

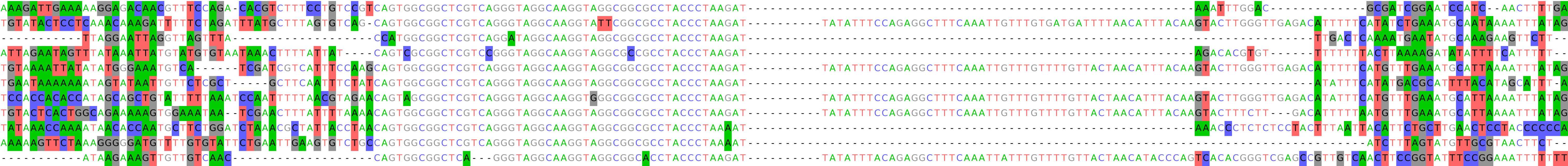
Start crop Point



End crop Point

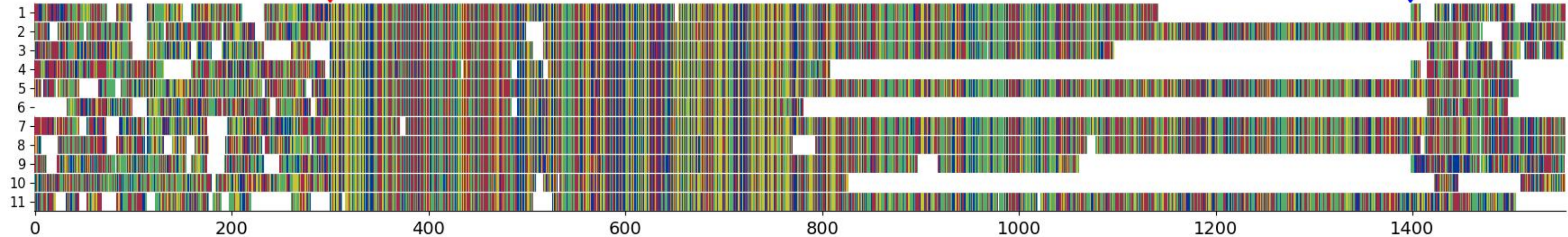


MSA length = 1099



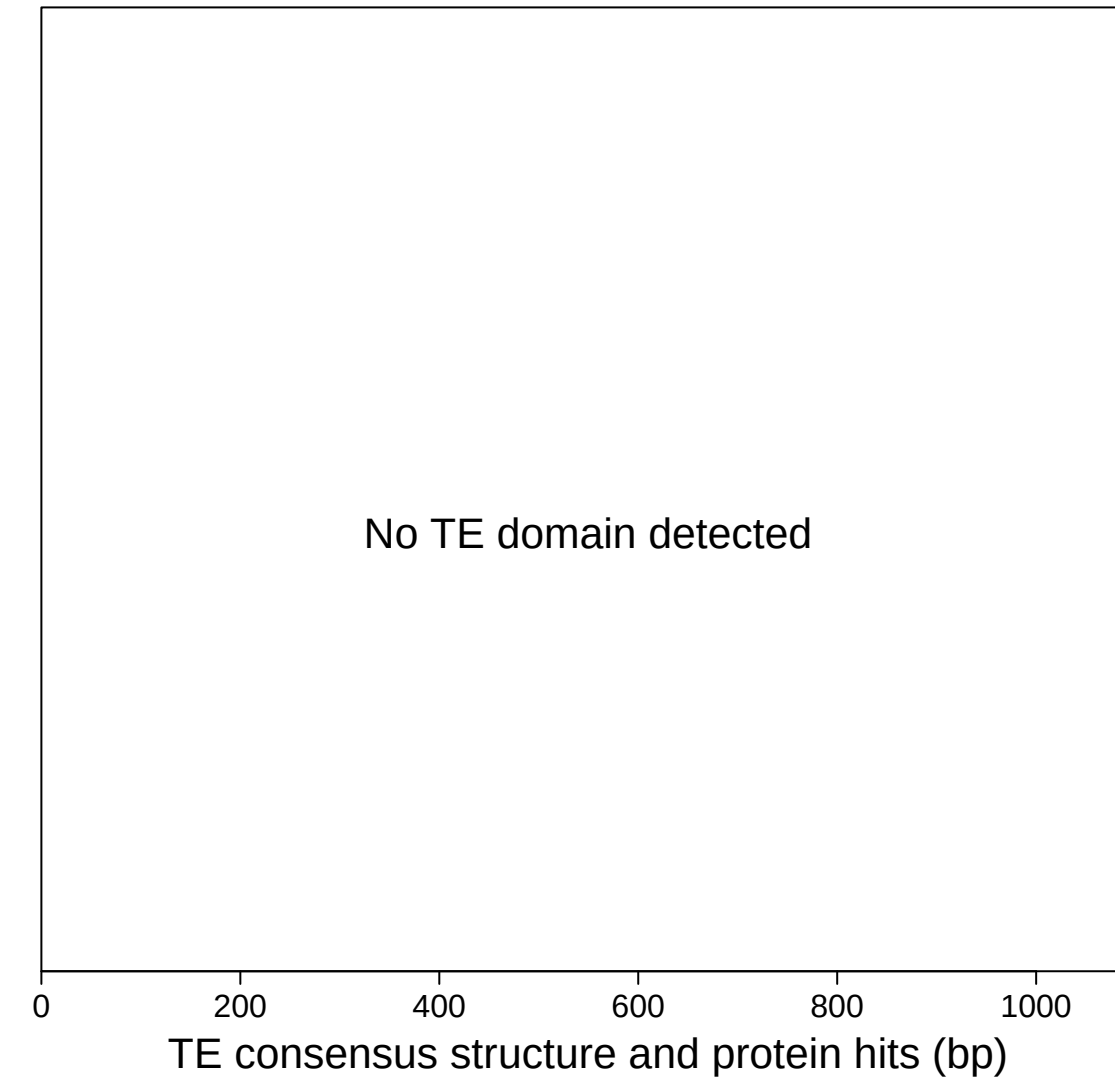
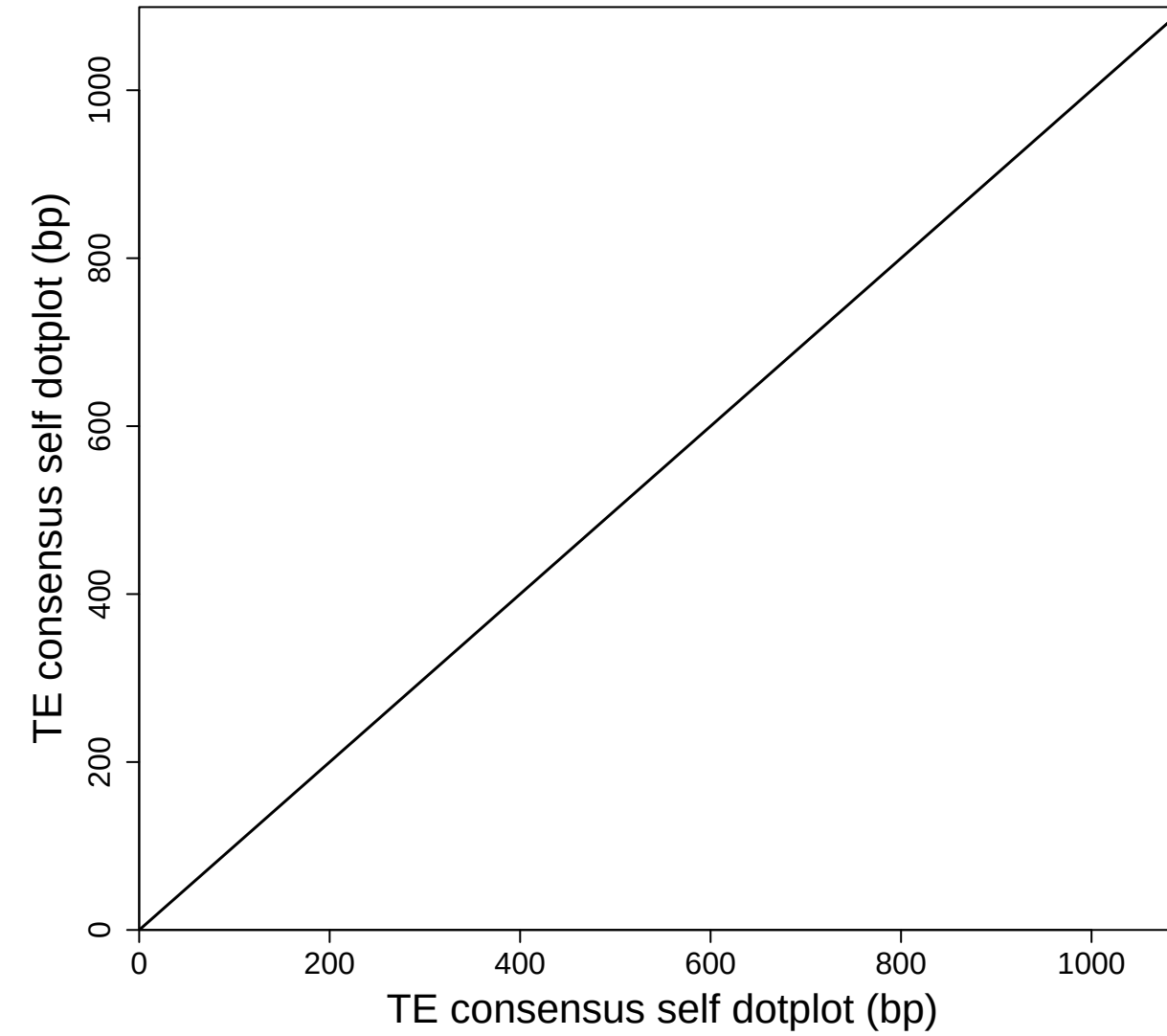
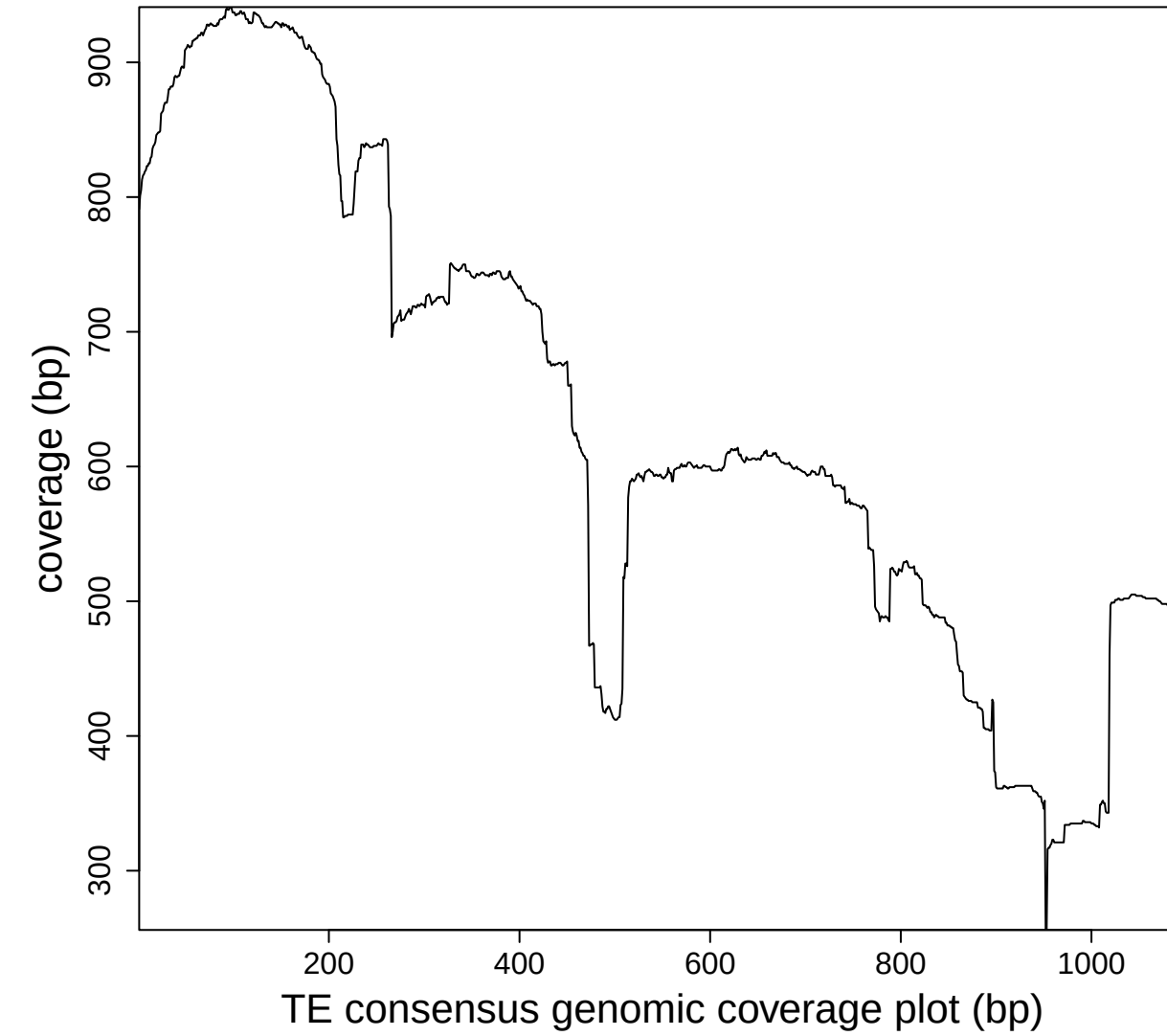
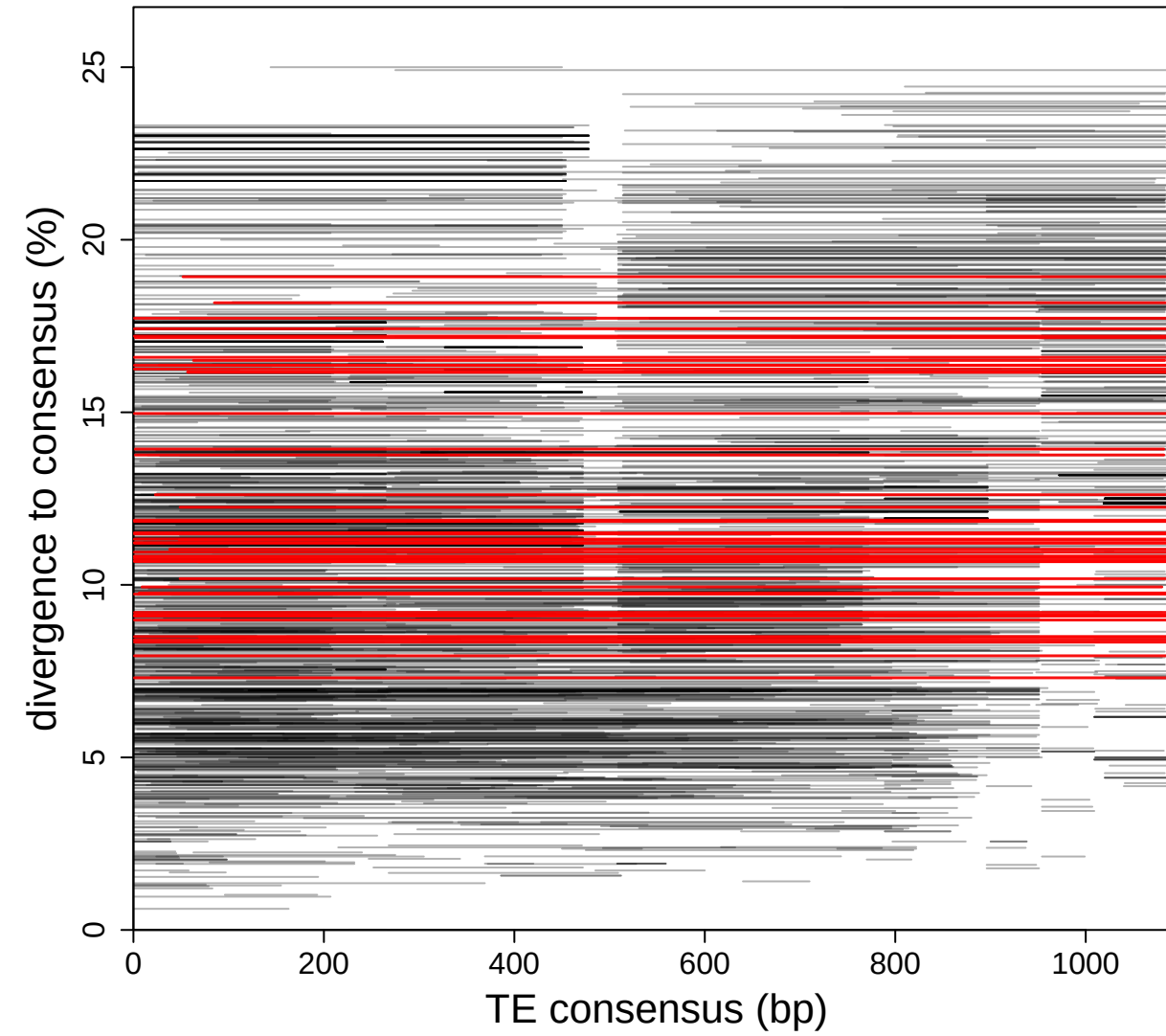
Start crop Point

End crop Point



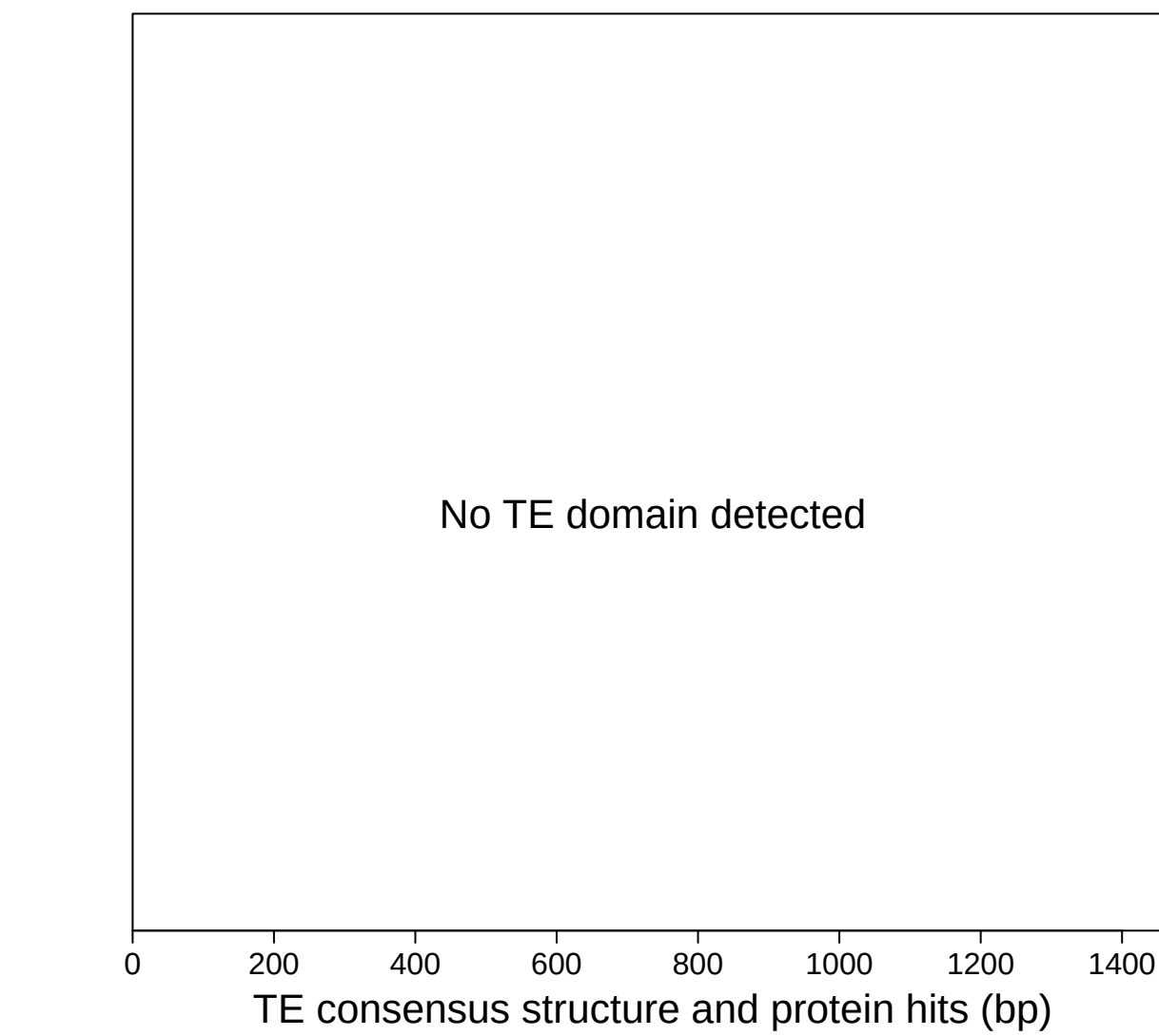
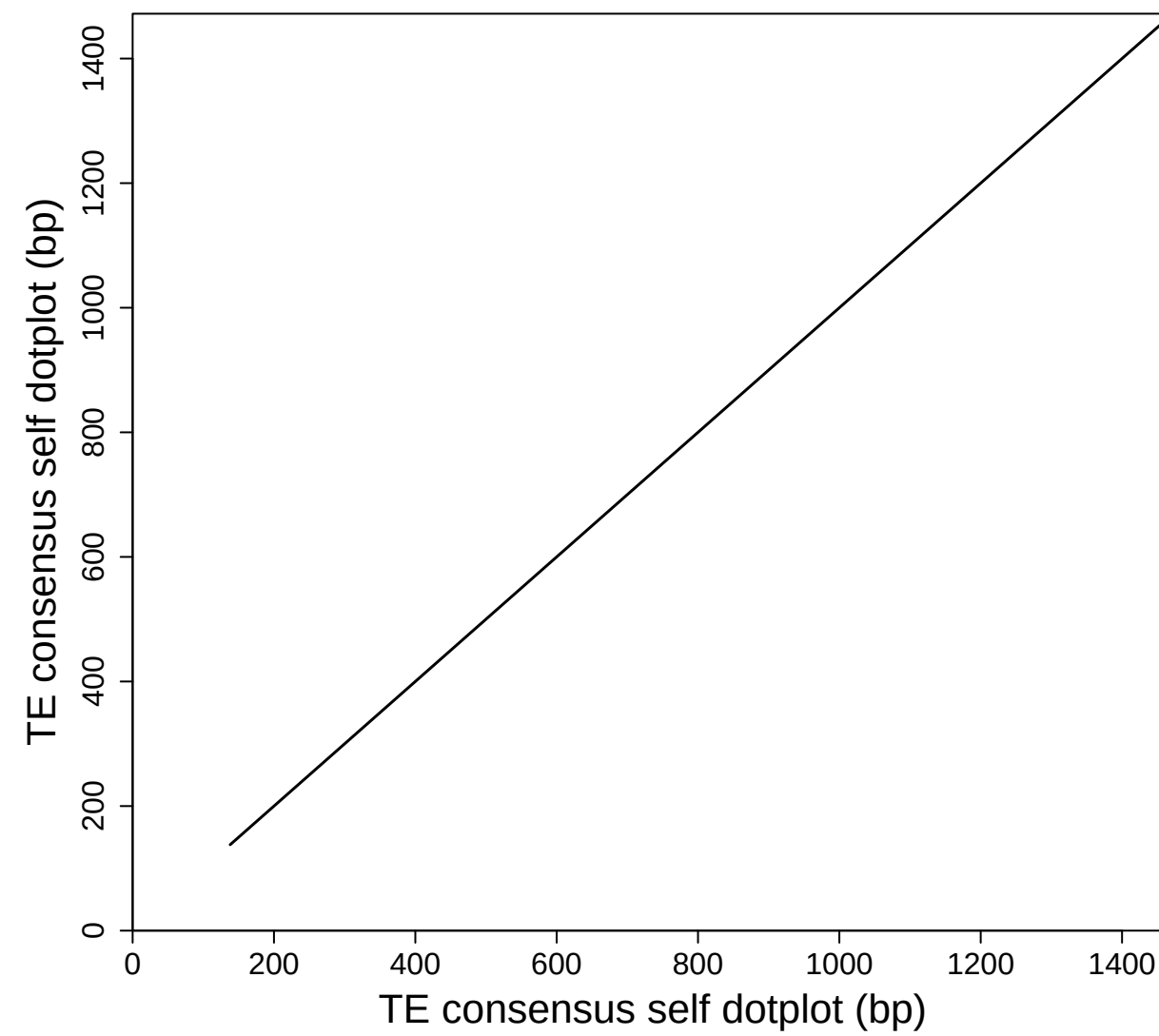
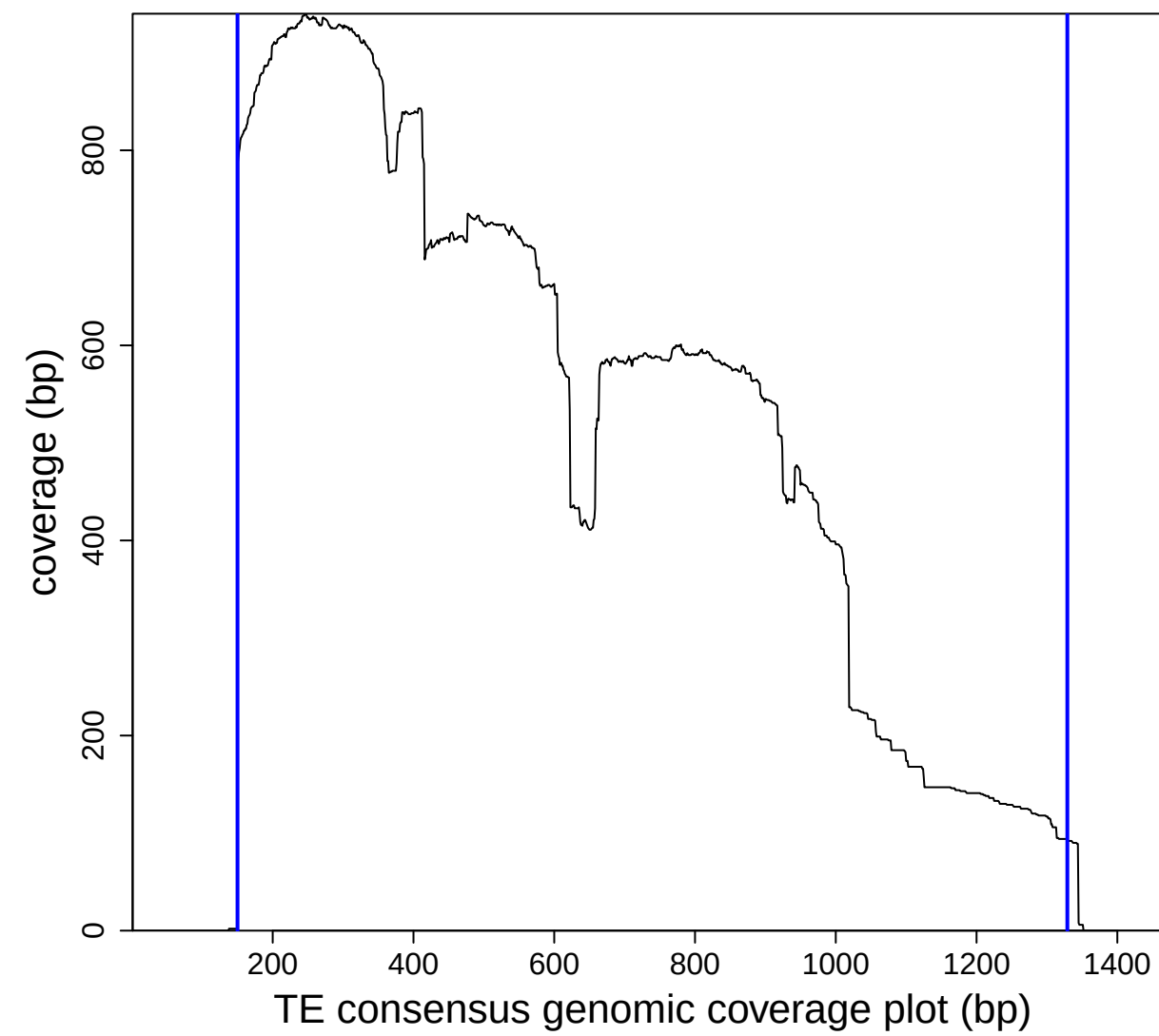
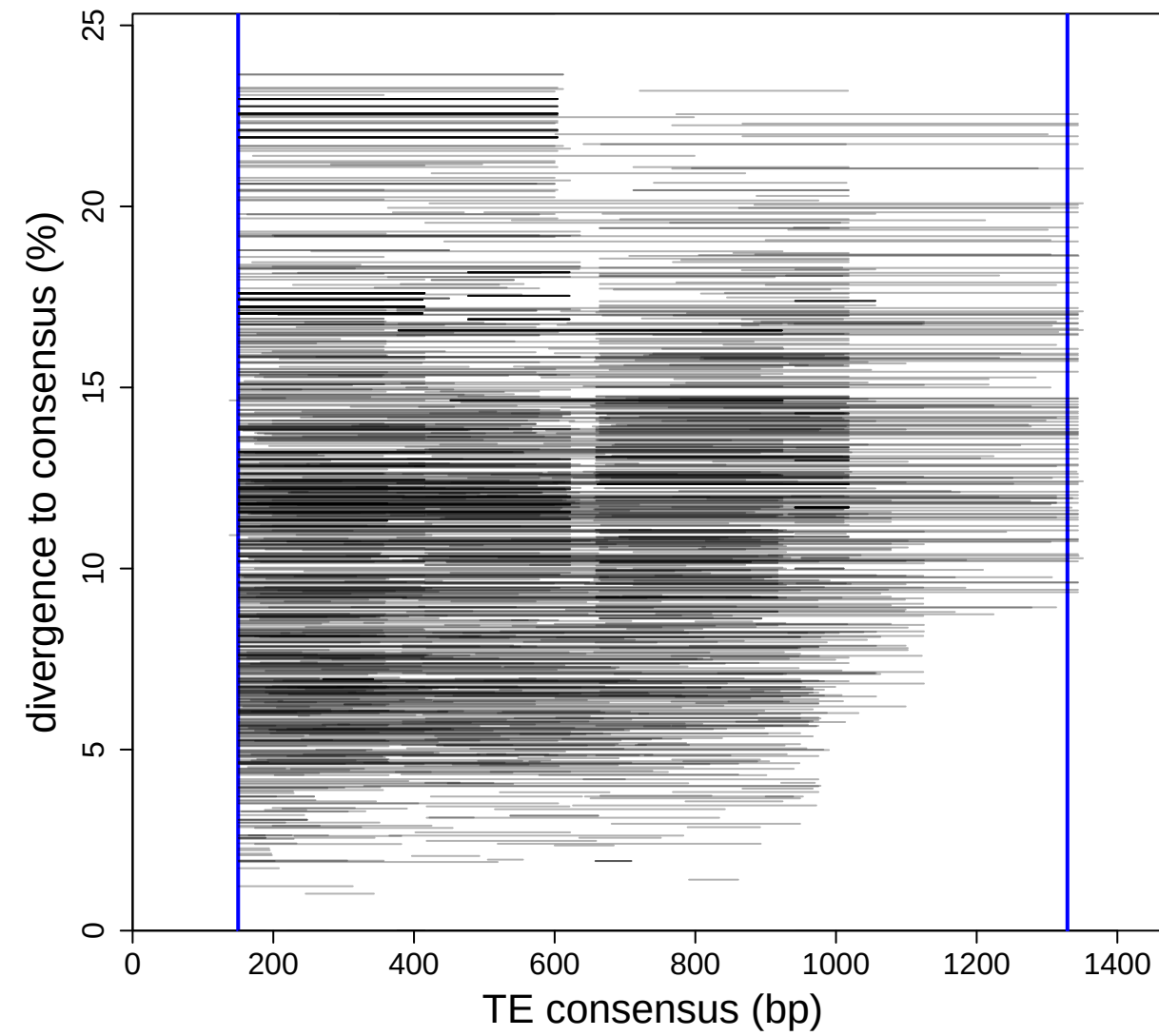
b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 1099bp; fragments: 2090; full length: 49 (≥ 989.1 bp)

After TEtrimmer 1099 bp

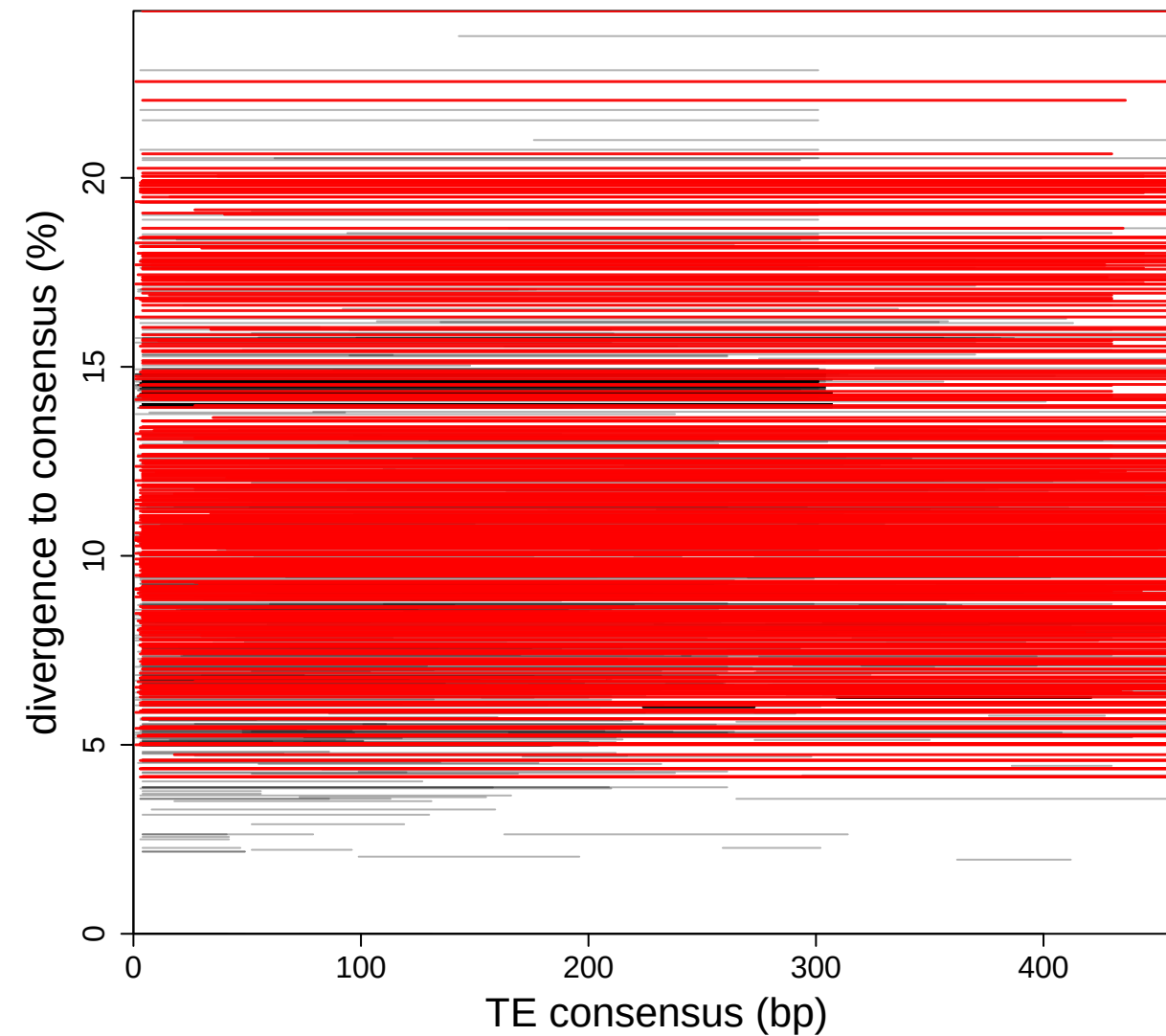


%.fasta.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 1479bp; fragments: 1679; full length: 0 (>=1331.1bp)

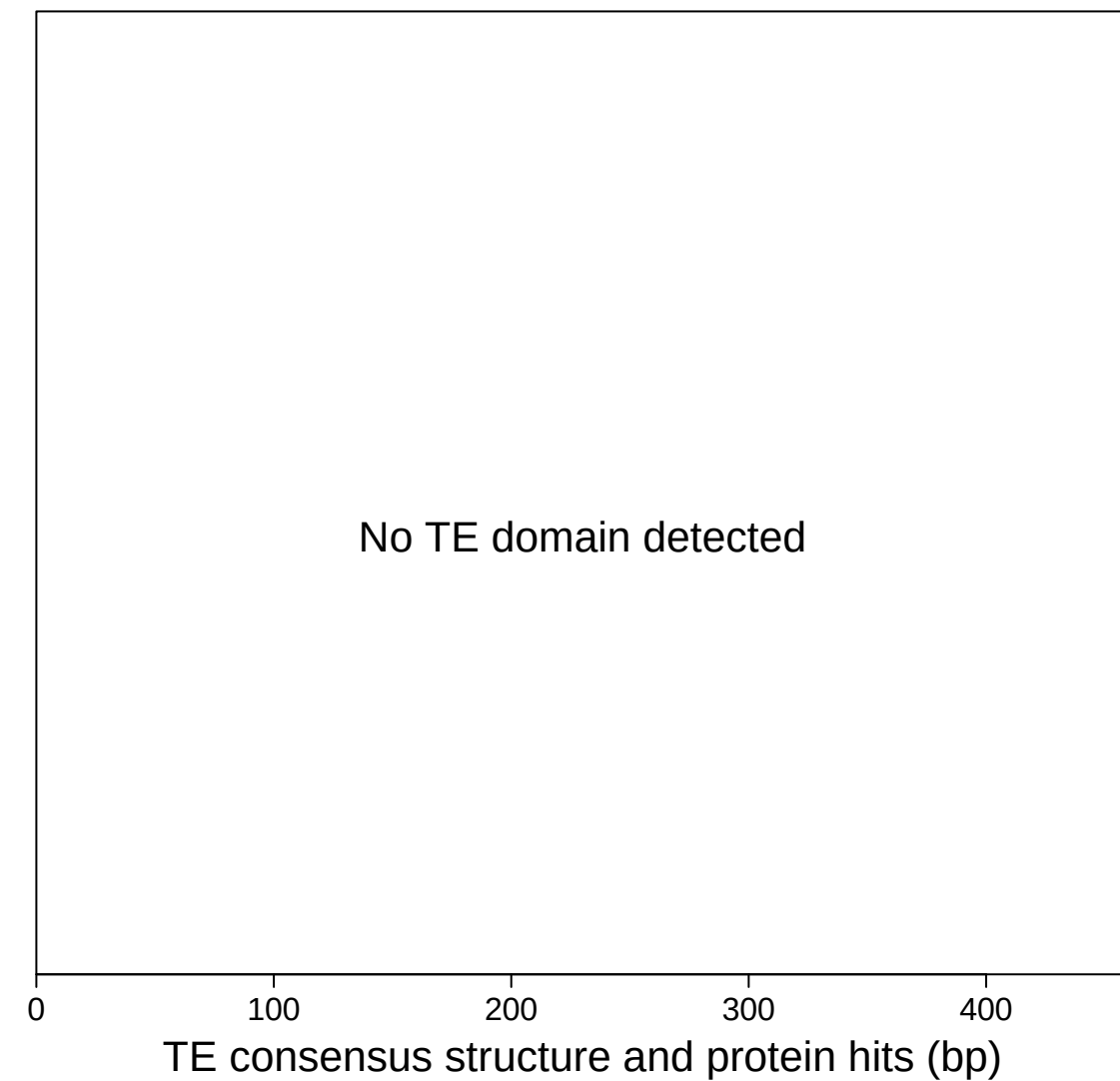
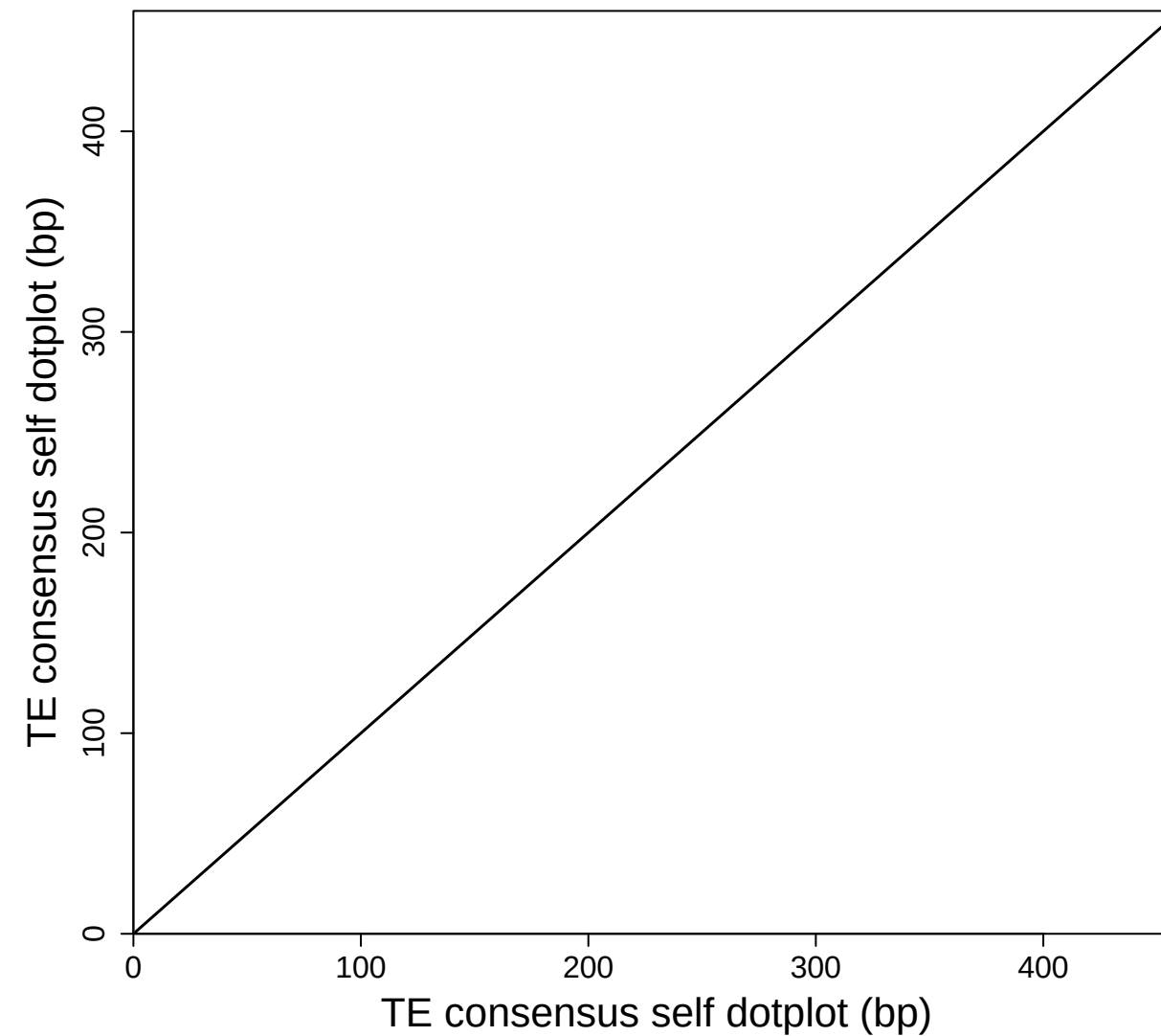
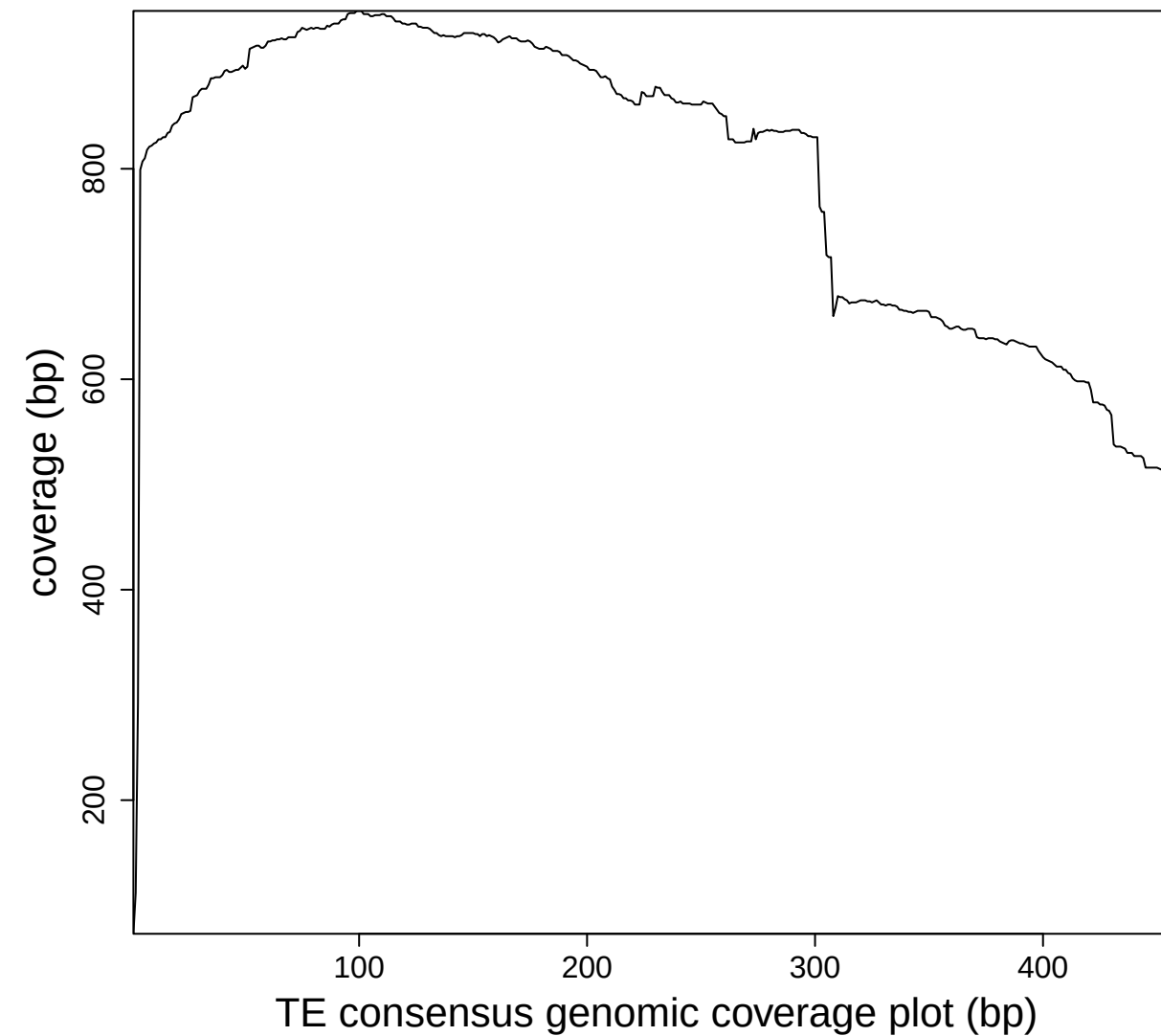
After TEtrimmer Extended plot Blue lines are boundaries



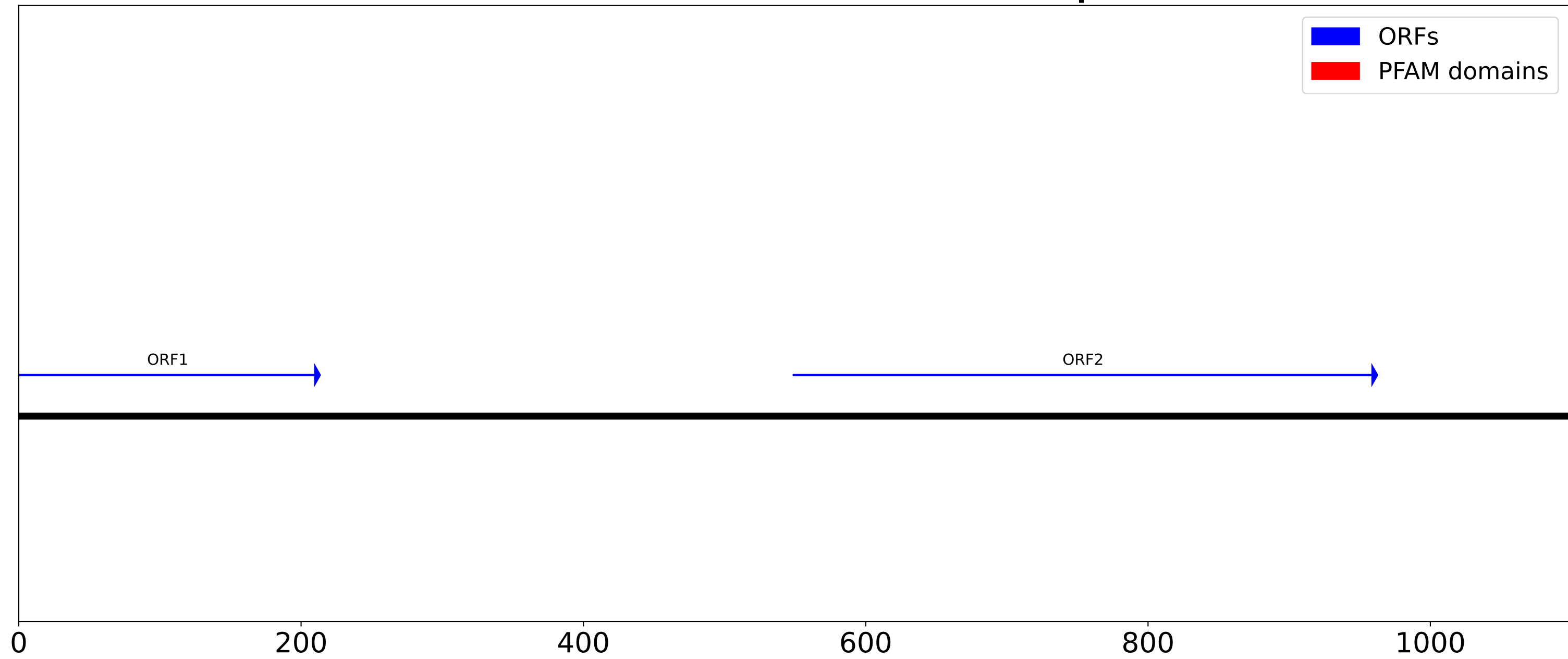
TE: rnd_1_family_67
size: 460bp; fragments: 1148; full length: 416 (≥ 414 bp)



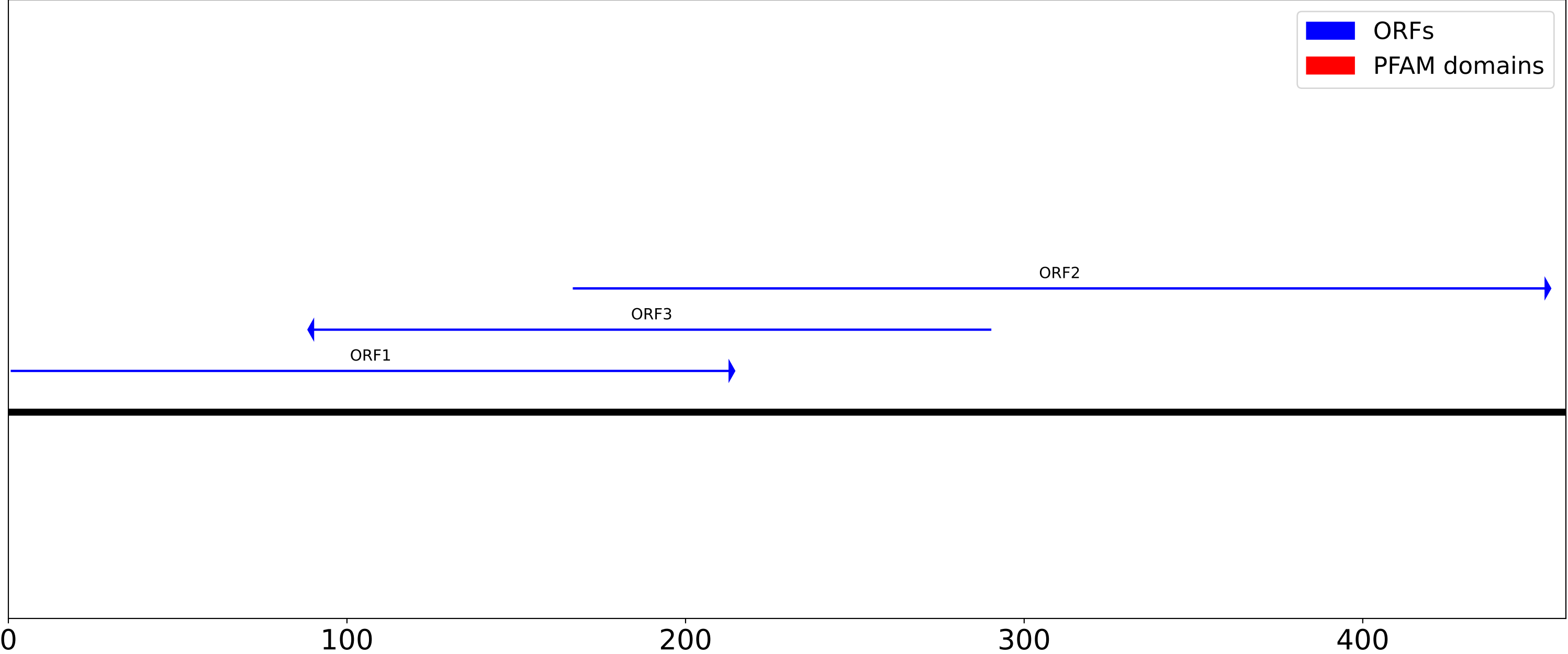
Before TEtrimmer 460 bp



After TEtrimmer ORF and PFAM domain plot



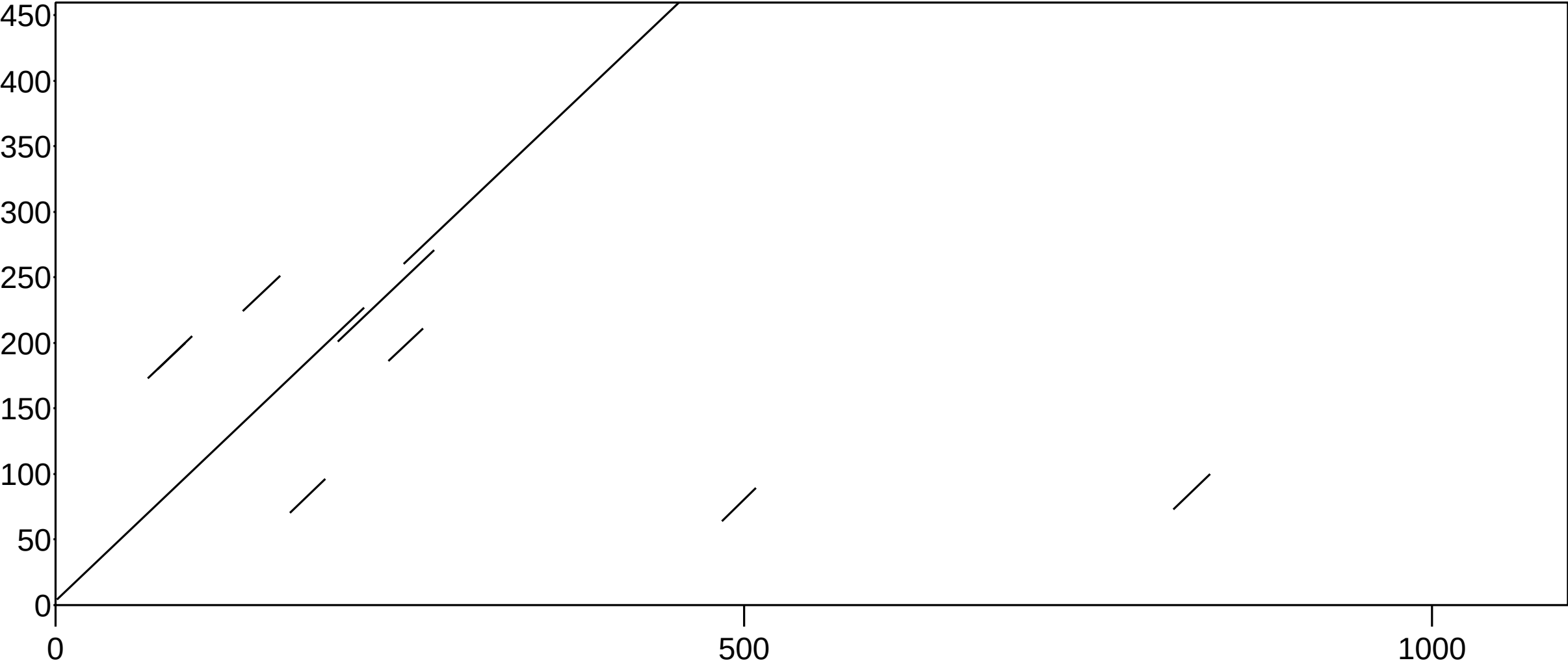
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)