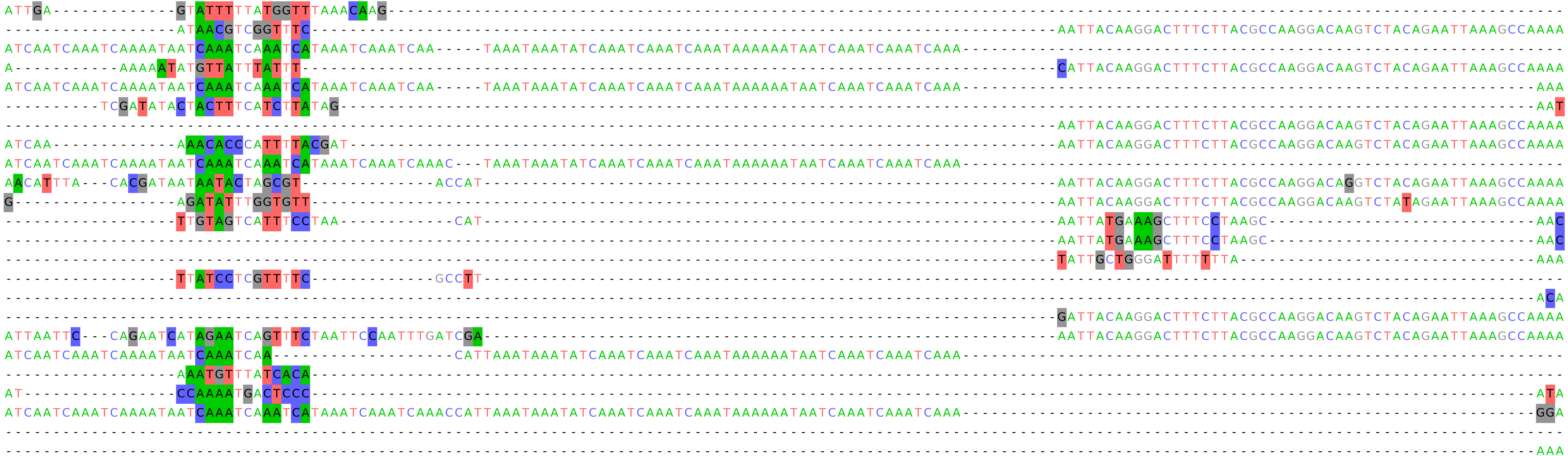


Start crop Point

End crop Point

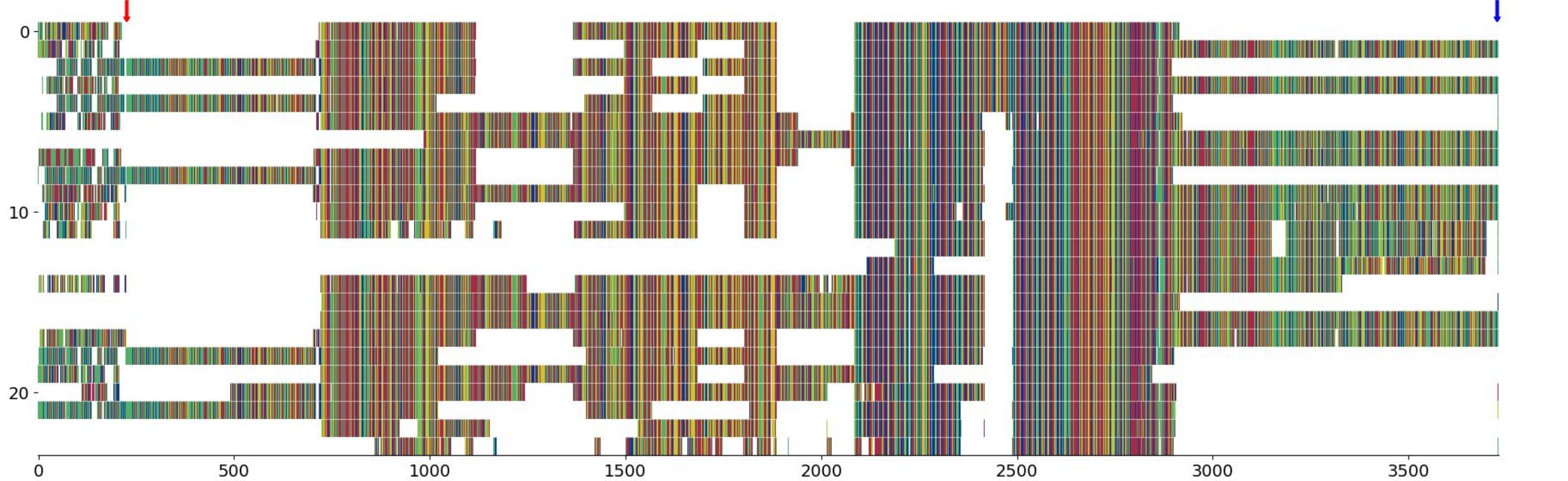


MSA length = 3502



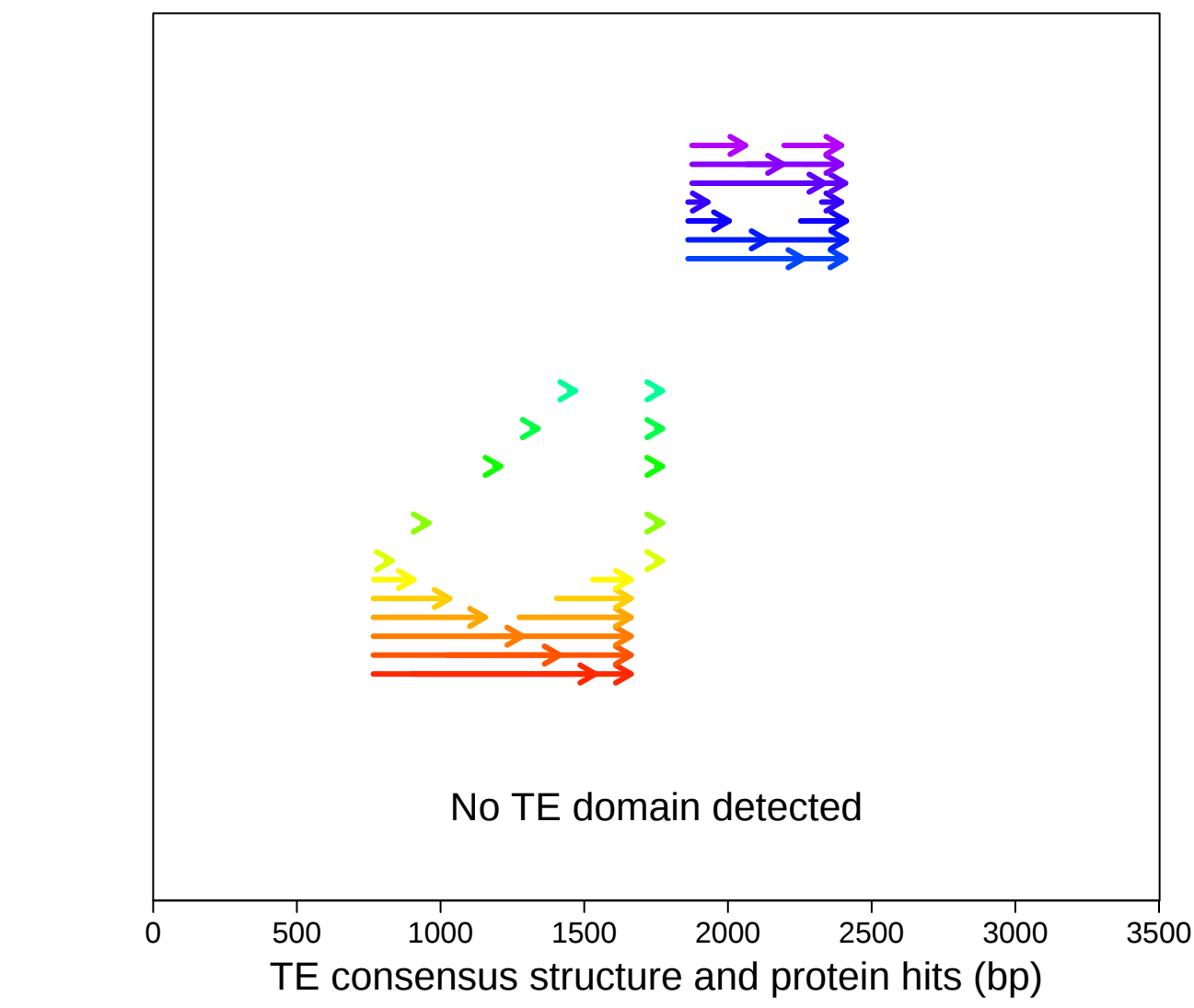
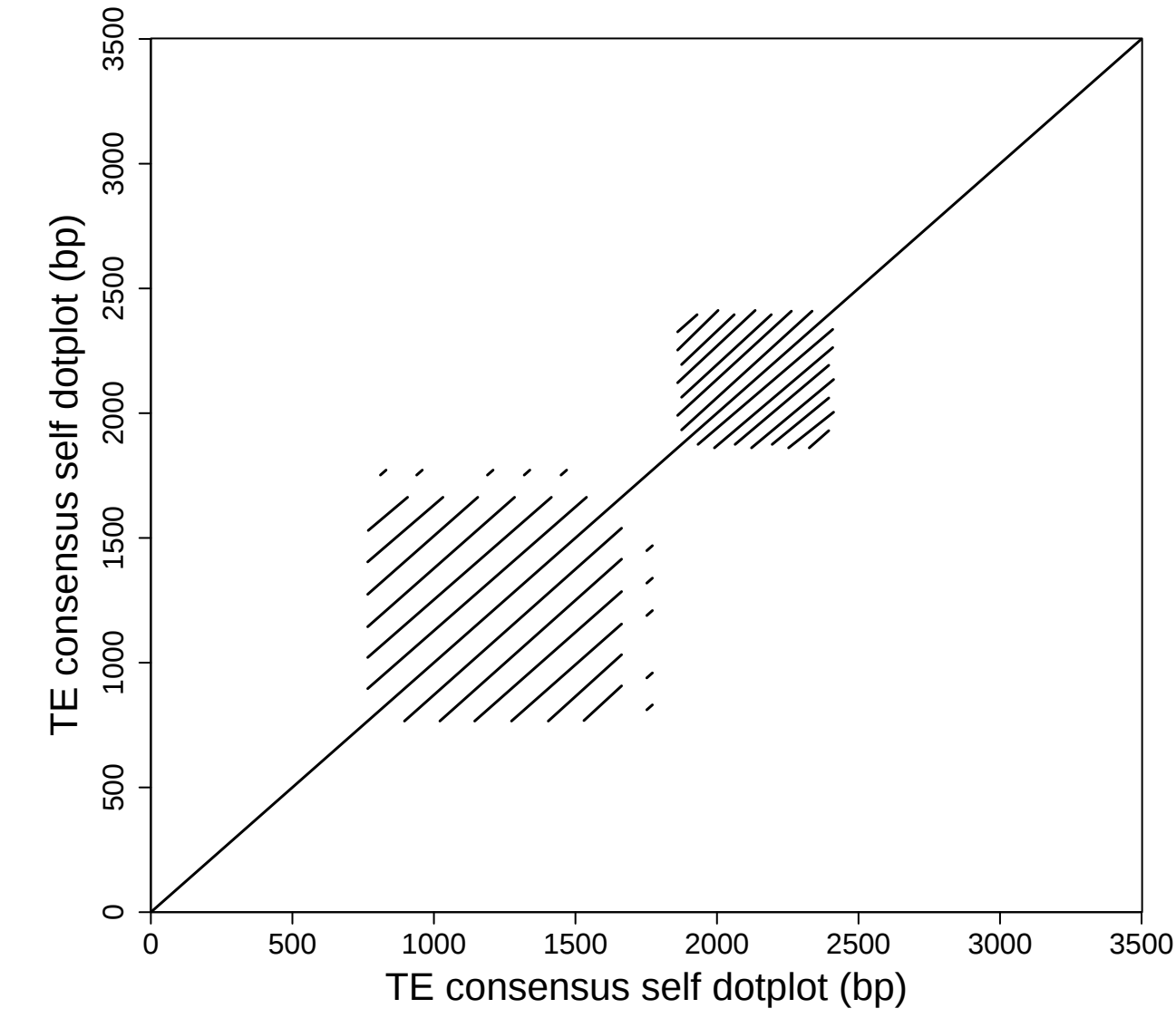
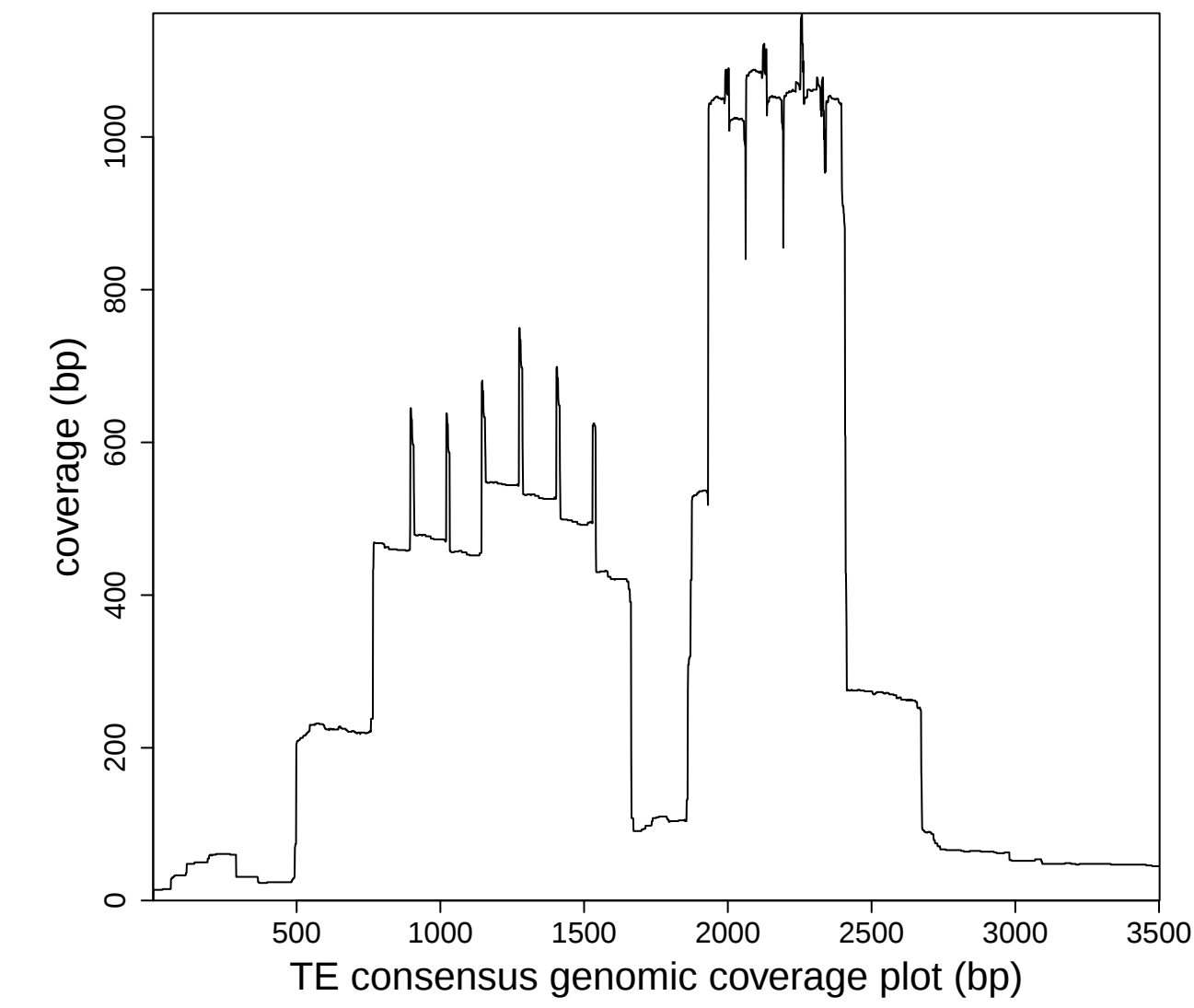
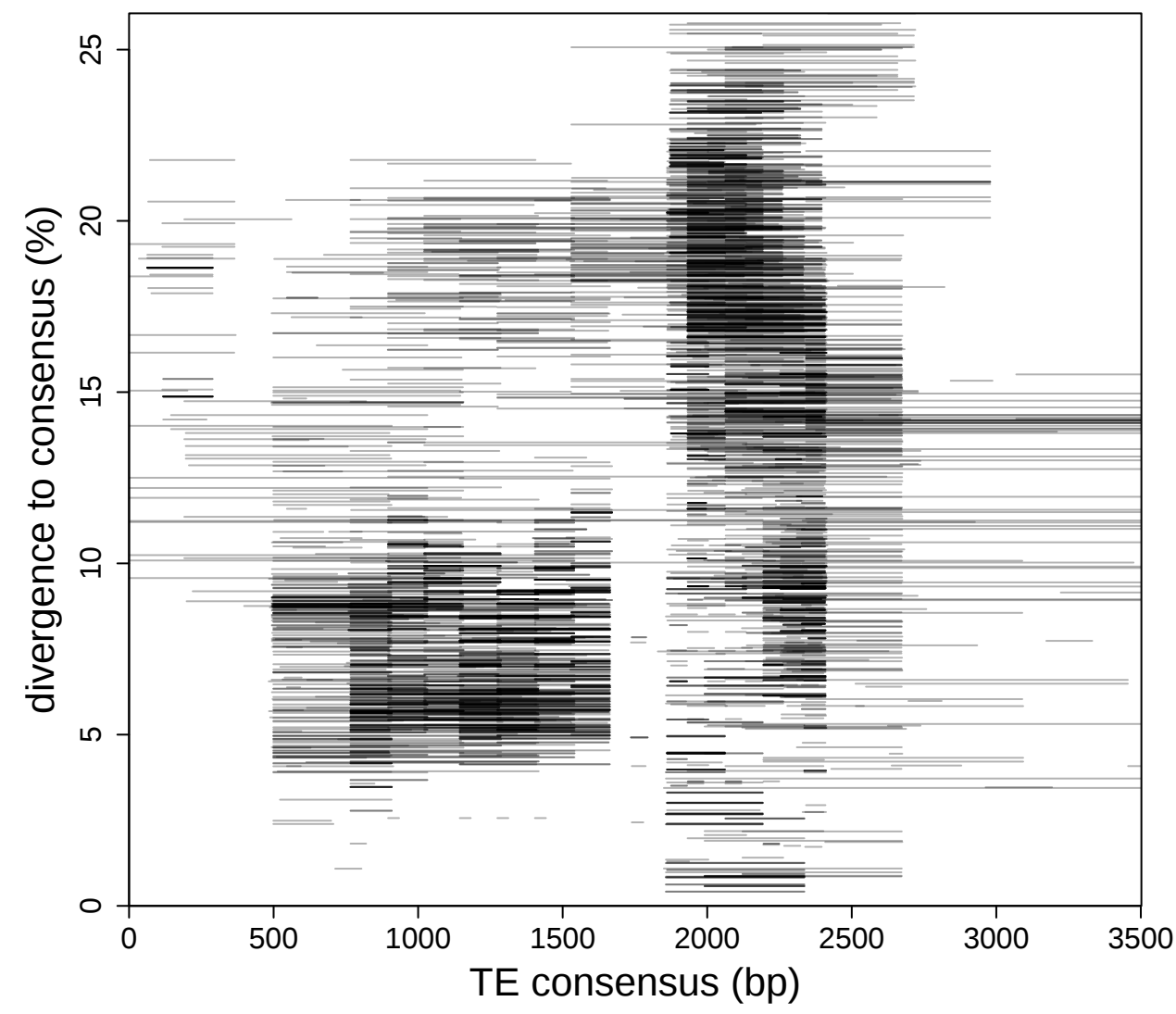
Start crop Point

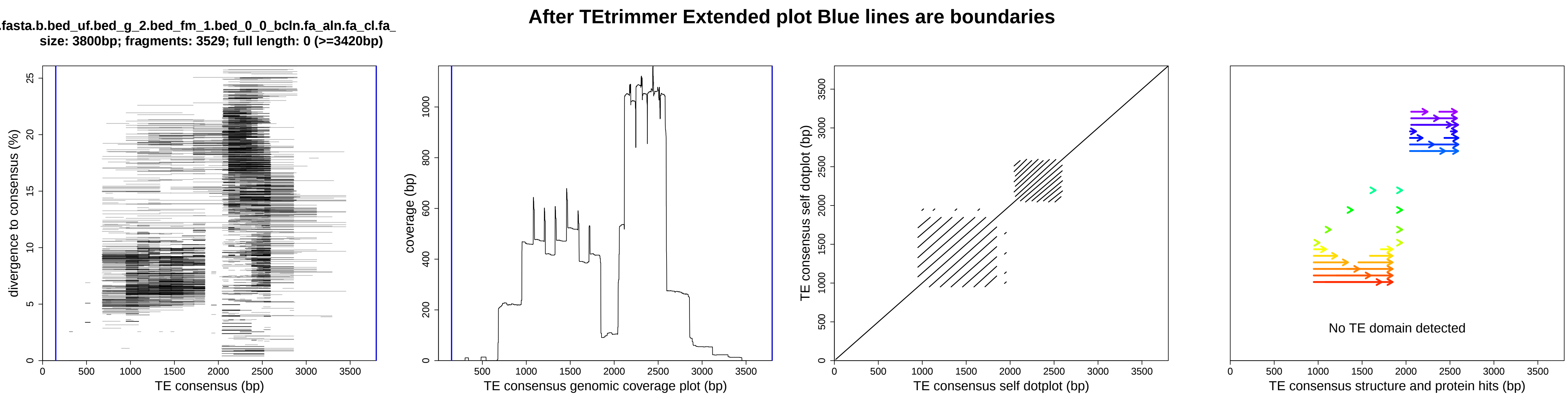
End crop Point



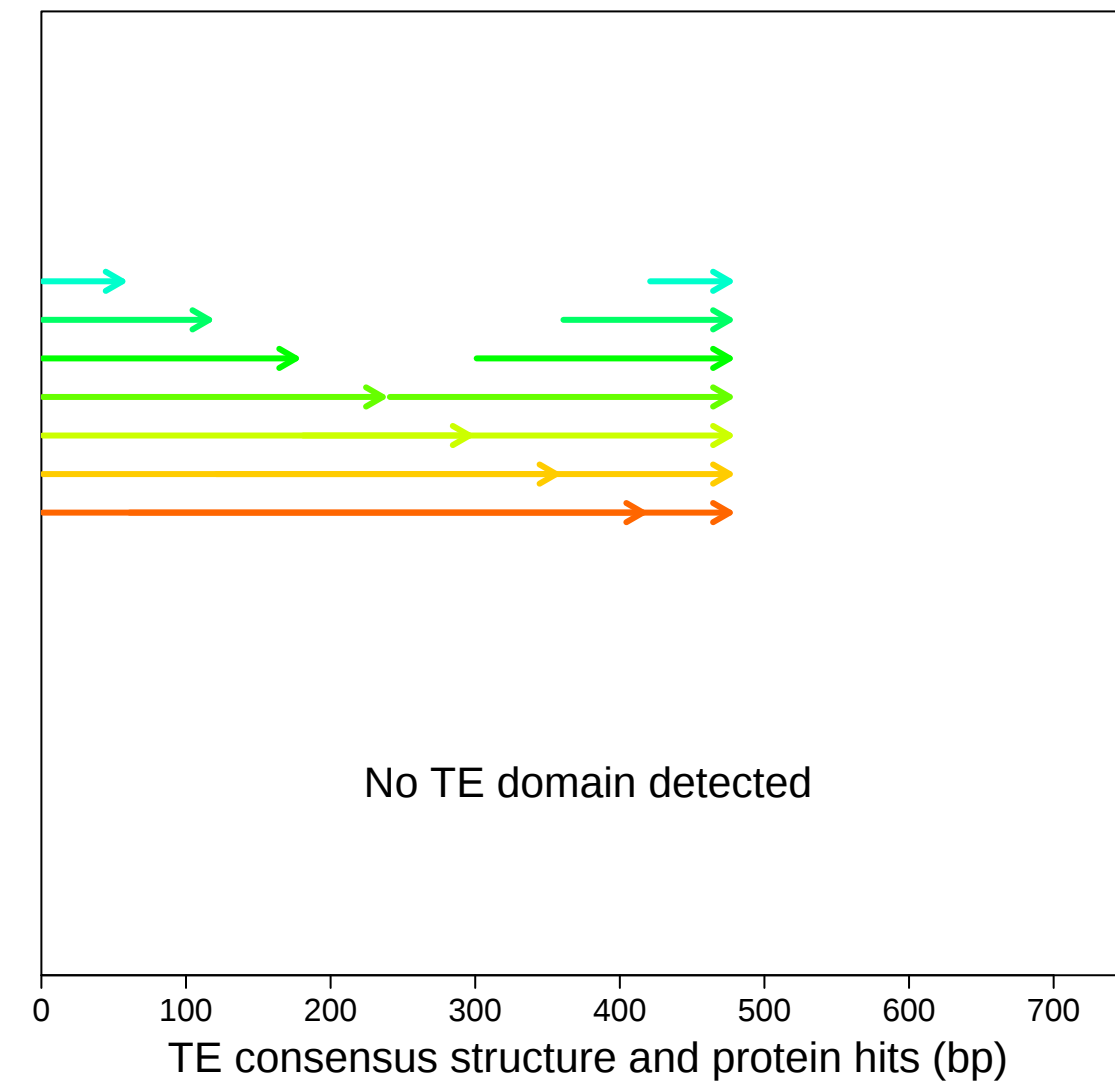
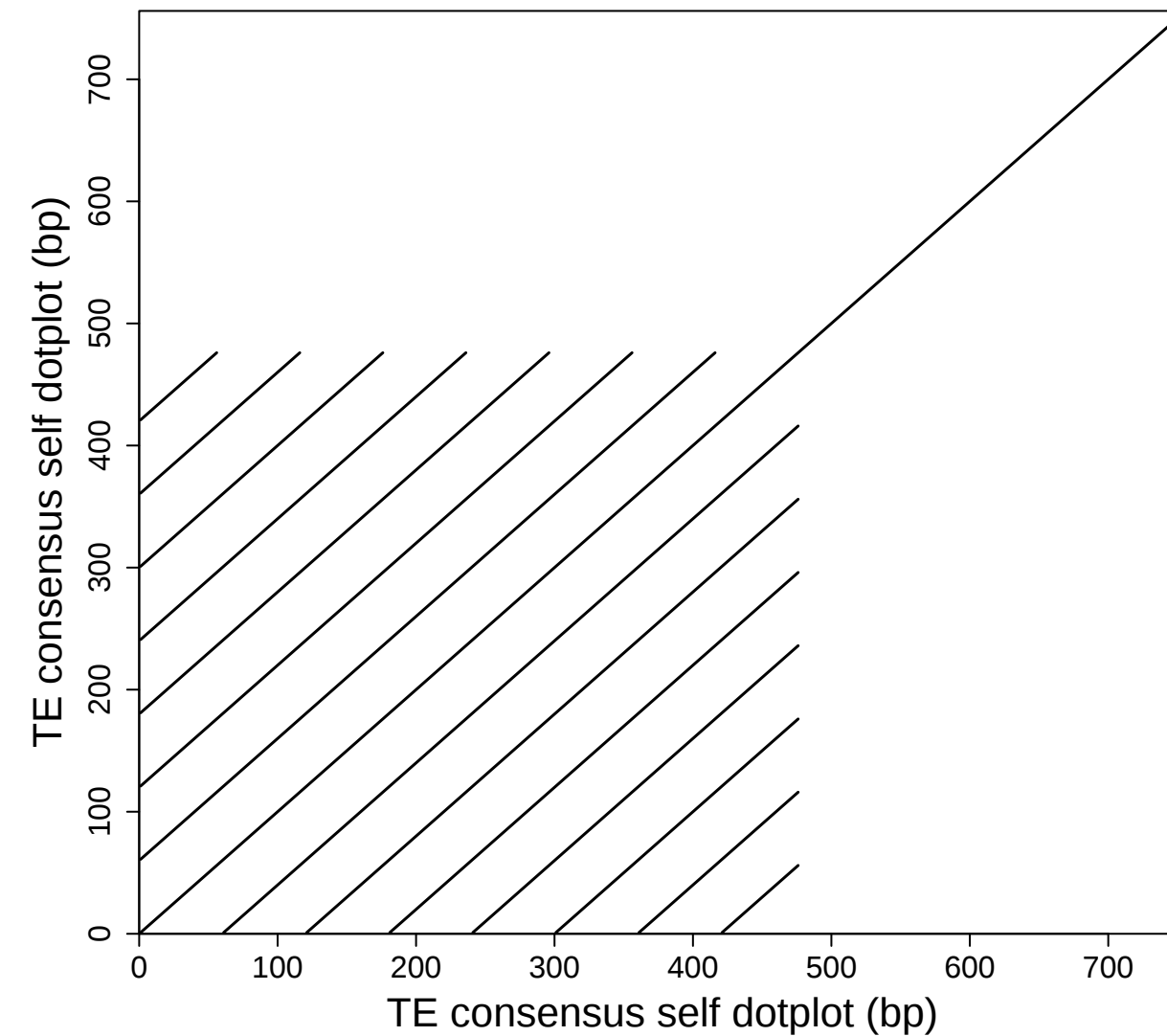
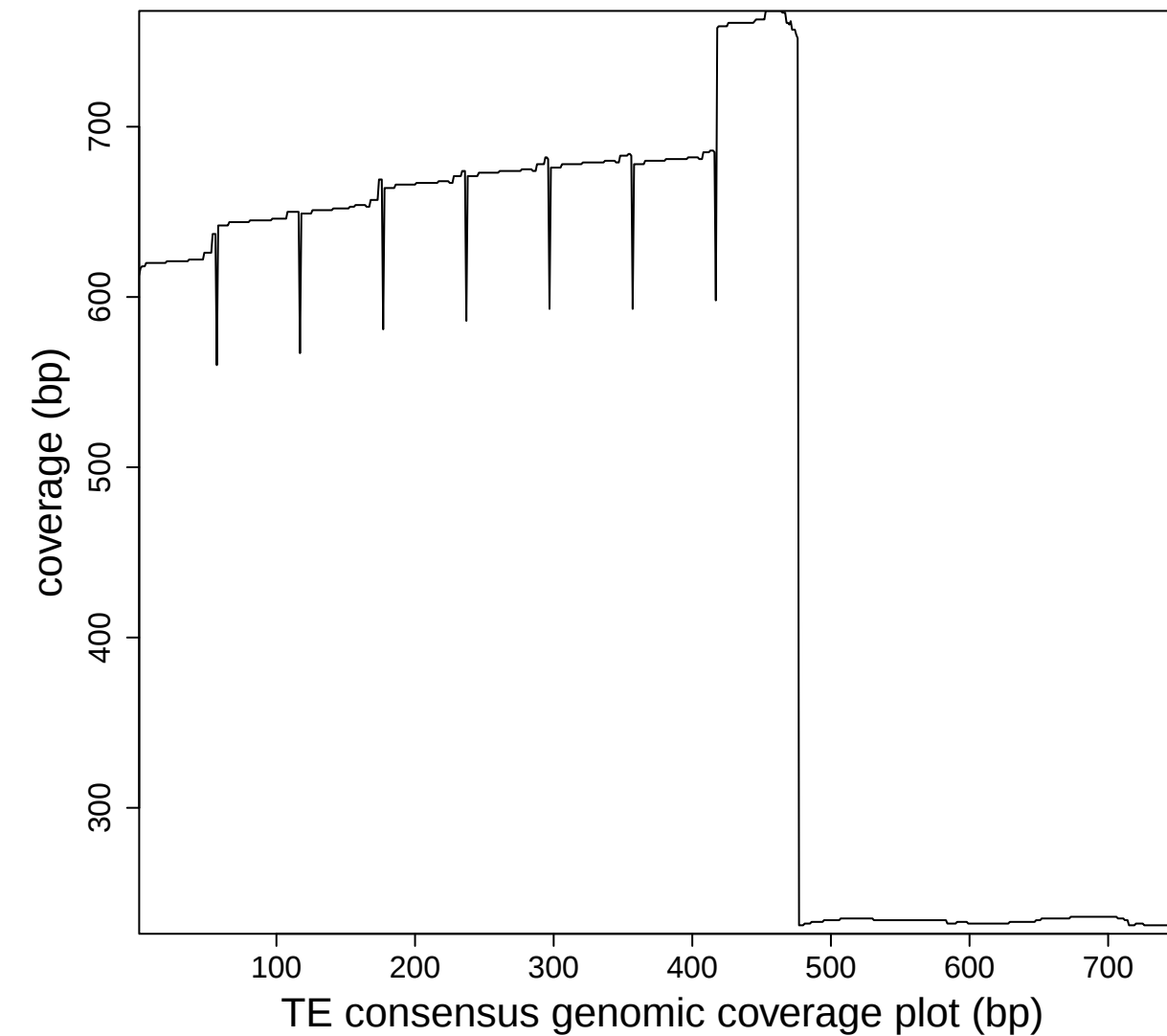
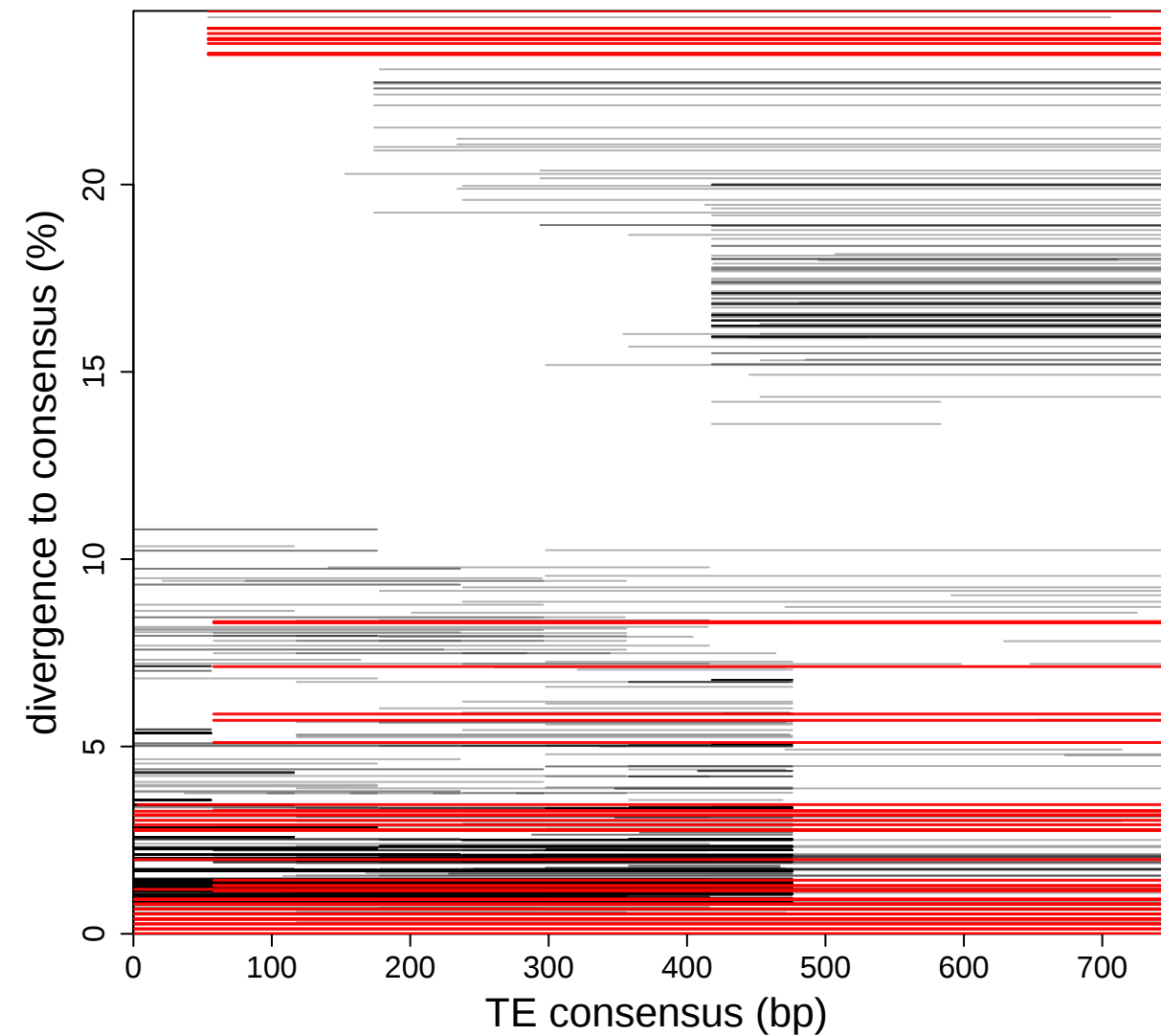
b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_
size: 3502bp; fragments: 3725; full length: 0 (>=3151.8bp)

After TEtrimmer 3502 bp



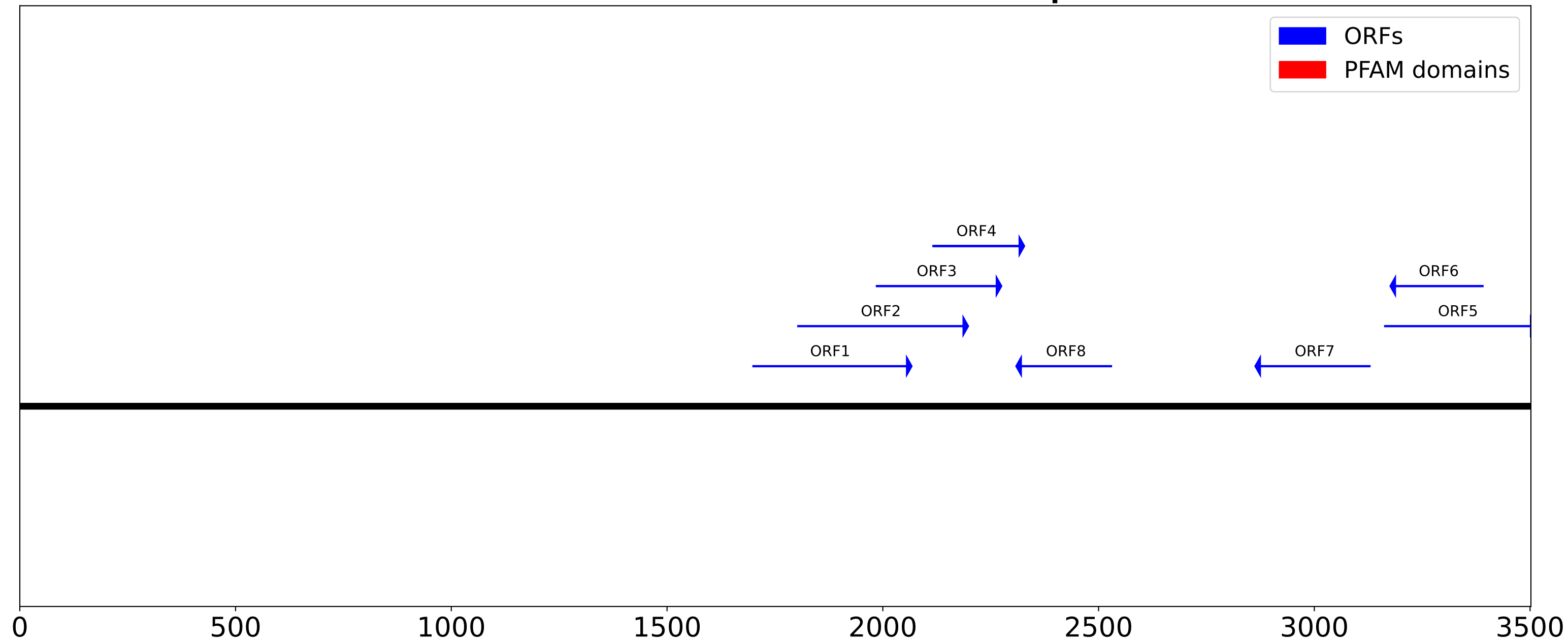


TE: ltr_1_family_66
size: 756bp; fragments: 1401; full length: 58 (≥ 680.4 bp)

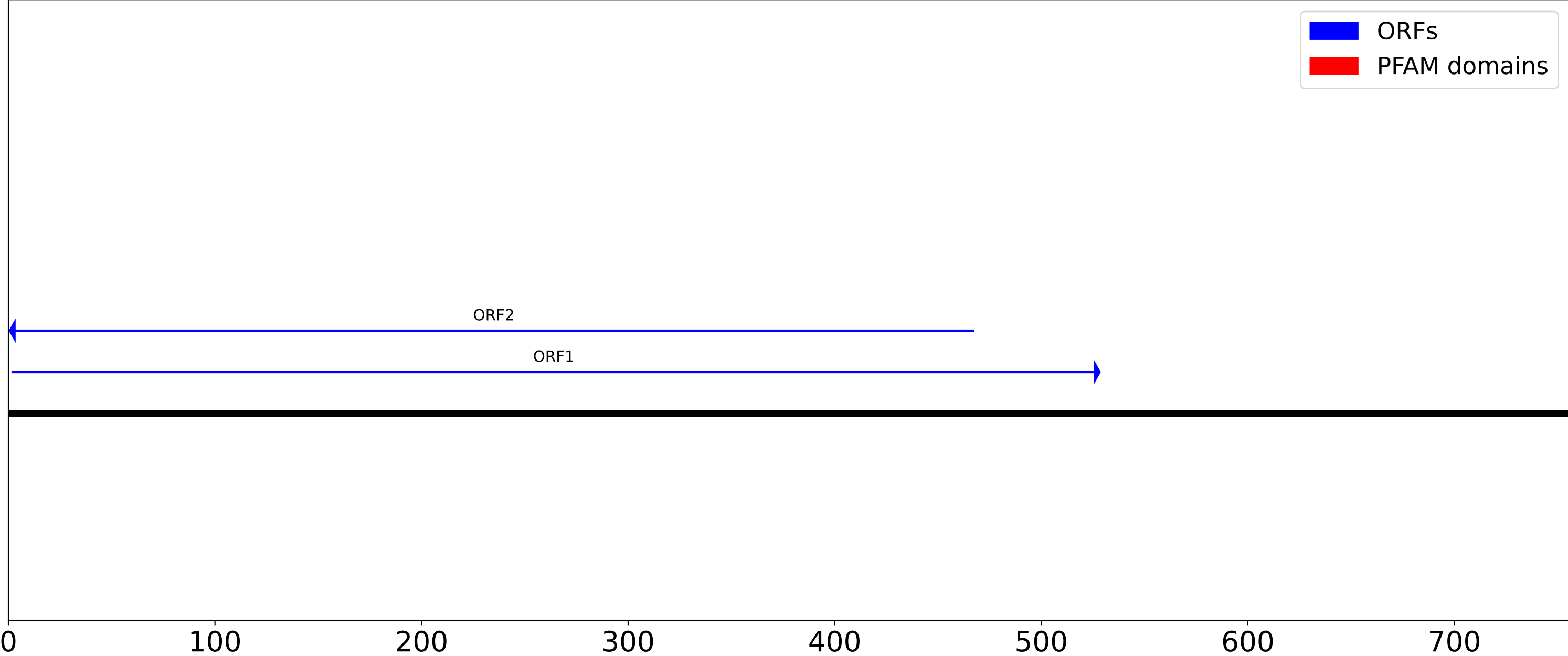


Before TEtrimmer 756 bp

After TEtrimmer ORF and PFAM domain plot



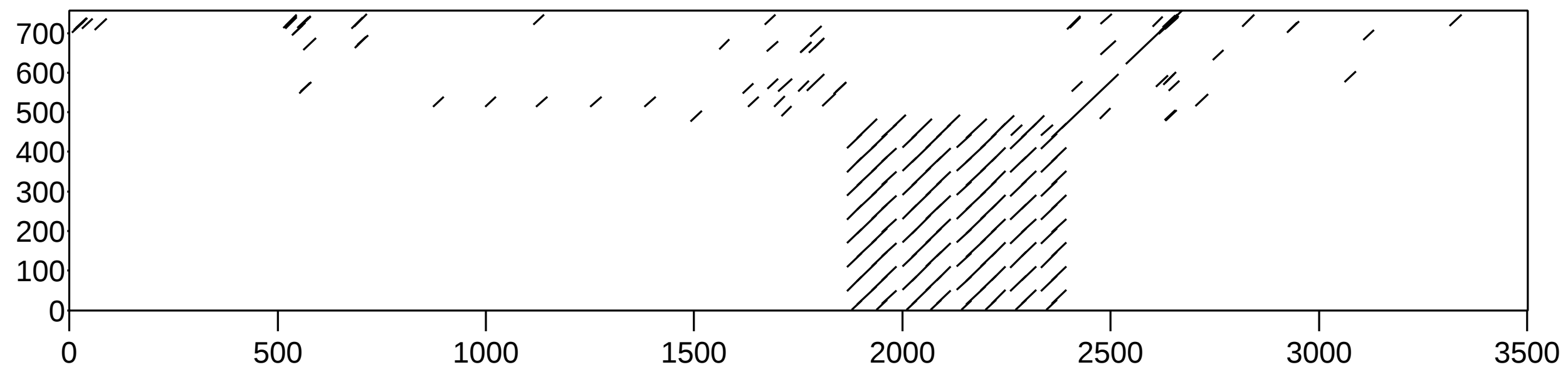
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

onsensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)