

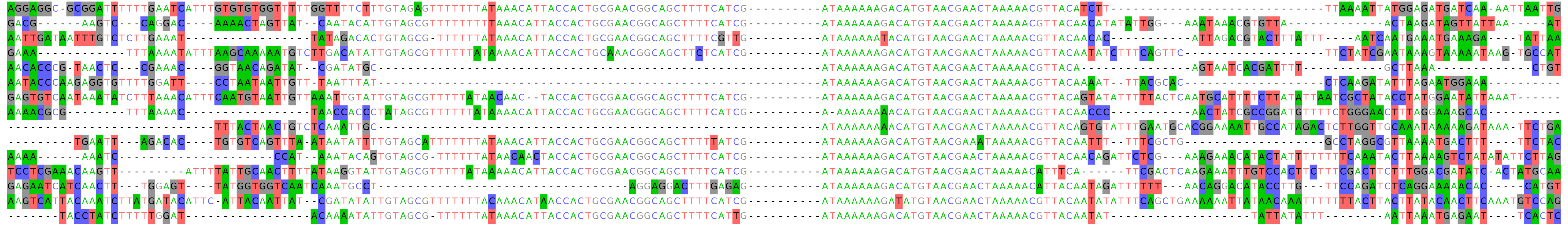
Start crop Point



End crop Point



MSA length = 1451



Start crop Point

End crop Point

0

10

0

250

500

750

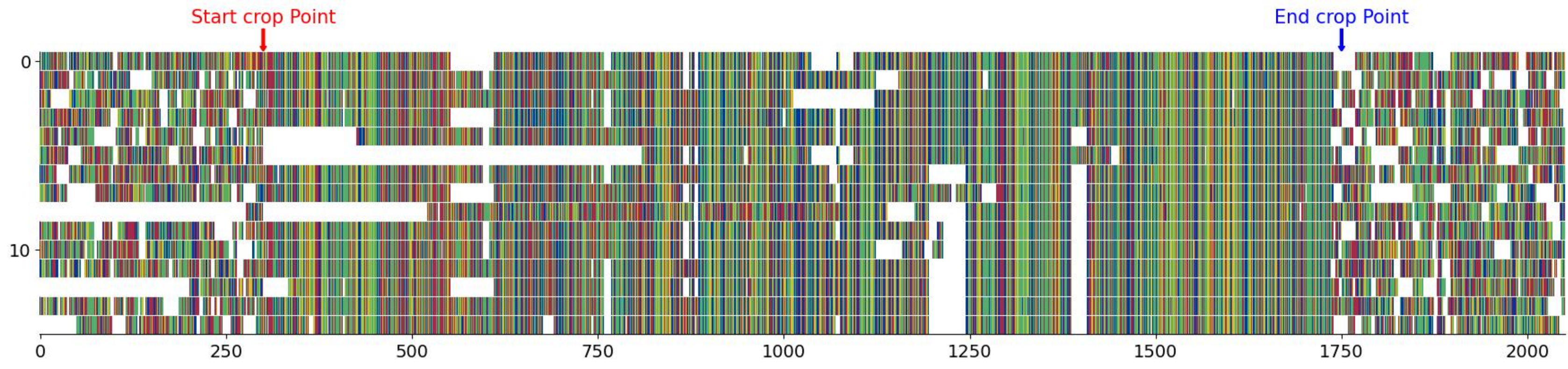
1000

1250

1500

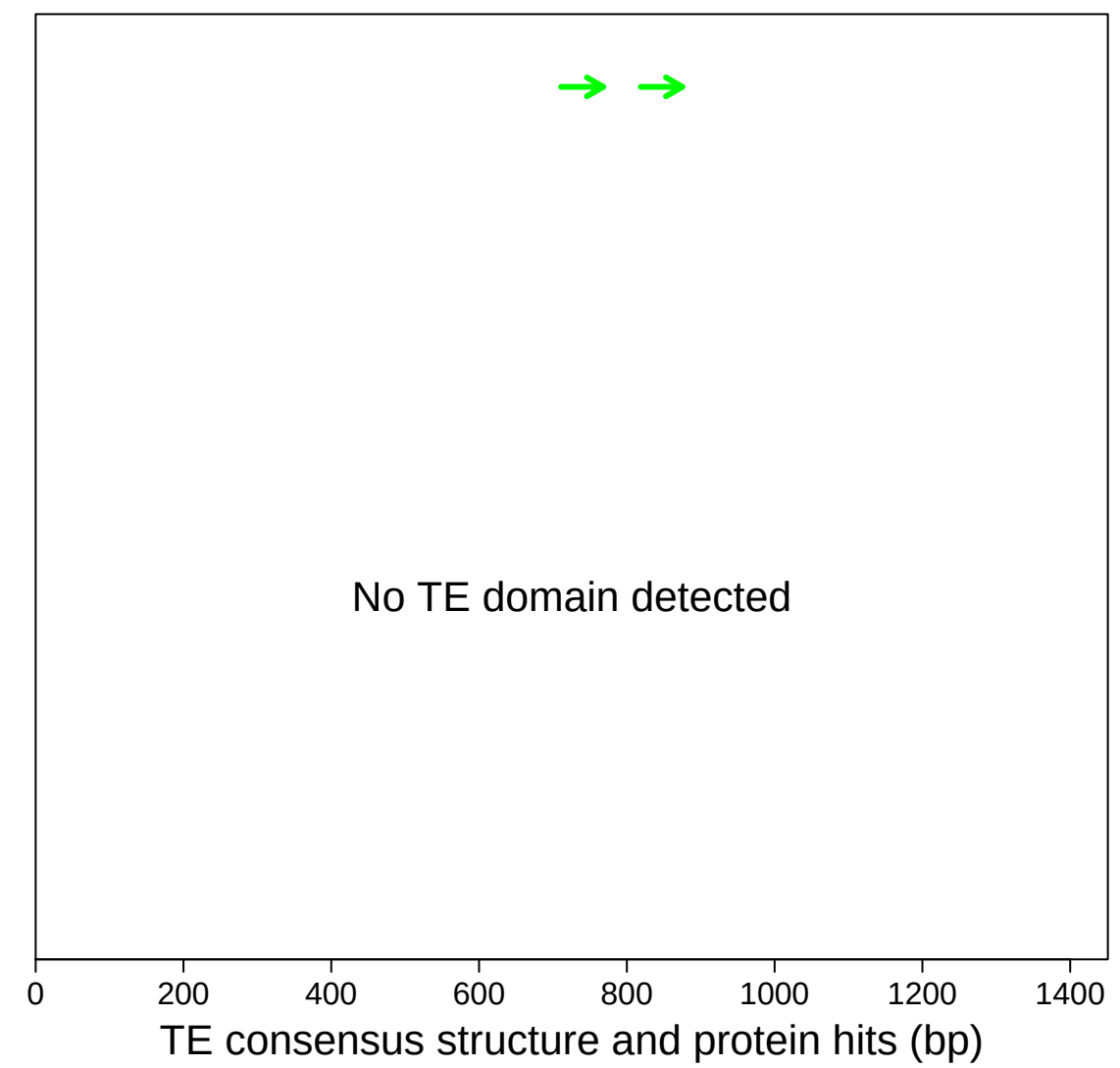
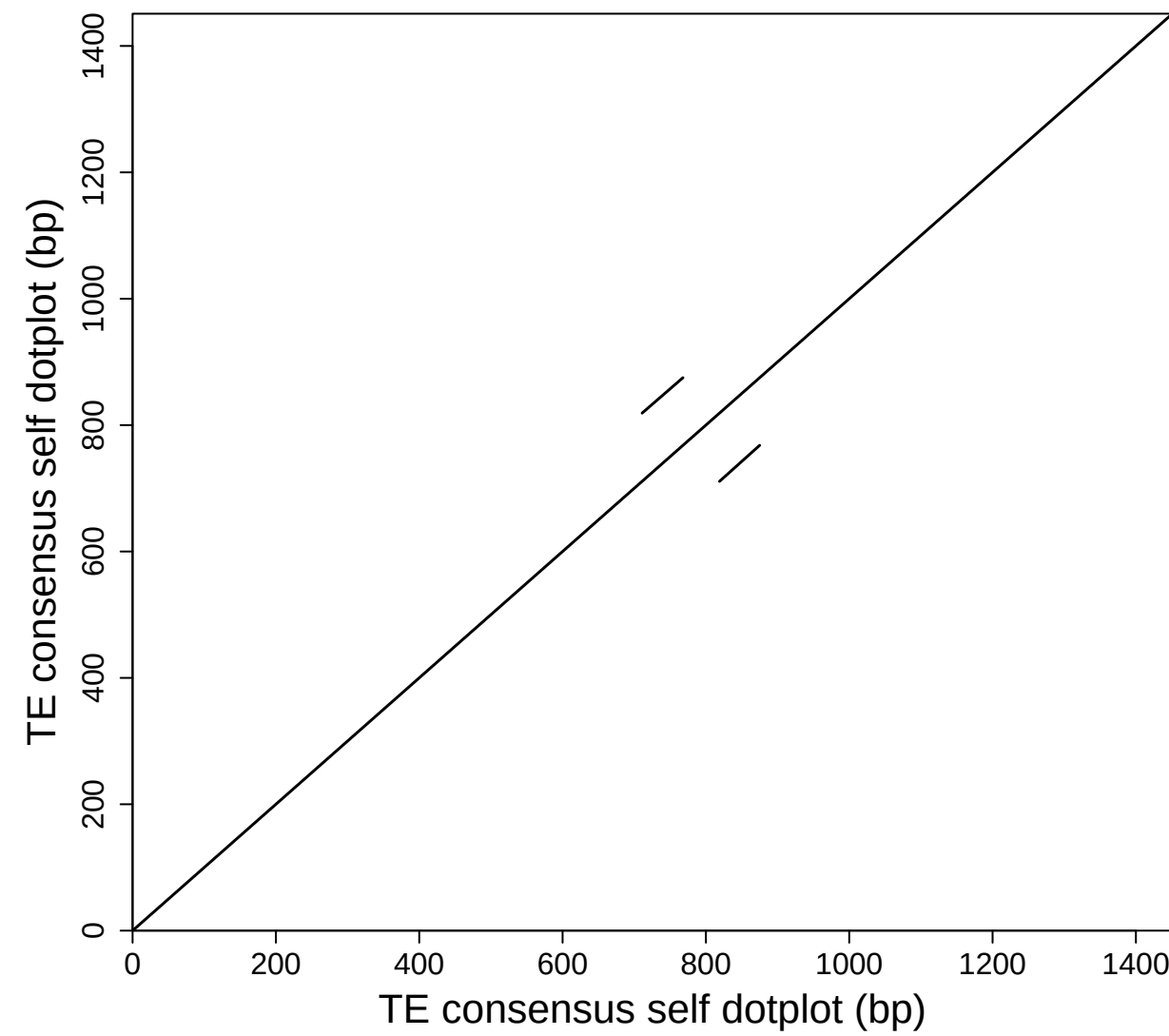
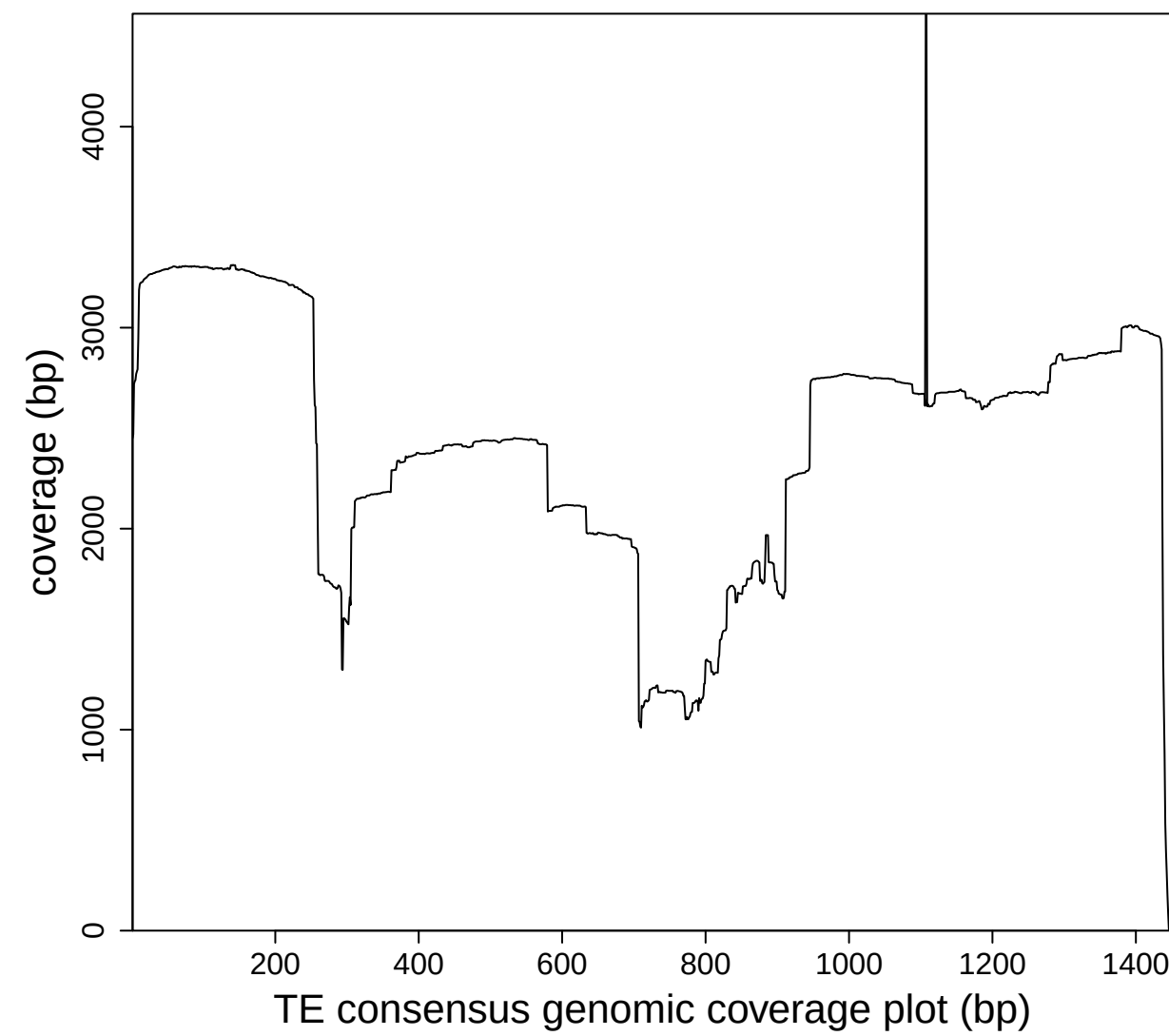
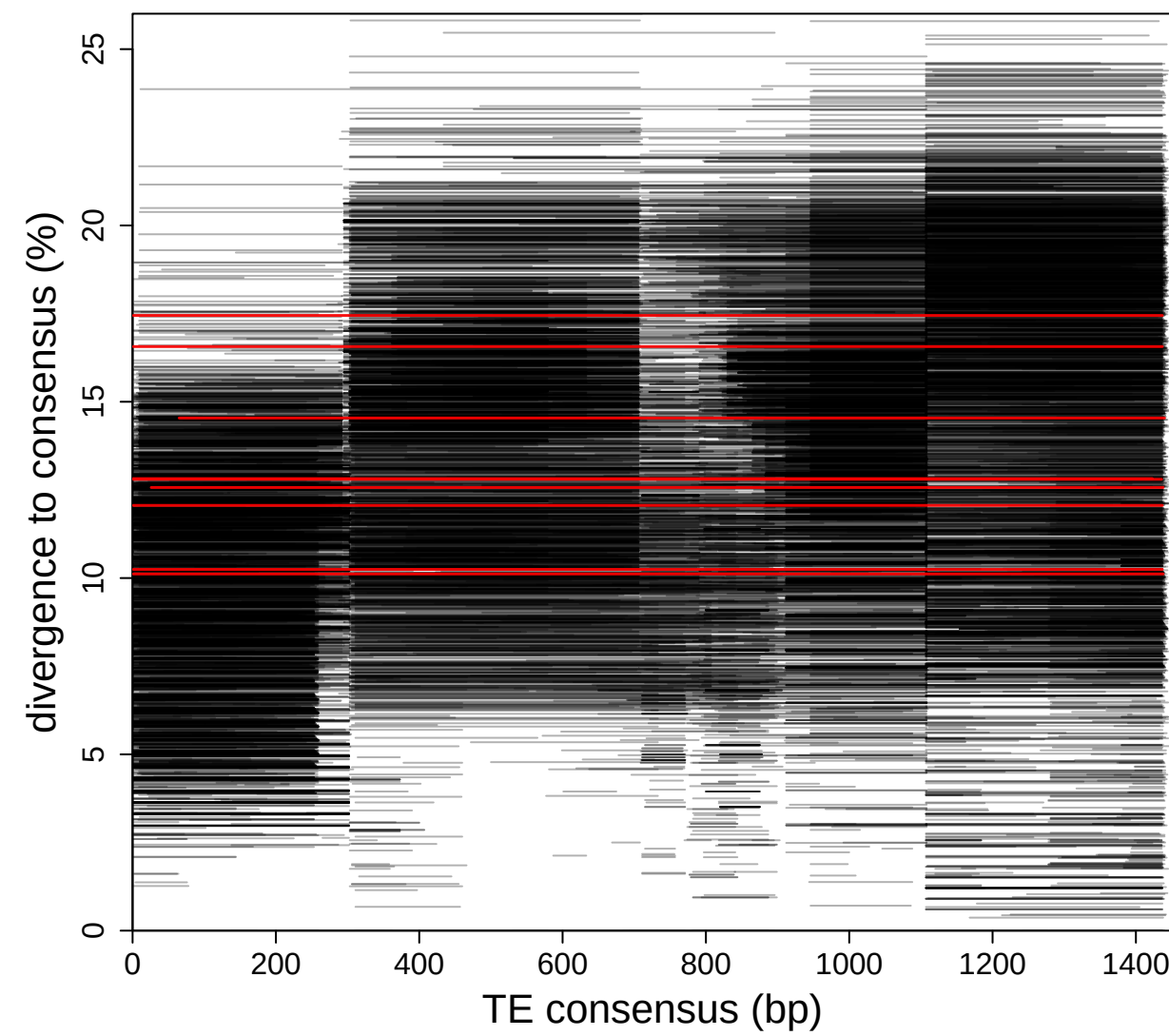
1750

2000



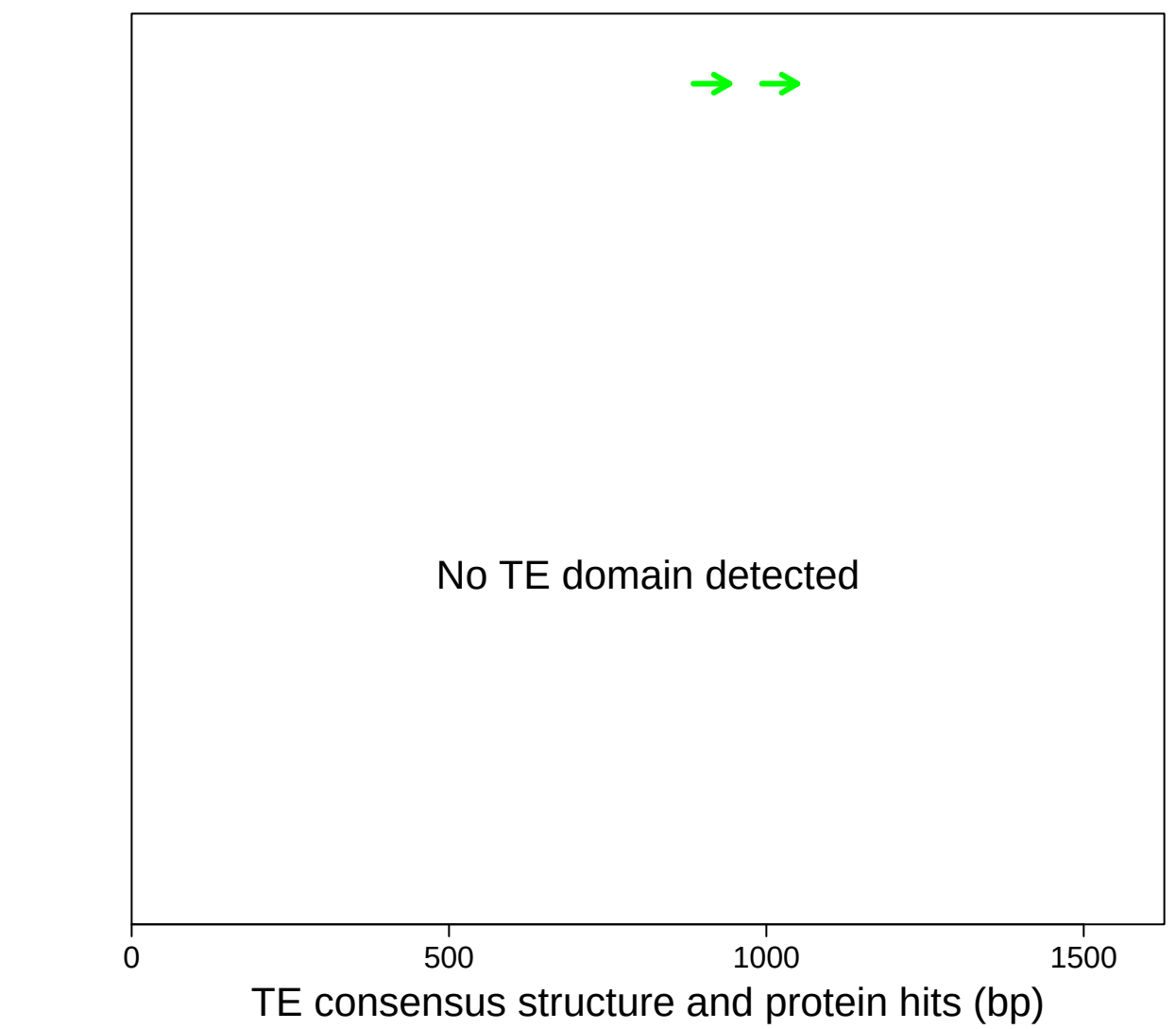
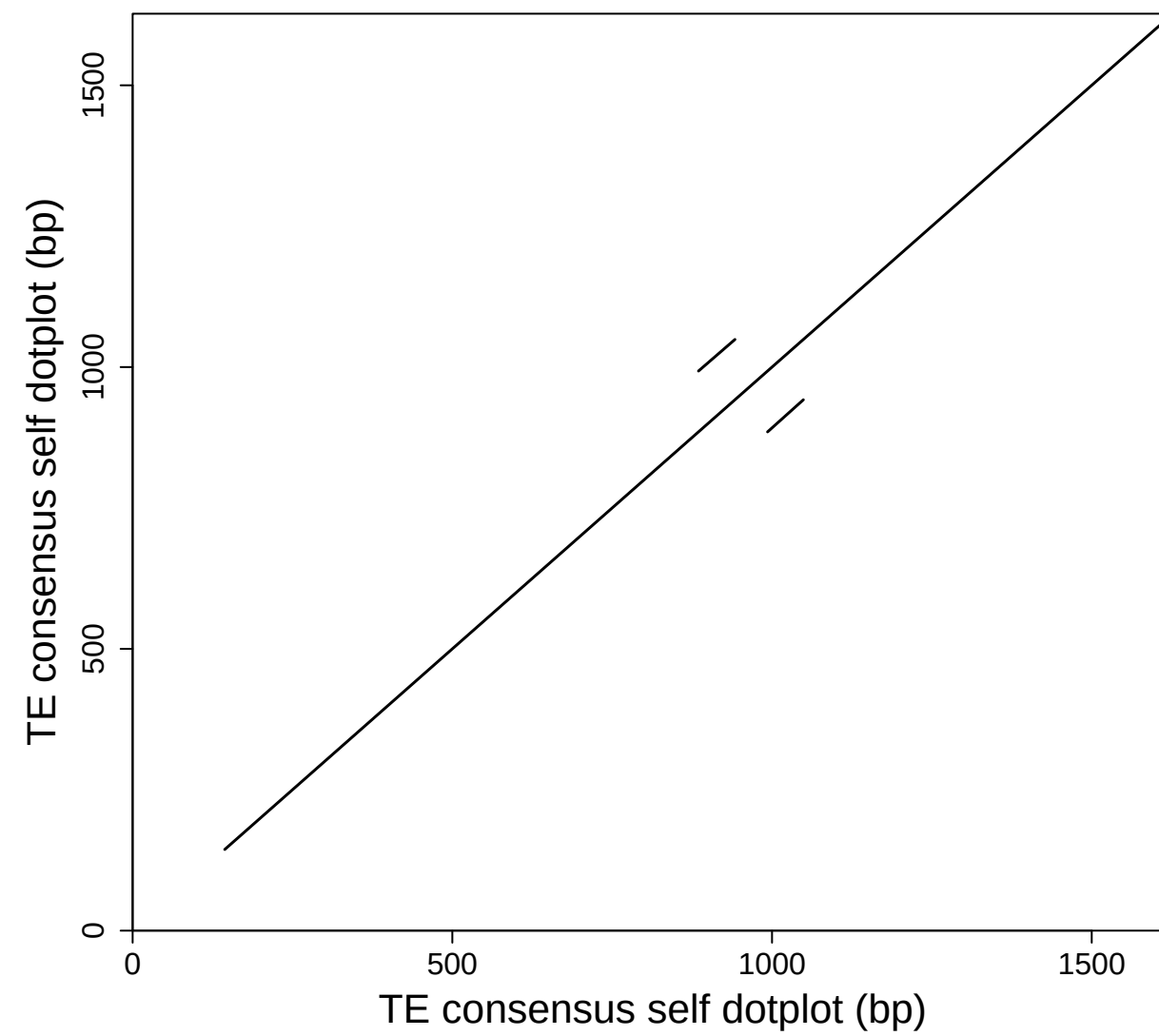
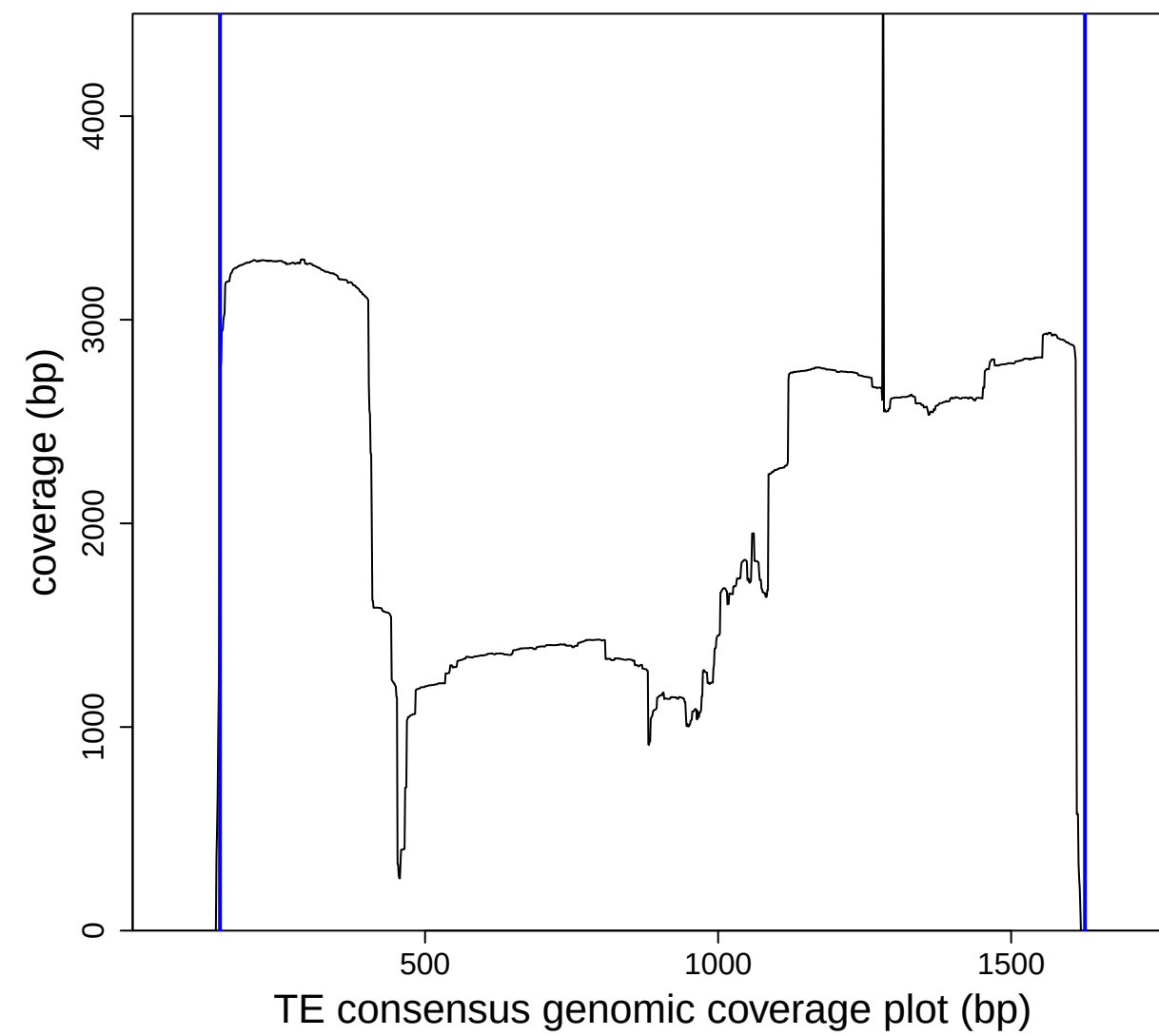
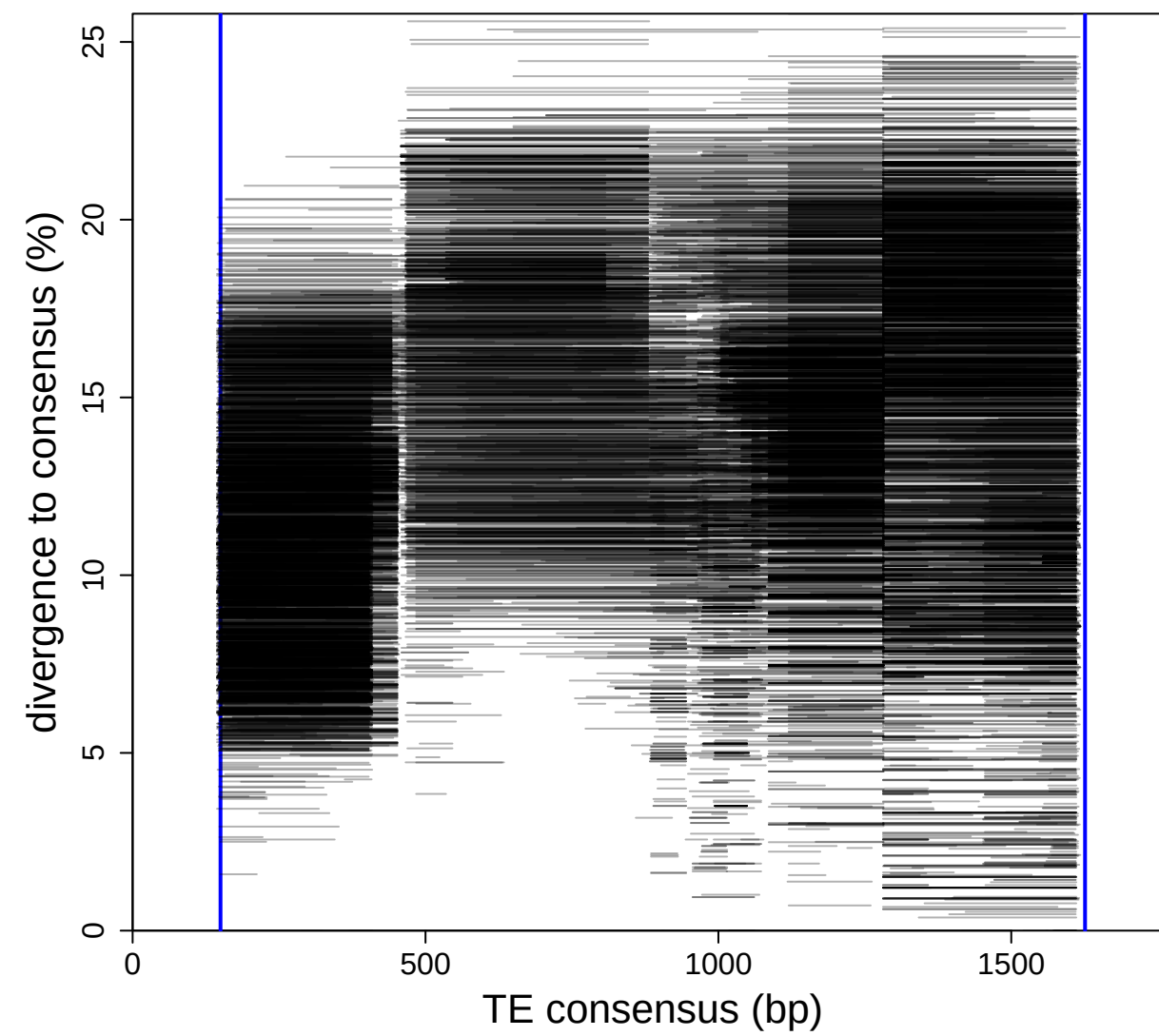
b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 1451bp; fragments: 11549; full length: 9 (>=1305.9bp)

After TETrimmer 1451 bp

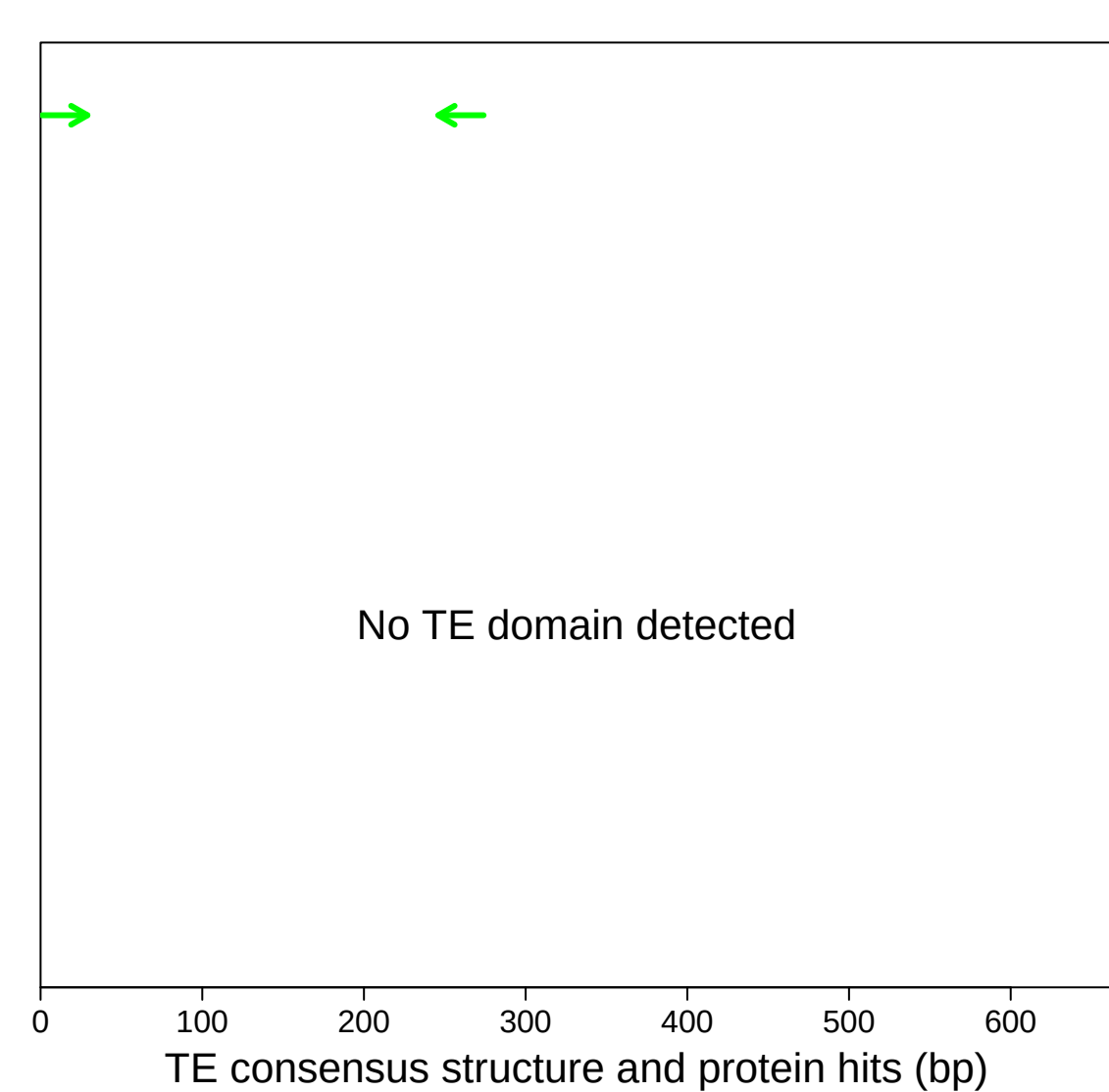
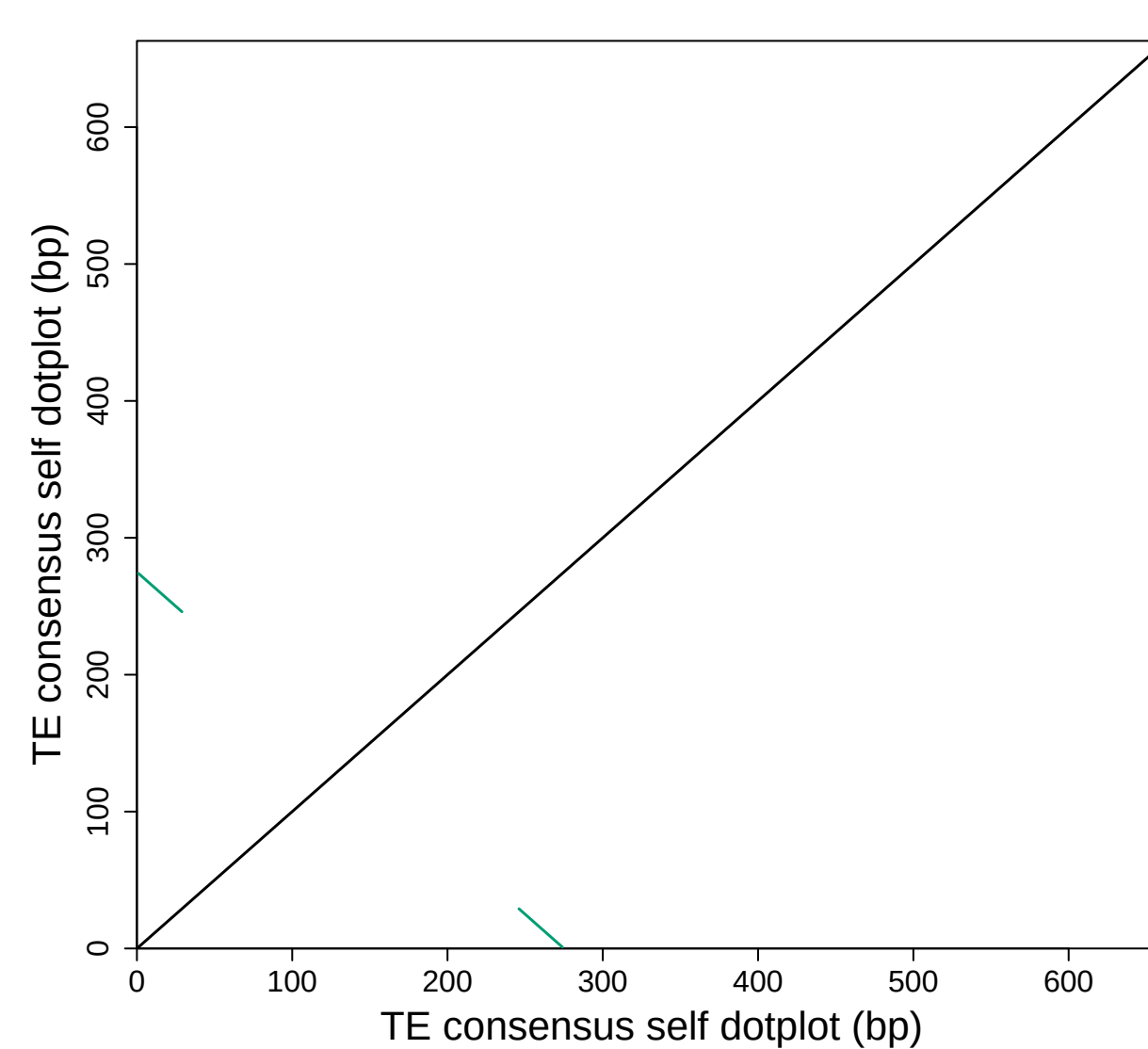
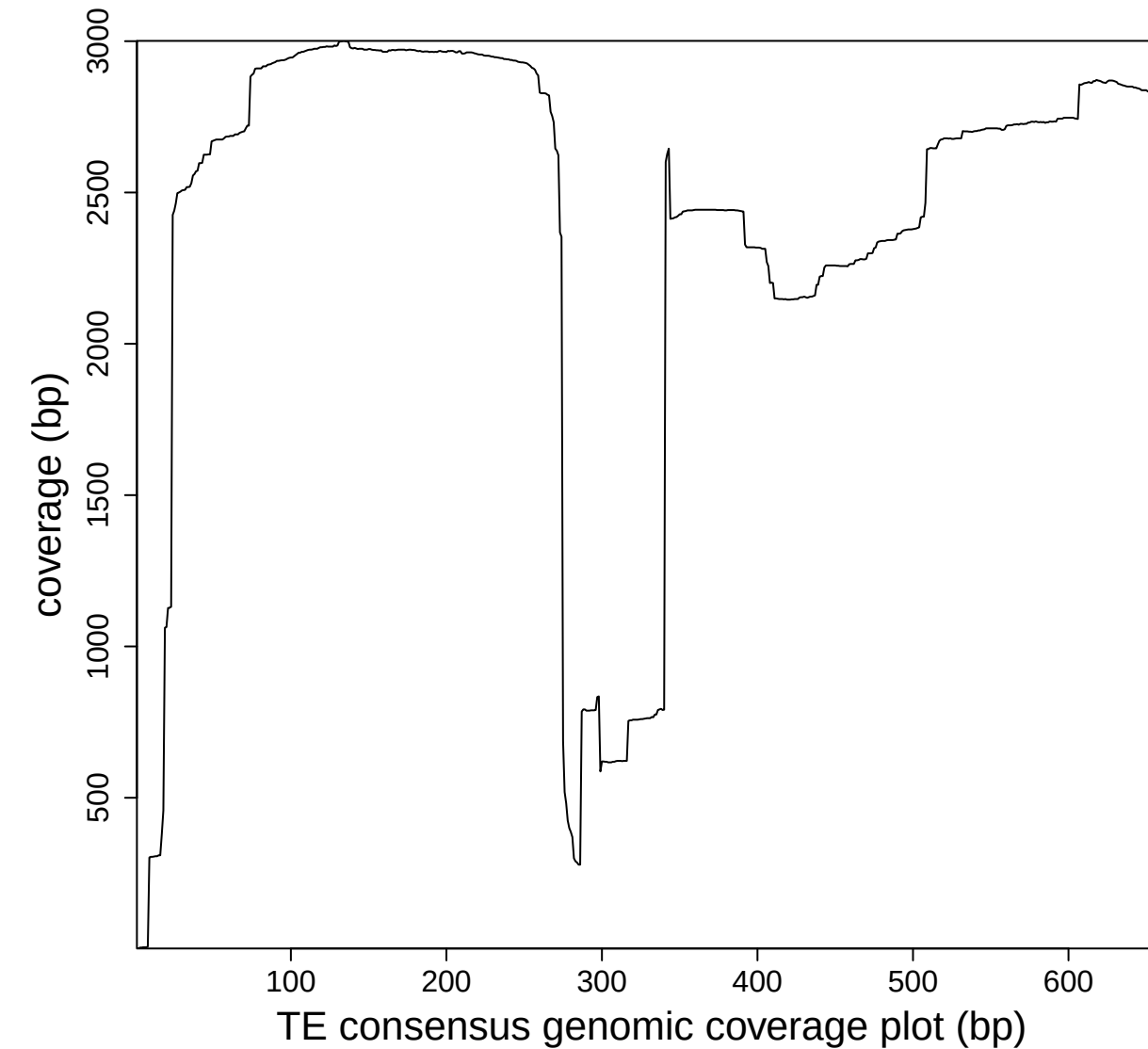
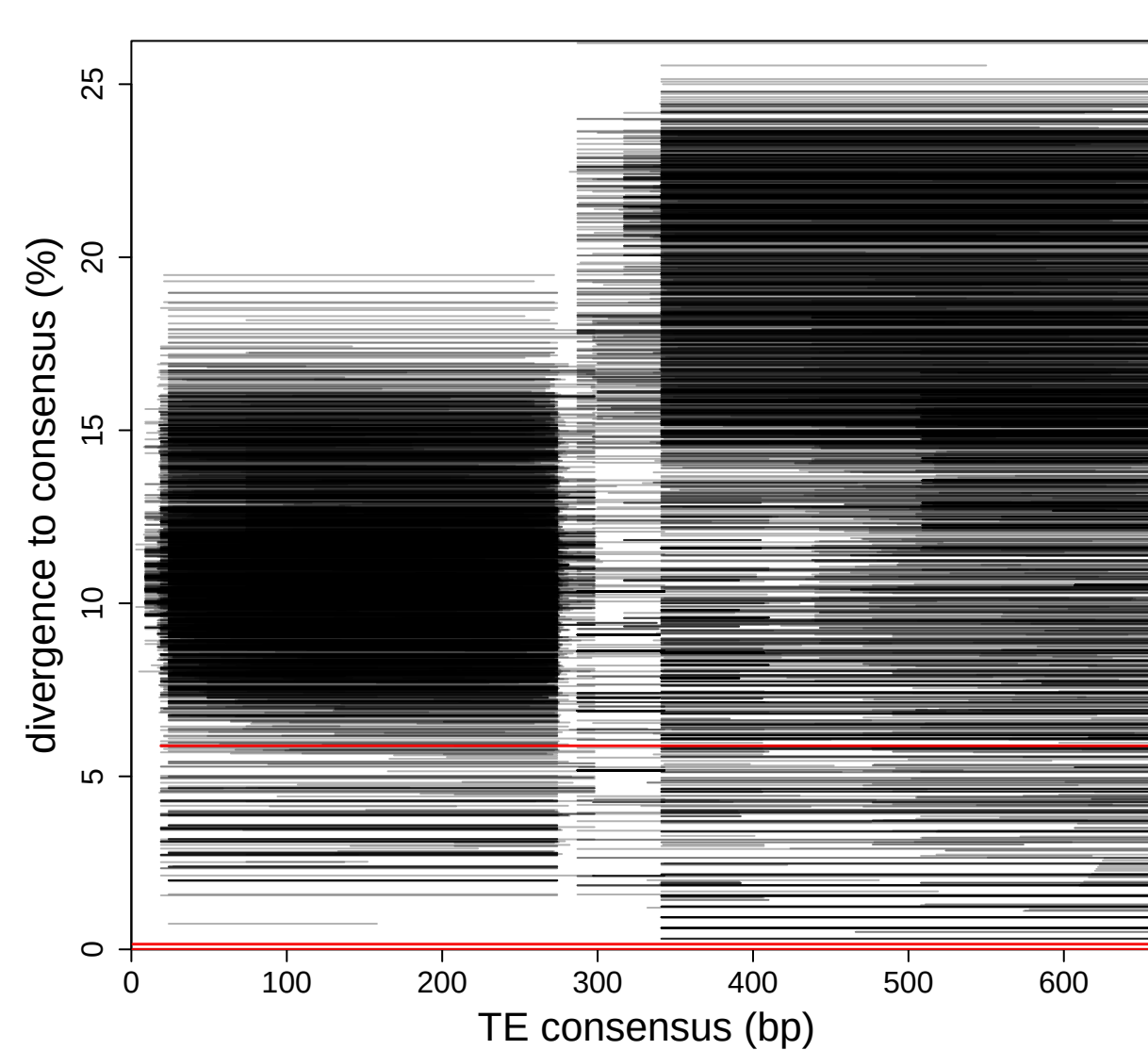


.fasta.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 1776bp; fragments: 10395; full length: 0 (>=1598.4bp)

After TEtrimmer Extended plot Blue lines are boundaries

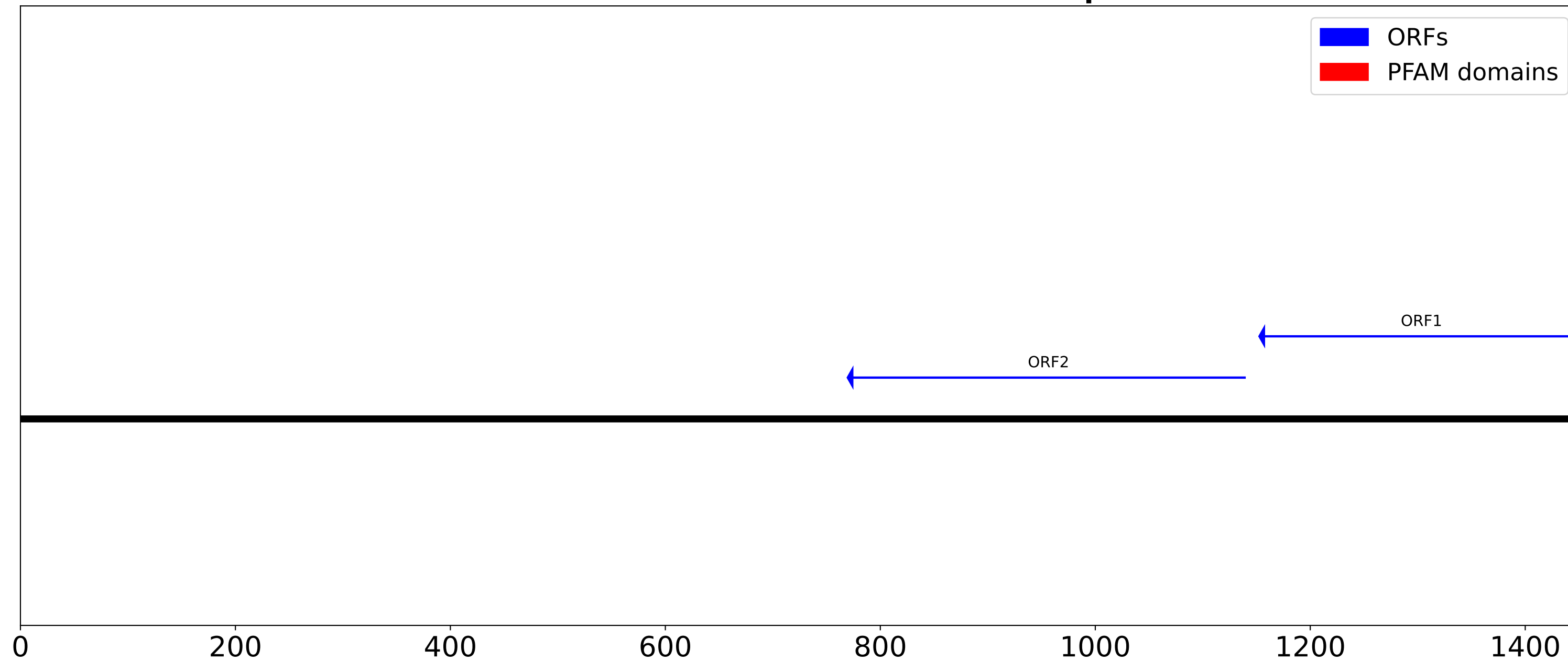


TE: ltr_1_family_257
size: 663bp; fragments: 6624; full length: 3 (≥ 596.7 bp)

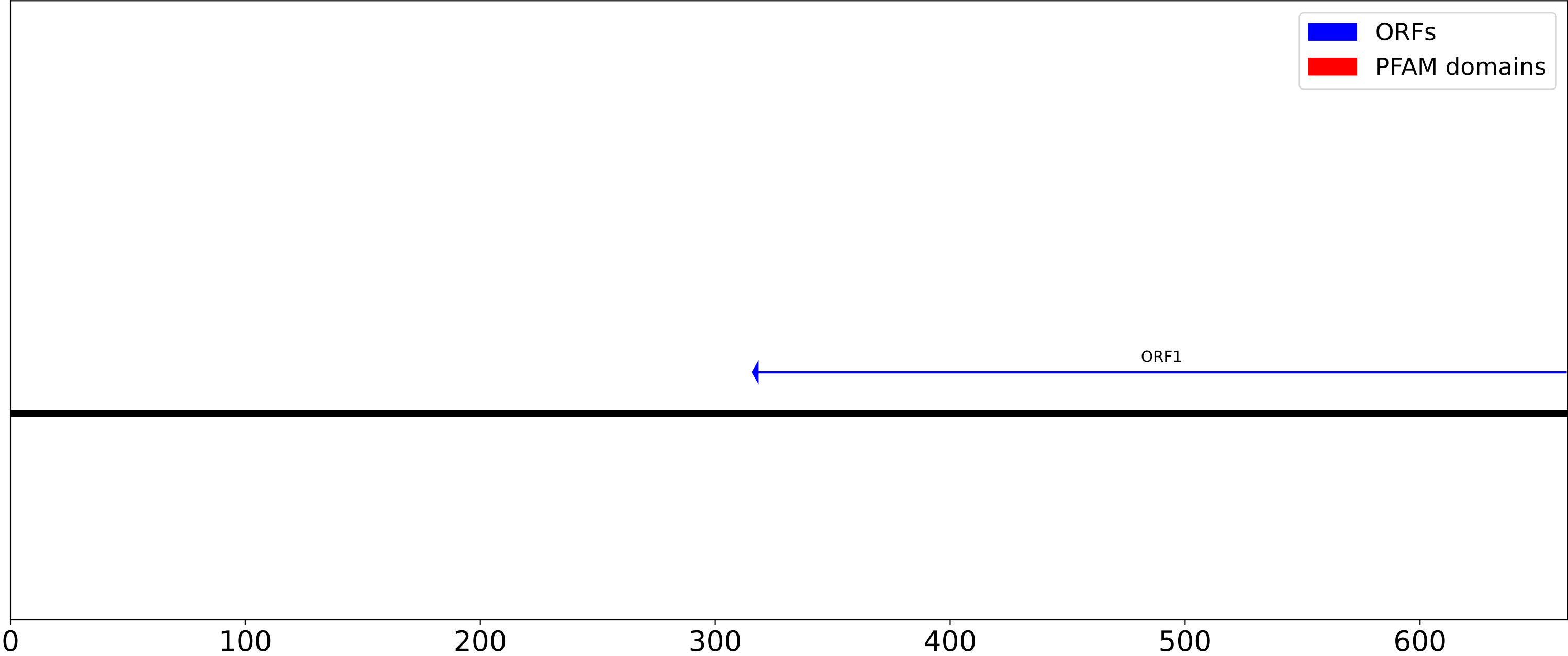


Before TEtrimmer 663 bp

After TEtrimmer ORF and PFAM domain plot



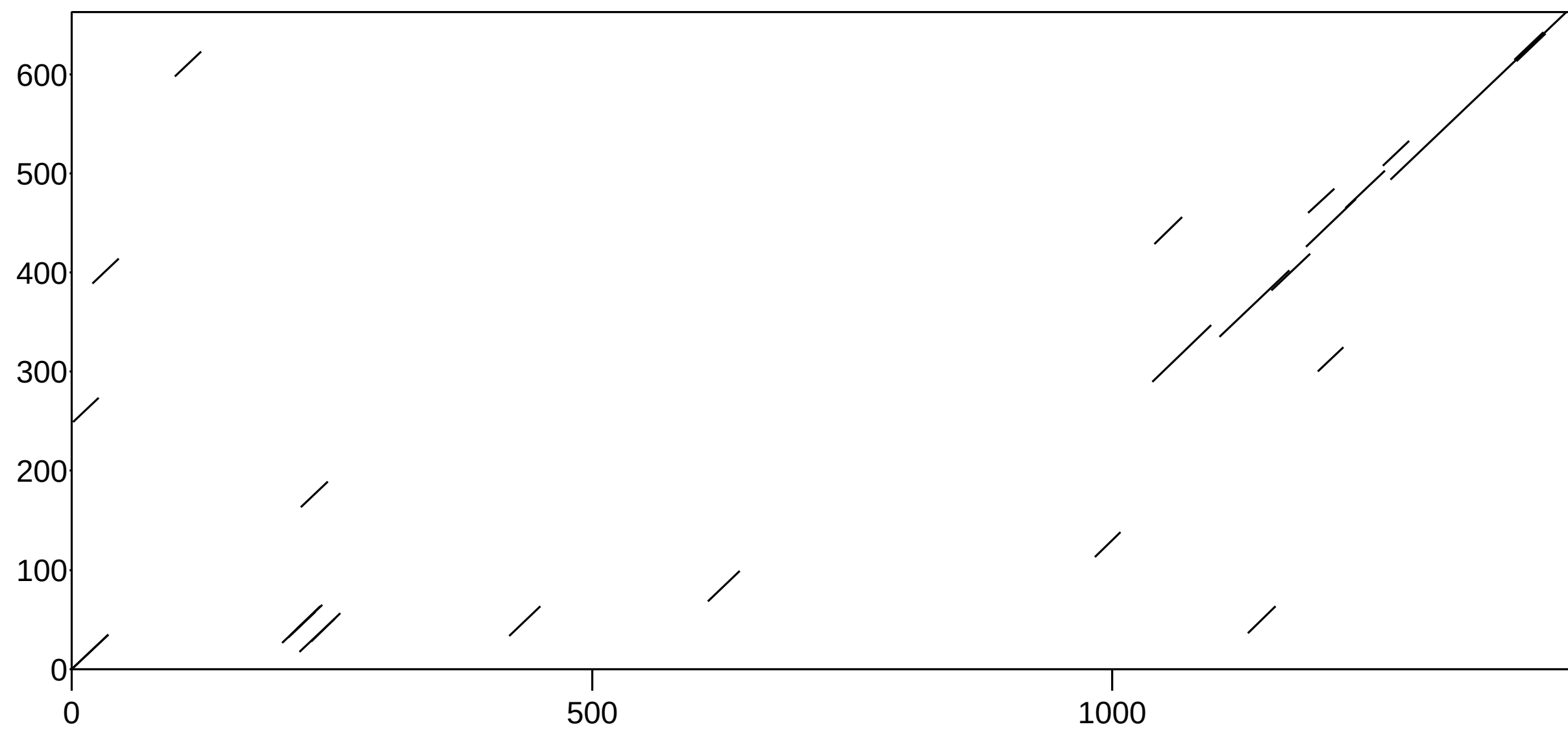
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)