

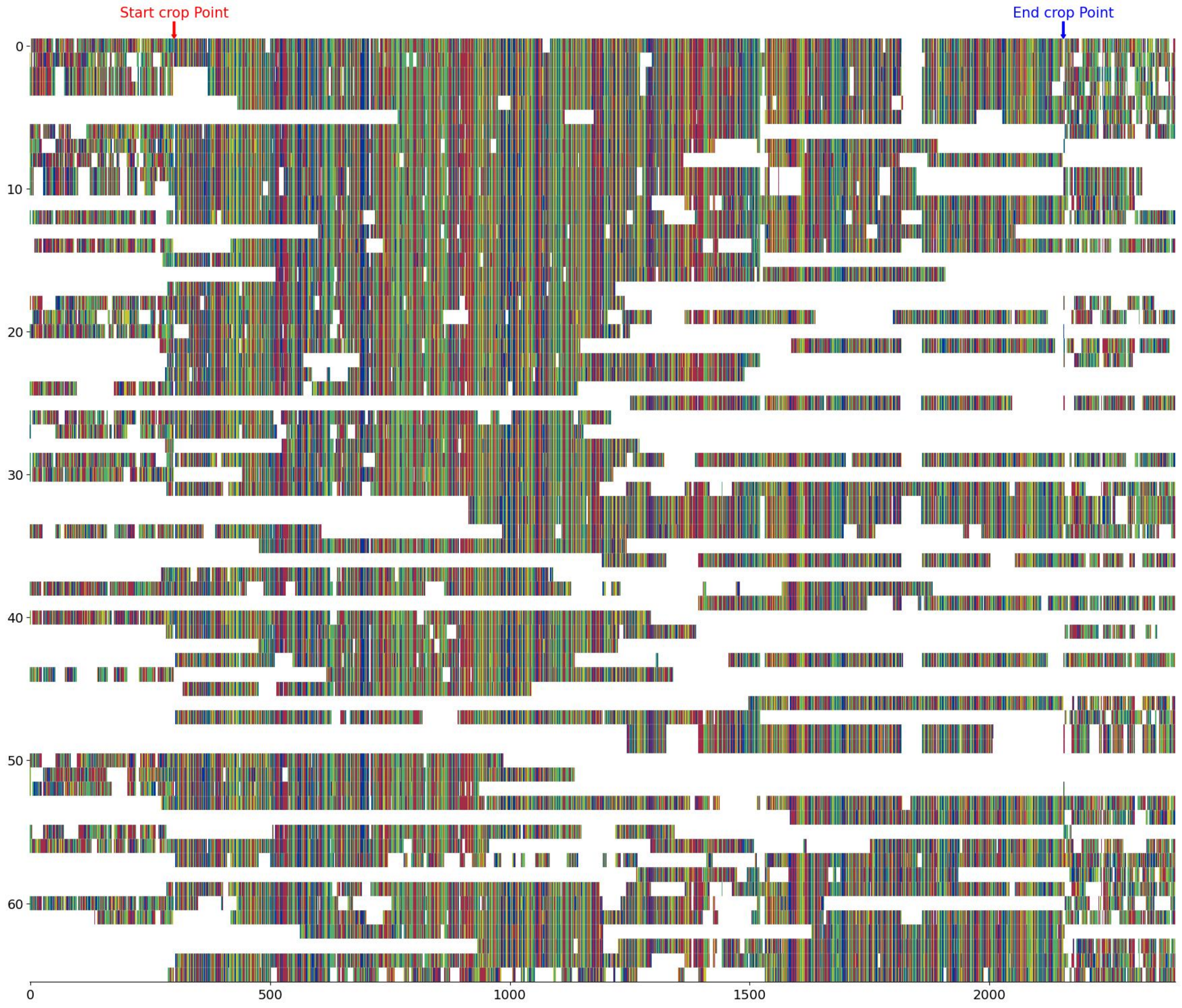
Start crop Point

End crop Point

Genomic tracks showing DNA sequence alignment (A, C, G, T) and variant calls (red and green markers) across a region. The tracks are organized into two main sections, each containing multiple rows of data. The top section displays a large block of sequence data with numerous variant calls. The bottom section shows a smaller block of sequence data with fewer variant calls. The tracks are labeled with coordinates (e.g., 1000000, 1000100, 1000200) and variant call format (VCF) strings (e.g., chr1:1000000:G>A:0.5).

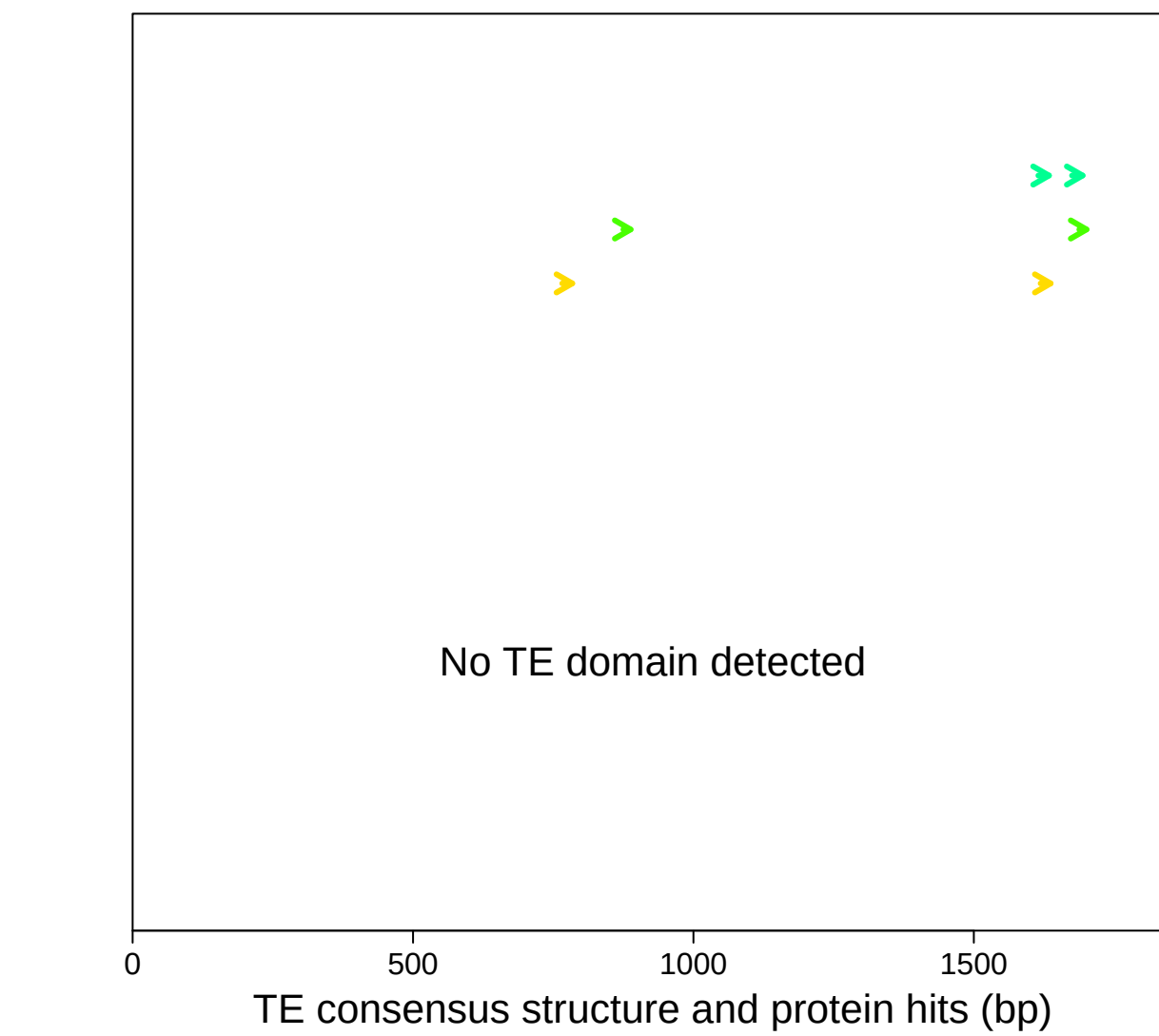
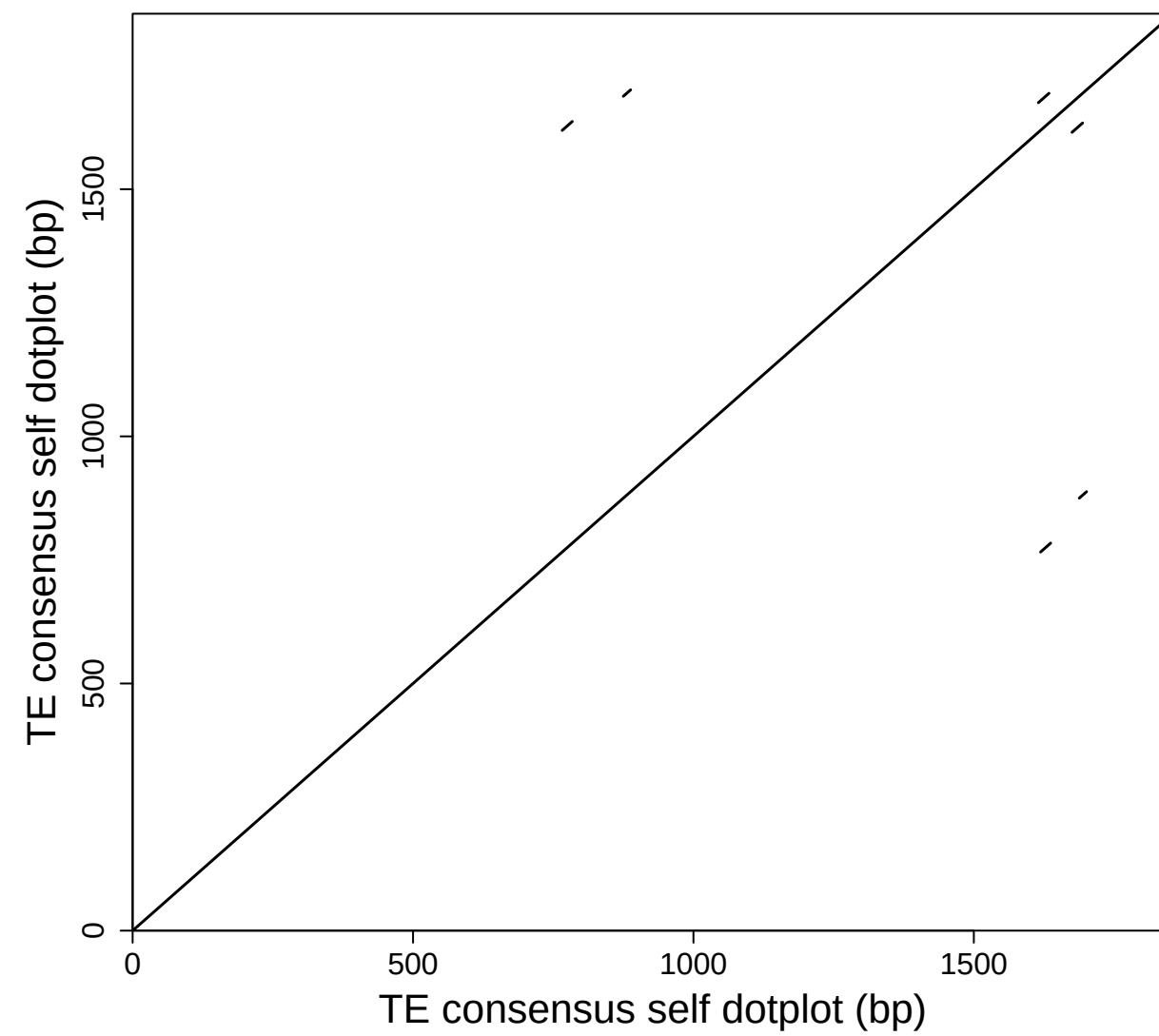
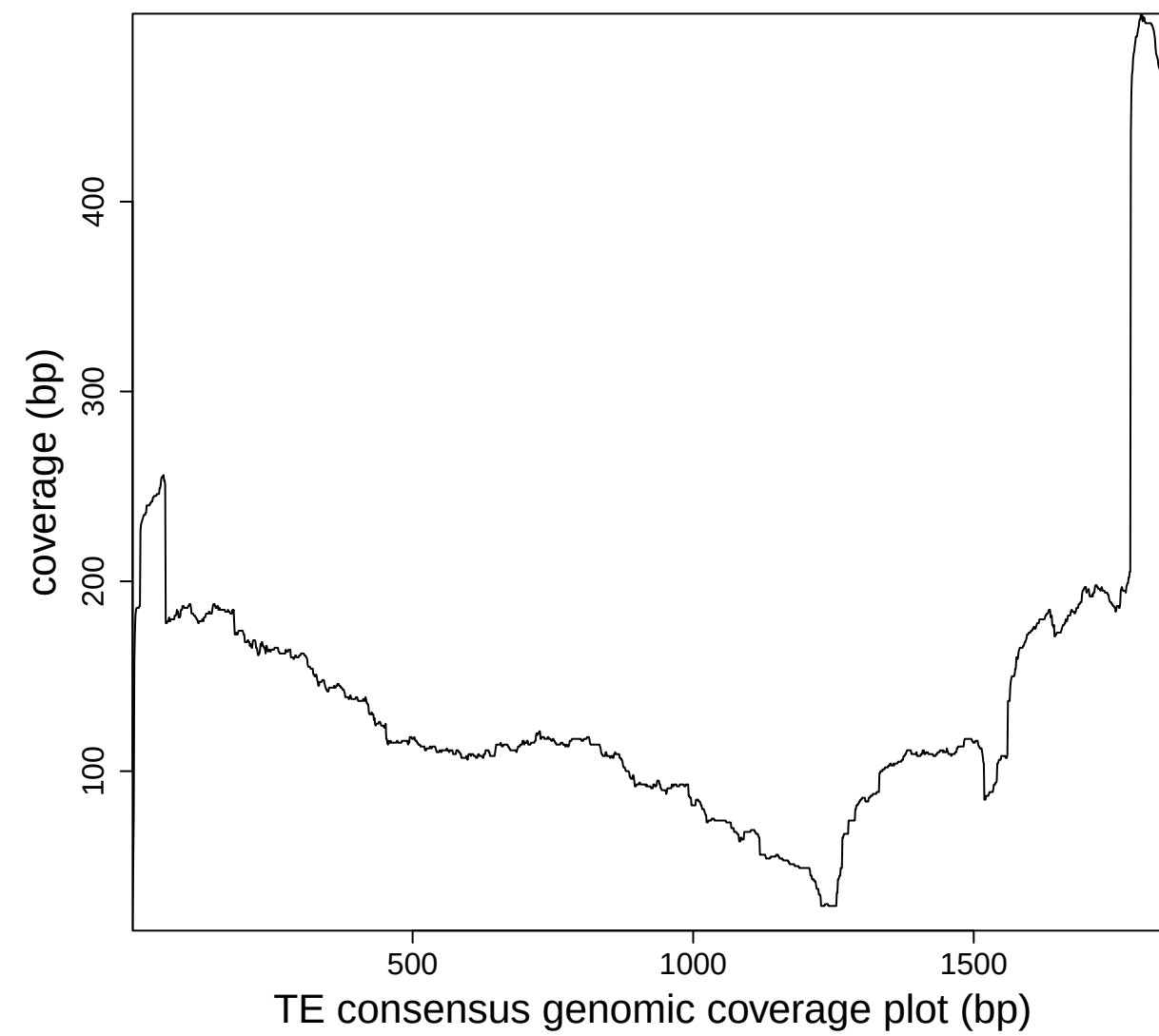
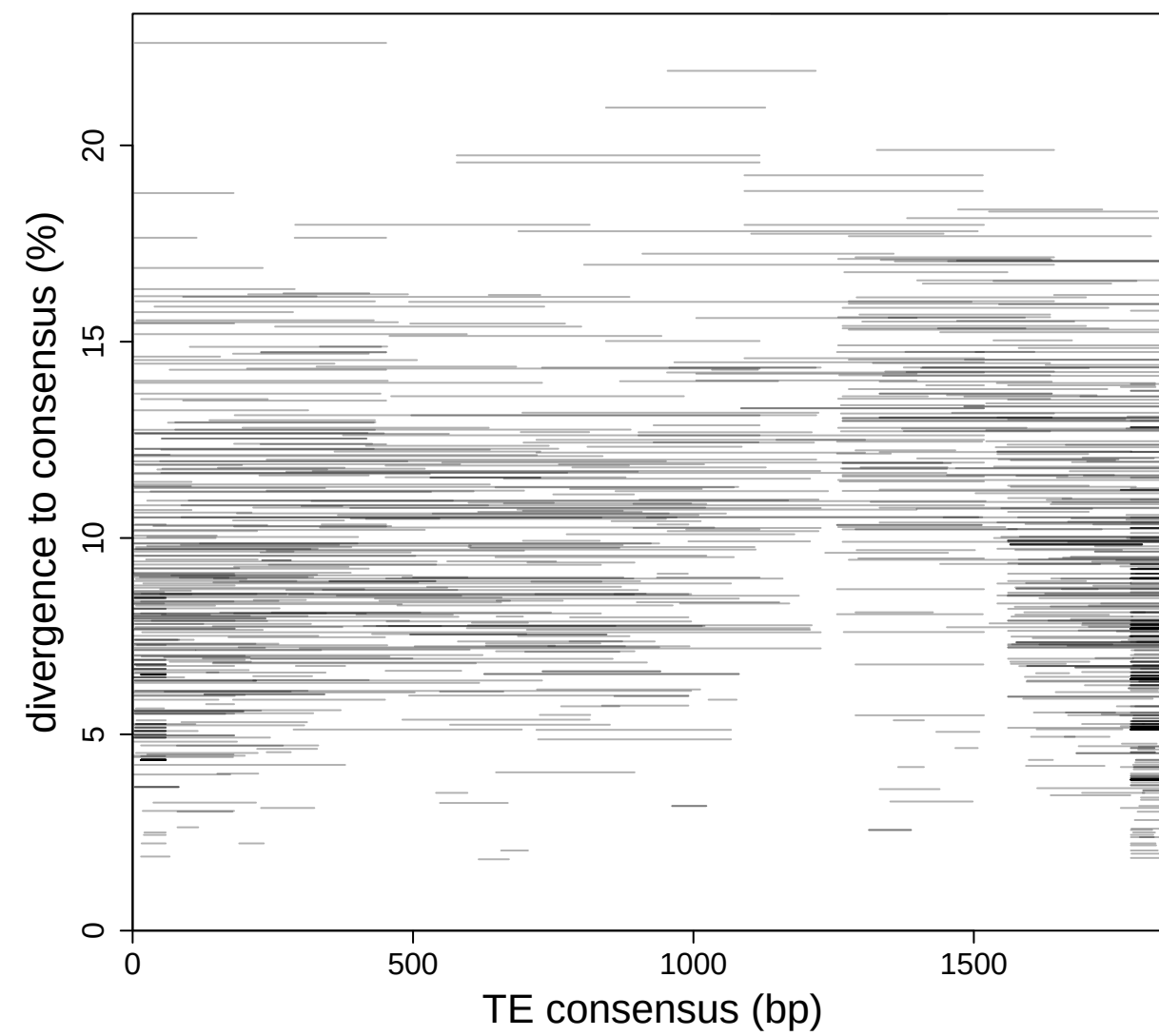
Start crop Point

End crop Point



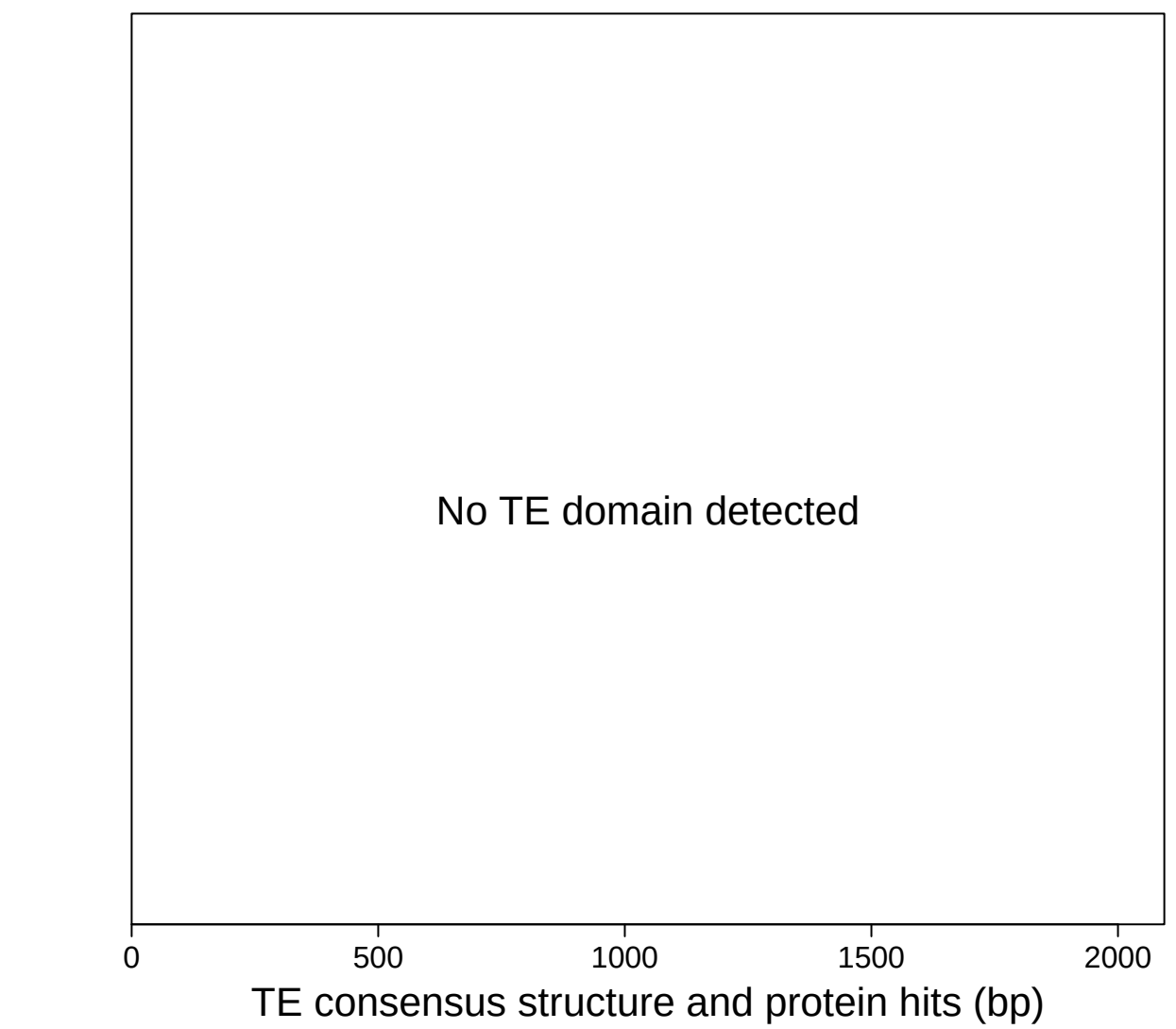
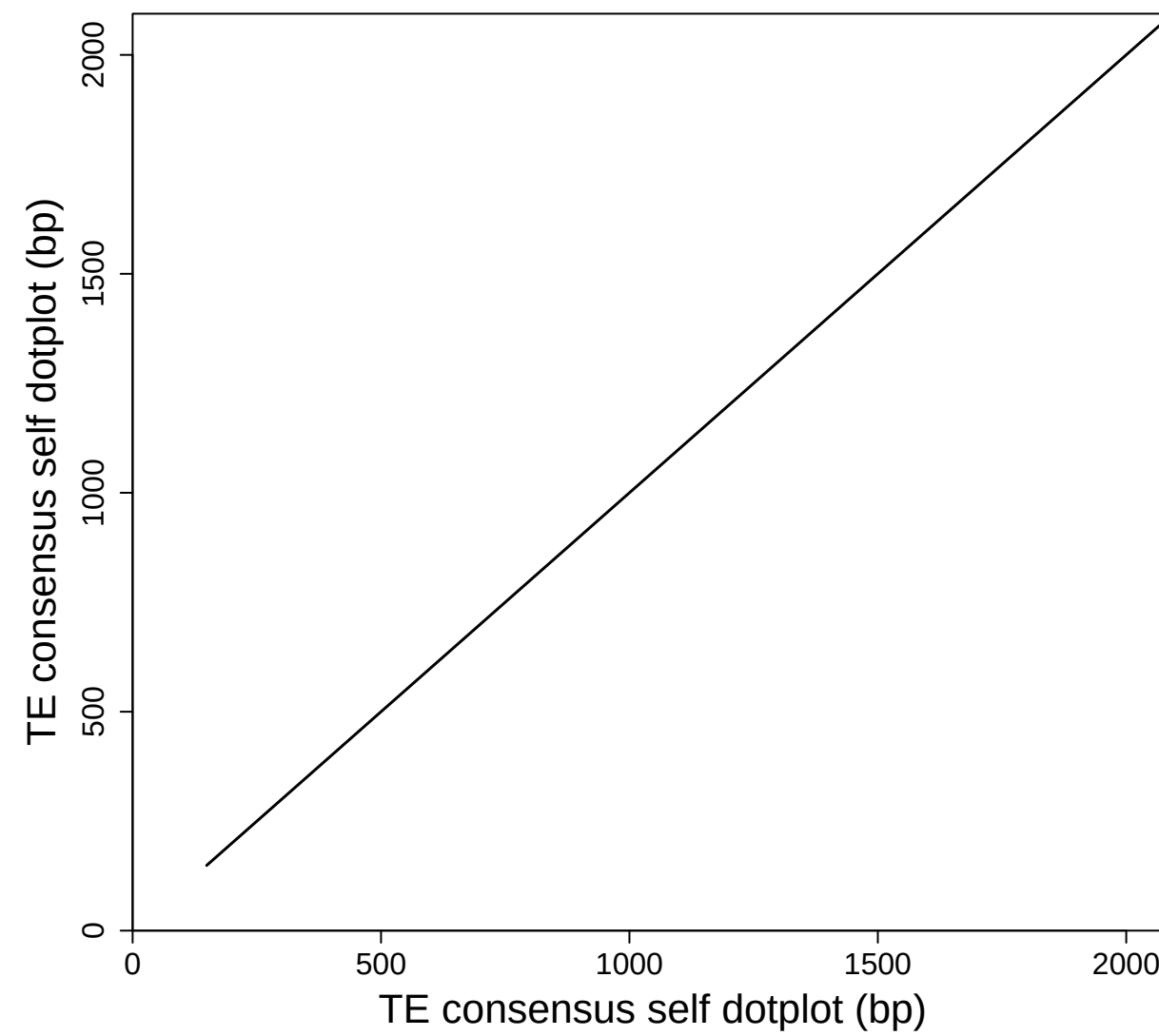
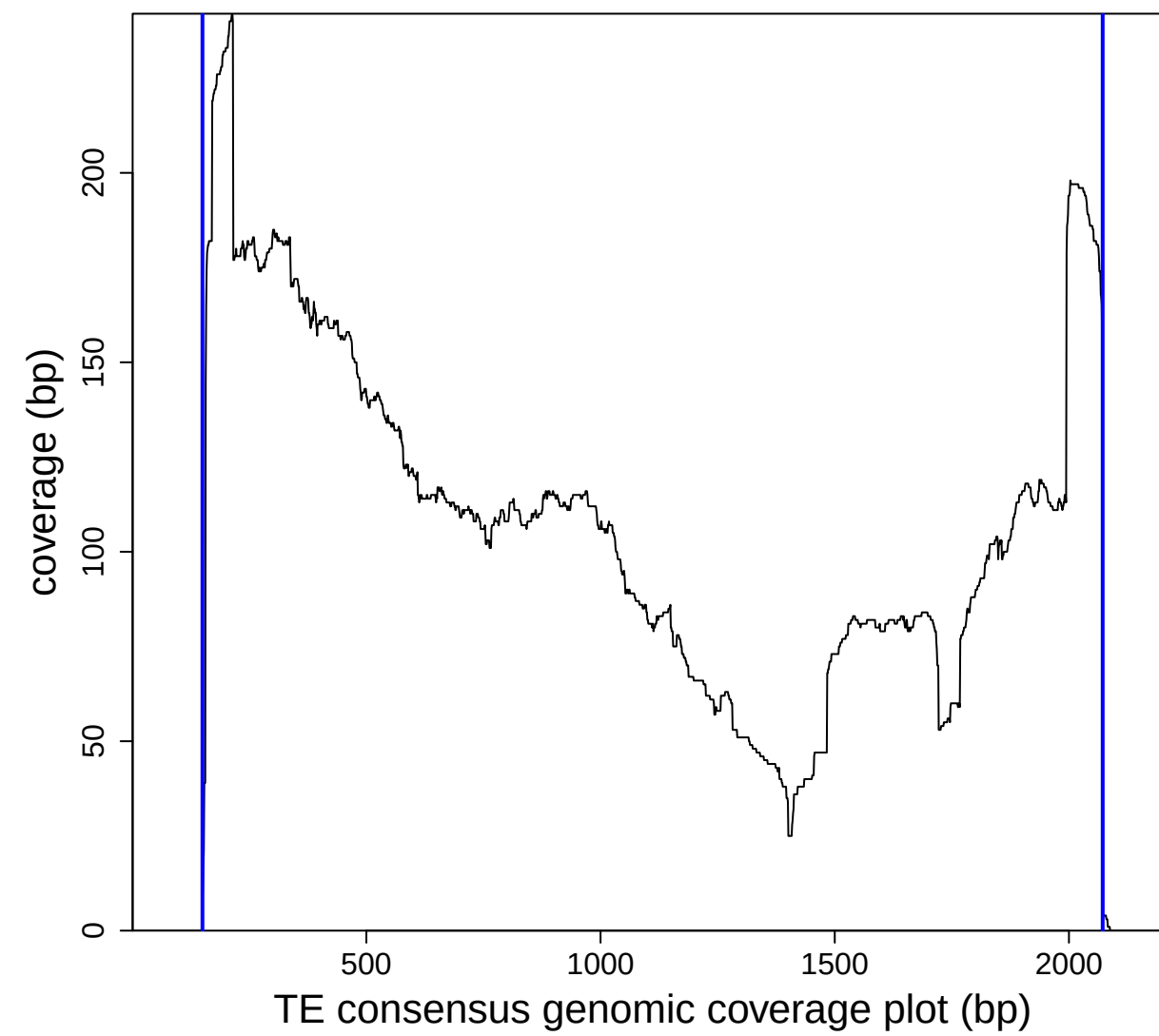
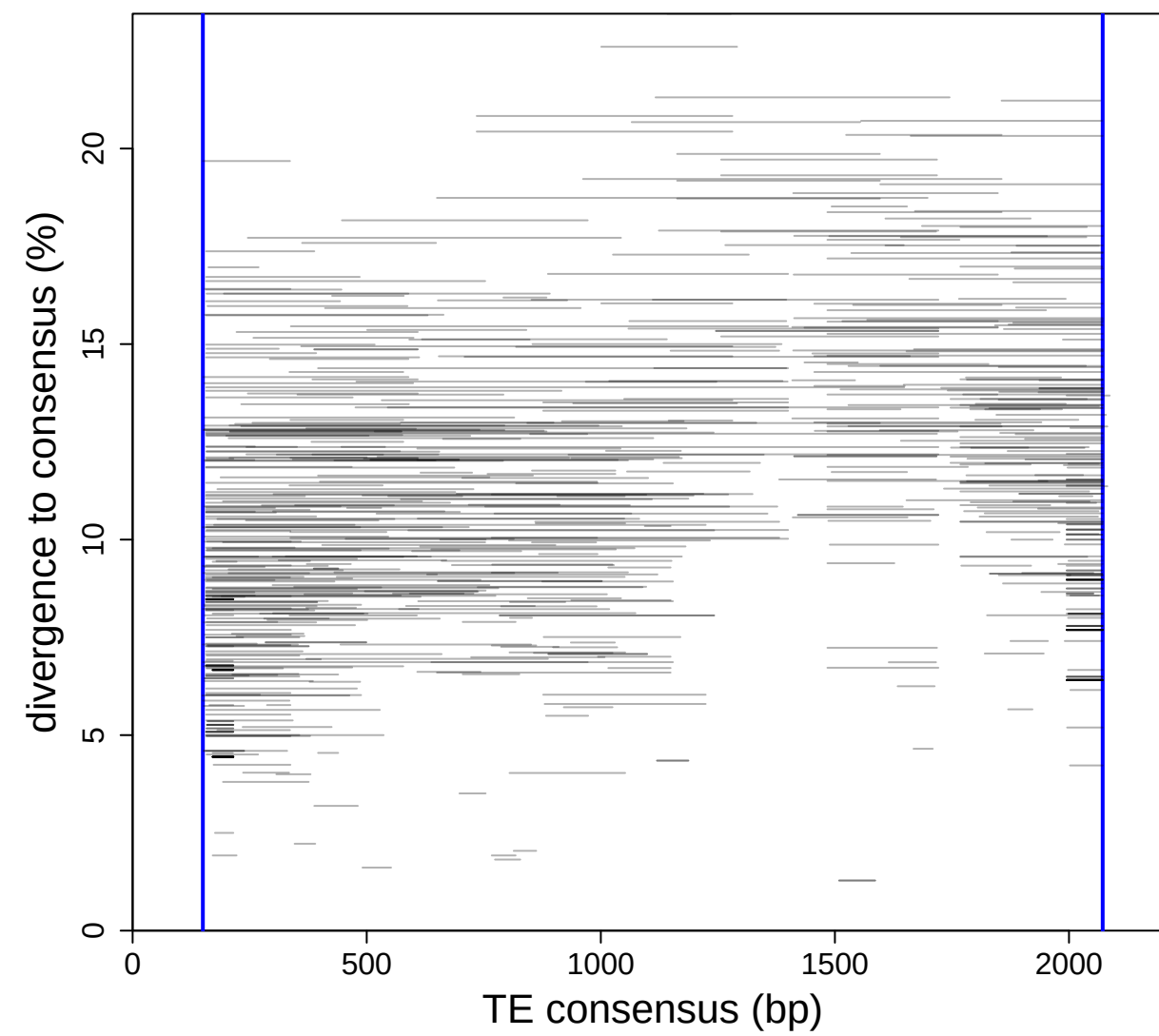
g_1.bed fm_1.bed 0 0 n.bed g_1.bed fm_2.bed 0 0 bcln.fa ε
size: 1855bp; fragments: 1099; full length: 0 (>=1669.5bp)

After TEtrimmer 1855 bp



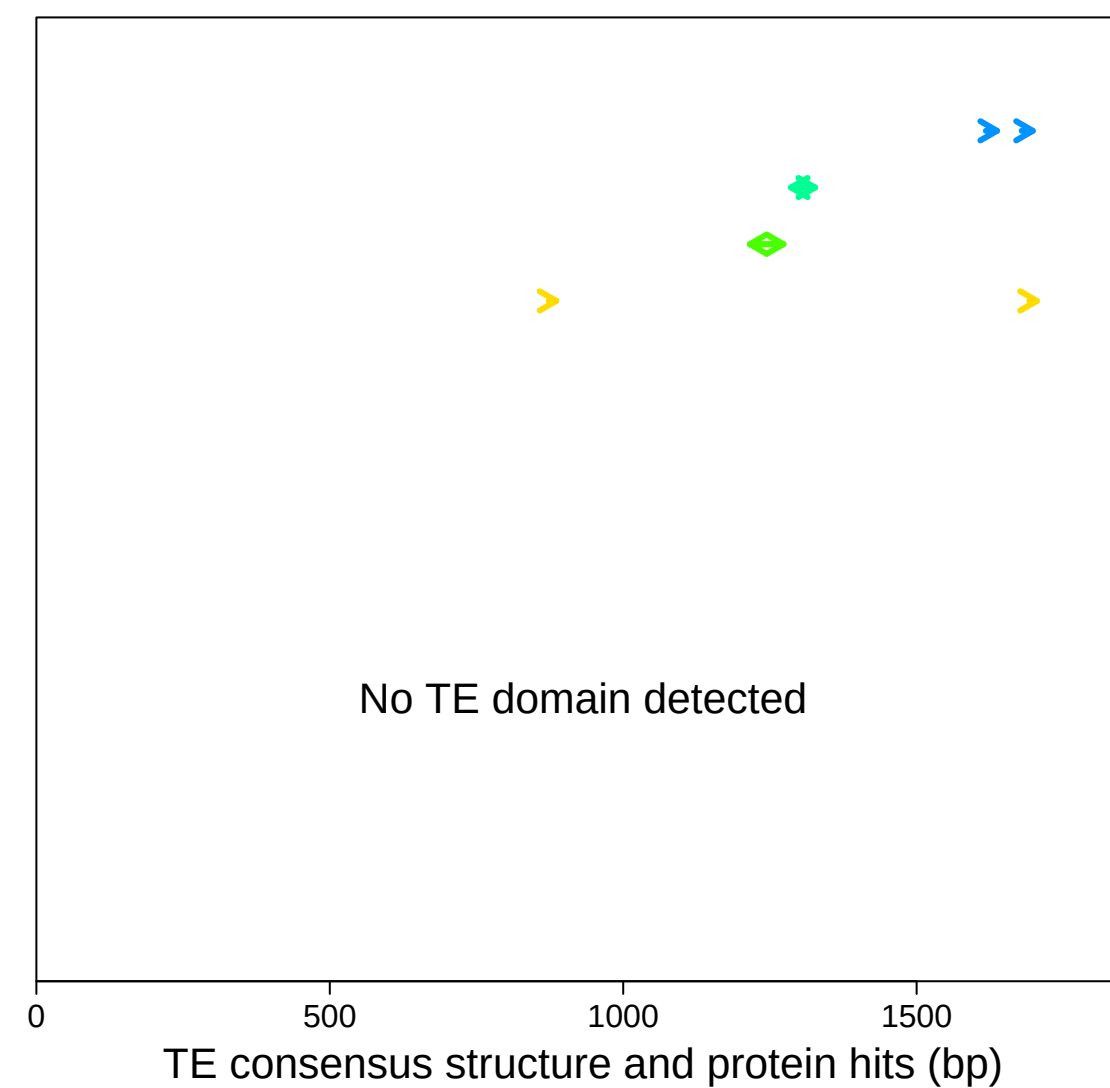
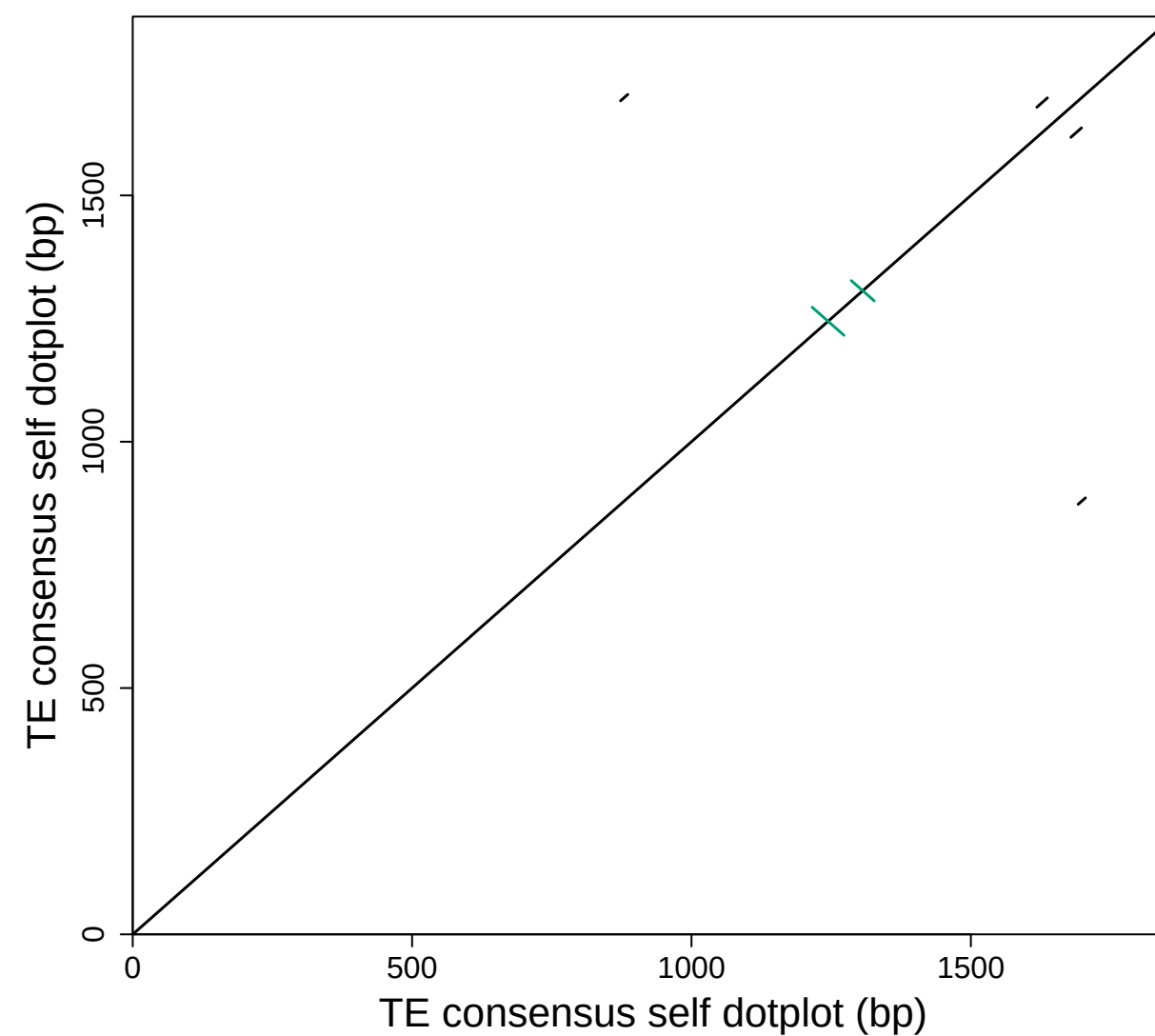
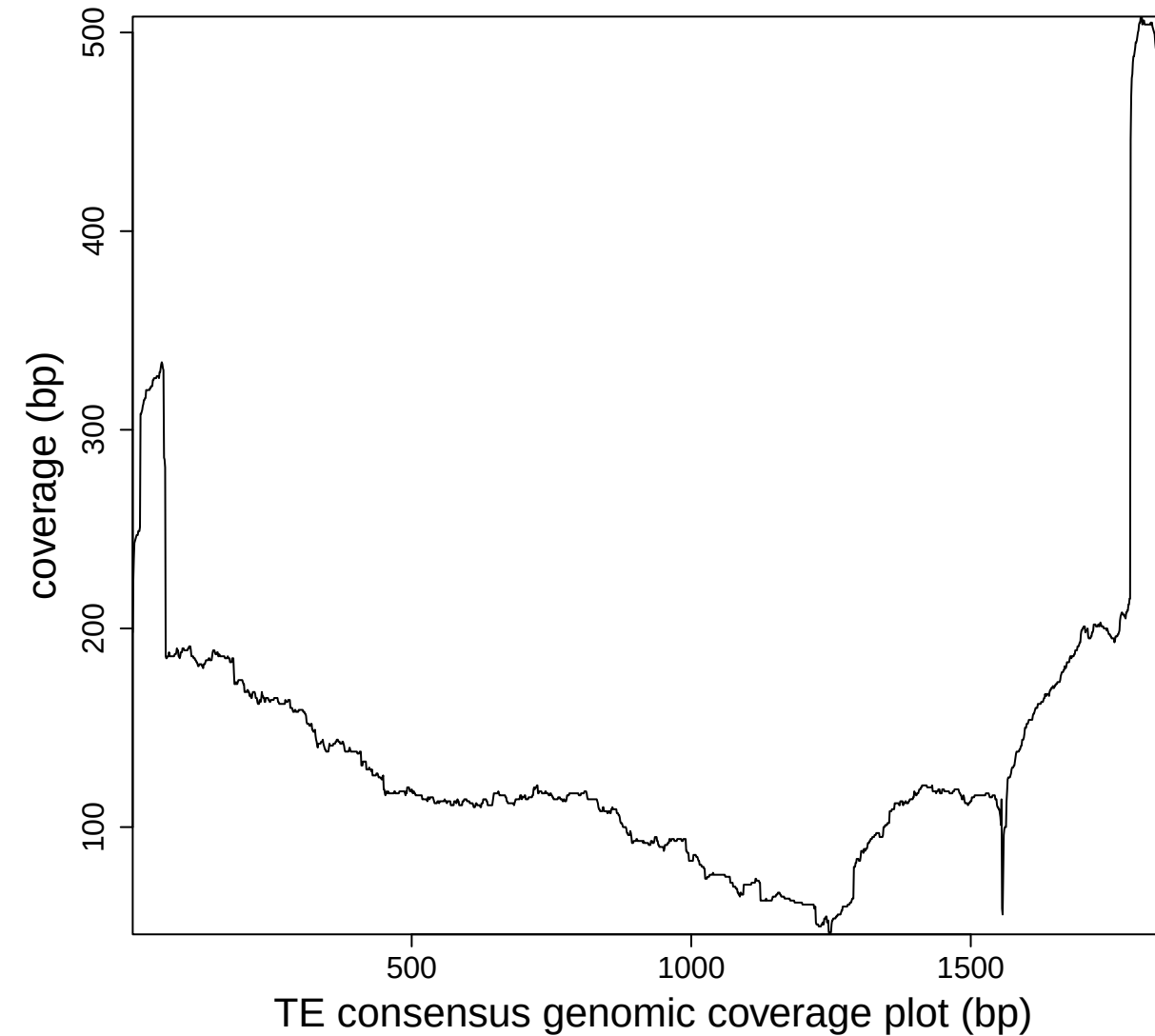
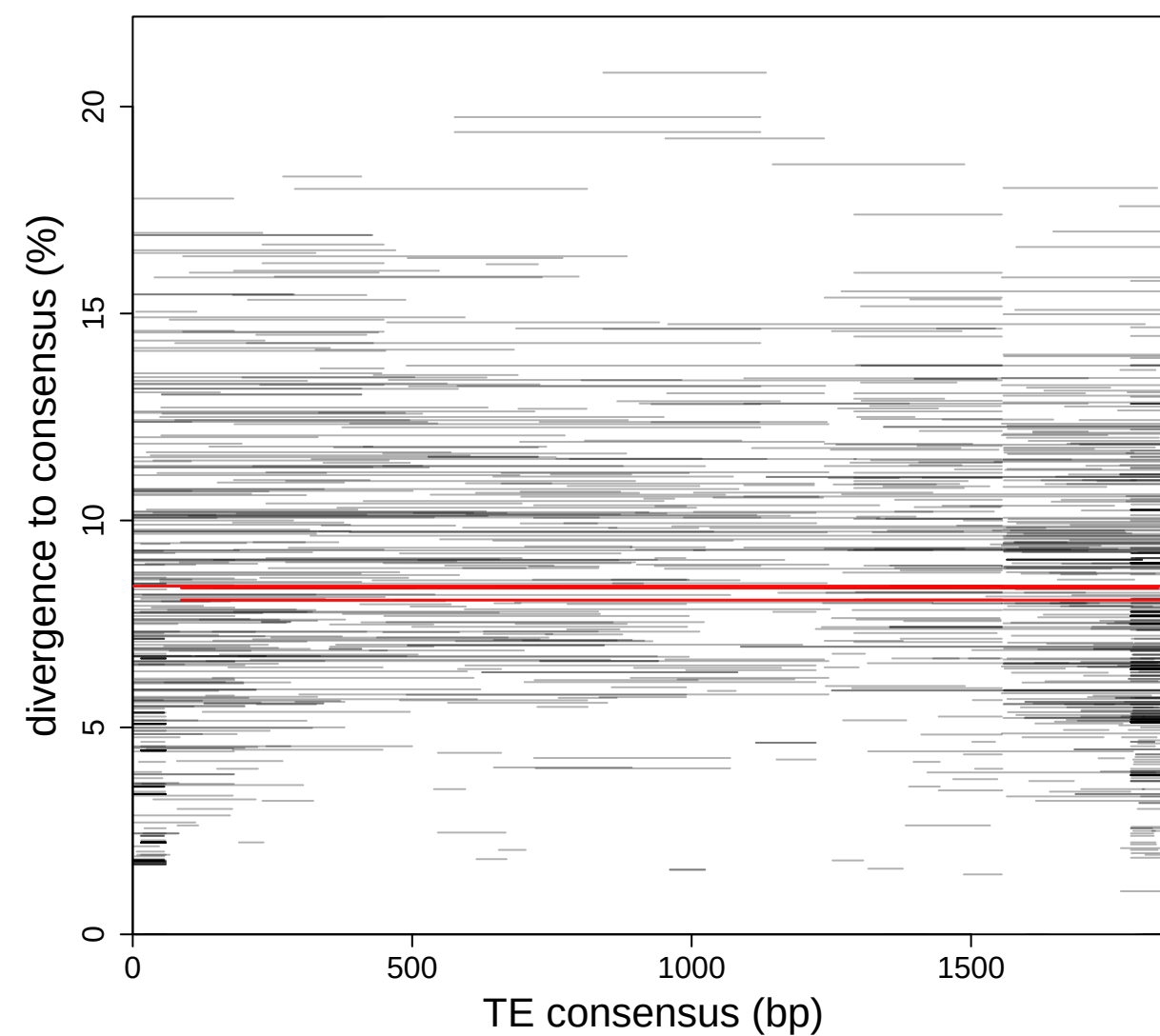
f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bc
size: 2222bp; fragments: 723; full length: 0 (>=1999.8bp)

After TEtrimmer Extended plot Blue lines are boundaries

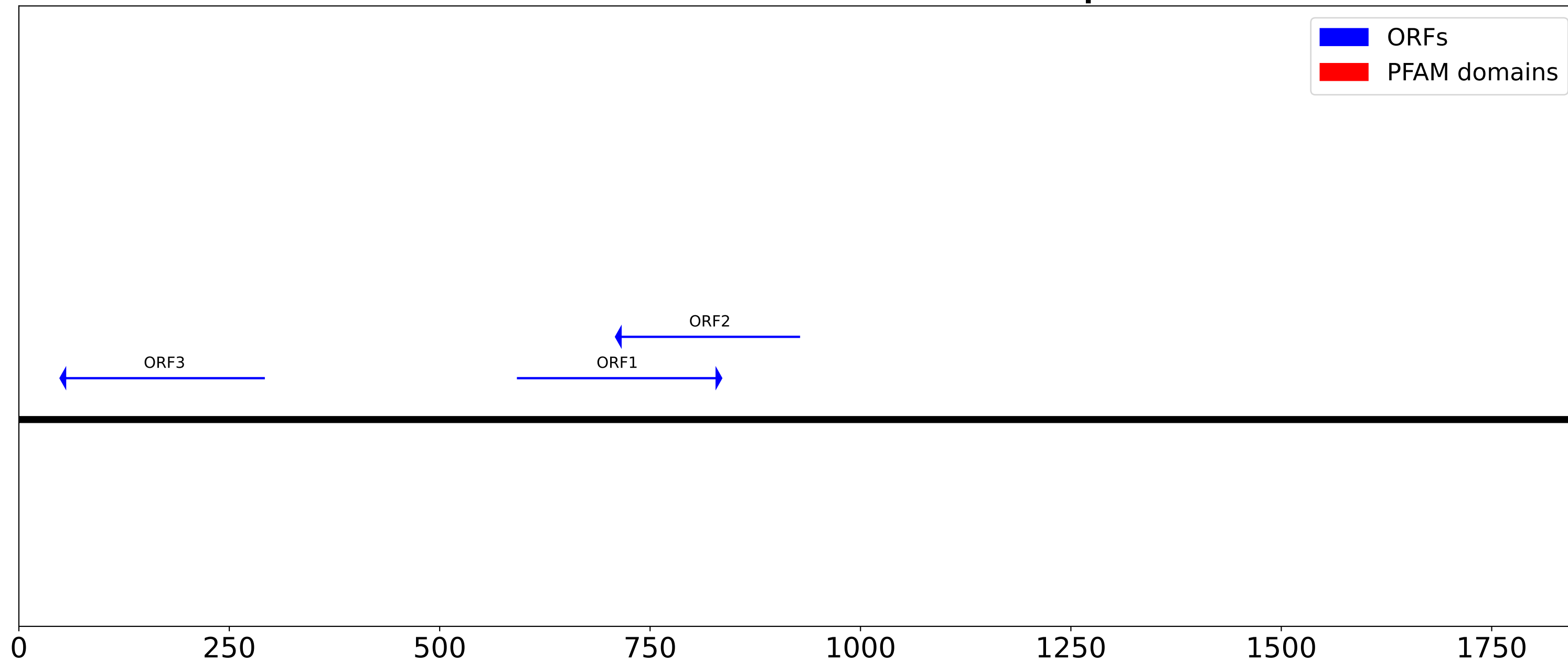


TE: rnd_5_family_3964
size: 1863bp; fragments: 1230; full length: 3 (≥ 1676.7 bp)

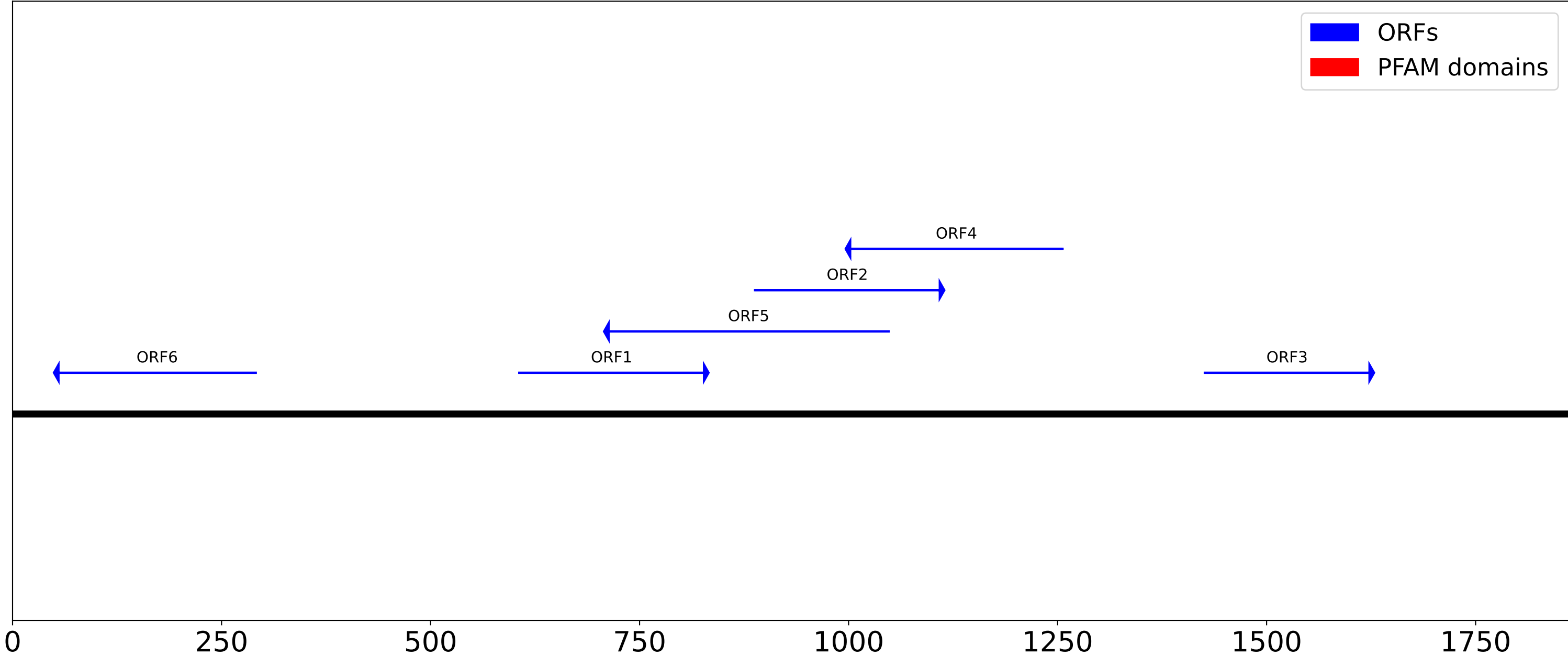
Before TEtrimmer 1863 bp



After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

