

Start crop Point



End crop Point



MSA length = 5672



Start crop Point

End crop Point

0

10

0

1000

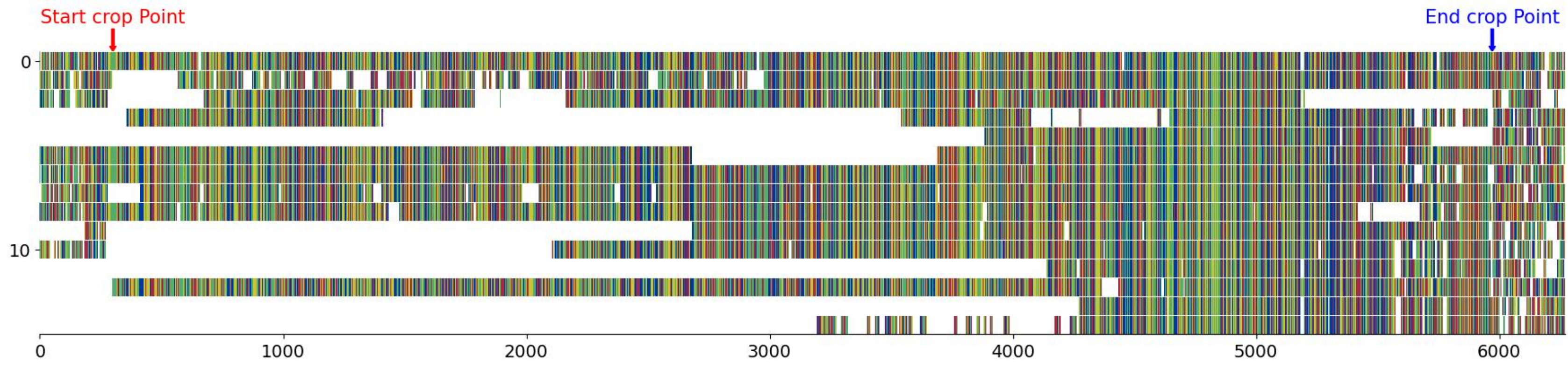
2000

3000

4000

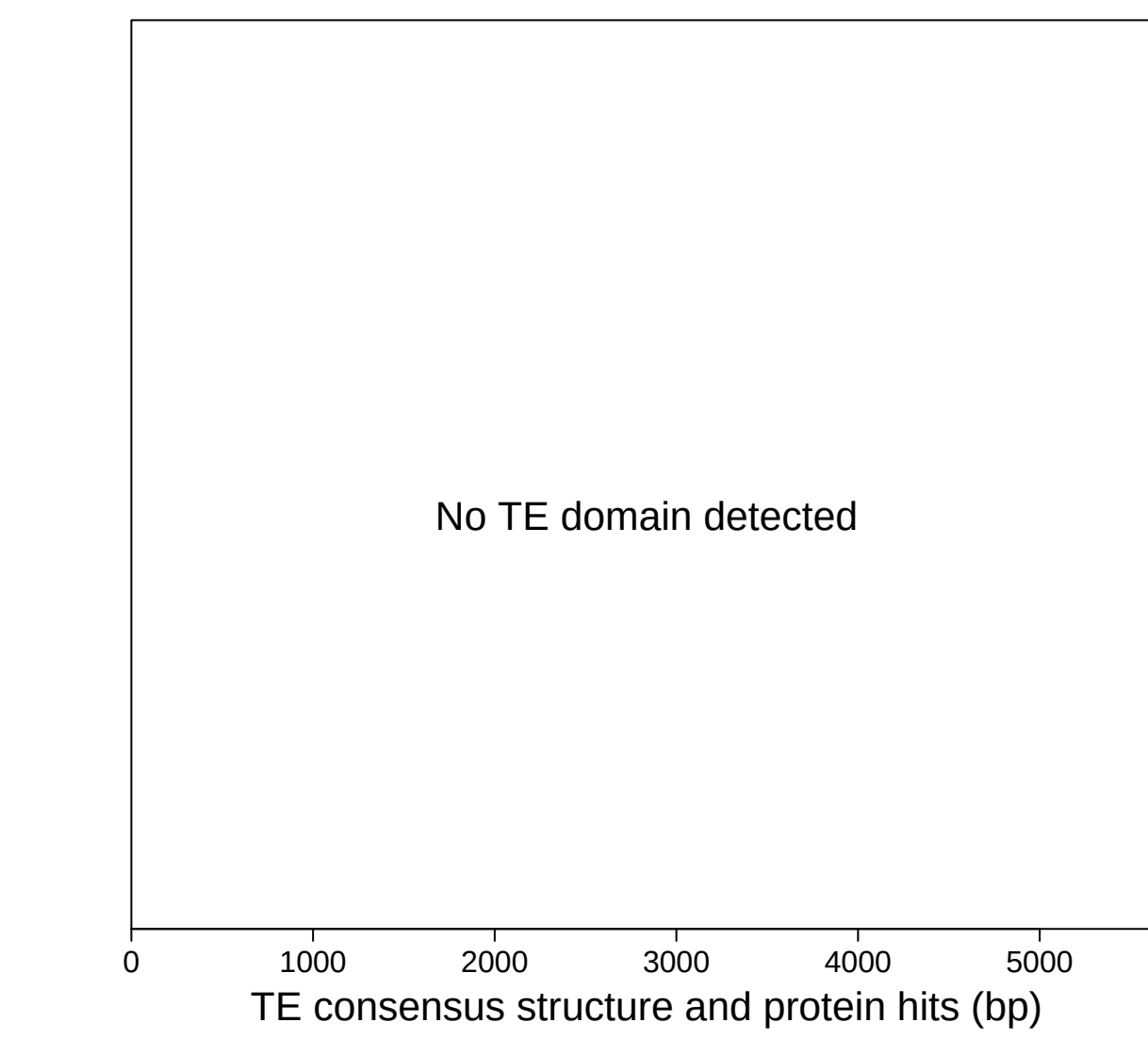
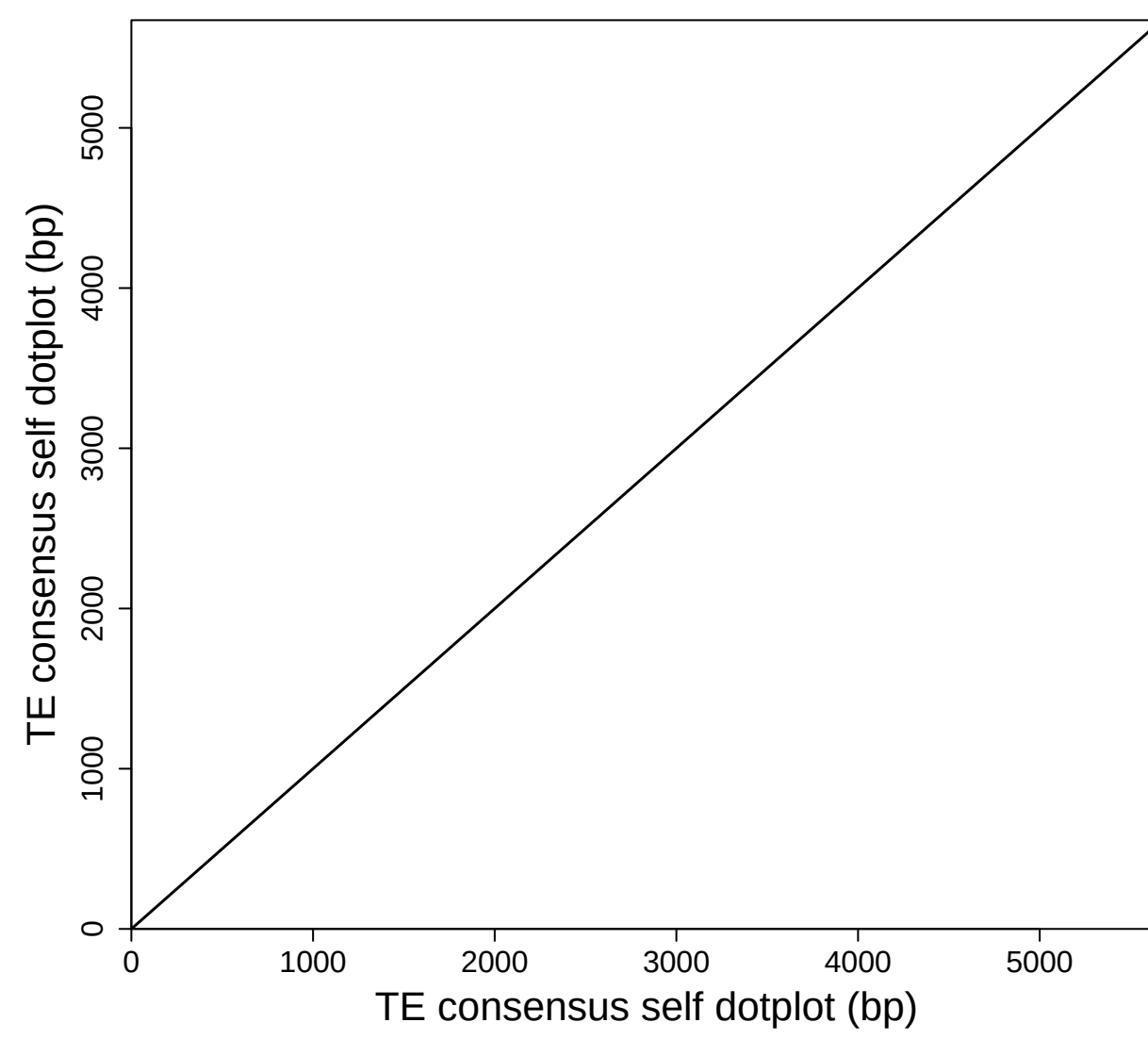
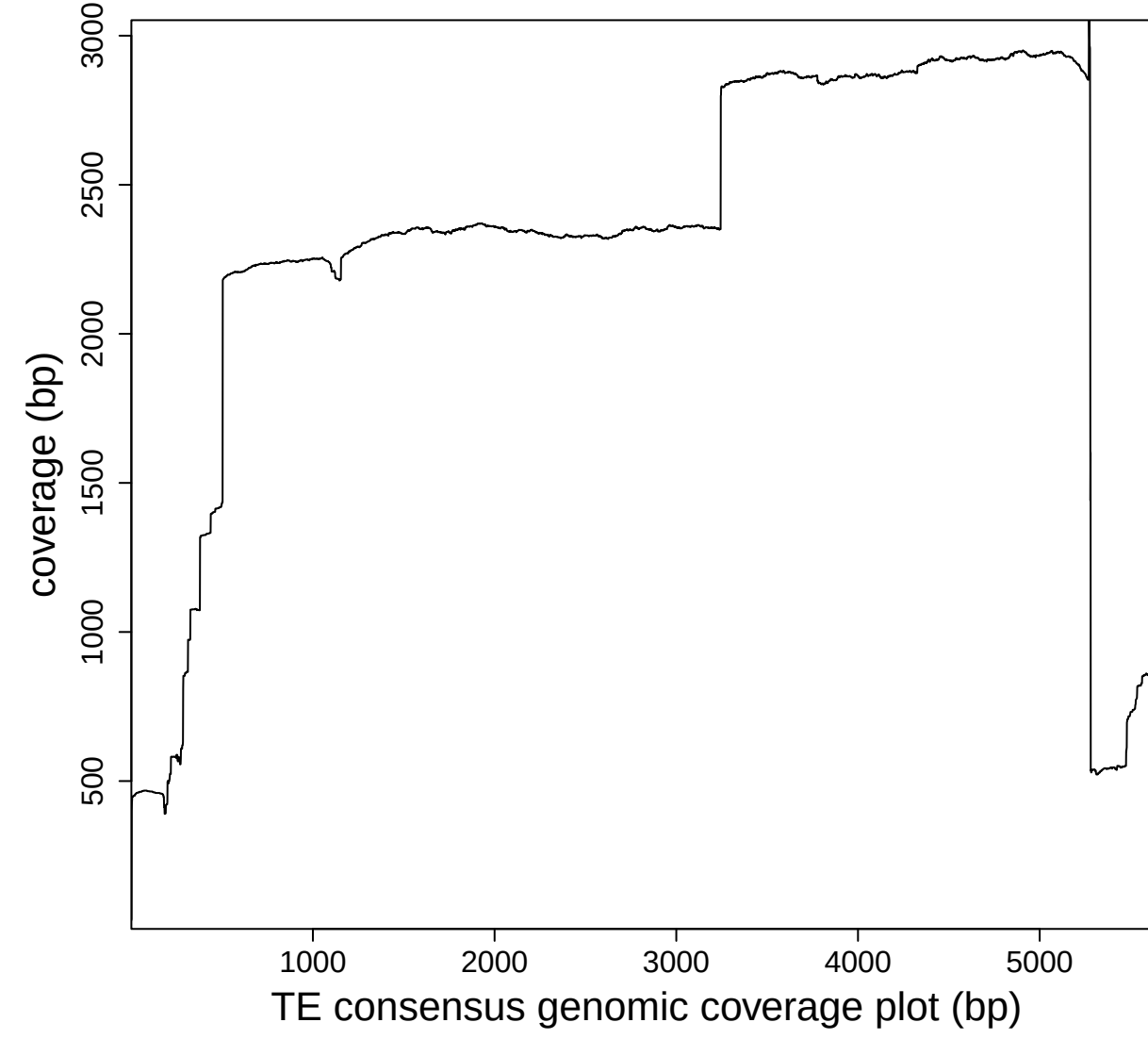
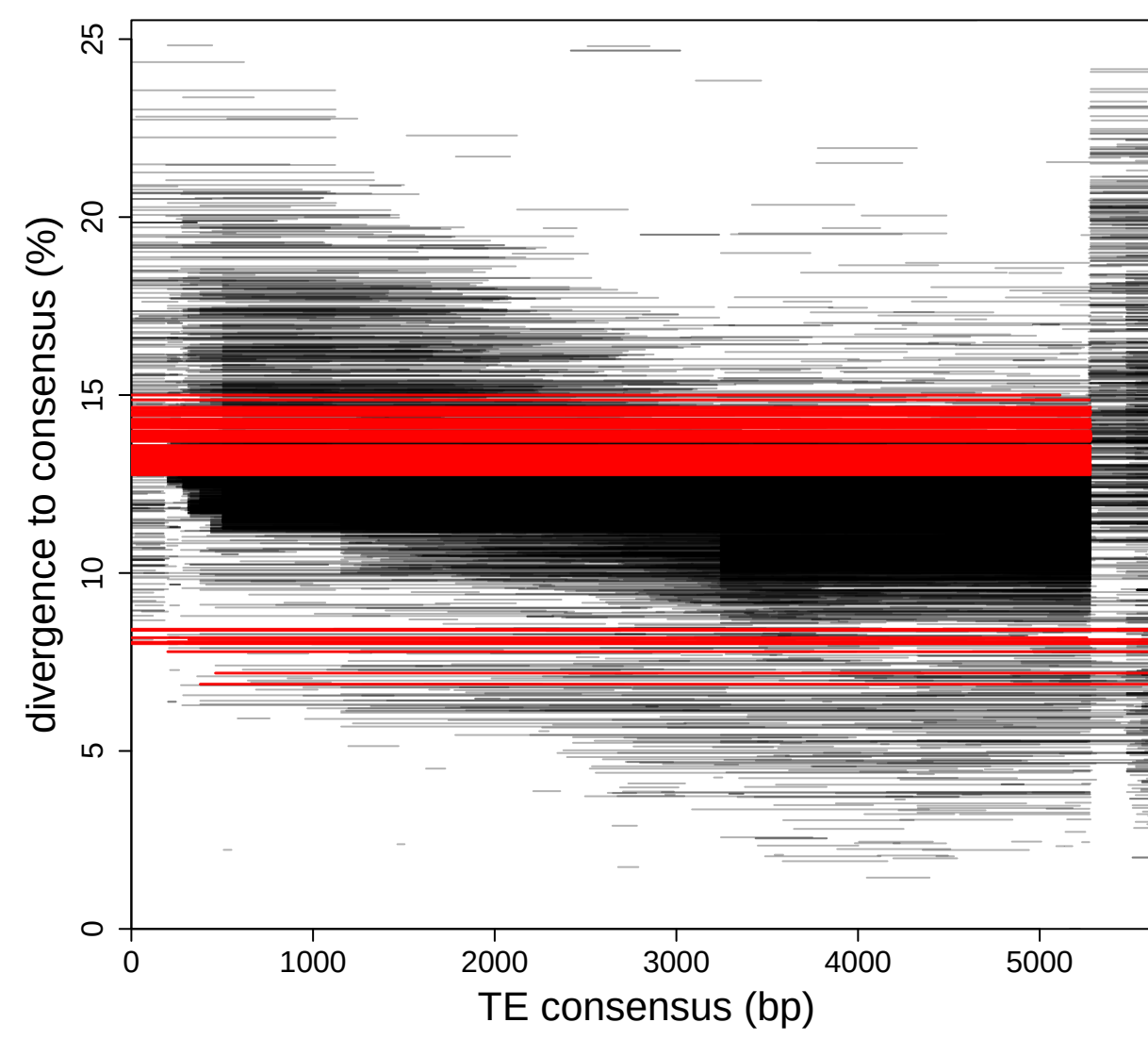
5000

6000



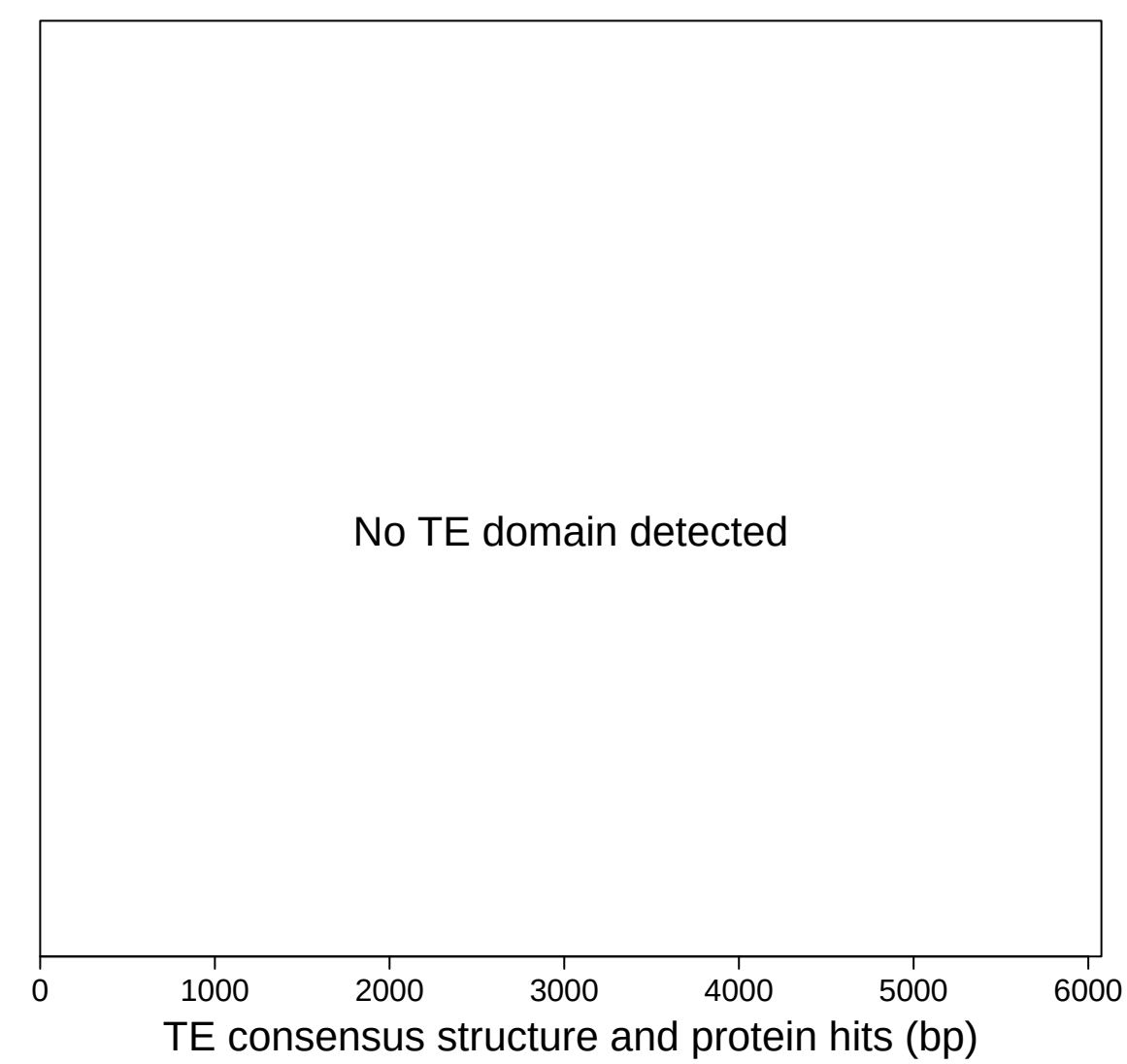
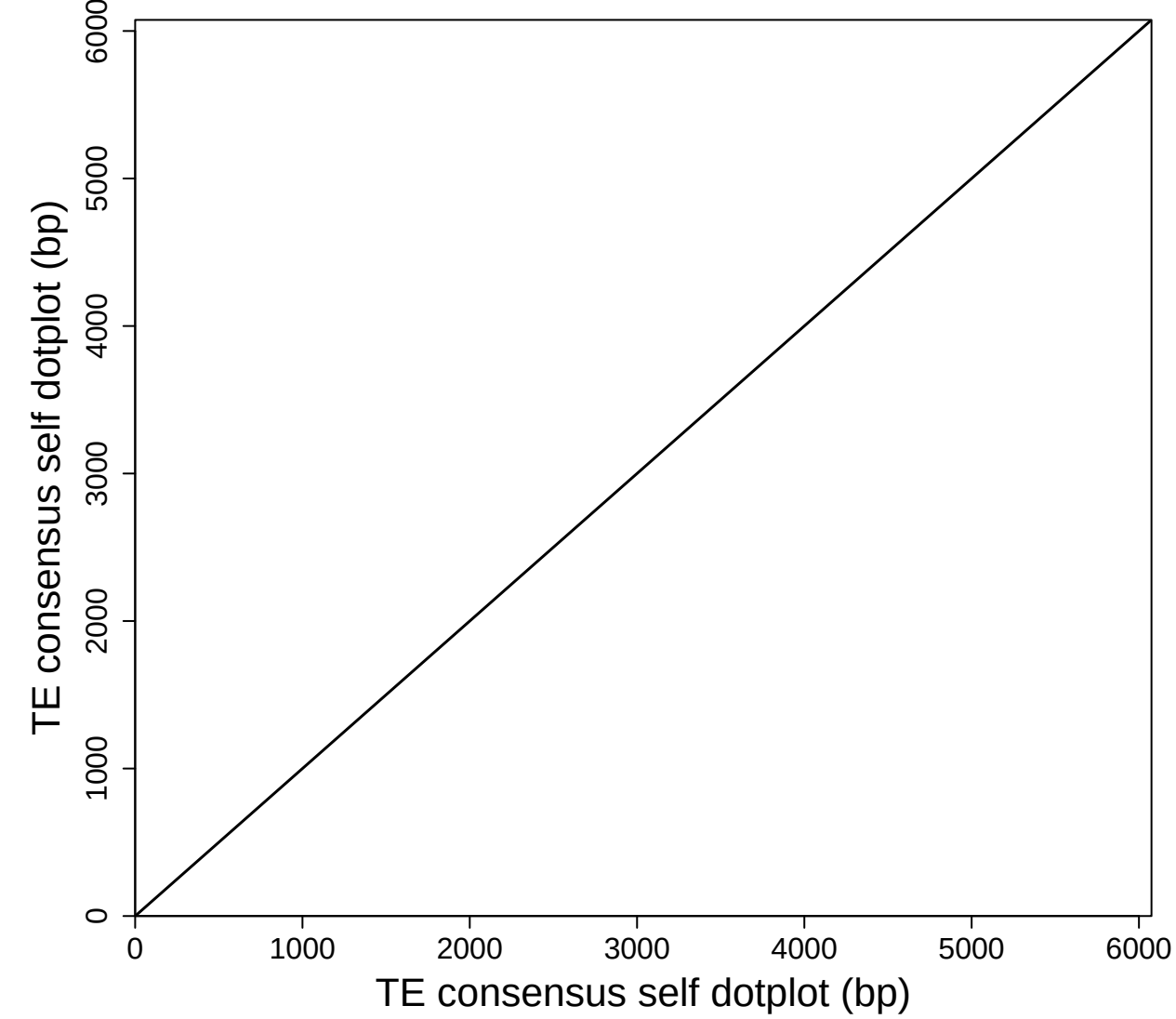
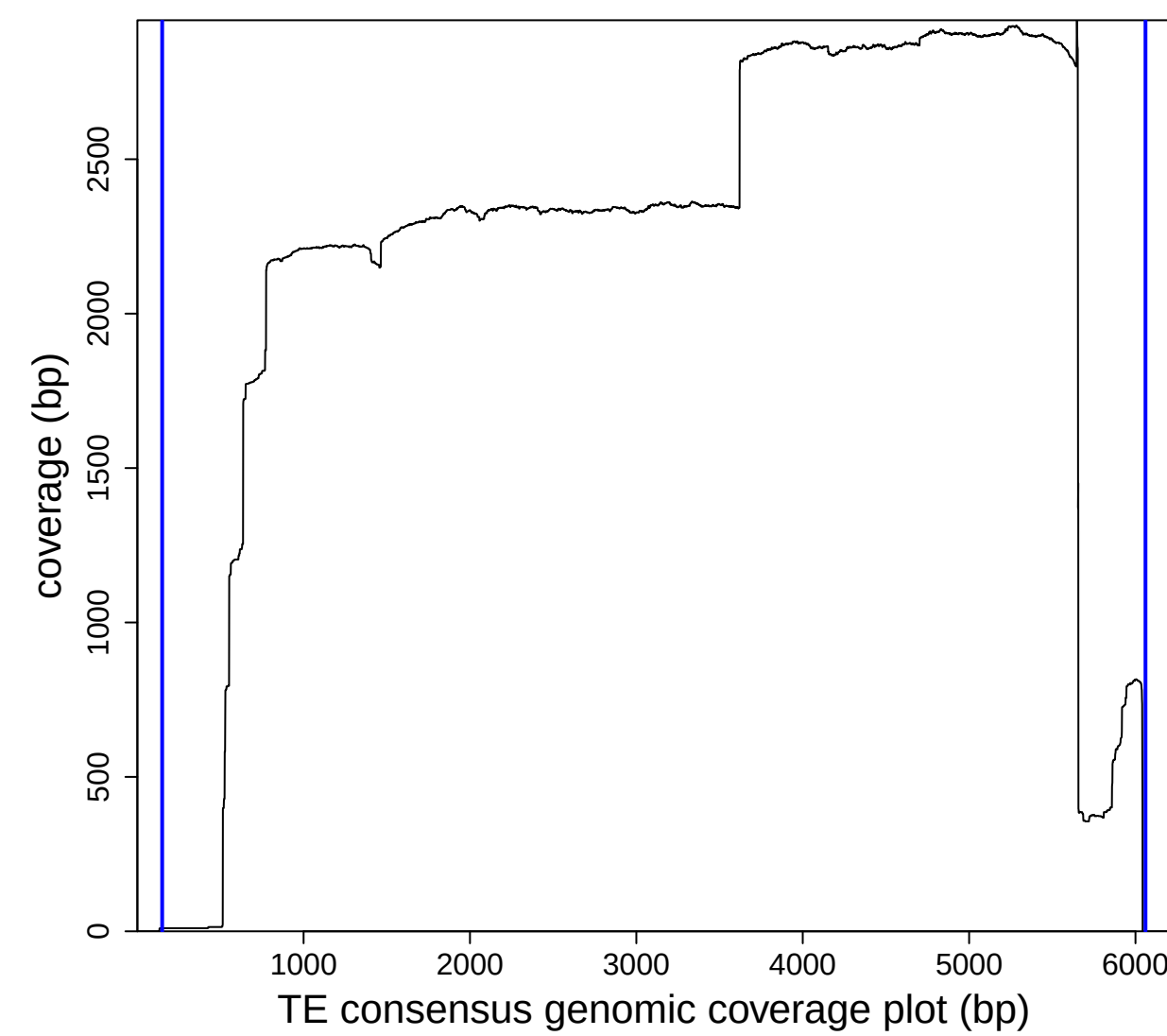
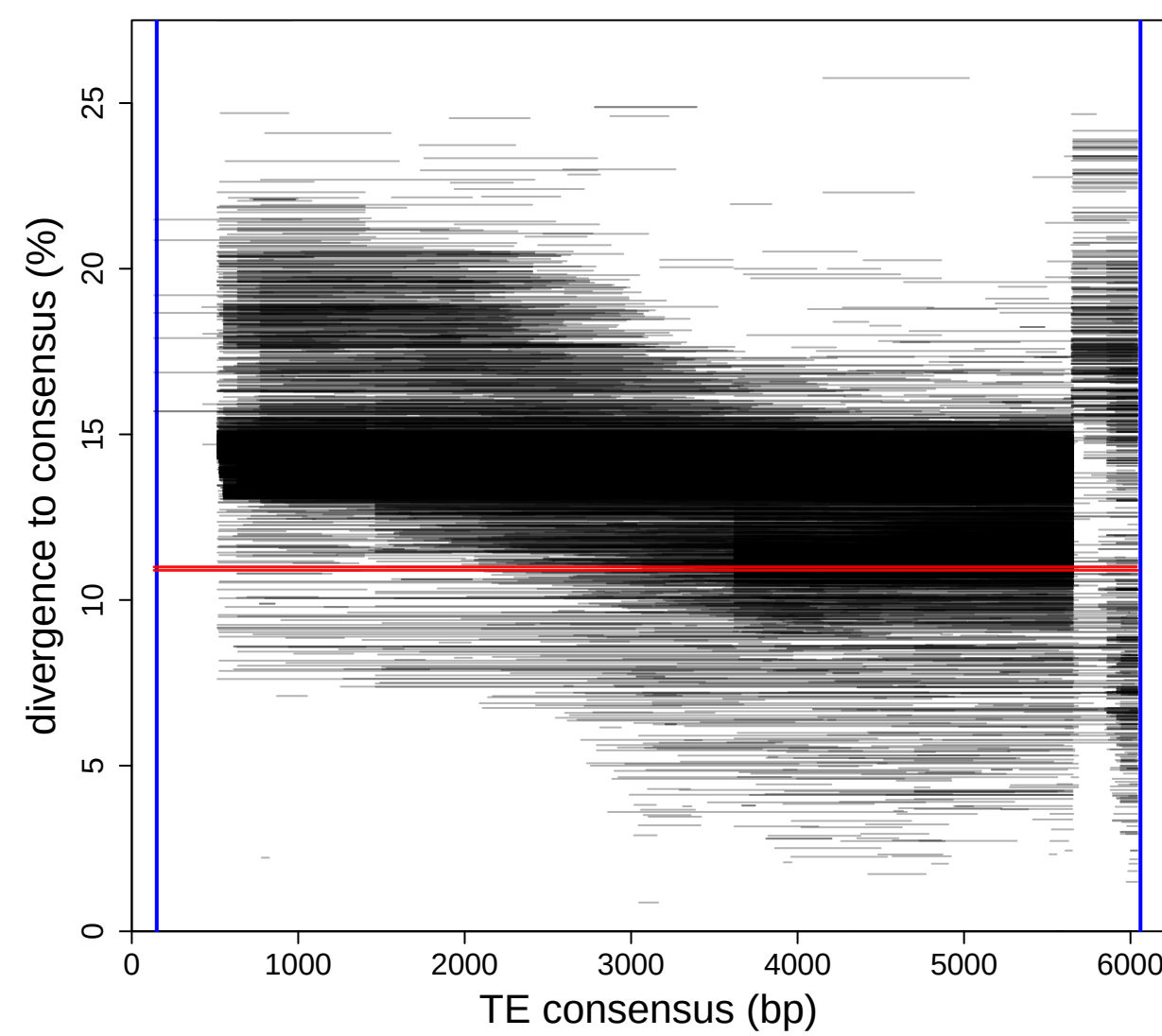
b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 5672bp; fragments: 5731; full length: 248 (≥ 5104.8 bp)

After TEtrimmer 5672 bp

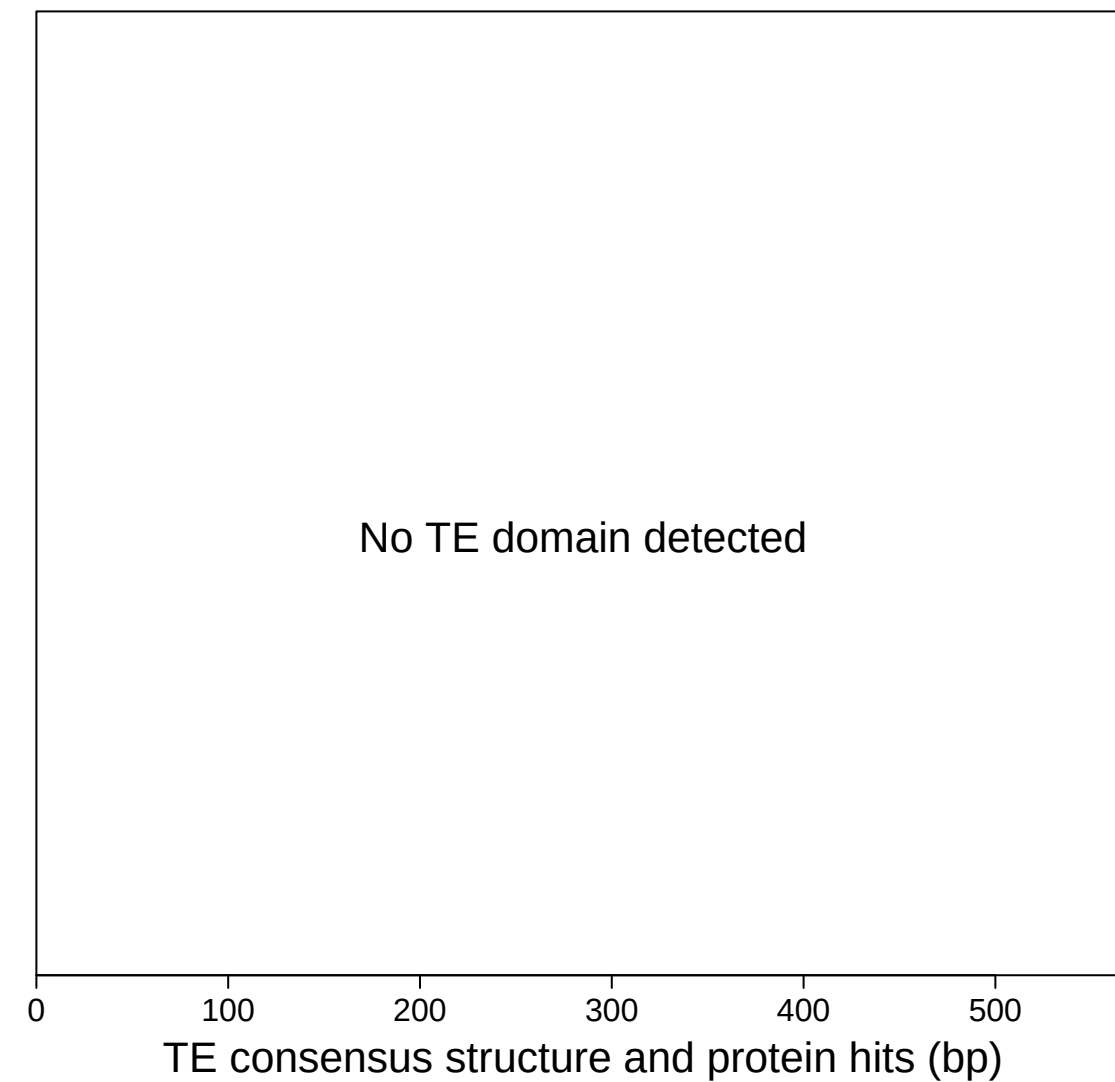
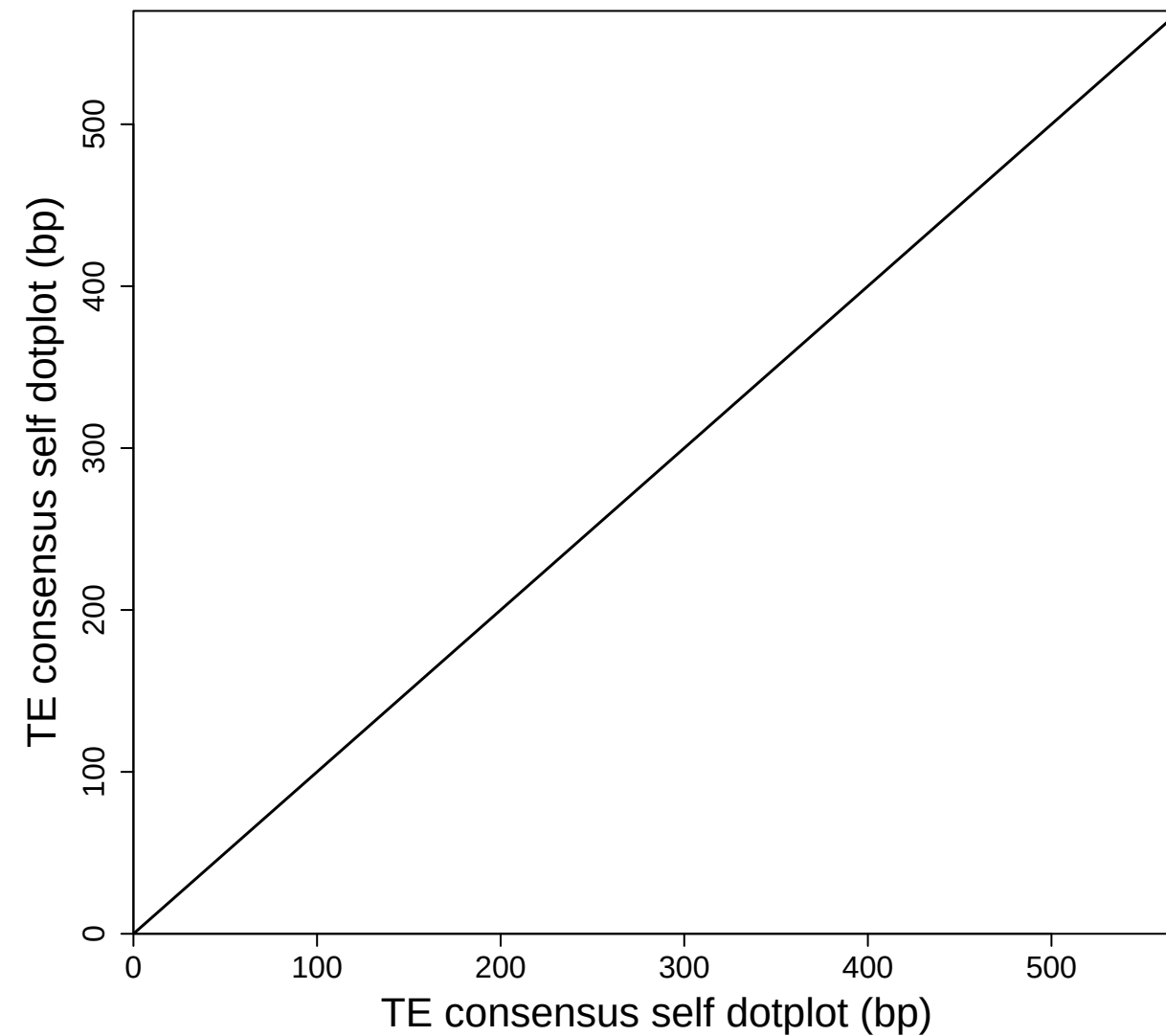
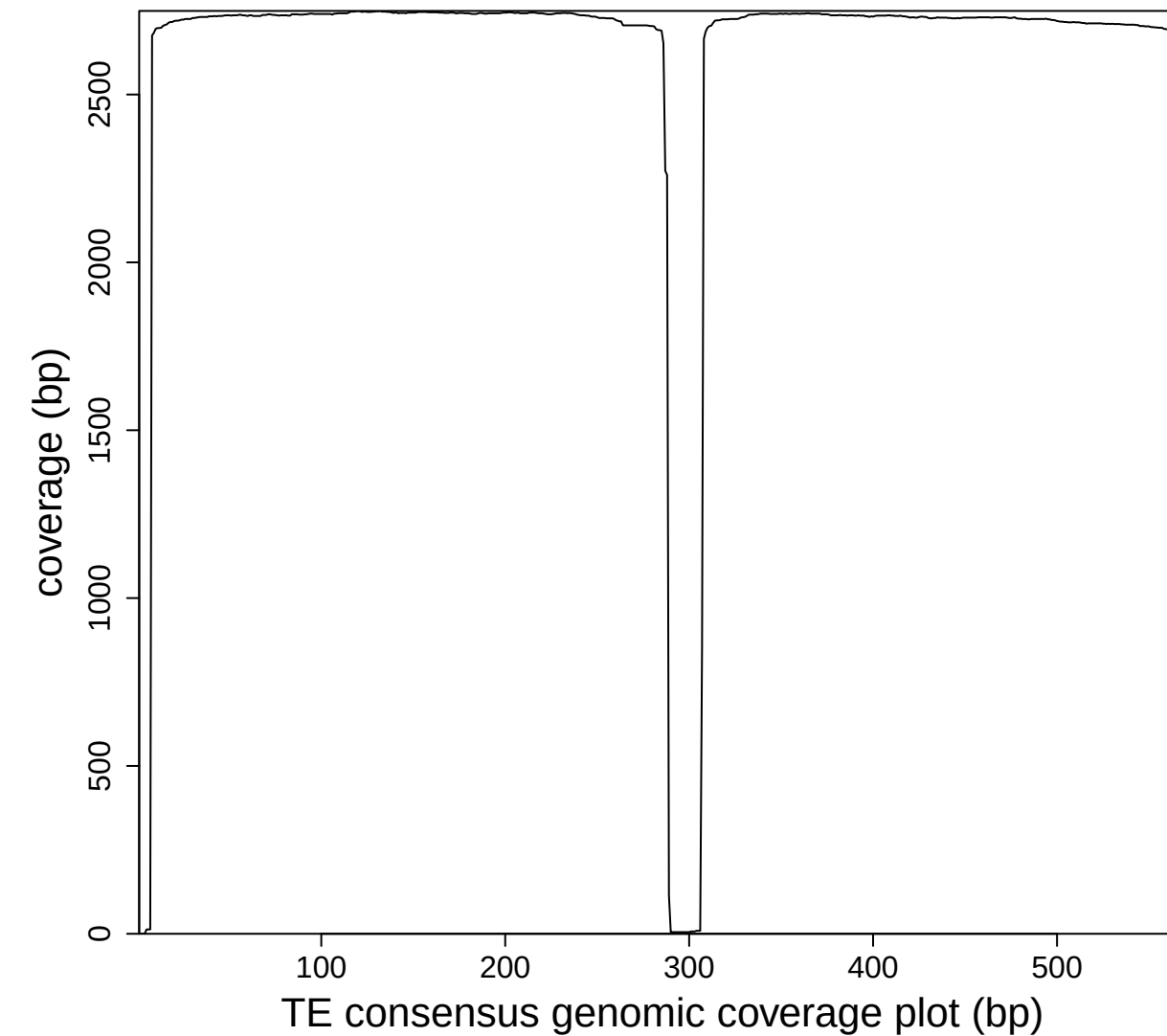
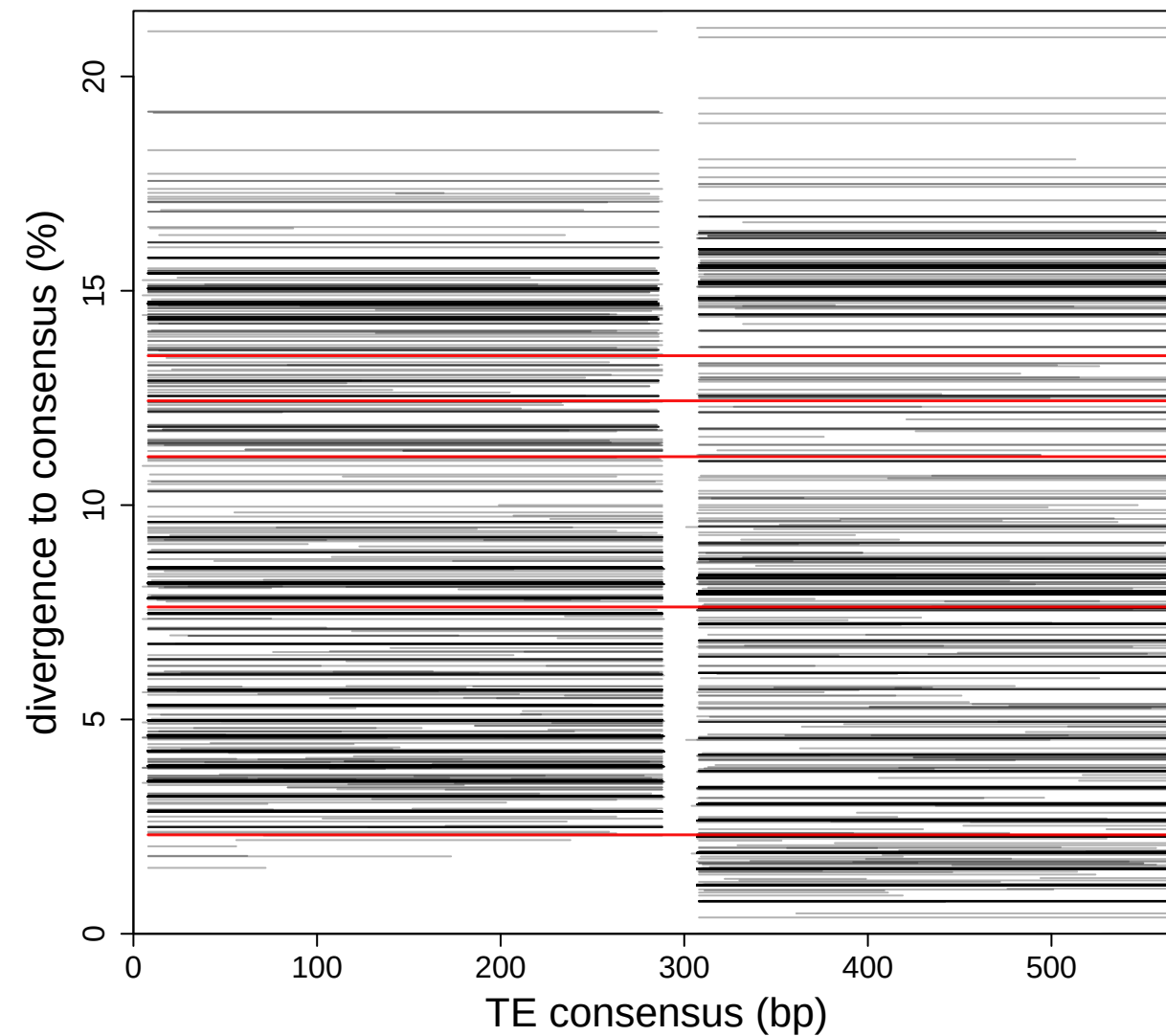


.fasta.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 6210bp; fragments: 5381; full length: 2 (>=5589bp)

After TEtrimmer Extended plot Blue lines are boundaries

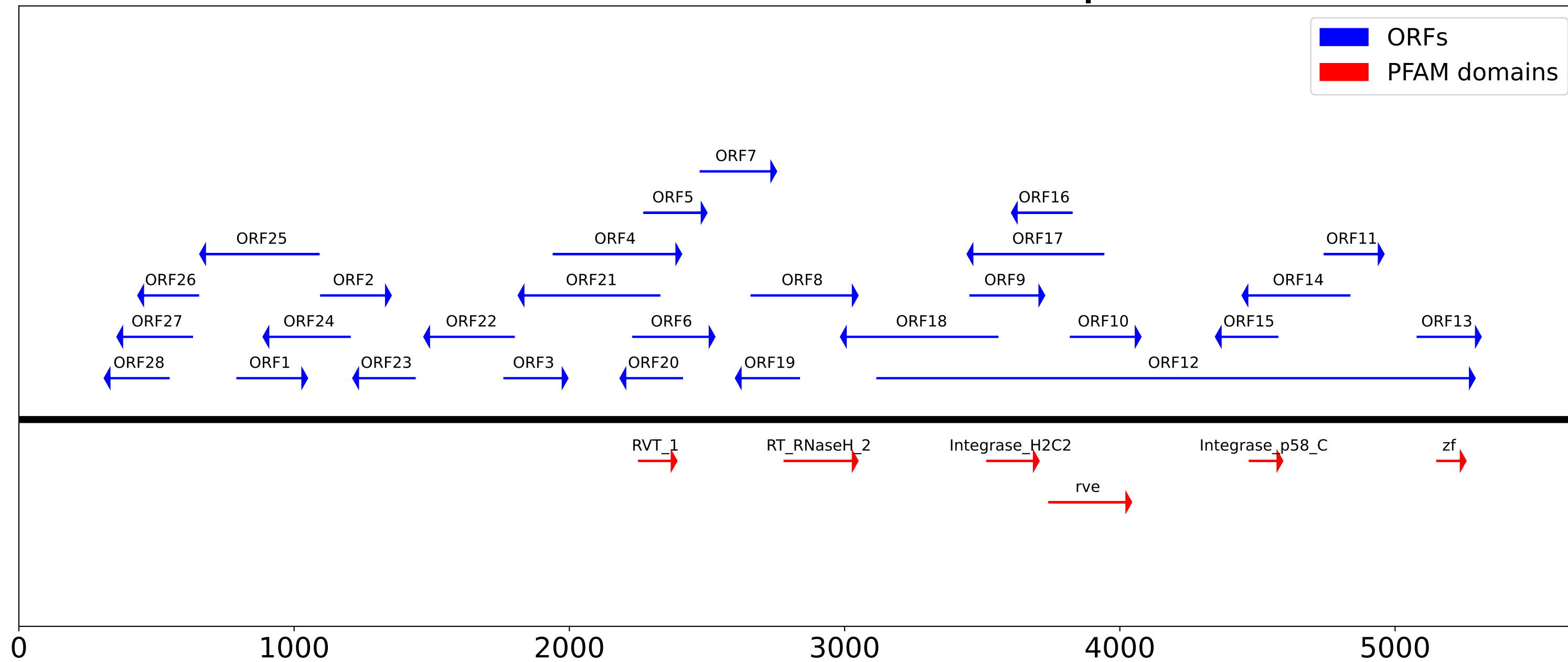


TE: ltr_1_family_450
size: 570bp; fragments: 5603; full length: 5 (≥ 513 bp)

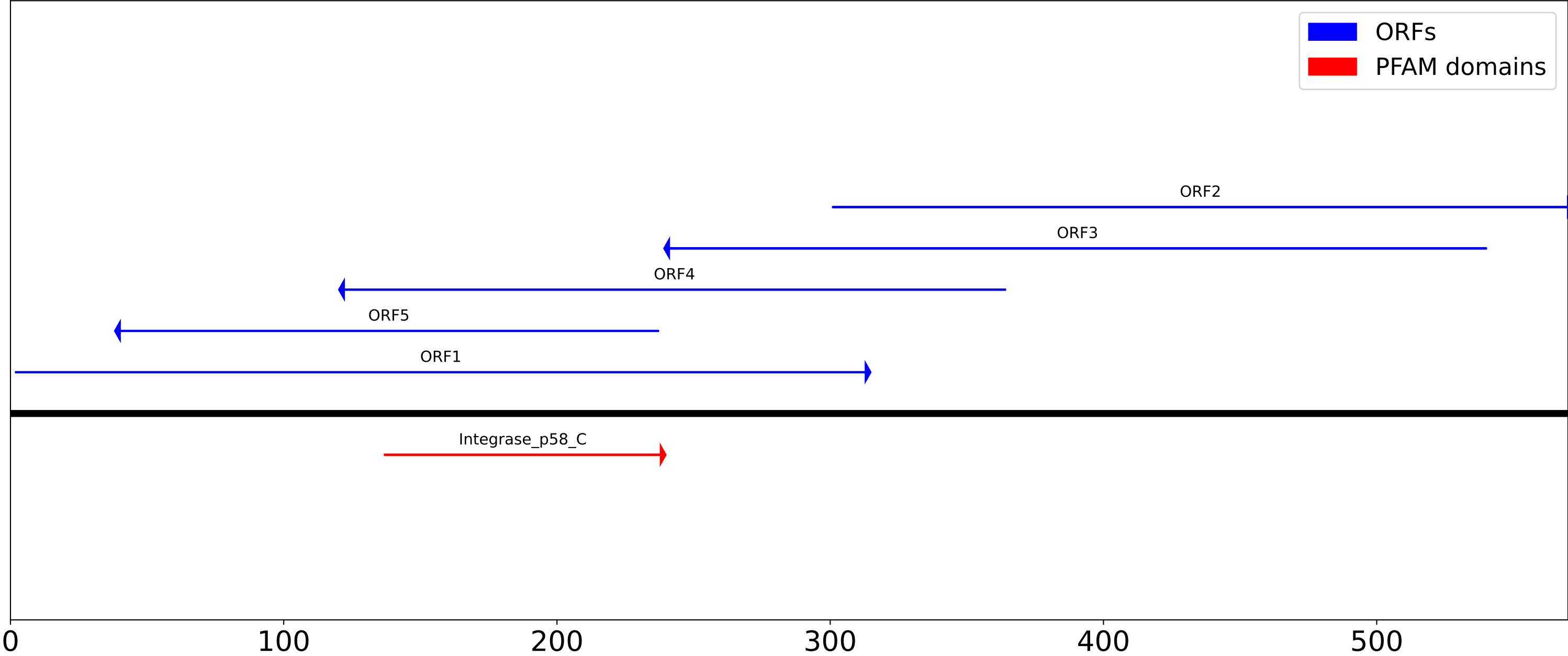


Before TEtrimmer 570 bp

After TETrimmer ORF and PFAM domain plot



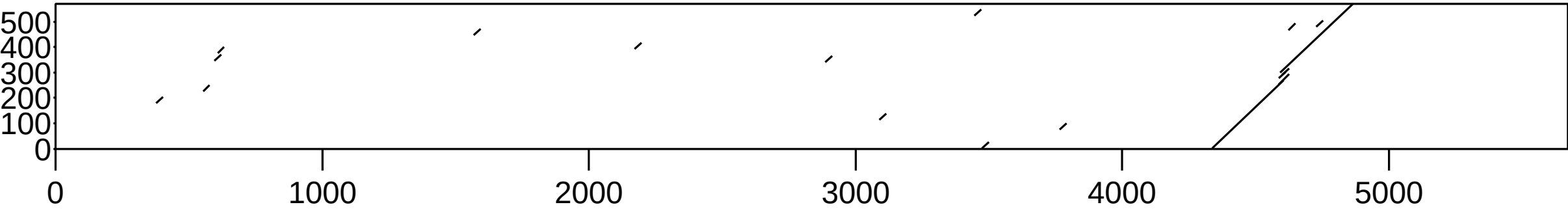
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)