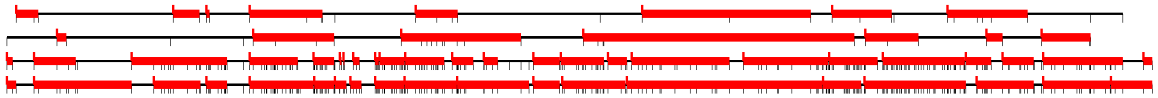
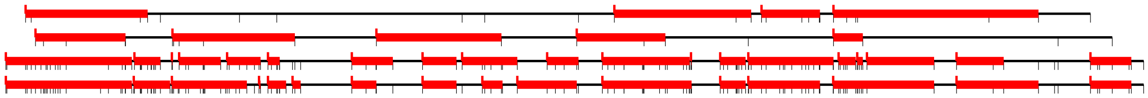
Haplotype blocks identified in simulated data

Figure 4. Schematic of the haplotype blocks found in simulations, using the Gabriel et al. (2002) block definition, with a slight modification (described in Wall and Pritchard 2003, AJHG, submitted). The parameters in the top line for each simulation were chosen to mimic Region 16b from the sub-Saharan African population in Gabriel et al. (2002). The parameters in the lower lines have (relative to the first line): eight-fold greater sample size; eight-fold greater marker density; and both eight-folder greater sample size and marker density, respectively. Red denotes haplotype blocks, while the lower tick-marks show the location of the markers typed in each population. The red upper tick-mark shows the left-most endpoint of each haplotype block. Below, we show the relative recombination rates (across the sequence) assumed in the simulations. Roughly 50% of all recombination events happen in the three hotspots. This is an expanded version of Figure 4 in Wall and Pritchard (2003, Nature Reviews Genetics, submitted).

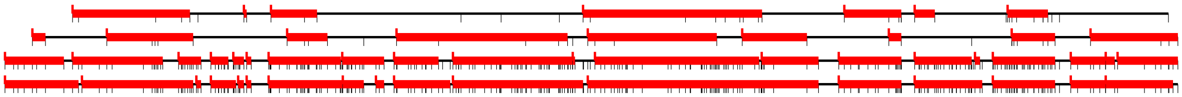
Simulation 1



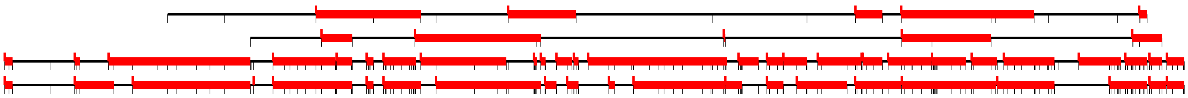
Simulation 2



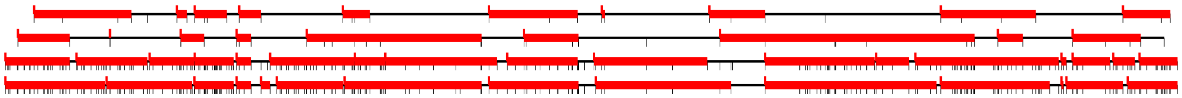
Simulation 3



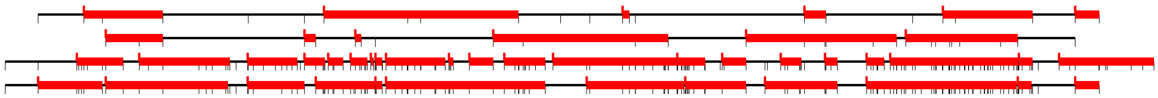
Simulation 4



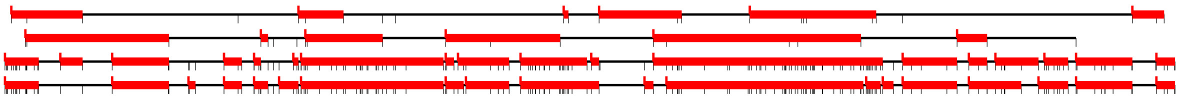
Simulation 5



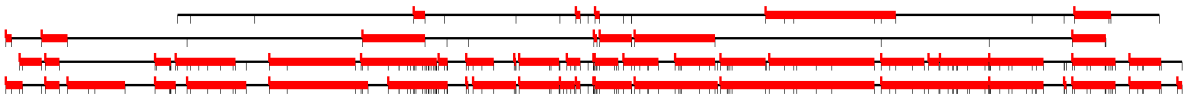
Simulation 6



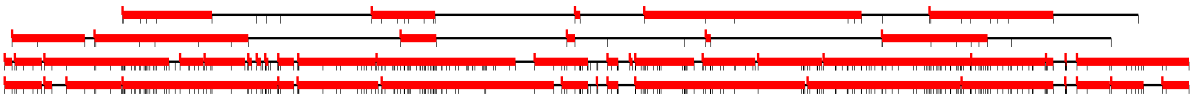
Simulation 7



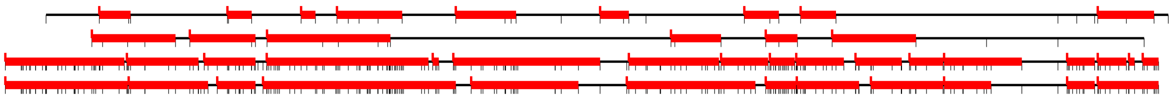
Simulation 8



Simulation 9



Simulation 10



Assumed Recombination Rate