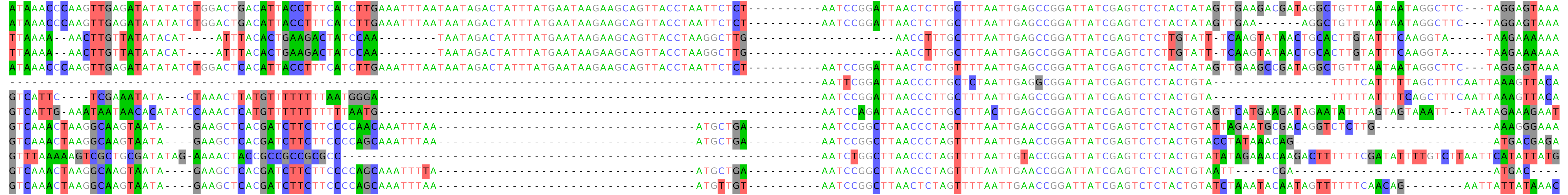


Start crop Point

End crop Point

MSA length = 1228



Start crop Point

End crop Point

0 -

10 -

0

250

500

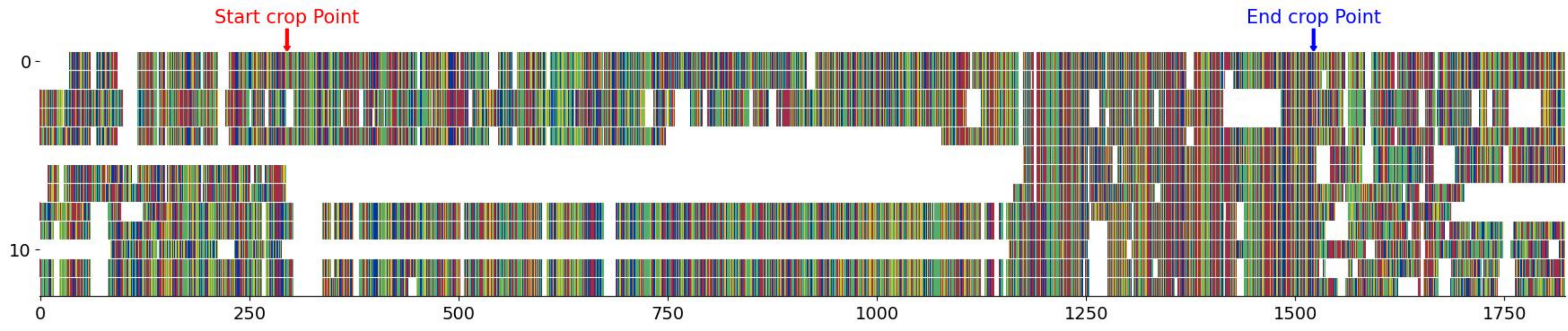
750

1000

1250

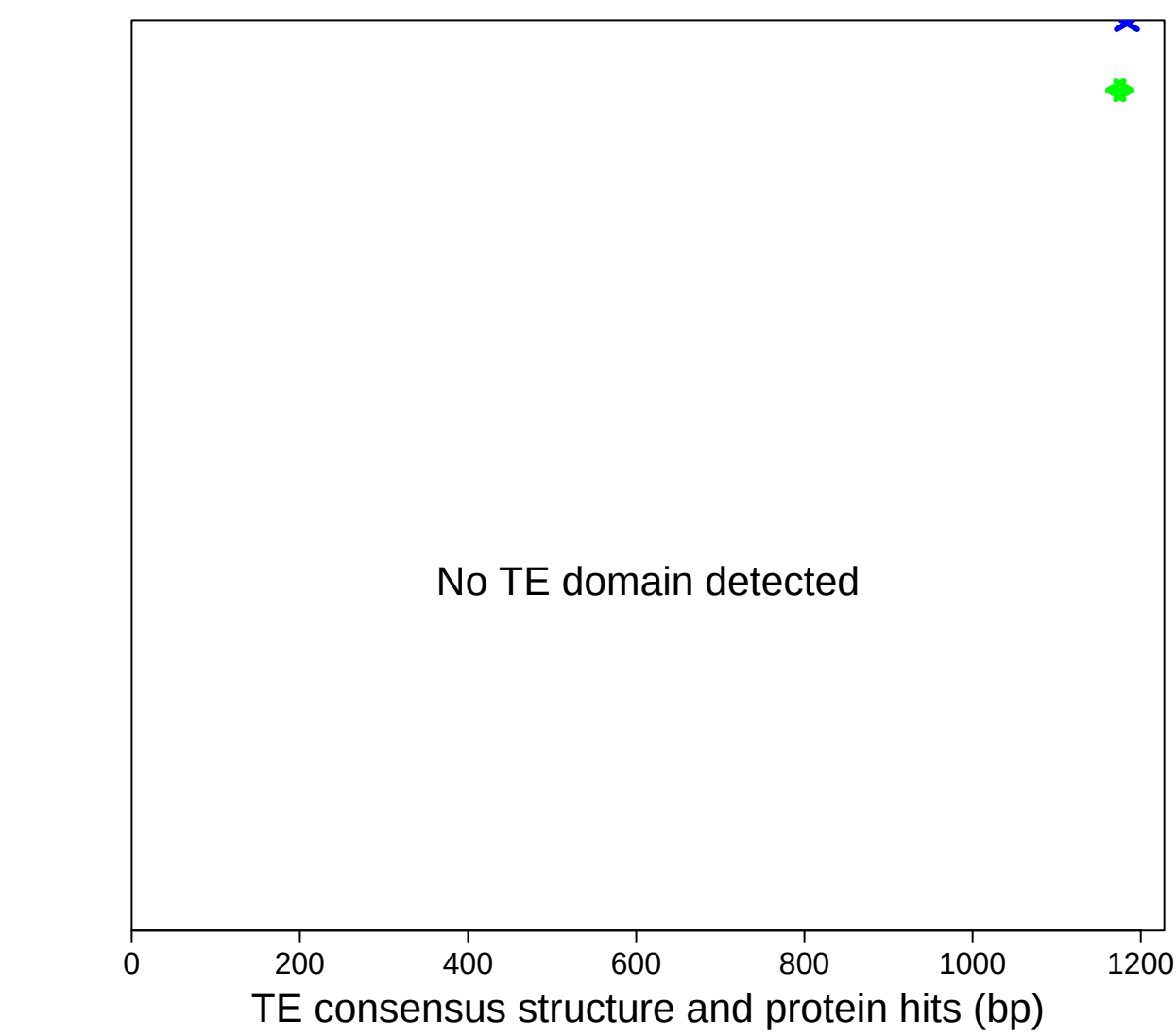
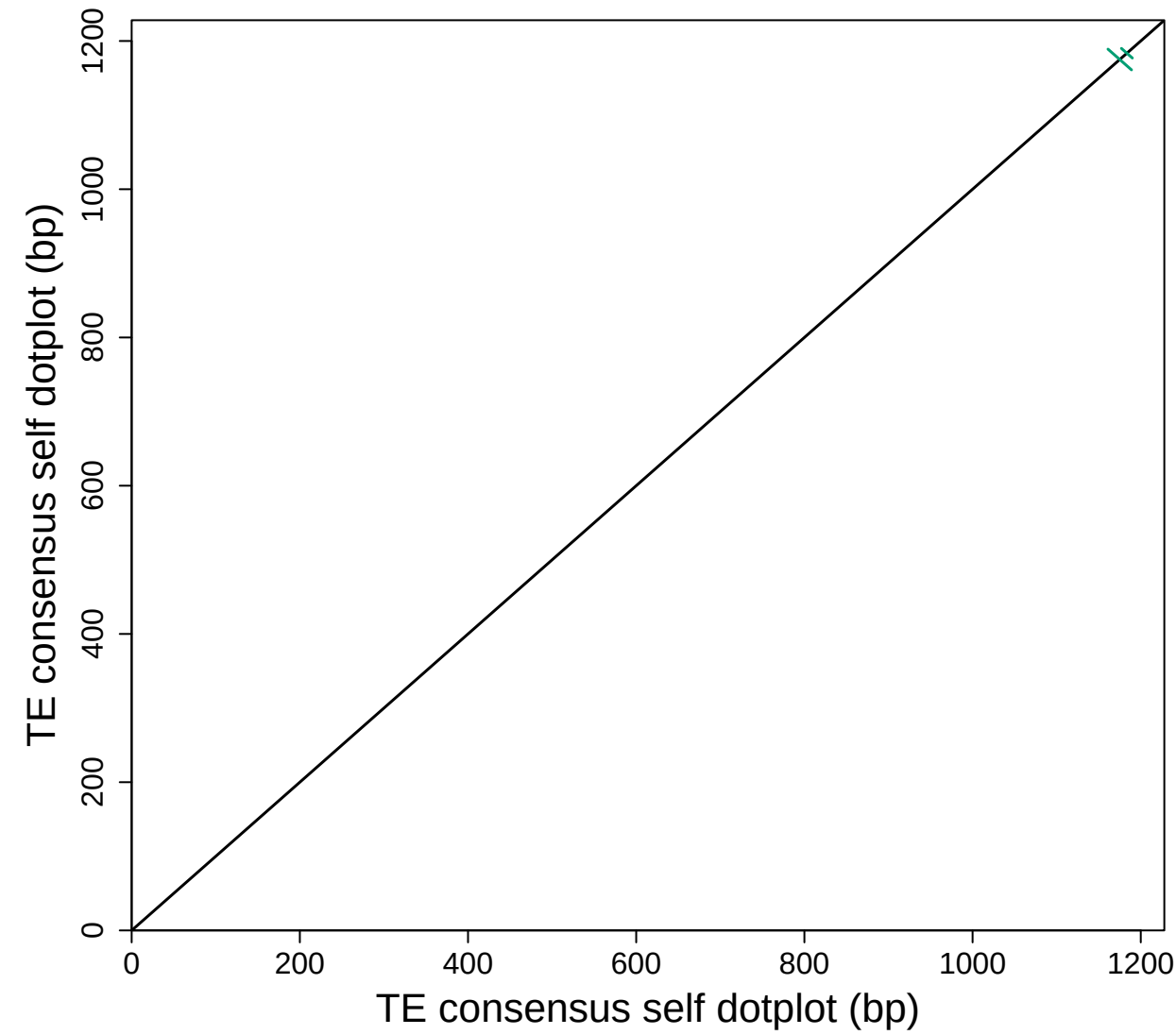
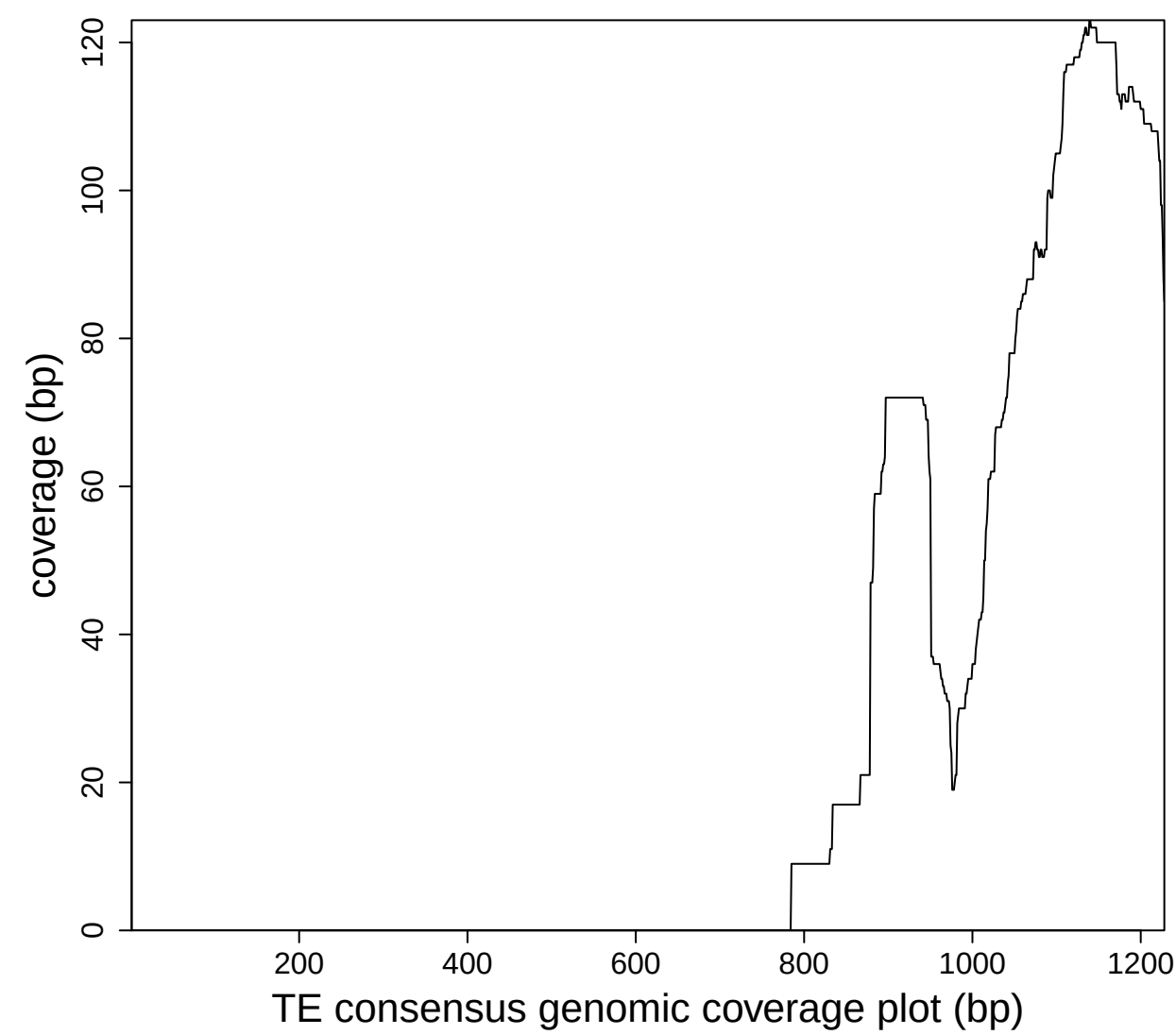
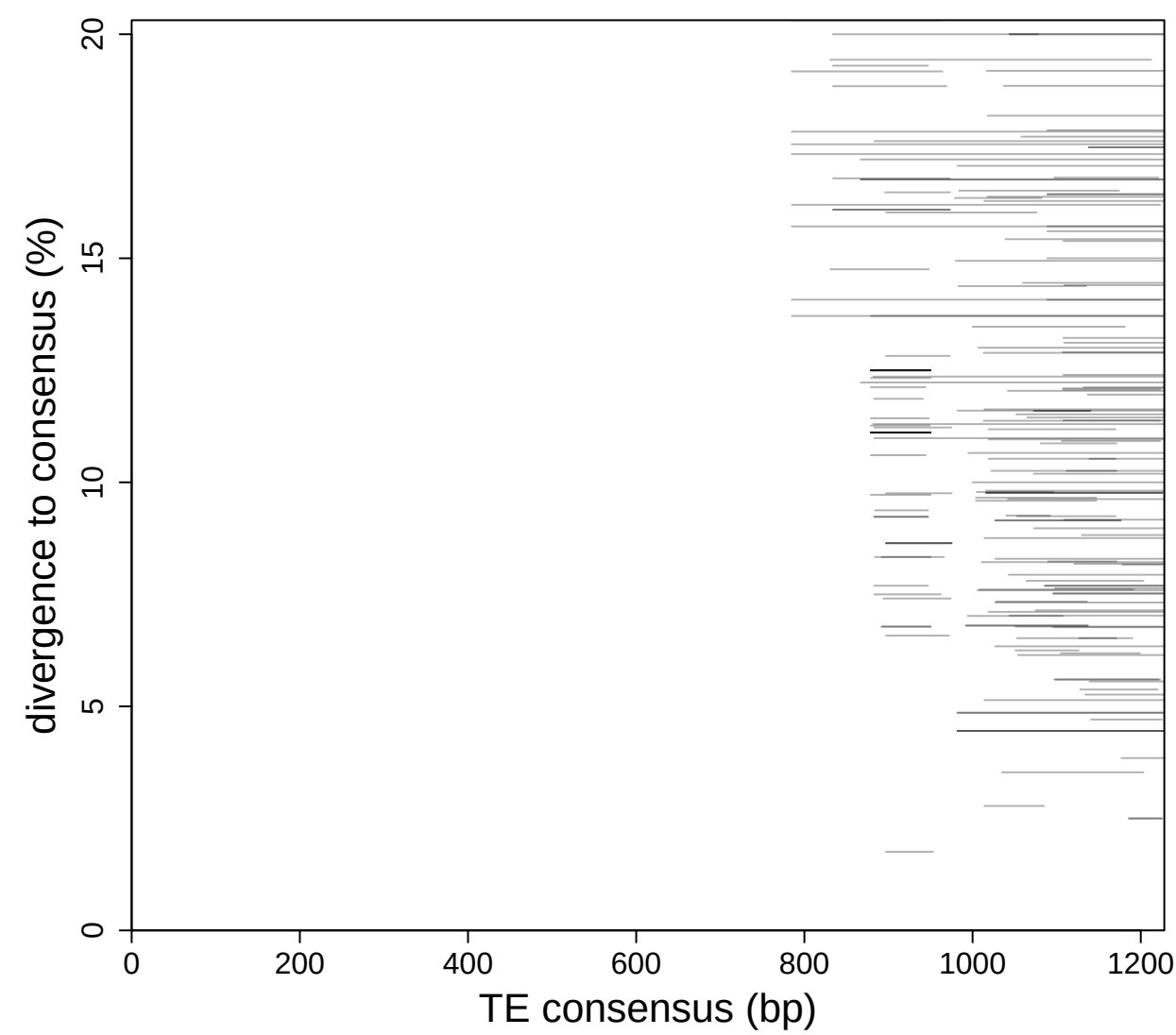
1500

1750



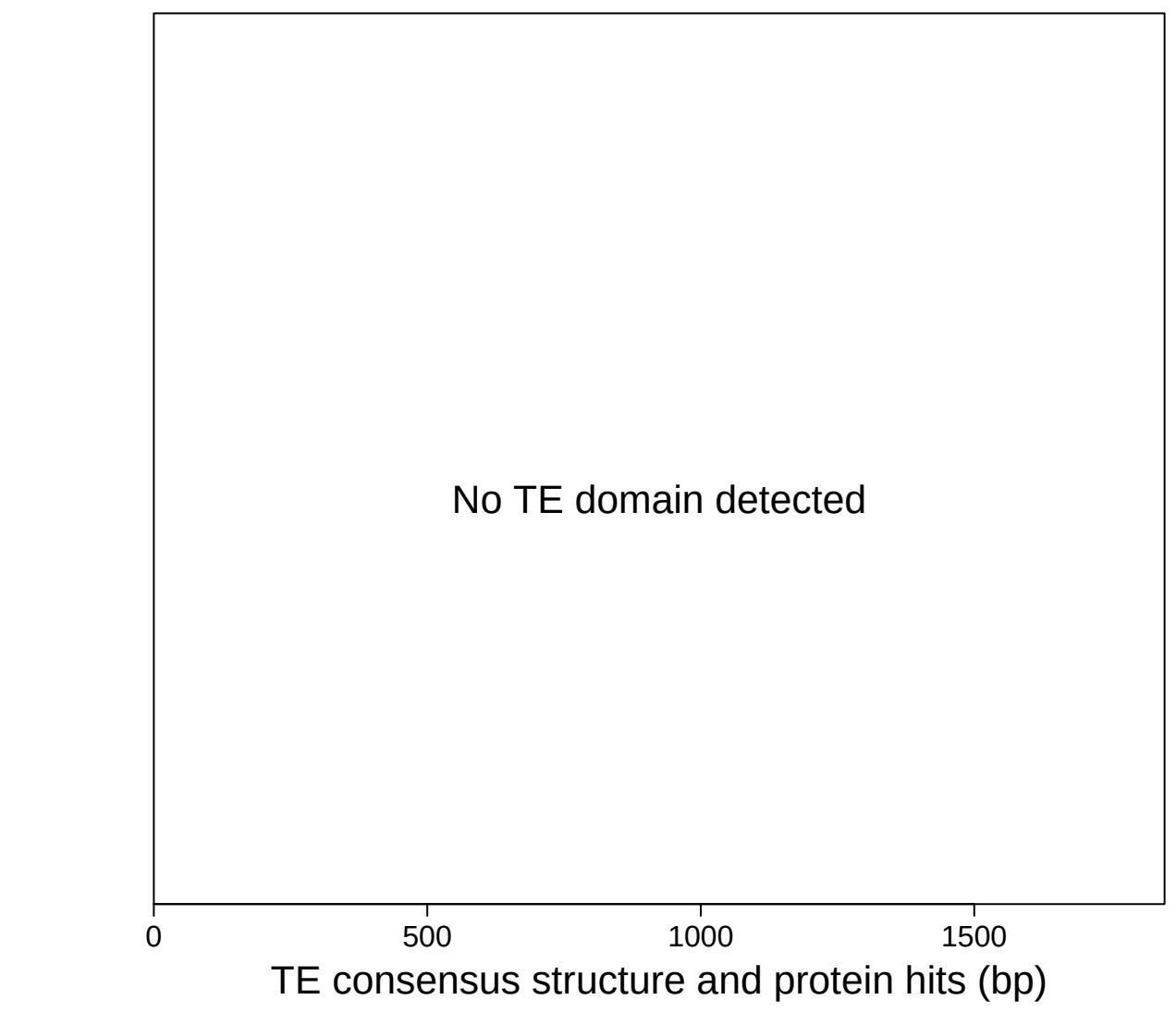
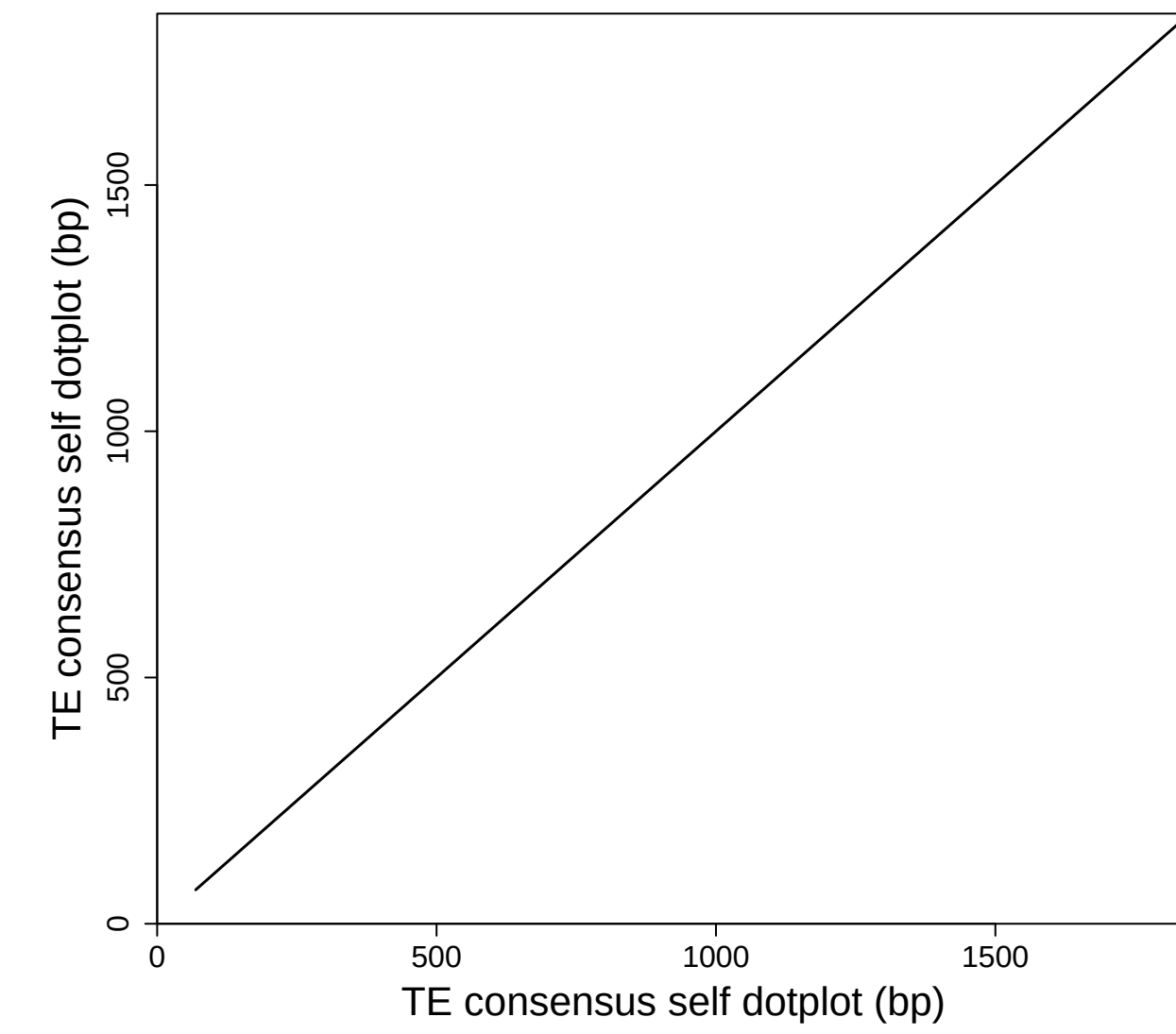
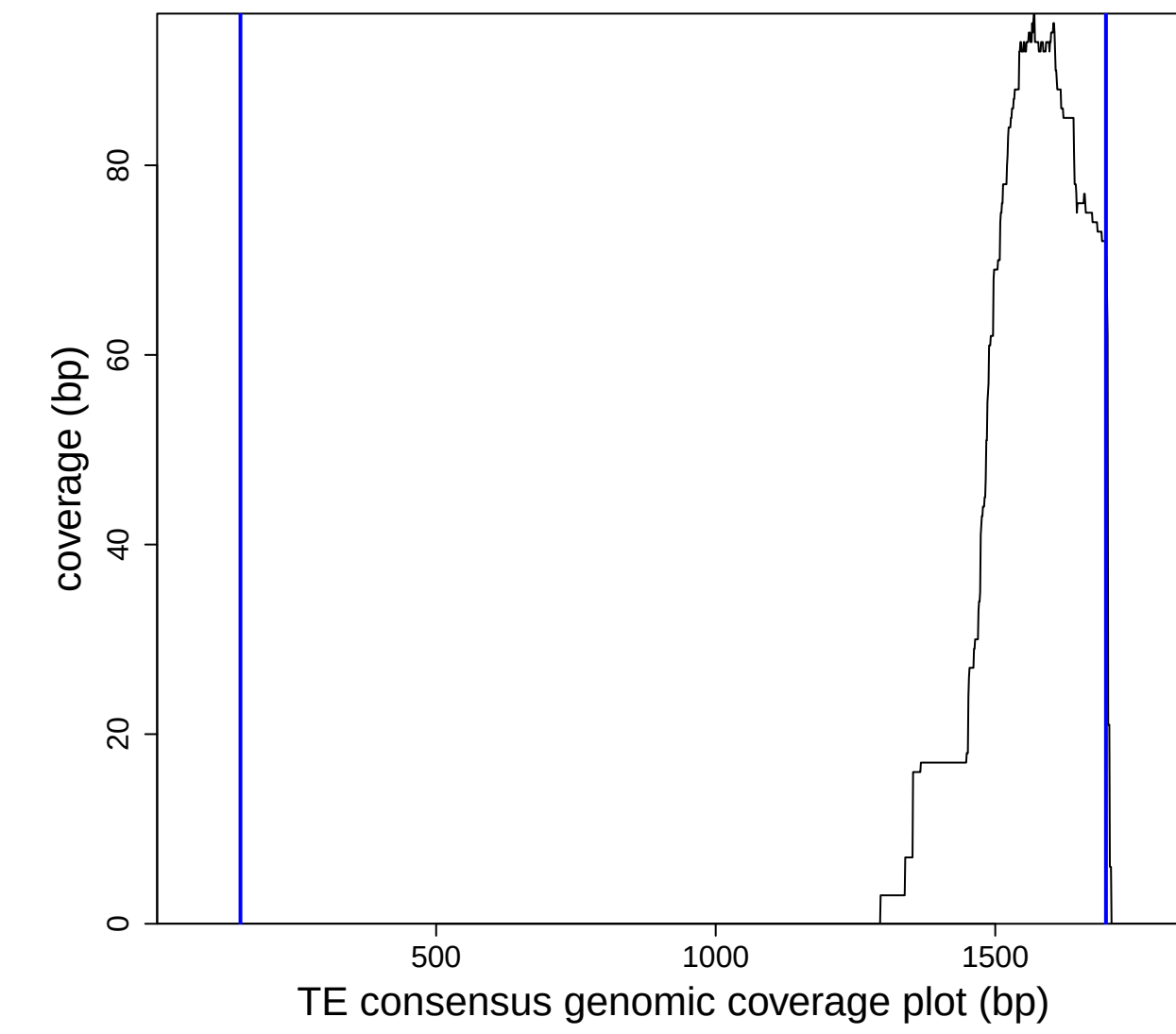
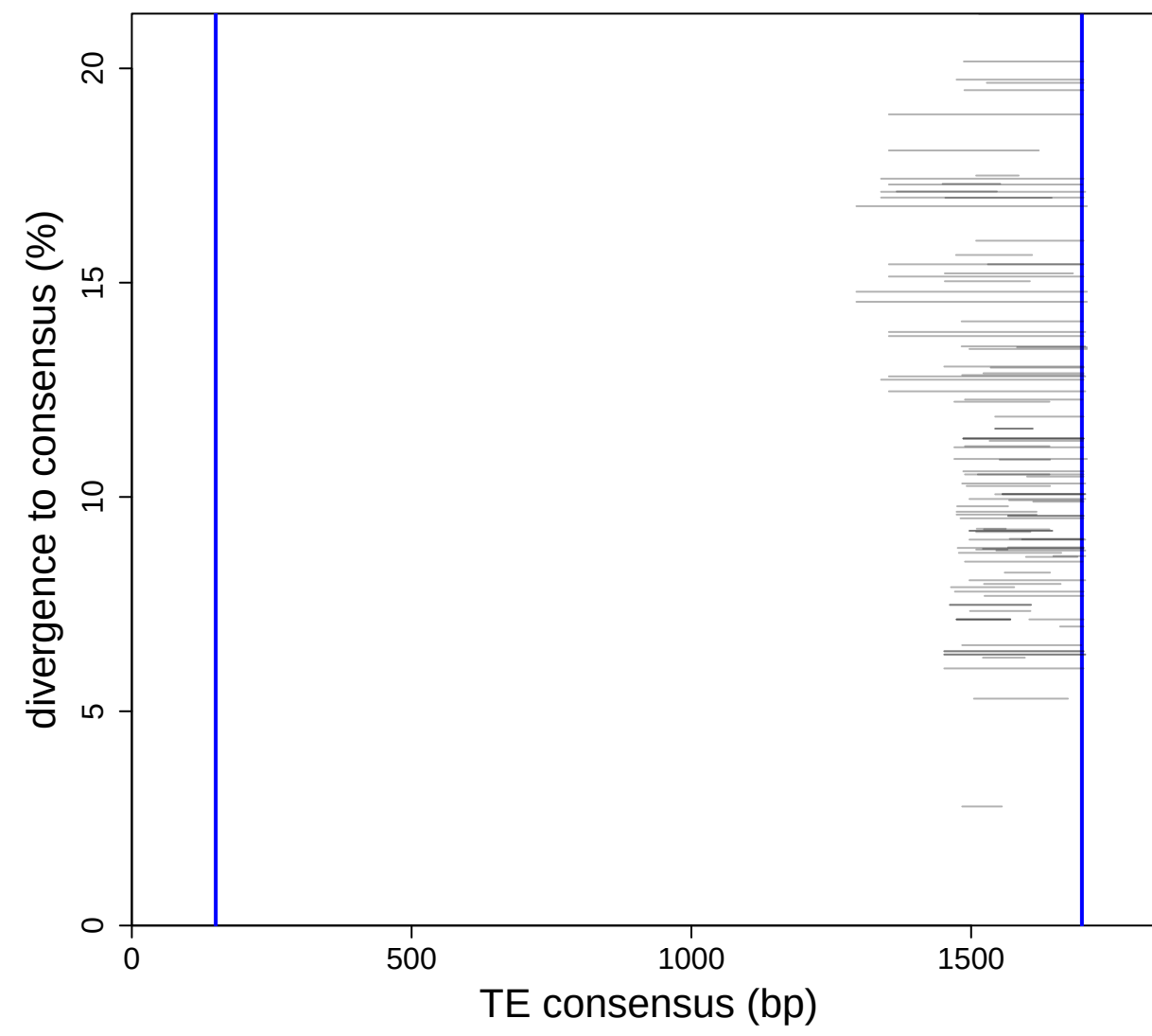
l.b.bed uf.bed g_1.bed fm_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 1228bp; fragments: 194; full length: 0 (>=1105.2bp)

After TEtrimmer 1228 bp

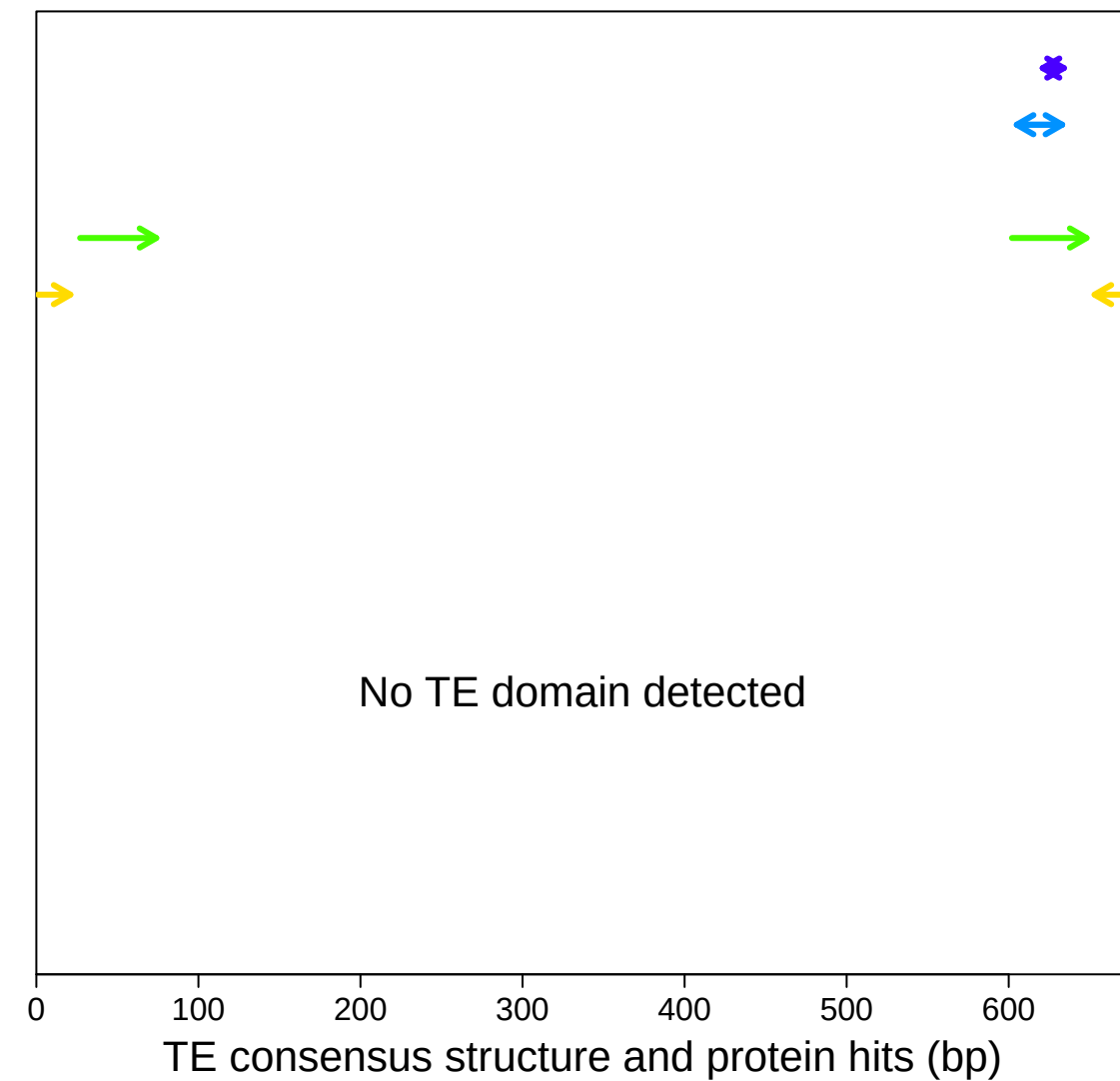
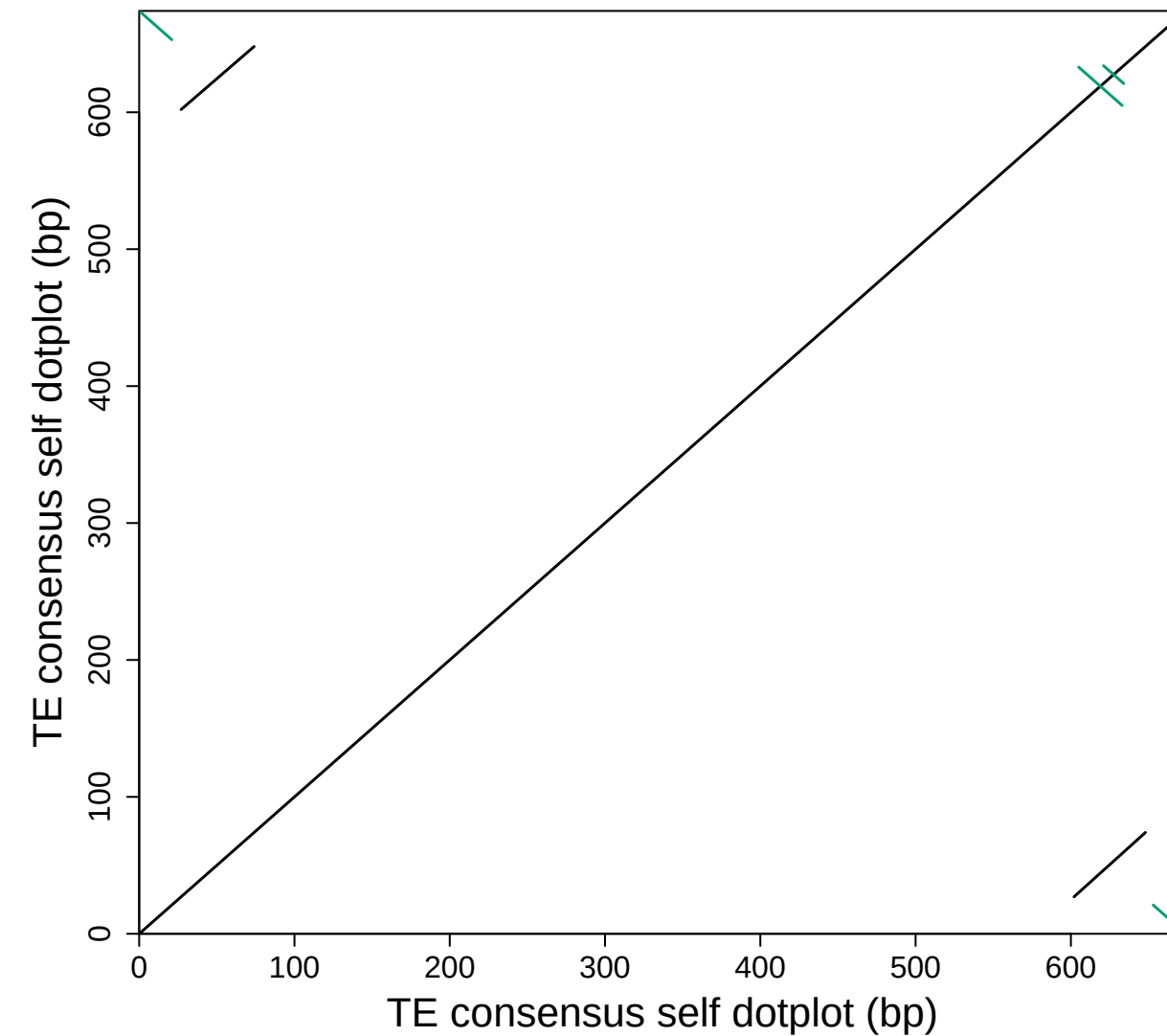
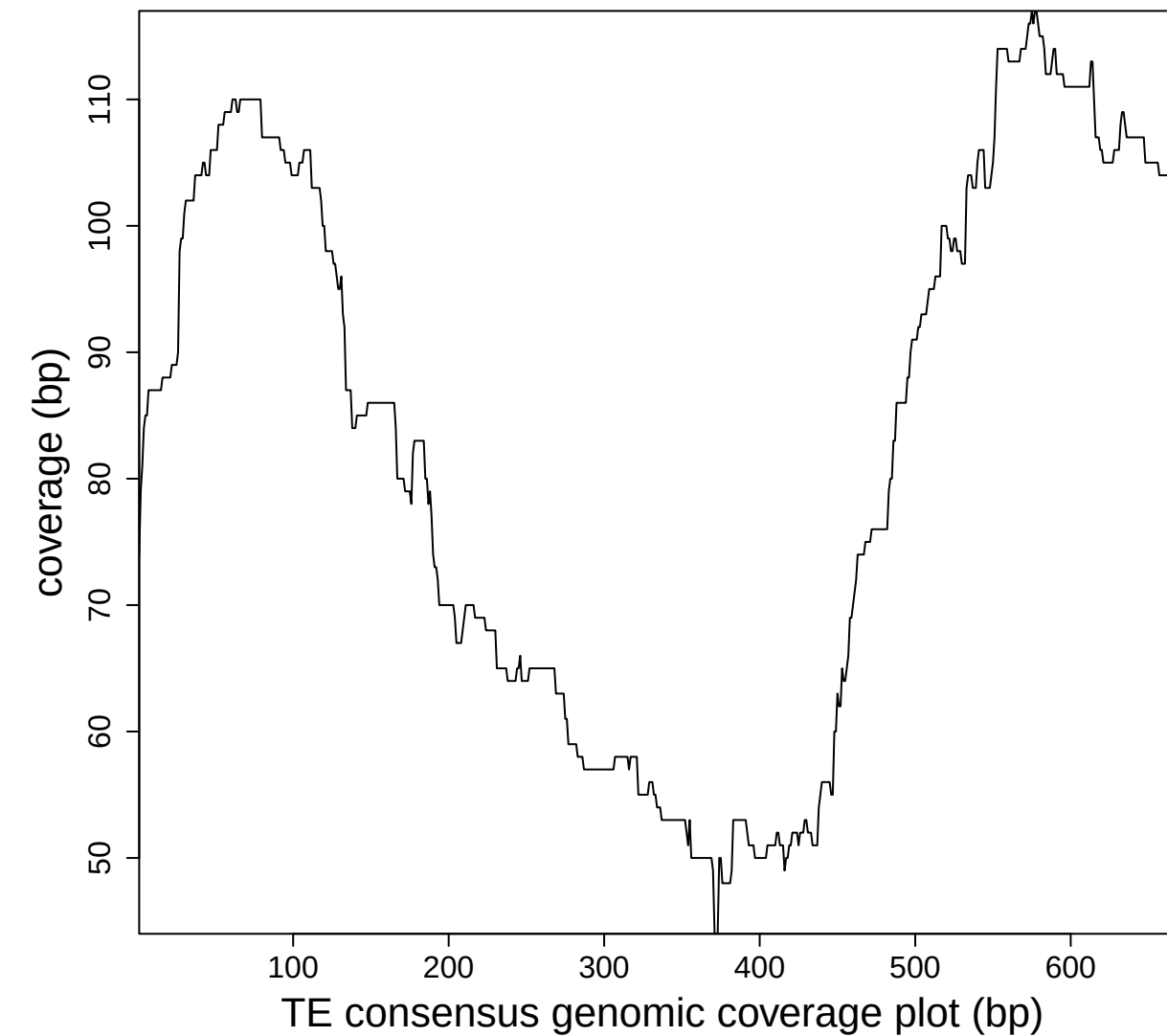
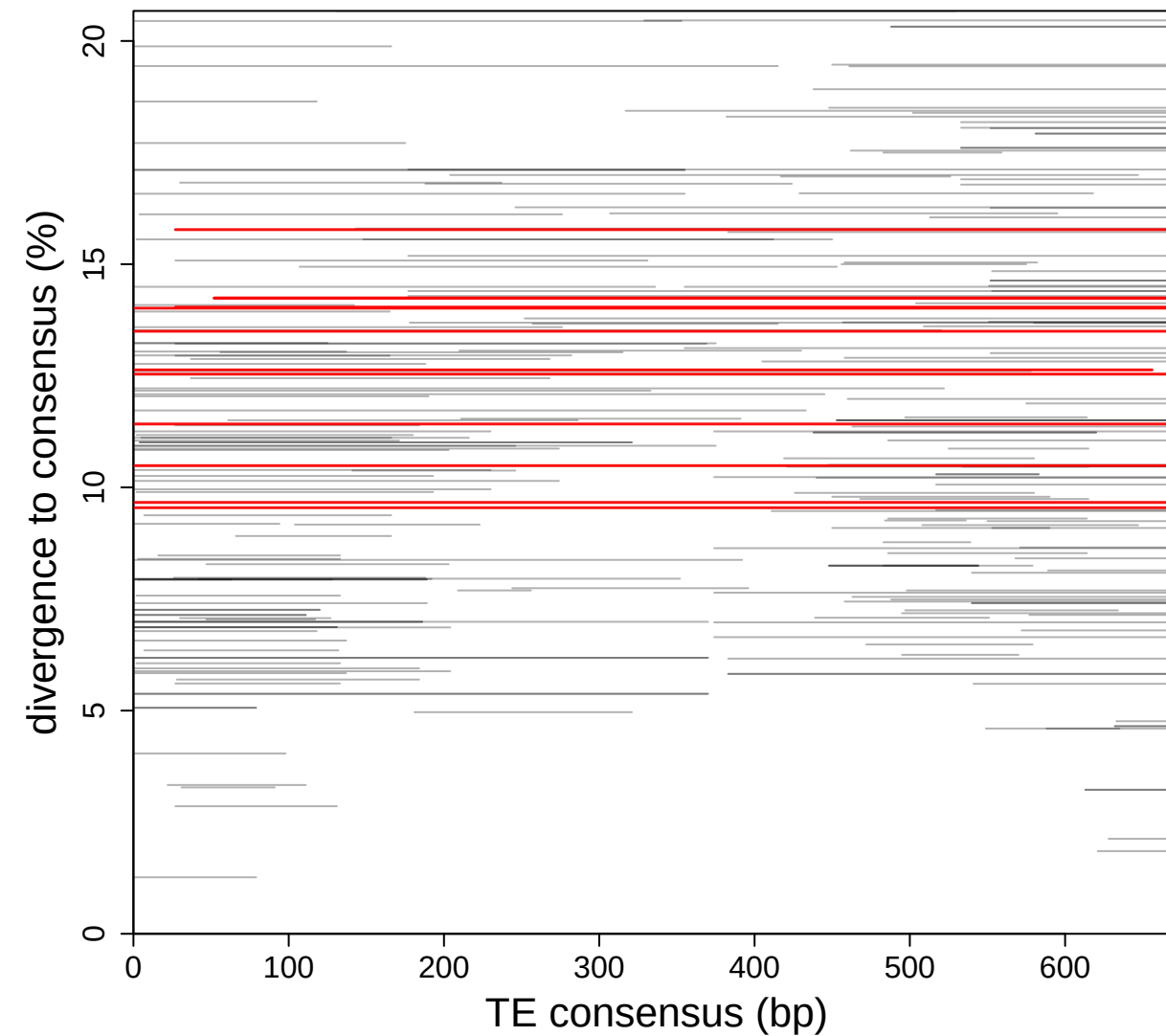


6.fasta.b.bed uf.bed g 1.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa
size: 1848bp; fragments: 110; full length: 0 (>=1663.2bp)

After TEtrimmer Extended plot Blue lines are boundaries

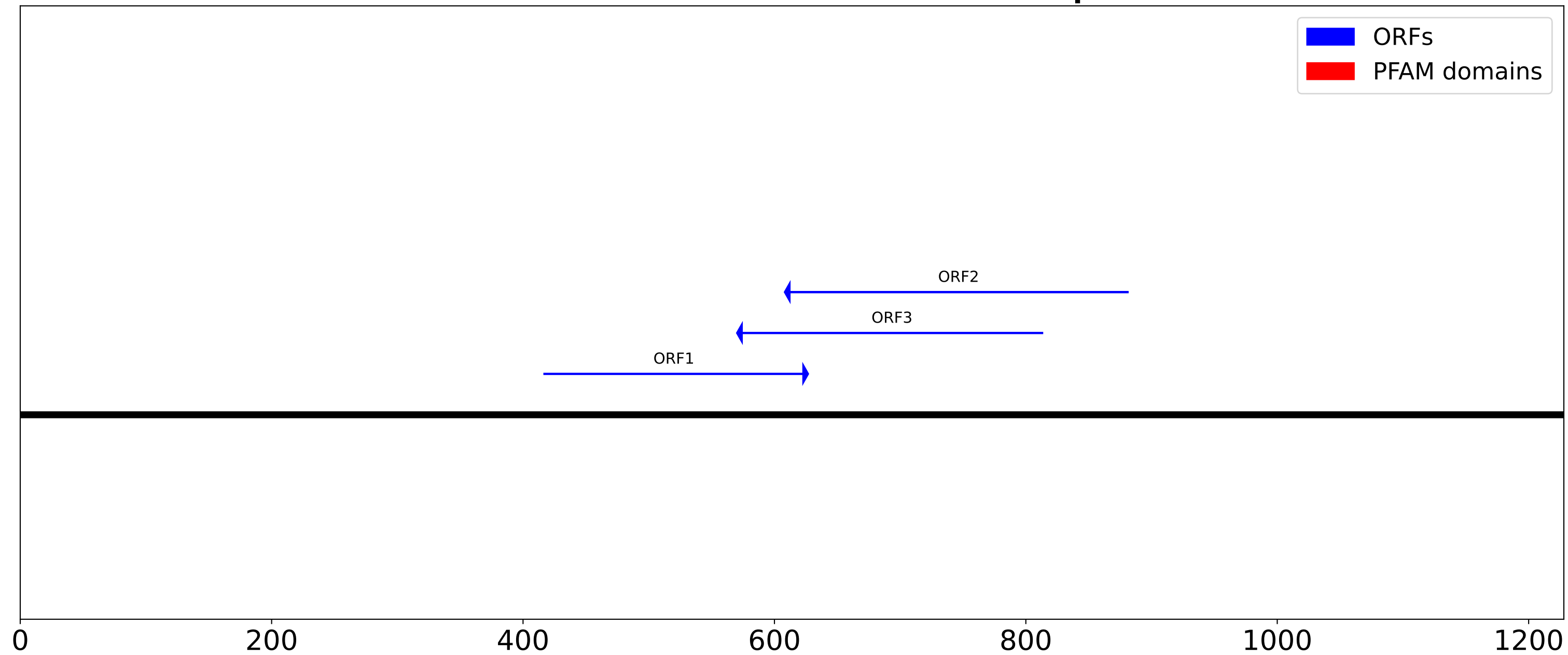


TE: rnd_4_family_466
size: 674bp; fragments: 250; full length: 12 (≥ 606.6 bp)

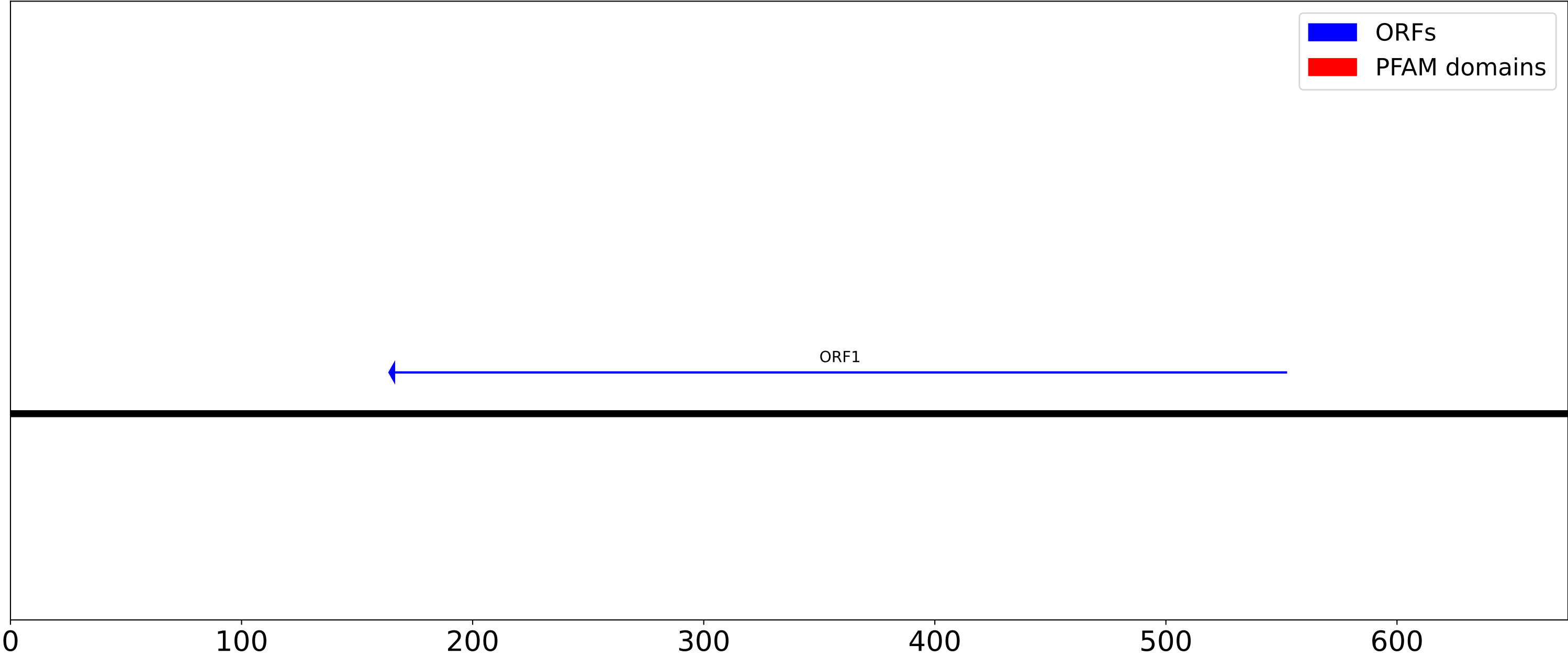


Before TEtrimmer 674 bp

After TEtrimmer ORF and PFAM domain plot



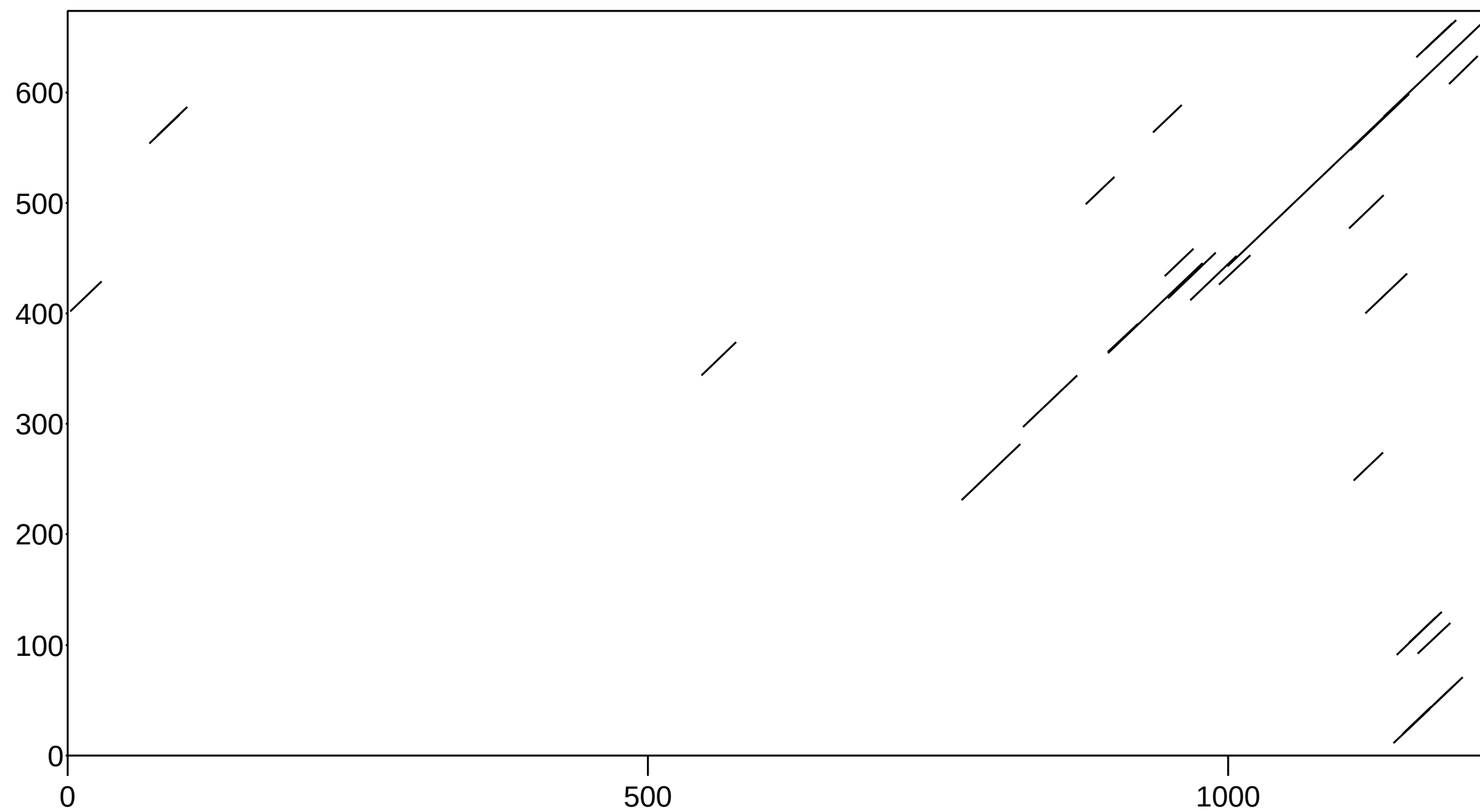
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)