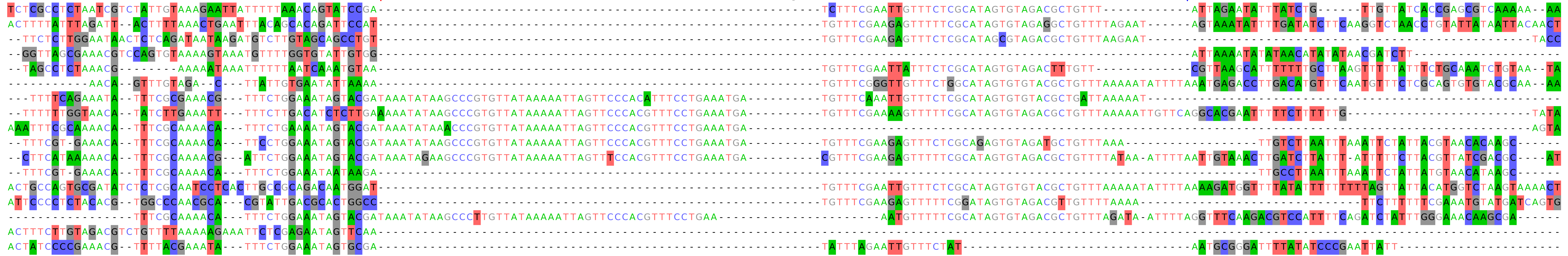


MSA length = 1359

Start crop Point



End crop Point



Start crop Point

End crop Point

0

10

0

250

500

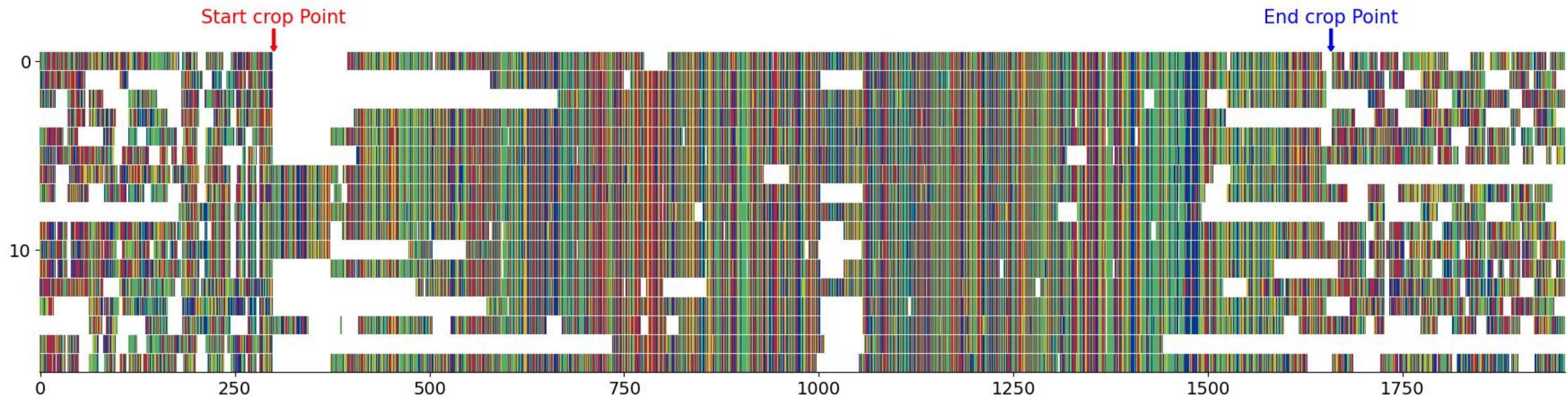
750

1000

1250

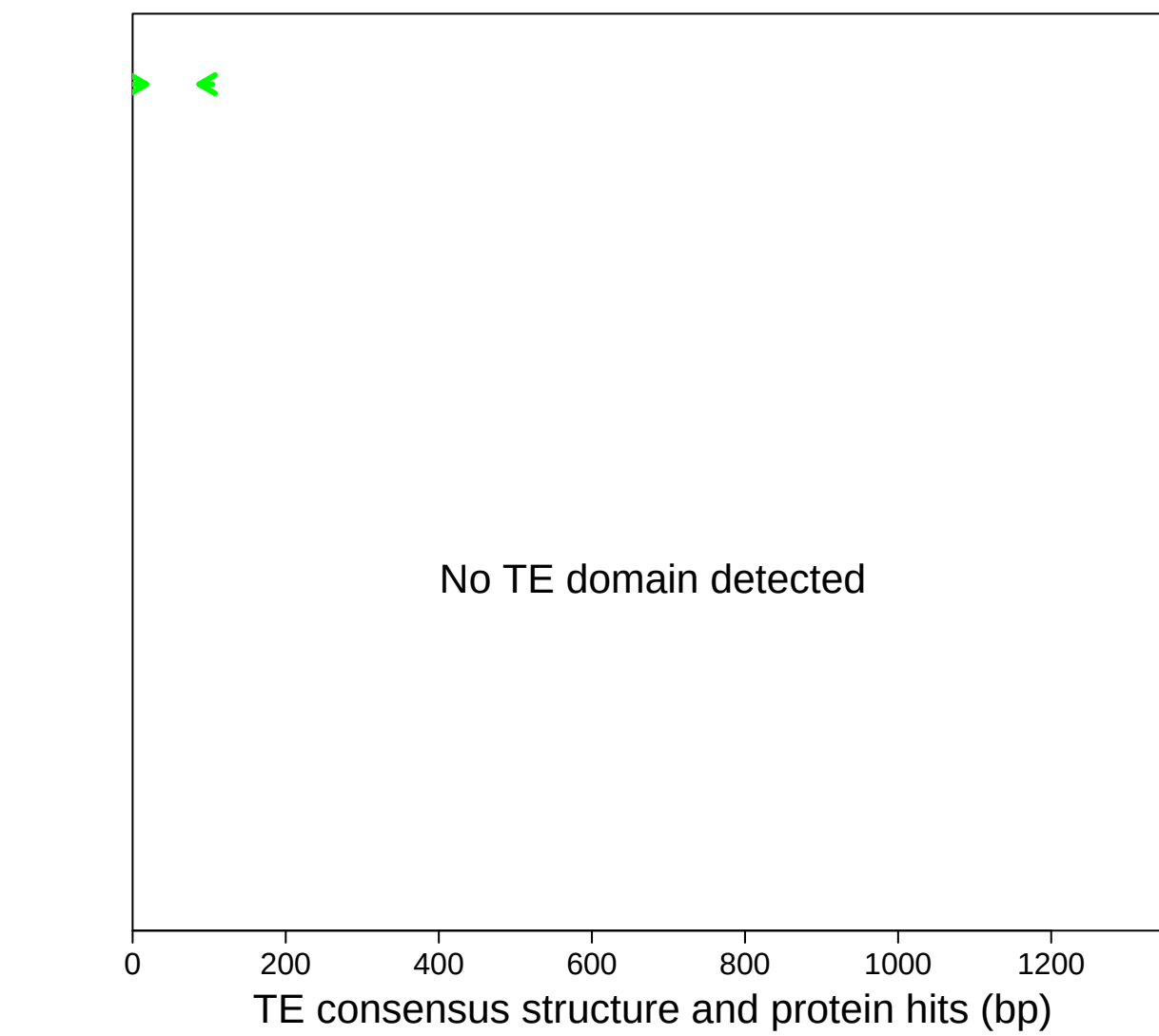
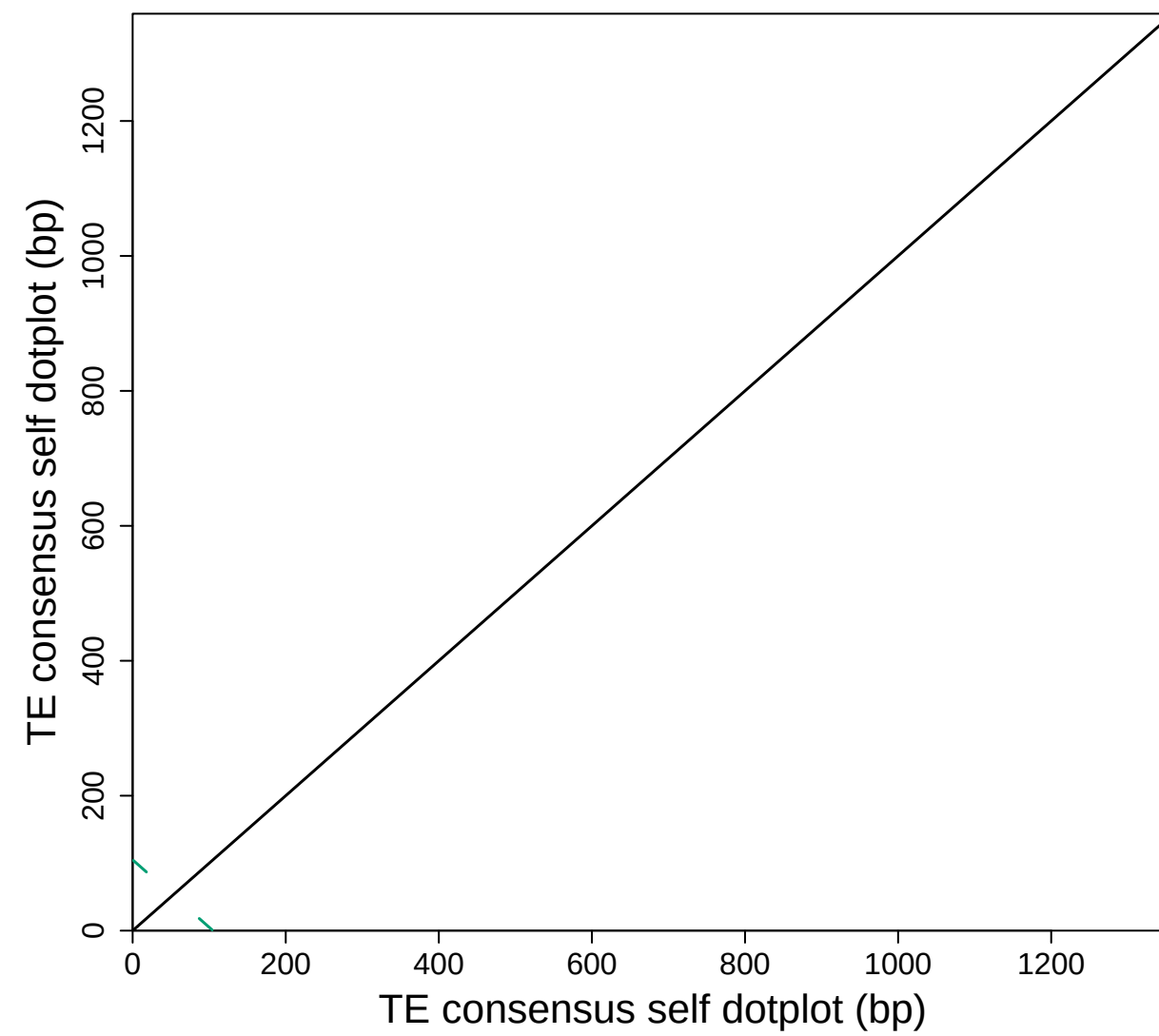
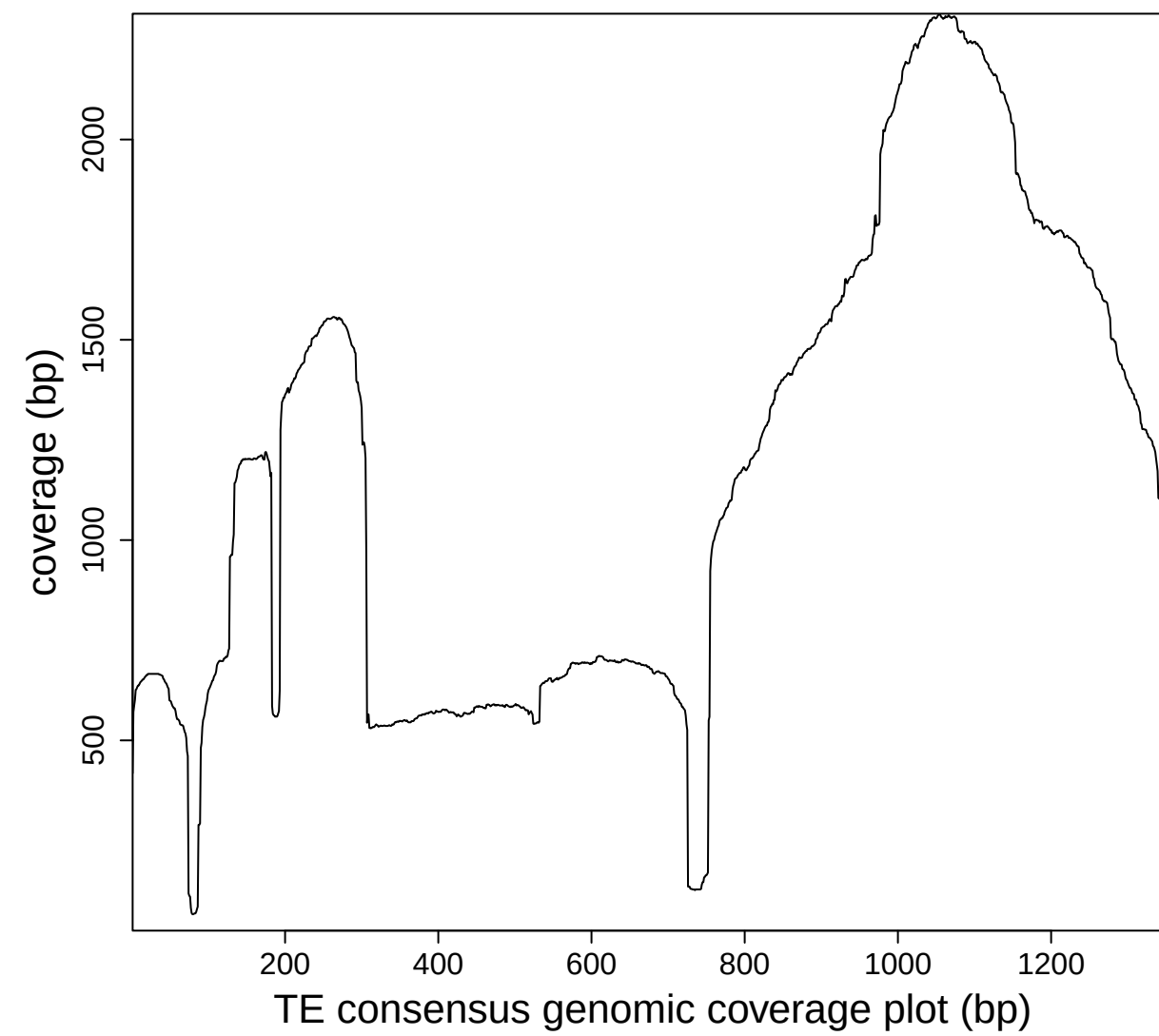
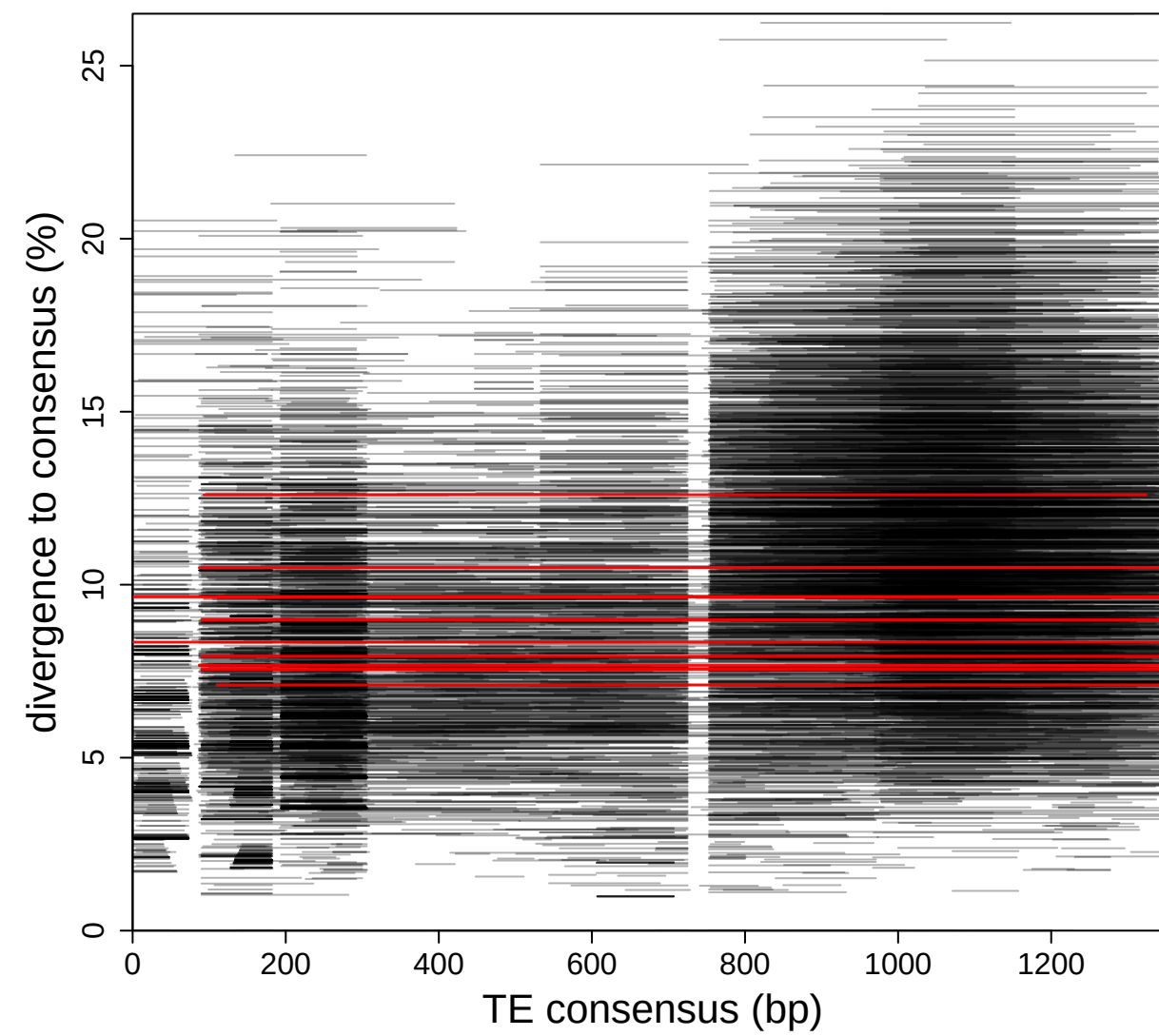
1500

1750



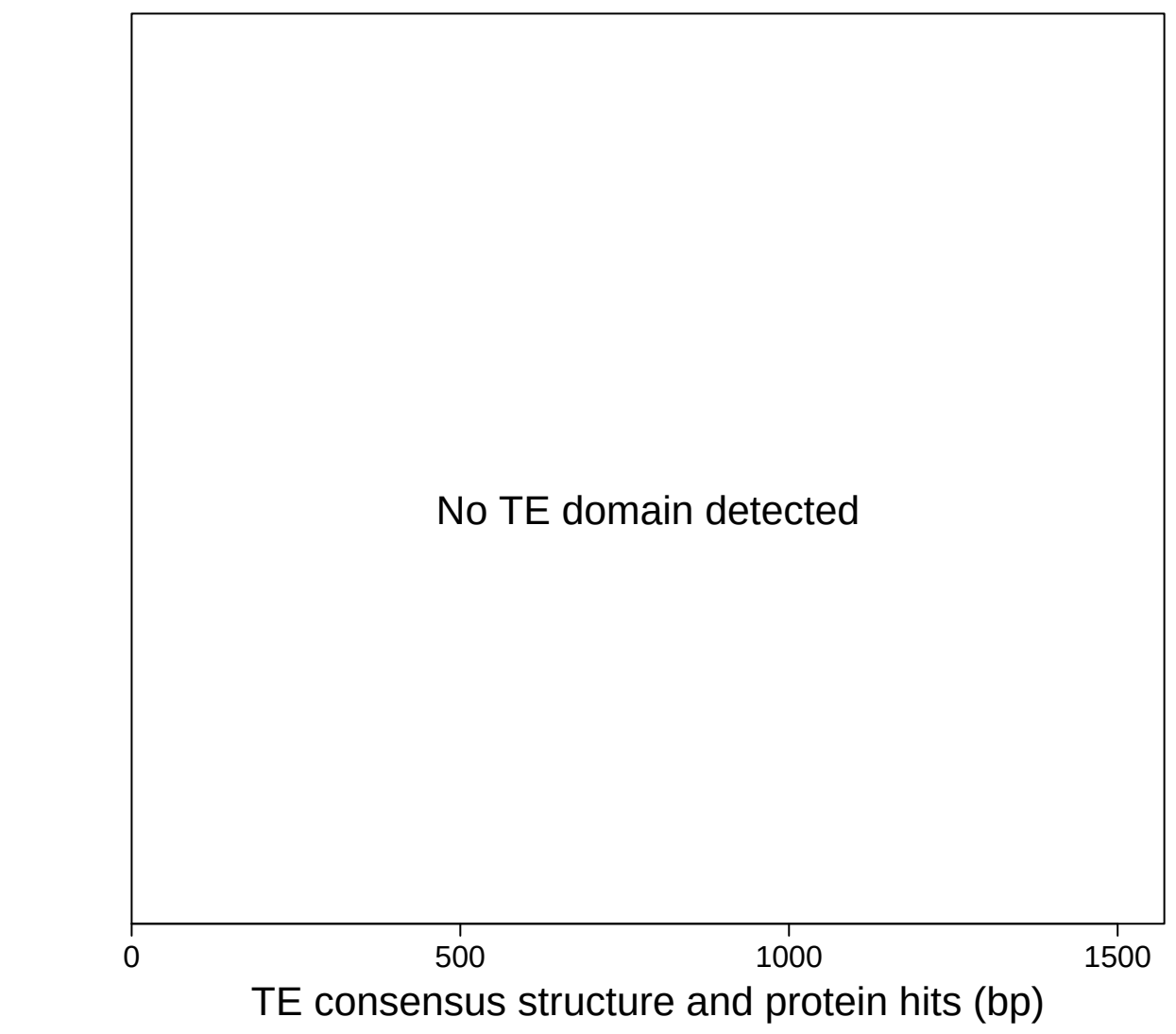
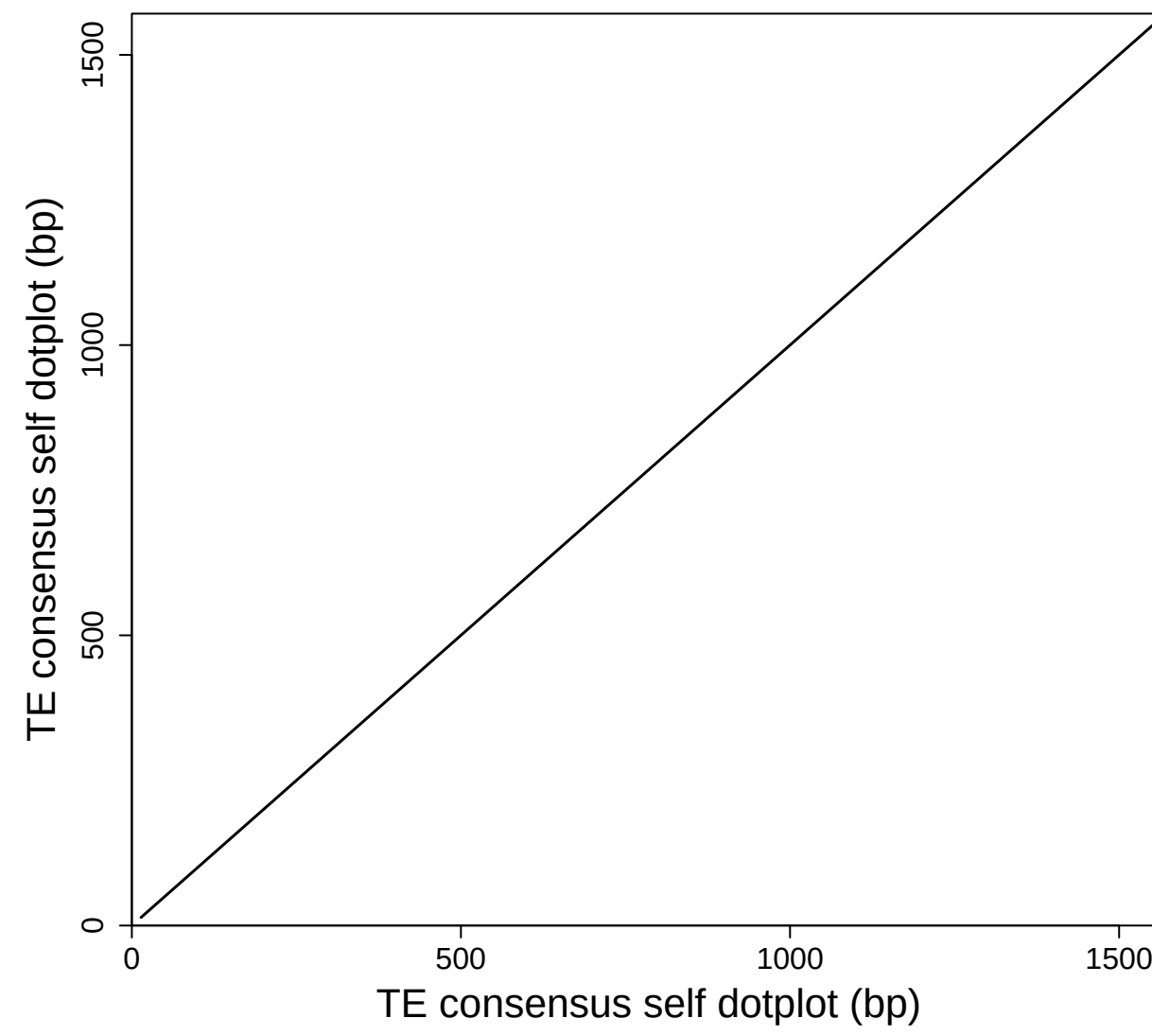
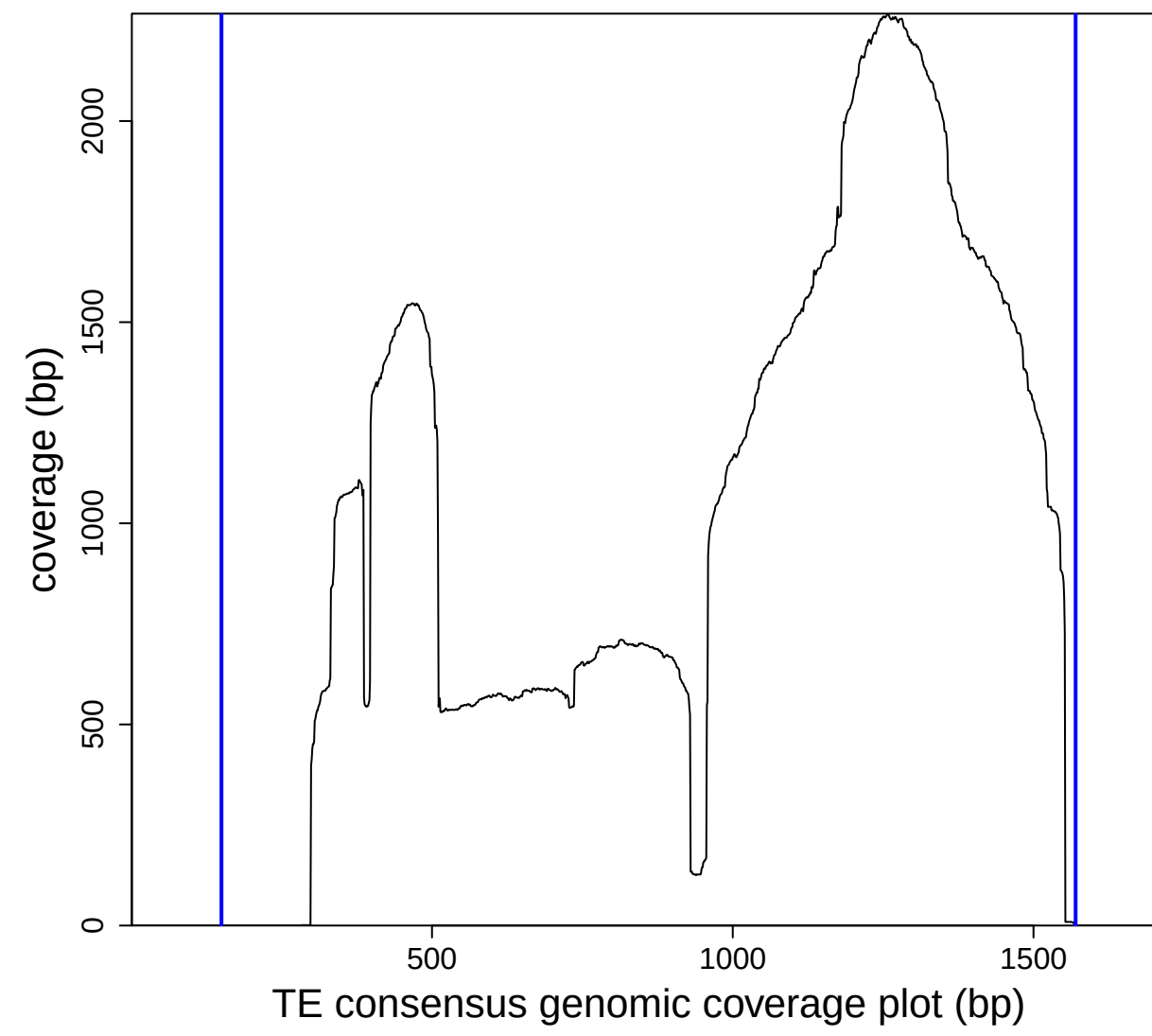
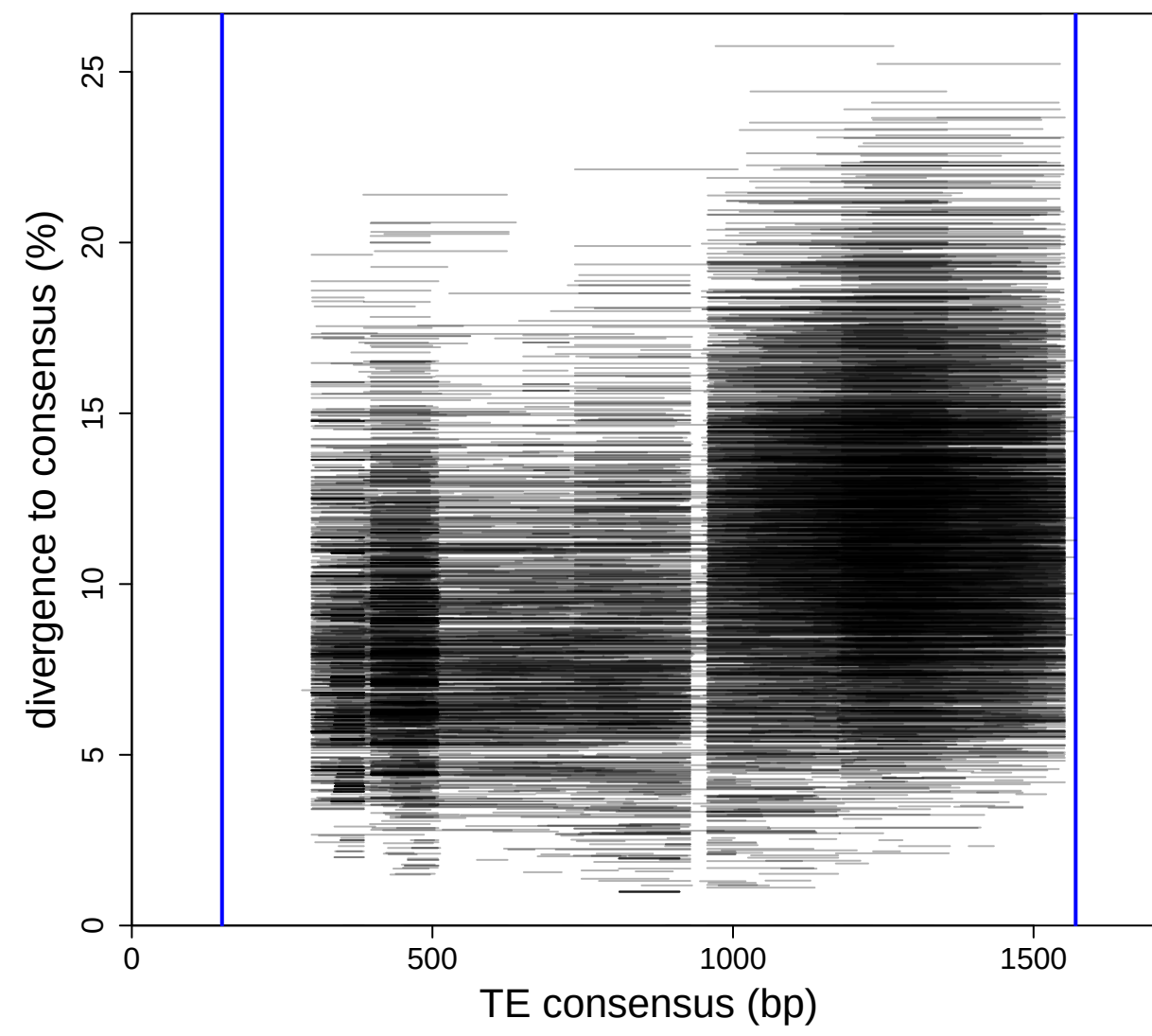
l.b.bed uf.bed g_2.bed fm_1.bed 0_0_bcln.fa aln.fa cl.fa gs.fa
size: 1359bp; fragments: 6485; full length: 11 (>=1223.1bp)

After TEtrimmer 1359 bp



2.fasta.b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa
size: 1720bp; fragments: 5617; full length: 0 (>=1548bp)

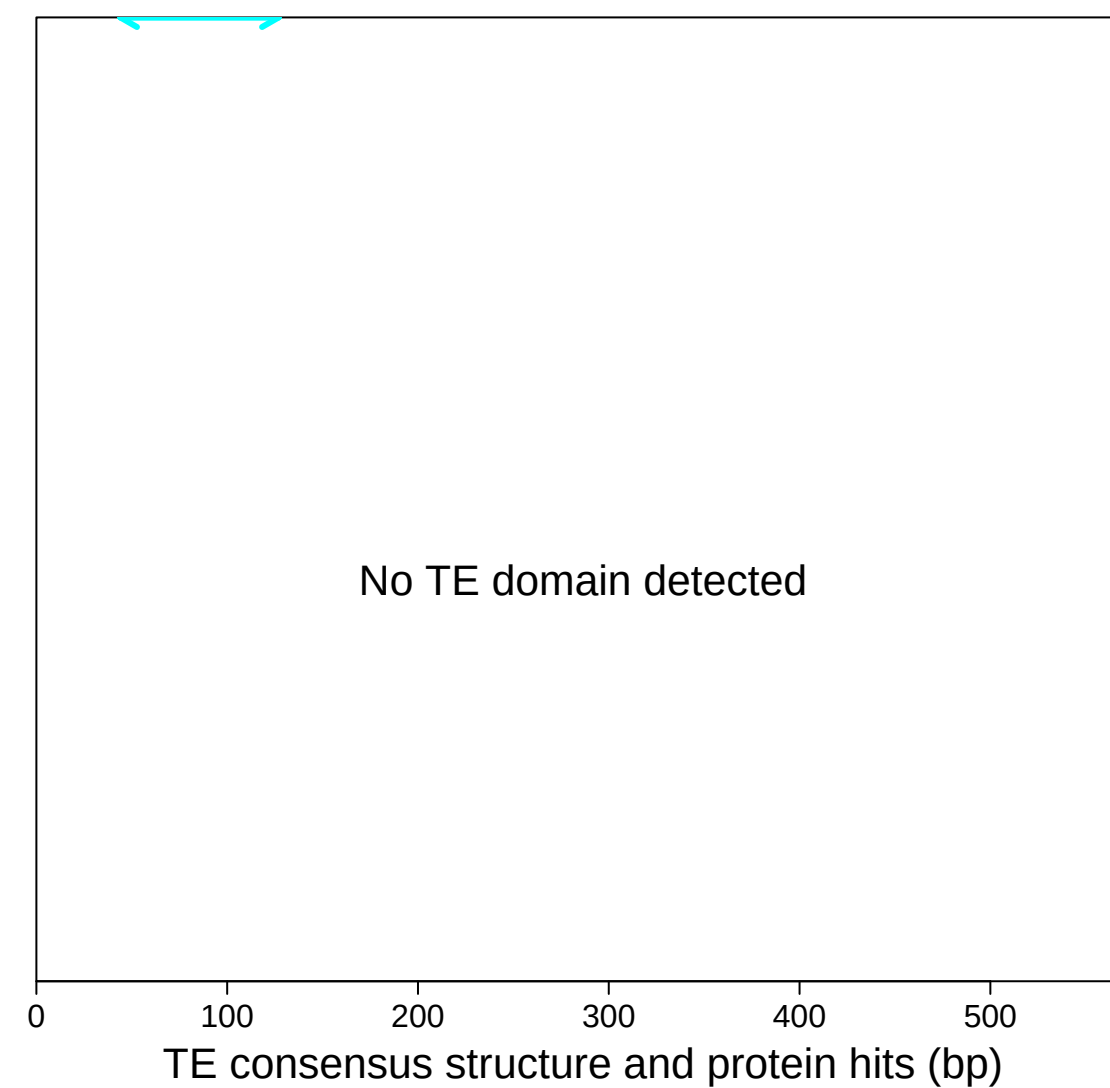
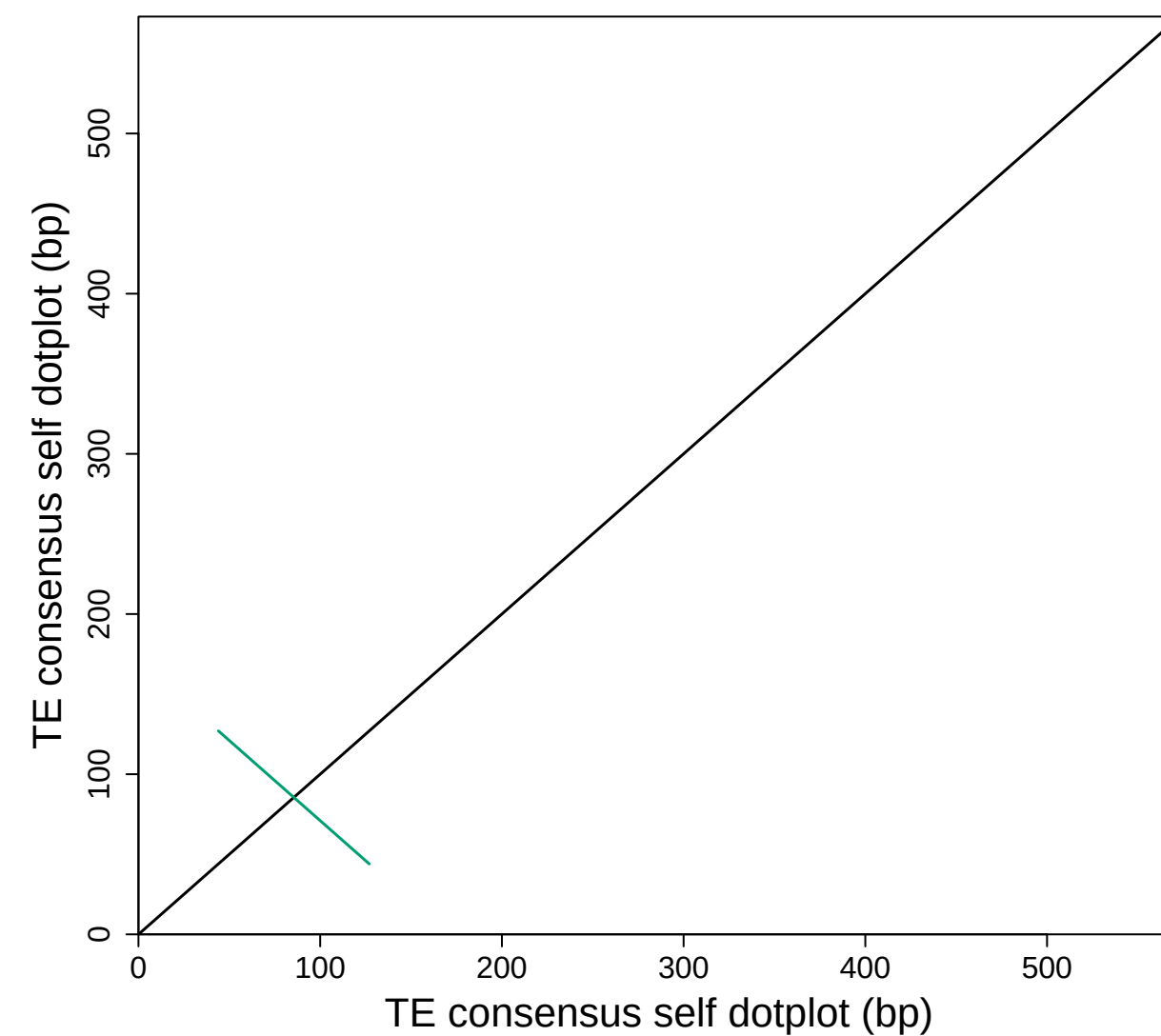
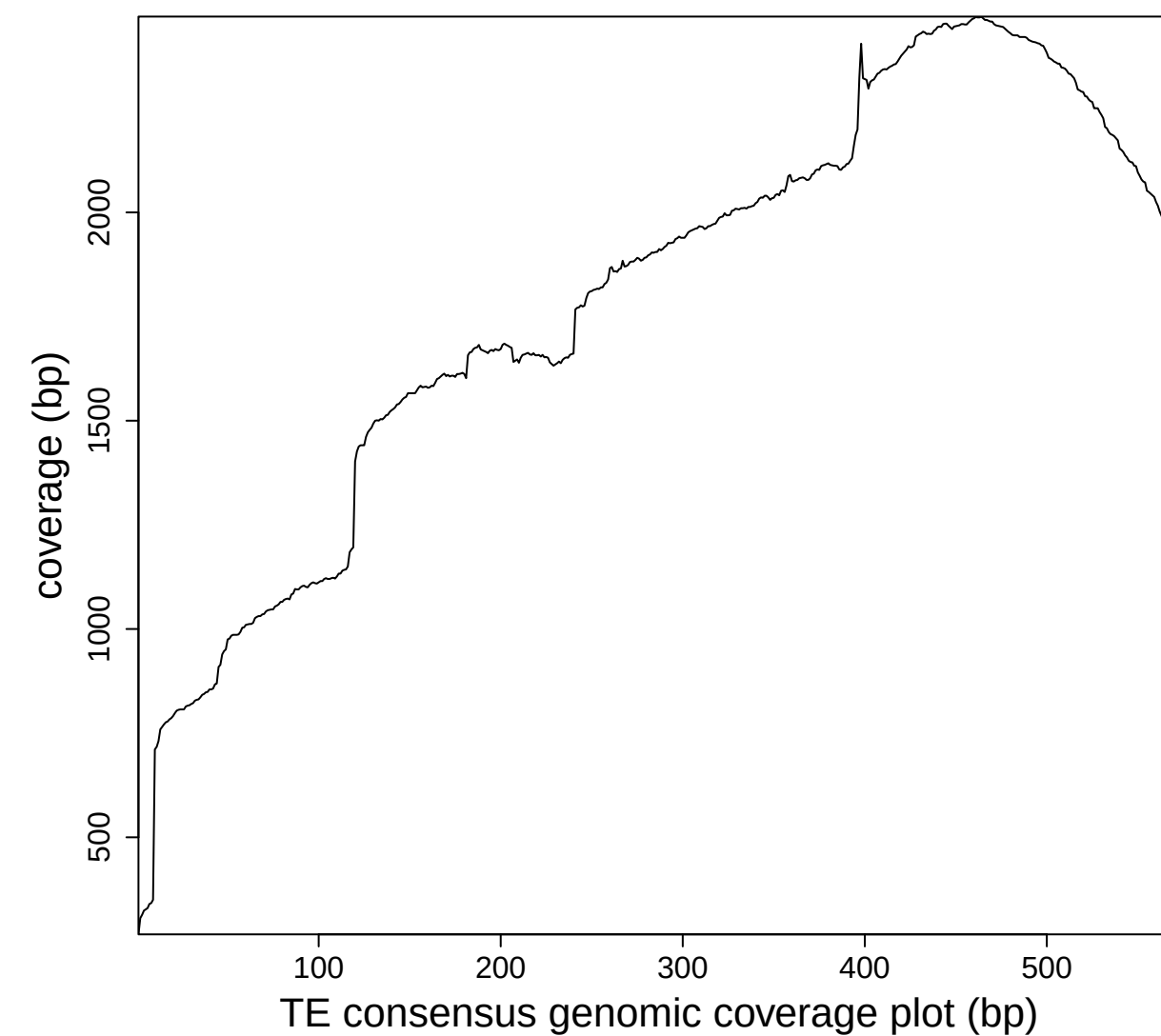
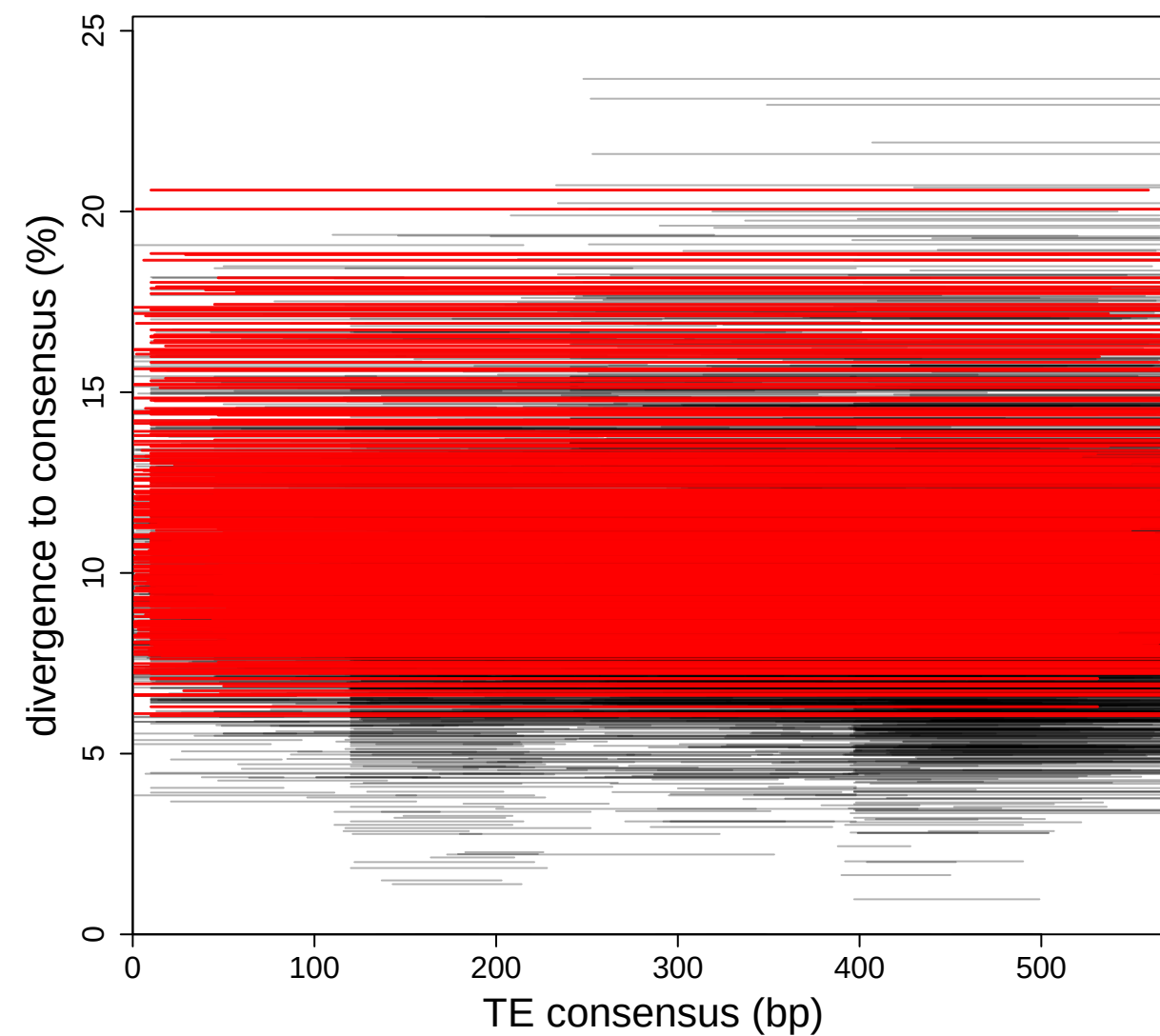
After TEtrimmer Extended plot Blue lines are boundaries



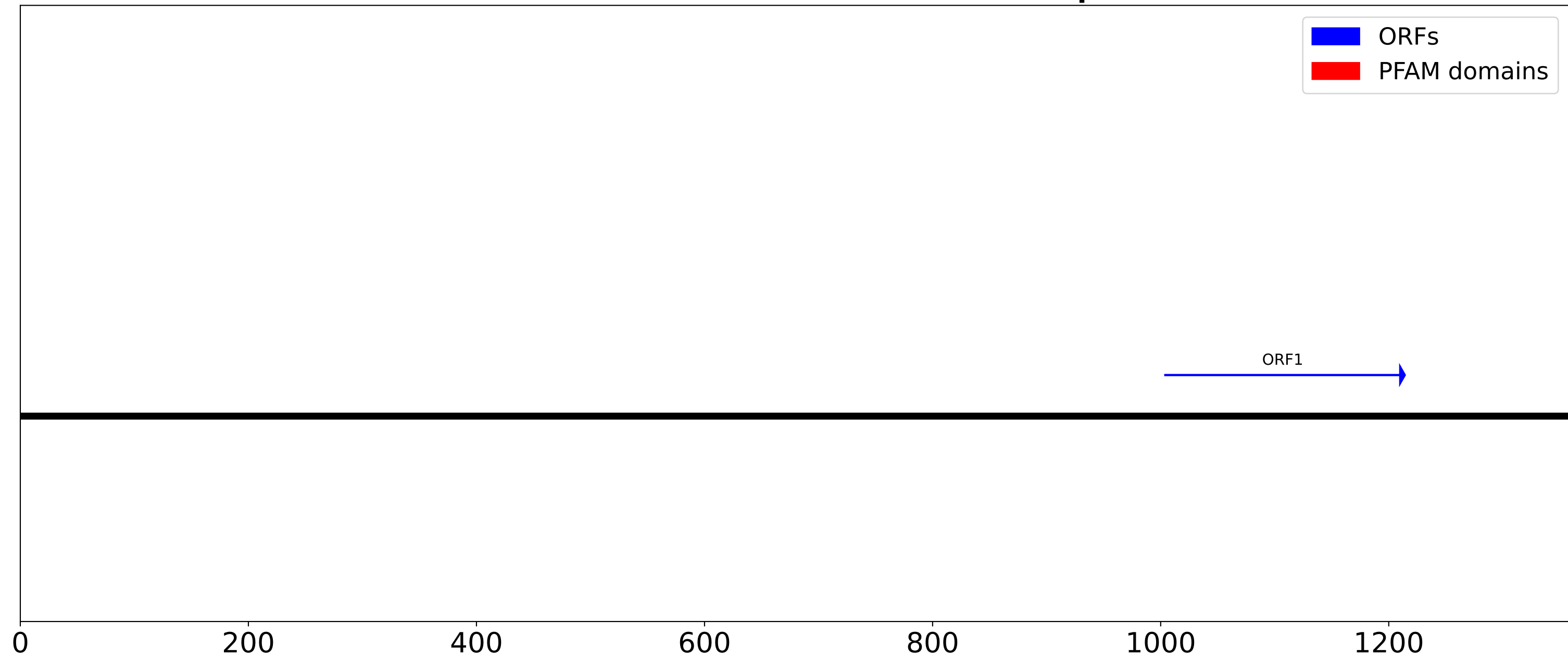
Before TEtrimmer 573 bp

TE: rnd_3_family_572

size: 573bp; fragments: 3521; full length: 413 (≥ 515.7 bp)



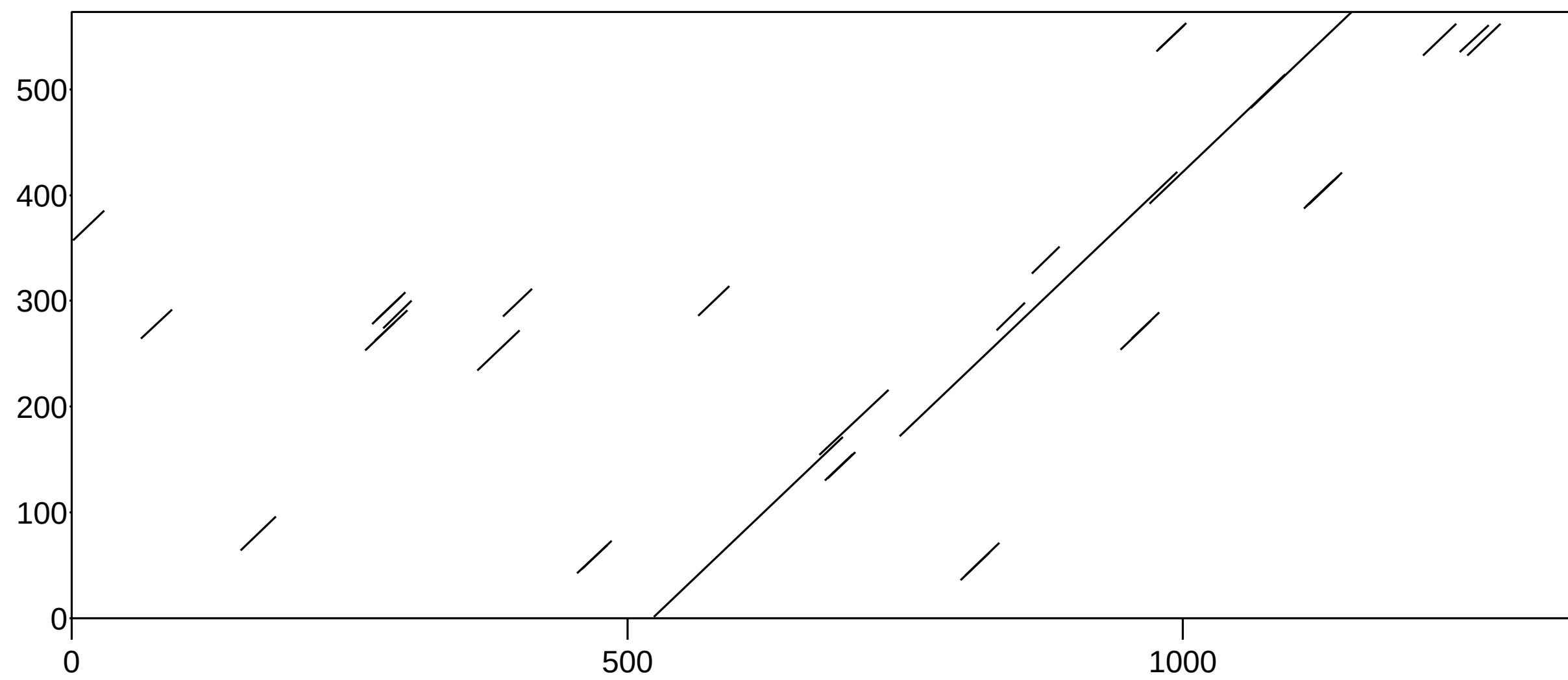
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)