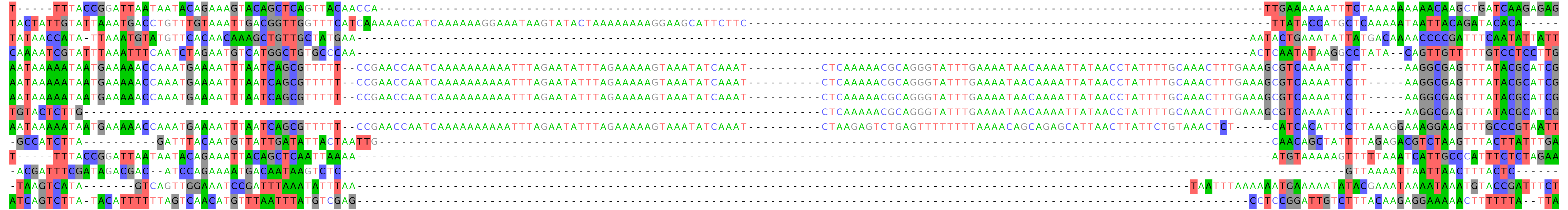


Start crop Point

End crop Point

MSA length = 2150



Start crop Point

End crop Point

0 -

10 -

0

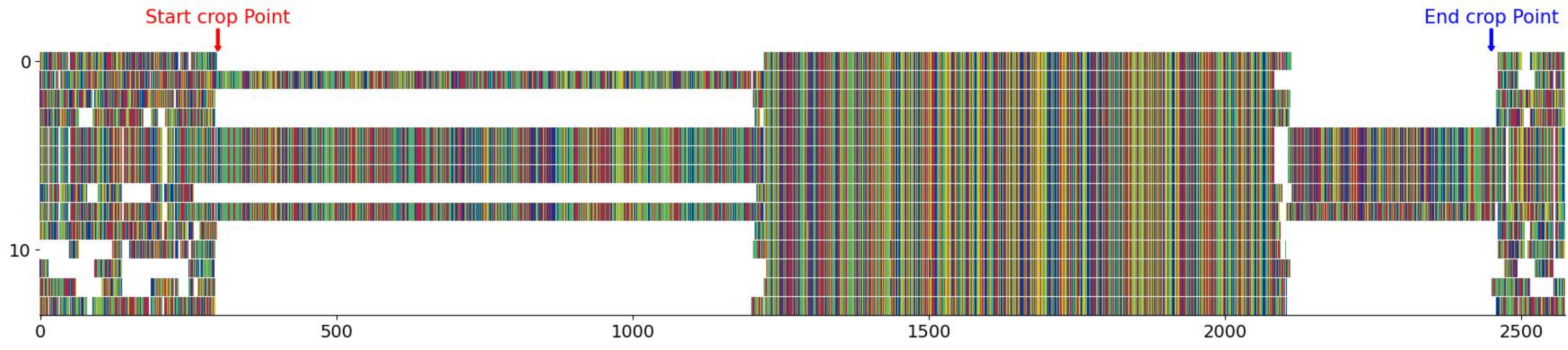
500

1000

1500

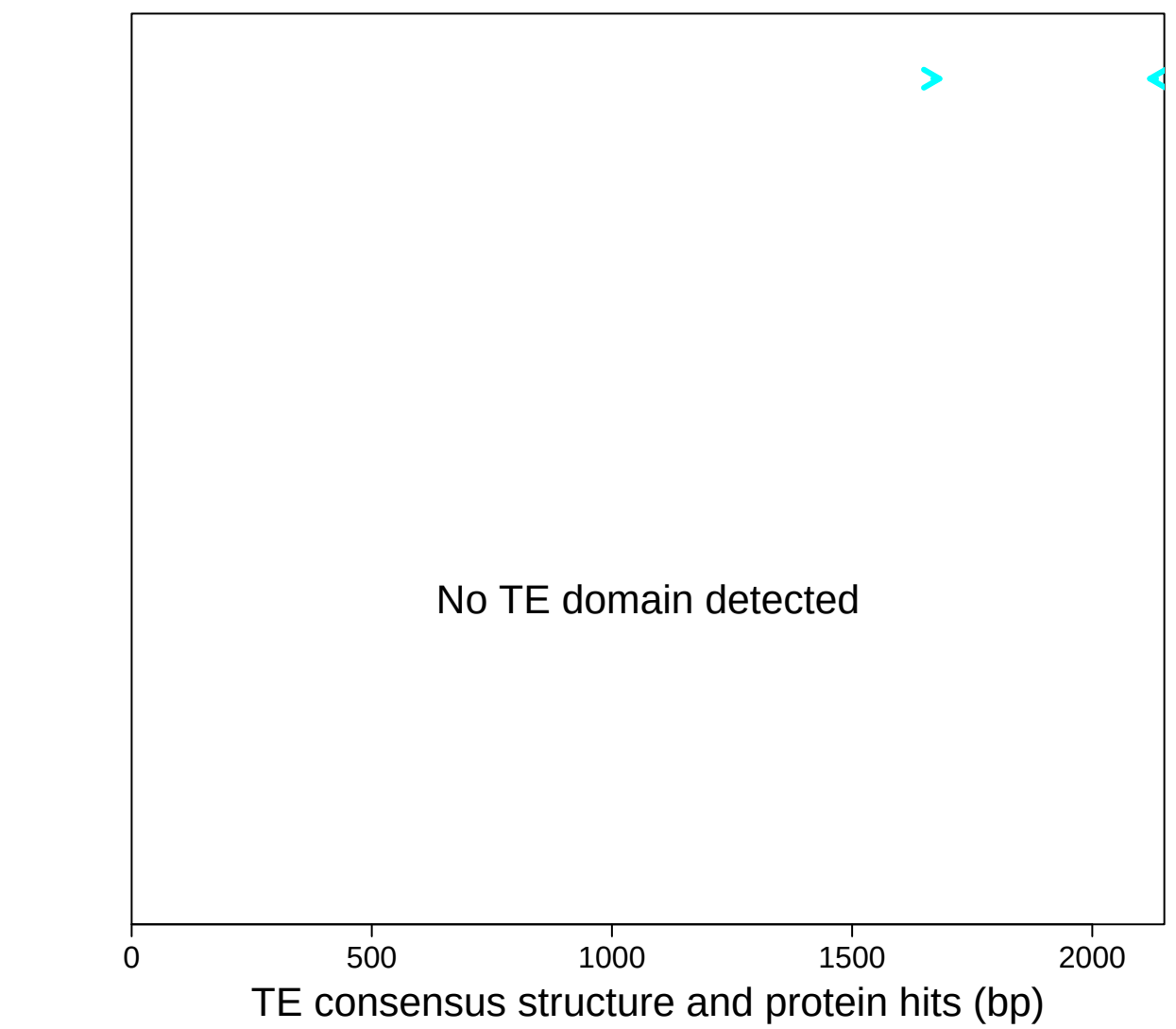
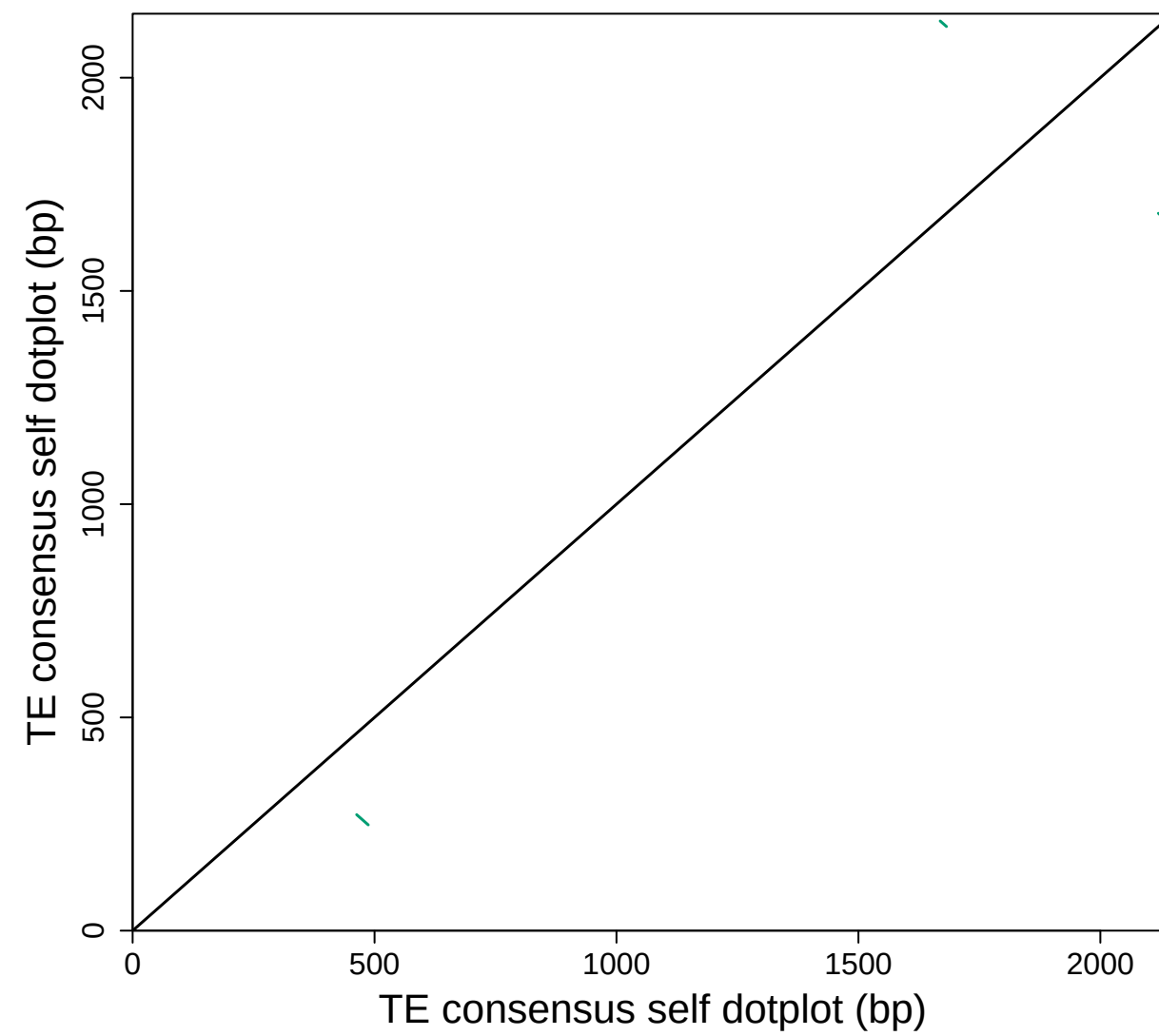
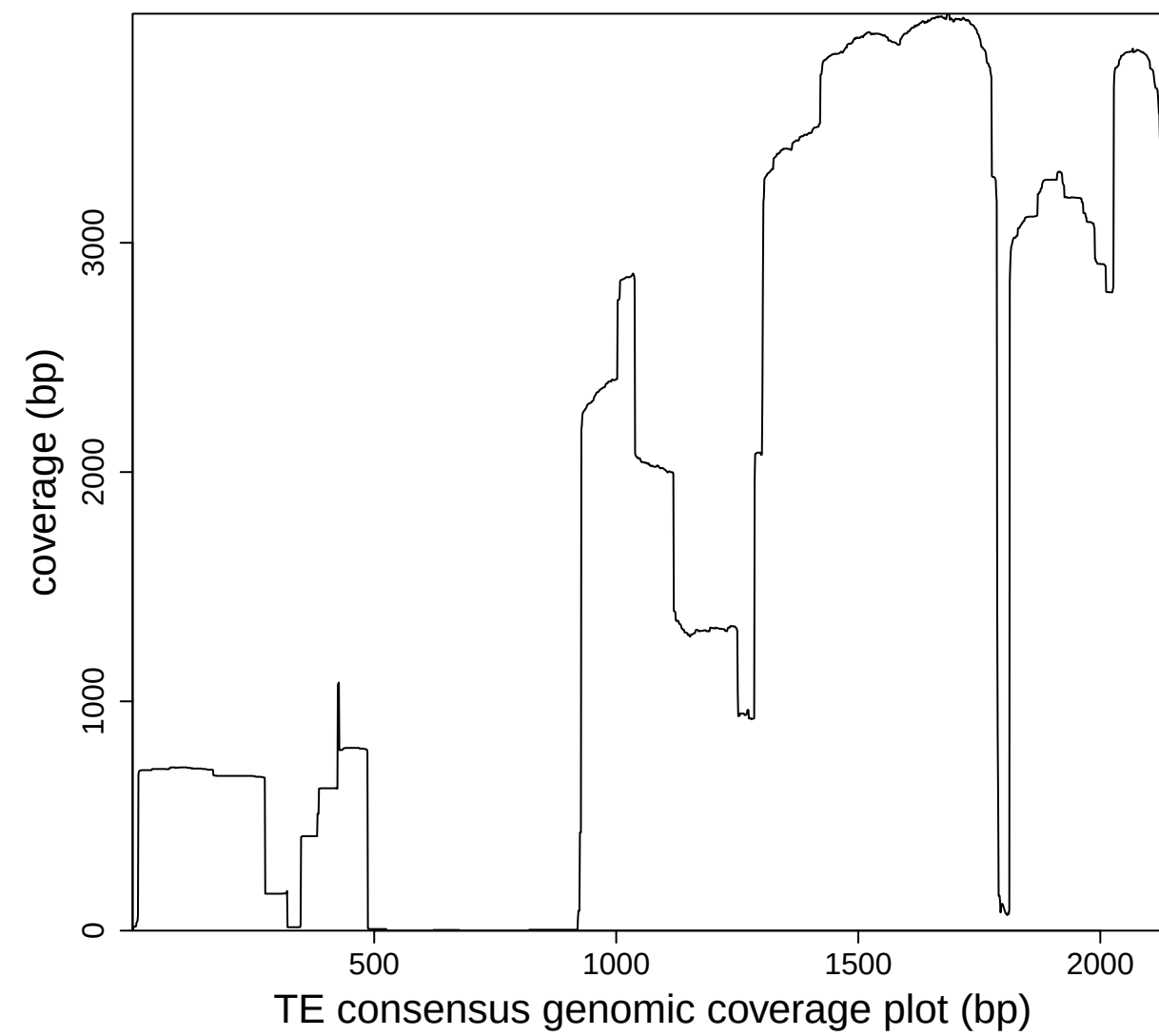
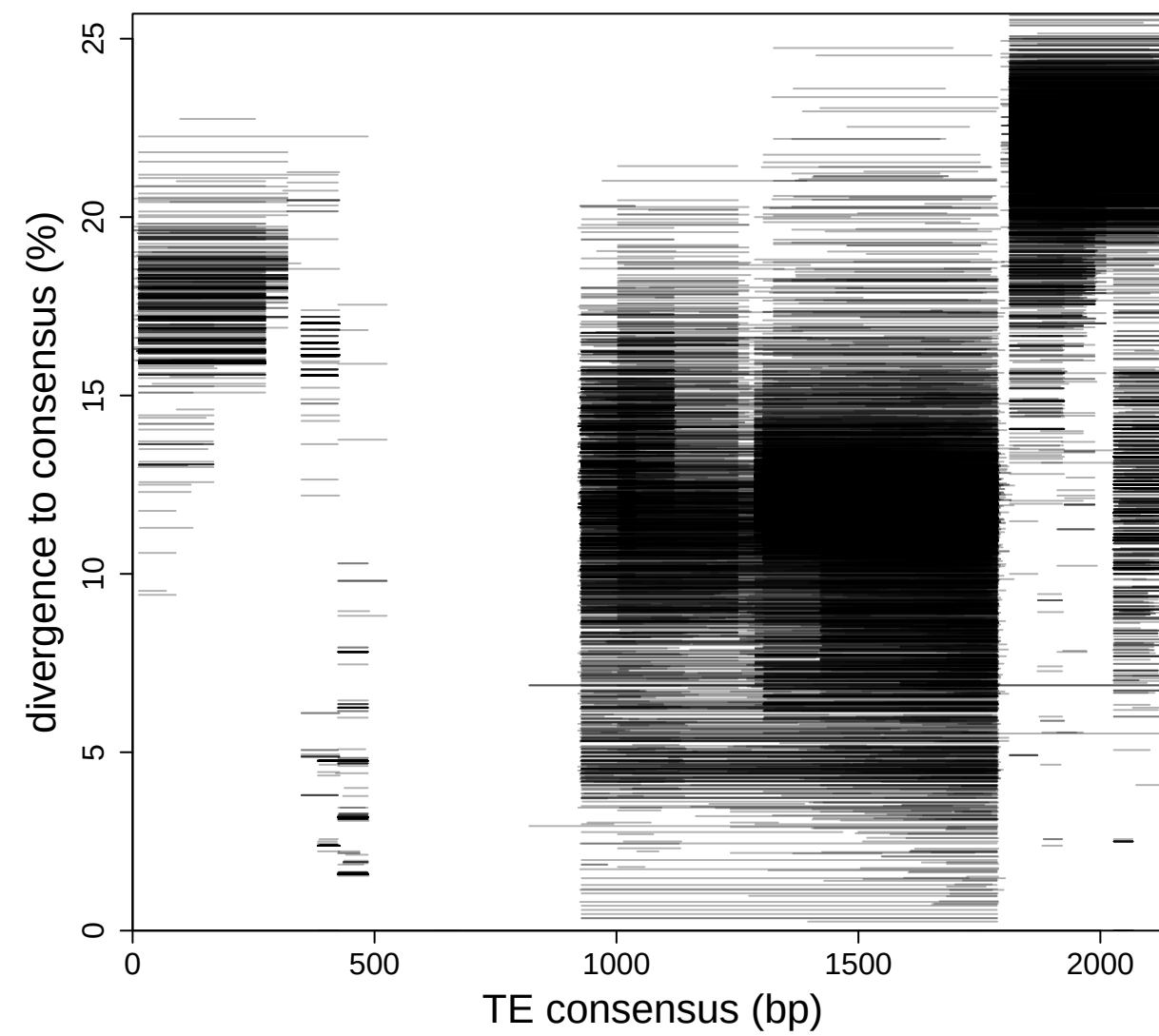
2000

2500



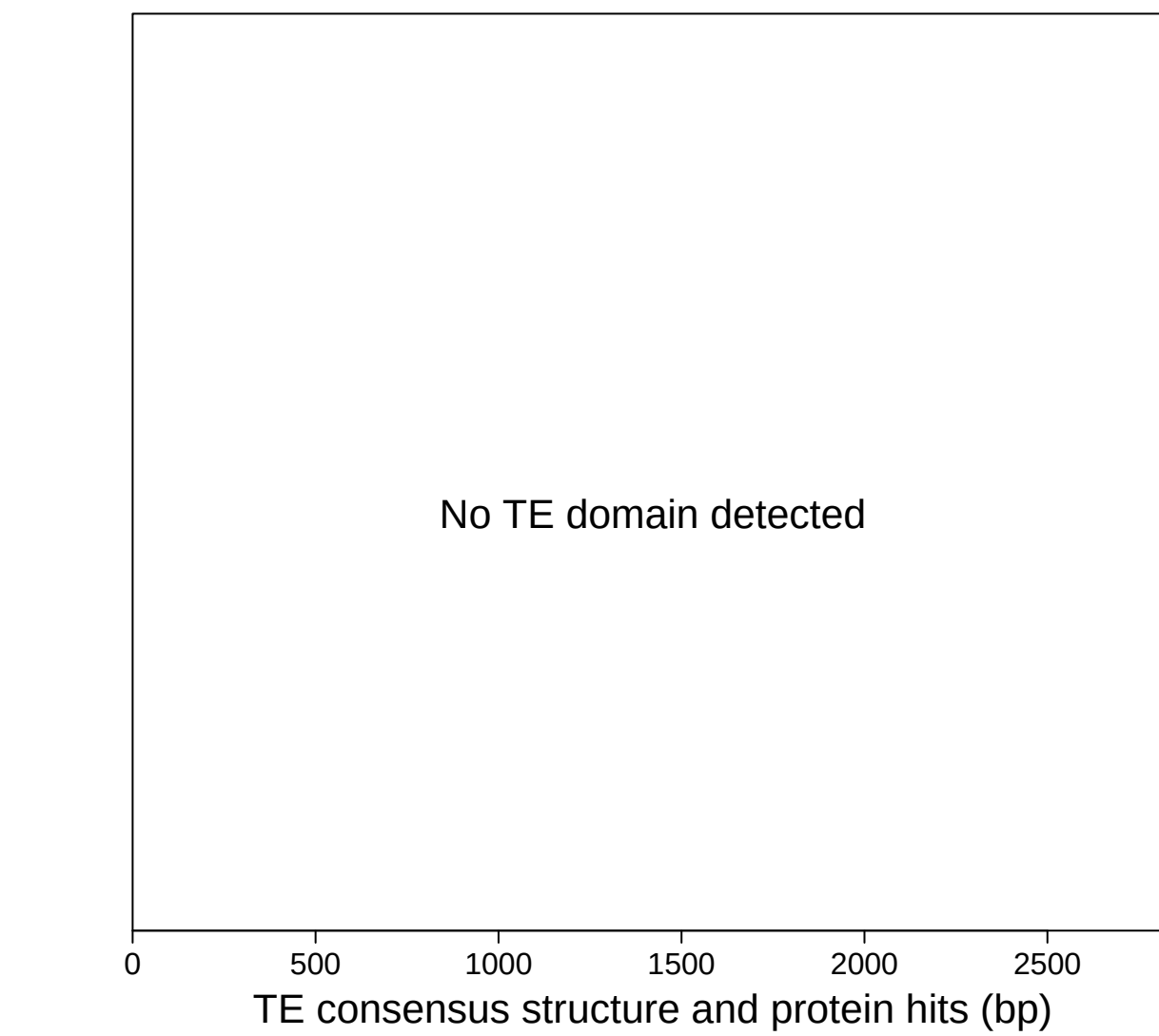
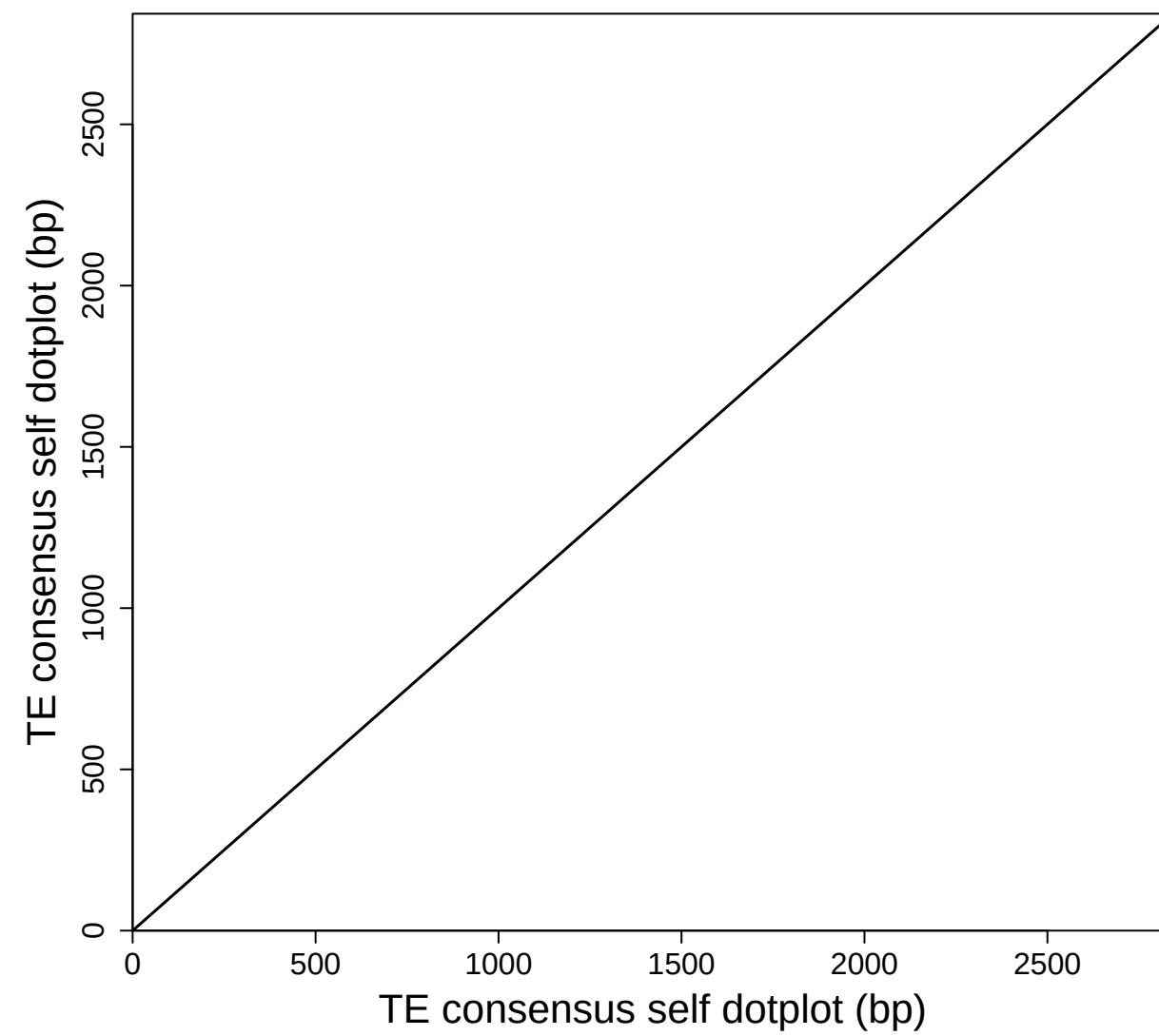
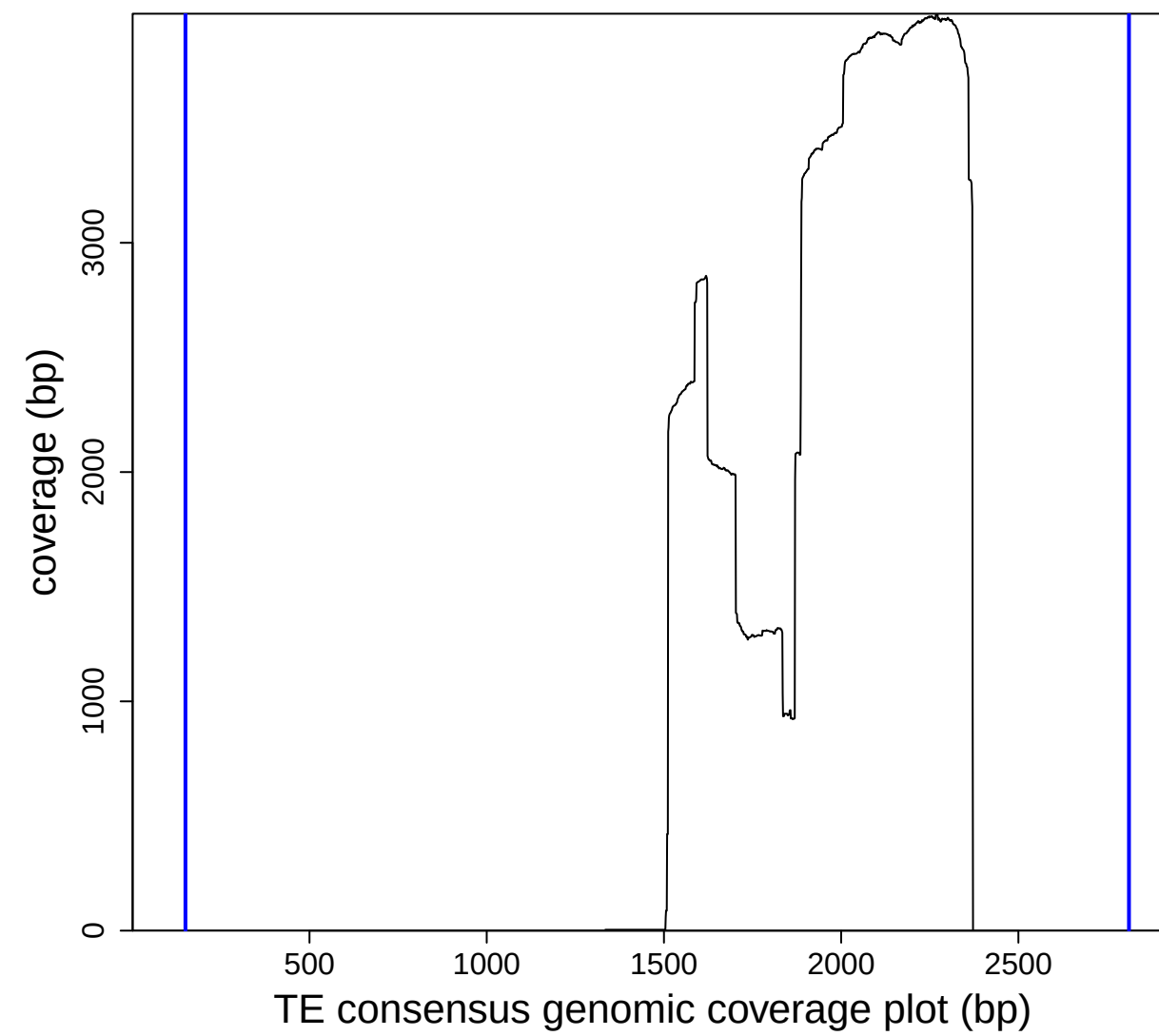
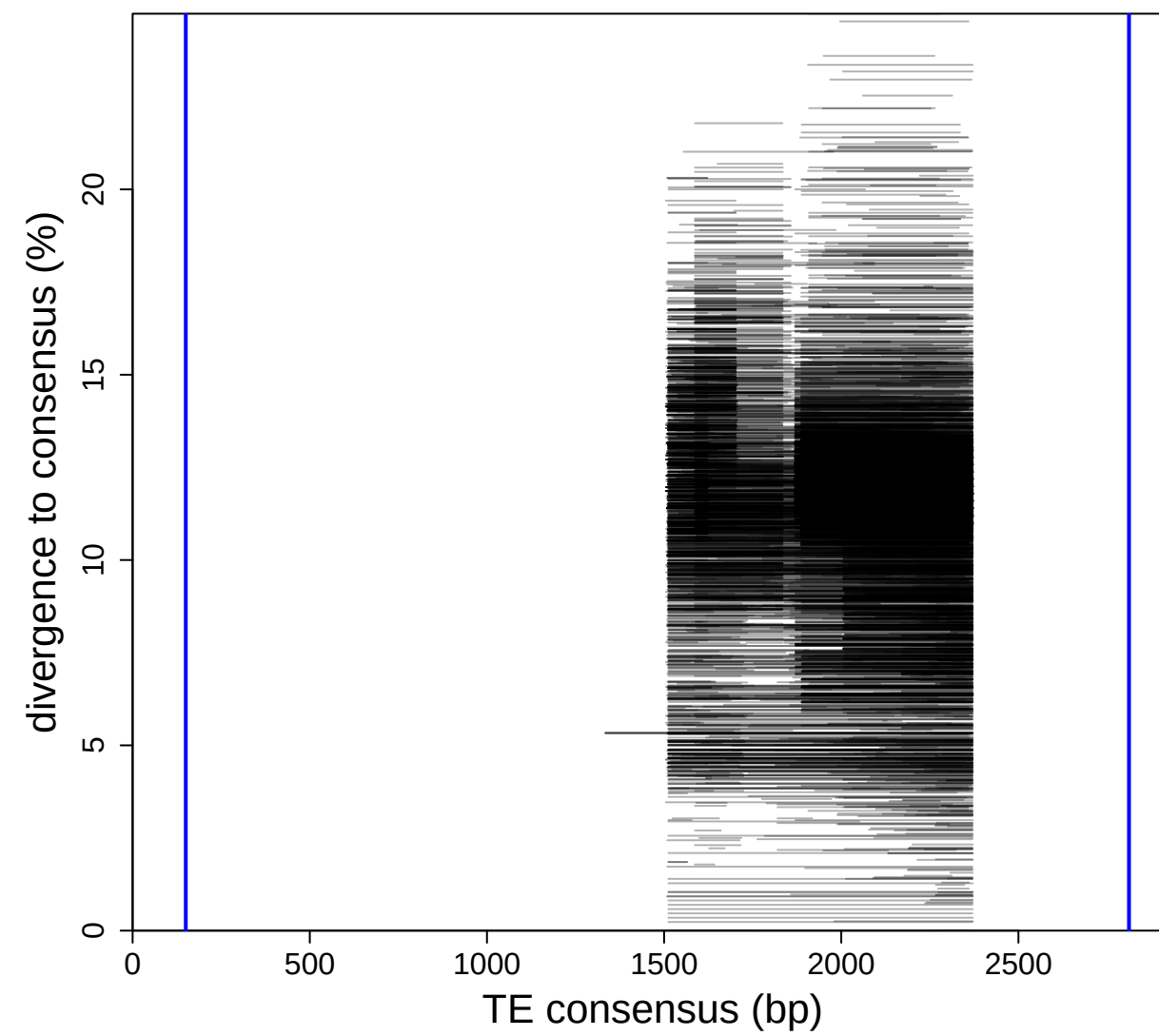
b.bed uf.bed g 3.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 2150bp; fragments: 13128; full length: 0 (>=1935bp)

After TEtrimmer 2150 bp



.fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 2936bp; fragments: 6574; full length: 0 (>=2642.4bp)

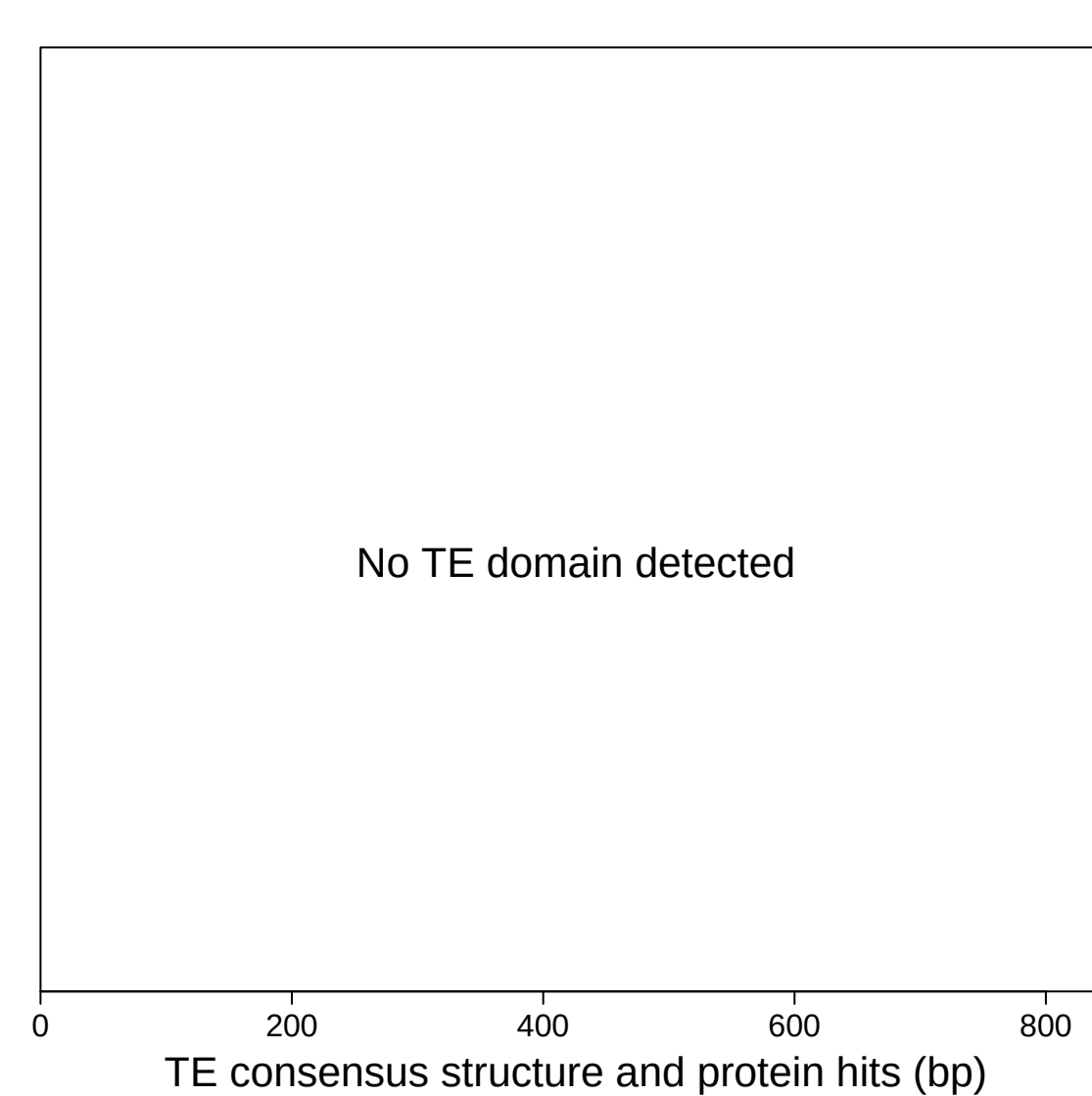
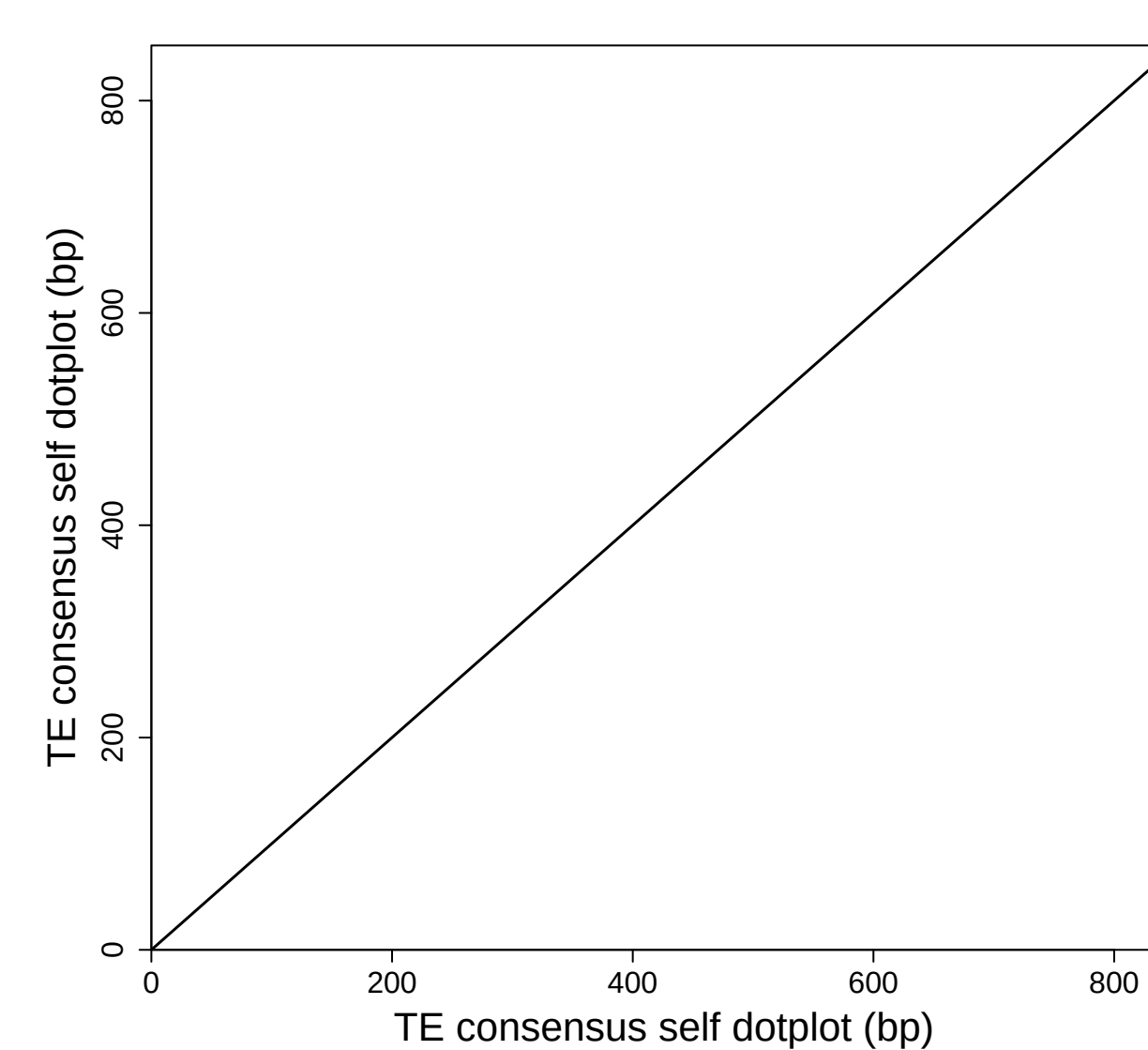
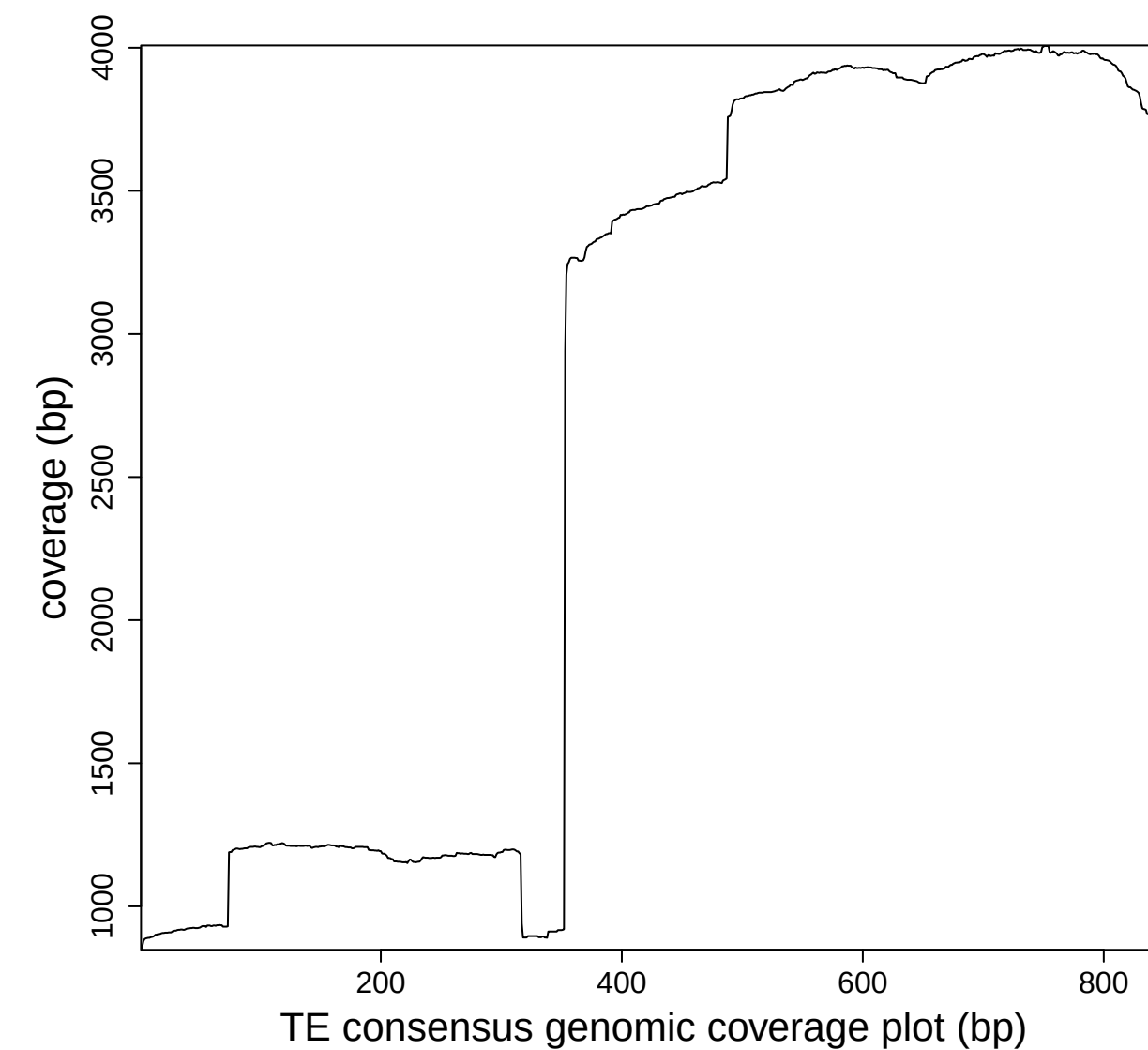
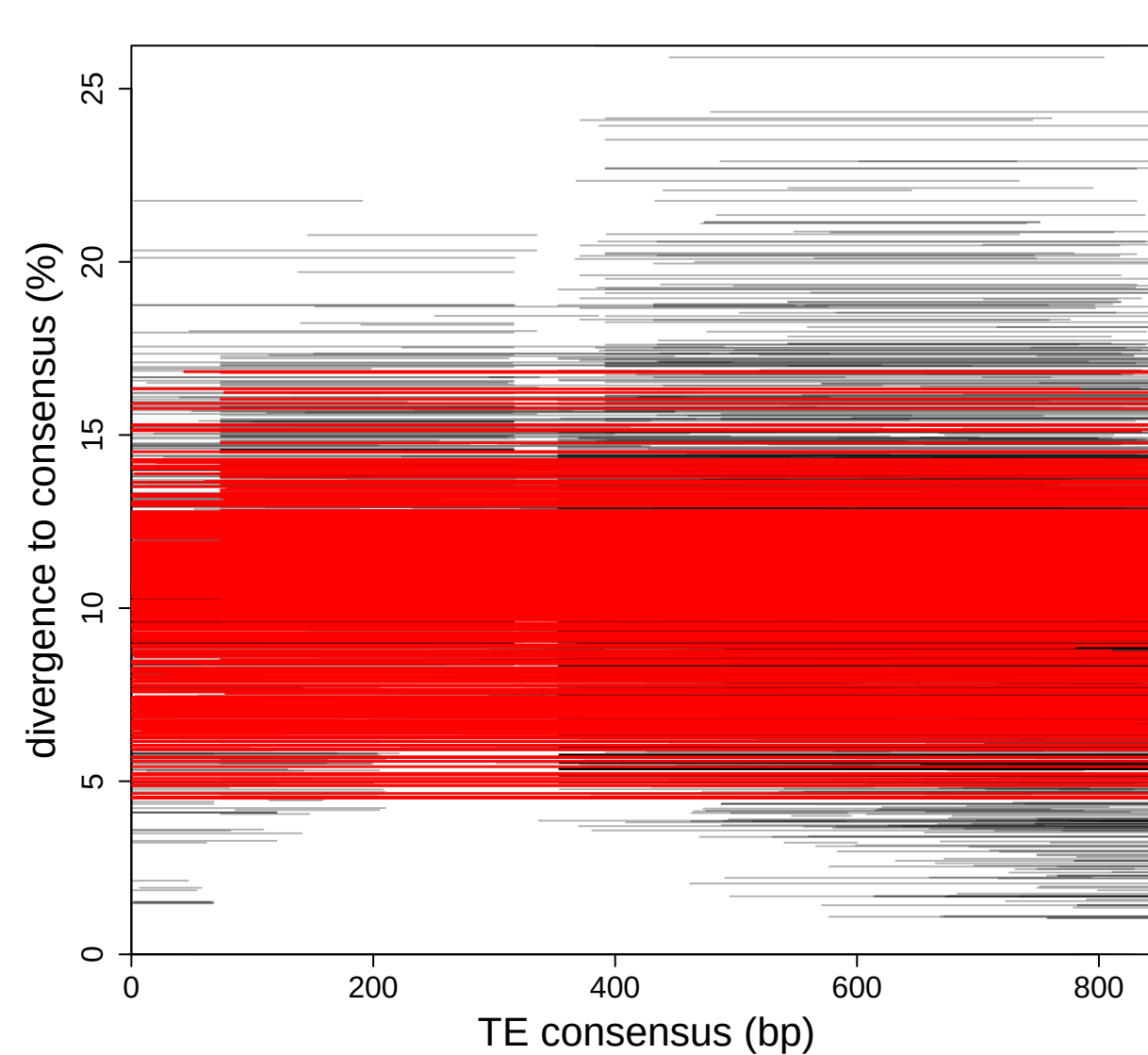
After TEtrimmer Extended plot Blue lines are boundaries



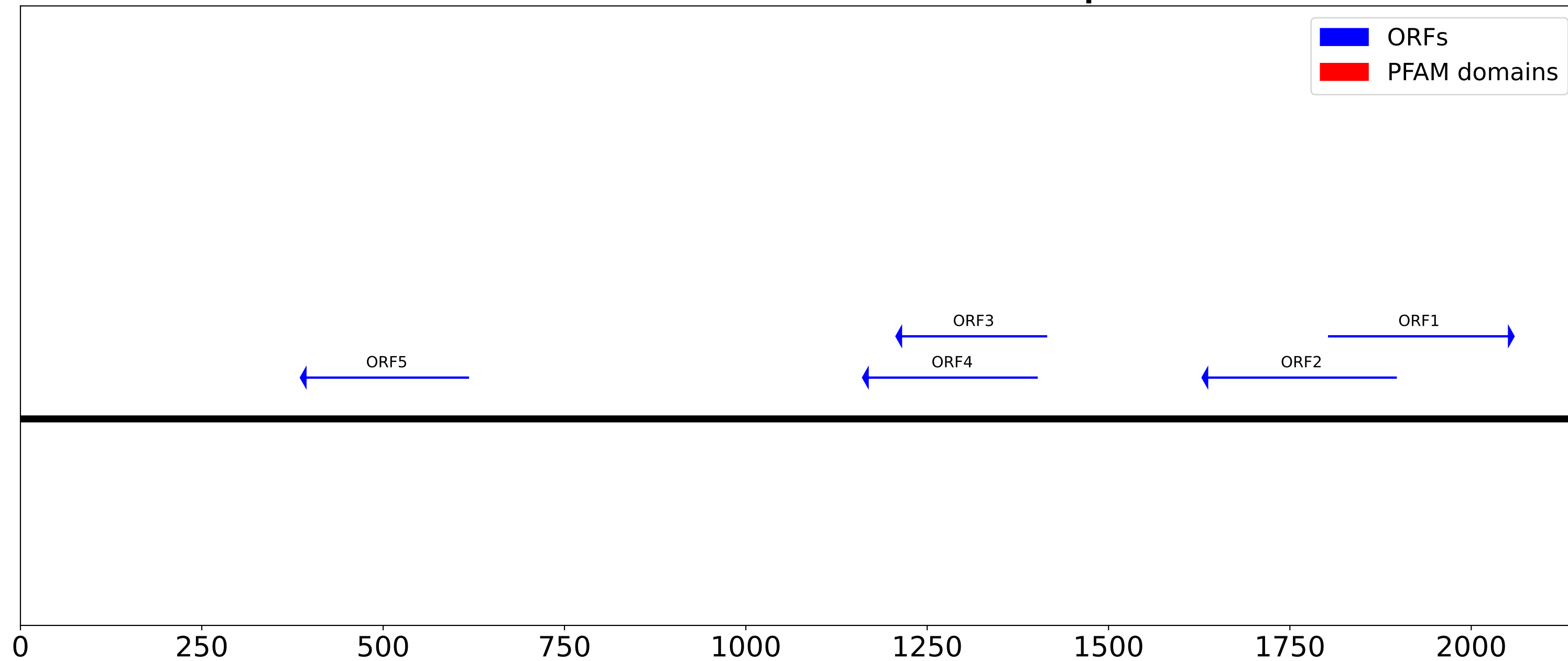
Before TEtrimmer 852 bp

TE: ltr_1_family_305

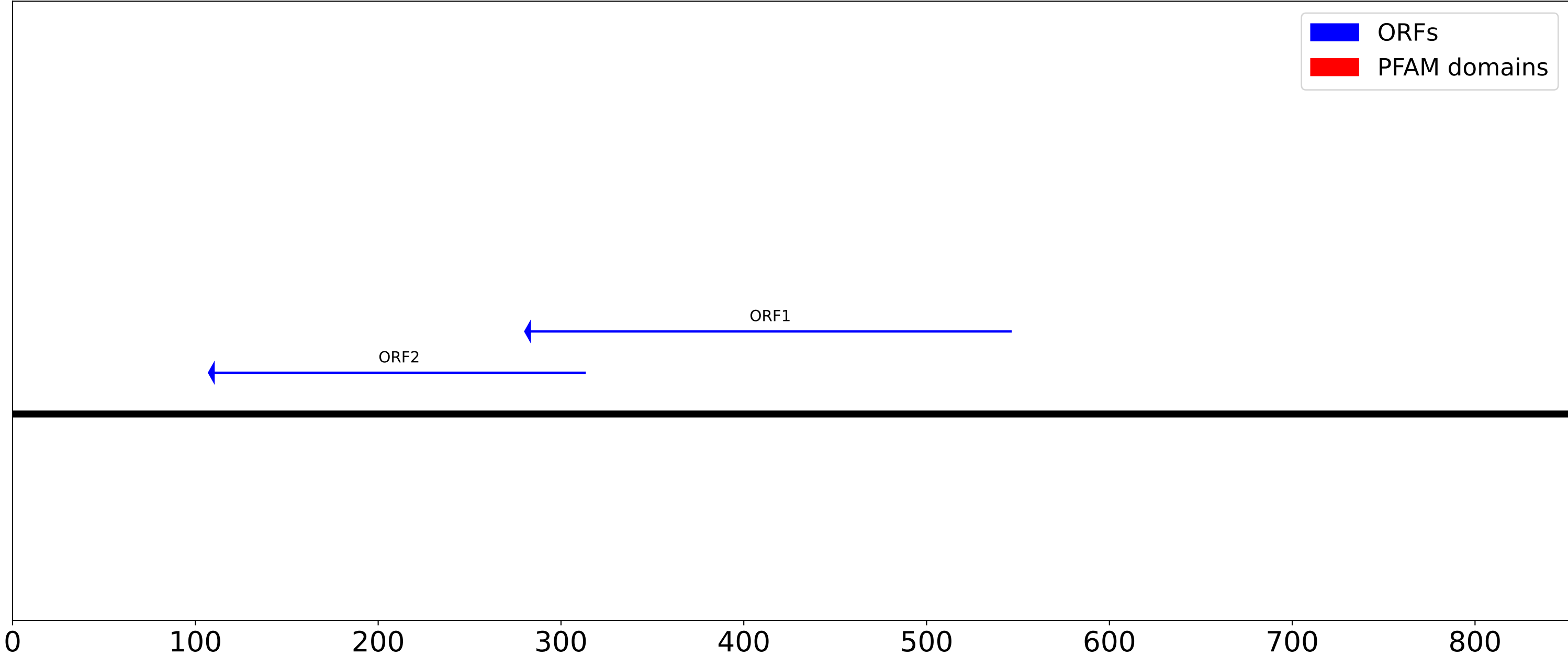
size: 852bp; fragments: 4960; full length: 608 (≥ 766.8 bp)



After TEtrimmer ORF and PFAM domain plot



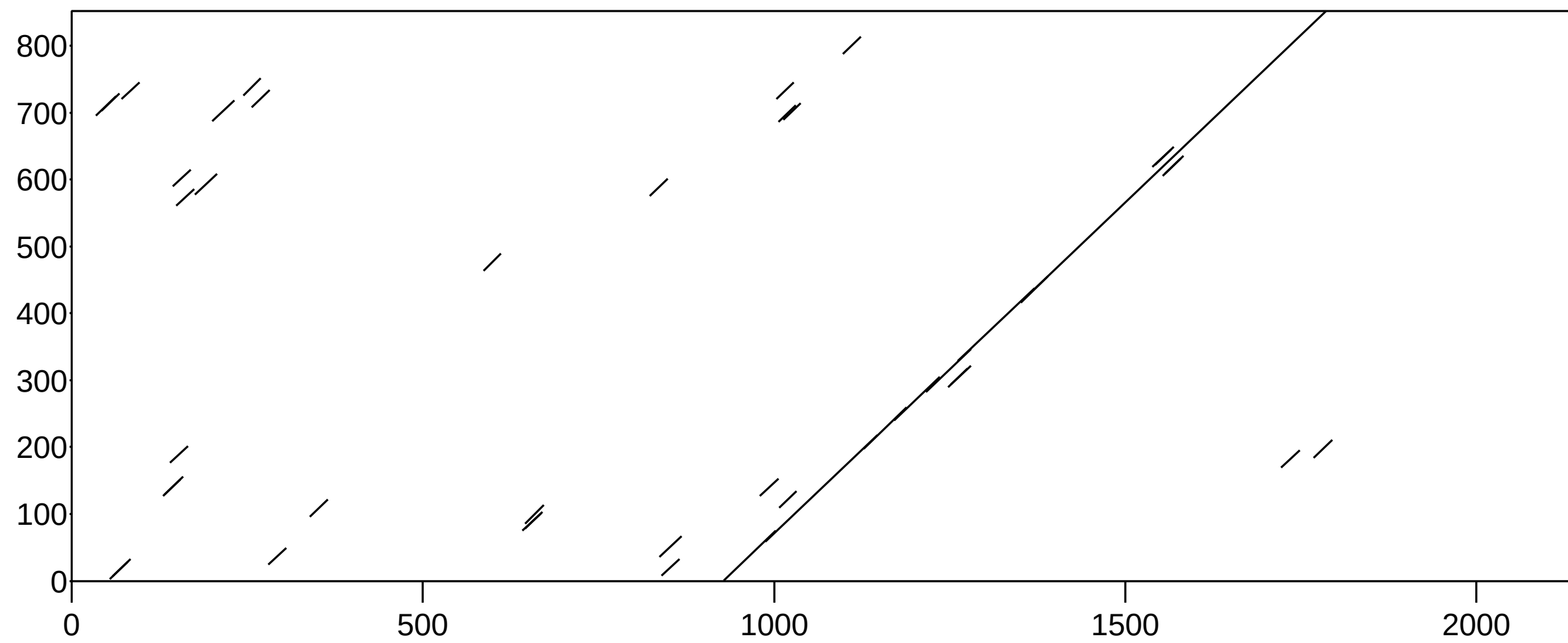
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)