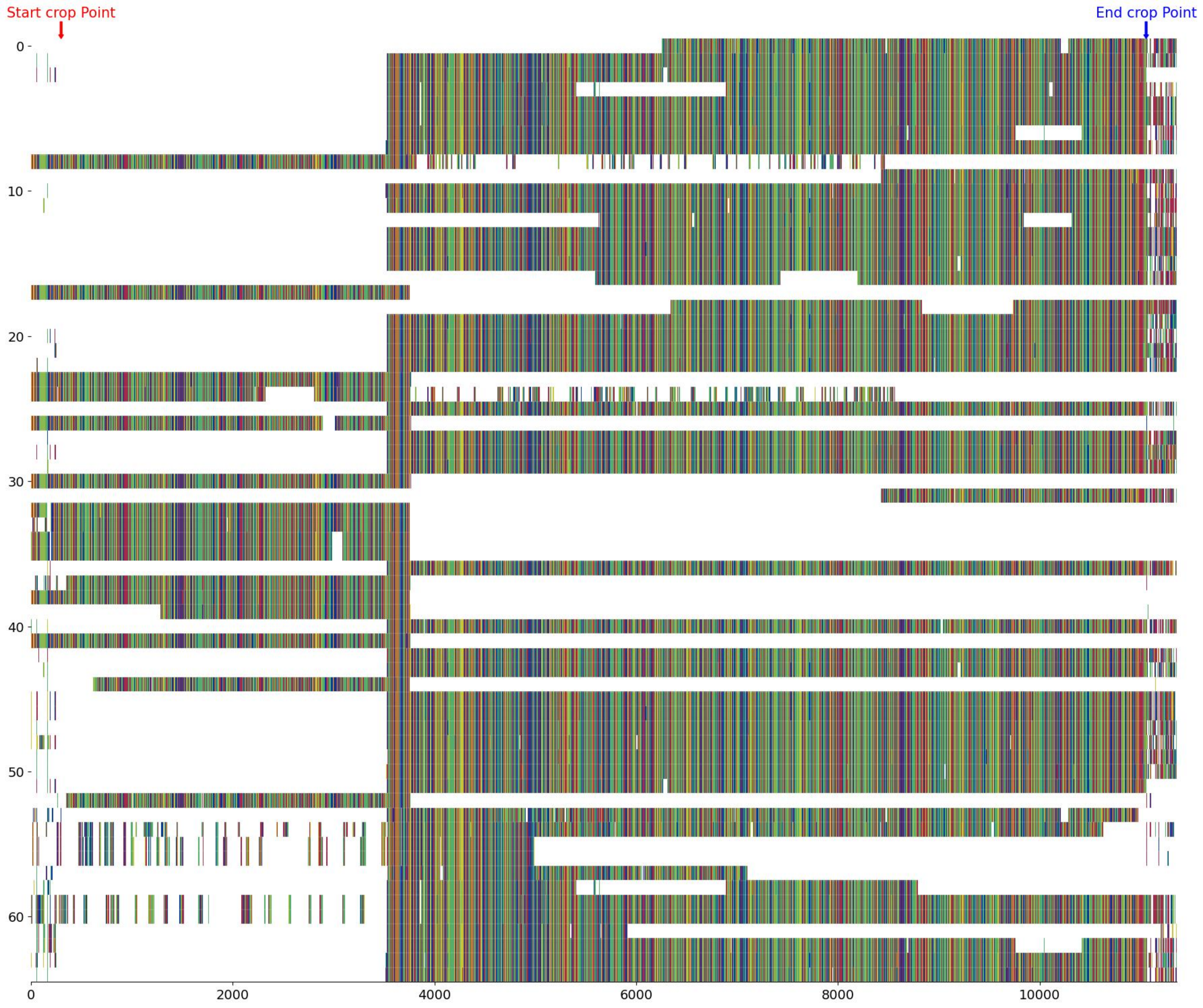




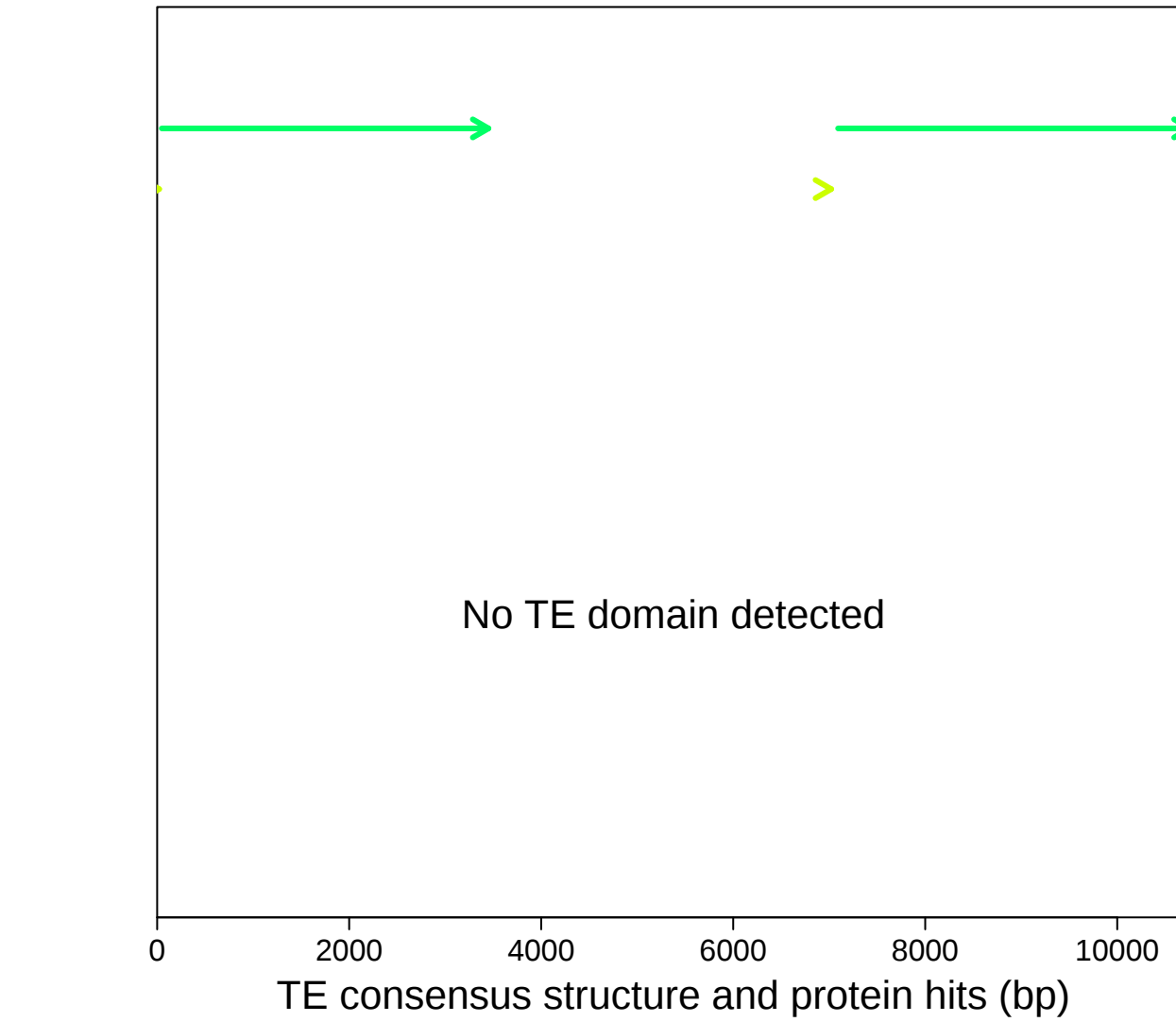
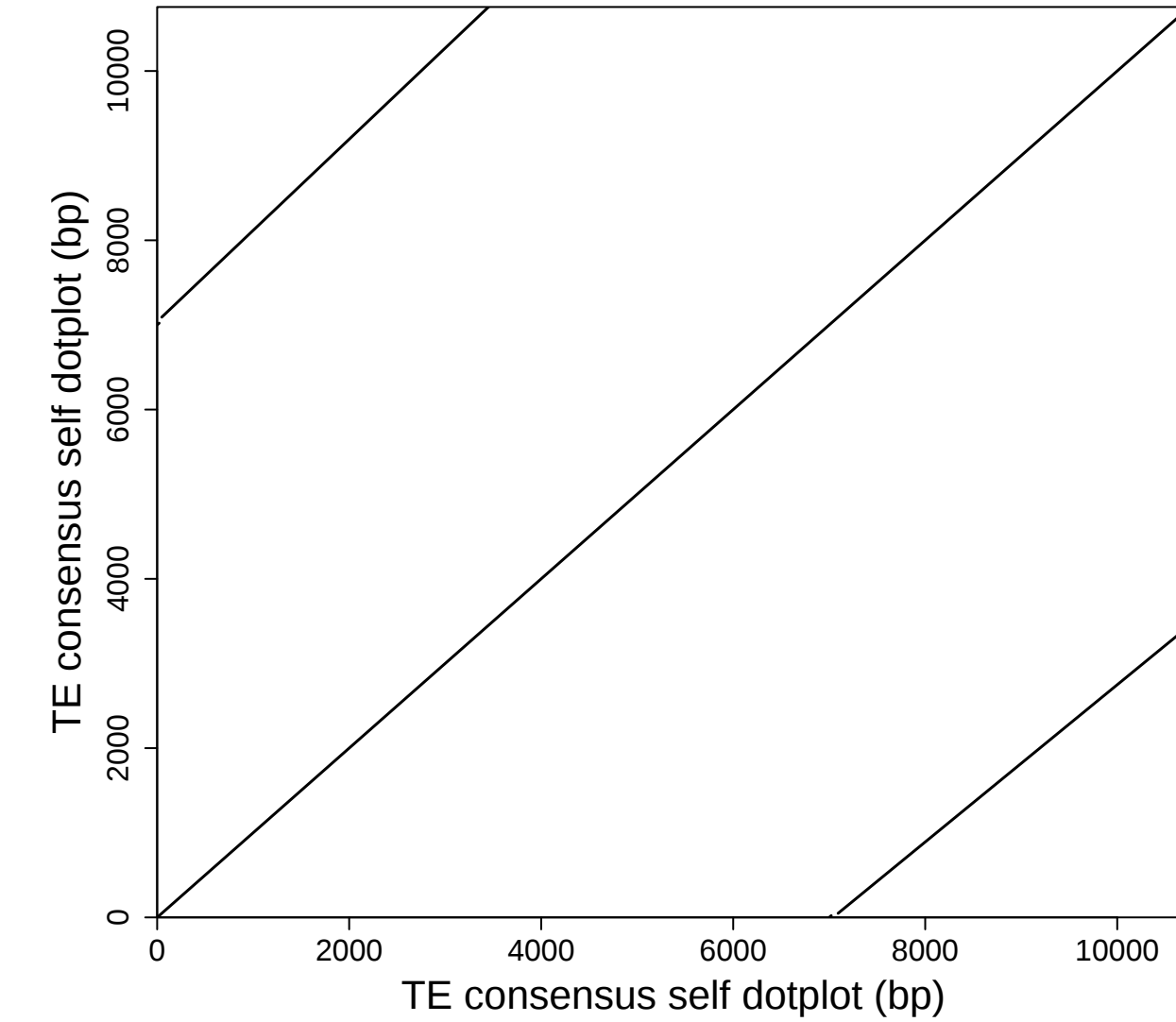
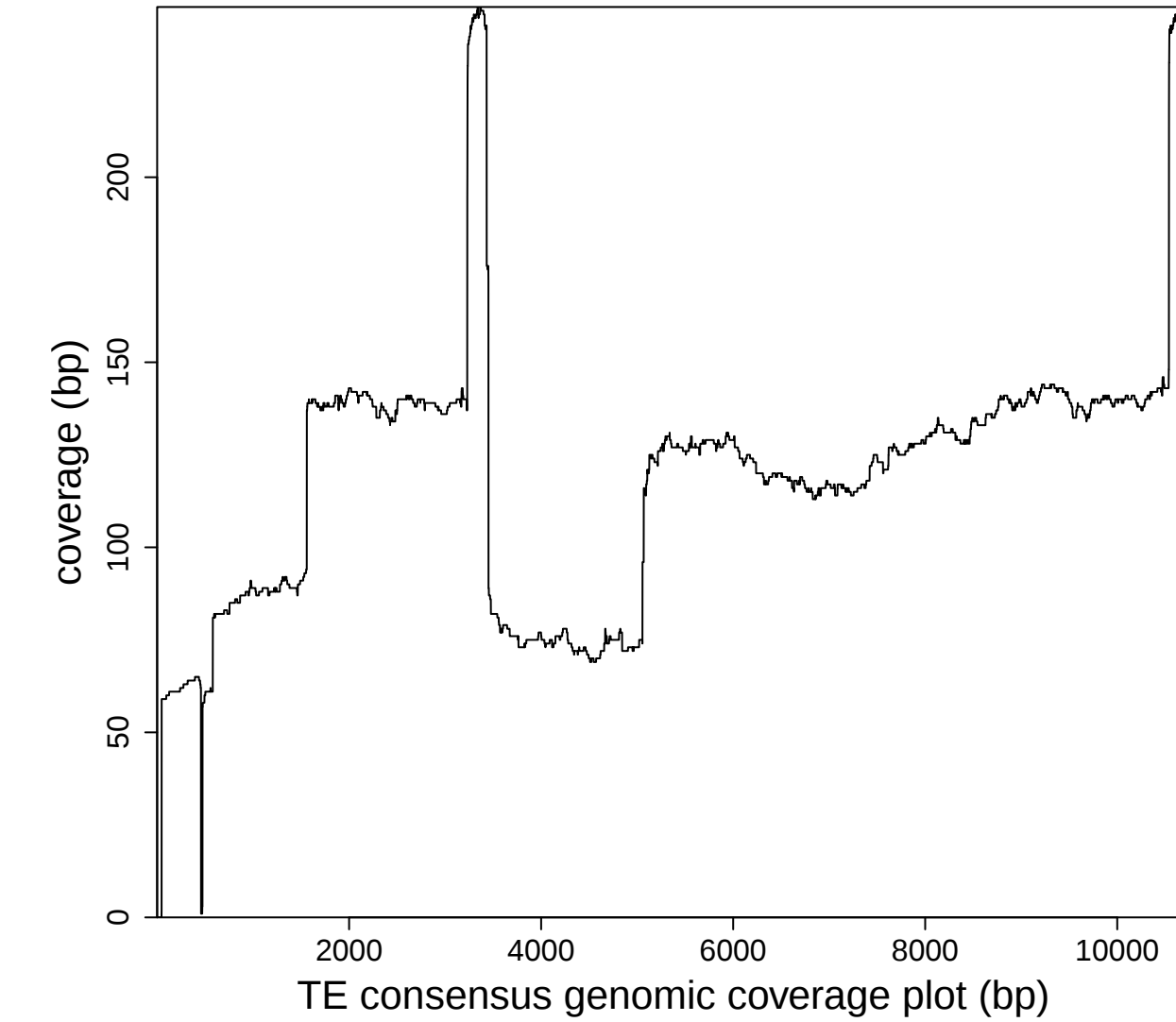
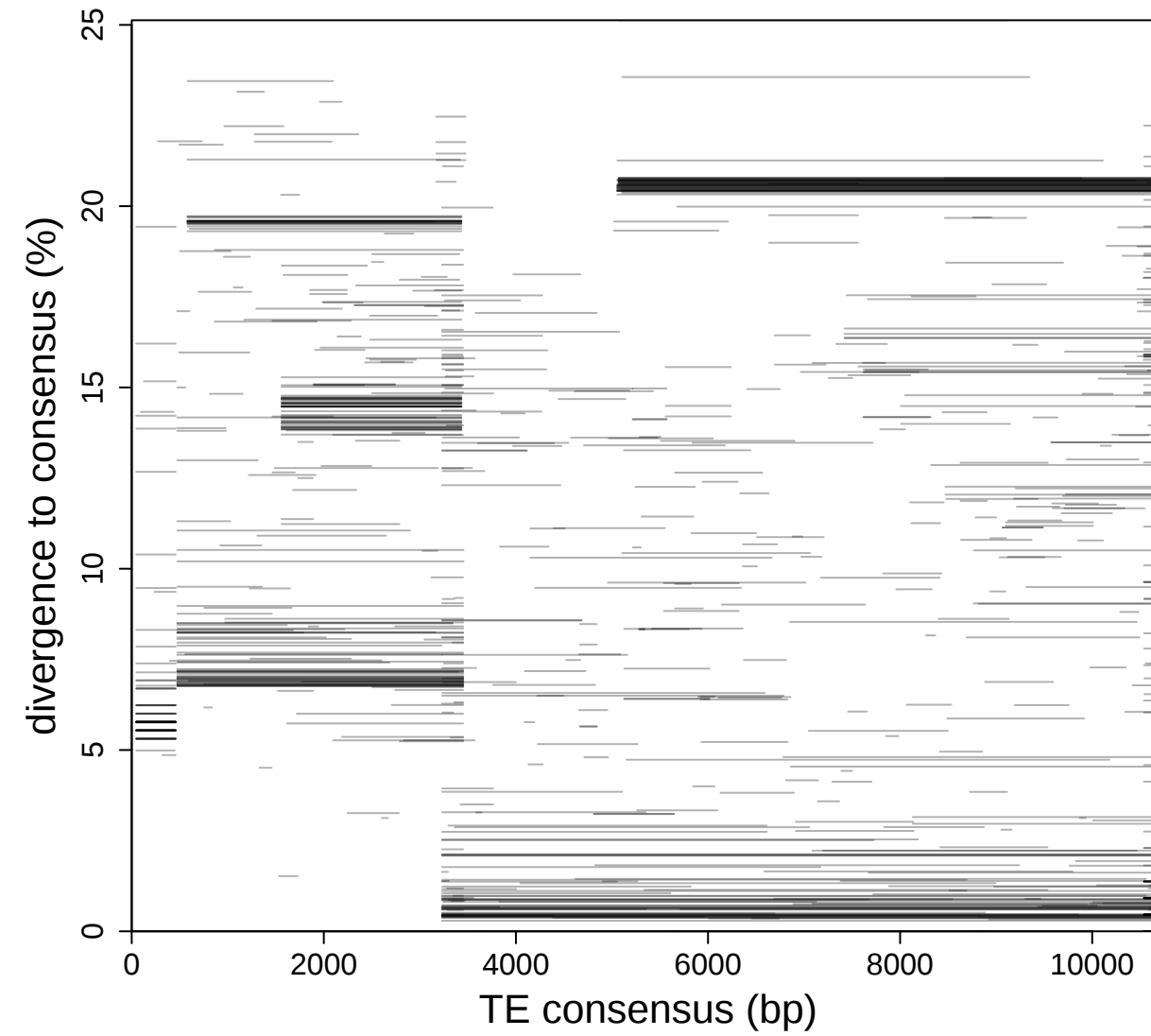
-----ATAA

Figure 1: Schematic representation of the 1000 Genomes Project. The figure displays a large number of genomic regions, each represented by a horizontal bar. The bars are color-coded to indicate the genetic ancestry of the individuals in the population: African (red), European (green), East Asian (blue), South Asian (orange), and Admixed American (purple). The bars are arranged in a grid, with each row representing a different individual and each column representing a different genomic region. The color of the bar indicates the primary ancestry of the individual, while the color of the segments within the bar indicates the ancestry of the specific genomic region. The figure illustrates the genetic diversity and admixture within the 1000 Genomes Project population.

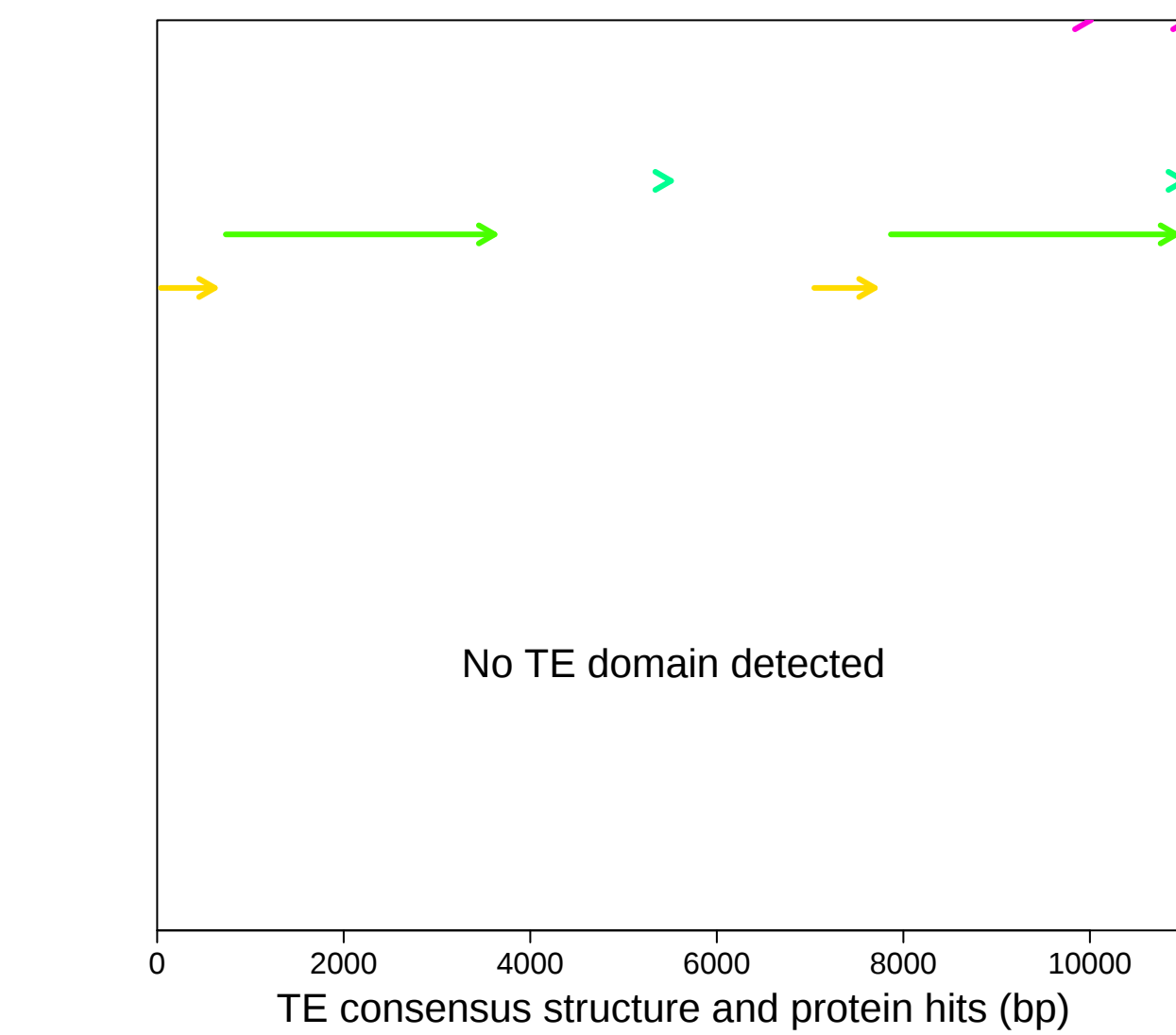
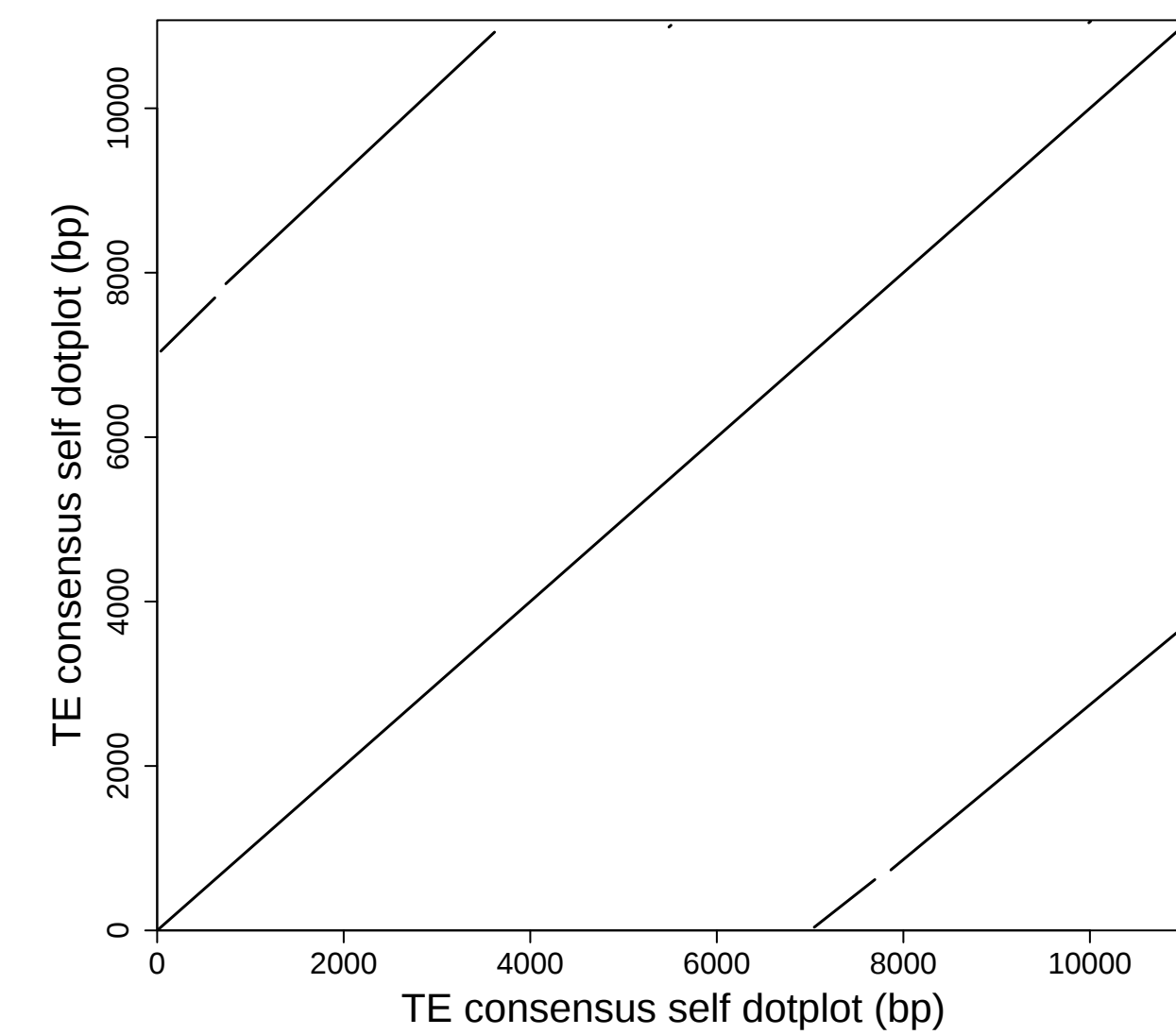
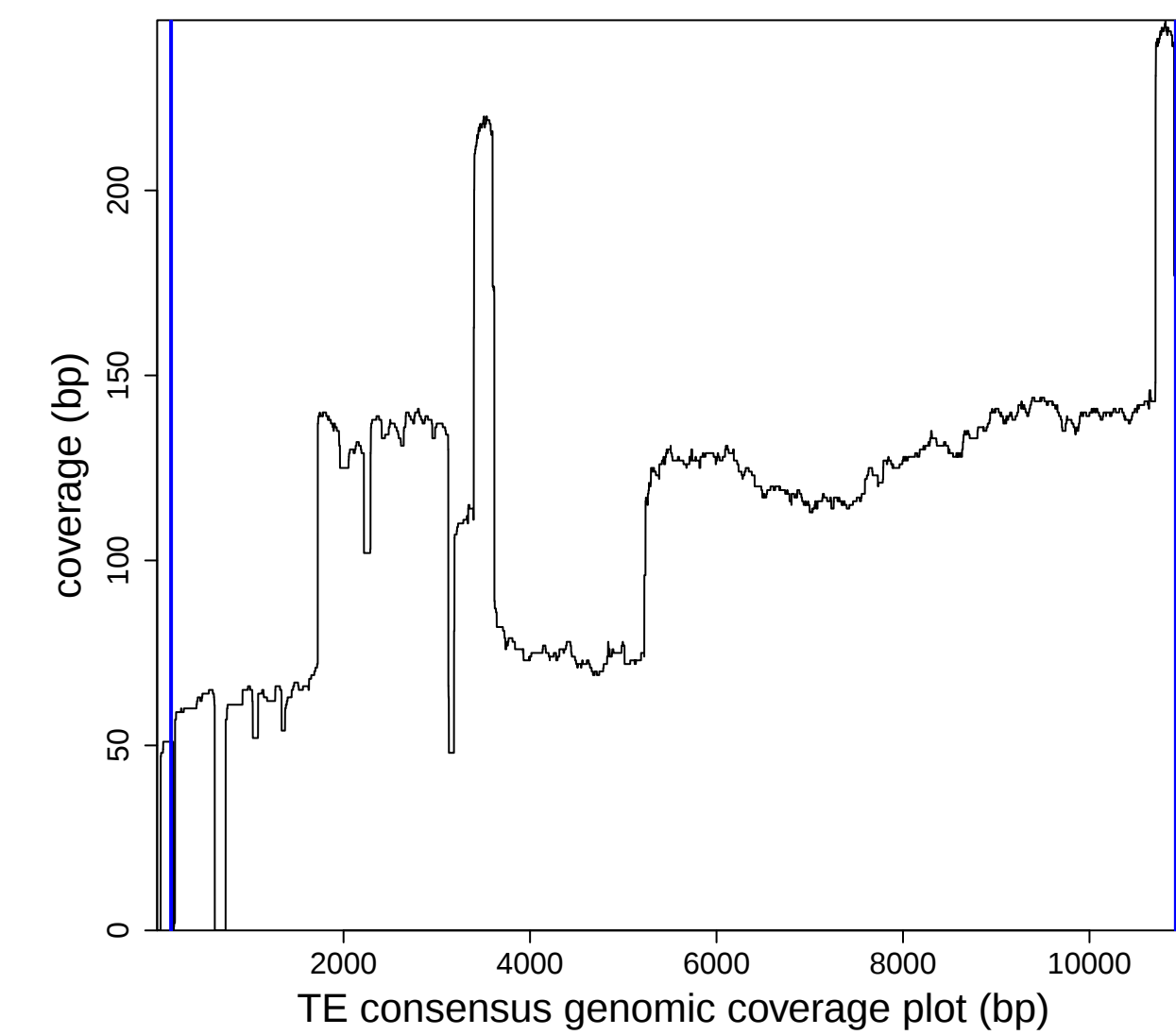
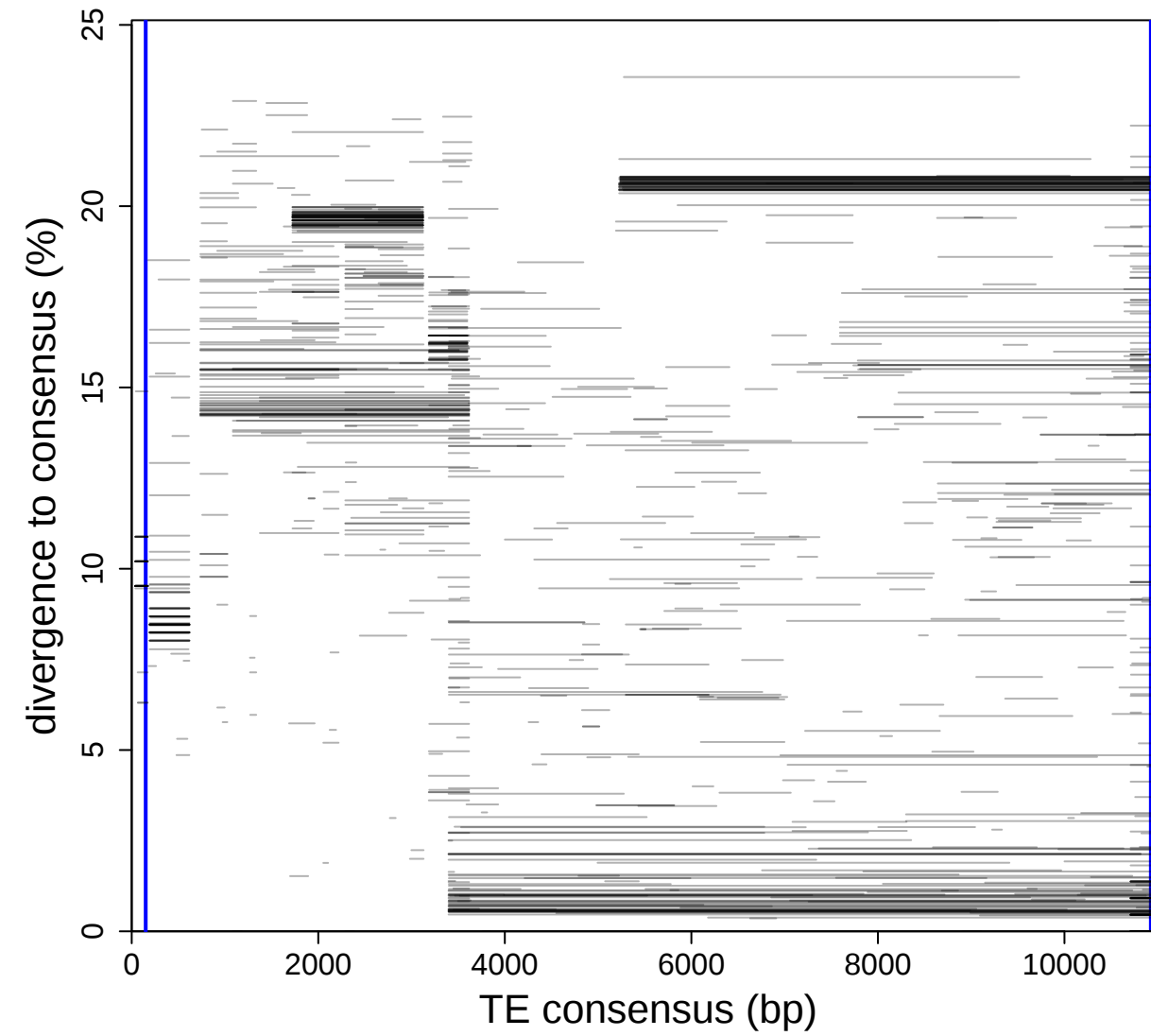


bed\_fm\_1.bed\_0\_0\_n.bed\_g\_1.bed\_fm\_2.bed\_0\_0\_bcln.fa\_aln.fa  
size: 10756bp; fragments: 810; full length: 0 (>=9680.4bp)

# After TEtrimmer 10756 bp

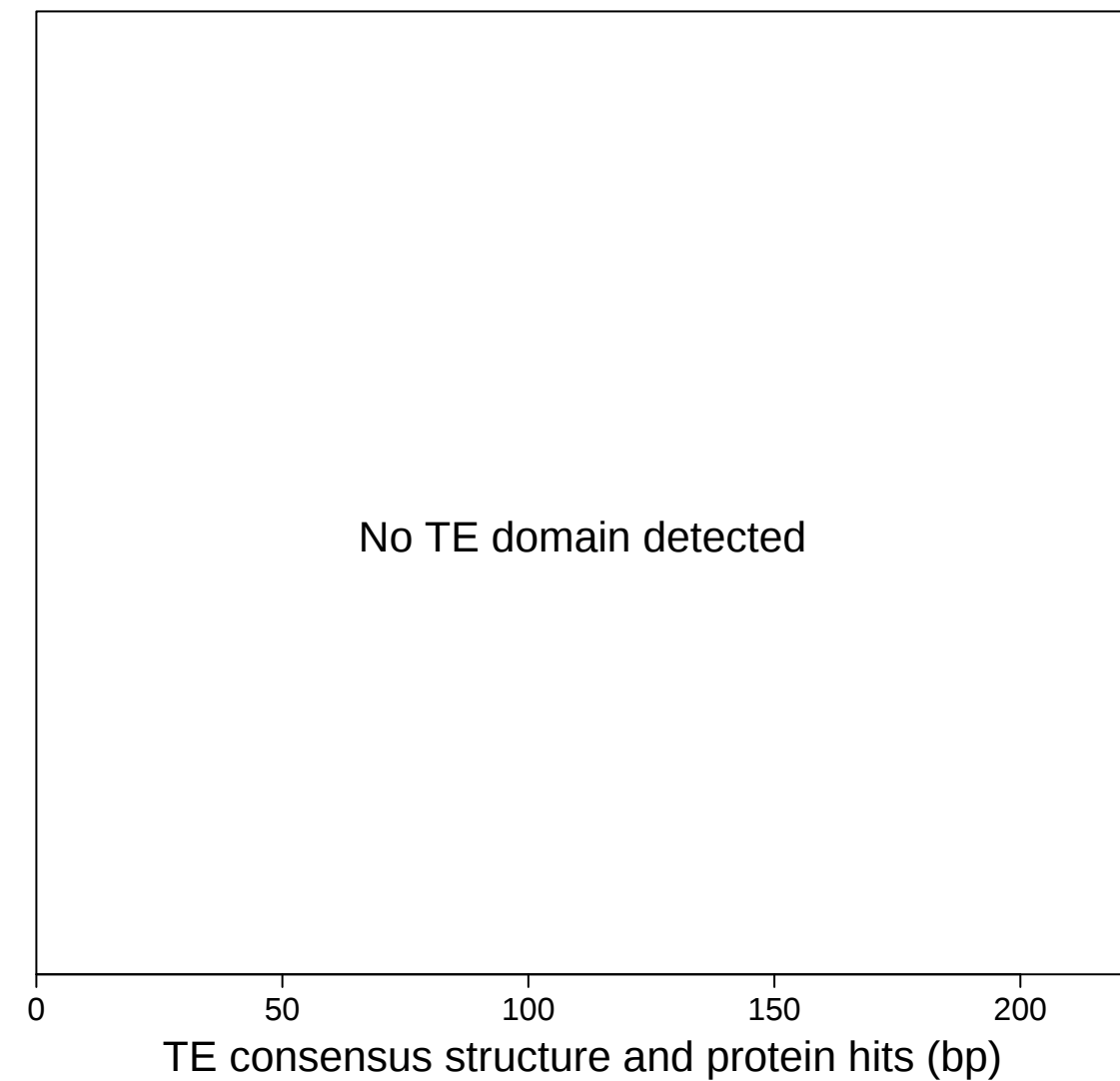
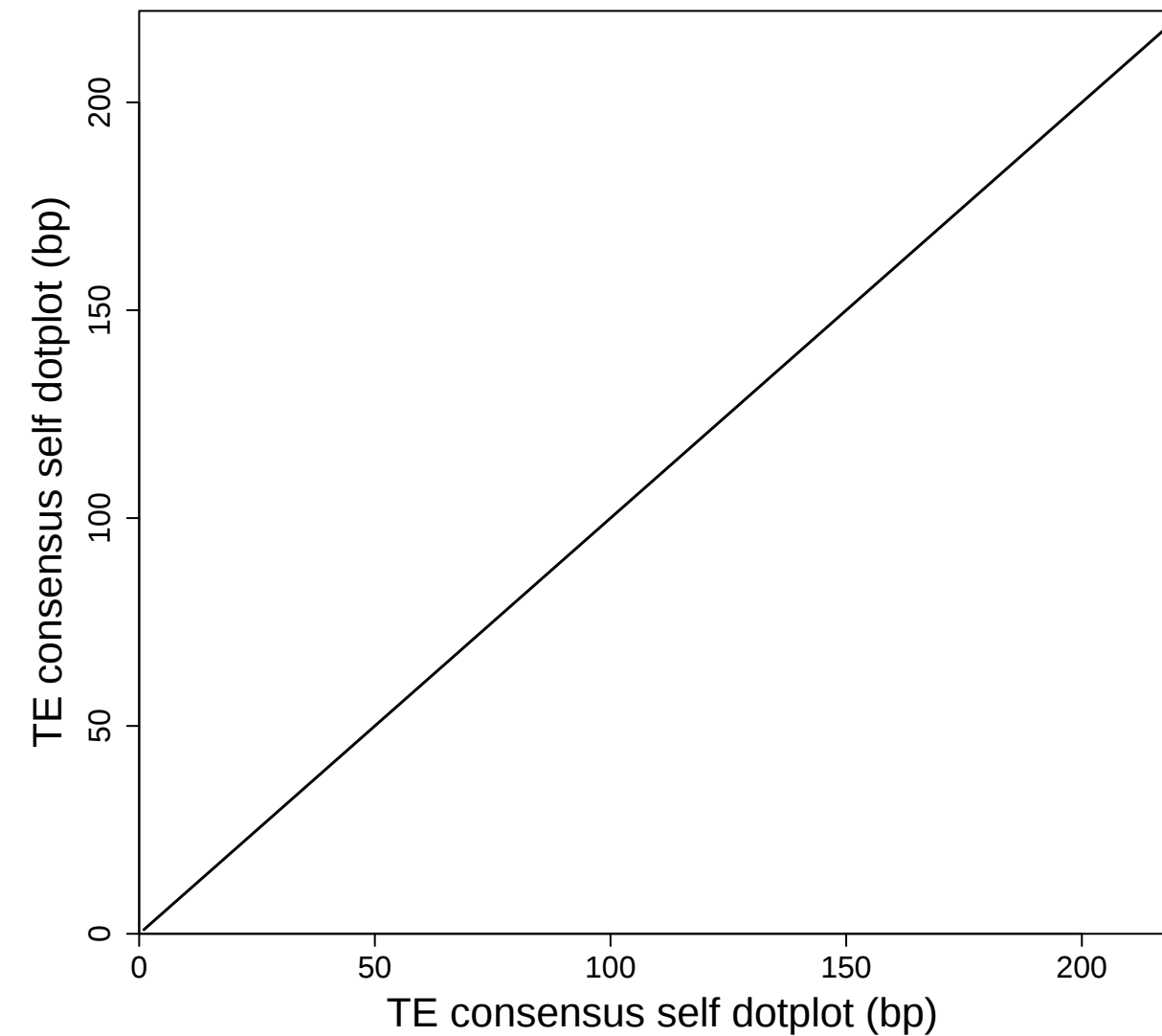
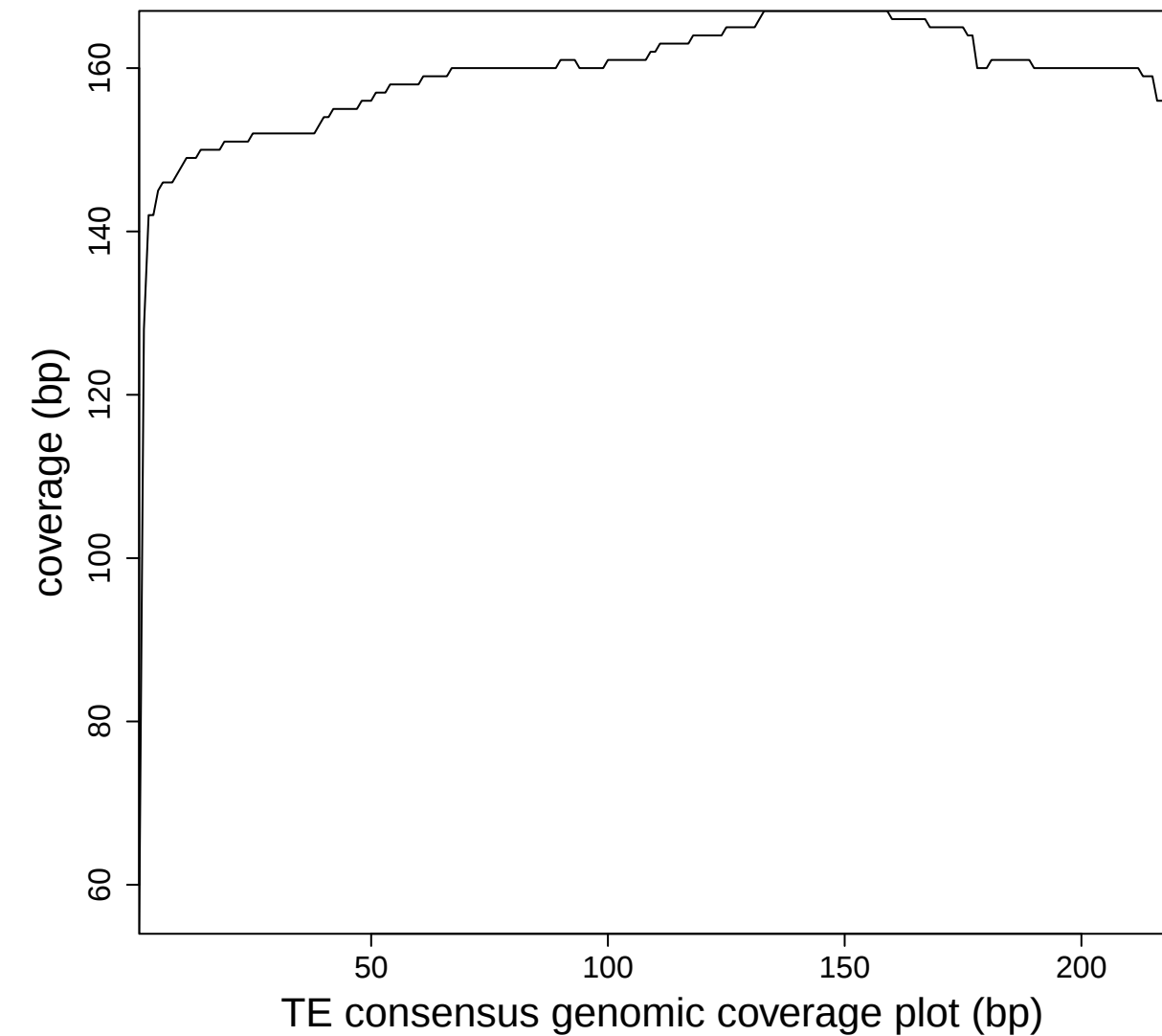
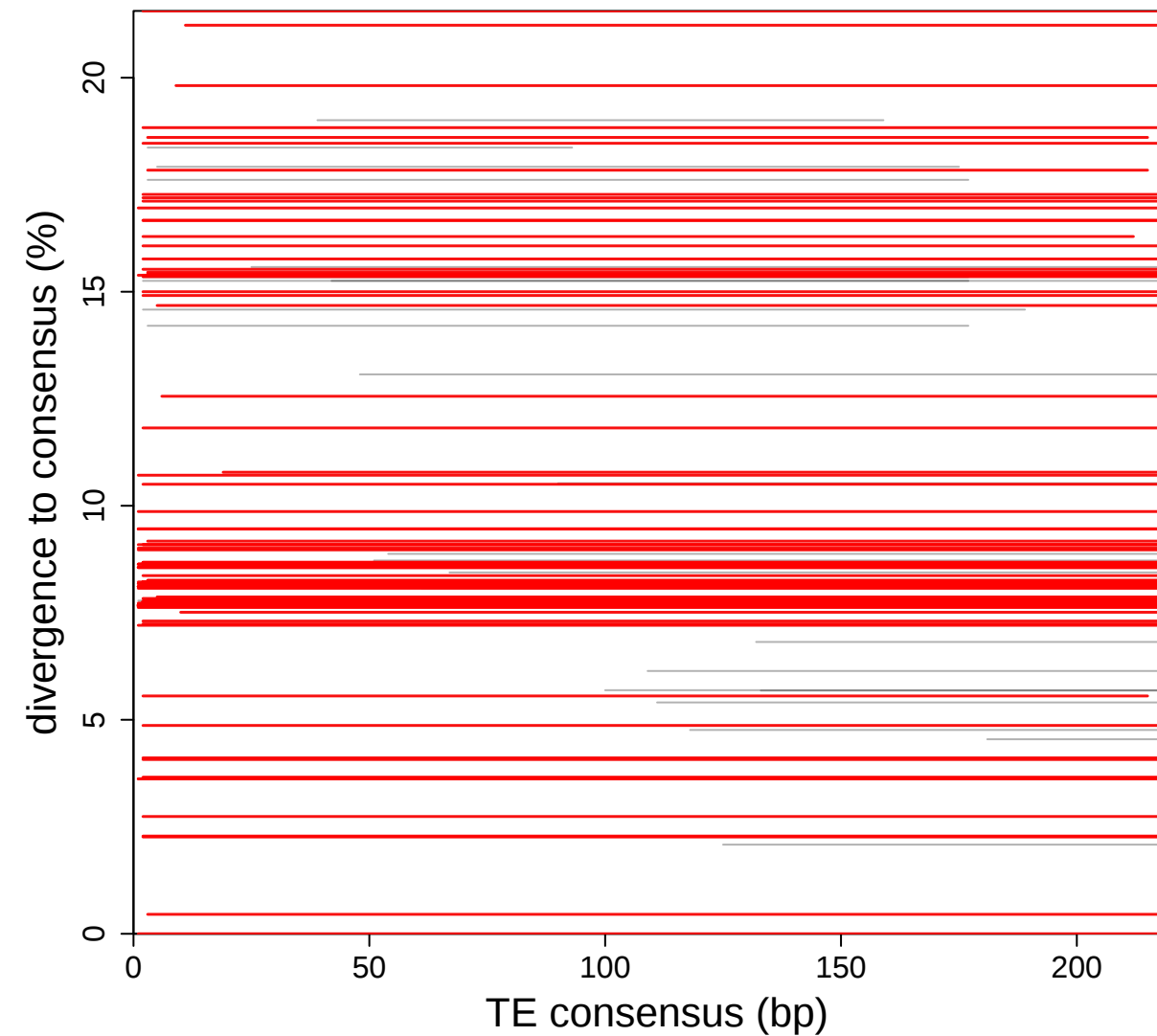


ed\_uf.bed\_g\_1.bed\_fm\_1.bed\_0\_0\_n.bed\_g\_1.bed\_fm\_2.bed\_0\_  
size: 11076bp; fragments: 963; full length: 0 (>=9968.4bp)



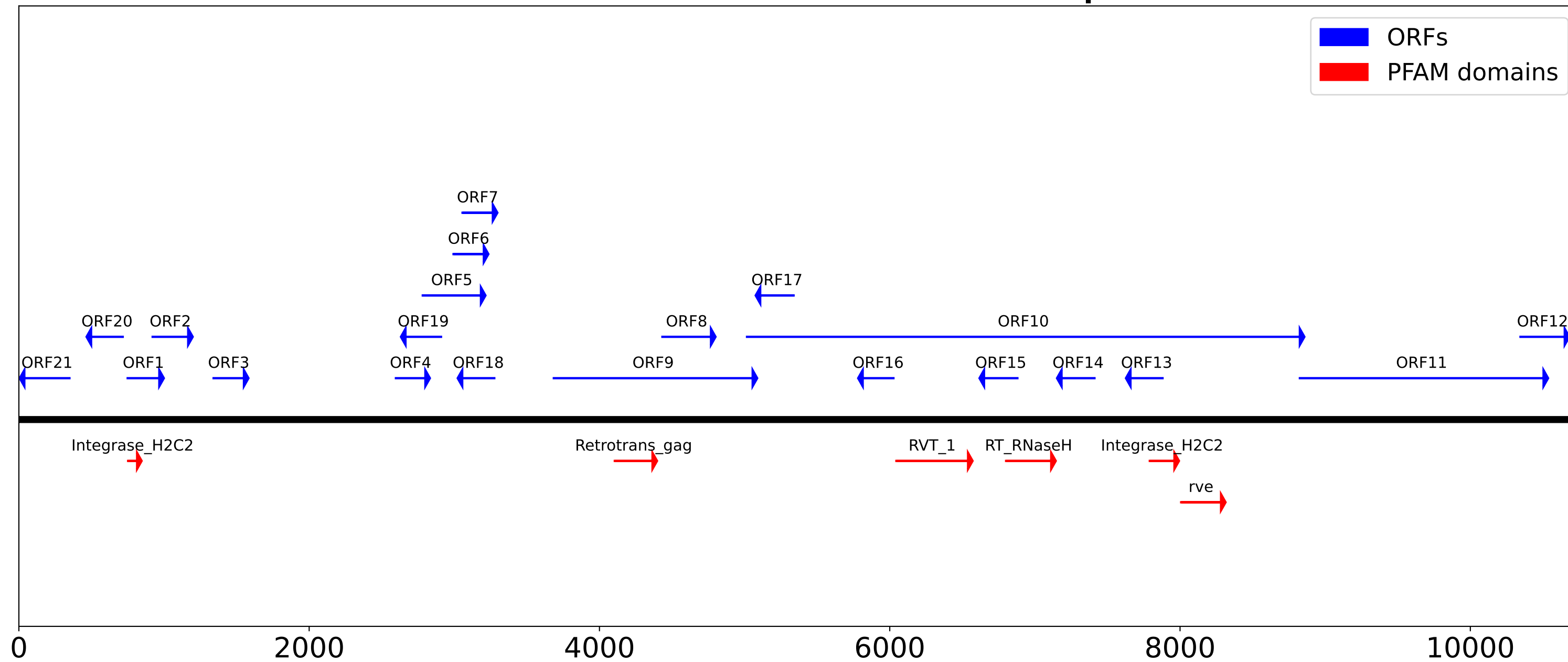
## After TEtrimmer Extended plot Blue lines are boundaries

TE: ltr\_1\_family\_180  
size: 222bp; fragments: 169; full length: 143 ( $\geq 199.8$ bp)



Before TEtrimmer 222 bp

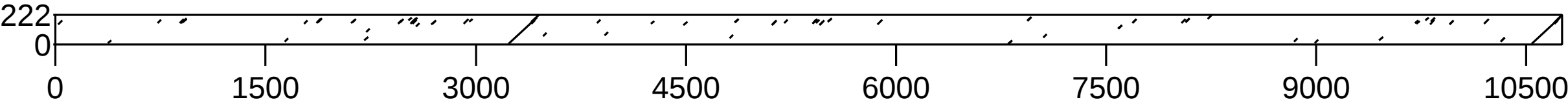
## After TEtrimmer ORF and PFAM domain plot



Dotplot

(windowsize = 25, threshold = 50.00 09/10/25)

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)