

MSA length = 6429

[illegible]

Start crop Point

End crop Point

0 -

10 -

0

1000

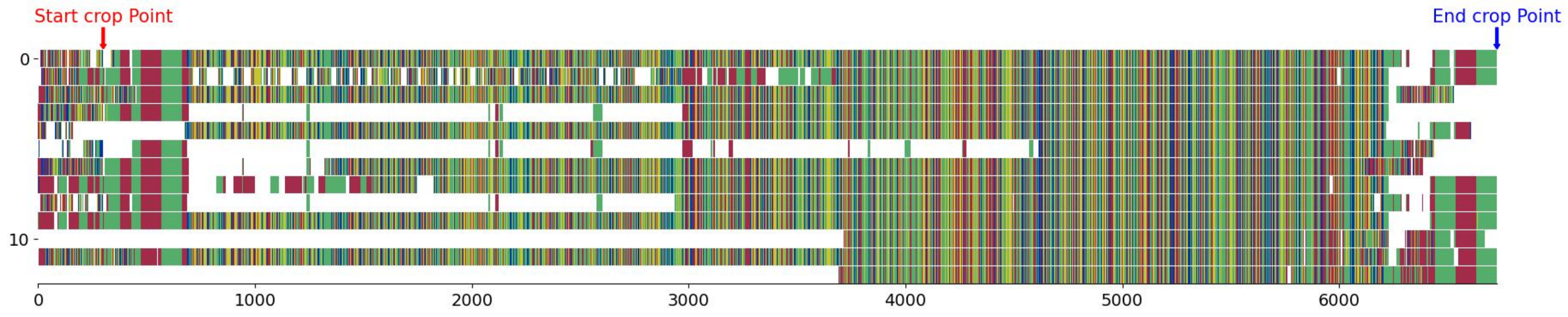
2000

3000

4000

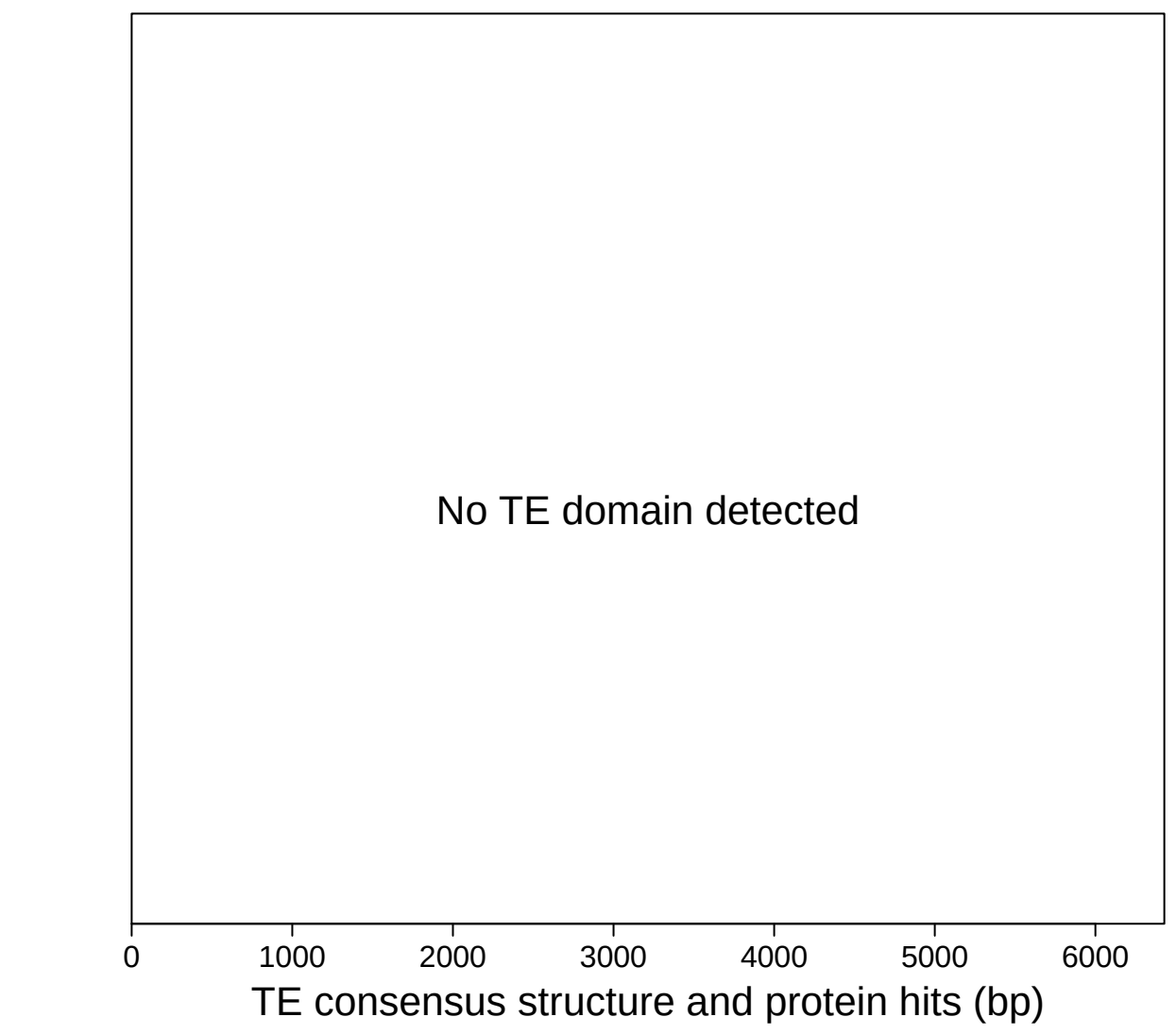
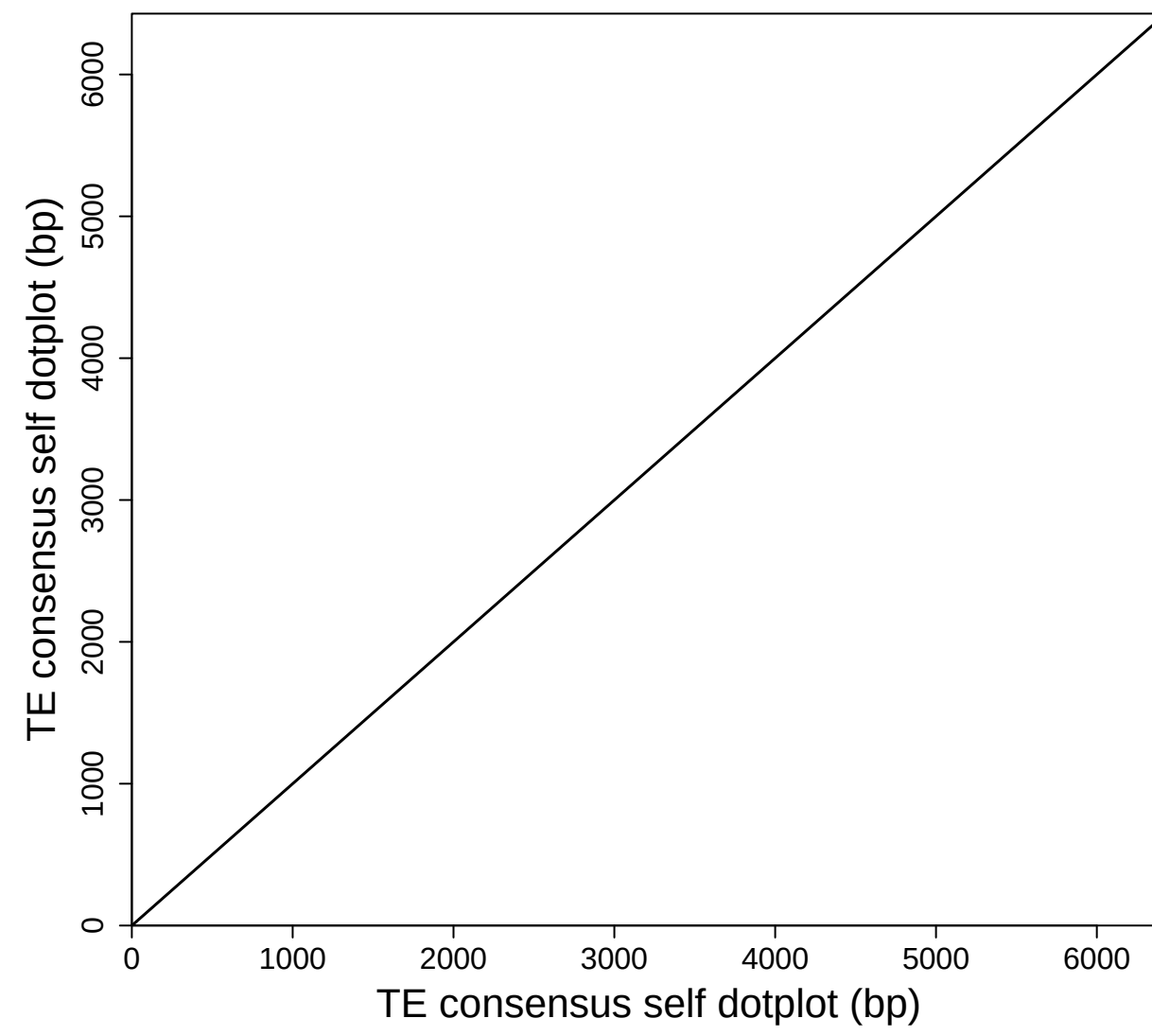
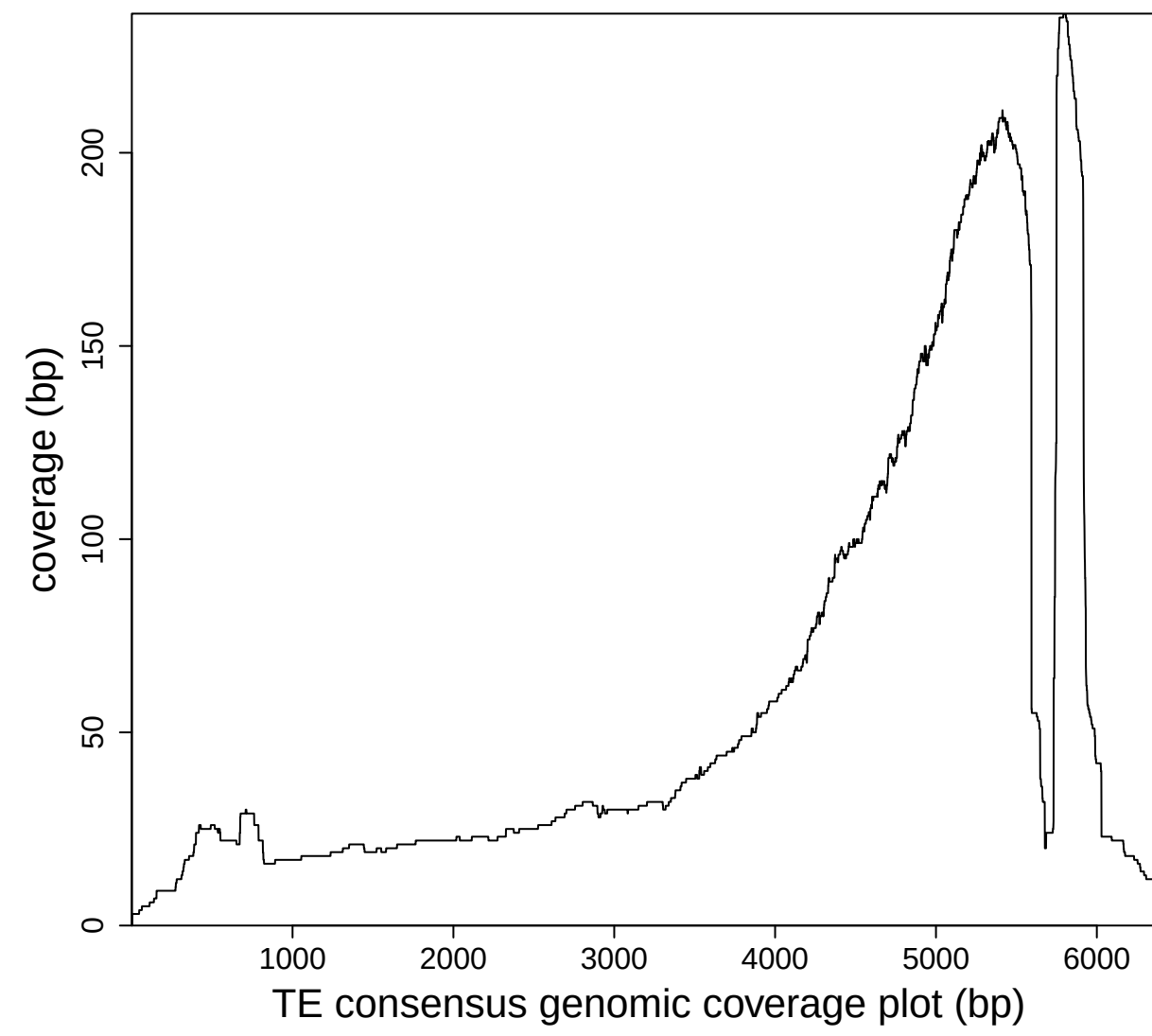
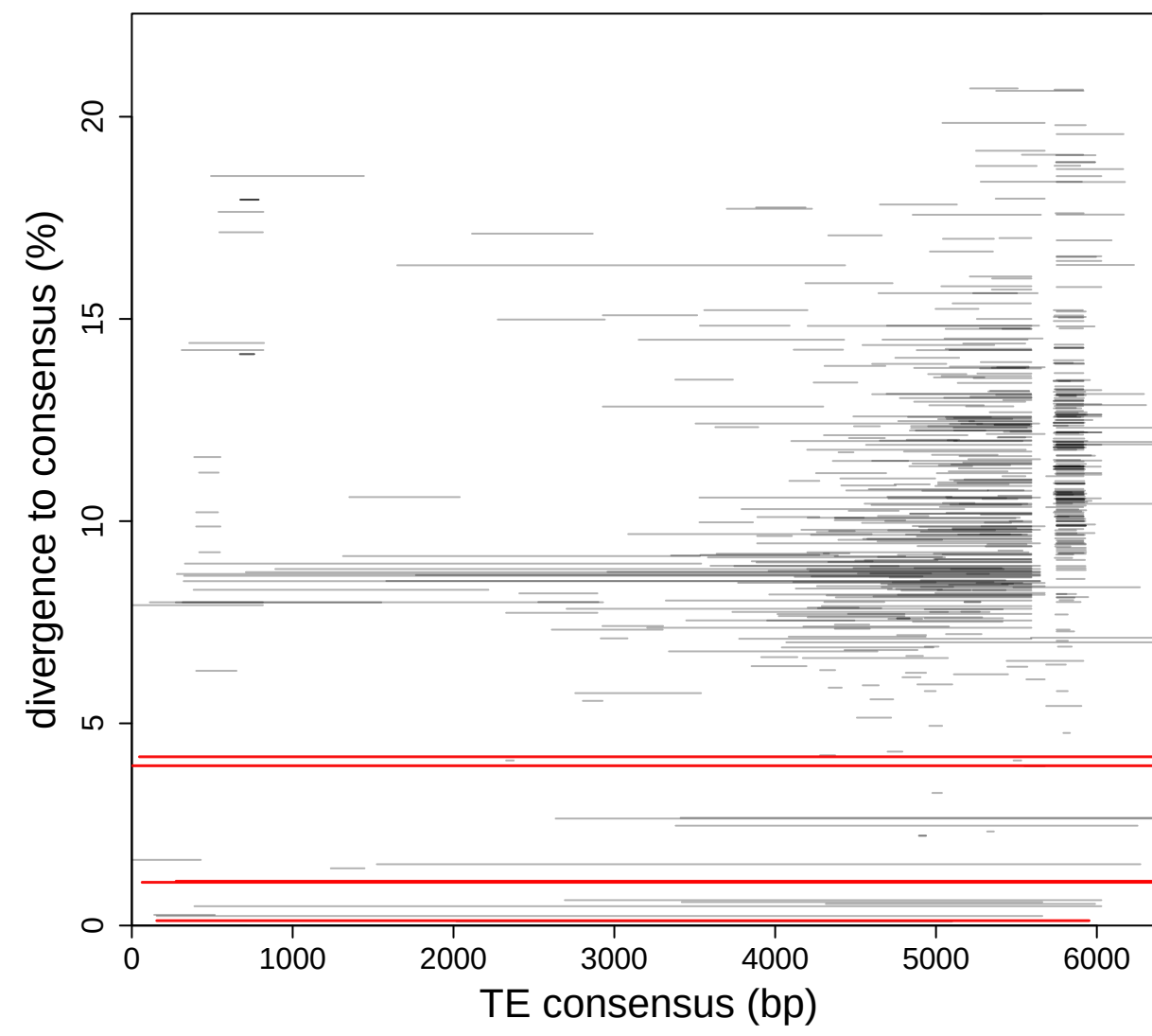
5000

6000



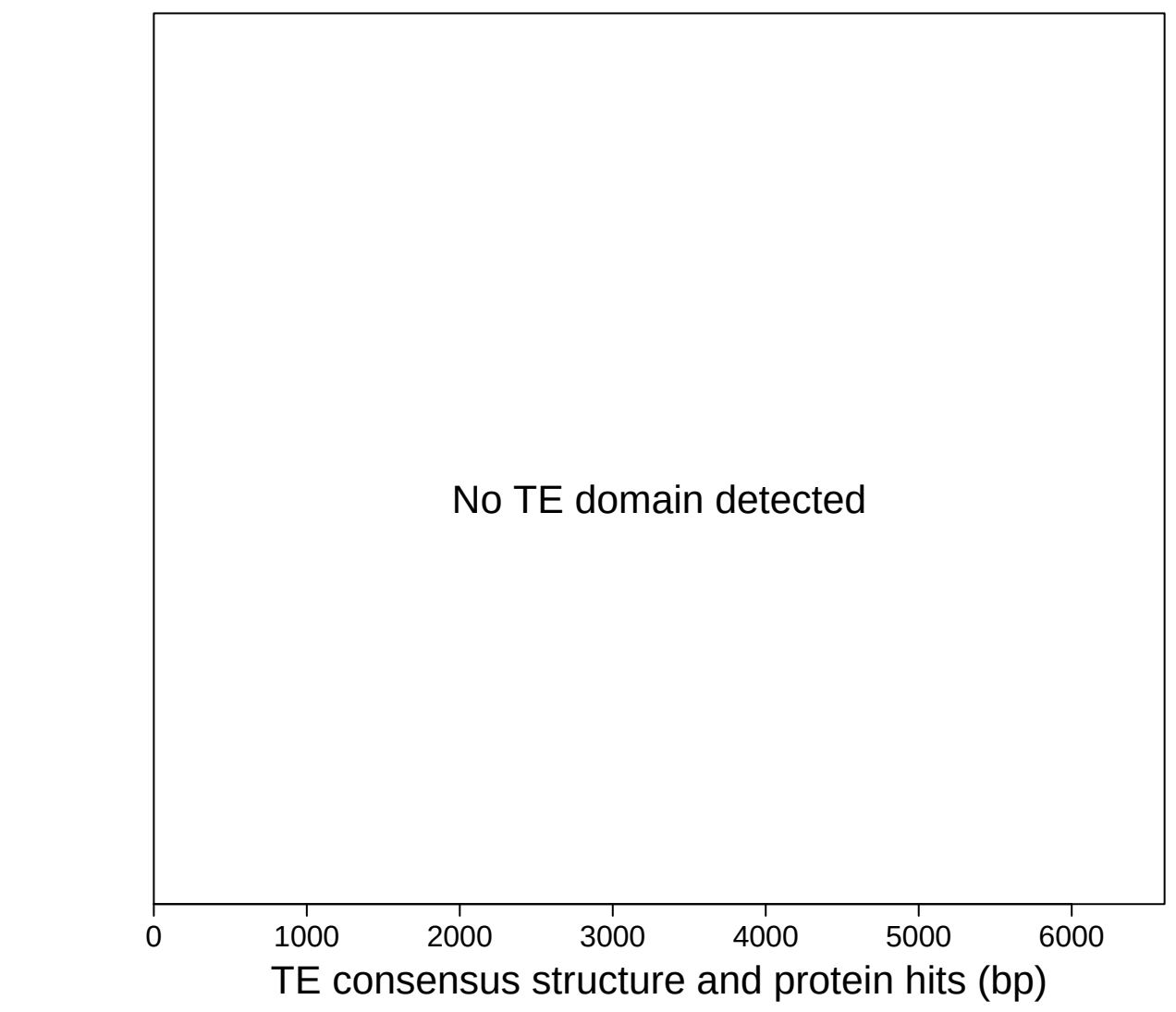
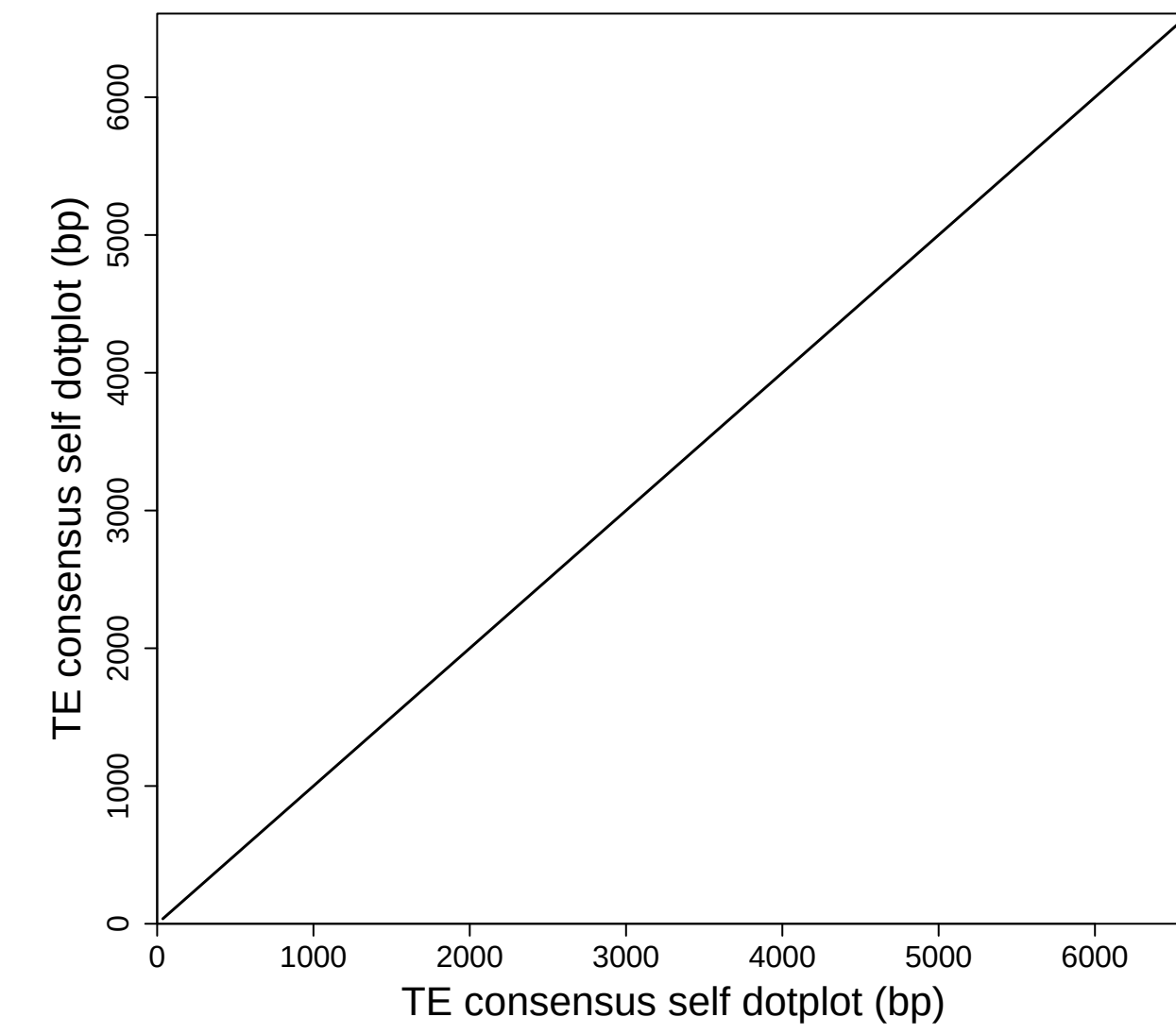
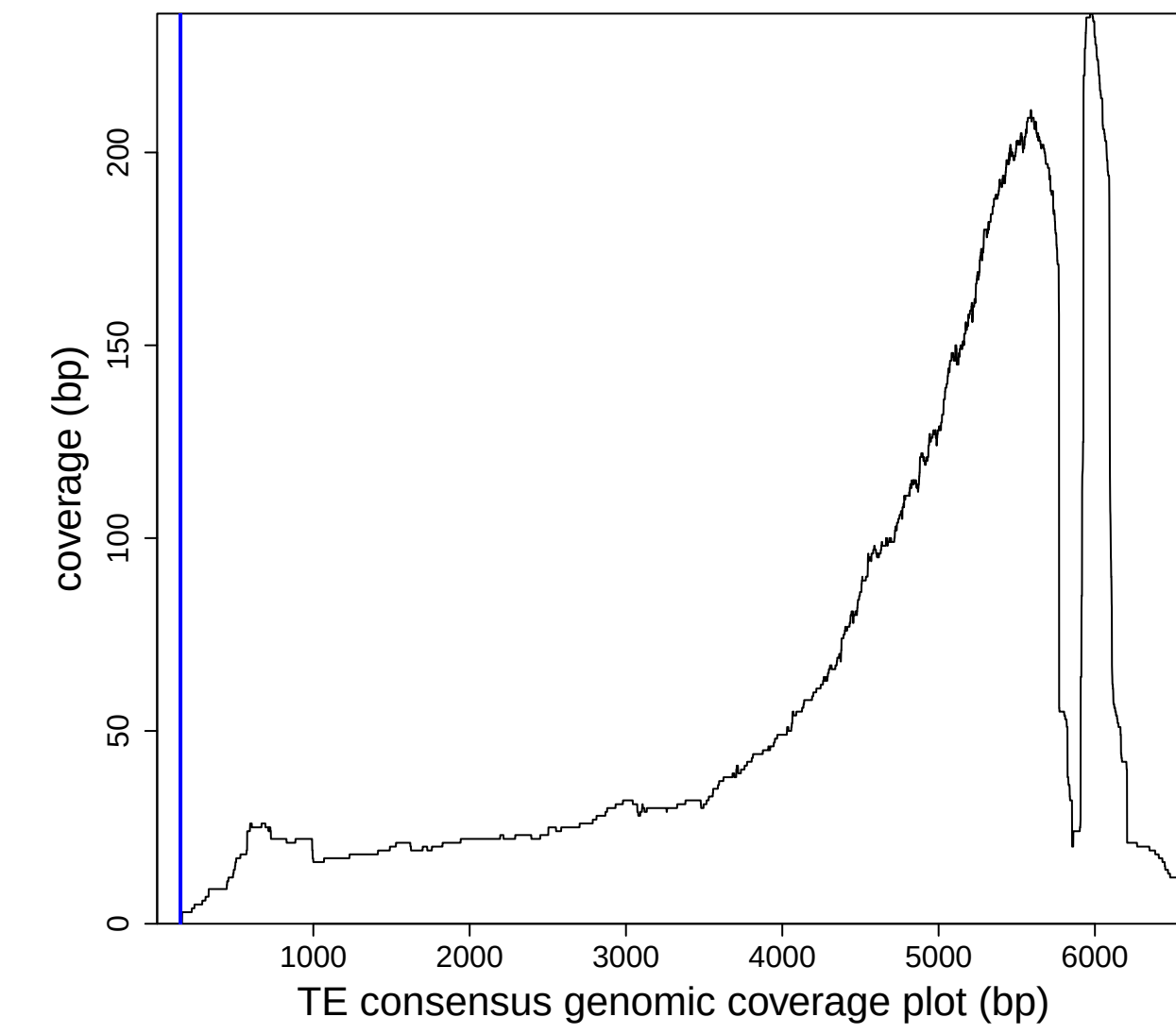
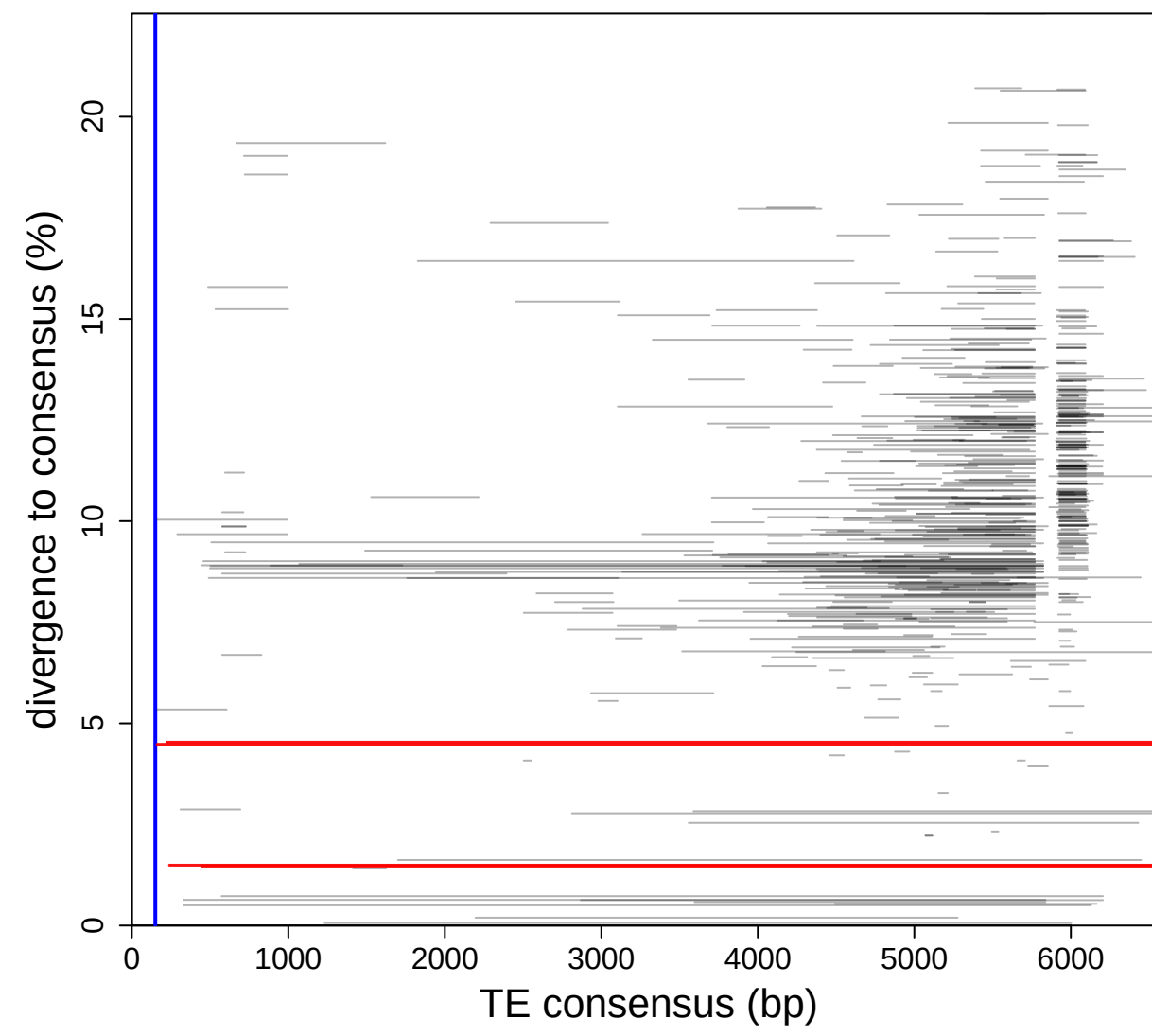
bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_c
size: 6429bp; fragments: 605; full length: 5 (≥ 5786.1 bp)

After TEtrimmer 6429 bp

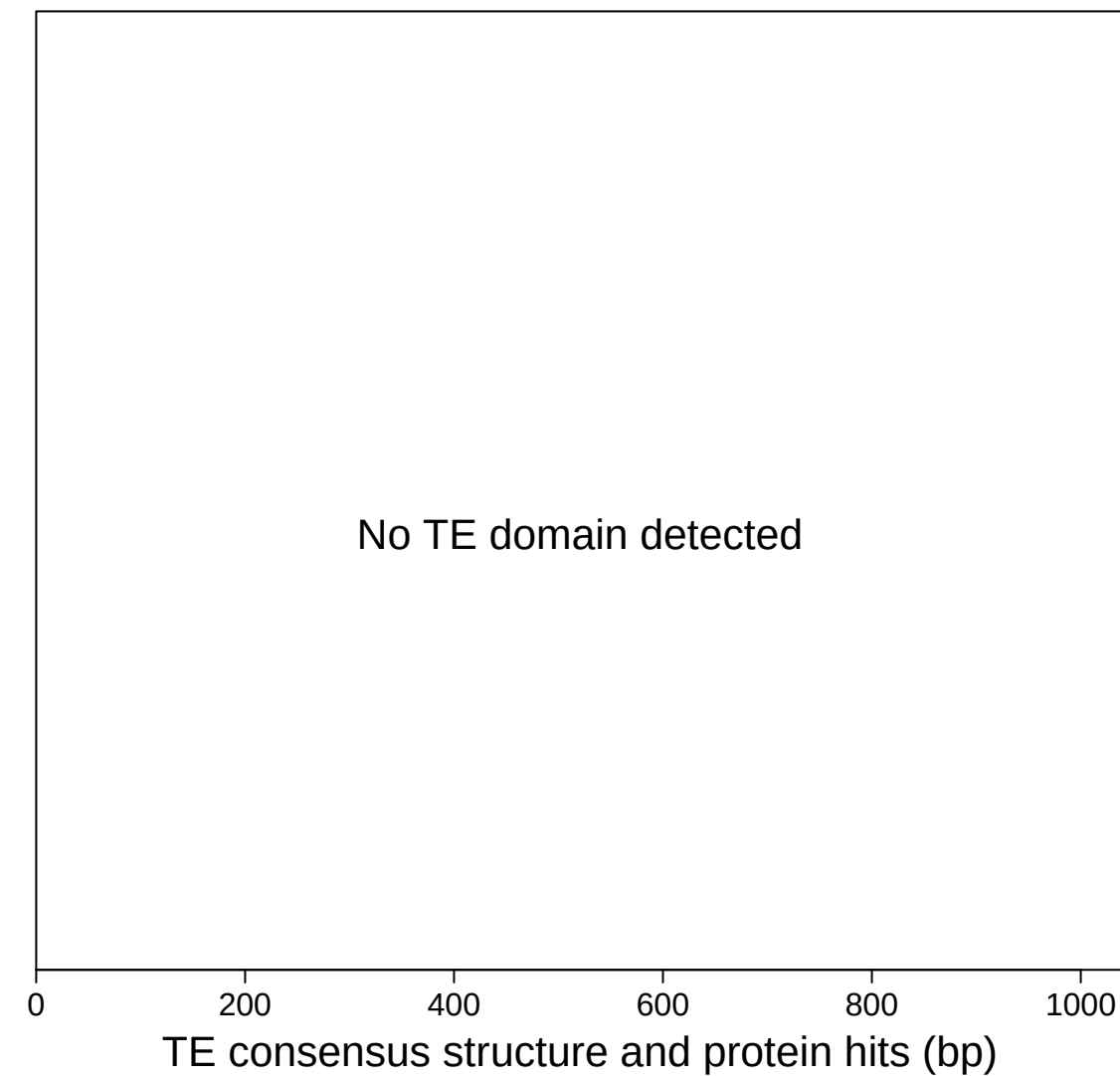
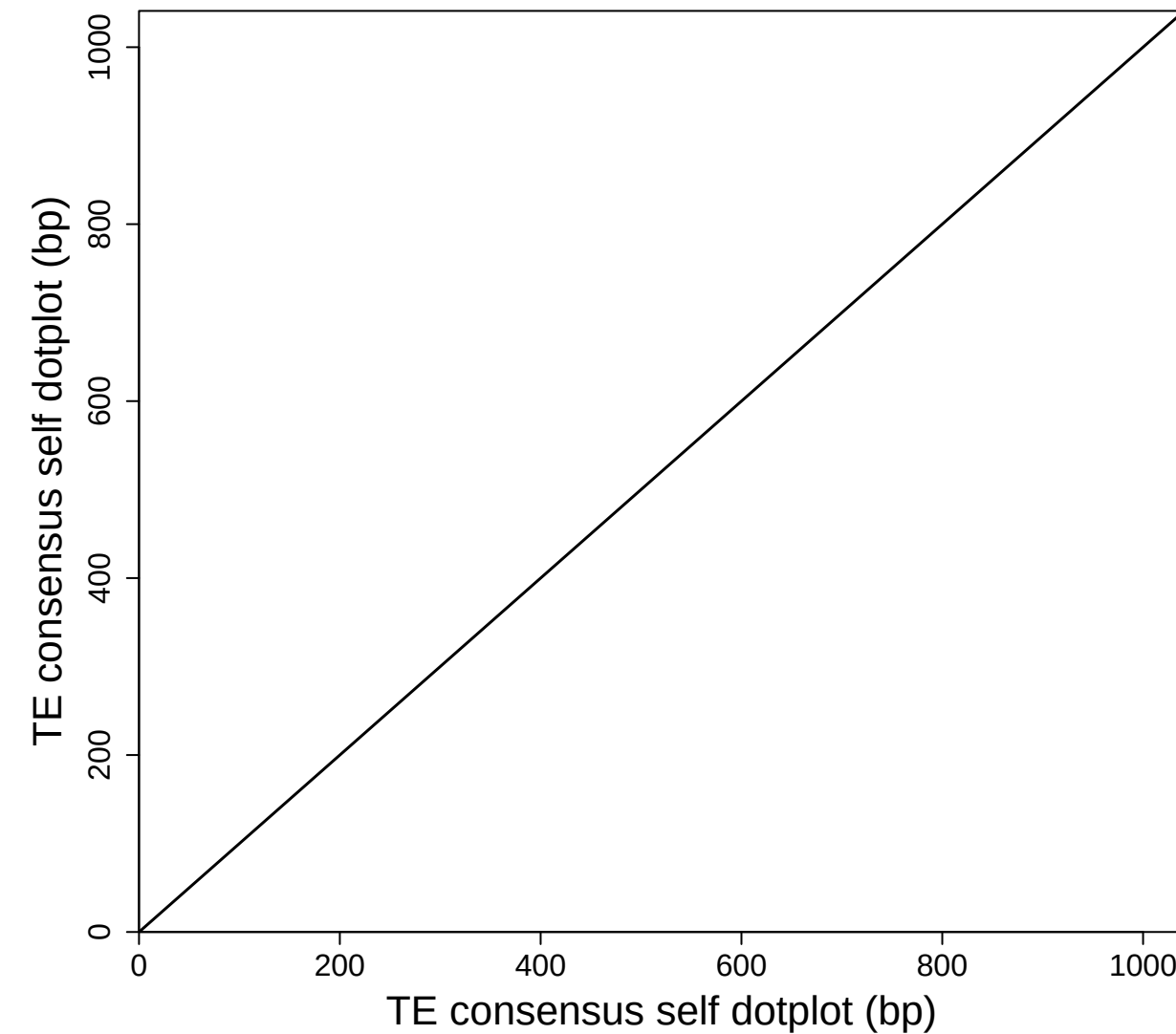
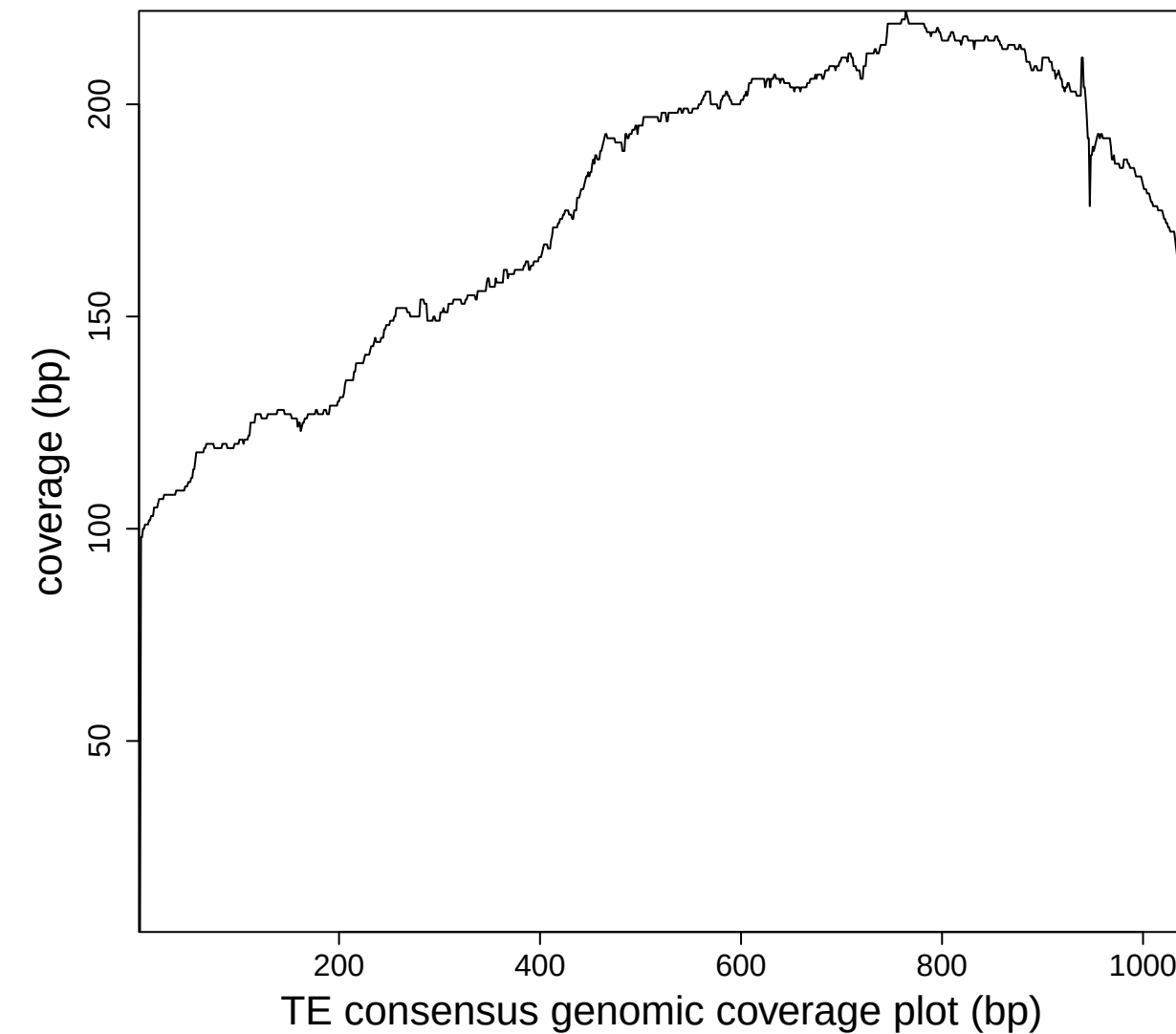
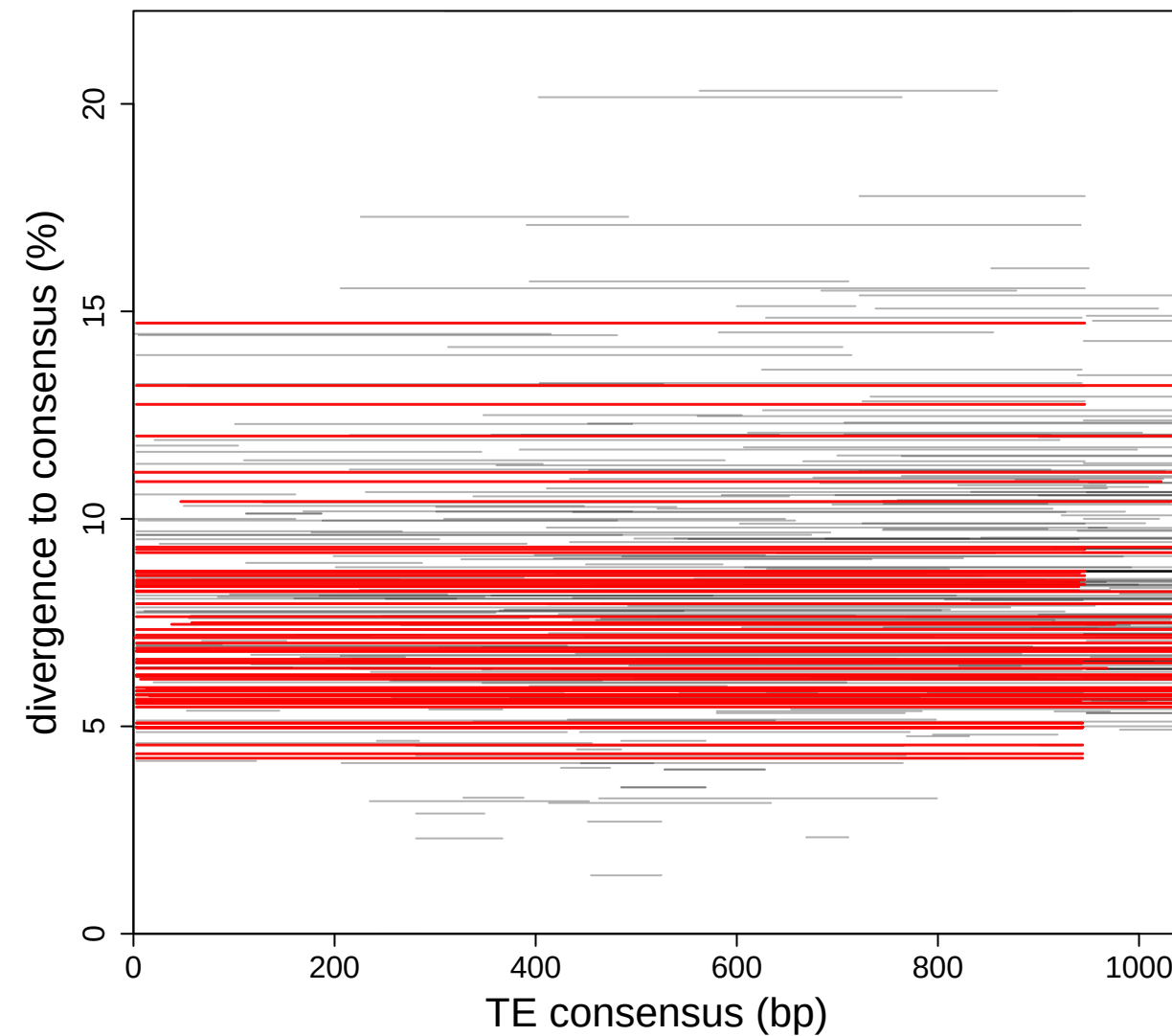


1.fasta.b.bed uf.bed g_3.bed fm_1.bed 0 0 bcIn.fa aln.fa cl.f
size: 6607bp; fragments: 597; full length: 4 (>=5946.3bp)

After TEtrimmer Extended plot Blue lines are boundaries

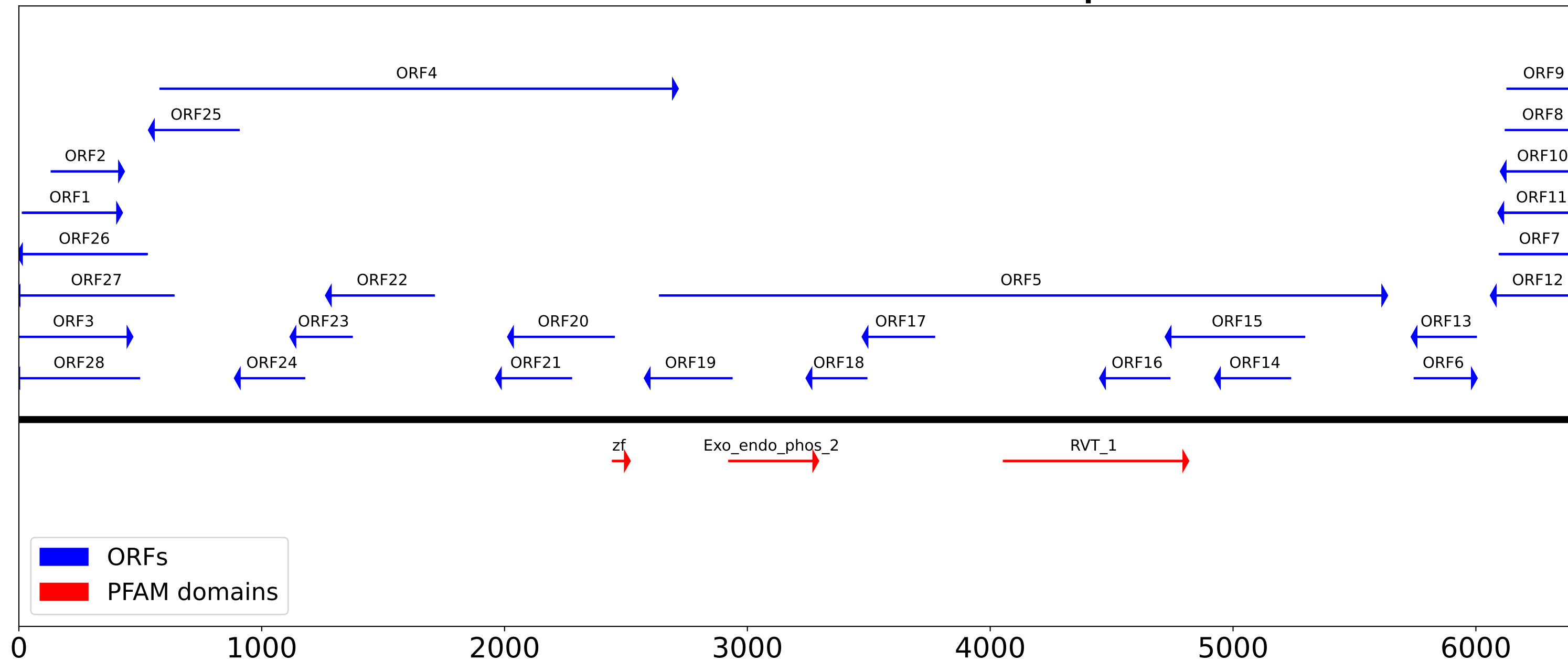


TE: rnd_5_family_7251
size: 1041bp; fragments: 388; full length: 72 (≥ 936.9 bp)

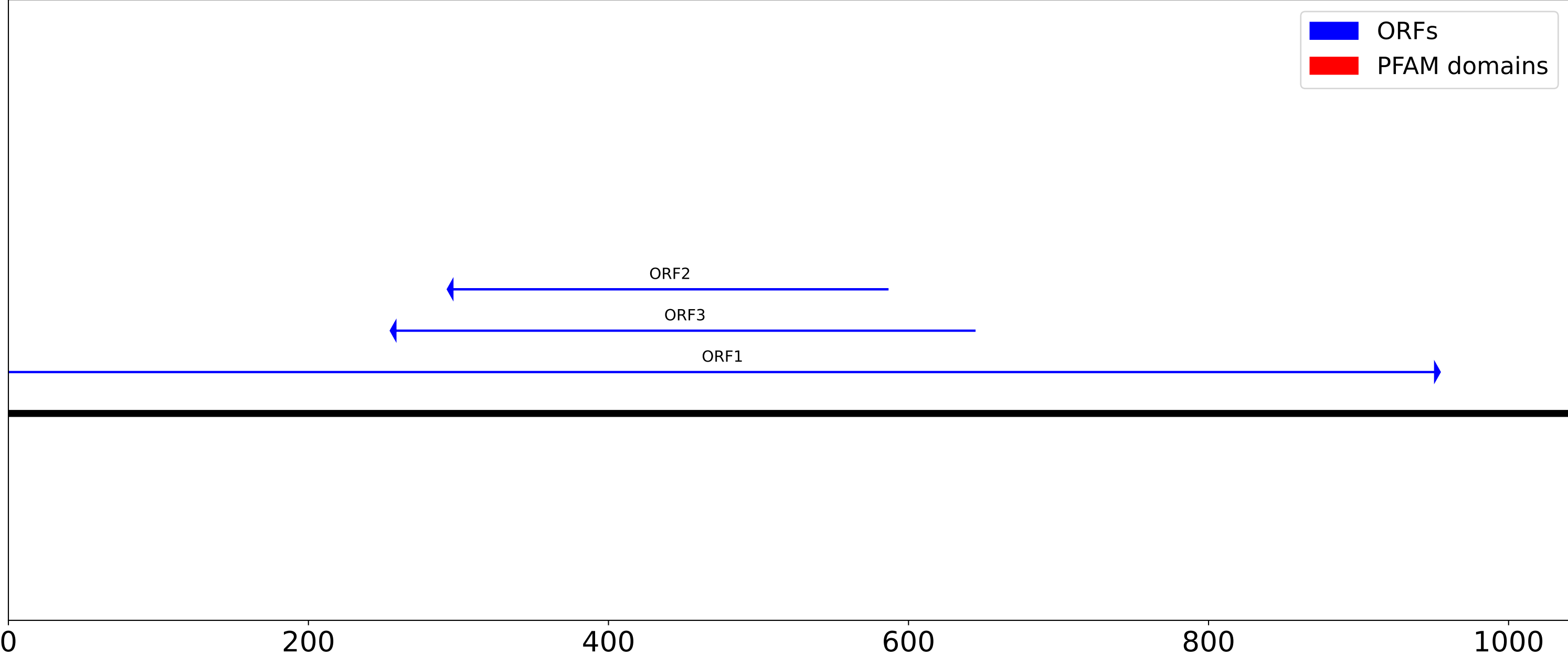


Before TEtrimmer 1041 bp

After TEtrimmer ORF and PFAM domain plot



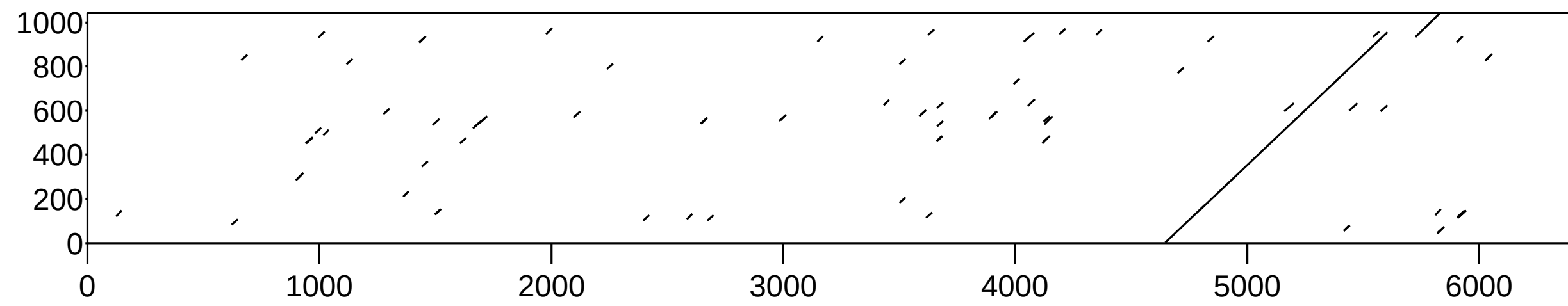
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

rsensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)