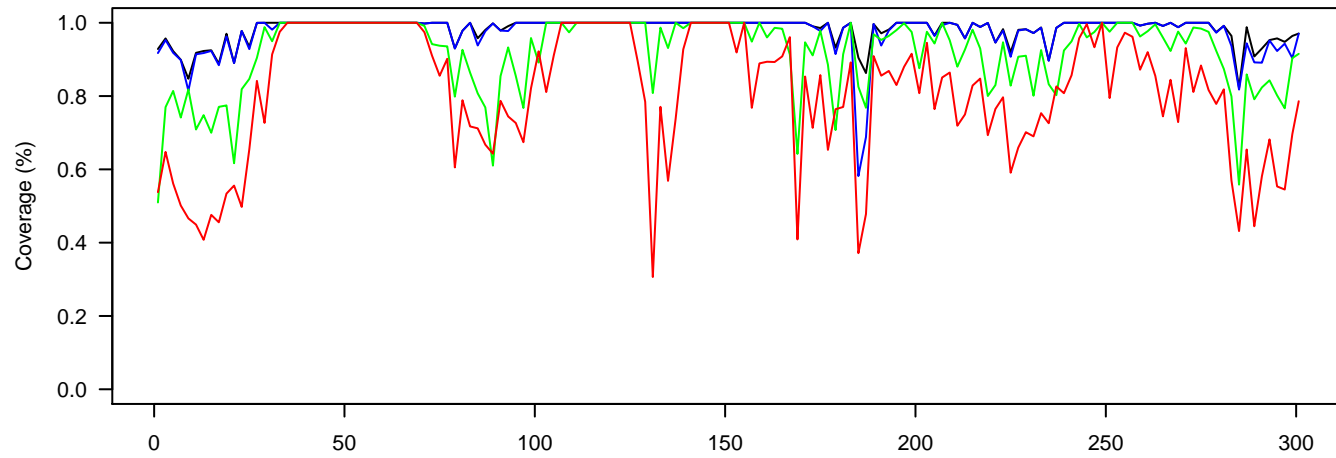
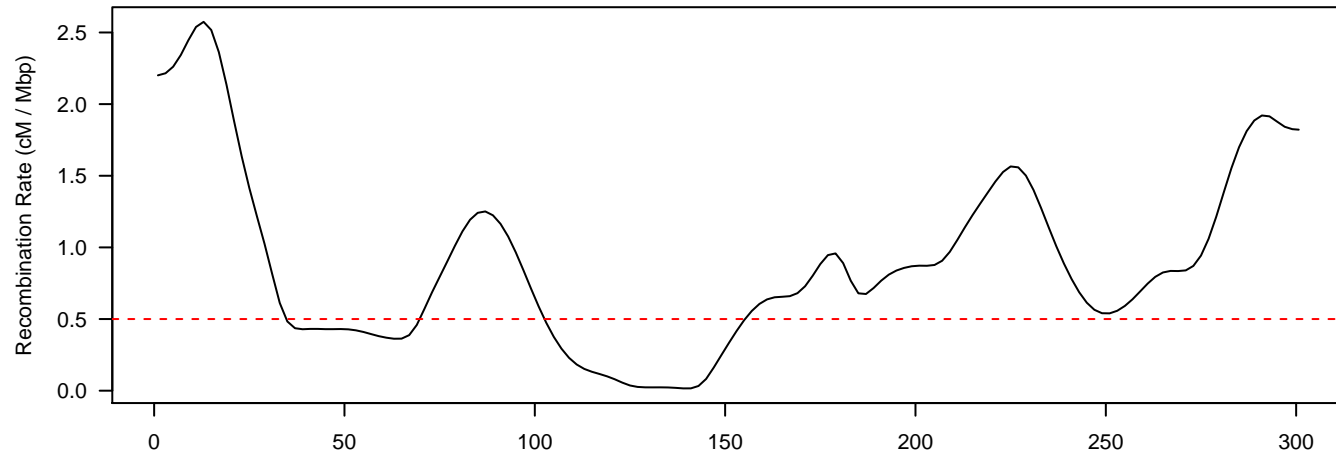
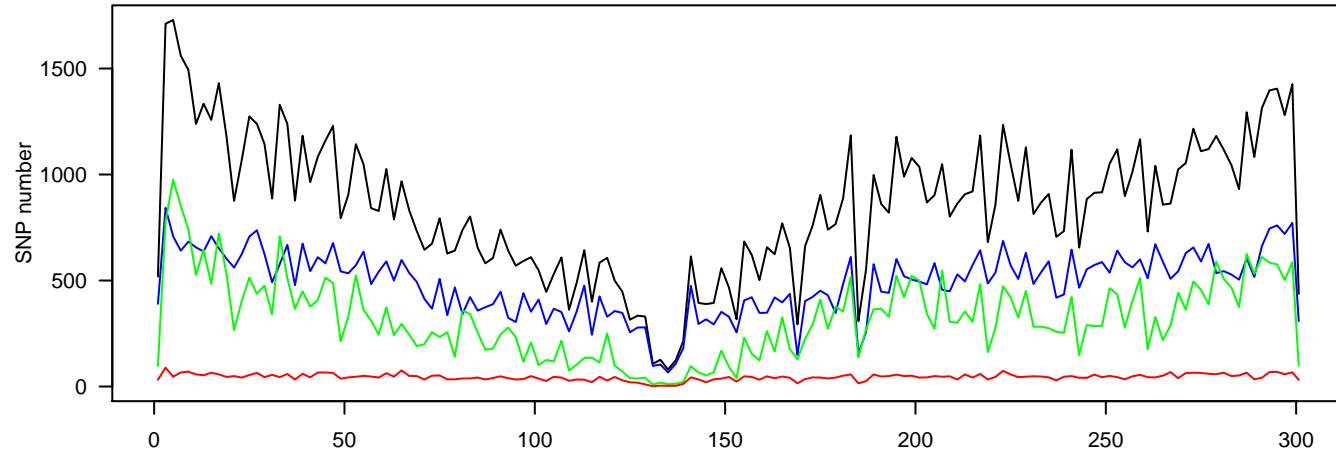
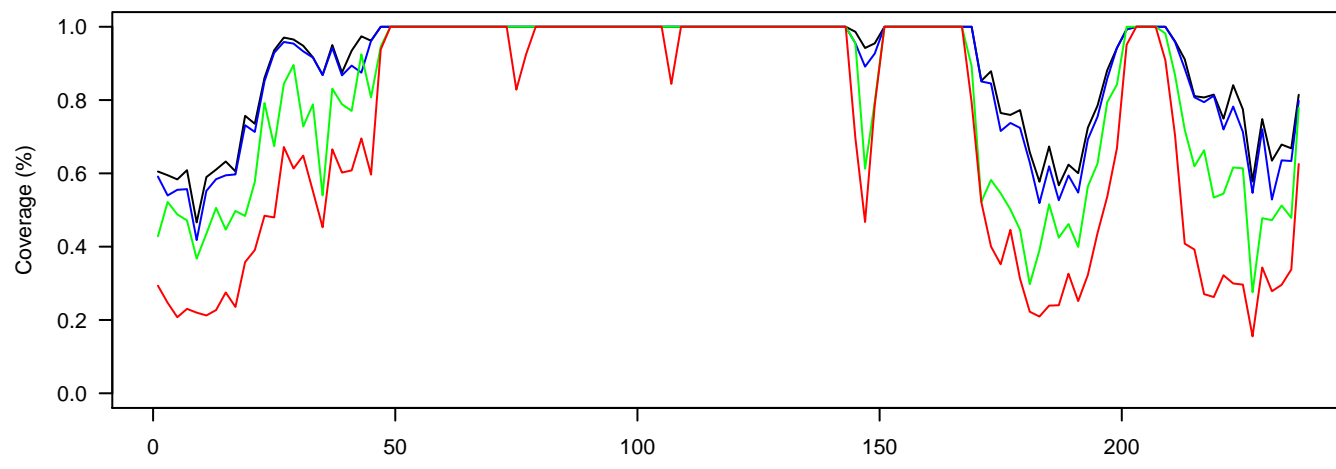
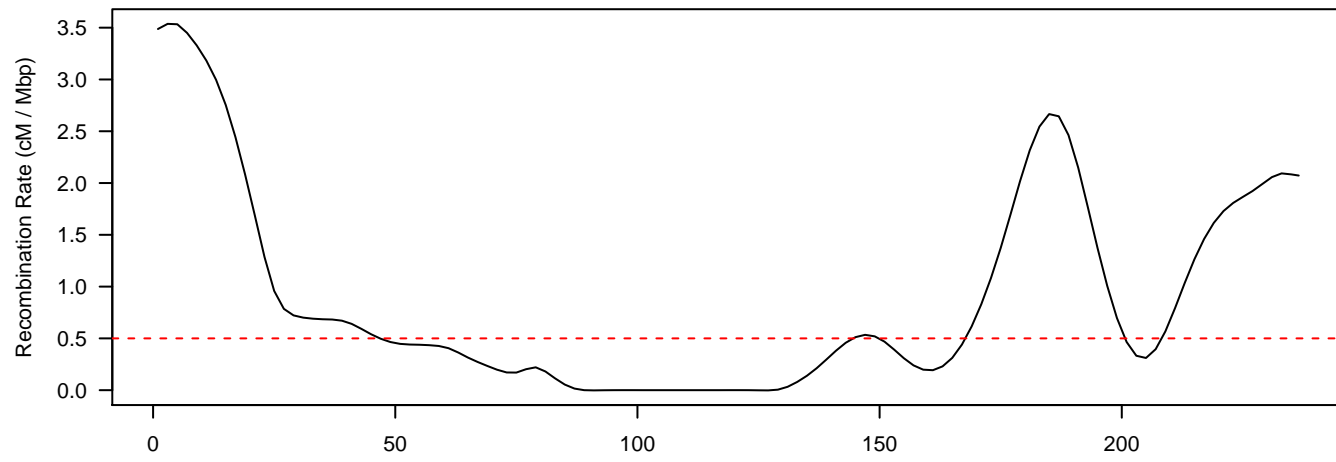
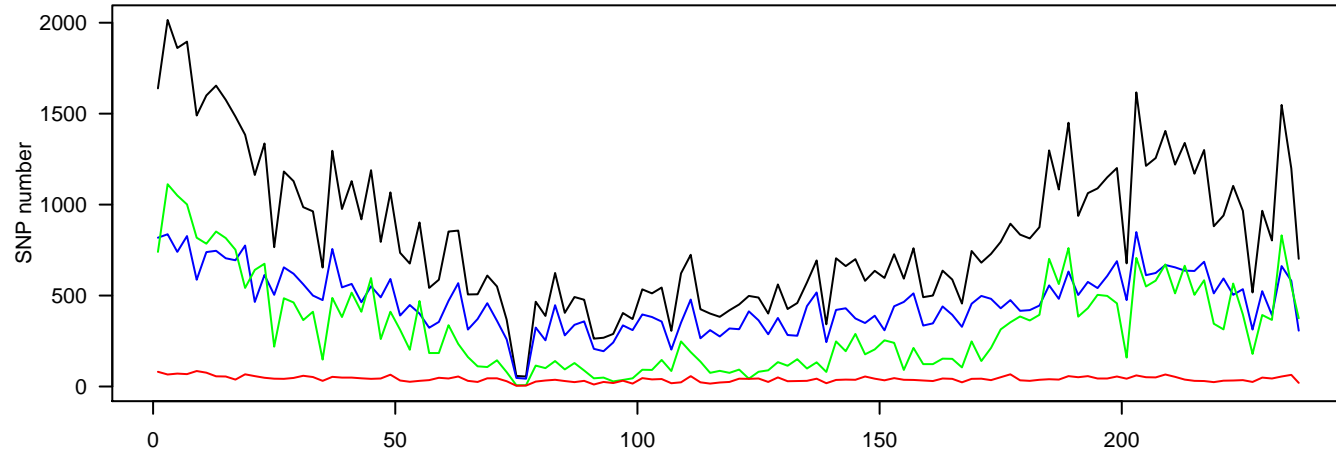


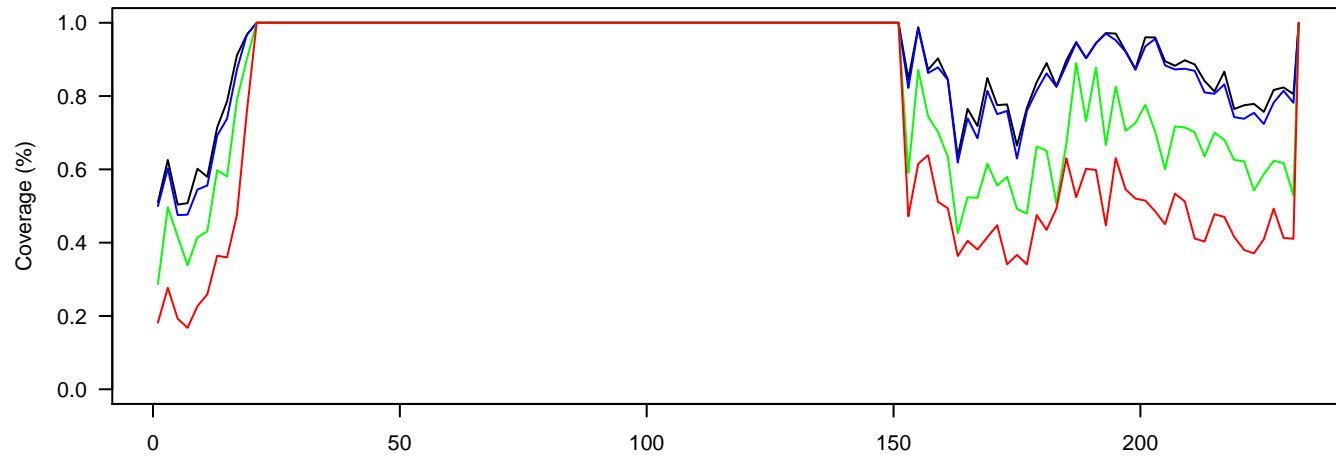
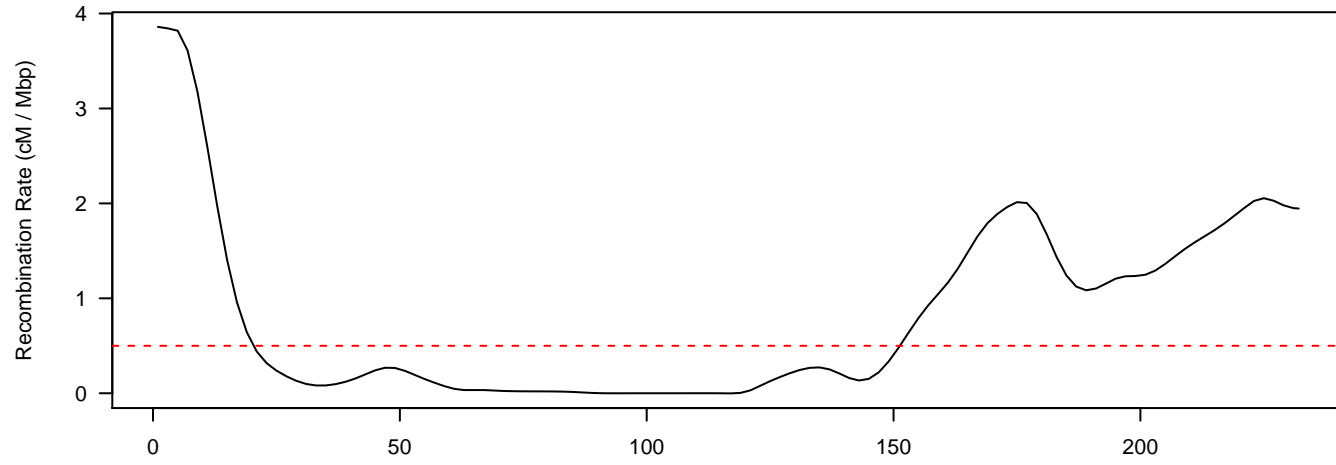
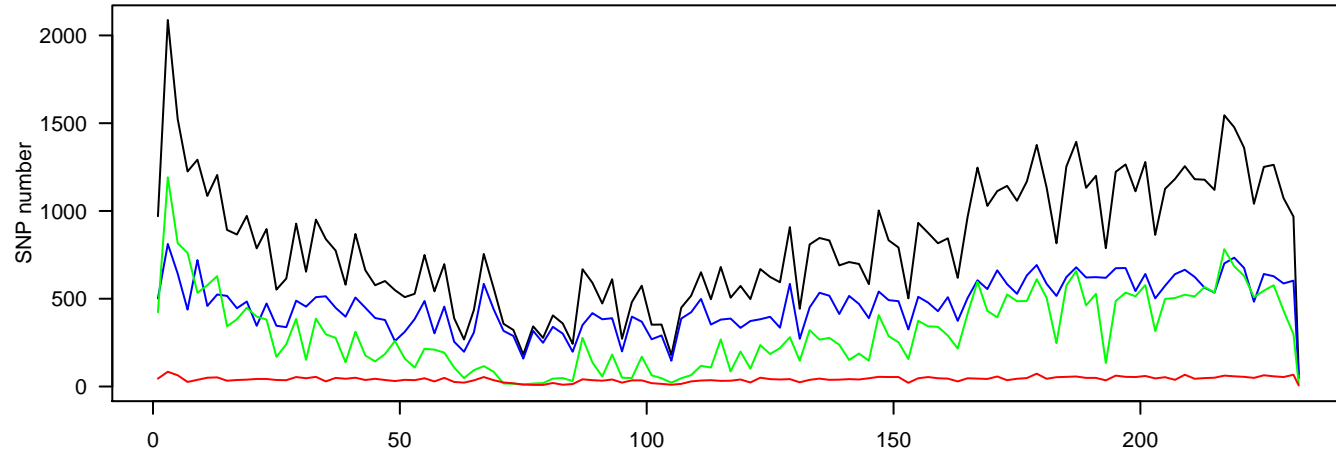
# Chromosome 1



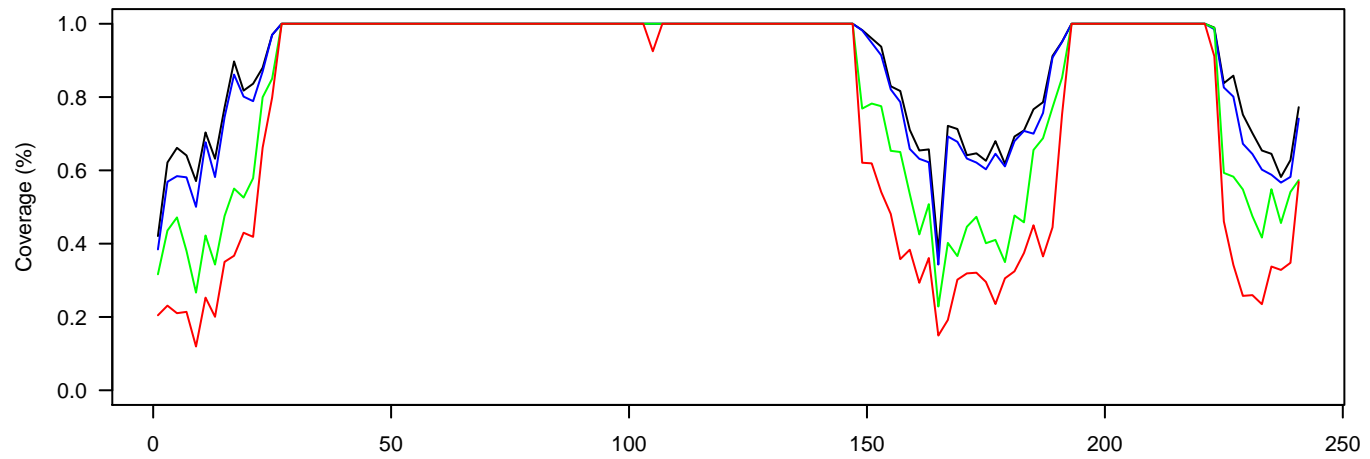
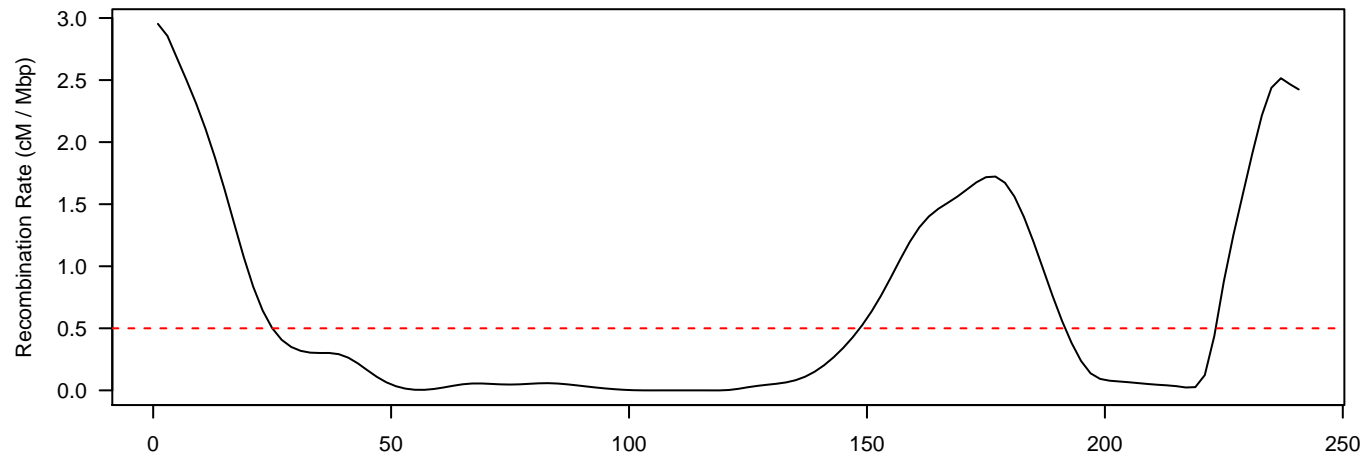
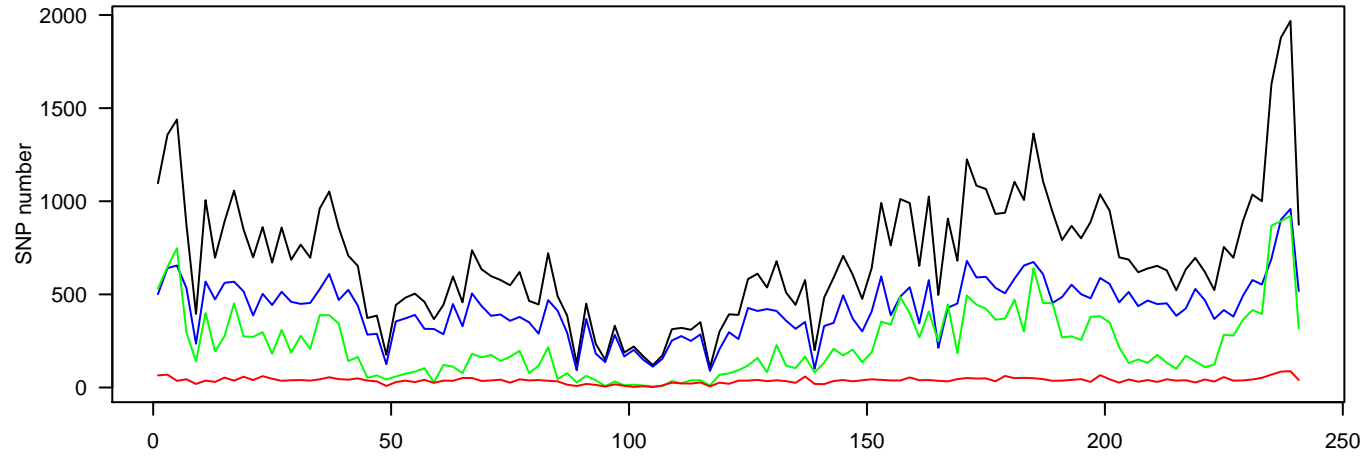
# Chromosome 2



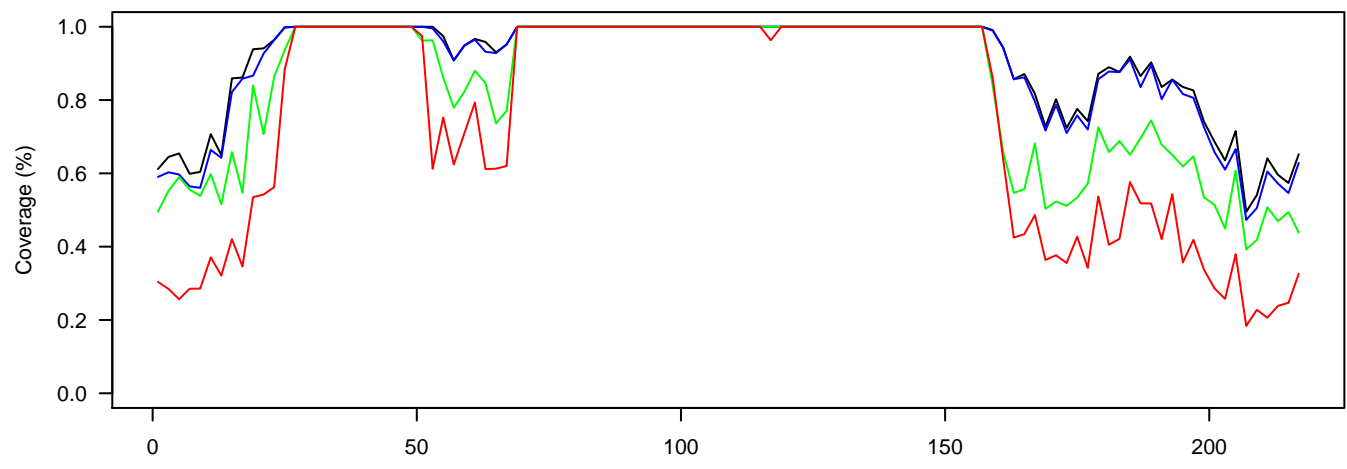
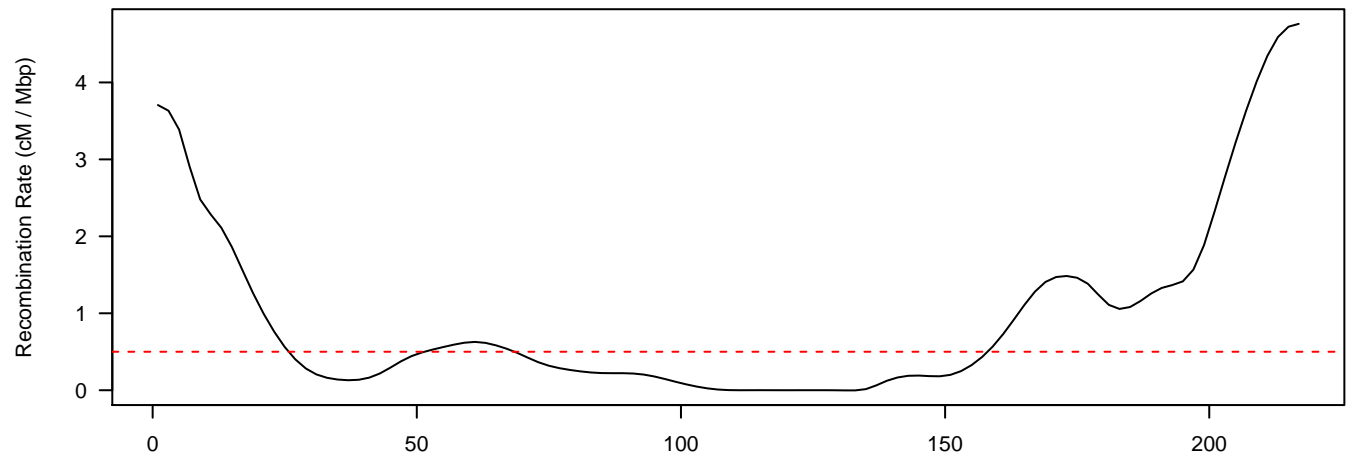
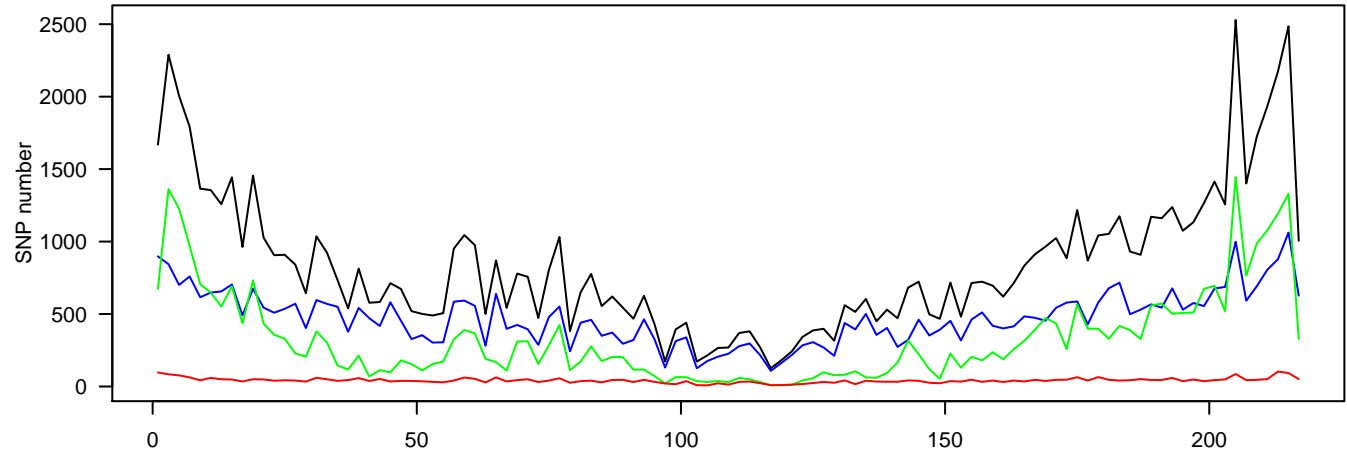
### Chromosome 3



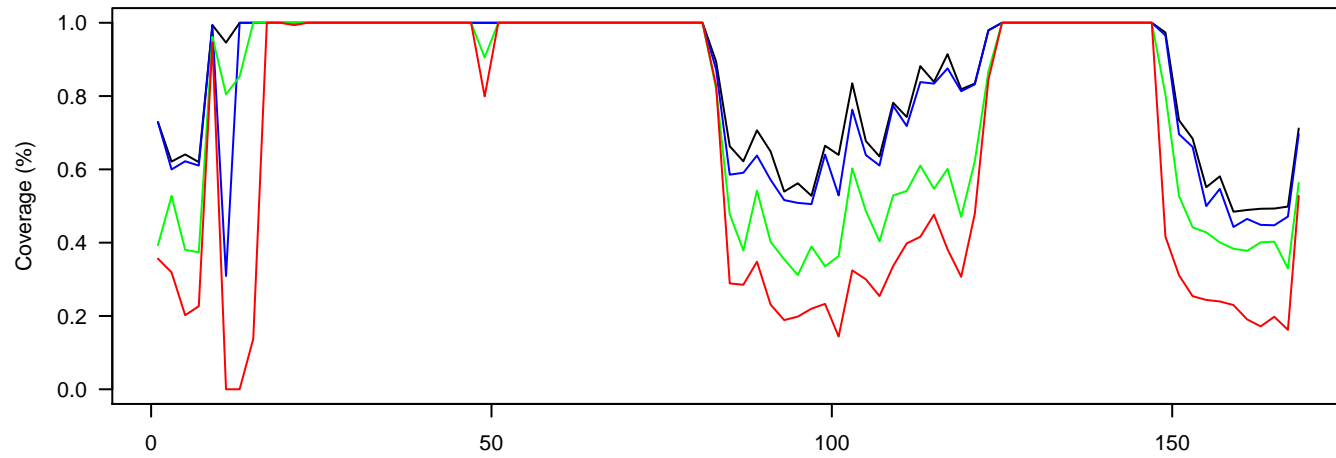
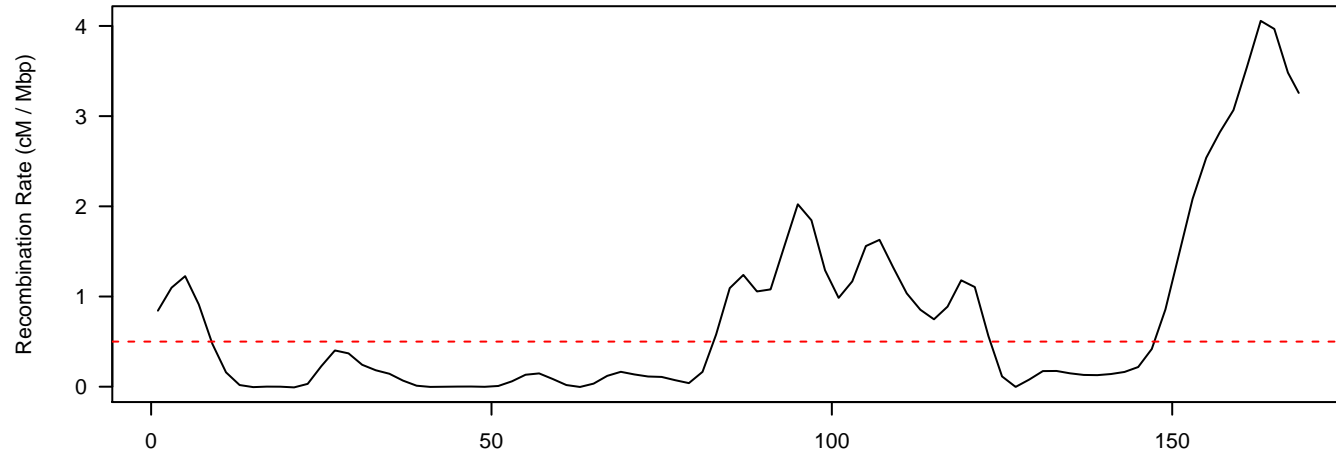
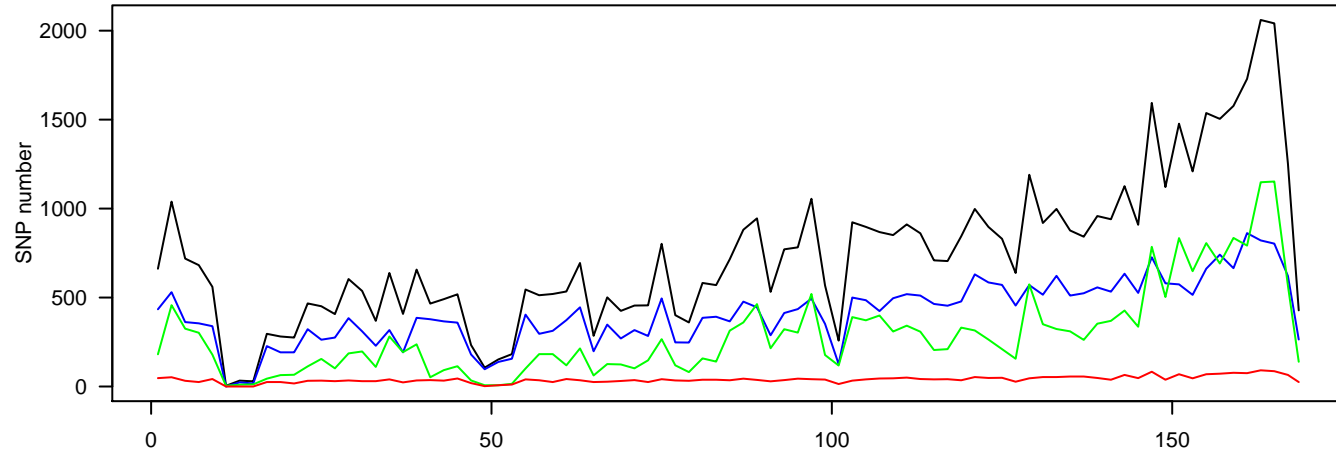
### Chromosome 4



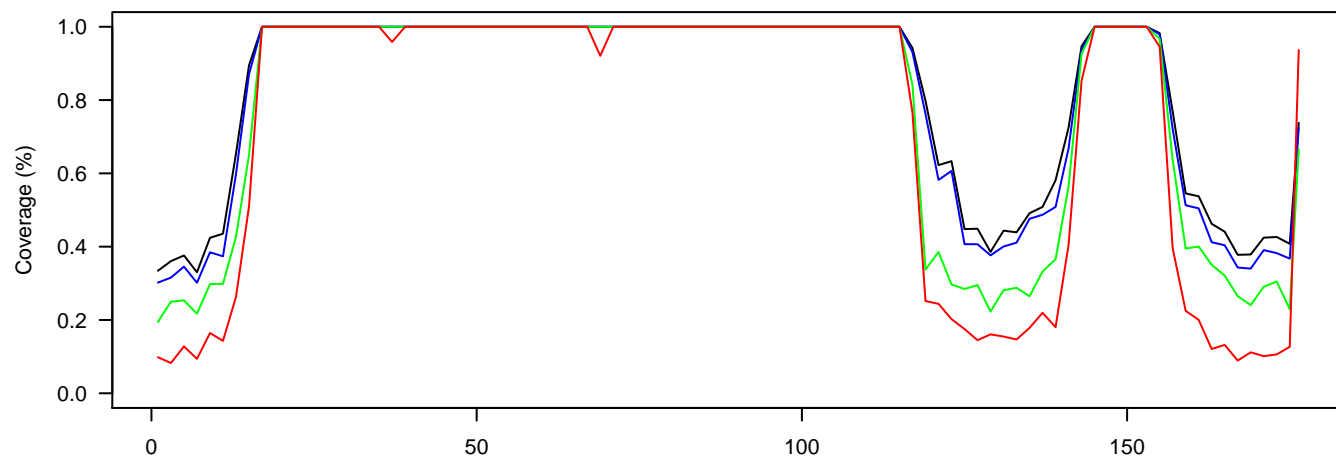
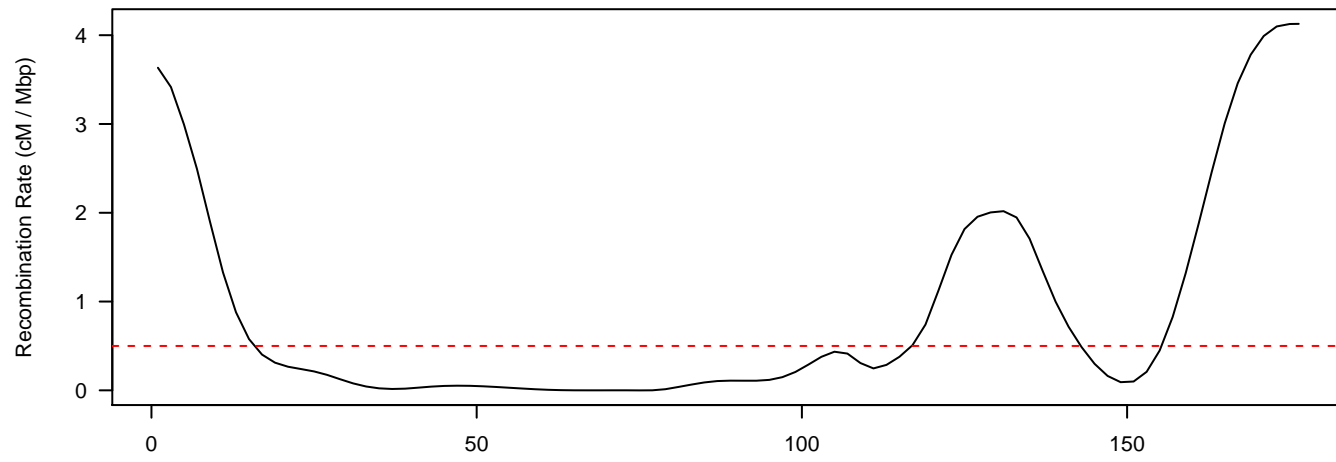
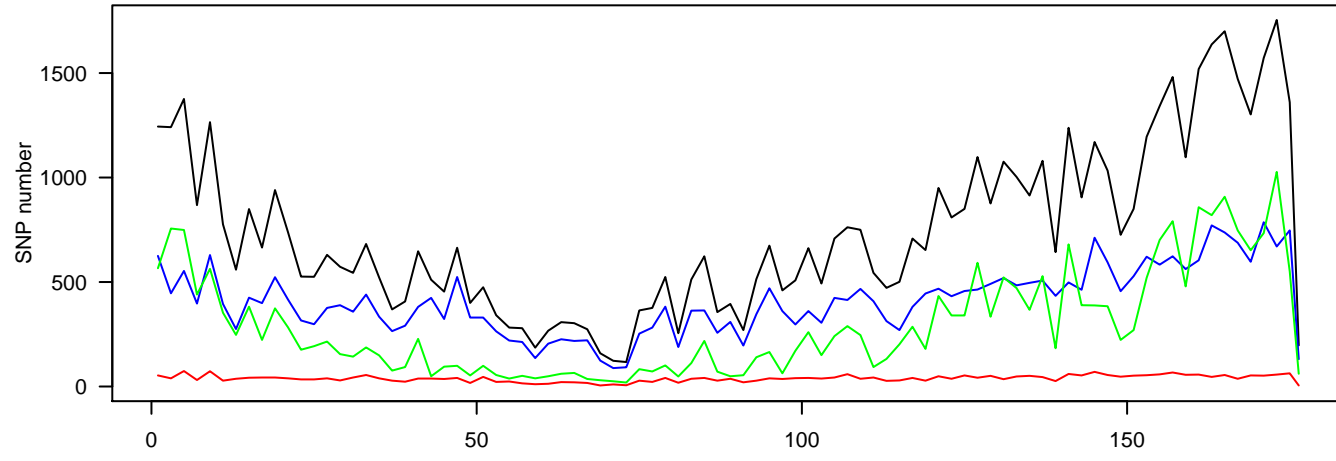
# Chromosome 5



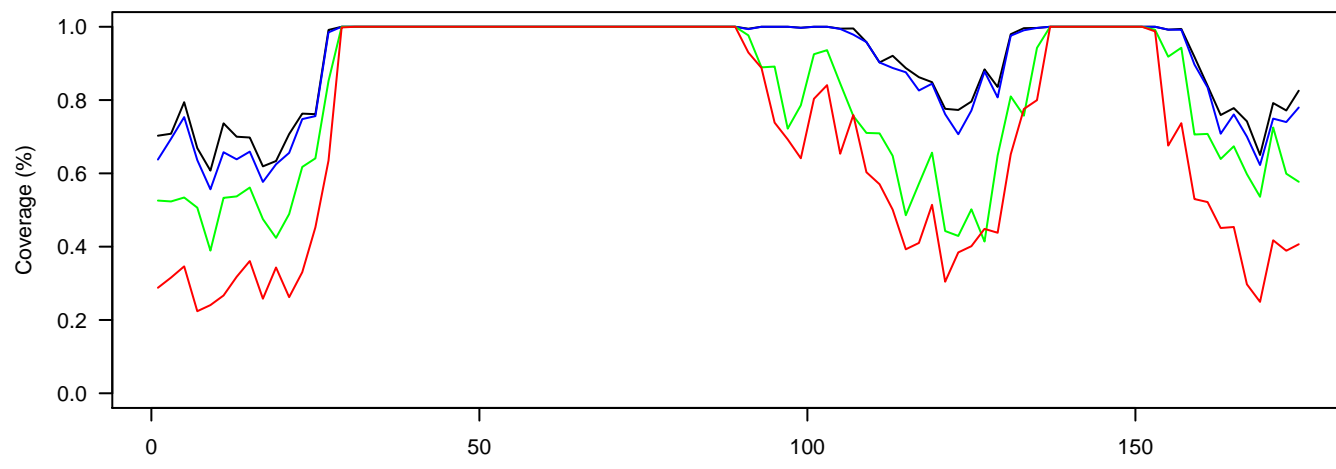
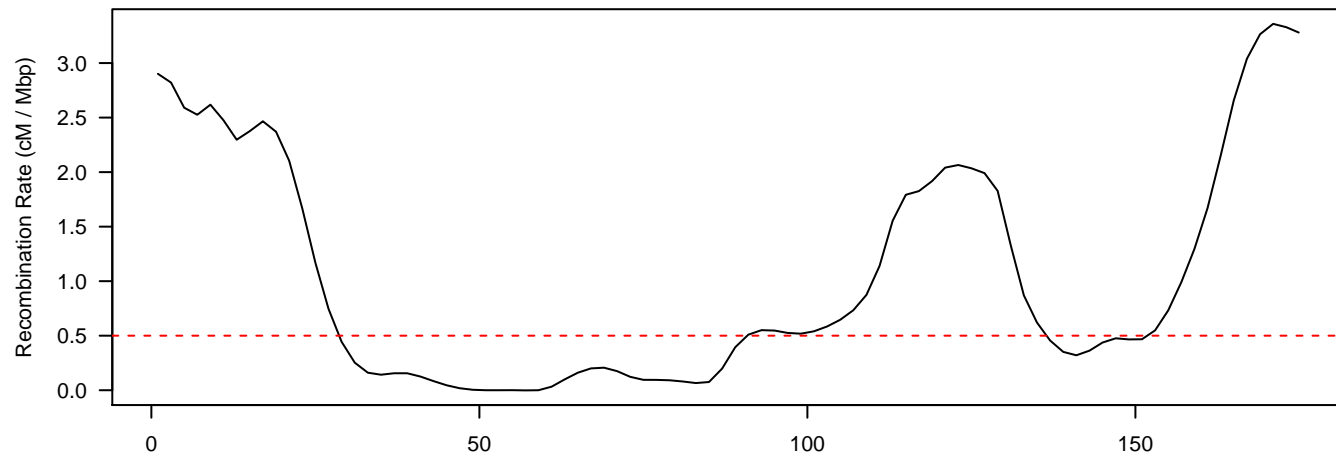
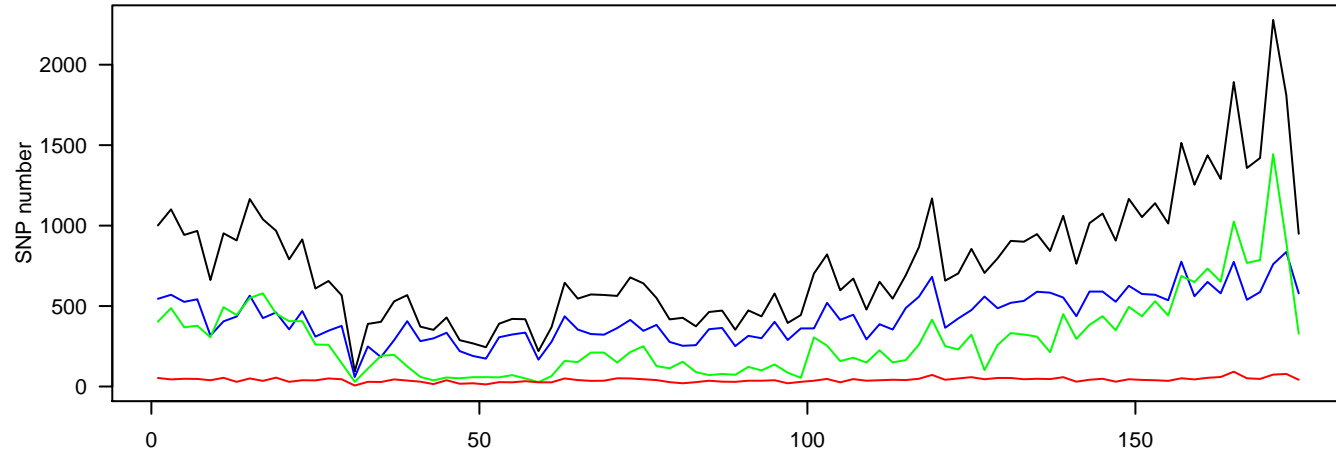
### Chromosome 6



# Chromosome 7

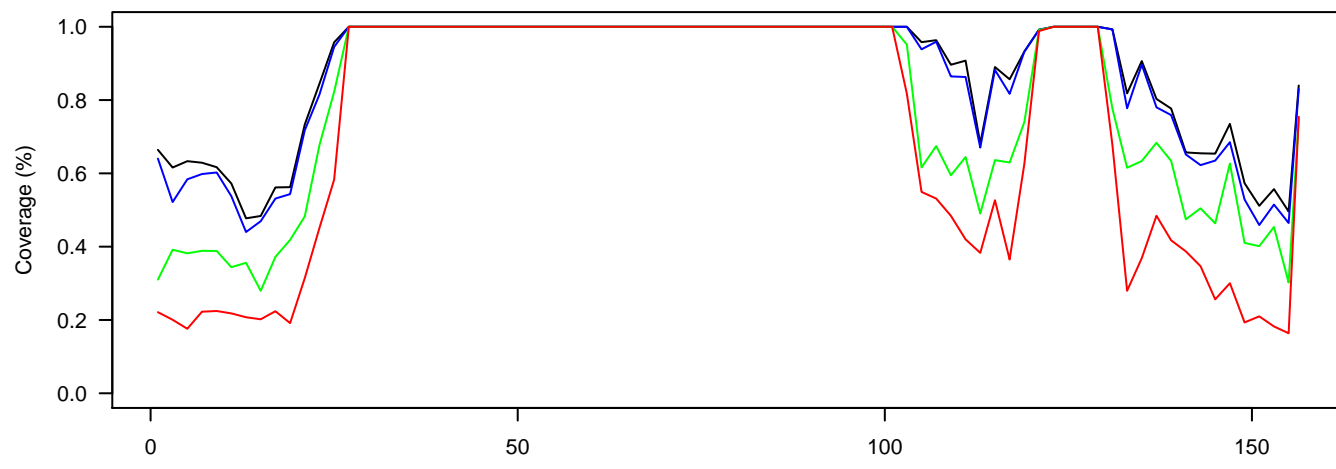
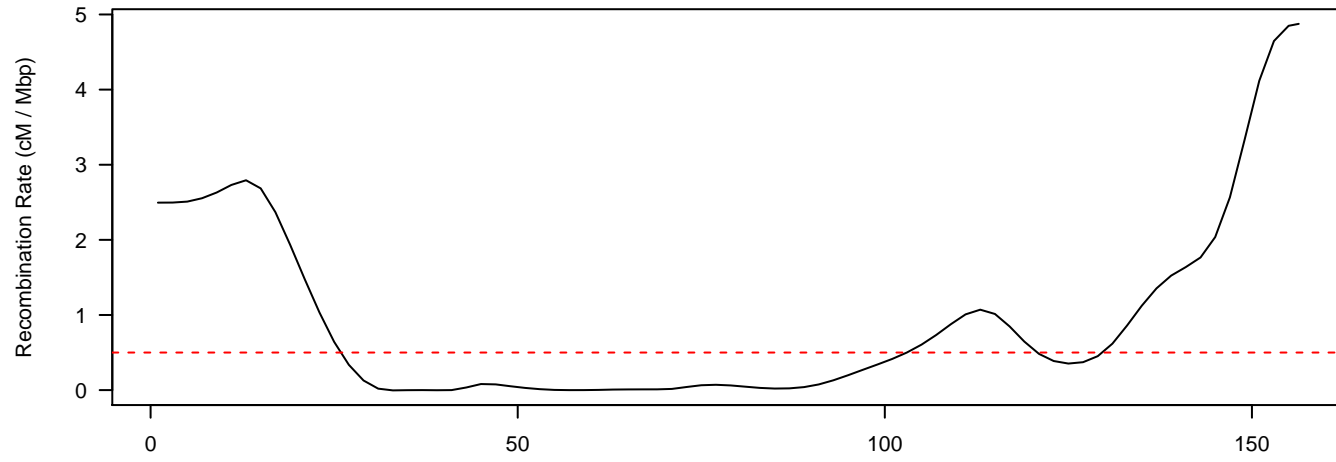
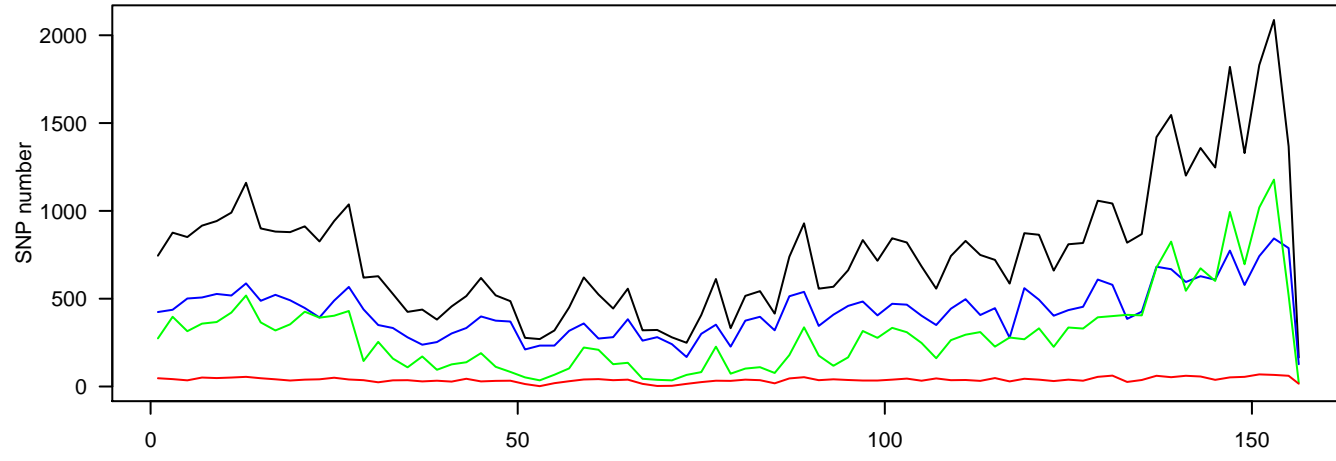


# Chromosome 8

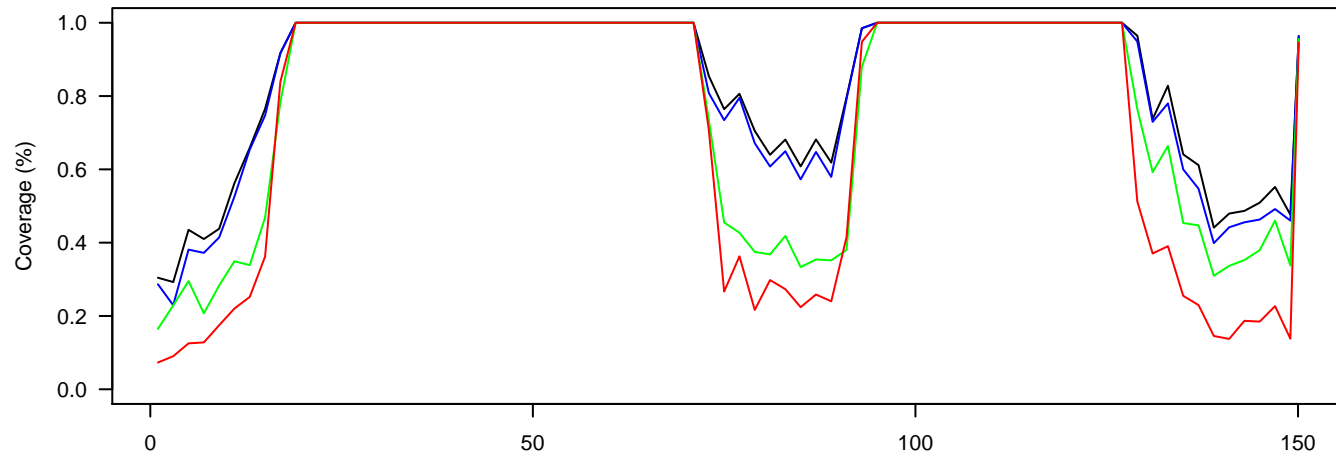
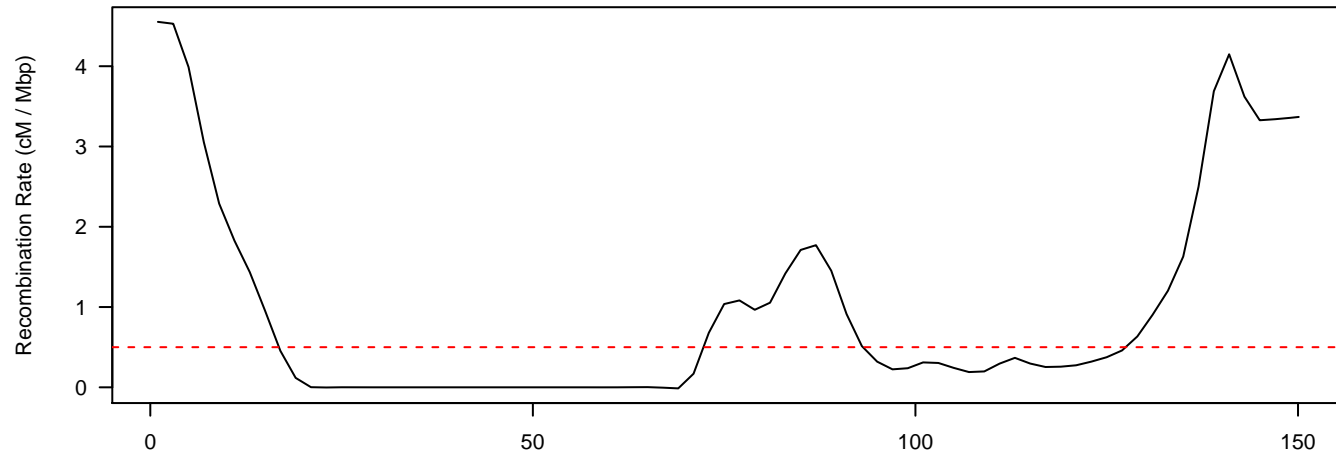
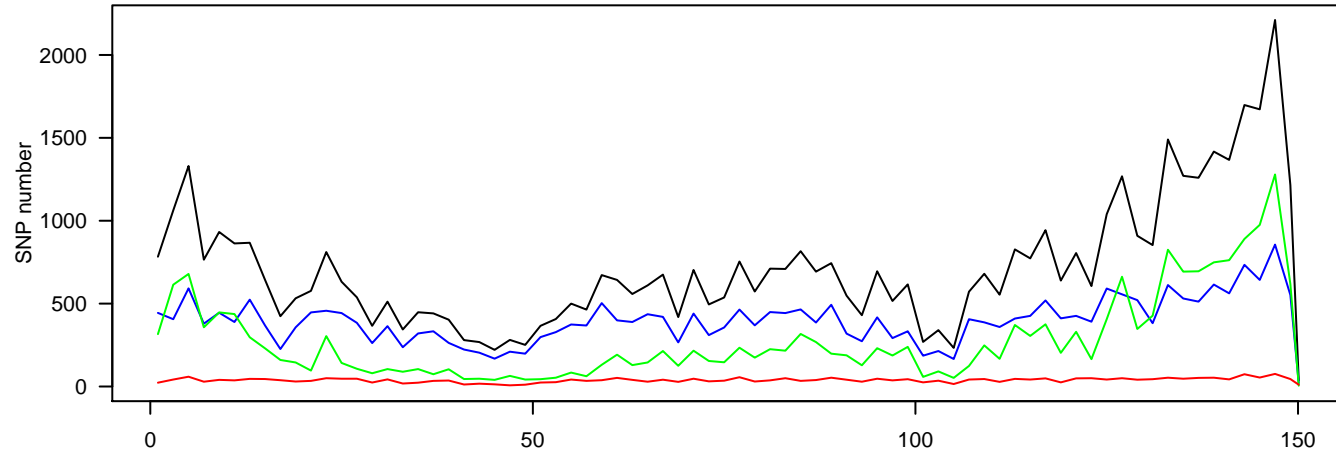




# Chromosome 9



# Chromosome 10



**Additional file 2 (.pdf):**

**Figure S2:** Variation of the markers density, the recombination rate and the genome coverage in non-overlapping 2 Mbp windows along each chromosome. The percentage SNP coverage (bottom) used the cumulated length of physical LD windows around each SNP. Markers have  $MAF \geq 5\%$ . Green, blue, red and black lines represent variation of GBS, 600K, 50K and combined technologies, respectively.