

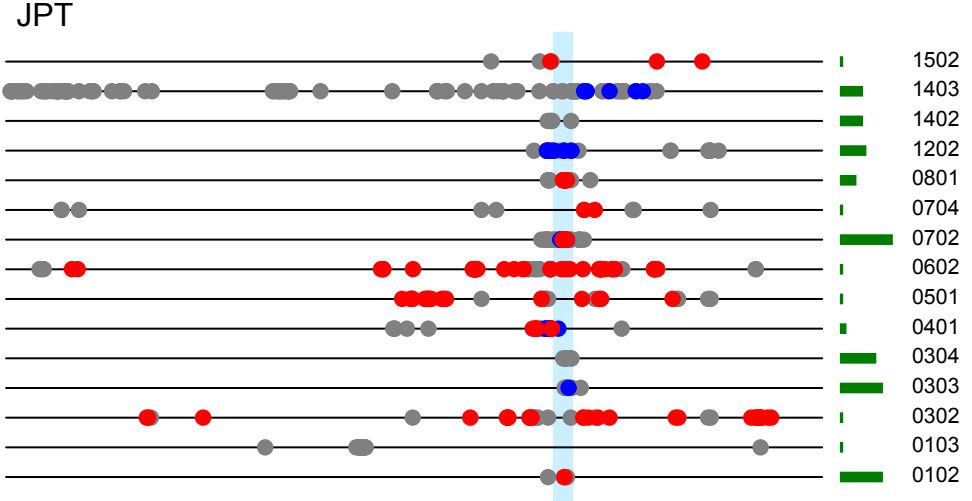
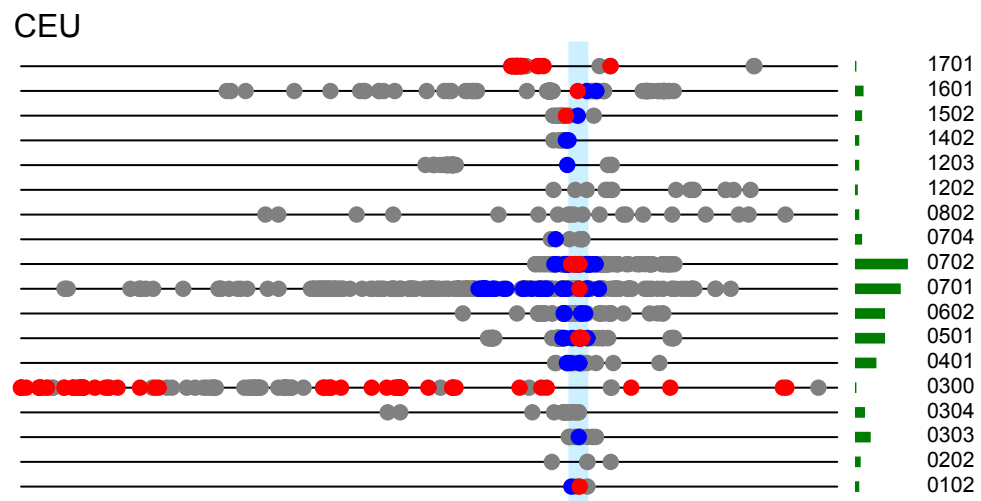
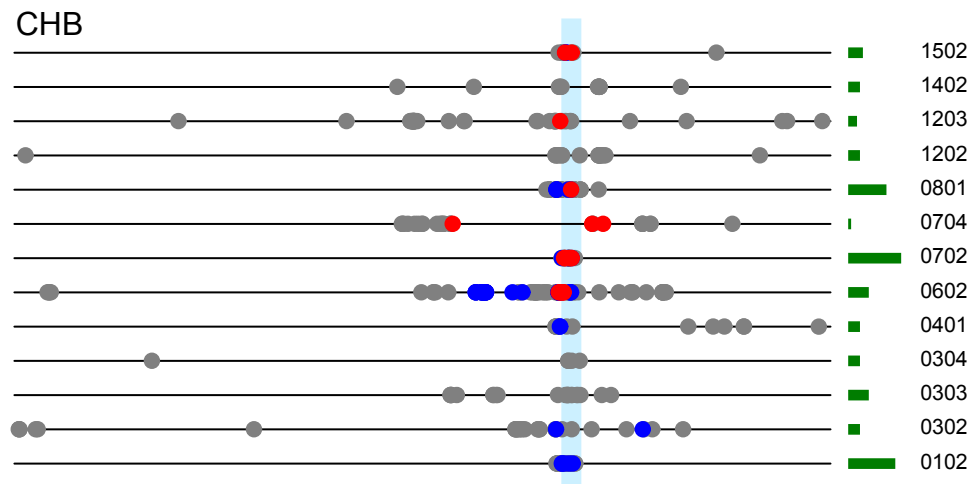
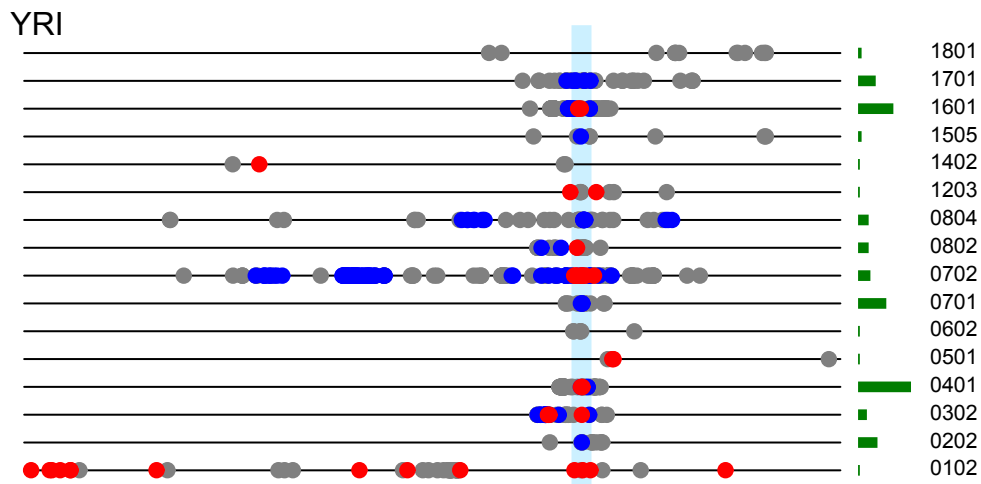
26 28 30 32 34

Position (Mb)

26 28 30 32 34

Position (Mb)

HLA-A



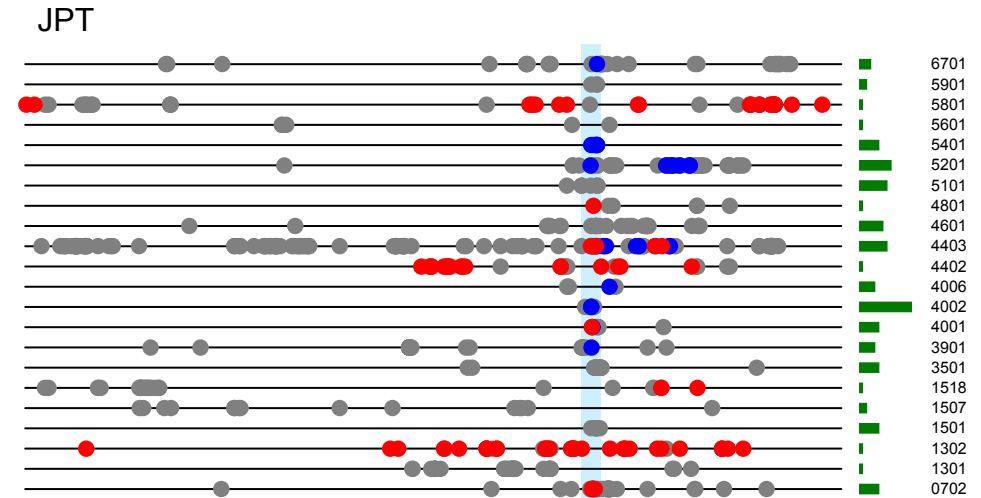
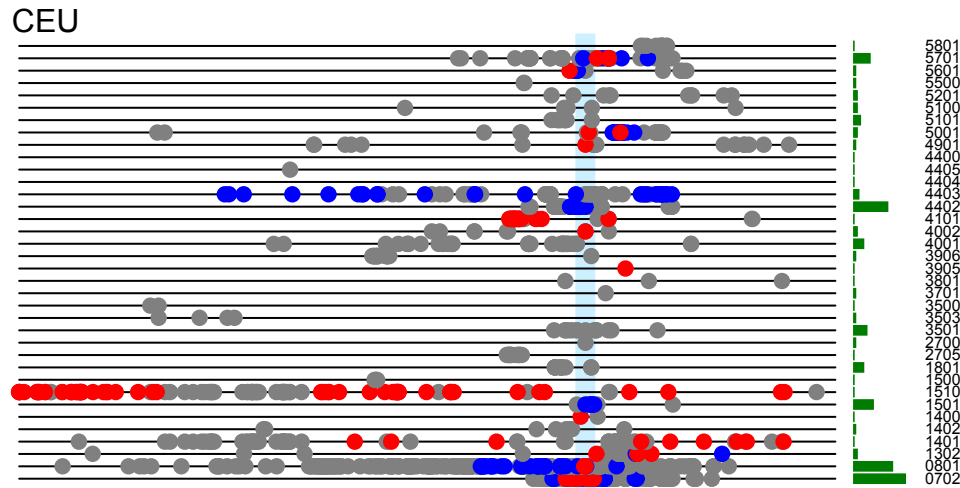
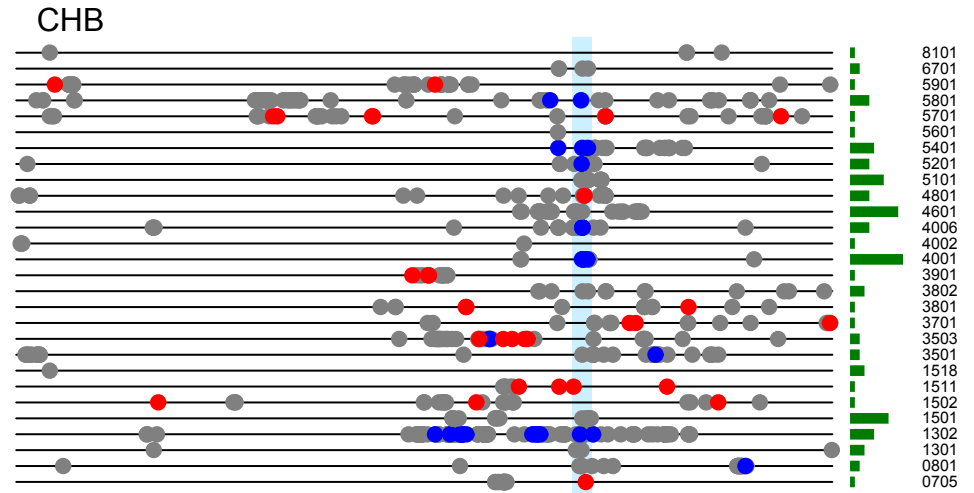
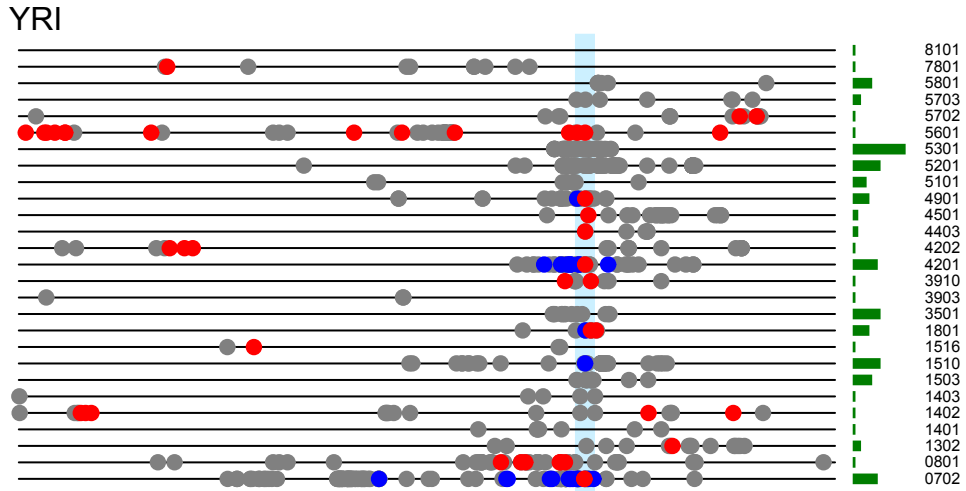
26 28 30 32 34

Position (Mb)

26 28 30 32 34

Position (Mb)

HLA-C



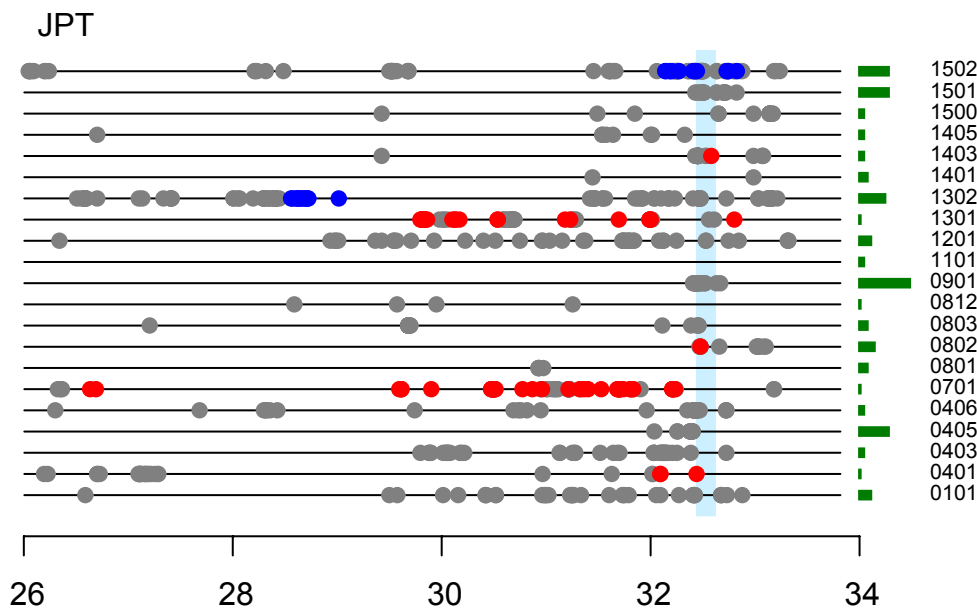
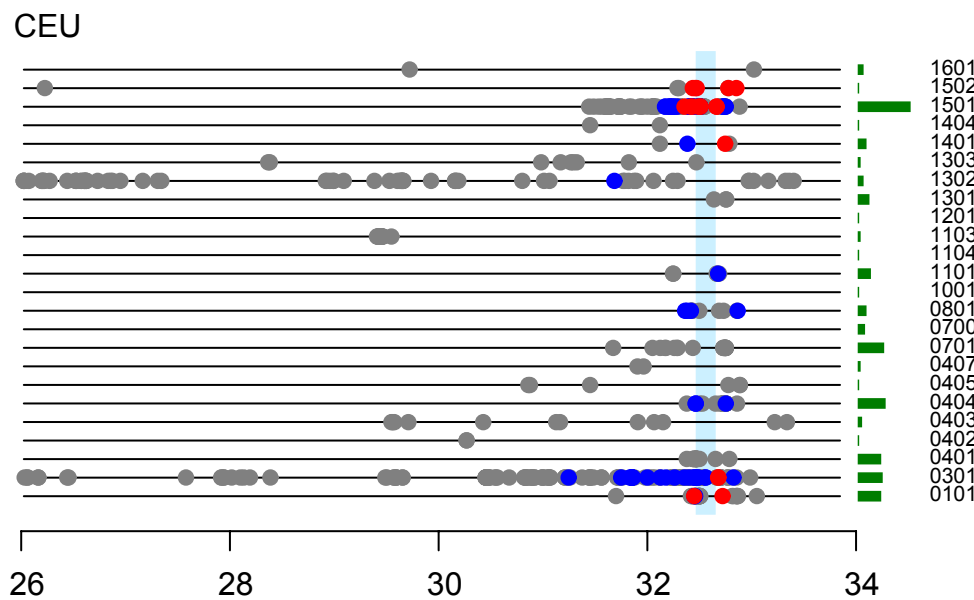
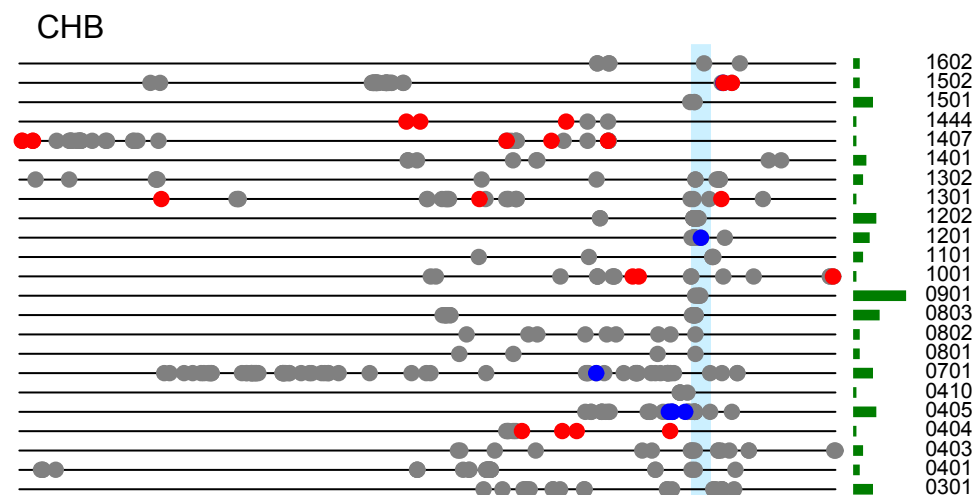
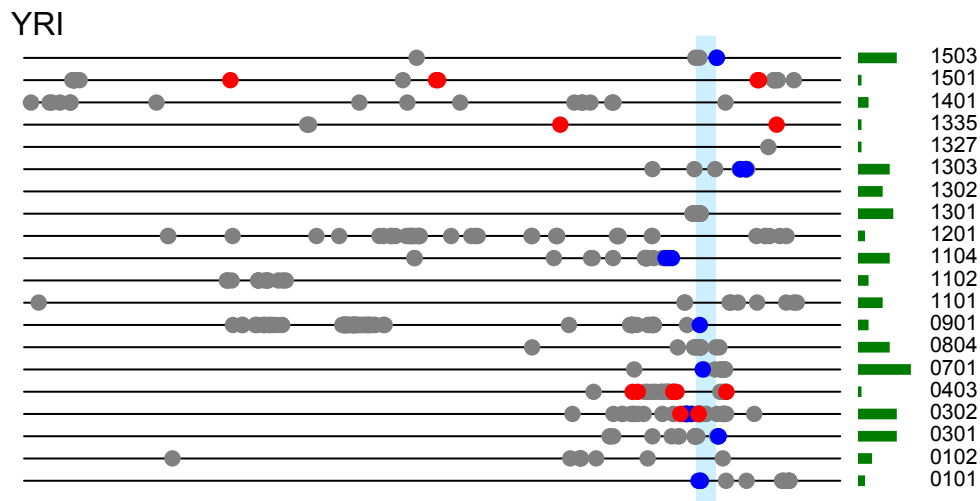
26 28 30 32 34

Position (Mb)

26 28 30 32 34

Position (Mb)

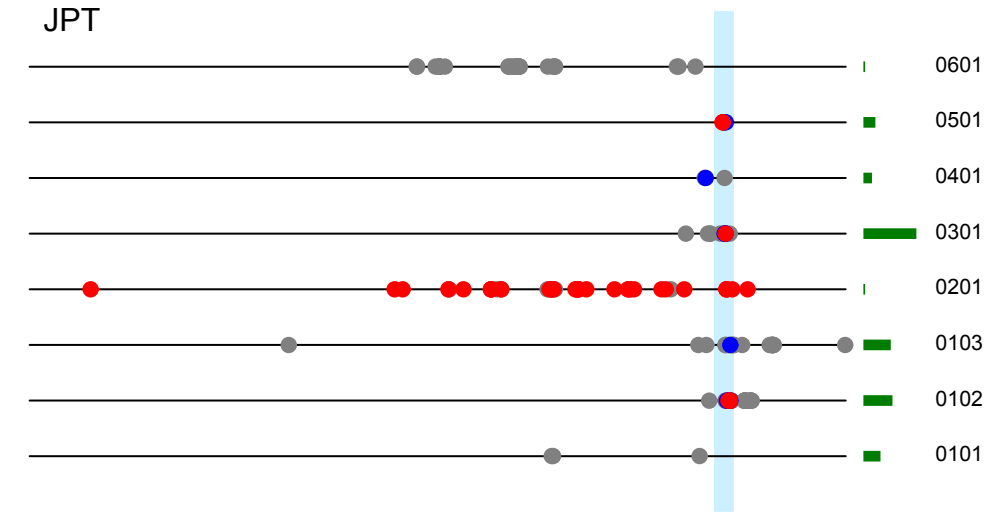
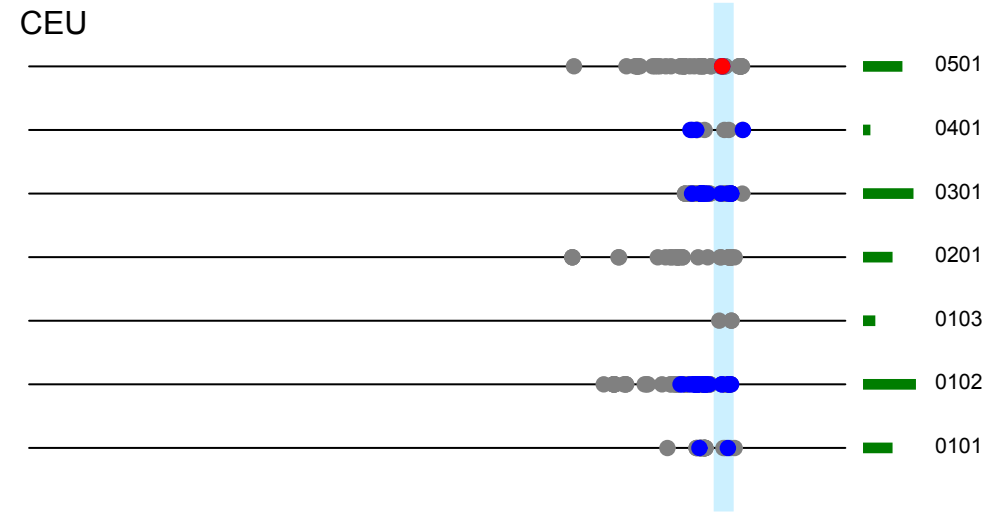
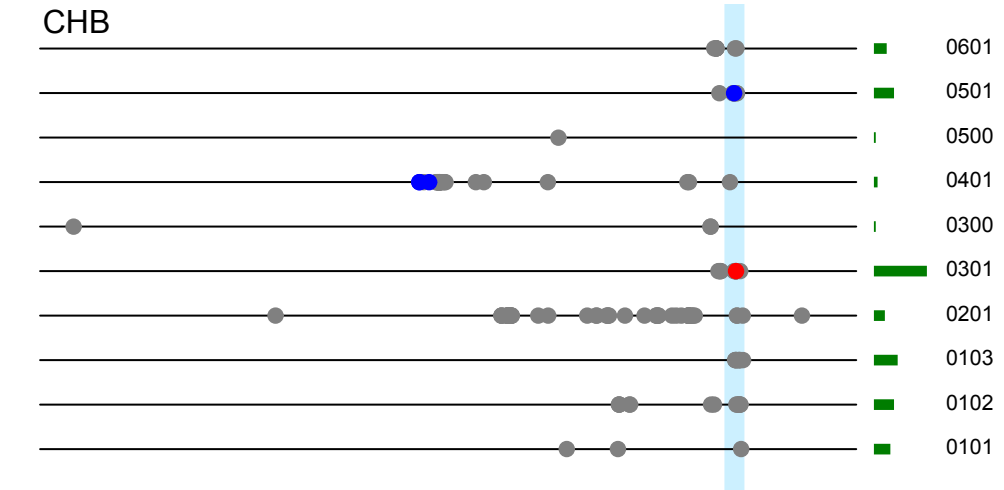
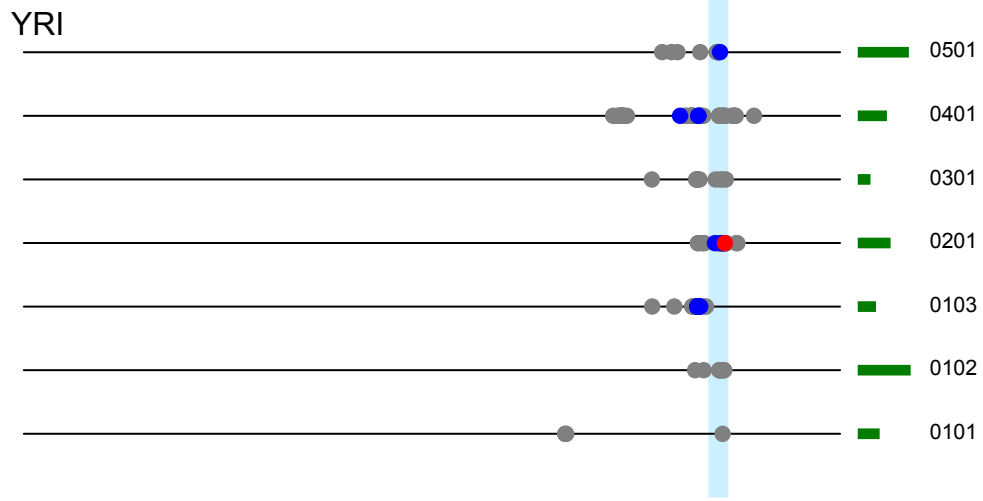
HLA-B



Position (Mb)

Position (Mb)

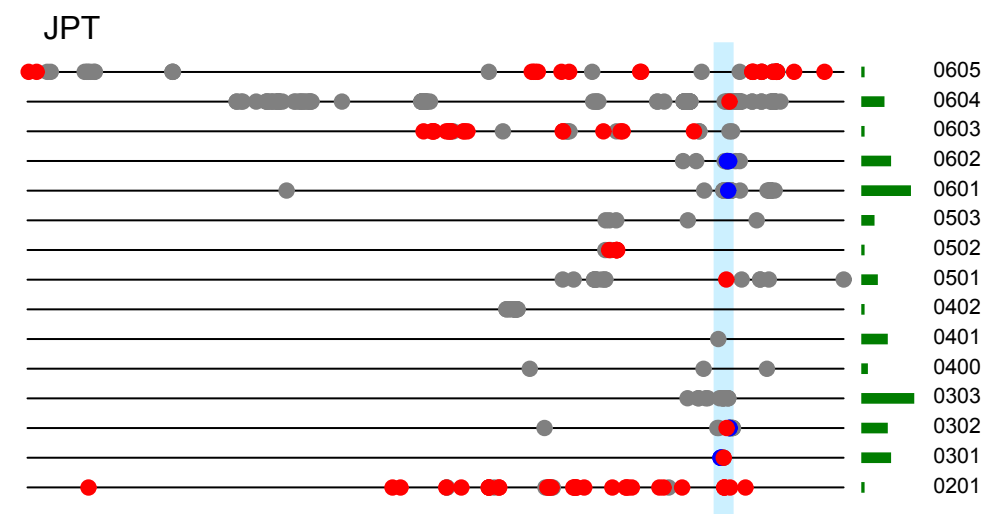
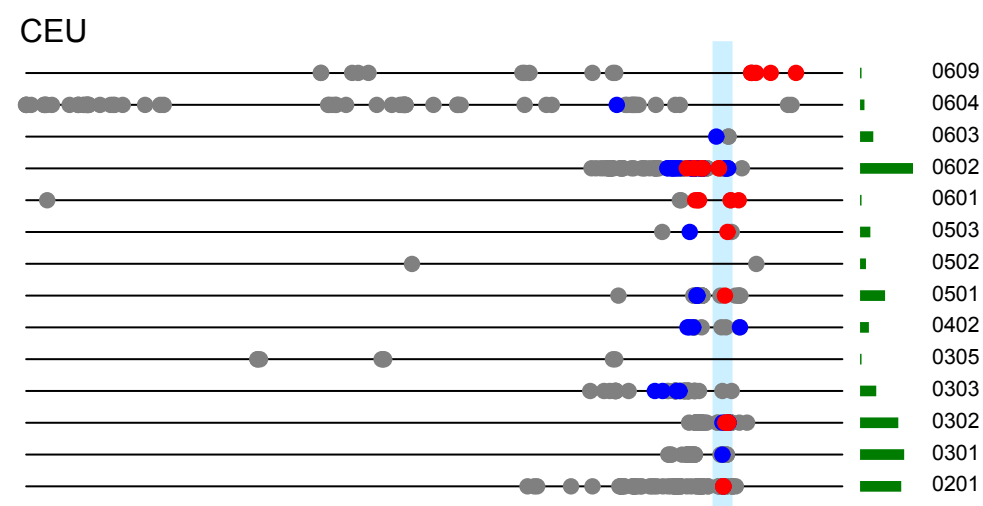
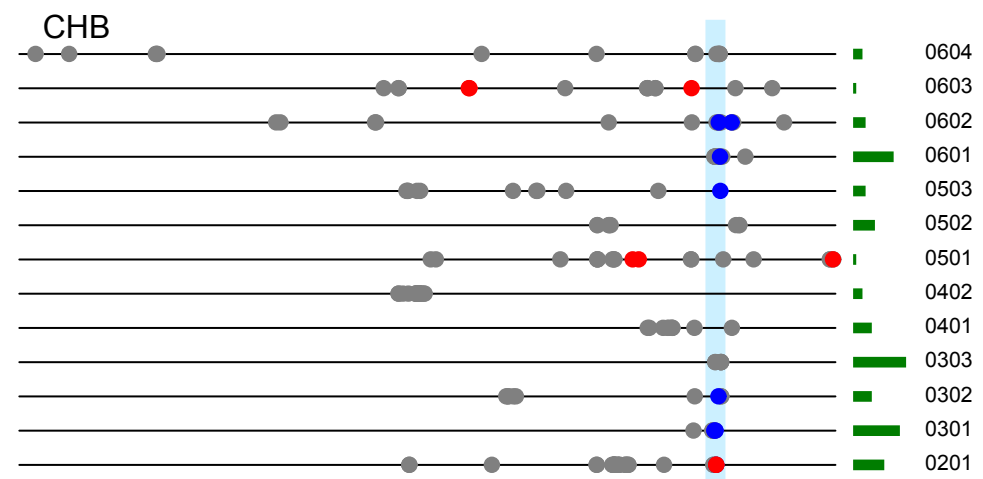
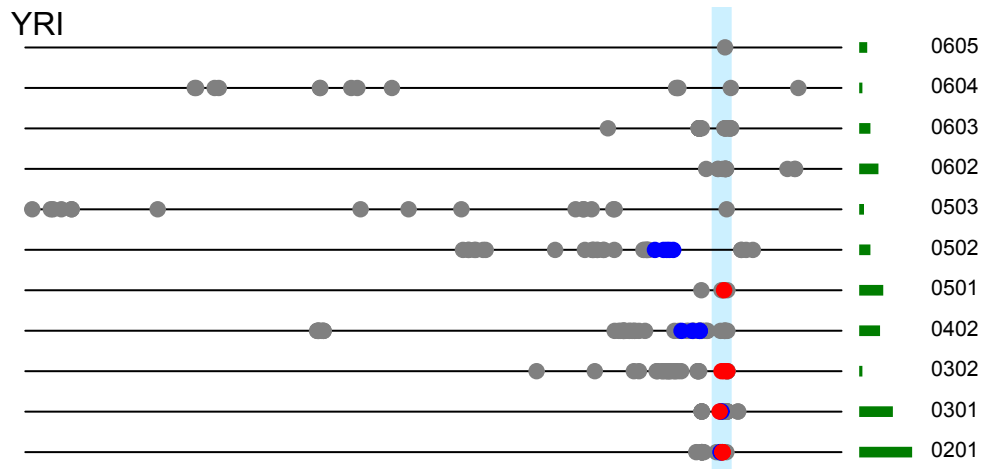
HLA-DRB



26 28 30 32 34
Position (Mb)

26 28 30 32 34
Position (Mb)

HLA-DQA



26 28 30 32 34
Position (Mb)

26 28 30 32 34
Position (Mb)

HLA-DQB

Supplementary Figure 1. Allelic association between SNPs across the 7.5 Mb extended MHC region and HLA types at each gene for the combined population data (using the 5,754 SNPs that were typed in all populations and are polymorphic across the combined population samples). **(a)** For *HLA-A* (the position of which is indicated by the vertical blue line), the position of SNPs across the 7.5 Mb region showing weak ($0.2 < r^2 < 0.5$; grey), moderate ($0.5 < r^2 < 0.8$; blue) and strong ($r^2 > 0.8$; red) association to each type that is present for each of the four populations. The size of the adjacent green bar indicates the relative frequency of each type in each population (types not present in a population are not shown). Parts **(b)** - **(f)** are for *HLA-C*, *HLA-B*, *HLA-DRB*, *HLA-DQA* and *HLA-DQB* respectively. All types found at least once in each population are shown.