

MSA length = 2774



Start crop Point

End crop Point

0

10

0

500

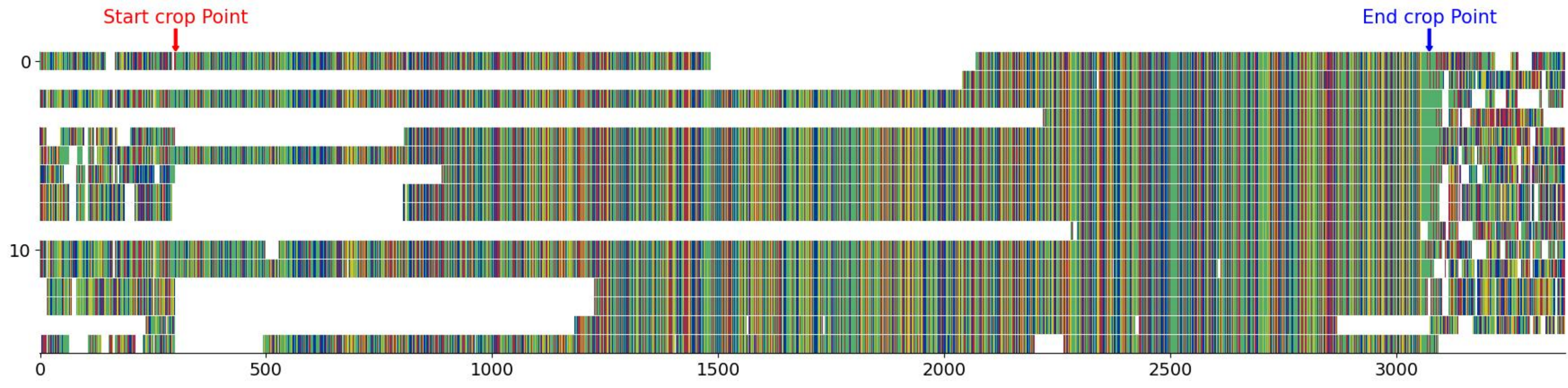
1000

1500

2000

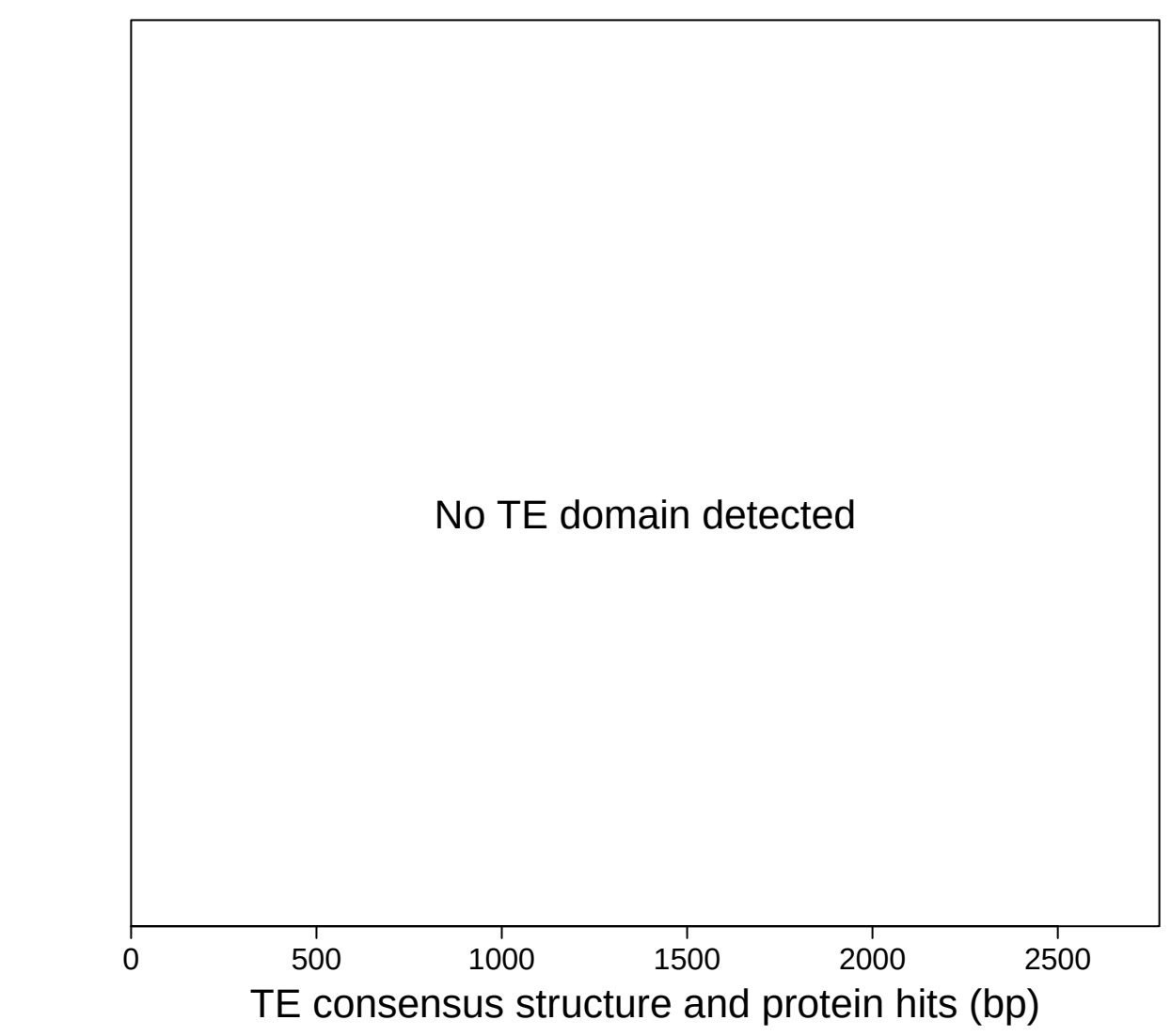
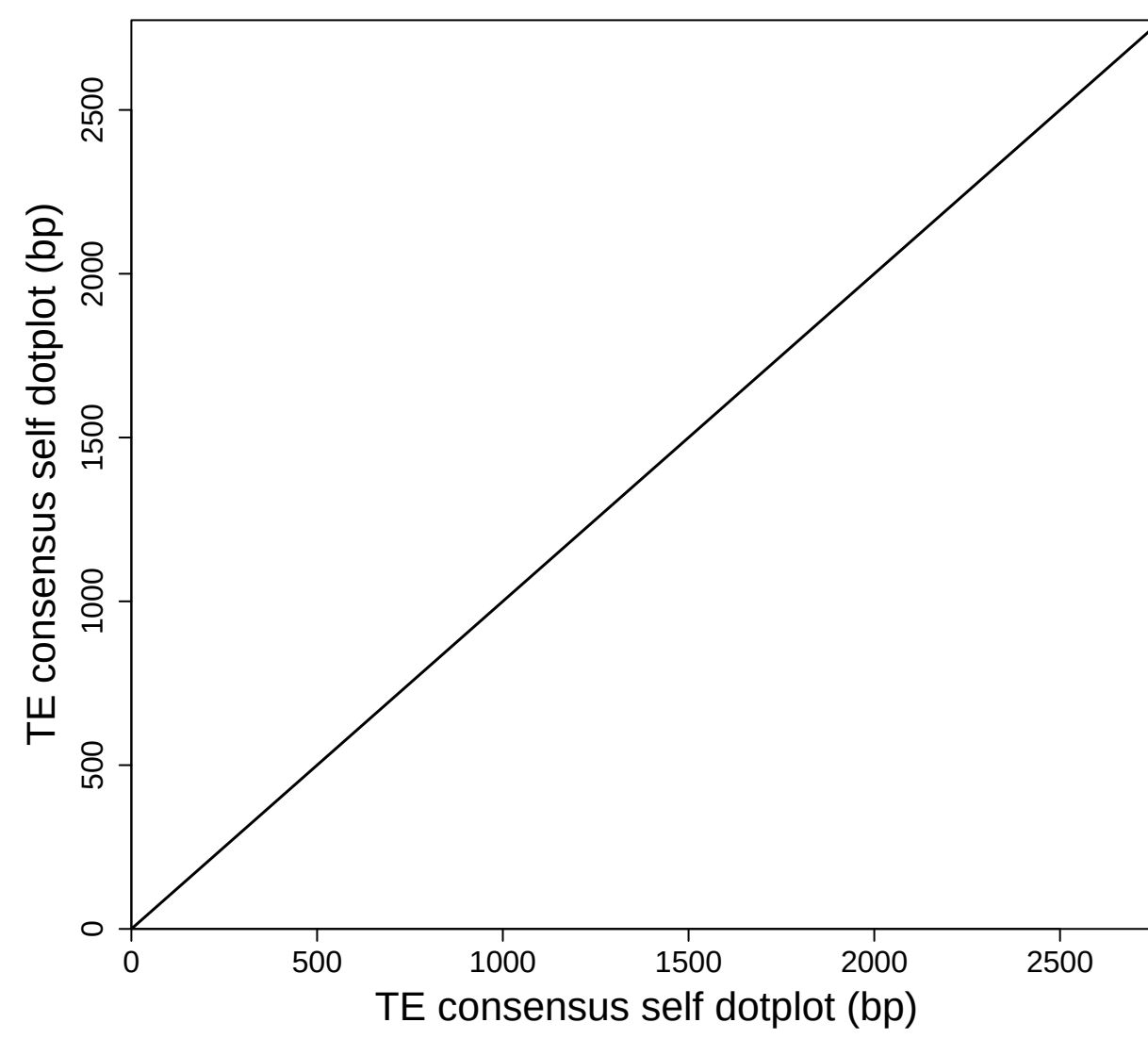
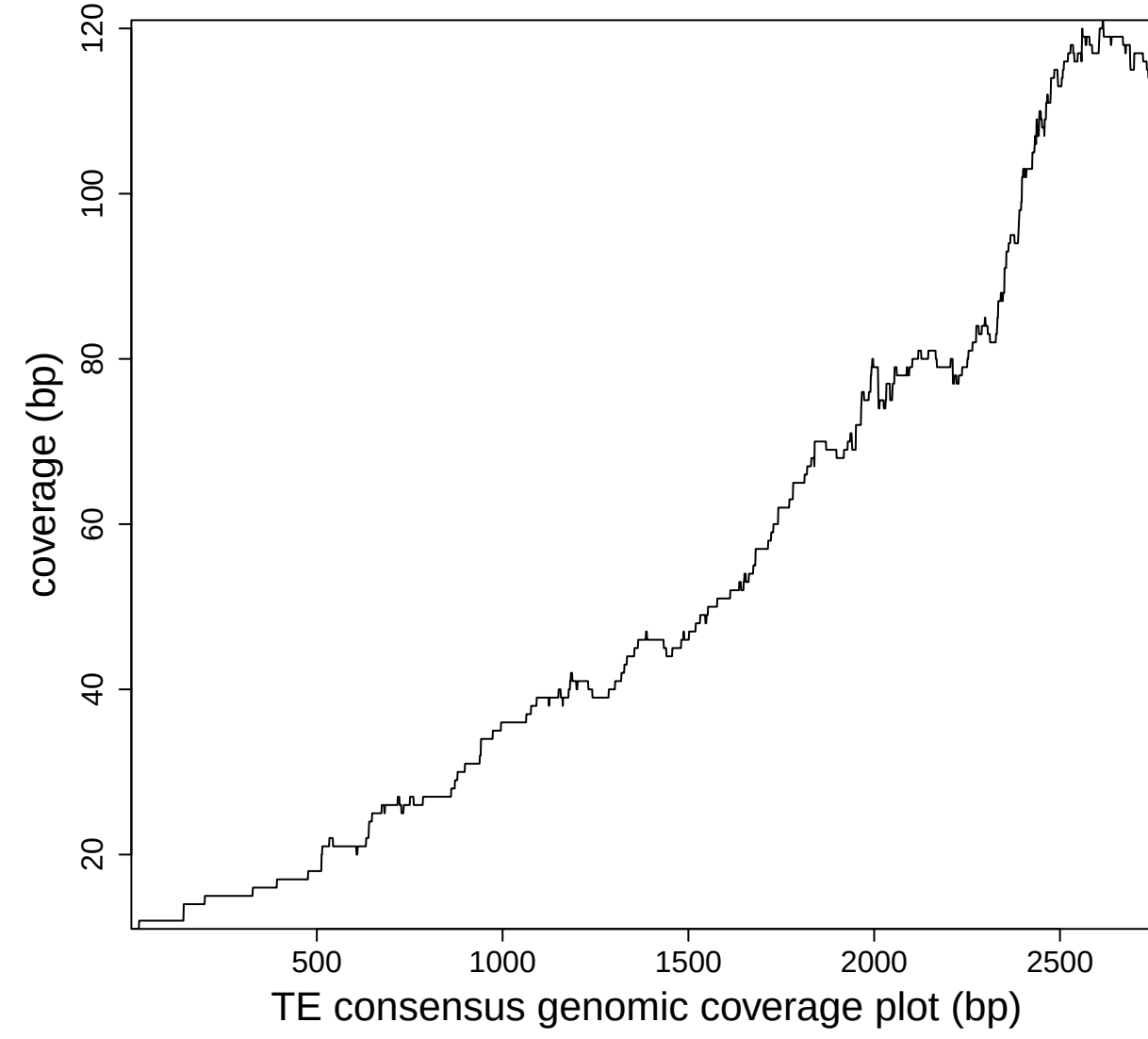
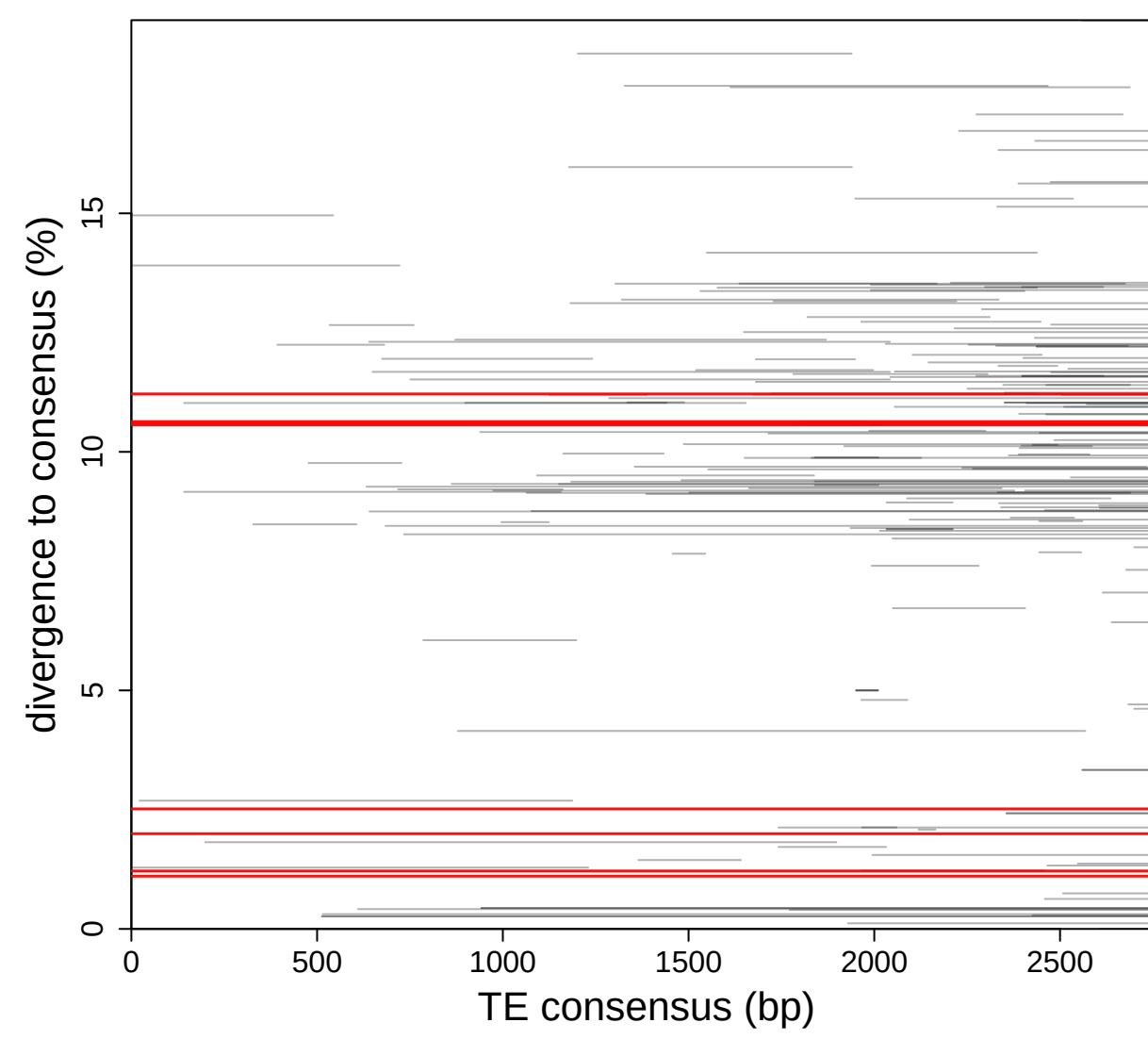
2500

3000



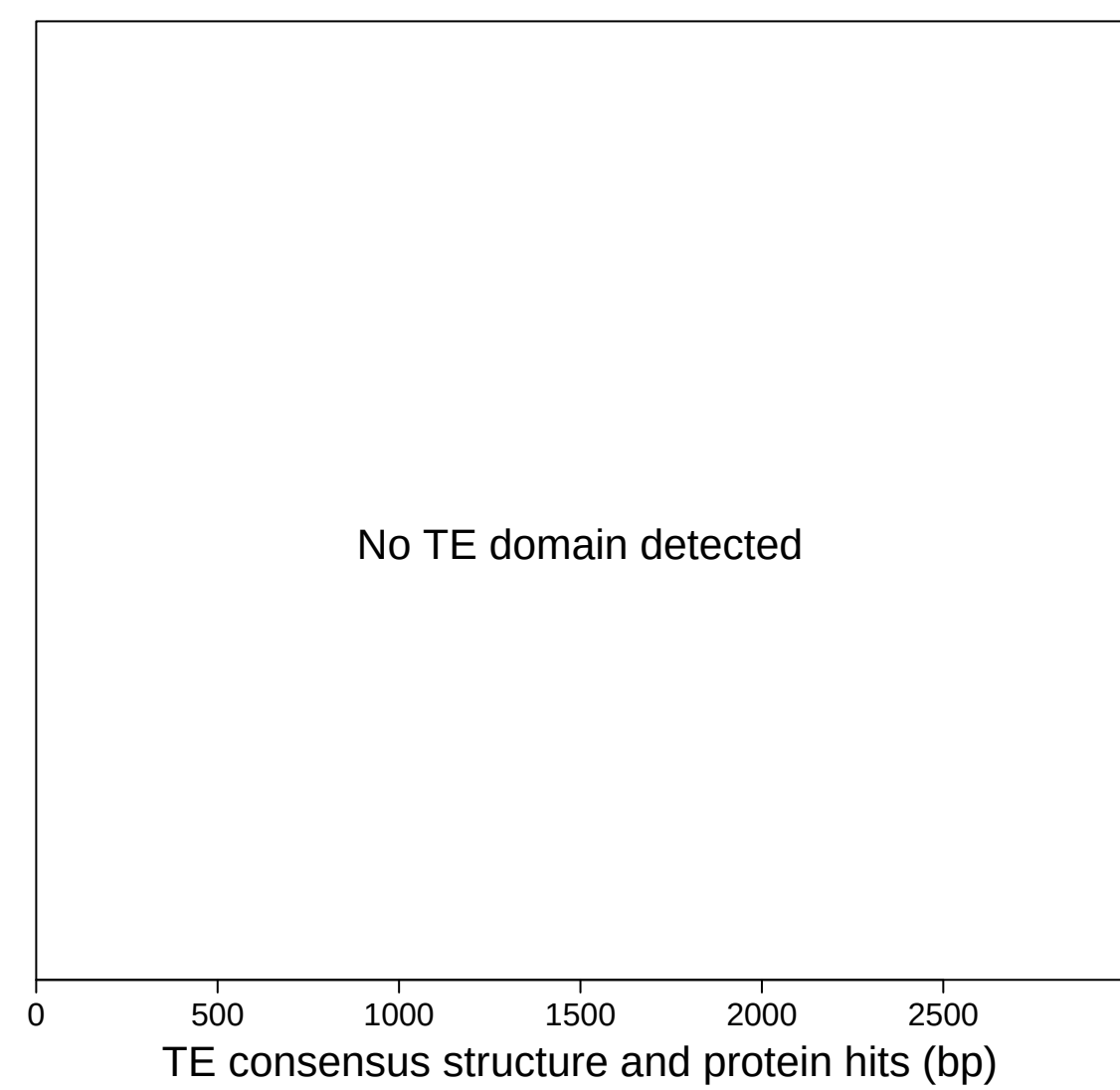
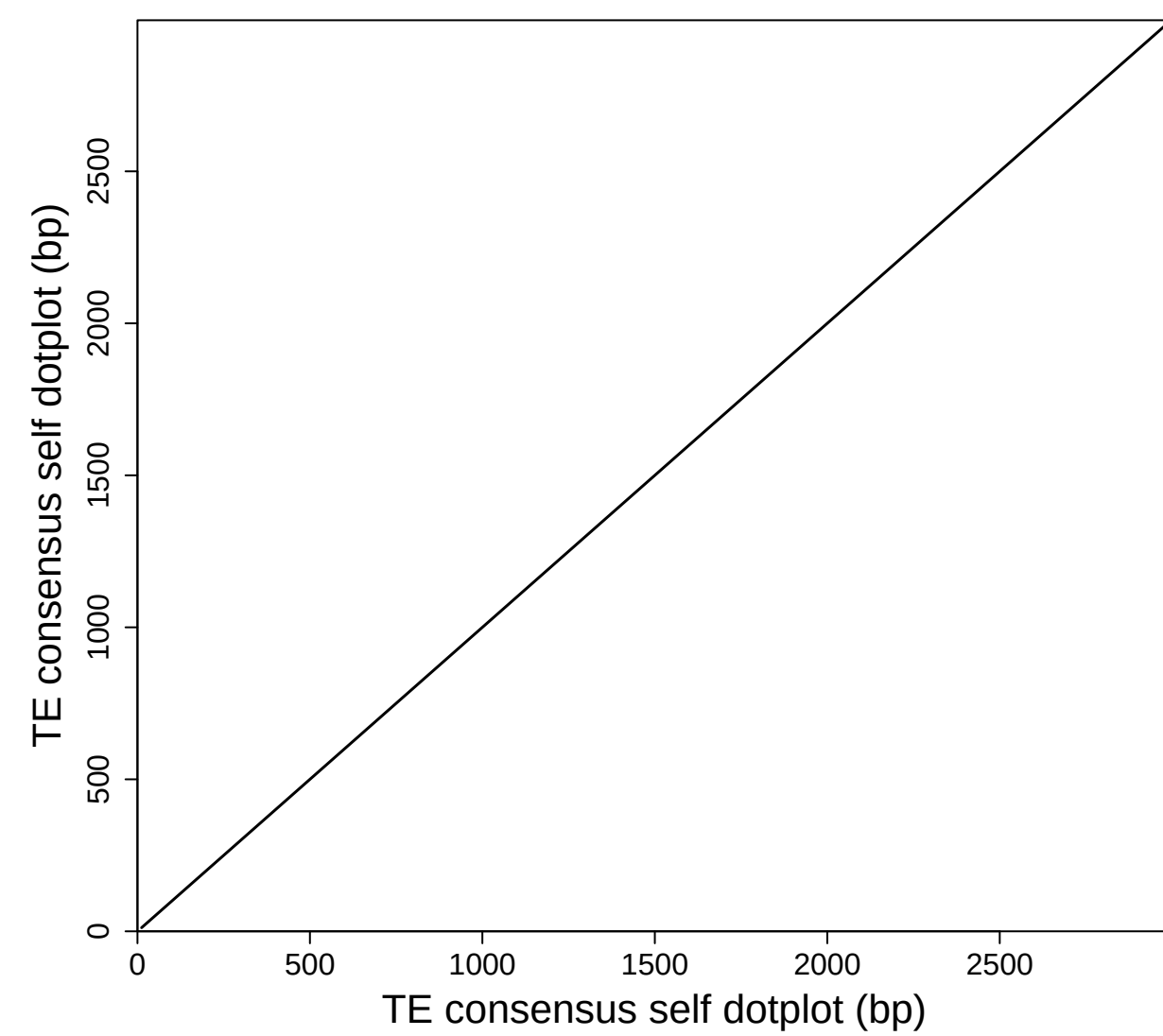
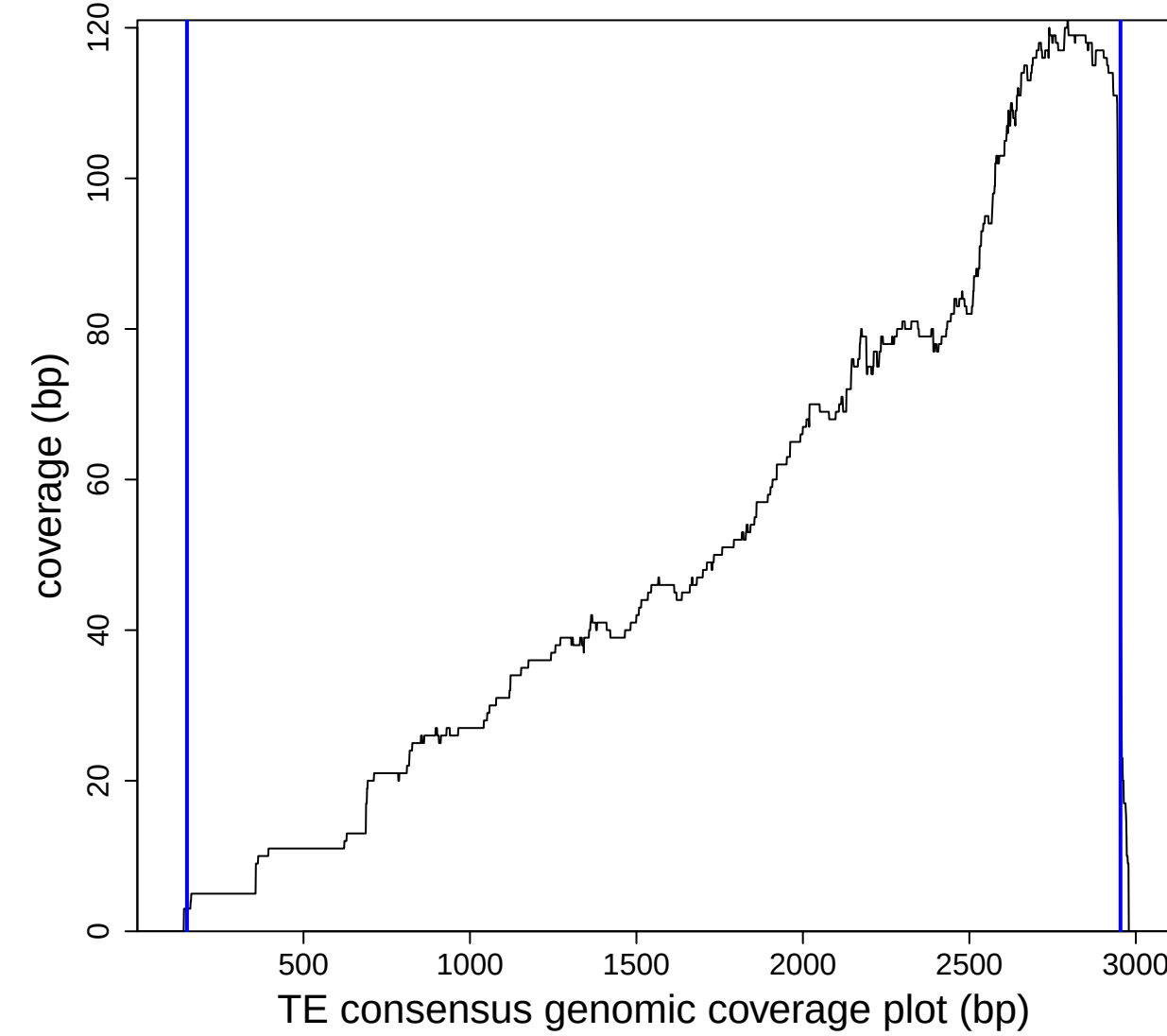
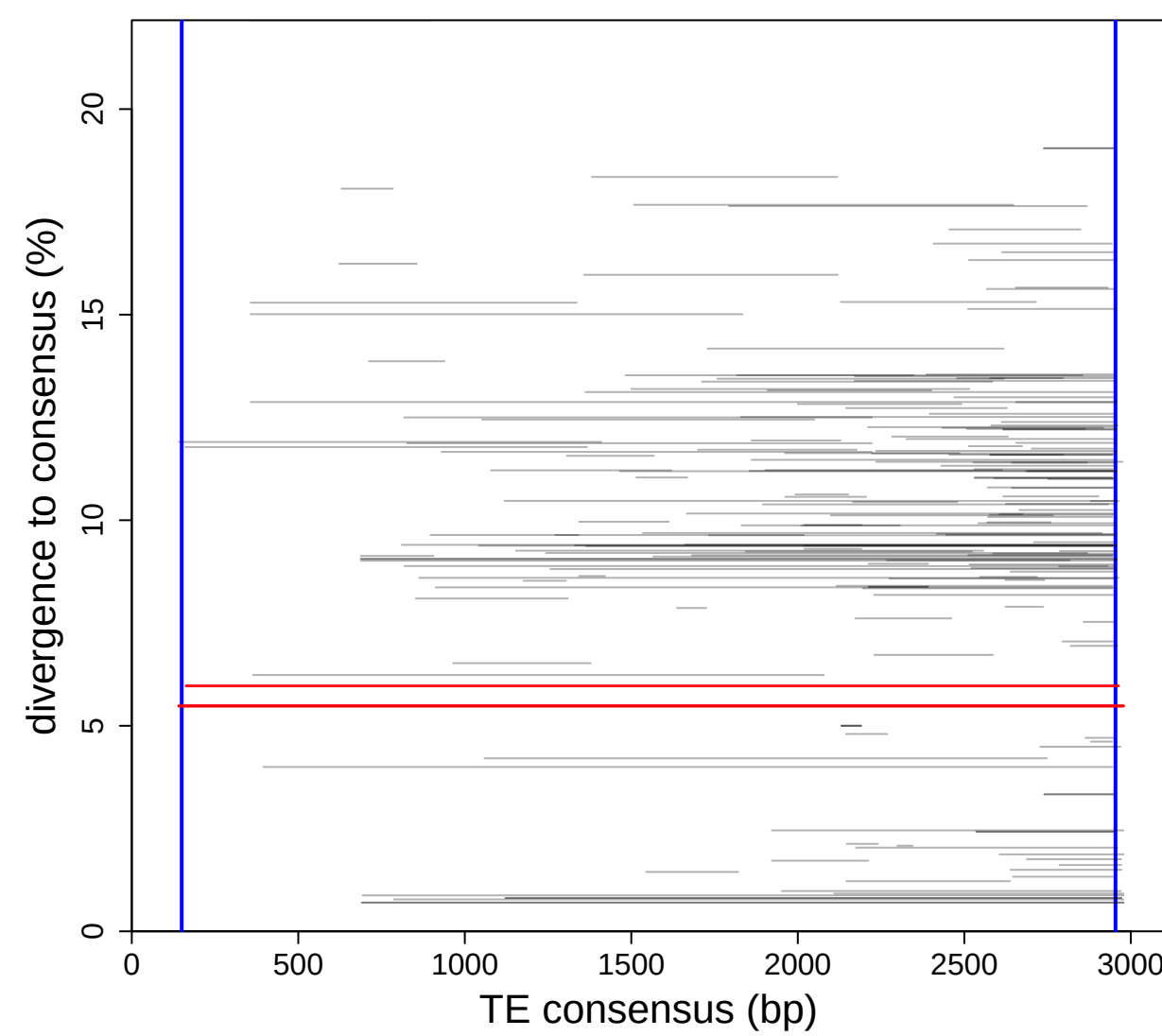
bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_c
size: 2774bp; fragments: 198; full length: 8 (>=2496.6bp)

After TEtrimmer 2774 bp

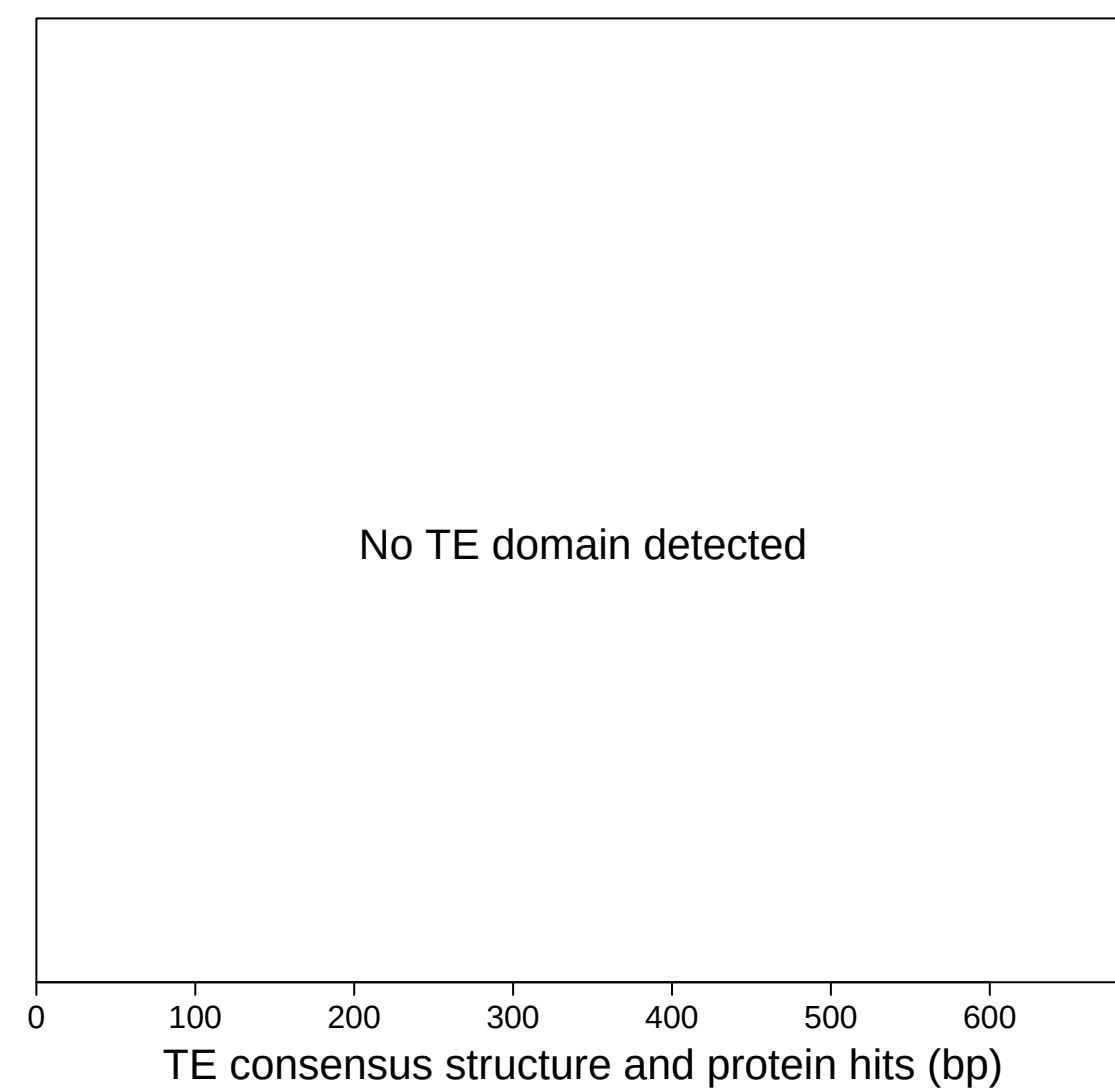
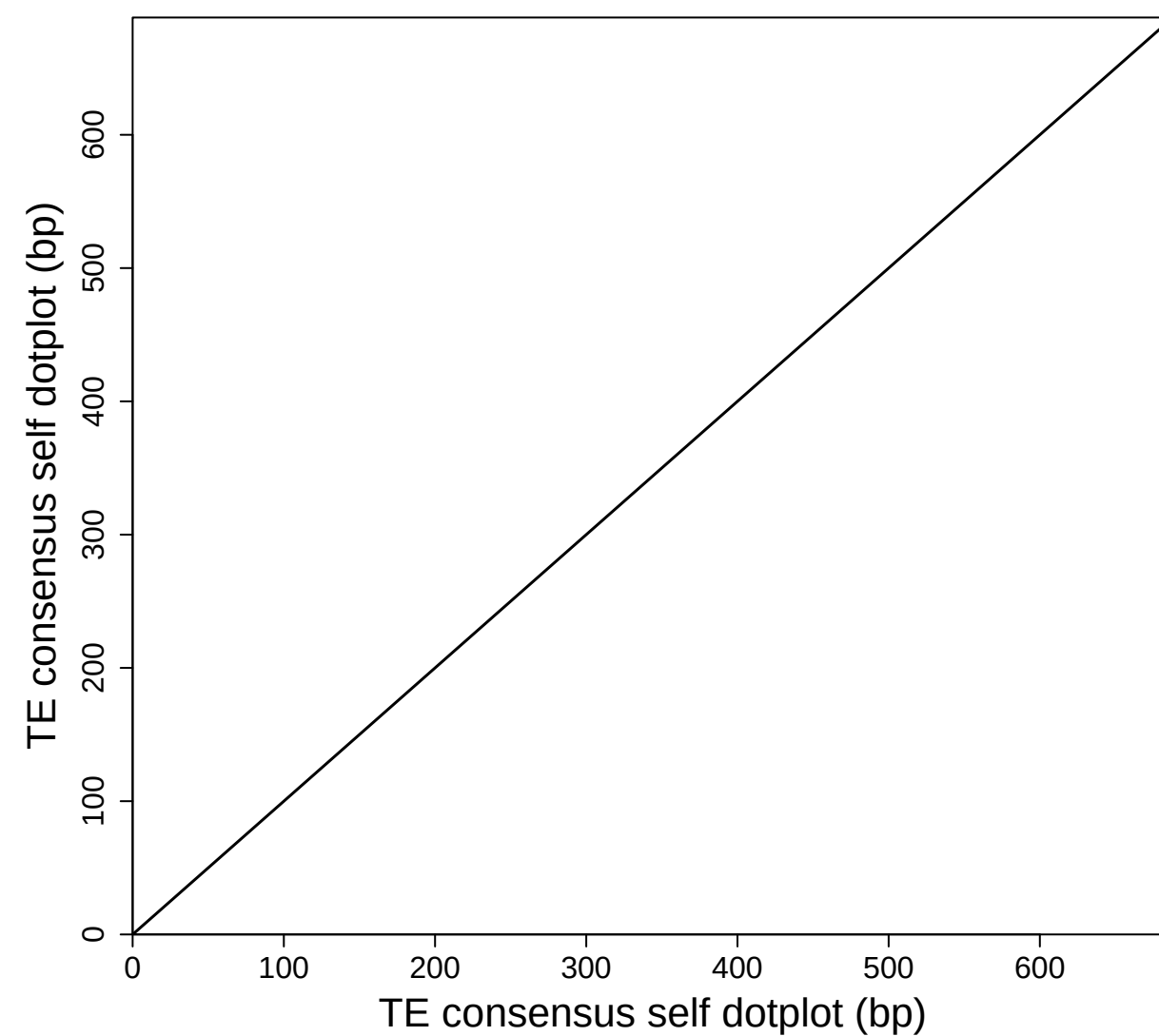
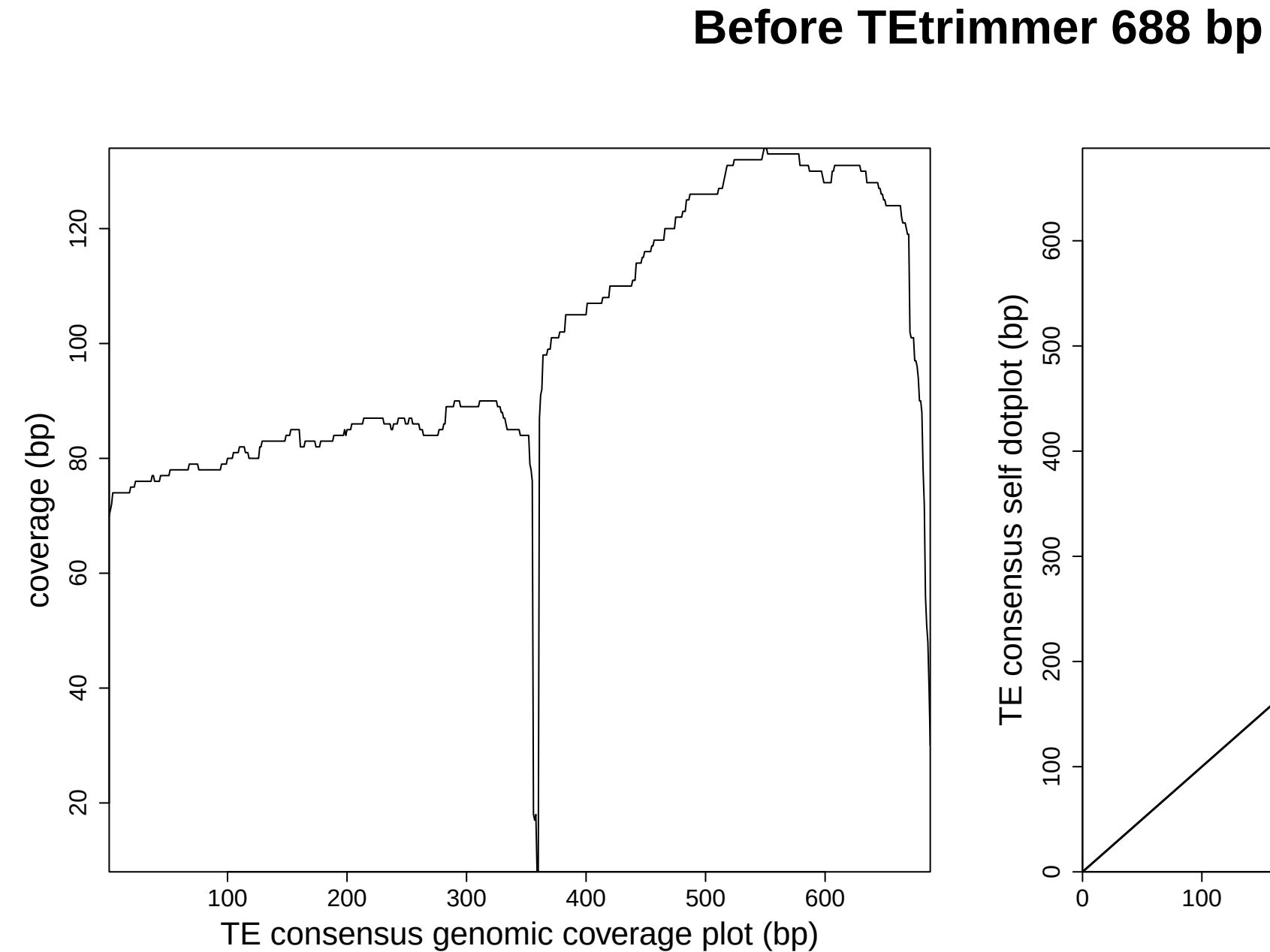
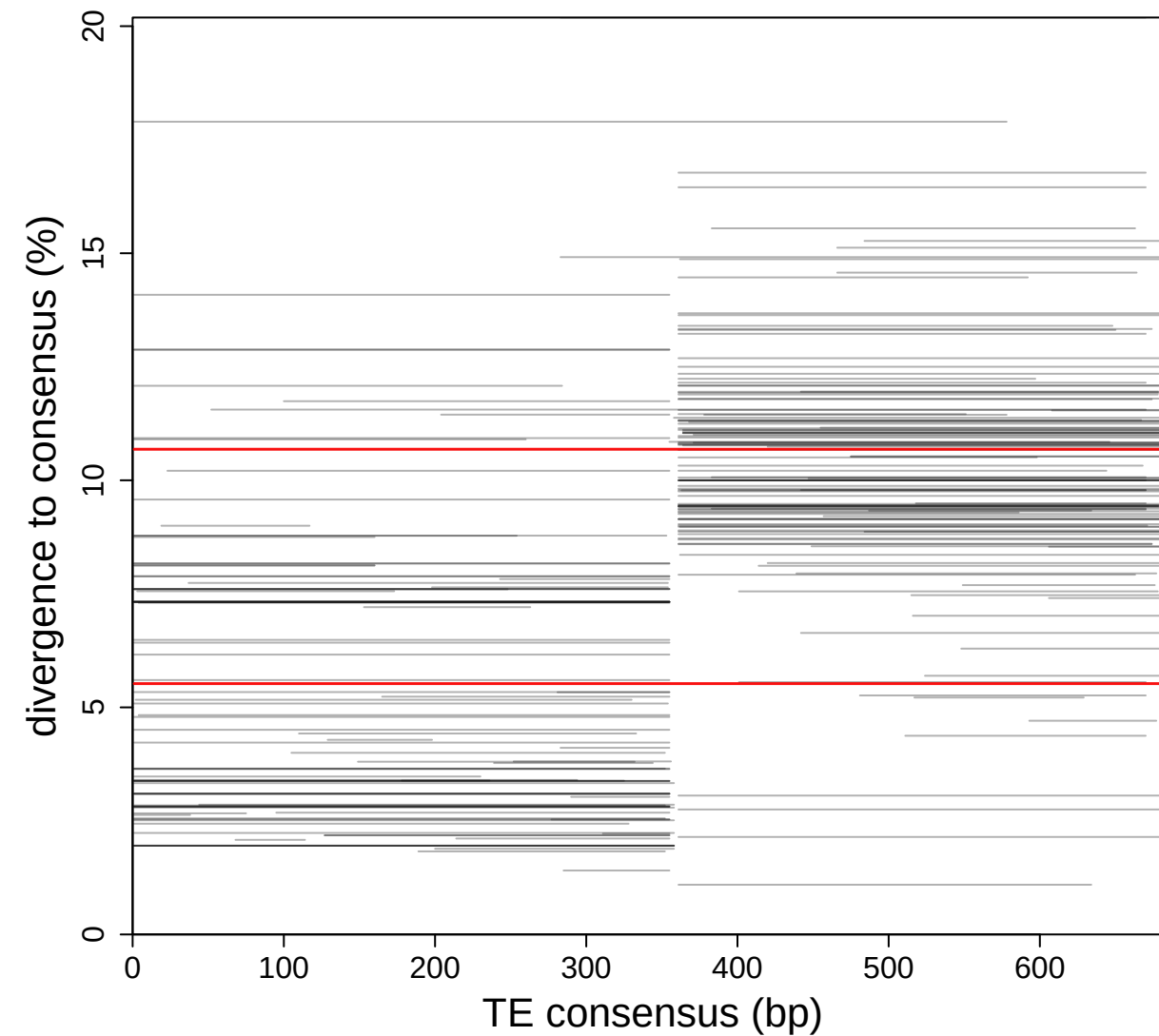


9.fasta.b.bed uf.bed g_2.bed fm_1.bed 0_0_bcln.fa aln.fa cl.f
size: 3104bp; fragments: 198; full length: 3 (>=2793.6bp)

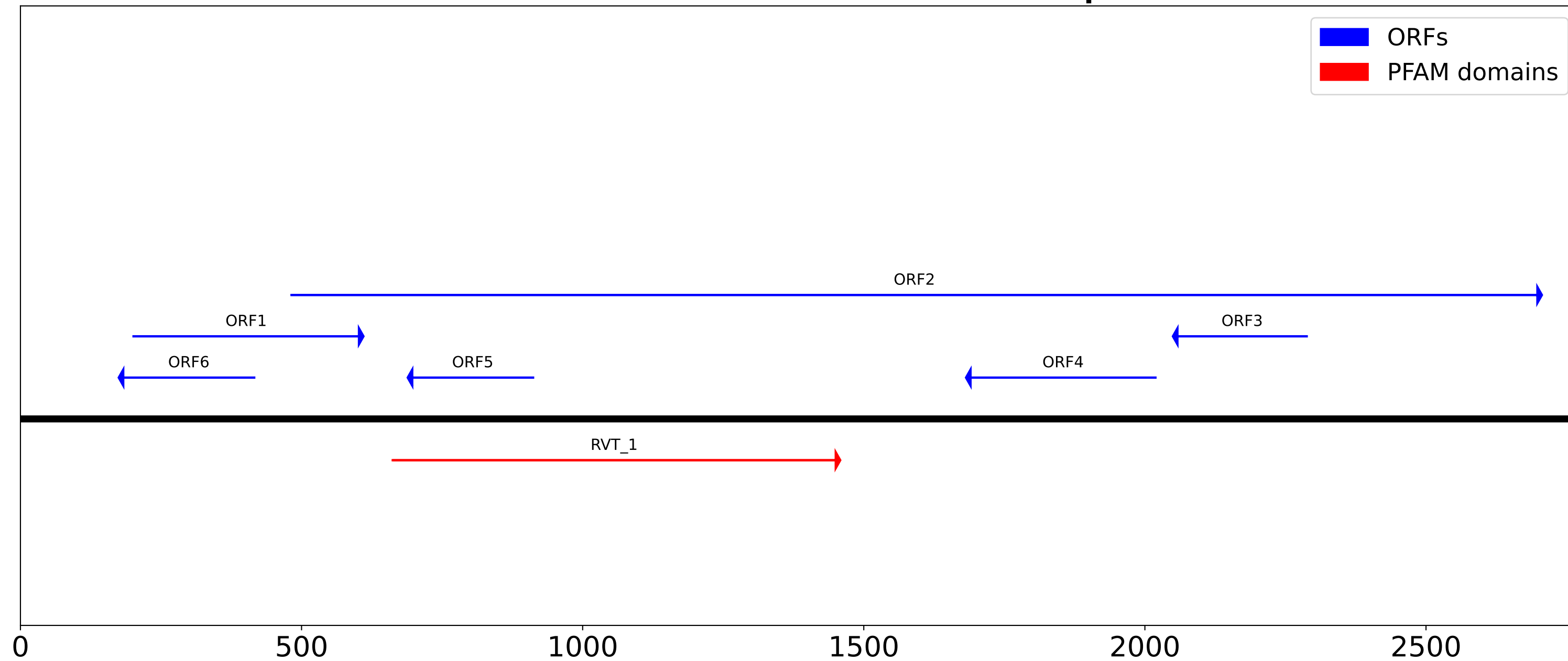
After TEtrimmer Extended plot Blue lines are boundaries



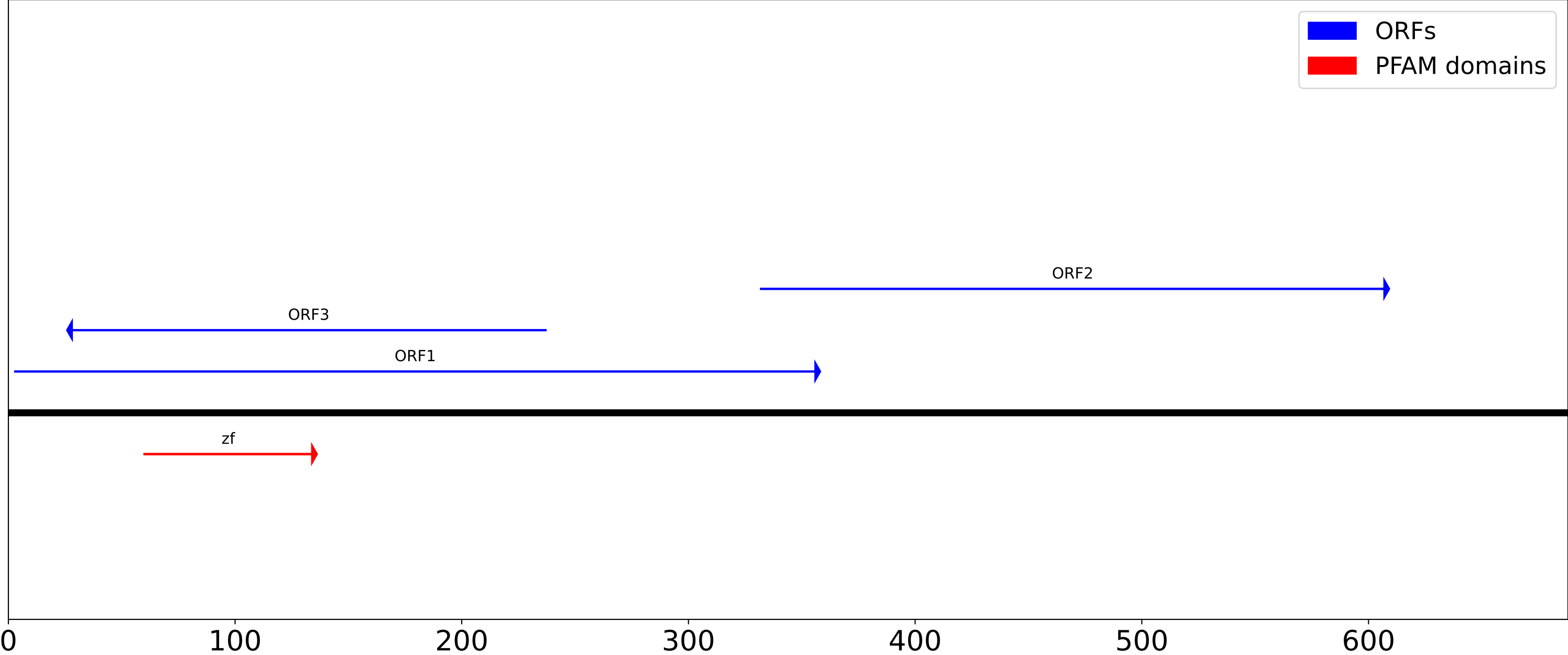
TE: rnd_5_family_7119
size: 688bp; fragments: 239; full length: 2 (≥ 619.2 bp)



After TEtrimmer ORF and PFAM domain plot



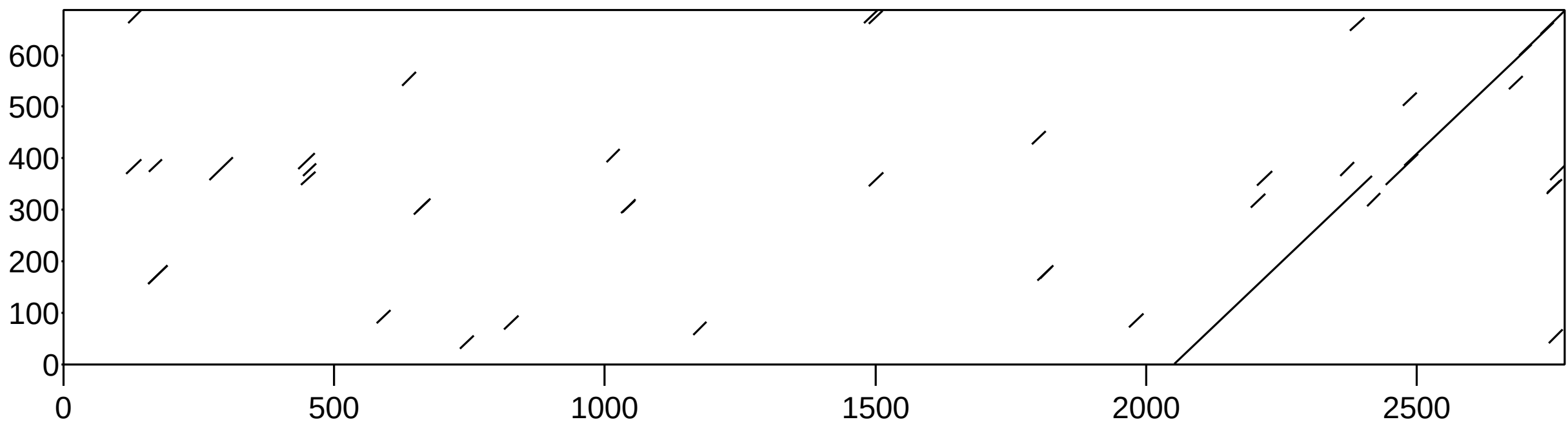
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)