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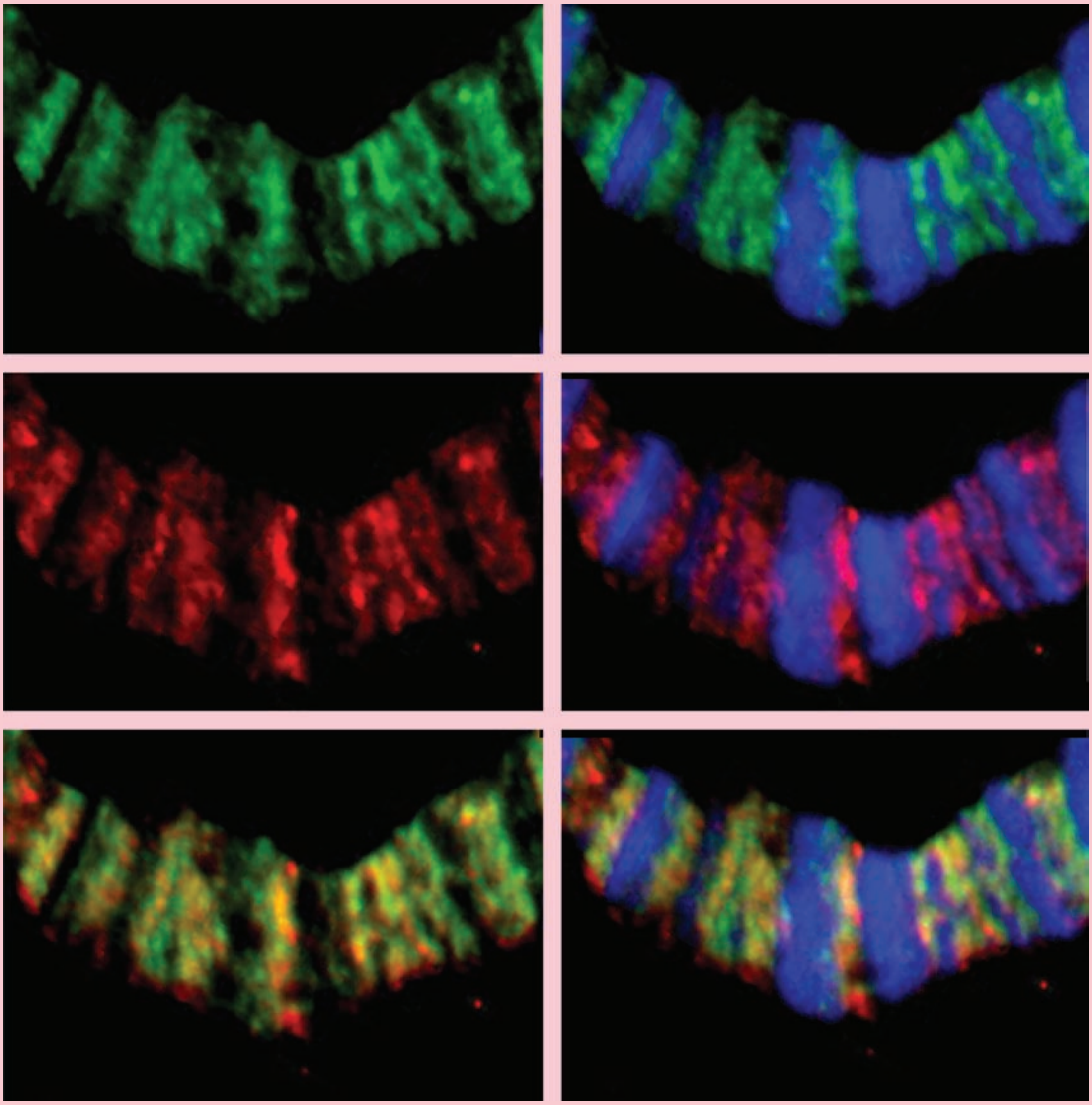

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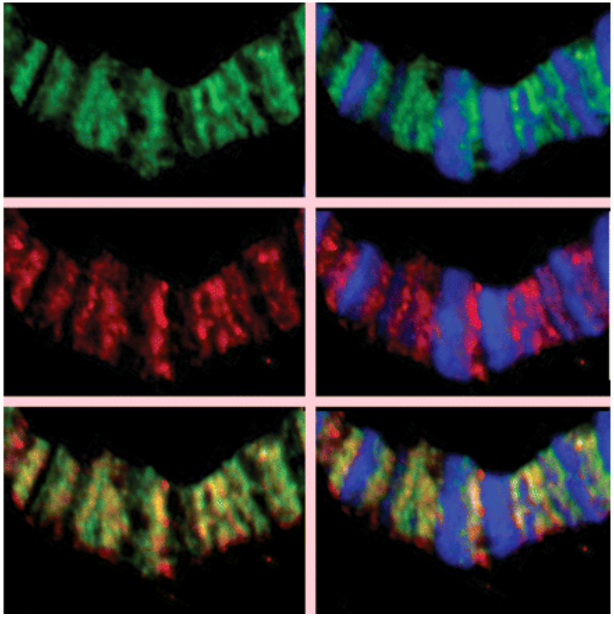
Cover image



Cover: SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamilya-like1 (SMARCAL1) and its homologues modulategene expression, particularly during stress responses. Although mutations of *SMARCAL1* are associated with Schimke immuno-osseous dysplasia, deficiency of the SMARCAL1 homologues in humans, mice and fruit flies is insufficient to cause disease without additional environmental or genetic perturbations of gene expression. On salivary polytene chromosomes, the *Drosophila* homologue Marcal1 (green) preferentially localizes totranscriptionally active or open chromatin, which is identified by trimethylatedhistone H3 lysine 4 (red), whereas compact chromatin is indicated by increased DAPI staining (blue). For further detail, see the article by Baradaran-Heravi, *et al*., pp. 2572–2587.

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Penetrance of biallelic *SMARCAL1* mutations is associated with environmental and genetic disturbances of gene expression

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Biallelic mutations of the DNA annealing helicase SMARCAL1 (SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin, subfamily a-like 1) cause Schimke immuno-osseous dysplasia (SIOD, MIM 242900), an incompletely penetrant autosomal recessive disorder. Using human, *Drosophila* and mouse models, we show that the proteins encoded by *SMARCAL1* orthologs localize to transcriptionally active chromatin and modulate gene expression. We also show that, as found in SIOD patients, deficiency of the *SMARCAL1* orthologs alone is insufficient to cause disease in fruit flies and mice, although such deficiency causes modest diffuse alterations in gene expression. Rather, disease manifests when *SMARCAL1* deficiency interacts with genetic and environmental factors that further alter gene expression. We conclude that the SMARCAL1 annealing helicase buffers fluctuations in gene expression and that alterations in gene expression contribute to the penetrance of SIOD.

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INTRODUCTION

With the discovery of incomplete penetrance in 1925 (1–3), it became apparent that not all individuals with identical mutant alleles necessarily manifest a trait. Incomplete penetrance has been attributed to genetic and environmental factors as well as to developmental stochastics (4–7). In its strictest sense, incomplete penetrance applies to the entire lifetime of the individual (8), although some traits initially considered incompletely penetrant are probably better described as having age-dependent penetrance (8,9).

Incomplete penetrance for autosomal recessive disorders is less commonly described than for autosomal dominant disorders, but it does occur (4,10–13). Examples of genetic and environmental modulators of incomplete penetrance in autosomal recessive disorders are illustrated by the following. The penetrance of the deafness phenotype in individuals with biallelic mutations of *DFNB26* can be suppressed by a dominant allele of the *DFNM1* locus (10). The penetrance of Bardet–Biedl syndrome can require the triallelic inheritance of mutations compromising BBSome complex assembly and vesicle trafficking to the ciliary membrane (11,14,15). In cystic fibrosis, the T7 polypyrimidine track variant in intron 8 of *CFTR* leads to more efficient splicing of exon 9 and reduces penetrance of the p.R117H mutation and cystic fibrosis to 0.03% for individuals with the compound heterozygous mutations p.[R117H; T7] + [ΔF508] (12,16,17). Suppression of phenylketonuria in individuals with biallelic mutations of *PAH* is possible through restriction of dietary phenylalanine (18). Lastly, the penetrance of hemochromatosis in individuals with biallelic mutations of *HFE* depends on a combination of genetic factors such as polymorphisms in iron metabolism genes and environmental factors affecting the iron load such as alcohol, dietary iron intake, age and gender (13,19). Despite this progress, however, the basis of incomplete penetrance remains undefined for most autosomal recessive disorders, including Schimke immuno-osseous dysplasia (SIOD).

Recently, two families have been reported in which siblings of affected individuals have incomplete penetrance of SIOD (20,21). SIOD is a multisystem disorder of renal failure, immunodeficiency, skeletal dysplasia, arteriosclerosis, migraine-like headaches, cerebral ischemia, bone marrow failure and hypothyroidism (22,23). It is associated with biallelic mutations in *SMARCAL1* that cause loss of SMARCAL1 enzymatic function (24–26). The SMARCAL1 enzyme recognizes single-stranded (ss)-to-double-stranded (ds) transitions in DNA (27) and functions as an annealing helicase (26). It also serves as a DNA stress response protein that participates in the maintenance of genomic integrity at stalled replication forks (28–32). Since components of DNA repair pathways frequently participate in transcription (33–40) and since variations in transcription can modulate trait penetrance (7), we hypothesized that SMARCAL1 also modulates transcription and that penetrance of SMARCAL1 deficiency results from further alteration of gene expression.

To test these hypotheses, we explored the effect of deficiency of the human, *Drosophila* and mouse *SMARCAL1* orthologs on gene expression and the interaction of such deficiency with environmental and genetic modifiers of transcription. We find that in humans, flies and mice, deficiency of the respective *SMARCAL1* ortholog alters expression of many genes and that in flies and mice deficiency of the respective ortholog is insufficient to cause disease in the absence of additional environmental or genetic insults.

RESULTS

Deficiency of *Marcal1* is insufficient for disease manifestations in *Drosophila*

To investigate whether deficiency of *SMARCAL1* orthologs is sufficient to cause disease, we developed a *Drosophila melanogaster* model. Similar to human *SMARCAL1*, the only fly ortholog *Marcal1* also encodes a DNA-specific ATPase (NP_608883.1, Marcal1) (Fig. 1A and B); it shares 32% amino acid identity and 44% amino acid similarity with SMARCAL1 (24). Like human SMARCAL1 and mouse Smarcal1 (25,41–43), Marcal1 is a nuclear protein and is highly expressed in the early embryo and developing tissues and gonads (Supplementary Material, Fig. S1).

By mobilizing *P-element KG9850* and screening for deletions of the *Marcal1* gene, we generated a loss-of-function *Marcal1* mutant that lacked 679 bp extending from the middle of the first exon into the second intron (NM_135039.1:c. 673_1258delinsATGATGAAATAACATCATTATATCGATTAACACAG, p.G225MfsX3, *Marcal1*^{del}, Supplementary Material, Fig. S2A). *Marcal1*$^{del/del}$ flies did not express *Marcal1* mRNA and protein (Supplementary Material, Fig. S2B and C), and surprisingly, like the unaffected individuals with biallelic *SMARCAL1* mutations (20,21), the mutant flies exhibited no morphologic differences when compared with wild-type flies and had a normal lifespan at 20°C.

Deficiency of murine *Smarcal1* is insufficient to cause disease

To address whether the absence of disease in *Marcal1*-deficient flies was attributable to the absence of tissues such as bones, mammalian kidneys and T cells, we generated mice deficient for *Smarcal1*. *Smarcal1* is the only *SMARCAL1* ortholog in mouse and encodes a DNA-specific ATPase (NP_061287.2, Smarcal1) (Fig. 1C) that has 72% amino acid identity and 78% amino acid similarity to the human SMARCAL1 (24). Using standard homologous recombination knockout technology, we deleted the first two coding exons of *Smarcal1* (NM_018817.2:c.172_989del, *Smarcal1*$^{del/del}$). These exons include the replication protein A binding site, nuclear localization signal and the first HARP domain (Supplementary Material, Figs S3–S5); deletion of the HARP domains has been associated with defective annealing helicase activity and disease in humans (24,44). When maintained on a mixed 75% 129SvEv and 25% C57BL/6 background, the *Smarcal1*$^{del/del}$ mice did not show developmental, growth or physical abnormalities or other signs of disease through 24 months (Supplementary Material, Fig. S6A–L). Analysis of lymphatic tissues showed that *Smarcal1*$^{del/del}$ mice had a reduction in their B-cell count but no T-cell deficiency (Supplementary Material, Fig. S6M–P). Similarly, when the *Smarcal1*^{del} allele was backcrossed onto a C57BL/6 background, the *Smarcal1*$^{del/del}$ mice did not

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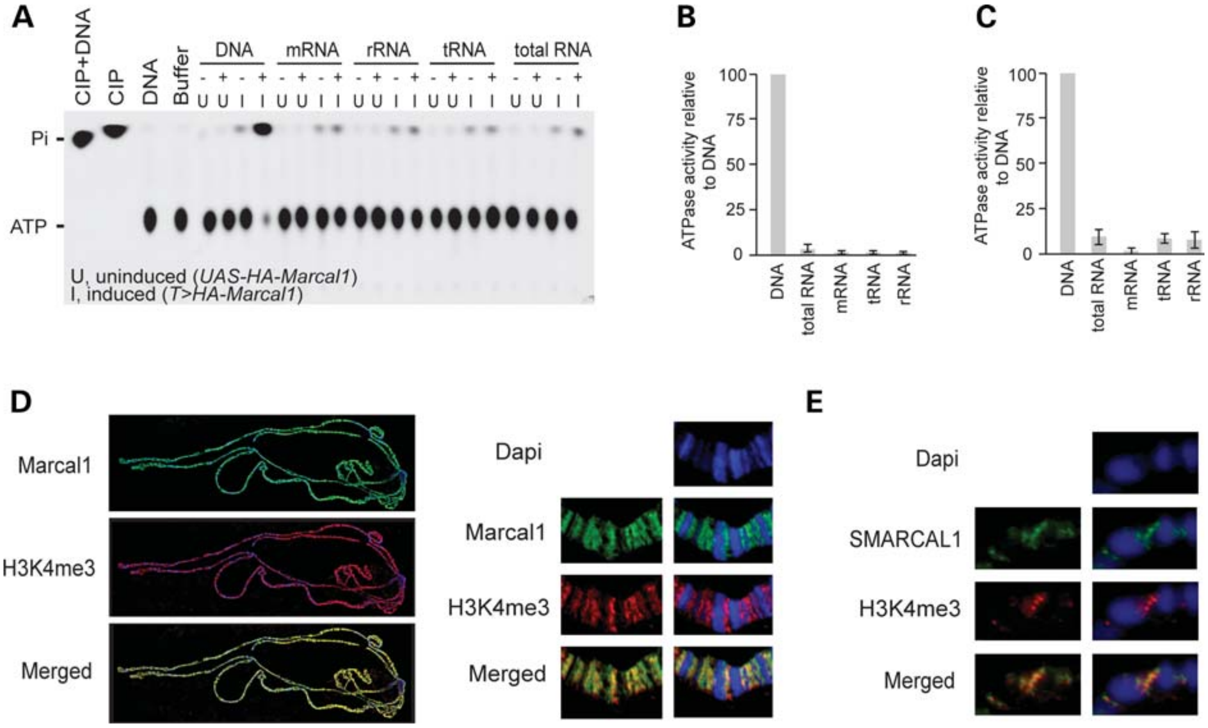

Figure 1. DNA specificity and chromatin binding of Marcal1, SMARCAL1 and Smarcal1. (**A**) Radiograph of a thin layer chromatography plate showing that Marcal1 has DNA-dependent ATPase activity. Purified hemagglutinin (HA)-tagged Marcal1 was immunoprecipitated from transgenic flies expressing HA-tagged Marcal1 under induction (I) of the tubulin-GAL4 driver. Control immunoprecipitates were prepared in parallel from transgenic flies carrying the *UAS-HA-Marcal1* transgene but not expressing it (U, uninduced). Both sets of immunoprecipitates were assayed for their ability to hydrolyze ATP to AMP and pyrophosphate (Pi) in the presence (+) or absence (−) of DNA, mRNA, rRNA, tRNA or total RNA. Calf intestinal phosphatase (CIP) was used as positive control, and the samples containing only DNA or buffer without immunoprecipitated enzyme were used as negative controls. (**B** and **C**) Plots showing the DNA-dependent ATPase activity of SMARCAL1 (B) and Smarcal1 (C) as measured by Kinase-Glo Luminescent Kinase Assay. For these assays, His-tagged SMARCAL1 and Smarcal1 were purified from HEK293 cells, using a nickel column, following the induction of expression with tetracycline. Nickel column elution fractions from uninduced cells were used as negative controls. Error bars represent 1 standard deviation. (**D**) Photographs showing immunofluorescence localization of HA-tagged Marcal1 on polytene chromosomes from *tub-GAL4*, *UAS-HA-Marcal1* flies. Note that Marcal1 (green) binds the interband regions and co-localizes with trimethyl-K4-histone H3 (H3K4me3; red). (**E**) Photographs showing immunofluorescence localization of human SMARCAL1 on polytene chromosomes from *MS1096-GAL4* and *UAS-SMARCAL1* flies. Note that SMARCAL1 (green) also binds the interband regions and co-localizes with H3K4me3 (red).

show developmental, growth or physical abnormalities and had the same immunologic phenotype as the mice on the mixed background (data not shown). Therefore, like the incomplete penetrance reported for the two human families (20,21), deficiency of the respective *SMARCAL1* ortholog in fruit flies and mice was insufficient to cause overt disease.

SMARCAL1 and Marcal1 bind open chromatin

To better understand the function of proteins encoded by *SMARCAL1* orthologs in the nucleus, we analyzed the association of SMARCAL1 and Marcal1 with chromatin. We used immunofluorescence to localize HA-tagged SMARCAL1 and Marcal1 on polytene chromosomes from third instar fruit fly larvae. Both SMARCAL1 and Marcal1 co-localize with trimethyl-K4 histone H3 and acetylated histone H4, which are markers of transcriptionally active chromatin (Fig. 1D and E and Supplementary Material, Fig. S7). To confirm and to define better this binding, we tagged Marcal1 on the N terminus with DNA adenine methyltransferase (Dam), which methylates adenine at GATC sequences (45); we judged the fusion protein to be functionally active since *in vivo* expression of Dam-Marcal1 induced extra wing veins similar to untagged Marcal1 or SMARCAL1 (25) (Fig. 2A and B and Supplementary Material, Fig. S8). Following transient expression of Dam-Marcal1 in *Drosophila* Kc167 cells, we found increased adenine methylation in regions enriched for trimethyl-K4 histone H3 and for acetylated histone H3 and H4 (Fig. 2C–E). The regions of increased adenine methylation also corresponded to accessible, transcriptionally active and early replicating chromatin (Fig. 2F–H and J). In contrast, adenine methylation was decreased in regions enriched for trimethyl-K27 histone H3 (Fig. 2I), a mark of inactive chromatin (46). The enrichment for adenine methylation spanned transcribed regions and was preferentially enriched in promoter regions compared with the rest of the gene (Fig. 2K and L).

To determine whether this preference for promoter regions might correlate with promoter proximal pausing or stalling of RNA polymerase II (RpII) (47), we compared our adenine methylation data with published RpII distribution in S2 cells (48) or *Toll*^{10b} embryos (49). This showed that adenine methylation was enriched in genes bound by RpII regardless of whether RpII was stalled or active and was underrepresented in genes without RpII binding. In contrast, transcriptionally inactive polycomb targets (46) were

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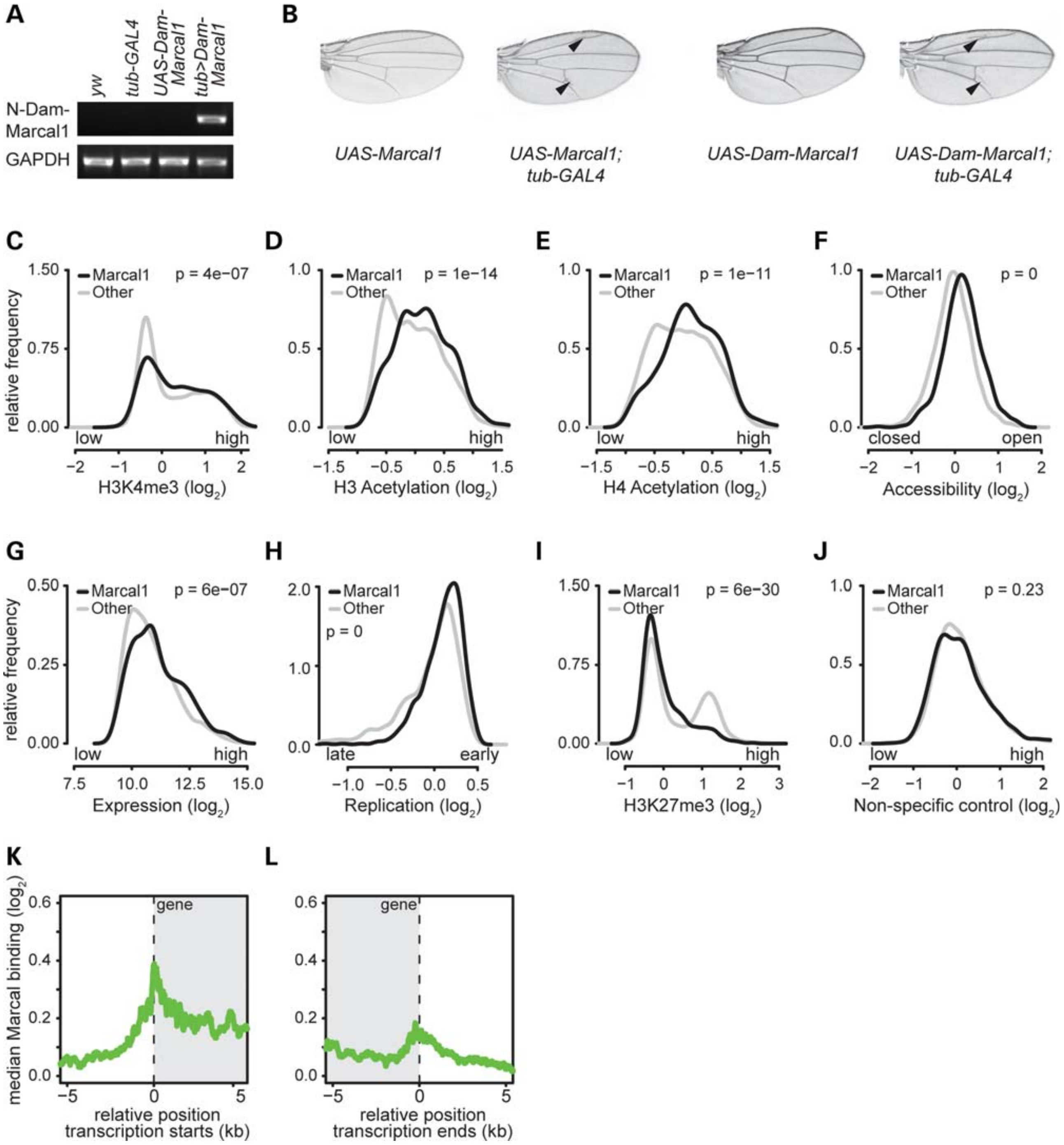

Figure 2. Expression of Marcal1 tagged with Dam on its N terminus methylates adenine in genomic regions of Kc167 cells with hallmarks of active transcription. (**A**) Photograph of an agarose gel showing that, by RT-PCR, *tub-GAL4* specifically induces expression of Dam-Marcal1 in transgenic *UAS-Dam-Marcal1;tub>GAL4* flies. (**B**) Expression of Dam-Marcal1 in *UAS-Dam-Marcal1;tub>GAL4* flies induces extra wing veins similar to those observed in *UAS-Marcal1;tub>GAL4* flies. (**C–J**) Density distribution plots showing relative frequencies (*y*-axes) of adenine methylation (Dam-Marcal1 target regions, black) and absence of adenine methylation (non-target regions, gray) for the indicated $\log_2$-transformed features: (C) trimethylation levels of lysine 4 of histone H3 (H3K4me3, a mark of actively transcribed chromatin), (D) acetylation levels of histone H3 (a mark of actively transcribed chromatin), (E) acetylation levels of histone H4 (a mark of actively transcribed chromatin), (F) chromatin accessibility (open and closed chromatin), (G) mRNA expression levels, (H) DNA replication timing, (I) trimethylation levels of lysine 27 of histone H3 (H3K27me3, a mark of non-transcribed genes) and (J) a non-specific antibody control (rabbit anti-IgG). The $\log_2$-transformed features were obtained from previously published genome-wide data (46,82–84). All *P*-values were calculated using the Mann–Whitney *U* test. (**K** and **L**) Alignment plots showing the $\log_2$-transformed median adenine methylation level (*y*-axes) relative to transcription start sites (K) and termination sites (L) of all target genes. The gray shading indicates the transcribed region. Transcription start and termination sites are at position 0 (dashed vertical lines). Note that Dam-Marcal1 preferentially targeted transcriptional start and termination sites.

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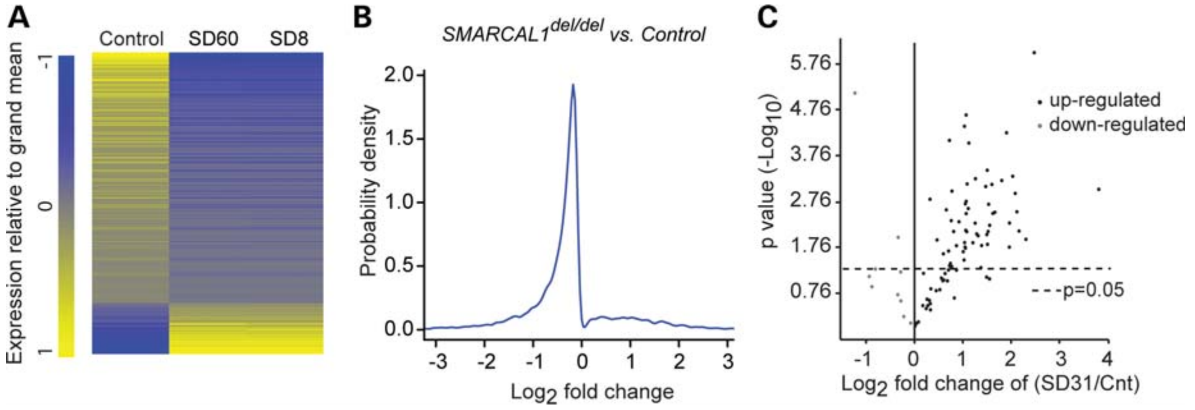

Figure 3. *SMARCAL1* deficiency alters gene expression. (**A**) Heat map of the $\log_2$ fold differences in RNA levels (q-value <0.05) between control and SIOD patient (SD8 and SD60) skin fibroblasts. The RNA levels were measured using Affymetrix Human Genome U133 Plus 2.0 arrays and are the average of three biologic replicates. (**B**) Density plot showing the distribution of the $\log_2$ fold differences in RNA levels (q-value <0.05) between control and SIOD fibroblasts. (**C**) Volcano plot comparing the expression of stress genes in control and SIOD (SD31) skin fibroblast cell lines after 1 h incubation at 43°C followed by 1 h incubation at 37°C. The plot is derived from three biologic replicates.

underrepresented among actively transcribed RpII genes (Supplementary Material, Table S1). Thus, Marcal1 likely has a broader role in transcription than modulating promoter proximal pausing or stalling of RpII.

Marcal1 and SMARCAL1 genetically interact with transcriptional components

To obtain genetic evidence that Marcal1 and SMARCAL1 are involved in transcription, we conducted a screen in *D. melanogaster* for enhancers and suppressors of the wing vein phenotype induced by expressing Marcal1 or SMARCAL1 under the control of the UAS promoter and the *tubulin*-GAL4 or *MS1096*-GAL4 drivers, respectively (Supplementary Material, Table S2) (25). We observed epistatic interactions with mutations of transcriptional regulators, including chromatin proteins, mediator complex members, RpII complex components and transcription initiation, elongation and termination factors (Supplementary Material, Table S2 and Fig. S9). Generally, but not always, loss-of-function mutations of transcriptional enhancers suppressed the wing vein phenotype, whereas loss-of-function mutations of transcriptional repressors enhanced the wing vein phenotype (Supplementary Material, Table S2).

SMARCAL1 deficiency alters gene expression in SIOD skin fibroblasts

To clarify whether the SMARCAL1 chromatin binding and its genetic interactions with transcriptional components were indicative of function, we checked whether deficiency of *SMARCAL1* altered gene expression. Using the Affymetrix Human Genome U133 Plus 2.0 Array, RNA derived from dermal fibroblasts of two SIOD patients (SD8 and SD60) showed significantly (q-value < 0.05) altered expression of 5644 genes ($\log_2$ median fold change of -0.255) (Fig. 3A and B; Supplementary Material, Fig. S10A and Table S3). Of these, 632 had >2-fold higher expression and 766 genes had >2-fold lower expression. The gene ontology (GO) biologic process annotations enriched among these differentially expressed genes included cellular and molecular metabolic processes, programmed cell death, cell cycle, signaling pathways and stress response (Supplementary Material, Tables S4 and S5).

Identification of the stress response was particularly intriguing since several patients with *SMARCAL1* deficiency have developed severe migraine-like headaches, transient weakness and transient paraplegia during hot weather (C.F.B., unpublished data). To test whether SMARCAL1 modulated expression of heat shock genes, we heat-stressed skin fibroblasts from a control individual and three SIOD patients (SD31, SD120 and SD123) for 1 h at 43°C. Using quantitative reverse-transcriptase PCR (qRT-PCR), we found that many heat stress response genes were significantly over- or under-expressed in the *SMARCAL1*-deficient fibroblasts (Fig. 3C; Supplementary Material, Fig. S11 and Table S6).

Marcal1 contributes to heat tolerance and modulates heat stress gene expression in *Drosophila*

Given the abnormal response to heat stress by SIOD patients and *SMARCAL1*-deficient skin fibroblasts, we hypothesized that heat stress modifies the penetrance of *Marcal1* deficiency. To test this, we reared *Marcal1*$^{del/del}$ and *yellow white* (*yw*) control flies at 20, 25 and 30°C. Although no differences were noted at 20°C, *Marcal1*$^{del/del}$ embryos and flies were significantly less viable at 25°C (<75% viability) and at 30°C (<20% viability) than *yw* control flies (Fig. 4A and B). Also, compared with *yw* flies, *Marcal1*$^{del/del}$ flies had abnormal expression of heat shock genes and proteins both at baseline and after 15 min at 37°C (Supplementary Material, Fig. S12).

The *Marcal1*$^{del/del}$ flies also laid smaller eggs than *yw* controls at 25°C but not at 20°C (Fig. 4C and D). At 20°C, the mean ($\pm$SD) egg volume was $0.0116 \pm 0.0018\ \mathrm{mm}^3$ for *yw* versus $0.0115 \pm 0.0015\ \mathrm{mm}^3$ for *Marcal1*$^{del/del}$ ($n = 100$, $P = 0.56$). In contrast, at 25°C the mean ($\pm$SD) egg volume

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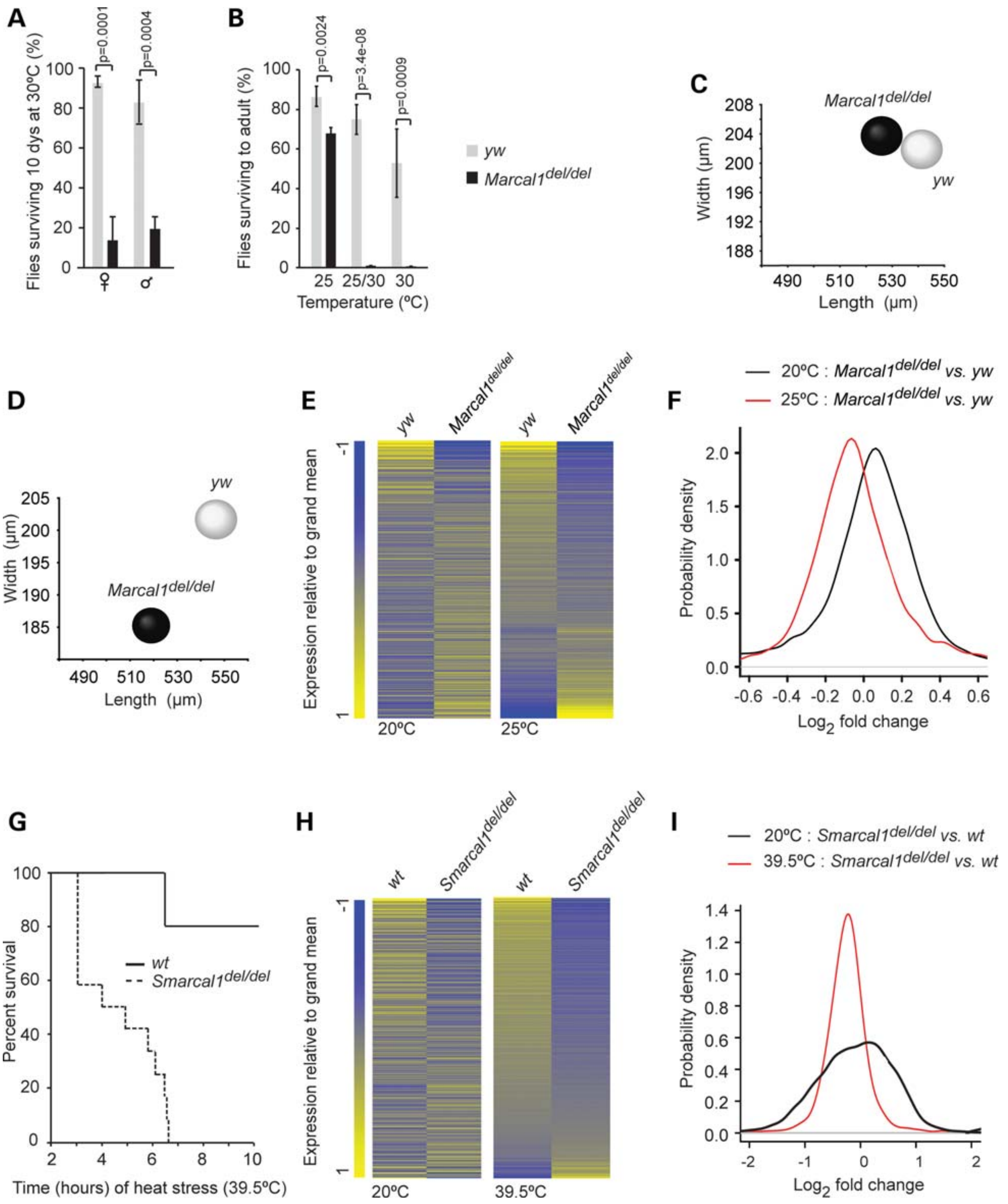

Figure 4. *Marcal1* and *Smarcal1* deficiencies increase susceptibility to heat stress. (**A**) Graph of the percent of *yw* control and *Marcal1*$^{del/del}$ flies surviving after 10 days at 30°C. Error bars represent 1 standard deviation. (**B**) Graph of the percent of *yw* control and *Marcal1*$^{del/del}$ embryos surviving through eclosion when raised at 25°C, when raised at 25°C for the first 5 days and then switched to 30°C or when raised at 30°C. Error bars represent 1 standard deviation. (**C** and **D**) Distribution plots of the dimensions of *yw* and *Marcal1*$^{del/del}$ eggs laid at 20°C (C) or at 25°C (D). (**E**) Heat maps of the $\log_2$ fold differences in all expressed mRNAs between *yw* and *Marcal1*$^{del/del}$ ovaries at 20°C and at 25°C. The RNA levels were measured using Affymetrix *Drosophila* Genome 2.0 Array and are the average of three biologic replicates. (**F**) Density plots showing the distribution of the $\log_2$ fold differences in gene expression between *yw* and *Marcal1*$^{del/del}$ ovaries at 20 and 25°C. (**G**) Survival curve for *Smarcal1*$^{+/+}$ ($n = 5$) and *Smarcal1*$^{del/del}$ ($n = 12$) mice maintained for 10 h at 39.5°C. (**H**) Heat map of the $\log_2$ fold differences for all expressed RNAs between *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ livers at 20 and 39.5°C. The RNA levels were derived from transcriptome sequencing and are the average of three biologic replicates. (**I**) Density plots showing the distribution of the $\log_2$ fold differences in RNA levels between *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ livers at 20 and 39.5°C.

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was $0.0117 \pm 0.0013\ \mathrm{mm}^3$ for *yw* versus $0.0094 \pm 0.0015\ \mathrm{mm}^3$ for *Marcal1*$^{del/del}$ ($n = 100$, $P = 7.45\mathrm{e}-21$).

To see whether this change in egg size correlated with altered gene expression, we compared RNA extracted from ovaries of *yw* and *Marcal1*$^{del/del}$ flies housed at 20°C with those housed at 25°C, using Affymetrix *Drosophila* Genome 2.0 Array. We found significant differences (q-value < 0.05) in the expression of 123 genes at 20°C and of 148 genes at 25°C; 81 genes were common in both groups. Furthermore, comparison of gene expression differences between *yw* and *Marcal1*$^{del/del}$ ovaries at 20 and 25°C showed a shift in the $\log_2$ median fold change from 0.01 at 20°C to −0.03 at 25°C (Fig. 4E and F). For both 20 and 25°C, the GO biologic process annotations enriched among genes differentially expressed between *yw* and *Marcal1*$^{del/del}$ ovaries included metabolic processes and response to stress (Supplementary Material, Tables S7–S9 and Fig. S10B).

Smarcal1 contributes to heat tolerance and modulates heat stress gene expression in mice

To test whether heat stress modified penetrance in the *Smarcal1*$^{del/del}$ mice, we housed the mice at 39.5°C. All *Smarcal1*$^{del/del}$ mice died within 6.5 h, whereas only 20% of wild-type (*Smarcal1*$^{+/+}$) mice died in 10 h (Fig. 4G). We used Illumina Next Generation Sequencing to characterize the transcriptomes of livers from *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice at an ambient temperature of 20°C or following 1 h at 39.5°C (Fig. 4H and I). At 20°C, 365 genes had >2-fold higher and 940 genes had >2-fold lower gene expression in *Smarcal1*$^{del/del}$ livers compared with *Smarcal1*$^{+/+}$ livers, and the affected genes mapped to multiple GO biologic process annotations, including cellular and molecular metabolic processes and gene expression (Supplementary Material, Tables S10–S12). Following 1 h at 39.5°C, 107 genes had >2-fold higher and 309 genes had >2-fold lower gene expression in *Smarcal1*$^{del/del}$ livers compared with *Smarcal1*$^{+/+}$ livers, and the median of gene expression differences between *Smarcal1*$^{del/del}$ liver and *Smarcal1*$^{+/+}$ liver shifted from a $\log_2$ median fold change of −0.06 at 20°C to −0.24 at 39.5°C (Fig. 4H and I). The genes with altered expression mapped to multiple GO biologic process annotations, including cellular and molecular metabolic processes, gene expression, stress response and immune response (Supplementary Material, Tables S13 and S14, and Fig. S10C).

To confirm the altered stress response identified in the liver transcriptome data, we used qRT-PCR to analyze heat shock gene expression in RNA isolated from the livers and brains of the 3 h heat-stressed *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice. This confirmed dysregulated expression of heat shock genes in both tissues (Supplementary Material, Table S15).

RpII inhibition decreases proliferation in *SMARCAL1*-deficient human fibroblasts

Having found that SMARCAL1, Marcal1 and Smarcal1 modulate gene expression during the heat stress response and are needed for heat tolerance, we hypothesized that other environmental and genetic factors altering transcription also induce penetrance when *SMARCAL1* orthologs are deficient. To test this, we incubated skin fibroblasts from a control individual and three SIOD patients (SD31, SD120 and SD123) for 48 h with 1 µg/ml of α-amanitin, a toxin that preferentially inhibits RpII (50,51). At this dose, SIOD fibroblasts proliferated significantly slower than control fibroblasts as measured by MTT assay and EdU incorporation by the Click-iT EdU assay (Fig. 5A); there was no difference in apoptosis or necrosis as judged by TUNEL assay and trypan blue staining (data not shown). Also, knockdown of the largest subunits of *RpII*, using shRNAs against *POLR2A* or *POLR2B* in SIOD fibroblasts, resulted in significantly decreased proliferation compared with a non-targeting shRNA or with knockdown of *RpII* components in control fibroblasts (Supplementary Material, Fig. S13A and B). This interaction between RpII and SMARCAL1 did not result from protein–protein interactions since SMARCAL1 did not co-precipitate with RpII (data not shown).

RpII mutations decrease the viability and increase gene expression changes in *Marcal1*$^{del/del}$ flies

Given the sensitivity of *SMARCAL1*-deficient cells to RpII inhibition and knockdown, we tested for analogous epistatic interactions in *Drosophila*. We introduced a single mutant allele of the largest subunit of *RpII* (*RpII215*^{3}, *RpII215*^{4}, *RpII215*^{8} or *RpII215*^{K1}) into the *Marcal1*$^{del/del}$ background (*RpII215*^{3}*/FM7;Marcal1*$^{del/del}$, *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$, *RpII215*^{8}*/FM7;Marcal1*$^{del/del}$ or *RpII215*^{K1}*/FM7;Marcal1*$^{del/del}$). Comparing the hatching of these embryos with *Marcal1*$^{del/del}$ and *RpII* heterozygous mutant embryos showed that these had a significantly reduced hatching rate at 20°C (Fig. 5B). This reduced hatching was not associated with increased apoptosis as measured by acridine orange staining or from altered protein–protein interactions between RpII215 and Marcal1 since Marcal1 did not co-precipitate with RpII215 (data not shown).

Besides reduced hatching, the introduction of a single mutant allele of *RpII215* into the *Marcal1*$^{del/del}$ background reduced the size of eggs relative to those of *Marcal1*$^{del/del}$ and *RpII215* heterozygous mutants (Fig. 5C). The mean (±SD) egg volume was $0.0116 \pm 0.0018\ \mathrm{mm}^3$ for *yw* versus $0.0115 \pm 0.0015\ \mathrm{mm}^3$ for Marcal1$^{del/del}$ ($n = 100$, $P = 0.56$), $0.0104 \pm 0.0015\ \mathrm{mm}^3$ for *RpII215*^{4}*/FM7* ($n = 100$, $P = 9.28\mathrm{e}-7$) and $0.0094 \pm 0.0016\ \mathrm{mm}^3$ for *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ flies ($n = 100$, $P = 1.03\mathrm{e}-13$).

To test whether this reduced egg size was associated with changes in gene expression, we used the Affymetrix *Drosophila* Genome 2.0 Array to compare gene expression in the ovaries of *Marcal1*$^{del/del}$, heterozygous *RpII215*^{4} (*RpII215*^{4}*/FM7*), *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ and *yw* flies. The introduction of the *RpII215*^{4} allele increased both the number of differentially expressed genes and the magnitude of the overall expression differences. A total of 744 genes were differentially (q-value < 0.05) expressed between *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ and *yw* ovaries compared with 123 genes between *Marcal1*$^{del/del}$ and *yw* ovaries. The $\log_2$ median fold change of expression differences for *Marcal1*$^{del/del}$ versus *yw* ovaries was 0.01, whereas for *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ versus *yw* ovaries, it was 0.07. The 744 differentially expressed genes mapped to multiple GO biologic process

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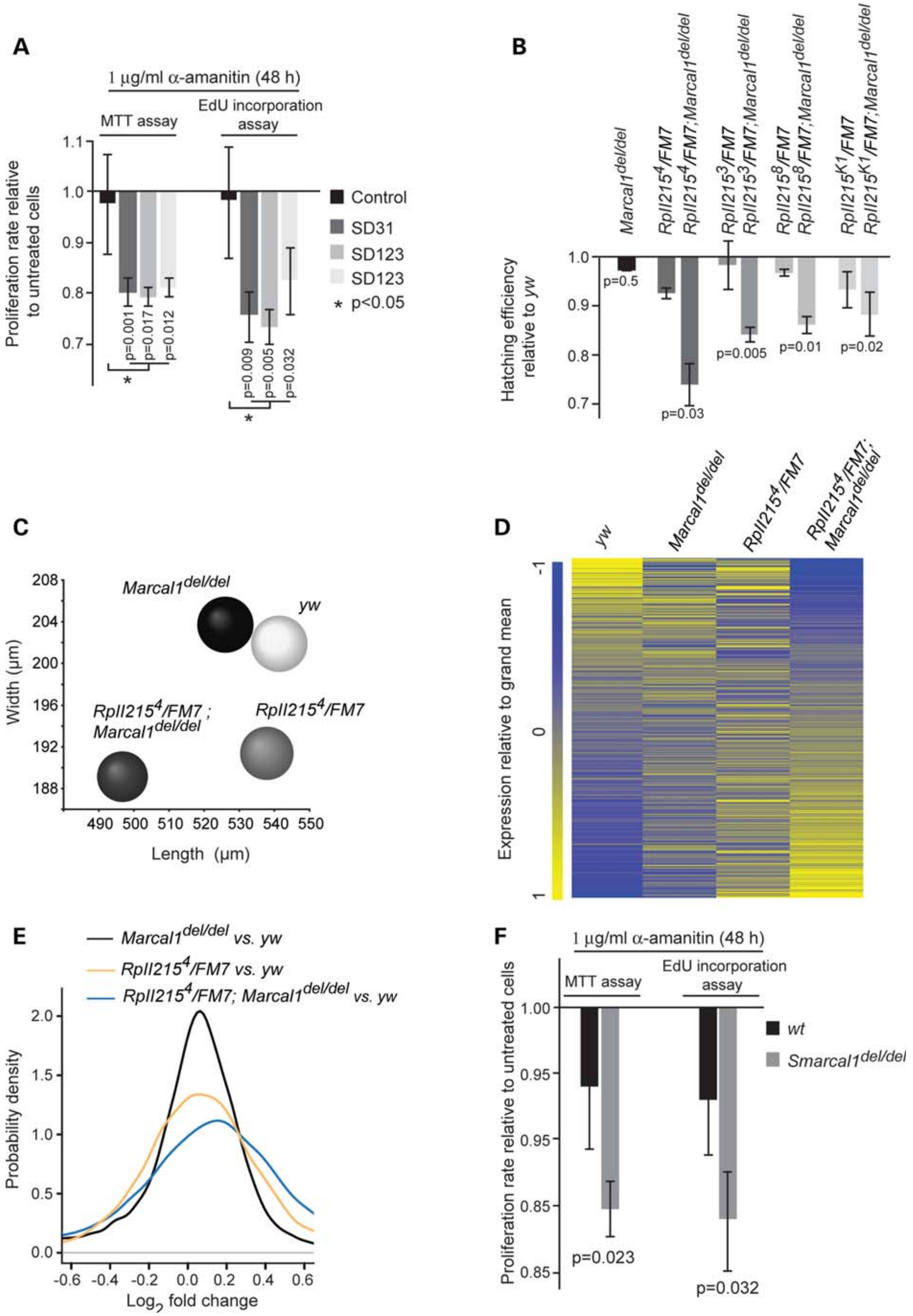

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annotations, including cellular and metabolic processes, cell cycle and response to stress (Fig. 5D and E and Supplementary Material, Tables S7 and S16).

Reciprocally, the introduction of the biallelic deletion of *Marcal1* into the background of the *RpII215*^{4} mutation also increased the number of differentially expressed genes and the magnitude of the overall expression differences. Comparison of gene expression in *RpII215*^{4}*/FM7* and *yw* ovaries identified 378 differentially (q-value < 0.05) expressed genes, and this increased to 744 for the comparison of *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ and *yw* ovaries. Also, the $\log_2$ median fold change of expression differences was 0.01 for *RpII215*^{4}*/FM7* versus *yw* and 0.07 for *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ versus *yw* ovaries. The 378 differentially expressed genes mapped to many GO biologic process annotations, including cellular and metabolic processes and gene expression (Fig. 5D and E and Supplementary Material, Tables S7 and S17).

RpII inhibition decreases proliferation in *Smarcal1*-deficient mouse embryonic fibroblasts

Having observed the interactions of SMARCAL1 and Marcal1 with RpII, we asked whether the inhibition of RpII function had a similar effect in *Smarcal1*$^{del/del}$ mouse embryonic fibroblasts (MEFs). When treated with 1 μg/ml α-amanitin, *Smarcal1*$^{del/del}$ MEFs proliferated significantly more slowly than *Smarcal1*$^{+/+}$ fibroblasts as measured by the MTT assay and EdU incorporation by the Click-iT EdU assay (Fig. 5F). Also, they exhibited no difference in apoptosis or necrosis as judged by the TUNEL assay and trypan blue staining (data not shown). Furthermore, knockdown of the largest subunit of *RpII*, using siRNAs against *Polr2a* in *Smarcal1*$^{del/del}$ MEFs, resulted in a significantly decreased proliferation rate compared with knockdown of *Polr2a* in *Smarcal1*$^{+/+}$ MEFs or with the treatment of *Smarcal1*$^{del/del}$ MEFs with a non-targeting siRNA (Supplementary Material, Fig. S13C and D).

RpII inhibition modifies the penetrance of *Smarcal1* deficiency and partially recapitulates SIOD in *Smarcal1*-deficient mice

Based on the preceding findings, we hypothesized that variations in gene expression are critical for expression of SIOD disease features. To test this *in vivo*, we injected *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice with either carrier (PBS, phosphate buffered saline) or α-amanitin (0.1 mg/kg/day) for 12 weeks. Although they did not develop T-cell deficiency (Supplementary Material, Fig. S14), the *Smarcal1*$^{del/del}$ mice injected with α-amanitin developed features of SIOD that were not observed in α-amanitin-treated *Smarcal1*$^{+/+}$ mice or in PBS-treated *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice (Fig. 6). First, they had length and weight growth restriction (Fig. 6A–C), and consistent with the growth restriction in SIOD, the mice had a disproportionately short spine (Fig. 6D and E). Second, as reported for SIOD growth plates (23,52), the distal femur growth plates were hypocellular, and chondrocytes in the proliferation and hypertrophic zones formed less organized columns (Fig. 6F–N). Finally, reminiscent of the early renal disease in SIOD, the treated *Smarcal1*$^{del/del}$ mice developed albuminuria (Fig. 6O).

DISCUSSION

We have shown that the proteins encoded by *SMARCAL1* orthologs localize to transcriptionally active chromatin, modulate gene expression and have epistatic interactions with transcription factors. We also found that, similar to the lack of penetrance for biallelic *SMARCAL1* mutations in humans, deficiency of the orthologs in fruit flies and mice is insufficient to cause disease in these organisms and that penetrance is associated with environmental or genetic insults that further modify gene expression. From these observations, we hypothesize that the annealing helicase function of SMARCAL1, Marcal1 or Smarcal1 maintains DNA topology to buffer variability in gene expression and thereby mitigates penetrance of pathologic traits arising from environmental and genetic insults (Fig. 7).

As an annealing helicase, SMARCAL1 resolves ss-to-ds DNA transitions (26). Such transitions occur during DNA replication, repair, recombination and transcription, and recent studies have shown that SMARCAL1 participates in the DNA stress response both at stalled replication forks and at double-strand DNA breaks repaired by recombination or end joining (28–32). However, since defects of DNA repair, replication and recombination have not been detected clinically in SIOD patients (53), we reasoned that, like many DNA repair enzymes (33–35,37,40,54), SMARCAL1 contributes to transcription and that its deficiency results in gene expression changes contributing to the pathophysiology of SIOD.

There are at least three non-exclusive models by which SMARCAL1 deficiency can alter gene expression. First, unrepaired DNA damage impedes RpII progression and impairs transcription (55). Second, like ERCC6, SMARCAL1 could be part of the transcriptional complex and thus its deficiency directly affects RpII transcription (34). Third, the DNA

Figure 5. Inhibition of RpII function causes penetrance of *SMARCAL1*, *Marcal1* and *Smarcal1* deficiency. (**A**) Graph showing the proliferation of α-amanitin-treated control and *SMARCAL1*$^{del/del}$ skin fibroblasts relative to untreated cells. The fibroblast cultures were treated with α-amanitin (1 μg/ml) for 48 h and proliferation was measured by the MTT and Click-iT EdU assays. (**B**) Graph showing the hatching rate at 20°C for *Marcal1*$^{del/del}$, *RpII215*$^{3\ or\ 4\ or\ 8\ or\ K1}$*/FM7* and *RpII215*$^{3\ or\ 4\ or\ 8\ or\ K1}$*/FM7;Marcal1*$^{del/del}$ embryos relative to the hatching rate of *yw* embryos. *FM7* is an X chromosome balancer. (**C**) Distribution plot of egg dimensions showing that *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ flies lay smaller eggs than *yw*, *Marcal1*$^{del/del}$ and *RpII215*^{4}*/FM7* flies. (**D**) Heat map comparing the $\log_2$ fold differences in all expressed mRNAs among *yw*, *Marcal1*$^{del/del}$, *RpII215*^{4}*/FM7* and *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ ovaries at 20°C. The RNA levels were measured using Affymetrix *Drosophila* Genome 2.0 Array and are the average of three biologic replicates. (**E**) Density plots showing the distribution of the $\log_2$ fold differences for transcripts depicted in (D). (**F**) Graph showing the proliferation of α-amanitin-treated *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ MEFs relative to untreated MEFs. The MEFs were treated with α-amanitin (1 μg/ml) for 48 h and proliferation was measured by the MTT and Click-iT EdU assays. Error bars in (A), (B) and (F) represent 1 standard deviation.

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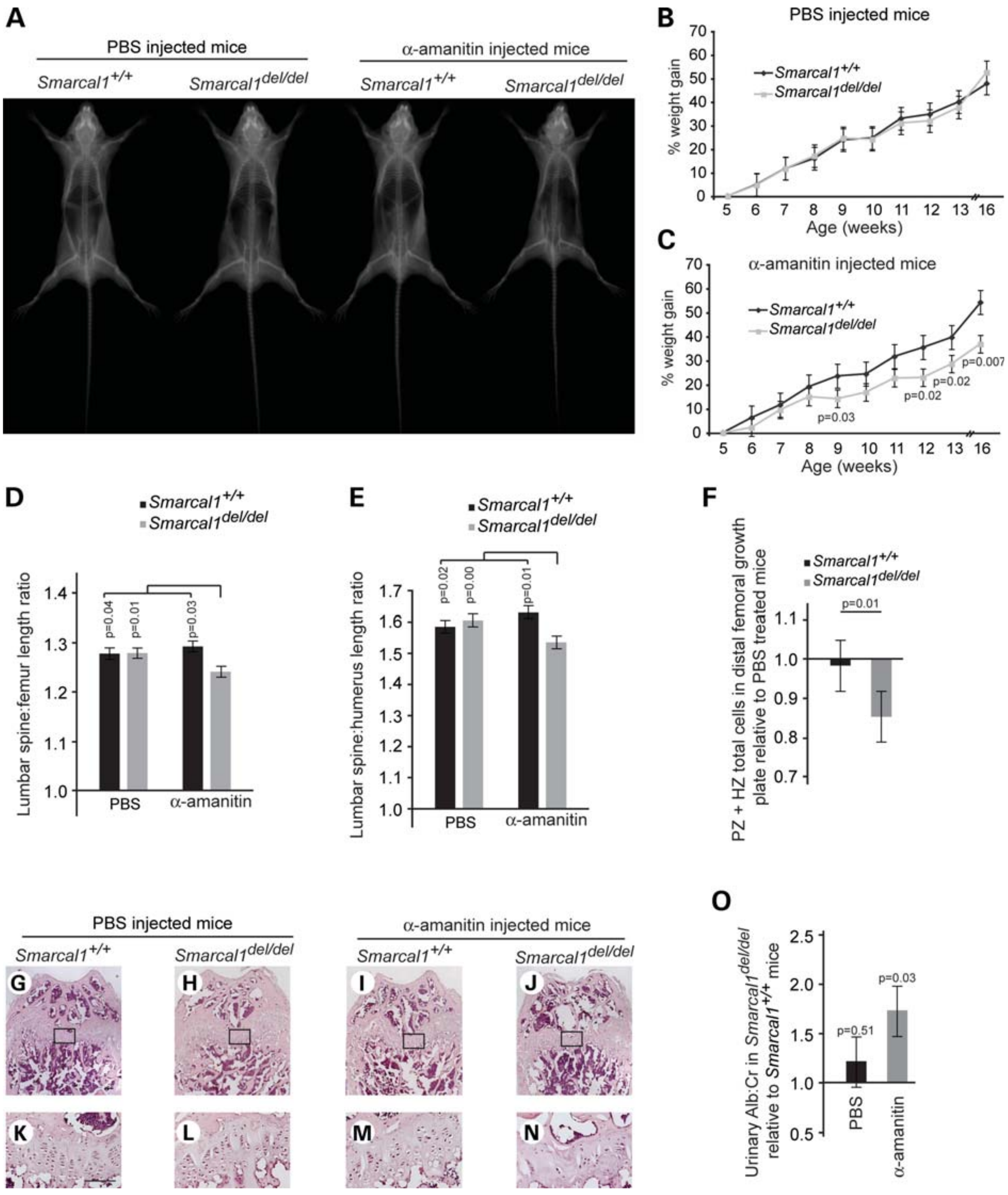

Figure 6. Treatment of *Smarcal1*$^{del/del}$ mice with α-amanitin partially recapitulates SIOD. (**A**) Radiographs of representative male mice after 12 weeks of daily intra-peritoneal (IP) injections with PBS or 0.1 mg/kg α-amanitin. (**B**) Growth curve showing that *Smarcal1*$^{+/+}$ ($n = 7$) and *Smarcal1*$^{del/del}$ ($n = 9$) mice gain weight equally when given daily IP injections of PBS. (**C**) Growth curve showing that *Smarcal1*$^{del/del}$ ($n = 9$) mice gain less weight than *Smarcal1*$^{+/+}$ ($n = 7$) mice when given daily ip-injections of 0.1 mg/kg α-amanitin. (**D** and **E**) Graphs showing the ratio of lumbar spine (L1–L6) length to femur length (D) or humerus length (E) for α-amanitin- and PBS-treated mice. Note that the α-amanitin treatment disproportionately shortened the lumbar spine of the *Smarcal1*$^{del/del}$ mice. (**F**) Plot of fold change in chondrocyte number in the proliferative (PZ) and hypertrophic (HZ) zones in the distal femoral growth plate of α-amanitin-treated mice, *Smarcal1*$^{del/del}$ ($n = 7$) and *Smarcal1*$^{+/+}$ ($n = 7$), relative to PBS-treated mice, *Smarcal1*$^{del/del}$ ($n = 7$) and *Smarcal1*$^{+/+}$ ($n = 6$). (**G–N**) Photographs of representative H&E staining of the distal femoral growth plate of *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ male mice treated with PBS or α-amanitin for 12 weeks. (K)–(N) Higher magnifications of the boxed areas on (G)–(J), respectively. Note the hypocellular growth plate and poorly organized columns of chondrocytes in the growth plate of the α-amanitin-treated *Smarcal1*$^{del/del}$ mouse. Bar = 100 µm. (**O**) Graph showing urine albumin excretion by *Smarcal1*$^{del/del}$ mice relative to *Smarcal1*$^{+/+}$ mice, following PBS or α-amanitin treatment. Bars in (B)–(F) and (O) represent standard errors.

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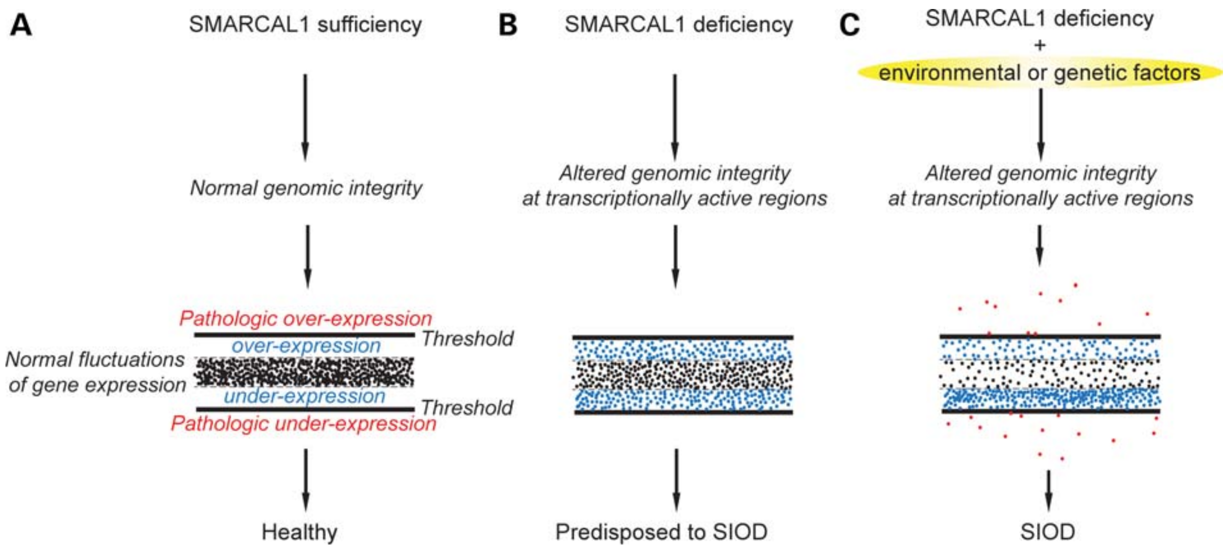

Figure 7. Model depicting the contribution of thresholded variations in gene expression to the penetrance of SIOD. (**A**) *SMARCAL1* orthologs buffer random fluctuations in gene expression by modulating DNA helicity within the promoter and across transcribed regions. (**B**) Deficiency of the *SMARCAL1* orthologs impairs maintenance of DNA structure within the transcriptionally active regions, and thereby alters gene expression. These alterations in gene expression are within a threshold of tolerance and compensated for such that few or no phenotypic features are apparent in humans and model organisms. (**C**) However, when transcription is further compromised by environmental or genetic factors that cause gene expression to pass a threshold, the organism is unable to compensate and manifests a phenotype.

structure maintained by SMARCAL1 modulates gene expression. Evidence against the first is the findings that (i) SIOD patients do not have ultraviolet light hypersensitivity (53), (ii) *SMARCAL1*-deficient fibroblasts do not have delayed recovery of mRNA synthesis following exposure to ultraviolet light or illudin S (C.F.B., unpublished data), and (iii) the proliferation rate of SMARCAL1-deficient cells is not detectably perturbed relative to control cells even though the transition from G2 to M phase is slightly delayed (28,31). Evidence against the second proposed mechanism includes (i) failure of SMARCAL1 homologues to co-purify or co-immunoprecipitate with RpII and transcription complexes studied (56–58) and (ii) failure of RpII to co-purify or co-immunoprecipitate with SMARCAL1 or Marcal1. We hypothesize, therefore, that the *SMARCAL1* orthologs influence gene expression through the maintenance of DNA structure.

SMARCAL1 could modulate RpII transcription through the maintenance of the topology and helicity of duplex DNA. In prokaryotes, changes in DNA helicity cause gene expression to be enhanced, repressed or unchanged (59), and the equilibrium between duplex DNA and strand opening modulates transcription factor binding and production of full-length RNA (60,61). Similarly, in eukaryotes, *in vitro* and *in vivo* studies of *MYC* expression show that transcription-induced supercoiling melts *MYC* far upstream element (FUSE) to enable binding by structure-sensitive regulatory proteins such as FUSE-binding protein (FBP) and FBP-interacting repressor (FIR) (62,63). Binding of FBP and FIR to FUSE modifies the rate of *MYC* promoter firing (62,63). Since negative supercoiling and positive supercoiling are generated upstream and downstream of the transcription bubbles (64,65), respectively, SMARCAL1, Marcal1 or Smarcal1 might contribute to the maintenance of DNA topology within and adjacent to transcribed regions. Deficiency of these orthologs would then alter gene expression as a consequence of the changes in DNA helicity or topology.

This model could also explain why, in contrast to transcription factors that bind conserved promoter elements, *SMARCAL1*, *Marcal1* and *Smarcal1* deficiencies do not consistently affect expression of homologous genes. Homologous genes in human, flies and mice frequently reside in different genomic neighborhoods or chromatin regions (66); therefore, the need for the SMARCAL1, Marcal1 and Smarcal1 to maintain duplex DNA around homologous genes might vary among species and thereby have differing effects on expression of homologous genes.

In summary, *SMARCAL1* deficiency is insufficient to cause SIOD, but the addition of environmental and genetic insults affecting transcription does cause penetrance and partial recapitulation of SIOD in model organisms. At both the molecular and genetic levels, SMARCAL1 plays a role in modulating gene expression. One model for the penetrance of biallelic mutations of *SMARCAL1* orthologs is shown in Figure 7. In this model, *SMARCAL1* orthologs modulate random fluctuations in gene expression and thereby potentiate or capacitate phenotypic changes induced by genetic or non-genetic insults, whereas the absence of the *SMARCAL1* orthologs creates a chromatin environment permissive for such insults, pushing gene expression beyond a threshold of disease (Fig. 7).

MATERIALS AND METHODS

Drosophila genetic studies

The y^{1};*P*{*SUPorP*}*Marcal1K*^{G09850}/*CyO* flies, which have a P element insertion in the *Drosophila* homologue of *SMARCAL1* (*Marcal1*) at 25B4, were obtained from the Bloomington

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Drosophila Stock Center (Bloomington, IN, USA). The loss-of-function mutant was obtained by imprecise P element excision (67); this deleted 679 bp nucleotides extending from the middle of the first exon into the second intron. The *Marcal1^{del}* flies were crossed to *w^{1118}* flies for eight generations, and the specificity of the small egg phenotype to the homozygous deletion of *Marcal1* in *Marcal1$^{del/del}$* flies was confirmed by failure of *Df(2L)Excel7793*, which has a breakpoint of 25B1;25B8, and *Df(2L)Excel7795*, which has a breakpoint of 25B3;25B9, to complement the *Marcal1^{del}* allele (68).

For expression of tagged and untagged *Marcal1* cDNAs, we generated five transgenic lines in *w^{1118}* flies, using the pUAST and pUASP vectors: (i) *UAST-Marcal1*, (ii) *UAST-HA-GFP-Marcal1*, (iii) *UAST-SMARCAL1*, (iv) *UASP-HA-GFP-Marcal1* and (v) *UAST-N-Dam-Marcal1*. All the other UAS lines, insertions and GAL4 lines used in this study were obtained from the Bloomington *Drosophila* Stock Center.

Using the SMARCAL1 and Marcal1 overexpression lines *MS1096-GAL4/MS1096-GAL4*; +/+; *pUAST-SMARCAL1/pUAST-SMARCAL1* and *pUAST-Marcal1/CyO*; *tubulin-GAL4/TM3, Sb^{1}* the F1 genetic screen was carried out at 28°C; all other crosses were performed at 20°C unless indicated otherwise in the text. For the wing phenotype analysis, images from 10 wings for each genotype were acquired using a Zeiss Axiovert 200 microscope and scored by two independent readers. The reference for the enhancement or the suppression of the wing veins was the average of SMARCAL1 or Marcal1 overexpression flies crossed to *w^{1118}* mutants of three different genetic backgrounds (Bloomington stocks 3605, 5905, 6326).

For egg hatching efficiency, three groups of 100 *yw*, *Marcal1$^{del/del}$*, *RpII215$^{3\ or\ 4\ or\ 8\ or\ K1}$/FM7* and *RpII215$^{3\ or\ 4\ or\ 8\ or\ K1}$/FM7;Marcal1$^{del/del}$* embryos were collected at 20°C. Hatching rates were calculated 45–48 h after egg deposition.

ATPase activity assay

The ATPase assay was performed with the purified Marcal1, SMARCAL1 and Smarcal1 proteins as previously described (25,69). See Supplementary Material for more details.

Immunofluorescence

Immunostaining of the *Drosophila* tissues and detection of human SMARCAL1 and mouse Smarcal1 were performed according to standard procedures as previously described (25,41,70,71). See Supplementary Material for more details.

High-dimensional (11-color) flow cytometry

Lymphoid tissues (spleen and thymus) from *Smarcal1$^{del/del}$* and *Smarcal1$^{+/+}$* mice were harvested in RPMI-1640 medium containing 10% FCS. The tissues were pressed through a 70 μm nylon cell strainer, suspended in 10 ml of PBS and incubated with red cell lysis buffer (150 mM NH_4Cl) for 5 min. After washing with 10 volumes of PBS, single-cell suspensions were stained with fluorochrome-conjugated anti-mouse B220, TCRaβ, CD4, CD8, CD44 and CD25 antibodies (BD Biosciences) (Supplementary Material, Table S18). 'Fluorescence-minus-one' controls were included to determine the level of non-specific staining and autofluorescence associated with subsets of cells in each fluorescence channel. Propidium iodide was added to all samples before data collection to identify dead cells. High-dimensional flow cytometry data were collected on an LSRII FACS instrument (BD Biosciences). The FLOWJO (TreeStar, San Carlos, CA, USA) software was used for fluorescence compensation and analysis.

Generation of Smarcal1 knock-out mice

Using standard homologous recombination knockout technology, we deleted the first two coding exons of *Smarcal1* (NM_018817.2:c.172_989del) and generated *Smarcal1$^{del/del}$* mice (see Supplementary Material for more details). Mice used in this study were housed, bred and euthanized according to accepted ethical guidelines approved by the Institutional Review Board of Baylor College of Medicine (Houston, TX, USA, IRB protocol: AN-2983) or the University of British Columbia (Vancouver, British Columbia, Canada, Animal Care Certificate: A10-0296).

Cell cultures

Human dermal fibroblasts from SIOD patients and unaffected individuals and fibroblasts from *Smarcal1$^{+/+}$* and *Smarcal1$^{del/del}$* embryos were cultured in DMEM (Gibco/Invitrogen) containing 15% fetal bovine serum (Gibco/Invitrogen) and 1% antibiotic/antimycotic (Gibco/Invitrogen) at 37°C and 5% CO_2. The SIOD patient fibroblasts had the following mutations in the SMARCAL1 protein or gene: SD8: p.[L397fsX40] + [?]; SD31: homozygous deletion of the first 5 exons of *SMARCAL1* (NT_005403.17:g.[67482574_67497178del] + [67482574_67497178del]); SD60: p.[E848X] + [E848X]; SD120: p.[R764Q] + [E848X]; and SD123: p.[R17X] + [R17X].

Heat stress

Drosophila: For assessing survival at 30°C, 200 flies of each genotype and sex (*yw* and *Marcal1$^{del/del}$*) were maintained in a temperature- and humidity-controlled incubator for 10 days. Surviving flies were tallied on day 10. To assess reproductive capacity, three groups of 100 *yw* and *Marcal1$^{del/del}$* embryos (300 in total for each genotype) were reared at different temperatures: group 1 was reared at 25°C; group 2 was reared at 25°C for the first 5 days and then shifted to 30°C (25/30°C); and group 3 was reared at 30°C. Flies surviving to adulthood were counted. For assessing gene or protein expression, ten 1–3-day-old female flies from each genotype (*yw* and *Marcal1$^{del/del}$*) were heat-stressed at 37°C in a water bath for 15, 30, 45 and 60 min with or without recovery for 1 h at room temperature. Mouse: Three groups of 4–5 *Smarcal1$^{+/+}$* and 4–12 *Smarcal1$^{del/del}$* female mice at 3–4 months of age were heat-stressed at 39.5°C for 1, 3 and 10 h as previously described (72). Human dermal fibroblasts: SIOD (SD31, SD120 and SD123) and control fibroblasts were heat-stressed for 1 h at 43°C followed by 1 h of recovery at 37°C as previously described (73).

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α-Amanitin treatment

Mice: Beginning at the age of 30 days, *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice (seven to nine per group) were injected intra-peritoneally daily with either PBS ($n = 9$ *Smarcal1*$^{del/del}$ and $n = 7$ *Smarcal1*$^{+/+}$) or 0.1 mg/kg α-amanitin (Sigma) ($n = 9$ *Smarcal1*$^{del/del}$ and $n = 7$ *Smarcal1*$^{+/+}$) diluted in PBS for 12 weeks. At the end of treatment, radiography was performed using the Faxitron X-ray cabinet. Human dermal fibroblasts: SIOD (SD31, SD120 and SD123) and control dermal fibroblasts were cultured in 96-well plates (3×10^3 cells/well). After 24 h, the medium was supplemented with 0 or 1 µg/ml α-amanitin and the cells were analyzed 48 h later for cell proliferation and viability, using the MTT assay as previously described (74). To measure proliferation with Click-iT EdU assay (Invitrogen), fibroblasts were cultured in the Lab-Tek 8 chambered cover glass system (7.5×10^3 cells/well). After 24 h, the medium was supplemented with 0 or 1 µg/ml α-amanitin, and after another 24 h, 10 µM EdU was added to each well. EdU detection and analysis was performed after 24 h, using Alexa Fluor 555 and Zeiss Axiovert 200 microscope, according to the manufacturer's protocol. Murine embryonic fibroblasts: Sensitivity of *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ fibroblasts to α-amanitin (0 and 1 µg/ml) was performed as described above for human fibroblasts.

RNA extraction and RT-PCR

RNA was extracted from the indicated tissue, using the RNeasy Mini Kit (Qiagen). cDNA synthesis was performed using SuperScript III First Strand Kit (Invitrogen) or qScript cDNA SuperMix (Quanta). Quantitative real-time RT-PCR was performed using the ABI 7500 Fast system, using the primers listed in Supplementary Material, Table S19 (see Supplementary Material for more details).

Urinary protein and creatinine measurement

Mouse urine samples were analyzed for total protein (Lowry Protein Assay Kit, Bio-Rad), creatinine (Creatinine Assay Kit, Cayman) or albumin (bromocresol green method). See Supplementary Material for more details.

Histopathology

Smarcal1$^{del/del}$ and *Smarcal1*$^{+/+}$ mice tissues were fixed in 4% PFA in PBS, paraffin-embedded and cut into 5 µm sections according to standard protocols (75). After H&E staining, tissues were analyzed using a Zeiss Axiovert 200 microscope. For distal femoral growth plate analysis, we counted all chondrocytes within the proliferative and hypertrophic zones and within 250 µm of the vertical midline.

Apoptotic analysis

Acridine orange staining for the detection of apoptotic cells in 20–23 h *Drosophila* embryos was performed as previously described (76). For human fibroblasts and MEFs, apoptotic cells were detected by TUNEL assay, using ApopTag Peroxidase In Situ Apoptosis Detection Kit (S7100, Chemicon).

RpII knock-down

Knock-down of the *RpII* genes encoding for the largest subunits of RpII in human fibroblasts and MEFs was carried out according to the Amaxa Biosystems optimized protocols (U-023 or A-023), using GFP-tagged shRNAs targeting *POLR2A* or *POLR2B* (SABiosciences) or Alexa Fluor 488-tagged siRNAs targeting *Polr2a* (Qiagen). See Supplementary Material for more details.

RNA sequencing and data analysis

For RNA sequencing, three samples of liver RNA were extracted from each group of 3–4-month-old *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ female mice at 20°C and after 1 h at 39.5°C. The RNA samples for each group were pooled, and RNA sequencing libraries were constructed and sequenced using the whole transcriptome shotgun sequencing procedure, as previously described (77–79). See Supplementary Material for details.

Microarray gene expression analyses

For gene expression array analysis of human cells, two samples of RNA were extracted from each of two SIODs (SD8 and SD60) and three of control skin fibroblast cell lines, labeled and hybridized to Affymetrix Human Genome U133 Plus 2.0 Arrays. For expression array analysis of *Drosophila* ovaries, three samples of RNA were extracted from *Drosophila* ovaries for each genotype at 20 and 25°C, labeled and hybridized to Affymetrix *Drosophila* Genome 2.0 Array. See Supplementary Material for details.

GO analysis

GO analysis was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 (80,81) (See Supplementary Material for more details).

Dam analysis of Marcal1 binding

We performed DamID as previously described (46) (see Supplementary Material for more details).

Statistics

Data are presented as mean ± SD unless otherwise stated. Comparisons were made using the two-tailed Student's *t*-test and Mann–Whitney *U* test. Differences were considered significant at a P-value of <0.05 or a q-value of <0.05.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at *HMG* online.

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Conflict of Interest statement. None declared.

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Penetrance of biallelic *SMARCAL1* mutations is associated with environmental and genetic disturbances of gene expression

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Supplementary Methods

Human subjects. Patients referred to this study gave informed consent approved by the Institutional Review Board of Baylor College of Medicine (Houston, TX, USA), the Hospital for Sick Children (Toronto, ON, Canada), or the University of British Columbia (H06-70283, Vancouver, BC, Canada). Also, the institutional review board of Stanford University School of Medicine approved the use of human tissue. The clinical data for patients were obtained from questionnaires completed by the attending physician as well as from the medical records.

Animal subjects. Mice used in this study were housed, bred, and euthanized in accordance with accepted ethical guidelines. These procedures were approved by the Institutional Review Board of Baylor College of Medicine (Houston, TX, USA, IRB protocol: AN-2983) or the University of British Columbia (Vancouver, BC, Canada, Animal Care Certificate: A10-0296).

Generation of *Smarcal1* KO construct. Recombineering was used to make a floxed allele of *Smarcal1* (Supplementary Material, Fig. S3). BAC DNA was transformed into the EL350 recombinogenic bacterial strain. The 5′ Homology Region (HR), 3′ HR, Exon 2 (Ex 2) HR, 5′ and 3′ Intron 1 (Int 1) HRs and 5′ and 3′ Intron 3 (Int 3) HRs were all PCR-amplified from RP22-273C7 BAC DNA and sequenced to exclude PCR-introduced mutations. The 5′ HR and 3′ HR were cloned into pBluescript (Invitrogen, Burlington, ON) containing a *thymidine kinase* (*tk*) negative selection cassette. The gap repair plasmid was linearized with Sal I to create a DNA double-strand break for gap repair, which was electroporated into EL350 cells transformed with the BAC. The mini-targeting vector was generated by ligating 5′ Int 1 HR upstream of the *loxP* floxed Neo cassette in plasmid PL452 and 3′ Int 1 HR downstream of the *loxP* floxed Neo cassette in PL452. The mini-targeting vector was then linearized with Not I and Sal I and co-electroporated with the gap repaired plasmid into EL350 cells to yield a plasmid with a floxed *Neo* cassette upstream of *Smarcal1* Exon 2. EL350 contains an arabinose-inducible *Cre Recombinase* gene. Following Cre Recombinase induction, a plasmid containing a *loxP* site upstream of Smarcal1 Exon 2 was retrieved. A second mini-targeting vector was created by ligating 5′ Int 3 HR upstream of the *FRT* flanked *Neo* cassette in plasmid PL451, and 3′ Int 3 HR downstream of the *FRT* flanked *Neo* cassette. PL451 also contains a *loxP* site downstream of the 3′ FRT site. The mini-targeting vector was linearized with Not I and Sal I and co-electroporated with the gap-repaired plasmid into EL350 cells to yield a plasmid with Exons 2 and 3 of *Smarcal1* floxed with *loxP* sites, a *Neo* positive selection cassette downstream of Exon 3 and a *tk* negative selection cassette. This conditional knockout construct was used for targeting *Smarcal1* in the murine genome. To test the functionality of the FRT sites and *loxP* sites, the Neo selection cassette was excised from the vector in bacteria expressing Flp recombinase and exons 2 and 3 were excised from the vector in cells expressing Cre recombinase (data not shown). The primers we used are shown in supplementary material, table S19.

***Smarcal1* gene targeting and Southern analysis.** The Darwin Core in the Department of Molecular and Human Genetics at the Baylor College of Medicine introduced the linearized conditional knockout construct into 129 SvEv Embryonic Stem (ES) cells by electroporation following standard techniques (1). Resistance to the antibiotic G418 and loss of the *tk* negative selection cassette was used to select ES cells in which the cKO construct inserted by homologous recombination within *Smarcal1*. Integration into the *Smarcal1* locus was confirmed by Southern analysis, using probes upstream of the 5′ loxP site and in Exon 4 (Supplementary Material, Fig. S4). The integration of the *Smarcal1* cKO construct into the endogenous *Smarcal1* genomic locus was screened by Southern analysis following XhoI and KpnI/PacI digestion of mouse SvEv embryonic stem cell genomic DNA. The 5′ Southern probe is *Smarcal1* exon 1 while the 3′ probe is exon 4 (Supplementary Material, Fig. S4). After restriction enzyme digestion overnight, DNA was separated on a 0.6% agarose gel in 0.5X TBE at 75 volts for 24 hours. The agarose gel was then exposed to UV radiation for 5 minutes, followed by a 10 minute wash in 0.25 N hydrochloric acid and a 10 minute wash in 0.4 N sodium hydroxide. The DNA was transferred to a nitrocellulose membrane overnight in alkaline transfer buffer (0.4 N sodium hydroxide and 1.0 M sodium chloride). The DNA was fixed to the membrane by soaking the membrane in neutralization buffer (0.5 M Tris-Cl, pH 7.2 and 1.0 M sodium chloride) for 15 minutes followed by UV irradiation. The membrane was placed in pre-hybridization buffer (0.2 M $NaPO_4$, pH 7.2; 1.0 mM EDTA; 1% BSA; 7% SDS; 15% formamide) and rocked for 4 hours at 65°C. Using the manufacturer's directions for the Rediprime II Random Prime Labeling System (Amersham/GE Healthcare), exon 4 of *Smarcal1* was labeled with alpha-P^{32} cytosine. The nitrocellulose membrane containing DNA was incubated with this labeled probe and fresh pre-hybridization buffer with rocking for 12 hours at 65°C. The nitrocellulose membrane was immersed in wash buffer ($NaPO_4$, EDTA, 7% SDS) three times for 30 minutes at 65°C. The membrane was subsequently exposed to film until development occurred at -80°C. Southern analysis was also used to identify mice after Cre recombinase removal of *Smarcal1* exons 2 and 3.

Generating Smarcal1 knock-out mice. In the conditional knockout allele, exons 2 and 3 of *Smarcal1* are floxed by *loxP* sites (*Smarcal1*^{loxP}). We observed germ-line transmission in 3 chimeric mice and established these 3 lines separately for analysis. Mice carrying a *GDF9-Cre* transgene (C57BL/6 background), which drives oocyte specific expression of Cre recombinase, were crossed to the *Smarcal1*$^{loxP/+}$ mice. Female mice carrying both the *GDF9-Cre* transgene and the *Smarcal1*^{loxP} excise exons 2 and 3 of Smarcal1 in the oocytes prior to fertilization (2). These female mice were backcrossed to *Smarcal1*$^{+/+}$ male mice (129SvEv background) to generate progeny heterozygous for a *Smarcal1* null allele (*Smarcal1*$^{del/+}$). *Smarcal1*$^{del/+}$ mice were intercrossed to generate *Smarcal1*$^{del/del}$ mice.

Backcrossing the *Smarcal1*^{del} allele onto the C57BL/6 background. We backcrossed the *Cre*-deleted mice into C57BL/6 background for eight generations. Apart from monitoring black coat color in backcrossed mice, we also analyzed the expression of IgM allotypes in B cells. Since B cells from 129SvEv mice express the IgM-a allotype and B cells from C57BL/6 mice express the IgM-b allotype, we followed IgM-b expression to determine purity of background. At eight generations, the backcrossed mice exclusively expressed IgM b allotype in their B cells suggesting that the backcrossed mice have a nearly homogeneous C57BL/6 background (data not shown).

Mouse PCR genotyping. One-centimeter mouse tail clippings were collected on postnatal day 21. Mouse tails were incubated overnight at 55°C in 800 µl tail lysis buffer (0.1 M Tris-HCl, pH 8.5; 5.0 mM EDTA, pH 8.0; 0.2% SDS; 200 mM NaCl) and 30 µl proteinase K solution. The following day, 500 µl of protein precipitation solution (Promega, Madison, WI) was added and solutions were centrifuged at maximum speed for 15 minutes to remove debris. The supernatant was transferred to a new tube, and genomic DNA was precipitated by adding an equal volume of isopropanol. The precipitate was centrifuged at maximum speed for 30 minutes at 4°C and was subsequently washed with 70% ethanol. The genomic DNA was resuspended in TE buffer.

Genotyping was performed by PCR (95ºC for 15 minutes, 30 cycles of 95°C for 1 minute, 60°C for 30 seconds, and 72°C for 1 minute) (Supplementary Material, Fig. S4). The PCR primers are listed in supplementary material, table S19.

Cloning and recombination of *Smarcal1* KO cDNA. The murine *Smarcal1* KO cDNA was cloned into the ECHO-adapted donor vector pUniBlunt/V5-His-Topo (Invitrogen) such that the V5-His$_6$ tag was added in frame to the carboxyl tail of the Smarcal1 protein as described (3). For expression of this cDNA in mammalian cells, this donor vector was recombined into the destination vector pcDNA5/FRT/TO-E as described (3).

RNA extraction. RNA was extracted from the indicated tissue using the RNeasy Mini Kit (Qiagen). Elimination of genomic DNA was performed using either on-column DNAase (Qiagen) or DNase I (Ambion) following RNA extraction at 37ºC for 1 hour. cDNA synthesis was performed using SuperScript III First Strand Kit (Invitrogen) or qScript cDNA SuperMix (Quanta Biosciences).

RT-PCR. *Human*: RT-PCR was performed as described(3, 4) using the primers listed in supplementary material, table S19. Quantitative real-time RT-PCR was performed using the ABI 7500 Fast system and PerfeCTa Sybr Fastmx Lrx 1250 (Quanta Biosciences) or a human heat shock proteins and protein folding array (SABiosciences) following the manufacturer's instructions. *Mouse*: For cloning, the *Smarcal1* cDNA was amplified by PCR using Platinum Taq DNA Polymerase (Invitrogen) with the primers listed in supplementary material, table S19 (94ºC for 5 minutes, 35 cycles of 94°C for 15 seconds, 55°C for 30 seconds and 68°C for 1 minute). Quantitative real-time RT-PCR was performed using the ABI 7500 Fast system and PerfeCTa Sybr Fastmx Lrx 1250 (Quanta Biosciences) or mouse heat shock PCR arrays (SABiosciences) following the manufacturer's instructions. *Drosophila*: For cloning the *Marcal1* cDNA was amplified by PCR using Platinum Taq DNA Polymerase (Invitrogen) with the primers listed in supplementary material, table S19 (94ºC for 5 minutes, 35 cycles of 94°C for 15 seconds, 55°C for 30 seconds and 68°C for 1 minute). PCR amplification of other cDNAs was done using HotStarTaq DNA Polymerase (Qiagen) with the primers listed in supplementary material, table S19 (94ºC for 15 minutes, 30 cycles of 94°C for 1 minute, 57°C for 1 minute and 72°C for 1 minute). Quantitative PCR was performed using the ABI 7500 Fast system and PerfeCTa Sybr Fastmx Lrx 1250 (Quanta Biosciences).

***RpII* knock-down.** Transfection of fibroblasts was carried out according to the Amaxa Biosystems Human Dermal Fibroblast Nucleofector Kit or the Amaxa Biosystems MEF Nucleofector Kit optimized protocol. For human dermal fibroblasts, we electroporated (Program U-023) 5.0µg of a plasmid expressing a GFP-tagged shRNA targeting *POLR2A* (insert sequence: AACGAGTTGGAGCGGGAATTT) or *POLR2B* (insert sequence: TCAGGTTCATGTTTGCAATCT) (SABiosciences) or 5.0µg of a plasmid expressing a GFP-tagged non-silencing shRNA (insert sequence: ggaatctcattcgatgcatac) (SABiosciences). For MEFs, we electroporated (Program A-023) 2.5µg of siRNA duplex 1 (Alexa-488-CAGAATCTGGCTACACTTAAA, Qiagen) or siRNA duplex 3 (Alexa-488-CTCAATGATGCTCGAGACAAA, Qiagen) targeting *Polr2a* or non-silencing siRNA duplex (Alexa-488-ACGUGACACGUUCGGAGAA, Qiagen). Thirty-six hours later, we selected transfected cells by fluorescent activated cell sorting and plated them at a concentration of $1x10^3$-

10^4 cells/100μl/well of 96-well Wallac cell culture plates. By quantitative real-time RT-PCR at 48 and 96 hours post-transfection, this method reduced expression of *POLR2A* by 50-80%, of *POLR2B* by 45-50%, and of *Polr2a* by 55-65% (siRNA duplex 1) or 70% (siRNA duplex 3). Cell viability and proliferation rate were assessed at 48, 72 and 96 hours post-transfection using the Cell Proliferation Reagent WST-1 (Roche, Laval, QC) according to the manufacturer's protocol and the relative proliferation rates were calculated for either the 24-hour (human fibroblasts) or 48-hour (mouse fibroblasts) intervals. The rate of cell growth in each group was compared for statistically significant differences using the two-tailed Student's *t*-test.

Marcal1 antibody generation. The polyclonal antibody to Marcal1 was generated in rabbit by injecting the amino terminus of Marcal1 (amino acids 1-400) and further purified by affinity purification.

Site directed mutagenesis. Site directed mutagenesis was performed as previously described (3) using primers listed in supplementary material, table S19.

Immunofluorescence. *Drosophila*: Polytene chromosomes of third instar larva were prepared and processed as described (5) and immunostaining of the polytene chromosomes, wing imaginal discs, embryos, eye discs, or testes were performed according to standard procedures (6). We used mouse anti-HA (1:200, Sigma), rabbit anti-acetyl-histone H4 (1:200, Upstate Biotechnology/Millipore), rabbit anti-trimethyl-K4-histone H3 (1:200, Upstate Biotechnology/Millipore) antibodies as primary antibodies. DNA was stained with 4',6-diamidino-2-phenylindole (1:1000, Sigma). Fluorophore-conjugated secondary antibodies were used to detect the primary antibodies. *Human*: Immunofluorescence studies for human SMARCAL1 were performed with an anti-SMARCAL1 antibody as previously described (3, 7). Expression of the *Smarcal1*^{del} cDNA lacking the first two coding exons with a 3' V5-tag in tetracycline-inducible T-Rex-293 cell line (Invitrogen) was detected by rabbit anti-V5 (1:250, Sigma) followed by a fluorophore-conjugated secondary antibody.

Immunoprecipitation. To check the physical interaction between Marcal1 or SMARCAL1 and RNA polymerase II, we used homozygous *tubulin-GAL4*, *UAS-HA-GFP-Marcal1* flies as well as T-REx-293 cells expressing V5-tagged SMARCAL1(3). The extracts of 100 flies were subjected to immunoprecipitation using monoclonal anti-HA agarose conjugate (Sigma). The T-Rex-293 nuclear extracts were incubated with rabbit anti-V5 agarose conjugate or mouse anti-RNA Polymerase II (CTD4H4, Covance) and immunoprecipitations were performed using Protein A or G agarose (Invitrogen), respectively. The immunoprecipitated proteins were detected by immunoblotting using rabbit anti-Marcal1 (1:2000), rabbit anti-SMARCAL1 (1:2000), and mouse anti-RNA Polymerase II (CTD4H4 or H14, 1:500; Covance).

Western blotting. Detection of Marcal1 was performed according to standard protocols (8) using rabbit anti-Marcal1 antibody (1:2000). Detection of SMARCAL1 and Smarcal1 were performed with an anti-SMARCAL1 antibody (4, 9).

ATPase activity assay. To assay ATPase activity, HA-GFP-Marcal1 was immunoprecipitated from protein extracts of *tub-GAL4*, *UAST-HA-GFP-Marcal1/TM6B* flies using the monoclonal anti-HA agarose conjugate (Sigma). His-tagged human SMARCAL1 and mouse Smarcal1 were purified from protein extracts of a stably transfected Flp-In T-Rex-293 cell lines (Invitrogen) using a His-Bind Purification Kit (Novagen/EMD). The ATPase assay was performed with the purified proteins as described (3, 10).

Urinary creatinine and albumin assays. Spot urine was collected from *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice injected with alpha-amanitin or PBS. Urinary creatinine measurement was performed using creatinine assay kit from Cayman Chemical Company (Ann Arbor) following the manufacturer's instruction. Urinary albumin measurement was performed using the bromocresol green method. Ten dilutions of albumin standards from 0 to 8 g/dl were prepared. Two microliters of standards and samples were added to a 96-well plate in duplicates and then 200 µl of albumin reagent (Sigma) was added and mixed. After incubation at room temperature for 1 minute, the absorbance was measured at 630 nm and the concentration was calculated. Finally, albumin/creatinine ratio was calculated for each sample.

Urinary protein and creatinine measurement. 24-hour urine was collected from *Smarcal1*$^{del/del}$ (n=4) and *Smarcal1*$^{+/+}$ (n=4) female mice at the age of 2 and 12 months using Nalgene metabolic cages. Protein measurement was performed in duplicate using Lowry proetein assay (Bio-Rad) following the manufacturer's instruction (Hercules). Urinary creatinine measurement was performed using creatinine assay kit from Cayman Chemical Company (Ann Arbor) following the manufacturer's instruction.

Microarray gene expression analysis in human cells. For analysis of gene expression in primary cultured human dermal fibroblasts, 5.0 µg of total RNA from two biologically independent replicates was extracted from two SIOD (SD8 and SD60) and three from a control skin fibroblast cell lines, labeled and hybridized to Affymetrix Human Genome U133 Plus 2.0 Arrays. CEL file data were normalized using the GCRMA package from the Bioconductor suite (11). Present-absent p values were calculated in R using the Affymetrix test statistic(12). Subsequent to deriving expression measures, an ANOVA model was fit to each genotype (Y=Genotype + Error), where Y is the normalized expression measure for a gene on a particular microarray. The model was fit using the LIMMA R package (13). Coefficients for the linear model were estimated by least squares method. Linear contrast scores were used to compare gene lists between the genotypes. Determination of up- and down-regulation of expression is made by computing a T-statistic for SIOD and control samples, and then adjusting the variance estimate using the empirical Bayes method as implemented in the LIMMA R Package. The p-values obtained are then converted to Q-values using the LBE R package (14, 15) to control the false discovery rate (FDR) at 0.05. A pair of lists was determined as well as linear contrast values ($\log_2$ fold changes) comparing the SIOD patients and the control. A Q-value cutoff of 0.05 was used to determine a pair of lists for the probe sets either overexpressed or underexpressed.

Microarray gene expression analysis in flies. For analysis of gene expression in flies, 5.0 µg of total RNA from three biologically independent replicates was extracted from 1) *yw*, 2) *Marcal1*$^{del/del}$, 3) *RpII215*^{4}*/FM7,* and 4) *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ ovaries at 20°C and from *yw* and *Marcal1*$^{del/del}$ at 25°C, labeled and hybridized to Affymetrix *Drosophila* Genome 2.0 arrays. Affymetrix cel file data were processed using the robust multi-array average (RMA) method as implemented in Bioconductor. The *yw* expression data from both the base and high temperature states were used to determine a set of "expressed" transcripts using the maximum RMA value for each probe set across all individual *yw* samples. Probe sets were identified as being expressed when the maximum RMA value was greater than or equal to six–a value determined by observation of the distribution of expression values in the *yw* samples. This analysis identified 6,437 probe sets, which were subsequently analyzed and visualized in the other genotypes. Linear contrast of the RMA values for each treatment was compared by first computing the mean of RMA values with each treatment group and then comparing different pairs of groups of interest. The heatmap was generated by sorting the differenced values and plotting each probe set. The density plots are kernel probability density estimates of the linear contrast scores for the ensemble of 6,437 probe sets, determined to be expressed in *yw*. FlyBase IDs provided by the Affymetrix website were used to query the FlyBase information.

RNA sequencing and data analysis. RNA was extracted from the liver of three *Smarcal1*$^{+/+}$ and three *Smarcal1*$^{del/del}$ female mice (3-4 months of age) at room temperature as well as after 1 hour at 39.5°C. The RNA sequencing libraries were constructed and sequenced using the whole transcriptome shotgun sequencing procedure, as previously described (16-18). The sequencing was performed using two lanes per genotype of an Illumina Genome Analyzer II following the manufacturer's instructions. Image analysis and base calling were done by the GA pipeline v1.0 (Illumina, Hayward, CA) using phasing and matrix values calculated from a control phiX174 library run on each flow cell. Raw quality scores were calibrated by alignment to the reference mouse genome (NCBI build 37, mm9) using ELAND (Illumina, Hayward, CA). Short read sequences obtained from the Illumina Genome Analyzer for each sample were mapped to the reference mouse genome (NBCI build 37, mm9) plus a database of known exon junctions (19) using MAQ in paired end mode (20). The exon junction sequences consisted of N-1 nucleotides of the donor exon 'spliced' to N-1 nucleotides of the acceptor exon for every known pair of exons in the mouse transcriptome, where N is the read length. This was designed to rescue reads that would not map to the mouse reference genome due to their spanning a splice site. The maximum insert size (-a parameter) to MAQ was 500. Mouse sequence summary count data were $\log_2$ scaled. All genes with a count per kilobase summary greater than 4 ($\log_2 > 2$) in either temperature condition in *Smarcal1*$^{+/+}$ samples were identified as well enough represented to be considered in our analysis. The mean $\log_2$ scaled expression summary (across both *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$) was determined for each temperature state. The deviation of each sample (computed by subtracting the observed value from the mean) for the base temperature condition was subsequently determined and plotted in the heatmap. For both heatmaps, the sort order was computed as follows: the difference between *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ in each treatment condition was divided by the $\log_2$ expression value in the *Smarcal1*$^{+/+}$ in the baseline temperature condition. The resulting scores for each treatment condition were averaged and then the genes were sorted according to this score for difference in the high temperature state. The density plots represent the distribution of expression difference values for each temperature state between the *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$. The same genes plotted in the heatmap are represented in the line plot (probability density estimate plot).

Gene Ontology (GO) analysis. GO analysis was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 (21, 22). Differentially expressed genes (q-value <0.05) between *yw* vs. *Marcal1*$^{del/del}$, *yw* vs. *RpII215*^{4}, and *yw* vs. *RpII215*^{4}*;Marcal1*$^{del/del}$ ovaries at 20°C, *yw* vs. *Marcal1*$^{del/del}$ ovaries at 25°C, differentially expressed genes (fold-change > 2) between *Smarcal1*$^{+/+}$ vs. *Smarcal1*$^{del/del}$ mouse livers at 20°C, *Smarcal1*$^{+/+}$ vs. *Smarcal1*$^{del/del}$ mouse livers at 39.5°C, and differentially expressed genes (q-value <0.05 and fold-change > 2) between control vs. SIOD fibroblasts, were analyzed for their enrichment in biological process GO biological process annotation terms at all levels.

DNA adenine methyltransferase analysis of Marcal1 binding. Full-length *Marcal1* was cloned into pNDamMyc such that Dam was fused in frame with the amino terminus of Marcal1. This construct was transfected into Kc167 cells as previously described (23). For microarray analyses, we used a 385K tiling array (NimbleGen Systems/Roche, Madison WI), which was designed by the group of Bas van Steensel (NKI – Amsterdam, The Netherlands). This array contained 60-mer oligomers roughly every 300 base pairs across the entire nonrepetitive part of the *Drosophila* genome (release 4.3). We made two independent biological replicate experiments that were differentially labeled and in parallel hybridized to the microarrays. The individual replicates were normalized, using Lowess Normalization methods. For each replicate, we defined Marcal1 binding sites as described (23). First, we removed random noise by calculating a running median with a window size of 15 consecutive probes (i.e. ~4.5 Kbp). We defined a Marcal1 binding site as: at least two consecutive probes along the DNA template that have a $\log_2$-transformed binding ratio (N-Dam-Marcal1/Dam) higher than an empirically determined threshold. This threshold was determined on randomly shuffled data, giving an estimate of the FDR. This FDR was defined as the number of binding sites in the random data / the number of sites in observed data. We chose a threshold that equals the standard deviation of $\log_2$-transformed binding ratios across all probes on the microarray, giving FDRs of ~1% and 0% for replicates 1 and 2, respectively, indicating that our definition of a binding site is highly stringent.

Next, we further increased confidence in our data by selecting only binding sites that were identified in both replicates. Finally, we identified target genes using the start and end coordinates of Marcal1 binding sites and FlyBase R4.3 gene annotation (www.flybase.org). As the minimal requirements for a target gene, we chose at least one nucleotide overlap with at least one Marcal1 binding site. We used this list of target genes to divide previously published data into target and non-target genes. These data sets include chromatin accessibility (24), gene expression (25), DNA replication timing(25), histone acetylation (26), histone methylation (23), and a non-specific antibody control (rabbit anti-IgG) (23). Data derived from Greil *et al*. (24) and Schubeler *et al*. (25, 26) compared 638 targets to 4718 non-targets, and data from Tolhius *et al*. (23) compared 1026 targets to 8964 non-targets. Density distribution plots, statistical tests, and alignment plots of Marcal1 binding around transcription start and termination sites of 1822 target genes were made with R (www.r-project.org).

Supplementary Figures

Supplementary Figure S1. Temporospatial expression of Marcal1 in *Drosophila* cells and tissues. (**A**) Photograph of S2 cells expressing GFP-tagged Marcal1. (**B**) Photograph of an ovarian nurse cell dissected from a transgenic fly expressing GFP-tagged Marcal1. (**C**) Photograph of immunofluorescently detected endogenous Marcal1 expression in the wing imaginal disc. The upper panel was treated with anti-Marcal1 serum and the lower panel with preimmune serum. (**D**) Northern blot analysis of *Marcal1* expression during *Drosophila* development.

Supplementary Figure S2. Generation of a fly model for the study of Marcal1 function. (**A**) Diagram showing that imprecise excision of P element *KG9850*, which is inserted within exon 1 of *Marcal1*, was used to generate a fly line deficient for Marcal1 ($Marcal1^{del/del}$). The mutation generated by this imprecise excision was c.673_1258delinsATGATGAAATAACATCA, p.225Mfs228X. (**B**) Northern blot analysis showing the absence of Marcal1 mRNA in $Marcal1^{del/del}$ flies. 3 µg of mRNA were used for Northern blot analysis. (**C**) Immunoblot analysis showing the absence of Marcal1 protein in $Marcal1^{del/del}$ flies. One *yw*, one $Marcal1^{del/del}$, and one *tub>GFP-Marcal1* (*tub-GAL4*, *UAS-HA-GFP-Marcal11*/*TM6B*) male fly (about 10 µg of protein of extract) were used. The rabbit polyclonal anti-Marcal1 antibody was used to probe the blot.

Supplementary Figure S3. Outline for deriving the *Smarcal1* knockout targeting vector from a bacterial artificial chromosome (BAC) via recombineering. The black triangles denote *LoxP* sites and the yellow triangles denote *FRT* sites.

Supplementary Figure S4. Generation of a *Smarcal1* deficient mouse. (**A**) Diagram of the restriction map for the *Smarcal1* gene after insertion of the cKO construct. *LoxP* sites are shown in black while *FRT* sites are shown in yellow. Insertion of the 5′ loxP site introduces an Xho I site and insertion of the neo cassette introduces a *PflF* I and *Pac* I site. Exons 2 and 3, which contain the initiating ATG site, nuclear localization signal, RPA binding site and a HARP domain, are removed when mice are crossed to Cre-expressing mice. The location of the Southern probes and the PCR genotyping primers are shown below the restriction maps. (**B**) Southern analysis was used to detect integration of the cKO construct, removal of neo cassette, and removal of exons 2 and 3. The expected restriction fragments for each digestion are shown in the table. (**C**) Southern analysis of *SvEv* embryonic stem (ES) cells after integration of the *Smarcal1* cKO construct. After restriction enzyme digestion with Kpn I and Pac I, probing with the 5′ probe shows an 18.5 kb band corresponding to the *Smarcal1* wild-type allele and a 4.2 kb band in those cells with the *Smarcal1 loxP* allele. Probing the membrane with the 3′ probe shows an 18.5 kb band corresponding to the *Smarcal1* wild-type allele and a 16.3 kb band corresponding to the *Smarcal1* floxed allele. The lanes marked with an asterisk represent ES cells that are heterozygous for the conditional allele (*Smarcal1*$^{+/loxP}$). (**D**) Depiction of the floxed *Smarcal1* allele used to generate the *Smarcal1*^{del} allele. The *Smarcal1*^{del} allele lacks exons 2 and 3 and thus encodes a protein with deletion of the amino terminal nuclear localization signal, RPA binding site and most of the first HARP domain. Noncoding exons are shown in yellow; exons encoding the HARP domains are shown in light blue; and exons encoding the SNF2 domain are shown in gray. (**E**) Southern analysis of mouse tail DNA after recombination of the *loxP* sites upon expression of Cre recombinase. Mice carrying a *GDF9-Cre* transgene(2), which drives oocyte specific expression of Cre recombinase, were crossed to the *Smarcal1*$^{loxP/+}$ mice to generate the *Smarcal1*^{del} allele. After restriction enzyme digestion with Kpn I and Xmn I, probing with the 3′ probe shows a 7.65 kb band corresponding to the *Smarcal1* wild-type allele and a 5.25 kb allele representing the knockout allele. The lanes marked with an asterisk represent mice that are heterozygous at the *Smarcal1* locus (*Smarcal1*$^{+/del}$). (**F**) PCR amplification products expected for genotyping of the *Smarcal1*^{LoxP} and *Smarcal1*^{del} alleles. (**G**) Results of the PCR genotyping for the floxed Smarcal1 allele (*Smarcal1*^{LoxP}). (**H**) Results of the PCR genotyping for the deleted Smarcal1 allele (*Smarcal1*^{del}).

Supplementary Figure S5. Expression analyses of the Smarcal1 deletion (*Smarcal1*^{del}) and wild type (*Smarcal1*$^{+}$) mRNA and protein. (**A**) Photograph of an agarose gel showing that by RT-PCR analysis of mRNA isolated from *Smarcal1*$^{+}$, *Smarcal1*$^{del/+}$ and *Smarcal1*$^{del/del}$ mouse embryonic fibroblasts (MEFs), the *Smarcal1*^{del} allele produces mRNA by splicing from exon 1 to 4. The PCR primer pair used had a forward primer in exon 1 and a reverse primer in exon 4. (**B**) Photograph of an immunoblot showing that the *Smarcal1*^{del} allele in MEFs does not produce Smarcal1 protein detectable by antiserum raised against the amino terminal of Smarcal1. □-tubulin is shown as a loading control. (**C**) Photograph of an immunoblot showing that expression of the wild type and deleted Smarcal1 with a carboxy terminal V5-tag in HEK 293 cells produces similar steady state levels of each protein. The proteins were detected using polyclonal anti-V5 serum. GAPDH is shown as a loading control. (**D**) Photographs showing that by immunofluorescent analysis, the Smarcal1^{+} and Smarcal1^{del} proteins localize to the nucleus. Bar = 20μm. (**E**) Graph of the DNA-dependent ATP hydrolysis activity of the Smarcal1^{del} protein relative to that of Smarcal1^{+} protein. Calf intestinal phosphatase was used as a positive control. The error bars represent one standard deviation.

Supplementary Figure S6. Phenotypic comparison of *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ mice. (**A**) Graphs comparing the body weights and lengths of newborn (P0) *Smarcal1*$^{+/+}$(n=20), *Smarcal1*$^{+/del}$ (n=55), and *Smarcal1*$^{del/del}$ (n=20) littermates. The error bars represent one standard deviation. None of the differences in these graphs are statistically significant. (**B**) Genotypes of the offspring of *Smarcal1*$^{+/del}$ x *Smarcal1*$^{+/del}$ parents. Note that the genotypes of the offspring have a Mendelian ratio both at birth and at weaning. (**C**) Graphs comparing the body weights and lengths for each sex of 6 month-old *Smarcal1*$^{+/+}$ (9 males and 21 females) and *Smarcal1*$^{del/del}$ (31 males and 24 females) littermates. The error bars represent one standard deviation. None of the differences in these graphs are statistically significant. (**D-G**) Photographs of representative H&E staining of the proximal tibia of 6 month-old *Smarcal1*$^{+/+}$ (**D** and **E**) and *Smarcal1*$^{del/del}$ (**F** and **G**) mice. Panels **E** and **G** are higher magnifications of the boxed areas on panels **D** and **F**, respectively. Note similar structure and cellularity of the growth plates between *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ mice. Bar = 100μm. (**H-K**) Photographs of representative H&E staining of the kidney cortex from 6 month-old *Smarcal1*$^{+/+}$ (**H** and **I**) and *Smarcal1*$^{del/del}$ (**J** and **K**) mice. Panels **I** and **K** are higher magnifications of the glomeruli boxed on panels **H** and **J**, respectively. Note similar glomeruli and tubular structures between *Smarcal1*$^{+/+}$ and *Smarcal1*$^{del/del}$ mice. Bar = 100 μm. (**L**) Graphs comparing the urinary excretion of protein over 24-hours by 2 and 12 month-old *Smarcal1*$^{+/+}$ (n=4) and *Smarcal1*$^{del/del}$ (n=4) mice. The protein excretion was normalized to the urinary creatinine. The error bars represent one standard deviation. (**M**) Plots show the representative FACS analysis of the thymus from *Smarcal1*$^{+/+}$ (n=3) and *Smarcal1*$^{del/del}$

(n=3) mice for different lymphocyte subsets. Thymocytes were initially analyzed for T-cell developmental stages based on CD4 and CD8 staining. Double negative (CD4$^-$CD8$^-$) cells were further resolved based on CD44 and CD25 expression into DN1 (CD44$^+$CD25$^-$), DN2 (CD44$^+$CD25$^+$), DN3 (CD44$^-$CD25$^+$) and DN4 (CD44$^-$CD25$^-$) fractions. (**N**) Quantification of lymphocyte subsets analyzed in panel m. The error bars represent one standard deviation. (**O**) Plots show the representative FACS analysis of the spleen from *Smarcal1*$^{+/+}$ (n=3) and *Smarcal1*$^{del/del}$ (n=3) mice for different lymphocyte subsets. Splenic B and T cells were initially resolved based on expression of B220 (CD45R) and TCRαβ. Subsequently, T cells (TCR□□) were further resolved into CD4$^+$ and CD8$^+$ T-cell subsets. Note that there is a significantly reduction of B cells (B220$^+$) in *Smarcal1*$^{del/del}$ spleen. The error bars represent one standard deviation.

Supplementary Figure S7. Photographs showing immunofluorescent co-localization of Marcal1 (green) with panacetyl-histone H4 (AcH4; red) on *Drosophila* polytene chromosomes. HA tagged Marcal1 was in transgenic flies (*tub-GAL4, UAS-HA-GFP-Marcal1*) and detected with an anti-HA monoclonal antibody.

Supplementary Figure S8. Photographs of *Drosophila* wings showing the extra wing veins induced by expression of Marcal1 (**A**) and SMARCAL1 (**B**). Marcal1 and SMARCAL1 expression were driven in transgenic flies by the GAL4-UAS system. No extra wing veins are observed with the UAS-Marcal1 or UAS-SMARCAL1 constructs alone or with the GAL4 drivers (*tubulin>GAL4* or *MS1096>GAL4*) alone. Also, note the absence of ectopic wing veins when the expressed protein product has no ATPase activity (*Marcal1*^{K275R} and *SMARCAL1*^{R586W}) (3, 27).

Supplementary Figure S9. Epistatic interaction of Marcal1 and SMARCAL1 overexpression with mutations of RNA polymerase II (RpII). Photographs of representative wings showing the effect of several *RpII215* and *RpII140* mutations on the extra wing vein phenotype. Quantification of wing margin scalloping in *C96-GAL4, UAS-Hrs* flies was used to control for nonspecific interactions between the various mutations and the GAL4-UAS system.

Supplementary Figure S10. Verification of microarray gene expression and transcriptome sequencing data by qRT-PCR. For each gene expression array and transcriptome experiment, genes involved in specific pathways that seemed to be deregulated in *SMARCAL1*-deficient cells or organisms were chosen for validation of mRNA levels by qRT-PCR. These pathways include cell cycle genes for the human gene expression array, egg development genes for the *Drosophila* gene expression array, and stress response genes for the mouse transcriptome. The RNA samples used for these validation studies were aliquots from the same biological replicates used for the gene expression array and transcriptome experiments. (**A**) Graphs of relative quotients (RQ) for steady state mRNA levels of 8 genes in cultured dermal fibroblasts derived from two SIOD patients (SD8 and SD60) and one unaffected control. The analysis was performed using human cell cycle PCR array (SABiosciences) and data was normalized to *B2M, HPRT1, RPL13A, GAPDH*, and *ACTB* mRNA levels and plotted relative to the unaffected control. (**B**) Graphs of the RQs for steady state mRNA levels of 7 genes in ovaries dissected from *Marcal*$^{del/del}$ and *yw* flies. The data was normalized to *Gapdh2* mRNA levels and plotted relative to the *yw* control flies. (**C**) Graphs of RQs for steady state mRNA levels of 7 genes in livers dissected from *Smarcal*$^{del/del}$ and *Smarcal1*$^{+/+}$ mice placed at an ambient temperature of 39.5ºC for 1 hour. The analysis was performed using the mouse heat shock PCR array (SABiosciences) and data was normalized to *Gusb, Hprt, Hsp90ab1, Gapdh*, and *Actb* mRNA levels and plotted relative to the unaffected control. All error bars represent one standard deviation.

Supplementary Figure S11. *SMARCAL1* deficiency causes abnormal expression of heat stress genes. Volcano plots of qRT-PCR comparison of stress gene expression in SIOD dermal fibroblasts (SD120 and SD123) to that in control unaffected dermal fibroblasts after one hour incubation at 43ºC followed by one hour incubation at 37°C. Each plot is based on three biological replicates.

Supplementary Figure S12. Effect of *Marcal1* deficiency on expression of heat stress genes and proteins in 1-3 day old *Drosophila* females. (**A**) Graphs showing qRT-PCR measurement of stress gene mRNA levels in *Marcal1*$^{del/del}$ flies relative to *yw* control flies. The duration of heat shock at 37ºC and recovery at 20ºC is shown above the graphs. The values in each graph represent the mean of three independent experiments assessed in triplicate. The data was normalized to *Gapdh2* mRNA levels. The error bars represent one standard deviation. (**B**) Photographs of immunoblots showing the expression of stress gene proteins in *Marcal1*$^{del/del}$ flies and *yw* control flies. The duration of heat shock at 37ºC and recovery at 20ºC is shown above. β-tubulin was used as a loading control. Abbreviations: *del*, *Marcal1*$^{del/del}$ flies; RQ, relative quotient.

Supplementary Figure S13. Effect of knocking down RpII components in *SMARCAL1* and *Smarcal1* deficient fibroblasts. (**A**) The ratio of WST-1 assay measurement of *SMARCAL1*$^{del/del}$ (SD31) and unaffected control dermal fibroblasts 72 and 96 hours following electroporation with non-targeting or *POLR2A*- and *POLR2B*-targeting shRNAs. The values in each graph represent the mean of 3 independent experiments and were normalized to the non-targeting values. (**B**) As measured by qRT-PCR, *POLR2A* and *POLR2B* mRNA levels were reduced approximately by 50-80% and 45-50%, respectively. The data was normalized to *GAPDH* mRNA levels and to the non-targeting control. (**C**) The ratio of WST-1 assay measurement of *Smarcal1*$^{del/del}$ and *Smarcal1*$^{+/+}$ MEFs 48 and 96 hours following electroporation with non-targeting or *Polr2a*-targeting siRNAs (*Polr2a-1* and *Polr2a-3*). The values in each graph represent the mean of 3 independent experiments and were normalized to the non-targeting values. (**D**) As measured by qRT-PCR, *Polr2a* mRNA levels were reduced approximately by 55-65% for siRNA duplex 1 and 70% for siRNA duplex 3. The data was normalized to *Gapdh* mRNA levels and to the non-targeting control. The error bars throughout represent one standard deviation.

Supplementary Figure S14. Treatment of *Smarcal1*$^{del/del}$ mice with α-amanitin does not recapitulate T-cell deficiency in SIOD. (**A**) Plots show the representative FACS analysis of the thymus from *Smarcal1*$^{+/+}$ (n=3) and *Smarcal1*$^{del/del}$ (n=5) mice treated with α-amanitin for different developmental T-cell subsets. Thymocytes were initially analyzed for T-cell developmental stages based on CD4 and CD8 staining. Double negative ($CD4^-CD8^-$) cells were further resolved based on CD44 and CD25 expression into DN1 ($CD44^+CD25^-$), DN2 ($CD44^+CD25^+$), DN3 ($CD44^-CD25^+$) and DN4 ($CD44^-CD25^-$) fractions. (**B**) Quantification of T-cell subsets analyzed in panel **A**. (**C**) Plots show the representative FACS analysis of the spleen from *Smarcal1*$^{+/+}$ (n=3) and *Smarcal1*$^{del/del}$ (n=5) mice treated with α-amanitin for different lymphocyte subsets. Splenic B and T cells were initially resolved based on expression of B220 (CD45R) and TCRαβ. Subsequently, T cells (TCRαβ) were further resolved into CD4$^+$ and CD8$^+$ T-cell subsets. (**D**) Quantification of T-cell subsets analyzed in panel **C**. Note that compared to untreated mice (Supplementary Material, Fig. S6), treatment with α-amanitin did not significantly alter the representation of the lymphocyte subsets. The error bars represent one standard deviation.

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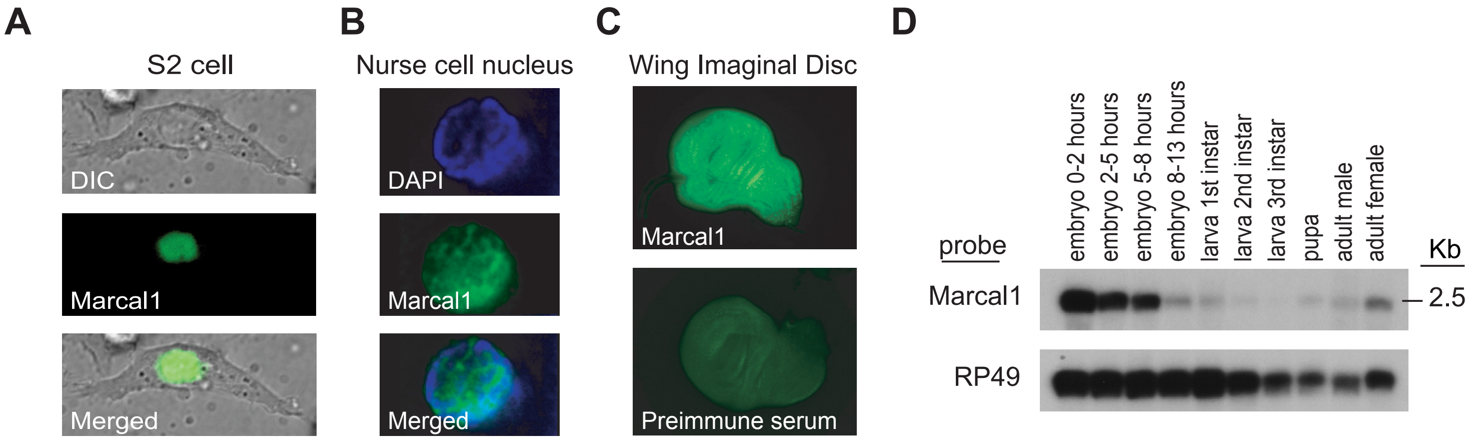

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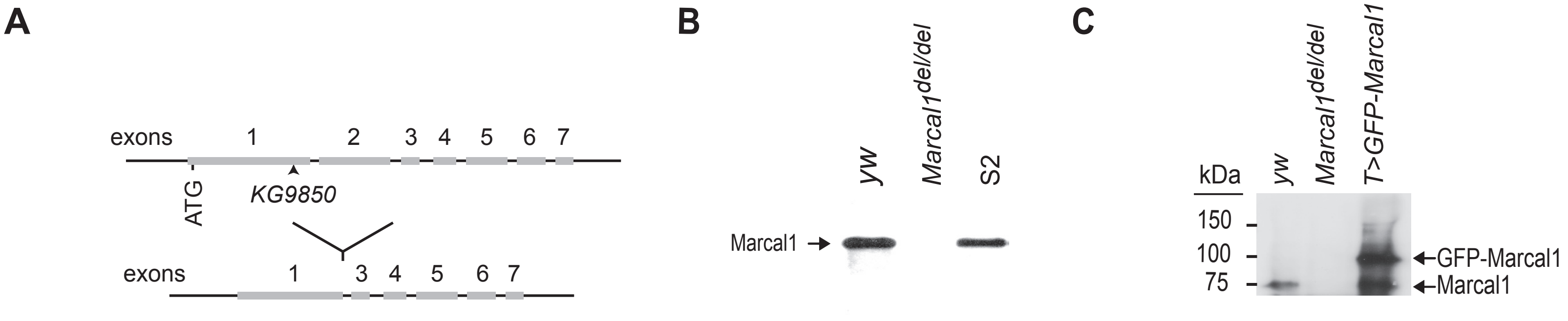

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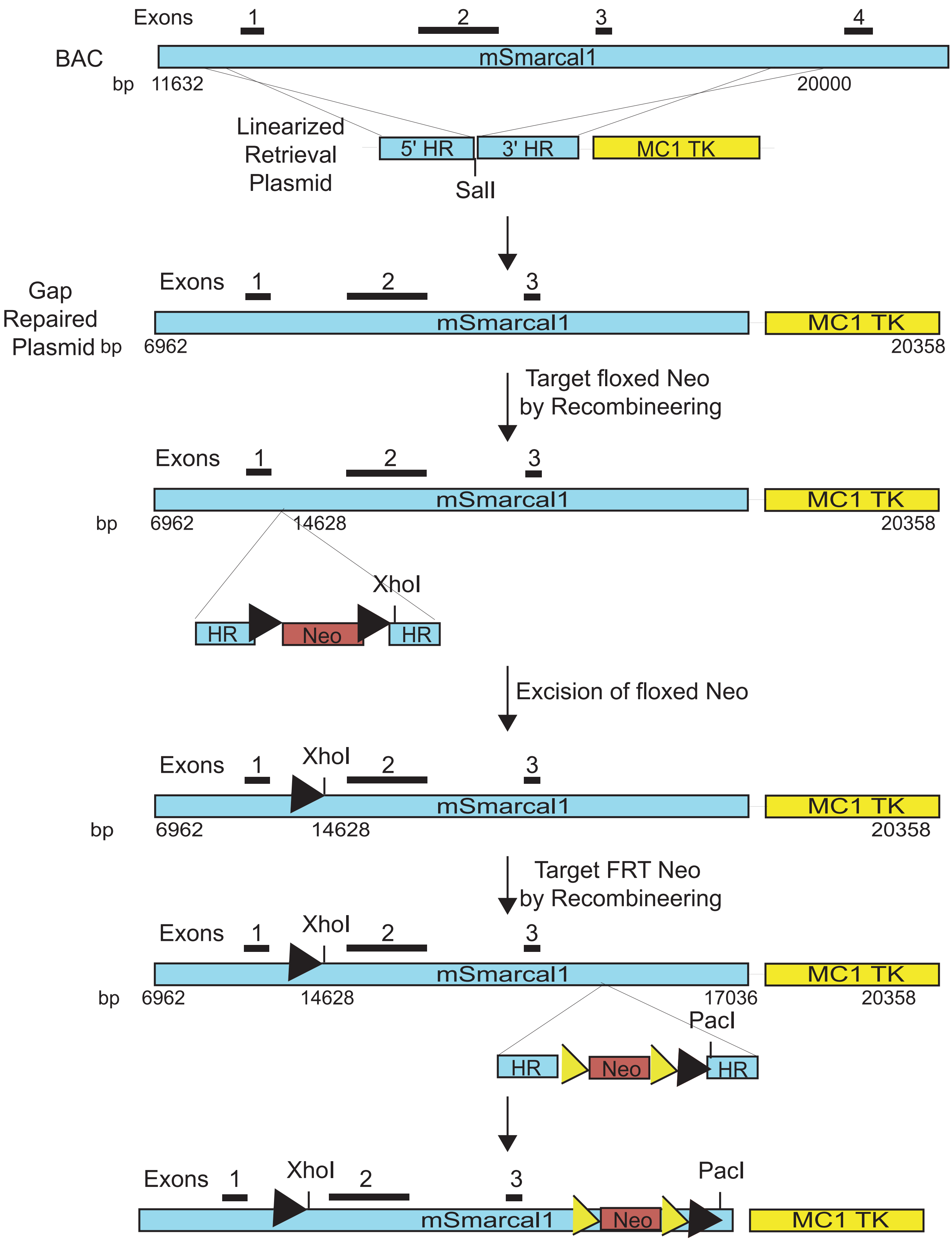

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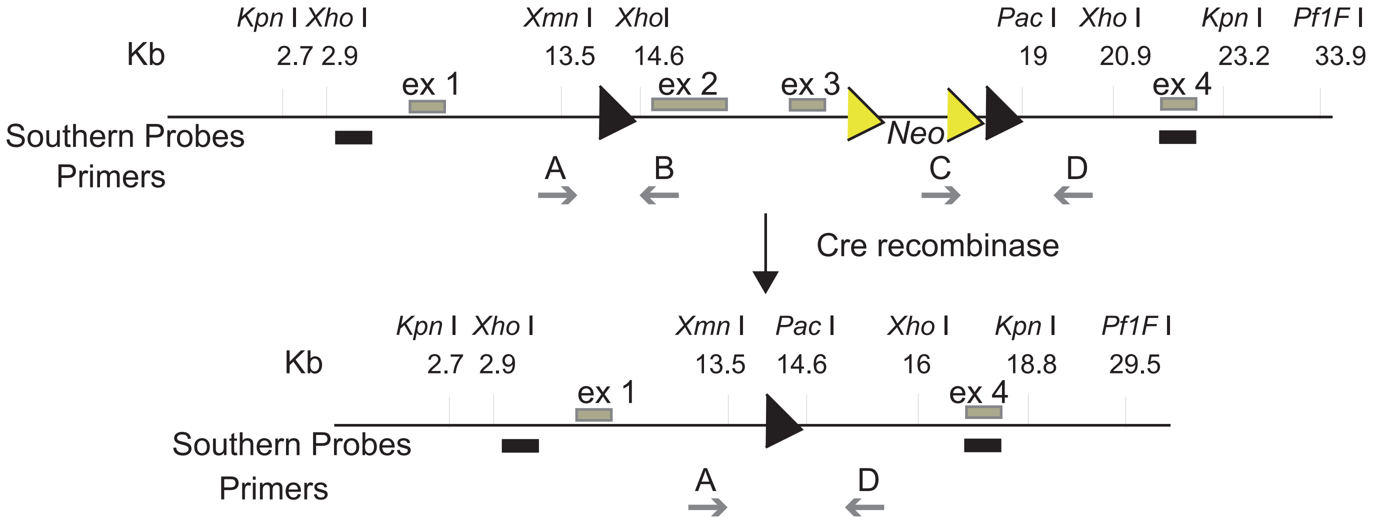
A

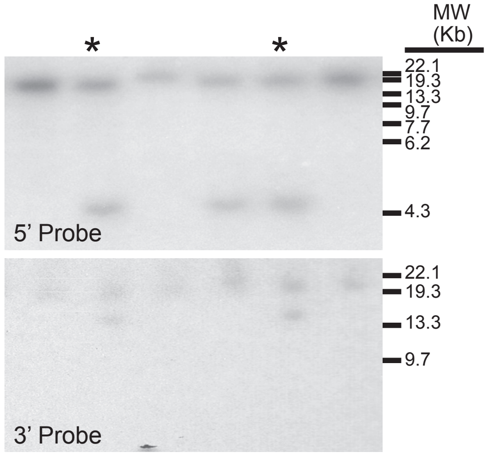


B

Fragment sizes (Kb) by Southern analysis for wild type (wt) and transgenic (Tg) *Smarcal1* alleles

	Genotype	Integration		Removal of *Neo*		Removal of Exons 2 & 3		
		Xho I	*Kpn* I/*Pac* I	Flp	*Kpn* I/*PflF* I	Cre	*Xho* I	*Kpn* I/*Xmn* I
5' Probe	wt	16	18.5	-	15.4	-	11.7	nd
	Tg	11.7	4.17	+	18.5	+	13.6	nd
3' Probe	wt	nd	18.5	-	5.2	-	nd	7.65
	Tg	nd	16.3	+	18.5	+	nd	5.25

C



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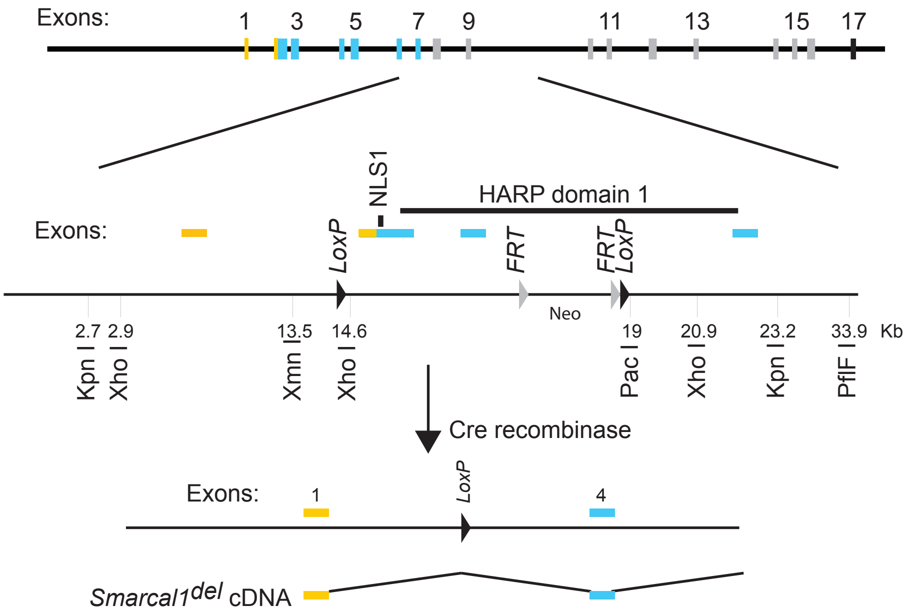

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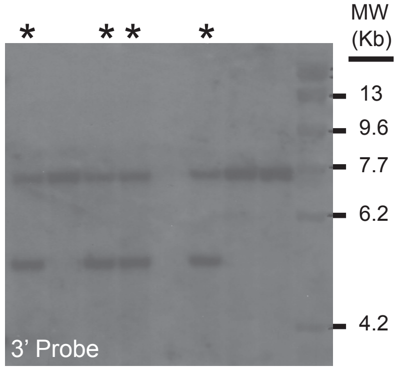
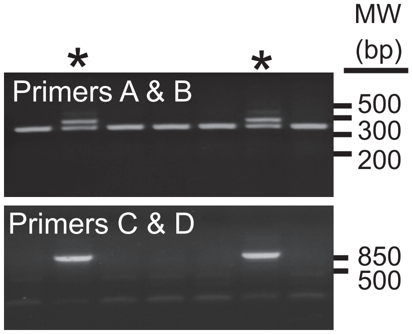


F

PCR products of wt and tg *Smarcal1* alleles

Primers	Genotype	*Smarcal1* allele	
		LoxP	del
A & B	wt	340 bp	340 bp
	Tg	374 bp	-
C & D	wt	-	-
	Tg	850 bp	-
A & D	wt	-	-
	Tg	-	637 bp

G



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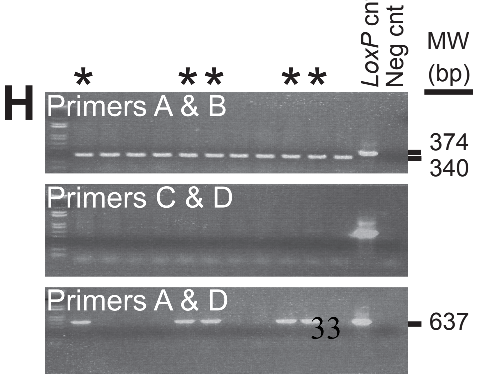

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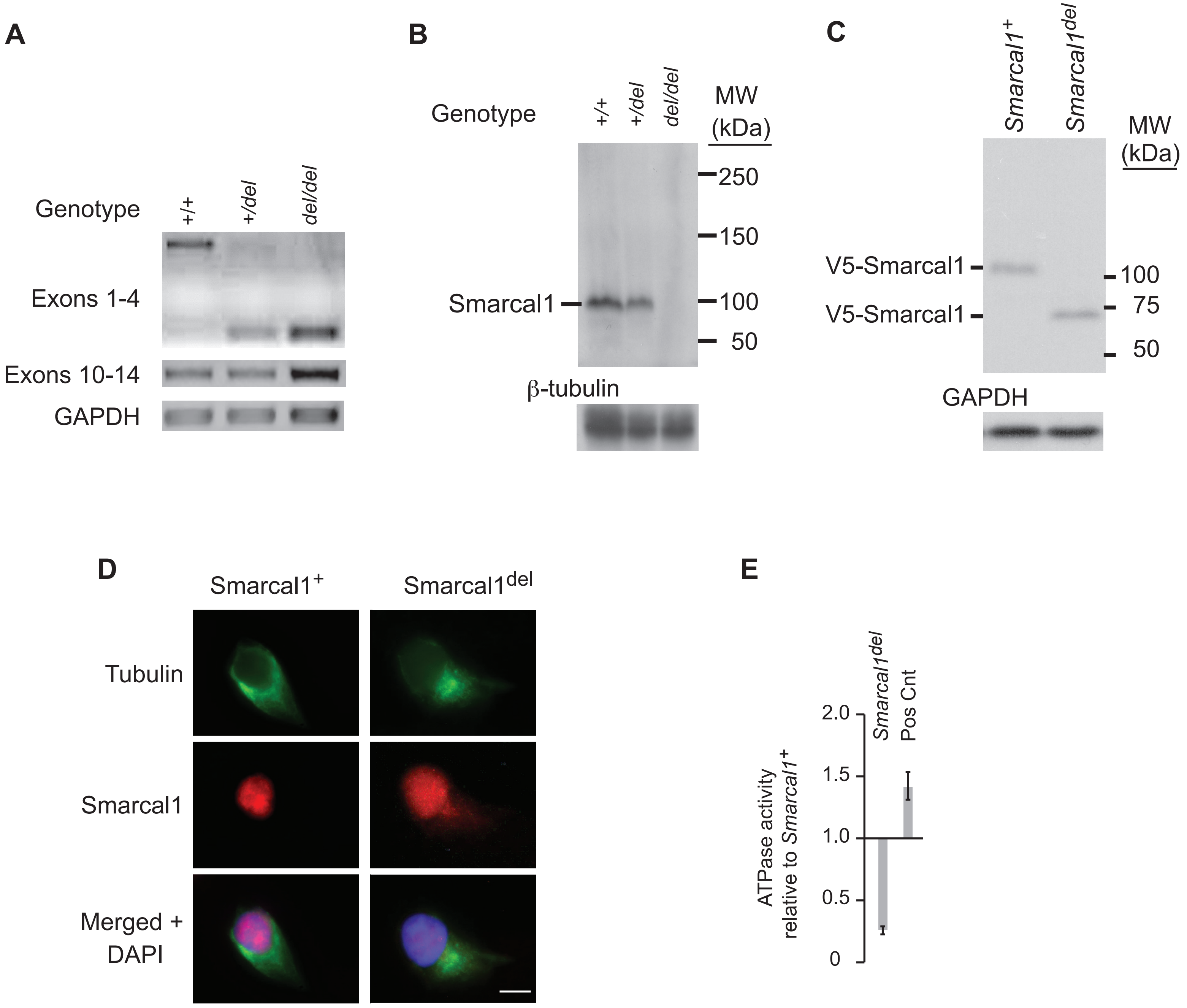

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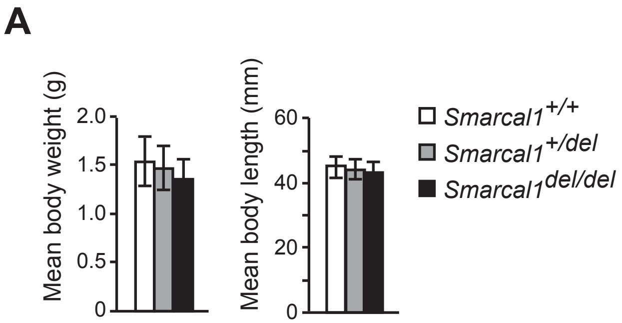
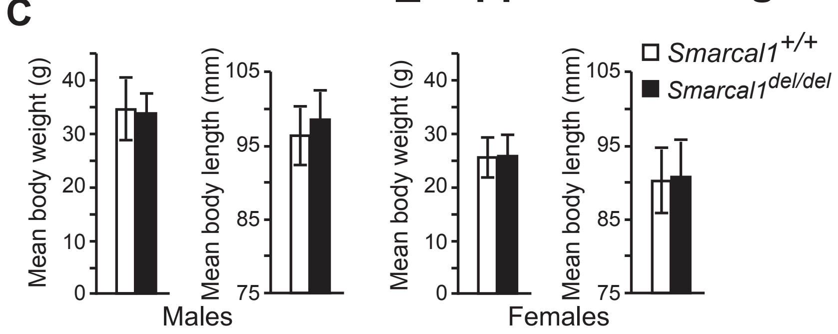
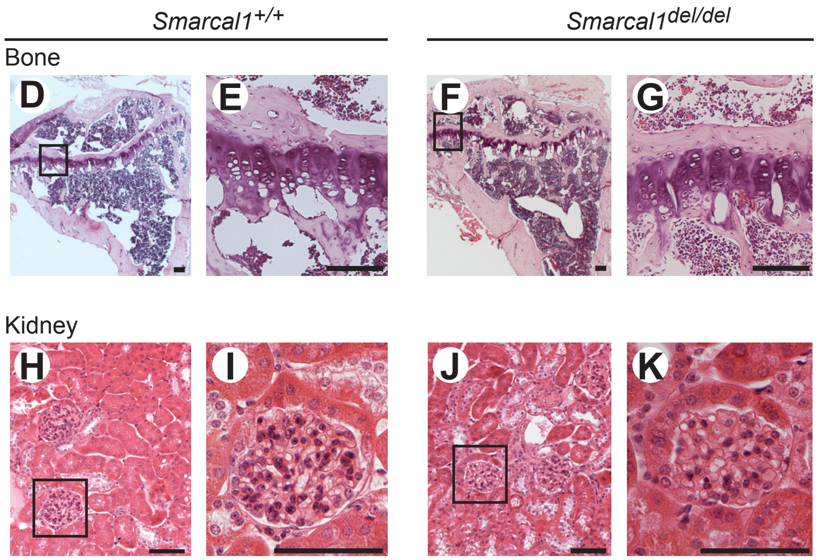
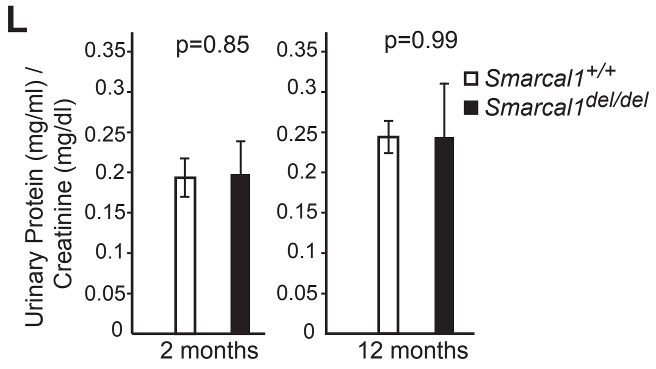


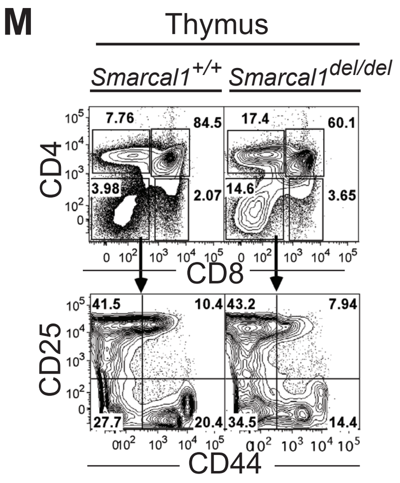
B

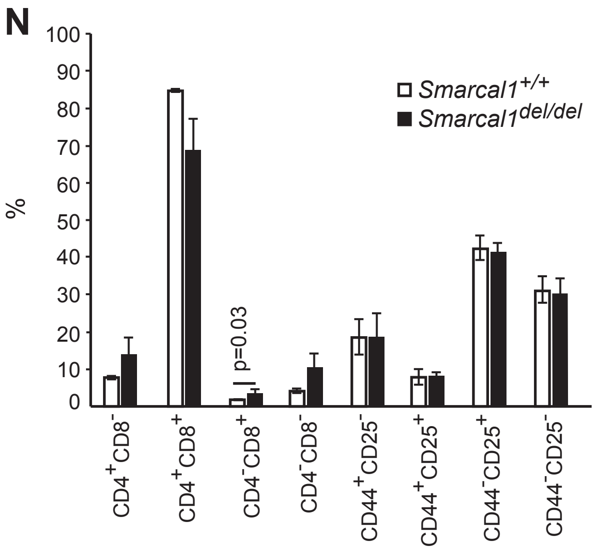
Smarcal1+/del X *Smarcal1+/del*	*P0*		*Weaned*	
	observed	expected	observed	expected
Smarcal1del/del	44	50	43	51
Smarcal1+/del	106	100	102	101
Smarcal1+/+	50	50	58	51
Total	200		203	
	p=0.58		p=0.32	

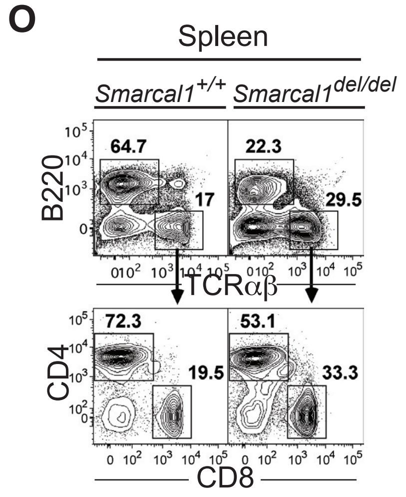


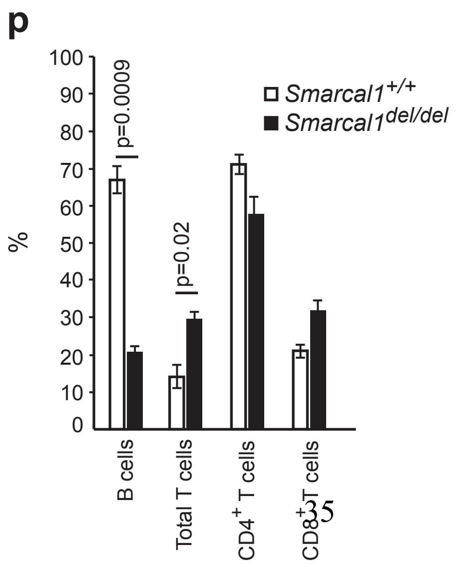


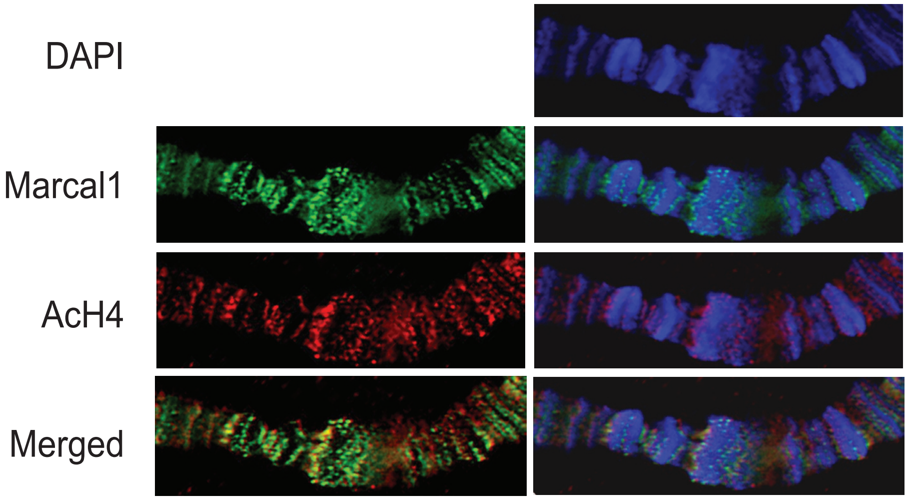








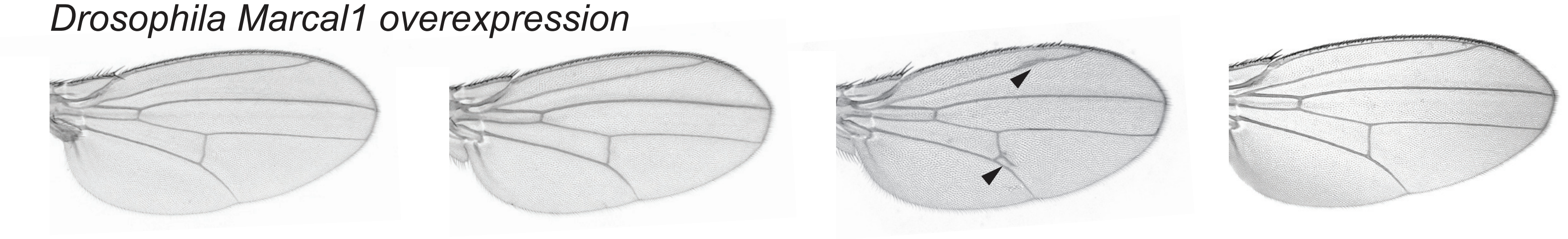



DAPI
Marcal1
AcH4
Merged

Baradaran-Heravi_Supplemental FigS8.

A

Drosophila Marcal1 overexpression



UAS-Marcal1

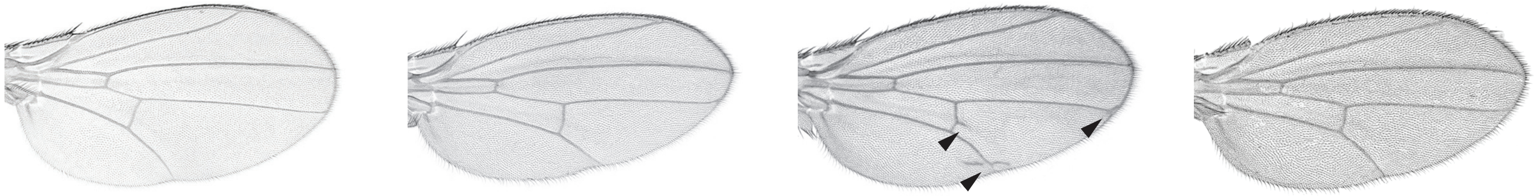
tubulin-GAL4

UAS-Marcal1;
tubulin-GAL4

UAS-Marcal1^{K275R}*;*
tubulin-GAL4

B

Human SMARCAL1 overexpression



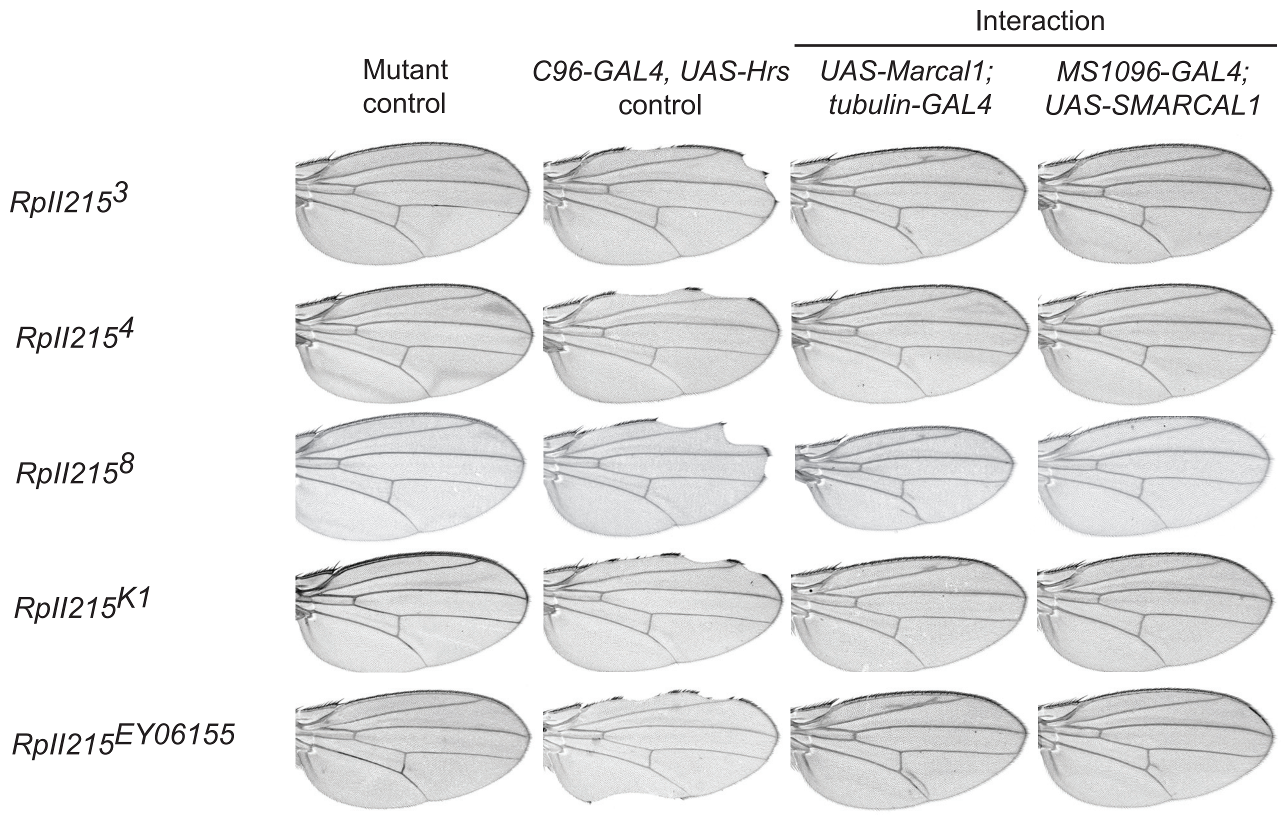
UAS-SMARCAL1

MS1096-GAL4

MS1096-GAL4;
UAS-SMARCAL1

MS1096-GAL4;
UAS-SMARCAL1^{R580W}

Baradaran-Heravi_Supplemental FigS9.



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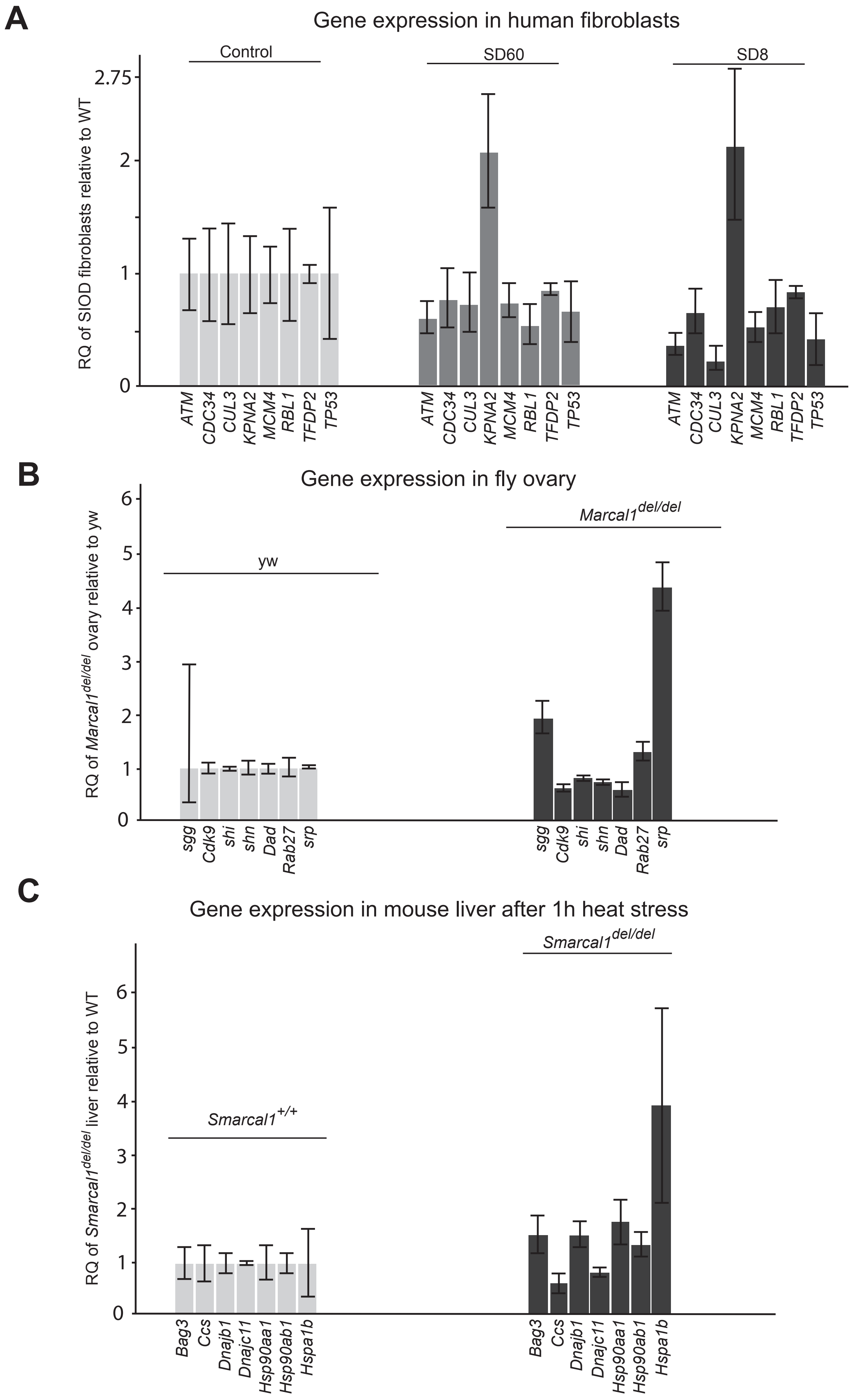

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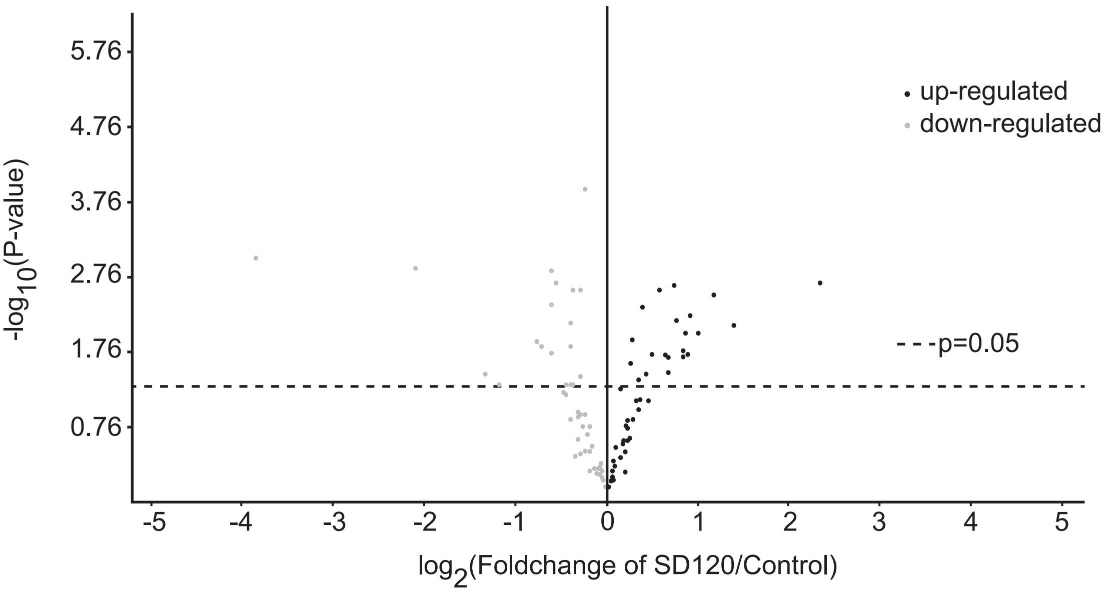

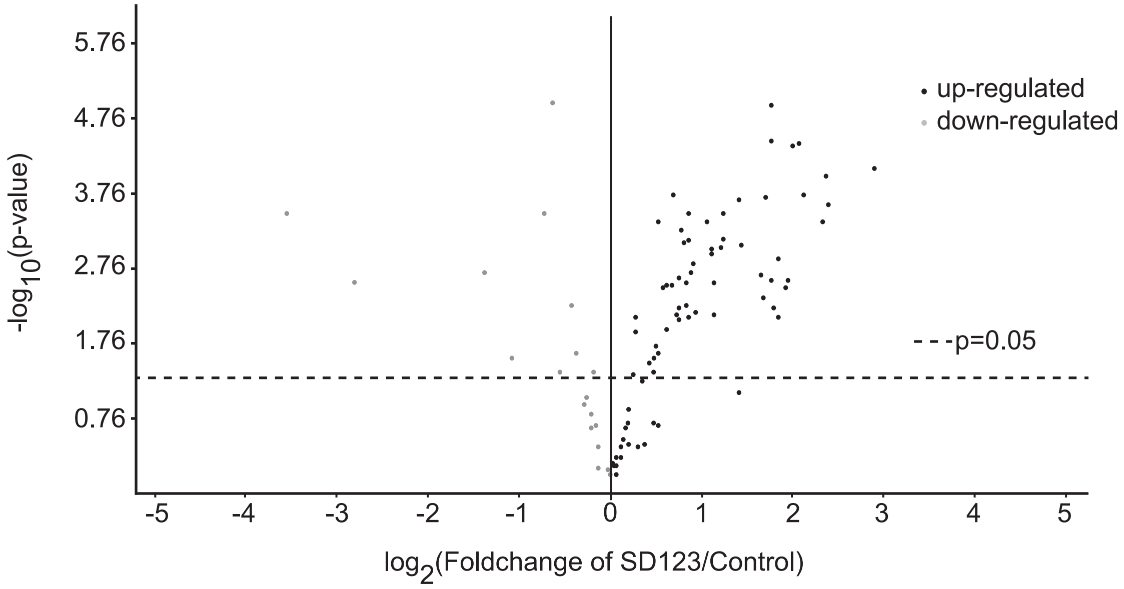

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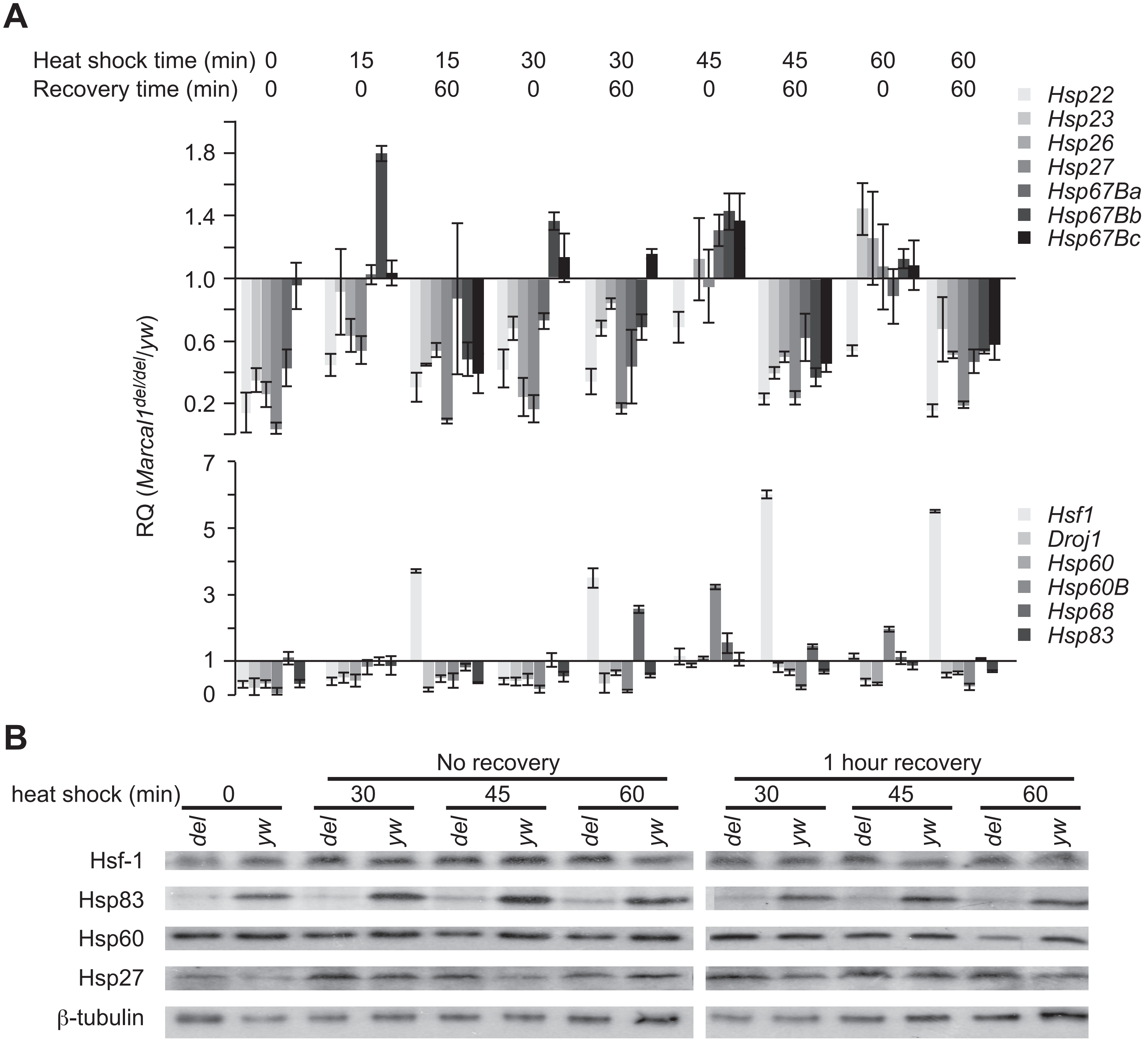

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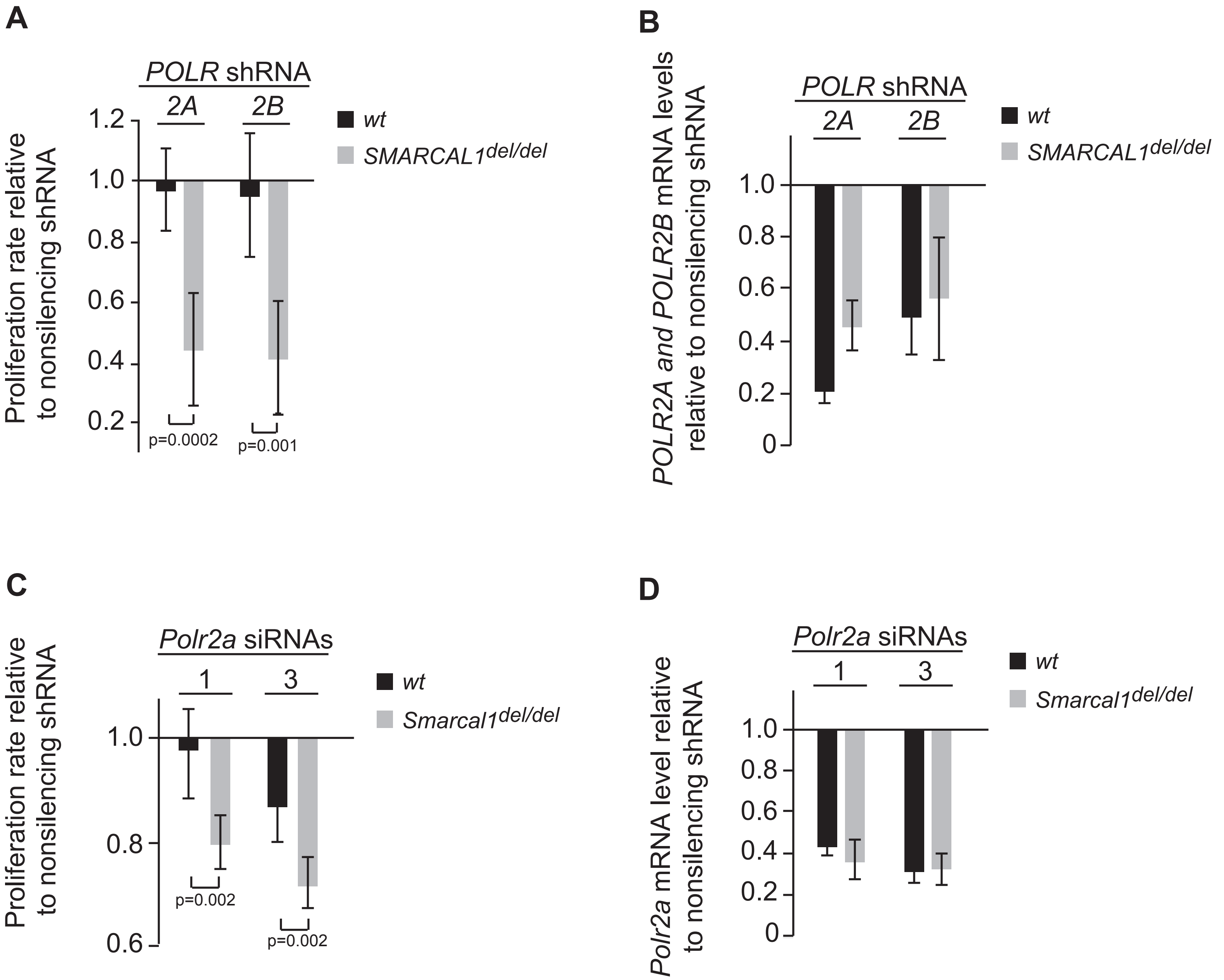

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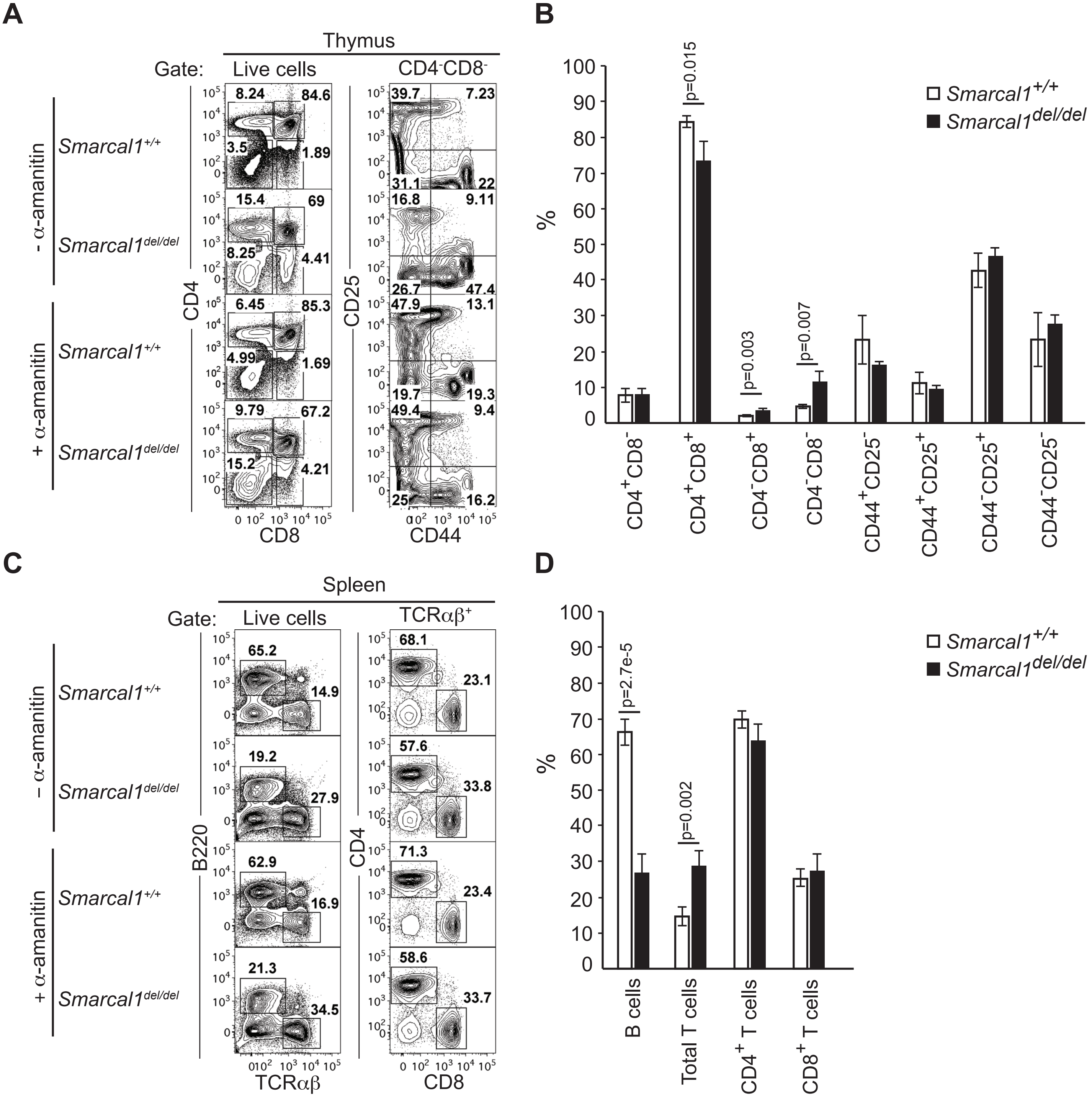

Supplementary Table S1 Distribution of RpII for Marcal1 and Pc target genes

Data		RpII absent			RpII stalled			RpII active			RpII undetermined		
Source	Profile	Observed (%)	Expected (%)	χ^2	Observed (%)	Expected (%)	χ^2	Observed (%)	Expected (%)	χ^2	Observed (%)	Expected (%)	χ^2
Toll10b	Marcal1	15	39	5E-69	21	11	6E-25	33	27	0.2	32	23	7E-09
	Pc	45	39	1	27	11	2E-45	11	27	1E-24	17	23	0.1
S2	Marcal1	28	55	2E-82	15	5	8E-41	42	29	3E-22	-	-	-
	Pc	64	55	7E-04	12	5	5E-11	13	29	7E-25	-	-	-

N.B. Expected is based on genome-wide distribution of RpII

P values from the χ^2 test were corrected for multiple testing, using Bonferroni correction

Supplementary Table S2 Suppressors and enhancers of ectopic wing veins induced by the overexpression of *Drosophila* Marcal1 and human SMARCAL1.

Gene	Allele	*Drosophila* Marcal1	Human SMARCAL1	Gene	Allele	*Drosophila* Marcal1	Human SMARCAL1
Nuclear Matrix and Chromatin Structure Interactors							
BEAF-32	*e00756*	E	E	*Nipped-B*	*02047*	S	S
	KG06904	S	0	*ord*	*1*	S	S
Lam	*91*	E	E	*san*	*KG04816*	0	0
	98	E	E	*SMC1*	*c00402*	E	E
	sz18	E	E	*su(Hw)*	*2*	S	S
LamC	*G00158*	S	S		*8*	S	S
	k11904	0	0		*e04061*	E	E
mei-S332	*1*	S	0	*Trl*	*s2325*	S	E
mod(mdg4)	*u1*	S	S		*KG08276*	S	S
	KG08515	S	S				
Chromatin Remodeling or Chromatin Structural Factors							
Acf1	*1*	0	0	*Pcaf*	*f02830*	S	0
	2	E	E		*f05456*	0	E
	EY08629	E	E		*C137T*	S	S
mod	*07570*	S	S		*E333st*	0	E
Nap1	*KG03959*	E	E		*Q186st*	S	0
	EY08596	E	E		*DeltaT280-F285*	S	S
	K01	E	E	*Sir2*	*17*	0	E
	K02	0	E		*2A-7-11*	E	E
nej	*P*	S	S	*Su(var)205*	*5*	E	E
	Q7	S	S	*Su(var)3-1*	*3*	S	S
nhk-1	*Z3-0437*	E	0	*Su(var)3-4*	*1*	S	E
Nipped-A	*NC116*	S	S		*2*	S	S
	NC186	S	S	*trr*	*1*	S	S
pr-set7	*1*	0	0		*3*	S	S
	EY04668	E	E		*4*	S	S
					EY06632	E	E
Mediator Complex							
Cdk8	*A162*	S	0	*MED18*	*e03853*	S	S
MED6	*EY05087*	E	E	*MED20*	*C6R20*	0	S
MED12 (Kto)	*1*	E	E		*f00955*	S	E
MED13 (skuld)	*2*	E	E	*MED23*	*KG00948*	E	0
	rK760	E	E	*MED24*	*BG01670*	E	E
	L7062	0	S	*MED28*	*e03165*	E	E
	EY07369	E	0	*MED29 (intersex)*	*1*	0	S
MED15	*f04180*	0	E		*KG04582*	0	0
MED17	*s2956*	E	E				
RNA Polymerase II Complex							
cul-4	*KG02900*	E	E	*RpII215*	*3*	0	0
	EP2518	S	0		*4*	S	S
RpII33	*1*	0	0		*8*	E	S
	k05605	0	S		*12*	E	E
RpII140	*wimp*	E	E		*102*	E	E
	S	S	S		*G0040*	0	S
					K1	S	S
					ts	S	E
					Ubl	E	S

					EY06155	E	E
RNA Polymerase II Initiation Factors							
pb (srb)	*1*	S	E	*Taf2 (TFIID)*	*c03353*	S	0
	10	S	S	*Taf4 (TFIID)*	*1*	E	S
	23	S	S		*e02502*	S	E
	27	S	0	*Taf5 (TFIID)*	*EY01764b*	E	0
Trf2	*PL28#1*	S	S	*Taf6 (TFIID)*	*1*	0	E
TfIIA-L	*e01040*	0	E		*f06930*	0	E
	d08487	S	E	*Taf10 (TFIID)*	*KG07031*	0	0
TfIIA-S	*E32*	S	E	*Taf10b (TFIID)*	*KG01574*	E	E
	E73	S	0	*Taf12L (TFIID)*	*KG00946*	E	S
	EY02323	E	S	*TfIIEα*	*e01382*	S	0
TfIIB	*DG14311*	S	E	*TfIIEβ*	*e00364*	S	E
caz (TFIID)	*EP1564*	E	E	*TfIIFα*	*d01485*	S	E
e(y)1 (TFIID)	*BG00948*	S	S	*TfIIFβ*	*j3C1*	E	S
mia (TFIID)	*B560*	S	S	*Cdk7 (TFIIH)*	*T170A*	E, blistered	E
	EY07883	E	E		*D136R*	E	E
Taf1 (TFIID)	*1*	S	S	*CycH (TFIIH)*	*KG02273*	E	E
	EP421	E	E	*hay (TFIIH, Xpb, Ercc3)*	*f00028*	0	E
RNA Polymerase II Elongation Factors							
Cdk9	*f05537*	E	E	*mus209 (PCNA)*	*02448*	S	S
CycT	*c04764*	S	S		*k00704*	0	S
	c06571	E	E		*EY09082*	E	E
dre4 (FACT, Spt16)	*EY01604*	E	S	*Spt4*	*k05316*	S	S
Elongin-B	*EP3132*	S	0	*Spt5*	*SIE-27*	S	S
	EY04022	E	E		*W049*	S, small	0
Elongin-C	*e01107*	S	0	*Spt6*	*G0063*	S	S
Mi-2	*DG12505*	S	0	*Su(Tpl) (ELL)*	*10*	S	S
	EY08138	E	E		*c00783*	0	0
	EY08696	E	E		*c03115*	S	0
					S-192	S	E
				TfIIS	*2*	S	0
RNA Polymerase II Transcription Termination Factors							
Ids	*1*	S	E	*Pcf11*	*k08015*	S	E
	A190	0	E	*Slbp*	*EP1045*	S	0
	e00889	S	E				
	Hor-1	E	E				
Regulators of DNA Replication Gene Transcription							
cdc2	*B47*	S	E	*Dp*	*49Fk-1*	0	S
	c03495	E	S		*a1*	S	S
	E1-23	E	E		*KG00660*	S	S
	E1-24	E	E		*EY09085*	E	E
	GT-000294	E	E	*E2f*	*07172*	S	S
CycA	*03946*	E	0		*i2*	0	S
	c05304	E	S		*KG03332*	S	S
	C8LR1	S	E		*EY14408*	E	0

	H170	S	S	*grh*	*06850*	E	E
	EY11746	E	S		*IM*	E	E
Dref	*KG09294*	0	S		*s2140*	E	S
	NP4719	0	0				
Regulators of Chromatin Condensation and Segregation							
barr	*k14014*	S	S	*mei-9*	*f01366*	S	S
	L305	S	S	*mei-P22*	*A054*	E	E
Cap-G (condensin)	*BG01873*	E	E		*P22*	E	E
	EP2346	E	E	*mei-W68*	*1*	S	S
gluon	*88-37*	S	0		*k05603*	S	S
	k08819	S	S	*pros*	*17*	S	S

Key: S = suppressor, 0 = Neither a suppressor nor an enhancer, E = enhancer.

Supplementary Table S3 Log_2 scale value of mRNAs expression in SIOD (SD8 and SD60) and control fibroblasts.

AffyID	Symbol	Control	SD8	SD60
204776_at	*THBS4*	14.73	3.05	2.77
213183_s_at	*CDKN1C*	7.89	2.35	2.3
226931_at	*TMTC1*	8.17	2.64	2.34
205549_at	*PCP4*	9.52	3.06	2.86
205226_at	*PDGFRL*	7.535	2.325	2.395
204712_at	*WIF1*	9.47	3.14	3.2
227949_at	*PHACTR3*	9.13	3.34	3.32
228750_at	*COL14A1*	7.96	3.02	2.98
221805_at	*NEFL*	6.99	2.55	2.75
205935_at	*FOXF1*	6.31	2.41	2.42
242137_at	*NA*	7.075	2.705	2.775
208096_s_at	*COL21A1*	7.235	2.685	2.985
220783_at	*MMP27*	5.75	2.35	2.22
219304_s_at	*PDGFD*	9.72	3.79	3.97
237860_at	*RBMS3*	6.61	2.68	2.66
206404_at	*FGF9*	5.255	2.185	2.175
239468_at	*MKX*	11.435	5.125	4.415
219454_at	*EGFL6*	5.88	2.45	2.47
221916_at	*NEFL*	7.97	3.51	3.47
1555106_a_at	*CTDSPL2*	5.86	2.6	2.56
229525_at	*THOC7*	6.87	2.91	3.15
232746_at	*CXCR7*	6.45	2.97	2.72
1557155_a_at	*ZIC1*	7.275	3.045	3.495
230418_s_at	*GALNTL1*	8.125	3.765	3.595
227816_at	*NTN1*	5.515	2.515	2.485
218995_s_at	*EDN1*	9.435	4.145	4.445
226322_at	*TMTC1*	9.04	4.45	3.95

225089_at	*USP40*	4.425	1.965	2.155
239503_at	*NA*	5.355	2.565	2.515
220306_at	*FAM46C*	5.46	2.62	2.59
235044_at	*CYYR1*	5.965	2.685	3.035
227857_at	*C20orf3*	7.5	3.48	3.72
239680_at	*NA*	6.265	3.125	3.005
229912_at	*SDK1*	5.07	2.51	2.51
210997_at	*HGF*	5.345	2.655	2.685
220386_s_at	*EML4*	7.39	3.57	3.88
1564630_at	*EDN1*	4.595	2.315	2.315
215450_at	*SNRPE*	8.38	4.37	4.19
203372_s_at	*SOCS2*	5.255	2.685	2.695
219616_at	*FLJ21963*	4.59	2.37	2.33
212777_at	*SOS1*	4.455	2.355	2.225
1568408_x_at	*NA*	4.58	2.36	2.37
221915_s_at	*RANBP1*	4.805	2.485	2.525
215813_s_at	*PTGS1*	11.095	5.875	5.765
228501_at	*GALNTL2*	6.33	3.46	3.2
210305_at	*PDE4DIP*	7.73	4.14	3.99
202283_at	*SERPINF1*	9.63	5.12	5.02
209646_x_at	*ALDH1B1*	9.325	5.015	4.825
228485_s_at	*SLC44A1*	8.68	4.61	4.6
237986_at	*MGC16121*	5.03	2.71	2.66
228707_at	*CLDN23*	8.345	4.675	4.265
211368_s_at	*CASP1*	5.295	2.745	2.925
213285_at	*TMEM30B*	4.915	2.675	2.625
207386_at	*CYP7B1*	5.775	3.265	2.965
225977_at	*PCDH18*	6.05	3.34	3.2
233191_at	*RUFY2*	5.64	2.92	3.19
209057_x_at	*CDC5L*	7.5	4.27	3.89
226865_at	*NA*	6.225	3.415	3.365

227610_at	*TSPAN11*	6.12	3.46	3.22
1555594_a_at	*MBNL1*	4.82	2.7	2.67
210454_s_at	*KCNJ6*	5	2.9	2.7
230164_at	*ZNF621*	4.57	2.5	2.68
207869_s_at	*CACNA1G*	5.61	3.27	3.11
210380_s_at	*CACNA1G*	6.22	3.55	3.53
215802_at	*TLE1*	5.325	3.035	3.015
241779_at	*MTX3*	7.17	4.26	3.91
230967_s_at	*USP7*	9.325	5.435	5.215
229505_at	*NAP1L4*	6.81	3.91	3.88
242809_at	*IL1RL1*	4.445	2.565	2.525
1554283_at	*CCRN4L*	5.775	3.295	3.335
1560047_s_at	*LOC439962*	5.725	3.345	3.275
204610_s_at	*CCDC85B*	6.505	3.715	3.825
228772_at	*HNMT*	6.94	4.16	3.88
214505_s_at	*FHL1*	6.28	3.69	3.62
227860_at	*CPXM1*	3.805	2.225	2.215
209829_at	*C6orf32*	10.8	6.12	6.47
213972_at	*FOXD1*	5.245	2.985	3.145
211064_at	*ZNF493*	5.33	3.22	3.04
204684_at	*NPTX1*	10.495	6.025	6.295
232926_x_at	*ANKRD19*	4.6	2.73	2.67
223556_at	*HELLS*	6.065	3.655	3.485
229204_at	*HP1BP3*	9.785	5.555	6.005
220786_s_at	*SLC38A4*	4.535	2.695	2.685
211348_s_at	*CDC14B*	6.715	4.135	3.855
239959_x_at	*PDE3B*	4.235	2.505	2.565
213642_at	*NA*	13.65	7.98	8.4
204841_s_at	*EEA1*	7.135	4.395	4.195
205732_s_at	*NCOA2*	5.52	3.4	3.24
1556066_at	*JMJD3*	3.465	2.085	2.085

213406_at	*WSB1*	3.94	2.35	2.41
232112_at	*RALGPS2*	4.555	2.835	2.685
208889_s_at	*NCOR2*	3.8	2.3	2.31
205128_x_at	*PTGS1*	13.13	8.15	7.83
210298_x_at	*FHL1*	4.005	2.445	2.435
213590_at	*SLC16A5*	8.195	4.855	5.125
210299_s_at	*FHL1*	8.635	5.405	5.115
214125_s_at	*NENF*	5.27	3.26	3.16
206765_at	*KCNJ2*	10.75	6.4	6.78
1560451_at	*PKN3*	3.73	2.27	2.3
237533_at	*LOC647049*	4.645	2.905	2.795
237954_x_at	*NA*	6.355	3.945	3.855
224321_at	*TMEFF2*	13.28	8.01	8.31
235887_at	*NA*	4.405	2.705	2.705
241927_x_at	*CDC34*	4.795	2.955	2.955
231248_at	*CST6*	3.835	2.375	2.345
1555272_at	*LOC285927*	9.375	5.805	5.745
218848_at	*THOC6*	3.69	2.3	2.25
221423_s_at	*YIPF5*	9.835	5.895	6.225
241975_at	*LOC399959*	5.53	3.42	3.41
225726_s_at	*PLEKHH1*	5.085	3.195	3.095
226811_at	*FAM46C*	7.54	4.53	4.79
201539_s_at	*FHL1*	4.4	2.65	2.8
202935_s_at	*FLJ37644*	10.32	6.36	6.41
233558_s_at	*FLJ12716*	7.87	4.72	5.02
214437_s_at	*SHMT2*	8.755	5.325	5.505
1555399_a_at	*DUSP16*	5.395	3.335	3.345
219427_at	*FAT4*	9.195	5.505	5.915
231650_s_at	*SEZ6L*	3.75	2.33	2.33
239461_at	*GALNTL2*	5.45	3.44	3.34
224580_at	*SLC38A1*	6.36	4.06	3.87

231174_s_at	*NA*	5.47	3.39	3.43
218748_s_at	*EXOC5*	5.115	3.125	3.255
228235_at	*MGC16121*	6.555	4.015	4.175
203961_at	*NEBL*	3.68	2.31	2.29
229042_s_at	*DYNC1H1*	4.515	2.785	2.885
228665_at	*CYYR1*	8.95	5.79	5.47
239247_at	*LOC401577*	3.83	2.4	2.42
1553635_s_at	*TCTEX1D1*	4.775	2.985	3.035
242196_at	*NA*	4.665	2.955	2.935
227545_at	*NA*	6.03	3.79	3.83
212868_x_at	*MAPKAPK5*	3.525	2.225	2.235
241902_at	*MKX*	4.505	2.865	2.835
214001_x_at	*FLJ20294*	12.215	7.785	7.675
213705_at	*NA*	10.25	6.57	6.46
222329_x_at	*NA*	5.215	3.225	3.405
1568377_x_at	*DEFB124*	4.425	2.835	2.805
220979_s_at	*ST6GALNAC5*	3.875	2.475	2.475
200908_s_at	*RPLP2*	12.26	7.6	8.04
215384_s_at	*MAP1A*	6.125	3.935	3.885
1552307_a_at	*C18orf17*	4.585	2.875	3.005
223925_s_at	*LOC767558*	8.13	5.26	5.16
205794_s_at	*NOVA1*	3.215	2.055	2.065
213561_at	*ASF1A*	3.75	2.39	2.43
1559585_at	*FLJ31033*	3.65	2.3	2.39
1559315_s_at	*LOC144481*	4.36	2.81	2.79
214283_at	*IFT20*	7.135	4.735	4.465
217580_x_at	*ARL6IP2*	4.39	2.84	2.82
231513_at	*NA*	12.735	7.965	8.495
209739_s_at	*PNPLA4*	4.095	2.645	2.655
1555970_at	*FBXO28*	4.98	3.27	3.17
232411_at	*NA*	4.205	2.735	2.715

229397_s_at	*GRLF1*	7.75	5.01	5.05
211347_at	*CDC14B*	6.49	4.2	4.22
204437_s_at	*FOLR1*	4.43	2.92	2.86
244066_at	*DENND4C*	5.185	3.425	3.345
1566163_at	*MEIS2*	4.415	2.885	2.875
229671_s_at	*C21orf45*	6.17	3.98	4.08
230867_at	*LOC131873*	3.415	2.235	2.225
233546_at	*LOC283075*	4.11	2.71	2.67
213813_x_at	*RNPS1*	10.205	6.865	6.475
204301_at	*KBTBD11*	3.75	2.45	2.46
235649_at	*ADAMTS8*	3.19	2.09	2.09
1568997_at	*NA*	4.425	2.955	2.855
214691_x_at	*FAM63B*	6.635	4.405	4.295
236335_at	*NA*	5	3.35	3.21
218858_at	*DEPDC6*	6.89	4.42	4.64
1559485_at	*C14orf103*	3.955	2.535	2.665
210333_at	*NR5A1*	3.635	2.395	2.385
229806_at	*QRICH1*	8.65	5.63	5.75
242972_at	*TRIM26*	4.085	2.735	2.635
243466_at	*NA*	4.415	2.955	2.865
231098_at	*NA*	4.205	2.785	2.745
219738_s_at	*PCDH9*	4.17	2.77	2.73
216875_x_at	*HAB1*	4.535	3.025	2.955
232497_at	*ZNF3*	4.675	3.145	3.035
228913_at	*LOC728913*	8.86	5.81	5.91
229584_at	*LRRK2*	4.185	2.775	2.765
1555772_a_at	*CDC25A*	4.21	2.79	2.79
213054_at	*KIAA0841*	4.525	3.055	2.955
241667_x_at	*FOXO1A*	4.04	2.71	2.65
218172_s_at	*DERL1*	9.38	6.15	6.29
244115_at	*FAM126A*	7.045	4.595	4.745

214057_at	*MCL1*	9.13	6.01	6.12
229458_s_at	*GALK1*	3.9	2.6	2.6
210984_x_at	*EGFR*	3.315	2.215	2.215
1570364_at	*ZNF564*	4.45	3.05	2.89
207570_at	*SHOX*	3.49	2.33	2.33
214149_s_at	*ATP6V0E1*	11.195	7.455	7.525
1552596_at	*GAS2L2*	3.725	2.495	2.485
1555097_a_at	*PTGFR*	4.64	3.08	3.16
243834_at	*TNRC6A*	5.335	3.625	3.555
1557840_at	*EFHB*	4.22	2.85	2.83
231798_at	*NOG*	11.52	7.61	7.92
214000_s_at	*RGS10*	5.265	3.505	3.585
1561500_at	*LOC348180*	4.595	3.145	3.045
239341_at	*VDP*	3.555	2.425	2.365
223640_at	*HCST*	5.025	3.435	3.345
204540_at	*EEF1A2*	3.89	2.63	2.63
214484_s_at	*OPRS1*	4.39	2.95	2.99
205111_s_at	*PLCE1*	5.805	4.025	3.825
214892_x_at	*C19orf29*	3.515	2.375	2.375
214041_x_at	*RPL37A*	8.955	5.905	6.215
218122_s_at	*SENP2*	5.93	4.13	3.9
213439_x_at	*RPIP8*	4.33	2.95	2.91
214313_s_at	*EIF5B*	6.515	4.425	4.415
205731_s_at	*NCOA2*	6.29	4.34	4.2
201718_s_at	*EPB41L2*	8.21	5.47	5.67
233496_s_at	*CFL2*	9.425	6.525	6.275
210113_s_at	*NLRP1*	3.345	2.265	2.265
232331_at	*PPARG*	3.99	2.71	2.72
1560866_at	*WNK2*	3.405	2.325	2.315
205330_at	*MN1*	8.655	6.045	5.735
221960_s_at	*RAB2A*	8.405	5.735	5.715

229689_s_at	*DLG5*	10.635	7.055	7.425
217257_at	*NA*	4.485	3.115	3.005
236389_x_at	*OIT3*	3.935	2.655	2.725
209159_s_at	*NDRG4*	3.51	2.4	2.41
210814_at	*TRPC3*	4.375	3.025	2.965
1552885_a_at	*NKX6-3*	3.69	2.52	2.54
202812_at	*GAA*	4.895	3.295	3.425
214807_at	*NA*	6.58	4.54	4.5
213621_s_at	*GUK1*	6.58	4.62	4.42
204189_at	*RARG*	2.795	1.915	1.915
225768_at	*NR1D2*	12.56	8.79	8.49
206410_at	*NR0B2*	3.21	2.23	2.19
204994_at	*MX2*	3.07	2.11	2.11
234773_x_at	*NA*	3.66	2.53	2.5
1556322_a_at	*TJAP1*	3.795	2.565	2.655
229787_s_at	*NA*	11.375	7.875	7.785
227349_at	*HELLS*	4.085	2.795	2.825
213652_at	*PCSK5*	7.595	5.305	5.165
1552856_at	*TMEM148*	3.54	2.44	2.44
221890_at	*ZNF335*	3.705	2.595	2.525
231387_at	*C6orf145*	8.665	6.095	5.865
1567252_at	*OR10D3P*	4.25	2.94	2.93
205297_s_at	*CD79B*	3.865	2.705	2.625
243135_x_at	*NA*	4.66	3.24	3.2
213488_at	*SNED1*	7.695	5.345	5.285
217315_s_at	*KLK13*	3.05	2.11	2.11
32402_s_at	*SYMPK*	3.335	2.315	2.315
229636_at	*CACNA2D2*	3.295	2.275	2.275
212362_at	*ATP2A2*	3.65	2.53	2.53
1567540_at	*SPAG10*	3.765	2.625	2.595
209692_at	*EYA2*	3.54	2.46	2.46

1559808_at	*PLEC1*	3.53	2.45	2.45
208791_at	*CLU*	3.715	2.595	2.565
230576_at	*BLOC1S3*	4.65	3.2	3.26
1555181_a_at	*ST3GAL3*	3.125	2.165	2.175
203071_at	*SEMA3B*	3.88	2.71	2.69
202374_s_at	*RAB3GAP2*	9.565	6.795	6.525
1559667_at	*NA*	4.86	3.43	3.34
230156_x_at	*CHD2*	6.33	4.43	4.39
230940_at	*REXO1*	3.595	2.505	2.495
209307_at	*SWAP70*	13.49	9.29	9.49
1554106_at	*ALS2CR16*	8	5.64	5.51
1563431_x_at	*CALM3*	11.305	7.945	7.815
218881_s_at	*FOSL2*	3.31	2.31	2.3
229784_at	*MGC16121*	8.165	5.745	5.635
223517_at	*FBXO44*	4.655	3.245	3.255
201427_s_at	*SEPP1*	12.005	8.395	8.365
205559_s_at	*PCSK5*	5.805	4.035	4.065
206140_at	*LHX2*	3.425	2.395	2.385
204795_at	*PRR3*	3.685	2.565	2.575
216116_at	*NCKIPSD*	2.945	2.065	2.055
232811_x_at	*PRICKLE1*	4.935	3.495	3.415
237236_x_at	*LOC731789*	3.53	2.49	2.45
213560_at	*GADD45B*	5.435	3.825	3.775
1569274_at	*LOC283551*	3.46	2.43	2.41
1563357_at	*NA*	5.01	3.47	3.55
1563902_at	*SPSB1*	3.495	2.485	2.415
243120_at	*NA*	3.54	2.48	2.48
227488_at	*MGC16121*	2.94	2.06	2.06
236908_at	*ACPL2*	3.91	2.73	2.77
241797_at	*NFIX*	3.545	2.495	2.485
1552306_at	*ALG10*	4.18	2.91	2.97

242336_at	*NA*	8.005	5.645	5.635
204939_s_at	*PLN*	3.95	2.78	2.79
1554918_a_at	*ABCC4*	3.26	2.3	2.3
230879_at	*BAG2*	5.92	4.07	4.28
AFFX-BioB-3_	*NA*	11.775	8.455	8.165
228871_at	*ALG14*	3.07	2.14	2.2
1569949_at	*GRK5*	2.25	1.58	1.6
231508_s_at	*NA*	10.385	7.405	7.275
203968_s_at	*CDC6*	3.835	2.735	2.695
227533_at	*RALGPS2*	8.39	6.07	5.79
235723_at	*BNC2*	3.33	2.33	2.37
225934_at	*MRPL20*	7.725	5.535	5.385
242592_at	*GPR137C*	6.035	4.195	4.345
225309_at	*PHF5A*	7.11	5.11	4.95
218406_x_at	*NENF*	4.38	3.09	3.11
216269_s_at	*ELN*	3.505	2.495	2.475
1570249_x_at	*GNB1*	3.62	2.52	2.6
239093_at	*C10orf65*	2.705	1.925	1.925
AFFX-r2-Ec-b	*NA*	12.135	8.685	8.515
236479_at	*NA*	3.465	2.465	2.455
205684_s_at	*DENND4C*	9.165	6.595	6.415
242484_at	*TTC9B*	3.415	2.415	2.425
202446_s_at	*PLSCR1*	9.965	7.125	7.035
243575_at	*MAST4*	3.355	2.375	2.375
242022_at	*PBX1*	6.76	4.88	4.72
223079_s_at	*GLS*	13.09	9.35	9.27
231988_x_at	*ZNF490*	5.28	3.82	3.69
237632_at	*HERC1*	4.335	3.105	3.085
237439_at	*USP43*	4.835	3.535	3.375
1553328_a_at	*SLC18A2*	3.075	2.185	2.195
243365_s_at	*AUTS2*	4.345	3.055	3.155

1555953_at	*SLC19A1*	3.84	2.72	2.76
1553647_at	*CDYL2*	4.245	3.015	3.035
206438_x_at	*C12orf38*	8.535	6.225	5.995
236439_at	*BCL6*	7.035	4.935	5.145
1554476_x_at	*ZNF808*	4.61	3.25	3.36
223481_s_at	*MRPL47*	7.025	5.155	4.935
1553686_at	*C18orf25*	3.415	2.455	2.445
205636_at	*SH3GL3*	3.085	2.205	2.215
238964_at	*NA*	3.55	2.54	2.56
203289_s_at	*C16orf35*	5.36	3.93	3.76
1557052_at	*NA*	4.075	2.955	2.905
222434_at	*ENAH*	10.68	7.59	7.77
218264_at	*BCCIP*	8.385	5.905	6.175
240556_at	*DCN*	7.255	5.125	5.315
227821_at	*LGI4*	3.685	2.655	2.645
1559343_at	*SNRPN*	6.965	5.035	5.005
231193_s_at	*NA*	10.495	7.625	7.495
219180_s_at	*PEX26*	6.44	4.59	4.69
217159_x_at	*SIGLEC7*	3.49	2.48	2.55
216943_at	*NA*	3.03	2.19	2.18
237056_at	*INSC*	4.32	3.12	3.12
232214_x_at	*ZNF554*	3.54	2.52	2.6
215720_s_at	*NFYA*	4.015	2.895	2.895
211123_at	*SLC5A5*	3.575	2.545	2.615
1563512_at	*NOS1AP*	3.67	2.66	2.64
242367_at	*SLC38A1*	3.875	2.845	2.755
229090_at	*LOC220930*	3.785	2.765	2.715
223121_s_at	*SFRP2*	3.565	2.585	2.575
217370_x_at	*FUS*	4.315	3.075	3.165
1555888_at	*EDD1*	4.86	3.56	3.48
1558450_at	*A2M*	3	2.17	2.18

1553586_at	*LOC283932*	3.68	2.66	2.67
204658_at	*TRA2A*	10.3	7.36	7.56
1557357_at	*LOC440944*	3.84	2.78	2.78
241210_at	*MYO1D*	3.355	2.435	2.435
232600_at	*ANKRD42*	6.66	4.71	4.93
216246_at	*NA*	13.325	9.585	9.735
1552271_at	*MGC24975*	2.855	2.045	2.095
1565730_at	*NA*	3.105	2.245	2.255
215436_at	*HSDL2*	4.24	3.15	3.01
208421_at	*NA*	3.57	2.59	2.59
1558011_at	*SMA5*	4.1	3.01	2.95
204112_s_at	*HNMT*	9.525	7.035	6.805
231016_s_at	*ARNT*	10.53	7.64	7.67
207968_s_at	*MEF2C*	2.79	2.03	2.03
228193_s_at	*RGC32*	3.565	2.595	2.585
244144_at	*SYNE1*	3.975	2.885	2.895
214267_s_at	*CADM4*	3.18	2.32	2.31
1568764_x_at	*PDCD6*	4.93	3.57	3.61
241015_at	*NA*	3.39	2.48	2.46
210129_s_at	*TTLL3*	3.33	2.41	2.45
213951_s_at	*PSMC3IP*	9.865	7.075	7.295
1564463_at	*LOC283711*	3.69	2.67	2.71
228473_at	*MSX1*	6.93	5.03	5.07
244709_at	*NA*	3.065	2.235	2.225
236351_at	*LOC389023*	3.4	2.48	2.48
230482_at	*ST6GALNAC5*	3.345	2.455	2.425
222585_x_at	*KRCC1*	7.215	5.375	5.145
216183_at	*TGM2*	2.755	2.005	2.015
37577_at	*ARHGAP19*	5.165	3.845	3.695
213640_s_at	*LOX*	3.19	2.35	2.31
202648_at	*RPS19*	10.31	7.65	7.42

224348_s_at	*H19*	3.325	2.425	2.435
241700_at	*ZFHX4*	3.79	2.76	2.78
1562081_a_at	*NA*	4.115	3.005	3.015
225762_x_at	*LOC284801*	5.13	3.78	3.72
205140_at	*FPGT*	6.13	4.45	4.53
228232_s_at	*VSIG2*	2.95	2.16	2.15
229931_at	*REPIN1*	3.49	2.58	2.52
201540_at	*FHL1*	14.81	10.91	10.78
202972_s_at	*FAM13A1*	3.2	2.32	2.37
213006_at	*KIAA0146*	3.88	2.85	2.84
1559696_at	*NA*	3.695	2.715	2.705
223791_at	*FAM27A*	3.42	2.5	2.5
AFFX-r2-Ec-b	*NA*	12.37	9.27	8.87
236324_at	*MBP*	3.055	2.235	2.235
240773_at	*TRIO*	3.935	2.925	2.855
228161_at	*RAB32*	3.01	2.21	2.2
206707_x_at	*C6orf32*	6.92	5.18	4.98
224579_at	*SLC38A1*	11.525	8.435	8.495
1569330_at	*NA*	3.105	2.285	2.275
219740_at	*VASH2*	3.11	2.29	2.29
209750_at	*NR1D2*	11.605	8.475	8.605
201081_s_at	*PIP5K2B*	4.955	3.665	3.635
218325_s_at	*DIDO1*	5.255	3.815	3.925
1554229_at	*LOC153222*	3.205	2.375	2.345
210321_at	*GZMH*	3.135	2.315	2.315
220285_at	*C9orf77*	3.215	2.365	2.375
1570366_x_at	*ZNF564*	3.41	2.52	2.5
221470_s_at	*IL1F7*	3.42	2.52	2.52
1552980_at	*HAS3*	3.815	2.805	2.825
212517_at	*ATRN*	9.73	7.07	7.27
232145_at	*USP39*	3.88	2.86	2.86

209437_s_at	*SPON1*	3.125	2.305	2.305
225123_at	*NA*	7.81	5.67	5.86
207872_s_at	*LILRA1*	3.51	2.59	2.59
1555558_at	*USP25*	3.945	2.925	2.895
1569728_at	*NA*	3.57	2.66	2.61
238669_at	*PTGS1*	11.56	8.58	8.5
244691_at	*SETD5*	3.745	2.765	2.765
1552274_at	*PXK*	8.37	6.08	6.3
219142_at	*RASL11B*	8.66	6.32	6.48
219577_s_at	*ABCA7*	3.83	2.84	2.83
212389_at	*SBF1*	3.21	2.38	2.37
204251_s_at	*CEP164*	5.985	4.385	4.465
210921_at	*NA*	3.405	2.525	2.515
210733_at	*TRAM1*	12.56	9.16	9.43
242856_at	*NA*	8.46	6.19	6.33
AFFX-r2-Ec-b	*NA*	12.415	9.375	9.005
1562235_s_at	*PBX1*	3.45	2.56	2.54
220442_at	*GALNT4*	3.105	2.325	2.275
1562477_at	*EBF2*	3.465	2.575	2.565
204415_at	*IFI6*	5.16	3.77	3.88
206105_at	*AFF2*	2.85	2.13	2.09
219205_at	*SRR*	7.375	5.435	5.505
224987_at	*C6orf89*	3.48	2.58	2.58
225604_s_at	*C9orf19*	7.65	5.72	5.62
1559812_at	*NA*	2.95	2.2	2.18
217053_x_at	*ETV1*	3.19	2.36	2.37
1559450_at	*NAALADL2*	3.685	2.755	2.725
1555063_at	*USP6*	4.095	3.075	3.005
AFFX-BioC-5_	*NA*	12.6	9.56	9.16
241896_at	*MACF1*	3.215	2.385	2.395
1559237_a_at	*NA*	3.05	2.27	2.27

236772_s_at	*NA*	9.81	7.42	7.17
223895_s_at	*EPN3*	3.705	2.775	2.745
1559535_s_at	*NA*	4.69	3.51	3.47
232609_at	*CRB3*	3.99	2.96	2.98
241165_at	*DCAMKL1*	3.68	2.75	2.73
222968_at	*NA*	11.37	8.59	8.35
224022_x_at	*WNT16*	9.98	7.36	7.51
223453_s_at	*DKFZP564J0863*	3.39	2.52	2.53
205769_at	*SLC27A2*	3.685	2.785	2.705
216139_s_at	*MAPK8IP3*	3.405	2.545	2.545
238335_at	*DNAJA5*	4.06	3.02	3.03
205598_at	*TRAIP*	2.83	2.11	2.11
244285_at	*KIF6*	3.64	2.72	2.72
1554258_a_at	*DNAJC5B*	3.055	2.285	2.275
212915_at	*PDZRN3*	13.445	10.025	10.065
1553235_at	*PCDHAC1*	3.105	2.325	2.325
231411_at	*LHFP*	10.63	7.84	8.05
231642_at	*C6orf201*	3.385	2.535	2.525
227744_s_at	*HNRPD*	4.385	3.215	3.345
211696_x_at	*HBB*	2.865	2.145	2.145
230214_at	*MRVI1*	8.485	6.335	6.355
210037_s_at	*NOS2A*	2.845	2.135	2.125
209970_x_at	*CASP1*	3.135	2.345	2.355
223906_s_at	*TEX101*	3.435	2.575	2.575
218237_s_at	*SLC38A1*	11.55	8.82	8.48
223910_at	*ERN2*	4.575	3.495	3.375
201787_at	*FBLN1*	9.51	7.25	7.01
205352_at	*SERPINI1*	8.915	6.815	6.565
241990_at	*RHOV*	3.77	2.84	2.82
240677_at	*NA*	2.86	2.12	2.16
208269_s_at	*ADAM28*	2.97	2.23	2.23

217473_x_at	*SLC11A1*	3.235	2.435	2.425
240167_at	*LOC152742*	3.91	2.95	2.91
1559702_at	*NA*	3.505	2.635	2.625
1557712_x_at	*NA*	5.265	3.975	3.915
208228_s_at	*FGFR2*	4.075	3.055	3.065
223905_at	*CCDC135*	3.05	2.29	2.29
207215_at	*HS322B1A*	3.315	2.495	2.495
206543_at	*SMARCA2*	6.04	4.49	4.59
217481_x_at	*FLJ45455*	3.675	2.765	2.755
204229_at	*SLC17A7*	2.93	2.22	2.19
208185_x_at	*NA*	3.805	2.875	2.845
1557124_at	*LOC440104*	3.4	2.56	2.56
201694_s_at	*EGR1*	12.04	9	9.11
207788_s_at	*SORBS3*	3.56	2.72	2.64
229803_s_at	*NA*	10.03	7.54	7.56
220532_s_at	*TMEM176B*	3.295	2.485	2.475
226672_s_at	*HDAC10*	4.23	3.2	3.18
209897_s_at	*SLIT2*	8.145	6.215	6.065
208920_at	*SRI*	6.51	4.99	4.83
205813_s_at	*MAT1A*	3.82	2.88	2.88
241765_at	*CPM*	5.225	3.935	3.945
244152_at	*SCHIP1*	3.34	2.52	2.52
239619_at	*ZNF395*	3.34	2.56	2.48
203222_s_at	*TLE1*	6.03	4.63	4.48
201404_x_at	*PSMB2*	4.545	3.475	3.385
224023_s_at	*C3orf10*	10.29	7.83	7.72
244571_s_at	*TTC12*	3.965	2.995	3.005
221550_at	*COX15*	5.795	4.405	4.355
236742_at	*ARFGEF1*	4.095	3.125	3.065
244353_s_at	*SLC2A12*	3.68	2.79	2.77
221715_at	*MYST3*	6.755	5.145	5.075

237604_at	*CNTFR*	3.71	2.85	2.77
205168_at	*DDR2*	9.835	7.485	7.385
242685_at	*GTPBP8*	3.45	2.61	2.61
230428_at	*THEM5*	3.31	2.51	2.5
1559924_at	*SLC38A2*	4.11	3.12	3.1
1558530_at	*LRTM2*	3.24	2.46	2.45
206249_at	*MAP3K13*	3.47	2.66	2.6
1565554_at	*LOC127841*	3.825	2.915	2.885
1552713_a_at	*SLC4A1*	3.17	2.41	2.41
229109_s_at	*BLVRA*	3.04	2.3	2.31
228278_at	*NFIX*	10.515	8.035	7.915
219703_at	*MNS1*	4.27	3.22	3.25
216794_at	*NA*	3.17	2.42	2.4
238534_at	*LRRFIP1*	3.48	2.68	2.6
214768_x_at	*HLA-C*	3.095	2.355	2.345
239613_at	*TMED3*	5.345	4.065	4.055
1559950_at	*LOC729689*	4.615	3.495	3.505
223495_at	*CCDC8*	10.22	7.65	7.87
222556_at	*ALG5*	2.795	2.125	2.115
220963_s_at	*C1orf89*	3.07	2.33	2.33
235683_at	*SESN3*	3.985	3.015	3.035
234332_at	*NUB1*	4.84	3.65	3.71
1555065_x_at	*USP6*	3.815	2.905	2.885
233112_at	*C9orf150*	3.705	2.795	2.845
238704_at	*NA*	4.69	3.54	3.6
242840_at	*DAB1*	3.16	2.39	2.42
233891_at	*NA*	3.335	2.545	2.525
206416_at	*ZNF205*	6.89	5.3	5.19
236940_at	*NA*	3.075	2.335	2.335
201813_s_at	*TBC1D5*	7.41	5.63	5.66
230451_at	*C1orf136*	3.54	2.69	2.7

223400_s_at	*PB1*	8.675	6.585	6.635
205505_at	*GCNT1*	7.715	5.935	5.815
215295_at	*DTNB*	2.995	2.275	2.275
206229_x_at	*PAX2*	4.365	3.325	3.325
242371_x_at	*NFAT5*	3.7	2.82	2.82
214422_at	*RAD23B*	3.53	2.66	2.72
229562_at	*RPL10A*	3.355	2.565	2.545
216385_at	*LOC220077*	3.525	2.685	2.685
230130_at	*SLIT2*	14.005	10.605	10.765
220119_at	*EPB41L4A*	3.02	2.31	2.29
221611_s_at	*PHF7*	4.635	3.555	3.525
235790_at	*CTAGE5*	3.05	2.37	2.29
207289_at	*MMP25*	5.135	3.885	3.955
235858_at	*CREBBP*	3.455	2.635	2.635
1565162_s_at	*MGST1*	8.08	6.06	6.29
228467_at	*PURB*	2.98	2.27	2.28
239666_at	*PYGO2*	3.375	2.605	2.555
241083_at	*DBC1*	3.74	2.87	2.85
205779_at	*RAMP2*	3.08	2.36	2.36
1555664_at	*NA*	3.09	2.37	2.37
1552516_a_at	*HIPK1*	3.135	2.405	2.395
209769_s_at	*GP1BB*	3.49	2.67	2.67
210456_at	*PCYT1B*	3.805	2.945	2.895
220758_s_at	*ROBO4*	3.135	2.405	2.395
220682_s_at	*KLHL5*	5.91	4.5	4.56
1569793_at	*SLC25A18*	3.615	2.775	2.765
230534_at	*ZNF678*	3.845	2.945	2.945
1556787_s_at	*PDE5A*	3.51	2.71	2.68
236796_at	*BACH2*	3.025	2.325	2.325
231366_at	*KIAA1505*	3.035	2.335	2.335
242081_at	*CENTB1*	3.79	2.89	2.93

209223_at	*IK*	3.1	2.37	2.39
208590_x_at	*GJA3*	3	2.3	2.3
219695_at	*SMPD3*	3.2	2.46	2.46
222665_at	*FAM82B*	7.245	5.645	5.485
235343_at	*NA*	3.335	2.575	2.545
224140_at	*NPCDR1*	3.28	2.52	2.51
1555452_at	*RALGPS1*	3.69	2.81	2.86
211546_x_at	*SNCA*	4.57	3.56	3.46
203010_at	*STAT5A*	3.09	2.33	2.41
225979_at	*PLEKHG2*	3.11	2.39	2.39
237784_at	*SUB1*	3.145	2.415	2.425
229619_at	*FOLR2*	4.08	3.16	3.11
210436_at	*CCT8*	3.12	2.4	2.4
221801_x_at	*NEFL*	4.225	3.285	3.205
232495_x_at	*CUGBP1*	3.065	2.345	2.375
236371_s_at	*TGS1*	3.145	2.435	2.415
222784_at	*SMOC1*	3.015	2.355	2.285
238268_at	*NA*	3.67	2.83	2.83
215182_x_at	*MYH9*	4.505	3.505	3.425
228404_at	*IRX2*	3.825	2.925	2.965
238238_at	*NA*	3.085	2.405	2.365
220272_at	*BNC2*	3.725	2.865	2.875
242458_at	*RALGPS2*	4.725	3.665	3.615
1570303_at	*NA*	3.955	3.045	3.055
1558238_at	*KIAA1856*	3.295	2.545	2.525
224087_at	*NA*	3.335	2.595	2.545
219162_s_at	*MRPL11*	4.595	3.545	3.535
222057_at	*NOL12*	3.505	2.745	2.655
1564066_at	*C6orf137*	6.04	4.71	4.61
213946_s_at	*OBSL1*	3.05	2.36	2.34
207677_s_at	*NCF4*	3.395	2.615	2.615

239530_at	*NA*	3.41	2.64	2.62
229381_at	*C1orf64*	4.03	3.11	3.11
222440_s_at	*THRAP3*	9.515	7.235	7.445
1553565_s_at	*DDAH1*	3.225	2.485	2.485
1561078_at	*NA*	2.89	2.23	2.23
215125_s_at	*UGT1A1*	3.32	2.57	2.56
1552725_s_at	*ADAMTS17*	2.955	2.265	2.295
1561581_at	*NA*	4.13	3.21	3.17
229437_at	*BIC*	5.71	4.38	4.45
220244_at	*LOH3CR2A*	4.375	3.375	3.385
1553828_at	*FAM55A*	3.1	2.4	2.4
200869_at	*RPL18A*	9.97	7.8	7.62
214216_s_at	*LARP5*	3.195	2.465	2.485
220095_at	*C9orf39*	2.845	2.205	2.205
233267_at	*SELENBP1*	2.745	2.125	2.125
222176_at	*PTEN*	3.115	2.415	2.415
206542_s_at	*SMARCA2*	11.415	8.865	8.795
239071_at	*RBBP4*	6.19	4.78	4.79
1561433_at	*LOC285103*	3.945	3.015	3.085
224145_s_at	*SPTBN4*	3.685	2.885	2.815
238170_at	*CEP63*	3.585	2.765	2.775
228872_at	*C9orf77*	3.575	2.785	2.755
229831_at	*CNTN3*	11.79	9.12	9.13
228243_at	*PAXIP1*	3.36	2.61	2.59
219442_at	*C16orf67*	2.85	2.21	2.21
206450_at	*DBH*	3.065	2.365	2.375
229047_at	*PLEKHB1*	5.095	3.965	3.935
1556659_at	*NA*	3.58	2.78	2.77
203498_at	*DSCR1L1*	9.715	7.545	7.525
215517_at	*PYGO1*	3.195	2.475	2.475
211904_x_at	*RAD52*	3.105	2.405	2.405

1561502_x_at	*LOC348180*	3.975	3.125	3.035
210075_at	*2-Mar*	3.38	2.63	2.61
211654_x_at	*HLA-DQB1*	3.005	2.325	2.325
228310_at	*ENAH*	10.34	7.89	8.15
215066_at	*PTPRF*	3.365	2.605	2.615
214115_at	*VAMP5*	8.86	6.93	6.83
220057_at	*XAGE1*	2.915	2.265	2.255
228850_s_at	*SLIT2*	12.11	9.45	9.37
239125_at	*NA*	3.185	2.475	2.465
1561863_a_at	*CRY1*	3.67	2.87	2.83
222487_s_at	*RPS27L*	10.575	8.195	8.235
222962_s_at	*MCM10*	3.13	2.44	2.42
216391_s_at	*ATXN8OS*	2.78	2.16	2.16
221383_at	*NMUR1*	3.33	2.59	2.59
218808_at	*DALRD3*	4.68	3.7	3.58
216911_s_at	*HIC2*	3.095	2.425	2.395
203604_at	*ZNF516*	9.28	7.32	7.12
1554469_at	*ZBTB44*	3.95	3.07	3.07
234431_at	*NA*	4.115	3.205	3.195
202980_s_at	*SIAH1*	8.715	6.735	6.825
1553055_a_at	*SLFN5*	3.51	2.74	2.73
222936_s_at	*C1orf121*	3.275	2.565	2.535
1556757_a_at	*ALS2CR11*	3.675	2.865	2.845
1561795_at	*NA*	3.285	2.555	2.565
243716_at	*NA*	3.35	2.62	2.6
240530_at	*SLC25A16*	3.15	2.46	2.45
207300_s_at	*F7*	6.39	5.05	4.9
1566884_at	*C17orf84*	2.9	2.27	2.25
201698_s_at	*SFRS9*	12.95	10	10.17
1556962_at	*ONECUT3*	4.835	3.795	3.745
1557817_a_at	*NA*	6.275	4.845	4.945

203373_at	*SOCS2*	12.16	9.42	9.53
203973_s_at	*CEBPD*	7.62	5.96	5.92
243712_at	*XIST*	2.63	2.05	2.05
229827_at	*BUB3*	3.54	2.76	2.76
216018_at	*RNF5*	2.675	2.105	2.075
240071_at	*NA*	2.93	2.28	2.29
201621_at	*NBL1*	10.285	7.955	8.085
1563283_at	*NA*	5.21	4.07	4.06
1553464_at	*FLJ40288*	3.57	2.83	2.75
211159_s_at	*PPP2R5D*	3.37	2.59	2.67
243425_at	*COX4NB*	3.305	2.595	2.575
242609_x_at	*ADCK4*	3.395	2.655	2.655
210924_at	*OLFM1*	3.16	2.47	2.45
231197_at	*PPP1R3F*	3.29	2.57	2.57
219618_at	*IRAK4*	5.3	4.07	4.21
220604_x_at	*FTCD*	4.72	3.66	3.7
213879_at	*NA*	13.51	10.64	10.46
206788_s_at	*CBFB*	7.315	5.755	5.665
230413_s_at	*AP1S2*	12.895	10.005	10.135
236611_at	*ZNF232*	4.135	3.195	3.275
231640_at	*LYRM5*	3.095	2.415	2.415
208867_s_at	*CSNK1A1*	8.155	6.335	6.405
214398_s_at	*IKBKE*	2.73	2.13	2.13
217413_s_at	*TNXB*	2.905	2.265	2.265
227236_at	*TSPAN2*	9.195	7.205	7.175
234110_at	*LOC283075*	3.505	2.755	2.725
222419_x_at	*UBE2H*	3.065	2.415	2.385
233545_at	*INPP5D*	3.41	2.67	2.66
217903_at	*STRN4*	3.13	2.44	2.45
203750_s_at	*RARA*	4.63	3.65	3.6
241470_x_at	*NA*	3.94	3.09	3.07

205597_at	*SLC44A4*	3.19	2.49	2.49
1553858_at	*ZBTB3*	6.925	5.485	5.365
1564603_at	*NUT*	2.755	2.155	2.155
240890_at	*CASP4*	3.925	3.075	3.065
241608_at	*SNTB2*	3.435	2.695	2.695
214101_s_at	*LOC728896*	11.45	9.04	8.89
202976_s_at	*RHOBTB3*	10.22	7.93	8.07
222942_s_at	*TIAM2*	6.16	4.84	4.8
223783_s_at	*GEMIN4*	3.215	2.525	2.515
1563961_at	*FHAD1*	3.155	2.475	2.465
210799_at	*HTR1B*	3.075	2.415	2.415
239535_at	*POMT2*	2.9	2.28	2.28
234958_at	*PPFIBP2*	3.45	2.71	2.71
207916_at	*RBM*	3.26	2.57	2.55
213722_at	*SOX2*	2.815	2.215	2.215
206582_s_at	*GPR56*	3.08	2.41	2.42
223477_s_at	*FLJ38663*	5.3	4.1	4.22
214435_x_at	*RALA*	12.705	10.045	9.885
220491_at	*HAMP*	6.11	4.83	4.76
237506_at	*TMEM177*	3.135	2.445	2.475
1561497_at	*NA*	3.565	2.815	2.795
233592_at	*ANKRD18B*	3.015	2.375	2.365
232642_at	*LOC90113*	3.37	2.66	2.64
229029_at	*NA*	2.89	2.25	2.29
235387_at	*GSTCD*	5.355	4.225	4.195
243709_at	*FLJ90709*	3.015	2.365	2.375
1556269_at	*MYT1*	3.58	2.86	2.77
242629_at	*RAB3B*	8.965	7.125	6.975
228803_at	*ORMDL1*	3.2	2.53	2.51
225564_at	*SPATA13*	10.3	8.07	8.14
213087_s_at	*EEF1D*	8.64	6.7	6.9

206759_at	*FCER2*	2.885	2.295	2.235
239980_at	*C22orf28*	3.465	2.735	2.715
239712_at	*C9orf93*	3.425	2.705	2.695
224313_at	*AASDHPPT*	2.785	2.185	2.185
1555713_at	*PNKD*	2.995	2.355	2.355
1562029_at	*NA*	3.14	2.48	2.48
241795_at	*RHEB*	5.485	4.335	4.315
201605_x_at	*CNN2*	9.035	7.105	7.135
218768_at	*NUP107*	10.85	8.56	8.54
212044_s_at	*RPL27A*	15.12	11.87	11.96
223577_x_at	*MALAT1*	13.15	10.3	10.44
231081_at	*FLJ40298*	3.2	2.54	2.5
202881_x_at	*NOL7*	3.02	2.39	2.38
234225_at	*NA*	3.41	2.68	2.7
214953_s_at	*APP*	12.42	9.74	9.86
240849_at	*FZR1*	4.785	3.745	3.815
234855_at	*ORF1*	3.92	3.14	3.05
236379_at	*EPB41*	3.105	2.445	2.455
33736_at	*STOML1*	8.375	6.695	6.535
1560131_at	*NA*	2.825	2.235	2.225
230170_at	*OSM*	3.145	2.485	2.485
207138_at	*PHF2*	3.53	2.79	2.79
202022_at	*ALDOC*	5.435	4.235	4.345
207569_at	*ROS1*	3.455	2.735	2.725
241445_at	*TMEM87B*	4.795	3.785	3.795
212257_s_at	*SMARCA2*	2.785	2.195	2.205
229242_at	*NA*	2.67	2.11	2.11
224977_at	*C6orf89*	9.835	7.765	7.775
219632_s_at	*TRPV1*	2.895	2.295	2.295
223493_at	*FBXO4*	7.15	5.6	5.7
201406_at	*RPL36A*	11.225	8.925	8.815

222022_at	*DTX3*	3.195	2.535	2.525
233278_at	*M-RIP*	3.095	2.445	2.455
240840_s_at	*C5orf35*	3.315	2.625	2.615
237713_at	*TACC2*	3.24	2.56	2.57
223541_at	*HAS3*	3.235	2.545	2.565
227298_at	*FLJ37798*	8.02	6.32	6.36
206590_x_at	*DRD2*	2.595	2.055	2.055
201867_s_at	*TBL1X*	5.975	4.685	4.785
237790_at	*FLJ33996*	3.27	2.58	2.6
223726_at	*KCNH3*	3.18	2.52	2.52
238297_at	*PHACTR1*	3.965	3.175	3.105
1555437_at	*EARS2*	3.83	3.03	3.03
221463_at	*CCL24*	2.935	2.325	2.315
235966_at	*DAB2IP*	5.48	4.33	4.35
238918_at	*NA*	2.845	2.245	2.245
226880_at	*NUCKS1*	14.68	11.59	11.66
224800_at	*WDFY1*	11.535	9.055	9.215
219271_at	*GALNT14*	2.8	2.22	2.22
37005_at	*NBL1*	11.85	9.41	9.36
228399_at	*OSR1*	3.385	2.665	2.705
1552491_at	*IDI2*	3.045	2.405	2.415
238816_at	*NA*	3.38	2.68	2.68
1565843_s_at	*BRPF3*	3.405	2.705	2.695
220519_s_at	*LIM2*	2.8	2.22	2.22
240494_at	*CTDSPL*	3.355	2.685	2.635
236643_s_at	*LOC645321*	4.025	3.225	3.155
233941_at	*C14orf166B*	3.205	2.545	2.545
1565823_at	*7-Sep*	11.205	9.005	8.775
203485_at	*RTN1*	3.445	2.725	2.735
210300_at	*REM1*	4.325	3.405	3.455
214072_x_at	*NENF*	5.79	4.6	4.59

1553713_a_at	*RHEBL1*	4.855	3.885	3.815
237310_at	*EXT1*	7.125	5.655	5.645
229648_at	*NA*	6.725	5.405	5.285
220725_x_at	*DNAH3*	5.955	4.765	4.695
244643_at	*NA*	2.75	2.19	2.19
1556014_at	*MESP2*	2.845	2.265	2.255
242636_at	*GCRG224*	2.94	2.34	2.34
244045_at	*NA*	3.37	2.68	2.67
244865_at	*HAX1*	3.88	3.06	3.11
218361_at	*GOLPH3L*	8.69	6.98	6.84
229621_x_at	*EBF3*	3.79	3.02	3.01
1566830_at	*LOC283104*	2.595	2.055	2.055
242239_at	*NSUN6*	7.235	5.775	5.725
222036_s_at	*MCM4*	8.97	7.13	7.13
224467_s_at	*PDCD2L*	3.25	2.59	2.58
235433_at	*APOOL*	9.455	7.425	7.615
1554743_x_at	*PMS1*	2.955	2.335	2.375
206125_s_at	*KLK8*	3.14	2.52	2.47
234654_at	*C20orf4*	3.62	2.88	2.88
233454_at	*C4orf15*	4.295	3.425	3.405
239674_at	*ARID1B*	3.375	2.725	2.655
228188_at	*FOSL2*	10.77	8.58	8.57
217406_at	*NA*	3.685	2.945	2.915
211650_x_at	*IL8*	2.755	2.195	2.195
227552_at	*1-Sep*	3.115	2.495	2.455
206800_at	*MTHFR*	3.16	2.52	2.52
206216_at	*SRPK3*	3.135	2.505	2.485
201766_at	*ELAC2*	5.1	4.02	4.1
205757_at	*ENTPD5*	3.34	2.66	2.66
229401_at	*IL17RE*	3.44	2.75	2.73
228594_at	*C5orf33*	10.42	8.18	8.42

236030_at	*RCOR2*	3.185	2.545	2.535
232754_at	*CENPQ*	3.515	2.815	2.785
231720_s_at	*JAM3*	2.685	2.145	2.135
216103_at	*ACOT11*	4.105	3.305	3.235
217462_at	*C11orf9*	3.765	3.025	2.985
244729_at	*NA*	3.515	2.815	2.785
1554895_a_at	*RHBDL2*	3.18	2.55	2.53
222328_x_at	*MEG3*	3.03	2.39	2.43
1563108_at	*LRRC62*	3.225	2.575	2.565
217579_x_at	*ARL6IP2*	4.65	3.69	3.73
219038_at	*MORC4*	9.4	7.49	7.51
213409_s_at	*RHEB*	7.595	5.975	6.145
217541_x_at	*ZNF816A*	3.545	2.855	2.795
205616_at	*NA*	3.345	2.685	2.655
208770_s_at	*EIF4EBP2*	9.51	7.48	7.7
241181_x_at	*NA*	5.015	4.025	3.975
227797_x_at	*LYRM2*	5.25	4.18	4.2
234344_at	*RAP2C*	5.05	4.03	4.04
239965_at	*MAGI1*	3.665	2.895	2.965
221373_x_at	*PSPN*	2.9	2.32	2.32
216679_at	*NA*	3.17	2.53	2.53
215402_at	*APPBP2*	3.68	2.94	2.94
205028_at	*TRO*	4.48	3.58	3.58
213789_at	*TBC1D25*	10.35	8.23	8.31
215281_x_at	*POGZ*	4.68	3.77	3.71
243078_at	*NA*	2.99	2.39	2.39
1553359_at	*FBXL18*	2.71	2.15	2.18
222374_at	*BTRC*	3.305	2.645	2.645
210431_at	*ALPPL2*	2.825	2.265	2.255
216417_x_at	*HOXB9*	3.725	2.975	2.985
215799_at	*NA*	2.89	2.31	2.31

1563549_a_at	*TMEM16H*	3.51	2.83	2.79
214091_s_at	*GPX3*	3.58	2.9	2.82
207101_at	*VAMP1*	3.69	2.95	2.95
223663_at	*CCDC88*	2.365	1.885	1.885
1554705_at	*SCARA5*	3.42	2.74	2.74
229329_s_at	*SSU72*	8.675	6.945	6.935
1557174_a_at	*IRAK1BP1*	4.02	3.22	3.22
1561181_at	*ARID5B*	2.825	2.235	2.295
242495_at	*SERF1A*	3.92	3.17	3.11
1555158_at	*NA*	2.705	2.165	2.165
1560800_at	*NA*	3.765	3.045	2.995
217248_s_at	*SLC7A8*	2.675	2.135	2.145
214549_x_at	*SPRR1A*	4.33	3.47	3.47
236042_at	*RAD52*	3.175	2.555	2.525
224445_s_at	*ZFYVE21*	11.005	8.905	8.735
214821_at	*SLC25A4*	2.73	2.19	2.19
1553582_a_at	*SPAG11*	3.52	2.84	2.81
203484_at	*SEC61G*	13.535	10.825	10.885
1555923_a_at	*C10orf114*	3.63	2.94	2.88
230666_at	*HOXA11S*	3.765	3.015	3.035
201442_s_at	*ATP6AP2*	2.92	2.34	2.35
1557755_at	*C14orf145*	3.605	2.895	2.885
202975_s_at	*RHOBTB3*	9.1	7.39	7.21
233747_at	*NA*	3.21	2.59	2.56
239933_x_at	*C14orf45*	3.315	2.655	2.655
231534_at	*CDC2*	3.02	2.43	2.41
226374_at	*CXADR*	3.15	2.53	2.53
1559467_at	*MTHFS*	5.88	4.77	4.67
229094_at	*LOC401431*	2.93	2.35	2.35
225796_at	*PXK*	10.77	8.72	8.57
1554212_s_at	*KCNS2*	7.375	5.975	5.855

231400_s_at	*NA*	2.655	2.135	2.135
219004_s_at	*C21orf45*	7.31	5.85	5.89
1557303_at	*NT5C*	2.675	2.145	2.155
215378_at	*SRA1*	4.06	3.27	3.25
230564_at	*SIPA1L3*	2.505	2.005	2.005
1563341_at	*KIF3A*	3.47	2.79	2.79
211366_x_at	*CASP1*	2.915	2.345	2.335
217904_s_at	*BACE1*	10.765	8.565	8.735
205194_at	*PSPH*	8.525	6.755	6.945
216537_s_at	*SIGLEC7*	3.085	2.485	2.475
1564257_at	*STAMBPL1*	5.165	4.175	4.125
229120_s_at	*CDC42SE1*	11.63	9.23	9.47
1559766_at	*NA*	2.795	2.255	2.245
1559534_at	*NA*	4.32	3.52	3.44
1567068_at	*OR4D1*	3.38	2.73	2.71
243029_at	*KREMEN1*	3.595	2.905	2.875
236571_at	*SLC2A3*	3.58	2.88	2.88
240584_at	*SHANK2*	3.165	2.545	2.545
238636_at	*NA*	4.84	3.9	3.9
205506_at	*VIL1*	3.095	2.495	2.485
238405_at	*GAB2*	3.88	3.15	3.1
233064_at	*LOC388494*	3.265	2.625	2.625
1554662_at	*C17orf47*	2.78	2.24	2.24
204984_at	*GPC4*	12.35	9.93	9.97
1562271_x_at	*ARHGEF7*	3.945	3.205	3.155
1557066_at	*LUC7L*	4.595	3.705	3.695
219990_at	*E2F8*	3.445	2.795	2.765
242485_at	*PTK2*	3.8	3.08	3.05
228197_at	*C1orf86*	2.86	2.3	2.3
237851_at	*NIBP*	3.83	3.13	3.05
238858_at	*TIFA*	2.79	2.25	2.25

211579_at	*ITGB3*	4.66	3.78	3.74
242368_at	*GTF2I*	3.235	2.595	2.625
232820_s_at	*FAM112A*	4.505	3.685	3.575
213479_at	*NPTX2*	3.23	2.61	2.6
1564444_at	*SLC24A3*	3.4	2.75	2.73
203166_at	*CFDP1*	10.095	8.235	8.045
217683_at	*HBG2*	2.935	2.365	2.375
215582_x_at	*MCM3AP*	6.145	4.905	5.015
230313_at	*TK2*	11.135	9.125	8.865
1555784_s_at	*IRAK1*	2.835	2.305	2.285
205500_at	*C5*	4.905	3.995	3.935
1569230_at	*TATDN1*	3.43	2.8	2.74
207151_at	*ADCYAP1R1*	3.44	2.77	2.79
216464_x_at	*GPR44*	2.71	2.19	2.19
217258_x_at	*IVD*	3.455	2.795	2.795
218221_at	*ARNT*	9.07	7.25	7.41
244394_at	*BLK*	2.8	2.26	2.26
1566256_s_at	*GPR180*	3.34	2.7	2.7
235875_at	*SLC1A4*	3.525	2.845	2.845
1553878_at	*GOT1L1*	3.57	2.89	2.88
243553_x_at	*LOC643749*	3.31	2.71	2.63
243766_s_at	*TEAD2*	4.335	3.505	3.495
207369_at	*NA*	3.135	2.535	2.535
236947_at	*SEMA3C*	3.155	2.565	2.535
234199_at	*SLC24A3*	2.62	2.12	2.12
229547_s_at	*WNK2*	4.325	3.525	3.475
228884_at	*LRRC27*	3.335	2.705	2.685
1569461_at	*KCNT1*	4.01	3.28	3.21
242668_x_at	*SPAG4L*	2.905	2.355	2.345
208454_s_at	*PGCP*	7.775	6.265	6.315
241114_s_at	*NA*	6.09	4.98	4.88

217432_s_at	*IDS*	3.03	2.46	2.44
216081_at	*LAMA4*	3.245	2.635	2.615
1555756_a_at	*CLEC7A*	3.28	2.66	2.65
243101_x_at	*C20orf160*	3.425	2.765	2.765
1558142_at	*TNRC6B*	11.77	9.52	9.54
243459_x_at	*PFTK1*	7.105	5.695	5.795
236338_at	*IRS2*	4.485	3.625	3.625
231950_at	*ZNF658*	3.605	2.925	2.915
208425_s_at	*TANC2*	3.55	2.88	2.87
220521_s_at	*ATG16L1*	3.49	2.8	2.85
208108_s_at	*AVPR2*	2.63	2.13	2.13
206618_at	*IL18R1*	3.03	2.47	2.43
240606_at	*ACACA*	3.76	3.06	3.02
1554004_a_at	*RGNEF*	3.175	2.575	2.565
1556111_s_at	*NA*	4.12	3.35	3.33
238663_x_at	*GRIA4*	3.33	2.7	2.68
239116_at	*ANKRD10*	3.325	2.695	2.685
215733_x_at	*CTAG2*	2.42	1.96	1.96
216254_at	*PARVB*	3.765	3.065	3.035
202938_x_at	*CTA-126B4.3*	2.72	2.2	2.2
1559611_at	*TMEM75*	2.95	2.39	2.39
202028_s_at	*RPL38*	14.575	11.855	11.775
1564905_at	*NA*	3.3	2.7	2.66
229304_s_at	*MLF1IP*	3.05	2.46	2.48
205011_at	*LOH11CR2A*	2.73	2.21	2.21
229465_s_at	*PTPRS*	11.73	9.47	9.54
235144_at	*NA*	4.03	3.26	3.27
212953_x_at	*CALR*	8.185	6.595	6.665
1552671_a_at	*SLC9A7*	3.49	2.83	2.83
1557129_a_at	*FAM111B*	3.99	3.26	3.21
214523_at	*CEBPE*	3.8	3.12	3.04

215153_at	*NOS1AP*	3.135	2.545	2.535
227225_at	*ZNF503*	4.305	3.485	3.485
228182_at	*ADCY5*	2.65	2.15	2.15
1563009_at	*LOC284930*	2.96	2.41	2.4
234117_at	*AAA1*	3.29	2.68	2.66
209184_s_at	*IRS2*	9.795	7.865	8.045
244548_at	*ARHGAP26*	3.265	2.645	2.645
210673_x_at	*TITF1*	4.68	3.8	3.79
239943_x_at	*PIGL*	3.83	3.12	3.1
222882_s_at	*C17orf59*	2.915	2.385	2.355
1562428_at	*LOC654780*	4.375	3.535	3.565
208321_s_at	*CABP1*	3	2.44	2.43
231278_at	*NA*	3.445	2.825	2.775
1560443_at	*SMCHD1*	4.175	3.385	3.395
215089_s_at	*RBM10*	8.5	6.97	6.83
224182_x_at	*SEMA6B*	2.76	2.24	2.24
1556494_at	*NA*	3.455	2.805	2.815
214773_x_at	*TIPRL*	10.35	8.32	8.5
214662_at	*WDR43*	9.245	7.405	7.605
213176_s_at	*LTBP4*	4.445	3.605	3.605
210073_at	*ST8SIA1*	3.815	3.135	3.065
1552646_at	*IL11RA*	3.495	2.855	2.825
228405_at	*RHPN1*	5.14	4.18	4.17
235941_s_at	*LOC401629*	3.195	2.595	2.595
212414_s_at	*6-Sep*	10.625	8.655	8.605
1556606_at	*NAV2*	2.68	2.18	2.17
205481_at	*ADORA1*	3.19	2.59	2.59
219076_s_at	*PXMP2*	7.89	6.5	6.33
208199_s_at	*ZFP161*	3.63	2.96	2.94
211577_s_at	*IGF1*	3.19	2.6	2.58
224965_at	*GNG2*	3.52	2.86	2.86

227681_at	*ZFP36L2*	3.135	2.555	2.555
224509_s_at	*RTN4IP1*	6.665	5.475	5.365
240508_at	*LOC400927*	2.635	2.135	2.135
209819_at	*HABP4*	3.475	2.865	2.795
223411_at	*MIF4GD*	7.39	5.95	6.07
244149_at	*MYL9*	2.715	2.205	2.215
238124_at	*MYOM3*	3.65	3.01	2.93
203811_s_at	*DNAJB4*	6.41	5.14	5.28
207303_at	*PDE1C*	2.865	2.325	2.335
1560296_at	*DST*	5.025	4.105	4.065
229837_s_at	*KCTD5*	2.865	2.335	2.325
213390_at	*C19orf7*	11.82	9.62	9.62
210228_at	*CSF2*	3.78	3.08	3.08
216866_s_at	*COL14A1*	2.84	2.32	2.31
220574_at	*SEMA6D*	2.9	2.38	2.34
219201_s_at	*TWSG1*	9.77	8.02	7.89
213302_at	*PFAS*	7.03	5.7	5.76
204808_s_at	*TMEM5*	10.8	8.81	8.79
241871_at	*CAMK4*	3.645	2.965	2.965
220410_s_at	*CAMSAP1*	3.02	2.46	2.46
234867_at	*NA*	3.275	2.675	2.665
216936_at	*NA*	3.165	2.595	2.575
240344_x_at	*LYRM7*	9.92	8.12	8.05
242185_at	*SFRS12*	2.995	2.445	2.435
214456_x_at	*SAA2*	3.305	2.685	2.695
208070_s_at	*REV3L*	11.46	9.32	9.36
206362_x_at	*MAP3K10*	4.2	3.43	3.41
234729_at	*SUMF2*	3.02	2.46	2.46
1557564_at	*ALKBH3*	3.185	2.605	2.595
208047_s_at	*NAB1*	4.155	3.345	3.435
1569891_at	*ATP5A1*	3.095	2.525	2.515

238173_at	*TCEA2*	2.93	2.39	2.39
231838_at	*C20orf119*	3.655	2.975	2.975
220684_at	*TBX21*	2.885	2.355	2.345
1560062_at	*SLC29A2*	3.225	2.645	2.605
225333_at	*ZNF496*	2.75	2.25	2.24
237913_at	*NA*	3.945	3.215	3.225
205275_at	*GTPBP1*	3.715	3.045	3.025
215077_at	*COL3A1*	3.335	2.745	2.695
216563_at	*ANKRD12*	8.24	6.79	6.65
1552325_at	*CCDC11*	4.31	3.56	3.47
242036_x_at	*ATP2B3*	3.35	2.76	2.7
217454_at	*LOC203510*	3.815	3.135	3.095
224538_s_at	*PARD6G*	3.135	2.545	2.565
241177_at	*NA*	3.605	2.945	2.945
225686_at	*FAM33A*	8.895	7.325	7.195
1558942_at	*ZNF813*	9.645	7.975	7.765
1556304_s_at	*NA*	3.6	2.95	2.93
223311_s_at	*MTA3*	6.405	5.265	5.195
1555902_at	*ARMCX5*	2.72	2.22	2.22
1568964_x_at	*SPN*	4.9	4.02	3.98
1563300_at	*LOC387826*	2.71	2.21	2.22
222462_s_at	*BACE1*	10.37	8.37	8.57
1562314_at	*NCOA1*	3.57	2.94	2.89
1554014_at	*CHD2*	6.97	5.7	5.69
1564438_at	*LOC729436*	3.415	2.795	2.795
203428_s_at	*ASF1A*	7.805	6.425	6.335
221071_at	*NA*	3.235	2.655	2.625
208167_s_at	*MMP16*	3.465	2.825	2.835
240350_at	*NA*	3.535	2.905	2.885
1559083_x_at	*LOC284600*	3.215	2.645	2.615
218379_at	*RBM7*	11.28	9.19	9.25

243849_at	*TMEM37*	5.07	4.15	4.14
207582_at	*PIN1L*	3.005	2.465	2.455
223425_at	*RAVER1*	2.94	2.4	2.41
244824_at	*NA*	3.18	2.61	2.59
221709_s_at	*C14orf131*	6.745	5.545	5.475
1567623_at	*ABLIM2*	2.865	2.345	2.345
201308_s_at	*11-Sep*	10.155	8.215	8.385
1568702_a_at	*WDR71*	3.19	2.6	2.61
1566896_at	*UNQ1887*	3.225	2.645	2.635
236504_x_at	*C6orf52*	3.315	2.725	2.705
1569857_s_at	*TPP2*	3.815	3.135	3.095
242658_at	*RAB11FIP3*	3.74	3.02	3.1
236222_at	*C3orf15*	2.86	2.35	2.33
234025_at	*NA*	2.86	2.34	2.34
1554967_at	*DIP2A*	2.72	2.22	2.23
34846_at	*CAMK2B*	2.66	2.18	2.17
222731_at	*ZDHHC2*	11.09	9.02	9.13
1558875_at	*SREBF1*	3.21	2.63	2.62
205754_at	*F2*	2.665	2.185	2.185
1566670_at	*C21orf124*	3.135	2.565	2.575
244858_at	*TGIF1*	3.07	2.52	2.51
1552887_at	*C10orf27*	3.445	2.835	2.805
221662_s_at	*SLC22A7*	3.125	2.555	2.565
220892_s_at	*PSAT1*	3.72	3.03	3.05
236720_at	*NA*	2.965	2.435	2.425
242740_at	*NA*	3.61	2.95	2.96
215746_at	*NOL14*	3.155	2.585	2.575
225684_at	*FAM33A*	12.49	10.34	10.11
212650_at	*EHBP1*	7.675	6.285	6.295
234464_s_at	*EME1*	9.155	7.545	7.455
202425_x_at	*PPP3CA*	11.005	9.085	8.955

244229_at	*PARVG*	3.21	2.64	2.62
1569341_at	*POLH*	4.1	3.37	3.35
243951_at	*ABCB1*	3.79	3.13	3.09
231710_at	*CAPS*	3.08	2.51	2.53
221408_x_at	*PCDHB12*	3.85	3.15	3.15
228203_at	*B3GNT1*	3.19	2.64	2.59
1553726_s_at	*C6orf170*	3.715	3.035	3.065
201137_s_at	*HLA-DPB1*	5.865	4.815	4.805
239718_at	*NA*	2.59	2.13	2.13
244495_x_at	*C18orf45*	7.81	6.32	6.49
1555196_at	*NA*	2.775	2.275	2.275
240591_at	*KCNIP4*	3.045	2.495	2.505
204248_at	*GNA11*	6.8	5.61	5.55
242180_at	*TSPAN16*	3.965	3.255	3.245
243161_x_at	*ZFP42*	3.34	2.75	2.73
212884_x_at	*TOMM40*	7.335	6.085	5.945
235406_x_at	*NA*	6.36	5.16	5.27
224153_s_at	*NA*	3.87	3.17	3.18
241038_at	*CHRM3*	3.165	2.605	2.595
1559406_at	*ANKRD18A*	2.945	2.425	2.415
229303_at	*NA*	9.61	7.94	7.84
239596_at	*SLC30A7*	6.735	5.535	5.525
230618_s_at	*NA*	13.56	11.01	11.27
202438_x_at	*IDS*	9.97	8.2	8.18
221681_s_at	*DSPP*	6.655	5.525	5.425
220459_at	*MCM3APAS*	3.46	2.85	2.83
239855_at	*PPM1L*	2.665	2.185	2.185
223580_at	*SPSB2*	5.03	4.15	4.11
239878_at	*IPMK*	3.885	3.205	3.175
238439_at	*ANKRD22*	2.755	2.265	2.255
1561531_at	*NA*	2.485	2.025	2.065

227877_at	*AXIIR*	2.895	2.365	2.385
231277_x_at	*DTWD2*	3.735	3.085	3.055
223578_x_at	*PRO1073*	9.895	8.225	8.045
241965_at	*LARP5*	3.075	2.535	2.525
215172_at	*PTPN20B*	3.285	2.705	2.695
220433_at	*PRRG3*	2.705	2.225	2.215
1552319_a_at	*KLK8*	4.275	3.525	3.505
1557275_a_at	*NA*	7.53	6.18	6.21
221925_s_at	*CSPP1*	3.755	3.115	3.065
1554953_a_at	*C21orf90*	3.165	2.595	2.615
208009_s_at	*ARHGEF16*	2.85	2.36	2.34
215646_s_at	*VCAN*	10.855	8.955	8.905
91682_at	*EXOSC4*	3.26	2.69	2.68
217316_at	*OR7A10*	3.62	2.98	2.98
220039_s_at	*CDKAL1*	3.125	2.575	2.565
214637_at	*OSM*	3.05	2.5	2.52
220443_s_at	*VAX2*	4.78	3.98	3.89
217061_s_at	*ETV1*	5.11	4.22	4.19
206148_at	*IL3RA*	2.86	2.39	2.33
215465_at	*ABCA12*	2.985	2.465	2.455
220780_at	*PLA2G3*	2.95	2.43	2.43
213633_at	*SH3BP1*	2.72	2.26	2.22
237555_at	*ING1*	3.85	3.17	3.17
238706_at	*PAPD4*	3.505	2.875	2.895
228731_at	*NA*	3.04	2.51	2.5
228625_at	*CITED4*	2.935	2.415	2.415
236297_at	*NA*	3.115	2.585	2.555
205277_at	*PRDM2*	5.145	4.205	4.275
239773_at	*GTPBP10*	3.19	2.63	2.63
223564_s_at	*GNB1L*	2.72	2.24	2.24
240243_at	*FGF2*	3.125	2.585	2.575

210686_x_at	*SLC25A16*	7.615	6.195	6.355
215705_at	*PPP5C*	3.545	2.925	2.925
215369_at	*LOC90120*	3.235	2.685	2.655
219955_at	*L1TD1*	3.06	2.54	2.5
243749_s_at	*NA*	3.155	2.625	2.575
1558167_a_at	*MGC16275*	3.54	2.94	2.9
222600_s_at	*UBE1L2*	10.14	8.38	8.34
209480_at	*HLA-DQB1*	3.525	2.905	2.905
232519_at	*NSFL1C*	2.61	2.15	2.15
233823_at	*KIAA1276*	3.005	2.485	2.475
238078_at	*SEC22A*	8.035	6.635	6.625
1566887_x_at	*NA*	9.725	7.945	8.095
216474_x_at	*TPSAB1*	2.585	2.125	2.125
204969_s_at	*RDX*	8.885	7.415	7.245
237761_at	*NEK6*	2.94	2.43	2.42
232589_at	*NA*	3.31	2.72	2.75
223979_x_at	*FTCD*	4.155	3.435	3.425
207635_s_at	*KCNH1*	2.875	2.375	2.375
1557961_s_at	*LOC642730*	9.73	8.07	7.99
212443_at	*NBEAL2*	2.65	2.19	2.19
243440_at	*NA*	3.02	2.52	2.47
1558770_a_at	*C17orf38*	2.66	2.2	2.2
232957_x_at	*NA*	3.985	3.315	3.265
219372_at	*IFT81*	9.645	7.955	7.975
1553710_at	*FLJ31659*	3.395	2.815	2.775
202971_s_at	*DYRK2*	11.47	9.49	9.45
1556925_at	*SMC3*	3.69	3.07	3.03
232470_at	*SNF1LK*	2.75	2.27	2.27
241951_at	*NA*	3.545	2.945	2.905
241647_x_at	*NA*	3.82	3.18	3.13
208189_s_at	*MYO7A*	2.545	2.125	2.085

241245_at	*SFRS4*	3.61	2.99	2.98
218778_x_at	*EPS8L1*	4.015	3.345	3.295
222938_x_at	*ENPP3*	2.605	2.155	2.145
229700_at	*ZNF738*	9.715	7.995	8.075
216112_at	*PKN2*	4.35	3.61	3.58
221723_s_at	*SLC4A5*	2.775	2.285	2.305
223327_x_at	*FLJ22795*	6.095	5.065	5.005
242916_at	*CEP110*	4.49	3.73	3.69
224600_at	*CGGBP1*	8.685	7.255	7.115
240215_at	*RAP1A*	2.845	2.355	2.345
212938_at	*COL6A1*	3.12	2.6	2.56
1566150_at	*CALML4*	3.25	2.69	2.69
235964_x_at	*C20orf118*	10.2	8.46	8.41
1561373_at	*LOC285796*	2.585	2.145	2.145
226631_at	*LOC399818*	8.48	7.1	6.94
242950_x_at	*SNX4*	3.03	2.53	2.49
240084_at	*CBX2*	3.39	2.78	2.84
1563250_at	*NA*	2.71	2.26	2.24
242376_at	*NA*	4.68	3.89	3.86
225400_at	*C1orf19*	3.045	2.515	2.535
236495_at	*PBEF1*	3.87	3.19	3.22
207578_s_at	*HTR4*	5.35	4.43	4.43
211128_at	*EDA*	2.31	1.91	1.91
224410_s_at	*LMBR1*	2.975	2.465	2.455
209764_at	*NA*	3.905	3.255	3.205
205325_at	*PHYHIP*	2.395	1.975	1.985
1569246_a_at	*C8orf74*	3.385	2.815	2.785
213048_s_at	*NA*	14.965	12.395	12.385
229216_s_at	*CSNK2A1*	2.775	2.295	2.295
205560_at	*PCSK5*	3.49	2.86	2.92
1561642_at	*PHACTR1*	3.465	2.845	2.885

228427_at	*ZNF395*	2.9	2.4	2.4
231355_at	*NA*	3.76	3.13	3.1
215214_at	*IGL@*	4.005	3.325	3.315
242849_at	*SASH1*	3.305	2.745	2.745
209528_s_at	*TELO2*	4.285	3.565	3.535
223053_x_at	*SSU72*	7.075	5.915	5.805
1556075_at	*BMPR2*	4.43	3.67	3.67
220538_at	*ADM2*	2.995	2.475	2.485
1556012_at	*KLHDC7A*	2.645	2.195	2.185
1569905_at	*HSD11B1L*	3.14	2.63	2.58
218887_at	*MRPL2*	3.265	2.705	2.705
233871_at	*NA*	3.71	3.08	3.07
229929_at	*SPSB4*	2.8	2.32	2.32
241248_at	*TNFSF11*	2.725	2.255	2.265
238777_x_at	*LOC728210*	2.8	2.32	2.32
240565_at	*ZFP28*	2.615	2.175	2.165
1558390_at	*ZNF599*	3.665	3.045	3.035
1562724_at	*LOC286114*	3.31	2.76	2.73
221975_s_at	*C21orf2*	3.27	2.7	2.72
208211_s_at	*ALK*	2.48	2.08	2.04
1561685_a_at	*LOC441178*	2.945	2.445	2.435
219884_at	*LHX6*	2.71	2.25	2.25
238277_at	*TNKS*	3.315	2.765	2.745
214666_x_at	*NA*	4.92	4.08	4.08
230872_s_at	*ARPC4*	3.315	2.775	2.735
1552409_a_at	*ODF4*	2.94	2.44	2.44
210705_s_at	*TRIM5*	10.425	8.705	8.595
1556319_at	*LOC283270*	2.775	2.295	2.305
232076_at	*ZNF707*	4.6	3.77	3.87
232187_at	*PALMD*	2.86	2.38	2.37
207593_at	*ABCG4*	2.94	2.44	2.44

227427_at	*GEFT*	5.4	4.5	4.46
214504_at	*ABO*	2.55	2.12	2.11
220554_at	*SLC22A7*	3.845	3.225	3.155
229745_x_at	*DACT3*	3.11	2.6	2.57
226940_at	*FAM69B*	2.72	2.26	2.26
1560962_at	*NA*	3.65	3.02	3.04
234271_at	*OTOP2*	2.84	2.38	2.34
217582_at	*KCNIP4*	3.54	2.97	2.91
216704_at	*TBCA*	3.245	2.705	2.695
1569690_at	*CCDC36*	3.7	3.1	3.06
214893_x_at	*HCN2*	4.195	3.495	3.485
217391_x_at	*NA*	3.005	2.505	2.495
1562415_a_at	*SPOCD1*	7.195	5.945	6.005
237548_at	*ZAK*	2.84	2.36	2.36
236730_at	*GIPC3*	2.62	2.18	2.18
241037_at	*NA*	3.645	3.035	3.015
215289_at	*ZNF419*	3.515	2.925	2.915
215135_at	*DNPEP*	4.195	3.485	3.495
240305_at	*DIP2C*	3.125	2.615	2.585
236736_at	*NA*	4.755	4.005	3.905
230221_at	*BAT5*	4.075	3.405	3.375
241201_at	*KIAA1530*	2.61	2.16	2.18
223069_s_at	*EML4*	3.45	2.88	2.86
210197_at	*ITPK1*	2.46	2.04	2.04
236794_at	*CTBP2*	3.305	2.745	2.745
203312_x_at	*ARF6*	9.975	8.395	8.195
243463_s_at	*RIT1*	11.055	9.125	9.265
214133_at	*MUC6*	3.485	2.895	2.905
244506_at	*TMTC1*	2.89	2.42	2.4
206077_at	*KEL*	2.76	2.3	2.3
207498_s_at	*CYP2D6*	2.88	2.41	2.39

209810_at	*SFTPB*	5.25	4.42	4.32
208652_at	*PPP2CA*	10.245	8.555	8.495
206654_s_at	*POLR3G*	3.525	2.925	2.935
230115_at	*DKFZp779M0652*	3.305	2.745	2.755
241455_at	*NA*	3.125	2.615	2.595
205170_at	*STAT2*	2.89	2.41	2.41
1562065_at	*NA*	3.47	2.91	2.87
225380_at	*LOC91461*	3.745	3.125	3.115
241030_at	*FSIP1*	3.055	2.545	2.535
206323_x_at	*OPHN1*	10.345	8.715	8.505
1566581_at	*CLPB*	3.375	2.835	2.795
220103_s_at	*MRPS18C*	3.57	2.98	2.96
227216_at	*RLTPR*	3.78	3.16	3.13
211184_s_at	*USH1C*	2.77	2.33	2.29
220544_at	*TSKS*	2.825	2.355	2.345
231851_at	*RAVER2*	3.425	2.855	2.845
1559618_at	*DTX1*	2.685	2.245	2.245
231681_x_at	*HIST3H2A*	2.97	2.47	2.47
235180_at	*STYX*	4.475	3.705	3.755
240432_x_at	*NA*	7.625	6.365	6.335
243638_at	*QKI*	3.25	2.71	2.71
211326_x_at	*HFE*	2.925	2.455	2.435
1556015_a_at	*MESP2*	2.245	1.875	1.865
217435_x_at	*NA*	2.835	2.355	2.355
201647_s_at	*SCARB2*	9.105	7.635	7.545
207862_at	*UPK2*	4.05	3.38	3.36
242857_at	*FARP2*	3.61	3.04	2.98
230891_at	*TUBE1*	3.445	2.875	2.865
1562074_a_at	*UNC13C*	3	2.5	2.5
1558440_at	*TMEM64*	2.975	2.485	2.475
209008_x_at	*KRT8*	3.325	2.755	2.785

229545_at	*C20orf42*	2.79	2.35	2.3
1554038_at	*LARP2*	2.65	2.21	2.21
208262_x_at	*MEFV*	2.68	2.24	2.24
233302_at	*BCL11B*	3.13	2.58	2.64
226904_at	*SLC6A8*	3.525	2.955	2.935
236010_at	*SH3D19*	3.73	3.13	3.09
221597_s_at	*HSPC171*	9.77	8.08	8.22
201263_at	*TARS*	11.87	10.02	9.79
209779_at	*C12orf31*	3.78	3.17	3.15
214347_s_at	*DDC*	3.6	3.02	2.98
214084_x_at	*NCF1*	2.8	2.34	2.33
239080_at	*NA*	3.61	3.01	3.01
236580_at	*NA*	2.855	2.375	2.385
218747_s_at	*TAPBPL*	3.135	2.595	2.645
226269_at	*GDAP1*	7.715	6.495	6.375
1555892_s_at	*LOC253039*	3.435	2.885	2.855
37424_at	*CCHCR1*	3.435	2.875	2.865
204110_at	*HNMT*	2.77	2.31	2.31
239445_at	*RAB6A*	2.835	2.375	2.375
236059_at	*C11orf61*	3.28	2.73	2.75
1555132_at	*NA*	2.705	2.265	2.255
224124_at	*ZRANB3*	3.245	2.735	2.685
1561961_at	*DKFZp686A1627*	3.235	2.705	2.685
209185_s_at	*IRS2*	12.65	10.67	10.47
229791_at	*CAPNS2*	3.25	2.72	2.71
238924_at	*LOC399761*	3.005	2.515	2.505
230307_at	*SLC25A21*	3.56	3.01	2.95
230662_at	*RNF187*	3.015	2.535	2.505
243200_at	*NA*	3.445	2.895	2.875
210193_at	*MOBP*	3.455	2.895	2.885
241834_at	*NA*	3.095	2.595	2.585

220319_s_at	*MYLIP*	3.745	3.125	3.125
237121_at	*NA*	3.44	2.88	2.88
1553915_at	*C10orf126*	3.565	2.995	2.965
1567036_at	*C20orf181*	3.085	2.595	2.575
216702_x_at	*ATP8A2*	3.93	3.28	3.29
1556182_x_at	*DRAP1*	3.145	2.635	2.625
1567590_at	*NA*	3.155	2.645	2.635
227205_at	*TAF1*	9.16	7.58	7.75
233277_at	*DLEU7*	2.46	2.06	2.06
1567256_at	*OR1J2*	3.525	2.955	2.935
233001_at	*SAMD10*	4.28	3.59	3.57
207787_at	*KRT33B*	2.66	2.23	2.22
1565860_at	*USP34*	2.71	2.27	2.27
233920_at	*MAD1L1*	2.58	2.16	2.16
233741_at	*FTCD*	3.03	2.53	2.53
213197_at	*ASTN1*	2.71	2.27	2.27
209433_s_at	*PAICS*	6.785	5.735	5.625
225072_at	*ZCCHC3*	2.95	2.46	2.47
211586_s_at	*ATP2B2*	2.73	2.28	2.3
205693_at	*TNNT3*	3.115	2.615	2.605
206011_at	*CASP1*	2.84	2.38	2.38
203783_x_at	*POLRMT*	2.605	2.185	2.175
237106_at	*SLC11A2*	3.625	3.045	3.035
232887_at	*hCG_1776018*	2.55	2.13	2.13
238048_at	*CLASP2*	2.95	2.48	2.47
212145_at	*MRPS27*	6.585	5.575	5.475
211407_at	*NDUFB7*	3.405	2.865	2.835
232163_at	*WDR19*	3.2	2.67	2.69
222129_at	*C2orf17*	10.845	9.095	9.075
243906_at	*OSTalpha*	3.83	3.24	3.18
231086_at	*BACE1*	3.91	3.24	3.31

1570430_at	*NA*	3.13	2.63	2.62
214105_at	*SOCS3*	2.72	2.28	2.28
201873_s_at	*ABCE1*	9.4	7.87	7.89
202473_x_at	*HCFC1*	2.84	2.37	2.39
1570633_at	*NA*	3.82	3.21	3.19
228575_at	*IL20RB*	3.25	2.72	2.73
1555103_s_at	*FGF7*	3.545	2.975	2.965
226001_at	*KLHL5*	12	10.01	10.12
233675_s_at	*LOC374491*	3.425	2.865	2.875
203294_s_at	*LMAN1*	6.61	5.53	5.56
231615_at	*C8orf70*	3.265	2.745	2.735
1564004_at	*DGKG*	3.555	3.005	2.955
222927_s_at	*CPLX3*	3.285	2.765	2.755
234342_at	*NA*	3.11	2.63	2.59
243975_at	*RTN4RL1*	3.165	2.665	2.655
220051_at	*PRSS21*	2.795	2.355	2.345
221038_at	*NA*	3.255	2.735	2.735
203253_s_at	*HISPPD1*	10.41	8.68	8.79
236770_at	*LOC283507*	2.715	2.275	2.275
222236_s_at	*DDEFL1*	5.24	4.44	4.36
1559481_at	*CHIC1*	3.085	2.595	2.585
1555474_at	*TTLL3*	3.46	2.93	2.88
223770_x_at	*MGC3207*	3.33	2.79	2.79
1563834_a_at	*C1orf62*	3.435	2.885	2.875
242082_at	*MMAB*	2.63	2.21	2.21
234947_s_at	*C10orf84*	9.98	8.32	8.44
201961_s_at	*RNF41*	3.015	2.525	2.535
208300_at	*PTPRH*	3.22	2.7	2.7
228746_s_at	*CDV3*	12.935	10.975	10.735
231273_x_at	*FRZB*	3.21	2.71	2.68
203940_s_at	*VASH1*	4.24	3.55	3.58

243410_at	*PTPN2*	2.77	2.33	2.33
224816_at	*C7orf20*	2.77	2.33	2.33
205009_at	*TFF1*	2.74	2.3	2.3
213671_s_at	*MARS*	10.37	8.62	8.8
1564294_at	*KIAA1128*	3	2.53	2.51
219712_s_at	*CARKL*	2.675	2.255	2.245
214589_at	*FGF12*	3.595	3.025	3.005
217222_at	*IGHG1*	2.655	2.235	2.235
213794_s_at	*NGDN*	7.76	6.47	6.57
1570138_at	*NA*	3.045	2.565	2.555
242603_x_at	*NA*	3.455	2.915	2.885
224501_at	*C1orf170*	3.075	2.575	2.585
1553823_a_at	*RTP1*	2.955	2.475	2.485
233937_at	*ZNF403*	2.785	2.335	2.345
205774_at	*F12*	2.465	2.065	2.065
205926_at	*IL27RA*	3.965	3.325	3.335
219487_at	*BBS10*	8.955	7.505	7.555
239101_at	*ITCH*	7.725	6.425	6.555
241361_at	*KIAA1833*	3.175	2.675	2.675
235129_at	*PPP1R1A*	2.9	2.46	2.41
234669_x_at	*HSA251708*	5.14	4.34	4.3
241381_at	*CXorf36*	2.935	2.475	2.465
212210_at	*INTS1*	3.105	2.615	2.605
223638_at	*NBPF3*	5.71	4.78	4.83
1563178_at	*NA*	2.65	2.23	2.23
219103_at	*DDEFL1*	4.03	3.38	3.4
1555843_at	*HNRPM*	2.595	2.185	2.175
1562292_at	*ANKRD30B*	4.03	3.41	3.37
1558631_at	*PPARA*	2.965	2.515	2.485
215712_s_at	*IGFALS*	3.2	2.7	2.69
232389_at	*WIPF3*	2.875	2.415	2.415

213139_at	*SNAI2*	13.695	11.435	11.625
1559265_at	*FLJ45187*	3.31	2.8	2.78
229142_s_at	*BBS1*	2.855	2.395	2.395
235664_at	*LOC729620*	3.16	2.66	2.66
1562038_at	*LIPC*	3.18	2.69	2.67
242747_at	*NA*	3.675	3.105	3.085
1562601_at	*UNQ6975*	2.92	2.47	2.44
206588_at	*DAZL*	3.145	2.655	2.635
210785_s_at	*C1orf38*	2.58	2.18	2.17
221023_s_at	*KCNH6*	3.185	2.665	2.705
219815_at	*GAL3ST4*	8.735	7.405	7.305
243084_at	*CALD1*	2.9	2.44	2.45
214222_at	*DNAH7*	5.095	4.245	4.335
218360_at	*RAB22A*	10.07	8.46	8.52
229954_at	*NA*	2.67	2.24	2.26
242190_at	*SDAD1*	3.735	3.165	3.135
204528_s_at	*NAP1L1*	14.395	12.225	12.045
230908_at	*NA*	2.865	2.405	2.415
217800_s_at	*NDFIP1*	10.29	8.62	8.72
237041_x_at	*RCOR1*	3.885	3.265	3.265
232775_at	*NA*	3.405	2.875	2.865
207771_at	*SLC5A2*	3.035	2.555	2.555
1562459_at	*NA*	3.655	3.105	3.045
240624_x_at	*NA*	4.155	3.535	3.465
209306_s_at	*SWAP70*	11.57	9.66	9.84
207618_s_at	*BCS1L*	7.595	6.395	6.405
210352_at	*BRD8*	2.475	2.095	2.085
212853_at	*DCUN1D4*	4.04	3.43	3.37
241490_s_at	*PGBD2*	2.94	2.48	2.48
231317_at	*TSNARE1*	3.025	2.575	2.525
205662_at	*EPPB9*	3.245	2.755	2.735

241903_at	*KCTD3*	4.07	3.43	3.43
231492_at	*NA*	3.145	2.645	2.655
233781_s_at	*RIF1*	3.445	2.925	2.895
1566097_at	*A2BP1*	2.505	2.115	2.105
237872_at	*LRFN2*	2.995	2.535	2.525
236874_at	*TSSK3*	3.245	2.745	2.745
202330_s_at	*UNG*	8.495	7.185	7.155
238060_s_at	*B4GALNT4*	3.47	2.92	2.94
217283_at	*NA*	3.025	2.555	2.545
206307_s_at	*FOXD1*	12.65	10.65	10.69
228339_at	*ECSM2*	3.025	2.545	2.545
208876_s_at	*PAK2*	10.62	9.02	8.91
221588_x_at	*ALDH6A1*	4.77	4.05	4.01
230639_at	*NA*	3.045	2.565	2.565
1553243_at	*ITIH5*	3.405	2.875	2.865
226456_at	*C16orf75*	6.535	5.565	5.465
227375_at	*ANKRD13C*	9.345	7.865	7.905
244090_at	*ITPR1*	4.61	3.88	3.9
226212_s_at	*NA*	3.58	3.05	3
236671_at	*COMT*	5.815	4.915	4.915
1566033_at	*CRTC3*	3.415	2.885	2.875
233067_at	*NA*	3.015	2.555	2.545
221719_s_at	*LZTS1*	2.72	2.3	2.29
222601_at	*UBE1L2*	9.215	7.735	7.825
231471_at	*ZNF638*	3.13	2.66	2.64
1561789_at	*DKFZP779L1068*	3.7	3.15	3.09
216000_at	*ASNS*	2.85	2.41	2.41
231736_x_at	*MGST1*	10.345	8.795	8.685
223345_at	*HDAC8*	5.3	4.49	4.47
202447_at	*DECR1*	11.24	9.59	9.41
244673_at	*KIAA1841*	3.38	2.84	2.88

208071_s_at	*LAIR1*	2.96	2.51	2.49
228094_at	*AMICA1*	3.12	2.63	2.65
217235_x_at	*NA*	3.36	2.84	2.84
220323_at	*CNTD2*	2.86	2.44	2.4
217017_at	*OSBPL10*	2.6	2.2	2.2
1556116_s_at	*PTPRS*	2.555	2.155	2.165
1553237_x_at	*PCDHAC1*	3.075	2.605	2.585
230460_at	*MYLK*	2.98	2.54	2.5
201142_at	*EIF2S1*	10.3	8.75	8.66
243744_at	*LOC348751*	3.23	2.73	2.73
233352_at	*WWC1*	3.275	2.785	2.755
217365_at	*PRAMEF5*	2.805	2.365	2.365
1559952_x_at	*LOC729689*	3.805	3.225	3.215
226052_at	*NA*	10.36	8.7	8.82
207230_at	*CDON*	3.22	2.75	2.7
237083_at	*NA*	3.475	2.945	2.935
218471_s_at	*BBS1*	6.565	5.525	5.575
207032_s_at	*CRISP1*	2.685	2.265	2.265
228636_at	*BHLHB5*	3.205	2.715	2.705
218553_s_at	*KCTD15*	4.755	4.015	4.025
215654_at	*BCAT2*	2.88	2.44	2.44
202692_s_at	*UBTF*	5.545	4.665	4.705
1553488_at	*TEKT5*	2.745	2.325	2.325
228578_at	*DRB1*	6.9	5.81	5.87
1561526_at	*NA*	3.07	2.59	2.6
208725_at	*EIF2S2*	5.155	4.315	4.405
220055_at	*ZNF287*	2.77	2.35	2.34
226878_at	*HLA-DOA*	2.705	2.285	2.285
223922_x_at	*MS4A6A*	2.43	2.05	2.05
216134_at	*FRMD4B*	3.345	2.835	2.825
1563039_at	*LARGE*	3.53	2.99	2.99

228093_at	*ZNF599*	3	2.52	2.56
206379_at	*EYA3*	3.04	2.59	2.56
207311_at	*DOC2B*	2.63	2.23	2.23
225636_at	*STAT2*	13.84	11.6	11.84
1565887_at	*TRPM7*	2.87	2.44	2.43
210272_at	*CYP2B7P1*	2.51	2.14	2.12
1555049_at	*C21orf29*	2.835	2.395	2.405
219291_at	*DTWD1*	10.475	8.825	8.925
217555_at	*SMC1A*	4.23	3.62	3.55
204968_at	*C6orf47*	7.365	6.245	6.245
230410_at	*NRP2*	3.05	2.59	2.58
1558553_at	*KIAA0182*	2.515	2.135	2.135
239241_at	*LOC727869*	4.535	3.845	3.835
203138_at	*HAT1*	11.39	9.58	9.72
225221_at	*NA*	11.355	9.545	9.695
241771_at	*RIMBP2*	2.78	2.36	2.36
1554110_at	*CDCP1*	3.225	2.735	2.725
219912_s_at	*ENPP3*	3.24	2.76	2.73
1555475_x_at	*TTLL3*	4.235	3.635	3.555
210477_x_at	*MAPK8*	2.51	2.13	2.13
1560671_at	*KIAA1652*	2.53	2.15	2.15
207637_at	*KIAA0789*	2.935	2.505	2.485
204746_s_at	*PICK1*	3.085	2.625	2.625
214098_at	*KIAA1107*	3.44	2.92	2.92
1552807_a_at	*SIGLEC10*	3.055	2.595	2.585
213349_at	*TMCC1*	7.39	6.31	6.23
1560086_at	*NA*	3.58	3.07	3.01
208466_at	*RAB3D*	2.91	2.47	2.47
233000_x_at	*NA*	2.93	2.49	2.49
244550_at	*TFDP1*	3	2.54	2.54
223693_s_at	*FLJ10324*	3.03	2.57	2.57

226408_at	*TEAD2*	6.415	5.395	5.485
227090_at	*PHF21A*	6.505	5.505	5.535
222000_at	*C1orf174*	11.07	9.33	9.44
234791_at	*GSH1*	3.005	2.555	2.535
226433_at	*RNF157*	3.475	2.965	2.935
230297_x_at	*SYNGAP1*	4.12	3.5	3.49
1569738_at	*NA*	3.02	2.56	2.56
1561454_at	*NA*	2.89	2.45	2.45
226800_at	*KIAA1799*	6.74	5.74	5.7
218353_at	*RGS5*	3.43	2.89	2.93
234681_s_at	*CHD6*	2.55	2.17	2.17
211798_x_at	*IGLJ3*	3.13	2.66	2.65
217251_x_at	*IVD*	2.91	2.49	2.45
1569604_at	*NA*	3.945	3.345	3.345
219381_at	*FLJ13231*	5.14	4.38	4.34
216551_x_at	*PLCG1*	5.76	4.88	4.89
1554062_at	*XG*	10.445	8.935	8.795
240999_at	*LOC401351*	3.075	2.615	2.615
243077_at	*FLJ16734*	3.405	2.915	2.855
1554510_s_at	*GHITM*	8.565	7.295	7.235
224498_x_at	*AXIN2*	2.8	2.38	2.38
237353_at	*CDKAL1*	3.54	3.02	2.99
234589_at	*TMEM106A*	2.565	2.185	2.185
219741_x_at	*ZNF552*	3.03	2.57	2.57
232357_at	*TTLL9*	2.51	2.13	2.13
1564112_at	*FAM71A*	2.48	2.11	2.1
1559848_at	*NSUN4*	3.47	2.95	2.95
1569879_a_at	*MEGF11*	2.39	2.03	2.03
207827_x_at	*SNCA*	8.035	6.835	6.805
207414_s_at	*PCSK6*	2.805	2.405	2.365
1561405_s_at	*PDIA3*	2.87	2.45	2.42

228379_at	*NUTF2*	8.855	7.545	7.495
239004_at	*SQSTM1*	2.865	2.415	2.445
1560133_at	*TNRC15*	3.47	2.94	2.95
233484_at	*NA*	3.06	2.6	2.6
223801_s_at	*APOL4*	3.795	3.255	3.185
233447_at	*RP11-506K6.3*	3.3	2.82	2.79
236141_at	*NBLA00301*	3.365	2.875	2.855
206705_at	*TULP1*	2.975	2.535	2.525
201451_x_at	*RHEB*	5.465	4.615	4.675
221969_at	*NA*	3.495	2.995	2.955
229392_s_at	*PIK3R2*	4.825	4.125	4.075
230423_at	*FOXD3*	2.81	2.39	2.39
201063_at	*RCN1*	13.85	11.72	11.82
226770_at	*MAGI3*	6.765	5.775	5.715
221224_s_at	*DCAKD*	5.35	4.55	4.55
1562274_at	*CDH13*	2.53	2.15	2.15
1553599_a_at	*SYCP3*	3.65	3.12	3.1
230530_at	*OSGIN1*	3.145	2.665	2.695
1553214_a_at	*CCDC7*	3.815	3.275	3.225
1555554_at	*RP11-49G10.8*	2.79	2.38	2.37
201055_s_at	*HNRPA0*	8.115	6.955	6.865
1559439_s_at	*C21orf58*	3.5	3	2.96
203375_s_at	*TPP2*	9.01	7.67	7.67
207822_at	*FGFR1*	3.325	2.835	2.815
1552524_at	*ART5*	2.73	2.33	2.32
216433_s_at	*PRDM2*	2.85	2.43	2.42
240158_at	*NA*	3.36	2.89	2.83
1558449_at	*MBTD1*	3.465	2.955	2.945
212840_at	*UBXD7*	10.955	9.305	9.365
238577_s_at	*NA*	2.905	2.475	2.465
1558856_at	*DMRTA2*	3.09	2.64	2.63

228540_at	*QKI*	3.54	2.99	3.05
235187_s_at	*C14orf135*	2.99	2.55	2.54
205642_at	*CEP110*	2.86	2.44	2.44
1552311_a_at	*RAXL1*	5.63	4.77	4.82
1563674_at	*FCRL2*	2.84	2.41	2.43
1554857_at	*ELMO2*	2.6	2.22	2.21
222911_s_at	*CXorf36*	2.875	2.465	2.445
202526_at	*SMAD4*	3.585	3.045	3.055
210657_s_at	*4-Sep*	2.84	2.43	2.41
242644_at	*TMC8*	3.355	2.865	2.845
212291_at	*HIPK1*	2.665	2.265	2.265
202725_at	*POLR2A*	5.28	4.47	4.53
211715_s_at	*BDH1*	3.145	2.685	2.675
1556240_at	*ATG7*	2.755	2.355	2.345
244488_at	*LSM14B*	2.55	2.18	2.16
239607_at	*GPR156*	4.71	4.01	4.02
211248_s_at	*CHRD*	2.795	2.375	2.375
230126_s_at	*JMJD2B*	3.435	2.935	2.925
207172_s_at	*CDH11*	7.665	6.585	6.475
241996_at	*RUFY2*	10.545	8.905	9.075
203061_s_at	*MDC1*	3.1	2.63	2.65
237455_at	*FLJ45825*	2.515	2.145	2.135
222783_s_at	*SMOC1*	2.495	2.135	2.125
231685_at	*SOX5*	3.04	2.6	2.59
218915_at	*NF2*	8.79	7.54	7.44
218763_at	*STX18*	9.275	7.955	7.875
236658_at	*NA*	2.96	2.52	2.53
1556595_at	*WWOX*	3.11	2.66	2.65
231143_at	*LOC642421*	2.88	2.46	2.46
242680_at	*NA*	3.075	2.625	2.615
230136_at	*LOC400099*	4.105	3.505	3.495

1557389_at	*SH3PXD2A*	2.815	2.405	2.395
238573_at	*NA*	9.815	8.405	8.345
229115_at	*DYNC1H1*	10.04	8.49	8.64
228083_at	*CACNA2D4*	3.01	2.57	2.57
210682_at	*LPO*	2.535	2.165	2.155
229043_at	*PAPD5*	11.06	9.39	9.49
224805_s_at	*C15orf17*	2.86	2.46	2.42
235529_x_at	*C20orf118*	10.82	9.29	9.19
222381_at	*PDCD6*	3.93	3.36	3.34
236776_at	*NA*	3.93	3.36	3.34
210507_s_at	*AVIL*	3.475	2.975	2.965
243697_at	*MOXD1*	2.99	2.56	2.54
207231_at	*DZIP3*	3.775	3.215	3.225
1566844_at	*PER4*	2.545	2.175	2.165
1553046_s_at	*GAL3ST2*	2.565	2.185	2.185
238313_at	*NA*	3.085	2.625	2.635
1570015_at	*RP11-165H20.1*	2.58	2.2	2.2
240567_at	*NA*	3.665	3.135	3.115
222766_at	*POLR3K*	3.54	3.03	3.01
1561611_at	*NA*	2.685	2.305	2.265
234727_at	*DNAH7*	2.58	2.2	2.2
204858_s_at	*ECGF1*	2.265	1.935	1.925
230792_at	*FAAH2*	2.69	2.31	2.28
237080_at	*SRGAP3*	3.56	3.04	3.04
1559629_at	*TMEM132D*	3.07	2.65	2.61
203439_s_at	*STC2*	11.995	10.145	10.355
219711_at	*ZNF586*	2.685	2.285	2.295
1556422_at	*ZFP28*	2.74	2.35	2.33
212230_at	*PPAP2B*	13.48	11.55	11.48
228949_at	*GPR177*	11.775	10.025	10.095
219934_s_at	*SULT1E1*	3	2.57	2.56

243091_at	*CRYZL1*	5.51	4.68	4.74
201611_s_at	*ICMT*	9.265	7.915	7.925
220505_at	*C9orf53*	2.825	2.405	2.415
204397_at	*EML2*	2.705	2.305	2.315
219674_s_at	*PRO2900*	5.625	4.815	4.795
223359_s_at	*PDE7A*	2.49	2.13	2.13
1555014_x_at	*NA*	4.635	3.985	3.935
220163_s_at	*HR*	2.695	2.305	2.295
1554241_at	*COCH*	13.38	11.54	11.34
222364_at	*NA*	7.815	6.615	6.745
235955_at	*MARVELD2*	3.46	2.93	2.99
228352_at	*UNC13D*	3.075	2.635	2.635
215587_x_at	*BTBD14B*	3.885	3.325	3.325
235592_at	*ELL2*	7.135	6.125	6.075
240795_at	*NA*	2.8	2.4	2.39
234419_x_at	*NA*	3.625	3.135	3.075
1556533_at	*C17orf52*	2.995	2.535	2.585
232235_at	*DSEL*	12.55	10.8	10.66
221293_s_at	*DEF6*	2.955	2.515	2.545
215383_x_at	*SPG21*	7.07	6.06	6.04
1554922_at	*ZNF678*	3.365	2.895	2.865
217374_x_at	*TRGV5*	2.65	2.27	2.27
1569557_at	*ZNF248*	3.235	2.795	2.745
202448_s_at	*ZER1*	2.375	2.035	2.035
218373_at	*AKTIP*	8.85	7.59	7.55
1569449_a_at	*CRSP2*	3.105	2.655	2.665
207099_s_at	*CHM*	2.695	2.315	2.315
215354_s_at	*PELP1*	6.275	5.345	5.395
242532_at	*NA*	2.92	2.5	2.5
238638_at	*SLC37A2*	5.275	4.545	4.485
231459_at	*SMG6*	2.595	2.215	2.215

211516_at	*IL5RA*	2.77	2.36	2.38
1559186_at	*PRKXP1*	3.435	2.935	2.935
231448_at	*Tenr*	2.91	2.51	2.47
1563821_at	*LOC170425*	2.855	2.445	2.435
212852_s_at	*TROVE2*	13.59	11.65	11.61
236490_at	*NA*	3.19	2.74	2.72
243912_x_at	*APOBEC3F*	3.505	3.025	2.975
242681_at	*CTNNBIP1*	3.095	2.665	2.635
1570593_at	*NA*	3.575	3.085	3.035
239076_at	*LOC441220*	4.58	3.92	3.92
234232_at	*KBTBD2*	3.095	2.645	2.655
226204_at	*GNB1L*	9.3	7.9	8.02
225442_at	*DDR2*	12.205	10.515	10.375
225118_at	*SETD8*	6.755	5.805	5.755
1554712_a_at	*GLYATL2*	2.89	2.49	2.46
225869_s_at	*UNC93B1*	2.735	2.355	2.325
242815_x_at	*FRMD4A*	3.425	2.955	2.905
1562352_at	*NA*	3.74	3.23	3.17
232502_at	*FLJ34077*	4.155	3.575	3.535
1563840_at	*EFTUD1*	3.07	2.65	2.61
228048_at	*C10orf41*	2.935	2.515	2.505
1559901_s_at	*C21orf34*	3.165	2.705	2.715
213563_s_at	*TUBGCP2*	5.095	4.375	4.345
201031_s_at	*HNRPH1*	14.305	12.155	12.345
1565876_x_at	*SMG6*	3.36	2.88	2.88
1560119_at	*LOC389634*	3.545	3.045	3.035
219186_at	*ZBTB7A*	4.45	3.84	3.78
1561990_at	*LOC157931*	2.325	1.985	1.985
216095_x_at	*MTMR1*	9.685	8.255	8.345
230186_at	*TMEM136*	2.92	2.5	2.5
210886_x_at	*TP53AP1*	2.975	2.545	2.565

230174_at	*LYPLAL1*	8.25	7.09	7.05
1560911_at	*NA*	2.89	2.46	2.49
217706_at	*LRRC51*	3.715	3.185	3.175
239276_at	*NA*	4.32	3.7	3.7
231198_at	*CDK6*	2.745	2.355	2.345
232373_at	*NOXA1*	2.81	2.41	2.4
243983_at	*MCF2L*	3.44	2.95	2.94
219580_s_at	*TMC5*	3.175	2.725	2.715
223844_at	*ADAMTS13*	2.79	2.4	2.38
234445_at	*C6orf12*	3.54	3.06	3.02
200698_at	*KDELR2*	13.44	11.51	11.53
1570022_at	*C3orf1*	3.07	2.63	2.63
243616_at	*NA*	3.195	2.745	2.725
239699_s_at	*PMS2L5*	4.46	3.82	3.83
220745_at	*IL19*	2.39	2.05	2.05
236179_at	*NA*	12.53	10.77	10.72
229886_at	*C5orf34*	4.165	3.565	3.565
1562576_at	*NA*	3.145	2.705	2.695
203255_at	*FBXO11*	10.365	8.955	8.825
235175_at	*GBP4*	3.275	2.815	2.815
239411_at	*ZNF496*	2.765	2.365	2.365
216849_at	*NA*	3.975	3.435	3.395
213753_x_at	*LOC642592*	7.72	6.68	6.56
219249_s_at	*FKBP10*	2.64	2.26	2.27
1560463_at	*NA*	2.51	2.15	2.15
205623_at	*ALDH3A1*	2.915	2.495	2.495
236839_at	*AUH*	3.84	3.3	3.29
204449_at	*PDCL*	10.075	8.645	8.635
1552399_a_at	*BRF1*	3.18	2.73	2.72
241043_at	*ORC5L*	3.53	3.03	3.03
244242_at	*NA*	2.85	2.45	2.45

231051_at	*SLC16A9*	2.845	2.445	2.445
220104_at	*ZC3HAV1*	3.07	2.63	2.64
206053_at	*ZNF510*	3.84	3.3	3.29
208251_at	*KCNC4*	2.56	2.2	2.2
239528_at	*PROM2*	3.98	3.45	3.38
210577_at	*CASR*	2.585	2.225	2.225
1561474_at	*NA*	2.85	2.46	2.44
233321_x_at	*LOC90834*	6.41	5.52	5.49
1566633_at	*NA*	3.085	2.655	2.635
214490_at	*ARSF*	2.605	2.245	2.235
217494_s_at	*PTENP1*	2.98	2.55	2.57
221197_s_at	*CHAT*	2.71	2.33	2.33
210864_x_at	*HFE*	2.645	2.265	2.265
213219_at	*ADCY2*	2.71	2.33	2.32
1565939_at	*C5orf22*	3.67	3.17	3.14
1553813_s_at	*TLE6*	2.915	2.505	2.495
234888_at	*CACHD1*	2.65	2.27	2.28
212217_at	*PREPL*	8.39	7.2	7.21
208771_s_at	*LTA4H*	10.695	9.235	9.145
1560207_at	*LOC644660*	3.195	2.755	2.725
241276_at	*NA*	2.86	2.46	2.46
240644_at	*NA*	2.745	2.365	2.355
1562853_x_at	*AGPAT3*	2.68	2.3	2.3
222180_at	*YES1*	3.38	2.88	2.92
206506_s_at	*SUPT3H*	3.505	3.015	3.005
214952_at	*NCAM1*	2.785	2.395	2.385
1562573_at	*CYP17A1*	3.855	3.325	3.305
220200_s_at	*SETD8*	3.325	2.865	2.855
217383_at	*PGK1*	2.85	2.45	2.45
1556553_at	*SLC45A4*	2.795	2.405	2.395
1560937_at	*RSU1*	3.41	2.92	2.94

216569_at	*NA*	3.11	2.68	2.66
211410_x_at	*KIR2DL5A*	2.44	2.08	2.12
204854_at	*LEPREL2*	3.735	3.235	3.195
1562260_at	*BRE*	3.16	2.73	2.71
235718_at	*SRL*	3.31	2.86	2.84
210046_s_at	*IDH2*	7.435	6.415	6.375
204777_s_at	*MAL*	2.73	2.35	2.35
201669_s_at	*MARCKS*	13.775	11.865	11.815
240393_at	*AES*	2.445	2.105	2.095
200646_s_at	*NUCB1*	3.13	2.71	2.68
229697_at	*HIRIP3*	3.27	2.83	2.79
218292_s_at	*PRKAG2*	3.515	3.025	3.015
206081_at	*SLC24A1*	6.41	5.5	5.52
206908_s_at	*CLDN11*	2.27	1.95	1.95
225668_at	*LOC134145*	3.635	3.125	3.135
234346_x_at	*ITGB4BP*	3.365	2.885	2.895
236224_at	*RIT1*	12.34	10.58	10.65
241581_at	*ERBB4*	2.84	2.44	2.44
212410_at	*EFHA1*	12.3	10.62	10.54
213565_s_at	*SMAD6*	5.615	4.835	4.825
232475_at	*C15orf42*	2.71	2.33	2.33
235011_at	*MAP3K2*	3.6	3.08	3.11
231616_at	*GYPA*	3.335	2.875	2.865
225415_at	*DTX3L*	7.59	6.52	6.54
215122_at	*TBX6*	3.29	2.84	2.82
234789_at	*NA*	3.58	3.09	3.07
210344_at	*OSBPL7*	2.85	2.45	2.45
208340_at	*CASP4*	3.065	2.645	2.635
228557_at	*L3MBTL4*	2.9	2.5	2.49
218568_at	*AGK*	9.36	8.07	8.04
218202_x_at	*MRPL44*	3.045	2.625	2.615

240081_at	*MYO5C*	3.56	3.07	3.05
244323_at	*BHLHB5*	3.545	3.075	3.025
1556826_s_at	*C1orf187*	3.635	3.155	3.105
225381_at	*LOC399959*	11.895	10.255	10.225
225885_at	*EEA1*	11.345	9.815	9.725
216509_x_at	*MLLT10*	3.16	2.71	2.74
1555749_at	*SF1*	2.89	2.5	2.48
206936_x_at	*NA*	7.315	6.265	6.335
242789_at	*PDE1A*	2.825	2.445	2.415
238004_at	*PGBD2*	4.525	3.915	3.885
222428_s_at	*LARS*	12.215	10.555	10.475
206918_s_at	*CPNE1*	8.06	7	6.89
215820_x_at	*SNX13*	3.805	3.285	3.285
201407_s_at	*PPP1CB*	11.775	10.095	10.215
228185_at	*ZNF25*	8.925	7.625	7.755
232770_at	*TUSC3*	2.89	2.5	2.48
234275_at	*ESR1*	2.985	2.575	2.565
220845_at	*ACOXL*	3.555	3.075	3.045
230553_at	*PRDM15*	3.255	2.815	2.805
223635_s_at	*SSBP3*	2.695	2.335	2.305
237532_at	*TNFRSF8*	2.65	2.29	2.29
243939_at	*NA*	2.585	2.225	2.235
231018_at	*LOC342979*	2.94	2.54	2.53
1569150_x_at	*PDLIM7*	2.8	2.41	2.42
230320_at	*TBRG1*	8.845	7.695	7.555
216195_at	*ANK2*	2.77	2.39	2.38
222679_s_at	*DCUN1D1*	9.88	8.57	8.47
212762_s_at	*TCF7L2*	9.215	7.985	7.925
236886_at	*NINJ2*	2.95	2.55	2.54
243403_x_at	*CPM*	3.19	2.77	2.73
1554706_at	*OR2L13*	3.175	2.765	2.715

1569805_at	*NA*	2.525	2.185	2.175
202602_s_at	*HTATSF1*	11.9	10.23	10.3
236867_at	*TRPV1*	4.5	3.88	3.88
221334_s_at	*FOXP3*	4.1	3.56	3.52
228443_s_at	*SETD8*	12.995	11.115	11.315
240836_at	*RPL27*	3.26	2.79	2.84
207649_at	*KRT37*	2.62	2.26	2.26
207019_s_at	*AKAP4*	3.19	2.75	2.75
236556_s_at	*LONRF1*	3.545	3.075	3.055
1563295_at	*NA*	2.665	2.305	2.305
227317_at	*LMCD1*	2.61	2.25	2.25
214293_at	*11-Sep*	11.555	10.025	9.915
1560386_at	*XPO1*	3.015	2.605	2.585
223281_s_at	*COX15*	8.74	7.57	7.51
231584_s_at	*NA*	3.185	2.745	2.745
1558938_at	*C14orf122*	3.51	3.03	3.03
215860_at	*SYT12*	4.035	3.495	3.455
203678_at	*MTMR15*	7.335	6.295	6.375
214191_at	*ICA1*	2.815	2.435	2.425
1563978_at	*LOC339457*	3.705	3.215	3.185
216614_at	*ITPR2*	3.125	2.705	2.695
237404_at	*PEX14*	2.715	2.345	2.335
220894_x_at	*PRDM12*	4.135	3.585	3.555
1563165_at	*LOC152845*	2.915	2.515	2.515
230107_at	*HM13*	2.72	2.34	2.35
1554037_a_at	*ZBTB24*	3.35	2.87	2.91
204179_at	*MB*	2.63	2.27	2.27
217802_s_at	*NUCKS1*	14.295	12.335	12.345
205800_at	*SLC3A1*	2.94	2.54	2.54
1553402_a_at	*HFE*	4.07	3.5	3.52
212327_at	*DKFZP686A01247*	10.52	9.17	8.99

233174_at	*NA*	3.115	2.685	2.705
232951_at	*CMTM7*	4.585	3.945	3.975
213682_at	*NUP50*	11.68	10.11	10.06
240328_at	*GNAO1*	2.585	2.225	2.235
241159_x_at	*ITFG1*	4.415	3.835	3.795
222187_x_at	*G3BP1*	3.42	2.96	2.95
214495_at	*CACNG2*	2.555	2.215	2.205
237218_at	*CCBL2*	2.79	2.41	2.41
1553462_at	*NA*	3.865	3.345	3.335
224936_at	*EIF2S3*	12.32	10.74	10.54
209078_s_at	*TXN2*	2.555	2.215	2.215
217557_s_at	*CPM*	3.73	3.25	3.2
209074_s_at	*FAM107A*	2.92	2.52	2.52
200630_x_at	*SET*	11.755	10.195	10.115
244095_at	*NA*	3.355	2.905	2.895
1559956_at	*SYT7*	3.69	3.2	3.18
239475_at	*ACPL2*	2.9	2.51	2.5
226038_at	*LONRF1*	8.37	7.27	7.19
219890_at	*CLEC5A*	2.535	2.195	2.195
214451_at	*TFAP2B*	3.23	2.8	2.78
242993_at	*PCK2*	3.27	2.82	2.84
236962_at	*PTBP2*	3.05	2.64	2.63
1557094_at	*NA*	3.595	3.125	3.095
229546_at	*FAM84A*	3.275	2.825	2.835
242873_at	*KLRK1*	2.77	2.39	2.39
203832_at	*SNRPF*	8.025	6.915	6.965
208458_at	*SCNN1D*	2.715	2.355	2.345
237977_at	*NA*	4.225	3.675	3.625
224073_at	*FLJ20464*	2.785	2.415	2.405
232097_at	*KIAA0737*	8.32	7.13	7.26
236223_s_at	*RIT1*	10.495	8.995	9.155

231850_x_at	*KIAA1712*	7.8	6.81	6.68
239382_at	*HPS1*	2.95	2.55	2.55
1554864_a_at	*SDC3*	2.735	2.375	2.365
230160_x_at	*DRAP1*	3.87	3.37	3.33
204579_at	*FGFR4*	3.11	2.7	2.68
233016_at	*NA*	3.15	2.74	2.71
238322_s_at	*TEAD2*	3.11	2.7	2.68
1560963_a_at	*NA*	2.85	2.48	2.46
1561850_at	*MGC15613*	2.69	2.33	2.32
209604_s_at	*GATA3*	2.655	2.285	2.305
232740_at	*MCM3APAS*	3.01	2.6	2.61
238723_at	*ATXN3*	4.92	4.27	4.25
233836_at	*TNRC6A*	2.8	2.42	2.42
1559029_at	*LOC286154*	2.96	2.56	2.56
1552927_at	*MAP3K7IP3*	3.73	3.25	3.21
200593_s_at	*HNRPU*	10.99	9.55	9.48
203425_s_at	*IGFBP5*	3.58	3.12	3.08
1561546_at	*NA*	3.065	2.655	2.645
1564074_at	*NA*	2.68	2.32	2.32
227504_s_at	*KIAA1276*	4.265	3.715	3.665
229701_at	*DNAJC9*	3.12	2.7	2.7
1569208_a_at	*DKFZP686A01247*	3.945	3.445	3.395
215238_s_at	*DOCK9*	2.8	2.43	2.41
1569668_at	*NA*	3.005	2.595	2.605
238127_at	*FLJ41484*	3.975	3.415	3.465
237262_at	*NA*	2.55	2.21	2.21
206372_at	*MYF6*	2.7	2.34	2.34
231101_at	*PPP2R5E*	10.555	9.205	9.065
208400_at	*GLP1R*	3.455	3.005	2.975
232631_at	*CDH6*	2.49	2.15	2.15
210185_at	*CACNB1*	3.69	3.2	3.19

237144_at	*LTBP3*	3.78	3.29	3.26
202711_at	*EFNB1*	2.84	2.46	2.46
1564385_at	*LOC219688*	2.93	2.54	2.53
229413_s_at	*PCGF3*	4.5	3.9	3.9
1568600_at	*CALML4*	2.89	2.53	2.48
208808_s_at	*HMGB2*	13.065	11.365	11.285
237988_at	*EIF1B*	3.345	2.915	2.885
212202_s_at	*TMEM87A*	11.345	9.845	9.815
221295_at	*CIDEA*	2.55	2.21	2.21
221871_s_at	*TFG*	10.34	8.89	9.03
205153_s_at	*CD40*	2.41	2.09	2.09
201405_s_at	*COPS6*	10.715	9.215	9.365
217530_at	*SLC34A1*	3.29	2.84	2.86
229301_at	*TUG1*	3.45	2.99	2.99
243711_at	*DDAH1*	3.6	3.13	3.11
237045_at	*FAM91A1*	5.73	4.95	4.99
233031_at	*ZEB2*	3.035	2.635	2.635
225799_at	*LOC541471*	10.53	9.05	9.21
204581_at	*CD22*	3.045	2.645	2.635
216284_at	*NA*	2.89	2.51	2.51
1558409_at	*IMMP2L*	3.195	2.795	2.745
215205_x_at	*NCOR2*	3.33	2.89	2.89
243448_at	*NA*	3.205	2.795	2.765
226944_at	*HTRA3*	6.18	5.4	5.32
234345_at	*NA*	2.89	2.51	2.51
230490_x_at	*RSU1*	12.285	10.655	10.645
1552509_a_at	*CD300LG*	2.585	2.245	2.245
240628_at	*CADM1*	2.755	2.375	2.415
207650_x_at	*PTGER1*	2.89	2.49	2.53
236605_at	*EIF3S12*	3.255	2.825	2.815
236235_at	*ITCH*	10.185	8.845	8.815

242982_x_at	*ITGB8*	2.825	2.445	2.445
1555034_at	*CLRN1*	3.01	2.61	2.61
1558889_at	*TTC28*	2.505	2.165	2.175
1553199_at	*WDR21C*	3.825	3.335	3.305
214431_at	*GMPS*	9.855	8.515	8.585
239213_at	*SERPINB1*	2.515	2.185	2.175
1561607_at	*NA*	2.75	2.39	2.39
219591_at	*CEND1*	2.72	2.36	2.36
216695_s_at	*TNKS*	2.91	2.53	2.52
226576_at	*ARHGAP26*	2.82	2.45	2.43
226304_at	*HSPB6*	3.165	2.745	2.745
213146_at	*JMJD3*	3.515	3.055	3.045
243119_at	*NUFIP2*	3.13	2.71	2.71
214282_at	*CP*	3.16	2.75	2.73
1554133_at	*RUFY2*	3.745	3.275	3.225
1560101_at	*SYDE2*	4.06	3.49	3.55
236062_at	*UBE2E1*	3.21	2.77	2.81
208557_at	*HOXA6*	3.28	2.85	2.84
204408_at	*APEX2*	3.275	2.835	2.845
1558956_s_at	*IFT80*	12.865	11.255	11.075
213965_s_at	*CHD5*	3.085	2.685	2.675
216770_at	*NA*	3.8	3.31	3.29
233355_at	*PRR17*	3.21	2.79	2.79
232041_at	*INADL*	2.43	2.11	2.11
237733_at	*RP11-125A7.3*	3.295	2.865	2.855
214170_x_at	*FH*	10.435	9.055	9.055
216981_x_at	*SPN*	2.47	2.15	2.14
212017_at	*LOC130074*	11.825	10.335	10.205
215279_at	*SVIL*	2.39	2.07	2.07
239979_at	*EPSTI1*	2.835	2.465	2.455
206540_at	*GLB1L*	3.35	2.92	2.9

217459_at	*NA*	2.8	2.44	2.43
203918_at	*PCDH1*	6.235	5.455	5.375
201785_at	*RNASE1*	2.865	2.485	2.485
1553957_at	*ZNF564*	6.965	6.005	6.095
1570372_at	*NA*	3.35	2.92	2.9
234096_at	*PACRG*	3.105	2.705	2.705
241359_at	*NA*	7.63	6.63	6.63
1553257_at	*GAL3ST3*	2.84	2.47	2.46
1557402_at	*NA*	2.85	2.48	2.46
244018_at	*SLC2A9*	2.985	2.575	2.605
1562396_at	*PP8961*	3.66	3.18	3.18
240792_at	*NCOR2*	2.885	2.505	2.505
239924_at	*LOC91316*	3.35	2.92	2.9
223779_at	*MGC10981*	2.565	2.235	2.225
209927_s_at	*C1orf77*	6.88	5.97	5.99
1557132_at	*WDR17*	3.325	2.915	2.865
203473_at	*SLCO2B1*	2.31	2.01	2.01
215165_x_at	*UMPS*	8.43	7.37	7.29
220457_at	*SAMD4B*	2.685	2.335	2.325
207561_s_at	*ACCN3*	2.75	2.39	2.39
227447_at	*SKIV2L2*	9.35	8.18	8.08
205517_at	*GATA4*	3.105	2.715	2.695
208912_s_at	*CNP*	9.985	8.745	8.615
231872_at	*LRRCC1*	3	2.61	2.6
225005_at	*PHF13*	9.48	8.17	8.31
207291_at	*PRRG4*	2.965	2.585	2.575
226844_at	*MOBKL2B*	2.6	2.27	2.25
1553906_s_at	*FGD2*	3.23	2.82	2.8
1561732_at	*NA*	3.47	3.02	3
241066_at	*ZNF449*	3.495	3.045	3.025
244637_at	*NA*	2.865	2.505	2.475

228030_at	*RBM6*	12.81	11.1	11.19
237069_s_at	*TRPM1*	2.685	2.335	2.345
220210_at	*CHRNA10*	2.705	2.355	2.345
240767_x_at	*VPS13A*	2.81	2.46	2.44
224694_at	*ANTXR1*	14.05	12.15	12.31
224748_at	*WDR68*	9.42	8.23	8.17
228219_s_at	*UPB1*	3.44	3.02	2.97
242247_at	*METT5D1*	4	3.47	3.49
206750_at	*MAFK*	2.565	2.225	2.225
217615_at	*LRRC37A*	2.725	2.355	2.385
240821_at	*NA*	3.6	3.15	3.13
234637_at	*KRTAP4-5*	2.665	2.335	2.315
243306_s_at	*GCC1*	3.26	2.85	2.83
1562446_at	*RP1-153G14.3*	2.8	2.44	2.44
215026_x_at	*SCNN1A*	5.23	4.55	4.55
209977_at	*PLG*	2.83	2.47	2.46
1570594_at	*TMEM45B*	3.125	2.735	2.705
1565915_at	*ZC3HAV1*	3.315	2.885	2.895
242845_at	*NA*	3.1	2.71	2.7
1556636_at	*NA*	3.355	2.925	2.915
226472_at	*PPIL4*	8.285	7.185	7.255
215917_at	*SNPH*	3.25	2.85	2.81
202029_x_at	*RPL38*	14.04	12.13	12.35
218688_at	*DAK*	2.83	2.47	2.46
228122_at	*CCDC66*	5.01	4.37	4.37
1562010_x_at	*NA*	4.65	4.08	4.02
242494_at	*PLCB1*	2.965	2.585	2.585
201657_at	*ARL1*	9.5	8.24	8.32
230839_at	*PRMT8*	2.445	2.145	2.115
1554171_at	*ZMYM3*	10.375	8.965	9.115
214638_s_at	*CCNT2*	5.33	4.68	4.62

1556175_at	*ABBA-1*	2.715	2.365	2.375
242427_at	*WAC*	3.625	3.165	3.155
235514_at	*SASP*	2.55	2.23	2.22
217509_x_at	*GRIK5*	5.985	5.255	5.185
218050_at	*UFM1*	13.795	11.985	12.045
208953_at	*LARP5*	8.695	7.575	7.575
228673_s_at	*EML4*	2.83	2.47	2.47
201602_s_at	*PPP1R12A*	8.055	7.015	7.025
232084_at	*SGTB*	3.055	2.665	2.655
207239_s_at	*PCTK1*	2.905	2.525	2.535
227064_at	*ANKRD40*	11.465	10.065	9.935
216084_at	*C9orf144*	3.055	2.665	2.655
215924_at	*DBC1*	3.12	2.73	2.71
217416_x_at	*NA*	3.25	2.83	2.83
213966_at	*HMG20B*	3.15	2.74	2.76
208450_at	*LGALS2*	2.595	2.265	2.255
205062_x_at	*ARID4A*	7.725	6.795	6.685
223802_s_at	*RBBP6*	5.695	4.965	4.975
229747_x_at	*MGC40489*	2.31	2.01	2.01
201775_s_at	*ATPAF1*	4.785	4.145	4.195
243246_at	*NAT12*	2.465	2.145	2.145
230315_at	*KLF3*	2.77	2.41	2.41
219359_at	*ATHL1*	4.37	3.79	3.83
228687_at	*ZNF777*	2.51	2.19	2.19
218646_at	*C4orf27*	11.63	10.13	10.17
242513_x_at	*KIAA2018*	3.255	2.835	2.835
221117_at	*NA*	2.98	2.6	2.6
228519_x_at	*CIRBP*	7.175	6.225	6.295
1561073_at	*TRPS1*	3.96	3.46	3.46
202276_at	*SHFM1*	11.96	10.4	10.47
179_at	*PMS2L11*	2.135	1.855	1.865

204293_at	*SGSH*	5.63	4.91	4.91
217662_x_at	*BCAP29*	9.835	8.605	8.555
242125_at	*CAPZA1*	2.72	2.38	2.38
232040_at	*LOC157860*	2.98	2.6	2.6
210063_at	*SARDH*	3.11	2.73	2.7
205901_at	*PNOC*	2.53	2.21	2.21
241718_x_at	*KIAA0947*	5.005	4.385	4.355
211304_x_at	*KCNJ5*	4.84	4.22	4.23
220266_s_at	*KLF4*	2.885	2.535	2.505
214243_s_at	*SERHL2*	2.675	2.345	2.325
1562433_at	*FLJ10489*	2.585	2.265	2.255
230061_at	*TM4SF18*	3.075	2.685	2.675
203168_at	*CREBL1*	3.68	3.22	3.21
1553397_at	*CCDC13*	3.805	3.325	3.315
1562955_at	*WDFY1*	2.62	2.29	2.27
230071_at	*11-Sep*	12.415	10.925	10.755
234169_at	*NA*	3.63	3.18	3.16
215807_s_at	*PLXNB1*	2.495	2.175	2.175
242454_at	*AMBP*	3.095	2.695	2.695
1555704_at	*CMTM3*	3.11	2.71	2.72
215244_at	*DGCR5*	2.56	2.24	2.24
227026_at	*HSMPP8*	9.235	8.135	7.985
1570345_at	*C9orf27*	3.775	3.315	3.275
211054_at	*INVS*	3.58	3.15	3.1
232608_x_at	*CARD14*	3.245	2.835	2.825
1558820_a_at	*C18orf34*	2.33	2.03	2.04
1553872_at	*MGC33894*	5.08	4.45	4.42
1561937_x_at	*NA*	2.37	2.07	2.07
206778_at	*CRYBB2*	2.475	2.165	2.155
1559591_s_at	*CHDH*	3.615	3.155	3.165
205409_at	*FOSL2*	2.58	2.26	2.25

241097_at	*RHOA*	3.13	2.74	2.72
232414_at	*LGALS8*	2.735	2.395	2.395
238701_x_at	*FLJ45803*	10.115	8.775	8.895
240595_at	*NA*	4.88	4.28	4.24
1561132_at	*DHX35*	2.68	2.34	2.34
238489_at	*NA*	3.355	2.955	2.915
1557452_at	*SSBP2*	2.72	2.38	2.38
216301_at	*NA*	3.125	2.715	2.745
237599_at	*ZNF30*	2.66	2.32	2.32
1556256_a_at	*APPBP1*	3.34	2.93	2.91
216160_at	*NA*	2.775	2.435	2.425
243114_at	*LOC648708*	2.57	2.25	2.25
1565746_at	*ZNF724P*	3.005	2.635	2.625
203209_at	*RFC5*	5.755	5.005	5.055
218792_s_at	*BSPRY*	2.7	2.36	2.36
241835_at	*NA*	3.235	2.855	2.815
228648_at	*LRG1*	2.99	2.62	2.6
222184_at	*NA*	4.395	3.845	3.835
1565911_at	*NA*	3.395	2.975	2.975
207585_s_at	*RPL36AL*	12.535	10.875	11.045
234347_s_at	*DENR*	2.52	2.2	2.21
243405_at	*TXNDC5*	8.635	7.515	7.585
1556938_a_at	*DYNLL1*	3.145	2.755	2.735
237889_s_at	*LOC553137*	2.57	2.25	2.25
1554873_at	*CSPP1*	3.47	3.05	3.01
226703_at	*KIAA1787*	3.005	2.635	2.615
223426_s_at	*EPB41L4B*	2.85	2.49	2.49
1556502_at	*RP11-151A6.2*	3.465	3.055	3.005
243971_x_at	*LOC731789*	2.605	2.285	2.275
234879_at	*NA*	2.615	2.285	2.295
232560_at	*UROS*	2.55	2.23	2.23

1560596_at	*GFPT1*	2.615	2.295	2.285
243958_at	*NA*	3.57	3.11	3.14
230035_at	*BOC*	5.045	4.415	4.405
230452_at	*FLJ42351*	2.605	2.295	2.265
228831_s_at	*GNG7*	4.075	3.555	3.585
228019_s_at	*MRPS18C*	8.15	7.1	7.17
240893_at	*FLJ22662*	2.7	2.36	2.36
230113_at	*NA*	3.18	2.79	2.77
218263_s_at	*ZBED5*	11.195	9.765	9.825
242537_at	*ZMYND8*	3.18	2.79	2.78
1562456_at	*NA*	2.745	2.405	2.405
228204_at	*PSMB4*	13.965	12.285	12.165
1562935_at	*NA*	2.89	2.54	2.52
1557569_at	*MPDU1*	3.295	2.885	2.875
211497_x_at	*NKX3-1*	2.535	2.225	2.205
206614_at	*GDF5*	4.905	4.275	4.305
225187_at	*KIAA1967*	4.545	3.985	3.975
223750_s_at	*TLR10*	3.065	2.695	2.665
222161_at	*NAALAD2*	3.17	2.78	2.77
244471_x_at	*PANX2*	2.505	2.185	2.185
1563120_at	*NA*	2.775	2.435	2.425
208944_at	*TGFBR2*	12.125	10.665	10.575
233374_at	*HIC2*	3.07	2.7	2.68
232088_x_at	*NA*	3.675	3.205	3.235
222376_at	*NA*	2.56	2.25	2.23
210135_s_at	*SHOX2*	10.815	9.505	9.445
220878_at	*NA*	2.75	2.41	2.41
205150_s_at	*KIAA0644*	2.88	2.52	2.52
237556_at	*LOC728804*	3.825	3.355	3.335
1560477_a_at	*SAMD11*	2.22	1.94	1.94
1554834_a_at	*RASSF5*	2.505	2.195	2.185

203248_at	*ZNF24*	3.265	2.865	2.855
207221_at	*F2RL3*	2.605	2.285	2.285
222219_s_at	*TLE6*	2.93	2.57	2.57
221225_at	*DCAKD*	3.475	3.035	3.045
1560974_s_at	*NOS1*	2.685	2.365	2.335
241605_at	*TRUB1*	3.1	2.72	2.71
224458_at	*C9orf125*	6.44	5.68	5.6
226054_at	*BRD4*	9.48	8.26	8.34
213511_s_at	*MTMR1*	8.89	7.75	7.83
230712_at	*NBPF1*	8.98	7.86	7.87
1554131_at	*KIAA1128*	3.815	3.325	3.355
212380_at	*KIAA0082*	3.34	2.91	2.93
203418_at	*CCNA2*	2.59	2.27	2.27
241671_x_at	*FLJ22536*	3.45	3.05	3
1557595_at	*GINS2*	6.585	5.755	5.775
207095_at	*SLC10A2*	2.965	2.585	2.625
1562392_at	*MRPL23*	2.54	2.23	2.22
237835_at	*NA*	2.975	2.625	2.605
213350_at	*RPS11*	15.945	13.895	14.045
229840_at	*IQSEC2*	4.265	3.765	3.715
212821_at	*SPTB*	2.805	2.465	2.465
1559915_at	*NA*	3.37	2.95	2.96
1557136_at	*ATP13A4*	3.315	2.925	2.895
242256_x_at	*NA*	3.955	3.495	3.445
1561221_x_at	*ZDHHC20*	2.525	2.205	2.205
241925_x_at	*NA*	2.97	2.61	2.61
239350_at	*MARVELD3*	2.705	2.365	2.375
1553094_at	*TAC4*	2.94	2.58	2.57
1552427_at	*ZNF485*	4.25	3.74	3.71
201614_s_at	*RUVBL1*	6.84	6.05	5.95
233152_x_at	*TNKS*	3.94	3.46	3.46

224570_s_at	*IRF2BP2*	12.455	10.825	11.005
237844_at	*LOC644010*	2.855	2.505	2.495
233532_x_at	*IFT52*	2.97	2.6	2.62
215574_at	*NA*	2.95	2.59	2.59
237726_at	*PLA2G6*	5.295	4.645	4.635
211396_at	*FCGR2C*	2.895	2.535	2.535
226959_at	*CAMK1D*	2.94	2.57	2.59
205124_at	*MEF2B*	2.725	2.385	2.385
216186_at	*C1orf21*	2.6	2.28	2.28
238639_x_at	*NA*	3.9	3.39	3.45
229625_at	*GBP5*	2.895	2.525	2.545
212333_at	*FAM98A*	12.71	11.22	11.08
230318_at	*SERPINA1*	2.375	2.075	2.075
1569600_at	*DLEU2*	3.515	3.105	3.055
235265_at	*ZNF650*	2.495	2.195	2.185
221685_s_at	*CCDC99*	10.94	9.55	9.65
225784_s_at	*KIAA1166*	2.565	2.245	2.245
240124_at	*NA*	2.63	2.31	2.31
234661_at	*CCDC57*	2.25	1.97	1.97
226238_at	*MCEE*	5.415	4.755	4.755
240676_at	*NA*	3.6	3.14	3.18
219067_s_at	*NSMCE4A*	7.51	6.61	6.57
236082_at	*PHLDB3*	2.715	2.385	2.375
204328_at	*TMC6*	2.515	2.225	2.195
1554285_at	*HAVCR2*	2.82	2.49	2.47
211473_s_at	*COL4A6*	2.555	2.235	2.245
221858_at	*TBC1D12*	10.15	8.98	8.85
205986_at	*AATK*	5.53	4.82	4.88
213160_at	*DOCK2*	5.15	4.55	4.5
230125_at	*GUSB*	3.33	2.94	2.92
240333_at	*NA*	2.77	2.43	2.43

228163_at	*ST6GALNAC4*	2.69	2.38	2.36
224198_at	*ELA1*	2.365	2.085	2.075
206179_s_at	*TPPP*	2.895	2.545	2.535
214141_x_at	*SFRS7*	9.615	8.505	8.395
1556650_at	*AUTS2*	3.11	2.73	2.73
1560987_a_at	*NA*	3.385	2.975	2.965
233053_at	*PB1*	5.78	5.08	5.08
209371_s_at	*SH3BP2*	2.425	2.125	2.125
209800_at	*KRT16*	2.705	2.385	2.375
202624_s_at	*CABIN1*	2.575	2.265	2.255
201949_x_at	*CAPZB*	12.98	11.35	11.45
1553398_at	*NA*	2.765	2.425	2.425
208354_s_at	*SLC12A3*	2.32	2.04	2.04
230667_at	*NA*	3.055	2.675	2.685
219188_s_at	*LRP16*	4.1	3.61	3.59
89476_r_at	*NPEPL1*	6.655	5.875	5.825
230990_at	*KIF13A*	2.33	2.05	2.05
223996_s_at	*MRPL30*	5.645	4.945	4.985
201133_s_at	*PJA2*	12.56	11.1	10.98
209612_s_at	*ADH1B*	2.7	2.37	2.38
231994_at	*CHDH*	3.29	2.88	2.9
202848_s_at	*GRK6*	2.8	2.46	2.46
219870_at	*ATF7IP2*	3.295	2.895	2.895
229687_s_at	*NA*	3.5	3.08	3.08
233063_s_at	*NA*	2.885	2.545	2.535
1558533_at	*KRBA2*	2.34	2.06	2.06
215609_at	*STARD7*	6.185	5.435	5.445
227911_at	*ARHGAP28*	2.81	2.47	2.47
37012_at	*CAPZB*	12.455	10.975	10.925
1562886_at	*NA*	3.37	2.98	2.95
1558620_at	*ZNF621*	7.79	6.8	6.9

224418_x_at	*PMCHL1*	2.385	2.105	2.105
215555_at	*C1orf63*	3.175	2.805	2.785
217762_s_at	*RAB31*	14.39	12.73	12.57
239685_at	*LOC283143*	2.755	2.415	2.415
236317_at	*SETBP1*	2.795	2.475	2.445
242423_x_at	*NA*	2.925	2.565	2.575
205952_at	*KCNK3*	2.725	2.405	2.395
215757_at	*PRKDC*	3.395	2.995	2.985
243594_x_at	*SPIRE2*	3.455	3.045	3.035
1570048_at	*DPH4*	3.2	2.8	2.84
211305_x_at	*FCAR*	2.855	2.515	2.515
204394_at	*SLC43A1*	2.695	2.375	2.375
229571_at	*CALM2*	5.185	4.535	4.585
229602_at	*NA*	5.595	4.905	4.935
240127_at	*FAM92A1*	3.105	2.745	2.715
224276_at	*ZNF33A*	2.84	2.5	2.5
235088_at	*LOC201725*	7.2	6.38	6.29
236522_at	*NFIA*	2.64	2.33	2.31
1552917_at	*IL29*	2.52	2.22	2.22
224425_x_at	*LOC440888*	2.64	2.32	2.32
216384_x_at	*LOC643287*	9.755	8.585	8.575
215773_x_at	*PARP2*	5.17	4.53	4.57
223921_s_at	*GBA2*	2.99	2.63	2.64
217341_at	*DNM1*	3.065	2.705	2.695
227647_at	*KCNE3*	2.775	2.435	2.435
243705_at	*DDHD1*	3.265	2.895	2.845
1556365_at	*RP3-398D13.1*	2.595	2.275	2.285
241945_at	*ALS2CR13*	3.19	2.81	2.81
227660_at	*ANTXR1*	8.03	7.06	7.07
1565856_at	*NA*	3.15	2.79	2.76
235991_at	*LOC606495*	3.285	2.895	2.875

240379_at	*PKP4*	2.7	2.38	2.38
236845_at	*TRIM62*	2.99	2.63	2.63
236709_at	*NA*	2.82	2.48	2.48
214197_s_at	*SETDB1*	3.355	2.975	2.935
239147_at	*ARSK*	6.425	5.655	5.665
239333_x_at	*NA*	7.585	6.715	6.645
217287_s_at	*TRPC6*	2.545	2.245	2.245
1553234_at	*ADAMTS18*	3.04	2.69	2.66
224433_s_at	*DDX54*	4.465	3.925	3.925
221155_x_at	*NA*	3.645	3.195	3.225
1562582_at	*LOC646405*	3.58	3.18	3.13
243288_at	*SMYD2*	2.82	2.49	2.48
217177_s_at	*NA*	3.115	2.745	2.735
207927_at	*HTR7*	3.595	3.175	3.165
211225_at	*FUT5*	5.07	4.47	4.47
1555748_x_at	*CD79B*	2.955	2.605	2.595
216390_at	*LCAT*	2.285	2.005	2.005
231084_at	*C10orf79*	2.985	2.635	2.625
1554683_a_at	*MGC50722*	3.145	2.765	2.765
223814_at	*TRNT1*	6.285	5.585	5.505
220353_at	*FAM86C*	2.69	2.37	2.37
1553352_x_at	*ERVWE1*	2.98	2.62	2.63
225717_at	*KIAA1715*	8.995	7.925	7.935
215855_s_at	*TMF1*	3.69	3.26	3.24
239844_x_at	*MGC33556*	3.075	2.725	2.695
215109_at	*RC3H1*	3.135	2.755	2.765
1570130_at	*SPATS2*	3.16	2.79	2.78
1560353_at	*FOXP1*	2.965	2.615	2.595
1566096_x_at	*ARHGEF12*	4.08	3.63	3.57
232681_at	*NA*	6.96	6.13	6.14
242350_s_at	*ST8SIA6*	2.795	2.465	2.455

230118_at	*NA*	2.64	2.32	2.33
240023_at	*NA*	2.425	2.135	2.145
232016_at	*MTMR15*	3.425	3.025	3.025
241947_at	*FAM113B*	2.765	2.445	2.435
244639_at	*TMBIM4*	3.425	3.035	3.015
208201_at	*DUX2*	2.84	2.51	2.5
222097_at	*MZF1*	2.925	2.595	2.575
232359_at	*RDH11*	3.5	3.1	3.07
200780_x_at	*GNAS*	13.32	11.68	11.81
226846_at	*PHYHD1*	3.56	3.12	3.16
216883_x_at	*PDE6D*	4.165	3.645	3.695
220967_s_at	*ZNF696*	3.35	2.93	2.97
225466_at	*FLJ36874*	7.885	6.945	6.955
237309_at	*FBXO4*	3.55	3.12	3.14
1569592_a_at	*F11*	3.415	3.035	2.995
219562_at	*RAB26*	2.435	2.155	2.155
234350_at	*NA*	3.72	3.29	3.27
237874_at	*RNF150*	3.015	2.665	2.655
1555844_s_at	*HNRPM*	14.77	13.07	12.99
234584_s_at	*ATE1*	5.9	5.16	5.24
230654_at	*NA*	3.2	2.83	2.81
239604_at	*RBMS3*	3.04	2.68	2.68
219472_at	*CENPO*	3.79	3.34	3.36
243758_at	*CCDC37*	3.315	2.935	2.905
221032_s_at	*TMPRSS5*	2.745	2.425	2.425
206781_at	*DNAJC4*	3.41	3.02	3
230921_s_at	*NA*	9.1	7.97	8.08
243825_at	*NA*	4.56	4.02	4.02
209359_x_at	*RUNX1*	4.295	3.795	3.795
236409_at	*LYPLAL1*	2.835	2.505	2.495
1563867_at	*LOC283194*	2.455	2.175	2.165

207127_s_at	*HNRPH3*	12.05	10.56	10.7
239312_at	*NA*	2.89	2.57	2.53
220464_at	*MCF2L*	3.38	2.99	2.97
209079_x_at	*PCDHGA1*	8.225	7.285	7.235
212652_s_at	*SNX4*	9.5	8.32	8.44
228588_s_at	*UBE2B*	13.525	11.915	11.965
1559149_at	*NA*	2.77	2.45	2.45
212981_s_at	*KIAA0738*	13.3	11.65	11.83
1553809_a_at	*C9orf71*	2.615	2.325	2.295
231575_at	*EGR4*	2.645	2.335	2.325
227680_at	*ZNF326*	10.2	8.98	9.03
1561240_at	*NA*	3.41	3.01	3.01
201603_at	*PPP1R12A*	13.925	12.245	12.335
204467_s_at	*SNCA*	3.42	3.02	3.02
227950_at	*UBE2H*	2.55	2.26	2.24
224778_s_at	*NA*	12.925	11.315	11.495
230324_at	*NCOA2*	3.655	3.215	3.245
213584_s_at	*CREBZF*	2.88	2.53	2.55
231797_at	*SIX4*	3.125	2.775	2.745
202294_at	*STAG1*	8.935	7.845	7.945
200981_x_at	*GNAS*	13.06	11.48	11.59
1561190_at	*CDKL3*	3.905	3.475	3.425
222684_s_at	*NOL10*	6.44	5.66	5.71
1555468_at	*NRP2*	2.945	2.605	2.605
226002_at	*GAB1*	3.225	2.865	2.825
241913_at	*KLHL8*	3.1	2.74	2.74
1560803_at	*DNAH3*	2.78	2.47	2.44
205849_s_at	*UQCRB*	12.87	11.46	11.28
1553229_at	*ZNF572*	2.89	2.55	2.55
242119_at	*PROX1*	2.465	2.175	2.185
212237_at	*ASXL1*	8.875	7.885	7.795

213402_at	*ZNF787*	2.68	2.35	2.38
243811_at	*NA*	3.155	2.815	2.775
207257_at	*EPO*	3.145	2.785	2.775
230556_at	*IMMP1L*	3.32	2.95	2.93
1553857_at	*IGSF22*	3.565	3.145	3.145
238460_at	*FAM83A*	2.815	2.485	2.495
1555429_at	*NA*	2.7	2.38	2.38
202820_at	*AHR*	9.405	8.365	8.245
237707_at	*FLJ20105*	2.375	2.095	2.095
214309_s_at	*C21orf2*	2.155	1.895	1.905
213236_at	*SASH1*	6.945	6.175	6.115
1552377_s_at	*FAM18B2*	3.165	2.805	2.795
236587_at	*NA*	3.29	2.92	2.9
1553499_s_at	*SERPINA9*	3.58	3.16	3.16
216142_at	*CALML4*	3.905	3.465	3.435
212636_at	*QKI*	12.185	10.845	10.695
211858_x_at	*GNAS*	12.465	11.025	11.015
242420_at	*PPP1R9A*	3.16	2.81	2.78
1556672_a_at	*RBM6*	3.035	2.685	2.675
207470_at	*DKFZp566H0824*	2.78	2.46	2.46
1563894_at	*LOC441178*	2.335	2.065	2.055
224566_at	*TncRNA*	13.375	11.725	11.915
235540_at	*GNRH1*	2.59	2.29	2.29
225775_at	*TSPAN33*	3.045	2.685	2.685
219748_at	*TREML2*	2.405	2.125	2.125
218600_at	*LIMD2*	2.845	2.525	2.515
237135_at	*NA*	2.735	2.415	2.415
217264_s_at	*SCNN1A*	8.08	7.16	7.12
236784_s_at	*APTX*	3.035	2.695	2.665
203269_at	*NSMAF*	12.455	11.105	10.925
1555894_s_at	*ABBA-1*	2.985	2.645	2.645

213719_s_at	*SMARCA4*	2.615	2.325	2.305
219769_at	*INCENP*	2.365	2.085	2.085
201069_at	*MMP2*	11.35	10.07	10
203517_at	*MTX2*	8.015	7.045	7.135
237554_at	*ACVR1*	3.205	2.815	2.845
212317_at	*TNPO3*	9.945	8.845	8.735
1552455_at	*PRUNE2*	2.745	2.435	2.425
244848_at	*CHD1L*	3.005	2.665	2.655
216894_x_at	*CDKN1C*	2.76	2.44	2.44
235524_at	*GARNL1*	2.605	2.305	2.305
242994_at	*NRD1*	2.545	2.255	2.245
204252_at	*CDK2*	7.17	6.32	6.37
231328_s_at	*FAM98C*	2.675	2.375	2.365
208888_s_at	*NCOR2*	2.43	2.15	2.15
207115_x_at	*MBTD1*	3.47	3.08	3.06
242315_at	*XYLT1*	2.735	2.425	2.415
1554940_a_at	*LOC388882*	2.465	2.185	2.185
216828_at	*NA*	2.97	2.62	2.63
230216_at	*C12orf51*	2.475	2.195	2.195
1562772_a_at	*DAND5*	3.24	2.86	2.87
233745_at	*PTOV1*	2.725	2.415	2.395
228199_at	*LOC729234*	2.665	2.375	2.355
203118_at	*PCSK7*	8.105	7.195	7.145
1563210_at	*ERBB2IP*	3.44	3.06	3.02
225302_at	*TXNDC10*	11.78	10.35	10.5
1560940_at	*NA*	3.605	3.215	3.165
209529_at	*PPAP2C*	2.325	2.065	2.065
243430_at	*SEZ6*	3.055	2.705	2.695
1561919_at	*C14orf101*	3.26	2.9	2.86
211704_s_at	*SPIN2B*	6.09	5.4	5.38
1564802_at	*NA*	3.055	2.705	2.695

212876_at	*B4GALT4*	10.405	9.265	9.155
212603_at	*MRPS31*	9.94	8.78	8.82
1556125_at	*GPATCH2*	2.675	2.375	2.375
240727_s_at	*NA*	3.12	2.76	2.76
240705_at	*CYP19A1*	3.145	2.805	2.765
206731_at	*CNKSR2*	2.825	2.505	2.495
232260_at	*NA*	2.79	2.46	2.48
202524_s_at	*SPOCK2*	2.535	2.245	2.235
215626_at	*DOCK9*	3.17	2.81	2.8
211894_x_at	*SEZ6L*	2.45	2.17	2.17
212273_x_at	*GNAS*	13.13	11.6	11.65
238522_at	*USP54*	2.565	2.275	2.265
208753_s_at	*NAP1L1*	11.985	10.555	10.665
201386_s_at	*DHX15*	10.475	9.245	9.305
230628_at	*EP400*	2.77	2.46	2.45
207517_at	*LAMC2*	3.31	2.95	2.91
229118_at	*NA*	2.81	2.5	2.48
216463_at	*NA*	3.345	2.985	2.945
234187_at	*NA*	2.425	2.145	2.145
1562944_at	*NA*	2.65	2.34	2.35
212125_at	*RANGAP1*	2.28	2.02	2.02
214190_x_at	*GGA2*	2.735	2.425	2.415
241095_at	*NA*	2.575	2.275	2.285
234881_at	*NA*	6.245	5.545	5.505
232990_at	*FAM104B*	3.285	2.905	2.915
211571_s_at	*VCAN*	8.2	7.26	7.26
1569796_s_at	*ATRNL1*	2.82	2.48	2.51
1553887_at	*FLJ40235*	2.645	2.345	2.345
227947_at	*PHACTR2*	12.225	10.805	10.845
224887_at	*GNPTG*	7.325	6.445	6.535
201496_x_at	*MYH11*	2.715	2.395	2.425

1553011_at	*TAF1L*	3.435	3.015	3.065
239611_at	*NPAS3*	2.63	2.33	2.33
242104_at	*NA*	3.17	2.81	2.81
213357_at	*GTF2H5*	9.745	8.675	8.605
202377_at	*LEPR*	11.855	10.445	10.575
214951_at	*SLC26A10*	2.585	2.295	2.285
228853_at	*STYX*	9.98	8.79	8.89
203034_s_at	*RPL27A*	12.12	10.67	10.81
202809_s_at	*INTS3*	8.5	7.48	7.59
208014_x_at	*AD7C-NTP*	2.64	2.34	2.34
239753_at	*LOC441383*	5.345	4.765	4.725
235646_at	*PIP5K1A*	2.795	2.475	2.475
237026_at	*SORBS1*	2.575	2.275	2.275
223965_at	*TRSPAP1*	2.81	2.5	2.48
244182_at	*NA*	5.855	5.175	5.215
219036_at	*CEP70*	3.23	2.85	2.88
207025_at	*GJA12*	3.25	2.89	2.88
209785_s_at	*PLA2G4C*	7.115	6.265	6.355
215486_at	*PRPS1L1*	3	2.68	2.65
213475_s_at	*ITGAL*	3	2.66	2.66
220500_s_at	*RABL2A*	3.38	3.01	2.98
204057_at	*IRF8*	3.33	2.95	2.95
234649_at	*POU2F1*	2.5	2.22	2.22
216043_x_at	*RAB11FIP3*	2.95	2.6	2.62
240285_at	*AQP2*	3.285	2.925	2.895
211837_s_at	*PTCRA*	2.84	2.52	2.52
202074_s_at	*OPTN*	10.78	9.57	9.55
200013_at	*RPL24*	13.905	12.365	12.295
1553793_a_at	*KIAA1109*	2.885	2.575	2.545
210548_at	*CCL23*	2.375	2.105	2.115
239454_at	*SCARF2*	2.775	2.465	2.455

227217_at	*WNK2*	2.575	2.285	2.275
227544_at	*C14orf83*	2.545	2.275	2.245
218155_x_at	*TSR1*	7.855	6.965	6.985
231631_at	*NA*	2.945	2.605	2.605
242858_at	*C14orf2*	2.8	2.48	2.48
213646_x_at	*TUBA1A*	12.475	11.105	11.035
1562449_s_at	*LARGE*	3.39	3.02	3
1561690_at	*SSBP2*	2.64	2.34	2.34
212633_at	*KIAA0776*	10.85	9.67	9.59
239850_at	*ZNF441*	2.8	2.48	2.49
229077_at	*KATNB1*	2.48	2.2	2.2
217898_at	*C15orf24*	11.91	10.64	10.5
240281_at	*RFT1*	2.48	2.2	2.2
232703_at	*GLUD1*	2.725	2.415	2.425
1559362_at	*KIAA0999*	2.965	2.635	2.625
233639_at	*POMGNT1*	2.735	2.435	2.425
206071_s_at	*EPHA3*	2.81	2.51	2.48
1557562_at	*GRIPAP1*	3.495	3.105	3.095
1553734_at	*AK7*	2.865	2.555	2.535
220980_s_at	*ADPGK*	9.05	8.05	8.01
234094_x_at	*DNAJA5*	3.535	3.155	3.115
228875_at	*C6orf189*	2.68	2.38	2.38
1552586_at	*TRPV3*	2.775	2.465	2.455
220336_s_at	*GP6*	3.125	2.775	2.765
234235_at	*NA*	2.945	2.615	2.605
230889_at	*LOC645321*	2.975	2.635	2.635
205458_at	*MC1R*	3	2.66	2.66
241073_at	*NA*	2.345	2.085	2.085
231107_at	*RSU1*	2.86	2.54	2.54
202729_s_at	*LTBP1*	13.615	12.025	12.155
1552889_a_at	*EXOC3L2*	4.65	4.15	4.11

208457_at	*GABRD*	2.185	1.945	1.945
222307_at	*LOC282997*	2.67	2.37	2.37
1552826_at	*SLC26A7*	3.165	2.815	2.795
230665_at	*NA*	2.67	2.37	2.37
202325_s_at	*ATP5J*	13.105	11.685	11.595
1559031_at	*EXOSC10*	2.75	2.45	2.44
244309_at	*LOC393076*	2.455	2.175	2.175
211066_x_at	*PCDHGC3*	8.96	7.99	7.92
226144_at	*REXO1*	2.395	2.125	2.135
1569339_s_at	*PAPLN*	3.2	2.83	2.86
232761_at	*COX4I2*	3.04	2.7	2.7
229979_x_at	*NA*	5.14	4.56	4.56
244717_x_at	*SV2B*	2.79	2.47	2.48
214031_s_at	*KRT7*	2.555	2.275	2.275
211493_x_at	*DTNA*	2.73	2.43	2.43
213188_s_at	*MINA*	9.765	8.655	8.705
210499_s_at	*PQBP1*	6.765	6.035	5.975
1559692_at	*NA*	2.795	2.485	2.475
1556099_at	*hCG_2025798*	3.175	2.825	2.815
1556136_at	*RP11-145H9.1*	3.165	2.805	2.805
238097_at	*FLJ41484*	3.315	2.955	2.945
241152_at	*NA*	3.62	3.24	3.2
227025_at	*PPHLN1*	2.815	2.505	2.495
1557476_at	*PFN4*	2.985	2.645	2.655
243966_at	*ZMYM5*	3.2	2.84	2.85
217347_at	*NA*	4.065	3.585	3.625
1552440_at	*ADMR*	3.475	3.105	3.085
1562414_at	*NA*	2.885	2.565	2.565
214296_x_at	*C19orf36*	3.855	3.435	3.425
228027_at	*GPRASP2*	10.205	9.115	9.025
203852_s_at	*SMN1*	9.085	8.095	8.065

222229_x_at	*hCG_26523*	9.655	8.635	8.515
211963_s_at	*ARPC5*	13.105	11.575	11.715
216387_x_at	*NA*	5.295	4.725	4.695
239938_x_at	*MEF2C*	3.61	3.22	3.19
226036_x_at	*CASP2*	3.035	2.715	2.675
238791_at	*ZNF100*	4.435	3.965	3.905
241366_at	*RBAK*	3.08	2.74	2.74
230070_at	*CNIH2*	2.39	2.13	2.13
202663_at	*WIPF1*	9.44	8.4	8.39
213467_at	*RND2*	2.83	2.52	2.51
244255_at	*LOC286114*	2.765	2.465	2.455
1570447_at	*FLJ44054*	2.775	2.465	2.475
1557651_x_at	*GALE*	4.57	4.04	4.09
200043_at	*ERH*	11.485	10.195	10.215
208984_x_at	*RBM10*	7.45	6.66	6.6
214889_at	*DKFZP564J102*	3.04	2.7	2.7
1570227_at	*COQ9*	3.035	2.695	2.705
202726_at	*LIG1*	2.51	2.24	2.22
217891_at	*C16orf58*	2.815	2.505	2.495
216740_at	*TRERF1*	2.84	2.53	2.52
244150_at	*SMC1A*	3.155	2.825	2.795
1558624_at	*CUTL1*	3.175	2.825	2.815
38269_at	*PRKD2*	4.955	4.415	4.405
230273_at	*C6orf165*	4.995	4.435	4.445
238010_at	*C1orf174*	2.85	2.54	2.53
232995_at	*PDGFD*	2.655	2.365	2.355
1553678_a_at	*ITGB1*	12.32	10.92	11
208615_s_at	*PTP4A2*	11.83	10.54	10.51
225060_at	*LRP11*	12.19	10.8	10.9
1566141_at	*GBF1*	2.59	2.31	2.31
1558795_at	*LOC728052*	3.4	3.03	3.01

227440_at	*ANKS1B*	2.46	2.19	2.18
244279_at	*FLJ10159*	2.465	2.195	2.185
216987_at	*IRF4*	3.155	2.815	2.805
209859_at	*TRIM9*	3.45	3.06	3.08
1562337_at	*OR7D2*	2.825	2.525	2.495
1556301_at	*NA*	3.015	2.675	2.675
235720_at	*CRIP3*	2.685	2.385	2.385
211909_x_at	*PTGER3*	6.035	5.345	5.395
238796_at	*YTHDC1*	2.805	2.505	2.495
213747_at	*AZIN1*	12.23	10.95	10.83
231480_at	*NA*	2.725	2.425	2.425
211489_at	*ADRA1A*	2.89	2.58	2.56
212761_at	*TCF7L2*	13.685	12.155	12.205
233377_at	*ARID5B*	3.27	2.93	2.89
201029_s_at	*CD99*	13.365	11.905	11.895
234099_at	*LAMA2*	2.37	2.11	2.11
216276_s_at	*ADAM3A*	3.65	3.27	3.23
218074_at	*FAM96B*	9.565	8.535	8.505
228067_at	*MGC42367*	2.87	2.55	2.56
216426_at	*LOC644540*	3.58	3.2	3.17
215980_s_at	*IGHMBP2*	4.605	4.115	4.095
1563181_a_at	*NA*	2.88	2.56	2.56
1557297_at	*ABCA13*	2.75	2.45	2.45
239686_at	*NA*	2.625	2.345	2.335
235838_at	*NLGN2*	2.525	2.245	2.245
237993_at	*CHCHD5*	3.65	3.25	3.25
1559678_s_at	*LOC730495*	3.1	2.76	2.76
207094_at	*IL8RA*	2.485	2.215	2.205
33323_r_at	*SFN*	3.28	2.93	2.91
202043_s_at	*SMS*	11.195	9.965	9.975
227560_at	*SFXN2*	3.3	2.92	2.96

1561243_at	*TMEM105*	2.8	2.5	2.5
228026_at	*SIKE*	9.195	8.255	8.135
227442_at	*COX18*	9.635	8.615	8.545
243473_at	*KIAA0999*	3.395	3.025	3.015
216162_at	*SBNO1*	2.715	2.425	2.415
219187_at	*FKBPL*	4.75	4.2	4.26
216498_at	*NA*	3.33	2.98	2.95
221549_at	*GRWD1*	6.695	5.965	5.955
244076_at	*RP11-130N24.1*	2.73	2.43	2.43
224886_at	*LOC339123*	6.365	5.695	5.635
220290_at	*AIM1L*	3.565	3.165	3.195
228718_at	*ZNF44*	7.12	6.37	6.31
222055_at	*FAHD2A*	2.875	2.555	2.555
244122_at	*MGST3*	2.505	2.235	2.225
221633_at	*NCAPH2*	2.705	2.415	2.405
1554473_at	*SRGAP1*	3.015	2.685	2.695
236708_at	*CAPZB*	4.22	3.74	3.78
221439_at	*RBBP9*	2.795	2.485	2.505
227276_at	*PLXDC2*	2.965	2.645	2.645
210404_x_at	*CAMK2B*	2.73	2.43	2.43
210030_at	*DOHH*	2.38	2.12	2.12
240409_at	*LOC283507*	2.865	2.555	2.545
212925_at	*C19orf21*	3.89	3.47	3.46
220859_at	*NA*	3.325	2.965	2.965
212188_at	*KCTD12*	13.195	11.705	11.815
221592_at	*RPL31*	2.19	1.95	1.95
237746_at	*SFRS11*	3.025	2.725	2.685
226707_at	*NAPRT1*	4.4	3.93	3.91
236034_at	*MCPH1*	2.74	2.45	2.43
234365_at	*NA*	2.615	2.335	2.335
220332_at	*CLDN16*	2.54	2.26	2.26

224565_at	*TncRNA*	13.585	12.065	12.155
210920_x_at	*EMID2*	3.36	2.98	3.01
230658_at	*SLC7A2*	2.875	2.565	2.555
244797_at	*NA*	2.41	2.15	2.15
242589_x_at	*DOCK5*	7.21	6.39	6.47
205265_s_at	*SPEG*	5.97	5.33	5.32
236038_at	*NA*	3.5	3.12	3.12
231544_s_at	*POLR3G*	3.13	2.8	2.78
209461_x_at	*WDR18*	2.525	2.245	2.255
1570156_s_at	*FMN1*	3.17	2.81	2.84
235411_at	*PGBD1*	4.555	4.065	4.055
203407_at	*PPL*	2.525	2.255	2.245
200061_s_at	*RPS24*	13.835	12.395	12.285
208713_at	*HNRPUL1*	9.535	8.545	8.475
1556894_at	*NT5DC2*	3.66	3.28	3.25
1566527_at	*CUTL2*	3.205	2.875	2.855
1569090_x_at	*FLJ35390*	2.8	2.5	2.5
203533_s_at	*CUL5*	10.795	9.585	9.675
244634_at	*FAM53B*	2.695	2.405	2.395
229804_x_at	*CBWD1*	8.615	7.665	7.725
219542_at	*NEK11*	5.53	4.91	4.95
223572_at	*HHATL*	2.4	2.14	2.14
1558881_at	*LOC145820*	2.565	2.285	2.285
37802_r_at	*FAM63B*	4.99	4.42	4.48
220215_at	*ZNF669*	5.25	4.72	4.66
1560492_at	*CRADD*	4.775	4.255	4.255
1557740_a_at	*NA*	4.005	3.575	3.565
234950_s_at	*RFWD2*	9.46	8.42	8.46
1560543_at	*GRK4*	3.59	3.22	3.2
219545_at	*KCTD14*	2.39	2.13	2.14
223851_s_at	*TNFRSF18*	2.77	2.47	2.47

202210_x_at	*GSK3A*	6.925	6.195	6.175
1563587_at	*CDH4*	2.875	2.575	2.565
208448_x_at	*IFNA16*	2.45	2.19	2.19
1563325_at	*NA*	2.745	2.445	2.445
215141_at	*NOL14*	2.325	2.085	2.085
204670_x_at	*HLA-DRB5*	2.275	2.035	2.035
213401_s_at	*TBL1X*	3.68	3.26	3.31
216506_x_at	*MLLT10*	2.895	2.585	2.595
244352_at	*NA*	3.515	3.155	3.115
227635_at	*RBBP6*	2.82	2.52	2.52
240906_at	*MRPS36*	3.075	2.745	2.755
1560889_a_at	*SEMA5A*	3.01	2.69	2.69
233966_at	*NA*	2.65	2.37	2.36
1568922_at	*SLC24A4*	2.695	2.415	2.405
243095_at	*NA*	4.11	3.66	3.68
224069_x_at	*P2RX2*	2.64	2.35	2.36
234565_x_at	*NA*	3.3	2.95	2.94
235178_x_at	*ESCO2*	3.37	3.02	3
1560638_a_at	*NA*	3.325	2.965	2.965
211130_x_at	*EDA*	2.61	2.33	2.33
220012_at	*ERO1LB*	3.4	3.03	3.04
207923_x_at	*PAX8*	2.59	2.31	2.31
209193_at	*PIM1*	5.885	5.285	5.235
1556846_at	*LOC646670*	2.79	2.5	2.49
1554017_at	*FLJ39378*	2.695	2.415	2.415
207680_x_at	*PAX3*	2.62	2.34	2.34
227470_at	*ZNF553*	5.08	4.57	4.51
228668_x_at	*FLJ36031*	2.875	2.575	2.575
219784_at	*FBXO31*	4.86	4.32	4.37
215599_at	*SMA4*	3.615	3.215	3.255
1563302_at	*NA*	4.275	3.845	3.795

219824_at	*SLC13A4*	2.695	2.415	2.405
240352_at	*NA*	2.865	2.565	2.555
219221_at	*ZBTB38*	11.035	9.895	9.825
238382_x_at	*COG5*	3.23	2.89	2.89
224724_at	*SULF2*	6.33	5.64	5.67
215389_s_at	*TNNT2*	3.4	3.03	3.05
1561854_at	*HBG2*	3.57	3.2	3.18
203152_at	*MRPL40*	7.43	6.65	6.64
209718_at	*NCAPH2*	5.82	5.19	5.22
239989_at	*C9orf39*	4.01	3.58	3.6
210292_s_at	*PCDH11X*	3.04	2.72	2.71
220302_at	*MAK*	2.565	2.295	2.285
1554694_at	*CCNY*	2.745	2.455	2.445
216434_at	*FLJ20699*	2.81	2.51	2.51
218046_s_at	*MRPS16*	6.305	5.665	5.615
209155_s_at	*NT5C2*	10.82	9.65	9.71
233282_at	*FIP1L1*	3.17	2.83	2.84
209573_s_at	*C18orf1*	2.565	2.295	2.285
216334_s_at	*CYP2A7P1*	3.295	2.965	2.935
1555816_at	*THSD4*	3.06	2.76	2.72
221849_s_at	*LOC90379*	3.005	2.695	2.685
160020_at	*MMP14*	8.18	7.28	7.36
1563853_at	*LOC283045*	2.165	1.935	1.945
205334_at	*S100A1*	2.83	2.54	2.53
217856_at	*RBM8A*	2.79	2.5	2.49
206777_s_at	*CRYBB2*	2.77	2.48	2.47
234315_at	*BACH1*	3.015	2.715	2.685
203380_x_at	*SFRS5*	12.035	10.755	10.785
207772_s_at	*PRMT8*	3.02	2.71	2.69
1569713_at	*NA*	2.585	2.305	2.315
243021_at	*LOC643965*	3.23	2.89	2.88

206460_at	*AJAP1*	2.745	2.455	2.465
1554583_a_at	*MGC50559*	2.315	2.065	2.075
218256_s_at	*NUP54*	10.61	9.56	9.42
242987_x_at	*NA*	3.265	2.935	2.905
221967_at	*NXPH4*	3.355	2.995	3.005
226442_at	*ABTB1*	2.515	2.245	2.255
1567622_at	*ABLIM2*	2.735	2.465	2.435
213655_at	*PAFAH1B1*	15.475	13.865	13.835
1557665_at	*NA*	3.16	2.83	2.81
222037_at	*MCM4*	4.105	3.645	3.695
1560921_at	*ZNF169*	2.63	2.36	2.35
212779_at	*KIAA1109*	10.655	9.585	9.485
228319_at	*FAM84A*	2.795	2.495	2.495
214675_at	*NUP188*	2.89	2.59	2.59
222677_x_at	*AURKAIP1*	3.515	3.135	3.165
233668_at	*EDIL3*	2.65	2.37	2.37
243174_at	*NA*	4.715	4.225	4.215
233205_at	*NA*	3.355	3.015	2.985
214329_x_at	*TNFSF10*	2.845	2.545	2.545
212836_at	*POLD3*	8.465	7.575	7.585
237241_at	*ECT2*	2.69	2.41	2.41
232144_at	*PBX1*	3.135	2.825	2.795
1556872_s_at	*IQSEC3*	2.3	2.06	2.06
207136_at	*ARR3*	2.545	2.285	2.275
233283_at	*MAX*	2.84	2.55	2.54
223815_at	*CCDC45*	3.2	2.84	2.88
208734_x_at	*RAB2A*	11.715	10.465	10.515
204598_at	*UBOX5*	5.035	4.515	4.505
1556607_at	*EHD4*	3.6	3.21	3.23
208865_at	*CSNK1A1*	13.8	12.39	12.33
220207_at	*LOC541469*	2.465	2.215	2.205

236711_at	*ZIC4*	2.69	2.42	2.4
1555904_at	*NA*	3.025	2.695	2.715
241545_x_at	*RBBP6*	3.67	3.28	3.3
212967_x_at	*NAP1L1*	13.365	11.965	11.975
202402_s_at	*CARS*	8.705	7.815	7.785
209638_x_at	*RGS12*	4.02	3.61	3.6
1559565_x_at	*TPST1*	2.9	2.61	2.59
1558475_at	*TNFSF5IP1*	2.615	2.335	2.335
219755_at	*CBX8*	3.07	2.75	2.75
234864_s_at	*TRPM6*	2.46	2.2	2.2
1558323_at	*NA*	4.735	4.225	4.255
231267_at	*C1orf76*	2.89	2.6	2.58
243004_at	*NA*	3.28	2.94	2.94
209617_s_at	*CTNND2*	2.89	2.59	2.59
203416_at	*CD53*	2.7	2.41	2.42
226694_at	*PALM2-AKAP2*	13.98	12.6	12.45
212639_x_at	*TUBA1A*	12.365	11.055	11.115
210599_at	*ZNF614*	3.14	2.82	2.82
240203_at	*NA*	3.28	2.95	2.92
231393_x_at	*NA*	7.585	6.805	6.805
214238_at	*NA*	2.845	2.555	2.545
1567333_at	*NA*	2.795	2.505	2.495
204427_s_at	*TMED2*	10.305	9.245	9.215
222563_s_at	*TNKS2*	3.165	2.855	2.825
1564338_at	*MKL1*	2.775	2.495	2.485
243155_at	*NA*	2.585	2.325	2.315
240070_at	*VSIG9*	2.605	2.335	2.325
223877_at	*C1QTNF7*	3.015	2.695	2.705
1567069_at	*OR4D1*	2.325	2.075	2.095
238483_at	*NA*	3.08	2.75	2.77
227806_at	*C16orf74*	2.83	2.54	2.53

211357_s_at	*ALDOB*	3.12	2.81	2.79
1554629_at	*EPHA7*	2.995	2.685	2.675
217149_x_at	*TNK1*	2.845	2.545	2.545
1554033_at	*FRMD4A*	3.025	2.715	2.705
236406_at	*ZNF324B*	2.835	2.545	2.535
207906_at	*IL3*	2.595	2.335	2.325
1564897_at	*NA*	2.28	2.04	2.05
1555146_at	*ATF2*	2.935	2.625	2.635
239112_at	*NA*	2.795	2.525	2.495
235898_at	*NA*	2.33	2.08	2.1
233525_s_at	*C9orf44*	3.185	2.875	2.845
220149_at	*FLJ22671*	3.68	3.3	3.3
217820_s_at	*ENAH*	12.93	11.64	11.55
209143_s_at	*CLNS1A*	8.9	7.94	8.02
237174_at	*NA*	2.53	2.27	2.27
230394_at	*TCP10L*	3.065	2.755	2.735
222160_at	*AKAP8L*	3.3	2.95	2.97
234003_at	*COVA1*	2.925	2.615	2.625
231573_at	*FATE1*	3.09	2.78	2.76
203263_s_at	*ARHGEF9*	2.725	2.435	2.445
212096_s_at	*MTUS1*	2.665	2.385	2.385
220791_x_at	*SCN11A*	2.97	2.67	2.67
229146_at	*C7orf31*	2.96	2.66	2.65
211988_at	*SMARCE1*	12.16	10.91	10.89
212931_at	*TCF20*	8.345	7.485	7.485
221672_s_at	*NIBP*	2.74	2.46	2.46
234206_at	*NA*	2.455	2.195	2.195
202846_s_at	*PIGC*	8.28	7.43	7.42
228696_at	*SLC45A3*	2.995	2.685	2.695
234887_at	*NA*	2.645	2.375	2.365
206961_s_at	*TRFP*	2.56	2.3	2.3

224390_s_at	*RGS8*	2.46	2.2	2.2
209645_s_at	*ALDH1B1*	2.675	2.395	2.405
1561692_at	*WWOX*	2.76	2.48	2.47
1560118_at	*NA*	2.86	2.57	2.56
229834_at	*NFIX*	3.1	2.78	2.78
241190_at	*NA*	3.12	2.81	2.79
36553_at	*ASMTL*	10.01	8.94	9.01
219191_s_at	*BIN2*	2.52	2.26	2.26
228117_at	*C22orf32*	2.935	2.635	2.625
222139_at	*KIAA1466*	2.745	2.465	2.465
228538_at	*ZNF662*	2.74	2.46	2.46
229432_at	*NAGS*	2.74	2.46	2.46
233806_at	*NA*	2.585	2.325	2.325
233908_x_at	*NA*	4.055	3.655	3.625
239280_at	*NA*	2.85	2.56	2.54
241349_at	*NA*	2.645	2.365	2.375
1555871_at	*KIAA1648*	2.625	2.365	2.355
208238_x_at	*NA*	6.955	6.225	6.245
241807_x_at	*NA*	2.92	2.62	2.62
241720_at	*ZNF326*	2.965	2.675	2.655
208921_s_at	*SRI*	11.48	10.35	10.25
229727_x_at	*NLF2*	3.205	2.885	2.875
206635_at	*CHRNB2*	5.735	5.135	5.165
1565672_at	*NA*	2.545	2.275	2.295
229287_at	*NA*	11.77	10.61	10.52
232328_at	*ZNF552*	2.645	2.375	2.365
224557_x_at	*P2RX2*	4.135	3.715	3.705
1552768_at	*CAMKK1*	2.56	2.3	2.3
1565558_at	*NA*	2.415	2.165	2.185
203772_at	*BLVRA*	3.1	2.79	2.78
240818_at	*NA*	2.805	2.525	2.525

216584_at	*NA*	5.24	4.72	4.68
236017_at	*CDKL3*	2.625	2.365	2.355
243355_at	*NA*	2.425	2.185	2.185
214536_at	*SLURP1*	2.37	2.13	2.13
231885_at	*KIAA1702*	3.065	2.745	2.755
217769_s_at	*POMP*	12.535	11.295	11.215
203983_at	*TSNAX*	11.76	10.56	10.56
213864_s_at	*NAP1L1*	13.245	11.885	11.895
212589_at	*RRAS2*	13.3	11.92	11.96
240043_at	*NA*	3.37	3.05	3.01
234761_at	*KIAA1530*	3.295	2.955	2.955
227370_at	*KIAA1946*	11.78	10.6	10.56
241009_at	*FOXN4*	2.56	2.3	2.3
219314_s_at	*ZNF219*	3.28	2.94	2.95
231682_at	*NA*	2.76	2.49	2.46
235460_at	*SNX22*	3.01	2.72	2.69
212139_at	*GCN1L1*	9.055	8.085	8.185
1553002_at	*DEFB105A*	2.68	2.42	2.39
242284_at	*LOC199899*	2.9	2.6	2.6
211517_s_at	*IL5RA*	3.08	2.78	2.75
224342_x_at	*LOC96610*	2.635	2.375	2.365
1559561_at	*FBXO18*	3.025	2.725	2.715
209447_at	*SYNE1*	8.65	7.77	7.77
217034_at	*HLA-C*	4.32	3.89	3.87
240321_at	*TCF4*	3.265	2.935	2.925
233402_at	*SNX24*	2.885	2.595	2.575
1555979_at	*FLJ39609*	2.845	2.565	2.555
1563425_at	*CLYBL*	3.395	3.045	3.055
211958_at	*IGFBP5*	3.565	3.205	3.205
238849_at	*ACY1*	2.53	2.27	2.27
244146_at	*DTWD1*	2.825	2.545	2.535

222168_at	*ALDH1A3*	2.985	2.685	2.685
216481_at	*GRIP2*	2.95	2.66	2.64
240441_at	*NA*	3.11	2.8	2.78
201353_s_at	*BAZ2A*	2.97	2.68	2.66
225599_s_at	*DKFZP779L1068*	9.43	8.45	8.49
229606_at	*NA*	14.75	13.28	13.22
216247_at	*LOC440992*	4.845	4.345	4.355
1555809_at	*CRISPLD2*	2.91	2.6	2.62
233967_at	*NA*	2.485	2.235	2.225
209236_at	*SLC23A2*	3.56	3.22	3.18
202110_at	*COX7B*	11.87	10.71	10.62
1556267_at	*C12orf28*	3.38	3.05	3.03
205073_at	*CYP2J2*	2.845	2.565	2.555
212816_s_at	*CBS*	2.825	2.535	2.545
1557145_at	*STK38*	3.22	2.9	2.9
222078_at	*NA*	3.355	3.015	3.015
1566787_at	*NA*	3.16	2.85	2.83
230234_at	*NA*	2.535	2.275	2.275
211646_at	*NA*	3.09	2.77	2.78
232852_at	*LDB2*	3.325	2.985	2.985
232731_x_at	*RAMP2*	2.655	2.395	2.385
1557657_a_at	*LOC400238*	2.55	2.3	2.29
232368_at	*BET3L*	3.34	3.02	2.99
1566881_at	*NA*	2.645	2.385	2.385
1555498_at	*NA*	3.12	2.82	2.79
207884_at	*GUCY2D*	2.24	2.02	2.02
201119_s_at	*COX8A*	10.685	9.655	9.555
1566541_at	*PRKCE*	2.855	2.575	2.575
209743_s_at	*ITCH*	3.84	3.46	3.45
201098_at	*COPB2*	13.56	12.27	12.13
228358_at	*SOX12*	2.56	2.29	2.32

214303_x_at	*MUC5AC*	2.65	2.39	2.39
1568618_a_at	*GALNT1*	14.06	12.73	12.56
238803_at	*HECTD2*	3.175	2.835	2.875
1554316_at	*PGLS*	2.79	2.51	2.51
1554553_s_at	*YIF1B*	2.21	1.99	1.99
244799_s_at	*NA*	2.695	2.425	2.415
1568752_s_at	*RGS13*	3.38	3.04	3.04
234043_at	*DYM*	3.35	3.01	3.01
1565713_at	*MYH9*	2.665	2.405	2.395
234496_x_at	*NYX*	4.305	3.885	3.855
1554452_a_at	*HIG2*	4.415	3.995	3.955
1565787_at	*ZCCHC7*	2.505	2.255	2.245
1559474_at	*SPEG*	2.355	2.115	2.115
222345_at	*NA*	2.81	2.54	2.52
234961_at	*NA*	3.13	2.83	2.8
208583_x_at	*HIST1H2AJ*	3.79	3.42	3.41
222089_s_at	*C16orf71*	2.655	2.395	2.385
201754_at	*COX6C*	12.66	11.4	11.4
237457_at	*EIF3S9*	2.64	2.38	2.38
220551_at	*SLC17A6*	2.55	2.29	2.29
226717_at	*LRRC51*	2.285	2.055	2.065
1557029_at	*HMMR*	2.39	2.15	2.15
234372_at	*NA*	2.675	2.415	2.405
220293_at	*C14orf161*	2.37	2.13	2.13
217131_at	*NA*	3.17	2.87	2.84
237739_at	*HBG1*	4.185	3.765	3.765
210880_s_at	*EFS*	3.025	2.735	2.715
211688_x_at	*KIR3DL2*	2.515	2.265	2.255
1564511_a_at	*FSTL4*	2.6	2.35	2.33
221844_x_at	*NA*	13.87	12.45	12.53
232233_at	*SLC22A16*	2.895	2.625	2.595

215296_at	*CDC42BPA*	5.63	5.07	5.06
243503_at	*NA*	2.59	2.33	2.33
1554577_a_at	*PSMD10*	6.585	5.895	5.955
214331_at	*TSFM*	5.425	4.875	4.895
244686_at	*TCOF1*	3.38	3.04	3.04
221966_at	*GPR137*	2.49	2.25	2.24
237776_at	*ZADH2*	2.385	2.145	2.145
201832_s_at	*VDP*	13.58	12.21	12.24
207154_at	*DIO3*	2.455	2.215	2.205
228881_at	*PARL*	2.22	2	2
228807_at	*NA*	2.59	2.34	2.33
228500_at	*THAP8*	2.655	2.395	2.385
217630_at	*ANGEL2*	3.38	3.04	3.04
1563263_at	*PLCG2*	2.275	2.055	2.055
216699_s_at	*KLK1*	2.885	2.605	2.605
211750_x_at	*TUBA1C*	13.06	11.71	11.81
1558327_at	*ZDHHC18*	2.735	2.465	2.455
222903_s_at	*CPEB1*	2.82	2.55	2.53
241333_x_at	*NA*	3.515	3.175	3.165
1566042_at	*NA*	3.105	2.805	2.795
209066_x_at	*UQCRB*	12.31	11.1	11.08
1555533_at	*GPR103*	2.605	2.355	2.345
241830_at	*C20orf112*	2.265	2.055	2.035
226553_at	*TMPRSS2*	2.84	2.56	2.56
220471_s_at	*MYCT1*	2.68	2.42	2.41
1570516_s_at	*HBG2*	2.195	1.975	1.975
228140_s_at	*PPP2R2C*	2.66	2.4	2.4
205127_at	*PTGS1*	2.335	2.095	2.095
1558280_s_at	*ARHGAP29*	2.845	2.555	2.575
242995_at	*XRN1*	3.855	3.475	3.475
238359_at	*NA*	3.665	3.305	3.305

220820_at	*NA*	3.315	2.985	2.995
233432_at	*LOC646982*	2.83	2.56	2.54
243122_at	*LOC729658*	2.995	2.695	2.695
1494_f_at	*CYP2A6*	2.77	2.5	2.49
1557520_a_at	*TMEM59*	3.235	2.925	2.905
237731_at	*LOC154092*	3.095	2.795	2.795
1554892_a_at	*MS4A3*	2.77	2.5	2.48
212265_at	*QKI*	13.845	12.485	12.475
1566171_at	*RFFL*	3.42	3.08	3.09
219524_s_at	*C20orf7*	3.42	3.08	3.08
211058_x_at	*TUBA1B*	13.63	12.24	12.33
218986_s_at	*FLJ20035*	5.555	4.985	5.035
203684_s_at	*BCL2*	2.595	2.335	2.335
206970_at	*CNTN2*	2.655	2.395	2.385
236486_at	*NA*	3.22	2.92	2.89
232898_at	*DAB2*	2.42	2.18	2.18
227915_at	*ASB2*	2.565	2.315	2.305
234898_at	*NA*	3.21	2.9	2.88
218041_x_at	*SLC38A2*	13.55	12.17	12.25
202150_s_at	*NEDD9*	2.8	2.52	2.52
240954_at	*CPT1B*	2.41	2.17	2.17
226397_s_at	*TBC1D7*	3.965	3.565	3.575
234385_at	*LOC339666*	2.975	2.685	2.675
1552304_at	*ALG10*	2.575	2.315	2.325
220276_at	*FLJ22655*	2.955	2.665	2.655
213840_s_at	*MRPS12*	2.79	2.52	2.5
1552398_a_at	*CLEC12A*	3.365	3.035	3.025
238967_at	*CLDN1*	3.52	3.17	3.18
40612_at	*DOPEY1*	5.28	4.76	4.76
1564854_at	*NA*	3.06	2.76	2.75
224438_at	*NA*	3.22	2.9	2.91

227608_at	*BSCL2*	8.16	7.38	7.34
225475_at	*MIER1*	8.865	8.005	7.975
202579_x_at	*HMGN4*	10.645	9.565	9.645
220374_at	*KLHL28*	2.665	2.395	2.405
1556699_at	*RBPMS*	2.865	2.585	2.575
1561731_at	*NA*	2.945	2.675	2.645
1567287_at	*OR5K1*	3.3	2.99	2.96
239149_at	*BRD4*	2.78	2.5	2.51
222005_s_at	*GNG3*	2.62	2.36	2.36
226029_at	*VANGL2*	2.69	2.42	2.44
208338_at	*P2RX3*	2.63	2.37	2.37
240618_at	*PTPRA*	2.47	2.23	2.23
230190_at	*NDFIP2*	2.44	2.2	2.2
1564705_at	*GLS2*	3.375	3.045	3.035
209316_s_at	*HBS1L*	7.35	6.64	6.62
237709_at	*NA*	2.39	2.15	2.15
219791_s_at	*NBLA00301*	2.24	2.02	2.02
235282_at	*SP2*	3.535	3.205	3.175
240634_x_at	*NA*	3	2.71	2.7
241429_at	*NA*	2.495	2.255	2.255
220760_x_at	*ZNF665*	5.73	5.19	5.15
231602_at	*PRRX2*	2.505	2.265	2.255
238038_at	*NA*	3.26	2.96	2.93
1567341_at	*FOXD4*	3.175	2.865	2.855
229724_at	*GABRB3*	2.335	2.105	2.115
1561988_at	*LOC286068*	2.335	2.115	2.105
1560697_at	*LOC283392*	2.71	2.45	2.44
240353_s_at	*C12orf54*	3.405	3.085	3.055
1562080_at	*NA*	3.21	2.9	2.88
205263_at	*BCL10*	13.32	12.04	11.99
220671_at	*CCRN4L*	2.365	2.135	2.125

223992_x_at	*ZCWPW1*	2.815	2.545	2.525
211072_x_at	*TUBA1B*	13.605	12.195	12.345
200882_s_at	*PSMD4*	11.91	10.74	10.76
1567374_at	*NA*	2.825	2.555	2.535
244081_at	*NA*	3.375	3.045	3.055
211101_x_at	*LILRA2*	2.745	2.485	2.475
241961_at	*SRD5A2L2*	3.115	2.825	2.805
1554745_at	*RALGPS1*	2.795	2.525	2.515
1562431_x_at	*NA*	3.695	3.355	3.315
224715_at	*WDR34*	4.745	4.315	4.255
1556055_at	*ATP11A*	3.27	2.93	2.97
217256_x_at	*NA*	9.475	8.575	8.525
238875_at	*ZC3H6*	3.2	2.88	2.89
211550_at	*EGFR*	3.13	2.83	2.83
229036_at	*TNRC6B*	9.695	8.775	8.725
241964_at	*NA*	2.285	2.065	2.065
1555926_a_at	*NA*	3.88	3.51	3.49
205233_s_at	*PAFAH2*	3.015	2.725	2.705
215055_at	*B3GNTL1*	4.76	4.3	4.3
221021_s_at	*CTNNBL1*	8.035	7.225	7.285
234651_at	*NA*	2.935	2.655	2.645
200930_s_at	*VCL*	2.805	2.525	2.535
232043_at	*GNG7*	3.32	3	3
226570_at	*ATP1B3*	4.32	3.92	3.88
1568844_at	*NA*	2.88	2.6	2.6
211582_x_at	*LST1*	2.395	2.175	2.145
1555823_at	*NA*	3.31	2.98	3
1559355_at	*NXPH2*	2.545	2.305	2.295
221286_s_at	*MGC29506*	3.975	3.595	3.585
235543_at	*NA*	3.145	2.835	2.845
237890_at	*DTNBP1*	2.745	2.485	2.475

241476_at	*NA*	2.5	2.26	2.25
241255_at	*NA*	2.605	2.355	2.345
232337_at	*B3GNT7*	2.25	2.03	2.03
219599_at	*PRO1843*	8.78	7.88	7.97
239308_at	*DYRK1A*	2.84	2.56	2.57
215547_at	*TSC22D2*	2.615	2.355	2.355
242831_at	*ATP8B2*	2.7	2.44	2.44
204108_at	*NFYA*	6.865	6.205	6.205
1570410_at	*CYGB*	3.08	2.79	2.77
220752_at	*LOC51145*	2.435	2.195	2.195
211403_x_at	*VCX2*	2.825	2.555	2.545
1556815_at	*H2AFY2*	3.67	3.32	3.3
203776_at	*GPKOW*	8.015	7.285	7.195
209768_s_at	*5-Sep*	2.91	2.65	2.61
208731_at	*RAB2A*	13.945	12.555	12.645
1561609_at	*NA*	3.03	2.74	2.73
213102_at	*ACTR3*	14.06	12.76	12.64
1562324_a_at	*NA*	2.94	2.66	2.66
237814_at	*NA*	3.025	2.745	2.715
239302_s_at	*MAP3K2*	2.825	2.545	2.545
206503_x_at	*PML*	2.565	2.325	2.325
209484_s_at	*NSL1*	11.745	10.575	10.645
243882_at	*NA*	3.185	2.885	2.875
243788_at	*PHF11*	3.08	2.79	2.78
216381_x_at	*AKR7A3*	3.05	2.76	2.75
1556608_a_at	*EHD4*	2.585	2.335	2.345
214405_at	*CUGBP2*	3.3	3	2.97
232638_at	*COL20A1*	2.885	2.615	2.595
215845_x_at	*NA*	2.725	2.465	2.465
214548_x_at	*GNAS*	12.91	11.64	11.7
1553740_a_at	*IRAK2*	2.7	2.45	2.43

205865_at	*ARID3A*	2.955	2.675	2.665
242203_at	*NA*	2.7	2.44	2.44
1559928_at	*PAPPA*	2.5	2.26	2.26
217088_s_at	*NCR1*	2.625	2.365	2.365
229622_at	*FLJ37034*	2.995	2.725	2.695
240632_at	*RAD51L1*	3.055	2.765	2.745
237849_at	*MAN1A1*	3.16	2.87	2.85
229112_at	*LOC285813*	3.89	3.49	3.53
1563135_at	*NA*	2.66	2.41	2.4
1554225_a_at	*NA*	2.69	2.43	2.43
1554589_at	*LENG9*	3.015	2.725	2.735
220706_at	*ADAMTS7*	2.615	2.365	2.355
226912_at	*ZDHHC23*	3.785	3.415	3.435
244100_at	*KIAA0350*	2.91	2.62	2.64
211931_s_at	*HNRPA3P1*	14.57	13.11	13.23
244842_x_at	*TUBGCP2*	4.78	4.31	4.33
206063_x_at	*YPEL1*	4.635	4.185	4.195
222444_at	*ARMCX3*	14.145	12.725	12.845
232718_at	*C8orf75*	2.355	2.125	2.135
210955_at	*CASP10*	3.11	2.81	2.81
216019_x_at	*PHLDB1*	2.405	2.165	2.175
1553115_at	*NKD1*	2.69	2.43	2.43
210179_at	*KCNJ13*	2.77	2.51	2.51
1554847_at	*ATP6V1B1*	3.075	2.775	2.775
1562751_at	*NA*	2.665	2.395	2.415
243512_x_at	*IMMP2L*	3.715	3.355	3.355
236806_at	*NA*	2.52	2.28	2.28
242075_at	*NT5C2*	3.055	2.775	2.745
212435_at	*TRIM33*	10.965	9.865	9.975
225035_x_at	*FAM39DP*	6.475	5.865	5.845
1570054_at	*NA*	3.305	2.985	2.985

220439_at	*RIN3*	2.86	2.59	2.58
210107_at	*CLCA1*	2.525	2.285	2.285
1569599_at	*SAMSN1*	2.91	2.64	2.63
223876_at	*SPATA16*	2.775	2.515	2.505
236096_at	*SIPA1L3*	2.255	2.035	2.035
1563157_at	*FOXP1*	2.765	2.505	2.495
226423_at	*PAQR8*	5.525	4.975	5.025
1557003_at	*FLJ25439*	2.5	2.26	2.26
242805_at	*CCNC*	3.57	3.23	3.23
221409_at	*OR2S2*	2.27	2.05	2.05
215086_at	*IBTK*	2.93	2.66	2.64
221609_s_at	*WNT6*	3.24	2.94	2.93
224792_at	*TNKS1BP1*	5.155	4.655	4.665
223845_at	*LOC144305*	2.52	2.29	2.27
235167_at	*LOC23117*	2.77	2.5	2.52
210770_s_at	*CACNA1A*	2.755	2.505	2.485
240342_at	*TRIM61*	4.485	4.065	4.065
212845_at	*SAMD4A*	12.15	10.99	11
233610_at	*LOC645355*	2.815	2.565	2.535
1568755_a_at	*NA*	2.74	2.48	2.47
210565_at	*GCGR*	2.04	1.85	1.84
241837_at	*ARID5B*	2.755	2.485	2.505
208655_at	*CCNI*	13.2	11.91	11.98
1570296_at	*NA*	2.85	2.58	2.57
244027_at	*ABCB7*	3.29	2.97	2.97
241768_at	*BCCIP*	3.275	2.965	2.945
218382_s_at	*U2AF2*	3.075	2.785	2.775
229124_at	*PROK1*	2.47	2.23	2.23
1554934_at	*RCBTB1*	3.13	2.84	2.82
203923_s_at	*CYBB*	3.035	2.755	2.745
1568739_at	*LOC285692*	3.03	2.76	2.73

204936_at	*MAP4K2*	2.99	2.72	2.7
236176_at	*LOC645757*	2.435	2.205	2.195
206345_s_at	*PON1*	2.515	2.275	2.275
241270_at	*RHBDF2*	2.78	2.51	2.53
208752_x_at	*NAP1L1*	12.83	11.56	11.66
239481_at	*RP1-32F7.2*	3.025	2.745	2.735
240051_at	*TPD52L3*	3.745	3.405	3.375
242942_at	*MGC15523*	3.115	2.815	2.815
240481_at	*TRAF3IP3*	3.125	2.825	2.825
201589_at	*SMC1A*	10.265	9.235	9.345
1560264_at	*MGST2*	2.57	2.33	2.33
234857_at	*NA*	2.33	2.11	2.11
208056_s_at	*CBFA2T3*	3.025	2.735	2.745
201222_s_at	*RAD23B*	10.97	9.96	9.9
227167_s_at	*RASSF3*	9.75	8.77	8.88
1553317_s_at	*GPR82*	3.005	2.725	2.715
242274_x_at	*SLC25A42*	3.53	3.2	3.19
1553099_at	*TIGD1*	3.86	3.49	3.51
1559871_s_at	*TDH*	3.3	3	2.97
219485_s_at	*PSMD10*	11.02	10.02	9.93
1561976_at	*C1orf167*	2.635	2.395	2.385
209251_x_at	*TUBA1C*	13.6	12.25	12.39
1561354_at	*NA*	2.595	2.355	2.355
224874_at	*POLR1D*	8.68	7.87	7.85
231560_at	*LRRC34*	3.3	3	2.97
243144_at	*NA*	2.795	2.535	2.525
1561445_at	*NA*	3.08	2.78	2.79
204646_at	*DPYD*	10.925	9.895	9.885
236282_at	*NA*	4.17	3.77	3.78
223117_s_at	*USP47*	11.15	10.11	10.08
237170_at	*NA*	3.12	2.83	2.82

218911_at	*YEATS4*	4.955	4.485	4.505
1557787_at	*NA*	2.97	2.69	2.69
1558334_a_at	*C22orf15*	3.455	3.115	3.155
1557590_at	*PARD6G*	2.56	2.33	2.31
1557236_at	*APOL6*	3.915	3.545	3.555
1566512_at	*LOC200169*	2.195	1.995	1.985
218847_at	*IGF2BP2*	9.045	8.205	8.175
220782_x_at	*KLK12*	2.645	2.395	2.405
222937_s_at	*MMP28*	2.455	2.215	2.225
232540_x_at	*CDR2*	5.57	5.06	5.04
221022_s_at	*PMFBP1*	2.53	2.29	2.29
204274_at	*EBAG9*	10.825	9.745	9.865
237962_x_at	*KIAA1267*	3.345	3.045	3.015
232082_x_at	*SPRR3*	2.34	2.12	2.12
236869_at	*PISD*	2.74	2.48	2.49
234686_at	*SUGT1*	3.49	3.17	3.16
240982_at	*CARS*	2.515	2.285	2.275
215445_x_at	*1-Mar*	3.935	3.565	3.575
212532_s_at	*LSM12*	10.785	9.815	9.725
212943_at	*KIAA0528*	9.77	8.88	8.82
1554813_at	*NA*	2.855	2.605	2.575
1569235_a_at	*LOC729303*	3.04	2.76	2.76
233089_at	*QRSL1*	3.24	2.95	2.92
1557666_s_at	*C9orf98*	2.705	2.445	2.445
1558595_at	*FLJ23861*	3.41	3.08	3.1
220924_s_at	*SLC38A2*	13.08	11.81	11.91
230938_x_at	*ATF5*	3.165	2.875	2.855
1559313_at	*FLJ35740*	2.935	2.655	2.655
1555348_at	*TFAP2E*	2.815	2.545	2.555
206286_s_at	*TDGF1*	3.285	2.985	2.975
1569610_at	*IQCH*	2.815	2.555	2.545

204681_s_at	*RAPGEF5*	3.515	3.195	3.185
230816_at	*NA*	2.815	2.565	2.545
211076_x_at	*ATN1*	2.58	2.34	2.34
1557560_at	*NA*	2.505	2.265	2.265
226917_s_at	*ANAPC4*	12.29	11.21	11.08
1560074_at	*PRKCA*	2.855	2.595	2.585
241209_at	*IQWD1*	3.345	3.035	3.015
230686_s_at	*SLC13A3*	2.745	2.485	2.485
1566916_at	*HPYR1*	2.765	2.515	2.505
1553020_at	*SMCR5*	2.695	2.445	2.435
1559921_at	*PECAM1*	2.475	2.235	2.245
209252_at	*HARS2*	6.515	5.925	5.895
243015_at	*CYP3A5*	2.955	2.685	2.675
223667_at	*FKBP7*	3.125	2.835	2.825
1569808_at	*NA*	3.5	3.17	3.19
1556499_s_at	*COL1A1*	15.625	14.085	14.245
239584_at	*NA*	2.37	2.15	2.15
1566186_at	*NA*	2.35	2.13	2.13
230977_at	*NPM2*	6.375	5.755	5.805
1561813_at	*NA*	2.79	2.54	2.52
226424_at	*CAPS*	3.7	3.36	3.35
206774_at	*FRMPD1*	2.625	2.385	2.385
241859_at	*NA*	3.25	2.95	2.94
1555547_at	*DNAJC6*	3.02	2.75	2.72
203762_s_at	*DYNC2LI1*	7.29	6.65	6.57
205572_at	*ANGPT2*	2.76	2.5	2.5
205938_at	*PPM1E*	2.495	2.265	2.255
1559065_a_at	*CLEC4G*	2.61	2.38	2.36
239534_at	*NA*	2.39	2.17	2.17
221217_s_at	*A2BP1*	2.55	2.31	2.31
224006_at	*NA*	3.23	2.93	2.93

240723_at	*EVL*	2.485	2.245	2.255
217390_x_at	*NA*	4.295	3.905	3.885
228755_at	*PERQ1*	2.605	2.365	2.355
213881_x_at	*SUMO2*	14.195	12.955	12.795
241577_at	*AFF3*	2.505	2.275	2.265
216031_x_at	*HN1L*	2.885	2.635	2.605
216153_x_at	*RECK*	7.31	6.61	6.65
1562329_at	*CSMD1*	3.115	2.835	2.825
202423_at	*MYST3*	9.155	8.295	8.325
226491_x_at	*PTBP1*	5.975	5.405	5.435
1555303_at	*NA*	3.195	2.895	2.895
234617_at	*OR52D1*	2.33	2.11	2.11
233108_at	*NA*	2.58	2.34	2.34
230054_at	*PRRT1*	2.715	2.445	2.475
230808_at	*FNTA*	3.975	3.615	3.605
1564295_at	*FLJ25917*	3.295	2.995	2.995
204988_at	*FGB*	2.855	2.605	2.585
202552_s_at	*CRIM1*	14.09	12.87	12.71
1566538_at	*MAGI1*	2.865	2.605	2.605
232627_at	*HGS*	3.63	3.29	3.29
232501_at	*NA*	2.59	2.35	2.35
1561529_at	*NA*	2.975	2.705	2.685
201616_s_at	*CALD1*	12.98	11.78	11.79
217519_at	*MACF1*	3.075	2.805	2.785
242129_at	*SIN3B*	2.235	2.025	2.045
206021_at	*SCAND2*	2.86	2.6	2.6
1568689_at	*LOC728853*	3.385	3.085	3.055
241575_at	*NA*	2.69	2.45	2.45
238545_at	*BRD7*	3.66	3.32	3.32
204985_s_at	*TRAPPC6A*	3.775	3.425	3.435
231595_at	*XLKD1*	2.295	2.075	2.075

231442_at	*ZPBP2*	2.6	2.36	2.36
220541_at	*MMP26*	2.235	2.035	2.035
1561037_a_at	*NA*	3.095	2.815	2.815
214189_s_at	*GGA2*	2.725	2.475	2.465
215702_s_at	*CFTR*	2.97	2.69	2.69
1569306_at	*NA*	2.99	2.73	2.7
228447_at	*CXYorf3*	2.6	2.36	2.36
214050_at	*CGGBP1*	4.65	4.23	4.22
242109_at	*SYTL3*	3.24	2.95	2.93
226841_at	*MPEG1*	2.315	2.095	2.095
228413_s_at	*SFRP1*	2.68	2.44	2.43
233792_at	*NA*	2.795	2.525	2.545
228498_at	*NA*	15.775	14.325	14.335
1570043_at	*NA*	3.25	2.95	2.95
225960_at	*ZNRF1*	3.43	3.11	3.12
210723_x_at	*MGC4771*	3.03	2.74	2.76
234022_at	*GALK2*	3.355	3.055	3.055
230105_at	*HOXB13*	2.475	2.255	2.255
214898_x_at	*MUC3B*	4.37	3.96	3.98
1570361_a_at	*TTC28*	3.645	3.305	3.305
232906_at	*KLHL20*	2.6	2.37	2.35
212651_at	*RHOBTB1*	9.665	8.775	8.785
1552627_a_at	*ARHGAP5*	3.305	3.005	3.005
217282_at	*MAN1A2*	3.015	2.745	2.725
1565282_at	*NA*	2.6	2.36	2.36
242152_at	*MTCP1*	2.99	2.72	2.7
215971_at	*C14orf135*	2.435	2.215	2.215
242531_at	*RRAGC*	3.05	2.78	2.76
201398_s_at	*TRAM1*	14.31	13.04	12.95
235237_at	*LOC203547*	2.705	2.465	2.465
210401_at	*P2RX1*	2.66	2.42	2.41

243839_s_at	*NA*	2.825	2.575	2.555
1560213_at	*HLA-A*	2.305	2.085	2.095
238615_at	*ERLIN2*	2.335	2.115	2.115
216975_x_at	*NPAS1*	2.985	2.715	2.705
1561469_at	*NA*	3.52	3.2	3.2
211046_at	*KCNH6*	3.205	2.925	2.895
219827_at	*UCP3*	2.86	2.61	2.59
241120_s_at	*CDC20B*	3.07	2.8	2.78
1565776_at	*ABCA1*	2.785	2.525	2.535
215386_at	*AUTS2*	2.525	2.295	2.285
241160_at	*NA*	2.725	2.485	2.475
206648_at	*ZNF571*	2.905	2.635	2.645
216684_s_at	*SS18*	4.43	4.05	4.01
1556232_at	*KIF6*	2.675	2.445	2.425
239136_at	*hCG_1818231*	2.85	2.59	2.59
243893_at	*KCNC3*	2.57	2.34	2.33
1556250_at	*ST18*	2.795	2.535	2.545
1557177_at	*OLFML1*	3.12	2.85	2.82
224911_s_at	*DCBLD2*	12.585	11.425	11.455
244133_at	*NA*	2.945	2.695	2.665
219517_at	*ELL3*	6.855	6.215	6.255
201326_at	*CCT6A*	12.435	11.315	11.285
240749_at	*NA*	3.07	2.79	2.79
1566185_at	*NA*	2.46	2.25	2.23
207022_s_at	*LDHC*	2.71	2.47	2.46
230853_at	*NA*	2.44	2.22	2.22
1566836_at	*NA*	2.85	2.6	2.58
228484_s_at	*FOXO1A*	2.375	2.155	2.155
1570250_at	*RP11-35N6.1*	3.02	2.75	2.74
235949_at	*TTC26*	3.74	3.41	3.39
220570_at	*RETN*	2.585	2.345	2.345

1559902_at	*MKL1*	2.675	2.435	2.425
1570433_at	*TMPRSS2*	2.265	2.065	2.065
239020_at	*FUT10*	2.965	2.705	2.695
227855_at	*ZNF219*	2.71	2.46	2.48
241475_at	*LOC286076*	2.7	2.46	2.45
219718_at	*FLJ10986*	2.485	2.265	2.255
220971_at	*IL25*	2.485	2.275	2.255
225918_at	*LOC146346*	10.945	9.905	9.995
240962_at	*ITGA9*	2.525	2.305	2.295
236743_at	*GOLGA7*	2.345	2.125	2.125
202760_s_at	*PALM2-AKAP2*	13.71	12.5	12.43
1560734_at	*OR4N4*	2.725	2.495	2.465
1562270_at	*ARHGEF7*	3.415	3.125	3.095
222115_x_at	*N-PAC*	2.795	2.545	2.535
238744_at	*ATPBD4*	2.755	2.505	2.515
206217_at	*EDA*	2.46	2.25	2.23
200810_s_at	*CIRBP*	14.15	12.87	12.87
236726_at	*NA*	2.84	2.58	2.58
209889_at	*SEC31B*	2.595	2.365	2.355
244338_at	*LDLRAD3*	3.025	2.755	2.745
224003_at	*TTTY14*	3.145	2.865	2.865
1569482_at	*NA*	3.69	3.37	3.34
1554801_at	*MGC27121*	2.86	2.61	2.6
1566889_at	*THADA*	2.63	2.4	2.39
238383_at	*C6orf58*	2.42	2.21	2.2
241450_at	*RSPO1*	2.47	2.25	2.25
214463_x_at	*HIST1H4K*	2.745	2.505	2.495
235527_at	*LOC284214*	3.12	2.85	2.83
206659_at	*FLJ14082*	2.715	2.485	2.465
1555053_at	*SYT9*	2.675	2.435	2.435
1570585_at	*LOC196264*	3.07	2.8	2.78

229486_s_at	*TMEM132A*	2.605	2.365	2.365
242182_x_at	*ITCH*	3.945	3.595	3.585
215804_at	*EPHA1*	2.595	2.365	2.355
1552787_at	*HELB*	3.15	2.88	2.85
1553868_a_at	*C5orf36*	3.58	3.26	3.26
1553074_at	*ASB11*	2.585	2.355	2.345
1559807_at	*SERF1A*	2.815	2.555	2.555
214400_at	*INSL3*	2.525	2.305	2.295
1569714_at	*ZFYVE20*	2.985	2.725	2.715
219018_s_at	*C14orf65*	7.425	6.745	6.775
236450_at	*TARSL2*	2.405	2.185	2.185
225054_x_at	*AMZ2*	3.075	2.805	2.785
233367_at	*LIFR*	3.205	2.935	2.915
243517_at	*NA*	2.595	2.355	2.355
226022_at	*SASH1*	13.245	12.005	12.115
223860_at	*NA*	2.525	2.305	2.305
208642_s_at	*XRCC5*	10.51	9.59	9.55
1564272_a_at	*KLHDC1*	3.39	3.1	3.07
210761_s_at	*GRB7*	2.365	2.145	2.155
202229_s_at	*CHERP*	2.375	2.155	2.165
235006_at	*MGC13017*	4.105	3.725	3.755
226906_s_at	*ARHGAP9*	3.255	2.975	2.945
244293_at	*NA*	3.36	3.07	3.05
241697_at	*NA*	2.44	2.23	2.21
229144_at	*KIAA1026*	7.015	6.425	6.355
239234_at	*OGDH*	3.535	3.235	3.205
235748_s_at	*MTHFD2L*	3.28	2.98	2.98
208375_at	*IFNA1*	2.745	2.505	2.495
201551_s_at	*LAMP1*	2.38	2.16	2.17
207236_at	*ZNF345*	2.97	2.71	2.71
1569481_s_at	*SNX22*	2.46	2.24	2.24

241969_at	*ARID5B*	2.875	2.625	2.605
227319_at	*NA*	8.72	7.91	7.97
229560_at	*TMSB4X*	2.595	2.355	2.365
1561099_at	*FLJ32756*	2.805	2.555	2.545
215760_s_at	*SBNO2*	2.69	2.44	2.46
1552338_at	*GSC*	2.105	1.915	1.925
217536_x_at	*NA*	3.77	3.42	3.45
1562776_at	*LOC339807*	2.64	2.41	2.4
238373_at	*H1FNT*	2.68	2.44	2.44
213014_at	*MAPK8IP1*	2.295	2.095	2.085
229046_s_at	*PLEKHB1*	2.61	2.38	2.37
237759_at	*CD48*	3.225	2.945	2.945
1557366_at	*FLJ36492*	3.655	3.345	3.325
204486_at	*KCNQ1*	2.9	2.65	2.63
224522_s_at	*DCAKD*	2.495	2.275	2.275
203277_at	*DFFA*	5.6	5.1	5.1
216238_s_at	*FGB*	2.775	2.535	2.525
221774_x_at	*FAM48A*	6.49	5.91	5.92
216456_at	*PCDH9*	2.345	2.145	2.135
211605_s_at	*RARA*	2.72	2.48	2.48
239083_at	*ZNF786*	3.41	3.11	3.1
217772_s_at	*MTCH2*	10.935	9.955	9.965
229358_at	*IHH*	2.4	2.19	2.18
236859_at	*RUNX2*	3.3	3.02	2.99
217063_x_at	*TRA@*	2.72	2.48	2.48
232717_at	*KALRN*	2.52	2.3	2.3
1561658_at	*PPP2R2B*	2.625	2.385	2.385
244060_at	*ADD2*	2.47	2.25	2.25
214542_x_at	*HIST1H2AI*	2.52	2.3	2.3
239944_at	*SERF1A*	2.475	2.255	2.255
202712_s_at	*CKMT1B*	2.53	2.31	2.3

210360_s_at	*MTSS1*	2.345	2.145	2.145
1563121_at	*NA*	2.29	2.09	2.09
216909_at	*RRP12*	2.505	2.285	2.285
45714_at	*HCFC1R1*	4.365	3.965	3.995
1559603_at	*GPR12*	2.405	2.185	2.195
213431_x_at	*SFI1*	4.655	4.235	4.245
200029_at	*RPL19*	12.14	11.03	11.1
1561165_a_at	*DEFB108B*	3.095	2.825	2.815
229191_at	*TBCD*	3.12	2.84	2.84
241247_at	*NA*	2.71	2.47	2.47
241876_at	*MDM4*	2.415	2.195	2.195
1566688_at	*NA*	2.29	2.09	2.09
238721_at	*MDH1B*	2.27	2.07	2.07
203752_s_at	*JUND*	12.91	11.72	11.82
204912_at	*IL10RA*	2.335	2.135	2.125
208272_at	*RANBP3*	3.67	3.33	3.36
209932_s_at	*DUT*	9.27	8.44	8.46
215017_s_at	*FNBP1L*	10.9	9.93	9.95
210824_at	*NA*	2.3	2.1	2.1
214938_x_at	*HMGB1*	14.645	13.395	13.295
1554156_a_at	*WFDC8*	2.565	2.345	2.345
235888_at	*NA*	2.905	2.655	2.645
204107_at	*NFYA*	2.625	2.375	2.405
1569683_at	*XYLB*	2.94	2.67	2.69
1562921_at	*LOC646927*	3.025	2.775	2.755
224100_s_at	*DPYSL5*	2.565	2.345	2.335
231026_at	*EFHC1*	2.19	1.99	1.99
221846_s_at	*CASKIN2*	4.255	3.855	3.895
200608_s_at	*RAD21*	11.685	10.705	10.615
242210_at	*ZNF24*	2.415	2.195	2.205
224448_s_at	*C6orf125*	8.57	7.79	7.83

234188_at	*RAB38*	2.55	2.33	2.33
233695_s_at	*CECR2*	2.865	2.605	2.615
229815_at	*NA*	3.845	3.515	3.495
230744_at	*NA*	8.005	7.285	7.325
1559002_at	*LOC340544*	2.47	2.24	2.26
240788_at	*ME1*	2.445	2.225	2.225
242077_x_at	*C6orf150*	3.6	3.27	3.29
234770_at	*NA*	2.71	2.47	2.47
1552544_at	*SERPINA12*	3	2.74	2.73
210816_s_at	*CYB561*	2.135	1.955	1.945
239193_at	*FUBP3*	2.605	2.375	2.385
229335_at	*CADM4*	3.035	2.775	2.765
213784_at	*RABL4*	2.23	2.03	2.03
1562546_at	*NA*	2.98	2.73	2.71
244067_x_at	*ZADH2*	3.21	2.93	2.93
237199_at	*TAF5L*	2.92	2.67	2.65
220695_at	*NA*	2.375	2.175	2.175
216548_x_at	*HMG4L*	2.51	2.29	2.29
215490_at	*C1orf69*	3.87	3.55	3.52
1569894_at	*PPP2R3C*	3.385	3.095	3.075
217636_at	*POLG*	2.615	2.395	2.385
209080_x_at	*TXNL2*	8.88	8.11	8.1
228249_at	*C11orf74*	6.59	6	6.02
236061_at	*PRDM15*	2.815	2.575	2.575
234095_at	*ATP8B1*	2.91	2.65	2.65
241637_at	*LOC645478*	4.015	3.665	3.655
1561918_at	*NA*	3.035	2.775	2.775
207145_at	*GDF8*	3.155	2.895	2.865
235503_at	*ASB5*	2.98	2.72	2.72
232246_at	*KIAA1648*	2.24	2.04	2.04
241615_x_at	*CD55*	2.615	2.395	2.395

215539_at	*NA*	3.345	3.065	3.035
220952_s_at	*PLEKHA5*	8.93	8.19	8.11
231689_at	*TRPM7*	2.385	2.185	2.175
238527_at	*NA*	2.905	2.655	2.635
231651_at	*ITGB3*	2.91	2.66	2.65
242512_at	*MYO9A*	4.61	4.19	4.23
1562697_at	*LOC339988*	2.59	2.37	2.37
217486_s_at	*ZDHHC17*	2.665	2.435	2.425
200902_at	*15-Sep*	13.86	12.71	12.6
228491_at	*KRT17*	2.74	2.5	2.5
1557744_at	*MYH7B*	2.58	2.36	2.35
221122_at	*HRASLS2*	3.2	2.94	2.9
1559583_at	*CD276*	2.585	2.365	2.365
231658_x_at	*RPL36*	3.69	3.38	3.36
201737_s_at	*6-Mar*	10.87	9.91	9.95
1565657_at	*CMTM6*	3.375	3.095	3.065
210660_at	*LILRA1*	2.815	2.575	2.575
210438_x_at	*TROVE2*	11.12	10.12	10.19
240620_at	*NA*	2.615	2.395	2.385
1560630_at	*NA*	2.335	2.135	2.135
1561015_at	*KLF3*	2.465	2.245	2.245
237891_at	*MDM2*	2.685	2.445	2.455
241331_at	*SKAP2*	2.445	2.235	2.225
208662_s_at	*TTC3*	13.355	12.155	12.245
217701_x_at	*ATRX*	3.17	2.89	2.89
216190_x_at	*ITGB1*	2.915	2.655	2.655
221866_at	*TFEB*	3.18	2.9	2.9
231789_at	*PCDHB14*	3.02	2.76	2.75
1557867_s_at	*C9orf117*	3	2.73	2.75
1568696_at	*ARMETL1*	2.655	2.445	2.415
1567627_at	*CD74*	2.505	2.285	2.285

223427_s_at	*EPB41L4B*	3.045	2.785	2.785
1569876_at	*C17orf57*	3.575	3.275	3.265
205349_at	*GNA15*	3.05	2.79	2.78
1557218_s_at	*FANCB*	2.955	2.705	2.695
210117_at	*SPAG1*	2.955	2.685	2.715
1559653_at	*GRTP1*	3.095	2.845	2.815
200026_at	*RPL34*	12.87	11.72	11.79
217197_x_at	*CG018*	2.55	2.33	2.33
230517_at	*REPIN1*	2.465	2.255	2.245
1568892_at	*NA*	2.975	2.725	2.705
217702_at	*IL27RA*	2.7	2.47	2.46
202569_s_at	*MARK3*	9.67	8.79	8.88
201795_at	*LBR*	10.26	9.41	9.34
241977_s_at	*RAB3C*	2.395	2.185	2.195
241555_at	*NA*	2.655	2.435	2.425
212034_s_at	*EXOC7*	9.425	8.615	8.595
221474_at	*MRLC2*	12.125	11.025	11.145
241576_at	*NA*	3.45	3.17	3.14
201050_at	*PLD3*	5.79	5.3	5.28
200909_s_at	*RPLP2*	10.305	9.445	9.395
1553254_at	*MAGEE2*	2.77	2.53	2.53
1570200_at	*HELB*	3.07	2.82	2.79
1569176_at	*TMPRSS12*	2.385	2.185	2.175
200963_x_at	*RPL31*	15.055	13.835	13.685
236002_at	*RPS2*	3.02	2.76	2.76
231970_at	*C14orf118*	4	3.68	3.64
238588_at	*CCNI*	4.32	3.94	3.95
201211_s_at	*DDX3X*	3.185	2.915	2.905
1564883_a_at	*TAS1R1*	2.275	2.075	2.085
240819_at	*NA*	2.925	2.675	2.665
243325_at	*GSTK1*	2.945	2.695	2.685

207158_at	*APOBEC1*	2.495	2.275	2.275
243696_at	*KIAA0562*	3.185	2.915	2.905
229282_at	*GATA6*	2.61	2.39	2.38
213849_s_at	*PPP2R2B*	2.945	2.695	2.685
241149_at	*KLHDC4*	2.32	2.12	2.12
215441_at	*LOC728759*	3.135	2.885	2.855
224120_at	*NA*	2.26	2.06	2.06
242439_s_at	*ASXL1*	6.795	6.215	6.215
1557753_at	*NA*	2.52	2.3	2.3
240277_at	*SLC30A7*	10.65	9.74	9.73
244644_at	*TMSB4X*	3.275	3.005	2.985
207573_x_at	*ATP5L*	9.34	8.5	8.59
230573_at	*SGK2*	3.06	2.8	2.8
1562300_at	*SLC8A3*	3.395	3.105	3.095
229799_s_at	*NCAM1*	2.59	2.37	2.37
205575_at	*C1QL1*	3.355	3.075	3.065
1569685_at	*NA*	2.39	2.19	2.19
44563_at	*WDR79*	4.48	4.11	4.09
1566576_at	*DPYSL5*	2.505	2.285	2.285
242432_at	*LRRC37A2*	3.245	2.975	2.955
231209_at	*C14orf73*	2.765	2.525	2.525
211238_at	*ADAM7*	2.715	2.485	2.475
200775_s_at	*HNRPK*	12.35	11.24	11.34
237744_at	*NA*	3.06	2.81	2.79
1558934_a_at	*NA*	3.695	3.365	3.395
212477_at	*CENTB2*	2.535	2.315	2.315
216216_at	*SLIT3*	2.975	2.705	2.725
1554103_at	*NA*	3.105	2.845	2.845
37953_s_at	*ACCN2*	2.42	2.22	2.21
216053_x_at	*RP13-401N8.2*	3.2	2.92	2.92
207770_x_at	*CSH2*	2.43	2.22	2.23

201450_s_at	*TIA1*	9.86	9.01	9.03
234752_x_at	*DMD*	3.325	3.055	3.035
232226_at	*LRRC4C*	2.82	2.59	2.57
221113_s_at	*WNT16*	2.505	2.295	2.285
233666_at	*TMEM106B*	2.81	2.58	2.56
235307_at	*LMTK2*	2.835	2.595	2.595
210883_x_at	*EFNB3*	2.675	2.445	2.455
1554696_s_at	*TYMS*	2.605	2.385	2.385
243979_at	*NA*	2.665	2.445	2.435
210848_at	*NA*	2.915	2.675	2.665
209740_s_at	*PNPLA4*	3.32	3.04	3.04
1558523_at	*C6orf60*	3.05	2.79	2.79
232993_at	*SYNJ1*	3.52	3.23	3.22
237204_at	*DPH1*	2.735	2.495	2.495
228808_s_at	*LOXL2*	2.17	1.99	1.99
201044_x_at	*DUSP1*	3.825	3.505	3.495
1555568_at	*MGC22265*	3.04	2.79	2.77
1553533_at	*JPH1*	2.715	2.485	2.475
225463_x_at	*LOC653519*	7.345	6.745	6.705
1561064_a_at	*NA*	2.635	2.415	2.405
240843_at	*PTPN2*	4.7	4.28	4.32
242626_at	*RP5-875H10.1*	2.455	2.245	2.265
229522_at	*HSPC105*	2.575	2.365	2.355
1557386_at	*LCT*	3.07	2.82	2.8
1554272_at	*LRAP*	2.89	2.65	2.64
234665_x_at	*HHLA3*	2.665	2.445	2.435
1557000_at	*ESPNL*	2.555	2.335	2.345
208956_x_at	*DUT*	12.165	11.125	11.135
207575_at	*GOLGA*	2.62	2.4	2.4
207023_x_at	*KRT10*	11.02	10.06	10.11
240010_at	*LMX1B*	2.82	2.59	2.57

239362_at	*NAPA*	2.705	2.485	2.475
205371_s_at	*DBT*	3.61	3.31	3.3
1560977_a_at	*BCL2L13*	2.64	2.42	2.42
1561079_at	*ANKRD28*	3.3	3.03	3.01
208877_at	*PAK2*	12.56	11.55	11.45
207527_at	*KCNJ9*	2.54	2.33	2.32
227168_at	*FLJ25967*	6.11	5.6	5.58
1566208_at	*TCEA1*	2.505	2.295	2.285
1555082_a_at	*NEK11*	2.785	2.555	2.535
226715_at	*FOXK1*	11.35	10.34	10.44
213210_at	*TAF6L*	2.82	2.59	2.57
1560070_at	*NA*	2.575	2.355	2.355
223372_at	*DNAJC4*	2.775	2.545	2.535
236499_at	*C1orf86*	4.215	3.835	3.875
1560639_at	*STMN3*	2.745	2.505	2.505
233701_at	*NRP1*	6.435	5.895	5.885
201701_s_at	*PGRMC2*	12.175	11.145	11.155
1564729_at	*NA*	2.63	2.41	2.41
202942_at	*ETFB*	7.985	7.345	7.275
230093_at	*TSGA2*	3.045	2.785	2.785
213728_at	*LAMP1*	12.96	11.86	11.87
226303_at	*PGM5*	3.135	2.875	2.875
1552842_at	*HS6ST3*	2.515	2.295	2.295
233711_at	*LOC645256*	3.13	2.88	2.85
1555180_at	*NA*	2.505	2.295	2.285
230555_s_at	*THRAP6*	2.38	2.18	2.18
206166_s_at	*CLCA2*	2.95	2.71	2.71
208695_s_at	*RPL39*	15.67	14.4	14.3
230248_x_at	*NA*	3.08	2.82	2.82
1554737_at	*FBN2*	2.475	2.265	2.275
216365_x_at	*IGL@*	2.285	2.095	2.085

234671_at	*KRTAP4-2*	2.645	2.425	2.425
228784_at	*ST3GAL2*	2.52	2.31	2.3
1569439_at	*NEDD4*	2.88	2.64	2.64
240204_at	*SNRPN*	2.83	2.6	2.58
234956_at	*LOC93444*	2.85	2.61	2.61
241341_at	*NA*	2.61	2.39	2.39
1569864_at	*SERAC1*	2.79	2.56	2.55
203862_s_at	*ACTN2*	3.08	2.82	2.82
1562712_at	*NA*	2.585	2.365	2.365
217471_at	*NA*	2.56	2.34	2.34
208693_s_at	*GARS*	13.22	12.11	12.12
206527_at	*ABAT*	2.675	2.455	2.445
210929_s_at	*AHSG*	3.25	2.97	2.98
1562371_s_at	*MGC26733*	2.735	2.515	2.505
231594_at	*NA*	2.555	2.345	2.335
203052_at	*C2*	2.66	2.44	2.44
243774_at	*MUC20*	3.52	3.23	3.21
230456_at	*OAF*	2.67	2.45	2.45
216712_at	*TMEM132A*	2.82	2.58	2.58
1554722_at	*TRPM3*	3.135	2.885	2.865
206005_s_at	*KIAA1009*	3.865	3.525	3.565
1557478_at	*KIAA1505*	2.9	2.65	2.66
202457_s_at	*PPP3CA*	12.23	11.18	11.24
1558448_a_at	*JMJD2B*	2.955	2.725	2.705
213231_at	*DMWD*	2.9	2.66	2.66
217191_x_at	*NA*	3.32	3.06	3.03
1554310_a_at	*EIF4G3*	2.695	2.475	2.475
213484_at	*NA*	2.685	2.465	2.455
211369_at	*NA*	3.295	3.025	3.015
239900_x_at	*NA*	3.69	3.38	3.39
229156_s_at	*ABP1*	2.86	2.63	2.61

212614_at	*ARID5B*	12.01	11	11.02
221149_at	*GPR77*	2.45	2.25	2.25
240068_at	*C21orf130*	3.165	2.905	2.905
234542_at	*ARHGEF12*	2.485	2.275	2.285
1566168_at	*LOC729986*	2.43	2.23	2.23
1555004_a_at	*RBL1*	2.7	2.48	2.47
240224_at	*PRDM10*	2.42	2.22	2.22
237343_at	*NA*	2.465	2.265	2.255
1561362_at	*NA*	3.765	3.445	3.455
211893_x_at	*CD6*	2.535	2.325	2.315
230671_at	*LOC389257*	3.515	3.225	3.215
210637_at	*TACR1*	2.235	2.055	2.055
1560209_at	*NA*	3.695	3.405	3.375
214284_s_at	*FGF18*	2.235	2.045	2.055
238782_at	*NA*	3.795	3.465	3.485
236036_at	*NA*	2.585	2.375	2.355
235628_x_at	*FLJ33630*	3.945	3.615	3.625
238409_x_at	*OXR1*	2.46	2.25	2.26
237659_at	*FLJ40288*	2.225	2.045	2.045
1557698_at	*CBWD1*	3.35	3.08	3.07
1558608_a_at	*PAPPA*	3.525	3.245	3.215
225917_at	*NA*	9.87	9.03	9.08
213687_s_at	*RPL35A*	10.23	9.34	9.43
1555688_s_at	*SLA2*	2.645	2.435	2.425
1561756_at	*NA*	2.48	2.28	2.28
242229_at	*NAPE-PLD*	4.365	4.015	3.995
223545_at	*FANCD2*	2.7	2.49	2.47
221212_x_at	*PB1*	3.66	3.37	3.35
238254_at	*ZNF677*	2.92	2.68	2.68
1568648_a_at	*LOC730087*	2.88	2.64	2.64
215798_at	*ALDH1L1*	4.34	3.98	3.98

200050_at	*ZNF146*	12.91	11.87	11.83
220644_at	*C1orf197*	2.56	2.35	2.34
222152_at	*PDCD6*	4.005	3.675	3.665
214044_at	*RYR2*	2.8	2.57	2.56
1552615_at	*ACACB*	6.12	5.64	5.59
226661_at	*CDCA2*	6.675	6.135	6.125
220493_at	*DMRT1*	2.785	2.565	2.555
209658_at	*CDC16*	10.835	9.905	9.975
240455_at	*NA*	3.075	2.815	2.825
212653_s_at	*EHBP1*	11.15	10.21	10.25
205146_x_at	*APBA3*	2.42	2.22	2.22
227321_at	*GATS*	2.63	2.41	2.41
243987_at	*NA*	2.63	2.42	2.41
240659_x_at	*C14orf106*	3.72	3.42	3.41
202502_at	*ACADM*	9.23	8.48	8.46
1557495_at	*NA*	3.755	3.465	3.435
1560618_at	*NA*	2.525	2.315	2.325
238291_at	*KIAA0776*	3.35	3.07	3.07
1556932_at	*NA*	2.43	2.23	2.23
1553127_a_at	*RNF168*	3.45	3.17	3.17
215397_x_at	*THSD4*	3.21	2.94	2.95
212971_at	*CARS*	12.18	11.16	11.2
234293_x_at	*NA*	2.605	2.395	2.385
239197_s_at	*EZH1*	4.66	4.28	4.28
218835_at	*SFTPA2*	2.44	2.24	2.24
205208_at	*ALDH1L1*	2.63	2.41	2.41
234316_x_at	*KLK12*	2.69	2.47	2.46
239117_at	*LOC643950*	2.285	2.105	2.105
1553103_at	*NFX1*	9.575	8.825	8.765
210546_x_at	*CTAG1B*	2.565	2.355	2.345
1553266_at	*CNOT6L*	3.025	2.795	2.765

233103_at	*NA*	2.535	2.335	2.335
1556038_at	*NA*	3.015	2.785	2.755
231010_at	*C4orf16*	2.38	2.18	2.19
232570_s_at	*ADAM33*	4.23	3.87	3.9
1555980_a_at	*FLJ39609*	3.105	2.855	2.845
207100_s_at	*VAMP1*	2.995	2.745	2.765
202217_at	*C21orf33*	10.99	10.14	10.04
223631_s_at	*C19orf33*	3.295	3.045	3.015
242249_at	*NA*	2.865	2.625	2.625
221607_x_at	*ACTG1*	15.08	13.77	13.91
238019_at	*LRG1*	2.755	2.545	2.525
244891_x_at	*PVT1*	2.75	2.53	2.53
1555978_s_at	*LOC727918*	2.67	2.46	2.44
206285_at	*NPHP1*	2.805	2.585	2.575
241232_x_at	*NA*	2.635	2.425	2.415
219058_x_at	*TINAGL1*	3.25	2.99	2.98
242788_at	*JMJD2D*	2.66	2.44	2.44
243631_at	*HSMPP8*	5.285	4.855	4.845
216767_at	*PARVA*	2.66	2.44	2.44
205742_at	*TNNI3*	2.495	2.295	2.295
228650_at	*NA*	9.09	8.32	8.38
229942_at	*BNC2*	6.975	6.405	6.415
206297_at	*CTRC*	4.025	3.705	3.695
238643_at	*NBL1*	2.16	1.98	1.98
207647_at	*CDY1*	3.085	2.835	2.825
215682_at	*LOC440792*	2.25	2.07	2.06
206815_at	*SPAG8*	3.42	3.15	3.13
235849_at	*SCARA5*	2.27	2.09	2.09
213980_s_at	*CTBP1*	10.305	9.425	9.505
211917_s_at	*PRLR*	2.68	2.46	2.46
237359_at	*NA*	2.555	2.355	2.345

1555774_at	*ZAR1*	2.86	2.63	2.62
235584_at	*LOC285033*	2.51	2.31	2.31
203601_s_at	*ZBTB17*	3.98	3.66	3.66
1566339_at	*CHD8*	3.105	2.855	2.845
229661_at	*SALL4*	2.555	2.355	2.355
233035_at	*NA*	3.055	2.805	2.825
32540_at	*PPP3CC*	2.73	2.5	2.51
214448_x_at	*NFKBIB*	6.225	5.715	5.725
226482_s_at	*F11R*	2.7	2.48	2.48
219693_at	*AGPAT4*	2.44	2.25	2.23
231734_at	*RBP2*	2.535	2.335	2.335
244847_at	*PKD2L2*	3.24	2.97	2.99
213539_at	*CD3D*	2.46	2.26	2.26
1554631_at	*ATM*	2.23	2.05	2.05
219534_x_at	*CDKN1C*	2.885	2.645	2.655
209766_at	*PRDX3*	2.415	2.215	2.225
237810_at	*CLDN6*	2.755	2.545	2.525
242970_at	*DIP2B*	2.915	2.675	2.675
232460_at	*NA*	2.58	2.38	2.37
241562_x_at	*NA*	2.94	2.71	2.7
205563_at	*KISS1*	2.435	2.245	2.235
236604_at	*BAHCC1*	2.71	2.49	2.49
229684_s_at	*ZNF644*	2.635	2.415	2.415
207955_at	*CCL27*	3.14	2.88	2.89
215304_at	*THSD4*	2.74	2.52	2.52
1555186_at	*CDKN1A*	2.29	2.11	2.1
1557816_a_at	*NA*	2.68	2.46	2.46
1559504_at	*FLJ35409*	3.325	3.065	3.055
240279_at	*WDFY2*	3.64	3.35	3.33
1559443_s_at	*LOC283888*	2.69	2.48	2.46
239094_at	*NA*	2.51	2.31	2.31

233676_at	*GPC6*	2.97	2.73	2.73
1560298_at	*NA*	2.73	2.51	2.51
218356_at	*FTSJ2*	9.565	8.835	8.765
215061_at	*LOC399818*	3.675	3.395	3.365
201254_x_at	*RPS6*	12.995	11.925	11.975
1554518_at	*GSTCD*	4.79	4.41	4.41
1556768_at	*NA*	2.56	2.35	2.36
221610_s_at	*STAP2*	2.41	2.22	2.21
230518_at	*EVA1*	3.075	2.825	2.835
210397_at	*DEFB1*	2.885	2.655	2.645
204991_s_at	*NF2*	3.105	2.865	2.855
222098_s_at	*MZF1*	3.04	2.8	2.8
207173_x_at	*CDH11*	13.535	12.415	12.485
215158_s_at	*DEDD*	9.53	8.77	8.76
215737_x_at	*USF2*	7.46	6.84	6.88
1554393_a_at	*ADC*	2.525	2.325	2.325
237950_s_at	*NA*	3.075	2.845	2.815
243846_x_at	*FLJ32810*	3.265	2.995	3.005
231702_at	*TDO2*	2.395	2.205	2.195
207768_at	*EGR4*	2.68	2.46	2.46
229811_at	*NA*	2.835	2.615	2.615
1553179_at	*ADAMTS19*	2.475	2.275	2.275
1566987_s_at	*LOC728850*	3.19	2.93	2.94
1562470_at	*C1orf83*	2.54	2.34	2.34
220659_s_at	*C7orf43*	5.99	5.51	5.51
230743_at	*HOXB5*	3.54	3.26	3.25
213945_s_at	*NUP210*	3.02	2.78	2.78
1553263_at	*USH1G*	2.53	2.32	2.34
233458_at	*POLR3E*	2.295	2.115	2.115
229945_at	*CYHR1*	2.615	2.415	2.405
214257_s_at	*SEC22B*	15.3	14.04	14.12

243348_at	*WDFY1*	2.795	2.565	2.575
1570414_x_at	*FLJ13197*	2.335	2.145	2.155
219794_at	*VPS53*	2.605	2.405	2.395
209919_x_at	*GGT1*	3.32	3.06	3.05
212772_s_at	*ABCA2*	3.08	2.84	2.83
219309_at	*CTA-216E10.6*	2.595	2.405	2.385
1564028_s_at	*FLJ40722*	2.47	2.28	2.27
240949_x_at	*GALNT10*	3.24	2.99	2.97
202762_at	*ROCK2*	11.525	10.605	10.605
224880_at	*RALA*	13.625	12.585	12.505
242105_at	*CCNE1*	2.51	2.31	2.31
223686_at	*TPK1*	2.945	2.715	2.695
240487_at	*NA*	2.695	2.485	2.475
210343_s_at	*SLC22A6*	2.99	2.76	2.75
233082_at	*ZNF630*	3.03	2.79	2.79
243895_x_at	*SMAD2*	2.875	2.655	2.645
1554707_at	*C9orf68*	3.07	2.84	2.82
205413_at	*MPPED2*	2.645	2.435	2.425
221433_at	*FGF21*	2.575	2.385	2.365
1556248_at	*MYRIP*	2.925	2.695	2.685
1559990_at	*CAMK1D*	2.955	2.715	2.715
1555214_a_at	*CLEC7A*	2.675	2.465	2.455
1566646_at	*LOC149086*	5.29	4.87	4.87
213293_s_at	*TRIM22*	9.84	9.08	9.03
1566426_at	*SBF2*	2.845	2.615	2.625
232900_at	*HERC2P7*	2.315	2.135	2.135
203948_s_at	*MPO*	2.31	2.13	2.13
239800_at	*NA*	3.03	2.79	2.79
237364_at	*ZNF529*	3.52	3.23	3.25
238944_at	*NA*	7.33	6.73	6.77
206780_at	*GAD2*	2.71	2.5	2.48

244168_s_at	*ULK4*	2.945	2.705	2.715
221180_at	*YSK4*	2.57	2.37	2.37
211846_s_at	*PVRL1*	2.435	2.245	2.225
233319_x_at	*PHACTR4*	6.275	5.775	5.775
216938_x_at	*DRD2*	2.52	2.32	2.32
1564590_a_at	*OFCC1*	2.54	2.34	2.34
211712_s_at	*ANXA9*	2.47	2.27	2.27
1558594_at	*LOC643382*	2.5	2.3	2.3
214060_at	*TAS2R5*	2.51	2.31	2.32
1563571_at	*LOC285463*	2.56	2.36	2.36
240198_at	*NA*	2.365	2.185	2.175
224067_at	*NA*	3.385	3.125	3.115
207244_x_at	*CYP2A6*	4.37	4.03	4.02
226623_at	*PHYHIPL*	2.76	2.54	2.54
224375_at	*NA*	12.515	11.555	11.505
1564165_at	*PRKRIP1*	4.5	4.15	4.14
217147_s_at	*TRAT1*	2.99	2.76	2.74
224424_x_at	*LOC644773*	2.395	2.215	2.205
238367_s_at	*MGC33556*	2.76	2.54	2.54
239745_at	*PAN3*	2.395	2.215	2.215
1564443_at	*DLEU2*	2.395	2.215	2.205
216656_at	*NA*	2.95	2.72	2.71
1555467_a_at	*CUGBP1*	2.83	2.61	2.6
230510_at	*HSPB9*	2.58	2.38	2.38
206433_s_at	*SPOCK3*	2.82	2.6	2.6
1555102_at	*FGF7*	3.33	3.07	3.07
230727_at	*PCGF2*	5.255	4.825	4.855
242962_at	*NA*	4.165	3.835	3.845
207263_x_at	*VEZT*	3.165	2.925	2.915
233913_at	*WFDC10A*	2.645	2.445	2.435
222758_s_at	*TMEM132A*	2.26	2.08	2.08

244017_at	*JAZF1*	2.635	2.435	2.435
44673_at	*SIGLEC1*	2.525	2.325	2.325
219846_at	*GON4L*	2.8	2.58	2.58
1552779_a_at	*SLC44A5*	3.05	2.82	2.81
211230_s_at	*PIK3CD*	2.745	2.525	2.535
214562_at	*HIST1H4L*	2.465	2.265	2.275
202393_s_at	*KLF10*	11.305	10.475	10.375
1557813_at	*SSBP2*	2.205	2.025	2.035
241337_at	*LOC728347*	2.705	2.495	2.485
1556149_at	*COMT*	2.31	2.13	2.13
217671_at	*RFX3*	2.505	2.305	2.315
1553258_at	*FLJ30679*	2.51	2.31	2.31
208370_s_at	*DSCR1*	13.11	12.13	12.05
218558_s_at	*MRPL39*	8.815	8.095	8.165
216316_x_at	*GK*	2.49	2.29	2.3
206466_at	*ACSBG1*	4.055	3.745	3.735
1565562_at	*FLJ21687*	5.795	5.325	5.355
222608_s_at	*ANLN*	9.7	8.97	8.92
1552370_at	*C4orf33*	2.865	2.655	2.635
239826_at	*C18orf45*	2.965	2.735	2.725
234253_at	*NA*	2.975	2.745	2.725
1561336_at	*DNASE1L3*	2.485	2.295	2.285
205814_at	*GRM3*	2.495	2.295	2.295
227959_at	*NA*	3.015	2.785	2.765
243876_at	*FNBP1*	2.83	2.61	2.61
231289_at	*NCOA1*	2.62	2.42	2.41
215313_x_at	*HLA-A*	12.38	11.4	11.43
239746_at	*KIAA1199*	2.685	2.485	2.475
217069_at	*MLL4*	2.695	2.495	2.485
215711_s_at	*WEE1*	2.415	2.225	2.235
230379_x_at	*PRKD3*	9.06	8.32	8.4

204296_at	*SLC4A5*	3.1	2.86	2.86
1566526_at	*LOC283688*	2.65	2.46	2.44
211921_x_at	*PTMA*	15.425	14.265	14.195
200873_s_at	*CCT8*	12.69	11.74	11.68
1568590_at	*ARL3*	2.525	2.335	2.325
241648_at	*ITSN2*	2.51	2.31	2.31
210130_s_at	*TM7SF2*	2.385	2.205	2.205
244839_at	*TTN*	3.07	2.84	2.82
1570529_at	*KIAA0020*	3.32	3.07	3.05
207473_at	*MLN*	2.385	2.205	2.205
205763_s_at	*DDX18*	9.76	9.02	8.98
241532_at	*RMND5A*	3.09	2.86	2.84
200066_at	*IK*	9.465	8.755	8.705
207017_at	*RAB27B*	3.14	2.91	2.89
217186_at	*NA*	2.735	2.525	2.515
229937_x_at	*LILRB1*	2.935	2.715	2.705
222371_at	*PIAS1*	3.39	3.13	3.13
1560657_at	*TIE1*	3.1	2.87	2.85
213583_x_at	*EEF1A1*	15.655	14.505	14.395
203668_at	*MAN2C1*	2.095	1.935	1.935
235800_at	*HSPA12A*	3.575	3.295	3.295
1564372_s_at	*CASC2*	2.58	2.38	2.38
220376_at	*LRRC19*	2.975	2.755	2.745
238860_at	*C6orf130*	5.44	5.03	5.01
222973_at	*UNC13B*	3.07	2.84	2.83
244364_at	*MYO3A*	2.44	2.26	2.25
207886_s_at	*CALCR*	3.04	2.81	2.8
210760_x_at	*TRIP11*	2.555	2.355	2.355
216062_at	*CD44*	3.205	2.975	2.955
231053_at	*NA*	2.31	2.13	2.13
227571_at	*NA*	2.39	2.21	2.21

201696_at	*SFRS4*	9.4	8.67	8.68
243073_at	*C6orf153*	2.505	2.305	2.305
241106_at	*SDCCAG10*	3.1	2.85	2.87
219802_at	*FLJ22028*	9.84	9.07	9.1
217129_at	*NA*	2.37	2.19	2.19
1552783_at	*ZNF417*	3.435	3.185	3.165
202618_s_at	*MECP2*	3.02	2.77	2.79
231818_x_at	*SLC20A2*	5.025	4.625	4.655
241188_at	*PIP3-E*	3.08	2.85	2.83
1561096_at	*LOC285419*	2.525	2.325	2.325
217475_s_at	*LIMK2*	2.715	2.515	2.505
219300_s_at	*CNTNAP2*	3.23	2.99	2.99
230402_at	*DUSP15*	3.205	2.975	2.955
242159_at	*NA*	3.17	2.93	2.92
220563_s_at	*SHANK1*	2.44	2.26	2.25
240171_at	*PTGS1*	3.11	2.87	2.87
229761_at	*LOC440173*	4.19	3.87	3.87
200699_at	*KDELR2*	13.165	12.155	12.165
239934_x_at	*HOXA11S*	3.325	3.075	3.065
224097_s_at	*F11R*	3.72	3.45	3.43
216397_s_at	*BOP1*	5.315	4.935	4.895
237112_at	*FAM102B*	3.29	3.04	3.03
234285_at	*SYNGAP1*	2.33	2.15	2.15
227248_at	*PLEKHH3*	2.705	2.505	2.505
1554176_a_at	*C3orf33*	2.89	2.67	2.67
216635_at	*NA*	2.525	2.315	2.335
1564654_at	*COL4A6*	2.455	2.275	2.275
237427_at	*NA*	2.62	2.42	2.42
234355_s_at	*PTCHD2*	2.06	1.9	1.9
1560758_at	*NA*	3.565	3.305	3.275
223190_s_at	*MLL5*	10.845	10.035	10.005

217152_at	*NA*	3.855	3.555	3.565
1561089_at	*NA*	2.655	2.455	2.445
1558745_at	*LOC92017*	2.73	2.53	2.52
226573_at	*DIRAS1*	3.455	3.205	3.185
204380_s_at	*FGFR3*	2.525	2.335	2.325
202163_s_at	*CNOT8*	10.24	9.43	9.48
205850_s_at	*GABRB3*	2.685	2.485	2.475
219666_at	*MS4A6A*	2.295	2.115	2.115
1555694_a_at	*KCNIP3*	2.195	2.035	2.025
222177_s_at	*SCAND2*	2.66	2.46	2.45
227561_at	*DDR2*	12.14	11.27	11.16
1564475_s_at	*LOC728723*	2.855	2.635	2.635
1563226_at	*MGC15523*	2.54	2.34	2.34
239387_at	*UVRAG*	3.045	2.815	2.805
219863_at	*HERC5*	3	2.78	2.78
1569238_a_at	*RAPGEF2*	2.86	2.64	2.64
1558474_at	*NA*	4.255	3.955	3.915
208674_x_at	*DDOST*	11.505	10.585	10.675
223022_s_at	*C6orf55*	9.375	8.635	8.685
200006_at	*PARK7*	13.005	11.995	12.045
229676_at	*PAPD1*	11.415	10.515	10.595
236039_at	*LYPD5*	2.37	2.19	2.19
210990_s_at	*LAMA4*	2.38	2.2	2.2
230367_at	*SMTNL1*	2.66	2.45	2.47
216172_at	*NA*	2.935	2.705	2.725
209901_x_at	*AIF1*	2.735	2.535	2.535
219199_at	*AFF4*	3.67	3.39	3.39
233805_at	*NA*	2.955	2.735	2.735
219569_s_at	*TMEM22*	9.83	9.09	9.09
1555397_at	*MYO1D*	2.71	2.52	2.5
210518_at	*CDH8*	3.38	3.13	3.11

1560733_at	*ALG5*	2.495	2.315	2.305
200705_s_at	*EEF1B2*	13.71	12.73	12.61
1569961_at	*NA*	2.545	2.345	2.345
200992_at	*IPO7*	13.75	12.7	12.72
1554604_at	*MBTPS2*	3.055	2.825	2.815
231245_s_at	*ADARB1*	2.455	2.275	2.265
207875_at	*NA*	3.025	2.805	2.795
236636_at	*NLGN1*	3.14	2.91	2.89
236588_at	*CFDP1*	3.045	2.815	2.805
216544_at	*RBMY2FP*	2.42	2.24	2.24
239831_at	*TMEM106C*	2.72	2.52	2.52
234552_at	*NA*	2.475	2.295	2.295
203316_s_at	*SNRPE*	12.545	11.605	11.605
227779_at	*ECSM2*	2.595	2.395	2.405
200673_at	*LAPTM4A*	14.455	13.365	13.355
1559384_at	*NA*	2.94	2.72	2.71
233910_at	*TMEFF2*	3.11	2.88	2.87
1562462_at	*DNAH10*	2.46	2.28	2.27
220581_at	*C6orf97*	4.22	3.89	3.91
200073_s_at	*HNRPD*	13.49	12.43	12.51
1552691_at	*ARL11*	2.875	2.665	2.655
38290_at	*RGS14*	3.23	2.99	2.99
213078_x_at	*AGPAT7*	2.355	2.175	2.175
210372_s_at	*TPD52L1*	2.4	2.23	2.21
221776_s_at	*BRD7*	7.4	6.87	6.81
1558899_s_at	*FLJ35946*	2.785	2.595	2.565
1556344_at	*LOC150051*	2.21	2.04	2.05
215872_at	*C14orf56*	2.265	2.085	2.095
240750_at	*C7orf44*	2.97	2.76	2.74
232613_at	*PB1*	2.94	2.72	2.72
1559437_at	*PRKRIP1*	3.315	3.085	3.055

223717_s_at	*ACRBP*	2.485	2.305	2.305
235329_at	*NOXO1*	2.48	2.3	2.3
234501_x_at	*PHTF1*	3.295	3.055	3.045
201973_s_at	*C7orf28B*	12.905	11.885	11.975
243925_at	*NA*	2.825	2.615	2.605
236780_at	*NA*	2.68	2.48	2.48
234792_x_at	*IGHV2-70*	2.465	2.285	2.285
238150_at	*FLJ27365*	2.64	2.45	2.43
235319_at	*NA*	2.495	2.315	2.315
230957_at	*NA*	2.7	2.51	2.49
205817_at	*SIX1*	2.555	2.365	2.355
1556999_at	*LOC285045*	2.545	2.355	2.345
1552504_a_at	*BRSK1*	2.99	2.77	2.76
1561320_at	*PAK6*	2.71	2.51	2.51
1561459_at	*NA*	2.44	2.26	2.26
206187_at	*PTGIR*	2.32	2.14	2.15
240553_at	*TESC*	2.49	2.31	2.3
1557305_at	*TACC1*	2.875	2.665	2.645
1565073_at	*NA*	2.72	2.53	2.51
231479_at	*TTC33*	2.935	2.715	2.715
207533_at	*CCL1*	2.615	2.415	2.415
244730_x_at	*ZSCAN16*	4.625	4.275	4.295
240673_at	*NA*	3.26	3.03	3.01
228610_at	*TM9SF3*	2.6	2.4	2.4
211333_s_at	*FASLG*	2.43	2.25	2.25
229628_s_at	*KIAA1529*	2.69	2.49	2.48
225100_at	*FBXO45*	7.905	7.305	7.315
234990_at	*NA*	2.67	2.47	2.47
1569543_at	*RSU1*	3.74	3.45	3.47
223026_s_at	*VPS29*	10.885	10.075	10.065
236967_at	*LOC645249*	2.335	2.155	2.155

233618_at	*NA*	2.39	2.21	2.21
1568762_at	*PDCD6*	3.125	2.885	2.885
240472_at	*NA*	3.795	3.495	3.525
1553466_at	*CXorf59*	2.12	1.96	1.96
240774_at	*NA*	3.23	3	2.98
228134_at	*NDE1*	2.13	1.97	1.97
207408_at	*SLC22A14*	2.61	2.42	2.4
207319_s_at	*CDC2L5*	3.095	2.865	2.855
220729_at	*NA*	2.86	2.65	2.64
230907_at	*GPRC5C*	2.46	2.28	2.28
212929_s_at	*FAM21C*	11.215	10.395	10.355
242763_at	*PKHD1L1*	3.15	2.92	2.91
218916_at	*ZNF768*	6.275	5.785	5.835
232970_at	*FAM86D*	2.525	2.345	2.345
210827_s_at	*ELF3*	3.065	2.845	2.835
226947_at	*GUSBL2*	5.435	5.015	5.045
224437_s_at	*C6orf55*	11.46	10.62	10.59
208204_s_at	*CAV3*	2.805	2.605	2.595
221758_at	*ARMC6*	6.45	5.97	5.97
234918_at	*GLTSCR2*	5.64	5.22	5.22
201980_s_at	*RSU1*	12.71	11.73	11.81
1559289_at	*TADA1L*	2.805	2.605	2.595
218685_s_at	*SMUG1*	2.495	2.315	2.305
1554148_a_at	*SLC33A1*	5.63	5.22	5.2
1559003_a_at	*LOC126661*	3.3	3.05	3.06
243153_at	*CDK5RAP2*	2.77	2.56	2.57
235517_at	*KCNIP4*	3.55	3.3	3.28
206181_at	*SLAMF1*	2.15	1.99	1.99
240684_at	*SIPA1L3*	2.89	2.68	2.67
216356_x_at	*BAIAP3*	3.675	3.395	3.395
204655_at	*CCL5*	2.285	2.115	2.125

219348_at	*MDS032*	6.105	5.625	5.675
239687_at	*BTBD12*	2.65	2.46	2.44
234056_at	*NA*	2.39	2.21	2.21
1562566_at	*LOC643749*	2.905	2.695	2.675
211751_at	*PDE4DIP*	2.765	2.565	2.555
232037_at	*PUNC*	2.785	2.585	2.575
208468_at	*SOX21*	2.325	2.155	2.145
205311_at	*DDC*	2.41	2.24	2.22
216057_at	*RAB3GAP2*	3.145	2.925	2.895
204499_at	*AGTPBP1*	2.66	2.46	2.46
211786_at	*TNFRSF9*	2.875	2.655	2.655
1557741_at	*UST*	3.15	2.93	2.9
1556204_a_at	*LOC730051*	2.78	2.58	2.58
215951_at	*TBC1D2B*	2.285	2.125	2.115
236181_at	*LOC389831*	3.345	3.095	3.105
219788_at	*PILRA*	3.175	2.945	2.935
207657_x_at	*TNPO1*	11.81	10.91	10.96
200089_s_at	*RPL4*	13.425	12.405	12.455
1569737_a_at	*CASKIN1*	2.45	2.27	2.27
226057_at	*CDGAP*	2.885	2.675	2.655
1557571_at	*VPS13D*	2.825	2.625	2.615
1555412_at	*FBXL21*	3.22	2.98	2.98
206553_at	*OAS2*	2.605	2.415	2.405
228052_x_at	*TCF3*	2.32	2.14	2.14
214537_at	*HIST1H1D*	2.47	2.3	2.28
1554885_a_at	*PRIM2A*	2.805	2.595	2.605
217175_at	*UGT2B15*	2.625	2.435	2.425
231122_x_at	*ZDHHC19*	2.94	2.71	2.73
1566456_at	*LOC729988*	2.52	2.34	2.34
232100_at	*IBRDC1*	2.99	2.76	2.78
212976_at	*NA*	2.885	2.675	2.665

209005_at	*FBXL5*	8.705	8.035	8.095
201097_s_at	*ARF4*	14.91	13.81	13.81
239816_at	*POLD3*	4.94	4.6	4.56
243885_x_at	*GFM1*	3.625	3.375	3.345
1553181_at	*DDX31*	2.26	2.1	2.1
231223_at	*CSMD1*	2.885	2.665	2.665
216630_at	*SEC14L1*	2.705	2.505	2.505
230837_at	*LOC647500*	3.04	2.83	2.81
234497_s_at	*NA*	2.775	2.575	2.565
216113_at	*ABI2*	2.7	2.5	2.5
1559522_at	*NA*	2.8	2.6	2.6
243158_at	*NT5C2*	2.41	2.23	2.24
204888_s_at	*NEURL*	2.11	1.95	1.95
231281_at	*TBC1D5*	2.73	2.52	2.54
1561652_at	*BECN1*	3.125	2.905	2.895
1555746_at	*CD79B*	3.165	2.935	2.925
211551_at	*EGFR*	2.515	2.335	2.335
223137_at	*ZDHHC4*	2.645	2.445	2.445
223781_x_at	*ADH4*	6.595	6.095	6.125
209598_at	*PNMA2*	2.44	2.26	2.26
214279_s_at	*NDRG2*	2.275	2.115	2.105
216785_at	*FKBP1B*	2.555	2.375	2.375
239609_s_at	*AGPAT7*	2.63	2.44	2.43
229902_at	*FLT4*	2.515	2.335	2.335
220901_at	*GPR157*	2.41	2.22	2.24
1556771_a_at	*BC038740*	2.855	2.645	2.655
203506_s_at	*MED12*	2.515	2.325	2.335
231612_at	*C4orf35*	2.535	2.355	2.345
230950_at	*NA*	2.645	2.455	2.445
244757_at	*CYP2R1*	3.295	3.065	3.045
244460_at	*PMP22CD*	2.465	2.295	2.275

231395_at	*NA*	2.28	2.12	2.12
1561587_at	*LOC284260*	2.5	2.33	2.31
239319_at	*LOC728342*	2.475	2.295	2.295
223775_at	*HHIP*	2.7	2.51	2.5
1553778_at	*WBSCR27*	2.575	2.395	2.385
1556334_s_at	*DSC1*	2.77	2.57	2.56
231671_at	*FGA*	2.335	2.165	2.155
1559110_at	*NA*	2.345	2.175	2.165
241102_at	*PBX1*	2.72	2.52	2.52
232822_x_at	*MGC16121*	2.885	2.675	2.665
240897_at	*NA*	2.4	2.23	2.22
241438_at	*RLF*	2.505	2.325	2.325
212132_at	*LSM14A*	12.62	11.65	11.75
206559_x_at	*EEF1A1*	15.56	14.49	14.36
216769_x_at	*C9orf150*	3.345	3.105	3.105
228010_at	*PPP2R2C*	2.79	2.58	2.6
238641_at	*FLJ43806*	2.945	2.715	2.735
239599_at	*NA*	2.595	2.415	2.405
242541_at	*ABCA9*	2.645	2.455	2.445
207596_at	*NA*	2.545	2.365	2.365
231614_at	*NOVA1*	2.99	2.78	2.76
211607_x_at	*EGFR*	2.625	2.435	2.425
204122_at	*TYROBP*	2.69	2.5	2.49
210576_at	*CYP4F8*	2.8	2.6	2.59
239884_at	*CADPS*	2.645	2.455	2.445
211878_at	*CPVL*	2.83	2.63	2.62
212734_x_at	*RPL13*	12.13	11.23	11.27
210808_s_at	*NOX1*	3.745	3.465	3.475
205655_at	*MDM4*	3.22	2.99	2.97
212213_x_at	*OPA1*	10.425	9.705	9.625
219138_at	*RPL14*	8.905	8.275	8.255

243679_at	*JPH3*	3.445	3.185	3.215
238499_at	*SLC45A3*	2.19	2.03	2.03
1561121_at	*IFT88*	3.07	2.86	2.84
231023_at	*ING1*	2.725	2.525	2.525
241162_at	*FARP1*	2.895	2.685	2.695
1559890_a_at	*ABI1*	3.54	3.28	3.28
206795_at	*F2RL2*	3.53	3.29	3.26
224597_at	*NA*	12.47	11.53	11.61
215663_at	*MBNL1*	3.015	2.805	2.785
206253_at	*DLG2*	3.04	2.82	2.82
242780_at	*VAPA*	3.94	3.64	3.67
1566323_at	*MAF*	2.98	2.76	2.76
220221_at	*VPS13D*	2.565	2.385	2.385
229337_at	*USP2*	2.76	2.56	2.56
1569785_at	*NA*	3.165	2.935	2.955
217593_at	*ZSCAN18*	3.41	3.16	3.17
201130_s_at	*CDH1*	2.41	2.24	2.23
218952_at	*PCSK1N*	2.365	2.185	2.195
227995_at	*NA*	2.23	2.07	2.07
212430_at	*RBM38*	4.505	4.185	4.175
238071_at	*LCN10*	2.945	2.725	2.725
234227_at	*FLJ13611*	3.05	2.84	2.83
217592_at	*ZSWIM1*	2.485	2.305	2.305
224644_at	*NA*	11.755	10.915	10.905
240447_at	*NA*	3.095	2.885	2.865
205331_s_at	*REEP2*	4.945	4.595	4.575
242649_x_at	*C15orf21*	2.835	2.645	2.625
237344_at	*FLJ45743*	2.385	2.215	2.205
234946_at	*NA*	3.245	3.015	3.005
219776_s_at	*NA*	2.37	2.2	2.19
217640_x_at	*C18orf24*	2.645	2.455	2.445

208636_at	*ACTN1*	13.11	12.14	12.2
211095_at	*NF1*	3.175	2.965	2.945
243653_at	*SHROOM3*	2.325	2.165	2.165
213780_at	*TCHH*	2.63	2.45	2.44
1552388_at	*FLJ30901*	2.285	2.125	2.125
238204_at	*LMOD1*	2.81	2.6	2.61
219932_at	*SLC27A6*	2.42	2.24	2.24
1563488_at	*TMEM132B*	2.57	2.39	2.38
223617_x_at	*ATAD3B*	5.08	4.71	4.73
242697_at	*ZNF540*	2.475	2.295	2.295
206699_x_at	*NPAS1*	3.65	3.39	3.38
217740_x_at	*RPL7A*	13.67	12.69	12.69
1563519_at	*TSC22D2*	3.505	3.255	3.245
205375_at	*MDFI*	3.36	3.12	3.12
234707_x_at	*IGLV1-44*	2.975	2.755	2.765
238300_s_at	*DAZAP2*	2.69	2.5	2.49
213677_s_at	*PMS1*	8.94	8.27	8.33
227287_at	*CITED2*	2.595	2.415	2.405
244156_at	*AGBL1*	3.01	2.8	2.78
217479_at	*FLJ45455*	3.265	3.035	3.025
1565581_at	*NA*	2.31	2.15	2.15
226910_at	*NA*	10.535	9.765	9.785
1553830_s_at	*MAGEA2*	2.465	2.285	2.295
201225_s_at	*SRRM1*	10.765	9.965	10.035
234138_at	*DAB1*	3.09	2.88	2.86
233310_at	*NA*	2.575	2.395	2.395
214385_s_at	*MUC5AC*	2.655	2.475	2.465
219921_s_at	*DOCK5*	2.79	2.59	2.59
237505_at	*ACAA2*	2.615	2.435	2.425
234012_at	*IGSF21*	3.475	3.235	3.225
202885_s_at	*PPP2R1B*	2.395	2.215	2.225

1561984_at	*NA*	2.42	2.24	2.24
238352_s_at	*CAPZB*	2.6	2.42	2.42
208386_x_at	*DMC1*	4.635	4.305	4.295
210885_s_at	*TRIM15*	2.46	2.29	2.28
207851_s_at	*INSR*	3.215	2.995	2.985
238344_at	*COPG2*	3.495	3.255	3.245
1558185_at	*CLLU1*	2.635	2.455	2.445
235312_s_at	*NRAP*	3.055	2.845	2.825
227011_at	*ZNF672*	2.5	2.32	2.32
240832_at	*NA*	2.61	2.42	2.43
1552412_a_at	*DEFB106A*	2.77	2.58	2.56
230507_at	*ATXN1*	3.01	2.8	2.78
1556909_at	*NA*	2.505	2.325	2.325
234614_at	*NA*	2.405	2.235	2.225
228566_at	*P15RS*	2.23	2.07	2.07
240492_at	*DKFZp686O1327*	2.935	2.725	2.735
236953_s_at	*RP11-50D16.3*	3.305	3.075	3.055
229918_at	*CCDC40*	2.695	2.495	2.505
1563858_at	*NA*	2.895	2.695	2.685
232365_at	*SIAH1*	2.895	2.695	2.685
1558691_a_at	*DOCK4*	2.83	2.63	2.63
234530_s_at	*C6orf12*	3.005	2.795	2.785
216318_at	*IGHA1*	3.265	3.035	3.025
1554145_a_at	*CCDC128*	2.415	2.245	2.235
235047_x_at	*BTBD14B*	5.715	5.315	5.305
225356_at	*TBX19*	11.54	10.75	10.69
1558410_s_at	*IMMP2L*	3.005	2.795	2.785
238650_x_at	*WDR89*	4.825	4.495	4.475
237825_x_at	*LOC647065*	3.535	3.275	3.285
1561105_at	*NA*	3.025	2.815	2.795
238839_at	*OTX1*	2.3	2.14	2.14

200634_at	*PFN1*	6.82	6.35	6.33
232207_at	*LOC285749*	2.78	2.57	2.59
213779_at	*EMID1*	5.41	5.03	5.02
232831_at	*LRFN5*	2.645	2.465	2.455
242393_x_at	*PARG*	2.63	2.45	2.44
1566865_at	*C7orf38*	2.86	2.67	2.65
244400_at	*VPS33A*	3.265	3.025	3.035
243905_at	*LOC387895*	2.57	2.39	2.38
1554259_at	*GPSM1*	2.04	1.89	1.9
1552390_a_at	*C8orf47*	2.965	2.755	2.765
1570255_s_at	*LOC375010*	2.965	2.765	2.755
1560910_at	*PPIL6*	2.77	2.58	2.57
242291_at	*EIF4ENIF1*	2.605	2.425	2.425
AFFX-hum_al	*NA*	16.15	15.08	14.94
219305_x_at	*FBXO2*	3.505	3.275	3.245
205834_s_at	*PART1*	2.62	2.44	2.43
237242_at	*LOC126536*	2.56	2.38	2.38
240356_s_at	*NA*	2.905	2.705	2.695
1556435_at	*LOC400622*	2.615	2.435	2.435
241973_x_at	*DPP7*	2.59	2.41	2.41
209097_s_at	*JAG1*	3.585	3.335	3.325
1562914_a_at	*FLJ25328*	2.115	1.965	1.975
214122_at	*PDLIM7*	2.705	2.515	2.505
1566643_a_at	*GNG7*	2.82	2.62	2.62
217348_x_at	*ARHGEF15*	2.88	2.67	2.69
1561906_at	*ASIP*	3.115	2.905	2.885
1566690_at	*NA*	2.185	2.025	2.025
242619_x_at	*SLC36A1*	2.655	2.475	2.465
236130_at	*MBD2*	2.425	2.245	2.255
211624_s_at	*DRD2*	2.745	2.545	2.555
229550_at	*KIAA1409*	2.29	2.13	2.13

205712_at	*PTPRD*	2.46	2.28	2.28
1557945_at	*TCTE3*	2.965	2.765	2.755
1563608_a_at	*KCNT1*	2.205	2.045	2.045
236093_at	*ZNF544*	4.32	4.02	4.02
1562981_at	*HBB*	2.355	2.205	2.185
205755_at	*ITIH3*	2.3	2.14	2.14
1557609_s_at	*TBC1D12*	3.345	3.125	3.095
1559350_at	*NA*	2.685	2.505	2.495
218893_at	*ISOC2*	3.795	3.535	3.525
229934_at	*NA*	2.445	2.275	2.265
AFFX-HUMR	*NA*	11.285	10.465	10.505
225265_at	*C2orf12*	13.09	12.13	12.22
234692_at	*BAI3*	2.765	2.565	2.565
1559849_at	*ZNF605*	3.365	3.135	3.115
238415_at	*UBE4B*	2.94	2.74	2.74
229234_at	*ZC3H12B*	2.935	2.735	2.735
223013_at	*TBL1XR1*	11.505	10.715	10.695
212195_at	*IL6ST*	14.365	13.325	13.405
228300_at	*CCDC103*	2.445	2.265	2.265
230593_at	*NA*	3.12	2.9	2.9
211604_x_at	*HAP1*	2.6	2.42	2.42
223863_at	*LOC114227*	2.82	2.63	2.62
233119_at	*FLJ14213*	2.205	2.045	2.045
216808_at	*LOC391703*	2.685	2.505	2.495
1561857_at	*TMEM110*	3.025	2.815	2.805
1556759_at	*NA*	2.94	2.75	2.73
210823_s_at	*PTPRS*	2.33	2.17	2.17
244728_at	*NA*	2.74	2.55	2.54
220906_at	*NA*	3.15	2.94	2.92
211461_at	*CSPG4LYP1*	2.65	2.47	2.47
211970_x_at	*ACTG1*	14.745	13.705	13.735

224984_at	*NFAT5*	11.565	10.775	10.755
208718_at	*DDX17*	14.535	13.505	13.535
1567219_at	*NA*	8.515	7.945	7.885
217858_s_at	*ARMCX3*	12.805	11.925	11.885
216482_x_at	*ZNF79*	2.26	2.1	2.1
229217_at	*SP3*	2.755	2.565	2.555
221982_x_at	*LAGE3*	5.11	4.77	4.73
232518_at	*PRIC285*	2.57	2.39	2.39
1566271_x_at	*GARNL1*	3.045	2.835	2.825
236438_at	*RABGEF1*	2.565	2.385	2.385
219322_s_at	*WDR8*	6.795	6.345	6.295
210643_at	*TNFSF11*	2.87	2.68	2.66
221699_s_at	*DDX50*	10.285	9.545	9.595
210583_at	*POLDIP3*	2.63	2.45	2.45
207008_at	*IL8RB*	3.245	3.025	3.015
211174_s_at	*CCKAR*	2.455	2.285	2.275
229775_s_at	*LOC730031*	2.34	2.18	2.18
209793_at	*GRIA1*	3.435	3.195	3.195
1565027_at	*OFCC1*	4.02	3.75	3.73
214428_x_at	*C4A*	5.065	4.715	4.705
238618_at	*NF2*	2.725	2.545	2.535
244153_at	*RHOT1*	3.85	3.59	3.58
244143_at	*NA*	2.94	2.73	2.74
237696_at	*NA*	3.22	3	3
218501_at	*ARHGEF3*	8.05	7.49	7.49
229184_at	*YSK4*	2.665	2.485	2.485
34260_at	*TELO2*	5.675	5.285	5.265
218872_at	*TESC*	2.355	2.195	2.195
234381_at	*IGL@*	4	3.72	3.72
236136_at	*PSCD3*	2.505	2.335	2.325
240833_at	*NIPSNAP3A*	2.505	2.325	2.325

213287_s_at	*KRT10*	12.035	11.245	11.155
224803_s_at	*LOC148413*	2.675	2.485	2.495
217246_s_at	*EPAG*	2.63	2.45	2.45
205864_at	*SLC7A4*	2.155	2.005	2.015
1556873_at	*RKHD2*	2.945	2.745	2.735
1555562_a_at	*ZCCHC7*	3.47	3.22	3.24
228897_at	*DERL3*	2.62	2.44	2.44
240267_at	*SYT6*	3.345	3.105	3.115
1559515_at	*XPA*	3.345	3.105	3.115
211265_at	*PTGER3*	2.83	2.64	2.63
1570046_at	*SCRG1*	3.03	2.83	2.82
225889_at	*AEBP2*	10.64	9.89	9.92
1558557_at	*MGC16824*	3.06	2.85	2.84
1561202_at	*NA*	3	2.8	2.79
241855_s_at	*CUL3*	2.935	2.735	2.735
224174_at	*TTTY11*	2.49	2.32	2.31
230852_at	*STAC3*	4.07	3.8	3.78
204694_at	*AFP*	2.69	2.52	2.5
215276_at	*WFDC8*	3.16	2.94	2.94
217594_at	*ZCCHC11*	3.335	3.105	3.115
214443_at	*PVR*	2.465	2.305	2.295
214655_at	*GPR6*	2.565	2.385	2.385
232866_at	*ZNF135*	2.455	2.295	2.285
225887_at	*C13orf23*	7.095	6.615	6.615
1556813_at	*ANKRD16*	2.525	2.345	2.355
208382_s_at	*DMC1*	2.64	2.46	2.46
1561170_at	*FLJ36131*	3.2	2.99	2.97
219995_s_at	*ZNF750*	2.95	2.76	2.74
236550_s_at	*ZNF311*	2.855	2.665	2.655
241014_at	*FLG*	3.21	2.99	2.99
207991_x_at	*ACRV1*	2.095	1.955	1.955

244263_at	*HDAC7A*	2.195	2.055	2.055
1560790_at	*FLJ36144*	2.83	2.64	2.63
208805_at	*PSMA6*	12.485	11.645	11.615
233719_s_at	*TASP1*	2.755	2.565	2.575
206646_at	*GLI1*	2.445	2.285	2.275
1560917_at	*ACAD9*	2.98	2.78	2.77
212267_at	*WAPAL*	10.115	9.435	9.425
202115_s_at	*NOC2L*	6.79	6.35	6.31
220550_at	*FBXO4*	2.94	2.74	2.73
238873_at	*NPC1*	3.115	2.905	2.895
1554613_a_at	*KIAA0226*	3.325	3.105	3.095
210630_s_at	*RAD52*	2.455	2.295	2.295
39817_s_at	*C6orf108*	6.47	6.04	6.02
215406_at	*TRIO*	2.46	2.3	2.3
1565832_at	*ANKRD15*	2.905	2.695	2.715
1560856_at	*NA*	2.93	2.73	2.73
201049_s_at	*RPS18*	14.475	13.495	13.495
242085_at	*C2orf18*	3.55	3.31	3.3
212705_x_at	*TSPAN4*	3.46	3.22	3.23
233143_at	*C20orf173*	2.435	2.265	2.275
220585_at	*HKDC1*	2.705	2.525	2.525
240696_at	*NA*	2.62	2.45	2.43
215202_at	*LOC91316*	2.295	2.135	2.135
232732_at	*NA*	2.755	2.575	2.565
229104_s_at	*GPR39*	2.86	2.67	2.66
200735_x_at	*NACA*	11.885	11.105	11.055
217200_x_at	*CYB561*	5.34	4.99	4.96
1568977_at	*RNASET2*	2.335	2.175	2.175
204990_s_at	*ITGB4*	3.665	3.425	3.425
237980_at	*LOC338864*	2.605	2.435	2.425
240332_at	*NA*	2.845	2.655	2.645

215852_x_at	*C20orf117*	3.155	2.945	2.935
1557964_at	*EIF4G2*	2.06	1.92	1.92
212010_s_at	*CDV3*	14.415	13.485	13.395
52940_at	*SIGIRR*	2.88	2.68	2.68
211050_x_at	*LOC643313*	2.3	2.14	2.14
217049_x_at	*PCDH11Y*	2.995	2.795	2.795
1567081_x_at	*CLN6*	2.42	2.26	2.26
202455_at	*HDAC5*	5.96	5.54	5.58
242519_at	*SEPP1*	2.895	2.705	2.695
239759_at	*NA*	2.39	2.23	2.23
1562830_at	*METT5D1*	2.305	2.145	2.145
206236_at	*GPR4*	3.01	2.81	2.81
226723_at	*CCDC23*	6.54	6.11	6.09
206633_at	*CHRNA1*	2.31	2.16	2.15
203713_s_at	*LLGL2*	2.605	2.435	2.425
209533_s_at	*PLAA*	7.905	7.365	7.375
1557206_at	*FLJ35848*	3.175	2.965	2.945
225159_s_at	*ELK4*	11.535	10.715	10.795
207436_x_at	*KIAA0894*	4.655	4.335	4.335
224108_at	*NA*	2.315	2.155	2.155
237132_at	*TJP2*	2.245	2.085	2.085
219424_at	*EBI3*	2.545	2.375	2.365
1565795_at	*DUOX1*	2.34	2.18	2.18
205591_at	*OLFM1*	2.885	2.685	2.685
221426_s_at	*OR3A3*	2.63	2.45	2.46
217994_x_at	*CPSF3L*	4.575	4.275	4.265
232380_at	*FLJ10986*	3.03	2.84	2.82
227845_s_at	*SHD*	2.275	2.115	2.115
213821_s_at	*IDS*	2.505	2.345	2.335
1566266_at	*NA*	3.025	2.835	2.815
221480_at	*HNRPD*	10.495	9.785	9.805

237798_at	*MSRA*	3.155	2.955	2.925
227661_at	*ANKRD11*	2.19	2.05	2.05
201094_at	*RPS29*	14.62	13.64	13.64
243782_at	*NA*	2.77	2.6	2.58
230271_at	*ONECUT2*	2.28	2.13	2.12
227393_at	*TMEM16J*	2.38	2.22	2.22
244696_at	*AFF3*	2.215	2.065	2.075
215115_x_at	*NTRK3*	2.195	2.055	2.055
232539_at	*NA*	4.955	4.625	4.615
61874_at	*C9orf7*	4.21	3.94	3.91
241313_at	*DOCK4*	2.12	1.98	1.98
233776_at	*PTPRA*	2.62	2.45	2.44
215381_at	*FRAP1*	2.38	2.22	2.22
232818_at	*FAM78B*	2.71	2.53	2.53
1568625_at	*NA*	2.505	2.345	2.335
1552474_a_at	*GAMT*	2.46	2.3	2.3
204877_s_at	*TAOK2*	2.675	2.505	2.485
206655_s_at	*GP1BB*	2.615	2.445	2.435
207487_at	*FLJ11996*	3.01	2.82	2.8
1569111_at	*SOX13*	2.565	2.385	2.395
237642_at	*MGC21675*	3.215	2.995	3.005
228666_at	*C15orf38*	2.775	2.595	2.595
1561010_a_at	*MAOB*	2.65	2.48	2.47
236699_at	*MBNL2*	2.39	2.23	2.23
38521_at	*CD22*	2.93	2.73	2.74
238938_at	*THADA*	2.61	2.44	2.43
1555548_at	*NDUFA10*	3.225	3.015	3.005
214182_at	*ARF6*	13.53	12.62	12.64
203788_s_at	*SEMA3C*	2.825	2.645	2.645
208314_at	*RRH*	2.42	2.26	2.26
220941_s_at	*C21orf91*	3.03	2.84	2.82

1559105_at	*LOC152084*	3.05	2.86	2.84
237422_at	*ARL6IP2*	3.115	2.905	2.915
235654_at	*NA*	2.69	2.52	2.5
1569560_at	*HIRA*	2.855	2.675	2.665
1559497_at	*NA*	2.855	2.675	2.665
1569426_at	*NA*	2.965	2.765	2.765
205359_at	*AKAP6*	2.265	2.115	2.105
212743_at	*RCHY1*	2.785	2.595	2.605
224005_at	*LOC727788*	2.255	2.105	2.115
239104_at	*CENTD1*	2.515	2.345	2.355
1565660_at	*FUT6*	3.785	3.545	3.515
238950_at	*NA*	2.545	2.375	2.385
231144_at	*SMARCD3*	2.4	2.24	2.24
1557012_a_at	*NA*	3.34	3.12	3.12
234101_at	*C3orf50*	2.605	2.435	2.425
225793_at	*LIX1L*	10.825	10.145	10.065
200651_at	*GNB2L1*	11.575	10.845	10.785
226915_s_at	*ARPC5L*	9.36	8.72	8.76
214987_at	*NA*	2.985	2.795	2.785
210376_x_at	*ELK1*	2.505	2.345	2.335
216296_at	*CLTA*	2.485	2.325	2.325
208024_s_at	*DGCR6*	4.955	4.645	4.615
241533_at	*LOC731656*	2.69	2.52	2.51
234231_at	*LOC197350*	2.43	2.27	2.27
232580_x_at	*PPM1B*	3.255	3.035	3.035
242992_at	*ZNF551*	2.585	2.415	2.405
241737_x_at	*NA*	2.8	2.62	2.62
204516_at	*ATXN7*	10.165	9.455	9.525
215538_at	*LARGE*	2.63	2.46	2.45
226347_at	*FUT11*	12.11	11.26	11.36
232962_x_at	*NA*	3.155	2.955	2.945

1566269_at	*GARNL1*	2.76	2.58	2.58
1552396_at	*WFDC6*	2.54	2.38	2.37
241517_at	*DDEF1*	2.525	2.365	2.365
1568867_x_at	*GPATCH8*	3.495	3.255	3.265
237754_at	*LOC730018*	2.16	2.02	2.02
205118_at	*FPR1*	3.13	2.93	2.93
201357_s_at	*SF3A1*	3.775	3.515	3.545
228916_at	*CWF19L2*	5.16	4.8	4.84
209096_at	*UBE2V2*	11.16	10.43	10.41
1566204_at	*NA*	2.765	2.595	2.575
237647_at	*GHRL*	2.34	2.18	2.18
1555650_at	*KLHL17*	2.045	1.905	1.905
208507_at	*OR7C2*	2.075	1.935	1.935
237211_x_at	*MORN3*	2.66	2.48	2.48
1568248_x_at	*SNORA71B*	2.38	2.22	2.23
1553341_at	*UROC1*	2.54	2.38	2.37
228968_at	*ZNF449*	8.79	8.18	8.24
224510_s_at	*CLPB*	2.52	2.35	2.36
201726_at	*ELAVL1*	10.605	9.915	9.895
202075_s_at	*PLTP*	2.52	2.36	2.35
234832_at	*ANTXR1*	2.45	2.3	2.28
1561584_at	*NA*	2.79	2.61	2.6
225083_at	*C6orf51*	13.68	12.83	12.73
236111_at	*NA*	2.915	2.725	2.715
241752_at	*SLC8A1*	2.45	2.29	2.29
223531_x_at	*GPR89A*	7.26	6.76	6.8
1562391_at	*B3GALNT2*	3.085	2.875	2.885
211620_x_at	*RUNX1*	2.67	2.49	2.49
210472_at	*MT1G*	2.635	2.465	2.455
1564352_at	*CECR3*	2.4	2.25	2.24
221238_at	*NSBP1*	3	2.81	2.79

233869_x_at	*DLG1*	3.65	3.4	3.42
231833_at	*PRR8*	2.565	2.395	2.405
237781_at	*HORMAD2*	2.56	2.4	2.39
56748_at	*TRIM10*	3.005	2.815	2.805
1558619_at	*SNHG7*	2.465	2.305	2.305
1552466_x_at	*C21orf100*	3.115	2.915	2.905
208347_at	*NA*	2.79	2.61	2.6
235785_at	*ATBF1*	2.4	2.24	2.24
240886_at	*CASR*	3.415	3.195	3.185
1570536_at	*NA*	2.2	2.05	2.06
237724_at	*RNF190*	2.54	2.38	2.38
238393_at	*BMPR2*	3.205	3.005	2.995
1570261_at	*MARS2*	2.69	2.52	2.51
221481_x_at	*HNRPD*	13.595	12.695	12.725
206945_at	*LCT*	2.5	2.34	2.34
211233_x_at	*ESR1*	2.2	2.06	2.05
224398_at	*NA*	2.68	2.51	2.5
242241_x_at	*WDR89*	3.655	3.425	3.405
40665_at	*FMO3*	2.43	2.27	2.27
235375_x_at	*TTC9B*	2.37	2.21	2.21
1552722_at	*ARPP-21*	3.04	2.84	2.84
1556405_s_at	*LOC374890*	2.48	2.32	2.32
1554676_at	*SRGN*	2.935	2.735	2.745
205745_x_at	*ADAM17*	8.995	8.445	8.385
1563841_at	*MEIS2*	2.76	2.58	2.58
236154_at	*NA*	2.97	2.77	2.77
206940_s_at	*POU4F1*	2.555	2.395	2.395
215921_at	*LOC23117*	2.595	2.435	2.425
224944_at	*TMPO*	8.6	8.06	8.02
1570337_at	*FIGLA*	2.325	2.175	2.165
1566438_at	*HS6ST3*	2.625	2.455	2.445

1560979_a_at	*NA*	3.07	2.87	2.87
207499_x_at	*UNC45A*	4.88	4.56	4.56
224061_at	*INMT*	2.565	2.395	2.405
239543_s_at	*NA*	2.865	2.685	2.685
1557771_at	*FHAD1*	2.985	2.795	2.785
237826_at	*HLA-A*	2.335	2.175	2.175
235910_x_at	*NA*	2.735	2.565	2.555
1564525_at	*NA*	3.185	2.975	2.985
1559756_at	*DKFZp667F0711*	3.11	2.91	2.9
1564052_at	*TREML4*	2.16	2.02	2.02
201994_at	*MORF4L2*	14.525	13.575	13.595
243733_at	*NEDD8*	3.22	3.01	3.02
1557835_at	*TMEM112*	2.19	2.04	2.06
233014_at	*IDI1*	4.515	4.215	4.225
213182_x_at	*CDKN1C*	2.71	2.53	2.53
1565763_at	*C13orf33*	2.24	2.1	2.1
1560978_at	*NA*	2.365	2.215	2.205
233424_at	*NRXN1*	3.535	3.315	3.305
1561144_at	*NCAPD2*	3.335	3.115	3.115
210453_x_at	*ATP5L*	10.145	9.475	9.505
207274_at	*CHRNE*	2.77	2.59	2.59
236773_at	*NA*	3.18	2.97	2.98
233284_at	*LYRM5*	2.885	2.705	2.695
231545_at	*OTP*	2.49	2.33	2.33
208373_s_at	*P2RY6*	2.81	2.63	2.63
242276_at	*C18orf2*	2.79	2.61	2.61
216647_at	*TCF3*	3.845	3.605	3.595
241878_at	*MTHFD1L*	2.285	2.145	2.145
243646_at	*C9orf41*	2.85	2.67	2.67
235219_at	*LOC116349*	3.945	3.685	3.695
207366_at	*KCNS1*	5.5	5.14	5.15

223744_s_at	*SIAE*	2.225	2.085	2.085
237481_at	*ACAD10*	3.165	2.955	2.965
1559681_a_at	*TRIM16L*	2.51	2.35	2.35
216110_x_at	*NA*	3.245	3.035	3.045
233090_at	*GPC6*	2.38	2.22	2.22
227811_at	*FGD3*	2.575	2.415	2.415
215511_at	*TCF20*	2.12	1.98	1.98
206353_at	*COX6A2*	2.355	2.205	2.195
1559843_s_at	*ABCA11*	3.19	2.98	2.99
239418_x_at	*ENTPD1*	3.325	3.095	3.115
211392_s_at	*PATZ1*	2.47	2.31	2.31
239647_at	*CHST13*	2.41	2.26	2.25
209166_s_at	*MAN2B1*	7.115	6.645	6.675
240123_at	*NA*	2.56	2.4	2.39
213428_s_at	*COL6A1*	14.37	13.49	13.4
208195_at	*TTN*	2.37	2.22	2.21
229353_s_at	*NUCKS1*	15.83	14.83	14.79
232305_at	*HMGCLL1*	3	2.81	2.8
208073_x_at	*TTC3*	12.76	11.98	11.9
201448_at	*TIA1*	10.85	10.13	10.18
224091_at	*NA*	2.79	2.62	2.61
223884_at	*OPTC*	2.57	2.41	2.41
220730_at	*FLJ12986*	2.685	2.505	2.515
207601_at	*SULT1B1*	2.525	2.365	2.365
224567_x_at	*MALAT1*	15.075	14.165	14.055
222952_s_at	*TLR7*	2.45	2.29	2.29
1563649_at	*NA*	3.335	3.125	3.105
202297_s_at	*RER1*	12.41	11.63	11.59
223371_s_at	*DNAJC4*	2.43	2.27	2.27
217238_s_at	*ALDOB*	2.435	2.275	2.275
1557842_at	*NA*	2.965	2.785	2.775

237538_at	*RSAD2*	2.635	2.475	2.475
226918_at	*JPH4*	2.455	2.295	2.295
1562342_at	*DACH1*	3.49	3.27	3.27
206340_at	*NR1H4*	2.635	2.475	2.465
244104_at	*MGAT3*	3.385	3.165	3.165
217553_at	*EEF1A1*	7.345	6.855	6.905
242952_at	*HDAC9*	3.315	3.105	3.095
1560446_at	*ZNF724P*	2.295	2.155	2.155
219858_s_at	*FLJ20160*	3.16	2.95	2.97
203551_s_at	*COX11*	9.005	8.445	8.415
224526_at	*FAM79B*	2.62	2.46	2.45
242322_at	*NA*	2.45	2.29	2.29
227206_at	*NDUFA10*	2.425	2.265	2.265
210633_x_at	*KRT10*	12.27	11.45	11.53
227589_at	*PITPNC1*	2.27	2.13	2.13
238502_at	*MORF4L2*	3.15	2.95	2.95
1563396_x_at	*NA*	3.015	2.825	2.805
237008_at	*NA*	2.47	2.31	2.31
239063_at	*NA*	2.815	2.635	2.635
206107_at	*RGS11*	2.33	2.19	2.18
227944_at	*PTPN3*	2.5	2.34	2.34
1561375_at	*NA*	2.415	2.255	2.265
205673_s_at	*ASB9*	2.8	2.62	2.62
1569751_at	*MGC51025*	2.8	2.62	2.62
1561595_x_at	*NA*	2.365	2.225	2.215
230546_at	*VASH1*	2.81	2.62	2.64
212998_x_at	*HLA-DQB1*	2.44	2.29	2.28
216793_x_at	*NA*	3.125	2.935	2.915
234720_s_at	*TOB2*	2.51	2.35	2.35
229980_s_at	*SNX5*	12.29	11.49	11.53
1569552_at	*PTPN18*	3.275	3.075	3.075

213441_x_at	*SPDEF*	2.19	2.05	2.05
220600_at	*TMEM103*	2.905	2.725	2.725
228074_at	*LOC162073*	2.3	2.16	2.16
216300_x_at	*RARA*	4.635	4.335	4.345
1566217_at	*A2BP1*	3.2	3	2.99
242446_at	*C6orf163*	3.075	2.885	2.875
243045_at	*SMYD1*	2.895	2.715	2.705
230989_s_at	*TSSK6*	2.34	2.19	2.2
1557512_at	*CLIP1*	2.84	2.66	2.66
215841_at	*GUCA1B*	2.325	2.185	2.175
209521_s_at	*AMOT*	2.675	2.515	2.505
208481_at	*ASB4*	2.805	2.625	2.625
236690_at	*RHBDD1*	2.52	2.37	2.36
211424_x_at	*METTL7A*	3.18	2.98	2.98
240548_at	*GTDC1*	3.23	3.02	3.04
215099_s_at	*RXRB*	2.485	2.325	2.325
229379_at	*AHDC1*	2.22	2.08	2.08
1556933_at	*SPIN1*	2.92	2.75	2.73
238225_at	*NA*	2.455	2.305	2.295
207449_s_at	*POFUT2*	2.51	2.35	2.35
218932_at	*C1orf181*	9.405	8.845	8.795
206620_at	*GRAP*	2.345	2.205	2.205
206447_at	*ELA1*	2.55	2.39	2.39
206645_s_at	*NR0B1*	2.515	2.365	2.355
235815_at	*TSHZ2*	2.405	2.245	2.255
216406_at	*NA*	2.92	2.74	2.74
239025_at	*RP11-262H14.4*	2.97	2.79	2.78
1552426_a_at	*TM2D3*	10.895	10.225	10.205
207189_s_at	*ZZEF1*	3.605	3.375	3.395
238281_at	*RBMS1*	2.345	2.205	2.205
222247_at	*DXS542*	2.295	2.155	2.155

230595_at	*LOC572558*	2.355	2.215	2.205
218571_s_at	*CHMP4A*	12.445	11.685	11.645
239279_at	*LZTR2*	2.975	2.795	2.785
242902_at	*LOC643160*	2.37	2.23	2.22
212413_at	*6-Sep*	6.42	6.02	6.02
238901_at	*SLAMF9*	2.88	2.7	2.7
213730_x_at	*TCF3*	9.1	8.54	8.54
1555707_at	*TNAP*	2.655	2.485	2.495
210629_x_at	*LST1*	2.285	2.145	2.145
225053_at	*CNOT7*	11.57	10.86	10.84
1560784_x_at	*NA*	2.6	2.44	2.44
1558392_at	*SYNE2*	2.785	2.605	2.605
242345_at	*tcag7.216*	2.65	2.49	2.49
205305_at	*FGL1*	2.715	2.555	2.545
1560204_at	*NT5DC4*	3.085	2.895	2.885
219124_at	*C8orf41*	6.495	6.085	6.095
235885_at	*MED12L*	2.97	2.8	2.78
202023_at	*EFNA1*	2.475	2.315	2.315
230589_at	*TRAF3IP2*	2.345	2.205	2.195
1558814_s_at	*TMED5*	2.63	2.47	2.47
244461_at	*SPECC1*	2.815	2.635	2.645
217157_x_at	*NA*	2.665	2.505	2.495
224996_at	*MGC34646*	12.415	11.665	11.635
1558343_at	*NA*	2.27	2.13	2.13
241875_at	*NA*	2.695	2.535	2.525
233401_at	*NRCAM*	2.86	2.68	2.68
244383_at	*NA*	3.025	2.845	2.845
231687_at	*C1orf173*	2.495	2.335	2.335
243446_at	*C14orf94*	2.355	2.215	2.215
232610_at	*PARP14*	2.55	2.4	2.39
1556808_at	*LOC121906*	2.28	2.14	2.14

238110_at	*SAPS2*	3.12	2.92	2.93
211542_x_at	*RPS10*	11.05	10.33	10.4
1557214_at	*NA*	2.54	2.38	2.38
233979_s_at	*ESPN*	2.89	2.71	2.71
232486_at	*LRFN1*	2.815	2.645	2.635
236218_at	*PHOSPHO1*	2.33	2.19	2.19
214251_s_at	*NUMA1*	2.97	2.79	2.79
211222_s_at	*HAP1*	2.485	2.325	2.325
200817_x_at	*RPS10*	11.125	10.445	10.445
241035_s_at	*NA*	2.495	2.335	2.335
219958_at	*C20orf46*	2.5	2.34	2.35
202403_s_at	*COL1A2*	15.5	14.59	14.49
218193_s_at	*GOLT1B*	12.415	11.625	11.675
204017_at	*KDELR3*	12.475	11.665	11.755
209404_s_at	*TMED7*	10.72	10.07	10.05
210940_s_at	*GRM1*	2.98	2.8	2.8
241452_at	*NA*	3.065	2.885	2.875
1557059_at	*LOC440902*	3.335	3.135	3.125
212800_at	*STX6*	5.915	5.555	5.555
217119_s_at	*CXCR3*	2.445	2.285	2.295
1561232_at	*NA*	2.27	2.13	2.13
202646_s_at	*CSDE1*	13.355	12.585	12.485
237720_at	*ASB4*	2.83	2.66	2.65
238503_at	*CNIH3*	2.955	2.775	2.775
220166_at	*CNNM1*	2.665	2.505	2.505
1554766_s_at	*PVT1*	2.865	2.695	2.685
1561702_at	*NA*	2.54	2.39	2.38
1558607_at	*PAPPA*	3.56	3.35	3.33
239644_at	*FLJ37440*	3.455	3.245	3.225
207114_at	*LY6G6C*	2.465	2.315	2.305
243127_x_at	*TRAP1*	3.56	3.34	3.34

210159_s_at	*TRIM31*	2.755	2.585	2.595
209119_x_at	*NR2F2*	5.045	4.745	4.735
240526_at	*ATP11A*	3.28	3.08	3.08
234845_at	*DKFZp761P0212*	2.95	2.77	2.76
209775_x_at	*SLC19A1*	2.26	2.12	2.12
1563072_at	*NA*	3.02	2.83	2.84
243563_at	*C1orf82*	3.095	2.915	2.905
244816_at	*NA*	2.51	2.36	2.35
239910_at	*PSG1*	2.395	2.255	2.245
237605_at	*NA*	2.95	2.78	2.76
237103_at	*SRC*	2.795	2.625	2.615
206333_at	*MSI1*	3.005	2.825	2.815
237362_at	*ZFP41*	2.625	2.465	2.465
224547_at	*NA*	2.385	2.245	2.235
230128_at	*IGL@*	2.93	2.76	2.74
230485_at	*LOC644844*	2.465	2.305	2.315
219245_s_at	*OGFOD2*	2.91	2.74	2.72
216575_at	*NA*	3.26	3.06	3.06
239911_at	*ONECUT2*	3.125	2.935	2.925
214990_at	*PIGO*	3.015	2.825	2.845
223175_s_at	*FEM1A*	7.315	6.855	6.885
229226_at	*MMS19L*	3.07	2.88	2.89
211951_at	*NOLC1*	12.14	11.36	11.44
236950_s_at	*LOC157381*	2.825	2.655	2.645
234015_at	*NAALADL2*	3.065	2.885	2.885
226299_at	*PKN3*	2.685	2.525	2.525
234156_at	*MICAL2*	3.94	3.7	3.7
1552518_s_at	*MTBP*	3.35	3.16	3.14
240882_at	*NA*	3.045	2.865	2.865
1569296_a_at	*LOC493754*	2.08	1.96	1.96
1560743_a_at	*ALS2*	2.99	2.81	2.81

231363_at	*LELP1*	3.26	3.07	3.05
1554810_at	*PLA2G4C*	3.165	2.965	2.975
231679_at	*NA*	2.62	2.46	2.46
242236_at	*NA*	2.605	2.445	2.445
239641_at	*FLI1*	2.68	2.52	2.52
234284_at	*GNG8*	2.68	2.53	2.51
219927_at	*FCF1*	2.865	2.695	2.685
1559566_at	*FBXO42*	2.835	2.655	2.665
1566473_a_at	*LOC647305*	3.155	2.955	2.965
1553799_at	*C15orf33*	2.93	2.76	2.75
233896_s_at	*PAPLN*	2.485	2.335	2.325
205246_at	*PEX13*	5.07	4.78	4.75
240038_at	*ELL2*	8.015	7.555	7.515
217285_at	*DGCR14*	2.2	2.06	2.07
208749_x_at	*FLOT1*	7.775	7.305	7.295
240119_at	*TEPP*	2.235	2.095	2.095
1566156_at	*NA*	2.065	1.945	1.945
227496_at	*LOC253842*	2.55	2.39	2.39
238561_s_at	*C8orf53*	2.59	2.43	2.43
1561334_at	*LOC285181*	2.505	2.355	2.345
210738_s_at	*SLC4A4*	3	2.82	2.82
1565836_at	*NA*	2.095	1.975	1.975
228973_at	*DLG2*	2.535	2.375	2.375
233229_at	*SCFD1*	2.57	2.41	2.42
1567014_s_at	*NFE2L2*	3.395	3.195	3.195
205245_at	*PARD6A*	3.185	2.995	2.985
1554564_a_at	*UNQ1887*	3.225	3.025	3.025
212709_at	*NUP160*	9.025	8.505	8.465
243234_at	*TBX3*	3	2.83	2.81
201896_s_at	*PSRC1*	2.94	2.75	2.77
211445_x_at	*NACAP1*	12.685	11.915	11.935

215474_at	*NSMCE2*	2.515	2.355	2.365
229188_s_at	*ZNRF2*	2.67	2.51	2.5
239327_at	*NA*	2.605	2.455	2.445
202830_s_at	*SLC37A4*	3.785	3.555	3.565
213715_s_at	*ANKRD47*	3.535	3.325	3.315
239511_s_at	*SFRS4*	3.2	3	3
235437_at	*NA*	2.745	2.585	2.585
1569963_at	*NA*	3.84	3.61	3.6
215332_s_at	*CD8B*	3.18	2.99	2.98
207979_s_at	*CD8B*	2.34	2.2	2.2
237278_x_at	*ATP2C1*	3.29	3.09	3.09
234473_at	*RP11-408E5.4*	2.915	2.745	2.725
1558764_at	*NA*	3.27	3.08	3.06
238217_at	*NA*	2.175	2.035	2.045
1554175_at	*CD300LB*	2.34	2.2	2.2
1552816_at	*C9orf121*	2.795	2.635	2.635
217359_s_at	*NCAM1*	2.3	2.16	2.16
221089_at	*NOX3*	2.445	2.305	2.305
222013_x_at	*FAM86A*	4.67	4.38	4.4
1557647_a_at	*NA*	2.67	2.51	2.51
238778_at	*MPP7*	2.71	2.55	2.55
1556821_x_at	*DLEU2*	2.89	2.72	2.71
243422_at	*C21orf66*	2.97	2.79	2.79
1555062_s_at	*GTPBP3*	3.075	2.905	2.885
206564_at	*OPRL1*	2.425	2.285	2.275
242528_at	*HOXA5*	2.405	2.265	2.265
1553911_at	*ZNF663*	2.59	2.44	2.43
222003_s_at	*DOCK6*	2.595	2.435	2.435
224408_at	*MCHR2*	2.39	2.25	2.25
1557685_at	*FLJ30277*	2.69	2.53	2.53
212263_at	*QKI*	8.885	8.355	8.345

1552594_at	*MDAC1*	3.08	2.89	2.91
223011_s_at	*OCIAD1*	10.755	10.085	10.135
223943_s_at	*GNG2*	2.545	2.385	2.395
1570331_at	*NA*	2.485	2.335	2.345
1570301_at	*NA*	2.6	2.44	2.44
240004_at	*GRM3*	2.27	2.13	2.13
1561663_at	*NA*	3.055	2.865	2.885
1556624_at	*CCDC92*	3.105	2.915	2.925
206647_at	*HBZ*	2.63	2.47	2.47
205914_s_at	*GRIN1*	2.35	2.21	2.21
237076_at	*NCSTN*	2.58	2.42	2.43
236203_at	*HLA-DQA1*	2.855	2.685	2.675
235210_s_at	*RPESP*	2.495	2.355	2.355
236682_at	*NA*	2.205	2.065	2.075
205151_s_at	*KIAA0644*	2.37	2.23	2.23
207954_at	*GATA2*	2.575	2.415	2.415
216795_at	*NA*	2.55	2.4	2.39
244703_x_at	*IPO9*	3.15	2.96	2.97
237269_at	*EVI1*	2.74	2.58	2.57
226835_s_at	*C20orf199*	7.31	6.86	6.89
228833_s_at	*LOC400027*	2.545	2.395	2.385
209961_s_at	*HGF*	2.505	2.355	2.365
241173_at	*NA*	3.61	3.4	3.39
1559063_at	*C21orf63*	2.66	2.5	2.5
231976_at	*LINS1*	2.565	2.415	2.405
206394_at	*MYBPC2*	2.335	2.195	2.195
1569772_x_at	*NA*	2.875	2.705	2.695
212923_s_at	*C6orf145*	12.04	11.28	11.36
230381_at	*C1orf186*	2.915	2.735	2.745
234882_at	*NA*	2.71	2.56	2.54
234216_at	*FLJ21408*	2.275	2.135	2.135

232756_at	*KALRN*	2.805	2.645	2.645
216259_at	*BMPER*	3.09	2.92	2.9
230110_at	*MCOLN2*	2.63	2.48	2.47
234102_at	*RASL11B*	2.3	2.16	2.16
233786_at	*NA*	2.925	2.755	2.745
213977_s_at	*CIZ1*	3.225	3.025	3.035
219598_s_at	*RWDD1*	12.28	11.56	11.56
234638_at	*LARGE*	2.28	2.14	2.14
243625_at	*CREB1*	3.235	3.035	3.045
244355_at	*KIAA0241*	2.62	2.47	2.46
234046_at	*NA*	3.155	2.985	2.965
207766_at	*CDKL1*	2.455	2.305	2.315
227972_at	*TOR2A*	4.265	4.005	4.015
213613_s_at	*CDC2L2*	2.31	2.17	2.17
1556461_at	*LOC730245*	3.265	3.075	3.065
234685_x_at	*KRTAP4-9*	2.235	2.095	2.105
233953_at	*GUCA1C*	2.575	2.425	2.415
1555192_at	*ZNF277P*	3.485	3.285	3.285
206991_s_at	*CCR5*	2.905	2.735	2.725
221418_s_at	*THRAP5*	2.68	2.53	2.52
1552490_at	*LACE1*	2.625	2.475	2.465
205944_s_at	*CLTCL1*	2.3	2.16	2.16
224759_s_at	*C12orf23*	13.97	13.14	13.16
235172_at	*GABPB2*	3.205	3.025	3.015
237649_at	*COPS4*	2.845	2.685	2.675
1566953_x_at	*SIRT5*	2.615	2.465	2.455
1552736_a_at	*NETO1*	2.68	2.52	2.52
238122_at	*RBM12B*	7.18	6.76	6.76
201400_at	*PSMB3*	8.25	7.74	7.8
205701_at	*IPO8*	2.37	2.24	2.22
1552349_a_at	*PRSS33*	2.37	2.23	2.23

231465_at	*NA*	2.465	2.325	2.325
229165_at	*MRPL12*	2.435	2.295	2.295
206658_at	*UPK3B*	2.7	2.54	2.54
223180_s_at	*C18orf55*	11.7	10.98	11.06
1560615_a_at	*RP11-529I10.4*	2.495	2.355	2.345
1563721_at	*NA*	2.955	2.785	2.775
240031_at	*MSRA*	2.975	2.805	2.785
222406_s_at	*PNRC2*	3.275	3.085	3.065
244068_at	*STS-1*	2.185	2.065	2.055
242101_at	*ESR2*	3.215	3.035	3.025
204424_s_at	*LMO3*	2.32	2.18	2.18
228154_at	*C19orf44*	2.33	2.19	2.19
1561387_a_at	*FAM55A*	3.02	2.85	2.84
220208_at	*ADAMTS13*	2.44	2.3	2.3
232212_at	*PLEKHA8*	3.63	3.41	3.42
237147_at	*RNF168*	3.285	3.095	3.085
239114_at	*SERGEF*	2.885	2.715	2.725
232562_at	*NA*	2.52	2.38	2.37
228504_at	*NA*	3.04	2.87	2.86
227573_s_at	*OBSL1*	2.585	2.435	2.425
1569496_s_at	*SPON2*	4.335	4.085	4.075
220053_at	*GDF3*	2.83	2.67	2.66
241052_at	*NA*	2.485	2.345	2.335
229716_at	*NA*	2.34	2.2	2.21
220232_at	*SCD5*	3.245	3.065	3.055
243891_at	*LOC196463*	2.44	2.3	2.3
208107_s_at	*LOC81691*	2.855	2.685	2.695
1554160_a_at	*ZNF446*	2.255	2.115	2.125
1565890_at	*C20orf82*	2.42	2.28	2.28
232199_at	*PPP1R3F*	2.1	1.98	1.98
210531_at	*NR2C1*	3.12	2.94	2.94

229039_at	*SYN2*	2.41	2.27	2.27
1559000_at	*C10orf108*	2.225	2.105	2.095
232845_at	*CDH23*	2.26	2.13	2.12
203307_at	*GNL1*	6.61	6.24	6.22
206814_at	*NGFB*	6.07	5.7	5.73
240599_x_at	*PHC3*	3.255	3.075	3.065
238273_at	*SLC13A4*	2.69	2.54	2.53
221076_at	*NA*	2.975	2.805	2.795
226070_at	*C9orf142*	4.105	3.865	3.865
215331_at	*MYH15*	2.275	2.135	2.135
222356_at	*TBL1Y*	3.41	3.21	3.21
210406_s_at	*RAB6C*	12.465	11.775	11.715
205683_x_at	*TPSAB1*	2.28	2.14	2.14
1564568_at	*ELL*	3.06	2.88	2.88
238161_at	*ZNF289*	2.62	2.46	2.46
239316_at	*LOC751071*	3.715	3.495	3.495
222847_s_at	*EGLN3*	2.72	2.56	2.56
1558698_at	*ZNF264*	2.855	2.695	2.685
204211_x_at	*EIF2AK2*	9.095	8.595	8.545
221547_at	*PRPF18*	8.875	8.365	8.345
1565844_at	*BRPF3*	2.64	2.48	2.49
240726_at	*PARD3B*	3.025	2.855	2.835
227885_at	*LOC400236*	2.845	2.685	2.685
216876_s_at	*IL17A*	2.92	2.76	2.75
221240_s_at	*B3GNT4*	3.255	3.075	3.065
242292_at	*DMRTC1*	2.975	2.805	2.795
216240_at	*PVT1*	2.325	2.185	2.185
1564490_at	*NA*	2.465	2.325	2.325
243067_at	*NME1*	2.45	2.31	2.31
1556318_s_at	*CAND1*	3.015	2.835	2.835
231038_s_at	*NA*	2.735	2.585	2.575

241751_at	*OFD1*	3.025	2.855	2.845
224708_at	*KIAA2013*	8.04	7.58	7.58
232864_s_at	*AFF4*	3.43	3.23	3.23
230999_at	*FLJ39051*	5.055	4.775	4.745
235929_s_at	*NA*	3.02	2.84	2.84
217358_at	*DNAJC16*	3.13	2.95	2.95
1554108_at	*NA*	2.905	2.745	2.735
215686_x_at	*TFAP2B*	2.895	2.735	2.725
224383_at	*RNF17*	2.935	2.775	2.765
239564_at	*NA*	2.82	2.66	2.66
213507_s_at	*KPNB1*	12.275	11.545	11.595
1569898_a_at	*NA*	2.06	1.94	1.94
235382_at	*FLJ90650*	2.565	2.425	2.415
228524_at	*ADCK5*	2.745	2.585	2.585
238172_at	*NDUFA10*	2.315	2.175	2.185
221698_s_at	*CLEC7A*	2.66	2.5	2.51
1558804_at	*NA*	2.84	2.69	2.67
217009_at	*PGK2*	2.79	2.62	2.64
1553076_at	*OFCC1*	2.76	2.61	2.59
244556_at	*LCP2*	2.5	2.36	2.36
234820_at	*MAS1L*	2.46	2.32	2.32
1552740_at	*C2orf15*	3.285	3.105	3.095
205031_at	*EFNB3*	2.235	2.105	2.115
210970_s_at	*IBTK*	12.84	12.13	12.07
217146_at	*JRK*	2.38	2.24	2.24
1557825_at	*NA*	2.08	1.96	1.96
230828_at	*GRAMD2*	3.025	2.845	2.845
215624_at	*TSC2*	2.275	2.145	2.135
243743_at	*HECW1*	2.9	2.74	2.73
1556842_at	*LOC286087*	2.845	2.695	2.675
239194_at	*WBSCR18*	3.13	2.95	2.95

1561213_at	*NA*	2.84	2.68	2.68
206436_at	*MPPED1*	2.43	2.29	2.29
207489_at	*FLJ12331*	2.43	2.29	2.29
208974_x_at	*KPNB1*	12.435	11.765	11.675
40640_at	*NCAPH2*	2.74	2.58	2.58
202061_s_at	*SEL1L*	10.99	10.38	10.35
237932_at	*NA*	3.42	3.22	3.22
1564235_at	*hCG_1994895*	2.315	2.175	2.185
219945_at	*DDX25*	2.67	2.52	2.51
240923_at	*COBLL1*	2.215	2.095	2.085
242103_at	*TMEM86A*	2.605	2.465	2.455
1558402_at	*NA*	3.05	2.88	2.87
241287_x_at	*C4orf15*	2.635	2.485	2.475
215534_at	*NA*	2.295	2.165	2.155
1558600_a_at	*PIP5K2B*	3.205	3.015	3.025
239645_at	*CCM2*	2.34	2.2	2.2
220601_at	*C16orf70*	2.73	2.57	2.57
210408_s_at	*CPNE6*	2.245	2.125	2.125
211077_s_at	*TLK1*	3.265	3.095	3.075
1564211_at	*C14orf64*	2.835	2.675	2.675
1552368_at	*CTCFL*	2.955	2.795	2.785
244831_at	*NA*	2.38	2.24	2.24
219046_s_at	*PKNOX2*	2.915	2.755	2.755
1564962_at	*ZNF92*	3.17	2.99	2.99
208929_x_at	*RPL13*	12.035	11.325	11.375
1555373_at	*C21orf114*	3.17	3	2.98
1560550_at	*NA*	2.595	2.455	2.445
215218_s_at	*WDR62*	2.665	2.515	2.505
208472_at	*IKZF4*	3.385	3.195	3.185
233256_at	*HIC2*	2.91	2.75	2.74
1555553_a_at	*SLC22A7*	2.19	2.07	2.07

227753_at	*TMEM139*	2.165	2.045	2.035
227849_at	*RP9*	2.445	2.305	2.305
234597_at	*NA*	2.855	2.695	2.685
1565728_at	*LOC284630*	2.92	2.76	2.76
1560102_at	*ARHGAP26*	3.085	2.915	2.895
210919_at	*PHLPP*	2.965	2.805	2.795
208275_x_at	*UTF1*	2.81	2.65	2.65
207735_at	*RNF125*	3.035	2.855	2.855
219456_s_at	*RIN3*	2.365	2.235	2.225
242095_at	*FLJ45825*	2.365	2.225	2.225
1570090_at	*EFHD1*	2.615	2.475	2.465
205816_at	*ITGB8*	2.695	2.545	2.535
1562648_at	*KIAA1212*	2.925	2.765	2.755
210961_s_at	*ADRA1D*	2.54	2.4	2.4
243172_at	*NA*	2.935	2.775	2.775
1556039_s_at	*NA*	3.17	3	2.98
236496_at	*DEGS2*	2.74	2.58	2.58
239865_at	*NA*	2.74	2.59	2.58
236416_at	*ARHGEF7*	3.035	2.855	2.865
1562895_at	*NA*	2.275	2.155	2.145
227231_at	*KIAA1211*	3.095	2.915	2.925
204689_at	*HHEX*	2.41	2.27	2.27
222290_at	*OR2A9P*	3.045	2.875	2.865
238990_x_at	*TRIM61*	6.595	6.215	6.225
230433_at	*LOC729970*	2.445	2.305	2.305
200017_at	*RPS27A*	13.725	12.975	12.915
1565802_at	*GTF2IRD2*	3.695	3.495	3.495
223741_s_at	*TTYH2*	2.44	2.31	2.3
231570_at	*C9orf138*	2.585	2.445	2.445
220181_x_at	*SLC30A5*	4.125	3.885	3.885
214383_x_at	*KLHDC3*	3.375	3.175	3.185

233332_at	*LOC121952*	2.42	2.28	2.28
237942_at	*SNRK*	3.28	3.1	3.09
211024_s_at	*TITF1*	2.85	2.69	2.69
242148_at	*BCL6B*	2.92	2.76	2.76
240865_at	*NA*	2.59	2.45	2.44
218475_at	*HTF9C*	3.27	3.1	3.08
207640_x_at	*NTN2L*	2.225	2.105	2.095
202005_at	*ST14*	2.71	2.55	2.55
205721_at	*GFRA2*	2.52	2.38	2.38
223740_at	*C6orf59*	2.42	2.28	2.29
229260_at	*C5orf15*	2.345	2.205	2.215
236189_at	*ANKRD50*	2.58	2.44	2.44
234069_at	*NA*	2.205	2.085	2.085
242551_at	*C18orf1*	2.685	2.535	2.525
216170_at	*CHCHD3*	2.41	2.27	2.27
200754_x_at	*SFRS2*	11.925	11.295	11.225
1563077_at	*NA*	2.83	2.68	2.66
214619_at	*CRHR1*	2.45	2.31	2.31
1555107_a_at	*KIAA1530*	2.325	2.185	2.195
205248_at	*DOPEY2*	2.46	2.32	2.32
233530_at	*FKBP1A*	2.59	2.45	2.45
1557790_at	*JRKL*	2.57	2.43	2.43
223977_s_at	*C18orf2*	2.9	2.75	2.73
232192_at	*LOC153811*	2.41	2.27	2.27
244501_at	*EVI5L*	2.55	2.41	2.4
209472_at	*CCBL2*	9.98	9.44	9.4
206293_at	*SULT2A1*	3.16	2.99	2.97
228958_at	*RPL27*	2.56	2.42	2.41
1564128_at	*QPRT*	2.735	2.585	2.575
205561_at	*KCTD17*	2.665	2.525	2.515
236497_at	*LOC729683*	2.635	2.495	2.495

234468_at	*NA*	2.78	2.62	2.63
231486_x_at	*NHLRC2*	2.8	2.65	2.64
1554492_at	*THADA*	3.105	2.925	2.925
226898_s_at	*SFPQ*	2.305	2.175	2.185
1563297_s_at	*NA*	2.355	2.225	2.215
239921_at	*tcag7.216*	2.825	2.675	2.665
215014_at	*NA*	3.23	3.04	3.06
224763_at	*RPL37*	8.485	7.985	8.025
232079_s_at	*TOMM40*	2.49	2.35	2.35
1556713_at	*FANCF*	2.665	2.525	2.515
216495_x_at	*IVD*	3.315	3.135	3.125
236871_s_at	*IQCF3*	3.385	3.205	3.195
237513_at	*TRY1*	2.42	2.29	2.28
239555_at	*LYN*	2.19	2.07	2.07
210234_at	*GRM4*	2.305	2.185	2.175
239196_at	*ANKRD22*	2.76	2.6	2.61
241123_at	*UPB1*	2.81	2.65	2.65
1567612_at	*NA*	2.805	2.655	2.645
220724_at	*FLJ21511*	2.81	2.66	2.64
1563878_a_at	*LOC338963*	2.815	2.655	2.655
222320_at	*CDC73*	3.27	3.08	3.1
1570412_at	*MED12L*	2.555	2.415	2.415
242557_at	*C6orf12*	2.795	2.645	2.635
229965_at	*PIK4CA*	2.355	2.215	2.225
205837_s_at	*GYPA*	3.055	2.895	2.885
233419_at	*NA*	2.58	2.44	2.44
231587_at	*LOC440838*	2.49	2.36	2.35
227342_s_at	*MYEOV*	2.365	2.235	2.225
1562214_at	*LOC151171*	2.015	1.895	1.895
216700_at	*TRIO*	2.235	2.115	2.115
1564426_x_at	*LOC389634*	2.805	2.655	2.645

234477_at	*IGHV2-70*	2.345	2.215	2.225
1553087_at	*C18orf12*	2.88	2.73	2.71
217389_s_at	*ATF5*	2.69	2.54	2.55
217681_at	*WNT7B*	2.195	2.075	2.075
1561590_a_at	*BC038740*	2.685	2.545	2.535
219574_at	*1-Mar*	2.645	2.505	2.495
1561834_a_at	*FLNB*	2.23	2.11	2.11
234602_x_at	*NA*	2.99	2.83	2.82
218925_s_at	*C11orf1*	3.05	2.89	2.88
1560738_at	*UBE3C*	3.115	2.945	2.935
233095_at	*NA*	2.725	2.575	2.565
216994_s_at	*RUNX2*	2.305	2.185	2.185
202463_s_at	*MBD3*	4.49	4.26	4.23
217758_s_at	*TM9SF3*	13.12	12.38	12.42
1570338_at	*D2HGDH*	2.675	2.525	2.535
215751_at	*RBM26*	2.715	2.565	2.575
234060_at	*NA*	2.57	2.43	2.43
207126_x_at	*UGT1A1*	2.56	2.42	2.42
210068_s_at	*AQP4*	2.375	2.245	2.235
237356_at	*ADAMTS18*	2.445	2.315	2.305
1559642_a_at	*C10orf56*	2.875	2.715	2.715
239795_at	*AXIN1*	2.88	2.72	2.72
243413_at	*TTC30B*	3.19	3.01	3.02
215583_at	*TMEM63A*	4.58	4.32	4.33
229712_at	*SNAPC3*	2.91	2.75	2.76
1561871_at	*NA*	2.275	2.155	2.155
240804_at	*GPR39*	2.735	2.575	2.585
232672_x_at	*MYEF2*	2.55	2.42	2.4
218744_s_at	*PACSIN3*	2.695	2.555	2.545
232327_at	*THSD7B*	2.77	2.61	2.62
1556354_s_at	*EPOR*	2.85	2.69	2.69

1555925_at	*NA*	2.95	2.8	2.78
1566932_x_at	*TFB2M*	2.47	2.33	2.34
214950_at	*IL9R*	2.58	2.44	2.44
240930_at	*CRAMP1L*	2.385	2.255	2.245
231204_at	*C4orf21*	3.075	2.915	2.905
244129_at	*NA*	2.335	2.205	2.215
1560683_at	*BCL8*	3.18	3.01	3
240720_at	*NA*	3.29	3.1	3.12
1568919_at	*NA*	2.67	2.53	2.52
209976_s_at	*CYP2E1*	2.695	2.545	2.555
227931_at	*NA*	10.045	9.505	9.495
243898_at	*RHBDD1*	2.705	2.565	2.555
241101_at	*NA*	2.44	2.31	2.3
241469_at	*SEC63D1*	2.795	2.635	2.635
239963_at	*NA*	3.175	2.995	3.005
223456_s_at	*TCHP*	3.155	2.975	2.985
1558930_at	*LOC728192*	2.455	2.315	2.315
1566251_at	*SH3GLP1*	3.455	3.275	3.265
230506_at	*C6orf164*	2.82	2.67	2.66
218630_at	*MKS1*	2.365	2.235	2.245
212783_at	*RBBP6*	9.015	8.515	8.525
221767_x_at	*HDLBP*	12.735	12.075	12.005
236783_at	*KCNIP4*	2.63	2.49	2.48
232850_at	*DCDC2*	2.57	2.43	2.43
207708_at	*ALOXE3*	2.235	2.115	2.115
215353_at	*ABP1*	2.865	2.715	2.695
227637_at	*TFCP2*	7.61	7.21	7.18
210491_at	*NA*	3.39	3.2	3.21
213801_x_at	*RPSA*	14.135	13.405	13.335
1566935_at	*TYRO3P*	2.665	2.525	2.515
236589_at	*NA*	2.89	2.74	2.73

1570326_at	*NA*	2.495	2.355	2.355
206154_at	*RLBP1*	2.145	2.025	2.025
219101_x_at	*ABHD8*	2.61	2.47	2.47
223549_s_at	*ESPN*	2.395	2.265	2.275
1557085_at	*PLAC1L*	2.795	2.645	2.635
1556400_at	*NA*	2.605	2.465	2.465
219943_s_at	*FLJ11850*	2.545	2.405	2.405
202072_at	*HNRPL*	2.765	2.615	2.625
220527_at	*MRPL20*	2.475	2.335	2.345
207684_at	*TBX6*	2.435	2.295	2.305
227056_at	*KIAA0141*	9.17	8.68	8.67
209813_x_at	*TRGV9*	2.325	2.205	2.205
207314_x_at	*KIR3DL2*	2.32	2.2	2.2
234994_at	*KIAA1913*	13.095	12.365	12.425
239941_at	*NA*	2.6	2.46	2.46
1554016_a_at	*C16orf57*	5.345	5.045	5.075
219086_at	*C14orf131*	2.845	2.695	2.685
230311_s_at	*PRDM6*	2.15	2.04	2.03
244385_at	*JMJD2C*	3.075	2.915	2.905
243881_at	*NA*	2.495	2.365	2.355
211056_s_at	*SRD5A1*	7.715	7.285	7.305
206779_s_at	*ASMT*	2.9	2.74	2.74
204030_s_at	*SCHIP1*	11.605	10.955	11.005
207475_at	*FABP2*	3.39	3.21	3.21
244191_at	*RPLP1*	2.475	2.345	2.335
217900_at	*IARS2*	9.98	9.46	9.43
218731_s_at	*VWA1*	2.48	2.35	2.34
1569915_at	*NA*	2.48	2.34	2.35
244538_at	*KCTD19*	2.565	2.435	2.425
229866_at	*NA*	3.36	3.18	3.18
231585_at	*VPS13A*	3.845	3.635	3.655

230218_at	*NA*	2.69	2.55	2.55
216305_s_at	*C2orf3*	4.305	4.075	4.065
1553174_at	*JPH2*	2.105	1.985	1.985
211599_x_at	*MET*	2.175	2.055	2.055
1561514_at	*LOC400655*	2.65	2.5	2.51
222169_x_at	*SH2D3A*	3.045	2.885	2.875
239318_at	*FAM118B*	2.25	2.13	2.13
218179_s_at	*FLJ12716*	8.24	7.8	7.8
1552588_a_at	*CNBD1*	2.57	2.44	2.43
210587_at	*INHBE*	2.58	2.44	2.44
1566480_x_at	*FLJ35848*	4.225	3.995	4.015
231938_at	*SGOL1*	3.135	2.965	2.975
200846_s_at	*PPP1CA*	6.945	6.565	6.575
211386_at	*MGC12488*	3.29	3.11	3.12
1559044_at	*EXOSC1*	3.075	2.915	2.915
202793_at	*MBOAT5*	5.22	4.95	4.94
211217_s_at	*KCNQ1*	2.72	2.58	2.58
211160_x_at	*ACTN1*	7.765	7.325	7.375
204846_at	*CP*	2.445	2.305	2.315
243458_at	*TNFAIP8*	3.34	3.15	3.17
233538_s_at	*CYBB*	2.295	2.175	2.175
217497_at	*ECGF1*	4.14	3.92	3.92
1569954_at	*C10orf112*	2.98	2.83	2.81
237627_at	*NA*	3.115	2.955	2.955
231580_at	*LOC729464*	2.61	2.47	2.47
237406_at	*NEK6*	2.475	2.345	2.335
202585_s_at	*NFX1*	3.64	3.45	3.44
220676_at	*ADAMTS8*	2.845	2.685	2.695
232355_at	*NA*	5.825	5.505	5.535
239407_at	*C21orf66*	2.37	2.25	2.25
216263_s_at	*NGDN*	2.915	2.755	2.765

243886_at	*LOC130355*	2.94	2.79	2.78
236677_at	*NGB*	2.355	2.235	2.235
1553169_at	*C20orf75*	2.205	2.085	2.085
241373_at	*ARIH2*	6.38	6.05	6.03
227625_s_at	*STUB1*	9.47	8.97	8.97
1555852_at	*PSMB9*	2.56	2.42	2.42
1563482_at	*DPYSL2*	2.64	2.5	2.5
240642_at	*NA*	2.32	2.2	2.2
230062_at	*KIAA1666*	2.775	2.635	2.625
220262_s_at	*EGFL9*	2.33	2.21	2.21
243137_at	*NA*	2.745	2.605	2.605
241723_at	*IQGAP2*	2.855	2.695	2.705
1562439_at	*NCOA3*	2.575	2.435	2.435
222068_s_at	*LRRC50*	2.415	2.285	2.295
220565_at	*CCR10*	2.64	2.5	2.5
203400_s_at	*TF*	2.465	2.335	2.325
220907_at	*GPR110*	2.72	2.58	2.57
1562282_at	*ZNF568*	3.675	3.485	3.465
1564707_x_at	*GLS2*	2.515	2.385	2.375
220771_at	*LOC51152*	3.175	3.015	3.005
235555_at	*NA*	2.98	2.83	2.82
232807_at	*C3orf40*	2.175	2.065	2.055
204207_s_at	*RNGTT*	5.905	5.605	5.575
1559641_at	*C10orf56*	2.69	2.55	2.55
233793_at	*ST6GALNAC5*	2.955	2.795	2.795
1556770_a_at	*FBXL13*	2.65	2.51	2.51
205645_at	*REPS2*	2.405	2.285	2.275
227772_at	*NA*	9.57	9.05	9.08
211736_at	*SP2*	2.65	2.51	2.51
1557309_at	*DENND1B*	2.99	2.84	2.83
241998_at	*LOC389073*	2.31	2.19	2.19

1557017_at	*NA*	3.005	2.855	2.835
227400_at	*NFIX*	6.195	5.875	5.875
210403_s_at	*KCNJ1*	2.26	2.14	2.14
204550_x_at	*GSTM1*	4.325	4.105	4.105
243862_at	*NA*	3.41	3.24	3.22
208080_at	*AURKA*	2.74	2.6	2.6
1562926_at	*NA*	2.73	2.59	2.59
1552865_a_at	*IFLTD1*	2.115	2.005	1.995
237418_at	*CDK5RAP2*	2.045	1.945	1.945
221142_s_at	*PECR*	2.515	2.375	2.375
234569_at	*NA*	2.4	2.28	2.27
233534_at	*KRTAP3-2*	3.07	2.91	2.91
35974_at	*LRMP*	2.78	2.63	2.64
243204_at	*NA*	3.04	2.88	2.88
203107_x_at	*RPS2*	13.505	12.795	12.805
206350_at	*APCS*	2.61	2.48	2.47
1553265_at	*SLC23A3*	2.81	2.67	2.67
244681_at	*C3orf46*	2.63	2.49	2.49
216759_at	*HRASLS2*	2.84	2.7	2.69
1554203_at	*C21orf9*	2.98	2.83	2.82
207080_s_at	*PYY*	2.34	2.22	2.22
228705_at	*CAPN12*	2.78	2.63	2.64
216386_at	*LOC220077*	2.415	2.295	2.285
242889_x_at	*LOC645431*	5.79	5.49	5.48
244468_at	*PDZK1*	2.805	2.665	2.655
206334_at	*LIPF*	2.595	2.455	2.455
230117_at	*VSTM2*	2.505	2.375	2.365
1555996_s_at	*EIF4A2*	2.485	2.355	2.365
1558292_s_at	*PIGW*	9.795	9.275	9.285
244747_at	*NPNT*	2.29	2.17	2.17
1562528_at	*RORA*	3.06	2.89	2.91

228055_at	*NAPSB*	2.125	2.015	2.005
1564887_at	*NA*	2.74	2.6	2.59
227209_at	*CNTN1*	3.08	2.92	2.92
214123_s_at	*NOL14*	2.96	2.8	2.81
1565820_x_at	*PHACTR4*	2.805	2.665	2.655
201240_s_at	*SPCS2*	14.285	13.535	13.555
225741_at	*THUMPD3*	6.88	6.5	6.54
1569486_at	*NA*	2.545	2.415	2.405
1562583_s_at	*LOC646405*	3.07	2.91	2.91
220828_s_at	*FLJ11292*	3.07	2.91	2.91
207879_at	*NA*	2.905	2.755	2.745
241326_at	*PAPOLA*	2.555	2.415	2.415
206906_at	*ICAM5*	2.095	1.995	1.995
1566739_at	*PLCE1*	2.745	2.605	2.605
1561206_at	*KLHL8*	3	2.84	2.84
207743_at	*PRO1880*	2.32	2.2	2.2
1561995_at	*NA*	2.105	1.995	2.005
1561894_at	*LOC653739*	2.82	2.68	2.67
1565774_at	*FAM38B*	2.47	2.35	2.34
230007_at	*JMJD1C*	3.12	2.96	2.96
1554786_at	*C20orf32*	2.745	2.605	2.605
233362_at	*ZNF341*	2.585	2.445	2.445
228934_x_at	*NA*	5.77	5.46	5.48
1556516_at	*C9orf93*	2.785	2.635	2.645
210128_s_at	*LTB4R*	2.78	2.63	2.64
209749_s_at	*ACE*	2.935	2.785	2.775
1569554_at	*ESR2*	2.81	2.67	2.66
227933_at	*LINGO1*	3.585	3.405	3.405
235189_at	*NARG2*	2.455	2.335	2.335
230358_at	*ZER1*	2.44	2.32	2.32
1561153_at	*CCDC134*	2.68	2.54	2.54

212137_at	*LARP1*	11.88	11.29	11.24
201530_x_at	*EIF4A1*	12.075	11.425	11.475
1553721_at	*RNF152*	2.925	2.775	2.765
216500_at	*NA*	5.165	4.905	4.895
218465_at	*TMEM33*	10.945	10.385	10.385
233368_s_at	*RBJ*	2.485	2.365	2.355
216363_at	*NA*	2.895	2.755	2.745
222828_at	*IL20RA*	2.79	2.65	2.65
1563061_at	*NA*	3.09	2.94	2.92
228682_at	*ENOPH1*	2.68	2.54	2.54
203780_at	*EVA1*	2.935	2.775	2.785
236245_at	*ODF3L1*	2.39	2.27	2.27
1570127_at	*NA*	2.825	2.685	2.685
235347_at	*LRCH3*	8.375	7.945	7.935
1568782_at	*RP2*	2.3	2.18	2.18
1555221_at	*NA*	2.155	2.045	2.035
1552674_at	*DIRC1*	3.05	2.9	2.89
206160_at	*APOBEC2*	2.895	2.755	2.745
1562811_at	*NA*	2.33	2.21	2.21
210379_s_at	*TLK1*	3.065	2.905	2.905
217236_x_at	*IGHG1*	2.455	2.335	2.335
213669_at	*FCHO1*	2.4	2.28	2.28
237578_at	*FLJ21963*	2.69	2.55	2.55
1557480_a_at	*DYSFIP1*	2.86	2.71	2.72
238603_at	*LOC254559*	2.475	2.355	2.345
212223_at	*IDS*	8.275	7.855	7.845
1569892_at	*NA*	2.77	2.64	2.62
1552938_at	*ZIC5*	2.835	2.695	2.695
1565852_at	*MBP*	2.515	2.395	2.385
1568871_at	*NA*	2.975	2.825	2.815
231212_x_at	*TPST1*	4.205	3.985	3.985

233474_at	*LOC284240*	2.35	2.23	2.23
225997_at	*MOBKL1A*	12.295	11.655	11.685
1565921_a_at	*NA*	2.525	2.405	2.395
227583_at	*POP4*	2.69	2.56	2.55
207837_at	*RBPMS*	3.5	3.32	3.32
237179_at	*PCMTD2*	2.955	2.805	2.795
234914_at	*ZNF7*	2.97	2.82	2.81
1553619_a_at	*TRIM43*	2.485	2.355	2.365
221137_at	*NA*	2.61	2.47	2.47
237085_x_at	*NA*	4.67	4.44	4.42
1554161_at	*SLC25A27*	2.945	2.795	2.785
240988_x_at	*NA*	2.415	2.295	2.295
243465_at	*TMEM140*	5.385	5.095	5.115
210033_s_at	*SPAG6*	2.285	2.165	2.165
211848_s_at	*CEACAM7*	2.67	2.54	2.53
229147_at	*NA*	2.655	2.525	2.515
231761_at	*FFAR1*	2.505	2.385	2.375
236064_at	*SLC25A35*	3.575	3.395	3.395
217193_x_at	*IL8*	2.89	2.75	2.74
1553625_at	*FAM98B*	3.365	3.185	3.195
229343_at	*GTSE1*	2.27	2.15	2.15
220944_at	*PGLYRP4*	2.105	2.005	2.005
242298_x_at	*KARS*	3.105	2.945	2.945
1561297_at	*WARS2*	2.25	2.13	2.13
230716_at	*LOC285733*	2.615	2.485	2.475
221163_s_at	*MLXIPL*	2.995	2.835	2.845
233780_at	*RIF1*	2.61	2.48	2.47
207832_at	*BAIAP2*	2.34	2.22	2.22
243821_at	*MRPS31*	2.7	2.56	2.56
1569539_at	*FILIP1L*	3.12	2.96	2.96
1560690_at	*NA*	2.35	2.23	2.23

241673_x_at	*NA*	2.885	2.745	2.735
1560773_at	*LOC645256*	2.515	2.395	2.395
236285_at	*NA*	2.42	2.29	2.3
229857_s_at	*KIAA1267*	2.575	2.445	2.435
1558398_at	*ANKRD24*	2.37	2.25	2.25
206057_x_at	*SPN*	2.265	2.145	2.145
203382_s_at	*APOE*	2.39	2.27	2.27
239523_at	*TUSC5*	2.925	2.785	2.775
220846_s_at	*PRKCZ*	2.255	2.135	2.145
239353_at	*NA*	2.43	2.31	2.31
227136_s_at	*C10orf46*	2.675	2.535	2.535
217890_s_at	*PARVA*	10.6	10.07	10.05
38157_at	*DOM3Z*	3.84	3.65	3.64
1552952_at	*RBMY2FP*	2.425	2.305	2.295
1555725_a_at	*RGS5*	2.84	2.7	2.7
1555116_s_at	*SLC11A1*	2.575	2.445	2.435
238283_at	*LOC151658*	2.77	2.63	2.63
235475_at	*SERP1*	2.595	2.455	2.465
215290_at	*LOC645323*	2.8	2.66	2.66
210954_s_at	*TSC22D2*	2.41	2.29	2.29
222241_at	*FAM125B*	2.78	2.64	2.64
240953_at	*ACPP*	2.535	2.415	2.405
230340_s_at	*WASL*	2.515	2.395	2.385
234430_at	*ANTXR1*	2.4	2.28	2.28
214762_at	*ATP6V1G2*	2.415	2.295	2.295
230682_x_at	*ABCC3*	2.47	2.35	2.35
1570357_at	*STX8*	2.555	2.435	2.435
234973_at	*SLC38A5*	3.465	3.285	3.285
1563187_at	*KCNH7*	3.03	2.88	2.87
1558518_at	*MAP3K7IP3*	2.77	2.63	2.63
236895_at	*SGPL1*	2.425	2.305	2.305

204557_s_at	*DZIP1*	8.44	8.01	8.03
1564319_at	*C19orf16*	2.625	2.495	2.485
231329_at	*ITPR1*	3.04	2.89	2.88
1569955_at	*NA*	2.43	2.31	2.31
211374_x_at	*NA*	3.895	3.695	3.695
240477_at	*ETV1*	3.07	2.91	2.91
1562051_at	*LOC284757*	2.77	2.63	2.63
233653_at	*NRG3*	2.83	2.69	2.69
224074_at	*VSX1*	2.605	2.475	2.465
236541_at	*NA*	2.47	2.35	2.35
231191_at	*ANKMY1*	2.46	2.34	2.33
234531_at	*FLJ11292*	3.025	2.875	2.865
210784_x_at	*LILRB3*	5.345	5.085	5.075
244306_at	*NRG3*	2.625	2.495	2.485
236188_s_at	*NAP1L4*	2.69	2.55	2.55
221980_at	*EMILIN2*	2.665	2.525	2.535
1564776_at	*LENG10*	2.645	2.505	2.505
212207_at	*THRAP2*	9.435	8.955	8.965
222091_at	*HPCAL4*	3.485	3.305	3.315
217036_at	*NA*	2.955	2.815	2.815
223275_at	*PRMT6*	5.355	5.105	5.075
1561175_at	*LOC283482*	2.53	2.41	2.41
35160_at	*LDB1*	2.975	2.825	2.835
244147_at	*KIAA1217*	2.81	2.67	2.67
234503_at	*CHCHD3*	2.915	2.775	2.765
243250_at	*ZDHHC13*	2.915	2.775	2.765
212934_at	*LOC137886*	7.13	6.78	6.77
204144_s_at	*PIGQ*	2.8	2.66	2.66
240001_at	*NA*	2.29	2.17	2.17
216968_at	*MASP2*	2.575	2.445	2.455
214471_x_at	*LHB*	2.505	2.385	2.375

232318_s_at	*LOC121838*	2.775	2.625	2.645
1559895_x_at	*NA*	3.1	2.95	2.94
239899_at	*FLJ31951*	2.145	2.045	2.035
208020_s_at	*CACNA1C*	2.435	2.315	2.315
231520_at	*SLC35F3*	2.44	2.32	2.32
1569779_at	*MICA*	2.73	2.59	2.59
241559_at	*TCEA1*	2.945	2.805	2.805
202614_at	*SLC30A9*	11.395	10.815	10.855
237525_at	*NA*	2.635	2.495	2.495
216887_s_at	*LDB3*	2.41	2.29	2.29
1555307_at	*TTF2*	2.72	2.59	2.58
219630_at	*PDZK1IP1*	2.24	2.13	2.12
210496_at	*NAG18*	3.25	3.09	3.09
219541_at	*LIME1*	4.795	4.545	4.565
205469_s_at	*IRF5*	2.305	2.185	2.185
1561856_at	*NA*	2.86	2.72	2.72
1563003_at	*ITGAX*	2.925	2.785	2.775
237289_at	*FAM119A*	9.045	8.615	8.585
233863_at	*NA*	2.33	2.21	2.21
1568660_a_at	*NA*	2.705	2.575	2.565
1569525_s_at	*NA*	3.195	3.035	3.035
242047_at	*PLEKHK1*	2.59	2.47	2.47
1567297_at	*OR13C4*	2.615	2.495	2.485
234456_at	*TRAPPC4*	2.155	2.055	2.055
238095_at	*GATA5*	2.725	2.595	2.585
1569504_at	*LILRB1*	2.79	2.65	2.65
243065_at	*PS1TP4*	2.665	2.535	2.525
239750_x_at	*VAPA*	3.74	3.55	3.57
222081_at	*NA*	2.255	2.145	2.135
1553607_at	*C21orf109*	3.065	2.905	2.915
236357_at	*NA*	2.305	2.185	2.185

1570299_at	*MAML2*	2.5	2.38	2.37
1561966_at	*NA*	2.36	2.24	2.24
241216_at	*KIF1B*	2.955	2.815	2.815
207091_at	*P2RX7*	2.245	2.125	2.125
208311_at	*GPR50*	2.285	2.175	2.165
1553642_at	*C9orf163*	2.145	2.045	2.045
205026_at	*STAT5B*	2.655	2.515	2.525
226711_at	*FOXN2*	10.355	9.835	9.845
1553151_at	*ATP6V0D2*	2.35	2.23	2.23
1559689_a_at	*GRAP*	2.585	2.465	2.455
214166_at	*SDHB*	2.34	2.22	2.22
1555822_at	*LOC641702*	2.43	2.31	2.31
214750_at	*PLAC4*	2.48	2.36	2.36
216598_s_at	*CCL2*	2.79	2.65	2.65
243756_at	*THSD7A*	2.41	2.29	2.29
207690_at	*ALX3*	2.225	2.125	2.115
1559932_at	*HEXA*	2.56	2.43	2.44
240222_at	*COPS8*	3.14	2.99	2.98
210714_at	*R3HDM1*	2.535	2.415	2.405
242778_at	*LPXN*	3.33	3.16	3.17
1553585_a_at	*MAGEA5*	2.525	2.405	2.405
216786_at	*LOC159110*	2.885	2.745	2.745
220667_at	*NA*	2.97	2.83	2.83
219581_at	*TSEN2*	3.175	3.015	3.015
35201_at	*HNRPL*	7.895	7.515	7.515
242643_x_at	*PHKB*	2.61	2.49	2.48
1562730_a_at	*SGCA*	2.47	2.35	2.35
244578_at	*LCP2*	2.45	2.33	2.33
234423_x_at	*NA*	2.265	2.145	2.155
213464_at	*SHC2*	3.125	2.965	2.975
1569833_at	*NA*	2.83	2.69	2.69

237580_at	*SYNE2*	2.995	2.855	2.845
1568686_at	*LOC158381*	2.735	2.595	2.595
208438_s_at	*FGR*	2.105	2.005	2.005
243529_at	*MARS2*	2.53	2.41	2.41
228015_s_at	*TRIM8*	2.4	2.28	2.28
222465_at	*C15orf15*	11.975	11.415	11.375
236759_at	*RIMS3*	2.39	2.27	2.27
1560024_at	*LOC388965*	2.96	2.82	2.82
205949_at	*CA1*	2.16	2.06	2.06
1563590_at	*PTPRE*	2.52	2.4	2.4
1558941_at	*ZNF704*	2.365	2.245	2.245
234313_at	*NCOR1*	2.685	2.545	2.555
1563379_at	*RORA*	2.37	2.25	2.25
1555319_at	*STAB1*	3.2	3.05	3.03
1567558_at	*TREML4*	2.56	2.44	2.44
1562743_at	*ZNF83*	2.375	2.255	2.255
238572_at	*MGC16211*	2.45	2.33	2.33
210123_s_at	*CHRNA7*	2.6	2.48	2.47
1564749_at	*NA*	2.575	2.455	2.445
237508_at	*CPEB3*	2.55	2.43	2.42
208154_at	*LOC51336*	2.32	2.21	2.2
231382_at	*FGF18*	2.295	2.185	2.175
237357_at	*LOC728119*	2.535	2.415	2.405
235491_at	*ZBTB10*	2.605	2.485	2.475
1563287_at	*NA*	2.485	2.365	2.365
213597_s_at	*CTDSPL*	2.375	2.255	2.255
244218_at	*SND1*	2.86	2.73	2.71
1552714_at	*CREG2*	2.57	2.45	2.44
1566253_at	*LRRC37B*	2.85	2.71	2.71
202707_at	*UMPS*	2.36	2.24	2.24
223873_s_at	*EPN1*	2.795	2.655	2.655

217676_at	*NA*	2.37	2.25	2.25
244077_at	*NEBL*	2.615	2.495	2.495
1557427_at	*NA*	2.94	2.8	2.8
208787_at	*MRPL3*	12.485	11.885	11.875
203781_at	*MRPL33*	10.65	10.14	10.13
238586_at	*TNK2*	2.315	2.195	2.195
237491_at	*MYH10*	2.57	2.45	2.44
217133_x_at	*CYP2B6*	2.52	2.4	2.4
207988_s_at	*ARPC2*	12.26	11.63	11.69
243118_at	*C6orf182*	6.31	6	6.01
218509_at	*LPPR2*	4.53	4.31	4.31
1565192_at	*NA*	2.79	2.65	2.65
1561222_at	*LOC283432*	3.185	3.035	3.025
233608_at	*RBMS3*	2.56	2.44	2.44
205723_at	*CNTFR*	3.465	3.305	3.295
227901_at	*AXIIR*	6.9	6.58	6.55
214186_s_at	*3.8-1*	3.145	2.995	2.985
237908_at	*LOC554203*	2.635	2.505	2.515
205852_at	*CDK5R2*	3	2.85	2.86
241695_s_at	*KLHL6*	2.58	2.46	2.46
208849_at	*NA*	2.825	2.685	2.685
216413_at	*NA*	2.725	2.595	2.585
215005_at	*EFCBP2*	2.55	2.43	2.43
233627_at	*MKL1*	2.735	2.605	2.595
223619_x_at	*PECR*	7.945	7.575	7.555
221327_s_at	*OPN1MW*	2.265	2.155	2.165
241663_at	*C3orf23*	2.395	2.275	2.275
232760_at	*TEX15*	2.665	2.545	2.535
229868_s_at	*GDF15*	2.725	2.595	2.585
1554717_a_at	*PDE4D*	2.53	2.41	2.41
1564413_at	*FLJ36116*	4.445	4.225	4.225

208833_s_at	*ATXN10*	10.865	10.355	10.335
202641_at	*ARL3*	10.73	10.2	10.22
222564_at	*POGK*	3.145	2.985	2.995
229558_at	*MGC16824*	6.195	5.905	5.895
1570190_at	*LSAMP*	2.95	2.82	2.8
212962_at	*SYDE1*	2.7	2.57	2.58
1556166_x_at	*NA*	2.56	2.44	2.44
232301_at	*UBE3B*	2.765	2.625	2.635
1562094_at	*MGC26963*	2.47	2.35	2.35
215696_s_at	*KIAA0310*	10.78	10.26	10.26
239465_at	*UQCRC2*	2.62	2.5	2.5
1554385_a_at	*PADI2*	2.455	2.335	2.335
1569061_at	*IQGAP3*	3.085	2.945	2.945
223756_at	*FLJ10081*	2.47	2.35	2.35
207200_at	*OTC*	2.295	2.195	2.185
1561733_at	*INPP5A*	2.605	2.485	2.485
208067_x_at	*UTY*	2.795	2.665	2.655
221993_s_at	*C16orf42*	2.655	2.525	2.535
1553861_at	*TCP11L2*	2.64	2.52	2.52
1556374_s_at	*TTC7B*	2.09	1.99	1.99
216709_at	*LOC400655*	2.685	2.565	2.555
237565_at	*GCC2*	2.51	2.39	2.39
1555336_a_at	*ITGA9*	2.275	2.175	2.165
215101_s_at	*CXCL5*	2.705	2.585	2.575
226380_at	*PTPN21*	8.745	8.345	8.305
1561916_at	*NA*	2.545	2.425	2.425
244570_at	*NA*	2.49	2.37	2.37
1569277_at	*ZNF91*	3.085	2.945	2.945
236810_at	*ITGB7*	2.55	2.43	2.42
1564010_at	*CAST*	2.19	2.09	2.09
216653_at	*DR1*	2.485	2.365	2.365

215032_at	*RREB1*	3.8	3.62	3.62
219404_at	*EPS8L3*	2.2	2.1	2.1
1562905_at	*NA*	3.34	3.18	3.18
224896_s_at	*TTL*	11.635	11.075	11.085
1556665_at	*TTC6*	2.665	2.545	2.535
205269_at	*LCP2*	2.93	2.8	2.78
232320_at	*LOC391142*	2.92	2.78	2.79
1562264_at	*LOC339685*	2.19	2.09	2.09
1562687_x_at	*hCG_1660379*	2.205	2.105	2.105
244030_at	*STYX*	2.675	2.545	2.555
215680_at	*KIAA1654*	2.43	2.31	2.31
200993_at	*IPO7*	12.355	11.775	11.775
239122_at	*NA*	2.1	2	2
224146_s_at	*ABCC11*	2.61	2.49	2.49
216627_s_at	*B4GALT1*	2.665	2.545	2.545
238210_at	*RYK*	2.4	2.28	2.28
1555719_a_at	*C3orf15*	2.94	2.8	2.8
244340_x_at	*NA*	4.085	3.885	3.895
233483_at	*LOC96597*	2.65	2.53	2.53
1555210_at	*DTWD1*	2.705	2.585	2.575
216715_at	*LOC442258*	3.08	2.93	2.94
1559394_a_at	*ROR1*	2.855	2.715	2.715
1562793_at	*NA*	3.26	3.1	3.11
240768_x_at	*UBXD2*	2.97	2.83	2.83
232190_x_at	*LOC115110*	5.25	5.02	4.99
224206_x_at	*MYNN*	7.11	6.76	6.78
233233_at	*RASSF3*	2.98	2.84	2.83
226361_at	*TMEM42*	4.67	4.45	4.45
238535_at	*CEP152*	3.045	2.905	2.895
242943_at	*ST8SIA4*	2.51	2.39	2.39
1558081_at	*RPL12*	2.415	2.295	2.295

208081_s_at	*ZNF442*	3.125	2.975	2.985
233716_at	*LOC645256*	3.135	2.995	2.995
1564333_a_at	*SORCS2*	2.45	2.33	2.33
243674_at	*NA*	3	2.86	2.86
1556996_at	*NA*	2.4	2.29	2.28
206711_at	*CXorf1*	2.37	2.26	2.25
1554069_at	*EPHA8*	3.48	3.33	3.31
230775_s_at	*SPG20*	2.26	2.16	2.16
238455_at	*NA*	2.575	2.455	2.445
1561706_at	*NA*	2.355	2.245	2.235
242455_at	*POU3F2*	2.845	2.705	2.715
234389_x_at	*NA*	2.425	2.315	2.305
1569909_at	*KRT6L*	3.07	2.92	2.93
1558868_a_at	*DSE*	2.445	2.325	2.335
215257_at	*ERGIC3*	2.65	2.53	2.53
244217_at	*A2BP1*	2.885	2.745	2.745
240236_at	*NA*	2.765	2.645	2.635
239266_at	*SNHG5*	2.98	2.84	2.84
208758_at	*ATIC*	8.14	7.75	7.77
244222_at	*NA*	3.17	3.03	3.02
213731_s_at	*TCF3*	2.29	2.19	2.19
232885_at	*LOC92482*	2.72	2.59	2.6
1560407_at	*MARK1*	2.71	2.59	2.58
211341_at	*POU4F1*	2.5	2.38	2.38
234408_at	*IL17F*	2.455	2.335	2.335
1569294_at	*RNF187*	2.11	2.01	2.01
220469_at	*COPE*	2.32	2.21	2.22
1561417_x_at	*LOC727792*	3.115	2.975	2.975
221118_at	*PKD2L2*	3.03	2.89	2.89
230883_at	*NA*	2.56	2.44	2.44
1555379_at	*MGC52498*	2.56	2.44	2.44

237000_at	*NA*	3.365	3.215	3.205
225124_at	*PPP1R9B*	3.49	3.33	3.33
238100_at	*AAK1*	2.6	2.48	2.48
227299_at	*CCNI*	4.525	4.305	4.315
208026_at	*HIST1H4F*	2.53	2.41	2.41
1555340_x_at	*RAP1A*	2.25	2.15	2.15
244625_at	*RERE*	2.775	2.645	2.655
237149_at	*NA*	2.64	2.52	2.52
205982_x_at	*SFTPC*	2.065	1.965	1.965
204325_s_at	*NF1*	3.43	3.27	3.27
243412_at	*EMR4*	3.03	2.89	2.89
235442_at	*CXorf56*	2.845	2.705	2.705
228994_at	*CCDC24*	2.455	2.335	2.345
1554495_s_at	*MTHFSD*	2.54	2.42	2.42
210466_s_at	*SERBP1*	12.355	11.755	11.805
1556867_at	*NA*	2.56	2.44	2.44
239119_at	*NA*	2.09	1.99	1.99
221244_s_at	*PDPK1*	2.225	2.125	2.125
1561721_a_at	*C12orf40*	3.03	2.89	2.89
219444_at	*BCORL1*	5.58	5.32	5.32
1552584_at	*IL12RB1*	2.57	2.45	2.45
221027_s_at	*PLA2G12A*	8.435	8.025	8.055
244553_at	*NA*	2.84	2.71	2.7
1554526_at	*OLFM3*	3.01	2.87	2.88
232743_at	*KIAA1833*	2.865	2.725	2.735
228409_at	*KIAA1881*	2.745	2.625	2.625
1563241_at	*PHF12*	3.11	2.97	2.96
230811_at	*CDK10*	2.525	2.405	2.405
1560742_at	*ALS2*	2.52	2.4	2.4
241311_at	*ST18*	2.505	2.385	2.385
213963_s_at	*SAP30*	2.945	2.815	2.805

241012_at	*LOC647336*	2.69	2.56	2.57
210936_at	*WDR1*	3.39	3.23	3.24
224063_at	*NLN*	2.7	2.58	2.57
236220_at	*NA*	2.625	2.505	2.505
210482_x_at	*MAP2K5*	2.325	2.225	2.225
240522_at	*BAIAP2L1*	2.795	2.675	2.665
219896_at	*DRD1IP*	2.21	2.11	2.11
238953_at	*SP2*	2.6	2.48	2.48
1564906_at	*SNHG4*	2.355	2.255	2.255
1559503_a_at	*LOC441666*	3.03	2.9	2.89
1569401_at	*CLEC12A*	2.815	2.695	2.685
227803_at	*ENPP5*	3.11	2.97	2.96
225336_at	*NA*	10.345	9.895	9.835
236287_at	*ZNF22*	2.775	2.655	2.645
240947_at	*TMEM16F*	2.715	2.595	2.585
232251_at	*NUDT16P*	2.56	2.45	2.44
244395_at	*FLJ41455*	3.02	2.88	2.88
233087_at	*FBXL17*	2.785	2.665	2.665
1562281_at	*TSPAN5*	2.66	2.54	2.54
1569819_at	*C15orf2*	2.355	2.255	2.245
236818_at	*NAALADL2*	2.495	2.375	2.375
1570473_at	*LOC338579*	3.08	2.94	2.93
237114_at	*HERC4*	2.995	2.855	2.855
227568_at	*HECTD2*	9.425	8.985	9.015
216403_at	*RP11-114G1.1*	2.485	2.365	2.375
1555141_a_at	*NHEDC1*	2.81	2.69	2.68
214958_s_at	*TMC6*	2.08	1.98	1.98
241086_at	*CROP*	2.96	2.82	2.82
220255_at	*FANCE*	6.845	6.515	6.535
207287_at	*FLJ14107*	2.68	2.56	2.56
215901_at	*ZNF81*	2.725	2.595	2.605

1559142_at	*MYST3*	2.835	2.705	2.715
1553101_a_at	*ALKBH5*	4.78	4.55	4.57
227716_at	*UBXD5*	2.995	2.855	2.855
224165_s_at	*IQCH*	2.95	2.81	2.81
1558678_s_at	*MALAT1*	15.61	14.91	14.9
214248_s_at	*TRIM2*	2.28	2.18	2.18
216516_at	*NA*	3.235	3.085	3.095
244784_at	*DHX57*	2.815	2.685	2.695
240621_at	*ATM*	2.31	2.21	2.21
234337_at	*TTLL9*	2.885	2.745	2.755
226187_at	*CDS1*	2.435	2.315	2.325
212629_s_at	*PKN2*	10.03	9.56	9.58
208085_s_at	*ARHGAP6*	2.365	2.265	2.265
215825_at	*NA*	2.795	2.675	2.665
228656_at	*PROX1*	2.415	2.315	2.305
233091_at	*ATAD3B*	2.335	2.235	2.235
1553847_a_at	*SPERT*	2.365	2.265	2.265
1561288_at	*NA*	2.71	2.59	2.58
220637_at	*FAM124B*	2.385	2.285	2.285
217696_at	*FUT7*	4.785	4.575	4.565
240355_at	*NA*	2.895	2.765	2.755
216812_at	*NA*	2.14	2.04	2.04
1554916_a_at	*JRK*	2.455	2.335	2.345
241919_x_at	*WDR31*	3.425	3.265	3.265
237123_x_at	*KLHL9*	3.08	2.94	2.94
1561881_at	*NA*	2.8	2.67	2.68
1560781_at	*C11orf47*	2.82	2.7	2.7
208659_at	*CLIC1*	12.09	11.58	11.52
240977_at	*LRCH1*	2.935	2.795	2.805
215554_at	*GPLD1*	2.6	2.48	2.48
1553888_at	*LDHAL6A*	2.55	2.43	2.44

1566999_at	*DTD1*	3.425	3.275	3.265
1561777_at	*C21orf34*	2.66	2.54	2.54
213751_at	*LOC284352*	2.6	2.48	2.48
238266_at	*NA*	2.555	2.435	2.445
221468_at	*XCR1*	2.265	2.165	2.165
1559410_at	*LOC389634*	2.525	2.415	2.405
227328_at	*CAMTA1*	7.475	7.125	7.155
207873_x_at	*SEZ6L*	2.36	2.26	2.26
215895_x_at	*ADFP*	2.835	2.705	2.715
207617_at	*DDX3X*	2.67	2.55	2.55
240436_at	*LOC650794*	2.36	2.26	2.26
1554733_at	*MGC24125*	2.76	2.64	2.64
231070_at	*IYD*	2.995	2.865	2.855
241623_at	*PTPN2*	2.565	2.445	2.445
217024_x_at	*SIRPA*	2.565	2.445	2.455
233134_at	*RPH3AL*	3.04	2.9	2.9
208881_x_at	*IDI1*	10.075	9.625	9.635
243193_at	*GPC3*	2.66	2.54	2.54
1564753_at	*LASS6*	2.975	2.835	2.835
230466_s_at	*RASSF3*	12.825	12.275	12.225
203555_at	*PTPN18*	4.21	4.03	4.02
240163_at	*RORA*	3.18	3.04	3.04
1555129_at	*NA*	2.16	2.06	2.06
1561278_at	*NA*	2.575	2.465	2.455
211129_x_at	*EDA*	2.24	2.14	2.14
230429_at	*ASPH*	2.365	2.265	2.265
233936_s_at	*ZNF403*	10.685	10.225	10.195
232194_at	*METTL4*	6.3	6.02	6.02
1552827_s_at	*SLC26A7*	2.73	2.61	2.61
228840_at	*AMOTL1*	4.32	4.12	4.12
243929_at	*ZNF533*	2.465	2.365	2.355

213267_at	*DOPEY1*	3.14	3	3
220656_at	*NARG1L*	3.1	2.96	2.96
1555504_at	*TYR*	2.965	2.835	2.825
215120_s_at	*SAMD4A*	3.095	2.965	2.955
221661_at	*SLC22A7*	2.815	2.695	2.685
216542_x_at	*F13B*	3.11	2.97	2.98
215051_x_at	*AIF1*	3.59	3.43	3.43
222546_s_at	*EPS8L2*	2.32	2.22	2.22
237473_at	*LOC728448*	2.18	2.08	2.08
236299_at	*ZNF496*	2.41	2.31	2.3
233149_at	*LOC729258*	2.385	2.285	2.275
240703_s_at	*HERC1*	2.605	2.495	2.485
1566955_at	*NA*	2.845	2.725	2.725
1562497_at	*MKL2*	2.515	2.395	2.395
1565805_at	*LOC728011*	2.175	2.075	2.075
233990_at	*FLJ12886*	2.405	2.305	2.305
207685_at	*CRYBB3*	2.22	2.12	2.12
216219_at	*AQP6*	3.18	3.04	3.04
215637_at	*TSGA14*	2.605	2.495	2.485
244127_at	*NA*	2.86	2.74	2.73
1563265_at	*HNF4A*	2.925	2.805	2.795
215339_at	*NKTR*	2.83	2.71	2.71
216745_x_at	*NA*	3.05	2.91	2.91
239796_x_at	*TIRAP*	2.865	2.745	2.745
244523_at	*MMD*	2.33	2.23	2.23
203892_at	*WFDC2*	2.135	2.035	2.035
217889_s_at	*CYBRD1*	7.045	6.735	6.745
224235_at	*NA*	2.87	2.75	2.74
1561523_at	*CCDC65*	2.915	2.795	2.785
242733_at	*HPGD*	2.67	2.55	2.55
204606_at	*CCL21*	2.35	2.25	2.25

241580_at	*KIAA1729*	2.71	2.59	2.59
239999_at	*C21orf34*	2.71	2.59	2.59
241126_at	*NA*	2.955	2.835	2.835
208973_at	*PRNPIP*	2.25	2.15	2.15
210917_at	*YES1*	2.74	2.62	2.62
1556210_at	*NA*	3.055	2.915	2.925
244767_at	*NA*	3.2	3.05	3.07
1566447_at	*CD6*	2.34	2.24	2.24
205094_at	*PEX12*	6.89	6.57	6.6
1558570_at	*LOC145783*	2.495	2.395	2.385
1558470_at	*MGC26733*	3.21	3.08	3.06
240052_at	*ITPR1*	2.535	2.425	2.415
213171_s_at	*MMP24*	3	2.86	2.87
244626_at	*CASZ1*	3.01	2.88	2.87
206493_at	*ITGA2B*	2.445	2.345	2.345
209971_x_at	*JTV1*	9.135	8.745	8.735
1554367_at	*FAM26C*	2.85	2.72	2.73
1563243_at	*DGCR5*	2.83	2.71	2.71
214851_at	*HNF4A*	2.195	2.095	2.095
1570320_at	*NA*	2.885	2.765	2.765
213200_at	*SYP*	3.64	3.48	3.48
219964_at	*ST7L*	2.555	2.445	2.435
224139_at	*C11orf76*	3.73	3.58	3.56
1562962_at	*NA*	3.36	3.22	3.21
205472_s_at	*DACH1*	2.7	2.58	2.58
1555142_at	*NHEDC1*	2.355	2.255	2.255
206313_at	*HLA-DOA*	2.33	2.23	2.23
1566869_at	*FRMD6*	2.29	2.19	2.19
1566846_at	*NA*	3.025	2.895	2.885
205186_at	*DNALI1*	2.33	2.23	2.23
229941_at	*LOC730112*	2.135	2.035	2.035

219095_at	*PLA2G4B*	2.29	2.19	2.19
209670_at	*TRAC*	4.6	4.4	4.4
1558144_at	*MEG3*	2.71	2.59	2.59
1557350_at	*G3BP1*	2.685	2.565	2.565
244079_at	*NA*	3.05	2.91	2.92
219803_at	*ANGPTL3*	2.595	2.475	2.475
221458_at	*HTR1F*	2.445	2.345	2.345
226645_at	*KLF2*	2.555	2.445	2.435
205015_s_at	*TGFA*	2.445	2.345	2.335
1558519_at	*FLJ23861*	2.81	2.69	2.69
205536_at	*VAV2*	2.535	2.415	2.425
233648_at	*SNF1LK2*	2.7	2.58	2.58
231004_s_at	*H1FX*	3.72	3.56	3.56
1566403_at	*SNORA68*	2.42	2.32	2.32
1561369_at	*NA*	2.71	2.59	2.59
207868_at	*CHRNA2*	5.58	5.35	5.33
1554305_at	*MGC20647*	2.455	2.355	2.355
243943_x_at	*C6orf52*	2.595	2.485	2.475
216329_at	*NA*	2.495	2.395	2.395
1562365_at	*LOC286177*	3.22	3.09	3.07
214183_s_at	*TKTL1*	2.33	2.23	2.23
244113_at	*NA*	2.26	2.16	2.16
227683_x_at	*NUDT4*	2.23	2.13	2.13
243583_at	*TCF7L2*	2.19	2.09	2.09
222066_at	*EPB41L1*	2.955	2.825	2.835
211775_x_at	*MGC13053*	2.925	2.805	2.795
233958_at	*NA*	2.565	2.445	2.455
1563407_x_at	*ATP4B*	2.24	2.14	2.14
206459_s_at	*WNT2B*	2.49	2.39	2.39
236972_at	*TRIM63*	2.63	2.52	2.51
219277_s_at	*OGDHL*	2.165	2.065	2.065

243678_at	*NA*	2.585	2.475	2.465
216388_s_at	*LTB4R*	2.6	2.48	2.48
1555853_at	*PSMB9*	2.42	2.32	2.32
234327_at	*NA*	2.165	2.065	2.065
1569454_a_at	*TMEM132D*	2.965	2.845	2.835
214481_at	*HIST1H2AM*	2.97	2.85	2.84
206402_s_at	*NPFF*	2.69	2.58	2.57
213855_s_at	*LIPE*	2.505	2.405	2.405
231071_at	*NA*	2.3	2.2	2.2
232395_x_at	*AGBL3*	2.945	2.825	2.825
212566_at	*MAP4*	11.765	11.245	11.275
225835_at	*SLC12A2*	9.245	8.845	8.845
244562_s_at	*NA*	2.42	2.32	2.32
236519_at	*C9orf135*	2.475	2.375	2.375
241495_at	*CCNL1*	2.935	2.815	2.815
215082_at	*ELOVL5*	2.71	2.59	2.59
1558154_at	*LLGL2*	2.9	2.78	2.78
234375_x_at	*NA*	3.2	3.07	3.06
203618_at	*FAIM2*	2.37	2.27	2.27
215742_at	*FBXW4*	2.515	2.415	2.415
238484_s_at	*NA*	2.8	2.68	2.68
216965_x_at	*SPG20*	2.605	2.495	2.485
216809_at	*CYLC1*	2.47	2.37	2.37
201916_s_at	*SEC63*	11.495	11.025	10.995
240164_at	*MUC4*	2.46	2.36	2.36
203396_at	*PSMA4*	13.12	12.56	12.56
224689_at	*MANBAL*	8.165	7.815	7.825
218487_at	*ALAD*	7.15	6.86	6.84
233485_at	*DDAH1*	2.535	2.435	2.425
234017_at	*LOC91948*	2.605	2.495	2.485
1567079_at	*CLN6*	2.975	2.855	2.855

212562_s_at	*CTSZ*	2.715	2.595	2.595
1569323_at	*PTPRG*	2.83	2.71	2.71
205939_at	*CYP3A7*	2.41	2.31	2.31
1561192_at	*C14orf143*	2.705	2.595	2.585
233327_at	*C6orf157*	2.555	2.445	2.455
216644_at	*NA*	2.86	2.74	2.74
1566984_at	*LOC728850*	2.74	2.62	2.63
1562290_at	*PPP2R2C*	3.095	2.965	2.955
217404_s_at	*COL2A1*	2.455	2.355	2.355
208041_at	*GRK1*	2.525	2.425	2.425
1555798_at	*DKFZp761D1918*	3.125	2.995	2.985
234541_s_at	*ARHGEF12*	2.33	2.23	2.23
1557754_at	*LOC401068*	2.615	2.505	2.495
229073_at	*LOC145786*	2.995	2.865	2.875
223526_at	*C18orf21*	7.345	7.045	7.035
1569783_at	*LOC401387*	2.985	2.865	2.865
214304_x_at	*DMN*	2.81	2.69	2.69
242227_at	*TCERG1*	2.36	2.26	2.26
1556877_at	*CTNNA3*	2.87	2.75	2.75
205971_s_at	*CTRB1*	2.97	2.85	2.85
238579_at	*C9orf85*	2.555	2.445	2.455
1560457_x_at	*LRG1*	2.92	2.8	2.8
221185_s_at	*IQCG*	2.34	2.24	2.24
1556247_a_at	*LRRC62*	2.515	2.405	2.415
220488_s_at	*BCAS3*	2.56	2.45	2.46
211468_s_at	*RECQL5*	2.495	2.395	2.395
207468_s_at	*SFRP5*	3.135	3.005	2.995
240921_at	*NA*	2.81	2.69	2.69
221945_at	*FBXO41*	3.075	2.955	2.955
243285_at	*EIF4B*	2.23	2.13	2.13
1558406_a_at	*EXPH5*	3	2.88	2.87

220549_at	*RAD54B*	2.785	2.665	2.665
1552969_a_at	*ZMYM6*	2.975	2.855	2.855
231065_at	*PDE6D*	2.755	2.635	2.635
1557907_x_at	*MUC12*	2.615	2.505	2.515
205203_at	*PLD1*	2.87	2.75	2.75
219535_at	*HUNK*	2.655	2.545	2.535
1565881_at	*GRLF1*	2.995	2.875	2.865
205147_x_at	*NCF4*	2.54	2.44	2.44
213091_at	*CRTC1*	2.565	2.455	2.465
239006_at	*SLC26A7*	3.105	2.985	2.975
244814_at	*UGCGL1*	2.9	2.78	2.78
218171_at	*VPS4B*	12.195	11.685	11.695
229818_at	*SVOP*	2.45	2.35	2.35
239701_at	*ENTPD1*	2.46	2.36	2.36
217303_s_at	*ADRB3*	2.5	2.4	2.4
232945_at	*FLJ32312*	3.17	3.03	3.04
210341_at	*MYT1*	3.195	3.055	3.065
216144_at	*ATXN7L1*	2.83	2.72	2.71
221769_at	*SPSB3*	2.95	2.82	2.83
1570276_a_at	*GATA4*	2.43	2.33	2.33
224753_at	*CDCA5*	2.83	2.71	2.71
244852_at	*DSEL*	2.93	2.81	2.81
1562923_at	*NA*	2.53	2.43	2.43
216469_at	*NA*	2.82	2.7	2.7
221313_at	*GPR52*	3.76	3.6	3.6
231437_at	*SLC35D2*	2.95	2.83	2.83
235607_at	*HNRPD*	2.82	2.7	2.7
231709_x_at	*MYO16*	2.865	2.755	2.745
222264_at	*BSCL2*	5.105	4.895	4.885
242766_at	*LOC391269*	2.51	2.41	2.41
213317_at	*CLIC5*	2.34	2.24	2.24

239681_at	*C17orf56*	2.92	2.8	2.8
201180_s_at	*GNAI3*	12.99	12.44	12.46
224029_x_at	*SCN11A*	3	2.88	2.88
215664_s_at	*EPHA5*	2.545	2.445	2.435
1566760_at	*FLJ34208*	2.5	2.4	2.4
215162_at	*GARNL1*	3.07	2.95	2.95
233989_at	*NA*	2.33	2.23	2.23
233509_at	*HERC4*	2.39	2.29	2.29
1557856_at	*DAD1*	2.48	2.38	2.38
1566551_at	*PDZRN3*	2.585	2.485	2.485
231356_at	*MBP*	3.095	2.975	2.965
228118_x_at	*MGC13114*	3.42	3.28	3.28
202183_s_at	*KIF22*	2.765	2.645	2.655
1559413_at	*TCP11L2*	3.11	2.99	2.99
239769_at	*CDH11*	2.4	2.3	2.3
1567682_x_at	*SNORA74A*	2.685	2.575	2.565
207077_at	*ELA2B*	2.52	2.42	2.42
1560201_at	*ZNF713*	2.91	2.79	2.79
241380_at	*FLJ41603*	2.96	2.84	2.84
1556110_at	*NA*	2.28	2.18	2.18
220402_at	*P53AIP1*	2.73	2.61	2.61
214294_at	*NFIA*	3.125	3.005	2.995
239966_at	*MEF2C*	2.845	2.725	2.725
240828_at	*JARID2*	2.325	2.225	2.225
215413_at	*EXOC7*	2.67	2.57	2.56
201371_s_at	*CUL3*	12.1	11.63	11.58
233751_at	*ATBF1*	2.44	2.34	2.34
240927_at	*NA*	2.715	2.595	2.605
213283_s_at	*SALL2*	3.5	3.36	3.36
244568_at	*SYNE2*	2.715	2.605	2.595
1569188_s_at	*RPL10*	2.855	2.745	2.735

206812_at	*ADRB3*	2.39	2.29	2.29
1562082_at	*NA*	2.795	2.675	2.675
231664_at	*SLC25A29*	2.81	2.7	2.69
210314_x_at	*TNFSF13*	2.355	2.255	2.255
1563162_at	*NA*	2.295	2.195	2.195
209181_s_at	*RABGGTB*	11.98	11.47	11.53
244592_at	*FLI1*	2.705	2.595	2.605
224683_at	*FBXO18*	8.585	8.245	8.235
212668_at	*SMURF1*	2.51	2.41	2.41
220854_at	*NA*	3.325	3.185	3.185
220965_s_at	*RSHL1*	2.55	2.45	2.45
217603_at	*ATP6V0A2*	2.51	2.41	2.41
241319_at	*EXOC6*	2.605	2.505	2.495
1553674_at	*LRRC44*	3.08	2.96	2.96
1555572_at	*CA6*	2.375	2.275	2.275
228214_at	*NA*	2.845	2.735	2.725
226286_at	*RBED1*	2.6	2.5	2.5
1556078_at	*LOC143286*	2.595	2.485	2.495
235621_at	*LOC653186*	3.665	3.525	3.525
1566963_at	*NA*	2.42	2.32	2.32
227983_at	*MGC7036*	7.97	7.64	7.66
1557631_at	*SLC25A4*	2.84	2.73	2.72
214324_at	*GP2*	2.635	2.535	2.535
1557630_s_at	*NA*	3.365	3.225	3.225
1568789_at	*C6orf107*	2.37	2.27	2.27
215259_s_at	*CADM4*	2.41	2.31	2.31
1569677_a_at	*C8orf45*	2.59	2.49	2.49
213811_x_at	*TCF3*	10.575	10.135	10.165
242623_x_at	*RP11-506K6.3*	2.895	2.775	2.775
237197_at	*LEMD1*	2.45	2.35	2.35
225823_at	*P117*	6.745	6.485	6.475

215968_at	*FAM55C*	3	2.88	2.88
229681_at	*NA*	2.62	2.52	2.52
219845_at	*BARX1*	2.41	2.31	2.31
214897_at	*KIAA0506*	2.625	2.525	2.525
205202_at	*PCMT1*	12.835	12.305	12.335
237787_at	*NA*	2.565	2.465	2.465
1554234_at	*KATNAL2*	2.53	2.43	2.43
211920_at	*CFB*	3.53	3.39	3.39
204992_s_at	*PFN2*	11.99	11.53	11.49
1558050_at	*EIF2B5*	3.12	3	3
1562775_at	*NUDT12*	2.885	2.765	2.765
1562973_at	*NA*	2.9	2.78	2.78
201524_x_at	*UBE2N*	10.465	10.055	10.045
234011_at	*MGC16384*	2.62	2.52	2.52
224520_s_at	*BEST3*	2.67	2.57	2.57
205292_s_at	*HNRPA2B1*	13.965	13.415	13.405
242802_x_at	*DTNA*	3.07	2.95	2.95
1561728_a_at	*LOC400238*	2.85	2.73	2.73
214853_s_at	*SHC1*	11.62	11.15	11.17
241402_at	*TSEN54*	3.435	3.295	3.295
236617_at	*WWOX*	2.37	2.27	2.27
205312_at	*SPI1*	2.68	2.58	2.58
219536_s_at	*ZFP64*	3.835	3.685	3.675
212376_s_at	*EP400*	6.435	6.185	6.175
1570213_at	*NA*	2.645	2.545	2.545
214705_at	*INADL*	3.06	2.94	2.94
241220_at	*KIAA1641*	2.91	2.8	2.79
208123_at	*KCNB2*	2.685	2.585	2.575
1557890_at	*LOC729178*	3.28	3.15	3.16
1552344_s_at	*CNOT7*	4.2	4.04	4.04
222258_s_at	*SH3BP4*	11.205	10.745	10.795

226655_at	*NA*	2.49	2.39	2.39
222456_s_at	*LIMA1*	2.775	2.675	2.665
215597_x_at	*MYST4*	2.96	2.85	2.84
218921_at	*SIGIRR*	2.615	2.515	2.515
239244_at	*NA*	2.755	2.655	2.655
1557593_at	*SPAG17*	2.945	2.825	2.835
1552825_at	*ZNF396*	2.72	2.62	2.62
1560915_at	*DPY19L1*	2.67	2.57	2.57
236510_at	*TRIM26*	2.5	2.4	2.4
1561612_at	*NA*	2.6	2.5	2.5
244256_at	*CACNA1E*	2.995	2.875	2.875
238378_at	*NA*	2.825	2.725	2.715
237947_at	*GTF2IRD1*	2.42	2.32	2.32
224158_s_at	*DKFZP779L1068*	2.925	2.805	2.805
203290_at	*HLA-DQA1*	2.475	2.375	2.375
239625_at	*NA*	2.75	2.65	2.65
243617_at	*LOC152485*	3.795	3.645	3.655
215877_at	*C14orf56*	2.545	2.445	2.445
210242_x_at	*MTHFS*	8.045	7.735	7.725
1569536_at	*C14orf58*	3.305	3.185	3.185
215763_at	*NA*	2.74	2.64	2.64
239150_at	*FLJ44379*	2.695	2.595	2.595
244231_at	*NA*	2.66	2.56	2.56
1552626_a_at	*TMEM163*	3.08	2.97	2.96
220455_at	*SLC16A8*	3.785	3.635	3.645
207542_s_at	*AQP1*	2.785	2.675	2.685
222336_at	*C4orf34*	3.12	3	3
243436_at	*NA*	2.79	2.69	2.69
232390_at	*NCAM2*	2.795	2.685	2.695
233121_at	*ZHX2*	2.895	2.785	2.775
226979_at	*MAP3K2*	11.715	11.295	11.245

242486_at	*CSNK1G1*	2.45	2.35	2.35
215428_at	*TJP1*	2.815	2.715	2.715
49077_at	*PPME1*	6.76	6.5	6.5
222023_at	*AKAP13*	3.19	3.07	3.07
211948_x_at	*BAT2D1*	6.005	5.775	5.785
228525_at	*NA*	3.31	3.19	3.19
1564029_at	*USP49*	2.57	2.47	2.47
236292_at	*RNF130*	4.325	4.155	4.175
238882_at	*LOC387647*	3.21	3.09	3.09
241390_at	*UGT2B7*	2.915	2.815	2.805
1556954_at	*LOC283854*	3.065	2.945	2.945
1562722_at	*FLJ40296*	3	2.88	2.89
233939_at	*REXO1*	3.965	3.825	3.815
233396_s_at	*CSRP2BP*	3.3	3.18	3.17
1568749_at	*NA*	2.695	2.595	2.595
210457_x_at	*HMGA1*	2.945	2.835	2.825
240360_at	*BRD4*	3.045	2.925	2.935
201073_s_at	*SMARCC1*	2.51	2.41	2.41
228823_at	*RASA4*	5.31	5.11	5.11
226816_s_at	*KIAA1143*	11.36	10.94	10.94
217266_at	*tcag7.350*	5.71	5.5	5.48
231307_at	*PAGE5*	2.78	2.68	2.68
208383_s_at	*PCK1*	3.23	3.11	3.11
215532_x_at	*ZNF492*	2.915	2.815	2.805
203032_s_at	*FH*	2.78	2.68	2.68
1560717_at	*NA*	2.915	2.815	2.815
220338_at	*RALGPS2*	3	2.89	2.88
211457_at	*GABARAPL3*	3.045	2.925	2.925
230809_at	*PCDHB14*	2.765	2.665	2.665
221888_at	*CC2D1A*	2.79	2.69	2.69
229386_at	*ID4*	2.65	2.55	2.55

204940_at	*PLN*	3.045	2.935	2.925
210558_at	*AKR1C4*	2.895	2.795	2.785
219215_s_at	*SLC39A4*	3.045	2.925	2.925
205940_at	*MYH3*	2.67	2.57	2.57
214351_x_at	*RPL13*	11.095	10.685	10.695
1553974_at	*LOC128977*	3.155	3.045	3.035
1562817_at	*NA*	3.075	2.965	2.955
243795_s_at	*LOC440900*	2.97	2.87	2.86
1562373_at	*ITPR1*	2.56	2.46	2.46
224431_s_at	*SUV420H2*	4.89	4.71	4.71
218623_at	*HMP19*	2.68	2.58	2.58
221869_at	*GM632*	3.955	3.815	3.815
240448_at	*KIAA0802*	2.885	2.785	2.785
1563690_at	*PPP4R1*	3.075	2.965	2.955
221078_s_at	*KIAA1212*	4.51	4.35	4.34
240072_at	*ASXL2*	2.655	2.555	2.555
224561_s_at	*MORF4L1*	12.6	12.16	12.13
207047_s_at	*CLCNKA*	2.74	2.64	2.64
1560347_at	*NA*	2.6	2.5	2.5
234570_at	*ZNF71*	3.28	3.16	3.16
222399_s_at	*TM9SF3*	11.215	10.795	10.825
236900_x_at	*LOC126661*	8.49	8.18	8.2
226200_at	*VARS2*	7.305	7.035	7.045
1557316_at	*STK24*	2.875	2.775	2.775
244181_at	*PIK3R1*	2.77	2.67	2.67
1569938_at	*SIRT5*	3.07	2.96	2.95
222323_at	*NA*	2.655	2.555	2.555
219617_at	*C2orf34*	4.86	4.67	4.69
213331_s_at	*NEK1*	9.91	9.56	9.54
207669_at	*KRT83*	2.585	2.485	2.485
1562142_at	*SKIV2L2*	3.15	3.03	3.03

244594_x_at	*KIAA0174*	3.065	2.955	2.945
1565549_at	*NA*	2.885	2.785	2.785
241308_at	*LOC729589*	2.84	2.74	2.74
237151_s_at	*MGC33657*	3.52	3.4	3.4
214567_s_at	*XCL2*	2.765	2.665	2.665
239805_at	*SLC13A2*	3.025	2.925	2.915
213339_at	*KIAA0495*	3.055	2.945	2.955
239920_at	*LOC728651*	3.705	3.575	3.565
1553765_a_at	*KLHL32*	2.985	2.885	2.885
231536_at	*TIAM1*	3.025	2.925	2.915
235604_x_at	*ZNF493*	3.14	3.02	3.03
234462_at	*NA*	2.83	2.73	2.73
207006_s_at	*CCDC106*	3.18	3.06	3.06
227253_at	*CP*	3.25	3.13	3.13
235145_at	*ZBTB7B*	4.455	4.295	4.295
221870_at	*EHD2*	9.61	9.27	9.27
1554704_at	*ATP8B3*	2.83	2.73	2.73
207128_s_at	*ZNF223*	4.435	4.275	4.275
240060_at	*SLC26A1*	3.39	3.27	3.27
209269_s_at	*SYK*	2.78	2.68	2.68
220345_at	*LRRTM4*	2.84	2.74	2.74
233307_x_at	*MGST3*	4.885	4.705	4.705
213981_at	*COMT*	6.665	6.435	6.425
1562823_at	*ROR1*	3.015	2.915	2.915
220328_at	*PHC3*	2.905	2.805	2.805
220976_s_at	*KRTAP1-1*	3.075	2.975	2.965
244096_at	*NA*	3.225	3.115	3.105
243863_at	*ZCWPW2*	2.9	2.8	2.8
1560964_at	*NA*	2.8	2.7	2.7
1566924_at	*NA*	2.82	2.72	2.72
213257_at	*SARM1*	5	4.82	4.82

237930_at	*LOC441204*	3.035	2.935	2.935
1559354_a_at	*FLJ25476*	2.705	2.605	2.605
214299_at	*TOP3A*	6.185	5.965	5.965
243760_at	*LOC650794*	5.625	5.435	5.415
215046_at	*FLJ23861*	4.895	4.735	4.725
219174_at	*IFT74*	8.455	8.155	8.185
211487_x_at	*RPS17*	13.99	13.51	13.51
1553978_at	*MEF2B*	5.37	5.2	5.18
216719_s_at	*RAB11FIP4*	3.02	2.92	2.92
239380_at	*C5orf27*	3.02	2.92	2.92
1568691_at	*NA*	3.71	3.58	3.59
243162_at	*PB1*	3.285	3.165	3.165
237104_at	*CTSS*	3.125	3.025	3.025
242791_at	*FBXO3*	3.235	3.125	3.135
215948_x_at	*ZMYM5*	6.065	5.865	5.855
240702_at	*HERC1*	2.885	2.785	2.785
240103_at	*NA*	2.85	2.75	2.75
209767_s_at	*5-Sep*	3.295	3.175	3.175
242654_at	*FANCC*	2.76	2.66	2.66
1569499_at	*TFDP2*	2.99	2.89	2.89
232983_s_at	*SERGEF*	3.1	3	3
208860_s_at	*ATRX*	9.105	8.795	8.815
239306_at	*C14orf93*	2.89	2.79	2.79
234040_at	*HELLS*	2.88	2.78	2.78
1558561_at	*HM13*	2.95	2.85	2.85
215321_at	*RPIB9*	3.115	3.015	3.015
219981_x_at	*ZNF587*	9.04	8.74	8.75
237756_at	*KLHL23*	2.965	2.865	2.865
241860_at	*STK17B*	2.82	2.72	2.72
236060_at	*NA*	3.25	3.15	3.14
239667_at	*SLC3A1*	3.12	3.02	3.02

204582_s_at	*KLK3*	2.92	2.82	2.82
244244_at	*CD300LG*	2.975	2.875	2.875
215565_at	*DTNB*	2.94	2.84	2.84
218830_at	*RPL26L1*	10.615	10.255	10.295
242825_at	*PAP2D*	3.05	2.95	2.95
1566515_at	*CWF19L2*	3.125	3.025	3.025
1569468_at	*MGC26356*	3.01	2.91	2.91
207131_x_at	*GGT1*	4.155	4.015	4.015
239585_at	*NA*	3	2.9	2.9
209704_at	*NA*	6.3	6.11	6.09
1559940_s_at	*FLJ16124*	3.17	3.07	3.07
240579_at	*NAG*	3.055	2.955	2.955
205510_s_at	*FLJ10038*	6.265	6.065	6.065
202682_s_at	*USP4*	8.88	8.59	8.61
1565743_at	*PFAAP5*	3.09	2.99	2.99
208540_x_at	*S100A11*	5.895	5.725	5.705
227713_at	*KATNAL1*	9.46	9.17	9.15
208584_at	*SNCG*	3.455	3.355	3.345
208857_s_at	*PCMT1*	11.33	10.98	10.97
1569422_at	*FAM129C*	3.345	3.245	3.245
1559061_at	*LOC253962*	4.075	3.955	3.945
243414_at	*PPIL2*	5.06	4.9	4.9
240918_at	*NA*	3.075	2.975	2.975
231794_at	*CTLA4*	3.1	3	3
211675_s_at	*MDFIC*	12.24	11.88	11.84
1558176_at	*LOC96610*	3.52	3.41	3.42
221098_x_at	*UTP14A*	3.535	3.435	3.425
217664_at	*JMJD2B*	3.05	2.95	2.95
200611_s_at	*WDR1*	9.75	9.44	9.46
206015_s_at	*FOXJ3*	10.54	10.23	10.21
200949_x_at	*RPS20*	10.96	10.61	10.63

243219_x_at	*NA*	3.195	3.095	3.095
222200_s_at	*BSDC1*	6.69	6.49	6.49
220564_at	*C10orf59*	3.47	3.37	3.37
200855_at	*TTC19*	3.38	3.28	3.28
225052_at	*MGC14327*	8.165	7.925	7.925
236737_at	*C17orf56*	3.65	3.54	3.55
201176_s_at	*ARCN1*	11.555	11.195	11.235
241507_x_at	*NA*	3.33	3.23	3.23
214338_at	*DNAJB12*	5.775	5.615	5.605
225549_at	*NA*	10.505	10.215	10.195
241054_at	*NA*	3.39	3.29	3.29
201960_s_at	*MYCBP2*	12.025	11.675	11.695
1562849_at	*SPECC1*	3.975	3.855	3.855
208286_x_at	*POU5F1*	5.795	5.645	5.625
209253_at	*SORBS3*	7.27	7.07	7.06
1559960_x_at	*NA*	4.055	3.935	3.945
218117_at	*RBX1*	8.46	8.22	8.22
217866_at	*FLJ12529*	7.04	6.85	6.84
201569_s_at	*SAMM50*	8.965	8.715	8.725
228401_at	*ATAD2*	7.2	7.01	6.99
224747_at	*UBE2Q2*	11.49	11.17	11.17
204765_at	*ARHGEF5*	6.265	6.085	6.095
235750_at	*C17orf65*	4.185	4.065	4.075
226669_at	*USP42*	8.825	8.595	8.605
212449_s_at	*LYPLA1*	10.88	10.59	10.61
213916_at	*ZNF20*	5.65	5.51	5.51
239706_x_at	*PSG1*	4.365	4.265	4.255
222042_x_at	*RKHD1*	4.375	4.275	4.265
225324_at	*CRLS1*	10	9.76	9.76
218364_at	*LRRFIP2*	9.79	9.56	9.55
222726_s_at	*EXOC5*	7.085	6.925	6.925

202184_s_at	*NUP133*	9.41	9.2	9.18
200011_s_at	*ARF3*	8.58	8.37	8.39
205762_s_at	*DUS4L*	4.205	4.105	4.105
235587_at	*LOC202781*	5.42	5.3	5.3
213508_at	*C14orf147*	7.77	7.59	7.59
201816_s_at	*GBAS*	8.265	8.075	8.095
224439_x_at	*RNF7*	9.265	9.065	9.065
233868_x_at	*ADAM33*	8.58	8.4	8.4
1563745_a_at	*LOC283050*	5.315	5.205	5.195
201244_s_at	*RAF1*	8.83	8.64	8.65
227308_x_at	*LTBP3*	5.07	4.97	4.97
223544_at	*TMEM79*	4.97	4.87	4.87
219074_at	*TMEM34*	9.11	8.94	8.92
238719_at	*NA*	8.185	8.045	8.035
219097_x_at	*C19orf42*	11.36	11.16	11.16
214532_x_at	*POU5F1P1*	6.315	6.195	6.205
223155_at	*HDHD2*	9.915	9.755	9.745
222733_x_at	*D21S2056E*	5.735	5.635	5.635
222848_at	*CENPK*	7.705	7.575	7.585
226354_at	*LACTB*	9.955	9.795	9.795
201966_at	*NDUFS2*	9.765	9.605	9.605
224726_at	*MIB1*	9.58	9.43	9.42
224830_at	*NUDT21*	8.975	8.855	8.855
200733_s_at	*PTP4A1*	11.255	11.115	11.115
222548_s_at	*MAP4K4*	11.225	11.125	11.125
222231_s_at	*LRRC59*	10.715	10.835	10.835
201552_at	*LAMP1*	12.49	12.64	12.65
226210_s_at	*MEG3*	11.685	11.845	11.835
227847_at	*EPM2AIP1*	8.665	8.785	8.795
227027_at	*NA*	9.4	9.53	9.55
200816_s_at	*PAFAH1B1*	11.44	11.61	11.62

222992_s_at	*NDUFB9*	8.54	8.68	8.67
203834_s_at	*TGOLN2*	5.65	5.75	5.75
235078_at	*NBEAL1*	9.05	9.22	9.24
207358_x_at	*MACF1*	9.915	10.105	10.125
223361_at	*C6orf115*	8.975	9.165	9.155
225210_s_at	*RPS6KA2*	9.115	9.315	9.305
203405_at	*DSCR2*	9.045	9.235	9.245
213838_at	*NOL7*	8.605	8.785	8.795
235413_at	*GGCX*	7.525	7.685	7.695
214305_s_at	*SF3B1*	9.475	9.685	9.705
209849_s_at	*RAD51C*	6.34	6.48	6.48
208841_s_at	*G3BP2*	11.4	11.66	11.66
213311_s_at	*TCF25*	7.79	7.97	7.97
53912_at	*SNX11*	6.085	6.225	6.225
212158_at	*SDC2*	12.235	12.545	12.525
239406_at	*ZNF193*	4.155	4.255	4.255
210524_x_at	*NA*	4.11	4.21	4.21
202664_at	*WIPF1*	10.835	11.115	11.115
221922_at	*GPSM2*	7.87	8.08	8.06
233268_s_at	*SELENBP1*	5.34	5.48	5.48
211933_s_at	*HNRPA3*	11.64	11.95	11.93
204656_at	*SHB*	5.395	5.535	5.545
219361_s_at	*ISG20L1*	7.815	8.015	8.025
226534_at	*KITLG*	11.54	11.83	11.86
225554_s_at	*ANAPC7*	7.43	7.64	7.62
217913_at	*VPS4A*	8.195	8.415	8.425
221743_at	*CUGBP1*	11.935	12.265	12.255
203244_at	*PEX5*	7.635	7.865	7.845
208726_s_at	*EIF2S2*	11.835	12.175	12.145
227331_at	*ITGB7*	3.985	4.095	4.105
204125_at	*NDUFAF1*	8.98	9.24	9.23

228348_at	*LINS1*	8.075	8.315	8.285
212297_at	*ATP13A3*	12.78	13.16	13.12
203644_s_at	*MON1B*	4.17	4.29	4.29
224184_s_at	*BOC*	6.31	6.49	6.5
222127_s_at	*EXOC1*	10.33	10.64	10.62
1558738_at	*NOL3*	4.435	4.565	4.575
201480_s_at	*SUPT5H*	5.2	5.36	5.37
224841_x_at	*CENPL*	9.245	9.545	9.545
236993_at	*NA*	2.925	3.025	3.025
219039_at	*SEMA4C*	6.375	6.585	6.575
213221_s_at	*SNF1LK2*	7.615	7.845	7.865
204246_s_at	*DCTN3*	8.745	9.045	9.045
238879_at	*NA*	7.355	7.615	7.585
236629_at	*C1orf69*	3.375	3.495	3.495
218524_at	*E4F1*	5.505	5.695	5.685
202845_s_at	*RALBP1*	8.075	8.355	8.355
46256_at	*SPSB3*	5.495	5.675	5.685
223072_s_at	*WBP1*	5.955	6.165	6.145
218178_s_at	*CHMP1B*	6.065	6.275	6.285
231045_x_at	*CTNND1*	7.655	7.925	7.915
230524_at	*MPI*	3.805	3.945	3.935
202605_at	*GUSB*	8.5	8.79	8.81
205294_at	*BAIAP2*	5.24	5.43	5.41
214789_x_at	*SFRS2B*	10.11	10.45	10.49
235923_at	*VTI1A*	3.525	3.645	3.645
212551_at	*CAP2*	7.015	7.265	7.285
204218_at	*C11orf51*	4.83	5.01	5
227541_at	*WDR20*	6.865	7.125	7.115
202565_s_at	*SVIL*	10.98	11.38	11.38
201479_at	*DKC1*	9.65	10.03	9.99
1558152_at	*TSPAN4*	8.455	8.785	8.755

218695_at	*EXOSC4*	4.975	5.165	5.145
240032_at	*NA*	3.2	3.32	3.32
223555_at	*GON4L*	4.28	4.44	4.44
203090_at	*SDF2*	6.75	7.02	7
233955_x_at	*CXXC5*	10.245	10.655	10.625
226276_at	*TMEM167*	9.16	9.51	9.52
225009_at	*CMTM4*	8.525	8.865	8.855
209064_x_at	*PAIP1*	8.435	8.755	8.755
218390_s_at	*C10orf84*	4.155	4.315	4.315
235232_at	*NA*	8.885	9.255	9.235
225455_at	*TADA1L*	4.8	5	4.99
202042_at	*HARS*	8.635	8.965	8.985
226697_at	*FAM114A1*	8.795	9.165	9.135
218267_at	*CINP*	5.29	5.51	5.51
220789_s_at	*TBRG4*	5.41	5.62	5.64
220042_x_at	*HIVEP3*	4.135	4.315	4.305
208855_s_at	*STK24*	12.775	13.295	13.325
212716_s_at	*EIF3S12*	10.03	10.47	10.43
225267_at	*KPNA4*	10.575	11.015	11.015
222471_s_at	*KCMF1*	8.075	8.395	8.435
208743_s_at	*YWHAB*	8.965	9.355	9.345
230905_at	*ZDHHC4*	3.13	3.27	3.26
202747_s_at	*ITM2A*	2.485	2.595	2.585
201322_at	*ATP5B*	10.185	10.665	10.615
200829_x_at	*ZNF207*	10.42	10.9	10.87
1554482_a_at	*SAR1B*	3.1	3.24	3.24
219108_x_at	*DDX27*	9.42	9.85	9.87
213242_x_at	*KIAA0284*	7.53	7.88	7.86
223396_at	*TMEM60*	9.27	9.71	9.68
236329_at	*FLJ33996*	2.315	2.415	2.425
209456_s_at	*FBXW11*	5.01	5.24	5.26

218070_s_at	*GMPPA*	6.185	6.475	6.455
202758_s_at	*RFXANK*	3.575	3.745	3.735
225334_at	*AS3MT*	9.625	10.105	10.065
233647_s_at	*CDADC1*	9.25	9.71	9.67
213391_at	*DPY19L4*	8.85	9.26	9.28
230230_at	*NA*	4.195	4.395	4.405
209462_at	*APLP1*	3.29	3.45	3.45
208614_s_at	*FLNB*	8.055	8.475	8.435
206042_x_at	*SNURF*	6.445	6.755	6.775
225127_at	*TMEM181*	10.825	11.375	11.345
231772_x_at	*CENPH*	2.86	3	3
209430_at	*BTAF1*	9.865	10.335	10.365
210025_s_at	*CARD10*	3.025	3.175	3.185
233088_at	*XYLT1*	2.285	2.405	2.405
231205_at	*DDEF1*	3.735	3.915	3.925
224698_at	*FAM62B*	9.7	10.18	10.19
227622_at	*PCF11*	7.16	7.52	7.52
202961_s_at	*ATP5J2*	9.1	9.58	9.54
226977_at	*LOC492311*	10.67	11.24	11.18
241348_at	*ZNF654*	7.79	8.17	8.21
212085_at	*SLC25A6*	9.785	10.315	10.265
209058_at	*EDF1*	10.285	10.805	10.845
223374_s_at	*B3GALNT1*	6.675	7.035	7.005
209717_at	*EVI5*	8.695	9.125	9.175
206958_s_at	*UPF3A*	7.905	8.305	8.335
229483_at	*UBE2H*	3.06	3.21	3.23
209317_at	*POLR1C*	7.95	8.39	8.35
210296_s_at	*PXMP3*	6.81	7.18	7.15
243309_at	*FLJ27352*	6.02	6.32	6.35
203944_x_at	*BTN2A1*	8.805	9.255	9.285
230167_at	*ADAMTS14*	4.95	5.2	5.22

209174_s_at	*QRICH1*	8.92	9.38	9.42
223258_s_at	*KIAA1333*	5.085	5.345	5.375
214820_at	*BRWD1*	5.3	5.58	5.58
226793_at	*TCP11L1*	6.64	7.01	6.98
223989_s_at	*REXO2*	7.88	8.28	8.32
217748_at	*ADIPOR1*	7.45	7.87	7.83
218160_at	*NDUFA8*	9.77	10.28	10.31
201046_s_at	*RAD23A*	7.9	8.34	8.3
209770_at	*BTN3A1*	6.28	6.6	6.64
204076_at	*ENTPD4*	10.35	10.91	10.94
224920_x_at	*MYADM*	6.925	7.305	7.305
235233_s_at	*NA*	8.13	8.59	8.59
229433_at	*RBM26*	4.765	5.035	5.015
227908_at	*TBC1D24*	8.385	8.875	8.825
202555_s_at	*MYLK*	10.04	10.58	10.62
208925_at	*CLDND1*	8.325	8.805	8.775
206592_s_at	*AP3D1*	9.98	10.57	10.51
219459_at	*POLR3B*	6.86	7.22	7.26
210564_x_at	*CFLAR*	5.235	5.515	5.545
213106_at	*ATP8A1*	2.82	2.98	2.98
209055_s_at	*CDC5L*	2.625	2.775	2.765
238075_at	*CHEK1*	7.63	8.05	8.09
213700_s_at	*PKM2*	5.955	6.295	6.295
208906_at	*BSCL2*	3.45	3.64	3.66
202401_s_at	*SRF*	7.175	7.575	7.615
212753_at	*PCGF3*	8.72	9.21	9.24
212205_at	*H2AFV*	9.42	9.97	9.95
1569973_at	*LOC441220*	3.245	3.435	3.445
204033_at	*TRIP13*	4.82	5.09	5.12
1557409_at	*SPG7*	3.505	3.715	3.705
228148_at	*ZNF584*	4.12	4.35	4.37

204173_at	*MYL6B*	7.19	7.59	7.63
227255_at	*PDIK1L*	5.575	5.915	5.905
1552301_a_at	*CORO6*	2.74	2.9	2.9
221782_at	*DNAJC10*	8.585	9.115	9.095
202721_s_at	*GFPT1*	6.27	6.66	6.64
213115_at	*ATG4A*	6.32	6.7	6.71
226406_at	*C18orf25*	8.96	9.52	9.49
212789_at	*NCAPD3*	4.95	5.25	5.25
219767_s_at	*CRYZL1*	7.285	7.755	7.705
222759_at	*SUV420H1*	5.995	6.365	6.355
200069_at	*SART3*	7.695	8.165	8.175
223187_s_at	*ORMDL1*	7.645	8.115	8.125
205677_s_at	*DLEU1*	7.32	7.77	7.79
228138_at	*ZSCAN25*	4.395	4.685	4.655
236192_at	*FNTA*	9.065	9.595	9.665
200769_s_at	*MAT2A*	2.325	2.475	2.465
218308_at	*TACC3*	4.14	4.39	4.41
209378_s_at	*KIAA1128*	6.405	6.805	6.815
201723_s_at	*GALNT1*	7.53	7.99	8.03
201460_at	*MAPKAPK2*	7.705	8.215	8.165
231019_x_at	*STK11*	6.015	6.385	6.415
227930_at	*EIF2C4*	6.79	7.22	7.24
201823_s_at	*RNF14*	7.86	8.38	8.34
226279_at	*PRSS23*	13.125	13.975	13.965
202196_s_at	*DKK3*	8.865	9.415	9.465
217794_at	*PRR13*	7.06	7.54	7.5
221069_s_at	*CCDC44*	6.26	6.67	6.65
65884_at	*MAN1B1*	6.465	6.865	6.905
204479_at	*OSTF1*	7.56	8.04	8.08
238165_at	*PDZRN3*	3.185	3.405	3.395
221881_s_at	*CLIC4*	6.26	6.66	6.69

54051_at	*PKNOX1*	7.32	7.83	7.78
208101_s_at	*URM1*	5.03	5.36	5.38
207791_s_at	*RAB1A*	9.475	10.075	10.145
201013_s_at	*PAICS*	8.65	9.22	9.24
209906_at	*C3AR1*	2.555	2.735	2.725
225558_at	*GIT2*	8.36	8.9	8.94
228503_at	*NA*	4.595	4.905	4.915
208972_s_at	*ATP5G1*	8.59	9.18	9.16
203403_s_at	*RNF6*	10.34	11.08	11
212747_at	*ANKS1A*	7.67	8.2	8.19
230047_at	*FLJ32810*	4.515	4.815	4.825
210559_s_at	*CDC2*	5.485	5.865	5.865
201527_at	*ATP6V1F*	8.42	9.01	8.99
36129_at	*RUTBC1*	8.15	8.73	8.69
201649_at	*UBE2L6*	5.77	6.17	6.16
225643_at	*C14orf32*	9.205	9.855	9.825
212908_at	*DNAJC16*	8.205	8.785	8.755
200978_at	*MDH1*	9.625	10.325	10.275
211096_at	*PBX2*	2.57	2.75	2.75
218286_s_at	*RNF7*	8.085	8.635	8.655
221024_s_at	*SLC2A10*	9.885	10.565	10.605
218156_s_at	*TSR1*	5.16	5.53	5.51
201732_s_at	*CLCN3*	7.665	8.235	8.185
225179_at	*NA*	8.71	9.35	9.31
219053_s_at	*VPS37C*	8.715	9.295	9.375
218119_at	*TIMM23*	5.59	5.99	5.99
226795_at	*LRCH1*	6.925	7.425	7.415
203773_x_at	*BLVRA*	8.555	9.155	9.185
209751_s_at	*SEDLP*	6.4	6.89	6.83
202777_at	*SHOC2*	9.44	10.11	10.13
224036_s_at	*LMBR1*	6.6	7.06	7.1

1554224_at	*NA*	2.81	3.02	3.01
209566_at	*INSIG2*	9.075	9.745	9.725
223020_at	*CLPTM1L*	7.9	8.46	8.5
221472_at	*SERINC3*	9.94	10.7	10.63
225452_at	*PPARBP*	7.53	8.12	8.06
244599_at	*ITGA4*	3.065	3.285	3.295
222976_s_at	*TPM3*	11.31	12.18	12.12
225881_at	*SLC35B4*	8.83	9.46	9.51
226883_at	*NA*	10.145	10.925	10.885
1553810_a_at	*KIAA1524*	3.44	3.69	3.71
223879_s_at	*OXR1*	2.785	2.985	2.995
213370_s_at	*SFMBT1*	4.675	5.025	5.035
206764_x_at	*MPPE1*	4.875	5.245	5.235
227639_at	*PIGK*	8.915	9.555	9.635
231576_at	*ETNK1*	9.345	10.005	10.085
211573_x_at	*TGM2*	2.34	2.52	2.52
200905_x_at	*HLA-E*	9.5	10.2	10.25
225264_at	*RARS2*	8.845	9.495	9.545
221695_s_at	*MAP3K2*	4.62	4.97	4.99
224951_at	*C12orf62*	8.795	9.485	9.455
211143_x_at	*NR4A1*	4.835	5.225	5.195
201226_at	*NDUFB8*	7.465	8.055	8.025
221875_x_at	*HLA-F*	7.605	8.215	8.185
202491_s_at	*IKBKAP*	8.56	9.22	9.22
226686_at	*ZCD2*	8.105	8.705	8.755
222700_at	*ARL6IP2*	7.115	7.645	7.695
203532_x_at	*CUL5*	5.255	5.635	5.685
218473_s_at	*GLT25D1*	7.87	8.46	8.51
225354_s_at	*SH3BGRL2*	2.995	3.235	3.235
242149_at	*NA*	2.985	3.215	3.225
239586_at	*FAM83A*	2.635	2.835	2.845

202281_at	*GAK*	6.255	6.765	6.735
232652_x_at	*SCAND1*	6.485	6.975	7.025
227996_at	*FARP1*	4.175	4.505	4.515
227213_at	*DEADC1*	2.97	3.2	3.21
222460_s_at	*NIP30*	8.175	8.825	8.835
229862_x_at	*ZBTB45*	5.135	5.545	5.555
239336_at	*THBS1*	9.025	9.755	9.735
222014_x_at	*MTO1*	8.645	9.345	9.335
235068_at	*ZDHHC21*	7.355	7.975	7.925
228275_at	*NA*	5.225	5.625	5.665
1556950_s_at	*SERPINB6*	3.565	3.855	3.845
212229_s_at	*FBXO21*	7.99	8.65	8.61
202774_s_at	*SFRS8*	6.775	7.335	7.325
202813_at	*TARBP1*	4.69	5.08	5.06
205618_at	*PRRG1*	8.695	9.405	9.385
229679_at	*FLJ40142*	5.7	6.15	6.17
238594_x_at	*NA*	3.48	3.75	3.78
224853_at	*SLAIN2*	3.515	3.805	3.795
202165_at	*PPP1R2*	8.905	9.615	9.675
233819_s_at	*ZNF294*	6.405	6.955	6.905
215227_x_at	*ACP1*	9.16	9.96	9.88
228571_at	*RBAK*	8.87	9.57	9.65
208631_s_at	*HADHA*	7	7.55	7.61
225110_at	*OGFOD1*	9.31	10.14	10.04
207431_s_at	*DEGS1*	8.03	8.67	8.74
201514_s_at	*G3BP1*	7.065	7.645	7.675
223391_at	*SGPP1*	9.115	9.905	9.855
214007_s_at	*TWF1*	5.785	6.295	6.235
238729_x_at	*SAV1*	3.32	3.6	3.6
203478_at	*NDUFC1*	8.91	9.63	9.7
214277_at	*COX11*	4.305	4.665	4.665

226224_at	*FOXK2*	6.435	6.985	6.965
204367_at	*SP2*	5.43	5.89	5.89
219157_at	*KLHL2*	9.64	10.5	10.42
212476_at	*CENTB2*	10.13	11.04	10.94
202584_at	*NFX1*	4.365	4.715	4.765
214794_at	*PA2G4*	2.725	2.945	2.975
1560648_s_at	*TSPYL1*	7.57	8.19	8.24
210104_at	*MED6*	5.035	5.455	5.465
40837_at	*TLE2*	5.42	5.89	5.88
216903_s_at	*CBARA1*	5.745	6.215	6.265
235432_at	*NPHP3*	8.98	9.77	9.75
223516_s_at	*C6orf49*	6.78	7.39	7.33
201674_s_at	*AKAP1*	2.865	3.115	3.105
208828_at	*POLE3*	6.27	6.82	6.8
212534_at	*NA*	8.04	8.72	8.76
226399_at	*NA*	8.035	8.725	8.745
218103_at	*FTSJ3*	7.52	8.21	8.15
208579_x_at	*H2BFS*	3.44	3.75	3.73
227304_at	*NA*	5.035	5.455	5.495
224298_s_at	*PHGDHL1*	6.36	6.92	6.92
217857_s_at	*RBM8A*	4.435	4.825	4.845
219169_s_at	*TFB1M*	6.79	7.41	7.37
209352_s_at	*SIN3B*	4.05	4.41	4.41
200045_at	*ABCF1*	7.65	8.33	8.33
229497_at	*ANKDD1A*	6.815	7.415	7.445
242719_at	*NA*	2.69	2.93	2.93
232432_s_at	*SLC30A5*	8.795	9.615	9.565
223255_at	*KIAA1333*	7.52	8.16	8.23
218904_s_at	*C9orf40*	5.435	5.905	5.955
232525_at	*SND1*	2.24	2.44	2.45
208688_x_at	*EIF3S9*	8.065	8.825	8.755

221229_s_at	*FLJ20628*	6.945	7.615	7.545
202405_at	*TIAL1*	7.585	8.295	8.245
202261_at	*VPS72*	7.67	8.41	8.33
218349_s_at	*ZWILCH*	6.355	6.915	6.955
217508_s_at	*C18orf25*	2.97	3.26	3.23
201635_s_at	*FXR1*	7.58	8.3	8.26
223273_at	*C14orf142*	5.2	5.69	5.67
208954_s_at	*LARP5*	7.885	8.645	8.575
209391_at	*DPM2*	3.545	3.875	3.865
227742_at	*CLIC6*	2.81	3.07	3.07
227617_at	*RP13-15M17.2*	6.04	6.59	6.62
223334_at	*TMEM126A*	9.505	10.445	10.365
229638_at	*IRX3*	10.795	11.845	11.785
211433_x_at	*KIAA1539*	5.775	6.325	6.305
222449_at	*TMEPAI*	10.925	12.025	11.895
210415_s_at	*ODF2*	3.35	3.67	3.67
212146_at	*PLEKHM2*	5.515	6.025	6.045
225953_at	*P15RS*	10.185	11.205	11.125
225106_s_at	*OGFOD1*	6.995	7.685	7.635
204083_s_at	*TPM2*	10.665	11.725	11.655
225749_at	*LOC283951*	5.335	5.835	5.875
225553_at	*NA*	10.415	11.425	11.405
219644_at	*CCDC41*	5.395	5.905	5.925
213453_x_at	*GAPDH*	11.09	12.19	12.14
203172_at	*FXR2*	4.655	5.115	5.105
204382_at	*NAT9*	6.14	6.76	6.72
214152_at	*CCPG1*	9.08	9.93	9.99
222986_s_at	*SCOTIN*	8.445	9.325	9.235
225610_at	*UHRF2*	9.94	10.87	10.97
228250_at	*FNIP1*	3.705	4.085	4.045
202355_s_at	*GTF2F1*	6.395	7.055	7.005

226232_at	*NA*	5.785	6.375	6.345
210756_s_at	*NOTCH2*	3.05	3.37	3.34
218515_at	*C21orf66*	8.225	9.075	9.005
223215_s_at	*C14orf100*	10.035	11.095	10.985
224679_at	*MESDC2*	7.4	8.16	8.13
203249_at	*EZH1*	5.825	6.395	6.445
234954_at	*NA*	3.72	4.11	4.09
201964_at	*SETX*	7.175	7.945	7.875
203212_s_at	*MTMR2*	6.565	7.205	7.255
222398_s_at	*EFTUD2*	8.165	8.955	9.055
244732_at	*NA*	3.29	3.63	3.63
222263_at	*SLC35E1*	4.615	5.105	5.085
238923_at	*SPOP*	5.095	5.625	5.615
220688_s_at	*MRTO4*	5.94	6.56	6.56
218624_s_at	*MGC2752*	6.245	6.865	6.935
229519_at	*FXR1*	8.295	9.205	9.115
229865_at	*FNDC3B*	7.295	8.065	8.045
220757_s_at	*UBXD1*	7.25	8.04	7.98
1557521_a_at	*NA*	5.265	5.815	5.825
211864_s_at	*FER1L3*	8.76	9.72	9.64
221036_s_at	*APH1B*	3.125	3.465	3.435
202530_at	*MAPK14*	8.115	8.995	8.945
210385_s_at	*ARTS-1*	6.695	7.355	7.435
217651_at	*NA*	2.65	2.91	2.94
203430_at	*HEBP2*	7.455	8.225	8.275
229555_at	*GALNT5*	7.04	7.81	7.76
209556_at	*NCDN*	2.195	2.425	2.435
211975_at	*ZNF289*	5.065	5.605	5.605
205671_s_at	*HLA-DOB*	2.165	2.405	2.395
210502_s_at	*PPIE*	4.035	4.455	4.455
229844_at	*NA*	7.93	8.79	8.76

209774_x_at	*CXCL2*	3.655	4.025	4.075
223060_at	*C14orf119*	8.535	9.395	9.505
202239_at	*PARP4*	6.19	6.86	6.84
241344_at	*GLB1*	7.395	8.215	8.165
225477_s_at	*NR2C2*	7.695	8.535	8.505
223486_at	*GTPBP8*	7.22	7.97	8.03
225295_at	*SLC39A10*	10.805	12.035	11.905
226973_at	*C20orf102*	3.54	3.92	3.92
242963_at	*MGC26963*	4.82	5.37	5.31
201345_s_at	*UBE2D2*	8.005	8.865	8.875
212686_at	*PPM1H*	3.18	3.52	3.52
218123_at	*C21orf59*	7.465	8.235	8.305
213766_x_at	*NCLN*	8.26	9.12	9.19
212795_at	*KIAA1033*	9.475	10.485	10.535
228174_at	*GOLGA1*	5.67	6.29	6.29
202471_s_at	*IDH3G*	3.94	4.36	4.39
219128_at	*C2orf42*	5.8	6.44	6.43
213133_s_at	*GCSH*	6.225	6.905	6.905
236044_at	*PPAPDC1A*	5.66	6.25	6.31
204132_s_at	*FOXO3A*	3.025	3.355	3.375
225231_at	*CBL*	7.95	8.83	8.83
238891_at	*NA*	4.04	4.5	4.46
1566956_at	*OR7E104P*	4.15	4.61	4.61
218151_x_at	*GPR172A*	7.38	8.15	8.25
216317_x_at	*RHCE*	2.58	2.87	2.85
213381_at	*C10orf72*	8.12	9.02	9.02
202496_at	*EDC4*	3.665	4.065	4.075
235119_at	*TAF3*	5.57	6.18	6.2
206142_at	*ZNF135*	4.31	4.8	4.78
242538_at	*TFDP1*	4.8	5.34	5.34
243016_at	*TYMS*	4.47	4.95	5

223042_s_at	*FUNDC2*	7.54	8.39	8.41
209467_s_at	*MKNK1*	3.425	3.805	3.815
201831_s_at	*VDP*	9.725	10.835	10.825
236569_at	*RAB14*	5.11	5.71	5.67
210568_s_at	*RECQL*	7.37	8.21	8.22
222530_s_at	*MKKS*	8.965	10.045	9.935
202417_at	*KEAP1*	7.395	8.225	8.255
219008_at	*C2orf43*	6.045	6.765	6.725
1560500_at	*NA*	3.425	3.845	3.805
1554021_a_at	*ZNF12*	5.315	5.905	5.965
210329_s_at	*SGCD*	7.515	8.385	8.395
213598_at	*DIMT1L*	5.7	6.36	6.37
212342_at	*YIPF6*	7.795	8.745	8.685
244462_at	*ZNF224*	3.455	3.845	3.875
222762_x_at	*LIMD1*	8.075	9.005	9.035
223594_at	*TMEM117*	8.035	8.935	9.025
229018_at	*C12orf26*	7.745	8.615	8.705
226754_at	*ZNF251*	4.695	5.265	5.235
202475_at	*TMEM147*	5.655	6.295	6.345
225508_at	*KIAA1468*	5.815	6.465	6.535
201702_s_at	*PPP1R10*	4.905	5.475	5.495
201985_at	*KIAA0196*	7.61	8.56	8.46
228655_at	*NA*	3.99	4.46	4.47
40465_at	*DDX23*	6.125	6.835	6.885
204928_s_at	*SLC10A3*	6.38	7.15	7.14
225772_s_at	*C12orf62*	5.92	6.65	6.62
218580_x_at	*AURKAIP1*	7.7	8.63	8.64
215994_x_at	*TBC1D9B*	6.3	7.04	7.09
220097_s_at	*TMEM104*	6.61	7.41	7.42
205283_at	*FCMD*	6.73	7.59	7.51
210407_at	*PPM1A*	6.485	7.265	7.295

226015_at	*ZNF12*	7.785	8.765	8.725
221833_at	*SIAH1*	6.21	6.95	7
204370_at	*CLP1*	6.67	7.5	7.48
218840_s_at	*NADSYN1*	5.66	6.36	6.35
227692_at	*GNAI1*	9.39	10.5	10.6
208736_at	*ARPC3*	8.63	9.65	9.73
201673_s_at	*GYS1*	6.225	7.015	6.985
231937_at	*NA*	3.135	3.535	3.505
209852_x_at	*PSME3*	4.9	5.52	5.49
221567_at	*NOL3*	3.575	4.005	4.035
201736_s_at	*6-Mar*	7.835	8.765	8.865
229127_at	*ATP5J*	8.06	9.06	9.06
207071_s_at	*ACO1*	7.325	8.235	8.245
209748_at	*SPAST*	8.195	9.235	9.195
201627_s_at	*INSIG1*	8.34	9.41	9.35
225401_at	*C1orf85*	5.805	6.515	6.535
235204_at	*ENTPD7*	7.99	8.97	9.01
218143_s_at	*SCAMP2*	6.72	7.59	7.53
1555730_a_at	*CFL1*	3.535	3.955	4.005
207721_x_at	*HINT1*	10.3	11.68	11.52
226577_at	*NA*	5.55	6.24	6.27
218105_s_at	*MRPL4*	2.63	2.95	2.98
203415_at	*PDCD6*	6.9	7.78	7.78
226854_at	*GTPBP5*	2.53	2.83	2.87
219809_at	*WDR55*	5.075	5.695	5.745
227486_at	*NT5E*	7.135	8.025	8.075
225244_at	*C1orf142*	6.98	7.91	7.84
201680_x_at	*ARS2*	7.235	8.135	8.185
226758_at	*LUC7L2*	8.67	9.82	9.75
204706_at	*INPP5E*	7	7.89	7.91
1569517_at	*LOC646482*	2.26	2.57	2.54

240834_at	*FAM105B*	4.845	5.465	5.495
213971_s_at	*SUZ12P*	6.405	7.265	7.215
218206_x_at	*SCAND1*	5.38	6.11	6.05
207035_at	*SLC30A3*	3.53	4	3.98
223067_at	*HSPC148*	8.69	9.81	9.85
216251_s_at	*TTLL12*	6.82	7.7	7.73
209836_x_at	*BOLA2*	6.53	7.36	7.41
208328_s_at	*MEF2A*	5.935	6.725	6.705
1568865_at	*FNTB*	2.48	2.81	2.8
209322_s_at	*SH2B1*	3.525	3.975	3.995
201522_x_at	*SNRPN*	7.315	8.325	8.255
222817_at	*HSD3B7*	4.11	4.66	4.65
212098_at	*LOC151162*	10.435	11.855	11.815
236778_at	*ATRX*	7.835	8.915	8.845
200824_at	*GSTP1*	6.6	7.51	7.45
218106_s_at	*MRPS10*	8.06	9.13	9.15
225429_at	*NA*	6.925	7.855	7.845
228211_at	*C9orf102*	3.205	3.615	3.645
224649_x_at	*CCNY*	6.135	6.995	6.915
210434_x_at	*JTB*	9.755	11.115	11.035
212390_at	*PDE4DIP*	6.98	7.9	7.94
213025_at	*THUMPD1*	8.095	9.195	9.165
205116_at	*LAMA2*	6.145	6.965	6.975
221473_x_at	*SERINC3*	8.19	9.35	9.23
213741_s_at	*KPNA1*	5.96	6.77	6.76
201433_s_at	*PTDSS1*	8.92	10.1	10.14
200837_at	*BCAP31*	8.1	9.17	9.23
208866_at	*CSNK1A1*	6.93	7.84	7.9
1560060_s_at	*VPS37C*	10.205	11.665	11.515
218095_s_at	*TMEM165*	10.14	11.53	11.52
218027_at	*MRPL15*	7.22	8.22	8.19

227193_at	*NA*	8.545	9.665	9.775
217742_s_at	*WAC*	7.045	8.045	7.975
222593_s_at	*SPATS2*	7.74	8.8	8.81
224881_at	*VKORC1L1*	5.885	6.705	6.675
218898_at	*FAM57A*	5.74	6.53	6.54
217437_s_at	*TACC1*	7.45	8.45	8.52
225498_at	*CHMP4B*	8.865	10.115	10.065
235531_at	*IL17RB*	5.06	5.75	5.77
201685_s_at	*KIAA0737*	7.22	8.27	8.17
218626_at	*EIF4ENIF1*	6.675	7.595	7.605
203364_s_at	*KIAA0652*	3.93	4.44	4.5
227418_at	*KIAA1826*	7.04	8.01	8.04
230465_at	*HS2ST1*	3.665	4.165	4.195
220160_s_at	*KPTN*	6.245	7.125	7.125
32088_at	*BLZF1*	5.96	6.83	6.77
236458_at	*NA*	2.335	2.655	2.665
44669_at	*LOC644096*	4.95	5.62	5.68
201057_s_at	*GOLGB1*	8.425	9.645	9.575
218831_s_at	*FCGRT*	5.195	5.935	5.925
231879_at	*COL12A1*	4.735	5.375	5.425
201607_at	*PWP1*	7.01	8.06	7.95
219279_at	*DOCK10*	5.985	6.775	6.875
219482_at	*SETD4*	5.755	6.585	6.555
225067_at	*ULK3*	2.49	2.85	2.84
210927_x_at	*JTB*	8.7	9.91	9.97
230578_at	*NA*	5.6	6.38	6.42
201568_at	*UQCRQ*	8.9	10.22	10.13
202395_at	*NSF*	8.335	9.555	9.515
230885_at	*SPG7*	5.505	6.245	6.335
215495_s_at	*SAMD4A*	2.76	3.17	3.15
223824_at	*C10orf59*	5.215	5.935	5.975

1569519_at	*NBPF11*	3.42	3.92	3.91
243948_at	*NA*	6.375	7.305	7.275
217043_s_at	*MFN1*	7.145	8.145	8.195
225760_at	*MYSM1*	7.22	8.31	8.21
211379_x_at	*B3GALNT1*	5.84	6.7	6.66
1566586_at	*NA*	2.91	3.33	3.33
203460_s_at	*PSEN1*	7.365	8.415	8.445
205547_s_at	*TAGLN*	10.565	12.195	12.005
201206_s_at	*RRBP1*	7.55	8.61	8.69
204360_s_at	*NAGLU*	6.33	7.29	7.21
226805_at	*C20orf142*	5.92	6.77	6.79
226501_at	*XPNPEP3*	7.215	8.235	8.275
218252_at	*CKAP2*	6.955	7.995	7.945
201146_at	*NFE2L2*	9.48	10.94	10.78
218163_at	*MCTS1*	8.405	9.615	9.635
228690_s_at	*NDUFA11*	8	9.16	9.17
218311_at	*MAP4K3*	7.45	8.51	8.56
224623_at	*LOC728554*	4.69	5.4	5.35
227001_at	*NPAL2*	8.74	10.08	9.95
218337_at	*RAI16*	5.065	5.835	5.775
238889_at	*FLJ21839*	5.3	6.05	6.11
222439_s_at	*THRAP3*	8.875	10.215	10.135
240592_at	*NCAPG*	6.835	7.835	7.835
205298_s_at	*BTN2A2*	6.955	8.015	7.945
204327_s_at	*ZNF202*	5.13	5.89	5.89
209092_s_at	*C17orf25*	7.05	8.05	8.13
227936_at	*TMEM68*	5.64	6.52	6.44
239682_at	*FLJ23861*	5.19	5.99	5.94
218197_s_at	*OXR1*	8.285	9.535	9.485
225055_at	*LOC728850*	7.59	8.66	8.76
214949_at	*NA*	8.01	9.26	9.12

207180_s_at	*HTATIP2*	5.595	6.475	6.385
223978_s_at	*CRLS1*	7.05	8.05	8.13
209356_x_at	*EFEMP2*	7.595	8.685	8.785
213020_at	*GOSR1*	6.57	7.53	7.57
225136_at	*PLEKHA2*	7.83	8.94	9.05
210959_s_at	*SRD5A1*	6.43	7.36	7.42
226515_at	*CCDC127*	5.545	6.375	6.365
232184_at	*ALS2*	7.16	8.19	8.28
209264_s_at	*TSPAN4*	4.085	4.705	4.695
217895_at	*PTCD3*	6.49	7.47	7.46
219499_at	*SEC61A2*	3.405	3.895	3.945
226572_at	*SOCS7*	6.56	7.51	7.57
217826_s_at	*UBE2J1*	6.78	7.74	7.86
239835_at	*KBTBD8*	4.77	5.46	5.52
221499_s_at	*STX16*	6.975	7.985	8.055
229325_at	*ZZZ3*	5.03	5.78	5.81
212725_s_at	*TUG1*	8.255	9.505	9.495
235072_s_at	*NA*	10.7	12.34	12.3
218056_at	*BFAR*	6.385	7.405	7.295
201861_s_at	*LRRFIP1*	8.94	10.27	10.33
208846_s_at	*VDAC3*	6.16	7.15	7.05
225730_s_at	*THUMPD3*	5.61	6.44	6.49
1552360_a_at	*TIRAP*	3.035	3.525	3.475
242033_at	*RNF180*	3.175	3.635	3.675
210719_s_at	*HMG20B*	5.125	5.885	5.955
201799_s_at	*OSBP*	6.07	6.99	7.02
222116_s_at	*TBC1D16*	8.185	9.445	9.445
227018_at	*DPP8*	6.77	7.75	7.88
219297_at	*WDR44*	8.375	9.655	9.695
212630_at	*EXOC3*	6.28	7.29	7.23
225853_at	*GNPNAT1*	8.775	10.225	10.075

213009_s_at	*TRIM37*	8.56	9.95	9.86
236515_at	*SAPS3*	6.875	7.965	7.935
207196_s_at	*TNIP1*	8.29	9.57	9.61
209233_at	*EMG1*	6.675	7.655	7.775
200704_at	*LITAF*	9.28	10.82	10.65
226732_at	*RBM33*	6.83	7.93	7.88
219520_s_at	*WWC3*	6.86	7.88	8
222993_at	*MRPL37*	5.395	6.205	6.295
201828_x_at	*FAM127A*	7.775	8.995	9.005
212482_at	*RMND5A*	6.6	7.63	7.65
217828_at	*SLTM*	9.495	10.935	11.055
229393_at	*L3MBTL3*	7.58	8.84	8.73
226241_s_at	*MRPL52*	7.32	8.44	8.53
201377_at	*UBAP2L*	7	8.05	8.19
213246_at	*C14orf130*	5.15	5.99	5.95
227852_at	*RP9*	5.38	6.29	6.2
208707_at	*EIF5*	4.175	4.875	4.825
209272_at	*NAB1*	7.925	9.265	9.145
208955_at	*DUT*	5.665	6.615	6.555
213637_at	*NA*	7.81	9.13	9
200607_s_at	*RAD21*	6.325	7.385	7.295
209864_at	*FRAT2*	2.565	2.975	2.985
225424_at	*GPAM*	6.54	7.61	7.58
226942_at	*PHF20L1*	6.115	7.085	7.105
200001_at	*CAPNS1*	8.365	9.695	9.725
224864_at	*SRA1*	7.385	8.655	8.515
203848_at	*AKAP8*	7.365	8.615	8.505
221705_s_at	*SIKE*	5.87	6.85	6.8
221780_s_at	*DDX27*	6.89	8.03	8
204244_s_at	*DBF4*	5.4	6.25	6.32
214783_s_at	*ANXA11*	7.025	8.135	8.225

218631_at	*AVPI1*	5.83	6.79	6.79
226579_at	*KNS2*	7.665	8.905	8.935
225451_at	*GRIPAP1*	4.15	4.81	4.85
218716_x_at	*MTO1*	7.355	8.625	8.495
209934_s_at	*ATP2C1*	7.215	8.445	8.345
228583_at	*LIN52*	6.755	7.935	7.805
226914_at	*ARPC5L*	9.425	11.035	10.905
200924_s_at	*SLC3A2*	7.155	8.385	8.285
225576_at	*C6orf72*	8.04	9.36	9.36
209234_at	*KIF1B*	6.005	6.945	7.035
202307_s_at	*TAP1*	6.56	7.64	7.65
225300_at	*C15orf23*	6.31	7.36	7.34
1555968_a_at	*NA*	5.24	6.15	6.05
224512_s_at	*LSMD1*	6.16	7.2	7.16
225827_at	*EIF2C2*	4.835	5.595	5.675
223381_at	*NUF2*	4.395	5.095	5.175
218246_at	*C1orf166*	6.68	7.78	7.81
1556131_s_at	*FBF1*	3.285	3.855	3.825
230241_at	*IFRG15*	5.8	6.75	6.8
225635_s_at	*LOC401504*	6.625	7.735	7.745
1561171_a_at	*FLJ36131*	3.19	3.76	3.7
230077_at	*SDHALP1*	6.3	7.32	7.4
236600_at	*SPG20*	6.825	8.015	7.945
202866_at	*DNAJB12*	7.645	8.955	8.905
203694_s_at	*DHX16*	6.65	7.75	7.79
200793_s_at	*ACO2*	5.595	6.575	6.495
233487_s_at	*LRRC8A*	6.215	7.265	7.255
238186_at	*NA*	2.795	3.285	3.255
227730_at	*NA*	4.24	4.94	4.98
225484_at	*TSGA14*	5.125	6.005	5.995
229517_at	*PTPDC1*	6.67	7.8	7.82

200721_s_at	*ACTR1A*	5.46	6.35	6.44
231823_s_at	*SH3PXD2B*	8.67	10.16	10.14
217822_at	*WBP11*	7.44	8.69	8.74
207812_s_at	*GORASP2*	9.175	10.685	10.795
209721_s_at	*HOM-TES-103*	6.56	7.71	7.65
209803_s_at	*PHLDA2*	10.51	12.25	12.37
215233_at	*JMJD6*	4.355	5.095	5.125
228005_at	*ZXDB*	5.46	6.36	6.44
225157_at	*MLXIP*	7.125	8.355	8.375
225493_at	*LOC144438*	7.62	8.96	8.92
221752_at	*SSH1*	8.445	9.855	9.965
221740_x_at	*LRRC37A*	5.64	6.65	6.59
231059_x_at	*SCAND1*	3.945	4.585	4.665
202986_at	*ARNT2*	5.56	6.56	6.49
209845_at	*MKRN1*	6.73	7.85	7.96
242851_at	*KIAA1919*	5.77	6.72	6.83
223527_s_at	*CDADC1*	6.37	7.46	7.52
208717_at	*OXA1L*	5.055	5.975	5.895
217893_s_at	*C1orf108*	7.92	9.29	9.34
213595_s_at	*CDC42BPA*	6.24	7.4	7.28
221107_at	*CHRNA9*	2.425	2.865	2.825
205217_at	*TIMM8A*	5.495	6.465	6.485
225669_at	*IFNAR1*	7.86	9.28	9.23
1552422_at	*C10orf25*	4.895	5.765	5.775
226734_at	*EIF4E2*	5.905	7.015	6.905
208097_s_at	*TXNDC1*	5.175	6.145	6.045
227247_at	*PLEKHA8*	6.62	7.76	7.84
1556061_at	*RPP30*	5.815	6.875	6.835
225716_at	*NA*	7.665	9.055	9.025
1555724_s_at	*TAGLN*	7.195	8.515	8.465
216088_s_at	*PSMA7*	6.855	8.025	8.125

212781_at	*RBBP6*	6.66	7.85	7.87
225158_at	*GFM1*	8.155	9.645	9.595
232008_s_at	*BBX*	7.46	8.78	8.82
224637_at	*NA*	8.025	9.415	9.545
202783_at	*NNT*	5.655	6.715	6.635
202625_at	*LYN*	5.525	6.545	6.505
221577_x_at	*GDF15*	4.62	5.48	5.45
227685_at	*TMF1*	7.625	9.095	8.945
218838_s_at	*TTC31*	6.13	7.19	7.31
227646_at	*NA*	8.265	9.835	9.735
225552_x_at	*CCNL2*	7.61	9.02	9
1555427_s_at	*SYNCRIP*	8.61	10.21	10.17
220349_s_at	*FLJ21865*	5.575	6.605	6.595
202527_s_at	*SMAD4*	6.94	8.29	8.15
1558279_a_at	*NA*	6.86	8.06	8.18
214151_s_at	*CCPG1*	7.47	8.87	8.83
204956_at	*MTAP*	6.04	7.2	7.12
209455_at	*FBXW11*	8.95	10.64	10.58
209202_s_at	*EXTL3*	4.355	5.115	5.205
222432_s_at	*CCDC47*	7.875	9.285	9.385
215749_s_at	*GORASP1*	5.23	6.23	6.19
230596_at	*NA*	2.88	3.4	3.44
202595_s_at	*LEPROTL1*	5.96	7.14	7.02
211031_s_at	*CLIP2*	4.085	4.875	4.845
202705_at	*CCNB2*	6.68	7.97	7.92
201500_s_at	*PPP1R11*	7.25	8.68	8.58
202731_at	*PDCD4*	4.485	5.335	5.355
224861_at	*GNAQ*	8.05	9.51	9.67
202642_s_at	*TRRAP*	5.75	6.9	6.8
206452_x_at	*PPP2R4*	5.4	6.5	6.38
217854_s_at	*POLR2E*	5.98	7.09	7.16

217627_at	*ZNF573*	6.14	7.29	7.35
226089_at	*RABL3*	3.835	4.575	4.575
228045_at	*NA*	6.835	8.115	8.185
212881_at	*PIAS4*	4.59	5.47	5.48
1555886_at	*PDSS2*	4.47	5.3	5.36
203262_s_at	*FAM50A*	6.43	7.69	7.66
208723_at	*USP11*	6.41	7.65	7.65
213011_s_at	*TPI1*	8.245	9.855	9.835
205437_at	*ZNF211*	5.315	6.405	6.295
212983_at	*HRAS*	4.565	5.505	5.415
213145_at	*FBXL14*	5.85	6.97	7.02
234672_s_at	*TMEM48*	7.66	9.09	9.23
209365_s_at	*ECM1*	6.145	7.365	7.335
202492_at	*ATG9A*	4.73	5.64	5.67
202754_at	*R3HDM1*	7.275	8.735	8.665
230664_at	*MGC39900*	4.835	5.745	5.815
227433_at	*KIAA2018*	6.14	7.32	7.36
208810_at	*DNAJB6*	6.99	8.43	8.3
207654_x_at	*DR1*	5.58	6.66	6.7
226474_at	*NLRC5*	7.51	9	8.98
212565_at	*STK38L*	8.455	10.115	10.125
213567_at	*NA*	7.13	8.57	8.52
212677_s_at	*CEP68*	5.1	6.08	6.13
217784_at	*YKT6*	5.55	6.61	6.7
227527_at	*MLL2*	7.74	9.22	9.34
227970_at	*GPR157*	4.795	5.775	5.735
228736_at	*HEL308*	5.655	6.825	6.755
226929_at	*MTHFR*	3.675	4.455	4.375
241709_s_at	*DOCK1*	3.675	4.435	4.395
213739_at	*NA*	3.335	4.015	3.985
212496_s_at	*JMJD2B*	6.97	8.45	8.29

221692_s_at	*MRPL34*	3.635	4.375	4.375
206364_at	*KIF14*	5.27	6.3	6.36
202096_s_at	*TSPO*	5.86	7.09	6.98
214578_s_at	*ROCK1*	6.285	7.595	7.495
204278_s_at	*EBAG9*	5.83	7.04	6.97
222732_at	*TRIM39*	5.62	6.81	6.71
229267_at	*ANAPC1*	5.54	6.67	6.65
200828_s_at	*RHOT1*	7.79	9.44	9.3
201132_at	*HNRPH2*	8.37	10.03	10.1
208698_s_at	*NONO*	6.735	8.035	8.165
201584_s_at	*DDX39*	6.87	8.31	8.23
1558529_s_at	*NA*	2.63	3.15	3.19
211928_at	*DYNC1H1*	7.485	9.045	8.965
235505_s_at	*NA*	5.96	7.24	7.13
217492_s_at	*PTENP1*	7.795	9.495	9.305
209724_s_at	*ZFP161*	4.105	4.915	4.975
227143_s_at	*BID*	6.175	7.455	7.455
223776_x_at	*TINF2*	5.755	6.995	6.885
212860_at	*ZDHHC18*	4.41	5.37	5.28
212083_at	*TEX261*	8.285	9.905	10.105
202838_at	*FUCA1*	5.09	6.2	6.1
209486_at	*SAS10*	7.97	9.72	9.54
1555216_a_at	*LOC645722*	5.15	6.18	6.27
47773_at	*FBXO42*	4.83	5.83	5.84
215629_s_at	*KIAA1799*	3.84	4.66	4.62
222048_at	*ADRBK2*	4.325	5.205	5.255
213694_at	*RSBN1*	6.815	8.285	8.195
45288_at	*ABHD6*	3.985	4.825	4.815
51774_s_at	*MGC13098*	4.165	5.005	5.085
218296_x_at	*MSTO1*	3.61	4.4	4.34
224657_at	*ERRFI1*	9.95	12.14	11.96

223058_at	*FAM107B*	7.2	8.68	8.76
205770_at	*GSR*	2.525	3.035	3.095
201440_at	*DDX23*	4.835	5.875	5.845
225222_at	*HIAT1*	8.495	10.405	10.195
224956_at	*NUFIP2*	7.71	9.43	9.28
220239_at	*KLHL7*	6.485	7.855	7.885
227129_x_at	*FLJ45340*	3.92	4.76	4.76
202301_s_at	*RSRC2*	7.725	9.365	9.405
228273_at	*NA*	7.665	9.375	9.275
224859_at	*CD276*	6.235	7.655	7.525
201626_at	*INSIG1*	9.825	12.025	11.895
1555543_a_at	*CLCC1*	4.245	5.195	5.135
213144_at	*GOSR2*	4.31	5.28	5.21
230091_at	*SRPK2*	5.9	7.11	7.25
233842_x_at	*C20orf43*	5.27	6.37	6.45
238823_at	*FMNL3*	4.745	5.735	5.825
218982_s_at	*MRPS17*	6.16	7.46	7.55
219819_s_at	*MRPS28*	5.815	7.095	7.095
209298_s_at	*ITSN1*	6.075	7.435	7.385
243648_at	*ZC3H11A*	6.165	7.555	7.485
208689_s_at	*RPN2*	8.13	9.84	9.98
226315_at	*CCDC16*	7.36	8.94	9.01
222573_s_at	*SAV1*	4.65	5.68	5.66
204970_s_at	*MAFG*	7.15	8.78	8.68
212123_at	*C10orf61*	5.48	6.66	6.73
223287_s_at	*FOXP1*	7.325	9.005	8.885
234982_at	*ZNF650*	7.31	9.02	8.84
204162_at	*KNTC2*	6.25	7.64	7.63
218089_at	*C20orf4*	5.32	6.49	6.51
1555780_a_at	*RHEB*	6.645	8.095	8.145
219001_s_at	*WDR32*	5.7	6.99	6.94

213161_at	*C9orf97*	6.515	8.035	7.905
202032_s_at	*MAN2A2*	5.74	6.96	7.08
243020_at	*FAM13A1OS*	3.39	4.14	4.15
204175_at	*ZNF593*	2.52	3.06	3.11
218845_at	*DUSP22*	6.88	8.49	8.35
219016_at	*FASTKD5*	5.505	6.755	6.695
224818_at	*SORT1*	7.205	8.795	8.825
244647_at	*NA*	3.72	4.55	4.56
202694_at	*STK17A*	5.97	7.36	7.26
208772_at	*ANKHD1*	6.33	7.72	7.79
218371_s_at	*PSPC1*	6.805	8.345	8.335
230508_at	*DKK3*	5.53	6.75	6.79
201114_x_at	*PSMA7*	7.92	9.64	9.77
239348_at	*USP31*	2.785	3.385	3.435
218514_at	*C17orf71*	5.865	7.145	7.235
1569167_at	*COMMD10*	2.59	3.2	3.14
224773_at	*NAV1*	7.005	8.685	8.495
208994_s_at	*PPIG*	6.565	7.995	8.125
204949_at	*ICAM3*	4.525	5.565	5.535
213383_at	*NA*	4.785	5.925	5.805
213954_at	*KIAA0888*	2.955	3.635	3.625
202084_s_at	*SEC14L1*	9.14	11.3	11.14
1566968_at	*SPRY4*	5.045	6.145	6.235
221853_s_at	*NOMO3*	7.34	9.12	8.92
206118_at	*STAT4*	2.53	3.11	3.11
210010_s_at	*SLC25A1*	3.625	4.465	4.435
202024_at	*ASNA1*	5.505	6.815	6.725
225112_at	*ABI2*	8.18	10.1	10.02
202304_at	*FNDC3A*	8.73	10.81	10.66
210330_at	*SGCD*	7.45	9.19	9.15
226536_at	*NSMCE2*	6.195	7.695	7.545

219057_at	*RABEP2*	2.725	3.335	3.385
204732_s_at	*TRIM23*	6.605	8.165	8.115
235696_at	*NA*	4.33	5.35	5.31
225850_at	*SFT2D1*	6.395	7.965	7.785
204478_s_at	*RABIF*	7.075	8.765	8.675
224770_s_at	*NAV1*	4.99	6.18	6.12
222212_s_at	*LASS2*	7.38	9.16	9.04
226161_at	*SLC30A6*	6.755	8.425	8.245
221452_s_at	*TMEM14B*	7.28	9.07	8.92
212906_at	*GRAMD1B*	5.43	6.64	6.78
226941_at	*NA*	6.84	8.53	8.39
221583_s_at	*KCNMA1*	3.8	4.68	4.72
219315_s_at	*C16orf30*	6.63	8.28	8.13
208424_s_at	*CIAPIN1*	5.86	7.28	7.23
204034_at	*ETHE1*	5.655	7.055	6.945
236635_at	*ZNF667*	4.36	5.43	5.37
230309_at	*BHMT*	4.805	5.905	5.995
227079_at	*DHX8*	5.475	6.825	6.735
1552329_at	*RBBP6*	3.645	4.565	4.475
224607_s_at	*SRP68*	7.375	9.215	9.095
229014_at	*FLJ42709*	5.945	7.355	7.415
212312_at	*BCL2L1*	5.71	7.04	7.14
231907_at	*NA*	5.63	7.04	6.95
212110_at	*SLC39A14*	10.345	12.835	12.855
225287_s_at	*TMEM55B*	5.745	7.155	7.125
222524_s_at	*SENP2*	4.39	5.47	5.44
224963_at	*SLC26A2*	7.16	8.95	8.85
217974_at	*TM7SF3*	5.26	6.57	6.51
224364_s_at	*PPIL3*	7.78	9.57	9.79
238733_at	*CPM*	5.285	6.655	6.515
201777_s_at	*KIAA0494*	3.13	3.9	3.89

1556000_s_at	*BTBD7*	6.435	8.115	7.925
227534_at	*C9orf21*	5.375	6.725	6.695
201541_s_at	*ZNHIT1*	5.49	6.81	6.89
227993_at	*METAP2*	7.075	8.895	8.775
1560821_at	*ARHGAP22*	3.08	3.83	3.85
227934_at	*NA*	7.3	9.14	9.1
204464_s_at	*EDNRA*	9.93	12.44	12.38
202883_s_at	*PPP2R1B*	6.495	8.155	8.075
223041_at	*CD99L2*	3.525	4.375	4.435
212305_s_at	*MIA3*	5.19	6.5	6.48
219238_at	*PIGV*	4.65	5.75	5.88
60084_at	*CYLD*	2.825	3.555	3.525
200820_at	*PSMD8*	6.45	8.12	8.02
208872_s_at	*REEP5*	6.225	7.825	7.745
227998_at	*S100A16*	7.945	9.885	10.035
221571_at	*TRAF3*	6.505	8.255	8.065
232095_at	*SRGAP2*	6.735	8.525	8.355
242550_at	*EIF3S9*	4.55	5.7	5.72
226183_at	*NA*	5.86	7.31	7.38
229572_at	*NA*	5.465	6.785	6.945
221511_x_at	*CCPG1*	6.42	8.01	8.11
212809_at	*NFATC2IP*	4.505	5.725	5.605
239784_at	*SMYD3*	4.625	5.825	5.795
236104_at	*NA*	6	7.53	7.56
236402_at	*NA*	4.81	6.09	6.01
225551_at	*C1orf71*	6.82	8.52	8.64
219874_at	*SLC12A8*	3.71	4.7	4.63
209939_x_at	*CFLAR*	6.51	8.26	8.12
1560878_at	*SYT15*	5.045	6.305	6.395
209311_at	*BCL2L2*	5.975	7.515	7.555
225973_at	*TAP2*	6.63	8.45	8.26

235238_at	*SHC4*	4.06	5.08	5.16
203063_at	*PPM1F*	5.77	7.3	7.25
227755_at	*NA*	7.02	8.87	8.85
209188_x_at	*DR1*	5.455	6.895	6.885
228569_at	*PAPOLA*	6.25	7.89	7.9
209520_s_at	*NCBP1*	4.205	5.245	5.365
205479_s_at	*PLAU*	8.395	10.575	10.615
219765_at	*ZNF329*	5.51	7.02	6.92
231835_at	*C1orf93*	5.34	6.69	6.82
223682_s_at	*MGC11102*	3.575	4.515	4.525
204163_at	*EMILIN1*	5.28	6.76	6.63
209653_at	*KPNA4*	4.86	6.17	6.15
202289_s_at	*TACC2*	7.41	9.42	9.4
222142_at	*CYLD*	3.205	4.085	4.055
222450_at	*TMEPAI*	9.34	11.85	11.87
202329_at	*CSK*	6.835	8.695	8.665
235260_s_at	*C4orf28*	3.26	4.14	4.15
238602_at	*DIS3L2*	3.715	4.685	4.755
227156_at	*TNRC8*	5.975	7.535	7.685
201104_x_at	*NBPF14*	5.845	7.385	7.495
222658_s_at	*APTX*	4.715	6.025	5.975
210664_s_at	*TFPI*	8.575	11.005	10.825
201344_at	*UBE2D2*	6.04	7.78	7.61
221563_at	*DUSP10*	6.195	7.805	7.985
1554140_at	*WDR78*	4.245	5.405	5.415
221437_s_at	*MRPS15*	4.47	5.65	5.77
228304_at	*NA*	3.065	3.955	3.855
226495_at	*VISA*	4.305	5.505	5.475
208821_at	*SNRPB*	6.3	7.96	8.12
239024_at	*SLC12A8*	5.56	7.08	7.12
225606_at	*BCL2L11*	4.09	5.22	5.24

225218_at	*ZFYVE27*	4.45	5.71	5.67
219655_at	*C7orf10*	5.205	6.565	6.735
226176_s_at	*USP42*	5.615	7.285	7.105
204169_at	*IMPDH1*	3.655	4.665	4.695
212714_at	*LARP4*	7.51	9.54	9.71
225391_at	*LOC93622*	4.925	6.385	6.235
1553768_a_at	*DCBLD1*	9.315	11.825	12.075
221839_s_at	*UBAP2*	5.985	7.665	7.675
217909_s_at	*MLX*	4.75	6.03	6.15
1554251_at	*HP1BP3*	5.38	6.93	6.87
203652_at	*MAP3K11*	3.565	4.615	4.545
218347_at	*TYW1*	4.615	5.855	6.015
230689_at	*NA*	5.515	7.035	7.145
222156_x_at	*CCPG1*	5.82	7.5	7.47
203513_at	*KIAA1840*	6.955	9.035	8.845
220370_s_at	*USP36*	4.04	5.21	5.19
218584_at	*FLJ21127*	5.07	6.49	6.56
200948_at	*MLF2*	6.005	7.655	7.825
226118_at	*ADCY3*	3.81	4.84	4.97
217825_s_at	*UBE2J1*	6.3	8.19	8.05
233878_s_at	*XRN2*	4.27	5.49	5.53
210145_at	*PLA2G4A*	7.27	9.3	9.44
210511_s_at	*INHBA*	10.595	13.785	13.535
202132_at	*WWTR1*	9.355	12.195	11.945
1555814_a_at	*RHOA*	4.155	5.285	5.425
1556551_s_at	*SLC39A6*	2.775	3.545	3.605
54970_at	*ZMIZ2*	6.565	8.545	8.415
209107_x_at	*NCOA1*	4.625	5.925	6.005
218973_at	*EFTUD1*	6.1	7.84	7.93
238421_at	*RC3H2*	3.705	4.785	4.785
200000_s_at	*PRPF8*	6.8	8.81	8.79

200720_s_at	*ACTR1A*	4.57	5.94	5.88
202111_at	*SLC4A2*	5.53	7.09	7.25
230799_at	*LOC388948*	5.48	7.1	7.1
212425_at	*SCAMP1*	4.415	5.705	5.735
201387_s_at	*UCHL1*	7.165	9.165	9.415
226175_at	*TTC9C*	4.36	5.67	5.65
203376_at	*CDC40*	5.91	7.74	7.6
222622_at	*LOC283871*	2.445	3.205	3.155
224430_s_at	*MTO1*	5.68	7.35	7.41
208800_at	*SRP72*	5.785	7.445	7.575
209044_x_at	*SF3B4*	4.965	6.485	6.415
1552354_at	*C19orf26*	2.8	3.61	3.67
203957_at	*E2F6*	5.475	7.195	7.065
225290_at	*ETNK1*	6.38	8.22	8.43
222490_at	*POLR3E*	5.93	7.75	7.75
225102_at	*MGLL*	8.27	10.8	10.82
235363_at	*NA*	3.815	4.995	4.965
202101_s_at	*RALB*	5.9	7.79	7.65
234998_at	*NA*	5.605	7.285	7.365
1560156_at	*CLEC2D*	3.285	4.305	4.295
217356_s_at	*PGK1*	6.675	8.835	8.645
243198_at	*TEX9*	3.66	4.74	4.86
227777_at	*C10orf18*	5.295	6.935	6.945
218159_at	*C20orf116*	6.035	7.965	7.895
209882_at	*RIT1*	7.095	9.205	9.435
221988_at	*CRSP7*	5.19	6.78	6.84
213279_at	*DHRS1*	5.875	7.615	7.815
229509_at	*MFSD8*	5.125	6.675	6.805
215235_at	*SPTAN1*	6.745	8.885	8.855
239437_at	*NA*	4.83	6.43	6.28
201005_at	*CD9*	6.985	9.305	9.075

210754_s_at	*LYN*	2.875	3.785	3.775
212756_s_at	*UBR2*	5.305	6.965	7.005
212528_at	*NA*	5.245	6.885	6.935
201765_s_at	*HEXA*	6.885	9.195	8.965
202236_s_at	*SLC16A1*	4.985	6.645	6.515
201285_at	*MKRN1*	6.785	9.055	8.865
243555_at	*EDNRA*	5.55	7.4	7.25
204668_at	*RNF24*	3.625	4.845	4.735
219148_at	*PBK*	6.435	8.475	8.545
204384_at	*GOLGA2*	5.545	7.305	7.375
222789_at	*RSBN1*	5.535	7.425	7.215
204725_s_at	*NCK1*	3.695	4.915	4.875
203235_at	*THOP1*	3.32	4.39	4.41
213895_at	*EMP1*	5.39	7.26	7.04
223104_at	*JAGN1*	6.085	8.045	8.095
212174_at	*AK2*	4.095	5.505	5.375
1555486_a_at	*FLJ14213*	4.655	6.255	6.125
204190_at	*USPL1*	5.15	6.82	6.88
236837_x_at	*LOC650794*	4.925	6.545	6.545
207483_s_at	*CAND1*	7.255	9.715	9.585
219239_s_at	*ZNF654*	3.27	4.31	4.39
243256_at	*MKNK1*	5.07	6.76	6.74
232946_s_at	*NADSYN1*	4.65	6.11	6.27
218051_s_at	*NT5DC2*	3.17	4.25	4.2
219798_s_at	*BCDIN3*	4.87	6.41	6.57
1552853_at	*FLJ32784*	2.54	3.39	3.38
223306_at	*EBPL*	6.015	8.005	8.025
215195_at	*PRKCA*	4.97	6.66	6.6
223575_at	*KIAA1549*	3.99	5.31	5.35
222777_s_at	*WHSC1*	4.88	6.46	6.57
225440_at	*AGPAT3*	5.055	6.815	6.695

236620_at	*RIF1*	6.045	8.055	8.075
215497_s_at	*WDTC1*	2.685	3.595	3.585
225747_at	*COQ10A*	4.04	5.32	5.48
202168_at	*TAF9*	5.285	7.155	7.015
222088_s_at	*SLC2A3*	4.95	6.71	6.55
229732_at	*HSZFP36*	4.555	6.185	6.015
218896_s_at	*C17orf85*	5.7	7.76	7.52
209412_at	*TMEM1*	5.63	7.59	7.52
228323_at	*CASC5*	5.1	6.89	6.79
206926_s_at	*IL11*	5.465	7.225	7.455
200900_s_at	*M6PR*	5.595	7.635	7.405
230779_at	*TNRC6B*	5.94	7.9	8.1
210191_s_at	*PHTF1*	4.96	6.69	6.67
218951_s_at	*PLCXD1*	5.505	7.425	7.395
224711_at	*YY1*	7.21	9.58	9.84
229441_at	*PRSS23*	6.64	8.98	8.93
222609_s_at	*EXOSC1*	5.315	7.195	7.145
212211_at	*ANKRD17*	5.075	6.785	6.915
203554_x_at	*PTTG1*	6.515	8.715	8.875
209605_at	*TST*	5.12	6.96	6.87
215482_s_at	*EIF2B4*	4.62	6.26	6.22
216212_s_at	*DKC1*	5.745	7.785	7.755
229240_at	*ZDHHC21*	3.765	5.015	5.165
224186_s_at	*RNF123*	3.765	5.025	5.175
212428_at	*KIAA0368*	6.295	8.555	8.475
204434_at	*SPATA2*	4.75	6.35	6.51
212548_s_at	*FRYL*	5.77	7.9	7.72
229873_at	*KCTD21*	4.115	5.595	5.545
213142_x_at	*LOC54103*	4.74	6.41	6.43
218312_s_at	*ZSCAN18*	5.04	6.83	6.85
242606_at	*NA*	4.955	6.625	6.835

201946_s_at	*CCT2*	5.565	7.615	7.505
202859_x_at	*IL8*	8.815	11.805	12.175
212912_at	*RPS6KA2*	5.86	7.98	7.97
211501_s_at	*EIF3S9*	6.005	8.165	8.205
205787_x_at	*LOC441155*	4.605	6.335	6.205
1556582_at	*NA*	3.71	5.05	5.05
231766_s_at	*COL12A1*	6.93	9.46	9.44
201066_at	*CYC1*	5.205	7.145	7.025
244832_at	*EDNRA*	5.38	7.24	7.43
223707_at	*MGC10850*	6.345	8.545	8.775
235205_at	*LOC346887*	5.55	7.51	7.67
200622_x_at	*CALM3*	5.44	7.42	7.46
228563_at	*GJA7*	5.665	7.645	7.875
211061_s_at	*MGAT2*	5.805	8.075	7.825
227741_at	*PTPLB*	6.16	8.4	8.48
201101_s_at	*BCLAF1*	5.52	7.5	7.65
208308_s_at	*GPI*	5.48	7.61	7.43
1555862_s_at	*MICALL2*	3.565	4.855	4.945
239355_at	*GMCL1*	5.425	7.495	7.405
201020_at	*YWHAH*	3.87	5.25	5.38
211762_s_at	*KPNA2*	7.075	9.765	9.675
227945_at	*TBC1D1*	4.73	6.51	6.51
244025_at	*NA*	3.255	4.435	4.515
218679_s_at	*VPS28*	4.905	6.675	6.815
1557450_s_at	*WHDC1L1*	5.165	7.005	7.205
226076_s_at	*MBD6*	3.575	4.895	4.945
239730_at	*NA*	3.44	4.79	4.69
224728_at	*ATPAF1*	4.565	6.275	6.335
226298_at	*RUNDC1*	4.84	6.65	6.71
238417_at	*PGM2L1*	6.065	8.455	8.285
222421_at	*UBE2H*	6.33	8.81	8.69

204570_at	*COX7A1*	6.085	8.415	8.425
240854_x_at	*NA*	5.44	7.48	7.57
212354_at	*SULF1*	9.39	13.01	12.97
205493_s_at	*DPYSL4*	3.74	5.26	5.09
232149_s_at	*NSMAF*	4.12	5.74	5.66
212065_s_at	*USP34*	3.05	4.26	4.21
238597_at	*ANKRD13C*	4.14	5.86	5.66
209797_at	*TMEM4*	6.185	8.615	8.565
204905_s_at	*EEF1E1*	6.08	8.33	8.59
203149_at	*PVRL2*	4.67	6.5	6.51
1561908_a_at	*HS3ST3B1*	7.86	10.91	10.97
225390_s_at	*KLF13*	6.945	9.835	9.535
1555326_a_at	*ADAM9*	3.625	5.005	5.095
220580_at	*BICC1*	2.445	3.425	3.395
212321_at	*SGPL1*	4.39	6.08	6.18
203742_s_at	*TDG*	4.53	6.3	6.36
222262_s_at	*ETNK1*	5.495	7.745	7.635
204283_at	*FARS2*	4.65	6.4	6.61
212079_s_at	*MLL*	2.87	3.98	4.04
221260_s_at	*FAM130A1*	5.905	8.405	8.135
224929_at	*TMEM173*	4.52	6.29	6.39
226391_at	*NDUFB2*	4.35	6.05	6.18
204160_s_at	*ENPP4*	4.02	5.61	5.71
234726_s_at	*TMEM168*	3.36	4.7	4.78
229492_at	*VANGL1*	3.7	5.22	5.22
209020_at	*C20orf111*	4.06	5.71	5.77
242294_at	*NA*	3.335	4.685	4.745
205514_at	*ZNF415*	4.1	5.85	5.75
213552_at	*GLCE*	5.855	8.325	8.235
205726_at	*DIAPH2*	5.625	8.085	7.855
226305_at	*LYNX1*	3.455	4.875	4.925

214439_x_at	*BIN1*	3.78	5.28	5.44
227844_at	*FMNL3*	2.62	3.67	3.77
213933_at	*PTGER3*	6.69	9.39	9.62
238437_at	*ZNF805*	4.065	5.855	5.705
242618_at	*TRIM26*	4.06	5.84	5.71
226897_s_at	*ZC3H7A*	4.555	6.555	6.395
219679_s_at	*WAC*	2.955	4.265	4.165
228257_at	*ANKRD52*	4.55	6.57	6.41
201042_at	*TGM2*	6.245	8.795	9.015
204772_s_at	*TTF1*	3.185	4.615	4.475
74694_s_at	*RABEP2*	4.88	7.08	6.88
214866_at	*PLAUR*	5.205	7.435	7.485
223651_x_at	*CDC23*	4.695	6.645	6.825
1553605_a_at	*ABCA13*	3.295	4.805	4.635
242705_x_at	*NA*	5.825	8.375	8.325
211009_s_at	*ZNF271*	5.19	7.49	7.4
204404_at	*SLC12A2*	4.415	6.445	6.255
204463_s_at	*EDNRA*	7.775	11.235	11.225
219006_at	*C6orf66*	5.66	8.31	8.06
1557852_at	*PHC2*	3.515	5.095	5.065
214453_s_at	*IFI44*	4.445	6.385	6.465
204021_s_at	*PURA*	5.555	8.185	7.925
227122_at	*ZNF564*	4.78	6.88	6.99
218556_at	*ORMDL2*	3.76	5.42	5.49
209408_at	*KIF2C*	4.55	6.5	6.71
225241_at	*CCDC80*	6.955	10.085	10.115
37079_at	*YDD19*	3.07	4.47	4.46
219342_at	*CASD1*	4.26	6.14	6.26
224469_s_at	*C14orf151*	3.975	5.865	5.715
1569263_at	*SLC16A3*	3.04	4.39	4.48
217861_s_at	*PREB*	4.135	6.105	5.995

235016_at	*REEP3*	3.32	4.96	4.77
1555789_s_at	*PHF23*	2.69	3.93	3.98
202063_s_at	*SEL1L*	3.78	5.57	5.55
219555_s_at	*CENPN*	4.88	7.16	7.2
213448_at	*MTX1*	4.44	6.6	6.44
236117_at	*NA*	3.86	5.62	5.73
204976_s_at	*AMMECR1*	5.435	8.135	7.885
1553718_at	*ZNF548*	6.95	10.44	10.03
223314_at	*NUPL1*	2.82	4.08	4.24
225582_at	*KIAA1754*	5.16	7.58	7.66
205924_at	*RAB3B*	3.99	6	5.78
209902_at	*ATR*	5.205	7.805	7.595
215617_at	*NA*	3.145	4.555	4.735
210845_s_at	*PLAUR*	5.775	8.665	8.435
236476_at	*MTCP1*	4.47	6.6	6.66
212353_at	*SULF1*	9.17	13.81	13.41
225791_at	*UBE2F*	4.065	6.045	6.035
221489_s_at	*SPRY4*	4.875	7.365	7.135
206376_at	*SLC6A15*	5.33	8.09	7.77
212051_at	*WIPF2*	5.25	7.76	7.86
201422_at	*IFI30*	4.38	6.45	6.59
209213_at	*CBR1*	3.37	5.08	4.98
228177_at	*CREBBP*	3.685	5.435	5.575
201467_s_at	*NQO1*	5.73	8.41	8.69
221477_s_at	*MGC5618*	6.9	10.37	10.23
212432_at	*GRPEL1*	5.115	7.755	7.545
225446_at	*BRWD1*	4.12	6.12	6.2
1565483_at	*EGFR*	6.955	10.515	10.275
226833_at	*CYB5D1*	4.23	6.35	6.31
208078_s_at	*ZEB1*	3.25	4.83	4.91
225915_at	*CAB39L*	4.87	7.21	7.41

238969_at	*C3orf55*	4.14	6.25	6.19
1552695_a_at	*SLC2A13*	4.89	7.46	7.24
230949_at	*SLC23A3*	2.54	3.81	3.83
230240_at	*DYRK3*	4.64	7.09	6.87
200615_s_at	*AP2B1*	4.35	6.51	6.59
1554423_a_at	*FBXO7*	4.21	6.25	6.42
210253_at	*HTATIP2*	3.16	4.77	4.75
213223_at	*RPL28*	4.285	6.455	6.475
202109_at	*ARFIP2*	3.52	5.22	5.42
205414_s_at	*KIAA0672*	5.415	8.165	8.225
1569868_s_at	*EME2*	4.755	7.265	7.155
218867_s_at	*C12orf49*	4.985	7.645	7.445
1568877_a_at	*ACBD5*	4.245	6.365	6.495
202263_at	*CYB5R1*	4.15	6.28	6.33
214099_s_at	*PDE4DIP*	2.705	4.165	4.055
230300_at	*NA*	5.645	8.635	8.545
208079_s_at	*AURKA*	5.85	8.85	9.02
205512_s_at	*AIFM1*	4.65	7.1	7.12
203162_s_at	*KATNB1*	5.29	8.2	8.02
209758_s_at	*MFAP5*	7.86	12.23	11.9
228555_at	*CAMK2D*	4.95	7.59	7.6
235251_at	*NA*	5.155	7.965	7.875
222806_s_at	*C11orf30*	3.35	5.18	5.12
201678_s_at	*C3orf37*	4.965	7.535	7.745
208627_s_at	*YBX1*	6.235	9.495	9.725
226331_at	*NA*	4.25	6.45	6.66
227067_x_at	*NBPF1*	4.56	7.17	6.91
237460_x_at	*LOC283551*	2.625	4.005	4.115
231319_x_at	*KIF9*	4.44	6.87	6.85
232441_at	*KRR1*	5.245	8.055	8.185
238756_at	*GAS2L3*	5.045	7.905	7.745

210621_s_at	*RASA1*	5.7	8.86	8.86
243931_at	*CD58*	3.73	5.69	5.9
210375_at	*PTGER3*	5.93	9.14	9.28
222587_s_at	*GALNT7*	3.94	6.16	6.11
231384_at	*NA*	3.72	5.91	5.69
203153_at	*IFIT1*	3.04	4.84	4.64
239863_at	*NA*	3.755	5.735	5.975
211756_at	*PTHLH*	6.485	10.265	9.985
217944_at	*POMGNT1*	4.31	6.88	6.62
223596_at	*SLC12A6*	2.86	4.57	4.39
228314_at	*LRRC8C*	3.315	5.275	5.145
212344_at	*SULF1*	6.245	9.745	9.895
204157_s_at	*KIAA0999*	3.995	6.415	6.165
209755_at	*NMNAT2*	2.1	3.27	3.33
231986_at	*RIMS1*	3.775	6.075	5.835
230645_at	*FRMD3*	6.665	10.725	10.255
222506_at	*LMBR1*	3.18	5.11	4.92
226273_at	*NA*	2.7	4.23	4.29
208699_x_at	*TKT*	3.09	4.93	4.82
242476_at	*NA*	4.42	6.87	7.17
238681_at	*GDPD1*	3.405	5.385	5.425
201009_s_at	*TXNIP*	4.84	7.76	7.64
219816_s_at	*RBM23*	4.485	7.295	6.995
225687_at	*FAM83D*	3.945	6.345	6.255
210236_at	*PPFIA1*	3.075	4.905	4.895
242286_at	*NA*	3.19	5.1	5.08
219558_at	*ATP13A3*	4.775	7.725	7.545
225834_at	*NA*	3.875	6.285	6.135
210563_x_at	*CFLAR*	4.395	7.155	6.985
1556773_at	*PTHLH*	4.64	7.37	7.55
203392_s_at	*CTBP1*	3.295	5.225	5.375

1559954_s_at	*DDX42*	4.415	7.025	7.215
226605_at	*SLC26A1*	4.73	7.75	7.54
211924_s_at	*PLAUR*	4.805	7.705	7.835
224685_at	*MLLT4*	4.42	7.01	7.35
225803_at	*FBXO32*	5.49	8.89	8.97
225926_at	*VTI1B*	3.98	6.6	6.39
228931_at	*COQ4*	4.81	7.87	7.87
229256_at	*PGM2L1*	5.95	9.87	9.66
201191_at	*PITPNA*	4.315	7.075	7.085
211595_s_at	*MRPS11*	3.22	5.27	5.33
203320_at	*SH2B3*	6.19	10.29	10.1
220202_s_at	*RC3H2*	3.66	6.03	6.05
241762_at	*FBXO32*	5.59	9.08	9.46
44065_at	*C12orf52*	3.75	6.33	6.1
202519_at	*MLXIP*	4.7	7.82	7.75
232345_at	*C18orf8*	2.805	4.595	4.735
228507_at	*NA*	5.49	9.02	9.44
212472_at	*MICAL2*	4.825	8.215	8.225
206167_s_at	*ARHGAP6*	4.31	7.16	7.53
218258_at	*POLR1D*	4.26	7.4	7.21
213524_s_at	*G0S2*	4.695	7.995	8.195
221523_s_at	*RRAGD*	3.12	5.38	5.42
222150_s_at	*LOC54103*	3.24	5.62	5.65
201394_s_at	*RBM5*	3.695	6.295	6.605
221667_s_at	*HSPB8*	5.11	8.95	8.91
224461_s_at	*AIFM2*	4.595	8.065	8.075
227006_at	*PPP1R14A*	3.035	5.435	5.235
32094_at	*CHST3*	4.255	7.385	7.635
224252_s_at	*FXYD5*	2.7	4.83	4.73
226278_at	*DKFZp313A2432*	4.365	7.845	7.635
238649_at	*PITPNC1*	4.33	7.71	7.76

237058_x_at	*SLC6A13*	3.55	6.48	6.34
1559067_a_at	*NA*	2.89	5.27	5.23
217901_at	*DSG2*	4.22	7.61	7.71
1564069_at	*NA*	2.545	4.675	4.545
202643_s_at	*TNFAIP3*	3.785	6.935	6.805
204962_s_at	*CENPA*	4.06	7.44	7.36
225328_at	*NA*	5.515	10.095	9.975
200806_s_at	*HSPD1*	3.79	7.11	6.75
206022_at	*NDP*	2.61	4.68	4.9
206298_at	*ARHGAP22*	4.99	9.28	9.14
228981_at	*TMEM169*	2.28	4.13	4.32
225863_s_at	*C19orf12*	3.89	7.37	7.17
224916_at	*TMEM173*	4.215	7.955	7.965
203764_at	*DLG7*	3.8	7.21	7.58
228499_at	*PFKFB4*	3.53	6.98	6.8
206943_at	*TGFBR1*	3.17	6.35	6.03
242389_at	*CROP*	4.125	7.985	8.385
213256_at	*3-Mar*	3.56	6.9	7.26
201695_s_at	*NP*	4.27	8.99	8.67
225345_s_at	*NA*	4.015	8.315	8.405
205282_at	*LRP8*	3.465	7.115	7.375
210367_s_at	*PTGES*	4.415	9.245	9.295
216235_s_at	*EDNRA*	3.355	7.065	7.055
202626_s_at	*LYN*	2.59	5.63	5.42
1552712_a_at	*NMNAT2*	2.665	5.865	5.555
216804_s_at	*PDLIM5*	3.35	7.18	7.24
206300_s_at	*PTHLH*	3.5	7.79	7.38
226368_at	*CHST11*	4.315	9.975	9.345
237563_s_at	*LOC440731*	2.715	6.345	6.335
226372_at	*CHST11*	3.225	7.925	7.395
1563947_a_at	*ERC1*	2.655	6.505	6.245

203066_at	*GALNAC4S-6ST*	3.24	8.21	7.95
231666_at	*PAX3*	2.62	6.72	6.4
212311_at	*KIAA0746*	2.16	5.95	5.89
205419_at	*EBI2*	2.63	8.27	7.79
228640_at	*NA*	2.39	8.05	8.48

Supplementary Table S4 Enrichment in biological process GO-terms (all levels) of upregulated expressed genes (q<0.05 and fold change >2) in SIOD compared to control human skin fibroblasts.

Term	**Count**	**PValue**	**Fold Enrichment**
GO:0009987~cellular process	401	3.81E-06	1.114107687
GO:0008152~metabolic process	292	0.002569399	1.118294973
GO:0044237~cellular metabolic process	265	2.59E-04	1.169510453
GO:0044238~primary metabolic process	265	0.005201134	1.121027209
GO:0043170~macromolecule metabolic process	229	9.89E-04	1.174529652
GO:0044260~cellular macromolecule metabolic process	216	2.30E-04	1.213241719
GO:0060255~regulation of macromolecule metabolic process	128	0.046000907	1.150244646
GO:0019538~protein metabolic process	123	0.001809831	1.281015565
GO:0016043~cellular component organization	115	4.26E-04	1.348248723
GO:0044267~cellular protein metabolic process	113	9.19E-05	1.405245307
GO:0048518~positive regulation of biological process	99	1.77E-04	1.426140875
GO:0048522~positive regulation of cellular process	90	3.81E-04	1.427053403
GO:0048519~negative regulation of biological process	82	0.005801357	1.325318531
GO:0048523~negative regulation of cellular process	75	0.008995627	1.323176524
GO:0006950~response to stress	72	0.033087325	1.251403031
GO:0006996~organelle organization	71	1.58E-04	1.561056908
GO:0007242~intracellular signaling cascade	57	0.022358971	1.329076037
GO:0043687~post-translational protein modification	54	0.023643914	1.337953114
GO:0008219~cell death	51	1.21E-06	2.077331933
GO:0016265~death	51	1.49E-06	2.062985718
GO:0033036~macromolecule localization	49	0.032408923	1.333670117
GO:0051641~cellular localization	47	0.006627596	1.483250465
GO:0016070~RNA metabolic process	45	0.019158633	1.404993409
GO:0042981~regulation of apoptosis	44	0.002250946	1.602733222
GO:0043067~regulation of programmed cell death	44	0.002678309	1.586942747
GO:0010941~regulation of cell death	44	0.002905771	1.58110124
GO:0031325~positive regulation of cellular metabolic process	43	0.016797479	1.431035458

GO:0008104~protein localization	43	0.017376476	1.42779048
GO:0009893~positive regulation of metabolic process	43	0.032409111	1.367330297
GO:0007049~cell cycle	42	0.003465433	1.585083629
GO:0051649~establishment of localization in cell	42	0.016008514	1.443691193
GO:0012501~programmed cell death	41	5.87E-05	1.965202274
GO:0006915~apoptosis	40	9.04E-05	1.945934024
GO:0009057~macromolecule catabolic process	39	0.017024787	1.462440429
GO:0044265~cellular macromolecule catabolic process	38	0.009034006	1.535006439
GO:0015031~protein transport	38	0.01909319	1.460472005
GO:0045184~establishment of protein localization	38	0.021206917	1.447177722
GO:0042127~regulation of cell proliferation	37	0.043581024	1.37686577
GO:0046907~intracellular transport	36	0.005863484	1.604729154
GO:0051246~regulation of protein metabolic process	35	5.15E-04	1.877327375
GO:0010605~negative regulation of macromolecule metabolic process	35	0.042952226	1.396486031
GO:0006396~RNA processing	34	0.001076341	1.820355466
GO:0051603~proteolysis involved in cellular protein catabolic process	34	0.00454528	1.6595574
GO:0044257~cellular protein catabolic process	34	0.005102412	1.651300895
GO:0030163~protein catabolic process	34	0.007935734	1.600859228
GO:0019941~modification-dependent protein catabolic process	32	0.007731843	1.632686108
GO:0043632~modification-dependent macromolecule catabolic process	32	0.007731843	1.632686108
GO:0022402~cell cycle process	30	0.018796618	1.555025153
GO:0043065~positive regulation of apoptosis	29	8.12E-04	1.975123034
GO:0043068~positive regulation of programmed cell death	29	9.10E-04	1.961438579
GO:0010942~positive regulation of cell death	29	9.82E-04	1.95242047
GO:0032268~regulation of cellular protein metabolic process	29	0.003414836	1.79177828
GO:0033554~cellular response to stress	29	0.030924616	1.500535167
GO:0016071~mRNA metabolic process	26	9.13E-04	2.057956712
GO:0006397~mRNA processing	25	2.75E-04	2.280865035
GO:0000278~mitotic cell cycle	25	0.00198551	1.978804531
GO:0051128~regulation of cellular component organization	25	0.02463692	1.598597547
GO:0022403~cell cycle phase	24	0.014968538	1.697756931

GO:0008283~cell proliferation	24	0.025690403	1.612090297
GO:0008380~RNA splicing	23	2.98E-04	2.371778388
GO:0043066~negative regulation of apoptosis	23	0.004995943	1.902782662
GO:0043069~negative regulation of programmed cell death	23	0.005812809	1.87628151
GO:0060548~negative regulation of cell death	23	0.006090459	1.871069617
GO:0007243~protein kinase cascade	21	0.028709615	1.662195806
GO:0006917~induction of apoptosis	19	0.026168464	1.738874481
GO:0012502~induction of programmed cell death	19	0.027214012	1.733457427
GO:0000279~M phase	19	0.033125271	1.691306486
GO:0044419~interspecies interaction between organisms	18	0.01720956	1.862733311
GO:0031399~regulation of protein modification process	18	0.024629861	1.786961108
GO:0010608~posttranscriptional regulation of gene expression	17	0.002389789	2.359560284
GO:0002520~immune system development	17	0.027336969	1.803866739
GO:0051301~cell division	17	0.045796846	1.687685491
GO:0048285~organelle fission	16	0.011981384	2.04620486
GO:0006511~ubiquitin-dependent protein catabolic process	16	0.018921815	1.936284764
GO:0010627~regulation of protein kinase cascade	16	0.02375317	1.881851056
GO:0048534~hemopoietic or lymphoid organ development	16	0.033108102	1.80223428
GO:0080134~regulation of response to stress	16	0.048419471	1.710149317
GO:0007067~mitosis	15	0.018694996	1.996793663
GO:0000280~nuclear division	15	0.018694996	1.996793663
GO:0000087~M phase of mitotic cell cycle	15	0.021450152	1.961136633
GO:0000398~nuclear mRNA splicing, via spliceosome	14	0.002222452	2.679792802
GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	14	0.002222452	2.679792802
GO:0000375~RNA splicing, via transesterification reactions	14	0.002222452	2.679792802
GO:0010035~response to inorganic substance	14	0.023503298	2.000040482
GO:0033043~regulation of organelle organization	14	0.034963921	1.889439165
GO:0010740~positive regulation of protein kinase cascade	13	0.011949331	2.279772405
GO:0051248~negative regulation of protein metabolic process	13	0.026591009	2.03594648
GO:0044087~regulation of cellular component biogenesis	12	0.009309886	2.474899188
GO:0018193~peptidyl-amino acid modification	12	0.022914376	2.169356078

GO:0006979~response to oxidative stress	12	0.024814323	2.142900516
GO:0006457~protein folding	12	0.040034652	1.985512343
GO:0032269~negative regulation of cellular protein metabolic process	12	0.044306334	1.95242047
GO:0051130~positive regulation of cellular component organization	12	0.045797201	1.941633617
GO:0009101~glycoprotein biosynthetic process	11	0.044035898	2.038920111
GO:0070647~protein modification by small protein conjugation or removal	11	0.047264982	2.01343361
GO:0043523~regulation of neuron apoptosis	10	0.003520201	3.254034117
GO:0010038~response to metal ion	10	0.032311256	2.270256361
GO:0030155~regulation of cell adhesion	10	0.044730063	2.137686646
GO:0007005~mitochondrion organization	10	0.04647877	2.122196163
GO:0051640~organelle localization	9	0.013115858	2.86496482
GO:0045937~positive regulation of phosphate metabolic process	9	0.020771924	2.635767635
GO:0010562~positive regulation of phosphorus metabolic process	9	0.020771924	2.635767635
GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	9	0.029700616	2.463334238
GO:0009791~post-embryonic development	8	0.011993542	3.209458307
GO:0007059~chromosome segregation	8	0.020337977	2.892474771
GO:0060191~regulation of lipase activity	8	0.02878751	2.692993752
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	8	0.047622255	2.41536553
GO:0042327~positive regulation of phosphorylation	8	0.047622255	2.41536553
GO:0043524~negative regulation of neuron apoptosis	7	0.00745701	4.019689203
GO:0051592~response to calcium ion	7	0.010715017	3.727348171
GO:0051656~establishment of organelle localization	7	0.029862946	2.971074629
GO:0031349~positive regulation of defense response	7	0.037918032	2.808276019
GO:0000302~response to reactive oxygen species	7	0.04241817	2.733388658
GO:0031647~regulation of protein stability	6	0.013549339	4.183758151
GO:0006944~membrane fusion	6	0.033795482	3.315430987
GO:0042542~response to hydrogen peroxide	6	0.041454286	3.137818613
GO:0016197~endosome transport	6	0.047097032	3.029617971
GO:0000186~activation of MAPKK activity	5	0.009538241	5.857261411
GO:0002831~regulation of response to biotic stimulus	5	0.016095999	5.049363285
GO:0006984~ER-nuclear signaling pathway	5	0.030268257	4.183758151

GO:0002711~positive regulation of T cell mediated immunity	4	0.013178866	7.809681881
GO:0002709~regulation of T cell mediated immunity	4	0.033143367	5.578344201
GO:0048538~thymus development	4	0.037432742	5.324783101
GO:0006829~zinc ion transport	4	0.046814116	4.881051176
GO:0001916~positive regulation of T cell mediated cytotoxicity	3	0.021717286	12.55127445
GO:0002839~positive regulation of immune response to tumor cell	3	0.02831063	10.98236515
GO:0002833~positive regulation of response to biotic stimulus	3	0.02831063	10.98236515
GO:0002834~regulation of response to tumor cell	3	0.02831063	10.98236515
GO:0002836~positive regulation of response to tumor cell	3	0.02831063	10.98236515
GO:0002837~regulation of immune response to tumor cell	3	0.02831063	10.98236515
GO:0001914~regulation of T cell mediated cytotoxicity	3	0.035590042	9.762102351
GO:0009435~NAD biosynthetic process	3	0.035590042	9.762102351
GO:0019359~nicotinamide nucleotide biosynthetic process	3	0.043501312	8.785892116
GO:0001953~negative regulation of cell-matrix adhesion	3	0.043501312	8.785892116

Supplementary Table S5 Enrichment in biological process GO-terms (all levels) of downregulated expressed genes (q<0.05 and fold change >2) in SIOD compared to control human skin fibroblasts.

Term	Count	PValue	Fold Enrichment
GO:0009987~cellular process	494	4.46E-09	1.130839368
GO:0008152~metabolic process	353	0.001386663	1.113882546
GO:0044238~primary metabolic process	333	6.81E-05	1.160661785
GO:0044237~cellular metabolic process	325	1.72E-05	1.181769473
GO:0043170~macromolecule metabolic process	288	8.74E-06	1.217060488
GO:0044260~cellular macromolecule metabolic process	271	1.65E-06	1.254163183
GO:0006807~nitrogen compound metabolic process	181	0.014593108	1.156038785
GO:0034641~cellular nitrogen compound metabolic process	179	0.00724506	1.176908638
GO:0009058~biosynthetic process	169	0.021436468	1.151314386
GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	167	0.008790601	1.182075602
GO:0044249~cellular biosynthetic process	165	0.020140687	1.156721644
GO:0019538~protein metabolic process	155	6.88E-05	1.330062856
GO:0010467~gene expression	153	0.002703185	1.231035986
GO:0009059~macromolecule biosynthetic process	143	0.005928128	1.218424357
GO:0034645~cellular macromolecule biosynthetic process	142	0.00602068	1.218509197
GO:0044267~cellular protein metabolic process	139	6.72E-06	1.424228501
GO:0016043~cellular component organization	132	0.001720248	1.275079551
GO:0048518~positive regulation of biological process	100	0.04314565	1.186911684
GO:0048519~negative regulation of biological process	99	0.002875626	1.318356257
GO:0048522~positive regulation of cellular process	96	0.013345635	1.254180723
GO:0048523~negative regulation of cellular process	92	0.00281572	1.337320564
GO:0006996~organelle organization	88	1.04E-05	1.594168528
GO:0051641~cellular localization	64	6.48E-05	1.664132037
GO:0016070~RNA metabolic process	64	8.77E-05	1.646390757
GO:0033036~macromolecule localization	63	0.004707418	1.412810981
GO:0051649~establishment of localization in cell	59	1.19E-04	1.67096826
GO:0006508~proteolysis	59	0.015287291	1.350725766

GO:0007049~cell cycle	56	6.29E-05	1.741334038
GO:0008104~protein localization	56	0.001470351	1.532058065
GO:0044248~cellular catabolic process	55	0.039031249	1.296040331
GO:0046907~intracellular transport	54	2.30E-06	1.983280646
GO:0015031~protein transport	51	8.20E-04	1.61499428
GO:0045184~establishment of protein localization	51	9.81E-04	1.600293421
GO:0022607~cellular component assembly	49	0.03380139	1.332994151
GO:0009892~negative regulation of metabolic process	48	0.006139044	1.484917817
GO:0009057~macromolecule catabolic process	47	0.009906301	1.452120337
GO:0022402~cell cycle process	46	1.93E-05	1.964559413
GO:0044265~cellular macromolecule catabolic process	46	0.004102933	1.531001474
GO:0010605~negative regulation of macromolecule metabolic process	46	0.005301377	1.512228976
GO:0031324~negative regulation of cellular metabolic process	45	0.006204503	1.508119658
GO:0043067~regulation of programmed cell death	45	0.040055776	1.337248958
GO:0010941~regulation of cell death	45	0.04235056	1.332326569
GO:0051603~proteolysis involved in cellular protein catabolic process	41	0.00198611	1.648877493
GO:0044257~cellular protein catabolic process	41	0.002190998	1.640674122
GO:0030163~protein catabolic process	41	0.003785536	1.590557067
GO:0019941~modification-dependent protein catabolic process	40	0.001617958	1.681527145
GO:0043632~modification-dependent macromolecule catabolic process	40	0.001617958	1.681527145
GO:0006396~RNA processing	39	0.001236903	1.720414381
GO:0006412~translation	38	3.71E-08	2.770201668
GO:0051246~regulation of protein metabolic process	38	0.002198151	1.679371341
GO:0006259~DNA metabolic process	36	0.002058718	1.716752812
GO:0016192~vesicle-mediated transport	36	0.014772651	1.508119658
GO:0000278~mitotic cell cycle	34	2.84E-05	2.217343497
GO:0022403~cell cycle phase	34	2.45E-04	1.981683802
GO:0009890~negative regulation of biosynthetic process	34	0.034713442	1.431792485
GO:0032268~regulation of cellular protein metabolic process	33	0.004526851	1.679930758
GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic a	33	0.013118819	1.555248397
GO:0051172~negative regulation of nitrogen compound metabolic process	33	0.01596552	1.534272022

GO:0010558~negative regulation of macromolecule biosynthetic process	33	0.030433277	1.455735246
GO:0031327~negative regulation of cellular biosynthetic process	33	0.041037632	1.419406737
GO:0051128~regulation of cellular component organization	32	0.004946304	1.685932893
GO:0016071~mRNA metabolic process	31	3.49E-04	2.021695542
GO:0034613~cellular protein localization	31	0.001922284	1.820017884
GO:0070727~cellular macromolecule localization	31	0.002104962	1.806829349
GO:0045595~regulation of cell differentiation	31	0.021870139	1.520380794
GO:0010629~negative regulation of gene expression	31	0.029362287	1.484181251
GO:0006397~mRNA processing	30	6.83E-05	2.255132199
GO:0008380~RNA splicing	29	1.91E-05	2.463970146
GO:0007010~cytoskeleton organization	29	0.014571112	1.604971379
GO:0034621~cellular macromolecular complex subunit organization	28	0.001893405	1.892542316
GO:0016481~negative regulation of transcription	28	0.04203877	1.471977357
GO:0006886~intracellular protein transport	27	0.006916062	1.741999177
GO:0032989~cellular component morphogenesis	26	0.02459913	1.580296669
GO:0000279~M phase	25	0.005188806	1.833580131
GO:0034622~cellular macromolecular complex assembly	24	0.006777963	1.821125625
GO:0043069~negative regulation of programmed cell death	24	0.025433379	1.613141918
GO:0060548~negative regulation of cell death	24	0.026055164	1.608660969
GO:0006325~chromatin organization	24	0.042046722	1.532058065
GO:0044419~interspecies interaction between organisms	23	0.003413072	1.96108846
GO:0007264~small GTPase mediated signal transduction	23	0.008230071	1.819632899
GO:0006519~cellular amino acid and derivative metabolic process	23	0.035545322	1.576670552
GO:0043066~negative regulation of apoptosis	23	0.037848088	1.567762808
GO:0000902~cell morphogenesis	23	0.039923928	1.558955152
GO:0006511~ubiquitin-dependent protein catabolic process	22	0.001119248	2.193628594
GO:0032535~regulation of cellular component size	22	0.004380449	1.95888605
GO:0001501~skeletal system development	22	0.024485677	1.664132037
GO:0006414~translational elongation	21	4.54E-09	5.017110942
GO:0000398~nuclear mRNA splicing, via spliceosome	21	5.04E-06	3.311949053
GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine a	21	5.04E-06	3.311949053

GO:0000375~RNA splicing, via transesterification reactions	21	5.04E-06	3.311949053
GO:0000087~M phase of mitotic cell cycle	20	0.00245136	2.154456654
GO:0044106~cellular amine metabolic process	20	0.049954855	1.582289477
GO:0006605~protein targeting	19	0.003619753	2.132411051
GO:0007067~mitosis	19	0.004602839	2.083947164
GO:0000280~nuclear division	19	0.004602839	2.083947164
GO:0048285~organelle fission	19	0.006936248	2.00204531
GO:0051169~nuclear transport	18	2.93E-04	2.748977605
GO:0030036~actin cytoskeleton organization	18	0.012866985	1.9218516
GO:0030029~actin filament-based process	18	0.022611851	1.80223428
GO:0006913~nucleocytoplasmic transport	17	7.44E-04	2.629541968
GO:0006260~DNA replication	17	0.005577274	2.158992353
GO:0006916~anti-apoptosis	17	0.011730717	1.991303626
GO:0010608~posttranscriptional regulation of gene expression	17	0.014481678	1.944116337
GO:0000904~cell morphogenesis involved in differentiation	17	0.04681793	1.68118257
GO:0051130~positive regulation of cellular component organization	16	0.008244027	2.133031119
GO:0009968~negative regulation of signal transduction	16	0.041107244	1.746962138
GO:0006520~cellular amino acid metabolic process	16	0.048692909	1.708312533
GO:0044087~regulation of cellular component biogenesis	14	0.006020286	2.379005658
GO:0032269~negative regulation of cellular protein metabolic process	14	0.036411103	1.87677113
GO:0051248~negative regulation of protein metabolic process	14	0.047054499	1.806517665
GO:0060348~bone development	13	0.004942309	2.55031617
GO:0048193~Golgi vesicle transport	13	0.008105847	2.394571671
GO:0006417~regulation of translation	13	0.011379132	2.289699919
GO:0051329~interphase of mitotic cell cycle	12	0.003513838	2.811252178
GO:0051325~interphase	12	0.004384042	2.731688437
GO:0001503~ossification	12	0.008055309	2.517904125
GO:0006333~chromatin assembly or disassembly	12	0.01621979	2.279991924
GO:0051493~regulation of cytoskeleton organization	12	0.025568552	2.129110106
GO:0043254~regulation of protein complex assembly	11	0.003970442	2.949211776
GO:0031400~negative regulation of protein modification process	11	0.025700206	2.230496301

GO:0042692~muscle cell differentiation	11	0.028433831	2.193628594
GO:0031398~positive regulation of protein ubiquitination	10	0.007776489	2.872608873
GO:0031396~regulation of protein ubiquitination	10	0.022583441	2.412991453
GO:0007498~mesoderm development	9	0.011191389	2.934719335
GO:0051028~mRNA transport	9	0.027340759	2.496198055
GO:0032956~regulation of actin cytoskeleton organization	9	0.030790635	2.440103717
GO:0065004~protein-DNA complex assembly	9	0.034527709	2.386475063
GO:0032970~regulation of actin filament-based process	9	0.036506704	2.360535117
GO:0009894~regulation of catabolic process	9	0.045181887	2.262179487
GO:0051348~negative regulation of transferase activity	9	0.045181887	2.262179487
GO:0050658~RNA transport	9	0.047544783	2.238858049
GO:0051236~establishment of RNA localization	9	0.047544783	2.238858049
GO:0050657~nucleic acid transport	9	0.047544783	2.238858049
GO:0051168~nuclear export	8	0.01156751	3.217321937
GO:0009116~nucleoside metabolic process	8	0.01616677	3.016239316
GO:0009896~positive regulation of catabolic process	7	0.01508882	3.447130647
GO:0000082~G1/S transition of mitotic cell cycle	7	0.027544912	3.016239316
GO:0030832~regulation of actin filament length	7	0.045400815	2.681101614
GO:0018209~peptidyl-serine modification	6	0.021467463	3.712294543
GO:0006888~ER to Golgi vesicle-mediated transport	6	0.028689536	3.447130647
GO:0030111~regulation of Wnt receptor signaling pathway	6	0.040465698	3.147380156
GO:0009156~ribonucleoside monophosphate biosynthetic process	5	0.013722009	5.245633593
GO:0009161~ribonucleoside monophosphate metabolic process	5	0.018370462	4.825982906
GO:0045732~positive regulation of protein catabolic process	5	0.023889125	4.468502691
GO:0000245~spliceosome assembly	5	0.041676657	3.770299145
GO:0006406~mRNA export from nucleus	5	0.045931594	3.656047656
GO:0046112~nucleobase biosynthetic process	4	0.018232464	6.894261294
GO:0060070~Wnt receptor signaling pathway through beta-catenin	4	0.03107872	5.677626948
GO:0006611~protein export from nucleus	4	0.036177914	5.362203229
GO:0006541~glutamine metabolic process	4	0.041678094	5.079982006
GO:0060260~regulation of transcription initiation from RNA polymerase II promoter	3	0.031246927	10.34139194

GO:0006563~L-serine metabolic process	3	0.040537411	9.048717949
GO:0008535~respiratory chain complex IV assembly	3	0.040537411	9.048717949

Supplementary Table S6 qRT-PCR measurement of mRNA levels of stress response genes in skin fibroblasts of three SIOD patients (SD31, SD120, and SD123) compared to control fibroblasts after 1 hour incubation at 43°C followed by 1 hour of recovery at 37°C.

Gene	**SD31**		**SD120**		**SD123**	
	Fold Change[1]	**p-value**	**Fold Change**[1]	**p-value**	**Fold Change**[1]	**p-value**
ATF6	1.2622	0.135459	1.1527	0.341137	1.1267	0.229573
BAG1	2.8363	0.000352	1.0019	0.966192	3.5748	0.001308
BAG2	2.6069	0.015457	1.3677	0.076477	1.7561	0.005454
BAG3	2.3752	0.005095	1.1335	0.246809	2.1359	0.000965
BAG4	1.7519	0.007574	-1.6417	0.015668	-1.4703	0.04208
BAG5	1.6503	0.000079	-1.3089	0.007806	1.0188	0.713173
CABC1	4.4718	0.00748	-1.1867	0.322074	3.1199	0.002126
CCS	1.6052	0.091673	1.5811	0.033582	1.6779	0.00864
CCT2	1.0555	0.71912	1.2794	0.07323	1.0454	0.731147
CCT3	1.1803	0.371998	1.2696	0.041069	-1.0921	0.802387
CCT4	1.2538	0.291481	1.0296	0.782612	-1.1474	0.155044
CCT5	1.703	0.044326	1.5918	0.021589	2.2955	0.000936
CCT6A	-1.2678	0.182014	1.3918	0.019737	-1.226	0.117257
CCT6B	2.4445	0.008641	2.232	0.003443	2.6615	0.000856
CCT7	1.121	0.318941	1.1537	0.159775	1.0567	0.589396
CRYAA	2.0308	0.031656	-1.6865	0.013274	1.1369	0.397599
CRYAB	2.7728	0.000798	1.1662	0.170989	2.3195	0.000731
DNAJA1	1.8902	0.004721	-1.0411	0.59516	1.4992	0.003205
DNAJA2	1.8288	0.015735	-1.0806	0.533833	1.1494	0.133854
DNAJA3	1.5186	0.086909	-1.3755	0.062798	-1.1313	0.21911
DNAJA4	1.6543	0.04226	1.1148	0.410201	4.9672	0.000418
DNAJC21	1.6838	0.004414	-1.3175	0.01605	1.8026	0.00075
DNAJB1	3.0693	0.003061	-1.3566	0.048129	2.3388	0.000324
DNAJB11	1.256	0.391398	1.556	0.019928	2.1741	0.002693
DNAJB12	1.5516	0.062903	-1.1573	0.2057	-1.0132	0.837028
DNAJB13	4.908	0.011193	2.574	0.008645	1.3815	0.192883
DNAJB14	2.4886	0.009531	-1.216	0.160202	1.3437	0.031363
DNAJB2	1.8237	0.053194	1.7778	0.017276	1.8953	0.006963
DNAJB5	1.5158	0.023366	-1.5119	0.00172	1.1922	0.007919
DNAJB6	2.309	0.013448	-1.2422	0.128193	1.5142	0.011459
DNAJB7	-1.8478	0.122297	-2.4916	0.034937	-11.5765	0.00032
DNAJB8	2.0308	0.031656	-1.6865	0.013274	1.1369	0.397599
DNAJB9	1.6876	0.047743	1.1626	0.134903	1.428	0.214447
DNAJC1	1.24	0.240858	1.066	0.507613	1.5821	0.002946
DNAJC10	2.0484	0.013372	1.2707	0.097916	1.373	0.027786
DNAJC11	1.3614	0.148716	-1.3231	0.129836	-1.0958	0.414228
DNAJC12	4.0663	0.00048	4.9156	0.002463	5.1697	0.000236
DNAJC13	2.8202	0.00894	-1.0573	0.651368	1.8742	0.001514
DNAJC14	1.6656	0.037315	-1.3898	0.060453	-1.0039	0.941755
DNAJC15	1.0088	0.875137	-1.2968	0.048745	1.834	0.001982
DNAJC16	2.0805	0.007253	-1.5147	0.00464	-1.1601	0.244467
DNAJC17	-1.1704	0.550877	-1.0757	0.647931	1.0509	0.727862

Gene	**SD31**		**SD120**		**SD123**	
	Fold Change[1]	**p-value**	**Fold Change**[1]	**p-value**	**Fold Change**[1]	**p-value**
DNAJC18	2.3974	0.000544	1.0137	0.761849	1.2689	0.05454
DNAJC19	2.0104	0.02115	-1.0308	0.732268	1.3744	0.042366
DNAJC3	1.6272	0.0203	-1.0526	0.483296	1.1837	0.045033
DNAJC4	2.1059	0.007588	1.213	0.134052	1.672	0.002261
DNAJC5	1.4992	0.089455	-1.0945	0.556829	1.0841	0.581058
DNAJC5B	-1.7485	0.05082	-13.9052	0.001171	-6.931	0.002672
DNAJC5G	2.7951	0.074388	-2.2499	0.04763	2.627	0.08139
DNAJC6	4.3437	0.002866	-4.2096	0.00158	5.0898	0.000102
DNAJC7	1.4678	0.079094	-1.2378	0.105793	1.0816	0.430962
DNAJC8	2.9316	0.082972	1.1456	0.606909	1.2251	0.402511
DNAJC9	-1.2187	0.059206	-1.297	0.002987	-1.6626	0.000321
HSF1	1.7037	0.001014	1.2039	0.012965	1.693	0.000554
HSF2	3.7187	0.000054	1.1685	0.245527	2.6181	0.000216
HSF4	3.0363	0.000718	1.3445	0.035484	-1.1376	0.042188
HSP90AA1	2.938	0.00552	1.0408	0.692262	3.2181	0.000208
HSP90AB1	2.1555	0.002423	1.0505	0.454187	1.8069	0.000318
HSP90B1	1.3814	0.011546	1.1989	0.025172	1.4283	0.000416
HSPA14	1.1383	0.063373	-1.0317	0.782365	1.1064	0.333144
HSPA1A	2.5847	0.046463	-1.2247	0.344951	2.1791	0.007469
HSPA1B	2.9215	0.005535	-1.4627	0.002436	1.7568	0.00079
HSPA1L	5.5563	0.000001	-1.2233	0.036845	3.9498	0.00004
HSPA2	2.8723	0.007686	-1.1206	0.283253	4.2841	0.000186
HSPA4	2.2979	0.002071	1.0027	0.932654	1.6326	0.007511
HSPA4L	3.8847	0.016677	-1.1327	0.339189	1.761	0.002674
HSPA5	3.8825	0.00498	1.6645	0.002534	7.3608	0.00008
HSPA8	1.5769	0.002565	-1.2295	0.00289	1.1998	0.01201
HSPA9	1.197	0.234855	1.0549	0.51817	-1.3069	0.023021
HSPB1	1.4327	0.141766	1.0467	0.748537	1.4403	0.023439
HSPB2	2.071	0.017525	-1.1902	0.111889	1.5279	0.002922
HSPB3	2.8403	0.014347	-1.5145	0.018669	3.3656	0.000012
HSPB6	-1.0588	0.751031	-1.1489	0.165979	-1.1973	0.092469
HSPB7	14.0196	0.000908	-1.3056	0.047857	3.3633	0.000037
HSPB8	-1.2165	0.248509	-1.0672	0.531006	-2.5981	0.00206
HSPD1	3.1641	0.002914	-1.2302	0.118704	1.6812	0.006083
HSPE1	2.0426	0.000039	1.0677	0.301475	1.6065	0.000192
HSPH1	4.2396	0.001114	1.0436	0.598721	4.093	0.000038
PFDN1	2.8813	0.001943	-1.2699	0.384879	1.2868	0.385838
PFDN2	1.2087	0.320503	1.2494	0.075045	1.3943	0.01892
SERPINH1	1.0267	0.771942	1.4885	0.003026	1.0247	0.744577
SIL1	1.2471	0.001528	1.1006	0.053786	1.1353	0.206732
TCP1	1.7705	0.214631	-1.1336	0.604575	1.0429	0.994102
TOR1A	2.0642	0.016952	1.1888	0.229031	1.7942	0.008074

Key: [1] Fold change of SMARCAL1-deficient fibroblast relative to control fibroblasts.

Supplementary Table S7 Log$_2$ scale value of mRNA expression in *yw, Marcal1*$^{del/del}$, *RpII215*^{4}*/FM7,* and *RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ fly ovaries at 20^{o}C and *yw* and *Marcal1*$^{del/del}$ ovaries at 25^{o}C.

AffyID	*FlyBase*	*yw* (20^{oC})	*Marcal1*$^{del/del}$ (20^{oC})	*RpII215*^{4}*/FM7* (20^{oC})	*RpII215*^{4}*/FM7;Marcal1*$^{del/del}$ (20^{oC})	*yw* (25^{oC})	*Marcal1*$^{del/del}$ (25^{oC})
1638332_at	FBgn0051926	7.78	9.94	7.63	6.62	7.48	10
1624061_at	FBgn0014076	10.66	12.74	11.16	10.32	10.62	12.69
1632351_at	FBgn0041252	9.17	11.19	9.05	7.8	8.44	11.08
1640516_at	FBgn0036938	7.71	9.71	8.19	7.29	7.43	9.33
1639210_at	FBgn0000644	9.05	10.99	9.87	8.95	8.94	10.87
1631343_at	FBgn0029696	7.78	9.72	8.69	6.45	7.42	9.41
1625398_at	FBgn0031754	8.18	10.11	9.32	8.52	8.37	9.39
1637929_a_at	FBgn0052602	8.38	10.28	9.44	7.86	8.14	10.2
1641113_at	FBgn0032789	10.07	11.74	10.52	8.64	9.57	11.82
1634091_at	FBgn0000358	12.38	14.01	11.37	11.95	12.31	13.98
1635548_s_at	FBgn0028536	7.99	9.59	7.34	7.52	6.08	8.32
1637395_at	FBgn0032788	9.51	11.1	9.71	7.86	8.78	11.19
1632106_at	FBgn0039754	7.82	9.31	8.86	7.73	7.44	9.05
1629380_at	FBgn0000356	11.78	13.26	10.63	10.52	11.63	13.33
1631556_at	FBgn0000357	12.15	13.61	10.66	10.24	11.71	13.8
1625897_s_at	---	7.45	8.9	8.17	6.69	6.69	8.92
1634351_at	FBgn0030653	7.31	8.74	7.25	7.67	7.14	8.35
1630377_at	FBgn0051928	8.43	9.81	8.45	7.88	8.28	10.25
1633465_at	FBgn0030043	10.52	11.88	10.9	8.76	9.16	11.4
1623852_at	FBgn0038395	9.75	11.1	10.17	9.51	9.18	11.21
1637407_at	---	8.24	9.57	9.43	8.08	9.06	9.76
1639805_at	---	8.45	9.75	9.11	8.14	8.07	9.8
1636357_at	FBgn0035768	9.86	11.13	10.07	8.85	8.72	11.19
1633471_at	FBgn0033521 /// FBgn003	7.4	8.66	7.71	5.18	7.17	8.06
1624660_at	---	7.05	8.27	7.81	7.78	6.99	7.99
1626846_s_at	FBgn0031914	7.66	8.86	8.44	7.41	6.89	8.62
1629407_at	FBgn0032126	8.27	9.45	9.04	7.4	6.59	8.92
1628474_at	---	8.52	9.69	8.34	7.69	7.74	8.27
1623883_at	---	6.99	8.12	7.27	7.62	7.16	7.9
1627195_at	FBgn0052642	7.29	8.42	6.7	5.78	6.47	8.61
1633305_at	FBgn0039678	7.44	8.52	7.68	7.68	7.56	8.08

1637806_at	FBgn0037661	6.47	7.55	7.16	6.78	7.12	7.82
1632979_at	FBgn0033381	8.96	10.04	10.04	9.94	8.97	9.93
1626467_a_at	FBgn0031111	8.96	10.04	9.42	8.14	7.77	9.96
1627844_at	FBgn0014469	9.41	10.48	10.35	10.31	9.44	10.28
1639036_at	FBgn0033699	8.62	9.69	9.67	8.63	8.67	9.79
1632984_s_at	---	7.18	8.23	7.45	6.76	7.11	7.95
1637707_at	FBgn0038469	8.99	10.05	9.3	7.75	7.27	10.12
1637261_at	FBgn0030045	10.42	11.47	10.13	9.45	8.86	11.51
1626856_at	FBgn0031974	6.95	7.98	8.05	7.83	7.89	8.35
1629229_a_at	FBgn0003507	8.47	9.49	8.91	7.53	7.28	9.28
1629673_at	FBgn0031554	7.19	8.21	7.22	5.44	5.76	7.97
1641158_a_at	FBgn0000427	11.03	12.03	11.15	10.42	10.53	12.1
1627352_at	---	8.27	9.27	9.94	9.03	7.95	9.01
1635576_at	---	9.63	10.61	9.77	8.79	9.29	9.83
1627880_at	FBgn0050334	7.21	8.17	6.14	5.83	7.43	7.45
1637843_at	FBgn0016724	8.84	9.8	7.84	8.07	8.27	8.68
1624810_at	FBgn0052774	8.49	9.45	8.74	6.8	6.4	9.73
1623681_at	FBgn0035697	8.32	9.27	8.61	6.33	6.17	9.28
1635060_at	FBgn0040733	7.71	8.64	7.59	7.34	7.44	8.28
1625651_at	FBgn0031359	6.75	7.67	7.16	7.68	7.19	7.91
1630842_s_at	FBgn0052641	8.83	9.75	8.97	8.99	8.89	9.68
1635503_at	FBgn0003983	13.24	14.13	13.42	13.2	13.22	14.15
1637835_at	FBgn0030510	8.13	9.02	8.16	8.28	8.39	8.89
1631628_s_at	FBgn0033521 /// FBgn003	8.14	9.03	8.67	8.5	8.26	8.42
1630441_at	FBgn0030439	8.06	8.95	8.15	6	6.53	8.46
1625046_at	FBgn0030067	7.82	8.7	9.23	9.05	7.71	9.11
1630767_at	FBgn0051262	8.58	9.46	8.92	9.24	8.94	9.16
1629271_at	FBgn0034494	9.87	10.74	9.91	10.91	9.94	10.75
1641398_s_at	FBgn0034657	8.21	9.07	8.73	9.08	8.32	9.18
1640031_at	FBgn0016122	9.22	10.08	9.64	9.17	9.06	9.92
1632992_at	FBgn0029568	10.43	11.28	10.42	8.73	8.98	11.44
1637731_at	FBgn0030042	9.42	10.27	9.31	7.74	8.07	9.9
1626286_at	FBgn0034495	7.67	8.52	7.4	8.75	7.55	8.3
1635742_s_at	FBgn0036715	7.9	8.74	8.26	7.59	6.73	8.49
1629061_s_at	FBgn0001228	7.46	8.29	8.99	8.4	8.57	8.62
1627171_at	---	9.71	10.54	9.96	9.83	9.93	10.54

1624747_at	FBgn0024920	9.5	10.31	10.21	10.34	9.84	10.33
1634468_at	FBgn0014417	9.27	10.07	9.69	10.11	9.33	10.14
1639035_at	FBgn0030931	6.65	7.45	6.52	7.14	7.38	7.75
1635847_at	FBgn0003979	13.12	13.92	13.52	12.95	12.91	14.08
1639415_at	---	7.56	8.35	7.55	7.17	7.55	7.41
1638233_at	---	9.2	9.98	9.6	9.58	9.1	9.76
1632499_at	FBgn0025390	8.52	9.3	8.28	6.67	7.23	9.23
1631098_at	FBgn0035868	6	6.77	7.15	6.65	7.07	7.35
1623044_at	FBgn0000355	13.42	14.19	12.13	12.9	13.38	14.29
1625075_at	FBgn0027570	7.84	8.61	7.9	6.87	7.01	8.41
1641211_at	FBgn0030044	10.34	11.1	9.54	9.55	8.53	11.26
1627340_at	FBgn0010309	7.89	8.64	8.25	7.96	7.65	8.68
1634658_a_at	FBgn0033765	8.84	9.58	9.56	9.67	8.15	9.13
1625263_at	---	9.44	10.18	10.18	10.43	9.62	10.09
1635173_at	FBgn0031681	7.33	8.07	8.23	7.11	6.61	8.09
1624885_at	---	7.28	8.01	7.41	5.98	6.07	8.17
1629569_at	FBgn0030555	7.24	7.97	6.97	7.39	7.48	7.95
1630539_at	FBgn0034410	7.76	8.48	7.77	8.27	7.7	8.44
1627964_s_at	FBgn0036116	7.2	7.92	7.44	6.42	6.1	7.8
1626088_at	FBgn0039902	7.17	7.88	7.38	7.77	7.44	7.88
1624067_at	FBgn0033887	8.35	9.05	8.54	7.13	7.28	8.76
1637774_s_at	FBgn0034063	8.28	8.98	8.18	8.57	8.17	8.9
1624800_at	FBgn0034354	10.2	10.88	10.4	10.73	9.56	10.07
1634890_at	---	9.55	10.23	9.83	10.04	10.08	10.41
1624729_at	FBgn0005630	6.77	7.45	7.45	7.22	7	7.51
1626442_at	---	9.48	10.15	10.18	9.64	9.7	10
1628759_a_at	FBgn0036814	8.52	9.19	8.62	8.58	8.32	9.26
1640551_at	FBgn0024909	6.6	7.26	6.91	7.06	7.73	7.85
1635928_a_at	FBgn0000489	7.81	8.47	8.58	7.75	7.73	8.36
1628758_at	FBgn0039856	6.57	7.23	7.11	7.9	7.44	7.59
1640112_at	FBgn0004629	9.46	10.12	10	9.28	9.42	9.93
1623569_at	FBgn0015351	6.92	7.55	7.09	7.33	7.04	7.25
1634584_at	---	7.71	8.34	8.15	8.06	8.05	8.34
1635390_s_at	FBgn0032889	8.71	9.34	8.98	9.39	9.14	9.18
1635701_at	FBgn0010039	8.35	8.98	9.03	9.18	9.09	9.6
1631231_at	FBgn0001085	7.96	8.59	8.51	8.41	7.66	8.5

1623364_at	FBgn0034761	8.16	8.79	10.07	8.89	7.82	8.61
1634872_at	FBgn0034266	7.42	8.05	7.53	8.19	7.1	7.7
1635200_at	FBgn0036332	6.03	6.65	6.64	7.04	7.65	7.57
1628114_s_at	FBgn0026379	7.89	8.51	8.34	8.55	8.38	8.81
1636174_at	FBgn0038020	7.17	7.79	7.8	8.5	8.81	8.69
1625658_at	FBgn0031909	8.55	9.16	8.94	9.12	8.98	9.32
1640002_at	FBgn0029924	9.17	9.77	9.12	9.82	8.94	9.28
1641651_at	FBgn0003980	12.83	13.43	12.97	12.33	12.32	13.56
1630593_at	---	7.07	7.66	6.56	6.41	7.13	8.41
AFFX-Dros-1	---	11.36	11.96	11.63	12.48	11.78	12
1625524_at	FBgn0031484	9.21	9.81	9.38	9.81	9.07	9.8
1626103_at	FBgn0000360	13.57	14.16	13.53	12.26	12.51	14.11
1633463_s_at	---	8.43	9.01	8.77	8	8.01	8.99
1637607_at	FBgn0033392	7.56	8.15	8.03	8.2	7.66	8.17
1633861_at	FBgn0037617	7.86	8.44	8.34	7.73	8.32	8.58
1636953_a_at	FBgn0036672	7.36	7.94	8.68	7.31	7.15	8.07
1641206_at	FBgn0015542	7.16	7.73	7.49	7.73	7.23	7.62
1631333_s_at	FBgn0052954	12.28	12.84	12.72	12.74	12.56	12.85
1630942_at	FBgn0034304	7.57	8.13	7.79	8.31	7.82	8.21
1629621_a_at	FBgn0025382	8.14	8.71	7.68	7.85	6.22	7.4
1635125_a_at	---	7.96	8.53	8.42	7.38	7.84	8.65
1630301_at	FBgn0031022	7.32	7.88	7.96	7.97	7.55	8
1640243_at	FBgn0032524	9.69	10.25	10.02	9.6	9.57	10.21
1626133_s_at	---	7.17	7.73	7.1	7.34	6.79	7.78
1635502_at	FBgn0034141	8.88	9.43	9.14	9.16	8.99	9.31
1630019_s_at	FBgn0035289	8.28	8.83	8.94	7.42	7.19	8.73
1641489_at	FBgn0053169	6.79	7.34	7.11	6.78	7.31	7.96
1629973_at	FBgn0038321	7.78	8.32	7.98	7.57	7.34	7.81
1636228_at	FBgn0000359	13.53	14.07	13.42	12.16	12.37	14.04
1634016_at	FBgn0037534	7.78	8.31	8.29	6.99	6.91	8.12
1625162_at	FBgn0035591	7.34	7.88	7.72	7.69	7.37	7.92
1627582_a_at	FBgn0050035	8.3	8.83	9.02	8.59	8.04	8.64
1640957_at	FBgn0041629	7.84	8.37	8.93	8.97	7.6	8.3
1628731_s_at	FBgn0033374 /// FBgn003	10.37	10.9	10.63	10.9	10.39	11.02
1636137_at	FBgn0015582	7.93	8.45	8.26	8.54	8.05	8.41
1634410_at	FBgn0036249	7.73	8.25	8.22	8.83	8.18	8.55

1638845_at	FBgn0037898	7.17	7.68	7.68	7.49	7.13	7.61
1637299_s_at	FBgn0036240	8.43	8.94	8.93	9.33	8.82	9
1633182_at	FBgn0051661	7.96	8.47	7.66	6.42	7.53	9.13
1633833_at	FBgn0038470	8.16	8.67	8.8	9.16	8.79	8.95
1634395_at	FBgn0035328	10.93	11.43	10.62	8.51	8.22	11.53
1623191_at	FBgn0032782	8.53	9.03	8.52	8.67	8.74	9
1627284_at	---	7.82	8.32	7.41	6.31	6.55	8.31
1640101_at	FBgn0034008	8.69	9.18	8.67	9.49	8.43	9.2
1631610_at	FBgn0032079	7.72	8.22	7.98	7.9	7.95	8.38
1639727_at	FBgn0027583	8.54	9.04	8.9	9.21	8.64	9.09
1630870_s_at	FBgn0031878	8.99	9.48	9.32	9.64	9.2	9.44
1637151_at	FBgn0020270	8.9	9.4	9.15	9.04	9	9.25
1633159_at	FBgn0039650	7.09	7.57	7.63	7.86	7.4	7.7
1633135_s_at	FBgn0042174	9.18	9.66	8.88	9.59	10.44	10.67
1638619_s_at	---	6.34	6.83	6.91	7.27	7.23	7.26
1639986_at	FBgn0036478	9.05	9.54	9.52	9.25	9.16	9.63
1635427_a_at	FBgn0026239	7.84	8.32	8.38	8.14	7.72	8.2
1640429_a_at	FBgn0033853	9.14	9.62	9.43	9.36	9.35	9.74
1626708_at	FBgn0020224	10.03	10.5	10.6	9.83	10.02	10.46
1626835_at	---	8.6	9.07	9.12	8.72	8.99	9.47
1639904_at	---	8.04	8.52	8.14	8.21	8	8.22
1625795_a_at	FBgn0034999	8.38	8.85	8.69	9.15	8.56	8.74
1625940_s_at	FBgn0004666	7.58	8.05	7.93	7.62	7.07	7.7
1635773_at	FBgn0035704	7.85	8.33	8.18	8.36	8.07	8.33
1626414_at	---	7.11	7.58	7.64	7.68	7.28	7.76
1625572_s_at	---	7.04	7.51	7.37	7.19	6.54	6.61
1624583_at	---	9.75	10.22	10.51	10.12	9.8	10.35
1637992_at	FBgn0039204	7.93	8.39	8.33	7.83	7.87	8.17
1622971_at	FBgn0034380	8.05	8.51	8.51	8.79	8.14	8.55
1625344_at	FBgn0026718	9.14	9.6	9.71	9.83	9.23	9.84
1633957_s_at	FBgn0038704	7.86	8.32	8.37	8.9	8.22	8.48
1626264_at	FBgn0031435	9.87	10.33	9.86	10.25	9.96	10.49
1630483_a_at	FBgn0035793	7.87	8.33	7.63	7.74	8.03	8.37
1627820_at	FBgn0050096	6.51	6.97	6.49	7.16	7.03	7.39
1624699_s_at	FBgn0000242	8.83	9.29	8.78	9.02	9.05	9.43
1637421_at	FBgn0022702	9.16	9.62	9.37	9.8	9.55	9.76

1624332_s_at	FBgn0027500 /// FBgn003	9.09	9.55	9.15	9.35	8.8	9.59
1624214_at	FBgn0034599	8.2	8.66	8.41	8.63	8.34	8.66
1636296_at	FBgn0037755	7.84	8.3	7.99	8.19	8.1	8.15
1638275_at	FBgn0030311	10.1	10.55	10.28	10.31	10.24	10.65
1627779_at	FBgn0035674	8.67	9.12	8.57	9.01	8.2	8.69
1641320_s_at	FBgn0029896	7.72	8.17	8.27	7.02	6.75	8.17
1635061_at	---	12.95	13.4	13.25	12.85	13.01	13.53
1631617_at	---	7.84	8.29	7.97	7.77	8.02	8.24
1637826_at	FBgn0032727	9.52	9.97	10.3	9.41	9.11	9.84
1623698_s_at	FBgn0015247	9.67	10.11	10.01	10.27	9.98	10.05
1640845_at	FBgn0037046	7.23	7.67	7.41	6.86	4.31	4.66
1632361_at	FBgn0031814	7.86	8.3	7.72	8.05	7.67	8.3
1624387_at	FBgn0050372	7.79	8.24	7.97	8.11	7.72	8.25
1623411_at	FBgn0005630	7.02	7.46	7.18	7.67	7.7	7.71
1628322_at	FBgn0015926	9.56	10.01	9.37	9.88	9.63	9.79
1627323_at	FBgn0034062	7.54	7.98	7.87	7.85	7.8	8.09
1632949_at	---	8.43	8.87	8.54	9.18	8.69	8.89
1626051_at	---	7.81	8.25	8.16	9.09	8.49	8.56
1623300_at	FBgn0035642	7.48	7.91	8.23	8.46	7.67	7.56
1626689_at	FBgn0031182	6.9	7.33	7.79	7.71	7.19	7.38
1636967_a_at	FBgn0038984	8.37	8.8	8.76	8.66	8.1	8.59
1624997_s_at	FBgn0026361	7.68	8.11	7.83	8.27	8.17	8.07
1627134_at	FBgn0026150	8.7	9.13	9.19	9.33	8.92	9.1
1636048_at	FBgn0039403	7.81	8.24	8.38	8.41	8.46	8.5
1636759_at	FBgn0034143	8.62	9.05	9.18	8.39	7.55	8.9
1640965_at	FBgn0037492	6.42	6.85	6.77	6.94	7.04	6.98
AFFX-Dros-1	---	11.88	12.31	12.01	12.67	12.15	12.42
1632876_a_at	FBgn0031319	8.13	8.56	7.74	8.04	7.97	8.38
1633022_at	FBgn0035526	6.86	7.28	7.16	7.48	7.17	7.14
1636899_s_at	FBgn0033448	7.45	7.88	7.89	7.14	7.17	7.75
1639654_at	---	7.77	8.2	8.35	8.47	7.64	8.27
1625113_s_at	FBgn0032363	9.18	9.61	9.7	9.24	9.48	9.93
1625997_s_at	---	8.92	9.35	8.73	6.69	7.88	8.71
1632432_at	FBgn0034903	8.52	8.95	8.2	7.9	7.49	8.83
1628330_at	---	6.89	7.31	6.86	6.94	7.16	7.35
1626820_at	FBgn0038477	7.02	7.44	7.62	8.09	7.39	7.44

1637300_at	FBgn0053199 /// FBgn003	7.51	7.93	8.39	8.14	7.97	8.24
1634052_s_at	FBgn0002781	7.32	7.74	7.31	7.62	7.6	7.98
1629865_s_at	FBgn0030115 /// FBgn003	6.82	7.23	6.95	7.35	7.17	7.13
1631024_s_at	FBgn0031192 /// FBgn003	7.06	7.47	7.35	7.61	7.4	7.38
1631330_at	FBgn0036008	9.11	9.53	9.88	9.99	9.67	9.87
1638783_at	FBgn0031357	9.4	9.81	9.34	9.97	9.47	9.8
1636902_at	---	7.86	8.27	7.94	8.3	8.28	8.13
1636254_s_at	FBgn0038192	8.85	9.26	9.38	9.65	9.14	9.56
1633547_a_at	FBgn0033613	10.27	10.68	11.25	10.79	10.09	10.81
1625722_at	FBgn0031534	9.34	9.76	9.83	10	9.7	9.77
1632283_at	FBgn0034186	7.1	7.52	7.46	7.91	7.47	7.44
1633051_at	FBgn0033374 /// FBgn003	9.66	10.07	9.81	10.12	9.6	10.08
1631188_a_at	FBgn0031762	7.01	7.42	7.31	7	6.59	7.15
1640485_at	FBgn0036142	7.35	7.76	7.64	8.01	7.81	7.84
1639604_at	FBgn0032231	9.57	9.97	9.58	10.26	9.9	9.98
1636815_a_at	FBgn0002973	9.22	9.62	9.67	9.38	9.42	9.68
1633462_at	FBgn0051365	9.21	9.61	9.33	9.24	9.32	9.52
1637570_at	FBgn0033816	8.6	9	9.08	9.09	8.89	9.03
1624550_at	FBgn0010287	8.21	8.61	8.41	8.77	8.56	8.86
1633455_at	FBgn0039702	7.73	8.13	7.65	7.98	7.9	8.14
1623109_at	FBgn0029929	9.57	9.97	9.97	10.15	9.51	10.1
1631777_a_at	FBgn0027342	9.49	9.89	9.85	9.83	9.6	9.93
1624571_s_at	FBgn0042218	10.61	11	10.67	10.9	10.48	10.73
1628796_at	---	6.39	6.79	7.08	6.9	7.26	7.25
1639059_s_at	FBgn0000615	11.7	12.1	11.81	12.06	11.96	12.04
1637197_at	---	8.08	8.48	8.23	8.53	8.4	8.47
1628662_at	FBgn0034786	8.46	8.85	8.57	8.62	8.44	8.69
1635263_at	---	8.41	8.8	8.74	9.19	8.52	8.53
1641700_at	---	7.94	8.33	7.81	7.99	8.24	8.32
1636412_at	FBgn0053208	8.6	8.99	8.91	9.01	9.47	9.62
1638425_at	FBgn0030654 /// FBgn003	7.28	7.66	7.22	7.58	7.31	7.62
1628929_s_at	FBgn0033434	8.98	9.37	9.3	8.99	9.01	9.41
1634549_at	---	10.46	10.84	9.93	10.21	10.43	10.71
1635987_at	FBgn0030041	7.36	7.74	6.49	5.94	6.37	6.86
1623731_at	FBgn0003751	7.24	7.62	7.39	7.73	7.57	7.77
1634428_at	FBgn0032154	8.48	8.86	8.88	9.2	8.7	8.87

1626497_at	---	8.52	8.89	8.62	8.88	8.65	8.99
1624381_at	FBgn0034924	7.97	8.35	7.61	7.56	7.91	8.44
1625044_at	FBgn0031663	9.95	10.33	9.58	10.46	9.87	10.22
1640257_at	FBgn0000326	7.35	7.72	7.75	7.92	7.77	7.85
1636709_at	FBgn0033265	7.18	7.56	7.41	7.49	7.57	7.69
1631419_at	FBgn0004047	12.6	12.97	12.09	11.23	12.01	12.82
1637405_at	---	7.1	7.47	7.51	7.92	7.16	7.18
1627182_at	FBgn0035694	10.92	11.29	11.23	10.42	10.47	11.4
1624200_at	FBgn0032934	7.17	7.54	7.3	7.97	7.53	7.56
1631672_at	FBgn0031421	7.26	7.63	7.05	7.61	7.33	7.62
1631564_at	FBgn0030366	6.97	7.34	7.07	6.97	7.14	7.45
1627315_s_at	FBgn0033075	9.15	9.52	9.45	9.19	9.27	9.57
1623193_at	---	9.47	9.84	9.88	10.12	9.66	9.67
1627786_s_at	---	8.99	9.36	8.71	8.75	8.92	9.25
1638166_at	---	9.65	10.02	10.12	9.59	9.77	10.16
1639117_a_at	FBgn0053096	8.74	9.11	8.72	9.08	8.55	8.78
1634208_a_at	FBgn0004879	8.03	8.39	8.13	8.4	8.25	8.74
1627507_at	FBgn0026570	7.3	7.66	7.72	7.81	7.47	7.83
1635618_at	FBgn0029944	9.57	9.93	9.87	9.94	9.64	10.08
1623682_a_at	FBgn0000253	11.75	12.11	12.05	12.37	11.99	12.23
1633191_at	FBgn0036519	7.34	7.71	7.66	7.84	7.47	7.83
1631208_at	---	8.21	8.57	8.69	8.78	8.39	8.65
1626880_at	FBgn0039691	8.84	9.2	9.4	9.48	9.1	9.17
1639582_at	FBgn0032686	8.77	9.13	9	9.1	8.82	9.22
1624680_a_at	---	7.97	8.32	8.43	8.77	8.37	8.39
1630781_at	FBgn0004811	9.26	9.62	9.28	9.23	9.25	9.62
1627512_at	FBgn0051915	7.7	8.06	8.04	8.25	7.72	8.08
1625968_at	FBgn0031139	9.9	10.26	10.16	9.89	9.79	10.02
1629033_at	FBgn0035204	9.27	9.62	9.53	9.93	9.48	9.6
1629600_at	FBgn0031356	9.13	9.49	9.13	9.31	9.15	9.46
1634349_at	---	9.05	9.41	9.58	9.21	9.24	9.71
1636939_at	FBgn0032728	7.29	7.65	7.75	7.97	7.59	7.75
1634403_at	FBgn0015567	7.3	7.66	8.1	7.52	6.97	7.65
1626182_a_at	FBgn0035945	9.01	9.36	9.2	9.65	9.37	9.51
1639113_at	FBgn0038639	7.98	8.33	8.18	8.28	8.24	8.36
1636919_at	FBgn0002736	10.67	11.02	10.78	11.08	10.36	11.02

1629869_s_at	FBgn0021953	7.13	7.48	7.46	6.76	6.68	7.53
1623088_at	FBgn0035461	7.5	7.85	7.53	8.4	7.88	7.91
1640798_a_at	FBgn0027108	9.65	10	10.25	10.13	9.77	10.55
1622943_s_at	FBgn0030323	8.48	8.82	8.52	9.07	8.66	8.85
1630130_at	FBgn0030432	10.84	11.19	10.8	10.77	10.54	10.99
1634277_at	FBgn0033186	7.07	7.42	7.22	7.62	7.22	7.44
1638252_at	FBgn0010441	8.37	8.72	8.6	8.95	8.78	8.8
1632875_at	FBgn0032705	9.13	9.48	9.33	9.74	9.04	9.38
1627214_s_at	FBgn0036519	6.95	7.29	7.06	7.13	7.11	7.31
1633728_at	FBgn0029825	8.03	8.37	8.04	8.66	7.63	8.05
1636849_at	FBgn0033698	7.94	8.29	8.59	8.43	7.96	8.14
1626850_s_at	FBgn0051953 /// FBgn003	8.44	8.78	8.62	9.06	8.62	8.65
1631062_at	FBgn0037383	7.62	7.96	8	8.13	7.93	8.17
1631037_at	FBgn0030501	9.46	9.8	9.85	9.95	9.65	9.88
1631525_at	FBgn0016970	9.11	9.45	9.15	9.39	9.12	9.34
1629748_s_at	FBgn0037541	6.61	6.95	7.1	7.3	7.02	7.03
1633422_a_at	FBgn0005630	7.25	7.59	7.51	7.84	7.45	7.55
1635762_at	FBgn0034270	8.09	8.43	7.66	7.98	8	8.49
1624275_at	FBgn0016984	7.49	7.83	7.44	7.81	7.54	7.87
1629227_at	---	7.02	7.35	7.77	7.85	7.09	7.48
1640818_at	FBgn0040079	8.98	9.32	9.1	9.34	9.16	9.21
1640240_s_at	FBgn0029763	9.46	9.8	9.97	10.26	9.74	9.97
1627576_at	FBgn0033348	7.93	8.27	8.07	8.54	8.26	8.41
1633727_s_at	FBgn0036896	7.48	7.81	8.11	7.64	7.62	7.96
1636302_s_at	---	7.39	7.73	7.61	7.7	7.05	7.53
1636961_a_at	FBgn0033631	11.1	11.44	11.1	10.95	11.04	11.52
1623536_s_at	FBgn0035542	7.56	7.89	8.22	7.34	7.39	7.82
1641326_at	FBgn0050118	7.62	7.95	8.22	7.94	7.44	7.85
1639185_at	FBgn0023509	6.77	7.1	7.44	7.53	7.21	7.34
1630786_at	FBgn0023395	8.77	9.11	8.87	9.41	9.1	9.26
1624010_a_at	FBgn0033607	7.67	8	7.99	8.33	8.11	8.15
1636244_s_at	FBgn0038803	10.15	10.48	10.72	10.32	9.88	10.66
1625354_at	FBgn0015571	7.75	8.09	7.98	7.76	7.67	7.79
1640060_at	FBgn0053096	9.02	9.35	8.98	9.22	8.79	8.92
1631614_at	FBgn0034351	7.86	8.2	8.11	8.19	7.84	8.32
1625310_at	FBgn0036565	8.16	8.49	8.12	8.44	8.49	8.75

1623179_at	FBgn0031549	7.39	7.72	7.89	8.14	7.67	7.66
1624302_at	FBgn0039730	8.39	8.72	8.14	8.52	8.36	8.74
1633384_at	FBgn0032921	9.01	9.34	9.18	9.19	8.99	9.42
1636929_at	---	7.81	8.14	8.31	8.44	8.25	8.35
1623505_s_at	---	12.84	13.17	12.59	12.92	12.77	12.96
1640554_at	FBgn0002781	7.56	7.89	7.34	7.65	7.55	7.81
1635945_at	FBgn0031439	7.56	7.88	7.74	7.58	6.82	7.65
1630005_at	---	12.29	12.62	11.79	12.07	12.12	12.36
1627460_at	FBgn0033683	9.85	10.18	9.84	9.81	9.74	9.88
1625759_at	FBgn0041627	7.43	7.75	7.72	8.39	7.82	7.37
1640327_at	FBgn0030912	6.91	7.24	7.54	8.26	7.07	7.01
1641532_at	---	8.62	8.95	9.49	9.65	8.89	9.13
1625348_s_at	FBgn0031664	8.78	9.1	9.09	9.52	9.14	9.1
1627431_at	FBgn0034009	8.42	8.75	8.51	8.55	8.5	8.96
1639318_at	---	9.98	10.31	10.19	10.27	9.88	10.1
1640096_at	---	8.01	8.33	8.08	8.22	8.11	8.22
1632946_at	---	9.96	10.28	9.97	10.31	10.29	10.34
1626702_at	FBgn0027343	6.74	7.06	6.89	6.82	7.16	7.29
1633557_at	FBgn0036569	7.06	7.38	7.29	7.26	7.23	7.38
1623404_at	FBgn0028932	7.13	7.45	7.75	7.46	7.38	7.64
1634041_at	---	9.99	10.31	10.43	10.35	10.16	10.29
1640431_at	FBgn0011774	8.67	8.99	8.75	9.29	8.97	9.08
1631099_at	FBgn0034748	7.78	8.1	8.15	8.44	8.12	8.12
1625367_at	FBgn0037734	6.96	7.28	7.24	7.49	7.23	7.42
1625083_at	FBgn0004400	8.79	9.11	9.34	9.1	9.05	9.12
1633716_at	FBgn0032845	7.32	7.64	7.62	7.74	7.6	7.84
1641055_at	FBgn0001224	7.59	7.91	7.26	7.55	9	8.94
1627278_s_at	FBgn0031187	7.58	7.9	8.21	8.17	7.88	8.03
1640665_at	FBgn0036192	7.24	7.56	7.29	7.5	7.29	7.53
1626215_at	FBgn0030240	7.34	7.66	6.96	7.3	7.24	7.46
1639916_at	FBgn0035276 /// FBgn003	7.42	7.74	7.64	7.51	7.68	7.71
1623037_a_at	FBgn0025698	8.55	8.86	9.08	8.96	8.49	8.64
1624970_s_at	FBgn0001980	8.68	9	9.14	9.32	8.99	9.01
1638621_at	FBgn0051648	8.21	8.52	8.43	8.93	8.41	8.6
1623985_at	---	8.71	9.02	8.82	9.03	8.92	9.19
1638352_at	FBgn0035073	7.33	7.64	7.69	8.05	7.55	7.57

1636660_at	FBgn0038446	9.41	9.73	9.6	9.83	9.66	9.72
1624156_at	FBgn0040259	8.29	8.6	8.89	9.04	8.65	8.81
1630640_at	FBgn0032161	8.33	8.64	8.32	9.11	8.47	8.62
1635088_at	FBgn0029975	10.7	11.01	10.62	10.59	10.61	10.88
1634165_at	FBgn0040364	7.71	8.02	8.53	7.23	7.09	7.59
1623022_at	FBgn0035312	7.83	8.14	7.73	8.44	7.77	8.35
1635997_a_at	FBgn0031842	9.66	9.97	9.52	9.61	9.48	10
1641360_at	FBgn0036356	8.58	8.89	8.5	8.86	8.7	8.8
1632837_at	FBgn0030008	7.26	7.57	7.29	7.62	7.71	7.65
1639085_at	FBgn0031972	7.79	8.1	7.75	8.24	7.94	8.14
1637336_at	FBgn0038974	7.5	7.81	7.96	8.3	7.9	7.93
1633766_at	FBgn0036564	7.76	8.07	7.72	8.24	7.82	7.83
1631342_at	FBgn0023212	10.42	10.72	10.45	10.58	10.57	10.84
1623058_at	---	8.7	9	9.01	8.87	8.9	9.1
1639937_at	FBgn0001995	9.75	10.05	9.94	9.97	9.9	10.09
1636805_a_at	FBgn0030680	7.72	8.02	7.55	7.54	7.64	8.14
1625919_at	FBgn0033549	9.15	9.45	8.89	9.42	9.02	9.28
1624897_at	---	8.33	8.63	8.01	8.24	8.24	8.73
1630409_at	FBgn0030500	9.07	9.37	9.38	9.79	9.4	9.31
1639398_at	FBgn0015240	8.98	9.29	9.12	9.26	9.09	9.3
1635368_at	FBgn0040366	7.87	8.17	8.1	8.44	8.32	8.47
1627257_at	FBgn0038763	8.93	9.23	8.92	8.94	9.04	9.26
1638410_at	FBgn0032644	9.06	9.36	9.26	9.52	9.19	9.38
1628492_at	FBgn0000109	8.58	8.88	8.69	8.9	8.69	8.97
1628788_a_at	FBgn0000499	8.87	9.17	8.8	9.09	9	9.07
1627665_at	FBgn0032997	9.69	9.98	9.92	10.17	10.01	10.14
1631034_at	---	10.56	10.86	10.41	10.94	10.8	10.88
1637768_at	FBgn0050100	8.26	8.56	9.03	9.22	8.45	8.73
1627646_at	---	8.22	8.51	8.58	8.69	8.57	8.71
1641097_at	FBgn0031379	8.3	8.6	8.51	8.77	8.42	8.69
1632352_a_at	FBgn0050007	6.93	7.23	7.08	7.39	7.12	7.14
1627956_x_at	FBgn0031054	6.84	7.14	6.78	7.22	7.03	7.4
1639048_a_at	FBgn0053199 /// FBgn003	7.42	7.72	8.34	7.99	7.79	8.2
1630808_at	---	9.21	9.5	9.53	9.6	9.77	9.78
1626323_s_at	FBgn0030205	10.11	10.4	10.39	10.37	10.23	10.52
1639946_at	FBgn0037880	8.21	8.5	8.18	8.51	8.2	8.39

1636736_s_at	---	7.77	8.06	7.3	7.56	8.03	8.06
1637444_s_at	FBgn0037822 /// FBgn002	8.22	8.51	7.88	8.36	8.3	8.41
1639592_at	FBgn0034724	8.29	8.58	9.09	8.26	7.93	8.52
1629709_at	FBgn0025874	8.01	8.31	8.19	8.59	8.32	8.38
1630411_at	FBgn0034527	8.1	8.4	8.37	8.23	8.25	8.59
1636574_s_at	FBgn0053056	7.71	8	7.56	7.47	7.84	8.07
1627052_at	FBgn0029936	7.68	7.97	7.85	8.51	8.05	7.94
1635849_at	FBgn0037251	9.35	9.65	9.09	9.24	9.15	9.46
1624565_a_at	FBgn0036032	7.46	7.75	7.44	7.71	7.51	7.67
1625283_at	FBgn0002781	7.13	7.42	7.19	7.48	7.31	7.44
1628037_at	FBgn0044030	6.9	7.19	7.37	7.43	7.19	7.13
1632151_at	FBgn0034817	7.94	8.23	8.53	8.26	8.05	8.13
1629145_at	FBgn0031107	7.6	7.89	8.06	7.9	7.98	8.07
1630414_at	FBgn0039135	10.02	10.31	9.87	10.28	10.47	10.38
1632011_at	---	8.97	9.25	8.59	8.73	9.18	9.16
1629408_s_at	FBgn0050387	8.78	9.06	9.19	9.23	8.82	9.25
1629879_at	FBgn0034523	7.15	7.44	7.64	8.02	7.8	7.46
1634767_at	FBgn0038407	8.6	8.89	9.18	8.8	8.1	8.83
1629894_at	FBgn0029913	7.67	7.95	7.48	7.65	7.79	7.91
1628456_at	---	7.77	8.06	7.86	8.36	7.84	8.02
1638663_at	FBgn0026571	10.55	10.83	10.92	10.52	10.41	10.73
1623358_at	FBgn0050381	7.46	7.74	7.41	7.41	7.57	7.67
1638217_at	FBgn0032799	9.81	10.09	10	10.12	9.88	10.03
1634814_at	FBgn0035877	7.4	7.69	7.75	7.64	7.38	7.55
1641655_at	FBgn0035334	9.62	9.9	9.97	10.06	9.92	9.92
1632672_at	FBgn0034083	8.31	8.59	8.41	7.72	8.16	8.56
1635222_at	FBgn0033463	6.9	7.19	7.26	7.44	7.27	7.27
1633523_at	FBgn0036271	8.43	8.71	8.39	8.58	8.43	8.61
1633448_at	FBgn0031640	8.3	8.58	8.17	8.7	8.39	8.49
1624181_at	FBgn0028469	9.58	9.86	9.52	9.55	9.52	9.63
1638933_at	FBgn0002901	7.95	8.23	8.02	8.45	8.19	8.27
1634001_at	FBgn0033607	8.93	9.21	9.32	9.52	9.29	9.4
1628438_at	FBgn0031752	7.42	7.7	7.6	7.72	7.64	7.83
1624247_at	FBgn0034908	7.28	7.56	7.67	7.74	7.57	7.58
1640930_at	FBgn0026317	9.02	9.3	9.34	9.37	9.3	9.5
1625183_at	FBgn0016930	7.13	7.41	7.09	6.71	6.84	7.2

1623993_at	FBgn0031287 /// FBgn003	7.81	8.09	7.96	8.77	8.08	8.08
1637133_x_at	FBgn0035552	8.28	8.56	8.31	7.71	7.96	8.66
1628638_at	FBgn0032671	9.01	9.29	9.18	9.31	9.13	9.3
1641253_at	FBgn0003501	9.5	9.78	9.5	9.47	9.35	9.63
1638935_at	FBgn0038099	10.12	10.4	10.18	10.4	10.26	10.35
1629725_at	FBgn0038270	7.66	7.94	7.72	7.89	8.09	8.22
1630824_a_at	FBgn0053145	9.05	9.33	9.26	9.74	9.18	9.47
1638112_at	FBgn0030274	8.88	9.16	9.1	9.38	9.22	9.36
1639346_at	FBgn0031815	8.69	8.97	8.75	9.12	8.96	9.23
1638244_s_at	FBgn0036043	8.78	9.06	8.72	9.31	8.49	8.96
1631363_at	FBgn0031886	8.96	9.24	9.02	9.69	9.19	9.34
1635754_at	---	9.21	9.49	9.58	9.38	9.4	9.68
1634193_at	FBgn0032251	8.53	8.8	8.61	8.86	9.01	9.19
1629691_at	FBgn0039358	10.14	10.42	10.42	9.6	10.43	10.42
1623725_at	FBgn0030995	7.46	7.74	7.37	7.61	7.38	7.35
1630537_a_at	---	9.02	9.3	8.97	9.06	9.15	9.35
1624580_at	FBgn0037696	7.6	7.88	7.8	8.1	7.85	7.93
1623552_s_at	FBgn0040030	9.64	9.91	9.84	9.92	9.35	9.41
1623873_at	FBgn0045073	10.12	10.39	10.25	10.47	10.22	10.34
1633436_at	FBgn0036105	7.38	7.65	7.16	7.54	7.83	7.9
1632731_at	FBgn0033924	8.15	8.42	8.26	8.76	8.37	8.61
1625731_at	FBgn0032127	10.51	10.79	10.31	8.19	8.18	10.68
1635874_at	FBgn0031265	7.21	7.48	7.59	7.31	7.3	7.35
1638897_at	FBgn0035027	8.59	8.86	8.95	9.07	8.85	8.87
1626123_at	---	7.59	7.86	7.14	7.09	7.63	7.7
1632281_at	FBgn0034598	8.41	8.68	8.69	8.6	8.53	8.96
1638278_s_at	FBgn0010246	7.36	7.64	8.31	7.77	6.98	7.72
1629427_at	FBgn0035942	7.56	7.83	7.58	7.97	7.73	7.75
1637397_a_at	FBgn0039206	7.66	7.93	7.72	7.8	7.97	7.98
1630884_at	---	10.31	10.58	10.42	10.64	10.63	10.79
1637547_at	FBgn0037709	9.08	9.35	9.45	9.4	9.1	9.28
1623769_at	FBgn0030968	8.11	8.38	8.25	8.13	8.16	8.4
1635013_s_at	FBgn0032848	7.82	8.09	8.05	8.27	8.08	8
1640280_at	FBgn0005630	7.92	8.19	8.1	8.29	7.86	8.07
1637175_at	FBgn0037356	9.2	9.47	9.06	9.23	9.22	9.32
1633836_a_at	FBgn0010470	9.81	10.08	10.39	9.6	9.1	10.03

1630542_at	FBgn0037382	8.31	8.58	8.61	8.75	8.54	8.52
1622968_at	---	7.75	8.02	8.12	8.23	7.96	7.93
1625747_at	FBgn0038747	9.34	9.61	9.44	9.57	9.39	9.73
1631784_at	FBgn0039291	9.02	9.28	8.97	9.51	9.12	9.24
1625879_at	FBgn0032884	9.33	9.6	9.63	9.67	9.51	9.91
AFFX-Dros-G	FBgn0001092	12.67	12.94	12.95	13.12	13.02	13.1
1628111_at	---	8	8.27	8.23	8.63	8.33	8.42
1639265_at	FBgn0039766	7.89	8.15	8.11	8.63	8.01	8.17
1635729_a_at	FBgn0003138	8.63	8.9	8.94	9.29	8.73	8.8
1627154_at	FBgn0034945	8.56	8.83	8.8	9.01	8.95	8.98
1640326_at	---	7.26	7.53	7.18	7.21	7.41	7.61
1635302_at	FBgn0002878	8.19	8.46	8.14	8.69	8.39	8.48
1635664_at	FBgn0011566	7.58	7.84	7.64	7.61	7.76	7.82
1623881_s_at	FBgn0029783	7.64	7.9	7.81	8.24	8.1	8.11
1640110_at	FBgn0030266	6.8	7.06	7.08	6.87	7.05	7.06
1635526_at	---	7.22	7.48	7.23	7.59	7.66	7.56
1640805_at	FBgn0033718	7.91	8.18	8.16	8.21	8.19	8.09
1628791_at	FBgn0035270	7.2	7.47	7.28	7.5	7.22	7.49
1629923_at	FBgn0031710	7.69	7.95	7.75	7.72	7.6	7.74
1623209_at	FBgn0036386	7.33	7.6	7.43	7.81	7.43	7.64
1640405_at	FBgn0010497	10.93	11.19	11.27	11.28	11.09	11.19
1635560_at	FBgn0032285	7.7	7.97	7.6	7.94	7.76	8.13
1641576_a_at	FBgn0038344	7.05	7.31	7.63	7.61	7.33	7.4
1625026_at	FBgn0040609	8.03	8.29	7.25	7.58	7.99	7.66
1633254_at	FBgn0032020	8.96	9.22	9.27	9.23	9.08	9.39
AFFX-r2-Bs-t	---	7.02	7.29	6.97	7.33	7.21	7.02
1638215_at	FBgn0037610	8.25	8.51	8.24	8.24	8.71	8.62
1625568_a_at	FBgn0034419	9.14	9.4	9.39	9.49	9.46	9.63
1636960_a_at	FBgn0033522	9.15	9.41	9.57	9.37	9.13	9.46
1628138_s_at	FBgn0029525	7.38	7.64	7.61	7.38	7.51	7.52
1634314_s_at	FBgn0001248	11.21	11.47	11.5	11.4	11.15	11.18
1639752_at	FBgn0030766	8.37	8.63	8.24	8.42	8.57	8.86
1632485_a_at	FBgn0015772	8.35	8.61	8.58	8.31	8.32	8.58
1624226_at	FBgn0038055	8.13	8.39	8.21	8.27	8.35	8.37
1638963_s_at	FBgn0034091	9.92	10.18	10.28	10.34	9.96	10.12
1628249_at	FBgn0036118	7.71	7.97	8.28	8.45	7.85	7.88

1626379_a_at	FBgn0040009	7.99	8.25	8.1	8.43	8.4	8.42
1628458_at	---	8.57	8.83	8.62	8.97	8.99	9.16
1635444_at	---	9.03	9.29	8.95	9.15	9.02	9.19
1633166_at	FBgn0033569	9.15	9.41	9.53	9.74	9.39	9.42
1628985_a_at	FBgn0013759	8.47	8.72	8.35	8.68	8.45	8.73
1628148_at	FBgn0025549	9.68	9.94	9.78	9.91	9.72	9.79
1623847_at	FBgn0034425	8.82	9.08	8.99	9.33	9.04	9.09
1628198_at	FBgn0002989	8.23	8.49	8.26	8.36	8.16	8.48
1641451_at	FBgn0035964	9.09	9.35	8.91	8.92	8.9	8.82
1631880_at	FBgn0030361	7.18	7.44	7	7.4	7.3	7.48
1622992_at	FBgn0002673	8.99	9.25	8.74	9.26	9.07	9.47
1628977_at	FBgn0034763	6.88	7.13	7.44	7.47	7.64	7.89
1626456_at	FBgn0052701	9.36	9.61	10.22	9.88	9.24	9.57
1630975_at	FBgn0030189	7.16	7.41	7.02	6.79	7.37	7.44
1637537_at	FBgn0000464	7.43	7.69	7.33	7.36	7.41	7.68
1633055_at	FBgn0031395	9.22	9.48	9.22	9.31	9.25	9.51
1641224_s_at	FBgn0030421	7.51	7.76	7.66	8.04	7.84	8
1623430_at	FBgn0019948	6.92	7.17	6.88	7.12	7.33	7.32
1639785_s_at	FBgn0015930	10.49	10.74	10.41	10.32	10.19	10.57
1635130_a_at	FBgn0019932	9.31	9.56	9.51	9.49	9.48	9.59
1641342_at	---	8.54	8.79	8.67	8.64	9.06	9.2
1633691_at	---	7.5	7.75	7.59	7.95	7.61	7.79
1626520_at	FBgn0025808	8.18	8.44	8.2	8.56	8.41	8.64
1634258_at	FBgn0002781	8.62	8.88	8.62	9.14	8.83	8.96
1639471_s_at	---	9.83	10.08	10.02	10.13	9.95	9.99
1635449_s_at	FBgn0000454	12.04	12.29	12.42	12.38	12.2	12.18
1637190_at	FBgn0035203	9.78	10.03	9.84	10.14	10.05	10
1637479_at	FBgn0003116	8.57	8.82	8.66	8.96	8.67	8.65
1623885_at	FBgn0015568	8.86	9.11	9.25	9.35	9.1	9.15
1640079_at	FBgn0028434	8.3	8.55	8.21	8.57	8.3	8.58
1630763_at	FBgn0035099	7.01	7.26	6.62	6.55	6.8	7.37
1623602_a_at	FBgn0014007	7.89	8.14	7.57	7.91	7.67	8.11
1637602_at	FBgn0023511	7.78	8.03	7.82	7.86	8.01	8.12
1630503_at	FBgn0038349	8.84	9.09	9.09	9.09	8.89	8.94
1629695_at	FBgn0038739	10.13	10.38	10.09	10.32	10.14	10.62
1627489_a_at	FBgn0034638	8.61	8.86	8.36	8.67	8.36	8.78

1635482_at	FBgn0031633	9.13	9.38	8.96	9.76	9.29	9.33
1632827_a_at	FBgn0004698	9.63	9.88	9.73	9.98	9.65	9.76
1624230_s_at	FBgn0003943	12.07	12.32	11.84	12.51	12.17	12.28
1634729_at	FBgn0032760	8.09	8.34	7.98	7.99	7.97	8.15
1626933_s_at	FBgn0035205	8.43	8.68	8.92	8.82	8.6	8.58
1637194_at	FBgn0034876	9.76	10.01	9.7	9.68	9.77	9.94
1630306_at	FBgn0035528	9.96	10.21	9.97	10.1	9.9	10.11
1633643_a_at	---	8.57	8.82	8.77	9.04	8.73	8.84
1639689_at	FBgn0002948	9.76	10.01	9.88	10.25	9.93	10.03
1631092_at	FBgn0037606	8.48	8.73	8.65	8.84	8.84	8.8
1638480_at	FBgn0014022	8.29	8.53	8.32	8.37	8.42	8.68
1640582_at	FBgn0035995	9.01	9.26	9.24	9.27	9.21	9.29
1639074_at	FBgn0035802	8.79	9.04	9.05	9.06	8.42	8.91
1637263_at	FBgn0038996	8.94	9.18	9.25	9.51	9.3	9.35
1641124_at	---	8.92	9.17	9.09	9.26	8.93	9.25
1636579_s_at	FBgn0004797	8.58	8.83	8.47	8.35	8.25	8.52
1638635_at	FBgn0035892	8.06	8.3	8.09	8.25	8.34	8.5
1626571_at	FBgn0035838 /// FBgn002	7.87	8.12	8.21	8.21	8.21	8.24
1635939_a_at	FBgn0031483	10.44	10.68	10.76	11.06	10.38	10.77
1632543_at	FBgn0033639	7.41	7.65	7.68	7.51	7.32	7.47
1624806_at	FBgn0041709	11.78	12.02	11.23	9.04	9.16	12.08
1625269_at	FBgn0035336	8.07	8.32	8.4	8.21	8.24	8.3
1628353_at	FBgn0001149	13.1	13.34	13.04	13.6	13.37	13.38
1639890_at	FBgn0039970	10.87	11.12	10.92	11.47	11.37	11.36
1626300_at	FBgn0031098	9.21	9.45	9.2	9.45	9.52	9.7
1637763_a_at	FBgn0033673	8.67	8.92	8.56	8.88	8.78	8.87
1635165_a_at	FBgn0035227	7.28	7.52	7.39	7.59	7.39	7.54
1636909_at	FBgn0029798	8.07	8.31	7.7	8	8.09	8.25
1630274_s_at	FBgn0035232	7.39	7.63	7.7	7.63	7.37	7.61
1639994_at	FBgn0029874	7.82	8.06	7.71	7.63	7.74	8.06
1633186_s_at	FBgn0035207	8.25	8.49	8.48	8.64	8.37	8.52
1638994_at	FBgn0036298	9.81	10.05	10.19	10.38	10.3	10.25
1641365_s_at	---	9.41	9.66	9.85	8.48	8.55	9.46
1626306_at	FBgn0026181	7.47	7.71	7.72	7.79	7.88	7.96
1636311_at	FBgn0001128	8.36	8.6	7.91	7.79	7.98	8.45
1626476_at	FBgn0051457	9.12	9.36	9.31	9.58	9.49	9.42

1627246_at	FBgn0020388	8.94	9.18	8.98	9.33	9.08	9.04
1629949_at	FBgn0037244	10.55	10.79	10.61	10.74	10.7	10.85
1635260_at	FBgn0027363	8.84	9.08	9.01	9.32	8.88	9.09
1625258_at	---	9.03	9.27	9.12	9.6	9.19	9.39
1629634_at	FBgn0029985	7.55	7.79	7.42	7.78	7.47	7.46
1625814_at	---	8.77	9.01	8.77	8.8	8.89	9.05
1639810_at	FBgn0004556	8.14	8.38	8.61	8.56	8.3	8.48
1628536_s_at	FBgn0039637	8.97	9.21	9.28	9.16	8.41	9.12
1624502_a_at	FBgn0037467	7.59	7.83	8.01	7.83	7.25	7.58
1629374_at	FBgn0004797	8.18	8.42	8.43	8.65	8.4	8.49
1623401_a_at	FBgn0033998	7.2	7.43	7.83	8.08	7.53	7.36
1633586_at	FBgn0036255	8.86	9.1	9.08	9.45	9.02	9.03
1627497_at	FBgn0035631	11.07	11.31	11.22	11.33	11.15	11.25
1631130_at	FBgn0038855	9.14	9.38	9.26	9.32	9.28	9.29
1636868_at	FBgn0032378	8.89	9.13	8.87	8.87	8.86	9.19
1638779_at	FBgn0043472	9.82	10.06	9.9	10.18	10.1	10.18
1634217_s_at	FBgn0024811	10.6	10.84	10.88	10.87	10.86	10.97
1633390_at	FBgn0030702	8.47	8.71	8.47	8.04	8.51	8.82
1631822_at	---	8.23	8.47	8.17	7.8	8.11	8.43
1637387_s_at	FBgn0013334	7.51	7.74	7.73	7.77	7.41	7.36
1638460_s_at	FBgn0031066 /// FBgn004	7.18	7.42	7.02	7.21	6.88	7.13
1631264_at	FBgn0035211	8.05	8.29	8.03	7.97	8.15	8.3
1635290_at	FBgn0024360	8.96	9.19	9.1	9.37	9.13	9.15
1623327_at	---	7.04	7.27	7.28	7.98	7	7.04
1626659_at	FBgn0039558	8.36	8.59	8.72	9.12	8.54	8.64
1635747_at	---	7.16	7.4	7.17	7.28	7.28	7.19
1626841_s_at	FBgn0000317	9.27	9.51	9.3	9.13	9.21	9.54
1639047_at	FBgn0043884	9.75	9.99	9.91	9.73	9.85	10.46
1638122_a_at	FBgn0031395	7.07	7.31	6.7	6.93	7.24	7.45
1623031_a_at	FBgn0040290	8.42	8.65	8.59	8.77	8.76	8.64
1638286_at	FBgn0005683	8.66	8.9	8.59	8.83	8.98	9.06
1636625_at	FBgn0034098	9.69	9.92	9.64	9.91	9.8	10.02
1624673_at	FBgn0032157	8.36	8.59	8.72	8.97	8.76	8.71
1640424_at	FBgn0037535	8.85	9.09	8.52	8.68	9.01	9.18
AFFX-r2-Bs-	---	7.46	7.69	7.79	8.26	7.49	7.4
1630369_a_at	FBgn0029867	10.24	10.47	10.39	10.6	10.51	10.55

1623403_s_at	FBgn0015024	10.6	10.83	11.05	10.94	10.69	11.1
1624320_at	FBgn0002707	6.91	7.14	7.16	7.23	7.4	7.43
1639825_at	---	8.59	8.82	8.18	9.63	6.48	7.42
1635713_at	FBgn0033661	8.9	9.13	9.33	8.68	8.88	9.2
1637264_at	FBgn0002924	8.85	9.08	9.07	9.28	9.16	9.09
1640131_a_at	FBgn0037897	8.62	8.85	8.63	8.59	8.67	8.71
1636673_s_at	FBgn0003870	7.95	8.18	8.44	7.88	7.62	8.21
1638167_at	FBgn0035155	8.57	8.8	8.3	8.35	8.3	8.67
1625813_at	FBgn0026573	7.12	7.35	6.97	7.22	7.02	7.12
1623830_at	FBgn0033890	8.89	9.12	8.98	9.33	9.29	9.22
1629794_at	FBgn0031872	8.39	8.62	8.14	8.69	8.55	8.78
1639587_s_at	FBgn0037144	8.56	8.79	8.51	8.76	8.91	8.87
1638763_at	FBgn0052030	7.27	7.5	7.61	7.84	7.55	7.61
1637160_at	FBgn0036908	9.95	10.18	10.19	10.16	10.12	10.22
1628382_at	FBgn0024285	9.49	9.72	9.94	10.09	9.76	9.82
1637226_at	---	9.31	9.53	9.77	9.9	9.46	9.49
1633294_at	FBgn0034931	7.67	7.9	6.82	7.41	6.53	7.15
1633293_at	FBgn0039099	9.7	9.93	9.97	9.94	9.63	9.7
1625500_at	FBgn0033273 /// FBgn001	7.66	7.89	7.86	8.13	7.9	7.92
1628721_at	FBgn0034490	8.67	8.89	8.8	8.09	8.17	8.74
1639182_at	FBgn0039920	7.69	7.92	7.56	7.63	7.16	7.25
1631899_a_at	FBgn0039145	8.83	9.06	9.14	9.29	9.07	9.15
1630514_at	---	9.04	9.26	9.04	9.35	9.11	9.34
1640265_a_at	FBgn0000032	10.14	10.37	10.26	10.32	10.54	10.52
1623357_at	FBgn0035752	7.22	7.45	7.45	7.23	7.21	7.18
1637473_s_at	FBgn0042125	8.38	8.61	8.3	8.58	8.71	8.79
1623264_at	FBgn0034854	8.61	8.84	8.57	8.42	8.68	8.79
1637163_at	FBgn0036486	9.42	9.65	9.44	10.28	9.76	9.74
1639419_at	---	11.44	11.67	11.46	11.36	11.29	11.46
1638294_at	FBgn0035843	8	8.23	8.13	8.31	8.28	8.22
1636471_at	FBgn0002781	7.49	7.72	7.73	7.58	7.33	7.64
1628809_at	FBgn0022699	7.31	7.53	7.69	7.92	7.87	7.62
1628896_a_at	---	8.81	9.03	8.75	8.9	9.26	9.28
1634563_at	FBgn0036684	8.84	9.06	8.85	9.14	8.83	8.95
1625427_at	FBgn0038304	8.18	8.4	8.39	8.52	8.33	8.4
1630269_s_at	---	8.26	8.49	8.56	8.6	8.48	8.6

1636774_at	FBgn0024698	8.91	9.13	8.96	8.89	8.89	9.01
1636732_at	FBgn0030316	7.68	7.9	7.77	7.85	8.01	7.94
1632732_at	FBgn0030242	9.84	10.06	9.56	9.88	9.96	10.06
1634906_at	FBgn0003721 /// FBgn000	9.71	9.93	9.84	9.98	9.56	9.85
1640870_s_at	FBgn0027070	9.23	9.45	8.17	9.47	9.4	9.37
1639133_at	FBgn0037469	9.17	9.39	8.92	9.23	9.26	9.49
1627823_at	---	9.06	9.29	9.38	9.38	9.15	9.43
1625564_at	FBgn0037574	8.42	8.65	8.2	8.39	8.62	8.86
1629180_at	FBgn0027791	9.32	9.54	9.3	9.49	9.28	9.48
1637691_at	FBgn0037844	10.92	11.14	10.82	11.11	11.3	11.35
1639388_a_at	FBgn0039958	10.35	10.57	10.41	10.6	10.46	10.4
1631407_a_at	FBgn0029879	8.61	8.84	8.76	9.13	8.71	8.88
1622930_a_at	FBgn0027873	8.34	8.56	8.56	8.63	8.54	8.54
1635321_at	FBgn0037819	8.91	9.14	9.51	8.83	8.95	9.05
1633814_at	FBgn0029866	8.53	8.75	8.64	8.74	8.16	8.26
1624994_at	FBgn0000996	10.61	10.83	10.79	10.93	10.77	10.8
1632119_s_at	FBgn0015788	10.73	10.95	10.88	10.77	10.6	10.89
1629515_at	FBgn0017558	9.63	9.85	9.6	9.48	9.66	9.65
1638729_at	FBgn0033921	8.78	9.01	8.92	9.14	9.09	9.15
1640133_at	FBgn0039860	8.21	8.43	8.03	8.47	8.41	8.53
1636034_at	FBgn0020306	10.13	10.35	10.22	10.07	9.75	10.08
1630997_at	FBgn0031979	7.75	7.97	8.2	8.45	7.98	8.05
1633515_s_at	FBgn0041171	9.79	10.01	10.17	10.05	9.98	10.17
1623643_s_at	FBgn0020414	7.68	7.9	7.88	7.66	7.16	7.46
1629777_at	FBgn0038166	9.52	9.74	9.44	9.53	9.62	9.66
1628429_at	FBgn0031049	11.72	11.94	11.76	11.7	11.77	11.98
1630358_at	FBgn0035388	9.21	9.43	9.42	9.23	9.35	9.66
1635225_at	FBgn0032759	7.4	7.62	7.59	7.98	7.52	7.58
1628560_at	---	10	10.22	10.22	10.39	10.26	10.25
1634334_at	FBgn0038927	8.52	8.74	8.62	8.74	8.67	8.65
1631675_a_at	FBgn0019948	9.03	9.25	9.1	9.08	9.11	9.26
1624613_at	---	9.49	9.71	9.68	9.43	9.37	9.65
1634303_at	FBgn0034453	9.61	9.82	9.81	10.01	9.86	9.99
1630918_at	---	8.09	8.31	8.01	8.19	8.33	8.24
1632602_s_at	FBgn0026611	9.55	9.77	9.61	9.73	9.46	9.64
1629820_at	FBgn0036771	7.48	7.7	7.47	7.78	7.81	7.81

1640159_at	FBgn0040369	7.62	7.83	7.64	7.61	7.11	7.69
1628667_at	FBgn0037877	7.42	7.64	7.8	7.92	7.68	7.78
1632316_at	FBgn0033883	9.3	9.52	9.38	9.38	9.27	9.49
1627538_at	FBgn0032400	13.03	13.25	12.85	12.95	13.07	13.25
1639790_at	FBgn0038536	7.5	7.72	7.64	7.83	7.82	7.81
1636106_s_at	FBgn0038535	9.84	10.06	10.16	10.25	9.82	10.09
1623460_at	---	8.55	8.76	8.75	9.01	8.82	8.79
1634524_s_at	FBgn0036955	8.97	9.18	9	9.2	9.07	9.16
1632043_a_at	---	8.14	8.36	8.22	8.4	8.4	8.29
1626506_at	FBgn0039212	9.11	9.33	9.2	9.29	9.03	9.21
1625841_at	FBgn0035537	7.84	8.06	7.77	8.5	8.01	8.08
1636332_at	FBgn0003721 /// FBgn000	10.92	11.13	11.32	10.45	10.44	11.11
1634112_a_at	FBgn0034345	11.13	11.35	11.28	11.34	11.12	11.29
1623644_s_at	FBgn0015521	13.92	14.13	14.14	14.14	14.06	14.11
1641554_at	FBgn0033539	8.65	8.87	8.51	8.51	8.77	8.84
1638409_at	FBgn0035147	8.65	8.86	8.89	8.2	8.16	8.67
1628512_at	FBgn0036763	7.51	7.73	7.85	8.08	7.84	7.91
1629889_s_at	FBgn0030362	8.16	8.37	9.19	8.88	8.84	8.89
1640364_at	FBgn0015776	11.23	11.45	11.4	11.4	11.32	11.56
1631304_a_at	FBgn0033401	8.49	8.71	8.66	8.92	8.63	8.6
1626945_at	FBgn0032005	10.29	10.51	10.44	10.67	10.45	10.54
1633473_s_at	FBgn0000064	7.66	7.88	8.27	7.54	7.64	7.4
1624077_at	FBgn0032031	7.44	7.66	7.64	7.64	7.57	7.69
1634922_s_at	FBgn0040384	8.46	8.67	8.64	8.71	8.68	8.73
1627812_s_at	FBgn0010252	10.61	10.83	10.68	10.96	10.71	10.99
1636775_at	---	7.02	7.23	7.54	6.96	6.57	6.92
1631190_at	FBgn0033993	6.59	6.81	6.42	7.23	7.1	7.17
1629159_at	FBgn0028919	8.52	8.74	8.46	8.93	8.59	8.72
1635538_at	FBgn0033259	8.01	8.22	8.14	8.18	8.19	8.22
1624188_at	FBgn0051392	7.16	7.37	7.01	7.42	7.46	7.35
1631745_at	FBgn0032398	9.75	9.96	10.09	10.07	9.91	10.05
1626115_at	FBgn0037540	7.97	8.18	7.65	7.87	8.04	8.19
1635643_at	FBgn0037364	9.33	9.54	9.57	9.86	9.66	9.62
1636267_at	FBgn0035209	10.12	10.34	9.89	10.3	9.76	9.73
1630523_at	FBgn0030100	8.29	8.5	7.76	8.04	8.64	8.7
1640979_at	FBgn0030484	8.25	8.46	9.01	9.37	8.54	8.17

1632917_at	FBgn0039258	9.44	9.65	9.43	9.7	9.35	9.5
1631688_at	FBgn0002641	9.01	9.22	8.92	9.32	8.99	9.01
1641023_at	FBgn0031006	8.36	8.58	8.69	8.72	8.58	8.71
1627764_at	FBgn0038325	9.02	9.23	9.06	9.11	9.01	9.15
1631263_at	FBgn0034600	9.03	9.24	9.32	9.71	9.2	9.29
1625358_s_at	FBgn0032885	7.54	7.75	7.16	8.01	7.91	7.73
1623347_at	FBgn0030551	12.32	12.53	12.16	12.46	12.42	12.44
1632916_at	---	8.28	8.49	8.34	8.47	8.61	8.52
1639111_at	FBgn0031378	8.87	9.08	8.97	9.44	9.11	9.29
1624427_at	FBgn0036292	8.22	8.43	8.22	8.43	8.53	8.5
1623102_at	---	10.47	10.68	9.99	10.29	10.44	10.43
1636912_at	FBgn0033616	9.12	9.33	9.13	9.34	9.31	9.45
1624847_at	FBgn0040534	9.56	9.77	9.74	9.86	9.68	9.84
1622906_at	FBgn0033630	8.8	9.01	8.57	7.4	8.39	9.02
1634191_at	FBgn0030870	10.38	10.58	10.28	10.28	10.22	10.34
1624935_at	FBgn0037578	9.09	9.3	9.03	9.39	9	9.12
1639409_at	FBgn0038590	6.98	7.19	7.31	7.53	7.06	7.16
1641316_at	FBgn0041147	7.55	7.76	7.66	7.64	7.63	7.72
1635811_at	FBgn0003302	8.84	9.05	8.63	8.61	8.78	9.05
1633778_at	FBgn0039487	8.94	9.14	9.32	9.24	8.88	9.23
1623122_at	FBgn0032032	7.89	8.1	7.89	8.12	7.92	8.04
1628493_at	---	7.41	7.62	7.51	7.11	7.17	7.87
1630112_at	FBgn0042213	7.89	8.09	8.29	8.25	8.03	8.2
1639975_at	FBgn0037713	7.42	7.63	7.13	7.92	7.3	7.49
1634604_at	FBgn0004643	9.67	9.88	9.67	10.08	9.89	9.86
1631309_at	FBgn0030966	7.58	7.79	7.85	8.11	7.85	7.94
1637329_a_at	---	8.42	8.63	8.58	8.74	8.61	8.59
1629545_at	FBgn0004045	13.11	13.31	13.18	12.6	12.62	13.36
1638738_s_at	FBgn0029092	11.34	11.55	11.4	11.61	11.22	11.52
1624463_s_at	---	8.25	8.46	8.22	8.54	8.05	8.41
1636337_s_at	FBgn0035375	8.71	8.92	9.04	8.96	8.72	9.03
1628377_s_at	FBgn0024832	9.74	9.94	9.87	10.04	9.75	9.88
1625679_at	FBgn0040715	9.37	9.58	9.75	9.85	9.44	9.61
1635329_at	FBgn0036133	9.96	10.17	9.88	9.95	9.99	10.15
1641048_a_at	FBgn0015600	9.25	9.46	9.34	9.16	9.22	9.55
1633129_at	FBgn0038583	7.85	8.06	7.92	8	7.83	7.95

1636872_at	FBgn0020766	8.72	8.92	8.71	8.78	8.55	8.66
1625024_at	FBgn0061476	8.88	9.09	9.04	9.44	9.3	9.4
1640198_at	FBgn0037082	8.11	8.32	8.03	8.28	8.49	8.44
1628530_at	FBgn0037045	9.01	9.21	8.68	8.94	8.97	8.97
1624122_a_at	FBgn0014015	8.52	8.72	8.49	8.44	8.57	8.93
1638031_at	FBgn0039639	7.2	7.4	7.42	7.34	7.38	7.42
1636295_at	FBgn0034177	7.16	7.36	7.27	7.45	7.18	7.4
1633333_a_at	FBgn0031968	8.16	8.36	7.7	8.11	7.94	7.79
1631674_at	---	9.48	9.69	9.8	9.45	9.49	9.72
1624658_at	FBgn0053158	7.49	7.69	7.67	7.74	7.65	7.42
1638020_at	FBgn0035679	7.8	8	8.12	8.25	7.83	7.82
1627953_at	FBgn0002781	7.97	8.18	8.01	8.3	8.05	8.19
1634161_at	FBgn0032389	7.79	8	8.05	8.21	8.46	8.57
1627640_at	FBgn0035105	9.31	9.51	9.18	9.24	9.31	9.47
1632184_at	FBgn0032204	8.55	8.76	8.44	8.87	8.86	8.92
1635177_at	---	10.84	11.05	10.89	11.05	10.97	10.96
1623826_at	FBgn0027052	9.76	9.97	9.69	9.85	9.9	10.13
1631273_at	FBgn0036988	8.49	8.69	8.15	8.26	8.52	8.62
1629325_at	---	8.96	9.16	8.92	8.72	9.17	9.39
1632187_at	FBgn0034184	7.89	8.09	8.01	8.35	7.94	7.89
1632652_s_at	FBgn0050022	7.71	7.91	7.97	7.87	7.77	7.89
1640177_at	FBgn0038772	10.17	10.37	10.29	10.49	10.45	10.57
1639310_at	FBgn0030963	9.14	9.35	9.11	9.89	9.54	9.44
1626997_at	FBgn0039449	8.06	8.26	7.95	8.17	8.48	8.48
1626224_s_at	FBgn0024689	8.37	8.57	8.54	8.68	8.37	8.54
1631712_at	FBgn0032042	8.89	9.09	8.76	8.96	9.03	9.29
1633801_s_at	FBgn0031738	7.43	7.63	7.61	7.85	7.41	7.54
1640653_at	FBgn0040057	8.64	8.85	9.21	8.96	9.28	9.52
1636245_at	---	7.39	7.6	7.73	7.47	7.53	7.66
1631466_at	FBgn0039601	8.84	9.04	9.02	9.08	8.96	8.89
1632928_at	FBgn0031812	9.24	9.44	8.96	9.41	9.4	9.52
1629796_s_at	FBgn0000316	9.95	10.15	9.96	10.29	10.04	10.01
1626082_at	FBgn0039642	8.16	8.37	8.48	8.33	8.31	8.5
1629036_at	---	8.33	8.53	8.24	8.65	8.73	8.76
1636847_s_at	FBgn0029152	9.8	10	9.95	10.17	9.81	10.09
1625519_at	FBgn0032643	9.65	9.85	9.79	9.88	9.71	9.89

1625185_at	FBgn0036261	7.67	7.87	7.47	7.6	7.68	8.01
1639253_at	FBgn0034451	10.32	10.52	10.34	10.6	10.3	10.52
1638544_at	FBgn0033429	8.18	8.38	8.36	8.28	8.08	8.24
1637166_at	---	9.39	9.59	9.47	9.85	9.44	9.66
1639608_at	FBgn0031091	10.37	10.57	10.43	10.56	10.8	10.79
1628204_at	FBgn0035703	7.07	7.27	7.3	7.39	7.32	7.33
1625833_at	FBgn0034808	9.03	9.23	8.88	8.84	9	9.26
AFFX-Dros-G	FBgn0001092	12.01	12.2	12.19	12.32	12.41	12.41
1626561_at	FBgn0036714	7.81	8.01	7.99	8.15	8.04	8
1627885_s_at	FBgn0036483	9.1	9.3	8.95	9.08	9	9.19
1635842_at	FBgn0036448	9.47	9.66	9.86	9.93	9.55	9.65
1626918_at	FBgn0035120	9.15	9.35	9.42	9.77	9.3	9.4
1640960_at	FBgn0039773	6.83	7.03	6.91	7.14	7.15	7.05
1624240_at	FBgn0010288	11.17	11.37	11.35	11.59	11.39	11.37
1623655_at	FBgn0005391	13.31	13.51	13.47	12.74	12.81	13.6
1635654_at	FBgn0030678	8.24	8.44	8.22	8.25	8.19	8.34
1628106_at	FBgn0035421	9.86	10.06	9.82	9.8	9.92	10.03
1631971_at	FBgn0036207	7.71	7.91	8.23	8.46	8.26	8.34
1634031_at	FBgn0035696	9.54	9.74	9.95	9.54	8.8	9.54
1630397_at	FBgn0039210	8.64	8.84	8.43	8.75	8.7	8.73
1635305_s_at	FBgn0013263	7.26	7.46	7.68	7.6	7.32	7.69
1636257_at	FBgn0036300	8.74	8.94	8.88	9.04	8.64	8.78
1637523_at	FBgn0029970	7.86	8.06	7.82	8.31	7.94	7.83
1627894_s_at	FBgn0013764	9.57	9.77	9.02	9.61	9.68	9.69
1629305_at	FBgn0010660	8.48	8.68	8.61	8.56	8.56	8.6
1632240_at	FBgn0040347	9.3	9.5	9.14	9.57	9.46	9.51
1624778_at	FBgn0020261	9.33	9.53	9.76	9.7	9.39	9.36
1624160_at	FBgn0031848	8.55	8.75	8.49	8.93	8.71	8.73
1624541_at	FBgn0031118	8.5	8.7	8.68	8.38	8.35	8.74
1634771_a_at	FBgn0030674	8.25	8.45	8.96	8.9	8.37	8.38
1637189_at	FBgn0038593	7.6	7.8	7.66	7.96	7.77	7.83
1634230_s_at	FBgn0011598	12.41	12.61	12.44	12.6	12.27	12.54
1624263_at	FBgn0039139	7.29	7.49	7.54	8	7.72	7.53
1631385_at	FBgn0030206	7.1	7.29	7.09	7.3	7.42	7.37
1632717_a_at	FBgn0031315	8.47	8.67	8.9	8.88	8.6	8.66
1628627_at	FBgn0033996	9.27	9.46	9.27	9.36	9.47	9.56

1631515_at	FBgn0039636	8.54	8.74	8.45	8.71	8.55	8.57
1624513_at	FBgn0035048	7.61	7.8	8.11	7.99	7.83	7.78
1630857_s_at	FBgn0024947	10.9	11.09	10.87	10.84	10.76	10.95
1629319_at	FBgn0032724	9.13	9.33	9.16	9.21	9.14	9.29
1637092_a_at	FBgn0034923	7.73	7.92	8.18	7.94	8.01	8.06
1629964_at	FBgn0036812	8.69	8.89	8.86	8.95	9	9.02
1639690_a_at	FBgn0016754	7.08	7.28	7.12	7.16	7.28	7.48
1628019_a_at	FBgn0039141	7.5	7.69	7.78	7.77	7.73	7.69
AFFX-Dros-1	---	11.43	11.63	11.49	11.85	11.5	11.82
1640470_s_at	---	10.27	10.47	10.66	10.59	10.44	10.53
1626355_at	FBgn0020756	8.21	8.4	8.42	8.33	8.44	8.36
1640341_s_at	FBgn0027836	9	9.19	9.35	9.71	9.49	9.43
1630451_at	---	8.68	8.87	8.82	8.8	8.72	8.74
1627651_a_at	FBgn0020278	9.1	9.3	9.13	8.96	9.23	9.43
1640001_at	---	8.99	9.18	9.32	9.18	9.05	9.17
1623177_at	---	9.01	9.2	8.93	8.89	9.01	9.16
1637671_a_at	FBgn0040777	10.4	10.6	10.64	10.48	10.47	10.61
1626175_at	---	8.54	8.73	8.57	8.78	8.71	8.67
1633458_at	FBgn0003655	11.02	11.22	10.97	11.23	11.1	11.19
1623375_at	FBgn0036480	7.16	7.35	7.36	7.82	7.42	7.41
1630991_at	FBgn0034455	10.31	10.5	10.25	10.62	10.33	10.45
1632747_at	FBgn0030507	9.05	9.24	9.06	9.57	9.23	9.25
1632222_a_at	FBgn0036428	10.97	11.17	10.98	11.14	10.94	11.17
1641198_at	FBgn0035294	7.84	8.03	7.89	7.93	7.93	8.12
1632680_at	FBgn0001970	8.48	8.67	8.48	9	8.41	8.37
1626898_at	FBgn0032348	9.11	9.31	9.13	9.39	9.23	9.13
1637174_s_at	FBgn0053008	7.38	7.57	7.23	7.73	7.32	7.51
1629144_at	FBgn0031607	7.75	7.95	7.89	8.16	8.03	7.94
1628932_at	FBgn0002781	8.12	8.31	8.06	8.55	8.39	8.54
1630729_at	---	7.39	7.58	7.46	7.52	7.53	7.36
1629113_a_at	---	7.86	8.05	8.02	8.1	8	8.08
1632748_at	FBgn0034402	7.53	7.72	7.67	7.96	7.69	7.7
1627580_at	FBgn0039016	7.4	7.59	7.58	7.62	7.56	7.53
1634147_a_at	---	7.73	7.92	7.93	8.16	8.06	7.88
1632777_at	FBgn0034033	7.85	8.04	8.17	7.93	8.07	8.16
1629019_s_at	FBgn0040660	11.95	12.15	12.18	12.3	12.12	12.13

1632301_at	FBgn0031818	9.24	9.43	9.12	9.19	9.35	9.46
1624375_at	---	9.79	9.98	9.56	9.81	9.75	10.08
1631183_at	---	7.02	7.21	7.49	6.74	6.7	7.24
1630124_at	FBgn0039560	6.67	6.86	6.74	7.25	7.2	7.15
1629625_at	FBgn0033613	8.87	9.06	9.47	9.19	9.02	9.24
1635487_at	FBgn0038463	8.37	8.56	8.58	8.96	8.51	8.52
1625447_at	FBgn0039680	8.71	8.9	8.85	9.37	8.86	8.83
1641178_s_at	FBgn0035181	8.97	9.16	9.16	9.37	9.27	9.29
1634430_at	FBgn0031186	8.85	9.04	8.91	9.08	8.87	9.19
1634714_at	---	8.36	8.55	8.56	8.62	8.58	8.59
1627930_s_at	FBgn0052280	7.8	7.99	8.56	7.08	7.32	7.85
1632110_at	FBgn0037711	7.81	8	7.81	8.09	8.13	8.1
1628550_a_at	FBgn0033377	8.61	8.8	8.98	9.03	8.66	8.75
1639589_at	FBgn0031398	8.32	8.5	8.2	8.39	8.34	8.34
1639264_at	FBgn0015075	8.41	8.59	8.82	8.9	8.51	8.47
1633758_at	FBgn0037848	8.14	8.33	7.81	7.97	8.12	8.18
1628660_at	FBgn0037151	7.95	8.14	7.89	8.61	8.33	8.25
1626807_a_at	FBgn0028703	7.61	7.8	7.68	7.97	7.42	7.88
1624537_s_at	FBgn0031420	8.39	8.58	8.41	8.58	8.48	8.56
1637634_at	FBgn0034204	8.42	8.61	8.37	8.24	8.32	8.59
1633665_at	---	9.2	9.39	9.2	9.54	9.43	9.47
1638200_at	FBgn0003048	7.85	8.04	7.68	7.7	7.97	8.02
1633835_s_at	FBgn0024991	9.79	9.97	9.77	9.89	9.7	9.82
1628271_at	FBgn0031418	9.64	9.83	9.06	9.88	9.72	9.68
1623664_at	FBgn0037044	8.23	8.42	8.41	8.39	8.53	8.45
1636040_at	FBgn0034583	10.19	10.37	10.17	10.38	10.02	10.26
1631721_at	FBgn0015025	6.98	7.17	6.96	7.31	7.35	7.15
1632099_s_at	FBgn0046704	9.16	9.34	9.2	9.23	9.3	9.35
1635652_at	FBgn0023458	8.64	8.82	8.81	8.69	8.62	8.64
1641168_s_at	FBgn0032961	11.19	11.37	11.52	11.72	11.56	11.63
1632417_a_at	FBgn0035944	10.39	10.57	10.43	10.67	10.47	10.58
1628825_at	FBgn0033998	8.21	8.4	8.46	8.55	8.15	8.37
1629663_at	FBgn0032979	10.25	10.43	10.33	10.54	10.41	10.57
1640361_at	FBgn0030956	11.05	11.23	10.88	11.2	11.13	11.23
1635422_s_at	FBgn0031774	7.61	7.79	7.52	7.96	8.08	8.04
1628601_at	FBgn0004380	7.71	7.89	7.78	8.12	8.02	7.86

1637667_at	FBgn0032034	9.23	9.41	9.28	9.57	9.31	9.44
1624535_at	FBgn0035114	10.99	11.17	10.64	11.2	11.09	11.18
1623805_at	FBgn0033352	8.21	8.39	8.01	8.11	8.14	8.4
1630657_at	FBgn0028647	7.47	7.65	7.68	7.9	7.63	7.62
1634784_at	FBgn0005596	8.71	8.89	8.84	8.85	8.85	8.93
1634942_at	FBgn0036460	9.85	10.03	10.27	9.81	10.08	10.17
1641134_at	FBgn0031713	8.7	8.89	8.77	8.96	8.87	8.82
1623798_at	FBgn0039169	7.81	7.99	7.71	7.69	8.06	8.05
1625655_at	FBgn0031436	9.6	9.78	10	9.95	9.73	9.8
1630024_at	FBgn0035851	7.85	8.04	7.88	8.01	7.77	7.91
1640200_at	FBgn0024242	9.24	9.42	9.18	8.8	8.95	9.29
1640660_at	FBgn0015818	9.36	9.55	9.72	9.68	9.71	9.83
1626249_s_at	FBgn0010382	10.24	10.42	9.9	10.24	10.27	10.58
1627865_a_at	---	7.26	7.44	7.79	7.26	6.91	7.44
1637437_at	FBgn0037794	7.41	7.59	7.83	7.91	7.81	7.89
1630703_at	FBgn0034181	11.33	11.52	11.49	11.52	11.36	11.46
1641444_a_at	FBgn0040285	8.78	8.96	8.83	8.69	8.91	9.1
1629921_a_at	FBgn0004837	8.87	9.05	8.68	8.94	8.81	9.07
1628655_at	FBgn0035969	9.66	9.84	9.97	9.96	9.81	9.83
1627150_at	FBgn0024987	9.54	9.73	9.82	9.76	9.62	9.92
1632640_at	FBgn0038360	8.7	8.88	8.65	8.67	8.81	8.77
1630912_at	FBgn0039698	8.44	8.63	8.44	8.49	8.4	8.51
1629851_at	FBgn0051998	9.01	9.19	9.01	9.12	8.7	8.89
1626763_a_at	FBgn0039269	10.42	10.6	10.42	10.71	10.72	10.74
1634543_at	FBgn0030646	7.5	7.68	7.62	7.98	7.68	7.68
1623590_s_at	FBgn0052438	8.56	8.74	8.78	9.02	8.81	8.76
1631278_a_at	FBgn0033695	8.28	8.46	8.56	8.88	8.4	8.5
1623678_at	FBgn0030692	9.29	9.47	9.83	9.94	9.38	9.45
1624277_at	FBgn0037716	8.43	8.61	8.38	8.74	8.43	8.56
1631388_at	---	7.96	8.14	8.03	8.14	7.86	7.98
1635340_at	FBgn0003891	9.45	9.63	9.85	9.65	9.51	9.75
1638315_s_at	FBgn0033716	8.93	9.11	9.22	9.16	9.27	9.35
1637107_at	FBgn0036052	8.34	8.52	8.41	8.45	8.29	8.53
1628463_at	FBgn0040494	9.83	10.01	9.77	10.57	9.96	10.04
1641596_at	FBgn0032751	6.99	7.17	6.92	6.85	7.04	7.19
1625544_s_at	---	7	7.17	7.04	6.98	7.6	7.5

1623902_at	---	10.22	10.4	10.52	10.32	10.25	10.41
1640830_at	---	10.26	10.44	10.31	10.58	10.56	10.6
1623506_s_at	FBgn0023177	10.09	10.27	10.22	10.62	10.25	10.2
1632667_s_at	FBgn0001092	12.82	13	13.01	13.2	13.1	13.15
1639341_at	FBgn0035449	9.55	9.73	9.34	9.46	9.41	9.67
1638722_at	FBgn0036621	7.96	8.14	7.82	7.88	7.94	8.2
1636533_at	FBgn0034217	6.9	7.08	7.15	7.66	7.35	7.59
1631460_s_at	FBgn0035047	9.64	9.81	9.22	9.73	9.72	9.83
1639051_at	FBgn0033554	8.28	8.45	8.37	8.58	8.15	8.4
1627090_at	FBgn0023180	8.52	8.7	8.58	8.58	8.58	8.51
1626888_at	FBgn0032485	9.62	9.8	9.71	9.76	9.7	10.07
1639280_at	FBgn0036733	8.53	8.71	8.88	9.54	8.87	8.8
1636363_s_at	FBgn0034282	10.17	10.35	10.39	10.92	10.48	10.44
1633355_at	FBgn0029664	8.02	8.2	8.7	9.24	8.29	8.29
1633573_a_at	---	7.83	8	7.91	7.64	7.9	7.84
1625271_at	FBgn0025684	8.46	8.63	8.18	8.34	8.41	8.52
1626840_a_at	FBgn0033914	9.41	9.59	9.73	9.66	9.6	9.62
1633845_at	FBgn0029858	8.33	8.51	8.23	8.64	8.25	8.31
1636164_s_at	FBgn0033005	10.7	10.87	10.99	11.01	10.94	11.04
1634078_at	FBgn0039631	8.01	8.19	7.89	8.25	8.26	8.24
1630835_a_at	FBgn0034002	7.54	7.72	7.35	7.71	7.48	7.52
1631875_at	FBgn0037321	8.63	8.8	8.54	8.87	8.86	9.12
1623688_at	FBgn0037027	8.73	8.9	8.84	9.17	8.91	8.88
1624190_at	FBgn0051637	8.42	8.6	8.44	8.66	8.67	8.85
1637453_at	FBgn0036842	10.27	10.45	10.28	10.44	10.31	10.46
1628959_at	FBgn0027658	7.86	8.03	7.98	8.14	7.69	7.98
1633429_at	FBgn0014340	8.22	8.4	8.34	8.72	8.39	8.39
1624604_a_at	FBgn0027595	8.06	8.24	7.83	8.38	8.2	8.22
1639184_at	FBgn0034940	8.49	8.67	8.51	8.69	8.53	8.55
1637718_at	FBgn0037876	7.15	7.33	7.23	7.51	7.21	7.39
1634501_at	FBgn0036512	8.6	8.77	8.57	8.65	8.57	8.55
1634385_at	FBgn0039731	7.92	8.09	7.94	8.44	8.2	8.24
1628451_at	---	8.69	8.86	8.22	8.32	8.61	8.84
1638415_at	---	12.82	12.99	13.15	13.11	13.07	13.11
1635684_a_at	FBgn0025726	7.37	7.54	7.33	7.39	7.56	7.88
1636299_at	FBgn0035036	7.2	7.38	7.38	7.63	7.45	7.4

1633731_at	FBgn0011737	9.18	9.35	9.21	9.47	9.29	9.36
1624515_at	FBgn0030932	11.71	11.88	11.43	11.65	11.7	11.64
1632704_at	FBgn0033812	9.64	9.81	9.61	9.63	9.66	9.76
1639145_s_at	FBgn0002921	9.95	10.12	10.3	10.3	9.97	10.09
1637555_at	FBgn0036197	10.41	10.59	10.65	10.7	10.44	10.44
1634654_at	FBgn0011230	9.72	9.9	10.19	10.17	9.89	9.93
1638590_at	---	8.47	8.65	8.53	8.8	8.64	8.65
1629956_at	FBgn0037472	9.72	9.89	9.54	9.72	9.71	9.91
1626421_at	FBgn0038735	7.09	7.27	7.47	7.57	7.48	7.45
1631575_at	---	8.96	9.14	9.05	9.19	9.13	9.12
1635044_at	FBgn0001225	12.96	13.13	12.63	13.2	13.28	13.18
1632094_at	FBgn0033690	9.3	9.47	9.4	9.46	9.47	9.57
1639728_at	FBgn0038401	8.91	9.08	9.02	9.21	9.05	9.07
1630166_s_at	FBgn0002638	11.57	11.74	11.72	11.94	11.67	11.66
1627562_at	FBgn0024958	8.31	8.49	8.7	8.42	8.57	8.44
1629578_at	FBgn0033902	10.79	10.96	11.36	11.08	11.17	11.03
1633347_at	---	7.82	8	8.03	8.41	8.22	8.26
1630176_at	FBgn0037660	7.34	7.51	7.48	7.69	7.53	7.69
1624923_s_at	---	9.52	9.7	9.47	9.1	9.39	9.77
1627598_at	FBgn0031233	9.29	9.46	9.41	9.59	9.37	9.38
AFFX-DapX-	---	7.63	7.81	8	8.33	7.74	7.42
1628807_at	FBgn0038344	8.95	9.13	9.25	9.19	9.09	9.19
1623972_a_at	FBgn0038745 /// FBgn003	9.89	10.06	10	10.1	10.01	10.13
1629266_s_at	FBgn0033886	11.13	11.3	11.11	11.41	11.31	11.21
1625080_at	FBgn0045828	12.25	12.42	12.49	12.63	12.39	12.42
1622932_s_at	FBgn0003447	9.82	9.99	9.88	10.15	9.78	9.91
1630132_at	---	11.2	11.37	11.5	11.44	11.44	11.29
1625244_at	FBgn0031604	9.02	9.19	8.97	9.11	8.95	9.08
1623631_at	---	9.42	9.59	9.47	9.64	9.57	9.49
1624594_at	FBgn0052484	9.33	9.5	9.34	9.51	9.28	9.38
1635938_s_at	FBgn0017561	9.68	9.85	8.84	8.74	9.76	10
1624343_at	FBgn0050443	8.68	8.85	8.86	8.75	8.8	8.84
1628016_s_at	---	8.51	8.68	8.76	8.91	8.47	8.52
1627067_at	FBgn0015614	11.38	11.55	11.31	11.3	11.5	11.6
1631640_a_at	FBgn0033566	9.51	9.68	9.37	9.92	9.69	9.64
1623247_at	FBgn0039296	8.45	8.62	8.51	8.75	8.63	8.71

1625599_at	---	8.97	9.14	8.88	9.36	9.28	9.23
1638463_at	FBgn0037656	7.36	7.53	7.51	7.71	7.61	7.68
1639046_at	---	9.64	9.81	9.78	9.63	9.73	9.81
1637926_s_at	FBgn0036855	9.19	9.36	9.43	9.35	9.34	9.42
1638834_a_at	FBgn0026873	8.85	9.02	9.27	9.27	9.24	9.19
1639347_s_at	FBgn0016131	8.95	9.12	9.71	9.46	9.07	9.43
1640143_at	FBgn0032819	8.17	8.34	8.4	8.07	8.23	8.35
1633527_a_at	---	8.86	9.03	8.79	8.97	8.97	9
1625264_s_at	FBgn0013770	12.77	12.94	12.72	12.73	12.75	12.8
1627455_at	FBgn0039067	8.24	8.4	8.32	8.88	8.46	8.5
1635018_at	FBgn0033935	7.95	8.11	7.78	8.15	8.12	7.99
1638313_at	FBgn0033677	10.34	10.5	10.17	10.37	10.55	10.71
1627377_at	FBgn0026431	8.49	8.65	8.54	9	8.87	8.62
1629155_at	FBgn0031310	9.11	9.28	9.35	9.41	9.21	9.23
1638539_at	FBgn0034422	9.16	9.32	9.39	9.5	9.06	9.39
1635168_at	FBgn0036991	8.79	8.95	8.75	9.06	9.13	9.07
1628548_at	---	9.33	9.49	9.08	9.44	9.61	9.62
1630052_s_at	FBgn0034089	9.65	9.81	9.9	10.14	9.85	9.88
1625201_s_at	FBgn0046225	7.18	7.34	7.62	7.89	7.5	7.57
1626701_at	FBgn0039357	8.12	8.29	8.1	7.57	8.02	8.24
1628558_at	FBgn0050022	7.96	8.13	8.08	8.11	7.99	8.14
1632271_a_at	FBgn0035253	10.35	10.51	10.2	10.27	10.53	10.67
1630882_s_at	FBgn0039338	9.33	9.5	9.56	9.69	9.54	9.54
1633883_at	FBgn0030787	9.93	10.09	9.54	9.8	10	10.05
1630123_at	FBgn0030145	7.42	7.58	7.71	8.04	7.76	7.72
1627248_at	FBgn0037705	7.74	7.9	8.28	7.86	7.98	8.25
1636741_s_at	FBgn0026418	10.54	10.71	10.78	10.99	10.81	10.74
1628701_a_at	---	7.82	7.99	7.99	7.84	7.81	7.42
1637733_at	FBgn0051063	9.48	9.64	9.67	9.64	9.52	9.57
1627938_at	FBgn0031611	6.85	7.01	7.16	7.02	7.06	6.7
1632936_at	FBgn0026616	8.77	8.94	8.77	8.9	8.72	9.06
1630701_at	FBgn0029980	9.17	9.33	9.17	9.44	9.47	9.43
1629198_at	FBgn0030047	7.65	7.82	7.84	8.24	7.88	7.75
1635101_at	FBgn0038418	7.09	7.25	7.07	7.17	7.3	7.15
1628404_at	FBgn0037537	9.21	9.38	9.28	9.22	9.18	9.34
1640859_at	FBgn0035627	8.51	8.68	8.34	8.87	8.78	8.68

1624611_a_at	FBgn0034753	13.33	13.5	13.27	13.46	13.42	13.52
1626359_at	FBgn0026876	8.55	8.72	8.84	9.32	8.92	8.82
1627382_at	FBgn0010638	11.79	11.96	11.93	11.64	11.71	12
1624755_a_at	FBgn0000711	9.77	9.93	10.01	10.12	9.97	9.97
1629095_a_at	FBgn0002719	10.15	10.31	10.56	10.28	10.12	10.2
1640289_a_at	---	9.63	9.8	9.99	10	10.27	10.45
1634839_at	---	8.2	8.36	8.17	8.39	8.53	8.51
1638598_at	FBgn0027592	8.56	8.73	8.64	9.04	8.86	8.83
1625165_at	---	7.87	8.03	7.91	8.31	8.18	8.18
1634818_s_at	FBgn0025704	8.8	8.96	8.75	8.71	8.59	8.55
1641671_at	FBgn0033273 /// FBgn001	9.86	10.03	10.01	10.25	10.01	10.04
1628634_at	FBgn0036695	8.74	8.9	8.44	8.68	8.73	8.8
1633886_at	FBgn0036107	9.66	9.83	9.7	9.86	9.74	9.74
1626549_at	FBgn0038274	7.82	7.98	8.07	8.37	8.17	7.95
1631836_at	FBgn0032763	7.46	7.63	7.36	7.7	7.86	7.8
1625068_a_at	FBgn0026777	11.41	11.57	11.4	11.7	11.59	11.65
1631009_at	FBgn0039559	9.81	9.98	9.93	10.09	10.03	9.99
1629963_at	FBgn0028563	10.32	10.48	10.25	10.12	10.33	10.44
1623728_at	FBgn0031270	7.75	7.92	7.82	8.25	8	8.05
1637617_at	FBgn0034403	11.03	11.19	11.2	11.4	11.18	11.21
1625177_at	FBgn0036922	7.88	8.04	7.68	8.04	8.21	8.17
1638748_at	FBgn0000575	9.52	9.69	9.88	9.33	9.38	9.94
1627013_at	FBgn0030289	9.28	9.44	9.01	9.26	9.3	9.29
1637739_at	FBgn0029820	8.6	8.76	8.52	8.7	8.6	8.52
1639189_at	FBgn0033984	8.75	8.91	8.34	8.61	8.69	9.1
1624726_s_at	FBgn0037138	9.89	10.06	10.14	9.9	9.83	10.11
1636297_at	FBgn0034964	8.14	8.31	8.5	8.49	8.44	8.27
1634411_at	FBgn0030874	8.36	8.53	8.43	8.65	8.51	8.52
1634107_at	---	9.08	9.24	9.34	9.24	9.24	9.17
1638339_at	FBgn0034430	9.9	10.06	10.03	10.26	10.07	10.12
1623918_at	---	9.32	9.48	9.24	9.3	9.42	9.45
1636221_a_at	FBgn0003716	9.8	9.97	9.87	9.68	9.89	9.94
1630013_s_at	FBgn0032224	9.95	10.11	9.97	10.02	9.96	10.11
1634963_at	FBgn0039907	9.13	9.3	9.17	9.17	9.13	9.34
1637217_at	FBgn0035324	7.89	8.05	8.27	8.42	8.25	7.98
1628368_at	FBgn0024291	10.56	10.73	10.47	10.61	10.63	10.74

1636788_a_at	FBgn0032515	9.24	9.4	9.15	9.84	9.53	9.39
1640315_at	FBgn0051241	7.68	7.84	7.71	8.17	7.88	7.84
1637110_at	FBgn0037028	7.82	7.98	8.1	8.1	7.67	7.7
1632418_s_at	FBgn0003165	10.29	10.45	10.34	10.28	10.34	10.47
1639581_at	FBgn0035462	7.31	7.47	7.29	7.95	7.55	7.55
1632783_a_at	FBgn0003612	9.57	9.73	9.61	10.02	9.7	9.72
1627359_at	FBgn0030596	7.02	7.18	7.73	6.08	5.79	7.46
1635587_s_at	FBgn0020312	8.87	9.03	8.71	8.99	8.9	9.09
1637606_at	FBgn0031535	10.36	10.52	10.14	10.36	10.43	10.47
1638846_at	---	9.42	9.58	9.43	9.4	9.47	9.71
1639410_at	FBgn0027095	10.05	10.21	10.42	10.29	10.16	10.39
1634672_at	FBgn0035947	10.18	10.34	10.65	10.58	10.31	10.36
1632206_at	FBgn0039459	9.12	9.28	8.66	8.77	9.43	9.23
1626940_at	FBgn0027548	9.27	9.43	9.35	9.16	9.24	9.21
1623493_at	FBgn0030420	6.75	6.91	6.67	7.17	7.1	6.89
1639038_at	FBgn0030654 /// FBgn003	8.04	8.2	7.92	8.15	8.02	7.98
1627204_at	FBgn0031308	7.97	8.13	8.36	8.16	8.02	8.02
1625681_at	FBgn0030141	8.76	8.92	9	9	9.06	9
1626844_at	FBgn0001222	10.9	11.06	10.87	11.18	11	11.14
1635547_a_at	FBgn0010803	9.22	9.38	9.3	9.59	9.31	9.38
1635343_a_at	FBgn0025676	7.4	7.56	8.01	8.08	8.27	8.26
1637536_at	FBgn0038633	7.35	7.5	7.7	7.26	7.27	7.61
1634000_a_at	FBgn0030345	10.03	10.19	9.79	10.03	10.02	10.12
1625422_at	FBgn0036614	7.9	8.06	7.99	8.34	8.17	8.09
1634859_at	FBgn0031951	8.19	8.34	8.24	8.52	8.23	8.68
1631328_s_at	FBgn0032474	9.99	10.15	9.59	9.72	9.85	9.87
1640441_at	---	10.18	10.34	10.35	10.37	10.13	10.29
1626278_at	FBgn0032453	11.48	11.64	11.63	11.87	11.68	11.76
1632852_s_at	FBgn0001142	11.24	11.4	11.46	11.46	11.34	11.53
1633253_s_at	FBgn0031474	9.18	9.34	9.39	9.48	9.41	9.54
1631831_at	---	7.36	7.52	7.44	7.83	7.62	7.49
1632605_at	FBgn0028552	7.99	8.15	7.97	8.27	8.38	8.24
1626985_a_at	FBgn0027509 /// FBgn003	10.28	10.44	10.46	10.66	10.41	10.58
1640644_at	FBgn0038745 /// FBgn003	10.16	10.31	10.45	10.31	10.26	10.47
1629954_at	FBgn0033962	8.73	8.88	9.1	8.84	8.73	8.93
1629109_at	FBgn0035848	9.14	9.3	9.1	9.5	9.19	9.28

1623458_at	FBgn0038438	9.41	9.57	9.44	9.3	9.6	9.71
1627845_at	FBgn0035906	10.21	10.37	10.46	10.44	10.36	10.34
1633847_at	FBgn0030056	11.22	11.38	11.2	11.38	11.36	11.33
1635570_a_at	FBgn0014467	7.45	7.6	7.29	7.33	7.29	7.3
1638162_s_at	FBgn0035357	9.06	9.22	9.17	9.34	9.1	9.2
1635887_at	FBgn0050094	7.66	7.82	7.85	7.82	7.85	7.82
1633335_at	FBgn0001965	8.42	8.57	8.42	8.58	8.63	8.61
1634895_s_at	FBgn0014010	10.06	10.22	10.36	10.34	10.23	10.59
1625742_at	FBgn0034913	10.34	10.5	10.44	10.55	10.61	10.57
1634858_s_at	FBgn0037917	8.49	8.65	8.74	8.88	8.82	8.91
1631357_at	---	8.34	8.49	7.95	7.87	8.09	8.11
1640452_at	FBgn0030411	8.35	8.51	8.19	8.64	8.54	8.5
1639205_s_at	FBgn0003742	10.09	10.25	9.98	10.1	10.02	10.31
1623975_at	FBgn0025185	8.16	8.32	8.36	8.83	8.54	8.49
1635344_at	FBgn0020018	8.4	8.55	8.25	8.69	8.51	8.34
1631630_at	---	9.82	9.97	9.8	10.25	9.93	9.95
1638140_at	FBgn0031659	8.72	8.87	8.9	9.08	8.72	8.8
1637532_s_at	FBgn0036975 /// FBgn003	10.72	10.87	10.91	10.96	10.65	10.76
1627629_at	FBgn0029868	10.08	10.23	10.54	10.34	10.22	10.37
1626752_at	FBgn0028530	8.49	8.64	8.62	8.85	8.51	8.57
1640173_at	---	8.63	8.79	8.66	8.86	8.84	8.75
1641575_at	FBgn0037963	9.57	9.73	9.77	9.56	9.39	9.75
1630355_a_at	FBgn0028932	7.23	7.38	7.65	7.35	7.48	7.52
1638175_at	FBgn0020272	8.82	8.97	8.94	9.21	8.84	8.75
1626180_at	FBgn0034794	9.36	9.52	9.46	9.83	9.41	9.39
1623069_s_at	FBgn0032775	8.81	8.96	8.93	8.91	8.56	8.55
1634009_at	FBgn0036472	8.45	8.61	8.39	8.22	8.63	8.57
1635743_at	FBgn0015838	8.83	8.98	9.12	8.86	9.21	9.45
1625750_at	FBgn0038830	9.77	9.92	10.05	9.8	9.89	10.01
1629045_s_at	---	7.82	7.97	7.74	7.92	7.83	7.83
1623383_at	FBgn0042131 /// FBgn001	9.97	10.13	10.28	10.2	10.03	10.01
1640791_at	FBgn0023216	7.86	8.01	8.25	8.57	8.15	8.19
1626813_at	---	11.07	11.22	11.2	11.46	11.19	11.18
1623582_at	FBgn0039179	9.3	9.45	9.4	9.49	9.51	9.61
1641331_at	FBgn0038769	6.95	7.1	6.76	6.97	7.12	7.02
1639034_at	FBgn0039687	8.65	8.8	8.9	9.07	8.88	8.91

1627843_at	FBgn0026148	8.55	8.7	8.51	8.83	8.97	8.88
1639999_at	FBgn0024993	8.4	8.55	8.35	8.67	8.85	8.71
1632130_s_at	FBgn0026370	7.07	7.22	7.55	7.51	7.76	8.17
1641317_at	---	9.87	10.02	10.09	10.4	10.03	10.16
1634074_a_at	FBgn0015565	12.18	12.33	11.29	11.58	12.13	12.16
1624138_at	FBgn0030855	8.24	8.39	8.61	8.56	8.39	8.35
1625855_at	FBgn0035149	8.91	9.06	9.03	9.04	8.97	8.95
1634690_at	FBgn0033881	9.52	9.67	9.62	10.13	9.83	9.81
1639055_at	FBgn0032101	9.69	9.84	9.81	9.35	9.84	9.97
1638354_at	FBgn0037293	8.71	8.86	8.83	8.92	8.89	8.91
1636695_at	FBgn0004462	8.75	8.9	9.23	9.6	8.79	8.94
1637559_at	FBgn0039126	9.87	10.02	9.95	10.25	10.02	10.07
1631984_at	FBgn0031282	7.63	7.78	7.59	7.89	7.69	7.75
1637525_s_at	FBgn0026409	12.44	12.59	12.63	12.69	12.63	12.59
1631051_at	FBgn0032883	7.9	8.05	8.02	8.29	8.08	8.12
1630660_at	---	10.2	10.35	10.35	10.83	9.52	9.92
1637973_a_at	FBgn0030431	9.38	9.53	9.43	9.54	9.38	9.37
1630167_at	FBgn0024841	10.79	10.94	10.56	10.52	10.74	10.65
1625119_at	FBgn0034249	7.66	7.81	7.55	7.92	7.71	7.75
1638848_at	FBgn0037792	8.62	8.77	8.9	9.02	8.8	8.89
1638930_s_at	FBgn0037117	7.86	8.01	7.69	7.71	7.97	8.12
1632739_at	FBgn0052536	8.1	8.25	7.54	7.54	7.2	7.41
1623293_at	FBgn0037018	9.32	9.47	9.43	9.58	9.34	9.43
1627509_s_at	FBgn0041150	10.26	10.41	10.25	10.43	10.36	10.37
1627009_at	FBgn0003527	8.88	9.03	9.02	9.08	9.12	9.03
1639574_a_at	FBgn0003218	7.6	7.74	7.77	8.06	7.92	7.82
1632433_at	FBgn0031194	7.99	8.14	8.19	8.64	8.29	8.36
1622983_a_at	FBgn0021761	9.81	9.96	9.95	10.07	9.89	9.89
1623061_at	FBgn0002036	7.87	8.02	7.83	8.2	7.96	7.86
1638267_s_at	FBgn0010504	8.56	8.71	8.68	8.65	8.18	8.43
1632818_at	FBgn0052281	7.73	7.88	8.27	8.26	7.81	7.98
1626719_a_at	FBgn0036141	9.88	10.03	9.86	10.15	10.01	10.04
1624211_at	FBgn0033638	8.38	8.53	8.07	8.06	8.29	8.5
1623239_at	FBgn0014269	9.04	9.19	9.1	9.47	9.29	9.29
1631993_s_at	FBgn0000064	10.93	11.07	11.29	11.26	11.08	11.24
1635531_at	FBgn0011705	10.54	10.69	10.32	10.06	10.42	10.74

1638095_at	FBgn0031227	8.73	8.88	8.91	9.08	8.63	8.89
1626347_at	FBgn0035337	8.52	8.66	8.64	8.48	8.62	8.73
1632510_at	FBgn0030973	8.65	8.79	8.98	9.27	8.89	8.8
1638216_at	---	8.08	8.23	8.07	7.86	7.89	8.03
1623434_at	FBgn0031590	10.32	10.46	10.38	10.53	10.23	10.31
1623235_at	---	7.87	8.02	8.12	8.33	8.08	7.97
1623943_at	FBgn0038462	10.5	10.65	10.17	10.29	10.77	10.7
1634844_at	FBgn0031092	9.38	9.53	9.81	9.63	9.45	9.51
1630406_at	FBgn0040513	7.13	7.28	7.12	7.36	6.93	7.02
1632403_at	FBgn0034346	7.8	7.94	7.68	7.81	7.75	7.86
1629123_at	FBgn0039141	9.22	9.37	9.47	9.15	9.27	9.47
1626385_s_at	---	9.76	9.91	9.89	10.17	9.9	10
1637130_at	---	10.08	10.23	10.16	10.17	10.13	10.32
1635796_a_at	FBgn0000251	10.93	11.07	10.74	10.88	11.01	11.11
1630803_at	---	9.16	9.31	9.23	9.39	9.26	9.23
1625172_s_at	FBgn0039890	9.96	10.1	10.06	10.22	10.19	10.21
1636991_s_at	FBgn0010435	7.84	7.99	8.04	7.03	7.1	7.82
1637601_at	FBgn0036509	8.44	8.58	8.74	8.31	8.18	8.52
1633292_a_at	FBgn0036272	10.28	10.43	10.59	10.77	10.51	10.65
1636255_s_at	FBgn0034117	9.64	9.78	9.43	9.54	9.52	9.69
1637244_at	---	7.71	7.85	7.66	8.02	7.74	7.68
1636210_at	FBgn0036354	8.77	8.91	8.49	9.36	8.97	8.96
1628283_at	FBgn0029999	8.57	8.71	8.57	8.79	8.65	8.48
1636801_at	FBgn0033352	8.99	9.13	9.22	9.05	9.07	8.98
1640813_at	FBgn0023536	8.04	8.19	8.22	8.29	8.2	8.08
1633764_a_at	FBgn0030813	7.25	7.4	7.58	7.9	7.59	7.69
1624480_at	---	9.16	9.3	9.42	9.47	9.24	9.06
1624684_at	FBgn0039401	8.14	8.28	8.2	8.45	8.28	8.19
1625549_at	FBgn0033842	8.55	8.69	8.49	9.16	8.57	8.65
1639873_at	FBgn0035901 /// FBgn003	7.47	7.62	7.15	7.45	7.51	7.5
1633174_at	FBgn0003525	11.39	11.53	11.25	11.73	11.51	11.68
1641424_at	FBgn0030768	8.6	8.75	8.75	9.08	8.93	8.86
1640576_a_at	FBgn0003015	10.32	10.46	10.52	10.61	10.15	10.36
1637799_at	FBgn0003257	9.79	9.94	10.08	9.92	9.87	9.93
1641687_at	FBgn0004908	8.44	8.59	8.82	8.82	8.62	8.62
1640268_at	FBgn0002781	7.84	7.98	7.56	7.76	7.74	7.89

1623130_at	---	7.05	7.19	6.97	7	7.03	7.19
1632233_at	FBgn0033316	9.15	9.3	9.25	9.45	9.27	9.2
1638179_at	FBgn0033209	11.2	11.35	11.15	10.67	11.11	11.24
1630774_s_at	FBgn0003371	7.34	7.48	8.28	7.87	7.29	7.71
1635904_s_at	FBgn0012049	10.32	10.47	10.33	10.24	10.34	10.47
1630887_a_at	FBgn0035500	10.54	10.69	10.54	10.64	10.53	10.7
1638358_s_at	FBgn0000242	7.49	7.63	7.05	7.36	7.54	7.63
1625590_a_at	FBgn0025720	9.91	10.05	9.7	9.99	9.98	10.07
1626553_at	FBgn0032702	9.04	9.18	9.22	9.24	9.17	9.24
1637319_at	FBgn0037781	7.8	7.94	7.6	8.17	8.15	7.93
1636628_at	FBgn0033486	9.79	9.93	9.83	10.02	9.92	9.97
1635634_at	FBgn0037102	8.8	8.94	9.05	8.99	9.04	9.08
1627567_at	FBgn0002914	8.64	8.78	8.84	9	8.88	8.81
1628743_at	FBgn0015229	9.89	10.03	9.96	10.01	9.9	10.09
1624539_at	FBgn0038870	8.43	8.58	8.51	8.48	8.38	8.47
1625137_at	FBgn0037967	8.27	8.41	8.19	8.71	8.44	8.37
1626304_at	---	11.22	11.36	11.11	11.09	11.12	11.32
1640741_at	FBgn0030806	7.11	7.25	7.25	7.64	7.4	7.45
1638014_at	FBgn0027617	7.58	7.72	7.93	8.25	7.66	7.8
1631849_at	FBgn0028375	8.98	9.12	8.9	8.92	9.01	9.18
1637546_at	FBgn0000100	13.59	13.73	13.71	13.48	13.59	13.7
1638104_a_at	FBgn0052951	8	8.14	8.71	8.13	8.04	8.17
1640796_a_at	FBgn0031119	9.02	9.16	9.08	9.28	9.26	9.41
1630027_s_at	FBgn0053113	12.29	12.43	12.23	12.2	12.09	12.5
1640187_a_at	FBgn0031115	8.53	8.67	8.58	8.81	8.52	8.58
1629117_at	FBgn0030930	9.2	9.34	9.15	9.06	9.16	9.3
1638680_at	FBgn0038857	8.88	9.02	9.12	9.14	9.01	9.08
1629797_at	FBgn0015797	8.42	8.56	8.45	8.26	8.5	8.54
1633491_s_at	---	8.76	8.9	8.6	8.45	8.88	8.94
1623335_a_at	FBgn0038326	10.2	10.34	10.24	10.15	10.11	10.28
1634408_at	FBgn0033971	9.01	9.15	9.09	8.9	8.85	9.12
1635476_at	FBgn0034614	8.67	8.81	9.02	9.16	9.07	8.93
1637758_at	FBgn0033584	8.89	9.03	9.09	9.31	8.85	9.02
1636465_at	FBgn0030659	8.04	8.18	8.16	8.38	8.32	8.18
1640713_at	FBgn0034919	9.3	9.44	9.65	9.69	9.54	9.63
1632489_a_at	FBgn0038425	8.54	8.68	8.7	8.83	8.69	8.72

1629001_at	FBgn0032454	9.3	9.44	9.47	9.5	9.4	9.45
1641115_at	FBgn0037482	9.1	9.24	9.33	9.54	9.18	9.29
1638527_a_at	FBgn0058196	10.35	10.49	10.35	10.57	10.53	10.63
1638605_at	FBgn0031893	8.95	9.09	8.83	9.1	9.29	9.1
1629124_at	FBgn0036248	9.44	9.58	9.59	9.83	9.73	9.8
1624901_at	FBgn0032907	8.33	8.47	8.44	8.67	8.87	8.74
1629941_a_at	FBgn0035829	10.52	10.66	10.5	10.66	10.71	10.85
1625806_at	FBgn0003134	9.28	9.42	9.44	9.33	9.39	9.51
1625672_s_at	---	7.39	7.53	6.36	6.33	6.88	7.17
1637830_s_at	FBgn0051145	7.04	7.18	7.45	6.6	6.53	6.93
1637810_at	FBgn0032446	8.07	8.21	7.97	8.17	8.2	8.22
1635967_at	FBgn0019662	7.29	7.43	7.3	7.27	7.24	7.31
1627478_at	FBgn0035347 /// FBgn003	8.7	8.84	9.15	8.75	8.73	8.86
1624231_s_at	FBgn0010348	11.3	11.44	11.72	11.58	11.36	11.55
1627888_at	FBgn0037875	9.71	9.85	9.7	9.74	9.61	9.86
1628801_at	---	7.36	7.5	7.6	7.73	7.65	7.58
1633338_at	---	9.37	9.51	9.45	9.64	9.56	9.63
AFFX-Dros-G	FBgn0001092	11.51	11.65	11.46	11.59	11.95	11.89
1634740_at	FBgn0030502	7.96	8.1	8.17	8.44	8.1	8.21
1634471_at	FBgn0053214	8.85	8.99	7.96	8.35	8.42	8.49
1639519_at	FBgn0032172	9.52	9.66	9.43	9.57	9.46	9.64
1637542_s_at	FBgn0052956	7.43	7.56	7.76	7.95	7.52	7.59
1641469_at	FBgn0032882	8.17	8.31	8.02	8.16	8.17	8.1
1637508_at	---	8.74	8.88	8.45	8.61	8.47	8.72
1637827_at	---	9.56	9.7	8.93	9.1	9.78	9.87
1627498_at	FBgn0053094	9.17	9.31	9.17	9.2	9.28	9.31
1623583_at	FBgn0031291	8.88	9.01	8.65	9.05	9.17	9.08
1636484_at	---	9.79	9.93	9.68	9.75	9.84	9.98
1639938_at	FBgn0036571	7.33	7.47	7.78	7.83	7.43	7.46
1628565_at	FBgn0031224	9.46	9.6	9.59	9.99	9.29	9.38
1631213_at	FBgn0031093	7.67	7.81	8.02	8.3	7.94	7.72
1628956_at	FBgn0026149	9.37	9.51	9.35	9.57	9.52	9.74
1641183_a_at	FBgn0032482	10.32	10.46	9.96	9.93	10.13	10.3
1630332_at	FBgn0031600	9.73	9.87	9.71	9.78	9.9	9.9
1633092_at	---	11.5	11.63	11.65	11.69	11.55	11.53
1625888_a_at	FBgn0035416	8.94	9.08	9.05	8.92	8.96	9.1

1640091_at	FBgn0030794	8.5	8.63	8.32	8.63	8.71	8.58
1633210_at	FBgn0035592	9.9	10.03	10.02	10	9.94	10.02
1626782_at	FBgn0032596	11.64	11.78	11.78	11.72	11.74	11.71
1633506_s_at	FBgn0036180	7.37	7.51	7.57	7.95	7.59	7.55
1629290_at	FBgn0025800	8.56	8.7	8.88	8.75	8.78	8.97
1638890_at	FBgn0021795	11.54	11.68	11.54	11.33	11.54	11.7
1634204_at	FBgn0012344	9.35	9.49	9.55	9.62	9.4	9.51
1640862_a_at	FBgn0015925	9.15	9.29	9.21	9.3	9.25	9.29
1633082_at	FBgn0038129	7.93	8.07	8.08	8.22	7.94	7.93
1623359_at	FBgn0003459	7.54	7.68	7.85	8.07	7.61	7.64
1629852_at	FBgn0035318	9.29	9.43	8.92	9.28	9.17	9.14
1626864_at	FBgn0033377	8.94	9.08	9.4	9.36	8.94	9.01
1636684_at	FBgn0051126	9.19	9.32	9.48	9.41	9.23	9.27
1639480_at	---	8.7	8.83	9.06	8.67	8.57	8.74
1628957_at	FBgn0001974	9.3	9.44	9.31	9.65	9.34	9.45
1638400_at	FBgn0033917	9.09	9.23	9.74	9.83	9.6	9.3
1636557_a_at	---	9.51	9.64	9.65	9.96	9.65	9.56
1624943_at	FBgn0030030	7.01	7.15	7.21	7.42	7.13	7.09
1639148_at	FBgn0032407	9.78	9.92	9.94	9.93	9.56	9.65
1632182_at	FBgn0030457	8.48	8.61	8.62	8.76	8.57	8.6
1634876_at	FBgn0032153	7.04	7.18	7.38	7.88	7.14	7.11
1640055_at	FBgn0034982	8.77	8.91	9.06	9.04	8.87	8.86
1628947_s_at	FBgn0002778	9.96	10.09	10.26	10.28	9.81	10.01
1640391_at	FBgn0000709	9.65	9.78	9.57	9.51	9.65	9.8
1639251_at	FBgn0039251	9.91	10.05	9.6	10.06	9.55	9.93
1624185_at	FBgn0037440	7.27	7.41	7.68	7.57	7.31	7.33
1633884_at	FBgn0034722	9.05	9.18	9.29	9.37	9.21	9.16
1623553_a_at	FBgn0039140	9.31	9.45	9.46	9.5	9.59	9.57
1632626_at	---	8.29	8.42	8.25	8.41	8.38	8.4
1636867_s_at	FBgn0038244	8.97	9.1	9.03	9.01	9.06	9.1
1634746_at	FBgn0035065	8.52	8.66	8.55	8.78	8.65	8.56
1633794_a_at	FBgn0031303	10.57	10.7	10.04	10.22	10.05	10.17
1638997_at	FBgn0050342	8.32	8.46	8.71	8.88	8.79	8.67
1632919_at	FBgn0038965	9.03	9.17	9.23	9.48	9.31	9.22
1634668_at	FBgn0019972	10.28	10.41	10.18	10.31	10.21	10.27
1631161_at	FBgn0011207	9.35	9.49	9.4	9.5	9.44	9.54

1626967_at	---	9.66	9.79	9.79	9.87	9.77	9.84
1635805_at	FBgn0034703	8.12	8.25	8.33	8.62	8.43	8.49
1630658_at	FBgn0052226	9.02	9.15	8.64	8.8	9.05	9.11
1633554_at	FBgn0000352	9.99	10.12	9.94	9.8	10.01	10.14
1627227_at	FBgn0014869	8.12	8.25	7.99	8.12	8.27	8.21
1638416_at	FBgn0015031	11.5	11.63	11.8	11.62	11.56	11.7
1640380_a_at	FBgn0035145	8.92	9.05	9.47	9.35	9.29	9.41
1634186_a_at	FBgn0039045	7.29	7.42	7.62	6.69	6.44	7.2
1633622_at	FBgn0031643	8.46	8.59	8.51	8.88	8.67	8.68
1628552_at	FBgn0038588	9.39	9.53	9.34	9.74	9.41	9.47
1627525_a_at	FBgn0028736	8.91	9.04	8.76	8.89	8.87	8.99
1638591_at	FBgn0032988	10.78	10.92	10.99	10.85	10.78	10.94
1629884_at	FBgn0051652	9.98	10.11	10.28	9.87	9.74	9.95
1627330_at	FBgn0032793	7.38	7.52	7.97	7.7	7.59	7.48
1626790_s_at	FBgn0020440	7.12	7.25	6.93	7.23	7.01	7.32
1640541_at	FBgn0005632	9.12	9.25	9.51	9.38	9.24	9.3
1639955_at	FBgn0022720	8.66	8.79	8.83	8.93	9.04	9
1623837_at	FBgn0031799	8.31	8.44	8.18	8.5	8.2	8.31
1624237_at	FBgn0034400	8.54	8.67	8.64	8.56	8.5	8.56
1638259_s_at	FBgn0027079	8.69	8.82	8.93	9.02	8.67	8.7
1631612_at	FBgn0040009	9.03	9.16	8.63	9.14	9.18	9.16
1639576_at	FBgn0004381	9.37	9.5	9.32	9.54	9.37	9.43
1626580_at	FBgn0026309	8.53	8.66	8.75	8.72	8.57	8.63
1625978_at	FBgn0032635	10.25	10.38	10.16	10.39	10.43	10.47
1624301_at	FBgn0035637	9.5	9.63	9.52	9.73	9.54	9.63
1629121_at	FBgn0032805	8.07	8.2	7.56	7.02	7.39	7.72
1629344_at	FBgn0039355	7.78	7.91	7.51	7.85	7.79	7.97
1624176_at	FBgn0035622	9.42	9.55	9.27	9.49	9.33	9.61
1632580_at	FBgn0033813	7.95	8.08	7.76	8.48	8.11	8.24
1640980_at	FBgn0038569	8.22	8.35	8.36	8.26	8.14	8.2
1628883_at	---	9.29	9.42	9.45	9.53	9.33	9.39
1631543_at	FBgn0027500 /// FBgn003	10.61	10.74	10.69	10.93	10.85	10.8
1632804_at	FBgn0038584	9.47	9.6	9.69	10.02	9.65	9.62
1634122_at	---	7.53	7.66	7.82	7.82	7.71	7.71
1635075_at	---	9.2	9.33	9.64	9.65	9.39	9.44
1639856_at	FBgn0032193	8.55	8.68	8.95	9.24	9.06	8.8

1637959_at	FBgn0038312	8.31	8.44	8.26	8.1	8.28	8.51
1641152_at	FBgn0031170	7.24	7.37	6.86	7.13	7.14	7.09
1630445_at	FBgn0010926	8.64	8.77	8.66	8.77	8.7	8.75
1639666_at	---	6.93	7.06	7.36	7.48	7.14	7.24
1633975_s_at	FBgn0033495	9.69	9.82	9.85	9.81	9.84	9.79
1634550_at	FBgn0037657	8.89	9.02	9.04	9.07	8.84	8.87
1640743_at	FBgn0000455	9.15	9.28	9.38	9.54	9.12	9.04
1641169_s_at	FBgn0031836	10.28	10.41	10.42	10.38	10.33	10.41
1635537_at	---	9.47	9.59	9.38	10.02	9.89	9.96
1638727_at	---	10.74	10.87	11.02	10.82	10.5	10.75
1636142_at	FBgn0030658	10.32	10.45	10.24	10.18	10.26	10.51
1638326_at	FBgn0038619	8.35	8.48	8.29	8.64	8.39	8.47
1636157_at	FBgn0035064	8.09	8.22	8.09	8.24	8.11	8.04
1623560_at	FBgn0037435	7.9	8.03	8.04	8.08	8.11	8.3
1635214_at	FBgn0002905	7.08	7.2	7.21	6.78	6.73	6.9
1623139_at	---	7.26	7.39	7.34	7.57	7.32	7.24
1639367_a_at	FBgn0033267	8.74	8.86	8.66	8.79	8.57	8.79
1625973_a_at	FBgn0040373	9.37	9.5	9.13	9.41	9.41	9.5
1624385_at	FBgn0037277	9.78	9.91	9.77	9.74	9.71	9.91
1629074_a_at	FBgn0036640	8.18	8.31	8.03	7.41	7.9	7.85
1640512_at	FBgn0028997	8.62	8.74	8.62	9.01	9.09	9.11
1625640_a_at	FBgn0039465	10.29	10.42	10.4	10.54	10.43	10.52
1638795_at	FBgn0034367	7.96	8.09	8.06	8.59	8.12	8.03
1631288_at	FBgn0030314	8.99	9.12	8.99	9.21	9.02	8.9
1627319_at	FBgn0029927	7.61	7.74	8.8	8.05	7.53	7.61
1626263_at	FBgn0036741	7.69	7.82	7.7	7.93	7.7	7.8
1628892_s_at	FBgn0036305	8.83	8.96	8.7	8.93	9.05	9.07
1638230_at	FBgn0029789	7.4	7.53	7.1	7.38	7.62	7.46
1634219_a_at	---	13.01	13.13	13.05	13.23	13.08	13.16
1626620_at	FBgn0027378	9.37	9.49	9.34	9.48	9.45	9.5
1640190_at	FBgn0035195	9.39	9.52	9.71	9.65	9.7	9.65
1628424_at	FBgn0039385	9.55	9.68	9.43	9.75	9.72	9.71
1628755_at	FBgn0037567	7.33	7.45	7.49	7.53	7.1	7.05
1625757_at	FBgn0051329 /// FBgn005	8.96	9.09	8.81	9.15	9.27	9.3
1635186_at	FBgn0036341	9.73	9.86	9.53	9.86	9.68	9.85
1627614_at	FBgn0033992	9.55	9.67	9.58	9.78	9.35	9.58

1641269_at	FBgn0028895	7.79	7.92	7.76	7.94	7.81	7.93
1626885_at	FBgn0030292	9.32	9.45	9.64	9.52	9.64	9.6
1636806_at	---	9.18	9.31	9.01	9.06	9.31	9.35
1637862_at	FBgn0038301	7.61	7.74	7.7	7.91	7.92	7.84
1636730_at	FBgn0029522	9.12	9.25	9.34	9.8	9.31	9.29
1633274_at	FBgn0031871	9.29	9.42	9.41	9.59	9.52	9.62
1641256_at	FBgn0036691	8.89	9.02	9.17	9.27	8.9	8.84
1629441_at	FBgn0036688	7.97	8.1	7.85	8.47	8.35	8.27
1629767_s_at	FBgn0004603	10.01	10.13	10.08	9.87	9.84	10.09
1639289_at	---	7.54	7.67	7.33	7.51	7.55	7.53
1637091_a_at	FBgn0037236	10.49	10.62	10.46	10.53	10.6	10.64
1625962_at	FBgn0003276	9.69	9.82	10.16	10.5	10.05	9.86
1635117_at	FBgn0001079	8.89	9.01	8.65	8.95	8.99	8.97
1625394_at	---	10.68	10.81	10.85	10.71	10.81	10.75
1632464_at	FBgn0039260	9.16	9.29	8.95	9.1	9.39	9.28
1634606_a_at	FBgn0027501	9.49	9.61	9.42	9.58	9.46	9.46
1641461_at	FBgn0028486	8.34	8.47	8.21	8.28	8.45	8.42
1638127_s_at	FBgn0030276	10.63	10.76	10.54	10.61	10.65	10.7
1627966_s_at	FBgn0034269	8.61	8.73	8.66	8.76	8.83	8.8
1640889_at	FBgn0030786	9.92	10.04	10.1	10.21	9.98	9.88
1632711_at	FBgn0035233	8.88	9.01	8.85	9.43	9.06	8.99
1640808_at	FBgn0034528	9.04	9.17	9.06	9	8.8	9.1
1632049_at	FBgn0032168	8.42	8.55	8.35	8.6	8.46	8.44
1639714_at	FBgn0001276	8.02	8.15	7.83	8.17	8.16	8.23
1634330_at	FBgn0002926	8.55	8.68	8.77	7.6	7.18	8.77
1624407_s_at	FBgn0015509	11.17	11.3	11.34	11.4	11.29	11.3
1626217_at	FBgn0016672	9.52	9.64	9.26	9.22	9.36	9.48
1639599_at	FBgn0031318	8.04	8.17	8.02	7.82	7.92	8
1631101_at	FBgn0036964	8.57	8.7	8.78	8.8	8.7	8.8
1627183_at	FBgn0015351	7.33	7.45	7.47	7.57	7.72	7.7
1640871_at	FBgn0025865	8.45	8.58	8.56	8.25	8.57	8.72
1635703_s_at	FBgn0013576	9.75	9.88	9.89	10.1	9.72	9.99
1625943_at	FBgn0038834	8.11	8.24	8.44	8.23	8.35	8.53
1634311_at	FBgn0030581	7.6	7.73	7.5	7.79	7.9	8.05
1627700_at	FBgn0039451	7.9	8.02	7.74	7.96	7.99	7.96
1629352_at	FBgn0010851	9.83	9.95	9.91	9.74	9.83	10.02

1641420_s_at	FBgn0037297	8.65	8.78	8.6	8.89	8.77	8.73
1633501_s_at	FBgn0004889	8.45	8.58	8.84	8.97	8.16	8.66
1640088_at	FBgn0027090	9.61	9.73	9.73	9.7	9.77	9.6
1623353_at	---	7.97	8.1	8.26	8.33	7.95	7.99
1641295_s_at	FBgn0022268	10.74	10.86	11.01	11.08	10.78	10.85
1638204_s_at	FBgn0026257	9.24	9.36	9.35	9.64	9.38	9.37
1639138_at	FBgn0039164	8.98	9.11	9.03	9.3	9.26	9.18
1639826_at	FBgn0052662	8.11	8.23	8.18	7.68	7.83	8.09
1639118_a_at	---	11.29	11.41	11.49	11.13	11.4	11.56
1633791_at	FBgn0031280	8.66	8.78	8.7	8.82	8.56	8.57
1631919_at	FBgn0031243	9.07	9.19	8.98	9.11	9.07	9.09
1633138_at	FBgn0052251	8.12	8.24	8.16	8.24	8.22	8.13
1640313_s_at	FBgn0019925	10.39	10.51	10.47	10.47	10.36	10.46
1627148_at	---	9.46	9.58	9.69	9.63	9.53	9.49
1635861_a_at	FBgn0032586	9.3	9.42	9.73	9.82	9.5	9.45
1631597_at	FBgn0038197	7.84	7.96	8.21	8.07	7.94	8.01
1635454_a_at	FBgn0037968	7.02	7.14	6.87	7.33	7.36	7.23
1641033_a_at	---	7.43	7.55	6.98	7.5	7.43	7.64
1624429_at	FBgn0035989	8.73	8.85	8.78	8.93	8.66	8.73
1641024_at	---	8.52	8.64	8.56	8.79	8.61	8.58
1627897_at	FBgn0038489	9.41	9.53	9.35	9.88	9.74	9.74
1629866_at	FBgn0025639	9.64	9.76	9.28	9.46	9.6	9.77
1632136_at	FBgn0039696	7.64	7.76	7.66	7.83	7.74	7.81
1629918_at	FBgn0033859	8.07	8.2	8.27	8.3	8.16	8.18
1626096_at	FBgn0038471	9.67	9.79	10.04	10.32	9.88	9.95
1627142_at	FBgn0037530	9.37	9.49	9.51	9.51	9.4	9.47
1627688_at	FBgn0034268	9.15	9.27	9.1	9.43	9.2	9.3
1636870_at	FBgn0037620	7.76	7.88	7.75	8.19	8.01	8.07
1627908_at	FBgn0037149	8.71	8.83	8.61	8.73	8.85	8.95
1625095_at	FBgn0037533	11.73	11.85	11.93	11.91	11.68	11.72
1636092_a_at	FBgn0004655	10.07	10.19	10.02	10.21	10.16	10.21
1632791_at	FBgn0052479	10.27	10.39	10.26	10.21	10.3	10.49
1640161_at	---	9.06	9.18	9.21	9.48	9.29	9.16
1641563_at	FBgn0037718	9.72	9.84	9.88	10.14	9.69	9.72
1624743_s_at	FBgn0005777	10	10.12	9.96	10.03	9.87	9.94
1623203_at	FBgn0032258	8.74	8.87	9.22	9.4	9.17	8.92

1641644_s_at	FBgn0000376	9.2	9.32	8.57	8.87	8.97	9.07
1635681_at	FBgn0029935	8.89	9.01	8.63	8.75	8.83	8.9
1623549_at	FBgn0039692	8.14	8.26	7.89	7.97	8.03	8.09
1636866_at	FBgn0038856	8.72	8.84	8.85	9.06	8.71	8.79
1635466_at	FBgn0011327	10.1	10.22	10.39	10.67	10.04	10.13
1624328_a_at	FBgn0011710	8.53	8.65	8.62	8.47	8.54	8.6
1625793_at	FBgn0015664	9.54	9.66	9.79	9.94	9.71	9.66
1624312_at	FBgn0031519	7.37	7.49	7.26	7.92	7.88	7.93
1637673_at	FBgn0038722	9.16	9.28	9.23	9.51	9.19	9.17
1630827_s_at	---	7.55	7.66	7.31	7.13	7.21	7.76
1632273_at	FBgn0039207	9.02	9.14	9.37	9.05	8.93	9.32
1640127_at	FBgn0036402	8.45	8.57	8.69	8.89	8.61	8.7
1630000_at	FBgn0030974	7.73	7.85	7.8	8.07	8	7.89
1627999_s_at	FBgn0014127	9.14	9.26	9.19	9.55	9.51	9.27
1629933_at	FBgn0029755	9.55	9.66	9.75	9.51	9.58	9.65
1632782_a_at	FBgn0038611 /// FBgn003	8.04	8.16	8.66	6.69	6.85	8.36
1624555_at	FBgn0004510	9.25	9.37	9.16	9.2	9.2	9.36
1640421_at	FBgn0036099	10.59	10.71	10.47	10.49	10.52	10.68
1628309_at	FBgn0031320	8.02	8.13	8.49	8.29	8.17	8.23
1634081_at	FBgn0027894	10.45	10.57	10.64	11.01	10.68	10.53
1637468_at	FBgn0028529	8.11	8.22	8.64	8.69	8.45	8.46
1628335_at	FBgn0036570	7.65	7.76	7.91	8.08	7.75	7.73
1637003_at	FBgn0029733	10.8	10.91	10.58	10.84	10.9	10.92
1640948_at	FBgn0036728	9.99	10.11	10.23	10.18	10.13	10.22
1638499_s_at	FBgn0033929	9.08	9.2	9.22	9.39	9.39	9.18
1641341_at	FBgn0031304	8.03	8.15	8.13	8.37	8.23	8.26
1633234_at	FBgn0031266	8.7	8.82	8.93	8.92	8.92	8.8
1640701_at	FBgn0038737	8.16	8.28	8.22	8.38	8.19	8.33
1641069_at	FBgn0037881	7.87	7.99	8.07	8.2	8.02	7.88
1623956_at	FBgn0024251	9.33	9.45	9.82	9.58	9.46	9.42
1624419_a_at	FBgn0010621	12.23	12.35	12.4	12.32	12.2	12.19
1628342_s_at	FBgn0027889	9.32	9.43	9.68	9.72	9.66	9.45
1626679_at	FBgn0038107	9.78	9.9	9.62	10	9.81	9.89
1626787_s_at	FBgn0038462	10.82	10.94	10.85	10.69	11.11	11.01
1625109_at	FBgn0004584	10.01	10.12	10	9.97	10.06	10.05
1634270_at	FBgn0032222	10.19	10.3	10.06	10.18	10.08	10.11

1626153_at	FBgn0003600	8.21	8.32	8.37	8.64	8.32	8.18
1629221_at	FBgn0027609	8.26	8.38	8.01	8.4	8.43	8.36
1625723_at	FBgn0037920	8.41	8.53	8.34	8.53	8.67	8.78
1624447_s_at	---	10.87	10.98	10.73	10.82	10.82	11.02
1639309_at	FBgn0038617	8.63	8.75	8.5	8.67	8.7	8.7
1640252_at	FBgn0038319	9.23	9.35	9.52	9.53	9.36	9.4
1635153_at	FBgn0039580	9.26	9.38	9.4	9.11	9.05	9.19
1625684_at	FBgn0037156	9.63	9.75	9.35	9.47	9.61	9.6
1635947_at	FBgn0040529	11.52	11.64	11.88	11.6	11.61	11.74
1624637_at	---	7.59	7.71	7.79	7.95	7.77	7.71
1640455_a_at	FBgn0038421	11.41	11.52	11.5	11.57	11.84	11.9
1641063_s_at	FBgn0032123	8.56	8.67	8.55	8.69	8.76	8.93
1626460_at	FBgn0024992	9.58	9.7	9.65	9.61	9.59	9.58
1640673_at	FBgn0026400	10.87	10.98	10.97	10.91	10.85	10.89
1630839_at	FBgn0014411	9.76	9.88	9.87	9.91	9.77	9.99
1632790_at	FBgn0033051	7.34	7.45	6.83	6.88	7.09	6.9
1636949_s_at	FBgn0033062	9.57	9.69	9.43	9.48	9.72	9.84
1625851_s_at	FBgn0005776	10.4	10.51	10.52	10.87	10.58	10.46
1641630_at	---	10.08	10.2	10.13	10.27	10.21	10.12
1631615_at	FBgn0026433	8.78	8.89	8.61	9.09	8.8	8.81
1623520_a_at	FBgn0032698	8.76	8.88	8.61	8.96	8.92	8.79
1628201_at	FBgn0025630	8.5	8.62	8.53	8.84	8.58	8.63
1630885_at	FBgn0031068	9.43	9.54	9.31	9.22	9.46	9.49
1640679_at	FBgn0033688	9.92	10.04	9.92	9.87	9.86	9.97
1623350_at	FBgn0010398	8.2	8.32	8.05	8.27	8.3	8.4
1631536_at	FBgn0040465	6.85	6.97	6.81	7.45	7.48	7.6
1637100_at	FBgn0004856	9.79	9.91	9.91	9.93	9.81	9.85
1637249_at	FBgn0032846	7.81	7.92	8.01	7.92	7.71	7.61
1636722_at	---	9.31	9.42	9.56	9.35	9.33	9.46
1639349_at	FBgn0030864	10.24	10.35	10.19	10.52	10.49	10.49
1632557_s_at	FBgn0031882	8.39	8.5	8.32	8.82	8.59	8.75
1634150_s_at	FBgn0015239	9.66	9.77	9.68	9.78	9.77	9.82
1640929_at	FBgn0036734	7.53	7.64	7.71	7.83	7.68	7.59
1635003_at	FBgn0027526	9.9	10.01	9.9	10.23	10.03	9.99
1630187_a_at	FBgn0030640 /// FBgn003	8.32	8.43	8.17	8.21	8.17	8.02
1631045_a_at	FBgn0037978	7.72	7.83	7.7	8.26	7.96	7.87

1634918_a_at	---	11.95	12.07	12.01	11.7	11.89	12.11
1638236_at	FBgn0032514	9.18	9.29	9.48	9.58	9.31	9.33
1635649_at	---	8.89	9	9.01	9.25	9.07	9.02
1638732_at	---	8.5	8.61	8.55	8.27	8.58	8.56
1632117_s_at	FBgn0004145	12.4	12.51	12.23	12.44	12.45	12.51
1623739_at	FBgn0011341	11.43	11.54	11.88	11.64	11.55	11.69
1629285_at	FBgn0037568	9.56	9.67	9.66	9.96	9.89	9.8
1624518_at	FBgn0025640	8.97	9.08	9.2	9.04	9.22	9.22
1641693_s_at	FBgn0052158	8.5	8.61	9.34	9.69	8.73	8.72
1625444_at	FBgn0042092	9.35	9.47	9.55	9.68	9.63	9.69
1637356_a_at	---	7.79	7.9	7.71	7.87	7.89	7.77
1624118_at	FBgn0015793	8.93	9.04	8.81	8.97	8.98	9.11
1638285_a_at	FBgn0025592	8.52	8.63	8.6	8.7	8.44	8.35
1623518_s_at	FBgn0051305 /// FBgn003	10.55	10.66	10.79	10.29	10.52	10.61
1629170_s_at	FBgn0015844	8.58	8.69	8.63	8.9	8.61	8.68
1633003_at	---	9.62	9.73	9.93	9.8	9.72	9.7
1622903_s_at	FBgn0030330	9	9.11	8.81	8.86	9.05	9.13
1641652_a_at	---	9.85	9.96	9.61	9.5	9.72	10
1625170_at	FBgn0035268	7.79	7.91	7.99	8.06	8.05	7.86
1640356_a_at	FBgn0035586	7.22	7.33	6.74	6.76	7.3	7.32
1627032_a_at	FBgn0027602	8.35	8.46	8.65	8.7	8.07	8.21
1641259_at	FBgn0013763	10.73	10.84	10.46	10.69	10.76	10.8
1628006_at	---	11.13	11.24	11.28	11.33	11.16	11.19
1637682_at	FBgn0026318	8.91	9.02	8.96	9.03	8.68	9.05
1632394_s_at	FBgn0031674	10.66	10.77	10.71	10.72	10.8	10.88
1623485_at	---	8.15	8.27	8.24	8.64	8.57	8.41
1641379_a_at	FBgn0039955	10.44	10.56	10.27	10.35	10.41	10.43
1623595_at	FBgn0032476	9.11	9.22	8.93	9.14	9.22	9.27
1632406_at	FBgn0031766	7.18	7.29	7.01	7.43	7.33	7.27
1625260_at	FBgn0030346	9.41	9.52	9.29	9.66	9.57	9.58
1636156_at	FBgn0036522	9.18	9.29	9.13	9.26	9.09	9.5
1640495_at	FBgn0010282	9.61	9.72	9.72	9.72	9.79	9.82
1637956_s_at	FBgn0045862	8.95	9.06	8.97	9.16	9.14	9.15
1625923_s_at	FBgn0024753	8.35	8.46	8.23	8.63	8.11	8.34
1628194_at	FBgn0023529	10.06	10.17	10.45	10.24	9.98	10.15
1629759_at	FBgn0042138	9.72	9.83	10.03	10.02	9.94	10.01

1633362_at	FBgn0038424	8.62	8.73	8.53	8.76	8.7	8.72
1639482_a_at	FBgn0052549	8.67	8.78	8.66	8.7	8.66	8.47
1627830_at	FBgn0022981	10.63	10.74	10.73	10.83	10.9	10.88
1623785_a_at	FBgn0003041	10.39	10.5	10.41	10.39	10.59	10.59
1635367_at	FBgn0004656	7.97	8.08	8.17	8	7.79	8.09
1641529_s_at	FBgn0037081	8.59	8.7	8.72	8.7	8.9	8.7
1636986_at	FBgn0001986	8.53	8.65	8.87	8.85	8.67	8.62
1636289_s_at	---	7.3	7.41	7.34	7.44	7.01	7.09
1634300_at	FBgn0025624	7.49	7.6	7.15	6.85	7.41	7.35
1637004_at	FBgn0033988	9.37	9.48	9.71	9.56	9.36	9.32
1627738_a_at	FBgn0002775	8.82	8.93	8.83	8.91	9.04	8.97
1630086_at	FBgn0029857	8.86	8.97	8.78	8.76	8.75	8.91
1629372_a_at	FBgn0028538	8.75	8.86	8.52	8.51	8.75	8.8
1633954_at	FBgn0038425	8.06	8.17	8.19	8.34	8.25	8.16
1626968_at	---	9.59	9.7	9.74	10.05	9.7	9.72
1633980_at	FBgn0035440	8.38	8.49	8.44	8.6	8.44	8.59
1635181_at	FBgn0038871	8.21	8.32	8.56	8.91	8.31	8.35
1628834_a_at	FBgn0020615	11.08	11.19	10.97	11.12	11.26	11.43
1634683_at	FBgn0011648	10.08	10.19	10.19	10.42	10.07	10.35
1635969_at	---	9.03	9.14	9.45	9.55	9.41	9.44
1631591_at	FBgn0051935	6.88	6.99	7.08	7.46	7.06	7.04
1629234_at	FBgn0053104 /// FBgn005	10.56	10.67	10.75	10.58	10.56	10.81
1631637_a_at	FBgn0015623	10.73	10.84	10.49	10.71	10.69	10.66
1636401_a_at	FBgn0020392	10.9	11.01	10.97	10.93	10.94	10.9
1630941_s_at	FBgn0003360	13.1	13.21	13.38	13.32	12.97	13.11
1623498_at	FBgn0039125	9.46	9.57	9.24	9.57	9.53	9.54
1638237_at	FBgn0038806	8.3	8.41	8.12	8.12	8.15	8.3
1636064_at	FBgn0037373	8.63	8.74	8.71	8.8	8.68	8.64
1639783_s_at	FBgn0005649	10.88	10.99	10.91	10.89	10.75	11.1
1632251_s_at	FBgn0032340	9.54	9.65	9.81	9.79	9.61	9.6
1630550_a_at	FBgn0032656	8.82	8.93	8.54	8.7	8.61	8.93
1630805_at	FBgn0014366	9.61	9.72	9.91	9.92	9.86	9.85
1626607_at	FBgn0035771	9.78	9.89	9.91	10.04	9.85	9.94
1625290_at	---	11.98	12.09	12.16	12.17	12.02	12.19
1634565_at	FBgn0032205	8.66	8.77	8.87	9.52	8.96	9.04
1633740_at	FBgn0030066	7.66	7.77	7.48	7.9	7.62	7.72

1625683_at	FBgn0039341	9.81	9.92	9.88	9.57	9.69	9.94
1636781_at	FBgn0033187	8.63	8.73	8.81	8.54	8.52	8.66
1632565_at	---	10.34	10.45	10.28	10.37	10.54	10.56
1628869_s_at	FBgn0039733	8.43	8.54	8.1	8.48	8.55	8.56
1630551_at	FBgn0036772	7.94	8.04	8.33	8.37	7.82	8.04
1631425_at	FBgn0036887	10.71	10.82	10.46	11.18	10.86	10.7
1637816_s_at	FBgn0003738	12.56	12.66	12.48	12.64	12.7	12.61
1636353_s_at	FBgn0037612	9.43	9.54	9.16	9.47	9.43	9.33
1640194_a_at	FBgn0040057	10.73	10.83	10.97	10.95	10.78	10.94
1637262_at	FBgn0038636	8.31	8.41	8.62	8.86	8.59	8.4
1638737_at	FBgn0030687	8.63	8.74	8.74	8.84	8.7	8.61
1638371_at	FBgn0051849	7.62	7.73	7.66	8	7.8	7.75
1633301_at	FBgn0031229	10.18	10.29	10.35	10.46	10.33	10.4
1629039_at	FBgn0034793	9.73	9.83	9.65	9.88	9.56	9.71
1627861_s_at	FBgn0010548	8.27	8.38	8.26	8.32	8.3	8.19
1638318_at	FBgn0033994	8.31	8.41	7.88	7.98	8.13	8.43
1630753_at	FBgn0030115 /// FBgn003	9.34	9.44	9.21	9.49	9.43	9.51
1625617_at	---	9.74	9.85	10	10.02	10.04	9.95
1636122_at	FBgn0030869	8.59	8.69	8.71	8.74	8.72	8.69
1634243_a_at	FBgn0039348	10.05	10.16	10.21	10.15	10.15	10.01
1640842_at	FBgn0032190	10.38	10.49	10.37	10.56	10.46	10.5
1641510_at	FBgn0021796	8.98	9.09	9	9.19	9.17	9.01
1630101_s_at	FBgn0024308	9.28	9.38	9.08	8.97	9.21	9.2
1640504_at	FBgn0040521	8.35	8.46	8.76	8.88	8.71	8.7
1623673_at	FBgn0037539	8.05	8.16	7.86	8.12	8.24	8.15
1633249_at	---	8.42	8.53	8.54	8.49	8.55	8.53
1628241_at	FBgn0032873	9.16	9.27	9.31	9.67	9.27	9.25
1639097_at	FBgn0000927	10.62	10.73	10.45	10.79	10.75	10.71
1636052_at	FBgn0001612	9	9.11	9.03	9.24	9.06	9.08
1640395_a_at	FBgn0016794	10.31	10.41	10.5	10.59	10.32	10.39
1627828_s_at	FBgn0005654	8.34	8.44	8.45	8.72	8.53	8.35
1634854_at	FBgn0025621	7.94	8.04	7.84	8.08	8	7.82
1630018_at	FBgn0003480	8.77	8.87	8.31	8.98	8.82	8.8
1640761_at	FBgn0028648	9.11	9.22	9.4	9.3	9.26	9.25
1636727_at	FBgn0030790	10.19	10.29	9.87	10.17	10.17	10.41
1639215_at	FBgn0024994	9.94	10.05	9.69	9.64	9.72	10.03

1624186_at	FBgn0036028	8.38	8.49	8.22	8.64	8.64	8.64
1636513_a_at	FBgn0001309	9.23	9.34	9.45	8.94	9.17	9.63
1636068_a_at	FBgn0046812	9.77	9.87	9.97	9.56	9.67	9.76
1636038_at	FBgn0037299	9.12	9.22	8.94	8.81	8.92	9.13
1634157_at	FBgn0025463	10.62	10.73	10.6	11.09	10.81	10.7
1631513_at	---	10.42	10.52	10.44	10.6	10.67	10.67
1628804_at	FBgn0034231	8.81	8.91	8.9	8.79	8.93	9.04
1638923_at	---	10.81	10.91	10.42	10.61	10.54	10.6
1626591_at	FBgn0052434	8.75	8.85	8.64	8.63	8.74	8.77
1635407_at	FBgn0052772	8.7	8.81	8.78	8.82	8.63	8.75
1627141_at	FBgn0039710	9.44	9.55	9.29	9.51	9.68	9.57
1632288_at	FBgn0026143	9.76	9.87	9.82	10.08	9.89	9.82
1623449_at	FBgn0032014	11.88	11.98	11.84	12.09	11.88	11.93
1640151_at	FBgn0033898	8.74	8.85	8.76	8.89	8.88	8.84
1628712_at	FBgn0030114	7.25	7.35	7.13	6.79	6.97	7.05
1638447_s_at	FBgn0033177	7.69	7.8	7.64	7.79	8.02	7.72
1625770_at	FBgn0035518	8.23	8.33	8.31	8.45	8.37	8.35
1625276_a_at	FBgn0000565	8.63	8.73	8.62	8.98	8.8	8.69
1638008_s_at	FBgn0039886	7.34	7.44	7.49	6.88	6.98	7.34
1627763_at	FBgn0051048	7.03	7.13	6.79	7.14	6.94	6.75
1624632_at	FBgn0011606	9.55	9.66	9.7	9.9	9.79	9.78
1632404_at	FBgn0028468	10.2	10.31	10.02	10.48	9.87	10.17
1628632_at	---	11.2	11.3	11.21	11.35	11.21	11.27
1624483_at	FBgn0036450	8.6	8.7	8.68	8.87	8.68	8.64
1632180_at	FBgn0033038	7.67	7.78	8.27	8.36	8.01	7.83
1624062_at	FBgn0035407	8.33	8.44	8.29	8.72	8.59	8.64
1639024_at	FBgn0037561	7.55	7.65	7.81	7.73	7.55	7.52
1636238_at	FBgn0035959	9.35	9.45	9.76	10.19	9.77	9.76
1634077_at	FBgn0030792	10.01	10.11	10.03	10.27	9.99	9.96
1632455_at	FBgn0031684	10.36	10.46	10.41	10.52	10.43	10.42
1628626_at	FBgn0052537	7.09	7.2	7.18	7.62	7.69	7.56
1637033_at	---	7.09	7.19	7.17	7.24	7.29	7.22
1637723_at	FBgn0002781	9.58	9.68	9.5	9.63	9.46	9.56
1633171_at	FBgn0031252	8.88	8.98	8.82	9.08	9.16	9.15
1628969_s_at	FBgn0033915	9.68	9.78	9.9	10.2	9.71	9.86
1638290_at	FBgn0052528	10.09	10.19	10.06	10.36	10.19	10.24

1637860_at	FBgn0004406	7.77	7.88	7.81	8.07	8.03	7.86
1634437_at	FBgn0036306	8.55	8.66	8.78	8.91	8.82	8.91
1625738_at	FBgn0037664	8.32	8.42	8.41	8.44	8.43	8.41
1627139_at	FBgn0033315	7.97	8.07	7.34	7.95	8.29	8.27
1627118_at	FBgn0033973	6.98	7.09	7.14	7.48	7.56	7.42
1626617_at	FBgn0000524	10.2	10.3	9.86	10.03	10.19	10.26
1638962_at	FBgn0030631	8.76	8.87	8.81	8.76	8.78	8.82
1636192_at	FBgn0036035	9.19	9.29	9.7	9.48	9.42	9.55
1627006_at	---	12.22	12.33	12.37	12.3	12.37	12.42
1623809_s_at	FBgn0030151	11.21	11.31	11.46	11.48	11.35	11.32
1635781_s_at	FBgn0038167	7.36	7.46	7.24	7.53	7.39	7.35
1638874_at	FBgn0025335	10.32	10.43	10.15	10.23	10.54	10.57
1635960_at	---	9.08	9.19	9.05	9.27	9.13	9.32
1627027_at	---	10.51	10.62	10.3	10.52	10.52	10.57
1638824_a_at	FBgn0004227	7.39	7.49	8.02	7.94	7.76	7.6
1623040_at	FBgn0039065	9.83	9.93	9.99	9.98	10.08	10.04
1625637_at	FBgn0035028	9.17	9.27	9.14	9.08	9.09	9.09
1641699_at	FBgn0026326	9.29	9.39	9.35	9.48	9.28	9.38
1628466_s_at	FBgn0028689	11.03	11.14	11.46	11.51	11.33	11.24
1639232_s_at	FBgn0040282	8.55	8.65	8.58	8.75	8.56	8.43
1628057_at	FBgn0028495	8.6	8.7	8.76	8.91	8.81	8.66
1627539_at	---	8.9	9	8.79	8.95	8.92	8.92
1640318_at	---	9.71	9.81	9.52	9.96	9.76	9.6
1641459_at	FBgn0025608	9.53	9.63	9.61	9.76	9.63	9.59
1634178_at	FBgn0030448	9.65	9.75	9.66	9.52	9.45	9.61
1623864_at	FBgn0036117	9.47	9.57	9.34	9.72	9.26	9.41
1630423_at	FBgn0034271	8.52	8.62	8.4	8.78	8.62	8.64
1639995_a_at	FBgn0033427	7.37	7.47	7.52	7.83	7.11	7.2
1631137_at	FBgn0036237	10.56	10.66	10.49	10.5	10.61	10.68
1629014_s_at	FBgn0037298	9.49	9.59	9.61	9.61	9.63	9.59
1634414_at	---	9.68	9.78	10.06	10.07	9.75	9.86
1623641_at	---	8.56	8.66	8.58	8.4	8.66	8.72
1638147_at	FBgn0030883	8.76	8.86	8.54	8.65	8.82	8.95
1638927_at	FBgn0035156	9.29	9.39	9.07	9.22	9.29	9.43
1629423_at	FBgn0028546	9.52	9.62	9.56	9.34	9.61	9.57
1627664_a_at	FBgn0030499	9.4	9.5	9.34	9.64	9.56	9.52

1627295_s_at	FBgn0010315	9.7	9.8	9.72	9.97	9.79	9.9
1630140_at	FBgn0032374	9.33	9.43	9.15	9.35	9.76	9.73
1631520_at	FBgn0033155	9.78	9.88	9.75	9.63	9.78	9.85
1639243_at	FBgn0033964	7.7	7.8	7.93	7.78	7.78	7.88
1631622_at	FBgn0034109	7.87	7.98	8.07	8.17	8.05	8.07
1628657_at	---	7.13	7.23	8.11	7.62	8.13	7.11
1637940_s_at	FBgn0035981	10.07	10.18	10	10.01	10	10.04
1628862_at	FBgn0027508	8.39	8.49	8.29	8.42	8.39	8.47
1629623_at	---	9.48	9.58	9.33	9.56	9.63	9.59
1632838_at	FBgn0020235	11.47	11.57	11.84	11.74	11.69	11.73
1625596_at	FBgn0020626	10.21	10.31	10.19	10.23	10.11	10.15
1636797_at	FBgn0021750	8.44	8.54	8.7	8.68	8.27	8.26
1626978_at	---	8.82	8.92	9.07	9.12	8.74	8.82
1630433_at	FBgn0037643	9.89	9.99	10.22	10.12	10.12	10.02
1622973_at	FBgn0038110	9.03	9.13	9.15	9.16	9.17	9.12
1632105_a_at	FBgn0026084	12.43	12.53	12.5	12.45	12.37	12.5
1626731_at	FBgn0010235	9.83	9.93	10	10.4	10.08	10.01
1631798_s_at	FBgn0039360	8.8	8.9	8.86	8.94	8.97	9.03
1638511_at	FBgn0010803	10.44	10.54	10.44	10.73	10.49	10.54
1636265_s_at	FBgn0003502	8.77	8.87	8.8	8.87	8.84	9.14
1634779_at	---	9.21	9.31	9.12	9.51	9.5	9.65
1629901_at	FBgn0039638	8.05	8.15	8.21	8.68	8.52	8.19
1636486_at	FBgn0004868	9.18	9.28	9.33	9.58	9.35	9.34
1641488_at	FBgn0035632	9.15	9.25	8.8	8.83	8.88	9.18
1637497_at	FBgn0036104	8.72	8.82	8.55	8.86	8.81	8.83
1628285_a_at	FBgn0017550	10.13	10.23	10.46	10.52	10.35	10.32
1627259_a_at	FBgn0003028	11.19	11.29	11.28	11.33	11.25	11.43
1627666_at	FBgn0037379	8.07	8.17	8.19	8.39	8.16	8.12
1632618_a_at	---	9.49	9.59	9.18	9.22	9.28	9.54
1625839_at	FBgn0042083	8.9	9	9.27	9.35	8.84	8.85
1641241_at	---	7.65	7.75	7.44	7.77	7.71	7.81
1624984_at	FBgn0037602	7.21	7.31	7.7	7.62	7.08	7.15
1625179_at	FBgn0039145	8.76	8.86	8.84	9.02	8.96	8.95
1639168_at	FBgn0037377	9.41	9.51	9.48	9.6	9.36	9.35
1624354_at	FBgn0013717	9.67	9.77	9.76	9.92	9.67	9.65
1639981_at	FBgn0015299	11.64	11.74	11.44	11.92	11.63	11.62

1629160_s_at	---	8.57	8.67	8.44	8.73	8.35	8.59
1632483_at	FBgn0004867	14.01	14.11	14.05	14.03	14.01	14.03
1623402_at	FBgn0032859	11.48	11.58	11.68	11.6	11.53	11.82
1633139_at	---	9.15	9.24	9.45	9.31	9.26	9.24
1638560_a_at	FBgn0033424	9.86	9.96	10.11	9.83	9.95	10.04
1625963_at	FBgn0039870	9.6	9.7	10.05	10.27	9.98	9.98
1624251_a_at	FBgn0031066 /// FBgn004	11.74	11.83	11.95	11.73	11.87	11.93
1628990_at	FBgn0001205	7.73	7.83	7.77	7.66	7.71	7.6
1640434_at	FBgn0033773	10.11	10.21	10.06	10.27	10.22	10.25
1625999_at	FBgn0037348	7.97	8.07	8.14	8.35	8.29	8.23
1630756_at	FBgn0029840 /// FBgn002	10.37	10.47	10.34	10.39	10.5	10.53
1627058_at	---	8.68	8.77	8.75	8.87	8.82	8.75
1641689_at	FBgn0033229	8.83	8.93	8.7	8.74	8.89	8.98
1637475_at	FBgn0030241	10.54	10.64	10.57	10.73	10.65	10.62
1627822_at	FBgn0029685	8.07	8.17	7.86	8.35	8.24	8.21
1625317_at	FBgn0034933	8.2	8.3	8.59	8.53	8.45	8.37
1638841_at	FBgn0034029	9.02	9.12	9.18	9.11	9.07	9.03
1625370_s_at	FBgn0050011	9.12	9.22	9.25	8.73	8.9	9.15
1631249_at	FBgn0036536	8.72	8.82	8.56	9.18	8.83	8.95
1629666_at	---	8.64	8.73	8.79	9.15	8.76	8.8
1640894_at	---	8.91	9.01	8.72	8.82	9.04	9.01
1641214_at	FBgn0032060	8.84	8.93	8.91	8.99	8.81	8.97
1624030_at	FBgn0023171	8.32	8.42	8.36	8.67	8.65	8.66
1629766_at	FBgn0051037	8.36	8.46	8.21	8.25	8.34	8.37
1628351_at	FBgn0029503	8.49	8.59	8.86	8.96	8.87	8.91
1635007_at	FBgn0040271	6.93	7.03	7.39	7.14	7.08	7.5
1623251_at	FBgn0037184	8.51	8.6	8.4	8.59	8.55	8.67
1635881_at	FBgn0039254	8.5	8.6	8.49	8.78	8.48	8.5
1638394_at	FBgn0034792	9.3	9.39	9.49	9.65	9.44	9.3
1640568_at	FBgn0027841	8.17	8.26	8.29	8.42	8.2	8.17
1637649_at	FBgn0033162	11.12	11.22	11.46	11.23	11.17	11.11
1638507_at	FBgn0035272	9.9	9.99	10.02	10.06	9.86	9.9
1626299_at	FBgn0004649	11.67	11.77	11.63	11.79	11.71	11.65
1637162_at	FBgn0039831	8.58	8.67	8.67	8.55	8.43	8.52
1628596_at	FBgn0034735	7.25	7.34	7.72	7.75	7.52	7.5
1639381_at	FBgn0033979	11.8	11.9	11.66	11.97	11.93	11.39

1638770_a_at	FBgn0039056	9.95	10.05	9.87	9.47	9.65	9.85
1635911_s_at	FBgn0030342	8.71	8.8	8.76	8.9	8.83	8.71
1637730_at	FBgn0036395	8.56	8.66	8.32	8.68	8.63	8.66
1630529_at	FBgn0031247	9.14	9.24	9.32	9.56	9.11	8.97
1636341_at	FBgn0001086	10.4	10.49	10.45	10.73	10.68	10.55
1623023_at	FBgn0039919	9.51	9.61	9.52	9.72	9.53	9.67
1623330_at	FBgn0035641	9.66	9.75	9.57	10.09	9.73	9.69
1624478_at	FBgn0025638	7.28	7.37	7.38	7.58	8.2	8.3
1632835_at	---	8.96	9.06	8.75	9.13	9.18	9.17
1637747_s_at	FBgn0033713	9.59	9.69	9.46	9.73	9.73	9.84
1637282_at	FBgn0038328 /// FBgn002	9.53	9.63	9.63	9.89	9.51	9.51
1626219_s_at	FBgn0040295	10.59	10.68	10.78	10.77	10.63	10.65
1639821_at	FBgn0031540	8.73	8.83	8.8	9.54	8.75	8.78
1627851_at	FBgn0034307	7.96	8.06	7.98	8.17	8	8.07
1636520_s_at	FBgn0035111	9.63	9.72	9.71	10.03	9.73	9.79
1641031_s_at	FBgn0039350	10.76	10.85	11.21	11.42	11.02	10.83
1631463_a_at	FBgn0000166	11.03	11.12	10.67	10.46	10.55	10.88
1630620_at	---	9.08	9.17	8.72	9.08	9.38	9.21
1625797_at	FBgn0030530	8.46	8.56	8.52	8.5	8.52	8.48
1628390_at	FBgn0036533	9.95	10.04	10.09	9.89	9.83	10.04
1627122_at	FBgn0052767	9.05	9.15	8.89	8.61	9	9.31
1636610_at	FBgn0036396	8.59	8.68	8.51	8.69	8.52	8.79
1632545_s_at	FBgn0034158	9.12	9.22	9.13	9.43	9.18	9.25
1627253_at	FBgn0015376	8.23	8.32	8.35	8.55	8.18	8.3
1627827_a_at	FBgn0026373	9.49	9.59	9.61	9.79	9.6	9.51
1632913_at	FBgn0030010	8.4	8.49	8.24	8.23	8.5	8.54
1626883_at	FBgn0033183	10.79	10.88	10.68	10.72	10.9	10.85
1634592_at	---	8.47	8.57	8.65	8.81	8.61	8.61
1636271_a_at	FBgn0053066	8.36	8.45	8.34	8.35	8.12	8.3
1626682_s_at	FBgn0031769	9.95	10.04	10.28	10.72	10.22	9.95
1635799_at	FBgn0030082	10.22	10.31	9.98	10.21	10.34	10.33
1637946_at	FBgn0035951	7.92	8.02	7.86	8.06	8.01	7.94
1638073_at	FBgn0030552	9.87	9.97	9.92	10.15	10.15	10
1627697_at	FBgn0033672	9.06	9.16	9.08	8.79	9.04	9.01
1637461_at	FBgn0031813	7.18	7.27	7.31	7.36	6.77	6.75
1627707_at	FBgn0037980	8.59	8.68	8.3	8.68	8.63	8.58

1627641_s_at	FBgn0040011	9.72	9.81	9.6	9.78	9.72	9.91
1640821_at	---	9.19	9.28	9.45	9.81	9.45	9.26
1639332_at	FBgn0025806	10.55	10.64	10.67	10.68	10.83	10.89
1637143_at	---	8.33	8.42	8.87	8.57	8.43	8.38
1632634_at	FBgn0037243	9.6	9.7	9.73	9.8	9.73	9.75
1637899_at	FBgn0033692	8.05	8.14	7.81	8.18	8.19	8.18
1628974_at	---	9.32	9.41	9.27	9.36	9.43	9.72
1628663_s_at	FBgn0030956	10.08	10.17	9.96	10.26	10.11	10.12
1637203_at	FBgn0037345	7.73	7.83	7.67	7.76	7.83	7.96
1628705_at	FBgn0039776	8.57	8.66	9.36	8.06	7.62	8.84
1630859_s_at	---	7.95	8.04	8.14	8.23	8.13	8.26
1640750_at	FBgn0032622	8.25	8.35	8.19	7.98	8.16	8.22
1631690_a_at	FBgn0034527	8.75	8.84	8.59	8.77	8.87	8.91
1634454_at	---	7.99	8.08	8.23	8.06	7.95	7.99
1634035_s_at	FBgn0061242	8.75	8.84	8.62	9.01	8.84	8.76
1634381_a_at	FBgn0031566	9.09	9.19	9.01	9	8.91	8.9
1631636_at	FBgn0032050	9.25	9.34	9.79	9.54	9.33	9.35
1636844_at	FBgn0029173	8.98	9.07	8.92	9.16	9.26	9.25
1638456_at	FBgn0033918	9.75	9.84	9.91	10	9.88	9.73
1623702_at	FBgn0029882	10.95	11.04	11.12	11.37	11.16	11.15
1638847_s_at	FBgn0003517	13.82	13.91	13.98	13.86	13.88	13.92
1623487_at	FBgn0016792	10.63	10.72	10.26	10.46	10.49	10.74
1640857_at	FBgn0039118	7.23	7.32	8.01	8.21	6.12	5.84
1624638_a_at	FBgn0037024	11.09	11.19	11.14	11.26	11.34	11.22
1625102_at	FBgn0038651	7.96	8.05	8.25	8.14	8.1	8.14
1626294_a_at	FBgn0051641	10.43	10.52	10.27	10.5	10.34	10.48
AFFX-DapX-	---	8.51	8.6	8.85	9.15	8.55	8.36
1629078_s_at	FBgn0020386	9.43	9.52	9.44	9.1	9.39	9.73
1632669_at	FBgn0014861	10.78	10.87	10.97	11.29	11.08	10.82
1625854_at	FBgn0037780	8.11	8.2	7.89	8.26	8.2	8.05
1629153_s_at	---	9.45	9.54	9.36	9.63	9.71	9.7
1632261_at	FBgn0052732	9.62	9.71	9.73	9.81	9.54	9.57
1628318_at	FBgn0037025	8.45	8.54	8.63	8.66	8.66	8.46
1640828_at	FBgn0037757	7.18	7.27	6.86	7.14	7.19	7.11
1628435_at	FBgn0003498	10.16	10.25	10.17	10.23	10.11	10.27
1640053_at	FBgn0035271	9.6	9.69	9.77	9.65	9.54	9.54

1627515_at	FBgn0032731	9.72	9.81	9.57	9.74	9.66	9.86
1638397_at	FBgn0034959	7.39	7.48	7.5	6.98	7.35	7.82
1639659_at	FBgn0021875	7.93	8.03	8.26	8.17	8.12	8.17
1634282_s_at	FBgn0026015	8.05	8.14	8.23	8.27	8.23	8.11
1623722_at	FBgn0015520	9.89	9.98	9.9	10.14	10.08	10.1
1624614_at	FBgn0038428	9.43	9.52	9.47	9.47	9.52	9.46
1635552_s_at	FBgn0051473	9.55	9.64	9.73	9.85	9.74	9.78
1627405_at	FBgn0035415	8.43	8.52	9	8.95	8.59	8.49
1634253_at	FBgn0030740	11.29	11.38	11.06	11.33	11.37	11.44
1639252_s_at	FBgn0039635	9.75	9.84	9.97	10.01	9.83	9.85
1623519_at	FBgn0000588	9.91	10	9.45	9.79	10.07	10.04
1632687_at	FBgn0036558	8.27	8.36	8.43	8.76	8.5	8.43
1632041_s_at	---	8.18	8.27	8.27	8.72	8.43	8.54
1626289_at	FBgn0020930	8.36	8.45	8.39	8.64	8.39	8.39
1631271_a_at	FBgn0026575	10.65	10.74	10.63	10.59	10.55	10.76
1629133_at	FBgn0029861	8.67	8.76	8.46	8.6	8.78	8.81
1630278_s_at	FBgn0004571	9.9	9.99	9.98	9.86	9.92	9.84
1632073_at	FBgn0036913	8.15	8.24	8.12	8.15	8.16	8.16
1627617_at	---	9.4	9.49	9.49	9.41	9.17	9.34
1635293_s_at	FBgn0036020	8.67	8.76	8.64	8.87	8.92	8.83
1628362_s_at	FBgn0029686	7.94	8.03	8.14	8.31	8.2	8.09
1632985_at	FBgn0035390	9.75	9.84	9.77	9.75	9.64	9.79
1638510_at	FBgn0034447	9.67	9.76	9.8	10.2	9.83	9.86
1640375_at	FBgn0026261	10.02	10.11	10.35	10.37	10.22	10.29
1627816_a_at	FBgn0052264	8.81	8.9	9.32	9.06	8.86	8.82
1625720_at	FBgn0039557	7.46	7.54	7.78	8.05	7.74	7.73
1624996_at	FBgn0039508	8.89	8.98	8.88	8.99	8.87	8.85
1627220_at	FBgn0017567	10.81	10.9	11.14	10.98	11.06	10.98
1636129_s_at	FBgn0031238	8.24	8.33	8.39	8.45	8.39	8.28
1632839_a_at	FBgn0037720	8.81	8.9	8.82	8.97	8.86	8.8
1627996_a_at	FBgn0037339	9.7	9.79	9.6	9.83	9.67	9.75
1631109_at	FBgn0034853	8.86	8.95	8.79	8.83	8.87	8.91
1630245_at	FBgn0003401	10.06	10.15	10.24	10.07	10.03	10.2
1634616_at	---	8.22	8.31	8.45	8.73	8.57	8.48
1639858_s_at	FBgn0026369	8.92	9.01	8.84	8.91	8.93	8.92
1623806_at	FBgn0037555	9.29	9.38	9.44	9.45	9.39	9.44

1633466_at	FBgn0036686	8.98	9.07	9.22	9.17	9.1	9.12
1640070_a_at	FBgn0039809 /// FBgn000	11.67	11.76	12.07	11.93	11.66	11.79
1637738_at	FBgn0038808	10.01	10.1	10.14	10.21	10.12	10.1
1634492_s_at	FBgn0037093	8.67	8.76	8.42	8.57	8.58	8.92
1638465_at	FBgn0037998	7.93	8.01	7.95	8.08	8	7.85
1637089_at	---	10.53	10.62	10.35	10.51	10.54	10.64
1625017_at	FBgn0034750	9.19	9.28	8.97	9.37	9.32	9.43
1624928_at	FBgn0036746	8.56	8.65	8.66	8.64	8.51	8.67
1637064_at	---	11.64	11.72	11.97	11.89	11.87	11.9
1640246_at	FBgn0022943	9.51	9.6	9.67	10.03	9.74	9.69
1635257_at	FBgn0031573	8.06	8.15	8.18	8.38	8.26	8.16
1637581_at	FBgn0005630	7.76	7.85	7.55	8.06	7.93	7.89
1629990_at	FBgn0031676	9.05	9.13	8.81	8.81	8.94	9.09
1623448_at	FBgn0038039	9.28	9.37	9.31	9.45	9.62	9.53
1633634_at	FBgn0001133	8.19	8.28	8.33	8.45	8.47	8.36
1631619_a_at	---	8.62	8.7	8.63	8.15	8.25	8.65
1625907_at	FBgn0034926	7.44	7.53	7.64	7.84	7.62	7.5
1635708_at	FBgn0023513	8.26	8.35	8.19	8.56	8.37	8.29
1632434_at	FBgn0013563 /// FBgn000	7.67	7.76	7.56	8.11	7.74	7.65
1624788_at	FBgn0038692	8.88	8.97	8.81	9.05	9.04	9.03
1627152_at	FBgn0033477	10.11	10.2	9.99	10.57	10.06	10.03
1629233_s_at	FBgn0037315	8.88	8.97	8.88	8.98	9.1	9.02
1637349_at	FBgn0028695	9.77	9.86	9.78	10.08	9.93	9.67
1622933_at	FBgn0034729	7.53	7.62	7.56	7.95	8.03	8.22
1641681_s_at	FBgn0035950	9.03	9.11	9.12	9.18	8.96	8.83
1641616_at	FBgn0010590	11.62	11.71	11.69	11.78	11.74	11.56
1632443_at	FBgn0035690	7.25	7.33	7.52	7.46	7.3	7.39
1634727_a_at	FBgn0003701	8.72	8.81	8.65	9.01	8.78	8.71
1634773_at	---	10.81	10.9	11	10.68	10.79	10.99
1627919_at	FBgn0024978	8.81	8.9	9.06	8.89	8.92	8.94
1633594_at	FBgn0028688	10.69	10.77	10.86	11.04	10.84	10.75
1640066_at	FBgn0037504	8.92	9.01	9.47	9.44	9.11	9.27
1629111_at	FBgn0037109	8.23	8.31	8.25	8.61	8.6	8.52
1626110_a_at	FBgn0030606	10.47	10.56	10.2	10.45	10.56	10.58
1622980_at	---	9.94	10.03	9.99	10.12	10.08	10.01
1630341_at	---	9.82	9.91	9.69	9.83	9.93	10

1640329_s_at	FBgn0036111	10.83	10.91	10.87	11.01	10.72	10.86
1640995_at	FBgn0038976	10.92	11.01	11.16	11.2	11.11	11.01
1639759_s_at	FBgn0010633	10.4	10.48	10.48	10.85	10.52	10.56
1627530_at	FBgn0032305	9.25	9.34	9.16	8.9	9.03	9.31
1639302_at	FBgn0036254	8.31	8.39	8.67	8.79	8.53	8.59
1626431_at	FBgn0036291	7.33	7.41	7.43	7.57	7.54	7.37
1639640_at	FBgn0052485	7.63	7.72	7.4	7.23	7.41	7.23
1640024_at	FBgn0039689	8.47	8.56	8.72	8.87	8.68	8.61
1633346_at	FBgn0036184	9.74	9.82	9.73	10.03	9.82	9.78
1625437_at	FBgn0042178	10.58	10.67	10.7	10.87	10.71	10.77
1623207_at	FBgn0035033	9.63	9.72	9.48	9.74	9.72	9.73
1631325_at	FBgn0003511	8.58	8.66	8.4	8.84	8.67	8.71
1636025_at	---	9.98	10.07	10.02	9.91	10.09	10.22
1630141_at	FBgn0033264	9.79	9.88	9.99	9.99	9.98	9.96
1634037_s_at	---	10.03	10.12	9.82	9.86	9.92	9.91
1630952_at	---	7.9	7.99	7.73	7.9	7.92	7.94
1636180_at	FBgn0040064	10.92	11	10.86	11.3	10.96	10.78
1623874_at	FBgn0031052	8.89	8.98	9.05	9.06	9.04	8.96
1629357_s_at	FBgn0023169	9.9	9.99	9.79	9.89	9.94	9.57
1628372_a_at	FBgn0005696	9.23	9.32	9.19	9.57	9.38	9.25
1624425_at	FBgn0032262	9.66	9.74	9.63	9.72	9.65	9.7
1633560_at	FBgn0040394	9.38	9.47	9.56	9.51	9.35	9.34
1635551_at	FBgn0034061	9.19	9.28	9.37	9.02	9.06	9.28
1627383_at	FBgn0000140	10.05	10.13	10.12	10.29	10.28	10.24
1639795_at	FBgn0029914	9.1	9.19	9.17	9.27	9.56	9.45
1631344_at	FBgn0027949	10.43	10.52	10.25	10.56	10.73	10.6
1625934_at	FBgn0037605	8.78	8.86	8.74	8.82	8.78	8.81
1627165_a_at	FBgn0039254	7.75	7.83	7.54	7.78	7.81	7.77
1632326_at	---	9.3	9.38	9.29	10.02	9.51	9.44
1641350_at	FBgn0033179	10.27	10.35	10.29	10.34	10.32	10.21
1640539_a_at	FBgn0037679	7.57	7.66	7.85	8.09	7.85	7.68
1625333_at	FBgn0053172	7.96	8.05	8.05	8.01	7.94	7.91
1624071_at	---	9.51	9.59	9.43	9.32	9.57	9.61
1637642_at	FBgn0030938	8.59	8.68	8.36	8.99	8.68	8.58
1637265_at	FBgn0035839	7.93	8.01	8.19	8.28	8.02	7.99
1632470_at	FBgn0036340	7.15	7.24	7.36	7.46	7.26	7.23

1629309_at	FBgn0032026	10.53	10.61	10.65	10.38	10.48	10.59
1625199_s_at	FBgn0010316	10.55	10.63	10.56	10.67	10.56	10.69
1640241_at	FBgn0035121	11.19	11.27	11.56	11.33	11.22	11.21
1626044_at	FBgn0036137	10.52	10.61	10.64	10.58	10.51	10.75
1637839_at	FBgn0030306	9.81	9.89	9.94	9.79	9.87	9.92
1630755_at	FBgn0031782	8.3	8.38	8.32	8.46	8.41	8.33
1639993_at	FBgn0027564	7.99	8.08	7.92	8.04	7.71	7.73
1633001_at	FBgn0030447	9.05	9.13	9.34	9.34	9.38	9.39
1627470_at	FBgn0003079	8.77	8.85	8.71	9.03	8.79	8.8
1624795_at	FBgn0037465	8.32	8.41	8.28	8.73	8.51	8.45
1624380_at	FBgn0039753	8.17	8.26	8.45	8.38	8.26	8.39
1629369_at	FBgn0035812	8.44	8.53	8.43	8.56	8.5	8.57
1627898_at	FBgn0020911	8.58	8.67	8.6	8.69	8.71	8.64
1640958_at	---	9.5	9.58	9.61	9.83	9.39	9.35
1641669_a_at	FBgn0036915	8.97	9.05	8.96	9.15	9.14	9.21
1623615_at	FBgn0030834	9.57	9.65	9.91	9.9	9.77	9.74
1632306_at	FBgn0037758	9.31	9.39	9.44	9.5	9.38	9.38
1628784_at	FBgn0037728	13.14	13.22	13.2	13.4	13.19	13.25
1631765_at	FBgn0004210	8.63	8.72	8.79	8.66	8.38	8.67
1640019_at	FBgn0011285	8.28	8.36	8.38	8.57	8.45	8.29
1628109_at	FBgn0030293	9.36	9.44	9.14	9.17	9.36	9.47
1630976_at	FBgn0003977	7.11	7.2	7.39	7.31	7.32	7.18
1634866_at	FBgn0030803	10.23	10.32	9.77	10.08	10.28	10.38
1626240_s_at	FBgn0038318	8.7	8.79	8.81	9	8.8	8.68
1627915_a_at	FBgn0001092	13.4	13.49	13.33	13.57	13.56	13.62
1633394_a_at	FBgn0035162	10.72	10.81	11.45	11.12	10.75	10.8
1624812_at	---	8.81	8.9	8.9	9.02	8.94	8.88
1623479_at	FBgn0015799	9.37	9.45	9.26	9.54	9.35	9.36
1624152_at	FBgn0039293	9.25	9.34	9.31	9.56	9.42	9.36
1639932_at	FBgn0014092	9.6	9.69	9.98	10.05	9.57	9.62
1625047_at	FBgn0022985	9.77	9.85	9.66	9.76	10.02	10.12
1639467_at	FBgn0052672	11.57	11.65	11.89	11.69	11.5	11.6
1638067_a_at	FBgn0031912	10.59	10.67	10.91	10.69	10.66	10.71
1639091_at	FBgn0028690	11.4	11.48	11.5	11.53	11.6	11.49
1627172_s_at	---	11.94	12.03	11.96	11.87	11.85	11.96
1624267_at	FBgn0035878	10.29	10.37	10.27	10.4	10.3	10.25

1626404_a_at	FBgn0000229	7.38	7.47	7.42	7.15	7.01	7.23
1630995_at	---	9.88	9.96	10.07	10.14	9.84	9.98
1624690_at	FBgn0036488	8.85	8.93	9.36	9.26	9.33	9.38
1639784_at	FBgn0020369	11.15	11.23	11.17	11.38	11.27	11.15
1636340_at	FBgn0037778	7.63	7.72	7.85	8.02	7.7	7.74
1629970_s_at	FBgn0015218	12.55	12.63	12.57	12.45	12.54	12.62
1637612_at	FBgn0036555	8.78	8.86	8.44	8.61	8.67	8.85
1637169_at	FBgn0031020	10.34	10.43	10.71	10.58	10.54	10.46
1628763_at	FBgn0035133	9.1	9.19	9.15	9.33	9.16	9.39
1638979_a_at	FBgn0002872	9.1	9.19	9.19	9.11	9.34	9.3
1626528_at	---	11.88	11.96	11.85	11.88	11.71	11.81
1634092_at	FBgn0036004	10.19	10.27	10.17	10.22	10.13	10.38
1625800_at	FBgn0037017	7.63	7.71	8	7.9	7.67	7.77
1635760_at	FBgn0015270	8.5	8.58	8.38	8.75	8.65	8.47
1635616_a_at	FBgn0039877	9.16	9.24	9.34	9.53	9.16	9.09
1634961_s_at	FBgn0020367	11.72	11.81	11.94	11.95	11.78	11.75
1640526_at	FBgn0037235	9.95	10.04	10.06	10.27	10.24	10.24
1622928_at	FBgn0038576	7.36	7.44	7.69	7.83	7.67	7.56
1632256_at	FBgn0010355	8.55	8.63	8.74	8.66	8.61	8.58
1627409_at	FBgn0030410	8.53	8.61	8.55	8.71	8.74	8.74
1641590_at	FBgn0038118	8.07	8.15	8.51	8.51	8.22	8.08
1623820_at	FBgn0035026	9.19	9.28	9.18	9.41	9.35	9.34
1630957_s_at	FBgn0037203	10.52	10.61	10.53	10.6	10.54	10.74
1634883_at	FBgn0032292	10.11	10.19	10	9.88	10.02	10.07
1626563_at	FBgn0010417	8.22	8.31	8.48	8.82	8.69	8.44
1624406_at	FBgn0032246	10.88	10.97	10.98	11.26	11.07	10.9
1637191_at	FBgn0021944	9.53	9.61	9.53	9.7	9.73	9.71
1626208_at	FBgn0001337	9.72	9.8	9.58	9.64	9.69	9.76
1625908_a_at	FBgn0020370	10.59	10.67	10.94	10.96	10.71	10.63
1628478_at	FBgn0034170	9.29	9.37	9.22	9.51	9.42	9.45
1634849_at	FBgn0032924	9.95	10.03	9.97	10.09	10	10.05
1630779_s_at	FBgn0027498	8.39	8.47	8.27	8.75	8.53	8.37
1638806_at	FBgn0038390	8.98	9.06	9.11	9.46	9.26	9.14
1635810_at	FBgn0032018	8.58	8.66	8.62	8.69	8.58	8.74
1633723_at	FBgn0039914	9.22	9.3	9.1	8.67	9.27	9.51
1635831_at	FBgn0031677	11.48	11.56	11.52	11.84	11.49	11.61

1631297_at	FBgn0020407	7.14	7.23	7.29	7.74	7.53	7.34
1627558_at	FBgn0037480	8.41	8.49	8.32	8.67	8.48	8.38
1638965_at	FBgn0025830	7.87	7.95	7.81	8.02	7.95	7.79
1641432_a_at	FBgn0016697	12.11	12.19	12.1	12.16	12.09	12.04
1624008_at	---	9.93	10.01	10.22	10.24	10.09	10.03
1632694_at	FBgn0031678	6.7	6.78	6.61	7.65	7.04	7.06
1632194_at	FBgn0039120	9.22	9.3	9.38	9.46	9.39	9.23
1629272_at	FBgn0031062	8.5	8.58	8.61	8.59	8.54	8.57
1623480_at	FBgn0037008	7.85	7.94	8.13	8.12	7.87	7.83
1641369_at	---	10.24	10.32	10.6	10.5	10.38	10.44
1640515_s_at	FBgn0028582	8.51	8.6	8.22	8.14	7.79	8.27
1628237_s_at	FBgn0032721 /// FBgn003	10.39	10.48	10.63	10.66	10.48	10.38
1624257_at	FBgn0030956	10.64	10.72	10.61	10.93	10.85	10.88
1634691_a_at	FBgn0050020	8.14	8.22	7.92	8.28	8.28	8.17
1624559_a_at	FBgn0034051	10.97	11.05	10.96	11.31	11.13	11.19
1638130_at	FBgn0038546	9.79	9.87	9.56	9.71	9.91	9.93
1632828_at	FBgn0029818	9.45	9.53	9.59	9.91	9.52	9.46
1636920_s_at	FBgn0035436	9.3	9.38	9.49	9.46	9.33	9.4
1627249_a_at	FBgn0001977	9.41	9.49	9.43	9.68	9.64	9.52
1632188_at	FBgn0041630	8.96	9.04	9.39	9.4	9.12	8.82
1639337_at	FBgn0034572	8.32	8.4	8.25	8.31	8.46	8.38
1632624_at	FBgn0000351	9.13	9.21	9.04	9.24	9.28	9.32
1632834_a_at	FBgn0036211 /// FBgn004	10.04	10.12	10.12	10.42	10.18	9.99
1629062_at	FBgn0037016	7.53	7.61	8.61	7.72	7.26	7.64
1630092_at	FBgn0032047	8.13	8.21	8.14	8.44	8.21	8.32
1637341_at	FBgn0028686	10.7	10.78	10.87	10.99	10.81	10.74
1627984_at	FBgn0035237	8.37	8.45	8.61	8.49	8.47	8.43
1633513_a_at	FBgn0034688	8.66	8.74	8.29	8.71	8.83	8.74
1641713_a_at	FBgn0039250	7.58	7.66	7.55	7.69	7.92	7.75
1632567_at	---	10.46	10.54	10.22	10.48	10.45	10.62
1632784_at	---	9.34	9.42	9.27	9.35	9.37	9.55
1637276_at	FBgn0011823	12.47	12.55	12.49	12.71	12.64	12.62
1628281_at	FBgn0017572	8.84	8.92	8.97	8.81	8.64	8.91
1635385_at	FBgn0039110	10.52	10.6	10.55	10.82	10.68	10.61
1625804_s_at	---	10.46	10.54	10.44	10.66	10.62	10.64
1637793_at	FBgn0037232	7.46	7.54	7.65	7.8	7.53	7.39

1634555_at	FBgn0037659	9.02	9.1	9.34	9.01	8.93	9.09
1625253_at	FBgn0040294	9.15	9.23	9.11	9.22	9.22	9.18
1640393_s_at	FBgn0040929	8.68	8.76	8.52	8.58	8.76	8.92
1628537_s_at	FBgn0035707	8.73	8.81	9.27	9.29	8.95	8.93
1632420_at	FBgn0035489	9.14	9.21	9.24	9.55	9.53	9.42
1640362_at	FBgn0026871	9.25	9.33	8.84	9.29	9.28	9.2
1631616_at	FBgn0040941	7.02	7.1	6.89	6.96	6.99	7.23
1640286_at	FBgn0042641	7.73	7.81	7.87	8.16	7.85	7.74
1630636_s_at	FBgn0030328	10.55	10.62	10.56	10.65	10.57	10.61
1640352_at	---	11.58	11.66	11.74	11.72	11.69	11.62
1634299_at	FBgn0032017	7.32	7.4	7.49	7.7	7.42	7.36
1626187_at	FBgn0038499	7.91	7.99	7.71	7.77	7.87	7.8
1638486_at	FBgn0010252	7.04	7.12	6.32	6.45	6.48	6.86
1630533_at	FBgn0034569	7.91	7.99	7.49	8.12	8.15	7.97
1627527_s_at	FBgn0030744	9.85	9.93	10.06	10.15	10.05	10.11
1629306_at	---	9.87	9.95	9.86	9.94	9.87	9.92
1632221_at	FBgn0031021	9.66	9.74	10.02	9.96	9.75	9.65
1635051_a_at	FBgn0031950	9.99	10.07	9.75	9.96	10.07	10.15
1631608_at	FBgn0039000	7.3	7.38	7.13	6.4	6.86	7.96
1625515_a_at	FBgn0003345	8.88	8.96	9.34	8.86	8.49	8.77
1638348_at	FBgn0051658	7.28	7.36	7.34	7.79	7.59	7.62
1632078_at	FBgn0038453	10.49	10.57	10.45	10.75	10.62	10.66
1639328_at	FBgn0030460	8.4	8.48	8.23	8.6	8.45	8.44
1628123_at	FBgn0030456	10.12	10.2	10.19	10.37	10.08	10.15
1628761_s_at	FBgn0038220	10.03	10.1	10.1	10.07	9.79	9.98
1629246_at	---	8.44	8.52	8.14	8.32	8.54	8.4
1629020_s_at	FBgn0000117	11.31	11.39	11.46	11.55	11.38	11.29
1629613_at	FBgn0038168	7.84	7.92	7.64	7.73	7.96	7.88
1639052_a_at	FBgn0035283	9.58	9.66	9.43	9.61	9.8	9.87
1632743_a_at	FBgn0002183	9.58	9.66	9.76	9.98	9.87	9.67
1639807_s_at	FBgn0032876	9.96	10.04	10.06	10.26	9.87	9.95
1628155_at	FBgn0001316	9.21	9.29	9.68	8.94	8.8	9.26
1633613_at	FBgn0035087	9.67	9.75	9.56	9.39	9.45	9.57
1641484_a_at	FBgn0003023	10.64	10.72	10.73	10.64	10.63	10.8
1623733_at	FBgn0023542	10.3	10.37	10.59	10.23	9.96	10.06
1630317_at	FBgn0039335	7.59	7.67	7.72	7.77	7.72	7.52

1639648_at	FBgn0015828	10.24	10.32	10.32	10.52	10.34	10.29
1635872_at	FBgn0010405	11.74	11.81	11.98	12.18	11.88	11.76
1624813_s_at	---	7.46	7.53	7.97	8.12	7.42	7.61
1638840_at	FBgn0037220	10.38	10.46	10.4	10.58	10.44	10.46
1633757_s_at	FBgn0032796	8.85	8.93	8.69	8.68	9.11	9.08
1627680_at	FBgn0033376	7.22	7.3	7.69	7.7	7.24	7.11
1636807_at	FBgn0027864	8.33	8.41	8.54	8.56	8.57	8.69
1627842_at	---	9.18	9.26	9.21	9.33	9.15	9.16
1626521_x_at	FBgn0034204	7.13	7.21	7.12	7.02	7.05	7.23
1637620_s_at	FBgn0035206	9.18	9.26	9.38	9.55	9.21	9.29
1632846_at	FBgn0031491	9.67	9.75	9.51	9.77	9.86	9.85
1631138_at	FBgn0030675	7.18	7.25	7.07	7.15	7.21	7.16
1639520_at	FBgn0033032	9.37	9.45	9.36	9.49	9.77	9.83
1638695_at	FBgn0030731	8.26	8.33	8.3	8.2	8.24	8.01
1640178_at	FBgn0010774	12	12.08	11.8	11.99	11.89	12.06
1628902_at	FBgn0038474	9.24	9.32	9.61	9.65	9.53	9.58
1628744_s_at	FBgn0032715 /// FBgn001	9.33	9.41	9.24	9.31	9.47	9.12
1629470_at	FBgn0039019	9.65	9.73	9.81	10.2	9.93	9.68
1635863_at	FBgn0035872	11.02	11.1	11.13	11.18	11.05	11.11
1626811_at	FBgn0039160	9.63	9.7	9.65	9.68	9.76	9.76
1639768_at	FBgn0031268	10.07	10.15	9.71	10.03	10.04	10.22
1634209_at	FBgn0003087	11.15	11.23	11.05	11.55	11.51	11.5
1633923_at	FBgn0030305	9.94	10.01	9.77	10.04	9.94	9.9
1636253_at	FBgn0036888	9.68	9.75	9.95	9.99	9.92	9.78
1639435_at	FBgn0027603	8.84	8.92	9.22	9.34	9.04	8.86
1640175_at	---	10.73	10.8	10.82	11.07	10.87	10.84
1633565_at	FBgn0033615	8.58	8.66	8.64	8.54	8.62	8.67
1632234_at	---	9.9	9.98	10.13	10.02	9.99	9.86
1634453_at	FBgn0001087	8.58	8.66	8.1	8.23	8.61	8.86
1627726_a_at	---	9.97	10.05	9.83	9.85	10	10.05
1627592_at	FBgn0034573	8.44	8.51	8.64	8.68	8.67	8.44
1629848_s_at	FBgn0037884	9.23	9.3	9.17	9.54	9.33	9.29
1639441_at	FBgn0005585	11.81	11.88	11.93	11.68	11.84	11.98
1634518_at	FBgn0035163	8.28	8.36	8	8.34	8.34	8.33
1623737_a_at	FBgn0015791	9.91	9.98	9.98	9.89	10.04	10.07
1624253_at	FBgn0052566	8.61	8.69	8.75	8.99	8.84	8.74

1634748_at	---	8.66	8.74	8.35	8.66	8.58	8.4
1634526_a_at	FBgn0003187	9.82	9.89	9.85	10.3	9.87	9.88
1639444_a_at	FBgn0039187	9.79	9.86	9.76	9.89	9.84	9.89
1636546_s_at	FBgn0030478	10.6	10.67	10.7	10.71	10.75	10.71
1628269_at	FBgn0000486	10.78	10.86	10.85	10.96	10.93	10.75
1637328_at	FBgn0025381	10.18	10.26	10.38	10.55	10.25	10.29
1640064_at	FBgn0052343	8.33	8.4	8.26	8.58	8.61	8.49
1637571_at	FBgn0036847	9.56	9.64	9.5	9.96	9.82	9.81
1638564_at	FBgn0038080	9.29	9.36	9.66	9.56	9.18	9.15
1636152_a_at	FBgn0030400 /// FBgn003	8.5	8.57	8.39	8.53	8.33	8.51
1634255_at	---	8.54	8.62	9.17	9.74	8.95	8.15
1623386_s_at	FBgn0029899	7.81	7.88	7.66	7.7	7.76	7.83
1637338_at	FBgn0032311	8	8.08	7.79	7.57	8.24	8.6
1628673_at	---	8.84	8.91	8.94	9.12	9	8.95
1638618_a_at	FBgn0030625	6.86	6.93	6.99	7.2	7.18	7.07
1624899_at	FBgn0003205	10.87	10.95	10.83	10.84	10.77	10.87
1630177_at	---	8.61	8.69	8.49	8.91	8.9	8.68
1626557_at	FBgn0024945	9.36	9.43	9.45	9.85	9.57	9.51
1630865_s_at	FBgn0039846	7.97	8.04	7.9	7.98	8.02	8.04
1630622_at	FBgn0037802	8.13	8.2	8.01	8.42	8.38	8.41
1627415_at	FBgn0039589	9.41	9.49	9.2	9.3	9.42	9.57
1632813_at	FBgn0037648	8.63	8.71	8.72	8.97	8.7	8.7
1641600_at	FBgn0032518	13.27	13.34	13.32	13.33	13.25	13.28
1636884_s_at	FBgn0032170	9.34	9.41	9.46	9.35	9.26	9.31
1626177_s_at	FBgn0034372	9.31	9.38	9.47	9.53	9.46	9.31
1637423_at	FBgn0036063	7.9	7.97	7.99	8.37	8.03	7.99
1623009_at	FBgn0028382	9.38	9.45	9.52	9.81	9.22	9.26
1637141_at	FBgn0032339	7.73	7.8	7.94	7.83	7.44	7.51
1634149_at	FBgn0027783	8.7	8.77	8.7	9.01	8.94	8.85
1630771_s_at	FBgn0002031	11.32	11.39	11.33	11.37	11.46	11.42
1629149_at	FBgn0036911	8.54	8.62	8.46	8.75	8.86	8.84
1636645_at	FBgn0034310	9.72	9.8	9.68	10.18	9.9	9.78
1633840_a_at	FBgn0033391	10.07	10.14	10.01	10.06	10.12	10.15
1623320_at	FBgn0040344	8.35	8.42	8.31	8.49	8.48	8.38
1639178_s_at	FBgn0016034	9.61	9.68	9.78	10.04	9.78	9.76
1626857_at	FBgn0039073	9.28	9.35	9.45	9.58	9.5	9.47

1634043_at	FBgn0034315	9.59	9.66	9.53	9.85	9.66	9.59
1625875_at	---	10.58	10.65	10.67	10.81	10.67	10.66
1638272_at	---	10.08	10.15	10.3	10.04	10.04	10.08
1624889_a_at	FBgn0021800	8.49	8.56	9.38	8.82	8.3	8.85
1630390_at	FBgn0034922	9.25	9.32	9.48	9.65	9.45	9.31
1634182_at	FBgn0035488	10.32	10.39	10.25	10.45	10.4	10.44
1631048_at	FBgn0029915	10.73	10.8	10.68	10.73	10.59	10.61
1632753_a_at	FBgn0031575	8.41	8.48	8.31	8.61	8.65	8.55
1641068_a_at	FBgn0003495	9.64	9.71	9.59	9.59	9.63	9.66
1626833_at	FBgn0039271	8.31	8.38	8.38	8.61	8.54	8.65
1627743_at	FBgn0036973 /// FBgn003	7.41	7.49	7.4	7.6	7.61	7.52
1633958_at	FBgn0019932	9.83	9.9	9.79	10.08	9.88	9.84
1627973_s_at	FBgn0053075 /// FBgn003	7.97	8.04	7.87	7.96	8.08	8.06
1633113_at	FBgn0036487	9.01	9.08	8.97	9.37	9.05	8.95
1639966_a_at	FBgn0032986	10	10.07	10.09	10.05	9.82	9.98
1631723_at	---	9.12	9.19	8.92	9.01	9.17	9.14
1623373_at	FBgn0029594	10.39	10.46	10.27	10.47	10.21	10.22
1632381_at	FBgn0043903	9.64	9.71	9.59	9.56	9.73	9.8
1632814_at	FBgn0003114	10.05	10.13	10.02	10.11	10.33	10.3
1628461_a_at	FBgn0034970	9.38	9.46	9.13	9.23	9.5	9.63
1641703_at	---	8.97	9.04	8.94	9.23	9	9
1627202_at	FBgn0043012	10.01	10.08	10.07	9.94	10.05	10.02
1625878_at	---	8.55	8.62	9	9.06	8.72	8.69
1625250_at	FBgn0038863	9.81	9.88	9.69	9.95	9.82	9.89
1630216_at	FBgn0026722	8.27	8.34	8.37	8.4	8.39	8.43
1631095_at	---	8.1	8.17	7.87	7.97	8.16	8.15
1622926_at	FBgn0032450	8.75	8.82	8.71	9.08	8.79	8.79
1625087_a_at	FBgn0052137	8.25	8.32	8.27	8.05	7.58	8.09
1627749_at	FBgn0032646	9.4	9.47	9.52	9.74	9.38	9.42
1639673_at	FBgn0030301	7.55	7.62	7.47	7.68	7.47	7.51
1623901_s_at	FBgn0038947	11.08	11.15	11.24	10.62	11.03	11.14
1627564_s_at	FBgn0019890	8.51	8.58	8.55	8.44	8.65	8.67
1631527_at	FBgn0036258	11.55	11.62	11.97	11.89	11.7	11.59
1627247_at	FBgn0035891	7.39	7.46	7.34	7.38	7.47	7.35
1624931_at	FBgn0026084	11.72	11.79	11.78	11.64	11.41	11.78
1635409_at	FBgn0011704	12.42	12.49	12.45	12.59	12.57	12.51

1640358_at	FBgn0032214	10.39	10.46	10.26	10.66	10.52	10.46
1627005_at	FBgn0015801	8.4	8.47	8.76	8.71	8.15	8.51
1641485_at	FBgn0004066	11.49	11.56	11.45	11.67	11.52	11.48
1639867_at	FBgn0000533	9.1	9.17	8.75	8.95	9.08	8.85
1637060_a_at	FBgn0037137	11.99	12.06	12.07	11.96	11.94	12.11
1630650_at	---	9.58	9.65	9.4	9.43	9.16	9.52
1624150_at	FBgn0029174	11.04	11.11	11.38	11.79	11.23	11.18
1627925_at	FBgn0032451	9.75	9.82	9.65	9.94	9.83	9.75
1630063_a_at	FBgn0040227	11.92	11.98	12.32	12.32	12	11.86
1636308_at	FBgn0035762	8.15	8.22	8.3	8.19	8.11	8.03
1630686_at	FBgn0030243	9.77	9.84	9.51	9.53	9.75	9.93
1627685_a_at	FBgn0014857	10.99	11.06	11.3	11.25	11.09	11.09
1631909_at	---	10.99	11.06	11.02	10.92	10.96	11.06
1639876_a_at	FBgn0000405	13.27	13.34	13.17	13.22	13.23	13.35
1629433_at	FBgn0035228	10.25	10.32	10.25	10.27	10.42	10.42
1633810_at	FBgn0036894	7.33	7.4	7.42	7.39	7.33	7.34
1629620_s_at	FBgn0014189	12.11	12.18	12.23	12.36	12.23	12.29
1632065_at	FBgn0037964	7.84	7.91	7.72	8.04	7.95	7.92
1629251_at	FBgn0051155	10.66	10.73	10.56	10.62	10.83	10.89
1639025_at	FBgn0039668	7.96	8.02	7.74	8.04	8.1	8.27
1632927_at	FBgn0037634	8.53	8.6	8.54	8.9	8.93	8.88
1635950_at	FBgn0004465	10.1	10.17	10.07	10.29	10.03	10.07
1633209_s_at	FBgn0034237	11.44	11.51	11.74	11.74	11.64	11.52
1625830_a_at	FBgn0026173	9.28	9.34	9.19	9.32	9.05	9.25
1625475_s_at	FBgn0004638	7.18	7.25	7.55	7.17	6.69	7.07
1633076_at	FBgn0034388	12.48	12.54	12.17	12.38	12.64	12.63
1630055_a_at	FBgn0033339	9.41	9.48	9.48	9.6	9.43	9.47
1626433_at	---	9.9	9.97	10.5	10.06	9.88	10.02
1627993_at	FBgn0037022	8.44	8.51	8.36	8.84	8.61	8.54
1641458_s_at	FBgn0025936	8.96	9.02	9.06	8.86	9.02	8.96
1638919_at	---	9.04	9.11	9.05	9.21	9.3	9.2
1632402_at	FBgn0037901	9.05	9.11	8.95	9.11	9.05	8.84
1632171_a_at	FBgn0031229	8.12	8.19	8.24	8.15	8.37	8.39
1640738_a_at	FBgn0011700	8.6	8.67	8.46	8.83	8.72	8.67
1639193_a_at	FBgn0039881	8.11	8.18	7.69	8.22	7.97	8
1630075_s_at	FBgn0030772	8.45	8.51	8.33	8.38	8.65	8.75

1641456_at	FBgn0032814	8.41	8.48	8.37	8.5	8.51	8.44
1636231_at	FBgn0029853	7.88	7.95	7.77	8.12	7.94	7.84
1641089_s_at	FBgn0039863	9.55	9.61	9.3	9.36	9.41	9.56
1627207_at	FBgn0031351	8.55	8.62	8.56	8.96	8.85	8.84
1636795_at	FBgn0028962	7.79	7.85	7.94	8.17	7.91	7.68
1626039_at	FBgn0038767	8.27	8.34	8.17	8.69	8.53	8.54
1627609_at	---	11.99	12.06	11.92	12.05	11.99	11.99
1639553_at	FBgn0032781	9.28	9.35	9.37	9.46	9.38	9.33
1633568_s_at	FBgn0040002	9.91	9.97	9.96	9.8	9.95	10.04
1640826_at	FBgn0037019	8.87	8.94	8.85	8.93	8.93	8.9
1640118_at	FBgn0034299	10.07	10.14	10.06	10.08	10.07	10.19
1623525_at	FBgn0003044	9.56	9.62	9.52	9.63	9.69	9.7
1635555_at	FBgn0032750	8.51	8.58	8.46	8.47	8.58	8.58
1628623_at	FBgn0040336	8.34	8.41	8.2	8.61	8.4	8.42
1635955_at	FBgn0031281	7.02	7.09	7.11	7.37	7.04	6.97
1624051_at	FBgn0038961	8.98	9.05	9.09	9.18	9.02	9.1
1633734_at	FBgn0027509 /// FBgn003	7.8	7.86	8.01	8.32	8.14	7.83
1624058_at	---	10.03	10.1	10	9.82	10.15	10.14
1631755_at	FBgn0037370	8.75	8.82	8.88	9.18	8.94	8.92
1635301_at	---	8.5	8.56	8.55	8.9	9.02	8.96
1639123_at	FBgn0025336	9.48	9.54	9.7	9.78	9.54	9.55
1631251_at	FBgn0052708	8.81	8.88	8.99	8.99	8.78	8.84
1629681_x_at	FBgn0029738	10.28	10.35	9.95	10.18	10.24	10.13
1639448_at	FBgn0039540	7.3	7.36	6.94	7.51	7.45	7.37
1634954_at	FBgn0030788	9.7	9.77	9.41	9.56	9.67	9.92
1639746_at	---	9.48	9.55	9.42	9.64	9.58	9.64
1637897_at	---	9.03	9.1	9.02	9.01	9.22	9.19
1634560_at	FBgn0010340	8	8.07	8.09	7.88	8.18	8.06
1628767_s_at	FBgn0039923	11.3	11.37	11.22	11.3	11.29	11.26
1639812_at	FBgn0038686	8.73	8.8	8.8	9.13	9.04	9
1639330_s_at	FBgn0031030	11.74	11.81	11.73	11.83	11.82	11.95
1631500_at	FBgn0002781	6.82	6.88	6.68	7.19	7.11	7.34
1634146_at	---	8.65	8.71	8.51	8.71	8.81	8.85
1637084_at	FBgn0038432	9.54	9.6	9.41	9.56	9.56	9.61
1632819_at	FBgn0051224	9.23	9.3	9.18	9.17	9.32	9.49
1632638_at	FBgn0030877	8.75	8.82	8.79	9.16	8.87	8.77

1626038_at	FBgn0042641	9.9	9.96	9.68	9.82	9.96	9.97
1640191_a_at	FBgn0036478	9.02	9.08	9.35	9.55	8.99	8.93
1628418_at	FBgn0000018	8.31	8.38	8.08	8.12	8.2	8.37
1629720_s_at	FBgn0052955	9.13	9.2	8.94	9	9.19	9.16
1623704_at	FBgn0028480	9.48	9.55	9.46	9.55	9.32	9.48
1638529_at	FBgn0004888	11.63	11.7	11.69	11.75	11.91	11.85
1627934_at	FBgn0031391	9.43	9.49	9.29	9.79	9.45	9.46
1635935_at	---	8.74	8.81	8.98	9.25	9.16	9.04
1638568_s_at	FBgn0001169	9.12	9.19	9.23	9.59	9.22	9.39
1624863_a_at	FBgn0027554	7.28	7.35	7.3	7.4	7.17	7.08
1632596_at	FBgn0037330	9.66	9.72	9.86	9.84	9.48	9.55
1639450_s_at	---	10.16	10.23	10.16	10.15	10.09	10.23
1623811_at	FBgn0026741	9.29	9.36	9.63	9.81	9.32	9.33
1628630_at	FBgn0032847	8.84	8.9	8.96	9.08	9.07	8.94
1627065_at	---	9.97	10.04	9.82	10.07	10.15	10.29
1629044_at	FBgn0028978	7.83	7.9	7.72	7.74	8.14	7.94
1622998_a_at	FBgn0035405	8.52	8.58	8.41	8.64	8.8	8.8
1633108_at	FBgn0036372	10.01	10.07	10	10	10.07	10.1
1628853_at	FBgn0030833	9.53	9.6	9.53	9.8	9.52	9.51
1635702_a_at	FBgn0030054	9.14	9.2	9.03	9.09	9.15	9.16
1631915_at	FBgn0040899	10.41	10.47	10.57	10.45	10.13	10.17
1627849_at	---	7.54	7.6	7.36	7.66	7.62	7.73
1639162_at	FBgn0020250	10.11	10.18	9.88	9.94	10.13	10.19
1623599_at	---	9.29	9.36	9.48	9.54	9.39	9.35
1625453_a_at	---	10.66	10.72	10.98	10.55	10.44	10.7
1634598_a_at	FBgn0033452	10.23	10.29	10.13	10.12	10.33	10.33
1636282_s_at	FBgn0010602	11.3	11.37	11.33	11.34	11.39	11.39
1626360_at	FBgn0038768	9.57	9.63	9.44	9.56	9.62	9.63
1631069_a_at	FBgn0053088	8.4	8.46	8.37	8.35	8.4	8.44
1630820_at	FBgn0039977	10.61	10.67	10.86	10.85	10.79	10.8
1624271_at	FBgn0034000	7.91	7.97	8.19	8.22	8.01	8.11
1639757_at	FBgn0025742	8.8	8.86	9	9.13	8.8	8.66
1632512_at	FBgn0039270	8.66	8.72	8.74	8.88	8.98	8.97
1627939_a_at	FBgn0024891	9.47	9.53	9.53	9.55	9.47	9.43
1629854_at	FBgn0030465	8.72	8.78	8.56	8.75	8.65	8.73
1628777_at	FBgn0033465	8.84	8.9	8.94	9.2	8.77	8.64

1628490_at	FBgn0039509	8.47	8.53	8.57	8.64	8.55	8.48
1633682_a_at	FBgn0052697	10.28	10.34	10.44	10.55	10.34	10.26
1627824_at	---	8.15	8.22	8.22	8.24	8.14	8.36
1641361_a_at	FBgn0036844	8.61	8.68	8.84	8.87	8.84	8.87
1625528_at	FBgn0031544	10.3	10.37	10.31	10.38	10.33	10.38
1630099_at	FBgn0033846	9.13	9.19	9.09	9.25	9.28	9.34
1624050_at	---	8.95	9.01	8.95	9.1	8.99	8.85
1637556_at	FBgn0039303	10.45	10.51	10.43	10.45	10.4	10.54
1624883_at	FBgn0032725	10.49	10.56	10.6	10.85	10.67	10.61
1626316_at	FBgn0030288	8.08	8.14	7.87	7.72	7.98	7.91
1637847_at	FBgn0032237	12.7	12.76	12.67	12.68	12.62	12.6
1633188_a_at	FBgn0026430	10.4	10.46	10.64	10.86	10.82	10.58
1631588_at	FBgn0004654	10.62	10.68	10.39	10.39	10.41	10.44
1636614_a_at	FBgn0040068	8.05	8.11	7.94	7.89	8.2	8.2
1640290_at	FBgn0030800	8.25	8.31	8.2	8.36	8.36	8.28
1637676_at	FBgn0034368	9.56	9.63	9.6	9.66	9.56	9.67
1635995_a_at	FBgn0037301	8.1	8.16	8.04	8.16	7.92	7.92
1634527_s_at	---	10.18	10.24	10.12	10.43	10.27	10.35
1635974_at	FBgn0015283	11.02	11.09	11.1	11.15	11.22	11.08
1626339_at	FBgn0033714	8.4	8.46	8.14	8.24	8.39	8.4
1624044_at	---	9.51	9.58	9.63	9.6	9.54	9.57
1624888_at	FBgn0035876	8.97	9.03	9.01	9.35	9.11	9.12
1636309_at	FBgn0037838	7.99	8.05	7.76	8.24	7.89	7.89
AFFX-r2-Dro	FBgn0000042	11.24	11.31	11.13	11.23	11.28	11.19
1626214_s_at	FBgn0027066	8.71	8.77	8.64	8.45	8.88	8.8
1631133_at	FBgn0024975	7.72	7.78	6.72	7.06	7.66	7.65
1631404_at	FBgn0037249	11.13	11.19	11.37	11.3	11.34	11.25
1641153_a_at	---	12.87	12.93	12.76	12.96	12.91	12.92
1632481_at	FBgn0035763	10.9	10.96	11.23	11.14	11.07	11.03
1634675_s_at	FBgn0029849	9.48	9.54	9.34	9.12	9.51	9.52
1630992_at	FBgn0039743	9.1	9.17	9.36	9.51	9.45	9.39
1640412_at	---	8.9	8.96	8.67	8.92	8.89	8.99
1637994_at	FBgn0033845	8.66	8.73	8.73	8.92	8.87	8.83
1632698_at	---	7.67	7.73	8.06	7.65	7.27	7.48
1622944_at	FBgn0033309	9.61	9.67	9.44	9.9	9.67	9.67
1626647_at	FBgn0017577	10.34	10.4	10.72	11.01	10.67	10.44

1626981_s_at	FBgn0033669	9.76	9.82	9.47	9.84	9.76	9.7
1625733_at	---	7.48	7.54	7.57	7.32	7.24	7.33
1623277_at	FBgn0016941	9.34	9.4	9.6	9.49	9.19	9.52
1636237_s_at	FBgn0030845	10.14	10.2	10.26	10.44	10.24	10.16
1624345_a_at	FBgn0038964	11.5	11.57	11.97	11.76	11.54	11.6
1629259_at	FBgn0035251	7.45	7.51	7.64	7.96	7.33	7.53
1635121_a_at	FBgn0034744	9.55	9.61	9.52	9.51	9.65	9.58
1631399_a_at	FBgn0029801	9.2	9.26	9.14	9.21	9.26	9.12
1629592_at	FBgn0030717	9.21	9.27	9.12	9.35	9.4	9.43
1635854_s_at	---	8.2	8.26	8.35	7.93	7.99	8.43
1641635_s_at	FBgn0035400	8.97	9.03	9.04	9.07	9	8.99
1631381_at	---	10.58	10.64	10.6	10.92	10.78	10.62
1633044_at	FBgn0034877	11.53	11.59	11.84	11.71	11.75	11.72
1635237_at	FBgn0030945	8.32	8.38	8.17	8.28	8.36	8.22
1623907_at	---	9.17	9.23	9.62	9.21	9.46	9.46
1626871_at	FBgn0029079	9.83	9.89	9.85	9.84	9.96	10.01
1626448_at	FBgn0040273	9.26	9.32	9.04	9.31	9.37	9.3
1630527_at	FBgn0037670	8.61	8.67	8.56	9.2	8.96	8.9
1625000_a_at	FBgn0052441	9.88	9.93	9.96	9.99	9.94	9.94
1637148_at	FBgn0025633	10.37	10.43	10.2	10.39	10.3	10.34
1630276_at	FBgn0031904	10.41	10.47	10.31	10.66	10.22	10.27
1627770_at	FBgn0010314	10.23	10.29	10.13	10.53	10.33	10.34
1640036_a_at	FBgn0028633	7.09	7.15	6.72	6.95	7.06	7.15
1637611_at	FBgn0026749	9.55	9.61	9.46	9.65	9.64	9.64
1640669_at	FBgn0039942	10.95	11.01	10.67	10.96	10.73	10.84
1624797_at	FBgn0030245	8.24	8.3	8.93	8.5	7.6	8
1640520_at	---	11.27	11.33	10.99	11.21	11.02	11.04
1627245_s_at	FBgn0039186	10.42	10.48	10.03	10.4	10.39	10.48
1629579_at	FBgn0032872	9.38	9.44	9.27	9.2	9.28	9.4
1639716_at	FBgn0026259	9.87	9.93	10.16	9.91	9.92	9.94
1628397_at	FBgn0033272	9.31	9.37	9.3	9.44	9.49	9.48
1633915_at	FBgn0037707	10.16	10.21	10.12	10.34	10.15	10.14
1625618_at	FBgn0030403	8.13	8.19	8.21	8.47	8.1	8.01
1633440_a_at	FBgn0032812	8.54	8.6	8.29	8.72	8.58	8.58
1635917_at	---	7.76	7.82	8.03	7.92	8.08	8.09
1626993_at	---	10.19	10.25	10.32	10.28	10.29	10.21

1634795_a_at	FBgn0023175	11.53	11.59	11.62	12	11.67	11.51
1622912_at	FBgn0030872	7.65	7.71	7	7.19	7.41	7.22
1624305_at	FBgn0028419	10.86	10.91	10.78	10.91	10.77	10.94
1630611_at	---	11.93	11.99	12.24	12.15	12.14	12.15
1633354_at	FBgn0031126	9.16	9.22	9.12	9.16	9	9.06
1637700_s_at	FBgn0034858	9.82	9.87	9.75	9.69	9.72	9.79
1634966_a_at	FBgn0010774	10.36	10.41	10.09	10.1	10.25	10.46
1641370_s_at	FBgn0025628	10.33	10.38	10.42	10.71	10.05	10.16
1625155_a_at	FBgn0028968	9.59	9.65	9.83	9.89	9.63	9.56
1634980_s_at	FBgn0036149	7.24	7.3	7.42	7.47	7.39	7.26
1637866_at	FBgn0032925	9.37	9.43	9.75	9.57	9.44	9.38
1627765_a_at	FBgn0034433	7.48	7.53	7.13	7.5	7.65	7.64
1631054_s_at	FBgn0039741	10.11	10.17	10.06	10.11	10.29	10.36
1622925_at	---	9.62	9.68	9.51	9.4	9.56	9.54
1625587_at	FBgn0034406	8.33	8.39	8.31	8.79	7.55	7.89
1632266_at	FBgn0025634	8.59	8.65	8.24	8.43	8.78	8.7
1635934_at	FBgn0015544	8.9	8.95	8.97	9.22	9.33	9.17
1623194_at	FBgn0033548	10.97	11.02	11.25	10.96	11.12	11.09
1638036_at	FBgn0004432	13.8	13.86	13.86	13.91	13.9	13.9
1639195_a_at	---	13	13.05	12.86	12.99	12.94	12.97
1625345_at	FBgn0028746	8.81	8.87	8.4	8.44	8.84	8.88
1638651_a_at	FBgn0038251	9.98	10.04	9.72	9.98	9.98	10.01
1628573_a_at	FBgn0019644	11.76	11.82	12.11	11.92	11.92	11.9
1630062_a_at	---	9.86	9.92	9.98	9.93	10.02	9.97
1629864_at	FBgn0024998	7.77	7.82	7.58	7.66	7.87	7.71
1624290_at	FBgn0034733	7.44	7.5	7.77	7.85	7.47	7.3
1632243_at	FBgn0037316	9.34	9.4	9.28	9.64	9.55	9.37
1632279_at	FBgn0010333	10.22	10.28	10.25	10.29	10.32	10.5
1635668_at	FBgn0034939	9.05	9.11	9.27	9.54	9.15	9.14
1638782_at	FBgn0034032	8.85	8.91	8.9	8.92	9.11	8.98
1630745_at	FBgn0030802	10.05	10.11	10.21	10.36	10.17	10.1
1639198_at	FBgn0033317	10.37	10.43	10.3	10.26	10.44	10.42
1629337_at	---	8.77	8.83	8.78	8.86	8.99	8.81
1628325_at	FBgn0052179	7.91	7.96	7.71	7.78	8.08	8.17
1629737_at	FBgn0015929	9.77	9.82	10.01	10.3	9.96	9.8
1640158_at	FBgn0032870	9.83	9.89	9.72	9.98	9.92	9.91

1632109_s_at	FBgn0025725	9.78	9.84	9.88	9.92	9.72	9.65
1631050_at	FBgn0032216	11.54	11.6	11.32	11.56	11.58	11.49
1630519_at	FBgn0015834	12.03	12.09	12.18	12.21	12.12	12.09
1635128_a_at	FBgn0000139	8.95	9.01	9.27	9.14	9.24	9.17
1640886_a_at	FBgn0001297	7.31	7.37	7.95	7.2	7.26	7.53
1639629_at	FBgn0015794	9.39	9.45	9.44	9.51	9.5	9.49
1630881_at	FBgn0035519	9.53	9.59	9.26	9.29	9.45	9.46
1639621_at	FBgn0034312	7.75	7.8	7.82	7.48	7.46	7.81
1637327_at	FBgn0031216	8.58	8.64	8.68	8.63	8.56	8.63
1636036_at	FBgn0035370	10.95	11	10.93	11.14	11.16	11.17
1632821_a_at	FBgn0028954	9.75	9.81	9.6	9.75	9.8	9.76
1637781_at	FBgn0038534	7.56	7.61	7.28	7.71	7.72	7.51
1623825_s_at	FBgn0039972	11.82	11.87	11.78	12.11	11.89	11.86
1634970_at	FBgn0037026	8.63	8.69	8.54	8.85	8.78	8.72
1631696_s_at	FBgn0034962	10.19	10.24	10.34	10.45	10.22	10.13
1630408_s_at	FBgn0030086	12.36	12.42	12.27	12.48	12.45	12.35
1631618_s_at	FBgn0030208	9.61	9.67	9.41	9.75	9.61	9.48
1638292_at	FBgn0037815	8.51	8.56	8.95	8.68	8.69	8.95
1625187_a_at	FBgn0025802	8.72	8.77	8.65	8.65	8.82	8.76
1633785_at	FBgn0027496	10.2	10.25	10.28	10.43	10.18	10.18
1624941_at	FBgn0050169	8.31	8.37	8.31	8.62	8.48	8.38
1633364_at	FBgn0036932	9.88	9.94	9.96	10.05	10.07	10.06
1628679_at	FBgn0037338	8.56	8.61	8.54	8.47	8.33	8.49
1634542_at	FBgn0035471	10.5	10.55	10.37	10.48	10.57	10.59
1633799_a_at	FBgn0035443	7.73	7.78	7.94	8.16	8.05	7.8
1627372_a_at	---	10	10.05	10.23	9.9	9.91	10.1
1629086_s_at	FBgn0017539	10.59	10.64	10.86	10.93	10.76	10.72
1633609_at	FBgn0031873	8.32	8.37	8.61	8.87	8.72	8.69
1633673_a_at	FBgn0010217	12.32	12.38	12.64	12.46	12.59	12.57
1630929_at	FBgn0025700	10.82	10.88	11.09	10.69	10.78	10.9
1623455_s_at	FBgn0030235	9.04	9.1	9.27	9.38	9.1	9.24
1626751_at	FBgn0035593	9.91	9.96	9.86	10.06	10.02	9.84
1637923_at	FBgn0051938	9.02	9.07	8.94	9.21	8.78	8.88
1623695_a_at	FBgn0036337	10.19	10.24	10.29	10.2	10.16	10.21
1633730_at	FBgn0030891	9.57	9.62	9.46	9.67	9.68	9.72
1631533_at	FBgn0013773	8.98	9.03	8.72	8.97	9.08	9.03

1626190_a_at	FBgn0038860	7.11	7.16	7.21	7.47	7.16	7.26
1634309_at	FBgn0038532	7.77	7.82	7.75	7.67	7.75	7.74
1639405_at	FBgn0026083	8.75	8.8	8.75	8.87	8.95	8.9
1635706_at	FBgn0036335	9.79	9.84	10	10.17	9.73	9.86
1637627_at	FBgn0004368	9.31	9.36	9.28	9.01	9.35	9.4
1630565_at	FBgn0031361	8	8.06	8.25	8.27	8.19	8.08
1634232_at	FBgn0032721 /// FBgn003	9.88	9.94	10.38	10.25	9.95	10
1640744_a_at	FBgn0034172	7.89	7.94	7.93	8.18	7.93	7.94
1636305_a_at	FBgn0038107 /// FBgn003	10.12	10.17	9.9	10.21	10.14	10.12
1641171_at	FBgn0032511	11.02	11.07	11.25	11.1	11.1	11.12
1639460_a_at	---	10.85	10.9	10.32	10.71	10.68	10.75
1624750_at	FBgn0033741	9.99	10.04	10.37	10.21	10.12	10.22
1626425_at	FBgn0014029	10.6	10.65	10.55	10.62	10.64	10.63
1630496_a_at	FBgn0015546	8.99	9.04	8.78	9.28	9.06	8.93
1624168_at	FBgn0030582	10.47	10.52	10.65	10.62	10.64	10.61
1640215_at	FBgn0038313	9.73	9.79	9.99	9.35	9.78	9.66
1637380_s_at	FBgn0016126	9.97	10.02	9.89	9.53	9.27	9.54
1637111_a_at	FBgn0013955	8.89	8.94	8.86	9.04	9.03	8.79
1629469_s_at	FBgn0036316	11.27	11.32	11.22	10.99	11.15	11.4
1635423_s_at	FBgn0001218	11.85	11.9	11.85	11.82	11.77	11.9
1639212_a_at	FBgn0036397	8.82	8.87	8.69	8.97	8.79	8.8
1633106_at	FBgn0035907	9.91	9.96	9.45	10.22	10.09	10.04
1636654_s_at	FBgn0031635	9.63	9.68	9.26	9.71	9.79	9.73
1633419_s_at	FBgn0052195 /// FBgn003	7.39	7.44	6.88	7.31	7.83	7.68
1640317_at	FBgn0004050	8.53	8.59	8.56	8.63	8.48	8.51
1636276_at	---	8.94	8.99	9.18	9.16	8.94	8.98
1639633_at	FBgn0033337	8.12	8.17	7.83	8.01	8	7.97
1625410_at	FBgn0036775	9.39	9.44	9.57	9.68	9.53	9.54
1635299_at	---	7.9	7.95	7.9	8.32	8.08	8.02
1626831_at	FBgn0032422	8.81	8.86	9.31	9.22	8.77	9.03
1623182_at	FBgn0032053	9.71	9.76	10.12	10.07	9.75	9.64
1627789_at	FBgn0029715	10.62	10.67	10.9	10.86	10.69	10.67
1631320_at	FBgn0022768	8.66	8.71	8.78	8.83	8.77	8.78
1641105_at	FBgn0013531	8.3	8.35	8.21	8.67	8.62	8.5
1636403_at	FBgn0037900	9.08	9.13	8.99	9.17	8.95	9.09
1636721_at	FBgn0003042	8.98	9.03	8.66	8.75	8.89	8.91

1630892_at	FBgn0034488	10.44	10.49	10.41	10.95	10.59	10.31
1631531_at	FBgn0038810	9.06	9.11	9.5	9.6	9.09	9
1631465_at	FBgn0036423	7.41	7.46	7.35	7.85	7.74	7.63
1637574_at	FBgn0027620	10.45	10.5	10.57	10	10.53	10.53
1637583_at	FBgn0033934	10.07	10.12	10.09	10.19	10.35	10.34
1636189_at	FBgn0003124	11.39	11.44	11.22	11.42	11.41	11.34
1640710_at	FBgn0028685	10.86	10.91	10.85	10.93	10.94	10.83
1623475_s_at	FBgn0003261	12.7	12.75	12.67	12.77	12.75	12.67
1633962_a_at	FBgn0023516	9.51	9.57	9.38	9.59	9.46	9.47
1622892_s_at	FBgn0035889	8.64	8.69	8.75	8.95	8.59	8.62
1633477_at	FBgn0034631	7.13	7.18	7.58	7.63	7.5	7.16
1632024_at	---	9.08	9.13	8.92	9.09	9.21	9.19
1632292_at	FBgn0040298	9.01	9.06	8.8	9.09	9.14	9.16
1638541_at	---	8.93	8.98	8.89	9.02	8.98	8.96
1638754_s_at	FBgn0034088	7.63	7.68	7.6	7.85	7.86	7.9
1628648_at	FBgn0027524	9.77	9.82	9.68	10.05	9.64	9.61
1635468_a_at	FBgn0036689	9.51	9.56	9.49	9.66	9.68	9.63
1631742_s_at	FBgn0002781	7.98	8.03	7.78	8.04	7.89	8.19
1624547_s_at	FBgn0004587	10.32	10.37	10.24	10.25	10.55	10.46
1629881_at	FBgn0028411	10.95	11	11.06	11.18	11.15	11.11
1625362_at	---	9.31	9.36	9.29	9.32	9.54	9.43
1635771_a_at	FBgn0052306	9.18	9.23	9.35	9.29	9.29	9.24
1629243_at	---	7.45	7.5	7.46	7.43	7.59	7.36
1628483_at	FBgn0030142	9.37	9.42	9.67	9.56	9.34	9.38
1639029_at	FBgn0002715	8.68	8.73	8.57	9.07	8.86	8.89
1637987_at	FBgn0039122	10.32	10.37	10.32	10.09	10.23	10.42
1638804_a_at	---	9.91	9.96	9.97	10.18	10.01	10.02
1636067_at	---	9.2	9.25	9.08	9.12	9.3	9.24
1641606_s_at	FBgn0037852	9.06	9.11	8.87	9.04	9.01	9.02
1638758_at	FBgn0029819	10.14	10.19	10.01	10.21	10.14	10.15
1625589_at	FBgn0033840	9.03	9.07	8.87	9.28	9.2	9.12
1625284_at	FBgn0039150	9.1	9.15	9.03	9.24	9.06	8.99
1639321_s_at	FBgn0003717	11.23	11.28	11.05	11.03	11.09	11.28
1635058_at	FBgn0038989	9.55	9.6	9.71	9.47	9.6	9.69
1638165_s_at	FBgn0052737	7.51	7.56	7.78	8.03	8.01	8.09
1631677_at	FBgn0030093	10.65	10.7	10.47	10.76	10.8	10.77

1634912_at	FBgn0002780	12.55	12.6	12.74	12.7	12.55	12.59
1637069_at	FBgn0035021	8.33	8.38	8.2	8.45	8.47	8.42
1630935_at	FBgn0033194	8.38	8.43	8.54	8.32	8.09	8.34
1628314_a_at	FBgn0030955	8.01	8.05	8.34	7.71	7.87	8.11
1639140_at	FBgn0034068	9.88	9.92	10	10.28	10	9.87
1628598_s_at	FBgn0037357	9.33	9.38	9.34	9.38	9.23	9.12
1641035_a_at	FBgn0039130	10.02	10.07	9.91	9.81	9.96	10.01
1623045_at	FBgn0025366	12.31	12.36	12.61	12.57	12.21	12.09
1634396_at	FBgn0038381	9.62	9.67	9.34	9.76	9.93	9.83
1625178_at	FBgn0051038	7.68	7.72	7.81	8.11	7.07	7.5
1638248_at	---	10.73	10.78	10.77	10.95	10.71	10.64
1632487_at	FBgn0037942	9.66	9.7	9.56	9.62	9.56	9.49
1638887_a_at	FBgn0034728	9.47	9.52	9.44	9.44	9.55	9.46
1629843_s_at	FBgn0029996	11.46	11.5	11.26	11.29	11.28	11.4
1631817_a_at	FBgn0034079	10.92	10.97	10.91	11.18	11.06	11.01
1624780_at	FBgn0040372	9.7	9.75	9.33	9.42	9.53	9.88
1624603_at	FBgn0036314	8.7	8.75	9.02	9.19	8.87	8.89
1637769_s_at	FBgn0000259	11.66	11.7	11.9	11.83	11.89	11.91
1625243_a_at	FBgn0000541	8.81	8.86	8.8	8.62	8.54	8.73
1634737_at	FBgn0038427	8.26	8.31	8.06	8.29	8.27	8.1
1632335_at	FBgn0039359	13.2	13.24	13.41	13.14	13.4	13.37
1626169_at	FBgn0024973	8.59	8.64	8.72	8.88	8.55	8.37
1641312_at	FBgn0001308	9.24	9.29	9.34	9.46	9.28	9.15
1640972_at	FBgn0010317	8.69	8.74	8.69	8.78	8.72	8.7
1624841_s_at	---	8.81	8.85	8.97	8.68	8.33	8.47
1633233_a_at	---	9.26	9.31	9.13	9.24	9.28	9.38
1630224_at	FBgn0034265	8.55	8.6	8.28	8.62	8.7	8.7
1633100_a_at	FBgn0011584	9.02	9.07	8.93	8.86	8.99	9.12
1633173_s_at	FBgn0052542	7.02	7.07	6.8	6.62	6.88	6.88
1636980_s_at	---	10.18	10.23	10.15	10.21	10.18	10.22
1639108_at	---	9.84	9.89	10.03	9.99	9.96	9.93
1623638_a_at	FBgn0035059	7.67	7.71	7.25	7.25	7.81	7.79
1639509_at	FBgn0022069	10.93	10.98	11.03	10.99	10.88	10.95
1623176_at	FBgn0032488	9.07	9.12	9.07	9.51	9.32	9.22
1628402_a_at	FBgn0032135	8.16	8.21	7.95	8.26	8.28	8.33
1623043_s_at	FBgn0035229	9.36	9.4	9.15	9.3	9.56	9.45

1640282_at	FBgn0036827	8.98	9.02	9.01	9.11	9.06	9.2
1627390_at	FBgn0037344	8.04	8.09	8.23	8.15	7.99	7.98
1627995_at	FBgn0032329	8.32	8.37	9.18	8.51	8.41	8.46
1637164_at	FBgn0037874	13.25	13.3	13.3	13.38	13.4	13.36
AFFX-r2-Bs-	---	8.65	8.7	8.95	9.35	8.74	8.59
1638857_at	FBgn0031493	9.11	9.15	9.3	9.28	9.24	9.16
1633336_at	---	8.97	9.02	9.09	8.92	9.01	8.97
1637352_a_at	FBgn0042135	9.63	9.67	9.47	9.46	9.69	9.77
1631212_at	FBgn0040339	9.95	9.99	9.88	10.02	9.86	9.86
1623496_at	FBgn0001330	8.18	8.22	8.45	8.39	8.23	8.16
1632980_at	FBgn0036824	10.57	10.61	10.91	10.68	10.53	10.79
1628248_at	FBgn0003334	10.67	10.72	10.46	10.55	10.61	10.84
1638446_a_at	FBgn0031492	8.62	8.66	8.72	8.92	8.8	8.67
1629694_at	FBgn0005648	7.06	7.1	6.86	7.77	7.02	7.27
1630732_at	FBgn0031456	8.09	8.13	7.93	8.13	8.24	8.27
1623967_at	FBgn0015296	9.46	9.51	9.46	9.52	9.73	9.62
1629795_at	---	8.85	8.9	8.63	8.8	8.77	8.82
1634316_at	FBgn0030246	9	9.04	9.26	9.2	9.11	9.02
1629809_at	FBgn0050491	8.21	8.25	8.2	8.11	7.98	8.05
1635909_at	---	8.36	8.4	8.68	8.58	8.27	8.41
1631733_at	FBgn0026089	9.95	10	10.05	10.1	9.97	9.84
1623545_at	FBgn0005655	11.78	11.82	11.98	12.06	12.09	11.91
1624386_at	FBgn0027057	9.24	9.28	9.39	9.49	9.48	9.32
1623086_at	FBgn0004913	9.82	9.86	9.82	10.09	10.01	9.87
1640661_at	---	7.85	7.9	8.01	7.96	7.88	7.95
1628445_at	FBgn0053213	8.98	9.02	8.95	9.32	9.09	8.87
1639878_at	FBgn0040666	9.8	9.84	9.97	9.98	9.78	9.84
1633784_at	FBgn0037638	8.86	8.91	8.98	9.07	8.91	8.87
1637554_a_at	FBgn0011763	9.98	10.03	10.07	10.05	9.98	10.03
1623855_s_at	FBgn0036187	8.45	8.49	8.44	8.45	8.43	8.46
1625204_a_at	FBgn0031995	8.93	8.98	8.71	8.79	8.8	8.77
1637038_at	FBgn0037569	8.21	8.25	8.15	8.3	8	8.01
1640121_a_at	FBgn0033380	8.71	8.76	8.79	9.08	8.92	8.93
1638624_at	FBgn0015781	8.88	8.92	9.03	9.12	8.95	9.16
1627197_at	FBgn0004574	8.65	8.69	8.62	8.92	8.91	8.69
1641607_at	---	9.23	9.27	8.92	9.08	9.26	9.06

1641328_at	FBgn0016119 /// FBgn000	11.82	11.86	12.23	12.07	11.98	11.98
1626947_s_at	FBgn0002521	11.16	11.21	11.02	11.3	11.11	11.21
1637841_at	FBgn0033199	8.56	8.6	8.27	8.53	8.44	8.51
1635827_s_at	FBgn0016917	10.15	10.19	10.15	10.15	10.23	10.25
1640138_at	FBgn0033017	11.38	11.42	11.33	11.57	11.45	11.4
1634619_at	FBgn0032147	7.85	7.89	7.8	7.75	7.13	7.45
1630213_at	FBgn0037255	8.65	8.7	9.01	9.35	8.86	8.7
1633331_at	FBgn0020306	10.53	10.57	10.52	10.42	10.35	10.63
1637142_at	FBgn0031824	9.38	9.43	9.4	9.78	9.5	9.23
1635239_at	FBgn0035164	8.8	8.85	9.06	9.32	8.88	8.76
1638186_a_at	FBgn0034542	8.77	8.82	8.73	8.99	8.78	8.65
1625691_at	FBgn0046687	9.4	9.44	9.15	9.11	9.2	9.37
1628943_at	FBgn0036299	9.2	9.24	9.1	9.27	9.24	9.25
1632051_at	---	8.84	8.88	8.7	8.82	9	8.96
1626158_s_at	FBgn0026630	9.85	9.9	9.74	9.86	9.95	10.1
1626899_at	---	8.97	9.02	9.14	9.26	9.07	9.03
1634871_s_at	---	8.8	8.84	8.54	8.7	8.61	8.74
1638526_a_at	FBgn0039240	8.51	8.55	8.5	8.49	8.62	8.54
1630911_s_at	FBgn0030719	10.72	10.76	10.94	10.86	10.76	10.8
1630731_at	FBgn0035414	7.54	7.59	7.23	7.59	7.76	7.71
1641566_s_at	FBgn0036816	10.93	10.98	11.12	11.21	10.99	11.12
1629005_a_at	FBgn0034971	9.26	9.3	9.21	8.83	9.28	9.24
1639086_s_at	FBgn0038145	12.51	12.55	12.5	12.62	12.55	12.59
1641584_at	FBgn0037922	10.09	10.13	9.8	10.42	10.25	10.21
1639378_at	FBgn0036850	8.49	8.53	8.27	8.74	8.62	8.65
1625426_at	FBgn0032171	8.87	8.91	8.57	8.78	8.87	8.87
1636544_at	FBgn0036489	8.97	9.01	8.97	8.71	8.59	8.88
1636926_s_at	FBgn0000250	11.51	11.56	11.28	11.47	11.62	11.59
1637814_s_at	FBgn0040308	9.11	9.16	9.2	9.25	9.33	9.3
1628017_a_at	FBgn0004419	13.24	13.29	13.07	13.23	13.34	13.31
1639555_at	FBgn0033802	9.9	9.94	9.92	10.02	9.74	10.06
1625480_at	FBgn0035586	8.28	8.33	8.24	8.11	8.3	8.32
1625125_at	FBgn0030612	9.55	9.59	9.55	9.55	9.73	9.66
1625107_at	FBgn0000221	8.01	8.05	7.5	7.86	7.75	7.84
1631090_a_at	FBgn0037234	8.51	8.55	8.58	8.74	8.64	8.78
1624032_at	FBgn0031670	11.47	11.52	11.28	11.58	11.46	11.46

1623648_s_at	FBgn0035226	9.18	9.22	9.59	9.4	9.19	9.23
1634390_s_at	FBgn0017565	13.2	13.24	13.39	13.44	13.32	13.27
1632547_at	---	12.79	12.83	12.66	12.92	12.81	12.84
1624496_at	FBgn0028554	11.08	11.13	11.01	11.06	10.99	11.11
1637470_at	FBgn0030753	9.62	9.66	9.75	9.92	9.75	9.72
1627021_at	FBgn0037622	7.99	8.04	7.83	8.28	8.13	8.09
1626135_s_at	FBgn0027588	10.34	10.38	10.52	10.43	10.24	10.32
1623952_a_at	FBgn0020887	10.34	10.38	10.24	10.24	10.17	10.36
1625763_at	FBgn0031263	11.07	11.11	11.41	11.35	10.87	10.86
1640295_a_at	FBgn0036518	9.34	9.38	9.46	9.59	9.14	9.22
1639121_at	FBgn0011745	10.71	10.75	10.82	10.94	10.76	10.69
1631940_s_at	FBgn0000283	11.11	11.15	11.1	11.07	11.15	11.21
1637552_s_at	FBgn0052423	8.39	8.43	8.61	8.58	8.31	8.61
1630340_at	FBgn0031638	9.16	9.2	8.92	9.18	9.22	9.28
1628011_a_at	FBgn0039544	8.89	8.93	8.71	8.88	9.03	9.03
1640822_s_at	FBgn0022987	6.98	7.02	6.92	7.16	7.02	7.14
1625898_s_at	FBgn0028717	9.25	9.29	9.24	9.4	9.43	9.35
1624568_at	---	7.79	7.83	7.24	7.55	7.3	7.09
1636599_at	FBgn0037491	8.86	8.9	8.81	8.94	8.88	8.91
1625032_s_at	FBgn0016038	9.61	9.65	9.57	9.82	9.65	9.59
1640561_at	FBgn0035916	9.44	9.48	9.35	9.7	9.61	9.56
1624023_at	FBgn0004103	10.24	10.29	10.58	10.55	10.61	10.57
1631430_at	FBgn0012058	8.29	8.33	8.6	8.78	8.56	8.33
1634700_at	FBgn0033342	11.24	11.28	11.39	11.53	11.47	11.29
1629647_at	FBgn0010612	12.29	12.33	12.45	12.54	12.38	12.34
1625081_at	FBgn0031498	8.02	8.06	7.86	8.13	8.06	8.02
1624097_s_at	FBgn0051151	8.47	8.52	8.57	8.59	8.53	8.59
1638113_at	---	8.48	8.52	8.55	8.48	8.39	8.57
1638765_at	FBgn0032016	9.56	9.6	9.57	9.9	9.68	9.53
1630156_at	---	10.1	10.14	10.41	10.19	10.09	10.11
1635358_at	FBgn0030003	9.05	9.09	9.15	9.39	9.34	9.17
1631427_s_at	FBgn0034691	8.81	8.85	8.87	8.97	8.85	8.81
1632724_at	FBgn0010215	10.65	10.69	10.74	10.92	10.79	10.79
1629968_s_at	FBgn0039381	8.78	8.82	8.52	8.95	8.67	8.59
1627254_at	FBgn0036510	9.49	9.53	9.56	9.64	9.72	9.65
1639892_at	FBgn0024289	7.02	7.06	6.91	5.9	6.2	6.29

1627900_at	---	9.21	9.25	9.72	9.29	9.31	9.23
1623333_a_at	---	7.87	7.91	7.97	7.82	7.88	7.78
1624826_at	FBgn0031990	8.56	8.6	8.65	8.36	8.45	8.51
1636816_s_at	FBgn0028916	9.05	9.09	9.05	9.26	9.13	9.05
1624858_at	FBgn0037878	10.03	10.07	10.02	10.29	10.26	10.13
1640377_s_at	FBgn0015286	11.51	11.55	9.97	10.21	11.26	11.39
1636681_at	FBgn0031183	8.75	8.79	8.41	8.55	8.77	8.73
1623481_at	FBgn0030703	10.57	10.6	9.66	10.14	10.54	10.63
1632236_at	---	9.47	9.51	9.38	9.47	9.37	9.34
1635871_at	FBgn0025724	9.29	9.33	9.5	9.42	9.29	9.25
1640872_at	---	9.04	9.08	9.24	9.11	9.02	9.03
1636371_at	FBgn0029686	9.01	9.05	8.85	9.05	9.08	9.26
1640589_at	---	9.1	9.14	9.28	9.31	9.22	9.23
1637065_a_at	FBgn0035276 /// FBgn003	8.02	8.06	8.08	8.39	8.04	8.08
1639242_a_at	FBgn0019960	9.15	9.18	9.54	9.6	9.47	9.28
1639586_at	FBgn0033206	9.05	9.09	8.86	9.15	8.95	9.06
1632163_at	FBgn0037747	9.59	9.63	9.16	9.72	9.77	9.77
1635638_s_at	FBgn0030412	9.14	9.18	9.07	8.83	9.31	9.28
1627221_at	FBgn0038574	9.53	9.57	9.52	9.68	9.56	9.63
1635378_at	FBgn0037098	8.09	8.13	8.08	7.97	8.03	8.12
1634733_at	FBgn0034804	10.39	10.43	10.37	10.18	10.13	10.2
1635564_at	FBgn0037150	9.05	9.08	8.8	8.87	8.98	8.94
1625144_at	FBgn0034704	8.56	8.6	8.59	8.73	8.71	8.43
1626280_a_at	FBgn0052956	10.09	10.13	10.22	10.47	10.34	10.22
1624520_a_at	FBgn0001078	10.49	10.53	10.29	10.23	10.19	10.49
1637257_at	---	9.78	9.82	9.75	9.67	10.02	9.76
1639721_at	FBgn0030228	8.5	8.53	8.09	8.41	8.4	8.39
1629629_at	FBgn0029958	9.96	10	9.91	10	9.95	9.97
1632338_a_at	FBgn0035651	9.59	9.63	9.46	9.4	9.55	9.52
1639514_at	FBgn0038811	8.37	8.41	8.64	8.24	8.24	8.38
1640271_s_at	FBgn0025741	10.88	10.92	10.68	10.59	10.64	10.99
1626162_s_at	FBgn0039672	8.84	8.88	9.24	9.21	9.16	8.98
1625038_s_at	FBgn0019686	11.89	11.93	11.9	11.97	11.94	11.94
1635778_at	FBgn0033766	7.85	7.89	8.02	7.91	8.11	7.96
1627003_at	FBgn0037359	8.16	8.2	8.13	8.35	8.4	8.41
1640007_at	FBgn0029718	10.56	10.59	10.69	10.73	10.47	10.46

1626259_at	FBgn0003575	8.77	8.8	8.88	8.84	8.86	8.76
1627452_a_at	FBgn0002441	8.84	8.87	8.48	8.72	8.93	8.83
1625014_at	---	9.52	9.56	9.39	9.37	9.63	9.6
1631125_at	FBgn0030353	11.19	11.23	11.18	11.25	11.27	11.33
1629924_at	FBgn0039280	7.39	7.43	7.43	7.46	7.61	7.49
1627702_at	FBgn0034431	9.77	9.81	9.7	9.89	9.96	9.79
1631964_at	FBgn0030012	7.72	7.76	7.56	7.8	7.84	7.63
1634159_s_at	---	8.96	9	8.89	8.76	9.01	9.14
1636735_s_at	FBgn0034946	9.46	9.49	9.11	9.29	9.51	9.54
1627794_a_at	FBgn0038327	8.26	8.3	8.33	8.49	8.49	8.35
1636548_at	FBgn0011211	12.31	12.35	12.62	12.56	12.48	12.39
1624014_at	FBgn0035965	8.56	8.6	8.49	8.53	8.59	8.57
1632370_at	FBgn0013347	10.57	10.6	10.59	10.74	10.68	10.58
1634383_a_at	FBgn0028425	10.08	10.12	10.41	10.16	10.08	10.13
1639632_at	FBgn0037489	9.23	9.26	9.58	9.45	9.44	9.41
1626565_at	FBgn0027599	8.87	8.91	8.77	9.06	8.86	8.84
1630983_s_at	---	8.77	8.8	9.4	9.29	9.14	9.15
1626154_at	FBgn0030053	8.29	8.32	8.28	8.4	8.51	8.39
1634199_at	---	10.18	10.22	10.07	10.32	10.28	10.19
1627945_at	---	8.47	8.5	8.3	8.29	8.37	8.52
1632955_at	FBgn0011754	8.42	8.45	8.39	8.49	8.54	8.48
1623869_at	---	7.26	7.3	7.2	7.49	7.43	7.46
1622984_at	FBgn0010213	10.83	10.87	11.13	10.98	11.07	10.91
1638801_at	---	9.96	10	9.8	10.05	9.98	9.96
1627116_at	FBgn0033261	9.05	9.09	9.17	9.39	9.3	9.3
1633602_at	FBgn0035624	8.35	8.38	8.34	8.46	8.5	8.53
1626621_at	FBgn0033474	10.09	10.12	10.07	10.49	10.2	10.08
1640311_s_at	FBgn0022238	10.95	10.98	10.8	10.87	10.85	11.06
1630668_a_at	FBgn0037374	9.37	9.41	9.29	9.28	9.48	9.51
1629920_at	FBgn0024889	10.42	10.45	10.36	10.42	10.48	10.39
1636886_at	FBgn0003483	10.09	10.13	10.14	10.31	10.06	10.08
1623285_at	FBgn0030245	9.66	9.69	9.26	9.17	9.56	9.64
1623231_at	FBgn0040228	8.29	8.33	8.34	8.61	8.37	8.34
1635761_at	FBgn0005642	9.82	9.86	9.56	9.83	10	9.93
1627546_at	FBgn0035769	9.47	9.51	9.23	9.43	9.46	9.42
1632123_at	FBgn0032915	9.14	9.17	9.43	9.22	9.16	9.13

1630705_at	FBgn0037843	8.74	8.78	8.66	8.73	8.88	8.91
1628482_at	FBgn0029959	8.98	9.01	8.91	8.94	9.15	9.08
1639392_at	---	10.68	10.72	10.9	10.61	10.58	10.7
1637557_a_at	FBgn0036357	9.26	9.3	9.22	9.58	9.34	9.13
1623021_at	FBgn0026380	11.86	11.9	11.9	12.03	11.85	11.72
1623366_at	FBgn0037608	9.43	9.47	9.71	9.73	9.55	9.45
1628044_at	FBgn0039115	9.72	9.76	9.87	9.99	9.9	9.96
1631240_at	FBgn0011336	10	10.04	10.22	9.75	9.6	9.98
1640462_at	FBgn0037933	9.72	9.76	9.69	9.87	9.75	9.75
1631996_at	FBgn0036613	9.1	9.14	9.54	9.72	9.41	9.27
1641714_at	FBgn0033543	7.2	7.23	7	6.89	7.41	7.2
1623955_at	FBgn0035953	8.15	8.19	8.34	8.34	8.28	8.25
1632355_at	---	9.34	9.37	9.2	9.23	9.58	9.75
1637410_s_at	FBgn0002121	8.25	8.28	8.58	8.96	8.11	8.46
1640456_at	FBgn0031606	8.06	8.09	8.23	8.43	8.2	7.9
1632663_at	FBgn0037134	9.83	9.86	9.6	10.2	10.07	9.93
1632384_at	FBgn0028926	7.68	7.72	7.76	7.65	7.96	7.83
1627020_at	FBgn0034535	8.85	8.88	8.95	8.88	8.98	8.94
1628613_a_at	FBgn0050492	9.66	9.69	9.62	9.22	9.61	9.76
1630688_at	FBgn0001233	13.42	13.46	13.6	13.68	13.53	13.47
1641648_at	FBgn0040396	9.88	9.92	10.08	10.42	10.04	10.01
1634504_a_at	---	9.73	9.76	9.62	9.63	9.71	9.67
1632736_at	FBgn0030944	9.37	9.41	9.36	9.42	9.43	9.28
1629841_at	FBgn0040298	8.17	8.21	8.71	8.64	8.22	8.3
1630637_s_at	FBgn0001219	13.42	13.45	13.52	13.48	13.46	13.39
1631579_a_at	FBgn0016081	8.3	8.33	8.45	8.46	8.43	8.27
1628710_at	FBgn0036919	8.92	8.96	8.79	8.82	8.95	8.96
1628321_at	FBgn0032354	9.29	9.32	8.9	9.38	9.54	9.45
1625775_a_at	FBgn0000382	9.03	9.07	8.76	8.93	9.03	9.15
1634168_s_at	FBgn0039163	10.17	10.21	10.25	10.33	10.25	10.26
1641027_at	FBgn0043458	8.77	8.8	8.86	8.93	8.73	8.82
1627492_at	FBgn0036578	9.76	9.79	9.95	9.97	9.79	9.82
1638614_at	FBgn0029525	9.23	9.27	9.32	9.04	9.24	9.16
1629021_at	FBgn0034989	8.98	9.02	9.13	9.24	9.03	8.92
1634434_at	---	8.51	8.54	8.34	8.45	8.57	8.53
1634695_at	FBgn0002542	9.98	10.01	9.77	10.13	10	9.9

1638030_at	FBgn0033104	8.26	8.29	8.3	8.31	8.47	8.25
1630984_at	FBgn0010217	11.73	11.77	11.76	11.72	11.61	11.72
1634696_at	FBgn0039004	8.68	8.72	8.89	9.24	8.85	8.76
1630823_at	---	8.67	8.71	8.96	8.84	8.8	8.7
1635667_at	FBgn0051108 /// FBgn005	9.72	9.75	9.5	9.75	9.76	9.66
1624431_at	FBgn0033085	8.87	8.9	9.19	9.06	8.86	8.87
1624894_s_at	FBgn0005776	10.09	10.13	10.2	10.3	10.16	10.16
1637650_at	FBgn0031256	9.85	9.88	9.82	10.35	9.96	9.87
1632844_s_at	FBgn0035236	9.84	9.87	9.75	9.71	9.88	9.9
1635892_at	FBgn0038577	9.95	9.98	9.95	10.4	9.93	9.63
1635123_at	---	9.37	9.4	9.22	9.23	9.43	9.31
1624639_at	FBgn0039626	7.59	7.62	7.64	7.72	7.7	7.74
1639761_s_at	FBgn0004921	11.5	11.53	11.67	11.42	11.49	11.59
1632577_a_at	FBgn0003600	10.87	10.9	11.2	11.16	11.12	11.02
1635630_a_at	FBgn0003475	8.98	9.02	8.77	8.95	9.04	9.13
1641196_at	FBgn0037737	9.26	9.29	9.21	9.46	9.23	9.3
1632146_a_at	FBgn0027579	10.71	10.75	10.63	10.56	10.34	10.5
1632258_s_at	FBgn0044823	9.55	9.58	9.71	9.95	9.91	9.77
1624779_at	FBgn0035524	10.23	10.26	10.56	10.52	10.23	10.28
1625866_at	FBgn0020645	6.94	6.97	6.73	6.84	7.05	7
1624693_at	FBgn0013749	11.65	11.68	11.68	11.81	11.69	11.76
1634687_at	FBgn0035541	10.25	10.28	10.54	10.29	10.21	10.21
1631687_at	FBgn0020620	8.27	8.31	7.97	8.24	8.38	8.56
1626543_at	FBgn0035869	8.95	8.98	8.77	8.95	9.08	9.07
1636006_at	FBgn0023510	9.3	9.33	9.3	9.21	9.23	9.31
1632998_at	FBgn0027490	8.33	8.36	8.24	8.5	8.49	8.38
1638711_at	FBgn0039175	9.34	9.37	9.57	9.54	9.57	9.38
1625994_a_at	FBgn0038474	9.58	9.61	9.79	9.91	9.79	9.8
1637509_s_at	FBgn0027360	11.08	11.11	11.2	11.15	11.19	11.07
1635915_at	FBgn0023167	10.79	10.82	11.03	10.91	10.71	10.84
1623572_at	FBgn0028974	7.16	7.19	6.98	7.55	7.27	7.17
1639853_at	FBgn0038252	11.48	11.52	11.46	11.72	11.68	11.69
1631078_at	FBgn0024177	11.27	11.3	11.32	11.5	11.55	11.55
1631620_at	---	10.73	10.76	11.03	11.09	10.83	10.66
1623647_at	FBgn0033349	10.57	10.6	10.68	10.87	10.66	10.53
1637783_at	FBgn0035435	7.74	7.77	7.28	7.76	7.93	7.83

1627394_s_at	FBgn0000097	9.26	9.29	9.11	8.97	8.9	9.18
1625836_at	FBgn0032149	8.43	8.46	8.74	8.41	8.51	8.44
1632559_at	FBgn0003268	8.34	8.37	8.24	8.58	8.48	8.27
1638257_at	FBgn0037342	8.96	8.99	8.86	9.09	9.16	9.12
1623053_a_at	FBgn0034345	10.04	10.07	10.03	9.86	10.05	10.08
1637887_at	FBgn0030321	10.48	10.51	10.59	10.33	10.32	10.39
1641297_at	FBgn0002431	10.4	10.43	10.58	10.3	10.4	10.44
1632318_at	FBgn0024365	8.95	8.98	8.93	9.03	8.79	8.89
1625972_at	---	7.42	7.45	7.88	7.6	7.07	6.68
1628141_at	---	10.06	10.09	10.08	8.82	9.94	10.11
1632713_at	FBgn0002962	12.33	12.36	12.07	12.31	12.25	12.3
1628161_at	FBgn0034118	9.73	9.76	10.03	10.12	10	9.89
1629977_at	FBgn0030743	10.29	10.32	10.48	10.66	10.66	10.47
1623726_at	FBgn0037611	8.58	8.61	8.42	9.05	8.72	8.53
1641438_at	---	8.79	8.82	8.83	9.06	8.85	8.75
1638929_at	FBgn0027529	10.05	10.08	10.07	10.06	9.82	9.99
1629432_at	FBgn0036990	9.75	9.78	10.03	9.97	9.73	9.77
1631577_a_at	---	11.19	11.22	11.37	11.32	11.35	11.4
1637954_at	FBgn0038049	10.11	10.14	10.08	10.37	10.13	10.13
1624134_a_at	FBgn0034650	9.99	10.02	9.75	10.04	10.17	10.14
1629887_at	FBgn0034021	10.28	10.31	10.22	10.4	10.25	10.24
1631479_at	FBgn0002283	10.3	10.33	10.05	10.03	10.3	10.38
1634307_at	FBgn0030685	10.35	10.38	10.39	10.24	10.4	10.53
1638052_at	---	11.41	11.44	11.47	11.58	11.7	11.68
1633417_at	---	12.17	12.2	12.04	12	12.21	12.18
1630543_at	---	8.2	8.23	8.31	8.4	8.56	8.47
1624521_a_at	FBgn0023537	10.69	10.71	11.04	10.92	11.02	10.91
1625421_at	FBgn0050377	9.96	9.99	9.98	9.85	9.84	9.77
1630606_at	FBgn0040475	8.8	8.82	8.79	8.98	8.82	8.81
1623900_a_at	FBgn0032382	8.21	8.24	7.91	8.55	8.14	7.78
1639206_at	FBgn0030700	7.31	7.34	7.05	7.37	7.27	7.24
1641707_at	FBgn0036136	9.89	9.92	9.88	10.14	9.86	9.7
1624361_s_at	FBgn0010488	11.65	11.68	11.85	11.93	11.74	11.67
1637149_s_at	FBgn0035498 /// FBgn002	10.16	10.19	10.12	9.96	10.03	10.11
1634289_at	FBgn0003210	8.41	8.44	8.68	8.67	8.32	8.5
1638593_a_at	FBgn0017566	9.33	9.36	9.56	9.72	9.42	9.23

1631006_a_at	FBgn0036353	9.33	9.36	9.37	9.45	9.4	9.39
1637720_at	FBgn0036819	7.4	7.43	7.27	7.76	7.57	7.55
1639715_at	---	9.11	9.14	8.94	9.04	8.94	9
1636679_at	FBgn0052296	7.22	7.25	7.65	7.62	7.31	7.15
1624012_at	FBgn0031231	10.38	10.41	10.33	10.58	10.25	10.24
1638837_a_at	FBgn0053066	8.26	8.29	8.23	8.18	8.02	8.15
1638690_at	FBgn0035639	10.47	10.5	10.38	10.48	10.49	10.55
1625945_a_at	FBgn0035137	8.42	8.45	7.89	8.3	8.34	8.55
1623271_a_at	FBgn0001281	10.51	10.54	10.66	10.56	10.53	10.61
1636071_a_at	FBgn0022942	8.98	9.01	8.73	8.97	9.03	8.92
1625481_a_at	FBgn0004795	11.39	11.42	11.25	11.14	11.33	11.41
1635979_at	---	9	9.03	8.86	8.89	9.04	9.03
1628323_s_at	FBgn0004646	8.38	8.41	9.17	8.49	7.84	8.27
1641058_at	FBgn0035529	9.93	9.96	9.97	9.83	10.04	9.99
1628901_at	---	9.32	9.34	9.18	9.13	9.63	9.65
1636073_at	---	8.89	8.92	9.09	8.92	8.8	8.84
1637489_at	FBgn0026079	7.82	7.85	8.39	8.01	7.7	7.62
1633363_at	FBgn0029689	9.23	9.26	9.13	9.33	9.23	9.07
1639228_at	FBgn0011741	9.4	9.43	9.38	9.36	9.43	9.3
1641676_at	FBgn0031298	8.58	8.61	8.46	8.65	8.66	8.64
1629401_s_at	FBgn0033426	7.42	7.45	7.69	7.57	7.51	7.37
1638012_at	FBgn0003292	8.22	8.25	7.83	8.26	8.45	8.35
1639951_at	FBgn0032871	8.61	8.63	8.5	8.37	8.32	8.46
1638297_at	FBgn0030099	7.85	7.87	7.79	7.88	7.82	7.65
1640659_s_at	FBgn0036685	9.25	9.28	9.44	9.62	9.26	9.29
1638208_at	FBgn0033783	10.08	10.11	10.08	9.92	10.06	10.09
1632840_s_at	FBgn0023441	9.21	9.24	9.29	9.01	9.11	9.14
1623306_at	FBgn0031105	9.06	9.09	9.43	9.16	9.23	9.14
1636225_at	FBgn0028980	9.06	9.08	8.88	9.2	9.3	9.27
1636553_at	FBgn0029813	6.85	6.88	7.34	7.27	7.17	6.99
1628008_a_at	FBgn0024923	11.91	11.94	12	12.23	11.89	11.75
1626738_at	FBgn0031300	8.21	8.24	8.37	8.35	8.43	8.24
1626483_at	---	9.12	9.15	9.08	9.24	9.11	9.06
1636291_at	FBgn0034646	10.09	10.12	10.17	10.46	10.19	10.14
1633698_at	FBgn0011455	11.1	11.13	11.46	11.34	11.27	11.31
1634096_at	FBgn0032114	11.5	11.53	11.48	11.65	11.58	11.47

1634705_at	FBgn0032701	8.49	8.52	8.79	8.45	8.42	8.4
1630115_at	FBgn0030694	8.6	8.63	8.87	8.95	8.8	8.7
1630384_at	FBgn0031875	9.35	9.38	9.27	9.57	9.55	9.34
1639522_at	FBgn0051950	8.48	8.51	8.51	8.78	8.58	8.49
1630290_at	FBgn0039211	9.14	9.17	9.11	9.16	9	9.12
1640599_at	FBgn0020513	10.32	10.35	10.68	10.53	10.42	10.4
1636160_at	FBgn0032863 /// FBgn005	8.41	8.44	8.38	8.41	8.62	8.43
1633008_at	FBgn0033121	9.19	9.22	8.95	9.06	9.2	9.18
1629655_at	FBgn0029512	11.25	11.28	11.33	11.76	11.54	11.35
1637027_s_at	FBgn0032801	7.54	7.57	7.35	7.27	7.72	7.71
1634739_a_at	FBgn0003071	9.71	9.74	9.62	9.52	9.8	9.62
1641318_at	FBgn0037687	9.13	9.16	9.23	9.41	9.2	9.02
1636464_at	FBgn0038269	8.18	8.21	8.45	8.49	8.29	8.17
1641309_s_at	FBgn0011604	9.4	9.43	9.5	9.63	9.53	9.43
1625713_at	FBgn0036330	8.19	8.22	7.95	8.44	7.6	7.32
1639494_at	FBgn0029004	8.4	8.42	8.61	9	8.46	8.44
1636243_at	FBgn0034921	8.96	8.99	9.01	9.32	9.28	9.21
1626755_at	FBgn0050085	9.62	9.65	9.45	9.68	9.73	9.59
1639663_at	FBgn0038316	9.07	9.09	8.98	9.24	9.21	9.17
1635016_at	FBgn0032054	8.69	8.72	8.62	8.7	8.8	8.68
1630557_at	FBgn0039306	9.53	9.55	9.71	9.67	9.63	9.64
1628785_at	FBgn0010830	9.88	9.91	9.77	9.94	9.98	9.97
1635377_at	FBgn0033884	8.71	8.74	8.67	8.91	8.79	8.83
1641226_a_at	FBgn0043884	9.67	9.7	9.85	9.95	9.73	9.69
1636029_s_at	FBgn0030718	10.54	10.57	10.54	10.47	10.61	10.52
1623472_at	FBgn0030805	8.96	8.99	8.89	9.22	9.15	9.1
1637101_at	FBgn0039861	7.7	7.73	7.72	7.89	7.82	7.85
1635342_at	FBgn0034654	11.14	11.17	11.17	11.35	11.22	11.08
1624744_a_at	FBgn0013718	8.83	8.85	9.11	9.01	8.68	8.94
1638864_at	FBgn0015789	10.95	10.97	10.71	10.58	10.86	10.95
1623108_at	FBgn0033081	11.59	11.62	11.45	11.75	11.72	11.65
1626454_at	FBgn0015625	11.37	11.39	11.19	11.43	11.26	11.35
1631766_at	FBgn0033751	9.63	9.66	9.63	9.69	9.78	9.59
1624390_a_at	FBgn0035110	9.62	9.65	9.88	9.89	9.82	9.78
1626615_at	---	7.75	7.77	7.59	7.92	7.78	7.69
1635021_at	FBgn0029088	8.44	8.47	8.27	8.24	8.5	8.49

1626370_at	FBgn0042107	8.84	8.86	8.93	8.92	8.8	8.63
1641568_a_at	FBgn0039265	9.98	10.01	10	10.33	10.16	10.13
1624157_at	FBgn0033734 /// FBgn003	10.56	10.59	10.15	10.79	10.31	10.21
1632897_at	FBgn0039188	8.9	8.92	8.76	8.71	8.83	8.89
1627173_at	FBgn0030076	8.84	8.86	8.79	8.96	8.83	8.65
1637359_at	FBgn0030608	11.92	11.94	11.44	11.59	11.66	11.68
1628595_at	FBgn0015321	10.08	10.11	9.87	10.19	10.29	10.34
1626801_at	FBgn0036290	9.83	9.85	9.91	9.99	10.03	10
1633961_s_at	---	10.31	10.33	10.17	10.17	10.24	10.4
1628420_s_at	FBgn0037944	8.42	8.45	8.07	8.37	8.53	8.61
1639763_at	---	9.84	9.86	10.05	10.2	9.99	9.92
1638229_at	FBgn0010741	11.4	11.43	11.44	11.41	11.39	11.32
1635473_at	FBgn0051713	7.73	7.76	7.87	7.97	7.83	7.76
1635208_at	FBgn0032467	8.86	8.88	8.9	8.94	8.81	8.75
1638784_s_at	---	7.76	7.78	7.7	8.05	7.92	7.92
1632670_at	FBgn0036389	9.71	9.74	9.78	9.49	9.59	9.59
1641188_a_at	FBgn0027574	8.22	8.25	8.12	8.26	8.29	8.33
1637220_s_at	FBgn0037655	10.34	10.36	10.39	10.61	10.41	10.26
1626653_a_at	FBgn0024891	8.77	8.79	8.7	8.58	8.77	8.75
1624392_s_at	FBgn0011672	9.17	9.19	9.31	9.55	9.35	9.42
1626817_at	FBgn0030789	8.3	8.33	8.37	8.28	8.29	8.39
1623633_at	FBgn0015359	9.86	9.89	10.14	10.12	10.09	10.02
1628913_at	FBgn0052365	8.64	8.67	8.57	8.75	8.65	8.67
1633918_s_at	FBgn0027515	10.16	10.18	10.08	10.21	10.06	10.1
1632548_a_at	FBgn0037207	9.48	9.51	9.34	9.48	9.7	9.71
1640333_at	FBgn0033055	9.06	9.08	8.95	9.17	9.13	9.02
1624365_at	FBgn0034308	9.01	9.03	8.74	8.81	8.99	8.82
1636639_at	FBgn0031260	10.25	10.27	10.48	10.15	10.13	10.41
1636336_at	FBgn0031189	8.67	8.69	8.74	8.57	8.66	8.76
1623807_a_at	---	9.81	9.84	10.07	10.02	9.94	9.77
1641246_at	FBgn0036038	7.44	7.46	7.75	7.92	7.73	7.57
1631139_a_at	FBgn0004811	9.67	9.7	9.31	9.44	9.68	9.8
1629150_at	FBgn0033035	10.85	10.88	10.82	10.94	11.03	10.97
1627462_a_at	FBgn0038735	7.07	7.1	7.36	7.42	7.39	7.19
1635843_at	FBgn0031773	8.49	8.51	8.64	8.6	8.52	8.55
1630076_at	FBgn0024352	11.87	11.89	12.05	12.03	11.94	11.95

1632364_at	---	9.13	9.16	9.46	9.78	9.24	8.96
1635996_at	FBgn0035911	9.86	9.88	9.62	9.89	9.73	9.68
1636514_at	FBgn0026323	9.61	9.64	9.38	9.38	9.51	9.48
1627062_s_at	FBgn0030571	8.5	8.53	8.35	8.57	8.61	8.65
1632475_at	FBgn0010909	9.28	9.3	9.41	9.43	9.45	9.47
1629632_at	FBgn0037689	7.86	7.88	7.7	7.64	7.93	7.83
1640288_s_at	FBgn0036974	11.71	11.73	11.8	11.86	11.73	11.63
1639447_at	FBgn0039829	8.54	8.56	8.96	8.67	8.64	8.6
1630721_s_at	FBgn0037218	10.4	10.43	10.3	10.16	10.49	10.55
1630246_at	FBgn0040890	9.95	9.98	9.66	9.62	9.86	9.8
1635588_at	---	8.98	9	9.26	9.35	9.14	9.12
1630416_at	FBgn0024887	9.01	9.03	8.96	9.11	9.17	9.18
1636977_at	FBgn0032880	8.91	8.93	9.2	9.17	9.02	9.03
1628240_at	FBgn0037010	10.06	10.09	10.07	10.21	10.11	10.06
1636858_at	FBgn0027106 /// FBgn000	8.64	8.66	8.29	8.61	8.5	8.51
1629844_s_at	FBgn0003200	10.08	10.11	9.95	10.02	10.07	10.13
1629602_at	FBgn0031044	9.21	9.24	9.05	9.03	9.32	9.39
1633965_at	FBgn0037001	10.33	10.35	10.8	10.65	10.59	10.38
1627589_s_at	FBgn0032078	10.22	10.24	10.11	9.72	9.91	10.05
1640445_at	FBgn0037374	9.78	9.8	9.68	9.43	9.75	9.88
1624208_s_at	FBgn0013750	9.9	9.93	9.83	9.85	9.89	10.2
1634887_at	FBgn0026567	11.07	11.1	11.06	10.91	11.06	11.12
1626320_at	FBgn0051344	8.74	8.76	8.73	8.86	8.77	8.86
1641235_at	FBgn0036906	7.36	7.38	6.98	7.21	7.65	7.58
1632484_at	FBgn0039767	10.44	10.46	10.22	10.54	10.52	10.54
1633163_at	FBgn0027792	9.15	9.18	9.16	9.14	9.21	9.03
1632202_at	FBgn0036286	9.01	9.03	8.81	8.92	9.02	9
1632220_s_at	FBgn0039792 /// FBgn000	13.8	13.82	13.92	13.9	13.85	13.79
1632576_at	FBgn0030871	9.26	9.28	9.15	9.4	9.62	9.41
1624685_at	FBgn0052190	9.03	9.06	9.43	9.17	9.16	9.22
1628172_at	FBgn0027948	10.57	10.59	10.78	10.69	10.77	10.73
1629930_s_at	FBgn0041342	8.71	8.73	8.92	8.69	8.57	8.62
1637442_at	FBgn0020245	8.81	8.83	8.74	8.6	8.67	8.69
AFFX-r2-Dro	FBgn0000042	10.68	10.71	10.46	10.44	10.54	10.51
1638310_at	FBgn0001565	10.44	10.46	10.64	10.59	10.72	10.55
1634863_at	FBgn0024558	7.83	7.85	7.82	8.31	8	7.89

1634917_at	FBgn0026372	13.81	13.83	14.1	14.04	13.96	13.92
1636606_at	FBgn0038524	9.19	9.21	8.74	8.94	9.18	9.09
1629217_at	FBgn0051258	9.42	9.44	9.55	9.67	9.73	9.58
1639953_at	FBgn0003015	12.35	12.38	12.43	12.33	12.11	12.3
1626972_at	FBgn0039634	10.02	10.04	9.9	9.99	9.96	9.97
1641233_a_at	FBgn0025937	7.88	7.9	7.88	8.18	7.88	7.76
1631286_at	FBgn0026738	9.36	9.39	9.3	9.5	9.45	9.49
1626196_at	FBgn0025678	10.32	10.34	10.21	10.34	10.35	10.35
1630090_at	---	8.08	8.1	8.18	8.54	8.36	8.19
1626033_at	FBgn0034110	8.07	8.09	8.22	8.17	8.15	8.12
1636561_at	FBgn0031413	7.83	7.85	7.75	7.81	8	7.8
1633660_at	FBgn0015271	9.38	9.4	9.32	9.51	9.44	9.24
1638884_at	FBgn0031384	6.95	6.97	7	6.98	7	7
1635828_at	FBgn0035499	11.27	11.29	11.33	10.93	10.96	11.22
1626191_at	FBgn0032717	7.07	7.09	6.96	7.02	7.11	7.07
1638999_at	---	7.22	7.24	6.91	7.08	7.29	7.17
1631334_at	FBgn0040335	9.43	9.45	9.26	9.06	9.36	9.44
1625112_at	FBgn0011715	10.83	10.85	10.72	11	10.9	10.8
1631196_at	---	9.65	9.67	9.81	9.89	9.93	9.89
1625295_at	FBgn0015402	7.94	7.96	7.74	8.1	8.11	8.08
1632421_at	FBgn0031817	8.43	8.45	8.26	8.16	8.58	8.36
1640977_at	FBgn0032393	9.44	9.46	9.52	9.7	9.53	9.44
1629286_s_at	FBgn0040918	9.68	9.7	9.58	9.6	9.63	9.9
1637993_at	---	8.43	8.46	8.38	8.56	8.62	8.51
1640612_at	FBgn0035285	9.03	9.05	9.06	9.12	9.17	9.12
1622981_at	FBgn0003964	8.94	8.96	8.86	9.07	9.08	9.1
1631519_at	FBgn0034496	7.82	7.84	8.01	8.06	7.85	7.81
1624705_a_at	FBgn0014163	10.81	10.83	10.82	10.78	10.74	10.91
1641278_at	FBgn0032236	10.34	10.36	10.57	10.5	10.57	10.63
1633222_at	FBgn0039417	8.85	8.87	8.66	8.68	9.02	8.93
1626785_at	FBgn0015268	12.95	12.97	12.98	13.09	13.12	13.05
1626163_s_at	FBgn0000042	13.13	13.15	13.05	13.18	13.09	13.01
1632771_at	FBgn0034727	9.59	9.61	9.76	9.81	9.78	9.65
1630492_at	FBgn0036513	9.72	9.74	9.57	9.89	9.69	9.53
1626199_at	FBgn0035238	8.85	8.87	8.94	8.87	8.97	9.15
1639023_at	FBgn0013998	7.93	7.95	8.23	8.51	8.13	7.76

1626988_at	FBgn0034179	7.06	7.08	7.39	7.78	7.58	7.8
1637106_at	FBgn0035866	9.89	9.91	9.74	9.89	9.94	9.96
1640089_at	FBgn0023143	11.27	11.29	11.37	11.45	11.32	11.39
1623715_at	FBgn0031898	8.72	8.74	9.02	9.27	9.02	8.81
1626143_a_at	---	7.27	7.29	7.04	6.99	7.4	7.27
1637678_at	FBgn0022344	10.19	10.21	10.46	10.26	10.15	10.22
1633625_s_at	FBgn0016696	9.91	9.93	9.63	9.73	9.83	9.83
1637988_at	FBgn0034248	9.56	9.58	9.8	9.73	9.55	9.42
1640042_at	FBgn0032295	10.18	10.2	10.09	10.27	10.28	10.2
1636286_at	FBgn0031708	9.52	9.54	9.34	9.45	9.31	9.33
1638001_a_at	FBgn0033675	8.47	8.49	8.55	8.79	8.65	8.67
1628497_at	FBgn0031344	8.17	8.19	8.08	8.33	8.49	8.24
1640928_at	FBgn0038587	12.21	12.23	12.49	12.48	12.44	12.38
1623370_at	FBgn0001990	8.42	8.44	8.33	8.66	8.61	8.56
1636935_at	---	10.72	10.74	10.66	10.79	10.79	10.9
1627868_at	FBgn0004901	10.36	10.38	10.43	10.49	10.45	10.44
1634822_a_at	FBgn0034729	8.09	8.1	8.16	8.44	8.59	8.5
1633680_at	FBgn0037809	7.54	7.56	7.64	7.86	7.82	7.9
1634670_at	FBgn0052714	10.53	10.55	10.47	10.47	10.28	10.8
1632765_at	FBgn0038303	8.15	8.17	8.24	8.27	8.3	8.12
1641075_at	FBgn0039302	10.52	10.53	10.63	10.41	10.42	10.41
1638970_at	FBgn0039404	9.13	9.15	9.08	9.16	9.11	9.22
1628061_at	FBgn0030616	13.27	13.29	13.45	13.45	13.41	13.35
1634979_at	FBgn0038601	10.14	10.16	10.29	10.21	9.93	10.02
1638370_s_at	FBgn0031071	10.51	10.53	10.18	10.11	10.39	10.56
1638090_at	FBgn0032162	8.89	8.9	8.71	9.03	8.92	8.78
1626076_at	FBgn0037700	9.86	9.88	9.95	10.17	9.96	9.97
1641436_at	FBgn0033740	8.99	9.01	8.84	8.85	9.02	8.92
1640476_at	FBgn0032169	8.75	8.76	8.61	8.83	8.74	8.7
1627364_s_at	FBgn0014027	13.84	13.86	13.87	13.93	13.91	13.79
1623405_at	FBgn0011692	10.19	10.21	10.1	10.35	10.22	10.17
1630247_at	FBgn0034734	7.52	7.53	7.65	7.38	7.53	7.44
1628960_s_at	FBgn0025635	9.81	9.83	9.68	9.94	9.9	9.83
1624064_at	FBgn0030738	10.11	10.13	10.05	10.31	10.16	10.15
1628991_at	FBgn0019830	9.66	9.68	9.83	9.85	9.64	9.6
1626513_at	FBgn0036846	9.01	9.03	8.96	9.14	9.13	9.05

1623408_s_at	FBgn0029676	11.2	11.22	11.32	11.42	11.35	11.26
1636861_at	FBgn0033925	8.93	8.95	8.76	8.92	9.01	8.98
1635365_at	FBgn0032250	9.19	9.21	9.16	9.29	9.3	9.39
1638161_at	FBgn0037202	9.26	9.28	9.27	9.35	9.16	9.03
1633418_at	FBgn0036741 /// FBgn003	9.76	9.78	9.47	9.48	9.72	9.79
1639011_a_at	FBgn0037329	8.77	8.79	8.76	8.75	8.94	8.83
1628279_s_at	FBgn0039929	11.11	11.13	11.3	11.43	11.09	11.29
1632195_at	FBgn0030435	9.46	9.47	9.22	9.2	9.53	9.53
1639731_at	FBgn0038564	9.56	9.58	9.3	9.5	9.52	9.61
1638342_at	FBgn0037378	10.09	10.11	10.19	10.23	10.03	9.94
1634881_at	FBgn0033029	9.17	9.19	9.21	9.32	9.05	9.24
1637369_at	---	9.19	9.21	9.31	9.44	9.33	9.3
1638822_at	FBgn0036484	9.42	9.44	9.42	9.52	9.67	9.55
1632931_at	---	10.28	10.3	10.12	10.32	10.24	10.46
1630794_at	FBgn0037371	8.84	8.85	8.71	9.01	9.04	8.91
1640689_a_at	---	10.92	10.94	11.02	11.2	10.99	10.93
1630953_at	FBgn0035692	10.78	10.79	10.92	10.75	10.77	10.87
1641300_s_at	---	12.52	12.54	12.24	12.43	12.55	12.6
1628425_at	---	7.81	7.82	7.46	8.66	7.84	7.7
1637808_a_at	FBgn0036533	8.92	8.94	8.78	8.65	8.81	8.91
1628938_at	---	8.55	8.56	8.54	8.49	8.29	8.36
1629116_at	---	11.77	11.79	11.76	11.8	11.85	11.87
1625827_s_at	FBgn0051992	11.22	11.24	11.09	11.18	11.18	11.26
1629466_at	FBgn0039069	8.53	8.55	8.69	9.06	8.72	8.54
1631517_at	FBgn0020633	10.85	10.87	11.25	11.45	11.08	10.85
1638476_s_at	FBgn0002777	8.65	8.66	8.15	8.11	8.68	8.73
1634393_s_at	FBgn0030268	10.16	10.18	10.08	10.33	10.34	10.25
1641462_at	FBgn0035323	8.49	8.51	8.68	8.53	8.53	8.41
1639645_at	FBgn0037669	9.78	9.8	9.88	10.16	10.07	9.89
1632274_at	FBgn0030671	9.39	9.4	9.32	9.44	9.35	9.4
1640099_at	FBgn0040066	8.11	8.12	8.42	8.62	8.07	8.27
1637298_at	FBgn0036760	9.75	9.77	9.55	9.79	9.79	9.73
1626353_at	FBgn0030352	9.28	9.3	9.1	9.19	9.09	9.12
1623580_at	FBgn0003884	13	13.02	13.08	13.2	12.96	13.08
1640989_at	FBgn0037779	9.6	9.62	9.6	9.53	9.63	9.54
1640346_at	---	9.94	9.96	9.8	10.2	10.23	10

1633528_s_at	---	10.82	10.84	10.83	10.92	10.86	10.86
1635774_at	FBgn0033233	9.31	9.33	9.27	9.32	9.32	9.25
1632908_s_at	FBgn0051072	8.41	8.43	8.44	7.92	8.33	8.3
1636708_at	FBgn0038195	9.95	9.97	9.8	9.78	10.07	10.04
1631106_s_at	FBgn0027086	10.04	10.05	10.56	10.46	10.23	10.06
1626449_s_at	FBgn0037346	12.54	12.55	12.45	12.5	12.53	12.53
1631594_s_at	FBgn0015279	9.26	9.28	9.4	9.39	9.29	9.2
1628846_at	FBgn0038549 /// FBgn003	8.12	8.14	7.96	8.04	8.04	7.92
1627301_s_at	FBgn0038575	10.42	10.43	10.16	10.6	10.56	10.5
1624464_s_at	FBgn0037925	9.25	9.27	9.34	9.09	8.72	8.9
1632551_at	FBgn0036982	8.31	8.32	7.95	8.2	8.14	8.15
1623692_s_at	FBgn0030318	8.9	8.91	8.86	8.94	8.6	8.56
1631493_at	FBgn0029093	11.66	11.68	11.54	11.45	11.61	11.57
1635247_at	FBgn0038675	9.01	9.02	8.84	9.22	9.26	9.19
1630738_s_at	FBgn0026379	7.54	7.55	7.45	7.59	7.1	7.07
1633878_at	FBgn0034240	7.88	7.89	7.58	7.47	7.83	7.71
1628615_at	FBgn0039116	8.79	8.81	9.04	9.15	8.95	8.92
1631313_at	FBgn0014930	9.34	9.35	9.51	9.39	9.45	9.45
1637515_s_at	FBgn0032956	9.16	9.17	9.14	9.48	9.35	9.35
1630079_at	FBgn0019637	8.74	8.76	8.81	8.9	8.83	8.6
1637214_a_at	FBgn0004243	9.69	9.7	9.69	9.45	9.76	9.67
1631088_at	FBgn0031094	9.51	9.52	9.49	9.58	9.6	9.45
1626049_at	FBgn0032052	9.5	9.51	9.26	9.52	9.52	9.43
1641733_a_at	FBgn0030657	7.47	7.49	7.4	7.88	7.43	7.36
1639224_at	FBgn0032906	10.66	10.68	10.56	11.14	10.95	10.74
1624763_at	FBgn0030396	9.17	9.18	9.18	9.2	9.24	9.22
1634609_at	FBgn0051111	8.8	8.81	8.72	9.21	9.09	8.93
1638411_at	FBgn0036800	9.02	9.04	8.96	9.47	9.2	9.18
1630178_at	FBgn0035402	9.33	9.34	9.34	9.56	9.33	9.1
1637517_s_at	FBgn0020647	8.45	8.46	8.43	8.65	8.49	8.33
1635645_at	FBgn0032881	7.92	7.93	8.07	8.22	8.01	7.88
1628487_s_at	FBgn0035107	10.16	10.17	9.93	10.11	10.19	10.1
1627109_at	FBgn0001220	11.22	11.23	11.47	11.22	11.24	11.34
1638431_at	---	7.96	7.98	7.86	7.93	7.58	7.5
1640497_at	FBgn0032742	10.25	10.26	10.25	10.43	10.54	10.34
1629082_at	---	10.68	10.69	10.72	10.88	10.76	10.69

1633763_at	FBgn0031458	9.48	9.49	9.34	9.48	9.63	9.58
1634924_at	---	9.88	9.89	9.91	9.88	9.9	10
1637053_at	FBgn0022213	11.04	11.05	11.06	11.36	11.19	11.03
1635659_at	FBgn0000377	8.83	8.85	9.16	9.2	8.99	8.8
1634212_at	FBgn0035136	8.4	8.41	8.23	8.39	8.42	8.32
1625197_at	FBgn0037346	10.4	10.42	10.36	10.27	10.05	10.24
1639905_at	FBgn0002021	8.95	8.96	9.06	9.39	8.9	8.87
1635491_s_at	FBgn0040340	10.18	10.2	10.47	9.92	9.81	10.26
1627926_at	FBgn0034058	9.9	9.92	9.66	10.14	9.96	9.89
1636033_at	FBgn0051368	7.49	7.51	7.94	7.8	7.82	7.59
1629696_a_at	FBgn0050497	9.49	9.51	9.74	9.52	9.01	9.31
1641346_at	FBgn0030112	9.11	9.13	8.77	8.83	9.37	9.31
1627528_at	FBgn0033900	7.33	7.35	7.79	7.68	7.34	7.33
1629040_at	FBgn0031881	8.16	8.18	8.4	8.34	8.33	8.25
AFFX-r2-Dro	FBgn0000042	13.18	13.19	13.1	13.28	13.11	13.04
1638520_at	FBgn0036059	9.24	9.25	9.2	9.24	9.4	9.54
1624086_at	FBgn0022097	11.99	12	11.82	12.02	12.02	11.72
1623326_a_at	FBgn0035473	11.31	11.33	11.43	11.38	11.38	11.35
1639816_at	FBgn0016132	9.54	9.55	9.32	9.43	9.54	9.54
1625324_at	FBgn0038053	9.22	9.24	9.11	9.22	9.21	9.2
1631029_at	FBgn0031880	7.35	7.36	7.24	7.49	7.26	7.24
1635421_at	FBgn0031106	9.85	9.87	9.51	9.66	9.62	9.68
1640509_s_at	FBgn0016031	9.61	9.62	9.65	9.28	9.66	9.66
1635079_at	FBgn0033225	8.18	8.19	8.78	8.68	8.56	8.33
1639806_at	---	9.91	9.92	9.9	9.94	9.86	9.97
1627244_at	FBgn0042180	10.44	10.46	10.04	10.22	10.4	10.42
1633297_at	---	8.9	8.91	8.52	9.12	9.03	8.97
1627911_at	FBgn0038673	9.13	9.14	9.35	9.51	9.23	9.24
1631191_at	FBgn0039554	8.7	8.72	8.68	8.91	8.7	8.69
1623339_at	FBgn0040833	8.96	8.97	9.1	9.38	9	8.97
1630671_s_at	FBgn0024246	8.14	8.16	8.12	8.2	8.04	8.05
1631019_at	FBgn0035918	10.05	10.07	9.91	10.3	10.12	10.07
1628297_a_at	FBgn0037746	9.12	9.13	8.88	9.28	9.2	9.11
1626673_s_at	---	10.57	10.58	10.68	10.7	10.68	10.68
1636626_s_at	FBgn0053071	10.96	10.97	11.02	10.77	10.82	10.88
1636482_at	FBgn0031739	9.59	9.61	9.48	9.62	9.58	9.69

1625163_at	FBgn0029117	8.94	8.96	8.99	9.04	9.01	8.99
1627314_s_at	FBgn0051864 /// FBgn003	9.5	9.51	9.22	9.38	9.46	9.38
1635692_s_at	FBgn0003748	9.59	9.6	9.97	9.42	9.27	9.28
1627018_s_at	FBgn0020235	11.38	11.39	11.66	11.58	11.61	11.52
1637618_at	FBgn0024230	8.79	8.8	8.58	8.84	8.84	8.86
1623853_at	FBgn0015000	9.1	9.11	8.94	9.15	9.3	9.25
1629279_at	FBgn0030858	8.53	8.54	8.57	8.86	8.68	8.5
1636126_at	FBgn0026573	8.53	8.54	8.14	8.29	8.41	8.76
1626056_a_at	FBgn0035766	9.47	9.48	9.68	9.73	9.56	9.52
1636948_a_at	---	9.96	9.97	10.3	10.23	10.07	9.92
1623365_at	FBgn0013753	9.41	9.42	9.13	9.6	9.45	9.52
1624078_at	FBgn0039153	7.76	7.77	7.67	8.02	8.04	7.89
1631719_at	---	8.99	9	8.81	9.27	9.1	8.98
1640577_a_at	FBgn0034261	8.46	8.48	8.31	8.51	8.57	8.41
1624831_at	---	8.76	8.77	8.73	9.14	8.96	8.88
1628831_at	FBgn0025615	9.82	9.83	9.8	10.02	9.95	9.87
1634972_at	FBgn0034215	10.26	10.27	10.33	10.38	10.21	10.24
1630227_a_at	FBgn0037703 /// FBgn003	9.81	9.82	9.54	9.76	9.63	9.73
1623291_at	---	9.58	9.59	9.8	9.49	10	9.76
1632309_at	FBgn0036148	9.22	9.23	9.32	9.33	9.39	9.21
1639917_at	---	8.37	8.38	8.15	8.23	8.3	8.44
1627114_at	FBgn0028507	9.58	9.59	9.6	9.81	9.76	9.68
1634065_s_at	FBgn0000579	12.86	12.87	12.72	13.18	12.89	12.81
1625141_at	---	10.13	10.14	10.3	10.21	10.29	10.19
1641427_at	FBgn0024236	9.96	9.97	9.9	9.93	10.1	10.18
1640633_s_at	FBgn0052425	10.27	10.28	10.16	10.43	10.35	10.29
1631131_a_at	FBgn0030170	8.47	8.49	8.1	8.54	8.62	8.35
1639770_at	---	8.68	8.69	8.68	8.71	8.89	8.92
1627111_at	FBgn0029148	11.07	11.08	11.46	11.16	11.02	11.05
1628509_at	FBgn0028541	9.89	9.9	10.08	10.17	10.06	10.02
1628521_at	FBgn0031661	9.13	9.14	8.99	9.05	9.07	9.17
1624649_a_at	FBgn0036697	9.47	9.48	9.34	9.27	9.45	9.64
1628311_at	FBgn0034065	8.39	8.4	8.66	8.39	8.4	8.4
1625470_s_at	FBgn0024273	7.25	7.26	7.12	7.48	7.51	7.48
1622979_a_at	FBgn0035871	10.73	10.74	10.5	10.75	10.61	10.62
1635250_at	FBgn0042107	8.17	8.18	7.92	8.23	8.33	8.26

1639568_at	FBgn0051285	7.18	7.19	7.29	7.46	6.97	6.94
1634023_at	FBgn0039407	8	8.01	8.04	7.98	8.08	8.02
1625110_at	FBgn0034577	10.68	10.69	10.73	10.57	10.58	10.63
1632904_at	FBgn0031868	8.13	8.14	7.78	8	8.43	8.62
1638047_at	FBgn0031499	8.4	8.41	8.09	8.49	8.58	8.6
1640185_at	FBgn0030263	9.2	9.21	9.17	9.51	9.5	9.29
1630792_at	FBgn0040075	10.1	10.11	10.41	10.16	10.12	10.08
1638500_at	FBgn0034537	9.3	9.31	9.19	9.26	9.38	9.43
1627104_at	FBgn0038597	7.87	7.88	8.54	8.1	7.94	7.68
1630453_at	FBgn0052267	10.99	11	10.87	11.01	11.04	11.15
1630208_at	FBgn0041588	8.69	8.7	8.67	8.64	8.74	8.69
1636842_at	FBgn0031996	9.29	9.3	9.32	9.54	9.46	9.33
1628950_at	FBgn0032684	7.29	7.3	7.36	7.43	6.94	7.33
1635824_at	FBgn0026080	8.97	8.98	8.82	8.88	8.92	8.91
1623819_at	FBgn0003346	10.26	10.27	10.33	10.4	10.54	10.45
1625573_at	FBgn0030480	10.26	10.27	10.41	10.37	10.19	10.23
1630023_at	---	9.71	9.72	9.51	9.35	9.6	9.66
1636765_at	FBgn0002781	7.17	7.18	7.12	7.59	7.6	7.48
1625746_at	FBgn0035152	7.83	7.84	7.94	7.9	8	8.15
1625845_s_at	FBgn0000412	11.83	11.84	11.83	11.81	11.79	11.83
1630078_a_at	FBgn0052000	9.92	9.93	9.97	9.85	9.63	9.92
1624529_at	FBgn0005533	13.66	13.67	13.77	13.8	13.81	13.75
1623302_at	FBgn0033891	7.82	7.83	7.85	7.98	8.01	7.9
1628014_at	FBgn0030853	9.68	9.69	10.18	9.85	9.84	9.73
1628264_a_at	FBgn0027375	8.01	8.02	8.18	8.25	8.26	8.06
1625633_a_at	FBgn0000116	10.41	10.42	10.7	10.96	10.39	10.42
1632397_at	FBgn0034498	9.04	9.05	9	8.97	9.04	9
1627280_s_at	FBgn0013726	11.11	11.12	11.15	11.31	11.02	11.07
1641291_at	FBgn0036762	10.04	10.05	10.38	10.5	10.31	10.14
1641329_at	FBgn0030967	8	8.01	7.9	7.87	8	8.01
1639135_at	FBgn0010391	10.23	10.24	10.41	10.15	10.09	10.07
1627977_at	FBgn0033454	8.9	8.91	9.2	9.27	8.98	8.87
1629819_s_at	FBgn0011260	10.81	10.82	11.08	11.01	10.95	10.92
1640610_at	FBgn0034694	7.69	7.7	7.73	8	7.83	7.72
1628422_s_at	---	10	10.01	9.87	9.9	9.88	9.98
1637679_s_at	FBgn0015320	11.11	11.12	11.13	11.35	11.2	11.27

1641193_s_at	FBgn0046214	13.13	13.14	13.18	13.21	13.15	13.13
1633380_at	FBgn0033473	8.97	8.98	9.33	9.38	9.13	9.06
1641373_at	FBgn0038585	10.26	10.27	10.4	10.37	10.12	10.21
1632822_at	---	8.68	8.69	8.66	8.64	8.73	8.69
1638875_at	---	9.65	9.65	9.69	9.69	9.57	9.69
1639355_s_at	---	9.33	9.34	9.88	9.23	9.18	9.59
1638570_a_at	FBgn0036213	13.96	13.97	13.9	13.89	13.92	13.87
1638351_s_at	FBgn0000556	14.4	14.41	14.44	14.52	14.45	14.42
1635603_at	FBgn0038043	10.53	10.54	10.64	10.78	10.66	10.64
1637967_at	---	10.85	10.86	10.86	10.85	11.02	10.98
1635314_at	FBgn0034534	9.42	9.43	9.57	9.6	9.62	9.56
1623632_s_at	FBgn0036115	10.59	10.6	10.73	10.48	9.87	10.38
1622948_at	---	9.18	9.19	9	9.29	9.33	9.26
1631832_at	FBgn0004687	11.58	11.59	11.81	11.56	11.54	11.67
1640090_a_at	FBgn0003423	10.23	10.24	10.39	10.04	10.08	10.26
1633856_at	---	9.74	9.75	10.11	10.02	9.79	9.7
1636496_at	---	10.04	10.05	10.03	9.99	9.9	10
1623670_at	FBgn0037142	7.13	7.14	7.26	7.55	7.22	7.13
1634176_a_at	---	9.23	9.24	9.19	9.29	9.46	9.37
1626657_a_at	FBgn0039003	7.76	7.77	7.74	7.94	7.79	7.54
1623257_a_at	FBgn0039997	9.83	9.83	9.94	9.93	9.98	9.92
1639443_at	FBgn0040600	7.25	7.26	7.8	7.31	7.26	7.24
1635399_s_at	---	8.02	8.03	7.9	8.04	7.97	8.07
1634652_a_at	FBgn0036516	8.44	8.45	8.42	8.47	8.58	8.64
1640558_a_at	FBgn0037556	9.73	9.74	9.35	9.61	9.73	9.82
1626371_at	FBgn0037756	11.44	11.45	11.58	11.58	11.51	11.59
1635756_at	---	9.12	9.13	9.24	9.27	9.27	9.39
1638201_at	FBgn0028967	12.26	12.27	12.16	12.5	12.5	12.39
1628027_a_at	FBgn0003178	11.95	11.96	11.93	12.23	12.14	11.86
1627502_at	FBgn0034674	8.81	8.82	8.93	9.13	9.04	8.98
1629607_at	FBgn0030915	8.84	8.85	8.65	8.75	9.08	9.05
1630798_at	FBgn0050077	7.32	7.33	7.54	7.53	7.32	7.26
1623936_at	---	11.26	11.26	11.24	11.33	11.16	11.18
1639771_at	FBgn0040236	9.12	9.13	9.05	9.06	9.15	9.07
1630743_at	FBgn0022347	10.49	10.5	10.38	10.72	10.55	10.55
1635621_at	---	9.35	9.36	9.4	9.58	9.52	9.46

1623222_s_at	FBgn0004828	12.23	12.24	11.95	11.98	12.31	12.23
1636997_at	FBgn0039189	8.67	8.68	8.63	8.77	8.65	8.62
1641491_at	---	12.89	12.9	13.05	13.17	13	12.88
1626998_at	FBgn0037619	7.58	7.59	7.51	7.6	7.91	7.94
1629452_at	FBgn0038868	8.47	8.48	8.47	8.17	8.37	8.47
1623138_at	FBgn0033676	10.46	10.46	10.25	10.34	10.4	10.56
1635280_at	FBgn0039349	9.43	9.44	9.32	9.65	9.5	9.35
1623857_at	---	9.11	9.12	8.91	9.3	9.43	9.3
1628112_at	---	8.7	8.7	8.61	8.79	8.87	8.77
1635253_a_at	FBgn0029721	10.7	10.71	10.95	10.93	10.85	10.79
1627270_at	FBgn0029865	10.35	10.36	10.1	10.31	10.4	10.37
1632047_at	FBgn0037263	6.7	6.7	6.73	7.21	7.34	7
1631878_at	FBgn0060451	12.01	12.02	12.11	11.99	12.16	12.12
1624815_at	FBgn0010278	9.28	9.29	9.45	9.49	9.54	9.49
1637736_a_at	FBgn0030930	8.81	8.82	8.67	8.76	8.77	8.64
1634172_at	FBgn0004915	10.6	10.61	10.49	10.73	10.66	10.71
1628160_a_at	FBgn0020306	9.04	9.05	8.76	8.96	8.68	8.95
1632440_at	---	12.47	12.47	12.53	12.64	12.53	12.45
1632513_at	FBgn0024542	9.33	9.33	9.34	9.84	9.55	9.47
1629464_a_at	FBgn0052473	10.28	10.29	10.35	10.45	10.25	10.35
1625944_a_at	FBgn0036574	9.64	9.65	9.78	9.77	9.76	9.74
1631248_at	FBgn0030062	8.46	8.46	8.97	8.57	8.41	8.5
1627863_at	FBgn0030752	8.9	8.91	8.67	8.67	8.98	8.92
1623573_s_at	FBgn0031883	10.59	10.6	10.54	10.6	10.5	10.4
1628324_at	FBgn0029893	9.6	9.61	9.6	9.49	9.63	9.71
1630466_at	FBgn0031864	9.26	9.27	9.57	9.4	9.37	9.2
1634020_at	---	9.83	9.83	9.8	9.48	9.5	9.63
1636066_s_at	---	7.01	7.02	7.15	7.07	6.96	6.9
1638439_a_at	FBgn0017545	14.33	14.33	14.35	14.41	14.35	14.31
1630932_at	FBgn0038106	8.63	8.64	8.79	8.92	8.79	8.72
1628920_at	FBgn0031048	11.45	11.45	10.63	11	11.29	11.13
1637737_at	FBgn0030184	11.68	11.68	11.96	11.81	11.85	11.78
1630448_at	FBgn0027514	8.41	8.42	8.26	8.62	8.43	8.29
1634489_at	FBgn0023517	10.84	10.85	10.81	11.03	11.03	10.84
1627308_s_at	FBgn0028697	14.08	14.08	14.16	14.18	14.17	14.14
1629650_at	FBgn0031536	8.06	8.06	7.97	8.04	7.96	7.88

1623606_at	FBgn0002593	14.1	14.1	14.15	14.11	14.13	14.15
1629943_at	FBgn0035879	7.78	7.79	7.94	8.05	7.9	7.81
1631861_at	FBgn0004106	11.44	11.44	11.46	11.78	11.69	11.64
1630623_a_at	FBgn0033382	8.92	8.92	8.09	8.78	8.77	8.8
1639970_at	FBgn0050422	8.42	8.42	8.34	8.58	8.6	8.39
1637068_at	FBgn0037855	8.58	8.59	8.58	8.7	8.56	8.6
1623387_at	---	9.57	9.58	9.46	9.75	9.68	9.57
1629151_at	FBgn0039837	9.74	9.74	9.49	9.93	9.75	9.6
1631073_at	FBgn0030529	9.91	9.92	9.97	9.73	9.82	9.95
1641306_at	FBgn0017428 /// FBgn000	8.22	8.23	8.27	8.12	8.22	8.05
1637379_at	FBgn0037340	8.79	8.79	8.95	8.98	8.83	8.8
1623543_at	FBgn0027539	9.86	9.87	9.85	9.91	9.9	9.93
1634211_at	---	7.83	7.84	7.58	7.51	7.71	7.95
1635481_a_at	FBgn0030946	8.24	8.25	7.91	8.09	8.17	8
1635052_a_at	FBgn0030474	7.88	7.89	7.98	8.01	7.78	7.74
1639801_at	FBgn0039943	10.38	10.39	10.21	10.21	10.36	10.35
1634601_at	FBgn0037583	10.04	10.04	9.95	10.45	10.18	9.96
1641540_a_at	---	9.85	9.85	9.52	9.46	9.73	9.73
1641608_at	FBgn0027568	8.88	8.88	8.92	9.19	8.8	8.68
1638693_s_at	FBgn0033226	8.7	8.7	8.62	8.66	8.88	8.72
1629902_at	FBgn0033795	7.92	7.93	8.1	8.25	8.11	7.9
1638189_s_at	FBgn0003310	9.3	9.31	9.32	9.15	9.18	9.34
1636677_s_at	FBgn0039635	9.12	9.12	9.13	9.34	8.98	8.9
1637503_at	FBgn0026441	7.37	7.38	7.3	7.58	7.44	7.27
1631194_at	FBgn0033990	8.47	8.47	8.45	8.67	8.62	8.57
1635066_at	FBgn0028500	8.27	8.27	8.5	8.5	8.3	8.27
1634013_at	---	10.53	10.53	10.78	10.8	10.63	10.52
1624193_s_at	FBgn0038473	9.99	10	10.31	10.18	10.14	10.08
1623470_at	FBgn0029158	9.29	9.29	9.31	9.4	9.4	9.4
1638998_at	FBgn0039632	8.88	8.88	8.54	8.81	8.86	8.77
1624141_at	FBgn0032194	9.09	9.1	9.5	9.35	9.35	9.36
1628210_at	FBgn0005695	11.06	11.07	10.98	11.05	11.11	11.12
1623020_at	FBgn0031360	9.5	9.51	8.86	9.45	9.5	9.34
1626266_at	FBgn0037481	9.15	9.16	9.19	9.49	9.26	9.24
1629576_at	FBgn0010342	10.42	10.43	10.09	10.51	10.57	10.49
1628131_at	FBgn0004463	8.14	8.14	8.5	8.02	8.15	8.07

1625781_at	FBgn0030996	10.02	10.02	9.89	9.98	10.02	10.01
1635252_a_at	FBgn0000667	10.08	10.08	9.97	9.87	10.22	10.08
1635688_at	FBgn0040850	7.23	7.24	6.8	6.55	6.6	7.21
1634533_at	FBgn0026316	10.05	10.06	9.98	9.9	9.91	9.98
1633032_s_at	FBgn0036043	10.16	10.17	10.13	10.28	9.97	10.17
1629478_at	---	10.63	10.64	10.73	10.98	10.64	10.55
1632794_a_at	FBgn0035437	9.25	9.25	9.09	9.09	9.19	9.2
1641718_at	FBgn0037347	7.77	7.77	7.75	7.79	8.01	8
1624937_at	FBgn0032620	9.77	9.77	9.79	9.82	9.76	9.98
1637411_s_at	FBgn0022361	8.61	8.61	8.58	8.75	8.53	8.43
1624189_at	FBgn0029822	9.1	9.1	8.92	8.98	9.21	9.3
1625034_s_at	FBgn0026620	10.24	10.25	10.23	10.32	10.15	10.22
1625748_s_at	FBgn0026192	9.18	9.18	9.1	8.96	8.9	8.97
1641252_at	FBgn0030506	7.68	7.69	7.78	8.19	7.86	7.62
1628840_at	FBgn0011236	9.51	9.51	9.55	9.28	9.4	9.33
1628636_a_at	FBgn0031078	9.55	9.55	9.71	9.74	9.74	9.48
1633083_at	FBgn0038426	9.18	9.18	9.42	9.38	9.22	9.12
1640528_at	FBgn0039352	8.72	8.72	8.6	8.79	8.56	8.75
1632197_at	FBgn0004925	11.01	11.01	11.35	11.12	11.16	11.04
1626247_at	FBgn0031314	7.74	7.75	7.73	8.12	7.99	7.68
1640491_at	FBgn0034245	12.03	12.03	12.05	12.08	12.03	11.95
1640104_at	FBgn0038277	13.92	13.92	13.88	13.92	13.92	13.87
1634820_at	FBgn0003150	11.15	11.15	11.49	11.4	11.3	11.13
1641355_a_at	FBgn0039857	13.62	13.62	13.74	13.72	13.74	13.66
1628427_a_at	FBgn0030391	9.08	9.08	8.94	9.16	9.12	9.15
1633973_at	---	10.59	10.6	11.03	10.84	10.62	10.72
1626544_at	---	9.77	9.77	9.76	9.76	9.61	9.62
1640230_at	---	8.57	8.57	8.84	8.8	8.64	8.74
1633287_at	FBgn0027619	10.99	10.99	11.15	10.97	11.13	11.18
1627832_at	FBgn0011232	8.9	8.9	8.7	9.08	8.98	8.98
1624006_at	FBgn0038760	7.05	7.05	7.13	7.34	7.29	7.12
1633320_at	FBgn0010747	9.24	9.24	9.27	9.36	9.4	9.23
1632332_at	FBgn0039427	9.34	9.35	9.35	9.35	9.36	9.62
1632776_at	FBgn0027053	10.03	10.03	10.2	10.29	10.27	10.05
1627778_a_at	FBgn0038306	9.35	9.35	9.46	9.22	9.26	9.32
1636176_at	FBgn0004926	11.79	11.79	12.04	11.84	11.89	11.85

1641147_s_at	FBgn0030735	8.92	8.93	8.88	8.95	9.06	8.99
1622895_at	---	8.97	8.98	9.26	9.1	9.09	9.17
1631965_at	FBgn0035854	8.52	8.52	8.64	8.49	8.24	8.34
1629790_at	FBgn0036334	12.18	12.18	12.33	12.29	12.27	12.27
1635508_at	---	8.39	8.4	8.65	8.52	8.38	8.42
AFFX-Dros-A	FBgn0000043	10.89	10.89	11.05	10.81	10.76	10.69
1630677_at	FBgn0034401	10.59	10.59	10.72	10.72	10.72	10.52
1631750_a_at	FBgn0016691	12.22	12.23	12.38	12.3	12.25	12.18
1637510_s_at	FBgn0041630	8	8	8.26	8.29	8.03	7.79
1627256_s_at	FBgn0037222	11.63	11.63	11.96	11.72	11.74	11.7
1638274_s_at	FBgn0035946	10.77	10.77	11.09	11.04	10.93	10.67
1626203_at	---	9.99	9.99	9.84	10.01	9.77	9.88
1623288_at	FBgn0002284	11.82	11.83	11.92	12.1	11.93	11.76
1637365_at	---	9.08	9.08	9.06	9.09	9	9.15
1627924_at	FBgn0003278	8.41	8.41	8.83	8.28	8.54	8.49
1623252_a_at	FBgn0029869	9.14	9.14	9.68	9.55	9.33	9.48
1631268_at	FBgn0015905	8.2	8.2	8.12	8.6	8.38	8.21
1623816_s_at	FBgn0037468	12.38	12.38	12.36	12.48	12.46	12.53
1624572_a_at	FBgn0040020	10.91	10.91	10.81	10.99	10.96	11.11
1623591_a_at	FBgn0040005	10.2	10.2	10.08	10.05	10.22	10.36
1641049_at	FBgn0000409	11.96	11.96	12.54	12.52	12.21	12.27
1632891_s_at	FBgn0004838	12.05	12.05	12.23	12.35	12.15	12.1
1625755_at	FBgn0035401	8	8	8.14	8.35	8.01	7.96
1635944_a_at	---	10.15	10.15	10.14	10.03	10.17	10.24
1624215_s_at	FBgn0024807	9.79	9.79	9.57	9.55	9.29	9.55
1637936_at	---	8.82	8.83	8.77	8.92	8.63	8.79
1640130_at	FBgn0051678	9.46	9.46	9.33	9.37	9.48	9.46
1637314_at	FBgn0003882	9.81	9.82	9.68	9.93	9.92	9.88
1627656_at	FBgn0001137	7.81	7.82	8.08	7.96	7.56	7.81
1624135_at	FBgn0042712	9.12	9.12	9.28	9.36	8.99	8.93
1636320_at	FBgn0031050	8.85	8.85	8.83	9.11	8.86	8.72
1624103_at	FBgn0030081	8.44	8.45	8.29	8.09	8.41	8.39
1627742_at	FBgn0036199	8.61	8.61	8.83	8.66	8.74	8.73
1640260_at	FBgn0000152	6.96	6.96	7.15	7.36	7.06	6.86
1625242_at	---	9.14	9.14	9	9.28	9.14	9.2
1629793_at	FBgn0030055	8.08	8.08	7.88	8.23	8.15	7.99

1632678_at	FBgn0033656	9.29	9.29	9.05	9.2	9.36	9.36
1629549_s_at	---	10.54	10.54	10.34	10.63	10.72	10.77
1632373_s_at	---	9.12	9.12	9.03	9.15	9.09	9.06
1640068_at	FBgn0037439	8.81	8.81	9.43	9.15	8.93	8.79
1637074_at	FBgn0037544	6.94	6.94	7.07	7.23	7.07	6.92
1641708_at	FBgn0039715	8.55	8.55	8.28	8.42	8.39	8.32
1639691_at	FBgn0052038	9.63	9.63	9.48	9.53	9.65	9.58
1639644_at	FBgn0027094	9.53	9.53	9.72	9.77	9.65	9.38
1638109_s_at	FBgn0035032	12.41	12.41	12.6	12.55	12.48	12.45
1633131_s_at	FBgn0042178	9.61	9.61	10.23	9.99	9.83	9.61
1632471_at	FBgn0029957	9.03	9.03	8.96	9.2	9.02	9.02
1640251_s_at	FBgn0000308	11.93	11.93	12.09	12.05	11.99	11.98
1641170_a_at	FBgn0037954	9.7	9.7	9.93	9.95	9.85	9.81
1623794_at	FBgn0039740	8.53	8.53	8.37	8.44	8.5	8.6
1635027_at	FBgn0051800	8.69	8.69	8.98	8.9	8.88	8.84
1635709_at	FBgn0025617	10.72	10.72	10.55	10.57	10.66	10.69
1630955_at	FBgn0031422	7.8	7.8	7.83	7.62	7.94	7.98
1634474_s_at	FBgn0036239	10.03	10.03	10.15	10.15	10.42	10.24
1632198_at	FBgn0035166	7.79	7.79	7.6	7.62	7.98	7.81
1633629_at	FBgn0031736	8.25	8.25	8.47	8.4	8.31	8.13
1636945_at	---	9.98	9.98	9.84	9.96	10.1	10.12
1629517_at	FBgn0031317	7.77	7.77	7.6	7.79	8.15	8.08
1626213_a_at	FBgn0015276	9.11	9.11	9.16	9.01	9.24	9.13
1626368_at	FBgn0002524	10.17	10.17	10.2	10.35	10.23	10.19
1636382_at	---	9.84	9.84	9.93	9.86	9.92	9.89
1634095_at	FBgn0028737	13.39	13.39	13.49	13.48	13.53	13.43
1637260_at	FBgn0039488 /// FBgn000	8.31	8.31	8.34	8.49	8.46	8.41
1628146_at	---	9.39	9.39	9.67	9.35	9.28	9.35
1625990_at	FBgn0037185	9.44	9.44	9.38	9.61	9.69	9.54
1636130_at	---	9.94	9.94	10.05	10.14	9.93	9.89
1638245_at	FBgn0031834	7.21	7.21	7.32	7.28	7.64	7.56
1625218_at	FBgn0037021	9.58	9.58	9.08	9.2	9.02	9.26
1627473_at	FBgn0033995	9.37	9.36	9.04	9.17	9.32	9.37
1629270_at	FBgn0003512	9.2	9.2	9.05	9.54	9.49	9.24
1635627_at	FBgn0027055	9.34	9.34	9.32	9.31	9.45	9.35
1633598_at	FBgn0052221	8.3	8.3	8	7.96	8.16	7.99

1633074_a_at	FBgn0011661	12.09	12.09	12.22	12.09	12.06	12.1
1640451_at	---	10.99	10.99	11.29	11.32	11.32	11.25
1627325_at	---	9.66	9.66	9.45	9.66	9.74	9.66
1627426_at	FBgn0033094	11.03	11.03	11.05	11.08	11.16	11.16
1630841_at	FBgn0031988	9.19	9.19	9.18	9.3	9.2	9.25
1633805_a_at	FBgn0003317	10.14	10.14	10.11	10.28	10.3	10.31
1623039_at	FBgn0033095	8.93	8.92	8.98	9.1	8.77	8.78
1640892_a_at	FBgn0000480	10.41	10.4	10.23	10.26	10.3	10.39
1636572_at	FBgn0031464	9.17	9.16	9.02	9.25	9.07	9.05
1627087_at	FBgn0023514	9.72	9.72	9.7	10	9.92	9.8
1631769_at	FBgn0003169	10.35	10.35	10.01	10.23	10.14	10.37
1626786_at	FBgn0033916	8.25	8.25	8.45	8.38	8.43	8.45
1638735_at	FBgn0033413	10.04	10.04	9.9	10.3	10.26	10.28
1641487_a_at	FBgn0020653	11.09	11.08	10.94	11.22	11.31	10.99
1637980_at	FBgn0000150	13.61	13.61	13.55	13.62	13.69	13.58
1636205_at	FBgn0038433	8.7	8.7	8.83	8.69	8.81	8.68
1629981_at	FBgn0010397	8.43	8.42	8.63	8.05	8.16	8.38
1640652_at	---	8.13	8.13	8.08	8.36	8.12	8.06
1637032_at	FBgn0039625	8.82	8.82	8.82	8.77	8.81	8.83
1636303_at	---	14.21	14.21	14.1	14.19	14.2	14.08
1635711_s_at	FBgn0011747	9.91	9.91	9.88	9.79	9.84	9.91
1640603_at	FBgn0052590	7.7	7.7	7.83	8.28	8.16	7.99
1629342_s_at	FBgn0039830	12.72	12.72	12.7	12.65	12.71	12.69
1638721_s_at	FBgn0029971	10.93	10.93	11.12	11.11	11.13	11.05
1623322_at	FBgn0033605	8.22	8.22	8.44	8.45	8.35	8.23
1625974_at	FBgn0024222	8.59	8.59	8.52	8.78	8.62	8.49
1623859_at	---	10.05	10.05	10.35	10.3	10.27	10.2
1629359_at	FBgn0032321	8.7	8.7	8.81	8.92	8.9	8.83
1628924_a_at	FBgn0034963	8.63	8.62	8.63	8.69	8.72	8.68
1623185_s_at	FBgn0011225	9.16	9.16	8.86	8.82	8.86	8.89
1633069_s_at	FBgn0037442	8.1	8.1	7.97	8.25	8.06	8.48
1631603_at	---	9.77	9.77	9.76	9.76	9.66	9.63
1626106_a_at	FBgn0027532	9.57	9.57	9.54	9.59	9.64	9.54
1634637_a_at	---	11.7	11.7	11.55	11.91	11.93	11.72
1636530_s_at	FBgn0003887	12.87	12.87	12.94	13.14	13.05	12.9
1636634_a_at	FBgn0032456	10.46	10.46	10.36	10.39	10.38	10.55

1638658_at	---	9.48	9.47	9.44	9.51	9.49	9.48
1631379_a_at	FBgn0033663	11.93	11.93	11.97	12.04	11.92	11.95
1634724_at	FBgn0038968	8.98	8.98	9.08	8.92	9.04	8.83
1630395_at	---	9.25	9.25	9.38	9.56	9.21	9.14
1628531_at	FBgn0028694	11.31	11.31	11.4	11.44	11.37	11.26
1628257_s_at	FBgn0035438	11.32	11.32	11.19	11.17	11.28	11.12
1623106_s_at	FBgn0020496	9.97	9.96	10.2	10.08	9.94	9.95
1639453_at	---	7.78	7.78	7.63	7.76	7.95	7.82
1632225_a_at	FBgn0029158	8.47	8.47	8.3	8.34	8.67	8.6
1627946_at	FBgn0039695	7.14	7.13	7.68	6.67	6.31	7.15
1641614_at	FBgn0033159 /// FBgn001	13.71	13.71	13.84	13.87	13.81	13.75
1624396_at	---	9.24	9.24	9.3	9.34	9.27	9.26
1638043_a_at	FBgn0028497	8.47	8.47	8.66	8.84	8.71	8.6
1629188_at	FBgn0036515	10.9	10.9	11.06	11.06	10.97	10.97
1627380_at	FBgn0010173	11.08	11.07	11.28	11.58	11.36	11.07
1627732_s_at	FBgn0050415	12.12	12.12	12.25	12.03	12.1	12.14
1629406_at	FBgn0041186	10.67	10.67	10.61	10.9	10.86	10.75
1638876_at	FBgn0028692	11.06	11.05	11.23	11.37	11.32	11.07
1637221_at	FBgn0032486	8.21	8.21	8.4	8.62	8.52	8.47
1633099_at	FBgn0031283 /// FBgn003	8.66	8.66	8.42	8.73	8.71	8.79
1636864_at	---	10.87	10.87	10.63	10.76	10.75	10.98
1639985_s_at	FBgn0000319	11.13	11.13	11.52	11.26	10.96	11.06
1637767_at	FBgn0032949	12.44	12.43	12.36	12.32	12.49	12.53
1625343_at	FBgn0036548	9.07	9.07	9.4	9.47	9.29	9.14
1637876_a_at	FBgn0036999	7.98	7.98	7.85	7.93	7.98	7.92
1626729_at	FBgn0034938	8.33	8.32	8.23	8.11	8.18	8.33
1633606_s_at	FBgn0053199 /// FBgn003	9.99	9.98	9.91	9.98	10.24	10.19
1625745_at	---	7.81	7.81	7.99	8.24	7.93	7.63
1638044_a_at	FBgn0039136	9.55	9.54	9.49	9.69	9.63	9.68
1627693_at	FBgn0037466	8.67	8.66	8.56	8.59	8.58	8.6
1626382_s_at	FBgn0035165	10.81	10.8	10.6	10.64	10.79	10.74
1639159_at	FBgn0036301	9.87	9.87	10.05	9.74	9.79	9.82
1633042_at	FBgn0038272	8.69	8.68	8.76	8.72	8.69	8.72
1630050_at	FBgn0033752	8.16	8.16	7.91	8.19	8.16	8.2
1630431_s_at	FBgn0033021	10.97	10.97	10.97	11.3	11.19	11.12
1635513_at	FBgn0037653	9.75	9.75	9.69	9.8	9.74	9.66

1628208_at	FBgn0036726	10.63	10.63	10.56	10.55	10.66	10.66
1626550_at	FBgn0052705	9.2	9.2	9.14	9.38	9.39	9.52
1630370_at	FBgn0038149	11.67	11.67	11.64	11.7	11.75	11.67
1630573_at	FBgn0036511	7.15	7.15	7.25	7.29	7.06	7.04
1630030_at	FBgn0033635	9.83	9.82	9.51	9.84	9.93	9.72
1631153_at	FBgn0003015	12.36	12.35	12.23	12.2	12.12	12.35
1629396_a_at	FBgn0031993	7.02	7.01	7	7.33	6.9	6.87
1639416_at	FBgn0033191	10.01	10	10.17	10.29	10.05	9.95
1637007_s_at	FBgn0030838	9.55	9.55	9.36	9.47	9.51	9.44
1623989_at	FBgn0032191	10.88	10.88	10.84	11.14	10.92	10.98
1624669_at	FBgn0038861	7.92	7.92	8.41	8.27	8.13	8
1632189_at	FBgn0023521	8.91	8.9	8.84	9.11	8.92	8.72
1625950_a_at	FBgn0033635	12.2	12.19	12.36	12.1	12.28	12.26
1624490_s_at	FBgn0001180	9.82	9.82	9.5	9.69	9.93	10.06
1625840_at	FBgn0037265	7.19	7.19	7.22	7.36	7.04	7.16
1623625_at	FBgn0039402	9.54	9.53	9.52	9.42	9.55	9.55
1627840_a_at	FBgn0005634	9.62	9.62	10.26	9.82	9.33	9.49
1635506_at	---	8.75	8.75	8.93	8.57	8.6	8.82
1633754_at	FBgn0036266	8.02	8.02	8.02	8.4	8.33	8.29
1633876_at	FBgn0032521	8.7	8.69	8.52	8.93	8.92	8.75
1632757_a_at	FBgn0037615 /// FBgn003	8.36	8.36	8.6	8.47	8.37	8.69
1626588_a_at	FBgn0032407	9.2	9.2	9.13	9.11	8.96	8.93
1639459_a_at	FBgn0013997	9.12	9.11	9.15	9.13	8.73	8.97
1631007_at	FBgn0011703	11.03	11.02	11.29	11.46	11.31	11.02
1636108_at	FBgn0036546	11.11	11.11	10.83	11.33	11.23	11.15
1637893_at	FBgn0021814	9.29	9.28	9.28	9.48	9.16	9.11
1627337_at	FBgn0031241	9.84	9.83	10.02	10.05	9.63	9.73
1631214_at	FBgn0033457	9.52	9.51	9.4	9.58	9.68	9.47
1623076_at	FBgn0052803	9.46	9.45	9.06	9.19	9.45	9.35
1634003_at	FBgn0052685	8.08	8.07	8.39	8.3	8.17	8.21
1635714_s_at	---	9.36	9.36	9.4	9.45	9.28	9.14
1625634_at	FBgn0010220	8.36	8.35	8.66	8.94	8.7	8.65
1626367_at	FBgn0032640	10.21	10.21	10.5	10.37	10.22	10.24
1630271_at	FBgn0011771	8.81	8.81	8.81	8.81	8.84	8.72
1631718_at	---	10.72	10.71	10.84	10.65	10.92	10.92
1637947_s_at	FBgn0050389	8.05	8.05	8.02	8.14	8.14	8.02

1627834_a_at	FBgn0000114	12.79	12.78	12.84	12.76	12.79	12.84
1634641_a_at	FBgn0033190	11.29	11.28	11.27	11.3	11.31	11.24
1635818_at	FBgn0032342	8.87	8.86	8.75	8.68	8.95	8.75
1625425_a_at	FBgn0034138	13.82	13.82	13.87	13.92	13.92	13.88
1623551_at	FBgn0036537	10.37	10.36	10.56	10.6	10.6	10.7
1635063_at	FBgn0016978	9.79	9.79	9.93	10.25	9.92	9.9
1640054_at	---	9.1	9.1	8.86	9.02	9.31	9.26
1625768_s_at	FBgn0005630	11.63	11.62	11.63	11.88	11.67	11.71
1629440_at	FBgn0031639	9.1	9.09	9.32	9.37	9.17	9.1
1625442_a_at	FBgn0003392	7.63	7.62	7.6	7.66	7.68	7.4
1635972_at	FBgn0035532	9.93	9.92	9.93	10.14	9.99	10.01
1628723_at	FBgn0011824	11.13	11.12	11.82	11.31	11.19	11.22
1636856_at	FBgn0041174	8.56	8.55	8.18	8.18	8.47	8.64
1627123_at	FBgn0031682	9.46	9.46	9.14	9.28	9.49	9.48
1641603_s_at	---	8.02	8.01	8.04	8.15	8.11	8.1
1626986_at	FBgn0038389	8.9	8.89	9.13	9.29	9.24	9.19
1627774_a_at	FBgn0010413	14.29	14.28	14.38	14.38	14.36	14.32
1640905_at	FBgn0034918	10.67	10.66	10.67	10.79	10.74	10.74
1635954_at	FBgn0029688	7.69	7.68	7.95	7.64	7.61	7.63
1624142_a_at	---	9	8.99	9.09	9.04	8.96	9
1638833_at	FBgn0030327	9.65	9.64	9.44	9.7	9.48	9.5
1639060_at	---	10.36	10.35	10.32	10.66	10.56	10.51
1634331_at	FBgn0021847	9.06	9.05	9.02	9.5	9.27	9.02
1636921_at	FBgn0010622	7.91	7.9	8.08	8.79	8.1	7.99
1636431_at	FBgn0033769	8.76	8.75	8.54	8.64	8.69	8.67
1626331_at	FBgn0033570	9.94	9.93	10.23	10.14	10	9.94
1623237_at	FBgn0031696	9.01	9	8.94	9.2	9.08	9.11
1638312_at	FBgn0033665	7.77	7.76	7.55	7.59	7.41	7.59
1637417_at	FBgn0032513	9.43	9.43	9.76	9.94	9.53	9.54
1624499_s_at	FBgn0030734	10.43	10.42	10.43	10.56	10.53	10.52
1636198_at	---	9.33	9.32	9.2	9.02	9.12	9.18
1641285_at	FBgn0015338	10.66	10.65	10.62	10.79	10.52	10.59
1632915_s_at	FBgn0053070	9.43	9.42	9.62	9.6	9.22	9.44
1632847_at	FBgn0036406	8.24	8.23	8.17	8.08	8.01	8.18
1638883_at	FBgn0029629	11.84	11.83	12.02	11.89	11.99	11.89
1634053_at	FBgn0030850	10.63	10.62	10.37	10.42	10.63	10.6

1633412_s_at	FBgn0029764	11.16	11.15	11.19	11.22	11.14	11.25
1626652_at	FBgn0022772	10.72	10.71	10.56	10.91	10.75	10.6
1640698_at	FBgn0031478	9.34	9.33	9.06	9.11	9.32	9.27
1638158_at	FBgn0038764	9.43	9.42	9.46	9.57	9.56	9.37
1630925_at	FBgn0028687	11.26	11.25	11.29	11.38	11.33	11.16
1638156_at	FBgn0001084	7.93	7.92	7.56	7.92	8.05	8.02
1626488_s_at	FBgn0028691	10.95	10.94	11	11.08	11.06	10.86
1638522_at	FBgn0030039	9.19	9.18	9.12	9.33	9.15	9.17
1624355_at	FBgn0015907	8.89	8.88	9.26	9.06	9.06	8.93
1628092_at	FBgn0031309	9.15	9.14	8.9	9.13	9.25	9.14
1632322_at	FBgn0038809	10.29	10.28	10.3	10.44	10.23	10.23
1632161_at	FBgn0026198	9.01	9	8.91	8.99	9.09	9.03
1626641_s_at	FBgn0027657	9.79	9.78	9.98	9.82	10.11	9.94
1640764_at	FBgn0003277	11.19	11.18	11.13	11.35	11.2	11.18
1640782_at	FBgn0033737	9.83	9.82	9.92	9.97	9.87	9.76
1628243_at	FBgn0028472	9.17	9.16	8.97	9.03	9.04	9.13
1633494_at	---	7.02	7.01	6.54	6.64	7	6.95
1631652_at	FBgn0038545	9.21	9.2	8.98	9.08	9.29	9.26
1632593_at	---	8.92	8.91	8.71	9.01	8.96	9
1638414_a_at	FBgn0036199	9.08	9.07	9.73	9.18	9.33	9.27
1638752_s_at	FBgn0051961	7.86	7.85	7.88	7.74	8.11	7.88
1636791_s_at	FBgn0036053	9.84	9.83	10.12	10.25	9.97	9.76
1635766_at	FBgn0000986	11.46	11.45	11.45	11.7	11.49	11.34
1627518_at	FBgn0039112	9.95	9.94	9.98	10.02	10.17	9.99
1630788_at	FBgn0015282	10.76	10.75	10.76	10.91	10.88	10.71
AFFX-r2-Dro	FBgn0000042	10.47	10.46	10.21	10.32	10.29	10.24
1639375_a_at	FBgn0037360	10.92	10.91	10.8	10.81	10.93	10.82
1641129_at	FBgn0004868	12.12	12.11	12.08	12.38	12.2	12.13
1637059_s_at	FBgn0015657	10.83	10.82	11.03	11.07	11.32	11.17
1628290_s_at	FBgn0032029	9.8	9.78	9.6	9.34	9.79	9.73
1629867_a_at	---	13.65	13.64	13.72	13.77	13.79	13.73
1636942_at	FBgn0031992	10.13	10.12	10.03	10.16	9.85	9.98
1638176_at	FBgn0034590	9.34	9.33	9.27	8.91	9.09	9.12
1641353_s_at	FBgn0052066 /// FBgn006	9.49	9.47	9.51	9.3	9.24	9.4
1634116_at	FBgn0037116	9.1	9.09	8.89	8.83	9.02	9
1640557_at	FBgn0020443	11.33	11.31	11.4	11.4	11.39	11.38

1626508_at	---	10.03	10.02	10.06	10.13	10.24	10.22
1623998_at	FBgn0037051	10.17	10.16	10.29	10.16	10.17	10.06
1628124_at	FBgn0029928	6.77	6.76	6.78	7.09	7.08	6.8
1630982_at	FBgn0034814	8.61	8.59	8.82	8.6	8.66	8.64
1634481_at	FBgn0030986	8.25	8.24	8.47	8.55	8.04	8.07
1637240_a_at	FBgn0034366	8.14	8.12	8.24	8.4	8.25	8.17
1640239_at	FBgn0050149	9.56	9.54	9.7	10.03	9.83	9.55
1638427_at	---	8.94	8.93	8.79	9	9.01	8.98
1640263_at	FBgn0031776	10.09	10.08	10.15	10.25	10.18	10.06
1641047_at	FBgn0032479	9.64	9.63	9.88	9.97	9.69	9.66
1633284_at	FBgn0034915	10	9.99	10.38	10.12	9.86	9.93
1626649_s_at	FBgn0051232	9.88	9.87	9.9	9.96	10.02	9.94
1641621_at	FBgn0029943	8.81	8.8	8.63	8.72	8.81	8.68
1634329_at	FBgn0052579	9.58	9.57	9.3	9.25	9.6	9.63
1627873_at	FBgn0038046	9.47	9.46	9.51	9.74	9.59	9.56
1624321_at	FBgn0014011	9.15	9.14	8.15	8.03	8.97	8.98
1626125_at	---	8.55	8.54	8.38	8.83	8.9	8.61
1641223_at	FBgn0036615	8.6	8.59	8.61	8.9	8.73	8.79
1636085_at	FBgn0037219	9.73	9.72	9.45	9.41	9.58	9.59
1626706_at	FBgn0040208	9.72	9.71	9.57	9.53	9.51	9.51
1640619_at	FBgn0027587	9.44	9.43	9.54	9.66	9.54	9.47
1634412_at	FBgn0039874	7.35	7.33	7.1	7.07	7.19	7.2
1632978_at	---	10.05	10.04	9.41	9.58	9.86	9.62
1632429_at	FBgn0015795	11.11	11.1	11.26	10.97	11.16	11.11
1631642_at	FBgn0038765	7.67	7.66	7.66	8.13	7.97	7.98
1634955_at	FBgn0011361	10.64	10.62	10.9	10.72	10.73	10.68
1633387_at	FBgn0031150	8.03	8.02	7.66	7.77	7.82	7.8
1628691_at	---	11.82	11.81	11.65	11.35	11.43	11.6
1626931_a_at	FBgn0039713	13.93	13.91	14.04	13.97	14.04	13.98
1631118_s_at	FBgn0013987	10.21	10.2	10.23	10.16	10.34	10.39
1624278_at	FBgn0036135	9.16	9.15	9.36	9.17	9.05	8.98
1638283_at	FBgn0038146	8.56	8.55	8.7	8.32	8.49	8.4
1636812_at	FBgn0035715	8.97	8.95	8.83	8.82	9.11	9.12
1624335_at	FBgn0031851	8.77	8.76	9.14	9.07	8.74	8.83
1630643_at	FBgn0032715 /// FBgn001	9.02	9	9.22	9.33	9.16	8.96
1634621_at	FBgn0039128	8.46	8.44	8.2	8.92	8.44	8.45

1631729_at	FBgn0035867	7.87	7.86	7.79	7.91	7.96	7.91
1639063_at	FBgn0032390	9.25	9.24	9.2	9.65	9.37	9.29
1631749_at	FBgn0030711	10.15	10.13	10.3	10.33	10.29	10.33
1623754_s_at	FBgn0024733	14.25	14.23	14.17	14.24	14.27	14.25
1627677_s_at	FBgn0036376	9.89	9.87	9.99	10.16	10.04	9.96
1625725_at	---	9	8.98	9.17	9.18	9.11	9.1
1634072_s_at	---	10.39	10.38	10.4	10.42	10.45	10.2
1628338_at	FBgn0029825	10.92	10.9	10.59	10.81	10.64	10.73
1627768_at	---	10.45	10.43	10.62	10.46	10.55	10.47
1630559_at	FBgn0034503	9.33	9.31	9.21	9.34	9.37	9.27
1635927_at	FBgn0037663	7.38	7.37	7.2	7.59	7.46	7.27
1626798_a_at	FBgn0000228	10.45	10.44	10.32	10.32	10.44	10.56
1625995_a_at	FBgn0004057	7.47	7.46	7.5	7.26	7.37	7.36
1630405_at	FBgn0004597	8.77	8.76	8.7	8.83	8.96	8.82
1633243_at	---	9.59	9.57	9.19	9.36	9.57	9.67
1632166_at	FBgn0024314	9.53	9.52	9.59	9.78	9.57	9.38
1622999_at	FBgn0011710	10.8	10.78	10.75	10.64	10.69	10.74
1630950_at	---	12.11	12.09	12.49	12.13	12.11	12.24
1641084_at	FBgn0035160	9.04	9.02	9.05	9.06	8.84	8.88
1636705_at	FBgn0026207	8.66	8.64	8.49	9.07	8.79	8.55
1639536_at	FBgn0029693	8.23	8.21	8.17	8.26	8.14	8.03
1630438_at	FBgn0052409	9.42	9.4	9.7	9.27	9.3	9.48
1628866_at	FBgn0032678	9.01	8.99	8.97	8.99	9.16	9.11
1633353_s_at	FBgn0033502 /// FBgn003	8.02	8	8.56	8.17	7.62	7.92
1627331_at	FBgn0010356	7.99	7.98	8.14	8.59	8.32	8.05
1639850_at	FBgn0040346	9.69	9.67	9.7	9.71	9.78	9.66
1629295_at	FBgn0029504	9.51	9.49	9.59	9.51	9.21	9.51
1628751_at	FBgn0033235	9.69	9.68	9.87	9.99	9.8	9.57
1632830_s_at	FBgn0001122	9.31	9.3	9.35	9.14	9.27	9.17
1630817_s_at	FBgn0032999	9.67	9.66	9.62	9.92	9.81	9.68
1635098_a_at	FBgn0030792	9.77	9.76	9.72	9.94	9.8	9.66
1641025_at	FBgn0030518	9.52	9.5	9.67	9.69	9.54	9.43
1628986_at	FBgn0033039	9.89	9.87	9.84	9.95	9.89	9.91
1623473_at	---	9.64	9.62	9.49	9.59	9.7	9.65
1639013_at	FBgn0036579	8.93	8.91	8.72	8.65	8.78	8.75
1637578_at	---	11.09	11.08	11.34	11.37	11.26	11.34

1633535_at	FBgn0028665	11.12	11.11	11.12	10.97	11.32	11.1
1635099_at	FBgn0038467	8.59	8.58	8.64	9.11	9.02	8.83
1630073_at	FBgn0037305	10.16	10.14	10.33	10.56	10.15	10
1636950_at	FBgn0039930	8.67	8.66	9.17	8.93	9.03	8.71
1633403_at	---	9.36	9.34	9.07	8.98	9.18	9.28
1638931_at	FBgn0033975	8.19	8.18	8.24	8.04	7.99	7.94
1628099_at	FBgn0040237	9.84	9.83	9.99	9.92	9.89	9.81
1640730_at	---	9.62	9.61	9.75	9.9	9.8	9.74
1624473_at	FBgn0011425	8.89	8.87	8.91	9.35	8.87	8.72
1637056_s_at	FBgn0034500	8.25	8.24	8.27	7.97	7.93	8.24
1631626_at	FBgn0000146	9.01	9	9.75	9.44	9.57	9.61
1637051_at	FBgn0036518	7.22	7.21	7.35	7.38	6.98	6.93
1627668_s_at	FBgn0052527	10.13	10.12	9.79	9.89	10.02	10.08
1622945_a_at	---	10.59	10.57	10.74	10.85	10.87	10.52
1640954_at	FBgn0036127	8.48	8.47	8.39	8.64	8.34	8.4
1641015_at	FBgn0025458	8.84	8.82	8.61	8.87	8.92	8.77
1634582_at	---	8.67	8.65	9.18	8.92	8.98	9.02
1635356_at	FBgn0033754	8.53	8.51	9.22	9.14	8.69	8.8
1634579_at	FBgn0043456	10.73	10.71	11.05	10.76	10.71	10.59
1639646_at	FBgn0050373	8.28	8.26	8.42	8.35	8.23	8.22
1638100_s_at	FBgn0035133	9.22	9.2	9.06	9.13	9	9.05
1629744_a_at	FBgn0010338	8.85	8.83	8.61	8.94	8.92	8.93
1638329_at	FBgn0000826	9.45	9.43	9.33	9.56	9.54	9.22
1634340_at	FBgn0027503	8.39	8.38	8.23	8.28	8.45	8.38
1624714_at	FBgn0010328	10.95	10.93	11.1	10.93	11.07	11.11
1636280_s_at	FBgn0038111	9.39	9.37	9.26	9.58	9.47	9.36
1628081_s_at	FBgn0038256	10.91	10.89	10.7	10.65	11	10.96
1627893_at	FBgn0036039	9.78	9.76	9.42	9.54	9.68	9.81
1639326_s_at	FBgn0040207	9.11	9.09	9.43	9.5	9.33	9.15
1629445_at	FBgn0010431	12.5	12.49	12.36	12.98	12.81	12.68
1627850_at	FBgn0035987	10.38	10.36	10.28	10.2	10.19	10.64
1635322_a_at	FBgn0033784	8.57	8.55	8.37	8.48	8.55	8.51
1627660_a_at	FBgn0039111	8.53	8.51	8.82	8.94	8.81	8.67
1630989_a_at	---	8.41	8.39	8	8.32	8.29	8.34
1624617_at	FBgn0033451	8.92	8.9	8.86	8.95	8.76	8.66
1624627_s_at	FBgn0039168	10.68	10.66	10.59	10.78	10.67	10.57

1623887_at	FBgn0033686	7.92	7.9	7.49	8.51	7.97	7.83
1629413_at	FBgn0031069	9.77	9.75	9.67	9.59	9.65	9.6
1627872_at	FBgn0035085	8.88	8.86	8.91	9.06	8.48	8.59
1630893_at	FBgn0033989	9.33	9.32	9.15	9.25	9.16	9.08
1623742_at	FBgn0039013	8.71	8.69	8.75	9.19	9.14	8.89
1636539_at	FBgn0028833	10.73	10.72	10.84	10.81	10.96	10.87
1623940_at	FBgn0037242	9.79	9.77	9.66	9.77	9.84	9.82
1627421_at	FBgn0030269	10.17	10.15	9.98	10.14	10.29	10.23
1632297_at	FBgn0035373	8.36	8.34	8.38	8.18	8.35	8.31
1624890_s_at	FBgn0031768	8.9	8.88	8.91	8.99	8.92	8.91
1636153_at	FBgn0034191	8.15	8.13	8.2	8.42	8.22	8.1
1635011_at	FBgn0036928	11.32	11.31	11.54	11.44	11.47	11.4
1636528_at	FBgn0039562	10.48	10.46	10.57	10.49	10.38	10.37
1635375_at	FBgn0038842	7.21	7.19	8.05	6.52	6.65	6.93
1637776_at	FBgn0032293	8.64	8.62	8.59	8.71	8.63	8.56
1635978_at	FBgn0053199 /// FBgn003	10.83	10.81	10.87	10.95	11	10.97
1628152_at	FBgn0024814	11.27	11.25	11.4	11.41	11.38	11.33
1632630_at	FBgn0030088	8.45	8.43	8.25	8.38	8.5	8.64
1635821_at	---	8.49	8.47	8.5	8.66	8.57	8.46
1629577_at	FBgn0035295	7.73	7.71	7.95	8.04	8.06	7.96
1630347_at	FBgn0036754	8.37	8.35	8.76	8.74	8.44	8.66
1636206_at	FBgn0035423	12.28	12.26	12.46	12.37	12.37	12.45
1633940_at	FBgn0037710	9.81	9.79	9.65	9.75	9.73	9.74
1634862_at	FBgn0032746	10.29	10.27	10.14	9.98	10.18	10.18
1627434_at	FBgn0035937	7.79	7.77	7.83	7.89	7.88	7.73
1638387_at	FBgn0041702	9.88	9.86	9.82	10.02	10.03	9.96
1638468_at	FBgn0050051	8.11	8.09	8.03	8.49	8.37	8.09
1631550_at	---	8.97	8.96	8.98	9.12	9.05	8.95
1631942_at	FBgn0036451	9.21	9.19	9.39	9.06	9.09	9.09
1635530_at	---	11.06	11.04	11.2	11.17	11.28	11.15
1632532_s_at	FBgn0010516	10.78	10.76	10.87	10.53	11.02	10.84
1626507_at	FBgn0030990	9.86	9.85	9.66	9.75	9.73	9.66
1624080_s_at	FBgn0024921	10.13	10.11	10.17	10.54	10.19	10.26
1628599_at	FBgn0031599	9.23	9.21	9.24	9.96	9.41	9.11
1640849_at	---	10.65	10.63	10.85	10.76	10.68	10.66
1637506_at	FBgn0052758	8.41	8.39	8.31	7.97	7.71	8.02

1629026_at	FBgn0002069	11.19	11.17	11.53	11.46	11.42	11.26
1631776_at	FBgn0037647	9.66	9.64	9.53	9.62	9.61	9.55
1633661_at	FBgn0031217	10.28	10.26	10.16	10.2	10.26	10.33
1632848_at	FBgn0030573	8.29	8.27	8.01	8.34	8.56	8.54
1640056_at	---	10.68	10.66	10.67	10.81	10.78	10.68
1639377_at	FBgn0010410	14.26	14.24	14.27	14.31	14.33	14.22
1631173_at	FBgn0030607	9.38	9.36	9.34	9.46	9.31	9.2
1641403_at	FBgn0035420	9.66	9.64	9.6	9.44	9.48	9.55
1641564_a_at	FBgn0004903	8.98	8.96	8.75	8.8	8.98	8.82
1627419_at	---	10.87	10.85	10.86	11.14	11.15	11.17
1640446_s_at	FBgn0002611	13.5	13.48	13.57	13.57	13.62	13.51
1626443_at	FBgn0026879	10.85	10.83	11.11	10.88	10.89	10.83
1624353_at	FBgn0052654	10.16	10.14	9.82	9.67	9.93	10.06
1625665_at	FBgn0036462	9.93	9.91	9.79	10.17	9.98	9.92
1638549_at	---	9.54	9.52	9.47	9.75	9.57	9.4
1630944_s_at	FBgn0030890	10.57	10.55	10.76	10.68	10.59	10.59
1637487_at	---	8.78	8.76	8.61	8.69	8.76	8.86
1627616_at	FBgn0040235	8.97	8.95	9.18	9.41	9.31	9.11
1637560_at	---	11.36	11.34	11.36	11.22	11.18	11.34
1640938_at	FBgn0035640	10.45	10.43	10.25	10.44	10.55	10.36
1627106_a_at	FBgn0032783	11.39	11.37	11.06	11.23	11.35	11.31
1631856_a_at	FBgn0021906	10.74	10.72	10.88	10.85	10.75	10.73
1632589_at	FBgn0031947	8.51	8.49	8.65	8.81	8.74	8.63
1636852_at	FBgn0030720	8.49	8.46	9.06	8.77	8.68	8.58
1623546_at	FBgn0022724	8.64	8.62	8.51	8.68	8.81	8.78
1636762_a_at	FBgn0025682	9.25	9.22	9.48	9.08	8.97	9.26
1640098_at	---	9.62	9.6	9.44	9.47	9.58	9.56
1626522_at	FBgn0015610	10.89	10.87	10.86	11.1	11.21	10.88
1634722_s_at	FBgn0026208	11.51	11.49	11.54	11.62	11.7	11.69
1629363_at	FBgn0038363	9.41	9.38	9.66	9.87	9.82	9.62
1633269_at	FBgn0031771	10.36	10.34	10.51	10.58	10.6	10.32
1638637_at	---	7.46	7.43	7.48	7.54	7.64	7.64
1640656_a_at	FBgn0004401	10.87	10.85	11.15	11.38	10.9	10.96
1634558_s_at	FBgn0001404	9.26	9.24	9.36	9.39	9.2	9.23
1640691_at	FBgn0034585	9.6	9.58	9.37	9.51	9.62	9.55
1623218_s_at	FBgn0037471	9.61	9.59	9.21	9.36	9.38	9.46

1639384_s_at	FBgn0034491	9.62	9.6	9.26	9.41	9.73	9.65
1629218_at	FBgn0026015	8.09	8.07	8.08	8.07	8.15	8.16
1630268_at	---	9.14	9.12	9.18	8.97	9.14	9.09
1633746_s_at	FBgn0000008	8.56	8.53	8.11	8.02	8.12	8.32
1639087_at	---	12.68	12.66	12.75	12.76	12.83	12.82
1633019_a_at	FBgn0040024	10.39	10.37	10.27	10.22	10.33	10.32
1630949_s_at	FBgn0041191	10.41	10.39	10.48	10.47	10.44	10.41
1634114_at	---	9.46	9.44	9.07	9.17	9.21	8.5
1633459_a_at	FBgn0020439	9.18	9.16	9.83	9.21	9.04	8.93
1625002_a_at	FBgn0038013	9.95	9.92	9.97	10.1	10.09	9.88
1626924_a_at	FBgn0004922	13.46	13.44	13.64	13.61	13.63	13.54
1638119_at	---	9.31	9.29	8.93	9.01	9.34	9.26
1626788_a_at	FBgn0039867	8.64	8.62	8.7	8.79	8.6	8.5
1630990_at	FBgn0004101	9.07	9.04	9.06	9.27	9.14	8.97
1626845_at	FBgn0037632	11.42	11.4	11.57	11.58	11.5	11.37
1624113_at	FBgn0033059	9.21	9.19	9.64	9.62	9.69	9.62
1633503_at	FBgn0037354	10.02	10	10	10.08	10.22	10.04
1631180_at	FBgn0039182	10.3	10.28	10.35	10.04	10.16	10.32
1630165_s_at	FBgn0022764	9.81	9.79	9.86	9.82	9.85	9.92
1627526_at	FBgn0033761	9.99	9.96	10.22	10.18	10.05	9.87
1638247_at	FBgn0031099	7.95	7.92	7.8	7.6	7.97	7.67
1627631_s_at	FBgn0013981	13.51	13.48	13.43	13.62	13.56	13.55
1632643_at	FBgn0032858	7.97	7.95	7.73	8.06	7.73	7.65
1634086_a_at	FBgn0005632	7.87	7.84	8.11	8.07	8	7.82
1637292_at	---	7.8	7.78	7.89	8.01	7.48	7.51
1629069_at	FBgn0035842	8.01	7.99	8.24	8.07	8.2	8.09
1628053_at	---	8.87	8.85	8.8	8.88	8.9	8.84
1637048_at	FBgn0030481	8.75	8.73	8.71	8.58	8.87	8.79
1641683_at	FBgn0031711	9.64	9.62	9.71	9.96	9.88	9.67
1637456_at	FBgn0027504	10.06	10.04	10.02	10.04	10.1	9.97
1629983_at	FBgn0030336	10.16	10.14	9.88	9.84	9.79	9.72
1626099_s_at	FBgn0038627 /// FBgn002	10.39	10.36	10.33	10.52	10.35	10.44
1634913_s_at	FBgn0031969	10.18	10.15	10.1	10.3	10.03	10.11
1638203_at	FBgn0036188	8.58	8.55	8.65	8.59	8.72	8.7
1634194_at	FBgn0003449	10.06	10.04	10.15	10.32	10.21	10.08
1625412_at	FBgn0035600	11.39	11.36	11.61	11.63	11.53	11.52

1624618_at	---	8.88	8.86	8.79	8.81	8.86	8.79
1634377_at	FBgn0037241	9.03	9.01	8.75	8.94	9.25	9.3
1625078_at	FBgn0022023	11.11	11.08	11.34	11.26	11.37	11.22
1640145_at	FBgn0010292	10.06	10.04	9.97	9.71	10.02	10.08
1636476_a_at	FBgn0037200	8.85	8.82	8.71	8.97	8.58	8.58
AFFX-Dros-A	FBgn0000043	10.56	10.53	10.63	10.05	10.35	10.27
1624906_at	FBgn0025366 /// FBgn002	13.98	13.96	14.06	14.06	14.03	13.99
1636636_at	FBgn0039252	9.17	9.15	9.31	9.44	9.37	9.03
1634655_at	FBgn0035059	8.7	8.68	8.29	8.58	8.75	8.66
1626117_at	---	9.52	9.49	9.36	9.53	9.54	9.44
1632178_at	FBgn0004875	9.64	9.62	9.43	9.32	9.36	9.69
1632503_at	FBgn0031662	9.12	9.1	9.14	9.08	9.05	9.04
1632815_at	FBgn0030701	8.82	8.8	8.89	8.95	9.03	8.88
1640078_at	FBgn0037121	9.74	9.71	10.07	9.82	9.73	9.81
1631198_at	FBgn0021995	8.96	8.94	9.75	9.15	9.02	8.92
1624533_s_at	FBgn0003862	8.3	8.27	8.44	7.92	8.39	8.36
1635856_at	FBgn0033712	7.1	7.08	7.05	6.99	7.17	7.34
1636075_at	FBgn0051453	9.31	9.28	9.38	9.6	9.47	9.23
1625223_a_at	FBgn0020249	10.84	10.82	11	10.97	10.98	10.88
1639895_at	---	10.71	10.68	10.51	10.68	10.82	10.62
1635278_at	FBgn0032217	10.23	10.21	10.11	10.12	10.26	10.18
1637269_at	---	7.3	7.28	8.54	8.28	7.86	7.86
1631837_at	FBgn0003732	11.69	11.67	11.75	11.58	11.81	11.76
1637875_a_at	FBgn0053084	8.01	7.99	8.18	8.2	8.33	8.33
1629321_at	FBgn0005386	7.35	7.33	7.32	7.35	7.47	7.34
1630851_s_at	FBgn0037314	11.83	11.81	11.9	11.91	11.88	11.73
1636281_at	---	8.29	8.26	8.4	8.34	8.12	8.29
1624154_at	FBgn0024227	9.07	9.05	8.86	9.58	9.22	8.98
1627566_a_at	FBgn0037303	10.86	10.84	10.79	10.82	10.97	10.85
1633161_at	FBgn0036818	7.29	7.26	7.19	7.42	7.51	7.4
1632152_at	FBgn0030521	11.43	11.41	11.55	11.12	11.42	11.31
1632894_at	FBgn0030109	9.56	9.54	9.47	9.54	9.46	9.41
1626743_at	FBgn0035787	7.16	7.13	7.13	7.26	7.16	7.13
1622898_a_at	FBgn0038307	10.3	10.27	10.43	10.42	10.36	10.34
1623225_s_at	FBgn0037094	10.11	10.08	10.14	10	10.02	9.93
1634989_at	FBgn0010100	10.64	10.61	10.98	10.89	10.78	10.68

1630239_at	FBgn0004236	12.15	12.13	12.04	12.22	12.29	12.19
1640943_at	FBgn0038948	9.19	9.17	9.03	8.89	9.37	9.16
1631979_at	FBgn0036333	9.4	9.38	9.51	9.66	9.45	9.34
1636773_a_at	FBgn0037384	9.86	9.83	9.84	10.02	10.02	9.95
1634173_at	FBgn0026761	8.78	8.76	9.15	9.37	8.89	8.79
1636845_at	FBgn0031656	10.01	9.99	10.24	10.14	10.17	10.1
1625490_at	---	9.4	9.38	8.95	8.9	9.15	9.03
AFFX-r2-Dro	FBgn0001128	10.52	10.49	10.34	10.58	10.83	10.66
1629598_at	FBgn0013269	11.43	11.41	11.75	11.57	11.53	11.53
1631015_s_at	FBgn0040061	14.19	14.16	14.14	14.19	14.27	14.2
1628814_s_at	FBgn0031453	11.72	11.7	11.91	11.67	11.83	11.8
1623564_at	FBgn0036643	8.9	8.87	8.59	8.78	8.8	8.59
1625496_at	---	9	8.98	9.2	9.04	8.91	8.89
1635628_s_at	FBgn0030724	10.8	10.77	10.82	10.54	10.85	10.81
1639963_at	FBgn0039623	9.17	9.14	8.97	8.98	9.18	9.28
1632280_at	FBgn0035374	9.74	9.71	9.86	9.92	9.76	9.68
1637251_a_at	FBgn0029118	8.58	8.55	8.64	8.41	8.68	8.64
1633664_at	FBgn0040239	9.44	9.42	9.17	9.44	9.56	9.58
1633579_at	FBgn0032229	9.61	9.58	9.88	9.69	9.74	9.52
1632007_at	FBgn0035807	10.12	10.1	9.91	10.02	10.07	10.08
1628180_at	FBgn0033507	9.48	9.46	9.88	9.63	9.61	9.62
1625603_at	FBgn0039137	7.76	7.73	7.53	7.54	7.51	7.58
1637466_at	FBgn0017549	9.71	9.69	9.6	9.77	9.81	9.83
1641298_at	FBgn0037926	8.41	8.38	8.68	8.4	8.3	8.25
1635143_at	FBgn0036813	9.64	9.61	9.55	9.36	9.75	9.72
1631739_at	FBgn0037351	13.96	13.93	14.02	13.95	13.98	13.93
1636887_s_at	FBgn0037120	8.92	8.9	8.99	9.22	9.32	9.45
1631199_at	FBgn0030514	8.7	8.67	8.6	8.82	8.74	8.67
1637144_a_at	FBgn0002645	10.19	10.16	10.16	10.37	10.09	10.16
1634189_at	FBgn0032700	8.53	8.51	8.47	8.86	8.51	8.5
1623422_a_at	FBgn0051908	10.13	10.1	10.01	10.09	10.19	10.15
1630825_at	FBgn0038862	8.75	8.72	8.81	9.1	8.72	8.75
1625571_at	FBgn0032215	9.36	9.34	9.25	9.43	9.49	9.58
1634944_at	FBgn0002174	8.81	8.79	9.05	8.93	8.91	8.8
1636440_at	FBgn0010620	9.65	9.62	9.88	10.01	9.55	9.64
1638975_at	FBgn0035109	7.43	7.41	7.24	7.62	7.55	7.38

AFFX-r2-Dro	FBgn0001128	6.72	6.69	6.38	6.45	7.07	6.85
1633745_a_at	FBgn0013733	9.14	9.11	9.22	8.77	8.8	9.06
1635211_at	---	8.55	8.53	8.32	8.21	8.38	8.59
1625801_s_at	FBgn0025637	12.09	12.06	12.04	12.05	12.29	12.2
1626693_at	---	13.95	13.92	13.97	13.99	14.06	14
1641560_at	FBgn0031438	9.86	9.83	9.91	10.09	10	9.83
1639788_at	FBgn0010426	11.31	11.29	11.23	11.13	11.29	11.23
1626237_at	FBgn0035411	11.08	11.05	10.93	10.87	10.89	11.03
1634528_at	FBgn0037743	7.45	7.42	7.66	7.57	7.43	7.39
1629685_at	FBgn0035356	7.75	7.72	7.87	7.72	7.82	7.77
1636638_s_at	FBgn0038570	10.58	10.55	10.78	10.61	10.8	10.56
1628215_s_at	---	8.17	8.14	8.06	7.99	8.08	8.34
1631367_at	FBgn0036127	8.8	8.78	8.88	9.16	9.04	8.84
1626340_at	---	9.16	9.13	9.48	9.41	9.1	8.93
1624675_at	FBgn0026076	10.42	10.39	10.4	10.43	10.56	10.52
1625150_s_at	FBgn0000559	13.62	13.59	13.75	13.76	13.66	13.54
1630144_at	FBgn0015617	9.28	9.25	9.34	9.25	9.42	9.35
1631684_at	FBgn0030759	8.69	8.66	8.36	8.49	8.75	8.57
1638701_at	FBgn0034948	9.88	9.85	9.93	10	10.12	10.06
1631954_at	FBgn0037894	9.63	9.6	9.75	9.75	9.66	9.58
1623686_at	---	7.97	7.94	8.11	8.37	8.42	8.19
1641654_a_at	FBgn0017581	11.08	11.05	11.03	10.96	11.11	10.91
1639941_at	FBgn0030137	8.4	8.37	8.64	8.77	8.68	8.57
1626534_at	FBgn0003714	10.74	10.71	10.73	10.84	10.65	10.54
1624782_a_at	FBgn0035601	12.04	12.01	12.06	12.05	12.15	12.08
1640433_a_at	FBgn0033636	8.94	8.91	8.95	8.88	8.99	8.98
1630614_s_at	---	10.44	10.41	9.62	8.83	9.13	9.82
1639499_at	FBgn0030344	8.94	8.91	9.16	9.06	8.86	8.92
1637066_at	FBgn0030683	9.12	9.09	8.62	9.03	9.26	9.12
1636587_at	FBgn0030969	9.43	9.4	9.24	9.39	9.56	9.49
1638344_at	FBgn0032477 /// FBgn003	8.06	8.03	8.05	8.3	8.1	7.98
1626313_at	FBgn0015374	10.1	10.07	10.31	10.42	10.31	10.31
1636446_at	FBgn0028837	9.23	9.2	9.14	9.31	9.42	9.27
1623607_at	---	8.92	8.89	8.82	8.99	8.99	8.89
1629252_at	FBgn0037282	9.14	9.11	8.88	9	8.88	8.97
1623379_at	---	8.22	8.19	7.67	8	8.26	8.15

1630816_at	FBgn0035853	10.26	10.23	10.2	10.32	10.31	10.26
1638652_at	FBgn0058006	8.83	8.8	8.94	8.82	9.13	8.53
1623268_a_at	---	8.48	8.45	8.67	8.48	8.43	8.42
1630455_at	FBgn0002607	13.99	13.96	14.07	14.04	14.04	13.99
1627988_at	FBgn0003279	13.63	13.6	13.74	13.64	13.66	13.57
1628980_s_at	FBgn0036058	9.76	9.73	9.71	9.8	9.56	9.74
1625537_at	FBgn0040397	7.76	7.73	7.68	7.48	7.37	7.67
1636766_at	FBgn0026585	9.48	9.45	9.89	9.31	9.47	9.56
1628221_at	FBgn0032449	7.7	7.67	7.17	7.41	7.31	7.27
1631541_at	FBgn0026170	12.74	12.71	12.72	12.8	12.79	12.77
1634262_s_at	FBgn0025674	9.53	9.5	9.34	9.45	9.61	9.38
1640492_at	FBgn0035588	9.2	9.17	9.2	9.1	9.08	8.97
1640997_at	FBgn0050122	10.54	10.51	10.52	10.41	10.52	10.58
1628937_s_at	FBgn0015778	10.32	10.29	10.31	10.11	10.27	10.42
1632676_s_at	FBgn0039644	11.68	11.65	11.79	11.68	11.68	11.77
1636770_at	---	10.26	10.23	10.55	10.31	10.31	10.2
1640142_at	FBgn0037529	9.69	9.65	10.08	9.83	9.88	9.73
1636020_s_at	FBgn0000054	10.27	10.23	10.25	10.56	10.56	10.5
1634421_at	FBgn0034073	9.07	9.04	8.88	8.64	8.96	8.89
1624020_at	FBgn0002781	8.84	8.81	8.89	8.89	8.96	8.83
1640655_s_at	---	9.15	9.12	8.92	9.11	8.97	8.91
1625076_at	FBgn0000114	12.8	12.77	12.67	12.69	12.78	12.85
1623650_a_at	FBgn0033050	9.27	9.24	9.26	9.59	9.56	9.49
1625117_at	FBgn0031046	9.81	9.78	9.58	9.39	9.73	9.75
1638270_at	FBgn0027054	10.3	10.27	10.39	10.56	10.46	10.33
1636044_at	FBgn0015816	8.45	8.41	8.55	8.59	8.34	8.21
1625233_at	---	8.46	8.43	8.64	8.6	8.8	8.7
1639477_s_at	FBgn0038224	12.1	12.07	12.25	12.13	12.17	12.09
1633967_at	FBgn0031657	9.27	9.24	9.54	9.19	9.4	9.47
1629382_at	---	9.99	9.95	9.72	9.84	10	9.96
1632390_at	FBgn0034443	10.07	10.04	9.85	9.89	9.95	10.01
1625217_at	FBgn0038578	7.71	7.67	7.79	8.23	7.91	7.68
1639312_at	---	13.81	13.77	13.9	13.81	13.87	13.8
1636822_s_at	FBgn0036401	11.26	11.23	11.19	11.29	11.36	11.31
1637966_at	FBgn0030018	10.21	10.18	10.01	10	10.12	10.28
1631227_at	FBgn0038858	8.9	8.87	8.98	9.1	8.92	8.87

1625902_at	FBgn0030638	8.68	8.64	8.64	8.77	8.71	8.52
1640746_at	FBgn0037731	9.27	9.24	9.74	9.49	9.42	9.42
1627458_at	---	9.23	9.19	9.32	9.31	9.36	9.24
1629501_at	FBgn0030673	7.3	7.27	7.03	7.32	7.61	7.45
1629593_at	FBgn0035475	8.02	7.99	7.68	7.95	8.36	8.16
1631994_a_at	FBgn0036122	7.45	7.42	7.57	7.89	7.35	7.11
1629018_a_at	FBgn0032000	9.41	9.37	9.4	9.4	9.52	9.51
1625377_at	---	9.3	9.27	9.3	9.19	9.08	9.19
1629345_at	FBgn0030943	10.05	10.01	10.07	10.05	10.2	10.11
1633517_at	FBgn0034313	10.24	10.21	10.26	10.36	10.28	10.35
1635596_at	FBgn0034210	8.9	8.87	8.71	8.94	8.86	8.85
1637917_s_at	FBgn0003870	9.15	9.12	8.74	8.74	8.63	8.9
1624364_at	FBgn0039566	9.14	9.11	9.25	9.31	9.2	8.98
1628278_at	FBgn0036375	8.72	8.69	8.46	8.62	8.78	8.65
1628306_at	FBgn0003744	10.07	10.04	9.94	10.13	10.14	10.11
1625019_at	FBgn0016762	7.76	7.73	7.9	7.69	7.83	7.69
1625051_at	FBgn0013343	9.34	9.31	9.41	9.39	9.35	9.33
1629148_a_at	---	9.48	9.44	9.32	9.55	9.53	9.41
1640594_at	FBgn0029823	11.07	11.04	11.53	11.46	11.28	10.86
1634975_at	FBgn0040284	12.01	11.97	11.91	12.18	12.04	12.01
1635039_at	FBgn0034707	6.93	6.9	6.71	7.21	7.15	6.82
1630916_at	FBgn0024326	7.04	7.01	7.44	7.18	6.98	7.12
1627866_at	FBgn0040268	8.48	8.45	8.48	8.53	8.5	8.47
1626902_a_at	FBgn0015790	11.27	11.24	11.26	11.28	11.25	11.19
1624656_s_at	FBgn0024983	8.53	8.5	8.58	8.62	8.44	8.39
1636056_at	FBgn0010409	14.05	14.02	14.1	14.08	14.14	14.08
1630996_s_at	FBgn0035432	8.89	8.86	9.29	8.98	8.71	8.67
1638155_at	FBgn0038314	7.6	7.56	7.93	8.33	7.82	7.66
1629384_at	FBgn0039654	7.85	7.82	8.24	8.38	7.98	7.77
1628488_at	FBgn0039492	9.25	9.21	9.14	9.06	9.23	9.15
1638059_at	FBgn0021825	9.37	9.33	9.41	9.65	9.57	9.4
1636322_at	FBgn0030035	8.79	8.76	8.94	9.17	8.79	8.68
1628319_s_at	---	8.96	8.92	8.68	8.51	8.74	8.88
AFFX-CreX-5	---	13.58	13.55	13.45	13.64	13.46	13.37
1623081_at	---	9.92	9.89	10.07	10.11	9.97	9.88
1630634_s_at	FBgn0015756	13.81	13.77	13.87	13.9	13.86	13.78

1623158_s_at	FBgn0030318	8.29	8.26	8.23	8.38	8.06	8.13
1640999_at	---	7.68	7.65	7.34	7.61	8.14	8.06
1625702_s_at	---	9.79	9.75	9.55	9.65	9.88	9.82
1639984_at	FBgn0040080	8.92	8.89	8.88	9.16	9.18	9.06
1634541_a_at	FBgn0033088	9.15	9.11	8.87	9.03	9.17	9.14
1631433_at	FBgn0036018	8.19	8.16	8.47	8.29	8.19	8.06
1630283_at	FBgn0035273 /// FBgn001	10.22	10.18	10.27	10.19	10.48	10.25
1636314_at	FBgn0010438	11.7	11.67	11.85	11.79	11.7	11.61
1638642_at	FBgn0031497	10.24	10.21	10.4	10.43	10.32	10.02
1633951_at	---	10.71	10.68	10.92	10.78	10.74	10.61
1632462_at	FBgn0037358	10.43	10.4	10.51	10.57	10.53	10.42
1625505_at	FBgn0035159	6.83	6.79	6.81	7.02	7.34	7.23
1623424_a_at	FBgn0011300	9.14	9.11	8.71	8.66	9.04	9.03
1633701_at	---	8.07	8.03	8.31	8.48	8.46	8.13
1628714_at	FBgn0033475	10.41	10.38	10.25	10.77	10.41	10.28
1624905_at	FBgn0034176	9.79	9.76	9.56	9.67	9.78	9.7
1631049_at	FBgn0011742	9.87	9.83	9.66	9.63	9.8	9.75
1635501_at	---	10.86	10.82	10.89	11.27	11.09	10.91
1640624_s_at	---	11.55	11.52	11.69	11.73	11.63	11.58
1632568_at	FBgn0037538	8.69	8.65	8.61	8.79	8.79	8.65
1625594_s_at	FBgn0022382	9.45	9.42	9.52	9.76	9.51	9.31
1630506_at	FBgn0031457	8.43	8.4	8.26	8.28	8.36	8.38
1629756_at	FBgn0027537	9.49	9.46	9.68	10	9.8	9.57
1634943_at	FBgn0015287	10.58	10.54	10.73	11.05	10.92	10.71
1628472_at	FBgn0028969	10.41	10.37	10.15	10.08	10.42	10.29
1628149_a_at	FBgn0044826	9.7	9.67	9.8	9.62	9.7	9.66
1636745_at	FBgn0037770	10.23	10.2	10.21	10.07	10.21	10.23
1624280_at	FBgn0030007	9.36	9.32	9.37	9.53	9.46	9.16
1630329_at	FBgn0030486	9.33	9.3	9.22	9.17	9.58	9.48
1630343_at	---	10.48	10.45	10.32	10.4	10.55	10.49
1634417_s_at	FBgn0035046	10.72	10.69	10.81	10.88	10.83	10.72
1629084_at	---	8.39	8.35	8.6	8.51	8.58	8.34
1625332_at	FBgn0033236	10.43	10.4	10.45	10.55	10.48	10.52
1633430_at	FBgn0010422	9.71	9.68	9.73	9.72	9.8	9.8
1625700_a_at	FBgn0011241	9.09	9.05	9.15	9.3	9.31	9.18
1641321_a_at	FBgn0036566	10.54	10.51	10.35	10.48	10.4	10.54

1638889_at	FBgn0029873	10.34	10.31	10.28	10.23	10.31	10.31
1624570_a_at	FBgn0011289	10.91	10.87	10.78	10.85	10.9	10.87
1623836_at	FBgn0011272	13.85	13.81	14	13.91	13.94	13.87
1631695_at	FBgn0040797	7.04	7	6.78	6.71	6.86	7
1633854_at	FBgn0011762	8.52	8.49	8.43	8.66	8.75	8.54
1625465_a_at	FBgn0038924	9.92	9.88	9.93	9.92	9.88	9.76
1635070_at	FBgn0035726	11.1	11.07	11.25	11.16	11.15	11.06
1633736_at	FBgn0032690	8.66	8.62	8.93	8.96	8.6	8.49
1629207_at	FBgn0032350	11.3	11.27	11.25	10.99	11.3	11.3
1641116_at	---	10.24	10.2	10.02	10.17	10.05	10.09
1635910_at	FBgn0037582	9.89	9.86	9.85	9.91	10.04	9.96
1625905_at	FBgn0035243	9.11	9.07	9	9.08	9	9.08
1624948_at	FBgn0037739	9.79	9.76	9.75	9.86	9.82	9.77
1624243_at	FBgn0032910	9.38	9.34	9.07	9.53	9.33	9.27
1638938_at	FBgn0026582	8.56	8.52	8.48	8.92	9	8.6
1625320_at	---	8.68	8.64	8.65	8.95	8.9	8.8
1631351_s_at	FBgn0030101	8.83	8.79	8.27	8.55	8.69	8.52
1640418_at	FBgn0002783	11.15	11.11	10.9	11.02	11.13	11.08
1640382_at	FBgn0030504	10.04	10	10.34	10.02	10.03	10.04
1637159_at	FBgn0030610	9.71	9.67	9.76	9.71	9.74	9.7
1640900_at	FBgn0038742	10.08	10.04	9.87	9.62	10.24	9.95
1640797_at	FBgn0032833	12.05	12.02	12.22	12.14	12.17	12.16
1632554_at	FBgn0037633	7.7	7.66	8.28	8.07	8.01	7.9
1627472_at	FBgn0000084	10.41	10.37	10.33	10.26	10.27	10.13
1628621_at	FBgn0039765	9.19	9.15	9.38	9.19	9.18	9.09
1624180_at	FBgn0030196	9.54	9.5	9.48	9.66	9.64	9.61
1638157_at	FBgn0038552	9.6	9.56	9.48	9.63	9.66	9.64
1625393_s_at	FBgn0036987	8.63	8.6	8.36	8.98	8.34	8.48
1626390_at	FBgn0032409	8.02	7.99	7.99	8.24	8.1	7.99
1634869_at	FBgn0025352	10.22	10.18	10.19	10.11	10.29	10.09
1638009_s_at	FBgn0037715	9.77	9.73	9.92	10.04	10.16	10.19
1638011_a_at	FBgn0016693	8.99	8.96	9.47	9.23	9.06	8.86
1623991_s_at	FBgn0033109	11.62	11.58	11.58	11.68	11.71	11.59
1638849_a_at	FBgn0029672	9.84	9.8	9.59	9.6	9.73	9.7
1633549_s_at	---	11.13	11.1	11.1	11.15	11.24	11.17
1634613_s_at	---	12.08	12.04	11.71	11.85	11.75	11.86

1635704_at	FBgn0030468	10.91	10.87	10.82	11.05	10.95	10.9
1633865_at	FBgn0037667	8.52	8.48	8.62	9.06	8.69	8.45
1630632_s_at	FBgn0029704	11.28	11.24	11.43	11.44	11.27	11.21
1638832_at	FBgn0033912	14.22	14.19	14.07	14.09	14.22	14.17
1628610_at	FBgn0031977	11.34	11.3	11.45	11.45	11.36	11.26
1627532_at	---	9.81	9.77	9.61	10.02	9.86	9.75
1639286_s_at	---	9.97	9.93	9.93	10.02	9.89	9.86
1632677_a_at	FBgn0034697	8.56	8.52	8.74	8.71	8.66	8.58
1623250_at	---	11.33	11.29	11.46	11.6	11.47	11.33
1624471_s_at	FBgn0000043	12	11.96	12.21	11.9	11.85	11.74
1641692_at	FBgn0039379	9.45	9.42	9.33	9.46	9.6	9.47
1634647_at	FBgn0037274	8.73	8.69	8.61	8.99	9.02	8.67
1638673_at	FBgn0010380	10.47	10.43	10.58	10.68	10.61	10.46
1627676_at	FBgn0037250	10.09	10.05	10.01	10.04	10.1	10.08
1626663_s_at	FBgn0027066	11.18	11.14	11.15	11.14	11.13	11.21
1624029_at	FBgn0035039	9.25	9.21	9.2	9.31	9.21	9.01
1625847_at	---	9.86	9.82	10	10.04	9.79	9.66
1627761_at	FBgn0036930	8.4	8.36	8.73	8.24	8.4	8.47
1625031_at	---	9.27	9.23	9.3	9.21	9.39	9.31
1641043_at	FBgn0035824	7.02	6.98	7.07	7.44	7.2	7.17
1630683_at	FBgn0028470	10.24	10.2	9.72	9.8	10.01	10.14
1629496_at	FBgn0026578	9.77	9.73	9.84	9.54	9.67	9.64
1641072_at	FBgn0037327	9.61	9.57	9.45	9.73	9.68	9.59
1627048_at	FBgn0032030	9.32	9.28	9.36	9.56	9.51	9.43
1623683_at	---	10	9.96	10.31	10.39	9.93	9.86
1633447_at	---	8.93	8.89	8.88	9.2	8.96	8.9
1633486_at	FBgn0030686	9.36	9.32	9.36	9.57	9.49	9.29
1639102_at	FBgn0017430	9.43	9.39	9.44	9.5	9.64	9.52
1623797_at	FBgn0036999	10.28	10.24	10.16	10.19	10.2	10.21
1630968_at	FBgn0035173	9.72	9.68	9.62	9.82	9.77	9.89
1637598_at	---	10.96	10.92	11.04	11.08	11.07	11.05
1625613_at	FBgn0014427	9.83	9.79	9.78	9.84	9.9	9.74
1637615_at	FBgn0033653	8.82	8.78	8.62	8.66	8.98	8.9
1635931_at	---	9.5	9.46	9.65	9.48	9.54	9.48
1636436_at	FBgn0011217	11.88	11.84	11.86	11.86	11.86	11.86
1641117_a_at	FBgn0031195	8.71	8.67	8.32	8.56	8.34	8.29

1623861_at	FBgn0000566	10.31	10.27	10.51	10.36	10.35	10.24
1624887_at	FBgn0037624	10.86	10.82	10.99	10.75	10.95	10.76
1638190_at	FBgn0037550	8.1	8.06	8.06	8.11	8.04	8.04
1622931_at	FBgn0035617	8.39	8.35	7.97	8.02	8.32	8.37
1623463_at	FBgn0011726	13.41	13.37	13.39	13.63	13.55	13.43
1639270_at	FBgn0034743	13.98	13.94	13.98	14	14.07	13.91
1636712_at	FBgn0032987	14.19	14.15	14.08	14.12	14.17	14.19
1631509_a_at	---	9.09	9.05	9.22	9.02	9.42	9.28
1629659_s_at	FBgn0003031	12.5	12.46	12.51	12.58	12.45	12.51
1629806_a_at	FBgn0052103	9.51	9.47	9.2	9.45	9.65	9.59
1635895_at	---	7.1	7.06	7.13	7.29	7.26	7.14
1629017_s_at	FBgn0005596	9.42	9.38	9.41	9.48	9.39	9.33
1638068_a_at	FBgn0033699	13.97	13.93	14	14	14.03	13.97
1627326_a_at	FBgn0032633	8.7	8.66	8.44	8.69	8.64	8.71
1631331_a_at	FBgn0038538	11.98	11.94	12.04	12.2	12.13	11.9
1631245_s_at	FBgn0036662	8.53	8.49	8.44	8.8	8.37	8.33
1638349_s_at	FBgn0034967	13.73	13.69	13.8	13.82	13.79	13.74
1639949_s_at	FBgn0011284	13.93	13.88	13.97	13.94	13.99	13.92
1635523_a_at	FBgn0036710	9.92	9.88	9.8	10	10.12	9.93
1636508_at	FBgn0013303	10.01	9.97	10.12	10.19	10.14	10.1
1631655_a_at	FBgn0052566	9.68	9.64	9.6	9.15	9.4	9.47
1625055_at	FBgn0014868	9.94	9.9	9.98	10.05	9.97	9.93
1634055_at	FBgn0024956	9.91	9.87	9.91	9.96	9.98	9.89
1640293_s_at	FBgn0037182	9.61	9.57	9.59	9.65	9.74	9.74
1627043_at	FBgn0037856	7.98	7.94	8.11	7.96	7.96	7.77
1635104_s_at	FBgn0053188	11.05	11	10.74	10.87	10.78	10.85
1637193_at	FBgn0034258	10.7	10.66	10.9	10.96	10.77	10.66
1631877_a_at	---	9.84	9.8	9.73	9.8	9.75	9.5
1622896_at	FBgn0038966	7.74	7.7	7.77	8.25	7.94	7.9
1623995_at	FBgn0037328	13.57	13.53	13.7	13.68	13.71	13.61
1623147_at	FBgn0051855	9.41	9.37	9.61	9.61	9.49	9.42
1637735_at	FBgn0033341	9.63	9.59	9.76	9.62	9.52	9.55
1629165_at	FBgn0038300	8.24	8.2	8.28	8.57	8.33	8.33
1636576_s_at	FBgn0004625	8.93	8.89	9.05	9.07	8.95	8.84
1625291_s_at	FBgn0042111	7	6.96	7.26	7.35	7.43	7.3
1632383_at	FBgn0037834	11.84	11.79	11.8	11.81	11.69	11.67

1628065_at	FBgn0038128	8.1	8.06	8.05	8.25	8.19	8.11
1635723_s_at	FBgn0053129	10.96	10.92	10.94	10.88	10.97	10.94
1633012_at	FBgn0031285	10.57	10.52	10.68	10.28	10.38	10.55
1641570_s_at	FBgn0051683	9.32	9.28	9.76	9.11	9.29	9.2
1627212_at	FBgn0003231	10.71	10.67	10.53	10.75	10.68	10.6
1639928_a_at	FBgn0050084	8.47	8.42	8.95	8.05	7.84	8.26
1632223_at	FBgn0020305	8.48	8.43	8.58	8.48	8.54	8.59
1627638_s_at	FBgn0003676	11.93	11.88	12.16	12.34	12.03	11.75
1640048_s_at	FBgn0052705	8.15	8.11	7.97	8.14	8.28	8.18
1633213_at	FBgn0005411	11.25	11.2	11.19	11.46	11.4	11.24
1629792_at	FBgn0040010	11.78	11.73	11.65	11.74	11.88	11.9
1630750_at	FBgn0034362	10.36	10.31	10.37	10.45	10.5	10.44
1640824_at	FBgn0037108	9.67	9.62	9.56	9.5	9.63	9.7
1628683_at	---	8.41	8.37	8.38	8.52	8.42	8.49
1625966_at	FBgn0039461	9.06	9.01	8.95	9.35	9.11	9.03
1639067_at	FBgn0028664	9.28	9.23	9.44	9.57	9.56	9.57
1627403_s_at	FBgn0025809	10.29	10.25	10.37	10.43	10.42	10.34
1634104_a_at	---	10.88	10.83	10.63	10.81	10.69	10.62
1628088_at	---	10.41	10.37	10.42	10.63	10.54	10.48
1636125_a_at	FBgn0040493	10.49	10.45	10.53	10.95	10.53	10.22
1626494_at	---	9.48	9.44	9.6	9.94	9.55	9.33
1635023_at	FBgn0030733	11.52	11.48	11.88	11.79	11.65	11.51
1638005_s_at	FBgn0016070	12.57	12.52	12.24	12.29	12.38	12.48
1627261_s_at	FBgn0015622	9.99	9.95	9.9	10.13	9.97	10.02
1629400_at	FBgn0035753	13.56	13.52	13.59	13.55	13.65	13.55
1630987_at	---	8.17	8.13	8.03	8.62	8.26	8.04
1628637_at	FBgn0033105	9.94	9.9	10.11	10.47	10.18	10.07
1623924_at	FBgn0033557	8.71	8.67	9.05	8.97	8.63	8.54
1635303_at	FBgn0010265	13.74	13.7	13.86	13.8	13.8	13.72
1639952_at	FBgn0028399	9.6	9.56	9.53	9.48	9.56	9.53
1629876_at	---	8.84	8.8	8.83	8.89	8.85	8.89
1627776_at	FBgn0039227	9.05	9	8.76	8.79	8.94	8.78
1628529_a_at	---	10.21	10.16	10.15	9.97	10.23	10.18
1630214_a_at	FBgn0039711	8.93	8.88	9	9.12	9.24	9.02
1629307_s_at	FBgn0010113	9.41	9.36	9.32	9.37	9.22	9.23
1627667_at	FBgn0035393	8.99	8.94	9.27	9.32	9.16	9.15

1623666_at	FBgn0036549	7.88	7.84	7.63	7.89	8.04	7.83
1639296_at	FBgn0031286	7.36	7.31	7.28	7.41	7.43	7.37
1623452_at	FBgn0036588	7.97	7.93	7.88	7.69	7.85	8.17
1629762_at	FBgn0038478	10.16	10.12	9.71	9.93	10.03	10.16
1638146_at	FBgn0020909	9.86	9.82	9.84	9.91	9.97	9.83
1624228_at	---	9.59	9.54	9.74	9.82	9.72	9.58
1625989_at	FBgn0032259	9	8.95	8.69	8.85	9.18	9.07
1626566_at	FBgn0035811	11.34	11.3	11.34	11.76	11.57	11.07
1636321_s_at	FBgn0039209	8.49	8.45	8.35	8.26	8.39	8.46
1627581_at	FBgn0033374 /// FBgn003	9.13	9.08	9.34	9.3	8.98	8.84
1634945_at	FBgn0032015	9.78	9.73	9.92	9.68	9.65	9.78
1636649_a_at	FBgn0035713	9.14	9.09	9.11	9.34	9.34	9.11
1625517_at	FBgn0017578	8.93	8.89	9.19	9.15	9.08	8.97
1639256_at	FBgn0032200	9.68	9.64	9.64	10	9.77	9.62
1625006_at	FBgn0030365	10.14	10.09	9.83	9.99	9.82	9.76
1632991_at	---	8.53	8.49	8.45	8.2	8.53	8.63
1632303_a_at	FBgn0039668	9.27	9.22	9.06	9.27	9.25	9.16
1623384_at	---	10.52	10.48	10.55	10.54	10.49	10.45
AFFX-Dros-A	FBgn0000043	10.85	10.81	10.97	10.45	10.74	10.66
1640184_at	FBgn0033122	8.72	8.67	8.46	8.61	8.87	8.72
1637905_s_at	FBgn0023528	9.57	9.52	9.69	9.85	9.69	9.51
1638575_at	FBgn0025815	10.67	10.63	10.94	11.1	10.84	10.62
1625466_at	FBgn0037478	9.05	9	8.98	9.16	8.92	8.87
1637284_at	FBgn0026056	8.76	8.71	8.64	8.88	8.83	8.9
1639358_at	FBgn0034035	8.46	8.41	8.59	8.5	8.34	8.37
1637424_at	FBgn0036295	8.96	8.92	8.86	9.02	8.99	9
1627410_at	FBgn0027356	8.73	8.68	9.13	8.98	8.81	8.83
1636596_at	FBgn0035722	9.79	9.75	9.94	9.57	9.51	9.5
1640968_a_at	---	10.28	10.23	10.37	10.08	10.19	10.23
1630470_s_at	FBgn0037261	10.84	10.8	10.66	11.09	10.98	10.8
1634094_a_at	FBgn0034878	9.13	9.09	9.33	9.46	9.35	9.07
1636191_a_at	FBgn0034529	7.24	7.19	7.15	7.21	7.33	7.25
1640480_at	FBgn0053051	8.31	8.26	9.2	8.67	8.31	8.24
1624971_at	FBgn0040383	7.65	7.6	7.92	7.98	7.03	7.01
1637342_s_at	FBgn0010551	12.24	12.2	12.31	12.23	12.27	12.24
1641465_at	FBgn0032445	8.99	8.94	9.21	9.1	9.16	9.1

1635389_s_at	FBgn0026415	10.88	10.83	10.68	10.88	10.84	10.75
1639722_s_at	FBgn0030745	7.1	7.06	7.38	7.15	7.52	7.3
1628202_at	FBgn0035540	8.84	8.79	8.69	8.88	8.99	8.82
1633389_at	FBgn0032465	9.11	9.07	9.06	9.09	9.27	9.2
1628167_s_at	FBgn0036967	9.46	9.41	9.37	9.6	9.59	9.63
1624482_at	---	10.25	10.21	10.44	10.49	10.27	10.08
1625488_s_at	FBgn0014020	10.26	10.21	10.28	10	9.77	10.14
1631046_s_at	FBgn0032976	9.78	9.73	9.98	9.73	9.54	9.74
1627916_s_at	FBgn0003204	11.5	11.45	11.31	11.27	11.31	11.41
1636358_a_at	FBgn0040057	10.47	10.42	10.48	10.22	10.53	10.57
1635647_at	FBgn0032877	8.79	8.74	8.68	8.66	8.99	8.98
1627944_a_at	FBgn0035318	8.18	8.13	8.22	8.37	8.33	8.08
1632816_at	FBgn0023506	9.17	9.13	9.12	9.38	9.28	9.17
1626337_at	FBgn0035063	8.76	8.71	9.12	8.89	8.64	8.59
1636922_at	FBgn0038057	7.71	7.66	8.19	8.09	7.83	7.79
1640915_at	FBgn0034802	11.73	11.68	11.76	11.62	11.72	11.77
1626942_at	FBgn0039273	9.06	9.01	8.88	9.08	9.39	9.39
1626079_a_at	FBgn0032955	10.82	10.77	10.83	11.03	10.97	10.85
1628629_at	FBgn0050038	8.64	8.59	8.66	8.73	8.75	8.56
1637990_s_at	FBgn0011205	8.37	8.32	8.44	8.53	8.36	8.24
1631406_at	FBgn0035024	9.06	9.01	9.18	9.19	9.18	9.01
1640015_at	FBgn0030960	7.65	7.6	7.48	7.46	7.7	7.64
1634868_at	FBgn0033899	8.55	8.51	8.44	8.41	8.55	8.53
1623716_at	FBgn0011744	10.71	10.66	10.8	10.96	10.83	10.64
1640394_s_at	FBgn0004107	10.7	10.65	10.26	10.49	10.64	10.53
1640574_at	FBgn0040080	12.53	12.49	12.52	12.47	12.46	12.46
1627002_at	FBgn0030121	7.6	7.55	8.13	8.41	7.98	7.75
1637715_a_at	FBgn0035247	9.23	9.19	9.24	9.36	9.3	9.24
1630131_at	FBgn0037842	8.92	8.87	8.99	8.94	9	8.99
1638607_s_at	FBgn0029176	13.12	13.07	13.21	13.17	13.24	13.14
1634304_a_at	FBgn0036958	9.03	8.98	8.79	8.87	9.18	9.21
1625128_a_at	---	11.72	11.67	11.96	11.82	11.86	11.82
1626823_a_at	FBgn0036505	9.71	9.67	9.44	9.61	9.81	9.7
1640672_at	FBgn0031830	11.46	11.41	11.77	11.77	11.63	11.48
1627970_at	---	8.02	7.97	8.02	7.8	8.12	8.18
1629995_at	FBgn0052104	7.63	7.58	7.77	7.76	7.66	7.47

1625169_at	FBgn0037317	8.95	8.91	8.9	9.2	9.15	9.04
1633605_at	FBgn0036889	8.78	8.73	8.56	8.57	8.7	8.66
1637308_at	FBgn0024364	9.11	9.06	9.25	9.17	9.37	9.29
1632098_at	FBgn0032138	10.92	10.87	11.26	11.1	11.11	10.8
1639370_at	FBgn0037368	9.27	9.22	9.19	9.31	9.33	9.34
1638323_at	FBgn0037614	10.31	10.26	10.06	9.98	10.36	10.39
1640748_at	FBgn0028708	9.66	9.61	9.41	9.78	9.99	9.88
1623906_at	FBgn0032189	9.43	9.38	9.23	9.55	9.67	9.58
AFFX-Dm-X(	---	14.2	14.15	14.07	14.25	14.12	13.99
1629859_s_at	FBgn0003969	9.56	9.51	9.72	9.72	9.71	9.56
1638830_at	FBgn0013746	10.23	10.18	10.39	10.53	10.42	10.36
1627056_a_at	FBgn0010607	9.17	9.12	9.05	9.37	9.2	9.22
1636351_at	FBgn0030239	10.17	10.12	10.04	10.31	10.23	10.07
1638185_at	FBgn0031188	9.48	9.43	9.31	9.59	9.57	9.44
1639202_a_at	FBgn0039025	8.32	8.27	8.7	8.67	8.45	8.15
1625060_at	FBgn0035254	7.94	7.89	8.08	7.99	8.13	8.09
1630930_a_at	FBgn0023441	8.65	8.6	8.71	8.15	8.38	8.61
1626481_a_at	FBgn0026619	9.02	8.97	9	8.95	8.91	8.9
1640897_at	FBgn0039875	8.43	8.38	8.52	8.43	8.24	8.37
1639957_s_at	FBgn0028696	13.7	13.65	13.63	13.74	13.78	13.68
1634904_s_at	---	9.89	9.84	9.79	9.69	9.84	9.8
1625494_at	FBgn0034114	8.2	8.15	7.67	8.32	8.18	8.1
1636190_at	FBgn0032033	8.43	8.38	8.45	8.57	8.52	8.43
1639072_at	FBgn0004864	9.2	9.15	9.26	9.16	9.08	9.22
1629012_at	FBgn0028388	10.94	10.89	10.97	11.01	11.07	10.85
1638868_at	FBgn0032929	10.07	10.02	10.11	10.33	10.19	10.03
1630735_at	FBgn0036853	10.24	10.19	9.98	10.21	10.14	10.05
1631151_at	FBgn0039563	9.46	9.41	9.44	9.57	9.41	9.39
1625297_at	FBgn0030668	8.4	8.35	8.39	8.32	8.4	8.3
1639725_at	---	8.91	8.86	8.9	8.86	8.78	8.67
1627034_a_at	FBgn0033086	8.55	8.5	8.52	8.5	8.31	8.29
1633822_at	FBgn0037087	10.04	9.99	10.08	10.06	10.05	10.01
1637629_a_at	FBgn0029157	9.31	9.26	8.82	8.94	9.58	9.42
1639552_s_at	FBgn0036959	8.19	8.14	8.29	8.27	8.36	8.25
1637180_at	FBgn0040778	7.38	7.33	7.08	7.65	7.68	7.65
1639893_s_at	FBgn0014026	13.59	13.54	13.53	13.47	13.67	13.49

1638671_at	---	7.14	7.09	7.54	7.56	7.34	7.35
1640523_at	FBgn0031660	10.22	10.17	10.37	10.26	10.09	10.03
1624439_at	FBgn0036642	11.04	10.99	11.06	11.03	11.16	10.96
1639719_at	FBgn0005648	8.51	8.46	8.65	8.81	8.17	8.44
1629882_at	FBgn0035902	7.27	7.22	6.92	7.71	7.54	7.52
1624963_at	FBgn0038549	8.32	8.26	8	8.27	8.41	8.34
1632914_at	FBgn0013548	9.15	9.1	8.66	9.28	9.24	8.97
1639635_s_at	FBgn0038297	10.4	10.35	10.14	10.15	10.18	10.17
1631387_at	FBgn0050344	8.91	8.86	9.16	9.01	8.91	8.93
1628903_s_at	FBgn0022764	7.82	7.77	7.95	7.77	7.83	7.68
1630057_at	FBgn0037603	8.53	8.48	8.34	8.03	8.54	8.51
1627545_at	---	9.16	9.11	9.29	9.26	9.27	9.15
1624776_a_at	FBgn0011361	10.82	10.76	11.04	11	10.85	10.84
1624205_at	---	11.75	11.7	11.8	11.83	11.88	11.77
1628282_at	FBgn0038488	7.84	7.79	7.85	8.23	8.17	7.91
1635394_at	---	10.78	10.73	10.72	10.7	10.63	10.67
1629662_at	FBgn0029714	9.9	9.85	9.8	9.91	9.86	9.84
1628299_at	FBgn0034925	9.99	9.94	9.97	10.07	10.2	10.11
1636080_a_at	---	7.48	7.43	7.83	7.21	6.73	7.4
1639614_s_at	---	14.49	14.44	14.44	14.48	14.47	14.44
1634909_at	---	9.09	9.04	9.48	9.37	9.42	9.25
1637951_at	FBgn0038235	8.03	7.98	8.29	8.28	8.28	8.2
1638667_a_at	FBgn0038065	10.9	10.84	10.82	10.71	10.79	10.83
1623073_s_at	FBgn0011760	12.23	12.18	12.21	12.11	12.14	12.23
1629916_at	---	10.23	10.18	9.98	10.06	10.23	10.1
1640962_s_at	FBgn0034894	10.08	10.02	9.7	9.9	10	9.97
1631645_at	FBgn0034987	8.87	8.82	8.84	8.96	8.86	8.83
1629241_at	FBgn0016698	8.59	8.53	8.82	8.71	8.81	8.59
1634197_at	FBgn0039882	7.55	7.5	7.5	7.72	7.76	7.78
1623645_a_at	FBgn0029778	8.31	8.26	8.26	8.43	8.45	8.35
1631074_at	FBgn0034084	8.56	8.51	8.26	8.93	8.95	8.89
1629248_at	---	9.47	9.42	9.43	9.37	9.43	9.54
1632134_s_at	FBgn0026597	9.35	9.3	9.14	9.14	9.18	9.36
1632482_at	FBgn0034914	10.14	10.09	10.06	10.36	10.2	10.11
1636691_a_at	FBgn0032475	10	9.94	9.77	9.88	9.89	9.92
1636173_s_at	FBgn0015765	8.96	8.91	9.06	8.97	8.96	9.02

1627505_at	FBgn0033232	8.67	8.61	8.55	8.53	8.84	8.73
1626781_at	FBgn0011826	9.9	9.84	9.98	10.13	10.06	10.07
1625386_at	FBgn0000413	11.07	11.02	11.05	11.03	11.08	11.09
1632850_at	FBgn0037073	10.06	10.01	10.11	9.98	9.97	9.91
1627864_at	FBgn0053130	8.17	8.12	8.02	7.91	8.14	8.25
1623374_a_at	FBgn0024238	9.46	9.4	9.4	9.5	9.15	9.36
1631648_at	FBgn0035827	10.25	10.2	10.16	10.21	10.39	10.21
1634764_at	FBgn0010078	14.41	14.35	14.2	14.19	14.32	14.27
1630901_a_at	FBgn0039261	10.16	10.1	10	10.17	10.17	10.12
1639151_a_at	---	9.9	9.85	9.72	9.67	9.88	9.9
1633870_at	FBgn0033101	9.83	9.78	9.61	9.35	9.86	9.58
1639208_at	FBgn0013756	9.7	9.65	9.53	9.48	9.57	9.56
1633751_at	FBgn0037543	9.56	9.5	9.82	9.56	9.51	9.38
1639357_at	FBgn0035141	8.31	8.26	8.14	8.39	8.51	8.38
1629387_s_at	FBgn0029095	7.24	7.18	7.84	7.51	7.57	7.45
1638197_at	FBgn0023508	8.83	8.78	8.33	8.5	8.7	8.59
1631772_a_at	FBgn0027951	8.67	8.62	8.28	8.4	7.91	8.15
1640415_at	FBgn0034951	9.63	9.57	9.59	9.49	9.44	9.42
1636161_at	FBgn0035153	8.98	8.93	9.17	9.11	9.05	9
1633277_at	FBgn0003941	13.5	13.45	13.6	13.57	13.61	13.51
1640083_at	FBgn0033460	9.02	8.97	8.93	9.01	9.03	8.91
1640700_at	FBgn0039712	9.62	9.57	9.49	9.67	9.7	9.62
1629868_s_at	FBgn0032130	8.15	8.1	8.05	8.1	8.29	8.36
1639602_s_at	FBgn0035850	9.78	9.73	9.77	9.69	9.76	9.67
1634461_at	---	9.62	9.56	9.33	9.38	9.47	9.47
1625556_at	FBgn0025186	9.72	9.66	9.67	9.74	9.63	9.6
1632269_at	FBgn0004913	13.78	13.73	13.84	13.85	13.89	13.78
1626147_s_at	FBgn0027842	10.23	10.17	10.24	10.29	10.16	9.99
1631028_s_at	FBgn0021979	10.43	10.37	10.42	10.55	10.51	10.33
1635116_a_at	FBgn0038108	8.69	8.63	8.47	8.54	8.61	8.51
1641372_at	FBgn0030553	7.85	7.8	8.13	7.99	8.39	8.33
1630772_at	FBgn0010768	7.19	7.13	7.1	6.7	6.93	7.14
1635619_a_at	FBgn0013765	9.43	9.38	9.08	9.32	9.42	9.23
1639567_at	---	9.13	9.08	8.88	9.06	9.19	9.11
AFFX-CreX-3	---	13.91	13.85	13.72	13.93	13.81	13.68
1623214_at	---	10.49	10.44	10.46	10.2	10.42	10.5

1625714_a_at	---	10.99	10.94	10.82	10.82	10.92	10.92
1638453_at	FBgn0034803	9.59	9.53	9.61	9.6	9.62	9.52
1632472_s_at	FBgn0038364	9.55	9.5	9.54	9.21	9.59	9.53
1634950_at	FBgn0038410	8.44	8.38	8.65	8.62	8.51	8.48
1625459_at	FBgn0034859	7.18	7.13	7.34	8.28	7.37	7.26
1632689_at	FBgn0026566	11	10.94	10.91	10.94	11.05	10.95
1624222_s_at	FBgn0030873	9.68	9.62	9.25	9.29	9.71	9.64
1637504_at	FBgn0030114	8.51	8.45	8.19	8.04	8.38	8.29
1634313_s_at	---	13.15	13.09	13.28	13.27	13.26	13.14
1638717_at	FBgn0029969	10.65	10.6	10.59	10.71	10.62	10.46
1627131_at	FBgn0028683	9.71	9.65	9.83	10.29	9.65	9.74
1628494_a_at	FBgn0024315	8.88	8.82	9	8.81	8.5	8.81
1638615_s_at	FBgn0039757	13.86	13.8	13.92	13.87	13.94	13.8
1640794_at	FBgn0031061	8.53	8.48	8.57	8.68	8.82	8.64
1633743_at	FBgn0004855	10.04	9.98	10.05	10.16	10.2	10.15
1630287_at	---	9.78	9.72	9.82	9.77	10.04	9.88
1639045_at	FBgn0037960	7.65	7.59	7.17	7.08	7.16	7.6
1626362_at	FBgn0031399	8.24	8.18	8.3	8.22	8.26	8.12
1632642_a_at	FBgn0031459	10.82	10.76	10.96	10.88	10.91	10.78
1641745_a_at	FBgn0038684	9.45	9.39	9.66	9.34	9.3	9.27
1629053_at	FBgn0034060	9.34	9.28	9.3	9.34	9.29	9.28
1628213_s_at	FBgn0043044	11.07	11.01	10.99	11.16	11.09	11.04
1633204_a_at	FBgn0036309	9.19	9.13	8.82	8.94	8.99	9.12
1633850_at	---	7.43	7.37	7.94	7.98	7.72	7.51
1623934_at	---	9.24	9.18	9.18	9.51	9.23	9.2
1626478_at	---	8.88	8.82	8.73	8.95	8.86	8.74
1636877_at	FBgn0035483	8.84	8.78	8.63	8.75	8.89	8.73
1639075_a_at	FBgn0037084	9.81	9.75	9.53	9.58	9.67	9.77
1625458_a_at	FBgn0035838 /// FBgn002	11.7	11.64	11.8	11.69	11.72	11.78
1638135_at	FBgn0030034	10.28	10.22	8.86	8.81	9.92	9.97
1637787_a_at	FBgn0033897	9.52	9.46	9.5	9.62	9.72	9.56
1628320_at	FBgn0037749	9.95	9.89	9.99	9.97	9.83	9.73
1640632_at	FBgn0014028	9.91	9.85	10.01	9.83	9.95	9.91
1630008_at	FBgn0039149	8.34	8.28	8.11	8.04	7.9	8.01
1629288_s_at	FBgn0030629	9.17	9.11	9.21	9.26	9.19	9.31
1634577_s_at	FBgn0030693	10.69	10.63	10.87	10.95	10.91	10.72

1624418_s_at	FBgn0035773	12.12	12.07	12.19	12.29	12.25	12.22
1638940_at	FBgn0030808	9.05	8.99	8.9	8.76	8.9	8.94
1633260_at	---	10.61	10.55	10.46	10.84	10.6	10.56
1633729_a_at	FBgn0035060	9.34	9.28	9.27	9.36	9.29	9.31
1626332_s_at	FBgn0035397	10.89	10.83	10.95	11.03	10.85	10.8
1631376_at	FBgn0003151	11.55	11.49	11.71	11.94	11.7	11.45
1636144_s_at	FBgn0039113	9.52	9.46	9.34	9.73	9.55	9.48
1641213_s_at	FBgn0037686	13.13	13.07	13.26	13.19	13.24	13.08
1629065_s_at	FBgn0015324	11.73	11.67	11.99	11.81	11.88	11.78
1630531_at	FBgn0038853	9.08	9.02	8.85	9.01	8.92	9.14
1627014_a_at	FBgn0051305 /// FBgn003	13.43	13.37	13.39	13.4	13.41	13.39
1636262_at	FBgn0036005	9.13	9.07	8.96	8.8	8.96	8.97
1636972_at	FBgn0036096	8.73	8.67	8.84	8.84	8.82	8.76
1631368_s_at	FBgn0027567	10.63	10.57	10.37	10.34	10.44	10.43
1628340_s_at	FBgn0011640	10.89	10.83	10.9	10.84	10.92	10.88
1632649_at	FBgn0032256	8.27	8.21	8.35	8.42	8.07	8.04
1631396_at	FBgn0015553	9.87	9.81	9.9	10.06	9.8	9.71
1635825_a_at	---	10.36	10.3	10.5	10.51	10.42	10.35
1637376_at	FBgn0050109	7.9	7.84	7.26	7.3	7.32	7.47
1630477_at	FBgn0002775	9.34	9.28	8.84	9.01	9.32	9.42
1639094_at	FBgn0034626	9.63	9.57	9.07	9.21	9.66	9.71
1632581_at	FBgn0033449	8.54	8.48	8.34	8.44	8.74	8.58
1636502_at	FBgn0038649	9.05	8.99	8.95	9.16	9.07	8.94
1633885_s_at	FBgn0037955	9.34	9.28	9.45	9.4	9.36	9.23
1632196_at	FBgn0020510	9.29	9.23	9.45	9.35	9.34	9.25
1626810_at	FBgn0030434	9.78	9.72	9.53	9.6	9.82	9.8
1628987_at	---	8.86	8.8	8.97	8.99	8.96	8.87
1626112_at	FBgn0011740	9.15	9.09	9.19	9.31	9.09	9.1
1640372_at	FBgn0028693	11.59	11.53	11.56	12.04	11.59	11.26
1639585_a_at	FBgn0019957	10.76	10.7	11.08	11.01	10.96	10.74
1638050_s_at	FBgn0005612	7.36	7.3	7.86	7.11	6.88	7.23
1639526_a_at	FBgn0024329	10.07	10.01	9.99	9.88	10.14	10.02
1629472_s_at	FBgn0037688	8.53	8.47	8.4	8.58	8.56	8.53
1636002_at	FBgn0025626	9.28	9.22	9.2	9.37	9.38	9.27
1629250_at	FBgn0035720	11.38	11.32	11.19	11.28	11.28	11.32
1626762_s_at	FBgn0000316	9.62	9.56	9.88	9.85	9.72	9.56

1631359_s_at	FBgn0028670	10.91	10.85	10.68	10.65	10.88	10.76
1624557_at	FBgn0025832	9.37	9.31	9.41	9.7	9.45	9.27
1641435_at	FBgn0033482	9.88	9.81	9.82	9.73	9.85	9.83
1629107_at	FBgn0005593	13.75	13.69	13.86	13.86	13.85	13.74
1638789_at	FBgn0020439	9.63	9.57	10.22	9.55	9.45	9.23
1638751_a_at	FBgn0030418	7.6	7.54	7.52	7.88	7.48	7.45
1626688_at	FBgn0030797	7.79	7.73	7.91	7.74	7.7	7.52
1633986_at	FBgn0038815	7.5	7.43	7.89	8.09	7.79	7.88
1639354_at	FBgn0037621	9.12	9.06	9.09	9.36	9.32	9.22
1635157_at	FBgn0035889	9.38	9.32	9.11	9.14	9.2	9.39
1634817_at	FBgn0003008	9.1	9.03	9.03	9.17	9.22	9.16
1635111_s_at	FBgn0033117	8.8	8.74	8.94	8.95	9	8.89
1632594_at	FBgn0033185	7.86	7.8	7.89	8.19	8.04	7.96
1635259_at	FBgn0002787	10.76	10.7	10.81	10.88	10.83	10.65
1639678_at	FBgn0039876	9.4	9.34	8.95	9.24	9.27	9.25
1634650_at	FBgn0031213	10.36	10.29	10.3	10.39	10.18	10.12
1641336_at	FBgn0032291 /// FBgn003	7.67	7.61	7.63	7.51	7.79	7.65
1625991_s_at	FBgn0035422	13.35	13.29	13.56	13.54	13.44	13.33
1634101_at	FBgn0029905	9.58	9.52	9.51	9.52	9.42	9.42
1634992_s_at	FBgn0037636	11.81	11.75	11.74	11.69	11.73	11.66
1626170_at	FBgn0033476	9.57	9.51	9.51	9.42	9.16	9.3
1628316_at	FBgn0038608	10.07	10	10.06	10.14	10.3	10.29
1629156_at	FBgn0052782	7.42	7.36	7.13	6.93	7.12	7.46
1633026_a_at	FBgn0051158	9.68	9.61	9.5	9.33	9.52	9.64
1640608_at	FBgn0023174	11.51	11.45	11.6	11.54	11.67	11.47
1640276_a_at	FBgn0024754	9.51	9.45	9.45	9.41	9.24	9.27
1631568_a_at	FBgn0003349	7.9	7.84	8.26	7.9	7.45	7.69
1623012_at	---	9.47	9.4	9.69	9.52	9.43	9.4
1629475_at	---	10.35	10.28	10.46	10.46	10.44	10.37
1630754_at	FBgn0037110	9.29	9.22	9.2	9.31	9.49	9.38
1625646_at	FBgn0039936	11.77	11.7	11.69	11.68	11.79	11.81
1639665_at	FBgn0037549	9.16	9.1	9.47	9.18	9.25	9.21
1626818_at	FBgn0032051	9.46	9.4	9.48	9.23	9.44	9.39
1630958_at	FBgn0036805	9.03	8.97	9.07	8.97	9.04	8.92
1630342_s_at	FBgn0038268	7.54	7.48	7.37	7.63	7.43	7.54
1627054_at	FBgn0003016	9.28	9.22	9.32	9.15	9.38	9.43

1638886_at	FBgn0037722	8.4	8.33	8.5	8.54	8.57	8.45
1629871_at	FBgn0033028	9.87	9.8	9.95	9.85	9.86	9.81
1641247_at	FBgn0031051	10.01	9.94	9.84	9.93	10.04	9.93
1641445_s_at	FBgn0030894	9.35	9.28	9.07	9.26	9.37	9.15
1636999_a_at	FBgn0043070	8.43	8.37	8.22	8.3	8.42	8.29
1639748_at	---	9.68	9.62	9.33	9.42	9.22	9.32
1626465_a_at	FBgn0010303	8.3	8.24	8.21	8.23	8.31	8.22
1626209_a_at	FBgn0029785	13.74	13.67	13.92	13.85	13.81	13.73
1633400_at	---	10.94	10.87	11.08	11.04	10.91	10.89
1637390_at	FBgn0023545	10.23	10.16	10.16	10.48	10.3	10.03
1636941_at	FBgn0036398	8.7	8.64	8.7	8.13	8.44	8.68
1624310_s_at	FBgn0036622	9.77	9.7	9.79	9.73	9.88	9.8
1631055_at	FBgn0000273	8.66	8.6	8.37	8.54	8.57	8.42
1629936_at	FBgn0023519	9.99	9.92	10.01	9.91	9.97	9.97
1634433_at	---	12.17	12.11	12.1	12.32	12.38	12.13
1627806_at	FBgn0037205	7.84	7.77	8.53	8.78	8.36	8.32
1628694_a_at	FBgn0020238	12.98	12.92	13.05	13.04	12.98	12.98
1640466_s_at	FBgn0033879	11.57	11.5	11.46	11.56	11.77	11.57
1627398_a_at	FBgn0001105	11.47	11.4	11.49	11.44	11.54	11.49
1638854_s_at	FBgn0036312	9.01	8.94	9.08	8.95	8.9	8.82
1638670_a_at	FBgn0039450	9.66	9.6	9.66	9.66	9.73	9.56
1624983_s_at	FBgn0010411	14	13.93	13.95	13.96	14.03	13.94
1635567_s_at	FBgn0032794	10.91	10.85	10.78	10.7	11.04	11.09
1624792_at	FBgn0030136	13.97	13.91	14.04	14.11	14.07	13.95
1624027_at	---	8.87	8.81	8.8	8.96	8.92	8.86
AFFX-r2-P1-c	---	14.27	14.2	14.15	14.33	14.19	14.1
1638937_at	FBgn0014906	10.77	10.71	10.52	10.79	10.72	10.66
1634320_at	---	10.73	10.66	10.76	10.79	10.76	10.63
1627044_s_at	FBgn0004551	10.03	9.96	10.14	10.08	10.03	9.93
1635608_at	FBgn0016685	12.78	12.72	12.72	12.76	12.65	12.72
1626768_at	FBgn0038854	7.41	7.34	7.65	8.01	7.65	7.4
1631807_at	FBgn0037708	7.84	7.77	7.7	7.55	7.52	7.48
1638731_at	FBgn0037911	8.67	8.6	8.45	8.66	8.74	8.6
1641305_at	FBgn0004872	9.85	9.78	10.08	9.69	9.57	9.67
1641004_a_at	FBgn0025683	10.21	10.14	10.21	9.89	9.59	9.81
1628717_a_at	FBgn0002873	8.76	8.69	8.43	8.34	8.68	8.46

1629690_at	FBgn0037918	7.93	7.86	7.92	8.01	7.96	7.76
1640082_at	FBgn0036801	9.95	9.88	9.81	9.73	9.83	10.01
1625824_at	FBgn0037231	10.32	10.25	10.25	10.2	10.32	10.21
1641130_at	FBgn0028539	8.95	8.88	8.89	8.94	8.85	8.82
1624330_s_at	FBgn0032197	10.53	10.46	10.44	10.71	10.63	10.46
1628820_at	FBgn0052521	7.26	7.19	6.8	6.68	7.1	7.08
1633964_at	FBgn0029706	8.8	8.73	8.8	9.02	8.86	8.89
1640765_at	FBgn0023094	10.32	10.25	9.91	10.19	10.32	10.18
1641017_at	FBgn0024188	9.95	9.88	10.01	10.16	10.01	9.94
1633399_at	FBgn0020129	7.9	7.83	8.04	7.76	7.97	7.74
1624284_a_at	FBgn0032745	9.01	8.95	9.14	9.42	9.11	9.07
1631488_at	FBgn0031077	7.26	7.2	7.29	7.02	6.95	7.01
AFFX-r2-Bs-	---	6.86	6.8	6.37	6.71	7.01	6.78
1622907_at	---	8.29	8.22	8.38	8.3	8.31	8.11
1629287_at	FBgn0036210	6.86	6.79	6.81	7.08	7.17	7.07
1625387_s_at	FBgn0025615 /// FBgn001	8.45	8.38	8.84	8.43	8.31	8.48
1624337_at	FBgn0004404	11.86	11.79	11.9	11.88	11.87	11.58
1627046_at	FBgn0031145	9.73	9.66	9.99	10.01	9.73	9.74
1627739_at	FBgn0040286	12.03	11.96	11.91	11.83	11.82	11.77
1623919_a_at	FBgn0038476	12.51	12.44	12.54	12.68	12.55	12.44
1635461_at	FBgn0034988	7.96	7.89	8.03	7.86	7.84	7.8
1629356_at	FBgn0019938	9.89	9.82	10.12	9.64	9.88	9.9
1623189_at	FBgn0035001	9.98	9.91	9.94	9.7	9.84	9.81
1635846_a_at	FBgn0004882	11.16	11.09	11.16	10.99	10.97	11.23
1632026_at	FBgn0028515	8.92	8.86	9.19	9.14	8.99	8.88
1635631_a_at	FBgn0027505	7.69	7.62	7.8	7.92	7.65	7.52
1627488_at	FBgn0038206	10.12	10.05	9.78	9.88	10.25	10.21
1631632_s_at	FBgn0000182	12.55	12.48	12.28	12.37	12.3	12.3
1627942_at	FBgn0038741	7.91	7.84	7.82	7.84	8.2	8.07
1630830_a_at	FBgn0037723	8.51	8.44	8.31	8.25	8.28	8.21
1631598_at	FBgn0029892	8.07	8	8.11	8.36	7.78	7.17
1631390_at	FBgn0038876	8.28	8.21	7.93	7.95	8.16	8.21
1638691_at	FBgn0052202	8.38	8.31	8.39	8.81	8.58	8.52
1634419_at	FBgn0031312	9.86	9.79	9.45	9.77	9.67	9.77
1627209_at	FBgn0030556	9.23	9.16	9.51	9.44	9.39	9.2
1616608_a_at	FBgn0001128	10.5	10.43	10.34	10.57	10.81	10.64

1629974_at	FBgn0011836	8.28	8.21	8.37	8.46	8.39	8.13
1640366_at	FBgn0038058 /// FBgn005	8.08	8.01	8.06	8.23	8.1	7.9
1634509_s_at	FBgn0004373	8.9	8.83	9.04	8.76	8.89	8.83
1635205_at	FBgn0037446	9.56	9.49	9.48	9.71	9.75	9.69
1623708_at	FBgn0039672	9.07	9	9.51	9.5	9.16	9
1628214_at	FBgn0017429	9.35	9.28	9.56	9.37	9.45	9.38
1628129_a_at	FBgn0052823 /// FBgn002	9.48	9.41	9.53	9.64	9.61	9.37
1634804_at	FBgn0031919	7.49	7.42	7.71	7.35	7.28	7.55
1631318_at	---	9.86	9.79	10.14	10.02	10.02	9.82
1636379_a_at	FBgn0020129	7.1	7.03	7.31	6.94	7.1	6.93
1623584_at	FBgn0032745	9.65	9.58	9.66	9.65	9.51	9.45
1635267_s_at	FBgn0035936	9.61	9.54	9.05	9.5	9.23	9.38
1628928_s_at	FBgn0025286	13.76	13.69	13.91	13.88	13.86	13.76
1641160_s_at	FBgn0037262	9.13	9.06	9.05	9.24	9.12	9.07
1630157_a_at	FBgn0030991	10.87	10.8	10.79	10.63	10.77	10.86
1627623_s_at	FBgn0000181	7.17	7.1	7.2	6.76	7.15	7.11
1623516_s_at	---	9.33	9.26	8.96	9.07	9.15	9.1
1636433_at	FBgn0030000	7.21	7.14	7.47	7.49	7.41	7.09
1636896_a_at	FBgn0031190	9.62	9.55	9.4	9.45	9.59	9.42
1637085_at	FBgn0013762	9.04	8.97	9.05	9.52	9.22	9.09
1628563_at	FBgn0053181	9.27	9.2	9.08	9.1	9.06	9.16
1636541_at	FBgn0042641	9.08	9.01	9.13	9.27	9.27	9.18
1633765_at	---	9.12	9.05	9.6	9.09	8.89	8.7
1624986_at	FBgn0037637	9.52	9.45	9.69	9.57	9.57	9.44
1626980_at	FBgn0025574	8.37	8.3	8.22	8.26	8.49	8.62
1624079_a_at	FBgn0039966	8.82	8.75	8.61	8.81	8.92	8.85
1640602_s_at	FBgn0042693	9.61	9.54	9.75	9.68	9.58	9.45
1628389_at	FBgn0038376	8.68	8.61	8.66	8.71	8.61	8.37
1624252_s_at	FBgn0037811 /// FBgn003	10.57	10.5	10.65	10.67	10.57	10.38
1636598_s_at	FBgn0040395	9.02	8.95	8.91	9.05	9.09	8.89
1637558_at	FBgn0033755	8.76	8.69	8.96	8.76	8.76	8.66
1628486_a_at	FBgn0033015	10.65	10.58	10.52	10.63	10.82	10.7
1636831_s_at	FBgn0000212	10.31	10.24	10.29	10.27	10.4	10.27
1640877_at	FBgn0031321	8.74	8.67	8.54	8.85	8.9	8.8
1626228_a_at	FBgn0034187	9.93	9.86	9.43	9.64	9.68	9.87
1632277_a_at	FBgn0026428	8.94	8.86	8.82	8.86	8.85	8.64

1624564_s_at	FBgn0004403	13.73	13.66	13.66	13.75	13.74	13.63
1639507_at	FBgn0037873	10.67	10.6	10.65	10.31	10.52	10.6
1637881_at	FBgn0032704	10.44	10.37	10.33	10.37	10.46	10.36
1625931_at	FBgn0040230	8.51	8.44	8.42	8.28	8.55	8.68
1641126_at	FBgn0030364	10.31	10.24	10.59	10.52	10.55	10.48
1629055_a_at	FBgn0031380	12.32	12.25	12.29	12.41	12.38	12.21
1624474_at	FBgn0038388	10.33	10.26	9.97	10.08	10.2	10.09
1629606_at	FBgn0035169	9.92	9.85	9.77	9.88	9.95	9.85
1633261_a_at	FBgn0031764	8.65	8.58	8.95	8.79	8.77	8.7
1628976_at	FBgn0031043	10.05	9.97	9.98	9.75	10.01	10.1
1625692_s_at	FBgn0034649	9.27	9.19	9.25	9	9.11	8.95
1639092_at	FBgn0039489	8.51	8.43	8.28	8.62	8.61	8.6
1631907_at	FBgn0036198	9.39	9.31	9.22	9.28	9.33	9.32
1627723_at	FBgn0037883	7.65	7.58	8.24	8.12	8.01	7.93
1639992_at	FBgn0038270	8.71	8.64	8.58	8.95	8.75	8.62
1626808_s_at	FBgn0014020	10.9	10.83	11.17	11.09	11.08	11.03
1637727_at	FBgn0035102	8.38	8.3	8.24	8.36	8.4	8.21
1633381_at	FBgn0030096	8.85	8.77	8.93	8.98	8.84	8.71
1632343_at	FBgn0020764	9.65	9.58	9.81	9.6	9.59	9.46
1641673_at	FBgn0027495	7.84	7.77	7.41	7.72	7.88	7.8
AFFX-Dros-e	FBgn0001942	13.05	12.98	13.13	13.11	13.07	12.99
1631973_at	FBgn0003022	10.6	10.52	10.56	10.68	10.87	10.63
1623926_at	FBgn0031242	10.26	10.19	10.24	10.01	10.11	10.19
1638412_at	---	8.19	8.12	8.16	8	8.22	8.09
1638070_at	---	9.56	9.49	9.65	9.4	9.52	9.5
1634362_a_at	---	11.12	11.05	10.92	10.71	10.9	10.99
1628603_at	FBgn0036825	13.69	13.61	13.82	13.81	13.81	13.68
1627465_at	FBgn0034726	9.21	9.13	9.35	9.46	9.53	9.38
1632962_at	FBgn0031980	13.7	13.62	13.84	13.87	13.8	13.73
1634133_at	FBgn0036920	9.59	9.52	9.57	9.71	9.67	9.57
1640527_at	---	10.75	10.68	10.81	10.73	10.61	10.62
1636837_at	FBgn0052179	9.22	9.15	9.24	9.02	9.23	9.25
1635248_at	FBgn0036267	8.57	8.49	8.29	8.47	8.17	8.37
1627983_at	FBgn0002506	10.07	10	10.45	10.6	10.26	10.06
1624165_a_at	FBgn0019947	9.32	9.24	9	8.96	9.21	9.26
1627634_at	FBgn0034398	11.51	11.44	11.48	11.6	11.72	11.59

1624504_s_at	FBgn0027786	10.36	10.29	10.38	10.32	10.5	10.39
1638871_at	---	10.78	10.7	10.52	10.59	10.55	10.59
1632158_a_at	FBgn0039066	9.11	9.04	8.84	9.05	9	8.94
1640051_s_at	FBgn0000258	12.5	12.43	12.53	12.54	12.53	12.52
1632763_at	FBgn0033974	9.43	9.36	9.52	9.62	9.63	9.47
1634281_at	FBgn0033556	9.28	9.2	9.47	9.67	9.54	9.41
1628547_at	FBgn0038038	8.69	8.61	8.6	8.7	8.38	8.3
1641502_a_at	FBgn0037063	9.35	9.27	8.89	9.22	9.31	9.24
1632438_at	FBgn0037372	9.36	9.28	9.17	9.59	9.21	9.11
1634530_at	FBgn0036608	7.48	7.4	7.16	7.29	7.29	7.17
1639544_at	FBgn0031008	9.97	9.89	10.18	10	10.27	10.07
1630717_s_at	FBgn0000289	9.87	9.8	9.81	9.7	9.94	9.98
1635527_at	---	8.18	8.1	8.21	7.91	8.02	8.01
1629373_at	FBgn0036994	9.49	9.42	8.98	9.24	9.49	9.42
1637015_s_at	FBgn0020255	12.21	12.13	12.21	12.31	12.17	12.02
1641332_at	FBgn0037074	7.18	7.1	7.02	6.99	7.22	7.16
1634823_at	FBgn0030572	9.43	9.35	9.66	9.68	9.42	9.35
1639692_s_at	FBgn0000462	9.47	9.4	9.59	9.8	9.56	9.44
1635745_a_at	FBgn0028479	10.97	10.9	11.16	11.26	11.09	10.75
1635903_at	FBgn0014006	9.42	9.34	9.28	9.31	9.35	9.28
1637623_at	---	10.75	10.67	10.59	10.61	10.3	10.38
1639551_at	FBgn0026262	10.63	10.55	10.35	10.28	10.41	10.46
AFFX-Dros-A	FBgn0000043	9.91	9.84	9.68	9.1	9.81	9.68
1627433_at	FBgn0034961	8.91	8.83	8.93	9.08	9.07	8.94
1624318_at	FBgn0010339	10.66	10.58	10.77	10.61	10.81	10.76
1639968_at	FBgn0033972	9.28	9.2	9.14	9.24	9.23	9.07
1639607_at	FBgn0037674	8.31	8.24	8.38	8.33	8.35	8.25
1635981_a_at	FBgn0037245	12.75	12.68	12.66	12.81	12.6	12.6
1625650_at	FBgn0037313	10.22	10.14	10.15	10.27	10.39	10.22
1632632_at	FBgn0028535	9.53	9.45	9.3	9.8	9.42	9.18
1630417_at	FBgn0010905	8.42	8.34	8.3	8.37	8.43	8.43
1637771_s_at	FBgn0033544	9.59	9.51	9.4	9.27	9.52	9.52
1627423_at	FBgn0039156	9.43	9.35	9.36	9.62	9.35	9.15
1639257_s_at	FBgn0037239	9.41	9.33	9.3	9.29	9.23	9.21
1628041_a_at	---	11.73	11.65	11.81	11.88	11.85	11.75
1624775_at	FBgn0032818	8.78	8.7	8.71	8.55	8.75	8.64

1628481_at	FBgn0037566	9.65	9.57	9.93	10.03	9.85	9.73
1632458_at	FBgn0033156	9.85	9.77	9.78	10.1	10.03	9.8
1637911_at	FBgn0030122	9.74	9.67	9.58	9.84	9.56	9.34
1633650_at	FBgn0038951	7.82	7.74	7.78	7.6	7.76	7.66
1632710_s_at	FBgn0038738	10.55	10.48	10.56	10.66	10.49	10.43
1640069_at	FBgn0034232	10.35	10.27	10.35	10.41	10.21	10.18
1640227_at	FBgn0028473	11.42	11.35	11.56	11.44	11.7	11.37
1636140_at	FBgn0031598	7.68	7.6	7.43	7.73	7.72	7.62
1639914_at	FBgn0038056	9.24	9.17	9.1	8.91	9.29	9.11
1628175_at	FBgn0037814	9.86	9.78	9.67	9.87	9.78	9.83
1632413_at	FBgn0032248	9.29	9.21	9.3	9.41	9.38	9.3
1631546_at	FBgn0034791	9.88	9.8	10	9.96	9.96	9.79
1640146_at	---	9.74	9.66	9.66	9.56	9.78	9.81
1630981_at	FBgn0037536	10.14	10.06	9.86	9.84	10.14	10.1
1636510_a_at	FBgn0039114	7.32	7.24	7.63	7.22	7.55	6.99
1641511_at	---	10.06	9.98	9.91	9.85	9.98	9.93
1634294_s_at	FBgn0030089	8.44	8.36	8.15	8.19	8.48	8.31
1636273_at	FBgn0033083	8.97	8.89	8.96	9.02	9.06	9.02
1624041_at	FBgn0033260	9.99	9.91	9.9	9.97	9.95	9.87
1636327_at	FBgn0051852	8.99	8.91	9.08	9.17	9.18	8.94
1631374_at	FBgn0024248	8.4	8.32	8.52	8.56	8.44	8.3
1636346_at	FBgn0036124	9.2	9.12	9.34	9.15	9.14	9.13
1632586_at	FBgn0036671	8.98	8.91	8.9	9	8.99	8.92
AFFX-r2-Dro	FBgn0001128	11.28	11.2	11.03	11.36	11.55	11.28
1624191_at	---	9.16	9.08	8.67	8.8	9.12	9.18
1624019_s_at	FBgn0002579	14.09	14.01	13.98	13.99	14.04	13.93
1634036_at	---	10.11	10.03	9.69	9.99	10	9.82
1635120_at	FBgn0034089	9.65	9.57	10.1	9.76	9.54	9.5
1641150_at	FBgn0027936	10.93	10.85	10.78	10.78	10.81	10.76
1633505_at	FBgn0039541	9.25	9.17	9.1	9.29	9.27	8.89
1637024_at	FBgn0028662	11.45	11.37	11.27	11.32	11.45	11.42
1641092_at	FBgn0035960	7.21	7.13	7.36	7.38	7.47	7.22
1626006_at	FBgn0010269	9.91	9.83	9.63	9.55	9.89	9.82
1641244_at	FBgn0011297 /// FBgn001	8.52	8.44	8.49	8.54	8.43	8.34
1633830_at	FBgn0032787	8.33	8.25	8.16	8.19	8.14	8.07
1630943_at	FBgn0036718	7.83	7.75	7.95	8.03	7.93	7.71

1639255_s_at	FBgn0027580	11.32	11.24	11.38	11.35	11.22	11.06
1629984_s_at	---	14.33	14.25	13.99	14.08	14.24	14.15
1629648_s_at	---	7.93	7.85	7.82	7.64	7.75	7.78
1628562_s_at	FBgn0002781	9.19	9.11	9.08	9.09	9.17	9.08
1637317_at	---	10.58	10.5	10.39	10.62	10.77	10.62
1641449_at	FBgn0034246	8.89	8.81	9.19	8.96	8.87	8.96
1636551_at	FBgn0037822 /// FBgn002	9.52	9.44	9.67	9.56	9.44	9.42
1625595_a_at	FBgn0030670	8.94	8.86	8.68	8.58	8.99	8.94
1633905_at	FBgn0035422	8.02	7.94	8.23	6.6	7.26	7.77
1634625_at	FBgn0027453	9.41	9.33	9.1	9.16	9.35	9.28
1628922_s_at	FBgn0015562	9.03	8.95	8.59	8.61	9.14	9.06
1636693_at	FBgn0030452	7.3	7.22	7.16	7.05	7.61	7.31
1635740_at	FBgn0015737	9.9	9.82	9.88	9.64	9.87	9.81
1626261_s_at	FBgn0033393	11.35	11.27	11.24	11.1	11.33	11.25
1632395_s_at	FBgn0028671	9.35	9.27	9.32	9.42	9.39	9.18
1641624_at	FBgn0051957	9.4	9.32	9.56	9.61	9.49	9.53
1636499_at	FBgn0039144	8.57	8.49	8.4	8.61	8.69	8.51
1641548_at	FBgn0035688	8.64	8.55	8.9	8.86	8.65	8.57
1629552_at	FBgn0027872	9.6	9.52	9.33	9.36	9.64	9.63
1623090_at	---	8	7.92	8.1	8.38	8.28	8.11
1623858_at	FBgn0027785	10.58	10.5	10.77	10.72	10.69	10.49
1632707_at	---	7.59	7.51	7.79	7.84	7.55	7.45
1635755_a_at	FBgn0036373	7.69	7.61	7.6	7.73	7.82	7.55
1640281_s_at	FBgn0035151	8.24	8.16	8.02	8.39	8.5	8.53
1636196_s_at	FBgn0030955 /// FBgn003	9.12	9.03	9.63	9.05	8.95	9.15
1630946_at	FBgn0004145	11.96	11.88	12.46	11.92	11.75	11.92
1635363_a_at	FBgn0032979 /// FBgn005	11.75	11.66	11.56	11.59	11.65	11.59
1634898_a_at	FBgn0027950	9.13	9.04	8.93	9.19	9.27	9.17
1625566_a_at	FBgn0032516	9.3	9.22	9.05	9.38	9.57	9.39
1635907_at	FBgn0037135	11.41	11.33	11.67	11.56	11.56	11.21
1630639_at	FBgn0039528	8.62	8.54	8.79	8.44	8.28	8.5
1623588_at	FBgn0024556	10.55	10.47	10.78	10.72	10.63	10.46
1630373_at	FBgn0028897	7.9	7.82	7.62	7.93	8.06	7.87
1627461_at	FBgn0032679	9.22	9.14	9.88	9.5	9.35	9.21
1637716_a_at	FBgn0003498	11.5	11.42	11.5	11.61	11.35	11.46
1631585_a_at	FBgn0033471	9.16	9.08	9.21	9.09	9.08	9.06

1640351_s_at	FBgn0038771	10.3	10.22	10.39	10.49	10.45	10.28
1640454_at	FBgn0027493	11.06	10.98	11.14	11.04	11.13	10.95
1624132_at	FBgn0035980	8.32	8.23	8.67	8.87	8.26	8.26
1637448_s_at	---	13.73	13.64	13.82	13.78	13.82	13.71
1630672_at	FBgn0013432	9.52	9.43	9.67	9.37	9.58	9.51
1633312_at	FBgn0037958	8.99	8.91	8.88	9.12	9.14	8.97
1639403_s_at	FBgn0029891	9.05	8.96	9.06	9.1	8.94	8.85
1623724_at	---	8.46	8.38	8.97	8.73	8.38	8.34
1634757_a_at	FBgn0014184	12.39	12.31	12.45	12.35	12.45	12.46
1640925_at	FBgn0034360	7.68	7.59	7.63	7.81	7.85	7.7
1635528_s_at	FBgn0031035	13.67	13.59	13.79	13.75	13.82	13.65
1623324_at	FBgn0002552	9.15	9.06	8.94	9.25	9.22	9.18
1637815_s_at	FBgn0044323	9.52	9.43	9.58	9.42	9.6	9.41
1626805_s_at	FBgn0011253	10.01	9.93	10.13	10.13	10.05	10.03
1635670_at	FBgn0031244	9.04	8.95	8.84	8.7	8.93	8.8
1628686_a_at	FBgn0003559	7.51	7.42	7.65	7.49	7.43	7.35
1638224_at	---	9	8.92	8.55	9.04	8.82	8.73
1628775_s_at	FBgn0024939	14.2	14.11	14.07	14.03	14.17	14.07
1637564_a_at	FBgn0038950	9.26	9.18	8.66	8.99	9.1	8.99
1626156_at	FBgn0032761	8.42	8.34	8.11	8.31	8.4	8.26
1630270_s_at	FBgn0020910	13.62	13.53	13.66	13.62	13.65	13.59
1637610_at	---	10.39	10.3	10.21	10.63	10.55	10.42
1632526_s_at	---	9.57	9.48	9.58	9.6	9.63	9.59
1625147_at	FBgn0039725	9.17	9.09	8.79	8.91	9.21	9.22
1628915_s_at	FBgn0027593	7.49	7.4	7.79	7.14	7.51	7.61
1629950_at	FBgn0030061	8.96	8.88	8.98	8.86	9.07	8.91
1640237_a_at	FBgn0001978	10.32	10.23	10.34	10.15	10.4	10.29
1632410_at	FBgn0035372	8.82	8.73	8.59	8.57	8.84	8.73
1635469_at	FBgn0037560	6.62	6.53	7.02	7.13	7.2	6.96
1627713_at	FBgn0030854	10.6	10.52	10.5	10.55	10.63	10.56
1634442_at	FBgn0003444	10.12	10.03	9.64	9.75	9.78	9.87
1641378_at	FBgn0028579	8.9	8.82	8.72	8.85	8.81	8.71
1630695_at	FBgn0039909	10.47	10.38	10.72	10.49	10.31	10.41
1628080_at	FBgn0030013	9.7	9.62	9.62	9.76	9.85	9.72
1640174_at	FBgn0025582	11.54	11.46	11.69	11.68	11.75	11.49
1635219_at	FBgn0039538	8.38	8.3	8.17	8.24	8.48	8.33

1640430_s_at	---	10.23	10.15	10.29	10.39	10.47	10.29
1635479_a_at	FBgn0052056	9.14	9.05	8.69	8.93	9.36	9.13
1631434_at	---	10.89	10.8	10.9	11.14	10.88	10.81
1629715_at	FBgn0037551	9.23	9.14	9.17	9	9.43	9.33
1637825_at	FBgn0033178	8.46	8.38	8.39	8.3	8.33	8.23
1628216_at	---	9.58	9.49	9.8	9.6	9.59	9.58
1626366_at	FBgn0027945	9.62	9.53	9.79	9.74	9.87	9.73
1627399_at	FBgn0033089	9.17	9.08	9.1	9.15	9.1	9.01
1627402_a_at	---	12.01	11.93	12.03	12.03	12.07	11.96
1636527_at	---	8.12	8.03	7.53	7.56	8.14	7.97
1633036_s_at	FBgn0052495 /// FBgn003	8.9	8.82	9.01	8.81	8.61	8.61
1629077_s_at	FBgn0037443	10.29	10.2	10.12	9.83	10.19	10.04
1630396_at	FBgn0038787	9.5	9.42	9.62	9.56	9.45	9.38
1637819_at	FBgn0032341	8.15	8.07	8.1	7.95	8.1	8.03
1630813_at	---	14.06	13.98	14.02	14.06	14.11	14
1640169_s_at	FBgn0001215	11.95	11.86	12.04	11.83	12.1	12.04
1627605_at	FBgn0024371	10.66	10.57	10.32	10.68	10.81	10.82
1637118_at	---	7.79	7.7	7.89	7.85	7.8	7.73
1631738_at	FBgn0032499	8.18	8.09	8.25	8.45	8.14	8.07
1636380_at	FBgn0024245	8.21	8.13	8.32	8.53	8.45	8.08
1627711_at	FBgn0010350	9.69	9.6	9.42	9.33	9.51	9.49
1638516_s_at	FBgn0032196	10.6	10.51	10.53	11.28	10.9	10.62
1637773_s_at	FBgn0036650	9.38	9.29	9.3	9.24	8.96	9.2
1632396_at	FBgn0033528	9.6	9.51	9.5	9.58	9.75	9.56
1640637_at	FBgn0036761	9.42	9.34	9.19	9.5	9.56	9.49
1630093_at	---	13.89	13.8	13.99	13.95	13.93	13.81
1629644_s_at	FBgn0039532	9.54	9.45	9.28	9.26	9.68	9.48
1637531_at	FBgn0030038	10.59	10.5	10.16	10.16	10.53	10.26
1623626_a_at	FBgn0024362	9.58	9.49	9.46	9.36	9.45	9.51
1632954_at	---	8.69	8.6	8.45	8.64	8.67	8.53
1625942_s_at	FBgn0011202	9.3	9.21	9	8.98	9.33	9.37
1632700_a_at	FBgn0033905	7.4	7.31	7.25	6.38	7.35	7.28
1624665_at	FBgn0032916	9.4	9.31	9.12	8.95	9.55	9.52
1631724_s_at	FBgn0035425	10.79	10.7	10.65	10.72	10.66	10.55
1624484_a_at	FBgn0015602	10.37	10.28	10.3	10.37	10.5	10.44
1622937_at	FBgn0036773	8.36	8.27	8.23	8.08	8.24	8.3

1625758_s_at	FBgn0025140	10.2	10.11	10.23	9.95	10.11	10.05
1628774_a_at	---	8.81	8.72	8.49	8.69	8.97	8.86
1629692_at	FBgn0034578	7.94	7.85	7.87	8.05	7.84	7.88
1634386_s_at	FBgn0016701	10.13	10.04	10.08	10.07	10.17	10.12
1633153_at	FBgn0031952	7.24	7.15	7.46	7.5	7.25	7.12
1628101_s_at	FBgn0030693	10.09	10	10.09	10.16	10.37	10.25
1635103_at	FBgn0023518	8.88	8.79	8.58	8.5	8.79	8.77
1634298_at	FBgn0031987	9.33	9.24	9.26	9.76	9.31	9.25
1641721_a_at	FBgn0039406	12.17	12.08	12.37	12.26	12.36	12.14
1630316_a_at	FBgn0023515	10.62	10.53	10.33	10.51	10.7	10.64
1623150_at	FBgn0003274	14.36	14.26	14.17	14.24	14.34	14.16
1623997_s_at	FBgn0038834	13.54	13.45	13.67	13.59	13.61	13.47
1640695_at	FBgn0039304	9.02	8.93	8.9	9.02	9.05	9.15
1633767_at	FBgn0037701	11.16	11.07	11.16	11.09	11.07	10.93
1641598_at	FBgn0041087	10.19	10.1	9.94	9.79	10.23	10.12
1635521_at	FBgn0035589	8.76	8.66	8.79	8.81	8.84	8.64
1630768_s_at	FBgn0033749 /// FBgn003	6.7	6.6	6.6	6.91	7.05	6.8
1630398_at	FBgn0032394	9.66	9.57	9.57	9.42	9.41	9.39
1628169_at	FBgn0039555	9.96	9.86	10.11	10.13	9.88	9.7
1625607_s_at	FBgn0011708	10.35	10.26	10.18	10.15	10.4	10.37
1638547_s_at	FBgn0035244	9.19	9.1	8.94	8.97	9.18	9
1625849_at	FBgn0029133	11.73	11.63	11.8	11.83	11.84	11.64
1632888_s_at	FBgn0032863 /// FBgn005	7.05	6.96	6.89	7.2	7.13	6.94
1625211_s_at	FBgn0025394	9.15	9.06	9.07	8.84	8.99	9.13
1639037_at	FBgn0035038	8.82	8.72	8.8	9.06	8.91	8.83
1630572_at	FBgn0011570	10.11	10.02	10.06	9.95	10.21	10.08
1630696_at	FBgn0037076	7.38	7.29	7.83	7.8	7.66	7.78
1632213_s_at	FBgn0038381	8.25	8.16	8.04	8.2	8.65	8.43
1625127_at	FBgn0004656	10.34	10.25	10.23	9.98	10.13	10.3
1635388_s_at	FBgn0010408	14.31	14.22	14.12	14.16	14.29	14.12
1637584_at	---	8.78	8.68	8.78	9.05	8.78	8.8
1625533_at	FBgn0000229	8.98	8.89	8.94	8.82	8.47	8.62
1637165_at	FBgn0038925	10.97	10.88	11.01	10.95	11.12	10.99
1624145_a_at	FBgn0028372	8.54	8.45	8.17	8.52	8.62	8.47
1640233_at	FBgn0034345	10.35	10.25	10.58	10.04	10.36	10.25
1624664_at	---	7.62	7.53	6.91	7.28	7.54	7.54

1636813_s_at	FBgn0038271	11.43	11.34	11.35	11.38	11.56	11.31
1626178_s_at	FBgn0036518	7.4	7.31	7.38	7.01	7.35	7.73
1628824_s_at	FBgn0029797	8.49	8.39	8.02	7.88	8.18	8.41
1630151_at	---	7.29	7.2	7.12	7.72	7.4	7.29
1631763_at	---	7.78	7.69	7.72	7.79	7.58	7.42
AFFX-r2-P1-	---	14.05	13.95	13.87	14.06	13.93	13.8
1622939_at	FBgn0020497	10.24	10.15	10.68	10.39	10.37	10.53
1638726_at	FBgn0010808	9.9	9.81	9.84	9.86	10.07	9.86
1623510_at	FBgn0035252	10.13	10.03	10.18	9.61	10.39	9.92
1641440_a_at	FBgn0036624	8.81	8.71	8.87	8.89	8.75	8.71
1628291_at	FBgn0039336	8.1	8.01	8.08	8.25	8.32	8.2
1639307_at	FBgn0038182	9.02	8.93	9.07	8.94	8.92	8.88
1631116_at	FBgn0015621	9.13	9.03	8.99	9.19	9.35	9.17
1638942_at	FBgn0050499	11.39	11.3	11.27	11.64	11.42	11.29
1631813_at	FBgn0029885	9.69	9.59	9.81	9.58	9.74	9.59
1638664_s_at	FBgn0001942	13.2	13.11	13.27	13.23	13.25	13.16
1639057_at	FBgn0036557	9.47	9.37	9.8	9.68	9.7	9.54
1640754_at	FBgn0036449	10.11	10.01	10.09	10.12	10.09	9.92
1625678_at	---	7.17	7.08	7.02	7.22	7.25	7
1633960_at	FBgn0038515	10.48	10.39	10.42	10.57	10.61	10.45
1627151_at	FBgn0035016	9.68	9.58	9.64	9.7	9.58	9.58
1628665_at	FBgn0036828	8.74	8.65	8.74	9.11	8.86	8.57
1635712_at	FBgn0030320	9.43	9.34	9.39	9.63	9.73	9.61
1637494_at	FBgn0023527	10.68	10.59	10.15	10.18	10.6	10.49
1633559_at	FBgn0033906	11.11	11.02	11.19	10.85	11.12	10.93
1634457_at	FBgn0031070	7.47	7.38	7.29	7.58	7.64	7.33
1637520_at	FBgn0031149	10.49	10.39	10.65	10.5	10.4	10.35
1624607_at	---	10.41	10.32	10.37	10.32	10.42	10.26
1630308_at	FBgn0029824	8.11	8.02	8.49	8.44	8.29	8.07
1634614_at	FBgn0023532	8.22	8.12	8.1	7.92	8.24	8.04
1627927_at	FBgn0034087	9.69	9.6	10.13	9.9	9.52	9.64
1626016_s_at	FBgn0011716	8.48	8.38	8.6	8.59	8.49	8.47
1635234_at	---	10.32	10.22	10.32	10.73	10.48	10.16
1632278_s_at	FBgn0050190	8.42	8.32	8.36	8.83	8.58	8.31
1624291_at	FBgn0036062	8.74	8.65	8.53	8.64	8.75	8.78
1626239_at	---	8.76	8.66	9.03	8.97	9.05	9.04

1623888_at	FBgn0039281	9.13	9.03	9.3	9.2	9.1	9.06
1626696_at	FBgn0000629	8.74	8.64	8.65	8.79	8.8	8.7
1636664_at	FBgn0037405	9.13	9.03	8.6	5.89	6.18	9.07
1641498_at	FBgn0037573	10.66	10.56	10.6	10.67	10.64	10.59
1626509_at	---	8.27	8.18	8.52	7.9	7.56	8.22
1623914_at	FBgn0017579	13.79	13.69	13.85	13.83	13.88	13.77
1632323_at	FBgn0038666	7.52	7.42	7.58	7.52	7.59	7.48
1629541_at	FBgn0040751	8.32	8.22	8.38	8.49	8.19	8.13
1631663_at	FBgn0039159	9.69	9.59	9.68	9.48	9.56	9.47
1639411_at	FBgn0052742	10.07	9.98	10.08	10.13	10.18	10.01
1633247_at	FBgn0039233	9.94	9.84	9.98	9.85	9.9	9.78
1631704_at	FBgn0039223	8.82	8.72	8.87	8.92	9.08	8.91
1639279_a_at	---	9.52	9.42	9.69	9.54	9.4	9.46
1632665_a_at	FBgn0030648	9.65	9.55	9.33	9.26	9.39	9.38
1626964_at	---	14.06	13.96	13.95	14.05	14.1	13.95
1639846_at	FBgn0040375	8.07	7.97	7.43	7.58	8.17	8.1
1640595_at	FBgn0036514	8.99	8.89	8.98	8.71	8.96	8.89
1639513_at	FBgn0037891	10.02	9.92	10.16	10.15	10.19	10.05
1633005_at	FBgn0029737	8.87	8.77	8.73	8.77	8.88	8.63
1639718_at	FBgn0042205	7.39	7.29	7.29	7.77	7.49	7.36
1632308_at	FBgn0032691	7.75	7.65	7.81	8.03	7.87	7.75
1638457_at	FBgn0037969	10.51	10.42	10.2	10.21	10.43	10.36
1635970_at	FBgn0028402	9.02	8.92	8.9	8.96	8.92	8.78
1627191_a_at	FBgn0000578	9.29	9.19	9.04	9.29	9.05	9.09
1640298_at	FBgn0030645	7.85	7.76	7.66	7.63	7.72	7.52
1641494_at	FBgn0034066	10.15	10.05	9.96	10.33	10.13	10.02
1641157_at	FBgn0033421	8.69	8.59	9.07	8.81	8.97	9.03
1627491_at	FBgn0001104	10.93	10.83	10.82	10.79	10.78	10.81
1632836_at	FBgn0052632	8.15	8.05	7.69	7.4	8.04	7.98
1624372_at	FBgn0031376	10.16	10.06	10.01	9.95	10.16	10.13
1634148_at	FBgn0036620	8.49	8.4	8.05	7.49	8.24	8.45
1634925_at	FBgn0030503	8.33	8.23	8.11	8.1	8.02	8.03
1624668_s_at	---	9.2	9.1	9.46	9.49	9.27	9.13
1628251_at	FBgn0053054	7.96	7.86	7.87	7.92	7.72	7.62
1624289_at	FBgn0036366	9.35	9.25	9.1	9.29	9.32	9.29
1633091_at	FBgn0030063	9.03	8.93	8.98	8.94	9.16	9.01

1636246_a_at	FBgn0036090	9.23	9.13	9	8.97	9.23	9.18
1626523_a_at	---	10.04	9.93	10.21	10.07	10.06	9.95
1629741_at	---	7.37	7.27	7.17	7.35	7.41	7.4
1631876_at	FBgn0028860	9.16	9.06	9.24	9.73	9.21	9.01
1623571_a_at	FBgn0032886	8.62	8.52	8.8	8.67	8.68	8.58
1623356_at	FBgn0037312	9.67	9.57	9.43	9.62	9.6	9.51
1625876_at	FBgn0039132	11.16	11.06	11.18	11.46	11.36	11.24
1635437_at	FBgn0039274	9.72	9.61	10	9.97	9.96	9.95
1639136_s_at	FBgn0004399	10.36	10.26	10.02	10.07	10.29	10.22
1632516_at	FBgn0031991	8.93	8.83	8.83	8.88	9	8.74
1631001_s_at	FBgn0034685	10.2	10.1	9.91	10.36	10.24	10.05
1634899_a_at	FBgn0036702	9.51	9.41	9.55	9.6	9.54	9.36
1630351_at	FBgn0051229	8.94	8.84	9.22	9.04	9.03	8.82
1640547_at	---	7.75	7.65	8.22	7.59	7.15	7.37
1626637_a_at	---	10.05	9.95	9.68	9.64	9.8	9.83
1626584_a_at	---	9.57	9.46	9.3	9.4	9.49	9.47
1637428_a_at	FBgn0003177	10.51	10.41	10.3	10.35	10.48	10.43
1632956_at	FBgn0040337	9.36	9.26	9.15	9.36	9.31	9.2
1629730_at	---	10.77	10.67	10.84	10.49	10.55	10.52
1640150_s_at	FBgn0033555 /// FBgn001	13.6	13.5	13.64	13.67	13.67	13.53
1639950_at	FBgn0036897	9.19	9.09	8.93	9.11	9.22	9.09
1630698_at	FBgn0029888	10.14	10.04	10.42	10.12	10.13	10.01
1628669_at	FBgn0034617	8.82	8.72	8.97	9.13	9.17	8.89
1629614_at	FBgn0051549	11.23	11.13	11.04	11.26	11.02	10.94
1637482_at	FBgn0015360	9.74	9.64	9.61	9.59	9.66	9.67
1626930_at	FBgn0027582	8.99	8.89	8.83	8.94	8.96	8.94
1638829_s_at	FBgn0002781	8	7.9	7.76	7.62	8.26	8.12
1638708_s_at	FBgn0037444	7.21	7.11	7.39	6.97	7.05	7
1630437_s_at	FBgn0034418	9.77	9.66	9.65	9.59	9.79	9.7
1624083_s_at	FBgn0005278	12.73	12.63	12.73	12.53	12.53	12.48
1635633_s_at	FBgn0033073	10.49	10.38	10.47	10.58	10.57	10.41
1639288_at	FBgn0033379	8.87	8.77	9.17	9.16	8.91	8.77
1627101_at	FBgn0041094	9.99	9.89	10.02	10.13	9.87	9.91
1640762_at	---	12.12	12.01	11.78	12.02	12.21	11.99
1637874_at	---	8.3	8.2	8.19	8.36	8.33	8.15
1628557_at	FBgn0033400	9.29	9.19	9.13	9.29	9.41	9.29

1632654_at	FBgn0032762	9.11	9.01	9.56	8.98	9.09	9.21
1635279_at	FBgn0040078	9.85	9.74	9.92	9.92	9.95	9.87
1638803_at	FBgn0014024	9.34	9.24	9.31	9.13	9.23	9.24
1626514_at	FBgn0038396	8.27	8.16	8.24	8.35	8.2	8.12
1638576_at	---	9.95	9.84	10.04	10.12	10.12	9.97
1641287_at	FBgn0037717	8.1	7.99	7.94	8.3	8.08	7.93
1641286_s_at	FBgn0015245	12.54	12.44	12.56	12.57	12.56	12.38
1638164_at	FBgn0037020	8.96	8.85	8.93	8.95	9.06	8.99
1634599_s_at	FBgn0011760	11.1	11	11.28	11.15	11.06	11.1
1634995_at	FBgn0034800	7.4	7.29	7.33	7.73	7.12	6.96
1629429_at	---	7.21	7.1	7	7.41	7.3	7.1
1625392_at	---	9.87	9.77	9.88	9.82	9.91	9.57
1625860_s_at	FBgn0037731	8.27	8.16	8.74	8.27	8.5	8.45
1625652_s_at	FBgn0039543	8.99	8.88	8.79	9.06	8.95	8.86
1625325_s_at	FBgn0052067	8	7.9	8.03	8.12	7.99	7.84
1623792_a_at	FBgn0000447	10.04	9.93	10.37	10.25	10.19	10.06
1635347_a_at	FBgn0030842	8.3	8.19	8.67	8.63	8.27	8.19
1640202_at	FBgn0020415	9.34	9.24	9.81	9.84	8.77	8.95
1630207_at	FBgn0032481	8.79	8.68	8.63	8.79	8.83	8.67
1623426_at	---	7.86	7.76	7.71	8.09	8.26	7.87
1636279_at	FBgn0001341	8.55	8.44	8.74	8.59	8.5	8.44
1633855_s_at	FBgn0031759	10.14	10.03	10.3	10.27	10.19	10.02
1638171_s_at	FBgn0031148	10.84	10.73	10.91	10.91	10.74	10.51
1638007_at	FBgn0039828	9.77	9.66	9.98	9.81	9.84	9.72
1629779_at	FBgn0020240	10.25	10.14	10.15	10.25	10.13	10.18
1637307_at	FBgn0051694	10.53	10.42	10.32	10.47	10.41	10.44
1628127_at	FBgn0038190	9.15	9.04	9.26	9.39	9.55	9.18
1630202_a_at	FBgn0033762	8.74	8.63	8.93	9.47	9.08	8.78
1625656_s_at	FBgn0034708	9.1	9	9	9.17	9.16	8.97
1628798_at	FBgn0029800	9.67	9.56	9.4	9.55	9.65	9.63
1628921_s_at	FBgn0002781	7.91	7.8	7.78	7.64	8.04	7.98
1634712_s_at	FBgn0020503	8.48	8.38	8.23	8.12	8.24	8.32
1626002_at	FBgn0014877	8.93	8.82	8.74	8.88	8.84	8.88
1635758_s_at	FBgn0025790	7.59	7.49	7.68	7.67	7.54	7.54
1628135_s_at	FBgn0025384	10.31	10.2	10.09	10.09	10.27	10.22
1641026_a_at	FBgn0002716	7.65	7.54	7.76	7.52	7.62	7.8

1634982_at	FBgn0038533	8.79	8.68	8.6	8.62	8.86	8.73
1639219_at	FBgn0032346	9.14	9.03	9.24	9.29	9.45	9.31
1628505_at	FBgn0037644	7.03	6.92	7.11	7.27	7.16	6.96
1636103_a_at	FBgn0037872	9.51	9.4	9.33	9.67	9.72	9.54
1623968_at	FBgn0032817	8.89	8.79	8.63	8.49	8.84	8.74
1627449_at	FBgn0035825	9	8.89	8.84	8.89	8.92	8.8
1624198_at	FBgn0037215	8.38	8.27	8.14	8.2	8.39	8.25
1629426_s_at	FBgn0040070	12.38	12.27	12.07	12.06	12.38	12.34
1640635_a_at	FBgn0020254	10.37	10.26	10.66	10.44	10.3	10.48
1635202_s_at	FBgn0032207	9.24	9.13	9.04	9.01	9.2	9.11
1630986_s_at	FBgn0042094	8.51	8.41	8.84	8.13	8.4	8.27
1635025_a_at	FBgn0029889 /// FBgn002	10.92	10.81	11.11	10.97	11.09	10.83
1627661_at	---	11.27	11.16	11.35	11	11.29	11.14
1641579_at	FBgn0036774	10.08	9.98	9.98	10.17	10.13	9.96
1625268_at	FBgn0036336	9.02	8.91	8.69	8.88	9.07	9.03
1635597_at	FBgn0028401	8.71	8.61	8.22	8.42	8.76	8.59
1632100_s_at	---	7.72	7.61	7.71	7.45	7.34	7.43
1627362_a_at	FBgn0003612	9.4	9.3	9.08	9.22	9.3	9.22
1631016_at	FBgn0052822	8.51	8.4	8.69	8.94	9.03	9.17
1630713_at	FBgn0011509	8.89	8.78	8.8	8.78	8.78	8.81
1641262_at	---	9.41	9.3	9.35	9.52	9.15	9.08
1640449_s_at	FBgn0031079	9.37	9.26	9.24	9.16	9.47	9.38
1631931_s_at	FBgn0010415	9.73	9.62	10	9.68	9.49	9.67
1635089_at	FBgn0034046	8.64	8.53	8.76	8.8	8.88	8.69
1634130_a_at	FBgn0036030	11.32	11.21	11.7	11.66	11.21	11.29
1633149_at	---	7.19	7.08	6.75	6.87	7.33	7.23
1631819_s_at	FBgn0016726	13.4	13.29	13.43	13.43	13.52	13.25
1638438_a_at	FBgn0003138	10.81	10.7	10.69	10.85	10.86	10.71
1632089_at	FBgn0025629	9.48	9.37	9.68	9.36	9.36	9.39
1623656_s_at	FBgn0046222	8.05	7.94	7.81	8.14	7.78	7.63
1631833_at	FBgn0002781	9.37	9.26	9.18	8.97	9.14	8.97
1629471_at	FBgn0029666	9.6	9.49	9.49	9.76	9.56	9.53
1625004_at	FBgn0042134	11.19	11.08	11.16	11.35	11.2	11.17
1637484_at	FBgn0039017	7.46	7.35	7.35	7.84	7.86	7.61
1625796_at	FBgn0031060	7.87	7.76	7.43	7.55	7.8	7.69
1624848_at	FBgn0027784	8.67	8.56	8.52	8.76	8.7	8.68

1639171_at	---	9.99	9.88	10.02	9.92	9.83	9.74
1629563_at	---	9.39	9.28	9.53	9.4	9.41	9.3
1631296_at	FBgn0039300	13.56	13.45	13.6	13.6	13.61	13.47
1624488_a_at	---	11.37	11.26	11.28	11.35	11.47	11.34
1637014_at	---	8.63	8.52	8.73	8.64	8.6	8.48
1630044_s_at	FBgn0038293	11.14	11.02	11.15	11.18	11.25	10.8
1631030_at	---	10.71	10.6	10.66	10.64	10.57	10.46
1637478_s_at	FBgn0011224	9.46	9.35	9.26	9.56	9.03	9.25
1637628_at	FBgn0034214	8.6	8.49	8.76	8.6	8.63	8.48
1628224_a_at	FBgn0020445	9.62	9.51	9.39	9.21	9.52	9.49
1639943_at	FBgn0034628	9.03	8.92	9.02	9.25	9.23	8.99
1627839_at	FBgn0035383	8.52	8.41	8.88	9.07	8.64	8.42
1640992_at	---	9.67	9.56	10.19	10.03	10.01	9.93
1624635_at	---	10.11	10	10.32	9.98	9.99	9.9
1628344_at	FBgn0000259	8.19	8.08	7.76	7.77	7.99	8.07
1638350_at	FBgn0032408	9.98	9.87	10.28	10.18	9.9	9.83
1630877_a_at	FBgn0031997	8.86	8.75	8.91	9.05	9.15	8.96
1641368_at	FBgn0032960	10.31	10.2	10.03	10.22	10.49	10.39
1624489_a_at	FBgn0023522	10.31	10.2	10.3	10.21	10.46	10.26
1629222_at	FBgn0014455	12.67	12.55	12.72	12.72	12.75	12.42
1633717_a_at	FBgn0035213	9.56	9.45	9.55	9.58	9.51	9.46
1629791_at	FBgn0038829	10.22	10.1	10.3	9.84	9.97	10.24
1623653_at	---	11.73	11.61	11.49	11.43	11.72	11.58
1634663_at	FBgn0030892	9.31	9.2	8.92	8.94	9.2	9.18
1625352_s_at	FBgn0033800	9.32	9.21	9.14	9.27	9.36	9.16
1641364_at	FBgn0030812	8.38	8.27	8.3	8.51	8.38	8.28
1629030_a_at	FBgn0027561	8.74	8.62	8.79	8.86	8.86	8.68
1640643_a_at	FBgn0027518	8.47	8.36	8.29	8.64	8.57	8.33
1625166_at	FBgn0040650	8.28	8.17	8.08	8.34	8.45	8.14
1631790_at	FBgn0030699	9.26	9.14	9.2	9.32	9.29	9.17
1626585_s_at	FBgn0019886	8.89	8.78	9.05	8.98	8.94	8.67
1633611_s_at	FBgn0052043	9.84	9.72	9.55	9.86	9.55	9.57
1632756_at	FBgn0030553	7.54	7.42	7.41	7.58	7.43	7.18
1629194_s_at	FBgn0000052	9.77	9.65	9.9	9.77	9.71	9.59
1631621_s_at	FBgn0001404	9.59	9.48	9.53	9.39	9.45	9.46
1631426_at	---	11.06	10.95	10.94	11.28	11.21	10.92

1634919_at	FBgn0033169	8.2	8.09	8.36	8.24	8.24	7.95
1630312_s_at	FBgn0036064	10.41	10.29	10.56	10.46	10.62	10.41
1635517_at	FBgn0033453	9.61	9.49	9.39	9.52	9.66	9.65
1636168_s_at	FBgn0032084	8.38	8.27	8.74	8.66	6.84	6.87
1627886_at	---	9.6	9.48	9.61	9.54	9.52	9.53
1637689_at	FBgn0032404	11.07	10.95	11.26	11.08	11.18	11
1633078_at	---	8.4	8.28	8.06	8.17	8.4	8.2
1624415_s_at	FBgn0037680	9.82	9.71	9.67	9.72	9.91	9.84
1639153_at	FBgn0033882	9.17	9.05	9.13	9.22	9.41	9.17
1628887_a_at	---	7.64	7.53	7.38	7.67	7.88	7.66
1631897_s_at	FBgn0033247	9.67	9.55	9.65	9.65	9.71	9.48
1627795_at	---	8.61	8.5	8.84	8.95	8.64	8.72
1625856_at	FBgn0000472	10.27	10.15	10.36	10.17	10.36	10.24
1627459_at	FBgn0031777	7.89	7.77	8.3	7.91	7.68	7.82
1623499_at	FBgn0033550	7.68	7.56	7.4	7.37	7.57	7.54
1639908_a_at	FBgn0036661	10.38	10.26	10.29	10.43	10.52	10.36
1626568_at	FBgn0038551	9.59	9.47	9.42	9.7	9.81	9.72
1623296_at	FBgn0052625	9.18	9.06	9.57	10.22	9.63	9.17
1628764_at	---	10.47	10.36	10.31	10.35	10.42	10.29
1633046_at	FBgn0031740	8.57	8.46	8.45	8.78	8.88	8.61
1633543_s_at	FBgn0010341	11.15	11.03	10.47	10.38	11.13	11.03
1632613_at	FBgn0028983	7.08	6.96	6.82	6.96	6.69	6.56
1625230_a_at	FBgn0051738	8.7	8.58	8.73	8.72	8.72	8.74
1624683_at	---	10.17	10.05	10.2	10.03	10.3	10.13
1628602_a_at	FBgn0032923	9.24	9.12	9.06	8.87	9.27	9.21
1640043_s_at	---	8.45	8.34	8.52	8.06	8.17	8.21
1641537_s_at	---	8.95	8.83	8.92	8.89	8.81	8.81
1637429_at	FBgn0034086	8.35	8.23	8.53	8.73	8.72	8.57
1637605_s_at	FBgn0035346	7.97	7.86	7.77	6.21	8.06	7.83
1630579_at	---	7.63	7.51	7.61	7.91	7.88	7.69
1626556_at	FBgn0038369	7.74	7.62	7.81	7.72	7.73	7.74
1641032_at	FBgn0035025	8.59	8.47	8.7	8.87	8.94	8.71
1635589_at	FBgn0039737	10.4	10.28	10.95	10.66	10.8	10.58
1623843_at	FBgn0038400	10.7	10.59	10.89	10.73	11.03	10.78
1634940_at	FBgn0020545	10.35	10.23	9.79	10.12	10.35	10.11
1636396_at	FBgn0015379	8.13	8.01	7.86	7.93	8.32	8.14

1627017_at	FBgn0024432	11.32	11.2	11.28	11.25	11.32	11.28
1640435_at	FBgn0026250	11.83	11.71	12.09	11.97	11.82	11.78
1636141_s_at	FBgn0001139	7.79	7.67	8.03	7.98	7.64	7.8
1630393_a_at	FBgn0031450	8.82	8.7	8.54	8.78	8.8	8.55
1630421_at	---	8.92	8.8	8.95	8.84	8.92	8.83
1626325_a_at	FBgn0033060	7.71	7.6	7.69	7.92	7.76	7.73
1633115_a_at	FBgn0026145	7.52	7.4	7.98	7.84	7.66	7.48
1629754_s_at	FBgn0013263	10.32	10.2	10.09	10.02	10.1	10.09
1641215_s_at	FBgn0033241	10.18	10.07	10.12	10.29	10.4	10.19
1639192_at	---	10.26	10.14	9.99	9.99	10.27	10.03
1630236_s_at	FBgn0034390	11.17	11.05	11.44	11.25	11.16	11.14
1634561_s_at	FBgn0052675	7.65	7.53	7.79	7.63	7.75	7.41
1637216_at	FBgn0036942	7.69	7.57	7.44	7.44	7.44	7.34
1623013_s_at	---	7.47	7.35	7.7	7.15	7.26	7.37
1629658_at	FBgn0032120	10.44	10.32	10.24	10.14	10.2	10.41
1623513_at	FBgn0030354	8.93	8.81	9.03	9.1	8.75	8.57
1629581_at	FBgn0035404	10.26	10.14	10.19	10.14	10.38	10.1
1626650_at	FBgn0002781	7.61	7.49	7.32	7.65	8.02	7.76
1637710_at	FBgn0004167	7.54	7.42	7.8	7.53	7.3	7.31
1638685_at	---	12.29	12.17	12.21	12.27	12.46	12.31
1640105_a_at	FBgn0033244	7.5	7.38	7.7	7.74	7.62	7.44
1631021_at	FBgn0039018	9.05	8.93	9.08	9.46	9.27	8.97
1628587_at	FBgn0035760	8.18	8.06	8.21	8.38	8.38	8.14
1636974_at	FBgn0041604	9.4	9.27	9.28	9.24	9.21	9
1635215_at	FBgn0029942	9.52	9.4	9.54	9.81	9.58	9.36
1624981_a_at	FBgn0035630	11.86	11.74	11.88	11.83	11.84	11.7
1631868_at	FBgn0029687	11.32	11.19	11.34	11.38	11.19	11.39
1626925_at	FBgn0013974	10.25	10.13	10.08	9.88	10.15	10.2
1635914_at	FBgn0032689	10.5	10.38	10.2	10.33	10.32	10.38
1627050_at	FBgn0032922	8	7.87	8.13	8.36	7.84	7.7
1626407_at	FBgn0032509	10.52	10.4	10.69	10.72	10.54	10.41
1634656_s_at	FBgn0064127	10.28	10.16	10.28	10.48	10.44	10.19
1635310_s_at	FBgn0051687	9.5	9.38	9.28	9.52	9.43	9.32
1639266_at	FBgn0030466	8.72	8.59	8.66	8.59	8.73	8.57
1638682_a_at	---	7.96	7.84	7.57	7.73	7.78	8.01
1629939_a_at	FBgn0035298	8.96	8.83	9.13	8.84	8.74	8.57

1633322_at	FBgn0030177	9.13	9.01	9.19	9.06	9.13	9.14
1635751_at	FBgn0052069	10.58	10.46	9.92	10.12	10.03	10.07
1624766_s_at	FBgn0011764	10.68	10.56	10.38	10.2	10.1	10.38
1632262_at	FBgn0036405	9.28	9.16	9.09	8.85	9.28	9.23
1636478_at	FBgn0031832	8.7	8.58	9.03	8.94	8.68	8.61
1629972_at	FBgn0030863	7.73	7.61	7.66	7.75	7.97	7.77
1627655_at	FBgn0050410	10.79	10.67	10.77	10.87	10.8	10.54
1639040_s_at	FBgn0034049	7.79	7.66	7.58	7.45	7.62	7.5
1630410_at	FBgn0052163	7.79	7.67	7.78	7.9	7.86	7.56
1634562_s_at	FBgn0034695	9.44	9.32	9.19	9.03	9.25	9.27
1634782_s_at	FBgn0015019	11.83	11.7	11.97	11.91	11.86	11.69
1634787_at	FBgn0052638	8.72	8.6	8.68	8.41	8.98	8.83
1640020_at	FBgn0030520	10.69	10.56	10.88	10.8	10.71	10.45
1633215_at	FBgn0035464	9.89	9.77	9.71	9.75	9.83	9.65
1638709_at	FBgn0024252	7.15	7.02	7.11	6.61	7.14	7.07
1630242_at	FBgn0051108 /// FBgn005	7.64	7.52	7.85	7.84	7.7	7.48
1639016_at	FBgn0030679	9.53	9.4	9.38	9.37	9.5	9.24
1632034_at	FBgn0037592	8.46	8.34	8.4	8.3	8.47	8.21
1639421_at	---	9.09	8.97	9.08	9	9.05	8.97
1631243_s_at	FBgn0010877	10.57	10.45	10.48	10.45	10.34	10.4
1626276_at	FBgn0035251	9.39	9.26	9.38	9.26	9.36	9.22
1636081_at	FBgn0051212	8.57	8.45	8.62	8.2	8.44	8.44
1640339_at	---	9.32	9.19	9.11	9.06	9.11	9.1
1628978_at	FBgn0034873	9.6	9.48	9.44	9.65	9.6	9.52
1639625_at	---	9.84	9.72	9.58	9.87	9.62	9.68
1641347_s_at	---	11.03	10.91	11.09	10.87	10.86	10.82
1639976_at	FBgn0033551	10.29	10.17	10.18	10.3	10.39	10.34
1631119_at	FBgn0035533	9.73	9.6	9.67	9.66	9.71	9.6
1633476_at	FBgn0034629	8.55	8.42	8.53	8.86	8.69	8.28
1627826_s_at	FBgn0033459	8.87	8.75	9.77	9.24	8.84	9.12
1623762_at	---	9.39	9.27	9.2	9.4	9.71	9.49
1629752_at	FBgn0032444	11.65	11.53	11.63	11.61	11.65	11.39
1641123_at	---	10.74	10.61	10.65	10.73	10.92	10.84
1633997_s_at	---	9.77	9.64	9.42	9.42	9.64	9.58
1625925_at	FBgn0051618	12.58	12.46	12.37	12.47	12.61	12.53
1640080_at	FBgn0032919	10.38	10.26	10.69	10.36	10.47	10.52

1630764_at	---	8.33	8.21	8.41	8.31	8.37	8.36
1628514_at	FBgn0031267	10.04	9.92	9.93	10.22	10.13	9.99
1624465_at	FBgn0014075	9.39	9.27	9.23	9.3	9.28	9.27
1631226_at	FBgn0028992	9.87	9.74	10.04	10.07	10.06	9.75
1622962_a_at	FBgn0031500	7.64	7.51	7.73	7.85	7.66	7.38
1625675_a_at	FBgn0034230	7.86	7.74	7.82	7.82	7.83	7.75
1633755_at	FBgn0038640	8.12	8	8.42	8.22	8.25	7.95
1635138_at	FBgn0004509	7.99	7.87	8.06	7.92	7.95	7.84
1633718_at	FBgn0032242	9.25	9.12	9.63	9.34	9.19	9.03
1640734_a_at	FBgn0038721	7.74	7.61	7.9	8.33	8.19	7.97
1637545_at	FBgn0030329	10.54	10.41	10.31	10.27	10.16	10.25
1629550_at	FBgn0037252	9.25	9.12	9.1	9.08	9.17	9.18
1623771_at	FBgn0029709	10.29	10.16	10.21	10.21	10.21	10.13
1635718_at	---	9.58	9.45	9.64	9.87	9.49	9.47
1631094_s_at	FBgn0032901	8.94	8.81	8.8	8.75	8.82	8.68
1633110_at	FBgn0038869	8.62	8.5	8.99	8.66	8.79	8.68
AFFX-r2-Ec-	---	12.36	12.23	12.49	12.7	12.14	11.84
1637597_a_at	FBgn0037652	10.52	10.39	10.54	10.55	10.45	10.37
AFFX-Dros-e	FBgn0001942	11.62	11.49	11.45	10.97	11.72	11.55
1632803_at	FBgn0024986	7.7	7.57	7.61	7.76	7.85	7.72
1629877_at	FBgn0051683	7.27	7.15	7.36	6.83	7.01	7.05
1633520_at	---	9.21	9.08	9.16	9.25	9.74	9.38
1639554_at	FBgn0023184	12.34	12.21	12.48	12.3	12.23	12.16
1626458_at	FBgn0038788	8.82	8.69	8.56	8.48	8.86	8.73
1634306_at	FBgn0004387	8.24	8.11	8.3	7.88	8.16	8.21
1637285_s_at	FBgn0029161	10.67	10.54	10.67	10.52	10.67	10.57
1632285_at	---	7.53	7.4	8.04	7.52	7.31	7.63
1640084_a_at	FBgn0033258	8.59	8.46	8.4	8.57	8.78	8.59
1636207_at	FBgn0031608	9.11	8.98	8.8	8.64	9.04	8.95
1639787_at	FBgn0037918	9.42	9.29	8.82	8.92	9.38	9.27
1631578_s_at	FBgn0031047	9.83	9.7	9.6	9.78	9.78	9.68
1626839_s_at	---	10.93	10.8	10.93	10.91	10.87	10.91
1627456_s_at	---	9.96	9.83	9.2	9.46	9.46	9.66
1624644_a_at	FBgn0039560	7.89	7.76	7.85	7.71	7.91	7.79
1631699_at	FBgn0031610	8.41	8.28	8.33	8.65	8.78	8.5
1636123_at	FBgn0032012	9.47	9.34	9.37	9.32	9.4	9.29

1631059_at	FBgn0003093	8.95	8.82	8.9	8.61	8.67	8.84
1627691_at	FBgn0022338	11.72	11.6	11.49	11.81	11.74	11.68
1634398_a_at	FBgn0000463	9.08	8.95	9.23	9.12	9.12	9.15
1640181_at	FBgn0036599	7.24	7.11	6.96	6.8	7.02	7.17
1629257_s_at	---	10.94	10.81	10.19	10.48	10.75	10.68
1624765_at	---	9.92	9.79	10.11	9.95	9.84	9.67
1631122_at	FBgn0039055	9.54	9.41	9.54	9.62	9.53	9.47
1635187_s_at	FBgn0039600	8.97	8.84	8.86	8.68	8.88	8.83
1627206_at	FBgn0029785	11.59	11.46	11.64	11.72	12.01	11.79
1625373_at	FBgn0038286	10.41	10.28	10.32	10.41	10.36	10.34
1636651_a_at	FBgn0004179	10.05	9.92	9.66	9.53	9.73	9.81
1625949_at	FBgn0001128	11.33	11.2	11.09	11.35	11.54	11.29
1639305_a_at	FBgn0019968	9.63	9.5	9.29	9.13	9.48	9.53
1629158_at	FBgn0032203	10.22	10.09	9.88	10.27	10.35	10.21
1626602_at	FBgn0020618	13.55	13.42	13.61	13.66	13.7	13.43
1624348_a_at	FBgn0035633	9.17	9.04	9.17	9.26	9.26	9.15
1635057_s_at	FBgn0031161	8.16	8.03	8.44	8.33	8.53	8.45
1635568_at	FBgn0034641	9.03	8.9	8.91	8.9	9.11	8.97
1634405_s_at	FBgn0014001	8.66	8.53	8.45	8.49	8.42	8.58
1632327_at	FBgn0038766	7.43	7.3	7.42	7.75	7.62	7.57
1631244_a_at	FBgn0005648	10.16	10.02	10.54	10.36	10.11	10.08
1639676_at	FBgn0032744	7.1	6.97	6.79	6.99	6.7	6.58
1630931_at	FBgn0031452	8.77	8.64	8.66	8.72	8.72	8.61
1636789_s_at	FBgn0050404	10.09	9.96	9.98	10.06	10.09	10.04
1640460_at	FBgn0036500	8.97	8.83	8.88	8.78	8.99	8.77
1629948_at	FBgn0035955	9.84	9.71	9.89	9.85	9.94	10.04
1627910_s_at	FBgn0037607	11.37	11.24	11.47	11.46	11.3	11.01
1632272_a_at	FBgn0039581	9.32	9.19	9.4	9.52	9.45	9.25
1623889_at	FBgn0035333	8.91	8.78	8.7	8.74	8.99	8.94
1636388_at	FBgn0031036	8.18	8.05	8.35	8.52	8.34	8.17
1632521_at	FBgn0029906	7.89	7.76	7.52	7.59	8.04	7.6
1630280_s_at	FBgn0030726	10.02	9.88	10.39	10.21	9.97	9.76
1639962_a_at	FBgn0019624	12.16	12.03	12.29	12.1	12.21	12.13
1627102_at	FBgn0030670	9.99	9.85	9.68	9.61	10	9.85
1632003_a_at	FBgn0004369	7.37	7.24	7.5	8.11	7.42	7.09
1631785_at	FBgn0004461	10.32	10.19	9.99	10.04	10.15	10.03

1634934_at	FBgn0036900	9.06	8.92	8.6	8.97	8.75	8.83
1629015_a_at	FBgn0025641	9.94	9.81	9.84	9.89	10.02	9.87
1623842_a_at	FBgn0011754	10.06	9.93	9.72	9.69	9.91	9.78
1635376_at	FBgn0030809	8.02	7.89	7.62	8.01	8.01	7.97
1629106_at	FBgn0029990	10.28	10.14	8.33	8	9.44	9.66
1630105_at	FBgn0035993 /// FBgn003	9.52	9.39	9.32	9.45	9.87	9.5
1627647_at	FBgn0037788	8.78	8.64	8.91	8.78	8.81	8.69
1635687_at	FBgn0033715	9.26	9.12	9.07	9.54	9.24	8.96
1627349_at	FBgn0010520	9.44	9.31	9.87	9.73	9.69	9.61
1632019_s_at	FBgn0028540	7.39	7.25	8.19	7.57	7.19	7.38
1631775_at	---	12.17	12.04	11.65	12.09	11.84	11.72
1636840_at	---	10.27	10.14	10.52	10.89	10.42	10.19
1624481_a_at	FBgn0051534	9.34	9.2	9.36	8.97	8.75	8.94
1634048_a_at	FBgn0027348	10.73	10.6	10.69	10.8	10.7	10.6
1636347_at	---	8.69	8.56	8.26	8.75	8.5	8.36
1627059_at	FBgn0025117	11.78	11.64	11.97	11.77	11.9	11.65
1638295_s_at	FBgn0037279	8.81	8.68	8.84	8.82	8.87	8.71
1631828_s_at	FBgn0033738	9.13	8.99	9.15	9.12	9.23	9
1640493_at	---	7.36	7.23	7.24	7.66	7.58	7.33
1633370_s_at	FBgn0030299	7.34	7.2	7.55	6.99	6.75	7.09
1630154_at	FBgn0035998	9.58	9.45	8.96	9.35	9.49	9.34
1634593_at	---	12.18	12.04	11.47	11.9	11.83	11.97
1626680_at	FBgn0032512	8.04	7.91	7.97	7.95	8.08	7.84
1635352_s_at	FBgn0020611	9.93	9.79	10.1	9.74	9.84	9.64
1637124_at	FBgn0024509	10.32	10.19	10.09	10.18	10.29	10.1
1638126_at	FBgn0033385	10.1	9.97	10.16	10.18	10.14	10.1
1632245_a_at	FBgn0028985	9	8.86	8.75	8.88	8.55	8.31
1631464_at	FBgn0038586	7.98	7.85	7.37	7.67	7.75	7.74
1624752_at	FBgn0036770	8.05	7.91	7.72	7.6	7.75	7.46
1635335_at	FBgn0027903	10.01	9.87	9.8	10.22	10.05	9.88
1631087_a_at	FBgn0037248	9.8	9.66	9.9	9.68	9.72	9.78
1635030_at	FBgn0033945	7.75	7.61	7.48	8.08	8.08	7.87
1637823_at	FBgn0030554	8.36	8.22	8.17	8.3	8.7	8.34
1625337_s_at	FBgn0002626	13.78	13.64	13.81	13.84	13.86	13.71
1622982_at	FBgn0024846	9.98	9.84	9.82	9.95	10.01	9.77
1639747_at	FBgn0050291	8.15	8.01	8.31	8.07	8.21	8.05

1634087_at	FBgn0035523	9	8.87	8.96	8.91	8.98	8.83
1638513_s_at	FBgn0039213	10.36	10.22	10.55	10.11	9.88	10.02
1638634_at	FBgn0052448	7.55	7.41	7.9	7.18	6.96	7.22
1630724_at	FBgn0039869	11.68	11.54	11.53	11.88	11.62	11.28
1635784_a_at	---	13.32	13.18	13.19	13.27	13.2	13.21
1628688_at	FBgn0039831	10.48	10.34	10.16	10.56	10.44	10.5
1633169_at	FBgn0024510	8.03	7.89	8.34	8.45	8.35	8.28
1629008_at	FBgn0038275	8.51	8.37	8.85	8.49	8.71	8.7
1639503_at	FBgn0003888	8.46	8.32	8.42	7.71	7.61	8.02
1624213_at	FBgn0039764	8.54	8.4	8.47	8.9	8.79	8.66
1625231_at	---	9.46	9.32	9.17	9.37	9.44	9.36
1622921_at	FBgn0052022	9.33	9.19	9.37	9.63	9.45	9.36
1637743_at	FBgn0037760	8.85	8.71	8.83	8.77	8.77	8.79
1626220_at	FBgn0035996	7.82	7.68	7.82	7.95	7.8	7.8
1640309_s_at	FBgn0010280	8.44	8.3	8.18	8.16	8.41	8.47
1635151_at	FBgn0029502	9.19	9.05	9.39	9.51	9.21	8.94
1627228_at	FBgn0030183	8.68	8.54	8.84	9.06	8.9	9.11
1635224_s_at	FBgn0001291	9.21	9.07	8.97	9.22	9.33	9.02
1635189_at	---	9.05	8.91	10.99	9.17	9.23	7.59
1639786_at	FBgn0034050	7.86	7.72	7.22	7.46	7.85	7.76
1626412_at	FBgn0035714	9.4	9.26	9.37	9.34	9.37	9.27
1638704_at	FBgn0030287	9.84	9.7	9.66	9.67	9.83	9.72
1632721_at	FBgn0021874	8.54	8.4	8.73	8.42	8.52	8.21
1633804_at	FBgn0036921	11.25	11.1	11.38	11.33	11.32	11.25
1630536_at	FBgn0002781	7.49	7.35	7.09	7.37	7.48	7.33
1637469_at	FBgn0053198	9.48	9.34	8.95	9.67	9.69	9.45
1633779_s_at	---	10.13	9.99	10.08	10.02	9.99	10.23
1632389_at	---	9.02	8.87	9.05	8.98	9.14	9.03
1625719_at	FBgn0002921	7.12	6.98	7.95	7.47	6.96	7.13
1628028_s_at	FBgn0029897	13.3	13.16	13.3	13.16	13.32	13.17
1641345_at	FBgn0036837 /// FBgn003	8.53	8.39	8.16	8.16	8.38	8.29
1627694_at	---	9.81	9.67	9.84	9.63	9.68	9.58
1639947_s_at	FBgn0033166	9.5	9.35	9.39	9.44	9.48	9.31
1636644_at	---	10.28	10.14	10.3	10.12	10.14	10.11
1623495_at	---	9.33	9.19	8.97	8.88	9.52	9.24
1627506_at	FBgn0000547	8.98	8.84	8.5	8.7	8.67	8.78

1634034_at	FBgn0036257	8.75	8.61	8.43	8.67	8.68	8.53
1631933_at	FBgn0037759	7.11	6.96	6.66	6.48	7.25	7.23
1623436_a_at	FBgn0010460	10.61	10.46	10.21	10.21	10.42	10.31
1626444_at	FBgn0003062	11.6	11.46	11.65	10.98	11.38	11.41
1638509_at	---	7.45	7.3	7.27	7.48	8.32	8.11
1639672_at	FBgn0030091	7.2	7.06	7	7.12	7.24	7.11
1634660_at	FBgn0039507	9.67	9.53	9.51	9.38	9.79	9.65
1623758_at	FBgn0032150	7.49	7.35	7.56	7.64	7.67	7.48
1633270_at	---	7.6	7.45	7.17	7.17	7.53	7.44
1625145_a_at	FBgn0030749	9.35	9.2	9.36	9.02	9.37	9.21
1636843_a_at	FBgn0037057	7.07	6.93	8.2	7.42	6.37	6.53
1624326_at	FBgn0028406	9.21	9.07	8.71	9.02	9.29	9.25
1629411_at	FBgn0037671	11.21	11.07	11.08	11.09	11.19	11.05
1631863_at	FBgn0028387	8.15	8.01	7.82	8.06	8.18	8.02
1630844_at	FBgn0028526	7.47	7.32	6.85	6.72	7.03	6.87
1626546_s_at	FBgn0036769	10.85	10.7	10.67	10.21	10.85	10.83
1626248_at	FBgn0037973	6.72	6.57	6.63	6.29	7.05	6.76
1629141_at	FBgn0013984	7.53	7.39	7.39	7.15	7.23	7.33
1636575_s_at	FBgn0033583	9.53	9.39	9.35	9.36	9.6	9.53
1634070_at	FBgn0025558	8.43	8.29	8.05	8.42	8.42	8.14
1634033_s_at	FBgn0025593	7.54	7.4	7.42	7.54	7.6	7.38
1623863_a_at	---	10.26	10.11	10.38	10.29	10.18	9.97
1639857_at	FBgn0052068	9.97	9.82	10.01	10.25	9.91	9.81
1636717_at	FBgn0038672	8.01	7.87	7.96	8.43	8.38	8.02
1625819_at	FBgn0005410	9.23	9.09	9.1	8.98	9.03	9.05
1628399_s_at	FBgn0004587	11.76	11.61	11.63	11.79	11.84	11.78
1625592_s_at	FBgn0037106	9.46	9.32	9.03	9.4	9.49	9.39
1625096_at	FBgn0036886	9.08	8.93	9.31	9.06	9.23	8.99
1628096_at	FBgn0038472	8.37	8.23	8.31	8.72	8.73	8.65
1629546_at	FBgn0038972	8.83	8.68	8.97	8.92	8.85	8.66
1637538_s_at	FBgn0034618	9.45	9.31	9.46	9.6	9.56	9.24
1625122_at	FBgn0039682	8.35	8.2	8.04	7.25	8.26	7.4
1627729_s_at	FBgn0028577	9.65	9.5	9.29	9.41	9.46	9.29
1641653_at	FBgn0024273	7.73	7.58	7.68	7.37	7.04	7.14
1641659_s_at	FBgn0039697	11.73	11.58	11.74	11.82	11.8	11.67
1638501_at	FBgn0036740	10.09	9.94	10.14	9.91	10.14	9.89

1627124_at	FBgn0030970	10.27	10.12	10.04	10.42	10.24	10.18
1633771_s_at	FBgn0037391	7.74	7.59	8	7.74	7.57	7.37
1629842_at	FBgn0004390	9.89	9.74	9.67	9.51	9.83	9.8
1630575_at	FBgn0039674	9.46	9.31	9.48	9.67	9.5	9.28
1635203_at	FBgn0040466	8.95	8.8	8.66	9.3	9.29	9.19
1641195_at	FBgn0038519	10.42	10.27	10.66	10.48	10.54	10.4
1625717_s_at	---	10.4	10.25	10.31	10.26	10.24	10.11
1639626_at	FBgn0039215	8.7	8.55	8.51	8.56	8.73	8.69
1625638_a_at	FBgn0001186	9.61	9.46	10	9.85	9.61	9.41
1626469_at	FBgn0033351	10.21	10.06	10.17	10.34	10.43	10.16
1640963_at	FBgn0052594 /// FBgn003	10.88	10.73	10.86	11.23	10.94	10.78
1631175_a_at	FBgn0032681	7.56	7.41	8.01	7.04	6.84	7.23
1628706_at	FBgn0030006	7.17	7.02	7.19	7.43	7.2	6.94
1635875_at	FBgn0002791	8.78	8.63	8.82	8.94	8.72	8.61
1638600_at	---	9.45	9.3	9.02	9.2	9.32	9.15
1627229_at	FBgn0033433	7.39	7.24	7.03	7.19	7.48	7.29
1632263_at	FBgn0033485	9.6	9.45	9.9	9.54	9.75	9.62
1630923_at	FBgn0036476	7.22	7.06	7.49	7.88	7.51	7.29
1637637_at	FBgn0003392	7.99	7.84	7.91	8.18	8.29	7.94
1629813_at	FBgn0039993	11.08	10.93	10.88	10.91	11.1	11.03
1637018_at	FBgn0030605	10.76	10.61	10.69	10.64	10.69	10.53
1631638_at	FBgn0030964	9.75	9.6	9.49	9.29	9.52	9.54
1624719_at	FBgn0029979	7.77	7.62	7.75	7.49	7.53	7.63
1624818_s_at	FBgn0010591	9.67	9.52	9.74	9.65	9.65	9.37
1631499_a_at	FBgn0003656	10.57	10.42	10.67	10.62	10.21	10.23
1626733_at	FBgn0032487	9.42	9.26	9.47	9.4	9.13	9.07
1634359_a_at	FBgn0032105	11.42	11.26	11.15	11.27	11.41	11.27
1640472_at	FBgn0035114	11.69	11.53	10.63	10.41	11.04	11.25
1640984_s_at	---	10.31	10.16	10.55	10.63	10.28	9.99
1632374_at	FBgn0030878	9.46	9.31	9.61	9.41	9.48	9.32
1626475_at	FBgn0032296	7.09	6.94	7.02	7.15	6.97	6.62
1625257_s_at	FBgn0051523	9.31	9.16	9.32	8.95	9.25	9.5
1633752_at	FBgn0052836	7.75	7.6	7.5	7.64	7.14	7.14
1623788_at	FBgn0034432	10.4	10.25	10.58	10.55	10.48	10.11
1632807_at	FBgn0040212	9.03	8.87	8.94	9.03	9.15	9.05
1631127_at	FBgn0036848	8.97	8.82	9.1	9.05	9.09	8.91

1634983_s_at	FBgn0052521	7.88	7.73	8.36	8.26	8.37	8.28
1632275_a_at	FBgn0032938	8.02	7.86	7.97	8.41	8.12	7.89
1635678_at	FBgn0034897	9.02	8.86	8.86	8.97	9.04	8.76
1630845_at	FBgn0003462	12.64	12.49	12.46	12.49	12.59	12.46
1639766_at	FBgn0003075	11.54	11.39	11.28	11.58	11.51	11.15
1625632_at	FBgn0024196	12.17	12.02	11.66	11.99	11.92	11.81
1632488_a_at	FBgn0053009	9.77	9.61	9.85	9.54	9.72	9.55
1633792_a_at	FBgn0003013	7.93	7.77	7.92	7.65	7.88	8.04
1630403_s_at	FBgn0037341	8.3	8.15	8.07	8.14	8.29	8.11
1641251_at	FBgn0035754	8.47	8.31	7.94	8.48	8.35	8.14
1625992_s_at	FBgn0035075	8.29	8.14	8.21	8.31	8.45	8.17
1638898_at	---	9.33	9.18	9.07	9.39	9.42	9.28
1640907_at	FBgn0001091	12.21	12.06	12.07	12.23	12.31	12.03
1630630_at	FBgn0034278 /// FBgn003	10.55	10.4	10.66	10.47	10.53	10.37
1640650_at	FBgn0024957	9	8.85	8.77	9.02	8.96	8.54
AFFX-Dros-e	FBgn0001942	12.8	12.64	12.76	12.58	12.86	12.65
1627856_at	FBgn0026417	7.81	7.66	7.97	8.04	7.49	7.32
1632142_at	FBgn0033571	10.41	10.25	10.3	10.82	10.56	10.25
1626806_at	FBgn0003741	8.46	8.3	8.61	8.34	8.5	8.34
1634824_a_at	FBgn0029941	10.71	10.55	10.32	10.49	10.61	10.46
1626405_at	FBgn0024732	8.68	8.52	8.24	9.24	8.76	8.63
1636186_s_at	FBgn0015221	12.15	11.99	12	11.85	12.08	12.01
1641330_at	FBgn0052212	8.26	8.1	7.7	7.62	7.88	7.9
1640247_at	FBgn0036666	9.5	9.34	9.47	9.29	9.39	9.23
1637608_at	FBgn0030057	8.73	8.57	8.6	8.65	8.53	8.38
1632517_at	FBgn0038115	8.29	8.13	8.09	8.18	7.78	7.6
1637978_at	FBgn0032790	8.64	8.49	8.35	8.36	8.63	8.39
1629104_at	FBgn0029997	8.2	8.04	8.26	8.34	8.19	8.01
1640321_at	---	7.16	7.01	7.31	6.82	6.89	6.76
1630174_s_at	FBgn0032195	8.42	8.27	8.48	8.45	8.44	8.35
1635428_at	FBgn0033948	8.75	8.59	8.32	8.71	8.92	8.84
1630530_at	FBgn0032059	8.68	8.52	8.64	8.88	9.07	8.78
1633011_at	FBgn0001994	7.6	7.44	7.53	7.56	7.46	7.6
1629942_at	---	9.79	9.63	9.78	9.87	9.92	9.96
1624021_a_at	FBgn0001624	9.23	9.07	9.04	8.92	9.1	9.14
1627550_a_at	FBgn0052587	8.88	8.72	8.83	8.34	8.51	8.56

1626218_s_at	FBgn0011818	9.4	9.24	8.94	9.01	9.3	8.98
1631040_at	FBgn0036302	8.92	8.76	8.82	9	8.98	8.63
1624065_at	FBgn0003514	10.79	10.63	10.96	10.66	10.61	10.59
1623287_at	FBgn0035267	8.55	8.39	8.59	8.67	8.36	8.43
1627788_at	FBgn0037943	8.78	8.62	8.85	8.66	8.68	8.65
1627511_at	FBgn0036165	8.44	8.28	8.4	8.31	8.72	8.71
1639524_at	FBgn0034378	9.58	9.42	9.08	9	9.26	9.34
1627267_at	FBgn0032694	8.23	8.07	8.42	8.38	7.76	8.03
1632973_at	FBgn0002781	8.21	8.05	7.71	7.98	8.24	7.99
1625551_at	FBgn0028426	7.25	7.09	7.53	7.59	7.55	7.23
1641737_a_at	FBgn0027616	7.05	6.89	6.41	6.97	6.8	6.8
1632971_at	---	8.84	8.68	8.83	8.55	9.02	8.78
1637798_at	FBgn0030451	10.15	9.99	10.13	10.09	10.09	9.87
1628423_at	FBgn0027541	9.45	9.28	9.2	9.35	9.46	9.24
1637705_at	FBgn0005427	8.62	8.46	8.68	8.43	8.25	8.49
1640457_s_at	---	7.78	7.62	8.56	8.58	8.09	7.64
1627239_s_at	FBgn0033837	8.11	7.95	7.87	7.84	8.09	8.11
1627612_a_at	FBgn0025864	9.88	9.71	9.75	9.92	9.88	9.67
1630031_at	FBgn0002590	13.11	12.95	13.32	13.02	13.2	13.03
1622941_at	FBgn0033529	10.58	10.41	10.7	10.61	10.7	10.53
1624727_s_at	FBgn0016756	9.38	9.22	9.32	9.23	9.37	9.16
1633599_a_at	FBgn0003067	7.63	7.46	7.05	6.27	7.43	6.23
1622995_at	---	9.26	9.1	9.36	9.17	9.33	9.15
1635542_at	---	10.79	10.62	10.5	10.46	10.62	10.57
1632415_s_at	FBgn0036534	8.09	7.92	8.03	8.04	7.88	7.84
1624037_s_at	FBgn0010280	8.98	8.82	9.11	8.96	8.86	8.99
1637467_at	FBgn0038047	6.87	6.71	6.62	6.69	7.34	6.76
1628589_at	---	11.61	11.45	11.63	11.71	11.75	11.5
1640009_at	FBgn0010812	7.47	7.3	7.63	7.58	7.68	7.23
1638796_at	FBgn0038723	10.18	10.01	10.02	10.02	10.08	9.86
1637982_at	FBgn0016687	11.65	11.48	11.72	11.88	11.93	11.58
1638092_a_at	FBgn0038369	9.75	9.58	9.67	9.56	9.76	9.58
1624300_s_at	FBgn0011817	9.91	9.74	9.24	9.77	9.82	9.66
1637172_at	FBgn0044030	10.27	10.1	10.02	10.06	10.11	10.05
1633025_at	FBgn0033808	8.87	8.7	8.78	8.86	8.94	8.69
1640998_at	FBgn0004811	7.54	7.37	7.45	7.83	7.72	7.54

1639430_at	FBgn0038908	8.43	8.26	8.56	8.75	8.49	8.29
1638359_s_at	FBgn0028953	7.14	6.98	7.44	6.8	6.71	7
1636883_s_at	FBgn0004362	11.23	11.06	11.08	11.18	10.96	11.03
1637302_s_at	---	8.57	8.4	8.71	8.3	7.86	8.06
1637383_at	FBgn0039249	6.88	6.71	7.01	6.56	7.02	6.72
1628952_s_at	FBgn0004509	8.75	8.58	8.52	8.63	8.68	8.46
1628738_at	FBgn0051251	7.85	7.69	7.52	8.07	8.03	7.94
1634164_at	---	10.77	10.6	10.04	10.37	10.3	10.23
1634100_at	FBgn0039965	9.98	9.81	9.78	10.06	10.04	9.85
1624837_at	FBgn0035805	8.77	8.6	9.12	8.93	8.74	8.53
1628618_at	FBgn0030669	9.35	9.19	9.15	9.29	9.47	9.21
1635566_s_at	FBgn0027338	8.11	7.94	7.47	7.59	7.41	7.27
1638485_s_at	FBgn0034371	8.56	8.39	8.29	8.43	8.7	8.44
1640220_a_at	FBgn0038683	9.43	9.26	9.16	9.27	9.2	9.12
1636978_at	FBgn0032600	9.9	9.73	9.79	9.77	9.95	9.9
1630795_at	FBgn0030037	9.61	9.44	9.65	9.72	9.71	9.5
1633798_at	FBgn0022959	10.87	10.7	11.02	10.9	10.98	10.68
1627376_at	FBgn0014018	9.05	8.88	9.06	8.99	9.07	8.77
1632525_at	FBgn0038191	10.02	9.85	10.01	9.94	9.95	9.78
1631093_at	FBgn0039627	8.71	8.54	8.9	8.68	8.84	8.72
1625134_at	FBgn0039044	9.21	9.04	9.07	8.99	9.27	9.11
1639803_at	FBgn0036576	8.12	7.95	7.81	7.54	7.92	7.64
1639484_at	FBgn0039854	8.66	8.49	8.85	8.72	8.87	8.56
1626675_at	---	7.62	7.45	7.73	8.13	7.87	7.54
1629537_s_at	FBgn0050394	7.34	7.17	7.53	7.18	7.26	7.22
1625126_at	FBgn0027522	8.25	8.08	8.24	8.27	8.24	8.04
1626725_at	FBgn0034936 /// FBgn003	9.55	9.38	9.58	9.54	9.56	9.37
1639600_at	FBgn0035248	7.54	7.37	7.58	7.42	7.54	7.52
1635563_at	FBgn0035900	7.02	6.84	6.93	6.65	6.46	6.43
1629525_at	FBgn0034543	8.71	8.54	8.65	8.6	8.61	8.51
1630469_a_at	FBgn0037470	10.14	9.97	9.77	9.79	9.92	9.8
1625680_a_at	FBgn0032455	10.79	10.62	10.57	10.95	10.89	10.65
1634374_at	FBgn0053138	10.33	10.15	10.13	10.52	10.3	9.82
1625414_at	FBgn0001941	10.45	10.28	10.18	10.27	10.29	10.3
1626575_at	FBgn0030286	8.64	8.47	8.4	8.38	8.73	8.45
1632556_s_at	FBgn0039665	9.49	9.31	9.06	9.1	9.6	9.42

1633382_s_at	FBgn0027529	7.5	7.32	7.63	7.35	7.14	7.25
1638609_s_at	FBgn0038016	9	8.82	9.03	8.92	9.09	8.76
1627287_at	FBgn0029831	8.07	7.89	8.14	8.41	8.72	8.39
1627627_at	FBgn0032822	8.42	8.25	8.26	8.56	8.32	8.14
1633021_s_at	FBgn0010905	9.59	9.42	9.5	9.38	9.72	9.59
1629176_at	FBgn0032841	9.58	9.4	9.55	8.75	9.33	9.16
1639566_s_at	---	8.05	7.88	8.41	7.42	7.85	7.93
1633231_a_at	FBgn0026758	9.23	9.05	8.96	8.92	8.95	8.73
1640267_at	FBgn0038454	7.83	7.65	7.69	7.66	7.77	7.81
1623312_s_at	FBgn0039272	10.03	9.85	9.7	9.91	9.92	9.71
1639972_at	FBgn0004087	10.67	10.49	10.35	10.72	10.47	10.14
1635429_at	---	9.93	9.76	9.92	10.04	10.05	9.97
1636559_s_at	FBgn0029134	12.53	12.36	12.22	12.56	12.46	12.14
1637663_at	FBgn0003687	9.36	9.19	8.98	9	9.48	9.3
1641396_a_at	---	10.25	10.07	10.14	10.08	10.25	10.11
1639954_at	FBgn0032261	8.67	8.49	8.92	8.81	8.56	8.38
1634798_at	FBgn0022246	8.45	8.27	8.64	8.52	8.36	8.25
1640924_a_at	FBgn0025681	8.88	8.7	8.51	8.55	8.81	8.75
1625857_at	FBgn0031998	9.34	9.16	9.14	8.65	9.21	9.15
1636182_a_at	FBgn0036317	7.77	7.59	7.51	7.7	7.89	7.64
1625464_at	FBgn0029870	10.34	10.16	10.2	10.18	10.37	10.15
1639619_a_at	FBgn0028516	9.29	9.11	9.66	9.3	9.13	9.2
1637643_at	FBgn0032117	6.77	6.59	7.01	6.78	7.07	6.96
1632267_a_at	FBgn0032198	11.94	11.76	12.04	11.74	11.95	11.8
1632259_at	FBgn0037971	9.74	9.56	9.18	9.45	9.44	9.36
1627448_at	FBgn0033428	10.39	10.21	10.43	10.43	10.3	10.04
1641541_a_at	FBgn0039969	11.49	11.31	11.45	11.23	11.58	11.42
1629559_s_at	---	7.66	7.48	7.81	6.97	7.25	7.35
1630025_at	FBgn0023526	8.88	8.7	8.81	8.74	8.79	8.67
1640510_at	FBgn0035765	11.1	10.92	10.89	10.83	11.04	11
1640300_at	---	7.01	6.82	7.01	6.97	6.77	6.62
AFFX-r2-Dro	FBgn0001128	10.59	10.41	10.23	10.19	10.77	10.51
1628726_s_at	FBgn0026376	9.54	9.35	9.1	9.23	9.24	9.47
1634021_a_at	FBgn0014870	7.18	7	7.84	7.15	6.94	7.04
1636647_s_at	---	10.33	10.15	10.56	10.64	10.47	10.1
1632479_at	FBgn0040623	10.38	10.2	10.19	9.92	10.16	10.11

1632191_s_at	FBgn0004873	7.21	7.02	7.83	7.41	7.16	6.91
1633956_s_at	FBgn0035266	9.92	9.74	9.79	9.7	10.07	9.95
1625315_at	FBgn0037011	9.35	9.17	9.49	9.14	9.16	9.04
1635637_at	FBgn0037609	9.4	9.22	8.97	9.25	9.49	9.25
1633690_at	FBgn0033903	7.36	7.17	7.81	7.53	7.34	7.38
1629479_a_at	FBgn0020303	11.63	11.45	11.7	11.27	11.5	11.37
1624164_s_at	FBgn0036144	7.02	6.83	6.78	6.86	6.61	7.03
1639061_at	FBgn0034975	8.06	7.87	7.94	7.73	7.92	7.83
1624560_at	FBgn0020254	9.6	9.41	9.27	9.04	9.12	9.48
1635581_at	FBgn0029937	8.1	7.91	7.98	8.24	8.21	7.98
1635393_s_at	FBgn0000568	7.12	6.93	7.05	6.22	6.62	6.27
1633931_a_at	FBgn0027779	10.69	10.5	10.6	10.41	10.73	10.46
1638947_at	FBgn0031651	9.3	9.11	9.4	9.34	9.29	9.16
1628229_at	FBgn0028990	8.82	8.64	8.58	8.71	8.91	8.64
1630080_at	FBgn0035997	10.37	10.19	10.32	10.25	10.35	10.26
1625443_a_at	FBgn0053054	7.96	7.77	7.99	8	7.65	7.53
1636406_at	FBgn0034643	8.7	8.52	8.72	8.57	8.91	8.73
1634135_at	FBgn0035444	9.25	9.06	9.13	9.2	9.31	9.06
1633911_a_at	FBgn0051550	8.33	8.15	8.28	8.07	8.03	7.94
1624244_at	FBgn0015806	8.71	8.53	9.09	8.61	8.35	8.54
1625340_at	FBgn0004227	8.27	8.09	8.06	7.66	7.87	8.19
1624530_at	FBgn0036980	11.17	10.98	10.78	10.83	11.05	10.98
1634245_at	---	7.05	6.86	7.43	7.65	7.18	7.02
1630440_at	FBgn0036916	8.37	8.18	8.73	8.5	8.59	8.43
1632728_at	---	8.52	8.33	8.54	8.47	8.73	8.65
1624340_at	---	9.85	9.66	9.76	9.73	9.88	9.58
1639211_at	---	10.78	10.6	9.59	9.76	10.33	10.15
1626271_at	FBgn0027528	7.17	6.98	7.73	7.39	7.39	7.24
1623594_at	FBgn0004133	7.05	6.86	7.24	6.76	6.51	6.52
1639245_x_at	FBgn0004657	9.31	9.13	9.22	8.85	9.2	9.37
1640322_at	FBgn0033580	7.06	6.87	6.97	6.91	7.13	7.01
1627782_at	---	8.67	8.48	8.93	8.61	8.58	8.34
1629101_a_at	FBgn0033019	9.97	9.78	9.62	9.46	10.04	9.86
1634302_s_at	FBgn0039640	10.75	10.57	10.91	11.09	10.78	10.59
1625844_s_at	FBgn0015903	7.32	7.13	7.03	7.12	7.18	7.08
1641000_a_at	FBgn0033844	9.73	9.54	9.72	9.52	9.53	9.48

1626769_s_at	FBgn0033224	9.5	9.31	9.44	9.59	9.51	9.36
1629903_at	---	10.38	10.19	10.38	10.61	10.69	10.25
1628516_at	FBgn0031603	7.51	7.32	7.59	7.43	7.56	7.31
1624183_a_at	FBgn0000634	10.4	10.21	10.17	10.21	10.18	10.14
1626236_at	FBgn0032703	9.41	9.22	9.39	9.27	9.31	9.17
1641747_s_at	FBgn0033010	9.27	9.08	8.82	8.81	8.95	9.08
1634218_at	FBgn0038828	10.34	10.15	9.68	9.77	10.19	10.2
1629388_s_at	FBgn0039745	9.39	9.2	9.38	9.19	9.33	9.15
1634321_s_at	FBgn0037376	8.98	8.79	8.58	8.91	9.31	9.07
1640841_at	FBgn0004177	10.71	10.52	10.86	11.02	10.7	10.6
1637223_s_at	FBgn0034504	9.51	9.32	9.47	9.26	9.27	9.21
1625249_at	FBgn0030090	9.18	8.99	8.94	8.86	9.05	8.81
1631205_a_at	FBgn0036182	12.1	11.91	11.82	12.1	12.32	12
1627265_at	FBgn0035202	7.96	7.77	7.55	8.21	8.04	7.83
1631355_at	---	9.28	9.09	9.41	9.28	9.36	9.1
1624715_at	FBgn0011361	10.98	10.79	11.15	11.13	10.91	10.75
1633795_a_at	---	7.49	7.3	7.9	6.26	6.42	6.94
1638839_at	FBgn0033998	9.53	9.34	9.4	9.45	9.48	9.33
1626760_at	FBgn0030178	8.32	8.12	8.35	8.55	8.52	8.26
1633563_at	FBgn0030245	7.69	7.5	8.35	8.1	7.73	7.55
1631083_at	FBgn0029609	9.29	9.09	8.98	8.91	9.18	9.04
1626710_at	---	8.39	8.2	8.29	8.62	8.6	8.32
1625131_s_at	FBgn0005671	11.36	11.16	11.34	11.24	11.53	11.33
AFFX-BioDn-	---	12.6	12.4	12.59	12.69	12.37	12.05
1634015_s_at	FBgn0038786	9.81	9.61	9.65	9.48	9.58	9.59
1635788_a_at	FBgn0037847	10.56	10.37	10.29	10.36	10.45	10.33
1640549_at	FBgn0023477	11.37	11.18	11.11	11.23	10.98	10.89
1639259_at	FBgn0033637	8.47	8.28	8.56	8.57	8.67	8.19
1641704_at	---	8.85	8.66	8.72	8.76	8.84	8.7
1628336_a_at	FBgn0010238	10.02	9.82	10.13	9.93	10.02	10.11
1632858_a_at	FBgn0037362	8.96	8.77	8.89	8.63	8.83	8.72
1626436_at	FBgn0035035	9.32	9.12	9.27	9.57	9.32	9.25
1626375_a_at	FBgn0029711	8.18	7.99	7.89	8	8.26	8.23
1633283_at	FBgn0037899	12.35	12.15	12.3	12.38	12.49	12.09
1628842_s_at	FBgn0039928	8.3	8.11	8.76	7.96	8.1	8.41
1638797_a_at	FBgn0037308	11.03	10.84	10.83	10.85	11.02	10.91

1633016_a_at	FBgn0003520	8.85	8.66	8.17	8.14	8.58	8.45
1639064_s_at	FBgn0010379	8.98	8.79	8.89	8.85	9	9.28
1631300_at	FBgn0010383	8.63	8.44	8.99	8.29	7.84	8.24
1638133_at	FBgn0022984	9.33	9.14	9.24	8.92	9.02	9.06
1641118_at	FBgn0029155	9.39	9.19	9.18	9.04	9.3	9.17
1624400_a_at	FBgn0013435	7.25	7.06	7.12	7.38	7.32	7.06
1630110_at	FBgn0033547	8.74	8.54	8.66	8.58	8.89	8.62
1630324_at	FBgn0034119	9.07	8.87	9.29	9.16	9.15	8.87
1634131_s_at	FBgn0023215	8.34	8.14	8.58	8.56	8.17	7.96
1635737_at	FBgn0033889	9.75	9.55	9.85	9.75	9.65	9.47
1641463_at	FBgn0032420	9.54	9.34	9.48	9.82	9.49	9.44
1633349_at	FBgn0010421	10.46	10.26	10.12	10.39	10.58	10.36
1640266_a_at	FBgn0034421	9.2	9	9.27	9.04	9.22	9.13
1634444_at	FBgn0033184	9.19	9	9.28	9.13	9.04	8.89
1637280_at	FBgn0039363	8.71	8.51	8.77	8.77	8.51	8.45
1631535_at	FBgn0004397	9.34	9.14	9.11	9.14	9.24	9.09
1639736_at	FBgn0030851	8.8	8.6	8.69	8.66	8.94	8.75
1631853_at	---	10.74	10.54	10.62	10.7	10.84	10.67
1637036_s_at	FBgn0003141	9.65	9.45	9.74	9.73	9.73	9.71
1640134_a_at	FBgn0032388	9.36	9.16	9.51	9.33	9.3	9.11
1640256_at	FBgn0000171	9.46	9.26	9.64	9.19	9.07	9.01
1629705_at	FBgn0036182	11.4	11.2	11.32	11.79	11.99	11.78
1641430_at	FBgn0034879	9.28	9.08	9.44	9.31	9.39	9.11
1625424_at	FBgn0037949	7.95	7.75	7.33	7.47	7.76	7.76
1624595_a_at	FBgn0010256	8.93	8.73	8.51	8.78	9.23	8.9
1635448_at	FBgn0005322	10.96	10.76	10.89	10.88	10.93	10.77
1629189_at	FBgn0031537	8.15	7.95	7.9	8.17	8.06	7.55
1633576_s_at	FBgn0022349	10.65	10.45	10.46	10.23	10.51	10.38
1629013_at	FBgn0029713	8.12	7.92	7.86	8.13	8.23	8.03
1634628_at	FBgn0050392	10.23	10.03	9.76	10.03	10.2	9.76
1634495_s_at	FBgn0005630	8.55	8.34	8.06	8.46	8.81	8.43
1634649_at	FBgn0004657	8.75	8.55	8.71	8.51	8.66	8.79
1624153_at	FBgn0035083	10.92	10.72	10.99	11.11	10.58	10.55
1638173_s_at	FBgn0031637	7.7	7.5	7.66	7.57	7.35	7.25
1623015_at	FBgn0038609	9.74	9.54	9.38	9.88	9.7	9.4
1629676_at	FBgn0028684	10.73	10.52	10.65	10.7	10.78	10.58

1630286_at	FBgn0000083	9.93	9.73	9.5	9.41	9.59	9.38
1628001_at	FBgn0032748	10.53	10.33	10.2	10.08	10.48	10.45
1637414_at	FBgn0028506	10.04	9.83	9.82	9.78	10.02	9.89
1627023_at	FBgn0039565	9.81	9.61	9.49	9.81	9.64	9.54
1633681_at	FBgn0037336	9.06	8.85	8.99	8.69	8.57	8.69
1629281_at	---	8.83	8.62	8.77	9.27	8.96	8.7
1628358_at	FBgn0028397	7.87	7.67	8.36	8.5	8.04	7.68
1640835_a_at	---	11.13	10.93	11.2	11.17	11.1	10.9
1635819_at	FBgn0014388	7.06	6.85	7.56	6.69	6.79	6.85
1629938_at	---	8.88	8.67	8.52	8.36	8.85	8.62
1635291_a_at	FBgn0017453	8.66	8.46	8.47	8.56	8.59	8.47
1631937_at	FBgn0051755	8.54	8.34	8.2	8.67	8.21	8.1
1634443_a_at	FBgn0016700	9.33	9.12	8.95	8.97	8.82	8.65
1635281_at	FBgn0033350	8.43	8.23	8.33	8.32	8.51	8.33
1626676_at	FBgn0025740	9.32	9.11	8.98	8.74	9.02	9.18
1625265_at	FBgn0035189	7.3	7.09	7.59	7.39	6.92	6.71
1628584_at	FBgn0036910	8.07	7.86	7.59	7.27	7.01	7.63
1632497_a_at	---	7.76	7.55	7.92	7.11	6.98	7.35
1622947_s_at	FBgn0004363	12.72	12.51	12.48	12.57	12.51	12.31
1639851_at	FBgn0040798	7.28	7.07	6.46	6.23	6.82	7
1638678_at	FBgn0034223	9.67	9.46	9.59	9.82	9.67	9.5
1636521_at	FBgn0026869	8.77	8.56	8.7	8.74	8.48	8.41
1628583_at	FBgn0051687	7.66	7.45	7.54	7.93	7.77	7.35
1639188_at	FBgn0038877	9.12	8.91	8.87	8.5	8.98	8.83
1639882_at	FBgn0037719	8.84	8.63	8.76	8.78	8.93	8.81
1639653_at	FBgn0036756	7.75	7.54	7.88	7.12	6.78	7.22
1627803_at	FBgn0039301	9.48	9.28	9.46	9.78	9.62	9.34
1626492_s_at	FBgn0001961	8.9	8.69	8.93	8.61	8.8	8.64
AFFX-r2-Ec-	---	12.98	12.77	13.02	13.22	12.75	12.43
1637983_s_at	FBgn0039109	9.05	8.84	9.27	8.88	8.92	8.98
1640363_a_at	FBgn0039464	9.28	9.07	9.32	9.88	9.83	9.4
1628363_at	FBgn0028373	8.78	8.57	9.04	8.43	7.96	8.42
1638550_s_at	FBgn0003074	11.02	10.81	10.87	11.05	11.06	10.67
1641599_at	---	11.71	11.5	11.02	11.05	11.15	11.02
1635137_a_at	FBgn0036212 /// FBgn003	9.63	9.42	9.66	9.31	9.51	9.28
1637286_a_at	FBgn0003209	9.49	9.28	9.32	9.4	9.23	9.07

1637125_at	FBgn0030060	10.09	9.87	9.9	10.3	10.24	9.67
1629115_s_at	FBgn0026178	8.67	8.45	8.54	8.39	8.38	8.22
1632658_a_at	FBgn0031192 /// FBgn003	7.52	7.31	7.07	7.17	7.29	6.94
1624139_at	FBgn0011754	9.82	9.6	9.51	9.39	9.6	9.5
1637401_at	FBgn0030528	8.75	8.53	8.35	8.31	8.76	8.51
1636354_at	FBgn0033160	9.29	9.07	9.63	9.63	9.59	9.24
1634978_at	FBgn0032140	8.3	8.08	8.01	7.25	7.7	8.01
1640199_at	FBgn0037332	9.16	8.95	8.96	9.1	9.09	8.95
1634704_at	---	7.28	7.07	7	7.27	7.18	6.89
1627004_at	FBgn0037071	8.84	8.62	8.58	8.87	8.93	8.77
1628815_at	---	9.98	9.76	9.71	9.45	9.7	9.6
1624686_a_at	FBgn0000479	8.64	8.43	8.77	8.86	8.55	8.38
1635447_at	FBgn0034225	7.66	7.44	7.58	6.9	7.1	7.44
1628117_at	FBgn0001226	12.4	12.18	12.18	12.7	12.62	12.23
1637079_at	FBgn0034300	9.66	9.45	9.28	9.29	9.35	9.45
1623605_a_at	FBgn0043364	9.62	9.41	9.37	9.13	9.4	9.22
1636003_at	FBgn0032430	8.3	8.09	8.66	8.46	8.2	7.93
1641293_at	FBgn0038736	7.59	7.38	7.5	7.43	7.57	7.36
1631237_s_at	FBgn0032036	9.52	9.3	9.33	9.07	9.38	9.05
1626314_at	FBgn0026158	10.13	9.91	10.35	9.93	10.13	9.87
1636026_at	FBgn0003471	9.2	8.98	9.54	9.07	9.09	8.84
1628795_s_at	FBgn0031779	7.7	7.49	7.6	7.84	7.64	7.47
1630118_s_at	FBgn0033739	7.48	7.26	7.49	7.57	7.6	7.6
AFFX-BioDn-	---	11.49	11.27	11.61	11.76	11.26	10.88
1632656_at	FBgn0030048	10.39	10.17	9.34	9.63	10.21	9.86
1637037_at	FBgn0000053	8.47	8.25	8.84	8.36	8.23	8.11
1629886_s_at	FBgn0000721	12.14	11.92	12.13	11.95	12.03	12.08
1631412_at	FBgn0029878	8.93	8.72	8.72	8.33	8.18	8.5
1623891_at	---	9.17	8.95	9.47	9.42	9.38	9
1638581_at	FBgn0031057	9.69	9.47	8.87	9.1	9.48	9.17
1629487_at	FBgn0019949	9.35	9.13	9.08	9.31	9.35	9.1
1636274_at	FBgn0030941	7.51	7.29	8.03	6.89	7.35	7.11
1626411_at	FBgn0029984	10.26	10.04	10.55	10.32	10.28	10.09
1638317_at	FBgn0030660	8.61	8.39	8.06	7.54	9.22	9.18
1626892_at	FBgn0032920	10.48	10.26	10.32	10.41	10.51	10.26
1636841_at	FBgn0033466	7.18	6.95	6.76	6.99	7.4	7.32

1624592_at	FBgn0032247	7.88	7.66	7.99	8.08	7.71	7.59
1624246_s_at	FBgn0039849 /// FBgn003	9.89	9.67	9.58	9.96	10.02	9.62
1637778_a_at	FBgn0039690	7.93	7.71	8.04	7.86	7.92	7.83
1639071_a_at	FBgn0020381	9.03	8.81	8.77	8.45	8.52	8.7
1634720_at	FBgn0030519	10.58	10.36	10.36	10.33	10.45	10.17
1638367_at	---	10.24	10.01	10.43	10.58	10.64	10.16
1636923_a_at	FBgn0033246	9.59	9.37	9.2	9.06	9.1	8.92
1633034_s_at	FBgn0015222	12.86	12.63	12.64	12.7	12.81	12.65
1635677_a_at	FBgn0014388	7.07	6.84	7.3	6.42	6.68	6.84
1633227_s_at	FBgn0032402	7.89	7.67	7.65	7.39	7.61	7.56
1635744_at	FBgn0032904	8.68	8.45	8.44	8.54	8.52	8.3
1636656_at	FBgn0036804	8.46	8.23	8.48	8.55	8.52	8.26
1624589_a_at	FBgn0028509	9.03	8.8	8.6	8.42	8.72	8.82
1640108_at	FBgn0035318	8.15	7.93	8.09	8.13	8.25	8.06
1635870_at	FBgn0030218	7.68	7.45	7.97	7.42	7.52	7.39
1639818_s_at	FBgn0015949	8.71	8.48	8.7	8.72	8.76	8.67
1638587_at	FBgn0003733	8.82	8.59	8.65	8.96	8.88	8.74
1628556_s_at	FBgn0010229	7.25	7.02	7.09	7.18	7.09	6.98
1639579_s_at	FBgn0031494 /// FBgn003	9.14	8.92	8.93	8.72	9.23	8.89
1632264_at	FBgn0030467	7.92	7.69	6.81	6.78	7.92	7.81
1641066_s_at	FBgn0032820	8.34	8.12	8.72	9.19	8.35	8.02
1640386_at	FBgn0004003	8	7.77	8.39	6.81	6.52	8.06
1626590_a_at	FBgn0033664	8.3	8.07	8.13	7.8	8.14	7.86
1626965_at	FBgn0032618	7.31	7.08	7.32	6.02	7.31	7
1631402_s_at	FBgn0010229	8.39	8.16	8.26	8.24	8.11	8.05
1632028_a_at	---	9.26	9.03	9.33	9.06	9.24	8.91
1628199_at	---	9.09	8.85	9	9.13	9.3	9.1
1625503_at	FBgn0052425	10.33	10.09	10.57	9.86	9.84	10.08
1633319_at	FBgn0035403	8.3	8.06	7.86	8.18	8.19	7.95
1629821_at	---	10.06	9.82	9.62	9.81	9.72	9.72
1630145_s_at	FBgn0029508	9.36	9.13	9.51	9.42	9.19	9.28
1634713_at	FBgn0034902	10.72	10.48	10.74	10.76	10.76	10.56
1636769_at	FBgn0032974	10.17	9.94	10.17	10.14	10.2	9.98
1630196_at	FBgn0025109 /// FBgn000	9.01	8.77	8.62	8.32	8.51	8.67
1625236_s_at	FBgn0040752	9.57	9.34	9.38	9.17	9.43	9.34
1639387_s_at	FBgn0015924	9.16	8.92	8.86	8.78	9.11	8.99

1636131_at	FBgn0038035	7.42	7.19	7.51	7.72	7.04	6.92
1633572_at	FBgn0033612	7.63	7.4	8.46	7.77	7.14	7.38
1640122_at	---	11.27	11.04	10.76	10.61	11.1	10.74
1637665_at	---	8.97	8.73	8.61	8.56	8.67	8.76
1631698_s_at	FBgn0026147	7.43	7.19	7.32	7.18	6.7	6.86
1628453_at	FBgn0030194	11.5	11.26	11.63	11.41	11.28	11.17
1641111_s_at	FBgn0028646	7.94	7.7	7.74	8.19	7.8	7.47
1632691_at	FBgn0004636	10.17	9.94	10.13	9.77	9.7	9.86
1641452_a_at	FBgn0041203	7.88	7.64	7.78	7.67	7.77	7.55
1630661_at	---	10.86	10.62	10.7	10.28	10.69	10.66
1634249_s_at	FBgn0021967	10.96	10.72	11.19	10.82	10.97	10.65
1638132_at	FBgn0039094	7.51	7.27	7.67	8.04	6.99	7.02
1623468_at	FBgn0035210	8.7	8.46	8.5	9.06	8.76	8.57
1628428_at	FBgn0025373	9.81	9.57	9.81	9.54	9.74	9.59
1634846_a_at	FBgn0031024	11.5	11.26	11.74	11.39	11.53	11.22
1641231_at	FBgn0033182	7.23	6.99	7.17	7.21	7.28	7.19
1627060_s_at	FBgn0010225	7.28	7.04	7.27	6.99	7.55	7.24
1635256_s_at	FBgn0035321	9.93	9.69	9.72	9.63	9.95	9.81
1633750_s_at	FBgn0031291	8.44	8.2	7.91	7.15	7.72	7.69
1641530_s_at	FBgn0033478	9.98	9.74	9.8	10.35	9.66	9.34
1628469_a_at	FBgn0052529	7.7	7.46	7.61	7.52	7.55	7.5
1633803_at	FBgn0003076	10.38	10.14	10.43	10.52	10.57	10.14
1638953_a_at	FBgn0035264 /// FBgn002	9.93	9.69	10.05	9.79	9.72	9.71
1631671_at	---	8.78	8.54	8.73	8.76	8.72	8.27
1631516_s_at	---	8.09	7.84	8.13	8.02	8	8.01
1629072_at	FBgn0003638	10.08	9.83	9.23	9.16	9.63	9.24
1636543_a_at	FBgn0039690	7.04	6.79	7.13	6.91	7.04	6.92
1624756_at	FBgn0027572	7.39	7.14	7.45	7.46	7.64	6.9
1638051_at	FBgn0032713	7.35	7.1	7.98	7.12	6.96	7.03
1641304_s_at	FBgn0037623	8.28	8.03	8.36	8.5	7.79	7.75
1637017_at	FBgn0037240	9.31	9.07	9.34	9.38	9.22	9.09
1625175_s_at	FBgn0031401	9.38	9.13	9.42	9.15	9.33	9.25
1634587_s_at	FBgn0036134	10.03	9.78	9.94	10	10	9.9
1624666_at	FBgn0037526	7.72	7.48	7.58	7.83	7.42	7.36
1629239_s_at	FBgn0039790	9.6	9.36	9.73	9.7	9.77	9.46
1623100_at	FBgn0027885	10.68	10.43	10.32	9.71	10.3	10.55

1631392_at	FBgn0039241	11.01	10.76	11.23	11.35	10.88	10.54
1638324_s_at	FBgn0038985	8.51	8.27	9.05	7.23	7.49	8.62
1638074_at	FBgn0035906	7.87	7.63	7.42	7.85	7.6	7.29
1631141_at	FBgn0025571	10.04	9.79	9.49	9.71	9.84	9.67
1625369_at	FBgn0038804	7.34	7.09	7.17	7.1	7.06	6.7
1624620_at	FBgn0004378	9.31	9.06	9.16	8.89	9.2	9
1637398_a_at	FBgn0000256	7.86	7.61	7.71	7.85	7.79	7.42
1626646_s_at	FBgn0036623	9.4	9.15	9.41	9.13	9.44	9.2
1630807_at	FBgn0039122 /// FBgn005	7.27	7.02	7.25	6.46	6.75	6.9
1625889_at	FBgn0020910	8.69	8.44	8.48	7.85	8.55	8.55
1640489_at	FBgn0038347	7.43	7.18	7.41	7.08	7.34	7.02
1623376_s_at	FBgn0013305	9.68	9.42	9.54	9.47	9.66	9.58
1630806_at	FBgn0000810	8.3	8.05	8.06	8.07	8	7.99
1631377_a_at	FBgn0022709	7.56	7.31	7.71	7.41	7.62	7.31
1635918_at	FBgn0052542	8.98	8.73	8.92	8.65	8.41	8.71
1623849_s_at	FBgn0039049	8.62	8.37	8.78	8.87	8.56	8.36
1626745_at	FBgn0029118	8.78	8.53	8.96	8.97	8.81	8.56
1628075_at	FBgn0015522	10.3	10.05	9.83	9.73	10.14	9.91
1634935_a_at	FBgn0033446	8.25	7.99	8.22	7.99	8.65	8.41
1626173_at	FBgn0010083	11.37	11.11	10.98	11.18	11.06	10.87
1635635_a_at	FBgn0015766	8.98	8.73	9.24	8.11	8.55	8.65
1638265_s_at	FBgn0051311	9.3	9.05	9.41	9.61	9.58	9.25
1626624_s_at	FBgn0041789	7.63	7.38	7.23	7.93	7.51	7.27
1627673_at	FBgn0003321	9.82	9.56	9.53	9.53	9.79	9.61
1641334_at	---	10.22	9.97	10.12	10.18	10.31	10.01
1625136_s_at	FBgn0032849	9.82	9.57	9.9	9.94	9.85	9.62
1634429_at	---	8.4	8.14	8.12	7.99	8.28	8.02
1641082_at	FBgn0030028	8.33	8.07	8.27	8.41	8.33	8.23
1641267_at	FBgn0003189	9.04	8.78	9.35	8.83	9.01	8.82
1641074_s_at	FBgn0011673	9.19	8.93	8.85	8.87	9.2	9.06
1637361_a_at	FBgn0025388	8.86	8.6	8.34	8.59	8.89	8.62
1632675_s_at	FBgn0039430	8.87	8.61	8.03	8.63	8.88	8.64
1640077_at	FBgn0030741	7.94	7.68	7.81	8.02	8.15	7.61
1639015_s_at	FBgn0001123	7.78	7.52	8.46	7.59	7.84	7.92
1640976_at	FBgn0029978	9.06	8.8	8.83	8.76	8.91	8.69
1624210_at	---	8.72	8.46	8.8	9.05	8.97	8.52

1631768_at	FBgn0022986	8.31	8.05	8.04	7.91	7.93	7.8
1639575_at	FBgn0033458	10.49	10.23	9.82	9.78	10.94	10.55
1635886_s_at	---	7.11	6.85	7.55	6.21	6.38	5.78
1636101_a_at	FBgn0051729	9.3	9.03	9.21	9.36	9.25	9.01
1626570_s_at	FBgn0025803	9.71	9.45	9.76	9.55	9.69	9.34
1636096_at	FBgn0030710	9.55	9.29	9.35	9.4	9.44	9.1
1633934_at	FBgn0037744	9.39	9.13	9.61	9.21	9.06	8.99
1633081_at	FBgn0031192 /// FBgn003	9.87	9.6	9.64	9.69	9.62	9.46
1625298_at	FBgn0031510	7.32	7.06	7.02	7.56	7.68	7.25
AFFX-BioC-3	---	10.4	10.14	9.96	10.07	10.1	9.71
1626707_a_at	FBgn0000083	10.6	10.33	10.62	10.41	10.4	10.16
1640834_at	FBgn0053002	10.27	10.01	10.18	10.2	10.32	9.97
1632952_at	FBgn0032160	10.39	10.12	10.24	10.32	10.41	10
1624873_at	FBgn0001296	9.62	9.35	10.32	9.2	8.7	9.27
1628339_a_at	FBgn0039737	8.45	8.19	8.48	8.3	8.95	8.46
1641518_a_at	FBgn0016977	8.59	8.32	8.38	7.96	8.24	8.23
1636468_a_at	FBgn0028744	9.06	8.79	9.19	8.76	8.94	8.77
1634845_at	FBgn0033127	9.77	9.5	9.33	9.76	9.75	9.44
1638060_at	FBgn0035720	8.57	8.3	7.68	7.54	7.93	7.98
1641506_at	---	11.95	11.68	11.16	11.34	11.57	11.32
1631223_at	FBgn0037369	9.57	9.3	9.64	9.89	9.62	9.24
1624119_at	FBgn0052486	8.86	8.59	8.68	8.52	8.59	8.59
1633386_s_at	---	6.16	5.89	5.68	4.64	7.31	5.4
1636809_at	FBgn0002525	9.63	9.36	9.6	9.31	9.32	9.14
1635062_at	FBgn0052743	8.12	7.85	7.69	7.4	7.95	7.75
1635900_at	FBgn0022073	10.18	9.91	10.25	9.64	10	9.92
1636947_at	FBgn0036424	8.41	8.14	8.44	7.83	8.06	8.25
1641207_s_at	FBgn0030817	11.68	11.41	11.63	11.73	11.8	11.67
1639877_at	FBgn0023181	9.08	8.81	9.04	9.56	9.26	8.77
1629568_at	---	8.38	8.11	8.56	8.4	8.3	8.15
1641556_a_at	FBgn0022153	8.61	8.34	8.38	8.33	8.56	8.36
1638653_a_at	FBgn0032469	7.82	7.55	8.07	7.7	7.12	7.43
1626393_at	FBgn0033375	8.38	8.1	8.08	8.05	7.96	7.98
1633488_at	FBgn0023129	9.68	9.41	9.61	9.72	9.91	9.59
1641279_at	FBgn0000173	9.2	8.92	9.18	8.66	8.87	9.02
1634156_at	FBgn0032208	10.16	9.89	10.21	9.81	10.09	9.94

1625710_at	---	9.46	9.19	9.22	9.32	9.47	9.1
1633054_at	FBgn0036696	10.4	10.12	10.3	10.32	10.18	9.94
1623770_at	FBgn0030482	8.16	7.89	8.29	7.88	7.39	7.22
1631149_s_at	FBgn0011638	11.28	11.01	10.95	11.07	11.07	10.9
1636958_s_at	---	9.76	9.48	9.8	9.62	9.73	9.41
1634522_s_at	FBgn0020389	8.02	7.75	7.97	7.7	7.96	7.53
1624378_at	FBgn0010110	8.87	8.59	8.72	8.69	8.67	8.34
1625744_at	---	10.88	10.6	11.37	11.59	11.19	11.51
AFFX-r2-Ec-	---	8.85	8.57	8.37	8.68	8.6	8.05
1624324_a_at	---	11.34	11.06	11.42	11.71	11.53	11.19
1632466_at	FBgn0032926	9.96	9.68	9.49	9.66	9.82	9.51
1627040_at	FBgn0027507	9.12	8.84	9.56	9.06	9.47	8.93
1633592_a_at	---	9.06	8.77	9.33	8.95	9.19	8.65
1629209_at	FBgn0038183	8.33	8.04	9.14	8.21	8	8.02
1635035_at	FBgn0036446	7.23	6.95	7.16	7.12	6.81	6.71
1632519_at	FBgn0034054	8.26	7.98	8.06	8.23	8.37	8.01
1625281_at	FBgn0027581	9.31	9.03	9.28	9.17	9.41	9.13
1626315_at	FBgn0030942	9.77	9.48	9.81	9.89	9.85	9.4
1631004_s_at	FBgn0003567	9.13	8.84	9.07	9.33	9.38	9.03
1623959_at	FBgn0031143	10.45	10.16	10.37	10.76	10.54	9.76
1635940_at	FBgn0032228	7.2	6.91	7.33	6.52	6.8	7.15
1632103_at	FBgn0037270	11.1	10.81	11.09	10.78	11.12	10.82
1634106_at	---	7.74	7.46	7.52	7.18	7.15	7.24
1627653_at	FBgn0052597	6.88	6.59	6.9	6.86	7.05	6.45
1629961_s_at	FBgn0010609	8.73	8.44	8.51	8.71	8.41	8.52
1632377_at	FBgn0034067	8.88	8.59	8.15	8.05	8.35	8.41
AFFX-r2-Ec-	---	10.67	10.38	10.26	10.47	10.36	9.88
1625895_a_at	FBgn0051211	8.22	7.93	7.51	7.45	7.63	7.6
1631258_at	FBgn0050005	9.77	9.48	9.73	9.49	9.85	9.53
1639527_at	FBgn0032243	8.6	8.31	8.43	8.36	8.52	8.36
1624075_at	FBgn0051495	7.19	6.9	7.61	7.82	7.5	6.77
1640922_a_at	FBgn0004914	9.35	9.06	9.36	9.31	9.44	9.31
1625792_s_at	---	10.57	10.27	10.41	10.92	10.82	10.42
1627854_at	FBgn0030737	8.81	8.51	8.75	8.61	8.17	8.13
1641022_a_at	FBgn0010383	8.01	7.72	7.96	7.41	7.28	7.31
1633143_s_at	---	7.45	7.16	7.19	6.75	6.52	6.7

1631595_at	---	10.24	9.95	10.39	9.85	10.15	9.93
1641289_at	FBgn0003498	11.25	10.95	11.65	10.85	10.74	11.01
1631549_s_at	FBgn0033836	8.54	8.25	8.29	8.46	8.6	8.18
1624331_at	---	9.58	9.28	9.74	9.66	9.56	9.25
1627796_s_at	FBgn0037444	9.79	9.49	9.82	9.6	9.69	9.5
1631565_a_at	FBgn0000370	10.87	10.57	11.41	11.13	11.21	10.91
1636771_at	---	9.15	8.85	9.18	9.28	9.21	8.91
1634188_a_at	FBgn0014396	7.69	7.39	7.85	7.28	7.68	7.58
1627015_at	FBgn0030026	8.98	8.68	8.68	8.85	8.82	8.46
1641078_s_at	FBgn0034025	9.35	9.05	9.11	8.83	9.14	9.03
1633379_s_at	FBgn0000338	9.21	8.91	9.24	8.93	9	9.05
1629905_s_at	---	7.29	6.99	7.92	7.52	7.02	7.28
1632135_a_at	FBgn0000662	9.93	9.63	9.53	10	9.94	9.67
1641685_at	FBgn0036735	8.34	8.04	8.44	8.19	8	8.05
1633468_x_at	---	7.53	7.23	7.07	7.01	7.39	7.24
1626749_a_at	FBgn0036837 /// FBgn003	11.04	10.74	10.67	10.77	10.92	10.87
1622950_a_at	FBgn0034611	9.93	9.63	10	9.42	9.78	9.56
1635808_s_at	FBgn0027610	8.94	8.64	9.21	9.24	9.06	8.67
1624913_s_at	FBgn0011818	8.59	8.29	8.16	8.4	8.51	8.16
1640793_at	FBgn0033951	9.28	8.98	9.32	9.47	9.61	9.27
1633760_at	FBgn0031877	7.31	7	7.47	7.27	7.41	7.07
1625697_at	---	7.17	6.86	6.15	4.12	6.93	6.18
1632963_at	FBgn0039561	9.02	8.72	8.69	8.67	8.85	8.88
1633225_at	FBgn0052278	9.93	9.62	10.02	9.67	9.72	9.53
1641281_at	FBgn0033581	9.5	9.19	9.33	9.69	9.68	9.15
1626352_at	---	7	6.7	6.82	6.41	6.72	6.32
1625027_a_at	FBgn0036545	9.61	9.31	8.58	9.23	9.56	9.2
1627493_at	FBgn0031913	10.53	10.23	10.74	9.92	10.28	9.84
1636301_s_at	FBgn0040108	9.6	9.29	9.92	9.68	9.49	9.61
1628132_at	FBgn0032517	7.22	6.92	7.12	6.93	7.25	6.88
1633843_at	FBgn0028952	7.58	7.27	7.19	7.39	7.71	7.57
1637785_at	FBgn0001332	10.8	10.49	10.77	11.18	10.94	10.56
1637402_at	---	8.55	8.24	8.26	8.46	8.63	8.32
1623954_s_at	FBgn0031025	9.77	9.46	9.82	10.04	10.03	9.53
1637491_s_at	FBgn0023507	7.3	6.99	7.73	7.16	7.37	6.69
1639233_at	FBgn0040234	7.74	7.43	7.64	7.57	7.78	7.46

1636928_s_at	FBgn0031174	9.38	9.08	9.55	9.48	9.14	9.11
1625445_s_at	FBgn0003396	8.43	8.12	8.71	8.33	8.31	8.26
1633232_at	---	7.81	7.5	7.76	7.1	7.6	7.58
1634222_at	FBgn0038953	7.87	7.56	7.85	8.66	7.89	7.49
1628873_s_at	FBgn0032940	9.99	9.68	9.85	9.53	9.68	9.49
1624070_at	FBgn0010408	9.48	9.16	9.29	8.79	9.5	9.22
1631013_at	---	10.06	9.75	9.89	9.64	9.8	9.74
1625196_a_at	FBgn0035497	8.52	8.21	8.38	8.4	8.6	8.37
1630318_at	---	9.05	8.74	8.65	8.91	9.33	8.89
1634572_at	FBgn0034259	12.34	12.03	12.34	12.16	12.35	12.04
1628352_a_at	FBgn0036892	7.31	7	7.53	7.33	7.24	6.93
1626579_at	FBgn0029925	9.54	9.23	9.11	9.51	9.79	9.25
1639306_s_at	FBgn0035142	9.17	8.86	9.45	8.99	8.99	8.81
1633454_s_at	FBgn0027621	7.01	6.69	6.58	6.63	6.5	6.39
1632958_a_at	FBgn0034648	7.84	7.52	7.72	7.61	8.08	7.7
1624742_a_at	FBgn0023211	11.21	10.89	11.3	10.96	11.23	11.04
1630653_a_at	FBgn0001145	7.44	7.13	7.38	6.36	7.04	6.64
AFFX-BioB-M	---	9.69	9.37	9.21	9.38	9.28	8.88
1641650_at	FBgn0015573	7.11	6.79	8.36	8.46	7.88	7.56
AFFX-r2-Ec-b	---	9.36	9.04	8.97	9.18	9.04	8.54
1637867_at	FBgn0031706	7.15	6.83	6.96	6.44	6.36	6.73
1624798_s_at	FBgn0004435	7.15	6.83	6.94	6.56	6.84	6.95
AFFX-BioC-5	---	10.42	10.1	9.82	9.95	10.1	9.64
1628276_s_at	---	9.5	9.18	9.76	9.46	9.3	9.31
1635238_s_at	FBgn0005536	7.16	6.84	7.45	6.96	6.93	6.72
1628143_a_at	FBgn0003244	8	7.68	8.13	7.72	7.73	7.81
AFFX-BioB-3	---	9.16	8.84	8.63	8.74	8.86	8.38
1627312_at	FBgn0002611	6.95	6.63	7.49	7.35	8.07	7.57
1635037_at	FBgn0035986	8.05	7.73	7.72	7.85	8.25	7.83
1632380_at	FBgn0002777	8.86	8.53	9.55	9.12	8.18	8.1
1632179_at	FBgn0014032	9.12	8.8	9.03	9.35	9.35	8.79
1622959_at	FBgn0033432	10.17	9.85	9.91	9.61	10.08	9.84
1638645_at	FBgn0031529	8.68	8.35	8.59	8.32	8.87	8.54
1628432_at	FBgn0039537	10.41	10.08	9.66	10.44	10.67	9.89
1631362_at	---	9.63	9.3	9.95	9.64	9.64	9.39
1628032_a_at	FBgn0051092	7.36	7.03	7.02	7.1	6.92	7.09

1638964_at	FBgn0037552	6.65	6.33	7.83	7.55	8.04	8.12
1631573_a_at	FBgn0016078	7.94	7.61	7.83	7.8	7.58	7.74
1627443_at	FBgn0029833	7.51	7.19	7.86	8.01	8.86	8.59
1630344_at	FBgn0032298	9.1	8.77	9.62	9.25	8.92	8.75
1626654_a_at	FBgn0039266	9.2	8.87	9.25	8.93	8.95	8.69
1634949_at	FBgn0010303	7.57	7.24	7.15	6.97	7.18	7.23
1627348_at	FBgn0038490	6.91	6.58	7.15	7.47	7.09	6.45
1623212_s_at	FBgn0041582	7.56	7.23	7.67	7.33	6.93	7.05
1623693_a_at	FBgn0020304	9.92	9.59	10.31	9.8	9.93	9.63
1641284_a_at	FBgn0039229	9.18	8.85	9.05	9.05	9.06	8.88
1632298_s_at	FBgn0024211	8.72	8.39	8.61	7.87	7.93	8.21
1631827_at	FBgn0033467	7.66	7.33	7.96	8.43	8.15	7.75
1630858_s_at	FBgn0039714	9.39	9.06	9.37	9.11	9.36	9.02
1624003_at	FBgn0032729	8.7	8.37	8.74	8.49	8.57	8.27
1639009_at	FBgn0030073	7.05	6.72	6.26	6.38	6.95	6.91
1625967_s_at	FBgn0024515	9.06	8.72	8.98	8.45	8.17	8.24
1631569_s_at	FBgn0013272	10.28	9.94	10.92	10.34	9.71	10.06
1623428_at	FBgn0040968	8.33	8	7.64	6.12	7.78	7.61
1629713_at	FBgn0035194	8.49	8.15	8.09	8.83	8.72	8.41
1636990_at	---	7.89	7.56	7.73	7.58	7.86	7.41
1633770_at	FBgn0037646	8.72	8.39	8.37	8.62	8.63	8.24
1631728_s_at	FBgn0024734	9.65	9.32	9.4	9.39	9.1	9.14
AFFX-r2-Ec-	---	11	10.67	10.45	10.71	10.67	10.17
1639769_at	---	10.65	10.31	10.74	10.44	10.31	10.04
1630365_at	FBgn0038259	7.03	6.69	7.16	6.64	6.85	6.79
1636315_at	FBgn0033195	7.19	6.85	6.77	7.29	7.31	7.02
1636505_at	---	10.93	10.59	10.85	10.72	10.97	10.66
1641272_at	FBgn0030130	8.71	8.37	8.47	7.9	7.84	8.23
1624856_at	FBgn0028525	9.27	8.93	8.6	8.38	9.06	9.1
1627773_a_at	FBgn0034405	10.77	10.43	10.55	10.2	10.9	10.68
1636694_at	FBgn0035590	8.39	8.05	8.35	8.61	8.55	8.07
1624503_at	FBgn0037012	7.58	7.24	7.98	6.84	6.78	7.45
1635372_a_at	FBgn0038294 /// FBgn002	9.2	8.86	9.94	9	8.76	8.92
1627184_at	---	8.14	7.8	8	7.7	7.76	7.73
1634250_at	FBgn0000044	10.45	10.1	11.81	9.99	10.36	10.58
1635583_s_at	FBgn0016797	7.29	6.95	8.14	7.67	7.15	6.96

1635558_s_at	FBgn0033802	8.98	8.64	9.03	8.7	8.44	8.33
1629088_at	FBgn0035993 /// FBgn003	9.11	8.76	8.74	8.88	8.86	8.9
1624475_at	---	9.97	9.63	10.35	10.19	10.19	9.52
1630378_at	FBgn0031358	8.34	7.99	7.89	8.35	8.49	7.91
1629023_s_at	---	10.81	10.46	10.74	11.04	11.05	10.76
1635040_a_at	FBgn0015933	9.89	9.54	9.62	9.6	9.74	9.62
1623388_at	FBgn0035084	7.15	6.8	6.87	6.9	6.52	6.32
1626349_at	FBgn0024510	9.77	9.42	10.07	9.7	9.73	9.45
1631058_s_at	---	10.93	10.58	10.8	10.91	11.07	10.68
1627132_at	FBgn0034379	7.37	7.02	7.25	7.61	7.9	7.32
1629758_at	---	7.75	7.4	7.56	7.67	7.94	7.58
1637499_s_at	FBgn0032587	8.95	8.6	8.81	8.61	8.79	8.63
1641549_at	FBgn0037892	9.23	8.88	9.25	9.21	9.22	8.79
1634576_at	FBgn0004647	8.41	8.06	8.02	7.84	8.17	8.17
1624054_at	FBgn0036752	7.37	7.02	8.23	7.49	7.17	6.74
1640775_a_at	FBgn0010222	8.69	8.34	9.33	8.82	8.64	8.38
1635768_at	FBgn0033814	10.18	9.82	9.97	9.57	9.78	9.78
1627216_s_at	---	9.42	9.07	9	8.71	9.56	9.29
1633487_at	FBgn0050109	9.25	8.89	9.01	8.98	9.33	8.95
1624857_at	FBgn0039969	6.97	6.61	6.77	6.39	7.01	7.04
1641381_s_at	FBgn0033609 /// FBgn003	9.41	9.05	9.1	9.12	9.48	9.22
1628580_a_at	FBgn0051536	7.23	6.87	7.45	6.78	6.68	6.59
1639485_at	---	9.63	9.27	9.68	9.49	9.96	9.53
1638819_at	FBgn0051712	9.23	8.87	8.98	9.13	9.14	8.86
1632063_s_at	FBgn0035558	8.08	7.72	8.23	8.19	8.1	8.32
1632339_s_at	FBgn0014141	9.48	9.12	9.28	8.67	8.95	9.07
1625334_at	---	11.51	11.15	11.28	11.23	11.55	11.06
1637256_at	---	7.72	7.36	7.88	7.78	7.76	7.37
1634736_at	FBgn0004873	9.73	9.37	9.7	9.49	9.86	9.47
1622908_a_at	FBgn0030073	7.35	6.99	5.6	5.7	6.69	6.44
1638256_at	FBgn0042713	8.5	8.13	8.44	8.57	8.69	8.44
1623875_at	FBgn0036000	8.39	8.03	8.43	8.12	8.38	8.28
1636943_s_at	---	10.33	9.97	10.19	10.65	10.17	9.82
1629965_at	FBgn0027513	9.02	8.65	8.38	8.7	9.06	8.59
AFFX-r2-Ec-b	---	9.51	9.14	9.03	9.4	9.21	8.66
1628398_at	FBgn0032167	7.89	7.52	7.8	6.99	7.62	6.91

1624919_at	FBgn0033734 /// FBgn003	8.71	8.34	8.57	8.29	8.26	8.23
1629511_at	FBgn0038983	9.28	8.91	9.4	8	8.46	9.13
1631455_at	FBgn0010649	7.9	7.53	7.82	7.77	7.82	7.44
1636648_s_at	---	7.29	6.92	6.63	5.99	6.87	6.8
1638630_at	FBgn0039751	8.09	7.72	7.73	8.08	8.05	7.67
1641620_s_at	FBgn0029903	9.21	8.83	8.7	8.47	8.56	8.55
1636787_s_at	FBgn0003691	9.85	9.47	9.73	9.6	9.43	9.24
1628385_a_at	FBgn0011656	9.13	8.76	9.02	9.07	9.1	8.86
1623589_a_at	FBgn0038983	7.55	7.18	7.51	5.75	6.78	7.42
AFFX-BioB-5	---	9.02	8.65	8.52	8.74	8.7	8.17
1636706_at	FBgn0033402	8.15	7.78	7.87	8.22	8.1	7.65
1639217_s_at	FBgn0010300	10.29	9.92	10	10.1	10.2	9.98
1626886_at	FBgn0035044	9.6	9.23	9.43	9.84	9.46	9.05
1633597_at	FBgn0038662	10.32	9.94	10.05	10.17	10.27	10.01
1635355_a_at	FBgn0021872	10.03	9.65	9.37	9.49	9.67	9.48
1634269_at	FBgn0031897	9.11	8.73	9.16	9.02	8.92	8.63
1638696_a_at	FBgn0035999	9.23	8.85	8.8	8.7	9.31	9.03
1633375_at	FBgn0035945	8.89	8.51	8.63	8.61	8.63	8.15
1640567_at	FBgn0031374	8.57	8.19	8.41	8.3	8.45	8.23
1637943_at	FBgn0017397	7.81	7.43	7.81	6.83	6.88	7.16
1634002_at	FBgn0040827	9.59	9.22	8.87	7.9	8.43	8.37
1622909_at	FBgn0020622	10.38	10	10.48	10.31	10.36	10.13
1623453_at	---	8.66	8.28	8.61	9.21	9.16	8.85
1640801_at	FBgn0017558	8.56	8.18	7.96	8.25	8.63	8.12
1640324_at	FBgn0000083	9.61	9.23	9.42	8.68	8.98	9.03
1624410_at	FBgn0034602	7.36	6.98	7.74	7.06	7.15	6.93
1636569_a_at	FBgn0033538	7.97	7.58	7.83	7.57	7.79	7.48
1632796_s_at	FBgn0000546	7.4	7.02	7.08	6.84	7.08	7.11
1625530_at	FBgn0032815	9.08	8.69	9.28	9.16	9.64	9.21
1641504_s_at	FBgn0034718	7.46	7.07	7.58	6.4	6.74	7.2
1623624_at	FBgn0038340	7.47	7.08	8.1	6.85	6.91	7.32
1638948_at	---	9.27	8.88	8.65	8.83	9.21	8.69
1625532_at	FBgn0000394	8.34	7.94	8.23	8.31	8.38	8.23
1641380_a_at	FBgn0040071	7.26	6.87	7.25	6.69	7.04	6.94
1630161_at	FBgn0020439	7.31	6.92	8.5	7.58	7.43	7.02
1634154_at	FBgn0029697	9.05	8.65	7.39	5.79	6.65	8.17

1634952_s_at	FBgn0034392	7.16	6.76	7.15	6.82	7.3	6.82
1630900_at	FBgn0026787	8.74	8.35	8.46	8.48	8.57	8.45
1634783_s_at	FBgn0031229	10.78	10.38	10.89	10.66	10.64	10.4
1638345_at	FBgn0000719	8.85	8.46	9.56	9.21	8.64	8.65
1636149_at	FBgn0028490	10.3	9.9	9.48	9.17	9.82	9.54
1625173_s_at	FBgn0036194	9.29	8.89	8.69	8.72	8.75	8.56
1641303_at	FBgn0000562	9.79	9.4	9.66	10.07	9.82	9.54
1625885_at	---	7.75	7.35	8.35	7.52	7.24	7.17
1638193_at	FBgn0039529	7.79	7.39	7.77	6.95	7.89	7.21
1630861_at	FBgn0034057	8.84	8.44	8.71	8.69	8.71	8.46
1635218_at	FBgn0036318	8.75	8.35	8.82	8.73	8.87	8.64
1622949_at	FBgn0003053	8.23	7.83	8.27	7.84	7.59	7.72
1624907_at	FBgn0029506	11.22	10.82	11.37	11.22	11.07	10.93
1635848_at	FBgn0025885	9.22	8.81	9.17	9.17	9.17	8.74
1634738_s_at	FBgn0051751	7.19	6.78	7.13	6.36	7.44	7.15
1623827_a_at	FBgn0011592	7.83	7.42	8.29	8.53	7.91	7.76
1640075_a_at	FBgn0036007	10.47	10.06	11.22	10.5	9.84	9.94
1634019_at	FBgn0033205	7.59	7.18	7.65	6.1	7.38	7.08
1640932_s_at	FBgn0052626	10.12	9.71	10.19	10.06	9.95	9.36
1627343_a_at	FBgn0036764	9.66	9.25	10.07	9.92	9.51	9.04
1630309_s_at	---	9.07	8.66	9.63	9.11	8.68	8.79
1629740_at	FBgn0051617	12.52	12.1	12.35	12.81	13.01	12.56
1627841_at	FBgn0034705	7.69	7.27	7.14	7.16	7.32	7.18
1636718_s_at	FBgn0031896	11.1	10.68	11.12	10.85	10.73	10.49
1637638_s_at	FBgn0032752	7.96	7.53	7.93	8	7.96	7.51
1625740_at	FBgn0031981	7.33	6.91	7.11	7.54	7.54	7.47
1640838_s_at	FBgn0027932	11.4	10.98	11.41	11.14	11.58	11.21
1635460_a_at	FBgn0002741	8.33	7.9	9.88	8.16	8.43	8.35
1630399_at	FBgn0039709	7.45	7.03	7.53	7.09	6.16	7.15
1625389_at	FBgn0035830	8.93	8.5	9.28	8.93	8.98	8.45
1624042_at	FBgn0004834	7.95	7.52	7.99	7.69	7.82	7.53
1630814_s_at	FBgn0030349	8.12	7.69	8.25	8.04	7.7	7.65
1638417_at	FBgn0051373	8.12	7.68	8.1	8.1	8.54	8.04
1635661_at	---	8.07	7.63	8.08	7.21	7.49	7.3
1634742_at	FBgn0022359	7.56	7.12	7.79	7.9	8.41	7.27
1637645_at	FBgn0029002	7.85	7.41	8.7	7.73	7.55	7.3

1632317_at	FBgn0031645	8.62	8.18	8.92	8.44	8.29	8.27
1638899_s_at	FBgn0030174	9.99	9.55	9.57	9.4	9.09	8.84
1623200_at	FBgn0011591	8	7.56	8.24	7.29	7.51	7.71
1635086_at	FBgn0029838	7.38	6.93	7.21	6.33	6.83	6.68
1640417_a_at	FBgn0033398	8.93	8.49	8.64	8.8	8.93	8.39
1641120_at	FBgn0034723	7.35	6.9	7.98	6.82	7.3	7.05
1636643_at	FBgn0035896	8.29	7.84	8.4	8.28	8.25	8.03
1639439_at	FBgn0030357	7.82	7.37	7.56	7.5	8.31	7.91
1628658_at	FBgn0024234	7.6	7.15	7.8	7.24	7.18	7.18
1634241_at	FBgn0037999	8.35	7.9	8.04	7.88	8.77	8.24
1634337_s_at	FBgn0053070	8.01	7.56	8.16	7.45	7.31	7.46
1628984_s_at	FBgn0010228	9.88	9.43	10.52	9.51	9.09	9.51
1626416_a_at	FBgn0011296	6.53	6.08	6.95	6.34	7.05	6.68
1626536_at	FBgn0035904	7.08	6.63	6.35	7.09	7.12	6.77
1630083_at	FBgn0015796	8.81	8.36	8.44	8.18	8.11	7.76
1624861_at	---	8.77	8.32	8.57	8.74	8.89	8.69
1636268_at	FBgn0040992	7.64	7.18	7.4	5.76	7.34	7.22
1636740_at	FBgn0011768	11.49	11.03	11.55	11.11	11.64	11.1
1632515_a_at	FBgn0032202	9.6	9.14	9.05	9.56	9.77	9.16
1639700_s_at	FBgn0030672	9.32	8.86	9.6	9.2	9.53	9.31
1639115_s_at	---	9.16	8.69	8.62	8.95	9.01	8.76
1638697_at	FBgn0034920	7.43	6.96	7.66	6.75	7.79	6.82
1631291_at	---	9.06	8.59	8.53	8.62	8.92	8.66
1628261_at	FBgn0036589	7.45	6.98	8.87	7.16	7.58	7.56
1626138_s_at	FBgn0005640	10.04	9.56	9.91	9.08	10.09	9.56
1629048_s_at	FBgn0036663	7.77	7.3	7.4	7.08	7.73	7.3
1629409_s_at	---	8.09	7.61	7.21	6.36	7.21	7.29
1622990_at	FBgn0032218	7.75	7.27	7.86	7.05	6.91	6.94
1627242_at	FBgn0011296	7.87	7.39	8.24	7.68	8.22	7.9
1638818_at	---	9.04	8.55	10.37	8.71	8.89	9.11
1639093_s_at	FBgn0032397	9.66	9.17	9.31	9.32	9.56	8.95
1633451_at	FBgn0052634	7.6	7.11	6.8	6.18	6.76	6.73
1638405_at	---	7.59	7.1	8.07	6.94	7.65	7.21
1634583_s_at	FBgn0031220	7.02	6.53	6.75	5.69	6.25	6.3
1626461_at	FBgn0036279 /// FBgn001	7.53	7.04	7.32	7.3	6.72	6.71
1633558_s_at	FBgn0035515	8.58	8.08	8.08	8.39	8.73	7.97

1625588_s_at	FBgn0036147	9.51	9.01	9.94	9.33	9.03	8.91
1638120_at	FBgn0027547	9.7	9.2	9.54	8.46	9.68	8.77
1632989_a_at	---	7.85	7.36	7.25	8.19	8.23	7.69
1626246_s_at	FBgn0024183	8.68	8.19	8.61	8.21	8.5	8.3
1632248_s_at	FBgn0039858	11.91	11.41	11.92	11.73	11.77	11.3
1625664_at	FBgn0036690	9.44	8.94	9.17	10.23	9.36	8.99
1633641_a_at	FBgn0034194	7.06	6.56	7.13	6.39	6.62	6.51
1638022_at	FBgn0035253	7.49	6.99	6.64	6.23	6.65	6.87
1625035_at	---	7.78	7.27	7.62	7.09	7.28	7.11
1637534_at	FBgn0041585	8.1	7.59	8.56	7.83	8.52	7.88
1635715_at	FBgn0051611	12.25	11.74	12.06	12.36	12.67	12.19
1631242_at	---	8.41	7.9	8.05	7.99	8.25	8.14
1639733_s_at	FBgn0032022	7.07	6.56	7.18	6.76	7	6.85
1631456_at	FBgn0036843	9.75	9.24	9.6	9.52	9.67	9.31
1640991_at	---	7.97	7.46	8.14	7.27	7.33	7.34
1629438_at	---	7.93	7.42	7.26	6.86	7.41	7.38
1627962_at	FBgn0051749	8.09	7.57	8.24	8.01	7.4	7.62
1631380_s_at	FBgn0002527	7.91	7.4	8.79	7.57	7.38	7.39
1627494_s_at	FBgn0011818	8.83	8.31	8.51	8.41	8.69	8.39
1639438_at	FBgn0005617	7.99	7.47	7.47	7.33	7.85	7.42
1635182_at	FBgn0011739	8.95	8.43	8.51	8.35	8.42	7.95
1629000_at	---	8.41	7.88	8.14	7.64	8.06	7.83
1628292_s_at	FBgn0015234	9.5	8.97	9.05	9.15	9.52	8.81
1623349_x_at	---	7.99	7.46	8.11	6.44	7.55	7.43
1631321_s_at	FBgn0051617	11.99	11.46	11.69	12.34	12.57	12.01
1629745_at	FBgn0038922	9.07	8.53	8.67	8.79	9	8.05
1625688_at	FBgn0037807	10.93	10.4	11.11	11.18	10.9	10.32
1634238_a_at	FBgn0036433	8.33	7.79	8.53	7.53	8.07	7.88
1623957_s_at	FBgn0010226	9.71	9.17	9.54	9.77	9.41	9.39
1625843_s_at	FBgn0052940	7.73	7.19	7.9	6.94	7.42	7.04
1624881_at	FBgn0024985	7.17	6.63	6.71	6.34	6.72	6.46
1640065_at	---	8.51	7.95	8.92	9.63	8.81	8.88
1641325_s_at	FBgn0004117	7.84	7.28	9.08	7.3	8.01	7.73
1638811_at	FBgn0036191	8.12	7.56	8.48	7.98	7.93	7.65
1640496_at	FBgn0024320	9.11	8.55	8.77	8.4	8.53	8.25
1641408_at	---	7.21	6.64	7.51	6.85	6.93	6.44

1626446_a_at	FBgn0002772	8.32	7.75	10.08	8.26	8.69	8.52
1625116_at	FBgn0001402	7.55	6.99	8.2	6.86	7.19	7.03
1626233_at	FBgn0031745	7.02	6.45	7.71	6.85	6.77	6.43
1639868_at	FBgn0031117	9.63	9.07	9.44	9.6	9.93	9.3
1624549_at	FBgn0027571	9.86	9.29	9.82	9.01	9.11	8.95
1626167_at	FBgn0033174	7.41	6.84	7.28	7.38	7.55	6.7
1634336_at	FBgn0000158	9.78	9.21	9.05	10.13	8.9	8.65
1625088_at	---	9.72	9.14	9.4	9.33	9.61	9.03
1641476_a_at	FBgn0025879	8.08	7.5	8.41	7.46	7.63	7.73
1641324_at	FBgn0002526	8.56	7.99	9.53	8.14	7.81	7.99
1633566_at	FBgn0038627 /// FBgn002	7.49	6.91	6.91	6.89	7.13	6.58
1636900_at	FBgn0032213	7.42	6.84	7.39	7.03	8.17	7.48
1627593_at	FBgn0014931	8.21	7.63	8.56	8.53	8.99	8.31
1631121_at	FBgn0030079	9.59	9.01	9.25	9.02	9.31	9.08
1640223_a_at	FBgn0001402	7.15	6.57	7.64	6.44	6.81	6.48
1629383_a_at	FBgn0035917	7.88	7.29	8.37	7.2	7.77	7.37
1633534_s_at	FBgn0037705	8.39	7.8	7.84	7.6	7.74	7.2
1633928_at	FBgn0030438	9.67	9.08	8.72	9.18	9.48	9.62
1623471_s_at	---	8.1	7.51	8.07	7.35	7.59	7.72
1629398_at	FBgn0032699	8.68	8.08	8.39	8.71	8.68	7.85
1637430_s_at	FBgn0030309	9.09	8.49	9.38	8.43	8.68	8.72
1623241_s_at	---	7.7	7.09	8.01	6.68	7.2	7.33
1632901_s_at	FBgn0000246	8.44	7.84	8.53	8.55	8.06	7.34
1638192_a_at	---	8.37	7.76	8	8.08	8.18	7.9
1629181_at	---	7.68	7.07	6.65	6.47	6.88	6.67
1636600_a_at	FBgn0038294 /// FBgn002	8.72	8.11	9.33	7.89	8.62	8.11
1623256_at	FBgn0034335	10.09	9.48	9.92	10.2	10.94	10.35
1636653_at	FBgn0002930	7.04	6.42	6.08	5.69	6.58	5.99
1636764_at	FBgn0051075	10.07	9.46	9.56	9.69	9.99	9.2
1638154_at	FBgn0017448	8.63	8.01	7.69	8.22	7.73	6.61
1639142_s_at	---	9.84	9.22	9.23	9.87	9.78	9.2
1628465_a_at	FBgn0029876	8.77	8.15	8.68	8.81	7.97	7.99
1632712_s_at	FBgn0038661	8.83	8.21	8.62	8.33	8.51	8.12
1635724_at	FBgn0038658	7.91	7.29	8.63	7.14	7.44	7.6
1636461_at	FBgn0023540	9.1	8.47	8.86	9.29	9.22	8.83
1637955_a_at	FBgn0033431	7.11	6.48	7.2	7.45	7.16	6.43

1626392_s_at	FBgn0011656	7.35	6.73	6.89	5.37	6.5	6.84
1633826_at	FBgn0031305	8.82	8.19	9.39	8.28	8	8.2
1626990_s_at	FBgn0026061	8.03	7.4	8.62	7.62	7.78	7.74
1640945_at	FBgn0005630	7.65	7.02	6.54	7.29	7.67	7.38
1639335_at	---	7.03	6.4	7.54	6.73	6.04	6.38
1630728_a_at	FBgn0033229 /// FBgn004	8.73	8.1	7	7.97	8.6	7.82
1632533_at	FBgn0025879	8.3	7.67	8.51	7.67	7.78	7.78
1640844_s_at	---	7.69	7.05	8.5	7.44	7.25	6.93
1631834_at	---	8.54	7.89	8.63	8.55	8.58	8.02
1635273_s_at	---	7.97	7.32	7.27	7.33	7.74	7.36
1629235_s_at	FBgn0004028	9.49	8.84	10.7	9.07	9.67	9.42
1636352_at	FBgn0031609	8.22	7.57	8.31	7.68	8.32	7.5
1640144_at	FBgn0034512	7.9	7.25	8.12	6.93	7.41	6.96
1639944_at	FBgn0038037 /// FBgn003	7.61	6.96	7.71	7.63	7.41	6.84
1637481_at	FBgn0029114	8.42	7.77	8.62	8.12	8.76	8.09
1641552_at	FBgn0010019	10.17	9.52	9.54	9.36	9.47	9.38
1634125_at	---	7.42	6.76	8.47	7.69	8.59	7.99
1624505_at	---	7.97	7.31	7.96	7.16	7.57	7.05
1632121_a_at	FBgn0035917	8.61	7.95	9.33	7.9	8.44	7.98
1628083_at	FBgn0028743	7.53	6.86	7.92	7.93	8.18	7.93
1635936_at	FBgn0039098	9.11	8.44	8.65	9.64	8.66	7.98
1633010_s_at	FBgn0026781	12.35	11.68	11.66	11.74	12.51	11.58
1636202_s_at	FBgn0001257	9.72	9.05	9.48	9	9.15	9.01
1633059_at	FBgn0033875	9.56	8.88	8.86	9	8.9	8.65
1630917_at	FBgn0031003	9.58	8.9	9.44	9.64	9.71	9.2
1634257_at	FBgn0030828	7.37	6.69	7.15	6.12	7.17	6.8
1624849_at	FBgn0040752	9.2	8.52	9.18	9.03	9.1	8.53
1623281_s_at	FBgn0061209	10.89	10.2	10.37	10.84	11.13	10.54
1633700_at	---	10.19	9.51	10.01	10.39	10.27	9.48
1635666_at	FBgn0061209	11.34	10.64	10.77	11.13	11.58	10.83
1637576_s_at	FBgn0033717	9.29	8.59	8.86	8.66	8.93	8.47
1636835_at	FBgn0030816	9.58	8.88	9.11	9.57	8.77	8.79
1627454_a_at	FBgn0010434	7.49	6.78	6.99	7.01	6.94	6.65
1638912_s_at	FBgn0001215	8.96	8.25	8.23	7.51	8.25	8.12
1636869_at	---	7.9	7.18	7.93	7.22	7.36	7.18
1640565_at	---	7.15	6.43	6.5	5.73	7.45	6.39

1626272_s_at	FBgn0037515	7.98	7.26	7.88	7.92	8.03	7.69
1630509_at	FBgn0002789	9.55	8.82	10.13	8.91	9.71	9.09
1635584_s_at	FBgn0003721 /// FBgn000	9.03	8.3	9.95	8.33	9.32	8.9
1626171_at	---	7.08	6.35	6.93	6.28	6.75	6.22
1632666_at	FBgn0002528	8.37	7.63	8.96	7.73	7.53	7.69
1625514_s_at	FBgn0041585	9.68	8.95	9.56	8.81	9.67	9.16
1627590_at	FBgn0032897	10.37	9.62	9.79	9.43	10.16	9.85
1638143_a_at	FBgn0032006	7.33	6.58	7.11	6.71	6.92	6.64
1628462_s_at	FBgn0025836	9.64	8.89	9.51	9.45	9.41	9.09
1623690_at	FBgn0038761	6.94	6.19	7.54	6.49	7.04	6.89
1624117_at	FBgn0032723	8.13	7.38	7.73	8.3	8.16	7.31
1637322_at	FBgn0003177	7.11	6.35	6.86	6.28	6.54	6.03
1627453_s_at	FBgn0005672	9.27	8.51	9.08	8.97	8.84	8.56
1629195_at	FBgn0032358	8.67	7.91	8.4	8.73	8.87	8.04
1634552_at	FBgn0041180	8.86	8.1	8.74	7.58	8.31	7.74
1626724_at	FBgn0052687	8.91	8.15	8.61	8.36	8.29	7.86
1628963_at	FBgn0033820	9.49	8.73	7.75	7.69	9.08	8.61
1631154_at	FBgn0033787	7.52	6.75	8.36	7.52	7.64	6.43
1632650_at	FBgn0027586	7.79	7.03	8.53	7.04	7.84	7.33
1624725_at	FBgn0037565	6.44	5.67	7.67	7.08	7.13	5.9
1629597_a_at	FBgn0034075	6.99	6.22	7.01	6.85	7.54	8.39
1636015_s_at	---	7.04	6.26	5.52	5.74	5.79	6.45
1630348_a_at	FBgn0037007	10.12	9.34	10.15	9.49	9.98	9.51
1641413_s_at	FBgn0034709	9.06	8.28	9.49	8.03	8.25	8.43
1626397_at	FBgn0005666	6.96	6.18	8.44	7.13	7.22	6.52
1623459_at	FBgn0028985	7.23	6.44	6.05	7.03	7.43	6.54
1636391_at	FBgn0034180	8.7	7.92	7.93	8.56	8.29	7.91
1632639_at	---	6.43	5.64	7.7	7.04	7.06	6.27
1638498_s_at	FBgn0033188	8.41	7.61	8.4	7.83	8.24	7.75
1631783_at	FBgn0031405	9.69	8.88	9.69	8.99	9.83	9
1635544_s_at	---	8.08	7.28	8.72	7.51	8.19	7.63
1639489_at	FBgn0034796	8.37	7.56	8.34	7.79	8.05	7.39
1623342_at	---	8.4	7.58	7.45	7	8.06	7.28
1640379_s_at	FBgn0034851	7.91	7.09	7.64	7.24	7.46	6.6
1635549_at	---	7.36	6.53	5.04	3.62	5.27	6.66
1639229_at	FBgn0016075	9.03	8.21	9.93	8.89	8.28	8.36

1632873_at	---	12.47	11.64	11.57	11.08	12.19	11.35
1623244_at	FBgn0035835	7.43	6.6	6.71	6.23	7.23	6.62
1635199_at	---	8.07	7.24	8.65	7.5	7.7	7.49
1629046_a_at	FBgn0033820	9	8.17	7.29	7.25	8.46	8.06
1633245_at	---	7.31	6.47	7.3	6.5	6.72	6.4
1623497_at	FBgn0002609	7.13	6.29	7.67	7.32	7.2	6.84
1630150_s_at	---	9.46	8.62	10.16	9.32	8.64	8.7
1640222_s_at	FBgn0032156	7.6	6.76	7.84	7.1	7.5	6.66
1631105_at	FBgn0027865	9.58	8.74	9.16	9.51	9.69	9.49
1624203_s_at	FBgn0001987	7.04	6.18	7.11	6.57	6.28	6.31
1632623_at	FBgn0000406	8.28	7.43	6.8	6.68	7.81	6.93
1630502_at	FBgn0011746	7.95	7.08	8.42	6.83	7.11	6.91
1625825_at	FBgn0026562	9.27	8.39	9.69	8.49	9	8.52
1631627_at	FBgn0034365 /// FBgn000	9.29	8.41	9.29	8.75	9.47	8.57
1633935_at	FBgn0050021	7.59	6.71	7.85	6.95	7.12	6.66
1641442_a_at	FBgn0001402	7.78	6.9	8.66	7.25	7.02	7.09
1630014_at	FBgn0034112	8.02	7.14	7.05	6.64	7	6.87
1636758_s_at	FBgn0033229 /// FBgn004	10.35	9.46	8.61	9.54	10.05	9.17
1624839_at	FBgn0001168	9.25	8.36	9.25	8.66	8.71	8.23
1637463_a_at	FBgn0002968	8.7	7.79	8.15	8.21	8.24	7.91
1633556_s_at	FBgn0020493	8.59	7.68	7.68	8.36	8.23	7.14
1631308_at	FBgn0034420	9.26	8.34	8.36	8.41	8.53	8.21
1632945_at	FBgn0051649	7.44	6.51	7.72	6.71	6.83	6.42
1635183_at	FBgn0024293	8.47	7.53	7.08	6.86	7.95	7.06
1639109_a_at	FBgn0023023	7.07	6.13	7.2	6.18	5.88	6.47
1636804_at	FBgn0040398	8.15	7.18	6.68	6.15	7.45	6.78
1634388_at	---	9.69	8.72	9.06	9.3	8.77	8.9
1625433_at	---	7.9	6.93	5.21	5.49	7.08	5.5
1633304_at	FBgn0030341	8.27	7.29	6.98	7.36	7.7	7.24
1636146_at	FBgn0002968	9.08	8.09	8.81	8.67	8.66	8.42
1623782_at	FBgn0033052	9.07	8.08	8.77	9.14	9.31	8.26
1633553_s_at	FBgn0035710	7.48	6.47	7.37	6.7	7.08	6.46
1623761_at	FBgn0030040	9.05	8.02	8.28	7.91	8.43	8.1
1629898_s_at	FBgn0034420	7.61	6.58	6.72	6.32	7.08	6.43
1636001_at	FBgn0034255	8.54	7.5	8.7	9.01	8.36	8.1
1638724_at	FBgn0028527	7.12	6.07	6.23	6.12	6.61	6.02

1633391_at	FBgn0038465	9.63	8.57	8.93	9.14	9.2	8.61
1627073_a_at	FBgn0038088	8.08	7.02	7.49	7.16	7.83	7.51
1626867_at	FBgn0051613	9.53	8.46	8.54	9.55	9.97	9.06
1636888_a_at	FBgn0016123	9.37	8.29	9.44	9.22	8.98	8.16
1627324_at	FBgn0005630	8.89	7.81	6.97	7.2	9.05	8.34
1638469_s_at	FBgn0023520	7.07	5.98	6.24	5.76	6.61	5.46
1629518_at	FBgn0032864	9.19	8.11	8.8	9.32	9.22	8.15
1634630_at	FBgn0026593	7.93	6.84	7.19	7.47	8.08	7.16
1629803_a_at	---	9.01	7.93	8.28	6.6	8.33	7.88
1624819_s_at	---	9.54	8.46	3.78	4.96	10.76	9.93
1630948_s_at	---	7.27	6.16	6.98	5.43	7.05	6.47
1636423_at	---	8.37	7.25	8.41	6.47	8.18	7.88
1635191_at	FBgn0029507	7.82	6.69	7.17	5.99	7.23	6.35
1641148_a_at	FBgn0012034	10.4	9.26	9.52	9.83	10.06	8.83
1635283_at	FBgn0028543	7.22	6.06	5.61	4.84	6.81	5.66
1632430_at	---	7.86	6.7	7.23	6.34	6.44	6.63
1626113_at	FBgn0035983	8.79	7.61	8.81	8.75	8.89	7.41
1640167_s_at	FBgn0030179 /// FBgn002	9.32	8.08	8.44	6.68	8.45	8.43
1629834_at	FBgn0036091	9.94	8.7	9.9	8.45	9.55	8.95
1637703_a_at	FBgn0041184	7.72	6.46	7.68	6.93	7.41	6.64
1624720_s_at	FBgn0032497	7.56	6.3	8.32	7.04	7.78	6.68
1638308_s_at	FBgn0051613	9.69	8.42	8.84	9.54	10.13	9.06
1640703_at	FBgn0050460	6.97	5.7	6.11	5.79	7.03	5.38
1640884_at	FBgn0029766	7.2	5.93	6.37	6.58	6.55	5.98
1641610_at	FBgn0030999	8.14	6.86	7.94	6.92	7.55	7.45
1641738_a_at	---	9.69	8.39	8.21	9.96	9.76	8.18
1631217_a_at	FBgn0010424	8.06	6.76	8.2	6.84	7.88	6.82
1638563_at	FBgn0039431	7.51	6.18	7.54	6.56	7.11	6.51
1637900_at	FBgn0039297	7.33	5.95	7.61	6.47	7.38	5.93
1628732_at	---	8.02	6.57	8.08	8.19	8.81	7.96
1633645_at	---	10.46	9	8.42	10.05	9.04	8
1633483_a_at	FBgn0031037	9.39	7.9	9.93	9.59	9.32	8.26
1635110_at	FBgn0033304	7.43	5.93	5.9	6.28	6.95	5.1
1629572_a_at	FBgn0026721	7.22	5.7	5.35	5.29	6.55	5.55
1626547_at	---	7.35	5.82	6.36	5.58	6.9	5.72
1629242_x_at	---	7.41	5.85	5.89	6.3	6.89	6.1

1631604_at	FBgn0031810	7.55	5.97	5.61	5.8	7.01	6.4
1634271_at	---	9.18	7.59	9.08	7.27	9.73	7.34
1635210_a_at	FBgn0003137	6.99	5.4	8.93	6.86	7.99	6.96
1633893_at	---	7.12	5.51	5.81	5	7.48	5.81
1639723_at	---	8.96	7.35	9.5	8.74	9.47	7.97
1640303_a_at	FBgn0035770	10.36	8.71	10.74	10.55	10.57	9.46
1628188_at	FBgn0023184	11.8	10.11	11.49	10.14	11.66	10.37
1641727_at	---	6.12	4.42	5.19	6.9	7.01	4.41
1635020_s_at	FBgn0016054	8.13	6.42	7.56	9.53	8.03	6.32
1630985_at	FBgn0050441	7.17	5.38	5.86	4.98	6.25	4.25
1630934_at	---	10.26	8.46	8.66	8.28	10.52	9.45
1638669_at	FBgn0034200	7.66	5.84	5.17	5.27	6.83	5.23
1626473_a_at	FBgn0032773	8.21	6.36	6.16	5.77	7.8	6.06
1632683_s_at	---	13.52	11.63	10.34	10.86	12.93	11.84
1626350_at	FBgn0015569	7.39	5.49	6.14	6.53	7.86	5.76
1632932_a_at	FBgn0053171	8.19	6.25	7.9	8.12	7.63	6.24
1639180_at	FBgn0033926	10.41	8.45	11.37	10.56	9.93	8.56
1630831_at	FBgn0038631	7.38	5.4	4.98	5.47	6.21	5
1626531_at	FBgn0031655	7.94	5.87	7.79	5.84	8.11	6.03
1638844_s_at	FBgn0031589	7.73	5.63	8.73	5.89	7.92	5.65
1634762_a_at	FBgn0034394	8.77	6.65	6.83	6.16	7.74	6.32
1627551_s_at	---	8.09	5.92	5.15	5.17	7.52	6.4
1640103_s_at	FBgn0031489	8.3	5.99	6.93	5.53	9.22	7.03
1628690_at	FBgn0031157	7.28	4.95	7.06	6.88	7.81	6.57
1629434_at	FBgn0035094	7.11	4.75	5.22	5.02	6.88	4.23
1641382_at	FBgn0011660	8.38	5.93	8.23	8.55	8.54	7.92
1641723_a_at	FBgn0035976	7.29	4.84	4.97	4.3	7.29	4.75
1625947_at	---	7.95	5.41	7.59	5.12	8.37	5.32
1625491_at	---	7.86	5.24	7.48	7.23	7.48	6.22
1641367_at	---	7.06	3.82	4.48	3	6.26	4.54
1637275_a_at	FBgn0033857	8.66	5.27	7.54	5.02	6.34	5.62
1628918_at	FBgn0032998	7.61	4.09	8.21	6.68	8.36	3.16
1639054_s_at	---	9	5.34	5.45	6.52	8.83	4.6
1633290_a_at	FBgn0028528	9.55	4.36	9.44	9.63	9.66	4.66

Supplementary Table S8 Enrichment in biological process GO-terms (all levels) of differentially expressed genes ($q<0.05$) between *Marcal1*$^{del/del}$ and *yw* ovaries at 20^{oC}.

Term	Count	PValue	Fold Enrichment
GO:0008152~metabolic process	50	0.077378231	1.168941048
GO:0016043~cellular component organization	24	0.04586477	1.453506787
GO:0006950~response to stress	9	0.073882931	2.00765625
GO:0009056~catabolic process	9	0.084881356	1.946818182
GO:0051716~cellular response to stimulus	7	0.037973165	2.776018519
GO:0006259~DNA metabolic process	6	0.052919286	2.907013575
GO:0033554~cellular response to stress	5	0.079115927	3.041903409
GO:0006281~DNA repair	4	0.067768971	4.199019608
GO:0006974~response to DNA damage stimulus	4	0.089674196	3.724347826

Supplementary Table S9 Enrichment in biological process GO-terms (all levels) of differentially expressed genes (q<0.05) between *Marcal1*$^{del/del}$ and *yw* ovaries at 25°C.

Term	**Count**	**PValue**	**Fold Enrichment**
GO:0008152~metabolic process	58	0.096794378	1.141870834
GO:0006950~response to stress	11	0.03703737	2.066359649
GO:0033036~macromolecule localization	11	0.053968425	1.933435929
GO:0008104~protein localization	10	0.027665154	2.300214823
GO:0009888~tissue development	10	0.054081143	2.030820294
GO:0002009~morphogenesis of an epithelium	8	0.011638694	3.205988304
GO:0060429~epithelium development	8	0.014511411	3.06956327
GO:0048729~tissue morphogenesis	8	0.018591517	2.92043469
GO:0002164~larval development	4	0.038431652	5.304024768
GO:0032787~monocarboxylic acid metabolic process	4	0.084146882	3.836954087
GO:0002168~instar larval development	3	0.097172331	5.635526316

Supplementary Table S10 Log_2 scale value of mRNA expression in *wt* and *Smarcal*$^{del/del}$ mouse livers at 20^{oC} and at 39.5^{oC}.

ENSEMBL	**SYMBOL**	***wt*** **(20^{oC})**	***Smarcal1***$^{del/del}$ **(20^{oC})**	***wt*** **(39.5^{oC})**	***Smarcal1***$^{del/del}$ **(39.5^{oC})**
ENSMUSG00000000001	*Gnai3*	5.91	5.22	5.51	5.19
ENSMUSG00000000031	*NA*	-2.33	-3.5	1.1	1.34
ENSMUSG00000000049	*Apoh*	11.01	10.64	10.65	10.75
ENSMUSG00000000056	*Narf*	4.51	3.92	4.33	4.11
ENSMUSG00000000058	*Cav2*	1.51	0.16	0.59	0.22
ENSMUSG00000000078	*Klf6*	2.24	1.3	2.36	2.05
ENSMUSG00000000085	*scmh1*	2.19	2.39	2.55	2.25
ENSMUSG00000000088	*Cox5a*	7.13	6.86	7.2	6.94
ENSMUSG00000000120	*Ngfr*	0.47	2.32	1.36	0.8
ENSMUSG00000000127	*Fert2*	1.7	1.2	1.77	1.2
ENSMUSG00000000131	*mKIAA0370*	4	4.25	4.16	3.88
ENSMUSG00000000134	*Tcfe3*	3.76	4	3.84	3.87
ENSMUSG00000000142	*Axin2*	1.61	1.9	1.67	1.51
ENSMUSG00000000148	*AA881470*	2.02	2.61	2.5	2.3
ENSMUSG00000000149	*Gna12*	5.51	6.13	6.18	6
ENSMUSG00000000154	*Slc22a18*	6.47	6.84	6.72	6.52
ENSMUSG00000000159	*Igsf5*	3.45	3.38	3.2	3.29
ENSMUSG00000000168	*Dlat*	4.41	4.12	4.22	3.67
ENSMUSG00000000171	*Sdhd*	7.19	6.96	7.13	6.88
ENSMUSG00000000184	*Ccnd2*	1.76	2.64	1.71	1.47
ENSMUSG00000000194	*Gpr107*	3.2	3.43	3.19	2.75
ENSMUSG00000000247	*Lhx2*	1.61	1.46	1.1	0.67
ENSMUSG00000000266	*Mid2*	0.69	0.35	1.11	0.69
ENSMUSG00000000275	*Trim25*	4.53	4.18	4.16	4.08
ENSMUSG00000000278	*Scpep1*	5.83	5.38	5.6	5.37
ENSMUSG00000000282	*Mnt*	1.54	2.15	1.76	1.06
ENSMUSG00000000290	*Itgb2*	1.58	2.01	1.98	1.3
ENSMUSG00000000296	*mD53*	3.12	2.09	3.02	2.6

ENSMUSG00000000301	*Pemt*	8.51	8.85	8.83	8.83
ENSMUSG00000000303	*Cdh1*	2.8	2.76	2.83	2.55
ENSMUSG00000000325	*Arvcf*	2.77	2.97	2.75	2.72
ENSMUSG00000000326	*Comt*	8.23	9.06	8.33	8.38
ENSMUSG00000000339	*BC051062*	2.93	2.71	2.53	2.53
ENSMUSG00000000340	*Dbt*	6.4	5.56	6.09	5.48
ENSMUSG00000000346	*Dazap2*	6.46	6.52	6.4	6.15
ENSMUSG00000000355	*Mcts1*	4.83	3.16	4.39	3.64
ENSMUSG00000000374	*Tmem1*	3.28	3.42	3.25	2.76
ENSMUSG00000000378	*Ccm2*	3.08	3.81	3.27	3.13
ENSMUSG00000000384	*Tbrg4*	3.82	4.48	4.34	4.04
ENSMUSG00000000385	*Tmprss2*	2.77	2.63	2.73	1.98
ENSMUSG00000000399	*Ndufa9*	6.84	6.85	6.91	6.57
ENSMUSG00000000420	*Galnt1*	4.87	4.3	4.37	3.8
ENSMUSG00000000439	*Mkrn2*	3.06	3.23	3.23	3.04
ENSMUSG00000000440	*Pparg*	2.07	1.49	2.5	1.86
ENSMUSG00000000441	*Raf1*	5.41	5.41	5.33	5.22
ENSMUSG00000000532	*Acvr1b*	1.66	2.07	2.11	1.34
ENSMUSG00000000538	*Tom1l2*	2.95	3.09	3.41	2.89
ENSMUSG00000000552	*Zfp385*	2.9	3.44	3.26	3.11
ENSMUSG00000000555	*Itga5*	3.1	4.32	3.09	3.24
ENSMUSG00000000561	*Wdr77*	3.76	4.42	4.01	3.6
ENSMUSG00000000563	*Atp5f1*	6.65	5.75	6.37	5.34
ENSMUSG00000000568	*Hnrpd*	4.15	4.06	4.35	3.76
ENSMUSG00000000581	*C1d*	4.21	3.03	3.92	3.22
ENSMUSG00000000594	*Gm2a*	7.08	6.85	7.33	6.96
ENSMUSG00000000600	*BC099422*	3.1	2.09	2.55	2.33
ENSMUSG00000000605	*Clcn4-2*	4.57	4.23	4.33	3.83
ENSMUSG00000000631	*Myo18a*	3.81	4.39	4.08	4.04
ENSMUSG00000000673	*Haao*	8.47	9.03	8.81	8.62
ENSMUSG00000000682	*Cd52*	3.05	1.99	3.84	2.99

ENSMUSG00000000686	*1300007F04Ri*	4.86	5.19	4.94	4.32
ENSMUSG00000000708	*Pcaf*	4.67	3.9	4.47	4
ENSMUSG00000000711	*AK206637*	4.26	4.29	4.21	4.01
ENSMUSG00000000738	*Spg7*	4.22	4.52	4.36	3.74
ENSMUSG00000000739	*Sult5a1*	4.82	3.59	3.56	3.52
ENSMUSG00000000740	*Rpl13*	1.11	0.86	1.21	0.99
ENSMUSG00000000743	*Chmp1a*	4.51	5.02	4.67	4.49
ENSMUSG00000000751	*Rpa1*	3.98	3.53	4.03	3.62
ENSMUSG00000000753	*Serpinf1*	9.2	9.61	9.4	9.35
ENSMUSG00000000759	*Tubgcp3*	1.71	1.46	1.34	1.17
ENSMUSG00000000776	*Polr3d*	1.86	3.07	2.22	2.25
ENSMUSG00000000782	*Tcf7*	1.68	2.15	2.27	1.65
ENSMUSG00000000787	*Ddx3x*	6.66	5.74	6.03	5.8
ENSMUSG00000000804	*Usp32*	3.46	2.37	3.02	2.36
ENSMUSG00000000811	*Txnrd3*	1.48	1.97	1.5	1.1
ENSMUSG00000000823	*NA*	2.38	2.61	2.58	2.29
ENSMUSG00000000826	*Dnajc5*	4.4	4.3	4.15	4.01
ENSMUSG00000000827	*Tpd52l2*	3.1	3.35	3.39	2.93
ENSMUSG00000000838	*Fmr1*	3.12	2.07	2.8	1.8
ENSMUSG00000000876	*Pxmp4*	6.62	6.59	6.03	5.97
ENSMUSG00000000881	*Dlg3*	2.65	2.54	2.58	1.95
ENSMUSG00000000902	*Smarcb1*	3.54	4.37	3.65	3.87
ENSMUSG00000000915	*Hip1r*	2.88	3.56	2.84	2.83
ENSMUSG00000000916	*Nsun5*	2.29	3.17	2.67	2.34
ENSMUSG00000000934	*Top1mt*	3.87	4.39	3.91	3.74
ENSMUSG00000000948	*Snurf*	2.75	2.75	2.69	2.14
ENSMUSG00000000957	*Mmp14*	3.69	4.57	3.7	4.15
ENSMUSG00000000958	*Slc7a7*	1.57	1.78	1.37	0.93
ENSMUSG00000000959	*Oxa1l*	5.61	6.19	6.03	6.05
ENSMUSG00000000976	*Heatr6*	1.72	2.2	2.13	1.99
ENSMUSG00000001016	*Ilf2*	3.26	2.82	3.44	3.04

ENSMUSG00000001017	*MNCb-1706*	4.2	3.73	4.02	3.56
ENSMUSG00000001018	*Snapap*	3.05	2.41	3.24	2.48
ENSMUSG00000001029	*Icam2*	0.95	1.32	1.23	1.36
ENSMUSG00000001036	*Epn2*	1.74	1.68	1.77	1.53
ENSMUSG00000001052	*Sec24b*	3.08	2.94	3.28	2.86
ENSMUSG00000001053	*C330016O10R*	1.02	2.87	1.2	1.02
ENSMUSG00000001054	*Rmnd5b*	3.15	4.05	3.67	3.16
ENSMUSG00000001056	*Nola2*	3.84	4.87	4.55	4.34
ENSMUSG00000001062	*NA*	3.33	3.59	3.23	3.05
ENSMUSG00000001065	*Zfp276*	3	3.29	3.33	2.98
ENSMUSG00000001089	*Luzp1*	2.57	2.16	2	2.02
ENSMUSG00000001095	*Slc13a2*	1.19	1.22	1.87	0.44
ENSMUSG00000001098	*Kctd10*	3	3.24	2.66	2.52
ENSMUSG00000001100	*Poldip2*	6.12	6.08	5.96	5.73
ENSMUSG00000001105	*Ift20*	5.58	5.2	5.74	5.64
ENSMUSG00000001119	*Col6a1*	1.01	1.49	1.27	1.31
ENSMUSG00000001123	*Lgals9*	9.28	9.32	9.11	9
ENSMUSG00000001127	*Araf*	4.2	4.81	4.34	4.14
ENSMUSG00000001128	*Cfp*	4.25	4.57	4.41	4
ENSMUSG00000001134	*Uxt*	1.32	-0.41	0.53	0.72
ENSMUSG00000001138	*Cnnm3*	2.99	3.33	2.96	2.33
ENSMUSG00000001143	*Lman2l*	3.68	3.8	3.36	3.52
ENSMUSG00000001150	*Mcm3ap*	2.19	2.47	2.2	2.28
ENSMUSG00000001151	*Pcnt*	1.2	0.86	1.18	0.82
ENSMUSG00000001155	*Ftcd*	7.12	7.51	7.46	7.29
ENSMUSG00000001156	*Mxd1*	1.02	1.07	1.45	1.19
ENSMUSG00000001157	*Gmcl1*	2.65	2.19	2.34	1.86
ENSMUSG00000001158	*2610209M04R*	3.69	3.14	3.69	2.81
ENSMUSG00000001173	*Ocrl*	1.25	1.07	1.25	0.74
ENSMUSG00000001175	*Calm1*	7.36	7.16	7.11	6.71
ENSMUSG00000001211	*Agpat3*	6.4	6.51	6.58	6.18

ENSMUSG00000001229	*Dpp9*	5.45	6.11	5.16	5.03
ENSMUSG00000001240	*Ramp2*	3.96	4.19	3.82	3.64
ENSMUSG00000001247	*Lsr*	6.51	7.35	6.56	6.58
ENSMUSG00000001248	*Gramd1a*	1.68	2.52	2.25	2.2
ENSMUSG00000001249	*Hpn*	7.74	8.38	8.28	8.06
ENSMUSG00000001280	*Sp1*	3.68	2.95	3.25	2.73
ENSMUSG00000001285	*Myg1*	3.6	4.21	4.09	4.01
ENSMUSG00000001289	*Pfdn5*	4.7	4.81	4.7	4.77
ENSMUSG00000001305	*Rrp15*	3.14	3.84	3.1	2.72
ENSMUSG00000001313	*Rnd2*	2.64	3.72	3.35	2.56
ENSMUSG00000001323	*Srr*	6.14	5.86	5.76	5.57
ENSMUSG00000001348	*Acp5*	6.28	6.76	6.5	6.53
ENSMUSG00000001366	*Fbxo9*	5.34	5.16	5.32	5.05
ENSMUSG00000001376	*1700034M03R*	2.14	1.58	1.89	1.73
ENSMUSG00000001379	*Apbb3*	3.35	2.93	2.92	2.71
ENSMUSG00000001380	*Hars*	4.59	4.96	4.39	4.53
ENSMUSG00000001383	*Zmat2*	5.45	5.11	5.13	5.3
ENSMUSG00000001403	*Ube2c*	-0.02	-0.47	1.35	-0.69
ENSMUSG00000001415	*Smg5*	3.24	3.86	3.45	3.46
ENSMUSG00000001416	*Cct3*	5.57	6.15	5.61	5.51
ENSMUSG00000001417	*Rhbg*	3.35	3.13	3.73	2.96
ENSMUSG00000001418	*0610031J06Ri*	5.41	5.94	5.65	5.59
ENSMUSG00000001419	*Mef2d*	2.88	3.31	3.18	3.15
ENSMUSG00000001424	*Snd1*	5.6	5.9	5.41	5.58
ENSMUSG00000001435	*Col18a1*	7.39	8.05	7.86	7.67
ENSMUSG00000001436	*Slc19a1*	2.22	3	2.95	2.47
ENSMUSG00000001440	*Kpnb1*	5.09	4.88	4.8	4.4
ENSMUSG00000001441	*Npepps*	3.59	3.13	3.68	3.12
ENSMUSG00000001445	*Mrpl10*	5.31	5.69	5.3	5.24
ENSMUSG00000001467	*Cyp51*	5.78	4.75	4.38	3.85
ENSMUSG00000001472	*Tcf25*	5.65	6.12	5.66	5.52

ENSMUSG00000001473	*Tubb6*	2.54	2.83	2.86	2.44
ENSMUSG00000001482	*Def8*	3.67	3.85	3.96	3.64
ENSMUSG00000001507	*Itga3*	1.07	1.27	1.32	1.2
ENSMUSG00000001518	*Itfg2*	1.74	2.49	2.4	2.15
ENSMUSG00000001524	*Gtf2h4*	2.86	3.69	3.47	3.26
ENSMUSG00000001525	*Tubb5*	5.47	5.9	5.57	5.65
ENSMUSG00000001542	*Ell2*	5.8	4.71	5.45	5.05
ENSMUSG00000001552	*Jup*	4.67	5.43	5.07	4.75
ENSMUSG00000001569	*Gm1040*	3.31	3.18	2.98	2.52
ENSMUSG00000001576	*Ergic1*	5.5	5.83	5.5	5.42
ENSMUSG00000001604	*Tcea3*	4.74	5.31	5.33	4.35
ENSMUSG00000001627	*Ifrd1*	3.63	2.88	3.88	4.12
ENSMUSG00000001630	*Stk38l*	1.55	0.94	1.73	1.51
ENSMUSG00000001632	*Brpf1*	2.24	2.81	2.46	2.43
ENSMUSG00000001663	*Gstt1*	7.54	8.01	7.86	7.56
ENSMUSG00000001665	*Gstt3*	7.16	6.88	7.27	6.79
ENSMUSG00000001666	*Ddt*	8.2	8.43	8.51	8.36
ENSMUSG00000001670	*Tat*	10.16	10.2	10.63	10.5
ENSMUSG00000001687	*Ubl3*	5.56	5.01	5.43	5.18
ENSMUSG00000001700	*Gramd3*	4.27	3.96	4.46	3.94
ENSMUSG00000001707	*Eef1e1*	3.52	3.14	3.54	3.28
ENSMUSG00000001729	*Akt1*	4.66	5.16	4.5	4.63
ENSMUSG00000001750	*Tcirg1*	3.76	4.14	3.85	3.47
ENSMUSG00000001751	*Naglu*	4.32	4.88	4.57	4.4
ENSMUSG00000001755	*Coasy*	5.87	6.32	5.99	5.83
ENSMUSG00000001761	*AK053708*	1.68	2.46	1.25	1.3
ENSMUSG00000001763	*Tspan33*	2.61	3.92	2.82	3.1
ENSMUSG00000001767	*Crnkl1*	3.09	2.43	2.49	1.83
ENSMUSG00000001768	*Rin2*	1.92	1.58	1.58	1.29
ENSMUSG00000001774	*Chordc1*	5.39	4.73	4.66	4.5
ENSMUSG00000001783	*D10Wsu52e*	5.3	5.3	5.08	5.02

ENSMUSG00000001785	*Pwp1*	3.04	3.17	3.01	2.84
ENSMUSG00000001786	*Fbxo7*	3.63	3.76	3.75	3.71
ENSMUSG00000001794	*Capns1*	6.29	6.73	6.48	6.38
ENSMUSG00000001802	*Lrp3*	2.23	2.96	2.61	2.64
ENSMUSG00000001829	*Clpb*	4.56	5.09	4.7	4.36
ENSMUSG00000001833	*7-Sep*	5.31	3.9	4.44	3.92
ENSMUSG00000001844	*Zdhhc4*	4.08	4.45	4.02	3.82
ENSMUSG00000001847	*Rac1*	5.79	6.18	5.89	5.7
ENSMUSG00000001855	*Nup214*	1.39	1.99	1.99	1.6
ENSMUSG00000001891	*Ugp2*	8.15	6.85	7.91	7.27
ENSMUSG00000001909	*Trmt1*	3.67	4.38	4.06	3.74
ENSMUSG00000001910	*Btbd14b*	3.1	3.7	3.13	3.06
ENSMUSG00000001911	*Nfix*	4.23	4.82	4.81	4.72
ENSMUSG00000001924	*Ube1x*	6.24	6.16	6.05	5.99
ENSMUSG00000001942	*Siae*	4.57	4.42	4.64	4.13
ENSMUSG00000001946	*Esam1*	3.04	3.77	3.16	3.14
ENSMUSG00000001948	*Spa17*	0.97	0.29	1.2	0.71
ENSMUSG00000001962	*D0HXS9928E*	3.55	4.11	3.7	3.91
ENSMUSG00000001964	*Emd*	3.51	3.71	3.68	3.75
ENSMUSG00000001983	*Ccdc44*	3.91	4.34	4.33	4.29
ENSMUSG00000001995	*Sipa1l2*	-0.6	0.16	1.34	1.07
ENSMUSG00000001999	*Blvra*	2.87	2.87	2.73	2.68
ENSMUSG00000002010	*Idh3g*	5.93	6.15	6.07	5.76
ENSMUSG00000002014	*Ssr4*	6.39	6.86	6.51	6.6
ENSMUSG00000002015	*Bcap31*	7.18	7	6.89	6.69
ENSMUSG00000002017	*2810405J04Ri*	4.24	3.66	3.76	3.37
ENSMUSG00000002028	*Mll1*	1.35	1.32	1.55	1.2
ENSMUSG00000002031	*1500035H01Ri*	4.61	4.74	4.9	4.99
ENSMUSG00000002032	*Tmem25*	3.2	3.58	3.72	3.36
ENSMUSG00000002043	*Trappc6a*	3.32	4.3	3.84	4.01
ENSMUSG00000002052	*Supt6h*	3.66	4.13	3.86	3.71

ENSMUSG00000002058	*Unc119*	1.21	2.16	0.62	1.37
ENSMUSG00000002064	*Sdf2*	4.58	5.23	5.13	5.34
ENSMUSG00000002083	*Bbc3*	1.5	3.28	2.57	2.31
ENSMUSG00000002102	*Psmc3*	6.1	6.4	6.16	6.01
ENSMUSG00000002103	*Acp2*	4.81	4.48	4.53	4.38
ENSMUSG00000002105	*Slc39a13*	2.37	3.08	2.45	2.3
ENSMUSG00000002107	*Cugbp2*	1.95	1.33	2.37	1.63
ENSMUSG00000002108	*Nr1h3*	6.27	6.75	6.54	6.27
ENSMUSG00000002109	*Ddb2*	3.47	2.5	2.88	2.61
ENSMUSG00000002111	*Sfpi1*	2.29	2.51	2.19	1.9
ENSMUSG00000002129	*Sf3a1*	3.47	3.83	3.65	3.65
ENSMUSG00000002147	*Stat6*	4.33	4.46	4.43	4.38
ENSMUSG00000002205	*Vrk3*	4.03	4.14	4.28	4.12
ENSMUSG00000002210	*1500002O20Ri*	1.18	2.22	1.96	1.9
ENSMUSG00000002221	*Paxip1*	2.58	2.72	2.8	2.46
ENSMUSG00000002222	*Rmnd5a*	5.32	4.57	5.17	4.69
ENSMUSG00000002227	*Mov10*	2.48	2.56	2.2	2.24
ENSMUSG00000002233	*Rhoc*	2.32	2.87	1.82	2.87
ENSMUSG00000002249	*Tead3*	2.03	2.88	2.72	2.51
ENSMUSG00000002250	*Ppard*	1.72	3.54	2.01	1.72
ENSMUSG00000002274	*Metrn*	1.55	2.37	2.24	2.24
ENSMUSG00000002279	*Tmem112*	4.9	5.47	5.09	4.95
ENSMUSG00000002280	*Narfl*	3.1	3.73	3.7	3.5
ENSMUSG00000002289	*Angptl4*	7.41	6.42	7.1	7.05
ENSMUSG00000002290	*NA*	2.04	2.15	2.27	3.39
ENSMUSG00000002307	*Daxx*	3.19	3.5	2.83	2.97
ENSMUSG00000002308	*Cd320*	1.84	2.29	2.21	1.96
ENSMUSG00000002319	*Ipo4*	3.74	4.45	3.87	3.8
ENSMUSG00000002320	*Tm9sf1*	4.73	5.16	4.83	4.7
ENSMUSG00000002325	*Isgf3g*	4.75	4.32	4.06	4.45
ENSMUSG00000002326	*Gmpr2*	3.6	3.67	3.53	3.47

ENSMUSG00000002329	*1810034K20Ri*	2.99	3.26	3.24	3.05
ENSMUSG00000002332	*Dhrs1*	6.4	6.91	6.28	6.32
ENSMUSG00000002342	*Tmem161a*	2.49	3.13	2.68	2.44
ENSMUSG00000002343	*Armc6*	1.43	2.81	1.91	1.48
ENSMUSG00000002345	*NA*	3.57	4.4	4.29	3.89
ENSMUSG00000002346	*Slc25a42*	4.91	5.26	5.7	5.34
ENSMUSG00000002365	*Snx9*	4.09	3.98	4.17	3.87
ENSMUSG00000002372	*Ranbp3*	3.62	4.48	4	3.89
ENSMUSG00000002379	*NA*	5.22	5.83	6.31	6.25
ENSMUSG00000002393	*Nr2f6*	4.91	6.28	5.6	5.33
ENSMUSG00000002395	*Use1*	4.18	4.47	4.49	4.83
ENSMUSG00000002396	*Ocel1*	2.71	4.17	3.42	3.09
ENSMUSG00000002409	*Dyrk1b*	2.67	3.02	3.2	2.58
ENSMUSG00000002413	*Braf*	1.85	1.05	1.5	1.18
ENSMUSG00000002416	*Ndufb2*	5.77	5.83	6.18	5.7
ENSMUSG00000002428	*Hltf*	1.69	0.47	1.28	0.48
ENSMUSG00000002455	*Prpf6*	4.23	4.46	4.3	4.03
ENSMUSG00000002475	*Abhd3*	5.57	5.14	5.42	5.26
ENSMUSG00000002477	*Snrpd1*	3.79	3.37	3.39	3.28
ENSMUSG00000002496	*Tsc2*	3.5	4.05	3.81	3.67
ENSMUSG00000002504	*Slc9a3r2*	3.47	4.48	3.5	3.6
ENSMUSG00000002524	*Puf60*	5.57	5.92	5.69	5.7
ENSMUSG00000002546	*Golga2*	3.6	3.78	3.72	3.33
ENSMUSG00000002550	*Uck1*	3.2	2.83	3.35	2.89
ENSMUSG00000002580	*1810046J19Rik*	6.29	5.8	6.01	5.95
ENSMUSG00000002588	*Pon1*	10.16	9.43	10.02	9.63
ENSMUSG00000002602	*Axl*	3.06	2.63	2.47	2.22
ENSMUSG00000002603	*Tgfb1*	2.41	2.85	2.75	2.21
ENSMUSG00000002608	*Ccdc97*	3.37	4.24	3.88	3.62
ENSMUSG00000002625	*Akap8l*	2.94	3.44	3.39	3.07
ENSMUSG00000002635	*Pdcd2l*	2.8	2.96	2.6	2.59

ENSMUSG00000002658	*Gtf2f1*	3.36	4.16	3.65	3.76
ENSMUSG00000002660	*Clpp*	5.26	5.98	5.73	5.5
ENSMUSG00000002661	*Alkbh7*	3.72	4.25	3.84	3.46
ENSMUSG00000002679	*Med6*	3.4	2.84	3.11	2.65
ENSMUSG00000002718	*Cse1l*	4.08	3.08	3.85	3.44
ENSMUSG00000002728	*Nat5*	2.86	1.88	2.61	2.34
ENSMUSG00000002731	*Prkra*	3.94	3.25	3.71	3.51
ENSMUSG00000002732	*Fkbp7*	2.11	1.81	2.2	1.94
ENSMUSG00000002733	*Plekha3*	3.91	3.74	3.7	3.48
ENSMUSG00000002741	*Ykt6*	5.16	5.35	4.96	4.84
ENSMUSG00000002748	*Baz1b*	3.64	3.5	3.66	3.63
ENSMUSG00000002763	*Pex6*	5.04	5.93	5.31	5.36
ENSMUSG00000002767	*Mrpl2*	4.56	5.39	4.92	4.82
ENSMUSG00000002768	*Mea1*	5.57	6.02	5.78	5.81
ENSMUSG00000002769	*Gnmt*	10.82	11.16	11.17	10.83
ENSMUSG00000002778	*Erd2.1*	6.5	6.55	6.51	6.42
ENSMUSG00000002781	*Tmem143*	3.55	3.54	3.77	3.44
ENSMUSG00000002797	*A030007L17Ri*	3.87	3.62	2.97	2.44
ENSMUSG00000002803	*Btbd6*	2.94	3.66	3.51	3.22
ENSMUSG00000002804	*Nudt14*	3.13	3.86	4.01	3.85
ENSMUSG00000002812	*Flii*	4.06	4.4	4.37	4.18
ENSMUSG00000002814	*Top3a*	1.17	1.07	1.13	0.83
ENSMUSG00000002820	*Atg4d*	3.81	4.44	4.36	4.13
ENSMUSG00000002825	*Qtrt1*	0.7	1.65	1.3	0.6
ENSMUSG00000002831	*S3-12*	1.8	0.07	1.4	0.79
ENSMUSG00000002833	*Hdgfrp2*	3.16	3.94	3.9	3.29
ENSMUSG00000002844	*Adprh*	2.43	2.45	2.43	1.62
ENSMUSG00000002845	*Tmem39a*	2.94	3.2	2.69	2.94
ENSMUSG00000002846	*4930455C21Ri*	4.61	4.37	4.51	4.27
ENSMUSG00000002847	*Pla1a*	4.45	4.25	4.37	4.26
ENSMUSG00000002871	*Gpr175*	3.11	3.55	3.36	2.79

ENSMUSG00000002881	*Nab1*	5.27	4.74	4.86	4.46
ENSMUSG00000002885	*Cd97*	3.32	3.66	2.88	2.8
ENSMUSG00000002897	*Il17ra*	3.15	3.42	3.28	2.99
ENSMUSG00000002908	*Kcnn1*	0.88	1.62	1.83	1.1
ENSMUSG00000002910	*Arrdc2*	3.47	4.33	4.06	3.82
ENSMUSG00000002944	*Cd36*	5.44	2.76	5.59	3.47
ENSMUSG00000002948	*Map2k7*	2.99	3.63	2.98	2.87
ENSMUSG00000002949	*Timm44*	4.65	4.97	4.86	4.64
ENSMUSG00000002957	*mKIAA0899*	5.06	5.05	4.77	4.66
ENSMUSG00000002963	*Pnkp*	3.53	3.99	3.91	3.75
ENSMUSG00000002968	*Med25*	4.16	5.37	4.81	4.41
ENSMUSG00000002980	*Bcam*	1.47	1.84	1.64	1.75
ENSMUSG00000002981	*Clptm1*	5.78	6.34	5.97	5.7
ENSMUSG00000002984	*Tomm40*	4.15	5.17	4.86	4.58
ENSMUSG00000002985	*Apoe*	12.38	13.05	13.23	13.03
ENSMUSG00000002992	*Apoc2*	8.72	9.03	9.51	9.56
ENSMUSG00000002996	*Hbp1*	5.61	4.9	5.26	4.92
ENSMUSG00000003031	*Cdkn1b*	3.38	2.7	3.5	3.19
ENSMUSG00000003033	*Ap1m1*	4.39	4.86	4.77	4.65
ENSMUSG00000003037	*Rab8A*	6.21	5.59	6.11	6.11
ENSMUSG00000003039	*2510049I19Rik*	5.6	5.63	5.77	5.64
ENSMUSG00000003053	*Cyp2c29*	10.02	9.66	9.99	9.94
ENSMUSG00000003062	*Stard3nl*	3.07	3.09	2.68	2.3
ENSMUSG00000003068	*lkb1*	4.77	5.61	5.23	5.01
ENSMUSG00000003072	*Atp5d*	6.85	7.71	7.52	7.35
ENSMUSG00000003099	*Ppp5c*	4.73	5.46	5.07	5.05
ENSMUSG00000003119	*Crkrs*	2.5	1.87	2.25	1.95
ENSMUSG00000003123	*Lipe*	2.01	2.86	2.88	2.32
ENSMUSG00000003131	*Pafah1b2*	3.86	3.29	3.24	3.09
ENSMUSG00000003134	*Tbc1d8*	3.65	3.29	3.77	3.56
ENSMUSG00000003135	*D1Bwg0212e*	3.35	3.07	3.08	2.57

ENSMUSG00000003154	*Foxj2*	1.73	2.24	2.13	1.88
ENSMUSG00000003161	*Sri*	4.27	4.07	3.68	3.46
ENSMUSG00000003166	*Dgcr2*	5.24	5.42	5.17	4.99
ENSMUSG00000003178	*Mical3*	1.07	1.27	1.74	1.56
ENSMUSG00000003184	*Irf3*	4.82	5.26	5.3	5.04
ENSMUSG00000003190	*Bcl2l12*	1.46	2.05	2.22	2.05
ENSMUSG00000003198	*BC011426*	1.31	0.9	1.71	1.01
ENSMUSG00000003199	*Mpnd*	5.5	6.2	5.85	5.61
ENSMUSG00000003200	*Sh3gl1*	3.5	4.2	3.66	3.37
ENSMUSG00000003208	*Ccdc94*	1.13	1.94	1.3	1.18
ENSMUSG00000003226	*Ranbp2*	4.2	3.45	3.78	3.29
ENSMUSG00000003233	*Dvl3*	2.07	3.33	2.62	2.82
ENSMUSG00000003234	*Abcf3*	4.27	4.69	4.47	4.35
ENSMUSG00000003235	*Eif2b5*	4.07	4.83	4.33	4.28
ENSMUSG00000003269	*Pscd2*	2.92	2.87	2.93	2.64
ENSMUSG00000003283	*Hck*	1.54	1.36	1.1	1.18
ENSMUSG00000003299	*MRPL4*	3.34	4.44	4.17	4.11
ENSMUSG00000003308	*Keap1*	4.31	5.05	4.46	4.55
ENSMUSG00000003316	*Glg1*	3.05	3.15	3.2	2.91
ENSMUSG00000003344	*NA*	3.93	4.71	4.2	3.93
ENSMUSG00000003345	*Csnk1g2*	5	5.7	5.13	4.91
ENSMUSG00000003346	*D10Bwg1364e*	4.71	5.76	5.08	5.01
ENSMUSG00000003348	*Mobkl2a*	1.43	2.08	1.17	0.67
ENSMUSG00000003355	*Fkbp11*	1.61	2.56	2.39	2.83
ENSMUSG00000003360	*Ddx23*	3.95	4.75	4.06	3.92
ENSMUSG00000003363	*Pld3*	3.55	4.3	4.12	3.83
ENSMUSG00000003378	*Grik5*	1.09	1.58	0.83	1.05
ENSMUSG00000003379	*Cd79a*	-0.39	-1.18	2.24	-2.3
ENSMUSG00000003380	*Pra1*	5.15	6.1	5.84	5.99
ENSMUSG00000003382	*Etv3*	1.98	1.96	1.68	1.48
ENSMUSG00000003402	*Prkcsh*	5.9	6.52	6.31	6.12

ENSMUSG00000003420	*Fcgrt*	7.1	7.33	7.14	7.07
ENSMUSG00000003421	*Nosip*	3.27	3.65	3.56	3.42
ENSMUSG00000003423	*Pih1d1*	4.73	5.08	4.93	4.7
ENSMUSG00000003426	*Rpl13a*	6.31	6.02	6.07	6.58
ENSMUSG00000003429	*Rps11*	5.99	6.03	5.92	5.74
ENSMUSG00000003435	*Supt5h*	4.27	5.11	4.79	4.58
ENSMUSG00000003437	*Paf1*	3.67	4.04	3.93	3.7
ENSMUSG00000003438	*AK212208*	4.71	5.35	4.83	4.64
ENSMUSG00000003444	*Med29*	1.62	1.24	1.2	1.81
ENSMUSG00000003458	*Ncstn*	4.39	4.98	4.72	4.43
ENSMUSG00000003464	*Pex19*	5.78	6.04	5.88	5.55
ENSMUSG00000003477	*Inmt*	7.81	8.05	7.67	7.96
ENSMUSG00000003518	*Dusp3*	4.35	3.98	4.4	4.15
ENSMUSG00000003526	*Prodh*	6.66	7.2	7.11	6.63
ENSMUSG00000003527	*Es2el*	1.76	2.12	2.03	1.49
ENSMUSG00000003528	*Slc25a1*	7.48	7.82	7.3	7.27
ENSMUSG00000003531	*Dgcr6*	5.01	5.68	5.49	5.2
ENSMUSG00000003546	*Klc4*	4.82	5.11	5.51	5.03
ENSMUSG00000003549	*Ercc1*	1.84	2.74	2.84	2.99
ENSMUSG00000003555	*Cyp17a1*	6.78	5.11	7.33	5.8
ENSMUSG00000003559	*As3mt*	6.06	5.15	5.74	5.24
ENSMUSG00000003573	*Homer3*	1.24	2.07	1.2	1.12
ENSMUSG00000003575	*Crtc1*	1	1.74	1.34	1.36
ENSMUSG00000003581	*Rnf215*	2.38	3.22	3.04	2.69
ENSMUSG00000003585	*Sec14l2*	8.26	8.36	8.07	7.84
ENSMUSG00000003604	*Aven*	3.95	4.09	3.85	3.64
ENSMUSG00000003617	*Cp*	8.44	8	8.36	8.01
ENSMUSG00000003623	*Crot*	8.47	8.25	7.43	7.27
ENSMUSG00000003644	*Rps6ka1*	3.32	3.88	3.6	3.53
ENSMUSG00000003660	*Ascc3l1*	3.87	4.11	4.07	3.86
ENSMUSG00000003662	*Ciao1*	4.81	5.04	5.07	4.96

ENSMUSG00000003680	*Taf6l*	0.77	1.55	1.58	1.54
ENSMUSG00000003721	*Insig2*	8.24	7.67	7.79	6.97
ENSMUSG00000003731	*Kpna6*	3.55	3.43	3.34	3.29
ENSMUSG00000003746	*Man1a*	6.56	5.84	6.27	5.82
ENSMUSG00000003752	*Itpkc*	1.69	2.42	2.06	1.54
ENSMUSG00000003759	*Sb1*	1.87	2.7	2.16	2.28
ENSMUSG00000003762	*Adck4*	3.53	4.23	3.92	3.84
ENSMUSG00000003778	*Brd8*	1.79	1.82	1.23	0.79
ENSMUSG00000003808	*Farsla*	2.15	2.96	2.33	2.23
ENSMUSG00000003809	*Gcdh*	8.3	8.14	8.37	7.98
ENSMUSG00000003810	*Mast2*	2.21	2.55	2.39	2.21
ENSMUSG00000003812	*Dnase2a*	2.15	3.1	2.73	2.92
ENSMUSG00000003813	*Rad23a*	4.6	5.1	5.15	4.97
ENSMUSG00000003814	*Calr*	9.12	9.24	8.77	8.82
ENSMUSG00000003824	*Syce2*	2.47	2.08	2.46	1.83
ENSMUSG00000003847	*Nfat5*	2.03	1.2	1.84	1.42
ENSMUSG00000003848	*Nob1*	2.71	2.67	2.9	2.81
ENSMUSG00000003849	*Nqo1*	3.95	3.16	3.39	2.87
ENSMUSG00000003868	*Ruvbl2*	2.4	3.77	3.03	2.83
ENSMUSG00000003873	*Bax*	3.7	4.12	3.96	3.52
ENSMUSG00000003923	*Tfam*	4.73	4.23	4.63	4.07
ENSMUSG00000003948	*Paqr11*	6.79	5.97	6.15	5.83
ENSMUSG00000003949	*Hlf*	4.28	3.47	4.2	3.72
ENSMUSG00000003955	*2310056P07Ri*	5.9	5.91	6.05	6.04
ENSMUSG00000003970	*Rpl8*	7.73	8.27	8.03	7.94
ENSMUSG00000004018	*Pog*	2.29	1.69	2.06	1.57
ENSMUSG00000004032	*Gstm5*	4.45	4.02	4.09	3.79
ENSMUSG00000004035	*Gstm7*	6.41	6.45	6.66	6.11
ENSMUSG00000004038	*Gstm3*	5.87	5.43	6.41	5.62
ENSMUSG00000004040	*Stat3*	4.76	5.17	4.98	4.77
ENSMUSG00000004043	*Stat5a*	2.3	2.94	2.4	1.79

ENSMUSG00000004044	*Ptrf*	1.28	1.07	0.97	0.93
ENSMUSG00000004054	*Map3k11*	4.12	4.91	4.33	4.45
ENSMUSG00000004056	*Akt2*	3.45	4.09	3.73	3.31
ENSMUSG00000004069	*Tid1*	6.43	6.18	6.35	6.12
ENSMUSG00000004070	*Hmox2*	6.12	5.59	5.82	5.84
ENSMUSG00000004071	*5730403B10Ri*	6.59	6.53	6.63	6.52
ENSMUSG00000004085	*B230120H23R*	0.95	0.54	1.68	0.76
ENSMUSG00000004096	*Cwc15*	5.86	5.53	5.62	5.69
ENSMUSG00000004099	*Dnmt1*	1.01	1.4	1.42	0.9
ENSMUSG00000004100	*Ppan*	2.21	3.34	2.3	2.33
ENSMUSG00000004105	*Angptl2*	2.29	2.58	2.18	2.29
ENSMUSG00000004187	*Kifc2*	0.33	0.56	1.5	1.35
ENSMUSG00000004207	*Psap*	8.01	8.25	8	7.93
ENSMUSG00000004221	*Ikbkg*	4.02	3.55	3.48	3.37
ENSMUSG00000004233	*Wars2*	1.07	1.57	1.13	1.16
ENSMUSG00000004263	*Atn1*	2.69	3.43	3.34	3.24
ENSMUSG00000004264	*Bcap37*	7.22	7.67	7.4	7.18
ENSMUSG00000004266	*Ptpn6*	3.36	3.82	3.56	3.21
ENSMUSG00000004268	*Emg1*	5.39	5.61	5.52	5.63
ENSMUSG00000004270	*Mboat5*	6.17	5.68	6.1	5.52
ENSMUSG00000004285	*Atp6v1f*	4.68	4.58	4.33	4.67
ENSMUSG00000004319	*Clcn3*	4.02	3.56	3.85	3.32
ENSMUSG00000004356	*NA*	1.62	1.98	1.79	1.48
ENSMUSG00000004364	*Cul3*	5.5	4.53	5.23	4.41
ENSMUSG00000004393	*Ddx56*	3.75	4.49	4.01	3.88
ENSMUSG00000004394	*Tmed4*	5.71	5.3	5.3	5.35
ENSMUSG00000004446	*Bid*	1.64	1.99	2.39	1.91
ENSMUSG00000004451	*Ralb*	2.66	2.98	2.69	2.67
ENSMUSG00000004460	*Dnajb11*	5.73	5.53	4.89	5.07
ENSMUSG00000004462	*Tbccd1*	3.74	3.87	3.78	3.61
ENSMUSG00000004530	*Coro1c*	2.57	2.75	2.59	2.48

ENSMUSG00000004535	*Tax1bp1*	6.33	5.61	6.1	5.64
ENSMUSG00000004552	*env*	5.22	5.58	5.29	5.33
ENSMUSG00000004558	*Ndrg2*	9.36	9.54	9.49	9.52
ENSMUSG00000004561	*Mett11d1*	3.46	3.37	3.48	3.43
ENSMUSG00000004562	*mFLJ00128*	1.62	2.78	2.27	1.93
ENSMUSG00000004565	*Pnpla6*	2.36	2.92	2.46	2.34
ENSMUSG00000004567	*Mcoln1*	3.61	4.1	3.74	3.61
ENSMUSG00000004568	*Arhgef18*	2.97	3.29	2.97	2.58
ENSMUSG00000004591	*AK082921*	4.19	3.3	3.86	3.3
ENSMUSG00000004610	*Etfb*	8.13	8.61	8.65	8.33
ENSMUSG00000004626	*Stxbp2*	3.48	4.26	3.67	3.33
ENSMUSG00000004631	*Sgce*	1.28	0.7	1.13	1.18
ENSMUSG00000004633	*Chn2*	3.57	3.04	3.74	3.87
ENSMUSG00000004642	*Slbp*	2.91	2	2.56	2.3
ENSMUSG00000004655	*Aqp1*	5.95	6.43	5.71	5.73
ENSMUSG00000004665	*Cnn2*	1.62	2.22	2.18	1.12
ENSMUSG00000004667	*Polr2e*	2.99	3.75	3.65	3.88
ENSMUSG00000004677	*Myo9b*	1.93	2.51	2.47	2.17
ENSMUSG00000004730	*Emr1*	3.38	2.51	2.19	2.12
ENSMUSG00000004748	*1700020C11Ri*	4.31	4.54	4.44	4.38
ENSMUSG00000004768	*Rab23*	1.8	1.72	1.64	1.15
ENSMUSG00000004771	*Rab11a*	6	5.5	5.78	5.34
ENSMUSG00000004788	*Eif2b2*	3.59	4.38	4.25	4.15
ENSMUSG00000004789	*Dlst*	6.96	6.8	6.82	6.31
ENSMUSG00000004798	*Ulk2*	4.14	3.99	4.06	3.73
ENSMUSG00000004814	*Ccl24*	1.52	0.94	1.26	1.14
ENSMUSG00000004815	*Dgkq*	2.57	2.48	2.66	2.44
ENSMUSG00000004837	*Grap*	1.33	2.21	2.02	1.54
ENSMUSG00000004843	*Chmp2b*	4.51	3.76	4.15	3.54
ENSMUSG00000004846	*Plod3*	3.38	4.12	3.56	3.58
ENSMUSG00000004849	*Ap1s1*	4.73	4.75	4.14	4.23

ENSMUSG00000004865	*SRPK1*	2.61	2.91	3	2.72
ENSMUSG00000004880	*Lbr*	1.89	1.81	1.88	1.75
ENSMUSG00000004895	*Prcc*	3.92	4.56	4.2	4.25
ENSMUSG00000004896	*BC023814*	1.62	1.85	1.91	1.71
ENSMUSG00000004897	*Hdgf*	6.63	6.79	6.51	6.36
ENSMUSG00000004929	*Thop1*	2.26	3.14	2.45	2.44
ENSMUSG00000004931	*Apba3*	4.24	5.33	4.73	4.39
ENSMUSG00000004934	*Pias4*	2.62	3.64	3.08	3.1
ENSMUSG00000004936	*Map2k1*	4.84	4.65	4.42	4.38
ENSMUSG00000004937	*Sgta*	5.04	5.91	5.43	5.37
ENSMUSG00000004945	*5730437N04Ri*	6.14	5.63	5.77	5.27
ENSMUSG00000004947	*Dtx2*	0.87	1.98	1.49	1.26
ENSMUSG00000004980	*Hnrnpa2b1*	6.59	5.83	5.95	5.57
ENSMUSG00000004994	*Ccdc130*	1.11	1.92	1.39	1.63
ENSMUSG00000004996	*2410018C20Ri*	3.06	4.22	3.42	3.25
ENSMUSG00000005034	*Prkacb*	4.63	3.74	4.13	3.75
ENSMUSG00000005043	*Sgsh*	1.26	2.07	1.6	1.56
ENSMUSG00000005054	*Cstb*	5.83	5.07	5.48	5.33
ENSMUSG00000005069	*Pex5*	5.47	5.85	5.53	5.42
ENSMUSG00000005078	*1200003C05Ri*	3.94	3.8	4.07	3.83
ENSMUSG00000005087	*Cd44*	1.37	0.28	0.84	0.77
ENSMUSG00000005089	*Slc1a2*	4.83	4.84	4.94	5.06
ENSMUSG00000005102	*Eif2ak4*	1.39	1.08	1.36	0.7
ENSMUSG00000005103	*Wdr1*	4.6	4.75	4.52	4.38
ENSMUSG00000005107	*Slc2a9*	4.02	4.12	4.03	3.85
ENSMUSG00000005125	*Ndrg1*	4.59	4.95	3.76	3.01
ENSMUSG00000005142	*Man2b1*	5.45	5.98	5.66	5.66
ENSMUSG00000005150	*1500041N16Ri*	3.29	3.87	3.52	3.17
ENSMUSG00000005161	*Prdx2*	4.85	4.13	4.97	5.09
ENSMUSG00000005198	*Polr2a*	3.25	3.31	3.53	3.33
ENSMUSG00000005204	*Senp3*	2.96	3.27	2.94	3.26

ENSMUSG00000005225	*Plekha8*	2.18	1.46	1.93	1.43
ENSMUSG00000005233	*Spbc25*	1.57	0.7	1.44	0.99
ENSMUSG00000005251	*Ripk4*	1	1.39	2	1.54
ENSMUSG00000005262	*Ufd1l*	4.5	4.27	4.34	4.2
ENSMUSG00000005268	*Prlr*	7.44	6.12	6.54	6.09
ENSMUSG00000005269	*Agxt2*	6.21	5.47	6.2	5.76
ENSMUSG00000005299	*Letm1*	5.38	5.65	5.52	5.26
ENSMUSG00000005312	*Ubqln1*	6.68	6.1	6.15	5.99
ENSMUSG00000005320	*Fgfr4*	4.5	5.23	4.89	4.83
ENSMUSG00000005338	*Cadm3*	1.38	1.86	1.55	1.38
ENSMUSG00000005354	*Txn2*	5.86	6.57	6.19	6.11
ENSMUSG00000005362	*Crbn*	4.65	3.73	4.3	3.78
ENSMUSG00000005370	*Msh6*	1.87	1.41	1.37	1.16
ENSMUSG00000005371	*Fbxo11*	3.65	2.96	3.48	2.87
ENSMUSG00000005373	*Mlxipl*	5.51	5.76	5.83	5.58
ENSMUSG00000005374	*Tbl2*	3.11	3.24	2.77	2.88
ENSMUSG00000005378	*Wbscr22*	4.01	4.47	4.02	4.07
ENSMUSG00000005397	*Nid1*	2.68	2.33	2.29	1.97
ENSMUSG00000005413	*Hmox1*	3.97	5.16	4.73	4.71
ENSMUSG00000005417	*AA536749*	3.01	3.22	3.16	2.95
ENSMUSG00000005442	*Cic*	2.09	3.14	2.65	2.57
ENSMUSG00000005469	*Prkaca*	4.9	4.93	5.14	5.03
ENSMUSG00000005481	*Ddx39*	2.83	3.21	2.86	2.52
ENSMUSG00000005483	*Dnajb1*	4.4	4.83	4.85	5.46
ENSMUSG00000005501	*Usp40*	2.96	2.54	2.98	2.36
ENSMUSG00000005505	*Kbtbd4*	3.31	3.63	3.42	3.1
ENSMUSG00000005506	*Cugbp1*	4.73	4	4.4	4.25
ENSMUSG00000005510	*Ndufs3*	4.32	3.95	4.47	4.3
ENSMUSG00000005514	*Por*	8.31	8.48	8.66	8.41
ENSMUSG00000005534	*Insr*	3.41	3.22	3.9	3.82
ENSMUSG00000005547	*Cyp2a5*	7.96	7.31	9.06	8.65

ENSMUSG00000005566	*Trim28*	4.8	5.62	5.07	5.02
ENSMUSG00000005575	*Ube2m*	5.22	5.85	5.46	5.39
ENSMUSG00000005580	*Adcy9*	2.7	2.76	3.19	2.79
ENSMUSG00000005609	*Ctr9*	3.25	3.55	3.3	3.33
ENSMUSG00000005610	*Eif4g2*	8.18	7.46	7.92	7.57
ENSMUSG00000005615	*Pcyt1a*	4.93	4.56	4.83	4.48
ENSMUSG00000005621	*Zfp592*	3.14	3.31	3.43	3.31
ENSMUSG00000005625	*Psmd4*	5.53	6.39	5.95	5.7
ENSMUSG00000005629	*Scnm1*	3.94	3.88	4.02	3.74
ENSMUSG00000005656	*Snx6*	4.1	3.41	3.78	3.31
ENSMUSG00000005674	*Tomm40l*	5.14	4.93	5.54	5.28
ENSMUSG00000005677	*Nr1i3*	6.62	6.53	6.86	6.65
ENSMUSG00000005681	*Apoa2*	13.53	12.99	13.69	14.03
ENSMUSG00000005682	*Usp52*	2.63	2.67	2.66	2.43
ENSMUSG00000005683	*Cs*	5.99	5.98	6.15	5.79
ENSMUSG00000005687	*Bcas2*	4.61	4.52	4.67	4.46
ENSMUSG00000005698	*Ctcf*	4.17	3.86	3.82	3.56
ENSMUSG00000005699	*Pard6a*	0.86	1.25	1.65	1.39
ENSMUSG00000005716	*Pvalb*	#NAME?	#NAME?	1.04	-0.12
ENSMUSG00000005718	*Tcfap4*	0.79	1.54	1.69	0.59
ENSMUSG00000005732	*Ranbp1*	4.12	4.26	4.47	4.36
ENSMUSG00000005774	*Rfx5*	1.3	0.92	1.33	1.09
ENSMUSG00000005779	*Psmb4*	6.98	7.32	7	6.76
ENSMUSG00000005802	*Slc30a4*	3.09	2.11	2.52	1.42
ENSMUSG00000005803	*Sqrdl*	7.13	7.01	7.03	6.51
ENSMUSG00000005804	*Pldn*	3.36	2.49	3.2	2.36
ENSMUSG00000005813	*Metap1*	4.32	4.13	4.3	4.2
ENSMUSG00000005823	*Gpr108*	3.58	4.01	4.07	3.73
ENSMUSG00000005836	*Gata6*	2.29	2.52	2.27	2.11
ENSMUSG00000005846	*Rsl1d1*	4.87	4.49	4.84	4.59
ENSMUSG00000005871	*Apc*	2.98	2.1	2.77	2.45

ENSMUSG00000005873	*Reep5*	2.39	2.34	2.13	2.26
ENSMUSG00000005881	*Ergic3*	6.13	6.8	6.44	6.35
ENSMUSG00000005882	*Uqcc*	3.63	3.8	3.99	3.84
ENSMUSG00000005886	*Ncoa2*	3.77	3.78	3.78	3.54
ENSMUSG00000005893	*Nr2c2*	3.01	2.07	2.59	2.29
ENSMUSG00000005897	*Nr2c1*	2.64	1.88	2.52	1.86
ENSMUSG00000005899	*Smpd4*	2.08	2.26	2.31	1.81
ENSMUSG00000005907	*Pex1*	3.08	2.76	3.3	2.88
ENSMUSG00000005936	*Kctd20*	3.74	3.29	3.58	3.18
ENSMUSG00000005949	*Ctns*	3.42	3.44	3.64	3.49
ENSMUSG00000005951	*Carkl*	5.16	5.09	5.48	5.14
ENSMUSG00000005973	*Rcn1*	2.99	2.14	2.34	2.07
ENSMUSG00000005980	*Dnase1*	1.05	0.84	1.04	0.89
ENSMUSG00000005981	*Trap1*	6.82	6.82	6.9	6.68
ENSMUSG00000005982	*1200013P24Ri*	6.09	5.9	6.05	5.82
ENSMUSG00000005983	*1700037C18Ri*	3.37	3.29	3.47	3.27
ENSMUSG00000006005	*Tpr*	3.86	3.61	3.88	3.33
ENSMUSG00000006010	*BC003331*	4.11	3.51	3.79	3.22
ENSMUSG00000006014	*NA*	3.75	3.55	3.68	3.5
ENSMUSG00000006019	*Dhx34*	0.95	1.75	1.39	0.64
ENSMUSG00000006021	*Kptn*	3.21	3.49	3.36	3.34
ENSMUSG00000006024	*Napa*	5.66	6.39	6.04	5.94
ENSMUSG00000006050	*Sra1*	5.9	6.31	6.3	6.11
ENSMUSG00000006057	*Atp5g1*	1.69	2.07	2.46	2.46
ENSMUSG00000006058	*Snf8*	3.97	4.05	4.57	4.57
ENSMUSG00000006095	*Tbcb*	4.2	4.24	3.97	4.09
ENSMUSG00000006127	*Pps*	2.54	3	3.03	2.63
ENSMUSG00000006134	*Crkl*	3.97	3.62	3.81	3.83
ENSMUSG00000006169	*Clint1*	3.84	3.63	3.37	3.21
ENSMUSG00000006191	*Cdkal1*	2.6	2.04	2.52	2.21
ENSMUSG00000006215	*Zbtb17*	1.85	2.46	2.09	1.7

ENSMUSG00000006218	*Gm693*	3.76	3.95	3.68	3.07
ENSMUSG00000006262	*Mobkl1a*	3.91	2.7	3.54	3
ENSMUSG00000006273	*Atp6v1b2*	5.15	4.56	4.78	4.45
ENSMUSG00000006276	*Eps15l1*	2.15	2.18	2.62	2.05
ENSMUSG00000006281	*Tep1*	1.36	1.55	1.31	1.04
ENSMUSG00000006289	*Osgep*	2.75	3.06	2.68	2.61
ENSMUSG00000006299	*Aamp*	5.98	6.89	6.44	6.35
ENSMUSG00000006301	*Tmbim1*	2.51	2.98	2.54	2.53
ENSMUSG00000006304	*Arpc2*	6.48	5.65	5.89	5.5
ENSMUSG00000006307	*Wbp7*	1.94	2.82	2.34	2.34
ENSMUSG00000006315	*Tmem147*	6.25	5.76	5.79	5.42
ENSMUSG00000006333	*Rps9*	4.86	5.14	5.09	4.84
ENSMUSG00000006335	*Tfpt*	2.86	3.34	2.45	2.73
ENSMUSG00000006356	*Crip2*	5.99	6.49	6.27	5.88
ENSMUSG00000006360	*Crip1*	3.26	2.37	3.53	4.4
ENSMUSG00000006373	*Pgrmc1*	9.5	9.18	9.37	8.9
ENSMUSG00000006378	*Gcat*	6.63	6.79	6.7	6.29
ENSMUSG00000006386	*Tek*	2.7	2.52	2.2	2.28
ENSMUSG00000006390	*Elovl1*	4.73	4.85	4.9	4.48
ENSMUSG00000006392	*Med8*	4.98	5.01	4.94	4.58
ENSMUSG00000006395	*Hyi*	5.38	5.02	5.6	4.63
ENSMUSG00000006412	*Pfdn2*	5.53	5.73	5.67	5.72
ENSMUSG00000006418	*Zfp313*	4.79	5.11	4.88	4.77
ENSMUSG00000006423	*NA*	3.17	2.24	2.8	2.14
ENSMUSG00000006442	*Srm*	3.56	4.84	3.97	4.13
ENSMUSG00000006445	*Epha2*	2.03	3.39	2.13	1.27
ENSMUSG00000006456	*Rbm14*	3.11	3.8	3.58	3.47
ENSMUSG00000006463	*Zdhhc24*	0.86	0.77	1.19	0.89
ENSMUSG00000006471	*Ndor1*	2	2.49	2.07	2.33
ENSMUSG00000006476	*Nelf*	5.14	5.25	4.96	4.81
ENSMUSG00000006494	*Pdk1*	5.75	4.64	5.32	4.44

ENSMUSG00000006498	*Ptbp1*	5.14	5.22	5.08	5.05
ENSMUSG00000006517	*Mvd*	2.23	2.51	1.93	1.92
ENSMUSG00000006519	*Cyba*	3.09	3.42	3.59	2.99
ENSMUSG00000006522	*Itih3*	8.56	9.1	8.64	8.58
ENSMUSG00000006526	*Tmem110*	2.31	3.23	2.94	2.61
ENSMUSG00000006527	*Sfmbt1*	2.7	2.22	2.41	2.04
ENSMUSG00000006529	*Itih1*	8.1	8.62	8.06	8.25
ENSMUSG00000006567	*Atp7b*	2.58	2.89	2.92	2.62
ENSMUSG00000006574	*Slc4a1*	-4.15	-2.21	1.34	-1.25
ENSMUSG00000006575	*Rundc3a*	1.88	2.41	2.57	1.83
ENSMUSG00000006585	*Cdt1*	0.45	0.62	2.18	1.12
ENSMUSG00000006589	*Aprt*	4.76	5.21	5.48	5.27
ENSMUSG00000006599	*p62*	4.6	3.61	4.04	3.78
ENSMUSG00000006611	*Hfe*	5.15	4.79	4.82	4.38
ENSMUSG00000006638	*Abhd1*	5.63	5.78	5.87	5.66
ENSMUSG00000006641	*Slc5a6*	0.67	0.77	1.96	1.37
ENSMUSG00000006673	*Qrich1*	4.29	4.27	4.33	4.2
ENSMUSG00000006676	*Usp19*	4.02	4.75	4.48	4.31
ENSMUSG00000006699	*Cdc42*	7.02	5.97	6.25	5.71
ENSMUSG00000006705	*Pknox1*	2.16	2.42	1.99	2.35
ENSMUSG00000006715	*Gmnn*	1.49	1.95	2.56	2.05
ENSMUSG00000006717	*Them2*	6.02	6.08	6.09	6.01
ENSMUSG00000006728	*Cdk4*	4.47	5.1	4.88	4.7
ENSMUSG00000006731	*B4galnt1*	6.03	6.83	6.45	6.43
ENSMUSG00000006732	*Mettl1*	2.96	4.04	2.75	3.08
ENSMUSG00000006736	*Tspan31*	7.89	7.88	7.95	7.62
ENSMUSG00000006740	*Kif5b*	4.17	3.34	3.66	3.45
ENSMUSG00000006763	*NA*	2.29	2.31	2.39	2.37
ENSMUSG00000006777	*Krt23*	2.91	1.71	3.89	2.4
ENSMUSG00000006782	*Cnp*	3.5	4.12	3.56	3.06
ENSMUSG00000006800	*Sulf2*	3.29	2.9	3.95	3.33

ENSMUSG00000006818	*Sod2*	7.61	7.26	7.53	7.39
ENSMUSG00000006850	*Tmco6*	1.64	2.03	1.92	1.66
ENSMUSG00000006906	*Stambp*	3.46	2.93	3.41	2.89
ENSMUSG00000006920	*Ezh1*	2.39	2.47	2.46	1.95
ENSMUSG00000006932	*Ctnnb1*	6.33	6.4	6.23	6.11
ENSMUSG00000006941	*Eif1b*	4.47	4.02	4.34	4.3
ENSMUSG00000006998	*Psmd2*	5.16	5.42	4.95	4.91
ENSMUSG00000007029	*Vars*	3.44	4.25	3.77	3.56
ENSMUSG00000007036	*Bat5*	4.11	4.67	4.39	4.13
ENSMUSG00000007038	*Neu1*	4.47	4.7	4.96	4.65
ENSMUSG00000007041	*Clic1*	3.99	4.29	3.93	3.75
ENSMUSG00000007050	*Lsm2*	3.33	4.21	4.41	4.09
ENSMUSG00000007338	*Mrpl49*	4.47	4.75	5.12	5.03
ENSMUSG00000007411	*Mark3*	4.3	4.13	4.09	3.9
ENSMUSG00000007415	*Gatad1*	5.06	4.56	4.7	4.39
ENSMUSG00000007458	*M6pr*	5.09	4.99	4.8	4.34
ENSMUSG00000007476	*Lrrc8a*	3.67	4.15	3.86	3.82
ENSMUSG00000007564	*Ppp2r1a*	4.97	5.75	5.32	5.31
ENSMUSG00000007570	*NA*	1.86	2.7	2.12	2.21
ENSMUSG00000007589	*Tinf2*	2.41	2.36	2.09	2.26
ENSMUSG00000007594	*Hapln4*	2.88	2.55	2.31	2.76
ENSMUSG00000007603	*Dus3l*	2.37	2.76	2.59	2.52
ENSMUSG00000007610	*Gtpbp3*	1.45	2.26	1.69	1.24
ENSMUSG00000007613	*Tgfbr1*	3.41	2.44	2.96	2.39
ENSMUSG00000007617	*Homer1*	1.32	-0.04	0.83	0.62
ENSMUSG00000007656	*AK076052*	4.46	3.24	3.96	3.75
ENSMUSG00000007659	*Bcl2l1*	4.99	5.24	4.57	4.73
ENSMUSG00000007670	*Khsrp*	3.51	3.82	4.15	3.86
ENSMUSG00000007721	*Ccdc124*	4.61	5.19	4.55	4.57
ENSMUSG00000007739	*Cct4*	6.34	5.71	6.05	5.61
ENSMUSG00000007777	*0610009B22Ri*	4.56	3.94	4.51	3.94

ENSMUSG00000007812	*Zfp655*	4.08	2.79	3.52	2.92
ENSMUSG00000007815	*Rhoa*	5.92	5.6	5.53	5.26
ENSMUSG00000007817	*Zmiz1*	2.94	3.56	3.14	2.67
ENSMUSG00000007833	*Aldh16a1*	4.35	4.78	4.76	4.45
ENSMUSG00000007836	*NA*	3.78	5.23	4.48	4.24
ENSMUSG00000007837	*Prrg2*	3.95	4.58	4.28	4.39
ENSMUSG00000007850	*Hnrph1*	4.64	4.03	4.46	4.06
ENSMUSG00000007867	*1700019E19Ri*	0.74	0.77	1.84	1.2
ENSMUSG00000007872	*Id3*	4.65	6.23	4.59	4.47
ENSMUSG00000007877	*Tcap*	#NAME?	#NAME?	2.47	2.28
ENSMUSG00000007880	*Arid1a*	3.26	3.59	3.55	3.45
ENSMUSG00000007891	*Ctsd*	7.56	7.99	7.88	7.64
ENSMUSG00000007892	*Rplp1*	3.97	4.64	4.59	4.97
ENSMUSG00000007950	*Abhd8*	0.7	2.05	1.17	1.49
ENSMUSG00000007987	*Rabl5*	1.75	2.09	2.49	1.88
ENSMUSG00000008035	*Mid1ip1*	4.09	4.69	4.36	4.65
ENSMUSG00000008036	*Ap2s1*	5.77	6.46	5.94	5.89
ENSMUSG00000008090	*Fgfrl1*	3.6	3.86	4.26	4.16
ENSMUSG00000008140	*2310044H10Ri*	5.27	5.95	5.8	5.57
ENSMUSG00000008167	*Fbxw9*	2.92	3.67	3.3	3.18
ENSMUSG00000008193	*Spib*	-2.66	-3.24	1.03	-2.83
ENSMUSG00000008200	*Fnbp4*	2.17	2.02	1.9	2.17
ENSMUSG00000008206	*Lass4*	0.66	1.67	1.28	1.22
ENSMUSG00000008226	*Scrn3*	4.16	3.92	3.99	3.88
ENSMUSG00000008301	*Rnuxa*	4.71	4.29	4.43	4.2
ENSMUSG00000008305	*Tle1*	4.34	4.18	4.14	4.07
ENSMUSG00000008333	*Snrpb2*	3.78	2.92	3.44	3.05
ENSMUSG00000008348	*NA*	3.3	3.54	3.91	3.71
ENSMUSG00000008373	*Prpf31*	1.33	2.13	1.67	1.77
ENSMUSG00000008384	*Sertad1*	1.28	2.34	2.45	2.16
ENSMUSG00000008393	*Carhsp1*	3.34	3.54	3.09	3.41

ENSMUSG00000008398	*Elk3*	2.09	2.33	1.85	1.68
ENSMUSG00000008429	*Herpud2*	4.46	4.51	4.56	4.22
ENSMUSG00000008435	*Rdh13*	1.69	1.92	1.81	1.95
ENSMUSG00000008475	*Arpc5*	5.83	4.84	5.64	5.69
ENSMUSG00000008540	*Mgst1*	10.13	9.61	10.13	9.69
ENSMUSG00000008575	*Nfib*	4.18	3.74	4.08	3.87
ENSMUSG00000008604	*Ubqln4*	4.42	5.07	4.41	4.67
ENSMUSG00000008668	*Rps18*	3.94	3.96	4.14	3.86
ENSMUSG00000008682	*Rpl10*	2.76	2.03	2.49	2.53
ENSMUSG00000008683	*Rps15a*	2.72	1.41	1.91	2.87
ENSMUSG00000008686	*NA*	1.4	-0.19	0.24	-0.21
ENSMUSG00000008690	*Ncaph2*	5.13	5.55	5.2	5.09
ENSMUSG00000008730	*Hipk1*	4.72	4.25	4.55	4.15
ENSMUSG00000008763	*Man1a2*	3.87	2.92	3.35	2.81
ENSMUSG00000008822	*Acyp1*	2.29	0.95	2.37	1.65
ENSMUSG00000008845	*Cd163*	2.98	1.54	2.55	1.41
ENSMUSG00000008855	*HDAC5*	3.19	4.15	3.68	3.29
ENSMUSG00000008859	*Rala*	4.18	3.77	3.81	3.62
ENSMUSG00000008892	*Vdac3*	2.03	2.58	2.61	2.21
ENSMUSG00000008958	*Vps72*	2.87	3.89	3.47	3.22
ENSMUSG00000008976	*Gabpa*	4.3	3.55	4.21	3.9
ENSMUSG00000009013	*Dynll1*	2.91	3.27	2.77	2.55
ENSMUSG00000009030	*Pdcl*	3.51	2.91	3.1	2.78
ENSMUSG00000009035	*Tmem184b*	3.68	3.83	4.08	3.63
ENSMUSG00000009073	*Nf2*	3.25	3.4	3.38	3.23
ENSMUSG00000009076	*Zmat5*	2.5	3.53	3.13	3.24
ENSMUSG00000009079	*Ewsr1*	2.21	2.43	2.38	2.12
ENSMUSG00000009090	*Ap1b1*	4.65	5.33	4.93	4.8
ENSMUSG00000009112	*Bcl2l13*	3.89	3.75	3.9	3.64
ENSMUSG00000009145	*Dqx1*	2.05	2.17	2.71	2.33
ENSMUSG00000009281	*Rarres2*	9.41	9.05	9.57	9.57

ENSMUSG00000009291	*Pttg1ip*	7.97	7.8	7.74	7.41
ENSMUSG00000009293	*Ube2g2*	5.24	5.98	4.91	5.07
ENSMUSG00000009376	*Met*	4.22	3.79	4.3	3.78
ENSMUSG00000009378	*Slc16a12*	5.05	4.65	4.48	4.32
ENSMUSG00000009406	*Elk1*	1.76	1.41	1.29	1.4
ENSMUSG00000009470	*Tnpo1*	3.95	3.04	3.8	3.27
ENSMUSG00000009535	*Rnmt*	3.05	2.34	2.24	1.81
ENSMUSG00000009549	*Srp14*	4.96	4.26	4.57	4.42
ENSMUSG00000009555	*Cdk9*	3.97	4.68	3.76	3.44
ENSMUSG00000009563	*Tor2a*	4.4	5.08	4.62	4.49
ENSMUSG00000009566	*Fpgs*	6.72	7.29	6.61	6.33
ENSMUSG00000009569	*Mkl2*	1.7	2.12	1.94	1.66
ENSMUSG00000009575	*Cbx5*	2.88	2.05	2.29	1.89
ENSMUSG00000009585	*Apobec3*	0.51	0.06	1.38	0.49
ENSMUSG00000009614	*Sardh*	8.26	8.5	8.37	7.97
ENSMUSG00000009621	*Vav2*	2.87	3.7	3.53	3.47
ENSMUSG00000009630	*Ppp2cb*	4.75	4.77	4.56	4.56
ENSMUSG00000009633	*G0s2*	5.91	6.17	5.21	5.12
ENSMUSG00000009640	*Dmap1*	2.83	3.46	3.17	2.96
ENSMUSG00000009646	*Pla2g12b*	5.87	6.22	5.82	5.75
ENSMUSG00000009647	*Ccdc109a*	2.97	2.81	2.95	2.61
ENSMUSG00000009654	*Oit3*	4.63	4.88	4.12	4.28
ENSMUSG00000009681	*Bcr*	3.37	3.8	3.71	3.47
ENSMUSG00000009687	*Fxyd5*	2.5	2.15	2.56	2.75
ENSMUSG00000009733	*Tcfcp2*	1.61	1.49	1.55	1.18
ENSMUSG00000009741	*NA*	4.63	4.31	4.65	4.51
ENSMUSG00000009772	*Nuak2*	2.29	2.89	1.93	1.58
ENSMUSG00000009828	*Ick*	2.57	2.38	1.98	1.47
ENSMUSG00000009863	*Sdhb*	8.01	7.94	8.24	7.74
ENSMUSG00000009894	*1110031B06Ri*	4.96	5.2	4.98	5.08
ENSMUSG00000009905	*Fvt1*	3.79	3.24	3.79	3.52

ENSMUSG00000009907	*Vps4b*	3.6	2.73	3.32	2.82
ENSMUSG00000009927	*Rps25*	1.41	0.29	0.83	0.91
ENSMUSG00000009995	*Taz*	4.17	3.9	4.1	3.92
ENSMUSG00000010025	*Aldh3a2*	7.87	7.03	7.35	6.93
ENSMUSG00000010045	*Tmem115*	3.88	4.67	4.2	4.23
ENSMUSG00000010047	*Hyal2*	5.11	5.41	5.03	4.66
ENSMUSG00000010048	*Ifrd2*	4.29	4.71	4.73	4.37
ENSMUSG00000010051	*Hyal1*	4.02	4.27	4.2	4.01
ENSMUSG00000010054	*Tusc2*	4.31	4.63	4.24	4.15
ENSMUSG00000010057	*Tusc4*	3.23	3.83	3.47	3.28
ENSMUSG00000010064	*Slc38a3*	9.46	10.03	9.85	9.72
ENSMUSG00000010067	*Rassf1*	1.55	1.86	1.6	1.54
ENSMUSG00000010095	*Slc3a2*	5.77	5.84	5.68	5.59
ENSMUSG00000010097	*Nxf1*	4.13	4.28	4.31	4.22
ENSMUSG00000010110	*Stx5*	5.3	5.65	4.98	4.6
ENSMUSG00000010122	*RP23-451A6.3*	6.31	6.17	6.32	5.82
ENSMUSG00000010175	*Prox1*	4.32	4.69	4.52	4.53
ENSMUSG00000010205	*Raver1*	3.48	3.99	3.83	3.48
ENSMUSG00000010277	*2610507B11Ri*	5.53	5.5	5.17	4.88
ENSMUSG00000010290	*AI597479*	2.59	2.04	2.47	1.81
ENSMUSG00000010307	*Tmem86a*	2.31	2.78	2.36	2.5
ENSMUSG00000010358	*Ifi35*	4.47	4.71	4.43	4.38
ENSMUSG00000010362	*Rdm1*	2.39	3.34	2.99	3.23
ENSMUSG00000010376	*Nedd8*	6.38	6.44	6.58	6.41
ENSMUSG00000010392	*Gosr1*	4.33	3.93	4.2	4
ENSMUSG00000010406	*Mrpl52*	6.2	5.87	6.38	6.32
ENSMUSG00000010453	*4632411B12Ri*	3.73	3.9	4.02	3.87
ENSMUSG00000010492	*Uckl1*	3.07	3.1	3.16	2.89
ENSMUSG00000010517	*Faf1*	4.62	4.12	4.3	3.96
ENSMUSG00000010538	*1700021C14Ri*	2.89	2.27	2.67	2.99
ENSMUSG00000010554	*Mett10d*	3	2.71	2.8	2.4

ENSMUSG00000010601	*Apol3*	5.23	5.05	5.03	5
ENSMUSG00000010607	*Pigyl*	4.26	4.56	5.58	6.25
ENSMUSG00000010608	*NA*	4.74	3.84	4.3	3.89
ENSMUSG00000010609	*Psen2*	6.29	6.72	6.44	6.05
ENSMUSG00000010651	*Acaa1b*	8.03	8.27	7.79	7.82
ENSMUSG00000010663	*Fads1*	8.49	8.01	7.81	7.64
ENSMUSG00000010755	*Cars*	3.53	4.12	3.32	3.12
ENSMUSG00000010797	*Wnt2*	2.02	1.58	1.04	1.45
ENSMUSG00000010911	*Apip*	3.79	3.54	4.12	3.69
ENSMUSG00000010914	*Pdhx*	3.3	3.22	3.6	3.24
ENSMUSG00000010936	*Vac14*	3.03	3.85	3.68	3.5
ENSMUSG00000011096	*Akt1s1*	4.01	4.77	4.33	4.13
ENSMUSG00000011114	*Tbrg1*	5.25	5.31	5.12	5.1
ENSMUSG00000011148	*Adssl1*	3.85	4.23	4.08	3.47
ENSMUSG00000011158	*Brf1*	2.14	2.82	2.64	2.32
ENSMUSG00000011179	*Odc1*	3.23	2.48	2.61	2.28
ENSMUSG00000011257	*Pabpc4*	1.63	1.49	2.05	1.64
ENSMUSG00000011263	*NA*	1.91	2.81	1.47	1.82
ENSMUSG00000011305	*2310076L09Ri*	6.86	6.31	5.93	5.14
ENSMUSG00000011306	*Sf4*	2.92	3.26	2.83	2.65
ENSMUSG00000011382	*Dhdh*	6.64	6.1	6.78	6.38
ENSMUSG00000011427	*Zfp790*	1.8	1.6	1.84	1.74
ENSMUSG00000011658	*Fuz*	2.64	3.35	2.7	2.67
ENSMUSG00000011752	*Pgam1*	0.87	0.78	1.41	1.06
ENSMUSG00000011831	*Evi5*	5.35	4.72	5.04	4.53
ENSMUSG00000011832	*B130050I23Ri*	1.05	1.48	0.88	0.83
ENSMUSG00000011837	*Snapc2*	3.05	3.36	3.27	2.88
ENSMUSG00000011877	*Git1*	2.36	3.18	2.77	2.45
ENSMUSG00000011884	*Gltp*	1.62	1.81	1.68	1.68
ENSMUSG00000011958	*Bnip2*	4.51	3.75	4.26	3.89
ENSMUSG00000011960	*Ccnt1*	2.64	2.55	2.81	2.8

ENSMUSG00000012076	*Brms1l*	0.95	-0.16	1.19	0.4
ENSMUSG00000012114	*Med15*	3.48	3.9	3.64	3.54
ENSMUSG00000012117	*Dhdds*	4.28	4.29	3.89	3.96
ENSMUSG00000012296	*Tjap1*	1.28	2.46	1.89	1.79
ENSMUSG00000012405	*Rpl15*	2.18	1.16	1.29	1.07
ENSMUSG00000012422	*Tmem167*	4.5	3.51	3.74	3.27
ENSMUSG00000012428	*Steap4*	6.39	6.58	5.78	5.77
ENSMUSG00000012429	*2810021B07Ri*	1.87	0.74	1.89	1.25
ENSMUSG00000012483	*Rpa3*	2.39	1.18	2.45	0.99
ENSMUSG00000012519	*Mlkl*	1.92	1.12	0.75	0.53
ENSMUSG00000012535	*Tnpo3*	4.9	4.5	4.47	4.19
ENSMUSG00000012640	*Zfp715*	2.3	1.31	1.61	1.04
ENSMUSG00000012848	*Rps5*	7.74	8.19	7.85	8.28
ENSMUSG00000013076	*Amotl1*	1.9	2.18	1.41	1.43
ENSMUSG00000013150	*Gfod2*	2.54	2.9	2.15	1.84
ENSMUSG00000013160	*Atp6v0d1*	6.21	5.87	6.02	5.9
ENSMUSG00000013465	*Nelfb*	3.56	4.48	3.84	3.64
ENSMUSG00000013495	*Tmem175*	2.48	2.53	2.52	1.99
ENSMUSG00000013539	*D16H22S680E*	5.74	5.76	6.2	5.82
ENSMUSG00000013593	*Ndufs2*	7.24	7.46	7.42	7.1
ENSMUSG00000013622	*0610007C21Ri*	5.9	6.03	5.94	5.79
ENSMUSG00000013646	*Sh3bp5l*	2.79	3.51	3.08	2.97
ENSMUSG00000013662	*Atad1*	5.43	4.55	5.2	4.46
ENSMUSG00000013663	*Pten*	5.89	5.1	5.53	5.07
ENSMUSG00000013698	*Pea15a*	3.48	3.53	2.95	3.2
ENSMUSG00000013707	*Tnfaip8l2*	0.16	0.61	1.13	-0.43
ENSMUSG00000013736	*Trnt1*	3.51	2.31	2.94	2.49
ENSMUSG00000013787	*Ehmt2*	3.86	4.66	4.29	4.11
ENSMUSG00000013822	*Elof1*	5.02	5.71	5.62	5.49
ENSMUSG00000013833	*Med16*	3.27	4.3	3.39	3.05
ENSMUSG00000013846	*St3gal1*	5.26	5.51	4.81	4.99

ENSMUSG00000013858	*mFLJ00277*	5.26	6.31	5.77	5.6
ENSMUSG00000013973	*Dedd*	4.16	4.23	4.21	4.04
ENSMUSG00000013997	*Nit1*	5.09	5.11	5.13	5.01
ENSMUSG00000014074	*Rnf168*	3.11	2.53	2.5	2.19
ENSMUSG00000014077	*Sid470*	5.93	7.03	5.5	6.59
ENSMUSG00000014164	*NA*	0.54	1.12	1.12	1.34
ENSMUSG00000014177	*Fam18b*	4.53	3.9	4.16	3.79
ENSMUSG00000014195	*mDj11*	4.84	4.99	4.94	4.81
ENSMUSG00000014226	*Cacybp*	5.35	4.8	4.79	4.55
ENSMUSG00000014232	*Cluap1*	1.96	2.21	2.29	2.23
ENSMUSG00000014243	*NA*	2.73	3.21	3.09	3.22
ENSMUSG00000014245	*Pigl*	2.12	2.45	2.49	2.15
ENSMUSG00000014294	*Ndufa2*	6.73	6.7	7.18	6.98
ENSMUSG00000014313	*Cox6c*	6.34	5.2	5.97	5.34
ENSMUSG00000014349	*Ube2z*	4.96	5.17	4.81	4.7
ENSMUSG00000014353	*Tmem87b*	3.8	2.73	3.39	2.61
ENSMUSG00000014355	*Anapc1*	2.94	2.67	2.94	2.29
ENSMUSG00000014361	*Mertk*	3.3	3.2	3.33	3.11
ENSMUSG00000014372	*Cyp2d10*	8.25	8.75	8.59	8.59
ENSMUSG00000014402	*Tsg101*	4.08	3.25	3.66	2.92
ENSMUSG00000014418	*Hps5*	2.32	2.05	2.26	1.64
ENSMUSG00000014426	*Map3k4*	2.23	2.74	2.66	2.34
ENSMUSG00000014470	*Rnf166*	2.31	3.1	2.96	2.84
ENSMUSG00000014496	*Ankrd28*	3.59	2.84	3.42	2.81
ENSMUSG00000014498	*Ankrd52*	2.75	3.31	3.07	3.17
ENSMUSG00000014503	*Pkd2l2*	2.58	1.91	2.23	1.53
ENSMUSG00000014504	*Srp19*	3.99	4.32	3.84	3.76
ENSMUSG00000014542	*Clec4f*	6.05	5.97	5.67	5.69
ENSMUSG00000014547	*Wdfy2*	1.71	2.15	2.09	1.66
ENSMUSG00000014550	*Zfyve20*	2.39	2.44	2.1	2.01
ENSMUSG00000014551	*Mrps25*	3.81	3.66	3.88	3.26

ENSMUSG00000014554	*Dguok*	3.39	3.28	3.59	3.49
ENSMUSG00000014599	*Csf1*	1.13	1.38	1.34	1.24
ENSMUSG00000014601	*6330569M22R*	2.83	3.18	2.69	2.69
ENSMUSG00000014606	*Slc25a11*	5.97	6.03	6.04	5.68
ENSMUSG00000014633	*2310061C15Ri*	4.26	3.77	3.89	3.85
ENSMUSG00000014668	*Chfr*	3.41	2.96	3.09	2.85
ENSMUSG00000014748	*Tex261*	5.44	5.44	5.46	5.07
ENSMUSG00000014763	*4932442K08Ri*	2.71	2.6	2.59	2.42
ENSMUSG00000014767	*Tbp*	2.9	2.33	2.48	2.66
ENSMUSG00000014769	*Psmb1*	7.21	7.12	7.14	7.07
ENSMUSG00000014771	*Pdcd2*	4.16	3.83	3.93	3.45
ENSMUSG00000014773	*Dll1*	0.86	1.85	1.16	1.01
ENSMUSG00000014791	*Elmo3*	2.92	3.76	3.07	3.15
ENSMUSG00000014850	*Msh3*	2.16	1.47	2.12	1.57
ENSMUSG00000014852	*Adamts13*	1.2	2.09	0.72	1.17
ENSMUSG00000014856	*Hspc171*	4.84	4.96	5.13	4.92
ENSMUSG00000014859	*E2f4*	3.72	4.62	4.07	4.01
ENSMUSG00000014867	*Surf4*	7.27	7.58	7.12	7.04
ENSMUSG00000014873	*Surf2*	3.65	3.45	3.69	3.48
ENSMUSG00000014905	*Dnajb9*	5.37	4.96	5.11	5.15
ENSMUSG00000014932	*Yes1*	3.61	2.3	3.19	2.43
ENSMUSG00000014956	*Ppp1cb*	6.18	5.25	5.74	5.18
ENSMUSG00000014959	*Gorasp2*	5.7	6.18	5.74	5.76
ENSMUSG00000014980	*5730449L18Ri*	0.74	1.83	1.02	0.72
ENSMUSG00000015002	*KIAA0143*	4.35	3.88	4.19	3.79
ENSMUSG00000015013	*Trappc2l*	3.64	3.77	3.95	4.38
ENSMUSG00000015016	*BC021611*	4.18	4.84	4.64	4.34
ENSMUSG00000015023	*Ddx19a*	3.39	3.3	3.58	3.11
ENSMUSG00000015027	*Galns*	1.3	1.67	1.69	1.28
ENSMUSG00000015083	*C8g*	8.38	8.5	8.62	8.37
ENSMUSG00000015085	*Entpd2*	1.31	1.66	0.8	1.25

ENSMUSG00000015087	*B230208H17R*	2.99	3.51	3.04	2.9
ENSMUSG00000015090	*Ptgds*	3.09	1.77	3.39	2.07
ENSMUSG00000015092	*Edf1*	6.29	6.14	6.48	6.36
ENSMUSG00000015094	*Npdc1*	1.37	2.23	2.07	1.42
ENSMUSG00000015095	*Fbxw5*	4.11	4.58	4.47	4.18
ENSMUSG00000015112	*Slc25a13*	7.29	6.45	6.99	6.51
ENSMUSG00000015120	*Ube2i*	1.45	1.68	1.37	1.38
ENSMUSG00000015126	*0610007P22Ri*	2.12	3.06	2.88	2.84
ENSMUSG00000015133	*Lrrk1*	1.32	1.65	1.6	1.69
ENSMUSG00000015143	*Actn1*	3.01	3.45	3.25	3.39
ENSMUSG00000015149	*Sirt2*	5.18	5.6	5.2	5.08
ENSMUSG00000015165	*Hnrnpl*	4.95	5.18	5.19	5.05
ENSMUSG00000015176	*Nolc1*	3.58	4.16	3.43	3.65
ENSMUSG00000015189	*Casd1*	4.07	3.71	3.91	3.28
ENSMUSG00000015202	*Cnksr3*	1.57	2.49	2.02	1.73
ENSMUSG00000015214	*Mtmr1*	3.68	3.18	3.49	3.05
ENSMUSG00000015224	*Cyp2j9*	1.14	0.92	0.24	0.51
ENSMUSG00000015243	*Abca1*	4.46	4.28	4.49	4.16
ENSMUSG00000015247	*Nipsnap3a*	6.14	5.68	5.66	5.4
ENSMUSG00000015289	*Lage3*	2.37	1.73	2.14	1.83
ENSMUSG00000015290	*Ubl4*	4.68	4.87	4.93	5.05
ENSMUSG00000015291	*Gdi1*	4.74	4.95	4.85	4.57
ENSMUSG00000015305	*Sash1*	3.5	3.3	3.34	3.1
ENSMUSG00000015312	*Gadd45b*	2.91	2.9	2.89	2.8
ENSMUSG00000015335	*Zdhhc12*	3.56	3.97	4.07	4.03
ENSMUSG00000015337	*Endog*	4.41	5.28	4.84	4.72
ENSMUSG00000015340	*AK153180*	2.98	1.77	2.58	2.12
ENSMUSG00000015341	*Golga7*	4.27	3.96	4.28	3.8
ENSMUSG00000015342	*Xk*	1.86	1.07	1	0.28
ENSMUSG00000015357	*Clpx*	7.51	6.85	6.25	5.6
ENSMUSG00000015363	*Trabd*	4.96	5.99	4.98	5.03

ENSMUSG00000015377	*1700027J05Ri*	1.34	1.52	1.37	1.45
ENSMUSG00000015461	*Crebl1*	3.45	4.33	3.61	4.07
ENSMUSG00000015474	*Ppt2*	4.69	5.07	4.93	4.84
ENSMUSG00000015478	*Rnf5*	5.47	5.98	5.47	5.59
ENSMUSG00000015488	*5930434B04Ri*	2.91	3.82	3.08	3.23
ENSMUSG00000015522	*Arnt*	3.41	3.13	3.22	2.96
ENSMUSG00000015536	*Mocs2*	6.78	6.47	6.7	6.31
ENSMUSG00000015542	*Nat9*	3.75	4.14	4.25	4.01
ENSMUSG00000015568	*Lpl*	3.21	3.02	2.94	2.83
ENSMUSG00000015575	*Atp6v0e*	5.34	5.61	5.68	5.45
ENSMUSG00000015597	*Zfp318*	2.65	2.18	2.57	2.18
ENSMUSG00000015605	*Srf*	2.7	3.56	3.08	2.92
ENSMUSG00000015653	*Steap2*	1.57	1.58	1.38	1.44
ENSMUSG00000015656	*Hspa8*	4.12	4.56	4.48	4.46
ENSMUSG00000015659	*Serac1*	1.12	0.78	1.28	0.89
ENSMUSG00000015668	*Pdzd11*	4.35	4.06	4.18	4.29
ENSMUSG00000015671	*Psma2*	5.06	5.11	4.92	4.68
ENSMUSG00000015672	*Mrpl32*	5.21	3.64	4.64	4.25
ENSMUSG00000015697	*Setdb1*	2.89	2.87	2.86	2.67
ENSMUSG00000015711	*Prune*	2.53	2.38	2.55	2.32
ENSMUSG00000015714	*Lass2*	7.9	7.4	7.57	7.15
ENSMUSG00000015733	*Capza2*	6.35	5.14	5.87	5.26
ENSMUSG00000015745	*Plekho1*	2.12	2.74	2.19	2.12
ENSMUSG00000015747	*Vps45*	2.7	2.35	2.41	1.93
ENSMUSG00000015748	*Prpf3*	2.38	2.05	2.13	2.14
ENSMUSG00000015749	*Anp32e*	3.72	3.71	3.07	3.02
ENSMUSG00000015750	*Aph1a*	3.95	2.89	3.75	2.83
ENSMUSG00000015755	*Map3k7ip2*	5.84	5.43	5.06	4.84
ENSMUSG00000015757	*Ppil4*	3.61	2.73	3.01	2.51
ENSMUSG00000015759	*Cnih*	6.22	5.29	5.66	5.21
ENSMUSG00000015776	*Med22*	3.5	4.24	3.82	3.75

ENSMUSG00000015790	*Surf1*	4.98	5.35	5.13	5.03
ENSMUSG00000015804	*Med28*	3.94	3.96	3.9	3.64
ENSMUSG00000015806	*Qdpr*	8.13	8.16	8.13	7.72
ENSMUSG00000015837	*Sqstm1*	7.53	8.1	7.56	7.53
ENSMUSG00000015839	*Nfe2l2*	4.91	4.68	5.02	4.78
ENSMUSG00000015843	*Rxrg*	1.32	1.77	2.13	1.63
ENSMUSG00000015846	*Rxra*	7.18	7.61	7.13	7.18
ENSMUSG00000015854	*Cd5l*	5.79	5.35	4.86	5.29
ENSMUSG00000015869	*NA*	4.95	5.33	5.35	5.05
ENSMUSG00000015882	*Lcorl*	1.04	-0.07	-0.04	-0.37
ENSMUSG00000015889	*Lta4h*	3.96	3.73	3.91	3.93
ENSMUSG00000015890	*NA*	7.16	7.18	6.94	6.69
ENSMUSG00000015932	*Dstn*	6.97	6.58	6.41	6.13
ENSMUSG00000015937	*H2afy*	5.4	5.5	5.34	5.21
ENSMUSG00000015942	*Gtf2ird2*	1.83	1.9	1.4	1.68
ENSMUSG00000015943	*Bola1*	3.53	4.18	4.11	4.06
ENSMUSG00000015950	*Ncf1*	1.7	1.52	1.33	0.83
ENSMUSG00000015961	*Adss*	4.77	4	4.59	3.91
ENSMUSG00000015966	*Il17rb*	2.06	2.08	2.27	2.03
ENSMUSG00000015968	*cacna1d*	1.93	1.2	2.04	1.65
ENSMUSG00000015970	*Chdh*	5.81	5.65	5.9	5.51
ENSMUSG00000015971	*Actr8*	3.98	4.02	3.87	3.93
ENSMUSG00000015994	*Fnta*	4.9	4.66	4.6	4.31
ENSMUSG00000016018	*Skiv2l2*	3.44	3.05	3.36	3.14
ENSMUSG00000016024	*Lbp*	6.33	6.63	6.54	6.31
ENSMUSG00000016028	*Celsr1*	2.96	2.48	2.39	2.1
ENSMUSG00000016128	*Stard13*	3.03	2.87	2.78	2.02
ENSMUSG00000016181	*AA408296*	1.35	1.66	1.44	1.65
ENSMUSG00000016194	*Hsd11b1*	9.03	9.16	9.17	8.94
ENSMUSG00000016239	*Lonrf3*	1.17	1.53	0.64	-0.07
ENSMUSG00000016252	*Atp5e*	6.9	6.99	7.04	7.01

ENSMUSG00000016253	*Th1l*	3.78	3.93	4.17	4.04
ENSMUSG00000016256	*Ctsz*	7.38	8.07	7.84	7.65
ENSMUSG00000016257	*Slmo2*	4.34	4.55	4.82	4.49
ENSMUSG00000016308	*Ube2a*	4.57	4.44	4.31	4.17
ENSMUSG00000016319	*Slc25a5*	6.86	6.4	6.86	6.18
ENSMUSG00000016344	*2700038C09Ri*	4.74	4.96	4.71	4.72
ENSMUSG00000016382	*Pls3*	5.47	5.16	4.98	4.65
ENSMUSG00000016409	*Nkap*	2.41	1.68	1.99	1.68
ENSMUSG00000016427	*Ndufa1*	7.12	6.8	7.45	7.52
ENSMUSG00000016477	*E2f3*	1.55	1.11	1.1	0.82
ENSMUSG00000016481	*Crry*	4	3.36	3.5	3.47
ENSMUSG00000016487	*Ppfibp1*	3.51	3.21	3.44	3.17
ENSMUSG00000016495	*5033414D02Ri*	1.9	0.5	1.37	0.64
ENSMUSG00000016503	*Gtf3a*	3.94	4.07	4.01	3.88
ENSMUSG00000016510	*Mtif3*	3.12	3.14	3.11	2.96
ENSMUSG00000016520	*Lnx2*	2.79	3.26	2.59	2.21
ENSMUSG00000016528	*Mapkapk2*	5.31	5.15	5.27	5.18
ENSMUSG00000016534	*Lamp2*	8.87	7.88	8.44	7.94
ENSMUSG00000016541	*Atxn10*	5.68	5.03	5.25	5.18
ENSMUSG00000016554	*Eif3d*	5.61	6.06	5.85	5.65
ENSMUSG00000016559	*H3f3b*	5.27	4.64	5.2	4.56
ENSMUSG00000016619	*Nup50*	3.95	3.69	3.74	3.6
ENSMUSG00000016637	*Rabl4*	2.58	3.24	2.86	3.76
ENSMUSG00000016664	*Pacsin2*	4.43	4.81	4.57	4.46
ENSMUSG00000016756	*Cmah*	4.49	3.97	4.26	3.87
ENSMUSG00000016757	*Ttll12*	2.68	3.52	2.91	2.73
ENSMUSG00000016758	*Bik*	-0.28	2.63	1.74	2.5
ENSMUSG00000016831	*mKIAA0737*	3.27	3.2	3.13	2.85
ENSMUSG00000016833	*Mrps18c*	4.44	2.78	3.87	3.67
ENSMUSG00000016921	*Sfrs6*	5.56	5.36	5.08	4.85
ENSMUSG00000016933	*Plcg1*	3.25	3.26	3.59	3.39

ENSMUSG00000016940	*Kctd2*	2.95	3.45	3.24	3.02
ENSMUSG00000016942	*Tmprss6*	7.85	8.45	7.96	7.79
ENSMUSG00000016946	*Kctd5*	1.18	1.74	1.16	0.95
ENSMUSG00000016984	*Etaa1*	1.9	0.96	1.35	0.7
ENSMUSG00000017009	*Sdc4*	8.14	8.74	8.13	8.23
ENSMUSG00000017057	*Il13ra1*	4.71	4.12	3.87	3.57
ENSMUSG00000017119	*Nbr1*	6.31	5.97	6.16	5.9
ENSMUSG00000017132	*CLM1-A*	3.65	3.73	4.24	4.14
ENSMUSG00000017144	*Rnd3*	3.23	2.84	2.46	2.59
ENSMUSG00000017176	*Nt5c3l*	1.08	1.3	0.86	0.55
ENSMUSG00000017188	*Ccdc56*	5.71	5.84	5.49	5.39
ENSMUSG00000017210	*Thrap4*	2.63	3.23	2.63	2.61
ENSMUSG00000017221	*Psmd3*	6.13	6.59	5.9	5.88
ENSMUSG00000017264	*Exosc10*	3.54	3.72	3.68	3.52
ENSMUSG00000017286	*Glod4*	5.58	4.95	5.33	4.81
ENSMUSG00000017288	*Vps53*	4.18	4.01	4.05	3.71
ENSMUSG00000017291	*Taok1*	3.45	2.19	2.98	2.3
ENSMUSG00000017299	*mTdIF1*	2.55	3.29	3.57	3.01
ENSMUSG00000017300	*Tnnc2*	#NAME?	#NAME?	2.63	2.85
ENSMUSG00000017307	*Acot8*	3.7	3.93	3.79	3.51
ENSMUSG00000017309	*Cd300lg*	3.88	3.98	3.54	3.43
ENSMUSG00000017344	*Vtn*	10.44	10.87	10.55	10.62
ENSMUSG00000017376	*Nlk*	2.04	1.62	2.31	1.82
ENSMUSG00000017386	*Traf4*	4.09	5.08	4.61	4.5
ENSMUSG00000017390	*Aldoc*	2.85	2.89	2.61	2.34
ENSMUSG00000017418	*Arl5b*	3.11	2.12	2.79	2.26
ENSMUSG00000017421	*Zfp207*	4.67	4.44	4.61	4.26
ENSMUSG00000017428	*Psmd11*	4.51	4.33	4.33	4.41
ENSMUSG00000017446	*C1qtnf1*	3.21	3.8	3.33	3.38
ENSMUSG00000017453	*Pipox*	8.05	8.01	8.11	7.92
ENSMUSG00000017466	*Timp2*	3.1	2.84	3.26	2.67

ENSMUSG00000017478	*5830416A07Ri*	3.11	3.76	3.34	3.08
ENSMUSG00000017485	*Top2b*	3.72	2.97	3.75	2.89
ENSMUSG00000017491	*Rarb*	0.69	0.71	1.59	0.95
ENSMUSG00000017493	*Igfbp4*	8.74	9.09	9.06	9
ENSMUSG00000017548	*Suz12*	3.84	2.77	3.1	2.51
ENSMUSG00000017561	*Cytor4*	2.32	1.95	2.14	2.12
ENSMUSG00000017615	*Tnfaip1*	4.21	4.33	4.07	3.93
ENSMUSG00000017639	*Rab11fip4*	1.71	2.57	2.24	1.79
ENSMUSG00000017664	*Slc35c2*	4.75	5.12	4.89	4.72
ENSMUSG00000017670	*Elmo2*	1.42	1.75	1.93	1.66
ENSMUSG00000017677	*Wsb1*	3.72	1.82	2.39	2.02
ENSMUSG00000017679	*5830472M02R*	2.91	2.28	2.22	2.06
ENSMUSG00000017686	*Rhot1*	4.65	3.73	4.24	3.86
ENSMUSG00000017707	*Serinc3*	7.25	6.87	6.99	6.68
ENSMUSG00000017713	*Tha1*	1.62	1.96	2.1	1.38
ENSMUSG00000017715	*Pgs1*	2.16	3.1	2.33	2.51
ENSMUSG00000017718	*Clast2*	7.33	7.52	7.05	6.66
ENSMUSG00000017721	*Pigt*	4.42	5.39	4.78	4.58
ENSMUSG00000017747	*Ghdc*	3.37	3.96	3.75	3.58
ENSMUSG00000017754	*Pltp*	4.07	4.33	4.18	4.25
ENSMUSG00000017756	*Slc12a7*	3.5	4.26	4.11	3.99
ENSMUSG00000017760	*Ctsa*	5.8	6.13	5.98	5.95
ENSMUSG00000017764	*Zswim1*	1.09	1.92	1.4	1.14
ENSMUSG00000017765	*Slc12a4*	2.12	2.97	2.14	2.58
ENSMUSG00000017774	*Myo1c*	3.59	3.9	3.34	3.4
ENSMUSG00000017776	*Crk*	5.01	4.45	4.63	4.17
ENSMUSG00000017778	*Cox7c*	5.18	4.21	5.36	4.99
ENSMUSG00000017781	*Pitpna*	5.31	5.31	5.3	5.16
ENSMUSG00000017801	*Mlx*	4.98	5.1	4.79	4.64
ENSMUSG00000017802	*1300010M03R*	5.72	5.89	5.75	5.49
ENSMUSG00000017830	*Dhx58*	2.12	2.33	1.54	1.94

ENSMUSG00000017831	*Rab5a*	5.04	4.05	4.62	4.33
ENSMUSG00000017837	*Nkiras2*	3.01	3.45	3.29	3.08
ENSMUSG00000017843	*Ppp2r5c*	4.11	3.97	3.7	3.42
ENSMUSG00000017858	*Ift52*	4.36	4.38	4.29	3.96
ENSMUSG00000017868	*Sgk2*	5.46	5.31	5.15	4.72
ENSMUSG00000017929	*B4galt5*	3.46	4.13	4	4.09
ENSMUSG00000017950	*Hnf4a*	8.2	8.82	7.91	8
ENSMUSG00000017978	*Cadps2*	2.17	1.58	1.73	1.49
ENSMUSG00000017999	*Ddx27*	3.34	4.12	3.43	3.33
ENSMUSG00000018001	*Pscd3*	1.36	1.04	1.2	0.75
ENSMUSG00000018040	*1110014J01Rik*	3.36	3.38	3.36	3.28
ENSMUSG00000018042	*Cyb5r3*	7.6	8.12	7.75	7.71
ENSMUSG00000018076	*Thrap2*	1.34	2	1.58	1.86
ENSMUSG00000018102	*Hist1h2bc*	6.75	6.82	6.77	6.64
ENSMUSG00000018143	*Mafk*	2.47	2.54	3.08	2.59
ENSMUSG00000018160	*Med1*	3.18	2.77	2.82	2.34
ENSMUSG00000018166	*Erbb3*	4.72	4.56	5.22	4.7
ENSMUSG00000018167	*Stard3*	3.03	3.8	3.22	3.55
ENSMUSG00000018171	*Tmem49*	6.41	5.4	5.73	5.39
ENSMUSG00000018189	*Uchl5*	4.5	3.67	4.06	3.68
ENSMUSG00000018196	*Glrx2*	4.37	4.69	4.38	4.13
ENSMUSG00000018209	*Stk4*	3.38	2.93	3.49	2.94
ENSMUSG00000018217	*Pmp22*	1.11	0.57	0.7	0.44
ENSMUSG00000018239	*Zcchc10*	2.04	0.99	1.64	1.46
ENSMUSG00000018286	*Psmb6*	6.09	6.84	6.59	6.32
ENSMUSG00000018287	*Spag7*	4.78	5.2	5	4.89
ENSMUSG00000018293	*Pfn1*	7.66	7.41	7.63	7.46
ENSMUSG00000018322	*Tomm34*	3.02	2.91	3.22	2.84
ENSMUSG00000018326	*Ywhab*	6.55	6.26	6.32	5.92
ENSMUSG00000018339	*Gpx3*	1.63	2.51	3	2.14
ENSMUSG00000018340	*Anxa6*	6.02	6.49	6.04	5.88

ENSMUSG00000018347	*Zkscan6*	1.24	1.4	1.09	0.7
ENSMUSG00000018363	*Smurf2*	4.2	3.58	3.69	3.54
ENSMUSG00000018372	*BC058545*	1.06	0.86	1.26	0.98
ENSMUSG00000018377	*Vezf1*	2.98	2.59	2.67	2.5
ENSMUSG00000018379	*Sfrs1*	4.42	3.54	4.03	3.58
ENSMUSG00000018381	*Abi3*	2.16	2.85	1.58	1.89
ENSMUSG00000018387	*Shroom1*	3.98	4.3	3.75	3.43
ENSMUSG00000018401	*Mtmr4*	4.32	4.57	3.69	3.56
ENSMUSG00000018412	*1700081L11Ri*	3.1	3.1	3.29	3.38
ENSMUSG00000018415	*4933439F18Ri*	4.32	4.15	4.16	3.89
ENSMUSG00000018417	*Myo1b*	6.75	6.02	6.51	5.95
ENSMUSG00000018425	*Dhx40*	4.56	3.95	4.3	3.93
ENSMUSG00000018427	*Ypel2*	2.88	2.53	2.57	1.86
ENSMUSG00000018428	*Akap1*	5.17	5.77	5.54	5.44
ENSMUSG00000018433	*Nol11*	2.85	2.94	2.75	2.52
ENSMUSG00000018442	*Derl2*	6.6	5.97	6.06	5.91
ENSMUSG00000018446	*C1qbp*	6.45	5.92	6.26	6.04
ENSMUSG00000018449	*Rpain*	3.32	3.9	3.91	3.9
ENSMUSG00000018459	*Slc13a3*	3.86	4.47	3.87	3.94
ENSMUSG00000018474	*Chd3*	3.24	3.49	3.29	2.99
ENSMUSG00000018476	*Jmjd3*	1.71	2.67	2.44	1.89
ENSMUSG00000018481	*Appbp2*	3.61	2.78	3.19	3.01
ENSMUSG00000018501	*Ncor1*	4.23	4.03	4.11	3.9
ENSMUSG00000018509	*NA*	3.26	3.82	3.84	3.79
ENSMUSG00000018541	*Ccdc49*	2.27	2.09	2.06	1.79
ENSMUSG00000018547	*Pip4k2b*	3.15	3.09	2.73	2.71
ENSMUSG00000018548	*Trim37*	2.36	2.12	2.15	1.88
ENSMUSG00000018559	*Dullard*	4.61	4.91	4.85	4.72
ENSMUSG00000018565	*Rai12*	3.98	4.55	4.03	4.17
ENSMUSG00000018567	*Gabarap*	8.3	7.91	8.16	8.06
ENSMUSG00000018572	*Phf23*	4.08	3.76	3.57	3.39

ENSMUSG00000018574	*Acadvl*	7.99	7.97	7.96	7.71
ENSMUSG00000018583	*G3BP*	3.96	3.66	3.73	3.51
ENSMUSG00000018585	*Atox1*	6.43	6.27	7.14	7
ENSMUSG00000018593	*Sparc*	6.1	6.39	5.95	5.93
ENSMUSG00000018599	*Smcr7*	3.04	3.43	3.39	3.06
ENSMUSG00000018604	*Tbx3*	3.18	3.39	3.1	3.45
ENSMUSG00000018648	*Dusp14*	2.15	1.95	2.43	1.22
ENSMUSG00000018651	*Tada2l*	1.64	1.79	1.55	1.22
ENSMUSG00000018659	*Pnpo*	6.66	6.57	6.44	6.36
ENSMUSG00000018661	*Cog1*	2.94	3.65	3.46	3.21
ENSMUSG00000018666	*Cbx1*	2.8	2.75	2.73	2.77
ENSMUSG00000018669	*Cdk5rap3*	4.32	5.27	4.49	4.62
ENSMUSG00000018672	*Copz2*	5.39	5.27	5.42	4.92
ENSMUSG00000018677	*Slc25a39*	7.83	8.66	8.22	7.95
ENSMUSG00000018678	*Sp2*	1.35	1.77	1.47	1.2
ENSMUSG00000018697	*Aatf*	3.16	3.32	3.49	2.96
ENSMUSG00000018707	*Dync1h1*	3.35	3.92	3.7	3.65
ENSMUSG00000018727	*D11Ertd636e*	1.07	1.36	2.7	1.44
ENSMUSG00000018733	*Pex12*	3.25	2.93	2.9	2.49
ENSMUSG00000018736	*Ndel1*	3.73	3.57	4.19	4.02
ENSMUSG00000018750	*Zbtb4*	1.73	1.82	1.81	1.86
ENSMUSG00000018752	*Tnfsf12-tnfsf13*	1.83	2.46	2.19	2.01
ENSMUSG00000018761	*Mpdu1*	5.45	5.75	5.53	5.54
ENSMUSG00000018765	*Fxr2*	4.2	4.66	4.33	4.33
ENSMUSG00000018770	*Atp5g3*	8.9	7.78	8.55	8.23
ENSMUSG00000018774	*Cd68*	2.65	2.92	3.02	2.72
ENSMUSG00000018796	*Acsl1*	8.55	8.94	8.04	8.14
ENSMUSG00000018800	*Abca5*	1.51	0.71	0.9	0.54
ENSMUSG00000018819	*Lsp1*	0.51	0.74	1.65	0.53
ENSMUSG00000018820	*Zfyve27*	2.05	2.37	2.27	2.34
ENSMUSG00000018821	*Avpi1*	3.52	4.24	4.18	4.29

ENSMUSG00000018841	*Rad51l3*	2.53	2.78	2.8	2.1
ENSMUSG00000018846	*Pank3*	4.15	2.55	3.46	2.87
ENSMUSG00000018848	*Rars*	4.49	4.19	4.38	4.19
ENSMUSG00000018849	*Wwc1*	3.84	4.56	3.89	4.18
ENSMUSG00000018858	*Ict1*	5.31	5.41	5.37	4.95
ENSMUSG00000018861	*Fdxr*	2.64	3.64	3.23	3.15
ENSMUSG00000018882	*Mrpl45*	4.38	4.55	4.61	4.49
ENSMUSG00000018893	*Mb*	#NAME?	#NAME?	3.67	4.03
ENSMUSG00000018899	*Irf1*	2.61	3.32	2.73	2.54
ENSMUSG00000018900	*Slc22a5*	4.17	3.43	3.68	2.82
ENSMUSG00000018906	*P4ha2*	1.98	2.09	2.66	2.59
ENSMUSG00000018909	*Arrb1*	2.15	2.15	1.56	1.93
ENSMUSG00000018920	*Cxcl16*	2.08	2.13	2.14	1.96
ENSMUSG00000018921	*Pelp1*	2.33	2.93	2.55	2.38
ENSMUSG00000018923	*Med11*	2.76	3.49	3.22	3.03
ENSMUSG00000018927	*Ccl6*	4.45	3.71	4.17	3.74
ENSMUSG00000018931	*Gtlf3b*	1.69	1.81	2.07	1.59
ENSMUSG00000018932	*Map2k3*	5.12	5.56	5.6	5.42
ENSMUSG00000018965	*Ywhah*	3.69	3.47	3.35	3.28
ENSMUSG00000018974	*Sart3*	2.17	2.71	2.22	2.05
ENSMUSG00000018995	*Nars2*	2.84	2.1	2.41	1.79
ENSMUSG00000018999	*Slc35b4*	3.69	3.96	3.7	3.43
ENSMUSG00000019039	*Dalrd3*	4.55	4.85	4.52	4.41
ENSMUSG00000019054	*Fis1*	5.42	5.93	5.81	5.53
ENSMUSG00000019055	*Plod1*	4.29	4.68	4.3	4.41
ENSMUSG00000019066	*Rab3d*	1.37	2.25	1.43	1.62
ENSMUSG00000019080	*Mfsd3*	2.44	3	2.53	2.63
ENSMUSG00000019082	*Slc25a22*	7.38	6.96	7.54	7.01
ENSMUSG00000019087	*Atp6ap1*	5.71	5.87	5.71	5.5
ENSMUSG00000019088	*Dnase1l1*	1.74	1.42	1.29	0.81
ENSMUSG00000019122	*Ccl9*	7.19	6.29	6.98	6.37

ENSMUSG00000019132	*BC005537*	6.86	6.08	6.47	5.88
ENSMUSG00000019139	*Isyna1*	1.38	1.58	1.61	1.27
ENSMUSG00000019143	*Hars2*	3.5	3.54	3.83	3.43
ENSMUSG00000019158	*Tmem160*	3.86	5.08	4.45	4.49
ENSMUSG00000019173	*Rab5c*	5.93	6.18	6.09	5.86
ENSMUSG00000019179	*Mdh2*	7.41	7.47	7.73	7.43
ENSMUSG00000019188	*Hm13*	5.59	6.04	5.63	5.67
ENSMUSG00000019189	*Rnf145*	1.89	2.42	2.24	2.51
ENSMUSG00000019194	*Scn1b*	0.67	2.17	1.56	1.75
ENSMUSG00000019210	*Atp6v1e1*	6.19	6.08	6.53	6.21
ENSMUSG00000019232	*Agxt2l1*	6.2	5.34	6.56	5.75
ENSMUSG00000019254	*Ppp1r12c*	2.92	3.84	3.29	3.31
ENSMUSG00000019256	*Ahr*	3.69	3.17	3.38	3.26
ENSMUSG00000019261	*Mtap1s*	0.56	2.32	1.27	1.16
ENSMUSG00000019295	*Tmem129*	4.09	4.2	4.15	3.92
ENSMUSG00000019297	*2610027L16Ri*	6.39	6.7	6.56	6.38
ENSMUSG00000019302	*Atp6v0a1*	4.71	5.14	4.81	4.54
ENSMUSG00000019312	*Grb7*	5.82	6.31	6.35	6.22
ENSMUSG00000019338	*Zfp687*	1.57	2.04	1.55	1.11
ENSMUSG00000019362	*D8Ertd738e*	5.97	6.73	6.74	6.8
ENSMUSG00000019368	*Sec14l4*	6.79	6.85	6.93	6.49
ENSMUSG00000019370	*Calm3*	4.16	4.61	4.34	3.99
ENSMUSG00000019373	*Cops3*	5.4	5.19	5.46	4.99
ENSMUSG00000019428	*SAM11*	6.9	7.74	7.07	6.81
ENSMUSG00000019432	*Bat1a*	3.96	4.67	4.47	4.06
ENSMUSG00000019433	*Gipc1*	2.48	3.73	3.09	3.07
ENSMUSG00000019437	*Tlcd1*	3.86	3.93	4.22	4.07
ENSMUSG00000019461	*Plscr3*	1.61	1.96	1.55	0.95
ENSMUSG00000019464	*Ptger1*	1.71	2.25	1.78	1.6
ENSMUSG00000019470	*Xab2*	2.74	3.76	3.11	2.79
ENSMUSG00000019471	*Cdc37*	5.73	6.25	5.87	5.69

ENSMUSG00000019478	*Rab4a*	4.69	5.11	5.19	5.08
ENSMUSG00000019487	*Trip10*	1.8	2.33	2.07	1.97
ENSMUSG00000019494	*COPS6*	6.45	6.75	6.69	6.37
ENSMUSG00000019505	*Ubb*	5.57	6.09	5.83	5.65
ENSMUSG00000019518	*Ap4m1*	2.73	2.8	2.89	3.07
ENSMUSG00000019528	*Gyg*	2.22	1.91	2.11	2.17
ENSMUSG00000019539	*Rcn3*	1.8	3.35	2.59	2.72
ENSMUSG00000019577	*Pdk4*	2.07	1.01	2.02	1.58
ENSMUSG00000019578	*Ubxd1*	4.58	5.11	5.15	4.94
ENSMUSG00000019579	*D17Wsu104e*	5.57	6.53	6.03	6
ENSMUSG00000019590	*Cyb561*	-0.33	1.47	1.09	0.48
ENSMUSG00000019659	*Ccdc12*	1.18	2.15	1.3	1.91
ENSMUSG00000019689	*1110001J03Rik*	5.48	5.29	5.72	5.56
ENSMUSG00000019710	*Mrpl24*	5.55	5.69	5.61	5.63
ENSMUSG00000019715	*Gle1l*	3.54	3.54	3.7	3.52
ENSMUSG00000019718	*2810055F11Ri*	3.83	2.75	3.74	3.26
ENSMUSG00000019726	*Lyst*	2.27	1.88	2.23	1.82
ENSMUSG00000019731	*Slc35e1*	4.57	4.86	4.55	4.42
ENSMUSG00000019732	*Calr3*	1.22	0.41	0.51	0.45
ENSMUSG00000019738	*Polr2i*	4.95	5.1	6.8	6.76
ENSMUSG00000019755	*Tmem189*	2.93	2.94	3.26	3.17
ENSMUSG00000019762	*Iyd*	6.55	6.24	6.59	6.28
ENSMUSG00000019763	*Rmnd1*	1.61	1.2	1.69	1.48
ENSMUSG00000019768	*Esr1*	4.05	3.63	2.59	2.09
ENSMUSG00000019774	*Mtrf1l*	2.29	2.06	2.28	2.05
ENSMUSG00000019777	*Hdac2*	2.88	2.5	2.62	2.18
ENSMUSG00000019779	*Frk*	1.82	1.01	1.3	0.75
ENSMUSG00000019782	*Rwdd1*	2	2.18	2.19	2.1
ENSMUSG00000019790	*Stxbp5*	1.58	1.46	1.62	1.26
ENSMUSG00000019791	*Hint3*	5.3	4.26	4.93	4.5
ENSMUSG00000019792	*Trmt11*	2.16	1.55	2.09	1.57

ENSMUSG00000019794	*Katna1*	3.26	2.78	2.95	2.63
ENSMUSG00000019795	*Pcmt1*	4.68	4.26	4.29	3.95
ENSMUSG00000019797	*1700021F05Ri*	3.94	3.14	3.74	3.22
ENSMUSG00000019802	*Sec63*	5.11	4.62	4.63	4.16
ENSMUSG00000019804	*Snx3*	6.55	6.26	6.38	6.14
ENSMUSG00000019806	*Aig1*	3.56	3.65	3.21	2.47
ENSMUSG00000019808	*Deadc1*	2.29	2.41	2.67	2.96
ENSMUSG00000019809	*Pex3*	4.48	3.75	4.44	4.06
ENSMUSG00000019810	*Fuca2*	1.33	0.86	1.48	1.18
ENSMUSG00000019813	*2410017P07Ri*	1.15	0.43	1.51	1.1
ENSMUSG00000019814	*Ltv1*	3.59	3.43	3.34	3.12
ENSMUSG00000019818	*Cd164*	8.06	7.12	7.43	6.93
ENSMUSG00000019820	*Utrn*	2.16	1.82	2	1.74
ENSMUSG00000019822	*Smpd2*	3.93	4.28	4.81	4.6
ENSMUSG00000019826	*Zbtb24*	2.43	2.35	2.28	2.1
ENSMUSG00000019832	*Rab32*	4.97	5.18	5.01	4.6
ENSMUSG00000019837	*Gtf3c6*	4.21	4.3	4.37	3.87
ENSMUSG00000019838	*Slc16a10*	5.64	5.29	5.66	5.35
ENSMUSG00000019841	*Sez4*	1.7	1.05	1.81	1.17
ENSMUSG00000019842	*Traf3ip2*	1.01	1.02	0.67	0.8
ENSMUSG00000019843	*Fyn*	1.99	2.43	1.76	1.64
ENSMUSG00000019849	*Prep*	3.81	4.15	4.03	3.82
ENSMUSG00000019851	*Perp*	6.61	5.86	5.91	5.57
ENSMUSG00000019854	*Reps1*	3.82	3.38	3.87	3.67
ENSMUSG00000019857	*Asf1a*	2.64	1.24	1.83	1.46
ENSMUSG00000019861	*Gopc*	3.52	3.11	3.34	2.76
ENSMUSG00000019863	*Qrsl1*	1.8	1.73	1.59	1.46
ENSMUSG00000019864	*Rtn4ip1*	3.86	3.7	3.95	3.17
ENSMUSG00000019866	*NA*	4.15	2.97	3.65	3.07
ENSMUSG00000019868	*Vta1*	3.65	3.88	3.98	3.67
ENSMUSG00000019872	*Smpdl3a*	5.1	4.65	4.91	4.69

ENSMUSG00000019873	*Reep3*	5.3	4.74	4.9	4.87
ENSMUSG00000019874	*Fabp7*	2.41	1.95	1.1	1.86
ENSMUSG00000019877	*Serinc1*	6.99	6.62	6.88	6.42
ENSMUSG00000019878	*Hsf2*	3.7	3	3.47	3.24
ENSMUSG00000019880	*Rspo3*	2.1	1.56	1.94	1.42
ENSMUSG00000019883	*Echdc1*	5.99	5.09	5.25	4.75
ENSMUSG00000019889	*Ptprk*	3.95	4.23	3.96	3.9
ENSMUSG00000019891	*Dcbld1*	1.5	1.63	1.36	1.48
ENSMUSG00000019897	*Ccdc59*	4.29	3.69	4.13	3.66
ENSMUSG00000019906	*Lin7a*	2.45	2.33	1.62	1.71
ENSMUSG00000019907	*Ppp1r12a*	2.88	2.61	2.8	2.5
ENSMUSG00000019916	*P4ha1*	2.93	2.67	2.91	3.24
ENSMUSG00000019917	*10-Sep*	2.89	2.05	2.72	2.08
ENSMUSG00000019920	*Lims1*	2.94	2.06	2.77	1.95
ENSMUSG00000019923	*Zwint*	4.66	4.6	4.36	4.25
ENSMUSG00000019927	*Ube2d1*	3.5	2.32	3.45	2.79
ENSMUSG00000019929	*Dcn*	7.38	7.09	7.2	7.16
ENSMUSG00000019935	*Slc17a8*	2.35	1.37	2.14	1.41
ENSMUSG00000019943	*Atp2b1*	3.33	3.08	3.35	3.12
ENSMUSG00000019944	*Rhobtb1*	5.04	4.76	4.45	4.05
ENSMUSG00000019947	*Arid5b*	4.2	2.91	3.44	3.49
ENSMUSG00000019948	*Actr6*	3.73	2.28	3.24	2.58
ENSMUSG00000019951	*mKIAA0701*	3.85	3.56	3.47	3.12
ENSMUSG00000019952	*Wdr51b*	1.84	1.49	1.95	1.73
ENSMUSG00000019960	*Dusp6*	4.22	3.81	3.49	4.16
ENSMUSG00000019961	*Tmpo*	2.84	2.85	2.85	2.54
ENSMUSG00000019969	*Psen1*	4.32	4.31	4.38	4.1
ENSMUSG00000019970	*Sgk*	3.66	4.05	3.4	3.34
ENSMUSG00000019977	*Hbs1l*	4.47	4.35	4.31	4.05
ENSMUSG00000019978	*Epb4.1l2*	1.67	1.93	1.48	1.33
ENSMUSG00000019984	*Sur2*	2.01	2.04	1.97	1.65

ENSMUSG00000019987	*Arg1*	10.44	10.21	10.66	10.83
ENSMUSG00000019988	*Nedd1*	2.42	1.52	2.24	1.78
ENSMUSG00000019989	*Enpp3*	3.31	3.07	3.7	3.5
ENSMUSG00000019990	*Pde7b*	1.88	0.87	0.99	1.21
ENSMUSG00000019996	*Mtap7*	2.73	3.17	3.13	2.89
ENSMUSG00000019997	*Ctgf*	2.98	2.62	2.93	2.67
ENSMUSG00000019998	*Stx7*	4.05	3.2	3.65	3.22
ENSMUSG00000020003	*Pex7*	5.91	5.72	5.78	5.34
ENSMUSG00000020009	*Ifngr1*	4.13	3.82	4.02	3.66
ENSMUSG00000020010	*Vnn3*	6.4	6.03	5.92	5.73
ENSMUSG00000020015	*Pctk2*	2.87	2.35	2.76	2.44
ENSMUSG00000020017	*Hal*	7.19	7.82	7.55	7.33
ENSMUSG00000020019	*Ntn4*	1.43	1.68	1.58	1.84
ENSMUSG00000020021	*Fgd6*	3.65	3.22	3.33	3.26
ENSMUSG00000020022	*Ndufa12*	5.68	5.54	5.85	5.98
ENSMUSG00000020023	*Tmcc3*	1.69	1.92	2.2	1.66
ENSMUSG00000020024	*Ccdc41*	1.87	1.02	1.64	1.07
ENSMUSG00000020027	*AK033206*	1.78	1.49	-0.9	-0.51
ENSMUSG00000020029	*AK202794*	6.67	5.8	6.43	5.99
ENSMUSG00000020034	*Tcp11l2*	4.07	3.47	3.92	3.56
ENSMUSG00000020037	*Rfx4*	0.52	0.5	1.02	0.32
ENSMUSG00000020038	*Cry1*	3.5	3.52	2.56	1.86
ENSMUSG00000020044	*Timp3*	4.08	3.31	3.63	3.48
ENSMUSG00000020048	*Hsp90b1*	8.73	8.6	8.01	7.91
ENSMUSG00000020051	*Pah*	9.64	9.14	9.75	9.33
ENSMUSG00000020053	*Igf1*	7.15	6.47	6.6	6.44
ENSMUSG00000020056	*Ccdc53*	4.54	4.08	4.76	4.37
ENSMUSG00000020059	*Sycp3*	3.24	0.84	2.67	1.51
ENSMUSG00000020063	*Sirt1*	2.34	1.27	2.25	1.55
ENSMUSG00000020064	*Herc4*	3.92	3.18	3.62	3.14
ENSMUSG00000020068	*3110049J23Ri*	6.28	6.48	6.26	5.95

ENSMUSG00000020069	*Hnrph3*	2.66	2.79	2.8	2.67
ENSMUSG00000020072	*Pbld*	6.81	6.87	7.24	6.9
ENSMUSG00000020074	*Ccar1*	4.38	3.79	3.85	3.12
ENSMUSG00000020075	*Ddx21*	4.04	3.9	4.03	3.82
ENSMUSG00000020076	*Ddx50*	3.82	2.65	3.14	2.72
ENSMUSG00000020077	*Srgn*	3.65	3.05	3.31	2.93
ENSMUSG00000020078	*Vps26a*	5.13	4.21	4.79	4.32
ENSMUSG00000020079	*Supv3l1*	3.4	3.53	3.89	3.66
ENSMUSG00000020083	*2010107G23Ri*	0.91	2.05	1.1	1.44
ENSMUSG00000020085	*Aifm2*	3.8	3.66	4.01	3.38
ENSMUSG00000020087	*NA*	4.47	5.56	5.16	5.11
ENSMUSG00000020088	*Sar1a*	5.96	5.18	5.39	5.55
ENSMUSG00000020089	*Ppa1*	7.16	6.7	7.07	6.47
ENSMUSG00000020091	*Eif4ebp2*	6.82	7.27	6.95	6.9
ENSMUSG00000020092	*X99384*	1.49	2.43	1.53	1.23
ENSMUSG00000020097	*Sgpl1*	4.82	4.75	4.6	4.3
ENSMUSG00000020098	*Pcbd1*	8.65	8.49	8.34	8.03
ENSMUSG00000020102	*Slc16a7*	5.47	4.32	5.08	4.43
ENSMUSG00000020105	*Lrig3*	1.45	1.67	1.89	1.86
ENSMUSG00000020107	*D10Ertd641e*	4.66	4.46	4.8	4.59
ENSMUSG00000020108	*Ddit4*	3.41	3	4.44	3.9
ENSMUSG00000020109	*Dnajb12*	4.93	5.33	5.2	5.14
ENSMUSG00000020111	*Cbara1*	4.6	4.76	4.46	4.28
ENSMUSG00000020114	*NA*	4.31	4.08	4.24	4.02
ENSMUSG00000020115	*Tbk1*	3.47	3.17	3.52	3.17
ENSMUSG00000020116	*Pno1*	4.99	4.65	4.78	4.36
ENSMUSG00000020122	*Egfr*	5.81	5.88	5.47	5.7
ENSMUSG00000020123	*Avpr1a*	5.14	5.28	4.2	4.16
ENSMUSG00000020124	*Usp15*	4.63	4.06	4.32	3.85
ENSMUSG00000020128	*Vps54*	4.29	3.54	3.9	3.41
ENSMUSG00000020130	*Tbc1d15*	4.69	3.79	4.31	3.87

ENSMUSG00000020131	*Pcsk4*	0.63	1.1	2.1	1.66
ENSMUSG00000020132	*Rab21*	5.14	3.78	4.62	4.04
ENSMUSG00000020133	*2310011J03Ri*	3.02	3.72	3.55	3.47
ENSMUSG00000020134	*Peli1*	3.22	2.82	3.41	3.17
ENSMUSG00000020137	*Thap2*	2.47	1.25	2.31	2.27
ENSMUSG00000020149	*Rab1A*	6.48	5.98	6.29	5.86
ENSMUSG00000020150	*Gamt*	7.23	7.57	7.65	7.4
ENSMUSG00000020152	*Actr2*	5.62	4.19	4.88	4.39
ENSMUSG00000020153	*Ndufs7*	5.52	6.53	6.24	5.91
ENSMUSG00000020154	*Ptprb*	3.03	3.21	2.81	2.95
ENSMUSG00000020156	*Mum1*	0.77	1.52	1.01	0.91
ENSMUSG00000020163	*Uqcr*	5.28	5.21	6.04	6.37
ENSMUSG00000020166	*Cnot2*	3.96	3.68	3.82	3.26
ENSMUSG00000020167	*Tcfe2a*	2.13	2.99	2.72	2.24
ENSMUSG00000020170	*Frs2*	2.59	2.18	2.71	2.42
ENSMUSG00000020171	*Yeats4*	4.32	4.08	4.27	3.68
ENSMUSG00000020173	*Cobl*	2.11	1.82	2.64	2.23
ENSMUSG00000020176	*Grb10*	2.23	0.97	2.15	0.93
ENSMUSG00000020180	*Snrpd3*	5.07	5.31	5.32	5.44
ENSMUSG00000020182	*Ddc*	4.99	4.73	4.83	4.24
ENSMUSG00000020183	*NA*	1.16	0.92	1.58	1.4
ENSMUSG00000020184	*Mdm2*	3.47	3.25	3.3	3.2
ENSMUSG00000020186	*Csrp2*	4.22	4.12	4.43	4.44
ENSMUSG00000020189	*Osbpl8*	3.44	2.12	3.21	2.5
ENSMUSG00000020190	*Mknk2*	6.01	6.65	6.69	6.45
ENSMUSG00000020196	*Cabin1*	1.44	2.46	2.67	2.54
ENSMUSG00000020198	*Ap3d1*	4.27	4.87	4.64	4.43
ENSMUSG00000020205	*Phlda1*	5.56	5.83	5.03	5.03
ENSMUSG00000020211	*Sf3a2*	3.41	4.33	4.03	4.04
ENSMUSG00000020219	*Timm13*	5.73	6.45	6.31	6.22
ENSMUSG00000020220	*NA*	3.16	3.01	3.04	2.86

ENSMUSG00000020224	*1190005P17Ri*	1.99	1.64	1.64	0.89
ENSMUSG00000020225	*AK162942*	6.28	5.92	6.18	5.79
ENSMUSG00000020228	*helB*	1.84	1.55	1.4	1.2
ENSMUSG00000020232	*Hmg20b*	3.52	3.96	3.9	3.65
ENSMUSG00000020234	*4930404N11Ri*	1.5	2.44	1.71	1.58
ENSMUSG00000020235	*Fzr1*	2.74	3.41	3.02	2.68
ENSMUSG00000020236	*Dohh*	3.4	4.34	3.97	3.93
ENSMUSG00000020238	*Ncln*	4.76	5.82	5.23	5.23
ENSMUSG00000020246	*Hcfc2*	2.51	2.15	2.01	1.79
ENSMUSG00000020248	*Nfyb*	2.88	2.21	2.53	2.46
ENSMUSG00000020250	*Txnrd1*	5.85	5.49	5.78	5.55
ENSMUSG00000020253	*Ppm1m*	1.79	1.95	1.89	1.43
ENSMUSG00000020255	*D10Wsu102e*	2.84	2.82	2.68	2.52
ENSMUSG00000020257	*Wdr82*	4.66	4.16	4.49	4.26
ENSMUSG00000020258	*6230410P16Ri*	5.62	6.36	6.02	5.81
ENSMUSG00000020260	*Pofut2*	3.7	3.96	3.86	3.29
ENSMUSG00000020261	*Slc36a1*	3.09	3.58	3.46	3.28
ENSMUSG00000020262	*Adarb1*	2.07	1.92	2.43	2.03
ENSMUSG00000020263	*Appl2*	2.51	2.35	2.74	2.4
ENSMUSG00000020265	*Sumo3*	5.94	5.89	5.53	5.32
ENSMUSG00000020267	*Hint1*	7.03	6.7	6.55	6.34
ENSMUSG00000020271	*mKIAA0696*	3.98	3.87	3.75	3.6
ENSMUSG00000020272	*Stk10*	0.37	1.35	1.06	-0.27
ENSMUSG00000020273	*Papolg*	1.18	0.65	1.12	0.38
ENSMUSG00000020277	*Pfkl*	4.08	4.97	4.28	4.38
ENSMUSG00000020280	*Ccdc139*	3.28	2.38	2.91	2.39
ENSMUSG00000020283	*Pex13*	5.62	4.79	5.35	5.04
ENSMUSG00000020284	*1810043G02R*	1.3	1.98	2.33	1.69
ENSMUSG00000020287	*Mpg*	2.31	2.1	1.9	1.53
ENSMUSG00000020288	*Ahsa2*	4.79	4.29	4.32	4.28
ENSMUSG00000020289	*Mpg*	2.43	2.89	2.83	2.28

ENSMUSG00000020290	*Xpo1*	3.18	1.93	2.93	1.7
ENSMUSG00000020300	*Cpeb4*	4.52	3.25	3.7	3.19
ENSMUSG00000020305	*Asb3*	1.27	0.89	1.28	0.88
ENSMUSG00000020307	*Cdc34*	4.62	5.29	4.73	4.88
ENSMUSG00000020308	*Gtrgeo22*	3.2	4.33	3.98	3.93
ENSMUSG00000020309	*2510006C20Ri*	4.95	4.08	4.92	4.48
ENSMUSG00000020311	*4933407N01Ri*	3.99	3.04	3.46	2.98
ENSMUSG00000020315	*Spnb2*	3.55	3.33	3.31	3.05
ENSMUSG00000020321	*Mdh1*	9.04	8.88	9.07	8.92
ENSMUSG00000020326	*Ccng1*	4.89	3.76	4.36	3.78
ENSMUSG00000020328	*Nudcd2*	4.38	4.02	4.07	3.63
ENSMUSG00000020329	*Polrmt*	2.98	3.72	3.28	3.27
ENSMUSG00000020346	*Mgat1*	4.7	5.32	4.71	4.56
ENSMUSG00000020349	*Ppp2ca*	6.63	6.72	6.7	6.33
ENSMUSG00000020357	*Flt4*	2.77	3.57	2.82	3.3
ENSMUSG00000020358	*Hnrpab*	6.22	6.05	5.9	5.77
ENSMUSG00000020359	*Agxt2l2*	3.53	3.16	3.32	3.04
ENSMUSG00000020361	*Hspa4*	5.85	5.71	5.67	5.36
ENSMUSG00000020362	*BC079836*	4.17	3.2	2.99	2.61
ENSMUSG00000020366	*Mapk9*	4.38	3.73	3.95	3.57
ENSMUSG00000020368	*Canx*	7.6	7.03	6.95	6.73
ENSMUSG00000020372	*Gnb2l1*	7.86	8.41	8.1	7.98
ENSMUSG00000020375	*Rufy1*	3.47	3.63	3.79	3.46
ENSMUSG00000020376	*Rnf130*	6.4	6	6.1	5.79
ENSMUSG00000020380	*Rad50*	1.74	1.23	1.29	0.67
ENSMUSG00000020381	*3010026O09Ri*	2.55	2.8	2.58	2.66
ENSMUSG00000020385	*Clk4*	3.44	2.66	3.79	4
ENSMUSG00000020386	*Sar1b*	8.18	7.37	7.88	7.41
ENSMUSG00000020387	*Phf15*	2.23	2.91	1.99	1.09
ENSMUSG00000020390	*Ube2b*	6.89	5.59	6.44	5.93
ENSMUSG00000020392	*Cdkn2aipnl*	4	4.01	4.1	3.8

ENSMUSG00000020393	*Kremen1*	1.69	2.26	2.39	1.82
ENSMUSG00000020397	*Med7*	3.81	3.35	3.61	3.44
ENSMUSG00000020400	*Tnip1*	1.99	2.76	2.49	2.24
ENSMUSG00000020402	*Vdac1*	7.12	6.65	6.86	6.58
ENSMUSG00000020409	*Slu7*	3.79	3.35	3.46	3.15
ENSMUSG00000020412	*Ascc2*	3.37	3.74	3.62	3.73
ENSMUSG00000020413	*Hus1*	1.66	1.38	1.29	0.56
ENSMUSG00000020422	*Tns3*	2.4	2.91	2.8	2.63
ENSMUSG00000020423	*Btg2*	1.87	2.03	1.85	1.59
ENSMUSG00000020427	*Igfbp3*	5.3	5.14	5.21	4.72
ENSMUSG00000020429	*Igfbp1*	5.87	4.24	6.04	5.97
ENSMUSG00000020430	*Pes1*	2.54	3.07	2.41	2.47
ENSMUSG00000020432	*Tcn2*	7.25	7.5	7.56	7.26
ENSMUSG00000020439	*Smtn*	1.04	1.63	1.03	1.09
ENSMUSG00000020440	*Arf5*	5.21	6.15	5.61	5.31
ENSMUSG00000020441	*2310033P09Ri*	2.44	2.79	2.45	2.33
ENSMUSG00000020444	*Guk1*	4	4.42	3.85	3.6
ENSMUSG00000020448	*Rnf185*	4.75	4.66	4.65	4.57
ENSMUSG00000020451	*Limk2*	0.89	0.8	1.17	0.9
ENSMUSG00000020454	*Eif4enif1*	3.09	3.45	3.34	3.21
ENSMUSG00000020455	*Trim11*	2.02	2.37	2.06	1.81
ENSMUSG00000020456	*Ogdh*	6.07	6.37	6.46	6.28
ENSMUSG00000020457	*Drg1*	5.44	5.19	5.49	5.19
ENSMUSG00000020458	*Rtn4*	5.49	3.82	4.51	3.8
ENSMUSG00000020459	*Mtif2*	3.95	3.44	3.86	3.33
ENSMUSG00000020460	*Rps27a*	0.84	1.71	1.25	0.6
ENSMUSG00000020462	*Ccdc104*	3.63	3.18	3.53	2.94
ENSMUSG00000020463	*Smek2*	4.42	3.57	3.94	3.37
ENSMUSG00000020464	*Pnpt1*	4.15	3.31	3.82	3.05
ENSMUSG00000020467	*Efemp1*	2.51	2.2	2.23	2.61
ENSMUSG00000020471	*Pold2*	2.17	3.13	2.51	2.48

ENSMUSG00000020472	*Zfp496*	3.37	3.7	3.6	3.47
ENSMUSG00000020476	*Dbnl*	3.7	4.48	3.88	3.86
ENSMUSG00000020477	*Mrps24*	5.71	5.86	5.54	5.56
ENSMUSG00000020482	*Ccdc117*	3.95	3.38	3.93	3.95
ENSMUSG00000020483	*Dynll2*	6.23	6.3	5.69	5.75
ENSMUSG00000020484	*Xbp1*	7.04	7.75	6.43	6.64
ENSMUSG00000020485	*Supt4h2*	2.94	1.84	2.84	2.51
ENSMUSG00000020486	*4-Sep*	0.98	1.82	1.55	1.3
ENSMUSG00000020495	*1200011M11Ri*	2.61	2.52	2.44	2.35
ENSMUSG00000020496	*NA*	5.69	6.46	5.63	5.59
ENSMUSG00000020513	*Tubd1*	0.67	0.88	1.17	0.97
ENSMUSG00000020514	*Mrpl22*	3.34	2.96	3.6	3.45
ENSMUSG00000020515	*Cnot8*	4.32	4.55	4.51	4.35
ENSMUSG00000020516	*RP23-467J12.2*	2.54	2.21	2.36	1.95
ENSMUSG00000020519	*Sap30l*	3.4	4.36	3.77	3.42
ENSMUSG00000020520	*Galnt10*	1.49	1.6	1.49	1.29
ENSMUSG00000020521	*0610013E23Ri*	4.95	3.61	4.09	3.7
ENSMUSG00000020522	*Mfap3*	2.25	2.25	2.29	1.9
ENSMUSG00000020523	*1810073G14Ri*	4.6	4.28	4.52	4.08
ENSMUSG00000020525	*Ppm1d*	1.84	1.65	1.84	1.34
ENSMUSG00000020526	*Znhit3*	2.13	2.18	2.4	2.15
ENSMUSG00000020527	*NA*	1.38	1.58	1.79	1.21
ENSMUSG00000020530	*Ggnbp2*	5.53	4.45	5.05	4.43
ENSMUSG00000020532	*Acaca*	1.84	1.33	2.02	1.62
ENSMUSG00000020534	*Shmt1*	7.02	7.16	6.99	7
ENSMUSG00000020536	*Llgl1*	1.04	2	1.17	1.1
ENSMUSG00000020537	*Drg2*	4.23	4.85	4.48	4.56
ENSMUSG00000020538	*Srebf1*	5.08	6.31	5.49	5.73
ENSMUSG00000020541	*Tom1l1*	3.43	2.3	3.07	2.65
ENSMUSG00000020544	*Cox11*	3.79	2.47	3.34	2.86
ENSMUSG00000020547	*Bzw2*	2.34	2.47	2.93	2.44

ENSMUSG00000020549	*Elac2*	3.72	4.52	3.89	3.91
ENSMUSG00000020553	*Pctp*	6.75	6.34	6.09	5.73
ENSMUSG00000020561	*Twistnb*	2.73	2.1	2.13	1.72
ENSMUSG00000020564	*Atxn7l1*	1.93	1.84	1.39	1.35
ENSMUSG00000020570	*Sypl*	5.57	4.58	5.08	4.67
ENSMUSG00000020571	*Pdia6*	7.13	7.49	6.65	6.87
ENSMUSG00000020572	*Pbef1*	4.71	4.4	4.6	4.41
ENSMUSG00000020576	*NA*	2.93	3.14	2.89	2.7
ENSMUSG00000020577	*Tspan13*	1.06	-0.84	1.04	0.32
ENSMUSG00000020580	*Rock2*	3.1	2.14	2.78	2.26
ENSMUSG00000020585	*Laptm4a*	7.17	6.66	6.83	6.45
ENSMUSG00000020590	*Snx13*	3.99	2.56	3.32	2.8
ENSMUSG00000020592	*Sdc1*	6.82	6.96	6.57	6.29
ENSMUSG00000020593	*Lpin1*	7.9	6.81	7.58	7.69
ENSMUSG00000020594	*Pum2*	4.55	3.78	4.19	3.73
ENSMUSG00000020604	*Arsg*	2.38	2.26	2.4	2.55
ENSMUSG00000020605	*Hs1bp3*	2.5	3.01	2.88	2.55
ENSMUSG00000020608	*Smc6*	3.15	2.08	2.51	2.11
ENSMUSG00000020609	*Apob*	9.3	8.56	8.8	8.31
ENSMUSG00000020610	*X83328*	2.59	2.57	2.41	2.41
ENSMUSG00000020611	*Gna13*	3.1	2.72	2.95	2.76
ENSMUSG00000020612	*Prkar1a*	5.61	5.24	5.42	5.14
ENSMUSG00000020614	*BC029169*	4.34	4.97	4.63	4.42
ENSMUSG00000020620	*Abca8b*	4.09	4.07	3.52	3.5
ENSMUSG00000020621	*Rdh14*	4.19	4.01	4.23	3.9
ENSMUSG00000020623	*Map2k6*	2.9	2.49	2.88	2.87
ENSMUSG00000020628	*Ttc15*	3.68	4.23	3.95	3.7
ENSMUSG00000020629	*Adi1*	7.1	6.63	6.86	6.42
ENSMUSG00000020630	*Rnaseh1*	1.5	1.63	1.56	1.55
ENSMUSG00000020631	*Atad2b*	2.94	1.88	2.47	1.93
ENSMUSG00000020634	*Ubxd4*	4.22	3.43	3.73	3.32

ENSMUSG00000020638	*Tyki*	1.84	1.09	0.03	1.04
ENSMUSG00000020640	*Itsn2*	2.48	2.03	2.46	2.19
ENSMUSG00000020641	*Rsad2*	2.43	0.93	1.33	1.57
ENSMUSG00000020644	*Id2*	6.51	5.97	5.94	5.52
ENSMUSG00000020647	*Ncoa1*	2.02	2.21	2.31	2.2
ENSMUSG00000020648	*Dus4l*	1.9	1.58	1.86	1.48
ENSMUSG00000020649	*Rrm2*	1.82	0.31	1.99	0.29
ENSMUSG00000020650	*Bcap29*	3.08	1.54	2.47	1.33
ENSMUSG00000020653	*Klf11*	2.46	2.15	2.18	1.87
ENSMUSG00000020659	*Cbll1*	2.89	1.83	2.18	2.07
ENSMUSG00000020661	*Dnmt3a*	1.11	1.27	1.24	1.19
ENSMUSG00000020664	*Dld*	6.87	5.68	6.3	5.58
ENSMUSG00000020669	*Sh3yl1*	2.79	2.07	2.3	2.61
ENSMUSG00000020671	*Rab10*	5.57	5.24	5.45	5.12
ENSMUSG00000020672	*Sntg2*	3.77	3.37	3.03	2.78
ENSMUSG00000020674	*Pxdn*	1.48	1.21	0.67	0.85
ENSMUSG00000020677	*Ddx52*	3.81	2.82	3.22	2.44
ENSMUSG00000020679	*Hnf1b*	2.69	3.68	3.26	3.02
ENSMUSG00000020680	*Taf15*	5.14	4.82	4.73	4.33
ENSMUSG00000020687	*Cdc27*	2.94	2.08	2.66	1.95
ENSMUSG00000020691	*Mettl2*	2.79	3.15	2.86	2.19
ENSMUSG00000020692	*Nle1*	0.8	2.27	1.53	1.65
ENSMUSG00000020694	*Tlk2*	3.08	2.32	2.86	2.45
ENSMUSG00000020696	*Rffl*	3.44	3.51	3.34	3.02
ENSMUSG00000020697	*Lig3*	3.09	3.03	2.9	2.71
ENSMUSG00000020700	*Map3k3*	3.03	3.18	2.88	2.65
ENSMUSG00000020705	*Ddx42*	3.82	3.42	3.28	3.04
ENSMUSG00000020706	*Ftsj3*	3.93	4.43	3.88	3.88
ENSMUSG00000020707	*Rnf135*	3.05	2.83	2.8	2.89
ENSMUSG00000020708	*Psmc5*	6.26	6.28	6.08	5.88
ENSMUSG00000020709	*Centa2*	4.53	4.46	4.44	4.1

ENSMUSG00000020715	*Ern1*	3.54	3.67	3.61	3.75
ENSMUSG00000020716	*NF1*	2.26	1.87	2.25	1.63
ENSMUSG00000020717	*Pecam1*	3.56	3.46	3.22	3.32
ENSMUSG00000020718	*Polg2*	1.79	1.37	2.22	1.4
ENSMUSG00000020719	*Ddx5*	5.65	4.7	5.47	5.01
ENSMUSG00000020720	*Psmd12*	6.02	5.89	5.58	5.49
ENSMUSG00000020721	*Helz*	1.2	1.43	1.36	0.94
ENSMUSG00000020733	*Slc9a3r1*	5.6	6.4	6.12	6.22
ENSMUSG00000020736	*Nt5c*	3.92	4.33	4.3	3.92
ENSMUSG00000020737	*Hn1*	2.89	3.44	2.82	2.53
ENSMUSG00000020739	*Nup85*	2.99	3.42	3.32	3.04
ENSMUSG00000020740	*mKIAA0154*	1.37	2.07	1.48	1.36
ENSMUSG00000020741	*1300001I01Rik*	6.43	7.01	6.57	6.34
ENSMUSG00000020743	*Mif4gd*	4.65	5.45	5.13	4.81
ENSMUSG00000020744	*Slc25a19*	2.87	2.41	2.85	3.01
ENSMUSG00000020745	*Pafah1b1*	4.77	3.91	4.2	3.83
ENSMUSG00000020747	*2310067B10Ri*	4.16	4.69	4.35	4.01
ENSMUSG00000020752	*Recql5*	1.52	2.26	2.13	1.83
ENSMUSG00000020755	*Sap30bp*	3.48	4.22	3.7	3.63
ENSMUSG00000020766	*Galk1*	4.49	5.31	4.56	4.7
ENSMUSG00000020770	*Unk*	1.46	1.69	1.68	1.23
ENSMUSG00000020773	*Trim47*	1.08	1.39	0.94	0.78
ENSMUSG00000020774	*Aspa*	3.53	2.14	3.29	2.06
ENSMUSG00000020775	*Mrpl38*	5.64	6.37	6.11	5.95
ENSMUSG00000020777	*muspaox*	9.2	8.89	9.09	8.88
ENSMUSG00000020780	*Srp68*	4.7	5.49	4.72	4.84
ENSMUSG00000020781	*Tsen54*	2.08	2.86	2.33	2.18
ENSMUSG00000020782	*Llgl2*	3.29	4.24	3.22	3.16
ENSMUSG00000020783	*1200014J11Rik*	3.2	2.75	2.51	2.53
ENSMUSG00000020790	*Ankhzn*	2.85	2.83	2.72	2.7
ENSMUSG00000020792	*Exoc7*	3.75	4.34	3.87	4.02

ENSMUSG00000020794	*Ube2g1*	4.98	3.84	4.77	4.1
ENSMUSG00000020801	*Med31*	2.89	2.13	2.99	2.4
ENSMUSG00000020802	*mKIAA1734*	1.51	2.62	1.88	1.85
ENSMUSG00000020803	*Txndc17*	5.84	6.05	6.1	5.82
ENSMUSG00000020806	*Rhbdf2*	2.05	3.09	2.12	1.85
ENSMUSG00000020810	*Cygb*	1.93	2.37	2.12	1.87
ENSMUSG00000020815	*1110005A03Ri*	2.44	2.53	2.38	1.98
ENSMUSG00000020817	*Rabep1*	4.3	3.55	3.97	3.34
ENSMUSG00000020818	*AK007898*	2.73	2.98	2.64	2.2
ENSMUSG00000020821	*Kif1c*	5.73	6.24	5.64	5.67
ENSMUSG00000020823	*Sec14l1*	2.37	2.42	2.19	2.19
ENSMUSG00000020827	*MINK*	3.67	4.45	4.08	4.11
ENSMUSG00000020829	*Slc46a1*	5.09	6.03	5.64	5.6
ENSMUSG00000020830	*Vmo1*	1.82	2.36	1.91	2.07
ENSMUSG00000020831	*D11Bwg0434e*	3.19	3.87	3.46	3.37
ENSMUSG00000020832	*Eral1*	3.6	4.32	4.23	4.04
ENSMUSG00000020834	*Dhrs13*	1.73	1.99	1.76	1.72
ENSMUSG00000020840	*Blmh*	4.55	4.31	4.73	4.33
ENSMUSG00000020841	*Cpd*	2.39	2.13	2.43	2.16
ENSMUSG00000020843	*Timm22*	3.17	2.91	3.31	3.08
ENSMUSG00000020849	*Ywhae*	7.84	7.24	7.7	7.38
ENSMUSG00000020850	*Prpf8*	5.4	5.78	5.46	5.32
ENSMUSG00000020857	*Nme2*	4.37	4.63	4.81	4.86
ENSMUSG00000020859	*BC096410*	4.31	3.52	3.86	3.41
ENSMUSG00000020863	*3300001P08Ri*	4.21	3.07	3.85	3.21
ENSMUSG00000020864	*Ankrd40*	4.33	4.18	4.42	4.1
ENSMUSG00000020865	*Abcc3*	6.32	7.05	6.6	6.66
ENSMUSG00000020868	*Xylt2*	2.71	3.67	3.04	3.19
ENSMUSG00000020869	*Lrrc59*	6.04	5.92	5.31	5.16
ENSMUSG00000020873	*Slc35b1*	5.32	5.69	4.75	4.85
ENSMUSG00000020876	*Snx11*	1.4	2.1	1.86	1.28

ENSMUSG00000020877	*Scrn2*	4.4	5.21	4.87	4.51
ENSMUSG00000020883	*Fbxl20*	2.97	2.58	3.07	2.54
ENSMUSG00000020884	*Asgr1*	8.5	8.43	8.52	8.41
ENSMUSG00000020888	*Dvl2*	5.79	5.96	5.87	5.55
ENSMUSG00000020889	*Nr1d1*	5.18	5.71	5.94	6.09
ENSMUSG00000020893	*Per1*	2.4	3.18	3.53	3.59
ENSMUSG00000020894	*Vamp2*	2.78	2.8	3.18	3.04
ENSMUSG00000020898	*1500010J02Rik*	0.98	1.47	1.84	1.2
ENSMUSG00000020899	*NA*	1.13	1.24	1.72	0.89
ENSMUSG00000020902	*Ntn1*	1.8	2.22	1.37	1.6
ENSMUSG00000020903	*Stx8*	1.4	1.77	1.73	1.57
ENSMUSG00000020910	*2310004I24Rik*	4.16	3.01	3.94	3.51
ENSMUSG00000020917	*Acly*	6.22	5.81	6.04	5.8
ENSMUSG00000020918	*Gcn5l2*	3.02	3.89	3.21	3.11
ENSMUSG00000020919	*Stat5b*	4.21	4.24	4.31	3.79
ENSMUSG00000020921	*Tmem101*	2.08	2.51	2.29	1.99
ENSMUSG00000020922	*Lsm12*	4.53	4.1	4.48	4.13
ENSMUSG00000020923	*Ubtf*	3.79	4.48	4.05	3.77
ENSMUSG00000020925	*Ccdc43*	2.92	2.37	2.62	2.23
ENSMUSG00000020926	*Adam11*	1.56	2.46	1.73	1.55
ENSMUSG00000020929	*Eftud2*	3.25	3.82	3.52	3.4
ENSMUSG00000020935	*Dcakd*	3.82	4.56	4.18	4.16
ENSMUSG00000020936	*Nmt1*	5.48	5.75	5.45	5.31
ENSMUSG00000020946	*Gosr2*	5.1	4.95	4.67	4.49
ENSMUSG00000020949	*Fkbp3*	5.1	3.61	4.3	3.75
ENSMUSG00000020952	*Scfd1*	4.72	4.03	3.99	3.46
ENSMUSG00000020953	*Coch*	-4.62	-3.62	1.09	-4.62
ENSMUSG00000020954	*Strn3*	3.83	3.44	3.5	3.25
ENSMUSG00000020955	*Ap4s1*	3.31	2.62	3.21	2.49
ENSMUSG00000020956	*6530401N04Ri*	3.11	3.03	3.24	3.03
ENSMUSG00000020962	*Gtf2a1*	2.87	1.95	2.65	2.13

ENSMUSG00000020964	*Sel1l*	5.48	5.63	5.14	4.96
ENSMUSG00000020973	*1110034A24Ri*	0.61	1.24	1.42	0.87
ENSMUSG00000020978	*Klhdc2*	4.95	4.37	4.87	4.37
ENSMUSG00000020982	*Sdccag1*	3.25	2.64	2.8	2.43
ENSMUSG00000020986	*Sec23a*	5.57	4.78	5.48	5.1
ENSMUSG00000020988	*L2hgdh*	3.33	2.63	3.15	2.88
ENSMUSG00000020993	*Trappc6b*	3.85	3.02	3.85	3.1
ENSMUSG00000020994	*Pnn*	3.33	3.01	3.21	2.75
ENSMUSG00000021000	*Ctage5*	7.39	6.79	7.61	7.11
ENSMUSG00000021003	*Galc*	1.08	1.21	1.36	0.67
ENSMUSG00000021009	*Ptpn21*	2.07	1.89	2.35	2.17
ENSMUSG00000021012	*Zc3h14*	4.13	3.54	4.05	3.69
ENSMUSG00000021013	*Ttc8*	1.14	0.79	1.09	0.54
ENSMUSG00000021018	*Polr2h*	1.65	2.16	1.96	2.06
ENSMUSG00000021022	*Ppp2r3c*	2.67	2.05	2.75	2.01
ENSMUSG00000021023	*NA*	2.85	2.61	2.93	2.65
ENSMUSG00000021024	*Psma6*	6.95	6.6	6.95	6.76
ENSMUSG00000021025	*Nfkbia*	5.5	5.66	5.89	5.58
ENSMUSG00000021027	*Garnl1*	1.06	0.8	1.01	0.27
ENSMUSG00000021028	*Mbip*	1.09	0.53	1.24	0.27
ENSMUSG00000021033	*Gstz1*	9.35	9.05	9.18	8.96
ENSMUSG00000021036	*Sptlc2*	3.49	3.13	3.29	3.09
ENSMUSG00000021037	*Ahsa1*	6.75	6.7	6.56	6.61
ENSMUSG00000021038	*AI413782*	3.17	2.91	3.36	2.65
ENSMUSG00000021039	*Snw1*	4.73	4.2	4.34	4.03
ENSMUSG00000021040	*1810035L17Ri*	5.82	4.97	5.93	5.69
ENSMUSG00000021044	*Adck1*	2.86	3.36	3.27	2.89
ENSMUSG00000021048	*Mthfd1*	6.46	6.81	6.66	6.41
ENSMUSG00000021051	*Ppp2r5e*	4.95	4.63	4.65	4.46
ENSMUSG00000021054	*Sgpp1*	5.13	4.6	4.75	4.58
ENSMUSG00000021065	*Fut8*	1.95	1.1	1.59	1.07

ENSMUSG00000021067	*Sav1*	3.33	3.07	3.18	2.72
ENSMUSG00000021069	*Pygl*	7.44	7.14	7.48	7.05
ENSMUSG00000021072	*Txndc1*	5.12	3.85	4.47	3.98
ENSMUSG00000021076	*Actr10*	5.18	4.87	4.82	4.56
ENSMUSG00000021079	*Timm9*	4.32	4.73	5.14	4.85
ENSMUSG00000021091	*Serpina3n*	8.37	8.69	8.66	8.59
ENSMUSG00000021094	*Dhrs7*	5.84	5.66	5.72	5.58
ENSMUSG00000021096	*Ppm1a*	6.05	6.1	5.94	5.68
ENSMUSG00000021097	*Clmn*	4.55	4.12	4.75	4.47
ENSMUSG00000021102	*Glrx5*	5.83	6.17	6.29	5.91
ENSMUSG00000021103	*Mnat1*	2.4	2.26	2.43	2.27
ENSMUSG00000021109	*Hif1a*	3.89	2.94	3.56	2.83
ENSMUSG00000021111	*Papola*	3.64	3.14	3.39	3.03
ENSMUSG00000021112	*Pals1*	2.9	1.37	2.33	1.56
ENSMUSG00000021113	*Snapc1*	1.62	0.39	1.04	0.34
ENSMUSG00000021114	*Atp6v1d*	4.98	4.85	5.34	4.86
ENSMUSG00000021115	*Vrk1*	1.74	1.21	1.71	0.85
ENSMUSG00000021116	*Eif2s1*	3.69	3.09	3.6	3.68
ENSMUSG00000021120	*Pigh*	2.85	2.12	2.23	1.77
ENSMUSG00000021124	*Vti1b*	5.39	4.26	4.68	4.41
ENSMUSG00000021127	*Zfp36l1*	6.17	5.6	5.85	5.73
ENSMUSG00000021133	*4933426M11Ri*	5.17	4.93	5.09	4.94
ENSMUSG00000021134	*Sfrs5*	4.55	4.09	4.8	4.5
ENSMUSG00000021135	*Slc10a1*	9.13	9.09	9.27	8.89
ENSMUSG00000021136	*Smoc1*	6.61	6.56	6.76	6.52
ENSMUSG00000021139	*Arip2*	4.12	3.8	4.05	3.66
ENSMUSG00000021140	*Pcnx*	2.72	2.67	2.67	2.28
ENSMUSG00000021143	*Pacs2*	2.16	2.6	2.76	2.24
ENSMUSG00000021144	*Mta1*	3.96	4.23	4.24	4.15
ENSMUSG00000021147	*Wdr37*	1.89	1.25	1.35	0.89
ENSMUSG00000021149	*Gtpbp4*	4.28	3.72	4.02	3.72

ENSMUSG00000021156	*Zmynd11*	4.1	3.59	3.92	3.72
ENSMUSG00000021171	*D12Ertd551e*	3.1	2.77	2.9	2.69
ENSMUSG00000021177	*Tdp1*	1.02	1.38	1.21	1.17
ENSMUSG00000021178	*Psmc1*	5.28	5.31	5.18	5.15
ENSMUSG00000021179	*NA*	1.81	2.18	2.1	1.34
ENSMUSG00000021185	*9030617O03Ri*	3.51	3.28	3.85	3.56
ENSMUSG00000021186	*Fbln5*	2.14	2.07	1.99	1.75
ENSMUSG00000021188	*NA*	2.65	1.96	2.1	1.69
ENSMUSG00000021189	*Atxn3*	2.82	2.1	2.51	1.81
ENSMUSG00000021190	*Lgmn*	5.15	5.24	4.9	4.91
ENSMUSG00000021192	*Golga5*	3.63	3.5	3.52	3.22
ENSMUSG00000021193	*Pitrm1*	4.5	4.25	4.49	3.94
ENSMUSG00000021208	*1810023F06Ri*	1.45	1.9	2.28	1.36
ENSMUSG00000021209	*8430415E04Ri*	2.66	1.23	2.27	1.77
ENSMUSG00000021210	*Akr1c6*	9.68	9.38	9.26	9
ENSMUSG00000021211	*Akr1c12*	5.36	4.99	5.29	4.94
ENSMUSG00000021213	*Akr1c13*	6.15	5.47	5.88	5.73
ENSMUSG00000021215	*Net1*	4.89	4.47	4.55	3.75
ENSMUSG00000021218	*Gdi2*	6.82	6.43	6.72	6.23
ENSMUSG00000021222	*Wdr21*	1.4	1.46	1.91	1.22
ENSMUSG00000021224	*Numb*	3.71	3.8	3.84	3.62
ENSMUSG00000021226	*Acot2*	3.33	2.54	3.1	2.37
ENSMUSG00000021228	*Acot3*	4.51	3.98	3.93	3.68
ENSMUSG00000021235	*Coq6*	3.17	3.6	3.35	3.14
ENSMUSG00000021236	*Entpd5*	6.5	5.85	6.2	5.67
ENSMUSG00000021238	*Aldh6a1*	8.6	7.85	8.21	7.77
ENSMUSG00000021240	*Abcd4*	3.27	3.64	4.01	3.43
ENSMUSG00000021241	*NA*	4.37	4.45	4.56	4.26
ENSMUSG00000021242	*Npc2*	6.53	6.56	6.25	6.57
ENSMUSG00000021243	*Fcf1*	1.59	1.21	1.23	1.65
ENSMUSG00000021244	*zap*	2.36	2.31	2.27	2.07

ENSMUSG00000021245	*Mlh3*	1.85	1.61	1.93	1.27
ENSMUSG00000021248	*Tmed10*	4.92	5.03	4.86	4.57
ENSMUSG00000021252	*0610007P14Ri*	6.36	5.64	5.98	5.5
ENSMUSG00000021254	*1700020O03Ri*	2.21	2.26	2.18	1.83
ENSMUSG00000021257	*Angel1*	1.69	2.5	1.75	1.37
ENSMUSG00000021258	*Ccnk*	3.71	3.77	3.79	3.83
ENSMUSG00000021264	*Yy1*	5.31	4.15	4.79	4.46
ENSMUSG00000021265	*Slc25a29*	0.59	1.97	1.21	0.89
ENSMUSG00000021266	*Wars*	3.01	3.67	3.2	3.11
ENSMUSG00000021270	*Hsp90aa1*	4.46	4.27	3.77	4.08
ENSMUSG00000021271	*NA*	1.34	1.74	0.82	0.29
ENSMUSG00000021273	*Fdft1*	3.7	3.79	3.07	3.22
ENSMUSG00000021275	*mKIAA0297*	1.46	1.26	1.01	0.63
ENSMUSG00000021276	*2810452K22Ri*	3.15	3.08	3.12	3.05
ENSMUSG00000021277	*Traf3*	1.7	1.8	1.4	1.49
ENSMUSG00000021279	*mKIAA1124*	3.96	4.3	4.34	4
ENSMUSG00000021281	*Tnfaip2*	2.41	3.77	2.19	1.83
ENSMUSG00000021282	*Eif5*	6.49	6.24	6.46	5.92
ENSMUSG00000021285	*Ppp1r13b*	2.26	2.78	2.27	2.26
ENSMUSG00000021286	*Zfyve21*	4.66	4.95	5.01	4.43
ENSMUSG00000021288	*Klc1*	1.63	2.41	2	1.93
ENSMUSG00000021290	*2010107E04Ri*	7.41	5.79	7.17	6.84
ENSMUSG00000021302	*Ggps1*	1.59	0.65	0.96	0.59
ENSMUSG00000021326	*Trim27*	3.5	4.01	3.84	3.46
ENSMUSG00000021327	*Zkscan3*	2.82	2.35	2.57	2.23
ENSMUSG00000021335	*Slc17a1*	3.91	3.43	3.78	3.15
ENSMUSG00000021336	*Slc17a4*	5.8	5.48	5.69	5.37
ENSMUSG00000021338	*Lrrc16*	1.26	1.32	1.04	1.32
ENSMUSG00000021339	*Mrs2l*	2.38	2.35	2.94	2
ENSMUSG00000021340	*Gpld1*	6.75	6.98	6.84	6.76
ENSMUSG00000021357	*Exoc2*	1.71	1.38	1.91	1.11

ENSMUSG00000021360	*Gcnt2*	2.42	2.22	2.57	2.55
ENSMUSG00000021361	*Tmem14c*	6.74	6.34	6.54	6.42
ENSMUSG00000021364	*Elovl2*	8.06	7.8	7.54	7.5
ENSMUSG00000021365	*Nedd9*	1.43	1.1	0.95	0.61
ENSMUSG00000021366	*Hivep1*	2.15	1.64	1.78	1.78
ENSMUSG00000021368	*Tbc1d7*	3.26	3.35	3.49	3.02
ENSMUSG00000021371	*Ccdc90a*	4.28	3.42	3.97	3.58
ENSMUSG00000021374	*Nup153*	3.35	2.96	3.15	3.07
ENSMUSG00000021375	*Kif13a*	1.55	2.14	2.04	1.91
ENSMUSG00000021376	*Tpmt*	6.47	3.75	6.24	5.03
ENSMUSG00000021377	*Dek*	4.85	3.82	4.43	3.69
ENSMUSG00000021385	*Ippk*	2.49	2.4	2.23	2.29
ENSMUSG00000021392	*Nol8*	2.93	2.16	2.59	2.25
ENSMUSG00000021395	*Spin1*	4.45	3.94	4.08	3.8
ENSMUSG00000021400	*Wrnip1*	4.45	4.72	4.42	4.21
ENSMUSG00000021408	*Ripk1*	4.16	3.88	3.84	3.47
ENSMUSG00000021411	*1300014I06Rik*	5.14	5.43	5.24	5
ENSMUSG00000021413	*Prpf4b*	3.77	2.93	3.4	2.87
ENSMUSG00000021415	*4933417A18Ri*	1.32	-0.5	1.07	-1.25
ENSMUSG00000021416	*1810022C23Ri*	3.86	2.08	3.55	1.58
ENSMUSG00000021417	*Peci*	7.33	7.15	7.35	7.12
ENSMUSG00000021418	*Rpp40*	2.56	2.46	2.58	2.19
ENSMUSG00000021420	*Fars2*	4.26	4.2	4.28	4.22
ENSMUSG00000021423	*Ly86*	2.49	1.65	2.4	1.89
ENSMUSG00000021427	*Ssr1*	6.41	5.2	5.64	5.13
ENSMUSG00000021428	*Riok1*	2.39	1.45	1.7	1.19
ENSMUSG00000021431	*6530403A03Ri*	4.67	3.69	4.49	4.11
ENSMUSG00000021432	*Slc35b3*	2.16	1.67	1.94	1.2
ENSMUSG00000021453	*Gadd45g*	3.65	5.06	3.63	3.93
ENSMUSG00000021457	*Syk*	0.43	0.46	1.3	-0.12
ENSMUSG00000021458	*2010111I01Rik*	1.43	1.91	2.05	1.82

ENSMUSG00000021460	*Auh*	3.24	3.33	3.16	2.68
ENSMUSG00000021466	*Ptch1*	2.88	3.29	3.06	2.91
ENSMUSG00000021468	*Sptlc1*	3.97	4.05	3.93	3.68
ENSMUSG00000021470	*0610007P08Ri*	2.26	1.68	2.23	1.83
ENSMUSG00000021474	*Sfxn1*	6.17	5.96	6.62	6.02
ENSMUSG00000021476	*Habp4*	4.07	4.08	4.36	4.38
ENSMUSG00000021477	*Ctsl*	8.99	8.67	9.08	8.61
ENSMUSG00000021481	*Zfp346*	1.19	1.6	0.9	0.23
ENSMUSG00000021482	*1110018J18Rik*	6.19	5.92	5.85	5.61
ENSMUSG00000021483	*Ccrk*	2.01	2.47	1.99	2.06
ENSMUSG00000021484	*Lman2*	6.46	7.31	6.63	6.44
ENSMUSG00000021485	*Mxd3*	1.3	1.7	1.01	1.23
ENSMUSG00000021486	*Prelid1*	5.03	5.79	5.54	5.12
ENSMUSG00000021488	*Nsd1*	3.27	2.88	3.18	3.02
ENSMUSG00000021492	*F12*	7.33	7.98	7.63	7.86
ENSMUSG00000021493	*Pdlim7*	1.26	1.64	2.02	1.96
ENSMUSG00000021494	*Ddx41*	3.96	4.62	4.33	4.17
ENSMUSG00000021495	*BC021381*	2.29	3.01	2.57	2.62
ENSMUSG00000021496	*Pcbd2*	3.99	4.22	4.02	3.9
ENSMUSG00000021497	*Txndc15*	6.16	5.92	5.83	5.62
ENSMUSG00000021500	*Ddx46*	3.69	3.45	3.7	3.14
ENSMUSG00000021501	*Caml*	3.83	3.74	3.85	3.93
ENSMUSG00000021504	*B4galt7*	2.55	2.94	2.48	2.48
ENSMUSG00000021509	*AU042651*	2.73	3.05	3.14	2.82
ENSMUSG00000021510	*A530054K11Ri*	1.17	0.1	0.51	0.28
ENSMUSG00000021514	*Zfp369*	1.19	1.31	1.3	1.55
ENSMUSG00000021518	*Ptdss1*	5.24	5.23	5.12	4.99
ENSMUSG00000021519	*Mterfd1*	4.67	3.64	4.38	3.95
ENSMUSG00000021520	*Uqcrb*	5.45	3.33	4.89	3.84
ENSMUSG00000021532	*Fastkd3*	2.23	2.43	2.02	1.89
ENSMUSG00000021537	*Cetn3*	4.82	4.05	4.47	4.02

ENSMUSG00000021539	*Lect2*	7.62	6.72	7.44	7.22
ENSMUSG00000021540	*Smad5*	3.28	2.88	3.01	2.72
ENSMUSG00000021546	*Hnrpk*	4.75	4.45	4.64	4.36
ENSMUSG00000021548	*Ccnh*	4	2.14	3.31	2.57
ENSMUSG00000021549	*Rasa1*	3.19	2.27	2.86	2.13
ENSMUSG00000021550	*NA*	3.45	3.47	3.35	3.21
ENSMUSG00000021552	*Gkap1*	2.64	1.76	2.47	1.78
ENSMUSG00000021555	*Mak10*	3.8	3.6	3.87	3.58
ENSMUSG00000021557	*Nna1*	2.15	1.84	1.91	1.41
ENSMUSG00000021559	*Dapk1*	4.36	4.42	4.26	3.65
ENSMUSG00000021573	*Tppp*	1.43	1.32	2.15	1.74
ENSMUSG00000021576	*Pdcd6*	5.9	5.62	6.06	5.77
ENSMUSG00000021577	*Sdha*	7.94	7.59	7.88	7.55
ENSMUSG00000021578	*Ccdc127*	2.91	2.2	2.46	2.27
ENSMUSG00000021579	*AI595366*	1.07	0.94	0.99	0.68
ENSMUSG00000021583	*Arts1*	5.45	4.42	5	4.58
ENSMUSG00000021585	*Cast*	3.37	2.64	3.16	2.8
ENSMUSG00000021589	*Rhobtb3*	1.49	1.27	1.61	1.09
ENSMUSG00000021591	*Glrx*	6.01	5.81	5.85	5.88
ENSMUSG00000021592	*Arsk*	2.26	1.86	2.22	1.67
ENSMUSG00000021594	*Srd5a1*	5.48	4.57	5.67	4.99
ENSMUSG00000021595	*Nsun2*	4.96	4.87	4.85	4.59
ENSMUSG00000021598	*Med10*	3.6	3.4	3.45	3.56
ENSMUSG00000021606	*Ndufs6*	5.2	4.38	5.3	5.01
ENSMUSG00000021607	*Mrpl36*	4.81	4.93	5.31	5.03
ENSMUSG00000021610	*Clptm1l*	6.09	6.23	5.81	5.55
ENSMUSG00000021611	*Tert*	1.17	0.69	1.54	0.77
ENSMUSG00000021615	*Xrcc4*	2.25	1.8	1.63	1.91
ENSMUSG00000021619	*Atg10*	2.32	1.49	1.73	1.11
ENSMUSG00000021620	*Acot12*	6.34	5.83	5.98	5.79
ENSMUSG00000021621	*Zcchc9*	3.08	2.67	2.96	2.67

ENSMUSG00000021622	*Ckmt2*	#NAME?	#NAME?	1.27	1.45
ENSMUSG00000021629	*Slc30a5*	4.35	3.84	4.04	3.49
ENSMUSG00000021635	*Rad17*	3.13	2.3	3.11	2.67
ENSMUSG00000021636	*Marveld2*	2.39	2.77	2.13	2.03
ENSMUSG00000021638	*Ocln*	3.38	3.04	3.5	2.98
ENSMUSG00000021639	*Gtf2h2*	2.87	1.74	2.45	1.57
ENSMUSG00000021643	*Serf1*	3.41	2.4	2.54	2.9
ENSMUSG00000021645	*Smn1*	2.49	2.31	2.7	2.59
ENSMUSG00000021646	*Mccc2*	5.46	5.25	5.61	4.89
ENSMUSG00000021650	*Ptcd2*	4.46	4.37	4.37	4.22
ENSMUSG00000021660	*Btf3*	2.64	2.95	2.69	2.46
ENSMUSG00000021661	*Ankra2*	2.28	1.74	2.38	2.22
ENSMUSG00000021665	*Hexb*	5.14	4.4	4.94	4.28
ENSMUSG00000021666	*Gfm2*	5.03	4.36	4.68	4.36
ENSMUSG00000021669	*Col4a3bp*	3.61	2.38	3.3	3.14
ENSMUSG00000021670	*Hmgcr*	4.51	3.77	4.53	4.39
ENSMUSG00000021671	*1200014M14R*	1.49	1.51	1.26	0.85
ENSMUSG00000021676	*Iqgap2*	6.75	6.15	6.71	6.33
ENSMUSG00000021681	*Aggf1*	3.83	3.93	3.78	3.56
ENSMUSG00000021686	*Ap3b1*	4.27	3.92	4.43	4.06
ENSMUSG00000021687	*Scamp1*	4.03	3.59	3.95	3.52
ENSMUSG00000021690	*Jmy*	2.54	2.14	2.54	2.07
ENSMUSG00000021693	*Kif2a*	2.19	0.95	1.24	0.79
ENSMUSG00000021694	*Ercc8*	1.41	0.86	1.3	1.37
ENSMUSG00000021701	*Plk2*	1.51	1.91	1.76	1.47
ENSMUSG00000021703	*Serinc5*	3.44	3.63	3.44	3.5
ENSMUSG00000021704	*NA*	0.84	0.22	1.14	1.22
ENSMUSG00000021706	*Zfyve16*	1.16	0.43	0.85	0.4
ENSMUSG00000021707	*Dhfr*	4.17	3.22	3.8	3.6
ENSMUSG00000021709	*Erbb2ip*	4.95	3.93	4.49	3.94
ENSMUSG00000021710	*Nln*	3.88	3.18	3.4	3.12

ENSMUSG00000021711	*2410002O22Ri*	4.54	3.8	4.32	3.85
ENSMUSG00000021712	*Trim23*	2.69	1.56	2.17	1.39
ENSMUSG00000021713	*Ppwd1*	2.81	1.51	2.79	1.91
ENSMUSG00000021715	*Sdccag10*	1.48	1.4	1.6	1.39
ENSMUSG00000021716	*3110031B13Ri*	4.39	3.29	4.06	3.19
ENSMUSG00000021731	*Mrps30*	4.57	4.26	4.44	4.11
ENSMUSG00000021733	*Slc4a7*	1.62	0.41	1.5	0.84
ENSMUSG00000021737	*Psmd6*	5.92	5.76	5.85	5.75
ENSMUSG00000021738	*Atxn7*	1.86	2.31	2.38	2.5
ENSMUSG00000021745	*Ptprg*	2.74	2.37	2.06	1.87
ENSMUSG00000021747	*4930452B06Ri*	0.75	-1.13	1.12	-1.96
ENSMUSG00000021748	*Pdhb*	5.1	4.88	5.45	5.29
ENSMUSG00000021751	*Acox2*	7.24	7.42	7.73	7.14
ENSMUSG00000021752	*Kctd6*	2.39	2.57	2.44	2.39
ENSMUSG00000021754	*Map3k1*	1.63	1.36	2.01	1.13
ENSMUSG00000021756	*Il6st*	5.49	5.37	5.36	5.22
ENSMUSG00000021759	*Ppap2a*	4.19	3.94	3.63	3.08
ENSMUSG00000021764	*Ndufs4*	6.15	5.81	6.42	5.44
ENSMUSG00000021770	*Samd8*	3.64	2.52	3.53	2.78
ENSMUSG00000021771	*Vdac2*	5.61	5	5.61	5.38
ENSMUSG00000021772	*Nkiras1*	4.69	3.47	4.57	3.41
ENSMUSG00000021773	*Comtd1*	1.5	2.72	1.97	2.14
ENSMUSG00000021774	*Ube2e1*	4.66	3.92	3.94	3.85
ENSMUSG00000021775	*Nr1d2*	4.28	2.82	4.34	3.96
ENSMUSG00000021779	*Thrb*	4.13	3.39	3.83	3.31
ENSMUSG00000021785	*Ngly1*	4.51	3.81	4.24	3.69
ENSMUSG00000021786	*Oxsm*	3.97	3.5	3.79	3.54
ENSMUSG00000021792	*5730469M10R*	6.44	5.83	6.13	5.56
ENSMUSG00000021794	*Glud1*	8.84	8.42	8.6	8.39
ENSMUSG00000021796	*Bmpr1a*	4.02	3.05	3.57	3.12
ENSMUSG00000021807	*2700060E02Ri*	4.06	3.98	3.88	4.04

ENSMUSG00000021809	*Nudt13*	2.21	1.97	2.13	1.89
ENSMUSG00000021810	*Ecd*	4.14	4.28	4.29	4
ENSMUSG00000021811	*Dnajc9*	2.39	1.55	1.63	1.41
ENSMUSG00000021814	*Anxa7*	5.35	5.72	5.09	5.26
ENSMUSG00000021816	*Ppp3cb*	4.05	3.24	3.82	3.15
ENSMUSG00000021819	*2310021P13Ri*	2.7	3.4	3.09	2.96
ENSMUSG00000021820	*Camk2g*	1.95	2.02	1.84	1.33
ENSMUSG00000021823	*Vcl*	3.08	3.04	3.42	3.06
ENSMUSG00000021824	*Ap3m1*	5.94	4.75	5.61	4.85
ENSMUSG00000021830	*Txndc16*	1.39	0.6	0.95	0.77
ENSMUSG00000021831	*Ero1l*	2.49	1.88	2.23	1.87
ENSMUSG00000021832	*Psmc6*	5.84	5.07	5.47	5.06
ENSMUSG00000021840	*C130032J12Ri*	3.76	4.26	4.27	4.14
ENSMUSG00000021843	*Ktn1*	2.49	1.53	2.09	1.51
ENSMUSG00000021846	*Peli2*	3.23	2.61	3.06	2.58
ENSMUSG00000021866	*Anxa11*	2.65	3.53	3.14	3.35
ENSMUSG00000021868	*Ppif*	5.27	5.65	6.09	5.37
ENSMUSG00000021870	*Slmap*	4.48	3.59	4.38	3.76
ENSMUSG00000021871	*Pnp*	6.25	6.35	6.3	6.03
ENSMUSG00000021876	*Rnase4*	9.59	9.68	9.63	9.51
ENSMUSG00000021877	*Arf4*	6.9	5.92	6.55	6.22
ENSMUSG00000021884	*Hacl1*	8.5	8.01	7.06	7.16
ENSMUSG00000021890	*Eaf1*	4.07	4.21	3.98	3.83
ENSMUSG00000021891	*Mettl6*	2.08	2.06	2.28	2.45
ENSMUSG00000021892	*Sh3bp5*	5.12	5.25	5.13	4.74
ENSMUSG00000021893	*Capn7*	4.21	3.55	3.83	3.37
ENSMUSG00000021895	*Arhgef3*	3.93	3.62	3.65	3.63
ENSMUSG00000021900	*Btd*	6.01	6.14	5.72	5.73
ENSMUSG00000021901	*Bap1*	3.84	4.34	4.03	3.95
ENSMUSG00000021902	*Phf7*	2.58	1.84	2.52	2.29
ENSMUSG00000021905	*Dph3*	2.98	2.78	2.91	2.86

ENSMUSG00000021906	*Oxnad1*	3.99	3.99	4.07	3.6
ENSMUSG00000021908	*NA*	2.07	2.03	1.94	1.84
ENSMUSG00000021910	*Nisch*	4.87	5.16	5.02	4.66
ENSMUSG00000021911	*Parg*	3.1	2.68	2.74	2.56
ENSMUSG00000021916	*Glt8d1*	2.49	1.8	2.29	1.61
ENSMUSG00000021917	*Spcs1*	5.78	5.75	5.72	5.46
ENSMUSG00000021918	*Nek4*	2.53	2.22	2.3	1.77
ENSMUSG00000021922	*Itih4*	9.83	10.28	9.95	9.98
ENSMUSG00000021928	*Ebpl*	6.68	6.74	6.76	6.83
ENSMUSG00000021929	*Kpna3*	4.5	3.88	4.15	3.6
ENSMUSG00000021930	*6330409N04Ri*	3.99	2.93	3.63	2.68
ENSMUSG00000021932	*Rnaseh2b*	2.61	1.88	2.49	2.13
ENSMUSG00000021936	*Mapk8*	2.55	1.73	2.27	1.86
ENSMUSG00000021938	*Pspc1*	1.55	1.19	1.79	1.43
ENSMUSG00000021939	*Ctsb*	9.14	8.8	9.06	8.75
ENSMUSG00000021943	*Gdf10*	1.16	-0.39	1.61	1.53
ENSMUSG00000021944	*Gata4*	3.07	3.87	2.85	2.91
ENSMUSG00000021945	*Zmym2*	3.18	2.48	2.86	2.53
ENSMUSG00000021947	*Cryl1*	3.74	4.2	4.13	3.53
ENSMUSG00000021948	*Prkcd*	1.84	1.76	1.8	1.44
ENSMUSG00000021951	*N6amt2*	2.54	2.63	2.92	2.75
ENSMUSG00000021957	*Tkt*	5.87	6.14	6.1	5.9
ENSMUSG00000021958	*2610028A01Ri*	1.84	2.48	1.52	1.76
ENSMUSG00000021959	*Lats2*	2.36	2.58	2.52	2.58
ENSMUSG00000021962	*SMIF*	1.23	0.98	0.99	1.03
ENSMUSG00000021963	*Sap18*	1.63	0.51	1.32	0.64
ENSMUSG00000021967	*Mrp63*	4.57	5.23	4.81	4.52
ENSMUSG00000021969	*Zdhhc20*	2.25	1.37	1.91	1.45
ENSMUSG00000021972	*Hmbox1*	1.63	1.53	1.49	1.41
ENSMUSG00000021973	*Efha1*	4.76	4	4.2	3.58
ENSMUSG00000021975	*Ints9*	1.66	2.09	2.09	2.01

ENSMUSG00000021978	*Extl3*	3.29	3.66	3.3	3.26
ENSMUSG00000021981	*Cab39l*	5.92	4.94	5.29	4.9
ENSMUSG00000021982	*Cdadc1*	5.37	4.78	5.02	4.79
ENSMUSG00000021987	*Mtmr6*	3.75	3.13	3.53	3.15
ENSMUSG00000021990	*NA*	2.8	2.67	3.05	2.74
ENSMUSG00000021993	*Mipep*	4.85	4.47	4.75	4.28
ENSMUSG00000021996	*Esd*	5.67	5	5.47	5.6
ENSMUSG00000021998	*Lcp1*	4.24	3.77	4.16	3.95
ENSMUSG00000021999	*Cpb2*	8.29	7.84	8.08	7.62
ENSMUSG00000022000	*Zc3h13*	2.22	2.18	2.15	1.68
ENSMUSG00000022003	*Slc25a30*	4.45	3.02	3.12	2.99
ENSMUSG00000022008	*1200011I18Rik*	2.98	1.76	2.4	1.97
ENSMUSG00000022009	*Nufip1*	1.86	0.98	1.45	0.92
ENSMUSG00000022010	*mKIAA1994*	3.14	3.47	3.45	3.15
ENSMUSG00000022013	*Dnajc15*	5.64	5.13	5.81	5.59
ENSMUSG00000022016	*NA*	3.74	2.58	3.26	2.67
ENSMUSG00000022019	*Tdrd3*	2.51	2.12	2.71	1.88
ENSMUSG00000022020	*Narg1l*	2.3	1.79	1.88	1.39
ENSMUSG00000022022	*Mtrf1*	2.34	2.36	2.45	2.41
ENSMUSG00000022023	*Wbp4*	3.14	2.68	2.99	2.46
ENSMUSG00000022024	*Sugt1*	4.91	4.62	4.67	4.11
ENSMUSG00000022025	*Lect1*	1.26	1.11	0.92	1.47
ENSMUSG00000022031	*Elp3*	3.21	3.75	3.49	3.03
ENSMUSG00000022035	*Ccdc25*	4.69	4.32	4.56	4.22
ENSMUSG00000022037	*Clu*	9.85	10.29	10.15	10.15
ENSMUSG00000022040	*Ephx2*	8.56	8.08	8.29	7.95
ENSMUSG00000022041	*Chrna2*	1.66	1.33	1.37	1.15
ENSMUSG00000022048	*Dpysl2*	1.08	0.1	1.42	1.18
ENSMUSG00000022051	*Bnip3l*	4.97	3.68	4.54	3.58
ENSMUSG00000022052	*Ppp2r2a*	2.85	2.01	2.25	2
ENSMUSG00000022057	*Adamdec1*	1.24	1.54	0.36	1.18

ENSMUSG00000022066	*Entpd4*	4.71	4.86	4.27	4.31
ENSMUSG00000022075	*Rhobtb2*	1.53	1.93	1.9	1.53
ENSMUSG00000022089	*Bin3*	3.3	3.22	3.16	2.85
ENSMUSG00000022091	*Sorbs3*	4.06	3.8	4.88	3.84
ENSMUSG00000022094	*Slc39a14*	6.45	6.38	5.93	5.88
ENSMUSG00000022095	*NA*	1.36	2.39	1.83	1.45
ENSMUSG00000022098	*mKIAA4159*	5.07	5.79	5.36	5.22
ENSMUSG00000022100	*Xpo7*	2.89	2.46	2.75	2.34
ENSMUSG00000022105	*Rb1*	1.92	0.73	1.97	1.32
ENSMUSG00000022106	*Rcbtb2*	3.28	3.17	3.19	3.02
ENSMUSG00000022108	*Itm2b*	9.5	9.15	9.34	9.09
ENSMUSG00000022109	*Med4*	2.41	2.48	2.1	2.31
ENSMUSG00000022110	*Sucla2*	7.05	6.17	6.58	5.99
ENSMUSG00000022111	*Uchl3*	2.88	1.53	1.79	1.47
ENSMUSG00000022119	*Rbm26*	2.63	1.99	2.5	2.16
ENSMUSG00000022122	*Ednrb*	2.93	1.82	2.44	2.32
ENSMUSG00000022124	*Fbxl3*	3.62	2.9	3.51	2.97
ENSMUSG00000022125	*Cln5*	4.58	3.7	4.38	3.98
ENSMUSG00000022130	*Tgds*	4.98	4.49	5	4.52
ENSMUSG00000022131	*Gpr180*	4.25	3.97	3.88	3.62
ENSMUSG00000022136	*Dnajc3a*	6.57	6.46	6.05	5.93
ENSMUSG00000022139	*Mbnl2*	4.3	3.96	4.04	3.87
ENSMUSG00000022141	*AK020398*	3.41	2.61	3.02	2.46
ENSMUSG00000022142	*Nup155*	2.54	2.27	2.53	2.05
ENSMUSG00000022148	*Fyb*	1.24	0.44	1.21	0.17
ENSMUSG00000022149	*C9*	7.28	6.99	7.05	6.77
ENSMUSG00000022150	*Dab2*	2.34	2.28	2.16	1.77
ENSMUSG00000022151	*Ttc33*	4.06	3.33	4.07	3.81
ENSMUSG00000022159	*Rab2b*	1.34	1.42	1.07	0.92
ENSMUSG00000022160	*Mettl3*	3.08	2.95	2.99	2.91
ENSMUSG00000022174	*Dad1*	6.75	7.52	7.7	7.57

ENSMUSG00000022175	*Lrp10*	4.38	5.13	4.91	4.83
ENSMUSG00000022177	*D14Ertd500e*	2.65	3.61	3.12	2.98
ENSMUSG00000022178	*Jub*	1.44	1.21	0.91	0.97
ENSMUSG00000022179	*4931414P19Ri*	1.36	1.74	1.87	1.55
ENSMUSG00000022181	*C6*	2.91	3.14	2.83	2.78
ENSMUSG00000022184	*Fbxo4*	3.37	2.66	2.63	2.64
ENSMUSG00000022185	*Acin1*	3.66	3.93	3.67	3.44
ENSMUSG00000022186	*Oxct1*	1.47	1.31	1.41	0.75
ENSMUSG00000022191	*Rnasen*	1.73	2	1.98	1.62
ENSMUSG00000022193	*Psmb5*	3.9	3.05	3.45	4.05
ENSMUSG00000022194	*Bcl2l2*	2.6	2.65	2.8	2.59
ENSMUSG00000022195	*6030458C11Ri*	2.83	2.44	3.07	2.79
ENSMUSG00000022198	*Pabpn1*	3.68	4.28	4.53	4.21
ENSMUSG00000022200	*Golph3*	6.12	5.15	5.7	5.46
ENSMUSG00000022201	*Zfr*	4.4	4.13	4.1	3.78
ENSMUSG00000022204	*Ngdn*	4.34	3.96	4.05	3.89
ENSMUSG00000022205	*Sub1*	6.12	5.41	6.05	6.27
ENSMUSG00000022210	*Dhrs4*	6.74	6.87	6.46	6.33
ENSMUSG00000022214	*Wdr23*	7.26	7.51	7.18	6.93
ENSMUSG00000022215	*1110028A07Ri*	2.51	1.92	2.58	2.08
ENSMUSG00000022216	*Psme1*	6.23	5.21	5.65	5.35
ENSMUSG00000022217	*1500005A01Ri*	3.6	3.66	4.05	3.61
ENSMUSG00000022218	*Tgm1*	1.54	2	2.1	2.57
ENSMUSG00000022219	*Cideb*	8.1	8.53	8.44	8.29
ENSMUSG00000022220	*Adcy4*	1.07	1.97	0.88	1.22
ENSMUSG00000022223	*2310014G06Ri*	3.98	4.16	3.97	3.51
ENSMUSG00000022228	*Zfp187*	4.27	3.08	4.18	3.74
ENSMUSG00000022234	*Cct5*	6.71	7.1	6.74	6.76
ENSMUSG00000022235	*Cmbl*	7.8	7.55	7.94	7.47
ENSMUSG00000022236	*Ropn1l*	3.53	3.68	3.99	3.76
ENSMUSG00000022237	*5730557B15Ri*	2.43	1.9	2.92	2.63

ENSMUSG00000022241	*Tars*	6.3	6.05	5.83	5.54
ENSMUSG00000022244	*Amacr*	6.18	6.44	6.11	5.84
ENSMUSG00000022246	*Rai14*	2.99	2.95	2.89	2.77
ENSMUSG00000022247	*Bxdc2*	4.53	4.05	4.12	3.6
ENSMUSG00000022248	*Rad1*	2.38	1.78	1.72	1.76
ENSMUSG00000022253	*1110020G09Ri*	6.44	5.76	5.87	5.37
ENSMUSG00000022255	*Mtdh*	5.09	4.27	4.74	4.19
ENSMUSG00000022257	*Laptm4b*	4.01	3.7	4.05	3.77
ENSMUSG00000022261	*Sdc2*	7.03	6.64	6.74	6.43
ENSMUSG00000022263	*Trio*	0.68	0.9	1.09	1.08
ENSMUSG00000022265	*Ank*	4.46	4.21	4.53	4.19
ENSMUSG00000022270	*1810015C04Ri*	7.13	5.61	6.33	5.42
ENSMUSG00000022272	*myo 10*	1.74	2.17	2.6	2.57
ENSMUSG00000022280	*Rnf19a*	3.89	2.91	3.14	2.72
ENSMUSG00000022283	*Pabpc1*	6.53	5.53	6.24	5.81
ENSMUSG00000022285	*Ywhaz*	5.02	4.42	4.82	4.44
ENSMUSG00000022295	*Atp6v1c1*	4.74	4.34	4.63	4.56
ENSMUSG00000022299	*Slc25a32*	4.69	3.08	4.24	3.48
ENSMUSG00000022300	*Wdsof1*	4.65	4.2	4.35	3.8
ENSMUSG00000022304	*Dpys*	7.6	7.57	7.61	7.47
ENSMUSG00000022307	*Oxr1*	5.17	4.16	4.73	4.26
ENSMUSG00000022312	*Eif3h*	5.67	5.81	5.71	5.66
ENSMUSG00000022313	*D530033C11R*	2.1	1.58	1.89	1.99
ENSMUSG00000022314	*Rad21*	4.72	4.51	4.65	4.3
ENSMUSG00000022323	*Hrsp12*	10.25	9.42	9.93	9.39
ENSMUSG00000022329	*Stk3*	2.9	1.97	2.52	2.15
ENSMUSG00000022332	*Khdrbs3*	4.02	3.8	3.96	3.76
ENSMUSG00000022336	*Eif3e*	4.42	3.89	3.87	3.78
ENSMUSG00000022337	*Ttc35*	5.43	3.79	5.02	4.34
ENSMUSG00000022338	*Eny2*	5.72	4.25	5.06	4.65
ENSMUSG00000022339	*Ebag9*	4.21	3.34	3.51	3.53

ENSMUSG00000022347	*A1bg*	9.83	7.43	8.43	5.72
ENSMUSG00000022350	*E430025E21Ri*	4	3.51	4.22	3.45
ENSMUSG00000022351	*Sqle*	5.09	4.23	3.94	3.46
ENSMUSG00000022353	*Mtss1*	5.82	6.15	5.85	5.94
ENSMUSG00000022354	*Ndufb9*	8.15	8.18	8.08	7.92
ENSMUSG00000022358	*Fbxo32*	1.04	0.44	0.92	0.53
ENSMUSG00000022359	*2410187C16Ri*	2.39	2.26	2.6	2.04
ENSMUSG00000022361	*Zhx1*	4.32	3.56	3.99	3.51
ENSMUSG00000022362	*9130401M01R*	2.73	3.5	3.19	2.81
ENSMUSG00000022365	*Derl1*	5	5.26	5.18	5
ENSMUSG00000022370	*Mrpl13*	6.15	5.28	5.82	5.21
ENSMUSG00000022371	*Col14a1*	3.54	3.33	3.22	3.16
ENSMUSG00000022372	*Sla*	0.82	0.03	1.02	0.29
ENSMUSG00000022377	*Ddef1*	2.27	2.33	2.57	1.9
ENSMUSG00000022378	*0910001A06Ri*	2.03	0.6	1.63	0.93
ENSMUSG00000022383	*Ppara*	5.77	5.44	5.54	5.45
ENSMUSG00000022386	*Trmu*	2.07	1.78	1.97	1.57
ENSMUSG00000022387	*mKIAA4191*	2.47	2.46	2.48	2.41
ENSMUSG00000022389	*Tef*	4.71	4.15	5.53	5.36
ENSMUSG00000022390	*Zc3h7b*	3.29	3.52	3.43	3.2
ENSMUSG00000022391	*Rangap1*	4.54	5.12	4.71	4.65
ENSMUSG00000022394	*L3mbtl2*	2.84	3.32	3.18	2.99
ENSMUSG00000022400	*Rbx1*	4.28	3.45	3.76	3.42
ENSMUSG00000022401	*Xpnpep3*	2.75	2.77	2.63	2.41
ENSMUSG00000022403	*St13*	7.07	6.18	6.56	6.4
ENSMUSG00000022404	*Slc25a17*	5.4	4.59	5.05	4.65
ENSMUSG00000022407	*Adsl*	2.47	3.1	2.73	2.29
ENSMUSG00000022412	*Smcr7l*	3.6	3.33	3.34	3.2
ENSMUSG00000022414	*Map3k7ip1*	0.5	1.4	1.08	0.35
ENSMUSG00000022419	*AK164741*	4.64	4.59	4.42	4.42
ENSMUSG00000022420	*Dnalc4*	2.11	2.45	2.32	2.16

ENSMUSG00000022425	*Enpp2*	4.67	4.36	4.85	4.62
ENSMUSG00000022426	*Josd1*	4.47	4.1	4.19	4.01
ENSMUSG00000022427	*Tomm22*	5.02	4.87	5.06	4.69
ENSMUSG00000022428	*Cby1*	2.3	2.45	3.04	3.12
ENSMUSG00000022433	*Csnk1e*	1.07	1.07	1.23	0.55
ENSMUSG00000022437	*Samm50*	5.77	5.78	5.68	5.41
ENSMUSG00000022443	*Myh9*	4.17	4.68	4.56	4.46
ENSMUSG00000022445	*Cyp2d26*	9.4	9.54	9.49	9.3
ENSMUSG00000022450	*Ndufa6*	7.38	7.62	7.78	8.05
ENSMUSG00000022451	*Twf1*	4.45	4.25	4.52	4.05
ENSMUSG00000022452	*1500032L24Ri*	6.28	6.7	6.53	6.41
ENSMUSG00000022453	*Naga*	4.37	4.95	4.68	4.62
ENSMUSG00000022462	*Slc38a2*	5.78	4.98	5.56	5.72
ENSMUSG00000022463	*Srebf2*	4.36	5.03	4.24	4.15
ENSMUSG00000022464	*Slc38a4*	8.65	7.99	8.84	8.23
ENSMUSG00000022466	*Rpap3*	1.47	1.6	1.59	1.49
ENSMUSG00000022471	*Xrcc6*	3.47	3.5	3.63	3.2
ENSMUSG00000022472	*D15Wsu75e*	4.79	5.02	5.03	4.91
ENSMUSG00000022473	*NA*	5.18	5.56	5.27	5.06
ENSMUSG00000022474	*Pmm1*	1.94	1.59	2.05	1.82
ENSMUSG00000022476	*Polr3h*	1.84	3.1	2.38	2.51
ENSMUSG00000022477	*Aco2*	5.96	5.68	6.28	5.89
ENSMUSG00000022488	*Nckap1l*	1.31	0.52	1.32	0.52
ENSMUSG00000022498	*Txndc11*	2.46	2.79	2.18	2.36
ENSMUSG00000022500	*Litaf*	5.63	5.59	5.32	4.97
ENSMUSG00000022503	*Nubp1*	3.85	4.49	3.82	3.72
ENSMUSG00000022505	*Emp2*	2.77	3.18	2.13	2.56
ENSMUSG00000022507	*1810013L24Ri*	3.96	3.66	3.81	3.82
ENSMUSG00000022508	*Bcl6*	1.84	4.66	4.59	3.37
ENSMUSG00000022512	*Cldn1*	5.24	4.97	4.99	4.78
ENSMUSG00000022514	*Il1rap*	4.39	4.73	4.5	4.76

ENSMUSG00000022515	*Anks3*	1.59	2.36	2.02	2.09
ENSMUSG00000022516	*Nudt16l1*	3.45	4.19	3.56	3.47
ENSMUSG00000022517	*mKIAA0544*	4.79	5.45	5.3	5.19
ENSMUSG00000022521	*Crebbp*	2.67	2.95	3.05	3.08
ENSMUSG00000022528	*Hes1*	2.94	3.2	2.12	1.91
ENSMUSG00000022529	*Zfp263*	2.76	1.93	2.2	2.1
ENSMUSG00000022533	*NA*	5.5	4.98	5.22	4.88
ENSMUSG00000022536	*3930401K13Ri*	5.47	5.77	5.55	5.35
ENSMUSG00000022538	*Lsg1*	3.02	3.35	2.94	3.05
ENSMUSG00000022540	*Rogdi*	3.46	4.36	3.51	3.4
ENSMUSG00000022544	*5730409G15Ri*	2.98	3.44	3.19	3.03
ENSMUSG00000022545	*Ercc4*	1.64	1.92	1.59	1.56
ENSMUSG00000022546	*Gpt1*	7.22	7.85	7.55	7.33
ENSMUSG00000022550	*Adck5*	3.32	5.1	3.47	3.55
ENSMUSG00000022551	*Cyc1*	7.58	7.63	7.57	7.31
ENSMUSG00000022552	*Sharpin*	4.62	4.69	4.72	4.35
ENSMUSG00000022553	*Maf1*	3.79	3.91	3.77	3.48
ENSMUSG00000022554	*Brp16*	1.28	2.15	1.82	1.87
ENSMUSG00000022555	*Dgat*	3.75	3.98	3.84	3.76
ENSMUSG00000022556	*Hsf1*	2.8	4.07	3.58	3.55
ENSMUSG00000022557	*Bop1*	3.68	4.65	3.84	3.87
ENSMUSG00000022558	*NA*	2.95	3.81	3.16	3.13
ENSMUSG00000022559	*Fbxl6*	2.8	3.81	3.23	2.91
ENSMUSG00000022560	*Gpr172b*	1.5	2.17	2.27	1.88
ENSMUSG00000022561	*Gpaa1*	3.86	4.5	3.82	3.8
ENSMUSG00000022562	*Oplah*	5.24	5.75	5.53	5.29
ENSMUSG00000022564	*Grina*	6.44	7.07	6.75	6.57
ENSMUSG00000022565	*Plec1*	2.27	2.9	2.79	2.68
ENSMUSG00000022568	*Scrib*	2.39	3.42	2.85	2.75
ENSMUSG00000022570	*Tsta3*	4.33	4.74	4.38	3.98
ENSMUSG00000022571	*Pycrl*	4.22	4.65	4.64	4.62

ENSMUSG00000022574	*Naprt1*	5.92	6.55	6.19	6.15
ENSMUSG00000022575	*Gsdmdc1*	4.2	4.11	3.96	3.55
ENSMUSG00000022579	*Gpihbp1*	4.23	4.99	4.61	4.57
ENSMUSG00000022587	*Ly6e*	8.52	8.62	8.8	8.37
ENSMUSG00000022591	*NA*	3.24	3.16	2.95	2.84
ENSMUSG00000022607	*Ptk2*	2.81	2.92	2.7	2.48
ENSMUSG00000022610	*Mapk12*	0.68	1.11	1.23	-0.14
ENSMUSG00000022614	*Tmem112b*	3.86	4.56	4.18	4.15
ENSMUSG00000022615	*Ecgf1*	6.29	6.98	6.56	6.29
ENSMUSG00000022617	*Chkb*	4.26	4.4	4.34	4.04
ENSMUSG00000022620	*Arsa*	2.54	3.1	3.23	3.19
ENSMUSG00000022629	*Kif21a*	4.05	3.24	3.67	3.46
ENSMUSG00000022634	*YAF2*	3.46	2.84	3.12	2.55
ENSMUSG00000022635	*Zcrb1*	4.36	3.79	3.9	3.56
ENSMUSG00000022636	*Alcam*	3.38	3.21	3.17	3.1
ENSMUSG00000022637	*Cblb*	1.5	1.17	1.53	1.44
ENSMUSG00000022656	*Pvrl3*	4.76	4.53	4.47	4.22
ENSMUSG00000022663	*Atg3*	6.06	5.96	5.89	5.55
ENSMUSG00000022664	*Slc35a5*	2.67	1.65	2.77	2.32
ENSMUSG00000022665	*Ccdc80*	2.55	2.72	2.17	2.39
ENSMUSG00000022668	*Gtpbp8*	3.02	2.16	3.08	2.15
ENSMUSG00000022671	*2410018G20Ri*	3.57	3.77	4.44	4.28
ENSMUSG00000022673	*Mcm4*	1.12	0.4	1.12	0.56
ENSMUSG00000022676	*Snai2*	2.49	1.76	2.84	2.2
ENSMUSG00000022677	*0610037P05Ri*	3.97	3.36	4.01	3.71
ENSMUSG00000022678	*Nde1*	2.93	3.23	3.36	2.95
ENSMUSG00000022679	*Mpv17l*	3.81	2.76	3.45	2.39
ENSMUSG00000022680	*Pdxdc1*	4.9	5.08	4.79	4.64
ENSMUSG00000022681	*Ntan1*	4.71	4.52	4.58	4.39
ENSMUSG00000022682	*Rrn3*	3.3	3.08	3.12	3.16
ENSMUSG00000022684	*Bfar*	4.94	4.88	5.11	4.77

ENSMUSG00000022685	*Parn*	2.94	2.83	2.88	2.86
ENSMUSG00000022698	*Nat13*	5.55	4.75	5.06	4.75
ENSMUSG00000022702	*Hira*	2.23	2.45	2.23	2.05
ENSMUSG00000022704	*Qtrtd1*	1.23	1.06	1.05	1.13
ENSMUSG00000022706	*Mrpl40*	5.11	4.3	4.8	4.58
ENSMUSG00000022707	*Gbe1*	5.81	4.68	5.47	5.22
ENSMUSG00000022708	*Zbtb20*	3.14	3.71	2.69	2.38
ENSMUSG00000022710	*Hausp*	4.67	4.1	4.31	4.03
ENSMUSG00000022711	*Pmm2*	5.36	5.48	5.48	5.22
ENSMUSG00000022718	*Dgcr8*	1.95	1.47	1.67	1.31
ENSMUSG00000022721	*Htf9c*	2.42	2.72	2.2	2.42
ENSMUSG00000022722	*Arl6*	1.87	0.91	1.75	1.59
ENSMUSG00000022723	*BC043118*	1.42	1.42	0.97	1.39
ENSMUSG00000022724	*Mina*	2.04	1.84	2.37	1.86
ENSMUSG00000022742	*Cpox*	6.93	6.29	6.99	6.41
ENSMUSG00000022744	*Cldnd1*	4.35	3.83	4.31	3.88
ENSMUSG00000022747	*St3gal6*	2.98	1.65	2.79	1.6
ENSMUSG00000022748	*2610528E23Ri*	1.42	1.81	1.58	1.59
ENSMUSG00000022749	*Tbc1d23*	3.45	2.41	3.17	2.45
ENSMUSG00000022750	*Klhl22*	2.62	2.93	2.81	2.56
ENSMUSG00000022751	*Nit2*	7.57	6.53	7.15	6.89
ENSMUSG00000022752	*Tomm70a*	5.26	4.63	4.95	4.35
ENSMUSG00000022757	*Tfg*	5.54	5.09	5.17	5.03
ENSMUSG00000022760	*Thap7*	2.76	3.83	3.69	3.71
ENSMUSG00000022761	*Lztr1*	3.45	3.92	3.79	3.59
ENSMUSG00000022765	*Snap29*	4.22	3.92	3.94	3.79
ENSMUSG00000022766	*Serpind1*	8.65	8.71	8.62	8.43
ENSMUSG00000022769	*Sdf2l1*	4.18	5.26	3.79	4.1
ENSMUSG00000022770	*Dlg1*	4.2	3.21	3.87	3.41
ENSMUSG00000022771	*Ppil2*	3.69	3.53	3.56	3.5
ENSMUSG00000022772	*Senp5*	3.04	2.17	2.43	2.19

ENSMUSG00000022774	*Ncbp2*	4.01	3.32	3.94	3.67
ENSMUSG00000022779	*Top3b*	2.65	2.63	2.6	2.09
ENSMUSG00000022781	*Pak2*	4.03	3.28	3.75	3.37
ENSMUSG00000022787	*Wdr53*	2.24	2.18	2.39	2.27
ENSMUSG00000022788	*Fgd4*	1.53	0.69	1.8	1.17
ENSMUSG00000022789	*Drp1*	4.38	3.48	3.98	3.38
ENSMUSG00000022790	*Igsf11*	4.34	3.42	3.75	3.09
ENSMUSG00000022791	*Tnk2*	2.48	3.35	2.47	2.41
ENSMUSG00000022792	*Yars2*	3.6	3.78	3.71	3.44
ENSMUSG00000022797	*Tfrc*	2.41	3.29	1.61	1.25
ENSMUSG00000022799	*Cdgap*	1.33	1.42	0.68	0.86
ENSMUSG00000022800	*Fyttd1*	3.8	2.45	3.37	2.69
ENSMUSG00000022801	*Lrch3*	1.9	1.39	1.73	1.32
ENSMUSG00000022807	*Osbpl11*	3.7	2.96	3.04	2.95
ENSMUSG00000022808	*Snx4*	3.68	2.82	3.38	2.94
ENSMUSG00000022809	*Nr1i2*	6.13	6.16	5.66	5.38
ENSMUSG00000022811	*Zfp148*	3.32	2.68	2.85	2.71
ENSMUSG00000022812	*Gsk3b*	3.43	2.84	3.48	3.02
ENSMUSG00000022814	*Umps*	4.83	4.44	4.79	4.69
ENSMUSG00000022816	*Fstl1*	1.16	0.85	1.12	0.53
ENSMUSG00000022817	*Itgb5*	4.62	5.04	4.59	4.49
ENSMUSG00000022820	*Ndufb4*	5.48	2.8	3.9	3.01
ENSMUSG00000022821	*Hgd*	9.11	8.99	9.22	8.73
ENSMUSG00000022827	*Rabl3*	3.91	3.51	3.93	3.7
ENSMUSG00000022828	*Gtf2e1*	2.83	2.72	2.7	2.37
ENSMUSG00000022831	*Hcls1*	1.32	1.75	1.8	1.35
ENSMUSG00000022836	*Mlyk*	3.89	4.07	3.98	3.96
ENSMUSG00000022841	*Ap2m1*	2.7	2.83	2.36	2.12
ENSMUSG00000022842	*Ece2*	0.93	1.45	1.33	1.23
ENSMUSG00000022843	*Clcn2*	3.94	4.68	4.14	3.87
ENSMUSG00000022844	*Pdia5*	4.84	5.66	4.83	5.04

ENSMUSG00000022847	*Thpo*	2.94	3.44	3.08	2.94
ENSMUSG00000022848	*Dirc2*	3.99	4.01	3.82	3.7
ENSMUSG00000022853	*Ehhadh*	7.93	7.5	7.53	7.49
ENSMUSG00000022855	*Senp2*	3.53	3.21	3.46	3.42
ENSMUSG00000022856	*Tmem41a*	3.36	3.87	4.02	3.7
ENSMUSG00000022858	*Sfrs10*	1.68	1.55	1.34	1.68
ENSMUSG00000022864	*D16Ertd472e*	1.89	0.87	1.14	1.12
ENSMUSG00000022865	*Cxadr*	4.26	2.93	3.8	3.34
ENSMUSG00000022867	*Usp25*	3.8	3.05	3.58	3.41
ENSMUSG00000022868	*Ahsg*	12.12	12.17	12.09	12.21
ENSMUSG00000022871	*Fetub*	8.81	9.32	9.17	9.25
ENSMUSG00000022875	*Kng1*	9.93	9.46	9.47	9.46
ENSMUSG00000022877	*Hrg*	9.7	9.68	10	9.83
ENSMUSG00000022881	*Rfc4*	1.12	0.48	1.66	1.48
ENSMUSG00000022884	*Eif4a2*	6.69	5.74	6.49	5.85
ENSMUSG00000022885	*St6gal1*	5.63	5.59	5.31	5.1
ENSMUSG00000022887	*Masp1*	5.65	5.19	5.28	5.05
ENSMUSG00000022889	*Mrpl39*	4.78	4.53	4.78	4.43
ENSMUSG00000022890	*Atp5j*	7.1	6.58	7.05	6.53
ENSMUSG00000022892	*App*	5	5.24	4.79	4.92
ENSMUSG00000022893	*Adamts1*	1.85	1.31	1.61	1.44
ENSMUSG00000022895	*Ets2*	3.63	3.77	3.41	3.32
ENSMUSG00000022897	*Dyrk1a*	3.17	2.66	3.18	2.88
ENSMUSG00000022898	*Dscr3*	4.04	4.16	3.95	3.49
ENSMUSG00000022905	*Kpna1*	4.63	4.14	4.34	3.92
ENSMUSG00000022906	*Parp9*	4.52	3.34	4.18	4.11
ENSMUSG00000022911	*Arl13b*	1.88	1.48	1.26	0.39
ENSMUSG00000022912	*Pros1*	4.7	4.03	4.1	3.84
ENSMUSG00000022913	*Dscr2*	4.57	4.69	4.41	4.45
ENSMUSG00000022914	*Brwd1*	1.62	1.17	1.44	1.1
ENSMUSG00000022940	*Pigp*	2.32	0.21	1.57	0.64

ENSMUSG00000022946	*Dopey2*	3.2	2.65	3.77	2.52
ENSMUSG00000022951	*Rcan1*	4.03	3.85	3.6	4
ENSMUSG00000022956	*Atp5o*	5.73	4.47	5.38	5.26
ENSMUSG00000022957	*Itsn1*	1.47	1.19	1.36	0.98
ENSMUSG00000022961	*mKIAA1019*	4.72	4.55	4.64	4.34
ENSMUSG00000022962	*Gart*	3.6	4	3.54	3.69
ENSMUSG00000022964	*Tmem50b*	2.25	2.69	2.23	1.92
ENSMUSG00000022965	*Ifngr2*	3.15	3.43	3.63	3.35
ENSMUSG00000022967	*Ifnar1*	4.01	3.97	3.83	3.53
ENSMUSG00000022969	*Il10rb*	2.38	2.77	2.67	2.34
ENSMUSG00000022971	*Ifnar2*	5.46	4.92	5.19	4.86
ENSMUSG00000022972	*1110004E09Ri*	3.42	3.64	3.44	3.48
ENSMUSG00000022973	*NA*	1.77	1.19	1.65	1.25
ENSMUSG00000022974	*NA*	2.36	1.79	2.32	1.99
ENSMUSG00000022978	*2610039C10Ri*	1.28	1.15	1.76	1.1
ENSMUSG00000022982	*Sod1*	7.28	7.58	7.44	7.27
ENSMUSG00000022983	*Sfrs15*	2.55	2.52	2.87	2.72
ENSMUSG00000022994	*Adcy6*	1.9	2.12	2.36	2.06
ENSMUSG00000022999	*Lmbr1l*	1.97	2.42	2.25	1.66
ENSMUSG00000023004	*Tuba1b*	1.48	1.24	1.37	1.33
ENSMUSG00000023007	*Hypc*	1.69	2	1.86	1.49
ENSMUSG00000023010	*Tegt*	9.47	9.67	9.43	9.28
ENSMUSG00000023018	*Smarcd1*	1.54	2.54	1.52	1.03
ENSMUSG00000023019	*Gpd1*	7.41	7.82	7.59	7.58
ENSMUSG00000023020	*2310016M24R*	4.87	5.07	4.84	5.03
ENSMUSG00000023022	*Lima1*	4.12	3.73	3.83	4.13
ENSMUSG00000023025	*D330037H05R*	3.71	2.27	3.03	2.64
ENSMUSG00000023027	*Atf1*	2.91	2.41	2.89	2.57
ENSMUSG00000023030	*Slc11a2*	2.5	2.83	2.77	2.08
ENSMUSG00000023031	*Ela1*	3.28	3.82	3.09	3.55
ENSMUSG00000023043	*Krt18*	6.04	6.63	6.33	6.12

ENSMUSG00000023044	*Csad*	4.27	6.5	5.01	5.4
ENSMUSG00000023045	*Soat2*	3.28	4.39	3.83	3.92
ENSMUSG00000023048	*Prr13*	5.01	5.41	5.81	5.81
ENSMUSG00000023050	*Map3k12*	4	3.74	4.18	3.8
ENSMUSG00000023051	*Tarbp2*	1.62	1.99	1.73	1.05
ENSMUSG00000023055	*Calcoco1*	4.01	3.9	4.72	4.36
ENSMUSG00000023057	*Fabp2*	6.14	5.27	5.8	5.1
ENSMUSG00000023067	*Cdkn1a*	5.91	6.58	3.89	3.38
ENSMUSG00000023068	*Nus1*	4.51	4.6	4.25	4.08
ENSMUSG00000023070	*Rgn*	10.06	9.05	9.55	9.18
ENSMUSG00000023072	*Ccdc123*	1.84	1.82	1.51	1.54
ENSMUSG00000023073	*Slc10a2*	4.62	3.84	3.62	4.02
ENSMUSG00000023074	*Mospd1*	2.26	1.41	2.81	1.98
ENSMUSG00000023075	*6330407G11Ri*	2.63	2.27	2.5	2.66
ENSMUSG00000023078	*Cxcl13*	2.01	0.2	2.47	0.9
ENSMUSG00000023079	*Gtf2ird1*	1.8	2.42	2.14	1.93
ENSMUSG00000023084	*NA*	1.87	2.13	2.27	1.94
ENSMUSG00000023087	*Ccrn4l*	3.9	3.93	4.62	5.08
ENSMUSG00000023089	*Ndufa5*	6.51	6.06	6.74	6.2
ENSMUSG00000023092	*Fhl1*	2.14	1.53	2.29	1.97
ENSMUSG00000023094	*Msrb2*	3.57	3.32	3.59	3.31
ENSMUSG00000023104	*Rfc2*	3.56	4.14	3.83	3.72
ENSMUSG00000023106	*Denr*	5.46	4.97	5.03	4.53
ENSMUSG00000023110	*Prmt5*	3.13	3.68	3.27	3.16
ENSMUSG00000023118	*NA*	4.07	4.78	4.57	4.38
ENSMUSG00000023122	*Sult1c2*	3.33	2.36	3.49	2.79
ENSMUSG00000023143	*Nagpa*	3.19	4.13	3.68	3.57
ENSMUSG00000023147	*Wrb*	1.19	0.76	1.1	1
ENSMUSG00000023150	*Ivns1abp*	5.63	5.15	5.29	4.81
ENSMUSG00000023156	*Rpp14*	3.34	2.81	3	2.96
ENSMUSG00000023170	*Gps2*	3.57	4.03	4.18	4.06

ENSMUSG00000023175	*Bsg*	8.19	8.55	8.6	8.35
ENSMUSG00000023176	*Cpn2*	7.15	7.81	7.21	7.17
ENSMUSG00000023186	*Loh11cr2a*	3.51	3	3.06	2.87
ENSMUSG00000023206	*Il15ra*	3.41	3.55	3.5	2.71
ENSMUSG00000023224	*Serping1*	8.89	9.26	9	9.03
ENSMUSG00000023232	*Serinc2*	-0.12	1.29	2.12	-0.16
ENSMUSG00000023243	*Kcnk5*	3.79	5.11	4.84	4.64
ENSMUSG00000023249	*Parp3*	3.25	3.58	3.07	3.09
ENSMUSG00000023262	*Acy1*	5.31	5.77	5.76	5.53
ENSMUSG00000023272	*Creld2*	4.68	5.67	3.59	4.28
ENSMUSG00000023277	*Twf2*	1.29	1.8	1.65	0.96
ENSMUSG00000023286	*Ube2j2*	0.99	1.07	1.39	0.8
ENSMUSG00000023307	*5-Mar*	5.16	4.46	4.98	4.56
ENSMUSG00000023330	*Dtwd1*	2.63	2.45	2.64	2.55
ENSMUSG00000023336	*Wfdc1*	2.43	2.1	2.17	1.94
ENSMUSG00000023341	*Mx2*	1.89	1.15	0.88	1.27
ENSMUSG00000023348	*Trip6*	2.69	3.39	2.91	2.68
ENSMUSG00000023349	*Clec4n*	1.11	0.34	1.58	0.47
ENSMUSG00000023353	*Centg3*	3.18	4.08	3.62	3.49
ENSMUSG00000023367	*Tmem176a*	7.55	7.81	7.58	7.43
ENSMUSG00000023393	*1700019H03Ri*	1.3	1.68	1.07	0.92
ENSMUSG00000023452	*Pisd*	4.06	4.26	4.21	3.75
ENSMUSG00000023456	*Tpi1*	7.24	7.45	7.31	7.07
ENSMUSG00000023460	*Rab12*	4.25	4.04	4.16	3.96
ENSMUSG00000023495	*Pcbp4*	2.93	3.63	3.36	3.61
ENSMUSG00000023572	*Ccndbp1*	3.5	3.7	3.69	3.68
ENSMUSG00000023707	*Ogfod2*	3.41	4.04	3.68	3.46
ENSMUSG00000023723	*Mrps23*	4.36	4.47	4.49	4.35
ENSMUSG00000023764	*Sfi1*	1.69	1.54	2.35	1.69
ENSMUSG00000023791	*Pigx*	3.75	3.79	4.48	4.05
ENSMUSG00000023795	*NA*	1.66	1.92	1.58	1.15

ENSMUSG00000023826	*Park2*	2.16	0.94	1.75	1.31
ENSMUSG00000023828	*Slc22a3*	1.51	0.64	1.57	0.62
ENSMUSG00000023829	*Slc22a1*	7.78	7.89	7.59	7.57
ENSMUSG00000023830	*Igf2r*	2.61	3.02	3.11	2.77
ENSMUSG00000023832	*Acat2*	4.8	4.63	4.23	3.94
ENSMUSG00000023845	*Lnpep*	2.48	1.29	1.97	1.5
ENSMUSG00000023846	*Riok2*	3.53	3.2	3.2	3.4
ENSMUSG00000023852	*Chd1*	3.27	2.74	3.22	2.86
ENSMUSG00000023861	*Brp44l*	2.62	2.77	3.05	3.08
ENSMUSG00000023883	*Phf10*	4.07	3.68	3.84	3.3
ENSMUSG00000023892	*Zfp51*	1.71	0.98	0.91	0.3
ENSMUSG00000023904	*Hcfc1r1*	5.58	5.84	6.46	6.64
ENSMUSG00000023905	*Tnfrsf12a*	2.37	2.77	2.71	2.58
ENSMUSG00000023913	*Pla2g7*	3.74	3.25	3.86	3.32
ENSMUSG00000023915	*Tnfrsf21*	1.4	2.05	2.01	1.8
ENSMUSG00000023919	*Cenpq*	2.36	1.23	2.29	1.15
ENSMUSG00000023921	*Mut*	6.85	6.37	6.65	6.2
ENSMUSG00000023923	*Tbc1d5*	2.28	2.4	2.5	2.29
ENSMUSG00000023932	*Cdc5l*	1.64	1.18	1.71	1.4
ENSMUSG00000023938	*Aars2*	2.45	3.33	2.86	2.65
ENSMUSG00000023939	*Mrpl14*	5.51	5.99	5.62	6.05
ENSMUSG00000023942	*Slc29a1*	7.51	7.66	7.5	7.49
ENSMUSG00000023944	*Hsp90ab1*	9.03	9.35	9.1	9.17
ENSMUSG00000023951	*Vegfa*	4.37	4.69	4.67	4.43
ENSMUSG00000023952	*Gtpbp2*	2.73	3.35	2.93	2.75
ENSMUSG00000023960	*Enpp5*	3.18	2.71	2.94	2.73
ENSMUSG00000023961	*Enpp4*	3.15	2.43	2.58	2.45
ENSMUSG00000023963	*Cyp39a1*	5.88	5.13	6.01	5.41
ENSMUSG00000023965	*NA*	3.5	3.4	3.06	2.87
ENSMUSG00000023967	*Mrps18a*	4.91	5.5	5.11	5.16
ENSMUSG00000023971	*BC011248*	3.6	4.23	4.19	4.04

ENSMUSG00000023973	*Tnrc5*	4.75	5.6	4.95	5.04
ENSMUSG00000023977	*Ubr2*	4.25	4.09	4.4	4.08
ENSMUSG00000023980	*Taf8*	1.79	2.51	2.16	2.1
ENSMUSG00000023982	*Guca1a*	0.69	1.18	1.14	1.48
ENSMUSG00000023988	*Bysl*	3.06	4.35	3.43	3.51
ENSMUSG00000023990	*Tcfeb*	1.04	1.94	1.92	1.78
ENSMUSG00000023991	*Foxp4*	2.53	3.28	3.32	3.22
ENSMUSG00000023994	*Nfya*	2.33	2.43	2.33	2.08
ENSMUSG00000024002	*Brd4*	3.5	3.45	3.59	3.55
ENSMUSG00000024006	*Stk38*	4.4	4.19	4.42	4.09
ENSMUSG00000024007	*Ppil1*	2.33	3.79	2.98	2.58
ENSMUSG00000024012	*AK189748*	5.69	6.42	5.85	5.81
ENSMUSG00000024014	*Pim1*	1.66	2.66	2.03	1.37
ENSMUSG00000024018	*NA*	2.91	3.02	2.76	2.89
ENSMUSG00000024019	*Rnf8*	3.48	3.56	3.41	3.27
ENSMUSG00000024026	*Glo1*	7.12	7.12	6.8	6.76
ENSMUSG00000024030	*Abcg1*	1.46	1.41	1.05	0.83
ENSMUSG00000024037	*wdr4*	1.76	2.5	1.98	1.95
ENSMUSG00000024038	*1500032D16Ri*	5.74	5.86	6.54	6.2
ENSMUSG00000024039	*Cbs*	8.39	8.97	8.4	8.18
ENSMUSG00000024042	*Snf1lk*	1.99	2.59	2.73	2.38
ENSMUSG00000024045	*Akap8*	3.54	3.01	3.46	3.01
ENSMUSG00000024048	*2900073G15Ri*	5.4	5.27	5.61	5.41
ENSMUSG00000024050	*Wiz*	2.1	2.74	2.56	2.55
ENSMUSG00000024052	*Lpin2*	6.23	5.55	6.32	6.19
ENSMUSG00000024054	*Smchd1*	2.04	1.41	1.89	1.43
ENSMUSG00000024055	*Cyp4f13*	5.43	5.85	5.65	5.61
ENSMUSG00000024063	*Lbh*	1.92	2.04	1.35	1.09
ENSMUSG00000024065	*Ehd3*	5.41	6.29	5.23	5.43
ENSMUSG00000024066	*Xdh*	4.99	5.27	4.99	5.18
ENSMUSG00000024067	*2810410M20R*	5.15	4.29	4.66	4.29

ENSMUSG00000024068	*Spast*	4.2	3.09	3.85	3.06
ENSMUSG00000024069	*Slc30a6*	3.01	3.31	3.31	2.89
ENSMUSG00000024070	*Prkcn*	4.59	4.75	5.09	4.97
ENSMUSG00000024072	*Yipf4*	4.32	3.87	4.31	3.79
ENSMUSG00000024073	*Birc6*	3.19	2.87	3.18	2.84
ENSMUSG00000024074	*Crim1*	1.35	1.97	1.57	1.83
ENSMUSG00000024077	*Strn*	1.59	1.53	1.25	1.51
ENSMUSG00000024078	*Ttc27*	2.3	2.64	2.42	2.24
ENSMUSG00000024079	*Eif2ak2*	3.29	2.13	2.49	2.27
ENSMUSG00000024081	*Cebpz*	4.14	4.32	4.07	3.77
ENSMUSG00000024082	*2410091C18Ri*	3.3	3.46	3.33	3.31
ENSMUSG00000024083	*Pja2*	3.6	3.57	3.33	3.28
ENSMUSG00000024084	*Qpct*	2.37	3.41	2.23	2.7
ENSMUSG00000024085	*Man2a1*	6.61	5.67	6.44	5.9
ENSMUSG00000024091	*Vapa*	6.41	5.73	6.32	5.85
ENSMUSG00000024095	*Hnrpll*	3.94	3.82	3.96	3.89
ENSMUSG00000024096	*Ralbp1*	3.9	3.88	3.71	3.48
ENSMUSG00000024097	*Sfrs7*	3.72	3.71	3.71	3.45
ENSMUSG00000024098	*Twsg1*	4.76	4.14	4.32	3.98
ENSMUSG00000024099	*Ndufv2*	7.78	7.17	7.6	7.26
ENSMUSG00000024101	*ORF19*	3.06	3.29	3.57	3.05
ENSMUSG00000024104	*D6Wsu116e*	4.08	4.08	4.27	3.8
ENSMUSG00000024118	*1600002H07Ri*	4.46	4.83	4.54	4.52
ENSMUSG00000024120	*Lrpprc*	5.07	4.8	5.37	4.97
ENSMUSG00000024121	*Atp6v0c*	2.38	1.64	2.44	2.31
ENSMUSG00000024122	*Pdpk1*	3.77	3.05	3.24	3.12
ENSMUSG00000024127	*Prepl*	4.63	4.86	4.75	4.65
ENSMUSG00000024130	*Abca3*	6.35	6.62	6.44	6.11
ENSMUSG00000024131	*Slc3a1*	5.59	5.95	5.65	5.55
ENSMUSG00000024132	*Dci*	7.21	7.48	7.45	7.24
ENSMUSG00000024135	*NA*	2.5	1.58	2.56	2.2

ENSMUSG00000024137	*E4f1*	1.38	2.23	1.68	1.14
ENSMUSG00000024140	*Epas1*	5.9	6.43	6.1	5.99
ENSMUSG00000024142	*Gbl*	1.56	2.15	1.84	1.84
ENSMUSG00000024143	*Rhoq*	2.21	1.48	2.37	1.75
ENSMUSG00000024145	*Pigf*	3.3	2.88	3.12	2.68
ENSMUSG00000024146	*Cript*	5.81	5.02	5.84	5.2
ENSMUSG00000024150	*Mcfd2*	7.36	7.42	7.25	7.09
ENSMUSG00000024151	*Msh2*	2.21	1.41	2.44	2.21
ENSMUSG00000024155	*NA*	4	2.39	3.5	2.44
ENSMUSG00000024158	*Hagh*	7.27	7.4	7.33	7.34
ENSMUSG00000024160	*Spsb3*	2.41	3.04	2.41	2.41
ENSMUSG00000024163	*Mapk8ip3*	1.35	2.1	1.32	1.47
ENSMUSG00000024164	*C3*	11.08	11.35	11.2	11.15
ENSMUSG00000024165	*Hn1l*	3.42	3.46	2.77	2.84
ENSMUSG00000024168	*BC054438*	3.4	4.05	3.29	3.15
ENSMUSG00000024169	*Ift140*	1.28	1.54	1.78	1.61
ENSMUSG00000024180	*Tmem8*	3.1	3.69	3.31	3.01
ENSMUSG00000024181	*Mrpl28*	5.46	5.75	5.61	5.49
ENSMUSG00000024182	*Axin1*	3.06	3.51	3.2	3.31
ENSMUSG00000024187	*Itfg3*	5.03	5.29	4.86	4.71
ENSMUSG00000024188	*Luc7l*	3	2.44	2.61	2.6
ENSMUSG00000024190	*Dusp1*	5.29	5.36	4.67	5.85
ENSMUSG00000024191	*Sec20*	3.51	3.73	4.01	3.67
ENSMUSG00000024193	*Phf1*	2.15	3.1	3.01	2.51
ENSMUSG00000024194	*Cuta*	5.75	6.08	6	5.94
ENSMUSG00000024197	*M6prbp1*	4.86	4.58	5.32	5.02
ENSMUSG00000024201	*mKIAA0876*	1.68	2.7	2.16	2.31
ENSMUSG00000024208	*2900010M23R*	4.79	4.62	6.02	5.18
ENSMUSG00000024212	*Mllt1*	2.8	3.68	3.27	3.34
ENSMUSG00000024213	*Nudt3*	3.85	3.57	3.85	3.54
ENSMUSG00000024218	*Taf11*	2.6	2.38	2.59	2.14

ENSMUSG00000024219	*Anks1*	2.62	2.73	2.97	2.74
ENSMUSG00000024220	*Zfp523*	2.49	3.25	2.65	2.63
ENSMUSG00000024222	*Fkbp5*	6.89	6.94	6.28	5.88
ENSMUSG00000024228	*Nudt12*	4.98	3.98	4.77	4.1
ENSMUSG00000024231	*Cul2*	4.1	3.69	3.79	3.3
ENSMUSG00000024234	*Papd1*	3.88	3.18	3.74	3.26
ENSMUSG00000024236	*Svil*	1.74	2.02	2.42	2.21
ENSMUSG00000024238	*Zfhx1a*	2.47	2.06	2.07	2.13
ENSMUSG00000024240	*Epc1*	2.03	2.19	2.56	2.22
ENSMUSG00000024241	*Sos1*	3.7	2.73	3.65	3.2
ENSMUSG00000024242	*Map4k3*	3.53	2.51	3.3	2.82
ENSMUSG00000024247	*AW548124*	3.1	4.22	3.39	3.75
ENSMUSG00000024248	*Cox7a2l*	4.86	4.84	5.02	4.84
ENSMUSG00000024251	*NA*	0.42	1.02	1.15	0.82
ENSMUSG00000024254	*Abcg8*	5.03	4.95	5.32	5.17
ENSMUSG00000024258	*Polr2d*	3.03	2.82	2.44	2.76
ENSMUSG00000024259	*Slc25a46*	5.02	3.66	4.62	3.81
ENSMUSG00000024260	*Sap130*	2.75	2.81	2.79	2.42
ENSMUSG00000024269	*AK171952*	2.79	2.65	2.33	1.97
ENSMUSG00000024271	*Elp2*	3.72	3.69	3.86	3.67
ENSMUSG00000024273	*2700062C07Ri*	1.99	2.44	1.99	2.51
ENSMUSG00000024276	*Zfp397*	2.87	1.82	2.27	1.7
ENSMUSG00000024277	*Mapre2*	2.24	2.31	2.59	2.49
ENSMUSG00000024283	*Wac*	4.4	4.14	4.41	4.26
ENSMUSG00000024286	*Ccny*	5.04	4.53	4.44	4
ENSMUSG00000024287	*Thoc1*	3.04	2.32	3.01	2.22
ENSMUSG00000024290	*Rock1*	4.01	2.65	3.45	2.75
ENSMUSG00000024292	*Cyp4f14*	7.65	7.66	7.58	7.35
ENSMUSG00000024293	*Esco1*	2.41	0.87	1.65	1.05
ENSMUSG00000024294	*Mib1*	3.31	3.11	3.17	3.08
ENSMUSG00000024298	*9030612M13R*	2.67	1.3	2.73	1.95

ENSMUSG00000024304	*Cdh2*	4.12	4.46	4.19	3.99
ENSMUSG00000024308	*Tapbp*	5.68	5.97	5.79	5.55
ENSMUSG00000024309	*H2-Ke2*	4.93	5.28	4.79	4.87
ENSMUSG00000024312	*Wdr46*	3.32	4.27	3.59	3.42
ENSMUSG00000024317	*Rnf138*	2.97	2.12	2.31	1.88
ENSMUSG00000024319	*Vps52*	3.33	3.9	3.6	3.29
ENSMUSG00000024325	*Ring1*	3.1	3.75	3.63	3.66
ENSMUSG00000024327	*Slc39a7*	5.18	6.17	5.29	5.41
ENSMUSG00000024331	*Dsc2*	4.19	3.66	4.08	3.83
ENSMUSG00000024335	*Brd2*	4.75	4.85	4.97	4.98
ENSMUSG00000024337	*Psmb9*	2.43	2.06	1.84	1.31
ENSMUSG00000024338	*Psmb8*	4.35	4.31	4.16	4.18
ENSMUSG00000024339	*Tap2*	3.26	3.57	3.08	3.07
ENSMUSG00000024346	*Pfdn1*	5.01	5.24	5.37	5.03
ENSMUSG00000024349	*NA*	1.18	0.35	0.47	0.59
ENSMUSG00000024350	*Dnajc18*	1.84	1.78	1.8	1.77
ENSMUSG00000024354	*Slc23a1*	5.51	4.92	5.14	4.52
ENSMUSG00000024357	*Sil1*	4.64	5.15	4.7	5.5
ENSMUSG00000024359	*Hspa9*	7.82	7.52	7.67	7.3
ENSMUSG00000024360	*Etf1*	6.01	5.21	5.44	5.14
ENSMUSG00000024369	*Rdbp*	4.07	4.79	4.02	3.94
ENSMUSG00000024370	*Cdc23*	2.58	2.25	2.18	1.8
ENSMUSG00000024371	*Cfb*	8.95	9.37	9.08	9.14
ENSMUSG00000024372	*C2*	5.38	5.27	5.14	5.09
ENSMUSG00000024378	*Stard4*	5.29	4.53	4.45	3.91
ENSMUSG00000024380	*Gypc*	3.57	3.64	3.66	3.3
ENSMUSG00000024381	*Bin1*	2.6	3.16	2.92	2.8
ENSMUSG00000024382	*Ercc3*	2.97	3.27	3.09	2.7
ENSMUSG00000024383	*Map3k2*	1.42	0.37	0.98	1.1
ENSMUSG00000024384	*Iws1*	2.56	2.28	2.48	1.85
ENSMUSG00000024386	*Proc*	7.91	8.76	8.33	8.24

ENSMUSG00000024387	*Csnk2b*	6.42	7.07	6.86	6.88
ENSMUSG00000024389	*Bat4*	1.42	2.25	2.44	2.25
ENSMUSG00000024391	*Apom*	8.59	8.46	8.53	8.51
ENSMUSG00000024392	*Bat3*	4.58	5.49	5.2	5.09
ENSMUSG00000024393	*Bat2*	4.46	5.39	4.95	4.95
ENSMUSG00000024395	*Lims2*	5.86	6.39	6.29	6.14
ENSMUSG00000024397	*Aif1*	1.92	0.91	1.59	0.96
ENSMUSG00000024399	*Ltb*	-0.74	-0.62	1.86	-2.43
ENSMUSG00000024400	*Wdr33*	3.35	2.92	3.25	3.07
ENSMUSG00000024404	*Riok3*	5.24	4.9	4.97	4.55
ENSMUSG00000024410	*3110002H16Ri*	3.94	3.87	4.26	3.88
ENSMUSG00000024413	*Npc1*	5.83	5.34	6.22	5.83
ENSMUSG00000024414	*Mrpl27*	3.3	4.08	3.64	3.74
ENSMUSG00000024422	*Dhx16*	3.43	4.07	3.62	3.55
ENSMUSG00000024423	*Impact*	2.72	1.78	1.72	1.65
ENSMUSG00000024424	*2810439F02Ri*	5.97	5.67	5.89	5.56
ENSMUSG00000024425	*Ndfip1*	7.97	7.03	7.56	6.98
ENSMUSG00000024426	*2610110G12Ri*	2.19	2.09	2.36	1.99
ENSMUSG00000024427	*Spry4*	2.51	2.51	1.32	1.47
ENSMUSG00000024429	*Gna-rs1*	2.82	3.75	3.07	3.14
ENSMUSG00000024430	*Cabyr*	0.43	0.16	1.07	0.8
ENSMUSG00000024431	*Nr3c1*	4.97	3.94	4.4	4.08
ENSMUSG00000024436	*Mrps18b*	3.63	4.63	4.19	4.22
ENSMUSG00000024437	*NA*	1.81	#NAME?	2.6	-3.65
ENSMUSG00000024440	*Pcdh12*	1.07	1.9	0.24	0.7
ENSMUSG00000024442	*0610009O20Ri*	4.26	4.62	4.68	4.35
ENSMUSG00000024446	*Rpp21*	3.58	3.84	4.18	4.3
ENSMUSG00000024451	*Centd3*	1.64	2.1	1.47	1.4
ENSMUSG00000024454	*Hdac3*	4.03	4.45	4.3	4.07
ENSMUSG00000024456	*BC029331*	4.48	4.64	4.39	4.16
ENSMUSG00000024457	*Trim26*	3.65	3.57	3.9	3.6

ENSMUSG00000024472	*NA*	1.57	1.17	1.22	1.03
ENSMUSG00000024474	*Ik*	4.86	5.13	4.92	4.76
ENSMUSG00000024477	*Pggt1b*	2.78	1.88	2.17	1.64
ENSMUSG00000024479	*Mal2*	5.15	4.68	4.6	4.14
ENSMUSG00000024480	*Ap3s1*	3.1	1.01	2.23	0.81
ENSMUSG00000024483	*Eif4ebp3*	4.14	4.11	4.5	4.32
ENSMUSG00000024487	*Yipf5*	5.02	4.21	4.51	4.1
ENSMUSG00000024491	*NA*	2.82	2.01	2.51	2.13
ENSMUSG00000024493	*Lars*	3.29	3.16	3.14	2.73
ENSMUSG00000024498	*Tcerg1*	2.32	1.69	2.06	1.64
ENSMUSG00000024507	*Hsd17b4*	7.75	7.48	7.64	7.34
ENSMUSG00000024513	*Mbd2*	4.95	4.66	4.75	4.47
ENSMUSG00000024515	*Smad4*	4.06	4.11	4.08	3.69
ENSMUSG00000024516	*Sec11c*	4.27	4.29	4.2	3.93
ENSMUSG00000024527	*Afg3l2*	4.97	5.16	5.21	4.93
ENSMUSG00000024528	*Srfbp1*	2.8	1.76	2.38	2.37
ENSMUSG00000024535	*Snx24*	2.59	1.37	2.33	1.92
ENSMUSG00000024537	*Tnfsf5ip1*	3.86	3.62	3.63	3.44
ENSMUSG00000024538	*Ppic*	1.14	0.94	0.94	1.33
ENSMUSG00000024539	*Ptpn2*	2.24	1.7	2.39	1.85
ENSMUSG00000024560	*Cxxc1*	4.04	4.81	4.53	4.34
ENSMUSG00000024561	*Mbd1*	4.07	4.4	3.96	4.15
ENSMUSG00000024563	*Smad2*	3.42	2.83	3.2	2.71
ENSMUSG00000024566	*Atp9b*	3.41	3.39	3.27	3.09
ENSMUSG00000024570	*1110032A13Ri*	4.07	4.63	4.58	4.21
ENSMUSG00000024571	*Txnl4a*	5.37	5.76	5.46	5.49
ENSMUSG00000024576	*Csnk1a1*	5.92	5.08	5.53	5.18
ENSMUSG00000024580	*Grpel2*	4.61	3.75	4.38	3.87
ENSMUSG00000024581	*Napg*	3.31	2.66	3.05	2.84
ENSMUSG00000024583	*Txnl1*	5.72	4.99	5.22	4.65
ENSMUSG00000024587	*Nars*	5.65	5.58	5.21	5.07

ENSMUSG00000024588	*Fech*	6.77	6.77	6.57	6.44
ENSMUSG00000024589	*Nedd4l*	5.07	4.76	4.51	4.04
ENSMUSG00000024590	*Lmnb1*	1.26	1.14	1.48	0.6
ENSMUSG00000024592	*NA*	3.8	2.39	3.56	2.63
ENSMUSG00000024594	*Prrc1*	3.79	3.72	3.49	3.26
ENSMUSG00000024597	*Slc12a2*	1.7	0.84	1.67	1.01
ENSMUSG00000024601	*Isoc1*	6.09	5.75	5.4	5.09
ENSMUSG00000024603	*Dctn4*	3.81	3.47	3.64	3.23
ENSMUSG00000024604	*Rbm22*	3.5	3.58	3.9	3.56
ENSMUSG00000024608	*Rps14*	6.13	7.44	7.16	6.86
ENSMUSG00000024610	*Cd74*	7.07	7.09	7.24	6.55
ENSMUSG00000024613	*Tcof1*	1.7	1.91	1.72	1.68
ENSMUSG00000024614	*Txndc10*	2.87	1.56	2.23	1.55
ENSMUSG00000024620	*Pdgfrb*	1.56	2.44	2.1	1.85
ENSMUSG00000024621	*Csf1r*	4.08	4.26	4.07	3.89
ENSMUSG00000024622	*A630042L21Ri*	2.51	2.93	2.65	2.58
ENSMUSG00000024639	*Gnaq*	3.01	2.64	2.92	2.69
ENSMUSG00000024642	*Tle4*	2.21	1.85	2.04	2.3
ENSMUSG00000024644	*Cndp2*	4.6	4.96	4.35	4.24
ENSMUSG00000024645	*1700034H14Ri*	4.25	3.48	3.79	3.36
ENSMUSG00000024646	*Cyb5*	10.16	10.29	10.34	10.62
ENSMUSG00000024654	*Asrgl1*	2.93	2.7	3.07	2.72
ENSMUSG00000024659	*AK170612*	0.83	1.42	1.14	1.41
ENSMUSG00000024661	*Fth1*	10.36	10.04	10.24	10.09
ENSMUSG00000024664	*Fads3*	0.6	1.34	1.06	1.04
ENSMUSG00000024665	*Fads2*	8.21	8.19	7.47	7.46
ENSMUSG00000024666	*Tmem138*	0.83	1.69	1.15	1.17
ENSMUSG00000024667	*2810441K11Ri*	2.22	1.28	1.9	1.73
ENSMUSG00000024668	*0610038F07Ri*	4.9	4.43	4.79	4.51
ENSMUSG00000024673	*Ms4a1*	-1.09	-3.07	1.73	-3.08
ENSMUSG00000024678	*Ms4a4d*	2.17	1.26	1.51	1.63

ENSMUSG00000024679	*Ms4a6d*	1.84	0.19	1.13	0.01
ENSMUSG00000024683	*Mrpl16*	5.74	4.9	5.4	5.3
ENSMUSG00000024687	*Osbp*	4.52	4.55	4.05	4.04
ENSMUSG00000024691	*4632417K18Ri*	1.35	0.26	0.72	-0.51
ENSMUSG00000024694	*Keg1*	6.41	6.45	5.69	6.13
ENSMUSG00000024695	*Zfp91*	5.12	4.29	4.72	4.31
ENSMUSG00000024712	*Rfk*	5.83	5.09	5.23	4.72
ENSMUSG00000024713	*NA*	1.84	1.9	1.95	1.66
ENSMUSG00000024725	*Ostf1*	4.64	4.41	4.65	4.42
ENSMUSG00000024730	*Ms4a8a*	1.74	0.81	0.81	0.92
ENSMUSG00000024732	*Ccdc86*	2.9	3.76	3.02	3.41
ENSMUSG00000024735	*Prpf19*	5.02	5.65	5.44	5.37
ENSMUSG00000024737	*Slc15a3*	1.64	1.92	0.83	0.8
ENSMUSG00000024740	*Ddb1*	5.98	6.2	6.05	6.07
ENSMUSG00000024742	*Fen1*	0.55	0.83	1.22	0.39
ENSMUSG00000024747	*Aldh1a7*	7.2	6.55	7.05	6.37
ENSMUSG00000024750	*Zfand5*	4.38	3.53	4.14	3.7
ENSMUSG00000024754	*Tmem2*	2.38	2.57	1.74	1.88
ENSMUSG00000024758	*Rtn3*	5.48	5.16	5.09	4.77
ENSMUSG00000024759	*5730596K20Ri*	5.23	4.04	4.65	4.22
ENSMUSG00000024761	*NA*	3.21	2.5	2.54	3.37
ENSMUSG00000024764	*NA*	2.56	2.81	2.85	2.42
ENSMUSG00000024766	*AI747699*	1.32	-1.07	0.38	-0.34
ENSMUSG00000024767	*Otub1*	4.36	5.23	5.22	5.16
ENSMUSG00000024769	*NA*	1.61	1.98	1.93	1.65
ENSMUSG00000024772	*Ehd1*	4.87	5.14	5.11	4.76
ENSMUSG00000024773	*Atg2a*	3.29	4.11	4.01	3.73
ENSMUSG00000024777	*Ppp2r5b*	2.23	3.03	2.71	2.59
ENSMUSG00000024778	*Fas*	4.15	3.42	3.48	3.06
ENSMUSG00000024780	*Cdc37l1*	4.89	3.72	4.28	3.73
ENSMUSG00000024781	*Lipa*	7.5	6.94	6.93	6.62

ENSMUSG00000024782	*Ak3*	8.35	7.83	8.05	7.69
ENSMUSG00000024785	*Rcl1*	5.77	5.99	6.1	6.09
ENSMUSG00000024787	*Snx15*	3.09	3.56	3.47	3.33
ENSMUSG00000024789	*Jak2*	2.84	2	2.69	1.89
ENSMUSG00000024790	*Sac3d1*	2.03	2.54	2.57	2.27
ENSMUSG00000024792	*Zfpl1*	3.23	3.98	3.63	3.43
ENSMUSG00000024797	*1110014N23Ri*	2.76	3.76	3.16	3.02
ENSMUSG00000024799	*Tm7sf2*	7	6.89	6.98	6.47
ENSMUSG00000024800	*Rpp30*	2.95	2.47	2.82	2.76
ENSMUSG00000024805	*Pcgf5*	2.73	2.05	2.56	2.14
ENSMUSG00000024807	*Syvn1*	4.69	6.25	5.03	5.04
ENSMUSG00000024811	*NA*	4.03	3.74	4.11	3.62
ENSMUSG00000024812	*Tjp2*	2.39	2.71	2.32	2.32
ENSMUSG00000024816	*1200004M23R*	3.48	3.28	3.65	3.23
ENSMUSG00000024817	*NIRF*	3.46	3.16	3.43	3.01
ENSMUSG00000024818	*Slc25a45*	4.17	3.8	4.02	3.75
ENSMUSG00000024824	*Rad9*	3.58	3.11	3.56	3.22
ENSMUSG00000024826	*Gja10*	3.88	4.18	3.96	3.95
ENSMUSG00000024827	*Gldc*	6.87	6.71	6.82	6.19
ENSMUSG00000024829	*Mrpl21*	2.41	2.02	2.09	2.85
ENSMUSG00000024830	*Rps6kb2*	2.99	3.67	3.4	3.2
ENSMUSG00000024833	*Pola2*	1.1	1.3	1.95	1.47
ENSMUSG00000024835	*Coro1b*	5.29	5.4	5.6	5.4
ENSMUSG00000024841	*2010003J03Ri*	4.06	4.63	4.51	4.42
ENSMUSG00000024843	*Chka*	4.69	5.22	3.38	3.17
ENSMUSG00000024844	*Banf1*	5.65	5.88	5.87	5.63
ENSMUSG00000024845	*Tmem134*	5.26	5.53	5.34	5.22
ENSMUSG00000024847	*Aip*	4.07	4.87	4.56	4.35
ENSMUSG00000024853	*Sf3b2*	5.3	5.46	5.37	5.21
ENSMUSG00000024854	*Pold4*	4.34	4.67	4.78	4.37
ENSMUSG00000024855	*Pacs1*	0.44	1.07	1.06	0.18

ENSMUSG00000024856	*Cdk2ap2*	5.26	6.28	5.46	5.46
ENSMUSG00000024858	*Adrbk1*	3.7	4.22	4.09	3.69
ENSMUSG00000024862	*Klc2*	1.5	2.5	2.31	1.87
ENSMUSG00000024863	*Mbl2*	8.5	8.29	8.28	8.18
ENSMUSG00000024866	*Acy3*	5.89	6.48	6.39	6
ENSMUSG00000024869	*Nudt8*	3.64	4.51	4.43	4.12
ENSMUSG00000024870	*Rab1b*	6.47	7.19	6.87	6.59
ENSMUSG00000024875	*Yif1a*	5.71	6.21	5.79	5.67
ENSMUSG00000024878	*Cbwd1*	2.02	1.34	1.79	1.79
ENSMUSG00000024887	*Asah2*	3.1	2.02	2.57	2.07
ENSMUSG00000024889	*Rce1*	3.15	3.81	2.68	2.54
ENSMUSG00000024892	*Pcx*	7.26	7.5	7.63	7.28
ENSMUSG00000024896	*Minpp1*	4.25	4.14	4.42	3.86
ENSMUSG00000024899	*Papss2*	7.4	6.91	7.12	6.5
ENSMUSG00000024900	*Cpt1a*	6.93	6.69	6.87	6.69
ENSMUSG00000024902	*Mrpl11*	4.97	5.11	5.18	4.96
ENSMUSG00000024906	*Mus81*	1.64	2.49	2.34	2.13
ENSMUSG00000024908	*Saps3*	5.08	4.59	4.73	4.22
ENSMUSG00000024911	*Fibp*	4.04	4.6	4.06	4
ENSMUSG00000024913	*Lrp5*	4.74	5.54	5.02	4.7
ENSMUSG00000024914	*Drap1*	5.48	6.01	5.52	5.54
ENSMUSG00000024921	*Smarca2*	4.35	4.12	4.51	4.16
ENSMUSG00000024924	*Vldlr*	3.31	2.36	2.51	1.71
ENSMUSG00000024925	*Rnaseh2c*	4.56	5.24	4.72	4.64
ENSMUSG00000024926	*Htatip*	2.93	3.23	2.96	2.75
ENSMUSG00000024927	*Rela*	4.81	5.69	5.13	5.16
ENSMUSG00000024939	*Mtvr2*	3.2	3.94	3.73	3.83
ENSMUSG00000024941	*Scyl1*	4.26	4.82	4.69	4.63
ENSMUSG00000024942	*Capn1*	2.81	3.18	2.85	2.77
ENSMUSG00000024943	*Smc5*	2.89	1.83	2.51	1.95
ENSMUSG00000024944	*Arl2*	2.15	2.44	2.66	2.41

ENSMUSG00000024947	*Men1*	3.62	3.86	3.78	3.57
ENSMUSG00000024948	*Map4k2*	1.67	2.23	1.71	1.51
ENSMUSG00000024949	*Sf1*	5.33	5.36	5.27	5.17
ENSMUSG00000024952	*Rps6ka4*	1.58	2.5	2.11	1.92
ENSMUSG00000024953	*Prdx5*	7.75	7.61	7.82	7.72
ENSMUSG00000024955	*Esrra*	3.06	4.02	4.18	3.76
ENSMUSG00000024958	*Gpr137*	2.67	3.35	3.15	2.93
ENSMUSG00000024959	*Bad*	3.41	3.83	3.69	3.41
ENSMUSG00000024960	*Plcb3*	2.22	3.06	2.63	2.52
ENSMUSG00000024962	*Vegfb*	3.54	4.07	3.51	3.58
ENSMUSG00000024963	*Dnajc4*	2.93	3.27	3.11	2.73
ENSMUSG00000024965	*BC032204*	0.5	1.19	1.62	0.63
ENSMUSG00000024966	*Stip1*	6.07	6.52	5.9	6.3
ENSMUSG00000024969	*Mark2*	2.45	2.88	3.02	3
ENSMUSG00000024974	*Smc3*	3.37	2.7	2.84	2.54
ENSMUSG00000024975	*Pdcd4*	6.14	5.56	5.99	5.39
ENSMUSG00000024976	*Shoc2*	4.47	3.77	4.18	3.83
ENSMUSG00000024978	*mKIAA1560*	5.61	5.57	5.44	5.05
ENSMUSG00000024981	*Acsl5*	7.72	7.15	7.29	6.84
ENSMUSG00000024982	*Zdhhc6*	4.79	4.75	4.75	4.4
ENSMUSG00000024983	*Vti1a*	2.6	1.93	2.29	2.03
ENSMUSG00000024985	*Tcf4*	2.38	2.06	2.74	2.55
ENSMUSG00000024986	*Hhex*	5.46	4.98	5.31	5.91
ENSMUSG00000024987	*Cyp26a1*	3.64	3.37	4.12	2.82
ENSMUSG00000024990	*Rbp4*	10.42	10.93	10.81	10.63
ENSMUSG00000024991	*Eif3s10*	5.7	5.48	5.55	5.05
ENSMUSG00000024993	*1810055E12Ri*	4	3.08	3.42	2.83
ENSMUSG00000024997	*Prdx3*	6.99	6.14	6.62	6.2
ENSMUSG00000024998	*PLC-epsilon*	1.42	0.9	1.09	0.8
ENSMUSG00000024999	*Noc3l*	1.51	0.65	1.53	0.67
ENSMUSG00000025003	*Cyp2c39*	9.59	8.82	9.35	8.97

ENSMUSG00000025004	*Cyp2c40*	6.78	5.8	5.99	5.26
ENSMUSG00000025006	*Sorbs1*	3.2	2.79	3.64	3.49
ENSMUSG00000025016	*Tm9sf3*	6.51	5.51	5.84	5.32
ENSMUSG00000025017	*Pik3ap1*	5.74	5.64	5.23	5.09
ENSMUSG00000025019	*mlr2*	2.07	0.54	1.47	1.17
ENSMUSG00000025024	*Smndc1*	3.37	2.02	3.17	2.6
ENSMUSG00000025025	*Mxi1*	2.96	2.86	2.93	2.58
ENSMUSG00000025026	*Add3*	2.65	2.55	2.4	2.1
ENSMUSG00000025027	*Xpnpep1*	3.96	4.47	4.24	3.96
ENSMUSG00000025034	*Trim8*	4.23	5.18	4.92	4.9
ENSMUSG00000025035	*Arl3*	4.17	4.15	4.2	4.23
ENSMUSG00000025036	*Sfxn2*	4.22	3.73	4.29	3.87
ENSMUSG00000025037	*Maoa*	2.28	1.7	1.93	1.42
ENSMUSG00000025039	*NA*	3.44	4.08	3.77	3.28
ENSMUSG00000025040	*Fundc1*	2.82	1.59	2.24	1.68
ENSMUSG00000025041	*Nt5c2*	3.49	3.48	3.46	2.9
ENSMUSG00000025044	*Msr1*	2.69	2.52	2.33	2.17
ENSMUSG00000025047	*Pdcd11*	2.29	2.96	2.78	2.41
ENSMUSG00000025049	*Taf5*	1.08	1	1.14	0.61
ENSMUSG00000025050	*Pcgf6*	2.79	2.55	2.37	2.52
ENSMUSG00000025059	*Gyk*	5.11	4.6	4.63	4.41
ENSMUSG00000025060	*Slk*	3.79	3.46	3.36	3.26
ENSMUSG00000025066	*6330577E15Ri*	5.13	4.35	4.89	4.63
ENSMUSG00000025068	*Gsto1*	7.22	6.58	6.89	6.6
ENSMUSG00000025075	*Habp2*	6.74	6.68	6.79	6.66
ENSMUSG00000025076	*Casp7*	4.16	3.79	4.12	3.59
ENSMUSG00000025077	*Dclre1a*	2.24	1.92	2.74	2.41
ENSMUSG00000025078	*Nhlrc2*	2.69	2.38	2.86	2.51
ENSMUSG00000025085	*Ablim1*	2.29	1.72	2.55	2
ENSMUSG00000025086	*Trub1*	2.52	3.05	3.26	2.67
ENSMUSG00000025089	*Gfra1*	6.51	5.92	6.49	5.87

ENSMUSG00000025102	*3110040N11Ri*	3.17	3.38	3.28	3.23
ENSMUSG00000025103	*Btbd1*	1.92	1.43	1.64	1.33
ENSMUSG00000025127	*Gcgr*	6.1	6.62	6.32	6.27
ENSMUSG00000025130	*P4hb*	9.18	9.53	9.07	9.01
ENSMUSG00000025132	*Arhgdia*	5.39	6.41	5.5	5.67
ENSMUSG00000025133	*Ints4*	3.45	3.43	3.52	3.18
ENSMUSG00000025134	*Thoc4*	3.09	3.23	3.37	2.88
ENSMUSG00000025135	*Anapc11*	1.93	2.77	2.62	2.49
ENSMUSG00000025137	*Pcyt2*	6.96	7.5	7.02	6.97
ENSMUSG00000025138	*Sirt7*	4.03	4.79	4.63	4.15
ENSMUSG00000025139	*Tollip*	4.84	4.63	4.58	4.41
ENSMUSG00000025142	*Aspscr1*	5.37	6.21	6.12	5.81
ENSMUSG00000025144	*Stra13*	4.92	5.22	5.2	5.02
ENSMUSG00000025145	*Lrrc45*	0.81	1.65	1.59	1.38
ENSMUSG00000025147	*Mmh*	3.86	4.43	4.16	4
ENSMUSG00000025151	*Maged1*	5.69	5.88	5.29	5.61
ENSMUSG00000025153	*Fasn*	5.58	5.49	5.78	5.65
ENSMUSG00000025155	*Dus1l*	4.78	5.2	5.23	4.93
ENSMUSG00000025156	*Gps1*	1.42	2.16	1.77	1.52
ENSMUSG00000025157	*Zdhhc16*	3.06	3.34	3.17	3.04
ENSMUSG00000025158	*Rfng*	3.64	4.08	3.75	3.5
ENSMUSG00000025159	*Mms19*	3.12	3.17	3.46	3.22
ENSMUSG00000025162	*Csnk1d*	4.77	4.98	4.6	4.48
ENSMUSG00000025169	*1110031I02Rik*	2.89	2.99	3.03	3.08
ENSMUSG00000025171	*Ubtd1*	2.64	3.12	2.72	2.65
ENSMUSG00000025173	*Wdr45l*	4.23	3.56	3.6	3.67
ENSMUSG00000025175	*Fn3k*	2.98	3.83	3.92	3.6
ENSMUSG00000025176	*0610010D20Ri*	6.47	6.69	6.38	6.31
ENSMUSG00000025178	*Pi4k2a*	4.23	4.82	4.62	4.38
ENSMUSG00000025184	*D19Ertd386e*	3.14	2.88	2.69	2.4
ENSMUSG00000025188	*ep*	1.09	1.83	1.34	1.36

ENSMUSG00000025190	*Got1*	8.91	8.36	8.72	8.21
ENSMUSG00000025193	*Cutc*	3.81	2.99	3.56	3.08
ENSMUSG00000025194	*Abcc2*	6.3	5.86	5.93	5.93
ENSMUSG00000025195	*Dnmbp*	2.92	2.89	3.04	3.09
ENSMUSG00000025196	*Cpn1*	7.88	8.22	7.96	7.96
ENSMUSG00000025197	*Cyp2c44*	8.03	8.25	7.99	8.23
ENSMUSG00000025198	*Erlin1*	4.55	4.37	4.4	4.13
ENSMUSG00000025199	*Chuk*	5.45	4.6	5.28	4.66
ENSMUSG00000025200	*Cwf19l1*	3.89	3.5	3.92	3.68
ENSMUSG00000025204	*Ndufb8*	7.19	7.52	7.53	7.1
ENSMUSG00000025207	*Sema4g*	6.55	7.18	6.93	6.81
ENSMUSG00000025208	*Mrpl43*	4.61	4.75	4.84	4.93
ENSMUSG00000025209	*Peo1*	3.88	4.38	3.96	3.65
ENSMUSG00000025217	*mKIAA4123*	2.54	2.2	2.53	2.1
ENSMUSG00000025218	*Poll*	1.95	2.51	2.17	2.01
ENSMUSG00000025220	*Mgea5*	4.28	3.74	4.22	3.42
ENSMUSG00000025223	*Ldb1*	3.57	4.07	4.02	4.02
ENSMUSG00000025224	*Gbf1*	3.86	4.36	3.97	3.87
ENSMUSG00000025225	*Nfkb2*	1.4	1.68	1.99	1.58
ENSMUSG00000025226	*Fbxl15*	2.19	2.57	2.61	2.06
ENSMUSG00000025227	*Tmem180*	2.08	2.29	2.21	2.29
ENSMUSG00000025228	*Actr1a*	4.97	5.39	5.23	5.01
ENSMUSG00000025232	*Hexa*	4.61	5.27	4.99	4.85
ENSMUSG00000025234	*Arih1*	4.67	3.98	4.31	3.93
ENSMUSG00000025236	*Adpgk*	3.12	3.25	3.67	3.27
ENSMUSG00000025237	*Parp6*	3.31	3.22	3.43	3.18
ENSMUSG00000025239	*limd1*	3.88	3.86	3.77	3.59
ENSMUSG00000025240	*Sacm1l*	5.04	4.27	4.7	4.36
ENSMUSG00000025241	*Fyco1*	3.31	3.14	3.38	3.13
ENSMUSG00000025245	*Lztfl1*	1.47	0.15	0.98	0.54
ENSMUSG00000025246	*Tbl1x*	4	3.58	3.54	3.42

ENSMUSG00000025255	*Zfhx4*	1.38	1.06	1.3	0.57
ENSMUSG00000025260	*Hsd17b10*	7.35	7.3	7.19	6.88
ENSMUSG00000025261	*Mule*	4.14	4.22	4.18	3.87
ENSMUSG00000025262	*ORF34*	1.39	0.71	1.01	0.54
ENSMUSG00000025264	*Tsr2*	2.72	2.1	2.14	2.11
ENSMUSG00000025266	*Gnl3l*	2.73	2.68	2.85	2.59
ENSMUSG00000025268	*Maged2*	1.04	1.61	1.22	1.36
ENSMUSG00000025270	*Alas2*	3.1	4.19	4.27	4.53
ENSMUSG00000025271	*Pfkfb1*	5.14	4.79	4.91	4.58
ENSMUSG00000025277	*Abhd6*	4.47	4.41	4.08	4.14
ENSMUSG00000025278	*Flnb*	3	3.57	3.34	3.5
ENSMUSG00000025279	*Dnase1l3*	5.5	5.66	5.31	5.33
ENSMUSG00000025280	*Polr3a*	1.8	2.18	2.39	1.78
ENSMUSG00000025283	*Sat1*	4.03	3.65	3.8	3.5
ENSMUSG00000025289	*Prdx4*	6.46	5.8	6.09	5.86
ENSMUSG00000025290	*Rps24*	3.8	2.88	3.65	3.08
ENSMUSG00000025314	*Ptprj*	3.26	2.95	2.94	2.6
ENSMUSG00000025316	*Banp*	2.07	3.17	2.57	2.39
ENSMUSG00000025317	*Car5a*	6.93	6.93	7.1	6.66
ENSMUSG00000025326	*mKIAA4216*	4.43	2.92	3.84	3.13
ENSMUSG00000025332	*Jarid1c*	4.37	4.87	4.44	4.37
ENSMUSG00000025337	*Sbds*	4.43	4.61	4.73	4.67
ENSMUSG00000025340	*Rabgef1*	3.57	3.17	3.34	3
ENSMUSG00000025347	*Mettl7b*	8.88	9.37	8.86	8.81
ENSMUSG00000025348	*Itga7*	1.24	1.8	2.04	1.52
ENSMUSG00000025349	*Bloc1s1*	4.28	5.07	5.08	4.42
ENSMUSG00000025350	*Rdh5*	3.76	4.24	4.6	4.2
ENSMUSG00000025353	*Ormdl2*	5.37	5.66	5.17	4.98
ENSMUSG00000025354	*Dnajc14*	4.32	4.36	4.25	3.97
ENSMUSG00000025355	*Mmp19*	5.6	5.25	5.25	4.84
ENSMUSG00000025357	*Dgka*	2.34	1.87	2.42	1.95

ENSMUSG00000025358	*Cdk2*	2.46	2.26	2.15	2.34
ENSMUSG00000025362	*Rps26*	5.47	5.72	5.81	5.86
ENSMUSG00000025364	*Pa2g4*	5.55	5.31	5.55	5.49
ENSMUSG00000025366	*Mbc2*	2.19	3.1	2.51	2.52
ENSMUSG00000025369	*Smarcc2*	4.94	5.05	5.13	5
ENSMUSG00000025371	*Chmp6*	3.26	3.86	3.18	3.45
ENSMUSG00000025372	*Baiap2*	3.29	4.45	3.62	3.37
ENSMUSG00000025373	*Rnf41*	1.76	2.01	1.92	1.66
ENSMUSG00000025374	*Obfc2b*	5.24	5.27	5.45	5.21
ENSMUSG00000025377	*2410002I01Rik*	2.2	2.79	2.82	2.32
ENSMUSG00000025379	*NA*	1.21	1.96	1.67	1.94
ENSMUSG00000025381	*Tmem4*	5.9	5.88	5.66	5.59
ENSMUSG00000025384	*2310003H01Ri*	0.84	1.91	1.55	1.11
ENSMUSG00000025393	*Atp5b*	9.75	9.66	9.73	9.42
ENSMUSG00000025395	*Prim1*	1.35	1.19	1.08	0.36
ENSMUSG00000025396	*Hsd17b6*	7.84	8.02	7.89	8.24
ENSMUSG00000025402	*Nab2*	2.59	3.53	3.21	2.76
ENSMUSG00000025403	*Shmt2*	6.89	7.47	7.34	7.07
ENSMUSG00000025404	*R3hdm2*	5	5.21	5.24	4.99
ENSMUSG00000025405	*Inhbc*	5.42	6.17	5.49	6.03
ENSMUSG00000025408	*Ddit3*	1.5	2.8	2.59	2.79
ENSMUSG00000025409	*Mbd6*	2.73	3.62	3.37	3.15
ENSMUSG00000025410	*Dctn2*	5.74	6.33	6.11	5.95
ENSMUSG00000025413	*Ttc4*	3.42	3.25	3.72	3.39
ENSMUSG00000025417	*Pip4k2c*	3.63	3.78	3.76	3.71
ENSMUSG00000025421	*Ier3ip1*	3.98	3.44	3.84	3.3
ENSMUSG00000025423	*Pias2*	3.99	3.61	3.96	3.76
ENSMUSG00000025428	*Atp5a1*	8.59	8.75	8.73	8.41
ENSMUSG00000025429	*Pstpip2*	2.3	1.6	1.86	1.78
ENSMUSG00000025436	*Xrcc6bp1*	0.56	1.73	1.26	0.77
ENSMUSG00000025437	*Vdu1*	4.18	3	3.76	3.36

ENSMUSG00000025439	*Clns1a*	4.05	3.96	3.97	3.84
ENSMUSG00000025451	*Paip1*	3.9	3.04	3.66	2.95
ENSMUSG00000025453	*Nnt*	5.53	4.57	4.92	4.6
ENSMUSG00000025464	*Paox*	1.57	1.48	1.46	1.26
ENSMUSG00000025465	*Echs1*	8.04	7.62	7.77	7.39
ENSMUSG00000025466	*1810014F10Ri*	3.59	3.23	3.62	3.66
ENSMUSG00000025470	*NA*	1.67	2.9	2.49	2.25
ENSMUSG00000025474	*Tubgcp2*	2.73	2.74	2.38	1.85
ENSMUSG00000025477	*Inpp5a*	3.59	3.49	3.49	3.42
ENSMUSG00000025479	*Cyp2e1*	12.32	11.54	12.03	11.87
ENSMUSG00000025481	*1190003J15Ri*	7.63	7.33	7.66	7.52
ENSMUSG00000025484	*Bet1l*	4.21	4.53	3.82	3.72
ENSMUSG00000025485	*Ric8*	3.18	3.83	3.66	3.55
ENSMUSG00000025486	*Sirt3*	5.39	5.89	5.93	5.99
ENSMUSG00000025487	*Psmd13*	5.78	5.57	5.6	5.41
ENSMUSG00000025491	*Ifitm1*	2.43	2.55	2.81	1.83
ENSMUSG00000025492	*Ifitm3*	8.74	8.81	8.88	8.75
ENSMUSG00000025494	*Sigirr*	3.82	4.36	4.11	4.06
ENSMUSG00000025495	*Ptdss2*	2.59	2.78	2.74	2.51
ENSMUSG00000025497	*Mupcdh*	5.14	6.05	5.77	5.56
ENSMUSG00000025498	*Irf7*	3.48	3.47	2.18	3.61
ENSMUSG00000025499	*Hras1*	3.16	3.65	3.28	3.18
ENSMUSG00000025503	*Taldo1*	5.79	6.08	6	5.61
ENSMUSG00000025504	*Eps8l2*	4.57	5.25	5	4.78
ENSMUSG00000025505	*Tmem80*	1.03	1.14	1.52	1.61
ENSMUSG00000025508	*Rplp2*	2.03	2.61	2.32	2.27
ENSMUSG00000025509	*Pnpla2*	6.1	6.39	6.76	6.27
ENSMUSG00000025510	*Cd151*	4.46	5.16	4.93	4.9
ENSMUSG00000025511	*Tspan4*	4.21	4.62	4.45	4.54
ENSMUSG00000025512	*Chid1*	3.37	3.82	3.46	3.23
ENSMUSG00000025521	*3110005G23Ri*	3.7	3.68	3.71	3.54

ENSMUSG00000025525	*AK086522*	4.79	4.11	4.57	4.15
ENSMUSG00000025531	*Chm*	2.79	1.48	2.16	1.56
ENSMUSG00000025532	*Crcp*	5.23	4.79	5.37	5.04
ENSMUSG00000025533	*Asl*	8.56	8.5	9.26	8.73
ENSMUSG00000025534	*Gusb*	3.36	3.3	3.24	3.21
ENSMUSG00000025538	*Sumf2*	2.63	3.11	2.69	2.39
ENSMUSG00000025544	*Tm9sf2*	6.47	5.81	6.11	5.69
ENSMUSG00000025545	*Clybl*	5.42	5.15	5.47	4.98
ENSMUSG00000025555	*Farp1*	2	2.62	2.03	2.25
ENSMUSG00000025558	*mKIAA1058*	1.61	1.47	1.5	1.4
ENSMUSG00000025571	*Tnrc6c*	1.63	1.92	2.07	2.11
ENSMUSG00000025572	*Tmc6*	1.31	2.45	1.92	1.61
ENSMUSG00000025574	*Tk1*	2.88	3.23	3.01	2.99
ENSMUSG00000025575	*Cant1*	3.06	3.5	3.4	3.06
ENSMUSG00000025577	*Cbx2*	2.17	2.69	2.31	1.59
ENSMUSG00000025578	*Cbx8*	1.93	2.39	2	1.51
ENSMUSG00000025579	*Gaa*	5.11	5.97	5.41	5.27
ENSMUSG00000025580	*Eif4a3*	2.99	3.88	3.32	3.49
ENSMUSG00000025583	*Raptor*	3.59	3.91	3.51	3.51
ENSMUSG00000025584	*Pde8a*	3.99	3.82	4.08	3.99
ENSMUSG00000025588	*Nat1*	1.5	-0.02	1.85	0.1
ENSMUSG00000025591	*1810029B16Ri*	1.29	0.89	0.65	0.38
ENSMUSG00000025607	*Copg2*	3.69	3.49	3.38	3.01
ENSMUSG00000025608	*Podxl*	2.04	2.28	0.74	1.16
ENSMUSG00000025609	*Mkln1*	4.78	4.42	4.65	4.12
ENSMUSG00000025612	*Bach1*	3.3	2.74	3.07	3.16
ENSMUSG00000025613	*Cct8*	6.4	6.49	6.32	6.13
ENSMUSG00000025616	*Usp16*	4.37	3.71	3.98	3.55
ENSMUSG00000025626	*Phf6*	1.72	0.55	1.48	0.75
ENSMUSG00000025630	*Hprt1*	5.76	5.18	5.48	4.89
ENSMUSG00000025645	*Ccdc51*	1.72	2.7	2.38	1.71

ENSMUSG00000025646	*NA*	1.89	2.07	1.71	1.29
ENSMUSG00000025647	*Scotin*	4.27	4.28	4.4	4.01
ENSMUSG00000025651	*Uqcrc1*	7.73	8.11	8.05	7.64
ENSMUSG00000025666	*Tmem47*	1.59	0.38	1.07	0.43
ENSMUSG00000025702	*8-Mar*	5.09	5.04	4.88	4.63
ENSMUSG00000025722	*NA*	3.39	3.54	3.64	2.84
ENSMUSG00000025724	*Sec11a*	4.86	4.91	4.86	4.6
ENSMUSG00000025728	*Pigq*	4.4	4.68	4.55	4.32
ENSMUSG00000025730	*Rab40C*	2.61	3.45	2.52	2.51
ENSMUSG00000025731	*0610011F06Ri*	6.55	7.06	6.75	6.95
ENSMUSG00000025732	*9530058B02Ri*	4.82	5.37	5.24	5.06
ENSMUSG00000025733	*Rhot2*	4.08	4.74	4.52	4.44
ENSMUSG00000025736	*2610003J06Ri*	5.61	6.03	5.47	5.55
ENSMUSG00000025737	*Wdr24*	2.84	3.44	3.03	2.96
ENSMUSG00000025742	*Prps2*	3.53	2.93	2.98	2.38
ENSMUSG00000025743	*Sdc3*	4.01	4.49	3.73	3.79
ENSMUSG00000025745	*Hadha*	7.65	7.67	7.75	7.52
ENSMUSG00000025757	*apg-1b*	3.73	3.1	3.27	3.27
ENSMUSG00000025759	*Mfsd8*	2.88	2.07	2.19	1.61
ENSMUSG00000025764	*Phf17*	3.53	3.71	3.85	3.71
ENSMUSG00000025766	*D3Ertd751e*	2.34	1.14	1.58	1.13
ENSMUSG00000025779	*Ly96*	3.55	2.89	3.52	2.75
ENSMUSG00000025780	*Itih5*	2.13	2.06	1.68	1.57
ENSMUSG00000025781	*Atp5c1*	6.56	6.49	6.77	6.34
ENSMUSG00000025782	*Taf3*	1.44	1.06	1.24	1.14
ENSMUSG00000025785	*Exosc7*	3.9	4.45	4.35	4.14
ENSMUSG00000025786	*GODZ*	3.68	3.53	3.2	3.3
ENSMUSG00000025788	*Chd2*	1.26	1.21	1.63	1.37
ENSMUSG00000025791	*Pgm2*	6.79	6.82	6.74	6.62
ENSMUSG00000025792	*Slc25a10*	6.91	7.02	6.96	6.6
ENSMUSG00000025793	*Hgs*	4.14	5.19	4.83	4.73

ENSMUSG00000025794	*Rpl14*	4.81	5.42	4.93	4.51
ENSMUSG00000025795	*Rassf3*	4.19	4.13	4.44	4.27
ENSMUSG00000025809	*Itgb1*	6.2	5.76	6.01	5.67
ENSMUSG00000025810	*Nrp1*	4.71	4.71	4.16	4.32
ENSMUSG00000025812	*Par3*	3.59	4.11	4.17	3.99
ENSMUSG00000025813	*Homer2*	3.85	3.97	3.8	3.94
ENSMUSG00000025815	*Dhtkd1*	6.06	5.56	5.94	5.56
ENSMUSG00000025817	*Nudt5*	3.52	3.15	3.59	3.03
ENSMUSG00000025823	*Pdia4*	6.93	7.11	6.19	6.38
ENSMUSG00000025825	*Iscu*	3.68	3.86	3.66	3.46
ENSMUSG00000025854	*BC004044*	3.26	4.54	4.2	4.29
ENSMUSG00000025856	*Pdgfa*	0.93	1.43	1.96	1.34
ENSMUSG00000025857	*Heatr2*	1.95	2.88	2.64	2.27
ENSMUSG00000025858	*1110007L15Ri*	3.07	3.43	3.16	3.15
ENSMUSG00000025860	*Birc4*	4.95	3.82	4.31	3.69
ENSMUSG00000025862	*SAP2*	4.57	3.27	3.93	3.43
ENSMUSG00000025868	*Higd2a*	6.29	6.47	6.38	6.47
ENSMUSG00000025869	*D13Wsu177e*	4.95	4.98	4.84	4.65
ENSMUSG00000025871	*4833439L19Ri*	4.85	4.75	5.21	4.85
ENSMUSG00000025872	*Thoc3*	3.73	4.13	3.84	3.52
ENSMUSG00000025873	*mKIAA0887*	4.63	4.69	4.78	4.53
ENSMUSG00000025878	*Uimc1*	3.08	2.82	3.02	2.55
ENSMUSG00000025880	*Smad7*	1.95	2.88	2.2	1.84
ENSMUSG00000025885	*Myo5b*	2.38	2.4	2.23	2.17
ENSMUSG00000025894	*Aasdhppt*	4.84	4.21	4.64	4.02
ENSMUSG00000025898	*Cwf19l2*	3.15	1.87	2.55	2.16
ENSMUSG00000025899	*Alkbh8*	2.17	0.84	1.59	1
ENSMUSG00000025903	*Lypla1*	7.04	5.58	6.33	5.74
ENSMUSG00000025907	*Rb1cc1*	3.69	2.36	3.3	2.46
ENSMUSG00000025911	*Adhfe1*	6.06	5.7	5.59	5.06
ENSMUSG00000025915	*Sgk3*	3.21	2.38	3.28	2.53

ENSMUSG00000025917	*Cops5*	6.09	5.55	5.59	5.23
ENSMUSG00000025920	*Stau2*	1.16	0.34	0.79	0.16
ENSMUSG00000025921	*Rdh10*	4.23	3.97	3.95	3.93
ENSMUSG00000025925	*Terf1*	2.98	2.2	2.69	1.7
ENSMUSG00000025933	*Tmem14a*	0.99	0.79	1.37	1.61
ENSMUSG00000025934	*Gsta3*	10.17	10.02	9.86	9.68
ENSMUSG00000025935	*Tram1*	6.47	5.97	6.21	6.04
ENSMUSG00000025937	*Lactb2*	7.55	6.22	7.01	6.59
ENSMUSG00000025939	*Ube2w*	4.29	3.33	4	3.56
ENSMUSG00000025940	*Tmem70*	5.12	4.52	4.95	4.58
ENSMUSG00000025949	*Pip5k3*	1.66	1	1.64	1.11
ENSMUSG00000025950	*Idh1*	8.11	7.38	7.52	7.08
ENSMUSG00000025956	*2310038H17Ri*	1.86	1.3	1.9	1.5
ENSMUSG00000025958	*Creb1*	2.16	1.58	1.79	1.39
ENSMUSG00000025962	*Fastkd2*	2.74	2.42	2.65	2.16
ENSMUSG00000025964	*Adam23*	2.23	2.2	2.06	1.94
ENSMUSG00000025967	*Eef1b2*	7.05	7.12	6.93	6.67
ENSMUSG00000025968	*Ndufs1*	6.43	5.87	6.33	5.83
ENSMUSG00000025969	*Nrp2*	2.46	2.15	2.37	2.01
ENSMUSG00000025971	*9430016H08Ri*	4.1	3.83	4.05	3.42
ENSMUSG00000025979	*Mobkl3*	4.65	3.56	3.96	3.39
ENSMUSG00000025980	*Hspd1*	5.8	5.45	5.62	5.2
ENSMUSG00000025981	*Coq10b*	3.17	2.25	4.22	3.86
ENSMUSG00000025982	*Sf3b1*	4.97	4.34	4.7	4.28
ENSMUSG00000025991	*Cps1*	9.96	10	10.23	9.94
ENSMUSG00000025993	*Slc40a1*	6.29	5.33	6.26	5.71
ENSMUSG00000025995	*Wdr75*	2.8	2.44	2.43	2.39
ENSMUSG00000026000	*Lancl1*	2.42	2.77	2.44	2.46
ENSMUSG00000026003	*Acadl*	7.81	7.22	7.56	7.03
ENSMUSG00000026004	*1110028C15Ri*	2.63	1.08	2.24	1.73
ENSMUSG00000026005	*Rpe*	4.58	3.33	3.9	3.69

ENSMUSG00000026014	*Raph1*	3.48	3.27	3.04	3.31
ENSMUSG00000026019	*Wdr12*	1.42	0.93	0.92	1.24
ENSMUSG00000026020	*Nol5*	3.56	3.1	2.72	2.87
ENSMUSG00000026021	*Sumo1*	3.21	2.27	3.41	3.24
ENSMUSG00000026024	*Als2*	4.68	4.95	4.46	4.32
ENSMUSG00000026027	*PAPK-A*	4.48	3.97	4.45	4.03
ENSMUSG00000026028	*Trak2*	2.59	2.35	2.79	2.53
ENSMUSG00000026029	*Casp8*	4.5	4.2	4.17	3.93
ENSMUSG00000026031	*Cflar*	4.07	3.51	3.85	3.55
ENSMUSG00000026032	*Ndufb3*	5.65	4.5	5.45	5.01
ENSMUSG00000026034	*Clk1*	4.89	3.81	5.36	4.78
ENSMUSG00000026035	*Ppil3*	2.46	1.71	2.47	2.19
ENSMUSG00000026036	*Nif3l1*	2.53	2.81	2.52	2.66
ENSMUSG00000026037	*Orc2l*	1.99	1.36	1.66	0.63
ENSMUSG00000026043	*mKIAA4231*	2.24	2.27	1.59	1.79
ENSMUSG00000026047	*Kdelc1*	1.96	1.32	2.12	2.03
ENSMUSG00000026048	*AK163166*	2.49	1.87	2.36	1.94
ENSMUSG00000026049	*NA*	2.68	1.19	2.14	1.24
ENSMUSG00000026064	*Ptp4a1*	2.6	0.54	2.32	1.7
ENSMUSG00000026072	*Il1r1*	3.49	3.7	2.88	3.66
ENSMUSG00000026074	*Map4k4*	1.59	1.5	1.41	1.06
ENSMUSG00000026077	*Npas2*	2.06	2.19	-1.06	-1.83
ENSMUSG00000026078	*Pdcl3*	4.01	4.32	4.1	3.91
ENSMUSG00000026082	*Rev1*	1.94	1.78	2.11	2.14
ENSMUSG00000026083	*Eif5b*	4.73	4.48	4.39	3.94
ENSMUSG00000026087	*Mrpl30*	5.37	5.11	5.34	5.14
ENSMUSG00000026088	*Mitd1*	3.03	2.48	2.34	2.6
ENSMUSG00000026094	*Stk17b*	2.26	1.22	1.94	0.87
ENSMUSG00000026095	*Asnsd1*	5.01	4.43	4.45	4.03
ENSMUSG00000026096	*Osgepl1*	3.61	2.69	3.23	2.72
ENSMUSG00000026097	*Ormdl1*	4.41	3.31	3.86	3.34

ENSMUSG00000026102	*Inpp1*	2.51	2.35	2.61	2.14
ENSMUSG00000026104	*Stat1*	4.59	3.35	3.82	3.83
ENSMUSG00000026107	*Nabp1*	2.55	0.92	2.41	2.25
ENSMUSG00000026111	*Unc50*	4.42	4.35	4.33	4.11
ENSMUSG00000026112	*6330578E17Ri*	5.14	4.8	5.01	4.76
ENSMUSG00000026113	*AK051424*	2.55	2.43	2.67	2.27
ENSMUSG00000026116	*Tmem131*	3.89	3.06	3.81	3.18
ENSMUSG00000026117	*Zap70*	2.38	3.02	2.81	2.41
ENSMUSG00000026123	*Plekhb2*	1.51	1.3	1.04	0.98
ENSMUSG00000026127	*Imp4*	4.59	4.83	4.51	4.39
ENSMUSG00000026131	*Bpag1*	2.11	1.98	2.45	2.16
ENSMUSG00000026142	*Rhbdd1*	3.54	3.65	3.35	3.3
ENSMUSG00000026150	*5230400G24Ri*	4.58	4.06	4.57	4.01
ENSMUSG00000026153	*4921533L14Ri*	2.78	1.83	2.76	2.49
ENSMUSG00000026154	*1110058L19Ri*	4.68	4.3	4.5	4.11
ENSMUSG00000026155	*Smap1*	4.78	4.17	4.47	3.74
ENSMUSG00000026156	*B3gat2*	2.82	2.49	2.68	1.98
ENSMUSG00000026158	*Ogfrl1*	2.67	2.24	2.29	1.67
ENSMUSG00000026159	*Hrb*	3.14	2.68	3.01	2.73
ENSMUSG00000026162	*Nhej1*	1.36	0.65	1.64	1.29
ENSMUSG00000026170	*Cyp27a1*	8.06	8.06	8.13	7.78
ENSMUSG00000026171	*Rnf25*	3.64	4.15	3.56	3.58
ENSMUSG00000026172	*Bcs1l*	3.6	3.63	3.6	3.18
ENSMUSG00000026174	*Rqcd1*	3.3	3.31	3.18	3
ENSMUSG00000026176	*Ctdsp1*	6.51	6.93	6.73	6.7
ENSMUSG00000026177	*Slc11a1*	1.76	2.31	1.64	1.38
ENSMUSG00000026179	*Pnkd*	5.97	6.27	6.16	5.78
ENSMUSG00000026181	*Ppm1f*	3.38	3.46	3.12	2.73
ENSMUSG00000026185	*Igfbp5*	1.64	1.82	1.42	1.59
ENSMUSG00000026187	*Xrcc5*	3.68	3.47	3.43	3.15
ENSMUSG00000026189	*Pecr*	7.94	7.99	7.81	7.52

ENSMUSG00000026192	*Atic*	3.8	4.28	3.79	3.7
ENSMUSG00000026193	*Fn1*	7.82	8.36	8.08	8.07
ENSMUSG00000026197	*Zfand2b*	4.11	4.42	4.61	4.23
ENSMUSG00000026198	*Abcb6*	5.35	5.61	5.37	5.17
ENSMUSG00000026199	*Ankzf1*	2.71	2.83	2.87	2.56
ENSMUSG00000026200	*NA*	0.79	1.15	1.09	0.53
ENSMUSG00000026201	*Stk16*	5.09	5.19	4.9	4.83
ENSMUSG00000026202	*Tuba4a*	7	7.58	6.76	6.93
ENSMUSG00000026203	*Dnajb10*	4.33	4.94	4.4	4.46
ENSMUSG00000026208	*Des*	1.38	1.86	2.54	2.54
ENSMUSG00000026209	*Dnpep*	4.55	5.41	4.91	4.59
ENSMUSG00000026213	*Stk11ip*	0.87	1.76	1.39	1.18
ENSMUSG00000026219	*Trip12*	4.66	3.95	4.44	3.99
ENSMUSG00000026222	*Sp100*	2.28	1.54	2.07	1.85
ENSMUSG00000026223	*Itm2c*	4.07	4.9	4.02	4.14
ENSMUSG00000026227	*NA*	4.79	5.39	4.8	4.81
ENSMUSG00000026229	*Psmd1*	6.23	6.24	5.95	5.73
ENSMUSG00000026234	*Ncl*	6.48	5.86	6.07	5.64
ENSMUSG00000026238	*Ptma*	1.84	1.16	1.44	1.43
ENSMUSG00000026239	*Pde6d*	2.68	2.36	2.77	2.15
ENSMUSG00000026240	*Cops7b*	2	2.39	2.17	2.27
ENSMUSG00000026245	*Farsb*	4.93	4.65	4.59	4.19
ENSMUSG00000026248	*Mrpl44*	4.34	4.56	4.55	4.43
ENSMUSG00000026254	*Eif4e2*	3.25	3.18	3.29	3.22
ENSMUSG00000026259	*Ngef*	3.73	4.07	4.37	4.09
ENSMUSG00000026260	*Ndufa10*	7.3	7.22	7.39	7.07
ENSMUSG00000026269	*Rnpepl1*	5.37	6.45	5.62	5.57
ENSMUSG00000026270	*Capn10*	3.76	4.39	3.9	3.77
ENSMUSG00000026272	*Agxt*	8.09	8.49	8.33	7.93
ENSMUSG00000026273	*Mterfd2*	2.59	2.49	2.81	2.8
ENSMUSG00000026275	*Ppp1r7*	4.43	4.22	4.04	3.58

ENSMUSG00000026276	*2-Sep*	5.37	4.53	5.1	4.52
ENSMUSG00000026277	*Stk25*	4.13	4.39	4.27	4.21
ENSMUSG00000026278	*Bok*	1.51	2.21	1.67	1.7
ENSMUSG00000026279	*Thap4*	1.55	1.98	1.83	1.55
ENSMUSG00000026280	*Atg4b*	4	4.32	4.2	4.19
ENSMUSG00000026281	*Dtymk*	3.13	2.39	2.39	2.41
ENSMUSG00000026283	*Ing5*	1.47	1.56	1.51	1.33
ENSMUSG00000026289	*Atg16l1*	3.66	3.84	3.71	3.73
ENSMUSG00000026295	*Spp2*	7.27	7.17	7.42	7.13
ENSMUSG00000026304	*Rab17*	4.24	4.39	4.74	4.39
ENSMUSG00000026305	*Lrrfip1*	2.65	2.77	2.87	2.56
ENSMUSG00000026307	*Scly*	5.86	6.27	5.79	5.79
ENSMUSG00000026309	*Ilkap*	4.08	4.37	4.19	3.83
ENSMUSG00000026315	*Serpinb8*	2.53	2.1	2.89	2.73
ENSMUSG00000026317	*Cln8*	4.2	4.3	4.41	4.45
ENSMUSG00000026319	*2310035C23Ri*	2.11	1.33	1.74	1.51
ENSMUSG00000026333	*Zh2c2*	2.67	1.55	1.54	1.82
ENSMUSG00000026335	*Pam*	3.6	3.31	3.13	2.95
ENSMUSG00000026339	*Ccdc93*	1.5	1.66	1.73	1.55
ENSMUSG00000026341	*Actr3*	3.9	2.76	3.38	2.82
ENSMUSG00000026342	*Slc35f5*	4.64	4.29	4.52	4.1
ENSMUSG00000026343	*NA*	1.26	1.29	1.49	1.12
ENSMUSG00000026344	*Lypd1*	0.4	0.72	1.02	0.02
ENSMUSG00000026348	*Acmsd*	5.02	3.46	5.24	3.87
ENSMUSG00000026349	*Ccnt2*	3.04	1.9	2.19	1.84
ENSMUSG00000026353	*Ubxd2*	5.46	5.29	4.88	4.65
ENSMUSG00000026356	*Dars*	5.38	4.97	5.38	4.81
ENSMUSG00000026360	*Rgs2*	2.8	1.29	1.34	1.2
ENSMUSG00000026361	*Cdc73*	3.54	2.6	2.87	2.78
ENSMUSG00000026365	*Cfh*	7.42	6.57	6.78	6.53
ENSMUSG00000026368	*F13b*	7.23	6.49	6.8	6.52

ENSMUSG00000026374	*Tsn*	4.08	3.74	4.2	3.7
ENSMUSG00000026377	*Mki67ip*	4.72	4.52	4.42	4.5
ENSMUSG00000026380	*Crtr-1*	1.26	0.76	0.8	0.13
ENSMUSG00000026383	*Epb4.1l5*	3.78	3.17	3.34	3.21
ENSMUSG00000026385	*Dbi*	9.02	8.77	9.09	9.12
ENSMUSG00000026389	*Steap3*	3.12	3.56	3.19	2.77
ENSMUSG00000026393	*Nek7*	5.02	4.53	4.73	4.29
ENSMUSG00000026395	*Ptprc*	1.12	0.58	1.67	-0.08
ENSMUSG00000026398	*Nr5a2*	4.43	4.45	4.23	4.25
ENSMUSG00000026399	*Cd55*	2.91	2.41	1.98	1.75
ENSMUSG00000026404	*Ddx59*	1.48	1.35	2.13	1.93
ENSMUSG00000026405	*C4bp*	7.63	7.11	7.37	7.21
ENSMUSG00000026409	*Pfkfb2*	2.16	2.22	1.84	1.88
ENSMUSG00000026411	*Tmem9*	3.71	3.66	3.66	3.34
ENSMUSG00000026417	*Pigr*	9.44	9.57	9.54	9.33
ENSMUSG00000026421	*Csrp1*	3.4	3.64	3.46	3.07
ENSMUSG00000026425	*Srgap2*	1.61	1.24	1.5	1.36
ENSMUSG00000026426	*Arl8a*	3.13	3.32	3.42	3.02
ENSMUSG00000026427	*Lgtn*	4.28	4.7	4.36	4.3
ENSMUSG00000026430	*Rassf5*	2.46	2.62	2.99	2.56
ENSMUSG00000026433	*Rab7l1*	3.1	3.21	3.55	3.44
ENSMUSG00000026434	*Nucks1*	5.49	4.34	5.15	4.64
ENSMUSG00000026435	*Slc45a3*	5.25	5.52	4.98	4.69
ENSMUSG00000026436	*Elk4*	3.09	2.42	3.46	2.72
ENSMUSG00000026437	*Pctk3*	4.42	4.4	4.97	4.7
ENSMUSG00000026439	*Rbbp5*	3.12	3.04	3.2	2.83
ENSMUSG00000026455	*Klhl12*	2.45	2.09	2.41	1.94
ENSMUSG00000026456	*Cyb5r1*	1.47	1.72	2.08	1.84
ENSMUSG00000026457	*Adipor1*	5.83	6.05	5.88	5.63
ENSMUSG00000026464	*Zc3h11a*	4.36	4.2	4.05	3.98
ENSMUSG00000026466	*Tor1aip1*	4.54	4.66	4.54	4.44

ENSMUSG00000026469	*Xpr1*	3.49	2.66	3.26	3
ENSMUSG00000026470	*Stx6*	2.07	2.66	2.29	2.16
ENSMUSG00000026471	*Mr1*	2.47	1.77	2.26	1.72
ENSMUSG00000026473	*Glul*	8.21	8.26	8.4	8.08
ENSMUSG00000026475	*Rgs16*	5.93	4.45	6.48	6.41
ENSMUSG00000026478	*Lamc1*	1.73	1.77	1.78	1.61
ENSMUSG00000026482	*Rgl1*	2.21	2.3	2.07	1.82
ENSMUSG00000026484	*Rnf2*	3.67	2.42	3.17	2.83
ENSMUSG00000026489	*Cabc1*	7.44	8.14	7.3	6.97
ENSMUSG00000026490	*NA*	2.45	2.28	2.31	1.83
ENSMUSG00000026491	*Ahctf1*	4.07	3.86	3.54	3.1
ENSMUSG00000026492	*Tfb2m*	1.59	1.17	1.51	1.22
ENSMUSG00000026495	*Efcab2*	1.56	0.36	1.73	-0.11
ENSMUSG00000026496	*Parp1*	3.74	4.27	3.78	3.73
ENSMUSG00000026499	*Acbd3*	3.95	3.54	3.41	3.14
ENSMUSG00000026500	*2310005N03Ri*	5.39	4.63	5.41	4.21
ENSMUSG00000026502	*5830417C01Ri*	3.23	2.64	2.82	2.28
ENSMUSG00000026509	*Capn2*	4.55	4.28	4.2	3.9
ENSMUSG00000026510	*Trp53bp2*	2.69	2.76	2.96	2.72
ENSMUSG00000026511	*Srp9*	4.63	3.84	4.31	3.73
ENSMUSG00000026516	*Nvl*	2.54	2.57	2.57	2.45
ENSMUSG00000026519	*Tmem63a*	3.38	3.25	3.26	2.74
ENSMUSG00000026520	*Pycr2*	1.74	2.98	2.24	2.16
ENSMUSG00000026526	*Fh1*	7.27	7.17	7.52	7.13
ENSMUSG00000026535	*Ifi202b*	1.81	1.05	0.56	0.7
ENSMUSG00000026542	*Apcs*	8.92	8.98	8.64	8.25
ENSMUSG00000026544	*Dusp23*	2.23	3.18	2.59	1.93
ENSMUSG00000026547	*Tagln2*	3.47	3.89	3.75	3.72
ENSMUSG00000026553	*Copa*	6.07	6.15	5.96	5.84
ENSMUSG00000026554	*Wdr42a*	5.22	5.56	5.28	4.98
ENSMUSG00000026558	*Uck2*	2.68	2.83	2.89	2.62

ENSMUSG00000026563	*Tada1l*	3.13	3.02	3.11	2.71
ENSMUSG00000026566	*Mpzl1*	1.45	1.43	0.88	0.94
ENSMUSG00000026568	*AK008044*	7.92	7.81	7.68	7.5
ENSMUSG00000026571	*NA*	4.49	4.56	4.04	4.04
ENSMUSG00000026574	*Dpt*	1.38	1.22	1.3	1.72
ENSMUSG00000026575	*Nme7*	2.2	1.28	2.09	1.88
ENSMUSG00000026576	*Atp1b1*	5.99	4.95	5.82	5.48
ENSMUSG00000026577	*Blzf1*	2.09	1.59	1.93	1.79
ENSMUSG00000026578	*4930455F23Ri*	1.95	1.66	2.25	1.21
ENSMUSG00000026579	*F5*	7.14	6.58	6.9	6.77
ENSMUSG00000026580	*Selp*	0.79	0.85	1.27	0.87
ENSMUSG00000026581	*Sell*	-0.32	-0.9	1.21	-1.69
ENSMUSG00000026584	*Scyl3*	3.48	3.16	3.18	2.84
ENSMUSG00000026585	*Kifap3*	2.06	1.6	2.01	1.53
ENSMUSG00000026589	*Sec16b*	5.34	5.22	4.94	4.5
ENSMUSG00000026594	*Ralgps2*	3.56	3.07	3.56	3.19
ENSMUSG00000026603	*Smyd2*	4.05	3.93	3.48	3.37
ENSMUSG00000026608	*Kctd3*	1.57	1.98	1.81	1.7
ENSMUSG00000026614	*Slc30a10*	4.75	4.54	3.96	3.68
ENSMUSG00000026615	*Eprs*	5.22	4.99	5.08	4.66
ENSMUSG00000026617	*Bpnt1*	5.5	5.28	5.52	5.28
ENSMUSG00000026618	*Iars2*	4.47	4.56	4.45	4.17
ENSMUSG00000026621	*Mosc1*	7.96	8.14	8.24	7.89
ENSMUSG00000026623	*Lpgat1*	5.5	4.97	5.23	4.76
ENSMUSG00000026626	*Ppp2r5a*	5.67	5.37	5.59	5.12
ENSMUSG00000026632	*NA*	1.79	1.84	1.75	1.2
ENSMUSG00000026634	*Angel2*	2.69	2.62	3.07	2.7
ENSMUSG00000026638	*Irf6*	4.18	4.31	3.65	3.28
ENSMUSG00000026640	*Plxna2*	1.84	2	2.41	2.19
ENSMUSG00000026641	*Usf1*	2.46	2.81	2.56	2.86
ENSMUSG00000026643	*Nmt2*	3.05	2.6	3.06	2.34

ENSMUSG00000026655	*3110001A13Ri*	5.66	4.49	5.16	4.78
ENSMUSG00000026656	*Fcgr2b*	5.31	5.03	4.92	5.13
ENSMUSG00000026659	*Dusp12*	2.66	2.56	2.57	2.42
ENSMUSG00000026662	*Sephs1*	3.49	3.14	3.05	3.06
ENSMUSG00000026663	*Atf6*	4.15	3.89	3.95	3.67
ENSMUSG00000026664	*Phyh*	10.06	9.68	10.06	9.69
ENSMUSG00000026667	*Uhmk1*	3.56	2.88	3.1	2.9
ENSMUSG00000026669	*Mcm10*	1.86	2.55	2.66	2.93
ENSMUSG00000026670	*Uap1*	5.11	4.8	4.77	4.58
ENSMUSG00000026672	*Optn*	5.49	5.49	5.59	5.3
ENSMUSG00000026675	*Hsd17b7*	3.56	3.53	3.31	3.33
ENSMUSG00000026678	*Rgs5*	5.24	4.19	4.82	4.26
ENSMUSG00000026687	*Aldh9a1*	7.96	7.6	7.6	7.04
ENSMUSG00000026688	*Mgst3*	5.35	5.63	5.63	6.03
ENSMUSG00000026691	*Fmo3*	8.24	8.46	8.07	7.53
ENSMUSG00000026692	*Fmo4*	3.06	1.66	3	2.52
ENSMUSG00000026694	*5630401D24Ri*	1.83	2.73	2.15	2.13
ENSMUSG00000026696	*Vamp4*	2.84	1.82	2.09	1.87
ENSMUSG00000026698	*Pigc*	2.64	2.24	2.62	2.48
ENSMUSG00000026701	*Prdx6*	8.86	8.46	8.57	8.24
ENSMUSG00000026705	*Klhl20*	1.96	1.5	1.85	1.14
ENSMUSG00000026709	*Dars2*	2.92	2.73	2.9	2.14
ENSMUSG00000026712	*Mrc1*	4.39	3.68	3.84	3.64
ENSMUSG00000026715	*Serpinc1*	10.34	10.44	10.45	10.37
ENSMUSG00000026718	*Stam*	3.12	2.27	2.64	2.19
ENSMUSG00000026721	*Rabgap1l*	2.57	1.42	2.07	1.39
ENSMUSG00000026723	*Trdmt1*	1.05	-0.11	0.63	0.23
ENSMUSG00000026727	*Rsu1*	4.69	4.35	4.53	4.27
ENSMUSG00000026728	*Vim*	3.68	3.14	3.51	3.39
ENSMUSG00000026729	*NA*	1.76	2	1.98	1.47
ENSMUSG00000026730	*Pter*	6.38	5.94	5.67	5.57

ENSMUSG00000026737	*Pip4k2a*	1.94	1.49	1.71	0.95
ENSMUSG00000026739	*Bmi1*	3.2	2.41	2.75	2.27
ENSMUSG00000026740	*Dnajc1*	4.34	3.5	4.05	3.69
ENSMUSG00000026743	*Mllt10*	3.3	3.13	3.25	2.91
ENSMUSG00000026749	*Nek6*	4.19	4.6	4.33	4.21
ENSMUSG00000026750	*Psmb7*	7.2	6.18	6.56	6.22
ENSMUSG00000026753	*Ppp6c*	5.19	4.45	4.97	4.7
ENSMUSG00000026754	*Golga1*	2.59	2.32	2.26	1.9
ENSMUSG00000026755	*Arpc5l*	4.72	4.28	4.7	4.36
ENSMUSG00000026761	*Orc4l*	3.04	1.58	2.59	1.85
ENSMUSG00000026766	*2010311D03Ri*	5.71	5.46	5.64	5.22
ENSMUSG00000026767	*2310047O13Ri*	4.07	2.86	3.92	3.58
ENSMUSG00000026771	*4921517N04Ri*	1.86	1.15	1.02	0.66
ENSMUSG00000026773	*Pfkfb3*	1.69	1.53	2.01	3.23
ENSMUSG00000026775	*Yme1l1*	5.52	4.39	5.12	4.47
ENSMUSG00000026781	*Acbd5*	5.97	4.96	5.62	5.39
ENSMUSG00000026784	*Pdss1*	1.51	1.04	1.4	0.61
ENSMUSG00000026786	*Apbb1ip*	0.66	-0.14	1.11	-0.05
ENSMUSG00000026788	*Zbtb43*	3.36	3.12	2.89	2.59
ENSMUSG00000026790	*Odf2*	1.49	1.72	2	1.32
ENSMUSG00000026791	*Slc2a8*	3.36	4.03	3.29	3.58
ENSMUSG00000026792	*Lrsam1*	1.95	2.18	2.52	2.03
ENSMUSG00000026796	*9130404D14Ri*	1.51	2.3	2.06	1.76
ENSMUSG00000026798	*Coq4*	3.69	4	3.55	3.3
ENSMUSG00000026799	*Med27*	2.53	2.71	2.87	2.76
ENSMUSG00000026803	*Ttf1*	2.08	1.92	1.95	1.88
ENSMUSG00000026806	*Ddx31*	1.28	1.87	1.3	1.33
ENSMUSG00000026810	*Dpm2*	4.09	4.49	4.18	4.35
ENSMUSG00000026811	*St6galnac6*	4.56	4.35	4.28	3.97
ENSMUSG00000026812	*Tsc1*	3	2.55	2.89	2.45
ENSMUSG00000026814	*Eng*	5.28	6.14	5.57	5.58

ENSMUSG00000026816	*Gtf3c5*	2.49	2.84	2.64	2.39
ENSMUSG00000026819	*Slc25a25*	6.19	6.3	6.02	6.06
ENSMUSG00000026820	*Ptges2*	3.85	4.74	4.38	4.24
ENSMUSG00000026822	*Lcn2*	6.04	5.54	6.25	4.66
ENSMUSG00000026827	*Gpd2*	3.77	2.46	3.43	2.83
ENSMUSG00000026836	*Acvr1*	2.46	2.68	2.25	2.32
ENSMUSG00000026839	*Upp2*	7.87	5.95	7.36	6.74
ENSMUSG00000026842	*Abl1*	2.29	2.84	2.67	2.49
ENSMUSG00000026843	*Fubp3*	2.68	2.45	2.54	2.57
ENSMUSG00000026848	*Tor1b*	3.22	3.68	3.78	3.64
ENSMUSG00000026849	*Tor1a*	4.38	4.97	4.95	4.95
ENSMUSG00000026851	*BC005624*	3.3	3.4	3.46	3.03
ENSMUSG00000026853	*Crat*	4.76	4.87	4.45	4.07
ENSMUSG00000026854	*Usp20*	0.79	1.38	1.33	1.28
ENSMUSG00000026856	*Dolpp1*	3.16	3.59	3.51	3.02
ENSMUSG00000026857	*2610205E22Ri*	1.66	2.91	2.69	2.19
ENSMUSG00000026858	*5730472N09Ri*	4.18	4.35	4.86	4.28
ENSMUSG00000026860	*Sh3glb2*	3.38	4.16	3.67	3.34
ENSMUSG00000026864	*Hspa5*	8.11	8.74	7.19	7.59
ENSMUSG00000026866	*Kynu*	6.71	5.86	6.7	6.09
ENSMUSG00000026867	*Gapvd1*	3.59	3.65	3.63	3.19
ENSMUSG00000026869	*Psmd5*	4.98	4.68	4.73	4.41
ENSMUSG00000026870	*D730039F16R*	4.69	4.74	4.56	4.32
ENSMUSG00000026872	*Zeb2*	1.61	0.59	1.28	0.66
ENSMUSG00000026874	*Hc*	7.57	7.46	7.38	7.37
ENSMUSG00000026878	*Rab14*	6.05	5.39	5.7	5.39
ENSMUSG00000026879	*Gsn*	2.55	3.37	3.31	3.06
ENSMUSG00000026880	*Stom*	5.74	5.13	5.44	5.26
ENSMUSG00000026883	*Dab2ip*	1.65	2.37	1.87	1.68
ENSMUSG00000026887	*Mrrf*	3.21	3.21	3.16	3.11
ENSMUSG00000026888	*Grb14*	5.24	4.82	5.07	4.7

ENSMUSG00000026889	*Rbm18*	3.87	3.11	3.34	3.28
ENSMUSG00000026890	*Lhx6*	1.3	0.82	1.83	0.15
ENSMUSG00000026893	*Gca*	1.01	0.09	1.43	0.63
ENSMUSG00000026895	*Ndufa8*	6.59	6.81	6.98	6.74
ENSMUSG00000026896	*Ifih1*	3.71	2.35	3.13	2.74
ENSMUSG00000026914	*Psmd14*	5.29	5.01	4.85	4.52
ENSMUSG00000026915	*Strbp*	3.91	3.14	3.62	2.85
ENSMUSG00000026917	*Wdr5*	4.25	4.09	4.2	4.06
ENSMUSG00000026918	*AK165817*	3.63	3.75	3.72	3.58
ENSMUSG00000026921	*Egfl7*	3.14	3.85	3.07	3.35
ENSMUSG00000026922	*Agpat2*	7.4	7.92	7.49	7.19
ENSMUSG00000026923	*Notch1*	1.86	3.29	1.95	2
ENSMUSG00000026924	*Sec16a*	4.21	4.37	4.28	4.11
ENSMUSG00000026925	*Inpp5e*	1.75	1.99	1.83	1.42
ENSMUSG00000026926	*Pmpca*	4.92	4.73	4.78	4.39
ENSMUSG00000026927	*Sdccag3*	4.44	4.67	4.45	4.33
ENSMUSG00000026932	*Btbd14a*	3.06	2.99	2.99	2.77
ENSMUSG00000026933	*NA*	0.95	1.18	1.01	1.03
ENSMUSG00000026938	*Fcna*	4.76	5.25	4.75	4.61
ENSMUSG00000026939	*Tmem141*	3.82	4.22	4.11	3.96
ENSMUSG00000026942	*Traf2*	2.32	3.18	2.51	2.6
ENSMUSG00000026944	*Abca2*	3.8	4.49	3.92	3.46
ENSMUSG00000026946	*Nmi*	4.05	2.9	3.77	3.85
ENSMUSG00000026958	*Dpp7*	3.45	4.04	3.79	3.91
ENSMUSG00000026960	*Arl6ip6*	2.68	1.92	3.18	2.51
ENSMUSG00000026965	*Anapc2*	4.2	4.73	4.27	4.08
ENSMUSG00000026966	*Ssna1*	3.57	3.98	3.67	3.8
ENSMUSG00000026970	*Rbms1*	3.8	2.95	3.33	3.11
ENSMUSG00000026974	*Zmynd19*	1.29	2.24	1.6	1.5
ENSMUSG00000026975	*Wdr85*	1.14	1.69	1.23	0.84
ENSMUSG00000026977	*7-Mar*	3.03	2.54	2.74	1.86

ENSMUSG00000026981	*Il1rn*	2.4	0.48	2.04	1.31
ENSMUSG00000026986	*Hnmt*	4.05	3.13	4.19	3.09
ENSMUSG00000026987	*Baz2b*	1.29	0.63	1.21	0.93
ENSMUSG00000026988	*Wdsub1*	1.25	1.45	1.1	0.75
ENSMUSG00000026991	*Pkp4*	4.62	5.12	4.94	4.85
ENSMUSG00000027001	*Dusp19*	2.92	1.64	2.57	1.88
ENSMUSG00000027002	*Nckap1*	5.93	5.38	5.65	5.04
ENSMUSG00000027006	*Dnajc10*	3.33	2.88	3.14	2.56
ENSMUSG00000027007	*Ssfa2*	4.9	4.62	4.8	4.54
ENSMUSG00000027010	*Slc25a12*	3.41	3.06	3.63	3.16
ENSMUSG00000027011	*Ube2e3*	4.33	3.5	4.09	3.56
ENSMUSG00000027012	*Dync1i2*	5.17	4.48	4.79	4.37
ENSMUSG00000027016	*Zfp533*	2.29	2.21	3.06	2.56
ENSMUSG00000027018	*Hat1*	2.54	2.14	2.53	1.8
ENSMUSG00000027030	*Stk39*	0.91	-0.17	1.53	0.23
ENSMUSG00000027035	*Lass6*	3.19	2.35	2.67	2.24
ENSMUSG00000027048	*Abcb11*	7.93	7.55	7.7	7.32
ENSMUSG00000027067	*Ssrp1*	4.37	4.96	4.55	4.58
ENSMUSG00000027074	*Slc43a3*	4.46	4.57	4.24	4.05
ENSMUSG00000027075	*Slc43a1*	2.96	3.22	3.21	2.77
ENSMUSG00000027076	*Timm10*	3.45	4.53	4.45	4.26
ENSMUSG00000027078	*Ube2l6*	5.75	5.73	5.59	5.53
ENSMUSG00000027079	*Clp1*	3.52	3.43	3.11	3.16
ENSMUSG00000027080	*Med19*	3.93	3.1	3.31	3.21
ENSMUSG00000027082	*Tfpi*	1.13	0.76	0.27	0.32
ENSMUSG00000027086	*Fastkd1*	3.87	3.11	4.07	3.42
ENSMUSG00000027087	*Itgav*	2.03	2.1	2.1	2.08
ENSMUSG00000027088	*Phospho2*	4.48	3.23	3.89	3.66
ENSMUSG00000027091	*Zc3h15*	4.45	3.92	3.93	3.63
ENSMUSG00000027099	*Mtx2*	4.23	3.68	4.21	3.63
ENSMUSG00000027104	*Atf2*	3.83	3.17	3.55	3.06

ENSMUSG00000027108	*Ola1*	4.9	3.94	4.38	3.88
ENSMUSG00000027109	*Sp3*	4.15	3.02	3.74	3.13
ENSMUSG00000027122	*2700007P21Ri*	1.91	0.98	1.66	1.39
ENSMUSG00000027130	*Slc12a6*	2.02	1.33	1.99	1.42
ENSMUSG00000027131	*Tmem85*	5.47	5.42	5.66	5.44
ENSMUSG00000027132	*2410042D21Ri*	1.55	0.31	1.05	0.59
ENSMUSG00000027133	*Nola3*	5.68	5.79	6.17	6.32
ENSMUSG00000027162	*Lin7c*	4.05	3.2	3.51	3.35
ENSMUSG00000027163	*Commd9*	3.34	3.48	3.5	3.54
ENSMUSG00000027164	*Traf6*	2.97	2.21	2.73	2.38
ENSMUSG00000027165	*B230118H07Ri*	3.63	3.52	3.67	2.87
ENSMUSG00000027166	*Dph4*	2.82	2.24	2.74	2.14
ENSMUSG00000027167	*Elp4*	2.98	2.81	2.85	2.06
ENSMUSG00000027170	*Eif3m*	3.22	3.07	3.03	2.74
ENSMUSG00000027173	*Depdc7*	4.12	3.9	4.18	4.07
ENSMUSG00000027175	*BC057381*	0.94	0.23	1.14	0.31
ENSMUSG00000027176	*Cstf3*	2.12	1.45	1.77	1.46
ENSMUSG00000027177	*Hipk3*	3.96	3.87	3.94	3.78
ENSMUSG00000027180	*Fbxo3*	4.48	3.88	4.29	4
ENSMUSG00000027184	*Caprin1*	6.55	6.07	6.22	5.61
ENSMUSG00000027185	*Nat10*	2.08	2.74	2.49	2.39
ENSMUSG00000027187	*Cat*	10.43	10.37	10.61	10.29
ENSMUSG00000027189	*Trim44*	4.18	3.92	3.94	3.68
ENSMUSG00000027193	*Api5*	4.92	4.41	4.66	4.2
ENSMUSG00000027194	*Ttc17*	3.47	3.46	3.6	3.42
ENSMUSG00000027195	*Hsd17b12*	6.64	6.08	6.15	5.59
ENSMUSG00000027198	*Ext2*	3.79	4.22	3.84	3.77
ENSMUSG00000027199	*Gatm*	3.19	2.58	2.61	2.02
ENSMUSG00000027200	*Sema6d*	2.13	1.79	1.47	1.2
ENSMUSG00000027203	*Dut*	2.49	2.49	2.55	2.04
ENSMUSG00000027206	*Cops2*	5.17	4.11	4.67	4.31

ENSMUSG00000027207	*Galk2*	3.63	3.37	3.49	3.16
ENSMUSG00000027215	*Cd82*	5.48	5.69	5.5	5.33
ENSMUSG00000027222	*Pex16*	5.89	5.93	5.97	5.81
ENSMUSG00000027227	*Sord*	7.97	8.63	8.11	8.51
ENSMUSG00000027243	*D230010M03R*	3.03	2.83	2.87	2.52
ENSMUSG00000027244	*D2Ertd391e*	4.6	4.91	4.55	4.36
ENSMUSG00000027245	*2310003F16Ri*	3.42	3.37	3.5	3.82
ENSMUSG00000027246	*Ell3*	0.61	-0.3	1.76	0.45
ENSMUSG00000027247	*Arhgap1*	2.16	2.49	2.16	1.88
ENSMUSG00000027248	*Pdia3*	8.62	8.16	7.9	7.7
ENSMUSG00000027249	*F2*	9.67	10.23	9.88	9.89
ENSMUSG00000027253	*Lrp4*	1.6	2.06	1.78	2.09
ENSMUSG00000027255	*Zfp289*	4.93	5.42	5.05	4.97
ENSMUSG00000027257	*Pacsin3*	4.34	4.92	4.41	4.36
ENSMUSG00000027259	*Adal*	3.75	2.64	3.41	2.68
ENSMUSG00000027261	*Hao1*	7.37	6.61	7.31	6.88
ENSMUSG00000027263	*Tubgcp4*	3.6	3.46	3.28	3.28
ENSMUSG00000027272	*Ubr1*	2.35	1.6	2.14	1.4
ENSMUSG00000027274	*Mkks*	3.8	3.76	3.96	3.55
ENSMUSG00000027282	*Mtch2*	5.79	5.35	5.47	5.05
ENSMUSG00000027285	*Cep27*	2.75	2.01	2.33	1.89
ENSMUSG00000027286	*Lrrc57*	2.83	2.28	2.8	2.52
ENSMUSG00000027287	*Snap23*	4.81	3.84	4.3	3.67
ENSMUSG00000027288	*Zfp106*	4.31	3.94	4.25	3.63
ENSMUSG00000027291	*Vps39*	2.54	3	3.04	2.81
ENSMUSG00000027293	*Ehd4*	1.31	1.77	1.36	1.01
ENSMUSG00000027300	*Ubox5*	1.93	2.37	1.87	1.29
ENSMUSG00000027303	*Ptpra*	4.03	3.79	3.77	3.36
ENSMUSG00000027304	*NA*	4.26	4.06	3.95	3.72
ENSMUSG00000027305	*Ndufaf1*	5.1	4.61	4.85	4.33
ENSMUSG00000027309	*4930402H24Ri*	1.88	2.14	2	2.06

ENSMUSG00000027312	*Atrn*	3.66	3.42	3.67	3.17
ENSMUSG00000027313	*Chac1*	2.05	1.95	1.32	2.14
ENSMUSG00000027324	*Rpusd2*	1.45	1.16	0.8	0.84
ENSMUSG00000027327	*1700037H04Ri*	2.14	2.92	2.15	2.41
ENSMUSG00000027332	*Ivd*	7.08	7.34	6.95	6.94
ENSMUSG00000027340	*svct2*	2.34	1.94	2.38	1.91
ENSMUSG00000027341	*5730494N06Ri*	2.39	1.2	2.13	1.38
ENSMUSG00000027342	*Pcna*	0.99	1.95	1.1	1.16
ENSMUSG00000027346	*Prei4*	5.02	3.01	4.72	3.66
ENSMUSG00000027349	*2610510H03Ri*	3.13	2.64	3.03	2.98
ENSMUSG00000027351	*Spred1*	2.92	1.74	1.98	1.77
ENSMUSG00000027357	*Crls1*	5.84	4.82	5.06	4.39
ENSMUSG00000027358	*Bmp2*	3.14	3.57	3.1	3.02
ENSMUSG00000027359	*Slc27a2*	9.13	8.69	9.02	9.01
ENSMUSG00000027360	*Hdc*	1.21	1.27	0.73	0.91
ENSMUSG00000027363	*mUBPY*	4.6	4.1	4.47	4.12
ENSMUSG00000027365	*Trpm7*	3.57	2.45	3.4	2.7
ENSMUSG00000027366	*2010106G01Ri*	5.59	5.15	5.18	4.48
ENSMUSG00000027367	*Stard7*	5.41	5.52	5.56	5.12
ENSMUSG00000027371	*Fahd2a*	3.5	3.94	3.56	3.51
ENSMUSG00000027374	*MRPS5*	3.49	3.52	4.03	3.52
ENSMUSG00000027376	*Prom2*	1.71	#NAME?	1.84	#NAME?
ENSMUSG00000027378	*Nphp1*	1.82	2.04	1.51	1.02
ENSMUSG00000027381	*Bcl2l11*	-0.01	0.62	1.32	0.89
ENSMUSG00000027384	*2310003L22Ri*	2.47	1.49	2.3	1.8
ENSMUSG00000027387	*Zc3h8*	0.58	0.91	1.31	0.58
ENSMUSG00000027394	*Ttl*	1.45	1.45	1.41	1.04
ENSMUSG00000027395	*Rpo1-2*	2.39	3.12	2.5	2.34
ENSMUSG00000027397	*Slc20a1*	3.05	3.32	3.71	3.83
ENSMUSG00000027404	*Snrpb*	4.97	5.79	5.4	5.32
ENSMUSG00000027405	*Nol5a*	3.02	3.75	2.9	2.96

ENSMUSG00000027406	*Idh3b*	7.29	7.42	7.43	7
ENSMUSG00000027411	*Vps16*	2.82	3.27	2.79	2.71
ENSMUSG00000027412	*Lpin3*	0.6	1.09	1.11	0.58
ENSMUSG00000027422	*Rrbp1*	6.07	6.33	5.68	5.95
ENSMUSG00000027423	*Snx5*	4.9	4.24	4.72	4.2
ENSMUSG00000027424	*8430406I07Rik*	1.94	2.24	2.05	1.72
ENSMUSG00000027425	*Csrp2bp*	3.22	3.63	3.3	3.23
ENSMUSG00000027427	*Polr3f*	2.27	1.61	1.88	1.53
ENSMUSG00000027428	*Rbbp9*	3.99	3.69	4.01	3.41
ENSMUSG00000027429	*Sec23b*	4.06	4.72	4.07	4.11
ENSMUSG00000027430	*Dtd1*	3.53	3.31	3.34	3.11
ENSMUSG00000027433	*Xrn2*	3.9	3.61	3.87	3.41
ENSMUSG00000027435	*Cd93*	1.83	1.15	1.13	1.13
ENSMUSG00000027439	*Gzf1*	4.92	4.47	4.45	3.97
ENSMUSG00000027447	*Cst3*	7.04	7.21	7.28	7.1
ENSMUSG00000027454	*NA*	1.56	1.62	1.44	0.97
ENSMUSG00000027455	*Nsfl1c*	3.35	3.88	3.36	3.14
ENSMUSG00000027465	*Tbc1d20*	4.53	4.65	4.65	4.4
ENSMUSG00000027466	*Rbck1*	4.29	5.02	4.41	4.37
ENSMUSG00000027472	*Pdrg1*	3.8	4.3	4.42	4.07
ENSMUSG00000027475	*Kif3b*	2.1	2	2.2	1.89
ENSMUSG00000027479	*Mapre1*	3.27	3.19	2.9	2.74
ENSMUSG00000027487	*Cdk5rap1*	2.21	2.33	2.18	1.61
ENSMUSG00000027488	*Snta1*	3.24	4.11	3.77	3.55
ENSMUSG00000027495	*2010011I20Rik*	6.03	6.07	5.88	5.96
ENSMUSG00000027498	*Cstf1*	3.53	3.39	3.47	3.22
ENSMUSG00000027502	*2410001C21Ri*	4.54	4.94	4.87	4.75
ENSMUSG00000027506	*Tpd52*	1.38	0.92	1.34	0.68
ENSMUSG00000027509	*Rae1*	3.1	3.33	3.12	3.32
ENSMUSG00000027510	*Rbm38*	0.31	2.01	2.5	2.25
ENSMUSG00000027513	*Pck1*	9.77	9.66	10.26	9.92

ENSMUSG00000027514	*Zbp1*	1.94	1.63	0.92	0.9
ENSMUSG00000027519	*Rab22a*	4.25	3.85	4.03	3.78
ENSMUSG00000027522	*Stx16*	3.04	2.76	2.79	2.55
ENSMUSG00000027523	*Gnas*	5.91	6.08	5.71	5.57
ENSMUSG00000027531	*Impa1*	4.94	4.67	4.77	4.28
ENSMUSG00000027534	*Snx16*	1.97	0.76	1.95	1.74
ENSMUSG00000027540	*Ptpn1*	3.24	3.51	3.18	3.22
ENSMUSG00000027546	*Atp9a*	4.68	5.33	4.56	4.66
ENSMUSG00000027551	*Zfp64*	1.44	2.16	1.58	1.42
ENSMUSG00000027552	*E2f5*	3.09	2.11	2.54	2.48
ENSMUSG00000027556	*Car1*	2.8	1.77	2.67	2
ENSMUSG00000027559	*Car3*	10.41	9.5	9.65	9.31
ENSMUSG00000027562	*Car2*	3.68	2.93	3.91	2.57
ENSMUSG00000027566	*Psma7*	6.94	6.52	6.42	6.26
ENSMUSG00000027569	*1600027N09Ri*	1.99	1.65	1.47	1.17
ENSMUSG00000027573	*2310003C23Ri*	4.04	3.82	3.95	3.67
ENSMUSG00000027575	*Arfgap1*	2.95	3.6	3.04	2.77
ENSMUSG00000027580	*BC006779*	3.67	3.91	3.41	3.36
ENSMUSG00000027582	*Zgpat*	2.53	2.71	2.47	2.21
ENSMUSG00000027589	*Pcmtd2*	4.44	3.31	4.3	3.8
ENSMUSG00000027593	*Raly*	5.06	5.75	5.55	5.47
ENSMUSG00000027597	*Ahcy*	3.81	3.38	3.77	3.01
ENSMUSG00000027598	*Itch*	5.28	4.4	4.83	4.28
ENSMUSG00000027599	*Armc1*	4.69	4.02	4.28	3.95
ENSMUSG00000027601	*Mtfr1*	5.41	5.08	5.43	4.98
ENSMUSG00000027602	*Map1lc3a*	5.75	6.19	5.78	5.97
ENSMUSG00000027605	*Acss2*	6.27	5.98	5.57	4.98
ENSMUSG00000027610	*Gss*	5.1	5.49	5.4	5.39
ENSMUSG00000027613	*Eif6*	4.53	5.1	4.88	4.94
ENSMUSG00000027615	*Hps3*	1.82	1.02	1.59	0.72
ENSMUSG00000027618	*Nfs1*	5.03	5.27	4.92	4.62

ENSMUSG00000027620	*Rbm39*	5.59	4.92	5.44	5
ENSMUSG00000027628	*0610011L14Ri*	3.82	4.21	3.91	3.86
ENSMUSG00000027630	*Tbl1xr1*	3.25	2.67	2.67	2.14
ENSMUSG00000027634	*Ndrg3*	2.7	2.53	2.62	2.4
ENSMUSG00000027636	*Sla2*	5.1	4.28	4.88	4.72
ENSMUSG00000027637	*1110008F13Ri*	7.4	6.47	7.08	6.87
ENSMUSG00000027639	*Samhd1*	2.66	2.06	2.32	1.99
ENSMUSG00000027642	*Rpn2*	6.59	6.67	6.44	6.34
ENSMUSG00000027649	*Ctnnbl1*	2.97	3.02	3.06	2.97
ENSMUSG00000027650	*2610036D13Ri*	2.37	2.69	2.67	2.5
ENSMUSG00000027651	*2610304G08Ri*	3.59	3.61	3.45	3.36
ENSMUSG00000027652	*B230339M05R*	2.45	1.91	2.25	1.92
ENSMUSG00000027655	*Dhx35*	1.66	1.76	1.81	1.08
ENSMUSG00000027660	*Skil*	2.43	2.25	1.23	1.21
ENSMUSG00000027663	*Zmat3*	1.18	1.03	1.49	1.03
ENSMUSG00000027665	*Pik3ca*	3.89	3.14	3.62	3.18
ENSMUSG00000027667	*Zfp639*	3.3	2.94	3.53	3
ENSMUSG00000027668	*Mfn1*	4.57	4.38	4.75	4.37
ENSMUSG00000027671	*Actl6a*	3.32	3.47	3.42	3.33
ENSMUSG00000027673	*Ndufb5*	7.07	6.41	6.73	6.1
ENSMUSG00000027677	*mKIAA1980*	1.7	0.51	1.05	0.58
ENSMUSG00000027678	*Ncoa3*	2.57	2.75	2.67	2.46
ENSMUSG00000027679	*Dnajc19*	2.68	2.15	2.63	2.19
ENSMUSG00000027680	*Fxr1h*	5.08	3.79	4.5	4.14
ENSMUSG00000027690	*Slc2a2*	7.34	6.63	7.7	7.27
ENSMUSG00000027695	*Pld1*	1.92	1.03	1.33	0.29
ENSMUSG00000027698	*Aadacl1*	3.82	3.24	3.7	2.92
ENSMUSG00000027706	*Tloc1*	7.26	6.42	6.67	6.36
ENSMUSG00000027708	*Dcun1d1*	3.35	2.15	2.8	2.37
ENSMUSG00000027709	*Mccc1*	5.1	5.03	5.44	4.88
ENSMUSG00000027710	*Acad9*	4.57	4.6	4.29	3.88

ENSMUSG00000027712	*Anxa5*	5.77	5.83	5.84	5.47
ENSMUSG00000027714	*Exosc9*	3.53	2.97	3.48	2.65
ENSMUSG00000027715	*Ccna2*	0.62	0.56	1.12	0.13
ENSMUSG00000027722	*Spata5*	1.42	0.96	1.2	1.01
ENSMUSG00000027739	*Rab33b*	2	1.78	2.07	1.62
ENSMUSG00000027742	*Cog6*	3.69	3.79	3.44	3.25
ENSMUSG00000027746	*Ufm1*	2.82	2.79	2.76	2.54
ENSMUSG00000027750	*Postn*	2.54	1.12	1.82	1.98
ENSMUSG00000027751	*D3Ertd300e*	2.42	2.16	2.51	1.92
ENSMUSG00000027752	*Exosc8*	3.21	2.68	3.14	2.43
ENSMUSG00000027761	*Aadac*	8.53	8.04	8.14	7.56
ENSMUSG00000027762	*Sucnr1*	3.9	3.5	3.46	1.92
ENSMUSG00000027763	*Mbnl1*	5.16	4.16	4.99	4.63
ENSMUSG00000027765	*P2ry1*	2.04	1.98	1.99	1.84
ENSMUSG00000027770	*Dhx36*	4.07	3.02	3.55	2.9
ENSMUSG00000027774	*Gfm1*	5.88	5.38	5.68	5.18
ENSMUSG00000027775	*Mfsd1*	5.81	5.15	5.53	5.35
ENSMUSG00000027778	*Ift80*	1.08	0.59	1.36	0.9
ENSMUSG00000027782	*Kpna4*	4.86	3.93	4.3	3.84
ENSMUSG00000027784	*Ppm1l*	2.24	1.92	1.9	1.77
ENSMUSG00000027787	*Nmd3*	4.6	3.68	4.4	3.79
ENSMUSG00000027792	*Bche*	6.41	4.71	5.51	4.86
ENSMUSG00000027796	*Smad9*	1.98	1.04	1.39	1.38
ENSMUSG00000027800	*Tm4sf1*	3.56	2.49	3.27	2.64
ENSMUSG00000027801	*Tm4sf4*	6.17	6.56	6.7	6.71
ENSMUSG00000027803	*Wwtr1*	2.74	1.96	2.81	2.22
ENSMUSG00000027804	*Ppid*	3.77	2.85	3.23	2.87
ENSMUSG00000027806	*Tsc22d2*	2.64	1.82	2.4	2.41
ENSMUSG00000027808	*D3Ucla1*	6.86	6.95	6.29	6.44
ENSMUSG00000027809	*Etfdh*	7.8	7.24	7.4	6.98
ENSMUSG00000027810	*Eif2a*	5.17	4.37	5.08	4.67

ENSMUSG00000027820	*Mme*	3.27	2.53	2.8	-0.46
ENSMUSG00000027822	*Slc33a1*	5.05	4.57	4.52	4.2
ENSMUSG00000027823	*Gmps*	4.6	3.9	4.11	3.91
ENSMUSG00000027828	*Ssr3*	6.6	6.01	6.2	5.81
ENSMUSG00000027829	*Ccnl1*	3.88	3.19	3.36	2.69
ENSMUSG00000027835	*Pdcd10*	2.12	-0.35	1.38	0.55
ENSMUSG00000027845	*Dclre1b*	1.09	0.85	0.74	1.05
ENSMUSG00000027848	*Olfml3*	1.43	1.49	1.7	1.15
ENSMUSG00000027852	*Nras*	3.05	3.36	2.68	2.21
ENSMUSG00000027854	*5730470L24Ri*	1.96	2.09	1.83	1.8
ENSMUSG00000027860	*Vangl1*	1.83	1.96	1.95	1.33
ENSMUSG00000027865	*Gdap2*	4.14	3.82	3.84	3.65
ENSMUSG00000027870	*Hao3*	6.12	5.32	5.63	4.75
ENSMUSG00000027875	*Hmgcs2*	10.57	10.21	10.67	10.37
ENSMUSG00000027878	*Notch2*	1.61	2.66	2.47	2.35
ENSMUSG00000027879	*Sec22b*	4.27	4.18	4.22	4.16
ENSMUSG00000027881	*Prpf38b*	4.18	4.1	4.07	3.71
ENSMUSG00000027882	*Stxbp3a*	3.61	2.57	3.55	2.81
ENSMUSG00000027883	*Gpsm2*	2.71	1.97	2.82	2.52
ENSMUSG00000027884	*Clcc1*	4.27	4.37	4.5	4.08
ENSMUSG00000027889	*Ampd2*	2.66	3.75	3.21	3.34
ENSMUSG00000027890	*Gstm4*	6.3	6.36	6.09	5.63
ENSMUSG00000027893	*Ahcyl1*	5.57	5.09	5.01	4.77
ENSMUSG00000027900	*Tmem77*	5.82	4.66	5.39	5.11
ENSMUSG00000027901	*Dennd2d*	1.24	0.8	1.68	0.96
ENSMUSG00000027905	*Ddx20*	2.99	2.52	2.7	2.36
ENSMUSG00000027931	*Npr1*	2.28	3.19	2.52	2.6
ENSMUSG00000027933	*Ints3*	3.31	3.73	3.57	3.18
ENSMUSG00000027935	*Rab13*	1.78	1.77	1.12	1.66
ENSMUSG00000027936	*Crtc2*	3.6	4.22	4.16	4
ENSMUSG00000027937	*Jtb*	5.41	5.3	5.1	4.89

ENSMUSG00000027940	*Tpm3*	3.41	3.35	2.92	3.25
ENSMUSG00000027942	*4933434E20Ri*	3.59	3.55	3.41	3.43
ENSMUSG00000027944	*Hax1*	3.43	3.58	3.74	3.51
ENSMUSG00000027947	*Il6ra*	5.42	5.72	5.54	5.52
ENSMUSG00000027951	*Adar*	3.03	2.69	2.64	3
ENSMUSG00000027952	*Pmvk*	4.81	5.63	4.6	4.66
ENSMUSG00000027953	*Rag1ap1*	3.4	3.42	3.56	3.15
ENSMUSG00000027954	*Efna1*	3.64	4.49	4.13	3.8
ENSMUSG00000027956	*Tmem144*	1.75	1.29	1.72	0.94
ENSMUSG00000027957	*Slc35a3*	4.72	3.74	4.15	3.68
ENSMUSG00000027958	*Hiat1*	4.5	4.05	4.15	3.66
ENSMUSG00000027962	*Vcam1*	3.55	2.29	3.41	1.89
ENSMUSG00000027963	*Extl2*	2.05	1.81	2.29	1.77
ENSMUSG00000027968	*Larp7*	2.25	2.24	2.32	1.73
ENSMUSG00000027981	*Amy1*	2.39	0.88	2.22	1.25
ENSMUSG00000027984	*Hadh*	8.23	8.38	8.22	7.88
ENSMUSG00000027993	*Trim2*	2.83	1.78	2.51	1.53
ENSMUSG00000027997	*Casp6*	4.84	4.64	4.89	4.44
ENSMUSG00000027998	*Plrg1*	4.32	4.19	3.96	3.79
ENSMUSG00000027999	*Pla2g12a*	3.75	4.36	3.8	3.97
ENSMUSG00000028001	*Fga*	10.87	11.22	10.93	10.83
ENSMUSG00000028003	*Lrat*	2.44	1.29	2.06	1.37
ENSMUSG00000028005	*Gucy1b3*	1.54	1.03	1.13	0.93
ENSMUSG00000028007	*Snx7*	3.46	3.3	3.15	2.65
ENSMUSG00000028008	*Accn5*	4	3.64	3.64	4.05
ENSMUSG00000028010	*Nola1*	2.15	3.14	2.38	2.8
ENSMUSG00000028011	*Tdo2*	10.54	9.52	10.27	9.81
ENSMUSG00000028013	*Ppa2*	4.99	5.11	5.18	4.6
ENSMUSG00000028015	*Ctso*	4.82	4.37	4.59	3.75
ENSMUSG00000028016	*Ints12*	2.92	2.33	2.68	2.39
ENSMUSG00000028018	*Gstcd*	1.47	0.31	0.66	0.47

ENSMUSG00000028019	*Pdgfc*	1.07	0.82	0.46	-0.14
ENSMUSG00000028024	*Enpep*	5.3	4.78	4.71	4.54
ENSMUSG00000028029	*Scye1*	4.86	4.61	4.54	4.56
ENSMUSG00000028030	*A630047E20Ri*	1.3	0.25	0.56	0.83
ENSMUSG00000028032	*Papss1*	2.3	3.01	1.66	2.07
ENSMUSG00000028034	*Fubp1*	2.47	2.51	2.78	2.41
ENSMUSG00000028035	*Dnajb4*	4.38	3.41	4.3	4.38
ENSMUSG00000028037	*Ifi44*	1.73	0	0.6	1.26
ENSMUSG00000028041	*Adam15*	-0.07	1.54	1.12	0.79
ENSMUSG00000028042	*Zbtb7b*	4.47	5.21	4.28	4.31
ENSMUSG00000028048	*Gba*	3.93	4.49	4.25	4.23
ENSMUSG00000028049	*Scamp3*	5.27	5.24	5.35	5.28
ENSMUSG00000028051	*Hcn3*	4.64	3.74	4.58	4.75
ENSMUSG00000028053	*Ash1l*	3.02	2.59	2.72	2.5
ENSMUSG00000028057	*Rit1*	3.39	3.46	3.28	2.96
ENSMUSG00000028060	*2810403A07Ri*	3.37	3.77	3.81	3.71
ENSMUSG00000028062	*Mapbpip*	5.91	6.4	6.38	6.24
ENSMUSG00000028063	*Lmna*	3.07	4.38	3.81	3.96
ENSMUSG00000028064	*Sema4a*	5.42	5.76	5.48	5.27
ENSMUSG00000028066	*Pmf1*	4.13	4.46	4.49	4.09
ENSMUSG00000028069	*Gpatch4*	2.81	4.02	2.87	2.83
ENSMUSG00000028070	*Apoa1bp*	5.91	6.28	6.29	5.97
ENSMUSG00000028073	*3110045G13Ri*	1.78	2.58	2.08	1.67
ENSMUSG00000028076	*Cd1d1*	7.33	6.5	6.74	6.32
ENSMUSG00000028080	*Lrba*	2.25	1.85	2.04	1.48
ENSMUSG00000028081	*Rps3a*	2.89	2.52	2.54	0.61
ENSMUSG00000028082	*Sh3d19*	4.73	4.24	4.54	4.39
ENSMUSG00000028085	*Pet112l*	4.67	4.18	4.53	4
ENSMUSG00000028086	*Fbxw6*	1.45	1.44	1.32	1.15
ENSMUSG00000028088	*Fmo5*	8.32	7.87	8.56	7.73
ENSMUSG00000028089	*Chd1l*	2.65	2.75	2.35	1.95

ENSMUSG00000028093	*Acp6*	4.78	4.76	4.73	4.61
ENSMUSG00000028096	*Gpr89*	4.57	4.97	4.44	4.45
ENSMUSG00000028098	*Zfp364*	5.04	4.27	4.62	4.51
ENSMUSG00000028099	*NA*	3.97	4.16	4.27	4
ENSMUSG00000028101	*Pias3*	1.56	1.94	1.87	1.19
ENSMUSG00000028104	*Polr3gl*	3.34	3.06	3.09	2.74
ENSMUSG00000028106	*4930535B03Ri*	2.29	2.25	2.46	2.3
ENSMUSG00000028107	*Tars2*	3.99	4.31	4.06	3.81
ENSMUSG00000028108	*Ecm1*	6.5	7.06	6.79	6.78
ENSMUSG00000028114	*mKIAA1627*	3.07	2.58	2.87	2.23
ENSMUSG00000028121	*Bcar3*	3.55	4.77	4.27	4.14
ENSMUSG00000028124	*Gclm*	6.83	6.96	6.82	6.74
ENSMUSG00000028126	*Pip5k1a*	2.27	2.42	2.46	2.52
ENSMUSG00000028127	*Abcd3*	7.73	6.69	7.12	6.42
ENSMUSG00000028128	*F3*	1.33	0.13	1.2	0.12
ENSMUSG00000028132	*Tmem56*	6.86	5.89	6.17	5.44
ENSMUSG00000028133	*Rwdd3*	1.09	0.89	0.45	-0.03
ENSMUSG00000028134	*Ptbp2*	1.71	1.39	1.64	1.18
ENSMUSG00000028136	*Snx27*	3.44	3.33	3.27	3
ENSMUSG00000028138	*Adh5*	8.04	7.68	7.85	7.48
ENSMUSG00000028140	*Mrpl9*	4.78	4.46	5.06	4.57
ENSMUSG00000028145	*Them4*	4.27	3.32	4.22	3.77
ENSMUSG00000028149	*Rap1gds1*	3.8	3.61	3.78	3.55
ENSMUSG00000028150	*Rorc*	4.16	4.1	4.41	4.18
ENSMUSG00000028156	*Eif4e*	3.25	2.87	3.18	2.71
ENSMUSG00000028158	*Mttp*	7.12	6.76	7.23	7.01
ENSMUSG00000028161	*Ppp3ca*	3.82	3.58	4.03	3.84
ENSMUSG00000028163	*Nfkb1*	3.34	3.34	3.42	3.03
ENSMUSG00000028164	*Manba*	2.51	2.15	2.71	2.1
ENSMUSG00000028165	*Cisd2*	3.48	2.49	3.12	2.68
ENSMUSG00000028167	*Bdh2*	3.75	3.5	3.79	3.52

ENSMUSG00000028173	*Gpr177*	1.31	0.87	1.57	0.47
ENSMUSG00000028179	*Cth*	8.91	8.22	8.7	7.99
ENSMUSG00000028180	*Zranb2*	4.02	3.36	3.88	3.46
ENSMUSG00000028184	*Lphn2*	2.86	3.26	3.08	2.98
ENSMUSG00000028185	*Dnase2b*	3.63	3.75	4.11	3.86
ENSMUSG00000028186	*Uox*	9.58	9.3	10.13	9.89
ENSMUSG00000028187	*Bxdc5*	4.2	4.32	4.49	4.11
ENSMUSG00000028189	*Ctbs*	2.83	2.04	2.69	2.49
ENSMUSG00000028191	*Bcl10*	3.24	2.41	2.7	2.6
ENSMUSG00000028194	*Ddah1*	6.46	6.31	6.62	5.9
ENSMUSG00000028195	*Cyr61*	2.12	2.27	2.87	3.13
ENSMUSG00000028199	*Cryz*	6.16	5.95	6.13	5.75
ENSMUSG00000028207	*Asph*	2.29	1.42	1.73	1.28
ENSMUSG00000028211	*Trp53inp1*	4.75	3.76	4.63	4.49
ENSMUSG00000028218	*6720467C03Ri*	3.09	2.81	3.11	2.38
ENSMUSG00000028221	*Tmem55a*	3.27	2.58	3.39	2.95
ENSMUSG00000028223	*Decr1*	7.43	6.5	6.95	6.51
ENSMUSG00000028224	*Nbn*	3.68	3.11	3.35	3.04
ENSMUSG00000028228	*Cpne3*	4.24	2.9	3.77	3.22
ENSMUSG00000028229	*2410005O16Ri*	4.69	4.05	4.75	3.9
ENSMUSG00000028232	*Tmem68*	2.12	1.18	2.04	1.72
ENSMUSG00000028233	*Tgs1*	1.86	1.5	1.72	1.16
ENSMUSG00000028234	*Rps20*	5.06	6.17	6.21	6.2
ENSMUSG00000028238	*Atp6v0d2*	3.41	2.48	2.78	2.07
ENSMUSG00000028240	*Cyp7a1*	4.68	1.55	6.77	6.02
ENSMUSG00000028243	*3110003A22Ri*	1.89	1.09	1.8	0.92
ENSMUSG00000028245	*Nsmaf*	2.63	2.55	2.92	2.11
ENSMUSG00000028247	*Coq3*	3.49	3.09	3.7	3.39
ENSMUSG00000028248	*NA*	2.38	1.83	2.44	1.96
ENSMUSG00000028249	*Sdcbp*	4.41	3.85	3.96	3.79
ENSMUSG00000028251	*NA*	4.71	3.78	4.59	3.98

ENSMUSG00000028252	*Ccnc*	3.66	2.38	3.33	2.76
ENSMUSG00000028256	*Odf2l*	1.93	0.85	1.63	1.02
ENSMUSG00000028261	*1110007M04Ri*	4.71	4.22	4.78	4.27
ENSMUSG00000028266	*Lmo4*	3.01	3.32	3.1	2.72
ENSMUSG00000028268	*Gbp3*	2.98	1.25	1.29	1.88
ENSMUSG00000028269	*Gbp1*	2.43	1.2	0.62	1.27
ENSMUSG00000028270	*Gbp2*	2.96	1.63	1.42	1.42
ENSMUSG00000028271	*Gtf2b*	3.88	3.5	3.62	3.36
ENSMUSG00000028273	*Pdlim5*	4.19	3.35	3.56	3.21
ENSMUSG00000028274	*Rngtt*	2.24	1.25	1.93	1.65
ENSMUSG00000028277	*Ube2j1*	4.41	4.46	4.48	4.44
ENSMUSG00000028282	*Casp8ap2*	1.17	-0.14	0.43	0.01
ENSMUSG00000028284	*Map3k7*	3.6	3.21	3.19	3.12
ENSMUSG00000028291	*2700059D21Ri*	3.99	3.63	4	3.7
ENSMUSG00000028292	*Rars2*	3.17	3.1	3.07	2.28
ENSMUSG00000028293	*Slc35a1*	4.12	3.95	3.95	3.35
ENSMUSG00000028295	*1810030N24Ri*	3.8	2.88	3.24	3.13
ENSMUSG00000028300	*3110043O21Ri*	2.36	1.82	2.23	1.82
ENSMUSG00000028307	*Aldob*	11.31	11.13	11.61	11.24
ENSMUSG00000028309	*mKIAA4116*	3.22	3.31	3.16	2.75
ENSMUSG00000028318	*Polr1e*	1.15	2.16	1.71	1.83
ENSMUSG00000028322	*Exosc3*	3.2	3.65	3.25	2.7
ENSMUSG00000028327	*1300002K09Ri*	6.13	6.25	5.67	5.55
ENSMUSG00000028328	*Tmod1*	2.14	1.53	2.21	1.78
ENSMUSG00000028329	*Xpa*	3.45	3.58	3.82	3.08
ENSMUSG00000028330	*AU014645*	3.62	3.7	3.65	3.47
ENSMUSG00000028331	*5830415F09Ri*	0.93	1.05	1.09	0.81
ENSMUSG00000028333	*Anp32b*	3.95	4.58	4.32	3.69
ENSMUSG00000028334	*Nans*	3.31	3.98	3.24	3.41
ENSMUSG00000028339	*Col15a1*	1.05	-0.87	0.84	-0.09
ENSMUSG00000028343	*Txndc4*	5.74	5	5.29	4.79

ENSMUSG00000028344	*inv*	2.16	2.56	2.64	2.81
ENSMUSG00000028345	*Tex10*	2.03	1.92	1.92	1.53
ENSMUSG00000028356	*Ambp*	10.65	10.72	10.39	10.69
ENSMUSG00000028359	*Orm3*	4.89	4.58	5.42	4.09
ENSMUSG00000028367	*Txn1*	7.71	6.64	6.72	6.19
ENSMUSG00000028381	*Ugcg*	3.3	2	3.07	3.16
ENSMUSG00000028382	*AK088920*	4.4	3.44	3.76	3.47
ENSMUSG00000028383	*Hsdl2*	6.23	5.25	5.78	5.36
ENSMUSG00000028385	*Snx30*	1.34	0.95	1.46	1
ENSMUSG00000028393	*Alad*	7.54	7.52	7.21	7.09
ENSMUSG00000028394	*Pole3*	3.62	3.64	3.63	3.42
ENSMUSG00000028397	*Jmjd2c*	1.63	1.37	1.54	1.45
ENSMUSG00000028398	*3110001D03Ri*	4.36	4.39	4.52	4.18
ENSMUSG00000028399	*Ptprd*	4.38	3.51	4	3.77
ENSMUSG00000028402	*Mpdz*	2.92	2.16	2.5	1.72
ENSMUSG00000028403	*Zdhhc21*	1.64	0.79	0.43	0.2
ENSMUSG00000028405	*Aco1*	6.5	6.54	6.36	6.06
ENSMUSG00000028407	*NA*	3.53	3	3.35	3.12
ENSMUSG00000028409	*Smu1*	4.96	5.2	4.9	4.7
ENSMUSG00000028410	*Dnaja1*	5.74	4.5	5.03	4.69
ENSMUSG00000028412	*Slc44a1*	3.44	3.5	3.24	2.78
ENSMUSG00000028413	*B4galt1*	4.29	3.47	3.19	3.3
ENSMUSG00000028414	*Fcmd*	1.39	-0.02	1.33	1.03
ENSMUSG00000028416	*Bag1*	6.14	6.14	5.78	5.63
ENSMUSG00000028419	*Chmp5*	5.13	4.69	5.08	4.61
ENSMUSG00000028420	*Tmem38b*	4.89	4.57	4.68	4.47
ENSMUSG00000028423	*Nfx1*	3.73	3.61	3.73	3.73
ENSMUSG00000028426	*Rad23b*	6.04	5.97	5.96	5.94
ENSMUSG00000028430	*Nol6*	2.67	3.84	3.1	3.2
ENSMUSG00000028431	*Ikbkap*	1.08	1.71	1.2	1.26
ENSMUSG00000028433	*Ubap2*	3	3.61	3.25	3.17

ENSMUSG00000028434	*NA*	4.92	4.79	4.76	4.53
ENSMUSG00000028436	*Wdr40a*	4.15	3.94	4.02	3.64
ENSMUSG00000028437	*Ubap1*	4.89	4.82	4.72	4.46
ENSMUSG00000028439	*2310028H24Ri*	1.31	1.8	1.27	0.56
ENSMUSG00000028443	*Nudt2*	3.88	3.26	3.63	3.58
ENSMUSG00000028444	*Cntfr*	0.78	1.61	1.9	1.37
ENSMUSG00000028445	*NA*	4.2	5.4	3.74	5.23
ENSMUSG00000028447	*Dctn3*	4.94	5.26	4.76	4.79
ENSMUSG00000028452	*Vcp*	3.95	3.71	3.4	1.71
ENSMUSG00000028454	*Pigo*	2.32	2.75	2.93	2.81
ENSMUSG00000028455	*Stoml2*	4.8	5.16	4.9	4.83
ENSMUSG00000028458	*Tesk1*	2.79	3.61	3.18	3.01
ENSMUSG00000028459	*Cd72*	0.73	1.28	1.45	0.37
ENSMUSG00000028461	*LOC622404*	5.84	6.11	6.26	6.11
ENSMUSG00000028464	*Tpm2*	1.28	1.36	2.8	2.26
ENSMUSG00000028465	*Tln1*	3.85	4.27	4.14	3.86
ENSMUSG00000028466	*Creb3*	4.57	5.24	5.2	5.04
ENSMUSG00000028467	*mKIAA1605*	1.56	2.22	2.01	1.45
ENSMUSG00000028468	*1110029E03Ri*	3.39	3.7	3.66	3.46
ENSMUSG00000028469	*Npr2*	3.87	4.1	3.97	3.45
ENSMUSG00000028470	*Hint2*	6.57	6.35	6.82	6.3
ENSMUSG00000028476	*Reck*	1.35	0.15	1.44	0.64
ENSMUSG00000028478	*Clta*	6.22	6.6	6.63	6.34
ENSMUSG00000028479	*Gne*	5.65	5.77	5.83	5.52
ENSMUSG00000028483	*Snapc3*	1.25	0.79	1.11	0.53
ENSMUSG00000028484	*Psip1*	2.9	1.91	2.48	1.81
ENSMUSG00000028494	*Adfp*	8.08	7.94	7.74	7.5
ENSMUSG00000028514	*NA*	3.35	3.32	3.36	3.08
ENSMUSG00000028517	*Ppap2b*	6.37	6.61	6.49	6.25
ENSMUSG00000028518	*Prkaa2*	3.16	2.94	3.11	2.94
ENSMUSG00000028521	*Slc35d1*	5	5.11	5.32	4.82

ENSMUSG00000028522	*Mier1*	4.3	3.29	4	3.38
ENSMUSG00000028525	*Pde4b*	1.61	1.17	0.94	1
ENSMUSG00000028527	*Ak3l1*	4.57	3.85	4.81	4.34
ENSMUSG00000028530	*Jak1*	5.07	4.82	4.8	4.62
ENSMUSG00000028536	*2610528J11Ri*	3.53	3.76	4.02	3.43
ENSMUSG00000028538	*St3gal3*	4.12	4.64	4.88	4.95
ENSMUSG00000028540	*Dph2*	1.28	1.9	1.3	1.44
ENSMUSG00000028542	*Slc6a9*	4.09	4.59	4.36	4.39
ENSMUSG00000028549	*Itgb3bp*	1.21	-0.17	1.17	0.02
ENSMUSG00000028550	*Atg4c*	3.52	2.95	3.31	2.89
ENSMUSG00000028551	*Cdkn2c*	1.17	0.21	1.61	0.53
ENSMUSG00000028552	*Eps15*	4.06	3.21	3.83	3.26
ENSMUSG00000028553	*Angptl3*	9.54	8.83	9.59	8.95
ENSMUSG00000028556	*Dock7*	1.5	1.07	1.19	1.02
ENSMUSG00000028557	*AK139182*	5.91	5.18	5.26	4.73
ENSMUSG00000028559	*Osbpl9*	5.64	5.3	5.63	5.27
ENSMUSG00000028560	*Usp1*	2.75	1.8	2.29	1.96
ENSMUSG00000028563	*Tm2d1*	1.8	0.9	1.63	1.3
ENSMUSG00000028565	*mKIAA1439*	5.1	4.44	4.94	4.6
ENSMUSG00000028567	*Txndc12*	5.34	5.27	5.27	5.16
ENSMUSG00000028572	*Hook1*	3.93	3.2	3.36	3.09
ENSMUSG00000028573	*2310009E04Ri*	5.27	5.16	5.28	4.83
ENSMUSG00000028576	*Ift74*	1.29	0.11	1.02	0.14
ENSMUSG00000028577	*Plaa*	3.69	3.3	3.28	2.9
ENSMUSG00000028578	*5830433M19R*	1.84	1.28	1.53	1.39
ENSMUSG00000028580	*Pum1*	3.85	3.7	4.02	3.8
ENSMUSG00000028581	*Laptm5*	3.67	3.84	3.96	3.85
ENSMUSG00000028582	*Cc2d1b*	1.86	2.21	2.12	1.8
ENSMUSG00000028597	*Gpx7*	1.02	0.58	0.93	0.67
ENSMUSG00000028599	*Tnfrsf1b*	3.79	3.71	4.11	4.15
ENSMUSG00000028601	*Echdc2*	5.43	6.09	5.96	5.72

ENSMUSG00000028603	*Scp2*	8.07	8.05	7.96	8.27
ENSMUSG00000028607	*Cpt2*	7.1	6.84	6.98	6.55
ENSMUSG00000028608	*0610037L13Ri*	3.24	3.89	3.5	3.46
ENSMUSG00000028609	*Magoh*	4.85	4.11	4.49	4.47
ENSMUSG00000028614	*Tmem48*	2.82	2.18	2.55	2.49
ENSMUSG00000028617	*Lrrc42*	2.72	3.25	3.13	3.33
ENSMUSG00000028618	*Tmem59*	8.03	7.43	7.9	7.62
ENSMUSG00000028619	*2210012G02Ri*	1.02	1.65	1.28	1.48
ENSMUSG00000028621	*mFLJ00377*	1.65	2.23	2	1.9
ENSMUSG00000028622	*Mrpl37*	4.87	5.26	5.19	4.92
ENSMUSG00000028629	*3110037I16Rik*	1.38	0.79	0.52	-0.52
ENSMUSG00000028630	*Dyrk2*	3.35	4.02	3.52	3.22
ENSMUSG00000028633	*Ctps*	0.69	1.29	1.28	1.2
ENSMUSG00000028636	*Ppcs*	3.06	3.13	3.15	3.15
ENSMUSG00000028639	*Ybx1*	5.41	4.58	4.89	4.34
ENSMUSG00000028641	*Lepre1*	2.48	3.19	2.62	2.83
ENSMUSG00000028643	*Ccdc23*	2.27	2.93	2.61	2.76
ENSMUSG00000028645	*Slc2a1*	2.46	3.15	2.28	1.93
ENSMUSG00000028646	*Rragc*	4.84	4.48	4.91	4.28
ENSMUSG00000028647	*amy-1*	4.51	2.7	3.63	3.2
ENSMUSG00000028649	*NA*	2.06	1.88	2.09	1.68
ENSMUSG00000028651	*Ppie*	3.02	3.51	3.12	3.45
ENSMUSG00000028653	*Trit1*	2.97	2.46	2.61	2.41
ENSMUSG00000028654	*Mycl1*	3.13	2.48	3.36	2.67
ENSMUSG00000028655	*Mfsd2*	6.56	6.65	6.93	6.64
ENSMUSG00000028656	*Cap1*	5.76	5.33	5.77	5.38
ENSMUSG00000028657	*Ppt1*	4.81	4.2	4.51	3.8
ENSMUSG00000028668	*Tceb3*	4.3	4.17	4.17	4.1
ENSMUSG00000028669	*1110049F12Ri*	3.7	3.77	3.78	3.36
ENSMUSG00000028670	*Lypla2*	4.92	5.94	5.18	5.17
ENSMUSG00000028671	*Gale*	2.3	2.58	1.56	1.41

ENSMUSG00000028672	*Hmgcl*	7.31	7.8	7.41	7.37
ENSMUSG00000028673	*Fuca1*	6.13	6.23	6.03	5.99
ENSMUSG00000028675	*Pnrc2*	5.06	4.5	5.17	4.52
ENSMUSG00000028676	*nssr 1*	1.78	0.41	0.95	0.56
ENSMUSG00000028677	*4931406I20Rik*	2.61	3.29	2.62	2.29
ENSMUSG00000028680	*Plk3*	4.1	3.83	4.91	5.33
ENSMUSG00000028683	*Eif2b3*	1.86	1.76	2.19	1.98
ENSMUSG00000028684	*Urod*	5.74	6.17	6.06	5.96
ENSMUSG00000028688	*Toe1*	2.25	2.18	1.43	1.52
ENSMUSG00000028689	*0610037D15Ri*	1.29	1.19	1.87	2.25
ENSMUSG00000028690	*Mmachc*	3.73	3.87	4.06	3.77
ENSMUSG00000028691	*Prdx1*	8.28	7.8	7.95	7.69
ENSMUSG00000028692	*Akr1a4*	8.14	8.53	8.22	8.03
ENSMUSG00000028693	*Nasp*	2.57	2.09	2.4	1.95
ENSMUSG00000028696	*Ipp*	2.66	2.23	2.4	2.23
ENSMUSG00000028700	*Pomgnt1*	2.77	3.54	2.9	3.01
ENSMUSG00000028703	*Lrrc41*	4.26	4.58	4.4	4.26
ENSMUSG00000028706	*Nsun4*	3.21	3.44	3.24	3.03
ENSMUSG00000028708	*Mknk1*	3.33	3.13	3.31	2.91
ENSMUSG00000028709	*Mobkl2c*	3.05	2.95	2.73	2.33
ENSMUSG00000028712	*NA*	2.66	2.94	2.4	2.86
ENSMUSG00000028713	*Cyp4b1*	3.42	3.75	3.12	3.45
ENSMUSG00000028715	*Cyp4a14*	10.18	9.24	9.73	8.96
ENSMUSG00000028716	*Pdzk1ip1*	0.77	1.52	1.32	0.73
ENSMUSG00000028719	*Cmpk*	5.73	4.37	5.22	4.73
ENSMUSG00000028729	*Ebna1bp2*	3.94	4.71	4.12	4.13
ENSMUSG00000028737	*Aldh4a1*	8.07	8.25	7.99	7.64
ENSMUSG00000028741	*Mrto4*	2.16	2.83	2.44	2.48
ENSMUSG00000028743	*Akr7a5*	6.53	7.18	6.82	6.92
ENSMUSG00000028744	*Pqlc2*	1.82	2.66	2.37	2.52
ENSMUSG00000028745	*Capzb*	6.1	5.9	6.02	5.86

ENSMUSG00000028755	*Cda*	2.7	3.68	2.86	2.71
ENSMUSG00000028756	*Pink1*	6.14	6.7	6.29	6.2
ENSMUSG00000028757	*Ddost*	6.31	6.97	6.23	6.18
ENSMUSG00000028759	*Hp1bp3*	4.79	4.5	4.65	4.46
ENSMUSG00000028760	*Eif4g3*	2.94	3.22	3.16	2.83
ENSMUSG00000028763	*NA*	0.93	1.99	1.41	1.51
ENSMUSG00000028766	*Akp2*	2.89	3.32	3.57	3.37
ENSMUSG00000028771	*Ptpn12*	3.93	3.64	3.66	3.36
ENSMUSG00000028772	*Zcchc17*	3.11	3.34	3.15	2.94
ENSMUSG00000028776	*arg1*	3.28	3.94	3.31	3.21
ENSMUSG00000028779	*Pef1*	4.56	5.35	4.89	4.69
ENSMUSG00000028788	*Ptp4a2*	5.82	4.7	5.37	4.91
ENSMUSG00000028790	*Khdrbs1*	3.28	2.7	2.87	2.63
ENSMUSG00000028792	*Ak2*	6.49	6.41	6.73	6.53
ENSMUSG00000028793	*NA*	4	4.1	4.23	3.99
ENSMUSG00000028795	*Ccdc28b*	1.21	1.83	2	1.78
ENSMUSG00000028796	*Phc2*	3.32	4.02	3.37	3.35
ENSMUSG00000028797	*2510006D16R*	5.49	5.86	5.53	5.45
ENSMUSG00000028798	*Eif3i*	6	6.45	6.12	6.06
ENSMUSG00000028799	*BC039093*	1.03	1.84	1.83	1.54
ENSMUSG00000028800	*Hdac1*	-0.66	-1.5	1.03	-0.49
ENSMUSG00000028803	*Npal3*	1.42	1.54	2.03	1.29
ENSMUSG00000028809	*Srrm1*	4.01	3.87	4.05	3.63
ENSMUSG00000028811	*Yars*	4.05	4.8	4.08	4.2
ENSMUSG00000028820	*Sfpq*	5.07	4.96	4.62	4.44
ENSMUSG00000028821	*Syf2*	4.78	5.12	5.13	4.78
ENSMUSG00000028822	*Tmem50a*	6.61	6	6.44	6.23
ENSMUSG00000028826	*Tmem57*	4.45	3.95	4.22	3.84
ENSMUSG00000028830	*AU040320*	3.14	3.29	3.25	3.1
ENSMUSG00000028833	*Ncdn*	2.07	3.13	2.7	2.44
ENSMUSG00000028837	*Psmb2*	6.65	6.6	6.52	6.33

ENSMUSG00000028838	*Extl1*	3.22	3.42	3.71	3.66
ENSMUSG00000028840	*Zfp593*	0.81	2.1	1.2	1.4
ENSMUSG00000028843	*Sh3bgrl3*	3.01	3.54	3.9	3.18
ENSMUSG00000028847	*Trappc3*	5.13	4.49	4.7	4.73
ENSMUSG00000028848	*Atpbd1b*	2.85	3.04	2.93	2.38
ENSMUSG00000028849	*Mtap7d1*	3.18	4	3.52	3.53
ENSMUSG00000028850	*Gpatch3*	1.06	1.93	1.3	1.26
ENSMUSG00000028851	*Nudc*	4.4	5.19	4.48	4.56
ENSMUSG00000028854	*Slc9a1*	2.18	2.62	2.52	2.29
ENSMUSG00000028857	*D4Ertd196e*	4.04	4.23	4.04	3.92
ENSMUSG00000028860	*slp1*	-3.25	-0.78	1.61	-0.74
ENSMUSG00000028861	*Mrps15*	5.69	5.05	5.4	5.23
ENSMUSG00000028863	*2310005N01Ri*	2.81	2.71	3.24	2.28
ENSMUSG00000028864	*Hgf*	2.66	1.77	2.3	2.15
ENSMUSG00000028868	*Wasf2*	3.54	3.51	3.5	3.31
ENSMUSG00000028869	*Gnl2*	3.71	3.77	3.85	3.4
ENSMUSG00000028878	*BC008163*	2.03	2.12	2.55	2.12
ENSMUSG00000028879	*Stx12*	4.08	3.24	3.72	3.25
ENSMUSG00000028882	*Ppp1r8*	3.17	3.87	3.47	3.17
ENSMUSG00000028884	*Rpa2*	1.09	1.67	2.24	1.53
ENSMUSG00000028886	*Eya3*	3.17	3.07	2.85	2.73
ENSMUSG00000028889	*Yrdc*	3.44	3.89	3.5	3.4
ENSMUSG00000028890	*Mtf1*	2.48	2.52	2.39	2.46
ENSMUSG00000028893	*Sesn2*	2.52	2.87	2.53	2.54
ENSMUSG00000028894	*Inpp5b*	3.86	3.9	4.24	3.96
ENSMUSG00000028896	*Rcc1*	3.9	3.26	2.67	3.09
ENSMUSG00000028898	*Trspap1*	3.47	3.4	3.3	3.03
ENSMUSG00000028899	*Taf12*	4.2	4.24	4.5	4.11
ENSMUSG00000028902	*Sf3a3*	3.8	3.71	3.29	3.03
ENSMUSG00000028906	*Epb4.1*	4.79	4.63	4.9	4.64
ENSMUSG00000028907	*Utp11l*	4.71	4.77	4.63	4.17

ENSMUSG00000028910	*Mecr*	4.75	5.13	4.92	4.72
ENSMUSG00000028911	*Sfrs4*	4.96	5	4.83	4.68
ENSMUSG00000028914	*Casp9*	3.02	3.04	2.79	2.13
ENSMUSG00000028917	*NA*	1.66	2.81	2.34	1.87
ENSMUSG00000028919	*Arhgef19*	3.09	4	4.12	2.89
ENSMUSG00000028920	*Fbxo42*	1.66	1.9	1.85	1.89
ENSMUSG00000028923	*Necap2*	2.07	2.52	2.17	2.2
ENSMUSG00000028932	*Psmc2*	6.05	6.15	6.02	5.91
ENSMUSG00000028936	*Rpl22*	6.42	6.64	6.65	7.19
ENSMUSG00000028937	*Acot7*	3.82	4.4	4.19	4.21
ENSMUSG00000028944	*Prkag2*	4.27	3.74	3.96	3.66
ENSMUSG00000028945	*Rheb*	5.52	5.44	5.41	5.04
ENSMUSG00000028948	*Nol9*	2.75	2.79	2.73	2.43
ENSMUSG00000028949	*Smarcd3*	0.03	0.33	1.13	0.39
ENSMUSG00000028952	*Zbtb48*	2.13	2	2.85	1.69
ENSMUSG00000028953	*Abcf2*	4.27	4.69	4.37	4.32
ENSMUSG00000028954	*Nub1*	4.18	3.98	4.15	3.94
ENSMUSG00000028955	*Vamp3*	3.25	2.65	3.23	2.92
ENSMUSG00000028957	*Per3*	-1.26	-1.21	1.54	1.46
ENSMUSG00000028958	*Tmub1*	2.4	2.65	3.02	2.95
ENSMUSG00000028959	*Fastk*	3.73	4.2	4.08	3.77
ENSMUSG00000028960	*Ube4b*	4.06	4.08	4.37	4.01
ENSMUSG00000028961	*Pgd*	4.53	4.69	4.34	4.22
ENSMUSG00000028962	*Slc4a2*	3.23	4.08	3.58	3.45
ENSMUSG00000028964	*Park7*	6.65	6.98	6.85	6.7
ENSMUSG00000028967	*Errfi1*	9.21	8.85	9.08	8.98
ENSMUSG00000028969	*Cdk5*	3.04	3.32	2.87	2.97
ENSMUSG00000028970	*Abcb1b*	2.44	2.04	2.28	1.87
ENSMUSG00000028973	*Abcb8*	3.52	4	3.72	3.26
ENSMUSG00000028974	*Dffa*	3.08	3.21	3.11	2.92
ENSMUSG00000028975	*Pex14*	5.15	5.59	5.53	5.12

ENSMUSG00000028976	*Slc2a5*	1.31	0.45	2.31	1.81
ENSMUSG00000028978	*Nos3*	1.07	1.32	0.08	0.03
ENSMUSG00000028979	*Masp2*	6.45	6.49	6.56	6.36
ENSMUSG00000028980	*H6pd*	7.25	7.78	7.4	7.19
ENSMUSG00000028982	*Slc25a33*	3.81	3.72	3.47	3.35
ENSMUSG00000028986	*Klhl7*	3.46	2.16	3	2.18
ENSMUSG00000028988	*Ctnnbip1*	2.22	2	2.49	1.86
ENSMUSG00000028990	*Lzic*	1.73	1.9	2.04	1.98
ENSMUSG00000028991	*Frap1*	3.28	3.3	3.52	3.21
ENSMUSG00000028992	*D4Cole1e*	3.25	2.99	3.32	3.18
ENSMUSG00000028995	*Drctnnb1a*	2.69	0.96	2.47	0.72
ENSMUSG00000028998	*Tomm7*	6.75	4.4	6.07	5.55
ENSMUSG00000028999	*Rint1*	1.82	2.16	1.72	1.92
ENSMUSG00000029003	*Mad2l2*	4.32	4.79	3.96	3.84
ENSMUSG00000029004	*NA*	3.43	2.83	3.35	2.99
ENSMUSG00000029007	*Agtrap*	1.12	1.1	-0.26	0.75
ENSMUSG00000029009	*Mthfr*	1.66	2.4	0.58	0.22
ENSMUSG00000029012	*Orc5l*	3.75	3.19	3.66	3.3
ENSMUSG00000029014	*Dnajc2*	2.6	1.45	2.17	1.1
ENSMUSG00000029016	*Clcn6*	1.09	1.21	0.01	0.5
ENSMUSG00000029017	*Pmpcb*	6.68	5.99	6.42	5.81
ENSMUSG00000029020	*Mfn2*	5.11	5.23	5.4	5.05
ENSMUSG00000029022	*D4Wsu114e*	1.24	1.65	2.1	1.47
ENSMUSG00000029028	*Lrrc47*	3.61	4.3	3.79	3.62
ENSMUSG00000029029	*DD57*	2.27	3.12	1.92	2.4
ENSMUSG00000029030	*1200015A19Ri*	5.25	5.59	5.27	4.97
ENSMUSG00000029033	*Centb5*	0.6	1.27	1.04	0.86
ENSMUSG00000029034	*Cpsf3l*	3.44	3.65	3.61	3.54
ENSMUSG00000029036	*AK154077*	3.61	4.4	4.21	3.87
ENSMUSG00000029038	*Ssu72*	4.67	4.66	4.68	4.59
ENSMUSG00000029047	*Pex10*	2.11	2.46	2.3	1.82

ENSMUSG00000029048	*Rer1*	6.72	6.59	7	7.06
ENSMUSG00000029050	*Ski*	3.22	3.9	3.8	3.69
ENSMUSG00000029053	*Prkcz*	1.04	0.69	1.42	1.42
ENSMUSG00000029056	*Pank4*	2.22	2.15	2.45	1.73
ENSMUSG00000029059	*2810405K02Ri*	4.34	5.07	4.8	4.64
ENSMUSG00000029060	*Mib2*	2.11	2.97	2.65	2.47
ENSMUSG00000029062	*Cdc2l1*	3.78	4.05	3.86	3.5
ENSMUSG00000029063	*Nadk*	7.19	7.07	6.9	6.81
ENSMUSG00000029064	*Gnb1*	5.42	5.36	5.24	5.01
ENSMUSG00000029066	*Mrpl20*	5.65	5.61	6.11	5.9
ENSMUSG00000029068	*Ccnl2*	4.5	4.44	4.34	4.01
ENSMUSG00000029070	*Mxra8*	1.68	2.03	1.79	1.61
ENSMUSG00000029071	*Dvl1*	4.31	4.92	4.74	4.53
ENSMUSG00000029073	*BC002216*	3.86	4.3	3.92	3.91
ENSMUSG00000029076	*Sdf4*	6.14	6.36	6.23	5.96
ENSMUSG00000029084	*Cd38*	3.67	2.85	3.12	2.65
ENSMUSG00000029086	*Prom1*	2.48	0.48	0.95	-1.41
ENSMUSG00000029089	*4933428G09Ri*	2.05	1.49	1.29	1.2
ENSMUSG00000029090	*NA*	3.98	4.03	3.93	3.61
ENSMUSG00000029098	*Acox3*	2.95	3.09	3.01	2.86
ENSMUSG00000029101	*Rgs12*	0.62	0.49	1.45	1.02
ENSMUSG00000029102	*Hgfac*	7.15	7.61	7.47	7.32
ENSMUSG00000029103	*Lrpap1*	4.96	5.22	4.89	4.75
ENSMUSG00000029104	*Hdh*	1.74	1.81	1.66	1.2
ENSMUSG00000029106	*Add1*	3.57	4.06	3.78	3.56
ENSMUSG00000029110	*Rnf4*	5.65	5.41	5.42	5.23
ENSMUSG00000029111	*Whsc2*	2.26	2.43	2.16	2.26
ENSMUSG00000029119	*Man2b2*	4.94	5.65	5.25	5.14
ENSMUSG00000029122	*Evc*	1.59	2.1	1.75	1.41
ENSMUSG00000029125	*Stx18*	3.13	2.89	2.86	2.77
ENSMUSG00000029128	*Rab28*	3.7	3.27	3.47	2.78

ENSMUSG00000029131	*Dnajb6*	0.76	1.24	1.64	1.47
ENSMUSG00000029135	*Fosl2*	0.13	1.43	1.17	1.05
ENSMUSG00000029136	*Rbks*	3.87	3.38	3.7	3.52
ENSMUSG00000029141	*Slc4a1ap*	2.74	2.76	2.95	2.62
ENSMUSG00000029142	*Mrpl33*	4.99	5.53	5.45	5.28
ENSMUSG00000029144	*Mpv17*	4.23	4.2	4.28	4.05
ENSMUSG00000029145	*Eif2b4*	3.84	4.62	4.37	4.28
ENSMUSG00000029146	*Snx17*	3.56	3.49	3.2	3.54
ENSMUSG00000029147	*Ppm1g*	4.91	5.39	5.09	5.03
ENSMUSG00000029148	*Nrbp1*	4.93	5.24	5.06	4.76
ENSMUSG00000029152	*Ociad1*	6.93	6.23	6.51	6.05
ENSMUSG00000029153	*Ociad2*	4.05	3.7	3.55	3.66
ENSMUSG00000029162	*Khk*	8.06	8.2	8.48	8.07
ENSMUSG00000029163	*Emilin1*	2.09	2.99	2.05	2.2
ENSMUSG00000029165	*Agbl5*	1.42	0.94	1.21	1.63
ENSMUSG00000029166	*Mapre3*	4.06	4.11	4.49	4.4
ENSMUSG00000029167	*Ppargc1a*	2.06	1.53	2.61	2.41
ENSMUSG00000029169	*Dhx15*	5.05	4.72	4.95	4.64
ENSMUSG00000029171	*Pgm1*	2.08	1.64	2.11	1.88
ENSMUSG00000029173	*Sepsecs*	5.08	4.32	4.66	4.07
ENSMUSG00000029175	*4930471M23R*	3.78	4.04	3.93	3.82
ENSMUSG00000029176	*Anapc4*	2.38	1.92	2.02	1.5
ENSMUSG00000029177	*Cenpa*	1.14	1.22	1.59	0.66
ENSMUSG00000029178	*Klf3*	4.1	4.7	4.73	4.66
ENSMUSG00000029185	*9130005N14Ri*	3.65	3.61	3.53	3.4
ENSMUSG00000029186	*Pi4k2b*	3.39	2.85	3.3	2.93
ENSMUSG00000029190	*D5Ertd579e*	3.63	3.1	2.98	2.6
ENSMUSG00000029191	*Rfc1*	3.08	2.49	2.94	2.57
ENSMUSG00000029192	*kiaa1322*	3.29	3.05	3.12	2.58
ENSMUSG00000029195	*Klb*	3.75	3.87	3.84	3.76
ENSMUSG00000029196	*NA*	3.69	3.8	3.49	3.44

ENSMUSG00000029198	*Grpel1*	6.88	7.06	6.83	6.66
ENSMUSG00000029199	*mLIP1*	5.03	4.4	4.61	4.37
ENSMUSG00000029201	*Ugdh*	6.43	5.72	6.07	5.34
ENSMUSG00000029202	*Pds5a*	4.02	3.71	3.93	3.52
ENSMUSG00000029203	*Hip2*	5.31	4.07	4.69	4.36
ENSMUSG00000029207	*Apbb2*	1.14	0.86	1.29	1.12
ENSMUSG00000029208	*Guf1*	2.63	1.82	2.16	1.39
ENSMUSG00000029213	*Commd8*	4.33	2.73	3.98	3.3
ENSMUSG00000029217	*Tec*	3.48	3.55	3.39	3.03
ENSMUSG00000029221	*Slc30a9*	4.71	4.04	4.77	4.13
ENSMUSG00000029227	*Fip1l1*	3.74	3.27	3.52	3.31
ENSMUSG00000029228	*Lnx1*	2.04	-0.13	2.53	1.52
ENSMUSG00000029229	*Chic2*	3.58	2.61	3.47	2.91
ENSMUSG00000029231	*Pdgfra*	1.17	0.94	1.33	0.71
ENSMUSG00000029233	*Srd5a2l*	2.79	3.27	2.96	2.89
ENSMUSG00000029234	*Tmem165*	3.05	1.97	2.58	1.52
ENSMUSG00000029238	*Clock*	3.99	3.15	3.34	2.73
ENSMUSG00000029246	*NA*	3.56	2.56	3.67	3.28
ENSMUSG00000029247	*Paics*	7.17	6.27	7.11	6.6
ENSMUSG00000029249	*Rest*	2.31	1.52	2.16	1.61
ENSMUSG00000029250	*Polr2b*	4.33	3.92	4.28	4.02
ENSMUSG00000029254	*stap-1*	1.9	-3.39	2.24	0.35
ENSMUSG00000029260	*Ugt2b34*	7.48	7.04	6.92	6.62
ENSMUSG00000029263	*Pigg*	2.51	2.06	2.7	2.16
ENSMUSG00000029265	*Dr1*	3.94	3.21	3.56	3.23
ENSMUSG00000029267	*Mtf2*	1.82	0.55	1.08	0.43
ENSMUSG00000029269	*Sult1b1*	4.89	3.53	4.27	3.58
ENSMUSG00000029270	*2900024C23Ri*	3.3	2.63	2.89	2.33
ENSMUSG00000029272	*Sult1e1*	2.67	-2.05	4.02	0.17
ENSMUSG00000029273	*Sult1d1*	7.9	5.85	7.61	6.52
ENSMUSG00000029276	*Glmn*	1.54	0.55	1.12	0.39

ENSMUSG00000029287	*Tgfbr3*	1.71	1.49	2	1.87
ENSMUSG00000029290	*Zfp326*	2.85	2.22	2.37	1.9
ENSMUSG00000029291	*Rufy3*	2.73	2.98	3.28	2.8
ENSMUSG00000029304	*Spp1*	4.11	4.02	3.75	3.88
ENSMUSG00000029309	*Sparcl1*	1.86	-1.03	2.02	0.95
ENSMUSG00000029310	*Nudt9*	4.78	5.02	4.6	4.59
ENSMUSG00000029311	*Hsd17b11*	6.32	6.27	6.16	6.08
ENSMUSG00000029313	*Aff1*	3.28	2.81	2.99	2.62
ENSMUSG00000029314	*A230097K15R*	4.55	4.05	4.4	3.59
ENSMUSG00000029319	*Coq2*	3.49	3.36	3.52	2.98
ENSMUSG00000029322	*Plac8*	1.83	1.58	2.16	2.12
ENSMUSG00000029326	*Enoph1*	1.37	1.78	1.85	1.4
ENSMUSG00000029328	*Hnrpdl*	3.38	3.17	3.8	3.13
ENSMUSG00000029333	*Rasgef1b*	4.01	3.72	4.38	4.74
ENSMUSG00000029338	*Antxr2*	3.22	2.8	3.07	2.49
ENSMUSG00000029344	*Tpst2*	4.57	5.16	4.6	4.45
ENSMUSG00000029345	*Tfip11*	3.23	3.91	3.6	3.5
ENSMUSG00000029346	*2810002G02R*	3.56	3.71	3.63	3.7
ENSMUSG00000029360	*NA*	2.76	3.23	2.9	2.79
ENSMUSG00000029363	*Rfc5*	1.01	1.29	1.13	1.11
ENSMUSG00000029364	*Wsb2*	3.88	4.51	3.89	3.77
ENSMUSG00000029366	*Dck*	1.57	0.35	1.86	1.13
ENSMUSG00000029368	*Alb*	15.02	15.24	15.06	15.19
ENSMUSG00000029369	*Afm*	8.48	7.77	8.03	7.94
ENSMUSG00000029370	*Rassf6*	2.79	2.54	3.07	2.32
ENSMUSG00000029372	*Ppbp*	-3.43	-2.85	1.35	-3.43
ENSMUSG00000029380	*Cxcl1*	-0.39	2	1.58	2.04
ENSMUSG00000029385	*Ccng2*	4.18	2.55	3.32	1.6
ENSMUSG00000029386	*Tctn2*	0.96	1.37	1.08	0.97
ENSMUSG00000029387	*Gtf2h3*	3.21	3.19	3.38	3.23
ENSMUSG00000029388	*Eif2b1*	4.26	4.65	4.47	4.33

ENSMUSG00000029389	*Ddx55*	1.39	1.45	1.4	1.23
ENSMUSG00000029390	*Tmed2*	3.51	2.85	3.33	3.07
ENSMUSG00000029397	*Rchy1*	4.67	4.71	4.6	4.22
ENSMUSG00000029401	*BC003324*	2.04	3.02	2.95	2.64
ENSMUSG00000029402	*6330548G22Ri*	1.76	2.4	1.99	2.03
ENSMUSG00000029403	*Cdkl2*	1.48	0.77	1.3	0.54
ENSMUSG00000029404	*Arl6ip4*	4.04	4.74	4.35	4.02
ENSMUSG00000029405	*G3bp2*	4.37	3.98	4.33	3.87
ENSMUSG00000029406	*Pitpnm2*	3.37	3.84	3.55	3.49
ENSMUSG00000029407	*Uso1*	5.41	5.21	4.92	4.62
ENSMUSG00000029415	*Sdad1*	2.14	1.99	1.85	1.64
ENSMUSG00000029416	*Slc15a4*	3.8	4.33	4.67	4.54
ENSMUSG00000029417	*Cxcl9*	3.86	2.42	3.06	3.21
ENSMUSG00000029422	*Rsrc2*	2.97	1.93	2.66	2.02
ENSMUSG00000029426	*Scarb2*	5.58	5.85	5.45	5.64
ENSMUSG00000029427	*Zcchc8*	3.17	2.9	3.18	2.66
ENSMUSG00000029428	*Stx2*	3.37	3.37	3.33	3.04
ENSMUSG00000029430	*Ran*	3.78	3.77	3.85	4.27
ENSMUSG00000029432	*Gbas*	2.15	2.13	2.29	2.11
ENSMUSG00000029433	*Diablo*	3.89	4.32	3.89	3.57
ENSMUSG00000029434	*Vps33a*	3.79	3.96	3.92	3.75
ENSMUSG00000029438	*Bcl7a*	0.85	1.39	1.1	0.79
ENSMUSG00000029439	*Sfrs8*	1.97	2.38	2.16	2.21
ENSMUSG00000029440	*Psmd9*	5.46	4.98	5.66	5.4
ENSMUSG00000029445	*Hpd*	11.36	11.16	11.52	11.1
ENSMUSG00000029446	*Psph*	1.73	2.41	1.64	1.88
ENSMUSG00000029447	*Cct6a*	5.85	5.77	5.64	5.72
ENSMUSG00000029454	*Mapkapk5*	4.28	3.91	4.17	3.99
ENSMUSG00000029455	*Aldh2*	9.67	10.05	10.07	10
ENSMUSG00000029456	*Acad10*	4.63	4.35	4.72	4.04
ENSMUSG00000029458	*Brap*	5.73	5.55	6.26	5.93

ENSMUSG00000029461	*B930006L02Ri*	3.67	3.25	3.51	3.44
ENSMUSG00000029462	*Vps29*	5.29	4.42	4.99	4.53
ENSMUSG00000029463	*1500011H22Ri*	1.63	1.42	1.76	1.18
ENSMUSG00000029464	*Atpbd1c*	2.82	3.31	3.1	3.04
ENSMUSG00000029465	*Arpc3*	5.41	5.55	5.74	5.45
ENSMUSG00000029466	*Anapc7*	2.16	2.65	2.56	2.27
ENSMUSG00000029467	*Atp2a2*	5.84	6.24	5.52	5.43
ENSMUSG00000029469	*Cdv1R*	1.04	0.97	1.37	0.76
ENSMUSG00000029470	*P2rx4*	3.73	4.01	3.79	3.56
ENSMUSG00000029471	*Camkk2*	1.34	2.01	1.48	1.58
ENSMUSG00000029472	*Anapc5*	5.18	4.99	4.89	4.71
ENSMUSG00000029474	*Rnf34*	2.69	2.76	2.68	2.37
ENSMUSG00000029475	*Fbxl10*	2.5	2.91	2.21	2.41
ENSMUSG00000029478	*Smrte*	2.01	3.09	3.18	2.82
ENSMUSG00000029480	*Dhx37*	2.15	2.75	2.3	2.12
ENSMUSG00000029482	*Aacs*	4.66	3.73	4.71	4.84
ENSMUSG00000029486	*Mrpl1*	3.79	2.76	3.33	2.56
ENSMUSG00000029499	*Pxmp2*	6.79	6.46	6.92	6.26
ENSMUSG00000029500	*Pgam5*	3.7	3.93	3.78	3.55
ENSMUSG00000029501	*D5Ertd585e*	3.53	2.84	3.54	3.14
ENSMUSG00000029502	*Golga3*	2.59	2.79	2.46	2.38
ENSMUSG00000029504	*Ddx51*	2.13	2.85	2.42	2.63
ENSMUSG00000029505	*Ep400*	2.31	2.75	2.45	2.41
ENSMUSG00000029507	*Pus1*	2.81	3.42	3.46	3.09
ENSMUSG00000029512	*Ulk1*	5.59	5.19	5.62	5.22
ENSMUSG00000029513	*Prkab1*	3.6	4.32	3.87	3.71
ENSMUSG00000029518	*Rab35*	3.88	4.21	3.89	3.82
ENSMUSG00000029524	*NA*	2.26	2.35	2.71	2.53
ENSMUSG00000029528	*Pxn*	4.01	4.37	3.99	3.8
ENSMUSG00000029534	*St7*	3.1	3.31	2.78	2.87
ENSMUSG00000029535	*Triap1*	4.26	4.25	4.09	4.22

ENSMUSG00000029536	*2010003O18Ri*	4.5	4.42	4.64	3.99
ENSMUSG00000029538	*Sfrs9*	3.78	3.86	3.75	3.5
ENSMUSG00000029545	*Acads*	7.13	7.35	7.19	6.82
ENSMUSG00000029547	*Ints1*	2.21	3.3	2.56	2.31
ENSMUSG00000029550	*Sppl3*	3.37	3.34	3.39	2.96
ENSMUSG00000029551	*Psmg3*	3.64	4.13	4.27	4.07
ENSMUSG00000029554	*Mad1*	1.86	2.33	2.87	2.71
ENSMUSG00000029556	*Hnf1a*	3.45	4.21	4.42	4.18
ENSMUSG00000029557	*Ftsj2*	2.57	3.25	2.88	2.59
ENSMUSG00000029559	*2210016L21Ri*	2.61	3.06	3.27	3.08
ENSMUSG00000029560	*Snx8*	2.42	3.34	3.19	3
ENSMUSG00000029561	*Oasl2*	1.71	1.71	1.12	2.06
ENSMUSG00000029569	*Tmem168*	3.34	2.36	2.74	2.29
ENSMUSG00000029571	*Tmem106b*	6.65	5.77	6.44	5.91
ENSMUSG00000029575	*Mmab*	3.07	2.73	2.43	2.19
ENSMUSG00000029577	*Ube3b*	4.77	5.03	4.77	4.35
ENSMUSG00000029578	*Wipi2*	4.98	5.32	4.81	4.72
ENSMUSG00000029580	*Actb*	7.47	7.91	7.72	7.52
ENSMUSG00000029587	*Zfp12*	1.73	1.89	1.72	1.5
ENSMUSG00000029591	*Ung*	0.47	0.99	1.43	1.51
ENSMUSG00000029592	*Usp30*	2.87	3.53	3.35	3.27
ENSMUSG00000029594	*Rbm19*	1.75	2.56	2.47	1.99
ENSMUSG00000029596	*Sdsl*	2.34	3.53	3.29	2.97
ENSMUSG00000029597	*Sds*	7.54	7.78	8.28	7.57
ENSMUSG00000029598	*1300012G16Ri*	5.08	6.17	5.76	5.71
ENSMUSG00000029599	*Ddx54*	3.63	4.88	4.26	4.11
ENSMUSG00000029600	*1110008J03Rik*	0.78	1.79	1.2	1.13
ENSMUSG00000029607	*4921520G13Ri*	1.27	1.37	1.49	1.23
ENSMUSG00000029610	*Jtv1*	3.44	3.75	3.69	4.06
ENSMUSG00000029613	*mKIAA1369*	4.8	4.66	5.02	4.68
ENSMUSG00000029614	*Rpl6*	3.71	4.53	4.21	3.55

ENSMUSG00000029616	*Erp29*	4.84	5.71	5.01	4.91
ENSMUSG00000029617	*AU022870*	4.98	4.19	4.42	3.97
ENSMUSG00000029621	*Arpc1a*	5.26	5.18	5.06	4.92
ENSMUSG00000029622	*Arpc1b*	4.07	3.84	3.72	3.59
ENSMUSG00000029623	*Pdap1*	5.7	4.87	4.95	4.98
ENSMUSG00000029624	*Ptcd1*	2.95	2.94	3.51	3.4
ENSMUSG00000029625	*Cpsf4*	3.5	3.95	4.02	4
ENSMUSG00000029627	*Zkscan14*	2.37	1.68	2.22	2.31
ENSMUSG00000029629	*Phf14*	2.58	2.08	2.57	2.05
ENSMUSG00000029630	*Cyp3a25*	7.41	6.85	7.48	6.81
ENSMUSG00000029632	*Ndufa4*	8.83	8.36	9.02	9.14
ENSMUSG00000029633	*NA*	3.77	3.36	3.63	3.18
ENSMUSG00000029634	*Rnf6*	3.83	4.23	3.9	3.79
ENSMUSG00000029635	*Cdk8*	2.79	1.96	2.57	2.14
ENSMUSG00000029638	*Glcci1*	1.1	0.68	1.37	1.13
ENSMUSG00000029640	*Usp12*	3.1	2.72	2.45	2.58
ENSMUSG00000029642	*Rpo1-3*	4.08	3.78	4.09	4.14
ENSMUSG00000029647	*Pan3*	2.84	2	3.11	2.39
ENSMUSG00000029648	*Flt1*	1.38	1.19	0.77	0.9
ENSMUSG00000029649	*Pomp*	7.54	6.42	7.36	7.08
ENSMUSG00000029650	*Slc46a3*	3.86	3.23	3.77	3.4
ENSMUSG00000029655	*BC037393*	2.82	1.57	2.09	1.58
ENSMUSG00000029656	*C8b*	6.29	7.05	6.44	6.42
ENSMUSG00000029657	*Hsp110*	5.34	5.7	5.24	5.89
ENSMUSG00000029661	*Col1a2*	1.45	1.63	1.43	1.44
ENSMUSG00000029664	*Tfpi2*	6.04	4.76	5.24	4.71
ENSMUSG00000029669	*Tspan12*	6.92	6.04	6.85	6.3
ENSMUSG00000029670	*Ing3*	1.65	1.27	1.18	1.02
ENSMUSG00000029672	*D6Wsu176e*	3.99	3.79	3.77	3.25
ENSMUSG00000029681	*BCL7B*	3.4	3.73	3.34	3.34
ENSMUSG00000029684	*Wasl*	5.2	3.99	4.84	4.37

ENSMUSG00000029686	*Cul1*	5.25	4.71	4.83	4.25
ENSMUSG00000029687	*Ezh2*	1.1	0.33	1.36	0.72
ENSMUSG00000029695	*Aass*	7.66	6.92	7.56	6.77
ENSMUSG00000029701	*Rbm28*	2.92	2.93	2.96	2.77
ENSMUSG00000029703	*1200011O22Ri*	1.8	2.72	2.32	1.78
ENSMUSG00000029705	*Cutl1*	1.88	2.35	2.45	2.18
ENSMUSG00000029708	*Gcc1*	2.15	2.12	2.09	2.06
ENSMUSG00000029710	*Ephb4*	3.47	4.38	3.6	3.66
ENSMUSG00000029713	*Gnb2*	5.41	6.15	5.56	5.5
ENSMUSG00000029714	*mKIAA4110*	2.09	2.5	2.41	1.93
ENSMUSG00000029715	*Pop7*	2.09	2.73	2.51	2.6
ENSMUSG00000029716	*Trfr2*	7.24	7.92	7.51	7.38
ENSMUSG00000029718	*Pcolce*	2.28	2.24	2.18	2.38
ENSMUSG00000029720	*Lrch4*	2.53	3.33	3.06	2.7
ENSMUSG00000029722	*Hrbl*	4.7	5.03	4.66	4.35
ENSMUSG00000029723	*Tsc22d4*	0.94	1.23	1.5	0.89
ENSMUSG00000029725	*2010007H12Ri*	2.59	3.87	3.87	3.64
ENSMUSG00000029726	*Mepce*	3.82	4.21	4.15	4.03
ENSMUSG00000029727	*Cyp3a13*	7.49	7.21	7.27	6.84
ENSMUSG00000029729	*Zkscan1*	3.47	2.89	3.33	2.98
ENSMUSG00000029730	*Mcm7*	1.62	1.23	1.82	1.71
ENSMUSG00000029735	*Tpk1*	3.52	3.19	3.23	2.82
ENSMUSG00000029759	*Pon3*	6.49	5.78	5.97	5.68
ENSMUSG00000029761	*Cald1*	6.93	6.1	6.35	5.97
ENSMUSG00000029763	*Exoc4*	2.03	1.93	1.84	1.95
ENSMUSG00000029767	*Calu*	6.06	5.37	5.45	5.05
ENSMUSG00000029771	*Irf5*	2.29	3.29	2.47	2.5
ENSMUSG00000029772	*4631427C17Ri*	2.65	2.26	2.49	2.06
ENSMUSG00000029775	*2410127E18Ri*	4.16	4.03	4.17	3.86
ENSMUSG00000029776	*Hibadh*	8.45	7.55	8.01	7.59
ENSMUSG00000029777	*Gars*	5.27	4.96	4.88	4.58

ENSMUSG00000029780	*Nt5c3*	4.87	3.54	4.55	3.76
ENSMUSG00000029781	*Fkbp9*	4.29	4.37	3.88	3.89
ENSMUSG00000029782	*2700094F01Ri*	2.58	2.78	2.68	2.47
ENSMUSG00000029787	*NA*	2.92	1.77	2.7	1.97
ENSMUSG00000029798	*NA*	2.35	0.87	1.51	0.84
ENSMUSG00000029802	*Abcg2*	4.52	3.87	4.31	3.84
ENSMUSG00000029810	*Tmem176b*	7.64	8.19	8	7.89
ENSMUSG00000029815	*NA*	2.51	2.39	2.7	2.26
ENSMUSG00000029817	*Tra2a*	4.34	4	3.61	3.64
ENSMUSG00000029823	*Luc7l2*	3.44	2.49	3.28	2.99
ENSMUSG00000029826	*Zc3hav1*	4.1	3.31	3.7	3.42
ENSMUSG00000029833	*Trim24*	4.06	3.87	3.56	3.51
ENSMUSG00000029840	*Mtpn*	5.94	5.52	5.67	5.47
ENSMUSG00000029859	*Epha1*	3.8	4.26	4.26	3.88
ENSMUSG00000029860	*Zyx*	4.39	5.37	4.82	4.48
ENSMUSG00000029863	*Casp2*	1.88	1.47	1.39	0.84
ENSMUSG00000029864	*Gstk1*	7.64	7.47	8.13	7.57
ENSMUSG00000029910	*Mad2l1*	2.02	0.79	1.81	1.43
ENSMUSG00000029911	*Ssbp1*	1.87	1.46	1.87	1.41
ENSMUSG00000029918	*Mrps33*	1.46	0.83	1.68	1.99
ENSMUSG00000029920	*mKIAA1122*	2.3	1.43	1.93	1.4
ENSMUSG00000029922	*Mkrn1*	2.88	2.84	3.09	2.56
ENSMUSG00000029924	*Slc37a3*	3.46	3.42	3.34	2.94
ENSMUSG00000029992	*Gfpt1*	2.74	2.68	2.12	1.89
ENSMUSG00000029993	*Nfu1*	2.82	1.89	2.74	2.43
ENSMUSG00000029994	*Anxa4*	4.95	4.77	4.66	4.55
ENSMUSG00000029998	*Pcyox1*	6.23	6.07	5.98	5.77
ENSMUSG00000029999	*Tgfa*	3.29	3.32	3.28	3.13
ENSMUSG00000030002	*Dusp11*	4.18	3.53	3.81	3.59
ENSMUSG00000030007	*AK153821*	6.09	6.38	6.04	6.06
ENSMUSG00000030008	*1700040I03Ri*	2.53	2.97	3.02	2.48

ENSMUSG00000030016	*Zfml*	3.45	2.42	3.15	2.52
ENSMUSG00000030019	*Fbxl14*	2.68	2.93	2.73	2.63
ENSMUSG00000030029	*Lrig1*	3.08	3.38	3.21	3.23
ENSMUSG00000030034	*Znhit4*	3.39	3.95	3.72	3.66
ENSMUSG00000030035	*Wbp1*	4.55	4.97	4.44	4.38
ENSMUSG00000030036	*Gcs1*	4.15	5.04	4.38	4.59
ENSMUSG00000030037	*NA*	5.11	5.12	5.26	4.78
ENSMUSG00000030042	*Pole4*	5.37	4.67	4.85	4.34
ENSMUSG00000030045	*Mrpl19*	2.94	3.32	2.84	2.79
ENSMUSG00000030055	*Rab43*	5.65	5.7	5.57	5.46
ENSMUSG00000030056	*Isy1*	3.85	3.5	3.34	2.99
ENSMUSG00000030057	*Cnbp*	7.63	7.15	7.39	6.97
ENSMUSG00000030058	*Copg*	4.64	4.81	4.38	4.43
ENSMUSG00000030059	*Tmf1*	3.75	3.25	3.07	2.86
ENSMUSG00000030060	*8430410A17Ri*	2.1	2.37	2.28	2.28
ENSMUSG00000030061	*Ube1c*	4.1	3.28	3.82	2.96
ENSMUSG00000030062	*Rpn1*	6.15	6.37	5.64	5.7
ENSMUSG00000030064	*Frmd4b*	4.21	3.66	3.89	3.39
ENSMUSG00000030067	*Foxp1*	2.55	2.25	2.22	1.67
ENSMUSG00000030068	*Eif4e3*	2.17	1.5	2	1.03
ENSMUSG00000030082	*Sec61a1*	6.23	6.61	5.82	6.06
ENSMUSG00000030083	*Abtb1*	3.17	4.28	3.9	3.76
ENSMUSG00000030086	*Chchd6*	1.99	2.52	2.55	2.55
ENSMUSG00000030087	*Klf15*	6.39	7.07	7.03	7.03
ENSMUSG00000030088	*Aldh1l1*	9.2	9.33	9.47	9.01
ENSMUSG00000030091	*Nup210*	1.18	2.17	1.39	1.37
ENSMUSG00000030094	*Xpc*	2.84	3.26	3.12	3.15
ENSMUSG00000030095	*Tmem43*	2.38	2.56	2.34	2.23
ENSMUSG00000030096	*Slc6a6*	4.29	4.41	4.39	4.31
ENSMUSG00000030101	*Sumf1*	4.38	4.24	4.17	4.1
ENSMUSG00000030102	*Itpr1*	3.76	3.76	3.82	3.52

ENSMUSG00000030103	*Bhlhb2*	5.42	5.35	6.28	6.58
ENSMUSG00000030104	*Edem1*	5.92	5.76	5.45	5.05
ENSMUSG00000030105	*Arl8b*	5.55	5.06	5.35	4.72
ENSMUSG00000030107	*Usp18*	3.73	2.52	2.66	3.44
ENSMUSG00000030108	*Slc6a13*	6.84	6.97	6.83	6.61
ENSMUSG00000030109	*Slc6a12*	6.03	6.07	6.1	5.62
ENSMUSG00000030113	*NA*	2.07	1.48	2.06	1.8
ENSMUSG00000030120	*Mlf2*	6.52	7.25	6.94	6.86
ENSMUSG00000030122	*Ptms*	8.45	9.13	8.79	8.63
ENSMUSG00000030123	*Plxnd1*	2.25	3.26	2.38	2.65
ENSMUSG00000030126	*NA*	3.51	3.01	3.67	3.75
ENSMUSG00000030127	*Cops7a*	5.35	5.55	5.52	5.15
ENSMUSG00000030131	*Mug2*	1.26	1.92	1.47	1.48
ENSMUSG00000030137	*Tuba8*	-1.19	0.18	1.16	-0.04
ENSMUSG00000030138	*Bms1*	3.06	2.99	2.91	2.74
ENSMUSG00000030157	*Clec2d*	5.98	4.35	5.38	5
ENSMUSG00000030159	*Clec1b*	3.4	1.93	3	2.49
ENSMUSG00000030161	*Gabarapl1*	8.07	8.52	8.72	8.51
ENSMUSG00000030166	*Rad52*	1.97	1.45	2.1	1.56
ENSMUSG00000030168	*Adipor2*	7.28	6.87	6.86	6.67
ENSMUSG00000030170	*Wnt5b*	1.17	1.48	1.83	1.77
ENSMUSG00000030172	*Erc1*	2.45	2.59	2.67	2.3
ENSMUSG00000030180	*NA*	2.18	1.56	2.03	1.75
ENSMUSG00000030188	*2010012C16Ri*	1.34	0.56	1.11	0.77
ENSMUSG00000030189	*Csda*	4.67	4.62	4.68	4.44
ENSMUSG00000030199	*Etv6*	2.59	2.48	2.88	2.44
ENSMUSG00000030201	*Lrp6*	3.86	3.31	3.51	3.13
ENSMUSG00000030203	*Dusp16*	4.27	4.04	3.84	3.62
ENSMUSG00000030204	*Ddx47*	4.35	4.34	4.44	4.26
ENSMUSG00000030207	*8430419L09Ri*	3.82	3.52	4.22	3.43
ENSMUSG00000030208	*Emp1*	1.12	1.27	0.33	0.42

ENSMUSG00000030213	*Atf7ip*	2.46	2.75	2.9	2.36
ENSMUSG00000030214	*1100001H23Ri*	5.39	4.99	4.92	4.74
ENSMUSG00000030216	*Wbp11*	4.63	4.51	4.62	4.58
ENSMUSG00000030218	*Mgp*	1.17	1.73	2	2.35
ENSMUSG00000030219	*Erp27*	0.42	0.68	1.63	-0.05
ENSMUSG00000030220	*Arhgdib*	2.98	2.97	3.38	2.72
ENSMUSG00000030222	*Rerg*	1.09	-0.33	0.69	0.07
ENSMUSG00000030224	*Strap*	6.02	5.06	5.46	5.2
ENSMUSG00000030225	*Dera*	6.12	5.94	5.96	5.66
ENSMUSG00000030228	*Pik3c2g*	3.35	2.36	3.1	2.26
ENSMUSG00000030231	*Plekha5*	2.53	2.7	2.79	2.39
ENSMUSG00000030232	*Aebp2*	2.95	2.19	2.53	1.98
ENSMUSG00000030236	*Slco1b2*	9.16	7.9	8.86	8.22
ENSMUSG00000030237	*Slco1a4*	6.52	5.6	6.68	5.84
ENSMUSG00000030243	*Recql*	1.49	1.25	1.34	1.27
ENSMUSG00000030244	*Gys2*	5.77	5.57	6.43	6.55
ENSMUSG00000030245	*Golt1b*	1.97	1.24	1.45	1.1
ENSMUSG00000030247	*Kcnj8*	1.58	1.02	1.57	1.14
ENSMUSG00000030249	*Abcc9*	2.87	2.27	2.37	2.15
ENSMUSG00000030259	*Rassf8*	3.47	3.21	3.04	3.02
ENSMUSG00000030264	*Thumpd3*	3.45	3.23	3.19	2.95
ENSMUSG00000030265	*Kras*	3.89	2.86	3.24	2.63
ENSMUSG00000030269	*1110061O04Ri*	3.81	4.06	3.98	3.58
ENSMUSG00000030271	*Ogg1*	0.74	1.8	1.74	1.8
ENSMUSG00000030272	*Camk1*	3.3	3.59	3.26	3.21
ENSMUSG00000030275	*NA*	4.24	4.04	4.14	3.74
ENSMUSG00000030281	*Il17rc*	4.3	4.91	4.43	4.06
ENSMUSG00000030282	*Cmas*	5.29	4.6	4.71	4.42
ENSMUSG00000030284	*Creld1*	4.54	5.18	4.92	4.71
ENSMUSG00000030286	*Tmem111*	5.46	5.32	5.23	5.09
ENSMUSG00000030287	*Itpr2*	2.62	2.49	2.93	2.65

ENSMUSG00000030291	*Med21*	3.68	3.39	3.71	3.33
ENSMUSG00000030298	*Sec13*	5.01	5.53	5.11	5.07
ENSMUSG00000030301	*Ccdc91*	3.74	3.75	3.82	3.74
ENSMUSG00000030303	*Mlstd1*	2.62	1.84	2.1	1.72
ENSMUSG00000030304	*Ergic2*	4.63	4.12	4.39	3.96
ENSMUSG00000030313	*D030011O10R*	4.82	4.02	4.6	4.15
ENSMUSG00000030314	*Atg7*	4.08	4.29	3.99	3.86
ENSMUSG00000030315	*Vgll4*	3.31	3.12	3.27	3.53
ENSMUSG00000030327	*Necap1*	5	4.28	4.81	4.46
ENSMUSG00000030330	*Ing4*	4.31	3.92	4.1	3.6
ENSMUSG00000030335	*bMRP64*	4.84	4.34	4.8	4.72
ENSMUSG00000030339	*Ltbr*	5.51	6.32	6	5.82
ENSMUSG00000030340	*Scnn1a*	3.37	3.66	4.07	3.95
ENSMUSG00000030341	*Tnfrsf1a*	5.94	6.18	6.02	6
ENSMUSG00000030342	*Cd9*	4	4.57	3.88	4.4
ENSMUSG00000030347	*D6Wsu163e*	2.52	2.42	2.55	2.44
ENSMUSG00000030352	*Tspan9*	3.78	4.04	3.64	3.68
ENSMUSG00000030357	*Fkbp4*	6.86	7.04	6.66	6.68
ENSMUSG00000030359	*Pzp*	10.14	10.31	10.14	10.19
ENSMUSG00000030374	*Strn4*	3.64	4.27	4.03	3.72
ENSMUSG00000030378	*2810007J24Ri*	8.88	7.21	8.06	7.16
ENSMUSG00000030382	*Slc27a5*	9	9.16	9.06	8.95
ENSMUSG00000030397	*mKIAA1860*	2.22	2.43	2.51	2.19
ENSMUSG00000030399	*Ckm*	#NAME?	-2.82	3.08	3.3
ENSMUSG00000030400	*Ercc2*	1.79	1.91	1.85	1.34
ENSMUSG00000030403	*Vasp*	2.97	2.93	2.99	2.67
ENSMUSG00000030407	*Qpctl*	2.97	3.09	3.21	2.82
ENSMUSG00000030409	*Dmpk*	2.28	2.65	2.72	2.37
ENSMUSG00000030410	*Dmwd*	3.02	3.71	3.41	3.32
ENSMUSG00000030417	*Pdcd5*	1.58	2.02	2.31	2.02
ENSMUSG00000030421	*C80913*	4.04	3.31	3.89	3.5

ENSMUSG00000030423	*Pop4*	3.89	3.71	3.48	3.55
ENSMUSG00000030424	*NA*	1.44	0.07	1	0.47
ENSMUSG00000030431	*2210411K11Ri*	2.38	4.23	3.39	3.07
ENSMUSG00000030432	*Rpl28*	0.75	1.71	1.71	1.42
ENSMUSG00000030435	*U2af2*	2.46	3.2	3	2.88
ENSMUSG00000030447	*Cyfip1*	3.95	3.78	3.76	3.56
ENSMUSG00000030451	*Herc2*	2.26	2.34	2.21	1.91
ENSMUSG00000030452	*Nipa2*	4.05	2.81	3.72	3.17
ENSMUSG00000030465	*Psd3*	2.8	1.62	2.62	2.1
ENSMUSG00000030469	*NA*	1.08	0.38	0.47	0.31
ENSMUSG00000030470	*Csrp3*	4.29	5.17	4.34	3.7
ENSMUSG00000030471	*Zdhhc13*	2.09	1.3	1.63	0.93
ENSMUSG00000030474	*Siglece*	1.86	1.67	1.69	0.78
ENSMUSG00000030483	*Cyp2b10*	6.48	2.86	4.91	2.87
ENSMUSG00000030494	*Rhpn2*	2.83	3.48	2.95	2.53
ENSMUSG00000030498	*Gas2*	4.38	3.33	4.23	3.33
ENSMUSG00000030499	*Kctd15*	2.11	2.69	2.15	2
ENSMUSG00000030505	*Prmt3*	2.46	2.9	2.12	2.28
ENSMUSG00000030509	*Asb7*	1.89	1.39	1.74	1.37
ENSMUSG00000030512	*Snrpa1*	3.75	3.67	3.61	3.34
ENSMUSG00000030513	*NA*	5.23	5.68	5.09	5.28
ENSMUSG00000030515	*Tarsl2*	2.84	2.39	2.91	2.45
ENSMUSG00000030516	*Tjp1*	3.35	2.7	3.36	2.84
ENSMUSG00000030521	*Mphosph10*	3.5	3.29	2.88	2.91
ENSMUSG00000030522	*Mtmr10*	3.77	3.27	3.88	3.55
ENSMUSG00000030527	*Crtc3*	1.8	2.36	2.12	2.11
ENSMUSG00000030530	*Furin*	7.01	7.37	7.45	7.3
ENSMUSG00000030532	*Hddc3*	3.73	3.82	3.44	3.37
ENSMUSG00000030533	*Unc45a*	2.04	2.8	2.65	2.4
ENSMUSG00000030534	*Vps33b*	1.59	1.69	1.77	1.76
ENSMUSG00000030536	*Iqgap1*	1.36	1.04	1.16	0.81

ENSMUSG00000030538	*Cib1*	4.68	5.2	5.35	5.23
ENSMUSG00000030539	*Sema4b*	1.71	2.38	2.34	1.9
ENSMUSG00000030541	*Idh2*	6.86	6.8	6.74	6.3
ENSMUSG00000030545	*Pex11a*	6.57	6.55	6.25	5.78
ENSMUSG00000030551	*Nr2f2*	3.31	2.78	3.51	3.31
ENSMUSG00000030555	*Ttc23*	4.94	4.2	5.08	4.72
ENSMUSG00000030556	*Lrrc28*	3.89	3.05	3.92	3.82
ENSMUSG00000030557	*Mef2a*	3.4	2.68	3.24	2.86
ENSMUSG00000030560	*Ctsc*	6.53	6	5.66	5.42
ENSMUSG00000030562	*Kox-1*	2.48	2.28	1.88	2.35
ENSMUSG00000030579	*Tyrobp*	3.92	3.79	4.03	3.47
ENSMUSG00000030587	*NA*	2.91	3.69	3.43	3.34
ENSMUSG00000030588	*Yif1b*	4.39	5.23	4.96	4.86
ENSMUSG00000030590	*1110006G06Ri*	1.12	1.86	1.49	1.51
ENSMUSG00000030591	*Psmd8*	6.56	7.08	6.69	6.7
ENSMUSG00000030595	*Nfkbib*	2.9	3.74	3.6	3.37
ENSMUSG00000030602	*Pak4*	2.47	3.37	2.76	2.45
ENSMUSG00000030603	*Psmc4*	6.25	6.66	6.22	6.14
ENSMUSG00000030605	*Mfge8*	2.28	2.84	3.31	2.46
ENSMUSG00000030609	*Isg20l1*	1.77	3.02	2.07	2.28
ENSMUSG00000030610	*Det1*	1.76	2.2	1.61	1.43
ENSMUSG00000030611	*Mrps11*	3.54	4.15	3.94	4
ENSMUSG00000030612	*Mrpl46*	4.04	4.46	4.37	4.24
ENSMUSG00000030613	*Ccdc90b*	2.94	2.24	2.87	1.88
ENSMUSG00000030614	*Tmem126b*	4.58	3.39	4.31	3.84
ENSMUSG00000030615	*Tmem126a*	4.95	4.46	4.67	4.56
ENSMUSG00000030619	*Eed*	3.61	2.41	3.34	3.08
ENSMUSG00000030623	*NA*	1.67	1.58	0.99	0.82
ENSMUSG00000030629	*Zfand6*	6.27	5.39	5.98	5.43
ENSMUSG00000030630	*Fah*	9.04	9.22	9.34	9.07
ENSMUSG00000030643	*Rab30*	4.08	2.89	4.17	3.3

ENSMUSG00000030647	*Ndufc2*	5.97	5.76	5.96	5.64
ENSMUSG00000030649	*3200002M19R*	1	1.1	1.22	0.91
ENSMUSG00000030652	*clk-1*	3.19	3.15	3.38	3.08
ENSMUSG00000030653	*Pde2a*	3.6	4.23	3.62	3.57
ENSMUSG00000030654	*Arl6ip1*	7.11	6.11	6.94	6.37
ENSMUSG00000030655	*2610207I05Rik*	2.92	1.93	2.47	2.13
ENSMUSG00000030659	*Nucb2*	1.29	0.98	0.9	0.75
ENSMUSG00000030660	*Pik3c2a*	3.12	2.03	2.67	2.24
ENSMUSG00000030662	*Ranbp5*	3.77	3.57	3.85	3.56
ENSMUSG00000030663	*1110004F10Ri*	4.19	4.1	4	3.72
ENSMUSG00000030664	*NA*	0.53	0.65	1.68	1.42
ENSMUSG00000030670	*Cyp2r1*	3.66	2.23	2.81	2.05
ENSMUSG00000030671	*Pde3b*	4.84	3.97	4.71	4.3
ENSMUSG00000030672	*Mylpf*	-1.55	-0.46	2.71	2.96
ENSMUSG00000030674	*Qprt*	6.52	6.89	6.61	6.3
ENSMUSG00000030678	*Maz*	4.68	5.51	4.86	4.9
ENSMUSG00000030680	*2900092E17Ri*	3.66	4	3.95	3.63
ENSMUSG00000030681	*Mvp*	3.29	4.18	3.63	3.46
ENSMUSG00000030682	*Cdipt*	4.73	5.68	5.12	4.95
ENSMUSG00000030685	*Kctd13*	0.97	1.53	2.05	1.42
ENSMUSG00000030688	*Stard10*	9.45	10.13	9.74	9.55
ENSMUSG00000030689	*Ccdc95*	1.97	2.59	2	2.21
ENSMUSG00000030691	*mKIAA0769*	3.58	2.62	3.42	3.05
ENSMUSG00000030695	*Aldoa*	5.15	5.62	5.65	5.37
ENSMUSG00000030697	*Ppp4c*	4.91	5.21	4.75	4.73
ENSMUSG00000030701	*Plekhb1*	4.13	3.93	3.65	3.27
ENSMUSG00000030703	*Gdpd3*	3.54	3.81	4.22	3.99
ENSMUSG00000030704	*Rab6*	5.06	3.91	4.71	4.28
ENSMUSG00000030706	*Mrpl48*	2.57	1.95	2.59	2.54
ENSMUSG00000030707	*Coro1a*	1.08	1.46	2.82	1.02
ENSMUSG00000030711	*Sult1a1*	8.85	8.15	8.71	8.16

ENSMUSG00000030714	*Ccdc101*	3.02	4.09	4.03	3.74
ENSMUSG00000030718	*Ppme1*	4.48	4.6	4.46	4.21
ENSMUSG00000030720	*Cln3*	2.23	2.77	2.55	2.38
ENSMUSG00000030724	*Cd19*	-2.31	#NAME?	1.29	#NAME?
ENSMUSG00000030726	*Pold3*	1.78	1.66	2.07	1.73
ENSMUSG00000030727	*Rabep2*	1.44	1.82	1.58	1.63
ENSMUSG00000030730	*Atp2a1*	-4.34	-3.96	3.47	3.23
ENSMUSG00000030731	*Syt3*	1.8	2.8	1.93	2.21
ENSMUSG00000030733	*Psmbeta*	3.54	4.17	4.04	4.05
ENSMUSG00000030737	*Slco2b1*	6.13	6.31	6.15	5.98
ENSMUSG00000030738	*Eif3c*	5.82	6.07	5.82	5.67
ENSMUSG00000030739	*Myh14*	1.81	2.42	2.15	1.76
ENSMUSG00000030741	*Spns1*	3.48	4.39	4.12	4.02
ENSMUSG00000030744	*Rps3*	6.36	6.93	6.76	6.7
ENSMUSG00000030747	*Dgat2*	8.57	8.77	8.66	8.72
ENSMUSG00000030748	*Il4ra*	3.05	3.83	3.68	3.27
ENSMUSG00000030750	*Nsmce1*	2.72	3.54	2.73	2.87
ENSMUSG00000030751	*Psma1*	6.63	6.37	6.44	6.03
ENSMUSG00000030753	*Prkrir*	4.97	3.91	4.29	4.03
ENSMUSG00000030754	*Copb1*	5.63	5.36	5.61	5.19
ENSMUSG00000030760	*Phca*	2.59	1.54	2.11	1.45
ENSMUSG00000030761	*Myo7a*	1.22	1.96	0.97	1.34
ENSMUSG00000030762	*Aqp8*	6.67	6.9	6.14	6
ENSMUSG00000030763	*Lcmt1*	2.67	2.68	2.62	2.38
ENSMUSG00000030766	*Arhgap17*	2.21	2.3	2.61	2.47
ENSMUSG00000030770	*Parva*	5.45	5.39	5.25	4.89
ENSMUSG00000030779	*Rbbp6*	3.31	2.55	3.02	2.69
ENSMUSG00000030780	*BC017158*	3.7	3.79	3.5	3.05
ENSMUSG00000030781	*Slc5a2*	2.21	2.34	1.87	1.47
ENSMUSG00000030785	*Cox6a2*	#NAME?	#NAME?	2.53	2.66
ENSMUSG00000030787	*Lyve1*	2.19	2	1.12	2.13

ENSMUSG00000030788	*Znf230*	4.76	3.94	4.3	3.7
ENSMUSG00000030795	*Fus*	3.64	4.08	4.08	3.93
ENSMUSG00000030798	*Cd37*	0.53	0.15	1.81	-1.35
ENSMUSG00000030801	*Myst1*	3.47	3.78	3.69	3.55
ENSMUSG00000030802	*Bckdk*	2.57	3.38	3.05	2.69
ENSMUSG00000030804	*Vkorc1*	7.78	8.17	7.93	7.9
ENSMUSG00000030805	*Stx4a*	3.94	4.38	3.77	3.65
ENSMUSG00000030815	*Phkg2*	3.35	3.95	3.63	3.33
ENSMUSG00000030816	*Rnf40*	3.45	4.01	3.68	3.61
ENSMUSG00000030822	*Prr14*	4.39	4.82	4.56	4.38
ENSMUSG00000030824	*Nucb1*	6.71	7.41	6.91	6.79
ENSMUSG00000030826	*Bcat2*	4.13	4.56	4.42	3.96
ENSMUSG00000030827	*Fgf21*	2.69	2.84	2.86	3.14
ENSMUSG00000030830	*Itgal*	1.88	1.78	1.62	1.53
ENSMUSG00000030834	*Abcc6*	4.13	4.51	4.45	4.38
ENSMUSG00000030835	*Nomo1*	3.94	4.52	4.07	3.95
ENSMUSG00000030842	*2400001E08Ri*	4.21	4.85	4.68	4.44
ENSMUSG00000030846	*Tial1*	3.7	2.97	3.54	3.04
ENSMUSG00000030847	*Bag3*	4.47	4.96	4.62	5.3
ENSMUSG00000030849	*Fgfr2*	2.58	3.07	2.94	3
ENSMUSG00000030850	*Ate1*	3.51	2.95	3.19	2.66
ENSMUSG00000030852	*Tacc2*	2.65	2.52	2.36	1.97
ENSMUSG00000030861	*Acadsb*	6.5	5.5	6.02	5.62
ENSMUSG00000030868	*Dctn5*	4.54	4.28	4.5	4.57
ENSMUSG00000030869	*Ndufab1*	2.75	1.95	2.75	2.71
ENSMUSG00000030870	*Ubfd1*	3.89	3.85	3.28	3.67
ENSMUSG00000030871	*Ears2*	2.83	3.76	2.67	2.47
ENSMUSG00000030872	*Gga2*	3.2	3.51	3.32	3.03
ENSMUSG00000030876	*Mettl9*	5.31	4.29	4.57	3.97
ENSMUSG00000030879	*Mrpl17*	5.8	6.66	6.2	5.9
ENSMUSG00000030880	*Polr3e*	2.24	2.77	2.46	2.52

ENSMUSG00000030881	*Arfip2*	2.18	2.95	2.25	2.39
ENSMUSG00000030882	*Fxc1*	1.04	1.37	1.62	1.79
ENSMUSG00000030884	*Uqcrc2*	8	7.58	7.97	7.54
ENSMUSG00000030887	*4930408O21Ri*	2.11	-0.19	0.93	0.13
ENSMUSG00000030888	*1500003O22Ri*	2.92	3.17	2.92	2.98
ENSMUSG00000030890	*Ilk*	4.82	4.73	5.01	4.95
ENSMUSG00000030894	*Tpp1*	5.68	5.73	5.82	5.62
ENSMUSG00000030895	*Hpx*	10.71	10.97	11	11.01
ENSMUSG00000030909	*Anks4b*	5.17	5.16	4.93	4.9
ENSMUSG00000030917	*Tmem159*	1.25	0.86	0.72	0.93
ENSMUSG00000030921	*Trim30*	1.05	-0.2	0.08	-0.45
ENSMUSG00000030922	*Lyrm1*	1.33	1.1	1.49	1.27
ENSMUSG00000030929	*Exod1*	4.53	3.28	4.27	3.46
ENSMUSG00000030930	*4631426J05Ri*	2.66	2.9	2.42	2.37
ENSMUSG00000030934	*Oat*	9.18	8.8	9.57	9.08
ENSMUSG00000030935	*Acsm3*	5.78	4.72	5.57	5.02
ENSMUSG00000030942	*Thumpd1*	3.74	3.4	3.47	3.21
ENSMUSG00000030946	*2310007H09Ri*	5.99	6.11	6.1	5.69
ENSMUSG00000030956	*A930008G19R*	2.13	2.02	2.85	2.47
ENSMUSG00000030960	*2010208K18Ri*	1.99	1.14	1.58	1.67
ENSMUSG00000030965	*C430003P19Ri*	3.99	3.66	3.94	3.64
ENSMUSG00000030966	*Trim21*	2.2	1.71	1.46	1.23
ENSMUSG00000030967	*Zranb1*	4.44	3.69	4.19	4.02
ENSMUSG00000030968	*NA*	1.58	1.11	0.36	1.07
ENSMUSG00000030972	*C730027J19Ri*	5.66	5.73	5.29	5.23
ENSMUSG00000030978	*Rrm1*	2.02	1.87	2.33	2.16
ENSMUSG00000030979	*Uros*	3.35	3.48	3.5	2.92
ENSMUSG00000030980	*Tsg118*	3.75	3.65	3.6	3.47
ENSMUSG00000030982	*9030624J02Ri*	3.25	3.45	3.58	3.3
ENSMUSG00000030983	*Bccip*	6.1	5.93	5.89	5.57
ENSMUSG00000030986	*Dhx32*	4.01	3.99	3.78	3.5

ENSMUSG00000030987	*Stim1*	4.19	4.54	4.38	4.28
ENSMUSG00000030990	*Frag1*	3.78	3.53	3.3	3.12
ENSMUSG00000031007	*Atp6ap2*	4.69	3.89	4.52	4.12
ENSMUSG00000031010	*Usp9x*	3.67	3	3.32	2.79
ENSMUSG00000031012	*Cask*	2.17	1.66	1.96	1.79
ENSMUSG00000031015	*Swap70*	1.04	1.49	1.89	1.58
ENSMUSG00000031016	*Wee1*	0.11	-0.6	1.46	1.39
ENSMUSG00000031021	*Tmem9b*	4.17	3.97	4.08	3.94
ENSMUSG00000031023	*D930014E17R*	4.17	3.81	3.76	3.7
ENSMUSG00000031024	*St5*	4.34	4.08	3.73	3.13
ENSMUSG00000031029	*Eif3f*	6.41	6.45	6.45	6.33
ENSMUSG00000031059	*Ndufb11*	5.65	5.88	6.2	6.02
ENSMUSG00000031060	*Rbm10*	1.56	2.13	1.88	1.39
ENSMUSG00000031065	*Pctk1*	3.34	3.33	3.28	2.98
ENSMUSG00000031068	*PICOT*	3.34	1.78	2.73	2.09
ENSMUSG00000031072	*Oraov1*	2.53	2.82	2.56	2.32
ENSMUSG00000031077	*Fadd*	3.02	3.36	3.23	3.31
ENSMUSG00000031078	*Cttn*	3.75	3.82	3.74	3.55
ENSMUSG00000031090	*Nadsyn1*	3.11	3.38	3.39	3.01
ENSMUSG00000031095	*Cul4b*	3.94	2.68	3.59	3
ENSMUSG00000031097	*Tnni2*	-4.02	#NAME?	2.89	3.84
ENSMUSG00000031109	*Enox2*	2.48	1.8	2.17	1.58
ENSMUSG00000031119	*Gpc4*	5.09	4.79	5.21	4.98
ENSMUSG00000031129	*Slc9a9*	1.48	1.39	0.64	0.64
ENSMUSG00000031134	*Rbmx*	2.42	1.84	2.02	1.67
ENSMUSG00000031138	*F9*	7.51	6.24	7.15	6.47
ENSMUSG00000031143	*Ccdc22*	2.58	3	2.96	3.1
ENSMUSG00000031147	*Pdzx*	3.32	4.19	3.82	3.71
ENSMUSG00000031148	*Gpkow*	3.18	2.41	2.71	2.5
ENSMUSG00000031149	*Praf2*	1.56	1.58	1.33	1.94
ENSMUSG00000031153	*Gripap1*	2.7	2.98	2.82	2.62

ENSMUSG00000031154	*Otud5*	3.67	3.65	3.87	3.5
ENSMUSG00000031156	*Slc35a2*	2.82	2.68	2.51	2.5
ENSMUSG00000031157	*Pqbp1*	4.19	4.34	4.34	4.1
ENSMUSG00000031158	*Timm17b*	5.37	5.59	5.43	5.28
ENSMUSG00000031161	*Hdac6*	2.19	2.53	2.32	2.57
ENSMUSG00000031166	*Wdr13*	3.25	3.24	2.73	2.61
ENSMUSG00000031168	*Ebp*	7.87	7.9	7.88	7.74
ENSMUSG00000031169	*Porcn*	1.45	2.29	1.57	1.38
ENSMUSG00000031171	*Ftsj1*	2.86	3.11	3.07	3.08
ENSMUSG00000031173	*Otc*	8.42	7.85	8.22	7.68
ENSMUSG00000031176	*Dynlt3*	5.88	4.71	5.43	4.88
ENSMUSG00000031196	*F8*	2.58	1.42	1.73	1.57
ENSMUSG00000031197	*Vbp1*	3.7	2.52	3.33	2.58
ENSMUSG00000031198	*Fundc2*	3.06	1.87	2.53	0.18
ENSMUSG00000031201	*Brcc3*	2.31	1.56	2.1	1.54
ENSMUSG00000031207	*Msn*	3.72	3.52	3.66	3.26
ENSMUSG00000031216	*Stard8*	2.7	2.71	2.22	1.96
ENSMUSG00000031217	*Efnb1*	3	3.71	2.87	2.85
ENSMUSG00000031221	*Igbp1*	5.63	5.54	5.46	5.46
ENSMUSG00000031226	*2610029G23Ri*	2.82	2.32	2.5	2.98
ENSMUSG00000031229	*Atrx*	2.77	1.96	2.23	1.59
ENSMUSG00000031231	*Cox7b*	6.22	6.9	6.86	7.65
ENSMUSG00000031232	*2610529C04Ri*	5.27	5.07	4.21	4.54
ENSMUSG00000031242	*2610002M06R*	3.01	2.36	2.49	1.89
ENSMUSG00000031245	*Nsbp1*	5.44	4.86	4.72	3.96
ENSMUSG00000031246	*Sh3bgrl*	6.21	4.46	5.54	4.8
ENSMUSG00000031256	*Cstf2*	2.4	2.18	2.33	1.96
ENSMUSG00000031266	*Gla*	2.27	1.47	2.08	1.56
ENSMUSG00000031271	*Serpina7*	3.55	3.04	2.68	2.09
ENSMUSG00000031278	*Acsl4*	3.94	3.29	3.69	3.31
ENSMUSG00000031286	*Glt28d2*	1.94	1.03	1.9	1.08

ENSMUSG00000031295	*Phka2*	2.6	2.54	2.36	2.46
ENSMUSG00000031299	*Pdha1*	6.23	5.51	6.09	5.53
ENSMUSG00000031303	*NA*	3.83	3.02	3.64	3.04
ENSMUSG00000031304	*Gm614*	0.37	-0.08	1.3	0.34
ENSMUSG00000031309	*Rps6ka3*	1.41	0.76	1.17	0.67
ENSMUSG00000031310	*Zmym3*	1.17	0.9	1.01	1.22
ENSMUSG00000031311	*Nono*	4.01	3.87	4.09	3.43
ENSMUSG00000031314	*Taf1*	1.78	1.29	1.53	1.1
ENSMUSG00000031320	*Rps4x*	3.91	5	4.79	3.95
ENSMUSG00000031327	*Chic1*	1.93	0.04	0.72	-0.18
ENSMUSG00000031328	*Flna*	2.11	2.34	1.95	2.06
ENSMUSG00000031333	*NA*	4.27	3.03	3.74	3.19
ENSMUSG00000031337	*Mtm1*	2.47	1.39	2.36	1.73
ENSMUSG00000031347	*Cetn2*	4.27	3.14	3.73	3
ENSMUSG00000031349	*Nsdhl*	6.25	5.48	5.66	4.96
ENSMUSG00000031352	*Hccs*	3.23	2.41	3.07	2.64
ENSMUSG00000031353	*Rbbp7*	4.21	3.74	3.72	3.46
ENSMUSG00000031357	*Syap1*	5.79	4.27	5.2	4.56
ENSMUSG00000031358	*Msl31*	4.7	3.76	4.36	3.82
ENSMUSG00000031360	*Ctps2*	2.14	1.72	1.56	1.42
ENSMUSG00000031365	*Zfp275*	2.21	2.04	1.88	1.43
ENSMUSG00000031371	*Uchl5ip*	2.97	3.27	2.83	2.08
ENSMUSG00000031373	*Car5b*	1.05	0.91	1.23	0.68
ENSMUSG00000031375	*Bgn*	6.41	6.54	6.57	6.34
ENSMUSG00000031378	*Abcd1*	3.4	3.74	3.99	3.3
ENSMUSG00000031379	*Pir*	3.97	4.02	3.97	3.9
ENSMUSG00000031381	*Piga*	1.1	1.17	0.81	0.92
ENSMUSG00000031386	*Hcfc1*	2.82	3.34	3.08	2.88
ENSMUSG00000031387	*Renbp*	1.06	1.61	1.41	1.16
ENSMUSG00000031388	*Ard1*	3.63	4.14	4.13	3.87
ENSMUSG00000031392	*IRAK1-S*	4.85	4.88	4.73	4.46

ENSMUSG00000031393	*Mecp2*	1.84	1.36	1.72	1.32
ENSMUSG00000031399	*1810037C20Ri*	2.57	3.53	3.32	3.02
ENSMUSG00000031400	*G6pdx*	1.36	1.74	1.03	1.17
ENSMUSG00000031402	*Mpp1*	3.72	3.48	3.74	3.46
ENSMUSG00000031403	*Dkc1*	3.31	3.58	3.41	2.8
ENSMUSG00000031422	*Morf4l2*	4.4	4.6	3.89	3.71
ENSMUSG00000031429	*Psmd10*	3.05	2.96	2.46	3.05
ENSMUSG00000031431	*Tsc22d3*	6.93	6.56	6.84	7.02
ENSMUSG00000031432	*Prps1*	4.19	4.21	4.28	3.89
ENSMUSG00000031433	*Rbm41*	1.01	-1.6	-0.36	-0.52
ENSMUSG00000031438	*Rnf128*	6.16	5.37	5.7	5.19
ENSMUSG00000031443	*F7*	6.26	6.86	6.32	6.19
ENSMUSG00000031444	*F10*	7.91	8.47	8.09	8.01
ENSMUSG00000031445	*Proz*	7.78	7.63	7.49	7.34
ENSMUSG00000031446	*Cul4a*	5.28	5.19	5.28	5.08
ENSMUSG00000031447	*Lamp1*	8.59	8.42	8.55	8.4
ENSMUSG00000031451	*Gas6*	4.18	4.88	3.83	3.93
ENSMUSG00000031453	*Rasa3*	2.1	2.27	2.88	2.52
ENSMUSG00000031458	*2410022L05Ri*	1.69	1.66	1.57	0.33
ENSMUSG00000031467	*Agpat5*	3.84	3.12	3.28	3.07
ENSMUSG00000031478	*Nek3*	0.19	0.45	1.31	-0.17
ENSMUSG00000031479	*Vps36*	4.38	3.81	3.75	3.61
ENSMUSG00000031482	*Slc25a15*	7.99	7.05	7.85	7.28
ENSMUSG00000031483	*Erlin2*	4.27	3.6	3.99	3.68
ENSMUSG00000031485	*Prosc*	5.89	5.53	5.83	5.63
ENSMUSG00000031487	*Brf2*	2.24	2.93	2.89	2.48
ENSMUSG00000031488	*Rab11fip1*	1.32	1.64	1.59	1.52
ENSMUSG00000031490	*Eif4ebp1*	4.76	5.76	5.45	5.34
ENSMUSG00000031502	*Col4a1*	2.71	3.49	2.97	2.83
ENSMUSG00000031503	*Col4a2*	2.15	2.72	2.5	2.17
ENSMUSG00000031504	*Rab20*	2.01	3.21	2.39	2.35

ENSMUSG00000031505	*0710008K08Ri*	5.45	5.86	5.56	5.44
ENSMUSG00000031508	*Ankrd10*	1.47	1.74	1.61	1.15
ENSMUSG00000031511	*Arhgef7*	2.06	2.63	2.22	1.99
ENSMUSG00000031513	*Leprotl1*	3.51	3.17	3.14	3.02
ENSMUSG00000031516	*Dctn6*	3.26	3.52	3.29	2.96
ENSMUSG00000031520	*Vegfc*	1.19	0.69	0.88	0.97
ENSMUSG00000031521	*Aga*	4.18	3.01	3.73	3.32
ENSMUSG00000031523	*Dlc1*	2.89	3.2	2.75	2.63
ENSMUSG00000031527	*Thex1*	2.75	1.71	2.41	2
ENSMUSG00000031529	*Tnks*	2.27	1.81	2.02	1.97
ENSMUSG00000031532	*Tmem66*	6.02	5.77	5.59	5.68
ENSMUSG00000031533	*Mrps31*	4.76	4.93	5.05	4.78
ENSMUSG00000031534	*AI316807*	4.56	4.12	4.21	3.86
ENSMUSG00000031536	*Polb*	3.86	3.52	4.14	3.63
ENSMUSG00000031537	*Ikbkb*	3.81	3.92	3.79	3.66
ENSMUSG00000031540	*Myst3*	2.66	2.24	2.54	2.33
ENSMUSG00000031545	*Agpat6*	6.36	6.45	6.09	5.78
ENSMUSG00000031546	*Gins4*	3.58	3.57	3.63	3.35
ENSMUSG00000031549	*Indol1*	5.99	5.76	6.47	6.18
ENSMUSG00000031555	*Adam9*	4.94	4.7	4.69	4.46
ENSMUSG00000031556	*Tm2d2*	5.84	6.32	5.86	5.61
ENSMUSG00000031557	*Plekha2*	1.09	0.65	0.79	0.38
ENSMUSG00000031561	*Odz3*	1.86	1.17	2.05	1.44
ENSMUSG00000031563	*BC040690*	1.83	1.67	2.12	1.79
ENSMUSG00000031568	*Rwdd4a*	3.97	3.72	3.78	3.75
ENSMUSG00000031570	*Ppapdc1*	4.05	4.1	3.4	3.15
ENSMUSG00000031575	*Ash2l*	2.78	3	3.11	2.79
ENSMUSG00000031577	*BC019943*	2.72	2.61	2.62	2.58
ENSMUSG00000031578	*Rbm13*	3.74	3.18	3.34	3.27
ENSMUSG00000031583	*Wrn*	1.78	0.9	1.56	1.59
ENSMUSG00000031584	*Gsr*	5.23	5.14	5.03	4.8

ENSMUSG00000031585	*Gtf2e2*	3.63	3.03	3.4	2.99
ENSMUSG00000031586	*Rbpms*	4.33	4.11	4.28	3.96
ENSMUSG00000031590	*Frg1*	4.53	3.4	4.38	3.78
ENSMUSG00000031591	*Asah1*	4.9	3.83	4.48	3.85
ENSMUSG00000031592	*pcm-1*	2.4	1.32	2.05	1.54
ENSMUSG00000031594	*Fgl1*	8.71	9.01	8.43	8.19
ENSMUSG00000031596	*Slc7a2*	7.27	6.24	7.14	6.54
ENSMUSG00000031600	*Vps37a*	3.73	2.56	3.35	2.97
ENSMUSG00000031601	*Cnot7*	3.88	2.71	3.41	2.83
ENSMUSG00000031604	*Sc4mol*	6.76	5.86	6.04	5.5
ENSMUSG00000031605	*Klhl2*	3.75	3.62	3.67	3.83
ENSMUSG00000031609	*Sap30*	1.32	1.78	1.85	1.08
ENSMUSG00000031613	*Hpgd*	7.77	6.83	7.05	6.77
ENSMUSG00000031616	*Ednra*	1.06	0.67	0.86	0.6
ENSMUSG00000031617	*Tmem34*	3.44	2.98	3.12	2.29
ENSMUSG00000031618	*Nr3c2*	0.1	-0.53	1.66	1.49
ENSMUSG00000031622	*NA*	3.13	3.67	3.1	3.19
ENSMUSG00000031626	*Sorbs2*	3.9	3.23	3.49	3.35
ENSMUSG00000031627	*Irf2*	5.45	5.2	5.54	5.23
ENSMUSG00000031628	*Casp3*	3.96	3.31	3.25	2.84
ENSMUSG00000031631	*4933411K20Ri*	2.92	2.1	2.51	2.1
ENSMUSG00000031633	*Slc25a4*	2.34	1.9	2.91	2.94
ENSMUSG00000031634	*1810047C23Ri*	4.94	4.36	4.78	4.42
ENSMUSG00000031640	*Klkb1*	6.89	6.47	6.8	6.54
ENSMUSG00000031641	*Cbr4*	4.55	4.32	4.29	3.7
ENSMUSG00000031644	*Nek1*	2.13	0.87	1.61	1
ENSMUSG00000031645	*F11*	5.82	5.44	5.77	5.47
ENSMUSG00000031652	*NA*	3	2.97	3.05	2.69
ENSMUSG00000031657	*Heatr3*	3.86	3.79	3.84	3.62
ENSMUSG00000031660	*Brd7*	4.37	4.36	4.5	4.06
ENSMUSG00000031661	*Nkd1*	1.13	2.53	2.13	2.18

ENSMUSG00000031665	*Sall1*	3.67	4.06	4.01	3.92
ENSMUSG00000031666	*Rbl2*	4.27	3.71	4.39	3.8
ENSMUSG00000031667	*Aktip*	2.99	2.49	2.93	2.48
ENSMUSG00000031668	*Eif2ak3*	2.12	2.83	2.16	2.18
ENSMUSG00000031671	*Setd6*	3.58	3.58	2.95	2.78
ENSMUSG00000031672	*Got2*	6.5	6.69	6.61	6.31
ENSMUSG00000031681	*Smad1*	2.03	2.02	2	1.77
ENSMUSG00000031683	*Lsm6*	2.1	2.07	2.07	1.81
ENSMUSG00000031684	*P7*	1.53	1.34	1.49	1.41
ENSMUSG00000031691	*Tnpo2*	3.64	3.95	3.91	3.63
ENSMUSG00000031696	*Vps35*	5.91	4.83	5.42	4.87
ENSMUSG00000031697	*Orc6l*	1.52	1.45	1.55	-0.1
ENSMUSG00000031700	*Gpt2*	7.62	7.16	7.94	7.16
ENSMUSG00000031701	*Dnaja2*	6.27	5.86	6.12	5.62
ENSMUSG00000031703	*Itfg1*	5.4	4.63	4.91	4.42
ENSMUSG00000031706	*Rfx1*	1.76	2.35	1.93	1.67
ENSMUSG00000031708	*Gpsn2*	7.58	7.82	7.85	7.74
ENSMUSG00000031711	*Zfp330*	2.17	2.35	2.28	2.23
ENSMUSG00000031714	*Gab1*	2.28	2	2.34	2.23
ENSMUSG00000031715	*Smarca5*	2.19	0.55	1.62	0.69
ENSMUSG00000031722	*Hp*	9.94	10.43	10.13	10.25
ENSMUSG00000031723	*Txnl4b*	3.26	3.28	3.24	3.16
ENSMUSG00000031725	*AU018778*	8.09	8.04	7.77	7.76
ENSMUSG00000031729	*mKIAA0174*	5.04	4.89	4.91	4.72
ENSMUSG00000031730	*Dhodh*	2.27	2.75	2.47	2.09
ENSMUSG00000031731	*Ap1g1*	5.41	4.98	4.98	4.77
ENSMUSG00000031750	*2010004A03Ri*	1.33	2.11	1.58	1.42
ENSMUSG00000031751	*Amfr*	7.32	7.51	7.01	6.94
ENSMUSG00000031753	*Cog4*	4.94	4.88	4.87	4.55
ENSMUSG00000031755	*Bbs2*	1.05	0.16	0.85	1.12
ENSMUSG00000031762	*Mt2*	8.79	8.06	8.56	8.24

ENSMUSG00000031765	*Mt1*	8.79	8.04	8.8	8.56
ENSMUSG00000031767	*Nudt7*	5.46	5.45	5.18	5.45
ENSMUSG00000031770	*Herpud1*	8.22	8.99	8.66	8.74
ENSMUSG00000031774	*2310065K24Ri*	3.89	4.37	4.11	4.02
ENSMUSG00000031775	*Pllp*	3.24	4.32	4.1	3.97
ENSMUSG00000031776	*Arl2bp*	1.04	1.24	1.47	0.7
ENSMUSG00000031781	*Ciapin1*	4.65	5.34	5.29	5.19
ENSMUSG00000031782	*Coq9*	5.96	6.24	6.16	6.01
ENSMUSG00000031783	*Polr2c*	1.66	1.89	2.09	1.88
ENSMUSG00000031788	*Kifc3*	1.56	2.84	1.68	1.55
ENSMUSG00000031790	*Mmp15*	3.12	3.47	3.74	3.61
ENSMUSG00000031791	*Tmem38a*	-0.03	0.52	1.02	0.86
ENSMUSG00000031792	*AA960436*	3.07	3.09	3.03	2.82
ENSMUSG00000031796	*Gtl3*	4.2	4.29	4.63	4.2
ENSMUSG00000031799	*Tpm4*	3.5	2.98	2.83	2.68
ENSMUSG00000031805	*Jak3*	1.02	1.48	1.38	0.37
ENSMUSG00000031807	*Pgls*	4.87	5.7	5.42	5.42
ENSMUSG00000031808	*Slc27a1*	1.39	2.21	2.04	1.34
ENSMUSG00000031811	*Fbxo31*	5.55	6.32	6.12	5.7
ENSMUSG00000031812	*Map1lc3b*	6.71	6.5	6.85	6.52
ENSMUSG00000031813	*1110012M11Ri*	5.05	5.98	5.87	5.73
ENSMUSG00000031816	*Mthfsd*	2.22	2.38	2.13	1.9
ENSMUSG00000031818	*Cox4i1*	8.06	8.74	8.61	8.6
ENSMUSG00000031819	*Cox4nb*	3.51	4.33	4.13	4
ENSMUSG00000031820	*5430437P03Ri*	5.18	5.97	5.64	5.39
ENSMUSG00000031822	*Gse1*	1.1	2.85	1.69	1.39
ENSMUSG00000031823	*Zdhhc7*	3.58	3.98	3.56	3.23
ENSMUSG00000031826	*Usp10*	4.82	5.38	5.16	4.93
ENSMUSG00000031827	*Cotl1*	2.99	3.61	3.56	2.88
ENSMUSG00000031828	*BC025816*	1.15	2.34	1.43	1.51
ENSMUSG00000031833	*NA*	2.87	3.73	3.43	3.21

ENSMUSG00000031834	*Pik3r2*	3.09	4.05	3.38	3.11
ENSMUSG00000031835	*Mbtps1*	4.78	4.88	4.63	4.54
ENSMUSG00000031838	*Ifi30*	4.32	4.56	4.86	4.34
ENSMUSG00000031839	*Hsbp1*	6.72	6.61	6.64	6.51
ENSMUSG00000031840	*Rab3a*	0.88	2.6	2.01	1.31
ENSMUSG00000031841	*Cdh13*	0.94	0.96	1.3	0.49
ENSMUSG00000031842	*Pde4c*	2.16	3.01	3.05	2.48
ENSMUSG00000031843	*Mphosph6*	1.47	0.36	0.13	-0.7
ENSMUSG00000031844	*Hsd17b2*	7.17	7.38	6.74	6.78
ENSMUSG00000031845	*Bcmo1*	2.87	2.6	3.09	2.57
ENSMUSG00000031848	*Lsm4*	3.48	3.84	4.04	3.59
ENSMUSG00000031851	*2310079N02Ri*	1.63	2.3	2.02	1.66
ENSMUSG00000031853	*BC021891*	1.28	1.29	1.19	0.55
ENSMUSG00000031858	*mKIAA0892*	3.48	3.87	3.48	3.12
ENSMUSG00000031862	*Atp13a1*	3.75	4.57	4.21	4.16
ENSMUSG00000031864	*Ints10*	1.46	1.7	1.42	0.79
ENSMUSG00000031865	*Dctn1*	2.75	3.45	3.4	2.98
ENSMUSG00000031871	*Cdh5*	3.38	3.72	3.17	3.37
ENSMUSG00000031875	*Cmtm3*	2.5	2.74	2.46	2.52
ENSMUSG00000031877	*2210023G05Ri*	4.76	4.59	4.9	4.36
ENSMUSG00000031878	*Appbp1*	3.9	3.13	3.75	2.95
ENSMUSG00000031879	*1110019N10Ri*	3.43	3.9	3.58	3.37
ENSMUSG00000031885	*Cbfb*	3.39	2.27	2.68	2.52
ENSMUSG00000031886	*Ces5*	6.43	6.13	6.27	6.05
ENSMUSG00000031887	*Tradd*	2.21	3.36	2.97	2.78
ENSMUSG00000031889	*D230025D16R*	5.35	4.63	4.93	4.79
ENSMUSG00000031897	*Psmb10*	4.35	4.89	4.15	4.42
ENSMUSG00000031901	*Dus2l*	2.17	2.63	2.16	2.02
ENSMUSG00000031902	*Nfatc3*	4.1	3.75	3.72	3.5
ENSMUSG00000031903	*Lypla3*	2.77	2.92	2.86	2.64
ENSMUSG00000031913	*Vps4a*	4.07	3.94	3.74	3.72

ENSMUSG00000031916	*Cog8*	4.56	4.75	4.41	4.17
ENSMUSG00000031917	*Nip7*	3.26	3.34	3.55	3.3
ENSMUSG00000031918	*Mtmr2*	2.81	2.51	2.65	2.37
ENSMUSG00000031921	*Terf2*	1.94	1.58	2.07	1.57
ENSMUSG00000031922	*Cep57*	2.99	1.82	2.5	2.05
ENSMUSG00000031924	*Cyb5b*	7.48	7.03	6.7	6.52
ENSMUSG00000031930	*Wwp2*	2.98	3.43	3.12	2.7
ENSMUSG00000031931	*Ankrd49*	2.85	1.99	2.63	2.12
ENSMUSG00000031935	*Med17*	3.09	3.11	2.94	2.75
ENSMUSG00000031938	*4931406C07Ri*	7.23	6.64	6.93	6.46
ENSMUSG00000031939	*Josd3*	2.19	1.03	2.01	1.09
ENSMUSG00000031948	*Kars*	5.59	5.65	5.43	5.28
ENSMUSG00000031950	*Gabarapl2*	2.21	3.64	3.23	3.11
ENSMUSG00000031953	*Tmem170*	2.92	2.3	2.7	2.14
ENSMUSG00000031954	*Cfdp1*	5.35	5.42	5.05	4.82
ENSMUSG00000031955	*Bcar1*	3.18	4.42	3.74	3.75
ENSMUSG00000031958	*Ldhd*	6.28	6.42	6.41	6
ENSMUSG00000031959	*Wdr59*	1.88	1.98	1.74	1.15
ENSMUSG00000031960	*Aars*	6.02	6.58	6.16	6.14
ENSMUSG00000031967	*Afg3l1*	5.13	4.9	4.83	4.47
ENSMUSG00000031969	*Acad8*	4.97	4.72	4.83	4.56
ENSMUSG00000031972	*Acta1*	#NAME?	-4.85	4.81	4.89
ENSMUSG00000031974	*Abcb10*	3.42	3.37	3.49	3.02
ENSMUSG00000031976	*AK122209*	1.45	1.52	1.27	1.23
ENSMUSG00000031977	*Galnt2*	4.51	4.68	4.19	3.91
ENSMUSG00000031979	*Cog2*	3.42	3.39	3.25	2.84
ENSMUSG00000031980	*Agt*	9.17	9.78	9.8	9.57
ENSMUSG00000031983	*2310022B05Ri*	2.94	3.29	3.16	2.52
ENSMUSG00000031984	*2810004N23Ri*	4.72	4.41	4.53	4.35
ENSMUSG00000031985	*AK148282*	4.76	5.08	4.77	4.48
ENSMUSG00000031986	*NA*	1.06	1.14	1.18	1.07

ENSMUSG00000031987	*Egln1*	4.03	4.29	3.94	4.12
ENSMUSG00000031988	*AK040818*	3.76	4.11	4.04	3.8
ENSMUSG00000031993	*Snx19*	3.46	3.42	3.54	3.27
ENSMUSG00000031996	*Aplp2*	7.28	6.85	7.03	6.81
ENSMUSG00000032000	*Birc3*	1.57	0.95	1.76	1.09
ENSMUSG00000032002	*Dcun1d5*	4.29	3.38	3.91	3.26
ENSMUSG00000032009	*Sesn3*	2.5	1.86	2.09	1.74
ENSMUSG00000032010	*Usp2*	3.34	3.26	4.42	4.46
ENSMUSG00000032012	*Pvrl1*	3.75	4.53	4.2	4.09
ENSMUSG00000032014	*Oaf*	7.06	7.53	7.59	7.51
ENSMUSG00000032018	*Sc5d*	7.56	6.9	6.58	6.5
ENSMUSG00000032026	*Rexo2*	6.22	6.4	6.11	5.78
ENSMUSG00000032028	*4432416J03Ri*	3.02	2.9	2.52	2.88
ENSMUSG00000032030	*Cul5*	2.83	2.13	2.61	1.96
ENSMUSG00000032035	*Ets1*	2.86	2.77	2.6	2.23
ENSMUSG00000032038	*St3gal4*	5.9	5.96	5.72	5.66
ENSMUSG00000032040	*Dcps*	3.83	4	3.93	3.81
ENSMUSG00000032041	*Tirap*	3.78	3.4	3.32	3.26
ENSMUSG00000032042	*Srpr*	5.84	6.25	5.67	5.73
ENSMUSG00000032044	*Rpusd4*	2.2	2.16	2.7	2.25
ENSMUSG00000032046	*NA*	4.69	4.53	4.38	4.11
ENSMUSG00000032047	*Acat1*	8.38	8.11	8.21	7.95
ENSMUSG00000032050	*Rdx*	6.49	5.87	6.24	5.82
ENSMUSG00000032051	*Fdx1*	6.42	6.56	6.5	6.48
ENSMUSG00000032053	*Pou2af1*	-1.78	-2.69	1.08	-3.67
ENSMUSG00000032058	*Ppp2r1b*	2.82	2.54	2.59	2.25
ENSMUSG00000032059	*Alg9*	2.84	3.06	2.82	2.57
ENSMUSG00000032060	*Cryab*	1.33	2.13	1.55	2.3
ENSMUSG00000032062	*2310030G06R*	3.69	3.44	3.54	3.34
ENSMUSG00000032065	*Tex12*	2.5	1	1.89	0.18
ENSMUSG00000032066	*Bcdo2*	2.98	3.5	3.49	3.36

ENSMUSG00000032067	*Pts*	5.04	4.71	5.17	4.55
ENSMUSG00000032076	*sgigsf*	3.15	2.82	3.28	2.84
ENSMUSG00000032077	*Bud13*	1.75	1.83	1.79	1.7
ENSMUSG00000032078	*Zfp259*	4.6	5.28	4.9	4.68
ENSMUSG00000032079	*Apoa5*	8.9	9.11	9.14	9.11
ENSMUSG00000032080	*Apoa4*	9.44	10.1	9.87	9.69
ENSMUSG00000032081	*Apoc3*	10.59	10.16	10.61	10.67
ENSMUSG00000032083	*Apoa1*	11.79	12.17	12.21	12.56
ENSMUSG00000032085	*Tagln*	2.26	2.41	2.57	2.35
ENSMUSG00000032086	*Bace*	3.78	4.06	3.71	3.44
ENSMUSG00000032092	*Mpzl2*	6.11	5.65	6.24	5.88
ENSMUSG00000032096	*Arcn1*	5.97	5.59	5.43	5.08
ENSMUSG00000032097	*Ddx6*	4.32	3.67	3.77	3.77
ENSMUSG00000032103	*Pus3*	1.84	1.7	1.57	0.93
ENSMUSG00000032109	*Nlrx1*	1.64	2.07	1.81	1.83
ENSMUSG00000032112	*Trappc4*	3.68	2.89	3.17	3.24
ENSMUSG00000032114	*Slc37a4*	7.27	7.33	7.76	7.51
ENSMUSG00000032115	*Hyou1*	5.57	6.61	4.78	5.45
ENSMUSG00000032116	*Stt3a*	5.54	5.11	4.79	4.69
ENSMUSG00000032119	*Mizf*	1.01	1.16	1.12	1.02
ENSMUSG00000032120	*Tmem24*	4.31	5.05	4.9	4.67
ENSMUSG00000032121	*1810021J13Ri*	2.23	1.73	2.12	2.36
ENSMUSG00000032123	*Dpagt1*	4.58	5.24	4.43	4.39
ENSMUSG00000032125	*Robo4*	2.08	2.96	2.14	2.14
ENSMUSG00000032126	*Hmbs*	4.94	4.82	4.56	4.4
ENSMUSG00000032127	*Vps11*	3.2	3.64	3.47	3.31
ENSMUSG00000032171	*Pin1*	3.25	4.17	3.62	3.43
ENSMUSG00000032175	*Tyk2*	2.53	2.88	2.41	2.2
ENSMUSG00000032178	*Ilf3*	1.85	2.16	2.17	2.22
ENSMUSG00000032179	*Bmp5*	2.58	1.49	1.92	1.32
ENSMUSG00000032180	*Tmed1*	3.62	4.13	3.79	3.73

ENSMUSG00000032182	*Yipf2*	3.97	4.71	4.28	4.22
ENSMUSG00000032184	*Lysmd2*	1.4	1.7	0.42	0.34
ENSMUSG00000032185	*Carm1*	3.88	4.58	4.4	4.39
ENSMUSG00000032187	*Smarca4*	3.86	4.55	4.21	3.94
ENSMUSG00000032193	*Ldlr*	4.83	5.23	5.22	5.09
ENSMUSG00000032194	*Ankrd25*	3.25	4.16	3.78	3.55
ENSMUSG00000032198	*Dock6*	1.23	1.86	1.24	1.13
ENSMUSG00000032199	*Grinl1a*	5.53	5.81	5.57	5.31
ENSMUSG00000032203	*NA*	3.93	3.61	3.72	3.58
ENSMUSG00000032204	*Aqp9*	7.43	7.36	7.56	7.3
ENSMUSG00000032207	*Lipc*	7.56	7.33	7.16	7.16
ENSMUSG00000032212	*Met*	3.78	3.37	3.37	3.2
ENSMUSG00000032215	*BC003885*	3.28	2.93	3.22	2.68
ENSMUSG00000032216	*Nedd4*	6.64	6.2	6.47	6.17
ENSMUSG00000032217	*Arkadia*	2.74	2.17	2.65	2.38
ENSMUSG00000032220	*Myo1e*	4.52	4.53	4.38	4.22
ENSMUSG00000032228	*Tcf12*	3.07	2.58	2.99	2.69
ENSMUSG00000032231	*Anxa2*	3.42	3.59	3.05	3.11
ENSMUSG00000032232	*Cgnl1*	3.99	4.17	4.09	4.01
ENSMUSG00000032235	*Narg2*	2.15	1.69	1.99	1.53
ENSMUSG00000032238	*Rora*	3.93	3.7	3.25	3.16
ENSMUSG00000032239	*rp9*	5.5	5.69	5.53	5.29
ENSMUSG00000032244	*Fem1b*	2.92	2.64	2.64	2.31
ENSMUSG00000032245	*Cln6*	1.24	1.95	2.14	2.26
ENSMUSG00000032249	*Anp32a*	6.79	6.87	7.19	6.98
ENSMUSG00000032252	*Glce*	3.31	2.81	2.91	2.55
ENSMUSG00000032253	*Phip*	1.3	0	1.2	0.3
ENSMUSG00000032261	*Sh3bgrl2*	4.11	3.93	3.74	3.77
ENSMUSG00000032263	*Bckdhb*	7.16	6.48	6.66	6.4
ENSMUSG00000032264	*Zw10*	2.74	3.09	3.04	2.61
ENSMUSG00000032265	*NA*	3.68	3.09	3.42	3.57

ENSMUSG00000032271	*Nnmt*	6.61	5.78	7.58	6.79
ENSMUSG00000032279	*Idh3a*	5.17	4.77	4.88	4.7
ENSMUSG00000032280	*Tle3*	0.09	1.71	1.13	1.44
ENSMUSG00000032288	*Imp3*	4.94	4.79	5.04	4.67
ENSMUSG00000032290	*Ptpn9*	3.5	3.61	2.62	2.65
ENSMUSG00000032293	*Ireb2*	4.66	3.71	4.38	3.97
ENSMUSG00000032294	*Pkm2*	1.44	1.69	1.51	1.42
ENSMUSG00000032295	*Man2c1*	3.12	3.58	3.12	3.15
ENSMUSG00000032298	*Neil1*	1.7	2.14	2.13	1.43
ENSMUSG00000032299	*Commd4*	4.32	4.72	4.43	4.15
ENSMUSG00000032300	*14-Sep*	2.8	3.05	2.62	2.55
ENSMUSG00000032301	*Psma4*	5.69	5.49	5.28	4.72
ENSMUSG00000032305	*2310046O06Ri*	2.05	1.95	2.19	1.8
ENSMUSG00000032306	*Mpi*	3.11	3.41	3.1	2.92
ENSMUSG00000032307	*Ube2q2*	2.72	1.92	2.54	2.1
ENSMUSG00000032308	*NA*	1.73	2.15	2.3	1.82
ENSMUSG00000032309	*Fbxo22*	5.6	5.21	5.46	5.1
ENSMUSG00000032310	*Cyp1a2*	9.15	9.24	9.44	9.25
ENSMUSG00000032311	*Nrg4*	0.94	-0.83	1.39	0.65
ENSMUSG00000032312	*Csk*	4.78	4.99	5.18	4.96
ENSMUSG00000032314	*Etfa*	7.26	6.64	7.22	6.73
ENSMUSG00000032316	*Clk3*	4.24	4.27	4.13	4.08
ENSMUSG00000032320	*Rcn2*	2.41	2.22	2.35	1.58
ENSMUSG00000032324	*Tspan3*	2.07	2.19	2	1.57
ENSMUSG00000032328	*Tmem30a*	6.56	5.85	5.86	5.19
ENSMUSG00000032329	*Hmg20a*	2.57	2.56	2.21	1.92
ENSMUSG00000032330	*Cox7a2*	7.18	6.8	7.37	6.94
ENSMUSG00000032336	*Nptn*	4.92	4.17	4.71	4.51
ENSMUSG00000032340	*Neo1*	2.03	1.94	2.19	1.97
ENSMUSG00000032342	*Mto1*	3.12	3.34	3.24	3.28
ENSMUSG00000032348	*Gsta4*	6.86	6.07	6.6	6.26

ENSMUSG00000032349	*Elovl5*	8.71	8.22	7.84	7.69
ENSMUSG00000032350	*Gclc*	6.79	6.89	6.4	6.44
ENSMUSG00000032353	*Tmed3*	3.38	4.76	3.04	3.57
ENSMUSG00000032359	*Ctsh*	8.01	7.46	7.72	7.64
ENSMUSG00000032363	*Adamts7*	0.47	2.28	1.22	1.58
ENSMUSG00000032366	*Perq1*	3.1	2.83	3.32	3.14
ENSMUSG00000032369	*Plscr1*	1.94	1.5	2.46	2.71
ENSMUSG00000032370	*Lactb*	4.92	4.28	4.62	4.21
ENSMUSG00000032372	*Plscr2*	5.1	4.17	5.15	4.72
ENSMUSG00000032376	*Usp3*	4.26	3.62	4.09	3.6
ENSMUSG00000032380	*DAPK2*	2.52	3.56	3.34	3.5
ENSMUSG00000032381	*5730536A07Ri*	5.71	5.06	5.38	5.1
ENSMUSG00000032382	*Snx1*	3.3	3.34	3.36	3.08
ENSMUSG00000032383	*Ppib*	7.83	7.93	7.7	7.48
ENSMUSG00000032386	*Trip4*	3.74	2.92	3.78	3.28
ENSMUSG00000032387	*Rbpms2*	4.91	5.04	5.23	5.13
ENSMUSG00000032388	*Spg21*	4.21	3.25	3.7	3.5
ENSMUSG00000032392	*Parp16*	3.31	3.33	3.59	3.27
ENSMUSG00000032393	*Dpp8*	4.53	4.12	4.19	3.92
ENSMUSG00000032396	*Dis3l*	3.41	3.43	3.34	3.26
ENSMUSG00000032397	*Tipin*	2.21	1.18	1.66	1.16
ENSMUSG00000032398	*Snapc5*	4.73	4.18	4.88	4.45
ENSMUSG00000032399	*Rpl4*	7.71	7.81	7.68	7.63
ENSMUSG00000032402	*Smad3*	2.14	3	2.52	2.62
ENSMUSG00000032403	*NA*	3.51	3.53	4.08	3.58
ENSMUSG00000032405	*Pias1*	2.95	2.76	2.84	2.84
ENSMUSG00000032407	*2610101N10Ri*	3.69	2.85	3	2.41
ENSMUSG00000032409	*NA*	1.18	0.48	1.02	0.35
ENSMUSG00000032410	*Xrn1*	1.25	0.59	0.94	0.38
ENSMUSG00000032411	*Tfdp2*	3.51	2.07	3.13	2.65
ENSMUSG00000032412	*Atp1b3*	4.24	3.52	4.05	3.6

ENSMUSG00000032415	*2610018I03Rik*	0.92	-0.08	1.01	1.16
ENSMUSG00000032418	*Mod1*	3.77	2.45	3.2	2.8
ENSMUSG00000032420	*Nt5e*	5.95	5.33	4.93	4.59
ENSMUSG00000032422	*Snx14*	3.74	2.74	3.58	3.01
ENSMUSG00000032423	*Syncrip*	3.34	2.44	2.91	2.37
ENSMUSG00000032424	*NA*	2.13	1.17	2.7	1.83
ENSMUSG00000032425	*NA*	1.6	1.29	1.4	1.29
ENSMUSG00000032431	*Crtap*	3.12	3.49	2.51	2.8
ENSMUSG00000032434	*Cmtm6*	5.46	5.95	5.23	4.94
ENSMUSG00000032435	*Dync1li1*	3.65	3.21	3.57	3.1
ENSMUSG00000032437	*Stt3b*	5.11	5.03	4.75	4.46
ENSMUSG00000032438	*NA*	0.28	2.45	1.9	1.78
ENSMUSG00000032440	*Tgfbr2*	1.75	1.77	2.1	1.7
ENSMUSG00000032456	*Nmnat3*	1.18	0.76	1.72	1.21
ENSMUSG00000032458	*Copb2*	6.1	5.67	5.88	5.66
ENSMUSG00000032459	*Mrps22*	4.4	4.31	4.06	3.82
ENSMUSG00000032462	*Pik3cb*	2.7	2	2.91	2.4
ENSMUSG00000032463	*Faim*	2.61	1.84	2.24	1.56
ENSMUSG00000032468	*Armc8*	1.96	2.18	2.32	2.24
ENSMUSG00000032469	*Dbr1*	2.64	2.08	2.1	1.87
ENSMUSG00000032470	*Mras*	0.48	1.1	1	0.61
ENSMUSG00000032475	*Nck1*	2.85	1.69	2.27	2.13
ENSMUSG00000032478	*Nme6*	2.75	3.16	3.11	3
ENSMUSG00000032479	*Mtap4*	3.51	3.39	3.3	3.14
ENSMUSG00000032480	*Dhx30*	2.95	3.85	3.23	3.17
ENSMUSG00000032481	*Smarcc1*	2.65	2.34	2.53	2.1
ENSMUSG00000032485	*Scap*	5.55	6.27	5.83	5.79
ENSMUSG00000032492	*Pthr1*	2.47	3.49	2.62	2.65
ENSMUSG00000032497	*Lrrfip2*	3	3.09	3.3	2.92
ENSMUSG00000032498	*Mlh1*	0.6	0.39	1.56	0.1
ENSMUSG00000032500	*Dclk3*	1.77	2.63	2.58	2.64

ENSMUSG00000032501	*Trib1*	3.39	3.37	3.49	3.38
ENSMUSG00000032504	*Pdcd6ip*	5.58	5.48	5.71	5.41
ENSMUSG00000032507	*Fbxl2*	0.92	0.22	1.09	0.19
ENSMUSG00000032508	*Myd88*	3.77	3.51	3.41	3.34
ENSMUSG00000032512	*Wdr48*	4.26	3.53	3.88	3.58
ENSMUSG00000032513	*Gorasp1*	4.14	4.5	4.24	4.16
ENSMUSG00000032515	*Axud1*	1.72	2.41	1.92	1.74
ENSMUSG00000032519	*Slc25a38*	4.22	4.77	4.22	4.05
ENSMUSG00000032525	*Nktr*	3.07	3.23	2.89	2.73
ENSMUSG00000032526	*Deb1*	5.24	4.75	5.49	5.37
ENSMUSG00000032527	*Pccb*	7.09	6.87	6.85	6.56
ENSMUSG00000032528	*Vipr1*	3.73	4.11	3.9	3.57
ENSMUSG00000032531	*Amotl2*	3.74	4.2	3.4	3.45
ENSMUSG00000032534	*Cep63*	2.6	2.37	2.23	2.15
ENSMUSG00000032536	*Trak1*	4.02	4.15	3.79	3.75
ENSMUSG00000032540	*Abhd5*	4.29	4.84	4.21	4.18
ENSMUSG00000032547	*Ryk*	4.57	4.31	4.36	4.24
ENSMUSG00000032548	*Slco2a1*	4.39	5.34	4.65	4.35
ENSMUSG00000032551	*1110059G10Ri*	3.31	2.97	3.21	2.91
ENSMUSG00000032553	*Srprb*	3.66	4.55	3.57	3.91
ENSMUSG00000032554	*Trf*	12.38	12.65	12.37	12.45
ENSMUSG00000032555	*Topbp1*	1.94	1.46	2.14	1.37
ENSMUSG00000032557	*Ube1dc1*	4.61	4.44	3.81	3.86
ENSMUSG00000032558	*Nphp3*	6.17	5.92	5.97	5.74
ENSMUSG00000032560	*NA*	3.78	3.16	3.43	3.06
ENSMUSG00000032562	*Gnai2*	6.04	6.48	6.15	6.09
ENSMUSG00000032563	*Mrpl3*	3.86	4.16	4.27	3.74
ENSMUSG00000032565	*Nudt16*	2.95	2.97	3.29	2.95
ENSMUSG00000032567	*Aste1*	1.34	0.7	1.63	1.33
ENSMUSG00000032570	*Atp2c1*	3.97	3.53	3.72	3.34
ENSMUSG00000032571	*Pik3r4*	2.25	2.55	2.6	2.43

ENSMUSG00000032575	*Armet*	6.21	7.4	5.32	6.2
ENSMUSG00000032578	*Cish*	3.88	1.33	-0.2	1.36
ENSMUSG00000032579	*Hemk1*	3.48	4.03	3.33	3.32
ENSMUSG00000032580	*Rbm5*	3.97	3.95	3.62	3.44
ENSMUSG00000032582	*Rbm6*	2.29	2.28	2.2	1.86
ENSMUSG00000032583	*Mon1a*	3.37	3.82	3.51	3.45
ENSMUSG00000032590	*Apeh*	4.74	5.42	4.99	5.03
ENSMUSG00000032591	*Mst1*	6.7	7.17	6.59	6.6
ENSMUSG00000032594	*Ihpk1*	4.56	4.48	4.63	4.46
ENSMUSG00000032596	*AK157941*	2.45	2.3	2.02	1.73
ENSMUSG00000032598	*Nckipsd*	1.27	1.86	1.21	1.08
ENSMUSG00000032599	*AK057615*	4.03	4.07	4.8	4.5
ENSMUSG00000032601	*Prkar2a*	5.42	5.17	5.06	4.81
ENSMUSG00000032602	*Slc25a20*	6.73	6.73	6.76	6.69
ENSMUSG00000032604	*Qars*	4.59	4.55	4.67	4.38
ENSMUSG00000032606	*Nicn1*	3.91	3.88	3.73	3.54
ENSMUSG00000032607	*Amt*	5.78	5.97	5.56	5.1
ENSMUSG00000032612	*mKIAA4155*	5.06	5.3	4.98	4.94
ENSMUSG00000032615	*Nt5m*	2.67	3.1	3.3	3.15
ENSMUSG00000032621	*Sfrs12*	2.93	2.15	2.57	2.3
ENSMUSG00000032624	*Eml4*	2.67	2.22	2.33	2.12
ENSMUSG00000032633	*Flcn*	3.72	3.68	4.29	3.75
ENSMUSG00000032637	*Atxn2l*	3.79	4.24	4.52	4.29
ENSMUSG00000032648	*Pygm*	-1.19	-0.14	1.09	1.28
ENSMUSG00000032652	*Crebl2*	5.17	4.83	4.8	4.34
ENSMUSG00000032667	*Pon2*	5.41	5.25	5.14	4.92
ENSMUSG00000032673	*2010316F05Ri*	4.33	3.22	4.4	4.13
ENSMUSG00000032679	*Cd59a*	4.62	5.57	4.62	5.3
ENSMUSG00000032688	*Malt1*	1.12	0.41	1.22	-0.05
ENSMUSG00000032698	*Lmo2*	1.77	2.2	2.61	1.66
ENSMUSG00000032702	*Ankrd15*	3.47	4.2	3.67	3.44

ENSMUSG00000032705	*Exdl2*	2.6	2.55	2.47	1.96
ENSMUSG00000032712	*2810474O19Ri*	2.73	2.19	2.47	1.96
ENSMUSG00000032714	*NA*	1.1	1.46	1.15	0.74
ENSMUSG00000032715	*Trib3*	2.46	3.15	3.15	2.53
ENSMUSG00000032724	*Abtb2*	2.16	3.09	2.92	2.62
ENSMUSG00000032725	*Folr2*	3.46	2.94	2.52	2.86
ENSMUSG00000032727	*Mier3*	2.51	1.4	2.12	1.62
ENSMUSG00000032733	*Sh3px3*	3.19	3.31	2.97	2.76
ENSMUSG00000032735	*Ablim3*	3.87	4.61	3.43	3.47
ENSMUSG00000032737	*Inppl1*	3.5	3.7	3.83	3.36
ENSMUSG00000032741	*calcium chann*	4.39	4.91	4.6	4.51
ENSMUSG00000032743	*D430042O09R*	1.93	2.27	2.19	1.88
ENSMUSG00000032745	*GPBP*	4.71	3.78	4.39	3.76
ENSMUSG00000032754	*Slc24a6*	4.44	4.88	4.81	4.36
ENSMUSG00000032757	*Bet1*	5.15	4.29	4.59	4.1
ENSMUSG00000032763	*Ilvbl*	4.09	4.28	4.12	3.83
ENSMUSG00000032766	*Gng11*	4.39	3.1	3.44	2.98
ENSMUSG00000032776	*Mctp2*	1.87	1.13	1.81	1.27
ENSMUSG00000032777	*Gtf3c1*	3.24	3.68	3.55	3.39
ENSMUSG00000032786	*Alas1*	7.26	6.06	6.61	7.3
ENSMUSG00000032788	*Pdxk*	3.65	3.48	4.28	3.93
ENSMUSG00000032802	*Srxn1*	4.23	4.57	4.32	3.91
ENSMUSG00000032803	*AK048941*	3.92	3.34	3.65	3.24
ENSMUSG00000032806	*Slc10a3*	1.65	1.59	1.6	1.46
ENSMUSG00000032808	*Cyp2c38*	7.22	6.42	7.07	6.66
ENSMUSG00000032812	*Centd2*	3.19	3.4	3.28	2.93
ENSMUSG00000032834	*Pwp2*	2.33	3	2.26	2.1
ENSMUSG00000032840	*2410131K14Ri*	2.68	2.9	2.82	2.86
ENSMUSG00000032842	*Abcc10*	0.62	1.26	1.23	0.62
ENSMUSG00000032855	*Pkd1*	1.35	1.69	1.57	1.19
ENSMUSG00000032860	*P2ry2*	2.46	3.1	2.98	3.14

ENSMUSG00000032867	*Fbxw8*	4.56	5.27	4.78	4.61
ENSMUSG00000032869	*Psmf1*	4.04	3.96	3.99	3.65
ENSMUSG00000032870	*Smap1l*	5.07	5.21	5.14	4.98
ENSMUSG00000032872	*Cyb5r4*	1.15	0.93	1.57	0.98
ENSMUSG00000032883	*Acsl3*	1.69	1.29	1.75	1.52
ENSMUSG00000032897	*Nfyc*	1.08	0.62	0.88	1.12
ENSMUSG00000032898	*Fbxo21*	4.73	5.54	5.75	5.5
ENSMUSG00000032902	*Slc16a1*	4.85	4.38	4.13	3.8
ENSMUSG00000032905	*Atg12*	3.75	3.34	4.1	3.62
ENSMUSG00000032913	*mKIAA0806*	1.06	0.48	0.71	-0.08
ENSMUSG00000032915	*Emr4*	1.79	0.87	0.93	0.91
ENSMUSG00000032932	*Stch*	4.27	3.46	3.24	3.09
ENSMUSG00000032939	*Nup93*	0.9	1.32	1.26	1.08
ENSMUSG00000032946	*Rasgrp2*	1.14	1.66	1.72	1.44
ENSMUSG00000032952	*Ap4b1*	3.38	3.46	3.44	3.36
ENSMUSG00000032959	*Pebp1*	5.01	5.12	5.2	5.06
ENSMUSG00000032965	*Ift57*	1.41	1.22	1.48	0.84
ENSMUSG00000032966	*FKBP12-T1*	5.43	5.49	5.33	5.13
ENSMUSG00000032977	*1810008A18Ri*	3.88	4.41	4.26	4.1
ENSMUSG00000032998	*Foxj3*	2.2	1.57	1.92	1.81
ENSMUSG00000033004	*Phr1*	1.98	1.72	1.94	1.45
ENSMUSG00000033009	*mKIAA1612*	2.42	2.45	2.34	2.33
ENSMUSG00000033014	*Trim33*	2.08	1.49	2.02	1.63
ENSMUSG00000033016	*Nfatc1*	1.65	1.79	2.03	1.73
ENSMUSG00000033020	*Polr2f*	5.3	5.57	5.22	5.43
ENSMUSG00000033021	*Gmppa*	3.65	4.21	3.55	3.42
ENSMUSG00000033022	*Cdo1*	10.26	10.27	10.25	9.93
ENSMUSG00000033029	*1700088E04Ri*	2.03	2.04	2.12	1.76
ENSMUSG00000033032	*Afap1l1*	1.59	1.56	0.41	0.56
ENSMUSG00000033039	*NA*	1.62	1.9	1.96	1.63
ENSMUSG00000033047	*Eif3eip*	6.17	6.19	5.91	5.8

ENSMUSG00000033054	*Npat*	1.36	0.37	1.13	0.5
ENSMUSG00000033055	*Ankrd54*	2.25	3.01	2.4	2.55
ENSMUSG00000033059	*Pygb*	1.05	1.1	0.93	0.91
ENSMUSG00000033060	*Lmo7*	2.25	2.03	2.68	2.33
ENSMUSG00000033065	*Pfkm*	2.42	3.05	3.34	3.03
ENSMUSG00000033068	*Entpd6*	2.68	3.12	2.58	2.27
ENSMUSG00000033075	*Senp1*	1.55	1.08	1.33	1.19
ENSMUSG00000033088	*Triobp*	1.69	2.28	2.14	1.92
ENSMUSG00000033096	*2310001A20Ri*	4.87	4.58	4.75	4.47
ENSMUSG00000033099	*Nol12*	3.08	4.24	3.51	3.45
ENSMUSG00000033102	*Cdc14b*	3.17	2.29	3.07	2.1
ENSMUSG00000033105	*Lss*	3.37	3.67	2.88	2.75
ENSMUSG00000033106	*Slc7a6os*	3.92	3.55	3.66	3.51
ENSMUSG00000033107	*Rnf125*	4.43	4.11	3.55	3.02
ENSMUSG00000033111	*3830406C13Ri*	3.37	2.58	3.36	2.79
ENSMUSG00000033114	*Slc35d2*	4.89	4.51	4.58	4.47
ENSMUSG00000033124	*Atg9a*	4.78	5.41	5.13	5.07
ENSMUSG00000033128	*Gga1*	3.65	4.76	4.46	4.43
ENSMUSG00000033147	*NA*	1.22	1.43	1.73	0.98
ENSMUSG00000033149	*Phldb2*	2.84	2.22	2.61	2.42
ENSMUSG00000033157	*Abhd10*	1.34	0.77	1.42	1.26
ENSMUSG00000033159	*1810031K17Ri*	4.69	4.91	5.5	5.13
ENSMUSG00000033161	*Atp1a1*	7.35	7.34	7.74	7.6
ENSMUSG00000033166	*Dis3*	2.02	1.98	1.91	1.06
ENSMUSG00000033170	*Card10*	1.66	2.83	2.55	2.46
ENSMUSG00000033174	*Mgll*	6.68	6.64	6.65	6.32
ENSMUSG00000033184	*NA*	6.21	5.68	5.59	5.37
ENSMUSG00000033186	*2410129H14Ri*	3.99	1.89	3.32	3.11
ENSMUSG00000033191	*Tie1*	2.09	2.95	2.49	2.67
ENSMUSG00000033216	*Eefsec*	4.5	4.82	4.59	4.25
ENSMUSG00000033220	*Rac2*	2.53	2.65	3.19	1.9

ENSMUSG00000033228	*Sfrs2ip*	3.8	3.48	3.75	3.39
ENSMUSG00000033237	*Arid2*	2.18	1.96	2.35	1.91
ENSMUSG00000033249	*Hsf4*	1.61	2.1	2.46	2.4
ENSMUSG00000033253	*NA*	0.85	1.54	1.13	0.96
ENSMUSG00000033256	*Shf*	1.34	2.28	2.59	1.93
ENSMUSG00000033257	*Ttll4*	1.82	1.46	1.52	1.28
ENSMUSG00000033272	*Slc35a4*	3.04	3.13	2.92	2.96
ENSMUSG00000033285	*Wdr3*	2.65	2.53	2.31	2.35
ENSMUSG00000033294	*Noc4l*	2.61	3.75	3.21	3.33
ENSMUSG00000033295	*Ptprf*	5.2	5.81	5	4.93
ENSMUSG00000033306	*Lpp*	2.02	1.37	1.25	0.82
ENSMUSG00000033307	*Mif*	2.93	4.04	3.58	3.68
ENSMUSG00000033308	*Dpyd*	7.74	6.96	7.46	7.06
ENSMUSG00000033313	*Fbxl8*	0.76	1.65	1.02	0.54
ENSMUSG00000033318	*Gstt2*	5.74	6.47	6.58	6.56
ENSMUSG00000033319	*Fem1c*	3.11	2.46	2.39	2.18
ENSMUSG00000033323	*Ctdp1*	2.25	2.28	2.07	2
ENSMUSG00000033326	*Jmjd2a*	2.68	3.16	2.71	2.35
ENSMUSG00000033335	*Dnm2*	4.01	4.7	4.4	4.36
ENSMUSG00000033352	*Map2k4*	4.82	4.31	4.69	4.35
ENSMUSG00000033355	*Rtp4*	4.38	3.61	3.74	4.13
ENSMUSG00000033365	*Ipo13*	2.71	3.67	3.08	2.95
ENSMUSG00000033373	*Fntb*	1.2	2.05	1.71	1.19
ENSMUSG00000033377	*Palmd*	4.43	4.09	4.1	3.69
ENSMUSG00000033379	*Atp6v0b*	5.83	5.81	6.15	6.24
ENSMUSG00000033382	*D030074E01R*	4.29	3.78	4.04	3.41
ENSMUSG00000033386	*Frrs1*	3.2	3.27	3.42	3.1
ENSMUSG00000033392	*Clasp2*	1.68	1.32	1.85	1.39
ENSMUSG00000033395	*Churc1*	5.42	5.33	5.21	5.36
ENSMUSG00000033400	*Agl*	3.51	3	3.14	2.89
ENSMUSG00000033411	*Ctdspl2*	1.28	-0.08	0.91	0.64

ENSMUSG00000033416	*1110038D17Ri*	6.73	7.15	6.5	6.26
ENSMUSG00000033417	*2700078E11Ri*	3.83	3.39	3.59	3.27
ENSMUSG00000033423	*Prnpip1*	4.52	5.06	4.62	4.59
ENSMUSG00000033427	*Upb1*	6.81	6.94	6.92	6.72
ENSMUSG00000033429	*Mcee*	6.03	5.98	6.32	6.07
ENSMUSG00000033430	*Terf2ip*	3.55	3.34	3.04	3.09
ENSMUSG00000033434	*Gtpbp6*	1.93	2.86	1.84	2.19
ENSMUSG00000033444	*mKIAA0376*	2.65	2.61	2.4	2.28
ENSMUSG00000033446	*P2ry5*	3.83	2.82	2.87	2.5
ENSMUSG00000033454	*Zbtb1*	1.79	1.33	1.5	1.1
ENSMUSG00000033475	*1110002E23Ri*	6.29	6.95	7.01	6.71
ENSMUSG00000033478	*AI450540*	3.38	3.76	3.81	3.89
ENSMUSG00000033487	*Fndc3a*	4.61	4.05	4.13	3.81
ENSMUSG00000033488	*BC026585*	4.42	4.58	4.28	3.98
ENSMUSG00000033499	*Larp5*	4.87	4.59	4.77	4.7
ENSMUSG00000033530	*NA*	3.15	3.28	3.41	3.23
ENSMUSG00000033533	*Acsm1*	7.97	8.02	7.94	7.64
ENSMUSG00000033540	*Idua*	2.58	2.94	2.77	2.7
ENSMUSG00000033542	*NA*	2.93	3.39	3.02	2.55
ENSMUSG00000033543	*Gtf2a2*	3.16	2.18	3.75	3.75
ENSMUSG00000033545	*Znrf1*	2.82	2.92	3.09	2.82
ENSMUSG00000033554	*Dph5*	2.08	1.98	1.78	1.54
ENSMUSG00000033557	*C530043G21R*	3.77	3.54	3.5	3.15
ENSMUSG00000033565	*Rbm9*	2.5	2.2	2.49	2.25
ENSMUSG00000033577	*Myo6*	3.17	2.28	3.15	2.65
ENSMUSG00000033589	*Reep4*	2.35	2.62	2.85	2.35
ENSMUSG00000033594	*Spata2L*	5.06	5.36	5.75	5.13
ENSMUSG00000033596	*Rfwd3*	1.78	1.42	1.83	1.08
ENSMUSG00000033610	*Pank1*	7.51	6.35	7.26	6.55
ENSMUSG00000033618	*Map3k13*	1.59	0.83	1.03	0.7
ENSMUSG00000033623	*Pcgf3*	2.68	2.27	2.67	2.53

ENSMUSG00000033624	*4930402E16Ri*	3.28	2.5	3.01	2.51
ENSMUSG00000033628	*Pik3c3*	3.12	2.8	3.15	2.7
ENSMUSG00000033629	*Ptplad1*	6.54	6.27	6.37	5.94
ENSMUSG00000033634	*Cml2*	8.05	8.22	7.99	7.93
ENSMUSG00000033653	*Vps8*	0.84	0.93	1.02	0.77
ENSMUSG00000033658	*Ddx19b*	1.97	1.6	1.07	1.38
ENSMUSG00000033671	*NA*	2.98	2.5	2.83	2.42
ENSMUSG00000033684	*Qsox1*	7.18	7.84	7.29	7.22
ENSMUSG00000033685	*Ucp2*	5.14	5.2	5.09	4.66
ENSMUSG00000033688	*1300017J02Ri*	8.29	8.36	8.22	8.18
ENSMUSG00000033701	*Acbd6*	3.84	4.21	4.18	4.18
ENSMUSG00000033703	*Fuk*	0.98	1.9	1.53	1.51
ENSMUSG00000033706	*Smyd5*	2.72	3.68	2.69	2.68
ENSMUSG00000033712	*NA*	2.52	2.8	2.81	2.56
ENSMUSG00000033713	*Foxn3*	2.96	2.41	3.01	2.69
ENSMUSG00000033715	*Akr1c14*	7.43	6.55	7.13	6.91
ENSMUSG00000033720	*Sfxn5*	3	2.54	3.44	2.93
ENSMUSG00000033728	*Lrrc14*	2.6	3.05	2.36	2.32
ENSMUSG00000033732	*Sf3b3*	3.45	3.99	3.81	3.65
ENSMUSG00000033735	*Spr*	5.54	6.31	6.06	5.8
ENSMUSG00000033739	*Fkbpl*	2.38	2.68	2.3	2.85
ENSMUSG00000033751	*Gadd45gip1*	4.41	5.28	4.76	4.6
ENSMUSG00000033760	*Rbm4b*	2.8	2.76	2.8	2.3
ENSMUSG00000033767	*D930015E06R*	2.98	3.01	3.54	2.87
ENSMUSG00000033769	*NA*	1.47	1.33	1.3	0.85
ENSMUSG00000033773	*Rpap2*	1.81	0.64	1.45	0.59
ENSMUSG00000033781	*Asb13*	5.31	4.67	5.04	4.85
ENSMUSG00000033790	*Tubgcp5*	1.65	1.18	1.45	0.95
ENSMUSG00000033793	*Atp6v1h*	5.3	4.48	4.95	4.48
ENSMUSG00000033799	*NA*	2.11	1.27	1.68	0.77
ENSMUSG00000033808	*Tmem87a*	2.16	1.66	1.84	1.41

ENSMUSG00000033809	*Alg3*	4.02	4.38	4.42	4.33
ENSMUSG00000033813	*Tcea1*	2.15	1.31	1.82	1.43
ENSMUSG00000033819	*Ppp1r16a*	3.56	4.28	4.1	3.87
ENSMUSG00000033831	*Fgb*	10.83	11.29	10.79	10.82
ENSMUSG00000033845	*Mrpl15*	5.89	5.48	5.8	5.44
ENSMUSG00000033855	*NA*	1.91	2.15	1.43	1.57
ENSMUSG00000033857	*D230014K01R*	0.94	1.23	1.24	0.69
ENSMUSG00000033860	*Fgg*	11.03	11.24	10.81	10.77
ENSMUSG00000033862	*Cdk10*	2.18	3.14	2.76	2.61
ENSMUSG00000033863	*Klf9*	6.12	5.47	5.49	5.21
ENSMUSG00000033871	*Ppargc1b*	1.49	1.42	1.72	1.32
ENSMUSG00000033880	*Lgals3bp*	5.64	5.49	5.43	5.71
ENSMUSG00000033885	*Pxk*	3.8	3.77	4.01	3.7
ENSMUSG00000033898	*BC026782*	7.37	6	6.96	6.46
ENSMUSG00000033909	*NA*	2.35	3.15	2.6	2.87
ENSMUSG00000033910	*Gucy1a3*	2.22	1.48	1.46	0.82
ENSMUSG00000033916	*Chmp2a*	6.18	6.58	6.51	6.29
ENSMUSG00000033917	*Mir16*	5.43	5.54	5.81	5.39
ENSMUSG00000033918	*Parl*	3.91	3.6	3.83	3.41
ENSMUSG00000033931	*Rbm34*	2.52	1.43	1.98	1.67
ENSMUSG00000033933	*Vhlh*	3.15	2.88	2.56	2.53
ENSMUSG00000033938	*Ndufb7*	6.25	6.84	6.91	7.05
ENSMUSG00000033940	*6720456B07Ri*	6	6.12	6.15	6.04
ENSMUSG00000033943	*Mga*	2.51	1.84	2.01	1.5
ENSMUSG00000033953	*Ppp3r1*	4.94	4.11	4.52	3.89
ENSMUSG00000033955	*Tnks1bp1*	3.11	3.6	3.64	3.55
ENSMUSG00000033960	*9430020K01Ri*	1.69	1.66	1.32	1.24
ENSMUSG00000033964	*Zbtb41*	2.66	1.86	2.29	1.83
ENSMUSG00000033965	*Slc16a2*	6.4	6.44	6.04	6.02
ENSMUSG00000033970	*Rfc3*	2.33	1.35	1.94	1.94
ENSMUSG00000033972	*6330416L07Ri*	1.4	0.43	0.55	0.7

ENSMUSG00000033983	*Coil*	1.52	1.48	1.06	0.2
ENSMUSG00000033985	*Tesk2*	2.94	3.13	2.8	2.9
ENSMUSG00000033991	*AK129128*	2.23	2.14	1.95	2.06
ENSMUSG00000034006	*Pqlc1*	5	5.81	5.61	5.88
ENSMUSG00000034007	*Scaper*	1.02	0.33	1.08	0.31
ENSMUSG00000034021	*Pds5b*	2.23	1.75	2.01	1.71
ENSMUSG00000034022	*Cpsf1*	3.46	4.26	3.78	3.54
ENSMUSG00000034024	*Cct2*	6.29	6.35	6.35	6.19
ENSMUSG00000034032	*Rpap1*	1.86	2.18	2.34	1.45
ENSMUSG00000034042	*Gpbp1l1*	4.06	3.31	3.86	3.37
ENSMUSG00000034064	*Ktelc1*	3.67	3.31	3.35	3.02
ENSMUSG00000034066	*Farp2*	3.28	3.14	3.38	3.04
ENSMUSG00000034075	*Zdhhc5*	4.93	5.15	5.08	4.92
ENSMUSG00000034083	*C130022K22R*	2.37	1.45	1.89	1.62
ENSMUSG00000034088	*Hdlbp*	7.41	7.06	7.16	7.07
ENSMUSG00000034101	*Ctnnd1*	5.26	4.85	5.08	4.85
ENSMUSG00000034105	*4632415K11Ri*	1.81	2.71	2.25	2.26
ENSMUSG00000034108	*Ccs*	6.92	7.34	6.93	6.68
ENSMUSG00000034109	*Golim4*	4.98	4.29	5.02	4.56
ENSMUSG00000034118	*Tpst1*	3.52	3.36	3.2	3.55
ENSMUSG00000034120	*Sfrs2*	5.55	5.15	5.11	4.82
ENSMUSG00000034126	*Pomt2*	3.17	3.47	3.3	3.36
ENSMUSG00000034135	*BC033915*	3.51	3.82	3.85	3.87
ENSMUSG00000034152	*Exoc3*	3.92	4.33	4.28	4.1
ENSMUSG00000034154	*Inoc1*	2.16	2.03	1.91	1.92
ENSMUSG00000034157	*mKIAA1737*	4.38	3.93	4.07	3.85
ENSMUSG00000034158	*Lrrc58*	4.32	3.68	4.16	4.02
ENSMUSG00000034160	*Ogt*	3.63	3	3.41	3.16
ENSMUSG00000034163	*Ccdc131*	2.41	1.93	2.61	1.94
ENSMUSG00000034165	*Ccnd3*	4.2	4.79	4.38	4.24
ENSMUSG00000034168	*6430527G18R*	3.04	4.12	3.53	3.41

ENSMUSG00000034171	*Faah*	6.01	6.02	6.02	5.74
ENSMUSG00000034173	*2410018M08R*	1.55	0.12	1.51	0.79
ENSMUSG00000034175	*Rhbdd3*	3.03	3.55	3.38	3.38
ENSMUSG00000034177	*Rnf43*	2.5	3.39	2.76	2.9
ENSMUSG00000034187	*Nsf*	2.6	2.67	2.96	2.37
ENSMUSG00000034189	*Hsdl1*	2.08	2.29	2.17	1.81
ENSMUSG00000034190	*Chmp7*	4.76	5.1	4.73	4.86
ENSMUSG00000034192	*Lsm3*	3.32	2.59	3.21	3.19
ENSMUSG00000034194	*NA*	2.33	3.17	2.39	2.35
ENSMUSG00000034201	*Gas2l1*	2.25	3.33	2.54	2.86
ENSMUSG00000034203	*Chchd4*	3.92	3.73	3.99	3.71
ENSMUSG00000034210	*4732418C07Ri*	3.16	2.62	2.91	2.53
ENSMUSG00000034211	*Mrps17*	4.16	4.24	4.52	4.03
ENSMUSG00000034216	*Vps18*	1.97	2.97	2.39	2.54
ENSMUSG00000034243	*NA*	3.33	3.17	3.23	2.82
ENSMUSG00000034245	*Hdac11*	4.81	4.72	4.8	4.72
ENSMUSG00000034247	*Plekhm1*	3.17	3.46	3.43	3.28
ENSMUSG00000034248	*Slc25a37*	2.84	2.86	3.5	3.1
ENSMUSG00000034252	*Senp6*	3.86	3.26	3.68	3.06
ENSMUSG00000034254	*Agpat1*	1.99	2.83	2.62	2.47
ENSMUSG00000034258	*Flvcr2*	1.72	1.93	1.46	1.47
ENSMUSG00000034259	*Exosc4*	3.47	4.59	4.07	4.22
ENSMUSG00000034263	*2010321M09R*	1.92	1.9	1.79	1.39
ENSMUSG00000034269	*mKIAA1757*	3.21	3.14	2.99	2.84
ENSMUSG00000034271	*Jundm2*	0.69	0.94	1.03	0.35
ENSMUSG00000034274	*Thoc5*	3.13	3.26	3.23	2.99
ENSMUSG00000034285	*Nipsnap1*	7.77	7.33	7.52	7.13
ENSMUSG00000034290	*Nek9*	4.14	4.21	4.07	3.87
ENSMUSG00000034292	*Traf3ip1*	1.41	1.88	1.87	1.48
ENSMUSG00000034297	*Med13*	3.15	1.95	2.71	2.3
ENSMUSG00000034300	*2810012G03Ri*	2.63	2.62	2.32	2.41

ENSMUSG00000034308	*4632417N05Ri*	6.18	6.53	6.08	5.83
ENSMUSG00000034312	*NA*	3.75	4.52	4.12	3.99
ENSMUSG00000034321	*Exosc1*	3.53	3.54	3.55	3.37
ENSMUSG00000034327	*Kctd9*	2.52	1.41	1.44	1.29
ENSMUSG00000034334	*NA*	1.89	1.78	1.84	2
ENSMUSG00000034341	*Wbp2*	6.01	6.76	6.6	6.54
ENSMUSG00000034345	*Gtf2h5*	5.03	4.76	5.09	5.05
ENSMUSG00000034349	*Smc4*	2.82	1.21	2.32	1.22
ENSMUSG00000034353	*RAMP1*	1.29	1.96	2.04	1.47
ENSMUSG00000034354	*mKIAA0371*	3.51	3.68	3.5	3.44
ENSMUSG00000034361	*Cpne2*	2.19	2.46	2.36	2.27
ENSMUSG00000034371	*Dak*	7.81	7.74	8.57	8.41
ENSMUSG00000034377	*Tulp4*	1	0.68	1.05	0.89
ENSMUSG00000034382	*AI661453*	1.47	2.74	2.32	2.04
ENSMUSG00000034390	*NA*	3.36	3.87	4.08	4.02
ENSMUSG00000034403	*Pja1*	4.2	4.64	4.26	4.13
ENSMUSG00000034412	*Tbc1d10a*	2.46	3.34	3.34	3.19
ENSMUSG00000034422	*Parp14*	3.05	2.08	2.58	2.76
ENSMUSG00000034424	*Gcsh*	6.25	5.75	5.9	5.43
ENSMUSG00000034429	*Zfp707*	3.13	3.52	3.54	3.31
ENSMUSG00000034430	*Zxdc*	2.13	1.97	2.26	2.05
ENSMUSG00000034432	*Cops8*	4.23	4.67	4.35	4.22
ENSMUSG00000034435	*Tmem30b*	3.1	4.31	3.74	3.71
ENSMUSG00000034442	*Trmt5*	2.66	2.44	2.4	2.42
ENSMUSG00000034445	*Cybasc3*	2.87	3.45	3.4	3.23
ENSMUSG00000034449	*BC022224*	4.34	5.11	4.96	4.52
ENSMUSG00000034450	*Gulo*	8.06	8.09	8.18	7.83
ENSMUSG00000034453	*Polr3b*	2.6	2.49	2.57	2.46
ENSMUSG00000034456	*Uroc1*	7.72	7.92	8.17	7.92
ENSMUSG00000034459	*Ifit1*	3.51	2.01	2.38	2.97
ENSMUSG00000034462	*Pkd2*	2.75	0.68	2.62	1.37

ENSMUSG00000034471	*Caskin2*	1.88	2.97	2	2.15
ENSMUSG00000034473	*Sec22a*	2.36	1.86	2.38	2.27
ENSMUSG00000034480	*Diap2*	2.41	1.12	1.94	1.22
ENSMUSG00000034484	*Snx2*	4.18	3.79	4.17	3.91
ENSMUSG00000034485	*Uaca*	1.47	1.89	1.96	1.53
ENSMUSG00000034487	*Kdelc2*	1.99	1.39	1.53	1.48
ENSMUSG00000034501	*1810048J11Rik*	1.52	1.37	1.66	1.11
ENSMUSG00000034509	*Mad2l1bp*	2.93	2.68	2.76	3.05
ENSMUSG00000034518	*Hmgb2l1*	1.61	1.38	1.37	0.81
ENSMUSG00000034522	*Zfp395*	1.97	3.31	2.88	2.79
ENSMUSG00000034525	*NA*	2.44	2.53	2.32	2.19
ENSMUSG00000034528	*Hsd17b13*	7.79	6.19	7.95	7.19
ENSMUSG00000034543	*Morc2a*	2.52	2.38	2.55	2.35
ENSMUSG00000034544	*Rsrc1*	2.78	2.3	2.37	1.91
ENSMUSG00000034557	*Zfyve9*	2.83	2.37	2.66	2.58
ENSMUSG00000034560	*A230046K03R*	3.05	2.16	2.59	2.21
ENSMUSG00000034563	*Ccpg1*	4.9	4.89	4.85	4.64
ENSMUSG00000034566	*Atp5h*	4.78	4.89	4.76	4.68
ENSMUSG00000034574	*Daam1*	3.54	3.21	3.47	3.15
ENSMUSG00000034575	*Pols*	2.93	3.25	3.3	3.14
ENSMUSG00000034584	*Exph5*	2.04	1.65	1.57	1.15
ENSMUSG00000034591	*Slc41a2*	1.1	0.61	0.7	-0.13
ENSMUSG00000034595	*NA*	0.72	1.33	1.4	1.02
ENSMUSG00000034602	*Mon2*	4.27	4.35	4.35	4.05
ENSMUSG00000034610	*Zcchc11*	2.61	1.89	3	2.36
ENSMUSG00000034616	*Ssh3*	1.8	2.62	2.46	1.9
ENSMUSG00000034617	*Mtrr*	1.52	1.63	1.53	1.62
ENSMUSG00000034620	*Tmem5*	3.29	2.84	2.94	2.65
ENSMUSG00000034621	*NA*	2.44	2.26	2.43	2.28
ENSMUSG00000034634	*Ly6d*	-0.76	-0.44	1.56	-0.79
ENSMUSG00000034636	*Zyg11b*	3.4	2.96	3.09	2.89

ENSMUSG00000034639	*NA*	1.94	1.65	1.8	1.86
ENSMUSG00000034640	*Tiparp*	2.26	0.78	1.48	-0.19
ENSMUSG00000034641	*4732429D16Ri*	1.05	1.45	-0.04	1.41
ENSMUSG00000034645	*NA*	1.39	0.57	0.64	1.03
ENSMUSG00000034659	*Tmem109*	4.08	4.88	4.22	4.28
ENSMUSG00000034663	*Bmp2k*	1.35	1.07	1.5	0.96
ENSMUSG00000034667	*Xpot*	3.7	3.27	3.6	3.15
ENSMUSG00000034673	*Pbx2*	2.95	3.22	3.13	3.02
ENSMUSG00000034684	*Sema3f*	1.32	1.75	1.04	1.24
ENSMUSG00000034707	*Gns*	6.37	6.39	6.47	6.2
ENSMUSG00000034708	*Grn*	7.04	7.32	7.49	7.08
ENSMUSG00000034709	*Ccdc128*	3.22	3.4	3.38	2.75
ENSMUSG00000034714	*Ttyh2*	4.59	5.19	5.04	4.97
ENSMUSG00000034723	*Txndc13*	2.54	1.38	2.37	1.59
ENSMUSG00000034724	*Cnot6l*	4.13	2.66	3.64	2.95
ENSMUSG00000034729	*Mrps10*	2.7	3.1	2.57	2.04
ENSMUSG00000034738	*Nostrin*	3.4	2.52	3.22	3.16
ENSMUSG00000034744	*Nagk*	3.18	3.47	3.04	2.5
ENSMUSG00000034757	*Tmub2*	3.96	4.41	4.38	4.2
ENSMUSG00000034761	*Map4k5*	2.52	1.6	2.38	2.17
ENSMUSG00000034771	*Tle2*	1.02	1.66	1.43	1.11
ENSMUSG00000034780	*B3galt1*	2.01	0.89	2.52	1.46
ENSMUSG00000034781	*Gna11*	4.87	5.33	5.17	5.1
ENSMUSG00000034783	*Cd207*	1.81	1.96	1.63	1.6
ENSMUSG00000034785	*Dio1*	5.66	5.87	4.91	5.94
ENSMUSG00000034786	*Gpsm3*	1.34	1.34	1.63	1.37
ENSMUSG00000034789	*Rab24*	3.53	4.04	4.05	3.98
ENSMUSG00000034793	*G6pc3*	1.61	2.47	2.39	1.86
ENSMUSG00000034795	*Ccdc122*	1.67	0.76	0.96	0.79
ENSMUSG00000034801	*NA*	2.92	2.07	3	2.58
ENSMUSG00000034807	*Glt25d1*	5	5.02	4.98	5.05

ENSMUSG00000034820	*5730453I16Rik*	3.25	3.11	3.14	2.97
ENSMUSG00000034826	*Nup54*	2.06	1.14	2.17	1.82
ENSMUSG00000034832	*NA*	1.1	1.35	1.38	1.06
ENSMUSG00000034837	*Gnat1*	0.11	0.57	1.53	0.86
ENSMUSG00000034845	*Plvap*	4.99	5.78	5.38	5.34
ENSMUSG00000034848	*Ttc21b*	0.99	0.08	1.04	0.29
ENSMUSG00000034850	*Tmem127*	4.08	4.3	4.16	4.01
ENSMUSG00000034853	*Acot11*	2.14	0.84	2.82	1.26
ENSMUSG00000034854	*F630110N24Ri*	1.58	2.52	1.78	1.64
ENSMUSG00000034858	*BC031353*	5.17	4.86	4.85	4.09
ENSMUSG00000034863	*NA*	0.07	0.55	1.21	-0.17
ENSMUSG00000034867	*Ankrd27*	2.82	3.01	3.22	2.85
ENSMUSG00000034868	*Mylc2b*	5.14	5.44	5.72	5.17
ENSMUSG00000034871	*BC026682*	1.48	0.52	2.5	0.45
ENSMUSG00000034875	*Nudt19*	5	4.73	5.1	4.71
ENSMUSG00000034880	*Mrpl34*	5.17	5.77	5.76	5.6
ENSMUSG00000034889	*2510012J08Rik*	2.38	3.45	2.49	2.73
ENSMUSG00000034892	*Rps29*	3.09	2.76	3.55	4.15
ENSMUSG00000034893	*Cog3*	2.58	2.76	2.3	2.32
ENSMUSG00000034902	*Pip5k1c*	2.78	3.7	3.31	3.12
ENSMUSG00000034903	*Cobll1*	4.12	3.52	4.06	3.68
ENSMUSG00000034908	*Sidt2*	6.44	6.91	6.03	6.04
ENSMUSG00000034911	*Ushbp1*	1.29	2.03	1.16	1.29
ENSMUSG00000034917	*Tjp3*	3.08	4.06	3.76	3.53
ENSMUSG00000034926	*Dhcr24*	8.47	8.86	8.68	8.47
ENSMUSG00000034928	*Rnf44*	4.26	4.6	4.56	4.47
ENSMUSG00000034930	*Rtkn*	1.39	2.1	2.09	1.8
ENSMUSG00000034931	*Dhx8*	3.04	3.23	3.18	2.94
ENSMUSG00000034932	*Mrpl54*	4.63	4.84	4.6	4.54
ENSMUSG00000034936	*Arl4d*	3.92	4.17	4.94	4.95
ENSMUSG00000034940	*Ap1gbp1*	2.54	1.98	2.1	1.87

ENSMUSG00000034947	*Tmem106a*	2.72	2.57	2.53	2.13
ENSMUSG00000034951	*Cog7*	3.45	3.99	3.32	3.1
ENSMUSG00000034957	*Cebpa*	7.27	8.01	7.49	7.39
ENSMUSG00000034973	*NA*	1.49	1.18	1.26	0.67
ENSMUSG00000034974	*Dapk3*	3.46	4.67	4.26	3.96
ENSMUSG00000034993	*Vat1*	3.8	4.56	4.18	4
ENSMUSG00000034994	*Eef2*	8.62	9.2	8.76	8.93
ENSMUSG00000034998	*Foxn2*	1.88	1.65	1.74	1.24
ENSMUSG00000035000	*Dpp4*	6.16	5.48	5.94	5.42
ENSMUSG00000035004	*Igsf6*	1.66	0.96	1.77	0.37
ENSMUSG00000035007	*Rundc1*	2.88	3.18	2.52	2.58
ENSMUSG00000035011	*Zbtb7a*	3.97	4.07	3.73	3.64
ENSMUSG00000035021	*NA*	2.35	2.18	2.24	2.1
ENSMUSG00000035024	*Ncapd3*	0.66	0.71	1.23	0.63
ENSMUSG00000035027	*Map2k2*	6.06	6.88	6.42	6.24
ENSMUSG00000035031	*C8a*	6.13	6.63	6.1	6.36
ENSMUSG00000035041	*Creb3l3*	7.88	7.48	7.78	7.49
ENSMUSG00000035042	*Ccl5*	1.06	-0.08	1.68	0.69
ENSMUSG00000035047	*Kri1*	2.19	2.84	2.77	2.45
ENSMUSG00000035048	*Anapc13*	6.04	5.82	6.19	6.09
ENSMUSG00000035049	*Rrp12*	0.6	2.22	1.02	1.51
ENSMUSG00000035051	*Dhx57*	1.62	1.83	1.65	1.33
ENSMUSG00000035064	*Eef2k*	1.18	1.82	1.63	1.57
ENSMUSG00000035069	*Oma1*	3.26	3.52	3.4	2.85
ENSMUSG00000035078	*Mtmr9*	3.9	3.89	3.66	3.45
ENSMUSG00000035086	*Becn1*	4.96	5.07	4.87	4.5
ENSMUSG00000035093	*3110001I20Rik*	4.15	3.7	3.92	3.69
ENSMUSG00000035104	*Tmem166*	5.66	5.42	5.85	5.39
ENSMUSG00000035105	*Egln3*	3.66	4.02	3.76	3.5
ENSMUSG00000035133	*Arhgap5*	4.64	3.25	3.69	3.01
ENSMUSG00000035139	*Secisbp2*	1.86	2.48	2.22	2.04

ENSMUSG00000035142	*Nubpl*	2.59	1.36	1.69	1.49
ENSMUSG00000035150	*Eif2s3x*	1.46	1.52	1.54	1.55
ENSMUSG00000035151	*Elmod2*	2.75	1.6	2.35	1.65
ENSMUSG00000035152	*Ap2b1*	4.22	4.4	4.08	3.9
ENSMUSG00000035161	*Ints6*	1.86	1.86	2.51	2.12
ENSMUSG00000035164	*NA*	1.17	0.37	1.26	1.25
ENSMUSG00000035168	*AK134490*	0.88	0.69	1.09	0.79
ENSMUSG00000035171	*1110059E24Ri*	3.47	2.8	3.56	2.92
ENSMUSG00000035172	*Plekhh3*	1.48	2.76	1.82	2.04
ENSMUSG00000035173	*A630007B06Ri*	2.32	1.6	2.05	1.53
ENSMUSG00000035181	*D930036F22R*	1.67	2.13	1.6	1.51
ENSMUSG00000035184	*NA*	1.62	2.2	1.96	1.94
ENSMUSG00000035198	*Tubg1*	3.18	3.87	3.94	4.08
ENSMUSG00000035199	*Arl6ip5*	5.12	5.05	5	4.75
ENSMUSG00000035202	*Kiaa0028*	7.33	7.11	7.11	6.27
ENSMUSG00000035203	*Epn1*	5.99	7	6.81	6.67
ENSMUSG00000035206	*3110056O03Ri*	1.98	3.16	2.94	2.61
ENSMUSG00000035212	*Leprot*	3.44	2.87	2.97	2.67
ENSMUSG00000035215	*Lsm7*	1.82	0.8	0.85	-0.23
ENSMUSG00000035227	*Spcs2*	4.96	4.76	4.19	4.06
ENSMUSG00000035234	*Ccdc98*	2.11	1.52	1.95	1.58
ENSMUSG00000035237	*Lcat*	9.07	9.52	9.17	9.08
ENSMUSG00000035242	*Oaz1*	3.6	2.83	3.03	3.09
ENSMUSG00000035245	*A130022J15Ri*	0.7	1.15	1.05	0.42
ENSMUSG00000035247	*NA*	4.75	4.7	4.73	4.5
ENSMUSG00000035248	*Zcchc6*	4.69	4.2	4.2	3.96
ENSMUSG00000035258	*Abi3bp*	1.47	0.63	1.15	0.9
ENSMUSG00000035266	*Hel308*	0.77	0.88	1.37	0.3
ENSMUSG00000035268	*Pkig*	3.13	3.31	3.27	2.86
ENSMUSG00000035273	*Hpse*	1.66	0.44	1.22	1.05
ENSMUSG00000035278	*Plekhj1*	4.24	4.81	4.62	4.57

ENSMUSG00000035284	*Vps13c*	2.33	1.85	2.35	1.86
ENSMUSG00000035297	*Cops4*	5.01	4.89	4.95	4.82
ENSMUSG00000035299	*Mid1*	1.35	1.12	1.27	1.19
ENSMUSG00000035310	*AI461788*	2.11	1.22	1.94	1.52
ENSMUSG00000035311	*Gnptab*	2	2.04	2.19	1.68
ENSMUSG00000035325	*NA*	5.67	6.04	6.1	5.9
ENSMUSG00000035329	*Fbxo33*	3.1	1.91	2.51	2.34
ENSMUSG00000035342	*Lzts2*	1.36	2.67	1.62	1.91
ENSMUSG00000035349	*Mia2*	6.12	5.22	5.92	5.37
ENSMUSG00000035351	*Nup37*	2.01	0.89	2.35	1.01
ENSMUSG00000035354	*Uvrag*	3.51	3.31	3.85	3.68
ENSMUSG00000035356	*Nfkbiz*	1.32	0.24	1.27	0.51
ENSMUSG00000035357	*Pdzrn3*	1.92	1.67	2.6	2.01
ENSMUSG00000035367	*Rmi1*	3.28	2.13	2.93	2.59
ENSMUSG00000035370	*Adat3*	3.2	3.84	3.41	3.43
ENSMUSG00000035372	*1810055G02Ri*	4.97	4.71	5.44	4.92
ENSMUSG00000035376	*Ptplb*	4.15	3.96	4.15	4.02
ENSMUSG00000035378	*Shq1*	1.06	1.46	1.05	1.1
ENSMUSG00000035382	*Pcsk7*	3.09	3.62	3.17	2.99
ENSMUSG00000035392	*Dennd1a*	2.83	3.28	3.3	3.13
ENSMUSG00000035397	*Klf16*	0.55	1.51	1.29	0.64
ENSMUSG00000035401	*AK009395*	2.25	2.38	2.36	2.19
ENSMUSG00000035413	*Tmem98*	4.6	4.08	4.47	3.44
ENSMUSG00000035437	*Rabgap1*	2.47	1.72	2.27	1.74
ENSMUSG00000035441	*Myo1d*	2.68	3.12	2.77	2.44
ENSMUSG00000035443	*mThy28*	4.02	4.03	3.81	3.52
ENSMUSG00000035451	*Foxa1*	3.23	3.01	2.73	2.75
ENSMUSG00000035459	*Stab2*	3.32	4.06	3.35	3.6
ENSMUSG00000035469	*Rcbtb1*	4.5	4	4.35	4.03
ENSMUSG00000035472	*Slc25a21*	3.56	2.2	2.9	2.39
ENSMUSG00000035473	*Galm*	6.7	6.44	6.72	6.47

ENSMUSG00000035476	*Map3k7ip3*	1.7	0.68	0.98	0.32
ENSMUSG00000035478	*Mbd3*	4.44	5.38	4.6	4.73
ENSMUSG00000035492	*NA*	2.31	1.72	2.34	1.91
ENSMUSG00000035493	*Tgfbi*	4.14	4.66	3.97	4.06
ENSMUSG00000035495	*BC057893*	3.15	2.92	3.07	2.97
ENSMUSG00000035498	*Cdcp1*	0.7	0.8	1.14	0.47
ENSMUSG00000035504	*Reep6*	8.47	9.05	8.89	8.76
ENSMUSG00000035505	*Cox18*	4.32	4.16	3.92	3.79
ENSMUSG00000035509	*Fbxl21*	0.96	1.6	1.3	1.29
ENSMUSG00000035517	*Tdrd7*	3.51	3.61	3.4	3.39
ENSMUSG00000035521	*Gnptg*	3.6	3.84	3.65	3.36
ENSMUSG00000035529	*Prdm4*	2.06	2.07	1.9	1.73
ENSMUSG00000035530	*Eif1*	5.33	4.94	5.76	5.55
ENSMUSG00000035540	*Gc*	12.29	12.07	12.19	12.11
ENSMUSG00000035545	*Leng8*	2.44	2.72	3.04	2.49
ENSMUSG00000035559	*BC051227*	3.87	4.33	4.28	3.99
ENSMUSG00000035561	*Aldh1b1*	5.88	5.97	6.08	5.54
ENSMUSG00000035569	*Ankrd11*	3.42	3.73	3.62	3.42
ENSMUSG00000035572	*Wdr32*	3.52	2.99	2.93	3.03
ENSMUSG00000035575	*Utp6*	4.02	3.55	3.75	3.38
ENSMUSG00000035585	*Tsen34*	2.06	2.94	2.32	2.08
ENSMUSG00000035595	*1600002K03Ri*	1.74	2.25	2.51	2.85
ENSMUSG00000035596	*Leng4*	4.42	4.73	4.57	4.29
ENSMUSG00000035597	*Prpf39*	2.84	1.7	2.38	1.65
ENSMUSG00000035601	*Rg9mtd3*	1.6	1.23	1.34	1.6
ENSMUSG00000035614	*NA*	2.53	1.64	2.42	1.9
ENSMUSG00000035620	*Ric8b*	2.78	2.62	2.17	2.31
ENSMUSG00000035621	*Midn*	3.58	4.42	4.33	3.95
ENSMUSG00000035623	*Rsf1*	1.69	0.84	1.55	0.97
ENSMUSG00000035629	*mKIAA0226*	2.27	2.49	2.58	2.46
ENSMUSG00000035632	*AK031165*	2.46	3.08	2.94	2.85

ENSMUSG00000035637	*Grhpr*	7.04	7.55	7.21	7.03
ENSMUSG00000035642	*1810020D17Ri*	3.84	3.92	4.57	4.39
ENSMUSG00000035649	*D4Wsu132e*	1.48	0.96	0.95	0.83
ENSMUSG00000035666	*Gtf3c4*	2.94	2.61	2.75	2.59
ENSMUSG00000035671	*Zswim4*	1.25	2.27	1.17	0.88
ENSMUSG00000035673	*Sbno2*	2.2	2.84	2.22	1.97
ENSMUSG00000035674	*Ndufa3*	5.37	5.42	5.93	6.05
ENSMUSG00000035686	*Thrsp*	7.52	6.46	7.97	7.84
ENSMUSG00000035692	*Isg15*	3.05	3.1	2.22	3.04
ENSMUSG00000035696	*Rnf38*	1.76	1.18	1.6	1.03
ENSMUSG00000035697	*Hmha1*	0.86	1.45	1.64	0.48
ENSMUSG00000035699	*Osta*	3	1.42	2.75	1.98
ENSMUSG00000035704	*Alg8*	2.93	2.56	2.79	2.94
ENSMUSG00000035711	*Dok3*	-0.63	0.01	1.08	-0.25
ENSMUSG00000035726	*Supt16h*	3.59	3.33	3.54	3.23
ENSMUSG00000035754	*Wdr18*	4.93	5.71	5.33	5.14
ENSMUSG00000035757	*1300018J18Ri*	5.67	5.8	5.81	5.46
ENSMUSG00000035759	*NA*	1.27	1.76	1.92	1.5
ENSMUSG00000035762	*Tmem161b*	1.95	0.89	2.07	0.97
ENSMUSG00000035764	*Fbxo45*	2.24	1.46	1.96	1.4
ENSMUSG00000035765	*Dym*	4.38	4.51	4.69	4.38
ENSMUSG00000035769	*Xylb*	6.31	6.15	6.57	6.36
ENSMUSG00000035770	*Dync1li2*	3.14	2.91	2.77	2.63
ENSMUSG00000035772	*MRP-S2*	4.37	5.29	5.17	5.14
ENSMUSG00000035776	*Cd99l2*	4.38	4.09	3.91	3.61
ENSMUSG00000035778	*Ggta1*	1.11	0.81	0.82	0.57
ENSMUSG00000035780	*Ugt2a3*	7.46	6.83	7.03	6.78
ENSMUSG00000035781	*C030046I01Ri*	4.92	5.21	5.1	4.94
ENSMUSG00000035783	*AK080187*	1.91	1.85	2.36	2.58
ENSMUSG00000035790	*1500031L02Ri*	2.33	2.03	2.12	2.01
ENSMUSG00000035798	*mKIAA0946*	2.06	1.55	1.4	0.99

ENSMUSG00000035811	*Ugt2b35*	5.28	5.11	4.91	4.89
ENSMUSG00000035824	*Tk2*	3.39	3.64	3.37	3.1
ENSMUSG00000035828	*Pim3*	4.99	5.4	5.63	5.53
ENSMUSG00000035834	*Polr3g*	2.82	1.94	2.3	1.72
ENSMUSG00000035836	*Ugt2b1*	8.1	7.37	7.7	7.48
ENSMUSG00000035840	*Lysmd3*	4.24	2.93	3.43	3.1
ENSMUSG00000035845	*Alg12*	1.93	2.79	2.07	1.8
ENSMUSG00000035847	*Ids*	3.26	2.58	2.95	2.78
ENSMUSG00000035851	*Ythdc1*	4.33	3.72	3.65	3.28
ENSMUSG00000035864	*Syt1*	2.93	2.27	2.53	1.94
ENSMUSG00000035868	*NA*	2	0.87	1.74	0.77
ENSMUSG00000035873	*Pawr*	2.4	1.87	2.23	2.01
ENSMUSG00000035875	*AI182371*	7.73	7.48	7.28	7.17
ENSMUSG00000035877	*Zhx3*	4.4	3.86	4	3.88
ENSMUSG00000035878	*C630028N24R*	5.78	4.62	5.85	5.1
ENSMUSG00000035885	*Cox8a*	7.08	7.7	7.7	7.68
ENSMUSG00000035890	*Rnf126*	3.75	4.83	4.56	4.33
ENSMUSG00000035898	*AK017645*	1.87	0.39	1.17	0.69
ENSMUSG00000035900	*BC021523*	1.65	2.09	1.44	0.98
ENSMUSG00000035901	*ORF37*	3.8	3.82	3.64	3.46
ENSMUSG00000035919	*Bbs9*	1.18	1.09	0.92	0.56
ENSMUSG00000035929	*NA*	3.7	3.52	3.45	3.5
ENSMUSG00000035933	*NA*	2.64	2.4	2.35	2.38
ENSMUSG00000035936	*Aldh5a1*	4.61	4.52	4.58	4.22
ENSMUSG00000035941	*mKIAA1417*	4.24	3.67	4.04	3.51
ENSMUSG00000035944	*AW124722*	4.69	5.26	4.72	4.96
ENSMUSG00000035948	*8430416H19Ri*	2.88	1.62	2.57	1.63
ENSMUSG00000035949	*Fbxw2*	3.91	3.56	3.81	3.55
ENSMUSG00000035953	*Tmem55b*	4.12	3.95	4.04	3.66
ENSMUSG00000035954	*mKIAA0716*	2.15	1.69	2.2	2
ENSMUSG00000035958	*AK140178*	3.53	2.4	3.49	2.75

ENSMUSG00000035960	*Apex1*	4.23	4.83	4.16	4.2
ENSMUSG00000035969	*Rusc2*	2.68	3.66	3.39	3.1
ENSMUSG00000035992	*Fnip1*	3.99	2.27	3.78	3.02
ENSMUSG00000036002	*B230312A22Ri*	2.21	2.54	2.22	1.91
ENSMUSG00000036019	*Tmtc2*	2.63	2.61	2.09	2.05
ENSMUSG00000036023	*Parp2*	2.92	2.18	2.7	1.97
ENSMUSG00000036026	*Tmem63b*	4.59	5.29	4.56	4.62
ENSMUSG00000036027	*NA*	0.54	-0.07	1.35	0.54
ENSMUSG00000036046	*5031439G07Ri*	3.47	3.67	3.74	3.19
ENSMUSG00000036053	*Fmnl2*	2.05	1.18	1.31	0.99
ENSMUSG00000036057	*Ptpn23*	2.13	2.99	2.65	2.58
ENSMUSG00000036061	*Smug1*	1.84	1.94	1.75	1.73
ENSMUSG00000036073	*Galt*	4.06	5.1	4.22	4.51
ENSMUSG00000036078	*Oprs1*	6.69	7.39	6.33	6.51
ENSMUSG00000036083	*Slc17a3*	4.25	4.22	3.99	3.89
ENSMUSG00000036087	*Slain2*	4.57	3.65	4.1	3.63
ENSMUSG00000036093	*Arl5a*	5.38	4.66	4.82	4.7
ENSMUSG00000036097	*6030443O07Ri*	2.08	1.56	1.93	1.67
ENSMUSG00000036098	*NA*	2.89	3.95	3.42	3.32
ENSMUSG00000036103	*Colec12*	4.48	4.28	4.04	3.52
ENSMUSG00000036104	*Rab3gap1*	3.8	3.79	3.8	3.32
ENSMUSG00000036106	*Arhgap8*	1.66	2.12	2.37	1.89
ENSMUSG00000036110	*Slc17a2*	5.66	5.34	5.19	5.29
ENSMUSG00000036112	*Metap2*	3.64	3.35	3.45	3.14
ENSMUSG00000036114	*2810432D09Ri*	3.84	4.49	3.81	4.03
ENSMUSG00000036120	*Rfxank*	2.6	3.57	2.84	2.75
ENSMUSG00000036138	*Acaa1a*	5.21	5.68	5.86	5.67
ENSMUSG00000036151	*Tm6sf2*	5.97	6.2	5.9	5.6
ENSMUSG00000036160	*Surf6*	2.48	2.89	2.27	2.3
ENSMUSG00000036167	*Pphln1*	2.33	2.61	2.46	2.12
ENSMUSG00000036180	*Gatad2a*	4.3	4.61	4.54	4.53

ENSMUSG00000036181	*Hist1h1c*	3.25	3.76	4.08	3.76
ENSMUSG00000036188	*Ankmy2*	2.87	2.65	2.8	2.48
ENSMUSG00000036197	*Glt8d3*	2.2	1.54	1.81	1.52
ENSMUSG00000036199	*Ndufa13*	7.39	7.34	7.57	7.4
ENSMUSG00000036202	*Rif1*	1.84	0.91	1.55	1.1
ENSMUSG00000036208	*BC027231*	2.12	1.87	2.27	1.68
ENSMUSG00000036214	*1700022C21Ri*	3.49	3.43	3.58	3.22
ENSMUSG00000036216	*Leap2*	6.96	6.65	7.1	6.53
ENSMUSG00000036241	*Ube2r2*	7.12	7.15	7.32	7.11
ENSMUSG00000036249	*Rbm43*	1.69	1.61	1.35	1.05
ENSMUSG00000036256	*Igfbp7*	6.63	6.42	6.31	6.22
ENSMUSG00000036257	*Pnpla8*	5.77	4.77	5.47	4.89
ENSMUSG00000036270	*Edc4*	2.53	2.88	2.52	2.38
ENSMUSG00000036275	*9530068E07Ri*	7.01	6.53	6.68	6.41
ENSMUSG00000036278	*Macrod1*	4.99	5.84	5.18	5.18
ENSMUSG00000036279	*NA*	4.79	3.76	4	3.36
ENSMUSG00000036281	*Snapc4*	0.82	1.7	1.4	0.95
ENSMUSG00000036282	*Nat12*	3.5	2.2	2.92	2.31
ENSMUSG00000036285	*2610024G14Ri*	3.14	3.45	3.05	2.95
ENSMUSG00000036291	*4932432K03Ri*	2.77	2	2.63	1.96
ENSMUSG00000036292	*Gramd1c*	3.11	2.21	3.07	2.12
ENSMUSG00000036299	*BC031181*	6.03	5.84	5.83	5.79
ENSMUSG00000036309	*Skp1a*	6.9	6.28	6.7	6.17
ENSMUSG00000036315	*Znrd1*	3.84	4	3.85	4.01
ENSMUSG00000036323	*Srp72*	5.7	5.05	5.22	4.85
ENSMUSG00000036327	*Qscn6l1*	1.64	1.77	1.64	1.37
ENSMUSG00000036333	*C330002I19Ri*	3.18	3.16	3.04	2.84
ENSMUSG00000036339	*6720456H20Ri*	2.95	1.77	2.51	1.99
ENSMUSG00000036352	*Ubadc1*	3.66	3.5	3.53	3.3
ENSMUSG00000036362	*P2ry13*	1.28	0.1	0.32	-0.34
ENSMUSG00000036368	*AW061290*	5.48	4.48	5.19	4.55

ENSMUSG00000036371	*Serbp1*	7.08	6.43	6.79	6.42
ENSMUSG00000036372	*NA*	5.29	4.79	5.13	5.23
ENSMUSG00000036376	*Abt1*	1.42	1.64	1.84	1.67
ENSMUSG00000036381	*P2ry14*	0.92	0	1.12	0.06
ENSMUSG00000036391	*Sec24a*	5.21	4.27	5.14	4.67
ENSMUSG00000036398	*Ppp1r11*	5.36	6.12	5.68	5.45
ENSMUSG00000036402	*Gng12*	4.26	3.79	3.92	3.63
ENSMUSG00000036427	*Gpi1*	5.32	5.39	5.79	5.41
ENSMUSG00000036430	*Tbcc*	2.41	3.16	2.76	2.22
ENSMUSG00000036432	*Siah2*	3.05	3.33	3.33	3.26
ENSMUSG00000036435	*Exoc1*	2.14	1.93	1.58	1.74
ENSMUSG00000036438	*Calm2*	5.66	5.36	5.63	4.88
ENSMUSG00000036442	*Thap11*	3.68	4.09	3.75	3.85
ENSMUSG00000036446	*Lum*	3.43	2.17	2.9	2.56
ENSMUSG00000036450	*Hif1an*	2.98	2.98	2.62	2.42
ENSMUSG00000036452	*Arhgap26*	1.5	1.4	1.44	1.15
ENSMUSG00000036461	*Elf1*	2.89	2.47	2.96	2.75
ENSMUSG00000036473	*Tbc1d24*	3.08	2.26	2.5	2.22
ENSMUSG00000036478	*Btg1*	5.05	4.63	4.75	4.31
ENSMUSG00000036492	*Rnf39*	2.62	2.95	2.78	2.78
ENSMUSG00000036499	*Eea1*	3.54	2.8	3.01	2.68
ENSMUSG00000036501	*2610024E20Ri*	4.08	3.47	3.8	3.33
ENSMUSG00000036503	*Rzf*	7.13	6.27	6.65	6.11
ENSMUSG00000036504	*Phpt1*	3.79	4.84	4.49	4.45
ENSMUSG00000036513	*Commd2*	3.91	3.58	3.92	3.41
ENSMUSG00000036528	*Ppfibp2*	2.99	2.8	3.74	3.26
ENSMUSG00000036529	*Sbf1*	3.4	4.17	3.65	3.5
ENSMUSG00000036534	*BC031853*	3.33	3.85	3.52	3.54
ENSMUSG00000036550	*NA*	4.3	3.85	4.13	3.76
ENSMUSG00000036555	*Iqce*	0.24	0.65	1.3	0.93
ENSMUSG00000036561	*Saps2*	3.39	3.9	3.76	3.52

ENSMUSG00000036565	*Ttyh3*	1.3	2.32	2.14	2.1
ENSMUSG00000036568	*NA*	1.84	1.85	1.84	1.91
ENSMUSG00000036570	*Fxyd1*	8.23	8.48	8.85	8.65
ENSMUSG00000036572	*Upf3b*	3.01	1.83	2.97	2.55
ENSMUSG00000036580	*Spg20*	4.41	4.28	4.1	3.68
ENSMUSG00000036585	*Fgf1*	6.24	5.86	5.91	5.46
ENSMUSG00000036591	*Arhgap21*	2.68	2.87	2.84	2.75
ENSMUSG00000036594	*H2-Aa*	6.08	5.49	6.06	5.3
ENSMUSG00000036606	*NA*	5.47	5.96	5.73	5.54
ENSMUSG00000036611	*2310005P05Ri*	2.45	2.61	3.09	2.84
ENSMUSG00000036613	*Tssc1*	1.96	2.67	2.5	2.07
ENSMUSG00000036615	*Rfxap*	2.59	2.74	2.38	2.63
ENSMUSG00000036620	*Mgat4b*	4.7	5.39	4.67	4.67
ENSMUSG00000036622	*Atp13a2*	2.57	3.38	2.92	2.85
ENSMUSG00000036632	*Alg5*	5.17	4.9	5.01	4.57
ENSMUSG00000036636	*Clcn7*	3.97	4.52	4.28	4.27
ENSMUSG00000036639	*Nudt1*	3.52	3.72	3.54	3.34
ENSMUSG00000036644	*Tbc1d9b*	4.52	5.13	4.53	4.54
ENSMUSG00000036646	*Man1b1*	4.26	4.41	4.14	4.07
ENSMUSG00000036649	*Slc45a4*	0.7	1.34	1.4	0.91
ENSMUSG00000036655	*Colec11*	4.68	4.54	4.55	4.56
ENSMUSG00000036678	*Aaas*	2.46	2.81	2.94	2.75
ENSMUSG00000036686	*Cc2d1a*	2.07	2.72	2.41	2.09
ENSMUSG00000036687	*Tmem184a*	2.11	2.23	2.58	2.23
ENSMUSG00000036693	*Nol14*	3.5	3.55	3.46	3.3
ENSMUSG00000036698	*Eif2c2*	1.19	1.25	1.04	0.9
ENSMUSG00000036707	*Cab39*	5.01	4.22	4.57	4.2
ENSMUSG00000036712	*Cyld*	2.55	1.65	2.29	1.59
ENSMUSG00000036721	*Zscan12*	1.91	1.11	1.7	1.3
ENSMUSG00000036733	*3100004P22Ri*	3.95	4.77	4.51	4.35
ENSMUSG00000036737	*Oxsr1*	3.8	3.57	3.45	3.19

ENSMUSG00000036748	*Cuedc2*	3.9	4.3	4.17	4.1
ENSMUSG00000036751	*Cox6b1*	8.29	8.13	8.75	8.6
ENSMUSG00000036752	*Tubb2c*	5.15	5.67	4.64	4.84
ENSMUSG00000036764	*Dnajc12*	2.89	2.99	2.81	2.72
ENSMUSG00000036775	*Decr2*	7.02	6.57	7	6.65
ENSMUSG00000036779	*NA*	3.85	3.5	3.99	3.77
ENSMUSG00000036781	*Rps27l*	7.37	4.81	6.72	6.24
ENSMUSG00000036782	*Klhl13*	2.73	2.3	2.26	1.58
ENSMUSG00000036810	*Tmem188*	3.13	2.38	2.91	2.36
ENSMUSG00000036813	*Entpd8*	5.36	5.52	5.47	5.22
ENSMUSG00000036817	*Unc84a*	2.28	2.41	2.29	2.01
ENSMUSG00000036819	*Jmjd4*	1.57	1.88	1.13	1.37
ENSMUSG00000036820	*Amdhd2*	2.54	3.27	2.97	2.57
ENSMUSG00000036822	*Topors*	3.71	3.3	3.39	3.02
ENSMUSG00000036825	*Ssx2ip*	1.92	1.88	2.16	1.81
ENSMUSG00000036826	*U2af1l4*	1.95	2.32	2.18	2.1
ENSMUSG00000036833	*Pnpla7*	4.67	4.96	5.02	4.93
ENSMUSG00000036835	*Psenen*	2.58	2.82	2.74	2.84
ENSMUSG00000036840	*Siah1a*	1.93	1	1.53	1.09
ENSMUSG00000036845	*Lin37*	2.45	3.12	3.05	2.26
ENSMUSG00000036850	*Mrpl41*	4.5	4.4	4.63	4.38
ENSMUSG00000036854	*Hspb6*	3.18	2.81	3.35	3.21
ENSMUSG00000036860	*Mrpl55*	3.35	4.01	4.41	3.99
ENSMUSG00000036863	*NA*	1.8	1.96	2.18	1.82
ENSMUSG00000036867	*Smad6*	1.62	3.28	2.1	1.87
ENSMUSG00000036873	*2410004B18Ri*	2.2	1.98	2.14	2.51
ENSMUSG00000036875	*Dna2l*	1.06	1.9	1.75	1.65
ENSMUSG00000036879	*Phkb*	3.52	2.66	3.01	2.6
ENSMUSG00000036880	*Acaa2*	9.47	9.37	9.27	9.06
ENSMUSG00000036885	*4631416L12Ri*	4.91	4.27	4.53	4.51
ENSMUSG00000036887	*C1qa*	5.06	5.41	5.25	4.92

ENSMUSG00000036890	*Gtdc1*	1.65	1.51	2.02	1.68
ENSMUSG00000036892	*Prodh2*	6.92	7.51	7.14	6.98
ENSMUSG00000036893	*Ehmt1*	2.95	3.11	2.89	2.89
ENSMUSG00000036896	*C1qc*	5.38	5.49	5.32	5.11
ENSMUSG00000036904	*Fzd8*	1.55	2.7	2.31	1.85
ENSMUSG00000036905	*C1qb*	6.14	5.99	5.84	5.71
ENSMUSG00000036908	*Unc93b1*	4.03	4.35	4.22	4.06
ENSMUSG00000036916	*Zfp280c*	0.85	0.23	1.06	0.46
ENSMUSG00000036918	*Ttc7*	3.76	4.06	4.51	4.35
ENSMUSG00000036932	*Aifm1*	6.15	5.59	5.98	5.37
ENSMUSG00000036934	*4921524J17Ri*	2.22	1.24	2.48	2.5
ENSMUSG00000036940	*Aof2*	2.81	2.79	3	2.63
ENSMUSG00000036941	*Elac1*	1.64	1.08	1.74	1.35
ENSMUSG00000036943	*Rab8B*	1.45	0.1	0.43	0.11
ENSMUSG00000036948	*BC037034*	2.44	2.97	2.92	2.48
ENSMUSG00000036955	*2510003E04Ri*	3.09	3.06	3.44	3.29
ENSMUSG00000036957	*Lrfn3*	2.11	2.87	1.68	1.74
ENSMUSG00000036959	*Bcorl1*	1.18	1.59	1.18	1.06
ENSMUSG00000036966	*Spryd3*	3.6	4.21	3.73	3.57
ENSMUSG00000036968	*2610019P18Ri*	1.98	2.09	1.53	1.79
ENSMUSG00000036975	*Tmem177*	2.45	2.69	2.52	2.01
ENSMUSG00000036980	*AK047944*	3.6	4.36	4.06	4
ENSMUSG00000036983	*Tfb1m*	3.38	3.19	3.38	2.71
ENSMUSG00000036985	*Zdhhc9*	6.17	6.16	6.38	6.08
ENSMUSG00000036986	*Pml*	3.11	3.48	3.33	3.33
ENSMUSG00000036989	*hac1*	1.76	2.1	2.29	1.99
ENSMUSG00000036990	*Otud4*	3.3	2.52	3	2.83
ENSMUSG00000036992	*Nxt1*	2.25	3.03	2.4	2.85
ENSMUSG00000036995	*Ddefl1*	0.55	1.94	1.07	1.57
ENSMUSG00000037003	*Tenc1*	3.93	4.74	4.32	4.1
ENSMUSG00000037007	*Zfp113*	1.52	0.83	1.23	0.7

ENSMUSG00000037013	*Ss18*	3.02	2.9	3.2	2.75
ENSMUSG00000037015	*Tmem185b*	3.19	2.47	2.9	2.17
ENSMUSG00000037017	*Zscan21*	2.53	2.56	2.57	2.55
ENSMUSG00000037019	*BC038156*	3.2	2.2	2.61	2.02
ENSMUSG00000037022	*Mmaa*	2.91	2.69	2.83	2.33
ENSMUSG00000037025	*Foxa2*	4.43	4.42	3.67	3.21
ENSMUSG00000037029	*Zfp146*	3.85	3.16	3.41	3.35
ENSMUSG00000037049	*Smpd1*	4.9	5.47	5.18	5.14
ENSMUSG00000037053	*Azgp1*	10.05	9.76	10.06	9.89
ENSMUSG00000037058	*Paip2*	6.05	5.45	5.75	5.3
ENSMUSG00000037062	*Sh3glb1*	5.64	5	5.62	5.02
ENSMUSG00000037071	*Scd1*	9.67	9.63	10.17	9.93
ENSMUSG00000037072	*15-Sep*	7.34	6.93	7.01	6.56
ENSMUSG00000037075	*Rnf139*	5.32	4.31	4.99	4.29
ENSMUSG00000037085	*Trmt12*	2.06	2.34	1.81	1.54
ENSMUSG00000037089	*Slc35b2*	3.57	4.27	4.06	3.98
ENSMUSG00000037095	*Lrg1*	7.68	8.61	8.44	7.56
ENSMUSG00000037096	*NA*	3.6	2.05	3.31	3.7
ENSMUSG00000037098	*NA*	2.19	2.79	2.68	2.43
ENSMUSG00000037103	*BC057552*	0.57	1.37	1.46	0.95
ENSMUSG00000037104	*Socs5*	1.96	1.82	1.72	1.26
ENSMUSG00000037108	*Zcwpw1*	1.25	1.66	1.88	1.42
ENSMUSG00000037110	*A230067G21R*	3.01	2.42	2.74	2.34
ENSMUSG00000037112	*Snf1lk2*	1.75	1.64	2.18	1.86
ENSMUSG00000037119	*D15Ertd621e*	5.15	4.55	4.84	4.36
ENSMUSG00000037134	*AI931714*	2.49	2.45	2.8	2.41
ENSMUSG00000037149	*Ddx1*	5.41	5.06	5.11	4.87
ENSMUSG00000037151	*Lrrc20*	1.21	2.02	2.24	1.69
ENSMUSG00000037152	*Ndufc1*	6.04	3.6	5.64	4.66
ENSMUSG00000037157	*Il22ra1*	0.72	1.93	2.08	0.96
ENSMUSG00000037166	*Ppp1r14a*	1.05	2.9	2.04	2.42

ENSMUSG00000037174	*Elf2*	3.67	3.77	3.56	3.27
ENSMUSG00000037190	*Cyb561d2*	2.61	3.27	3.03	3.16
ENSMUSG00000037197	*Rbm17*	4.06	3.91	3.94	3.49
ENSMUSG00000037204	*9430023L20Ri*	4.39	4.94	4.8	4.31
ENSMUSG00000037210	*BC037112*	2.59	2.4	2.6	2.49
ENSMUSG00000037211	*Spry1*	1.5	2.28	1.69	1.66
ENSMUSG00000037214	*Thap1*	1.5	2.35	2.1	1.94
ENSMUSG00000037216	*Lipt1*	2.18	1.99	2.06	1.98
ENSMUSG00000037221	*Mospd3*	4.65	5.9	5.39	5.33
ENSMUSG00000037234	*Hook3*	2.62	1.35	2.12	1.89
ENSMUSG00000037235	*Mxd4*	4.67	5.41	4.82	4.69
ENSMUSG00000037236	*Matr3*	5.06	3.65	4.52	3.8
ENSMUSG00000037242	*Clic4*	5	5	4.41	4.86
ENSMUSG00000037251	*4930444A02Ri*	2.13	2.49	2.3	1.49
ENSMUSG00000037253	*Mex3c*	3.31	2.69	2.97	2.46
ENSMUSG00000037254	*Itih2*	9.28	9.09	9.13	9.24
ENSMUSG00000037257	*2310007F21Ri*	3.76	3.65	4.13	3.77
ENSMUSG00000037260	*Hgsnat*	4.92	4.97	4.95	4.98
ENSMUSG00000037262	*Kin*	3.22	2.92	3.06	2.44
ENSMUSG00000037266	*D4Wsu53e*	6.14	5.5	6.33	5.57
ENSMUSG00000037270	*NA*	3.27	2.77	2.98	2.2
ENSMUSG00000037275	*Gemin5*	1.64	2.29	1.66	1.59
ENSMUSG00000037278	*Tmem97*	5.56	4.69	5.14	4.92
ENSMUSG00000037286	*Stag1*	3.23	2.59	2.93	2.45
ENSMUSG00000037287	*Tbcel*	4.19	3.93	4.16	3.95
ENSMUSG00000037291	*NA*	1.54	0.79	1.23	0.4
ENSMUSG00000037295	*Ldlrap1*	3.77	4.07	4.05	3.82
ENSMUSG00000037296	*Lsm1*	3.74	3.01	3.57	3.51
ENSMUSG00000037300	*Ttc13*	4.17	3.92	4.03	3.65
ENSMUSG00000037316	*Bag4*	4.09	3.5	3.93	3.46
ENSMUSG00000037321	*Tap1*	3.16	2.77	3.06	2.97

ENSMUSG00000037325	*Bbs7*	1.2	0.1	1.27	0.18
ENSMUSG00000037326	*Solh*	2.43	3.28	2.91	2.82
ENSMUSG00000037331	*NA*	4.93	5.23	5.04	5.01
ENSMUSG00000037339	*2410018C17Ri*	1.39	1.63	1.6	1.49
ENSMUSG00000037343	*Taf2*	2.72	2.41	2.51	2.32
ENSMUSG00000037344	*Slc12a9*	1.13	1.94	1.75	1.78
ENSMUSG00000037348	*Paqr7*	2.7	3.33	4.15	3.64
ENSMUSG00000037349	*Nudt22*	2.36	3.35	3.51	3.55
ENSMUSG00000037351	*Actr1b*	4.86	5.35	5.05	4.88
ENSMUSG00000037353	*Letmd1*	3.89	4.27	4.4	4.24
ENSMUSG00000037355	*4933407H18Ri*	1.08	-0.14	0.87	0.2
ENSMUSG00000037361	*0610009D07Ri*	4.78	4.49	4.71	4.52
ENSMUSG00000037364	*Ars2*	3.99	4.42	4.07	3.82
ENSMUSG00000037366	*Pafah2*	5.86	5.93	6.2	5.49
ENSMUSG00000037369	*Utx*	2.6	2.02	2.63	2.2
ENSMUSG00000037370	*Enpp1*	3.37	2.74	3.2	2.78
ENSMUSG00000037373	*Ctbp1*	4.81	4.99	4.86	4.46
ENSMUSG00000037376	*Trmt6*	1.75	2.18	1.46	1.82
ENSMUSG00000037395	*Rcor3*	2	1.4	1.58	0.85
ENSMUSG00000037400	*Atp11b*	4.13	3.26	3.99	3.28
ENSMUSG00000037405	*H1f0*	2.22	2.65	2.37	2.46
ENSMUSG00000037406	*Htra4*	1.67	1.72	1.09	-0.24
ENSMUSG00000037408	*Cnnm4*	1.08	1.61	1.71	1.54
ENSMUSG00000037410	*Tbc1d2b*	3.45	3.66	3.35	3.7
ENSMUSG00000037415	*Ranbp10*	4.63	4.75	4.6	4.33
ENSMUSG00000037416	*Dmxl1*	2.27	1.12	1.92	1.31
ENSMUSG00000037426	*Depdc5*	1.45	1.39	1.6	1.65
ENSMUSG00000037434	*Slc30a1*	3.58	3.24	3.68	3.15
ENSMUSG00000037440	*Vnn1*	5.39	4.18	4.55	4.18
ENSMUSG00000037443	*Ccdc21*	2.5	2.67	3.86	2.58
ENSMUSG00000037455	*NA*	1.14	0.85	1.05	1

ENSMUSG00000037458	*Azin1*	5.23	3.62	5.05	4.56
ENSMUSG00000037461	*Ints7*	2.45	3.01	2.58	2.55
ENSMUSG00000037465	*Klf10*	4.67	3.72	3.99	3.79
ENSMUSG00000037470	*Ugcgl1*	4.29	4.5	4.15	4.03
ENSMUSG00000037475	*Thoc2*	3.29	1.75	2.68	1.9
ENSMUSG00000037486	*Asxl2*	2.28	1.5	1.66	1.3
ENSMUSG00000037487	*mKIAA0896*	3.96	3.62	4.14	3.71
ENSMUSG00000037493	*Cib2*	1.95	1.98	1.79	1.26
ENSMUSG00000037499	*Nenf*	2.48	3.11	2.87	2.66
ENSMUSG00000037503	*BC043098*	4.35	4.37	4.21	4
ENSMUSG00000037513	*Samd4b*	3.34	3.74	3.46	3.51
ENSMUSG00000037514	*Pank2*	3.65	2.79	3.21	3.13
ENSMUSG00000037519	*NA*	3.71	3.17	3.4	3.06
ENSMUSG00000037523	*D430028G21R*	5.61	6.42	5.81	5.81
ENSMUSG00000037525	*Bcdin3d*	1.18	1.94	1.4	1.01
ENSMUSG00000037526	*D14Ertd436e*	3.33	2.9	3.44	3.3
ENSMUSG00000037531	*Mrpl47*	4.12	3.48	4.16	3.51
ENSMUSG00000037533	*Rapgef6*	2.07	1.49	2.09	1.58
ENSMUSG00000037536	*Fbxo34*	2.49	2.13	2.58	2.56
ENSMUSG00000037541	*Shank2*	1.51	1.66	0.69	0.76
ENSMUSG00000037542	*Aldh8a1*	7.91	7.71	7.92	7.61
ENSMUSG00000037548	*H2-DMb2*	-1.34	-1.64	1	-2.22
ENSMUSG00000037552	*Plekhg2*	0.9	1.49	1.31	0.99
ENSMUSG00000037553	*Zdhhc18*	3	3.59	3.52	3.32
ENSMUSG00000037563	*Rps16*	2.15	2.73	2.99	3.18
ENSMUSG00000037573	*Tob1*	6.22	6.03	5.97	5.85
ENSMUSG00000037580	*Gch1*	6.2	5.98	6.32	6.04
ENSMUSG00000037581	*Rps6kc1*	0.93	1.48	1.05	0.99
ENSMUSG00000037583	*Nr0b2*	4.3	6.16	3.91	4.32
ENSMUSG00000037600	*1810019J16Ri*	0.79	1.97	1.6	1.24
ENSMUSG00000037601	*Nme1*	5.94	5.94	5.89	5.65

ENSMUSG00000037608	*Bclaf1*	4.19	2.89	3.37	2.72
ENSMUSG00000037621	*Atoh8*	2.94	5.09	3.86	3.78
ENSMUSG00000037622	*Wdtc1*	5.55	5.99	6.33	5.71
ENSMUSG00000037640	*Zfp60*	1.76	1.26	1.44	0.74
ENSMUSG00000037643	*Prkci*	3.08	2.26	2.68	2.25
ENSMUSG00000037646	*NA*	1.81	1.45	1.74	1.22
ENSMUSG00000037649	*H2-DMa*	2.67	2.05	2.35	1.37
ENSMUSG00000037652	*Phc3*	1.12	0.75	1.24	1.13
ENSMUSG00000037656	*Slc20a2*	5.22	5.41	5.43	5.02
ENSMUSG00000037664	*Cdkn1c*	2.4	1.5	2.41	1.65
ENSMUSG00000037669	*1110057K04Ri*	4.77	4.4	4.72	4.48
ENSMUSG00000037674	*Rfxdc2*	2.01	1.1	1.37	1
ENSMUSG00000037679	*2610204M08R*	3.63	4.42	3.86	3.75
ENSMUSG00000037686	*A530050D06R*	5.41	6.13	6.09	5.82
ENSMUSG00000037692	*Ahdc1*	1.74	2.72	2.2	1.94
ENSMUSG00000037697	*AK036369*	2.01	0.94	2.21	1.83
ENSMUSG00000037703	*Prosapip1*	3.33	3.78	3.75	3.52
ENSMUSG00000037706	*Cd81*	7.64	7.57	7.63	7.4
ENSMUSG00000037709	*D430015B01R*	3.81	3.37	4.57	4.13
ENSMUSG00000037710	*Cisd1*	6.79	6.75	7.07	6.82
ENSMUSG00000037712	*Plekhc1*	5.71	5.26	5.42	5.34
ENSMUSG00000037720	*Tmem33*	4.92	4.12	4.4	4.08
ENSMUSG00000037722	*Gnpnat1*	4.3	3.32	4.06	3.41
ENSMUSG00000037730	*Mynn*	2.18	1.24	1.74	1.54
ENSMUSG00000037740	*Mrps26*	3.38	3.89	4.04	3.9
ENSMUSG00000037742	*Eef1a1*	7.95	7.83	8.1	8.05
ENSMUSG00000037750	*BC017647*	3.39	3.29	3.29	3.21
ENSMUSG00000037752	*Xkr8*	1.42	1.55	1.74	0.98
ENSMUSG00000037761	*Actr5*	1.41	2.25	1.56	1.63
ENSMUSG00000037762	*Slc16a9*	1.13	0.89	0.13	-0.28
ENSMUSG00000037773	*A930025D01R*	2.58	3.13	2.92	2.64

ENSMUSG00000037780	*Mbl1*	6.93	7.15	6.82	6.7
ENSMUSG00000037787	*2810002N01Ri*	4.37	4.65	4.25	4.33
ENSMUSG00000037788	*AW146242*	1.09	0.62	0.6	0.44
ENSMUSG00000037791	*Phf12*	2.97	3.17	3.25	2.93
ENSMUSG00000037795	*B3bp*	3.29	2.4	3.13	2.47
ENSMUSG00000037797	*Adh4*	5.64	5.9	5.43	5.46
ENSMUSG00000037798	*Mat1a*	10.58	10.71	10.83	10.42
ENSMUSG00000037805	*Rpl10a*	0.54	1.43	1.17	1
ENSMUSG00000037808	*2810485I05Rik*	2.1	0.75	1.74	1.17
ENSMUSG00000037814	*Larp2*	5.66	5.39	5.3	5.06
ENSMUSG00000037815	*Ctnna1*	5.35	5.32	5.36	5.06
ENSMUSG00000037818	*3110057O12Ri*	3.3	2.38	3.23	2.6
ENSMUSG00000037820	*Tgm2*	5.44	6.07	5.1	5.25
ENSMUSG00000037822	*1110003E01Ril*	5.2	5.43	5.23	4.8
ENSMUSG00000037824	*Tspan14*	4.31	4.59	4.28	4.1
ENSMUSG00000037826	*Ppm1k*	5.18	4.24	5.01	4.38
ENSMUSG00000037845	*D630004A14R*	1.48	0.99	1.24	1.09
ENSMUSG00000037847	*BC016495*	4.11	2.97	4.65	4.04
ENSMUSG00000037851	*Iars*	3.45	3.55	3.07	3.07
ENSMUSG00000037857	*Nufip2*	3.33	2.2	3.06	2.79
ENSMUSG00000037872	*Darc*	1.85	2	1.75	1.92
ENSMUSG00000037876	*NA*	3.24	2.61	2.81	2.51
ENSMUSG00000037885	*Stk35*	2.44	2.3	2.68	2.43
ENSMUSG00000037894	*H2afz*	0.25	1.11	1.76	1.9
ENSMUSG00000037896	*Rcor1*	2.7	2.74	2.6	2.48
ENSMUSG00000037902	*Sirpa*	2.46	2.42	2.87	1.96
ENSMUSG00000037905	*Bri3bp*	3.46	4.26	3.88	3.87
ENSMUSG00000037916	*Ndufv1*	6.74	6.97	7.01	6.67
ENSMUSG00000037926	*Ssh2*	1.72	2.04	2	1.57
ENSMUSG00000037933	*Bicd2*	2.12	2.19	1.79	1.55
ENSMUSG00000037935	*Smarce1*	2.53	1.68	1.99	1.93

ENSMUSG00000037936	*Scarb1*	7.12	7.56	7.6	7.4
ENSMUSG00000037938	*Chchd5*	3.36	3.94	4.22	4.08
ENSMUSG00000037942	*Crp*	8.27	8.53	8.13	8.07
ENSMUSG00000037949	*Tmem16k*	2.44	2.9	2.45	2.49
ENSMUSG00000037957	*Wdr20a*	2.4	2.29	2.3	2.32
ENSMUSG00000037958	*Ccdc55*	3.18	2.66	2.67	2.36
ENSMUSG00000037960	*1110007C09Ri*	2.93	3.18	3.46	3.17
ENSMUSG00000037965	*Zc3h7a*	3.01	2.66	2.89	2.14
ENSMUSG00000037966	*Ninj1*	6.59	7.57	6.51	6.58
ENSMUSG00000037971	*1110032A03Ri*	3.97	3.99	4.09	3.83
ENSMUSG00000037982	*NA*	1.95	2	1.49	1.41
ENSMUSG00000037992	*Rara*	2.33	3.68	3.23	2.81
ENSMUSG00000037993	*Dhx38*	2.68	3.61	2.82	2.73
ENSMUSG00000037997	*Parp11*	1.22	0.91	0.96	0.7
ENSMUSG00000037999	*NA*	2.09	1.34	1.56	0.76
ENSMUSG00000038000	*Acd*	3.16	3.92	4.05	3.72
ENSMUSG00000038002	*NA*	1.43	1.57	1.76	1.53
ENSMUSG00000038005	*NA*	2.81	2.23	2.49	2.17
ENSMUSG00000038007	*Asah3l*	3.25	2.85	2.93	3.01
ENSMUSG00000038009	*2810451A06Ri*	6.34	6.43	6.34	6.28
ENSMUSG00000038013	*Wipf2*	2.24	2.11	2.32	1.95
ENSMUSG00000038014	*BC010304*	5.95	5.82	5.92	5.58
ENSMUSG00000038023	*Atp6v0a2*	3.75	3.65	3.84	3.47
ENSMUSG00000038024	*Dennd4c*	2.26	1.87	2	1.89
ENSMUSG00000038025	*Phf2*	2.67	3.33	3.03	3.04
ENSMUSG00000038028	*9630033F20Ri*	2.09	2.36	1.82	2.08
ENSMUSG00000038034	*Igsf8*	1.39	2.28	1.86	2.17
ENSMUSG00000038039	*Gcc2*	3.24	2.37	2.53	2.19
ENSMUSG00000038046	*Rnmtl1*	2.67	2.51	2.73	2.37
ENSMUSG00000038055	*Dexi*	3.12	3.67	3.84	3.68
ENSMUSG00000038056	*Mll3*	2.08	1.58	2	1.61

ENSMUSG00000038058	*Nod1*	1.58	2.22	2.09	1.6
ENSMUSG00000038068	*Rnf144b*	4.33	3.94	3.37	3.37
ENSMUSG00000038069	*Cdkn2aip*	2.81	2.45	2.94	2.49
ENSMUSG00000038072	*Galnt11*	3.62	3.44	3.46	3.13
ENSMUSG00000038074	*Fkbp14*	1.22	0.67	0.52	0.34
ENSMUSG00000038079	*Als2cr4*	1.34	0.43	0.91	0.11
ENSMUSG00000038080	*Aof1*	3.7	2.88	3.71	3.08
ENSMUSG00000038084	*Opa1*	5.27	4.76	5.08	4.69
ENSMUSG00000038095	*Sbno1*	3.69	3.22	3.41	3.05
ENSMUSG00000038102	*D030016E14R*	3.13	3.21	3.51	3.2
ENSMUSG00000038116	*Phf20*	2.08	1.57	1.78	1.28
ENSMUSG00000038121	*4933403F05Ri*	4.49	3.2	4.09	3.48
ENSMUSG00000038127	*Ccdc50*	3.41	2.35	2.82	2.09
ENSMUSG00000038145	*Snrk*	3.78	4.11	4	4.07
ENSMUSG00000038147	*Cd84*	1.05	1.26	1.51	0.76
ENSMUSG00000038150	*Ormdl3*	5.52	5.74	5.54	5.26
ENSMUSG00000038160	*Atg5*	5.33	4.58	5.25	4.66
ENSMUSG00000038167	*Plekhg6*	1.75	2.38	2.89	2.6
ENSMUSG00000038170	*Pde4dip*	3.7	3.77	3.8	3.71
ENSMUSG00000038171	*Rbm12*	1.06	1.17	0.9	0.7
ENSMUSG00000038172	*1810054D07R*	2.74	1.96	2.31	1.87
ENSMUSG00000038174	*BC049806*	3.17	1.8	2.46	1.82
ENSMUSG00000038175	*Mylip*	3.26	3.03	3.25	3.04
ENSMUSG00000038178	*Slc43a2*	1.69	2.25	1.13	1.55
ENSMUSG00000038181	*NA*	2.13	3.05	2.63	2.68
ENSMUSG00000038188	*Scarf1*	1.46	1.87	1.5	1.32
ENSMUSG00000038193	*Hand2*	1.93	1.78	2.02	1.8
ENSMUSG00000038195	*Rilp*	4.19	4.55	4.6	4.38
ENSMUSG00000038206	*Fbxo8*	5.51	4.73	5.36	4.78
ENSMUSG00000038212	*Hiatl1*	4.17	3.31	3.85	3.54
ENSMUSG00000038213	*Tapbpl*	3.46	3.74	3.38	3.2

ENSMUSG00000038215	*BC088983*	2.15	1.44	1.94	1.55
ENSMUSG00000038217	*2010305C02Ri*	5.63	5.42	5.23	4.54
ENSMUSG00000038224	*Serpinf2*	8.95	9.53	9	8.95
ENSMUSG00000038225	*Ccdc111*	1.23	0.44	1.21	0.47
ENSMUSG00000038233	*C730027P07R*	2.29	1.91	1.68	0.97
ENSMUSG00000038235	*F11r*	5.08	5.71	5.48	5.32
ENSMUSG00000038240	*Pdss2*	3.08	3.16	3.07	2.85
ENSMUSG00000038244	*mKIAA0750*	2.05	2.34	1.89	1.65
ENSMUSG00000038250	*Usp38*	4.24	3.24	3.38	3.2
ENSMUSG00000038267	*3110004L20Ri*	4.53	4.89	4.7	4.56
ENSMUSG00000038268	*Ovca2*	3.55	3.72	3.41	3.28
ENSMUSG00000038274	*Fau*	2.22	3.64	3.8	3.24
ENSMUSG00000038279	*Nol1*	3.3	4.28	3.63	3.72
ENSMUSG00000038280	*gl*	2.7	2.05	2.84	2.08
ENSMUSG00000038286	*Bphl*	7.63	6.93	7.53	7.03
ENSMUSG00000038290	*Smg6*	2.79	2.86	3.07	2.65
ENSMUSG00000038291	*Snx25*	2.56	2.67	2.7	2.37
ENSMUSG00000038298	*Pdzk1*	5.23	5.53	5.12	5.09
ENSMUSG00000038299	*Wdr36*	4	3.46	3.98	3.4
ENSMUSG00000038301	*Snx10*	4.71	3.05	3.83	3.49
ENSMUSG00000038302	*Lace1*	3.22	2.39	3.35	2.96
ENSMUSG00000038312	*Edem2*	4.83	5.32	4.87	4.87
ENSMUSG00000038323	*NA*	3.38	2.49	2.68	2.28
ENSMUSG00000038324	*Trpc4ap*	5.76	6.13	5.81	5.61
ENSMUSG00000038332	*Sesn1*	2.61	2.5	2.68	2.25
ENSMUSG00000038335	*Tsr1*	5.08	5.06	4.84	4.62
ENSMUSG00000038342	*Mlxip*	1.56	1.72	1.22	1.22
ENSMUSG00000038344	*4932441K18Ri*	2.1	1.08	1.61	1.04
ENSMUSG00000038346	*Zfp384*	2.23	2.48	2.58	2.2
ENSMUSG00000038351	*Sgsm2*	1.76	1.91	1.31	1.28
ENSMUSG00000038365	*Fbxo25*	2.36	2.18	2.08	1.82

ENSMUSG00000038366	*Lasp1*	5.14	5.31	4.95	4.7
ENSMUSG00000038368	*BC057079*	1.08	1.1	0.94	0.76
ENSMUSG00000038369	*Ncoa6*	2.69	2.57	2.87	2.54
ENSMUSG00000038370	*Pcp4l1*	6.27	6.07	5.97	5.85
ENSMUSG00000038371	*NA*	3.29	2.51	3.07	2.49
ENSMUSG00000038374	*Rbm8a*	4.56	4.47	4.19	4.29
ENSMUSG00000038375	*Trp53inp2*	7.16	7.55	7.03	6.87
ENSMUSG00000038383	*Pigu*	3.79	3.62	3.27	3.33
ENSMUSG00000038384	*NA*	2.43	3.64	2.96	2.81
ENSMUSG00000038387	*Rras*	4.49	5.14	4.4	4.49
ENSMUSG00000038388	*Mpp6*	5.84	5.17	5.2	4.83
ENSMUSG00000038393	*Txnip*	5.89	5.46	5.26	5.5
ENSMUSG00000038398	*Upf3a*	2.6	3.25	2.99	2.53
ENSMUSG00000038403	*NA*	5.25	5.29	5.02	4.15
ENSMUSG00000038406	*Scaf1*	3.27	4.16	3.64	3.51
ENSMUSG00000038412	*Higd1a*	3.99	3.46	4.61	5.22
ENSMUSG00000038415	*Foxq1*	2.69	3.52	2.23	2.52
ENSMUSG00000038416	*Cdc16*	3.86	3.65	3.83	3.2
ENSMUSG00000038417	*Fig4*	2.86	2.7	2.75	2.24
ENSMUSG00000038418	*Egr1*	1	0.79	2.8	1.9
ENSMUSG00000038422	*Hdhd3*	3.64	4.37	3.97	4.28
ENSMUSG00000038425	*Poli*	1.53	1.82	1.24	1.37
ENSMUSG00000038429	*Usp5*	4.44	5.14	4.65	4.54
ENSMUSG00000038437	*Mllt6*	1.77	2.3	2.03	1.99
ENSMUSG00000038446	*NA*	3.82	3.23	3.88	3.38
ENSMUSG00000038451	*Spsb2*	2.21	2.9	2.88	2.67
ENSMUSG00000038459	*2210412D01Ri*	5.87	5.82	5.61	5.35
ENSMUSG00000038462	*Uqcrfs1*	7.38	7.59	7.64	7.3
ENSMUSG00000038467	*Chmp4b*	5.25	6.01	5.48	5.18
ENSMUSG00000038481	*mKIAA1028*	1.65	0.49	1.38	0.73
ENSMUSG00000038482	*Tfdp1*	2.32	2.39	2.47	1.91

ENSMUSG00000038485	*Socs7*	2.08	1.89	1.71	1.77
ENSMUSG00000038489	*NA*	1.08	2.49	1.88	2.08
ENSMUSG00000038495	*Otud7b*	2.69	2.52	2.59	2.6
ENSMUSG00000038497	*Tmco3*	1.78	1.69	1.63	1.15
ENSMUSG00000038500	*Prr3*	0.82	1.45	1.79	1.11
ENSMUSG00000038502	*Ptov1*	4.3	5.25	4.82	4.69
ENSMUSG00000038503	*Mesdc2*	4.77	5.37	4.64	4.58
ENSMUSG00000038506	*Dcun1d2*	2.83	2.46	2.99	3.04
ENSMUSG00000038507	*Parp12*	4.02	3.3	3.82	3.78
ENSMUSG00000038508	*Gdf15*	0.57	1.58	1.11	0.6
ENSMUSG00000038510	*Bxdc1*	2.09	1.14	1.73	1.67
ENSMUSG00000038515	*Grtp1*	3.79	3.82	3.91	3.68
ENSMUSG00000038517	*Tbkbp1*	1.25	2.21	2.39	1.8
ENSMUSG00000038518	*Jarid2*	1.6	1.42	1.73	1.45
ENSMUSG00000038520	*Tbc1d17*	3.91	4.42	4.49	4.3
ENSMUSG00000038521	*C1s*	6.79	6.67	6.51	6.58
ENSMUSG00000038522	*AI317395*	5.08	4.95	5.14	4.81
ENSMUSG00000038525	*Armc10*	1.27	0.8	1.44	0.59
ENSMUSG00000038526	*Car14*	5.72	4.86	5.85	4.83
ENSMUSG00000038527	*C1rl*	6.05	6.37	6.28	6.21
ENSMUSG00000038530	*Rgs4*	1.08	1.02	1.54	1.6
ENSMUSG00000038533	*Cbfa2t2*	1.74	1.51	1.86	1.56
ENSMUSG00000038535	*Suhw4*	2.31	1.39	2.1	1.55
ENSMUSG00000038538	*D130059P03R*	1.29	1.38	1.53	1.44
ENSMUSG00000038539	*Atf5*	7.53	7.91	7.65	7.5
ENSMUSG00000038542	*Pcid2*	3.07	3.29	2.85	2.78
ENSMUSG00000038544	*1110054O05Ri*	1.46	0.83	0.83	0.49
ENSMUSG00000038546	*Ranbp9*	4.08	3.99	3.76	3.65
ENSMUSG00000038550	*Gm129*	1.72	1.07	2.97	2.95
ENSMUSG00000038552	*Fndc4*	4.52	4.61	4.51	4.37
ENSMUSG00000038563	*Eftud1*	2.17	2.36	2.31	2.14

ENSMUSG00000038564	*Ift172*	1.64	2.09	1.77	1.73
ENSMUSG00000038569	*Rad9b*	3.65	2.2	3.55	2.68
ENSMUSG00000038576	*Susd4*	2.02	2.55	1	2.53
ENSMUSG00000038578	*NA*	1.63	1.66	1.11	1.18
ENSMUSG00000038582	*Pptc7*	4.62	3.64	4.44	3.93
ENSMUSG00000038591	*Colec10*	5.09	4.09	4.2	3.89
ENSMUSG00000038594	*NA*	3.3	2.82	3.43	3.34
ENSMUSG00000038604	*2310066E14Ri*	1.9	2.36	1.89	1.89
ENSMUSG00000038607	*Gng10*	4.18	2.52	3.09	2.71
ENSMUSG00000038611	*AA673488*	2.54	2.89	2.6	2.68
ENSMUSG00000038612	*Mcl1*	5.64	5.17	6.02	5.42
ENSMUSG00000038615	*Nfe2l1*	5.43	5.55	5.35	5.07
ENSMUSG00000038618	*Rassf7*	3.82	4.49	4.08	3.74
ENSMUSG00000038619	*Ensa*	3.93	3.91	3.97	3.68
ENSMUSG00000038622	*Med30*	2.67	2.21	2.44	1.8
ENSMUSG00000038628	*Polr3k*	3.28	2.63	3	2.57
ENSMUSG00000038633	*Degs1*	6.25	5.34	5.79	5.54
ENSMUSG00000038637	*Lrrc56*	0.63	0.99	1.4	0.9
ENSMUSG00000038641	*Akr1d1*	7.51	6.54	7.07	6.43
ENSMUSG00000038642	*Ctss*	5.24	3.82	4.76	4.27
ENSMUSG00000038646	*2610204K14Ri*	1.89	0.98	1.77	1.3
ENSMUSG00000038648	*Creb3l2*	2.24	2.97	2.33	2.66
ENSMUSG00000038650	*Rnh1*	5.77	5.86	5.86	5.75
ENSMUSG00000038656	*Cyp3a16*	8.63	4.8	6.45	4.01
ENSMUSG00000038658	*C030046E11Ri*	2.99	2.37	2.98	2.63
ENSMUSG00000038664	*NA*	2.03	2.08	2.17	1.57
ENSMUSG00000038671	*Arfrp1*	3.79	3.81	3.47	3.5
ENSMUSG00000038683	*Pak1ip1*	4.55	4.67	4.71	4.53
ENSMUSG00000038685	*Rtel1*	1.77	1.89	1.79	1.56
ENSMUSG00000038690	*AK164124*	8.27	6.68	8.27	8.4
ENSMUSG00000038695	*Josd2*	2.64	3.96	3.54	3.18

ENSMUSG00000038696	*Mapkap1*	4.31	4.08	4.33	3.93
ENSMUSG00000038697	*Taf5l*	2.96	2.84	2.69	2.43
ENSMUSG00000038704	*0610012D14Ri*	6.4	7.02	6.87	6.7
ENSMUSG00000038705	*Gmeb2*	2.49	2.55	2.55	2.34
ENSMUSG00000038708	*Golga4*	4.12	4.01	3.79	3.6
ENSMUSG00000038712	*4930504E06Ri*	5.17	5.64	5.59	5.35
ENSMUSG00000038722	*Bud31*	5.76	5.49	5.89	5.78
ENSMUSG00000038733	*Wdr26*	5.14	4.66	4.67	4.5
ENSMUSG00000038736	*Nudcd1*	2.74	1.82	2.13	2.13
ENSMUSG00000038742	*Angptl6*	3.23	3.9	3.59	3.76
ENSMUSG00000038745	*Nlrp6*	4.89	5.42	4.97	4.93
ENSMUSG00000038754	*Elovl3*	2.34	1.11	0.52	-0.06
ENSMUSG00000038759	*NA*	1.54	1.48	1.67	1.29
ENSMUSG00000038762	*Abcf1*	4.6	5.34	4.97	4.74
ENSMUSG00000038764	*Ptpn3*	3.09	3.17	3.19	2.95
ENSMUSG00000038766	*Gabpb2*	2.55	2.1	2.25	1.96
ENSMUSG00000038768	*9130409I23Rik*	3.48	1.77	3.14	2.19
ENSMUSG00000038773	*Jmjd1b*	2.24	2.36	2.32	1.95
ENSMUSG00000038774	*NA*	2.77	2.16	2.57	2.2
ENSMUSG00000038776	*Ephx1*	7.6	8.31	7.91	7.98
ENSMUSG00000038780	*Smurf1*	2.23	2.59	2.69	2.52
ENSMUSG00000038781	*Stap2*	4.5	4.89	4.9	4.65
ENSMUSG00000038784	*Cnot4*	2.55	2.09	2.56	2.41
ENSMUSG00000038803	*2310016E02Ri*	4.75	5.02	5.03	5.19
ENSMUSG00000038806	*BC031781*	2.69	2.25	2.55	2.53
ENSMUSG00000038811	*Gngt2*	1.45	1.29	1.36	1.13
ENSMUSG00000038812	*0610038D11Ri*	1.76	2.45	2.01	1.91
ENSMUSG00000038827	*BC026590*	1.27	1.23	1.12	1.1
ENSMUSG00000038828	*1110039B18Ri*	4.87	5.55	4.9	4.78
ENSMUSG00000038831	*Ralgps1*	1.34	-0.13	0.45	0.21
ENSMUSG00000038838	*Vars2*	2.77	3.3	2.83	2.71

ENSMUSG00000038844	*Kif16b*	2.16	1.44	1.81	1.39
ENSMUSG00000038845	*Phb*	2.57	2	2.25	1.74
ENSMUSG00000038848	*Ythdf1*	4.49	4.08	4.24	4.12
ENSMUSG00000038859	*Baiap2l1*	4.88	4.26	4.89	4.38
ENSMUSG00000038861	*Pi4kb*	3.98	4.24	3.99	4
ENSMUSG00000038866	*NA*	3.47	3.15	3.3	2.9
ENSMUSG00000038871	*Bpgm*	3.15	3.26	3.51	3.65
ENSMUSG00000038872	*Zfhx3*	0.79	0.48	1.43	0.96
ENSMUSG00000038876	*Rnf146*	4.31	3.93	3.9	4.01
ENSMUSG00000038880	*Mrps34*	4.91	5.23	5.3	5.4
ENSMUSG00000038884	*A230050P20Ri*	3.39	3.72	3.46	3.5
ENSMUSG00000038886	*Man2a2*	2.9	3.13	2.39	2.75
ENSMUSG00000038888	*Atpbd3*	1.43	1.91	1.21	1.41
ENSMUSG00000038894	*Irs2*	2.35	2.64	2.3	1.98
ENSMUSG00000038895	*Zfp653*	1.21	1.48	0.97	1.48
ENSMUSG00000038902	*Pogz*	1.79	2.03	2.2	1.99
ENSMUSG00000038903	*Ccdc68*	1.07	1.25	1.28	1.5
ENSMUSG00000038909	*Myst2*	3.95	3.82	3.67	3.6
ENSMUSG00000038910	*Plcl2*	2.82	2.7	3.08	2.55
ENSMUSG00000038914	*Dido1*	1.8	1.67	1.97	1.88
ENSMUSG00000038949	*9630058J23Ri*	2.49	2.22	2.77	2.07
ENSMUSG00000038954	*Supt3h*	2.5	2.31	1.82	1.41
ENSMUSG00000038957	*Edc3*	2.92	3.17	2.56	2.65
ENSMUSG00000038965	*Ube2l3*	5.77	5.61	5.51	5.22
ENSMUSG00000038967	*Pdk2*	6.79	6.94	7.55	7.14
ENSMUSG00000038970	*Lmtk2*	2.41	2.37	2.66	2.3
ENSMUSG00000038975	*Rabggtb*	5.07	4.75	5.14	5.01
ENSMUSG00000038976	*Ppp1r9b*	1.64	2.11	2.1	1.59
ENSMUSG00000038982	*Muted*	4.3	4.18	4.11	3.82
ENSMUSG00000038990	*Cables2*	3.55	3.89	3.54	3.37
ENSMUSG00000038991	*Txndc5*	6.07	6.55	5.55	5.75

ENSMUSG00000039000	*mKIAA0010*	4.48	3.9	4.17	3.73
ENSMUSG00000039001	*Rps21*	5.74	4.34	5.85	6.65
ENSMUSG00000039004	*Bmp6*	2.07	2.08	1.67	1.5
ENSMUSG00000039007	*HLS2*	5.6	5.29	5.3	5.04
ENSMUSG00000039016	*Timm8b*	5.5	5.4	5.74	5.59
ENSMUSG00000039018	*Mtg1*	3.3	3.32	3.39	3.36
ENSMUSG00000039031	*Arhgap18*	2.35	1.59	2.24	1.59
ENSMUSG00000039033	*Tasp1*	1.16	1.72	1.47	1.12
ENSMUSG00000039041	*Adrm1*	2.77	3.59	3.41	3.11
ENSMUSG00000039043	*2610034B18Ri*	2.21	2.28	2.48	1.92
ENSMUSG00000039046	*Usp6nl*	2.71	1.89	2.29	2.14
ENSMUSG00000039047	*Pigk*	4.18	3.86	3.98	3.66
ENSMUSG00000039048	*Foxred1*	3.78	3.84	3.98	3.72
ENSMUSG00000039050	*Osbpl2*	4.2	4.13	4.43	4.15
ENSMUSG00000039055	*Eme1*	1.77	1.17	1.48	1.28
ENSMUSG00000039062	*Anpep*	5.88	6.37	6.16	6.16
ENSMUSG00000039063	*Echdc3*	6.1	6.15	6.18	5.74
ENSMUSG00000039065	*A930016P21Ri*	1.92	2.93	2.55	2.24
ENSMUSG00000039067	*Psmd7*	5.95	6.29	5.87	5.6
ENSMUSG00000039068	*Zzz3*	2	1.84	1.93	1.72
ENSMUSG00000039069	*Gtpbp5*	3.4	3.98	3.62	3.59
ENSMUSG00000039087	*Rreb1*	2.79	3.01	2.83	2.86
ENSMUSG00000039089	*L3mbtl3*	0.91	0.88	1.62	1.19
ENSMUSG00000039096	*Rsad1*	0.96	0.67	1.2	0.87
ENSMUSG00000039100	*6-Mar*	6	5.36	5.54	5.03
ENSMUSG00000039105	*Atp6v1g1*	4.19	3.33	3.77	2.76
ENSMUSG00000039108	*Lsm14b*	3.7	3.71	3.61	3.37
ENSMUSG00000039114	*Nrn1*	8.19	7.74	8.1	7.92
ENSMUSG00000039115	*Itga9*	2.7	2.94	2.1	1.96
ENSMUSG00000039117	*Taf4a*	2.35	2.37	2.49	2.14
ENSMUSG00000039128	*Cdc123*	4.87	5.03	4.8	4.72

ENSMUSG00000039130	*Zc3hc1*	2.71	2.91	2.79	2.95
ENSMUSG00000039145	*Camk1d*	4.32	3.9	3.67	3.2
ENSMUSG00000039148	*Sart1*	2.76	3.12	2.92	2.6
ENSMUSG00000039156	*Stim2*	2.66	2.41	2.49	2.5
ENSMUSG00000039157	*C230093N12R*	1.93	2.58	2.82	2.65
ENSMUSG00000039159	*Ube2h*	3.25	2.13	3.01	2.63
ENSMUSG00000039163	*2010110K16Ri*	4.86	4.39	4.98	4.4
ENSMUSG00000039166	*Akap7*	1.76	1.18	1.54	0.75
ENSMUSG00000039167	*Eltd1*	3.16	2.31	2.28	2.15
ENSMUSG00000039168	*Dap*	7.79	7.99	7.59	7.53
ENSMUSG00000039176	*Polg*	3.96	4.22	4.08	3.75
ENSMUSG00000039178	*Tbc1d19*	0.82	0.69	1.59	1.05
ENSMUSG00000039182	*AW209491*	3.75	3.13	3.48	3.43
ENSMUSG00000039183	*Nubp2*	4.57	5.22	4.77	4.83
ENSMUSG00000039187	*Fanci*	1.69	0.65	1.37	0.75
ENSMUSG00000039191	*Rbpj*	1.03	0.92	0.62	0.06
ENSMUSG00000039195	*1110008P14Ri*	4.69	5.71	5.02	5.1
ENSMUSG00000039196	*Orm1*	9.14	8.55	9.02	8.95
ENSMUSG00000039197	*Adk*	9.06	8.57	9.04	8.61
ENSMUSG00000039199	*Zdhhc1*	0.15	1.18	1.11	0.72
ENSMUSG00000039201	*Tbc1d25*	1.13	1.62	1.11	1.68
ENSMUSG00000039202	*Abhd2*	6.16	6.4	5.45	5.58
ENSMUSG00000039205	*Ciz1*	2.86	3.27	3.14	2.8
ENSMUSG00000039206	*Daglb*	2.38	2.95	2.83	2.62
ENSMUSG00000039210	*Gpatch2*	2.23	2.41	2.13	1.64
ENSMUSG00000039217	*Il18*	4.68	3.37	3.91	3.08
ENSMUSG00000039218	*Srrm2*	5	5.31	5.13	4.91
ENSMUSG00000039219	*Arid4b*	2.98	1.38	2.38	1.83
ENSMUSG00000039220	*Ppp1r10*	2.84	2.66	3.72	3.97
ENSMUSG00000039221	*Rpl22l1*	4.79	1.48	3.61	3.04
ENSMUSG00000039230	*Tbcd*	2.96	3.48	3.09	2.9

ENSMUSG00000039231	*Suv39h1*	2.43	2.19	2.07	1.6
ENSMUSG00000039233	*Tbce*	3.24	2.97	2.78	2.55
ENSMUSG00000039234	*Sec24d*	5.25	5.31	4.94	4.66
ENSMUSG00000039236	*Isg20*	0.11	0.44	1.05	1.19
ENSMUSG00000039238	*Zfp750*	1.61	1.74	1.81	2.12
ENSMUSG00000039242	*B3galnt2*	3.27	3.19	3.42	2.82
ENSMUSG00000039244	*E130309D02R*	3.64	3.96	3.72	3.75
ENSMUSG00000039246	*Lyplal1*	5.16	4.22	4.8	4.07
ENSMUSG00000039253	*BC032265*	2.16	2.27	2.69	2.54
ENSMUSG00000039254	*Pomt1*	3.34	3.48	3.19	3.1
ENSMUSG00000039262	*5830434P21Ri*	3.11	3.7	3.31	3.39
ENSMUSG00000039263	*Npepl1*	4.88	5.47	5.07	4.96
ENSMUSG00000039270	*Megf9*	5.4	4.11	4.18	3.39
ENSMUSG00000039275	*Foxk2*	2.36	2.58	2.16	2.79
ENSMUSG00000039282	*Shprh*	1.67	0.88	1.44	0.74
ENSMUSG00000039285	*Azi2*	4.12	3.89	3.82	3.53
ENSMUSG00000039286	*Fndc3b*	2.73	2.43	1.85	1.72
ENSMUSG00000039294	*BC017643*	2.71	2.61	2.43	1.97
ENSMUSG00000039307	*Hexdc*	1.08	1.55	1.85	1.27
ENSMUSG00000039308	*Ndst2*	3.32	3.61	3.21	2.94
ENSMUSG00000039318	*NA*	2.93	2.77	2.55	2.37
ENSMUSG00000039323	*Igfbp2*	7.79	8.63	8.06	8.36
ENSMUSG00000039345	*BC024814*	2.95	3.15	2.49	2.81
ENSMUSG00000039349	*C130074G19R*	6.35	6.42	6.29	6.18
ENSMUSG00000039354	*Smarcal1*	2.65	3.1	2.59	2.76
ENSMUSG00000039356	*Exosc2*	2.94	3.69	2.98	3.18
ENSMUSG00000039357	*Fut11*	1.28	0.78	0.73	0.48
ENSMUSG00000039361	*mKIAA4114*	5.75	4.77	5.35	4.99
ENSMUSG00000039367	*Sec24c*	5.08	5.36	5.06	4.85
ENSMUSG00000039377	*Hlx*	0.63	1.54	1.34	1.74
ENSMUSG00000039382	*Wdr45*	4.7	4.97	4.69	4.81

ENSMUSG00000039395	*Mreg*	4.83	4.68	4.78	4.33
ENSMUSG00000039405	*Prss23*	1.07	0.88	0.85	0.51
ENSMUSG00000039414	*Heatr5b*	1.76	1.55	1.9	1.69
ENSMUSG00000039427	*Alg1*	4.2	4.65	4.25	4.21
ENSMUSG00000039428	*Tmem135*	5.08	4.08	4.38	4.06
ENSMUSG00000039431	*Mtmr7*	1.41	1.23	1.73	1.23
ENSMUSG00000039438	*BC021608*	8.27	9	9	8.86
ENSMUSG00000039449	*Prpf18*	3.85	3.49	3.84	3.29
ENSMUSG00000039450	*Dcxr*	6.95	7.69	7.41	7
ENSMUSG00000039452	*Snx22*	5.57	5.88	5.51	5.33
ENSMUSG00000039456	*mKIAA0136*	2.26	1.68	2.44	2.26
ENSMUSG00000039457	*Ppl*	2.38	2.79	2.66	2.17
ENSMUSG00000039458	*Mtmr12*	1.8	1.94	1.49	1.23
ENSMUSG00000039461	*Tcta*	4.19	3.95	3.95	3.72
ENSMUSG00000039463	*NHE8*	3.81	4.39	3.77	3.69
ENSMUSG00000039473	*Ubn1*	3.36	3.58	3.32	3.25
ENSMUSG00000039474	*Wfs1*	1.65	2.76	2.3	2.06
ENSMUSG00000039477	*Zfp469*	1.12	2.34	1.84	1.95
ENSMUSG00000039480	*Nt5dc1*	3.56	2.54	3.05	2.57
ENSMUSG00000039483	*Asb6*	1.35	1.89	1.3	1.08
ENSMUSG00000039485	*Tspyl4*	2.14	2.24	2.09	1.15
ENSMUSG00000039497	*Dse*	2.18	1.62	1.24	1.39
ENSMUSG00000039501	*Znfx1*	3.09	3.47	3.18	3.28
ENSMUSG00000039509	*Nup133*	2.14	2.47	2.85	2.43
ENSMUSG00000039512	*F830021D11R*	2.29	2.45	2.51	2.03
ENSMUSG00000039515	*Ppp2r4*	4.74	5.35	4.79	4.53
ENSMUSG00000039519	*Cyp7b1*	4.73	4.21	4.16	3.74
ENSMUSG00000039523	*BC046331*	1.84	2.26	2.11	1.96
ENSMUSG00000039529	*Atp8b1*	2.96	3.15	3.24	2.99
ENSMUSG00000039530	*Tusc3*	2.63	2.54	3.24	2.68
ENSMUSG00000039531	*2700019D07R*	1.24	1.07	1.23	0.69

ENSMUSG00000039533	*Mmd2*	3.21	2	3.07	2.33
ENSMUSG00000039536	*Stau1*	5.53	5.25	5.24	5.17
ENSMUSG00000039552	*NA*	1.92	1.47	1.12	0.13
ENSMUSG00000039568	*NA*	3.71	4.49	4.27	4.28
ENSMUSG00000039599	*AA536717*	2.78	2.91	2.87	2.65
ENSMUSG00000039601	*Rcan2*	3.83	2.23	3.33	1.52
ENSMUSG00000039615	*Stub1*	5.55	6.31	5.62	5.73
ENSMUSG00000039616	*Mocos*	4.88	4.67	4.66	4.24
ENSMUSG00000039617	*NA*	1.69	1.23	1.18	1.67
ENSMUSG00000039623	*C330006K01R*	1.15	1.89	2.34	2.01
ENSMUSG00000039628	*Hs3st6*	-0.89	1.69	1.21	1.03
ENSMUSG00000039630	*Hnrnpu*	6.21	5.55	5.72	5.33
ENSMUSG00000039634	*Zfp189*	2.21	1.33	1.55	1.65
ENSMUSG00000039637	*Coro7*	2.63	3.06	2.74	2.36
ENSMUSG00000039640	*Mrpl12*	6	6.28	6.52	6.67
ENSMUSG00000039646	*Vasn*	1.74	3.43	2.48	2.88
ENSMUSG00000039648	*Ccbl1*	5.16	6.05	4.88	5.12
ENSMUSG00000039652	*Cpeb3*	1.77	0.83	1.93	1.49
ENSMUSG00000039653	*Baat*	7.55	7.03	7.04	6.86
ENSMUSG00000039656	*Rxrb*	3.73	4.21	4.03	4.02
ENSMUSG00000039660	*D2Wsu81e*	3.39	4.16	3.79	3.69
ENSMUSG00000039662	*Icmt*	3.27	3.59	3.32	3.38
ENSMUSG00000039670	*1810049H13R*	2.87	3.32	3.91	3.31
ENSMUSG00000039671	*Prkcbp1*	1.65	1.73	1.77	1.5
ENSMUSG00000039678	*Tbc1d13*	3.76	4.01	3.81	3.68
ENSMUSG00000039680	*Mrps6*	4.19	3.91	4.06	3.62
ENSMUSG00000039682	*Lap3*	7.46	7.49	7.44	7.25
ENSMUSG00000039686	*Zer1*	2.77	3.39	3.22	3.13
ENSMUSG00000039701	*Usp53*	1.67	0.95	1.39	1.26
ENSMUSG00000039703	*Nploc4*	5.34	5.63	5.31	5.22
ENSMUSG00000039704	*Lmbrd2*	4.08	2.89	3.5	3.11

ENSMUSG00000039706	*Ldb2*	1.35	1.44	1.08	1.37
ENSMUSG00000039713	*mKIAA0720*	0.65	1.83	1.63	1.44
ENSMUSG00000039715	*Wdr34*	1.41	2.59	2.04	1.84
ENSMUSG00000039725	*2810408M09R*	1.49	2.28	2.48	2.01
ENSMUSG00000039735	*Fnbp1l*	2.36	2.03	2.02	1.47
ENSMUSG00000039737	*Prkrip1*	2.12	2.01	2.42	2.09
ENSMUSG00000039740	*Alg2*	2.7	3.64	2.59	2.96
ENSMUSG00000039745	*Htatip2*	4.73	4.94	4.77	4.74
ENSMUSG00000039752	*NA*	1.86	3.28	2.75	2.55
ENSMUSG00000039753	*Fbxl5*	4.13	3.76	3.97	3.58
ENSMUSG00000039754	*Alkbh4*	1.45	1.57	1.31	1.91
ENSMUSG00000039756	*Dnttip2*	4.17	3.57	3.78	3.5
ENSMUSG00000039759	*Thap3*	1.79	2.92	2.48	2.17
ENSMUSG00000039763	*ORF28*	2.71	2.44	3.01	2.47
ENSMUSG00000039768	*Dnajc11*	3.03	3.72	3.62	3.59
ENSMUSG00000039770	*Ypel5*	5.18	3.72	4.94	4.4
ENSMUSG00000039771	*Polr2j*	4.08	4.36	4.47	4.49
ENSMUSG00000039782	*cpeb2*	4.62	2.72	4.26	3.27
ENSMUSG00000039783	*Kmo*	7.19	6.65	6.91	6.48
ENSMUSG00000039789	*Zfp597*	1.73	0.58	1.31	0.82
ENSMUSG00000039795	*Zfand1*	1.13	1.01	1.33	1.36
ENSMUSG00000039804	*Ncoa5*	2.71	3	2.36	2.34
ENSMUSG00000039809	*Gabbr2*	2.9	3.36	2.4	2.76
ENSMUSG00000039810	*Zc3h10*	2.12	2.77	2.44	2.43
ENSMUSG00000039826	*Trub2*	2.47	2.92	2.62	2.8
ENSMUSG00000039828	*Wdr70*	1.05	0.74	0.95	0.88
ENSMUSG00000039831	*Arhgap29*	4.85	3.54	3.94	3.67
ENSMUSG00000039834	*Zfp335*	2.33	2.97	2.47	2.43
ENSMUSG00000039840	*NA*	2.73	2.56	2.76	2.26
ENSMUSG00000039841	*Zfp800*	2.09	0.8	1.64	1.2
ENSMUSG00000039844	*Rapgef1*	3.8	4.42	4.02	3.96

ENSMUSG00000039849	*F730014I05Ri*	3.01	3.61	3.37	3.05
ENSMUSG00000039852	*Rere*	2.6	2.62	2.91	2.77
ENSMUSG00000039853	*Trim14*	3.84	4.22	3.71	3.45
ENSMUSG00000039865	*Slc44a3*	2.24	2.04	1.95	1.43
ENSMUSG00000039878	*Slc39a5*	0.97	0.18	1.36	0.41
ENSMUSG00000039879	*Heca*	4.23	3.56	3.98	3.44
ENSMUSG00000039886	*Tmem120a*	5.62	5.4	5.96	5.37
ENSMUSG00000039887	*Alg14*	4.44	4.03	4.1	3.55
ENSMUSG00000039901	*9130011E15Ri*	2.15	2.11	2.49	2.03
ENSMUSG00000039908	*Slc26a11*	1.41	1.66	2	1.61
ENSMUSG00000039910	*Cited2*	3.65	4.22	3.85	3.41
ENSMUSG00000039914	*Coq10a*	3.34	3.44	3.7	3.49
ENSMUSG00000039917	*Rhbdd2*	3.33	3.74	3.45	3.2
ENSMUSG00000039934	*A530088I07Ri*	2.93	2.71	2.8	2.62
ENSMUSG00000039952	*Dag1*	5.22	5.17	5.03	4.9
ENSMUSG00000039953	*Clstn1*	1.04	1.46	0.71	0.85
ENSMUSG00000039956	*Mrap*	5.28	6.13	5.84	5.92
ENSMUSG00000039958	*4833442J19Ri*	3.61	3.76	4.15	3.75
ENSMUSG00000039959	*Hip1*	1.43	1.19	0.5	0.5
ENSMUSG00000039960	*Rhou*	5.39	5.09	5.15	4.86
ENSMUSG00000039967	*NA*	2.34	0.87	1.44	0.36
ENSMUSG00000039968	*Rsbn1l*	1.96	1.16	1.66	0.94
ENSMUSG00000039976	*Tbc1d16*	1.48	1.63	1.62	1.71
ENSMUSG00000039982	*Dtx4*	3.32	3.03	2.41	1.95
ENSMUSG00000039983	*Ccdc32*	2.05	2.54	2.34	2.27
ENSMUSG00000039987	*Phtf2*	0.93	0.94	1.07	0.91
ENSMUSG00000039988	*Ankrd13c*	4.05	3.32	4.13	3.59
ENSMUSG00000039989	*Cbx4*	2.61	3.66	3.13	2.35
ENSMUSG00000039990	*2700050L05Ri*	2.78	2.45	2.46	2.57
ENSMUSG00000039997	*Ifi203*	1.82	0.7	1	0.75
ENSMUSG00000040006	*BC013529*	5.18	4.44	4.78	4.32

ENSMUSG00000040007	*Bahd1*	1.98	2.81	2.29	2.15
ENSMUSG00000040010	*Slc7a5*	0.58	1.49	1.21	0.96
ENSMUSG00000040017	*Saa4*	8.82	8.63	9.17	8.65
ENSMUSG00000040018	*Cox15*	4.11	4.06	4.02	3.76
ENSMUSG00000040021	*NA*	3.39	2.65	3.17	3
ENSMUSG00000040025	*Ythdf2*	3.71	3.28	3.25	3.09
ENSMUSG00000040026	*Saa3*	1.46	2.17	1.7	1.86
ENSMUSG00000040028	*Elavl1*	4.78	3.96	4.41	4.27
ENSMUSG00000040029	*Ipo8*	4.38	3.98	4.13	3.74
ENSMUSG00000040033	*Stat2*	4.03	4.28	3.83	4.14
ENSMUSG00000040034	*Nup43*	1.57	1.43	1.47	0.96
ENSMUSG00000040040	*Ift88*	1.07	0.84	1.15	0.67
ENSMUSG00000040043	*Rbms2*	2.4	2.09	2.31	2.22
ENSMUSG00000040044	*Orc3l*	3.74	3.3	3.58	3.07
ENSMUSG00000040048	*Ndufb10*	7.1	7.29	7.91	8.2
ENSMUSG00000040054	*TIP5*	2.83	2.86	2.74	2.59
ENSMUSG00000040078	*NA*	4.27	2.66	3.02	3.76
ENSMUSG00000040097	*Flywch1*	3.16	3.58	3.1	3.15
ENSMUSG00000040102	*Klhdc5*	1.5	1.24	1.59	0.79
ENSMUSG00000040105	*Ppapdc2*	3.24	3.14	3.46	2.68
ENSMUSG00000040112	*Mrps35*	4.72	4.79	4.68	4.54
ENSMUSG00000040123	*Zmym5*	3.61	2.08	3.16	2.69
ENSMUSG00000040127	*Sdro*	5.83	4.92	5.47	4.79
ENSMUSG00000040128	*Pnrc1*	6.02	6.17	5.9	5.32
ENSMUSG00000040134	*Rdh7*	9.47	9.53	9.5	9.31
ENSMUSG00000040146	*Rgl3*	3.04	3.63	3.8	3.47
ENSMUSG00000040147	*Maob*	7.95	7.28	7.68	7.09
ENSMUSG00000040151	*Hs2st1*	2.4	1.84	1.97	1.79
ENSMUSG00000040167	*Ikzf5*	1.66	0.43	1.13	0.83
ENSMUSG00000040170	*Fmo2*	3.92	3.85	3.61	3.87
ENSMUSG00000040174	*Alkbh3*	3.3	3.37	3.69	3.16

ENSMUSG00000040177	*2310057M21R*	0.8	1.22	1.02	1.15
ENSMUSG00000040181	*Fmo1*	7.86	7.27	7.5	7.16
ENSMUSG00000040188	*Scamp2*	3.83	4.1	3.89	3.62
ENSMUSG00000040212	*Emp3*	1.72	2.01	1.43	1.73
ENSMUSG00000040213	*Ccbl2*	7.29	7.2	6.51	6.53
ENSMUSG00000040225	*Bat2d*	2.89	2.59	2.89	2.49
ENSMUSG00000040234	*Tm7sf3*	4.63	4.93	4.71	4.61
ENSMUSG00000040236	*Trappc5*	4.15	4.79	4.98	4.98
ENSMUSG00000040242	*Fgfr1op2*	4.28	3.53	3.91	3.59
ENSMUSG00000040249	*Lrp1*	5.73	6.46	5.99	5.77
ENSMUSG00000040250	*4933424B01Ri*	2.83	2.93	3	2.89
ENSMUSG00000040253	*Gbp6*	3.06	2.03	1.13	1.58
ENSMUSG00000040263	*Klhdc4*	1.7	2.22	1.86	1.64
ENSMUSG00000040268	*Plekha1*	1.94	1.65	1.79	1.42
ENSMUSG00000040269	*Mrps28*	4.4	4.33	4.29	4.04
ENSMUSG00000040274	*Cdk6*	1.18	0.8	1.24	0.93
ENSMUSG00000040280	*Ndufa4l2*	0.03	0.19	1.57	1.34
ENSMUSG00000040282	*BC052040*	1.23	0.65	1.11	0.56
ENSMUSG00000040296	*Ddx58*	3.62	3.28	3.29	3.43
ENSMUSG00000040297	*NA*	2.61	1.44	2.12	1.13
ENSMUSG00000040302	*C030048B08R*	2.19	1.36	1.9	1.77
ENSMUSG00000040321	*Zfp770*	2.11	1.08	1.71	1.3
ENSMUSG00000040323	*NA*	1.43	0.99	1.47	1.9
ENSMUSG00000040325	*Vprbp*	3.24	3.24	3.23	3.01
ENSMUSG00000040331	*NA*	4.89	4.12	4.75	4.14
ENSMUSG00000040350	*Trim7*	0.69	0.59	1.03	0.63
ENSMUSG00000040351	*mKIAA1386*	3.13	2.58	2.79	2.46
ENSMUSG00000040354	*Mars*	4.49	5.2	4.57	4.7
ENSMUSG00000040356	*Skiv2l*	3.93	4.66	4.31	4.09
ENSMUSG00000040359	*mKIAA0776*	3.53	3.38	2.91	2.78
ENSMUSG00000040363	*Bcor*	1.66	2.71	1.74	1.35

ENSMUSG00000040365	*Trim41*	3.08	3.42	3.19	2.76
ENSMUSG00000040370	*Lyrm5*	5.45	3.93	5.06	3.98
ENSMUSG00000040374	*Pxmp3*	5.23	4.42	4.94	4.44
ENSMUSG00000040383	*Aqr*	2.79	2.82	2.91	2.74
ENSMUSG00000040385	*Ppp1ca*	7.26	7.33	7.18	6.85
ENSMUSG00000040390	*Map3k10*	1.56	2.28	1.9	1.96
ENSMUSG00000040396	*Abhd13*	3.17	2.61	2.62	2.38
ENSMUSG00000040407	*Akap9*	2.42	1.92	2.2	1.9
ENSMUSG00000040410	*Fbxl4*	3.5	3.49	3.48	3.23
ENSMUSG00000040413	*Timd2*	5.87	5.39	5.88	5.62
ENSMUSG00000040414	*Slc25a28*	3.33	3.74	3.79	3.68
ENSMUSG00000040423	*Rc3h1*	2.23	1.81	2.25	1.79
ENSMUSG00000040430	*Pitpnc1*	2.72	2.24	3.25	2.9
ENSMUSG00000040433	*Zbtb38*	2.22	1.91	1.82	1.83
ENSMUSG00000040435	*Myd116*	2.65	2.81	2.69	2.76
ENSMUSG00000040441	*NA*	4.2	4.92	4.58	4.55
ENSMUSG00000040446	*BC021395*	1.88	1.12	1.59	1.29
ENSMUSG00000040447	*NA*	3.86	4.06	4.51	3.79
ENSMUSG00000040451	*Sgms1*	2.69	2.25	2.38	2.05
ENSMUSG00000040455	*Usp45*	2.54	1.45	2.25	1.88
ENSMUSG00000040459	*9430010O03Ri*	4.65	3.55	3.94	3.9
ENSMUSG00000040462	*Os9*	6.76	7.44	7.05	6.94
ENSMUSG00000040463	*Mybbp1a*	3.72	4.69	4.21	4.08
ENSMUSG00000040464	*Gtpbp10*	2.27	1.04	2.01	1.45
ENSMUSG00000040466	*Blvrb*	6.2	7.01	6.36	6.5
ENSMUSG00000040471	*Ggt6*	3.45	4.09	4.09	3.54
ENSMUSG00000040472	*Rabggta*	3.63	3.91	4.04	3.95
ENSMUSG00000040479	*Dgkz*	3.15	3.86	3.6	3.3
ENSMUSG00000040481	*Bptf*	2.36	2.05	2.25	2.09
ENSMUSG00000040482	*Dom3z*	3.05	4.12	3.51	3.67
ENSMUSG00000040488	*Ltbp4*	2.74	3.72	3.13	3.29

ENSMUSG00000040498	*2210010C17Ri*	1.67	3.21	2.97	3.13
ENSMUSG00000040505	*Abcg5*	4.89	4.93	4.95	5.16
ENSMUSG00000040506	*D030051N19R*	3.13	3.45	3.14	3
ENSMUSG00000040511	*Pvr*	1.55	1.26	1.55	1.23
ENSMUSG00000040520	*Manea*	3.59	2.05	3.13	2.56
ENSMUSG00000040521	*Tsfm*	2.83	3.2	2.81	2.68
ENSMUSG00000040524	*Zfp609*	1.5	1.75	1.54	1.76
ENSMUSG00000040525	*Cblc*	3.24	4.17	3.68	3.42
ENSMUSG00000040532	*Abhd11*	4.73	4.65	4.73	4.41
ENSMUSG00000040536	*Efcbp1*	3.78	2.91	3.45	3.11
ENSMUSG00000040548	*Tex2*	5.87	5.66	5.74	5.59
ENSMUSG00000040549	*mKIAA0097*	2.02	1.49	1.91	1.43
ENSMUSG00000040550	*Otud6b*	3.44	2.92	3.26	2.85
ENSMUSG00000040557	*Wbscr27*	2.42	2.91	2.23	2.34
ENSMUSG00000040560	*NA*	2.54	2.24	2.75	2.42
ENSMUSG00000040562	*Gstm2*	5.62	4.6	5.79	5.02
ENSMUSG00000040564	*Apoc1*	11.88	11.23	12.26	11.95
ENSMUSG00000040565	*Btaf1*	2.71	1.99	2.42	1.9
ENSMUSG00000040583	*Cyp2b13*	6.85	-5.23	4.18	-5.23
ENSMUSG00000040584	*Abcb1a*	0.87	0.28	1.01	0.09
ENSMUSG00000040592	*Cd79b*	-0.74	-0.66	2.4	-0.94
ENSMUSG00000040599	*Mis12*	3.43	2.78	3.01	2.93
ENSMUSG00000040605	*Bace2*	2.16	2.56	2.01	1.59
ENSMUSG00000040612	*NA*	4.23	4.64	4.07	4.09
ENSMUSG00000040613	*Apobec1*	3.53	3.15	3.4	2.88
ENSMUSG00000040616	*Tmem51*	3.38	4.33	3.58	3.74
ENSMUSG00000040620	*Dhx33*	2.86	3.13	2.78	2.59
ENSMUSG00000040648	*mKIAA0433*	5.18	4.07	4.53	3.77
ENSMUSG00000040651	*NA*	2.5	1.77	2.44	1.87
ENSMUSG00000040652	*Oaz2*	2	2.27	2.54	2.03
ENSMUSG00000040658	*BC048355*	3.29	3.97	3.91	3.44

ENSMUSG00000040659	*Efhd2*	4.82	5.81	4.92	5.32
ENSMUSG00000040660	*Cyp2b9*	7.96	-3.23	5.65	-3.65
ENSMUSG00000040661	*Rad54l2*	3.22	2.81	3.11	2.76
ENSMUSG00000040667	*Nup88*	3.79	3.49	3.82	3.35
ENSMUSG00000040681	*Hmgn1*	5.04	3.82	4.34	3.42
ENSMUSG00000040687	*Madd*	1.72	2.23	2.36	2.04
ENSMUSG00000040688	*Tbl3*	3.2	3.98	3.68	3.54
ENSMUSG00000040697	*Dnajc16*	2.46	2.64	2.36	2.26
ENSMUSG00000040699	*Limd2*	3.74	3.63	3.63	3.06
ENSMUSG00000040701	*Ap1g2*	1.51	2.26	2.13	1.88
ENSMUSG00000040705	*NA*	#NAME?	-4.89	1.75	1.95
ENSMUSG00000040706	*Agmat*	6.94	7.5	7.28	6.99
ENSMUSG00000040712	*Camta2*	2.69	3.47	3.25	3.19
ENSMUSG00000040713	*Creg1*	8.51	8.04	8.3	8.02
ENSMUSG00000040715	*Ddi2*	6.66	7.04	6.55	6.41
ENSMUSG00000040720	*1110037F02Ri*	2.39	2.21	2.34	2.05
ENSMUSG00000040721	*Zfhx2*	0.62	1.45	1.26	1.57
ENSMUSG00000040722	*Scamp5*	2.47	2.61	2.43	2.23
ENSMUSG00000040723	*Rcsd1*	2.17	2.49	1.98	1.4
ENSMUSG00000040725	*Hnrpul1*	4.69	5.07	5.05	4.76
ENSMUSG00000040731	*Eif4h*	6.41	6.77	6.39	6.3
ENSMUSG00000040732	*Erg*	1.45	1.29	1.25	1.02
ENSMUSG00000040738	*Ints8*	2.84	2.15	2.44	2.12
ENSMUSG00000040740	*Slc25a34*	2.13	1.92	1.98	1.36
ENSMUSG00000040746	*Rnf167*	5.3	5.77	5.85	5.51
ENSMUSG00000040747	*Cd53*	3.53	1.85	2.88	1.81
ENSMUSG00000040760	*Appl1*	1.69	0.75	1.64	0.61
ENSMUSG00000040761	*Spen*	2.07	2.62	2.4	2.28
ENSMUSG00000040767	*3300001G02R*	1.33	1.52	2.15	1.69
ENSMUSG00000040771	*AI314976*	3.75	3.71	3.91	3.54
ENSMUSG00000040774	*Cept1*	5.62	5.14	5.12	4.55

ENSMUSG00000040782	*Rfwd2*	1.67	0.96	1.51	0.88
ENSMUSG00000040785	*mKIAA4119*	2.58	1.36	2.07	1.61
ENSMUSG00000040795	*Iqcc*	2.44	2.12	1.78	1.65
ENSMUSG00000040811	*NA*	1.11	1.85	1.16	0.85
ENSMUSG00000040813	*Tex264*	6.08	6.7	6.45	6.28
ENSMUSG00000040818	*A630054L15Ri*	3.16	2.19	2.66	2.5
ENSMUSG00000040820	*Hlcs*	2.13	1.81	2.18	1.99
ENSMUSG00000040822	*1700123O20Ri*	4.55	4.84	4.79	4.66
ENSMUSG00000040824	*Snrpd2*	4.36	4.26	4.1	4.54
ENSMUSG00000040842	*D4Ertd22e*	4.73	5.18	5.07	4.93
ENSMUSG00000040843	*Tiprl*	4.12	3.21	3.76	3.52
ENSMUSG00000040848	*Sft2d2*	5	4.76	4.68	4.45
ENSMUSG00000040850	*Psme4*	5.28	4.62	4.65	4.23
ENSMUSG00000040855	*Reps2*	3.64	2.82	3.5	2.86
ENSMUSG00000040857	*Erf*	2.74	3.31	3.49	3.07
ENSMUSG00000040859	*Bsdc1*	5.25	5.66	5.45	5.13
ENSMUSG00000040865	*A430093A21Ri*	1.22	0.37	0.99	0.9
ENSMUSG00000040883	*BC010787*	8.64	8.95	9.08	9.05
ENSMUSG00000040888	*Gfer*	4.06	4.38	4.23	4.12
ENSMUSG00000040891	*Foxa3*	4.17	4.91	4.55	5.04
ENSMUSG00000040904	*D11Bwg0434e*	6.14	6.9	7.01	6.9
ENSMUSG00000040913	*Fbxw4*	2.88	3.46	3.04	2.73
ENSMUSG00000040918	*Slc19a2*	6.01	5.67	5.84	5.44
ENSMUSG00000040928	*S100pbp*	2.65	2.12	2.1	1.61
ENSMUSG00000040938	*Slc16a11*	1.49	2.52	2.02	2.38
ENSMUSG00000040940	*mFLJ00369*	3.23	4.32	3.79	3.58
ENSMUSG00000040943	*E130014J05Ri*	1.23	0.75	0.99	0.26
ENSMUSG00000040945	*Rcc2*	2.69	3.27	3.26	3
ENSMUSG00000040952	*Rps19*	1.32	0.9	1.43	1.73
ENSMUSG00000040957	*Cables1*	0.59	1.14	1.9	1.25
ENSMUSG00000040963	*Asgr2*	7.99	7.87	8.19	7.95

ENSMUSG00000040964	*mKIAA1626*	1.93	3	2.21	2.04
ENSMUSG00000040997	*Abhd4*	5.04	5.35	5.02	4.87
ENSMUSG00000041003	*Nbeal1*	1.03	-0.61	0.42	0.19
ENSMUSG00000041012	*Cmtm8*	5.27	5.24	5.96	5.68
ENSMUSG00000041025	*C79267*	2.29	3.16	2.56	2.63
ENSMUSG00000041028	*Ghitm*	7.83	7.26	7.52	7.06
ENSMUSG00000041035	*5330431N19Ri*	3.03	3.39	3.33	3.2
ENSMUSG00000041037	*Irgq*	2.62	3.2	2.66	2.67
ENSMUSG00000041040	*Als2cr13*	2.3	1.43	1.74	1.12
ENSMUSG00000041044	*Lrit1*	1.16	-1.91	1.52	1.29
ENSMUSG00000041057	*NA*	3.55	3.48	3.11	3.21
ENSMUSG00000041058	*Wwp1*	4.92	4.09	4.36	4
ENSMUSG00000041075	*Fzd7*	2.87	2.74	2.36	1.97
ENSMUSG00000041079	*Rwdd2b*	2.61	2.59	2.74	2.46
ENSMUSG00000041084	*2310008M10R*	6.04	5.77	5.22	5.52
ENSMUSG00000041096	*Tspyl2*	1.25	0.99	0.67	0.3
ENSMUSG00000041115	*Iqsec2*	1.4	1.49	1.75	1.57
ENSMUSG00000041119	*Pde9a*	3.49	3.37	4.03	3.54
ENSMUSG00000041124	*8430410K20Ri*	4.01	3.24	3.47	3
ENSMUSG00000041126	*NA*	3.87	3.89	4.06	3.76
ENSMUSG00000041130	*Zfp598*	4.31	5.1	4.62	4.62
ENSMUSG00000041132	*B230342M21R*	5.48	5.39	5.4	5.2
ENSMUSG00000041133	*SmcB*	4.37	4.08	4.2	3.93
ENSMUSG00000041135	*Ripk2*	2.14	1.51	2.41	2.14
ENSMUSG00000041143	*Tmco4*	2.13	2.77	2.6	2.41
ENSMUSG00000041161	*NA*	1.82	2.3	2.19	2.01
ENSMUSG00000041164	*Zmiz2*	3.22	4.33	3.9	3.79
ENSMUSG00000041168	*Lonp1*	6.01	6.47	6.2	5.9
ENSMUSG00000041180	*Hectd2*	5.97	4.48	4.86	4.46
ENSMUSG00000041187	*Prkd2*	1.21	1.57	1.04	1.01
ENSMUSG00000041203	*2310036O22Ri*	6.01	6.22	5.99	5.95

ENSMUSG00000041215	*Yeats2*	1.15	1.29	1.07	0.76
ENSMUSG00000041216	*Rlbp1l1*	1.53	0.11	1.07	0.44
ENSMUSG00000041220	*Elovl6*	4.58	3.28	4.06	3.63
ENSMUSG00000041225	*Arhgap12*	3.03	2.06	2.84	2.28
ENSMUSG00000041229	*Phf8*	1.03	1.05	1.17	1.07
ENSMUSG00000041231	*Ublcp1*	1.74	1.51	2.07	1.63
ENSMUSG00000041235	*Chd7*	2.02	2	2.14	1.81
ENSMUSG00000041236	*Vps41*	4.71	4.1	4.3	3.79
ENSMUSG00000041237	*Pklr*	6.84	6.45	6.8	7
ENSMUSG00000041238	*Rbbp8*	1.8	1.4	1.7	1.06
ENSMUSG00000041241	*0610009K11Ri*	3.65	4	4.1	3.75
ENSMUSG00000041258	*NA*	1.89	1.78	1.77	1.26
ENSMUSG00000041261	*Car8*	4.68	4.51	4.52	4.31
ENSMUSG00000041263	*Rusc1*	1.25	1.73	1.47	1.47
ENSMUSG00000041264	*Uspl1*	3.58	3.64	3.34	3.49
ENSMUSG00000041268	*NA*	2.25	1.38	2.19	1.61
ENSMUSG00000041272	*Tox*	3.19	2.72	2.26	1.95
ENSMUSG00000041278	*Ttc1*	3.86	3.61	3.81	3.69
ENSMUSG00000041297	*Cdc2l5*	3.26	2.8	2.94	2.78
ENSMUSG00000041303	*Gtf3c3*	1.74	1.21	1.75	1.21
ENSMUSG00000041308	*Sntb2*	1.45	1.22	1.17	0.89
ENSMUSG00000041319	*Thoc6*	1.75	2.14	2.03	2.14
ENSMUSG00000041324	*Inhba*	1.31	0.71	0.91	1.66
ENSMUSG00000041328	*Pcf11*	2.68	1.76	2.58	2.04
ENSMUSG00000041341	*Atg2b*	2.89	2.7	2.98	2.56
ENSMUSG00000041346	*Wdr79*	2.29	2.96	2.51	2.28
ENSMUSG00000041354	*Rgl2*	1.84	2.42	2.22	1.88
ENSMUSG00000041355	*Ssr2*	6.59	6.33	6.03	6.09
ENSMUSG00000041360	*D19Bwg1357e*	3.29	3.55	3.31	3.2
ENSMUSG00000041362	*4930506M07R*	3.21	3.23	3.34	3.13
ENSMUSG00000041375	*Ccdc9*	1.84	2.77	2.44	2.23

ENSMUSG00000041378	*Cldn5*	1.7	2.91	1.45	2.05
ENSMUSG00000041390	*Mdfic*	3.19	2.27	2.59	1.86
ENSMUSG00000041396	*2810422O20Ri*	1.73	1.65	1.72	1.33
ENSMUSG00000041406	*BC055324*	1.47	0.38	1.4	0.79
ENSMUSG00000041408	*Wapal*	4.93	4.3	4.37	3.77
ENSMUSG00000041415	*Dicer1*	3.02	2.81	3.01	2.57
ENSMUSG00000041417	*Pik3r1*	4.56	3.97	4.31	4.29
ENSMUSG00000041426	*Hibch*	6.09	5.18	5.82	5.17
ENSMUSG00000041429	*Nthl1*	1.33	2.48	2.44	2.52
ENSMUSG00000041438	*Cirh1a*	3.68	4	3.87	3.68
ENSMUSG00000041439	*2210010L05Ri*	1.25	1.48	1.46	1.49
ENSMUSG00000041444	*Grit*	1.35	1.47	1.34	1.26
ENSMUSG00000041445	*Mmrn2*	2.43	2.87	2.53	2.71
ENSMUSG00000041459	*Tardbp*	5.15	4.58	4.87	4.5
ENSMUSG00000041471	*3110001K24Ri*	5.08	3.84	4.49	4.21
ENSMUSG00000041481	*Serpina3g*	3.08	2.26	2.21	1.85
ENSMUSG00000041483	*Zfp281*	3.42	2.62	3.36	2.83
ENSMUSG00000041488	*Stx3*	2.15	1.58	1.65	1.15
ENSMUSG00000041506	*Rrp9*	1.93	3.22	2.82	2.91
ENSMUSG00000041515	*Irf8*	1.3	1.64	1.78	1.41
ENSMUSG00000041528	*Kpc1*	3.91	4.47	4.3	4.02
ENSMUSG00000041530	*Eif2c1*	3.06	2.86	2.68	2.46
ENSMUSG00000041540	*Sox5*	1.92	1.01	2.21	2.24
ENSMUSG00000041548	*Hspb8*	7.65	8.04	7.45	7.61
ENSMUSG00000041560	*Gltscr2*	4.56	5.24	4.76	4.9
ENSMUSG00000041570	*Camsap1l1*	2.57	1.79	2.2	1.97
ENSMUSG00000041571	*Sepw1*	6.81	7.38	7.41	6.88
ENSMUSG00000041577	*Prelp*	4.86	5.32	5.02	5.07
ENSMUSG00000041594	*Tmtc4*	1.06	0.37	1.33	0.99
ENSMUSG00000041598	*Cdc42ep4*	4.65	5.36	4.8	4.79
ENSMUSG00000041623	*D11Wsu47e*	1.34	1.61	1.32	0.7

ENSMUSG00000041625	*BC006662*	5.96	6.04	5.72	5.71
ENSMUSG00000041629	*D11Wsu99e*	2.79	2.6	2.92	2.88
ENSMUSG00000041632	*Mrps27*	4.54	4.88	4.16	4.09
ENSMUSG00000041638	*Gcn1l1*	2.86	3.64	3.38	3.12
ENSMUSG00000041645	*Ddx24*	4.52	4.64	4.56	4.33
ENSMUSG00000041650	*Pcca*	5.56	4.79	5.45	4.93
ENSMUSG00000041654	*Slc39a11*	3.32	3.52	3.05	2.74
ENSMUSG00000041660	*Bbox1*	6.34	5.75	6.19	5.75
ENSMUSG00000041671	*Pyroxd1*	2.55	2.05	2.74	1.97
ENSMUSG00000041684	*Bivm*	2.8	1.68	2.5	1.95
ENSMUSG00000041685	*Fcho2*	3.68	2.21	2.99	2.19
ENSMUSG00000041688	*Amot*	1.14	0.53	0.28	0.27
ENSMUSG00000041697	*Cox6a1*	7.44	8.17	8.13	8.08
ENSMUSG00000041698	*Slco1a1*	5.37	5.62	5.12	5.71
ENSMUSG00000041702	*Btbd7*	1.93	1.74	1.93	1.61
ENSMUSG00000041712	*5730410I19Rik*	3.45	3.38	3.32	3.28
ENSMUSG00000041716	*Moap1*	1.58	1.77	2.05	1.76
ENSMUSG00000041717	*Golt1a*	3.42	3.6	3.67	3.43
ENSMUSG00000041720	*Pik4ca*	3.25	3.43	3.35	3.17
ENSMUSG00000041733	*Coq5*	4.98	4.97	5	4.72
ENSMUSG00000041736	*Tspo*	5.31	5.46	5.66	5.51
ENSMUSG00000041740	*Rnf10*	6.36	6.66	6.37	6.11
ENSMUSG00000041747	*Utp15*	2.07	1.63	1.93	1.97
ENSMUSG00000041748	*NA*	3.18	2.76	3.15	2.93
ENSMUSG00000041750	*Cd1d2*	1.97	2.01	2.09	2.41
ENSMUSG00000041757	*Plekha6*	3.41	3.73	3.52	3.38
ENSMUSG00000041762	*Gpr155*	3.08	2.83	3.27	2.88
ENSMUSG00000041763	*Tpp2*	3.88	3.2	3.68	3.12
ENSMUSG00000041765	*Ubac2*	4.43	4.66	4.64	4.53
ENSMUSG00000041769	*Ppp2r2d*	5.13	4.6	4.6	4.15
ENSMUSG00000041773	*Enc1*	1.56	1.09	0.82	0.24

ENSMUSG00000041775	*Mapk1ip1*	2.65	2.34	2.46	2.1
ENSMUSG00000041779	*Tram2*	1.42	1.78	2.1	2.05
ENSMUSG00000041781	*Cpsf2*	2.87	2.96	2.87	2.45
ENSMUSG00000041782	*Lad1*	2.3	3.34	3.06	2.08
ENSMUSG00000041798	*Gck*	6.26	7.85	6.29	6.93
ENSMUSG00000041815	*Poldip3*	4.77	4.58	4.77	4.18
ENSMUSG00000041827	*Oasl1*	1.22	1.23	0.71	1.64
ENSMUSG00000041828	*Abca8a*	5.1	4.95	4.73	4.71
ENSMUSG00000041837	*Pdcd7*	1.93	2.23	2.15	1.94
ENSMUSG00000041840	*Ccdc5*	1.79	1.38	2.28	1.28
ENSMUSG00000041841	*Rpl37*	1.77	1.9	2.59	2.41
ENSMUSG00000041845	*Rhod*	3.74	4.02	3.21	3.3
ENSMUSG00000041846	*Smek1*	4.72	3.57	4.1	3.82
ENSMUSG00000041849	*NA*	3.07	2.26	3.13	2.6
ENSMUSG00000041852	*Tcf20*	2.52	2.42	2.51	2.18
ENSMUSG00000041859	*Mcm3*	1.17	1.27	1.49	1
ENSMUSG00000041870	*Ankrd13a*	4.37	4.13	4.01	3.53
ENSMUSG00000041879	*Ipo9*	3.25	3.22	2.96	2.83
ENSMUSG00000041881	*Ndufa7*	5.32	5.69	5.56	5.48
ENSMUSG00000041890	*Git2*	2.32	2.5	2.54	2.42
ENSMUSG00000041891	*Lman1*	6.63	5.87	6.27	5.83
ENSMUSG00000041895	*Wipi1*	2.24	2.66	2.44	2.43
ENSMUSG00000041915	*Ammecr1l*	4.78	4.37	4.49	4.54
ENSMUSG00000041920	*Slc16a6*	2.04	1.88	1.44	1.01
ENSMUSG00000041921	*Metapl1*	4	4.29	4.18	3.66
ENSMUSG00000041926	*Rnpep*	3.62	4.22	4.33	4.01
ENSMUSG00000041930	*BC057022*	-0.28	1.61	1.56	1.02
ENSMUSG00000041935	*AW549877*	3.49	2.46	3.06	2.49
ENSMUSG00000041936	*Agrn*	2.21	2.52	2.02	2
ENSMUSG00000041939	*Mvk*	3.91	4.68	3.36	3.18
ENSMUSG00000041949	*Tmco7*	0.95	1.55	1.33	1.44

ENSMUSG00000041957	*Pkp2*	4.35	3.96	4.14	3.7
ENSMUSG00000041958	*Pigs*	3.04	3.94	3.49	3.14
ENSMUSG00000041959	*S100a10*	7.28	6.68	7.08	6.65
ENSMUSG00000041961	*Znrf3*	1.28	1	1.55	1.34
ENSMUSG00000041966	*4833418A01Ri*	1.78	1.23	1.43	0.96
ENSMUSG00000041974	*2310008H04Ri*	1.9	1.27	1.56	0.88
ENSMUSG00000041975	*Mettl8*	3.25	2.76	3.07	2.67
ENSMUSG00000041977	*Arhgef11*	3.32	3.56	3.73	3.46
ENSMUSG00000041992	*Rapgef5*	1.07	0.9	0.58	0.31
ENSMUSG00000041995	*Zbed3*	2.2	2.05	2.5	1.9
ENSMUSG00000041997	*Tlk1*	4.62	4.03	4.43	3.94
ENSMUSG00000042010	*Acacb*	4.44	4.17	4.11	3.27
ENSMUSG00000042015	*Wdr41*	3.13	2.9	3.09	2.67
ENSMUSG00000042032	*Mat2b*	3.43	2.88	3.49	3.11
ENSMUSG00000042041	*2010003K11Ri*	3.52	3.59	4.23	3.96
ENSMUSG00000042042	*Galnact2*	2.47	1.89	2.35	1.47
ENSMUSG00000042043	*Tbca*	4.13	1.41	3.26	2.95
ENSMUSG00000042046	*Ripk5*	1.97	1.61	1.55	1.22
ENSMUSG00000042055	*Brwd2*	3.35	2.94	3.55	2.87
ENSMUSG00000042063	*mKIAA4205*	2.24	2.06	1.84	1.59
ENSMUSG00000042066	*Tmcc2*	0.71	1.38	1.27	1.18
ENSMUSG00000042073	*Abhd14b*	6.95	7.45	7.61	7.24
ENSMUSG00000042079	*Hnrpf*	2.56	2.56	2.98	2.45
ENSMUSG00000042082	*Arsb*	3.41	2.96	3.38	2.8
ENSMUSG00000042099	*Ankrd47*	1.17	2.05	1.04	1.21
ENSMUSG00000042102	*Dmgdh*	8.39	7.67	8.34	7.57
ENSMUSG00000042105	*Inpp5f*	2.48	2.47	2.54	2.34
ENSMUSG00000042111	*Ccdc115*	2.65	2.8	2.94	2.66
ENSMUSG00000042118	*Bhmt2*	7.77	7.59	7.61	7.11
ENSMUSG00000042121	*Ssh1*	1.8	2.3	2.14	1.93
ENSMUSG00000042129	*Rassf4*	1.45	0.83	1.32	0.95

ENSMUSG00000042133	*Ppig*	3.35	2.61	3	2.23
ENSMUSG00000042138	*BC024479*	1.39	1.2	1.41	0.83
ENSMUSG00000042148	*Cox10*	2.85	3.18	3.7	3.24
ENSMUSG00000042165	*NA*	1.25	2.14	1.95	2.89
ENSMUSG00000042167	*Papd4*	1.85	1.05	1.92	1.53
ENSMUSG00000042178	*Armc5*	2.02	3.27	2.6	2.29
ENSMUSG00000042185	*Nfrkb*	1.2	1.61	1.55	1.41
ENSMUSG00000042198	*Chchd7*	3.15	3.04	3.3	2.88
ENSMUSG00000042202	*A530082C11Ri*	4.56	3.77	4.57	4.11
ENSMUSG00000042203	*Tbc1d22b*	0.94	1.72	1.23	1.17
ENSMUSG00000042207	*Jarid1b*	2.17	2.17	2.43	2.02
ENSMUSG00000042208	*0610010F05Ri*	2.55	1.6	2.5	1.93
ENSMUSG00000042210	*Abhd14a*	2.23	2.04	2.52	2.25
ENSMUSG00000042211	*Fbxo38*	3.53	3.15	3.27	3.03
ENSMUSG00000042213	*Anubl1*	4.42	2.61	3.31	2.67
ENSMUSG00000042228	*Lyn*	3.5	3.53	3.6	3.41
ENSMUSG00000042229	*Rabif*	3.43	3.21	3.09	2.83
ENSMUSG00000042246	*Tmc7*	1.04	0.73	0.8	0.31
ENSMUSG00000042248	*Cyp2c37*	8.64	7.87	7.83	7.55
ENSMUSG00000042251	*4732466D17Ri*	7.06	6.96	6.84	6.6
ENSMUSG00000042271	*Nxt2*	4.41	3.07	3.98	3.36
ENSMUSG00000042275	*Pelo*	3.29	3.61	3.07	3.42
ENSMUSG00000042284	*Itga1*	2.82	2.24	2.52	2.41
ENSMUSG00000042286	*Stab1*	3.29	4.11	3.22	3.24
ENSMUSG00000042289	*Hsd3b7*	7.77	8.43	7.82	7.66
ENSMUSG00000042292	*Mkl1*	1.56	2.4	2.01	2.1
ENSMUSG00000042293	*NA*	4.54	5.07	5.25	4.96
ENSMUSG00000042298	*Ttc19*	2.78	2.23	2.73	2.2
ENSMUSG00000042302	*Ehbp1*	1.86	1.27	1.74	0.65
ENSMUSG00000042303	*Sgsm3*	1.88	2.47	2.23	2.17
ENSMUSG00000042305	*Tmem183a*	6.17	5.49	5.73	5.28

ENSMUSG00000042308	*Setd1a*	2.52	2.94	2.46	2.33
ENSMUSG00000042312	*S100a13*	5.37	3.64	5.63	5.7
ENSMUSG00000042323	*Pbrm1*	3.6	2.68	3.57	2.93
ENSMUSG00000042328	*AK008458*	2.64	2.6	3.06	2.16
ENSMUSG00000042333	*Tnfrsf14*	2.82	2.48	2.74	2.28
ENSMUSG00000042340	*Ctf1*	2.11	2.12	1.96	1.55
ENSMUSG00000042348	*Arl15*	2.73	1.83	2.85	2.02
ENSMUSG00000042349	*Ikbke*	2.43	2.69	2	1.8
ENSMUSG00000042350	*1110018G07Ri*	3.91	3.64	4	3.53
ENSMUSG00000042354	*Gnl3*	4.31	3.73	4.07	3.87
ENSMUSG00000042363	*1110067D22Ri*	4.59	4.04	3.34	2.16
ENSMUSG00000042364	*Snag1*	3.35	3.09	3.19	3.07
ENSMUSG00000042369	*Rbm45*	3.18	2.67	2.63	2.65
ENSMUSG00000042380	*BC003266*	3.73	4.43	4.01	4.1
ENSMUSG00000042389	*Tsen2*	1.22	2.26	1.91	1.76
ENSMUSG00000042390	*Gatad2b*	2.93	2.81	2.87	2.66
ENSMUSG00000042396	*Rbm7*	5.09	3.79	4.57	4.35
ENSMUSG00000042404	*Dennd4b*	0.09	0.8	1.06	0.14
ENSMUSG00000042406	*Atf4*	5.91	6.36	6.24	6.22
ENSMUSG00000042408	*Zmym6*	1.46	0.17	1.6	0.95
ENSMUSG00000042410	*Agps*	2.39	1.49	2.1	1.42
ENSMUSG00000042419	*Nfkbil1*	1.58	2.37	2.71	2.31
ENSMUSG00000042423	*NA*	3.64	4.15	3.88	3.79
ENSMUSG00000042426	*Dhx29*	2.09	1.96	1.98	1.76
ENSMUSG00000042429	*Adora1*	3	3.41	3.6	3.42
ENSMUSG00000042444	*B230380D07R*	1.59	1.1	1.86	1.12
ENSMUSG00000042446	*NA*	1.63	0.56	1.09	0.63
ENSMUSG00000042447	*BC020002*	1.99	1.52	1.52	1.38
ENSMUSG00000042451	*Mybph*	1	1.09	1.78	1.58
ENSMUSG00000042453	*Reln*	2.97	3.25	2.61	3.05
ENSMUSG00000042460	*C1galt1*	4.04	3.31	3.47	3.03

ENSMUSG00000042462	*2410015N17Ri*	4.83	4.94	5.66	5.17
ENSMUSG00000042472	*Zfp410*	3.25	3.36	3.05	2.98
ENSMUSG00000042473	*Tbc1d8b*	3.02	2.22	2.37	2.17
ENSMUSG00000042474	*Faim3*	-2.38	-2.97	1.27	-2.38
ENSMUSG00000042476	*Abcb4*	6.92	6.26	6.62	6.14
ENSMUSG00000042485	*Mustn1*	2.27	2.97	2.91	3.07
ENSMUSG00000042487	*Leo1*	3.55	3.61	2.72	2.45
ENSMUSG00000042492	*Tbc1d10b*	2.21	2.47	2.32	2.2
ENSMUSG00000042502	*Cd2bp2*	2.87	3.77	3.51	3.53
ENSMUSG00000042505	*Acn9*	1.67	1.06	1.14	0.71
ENSMUSG00000042506	*Usp22*	3.68	3.66	3.73	3.18
ENSMUSG00000042507	*NA*	1.55	1.88	1.62	1.17
ENSMUSG00000042508	*Dmtf1*	3.1	2.53	2.67	2.36
ENSMUSG00000042510	*AA986860*	1.3	1.89	1.42	1.76
ENSMUSG00000042520	*Ubap2l*	3.8	4.04	4.11	3.8
ENSMUSG00000042524	*Unc84b*	4.68	4.83	5.19	4.93
ENSMUSG00000042535	*Gtpbp1*	3.25	3.63	3.6	3.36
ENSMUSG00000042541	*Shfm1*	6.06	6.13	6.25	5.94
ENSMUSG00000042548	*Asxl1*	2.51	2.46	2.16	2.04
ENSMUSG00000042557	*Sin3a*	3.64	3.4	3.12	3.08
ENSMUSG00000042558	*Adprhl2*	2.88	3.67	2.88	2.85
ENSMUSG00000042569	*Dhrs7b*	3.05	3.13	3.16	2.92
ENSMUSG00000042570	*Mier2*	2.23	3.03	2.13	2.08
ENSMUSG00000042572	*Ube2q1*	4.2	4.53	4.24	4.26
ENSMUSG00000042589	*Cutl2*	2.21	1.69	0.21	1.89
ENSMUSG00000042590	*Ipo11*	2.66	2.39	2.41	1.94
ENSMUSG00000042594	*Sh2b3*	2.87	3.2	3.36	2.88
ENSMUSG00000042595	*BC031748*	1.01	0.04	0.65	-0.02
ENSMUSG00000042599	*Jhdm1d*	1.95	0.78	1.7	0.95
ENSMUSG00000042605	*Atxn2*	4.45	4.56	4.97	4.64
ENSMUSG00000042608	*Stk40*	4.18	4.84	4.01	4.14

ENSMUSG00000042613	*Pbxip1*	1.49	2.1	2.17	1.97
ENSMUSG00000042622	*Maff*	1.73	0.37	1.94	1.17
ENSMUSG00000042625	*Safb2*	3.16	3.75	3.46	3.03
ENSMUSG00000042626	*Shc1*	3.84	3.89	3.59	3.54
ENSMUSG00000042628	*Zfyve1*	4.86	4.81	4.96	4.51
ENSMUSG00000042632	*Pla2g6*	3.94	4.16	4.42	3.71
ENSMUSG00000042638	*Gucy2c*	0.71	-0.22	1.03	-0.08
ENSMUSG00000042642	*Flad1*	4.42	4.96	4.65	4.53
ENSMUSG00000042647	*NA*	1.94	1.86	2.45	1.87
ENSMUSG00000042650	*Alkbh5*	5.06	5.06	5.2	5.03
ENSMUSG00000042659	*Arrdc4*	3.27	2.79	3.35	3.02
ENSMUSG00000042660	*Wdr55*	3.38	4.05	3.34	3.43
ENSMUSG00000042670	*Immp1l*	2.2	0.06	1.23	1.23
ENSMUSG00000042675	*Ypel3*	4	4.12	4.37	4.23
ENSMUSG00000042680	*Gm944*	3.63	3.7	3.74	3.59
ENSMUSG00000042682	*Selk*	4.86	4.08	4.46	4.04
ENSMUSG00000042688	*Mapk6*	4.21	3.42	3.96	3.42
ENSMUSG00000042694	*Obfc1*	1.09	1.05	1.27	1.09
ENSMUSG00000042699	*Dhx9*	4.43	3.74	4.22	3.91
ENSMUSG00000042700	*Sipa1l1*	2.62	2.76	2.68	2.6
ENSMUSG00000042705	*Commd10*	3.07	2.83	2.04	2.27
ENSMUSG00000042709	*Atpaf2*	4.28	4.26	4.03	3.93
ENSMUSG00000042712	*Wbp5*	4.23	2.88	3.66	3.44
ENSMUSG00000042719	*C330023M02R*	3.39	3.13	2.8	2.37
ENSMUSG00000042726	*Trafd1*	3.92	4.04	4.07	3.95
ENSMUSG00000042729	*Wdr74*	4.03	4.61	4.26	4.3
ENSMUSG00000042737	*Dpm3*	3.8	3.83	3.94	4.27
ENSMUSG00000042742	*B630005N14R*	2.06	1.69	1.49	1.15
ENSMUSG00000042744	*NA*	1.72	1.97	2.05	1.69
ENSMUSG00000042745	*Id1*	2.18	3.42	1.73	1.22
ENSMUSG00000042747	*Krtcap2*	5.95	5.66	6.05	6.1

ENSMUSG00000042770	*Hebp1*	7.68	8.13	8.18	7.96
ENSMUSG00000042772	*Smg7*	3.63	3.19	3.68	3.48
ENSMUSG00000042790	*D130054N24R*	3.74	3.34	3.74	3.21
ENSMUSG00000042797	*Aqp11*	5.71	5.07	6.18	5.36
ENSMUSG00000042814	*Mcts2*	1.8	2.11	2.49	2.42
ENSMUSG00000042831	*Alkbh6*	2.83	3.14	2.82	2.96
ENSMUSG00000042834	*D0H4S114*	2.44	2.68	1.34	1.16
ENSMUSG00000042874	*NA*	2.72	4.11	2.88	2.87
ENSMUSG00000042878	*Ccdc85b*	1.68	3.14	2.21	2.61
ENSMUSG00000042903	*Foxo4*	3.89	4.23	3.74	3.68
ENSMUSG00000042922	*NA*	2.18	2.89	2.64	2.52
ENSMUSG00000042962	*NA*	5.63	3.78	5.15	6.04
ENSMUSG00000042969	*NA*	1.12	1.42	1.91	1.8
ENSMUSG00000042978	*Sbk1*	3.57	3.8	4.34	4.13
ENSMUSG00000042988	*Notum*	3.89	4.77	4.74	4.56
ENSMUSG00000042992	*Loh12cr1*	2.54	2.93	2.86	2.77
ENSMUSG00000042997	*8030451K01Ri*	2.93	2.65	2.81	2.57
ENSMUSG00000043008	*Klhl6*	0.76	0.96	1.14	0.1
ENSMUSG00000043013	*Onecut1*	3.56	2.82	1.62	3.07
ENSMUSG00000043019	*EDEM3*	3.9	3.39	3.46	2.94
ENSMUSG00000043059	*Zfp513*	2.13	2.32	1.83	2.07
ENSMUSG00000043061	*Tmem18*	3.53	3.28	3.43	3.13
ENSMUSG00000043067	*Dpy19l1*	4.01	3.35	3.77	3.53
ENSMUSG00000043068	*2310031A18Ri*	2.74	4.18	3.34	3.18
ENSMUSG00000043085	*Tmem82*	4.11	4.89	4.45	4.55
ENSMUSG00000043090	*D330038O06R*	1.31	1.52	1.58	1.01
ENSMUSG00000043091	*Tuba1c*	2.94	3.15	2.57	2.53
ENSMUSG00000043131	*Mobkl1b*	4.85	4.31	4.43	4.01
ENSMUSG00000043140	*Tmem186*	2.77	3.02	3.17	2.55
ENSMUSG00000043146	*NA*	2.36	2.57	2.12	2.17
ENSMUSG00000043154	*NA*	2.69	1.66	2.42	2.01

ENSMUSG00000043162	*Pigy*	4.85	5.38	4.96	4.63
ENSMUSG00000043183	*4732471D19Ri*	0.66	1.04	1.1	0.99
ENSMUSG00000043190	*Rfesd*	2.13	1.1	2.17	1.48
ENSMUSG00000043192	*NA*	3.9	3.08	3.7	4.54
ENSMUSG00000043207	*Zmpste24*	5.34	4.72	5.03	4.57
ENSMUSG00000043241	*Upf2*	2.99	2.48	2.86	2.32
ENSMUSG00000043252	*Tmem64*	4.82	3.88	4.22	3.66
ENSMUSG00000043257	*Pigv*	1.85	2.11	2.07	1.84
ENSMUSG00000043270	*NA*	1.17	0.24	0.86	1.24
ENSMUSG00000043279	*Trim56*	1.57	1.22	1.28	1.43
ENSMUSG00000043284	*Tmem11*	4.44	4.71	4.65	4.63
ENSMUSG00000043290	*Zfp784*	1.15	1.9	1.69	1.2
ENSMUSG00000043300	*B3galnt1*	1.35	-0.22	0.87	1.02
ENSMUSG00000043311	*D17H6S53E*	2.94	2.95	2.75	2.52
ENSMUSG00000043323	*2410025L10Ri*	1.25	2.02	1.93	1.71
ENSMUSG00000043336	*NA*	1.45	1.05	1.69	1.18
ENSMUSG00000043391	*2510009E07Ri*	1.91	1.51	1.49	1.15
ENSMUSG00000043411	*Usp48*	2.52	2.43	2.31	2.04
ENSMUSG00000043415	*NA*	1.95	1.69	1.87	1.07
ENSMUSG00000043421	*2310016C08Ri*	1.16	1.29	0.75	0.4
ENSMUSG00000043424	*NA*	2.55	1.01	0.85	2.28
ENSMUSG00000043432	*Leng9*	1.86	1.83	2.06	1.69
ENSMUSG00000043445	*1700012G19Ri*	2.93	4.01	3.34	3.5
ENSMUSG00000043484	*NA*	2.48	1.24	0.68	1.43
ENSMUSG00000043488	*NA*	1.53	-0.61	1.5	0.64
ENSMUSG00000043510	*Hscb*	2.14	2.47	2.67	2.32
ENSMUSG00000043535	*Setx*	2.23	1.52	2.01	1.18
ENSMUSG00000043574	*NA*	1.52	-0.26	-0.26	0.4
ENSMUSG00000043587	*Acpl2*	0.24	0.11	1.07	0.36
ENSMUSG00000043618	*NA*	4.93	4.81	4.44	4.84
ENSMUSG00000043681	*2200001I15Rik*	3.09	2.48	4.73	5.54

ENSMUSG00000043683	*Fem1a*	3.73	4.19	3.52	3.4
ENSMUSG00000043687	*1190005I06Rik*	1.94	2.52	2.7	3.01
ENSMUSG00000043688	*NA*	2.62	3.19	2.76	2.67
ENSMUSG00000043702	*E430028B21Ri*	2.58	3.18	2.52	2.67
ENSMUSG00000043716	*Rpl7*	4.32	4.41	4.41	3.61
ENSMUSG00000043733	*Ptpn11*	4.44	4.62	4.39	4.25
ENSMUSG00000043770	*NA*	4.57	4.45	5.71	5.91
ENSMUSG00000043773	*NA*	1.31	0.8	1.28	-0.15
ENSMUSG00000043789	*NA*	3.23	3.46	3.76	3.6
ENSMUSG00000043801	*NA*	4.23	4.65	4.31	5.04
ENSMUSG00000043831	*Lysmd4*	2.6	2.8	2.05	2.28
ENSMUSG00000043832	*Clec4a3*	1.27	0.55	0.92	0.43
ENSMUSG00000043858	*Nup62*	3.37	3.69	3.19	3.4
ENSMUSG00000043866	*Taf10*	4.69	4.58	4.36	4.32
ENSMUSG00000043872	*Zmym1*	1	0.05	0.7	0.63
ENSMUSG00000043881	*Kbtbd7*	2.81	1.9	2.42	2.04
ENSMUSG00000043885	*Slc36a4*	1.39	0.92	0.63	1.1
ENSMUSG00000043895	*Edg5*	0.98	1.4	1.45	1.37
ENSMUSG00000043909	*Trp53bp1*	2.14	2.06	1.87	1.65
ENSMUSG00000043923	*Ccdc84*	3.18	3.07	2.99	3.08
ENSMUSG00000043940	*mKIAA0993*	2.03	2.14	2.24	2.02
ENSMUSG00000043962	*Thrap3*	2.73	2.35	2.8	2.21
ENSMUSG00000043964	*Orai3*	3.73	3.93	3.62	3.63
ENSMUSG00000043987	*Cep164*	0.89	1.74	1.87	1.93
ENSMUSG00000043991	*Pura*	2.94	3.76	3.23	2.82
ENSMUSG00000043998	*NA*	5.42	5.35	5.2	5.1
ENSMUSG00000044005	*Gls2*	8.15	7.89	8.13	7.48
ENSMUSG00000044018	*Mrpl50*	5.88	5.18	5.6	5.17
ENSMUSG00000044026	*Tmem20*	4.72	3.55	4.44	4.01
ENSMUSG00000044030	*Irf2bp1*	2.93	3.94	3.41	3.45
ENSMUSG00000044037	*Als2cl*	2.8	2.86	2.87	2.44

ENSMUSG00000044066	*Cep68*	2.4	2.62	2.49	2.23
ENSMUSG00000044068	*Zrsr1*	3.2	2.52	2.92	2.92
ENSMUSG00000044071	*AI851790*	1.66	-0.73	0.6	-1.36
ENSMUSG00000044080	*S100a1*	7.03	7.08	7.47	7.34
ENSMUSG00000044098	*Rsbn1*	1.67	0.63	0.96	0.45
ENSMUSG00000044134	*A230106M15R*	2.54	3.21	3.06	2.24
ENSMUSG00000044139	*BC039632*	1.91	2.14	2.25	2.12
ENSMUSG00000044145	*NA*	-0.7	0.09	1.1	1.43
ENSMUSG00000044147	*Arf6*	5.04	5.01	4.83	4.72
ENSMUSG00000044148	*1810030O07Ri*	2.63	2.32	2.31	1.52
ENSMUSG00000044149	*Nkrf*	1.88	0.99	1.19	0.84
ENSMUSG00000044155	*Lsm8*	2.54	2.11	2.47	2.55
ENSMUSG00000044167	*Foxo1*	4.24	4.5	4.9	4.87
ENSMUSG00000044197	*Gpr146*	4.09	4.47	4.9	4.61
ENSMUSG00000044206	*Vsig4*	4.92	4.09	4.27	3.54
ENSMUSG00000044211	*NA*	3.05	2.36	3.01	3.86
ENSMUSG00000044221	*Grsf1*	6	5.29	5.91	5.53
ENSMUSG00000044224	*NA*	2.19	2.82	2.32	2.21
ENSMUSG00000044252	*Osbpl1a*	5.87	4.54	5.29	5.19
ENSMUSG00000044254	*Pcsk9*	2.82	4.16	2.54	3.61
ENSMUSG00000044258	*Ctla2a*	1.72	0.86	2.63	1.8
ENSMUSG00000044279	*Crb3*	3.42	4.01	3.84	3.39
ENSMUSG00000044308	*Zfp650*	4.97	4.16	4.35	4.08
ENSMUSG00000044328	*Trp53i13*	1.79	2.71	1.86	1.46
ENSMUSG00000044330	*NA*	0.21	-0.44	1.51	1
ENSMUSG00000044339	*Alkbh2*	1.44	1.83	1.87	1.53
ENSMUSG00000044340	*NA*	2.83	2.85	3.18	2.97
ENSMUSG00000044345	*NA*	3.53	3.76	4.23	4.21
ENSMUSG00000044350	*9030625A04Ri*	3.08	2.85	2.29	2.28
ENSMUSG00000044359	*P2ry4*	2.75	1.89	3.01	2.46
ENSMUSG00000044361	*Eppk1*	1.28	1.83	2.33	1.71

ENSMUSG00000044393	*Dsg2*	3.38	3.83	3.29	2.94
ENSMUSG00000044408	*1110002B05Ri*	5.36	4.57	5.14	4.45
ENSMUSG00000044424	*NA*	3.87	3.39	3.74	3.79
ENSMUSG00000044433	*2310057J16Ri*	2.31	3.24	2.74	2.72
ENSMUSG00000044434	*NA*	1.38	0.59	1.37	2.46
ENSMUSG00000044442	*N6amt1*	1.24	0.94	1.06	0.47
ENSMUSG00000044447	*Dock5*	1.42	1.22	2.03	1.65
ENSMUSG00000044452	*NA*	1.99	1.77	1.93	1.75
ENSMUSG00000044456	*Rin3*	3.49	4.19	4.11	4.01
ENSMUSG00000044465	*4632419K20Ri*	1.83	2.79	2.24	1.98
ENSMUSG00000044468	*NA*	2.31	3.05	2.66	2.71
ENSMUSG00000044469	*Tnfaip8l1*	4.58	5.37	4.71	4.43
ENSMUSG00000044475	*Ascc1*	4.13	3.61	3.78	3.8
ENSMUSG00000044477	*Zfand3*	5.03	5.24	5.22	5.12
ENSMUSG00000044496	*2510039O18Ri*	4.04	4.77	4.2	4.02
ENSMUSG00000044501	*Zfp758*	1.66	-0.37	0.79	0.5
ENSMUSG00000044502	*2310022M17R*	3.36	3.67	3.53	3.14
ENSMUSG00000044533	*Rps2*	2.96	3.59	3.48	3.4
ENSMUSG00000044534	*Ccbp2*	1.09	1.46	1.04	0.49
ENSMUSG00000044600	*9130011J15Ri*	5.53	5.55	5.7	5.59
ENSMUSG00000044617	*Zbtb39*	1.81	2.1	1.65	1.54
ENSMUSG00000044627	*2900010J23Ri*	6.84	6.13	6.39	5.89
ENSMUSG00000044641	*Pard6b*	2	2.16	1.94	1.72
ENSMUSG00000044661	*NA*	4.76	4.15	4.43	4.22
ENSMUSG00000044674	*Fzd1*	2.12	2.1	2.18	1.53
ENSMUSG00000044676	*Zfp612*	1	0.42	1.3	1.15
ENSMUSG00000044700	*D4Ertd429e*	2.24	3.05	2.77	2.46
ENSMUSG00000044709	*Gemin7*	3.58	4.02	3.89	3.59
ENSMUSG00000044712	*NA*	1.24	0.3	0.44	-0.13
ENSMUSG00000044715	*4933433P14Ri*	3.05	2.32	3.28	2.76
ENSMUSG00000044730	*9930104L06Ri*	0.89	1.61	1.08	0.35

ENSMUSG00000044734	*Serpinb1a*	3.73	2.11	2.78	1.26
ENSMUSG00000044749	*Abca6*	6.09	5.46	6.18	5.5
ENSMUSG00000044751	*NA*	2.18	2.11	2.4	3.01
ENSMUSG00000044763	*Rg9mtd1*	4.18	3.22	3.84	3.26
ENSMUSG00000044768	*D1Ertd622e*	3.68	2.82	3.21	2.79
ENSMUSG00000044783	*6430706D22Ri*	3.44	2.82	3.45	2.97
ENSMUSG00000044786	*Zfp36*	5.51	6.02	6.04	5.93
ENSMUSG00000044788	*Fads6*	3.61	4.22	3.93	4.01
ENSMUSG00000044791	*Setd2*	3.59	3.03	3.31	3.03
ENSMUSG00000044792	*Isca1*	4.24	3.83	4.25	3.97
ENSMUSG00000044795	*Cyb5d1*	1.6	1.67	1.4	1.34
ENSMUSG00000044811	*Cd300d*	1.36	1.19	1.44	1.37
ENSMUSG00000044813	*NA*	4.06	4.96	4.13	4.49
ENSMUSG00000044820	*AY074887*	0.13	2.22	1.63	1.4
ENSMUSG00000044857	*Lemd2*	3.3	4.2	3.89	3.71
ENSMUSG00000044864	*Ankrd50*	1.43	1.07	1.12	0.86
ENSMUSG00000044867	*Gimap1*	0.26	0.92	1.38	-0.16
ENSMUSG00000044873	*NA*	0.88	-1.72	1.1	0.65
ENSMUSG00000044876	*Zfp444*	2.92	3.54	3.38	3.18
ENSMUSG00000044881	*AK171117*	2.42	2.75	2.52	2.32
ENSMUSG00000044894	*Uqcrq*	6.22	6.34	6.52	6.51
ENSMUSG00000044934	*Zfp367*	1.43	0.95	1.54	0.9
ENSMUSG00000044950	*NA*	1.46	0.9	0.91	1.2
ENSMUSG00000044952	*Kctd21*	2.54	2.68	2.27	2.75
ENSMUSG00000044965	*NA*	4.95	5.16	5.07	5.19
ENSMUSG00000044976	*Wdr72*	1.68	2.26	1.02	0.99
ENSMUSG00000044986	*Tst*	7.85	8.55	7.95	7.54
ENSMUSG00000044991	*NA*	2.06	2.02	3.01	2.16
ENSMUSG00000045038	*Prkce*	1.79	2.22	1.22	1.74
ENSMUSG00000045039	*NA*	0.8	1.77	1.45	1.22
ENSMUSG00000045078	*Rnf216*	3.18	3.14	3.16	3.05

ENSMUSG00000045087	*Edg8*	0.87	0.98	1.87	1.29
ENSMUSG00000045092	*Edg1*	5.06	5.25	4.72	4.56
ENSMUSG00000045094	*4933429F08Ri*	3.39	3.27	2.74	2.47
ENSMUSG00000045095	*Magi1*	2.41	2.68	2.05	2.23
ENSMUSG00000045098	*Suv420h1*	2.4	1.9	2.18	1.99
ENSMUSG00000045100	*Slc25a26*	2.72	2.77	2.69	2.62
ENSMUSG00000045103	*dystrophin*	1.77	0.48	1.85	1.41
ENSMUSG00000045107	*NA*	2.3	2.41	2.2	2.57
ENSMUSG00000045110	*NA*	3.94	3.39	3.75	3.28
ENSMUSG00000045128	*Rpl18a*	1.33	2.46	2.32	2.56
ENSMUSG00000045140	*Pigw*	1.44	0.24	1.24	0.67
ENSMUSG00000045160	*Bola3*	5.33	4.42	5.23	4.79
ENSMUSG00000045176	*2310047M10R*	2.45	2.32	2.38	2.22
ENSMUSG00000045180	*Shroom2*	2.97	2.84	2.13	2.23
ENSMUSG00000045193	*Cirbp*	1.78	1.63	2.23	1.71
ENSMUSG00000045205	*Dpy19l4*	2.37	1.57	1.88	0.99
ENSMUSG00000045210	*AK031819*	3.8	2.8	3.05	2.92
ENSMUSG00000045211	*Nudt18*	1.99	2.65	2.06	2.46
ENSMUSG00000045216	*Hs6st1*	6.09	6.38	6.36	6.37
ENSMUSG00000045237	*1110012L19Ri*	2.98	2.81	3.68	3.88
ENSMUSG00000045248	*Med26*	1.47	1.98	1.56	1.53
ENSMUSG00000045251	*Zfp688*	1.04	1.7	1.08	1.21
ENSMUSG00000045252	*Zfp574*	2.93	3.89	3.28	3.41
ENSMUSG00000045257	*Morn2*	3.75	3.15	3.97	4.06
ENSMUSG00000045259	*Klhdc9*	2.09	1.52	2.1	1.45
ENSMUSG00000045268	*Zfp691*	2.45	2.15	2.44	2.11
ENSMUSG00000045282	*Tmem86b*	6.68	6.92	7.03	6.65
ENSMUSG00000045287	*Rtn4rl1*	2.36	3.93	3.33	3.22
ENSMUSG00000045294	*Insig1*	5.71	5.73	5.65	5.51
ENSMUSG00000045302	*Preb*	5.41	6.27	5.51	5.69
ENSMUSG00000045312	*Lhfpl2*	1.27	1.72	1.28	0.95

ENSMUSG00000045314	*Ankrd56*	2.01	2.91	1.54	1.29
ENSMUSG00000045316	*Fahd1*	4.59	5.08	5.04	4.82
ENSMUSG00000045319	*5430407P10Ri*	3.21	3.85	3.21	3.08
ENSMUSG00000045359	*NA*	1.69	2.04	1.15	-0.34
ENSMUSG00000045365	*NA*	2.58	3.35	2.42	2.93
ENSMUSG00000045374	*NA*	3.35	3.79	3.89	3.3
ENSMUSG00000045377	*Tmem88*	1.92	2.52	1.71	2.22
ENSMUSG00000045382	*Cxcr4*	-1.72	-0.86	2.05	0.07
ENSMUSG00000045391	*NA*	1.65	-0.7	0.99	1.32
ENSMUSG00000045392	*Olfr1033*	2.22	0.71	1.15	0.72
ENSMUSG00000045406	*NA*	1.89	2.64	1.95	2.37
ENSMUSG00000045409	*Trim39*	1.89	2.21	1.78	2.08
ENSMUSG00000045410	*Akr1e1*	5.04	4.77	4.8	4.33
ENSMUSG00000045414	*1190002N15Ri*	3.64	2.85	3.56	3.12
ENSMUSG00000045427	*Hnrph2*	2.97	2.6	2.88	2.55
ENSMUSG00000045435	*Tmem60*	4.11	2.75	3.95	3.36
ENSMUSG00000045438	*Cox19*	4.85	4.78	5.08	4.83
ENSMUSG00000045441	*Gprin3*	2.94	2.02	2.56	2.05
ENSMUSG00000045472	*NA*	3.24	4.17	3.51	3.55
ENSMUSG00000045482	*Trrap*	1.78	2.16	2	1.62
ENSMUSG00000045503	*Sys1*	4.43	4.95	4.44	4.36
ENSMUSG00000045538	*Ddx28*	3.19	3.38	2.95	2.9
ENSMUSG00000045546	*Rnf113a2*	2.57	2.42	2.83	2.84
ENSMUSG00000045551	*Fpr1*	1.99	1.58	1.31	1.09
ENSMUSG00000045576	*St7l*	3.61	3.03	3.2	3.21
ENSMUSG00000045594	*Glb1*	1.86	1.47	2.05	1.54
ENSMUSG00000045598	*Zfp553*	1.78	2.22	1.97	2.04
ENSMUSG00000045624	*Esf1*	3.54	2.82	2.75	2.28
ENSMUSG00000045636	*Mtus1*	5.68	5.43	5.47	5.17
ENSMUSG00000045639	*mKIAA0326*	1.8	2.03	2.15	1.73
ENSMUSG00000045658	*5033414K04Ri*	6.21	5.87	6.02	5.51

ENSMUSG00000045659	*Plekha7*	0.35	1.23	1.03	0.64
ENSMUSG00000045664	*Cdc42ep2*	1.28	1.79	0.53	0.75
ENSMUSG00000045665	*D15Mgi27*	3.59	4.63	4.26	4.08
ENSMUSG00000045671	*Spred-2*	1.64	1.89	1.54	1.11
ENSMUSG00000045680	*Tcf21*	1.54	2.32	2.1	1.59
ENSMUSG00000045690	*NA*	1.62	2.3	2.09	2.65
ENSMUSG00000045691	*Thtpa*	3.7	3.98	3.81	3.61
ENSMUSG00000045730	*Adrb2*	0.74	-0.56	1.02	-0.8
ENSMUSG00000045744	*9930021D14Ri*	1.52	2.34	2.07	2
ENSMUSG00000045752	*Tssc4*	2.73	3.73	3.29	3.2
ENSMUSG00000045767	*B230219D22R*	4.07	3.63	3.9	3.62
ENSMUSG00000045775	*Slc16a5*	3.88	4.02	4.06	3.76
ENSMUSG00000045776	*Lrtm1*	3.6	1.75	3.24	1.39
ENSMUSG00000045795	*Whdc1*	3.64	4.46	4.27	4
ENSMUSG00000045817	*Zfp36l2*	4.23	3.91	4.14	3.8
ENSMUSG00000045826	*Ptprcap*	-0.91	-0.62	1.65	-0.91
ENSMUSG00000045827	*Serpinb9*	2.42	1.86	1.51	0.67
ENSMUSG00000045854	*Lyrm2*	3.7	2.53	3.95	3.4
ENSMUSG00000045867	*Cradd*	3.77	4.15	3.85	3.91
ENSMUSG00000045875	*Adra1a*	0.61	-0.1	1.46	1.03
ENSMUSG00000045886	*NA*	2.69	1.57	2.95	3.78
ENSMUSG00000045896	*Paip2b*	3.71	3.45	3.32	2.89
ENSMUSG00000045917	*6330416G13Ri*	1.22	1.16	1.01	0.68
ENSMUSG00000045930	*Clec14a*	3.18	3.62	3.27	2.95
ENSMUSG00000045932	*Ifit2*	1.28	0.04	-0.54	0.02
ENSMUSG00000045934	*Mtmr11*	1.96	1.45	1.95	0.87
ENSMUSG00000045948	*Mrps12*	4.61	4.74	4.5	4.75
ENSMUSG00000045954	*Sdpr*	3.6	3.14	2.85	2.79
ENSMUSG00000045962	*Wnk1*	4.25	3.93	4.1	3.8
ENSMUSG00000045969	*Ing1*	3.1	3.43	2.85	2.43
ENSMUSG00000045973	*Mcart1*	4.34	3.79	4.02	4.38

ENSMUSG00000045975	*5830404H04Ri*	5.91	5.71	5.64	5.41
ENSMUSG00000045980	*Tmem104*	2.21	3.02	2.66	2.55
ENSMUSG00000045983	*Eif4g1*	6.51	6.88	6.62	6.56
ENSMUSG00000045991	*Onecut2*	4.51	3.62	4.1	3.62
ENSMUSG00000045996	*Polr2k*	1.31	-0.87	1.61	1.04
ENSMUSG00000045999	*NA*	6.71	7.45	7.25	7.01
ENSMUSG00000046010	*Ccdc16*	2.93	2.19	2.71	2.24
ENSMUSG00000046020	*Pofut1*	2.26	2.34	1.82	1.59
ENSMUSG00000046027	*Stard5*	4.74	4.91	5.24	4.86
ENSMUSG00000046032	*Snx12*	3.89	3.19	3.3	3.08
ENSMUSG00000046034	*BC087945*	5.16	5.18	5.09	4.83
ENSMUSG00000046062	*Ppp1r15b*	5.12	4.9	5.27	5.17
ENSMUSG00000046070	*Igfals*	6.33	6.86	5.73	5.97
ENSMUSG00000046079	*Lrrc8d*	3.97	3.45	3.81	3.28
ENSMUSG00000046085	*NA*	0.52	1.56	1.36	1.48
ENSMUSG00000046096	*NA*	2.72	1.81	1.77	1.93
ENSMUSG00000046110	*LOC574418*	3	2.95	2.96	2.63
ENSMUSG00000046138	*9930021J03Ri*	3.13	3.05	3.04	3.1
ENSMUSG00000046139	*AV312086*	3.44	3.29	3.29	3.08
ENSMUSG00000046153	*NA*	3.25	1.88	2.45	3.59
ENSMUSG00000046179	*E2f8*	2.21	2.06	1.49	1.44
ENSMUSG00000046185	*Zfp84*	1.66	1.29	1.41	1.49
ENSMUSG00000046201	*NA*	3.29	2.15	2.77	2.51
ENSMUSG00000046229	*Scand1*	4.41	5.96	5.88	5.56
ENSMUSG00000046230	*Vps13a*	1.44	0.29	1.29	0.65
ENSMUSG00000046280	*She*	1.25	0.92	0.12	0.63
ENSMUSG00000046311	*Zfp62*	2.53	1.94	2.28	1.79
ENSMUSG00000046312	*AI464131*	4.32	4.69	4.54	4.55
ENSMUSG00000046314	*Stxbp6*	2.32	1.15	1.85	1.74
ENSMUSG00000046318	*mKIAA1983*	1.06	0.24	0.84	0.59
ENSMUSG00000046324	*Ermp1*	3.06	2.78	3.11	2.51

ENSMUSG00000046329	*Slc25a23*	7.42	7.48	7.41	7.44
ENSMUSG00000046330	*Rpl37a*	2.81	2.11	2.17	2.16
ENSMUSG00000046334	*NA*	1.53	-1.46	0.61	1.24
ENSMUSG00000046351	*Zfp322a*	2.39	1.51	1.95	1.39
ENSMUSG00000046352	*Gjb2*	7.28	7.3	7.6	7.57
ENSMUSG00000046364	*Rpl27a*	2.46	2.87	2.28	1.24
ENSMUSG00000046379	*NA*	2.6	1.1	3.39	2.06
ENSMUSG00000046402	*Rbp1*	4.18	4.96	4.35	4.92
ENSMUSG00000046404	*Yod1*	2.95	1.32	2.35	2.39
ENSMUSG00000046441	*BC025546*	1.19	-0.13	0.95	0.47
ENSMUSG00000046447	*Camk2n1*	5.9	5.35	5.95	5.55
ENSMUSG00000046470	*Sox18*	1.74	3.1	1.39	1.46
ENSMUSG00000046516	*Cox17*	2.51	2.53	2.84	2.71
ENSMUSG00000046519	*Golph3l*	2.57	1.81	1.83	1.54
ENSMUSG00000046532	*Ar*	1.45	0.42	1.22	0.52
ENSMUSG00000046546	*BC022623*	1.16	1.81	1.38	1.26
ENSMUSG00000046556	*Zfp319*	1.39	1.71	1.73	1.56
ENSMUSG00000046562	*Unc119b*	3.69	4.36	3.7	3.71
ENSMUSG00000046567	*4930430F08Ri*	2.81	1.19	2.52	1.77
ENSMUSG00000046573	*Lyrm4*	4.28	3.84	4.27	3.57
ENSMUSG00000046574	*mKIAA1205*	1.14	2.23	1.85	1.65
ENSMUSG00000046598	*Bdh1*	6.98	7.22	6.9	6.8
ENSMUSG00000046603	*D9Ertd402e*	3.33	2.81	2.96	2.55
ENSMUSG00000046605	*B3gntl1*	1.11	1.56	1.08	0.76
ENSMUSG00000046635	*NA*	2.92	3.44	3.88	3.22
ENSMUSG00000046667	*Rbm12b*	1.58	0.64	1.99	1.29
ENSMUSG00000046668	*Cxxc5*	5.02	5.44	5	4.62
ENSMUSG00000046671	*2410166I05Rik*	5.36	5.82	5.57	5.19
ENSMUSG00000046675	*D230037D09R*	1.67	1.17	1.45	1.32
ENSMUSG00000046679	*C87436*	2.82	2.7	2.57	2.64
ENSMUSG00000046687	*NA*	7.06	6.8	7.43	7.66

ENSMUSG00000046688	*T2bp*	2.28	1.01	3.08	2.01
ENSMUSG00000046691	*5830457O10Ri*	4.76	4.43	4.54	4.58
ENSMUSG00000046706	*NA*	0.66	0.37	1.1	2.09
ENSMUSG00000046707	*Csnk2a2*	4.1	3.68	4	3.77
ENSMUSG00000046718	*Bst2*	7.13	6.94	7.15	7.34
ENSMUSG00000046721	*NA*	0.46	0.79	1.54	0.65
ENSMUSG00000046722	*Cdc42se1*	3.24	3.45	3.49	3.57
ENSMUSG00000046727	*0610010O12Ri*	2.64	2.66	3.01	2.7
ENSMUSG00000046753	*Ccdc66*	1.39	1.36	1.33	0.91
ENSMUSG00000046756	*Mrps7*	5.08	5.41	5.18	5.24
ENSMUSG00000046761	*AA409316*	2.19	2.64	2.51	2.2
ENSMUSG00000046785	*Epm2aip1*	2.18	1.41	1.89	1.1
ENSMUSG00000046791	*2410016O06Ri*	2.04	2.16	1.89	1.93
ENSMUSG00000046792	*Zfp787*	3.13	3.74	3.28	3.41
ENSMUSG00000046794	*Ppp1r3b*	7	7.03	6.74	6.85
ENSMUSG00000046798	*Cldn12*	5.24	4.36	4.89	4.41
ENSMUSG00000046805	*Mpeg1*	4.27	3.16	3.39	3.29
ENSMUSG00000046806	*3110062M04Ri*	2.85	2.8	2.87	2.54
ENSMUSG00000046808	*Atp10d*	1.95	0.59	1.82	0.58
ENSMUSG00000046811	*C730027E14Ri*	5.64	6.5	6.1	6.02
ENSMUSG00000046814	*Gchfr*	6.74	7.45	7.39	7.71
ENSMUSG00000046822	*Slc39a3*	2.2	2.81	2.19	2.05
ENSMUSG00000046840	*NA*	1.88	2.02	2.33	2.42
ENSMUSG00000046841	*Ckap4*	1.24	0.98	0.9	0.51
ENSMUSG00000046861	*Hectd3*	4.17	4.39	4.56	4.13
ENSMUSG00000046862	*4732496O08Ri*	1.76	1.68	1.27	1.12
ENSMUSG00000046865	*Fbl*	1.01	1.36	1.6	1.86
ENSMUSG00000046873	*Mbtps2*	1.22	0.71	1.02	0.41
ENSMUSG00000046879	*Irgm*	5.48	4.87	4.74	4.89
ENSMUSG00000046897	*Znf740*	3.01	2.87	2.93	2.6
ENSMUSG00000046909	*1110002N22Ril*	3.49	3.34	3.1	2.64

ENSMUSG00000046916	*Myct1*	1.52	0.81	1.12	1.05
ENSMUSG00000046947	*Adck2*	3.05	3.17	3.09	2.93
ENSMUSG00000046949	*Nqo2*	6.45	5.9	6.45	6.02
ENSMUSG00000046959	*Slc26a1*	6.66	6.87	6.93	6.76
ENSMUSG00000046962	*Zfp295*	1.54	1.55	1.35	1.17
ENSMUSG00000046982	*Tshz1*	3.14	2.87	3.24	2.84
ENSMUSG00000046985	*Tapt1*	4.88	4.31	4.87	4.57
ENSMUSG00000047030	*Spata2*	2.13	2.75	2.16	2.68
ENSMUSG00000047036	*Zfp445*	3.49	2.99	3.04	2.72
ENSMUSG00000047037	*Nipa1*	1.64	0.93	0.51	0.19
ENSMUSG00000047044	*D030056L22Ri*	2.05	1.18	2.35	1.29
ENSMUSG00000047045	*Tmem164*	1.5	1.67	1.21	1.1
ENSMUSG00000047067	*Dusp28*	2.55	2.99	2.88	2.52
ENSMUSG00000047084	*fi58gm*	4.46	4.2	4.32	4.2
ENSMUSG00000047090	*1110012D08Ri*	4.37	3.87	4.04	3.66
ENSMUSG00000047098	*Rnf31*	2.77	3.09	2.39	2.43
ENSMUSG00000047109	*Cldn14*	2.42	3.67	1.99	3.05
ENSMUSG00000047112	*NA*	4.42	5.42	5.16	4.94
ENSMUSG00000047123	*Ticam1*	3.64	4.09	3.63	3.26
ENSMUSG00000047126	*Cltc*	5.88	5.59	5.67	5.3
ENSMUSG00000047139	*Cd24a*	0.11	-0.48	2.67	0.97
ENSMUSG00000047141	*Zfp654*	3.48	1.9	2.8	1.89
ENSMUSG00000047150	*1700001C19Ri*	1.96	2.24	2.3	2.31
ENSMUSG00000047153	*9130227C08Ri*	3.18	3.58	3.03	2.57
ENSMUSG00000047166	*Tigd5*	0.68	1.87	1.53	1.24
ENSMUSG00000047180	*Lincr*	1.11	1.28	1.06	0.5
ENSMUSG00000047187	*Rab2*	6.04	5.35	5.63	5.29
ENSMUSG00000047213	*Ythdf3*	5.04	3.78	4.57	4.12
ENSMUSG00000047221	*AI847670*	2.07	1.83	2.06	1.51
ENSMUSG00000047228	*BC048546*	0.79	-1.87	1.32	-1.21
ENSMUSG00000047230	*Cldn2*	4.28	4.96	4.32	4.62

ENSMUSG00000047238	*Mageh1*	0.47	1.11	1.45	1.37
ENSMUSG00000047248	*AU020772*	1.93	1.69	1.95	1.75
ENSMUSG00000047250	*Ptgs1*	3.09	2.32	2.4	1.99
ENSMUSG00000047260	*Tmem93*	5.54	6.06	6.13	5.99
ENSMUSG00000047264	*Zfp358*	3.11	3.9	3.22	3.3
ENSMUSG00000047284	*0610025P10Ri*	2.49	2.73	2.45	2.15
ENSMUSG00000047308	*NA*	0.49	1.79	1.35	1.61
ENSMUSG00000047368	*5730446C15Ri*	3.84	2.68	3.14	2.87
ENSMUSG00000047371	*Zfp768*	3.82	3.81	3.64	3.62
ENSMUSG00000047379	*B3gnt1*	3.65	4.04	3.74	3.71
ENSMUSG00000047388	*BC060631*	2.14	2.38	2.24	1.81
ENSMUSG00000047394	*2010001J22Ri*	1.89	2.87	2.31	1.43
ENSMUSG00000047407	*Tgif1*	2.9	3.21	3.09	2.49
ENSMUSG00000047409	*Ctdspl*	1.22	1.54	1.28	1.04
ENSMUSG00000047412	*Zbtb44*	3.85	2.94	3.56	3.26
ENSMUSG00000047417	*Rexo1*	2.7	3.48	2.96	2.75
ENSMUSG00000047423	*AI837181*	4.1	4.75	4.31	3.92
ENSMUSG00000047446	*Arl4a*	5.08	4.58	4.38	3.76
ENSMUSG00000047454	*Gphn*	5.44	5.38	5.61	5.25
ENSMUSG00000047459	*Dynlrb1*	6.88	6.85	7.21	7.17
ENSMUSG00000047466	*8030462N17Ri*	1.78	1.61	1.49	1.74
ENSMUSG00000047492	*Inhbe*	4.97	5.1	4.62	4.48
ENSMUSG00000047496	*Rnf152*	1.48	0.43	1.47	0.87
ENSMUSG00000047514	*Tspyl1*	4.44	4.02	3.81	3.54
ENSMUSG00000047517	*Dmbt1*	2.2	0.33	-0.62	0.62
ENSMUSG00000047539	*Fbxo28*	2.07	1.73	1.87	1.68
ENSMUSG00000047547	*Cltb*	4.83	5.28	4.87	4.81
ENSMUSG00000047554	*Tmem41b*	1.73	0.9	1.46	0.87
ENSMUSG00000047603	*Zfp235*	0.86	0.48	1.02	0.61
ENSMUSG00000047613	*A430005L14Ri*	4.21	4.43	4.47	4.23
ENSMUSG00000047617	*BC029214*	4.06	4.47	3.81	3.83

ENSMUSG00000047631	*Apof*	8.25	8.28	8.32	8.4
ENSMUSG00000047635	*2810006K23Ri*	2.58	2.46	2.55	2.24
ENSMUSG00000047638	*Nr1h4*	6.24	5.64	6.19	6
ENSMUSG00000047648	*Fbxo30*	2.68	1.98	2.29	1.83
ENSMUSG00000047649	*Cd3eap*	1.81	2.98	1.76	2.23
ENSMUSG00000047656	*Trpt1*	0.99	1.66	1.28	1.16
ENSMUSG00000047675	*LOC10004218*	5.33	4.99	4.96	4.56
ENSMUSG00000047694	*Yipf6*	3.94	2.68	3.52	2.83
ENSMUSG00000047710	*D8Ertd457e*	2.03	1.94	1.92	1.53
ENSMUSG00000047714	*Ppp1r2*	2.04	1.36	1.77	1.47
ENSMUSG00000047719	*Ubiad1*	4.02	4.26	3.89	3.74
ENSMUSG00000047721	*Bola2*	3.58	4.52	4.12	4.46
ENSMUSG00000047728	*NA*	7.21	6.9	6.83	6.57
ENSMUSG00000047731	*D19Wsu162e*	7.41	7.53	7.3	7.04
ENSMUSG00000047735	*NA*	2.43	1.09	1.63	1.04
ENSMUSG00000047777	*Phf13*	1.19	1.9	1.66	1.47
ENSMUSG00000047789	*9130023D20Ri*	1.53	1.12	1.52	1.33
ENSMUSG00000047793	*Sned1*	0.94	1.02	1.13	0.91
ENSMUSG00000047797	*Gjb1*	8.72	9.38	8.71	8.72
ENSMUSG00000047804	*Akap10*	1.63	1.43	1.64	1.27
ENSMUSG00000047822	*EG624219*	4.2	6.17	4.3	4.54
ENSMUSG00000047824	*Pygo2*	2.76	3.42	2.98	2.84
ENSMUSG00000047832	*Cdca4*	1.7	1.44	1.3	1.55
ENSMUSG00000047843	*Bri3*	3.28	4.12	4.02	3.81
ENSMUSG00000047866	*Lonp2*	7.02	6.84	6.89	6.52
ENSMUSG00000047867	*Gimap6*	1.83	1.82	1.88	1.53
ENSMUSG00000047879	*Usp14*	4.67	3.35	3.84	3.18
ENSMUSG00000047881	*Rell1*	2.45	2.37	1.91	1.79
ENSMUSG00000047888	*Tnrc6b*	2.27	1.75	2.37	1.89
ENSMUSG00000047907	*Tshz2*	2.11	1.89	1.69	1.55
ENSMUSG00000047909	*Ankrd16*	1.49	1.85	1.21	1.24

ENSMUSG00000047921	*1810044A24Ri*	2.5	2.62	2.42	2.22
ENSMUSG00000047945	*Marcksl1*	2.16	2.9	2.53	2.51
ENSMUSG00000047963	*Stbd1*	4.31	5.55	4.68	5.28
ENSMUSG00000047989	*D030070L09Ri*	2.92	3.28	3	2.79
ENSMUSG00000048000	*Tnrc15*	3.39	3.35	3.21	2.97
ENSMUSG00000048007	*Timm8a1*	1.92	1.27	2.04	1.12
ENSMUSG00000048039	*Isg20l2*	3.48	3.27	2.91	3.29
ENSMUSG00000048047	*Zbtb33*	2.9	1.9	2.19	1.79
ENSMUSG00000048058	*Ldlrad3*	2.25	2.04	2.98	2.64
ENSMUSG00000048076	*Arf1*	6.32	5.9	6.05	5.91
ENSMUSG00000048087	*NA*	2.35	1.9	1.29	2.66
ENSMUSG00000048100	*Taf13*	3.04	2.38	2.91	2.45
ENSMUSG00000048106	*NA*	1.95	1	0.96	0.89
ENSMUSG00000048109	*Rbm15*	2.58	2.24	2.24	2.3
ENSMUSG00000048118	*Arid4a*	2.68	2.36	2.5	2.29
ENSMUSG00000048120	*Entpd1*	2.18	1.95	1.4	1.23
ENSMUSG00000048149	*NA*	2.3	1.73	1.96	2.37
ENSMUSG00000048154	*NA*	1.6	2.21	1.74	1.72
ENSMUSG00000048163	*Selpl*	0.61	0.69	1.11	0.18
ENSMUSG00000048164	*NA*	1.71	1.6	2.05	2.35
ENSMUSG00000048170	*1110007A13Ri*	3.99	3.96	4.07	3.83
ENSMUSG00000048175	*Asb8*	3.81	4.46	3.97	3.87
ENSMUSG00000048186	*E130319B15Ri*	1.71	1.67	1.69	1.67
ENSMUSG00000048217	*Nags*	5.36	6.25	5.53	5.42
ENSMUSG00000048218	*Amigo2*	3.39	2.51	3.22	2.51
ENSMUSG00000048222	*Mfap1b*	1.45	0.34	1.08	0.9
ENSMUSG00000048234	*AK040602*	6.41	5.73	5.93	5.32
ENSMUSG00000048249	*A930001N09Ri*	2.83	1.45	2.26	1.66
ENSMUSG00000048264	*Dip2c*	1.68	1.24	1.76	1.46
ENSMUSG00000048271	*Prr8*	2.93	2.45	2.7	2.36
ENSMUSG00000048277	*Clast2*	5.32	6.25	5.81	5.82

ENSMUSG00000048307	*Ankrd46*	4.49	4.42	4.6	4.32
ENSMUSG00000048310	*Pskh1*	3.99	4.36	4.12	4.07
ENSMUSG00000048316	*NA*	3.77	4.42	3.67	3.76
ENSMUSG00000048332	*Lhfp*	2.06	2.2	1.87	1.87
ENSMUSG00000048351	*2010305A19Ri*	3.99	4.15	4.35	4.37
ENSMUSG00000048365	*NA*	3.15	3.31	3.17	2.9
ENSMUSG00000048371	*4833426J09Rik*	3.6	3.16	2.92	2.62
ENSMUSG00000048376	*F2r*	3.14	2.72	2.63	2.38
ENSMUSG00000048379	*Socs4*	2.76	1.77	2.28	1.93
ENSMUSG00000048429	*1810026J23Rik*	4.79	4.81	4.64	4.42
ENSMUSG00000048439	*Nupl2*	1.5	1.39	1.37	0.6
ENSMUSG00000048486	*D930001I22Ri*	4.56	4.74	4.76	4.52
ENSMUSG00000048489	*8430408G22Ri*	5.62	5.95	6.4	6.1
ENSMUSG00000048490	*Nrip1*	1.92	1.35	1.93	1.4
ENSMUSG00000048495	*1110034B05Rik*	2.37	1.34	2.11	0.89
ENSMUSG00000048498	*Cd300e*	1.36	0.19	-0.89	-0.05
ENSMUSG00000048546	*Tob2*	4.77	5.01	4.94	4.93
ENSMUSG00000048550	*Thnsl1*	0.67	0.19	1.26	0.15
ENSMUSG00000048578	*2410014A08Ri*	5.3	5.72	4.69	4.82
ENSMUSG00000048581	*E130311K13Ri*	2.3	1.76	2.11	1.74
ENSMUSG00000048647	*Exdl1*	1.49	-0.48	0.99	-1.03
ENSMUSG00000048661	*Lemd3*	1.93	1.1	1.43	1.19
ENSMUSG00000048668	*5930416I19Rik*	1.65	2.05	1.64	1.4
ENSMUSG00000048701	*NA*	2.91	3.02	3.01	2.89
ENSMUSG00000048706	*D4Bwg0951e*	5.83	5.59	5.87	5.9
ENSMUSG00000048720	*Tbc1d12*	2.34	0.81	1.75	1.1
ENSMUSG00000048731	*Ggnbp1*	1.96	2.3	2.3	2.37
ENSMUSG00000048755	*Mcat*	3.79	4.27	4.05	3.75
ENSMUSG00000048756	*Foxo3a*	3.52	3.39	3.79	3.49
ENSMUSG00000048758	*Rpl29*	-1.29	-2.65	1.88	-1.15
ENSMUSG00000048769	*H1f0*	6.03	6.83	6.7	6.6

ENSMUSG00000048772	*Tmem53*	4.17	4.79	4.21	4.36
ENSMUSG00000048782	*Insc*	2.74	3.78	2.31	2.31
ENSMUSG00000048787	*Dcun1d3*	2.9	1.79	2.05	2.07
ENSMUSG00000048796	*Cyb561d1*	1.07	1.49	0.98	0.78
ENSMUSG00000048799	*Ccdc100*	2.62	2.5	2.7	2.14
ENSMUSG00000048826	*Dact2*	2.52	3.67	2.7	2.35
ENSMUSG00000048832	*Vps37c*	2.74	3.47	2.82	2.8
ENSMUSG00000048833	*NA*	4.67	4.49	4.21	3.98
ENSMUSG00000048856	*AI132487*	8.29	8.48	8.91	8.63
ENSMUSG00000048874	*Phf3*	3.85	3.38	3.67	3.57
ENSMUSG00000048878	*Hexim1*	4.27	4.45	4.22	4.09
ENSMUSG00000048897	*Zfp710*	1.8	2.47	2.19	2.12
ENSMUSG00000048910	*NA*	1.78	2.42	2.02	1.98
ENSMUSG00000048911	*Rnf24*	1.34	0.72	1.07	0.9
ENSMUSG00000048916	*NA*	2.96	2.51	2.88	3.64
ENSMUSG00000048920	*Fkrp*	2.78	2.95	2.54	2.2
ENSMUSG00000048924	*Ccdc125*	1.66	1.46	1.31	1.13
ENSMUSG00000048930	*Tada3l*	1.6	2.56	2.22	2.06
ENSMUSG00000048949	*NA*	1.26	0.24	-0.07	0.99
ENSMUSG00000048970	*C1galt1c1*	4.45	3.31	4.3	4.1
ENSMUSG00000049037	*Clec4a1*	1.36	0.44	1.15	0.53
ENSMUSG00000049038	*Mterfd3*	1.67	-0.09	1.46	-0.21
ENSMUSG00000049044	*cAMP-GEFII*	6.22	5.83	5.31	5.32
ENSMUSG00000049076	*Centb2*	3.05	2.41	2.73	2.23
ENSMUSG00000049086	*Bmyc*	0.68	2.04	2.06	1.79
ENSMUSG00000049090	*Zadh2*	5.72	5.25	5.45	5.07
ENSMUSG00000049091	*Sephs2*	9.22	9.36	9.15	8.92
ENSMUSG00000049106	*Wdr22*	3.44	3.54	3.2	3.25
ENSMUSG00000049115	*Agtr1a*	6.75	6.34	6.44	6.01
ENSMUSG00000049124	*NA*	1.05	-0.63	2.36	2.83
ENSMUSG00000049152	*Ugt3a2*	8.12	7.66	7.73	7.48

ENSMUSG00000049164	*Zfp518*	2.01	0.47	1.09	0.35
ENSMUSG00000049232	*Tigd2*	3.24	1.89	2.8	2.08
ENSMUSG00000049246	*NA*	1.88	2.15	2.3	2.93
ENSMUSG00000049266	*NA*	3.78	2.89	3.61	2.76
ENSMUSG00000049287	*A230051G13R*	2.39	2.89	2.35	2.12
ENSMUSG00000049288	*NA*	1.32	0.65	-0.14	0.43
ENSMUSG00000049295	*Zfp219*	2.5	3.48	2.59	3
ENSMUSG00000049299	*Trappc1*	5.39	4.99	5.35	5.09
ENSMUSG00000049300	*Prmt6*	1.46	1.28	0.86	0.83
ENSMUSG00000049305	*Ccdc71*	3.36	3.98	3.25	3.22
ENSMUSG00000049313	*Sorl1*	1.23	1.61	1.77	1.17
ENSMUSG00000049321	*Zfp2*	1.32	0.89	1.06	0.87
ENSMUSG00000049323	*Smcr8*	2.81	2.65	2.55	2.37
ENSMUSG00000049327	*Setd8*	3.67	3.46	3.78	3.25
ENSMUSG00000049329	*NA*	4.15	3.25	3.73	3.85
ENSMUSG00000049339	*BC038286*	6.7	7.06	6.69	6.59
ENSMUSG00000049354	*Wdr68*	2.78	3.41	3.06	3.26
ENSMUSG00000049382	*Krt8*	4.57	5.19	4.66	4.2
ENSMUSG00000049396	*Gemin4*	1.94	2.2	2.03	1.86
ENSMUSG00000049401	*Ogfr*	4.15	4.56	4.24	4.45
ENSMUSG00000049404	*NA*	5.44	5.44	4.86	5.13
ENSMUSG00000049421	*Zfp260*	3.76	2.87	3.09	2.77
ENSMUSG00000049422	*Ndg2*	8.79	9.23	9.04	8.98
ENSMUSG00000049439	*Cyp20a1*	3.2	3.18	3.2	2.71
ENSMUSG00000049470	*Aff4*	4	3.33	3.64	3.26
ENSMUSG00000049477	*NA*	2.49	2.14	2.18	3.26
ENSMUSG00000049482	*2310061F22Ri*	1.22	2.43	1.59	1.59
ENSMUSG00000049489	*1810009O10Ri*	2.87	2.9	2.95	2.37
ENSMUSG00000049494	*NA*	2.78	1.21	1.91	2.65
ENSMUSG00000049502	*Dtx3l*	4.49	3.31	4.11	3.82
ENSMUSG00000049504	*2810046L04Ri*	1.81	1.88	1.93	1.49

ENSMUSG00000049516	*Spty2d1*	2.67	2.45	2.2	2.49
ENSMUSG00000049521	*Cdc42ep1*	3.72	5.45	4.2	4.62
ENSMUSG00000049550	*Clip50*	3.79	3.12	3.45	3.11
ENSMUSG00000049553	*Rpo1-4*	2.35	2.84	2.28	2.21
ENSMUSG00000049555	*Tmie*	3.31	3.14	3.6	2.65
ENSMUSG00000049577	*Zfpm1*	3.81	5.06	4.58	4.75
ENSMUSG00000049580	*Tsku*	4.82	5.63	4.88	5.89
ENSMUSG00000049600	*Zbtb45*	1.1	1.98	1.26	1.02
ENSMUSG00000049606	*Zfp644*	2.31	1.35	2.07	1.35
ENSMUSG00000049624	*Slc17a5*	4.03	3.44	3.79	3.47
ENSMUSG00000049630	*C1ql3*	1.63	0.34	1.32	0.49
ENSMUSG00000049643	*2310022A10Ri*	1.73	1.84	1.69	1.61
ENSMUSG00000049647	*Purb*	3.82	2.63	3.24	2.55
ENSMUSG00000049657	*Zbtb5*	1.54	1.92	1.26	1.05
ENSMUSG00000049658	*Bdp1*	2.41	1.28	1.89	1.61
ENSMUSG00000049659	*Aftph*	4.39	3.87	4.1	3.87
ENSMUSG00000049672	*Zfp161*	0.98	1.13	1	0.82
ENSMUSG00000049680	*2010005J08Ri*	2.94	3.48	2.92	2.96
ENSMUSG00000049685	*Cyp2g1*	2.16	0.71	0.06	-0.27
ENSMUSG00000049686	*Orai1*	3.58	4.52	3.98	3.97
ENSMUSG00000049717	*Lig4*	1.09	0.34	0.47	0.18
ENSMUSG00000049734	*Trex1*	2.1	2.43	2.14	2.21
ENSMUSG00000049739	*Zfp646*	1.98	2.33	1.98	2.27
ENSMUSG00000049742	*NA*	-0.94	-1.18	1.11	0.58
ENSMUSG00000049751	*Rpl36al*	4.28	4.16	4.26	4.5
ENSMUSG00000049755	*Zfp672*	2.69	2.79	2.65	2.44
ENSMUSG00000049760	*2410015M20R*	6.73	6.72	6.98	6.99
ENSMUSG00000049764	*Zfp280b*	1.4	1.63	1.4	1.41
ENSMUSG00000049775	*Tmsb4x*	6	5.61	6.04	5.47
ENSMUSG00000049791	*Fzd4*	2.76	2.42	2.79	2.27
ENSMUSG00000049792	*Bag5*	3.32	3.35	3	3.22

ENSMUSG00000049800	*Sertad2*	2.78	2.07	2.74	2.44
ENSMUSG00000049804	*NA*	1.78	0.87	0.73	0.3
ENSMUSG00000049807	*Arhgap23*	1.98	2.73	1.99	1.7
ENSMUSG00000049832	*NA*	3.75	4.01	3.81	4.57
ENSMUSG00000049858	*Suox*	7.13	6.93	7	6.48
ENSMUSG00000049878	*Rlf*	2.32	1.13	1.77	1.48
ENSMUSG00000049881	*NA*	1.72	1.65	1.67	1.94
ENSMUSG00000049882	*Gm71*	3.46	3.18	3.1	2.34
ENSMUSG00000049883	*NA*	2.9	4.11	3.82	4.19
ENSMUSG00000049922	*Slc35c1*	3.49	3.76	3.35	3.28
ENSMUSG00000049932	*H2afx*	2.76	3.09	2.79	2.83
ENSMUSG00000049940	*NA*	5.03	5.09	4.76	4.53
ENSMUSG00000049950	*Rpp38*	1.6	2.09	1.94	1.56
ENSMUSG00000049957	*Ccdc137*	1.68	2.12	1.61	1.55
ENSMUSG00000049960	*Mrps16*	4.62	5.31	5.25	5.24
ENSMUSG00000049969	*Plekhf2*	3.25	2.33	2.92	2.38
ENSMUSG00000049971	*Glt1d1*	4.18	3.64	4.05	3.72
ENSMUSG00000049988	*Lrrc25*	0.96	1.31	1.11	0.41
ENSMUSG00000049992	*NA*	0.89	0.39	1.46	0.49
ENSMUSG00000050002	*5133401N09Ri*	4.22	4	4.01	4.05
ENSMUSG00000050017	*Pitpnb*	5.77	5.43	5.41	5.19
ENSMUSG00000050029	*Rap2c*	4.43	3.55	3.87	3.3
ENSMUSG00000050043	*Txndc14*	3.53	2.95	3.38	3.04
ENSMUSG00000050052	*2610019F03Ri*	1.84	1.95	2.04	1.99
ENSMUSG00000050069	*Grem2*	1.92	1.1	2.24	2.34
ENSMUSG00000050077	*NA*	1.55	1.05	1.37	1.41
ENSMUSG00000050079	*Rspry1*	2.46	2.34	2.42	1.95
ENSMUSG00000050088	*1600012H06Ri*	4.65	3.57	4.07	3.42
ENSMUSG00000050103	*A530016O06R*	6.34	5.03	5.47	5.22
ENSMUSG00000050144	*Slc25a44*	5.88	5.98	5.66	5.47
ENSMUSG00000050148	*Ubqln2*	3.22	3.5	3.34	3.18

ENSMUSG00000050157	*Gm867*	3.82	2.73	3.02	3.49
ENSMUSG00000050174	*Nudt6*	2.56	3.23	2.87	2.88
ENSMUSG00000050188	*Lsm10*	3.9	3.87	4.06	3.6
ENSMUSG00000050199	*Lgr4*	4.48	3.88	4.32	3.99
ENSMUSG00000050213	*Snip1*	2.72	3.02	2.79	2.52
ENSMUSG00000050229	*Pigm*	1.46	1.25	1.02	0.73
ENSMUSG00000050234	*Gja4*	1.28	2.39	1.82	1.71
ENSMUSG00000050244	*Heatr1*	1.97	2.48	1.95	1.68
ENSMUSG00000050270	*A730055C05R*	3.5	3.39	3.75	3.22
ENSMUSG00000050299	*NA*	4.06	3.85	3.8	4.48
ENSMUSG00000050310	*4921505C17R*	2.07	1.27	1.85	1.24
ENSMUSG00000050312	*Nsun3*	2.87	1.84	2.53	2.08
ENSMUSG00000050323	*2310030N02R*	4.03	3.43	3.96	3.65
ENSMUSG00000050324	*NA*	2.5	2.09	2.54	1.95
ENSMUSG00000050335	*Lgals3*	2.2	2.23	2.23	2.34
ENSMUSG00000050347	*NA*	1.75	0.45	2.75	3.57
ENSMUSG00000050373	*5730407K14R*	2.84	3.16	3.31	2.72
ENSMUSG00000050390	*C77080*	4.58	5.07	5.26	5.1
ENSMUSG00000050428	*Fbxo46*	1.12	1.6	1.76	1.69
ENSMUSG00000050440	*Hamp1*	11.04	10.58	11.21	11.34
ENSMUSG00000050445	*Cyp8b1*	7.59	7.81	7.82	7.48
ENSMUSG00000050471	*Ppp4r1l*	2.07	2.18	2.06	2.32
ENSMUSG00000050493	*BC030183*	2.5	3.69	2.78	3.27
ENSMUSG00000050530	*9630050M13R*	1.24	1.58	0.91	0.58
ENSMUSG00000050541	*Adra1b*	4.39	4.73	4.14	3.83
ENSMUSG00000050549	*5730508B09R*	1.97	1.21	1.94	0.22
ENSMUSG00000050550	*NA*	3.14	2.65	1.75	2.25
ENSMUSG00000050552	*0910001L09R*	5.76	6.01	5.98	5.83
ENSMUSG00000050565	*Tor1aip2*	5	4.24	4.56	4.4
ENSMUSG00000050567	*Maml1*	2.63	2.84	2.68	2.58
ENSMUSG00000050608	*NA*	6.46	6.39	6.6	6.5

ENSMUSG00000050619	*NA*	2.27	1.67	2.08	1.64
ENSMUSG00000050627	*Gpd1l*	4.07	3.81	3.8	3.81
ENSMUSG00000050663	*Trhde*	2.08	1.16	1.87	1.52
ENSMUSG00000050668	*2310002B06Ri*	3.29	2.41	2.8	2.36
ENSMUSG00000050697	*Prkaa1*	3.07	1.81	2.58	2.22
ENSMUSG00000050705	*NA*	4.48	4.61	5.1	4.78
ENSMUSG00000050708	*Ftl1*	8.09	8.15	8.51	8.7
ENSMUSG00000050721	*Plekhq1*	1.63	2.14	1.87	1.64
ENSMUSG00000050730	*NA*	4.12	3.73	4.01	3.85
ENSMUSG00000050732	*Vamp8*	6.69	7.26	7.02	7
ENSMUSG00000050777	*Tmem37*	5.44	6.48	5.87	5.64
ENSMUSG00000050812	*AI314180*	4.69	4.37	4.58	4.36
ENSMUSG00000050846	*Zfp623*	3.31	3.17	2.98	3.26
ENSMUSG00000050854	*Tmem125*	1.91	2.19	2.13	1.74
ENSMUSG00000050856	*Atp5k*	4.91	3.67	4.41	4.64
ENSMUSG00000050860	*Phospho1*	2.93	3.63	2.26	2.82
ENSMUSG00000050890	*Pdik1l*	2.63	1.8	2.24	1.73
ENSMUSG00000050891	*Tatdn1*	2.89	1.6	2.69	1.93
ENSMUSG00000050904	*NA*	2.85	2.81	2.88	3.49
ENSMUSG00000050908	*BC068110*	1.74	2.08	1.5	1.36
ENSMUSG00000050912	*Tmem123*	4.28	3.97	4.4	3.86
ENSMUSG00000050931	*Sgms2*	3.75	3.3	3.94	3.71
ENSMUSG00000050947	*Amigo1*	1.96	2.23	2.04	2.2
ENSMUSG00000050951	*NA*	0.24	1.6	1.87	1.59
ENSMUSG00000050953	*Gja1*	1.98	1.3	1.94	1.76
ENSMUSG00000050965	*Prkca*	2.18	1.59	2.02	1.6
ENSMUSG00000050989	*Sepn1*	1.16	1.71	1.25	1.37
ENSMUSG00000051000	*9930021J17Ri*	0.74	0.84	1.79	0.62
ENSMUSG00000051007	*Pddc1*	3.97	3.61	3.9	3.58
ENSMUSG00000051041	*Olfml1*	2.88	2.24	1.88	2.33
ENSMUSG00000051043	*Gprc5c*	5.27	5.34	5.3	5.1

ENSMUSG00000051065	*1600021P15Ri*	3.92	3.18	3.79	3.01
ENSMUSG00000051076	*Vtcn1*	1.1	-1.46	0.56	-2.71
ENSMUSG00000051082	*NA*	2.46	3.31	2.88	2.77
ENSMUSG00000051098	*2900024O10Ri*	1.78	0.32	1.74	1.11
ENSMUSG00000051124	*Gimap9*	3.77	3.33	2.91	2.53
ENSMUSG00000051133	*NA*	2.73	3.58	1.96	2.81
ENSMUSG00000051147	*Nat2*	4.19	3.13	3.74	3.23
ENSMUSG00000051149	*Adnp*	4.39	3.78	4.18	3.7
ENSMUSG00000051154	*Commd3*	6.29	5.82	5.67	5.67
ENSMUSG00000051166	*Eml5*	1.27	0.22	0.86	0.63
ENSMUSG00000051169	*NA*	2.99	4.26	3.82	3.69
ENSMUSG00000051177	*Plcb1*	1.66	0.82	1.68	1.16
ENSMUSG00000051184	*Zfp524*	3.32	3.89	3.93	3.92
ENSMUSG00000051185	*Tmem157*	3	2.34	2.87	2.37
ENSMUSG00000051186	*NA*	3	3.39	3.81	3.32
ENSMUSG00000051223	*Bzw1*	5.55	5.26	5.25	4.74
ENSMUSG00000051226	*NA*	8.37	7.25	7.87	6.93
ENSMUSG00000051232	*AI316787*	3.11	2.66	3.36	2.81
ENSMUSG00000051234	*Rnf7*	3.84	2.42	3.11	2.7
ENSMUSG00000051236	*Msrb3*	2.59	2.11	2.06	2.08
ENSMUSG00000051238	*NA*	1.57	2.05	1.49	1.33
ENSMUSG00000051255	*NA*	2.47	2.59	2.01	1.57
ENSMUSG00000051256	*Jagn1*	4.64	5.06	4.61	4.66
ENSMUSG00000051285	*Pcmtd1*	5.46	4.09	5.1	4.36
ENSMUSG00000051306	*Usp42*	1.55	1.65	1.24	1.04
ENSMUSG00000051316	*Taf7*	2.71	1.84	2.37	1.85
ENSMUSG00000051319	*NA*	4.99	4.63	5.48	5.19
ENSMUSG00000051329	*Nup160*	1.13	1.07	1.38	0.84
ENSMUSG00000051339	*2900026A02Ri*	4.16	5.06	4.6	4.71
ENSMUSG00000051346	*Spryd4*	5.16	5.16	4.86	4.64
ENSMUSG00000051351	*Zfp46*	0.12	0.81	1.11	0.44

ENSMUSG00000051355	*Commd1*	5.14	4.19	4.59	4.63
ENSMUSG00000051359	*Ncald*	2.87	2.9	2.26	2.37
ENSMUSG00000051375	*Pcdh1*	4.8	5.94	5.45	5.4
ENSMUSG00000051390	*Zbtb22*	3.04	3.82	3.31	2.75
ENSMUSG00000051391	*Ywhag*	5.44	5.69	5.5	5.61
ENSMUSG00000051396	*Hspa14*	3.42	3.4	3.57	3.37
ENSMUSG00000051403	*BC024868*	4.78	5.62	5.14	5.22
ENSMUSG00000051413	*Plagl2*	1.02	1.01	0.99	0.8
ENSMUSG00000051427	*4930562D19Ri*	1.71	1.96	2.1	1.82
ENSMUSG00000051428	*NA*	1.31	1.32	1.22	1.54
ENSMUSG00000051439	*Cd14*	1.85	1.65	1.7	1.7
ENSMUSG00000051451	*BC051589*	2.55	1.74	2.2	1.67
ENSMUSG00000051452	*OTTMUSG000*	3.96	3.31	3.23	2.6
ENSMUSG00000051469	*AK088914*	3.92	2.82	2.83	2.57
ENSMUSG00000051483	*Cbr1*	6.78	6.88	6.54	6.59
ENSMUSG00000051495	*NA*	4.2	4.69	4.64	4.46
ENSMUSG00000051502	*2700038N03Ri*	0.49	1.39	1.98	2.21
ENSMUSG00000051510	*Mafg*	4.01	4.3	3.73	3.52
ENSMUSG00000051518	*Rps19bp1*	3.95	4.47	4.59	4.33
ENSMUSG00000051554	*NA*	3.78	2.51	3.17	3.1
ENSMUSG00000051557	*NA*	1.95	2.35	2.41	2.1
ENSMUSG00000051578	*Cmtm4*	3.32	3.21	2.82	2.97
ENSMUSG00000051579	*Tceal8*	5.25	4.23	4.98	4.82
ENSMUSG00000051586	*NA*	1.77	1.8	2.4	2.07
ENSMUSG00000051615	*Rap2a*	2.78	2.61	3.13	2.91
ENSMUSG00000051650	*B3gnt2*	3.44	3.15	3.53	3.17
ENSMUSG00000051652	*Lrrc3*	4.57	5.26	4.71	5.06
ENSMUSG00000051669	*AU021092*	1.06	1.08	1.33	0.53
ENSMUSG00000051671	*1810063B05Ri*	4.77	4.29	5.18	4.42
ENSMUSG00000051674	*Dcun1d4*	3.62	3.12	3.49	3.2
ENSMUSG00000051675	*Trim32*	2.25	2.2	1.96	1.71

ENSMUSG00000051682	*Treml4*	1.62	1.47	1.19	1.11
ENSMUSG00000051695	*Pcbp1*	6.29	7.05	6.43	6.49
ENSMUSG00000051705	*Senp8*	0.69	0.2	1.17	-0.26
ENSMUSG00000051716	*Apon*	7.93	8.17	8.05	7.94
ENSMUSG00000051721	*BC068281*	1.49	1.21	1.64	1.48
ENSMUSG00000051730	*Mettl5*	2.59	1.93	2.64	2.24
ENSMUSG00000051748	*1100001G20Ri*	9.68	9.41	9.95	9.57
ENSMUSG00000051761	*NA*	4.34	5.26	5.08	4.19
ENSMUSG00000051768	*Xrcc1*	2.17	2.68	2.88	2.81
ENSMUSG00000051786	*NA*	3.43	3.56	3.52	3.17
ENSMUSG00000051811	*Cox6b2*	5.06	4.81	5.27	5.16
ENSMUSG00000051839	*Gypa*	-4.19	#NAME?	1.22	-1.02
ENSMUSG00000051853	*Arf3*	4.59	5.02	4.42	4.42
ENSMUSG00000051864	*Tbc1d22a*	3.23	3.23	3.44	3.06
ENSMUSG00000051907	*NA*	0.32	0.6	1.93	0.64
ENSMUSG00000051910	*Sox6*	1.79	1.49	1.69	1.2
ENSMUSG00000051934	*Spats2*	1.52	1.13	1.48	1.31
ENSMUSG00000051977	*NA*	1.06	0.28	1.23	0.56
ENSMUSG00000051978	*Erich1*	1.05	0.95	0.82	0.63
ENSMUSG00000051984	*Sec31b*	1.29	0.9	1.49	0.87
ENSMUSG00000051989	*1190017O12Ri*	2.85	3.15	3	3
ENSMUSG00000052024	*NA*	4.98	4.22	4.52	5.39
ENSMUSG00000052033	*Pfdn4*	3.02	1.49	2.66	2.56
ENSMUSG00000052040	*Klf13*	3.51	3.91	3.67	3.28
ENSMUSG00000052056	*Zfp217*	1.13	1.49	1.28	0.93
ENSMUSG00000052085	*Dock8*	3.16	2.81	2.87	2.48
ENSMUSG00000052102	*Gnpda1*	3.38	3.52	3.51	3.59
ENSMUSG00000052117	*D630039A03R*	2.84	2.86	1.65	1.11
ENSMUSG00000052131	*Akr1b7*	0.94	0.28	1.32	-0.09
ENSMUSG00000052139	*Bre*	4.11	3.7	3.94	3.66
ENSMUSG00000052144	*Ppp4r2*	3	2.04	2.39	1.92

ENSMUSG00000052151	*Ppap2c*	3.41	4.46	3.8	3.79
ENSMUSG00000052154	*NA*	0.39	2.34	1.37	1.55
ENSMUSG00000052155	*Acvr2a*	3.66	2.55	3.2	2.72
ENSMUSG00000052160	*Pld4*	2.23	2.33	2.1	2.26
ENSMUSG00000052192	*NA*	0.59	1.04	1.01	2.03
ENSMUSG00000052214	*Opa3*	4.9	5.37	5.06	4.88
ENSMUSG00000052229	*Gpr17*	1.02	1.36	1.14	0.97
ENSMUSG00000052253	*Zfp622*	4.18	4.27	4.25	4.11
ENSMUSG00000052293	*Taf9*	3.34	3.09	3.42	2.81
ENSMUSG00000052296	*Saps1*	5.12	5.63	5.43	5.28
ENSMUSG00000052298	*Cdc42se2*	2.84	2.96	2.75	2.31
ENSMUSG00000052299	*Zfp294*	3.22	2.64	3.21	2.58
ENSMUSG00000052302	*NA*	1.03	-0.17	2.24	1.17
ENSMUSG00000052305	*NA*	5.14	6.69	7.45	7.67
ENSMUSG00000052310	*Slc39a1*	4.7	4.87	4.73	4.51
ENSMUSG00000052337	*Immt*	5.77	5.55	5.47	5.14
ENSMUSG00000052369	*AK177749*	3.9	4.17	4.04	3.64
ENSMUSG00000052384	*Lrrc33*	1.49	1.5	1.37	1.11
ENSMUSG00000052392	*Acot4*	4.95	3.98	4.17	3.94
ENSMUSG00000052395	*Rft1*	3.32	3.02	3.21	2.94
ENSMUSG00000052397	*Vil2*	1.32	1.67	1.74	1.37
ENSMUSG00000052406	*Rexo4*	2.72	3.24	2.68	2.78
ENSMUSG00000052414	*Atf7*	1.64	1.38	1.59	1.43
ENSMUSG00000052419	*NA*	4.41	4.48	4.67	4.67
ENSMUSG00000052423	*B4galt3*	2.29	2.36	2.4	2.59
ENSMUSG00000052428	*Tmco1*	6.69	6.13	6.52	5.84
ENSMUSG00000052429	*Prmt1*	2.61	3.29	3.01	3.04
ENSMUSG00000052439	*NA*	1.04	0.29	0.15	-0.66
ENSMUSG00000052446	*NA*	2.33	1.76	1.42	0.65
ENSMUSG00000052456	*Asna1*	4.9	5.62	5.16	5.01
ENSMUSG00000052459	*Atp6v1a*	4.69	4.2	4.4	3.97

ENSMUSG00000052488	*Cherp*	3.26	3.92	3.48	3.35
ENSMUSG00000052520	*Cyp2j5*	8.38	7.54	8.01	7.57
ENSMUSG00000052533	*mKIAA0169*	1.09	1.85	1.76	1.41
ENSMUSG00000052534	*Pbx1*	2.31	2.27	2.64	2.49
ENSMUSG00000052539	*Magi3*	2.89	2.94	2.93	2.6
ENSMUSG00000052562	*C730048C13R*	5.01	4.07	4.86	4.22
ENSMUSG00000052563	*NA*	0.74	2.12	1.28	0.67
ENSMUSG00000052566	*Hook2*	2.47	2.82	3.01	2.73
ENSMUSG00000052593	*Adam17*	3.7	3.27	3.35	3.01
ENSMUSG00000052595	*1810073H04Ri*	6.03	5.45	5.81	5.5
ENSMUSG00000052605	*Isoc2b*	3.84	3.66	4.28	3.99
ENSMUSG00000052609	*Plekhg3*	2.94	3.68	3.9	3.93
ENSMUSG00000052632	*Ddef2*	2.27	1.85	1.84	1.05
ENSMUSG00000052656	*Rnf103*	5.14	4.16	5.15	4.44
ENSMUSG00000052673	*NA*	-0.2	1.97	1.16	1.22
ENSMUSG00000052676	*Zmat1*	2.07	0.84	2.22	1.24
ENSMUSG00000052681	*Rap1b*	5.69	4.75	5.04	4.68
ENSMUSG00000052684	*Jun*	1.33	1.77	2.61	2.63
ENSMUSG00000052707	*Tnrc6a*	3.22	2.82	3.27	2.61
ENSMUSG00000052712	*BC004004*	6.25	6.04	5.92	5.43
ENSMUSG00000052714	*NA*	3.08	0.68	2.81	2.12
ENSMUSG00000052738	*Sucla1*	7.6	7.44	7.76	7.26
ENSMUSG00000052747	*NA*	5.31	5.09	5.19	4.89
ENSMUSG00000052748	*1200016B10Ri*	3.36	2.46	3.05	2.81
ENSMUSG00000052751	*Repin1*	4.48	5.11	4.35	4.19
ENSMUSG00000052752	*Traf7*	2.21	2.71	2.24	2.08
ENSMUSG00000052757	*NA*	5.01	2.67	4.02	3.23
ENSMUSG00000052763	*Zfp212*	2.08	2.34	2.1	1.42
ENSMUSG00000052794	*1700030K09Ri*	1.01	1.49	1.03	0.46
ENSMUSG00000052800	*NA*	3.07	3.7	3.9	4.05
ENSMUSG00000052825	*NA*	4.43	3.54	3.63	4.05

ENSMUSG00000052833	*Sae1*	5.22	5.32	5.35	5.5
ENSMUSG00000052837	*Junb*	2.26	3.74	3.31	2.86
ENSMUSG00000052894	*NA*	3.71	3.17	3.18	4.2
ENSMUSG00000052906	*Ubxd6*	4.45	4.26	4.32	4.07
ENSMUSG00000052914	*Cyp2j6*	5.83	4.59	5.34	4.74
ENSMUSG00000052915	*4121402D02Ri*	3.95	3.92	3.68	3.63
ENSMUSG00000052917	*Senp7*	1.01	0.41	0.75	0.23
ENSMUSG00000052926	*Rnaseh2a*	3	2.97	3.35	3.15
ENSMUSG00000052928	*Gm672*	3.03	3.54	2.85	3.01
ENSMUSG00000052934	*NA*	5.8	5.01	5.96	5.34
ENSMUSG00000052957	*Gas1*	1.84	3.1	2.05	1.8
ENSMUSG00000052962	*Mrpl35*	3.66	2.6	2.97	2.75
ENSMUSG00000052974	*Cyp2f2*	8.86	8.91	9.27	9.25
ENSMUSG00000052997	*Sae2*	4.05	3.61	3.69	3.45
ENSMUSG00000053012	*Krcc1*	5.57	4.61	5.17	4.42
ENSMUSG00000053051	*NA*	3.09	2.62	3.06	2.93
ENSMUSG00000053062	*Jam2*	2.44	1.98	2.17	2.11
ENSMUSG00000053090	*NA*	2.52	2	2.26	1.7
ENSMUSG00000053094	*0610007L01Ri*	4.88	5.19	4.84	4.72
ENSMUSG00000053110	*Yap1*	4.74	4.84	4.77	4.64
ENSMUSG00000053119	*Vps24*	4.41	4.34	4.32	4.17
ENSMUSG00000053134	*Supt7l*	2.18	2.43	2.23	2.07
ENSMUSG00000053158	*Fes*	1.63	1.74	2.33	1.56
ENSMUSG00000053168	*9030619P08Ri*	6.56	4.74	4.97	5.01
ENSMUSG00000053175	*Bcl3*	3.72	5.23	3.83	4.23
ENSMUSG00000053219	*Raet1e*	1.87	0.5	1.94	0.7
ENSMUSG00000053226	*SP1*	0.6	1.25	1.18	0.75
ENSMUSG00000053253	*Ndfip2*	5.18	4.04	4.7	4.28
ENSMUSG00000053279	*Aldh1a1*	9.11	9.04	9.08	8.54
ENSMUSG00000053286	*1190005F20Ri*	3.85	3.35	3.63	3.54
ENSMUSG00000053289	*NA*	2.71	2.69	2.25	2.03

ENSMUSG00000053291	*Rab4b*	3.45	3.29	3.46	3.6
ENSMUSG00000053293	*Pom121*	2.43	2.93	2.79	2.84
ENSMUSG00000053303	*BC014805*	7.13	6.62	6.09	6.01
ENSMUSG00000053317	*Sec61b*	4.95	3.45	4.81	5.28
ENSMUSG00000053329	*D10Jhu81e*	6.39	6.86	6.67	6.41
ENSMUSG00000053332	*NA*	4.35	3.86	4.05	4.45
ENSMUSG00000053333	*Dis3l2*	2.54	2.58	2.37	2.35
ENSMUSG00000053334	*D5Ertd40e*	2.14	3.25	2.38	2.4
ENSMUSG00000053347	*4930432O21Ri*	2.66	1.07	1.82	1.26
ENSMUSG00000053353	*NA*	0.58	1.07	1.5	1.65
ENSMUSG00000053358	*NA*	1.36	2.28	1.92	1.13
ENSMUSG00000053390	*C920016K16R*	1.46	1.04	0.7	0.45
ENSMUSG00000053407	*NA*	0.79	1.83	1.63	1.47
ENSMUSG00000053411	*Cbx7*	0.98	1.85	1.65	1.66
ENSMUSG00000053436	*Mapk14*	5.35	5.34	5.42	5.32
ENSMUSG00000053453	*Thoc7*	5.49	4.46	5.22	4.56
ENSMUSG00000053460	*Ggcx*	5.55	5.43	5.34	5.11
ENSMUSG00000053470	*Jmjd1a*	2.37	1.81	2.49	2
ENSMUSG00000053474	*NA*	4.21	5.28	5.01	5.18
ENSMUSG00000053477	*Tcf4*	1.3	1.22	1.65	1.7
ENSMUSG00000053483	*Usp21*	2.97	3.42	3.1	2.75
ENSMUSG00000053510	*Nrd1*	5.09	4.92	5.01	4.52
ENSMUSG00000053536	*Cstf2t*	3.83	3.27	3.44	2.97
ENSMUSG00000053559	*BC004728*	4.43	4.86	4.22	4.12
ENSMUSG00000053560	*Ier2*	3.74	4.94	3.96	4.05
ENSMUSG00000053565	*Eif3k*	5.6	5.98	6.1	6.36
ENSMUSG00000053581	*Zfand2a*	2.59	2.62	2.39	2.53
ENSMUSG00000053588	*NA*	2.34	3.2	2.65	3.05
ENSMUSG00000053600	*Zfp472*	0.89	0.72	1.02	0.28
ENSMUSG00000053603	*NA*	0.44	1.63	2.21	1.81
ENSMUSG00000053604	*Rpia*	1.3	0.41	1.75	0.85

ENSMUSG00000053613	*NA*	0.76	1.87	1.97	1.66
ENSMUSG00000053617	*Sh3pxd2a*	1.6	1.63	1.93	1.93
ENSMUSG00000053641	*NA*	1.6	0.42	1.75	1.21
ENSMUSG00000053644	*Aldh7a1*	8.03	7.93	8.09	7.72
ENSMUSG00000053646	*Plxnb1*	0.32	1.26	1.48	0.82
ENSMUSG00000053664	*NA*	2.11	1.51	2.69	1.99
ENSMUSG00000053684	*BC048403*	0.92	1.56	1.55	1.22
ENSMUSG00000053714	*NA*	0.51	1.58	1.7	1.01
ENSMUSG00000053716	*Dusp7*	1.65	2.13	1.64	1.42
ENSMUSG00000053730	*Tmem39b*	1.66	2.35	1.87	1.74
ENSMUSG00000053754	*Chd8*	2.85	3.02	2.8	2.46
ENSMUSG00000053768	*Chchd3*	6	5.5	5.92	5.6
ENSMUSG00000053774	*NA*	2.6	2.03	2.35	2.17
ENSMUSG00000053799	*Exoc6*	3.6	2.66	3.44	3.14
ENSMUSG00000053801	*Grwd1*	1.99	3.64	2.9	2.85
ENSMUSG00000053819	*mKIAA4163*	1.4	0.08	1.57	0.6
ENSMUSG00000053835	*H2-T24*	2.67	2.38	2.2	2.55
ENSMUSG00000053838	*Nudcd3*	4.2	4.48	4.31	4.18
ENSMUSG00000053841	*Txlna*	3.39	3.94	3.1	2.99
ENSMUSG00000053846	*Lipg*	3.32	1.5	3.03	2.92
ENSMUSG00000053870	*Fpgt*	3.08	1.95	2.35	2.18
ENSMUSG00000053877	*NA*	3.34	3.46	3.52	3.39
ENSMUSG00000053886	*NA*	2.7	2.57	3.1	2.18
ENSMUSG00000053897	*Slc39a8*	4.84	4.35	4.13	4.2
ENSMUSG00000053898	*Ech1*	8.2	7.78	8.26	7.94
ENSMUSG00000053906	*NA*	3.47	4.26	3.79	3.6
ENSMUSG00000053907	*Mat2a*	5.14	4.78	5.03	4.61
ENSMUSG00000053929	*Cyhr1*	4.11	4.97	4.48	4.4
ENSMUSG00000053931	*Cnn3*	5.47	5.11	5.3	4.96
ENSMUSG00000053935	*NA*	2.35	1.29	2.11	1.5
ENSMUSG00000053950	*NA*	1.37	1.56	1.69	1.77

ENSMUSG00000053964	*Lgals4*	1.71	1.19	1.96	0.4
ENSMUSG00000054008	*Ndst1*	5.16	5.36	5.2	5.04
ENSMUSG00000054021	*Sirt5*	3.13	2.81	3.02	2.48
ENSMUSG00000054027	*Nt5dc3*	2.88	2.93	2.8	2.82
ENSMUSG00000054051	*Ercc6*	1.12	0.5	0.9	0.69
ENSMUSG00000054072	*Iigp1*	7.68	6.3	6.49	6.47
ENSMUSG00000054079	*Utp18*	2.59	2.61	2.61	2.03
ENSMUSG00000054083	*Capn12*	3.54	2.48	3.4	3.1
ENSMUSG00000054091	*1810037I17Rik*	3.55	3.13	3.6	3.12
ENSMUSG00000054111	*NA*	1.96	2.72	3.21	2.99
ENSMUSG00000054178	*NA*	1.51	0.46	0.92	-0.09
ENSMUSG00000054191	*Klf1*	0.24	0.36	1.45	0.22
ENSMUSG00000054199	*NA*	1.1	1.87	1.43	1.16
ENSMUSG00000054226	*Tprkb*	5.74	5.46	5.93	5.56
ENSMUSG00000054237	*5730455O13Ri*	2.65	1.92	2.82	2.15
ENSMUSG00000054252	*Fgfr3*	2.81	3.08	2.94	2.76
ENSMUSG00000054263	*Lifr*	6.94	6.72	6.2	6.2
ENSMUSG00000054277	*Arfgap3*	1.95	2.49	1.69	1.65
ENSMUSG00000054280	*C330019G07R*	2.72	2.32	2.16	1.94
ENSMUSG00000054302	*Eapp*	4.57	4.47	4.38	4.03
ENSMUSG00000054309	*Cpsf3*	4.68	4.66	4.67	4.31
ENSMUSG00000054312	*Mrps21*	4.31	4.43	4.56	4.69
ENSMUSG00000054364	*Rhob*	3.78	5.03	4.21	4.2
ENSMUSG00000054387	*Mdm4*	2.58	1.72	2.01	1.29
ENSMUSG00000054404	*Slfn5*	2.14	1.32	0.84	1.02
ENSMUSG00000054405	*Dnajc8*	3.73	3.07	3.28	3.07
ENSMUSG00000054408	*Spcs3*	4.67	4.7	4.63	4.37
ENSMUSG00000054414	*Slc30a7*	2.89	2.8	2.78	2.9
ENSMUSG00000054417	*Cyp3a44*	7.3	4.6	5.41	4.26
ENSMUSG00000054422	*Fabp1*	10.46	10.09	10.26	10.23
ENSMUSG00000054426	*NA*	2.73	3.15	3.86	3.41

ENSMUSG00000054428	*Atpif1*	5.23	5.08	5.09	4.77
ENSMUSG00000054435	*Gimap4*	3.29	3.02	2.83	2.64
ENSMUSG00000054452	*Aes*	8.88	9.42	9.16	8.97
ENSMUSG00000054455	*Vapb*	5.67	5.63	5.46	5.23
ENSMUSG00000054469	*Lycat*	4.85	4.22	4.64	4.28
ENSMUSG00000054474	*Thnsl2*	5.21	5.23	5.34	4.72
ENSMUSG00000054477	*Kcnn2*	4.53	4.67	4.84	4.64
ENSMUSG00000054484	*Tmem62*	2.97	2.51	2.93	2.17
ENSMUSG00000054499	*Dedd2*	3.88	4.94	4.96	4.8
ENSMUSG00000054509	*NA*	2.18	2.01	2.66	2.29
ENSMUSG00000054517	*Trim65*	1.67	1.83	1.74	1.69
ENSMUSG00000054519	*BC050078*	1.29	0.33	0.84	0.44
ENSMUSG00000054520	*Sh3bp2*	2.67	3.02	2.75	2.7
ENSMUSG00000054545	*Ugt1a10*	7.73	7.17	7.44	7.24
ENSMUSG00000054574	*NA*	2.21	1.41	2.16	1.41
ENSMUSG00000054588	*LOC626578*	1.57	0.01	-0.97	-0.5
ENSMUSG00000054604	*Cggbp1*	4.98	3.8	4.38	3.97
ENSMUSG00000054611	*Fbxl11*	3.84	3.69	3.59	3.55
ENSMUSG00000054612	*Mgmt*	3.65	3.46	3.66	3.49
ENSMUSG00000054619	*Mettl7a*	7.1	6.73	7.04	7.08
ENSMUSG00000054630	*Ugt2b5*	7.71	7.37	7.44	7.32
ENSMUSG00000054648	*1200003I07Rik*	3.13	2.65	2.8	2.37
ENSMUSG00000054676	*1600014C10Ri*	6.69	7.84	7.35	7.44
ENSMUSG00000054690	*Emcn*	0.72	0.57	1.21	0.68
ENSMUSG00000054693	*Adam10*	3.93	2.94	3.48	2.86
ENSMUSG00000054715	*Zscan22*	1.61	2.06	1.53	1.43
ENSMUSG00000054716	*Zfp771*	2.99	4.49	3.48	3.38
ENSMUSG00000054720	*Lrrc8c*	1.22	0.2	0.85	0.17
ENSMUSG00000054723	*AI662250*	2.81	3.4	3.08	3
ENSMUSG00000054733	*Msra*	6.64	6.7	6.64	6.51
ENSMUSG00000054757	*Akr1c20*	6.5	5.71	5.73	5.58

ENSMUSG00000054766	*AK031561*	3.48	2.55	3.14	2.64
ENSMUSG00000054792	*Klhl18*	1.59	1.85	1.79	1.51
ENSMUSG00000054793	*Cadm4*	1.03	2.88	1.36	2.11
ENSMUSG00000054808	*Actn4*	6.24	6.61	6.46	6.27
ENSMUSG00000054814	*Usp46*	2.74	1.87	2.55	1.82
ENSMUSG00000054823	*Whsc1l1*	2.52	2.69	2.19	2.06
ENSMUSG00000054827	*Cyp2c50*	8.7	7.73	8.18	8.09
ENSMUSG00000054843	*Atrnl1*	3.42	3.07	2.95	2.77
ENSMUSG00000054855	*Rnd1*	2.64	3.13	3.03	2.29
ENSMUSG00000054874	*Pcnxl3*	2.96	3.66	3.19	3.14
ENSMUSG00000054889	*NA*	4.38	4.04	4.18	3.69
ENSMUSG00000054894	*Atp5s*	2.08	0.71	1.58	0.83
ENSMUSG00000054920	*Klhl5*	2.78	2.74	2.88	2.42
ENSMUSG00000055013	*Centg2*	0.57	0.83	1.16	1.01
ENSMUSG00000055024	*Ep300*	2.93	2.77	3.08	3.02
ENSMUSG00000055027	*Smyd1*	1.99	1.78	1.52	1.36
ENSMUSG00000055041	*Commd5*	3.23	3.75	3.51	3.36
ENSMUSG00000055044	*Pdlim1*	3.12	3.91	3.17	3.37
ENSMUSG00000055053	*Nfic*	4.08	5.05	4.85	4.62
ENSMUSG00000055065	*Ddx17*	5.03	5.03	5.06	5.38
ENSMUSG00000055116	*Arntl*	3.88	3.88	2.38	1.62
ENSMUSG00000055128	*Cgrrf1*	5	4.44	4.95	4.61
ENSMUSG00000055148	*Klf2*	2.11	3.01	2.12	2.25
ENSMUSG00000055172	*C1r*	5.06	4.64	4.77	4.65
ENSMUSG00000055178	*NA*	5.42	4.14	5.12	4.39
ENSMUSG00000055200	*Sertad3*	2.04	2.24	2.03	1.66
ENSMUSG00000055204	*Ankrd17*	3.83	3.28	3.5	3.12
ENSMUSG00000055228	*8430426H19Ri*	1.49	0.48	1.2	0.17
ENSMUSG00000055239	*Kcmf1*	5.67	5.44	5.62	5.39
ENSMUSG00000055240	*Zfp101*	1.63	0.38	1.32	0.25
ENSMUSG00000055296	*D730040F13R*	2.19	1.41	2.21	1.88

ENSMUSG00000055301	*Adh7*	2.68	2.36	2.53	2.46
ENSMUSG00000055302	*Mrfap1*	5.21	5.37	5.27	5.07
ENSMUSG00000055312	*0610012H03Ri*	5.05	4	4.73	3.37
ENSMUSG00000055319	*Sec23ip*	3.78	3.71	3.39	3.38
ENSMUSG00000055320	*Tead1*	1.04	0.06	0.47	0.13
ENSMUSG00000055322	*NA*	4.67	5.24	4.78	4.69
ENSMUSG00000055334	*Snupn*	2.11	2.25	2.09	1.79
ENSMUSG00000055371	*Stam2*	2.6	2.35	2.53	2.12
ENSMUSG00000055396	*NA*	2.41	2.63	2.87	2.78
ENSMUSG00000055401	*Fbxo6*	4.23	4.76	4.36	3.96
ENSMUSG00000055424	*NA*	0.24	1.45	1.78	1.25
ENSMUSG00000055435	*Maf*	3.85	3.26	3.88	3.58
ENSMUSG00000055436	*Sfrs11*	3.78	3.38	3.78	3.13
ENSMUSG00000055440	*NA*	5.16	5.74	5.06	5
ENSMUSG00000055447	*Cd47*	5.92	5.67	5.89	5.59
ENSMUSG00000055491	*Pprc1*	2.01	2.59	1.98	2.42
ENSMUSG00000055493	*AK041609*	0.91	1.14	1.13	0.26
ENSMUSG00000055531	*Cpsf6*	3.21	3.1	3.04	2.77
ENSMUSG00000055538	*NA*	5.5	5.43	5.62	5.39
ENSMUSG00000055546	*Timd4*	2.82	1.99	1.96	1.91
ENSMUSG00000055553	*Uba52*	4.02	4.74	4.5	4.35
ENSMUSG00000055593	*NA*	2.35	1.42	1.74	1.85
ENSMUSG00000055652	*Klhl25*	2.78	3.99	3.11	3.08
ENSMUSG00000055660	*Mettl4*	2.15	1.25	1.91	1.39
ENSMUSG00000055670	*Zzef1*	2.64	2.82	2.67	2.38
ENSMUSG00000055681	*Cope1*	6.01	6.84	6.34	6.16
ENSMUSG00000055707	*Klhl26*	2.01	2.42	2.32	2.05
ENSMUSG00000055720	*Ubl7*	4.89	5.15	5.33	5.03
ENSMUSG00000055723	*Rras2*	3.47	2.86	3.43	2.88
ENSMUSG00000055725	*Paqr3*	2.25	1.98	2.34	1.97
ENSMUSG00000055730	*Ces6*	6.91	7.15	7.09	7.27

ENSMUSG00000055737	*Ghr*	7.31	6.76	6.98	6.71
ENSMUSG00000055755	*NA*	0.86	2.02	1.28	1.29
ENSMUSG00000055760	*Gemin6*	1.47	0.49	1.56	1.09
ENSMUSG00000055762	*Eef1d*	2.63	3.18	3.14	2.98
ENSMUSG00000055771	*NA*	1.58	0.84	1.18	2.09
ENSMUSG00000055782	*Abcd2*	4	3.74	2.95	3.08
ENSMUSG00000055799	*Tcf3*	2.24	2.49	2.26	2.34
ENSMUSG00000055802	*NA*	1.45	1.39	2.78	2.07
ENSMUSG00000055817	*Mta3*	1.02	1.07	1.14	0.79
ENSMUSG00000055835	*Zfp1*	2.01	1.62	2	1.5
ENSMUSG00000055839	*Tceb2*	5.06	4.13	4.96	4.7
ENSMUSG00000055849	*NA*	3.59	3.4	3.36	2.71
ENSMUSG00000055850	*Rnf181*	5.63	5.73	5.74	5.6
ENSMUSG00000055862	*9030607L17Ri*	1.36	2.02	1.9	1.73
ENSMUSG00000055866	*Per2*	0.63	1.22	2.33	2.73
ENSMUSG00000055900	*Tmem69*	4.12	2.98	4.08	3.81
ENSMUSG00000055912	*Tmem150*	5.33	5.42	5.4	5.28
ENSMUSG00000055917	*Zfp277*	2.53	1.81	2.59	2.08
ENSMUSG00000055932	*Fto*	3.74	4.06	3.84	3.64
ENSMUSG00000055943	*2900064A13Ri*	5.96	5.77	5.72	5.32
ENSMUSG00000055968	*NA*	0.14	2.39	1.87	1.2
ENSMUSG00000055980	*AK141842*	1.56	2.15	1.76	1.92
ENSMUSG00000055991	*Zkscan5*	2.94	2.86	2.42	2.43
ENSMUSG00000056025	*mCLCA1*	1.18	0.59	1.55	0.54
ENSMUSG00000056032	*NA*	2.58	0.41	2.31	0.59
ENSMUSG00000056035	*Cyp3a11*	10.39	9.6	10.22	9.96
ENSMUSG00000056054	*S100a8*	0.85	1.69	1.3	0.22
ENSMUSG00000056071	*S100a9*	1.7	1.74	1.9	1.52
ENSMUSG00000056076	*Eif3b*	5.66	5.99	5.7	5.65
ENSMUSG00000056091	*St3gal5*	7.89	7.58	7.54	7.43
ENSMUSG00000056116	*H2-T22*	4.55	4.77	4.52	4.4

ENSMUSG00000056121	*Fez2*	3.98	4.03	3.69	3.55
ENSMUSG00000056131	*Pgm3*	2.37	1.86	1.8	1.46
ENSMUSG00000056148	*Rdh9*	4.87	5.06	4.88	5
ENSMUSG00000056153	*Cis4*	1.84	1.56	1.25	1.02
ENSMUSG00000056167	*Cnot10*	2.86	2.8	2.92	2.91
ENSMUSG00000056199	*NA*	4.25	3.55	3.15	3.67
ENSMUSG00000056201	*Cfl1*	6.34	6.28	6.47	6.23
ENSMUSG00000056204	*Pgpep1*	4.65	5.02	4.88	4.64
ENSMUSG00000056209	*Npm3*	1.06	1.15	0.92	0.62
ENSMUSG00000056211	*R3hdm1*	2.89	2.6	2.83	2.53
ENSMUSG00000056216	*Cebpg*	4.59	4.62	4.13	4.54
ENSMUSG00000056228	*NA*	2.94	3.07	2.51	2.37
ENSMUSG00000056260	*4933421E11Ri*	2.22	1.06	2.21	1.56
ENSMUSG00000056268	*Dennd1b*	1.31	1.05	1.44	0.51
ENSMUSG00000056305	*Usp39*	3.92	3.85	3.97	3.94
ENSMUSG00000056310	*Tyw1*	1.23	1.82	1.69	1.58
ENSMUSG00000056313	*1810011O10Ri*	5.04	4.79	5.43	5.33
ENSMUSG00000056328	*Myh1*	#NAME?	#NAME?	1.98	1.68
ENSMUSG00000056342	*NA*	3.38	2.86	2.9	2.58
ENSMUSG00000056383	*AI987944*	2.89	1.86	2.36	2.01
ENSMUSG00000056412	*NA*	1.65	1.42	1.81	1.9
ENSMUSG00000056429	*Tgoln2*	6.7	6.35	6.53	6.07
ENSMUSG00000056438	*NA*	5.45	6.14	6.07	6.06
ENSMUSG00000056487	*LOC554292*	0.29	-4.72	1.12	-3.79
ENSMUSG00000056492	*Gpr116*	3.58	3.42	3.23	3.08
ENSMUSG00000056493	*Foxk1*	2.6	2.73	2.73	2.55
ENSMUSG00000056501	*Cebpb*	5.04	6.05	6.09	5.93
ENSMUSG00000056515	*Rab22B*	1.21	0.89	0.78	0.79
ENSMUSG00000056536	*Pign*	1.4	0.18	0.95	-0.05
ENSMUSG00000056537	*Rnf12*	3.38	2.54	2.88	2.57
ENSMUSG00000056550	*NA*	4.39	3.87	4.6	5.85

ENSMUSG00000056552	*E130120F12Ri*	1.52	0.26	1.02	0.34
ENSMUSG00000056579	*NA*	3.9	3.55	3.71	3.16
ENSMUSG00000056608	*Chd9*	2.49	1.74	2.03	1.89
ENSMUSG00000056612	*Ppp1r14b*	2.16	2.85	2.64	1.96
ENSMUSG00000056629	*Fkbp2*	6.96	6.6	6.69	6.84
ENSMUSG00000056643	*NA*	1.3	3.18	1.8	0.64
ENSMUSG00000056652	*NA*	2.6	3.12	2.48	2.96
ENSMUSG00000056665	*4930572J05Ri*	1.37	1.98	2.2	1.53
ENSMUSG00000056666	*Retsat*	7.4	7.69	7.52	6.87
ENSMUSG00000056671	*Prelid2*	3.6	3.87	2.99	2.95
ENSMUSG00000056692	*D17Wsu92e*	6.7	7.09	6.8	6.79
ENSMUSG00000056698	*Rbed1*	3.95	3.66	4.38	3.63
ENSMUSG00000056708	*Ier5*	0.72	2.37	1.33	0.96
ENSMUSG00000056718	*NA*	1.06	0.92	0.63	0.7
ENSMUSG00000056749	*Nfil3*	5.14	5.58	3.98	3.78
ENSMUSG00000056763	*Cspp1*	1.82	1.63	1.92	1.31
ENSMUSG00000056770	*Setd3*	3.64	2.77	3.47	3.26
ENSMUSG00000056820	*Tsnax*	3.83	3.57	3.53	3.32
ENSMUSG00000056851	*hnRNP X*	7.24	7.51	7.52	7.34
ENSMUSG00000056880	*NA*	1.56	1.11	1.8	2.93
ENSMUSG00000056888	*Glipr1*	2.46	2.36	2.46	1.75
ENSMUSG00000056899	*Immp2l*	5.74	5.06	5.27	4.93
ENSMUSG00000056917	*Sipa1*	1.79	2.52	1.97	1.73
ENSMUSG00000056938	*Acbd4*	4.16	4.69	4.34	4.12
ENSMUSG00000056941	*Commd7*	3.56	3.81	3.19	3.43
ENSMUSG00000056951	*Rbm4*	2.55	3.01	2.74	2.69
ENSMUSG00000056952	*Tatdn2*	3.53	4.11	3.7	3.62
ENSMUSG00000056962	*mKIAA0585*	3.05	3.64	3.43	3.5
ENSMUSG00000056973	*Ces3*	8.38	8.52	7.9	8.02
ENSMUSG00000056978	*Hamp2*	9.74	9.29	10.29	9.88
ENSMUSG00000056989	*NA*	1.75	#NAME?	2.07	1.1

ENSMUSG00000056999	*Ide*	4.78	4.14	4.36	4.11
ENSMUSG00000057037	*Cfhr1*	7.05	6.21	6.64	6.15
ENSMUSG00000057054	*AI842396*	3.29	3.06	3.45	3.07
ENSMUSG00000057068	*Gm1381*	3.03	2.98	2.68	3.23
ENSMUSG00000057069	*Ero1lb*	2.46	2.5	2.04	2.22
ENSMUSG00000057074	*Ces1*	6.4	5.34	5.87	5.7
ENSMUSG00000057088	*NA*	5.79	6.11	6.01	6
ENSMUSG00000057101	*Zfp180*	3.19	3.2	3.01	3.03
ENSMUSG00000057103	*Cml1*	6.66	7.05	6.68	6.74
ENSMUSG00000057110	*NA*	2.38	1.55	2.08	1.28
ENSMUSG00000057113	*Npm1*	3.89	2.78	3.51	3.29
ENSMUSG00000057130	*Txnl4a*	5.05	4.72	4.79	5.01
ENSMUSG00000057133	*Chd6*	1.41	0.91	1.31	0.88
ENSMUSG00000057134	*Gm237*	1.89	3.36	2.38	2.42
ENSMUSG00000057137	*Tmem140*	4.15	4.11	4.26	3.88
ENSMUSG00000057143	*9230105E10Ri*	1.97	0.26	0.95	0.53
ENSMUSG00000057147	*Atpbd4*	1.67	1.58	1.72	1.31
ENSMUSG00000057176	*Gm166*	0.57	0.94	1.3	1.06
ENSMUSG00000057177	*Gsk3a*	4.61	5.3	5.36	5.15
ENSMUSG00000057181	*5730455P16Ri*	2.24	2.37	2.17	2.33
ENSMUSG00000057191	*AB124611*	1.75	1.37	1.46	1.26
ENSMUSG00000057193	*Slc44a2*	2.42	2.72	2.56	2.46
ENSMUSG00000057220	*NA*	-0.27	-1.39	1.98	-0.23
ENSMUSG00000057228	*Aadat*	6.77	5.54	6.54	5.77
ENSMUSG00000057229	*2310004L02Ri*	4.94	5.11	5.66	5.31
ENSMUSG00000057234	*Mett5d1*	1.61	-0.15	1.4	0.95
ENSMUSG00000057236	*Rbbp4*	5.55	5.34	5.46	5.26
ENSMUSG00000057254	*BC066107*	1.8	1.07	1.05	0.02
ENSMUSG00000057265	*2900006K08Ri*	4.35	3.84	4.18	3.81
ENSMUSG00000057278	*Snrpg*	0.69	0.96	1.25	1.12
ENSMUSG00000057315	*Arhgap24*	1.74	1	1.58	1.24

ENSMUSG00000057322	*Rpl38*	0.62	0.46	1.39	0.65
ENSMUSG00000057342	*Sphk2*	4.03	4.39	4.33	3.89
ENSMUSG00000057346	*2310016F22Ri*	5.34	5.31	5.42	5.75
ENSMUSG00000057356	*NA*	6.2	4.85	5.4	5.8
ENSMUSG00000057363	*Uxs1*	2.44	1.96	2.04	1.29
ENSMUSG00000057367	*Birc2*	3.23	2.27	2.84	2.2
ENSMUSG00000057375	*Yipf1*	4.57	5.04	4.75	5
ENSMUSG00000057388	*Mrpl18*	4.54	4.52	4.69	4.59
ENSMUSG00000057396	*Zfp759*	1.75	0.99	0.75	-0.48
ENSMUSG00000057400	*Es1*	10.32	10.32	10.31	10.22
ENSMUSG00000057406	*Whsc1*	1.04	0.77	0.65	0.4
ENSMUSG00000057409	*KRAZ1*	1.78	1.08	1.26	0.55
ENSMUSG00000057411	*BC008155*	4.03	4.79	4.54	4.45
ENSMUSG00000057421	*Las1l*	3.89	4.36	4.04	3.77
ENSMUSG00000057465	*Saa2*	4.17	4.7	5.3	5.3
ENSMUSG00000057469	*E2f6*	3.54	3.65	3.66	3.19
ENSMUSG00000057497	*2010309E21Ri*	4.98	4.84	4.88	4.26
ENSMUSG00000057506	*NA*	1.06	1.02	1.02	1.11
ENSMUSG00000057522	*Spop*	6.08	5.84	5.71	5.37
ENSMUSG00000057530	*Ece1*	6.14	6.42	6.47	6.41
ENSMUSG00000057531	*Dtnbp1*	4.88	5.37	5.25	4.97
ENSMUSG00000057541	*mKIAA1897*	1.24	1.11	1.1	1.06
ENSMUSG00000057551	*Zfp75*	2.65	2.34	2.33	1.97
ENSMUSG00000057554	*Lgals8*	5.68	5.2	5.65	5.2
ENSMUSG00000057561	*Eif1a*	5.39	5.59	4.88	4.84
ENSMUSG00000057572	*Zbtb8os*	1.42	0.37	0.67	0.78
ENSMUSG00000057594	*Arl16*	1.68	2.19	1.94	1.8
ENSMUSG00000057637	*Prdm2*	2.99	2.58	3.11	2.94
ENSMUSG00000057649	*Brd9*	1.82	2.36	2.49	1.98
ENSMUSG00000057667	*Bloc1s3*	1.77	1.7	1.37	0.93
ENSMUSG00000057672	*Pkn1*	2.65	3.28	2.88	2.8

ENSMUSG00000057691	*NA*	2.74	3.09	2.9	2.69
ENSMUSG00000057722	*Lepr*	1.31	0.9	0.75	0.76
ENSMUSG00000057738	*Spna2*	4	4.33	4.24	3.96
ENSMUSG00000057778	*Cyb5d2*	3.71	3.86	3.44	3.4
ENSMUSG00000057788	*Ddx49*	3.48	4.24	3.48	3.59
ENSMUSG00000057789	*Bak1*	2.52	2.73	2.87	2.62
ENSMUSG00000057796	*NA*	4.62	3.83	3.47	2.7
ENSMUSG00000057808	*NA*	1.48	0.48	1.11	1.27
ENSMUSG00000057835	*Zfp119*	1.57	0.29	0.43	0.13
ENSMUSG00000057841	*Rpl32*	5.69	6.25	5.82	5.84
ENSMUSG00000057858	*D19Ertd737e*	1.58	0.64	1.42	0.82
ENSMUSG00000057863	*Rpl36*	0.57	1.12	1.13	1.18
ENSMUSG00000057880	*Abat*	7.51	7.15	7.37	6.69
ENSMUSG00000057924	*NA*	2.07	0.45	1.35	0.18
ENSMUSG00000057933	*Gsta2*	4.2	2.83	5.03	3.56
ENSMUSG00000057963	*Itpk1*	3.51	3.75	3.72	3.26
ENSMUSG00000057982	*Zfp809*	3.35	2.72	3.39	2.8
ENSMUSG00000058013	*11-Sep*	2.58	2.52	2.32	1.75
ENSMUSG00000058022	*9530008L14Ri*	6.5	5.54	6.06	5.68
ENSMUSG00000058056	*Palld*	2.9	3.85	3.15	3.7
ENSMUSG00000058057	*ENSMUSG000*	1.77	#NAME?	1.79	#NAME?
ENSMUSG00000058064	*NA*	4.22	3.78	2.78	3.63
ENSMUSG00000058076	*Sdhc*	7.36	7.47	7.52	7.15
ENSMUSG00000058093	*NA*	1.48	0.38	0.81	-0.01
ENSMUSG00000058099	*Nfam1*	0.64	1.52	1.11	0.95
ENSMUSG00000058126	*NA*	2.39	0.03	2.24	0.92
ENSMUSG00000058135	*Gstm1*	8.53	8.96	8.97	8.87
ENSMUSG00000058140	*NA*	2.59	3.37	2.83	2.71
ENSMUSG00000058152	*4833446K15Ri*	1.18	1.15	1.02	0.9
ENSMUSG00000058173	*Fn5*	2.46	2.83	2.43	2.65
ENSMUSG00000058192	*2210010B09Ri*	1.04	0.54	0.66	0.35

ENSMUSG00000058207	*Serpina3k*	11.17	11.28	11.09	11.5
ENSMUSG00000058216	*BC021614*	4.64	4.95	5.37	5.01
ENSMUSG00000058230	*Grlf1*	4.49	4.7	4.46	4.38
ENSMUSG00000058239	*Usf2*	4.74	5.01	4.49	4.47
ENSMUSG00000058240	*Cryzl1*	2.84	2.97	2.28	2.55
ENSMUSG00000058254	*Tspan7*	2.67	2.81	2.19	2.44
ENSMUSG00000058258	*Idi1*	1.87	0.85	0.24	-0.48
ENSMUSG00000058267	*Mrps14*	4.33	3.73	3.95	3.53
ENSMUSG00000058291	*Zfp68*	2.94	2.46	2.68	2.11
ENSMUSG00000058301	*Upf1*	3.9	4.62	4.41	4.35
ENSMUSG00000058317	*Ube2e2*	4.04	4.05	3.73	3.41
ENSMUSG00000058318	*Phf21a*	1.61	1.61	1.72	1.47
ENSMUSG00000058325	*Dock1*	2.01	2.15	1.85	1.76
ENSMUSG00000058351	*NA*	2.61	3.68	3.89	3.43
ENSMUSG00000058355	*Abce1*	5.14	4.74	4.82	4.47
ENSMUSG00000058357	*NA*	4.73	4.13	4.49	6.51
ENSMUSG00000058388	*Phtf1*	1.5	1.03	0.83	1.14
ENSMUSG00000058392	*Rrp1b*	1.01	1.19	0.77	1.02
ENSMUSG00000058396	*Admr*	4.79	5.51	4.49	4.68
ENSMUSG00000058407	*Txndc9*	4.25	3.87	4.34	3.66
ENSMUSG00000058440	*Nrf1*	1.13	1.62	1.23	1.19
ENSMUSG00000058443	*NA*	0.63	1.3	1.7	1.3
ENSMUSG00000058444	*Map2k5*	3.22	3.27	3.68	3.23
ENSMUSG00000058446	*Znrf2*	4.77	3.75	4.29	3.99
ENSMUSG00000058454	*Dhcr7*	5.92	5.83	5.49	5.07
ENSMUSG00000058486	*Wdr91*	2.83	3.34	2.77	2.27
ENSMUSG00000058492	*NA*	7.99	7.47	7.61	8.68
ENSMUSG00000058503	*5830415L20Ri*	2.5	1.56	2.05	1.85
ENSMUSG00000058523	*Mup5*	2.58	-0.32	-1.12	1.66
ENSMUSG00000058542	*NA*	1.06	1.35	0.62	0.88
ENSMUSG00000058546	*Rpl23a*	2.24	2.46	2.57	2.34

ENSMUSG00000058569	*Tmed9*	5.34	5.63	5	5.26
ENSMUSG00000058586	*Serhl*	3.99	4.15	4.06	3.99
ENSMUSG00000058587	*Tmod3*	3.92	3.14	3.45	3.1
ENSMUSG00000058594	*Fbxo18*	3.49	3.41	3.49	2.98
ENSMUSG00000058600	*Rpl30*	1.46	1.05	1.81	1.28
ENSMUSG00000058603	*NA*	0.87	1.45	1.5	0.97
ENSMUSG00000058624	*Gda*	3.78	2.59	3.08	2.44
ENSMUSG00000058638	*Zfp110*	3.7	2.92	3.16	3.08
ENSMUSG00000058655	*Eif4b*	6.04	6.62	6.29	6.29
ENSMUSG00000058672	*Tubb2a*	5.77	6.4	4.22	4.5
ENSMUSG00000058690	*mKIAA1128*	3.44	2.7	3.27	2.91
ENSMUSG00000058704	*Memo1*	4.5	3.55	3.49	3.69
ENSMUSG00000058706	*NA*	4.12	3.95	4.02	3.79
ENSMUSG00000058709	*Egln2*	4.55	5.64	4.91	4.91
ENSMUSG00000058715	*Fcer1g*	4.14	3.09	3.72	3.3
ENSMUSG00000058748	*BC003267*	1.86	0.8	0.67	0.34
ENSMUSG00000058756	*Thra*	3.15	4.14	3.76	3.73
ENSMUSG00000058761	*NA*	3.85	3.21	3.92	3.74
ENSMUSG00000058793	*Cds2*	4.15	4.54	4	4.18
ENSMUSG00000058799	*Nap1l1*	2.9	2.68	2.57	1.9
ENSMUSG00000058812	*NA*	1.65	1.66	2.28	2.13
ENSMUSG00000058833	*2810428I15Rik*	4.52	5.55	5.14	4.87
ENSMUSG00000058835	*Abi1*	4.51	4.34	4.51	4.14
ENSMUSG00000058886	*Deaf1*	2.8	3.4	3.34	3.13
ENSMUSG00000058905	*NA*	0.58	-0.04	1.23	0.61
ENSMUSG00000058921	*Slc10a5*	4.22	3.79	3.73	3.75
ENSMUSG00000058927	*NA*	2.44	2.35	3.03	3.33
ENSMUSG00000058942	*NA*	1.02	0.23	0.96	0.55
ENSMUSG00000058952	*Cfi*	8.49	8.53	8.35	8.37
ENSMUSG00000058979	*Cecr5*	3.62	4.2	3.91	3.66
ENSMUSG00000058997	*NA*	5.46	4.6	5.35	4.47

ENSMUSG00000059005	*Hnrpa3*	1.74	1.52	0.88	0.82
ENSMUSG00000059013	*Sh2d3c*	1.59	2.62	1.99	1.64
ENSMUSG00000059027	*NA*	2.01	0.93	2.01	1.14
ENSMUSG00000059039	*NA*	0.09	2.29	1.24	1.68
ENSMUSG00000059040	*EG433182*	1.59	2.81	1.69	1.83
ENSMUSG00000059070	*Rpl18*	0.68	2.3	1.97	1.11
ENSMUSG00000059089	*Fcgr4*	3.09	1.74	2.09	2.81
ENSMUSG00000059119	*Nap1l4*	4.56	4.83	4.56	4.33
ENSMUSG00000059142	*A630033E08Ri*	1.6	-0.08	0.57	0.19
ENSMUSG00000059144	*NA*	1.09	1.84	1.85	1.84
ENSMUSG00000059149	*Mfsd4*	2.06	1.76	2.25	1.7
ENSMUSG00000059182	*Skap2*	3.67	3.15	3.4	2.92
ENSMUSG00000059183	*Mtfmt*	1.8	1.63	2.05	1.23
ENSMUSG00000059208	*Hnrpm*	4.92	5.15	4.88	4.75
ENSMUSG00000059248	*9-Sep*	5.15	4.93	5.08	4.55
ENSMUSG00000059249	*NA*	3.02	2.47	3.85	2.53
ENSMUSG00000059263	*Usp47*	4.76	4.62	4.74	4.35
ENSMUSG00000059273	*mKIAA1064*	2.36	3	3.09	2.86
ENSMUSG00000059277	*R74862*	1.03	1.03	1.08	0.29
ENSMUSG00000059278	*Lsmd1*	4.86	5.47	4.98	5.42
ENSMUSG00000059288	*Cdyl*	1.4	0.91	1.23	1.13
ENSMUSG00000059316	*Slc27a4*	3.85	4.53	4.07	4.1
ENSMUSG00000059325	*Hopx*	4.9	4.16	5.03	4.77
ENSMUSG00000059326	*Csf2ra*	0.27	1.11	1.14	0.57
ENSMUSG00000059355	*BC056474*	3.3	4.12	4.06	3.78
ENSMUSG00000059363	*Fxn*	2.97	3.8	3.69	3.71
ENSMUSG00000059409	*Ppp2r5d*	4.17	4.55	4.35	4.37
ENSMUSG00000059423	*MGC67181*	1.66	1.02	0.58	0.13
ENSMUSG00000059434	*Gckr*	6.27	5.96	6.36	5.99
ENSMUSG00000059436	*Myn*	4.24	3.49	4.09	4.09
ENSMUSG00000059439	*Bcas3*	2.39	3.04	3.05	2.85

ENSMUSG00000059447	*Hadhb*	3.31	2.74	3.23	2.36
ENSMUSG00000059456	*Ptk2b*	3.72	3.46	4.26	3.72
ENSMUSG00000059474	*Mbtd1*	2.2	0.85	1.76	1.19
ENSMUSG00000059475	*Zfp426*	2.06	1.64	2.1	1.6
ENSMUSG00000059479	*B3gnt8*	4.86	5.58	5.21	4.87
ENSMUSG00000059481	*Plg*	9.85	10.47	10.14	10.12
ENSMUSG00000059482	*2610301B20Ri*	2.27	1.72	1.72	1.2
ENSMUSG00000059486	*Kbtbd2*	3.05	2.04	2.8	2.61
ENSMUSG00000059495	*Arhgef12*	4.44	4.07	4.27	4.12
ENSMUSG00000059498	*Fcgr3*	3.02	2.2	3.1	2.63
ENSMUSG00000059518	*Znhit1*	4.29	4.89	4.9	4.75
ENSMUSG00000059534	*1110020P15Ri*	6.71	6.42	7.1	7.34
ENSMUSG00000059552	*p53*	3.64	4.08	3.92	3.7
ENSMUSG00000059554	*Ccdc28a*	2.68	2.12	3.22	2.89
ENSMUSG00000059555	*A830007P12Ri*	1.71	1.94	1.63	1
ENSMUSG00000059586	*Nsmce2*	2.85	2.37	2.52	2.39
ENSMUSG00000059588	*Calcrl*	3.1	2.18	2.36	2.14
ENSMUSG00000059605	*NA*	1.37	0.65	1.12	0.45
ENSMUSG00000059634	*NA*	5.39	6.12	6.15	6.12
ENSMUSG00000059669	*Taf1b*	1.91	1.44	1.47	1
ENSMUSG00000059689	*Zfp637*	3.76	4.06	3.84	3.72
ENSMUSG00000059708	*Sfrs17b*	1.19	0.88	0.35	0.35
ENSMUSG00000059714	*Flot1*	3.41	4.23	3.62	3.51
ENSMUSG00000059734	*Ndufs8*	6.66	7.07	7.07	6.56
ENSMUSG00000059743	*Fdps*	4.2	4.08	3.18	2.47
ENSMUSG00000059751	*NA*	2.99	4.06	3.88	4.38
ENSMUSG00000059772	*Giyd2*	1.86	2.35	2.38	2.31
ENSMUSG00000059775	*NA*	0.6	1.04	1.07	1.56
ENSMUSG00000059796	*Eif4a1*	4.23	3.74	3.95	3.73
ENSMUSG00000059807	*NA*	6.9	6.8	6.23	5.92
ENSMUSG00000059811	*Arl6ip2*	6.48	5.75	6.15	5.85

ENSMUSG00000059820	*AU019823*	3.27	2.24	2.56	2.04
ENSMUSG00000059824	*Dbp*	1.22	0.62	4.95	5.29
ENSMUSG00000059834	*Sclt1*	1.1	0.53	1.21	0.27
ENSMUSG00000059839	*9630025I21Rik*	2.31	1.83	1.87	1.24
ENSMUSG00000059851	*Suv420h2*	2.1	2.65	2.24	2.11
ENSMUSG00000059866	*Tnip2*	0.86	0.8	1.19	0.91
ENSMUSG00000059878	*Zfp422*	2.79	2.74	2.93	2.54
ENSMUSG00000059883	*Irak4*	1.36	1.76	1.41	1.57
ENSMUSG00000059890	*Ube4a*	4.92	4.24	4.52	4.13
ENSMUSG00000059895	*Ptp4a3*	1.24	2.72	1.98	2.38
ENSMUSG00000059897	*D10627*	1.97	0.27	1.04	0.18
ENSMUSG00000059908	*Mug1*	8.6	9.03	8.93	9.04
ENSMUSG00000059920	*4930453N24Ri*	3.96	2.37	3.31	2.91
ENSMUSG00000059923	*Grb2*	4.41	4.38	4.43	4.2
ENSMUSG00000059939	*9430015G10Ri*	1.33	1.54	1.12	1.55
ENSMUSG00000059981	*NA*	2.96	3.52	3.11	3.01
ENSMUSG00000059995	*Atxn7l3*	3.55	3.77	3.44	3.31
ENSMUSG00000060002	*Chpt1*	5.01	3.94	4.76	3.98
ENSMUSG00000060012	*Kif13b*	2.64	3	2.95	2.76
ENSMUSG00000060029	*NA*	2.44	1.81	2.2	1.65
ENSMUSG00000060032	*H2afj*	4.61	5.68	5.49	5.47
ENSMUSG00000060036	*Rpl3*	1.85	3.22	1.74	2.1
ENSMUSG00000060038	*Dhps*	2.32	2.9	2.67	2.58
ENSMUSG00000060063	*Alox5ap*	2.49	2.49	2.43	1.71
ENSMUSG00000060068	*NA*	1.26	1.1	1.8	1.46
ENSMUSG00000060090	*Rp2h*	1.94	0.84	1.22	0.75
ENSMUSG00000060098	*mKIAA1933*	2.52	3.19	2.94	2.66
ENSMUSG00000060121	*Sip1*	3.44	3.11	3.55	3.14
ENSMUSG00000060126	*Tpt1*	3.51	5.05	4.56	3.96
ENSMUSG00000060147	*Serpinb6a*	3.66	2.98	3.26	3.23
ENSMUSG00000060149	*BC002059*	2.16	0.34	1.83	0.76

ENSMUSG00000060152	*Pop5*	4.38	4.82	4.75	4.76
ENSMUSG00000060166	*Zdhhc8*	0.88	1.86	1.85	1.58
ENSMUSG00000060177	*Klk1b22*	1.09	0.16	1.52	-0.91
ENSMUSG00000060181	*Slc35e3*	1.6	1.29	1.37	1.06
ENSMUSG00000060216	*Arrb2*	2.43	3.32	2.93	2.92
ENSMUSG00000060224	*4833409A17Ri*	3.97	3.94	4.44	3.85
ENSMUSG00000060244	*Refbp2*	1	1.35	1.33	0.42
ENSMUSG00000060261	*Diws1t*	5.03	5.35	5.16	4.99
ENSMUSG00000060279	*Ap2a1*	3.58	4.4	4.06	4.09
ENSMUSG00000060301	*2610008E11Ri*	2.17	1.45	1.45	0.83
ENSMUSG00000060317	*C730036D15R*	6.65	6.5	5.93	6.1
ENSMUSG00000060373	*Hnrnpc*	4.99	4.29	4.65	4.62
ENSMUSG00000060376	*Bckdha*	6.97	7.69	7.38	7.11
ENSMUSG00000060407	*Cyp2a12*	8.48	8.5	8.59	8.41
ENSMUSG00000060419	*NA*	3.47	2.31	2.97	3.88
ENSMUSG00000060427	*AI449175*	2.72	2.48	2.46	2.08
ENSMUSG00000060429	*Sntb1*	4.05	4.21	3.87	3.79
ENSMUSG00000060438	*NA*	0.43	1.4	1.11	1.88
ENSMUSG00000060450	*Triad2*	5.18	5.01	5.34	4.82
ENSMUSG00000060459	*Kng2*	7.12	6.68	6.79	6.54
ENSMUSG00000060466	*NA*	1.57	0.86	1.77	1.35
ENSMUSG00000060470	*Gpr97*	1.55	1.74	0.78	1.24
ENSMUSG00000060475	*Wtap*	3.03	2.51	2.58	2.45
ENSMUSG00000060477	*Irak2*	2.64	2.83	2.66	2.55
ENSMUSG00000060510	*NA*	2.47	1.22	2.04	1.69
ENSMUSG00000060512	*0610040J01Ri*	4.22	4.62	4.67	4.65
ENSMUSG00000060519	*Tor3a*	2.73	2.83	2.08	1.66
ENSMUSG00000060538	*1110032O16Ri*	4.1	4.65	4.6	4.65
ENSMUSG00000060550	*H2-Q7*	2.57	3.19	2.72	2.55
ENSMUSG00000060579	*Fhit*	2.31	2.61	2.63	2.35
ENSMUSG00000060586	*H2-Eb1*	5.4	4.85	5.39	4.73

ENSMUSG00000060591	*Ifitm2*	7.19	7.8	7.85	7.56
ENSMUSG00000060600	*ENO3*	0.18	0.99	1.53	1.79
ENSMUSG00000060601	*Nr1h2*	4.49	5.25	4.76	4.72
ENSMUSG00000060613	*Cyp2c70*	9.42	8.96	9.14	8.74
ENSMUSG00000060628	*NA*	6.39	4.58	5.71	5.11
ENSMUSG00000060636	*Rpl35a*	3.39	3.23	3.31	2.94
ENSMUSG00000060639	*Hist1h4i*	2.37	2.38	2.66	2.42
ENSMUSG00000060647	*NA*	2.23	1.99	1.99	1.65
ENSMUSG00000060657	*4921513D23Ri*	4.18	3.71	3.9	3.72
ENSMUSG00000060675	*Hrasls3*	1.68	1.46	1.25	1.36
ENSMUSG00000060679	*Mrps9*	4.1	3.83	4.22	3.56
ENSMUSG00000060681	*mKIAA0267*	2.11	1.57	1.62	1.11
ENSMUSG00000060703	*Cd302*	8.03	7.93	7.9	7.56
ENSMUSG00000060708	*Cno*	2.67	3.62	2.26	2.7
ENSMUSG00000060730	*NA*	1.43	1.28	0.88	1.29
ENSMUSG00000060733	*Ipmk*	4.71	3.95	4.44	4.15
ENSMUSG00000060739	*5730427N09Ri*	2.92	2.74	2.34	1.17
ENSMUSG00000060743	*H3f3a*	3.38	1.47	3.12	2.89
ENSMUSG00000060802	*B2m*	10.75	9.85	10.7	10.68
ENSMUSG00000060803	*Gstp1*	4.66	5.94	5.6	5.95
ENSMUSG00000060807	*Serpina6*	8.56	8.41	8.51	8.46
ENSMUSG00000060814	*NA*	1.55	2.88	1.88	1.26
ENSMUSG00000060862	*Zbtb40*	1.76	2.16	1.55	1.5
ENSMUSG00000060904	*Arl1*	4.97	4.25	4.35	4.19
ENSMUSG00000060923	*Acyp2*	1.31	-0.38	0.37	1.27
ENSMUSG00000060935	*AI597468*	3.06	1.67	1.87	1.21
ENSMUSG00000060938	*Rpl26*	4.07	4.54	3.87	3.57
ENSMUSG00000060950	*6720458F09Ri*	0.84	2.47	1.25	1.44
ENSMUSG00000060961	*Slc4a4*	3.85	3.95	3.66	3.33
ENSMUSG00000060981	*Hist1h4h*	2.23	2.05	3.28	3.35
ENSMUSG00000060992	*Copz1*	6.97	7.14	6.77	6.56

ENSMUSG00000061024	*Rrs1*	3.16	2.88	2.78	2.97
ENSMUSG00000061028	*Sfrs16*	1.03	1.96	1.32	1.02
ENSMUSG00000061032	*Rrp1*	5.16	5.51	5.24	4.85
ENSMUSG00000061046	*Haghl*	0.37	2.04	1.77	1.36
ENSMUSG00000061079	*Zfp143*	1.62	1.7	1.34	1.39
ENSMUSG00000061111	*BC003940*	3.15	4.07	3.58	3.72
ENSMUSG00000061118	*Wbscr18*	4.44	4.77	4.6	4.35
ENSMUSG00000061119	*Prcp*	2.26	2.12	2.27	2.19
ENSMUSG00000061130	*Ppm1b*	3.9	3.6	3.52	3.37
ENSMUSG00000061136	*Prpf40a*	4.24	3.25	3.84	3.32
ENSMUSG00000061175	*NA*	2.7	2.32	3.94	3.42
ENSMUSG00000061207	*Stk19*	0.92	1.85	1.51	1.95
ENSMUSG00000061232	*H2-K1*	9.09	9.33	9.2	8.97
ENSMUSG00000061244	*Exoc5*	3.52	2.18	2.73	2.38
ENSMUSG00000061273	*Tmem32*	4.06	3.15	3.51	2.98
ENSMUSG00000061286	*Exosc5*	4.27	5	4.76	4.56
ENSMUSG00000061288	*Taok3*	4.09	4.07	4.36	4.1
ENSMUSG00000061292	*NA*	4.54	3.93	4.84	4.66
ENSMUSG00000061306	*1810073N04Ri*	4.85	5.57	4.9	4.85
ENSMUSG00000061313	*NA*	2.85	2.07	2.96	2.67
ENSMUSG00000061353	*Cxcl12*	5.73	5.38	5.47	5.36
ENSMUSG00000061360	*Phf5a*	4.86	5.45	5.22	5.16
ENSMUSG00000061374	*Fiz1*	3.53	3.68	3.69	3.7
ENSMUSG00000061410	*Zcchc14*	3.2	3.36	3.55	3.35
ENSMUSG00000061436	*Hipk2*	2.72	2.61	2.83	2.85
ENSMUSG00000061455	*Stx17*	2.98	2.43	2.73	2.51
ENSMUSG00000061458	*Nol10*	1.58	1.92	1.83	1.58
ENSMUSG00000061461	*NA*	2.04	1.65	2.18	2.18
ENSMUSG00000061474	*Mrps36*	0.95	0.83	2.1	2.92
ENSMUSG00000061477	*Rps7*	2.54	2.94	3.28	2.58
ENSMUSG00000061479	*Snrpa*	3.24	3.42	3.71	3.72

ENSMUSG00000061518	*LOC10004034*	5.48	6.04	6.3	5.9
ENSMUSG00000061536	*Sec22c*	1.89	1.25	2.43	1.78
ENSMUSG00000061540	*Orm2*	5.04	5.39	5.77	5.11
ENSMUSG00000061555	*Vamp5*	1.18	1.62	1.56	1.58
ENSMUSG00000061559	*Wdr61*	4.21	3.22	3.77	3.58
ENSMUSG00000061589	*Dot1l*	2	2.46	2.09	1.82
ENSMUSG00000061607	*Mdc1*	1.53	1.18	1.75	1.22
ENSMUSG00000061631	*NA*	0.61	1.15	1.71	3.21
ENSMUSG00000061650	*Med9*	3.05	3.5	3.26	3.65
ENSMUSG00000061665	*Cd2ap*	3.4	2.31	3.17	2.75
ENSMUSG00000061689	*Dlgap4*	1.55	1.77	1.58	1.69
ENSMUSG00000061723	*Tnnt3*	#NAME?	#NAME?	3.26	3.49
ENSMUSG00000061731	*Ext1*	2.9	2.79	3.06	2.64
ENSMUSG00000061740	*Cyp2d22*	6.75	7.47	7.1	7.38
ENSMUSG00000061751	*NA*	1.36	1.09	2.13	1.75
ENSMUSG00000061755	*A230054D04R*	2.27	1.82	1.9	1.44
ENSMUSG00000061759	*1700052N19Ri*	2.41	2.45	2.5	2.33
ENSMUSG00000061778	*Mospd2*	4.1	3.35	4.1	3.28
ENSMUSG00000061808	*Ttr*	11.99	12.73	12.83	12.28
ENSMUSG00000061825	*Ces2*	2.04	-0.03	1.8	0.5
ENSMUSG00000061838	*Suclg2*	5.51	4.93	5.42	4.5
ENSMUSG00000061859	*Inadl*	1.41	1.54	1.42	1.04
ENSMUSG00000061887	*Ssbp3*	3.71	4	4.6	4.28
ENSMUSG00000061898	*Rbak*	0.91	0.45	1.03	0.49
ENSMUSG00000061904	*Slc25a3*	8.17	8.02	8.03	7.64
ENSMUSG00000061947	*Serpina10*	7.5	7.59	7.2	7.34
ENSMUSG00000061950	*Ppp4r1*	3.53	3.66	3.41	3.34
ENSMUSG00000061959	*Es22*	6.59	6.31	6.59	6.32
ENSMUSG00000061979	*Wbscr16*	2.9	3.52	3.24	2.96
ENSMUSG00000061981	*Flot2*	4.79	5.36	4.57	4.51
ENSMUSG00000061983	*Rps12*	0.26	1.38	1.73	1.42

ENSMUSG00000062006	*Rpl34*	1.91	0.7	2.24	1.96
ENSMUSG00000062014	*Gmfb*	4.23	3.05	3.7	2.81
ENSMUSG00000062019	*NA*	5.84	5.52	5.49	5.91
ENSMUSG00000062031	*Athl1*	3.83	4.47	4.12	4.08
ENSMUSG00000062040	*Zfp27*	1.43	1.16	0.73	0.71
ENSMUSG00000062054	*Iah1*	7.16	7.15	7.35	7.01
ENSMUSG00000062070	*Pgk1*	3.72	3.28	3.64	2.98
ENSMUSG00000062075	*Lmnb2*	1.66	2.08	1.67	1.55
ENSMUSG00000062078	*Qk*	3.24	2.72	3.01	2.72
ENSMUSG00000062098	*Btbd3*	1.17	0.59	0.82	0.28
ENSMUSG00000062101	*BC031441*	1.25	0.32	0.78	-0.29
ENSMUSG00000062110	*Scfd2*	1.29	1.72	1.56	1.43
ENSMUSG00000062116	*5730403M16R*	2.63	2.2	2.55	2.41
ENSMUSG00000062127	*Cttnbp2nl*	1.05	0.97	0.93	0.57
ENSMUSG00000062169	*Cnih4*	2.5	2.18	2.4	2.06
ENSMUSG00000062181	*EG13909*	7.39	6.9	6.9	6.83
ENSMUSG00000062190	*Lancl2*	1.69	1.43	1.41	1
ENSMUSG00000062198	*2700097O09Ri*	2.03	2.02	2.39	1.75
ENSMUSG00000062202	*Btbd9*	3.17	2.93	2.9	2.51
ENSMUSG00000062203	*Gspt1*	6.06	5.11	5.62	5.25
ENSMUSG00000062232	*Rapgef2*	1.48	1.46	1.56	1.54
ENSMUSG00000062234	*Gak*	4.56	4.91	4.85	4.68
ENSMUSG00000062260	*AA415398*	1.77	1.33	2.06	1.99
ENSMUSG00000062300	*Pvrl2*	3.4	4.4	3.67	3.79
ENSMUSG00000062352	*Itgb1bp1*	3.35	3.46	3.64	3.74
ENSMUSG00000062373	*Tmem65*	1.93	0.89	1.41	1.14
ENSMUSG00000062376	*2010012O05Ri*	3.02	3.57	3.42	2.87
ENSMUSG00000062381	*Vps28*	5.91	6.49	6.29	6.06
ENSMUSG00000062397	*Zfp706*	5.91	4.47	5.31	4.85
ENSMUSG00000062410	*Hsd3b3*	6.06	4.45	5.49	5.44
ENSMUSG00000062421	*Arf2*	2.26	2.37	1.9	1.86

ENSMUSG00000062480	*Acat3*	7.26	6.92	6.89	6.45
ENSMUSG00000062515	*Fabp4*	3.48	2.36	3	2.91
ENSMUSG00000062526	*Mppe1*	2.39	2.09	2.48	2.05
ENSMUSG00000062563	*Cys1*	0.74	2.07	1.74	1.38
ENSMUSG00000062580	*Timm17a*	3.51	2.52	3.08	3.09
ENSMUSG00000062585	*Cnr2*	1.44	1.79	1.35	1.87
ENSMUSG00000062604	*Srpk2*	2.66	1.21	2.32	1.88
ENSMUSG00000062619	*2310039H08Ri*	4.65	4.93	5.2	4.96
ENSMUSG00000062624	*Cyp2c67*	6.03	5.43	6.02	6.01
ENSMUSG00000062627	*Mysm1*	2.03	0.91	1.54	1.2
ENSMUSG00000062646	*mFLJ00088*	3.23	1.95	3.18	1.79
ENSMUSG00000062647	*Rpl7a*	4.16	4.28	4.08	4.08
ENSMUSG00000062691	*NA*	4.46	3.65	4.04	3.89
ENSMUSG00000062729	*Ppox*	2.83	3.19	2.79	2.73
ENSMUSG00000062761	*Zfp512*	1.53	2.08	2	1.85
ENSMUSG00000062762	*Ei24*	8.13	7.08	7.4	6.81
ENSMUSG00000062797	*l7Rn6*	5.1	3.93	4.49	4.43
ENSMUSG00000062822	*4833420G17Ri*	1.84	0.4	2.57	1.44
ENSMUSG00000062895	*NA*	4.75	1.52	3.84	5.34
ENSMUSG00000062901	*Klhl24*	4.66	3.05	4.2	3.21
ENSMUSG00000062906	*Hdac10*	2.52	2.61	2.14	2.04
ENSMUSG00000062908	*Acadm*	8.04	7.11	7.81	7.47
ENSMUSG00000062929	*Cfl2*	5.95	5.35	5.5	4.96
ENSMUSG00000062931	*NA*	1.29	1.08	0.64	0.2
ENSMUSG00000062937	*Mtap*	5.24	4.2	4.8	4.26
ENSMUSG00000062946	*NA*	0.56	0.24	1.6	0.5
ENSMUSG00000062949	*Atp11c*	5.72	4.65	5.25	4.58
ENSMUSG00000062960	*Kdr*	3.56	3.98	3.21	3.47
ENSMUSG00000062963	*Ufc1*	6.07	5.95	5.67	5.56
ENSMUSG00000062980	*A430107O13R*	3.73	3.3	3.69	3.53
ENSMUSG00000062981	*D10Ertd322e*	3.64	3.35	3.62	3.73

ENSMUSG00000062997	*Rpl35*	0.35	0.34	1.06	0.77
ENSMUSG00000063015	*Ccni*	6.07	5.23	5.72	5.15
ENSMUSG00000063019	*Manbal*	3.16	3.6	3.26	3.38
ENSMUSG00000063049	*Ing2*	2.44	1.88	1.77	1.45
ENSMUSG00000063052	*Lrrc40*	2.62	1.73	2.22	1.83
ENSMUSG00000063065	*Mapk3*	4.3	4.89	4.54	4.5
ENSMUSG00000063077	*Kif1b*	4.34	4.01	4.35	3.93
ENSMUSG00000063108	*mKIAA4196*	1.31	0.79	0.88	0.23
ENSMUSG00000063145	*Bbs5*	1.22	0.68	2.07	0.91
ENSMUSG00000063171	*NA*	3.11	3.76	3.77	3.73
ENSMUSG00000063172	*2900042B11Ri*	2.07	1.17	2.08	1.55
ENSMUSG00000063179	*Pstk*	2.91	1.68	2.59	2.26
ENSMUSG00000063200	*Nol7*	4.88	4.3	4.51	3.85
ENSMUSG00000063229	*Ldha*	7.43	8.04	7.64	7.41
ENSMUSG00000063232	*Serpina11*	6.42	7.36	6.2	6.83
ENSMUSG00000063235	*Ptpmt1*	5.35	5.42	5.47	5.05
ENSMUSG00000063236	*1110038F14Ri*	2.61	2.55	2.65	2.57
ENSMUSG00000063253	*Scoc*	1.77	-0.23	0.61	0.12
ENSMUSG00000063268	*Plec1*	2.6	2.91	2.72	2.51
ENSMUSG00000063273	*Narg1*	4.19	3.38	3.81	3.24
ENSMUSG00000063275	*Ptpla*	1.45	1.66	1.47	1.22
ENSMUSG00000063281	*Zfp35*	3.33	2.97	2.87	2.42
ENSMUSG00000063316	*Rpl27*	0.25	1.53	1.44	1.12
ENSMUSG00000063317	*NA*	1.13	0.53	0.66	0.99
ENSMUSG00000063320	*NA*	3.26	3.54	3.96	3.71
ENSMUSG00000063334	*Krr1*	3.75	3.42	3.52	3.3
ENSMUSG00000063354	*Slc39a4*	4.83	5.56	5.06	5.27
ENSMUSG00000063358	*Mapk1*	5.45	5.1	5.43	5.07
ENSMUSG00000063362	*Alg11*	3.42	2.99	3.14	2.78
ENSMUSG00000063382	*Bcl9l*	3.19	4.56	3.68	3.5
ENSMUSG00000063388	*NA*	4.46	-0.45	0.88	1.06

ENSMUSG00000063406	*Tmed5*	4.48	3.28	3.88	3.24
ENSMUSG00000063410	*Stk24*	3.63	3.78	3.78	3.39
ENSMUSG00000063415	*Cyp26b1*	1.31	1.51	1.57	1.25
ENSMUSG00000063428	*Ddo*	3.56	3.02	3.58	3.41
ENSMUSG00000063439	*B9d2*	1.95	2.01	2.68	2.31
ENSMUSG00000063445	*Nmral1*	1.73	1.83	1.59	1.99
ENSMUSG00000063450	*Syne2*	1.71	1.76	2.1	1.89
ENSMUSG00000063457	*Rps15*	6.57	7.08	7.02	7.55
ENSMUSG00000063488	*NA*	1.76	1.26	1.9	1.22
ENSMUSG00000063495	*NA*	3.51	1.55	2.4	3.05
ENSMUSG00000063511	*Snrp70*	3.49	4.18	3.57	3.47
ENSMUSG00000063524	*Eno1*	3.61	3.36	4.4	3.03
ENSMUSG00000063550	*Nup98*	2.6	2.39	2.48	2.42
ENSMUSG00000063558	*Aox1*	4.11	4.21	3.93	3.93
ENSMUSG00000063576	*Klhdc3*	5.08	5.56	5.32	5.26
ENSMUSG00000063656	*NA*	4.88	4.48	4.53	4.44
ENSMUSG00000063659	*Zfp238*	3.07	2.91	2.86	2.57
ENSMUSG00000063683	*Glyat*	6.27	5.76	5.88	5.93
ENSMUSG00000063684	*NA*	2.84	1.7	2.4	3.29
ENSMUSG00000063696	*NA*	2.46	3.78	3.36	3.25
ENSMUSG00000063704	*Mapk15*	1.56	2.33	1.36	1.3
ENSMUSG00000063727	*Tnfrsf11b*	1.94	1.35	1.68	1.58
ENSMUSG00000063730	*Hsd3b2*	2.48	3.23	2.5	3.01
ENSMUSG00000063739	*NA*	1.37	1.34	2.23	0.9
ENSMUSG00000063757	*4632433K11Ri*	0.83	1.55	1.38	0.89
ENSMUSG00000063760	*NA*	4.19	3.4	3.29	3.71
ENSMUSG00000063785	*Utp14a*	3.37	2.83	3.49	3.26
ENSMUSG00000063787	*Chchd1*	5.43	4.13	5.19	5.11
ENSMUSG00000063800	*Prpf38a*	2.83	2.37	2.89	2.52
ENSMUSG00000063801	*Ap3s2*	2.94	3.13	3.04	3.03
ENSMUSG00000063802	*1500019G21Ri*	3.89	4.83	4.19	4.12

ENSMUSG00000063808	*Gpatch1*	1.98	1.83	1.79	1.44
ENSMUSG00000063849	*Ppcdc*	2.33	2.67	2.38	2.4
ENSMUSG00000063856	*Gpx1*	10.47	10.39	10.17	10.11
ENSMUSG00000063870	*mKIAA4075*	4.59	4.66	4.56	4.2
ENSMUSG00000063882	*Uqcrh*	6.9	6.41	7.09	7.04
ENSMUSG00000063884	*Ptcd3*	4.55	3.7	4.13	3.59
ENSMUSG00000063886	*NA*	2.05	2.38	2.32	2.23
ENSMUSG00000063888	*Rpl7l1*	5.26	5.65	5.08	5.27
ENSMUSG00000063889	*Crem*	3.55	2.78	2.73	2.74
ENSMUSG00000063894	*Zfp192*	1.82	1.11	1.36	0.56
ENSMUSG00000063895	*Nupl1*	2.8	2.55	2.71	2.19
ENSMUSG00000063902	*NA*	4.69	4.31	4.22	5.13
ENSMUSG00000063904	*Dpp3*	4.66	4.94	4.74	4.75
ENSMUSG00000063929	*Cyp4a32*	2.3	2.35	1.36	2.44
ENSMUSG00000063931	*Pepd*	5.11	5.47	5.22	4.9
ENSMUSG00000063952	*Brpf3*	3.04	3.34	3.24	3.25
ENSMUSG00000063972	*Nr6a1*	1.41	1.07	1.85	1.48
ENSMUSG00000064021	*NA*	0.7	1.04	1.41	2.62
ENSMUSG00000064030	*Wibg*	3.08	4	3.4	2.93
ENSMUSG00000064037	*Xab1*	2.58	2.92	2.59	2.42
ENSMUSG00000064068	*Mtx1*	4.39	4.49	4.28	4.31
ENSMUSG00000064090	*Vrk2*	1.98	1.86	2.09	1.61
ENSMUSG00000064105	*Cnnm2*	2.27	2.28	2.57	2.16
ENSMUSG00000064120	*Mocs1*	6.38	6.6	6.66	6.38
ENSMUSG00000064127	*Med14*	1.87	1.34	1.89	1.55
ENSMUSG00000064138	*NA*	2.75	2.06	2.06	1.64
ENSMUSG00000064145	*Ari2*	3.28	3.13	2.94	2.8
ENSMUSG00000064163	*NA*	3.92	3.4	4.32	4.66
ENSMUSG00000064181	*Rab3ip*	4.79	4.38	4.63	4.17
ENSMUSG00000064210	*Tmem16f*	2.12	1.72	1.51	1.26
ENSMUSG00000064215	*ISG12a*	5.49	5.93	5.45	5.68

ENSMUSG00000064225	*Paqr9*	5.75	6.36	5.3	5.08
ENSMUSG00000064254	*Ethe1*	6.08	6.56	6.05	5.6
ENSMUSG00000064262	*Gimap8*	1.44	0.71	0.65	0.36
ENSMUSG00000064267	*Hvcn1*	0.48	0.66	1.55	0.47
ENSMUSG00000064284	*2210021J22Ri*	1.22	2.44	2.34	2.36
ENSMUSG00000064289	*Tank*	3.21	2.08	2.84	2.33
ENSMUSG00000064294	*Aox3*	6.14	5.84	5.78	5.85
ENSMUSG00000064302	*Clasp1*	2.14	1.63	1.94	1.9
ENSMUSG00000064307	*NA*	1.74	1.94	1.68	1.48
ENSMUSG00000064326	*Siva1*	0.58	1.78	1.62	0.52
ENSMUSG00000064373	*Sepp1*	11.57	11.49	11.69	11.43
ENSMUSG00000064405	*NA*	1.35	-0.13	0.56	0.34
ENSMUSG00000064441	*NA*	#NAME?	-2.68	1.67	-0.05
ENSMUSG00000064493	*NA*	4.73	2.34	3.66	1.83
ENSMUSG00000064540	*NA*	3.08	3.06	3.4	2.4
ENSMUSG00000064615	*NA*	1.01	-0.19	0.24	#NAME?
ENSMUSG00000064637	*NA*	4.22	4.24	3.52	2.9
ENSMUSG00000064647	*NA*	0.81	0.44	1.2	#NAME?
ENSMUSG00000064725	*NA*	1.32	1.2	-0.91	0.54
ENSMUSG00000064791	*NA*	1.67	2.1	3.38	2.38
ENSMUSG00000064797	*NA*	3.3	2.15	2.7	-0.57
ENSMUSG00000064816	*NA*	1.46	1.97	-0.76	#NAME?
ENSMUSG00000064949	*NA*	1.23	0.68	0.91	0.29
ENSMUSG00000064981	*NA*	1.71	-0.85	0.46	-1.1
ENSMUSG00000064995	*NA*	0.52	-0.78	1.38	0.4
ENSMUSG00000065037	*NA*	3.6	4.51	5.79	5.01
ENSMUSG00000065087	*NA*	1.24	-1.33	-1.33	-0.71
ENSMUSG00000065105	*NA*	2.3	2.68	2.58	0.43
ENSMUSG00000065124	*NA*	1.11	-0.58	-0.42	-1.14
ENSMUSG00000065126	*NA*	-0.81	0.43	1.23	1.05
ENSMUSG00000065265	*NA*	1.21	0.55	1.5	-0.89

ENSMUSG00000065331	*NA*	-0.13	-0.1	1.43	-1.1
ENSMUSG00000065407	*NA*	5.63	6.57	6.23	6.3
ENSMUSG00000065455	*NA*	0.12	2.12	1.13	1.93
ENSMUSG00000065463	*NA*	1.64	-0.68	0.82	0.14
ENSMUSG00000065475	*NA*	0.29	1.2	1.49	-0.16
ENSMUSG00000065487	*NA*	1.4	2.73	2.32	2.42
ENSMUSG00000065529	*NA*	2.24	2.5	2.35	2.61
ENSMUSG00000065548	*NA*	0.61	1.85	1.13	1.02
ENSMUSG00000065591	*NA*	1.32	-1.1	-0.19	-1.25
ENSMUSG00000065663	*NA*	1.29	-0.97	0.17	#NAME?
ENSMUSG00000065862	*NA*	1.85	1.17	0.63	0.69
ENSMUSG00000065870	*NA*	#NAME?	-2.08	1.37	-1.08
ENSMUSG00000065887	*NA*	3.91	1.54	2.97	3.08
ENSMUSG00000065954	*Tacc1*	3.58	3.95	3.41	3.51
ENSMUSG00000065979	*C530044N13R*	5.49	5.4	5.55	5.25
ENSMUSG00000065987	*Cd209b*	1.31	1.52	0.78	0.73
ENSMUSG00000065990	*Aurkaip1*	5.68	5.71	5.92	5.68
ENSMUSG00000066026	*Dhrs3*	7.35	7.57	7.47	7.31
ENSMUSG00000066036	*Zubr1*	3.84	4.05	3.99	3.73
ENSMUSG00000066037	*Hnrnpr*	2.5	2.05	1.98	1.58
ENSMUSG00000066042	*Med18*	1.16	0.06	0.71	0.63
ENSMUSG00000066043	*Phactr4*	4.3	4.12	4.06	3.94
ENSMUSG00000066048	*NA*	2.59	2.49	2.77	1.83
ENSMUSG00000066072	*Cyp4a10*	9.28	8.71	8.91	7.97
ENSMUSG00000066148	*Prpf4*	2.47	2.1	2.24	2.21
ENSMUSG00000066149	*Cdc26*	2.07	1.74	1.7	2.25
ENSMUSG00000066150	*Slc31a1*	6.68	6.12	6.35	5.95
ENSMUSG00000066151	*NA*	2.96	3.3	3.38	3.15
ENSMUSG00000066152	*Slc31a2*	2.94	2.78	2.81	2.71
ENSMUSG00000066153	*OTTMUSG000*	1.4	0.1	1.28	1.42
ENSMUSG00000066154	*Mup3*	9.17	8.96	8.65	9.44

ENSMUSG00000066175	*NA*	1.31	2.76	2.46	3.09
ENSMUSG00000066232	*Ipo7*	5.56	4.87	5.3	4.76
ENSMUSG00000066233	*Tmem42*	2.84	3.01	2.95	2.4
ENSMUSG00000066235	*C85492*	0.71	1.4	1.36	1.57
ENSMUSG00000066278	*Vps37b*	3.18	3.9	3.24	3.01
ENSMUSG00000066306	*Numa1*	3.31	3.66	3.56	3.38
ENSMUSG00000066319	*Rtp3*	4.61	4.68	4.69	4.81
ENSMUSG00000066324	*Impad1*	4.31	3.27	3.83	3.31
ENSMUSG00000066357	*Wdr6*	1.73	2.48	2.44	2.21
ENSMUSG00000066361	*Serpina3c*	4.06	4.52	3.9	3.68
ENSMUSG00000066362	*NA*	1.28	2.08	0.72	1.87
ENSMUSG00000066363	*Serpina3f*	2.68	1.29	1.28	0.97
ENSMUSG00000066366	*Serpina1a*	8.16	8.29	8.49	8.61
ENSMUSG00000066406	*NA*	2.15	1.83	2.86	2.63
ENSMUSG00000066415	*NA*	3.9	3.32	3.56	3.24
ENSMUSG00000066440	*Zfyve26*	2.85	2.64	3.04	2.68
ENSMUSG00000066441	*Rdh11*	5.73	5.33	4.83	4.55
ENSMUSG00000066442	*Mthfs*	1.59	0.83	1.43	1.21
ENSMUSG00000066491	*NA*	4.25	3.24	3.88	5.45
ENSMUSG00000066513	*Klk1b4*	0.89	0.09	1.49	1.26
ENSMUSG00000066551	*Hmgb1*	1.27	0.29	1.36	1.02
ENSMUSG00000066553	*NA*	3.31	0.27	3.88	4.02
ENSMUSG00000066568	*Lsm14a*	4.32	3.83	3.98	3.74
ENSMUSG00000066571	*4931406P16Ri*	2.06	1.72	1.91	1.99
ENSMUSG00000066595	*Flvcr1*	1.19	0.79	1.23	0.25
ENSMUSG00000066621	*mKIAA1358*	1.06	1.76	1.43	0.95
ENSMUSG00000066637	*Ttc32*	3.98	2.17	3.65	3.09
ENSMUSG00000066640	*Fbxl18*	0.88	1.1	1.04	0.88
ENSMUSG00000066647	*EG330503*	1.11	0.51	0.88	0.47
ENSMUSG00000066687	*Zbtb16*	4.17	4.23	3.68	3.53
ENSMUSG00000066705	*Fxyd6*	0.73	1.27	1.17	1.62

ENSMUSG00000066735	*Vkorc1l1*	0.97	0.67	1.48	0.95
ENSMUSG00000066757	*NA*	2.67	1.55	2.04	3.07
ENSMUSG00000066798	*Zbtb6*	2.06	0.42	1.44	1.04
ENSMUSG00000066839	*Ecsit*	5.05	5.53	5.3	5.12
ENSMUSG00000066880	*Zfp617*	1.66	0.34	1.6	0.45
ENSMUSG00000066892	*Fbxl12*	1.1	1.02	1.45	1.45
ENSMUSG00000066900	*Suds3*	5.47	5.96	5.69	5.57
ENSMUSG00000066944	*NA*	0.95	1.39	1.14	1.69
ENSMUSG00000066952	*NA*	2.08	2.17	1.65	1.36
ENSMUSG00000066979	*Bub3*	3.89	4.63	4.28	4.19
ENSMUSG00000067071	*Hes6*	4.22	5.03	4.27	4.57
ENSMUSG00000067085	*NA*	3.68	4.27	4.15	3.9
ENSMUSG00000067124	*NA*	2.22	2.57	2.76	2.47
ENSMUSG00000067144	*Slc22a7*	3.23	3.07	3.62	3.06
ENSMUSG00000067148	*Rpo1-1*	4.13	4.84	4.49	4.35
ENSMUSG00000067149	*Igj*	0.43	1.48	3.87	1.27
ENSMUSG00000067150	*Xpo5*	2.5	2.68	2.66	2.51
ENSMUSG00000067189	*NA*	1.03	0.22	1.73	1.38
ENSMUSG00000067194	*Eif1ay*	5.48	4.16	4.71	3.91
ENSMUSG00000067212	*H2-T23*	6.1	6.69	6.47	6.36
ENSMUSG00000067219	*Npal1*	2.95	1.15	2.99	1.43
ENSMUSG00000067225	*Cyp2c54*	8.24	7.63	7.57	7.46
ENSMUSG00000067235	*H2-Q10*	9.43	9.65	9.54	9.43
ENSMUSG00000067274	*Arbp*	4.7	5.33	5.2	4.93
ENSMUSG00000067279	*Ppp1r3c*	6.26	6.11	5.48	4.96
ENSMUSG00000067284	*Hspa1b*	0.18	2.13	2.47	4.53
ENSMUSG00000067336	*Bmpr2*	2.63	2.51	2.51	2.53
ENSMUSG00000067365	*Tmem128*	3.81	3.11	3.73	3.44
ENSMUSG00000067367	*Lyar*	3.25	3.23	3.4	2.85
ENSMUSG00000067369	*4732479N06Ri*	3.6	3.27	3.32	2.53
ENSMUSG00000067424	*Zfp563*	1.15	0.26	0.77	0.16

ENSMUSG00000067480	*OTTMUSG000*	2.8	0.88	2.79	1.66
ENSMUSG00000067567	*Hdac8*	1.11	0.43	1.54	1.41
ENSMUSG00000067579	*NA*	2.32	3	3.08	3.35
ENSMUSG00000067586	*Edg3*	1.04	0.74	0.79	0.15
ENSMUSG00000067608	*NA*	2.54	1.31	2.61	1.6
ENSMUSG00000067653	*Ankrd23*	-0.71	-0.43	1.02	0.47
ENSMUSG00000067656	*NA*	3.87	2.37	3.19	2.94
ENSMUSG00000067713	*Prkag1*	4.33	5.02	4.57	4.43
ENSMUSG00000067722	*NA*	3.89	4.08	4.31	4.17
ENSMUSG00000067736	*NA*	3.54	0.24	0.89	0.89
ENSMUSG00000067787	*Blcap*	4.17	4.46	4.26	3.73
ENSMUSG00000067813	*Xkr9*	3.27	1.73	2.84	2.48
ENSMUSG00000067818	*NA*	1.42	1.97	1.98	2.1
ENSMUSG00000067825	*Pex26*	3.14	3.42	3.22	2.98
ENSMUSG00000067847	*2010100O12R*	4.37	5.32	6.75	6.67
ENSMUSG00000067851	*Arfgef1*	4.96	4.25	4.61	4.01
ENSMUSG00000067870	*NA*	2.29	2.52	2.03	3.33
ENSMUSG00000067873	*Htatsf1*	3.82	3.42	3.45	2.7
ENSMUSG00000067889	*Spnb3*	3.32	3.94	4.09	3.65
ENSMUSG00000067928	*Zfp760*	1.1	0.34	0.86	-0.32
ENSMUSG00000067931	*BC049807*	1.26	0.6	1	0.92
ENSMUSG00000067942	*Zfp160*	1.83	0.43	0.9	0.13
ENSMUSG00000067995	*Gtf2f2*	2.98	2.76	2.79	2.61
ENSMUSG00000068011	*NA*	3.08	3.42	3.48	3.38
ENSMUSG00000068015	*Lrch1*	1.87	1.98	2.05	1.99
ENSMUSG00000068036	*Mllt4*	2.43	2.47	2.81	2.58
ENSMUSG00000068039	*AK163149*	7.33	7.1	7.04	6.77
ENSMUSG00000068040	*Tm9sf4*	4.8	5.06	4.8	4.73
ENSMUSG00000068083	*Cyp2d40*	5.07	5.17	5.07	5.03
ENSMUSG00000068086	*Cyp2d9*	5	5.81	5.33	6.35
ENSMUSG00000068101	*Cenpm*	2.22	2.4	2.4	1.8

ENSMUSG00000068134	*Zfp120*	2.56	1.26	1.78	0.93
ENSMUSG00000068184	*NA*	4.79	3.52	4.2	3.7
ENSMUSG00000068188	*NA*	4	3	4.1	3.32
ENSMUSG00000068206	*Pick1*	2.16	2.89	2.6	2.2
ENSMUSG00000068220	*Lgals1*	2.93	2.55	3.45	4.05
ENSMUSG00000068240	*NA*	3.66	3.8	3.76	5.65
ENSMUSG00000068246	*NA*	4.34	4.09	3.93	4.35
ENSMUSG00000068250	*NA*	1.98	0.53	1.79	1.18
ENSMUSG00000068264	*2310035K24Ri*	3.52	3.66	4.07	3.76
ENSMUSG00000068267	*Cenpb*	4.35	5.01	4.57	4.38
ENSMUSG00000068284	*Gm608*	3.16	2.79	2.94	2.72
ENSMUSG00000068290	*2600009E05Ri*	6.95	6.55	6.78	6.58
ENSMUSG00000068299	*1700019G17Ri*	1.19	1.39	0.97	0.63
ENSMUSG00000068303	*NA*	2.77	3.17	3.11	3.09
ENSMUSG00000068328	*Aup1*	6.94	7.29	7.21	6.97
ENSMUSG00000068329	*HtrA2*	3.04	3.79	2.98	2.85
ENSMUSG00000068391	*Chrac1*	4.27	4.21	4.22	4.02
ENSMUSG00000068479	*Mfap1a*	1.77	0.6	1.24	0.43
ENSMUSG00000068551	*Zfp467*	1.91	2.45	2.62	2.29
ENSMUSG00000068566	*Myadm*	3.28	3.58	3.33	2.97
ENSMUSG00000068580	*Zfyve19*	3.36	3.41	3.32	3.29
ENSMUSG00000068587	*NA*	3.28	2.35	2.95	2.53
ENSMUSG00000068606	*EG225594*	1.92	-0.79	-1.1	-0.75
ENSMUSG00000068663	*Clec16a*	2.86	2.8	2.47	2.47
ENSMUSG00000068706	*NA*	4.04	3.34	3.98	4.83
ENSMUSG00000068732	*2010200O16Ri*	4.42	4.02	4.25	3.82
ENSMUSG00000068735	*Trp53i11*	1.48	2.27	2.44	2.21
ENSMUSG00000068739	*Sars*	5.1	5.79	5.38	5.34
ENSMUSG00000068742	*Cry2*	3.26	3.96	3.94	3.67
ENSMUSG00000068749	*Psma5*	1.37	1.31	1.52	0.97
ENSMUSG00000068762	*Gstm6*	5.49	5.75	5.69	5.32

ENSMUSG00000068798	*Rap1a*	3.8	2.52	3.21	2.81
ENSMUSG00000068823	*Csde1*	6.15	5.34	5.78	5.29
ENSMUSG00000068856	*Sf3b4*	2.8	2.51	2.04	1.74
ENSMUSG00000068874	*Selenbp1*	6.47	6.77	6.65	6.48
ENSMUSG00000068876	*NA*	2.15	1.85	2.03	1.43
ENSMUSG00000068877	*Selenbp2*	3.25	0.37	3.12	2.05
ENSMUSG00000068882	*Ssb*	5.29	4.33	4.78	4.2
ENSMUSG00000068910	*NA*	3.96	4.18	3.74	3.92
ENSMUSG00000068917	*Clk2*	2.15	2.36	2.41	2.24
ENSMUSG00000068921	*Dap3*	5.2	4.63	5.15	4.58
ENSMUSG00000068922	*Msto1*	1.86	2.78	2.71	2.07
ENSMUSG00000069020	*Urm1*	3.77	3.75	3.72	3.56
ENSMUSG00000069089	*Cdk7*	3.1	2.6	3.14	3.02
ENSMUSG00000069094	*Pde7a*	0.83	0.2	1.01	0.04
ENSMUSG00000069135	*Fgfr1op*	3.28	2.57	3	2.63
ENSMUSG00000069204	*Zfp748*	1.34	0.15	0.33	0.15
ENSMUSG00000069206	*C330011K17Ri*	1.91	1.22	1.74	1.2
ENSMUSG00000069208	*BC012278*	3.84	2.75	3.39	3.04
ENSMUSG00000069237	*C78339*	4.56	3.82	4.09	3.51
ENSMUSG00000069255	*Dusp22*	3.28	2.57	2.77	2.15
ENSMUSG00000069324	*NA*	2.92	1.99	3.42	1.38
ENSMUSG00000069394	*Pcdhga2*	2.27	2.52	2.28	2.37
ENSMUSG00000069456	*Rdh16*	5.62	5.04	5.43	4.93
ENSMUSG00000069495	*Epc2*	2.95	2.28	2.53	2.29
ENSMUSG00000069516	*Lyzs*	5.09	5.32	5.5	5.05
ENSMUSG00000069520	*Tmem19*	5.83	6.11	5.35	5.54
ENSMUSG00000069539	*Scyl2*	4.24	3.84	3.96	3.72
ENSMUSG00000069564	*NA*	3.57	2.49	3.38	2.45
ENSMUSG00000069565	*Dazap1*	3.93	3.81	4.44	4.24
ENSMUSG00000069618	*NA*	0.96	1.24	1.84	1.48
ENSMUSG00000069633	*Pex11g*	2.88	4	3.49	3.62

ENSMUSG00000069637	*NA*	5.21	4.86	5.05	4.38
ENSMUSG00000069662	*Marcks*	3.66	2.51	3.26	2.64
ENSMUSG00000069668	*Sult3a1*	9.93	7.14	9.33	8.27
ENSMUSG00000069678	*Pcgf1*	0.78	1.72	1.43	1.17
ENSMUSG00000069682	*NA*	1.77	1.48	1.22	1.56
ENSMUSG00000069729	*Arid1b*	1.66	2.02	2.36	1.99
ENSMUSG00000069733	*Ube2u*	2.95	1.31	2.48	-0.93
ENSMUSG00000069744	*Psmb3*	2.52	2.98	3.06	2.32
ENSMUSG00000069769	*Msi2*	2.55	1.62	2.22	1.81
ENSMUSG00000069792	*OTTMUSG000*	4.92	4.71	4.55	4.38
ENSMUSG00000069805	*Fbp1*	9.81	9.66	10	9.82
ENSMUSG00000069808	*2310047D13Ri*	1.56	0.98	1.39	1.02
ENSMUSG00000069825	*Spata22*	1.06	0.03	0.06	0.15
ENSMUSG00000069835	*Sat2*	3.2	3.77	3.49	3.4
ENSMUSG00000069844	*Sco1*	3.31	2.19	2.91	2.36
ENSMUSG00000069874	*Iigp2*	4.76	3.53	3.32	3.9
ENSMUSG00000069895	*D8Ertd587e*	2.6	2.51	2.41	2.38
ENSMUSG00000069899	*NA*	2.77	1.81	2.07	2.54
ENSMUSG00000069917	*Hba-a2*	1.14	4	4.81	5
ENSMUSG00000069919	*Hba-a2*	1.48	4.43	5.22	5.45
ENSMUSG00000069920	*C76566*	3.08	1.91	2.72	2.39
ENSMUSG00000069922	*NA*	8.8	8.61	8.39	8.75
ENSMUSG00000069972	*NA*	1.59	2.26	2.44	0.93
ENSMUSG00000070002	*Ell*	3.62	3.85	3.97	3.72
ENSMUSG00000070003	*Ssbp4*	0.86	1.3	1.26	1.11
ENSMUSG00000070044	*BC035537*	3.07	2.75	2.49	2.21
ENSMUSG00000070047	*Fat1*	1.67	1.88	2.04	1.7
ENSMUSG00000070056	*Mfhas1*	3.06	3.64	3.23	3.32
ENSMUSG00000070283	*4733401H18Ri*	3.63	4.26	3.69	3.84
ENSMUSG00000070284	*Gmppb*	3.33	4.25	3.69	3.7
ENSMUSG00000070305	*Mpzl3*	1.89	1.29	1.66	1.33

ENSMUSG00000070315	*NA*	2.72	3.02	2.94	3.02
ENSMUSG00000070319	*Eif3g*	5.15	6.24	5.84	5.82
ENSMUSG00000070327	*Rnf213*	2.58	2	2.25	2.3
ENSMUSG00000070343	*NA*	-0.53	-0.9	1.05	-0.12
ENSMUSG00000070348	*Ccnd1*	3.78	4.39	3.69	3.76
ENSMUSG00000070371	*Prss36*	1.09	1.43	1.37	1.02
ENSMUSG00000070392	*Hist2h3c1*	2.87	2.26	2.74	2.13
ENSMUSG00000070394	*1810027O10Ri*	7.42	6.37	7.27	7.01
ENSMUSG00000070397	*Tmem102*	2.65	2.87	2.73	2.13
ENSMUSG00000070407	*Hs3st3b1*	4.6	4.47	4.62	4.34
ENSMUSG00000070420	*Zfp498*	1.85	1.43	1.69	1.55
ENSMUSG00000070426	*Rnf121*	3.1	2.74	2.94	2.64
ENSMUSG00000070427	*Il18bp*	3.64	3.06	3.07	2.56
ENSMUSG00000070436	*Serpinh1*	3.21	3.81	2.65	3.28
ENSMUSG00000070473	*Cldn3*	5.03	6.44	6.02	5.9
ENSMUSG00000070488	*NA*	2.49	1.61	2.15	2.97
ENSMUSG00000070493	*Chchd2*	6.1	5.38	5.73	4.91
ENSMUSG00000070497	*NA*	4.65	3.04	4.37	5.19
ENSMUSG00000070520	*Ndnl2*	1.61	1.85	1.74	1.74
ENSMUSG00000070528	*NA*	1.49	0.39	1.6	1.17
ENSMUSG00000070544	*Top1*	5.21	4.33	4.82	4.42
ENSMUSG00000070572	*NA*	1.1	1.16	0.99	2.57
ENSMUSG00000070576	*Mn1*	2.22	3.08	2.97	2.79
ENSMUSG00000070594	*EG214403*	6.52	5.87	6.38	5.85
ENSMUSG00000070643	*sox-13*	1.31	1.78	2.09	1.67
ENSMUSG00000070644	*Etnk2*	7.82	7.57	7.84	7.27
ENSMUSG00000070645	*Ren1*	2.4	1.96	3.49	1.81
ENSMUSG00000070661	*Rnf186*	1.93	2.17	1.92	0.88
ENSMUSG00000070690	*NA*	2.87	3.16	2.71	3.04
ENSMUSG00000070697	*Utp3*	4.69	4.24	4.43	4.13
ENSMUSG00000070699	*SerRSmt*	2.77	3.37	2.96	2.83

ENSMUSG00000070704	*Ugt2b36*	8.76	8.03	8.57	8.18
ENSMUSG00000070705	*NA*	1.48	0.81	1.08	0.65
ENSMUSG00000070730	*1200015F23Ri*	5.21	5.45	5.28	5.06
ENSMUSG00000070733	*Fryl*	1.33	1.02	1.66	1.11
ENSMUSG00000070737	*LOC10003996*	3.17	2.71	2.94	2.89
ENSMUSG00000070738	*NA*	2.58	2.97	2.82	2.62
ENSMUSG00000070780	*BC013481*	4.36	3.73	4.4	4.21
ENSMUSG00000070810	*EG629219*	4.15	0.22	4.01	0.78
ENSMUSG00000070811	*C730007P19R*	7.02	2.8	6.61	3.49
ENSMUSG00000070873	*EG232801*	2.33	1.36	1.81	1.41
ENSMUSG00000070889	*NA*	1.66	1.42	1.61	1.31
ENSMUSG00000070923	*Klhl9*	4.58	3.48	4.03	3.39
ENSMUSG00000070934	*Rraga*	5.02	4.72	4.71	4.42
ENSMUSG00000070939	*Tgfbrap1*	3.24	3.31	3.64	3.48
ENSMUSG00000070953	*Rabepk*	2.33	2.73	2.16	2.46
ENSMUSG00000070960	*NA*	2.84	1.88	1.34	2.38
ENSMUSG00000070972	*2010203O07R*	3.72	2.73	3.19	2.81
ENSMUSG00000070985	*NA*	5.39	4.6	4.82	4.87
ENSMUSG00000071014	*Ndufb6*	6.09	6.31	6.49	5.9
ENSMUSG00000071035	*NA*	2.64	2.08	1.91	3.13
ENSMUSG00000071042	*Rasgrp3*	1.19	1.24	1.22	0.98
ENSMUSG00000071054	*NA*	3.68	4.29	4.06	3.97
ENSMUSG00000071072	*Ptges3*	4.4	3.74	4.49	3.99
ENSMUSG00000071074	*Yipf3*	6	6.57	6.01	6.06
ENSMUSG00000071076	*Jund1*	4.55	6.11	5.74	5.62
ENSMUSG00000071078	*2310073E15Ri*	3.41	3.76	2.96	3.38
ENSMUSG00000071083	*NA*	1.86	-0.16	0.06	0.27
ENSMUSG00000071107	*NA*	3.73	2.57	2.97	2.74
ENSMUSG00000071141	*NA*	2.25	1.61	2.01	3.44
ENSMUSG00000071151	*NA*	3.57	3.04	3.15	4.2
ENSMUSG00000071172	*Sfrs3*	3.06	3.04	2.92	2.22

ENSMUSG00000071177	*Serpina1d*	9.97	10.14	10.64	10.77
ENSMUSG00000071178	*Serpina1b*	10.53	10.7	10.92	11.14
ENSMUSG00000071180	*2810008M24R*	4.22	3.08	3.55	3.17
ENSMUSG00000071204	*NA*	2.6	2.68	2.84	2.7
ENSMUSG00000071222	*NA*	0.83	0.04	1.27	1.71
ENSMUSG00000071226	*NA*	1.98	1.52	2.14	1.62
ENSMUSG00000071253	*Slc25a16*	5.45	5.1	5.18	4.97
ENSMUSG00000071256	*Zfp213*	0.48	1.87	1.34	1.85
ENSMUSG00000071266	*1300003B13Ri*	3.05	1.4	2.6	2.02
ENSMUSG00000071267	*NA*	2.43	1.43	1.77	1.48
ENSMUSG00000071281	*NA*	1.58	0.48	1.2	0.47
ENSMUSG00000071284	*NA*	1.93	0.33	1.08	-0.77
ENSMUSG00000071285	*Zfp87*	2.13	1.64	1.95	2.44
ENSMUSG00000071286	*NA*	1.92	1.54	1.34	0.8
ENSMUSG00000071291	*Zfp817*	2.3	0.86	2	0.55
ENSMUSG00000071335	*NA*	4.41	4.07	3.9	3.59
ENSMUSG00000071345	*NA*	6.63	7.04	6.9	6.77
ENSMUSG00000071350	*Setdb2*	2.34	2.17	2.54	2.02
ENSMUSG00000071351	*NA*	1.75	0.13	-0.08	1.67
ENSMUSG00000071358	*NA*	2.07	0.53	2.01	1.58
ENSMUSG00000071359	*Tbpl1*	2.94	2.09	2.91	2.79
ENSMUSG00000071369	*Map3k5*	4.74	4.2	3.7	3.4
ENSMUSG00000071379	*Hpcal1*	2.7	3.24	3.31	3.02
ENSMUSG00000071415	*Rpl23*	4.35	3.93	4.13	3.34
ENSMUSG00000071451	*NA*	2.37	3.74	3.83	3.94
ENSMUSG00000071454	*dtn-b*	3.94	4.26	3.93	3.78
ENSMUSG00000071456	*NA*	0.93	0.97	1.65	1.37
ENSMUSG00000071477	*Zfp777*	1.47	2.38	2.04	1.29
ENSMUSG00000071528	*Usmg5*	4.58	4.59	4.82	4.07
ENSMUSG00000071533	*Pcnp*	3.45	2.33	2.97	2.41
ENSMUSG00000071543	*NA*	1.57	1.92	0.57	0.91

ENSMUSG00000071547	*Nt5dc2*	2.71	3.32	2.81	2.47
ENSMUSG00000071551	*Akr1c19*	4.25	3.33	3.39	3.45
ENSMUSG00000071584	*NA*	3.91	3.7	4.31	4.15
ENSMUSG00000071632	*2510002D24Ri*	3.43	3.72	3.11	3.21
ENSMUSG00000071633	*EG240549*	7.16	7.05	6.54	6.25
ENSMUSG00000071637	*Cebpd*	2.21	3.08	2.76	3.01
ENSMUSG00000071640	*Stxbp3b*	0.76	-0.75	1.03	0.95
ENSMUSG00000071644	*Eef1g*	2.8	2.26	2.4	2.55
ENSMUSG00000071645	*Tut1*	2.47	2.93	2.63	2.65
ENSMUSG00000071646	*Mta2*	4.66	4.73	4.56	4.41
ENSMUSG00000071647	*Eml3*	2.55	3.37	2.99	2.69
ENSMUSG00000071648	*Rom1*	1.24	1.17	0.96	0.15
ENSMUSG00000071649	*B3gat3*	4.73	5.18	4.83	4.72
ENSMUSG00000071650	*Ganab*	6.43	6.63	6.26	6.19
ENSMUSG00000071652	*Ints5*	2.68	3.13	2.6	2.93
ENSMUSG00000071653	*1810009A15Ri*	3.74	4.36	3.85	3.98
ENSMUSG00000071654	*NA*	4.38	4.95	4.8	4.71
ENSMUSG00000071655	*AK172428*	6.98	6.73	6.76	6.6
ENSMUSG00000071657	*Gng3lg*	5.35	5.78	5.32	5.22
ENSMUSG00000071659	*Hnrpul2*	4.76	4.7	4.49	4.18
ENSMUSG00000071660	*Ttc9c*	3.19	2.61	3.08	2.9
ENSMUSG00000071662	*Polr2g*	4.21	3.28	4.33	4.26
ENSMUSG00000071711	*Mpst*	5.44	6.27	5.96	5.71
ENSMUSG00000071713	*Csf2rb*	1.1	0.92	1.17	0.53
ENSMUSG00000071757	*Zhx2*	1.98	2.33	2.53	2.27
ENSMUSG00000071791	*NA*	5.44	4.24	4.7	6.1
ENSMUSG00000071856	*Mcc*	2.6	1.9	2.57	2.37
ENSMUSG00000072030	*NA*	1.57	3.04	3.01	2.1
ENSMUSG00000072082	*Ccnf*	1.09	1.7	1.41	1.62
ENSMUSG00000072115	*Ang*	7.59	8.01	8.15	8.15
ENSMUSG00000072294	*Klf12*	3.51	2.63	3.14	3.03

ENSMUSG00000072407	*NA*	2.8	2.94	3.6	4.28
ENSMUSG00000072493	*NA*	1.09	1.46	1.15	0.96
ENSMUSG00000072494	*NA*	-0.06	0.25	1.11	1.37
ENSMUSG00000072501	*Phf20l1*	2.81	1.71	2.39	2.01
ENSMUSG00000072565	*NA*	2.23	1.71	2.04	3.19
ENSMUSG00000072568	*NA*	3	2.69	2.77	1.86
ENSMUSG00000072582	*Ptrh2*	2.55	2.35	2.33	2.23
ENSMUSG00000072593	*NA*	1.47	1.41	1.62	1.73
ENSMUSG00000072594	*NA*	3.54	3.13	3.41	4.93
ENSMUSG00000072620	*Slfn2*	1.81	1.11	1.39	1.26
ENSMUSG00000072625	*Gdf2*	3.62	3.78	3.64	3.52
ENSMUSG00000072629	*NA*	1.16	1.78	1.39	1.41
ENSMUSG00000072641	*NA*	2.77	1.01	0.22	1.78
ENSMUSG00000072657	*NA*	5.37	4.9	5.58	4.64
ENSMUSG00000072664	*Ugt3a1*	4.73	3.93	4.42	3.71
ENSMUSG00000072673	*NA*	4.24	4.67	4.37	3.84
ENSMUSG00000072682	*NA*	3.19	2.91	3.18	2.67
ENSMUSG00000072684	*NA*	4.4	3.96	3.99	3.52
ENSMUSG00000072692	*NA*	2.38	0.85	2.39	4.12
ENSMUSG00000072693	*NA*	3.98	2.93	4.15	3.5
ENSMUSG00000072698	*NA*	4.39	2.65	4.45	3.75
ENSMUSG00000072704	*NA*	6	5.01	5.72	5.22
ENSMUSG00000072734	*NA*	-0.17	0.33	1.25	1.04
ENSMUSG00000072772	*Grcc10*	6.43	6.59	6.68	6.75
ENSMUSG00000072788	*NA*	2.69	2.92	2.76	2.12
ENSMUSG00000072809	*NA*	1.65	1.48	0.85	0.81
ENSMUSG00000072825	*AW555464*	2.77	3.91	3.32	3.37
ENSMUSG00000072836	*NA*	0.65	0.51	1.21	0.05
ENSMUSG00000072837	*NA*	4.78	5.07	5.16	4.96
ENSMUSG00000072847	*NA*	1.17	0.62	1.45	0.54
ENSMUSG00000072849	*Serpina1e*	6.94	8.63	7.05	8.2

ENSMUSG00000072853	*NA*	3.22	3.57	2.7	3.32
ENSMUSG00000072889	*Nfxl1*	1.8	2.29	1.62	1.67
ENSMUSG00000072896	*NA*	1.16	1.28	0.96	1.33
ENSMUSG00000072933	*NA*	5.15	5.91	5.15	5.06
ENSMUSG00000072941	*Sod3*	5.7	5.81	6.05	5.79
ENSMUSG00000072946	*Zadh1*	5.28	4.86	5.24	4.88
ENSMUSG00000072949	*Acot1*	6.62	5.71	5.85	5.15
ENSMUSG00000072955	*LOC666244*	1.47	0.51	0.95	0.32
ENSMUSG00000073002	*Vamp5*	1.24	1.78	1.63	1.79
ENSMUSG00000073005	*NA*	0.96	-1.81	1.13	#NAME?
ENSMUSG00000073019	*NA*	2.24	2.38	1.62	0.96
ENSMUSG00000073074	*NA*	2.44	1.4	2.04	2.4
ENSMUSG00000073096	*Lrrc61*	6.13	5.98	6.36	6.34
ENSMUSG00000073114	*NA*	2.58	2.27	2.35	1.9
ENSMUSG00000073126	*Atxn7l4*	2.18	1.58	2.04	1.88
ENSMUSG00000073131	*2610030H06Ri*	3.57	2.34	3.11	2.33
ENSMUSG00000073139	*AK197085*	4.59	3.86	4.29	3.84
ENSMUSG00000073143	*NA*	3.27	2.15	2.82	2.19
ENSMUSG00000073147	*NA*	0.85	1.45	1.4	1.79
ENSMUSG00000073155	*NA*	4.82	5.62	5.1	5.29
ENSMUSG00000073198	*NA*	2.23	0.65	1.25	1.87
ENSMUSG00000073228	*NA*	1.72	1.27	1.55	0.99
ENSMUSG00000073240	*NA*	2.86	2.82	2.24	2.8
ENSMUSG00000073291	*NA*	1.72	1.64	0.46	0.91
ENSMUSG00000073387	*Med20*	2.8	3	2.89	2.82
ENSMUSG00000073393	*NA*	1.62	1.16	1.6	1.15
ENSMUSG00000073406	*H2-Bl*	2.26	2.45	2.12	2.51
ENSMUSG00000073409	*H2-Q6*	2.14	2.43	2.56	2.23
ENSMUSG00000073411	*H2-B2*	7.61	8.03	7.77	7.69
ENSMUSG00000073412	*Lst1*	1.08	1.27	2.12	2.98
ENSMUSG00000073416	*NA*	1.43	2.39	3.61	5.24

ENSMUSG00000073418	*C4b*	7.34	8.18	7.64	7.68
ENSMUSG00000073421	*H2-Ab1*	5.61	5.25	5.58	5.18
ENSMUSG00000073422	*H2-Ke6*	5.53	5.75	5.68	5.48
ENSMUSG00000073423	*Zfp414*	1.84	2.16	2.22	1.84
ENSMUSG00000073424	*Cyp4f15*	6.29	6.69	6.64	6.34
ENSMUSG00000073435	*Nme3*	4.02	4.98	4.43	4.37
ENSMUSG00000073436	*NA*	1.63	2.5	1.65	1.7
ENSMUSG00000073437	*NA*	4.73	5.16	5.06	4.64
ENSMUSG00000073440	*NA*	4.25	2.77	3.24	2.93
ENSMUSG00000073463	*NA*	2.29	0.31	1.68	1.2
ENSMUSG00000073468	*5630401J11Rik*	0.74	0.92	1.69	0.92
ENSMUSG00000073469	*Rnaset2a*	1.96	1.57	2.09	1.88
ENSMUSG00000073481	*Mosc2*	7.98	8.39	8.32	8.05
ENSMUSG00000073520	*NA*	4.03	2.68	3.34	2.91
ENSMUSG00000073527	*NA*	2.96	2.81	3	1.94
ENSMUSG00000073534	*NA*	1.08	1.89	0.81	1.18
ENSMUSG00000073542	*Cep76*	1.34	0.61	1.31	1.35
ENSMUSG00000073543	*Chmp1b*	4.33	4.13	4.17	4.22
ENSMUSG00000073552	*NA*	2.03	2.09	1.72	2.32
ENSMUSG00000073555	*EG240327*	5.76	3.59	5.18	4.02
ENSMUSG00000073563	*Csnk1g3*	3.87	3.15	3.82	3.08
ENSMUSG00000073565	*Prr16*	4.79	3.96	4.09	3.89
ENSMUSG00000073599	*1110006O17Ri*	0.87	1.08	1.1	0.67
ENSMUSG00000073600	*NA*	1.3	1.71	1.77	1.39
ENSMUSG00000073609	*D2hgdh*	1.83	2.19	2.12	1.56
ENSMUSG00000073611	*NA*	2.93	3.15	2.85	2.66
ENSMUSG00000073616	*NA*	5.74	4	4.81	4.78
ENSMUSG00000073633	*Fbxo36*	3.09	2.98	3.3	3.03
ENSMUSG00000073635	*NA*	1.16	-0.11	0.34	-0.08
ENSMUSG00000073638	*NA*	1.88	1.37	1.79	0.98
ENSMUSG00000073639	*Rab18*	6.39	5.52	5.91	5.58

ENSMUSG00000073643	*Wdfy1*	2.98	2.55	3.11	2.48
ENSMUSG00000073647	*NA*	1.46	0.63	0.34	1.33
ENSMUSG00000073651	*NA*	2.41	2.39	1.91	2.35
ENSMUSG00000073652	*NA*	2.86	3.51	3.43	3.42
ENSMUSG00000073664	*AK041465*	1.59	0.36	0.99	0.48
ENSMUSG00000073676	*Hspe1*	5.26	5.53	5.5	5.26
ENSMUSG00000073678	*NA*	1.54	0.48	1.89	0.69
ENSMUSG00000073684	*2610002J02Ri*	1.42	2.87	2.6	2.46
ENSMUSG00000073700	*Klhl21*	4.33	4.55	4.67	4.26
ENSMUSG00000073702	*M75*	1.23	0.04	0.67	0.34
ENSMUSG00000073707	*NA*	1.88	1.48	1.88	1.52
ENSMUSG00000073719	*NA*	3.67	4	3.52	3.58
ENSMUSG00000073725	*Lmbrd1*	4.52	4	4.37	3.96
ENSMUSG00000073731	*NA*	3.67	4.24	3.86	3.78
ENSMUSG00000073738	*NA*	3.2	3.2	1.4	2.82
ENSMUSG00000073755	*5730409E04Ri*	1.58	1.52	1.42	1.39
ENSMUSG00000073775	*Kti12*	3.85	4.91	3.89	4.09
ENSMUSG00000073778	*NA*	1.03	1.44	0.91	0.75
ENSMUSG00000073787	*NA*	2.82	2.98	3.38	3.25
ENSMUSG00000073792	*Alg6*	2.09	1.01	1.44	1.23
ENSMUSG00000073832	*Mup1*	0.84	0.16	1.51	2.33
ENSMUSG00000073835	*NA*	2.03	-2.5	1.37	1.11
ENSMUSG00000073838	*Tufm*	2.48	2.96	3	2.99
ENSMUSG00000073849	*NA*	1.51	2.11	2.2	1.65
ENSMUSG00000073852	*NA*	4.16	3.61	3.53	2.57
ENSMUSG00000073859	*NA*	3.24	1.71	1.89	2.08
ENSMUSG00000073889	*Il11ra1*	1.97	2.48	1.7	1.53
ENSMUSG00000073910	*Mobkl2b*	3.57	3.5	3.92	3.63
ENSMUSG00000073940	*Hbb-b1*	2.5	4.96	5.83	6.07
ENSMUSG00000073982	*Rhog*	4.1	4.4	4.42	4.21
ENSMUSG00000073985	*NA*	0.25	0.94	1.65	0.13

ENSMUSG00000073987	*Ggh*	4.52	3.77	4.19	3.57
ENSMUSG00000073988	*Ttpa*	8.67	7.13	8.02	7.33
ENSMUSG00000074005	*NA*	4.67	4.94	4.88	4.26
ENSMUSG00000074030	*Exoc8*	1.57	2.18	1.42	1.43
ENSMUSG00000074040	*NA*	0.59	1.65	1.23	1.54
ENSMUSG00000074044	*NA*	1.96	3.16	3.8	3.19
ENSMUSG00000074052	*BC048644*	4.3	4.54	4.5	4.18
ENSMUSG00000074054	*NA*	1.22	0	0.17	1.11
ENSMUSG00000074063	*Osgin1*	4.14	5.52	4.5	5.09
ENSMUSG00000074064	*Mlycd*	5.73	6.38	6.09	5.92
ENSMUSG00000074071	*EG434197*	2.98	2.8	3.65	3.2
ENSMUSG00000074085	*NA*	2.4	2.98	2.79	2.54
ENSMUSG00000074088	*Wdr57*	2.54	2.88	2.91	2.3
ENSMUSG00000074093	*NA*	3.42	2.59	2.48	2.21
ENSMUSG00000074102	*NA*	2.94	2.76	3.3	3.35
ENSMUSG00000074106	*NA*	2.31	3.8	3.42	2.8
ENSMUSG00000074115	*Saa1*	5.59	6.38	6.21	5.71
ENSMUSG00000074129	*Flt3l*	1.45	1.9	2.1	1.4
ENSMUSG00000074141	*Il4i1*	1.15	2	1.34	1.76
ENSMUSG00000074151	*AI451557*	1.81	0.73	1.47	0.79
ENSMUSG00000074157	*NA*	4.24	3.55	4.03	3.67
ENSMUSG00000074166	*AW146154*	1.15	0.3	0.47	-0.24
ENSMUSG00000074170	*Plekhf1*	3.29	2.71	3.8	3.13
ENSMUSG00000074182	*2410019A14Ri*	1.96	2.04	1.85	1.37
ENSMUSG00000074203	*NA*	2.61	3.41	3.16	3.03
ENSMUSG00000074207	*Adh1*	10.46	10.57	10.06	10.13
ENSMUSG00000074210	*0610010E21Ri*	2	2.65	2.75	2.56
ENSMUSG00000074211	*NA*	3.35	4.04	4.12	3.9
ENSMUSG00000074212	*NA*	2.63	2.41	2.25	2.27
ENSMUSG00000074218	*Cox7a1*	1.81	1.66	2.14	3
ENSMUSG00000074219	*NA*	-0.26	0.85	1.67	1.68

ENSMUSG00000074221	*Zfp568*	1.47	1.7	1.64	1.18
ENSMUSG00000074227	*Spint2*	5.84	6.66	6.16	6.03
ENSMUSG00000074238	*BC002199*	4.26	3.62	3.94	3.57
ENSMUSG00000074246	*NA*	3.96	4.47	4.37	4.69
ENSMUSG00000074247	*NA*	3.42	4.2	3.16	3.27
ENSMUSG00000074254	*Cyp2a4*	7.71	7.66	8.01	8.05
ENSMUSG00000074264	*Amy1*	7.85	6.96	7.61	7.14
ENSMUSG00000074269	*NA*	1.59	2.33	1.42	1.35
ENSMUSG00000074272	*Ceacam1*	6.35	5.97	6.3	5.88
ENSMUSG00000074280	*NA*	#NAME?	3.6	1.68	1.38
ENSMUSG00000074284	*NA*	3.31	2.97	3.47	3.71
ENSMUSG00000074285	*NA*	4.01	3.46	4.52	3.99
ENSMUSG00000074336	*Apoc4*	9.82	10.22	10.46	10.28
ENSMUSG00000074360	*NA*	1.36	1.35	1.82	0.96
ENSMUSG00000074363	*NA*	0.53	1.22	1.04	1.14
ENSMUSG00000074373	*NA*	9.33	9.99	9.74	9.52
ENSMUSG00000074375	*NA*	1.14	#NAME?	4.38	#NAME?
ENSMUSG00000074377	*NA*	2.03	-2	2.5	-1
ENSMUSG00000074396	*Pex11b*	3.89	3.85	3.81	3.61
ENSMUSG00000074398	*NA*	4.16	3.51	3.67	3.97
ENSMUSG00000074405	*6430526N21Ri*	1.24	2.13	1.74	1.76
ENSMUSG00000074406	*Zfp628*	1.12	1.8	1.26	1
ENSMUSG00000074457	*S100a16*	4.38	4.85	4.29	4.19
ENSMUSG00000074460	*NA*	1.7	2.34	1.75	2.18
ENSMUSG00000074466	*NA*	1.19	1.06	1.28	1.66
ENSMUSG00000074476	*Spc24*	2.7	2.97	2.76	2.59
ENSMUSG00000074479	*NA*	5.21	2.46	4.43	3.84
ENSMUSG00000074482	*NA*	2.35	1.62	2	1.68
ENSMUSG00000074491	*Clec4g*	5.11	5.8	5.19	5.17
ENSMUSG00000074498	*NA*	4.97	4.98	5.34	4.83
ENSMUSG00000074513	*Arfip1*	4.09	2.87	3.38	2.95

ENSMUSG00000074557	*NA*	1.37	1.1	0.84	-1.33
ENSMUSG00000074576	*NA*	1.72	2.06	2.03	1.48
ENSMUSG00000074578	*1500012F01Ri*	3.91	3.67	4.61	4.41
ENSMUSG00000074582	*Arfgef2*	3.55	3.82	3.72	3.45
ENSMUSG00000074598	*NA*	2.68	0.44	0.95	-1.48
ENSMUSG00000074622	*Mafb*	5.86	5.16	6.02	5.85
ENSMUSG00000074623	*Gm826*	2.5	1.09	2.68	1.65
ENSMUSG00000074634	*EG633640*	2.13	0.25	1.63	1.39
ENSMUSG00000074636	*NA*	2.09	0.23	0.56	1.73
ENSMUSG00000074639	*BC089597*	7.91	7.49	7.68	7.4
ENSMUSG00000074642	*NA*	3.05	2.72	2.62	2.89
ENSMUSG00000074643	*Rbm12*	3.14	2.87	2.82	2.27
ENSMUSG00000074649	*NA*	1.75	1.42	2.06	1.57
ENSMUSG00000074656	*Eif2s2*	3.31	2.57	2.69	2.49
ENSMUSG00000074661	*NA*	0.42	-0.55	1.18	0.28
ENSMUSG00000074698	*Csnk2a1*	4.43	3.83	4.21	3.55
ENSMUSG00000074700	*NA*	1.3	-0.69	1.17	0.53
ENSMUSG00000074732	*NA*	1.78	0.86	1.23	0.53
ENSMUSG00000074733	*NA*	2.09	1.54	2.02	1.97
ENSMUSG00000074743	*Thbd*	1.5	1.58	1.02	1.15
ENSMUSG00000074746	*Pdzd8*	3.53	3.19	3.41	3.11
ENSMUSG00000074748	*4921506J03Ri*	5.19	5.76	5.31	5.19
ENSMUSG00000074749	*Gm114*	3.5	3.58	3.67	3.45
ENSMUSG00000074754	*Gm561*	4.79	4.1	5.25	4.82
ENSMUSG00000074768	*BHMT*	5.7	5.16	5.92	4.85
ENSMUSG00000074781	*Ube2n*	2.33	1.39	1.7	1.43
ENSMUSG00000074782	*NA*	1.32	1.23	1.79	1.88
ENSMUSG00000074785	*Plxnc1*	3.05	2.78	2.35	2.3
ENSMUSG00000074794	*mKIAA1376*	5.38	4.5	5.1	4.46
ENSMUSG00000074797	*Itpa*	3.07	2.68	3.06	2.76
ENSMUSG00000074807	*NA*	0.8	2.46	1.79	2.24

ENSMUSG00000074824	*NA*	1.48	0.27	0.89	0.27
ENSMUSG00000074825	*NA*	2.14	1.91	1.95	1.48
ENSMUSG00000074828	*NA*	7.19	6.8	7.01	6.84
ENSMUSG00000074861	*NA*	1.26	1.62	1.88	1.69
ENSMUSG00000074873	*NA*	1.05	0.38	1	0.39
ENSMUSG00000074874	*NA*	2.31	0.84	1.35	1.37
ENSMUSG00000074876	*NA*	1.25	2.69	2.13	1.93
ENSMUSG00000074880	*NA*	2.73	3.36	2.79	2.61
ENSMUSG00000074882	*Cyp2c68*	7.01	6.5	6.5	6.29
ENSMUSG00000074884	*Serf2*	4.07	3.72	4.28	3.94
ENSMUSG00000074886	*Grk6*	2.67	2.91	2.98	2.43
ENSMUSG00000074890	*NA*	1.86	2.3	2.02	1.77
ENSMUSG00000074896	*Ifit3*	2.36	1.88	1.45	2.42
ENSMUSG00000074903	*NA*	1.1	0.54	0	1.5
ENSMUSG00000074909	*Ranbp6*	2.7	2.12	2.36	1.92
ENSMUSG00000074910	*NA*	1.12	-0.82	0.37	0.59
ENSMUSG00000074917	*NA*	3.58	3.92	2.52	1.97
ENSMUSG00000074922	*2900009I07Rik*	3.59	4.37	3.99	3.86
ENSMUSG00000074925	*NA*	0.58	1.01	1.24	0.7
ENSMUSG00000074931	*NA*	1.23	1.16	0.89	2.06
ENSMUSG00000074940	*NA*	3.09	1.25	2.74	2.29
ENSMUSG00000074984	*NA*	2.83	0.82	1.19	1.37
ENSMUSG00000074994	*NA*	2.67	1.91	2.34	2.06
ENSMUSG00000075000	*Nrbf2*	2.67	2.72	2.39	2.3
ENSMUSG00000075010	*NA*	7.82	6.33	7.07	7.34
ENSMUSG00000075043	*0610006I08Rik*	4.45	4.83	4.54	4.28
ENSMUSG00000075053	*NA*	1.64	0.49	1.34	1.8
ENSMUSG00000075054	*1600012F09Ri*	1.45	1.15	1.7	1.97
ENSMUSG00000075216	*NA*	3.71	3.42	4.08	3.78
ENSMUSG00000075225	*5033413D22Ri*	2.07	1.44	1.2	0.49
ENSMUSG00000075227	*Znhit2*	4.01	4.69	4.44	4.42

ENSMUSG00000075229	*Ccdc58*	3.99	3.72	4.35	3.84
ENSMUSG00000075232	*Amd2*	1.47	0.9	1.33	1
ENSMUSG00000075254	*Heg1*	1.76	2.03	1.68	1.34
ENSMUSG00000075256	*Cerkl*	1.78	0.48	1.48	0.76
ENSMUSG00000075273	*Ttc30b*	1.72	0.73	1.19	0.67
ENSMUSG00000075279	*NA*	3.32	2.86	3.09	3.91
ENSMUSG00000075284	*Wipf1*	1.12	0.76	0.93	0.65
ENSMUSG00000075285	*NA*	6.05	4.51	5.23	4.93
ENSMUSG00000075324	*Fign*	0.82	0.47	1.29	0.98
ENSMUSG00000075327	*Zbtb2*	1.57	1.04	1.25	0.85
ENSMUSG00000075368	*NA*	2.88	2.16	2.67	0.33
ENSMUSG00000075376	*Rc3h2*	2.56	1.27	2.14	1.44
ENSMUSG00000075391	*NA*	5.64	5.66	5.46	6.18
ENSMUSG00000075401	*NA*	2.87	3.04	3.01	2.74
ENSMUSG00000075411	*NA*	0.33	1.64	1.5	-0.46
ENSMUSG00000075415	*Fnbp1*	0.96	1.02	1.25	0.9
ENSMUSG00000075417	*NA*	1.01	2.14	1.83	2.01
ENSMUSG00000075419	*Dolk*	3.52	4.03	3.32	3.04
ENSMUSG00000075463	*NA*	0.45	1.31	1.3	1.48
ENSMUSG00000075467	*D2Bwg1335e*	3.96	4.87	4.35	3.93
ENSMUSG00000075470	*Alg10b*	3.76	3.3	3.33	3.01
ENSMUSG00000075472	*NA*	4.73	2.68	3.92	3.49
ENSMUSG00000075486	*Commd6*	5.55	5	5.27	5.12
ENSMUSG00000075507	*NA*	2.27	1.67	2.04	1.73
ENSMUSG00000075511	*NA*	1.22	0.9	1.67	0.99
ENSMUSG00000075514	*NA*	0.59	0.7	1.15	0.59
ENSMUSG00000075517	*NA*	5	5.25	5.04	4.83
ENSMUSG00000075528	*Aarsd1*	2.69	3	2.95	2.51
ENSMUSG00000075536	*NA*	0.06	-0.3	1.03	0.12
ENSMUSG00000075543	*Prhoxnb*	5.75	6.15	5.53	5.81
ENSMUSG00000075551	*Cyp3a41a*	2.1	0.26	0.77	-0.81

ENSMUSG00000075552	*NA*	4.54	0.75	3.84	2.59
ENSMUSG00000075558	*NA*	-0.23	1.33	1.51	1.03
ENSMUSG00000075562	*NA*	2.44	3.96	3.8	3.35
ENSMUSG00000075576	*NA*	1.08	1.67	0.88	1.18
ENSMUSG00000075577	*NA*	2.49	3.04	2.55	2.65
ENSMUSG00000075578	*NA*	0.8	2.51	1.2	1.35
ENSMUSG00000075582	*NA*	6.55	7.12	6.93	7.05
ENSMUSG00000075590	*Nrbp2*	4.08	4.74	4.57	4.38
ENSMUSG00000075591	*NA*	4.11	3.37	3.62	4.51
ENSMUSG00000075595	*Zfp652*	3.3	2.75	2.96	2.62
ENSMUSG00000075602	*Ly6a*	4.06	2.99	3.39	3.33
ENSMUSG00000075700	*2810407C02Ri*	6.23	4.98	5.64	5.22
ENSMUSG00000075701	*H47*	5.77	5.9	5.36	5.42
ENSMUSG00000075702	*Selm*	0.45	0.5	1.04	0.34
ENSMUSG00000075703	*D5Wsu178e*	4.29	3.82	3.76	3.11
ENSMUSG00000075704	*Txnrd2*	4.41	4.99	4.44	4.33
ENSMUSG00000075705	*Sepx1*	7.41	7.99	7.98	7.94
ENSMUSG00000075706	*GPx4*	3.85	3.26	3.97	3.58
ENSMUSG00000075876	*NA*	1.02	0.95	2.49	0.64
ENSMUSG00000075924	*NA*	2.07	2.12	2.71	2.35
ENSMUSG00000076004	*NA*	7.23	8.71	7.8	7.2
ENSMUSG00000076036	*NA*	10.61	10.55	10.97	11.09
ENSMUSG00000076060	*NA*	4.45	4.52	3.85	3.89
ENSMUSG00000076128	*NA*	4.96	4.79	4.98	5.07
ENSMUSG00000076130	*NA*	1.47	2.98	1.34	-0.68
ENSMUSG00000076138	*NA*	9.02	7.91	9.01	8.63
ENSMUSG00000076258	*NA*	9.46	10.02	9.76	8.91
ENSMUSG00000076270	*NA*	3.44	3.05	3.46	2.67
ENSMUSG00000076275	*NA*	-0.75	#NAME?	1.3	-0.53
ENSMUSG00000076281	*NA*	4	4.76	3.68	2.96
ENSMUSG00000076372	*NA*	4.55	3.33	4.14	3.12

ENSMUSG00000076387	*NA*	1.89	2.34	2.78	2.93
ENSMUSG00000076432	*Ywhaq*	2.89	2.68	2.9	2.37
ENSMUSG00000076435	*BC018371*	5.02	4.16	5.14	4.48
ENSMUSG00000076437	*2700094K13Ri*	1.38	2.27	1.82	2.05
ENSMUSG00000076441	*Ass1*	7.83	7.06	8.38	8.26
ENSMUSG00000076454	*NA*	1.23	2.74	0.92	1
ENSMUSG00000076502	*NA*	-2.86	-0.53	1.23	-2.86
ENSMUSG00000076509	*NA*	0.92	-0.01	2.2	0.16
ENSMUSG00000076515	*NA*	-0.82	-0.04	1.86	#NAME?
ENSMUSG00000076516	*NA*	0.28	0.94	2.48	1.05
ENSMUSG00000076520	*NA*	-0.66	-1.84	1.86	-2.51
ENSMUSG00000076521	*NA*	-2.86	#NAME?	1	#NAME?
ENSMUSG00000076522	*NA*	0.76	-1.4	1.78	#NAME?
ENSMUSG00000076523	*NA*	-0.87	#NAME?	1.31	#NAME?
ENSMUSG00000076527	*NA*	-2.79	-2.79	1.01	#NAME?
ENSMUSG00000076536	*NA*	-2.78	#NAME?	1.33	#NAME?
ENSMUSG00000076560	*NA*	-2.84	-2.84	1.57	-1.99
ENSMUSG00000076563	*NA*	#NAME?	-2.79	1.52	#NAME?
ENSMUSG00000076564	*NA*	-1.96	#NAME?	1.32	#NAME?
ENSMUSG00000076566	*NA*	-1.79	-0.96	1.4	-2.05
ENSMUSG00000076579	*NA*	-2.87	#NAME?	1.08	#NAME?
ENSMUSG00000076580	*NA*	-1.37	#NAME?	2.18	-2.02
ENSMUSG00000076583	*NA*	-1.87	-1.28	1.03	-2.87
ENSMUSG00000076585	*NA*	-2.79	-1.35	1.06	-0.94
ENSMUSG00000076590	*NA*	#NAME?	#NAME?	1.3	#NAME?
ENSMUSG00000076592	*NA*	-0.47	-0.79	1.29	-0.51
ENSMUSG00000076600	*NA*	-0.16	-1.36	1.13	#NAME?
ENSMUSG00000076604	*NA*	1.32	2.65	4.31	-1
ENSMUSG00000076605	*NA*	2.51	0.53	4.42	1.41
ENSMUSG00000076607	*NA*	1.26	1.35	3.22	-0.79
ENSMUSG00000076608	*NA*	-0.75	1.19	3.39	-1

ENSMUSG00000076609	*NA*	5.49	5.57	7.76	4.93
ENSMUSG00000076610	*NA*	1.62	3.52	3.39	2.74
ENSMUSG00000076612	*NA*	-3.33	-0.76	1.02	-0.17
ENSMUSG00000076613	*NA*	-1.47	0.62	1.47	0.25
ENSMUSG00000076616	*NA*	-0.95	-3.95	2.49	-1.38
ENSMUSG00000076617	*NA*	3.23	2.75	6.23	2.22
ENSMUSG00000076618	*NA*	#NAME?	1.81	2.6	-0.71
ENSMUSG00000076619	*NA*	0.2	0.32	2.45	0.25
ENSMUSG00000076672	*NA*	-4.45	-2.81	1.34	-2.81
ENSMUSG00000076687	*NA*	#NAME?	#NAME?	1.14	#NAME?
ENSMUSG00000076928	*NA*	0.81	0.24	1.79	-0.41
ENSMUSG00000076929	*NA*	-0.84	-1.09	2.44	-0.22
ENSMUSG00000076930	*NA*	-0.6	#NAME?	2.6	#NAME?
ENSMUSG00000076931	*NA*	-0.39	-0.84	3.1	0.11
ENSMUSG00000076933	*NA*	-0.79	0.66	3.46	0.18
ENSMUSG00000076934	*NA*	#NAME?	-0.99	2.13	-0.13
ENSMUSG00000076937	*NA*	-0.66	1.04	2.72	#NAME?
ENSMUSG00000076938	*NA*	#NAME?	0.16	3.08	#NAME?
ENSMUSG00000077220	*NA*	2.98	#NAME?	-0.83	-0.76
ENSMUSG00000077222	*NA*	-1.07	-0.22	1.2	0.07
ENSMUSG00000077346	*NA*	3.6	2.67	3.12	3.18
ENSMUSG00000077370	*NA*	2.68	2.46	5.18	3.52
ENSMUSG00000077394	*NA*	1.46	#NAME?	-0.86	-0.86
ENSMUSG00000077450	*Rab11b*	4.96	4.15	4.62	4.29
ENSMUSG00000077493	*NA*	2.21	-0.9	2.81	0.45
ENSMUSG00000077625	*NA*	3.17	2.1	3.1	2.94
ENSMUSG00000077637	*NA*	2.16	1.98	1.79	0.91
ENSMUSG00000077705	*NA*	3.56	2.68	2.61	2.95
ENSMUSG00000077709	*NA*	2.05	1.04	1.55	1.16
ENSMUSG00000077924	*NA*	3.54	4.3	2.91	3.23
ENSMUSG00000078081	*NA*	2.11	2.24	2.18	2.49

ENSMUSG00000078092	*NA*	5.23	4.67	5.06	4.66
ENSMUSG00000078103	*NA*	2.87	0.45	2.83	2.92
ENSMUSG00000078104	*EG329070*	2.4	2.03	2.66	2.41
ENSMUSG00000078105	*NA*	6.29	7.29	6.72	6.59
ENSMUSG00000078108	*NA*	2.21	1.61	1.86	2.17
ENSMUSG00000078124	*NA*	3.23	4.07	3.3	3.19
ENSMUSG00000078135	*Eid1*	3.98	3.56	3.54	3.15
ENSMUSG00000078143	*NA*	5.09	4.24	4.58	3.97
ENSMUSG00000078152	*NA*	4.21	3.05	3.5	3.31
ENSMUSG00000078153	*NA*	3.08	3.48	3.01	3.49
ENSMUSG00000078173	*AK053703*	1.25	1.62	1.53	1.33
ENSMUSG00000078174	*NA*	1.98	2.34	3.29	2.82
ENSMUSG00000078178	*NA*	3.24	3.47	2.93	3.14
ENSMUSG00000078183	*NA*	1.03	-0.47	0.44	0.6
ENSMUSG00000078188	*NA*	4.38	4.5	4.76	4.55
ENSMUSG00000078193	*NA*	2.12	2.66	2.5	1.83
ENSMUSG00000078201	*C730025P13R*	2.65	3.51	2.91	3.03
ENSMUSG00000078226	*NA*	2.61	2.05	2.45	2.52
ENSMUSG00000078234	*Klhdc7a*	0.83	1.46	1.87	1.71
ENSMUSG00000078250	*NA*	5.82	5.47	5.71	5.45
ENSMUSG00000078282	*NA*	1.08	-2.11	-0.03	-1
ENSMUSG00000078284	*NA*	2.16	-0.03	1.29	1.01
ENSMUSG00000078285	*Plekha6*	3.59	3.78	3.67	3.68
ENSMUSG00000078303	*NA*	10.28	10.18	10.09	9.06
ENSMUSG00000078317	*F8a*	2.15	2.28	2.09	1.9
ENSMUSG00000078348	*Sf3b5*	3.64	4.54	4.49	4.52
ENSMUSG00000078364	*NA*	3.13	1.86	3.27	2.92
ENSMUSG00000078373	*NA*	1.54	1.42	1.61	1.08
ENSMUSG00000078429	*Ctdsp2*	3.73	3.98	4.03	3.82
ENSMUSG00000078440	*Dohh*	2.73	3.59	3.3	3.22
ENSMUSG00000078441	*Scamp4*	4.53	5.15	4.73	4.76

ENSMUSG00000078445	*NA*	1.01	1.49	1.27	1.31
ENSMUSG00000078449	*NA*	4.62	3.61	3.82	3.97
ENSMUSG00000078452	*Raet1a*	4.11	1.82	3.63	1.58
ENSMUSG00000078453	*3110003A17Ri*	3.22	2.07	2.98	2.77
ENSMUSG00000078480	*NA*	2.15	1.34	2.3	2.14
ENSMUSG00000078482	*NA*	1.23	-0.36	0.61	1.99
ENSMUSG00000078484	*Klhl17*	1.28	2.13	1.9	1.38
ENSMUSG00000078515	*NA*	6.66	7.04	6.55	6.41
ENSMUSG00000078517	*C230096C10R*	2.51	3.29	3.41	3.37
ENSMUSG00000078525	*NA*	0.85	0.98	1.96	2.45
ENSMUSG00000078548	*NA*	5.1	4.49	4.81	4.4
ENSMUSG00000078560	*NA*	2.85	3.38	2.91	3.36
ENSMUSG00000078563	*NA*	3.49	1.85	1.76	3.15
ENSMUSG00000078566	*Bnip3*	6	5.35	5.87	5.82
ENSMUSG00000078567	*NA*	1.97	2.59	2.34	2.39
ENSMUSG00000078570	*NA*	3.36	3.96	3.26	3.44
ENSMUSG00000078571	*NA*	2.29	2.6	2.57	2.32
ENSMUSG00000078572	*NA*	3.8	4.16	4.47	3.84
ENSMUSG00000078578	*Ube2d3*	5.86	4.72	5.54	5.05
ENSMUSG00000078580	*E430018J23Ri*	1.41	1.42	1.1	1.08
ENSMUSG00000078584	*AU022252*	5.4	5.18	5.34	5.14
ENSMUSG00000078588	*B4galt2*	1.7	2.04	1.84	2
ENSMUSG00000078607	*NA*	1.06	1.21	2.1	0.76
ENSMUSG00000078612	*NA*	1.07	0.64	1.24	0.48
ENSMUSG00000078619	*Smarcd2*	5.34	5.58	5.51	5.09
ENSMUSG00000078622	*Ccdc47*	5.4	4.41	4.75	4.42
ENSMUSG00000078645	*4930504E06Ri*	2.79	3.98	3.53	3.53
ENSMUSG00000078650	*G6pc*	8.57	7.73	7.95	8.14
ENSMUSG00000078652	*Psme3*	5.26	5.58	5.52	5.28
ENSMUSG00000078653	*Cntd1*	2.78	2.03	2.42	1.68
ENSMUSG00000078656	*Vps25*	5.99	6.25	6.14	5.96

ENSMUSG00000078667	*NA*	1.69	1.82	1.74	1.77
ENSMUSG00000078670	*NA*	1.88	2.03	1.15	1.53
ENSMUSG00000078671	*Chd2*	1.33	0.39	1.09	-0.03
ENSMUSG00000078672	*OTTMUSG000*	1.45	1.45	2.43	2.15
ENSMUSG00000078674	*Mup2*	1.4	-0.82	0.35	0.97
ENSMUSG00000078675	*Mup2*	2.22	-0.31	1.34	1.98
ENSMUSG00000078676	*Casc3*	3.27	3.51	3.18	3.17
ENSMUSG00000078680	*Mup2*	7.41	5.96	6.62	7.43
ENSMUSG00000078681	*Tm2d3*	3.98	4.33	3.79	3.8
ENSMUSG00000078685	*NA*	2.39	-1.64	1.23	1.08
ENSMUSG00000078686	*Mup2*	5.81	2.71	5.12	6.05
ENSMUSG00000078695	*Mel13*	4.5	4.53	4.66	4.36
ENSMUSG00000078697	*NA*	3.66	5.11	4.32	4.12
ENSMUSG00000078699	*NA*	3.28	4.43	4.02	4.09
ENSMUSG00000078713	*1110019J04Rik*	2.47	2.38	2.47	2.29
ENSMUSG00000078719	*LOC10003967*	3.45	3.8	3.93	3.72
ENSMUSG00000078761	*Ankrd50*	1.78	1.8	1.51	1.38
ENSMUSG00000078765	*U2af26*	3.39	3.82	3.7	3.65
ENSMUSG00000078772	*NA*	3.29	2.63	3	2.75
ENSMUSG00000078784	*1810022K09Ri*	3.56	1.27	2.48	2.13
ENSMUSG00000078786	*NA*	2.07	2.51	2.61	2.6
ENSMUSG00000078789	*NA*	3.69	4.04	3.92	3.74
ENSMUSG00000078798	*C730007P19R*	7.43	0.57	7.78	1.66
ENSMUSG00000078799	*NA*	4.73	-0.38	5.49	1.22
ENSMUSG00000078812	*Eif5a*	7.02	7.19	7.17	6.93
ENSMUSG00000078813	*Leng1*	3.17	3.36	2.96	3.2
ENSMUSG00000078851	*Hist3h2a*	0.72	1.7	1.96	0.99
ENSMUSG00000078852	*Zfp672*	1.66	1.33	1.76	1.8
ENSMUSG00000078853	*Igtp*	5.83	4.53	4.34	4.82
ENSMUSG00000078861	*NA*	1.51	-0.24	0.62	0.17
ENSMUSG00000078866	*NA*	1.42	0.33	1.86	1.26

ENSMUSG00000078900	*NA*	3.78	3.63	3.55	3.73
ENSMUSG00000078908	*Mon1b*	2.47	2.62	2.34	2.26
ENSMUSG00000078914	*NA*	2.53	1.57	2.2	3.61
ENSMUSG00000078916	*NA*	4.7	3.85	3.86	4.78
ENSMUSG00000078919	*Dpm1*	5.33	4.72	5.3	4.74
ENSMUSG00000078920	*Ifi47*	3.35	3.03	2.48	2.35
ENSMUSG00000078923	*Ube2v1*	0.8	1.71	1.08	0.61
ENSMUSG00000078931	*AK209600*	4.91	5.01	4.67	4.35
ENSMUSG00000078936	*2410002O22Ri*	2.12	1.82	2.46	2.48
ENSMUSG00000078939	*NA*	4.23	3.77	4.18	4.41
ENSMUSG00000078941	*Taf9*	4.19	3.21	4.06	3.49
ENSMUSG00000078946	*NA*	1.99	0.21	1.11	0.45
ENSMUSG00000078960	*AK044623*	2.26	2.73	2.26	2.6
ENSMUSG00000078961	*NA*	1.15	1.19	1.49	1.84
ENSMUSG00000078964	*LOC382044*	7.22	6.95	6.8	6.74
ENSMUSG00000078970	*Wdr92*	2	2.14	2.34	2.01
ENSMUSG00000078983	*NA*	3.26	2.76	3.22	3.08
ENSMUSG00000079002	*C030006K11Ri*	4.06	4.96	4.6	4.75
ENSMUSG00000079003	*Samd1*	2.84	3.25	3.34	2.89
ENSMUSG00000079004	*NA*	1.1	2.09	2.49	2.77
ENSMUSG00000079012	*Serpina3m*	9.17	9.15	9.28	9.56
ENSMUSG00000079015	*Serpina1c*	9.46	9.6	9.75	9.99
ENSMUSG00000079017	*Isg12*	3.11	2.49	2.76	3.36
ENSMUSG00000079036	*Alkbh1*	1.53	1.32	1.43	1.34
ENSMUSG00000079037	*Prnp*	4.3	3.92	4.14	3.39
ENSMUSG00000079040	*NA*	2.51	2.74	2.88	2.82
ENSMUSG00000079043	*Fastkd5*	3	2.47	2.65	2.78
ENSMUSG00000079057	*Cyp4v3*	7.7	7.17	7.48	7.17
ENSMUSG00000079065	*NA*	1.72	-0.22	-0.03	0
ENSMUSG00000079068	*NA*	1.17	1.45	1.7	3.54
ENSMUSG00000079104	*AU021838*	4.52	4.24	4.3	3.99

ENSMUSG00000079111	*Kdelr2*	5.97	5.84	5.89	5.75
ENSMUSG00000079139	*NA*	1.78	1.68	1.08	1.47
ENSMUSG00000079144	*A130010J15Ri*	2.15	2.02	2.03	1.87
ENSMUSG00000079145	*NA*	5.7	4.92	5.58	4.83
ENSMUSG00000079149	*Atp11a*	1.08	0.73	0.86	0.03
ENSMUSG00000079164	*Tlr5*	1.59	1.37	1.49	1.72
ENSMUSG00000079165	*Lrch4*	1.99	2.79	2.71	2.25
ENSMUSG00000079179	*NA*	1.65	1.92	2.21	2.02
ENSMUSG00000079184	*Mphosph8*	3.88	2.92	3.22	2.7
ENSMUSG00000079185	*NA*	1.53	1.04	1.97	1.57
ENSMUSG00000079188	*NA*	-0.09	0.26	1.8	2.22
ENSMUSG00000079197	*Psme2*	3.03	2.98	3.26	3.24
ENSMUSG00000079215	*Zfp664*	3.39	3.43	3.05	2.96
ENSMUSG00000079227	*Ccr5*	1.69	0.7	0.68	-0.07
ENSMUSG00000079252	*Ifrg15*	5.44	4.77	5.29	4.88
ENSMUSG00000079283	*2310009B15Ri*	1.41	1.29	1.69	2.1
ENSMUSG00000079297	*NA*	3.11	2.01	2.35	3.34
ENSMUSG00000079316	*Rab9*	6.05	4.91	5.54	5.37
ENSMUSG00000079317	*Trappc2*	1.09	-0.83	0.44	-0.69
ENSMUSG00000079334	*Hyal1*	4.56	5.26	5.11	4.81
ENSMUSG00000079343	*EG317677*	2.18	-5.73	1.82	-4.15
ENSMUSG00000079351	*NA*	2.59	1.44	1.98	1.32
ENSMUSG00000079355	*Ccrl1*	5.22	5.27	5.1	4.82
ENSMUSG00000079357	*NA*	2.69	1.57	2.3	1.51
ENSMUSG00000079362	*Mpa2l*	1.82	0.09	-0.61	-1.19
ENSMUSG00000079363	*Gbp4*	1.34	-0.74	-1.69	-1.21
ENSMUSG00000079366	*NA*	2.45	2.29	2.38	1.91
ENSMUSG00000079411	*Alg13*	1.4	0.3	1.21	0.8
ENSMUSG00000079415	*Zfp91-cntf*	4.01	3.96	4.02	3.8
ENSMUSG00000079419	*Ms4a6c*	2.16	0.14	1.04	1.14
ENSMUSG00000079426	*Arpc4*	5.37	5.82	5.88	5.83

ENSMUSG00000079427	*NA*	3.4	2.49	3.15	2.92
ENSMUSG00000079437	*1810059G22Ri*	4.25	4.63	4.49	4.21
ENSMUSG00000079447	*AI661453*	1.95	2.89	2.51	2.35
ENSMUSG00000079468	*NA*	2.14	0.7	1.66	1.36
ENSMUSG00000079469	*Pigb*	2.37	2.86	2.55	2.42
ENSMUSG00000079477	*Rab7*	6.16	5.85	6.02	5.76
ENSMUSG00000079478	*Sssca1*	3.69	4.05	3.97	3.54
ENSMUSG00000079484	*Phyhd1*	5.44	5.34	5.39	5.19
ENSMUSG00000079487	*Med12*	2	2.1	2.51	2.3
ENSMUSG00000079488	*AK018679*	4.94	4.5	5.25	5
ENSMUSG00000079491	*H2-T10*	2.13	1.76	1.4	1.72
ENSMUSG00000079498	*Wdr9*	1.07	0.91	0.98	0.75
ENSMUSG00000079505	*NA*	2.91	3.24	3.09	2.96
ENSMUSG00000079507	*H2-Q1*	1.26	0.23	1.02	0.14
ENSMUSG00000079509	*Zfx*	2.2	1.04	1.8	1.42
ENSMUSG00000079511	*Ccdc142*	2.82	2.92	2.9	2.63
ENSMUSG00000079529	*Mtcp1*	1.35	0.29	1.2	0.71
ENSMUSG00000079547	*H2-DMb1*	1.54	1.22	0.63	1.64
ENSMUSG00000079551	*Cflar*	2.58	2.42	3.29	3.07
ENSMUSG00000079552	*St3gal6*	0.6	-1.44	1.07	0.66
ENSMUSG00000079555	*BC023882*	1.83	0.47	1.36	0.24
ENSMUSG00000079557	*2-Mar*	5.01	5.53	5	4.91
ENSMUSG00000079562	*Maea*	4.47	4.77	4.51	4.22
ENSMUSG00000079563	*Pglyrp2*	6.05	6.25	6.22	5.89
ENSMUSG00000079605	*Zbtb9*	2.36	2.41	2.13	1.93
ENSMUSG00000079611	*NA*	3.36	3.65	3.34	2.64
ENSMUSG00000079614	*Seh1l*	4.48	3.6	3.93	3.69
ENSMUSG00000079641	*Rpl39*	1.64	0.86	1.4	0.88
ENSMUSG00000079658	*Tceb1*	5.12	3.77	4.46	4.06
ENSMUSG00000079659	*4930420K17Ri*	5.9	5.37	5.95	5.2
ENSMUSG00000079671	*NA*	1.95	1.29	1.36	0.57

ENSMUSG00000079677	*NA*	3.95	4.85	4.48	4.33
ENSMUSG00000079681	*Glp1*	2.37	3.28	2.91	2.74
ENSMUSG00000079716	*NA*	2.73	2.31	2.42	1.63
ENSMUSG00000079737	*3110001I22Rik*	1.17	0.93	1.58	1.37
ENSMUSG00000079738	*NA*	1.1	0.39	0.86	0.31
ENSMUSG00000079869	*NA*	4.05	3.47	3.16	3.29
ENSMUSG00000079880	*NA*	1.85	-0.03	0.68	-1.33
ENSMUSG00000079914	*NA*	3.7	3.66	3.65	3.44
ENSMUSG00000079936	*NA*	5.89	6.61	6.62	6.47
ENSMUSG00000079954	*NA*	2.07	1.44	1.47	1.67
ENSMUSG00000079961	*NA*	3.5	3.01	3.25	2.21
ENSMUSG00000079971	*NA*	3.73	3.9	3.87	3.59
ENSMUSG00000079985	*NA*	1.07	1.55	1.24	-0.38
ENSMUSG00000079986	*NA*	5.4	5.96	4.65	4.92
ENSMUSG00000079989	*NA*	4.3	2.98	3.59	3.21
ENSMUSG00000079990	*NA*	3.55	3.86	3.38	3.43
ENSMUSG00000080018	*NA*	1.38	1.26	1.16	0.98
ENSMUSG00000080025	*NA*	5.54	5.71	5.61	5.01
ENSMUSG00000080049	*Exosc6*	2.32	2.84	2.28	2.28
ENSMUSG00000080058	*NA*	4.73	6.54	5.99	5.86
ENSMUSG00000080124	*NA*	1.61	1.1	0.02	-0.19
ENSMUSG00000080125	*AK171116*	2.74	2.35	2.99	2.44
ENSMUSG00000080136	*NA*	3.76	4.41	3.82	3.84
ENSMUSG00000080153	*NA*	2.9	1.04	1.27	2.13
ENSMUSG00000080225	*NA*	1.44	2.18	2.04	1.23
ENSMUSG00000080229	*NA*	1.57	0.96	1.29	0.76
ENSMUSG00000080238	*Ubp1*	4.35	4.07	4.39	4.17
ENSMUSG00000080242	*NA*	3.29	3.76	3.8	4.03
ENSMUSG00000080268	*Brms1*	3.46	4.14	3.95	3.82
ENSMUSG00000080374	*NA*	4.14	4.57	5.13	4.08
ENSMUSG00000080395	*NA*	7.86	5.83	7.11	8.57

ENSMUSG00000080404	*NA*	5.67	6.09	4.86	5.27
ENSMUSG00000080457	*NA*	4.3	4.42	2.82	4.51
ENSMUSG00000080512	*NA*	8.14	7.29	7.44	7.87
ENSMUSG00000080533	*NA*	1.8	2.95	1.68	2.63
ENSMUSG00000080552	*NA*	1.03	1.36	2.02	1.14
ENSMUSG00000080587	*NA*	1.58	-1.21	-0.82	-0.97
ENSMUSG00000080643	*NA*	4.24	5.63	6.6	4.9
ENSMUSG00000080738	*NA*	6.56	5.18	5.31	7.07
ENSMUSG00000080772	*NA*	1.84	0.74	1.51	2.28
ENSMUSG00000080824	*NA*	2.07	0.53	2.01	1.58
ENSMUSG00000080848	*NA*	3.22	2.7	3.43	4.68
ENSMUSG00000080893	*NA*	5.26	5	5.33	5.26
ENSMUSG00000080904	*NA*	8.22	6.63	7.32	7.75
ENSMUSG00000080907	*NA*	0.19	0.79	1.17	1
ENSMUSG00000080921	*NA*	3.92	3.4	4.32	4.66
ENSMUSG00000080935	*NA*	4.98	4.22	4.52	5.39
ENSMUSG00000080973	*NA*	1.17	-0.26	0.3	1.82
ENSMUSG00000080989	*NA*	2.18	1.84	1.59	1.71
ENSMUSG00000080991	*NA*	3.51	1.54	2.39	3.05
ENSMUSG00000081049	*NA*	2.92	0.45	2.05	2.72
ENSMUSG00000081051	*NA*	4.53	4.71	5.38	6.02
ENSMUSG00000081059	*NA*	2.75	1.56	1.66	3.09
ENSMUSG00000081094	*NA*	0.55	0.16	1.01	1.2
ENSMUSG00000081121	*NA*	2.07	0.71	1.26	2.32
ENSMUSG00000081149	*NA*	2.33	1.78	1.67	2.24
ENSMUSG00000081164	*NA*	1.04	0.49	-2.15	0.23
ENSMUSG00000081204	*NA*	2.78	1.21	1.91	2.64
ENSMUSG00000081223	*NA*	2.23	2.93	2.69	3.24
ENSMUSG00000081272	*NA*	3.09	3.2	2.75	3.39
ENSMUSG00000081277	*NA*	3.5	1.89	2.46	2.99
ENSMUSG00000081344	*NA*	4.65	3.04	4.37	5.19

ENSMUSG00000081370	*NA*	1.08	0	0.24	1.59
ENSMUSG00000081393	*NA*	3.99	3.34	3.78	3.76
ENSMUSG00000081411	*NA*	3.24	2.74	1.84	2.34
ENSMUSG00000081413	*NA*	2.25	1.56	2.54	1.67
ENSMUSG00000081419	*NA*	3.67	3.12	3.13	4.15
ENSMUSG00000081476	*NA*	2.02	1.99	1.85	2.46
ENSMUSG00000081485	*NA*	4.75	1.52	3.84	5.34
ENSMUSG00000081512	*NA*	2.3	2.85	2.07	2.2
ENSMUSG00000081519	*NA*	2.37	1.62	1.75	1.92
ENSMUSG00000081534	*4930570C03Ri*	5.17	5.55	5.27	5.05
ENSMUSG00000081603	*NA*	2.58	0.28	1.42	1.55
ENSMUSG00000081669	*NA*	2.19	1.51	1.99	3.07
ENSMUSG00000081715	*NA*	3.51	2.68	2.59	4.18
ENSMUSG00000081726	*NA*	0.7	1.04	1.41	2.62
ENSMUSG00000081727	*NA*	0.96	1.6	1.75	2
ENSMUSG00000081729	*NA*	3.76	3.13	2.76	3.68
ENSMUSG00000081772	*NA*	2.18	0.78	1.64	1.49
ENSMUSG00000081780	*NA*	1.74	0.04	1.08	1.35
ENSMUSG00000081787	*NA*	1.23	1.16	0.89	2.06
ENSMUSG00000081824	*NA*	5.37	4.26	5.25	5.69
ENSMUSG00000081867	*NA*	2.83	3.78	3.65	3.71
ENSMUSG00000081888	*NA*	2.65	2.34	1.59	3.27
ENSMUSG00000081944	*NA*	0.92	0.66	1.44	0.4
ENSMUSG00000081952	*NA*	1.36	1.6	1.86	2.28
ENSMUSG00000081956	*NA*	2.52	1.71	2.8	2.42
ENSMUSG00000081988	*NA*	2.5	1.36	2	1.5
ENSMUSG00000082044	*NA*	1.93	1.61	2.23	2.12
ENSMUSG00000082100	*NA*	3.88	4.29	4.41	5.41
ENSMUSG00000082192	*NA*	2.38	2.32	2.11	3.49
ENSMUSG00000082209	*NA*	3.61	3.75	3.59	4.53
ENSMUSG00000082232	*NA*	2.14	1.91	2.29	2.38

ENSMUSG00000082272	*NA*	2.49	2.03	2.19	3.8
ENSMUSG00000082286	*NA*	3.7	4.32	4.21	3.69
ENSMUSG00000082292	*NA*	2.14	1.13	0.54	0.97
ENSMUSG00000082293	*Bhmt*	6.66	6.07	6.69	5.09
ENSMUSG00000082319	*NA*	1.39	1.51	1.08	2.23
ENSMUSG00000082321	*NA*	2.09	0.23	0.56	1.73
ENSMUSG00000082363	*NA*	3.52	0.4	2.54	3.45
ENSMUSG00000082385	*NA*	3.28	2.13	2.84	3.74
ENSMUSG00000082409	*NA*	1.75	1.09	1.54	3.1
ENSMUSG00000082425	*NA*	3.78	1.7	3.72	2.92
ENSMUSG00000082431	*NA*	1.41	1.91	1.31	1.71
ENSMUSG00000082454	*NA*	2.49	1.61	2.15	2.97
ENSMUSG00000082519	*NA*	3.8	2.39	3.21	2.82
ENSMUSG00000082530	*NA*	0.95	1.05	1.64	3.45
ENSMUSG00000082536	*NA*	4.56	3.36	3.93	5.2
ENSMUSG00000082654	*NA*	2.3	1.73	1.96	2.37
ENSMUSG00000082674	*NA*	2.84	1.87	2.26	3.15
ENSMUSG00000082675	*NA*	1.57	0.57	1.05	2.22
ENSMUSG00000082676	*NA*	1.17	-0.06	1.2	0.2
ENSMUSG00000082697	*NA*	3.12	1.36	1.01	1.2
ENSMUSG00000082702	*NA*	1.31	0.87	0.59	0.37
ENSMUSG00000082787	*NA*	1.68	1.84	1.6	3.23
ENSMUSG00000082811	*NA*	1.21	1.13	1.96	1.71
ENSMUSG00000082836	*NA*	1.58	1.36	1.6	2.71
ENSMUSG00000082876	*NA*	1.32	0.32	0.85	1.06
ENSMUSG00000082908	*NA*	2.77	3.02	2.95	3.76
ENSMUSG00000082935	*NA*	2.7	1.64	2.35	2.38
ENSMUSG00000082992	*NA*	2.96	-0.95	2.01	-0.61
ENSMUSG00000082998	*NA*	1.46	0.07	0.6	2.26
ENSMUSG00000083003	*NA*	1.22	1.49	2.24	2.89
ENSMUSG00000083012	*2810453I06Rik*	1.9	2.42	2.18	2.07

ENSMUSG00000083097	*NA*	1.2	0.88	0.79	1.83
ENSMUSG00000083179	*NA*	2.78	0.31	1.55	1.77
ENSMUSG00000083194	*NA*	2.85	2.37	3.05	2.15
ENSMUSG00000083240	*NA*	2.88	2.16	2.67	0.33
ENSMUSG00000083282	*Ctsf*	3.77	4.48	3.89	4.06
ENSMUSG00000083325	*NA*	1.32	0.21	0.91	1.28
ENSMUSG00000083327	*NA*	4.97	5.16	4.18	5.59
ENSMUSG00000083354	*NA*	3.03	3.56	3.4	3.08
ENSMUSG00000083370	*NA*	3.45	4.01	3.99	4.25
ENSMUSG00000083405	*NA*	4.35	4.56	4.66	4.77
ENSMUSG00000083443	*NA*	1.33	1.88	1.39	2.47
ENSMUSG00000083476	*NA*	1.79	1.07	-0.19	2.29
ENSMUSG00000083478	*NA*	2.35	0.51	0.97	-1.53
ENSMUSG00000083480	*NA*	2.34	2.24	2.87	3.03
ENSMUSG00000083497	*NA*	6.68	6.66	6.4	7.16
ENSMUSG00000083557	*NA*	1.17	0.24	0.86	1.24
ENSMUSG00000083563	*NA*	2.97	0.83	0.69	0.73
ENSMUSG00000083567	*NA*	2.3	1.15	1.2	1.15
ENSMUSG00000083621	*NA*	2.42	1.27	1.67	3.78
ENSMUSG00000083626	*NA*	2.62	0.91	2.35	2.6
ENSMUSG00000083694	*NA*	2.18	2.11	2.39	3.01
ENSMUSG00000083696	*NA*	3.02	1.83	1.54	1.51
ENSMUSG00000083736	*NA*	1.05	-0.84	0.44	1.21
ENSMUSG00000083758	*NA*	3.8	3.48	3.53	3.26
ENSMUSG00000083773	*NA*	4.5	-3.32	4.68	-4.32
ENSMUSG00000083798	*NA*	2.06	-3.67	2.11	#NAME?
ENSMUSG00000083800	*NA*	5.47	4.26	4.72	6.12
ENSMUSG00000083829	*NA*	2.43	2.87	1.87	1.6
ENSMUSG00000083840	*NA*	5.84	5.52	5.49	5.91
ENSMUSG00000083844	*NA*	2.86	2.92	2.82	3.27
ENSMUSG00000083863	*NA*	1.94	0.48	1.13	1.28

ENSMUSG00000083892	*NA*	1.23	-0.81	0.02	-0.66
ENSMUSG00000083899	*NA*	2.11	0.84	0.69	2.28
ENSMUSG00000083902	*NA*	2.56	1.79	2.03	2.38
ENSMUSG00000083992	*NA*	4.78	2.98	3.59	4.97
ENSMUSG00000084013	*NA*	3.56	3.18	2.61	4.33
ENSMUSG00000084067	*NA*	1.56	-2.61	0.52	-0.61
ENSMUSG00000084093	*NA*	0.67	1.22	1.89	1.09
ENSMUSG00000084098	*NA*	3.08	2.62	2.8	3.56
ENSMUSG00000084099	*NA*	2.16	2.7	1.7	3.18
ENSMUSG00000084128	*Rbm35b*	4.7	5.46	5.09	4.95
ENSMUSG00000084132	*NA*	1.71	0.28	1.74	0.62
ENSMUSG00000084159	*NA*	3.32	2.21	2.47	3.64
ENSMUSG00000084215	*NA*	1.72	2.1	1.73	1.98
ENSMUSG00000084241	*NA*	1.56	-0.01	0.85	0.92
ENSMUSG00000084289	*NA*	3.83	3.36	3.29	4.79
ENSMUSG00000084319	*NA*	6.2	4.85	5.4	5.8
ENSMUSG00000084329	*NA*	2.59	2.29	1.9	2.52
ENSMUSG00000084347	*NA*	1.82	2.59	2.43	2.92
ENSMUSG00000084349	*NA*	2.76	2.38	2.58	3.45
ENSMUSG00000084384	*NA*	3.25	1.88	2.45	3.59
ENSMUSG00000084398	*NA*	2.41	1.53	2.65	2.78
ENSMUSG00000084416	*NA*	0.61	1.15	1.71	3.21
ENSMUSG00000084479	*NA*	1.19	-0.19	0.56	-3.12
ENSMUSG00000084514	*NA*	0.67	1.7	1.79	1.74
ENSMUSG00000084516	*NA*	4.42	3.07	4.32	4.38
ENSMUSG00000084523	*NA*	4.2	1.8	4.06	4.1
ENSMUSG00000084565	*NA*	-0.83	1.61	2.51	1.5
ENSMUSG00000084590	*NA*	4.08	3.44	4.15	3.61
ENSMUSG00000084616	*NA*	1.86	1.07	-0.43	-0.84
ENSMUSG00000084691	*NA*	#NAME?	-0.57	1.43	1.02
ENSMUSG00000084708	*NA*	1.02	-1.53	-0.53	-0.87

ENSMUSG00000084724	*NA*	5.37	5.03	4.64	4.16
ENSMUSG00000084735	*NA*	10.99	11.01	11.14	10.97

Supplementary Table S11 Enrichment in biological process GO-terms (all levels) of upregulated expressed genes (fold change >2) between *Smarcal1*$^{del/del}$ and *wt* mouse livers at 20^{oC}.

Term	**Count**	**PValue**	**Fold Enrichment**
GO:0009987~cellular process	168	0.002641961	1.137409509
GO:0008152~metabolic process	126	0.041472607	1.124285553
GO:0044238~primary metabolic process	119	0.005718276	1.200130932
GO:0044237~cellular metabolic process	110	0.018369419	1.176415284
GO:0043170~macromolecule metabolic process	104	0.001672704	1.274839867
GO:0044260~cellular macromolecule metabolic process	95	0.001393976	1.308129879
GO:0010467~gene expression	77	1.23E-08	1.87599573
GO:0034641~cellular nitrogen compound metabolic process	77	2.61E-05	1.553360716
GO:0006807~nitrogen compound metabolic process	77	7.25E-05	1.509131734
GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	71	8.23E-05	1.54368359
GO:0009058~biosynthetic process	69	0.001702868	1.405095868
GO:0019222~regulation of metabolic process	68	8.38E-04	1.447802897
GO:0044249~cellular biosynthetic process	68	0.001191447	1.429340981
GO:0034645~cellular macromolecule biosynthetic process	63	4.07E-05	1.645638987
GO:0009059~macromolecule biosynthetic process	63	4.50E-05	1.640167203
GO:0060255~regulation of macromolecule metabolic process	63	0.00102386	1.46809609
GO:0031323~regulation of cellular metabolic process	63	0.002514426	1.416454519
GO:0080090~regulation of primary metabolic process	62	0.001479369	1.453444433
GO:0032502~developmental process	59	0.010833413	1.347315795
GO:0010468~regulation of gene expression	57	0.001966547	1.469909301
GO:0007275~multicellular organismal development	57	0.004506159	1.416267232
GO:0031326~regulation of cellular biosynthetic process	56	0.00455405	1.421877148
GO:0009889~regulation of biosynthetic process	56	0.004919706	1.416708774
GO:0010556~regulation of macromolecule biosynthetic process	55	0.003461829	1.446926568
GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic proce	54	0.004396992	1.437523754
GO:0051171~regulation of nitrogen compound metabolic process	54	0.005191711	1.426009019
GO:0045449~regulation of transcription	53	0.002262042	1.490729513

GO:0006350~transcription	49	1.30E-04	1.732110361
GO:0048856~anatomical structure development	47	0.02301666	1.356692178
GO:0048731~system development	43	0.04103519	1.328794751
GO:0048518~positive regulation of biological process	40	0.001247878	1.678198701
GO:0030154~cell differentiation	38	0.009112483	1.517063816
GO:0048869~cellular developmental process	38	0.016942011	1.454934675
GO:0048513~organ development	37	0.033211865	1.393646639
GO:0048522~positive regulation of cellular process	36	0.001771508	1.708329996
GO:0006950~response to stress	32	0.003969109	1.692939636
GO:0048523~negative regulation of cellular process	32	0.004381093	1.681577625
GO:0048519~negative regulation of biological process	32	0.018742393	1.511644441
GO:0042981~regulation of apoptosis	28	2.13E-07	3.171583115
GO:0043067~regulation of programmed cell death	28	2.77E-07	3.131938326
GO:0010941~regulation of cell death	28	3.05E-07	3.115249489
GO:0007242~intracellular signaling cascade	28	0.00138857	1.916814713
GO:0016070~RNA metabolic process	25	1.43E-04	2.365512331
GO:0043065~positive regulation of apoptosis	19	8.82E-08	4.798937758
GO:0043068~positive regulation of programmed cell death	19	9.95E-08	4.760546256
GO:0010942~positive regulation of cell death	19	1.12E-07	4.722764142
GO:0009790~embryonic development	19	0.020838927	1.77632323
GO:0051716~cellular response to stimulus	18	0.007637899	2.027873736
GO:0009605~response to external stimulus	18	0.026914448	1.761715308
GO:0048468~cell development	17	0.034895793	1.742813471
GO:0006357~regulation of transcription from RNA polymerase II promoter	17	0.037331128	1.728667258
GO:0006396~RNA processing	16	0.004303463	2.293410216
GO:0033554~cellular response to stress	15	0.005324625	2.325696777
GO:0043009~chordate embryonic development	15	0.007488582	2.23178503
GO:0009792~embryonic development ending in birth or egg hatching	15	0.008095696	2.210779995
GO:0031324~negative regulation of cellular metabolic process	15	0.024559617	1.921434556
GO:0009892~negative regulation of metabolic process	15	0.046216925	1.759515913
GO:0031327~negative regulation of cellular biosynthetic process	14	0.019983076	2.039401701

GO:0009890~negative regulation of biosynthetic process	14	0.021588102	2.020605372
GO:0012501~programmed cell death	14	0.03909713	1.854001546
GO:0006917~induction of apoptosis	13	1.46E-05	4.876071645
GO:0012502~induction of programmed cell death	13	1.46E-05	4.876071645
GO:0010558~negative regulation of macromolecule biosynthetic process	13	0.035038155	1.948095609
GO:0001701~in utero embryonic development	12	0.003666728	2.815225462
GO:0006412~translation	12	0.013128177	2.356317236
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	11	0.003909218	2.982798406
GO:0007264~small GTPase mediated signal transduction	11	0.008344968	2.670645084
GO:0006974~response to DNA damage stimulus	11	0.016570406	2.400788961
GO:0045892~negative regulation of transcription, DNA-dependent	11	0.02551341	2.237098804
GO:0051253~negative regulation of RNA metabolic process	11	0.026733462	2.222665909
GO:0034470~ncRNA processing	10	9.56E-04	3.964478894
GO:0034660~ncRNA metabolic process	10	0.005046953	3.100929036
GO:0001944~vasculature development	10	0.018670222	2.505550661
GO:0001568~blood vessel development	9	0.04153762	2.310446306
GO:0046578~regulation of Ras protein signal transduction	8	0.025696357	2.768564266
GO:0048514~blood vessel morphogenesis	8	0.038985868	2.530859253
GO:0006351~transcription, DNA-dependent	7	0.01325368	3.594027587
GO:0032774~RNA biosynthetic process	7	0.015334994	3.479931473
GO:0009991~response to extracellular stimulus	7	0.01950439	3.296777185
GO:0002460~adaptive immune response based on somatic recombination of immune receptors	6	0.010847465	4.474197609
GO:0002250~adaptive immune response	6	0.010847465	4.474197609
GO:0035023~regulation of Rho protein signal transduction	6	0.011930806	4.370146501
GO:0051789~response to protein stimulus	6	0.012499086	4.319914932
GO:0031667~response to nutrient levels	6	0.036506779	3.268109558
GO:0009451~RNA modification	5	0.00433406	7.456996014
GO:0006959~humoral immune response	5	0.010565775	5.799885789
GO:0007050~cell cycle arrest	5	0.012721112	5.494628642
GO:0042770~DNA damage response, signal transduction	5	0.012721112	5.494628642
GO:0001666~response to hypoxia	5	0.018785915	4.893653634

GO:0070482~response to oxygen levels	5	0.019775435	4.818366655
GO:0008033~tRNA processing	5	0.02520166	4.474197609
GO:0030330~DNA damage response, signal transduction by p53 class mediator	4	0.003181089	13.18710874
GO:0008630~DNA damage response, signal transduction resulting in induction of apoptosis	4	0.005548627	10.89369853
GO:0007266~Rho protein signal transduction	4	0.008747268	9.279817262
GO:0008629~induction of apoptosis by intracellular signals	4	0.017840719	7.158716174
GO:0002455~humoral immune response mediated by circulating immunoglobulin	4	0.017840719	7.158716174
GO:0031668~cellular response to extracellular stimulus	4	0.034479228	5.567890357
GO:0009266~response to temperature stimulus	4	0.047250824	4.912844433
GO:0042771~DNA damage response, signal transduction by p53 class mediator resulting in ind	3	0.020182964	13.42259283
GO:0002886~regulation of myeloid leukocyte mediated immunity	3	0.023047212	12.5277533
GO:0006400~tRNA modification	3	0.026067652	11.74476872
GO:0045682~regulation of epidermis development	3	0.032554682	10.43979442
GO:0032764~negative regulation of mast cell cytokine production	2	0.031536926	62.63876652
GO:0042092~T-helper 2 type immune response	2	0.031536926	62.63876652
GO:0002701~negative regulation of production of molecular mediator of immune response	2	0.046932062	41.75917768
GO:0002719~negative regulation of cytokine production during immune response	2	0.046932062	41.75917768
GO:0032763~regulation of mast cell cytokine production	2	0.046932062	41.75917768

Supplementary Table S12 Enrichment in biological process GO-terms (all levels) of downregulated expressed genes (fold change >2) between *Smarcal1*$^{del/del}$ and *wt* mouse livers at 20^{oC}.

Term	Count	PValue	Fold Enrichment
GO:0009987~cellular process	391	1.17E-05	1.131659221
GO:0008152~metabolic process	343	5.69E-13	1.308372903
GO:0044238~primary metabolic process	293	4.96E-08	1.263224745
GO:0044237~cellular metabolic process	290	1.99E-10	1.325858896
GO:0043170~macromolecule metabolic process	231	1.85E-04	1.210502283
GO:0044260~cellular macromolecule metabolic process	218	6.15E-06	1.283261278
GO:0009058~biosynthetic process	159	4.32E-06	1.384156914
GO:0044249~cellular biosynthetic process	155	4.28E-06	1.392803878
GO:0006807~nitrogen compound metabolic process	152	5.89E-04	1.273536365
GO:0034641~cellular nitrogen compound metabolic process	148	6.43E-04	1.276364287
GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	141	2.93E-04	1.310540322
GO:0019222~regulation of metabolic process	128	0.034484236	1.165042677
GO:0010467~gene expression	126	6.91E-04	1.312329833
GO:0034645~cellular macromolecule biosynthetic process	122	1.94E-04	1.362338986
GO:0009059~macromolecule biosynthetic process	122	2.29E-04	1.357809181
GO:0060255~regulation of macromolecule metabolic process	121	0.015912722	1.205398479
GO:0080090~regulation of primary metabolic process	119	0.023253486	1.192573187
GO:0019538~protein metabolic process	115	0.034991225	1.177607818
GO:0010468~regulation of gene expression	110	0.019242851	1.212661818
GO:0031326~regulation of cellular biosynthetic process	109	0.03676522	1.183128406
GO:0009889~regulation of biosynthetic process	109	0.039317286	1.178827859
GO:0051171~regulation of nitrogen compound metabolic process	107	0.023060951	1.20793517
GO:0010556~regulation of macromolecule biosynthetic process	107	0.025084653	1.203369266
GO:0006810~transport	106	0.021882276	1.211974571
GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic proces	106	0.025307516	1.206308731
GO:0051234~establishment of localization	106	0.026288695	1.203750825
GO:0044267~cellular protein metabolic process	105	9.52E-04	1.346583653

GO:0045449~regulation of transcription	103	0.013613902	1.238487252
GO:0006350~transcription	89	0.002767204	1.344933534
GO:0006464~protein modification process	60	0.039632935	1.275132275
GO:0009056~catabolic process	54	0.012234347	1.390384615
GO:0033036~macromolecule localization	48	0.012274357	1.424981523
GO:0044248~cellular catabolic process	47	0.006673421	1.484145702
GO:0006629~lipid metabolic process	46	2.25E-04	1.769795658
GO:0009057~macromolecule catabolic process	45	1.04E-04	1.842507645
GO:0030163~protein catabolic process	43	1.08E-05	2.070943245
GO:0044265~cellular macromolecule catabolic process	43	9.07E-05	1.890713373
GO:0051603~proteolysis involved in cellular protein catabolic process	41	2.14E-05	2.055971702
GO:0044257~cellular protein catabolic process	41	2.45E-05	2.044485827
GO:0008104~protein localization	39	0.035654369	1.386896857
GO:0019941~modification-dependent protein catabolic process	38	7.88E-05	2.003062117
GO:0043632~modification-dependent macromolecule catabolic process	38	7.88E-05	2.003062117
GO:0007049~cell cycle	36	0.007789552	1.577741408
GO:0015031~protein transport	36	0.018992568	1.480798771
GO:0045184~establishment of protein localization	36	0.020583667	1.469512195
GO:0044255~cellular lipid metabolic process	28	0.022949004	1.555555556
GO:0022402~cell cycle process	24	0.022339819	1.635284139
GO:0022403~cell cycle phase	21	0.021679455	1.714430894
GO:0000278~mitotic cell cycle	19	0.004626069	2.085154827
GO:0055086~nucleobase, nucleoside and nucleotide metabolic process	19	0.012146806	1.891367204
GO:0051301~cell division	18	0.03441481	1.715302491
GO:0008610~lipid biosynthetic process	18	0.038563972	1.69122807
GO:0009117~nucleotide metabolic process	17	0.023018101	1.843004948
GO:0006753~nucleoside phosphate metabolic process	17	0.023018101	1.843004948
GO:0006511~ubiquitin-dependent protein catabolic process	14	0.002354923	2.658786446
GO:0070647~protein modification by small protein conjugation or removal	13	4.84E-04	3.347222222
GO:0008202~steroid metabolic process	13	0.017438114	2.162180814
GO:0009165~nucleotide biosynthetic process	13	0.02979772	2.00063857

GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	13	0.035923876	1.944754811
GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	13	0.035923876	1.944754811
GO:0032446~protein modification by small protein conjugation	10	0.002625486	3.389592124
GO:0009152~purine ribonucleotide biosynthetic process	10	0.018414059	2.502596054
GO:0009260~ribonucleotide biosynthetic process	10	0.02281297	2.412412412
GO:0022900~electron transport chain	10	0.024020833	2.390873016
GO:0009150~purine ribonucleotide metabolic process	10	0.033774613	2.250233427
GO:0009259~ribonucleotide metabolic process	10	0.044069951	2.142222222
GO:0016567~protein ubiquitination	9	0.003033492	3.651515152
GO:0009206~purine ribonucleoside triphosphate biosynthetic process	9	0.022608486	2.591397849
GO:0009201~ribonucleoside triphosphate biosynthetic process	9	0.022608486	2.591397849
GO:0009145~purine nucleoside triphosphate biosynthetic process	9	0.023937549	2.563829787
GO:0009142~nucleoside triphosphate biosynthetic process	9	0.025320479	2.536842105
GO:0009205~purine ribonucleoside triphosphate metabolic process	9	0.034801002	2.386138614
GO:0009199~ribonucleoside triphosphate metabolic process	9	0.036586194	2.362745098
GO:0009144~purine nucleoside triphosphate metabolic process	9	0.04434035	2.273584906
GO:0045454~cell redox homeostasis	8	0.008026038	3.455197133
GO:0051236~establishment of RNA localization	8	0.011197479	3.245791246
GO:0050657~nucleic acid transport	8	0.011197479	3.245791246
GO:0050658~RNA transport	8	0.011197479	3.245791246
GO:0006403~RNA localization	8	0.012114748	3.1973466
GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	8	0.020105616	2.894894895
GO:0006754~ATP biosynthetic process	8	0.033055356	2.612466125
GO:0051028~mRNA transport	7	0.02751857	3.023297491
GO:0046777~protein amino acid autophosphorylation	7	0.035972482	2.84006734
GO:0051325~interphase	6	0.04063239	3.150326797
GO:0030518~steroid hormone receptor signaling pathway	4	0.041583328	5.100529101
GO:0060322~head development	4	0.041583328	5.100529101
GO:0030521~androgen receptor signaling pathway	3	0.025712762	11.47619048

Supplementary Table S13 Enrichment in biological process GO-terms (all levels) of upregulated expressed genes (fold change >2) between *Smarcal1*$^{del/del}$ and *wt* mouse livers at 39.5^{oC}.

Term	**Count**	**PValue**	**Fold Enrichment**
GO:0008152~metabolic process	23	0.003300414	1.552882241
GO:0044237~cellular metabolic process	20	0.007034519	1.618462239
GO:0044238~primary metabolic process	20	0.014637179	1.526216927
GO:0043170~macromolecule metabolic process	18	0.01055318	1.669549902
GO:0044260~cellular macromolecule metabolic process	17	0.00816963	1.771253755
GO:0009058~biosynthetic process	13	0.013022419	2.0031101
GO:0010467~gene expression	12	0.00933004	2.212213147
GO:0044249~cellular biosynthetic process	12	0.027232697	1.908590604
GO:0034645~cellular macromolecule biosynthetic process	11	0.016557519	2.174159021
GO:0009059~macromolecule biosynthetic process	11	0.016931463	2.166929897
GO:0044267~cellular protein metabolic process	10	0.019537026	2.2699553
GO:0009057~macromolecule catabolic process	6	0.009614252	4.348318043
GO:0006412~translation	5	0.003791732	7.428944619
GO:0044257~cellular protein catabolic process	5	0.022593811	4.413097455
GO:0030163~protein catabolic process	5	0.025292651	4.262290168
GO:0044265~cellular macromolecule catabolic process	5	0.03383289	3.891351943
GO:0001889~liver development	3	0.003443706	33.06744186
GO:0006351~transcription, DNA-dependent	3	0.025489793	11.65491803
GO:0032774~RNA biosynthetic process	3	0.027060159	11.28492063

Supplementary Table S14 Enrichment in biological process GO-terms (all levels) of downregulated expressed genes (fold change >2) between *Smarcal1*$^{del/del}$ and *wt* mouse livers at 39.5^{o}C.

Term	Count	PValue	Fold Enrichment
GO:0008152~metabolic process	103	0.016272015	1.172058164
GO:0050896~response to stimulus	45	0.005603062	1.475047604
GO:0002376~immune system process	34	7.00E-10	3.433614114
GO:0048518~positive regulation of biological process	27	0.048865517	1.444617955
GO:0006955~immune response	23	9.55E-08	3.90082063
GO:0007242~intracellular signaling cascade	22	0.004868256	1.92066065
GO:0048583~regulation of response to stimulus	19	1.58E-07	4.599267961
GO:0002682~regulation of immune system process	18	5.61E-07	4.465454672
GO:0002684~positive regulation of immune system process	16	4.33E-08	6.20442893
GO:0050776~regulation of immune response	15	1.14E-07	6.273457262
GO:0002520~immune system development	15	1.95E-05	4.061797753
GO:0007049~cell cycle	14	0.041924611	1.830357307
GO:0048534~hemopoietic or lymphoid organ development	13	2.09E-04	3.695609581
GO:0032879~regulation of localization	13	0.004894491	2.557798749
GO:0042981~regulation of apoptosis	13	0.043815882	1.877877563
GO:0043067~regulation of programmed cell death	13	0.047401685	1.854404093
GO:0010941~regulation of cell death	13	0.048998886	1.844522721
GO:0050778~positive regulation of immune response	12	1.03E-06	7.048413748
GO:0048584~positive regulation of response to stimulus	12	2.12E-05	5.153678869
GO:0006952~defense response	12	0.024600279	2.13969703
GO:0051249~regulation of lymphocyte activation	11	1.26E-05	6.102098939
GO:0002694~regulation of leukocyte activation	11	2.27E-05	5.705858748
GO:0050865~regulation of cell activation	11	2.53E-05	5.632706713
GO:0001775~cell activation	11	0.001033108	3.571960354
GO:0002253~activation of immune response	10	1.18E-06	9.288607264
GO:0051251~positive regulation of lymphocyte activation	10	2.51E-06	8.498087497
GO:0002696~positive regulation of leukocyte activation	10	3.88E-06	8.068891159

GO:0050867~positive regulation of cell activation	10	4.58E-06	7.909111136
GO:0045321~leukocyte activation	10	0.00169721	3.647580935
GO:0030097~hemopoiesis	10	0.004225054	3.182550696
GO:0046649~lymphocyte activation	9	0.002706634	3.764074357
GO:0043065~positive regulation of apoptosis	9	0.012474879	2.898944364
GO:0043068~positive regulation of programmed cell death	9	0.013084144	2.875752809
GO:0010942~positive regulation of cell death	9	0.013697532	2.852929374
GO:0008284~positive regulation of cell proliferation	9	0.025881579	2.531472543
GO:0002460~adaptive immune response based on somatic recombination of immune receptors bu	8	8.32E-05	7.607811664
GO:0002250~adaptive immune response	8	8.32E-05	7.607811664
GO:0002697~regulation of immune effector process	8	1.12E-04	7.262002043
GO:0080134~regulation of response to stress	8	0.009212006	3.399234999
GO:0007243~protein kinase cascade	8	0.028380712	2.707865169
GO:0000278~mitotic cell cycle	8	0.033158027	2.619082704
GO:0050851~antigen receptor-mediated signaling pathway	7	4.88E-06	15.53261548
GO:0002429~immune response-activating cell surface receptor signaling pathway	7	1.07E-05	13.63839408
GO:0002768~immune response-regulating cell surface receptor signaling pathway	7	1.63E-05	12.70850358
GO:0002699~positive regulation of immune effector process	7	2.12E-05	12.15595994
GO:0002757~immune response-activating signal transduction	7	2.72E-05	11.64946161
GO:0050671~positive regulation of lymphocyte proliferation	7	3.45E-05	11.18348315
GO:0032946~positive regulation of mononuclear cell proliferation	7	3.45E-05	11.18348315
GO:0070665~positive regulation of leukocyte proliferation	7	4.33E-05	10.75334918
GO:0002764~immune response-regulating signal transduction	7	4.33E-05	10.75334918
GO:0050864~regulation of B cell activation	7	5.98E-05	10.16680286
GO:0002703~regulation of leukocyte mediated immunity	7	2.32E-04	7.988202247
GO:0042113~B cell activation	7	4.18E-04	7.168899453
GO:0050670~regulation of lymphocyte proliferation	7	4.79E-04	6.989676966
GO:0032944~regulation of mononuclear cell proliferation	7	4.79E-04	6.989676966
GO:0070663~regulation of leukocyte proliferation	7	5.47E-04	6.81919704
GO:0050863~regulation of T cell activation	7	0.002293823	5.177538494
GO:0002252~immune effector process	7	0.004917707	4.437890137

GO:0002521~leukocyte differentiation	7	0.008689088	3.937846178
GO:0010627~regulation of protein kinase cascade	7	0.013010348	3.607575208
GO:0009967~positive regulation of signal transduction	7	0.020681219	3.251012542
GO:0010647~positive regulation of cell communication	7	0.030931302	2.958593425
GO:0007067~mitosis	7	0.031660108	2.943021881
GO:0000280~nuclear division	7	0.031660108	2.943021881
GO:0000087~M phase of mitotic cell cycle	7	0.03454287	2.882341017
GO:0048285~organelle fission	7	0.036832348	2.838447499
GO:0050853~B cell receptor signaling pathway	6	5.16E-07	34.23515249
GO:0050871~positive regulation of B cell activation	6	8.92E-05	12.95384148
GO:0016064~immunoglobulin mediated immune response	6	0.001107776	7.607811664
GO:0019724~B cell mediated immunity	6	0.001276053	7.373725151
GO:0002706~regulation of lymphocyte mediated immunity	6	0.001276053	7.373725151
GO:0002449~lymphocyte mediated immunity	6	0.002557754	6.306475458
GO:0002443~leukocyte mediated immunity	6	0.005050415	5.385304886
GO:0043408~regulation of MAPKKK cascade	6	0.006077862	5.153678869
GO:0031347~regulation of defense response	6	0.009273909	4.653321697
GO:0030098~lymphocyte differentiation	6	0.01395435	4.204316972
GO:0016053~organic acid biosynthetic process	6	0.031544275	3.399234999
GO:0046394~carboxylic acid biosynthetic process	6	0.031544275	3.399234999
GO:0006260~DNA replication	6	0.041482863	3.153237729
GO:0030888~regulation of B cell proliferation	5	6.36E-04	12.48156601
GO:0002705~positive regulation of leukocyte mediated immunity	5	0.001495156	9.985252809
GO:0002708~positive regulation of lymphocyte mediated immunity	5	0.001495156	9.985252809
GO:0030183~B cell differentiation	5	0.002519638	8.68282853
GO:0006959~humoral immune response	5	0.004521448	7.396483562
GO:0002822~regulation of adaptive immune response based on somatic recombination of immun	5	0.005151322	7.132323435
GO:0002819~regulation of adaptive immune response	5	0.005151322	7.132323435
GO:0050727~regulation of inflammatory response	5	0.005487218	7.007194954
GO:0050870~positive regulation of T cell activation	5	0.009185436	6.051668369
GO:0002526~acute inflammatory response	5	0.018381732	4.930989041

GO:0010740~positive regulation of protein kinase cascade	5	0.024110205	4.538751277
GO:0032101~regulation of response to external stimulus	5	0.039684279	3.877768081
GO:0042330~taxis	5	0.047201078	3.664312957
GO:0006935~chemotaxis	5	0.047201078	3.664312957
GO:0030890~positive regulation of B cell proliferation	4	0.002453711	14.52400409
GO:0002889~regulation of immunoglobulin mediated immune response	4	0.006014582	10.65093633
GO:0002712~regulation of B cell mediated immunity	4	0.006014582	10.65093633
GO:0002824~positive regulation of adaptive immune response based on somatic recombination o	4	0.008549035	9.397884997
GO:0046634~regulation of alpha-beta T cell activation	4	0.008549035	9.397884997
GO:0002821~positive regulation of adaptive immune response	4	0.008549035	9.397884997
GO:0042102~positive regulation of T cell proliferation	4	0.009266223	9.129373997
GO:0002455~humoral immune response mediated by circulating immunoglobulin	4	0.009266223	9.129373997
GO:0046651~lymphocyte proliferation	4	0.015257265	7.607811664
GO:0032943~mononuclear cell proliferation	4	0.016254455	7.430885811
GO:0070661~leukocyte proliferation	4	0.016254455	7.430885811
GO:0043410~positive regulation of MAPKKK cascade	4	0.020602171	6.798469998
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	4	0.028205284	6.028831885
GO:0031349~positive regulation of defense response	4	0.033992386	5.605755963
GO:0045619~regulation of lymphocyte differentiation	4	0.03552811	5.509104998
GO:0051052~regulation of DNA metabolic process	4	0.03552811	5.509104998
GO:0042129~regulation of T cell proliferation	4	0.037099138	5.415730337
GO:0043406~positive regulation of MAP kinase activity	4	0.037099138	5.415730337
GO:0007059~chromosome segregation	4	0.04547771	4.992626404
GO:0051605~protein maturation by peptide bond cleavage	4	0.047256716	4.915816768
GO:0048585~negative regulation of response to stimulus	4	0.047256716	4.915816768
GO:0046641~positive regulation of alpha-beta T cell proliferation	3	0.006493239	23.96460674
GO:0002863~positive regulation of inflammatory response to antigenic stimulus	3	0.010982563	18.43431288
GO:0007159~leukocyte adhesion	3	0.012708992	17.11757624
GO:0002714~positive regulation of B cell mediated immunity	3	0.012708992	17.11757624
GO:0002891~positive regulation of immunoglobulin mediated immune response	3	0.012708992	17.11757624
GO:0046640~regulation of alpha-beta T cell proliferation	3	0.012708992	17.11757624

GO:0002886~regulation of myeloid leukocyte mediated immunity	3	0.014545318	15.97640449
GO:0009067~aspartate family amino acid biosynthetic process	3	0.01648857	14.97787921
GO:0045577~regulation of B cell differentiation	3	0.01648857	14.97787921
GO:0002861~regulation of inflammatory response to antigenic stimulus	3	0.020684244	13.31367041
GO:0048535~lymph node development	3	0.022931001	12.61295092
GO:0051053~negative regulation of DNA metabolic process	3	0.025273351	11.98230337
GO:0009066~aspartate family amino acid metabolic process	3	0.030234083	10.89300306
GO:0000018~regulation of DNA recombination	3	0.035545458	9.985252809
GO:0050729~positive regulation of inflammatory response	3	0.035545458	9.985252809
GO:0002637~regulation of immunoglobulin production	3	0.0383263	9.585842697
GO:0046635~positive regulation of alpha-beta T cell activation	3	0.041187296	9.217156439
GO:0042098~T cell proliferation	3	0.047140192	8.558788122
GO:0051307~meiotic chromosome separation	2	0.036884021	53.25468165
GO:0051304~chromosome separation	2	0.036884021	53.25468165
GO:0032413~negative regulation of ion transmembrane transporter activity	2	0.048875547	39.94101124
GO:0032410~negative regulation of transporter activity	2	0.048875547	39.94101124

Supplementary Table S15 qRT-PCR measurement of mRNA levels of stress genes in the brain and liver of mice following 3 hours of heat shock at 39.5ºC.

Gene	Brain		Liver	
	Fold change[*]	p-value	Fold change[*]	p-value
Dnajc21	0.5539	0.103303	0.6619	0.01114
Atf6	1.6647	0.005168	0.6862	0.226613
Bag1	0.8096	0.073824	1.056	0.825353
Bag2	0.6678	0.098269	0.3263	0.008426
Bag3	1.2282	0.69129	12.4831	0.001895
Bag4	0.7621	0.177136	0.4633	0.010735
Bag5	0.9877	0.933817	0.3471	0.002917
Cabc1	0.9734	0.799302	1.9504	0.053862
Ccs	1.0806	0.855899	1.8411	0.070995
Cct2	1.3147	0.151575	0.8364	0.516403
Cct3	0.9056	0.328878	0.8311	0.102503
Cct4	1.344	0.133211	1.0124	0.868098
Cct5	1.1644	0.031368	1.1865	0.126963
Cct6a	1.1063	0.367545	0.8571	0.116482
Cct6b	0.5358	0.394047	0.5841	0.325782
Cct7	1.005	0.843311	0.723	0.049662
Cryaa	0.7794	0.396386	0.8414	0.448701
Cryab	0.6529	0.13472	0.9309	0.514309
Dnaja1	1.4577	0.001304	1.6457	0.104811
Dnaja2	0.8556	0.220376	0.4867	0.052802
Dnaja3	0.7889	0.053368	0.4787	0.130644
Dnaja4	1.8024	0.005696	1.3622	0.394316
Dnajb1	2.7974	0.003117	9.8775	0.000192
Dnajb2	0.6692	0.023008	0.8844	0.465361
Dnajb11	0.2557	0.339799	0.1911	0.127867
Dnajb12	0.9954	0.900606	0.7651	0.162726
Dnajb13	0.7095	0.428443	0.9409	0.473346
Dnajb14	0.7177	0.071358	0.4677	0.028752
Dnajb5	3.126	0.006149	0.2583	0.061209
Dnajb6	0.9888	0.850383	0.6414	0.007803
Dnajb7	0.6096	0.42118	2.3162	0.067284
Dnajb8	0.5007	0.377314	0.8587	0.44971
Dnajb9	0.6582	0.00112	1.3041	0.458707
Dnajc1	1.4859	0.005896	0.7579	0.235999
Dnajc10	0.9356	0.361546	0.3696	0.002008
Dnajc11	0.9057	0.477053	0.7642	0.245459
Dnajc12	0.4137	0.021857	0.8988	0.572277
Dnajc13	0.8298	0.177084	0.422	0.004247
Dnajc14	1.0748	0.374884	0.5152	0.001132
Dnajc15	0.7344	0.144963	1.4294	0.246661
Dnajc16	0.7201	0.053174	0.5555	0.090918
Dnajc17	1.1979	0.177347	0.8909	0.519996
Dnajc18	0.8688	0.336257	0.4949	0.0002
Dnajc19	0.8057	0.117401	1.0616	0.917233
Dnajc3	0.711	0.103528	0.8585	0.574645
Dnajc4	0.6764	0.184894	1.273	0.016873
Dnajc5	1.1447	0.283714	0.5081	0.014792
Dnajc5b	0.7204	0.388559	0.8587	0.44971
Dnajc5	1.1447	0.283714	0.5081	0.014792
Dnajc5b	0.7204	0.388559	0.8587	0.44971
Dnajc5g	0.5655	0.379182	0.8058	0.445654
Dnajc6	0.967	0.607897	0.1212	0.025154
Dnajc7	1.294	0.026786	0.7721	0.184159
Dnajc8	0.4721	0.033914	0.5724	0.41244
Dnajc9	0.6716	0.097667	0.3377	0.145668
Hsf1	0.6871	0.09983	0.4489	0.002501
Hsf2	0.924	0.514831	1.481	0.214062
Hsf4	0.701	0.260822	0.5157	0.077468
Hsph1	1.2425	0.213459	2.6855	0.000429
Hsp90aa1	0.9517	0.654922	1.2593	0.732777
Hsp90ab1	1.1284	0.031751	1.0249	0.986762
Hsp90b1	0.8877	0.325235	1.0267	0.755551
Hspa14	0.827	0.376506	0.5518	0.043781
Hspa1a	19.8949	0.000918	504.2773	0.000067
Hspa1b	18.4604	0.000675	232.0417	0.000392
Hspa1l	0.7101	0.109201	1.7557	0.032631
Hspa2	1.9834	0.03778	1.2014	0.718687
Hspa4	1.2709	0.057047	0.4114	0.028217
Hspa4l	0.4652	0.063573	0.8071	0.385973
Hspa5	1.0546	0.813525	1.4061	0.086402
Hspa8	1.5838	0.00096	2.3528	0.000481
Hspa9	0.832	0.654396	0.7577	0.261593
Hspb1	2.3665	0.003963	3.8697	0.001453
Hspb2	1.1072	0.70863	0.4993	0.330753
Hspb3	1.2617	0.722348	0.4965	0.373041
Hspb6	0.7388	0.265384	0.5696	0.130521
Hspb7	0.7674	0.212276	0.6188	0.364641
Hspb8	0.546	0.168098	1.9018	0.04364
Hspd1	1.285	0.004456	1.7756	0.029237
Hspe1	1.1327	0.213775	1.4252	0.249831
Pfdn1	0.9881	0.870701	1.2651	0.259957
Pfdn2	0.7737	0.063529	0.9846	0.870173
Serpinh1	1.4643	0.182529	0.63	0.493928
Sil1	1.2234	0.342094	1.7865	0.015409
Tcp1	1.3309	0.018088	1.0342	0.721104
Tor1a	1.2889	0.019206	0.9866	0.968326
Gusb[$]	0.5093	0.006591	0.8001	0.270133
Hprt1[$]	0.955	0.343731	1.0434	0.661078
Hsp90ab1[$]	1.1395	0.020618	1.0932	0.688567
Gapdh[$]	1.1904	0.007638	1.417	0.083667
Actb[$]	1.5157	0.004774	0.7732	0.352965

Key: [*] Fold change of *Smarcal1*$^{del/del}$ relative to *wt*; [$] control genes; blue shading, genes that have significantly different expression just in the brain of *Smarcal1*$^{del/del}$ compared to *wt* ; pink shading, genes that have significantly different expression just in the liver of *Smarcal1*$^{del/del}$ compared to *wt*

Supplementary Table S16 Enrichment in biological process GO-terms (all levels) of differentially expressed genes (q<0.05) between *RpII215^{4}/FM7;Marcal1$^{del/del}$* and *yw* fly ovaries.

Term	Count	PValue	Fold Enrichment
GO:0009987~cellular process	350	7.11E-08	1.182962437
GO:0008152~metabolic process	300	2.90E-05	1.168941048
GO:0044238~primary metabolic process	250	8.69E-05	1.195140191
GO:0044237~cellular metabolic process	223	2.26E-05	1.242854726
GO:0043170~macromolecule metabolic process	191	0.027556497	1.121973063
GO:0065007~biological regulation	171	0.012492805	1.158556378
GO:0044260~cellular macromolecule metabolic process	169	1.09E-04	1.281200439
GO:0050789~regulation of biological process	160	0.005729838	1.191211236
GO:0050794~regulation of cellular process	148	0.010568064	1.184387145
GO:0016043~cellular component organization	140	4.61E-06	1.413131599
GO:0051179~localization	118	0.009257764	1.225732441
GO:0006807~nitrogen compound metabolic process	115	8.13E-04	1.320637602
GO:0034641~cellular nitrogen compound metabolic process	111	5.10E-05	1.425098921
GO:0051234~establishment of localization	102	0.00849426	1.256228433
GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	99	2.04E-04	1.41339
GO:0006810~transport	97	0.016600255	1.234697456
GO:0006996~organelle organization	81	1.39E-04	1.502611746
GO:0043412~biopolymer modification	61	4.57E-04	1.557361707
GO:0006464~protein modification process	58	5.60E-04	1.568270202
GO:0033036~macromolecule localization	53	1.71E-05	1.843721572
GO:0007049~cell cycle	52	0.002722216	1.50646645
GO:0044085~cellular component biogenesis	49	0.006815028	1.459842794
GO:0043687~post-translational protein modification	48	9.74E-04	1.616226415
GO:0051641~cellular localization	47	0.001688624	1.585546629
GO:0016070~RNA metabolic process	47	0.002271936	1.561925822
GO:0065008~regulation of biological quality	47	0.013660778	1.414425239
GO:0009056~catabolic process	46	7.73E-04	1.658400673

GO:0048519~negative regulation of biological process	46	0.02861235	1.359119757
GO:0022402~cell cycle process	45	0.008840369	1.468121572
GO:0008104~protein localization	43	3.21E-05	1.957578656
GO:0006796~phosphate metabolic process	43	0.024241749	1.392687538
GO:0006793~phosphorus metabolic process	43	0.024241749	1.392687538
GO:0007010~cytoskeleton organization	42	0.002320114	1.61188172
GO:0022607~cellular component assembly	42	0.025399639	1.393169145
GO:0022403~cell cycle phase	41	0.011826147	1.47515961
GO:0048523~negative regulation of cellular process	41	0.03795045	1.359998451
GO:0051649~establishment of localization in cell	40	0.002594879	1.626044039
GO:0048699~generation of neurons	40	0.010288425	1.49650594
GO:0000279~M phase	40	0.010691232	1.493375174
GO:0006950~response to stress	40	0.011361063	1.487152778
GO:0022008~neurogenesis	40	0.020110822	1.430527722
GO:0007017~microtubule-based process	38	0.002135805	1.670299672
GO:0000902~cell morphogenesis	36	0.022882898	1.453506787
GO:0044248~cellular catabolic process	35	0.002475963	1.70191871
GO:0000278~mitotic cell cycle	34	0.00307323	1.69485568
GO:0050793~regulation of developmental process	33	6.51E-04	1.881509585
GO:0000226~microtubule cytoskeleton organization	32	5.86E-04	1.916331096
GO:0046907~intracellular transport	32	0.001329529	1.824494143
GO:0016192~vesicle-mediated transport	32	0.030243692	1.460528559
GO:0051716~cellular response to stimulus	31	2.35E-04	2.048966049
GO:0051128~regulation of cellular component organization	31	3.88E-04	1.990002998
GO:0048518~positive regulation of biological process	31	0.01176345	1.589715038
GO:0030030~cell projection organization	31	0.021537837	1.515673516
GO:0051276~chromosome organization	29	0.002171798	1.835209811
GO:0051239~regulation of multicellular organismal process	29	0.002398442	1.822285798
GO:0045184~establishment of protein localization	29	0.002512304	1.815891813
GO:0006629~lipid metabolic process	29	0.003934782	1.760303288
GO:0006396~RNA processing	29	0.008777374	1.658747329

GO:0006259~DNA metabolic process	28	9.92E-05	2.261010558
GO:0009057~macromolecule catabolic process	28	0.003317298	1.803910951
GO:0015031~protein transport	27	0.006769389	1.733228417
GO:0048858~cell projection morphogenesis	27	0.035267791	1.505742188
GO:0032990~cell part morphogenesis	27	0.049511237	1.455702417
GO:0048667~cell morphogenesis involved in neuron differentiation	26	0.018881001	1.611082176
GO:0009966~regulation of signal transduction	26	0.023674724	1.578202948
GO:0000904~cell morphogenesis involved in differentiation	26	0.033093738	1.531325633
GO:0048522~positive regulation of cellular process	26	0.042167891	1.49193462
GO:0010646~regulation of cell communication	26	0.042167891	1.49193462
GO:0043933~macromolecular complex subunit organization	25	0.025116097	1.587707592
GO:0048812~neuron projection morphogenesis	25	0.030173439	1.559950466
GO:0031175~neuron projection development	25	0.030993553	1.554515099
GO:0045595~regulation of cell differentiation	24	2.49E-04	2.315135135
GO:0007051~spindle organization	24	0.003623308	1.903555556
GO:0010324~membrane invagination	23	0.031610381	1.590907623
GO:0006897~endocytosis	23	0.031610381	1.590907623
GO:0016071~mRNA metabolic process	22	0.010804123	1.792732116
GO:0044265~cellular macromolecule catabolic process	22	0.014372148	1.744925926
GO:0009605~response to external stimulus	21	0.00621043	1.921858974
GO:0030163~protein catabolic process	21	0.00817114	1.8738125
GO:0033554~cellular response to stress	20	0.004358407	2.027935606
GO:0006397~mRNA processing	20	0.012084936	1.839776632
GO:0006909~phagocytosis	20	0.014066487	1.811759729
GO:0051726~regulation of cell cycle	19	0.005198615	2.042595382
GO:0044255~cellular lipid metabolic process	19	0.013769279	1.852846084
GO:0006911~phagocytosis, engulfment	19	0.016878101	1.813213012
GO:0007052~mitotic spindle organization	19	0.023601968	1.747787801
GO:0007409~axonogenesis	19	0.028265593	1.712478956
GO:0034621~cellular macromolecular complex subunit organization	19	0.035028892	1.670299672
GO:0007059~chromosome segregation	18	2.53E-04	2.745512821

GO:0042592~homeostatic process	18	0.009510974	1.970705521
GO:0044257~cellular protein catabolic process	18	0.027037229	1.755327869
GO:0051603~proteolysis involved in cellular protein catabolic process	18	0.027037229	1.755327869
GO:0032879~regulation of localization	17	1.08E-04	3.064436027
GO:0016311~dephosphorylation	17	3.40E-04	2.783295107
GO:0019941~modification-dependent protein catabolic process	17	0.026868496	1.795142998
GO:0043632~modification-dependent macromolecule catabolic process	17	0.028195026	1.784583333
GO:0060284~regulation of cell development	16	0.006283738	2.179643766
GO:0022603~regulation of anatomical structure morphogenesis	16	0.033909195	1.784583333
GO:0007067~mitosis	15	0.033572894	1.833476027
GO:0000087~M phase of mitotic cell cycle	15	0.037073808	1.808699324
GO:0000280~nuclear division	15	0.037073808	1.808699324
GO:0048285~organelle fission	15	0.046957866	1.749591503
GO:0006470~protein amino acid dephosphorylation	14	5.70E-04	3.046849593
GO:0019725~cellular homeostasis	14	0.008806922	2.250825826
GO:0006974~response to DNA damage stimulus	14	0.011710995	2.172536232
GO:0009968~negative regulation of signal transduction	13	0.011212454	2.274468954
GO:0006281~DNA repair	13	0.011212454	2.274468954
GO:0010648~negative regulation of cell communication	13	0.012070809	2.252386731
GO:0033043~regulation of organelle organization	13	0.018324001	2.128402141
GO:0022604~regulation of cell morphogenesis	13	0.03372718	1.949544818
GO:0006403~RNA localization	13	0.04651578	1.855966667
GO:0000398~nuclear mRNA splicing, via spliceosome	13	0.048932949	1.841236772
GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	13	0.048932949	1.841236772
GO:0006260~DNA replication	12	0.01781505	2.230729167
GO:0007346~regulation of mitotic cell cycle	12	0.020496925	2.185204082
GO:0007264~small GTPase mediated signal transduction	12	0.040774274	1.964678899
GO:0045454~cell redox homeostasis	11	6.03E-04	3.703852201
GO:0060341~regulation of cellular localization	11	0.004245002	2.88682598
GO:0044087~regulation of cellular component biogenesis	11	0.013258339	2.453802083
GO:0019637~organophosphate metabolic process	11	0.043964131	2.023754296

GO:0051049~regulation of transport	10	0.002427666	3.367138365
GO:0006261~DNA-dependent DNA replication	10	0.004043948	3.130847953
GO:0046486~glycerolipid metabolic process	10	0.005731113	2.974305556
GO:0006644~phospholipid metabolic process	10	0.044237619	2.124503968
GO:0045132~meiotic chromosome segregation	9	0.01329798	2.817763158
GO:0050657~nucleic acid transport	9	0.02332665	2.549404762
GO:0050658~RNA transport	9	0.02332665	2.549404762
GO:0051236~establishment of RNA localization	9	0.025406222	2.509570312
GO:0050767~regulation of neurogenesis	9	0.032413809	2.397201493
GO:0002164~larval development	9	0.035016101	2.361948529
GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	9	0.035016101	2.361948529
GO:0051169~nuclear transport	9	0.046827578	2.230729167
GO:0006913~nucleocytoplasmic transport	9	0.046827578	2.230729167
GO:0031023~microtubule organizing center organization	8	0.014725806	3.037588652
GO:0002168~instar larval development	8	0.01643681	2.974305556
GO:0045995~regulation of embryonic development	8	0.029728228	2.64382716
GO:0006650~glycerophospholipid metabolic process	8	0.029728228	2.64382716
GO:0032880~regulation of protein localization	7	0.017794576	3.287390351
GO:0048193~Golgi vesicle transport	7	0.031122715	2.905135659
GO:0051297~centrosome organization	7	0.031122715	2.905135659
GO:0010627~regulation of protein kinase cascade	7	0.034401593	2.839109848
GO:0007127~meiosis I	7	0.037895519	2.776018519
GO:0000070~mitotic sister chromatid segregation	7	0.041607995	2.71567029
GO:0000819~sister chromatid segregation	7	0.045541974	2.657890071
GO:0048585~negative regulation of response to stimulus	6	0.006380093	4.867045455
GO:0051050~positive regulation of transport	6	0.013259737	4.118269231
GO:0022411~cellular component disassembly	6	0.018078793	3.824107143
GO:0010769~regulation of cell morphogenesis involved in differentiation	6	0.023929637	3.569166667
GO:0010975~regulation of neuron projection development	6	0.023929637	3.569166667
GO:0030261~chromosome condensation	6	0.023929637	3.569166667
GO:0046822~regulation of nucleocytoplasmic transport	6	0.034779589	3.24469697

GO:0032386~regulation of intracellular transport	6	0.038972833	3.149264706
GO:0006270~DNA replication initiation	5	0.008043526	5.948611111
GO:0010741~negative regulation of protein kinase cascade	5	0.015787154	4.957175926
GO:0050770~regulation of axonogenesis	5	0.015787154	4.957175926
GO:0007426~tracheal outgrowth, open tracheal system	5	0.027058084	4.249007937
GO:0043269~regulation of ion transport	4	0.003060597	11.89722222
GO:0032508~DNA duplex unwinding	4	0.00787683	8.922916667
GO:0032392~DNA geometric change	4	0.00787683	8.922916667
GO:0035099~hemocyte migration	4	0.039881238	5.098809524
GO:0043624~cellular protein complex disassembly	4	0.039881238	5.098809524
GO:0043241~protein complex disassembly	4	0.039881238	5.098809524
GO:0033044~regulation of chromosome organization	4	0.047840666	4.758888889
GO:0034765~regulation of ion transmembrane transport	3	0.017362884	13.384375
GO:0034762~regulation of transmembrane transport	3	0.017362884	13.384375
GO:0032412~regulation of ion transmembrane transporter activity	3	0.017362884	13.384375
GO:0051924~regulation of calcium ion transport	3	0.017362884	13.384375
GO:0032409~regulation of transporter activity	3	0.017362884	13.384375
GO:0022898~regulation of transmembrane transporter activity	3	0.017362884	13.384375
GO:0010959~regulation of metal ion transport	3	0.027873818	10.7075
GO:0032837~distributive segregation	3	0.027873818	10.7075
GO:0006268~DNA unwinding during replication	3	0.040280429	8.922916667
GO:0006415~translational termination	3	0.040280429	8.922916667

Supplementary Table S17 Enrichment in biological process GO-terms (all levels) of differentially expressed genes (q<0.05) between *RpII215*^{4}*/FM7* and *yw* fly ovaries.

Term	Count	PValue	Fold Enrichment
GO:0009987~cellular process	181	1.57E-04	1.179297493
GO:0008152~metabolic process	161	2.29E-04	1.209314112
GO:0044238~primary metabolic process	125	0.022834886	1.151942353
GO:0044237~cellular metabolic process	124	4.59E-05	1.332229605
GO:0044260~cellular macromolecule metabolic process	89	0.003132667	1.300655468
GO:0050789~regulation of biological process	84	0.031554616	1.205563179
GO:0016043~cellular component organization	66	0.019002973	1.284222864
GO:0006807~nitrogen compound metabolic process	57	0.042133297	1.261834985
GO:0034641~cellular nitrogen compound metabolic process	55	0.012305381	1.361214643
GO:0010467~gene expression	51	0.019970999	1.346494189
GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic proces	50	0.014752062	1.376064257
GO:0043412~biopolymer modification	31	0.018527719	1.525679255
GO:0048519~negative regulation of biological process	28	0.015566646	1.594776457
GO:0007389~pattern specification process	27	0.001468989	1.935090361
GO:0033036~macromolecule localization	27	0.003662632	1.810610865
GO:0044085~cellular component biogenesis	27	0.024350343	1.550656717
GO:0003002~regionalization	26	0.00144818	1.970136051
GO:0016070~RNA metabolic process	26	0.012464648	1.665627127
GO:0006796~phosphate metabolic process	26	0.016586938	1.623306292
GO:0006793~phosphorus metabolic process	26	0.016586938	1.623306292
GO:0048523~negative regulation of cellular process	24	0.038173228	1.534644153
GO:0008104~protein localization	22	0.00482586	1.930702401
GO:0007444~imaginal disc development	21	0.01614927	1.753479939
GO:0016310~phosphorylation	21	0.021749883	1.699844082
GO:0006396~RNA processing	20	0.001736517	2.205231181
GO:0035220~wing disc development	18	0.003229869	2.203661622
GO:0048736~appendage development	15	0.012058473	2.097658928

GO:0007560~imaginal disc morphogenesis	15	0.036210253	1.816986255
GO:0048563~post-embryonic organ morphogenesis	15	0.036210253	1.816986255
GO:0048569~post-embryonic organ development	15	0.049294478	1.73745487
GO:0002009~morphogenesis of an epithelium	14	0.01361855	2.1405444
GO:0060429~epithelium development	14	0.018897383	2.049457404
GO:0035107~appendage morphogenesis	14	0.023418194	1.990175578
GO:0048737~imaginal disc-derived appendage development	14	0.024129689	1.981985555
GO:0048729~tissue morphogenesis	14	0.027116667	1.949888623
GO:0045595~regulation of cell differentiation	13	0.007439984	2.417410181
GO:0007476~imaginal disc-derived wing morphogenesis	13	0.024419573	2.051471943
GO:0007472~wing disc morphogenesis	13	0.026027967	2.032822198
GO:0035120~post-embryonic appendage morphogenesis	13	0.033956683	1.952929622
GO:0035114~imaginal disc-derived appendage morphogenesis	13	0.044715196	1.871217086
GO:0034621~cellular macromolecular complex subunit organization	12	0.033607907	2.033592498
GO:0007167~enzyme linked receptor protein signaling pathway	11	0.009320195	2.609777039
GO:0009891~positive regulation of biosynthetic process	10	0.033453144	2.248471008
GO:0031328~positive regulation of cellular biosynthetic process	10	0.033453144	2.248471008
GO:0031325~positive regulation of cellular metabolic process	10	0.047008098	2.110528002
GO:0022613~ribonucleoprotein complex biogenesis	9	0.00574828	3.293770828
GO:0016331~morphogenesis of embryonic epithelium	9	0.022953709	2.580120482
GO:0006403~RNA localization	9	0.028449931	2.476915663
GO:0006730~one-carbon metabolic process	8	0.006261493	3.621221729
GO:0009968~negative regulation of signal transduction	8	0.028229202	2.69816521
GO:0010648~negative regulation of cell communication	8	0.029569966	2.671969431
GO:0032259~methylation	7	0.004072624	4.543608396
GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	7	0.013572868	3.541341838
GO:0043414~biopolymer methylation	6	0.007662472	4.800224152
GO:0017145~stem cell division	6	0.015523668	4.047247815
GO:0008356~asymmetric cell division	6	0.02575562	3.558786872
GO:0050657~nucleic acid transport	6	0.035215408	3.276343469
GO:0050658~RNA transport	6	0.035215408	3.276343469

GO:0051236~establishment of RNA localization	6	0.037333192	3.225150602
GO:0042254~ribosome biogenesis	6	0.037333192	3.225150602
GO:0035222~wing disc pattern formation	6	0.04657453	3.035435861
GO:0007173~epidermal growth factor receptor signaling pathway	5	0.019532476	4.778000892
GO:0006364~rRNA processing	5	0.027717191	4.300200803
GO:0016072~rRNA metabolic process	5	0.030037905	4.195317857
GO:0006446~regulation of translational initiation	4	0.014180198	7.644801428
GO:0007179~transforming growth factor beta receptor signaling pathway	4	0.027686318	5.982888074
GO:0033227~dsRNA transport	4	0.034474406	5.504257028
GO:0008213~protein amino acid alkylation	4	0.046111135	4.914515204
GO:0006479~protein amino acid methylation	4	0.046111135	4.914515204
GO:0022411~cellular component disassembly	4	0.046111135	4.914515204
GO:0048096~chromatin-mediated maintenance of transcription	3	0.032228518	10.32048193
GO:0045815~positive regulation of gene expression, epigenetic	3	0.038650506	9.382256298

Supplementary Table S18 Antibodies used for flowcytometry.

Antigen	**Species specificity**	**Clone**	**Conjugation**
TCRβ	Mouse	H57-597	APC
CD4	Mouse	GK1.5	APCCy7
CD8	Mouse	53-6.7	Pacific Blue
CD44	Mouse	IM7	PerCPCy5.5
CD25	Mouse	PC61	PE
B220	Mouse	RA3-6B2	Alexa 700

Supplementary Table S19 Oligonucleotide primers.

Primer	Sequence
Marcal1 cloning	
Coding-F	ATGTCCACTTGCAGTTCATCCGAGATAGC
HA-coding-F	ATGTACCCATACGACGTCCCAGACTACGCTATGTCCACTTGCAGTTCATCCGAGATAGC
Coding-R	CTAAATATCTAATTCCAAAAAAGCCTCATC
Marcal1 mutagenesis	
K275R	
5′ primer	GAAATGGGCCTGGGCAGAACCTATCAGGCCTTG
3′ primer	CAAGGCCTGATAGGTTCTGCCCAGGCCCATTTC
Marcal1 deletion identification	
5′-primer	TCAATTGATGTCGCAGCATGTCCACTT
3′-primer-1	CCAGATACGGGTTTGGCCATCGTAGCACTT
3′-primer-2	GGTGATTAGCACCTTGGCCTCACCCACATA
3′-primer-3	AGGACGACAGTCTCACTGCGGATGGAAGAA
3′-primer-4	TTCCTGAATTGCAGGCTTTTAGGGAGAGCA
3′-primer-5	GCCGCGATATCCGACTCAGCCTTGTTTACT
3′-primer-6	GCCAGGTCACATGAAACCGGCTATCTGAAA
Drosophila heat shock RT-PCR primers	
Hsp83	
5′ primer	GGGTTTCTACTCCGCCTACC
3′ primer	CAGTCGTTGGTCAGGGATTT
Hsp68	
5′ primer	GACAACGGCAAACCAAAGAT
3′ primer	GCGTCAATCTCCAAAGAAGC
Hsp67Ba	
5′ primer	ATCGCCATCATCCGTACAAT
3′ primer	CTGCGCATCCTTATCCTTCT
Hsp67Bb	
5′ primer	GAAGGAAGAGCTCCAGCAGA
3′ primer	ATTCATTCCAGGAGCCTTTG
Hsp67Bc	
5′ primer	CCACGATATGTTCCCGAATC
3′ primer	GAACTCCATCCTCCGACAAA
Hsp60	
5′ primer	GAGGTTATCGAGGGCATGAA
3′ primer	TACTCGGAGGTGGTGTCCTC
Hsp60B	
5′ primer	CAAAGTGGGTCCAAGAGGAA
3′ primer	CGCATTTCCAAAAGTCCTGT
Hsp27	
5′ primer	GAGGATGACTTCGGTTTTGG
3′ primer	ACTTGGCCTGTTCCTTGCT
Hsp26	
5′ primer	GATGGTGCCCTTCTATGAGC
3′ primer	CCTTGGGATTCTCCTTCACA
Hsp23	
5′ primer	GTGTCGAAAATCGGAAAGGA
3′ primer	CCTTGGGATTCTCCTTCACA

Hsp22	
5′ primer	TGCGTTCCTTACCGATGTTT
3′ primer	ACCTTGTCCGCCTCGTATC
Hsf	
5′ primer	CCGCTGGCGGTAATATTCTA
3′ primer	CCCAAATTTTGTTGCTGGT
DnaJ-1 (Droj1)	
5′ primer	CCACATTTGCCCAGTTCTTT
3′ primer	TTGTCGCGAATGATGAAGAC
Gapdh2	
5′ primer	ATCGTCGAGGGTCTGATGAC
3′ primer	TCAGCTTCACGAACTTGTCG
Drosophila RT-PCR primers for microarray verifiacation	
sgg	
5′ primer	AGCTGAACGACCTGTGGCCC
3′ primer	TCGCGACCTGTCGTCTCCCA
Cdk9	
5′ primer	GGCCAAGGCACCTTCGGAGAG
3′ primer	GTGGCCTTGGTGCGGCAGAT
shi	
5′ primer	TGAAACGATTTGGAAGCGGAGTGTGG
3′ primer	AGCGCACTGCGATTTGGGCTT
shn	
5′ primer	ACCTCCGGCAACGAAAGCGG
3′ primer	TAACGGGCCTGCTGTTGGCG
Dad	
5′ primer	CAGCACGTCCAGAGCCACCG
3′ primer	GGCGGGACAAGTGGGCAGTC
Rab27	
5′ primer	CGCGACGCCATGGGTTTCCT
3′ primer	CCGCGTTCTCGATCCGCTCC
srp	
5′ primer	CGTCGGGAACGGCAGCAACT
3′ primer	TGGTCAGTGGCCGTGGGACA
Drosophila N-Dam-Marcal1 RT-PCR primers	
5′ primer	GGCACACGTAAAAAGGTGGA
3′ primer	GGACCGCTCCTGTTGATCT
Smarcal1 cloning	
Coding-F	ATGTCCTTGCCACTTACAGAGGAGCAG
Coding-R	TTAAAGAAAATACTTTATTTCAATGAGC
Smarcal1 KO construct primers	
5′ HR-F	CGGGGTACCCAGAACGGAACAACCGCTAAGGAAG
5′ HR-R	ACGCGTCGACGGGACCTTCGAGGATATTCGTCTCC
3′ HR-F	ACGCGTCGACTGCATCGCTGTCCTCTCATTCTCTC
3′ HR-R	ATAAGAATGCGGCCGCGGCACAGTGACATGCCCTGTAATTC
Left Int 1-F	ACGCGTCGACGGGCTGGGCCAAACCCTAACTAGAA
Left Int1-R	GGAATTC*GCTCTTC*CTCACTACATTTCTGTTGAATCTGCAGGTGACCAA
Right Int 1-F	CGCGGATCCGATGGAAGGCAAGGGGAAAATTTAGTGTGCAG

Right Int 1-R	ATAAGAATGCGGCCGCAAAACGTACGTCCACCATGTTTGATT
Left Int 1-F	ACGCGTCGACTTCACCTGCAGCGGAAAGTTAGCAG
Left Int 1-R	CCGGAATTCCAGGGCAGACTCGGAAGATGGGGTACA
Right Int 3-L	CGCGGATCC*TTAATTAA*TGTCGGTGTTTCTGTCCTCTTGTCCTG
Right Int 3-R	ATAAGAATGCGGCCGCCATCAGGAAGGCTGAGAGCCACTG
Smarcal1 genotyping primers	
Primer A	GGTGATGTGTGTTGGTTGAGTTGAA
Primer B	TCAGACAGAAATAGACTGGCCAATGA
Primer C	GGCACAGTGACCCTTGTCCCCAGTTCTCC
Primer D	GCTACAGGGGAAACCAAGCCTGCACACG
Mouse RNA polymerase II large subunit RT-PCR primers	
Polr2a	
5′ primer	GGAGGGTGATGAGGATCTGA
3′ primer	GCCCAACACAAAACACTCCT
Polr2b	
5′ primer	GTATTGAACCGCCTGACGTT
3′ primer	TCCAAAATTGGAGAGGGTTG
Human SMARCAL1 RT-PCR primers	
5′ primer	CGCCTGACAGCTGGCCTGATC
3′ primer	TTGGCAACCTTTAGGACCGGCATAG
Human GAPDH RT-PCR primers	
5′ primer	CTTTTGCGTCGCCAGCCGAG
3′ primer	GGTGACCAGGCGCCCAATACG
Human RNA polymerase II large subunit RT-PCR primers	
POLR2A	
5′ primer	CGCTTAAGCCTTCCAACAAG
3′ primer	GAGGACGACCTTGCTGTCTC
POLR2B	
5′ primer	AAGAACCGCCACGATATTTG
3′ primer	TTGACCGCAACATAATTGGA

- Underlined and italicized bases represent restriction enzyme sites that were introduced into the DNA.