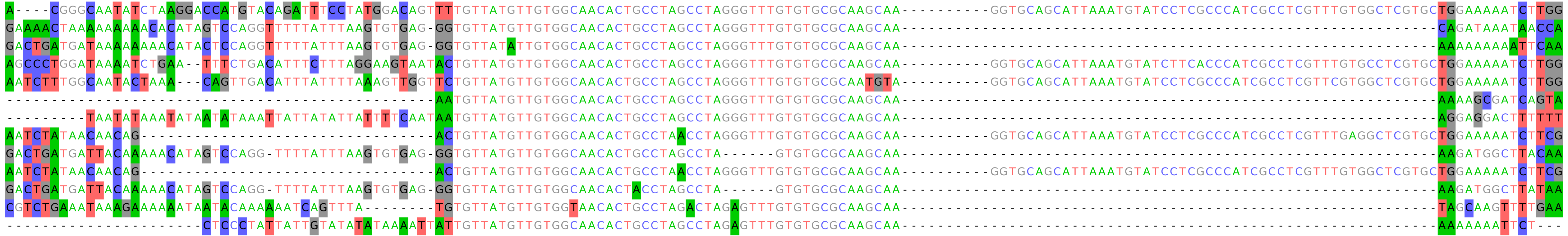
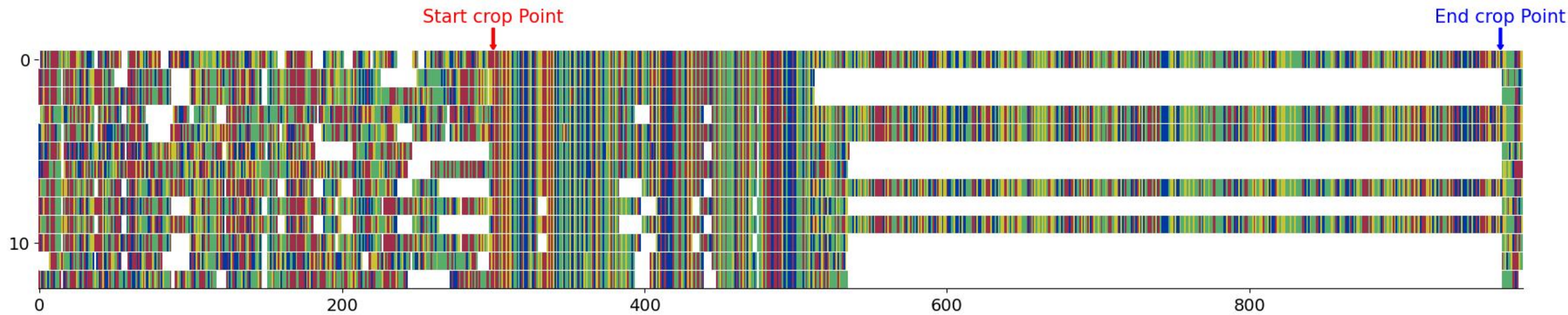


Start crop Point

End crop Point

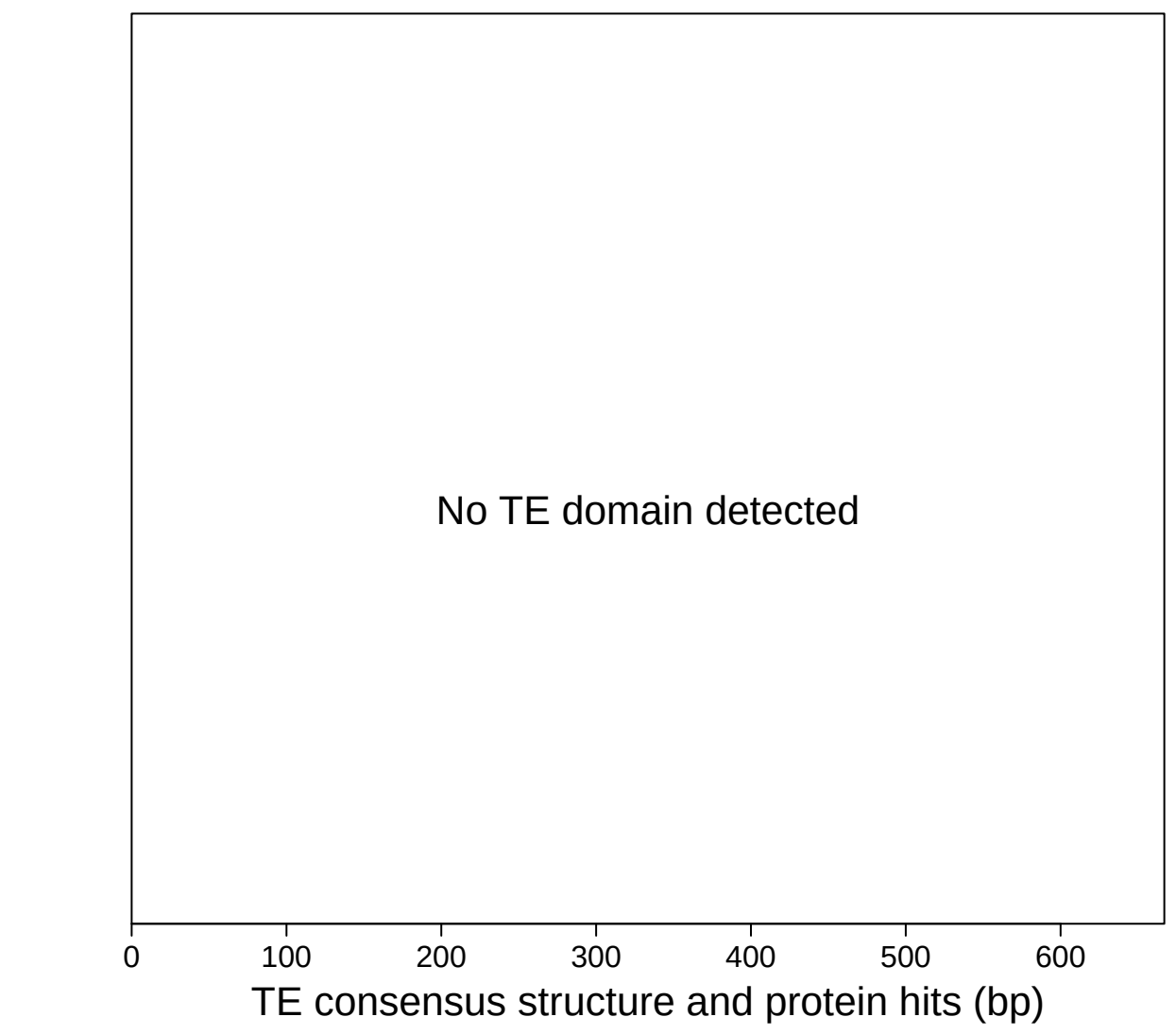
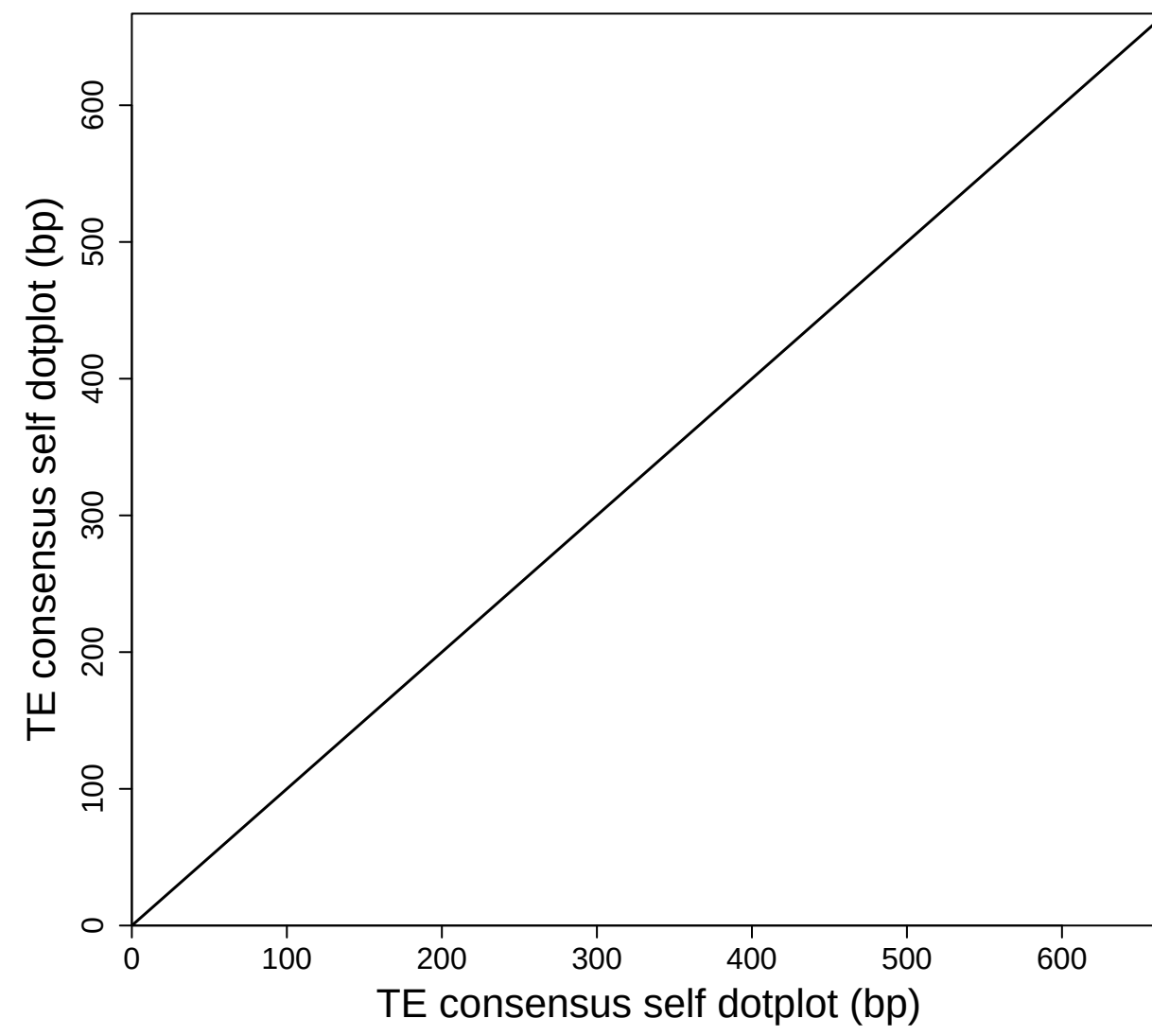
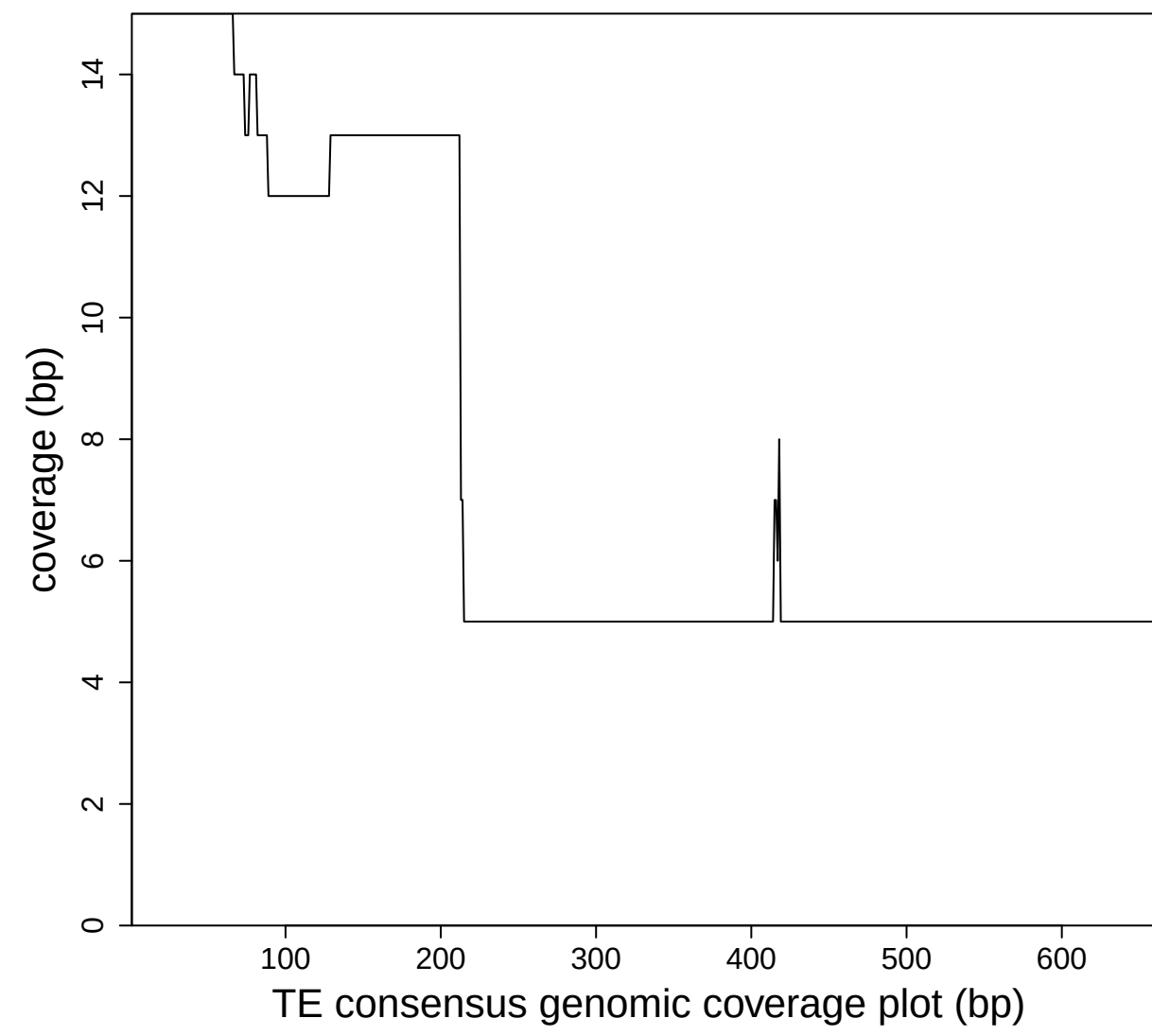
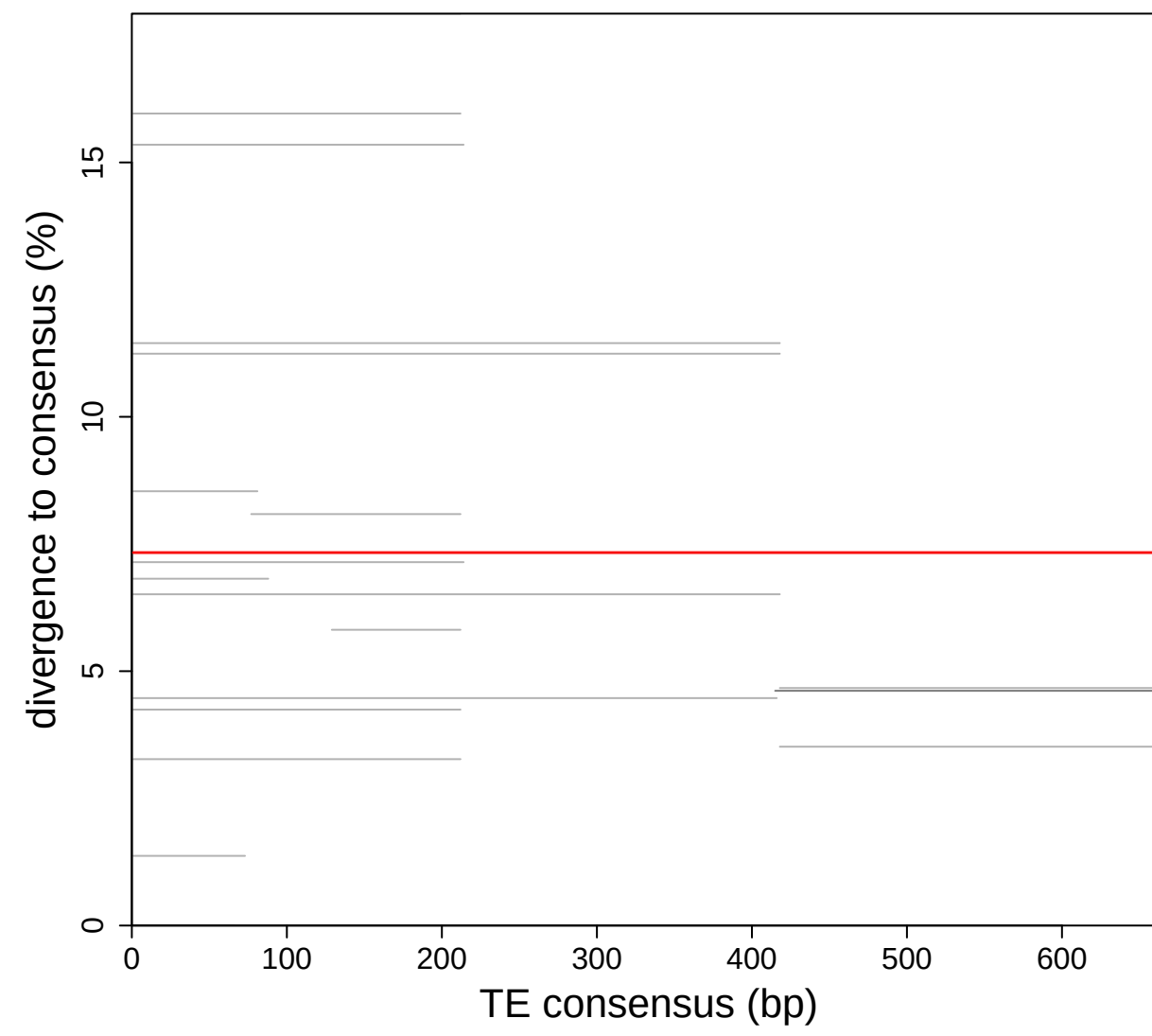
MSA length = 667





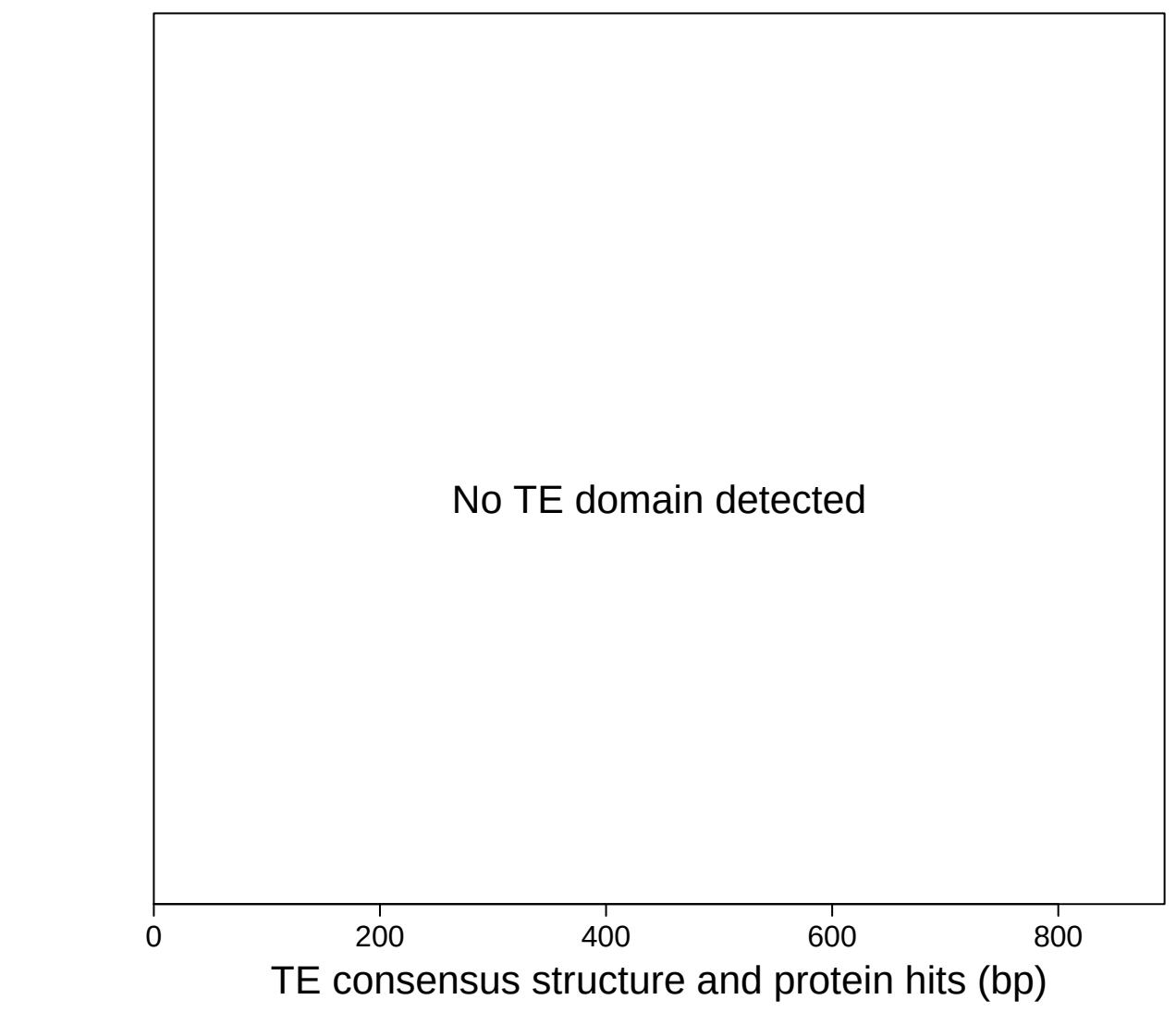
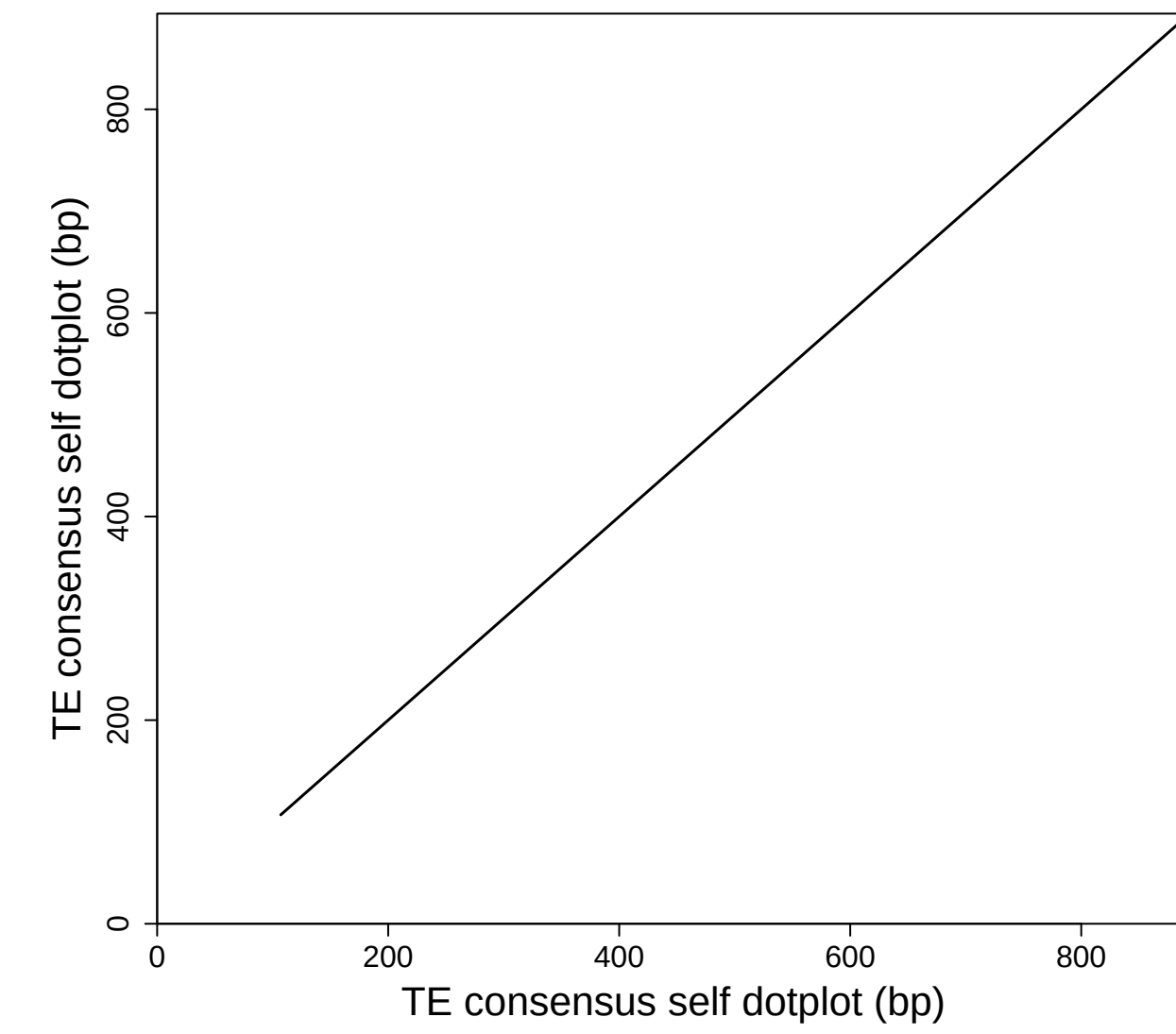
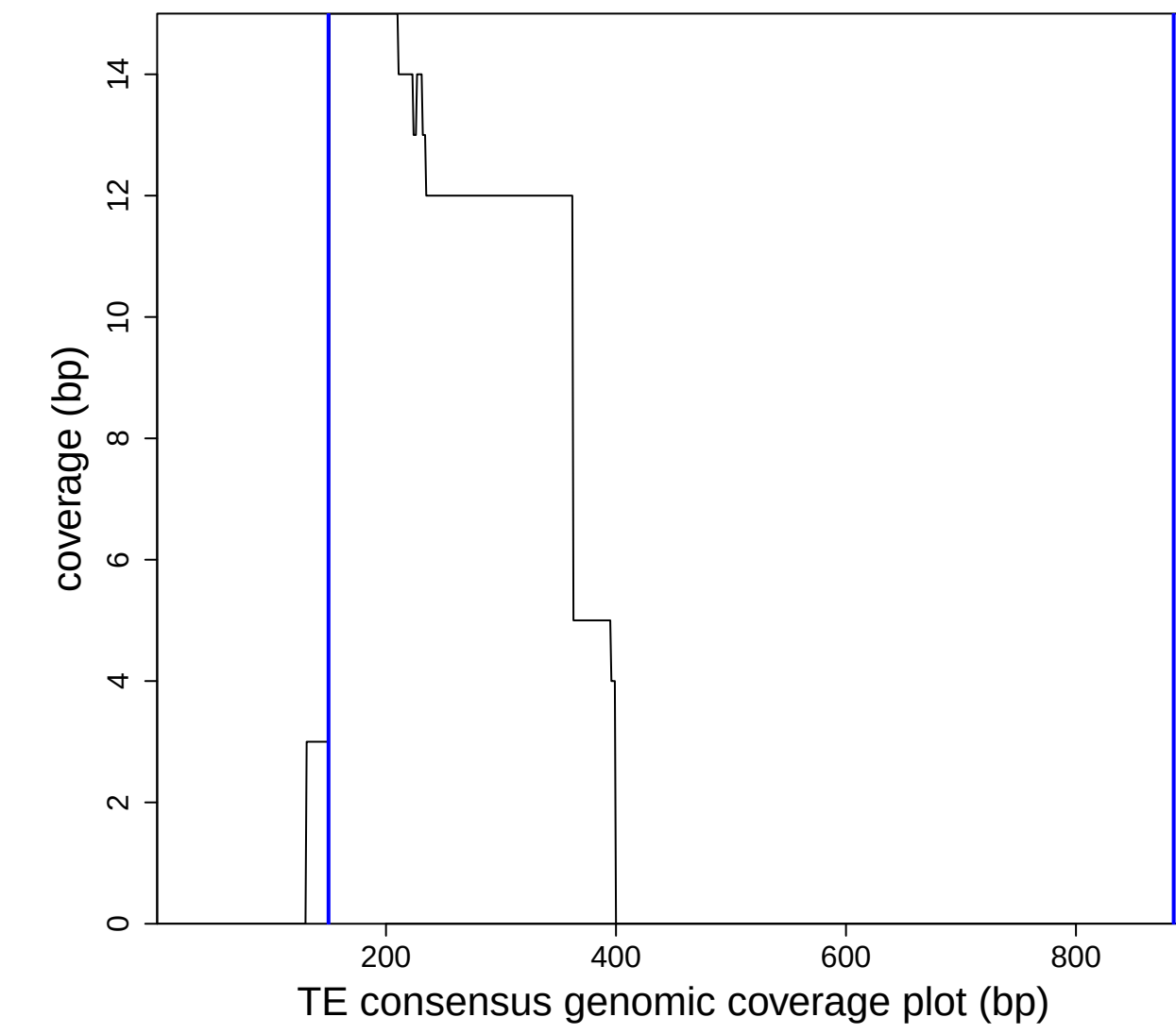
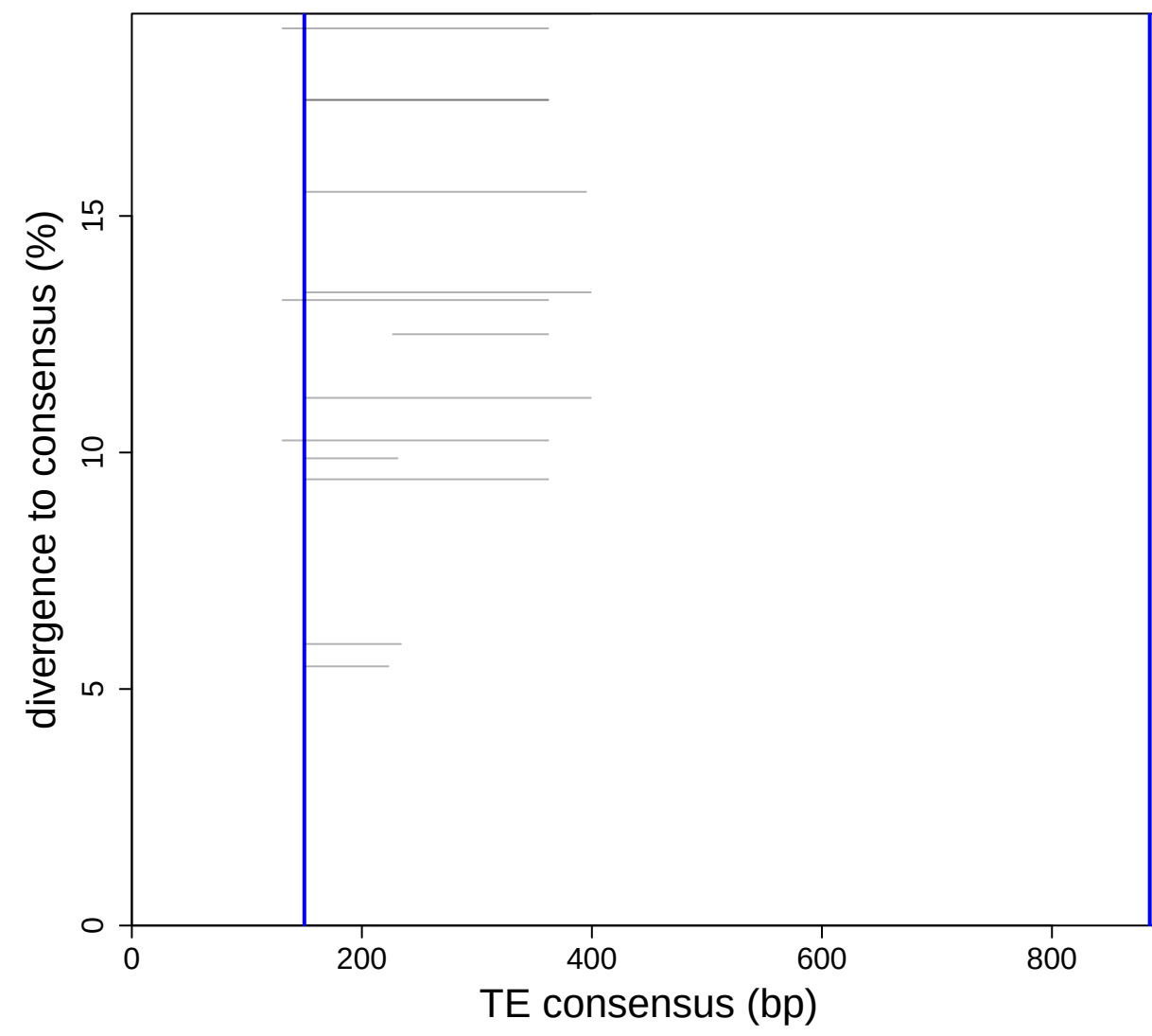
b.bed_uf.bed_g_1.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa
size: 667bp; fragments: 21; full length: 1 (>=600.3bp)

After TEtrimmer 667 bp

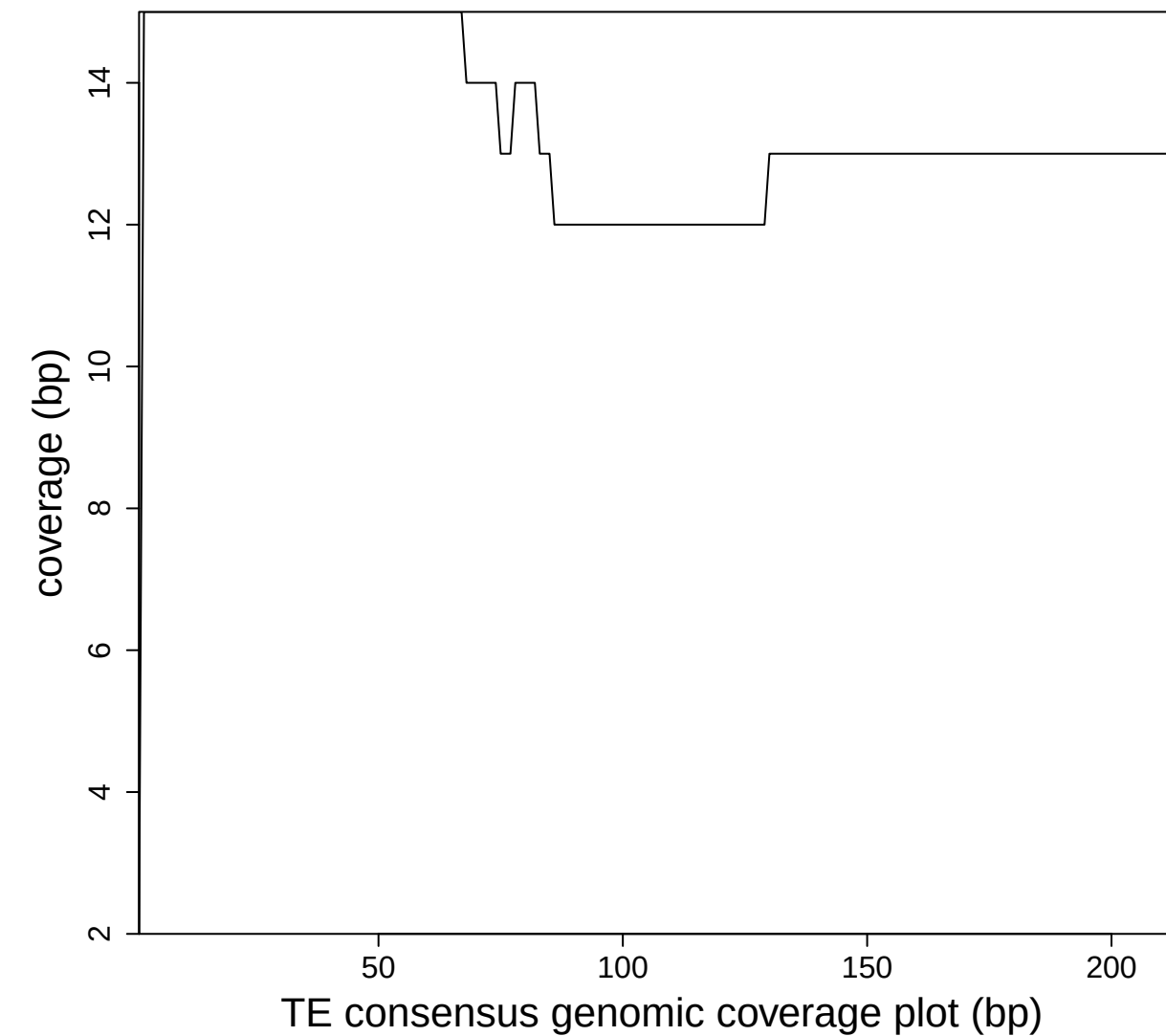
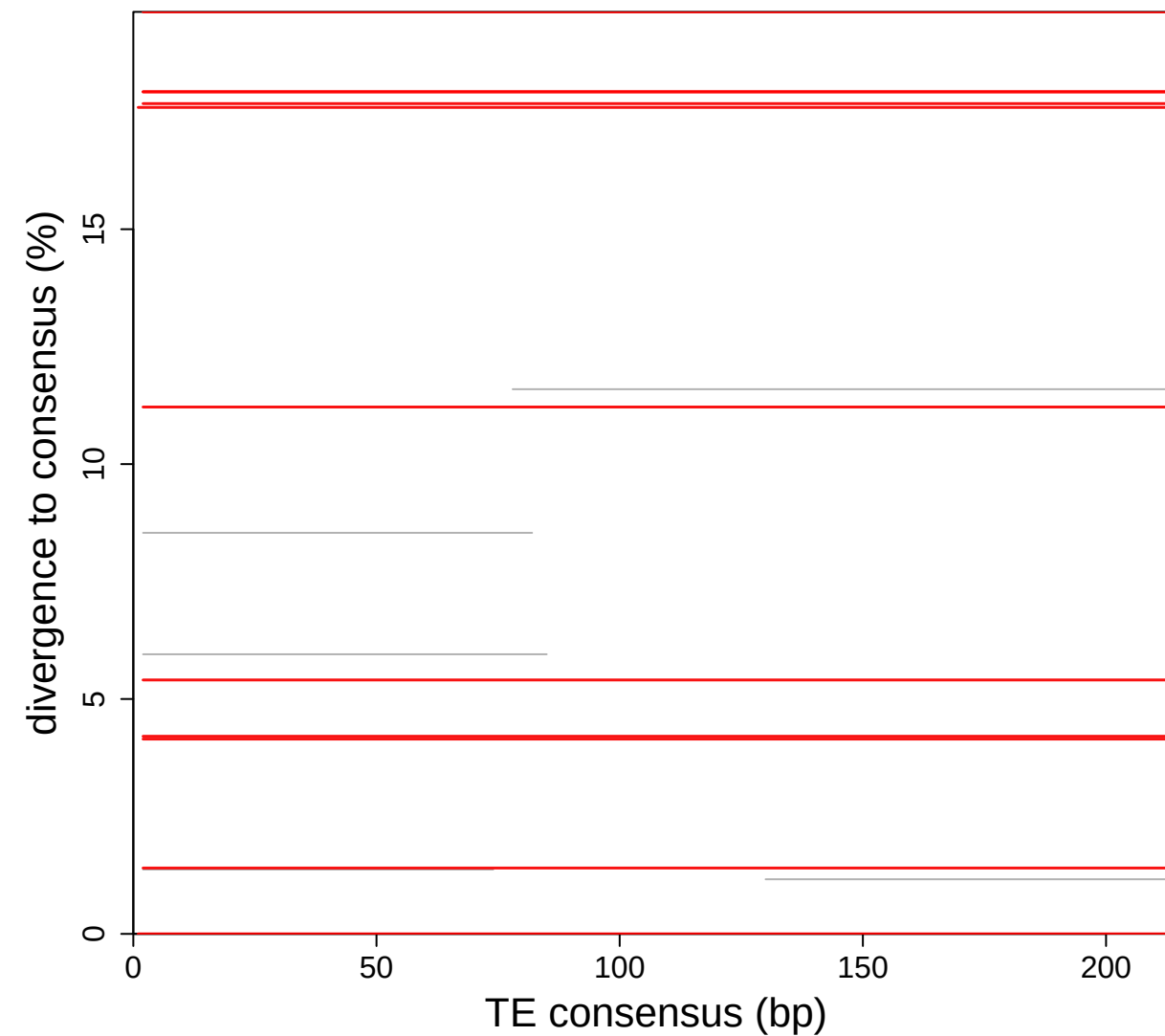


.fasta.b.bed_uf.bed_g_1.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 899bp; fragments: 16; full length: 0 (>=809.1bp)

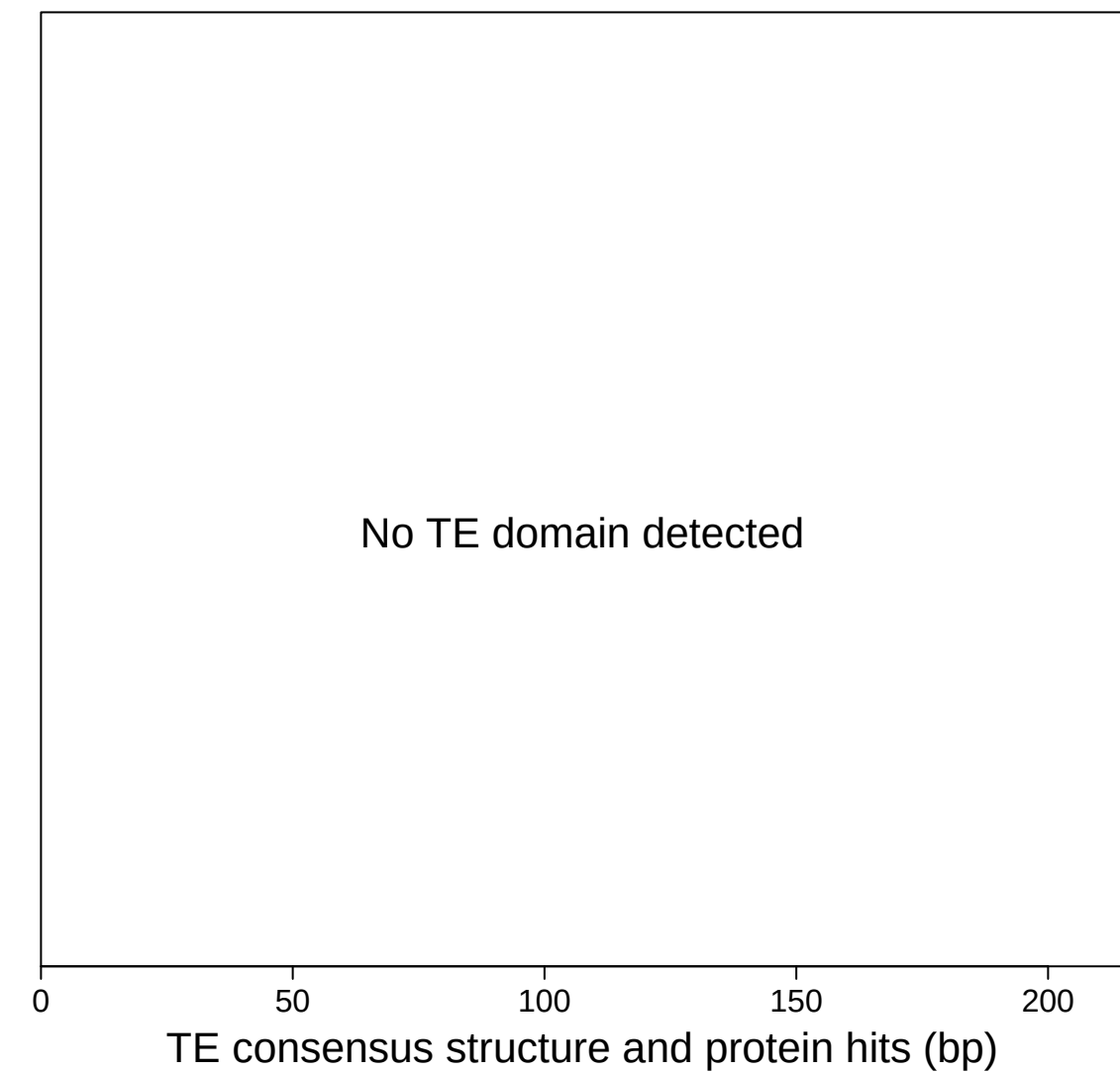
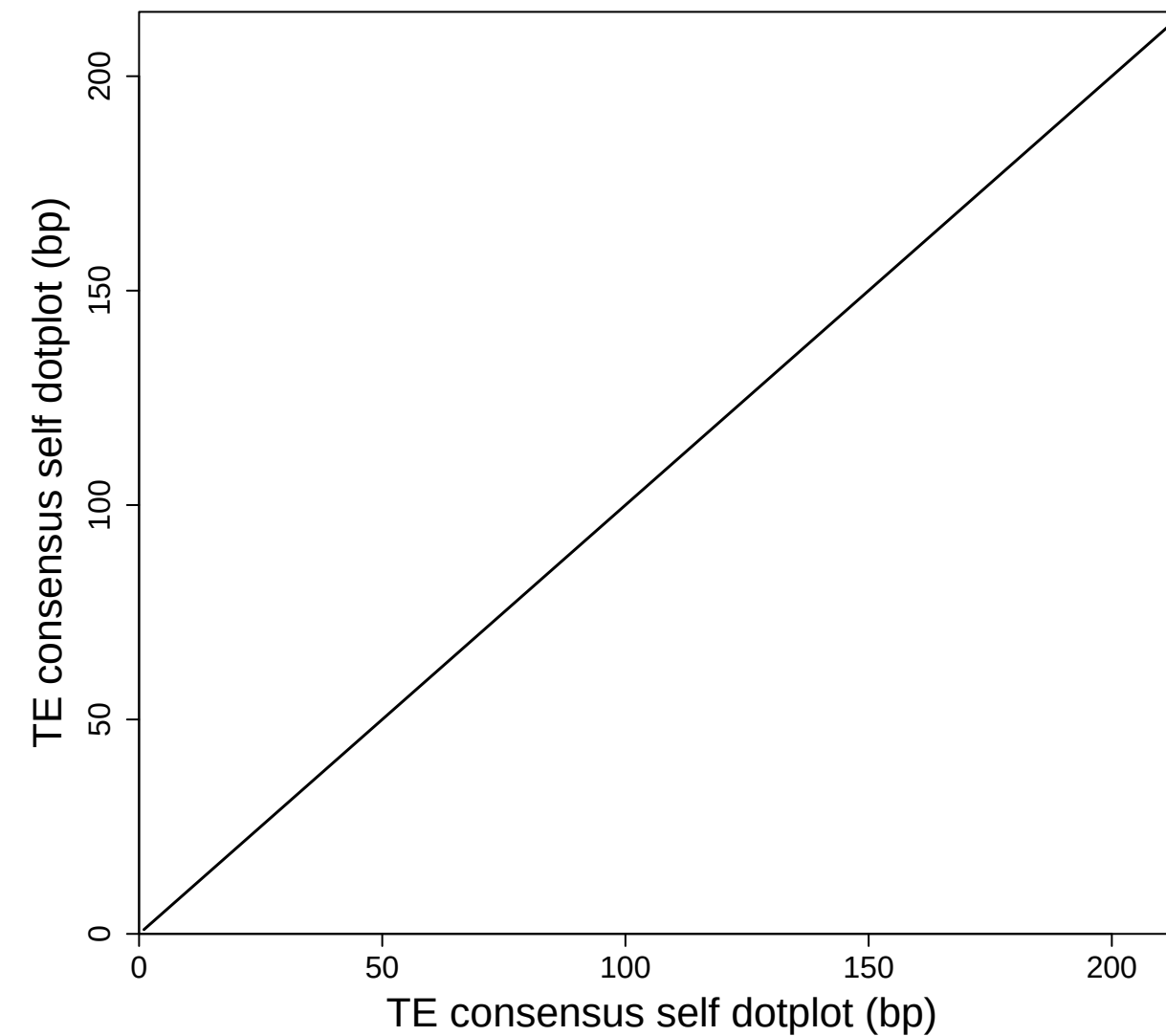
After TEtrimmer Extended plot Blue lines are boundaries



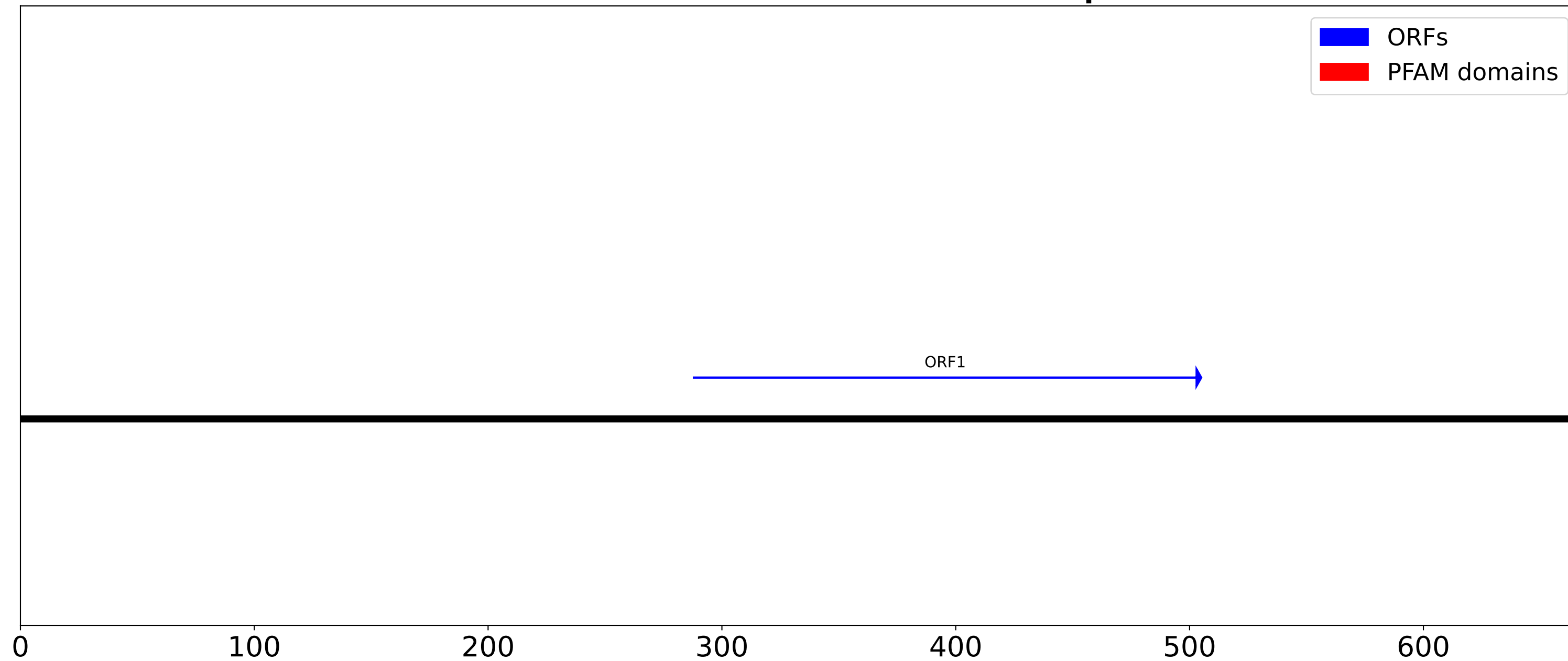
TE: ltr_1_family_239
size: 215bp; fragments: 17; full length: 11 (≥ 193.5 bp)



Before TEtrimmer 215 bp



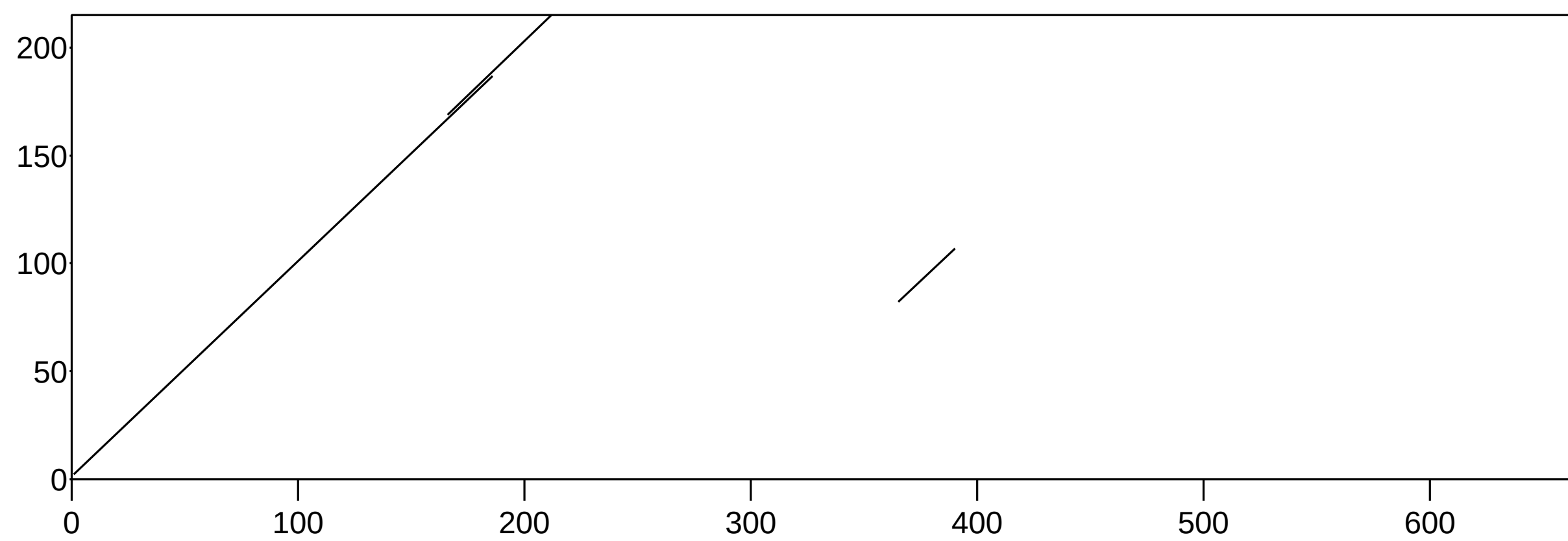
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)