

Start crop Point



End crop Point



MSA length = 1643



Start crop Point

End crop Point

0 -

10 -

0

250

500

750

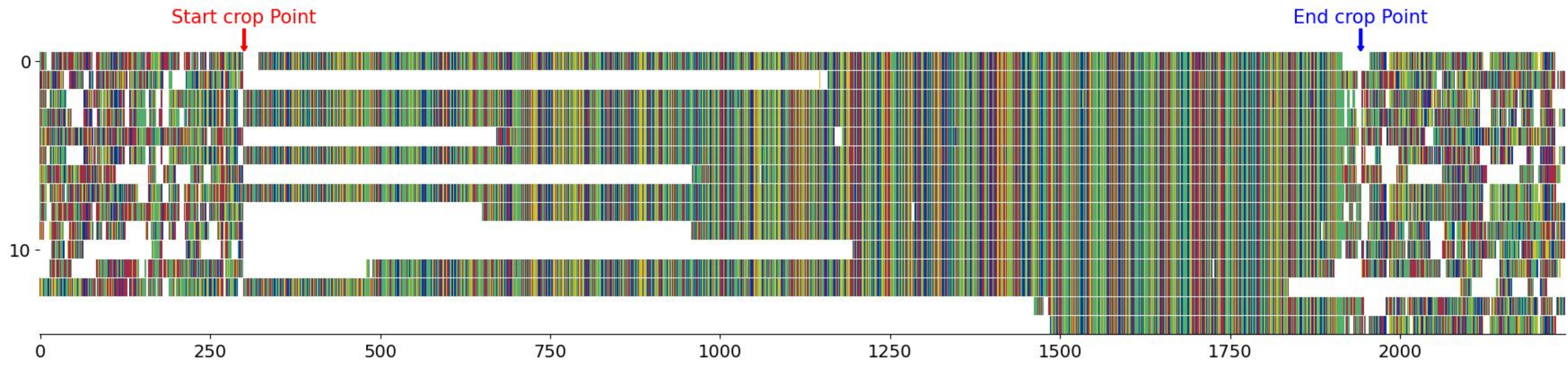
1000

1250

1500

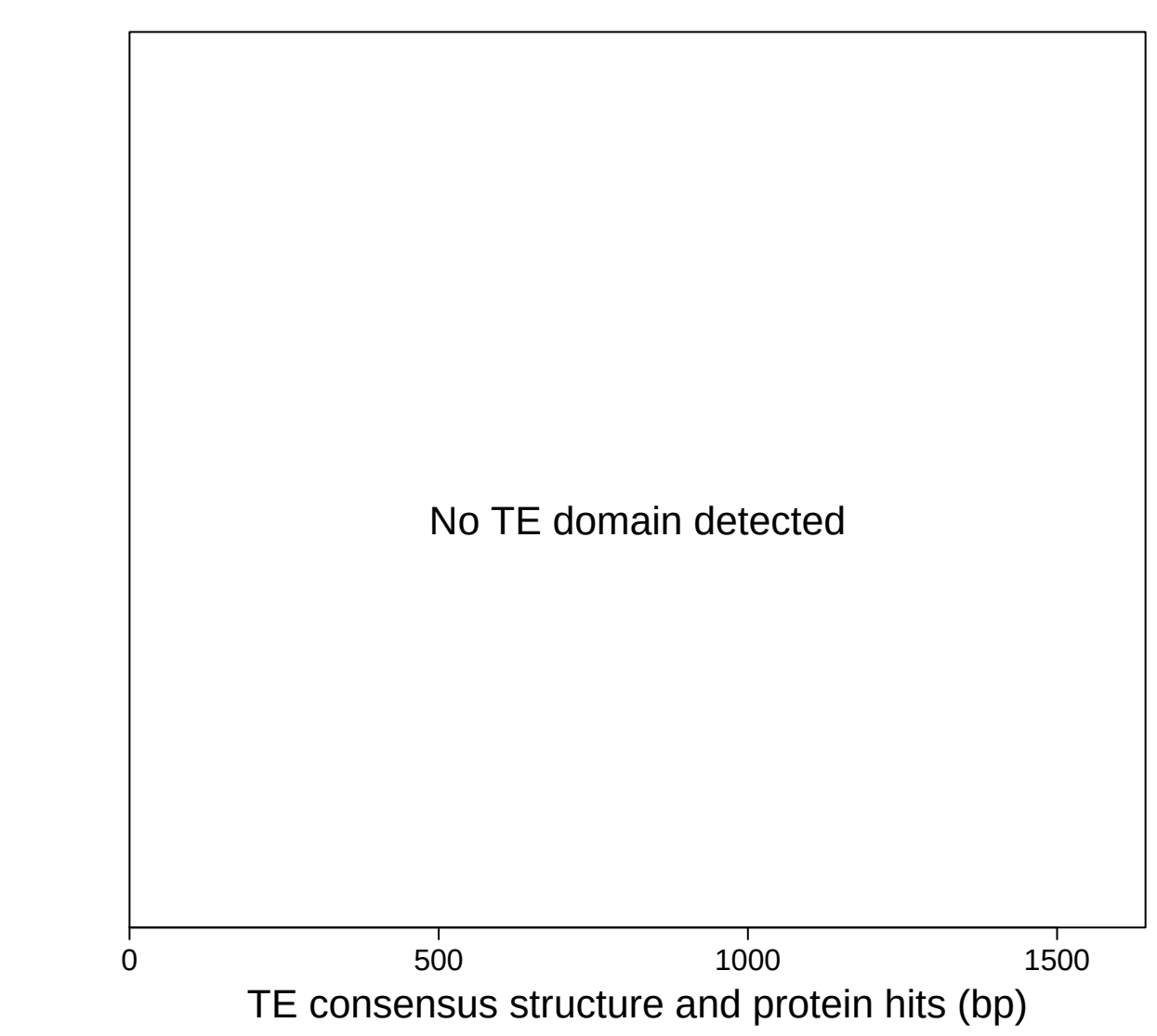
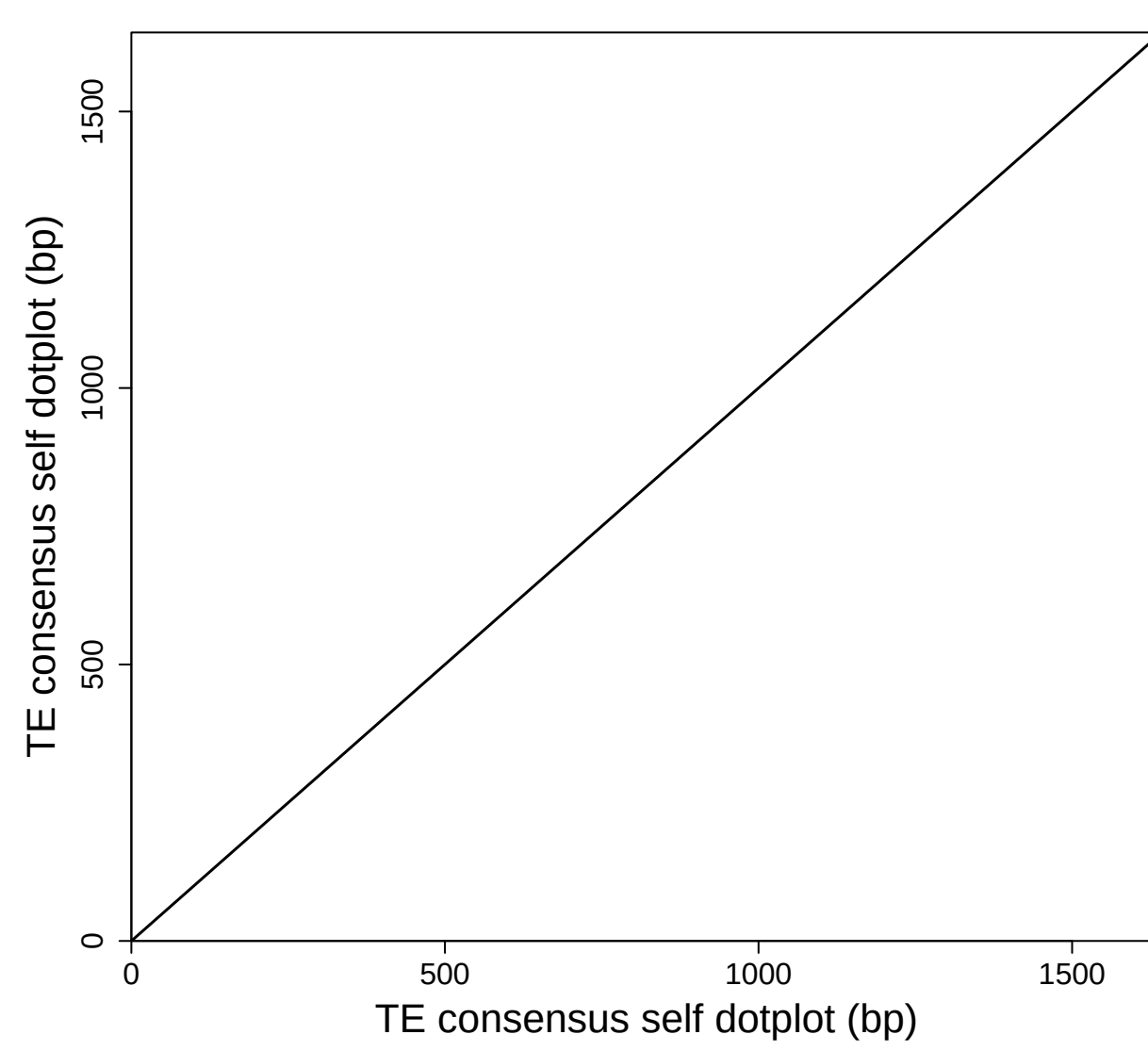
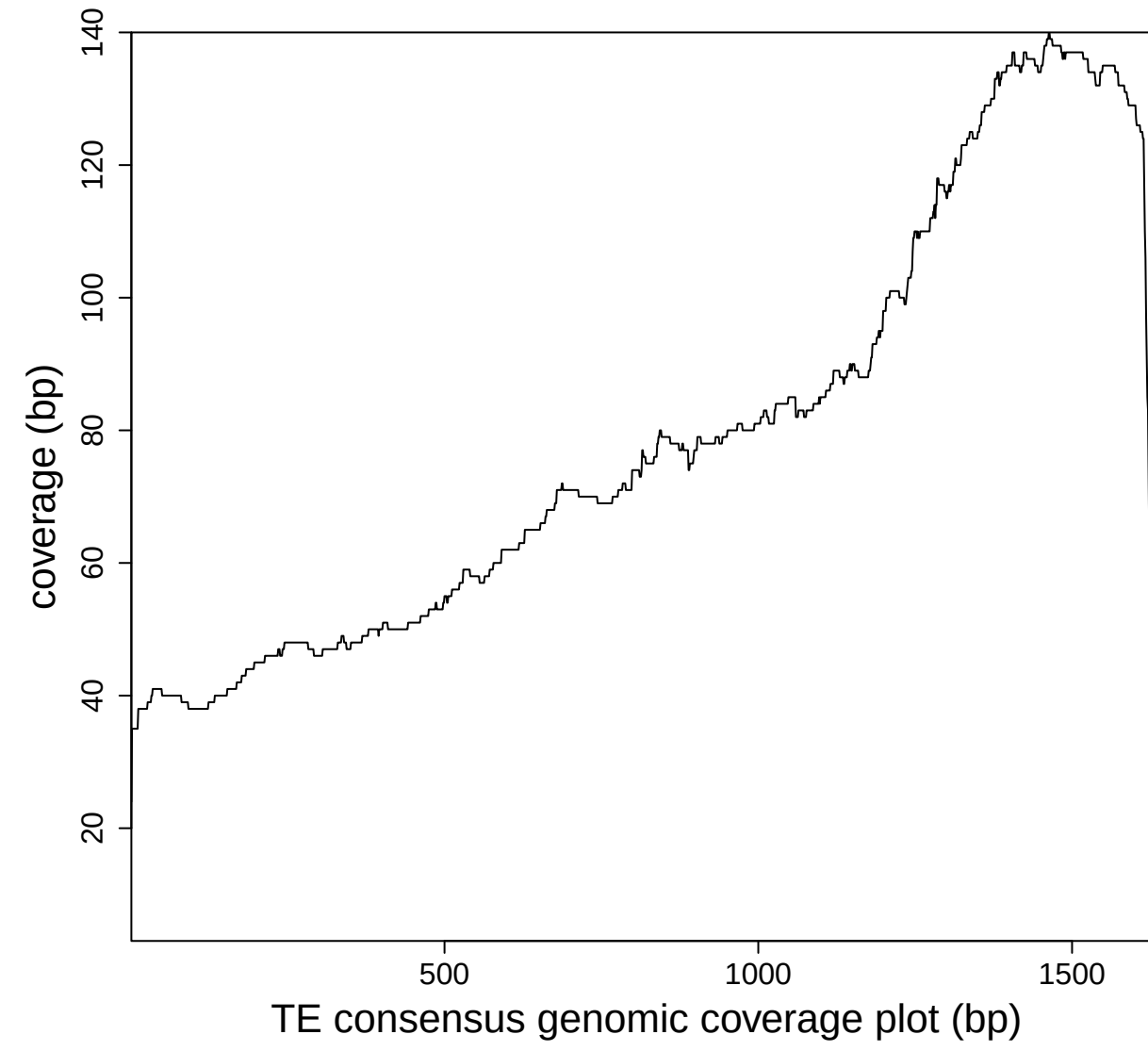
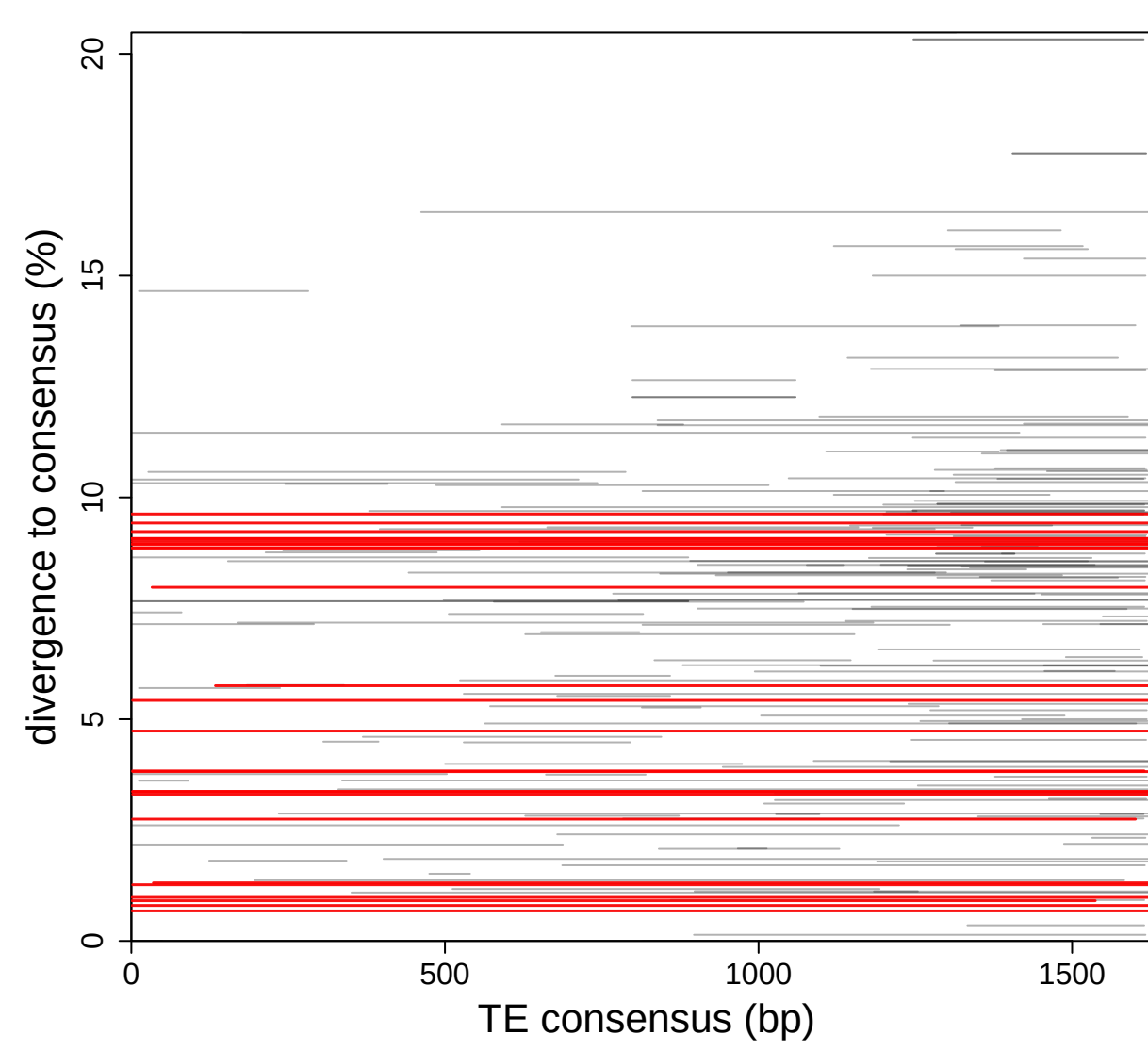
1750

2000



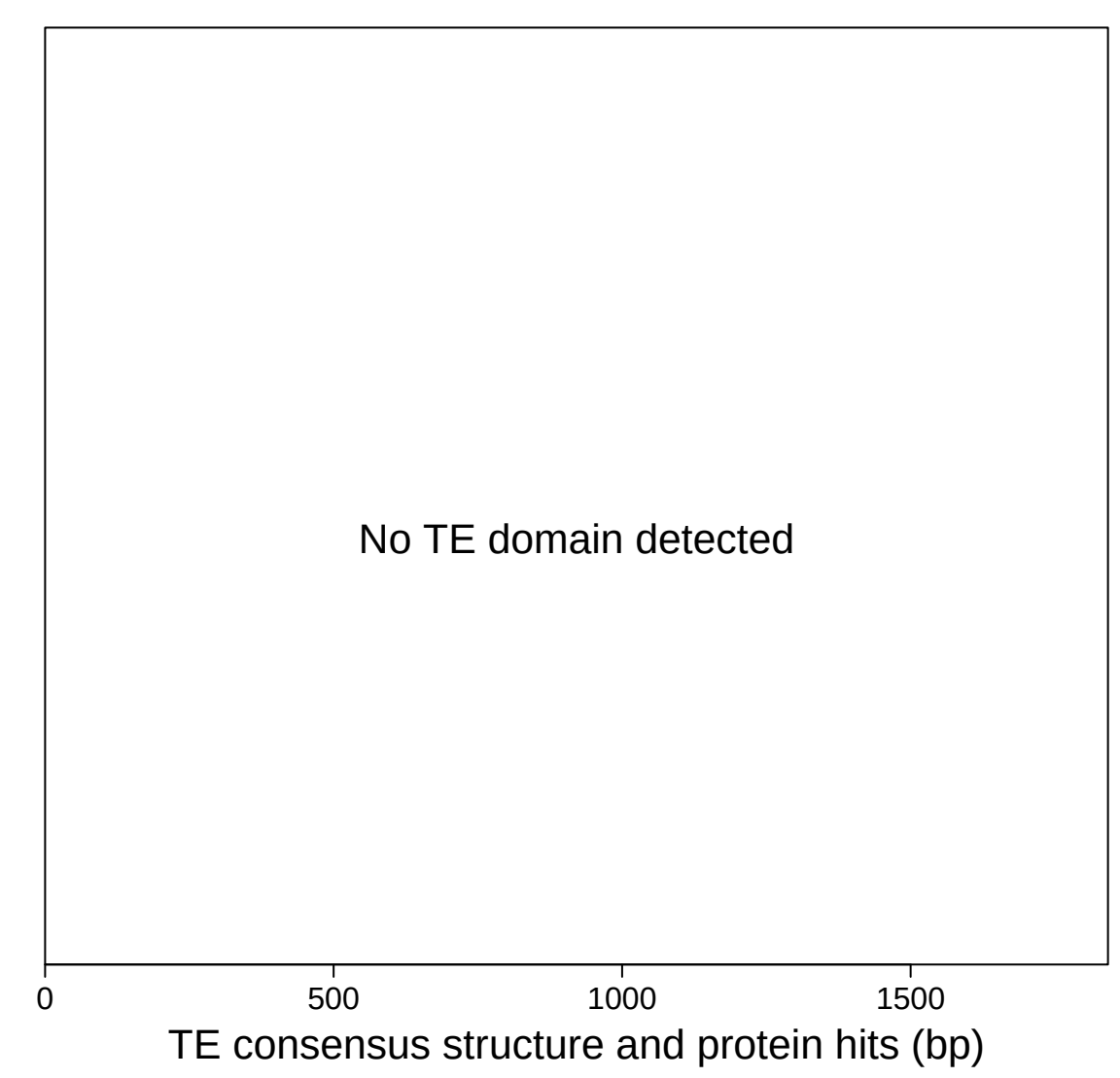
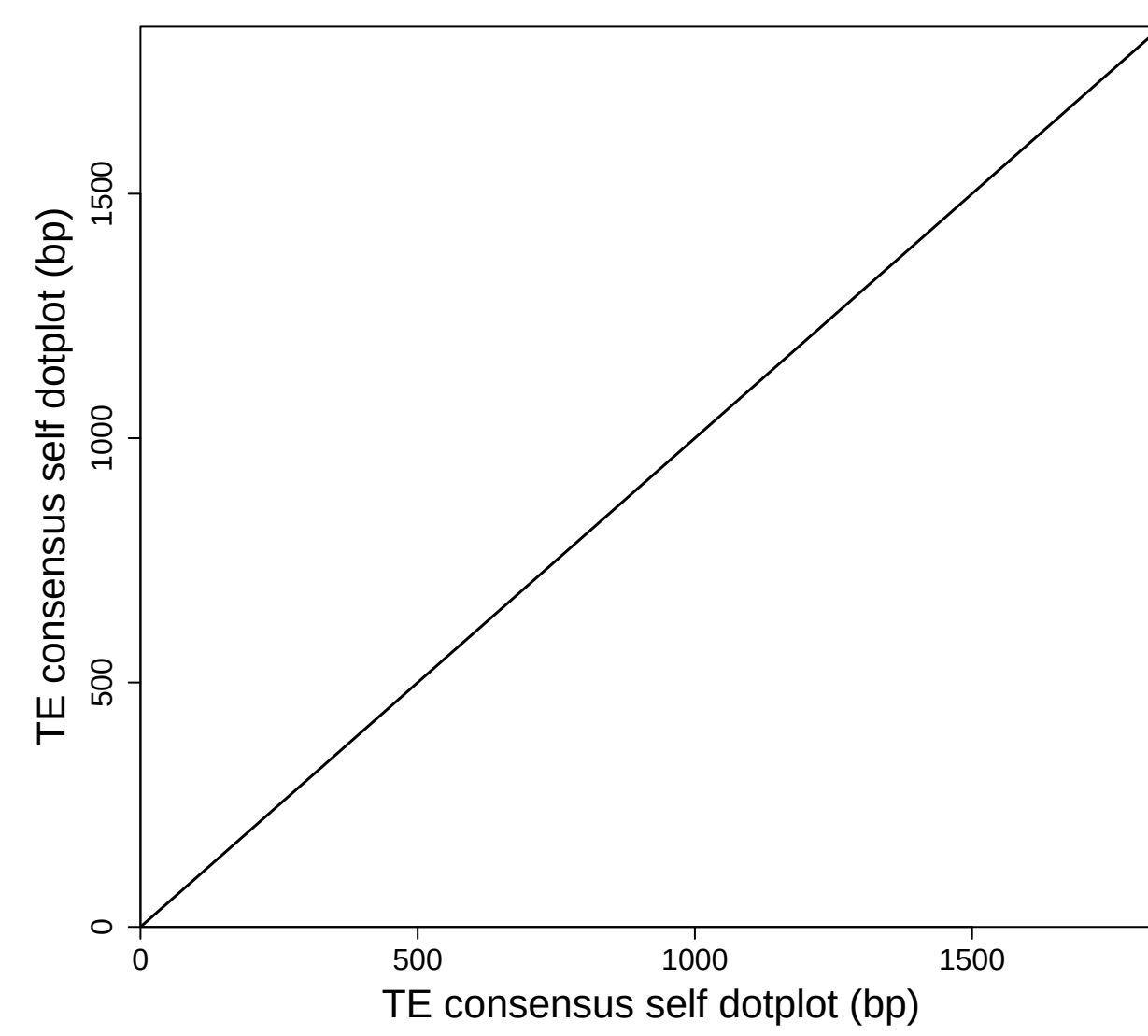
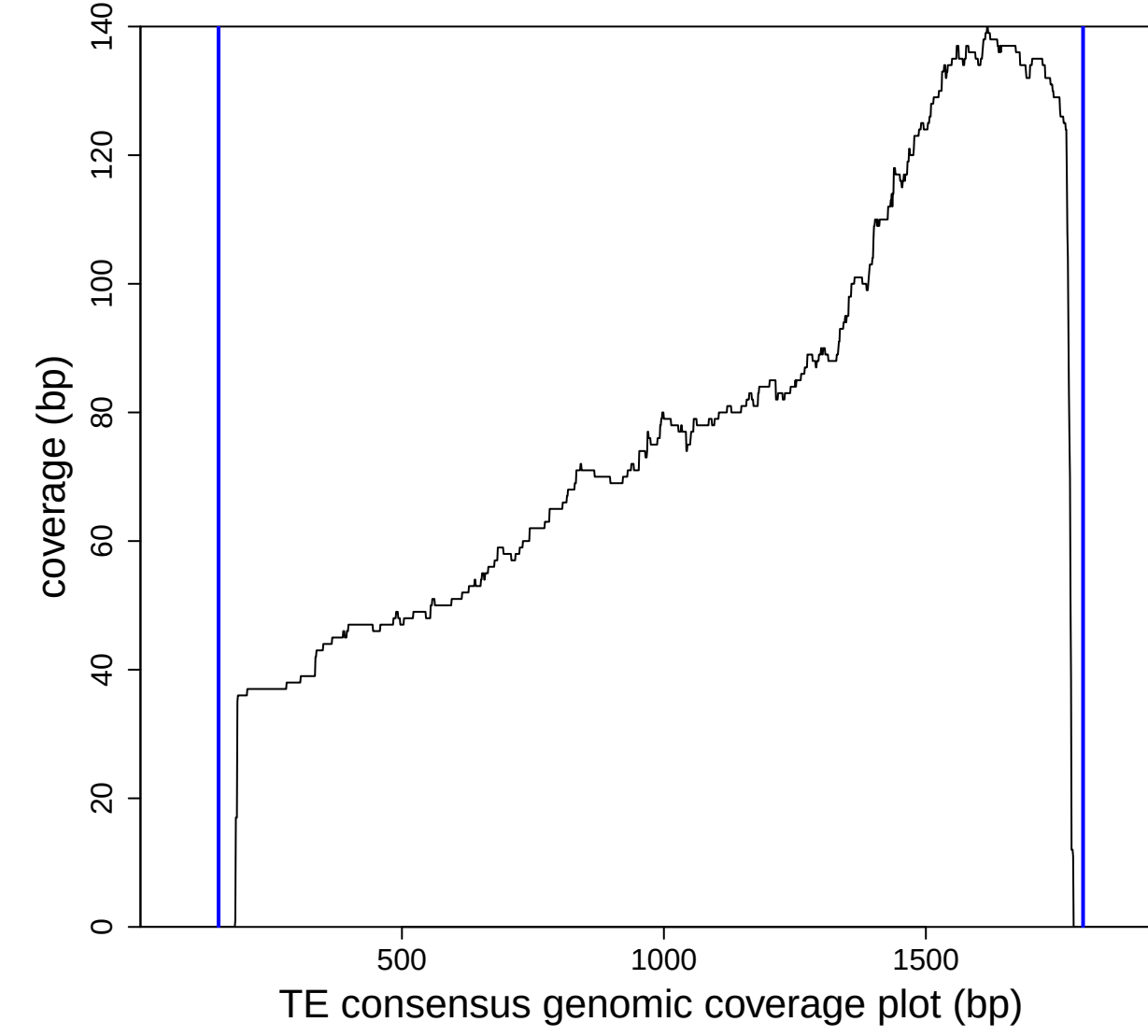
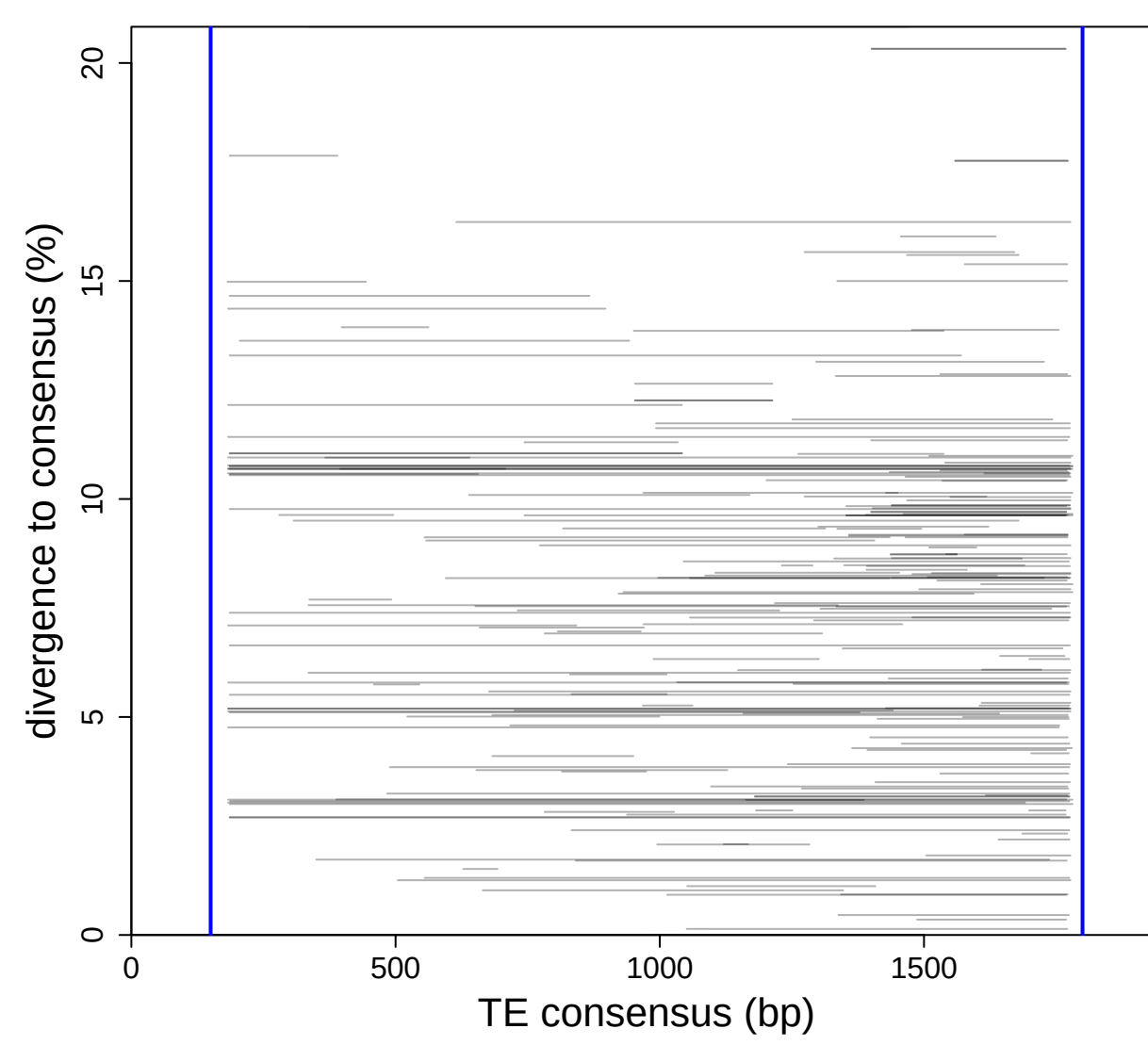
bed_uf.bed g_3.bed fm_1.bed 0_0 bcln.fa aln.fa cl.fa gs.fa c
size: 1643bp; fragments: 213; full length: 26 (≥ 1478.7 bp)

After TEtrimmer 1643 bp

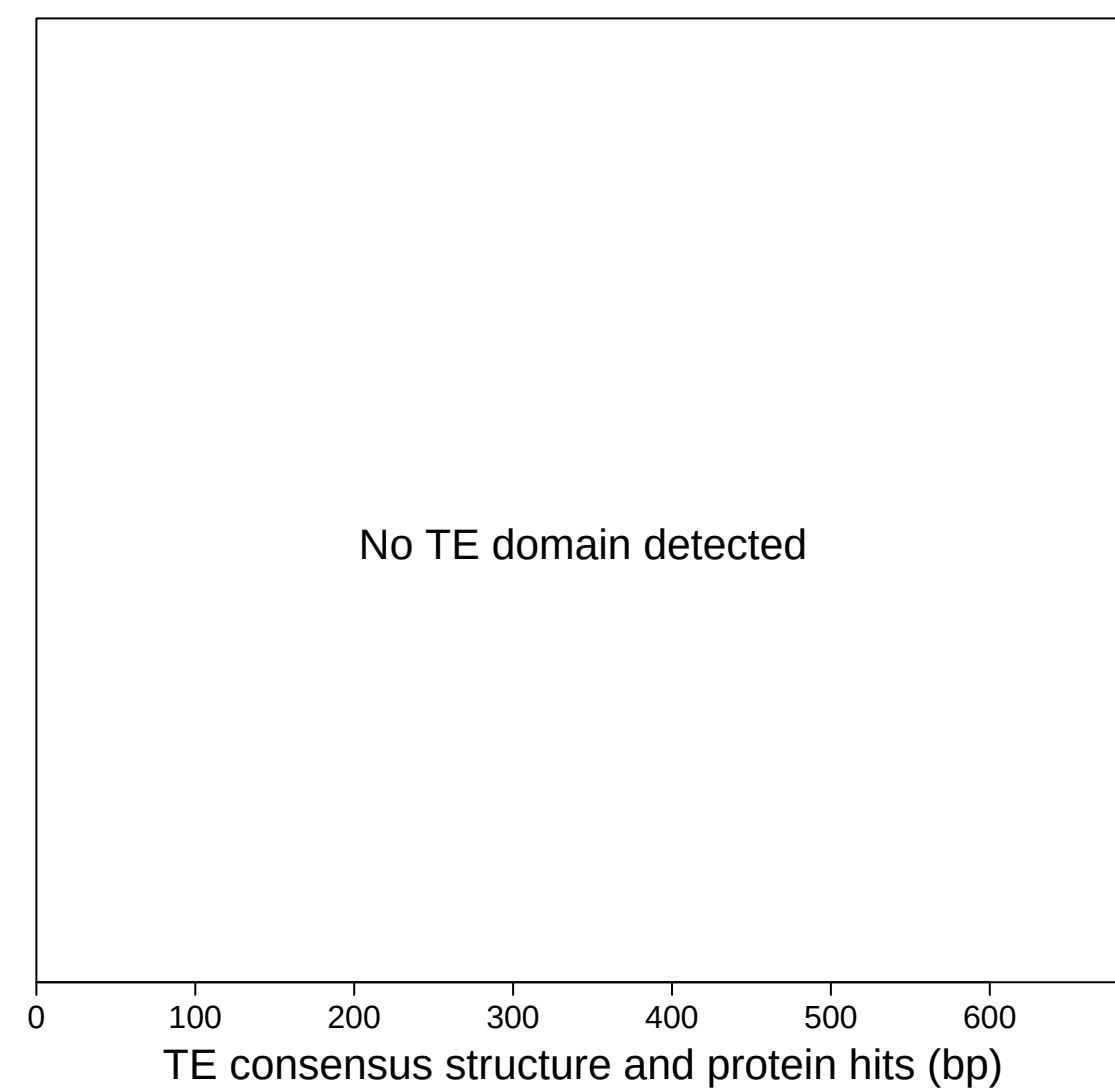
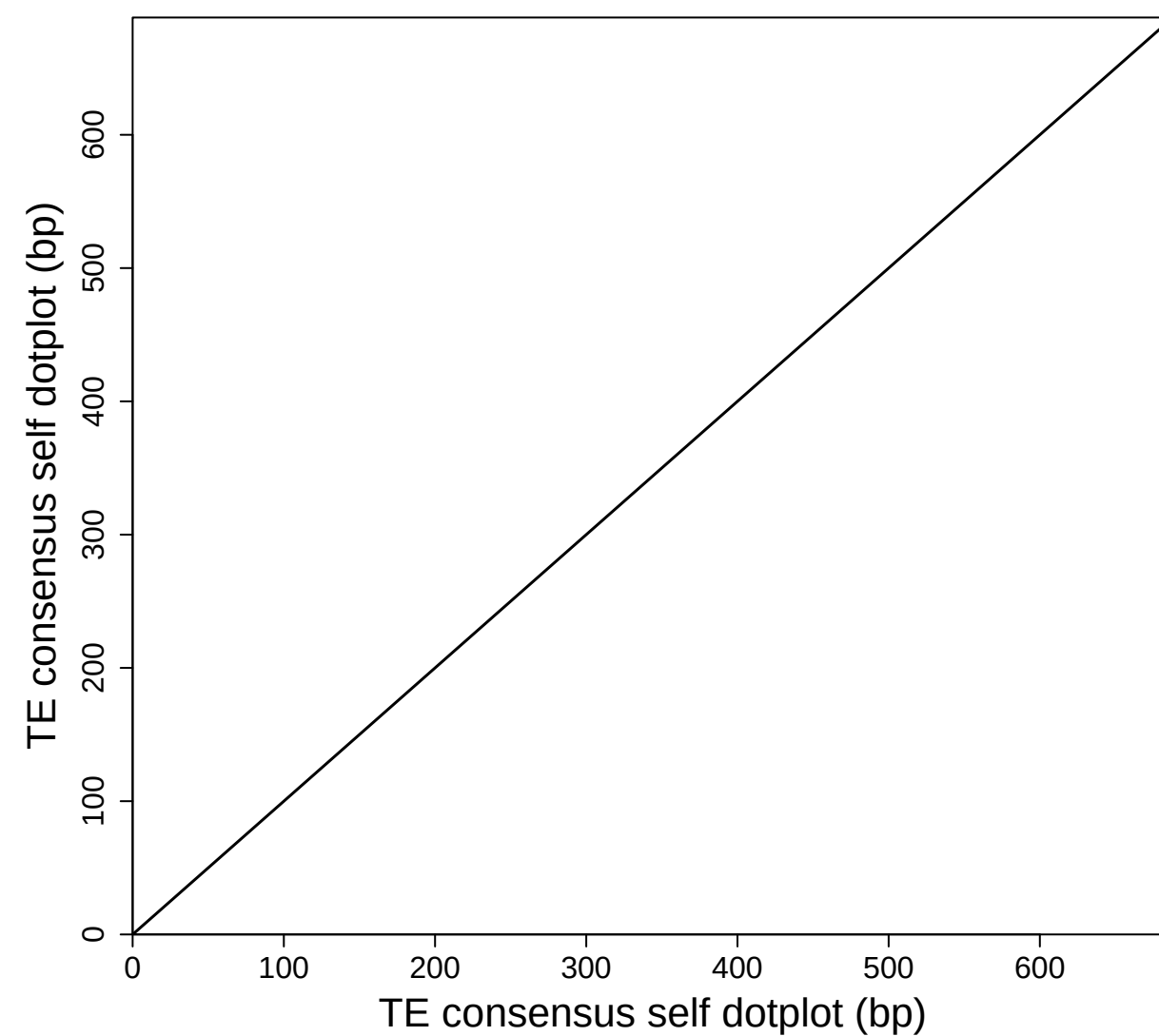
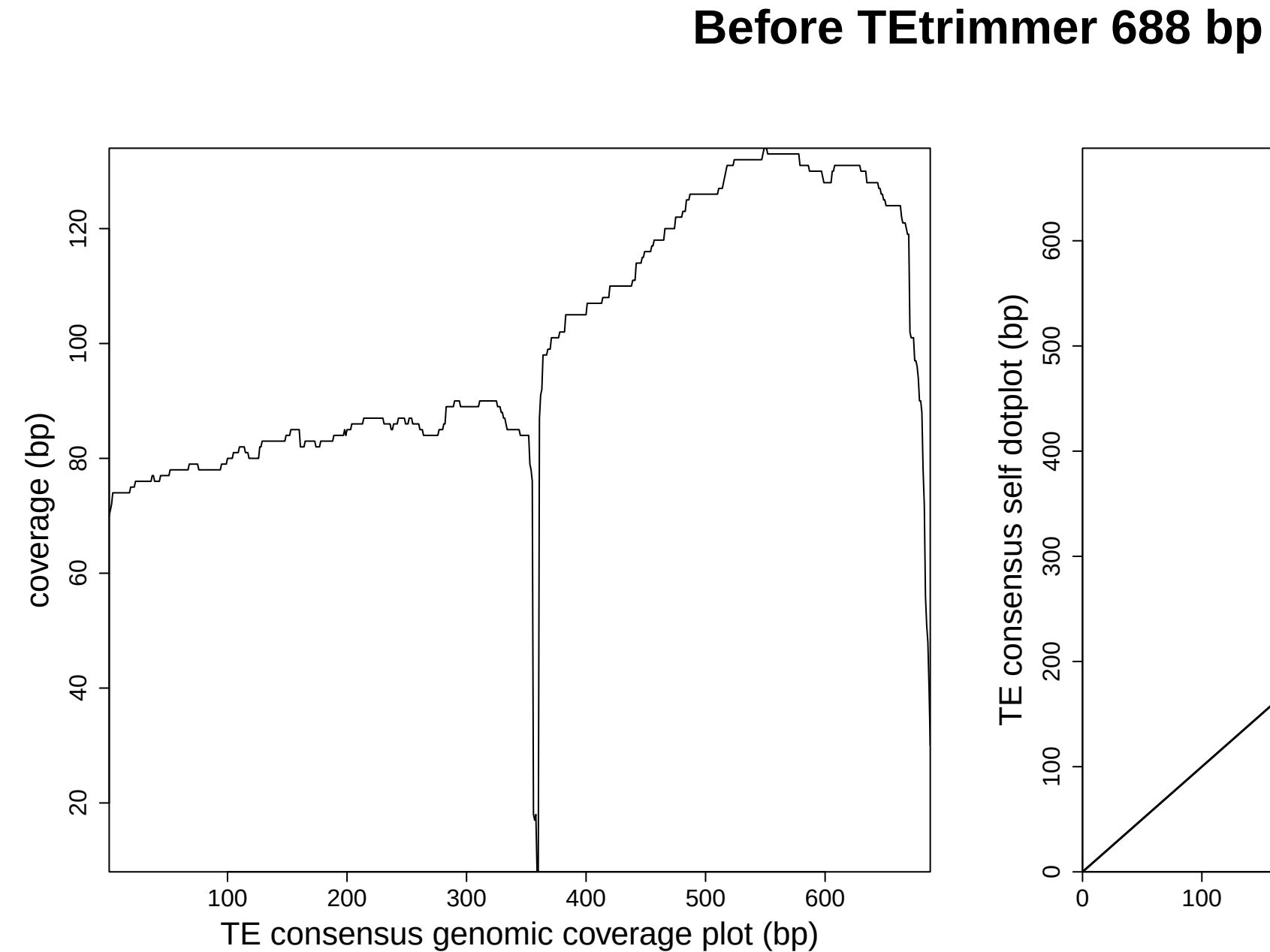
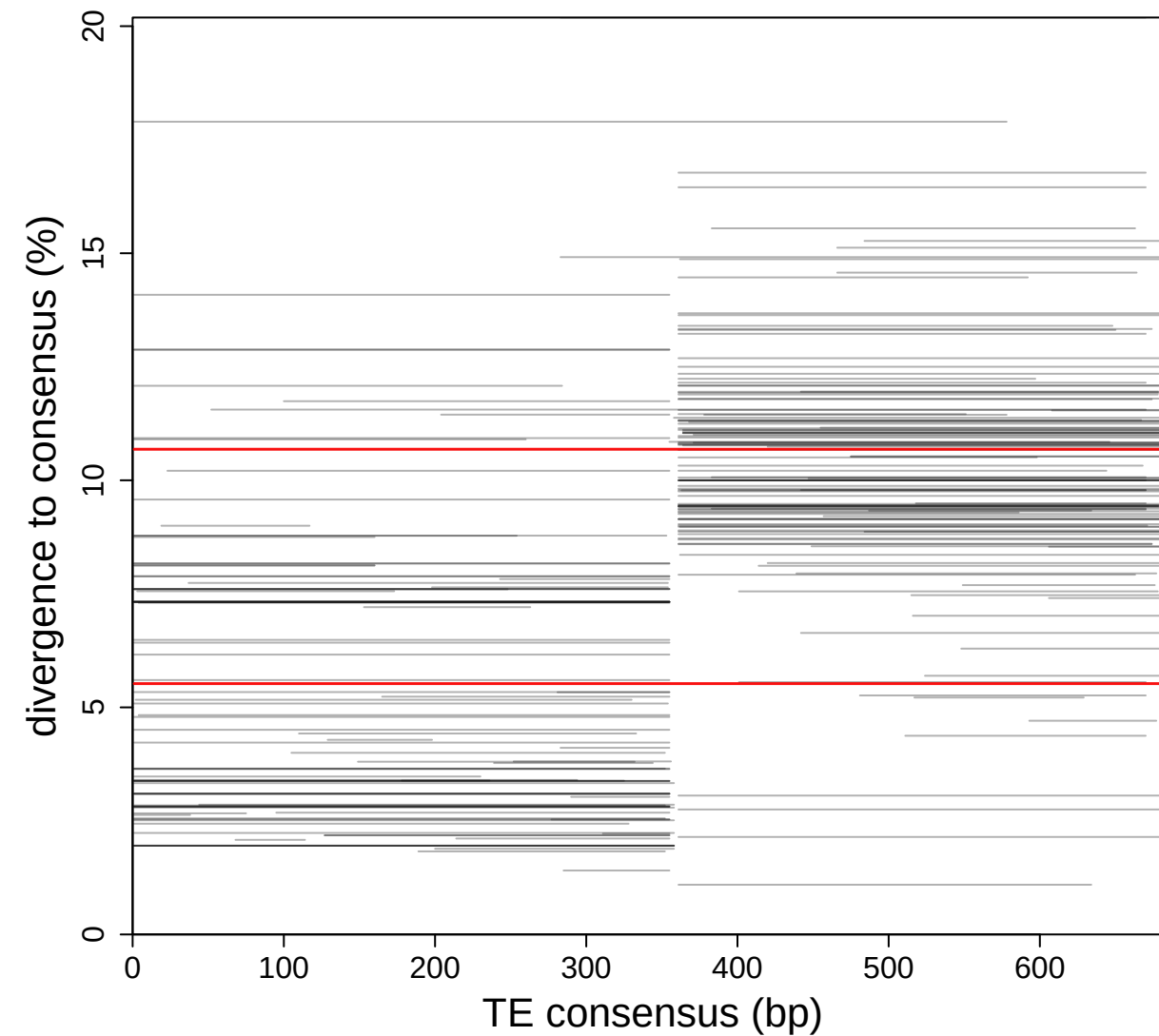


9.fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.f
size: 1950bp; fragments: 209; full length: 0 (>=1755bp)

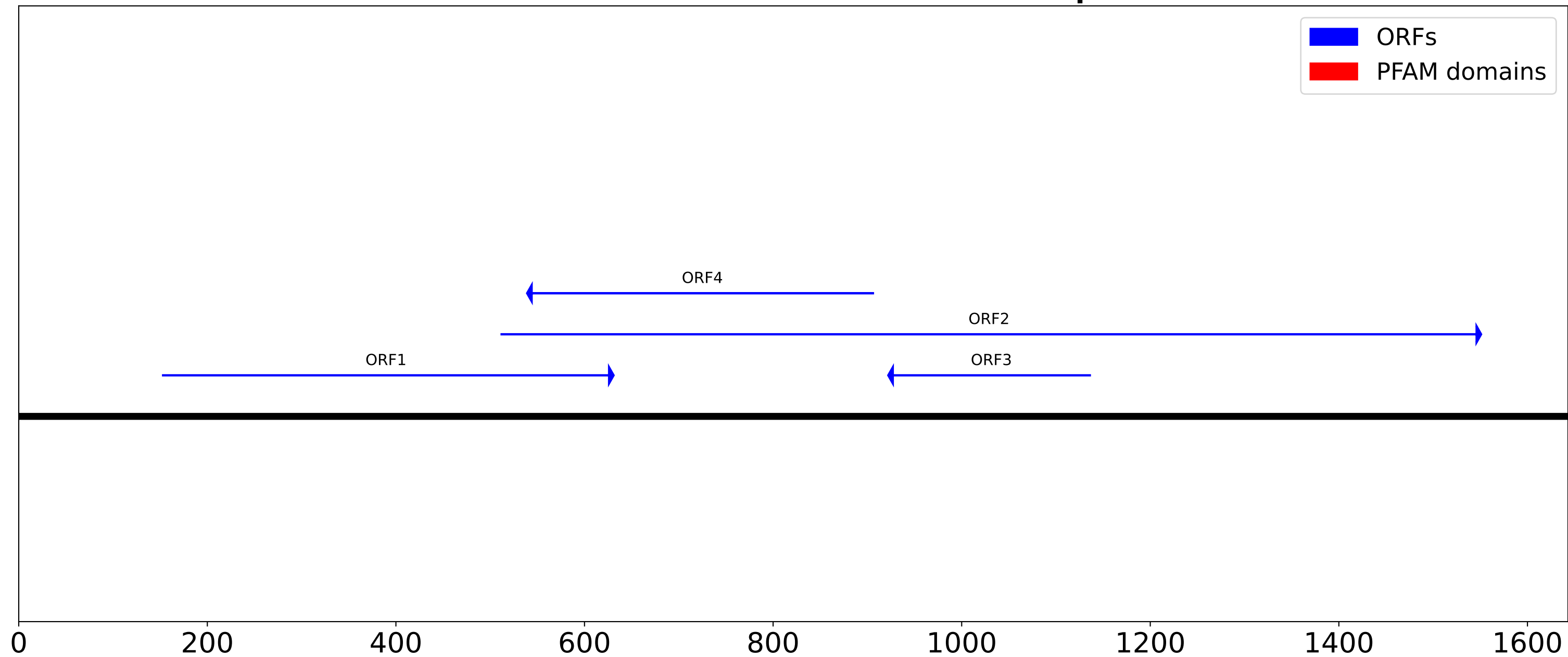
After TEtrimmer Extended plot Blue lines are boundaries



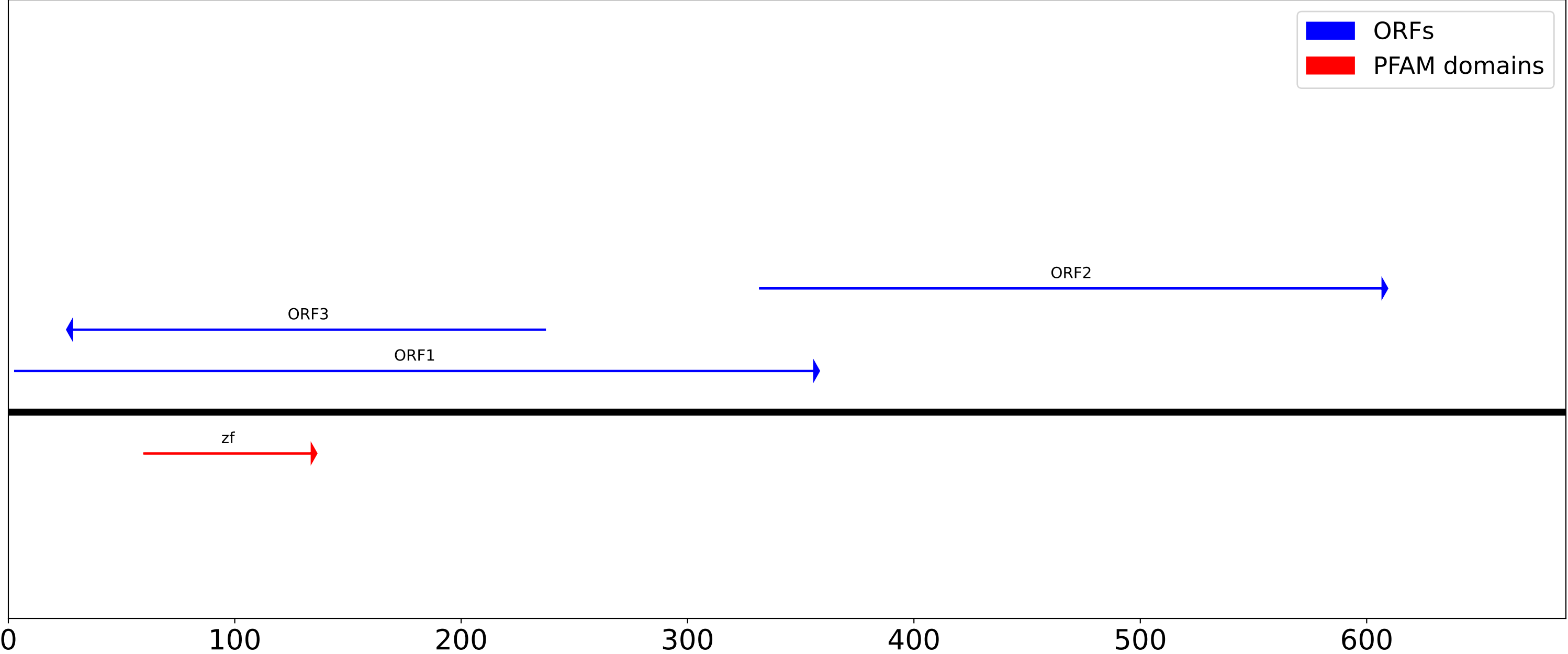
TE: rnd_5_family_7119
size: 688bp; fragments: 239; full length: 2 (≥ 619.2 bp)



After TEtrimmer ORF and PFAM domain plot



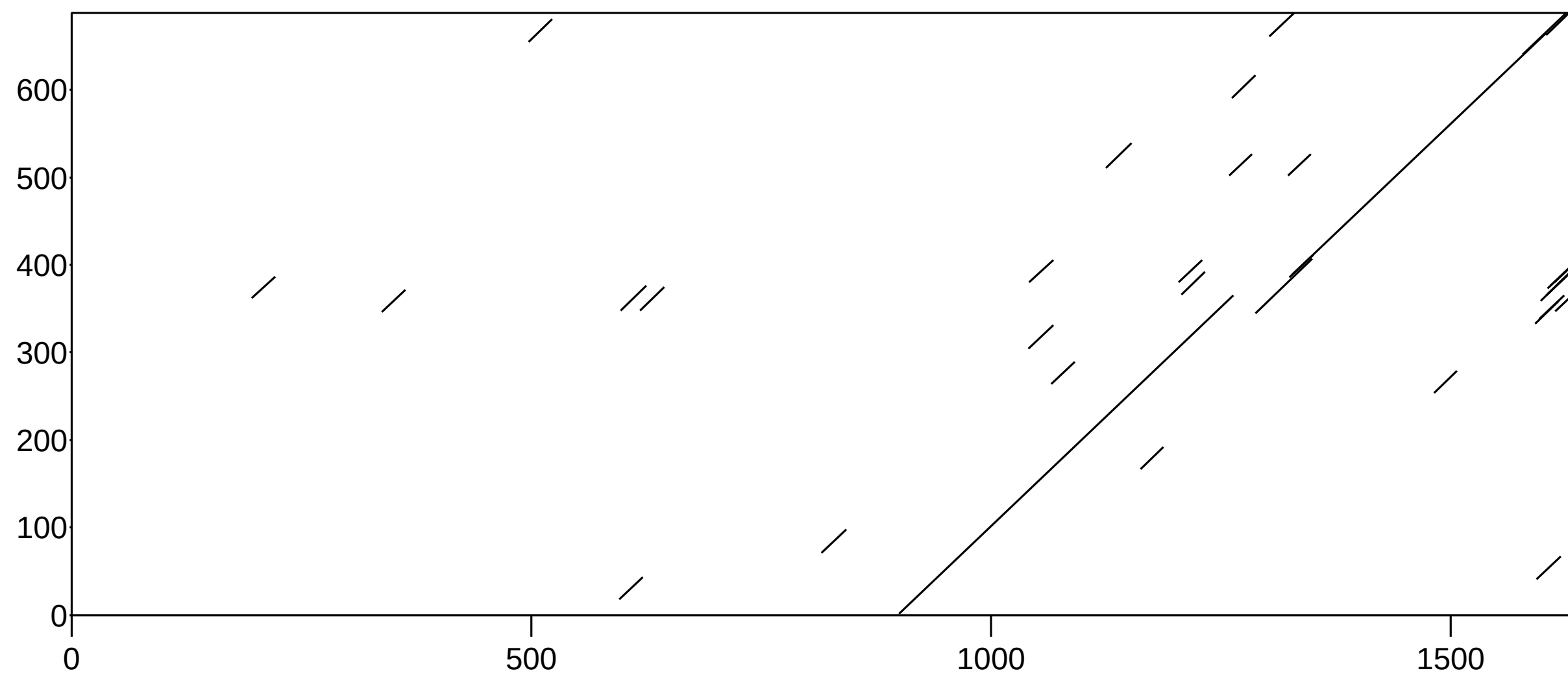
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)