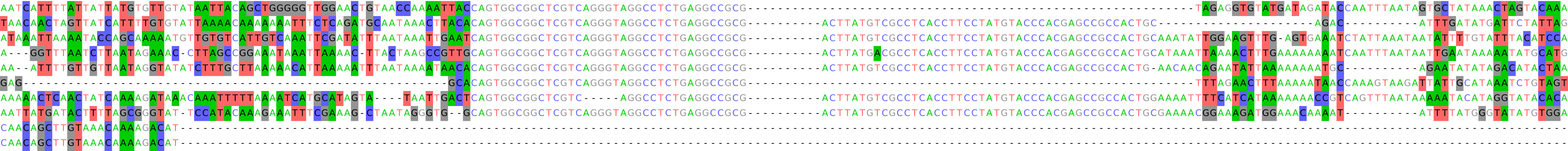


MSA length = 3360

Start Crop Point

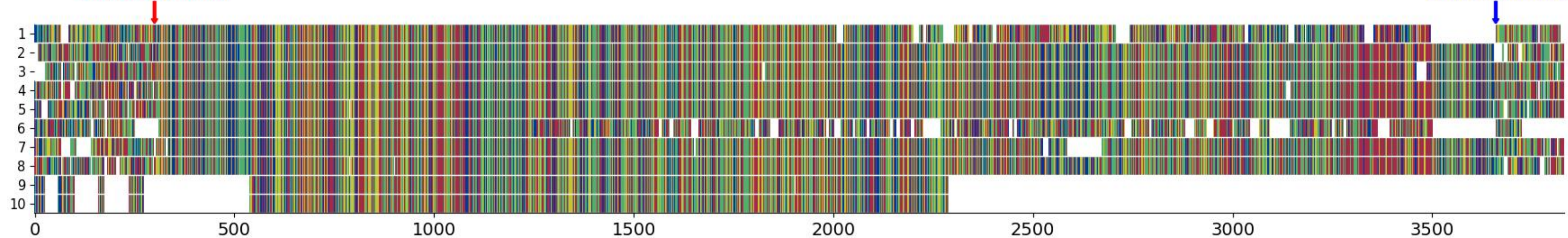


End Crop Point



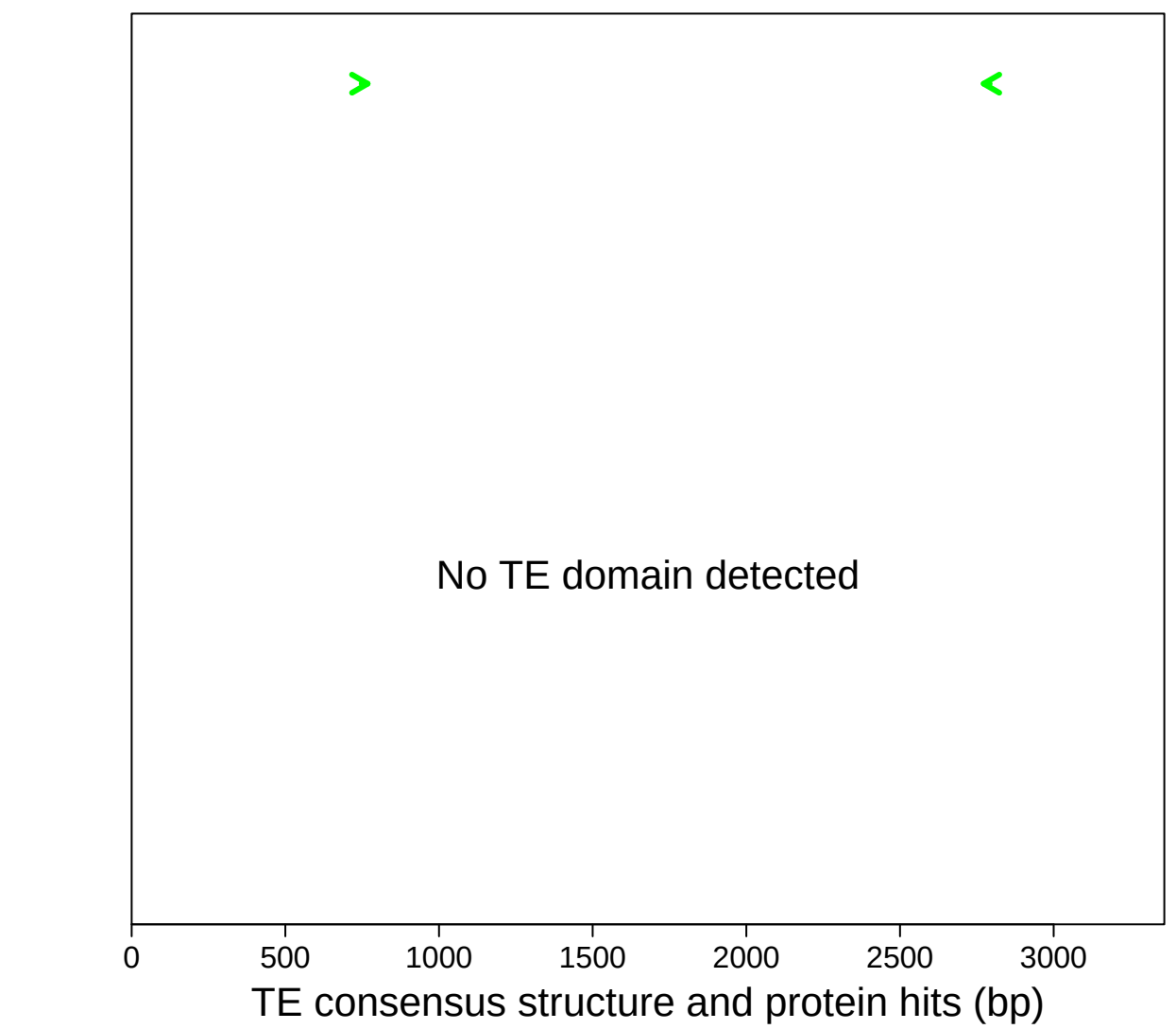
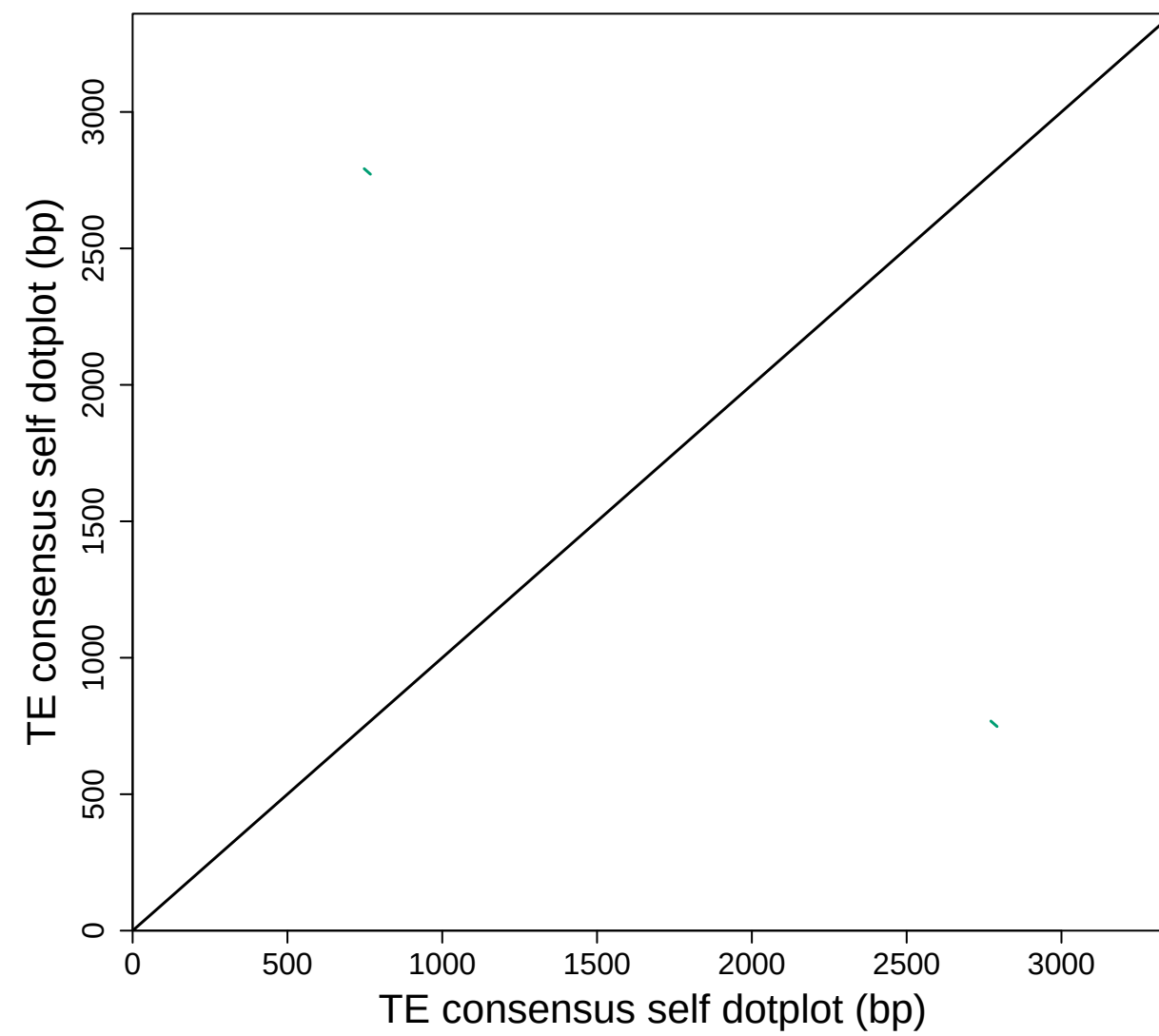
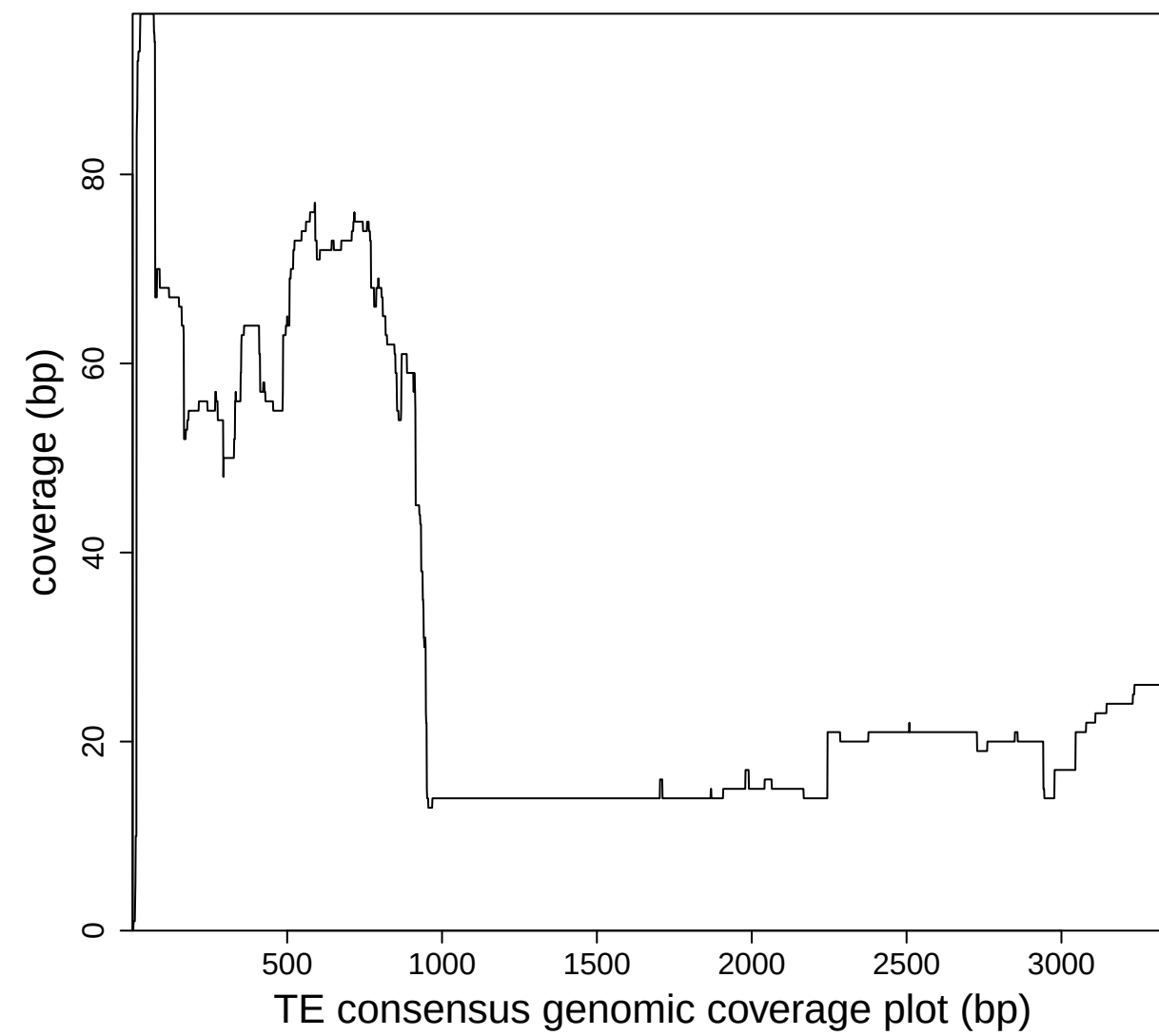
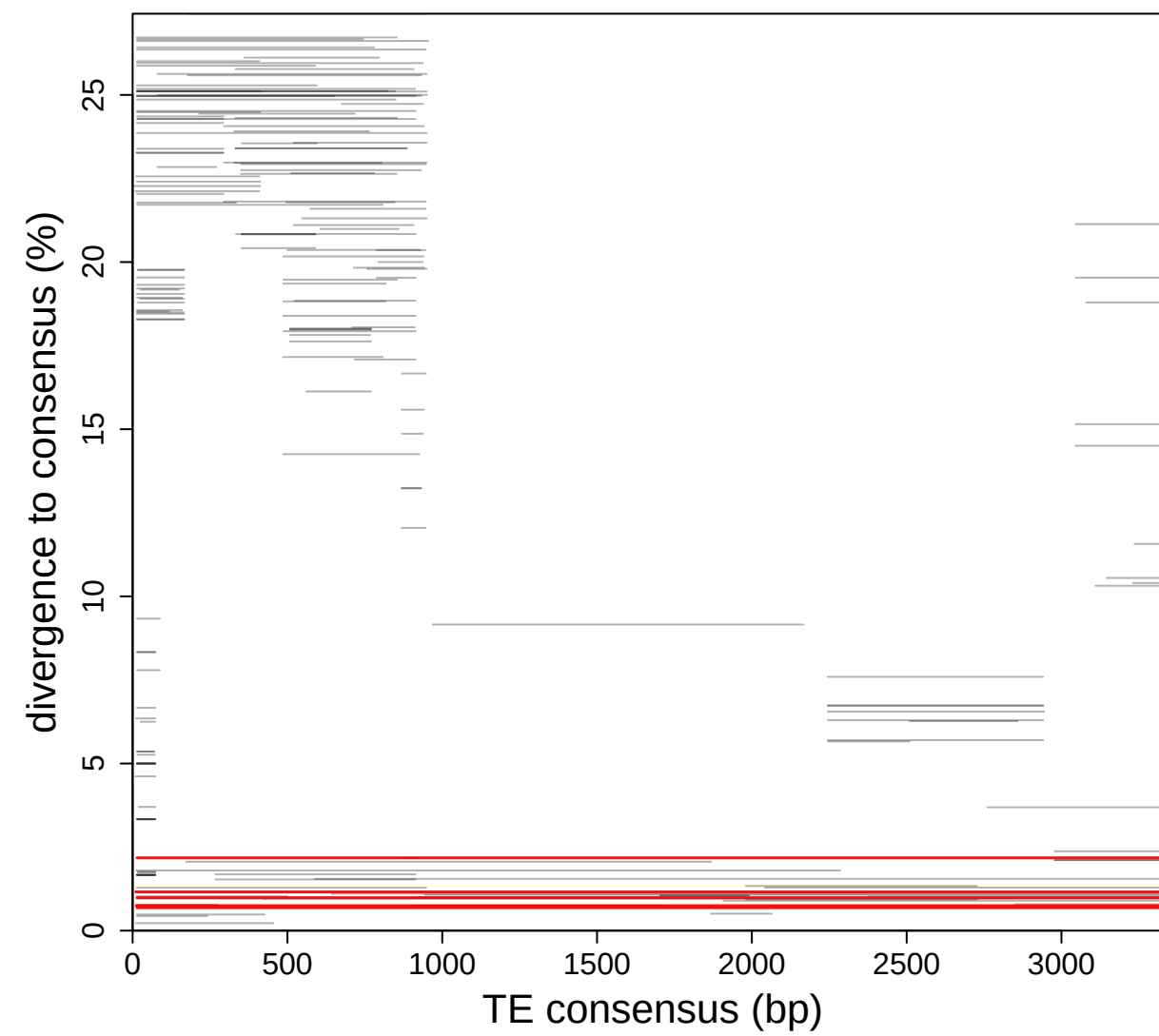
Start crop Point

End crop Point



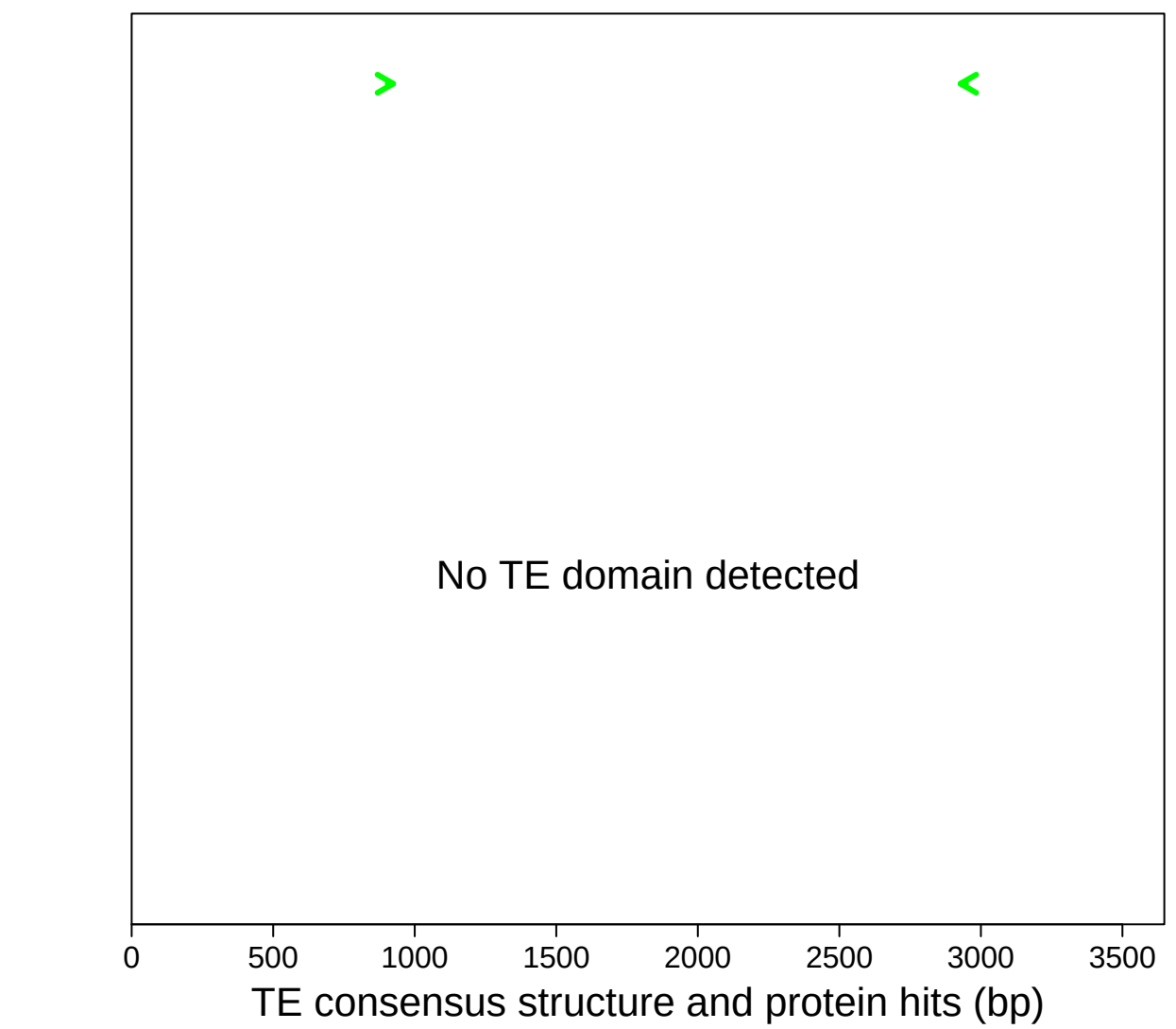
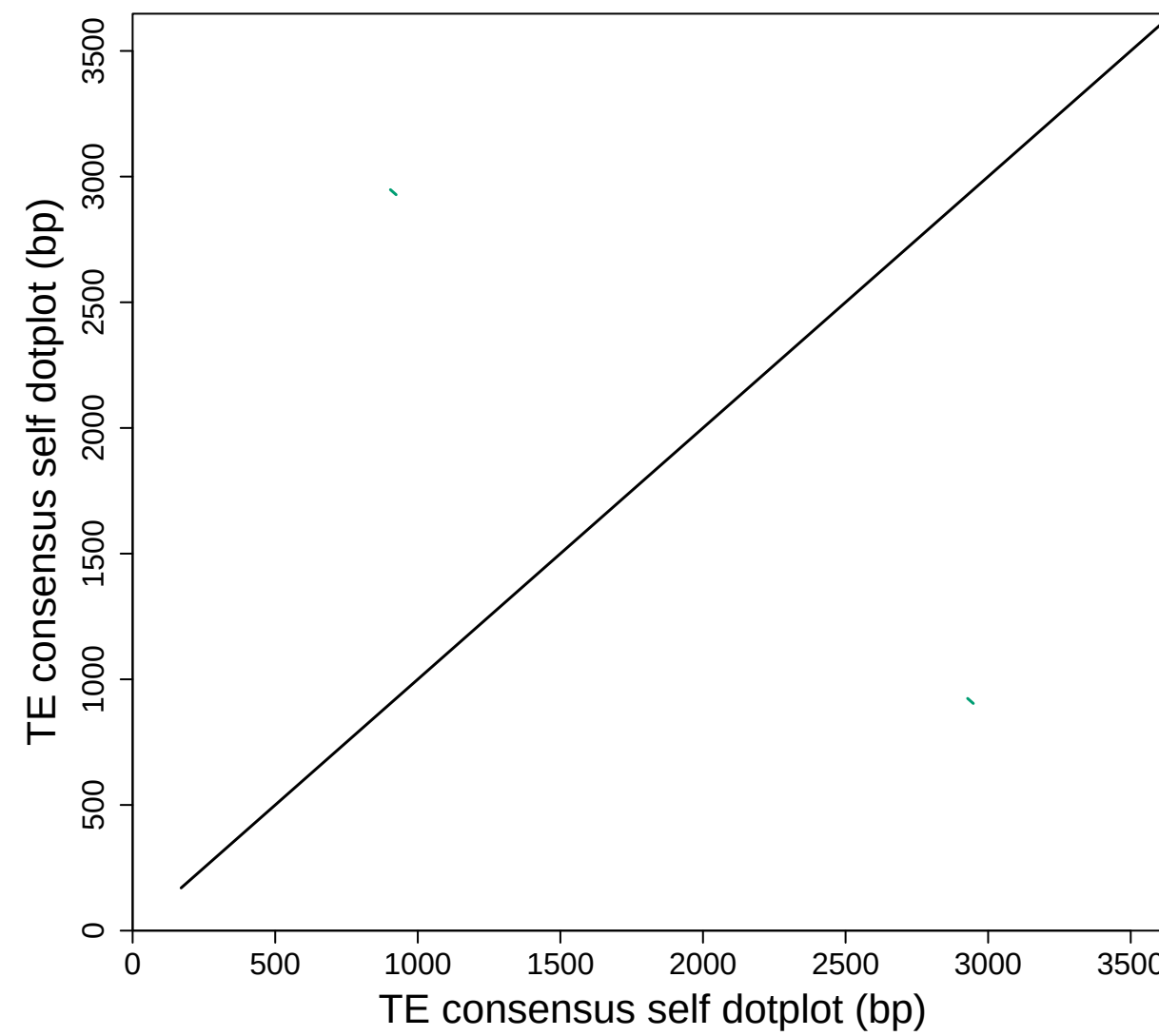
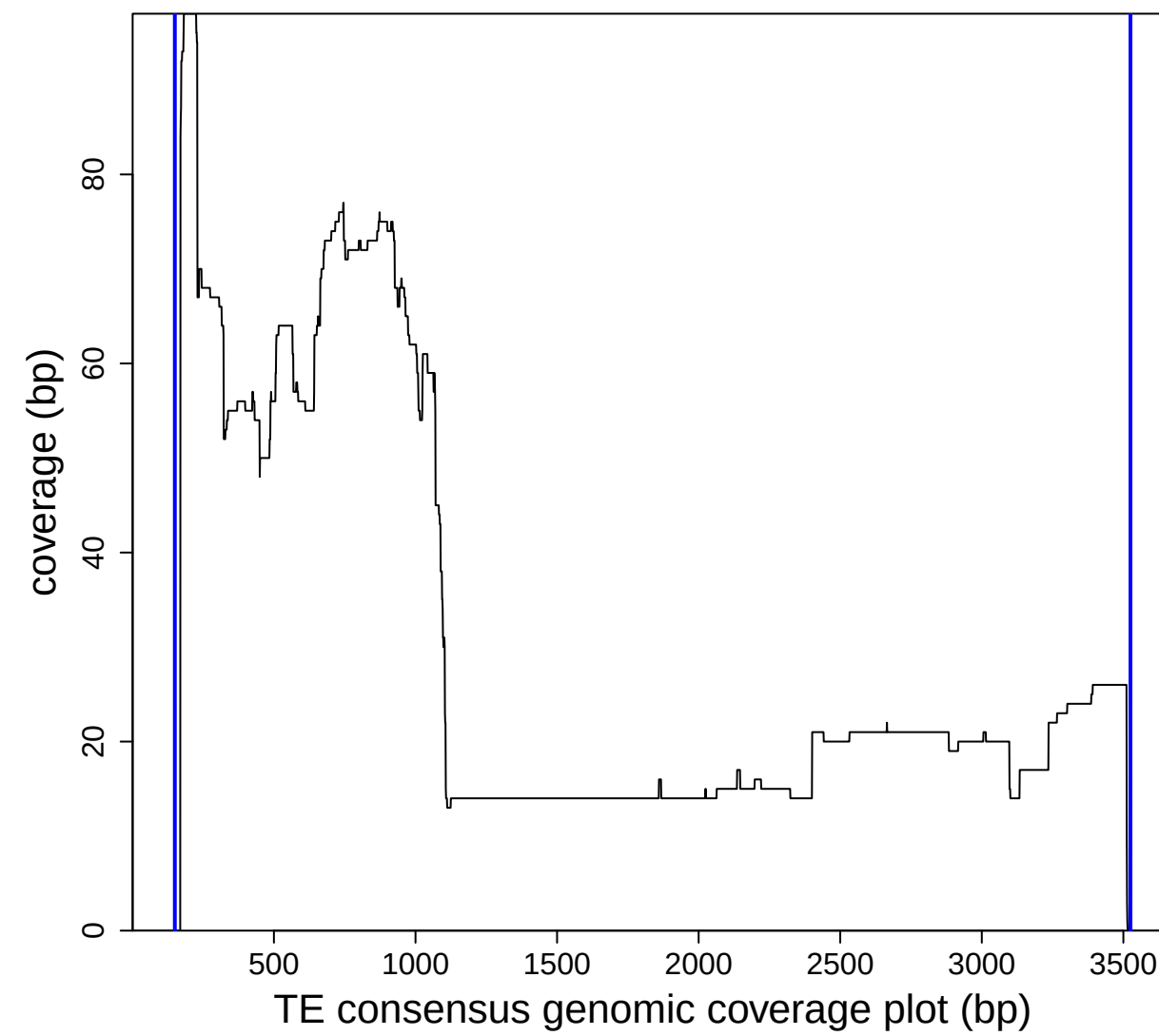
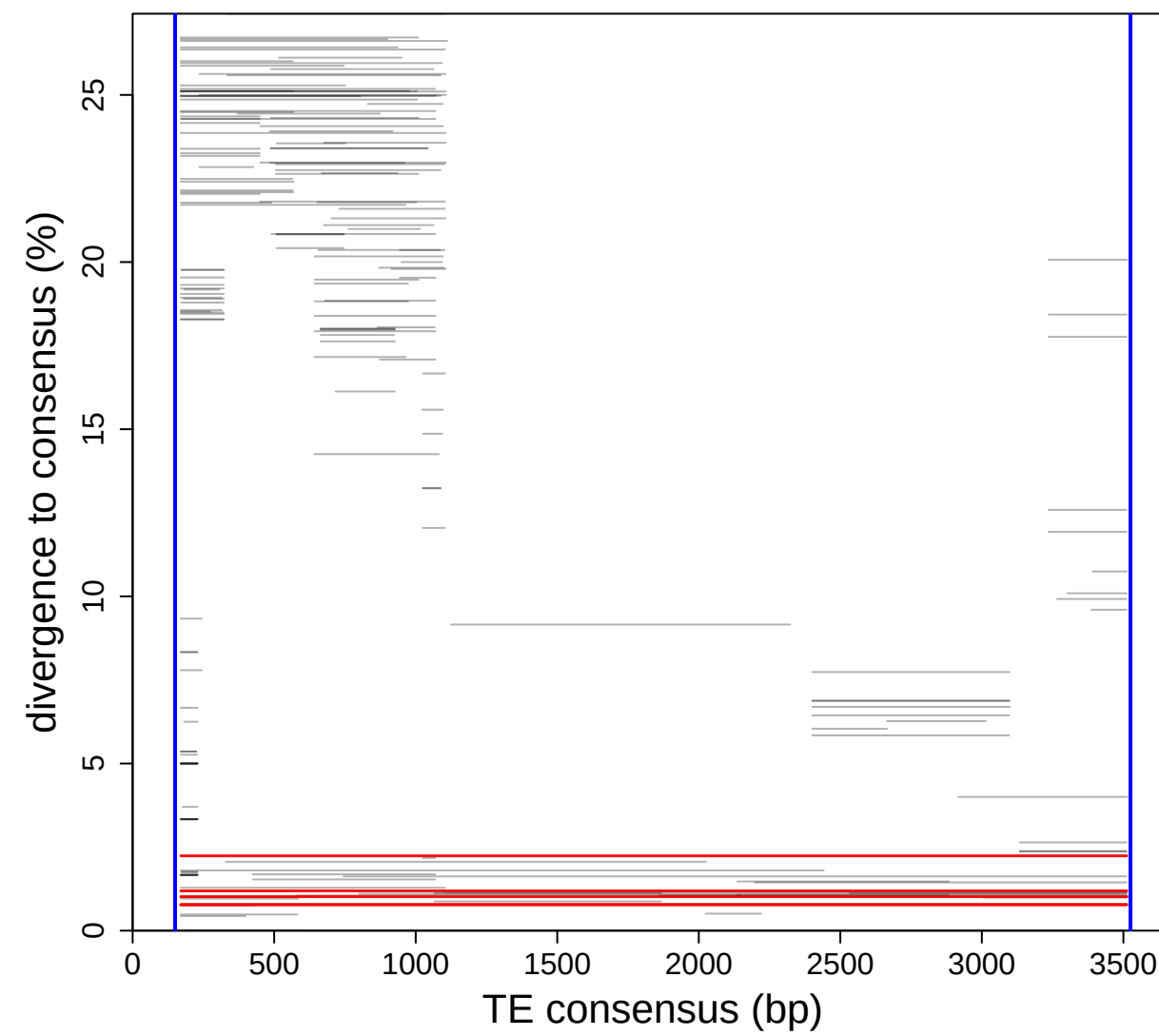
l.b.bed uf.bed g_2.bed fm_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 3360bp; fragments: 199; full length: 5 (>=3024bp)

After TEtrimmer 3360 bp

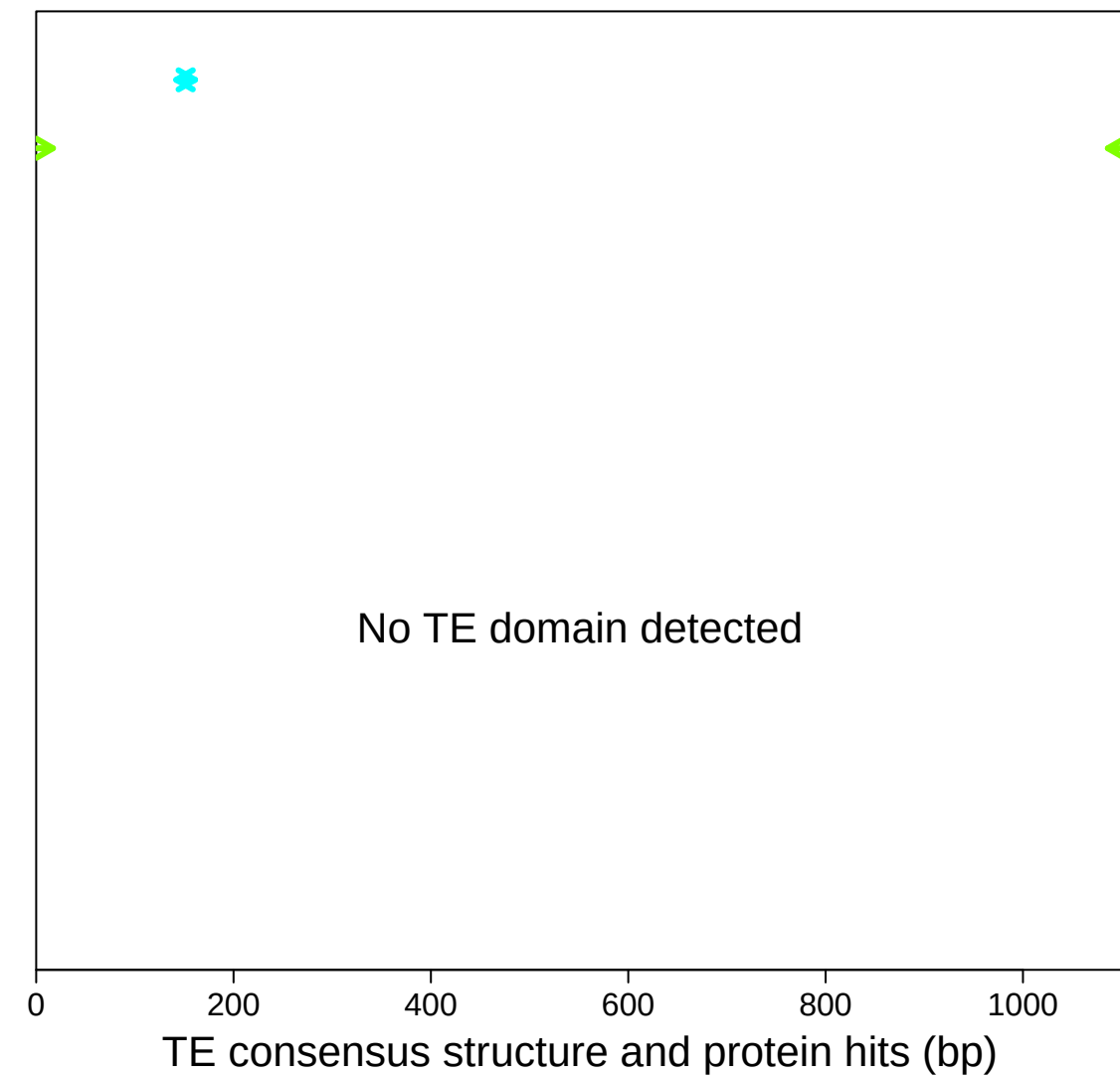
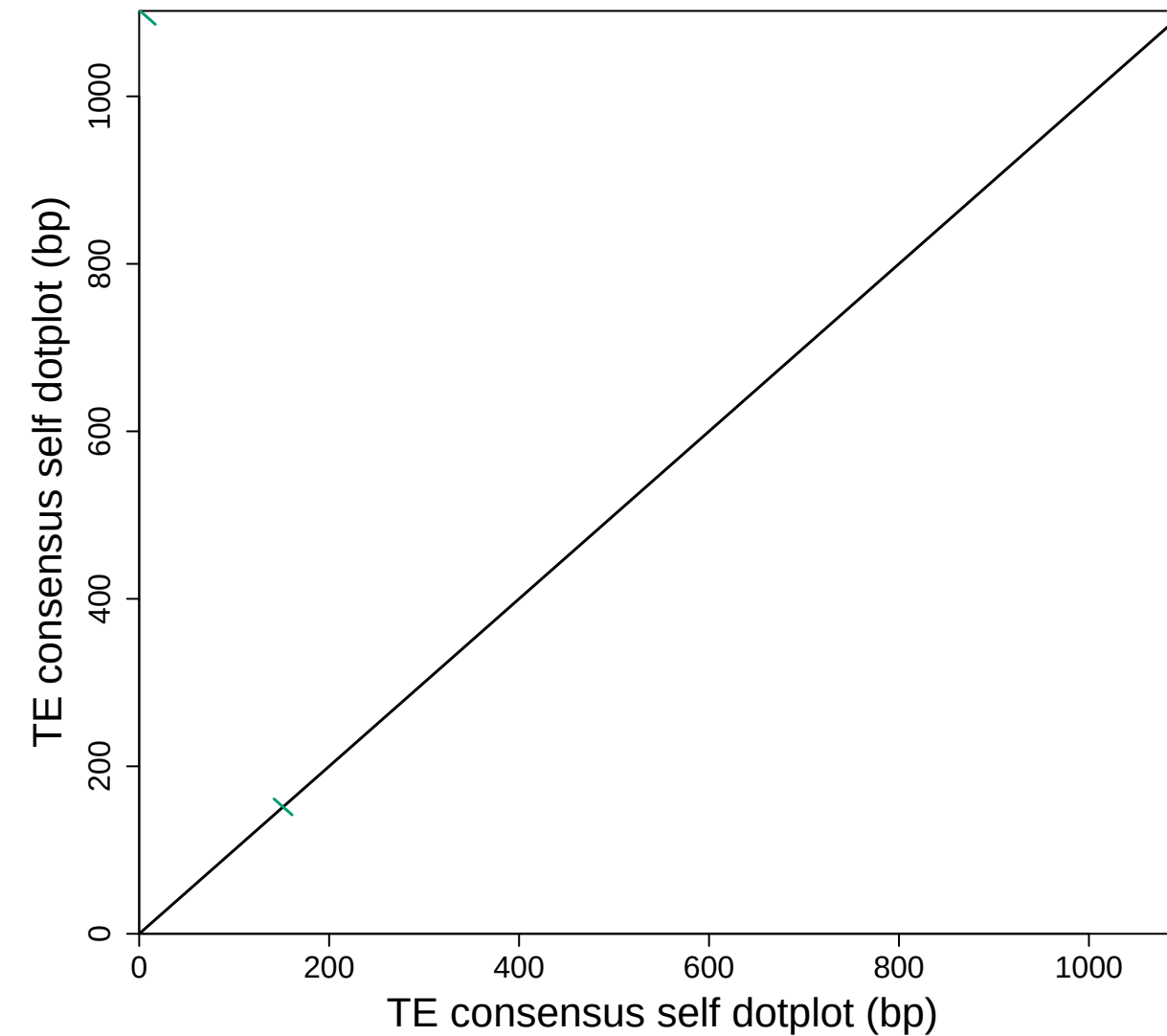
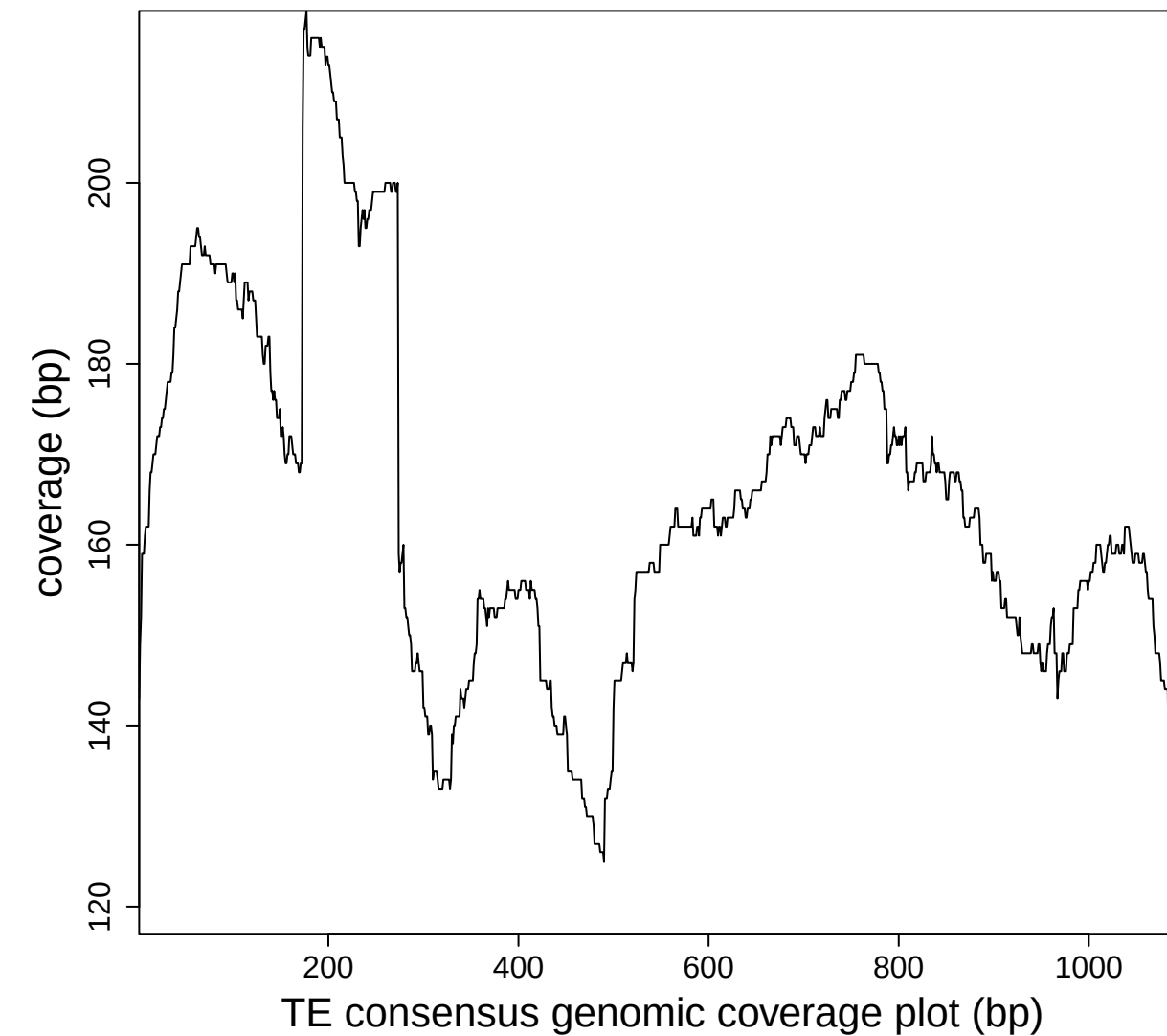
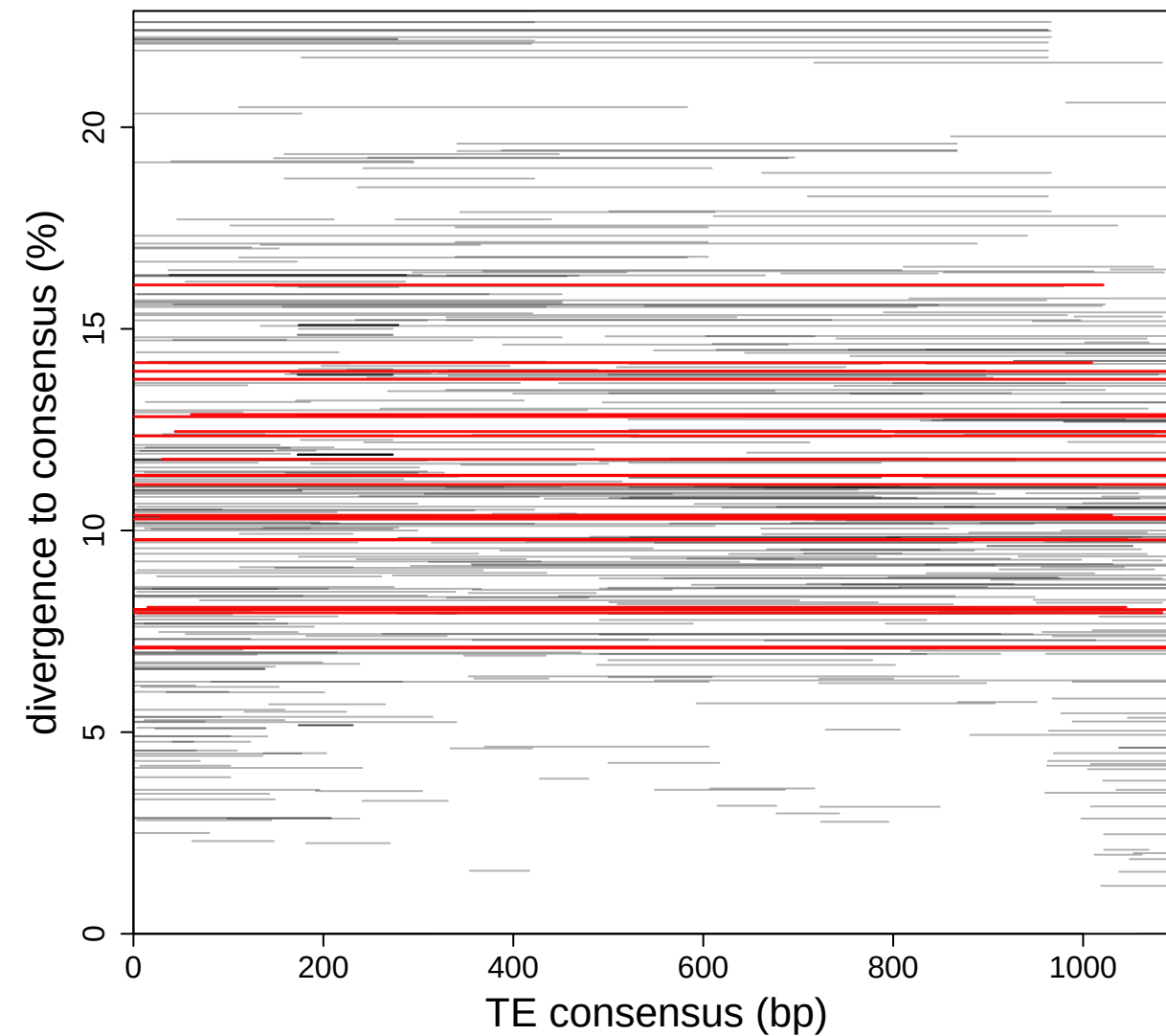


7.fasta.b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa
size: 3675bp; fragments: 199; full length: 5 (>=3307.5bp)

After TEtrimmer Extended plot Blue lines are boundaries

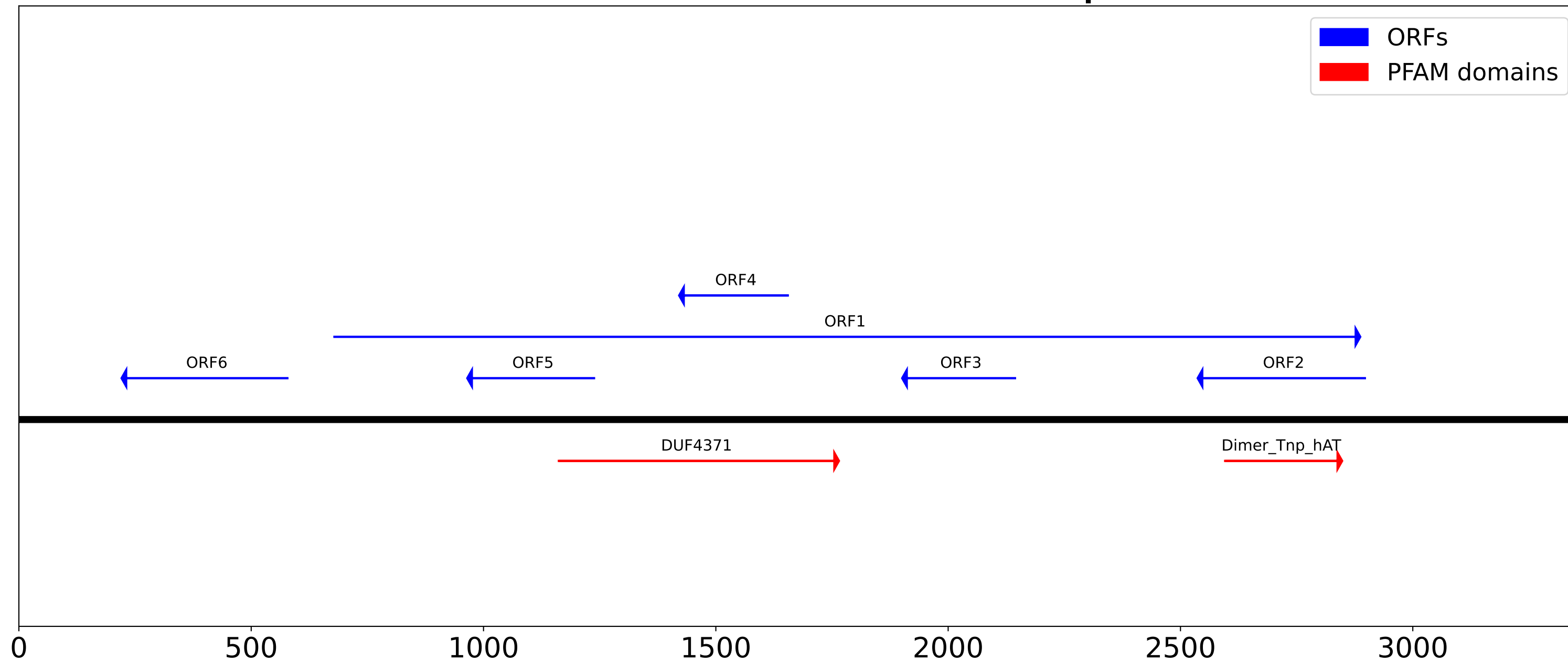


TE: rnd_5_family_777
size: 1102bp; fragments: 542; full length: 23 (≥ 991.8 bp)

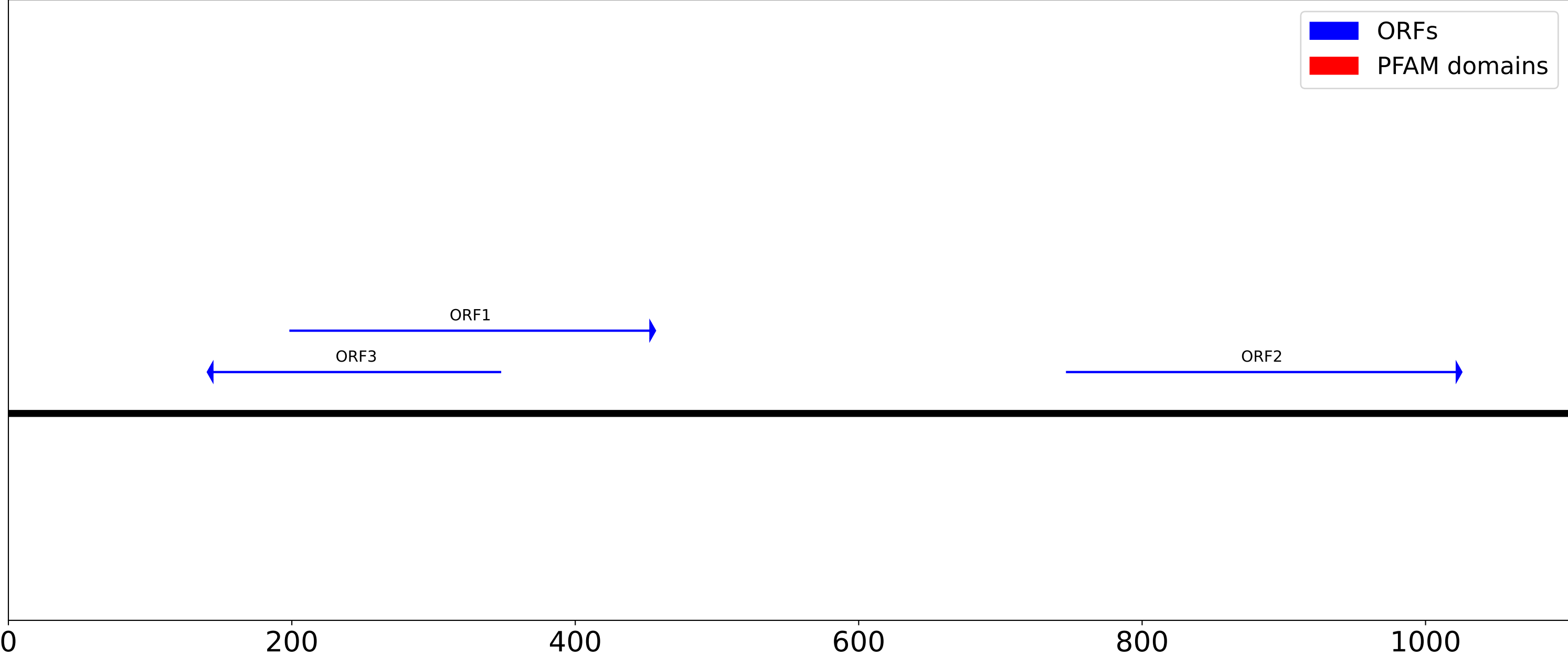


Before TEtrimmer 1102 bp

After TEtrimmer ORF and PFAM domain plot



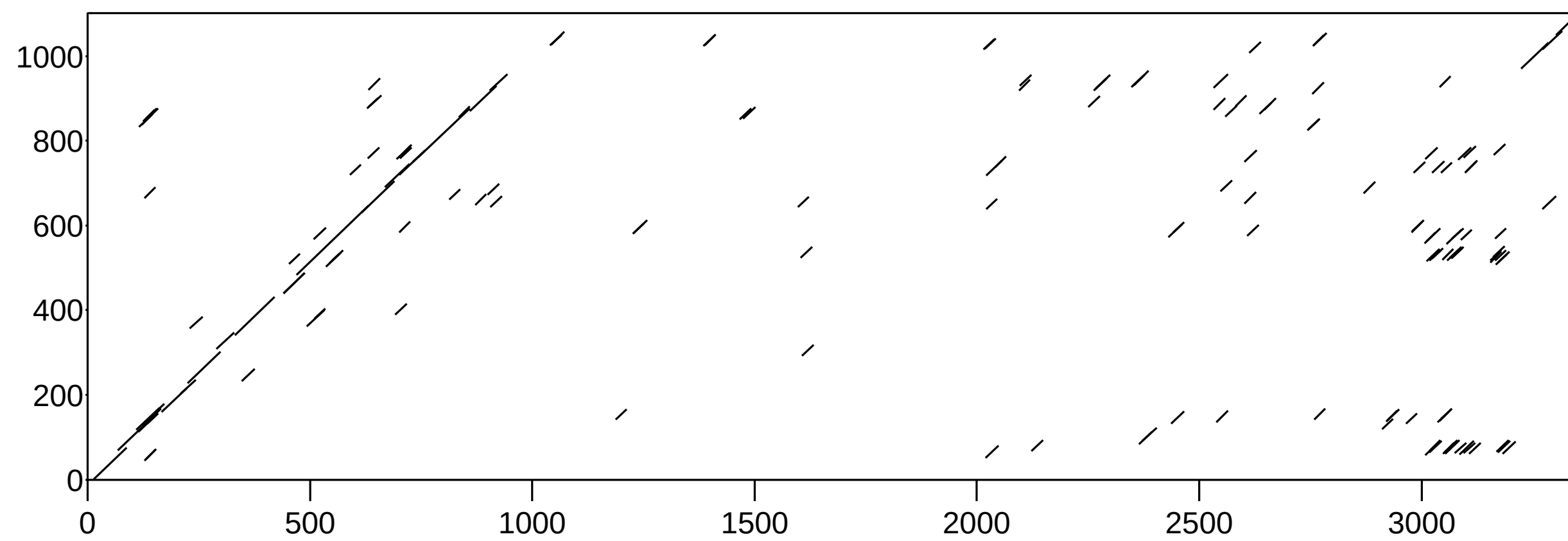
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)