

Start crop Point



End crop Point



MSA length = 2375



Start crop Point

End crop Point

0

10

0

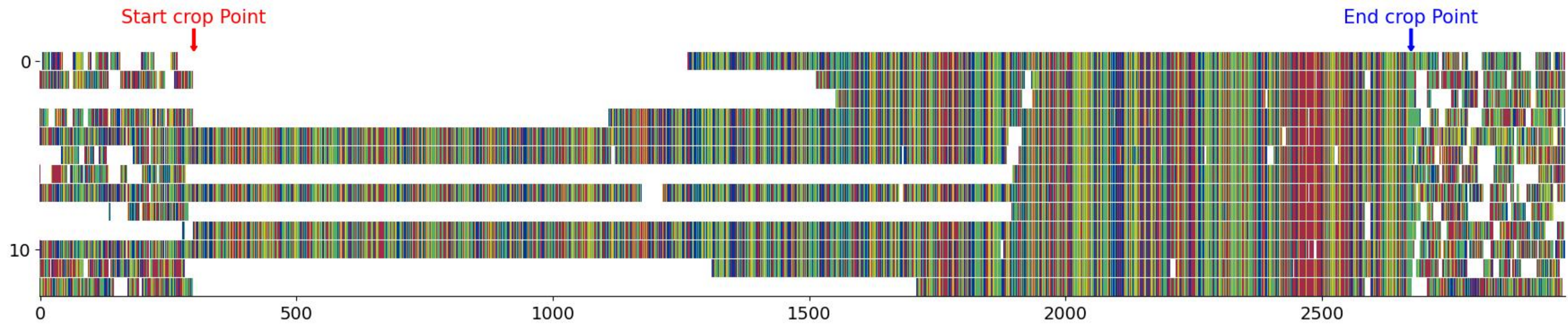
500

1000

1500

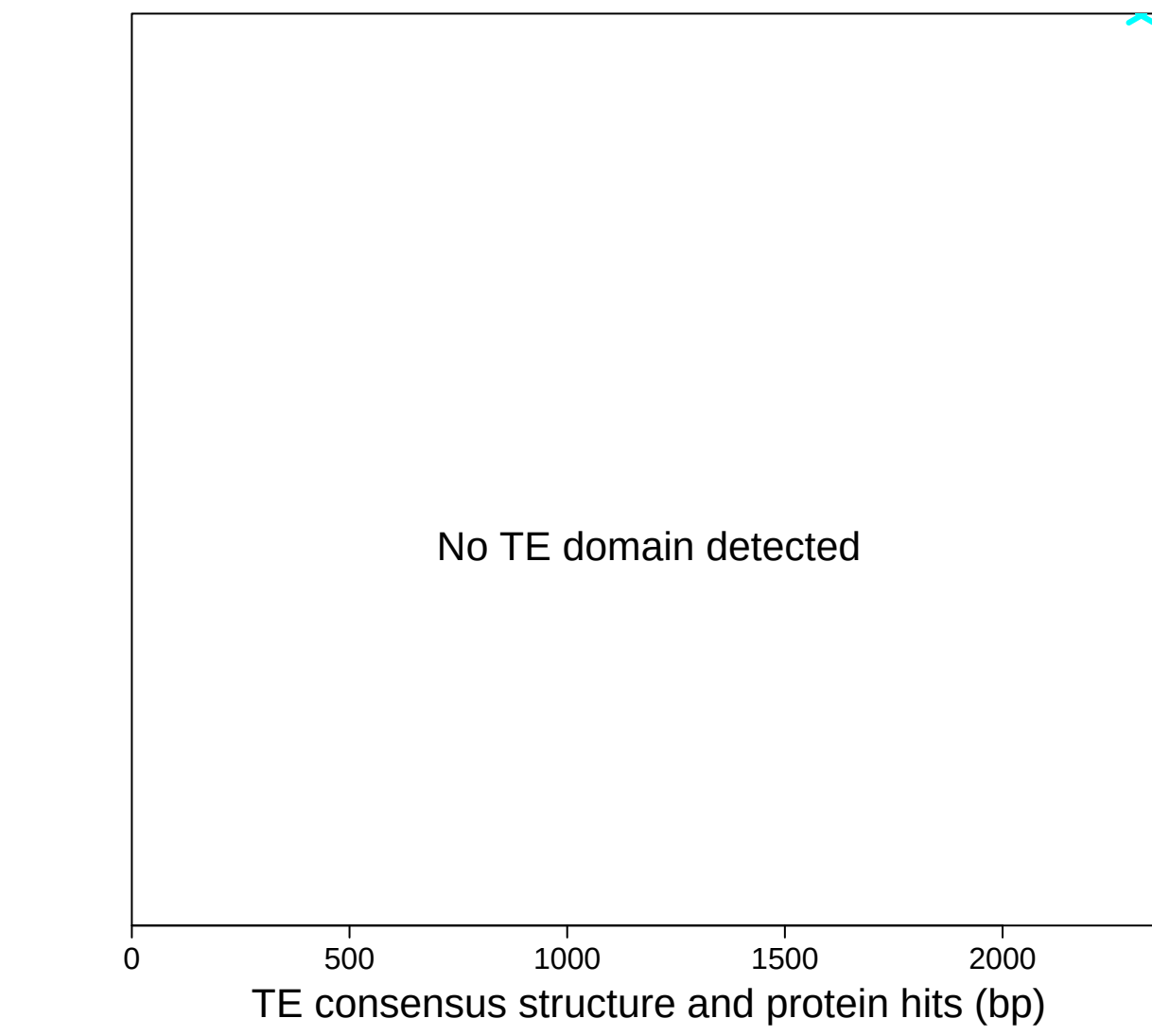
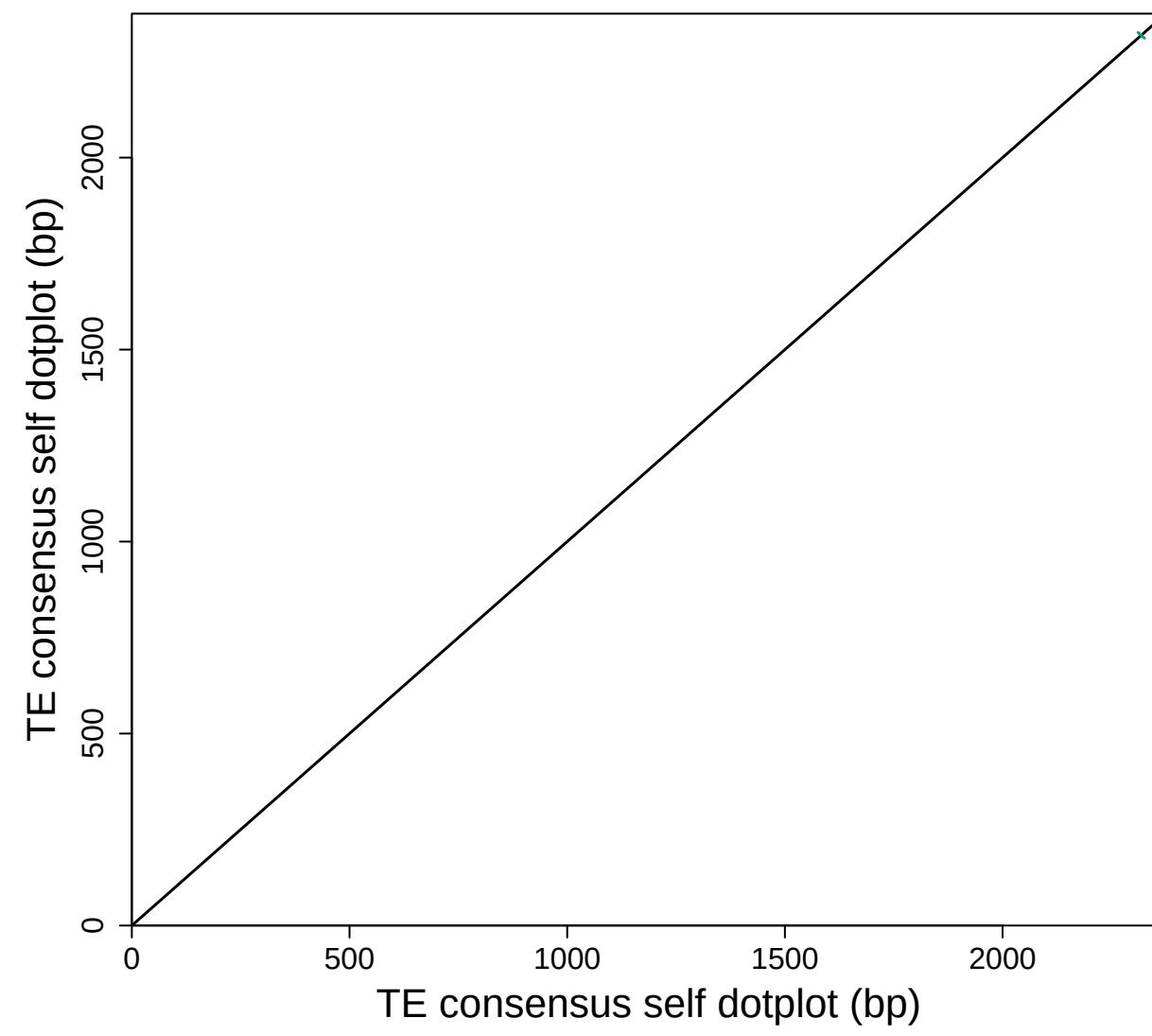
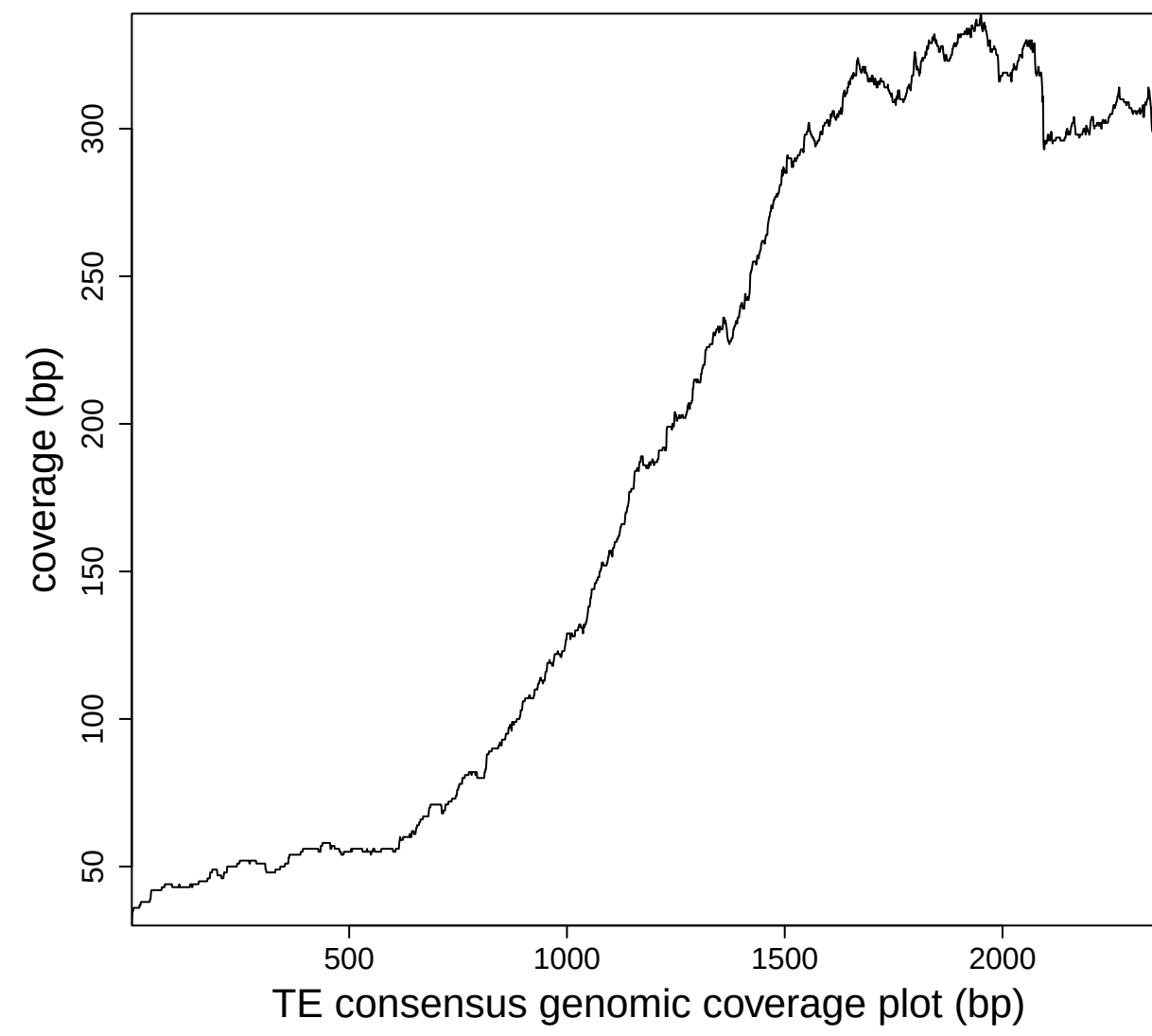
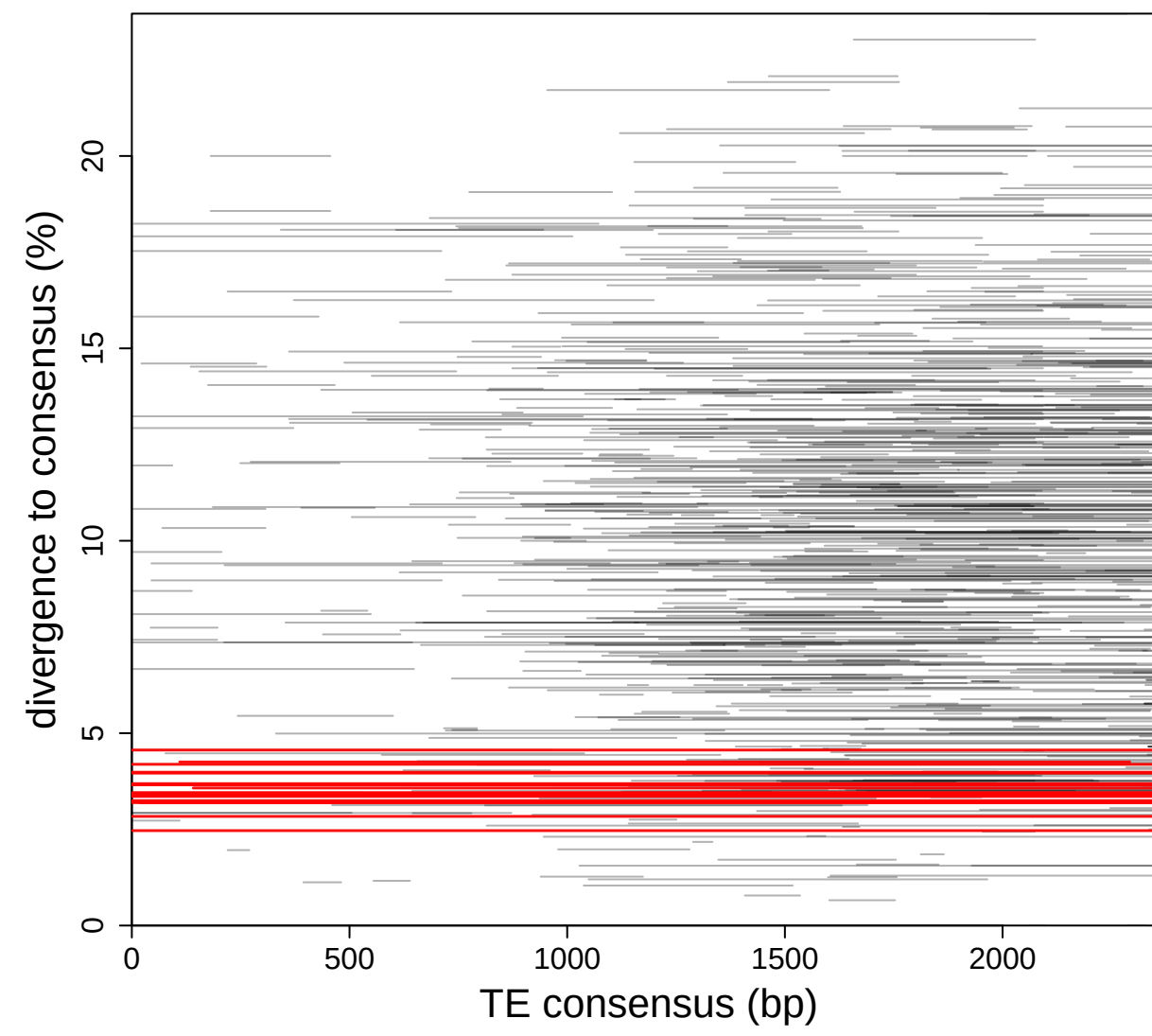
2000

2500



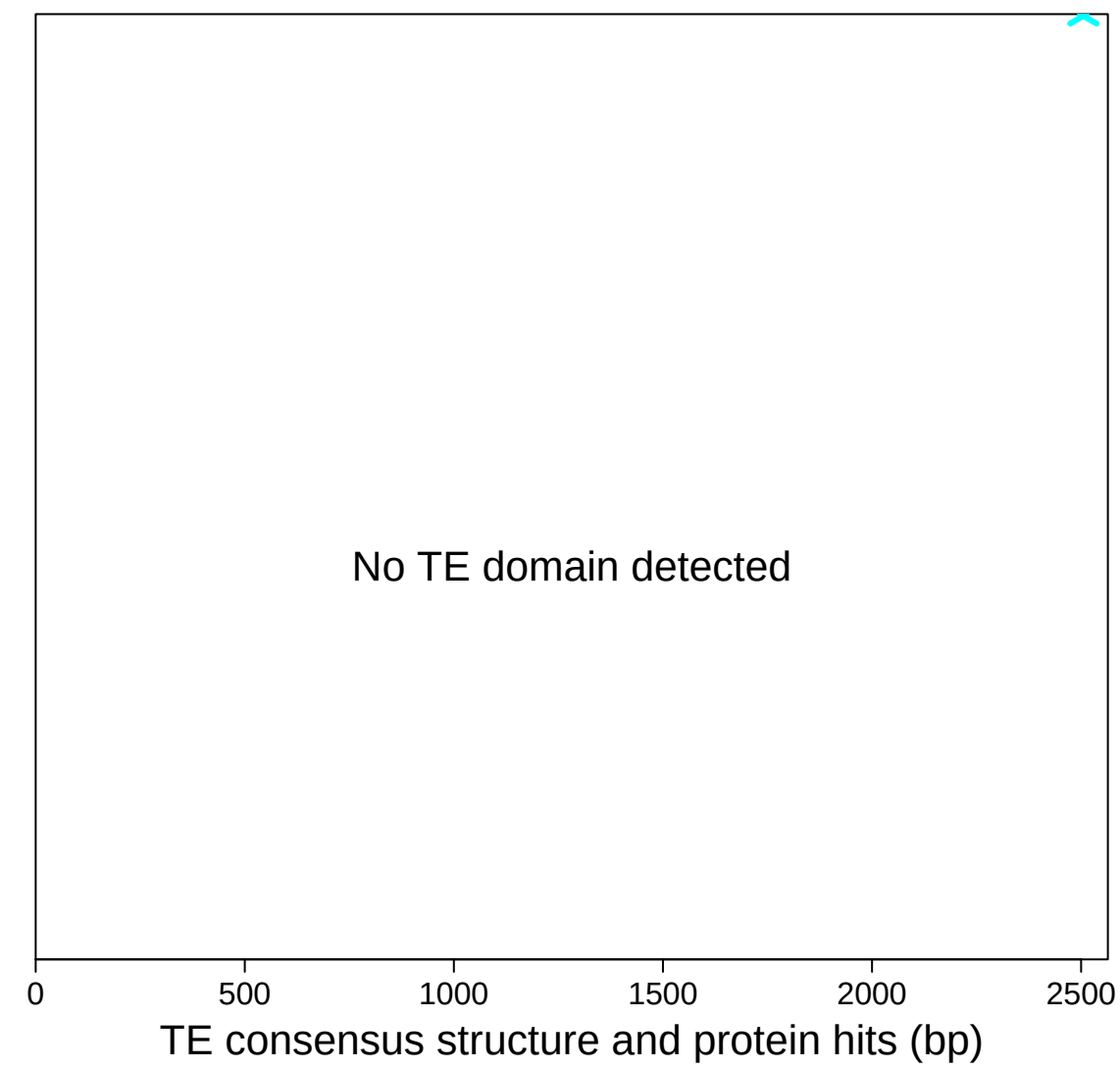
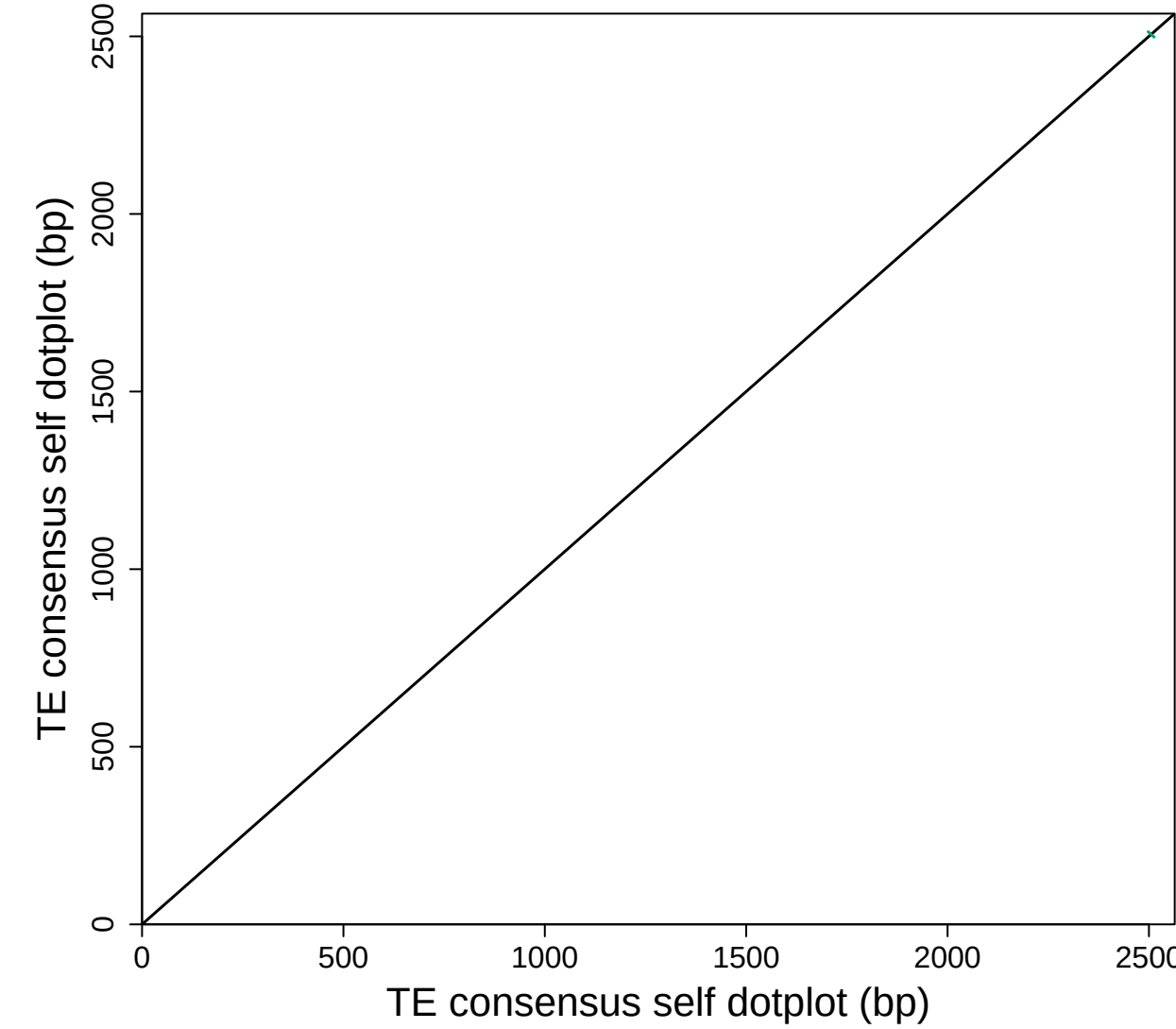
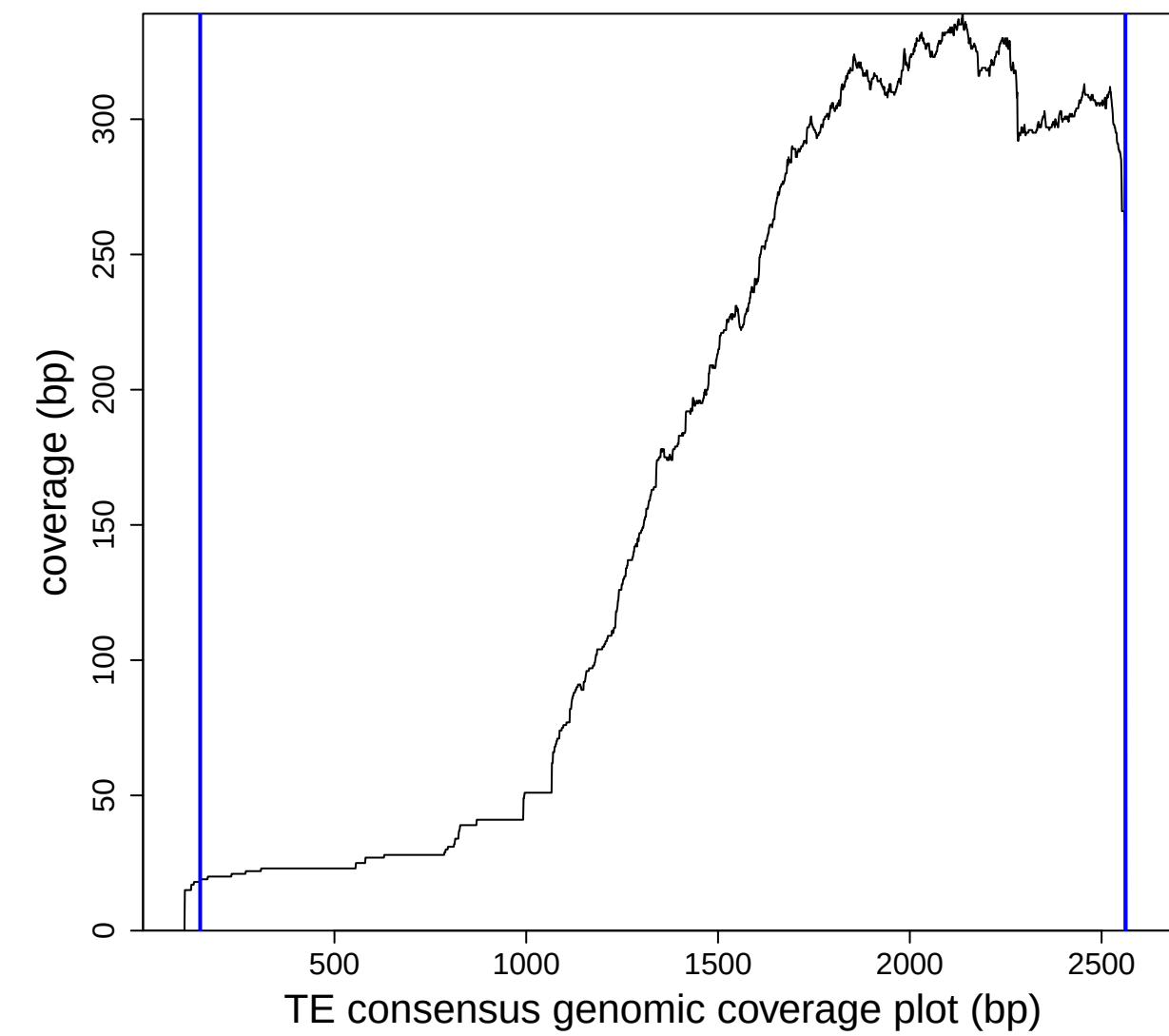
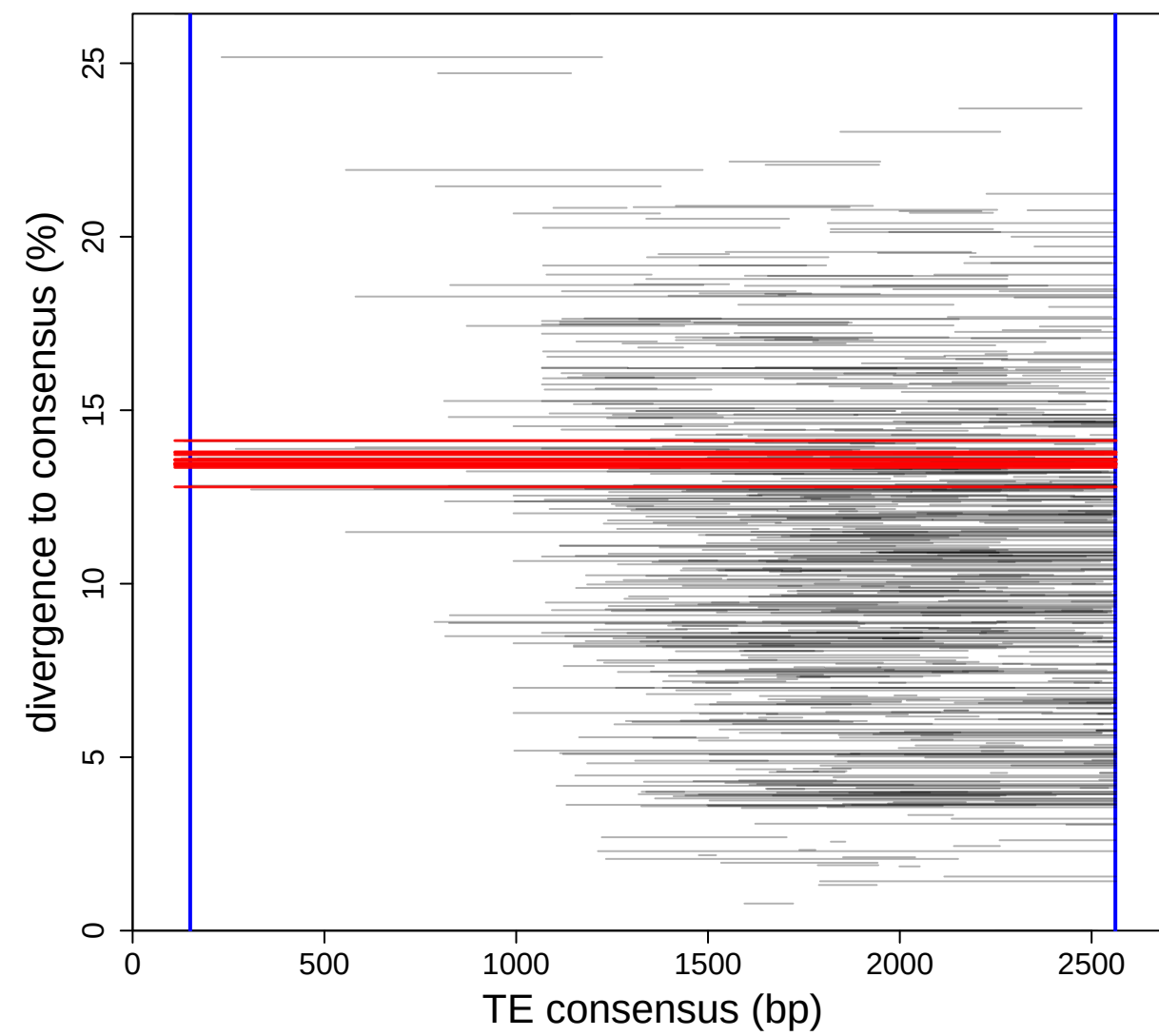
bed_uf.bed g_2.bed fm_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c
size: 2375bp; fragments: 783; full length: 21 (≥ 2137.5 bp)

After TEtrimmer 2375 bp

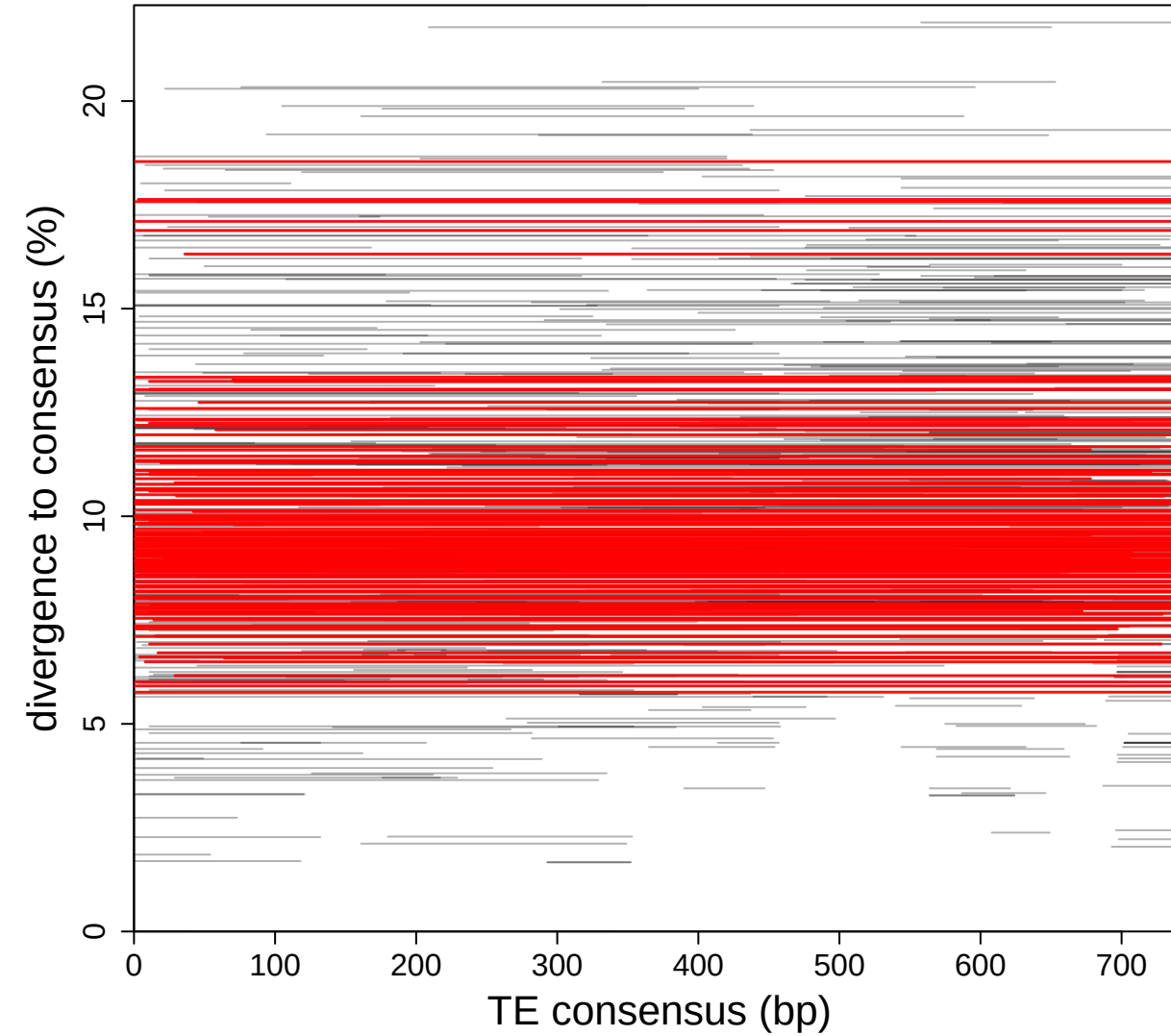


4.fasta.b.bed uf.bed g_2.bed fm_1.bed 0 0 bcIn.fa aln.fa cl.f
size: 2712bp; fragments: 712; full length: 14 (>=2440.8bp)

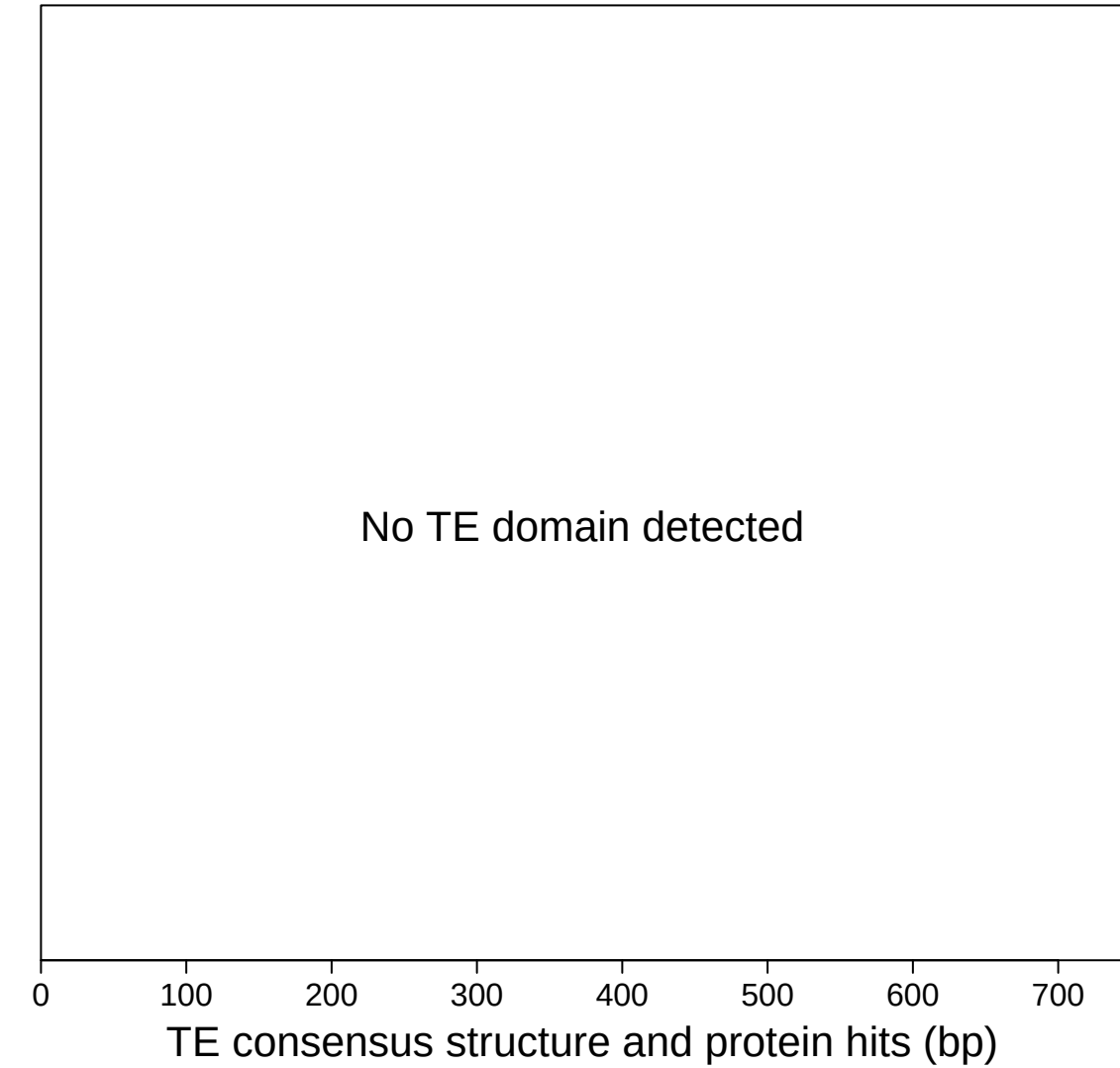
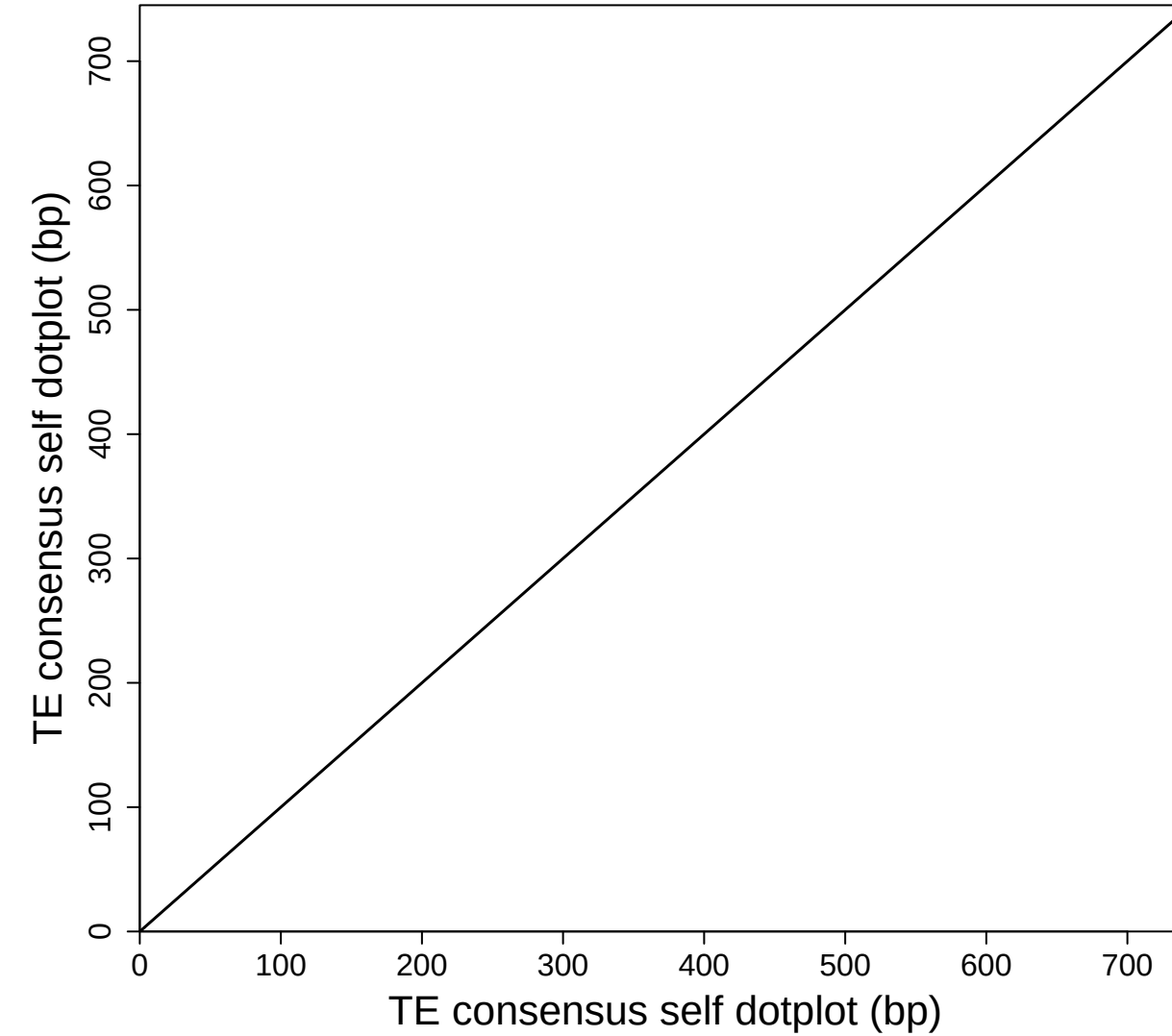
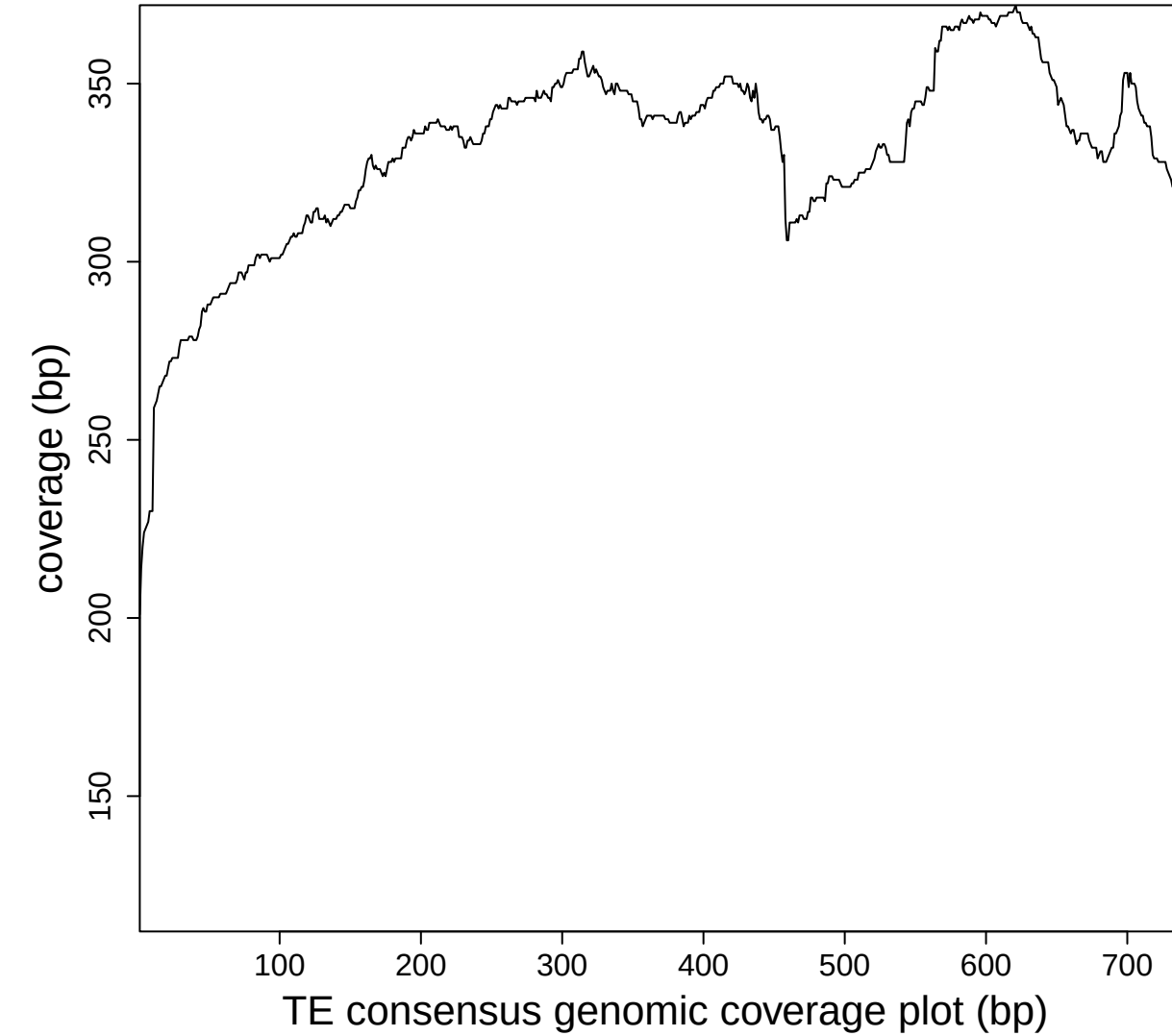
After TEtrimmer Extended plot Blue lines are boundaries



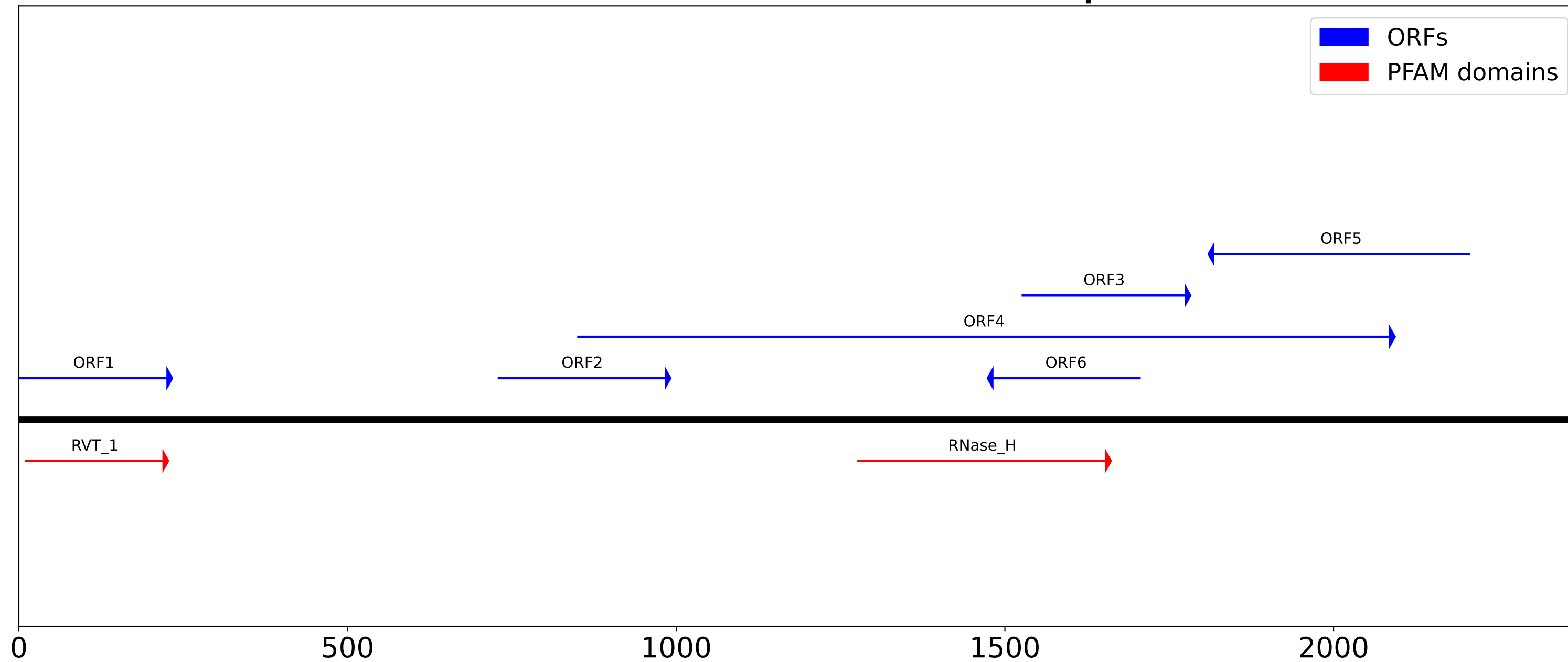
TE: rnd_4_family_3624
size: 745bp; fragments: 659; full length: 147 (≥ 670.5 bp)



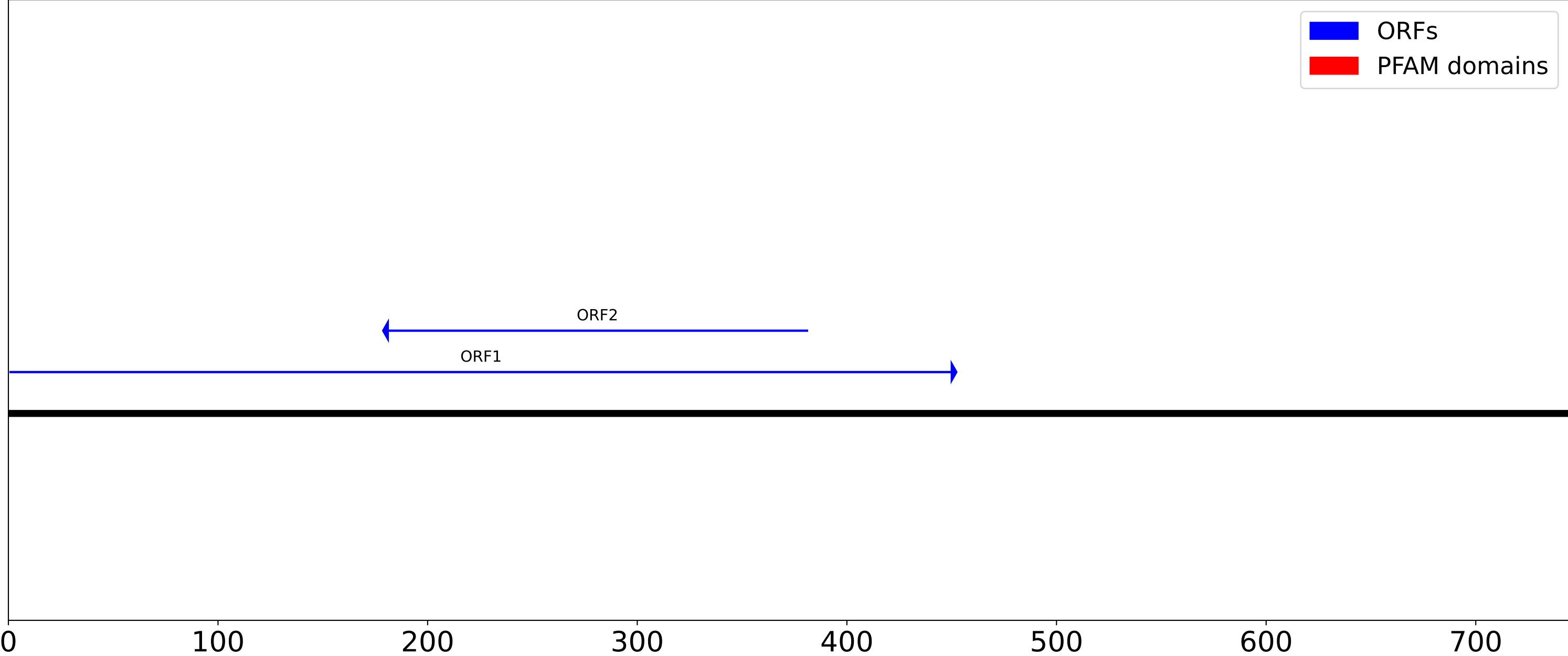
Before TEtrimmer 745 bp



After TEtrimmer ORF and PFAM domain plot



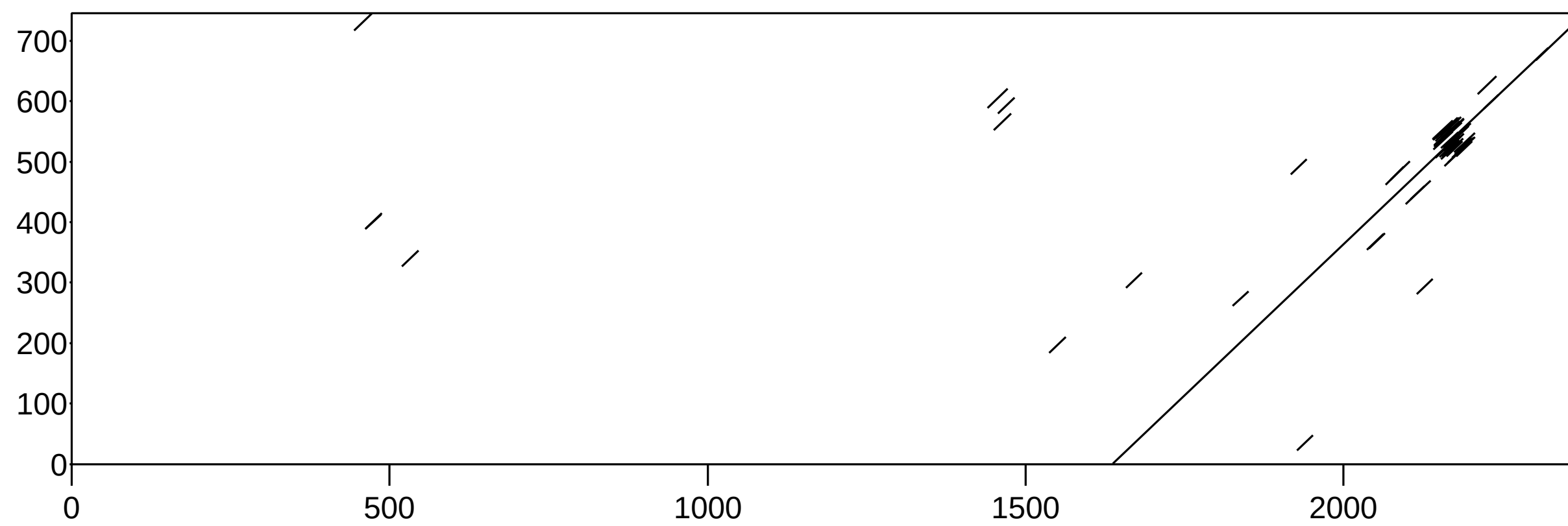
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)