

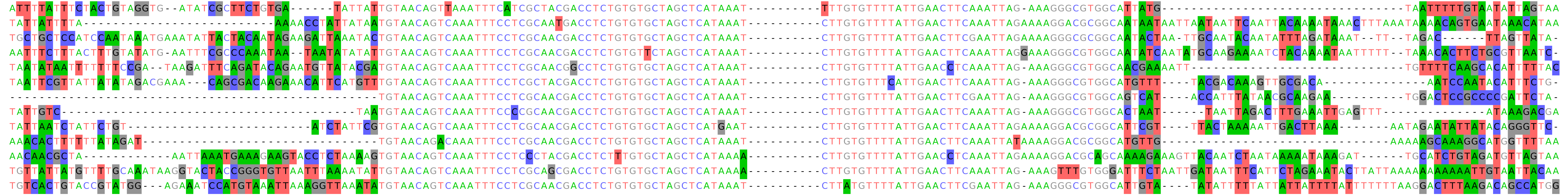
Start crop Point



End crop Point



MSA length = 1941



Start crop Point

End crop Point

0

10

0

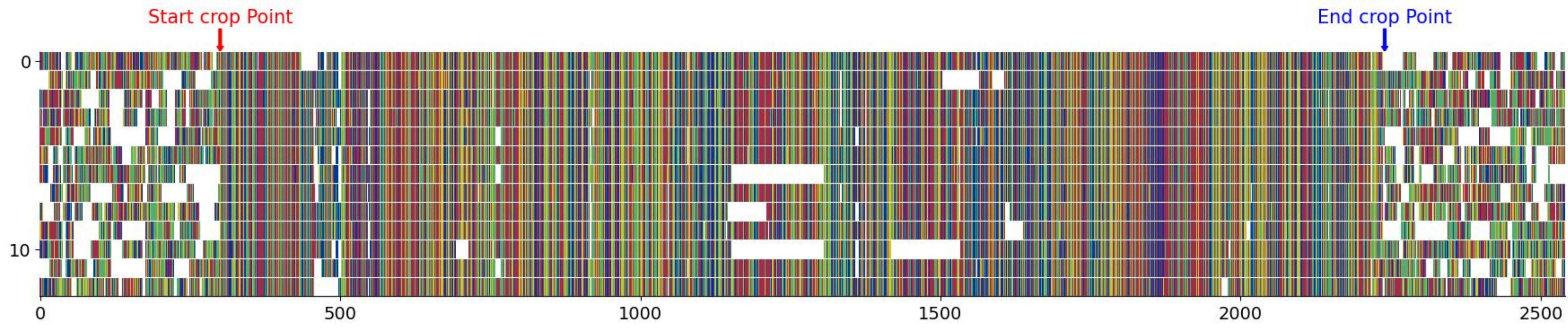
500

1000

1500

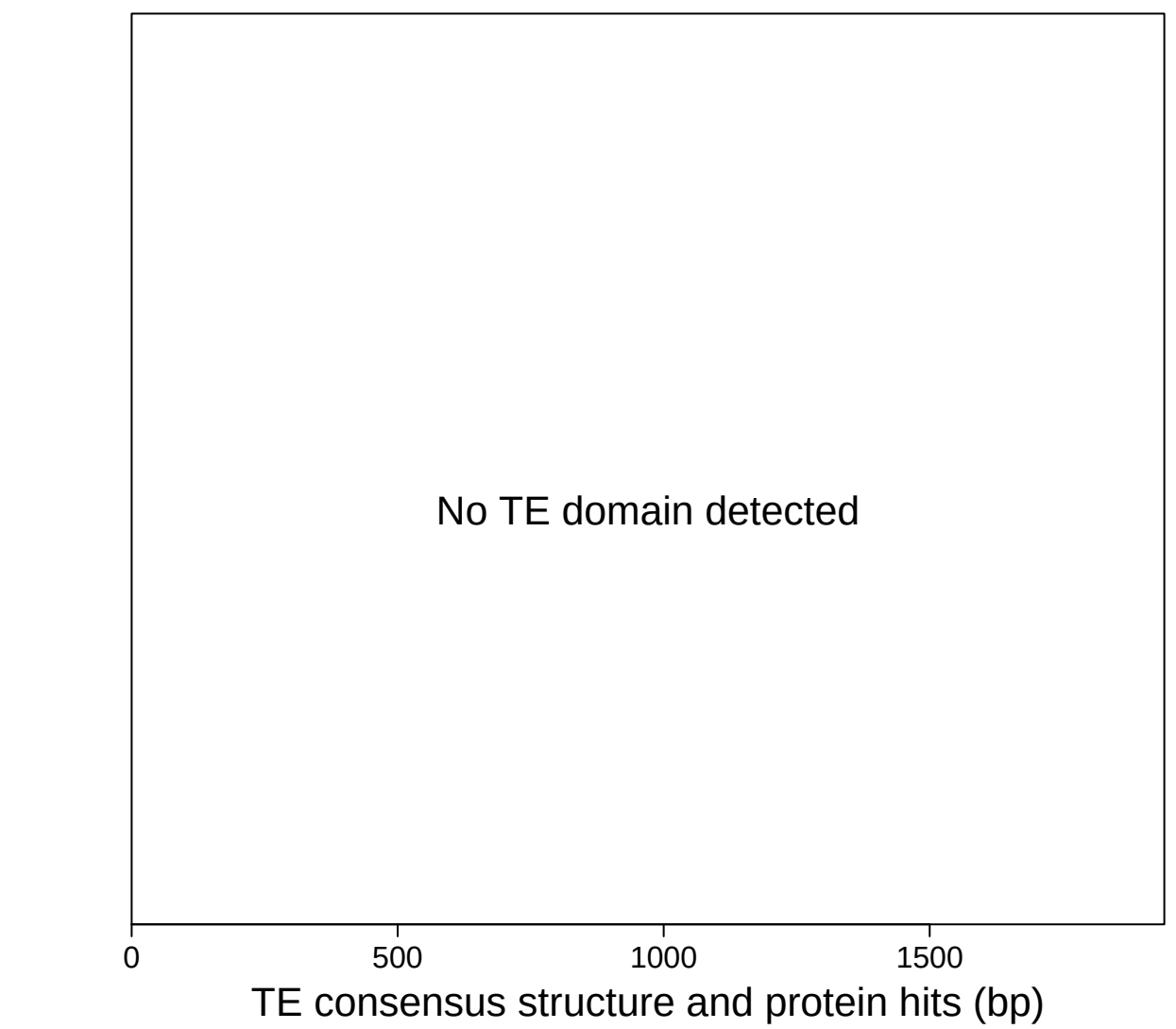
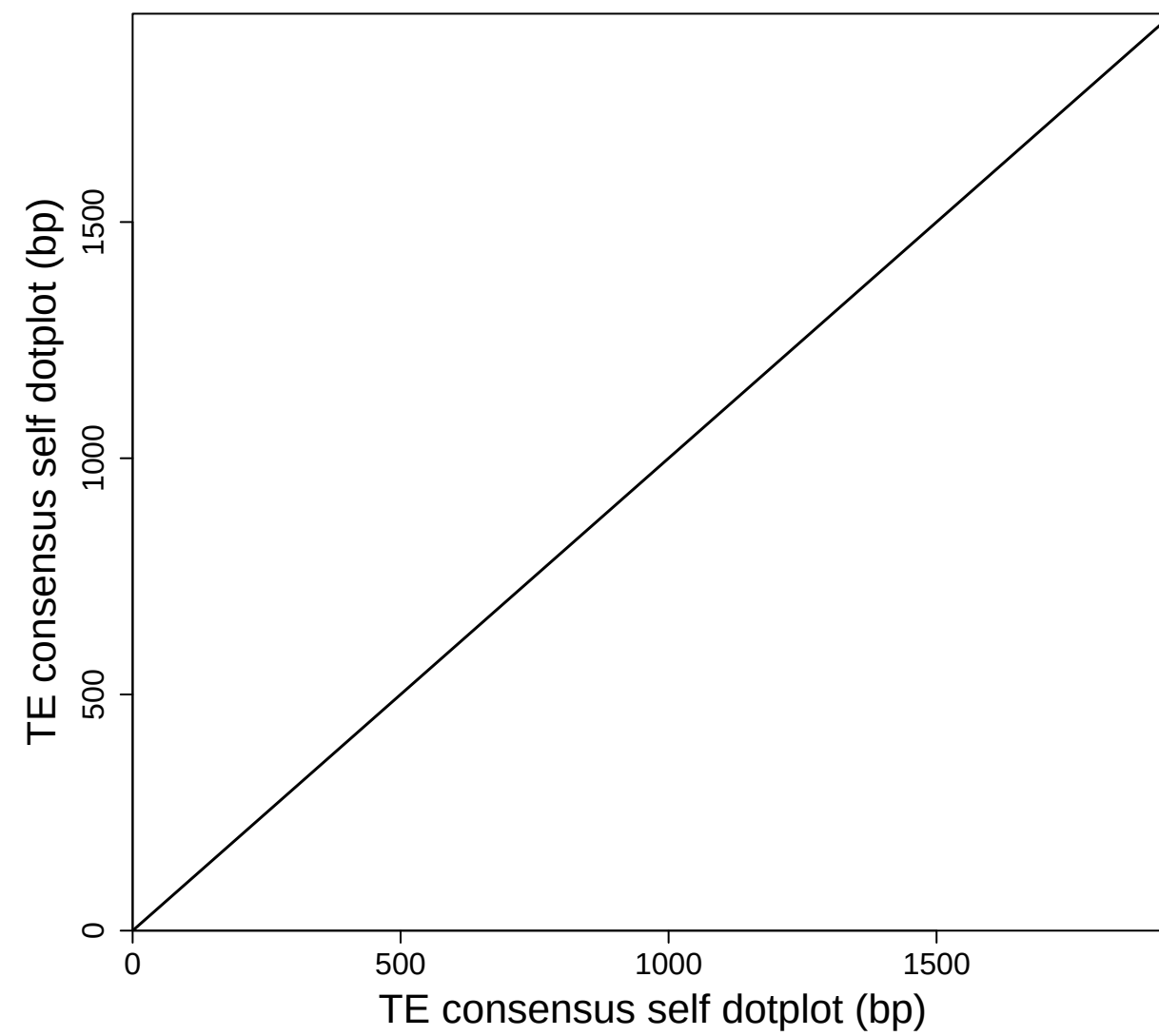
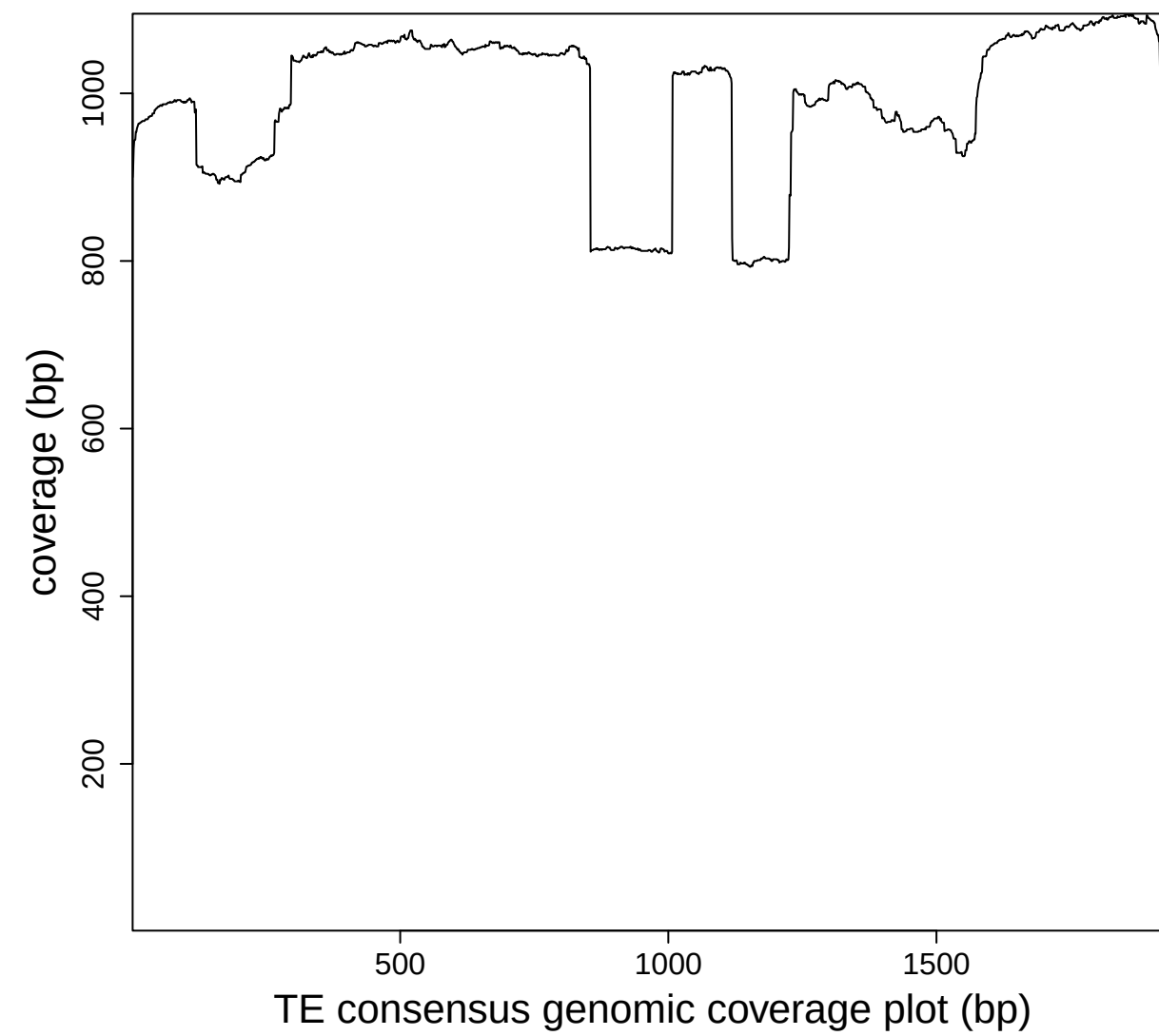
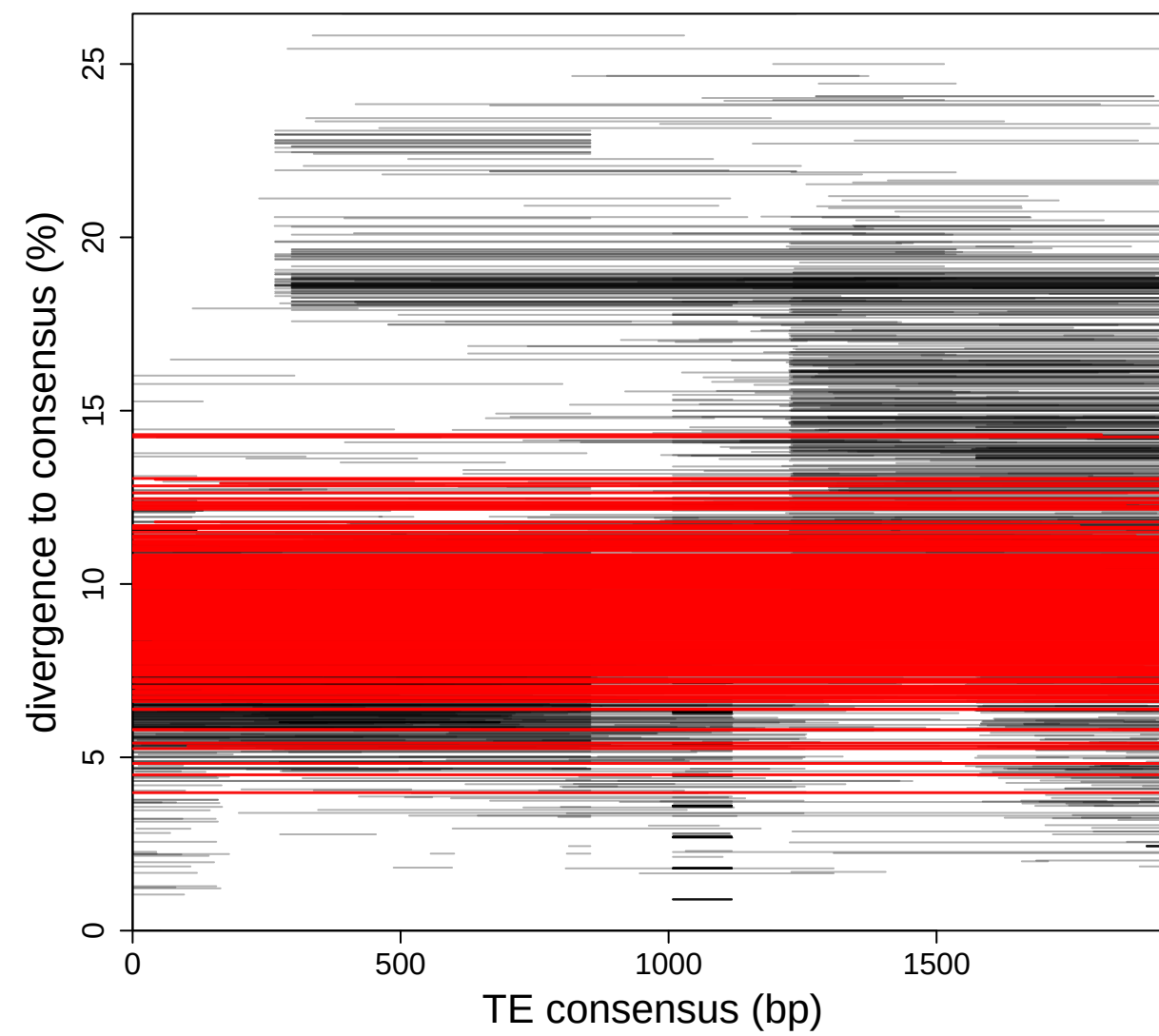
2000

2500



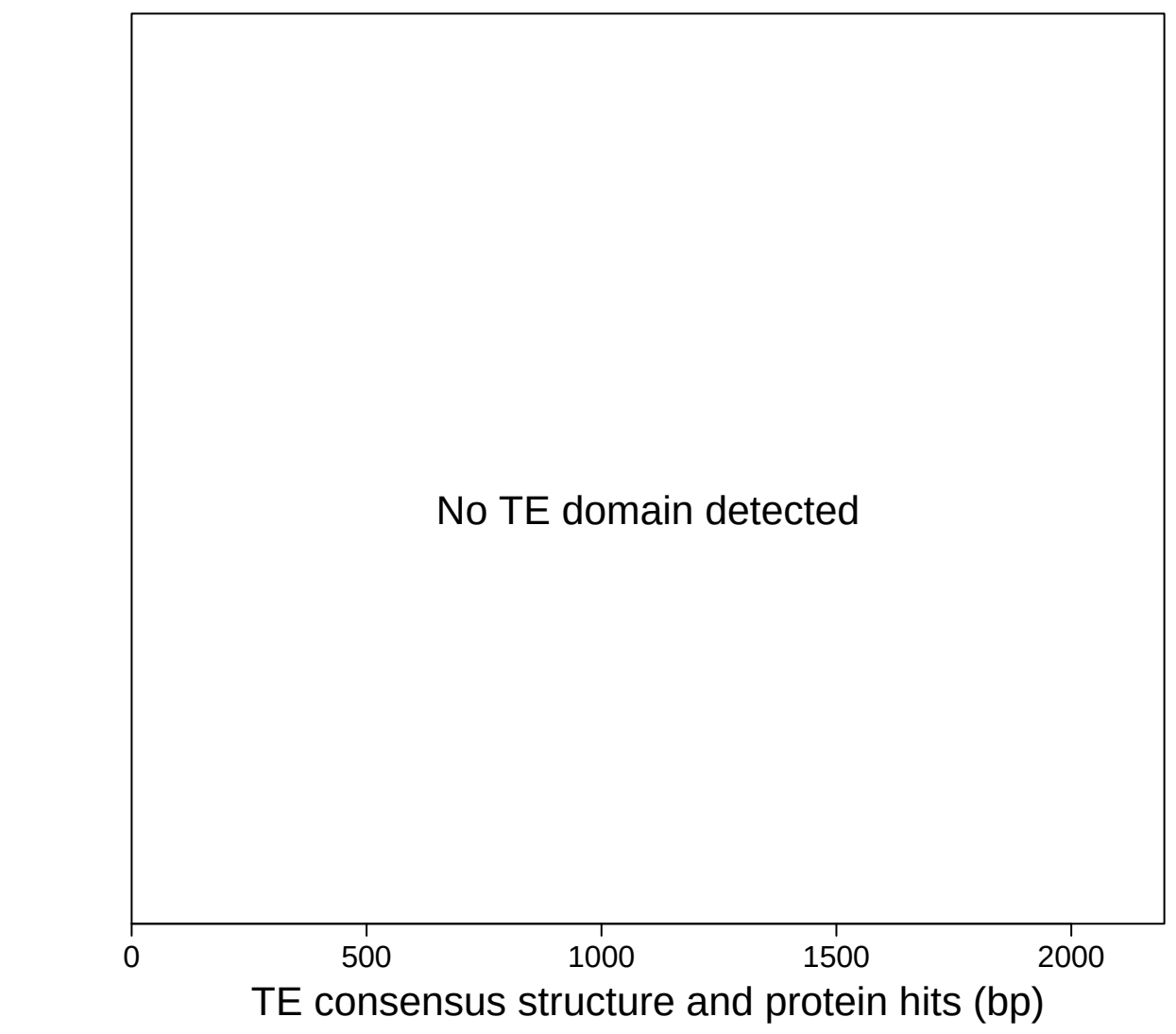
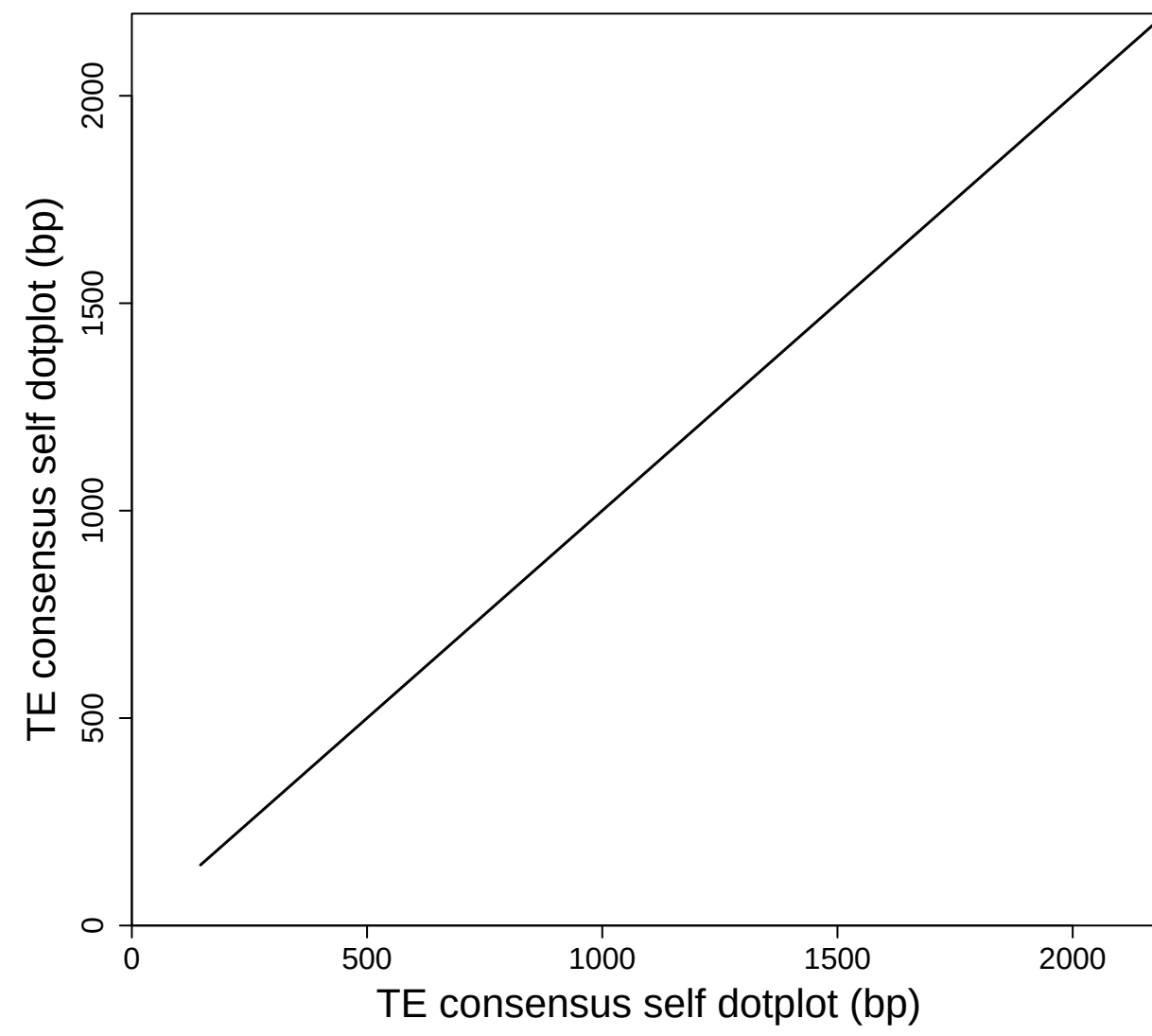
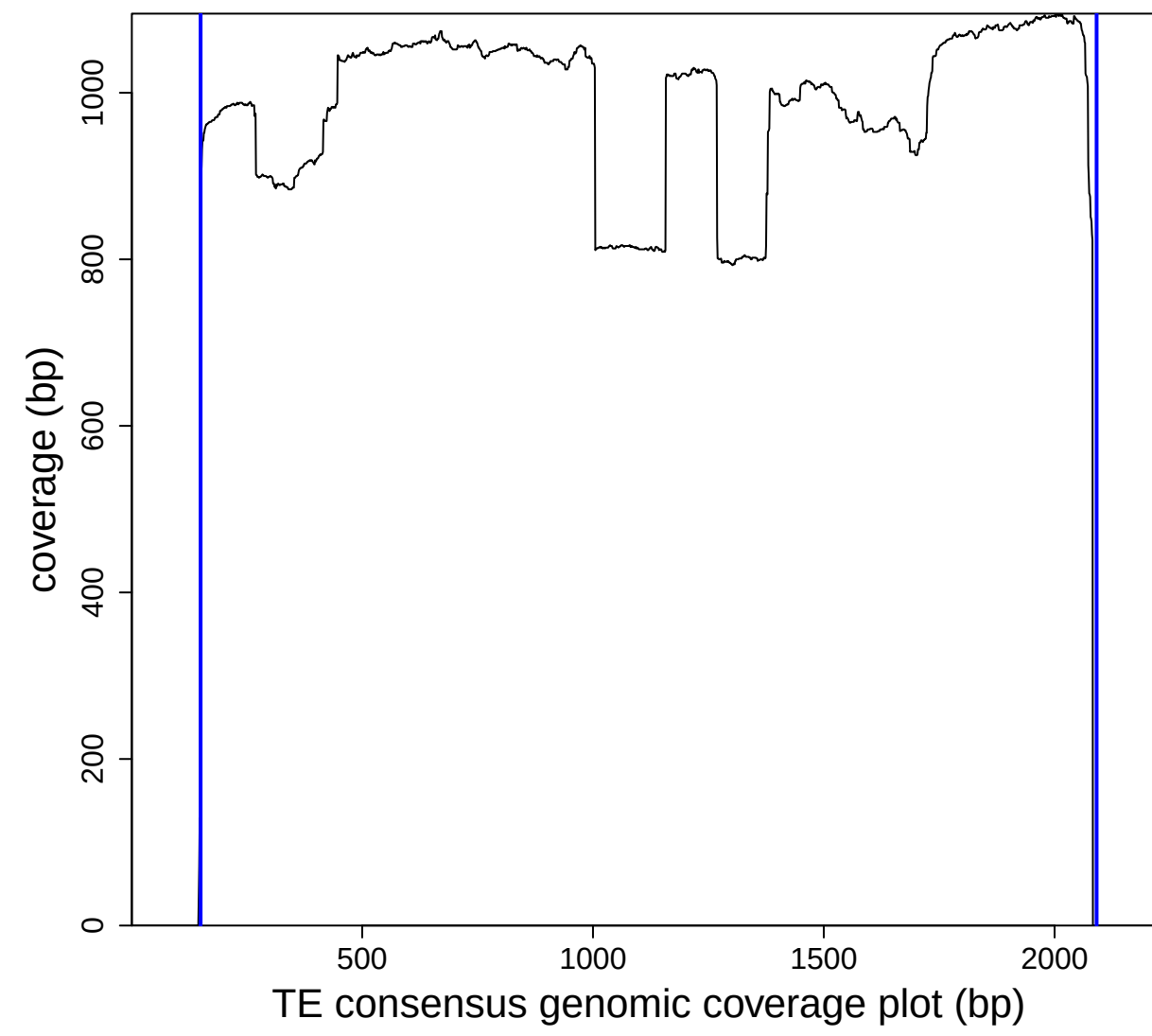
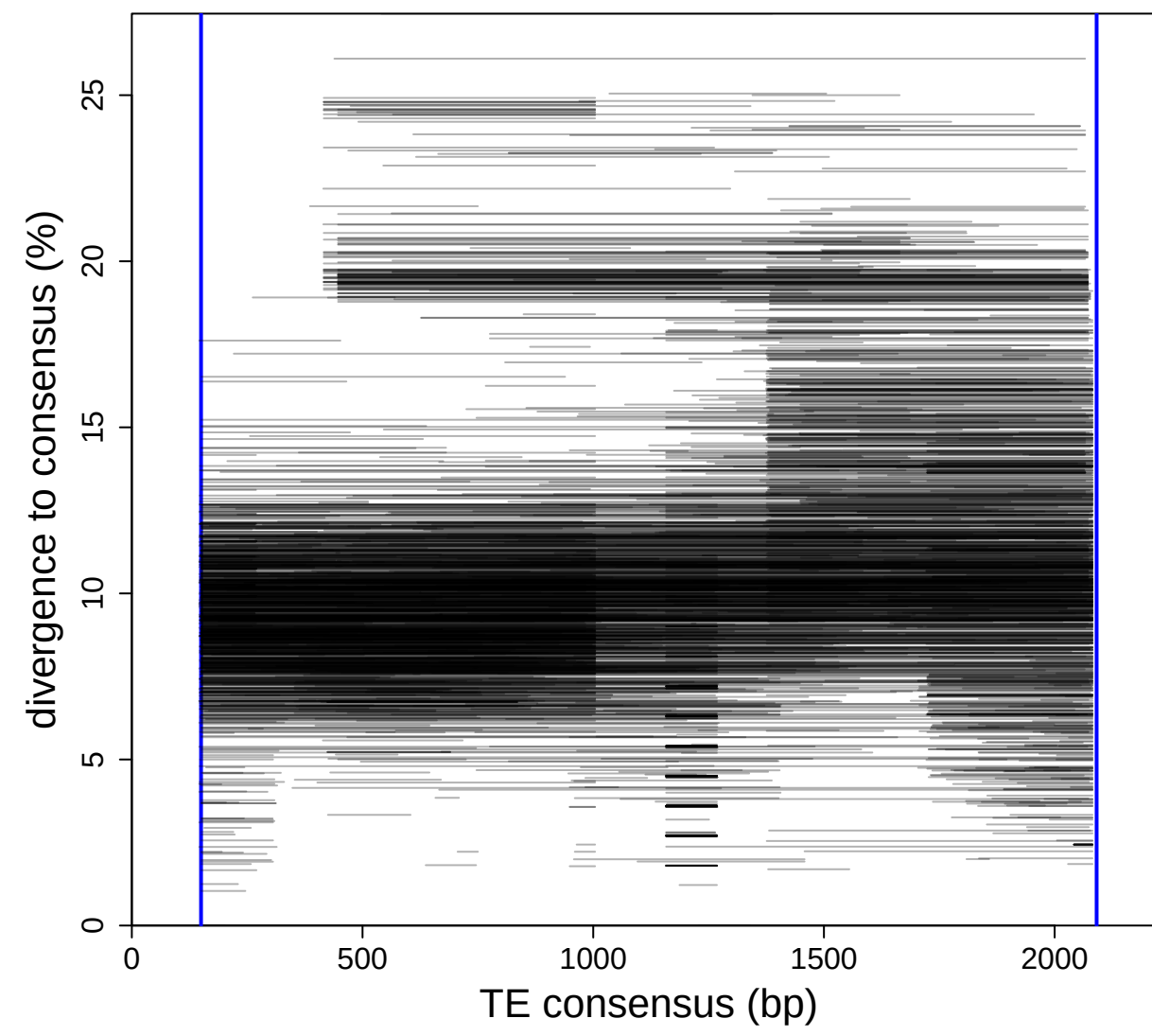
.b.bed uf.bed g_1.bed fm_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 1941bp; fragments: 2397; full length: 323 (≥ 1746.9 bp)

After TEtrimmer 1941 bp



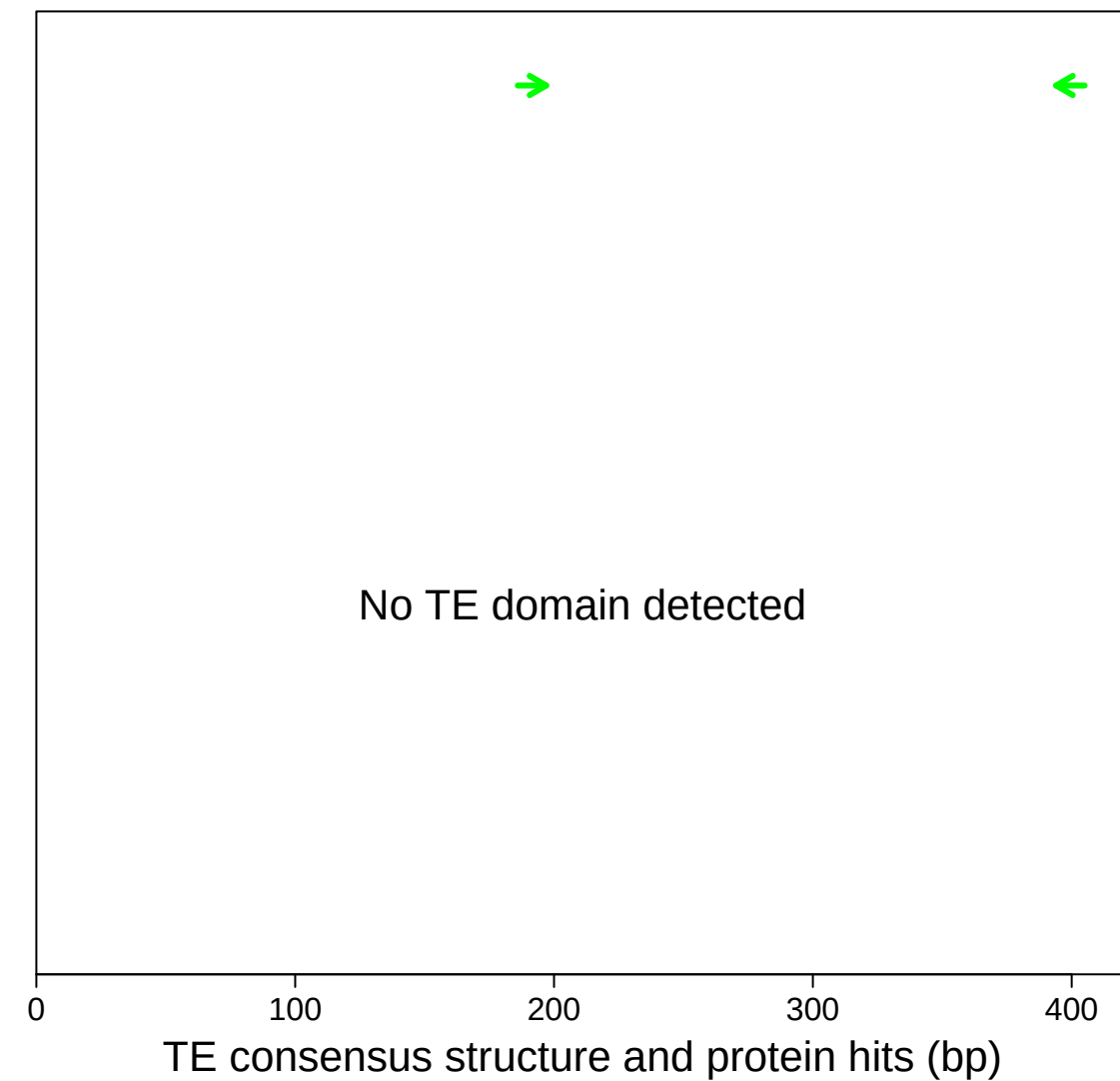
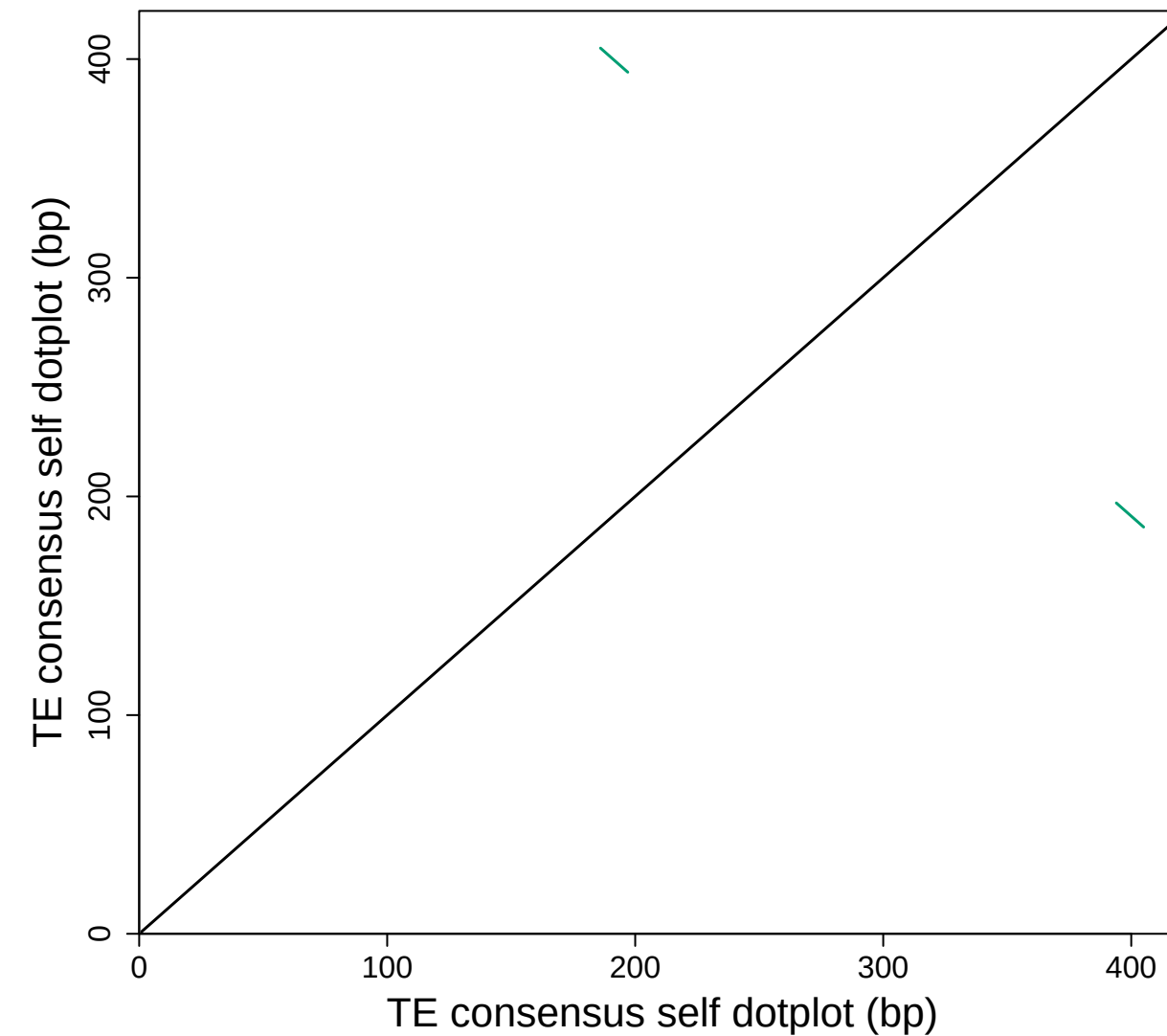
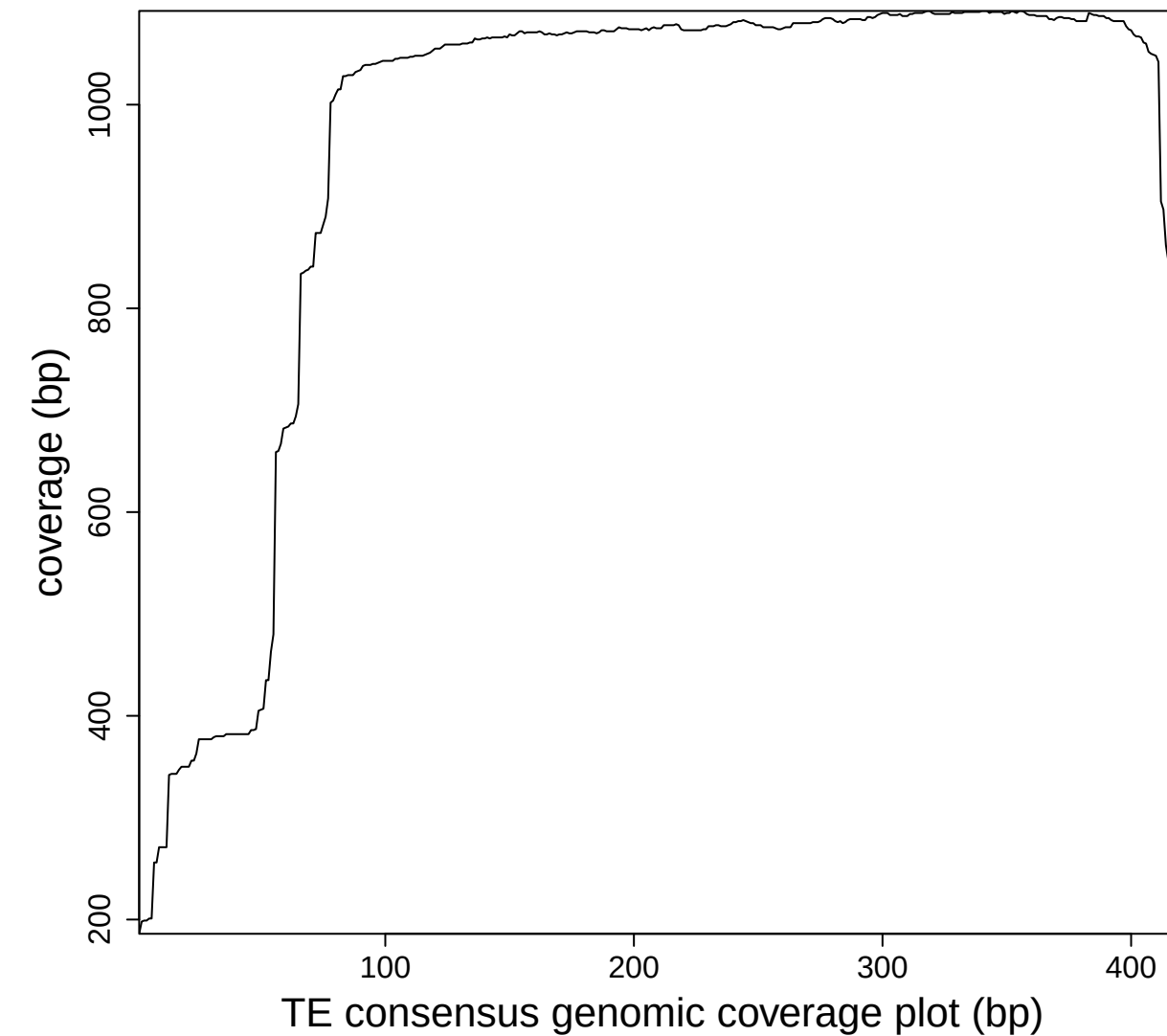
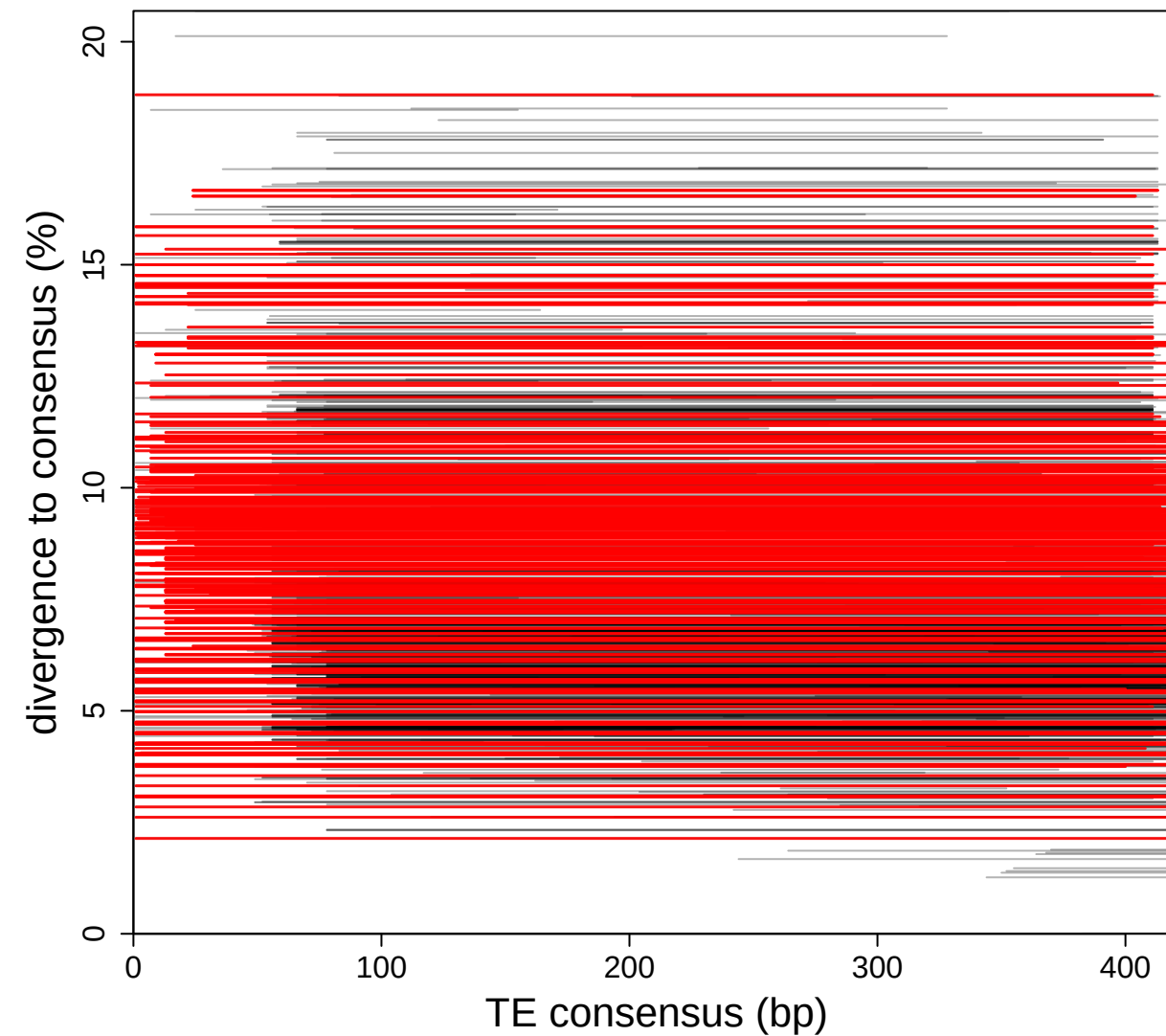
8.fasta.b.bed uf.bed g 1.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa
size: 2241bp; fragments: 2396; full length: 0 (>=2016.9bp)

After TEtrimmer Extended plot Blue lines are boundaries

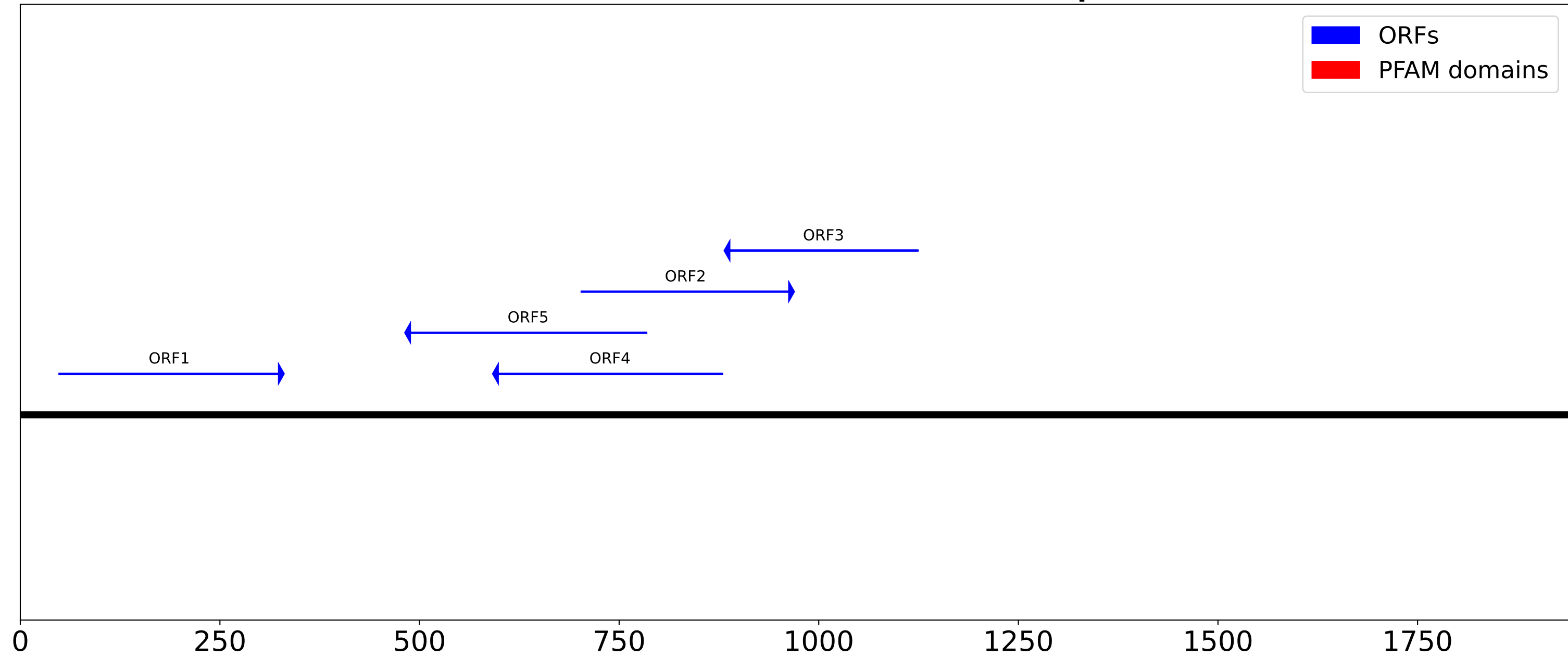


TE: rnd_1_family_228
size: 422bp; fragments: 1194; full length: 343 (>=379.8bp)

Before TEtrimmer 422 bp



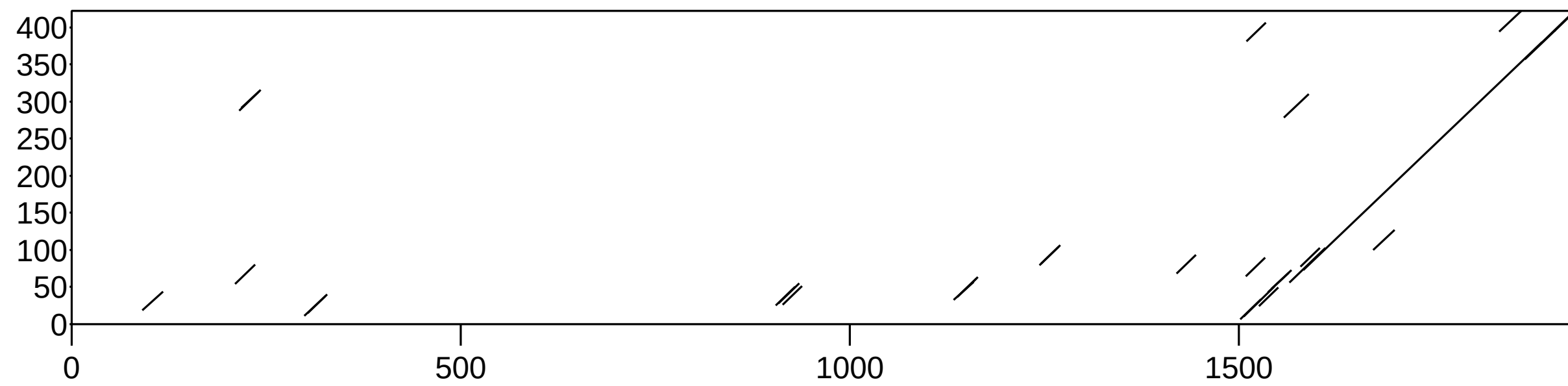
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

onsensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)