

Start crop Point



End crop Point



MSA length = 1591



Start crop Point

End crop Point

0 -

10 -

0

250

500

750

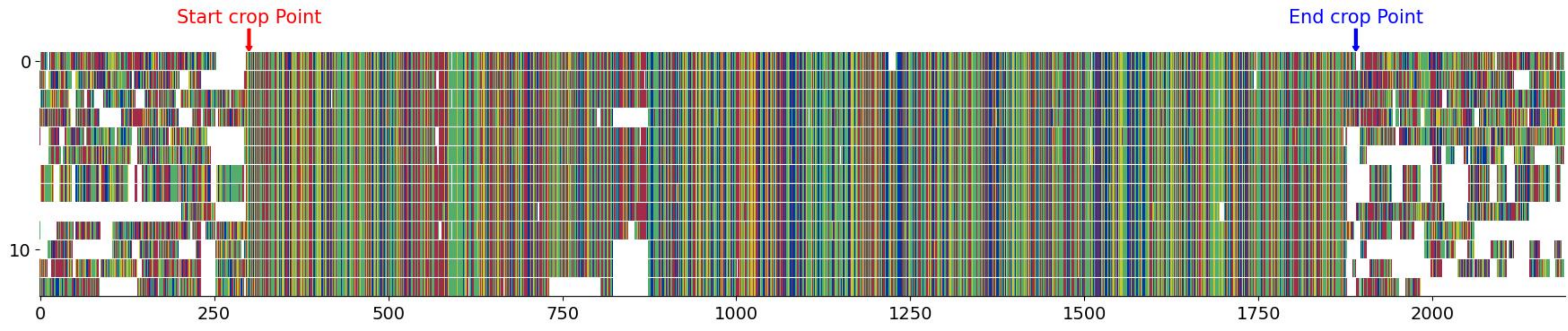
1000

1250

1500

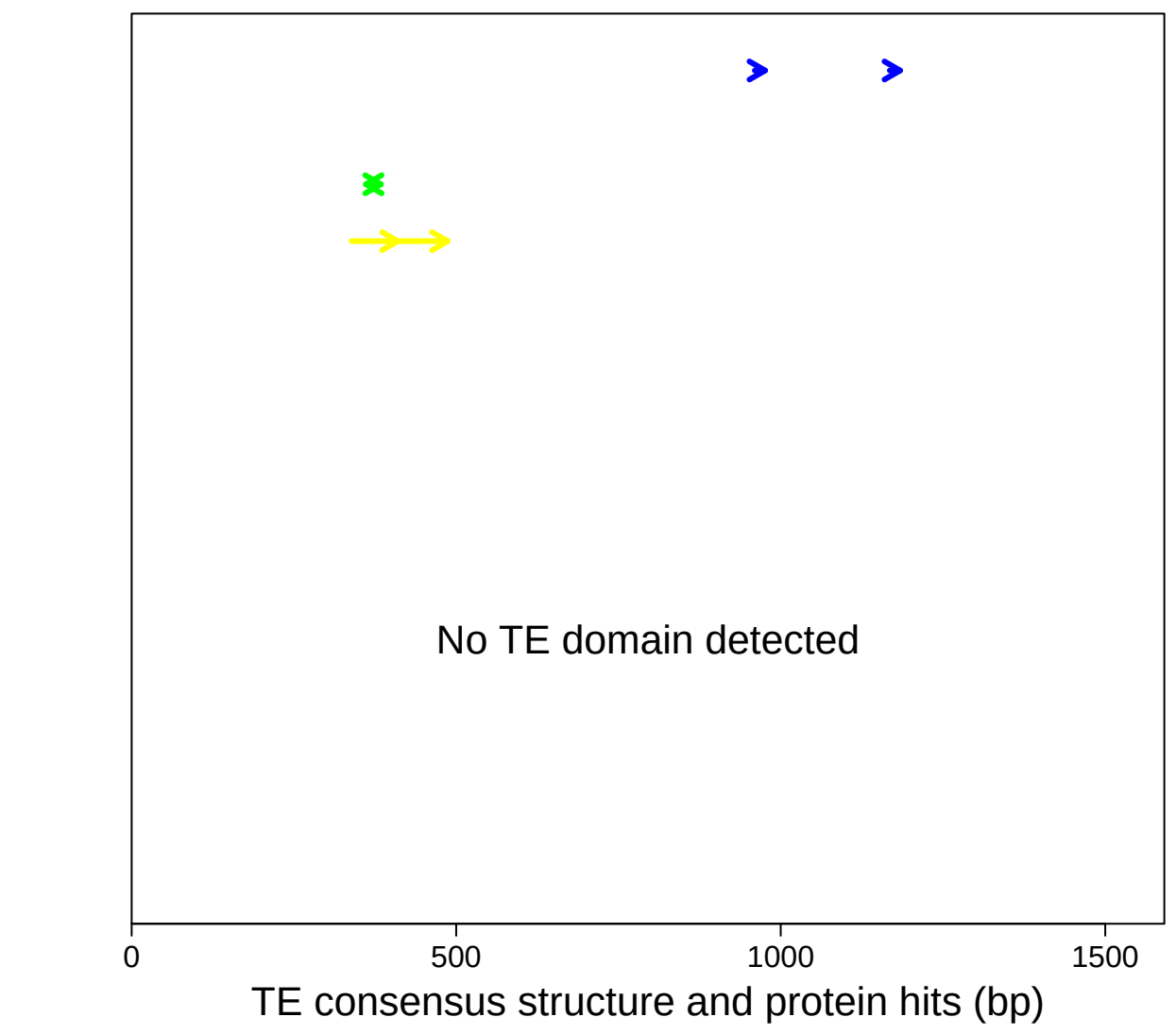
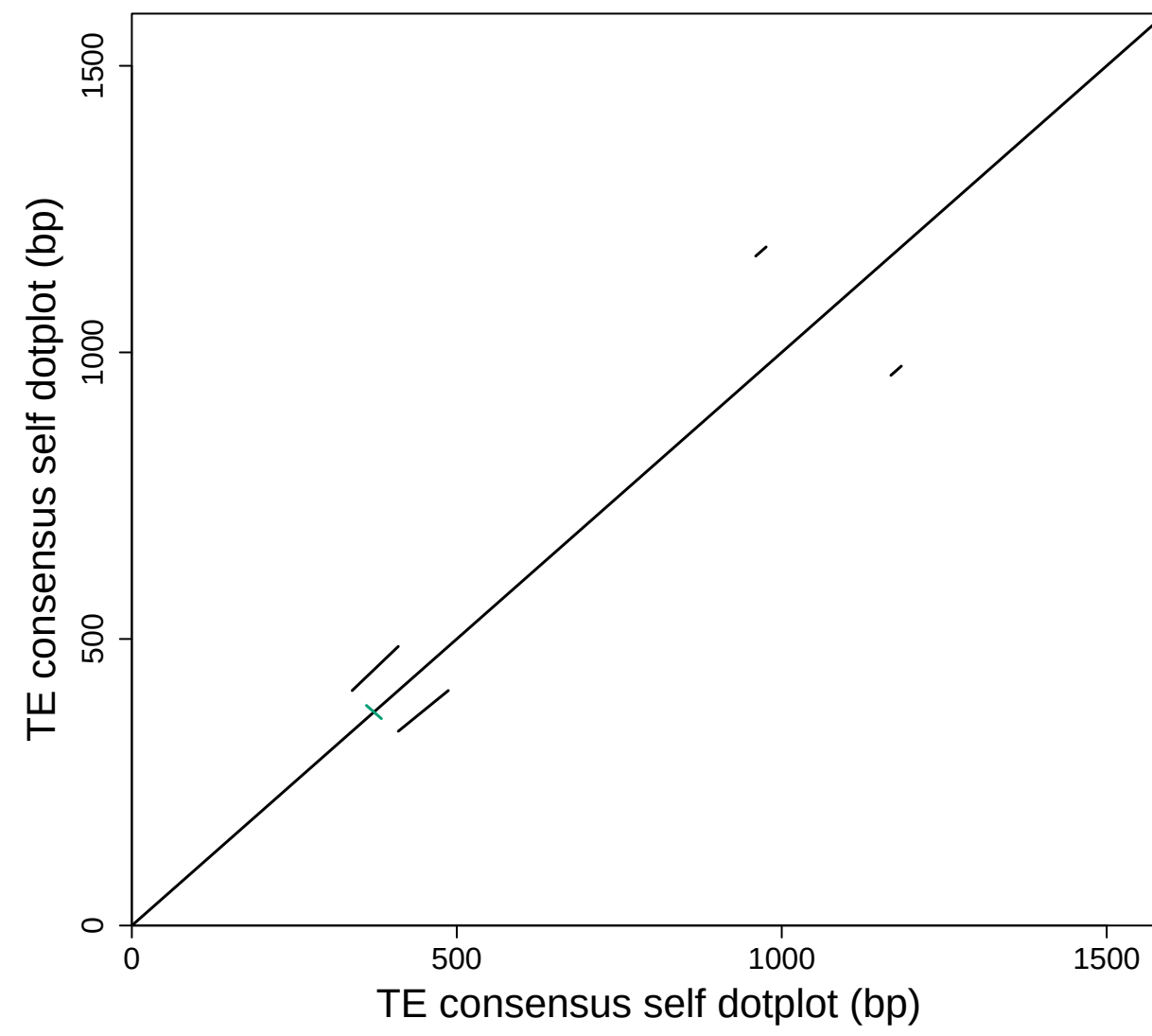
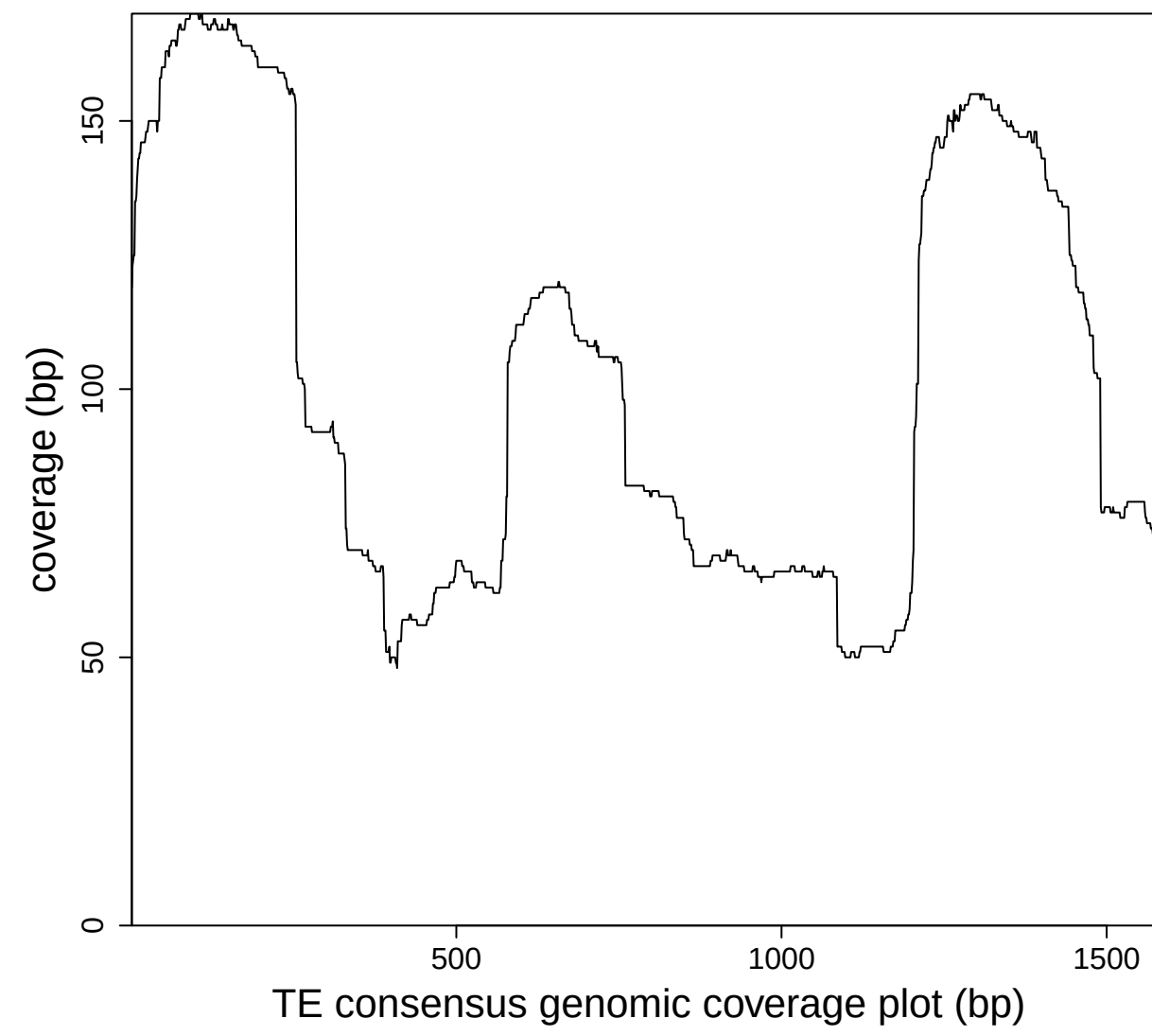
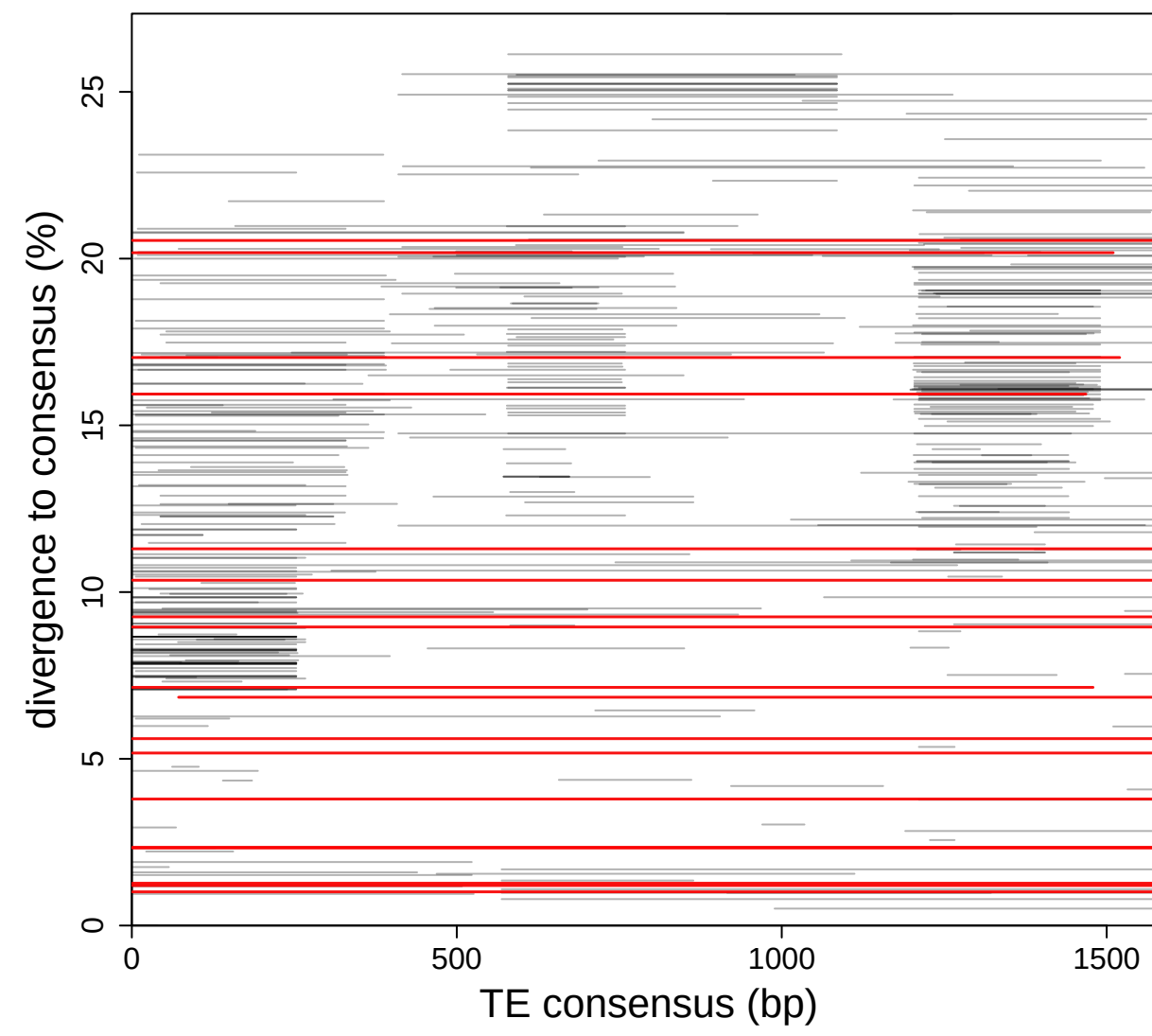
1750

2000



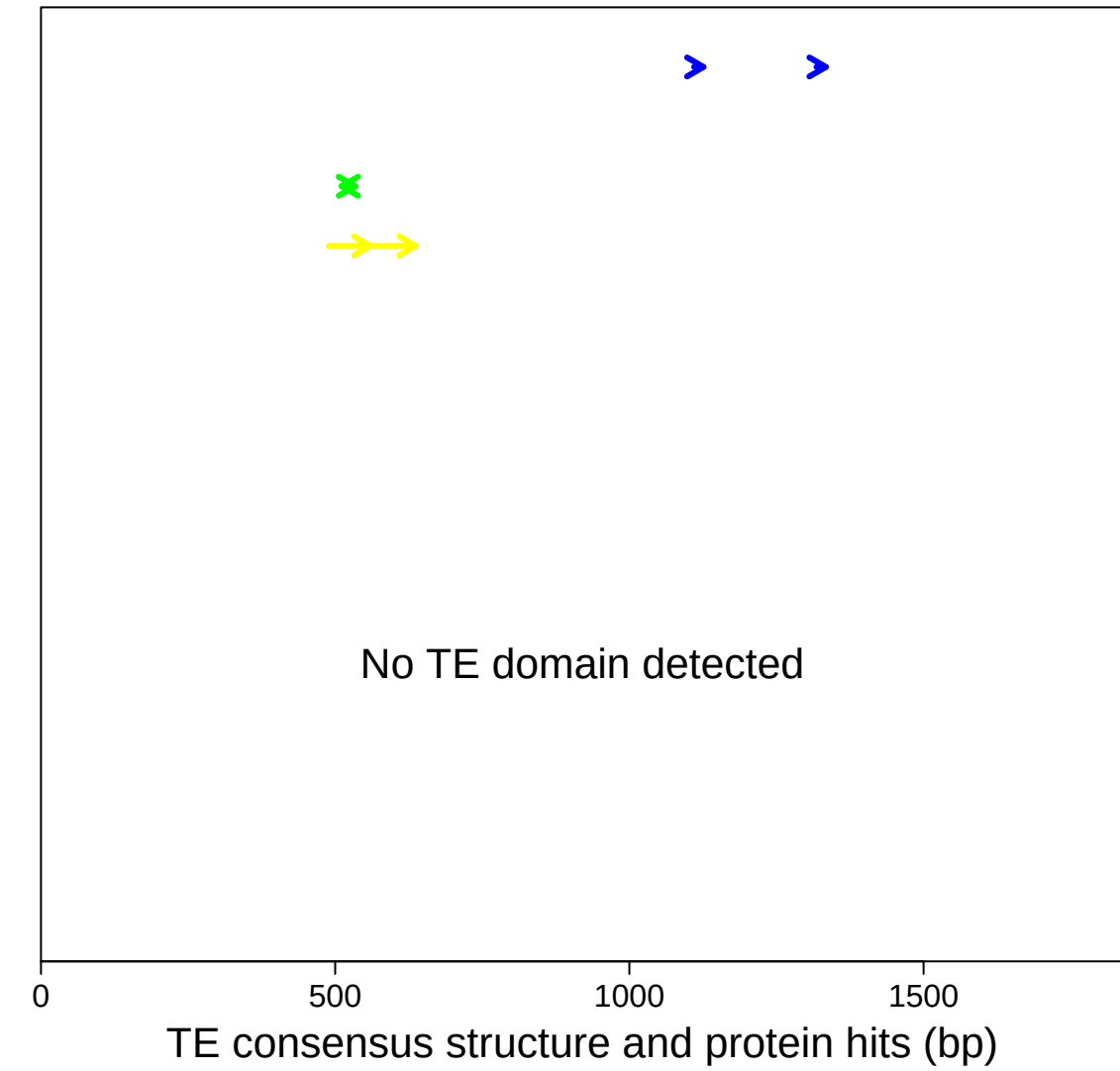
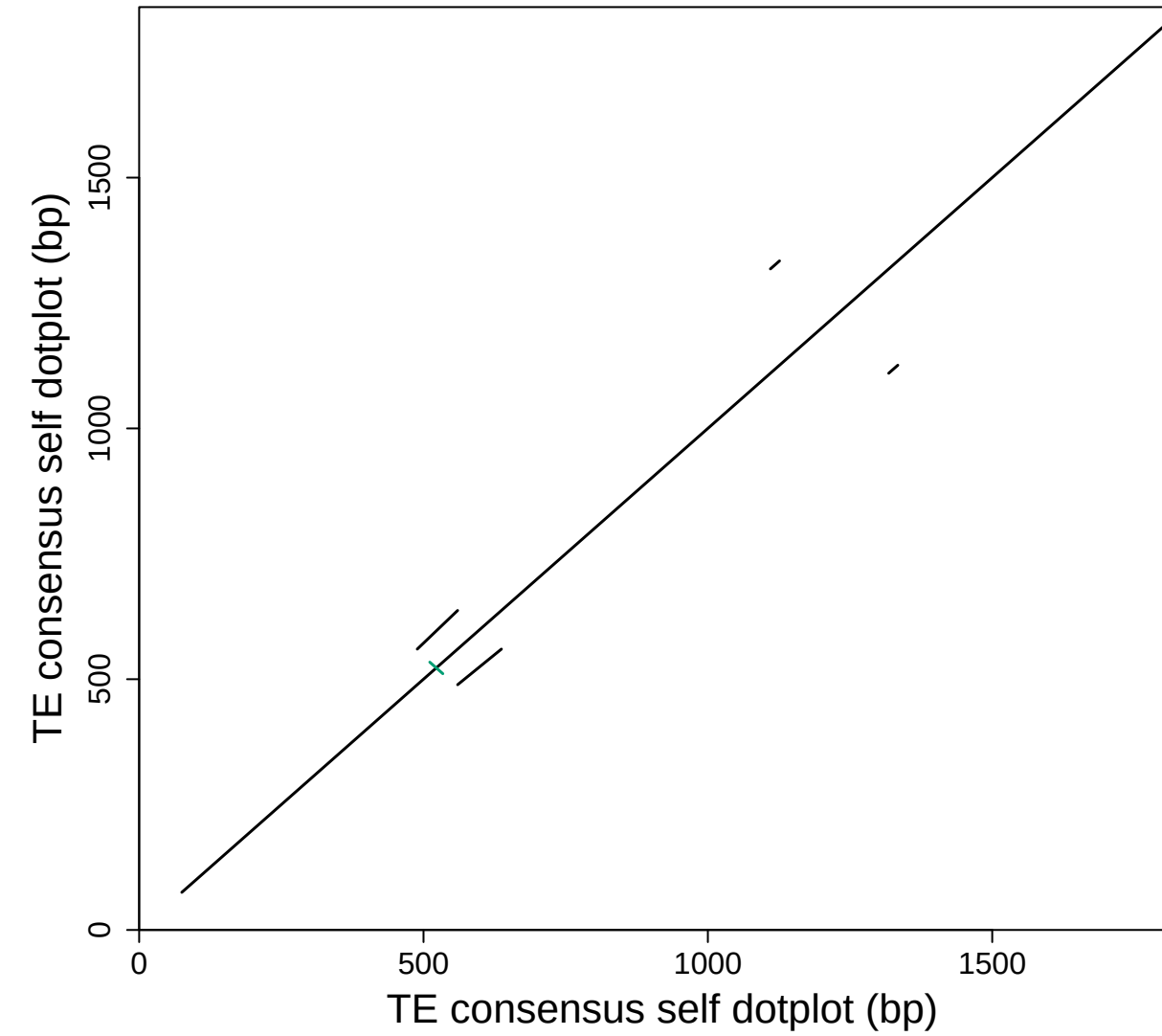
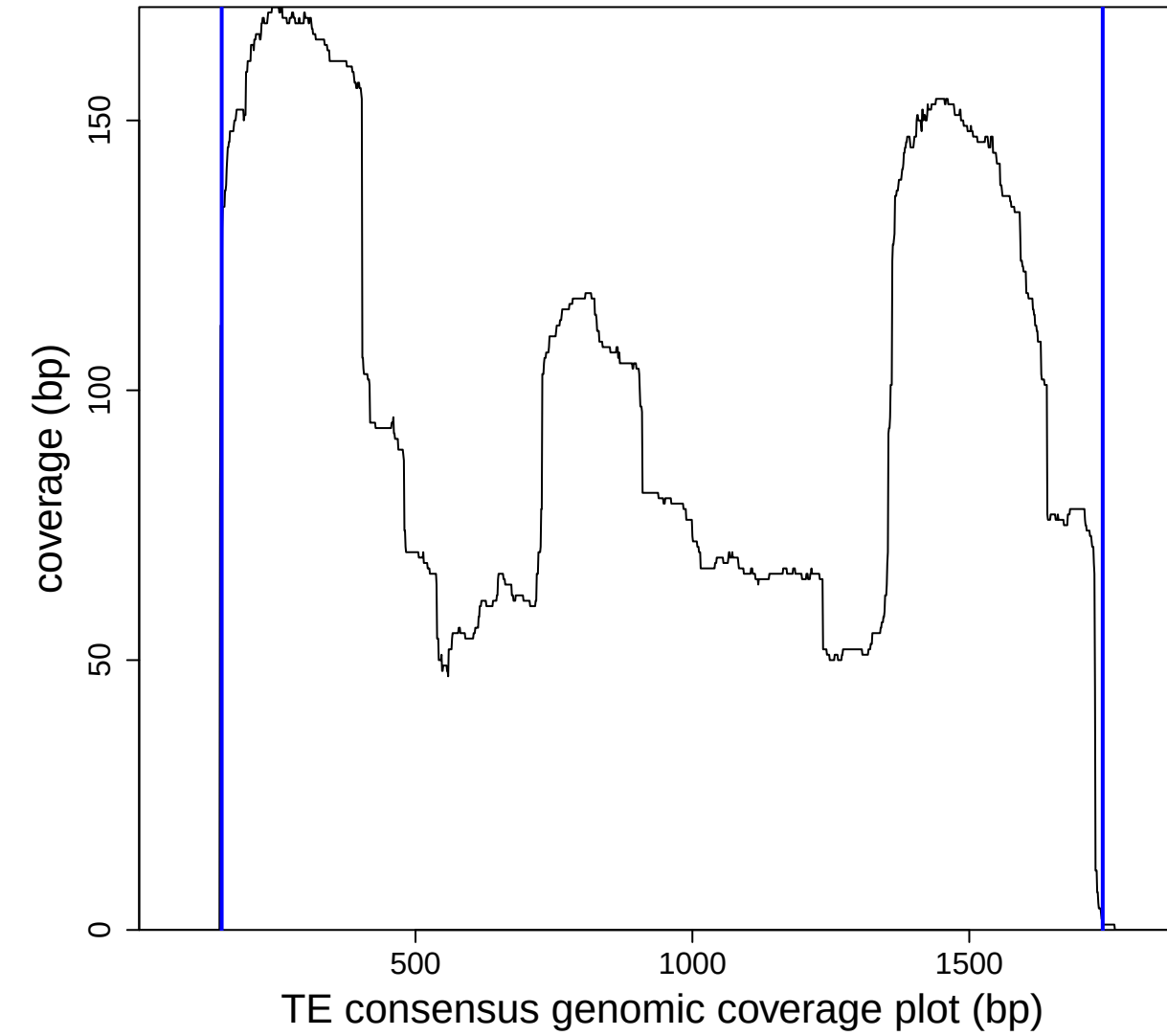
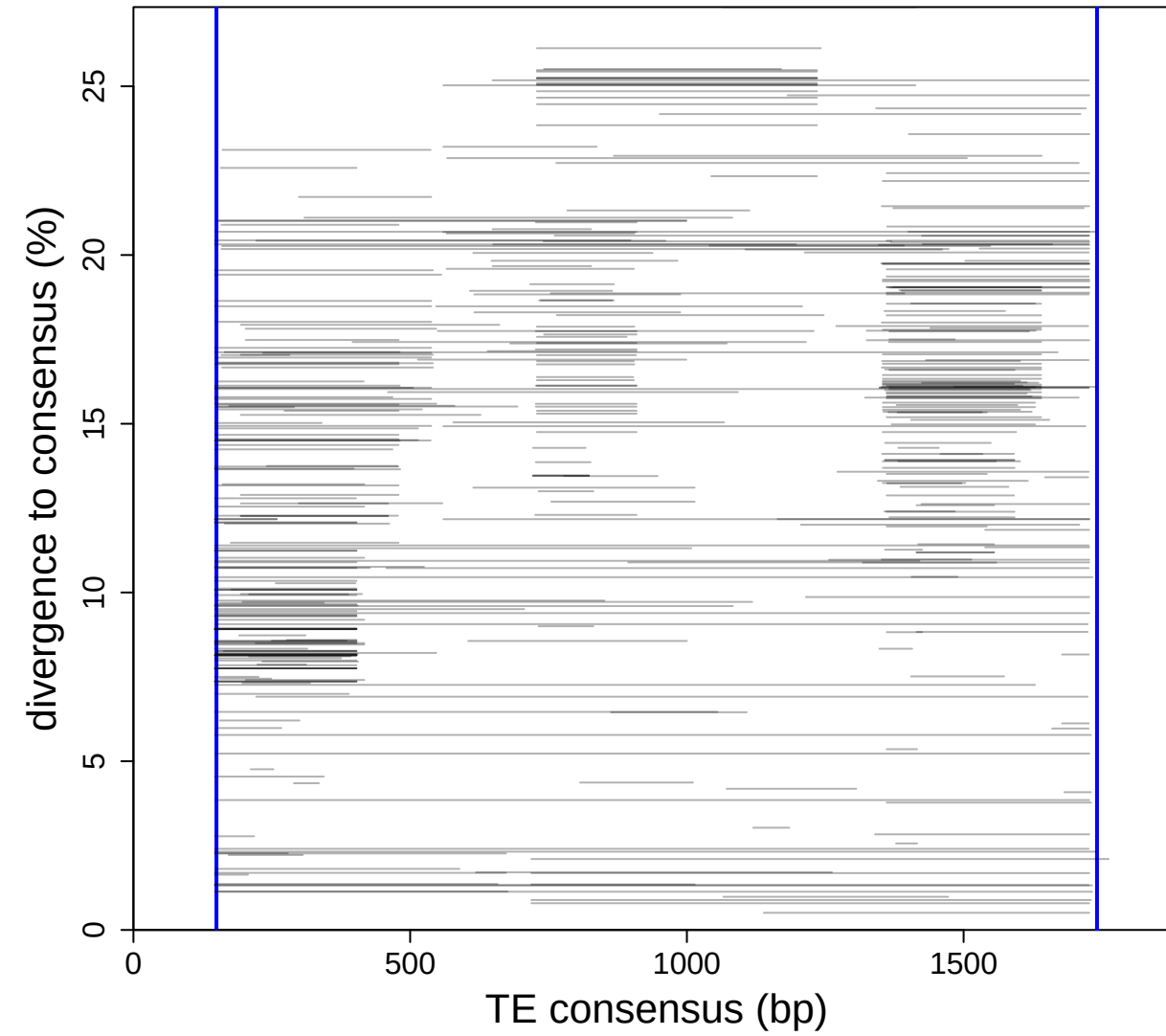
l.b.bed uf.bed g_2.bed fm_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 1591bp; fragments: 417; full length: 18 (≥ 1431.9 bp)

After TEtrimmer 1591 bp

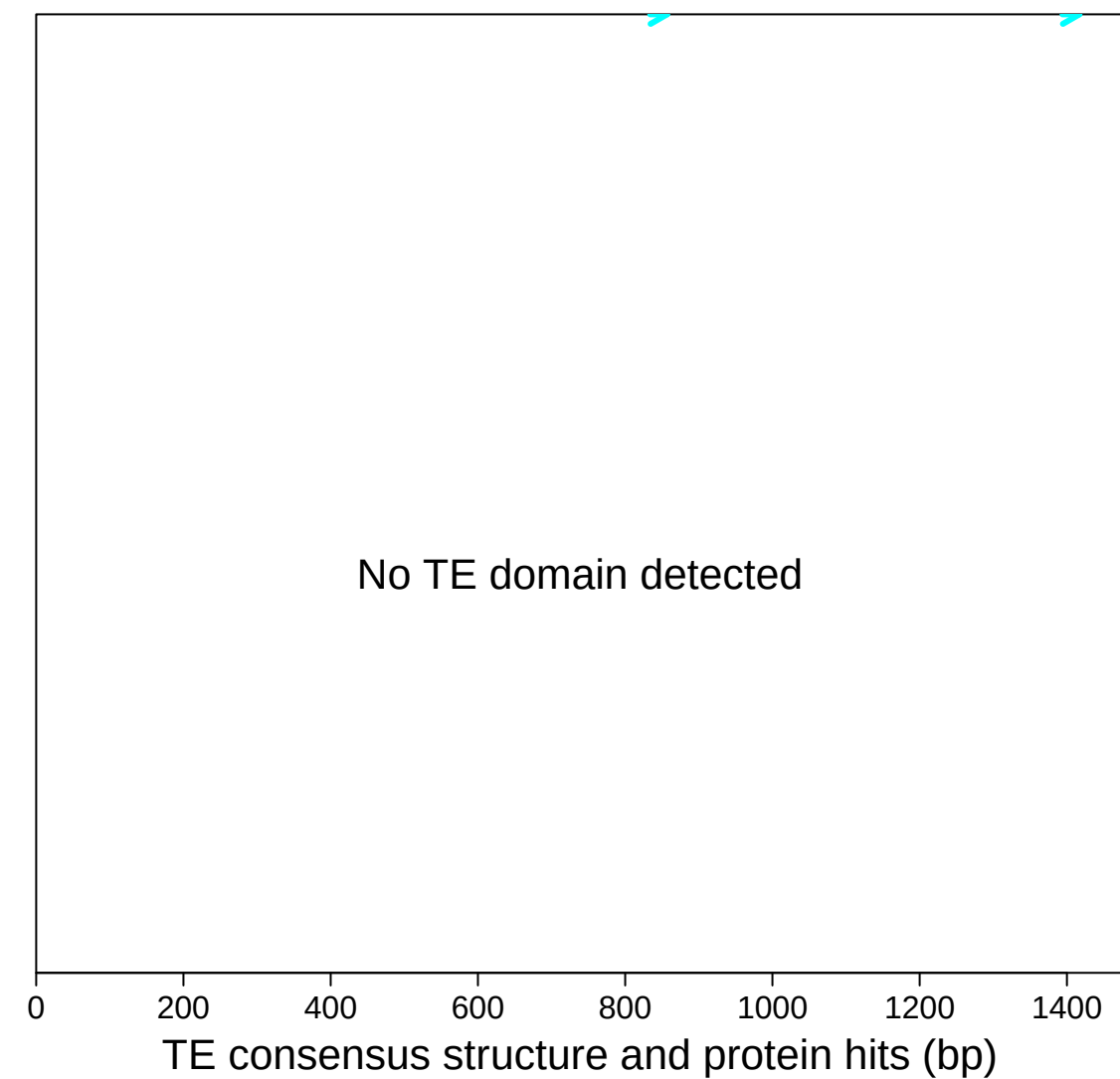
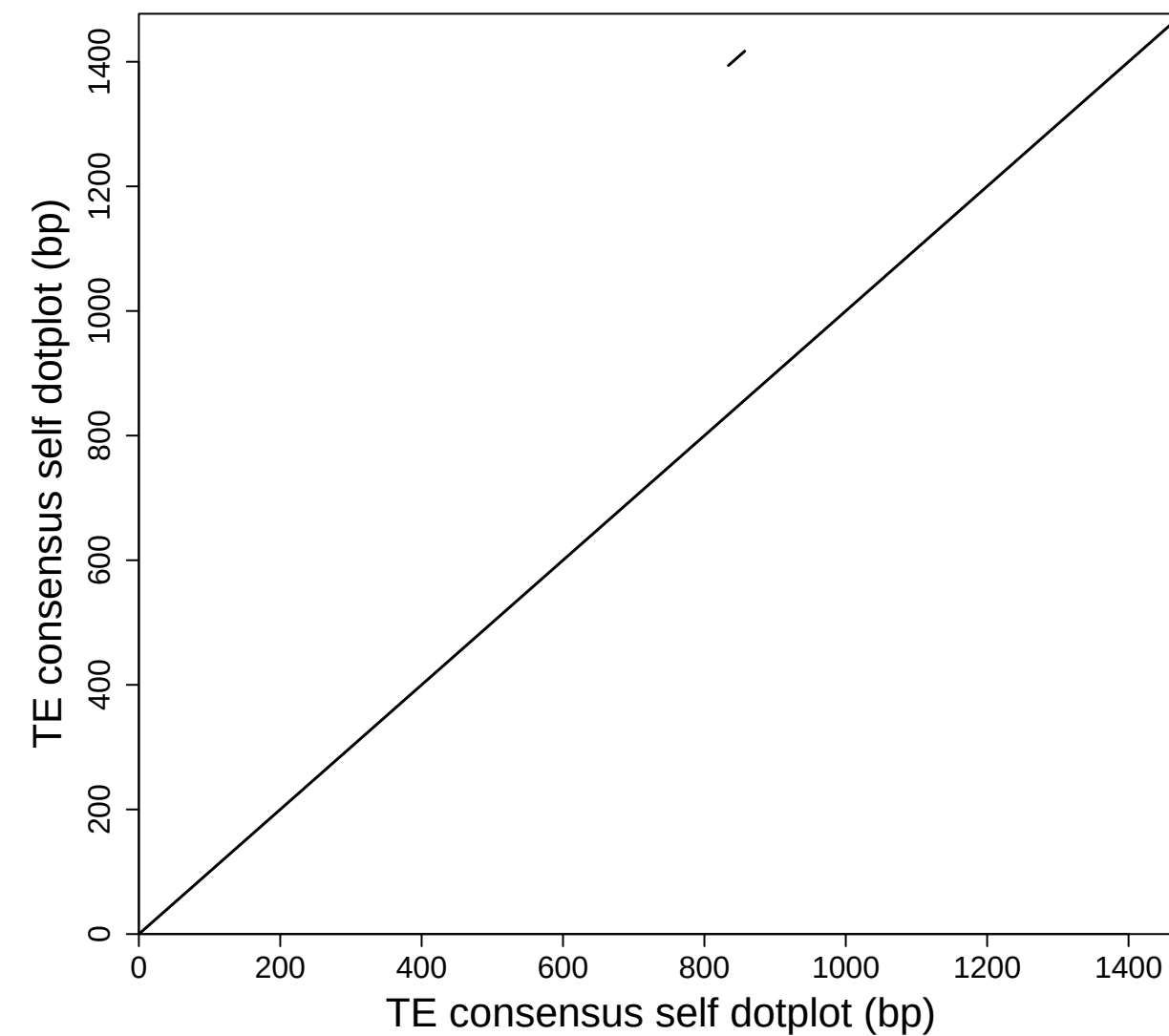
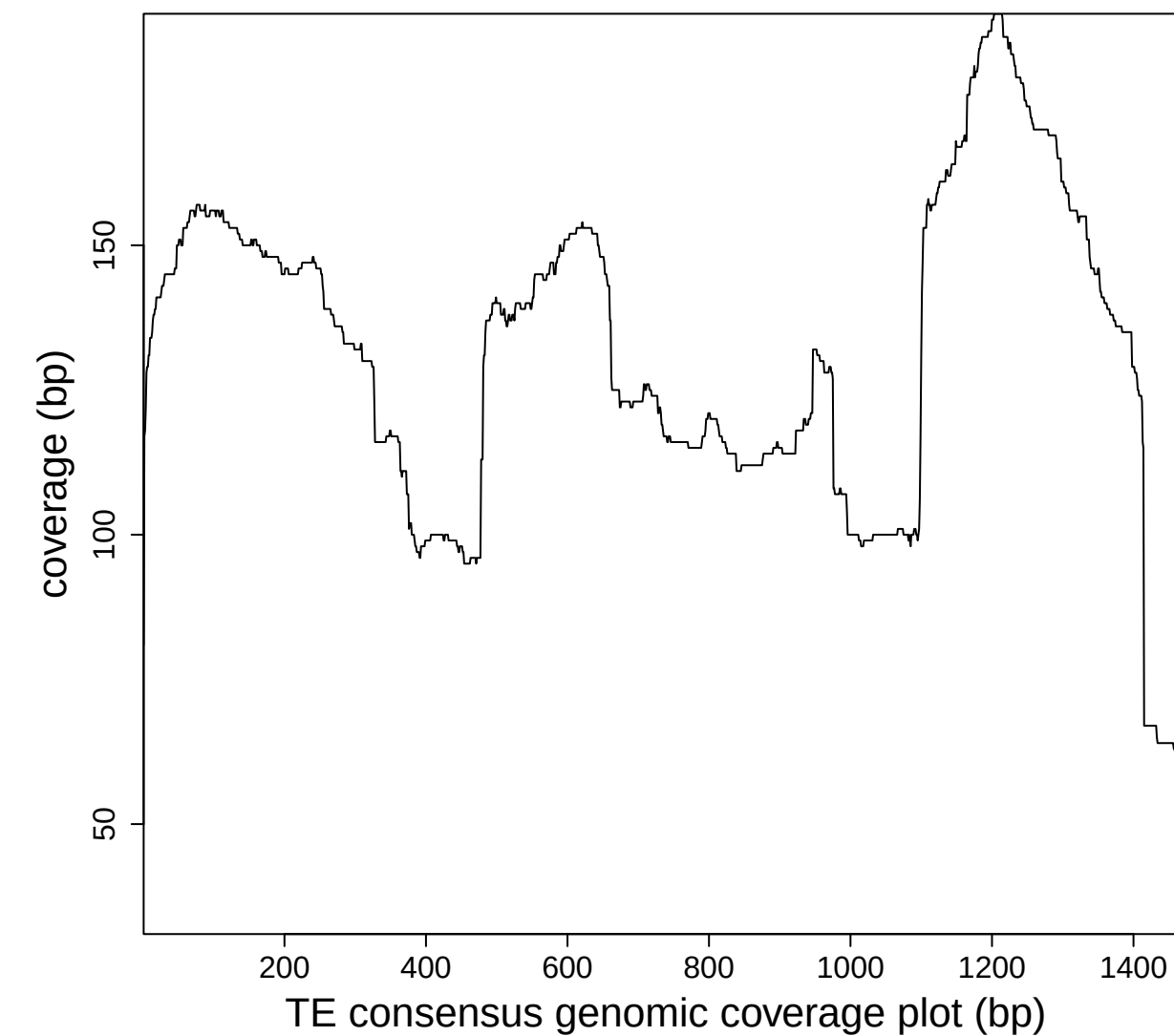
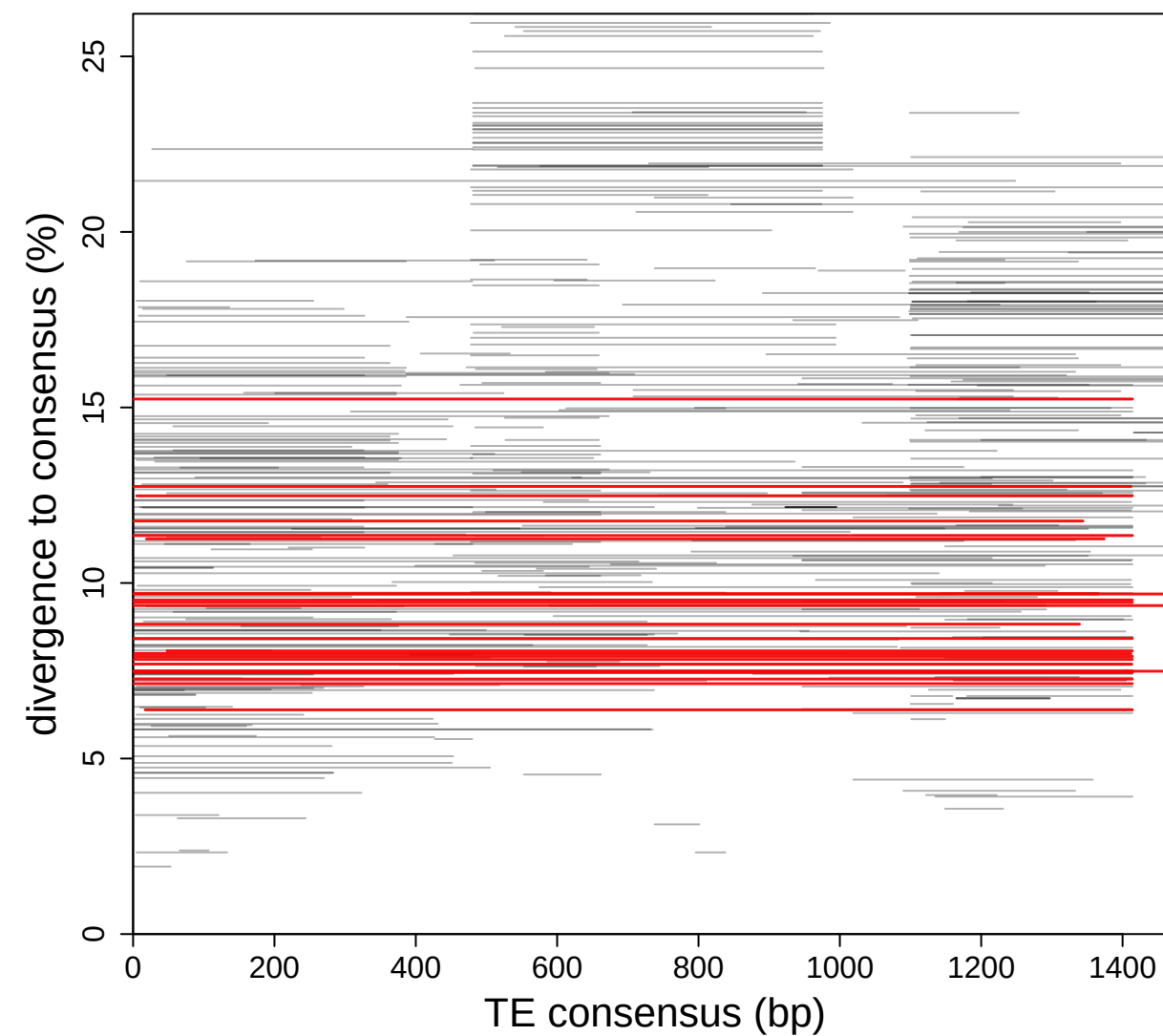


6.fasta.b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa
size: 1891bp; fragments: 416; full length: 0 (>=1701.9bp)

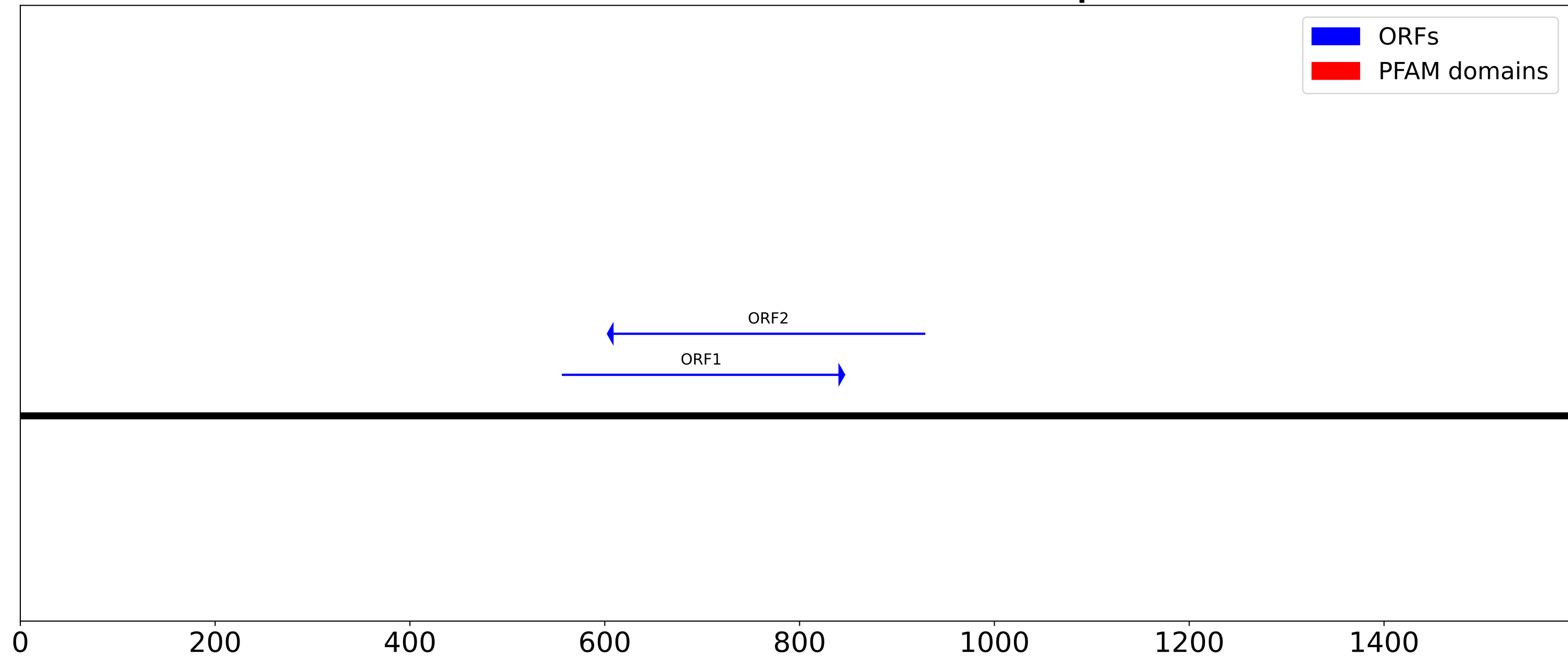
After TEtrimmer Extended plot Blue lines are boundaries



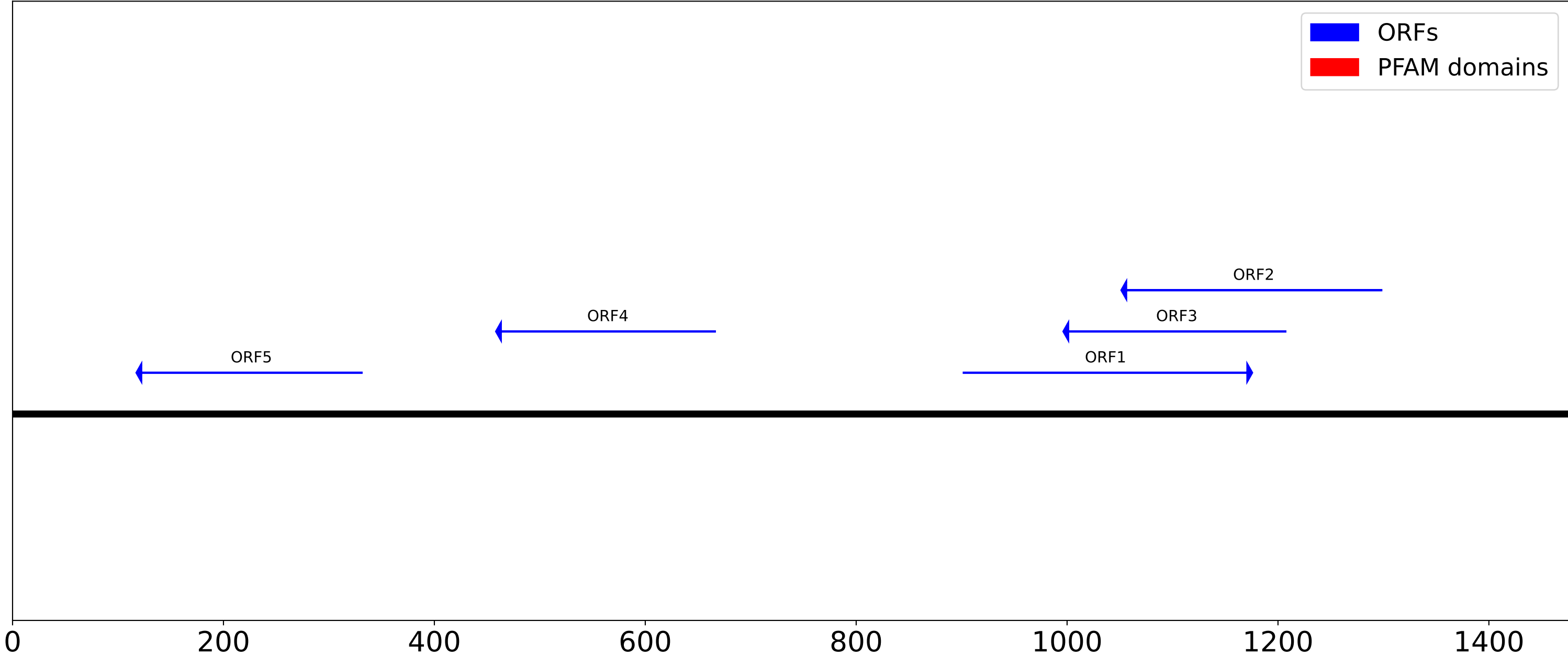
TE: rnd_5_family_106
size: 1477bp; fragments: 433; full length: 24 (≥ 1329.3 bp)



After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

