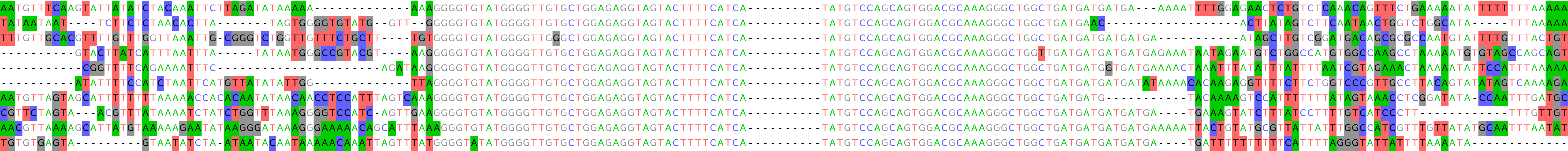


Start Crop Point

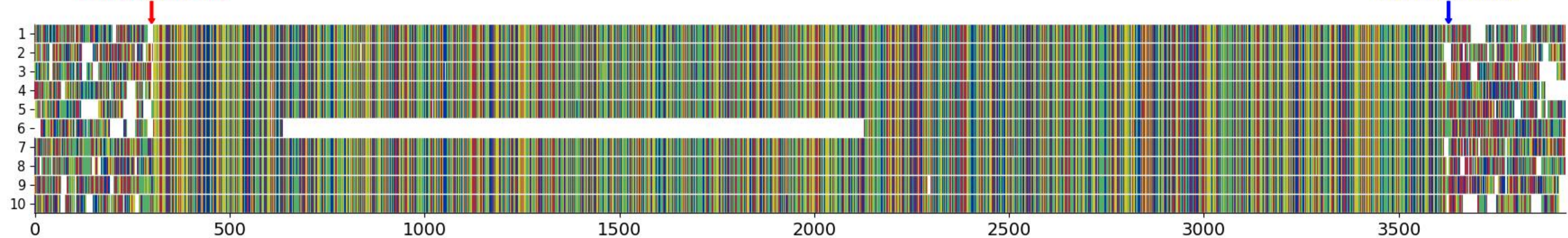
End Crop Point

MSA length = 3329



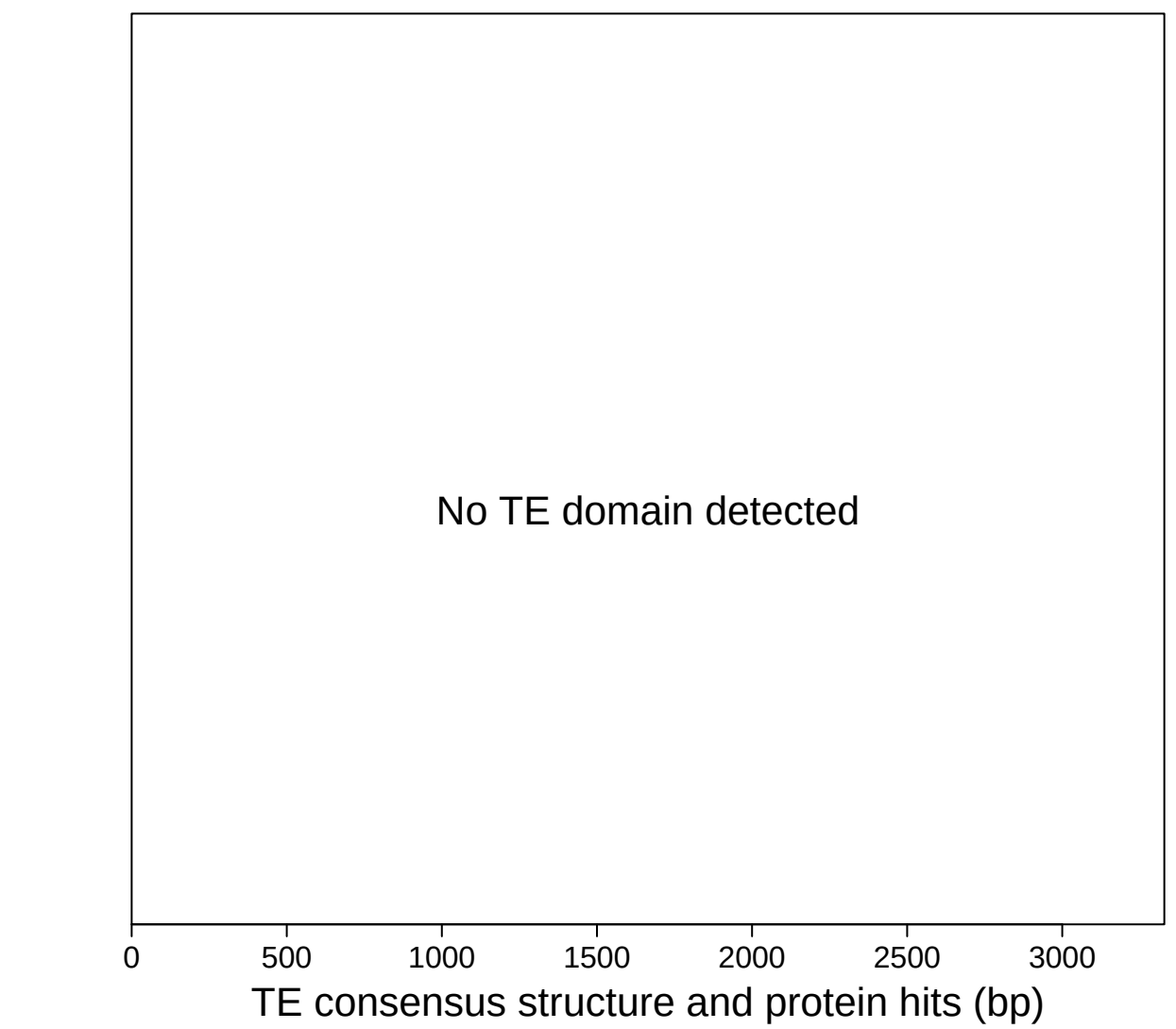
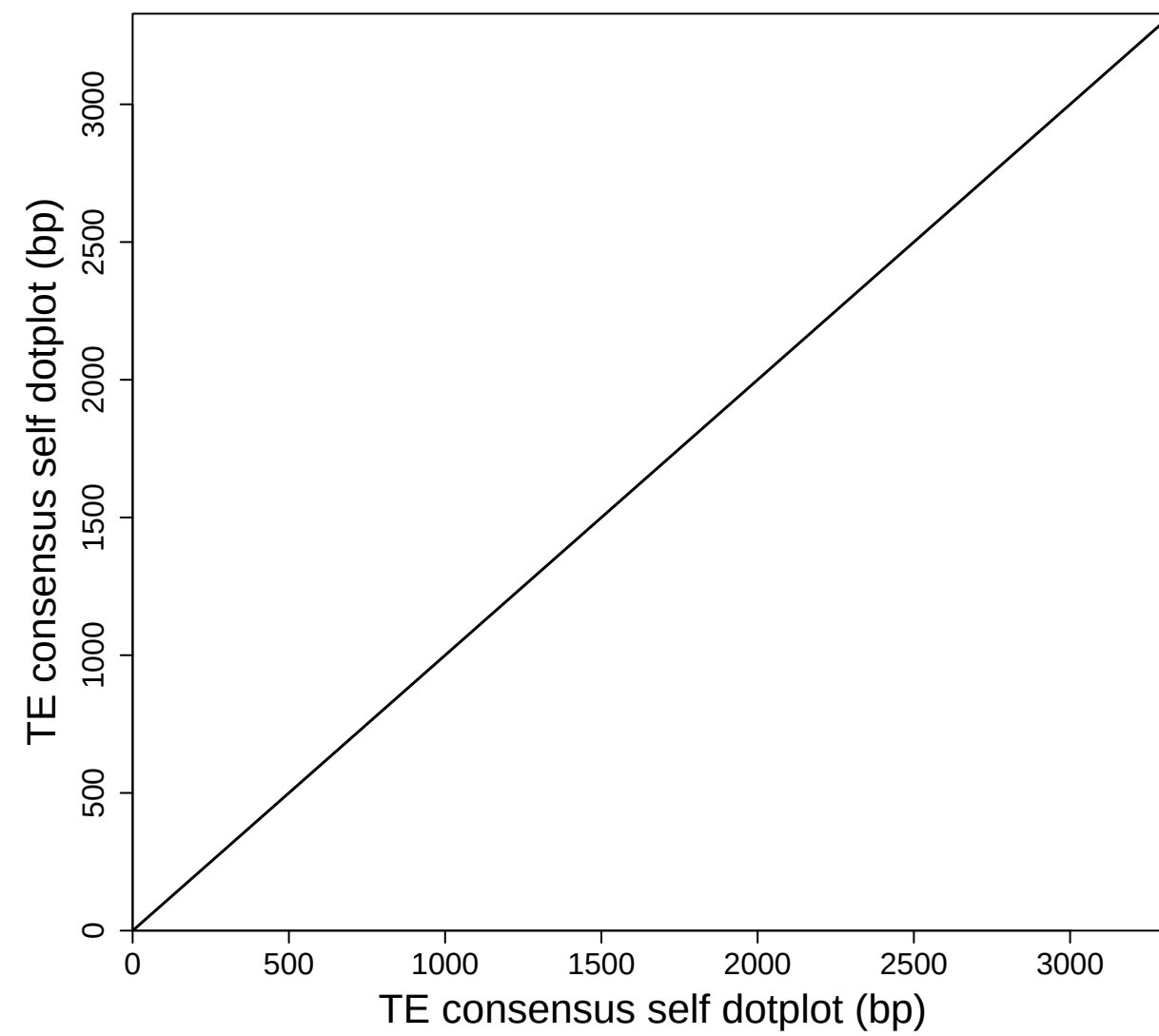
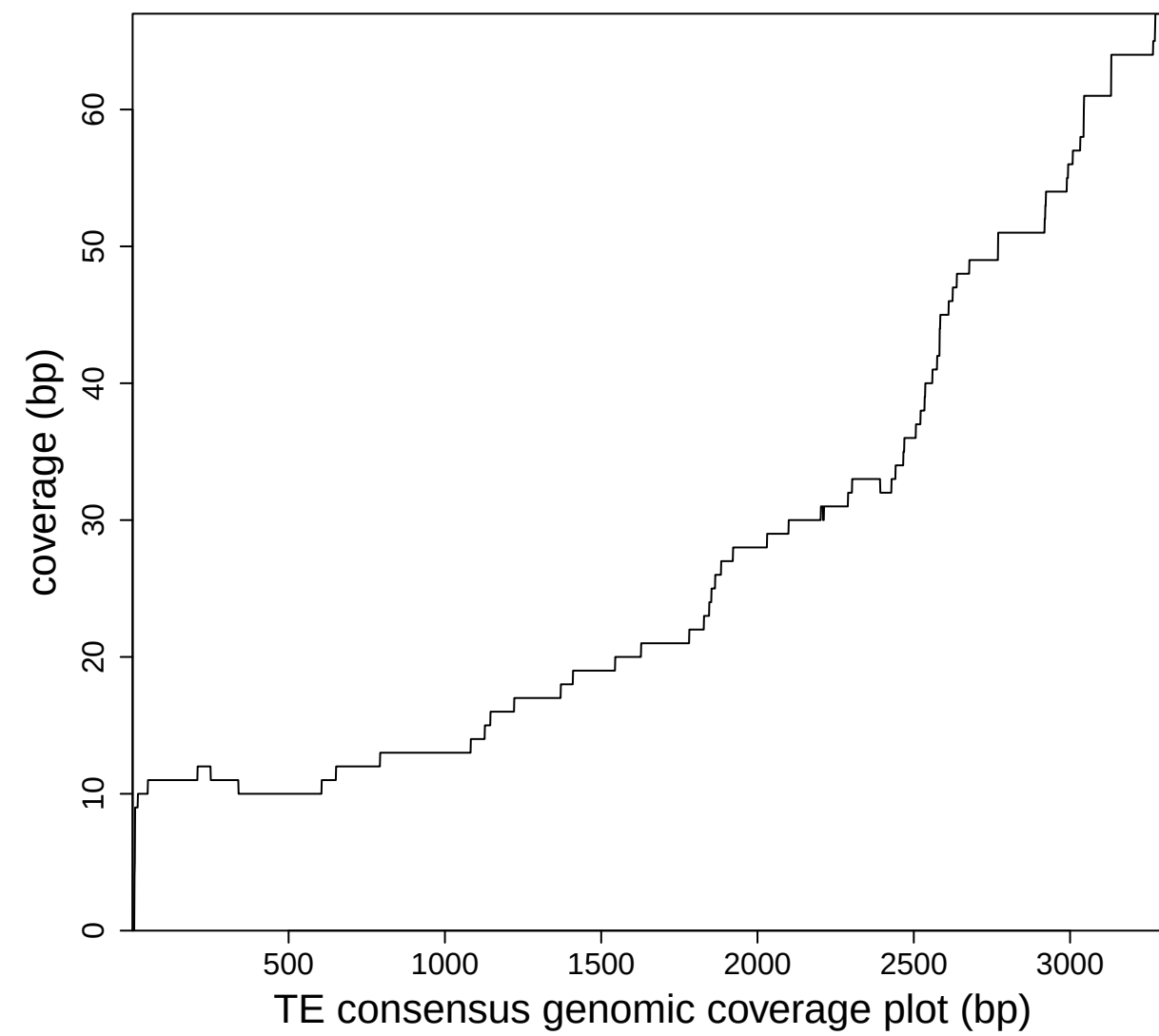
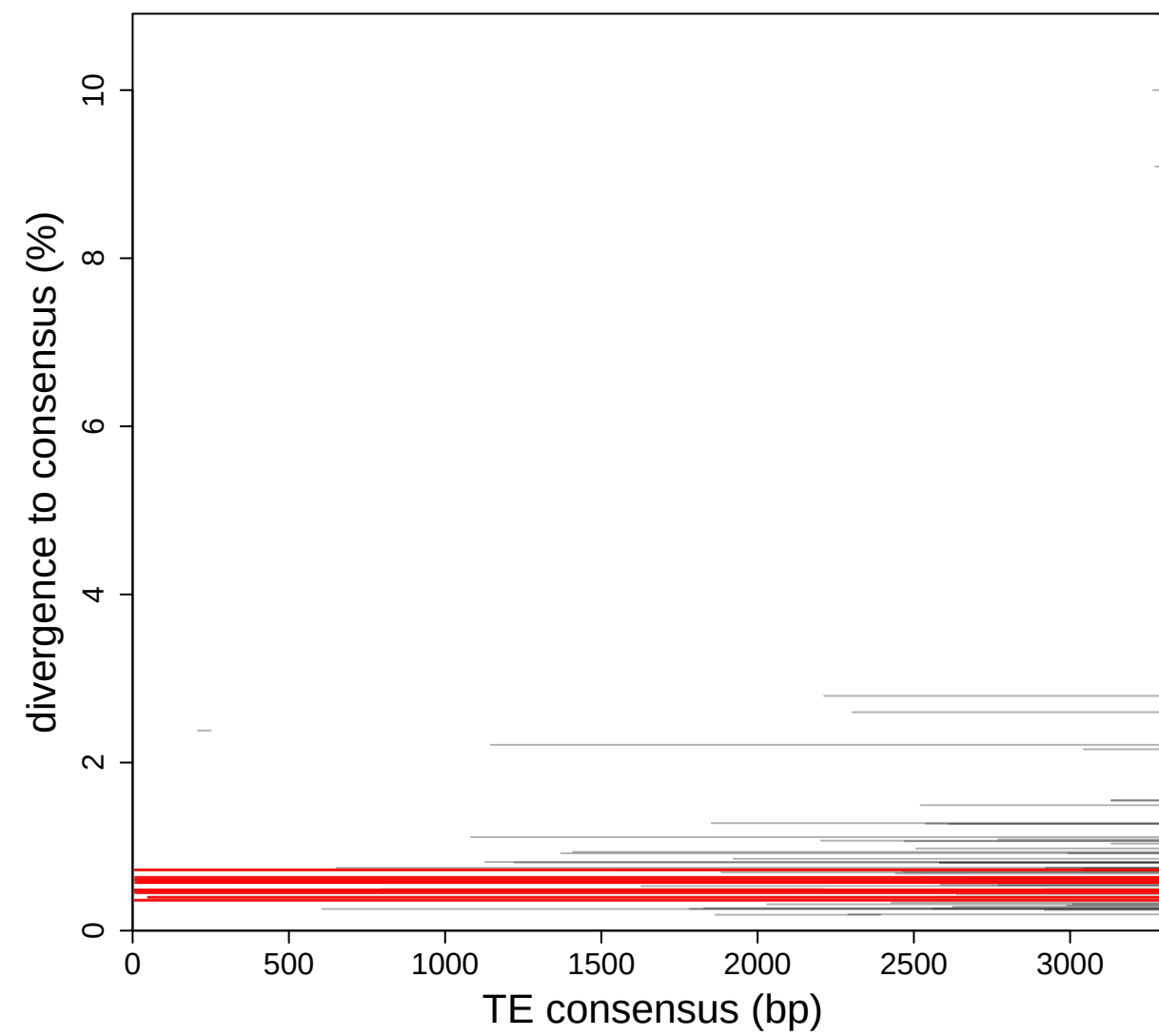
Start crop Point

End crop Point



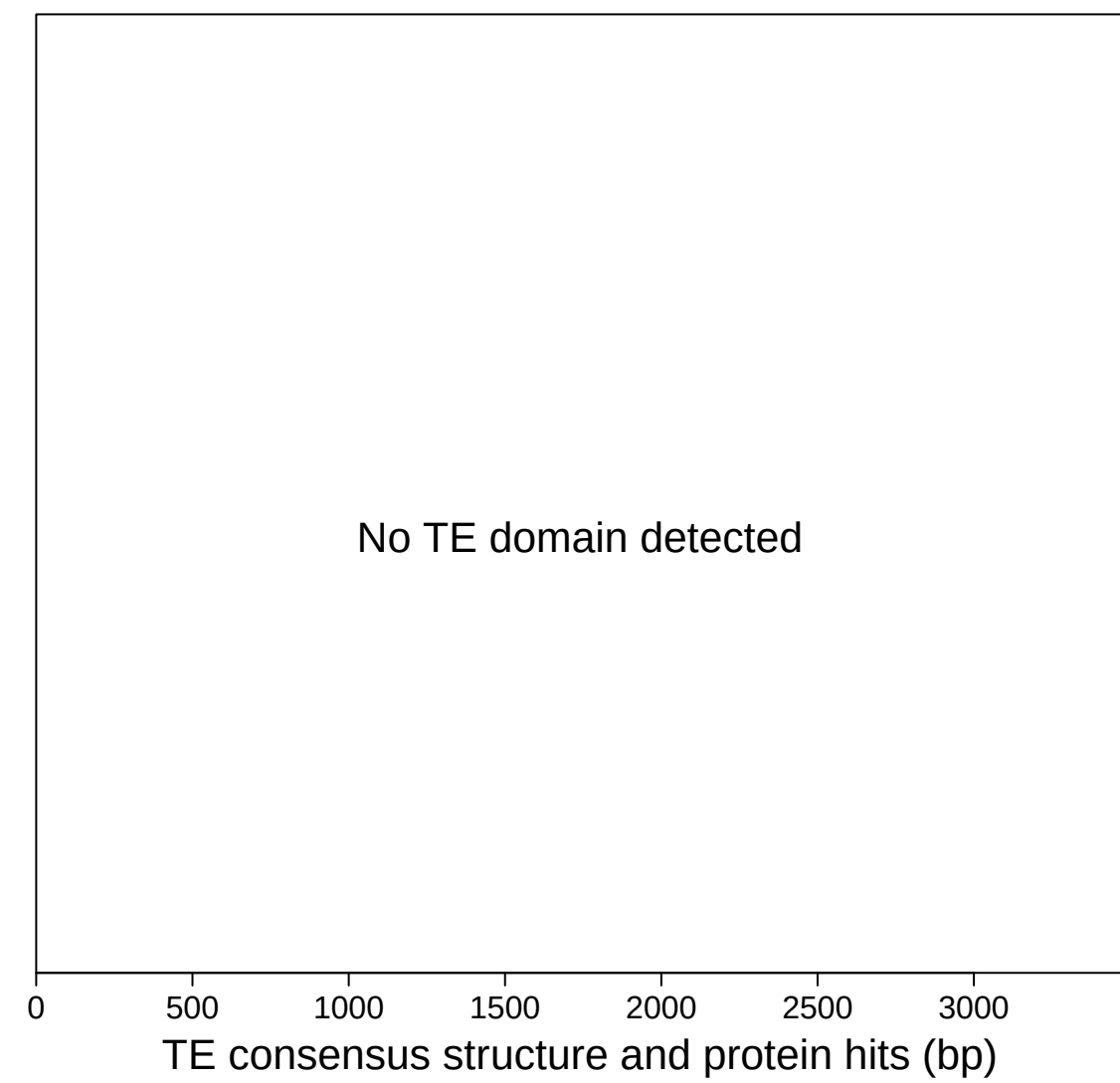
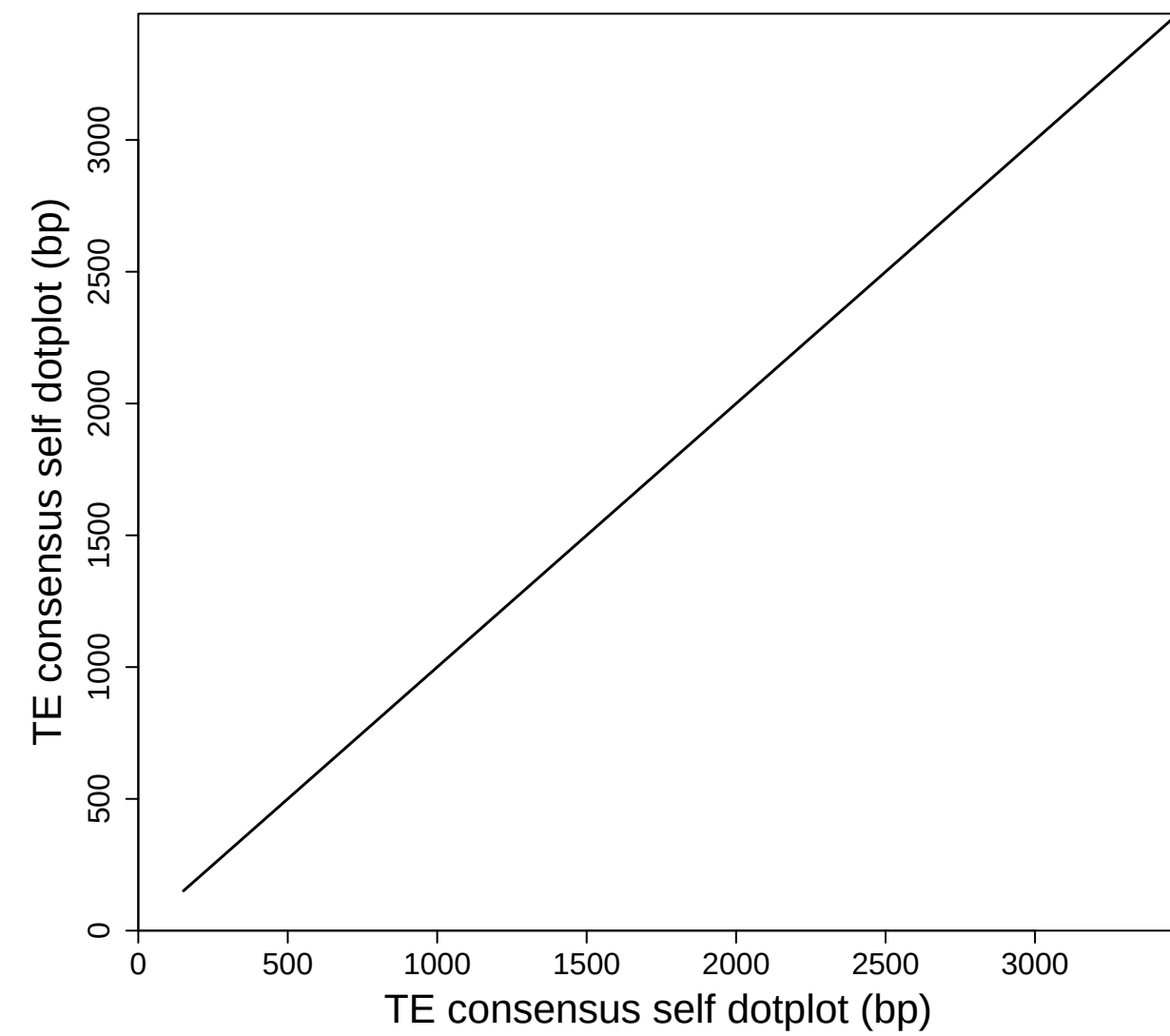
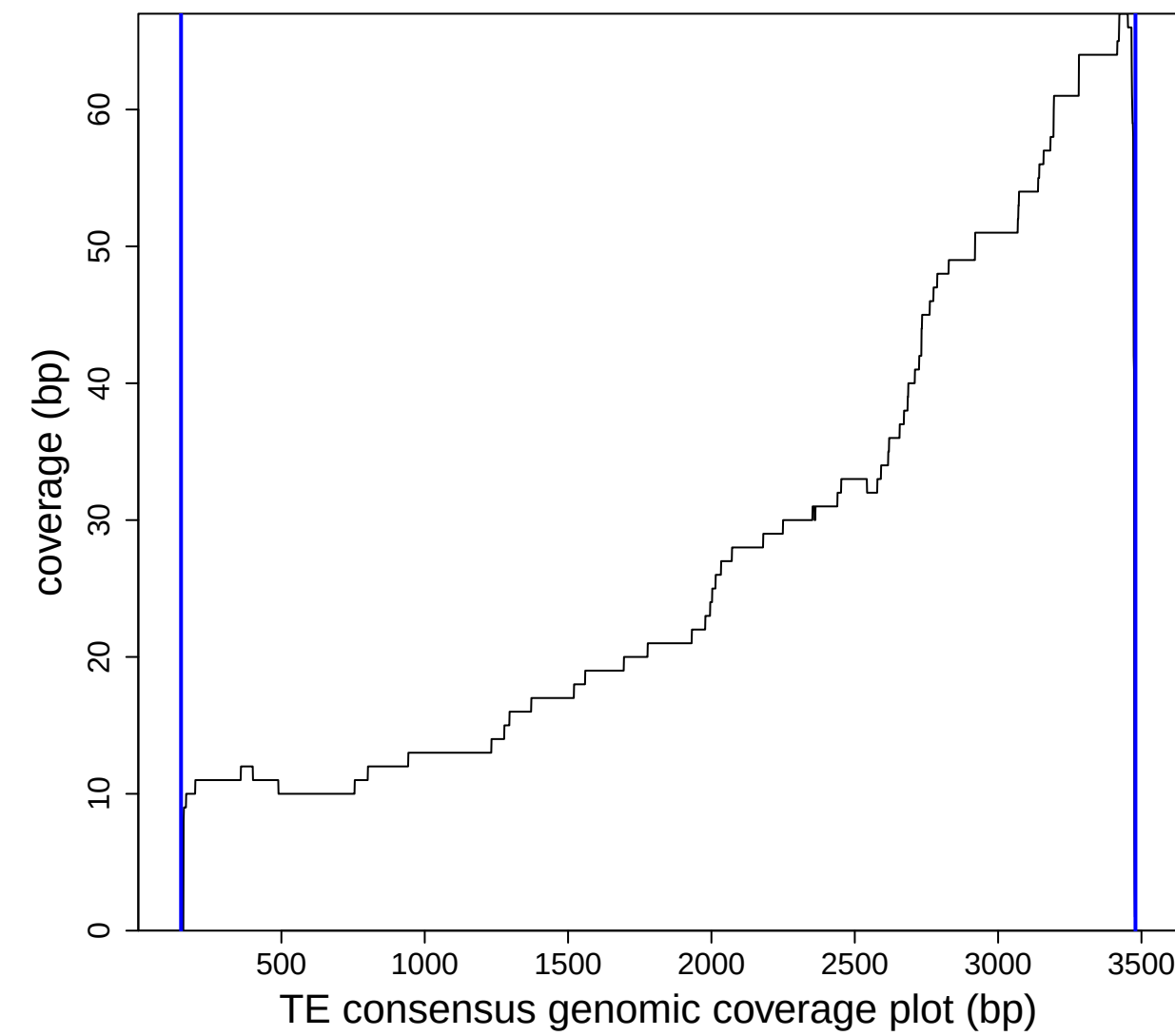
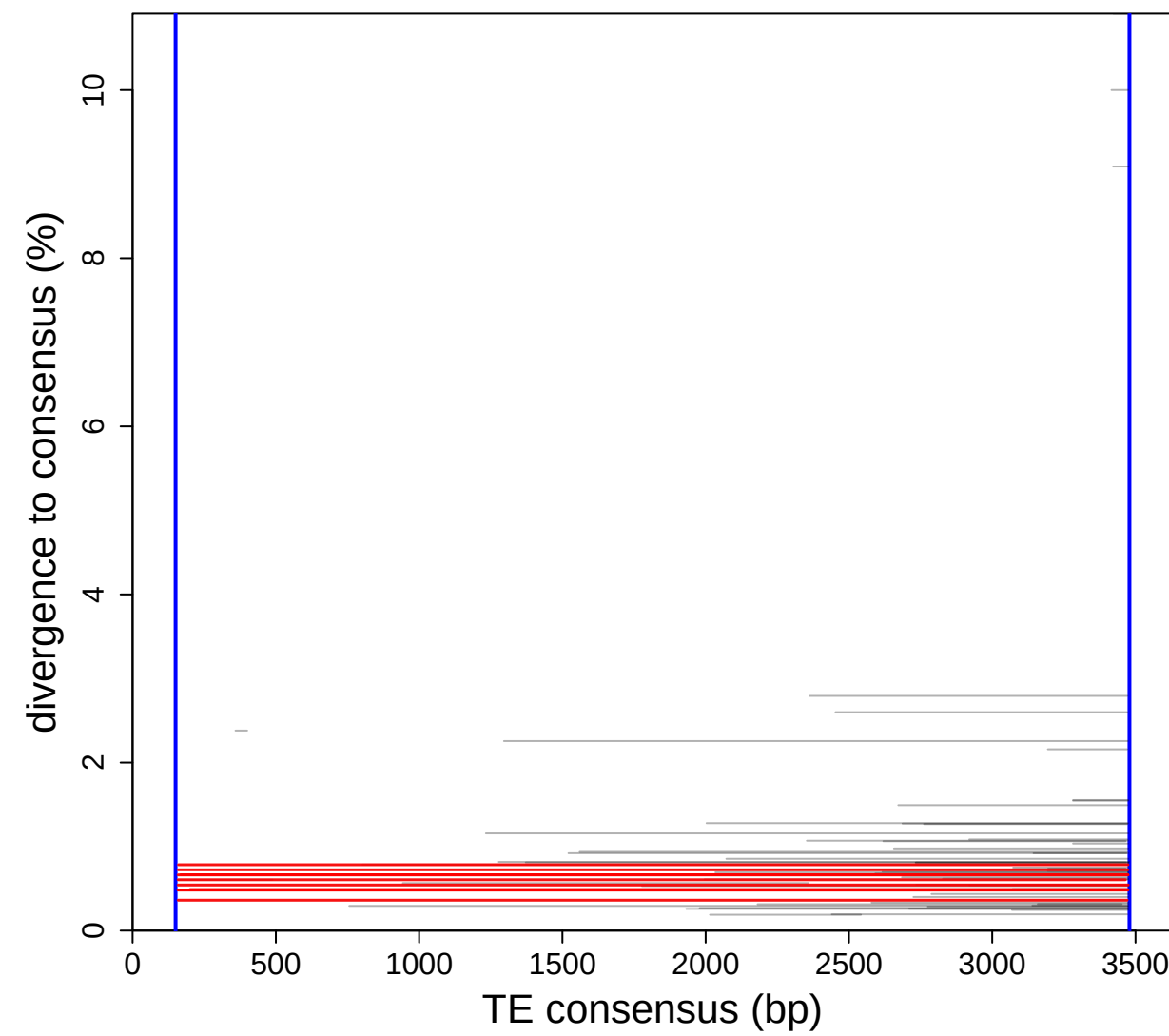
bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_c
size: 3329bp; fragments: 71; full length: 10 (>=2996.1bp)

After TEtrimmer 3329 bp

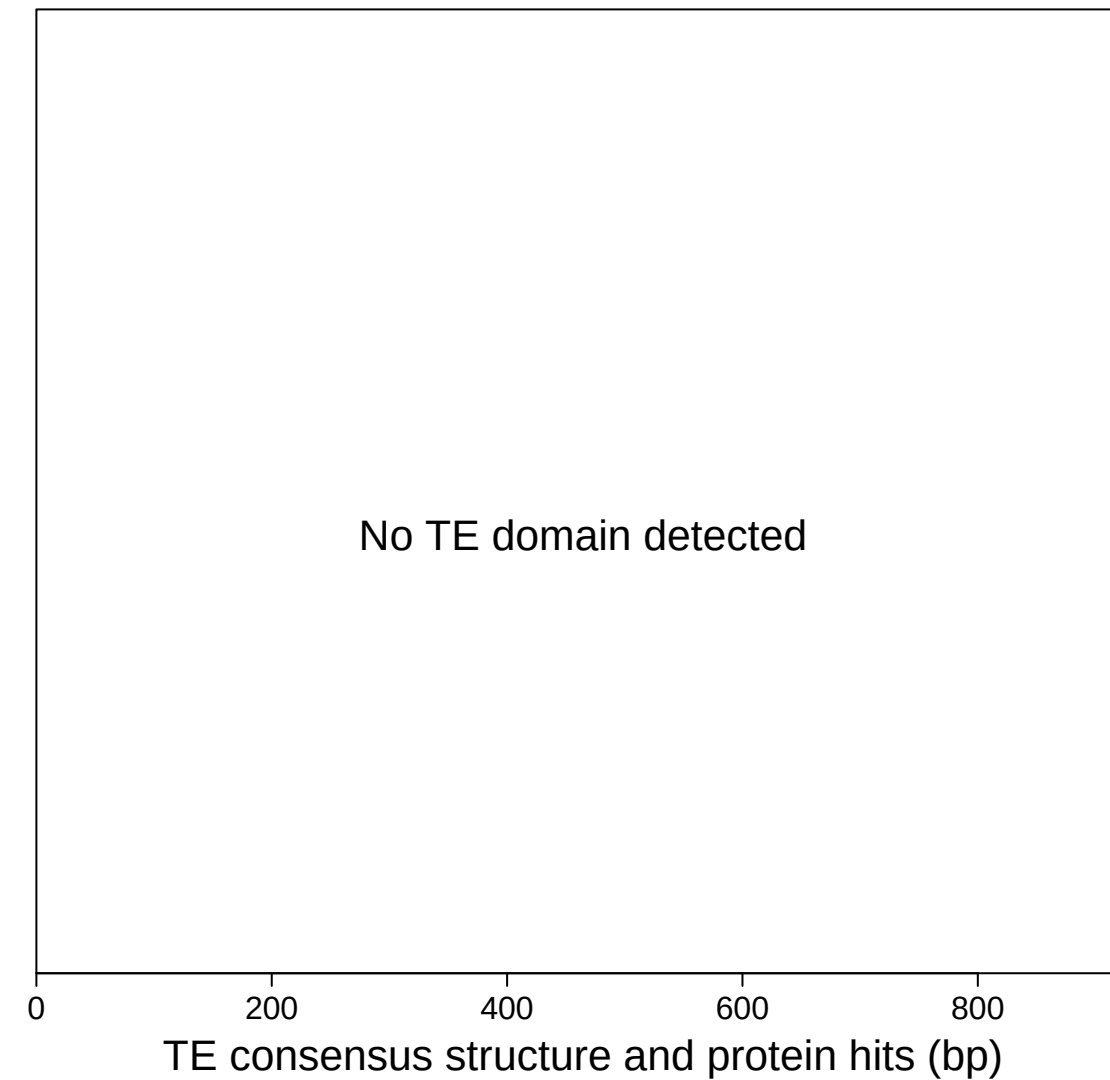
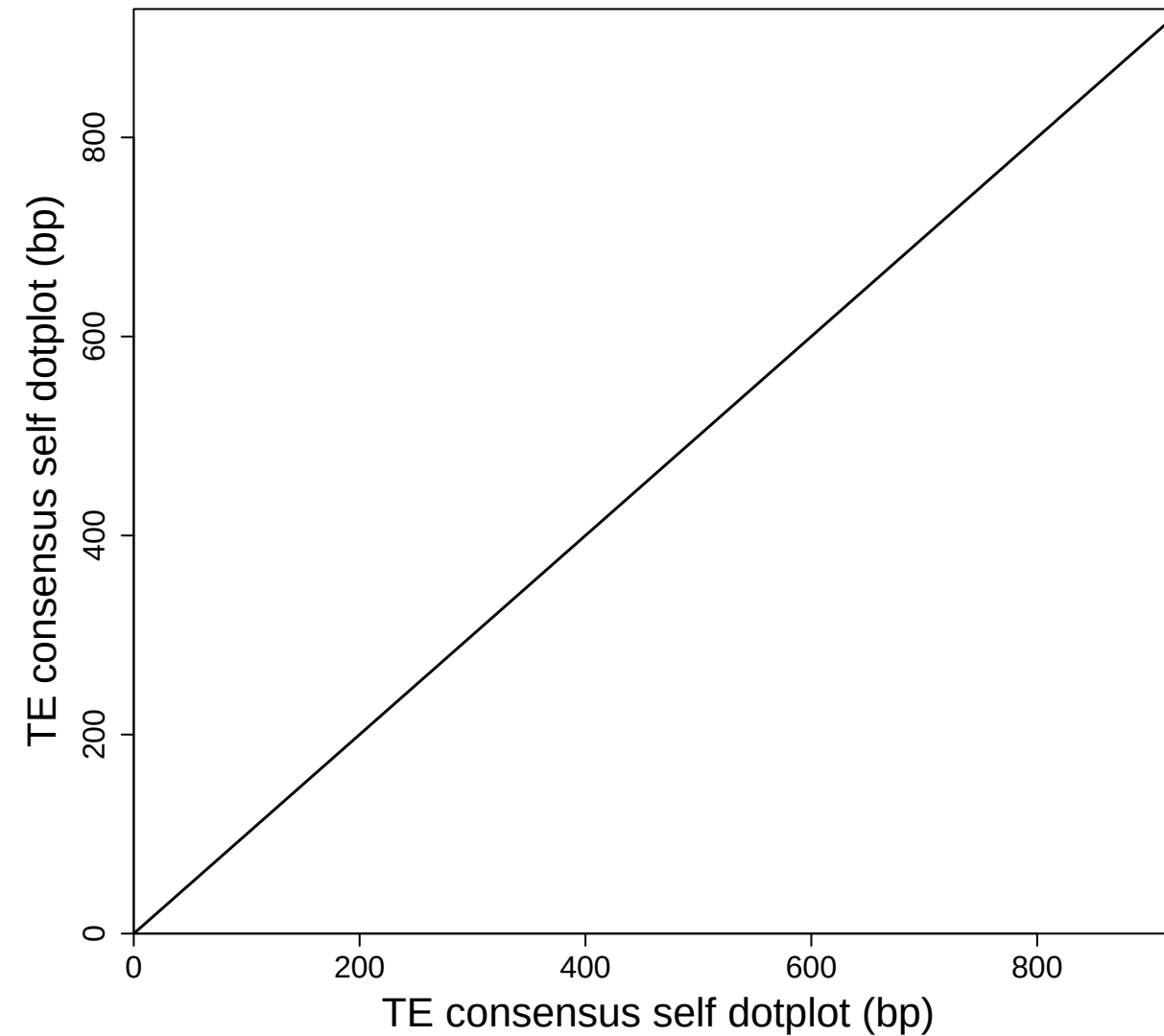
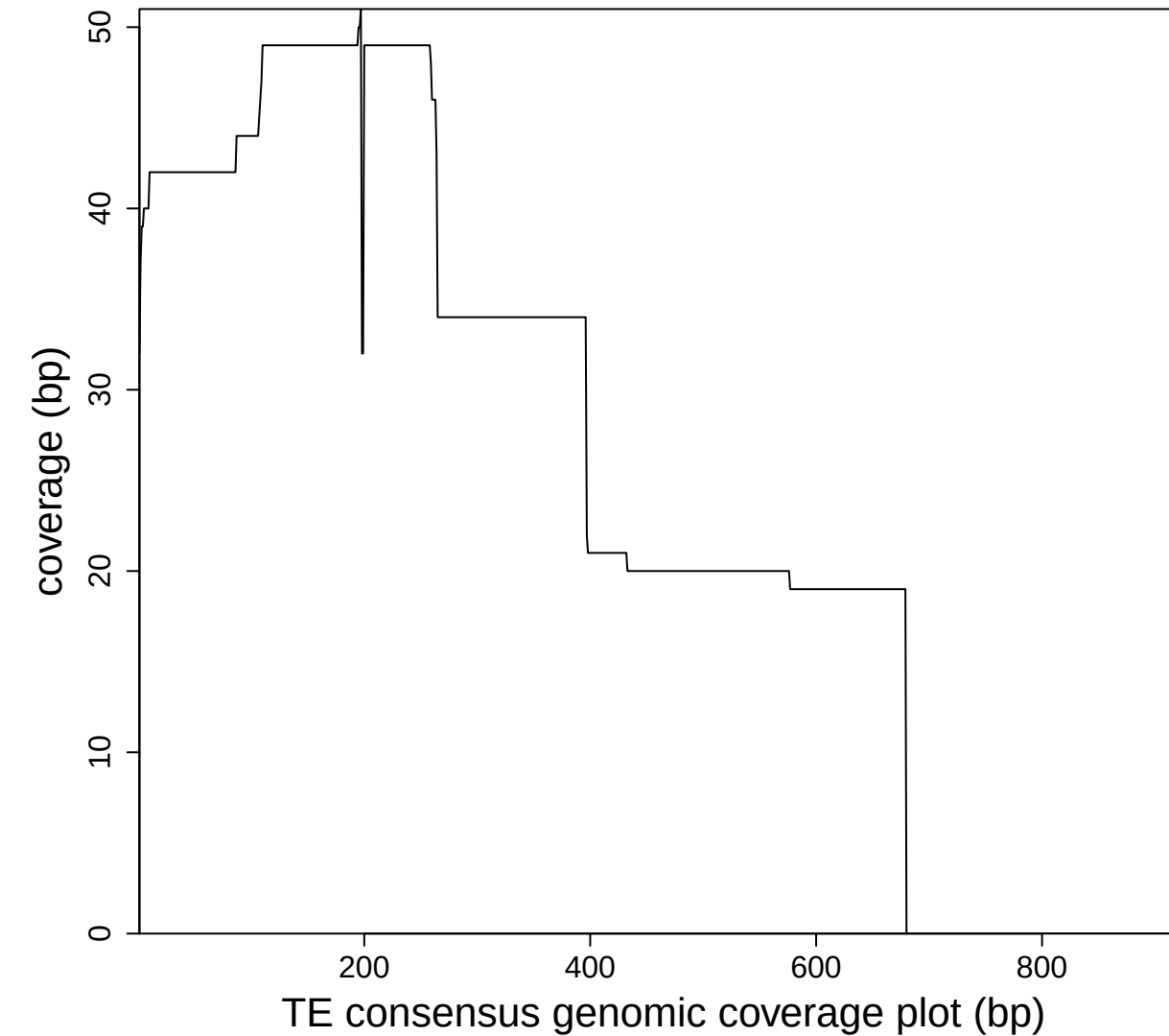
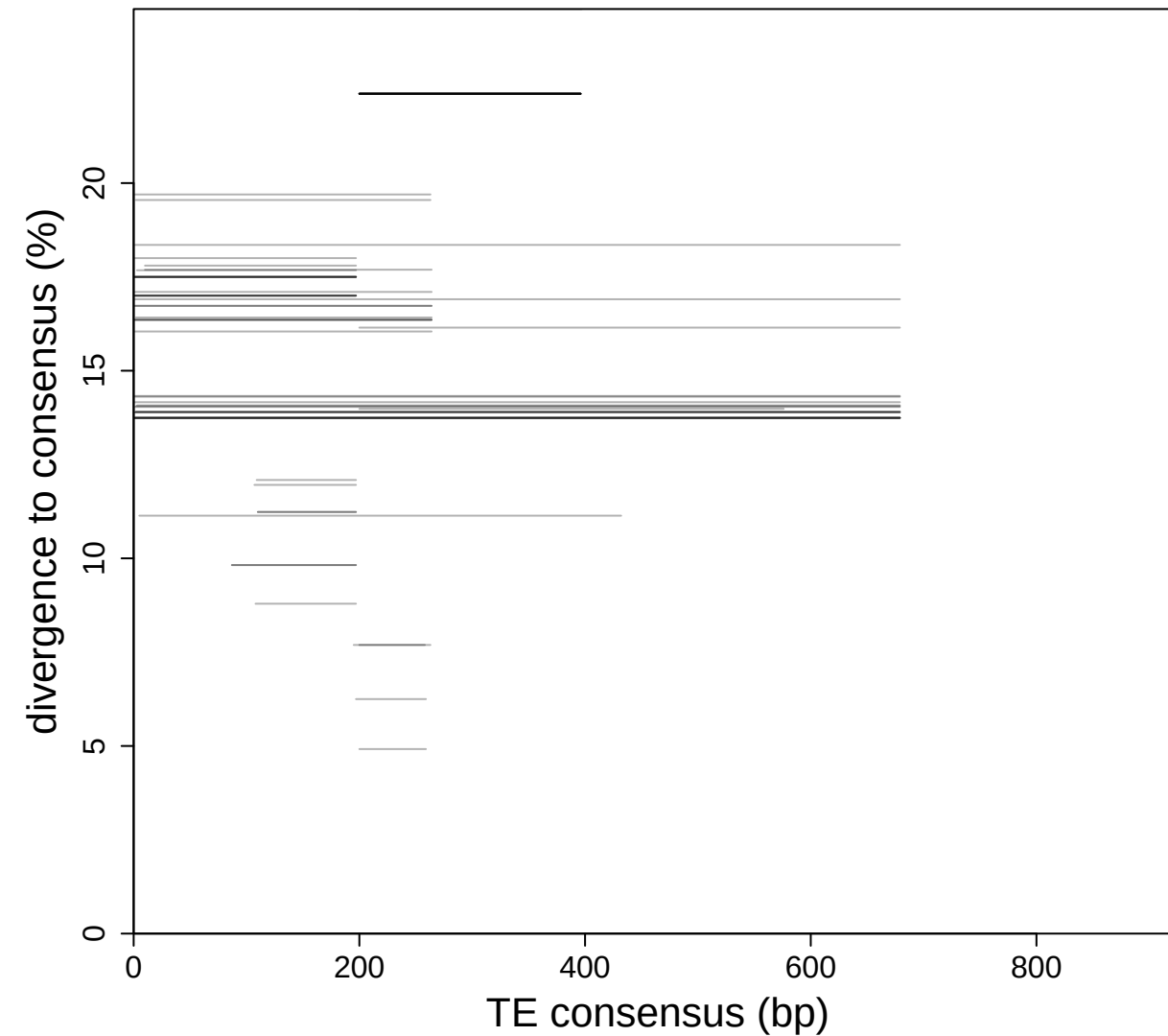


96.fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.1
size: 3629bp; fragments: 71; full length: 10 (≥ 3266.1 bp)

After TEtrimmer Extended plot Blue lines are boundaries

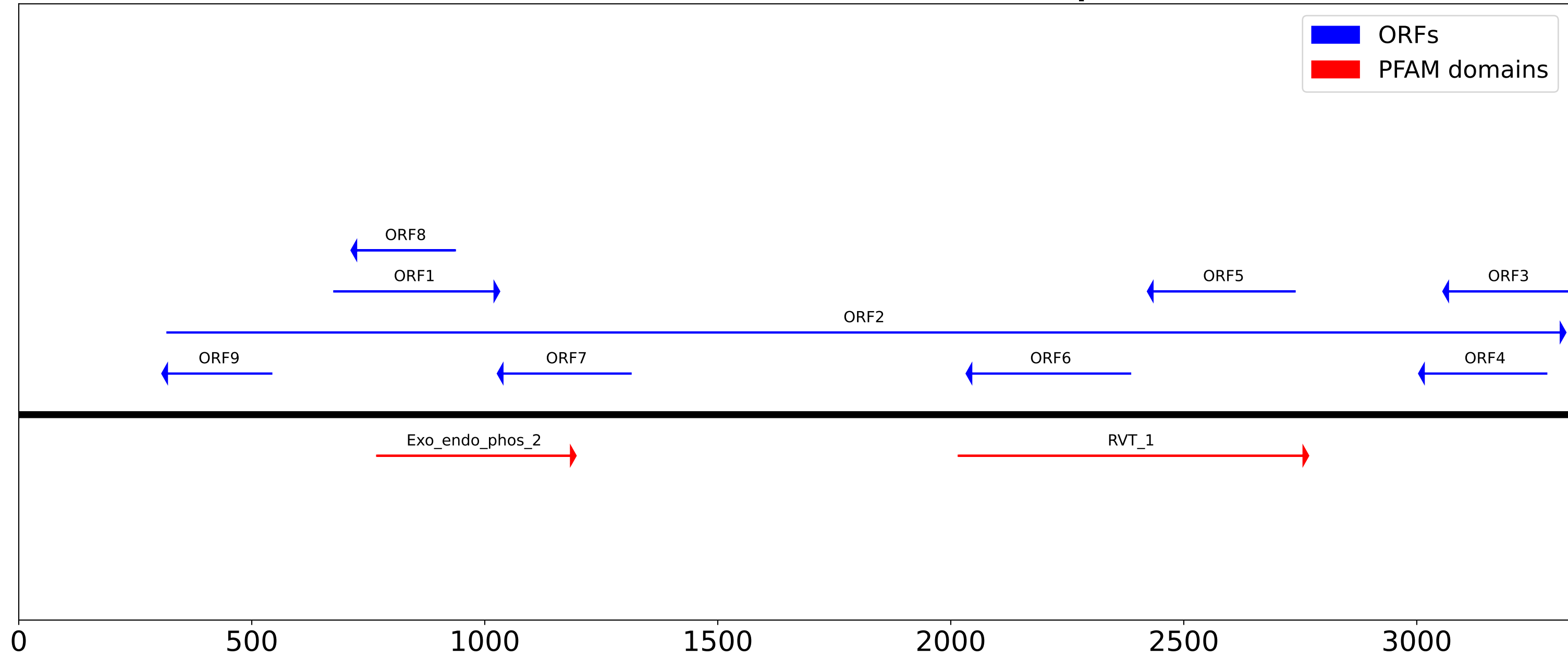


TE: rnd_5_family_10596
size: 929bp; fragments: 68; full length: 0 (≥ 836.1 bp)

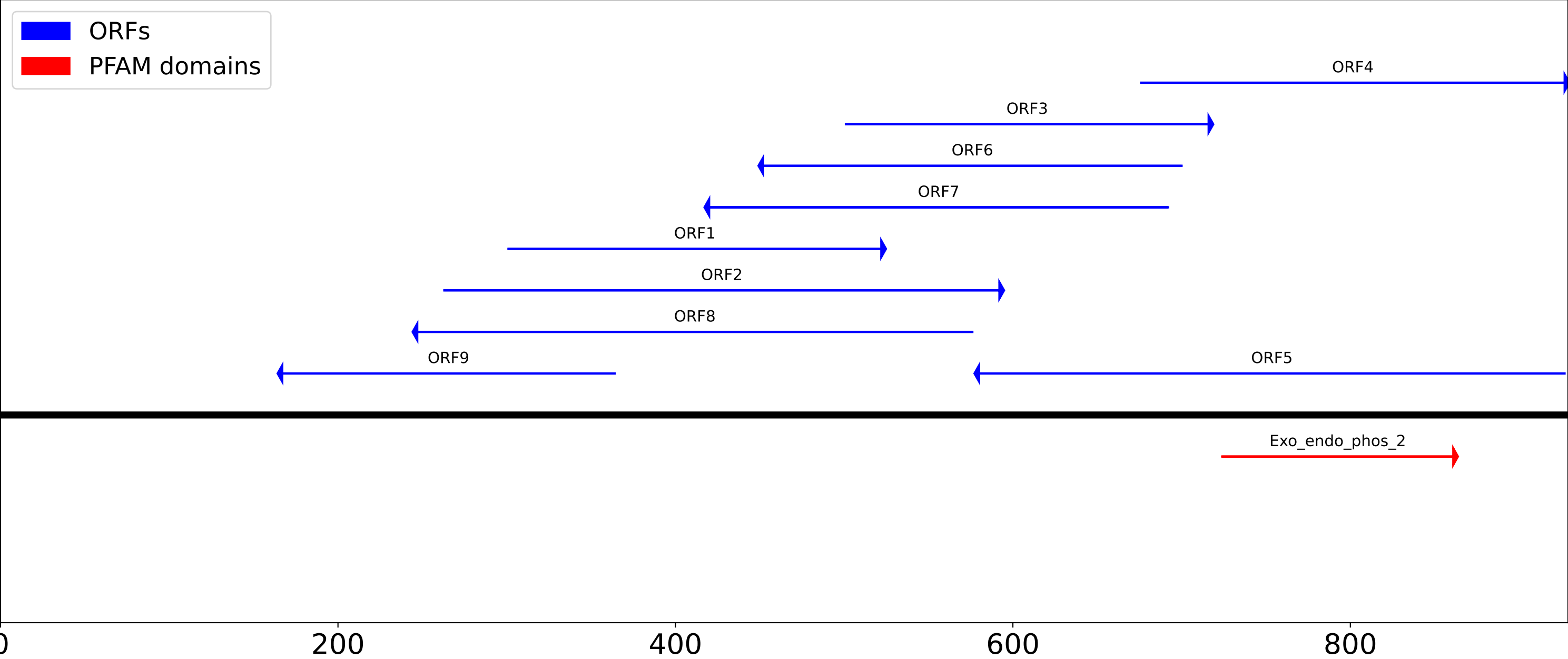


Before TEtrimmer 929 bp

After TEtrimmer ORF and PFAM domain plot



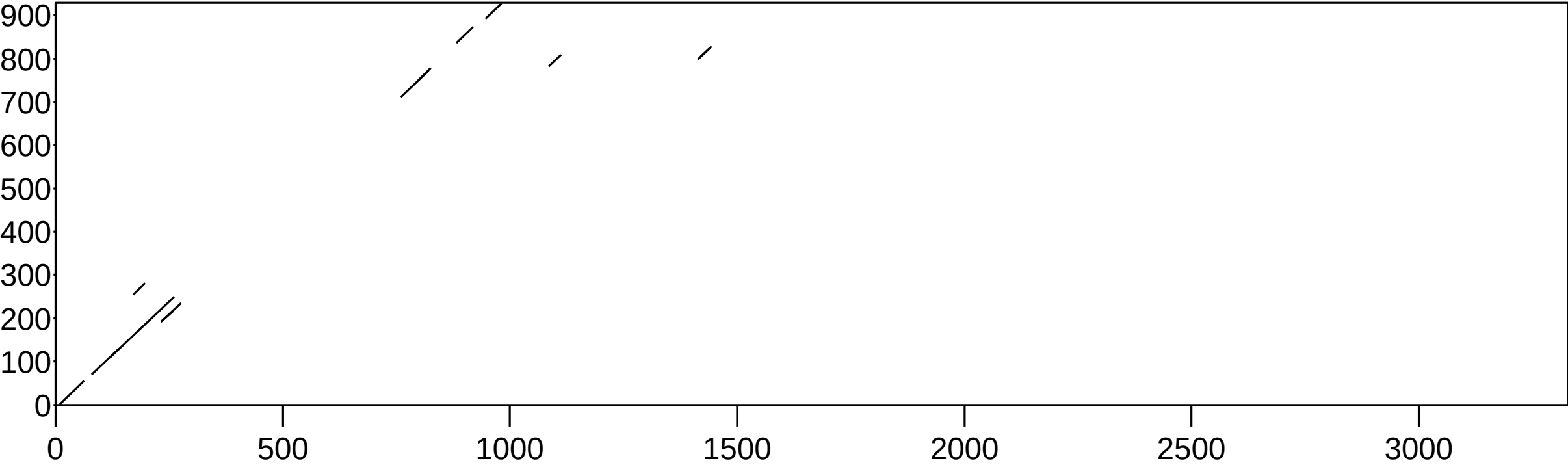
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)