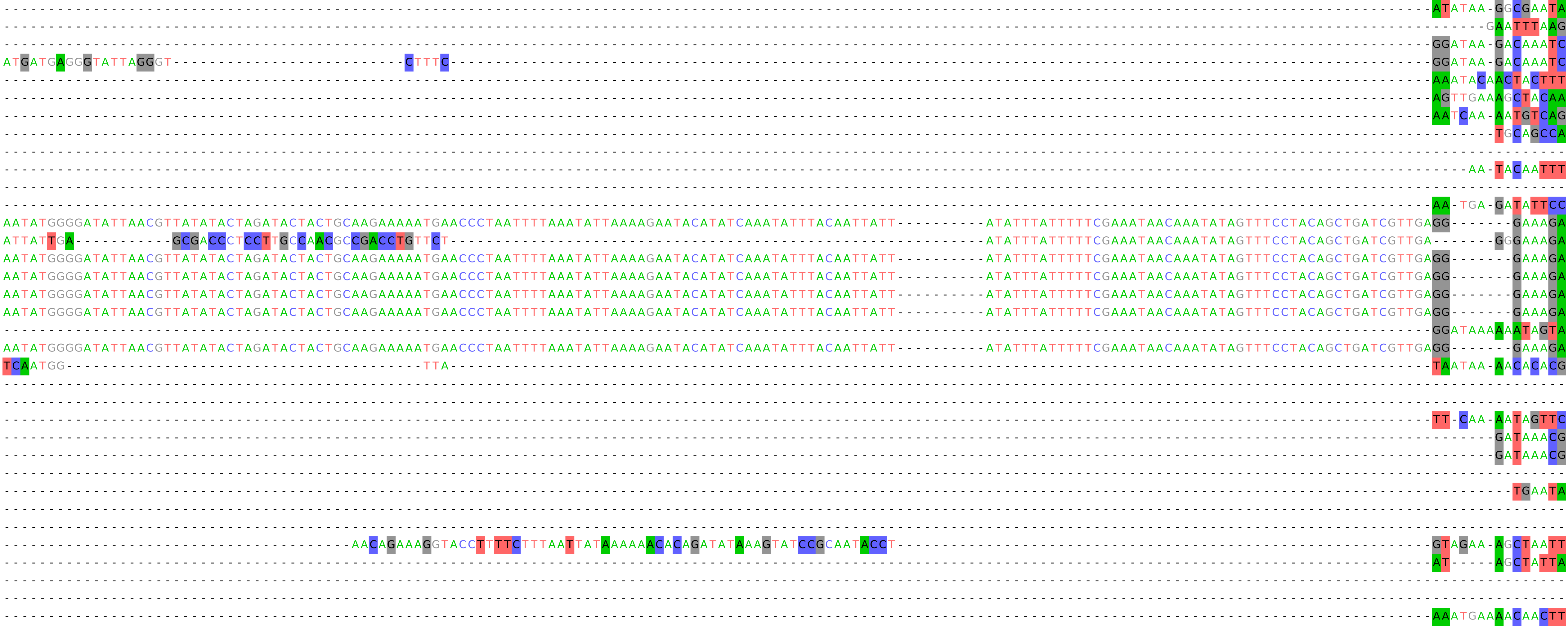
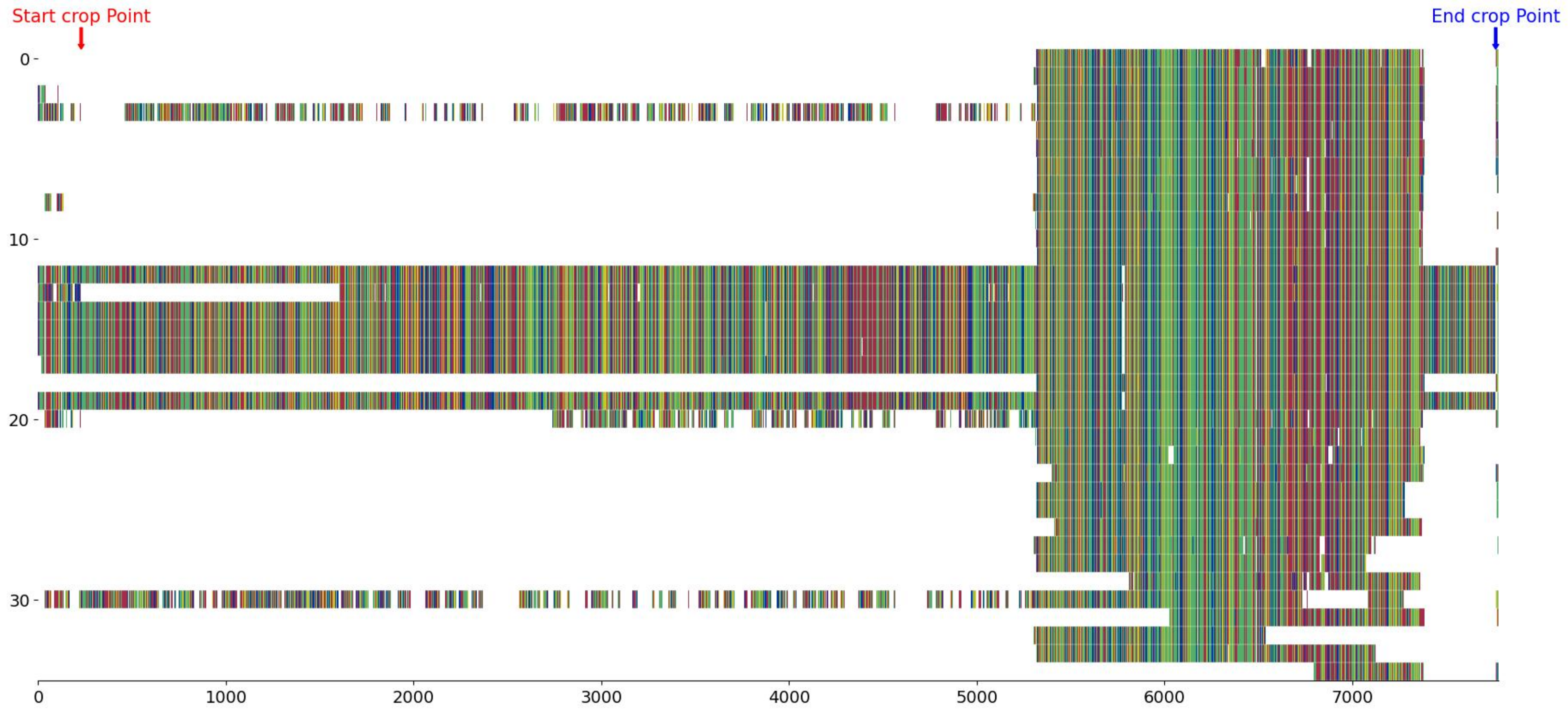


Start crop Point

End crop Point

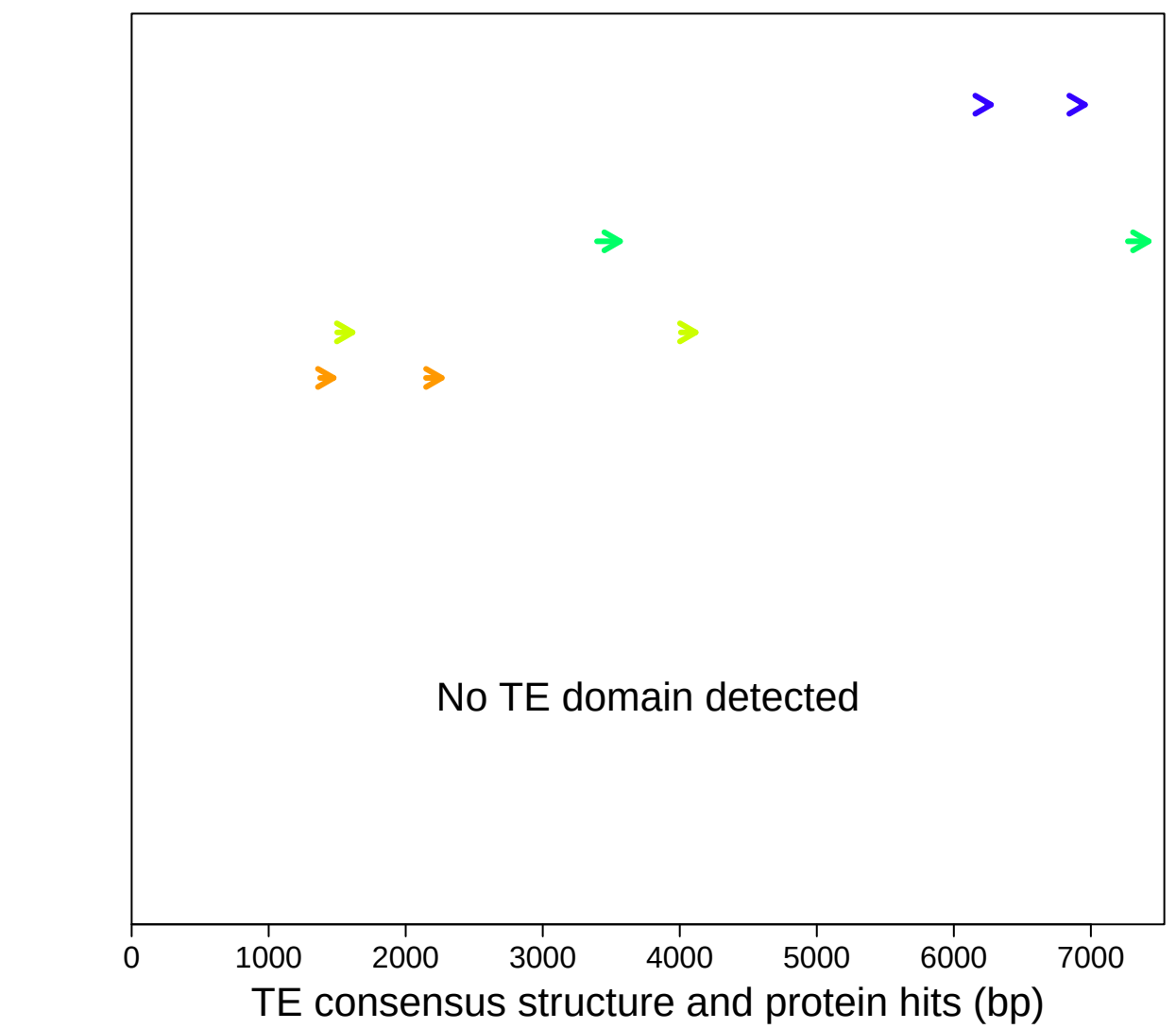
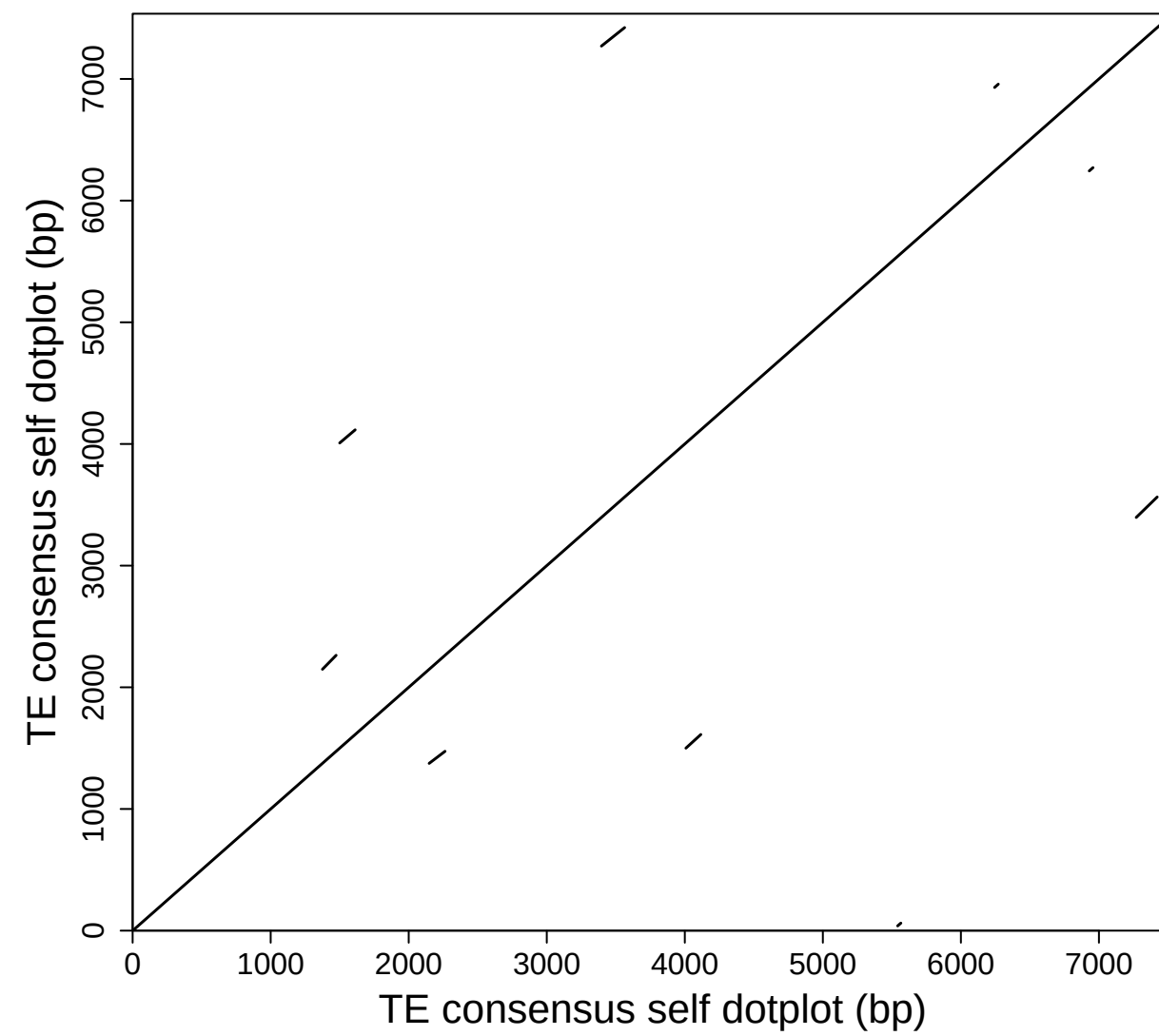
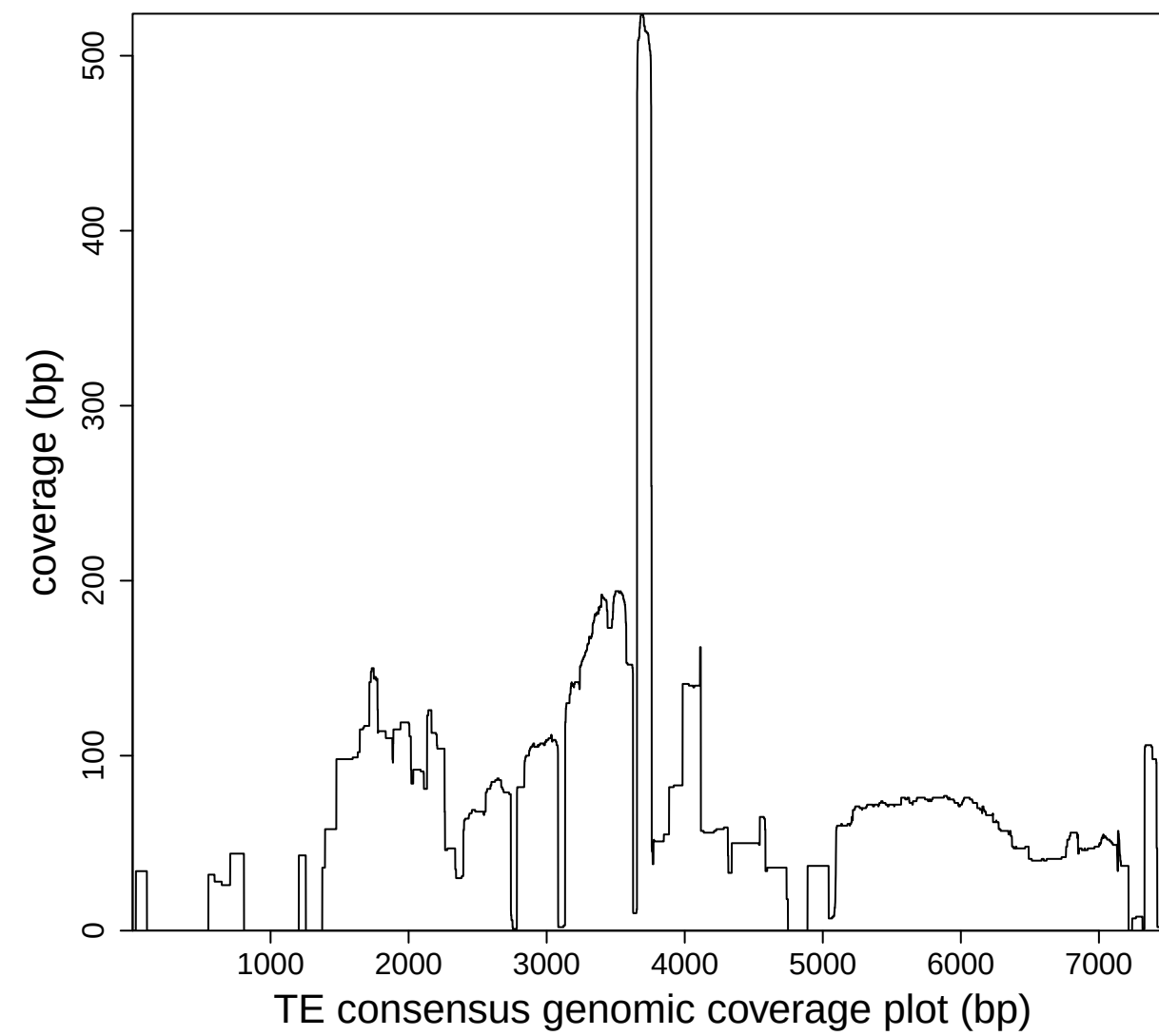
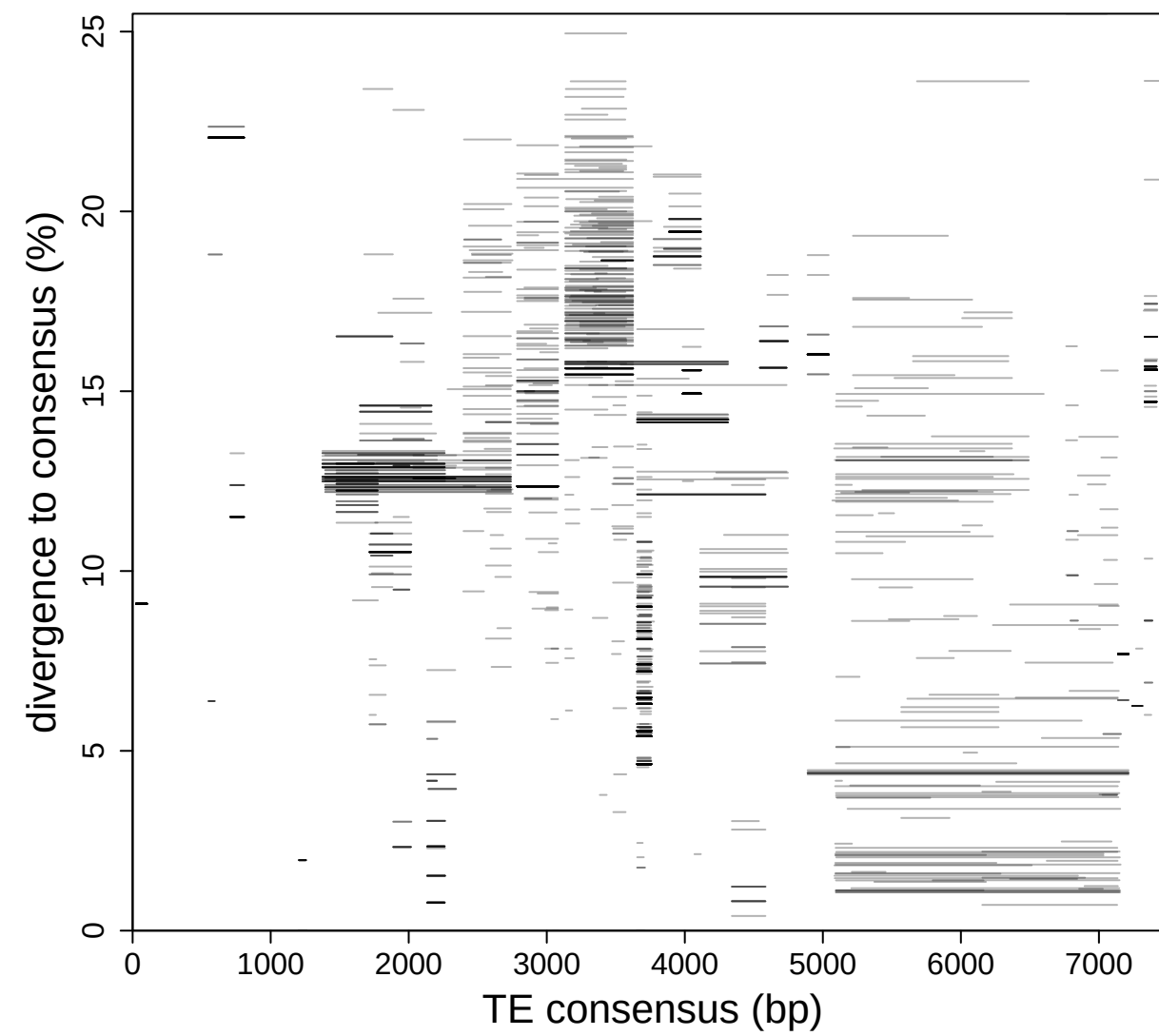
MSA length = 7536





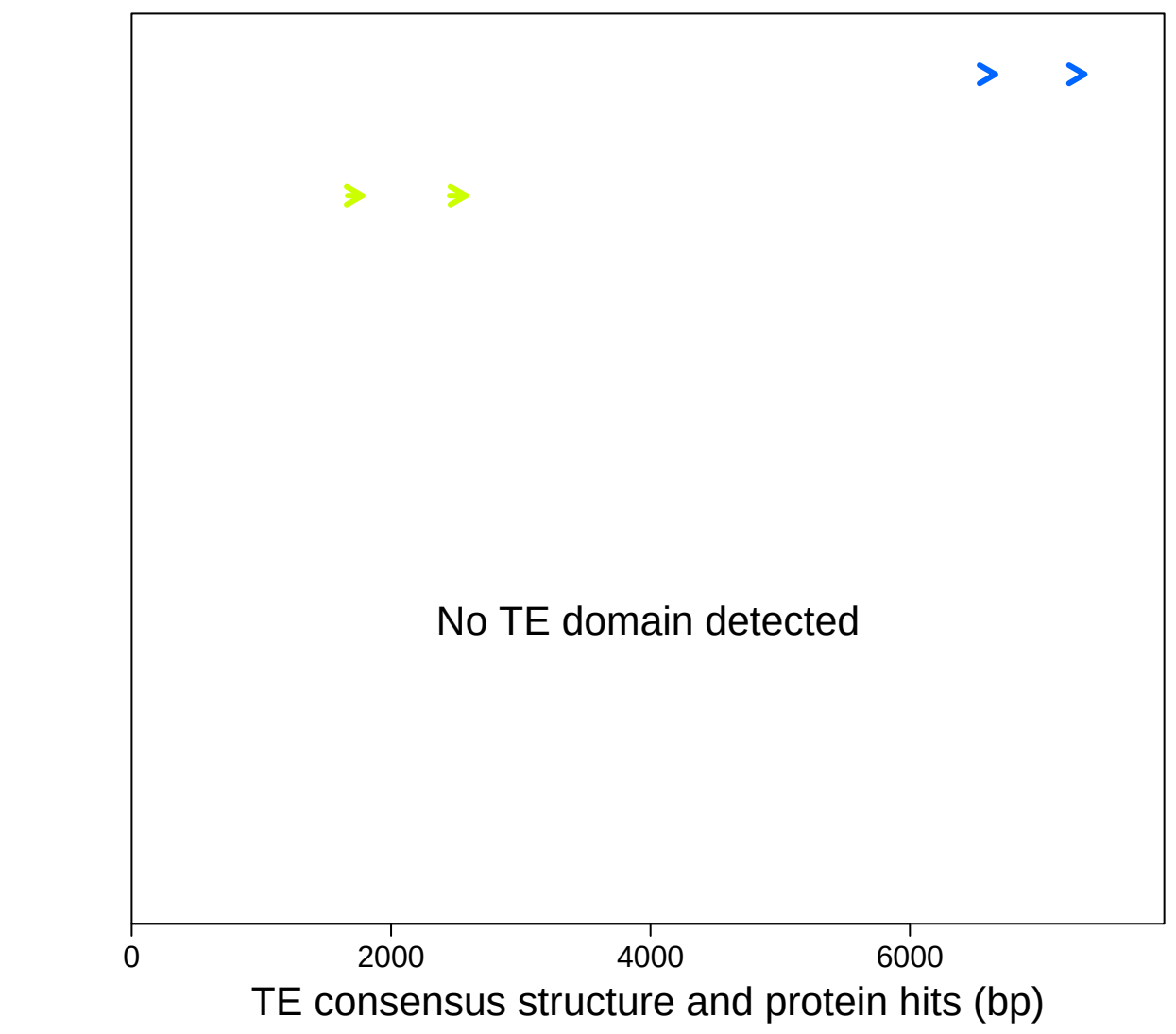
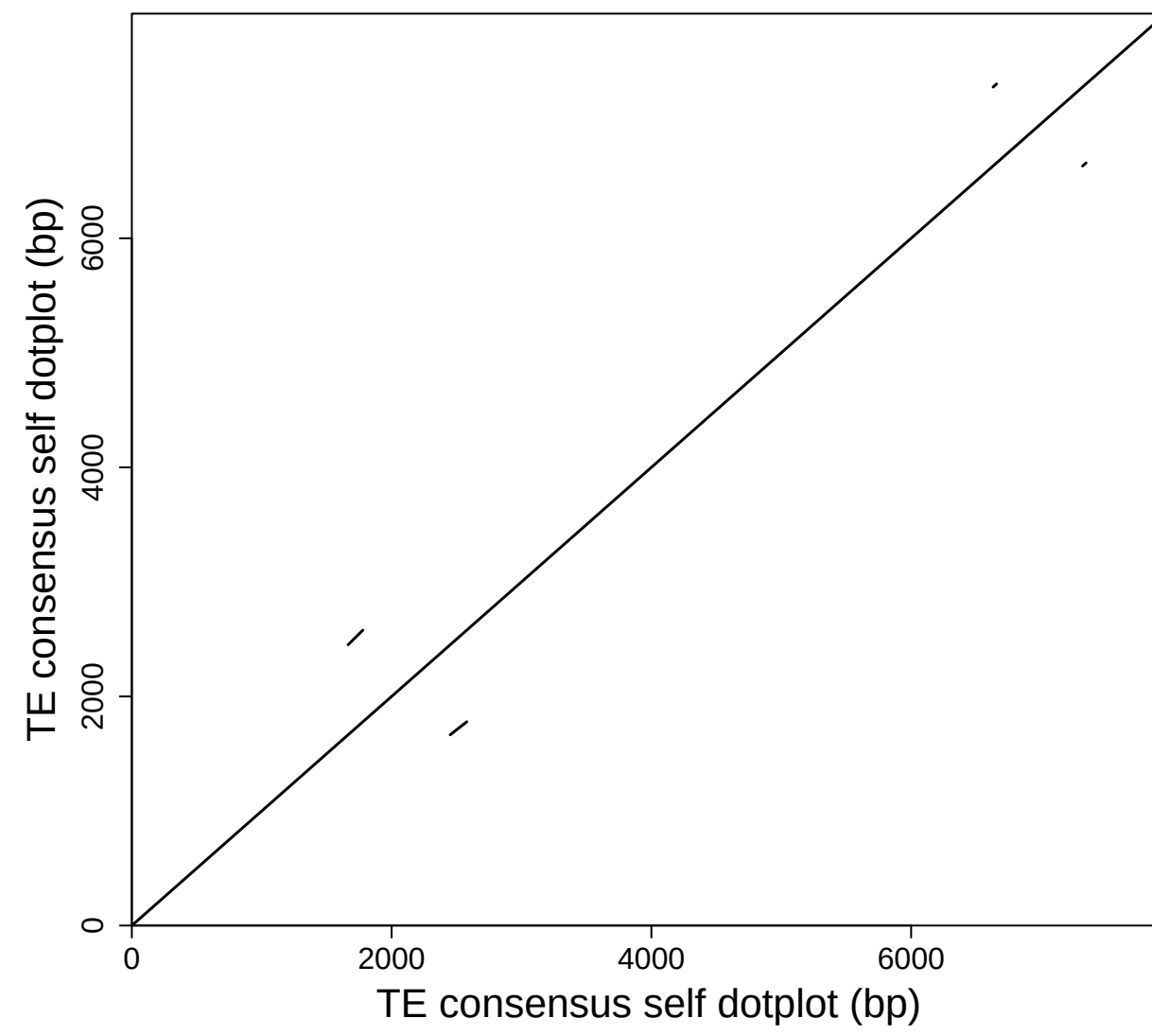
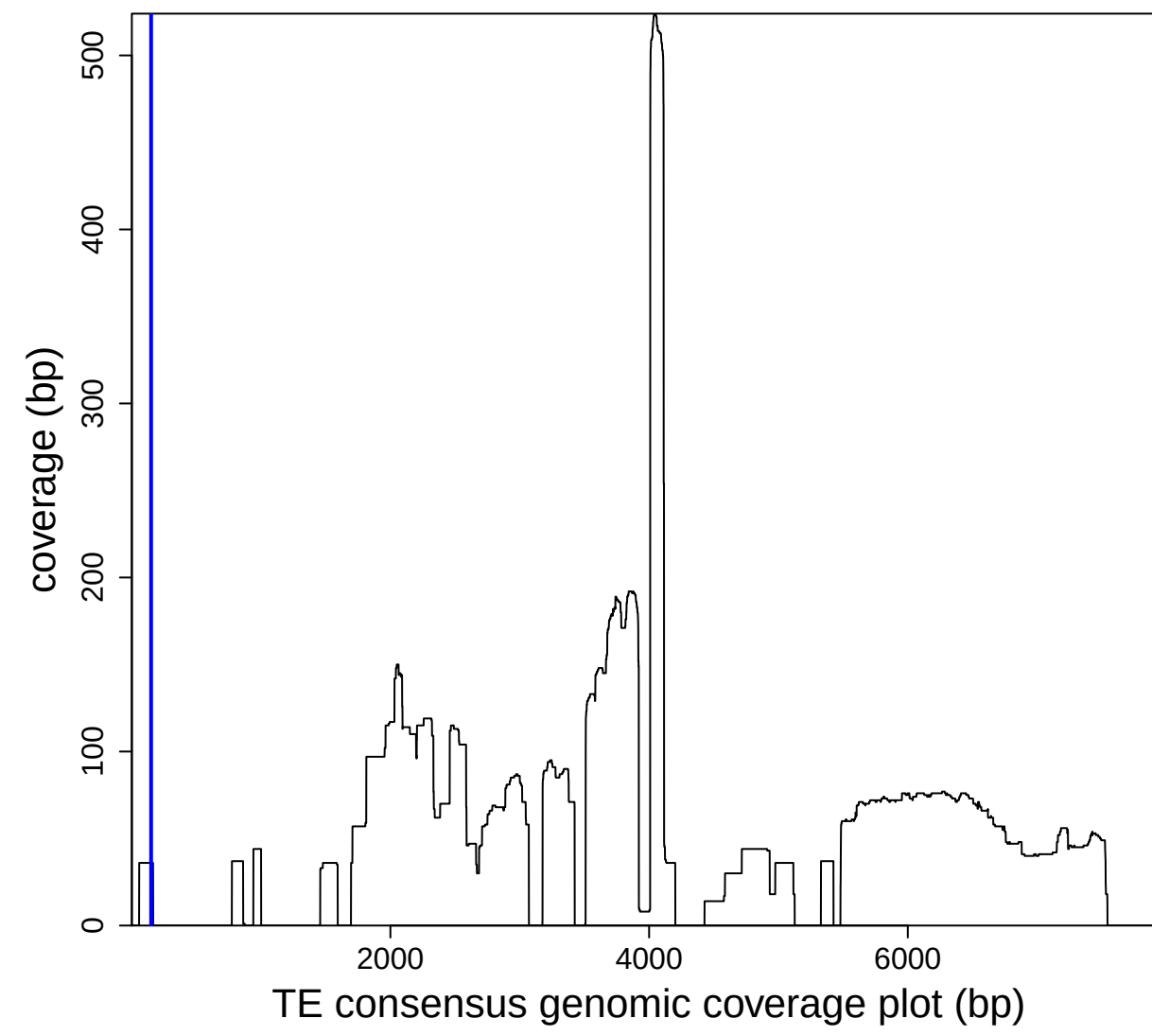
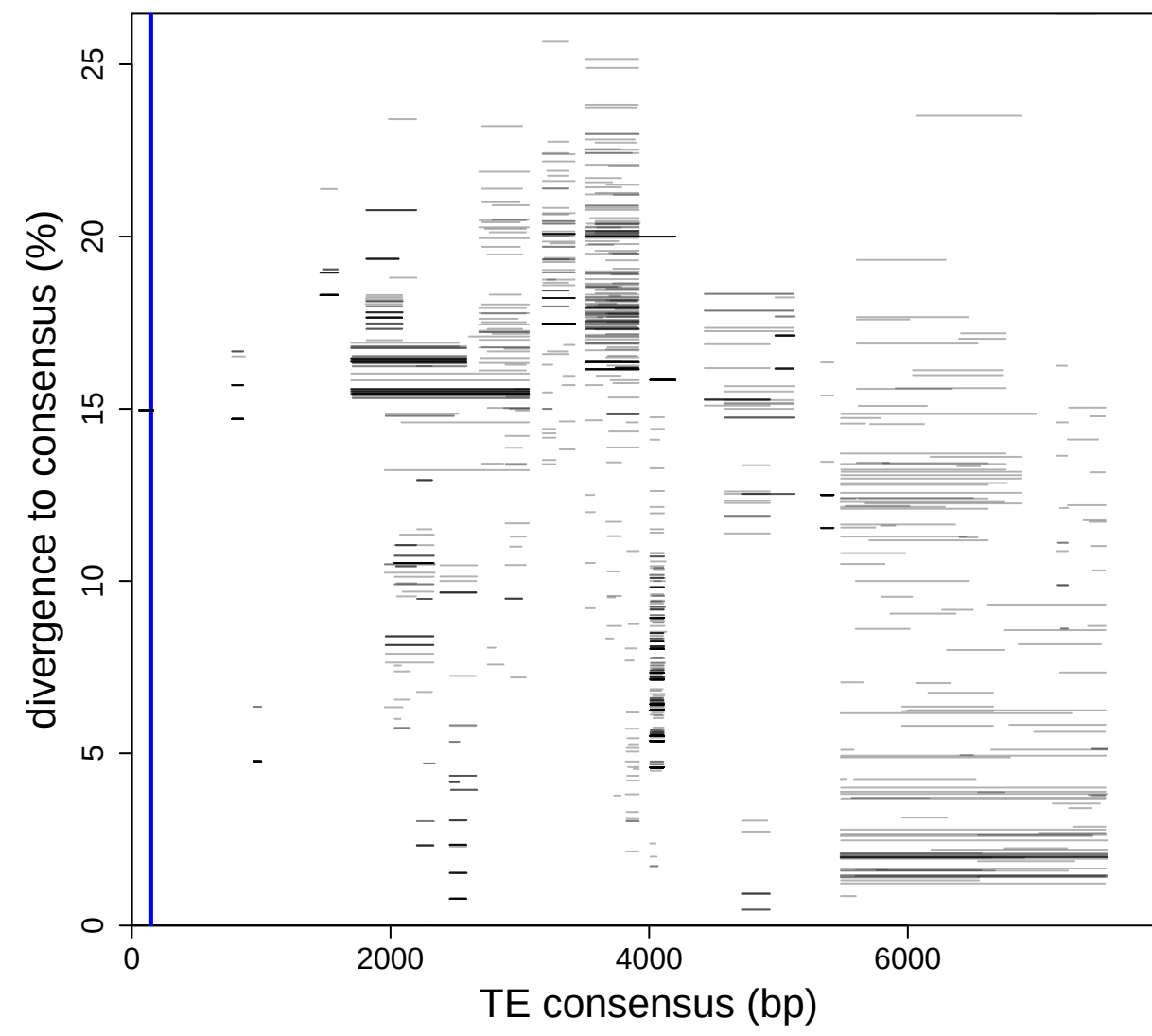
bed uf.bed g 1.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c
size: 7536bp; fragments: 2210; full length: 0 (>=6782.4bp)

After TEtrimmer 7536 bp



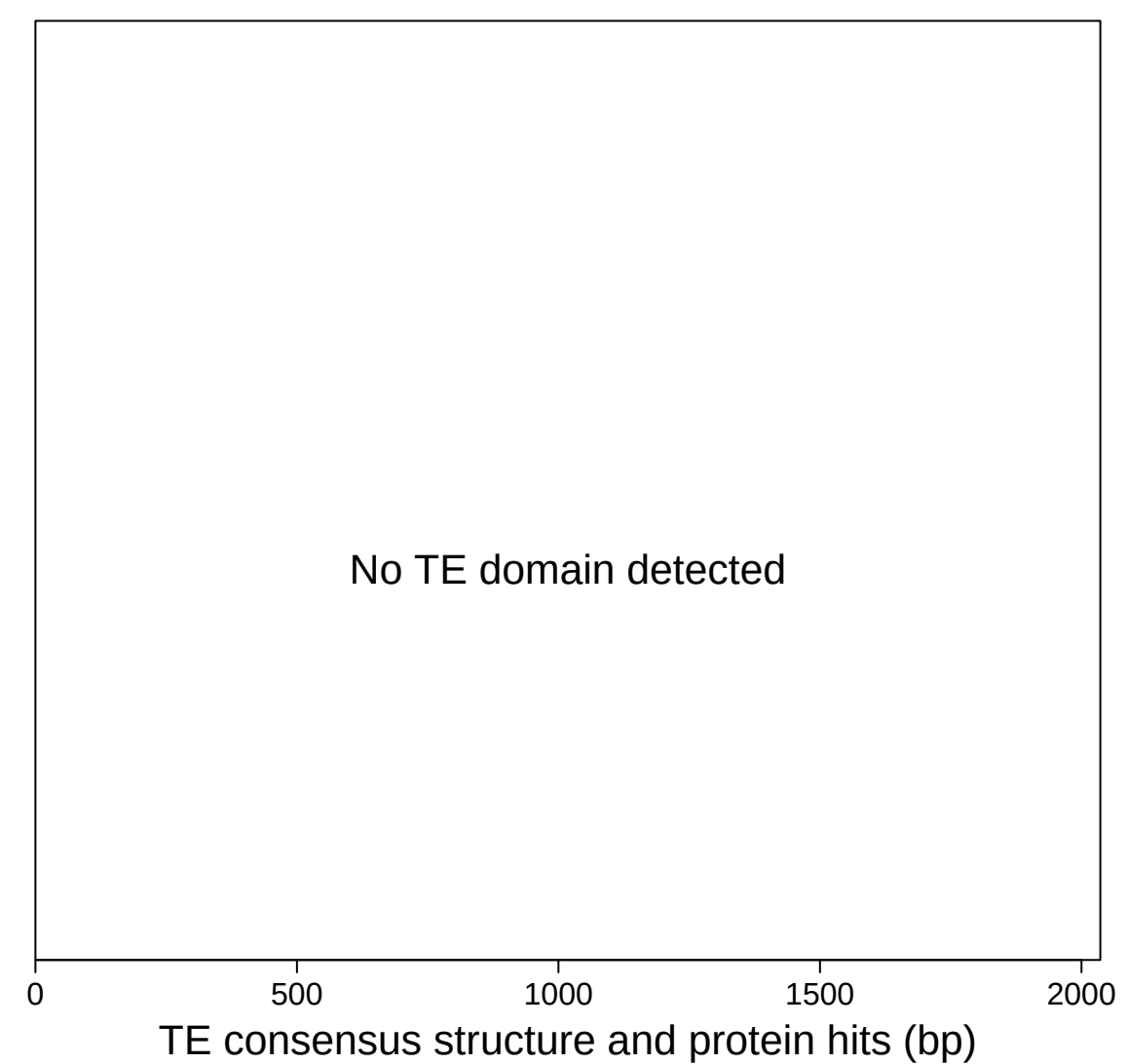
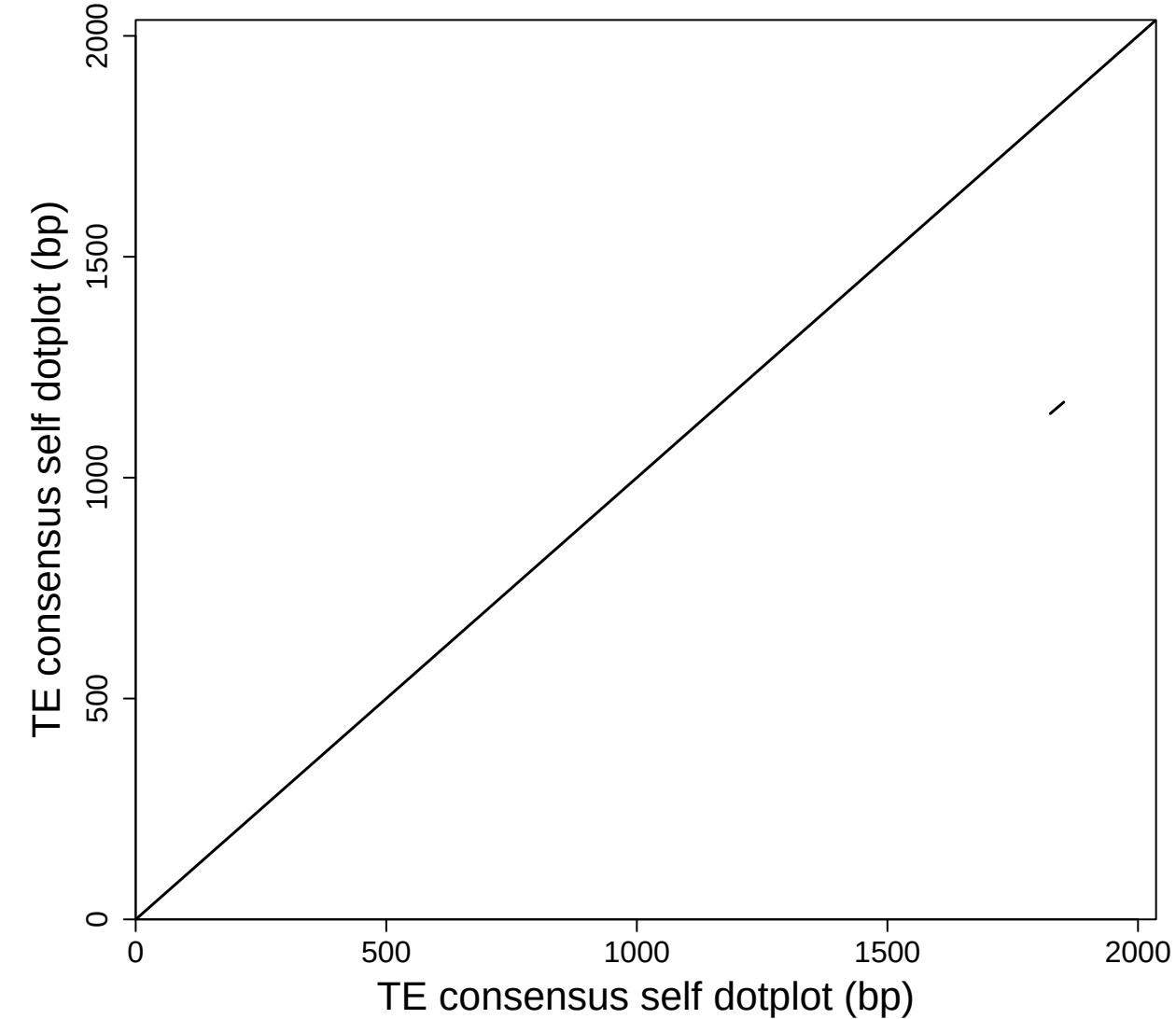
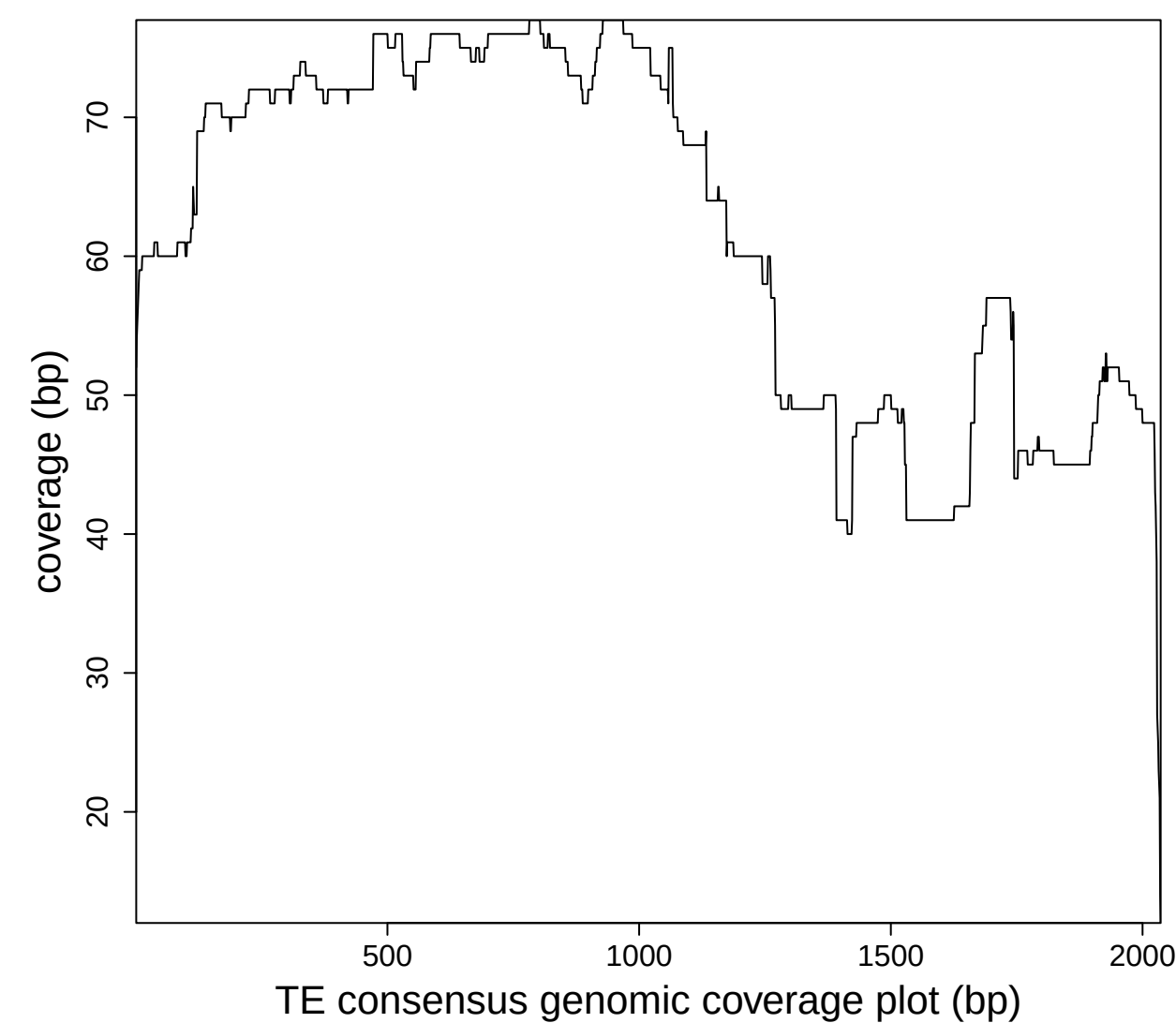
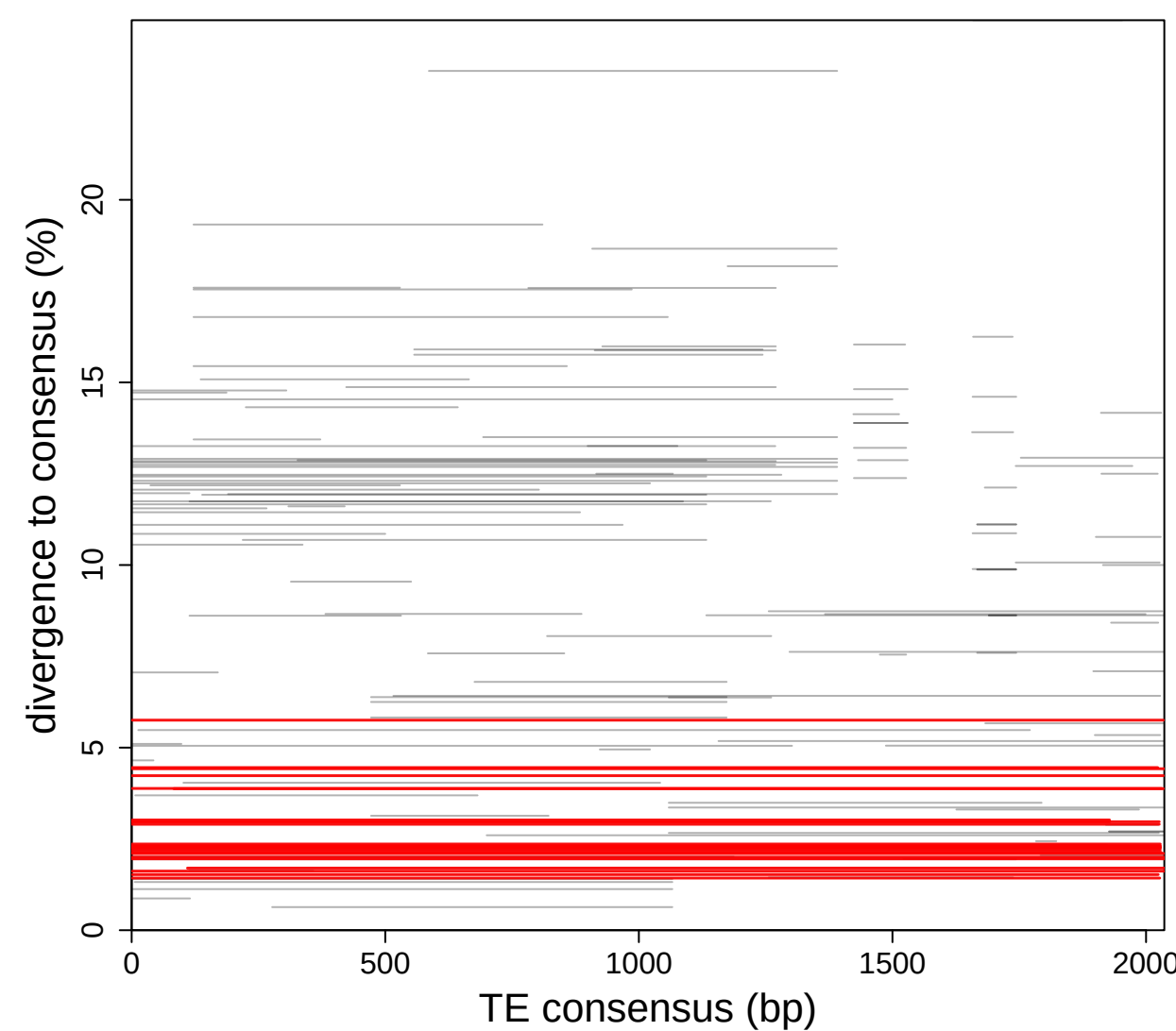
0.fasta.b.bed uf.bed g_1.bed fm_1.bed 0_0_bcln.fa aln.fa cl.f
size: 7995bp; fragments: 1526; full length: 0 (>=7195.5bp)

After TEtrimmer Extended plot Blue lines are boundaries

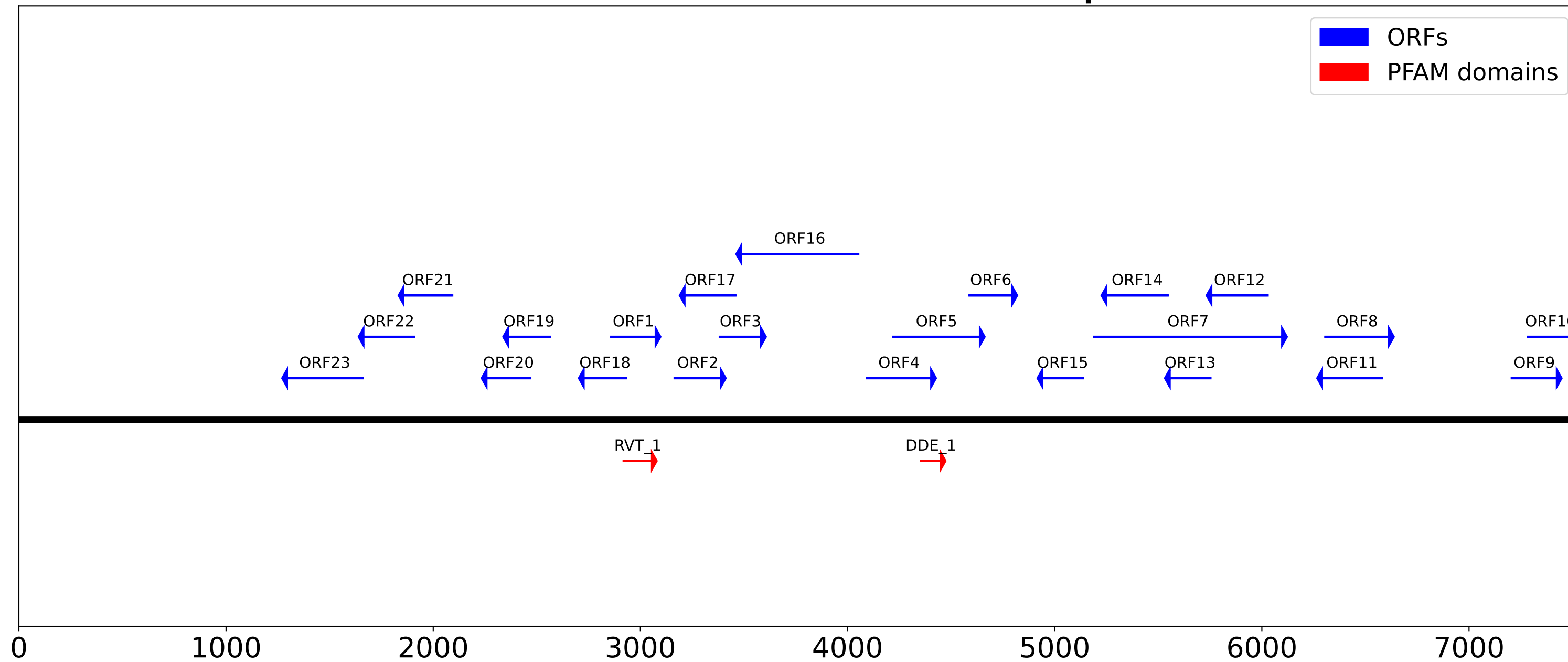


TE: rnd_5_family_4690
size: 2036bp; fragments: 158; full length: 26 (≥ 1832.4 bp)

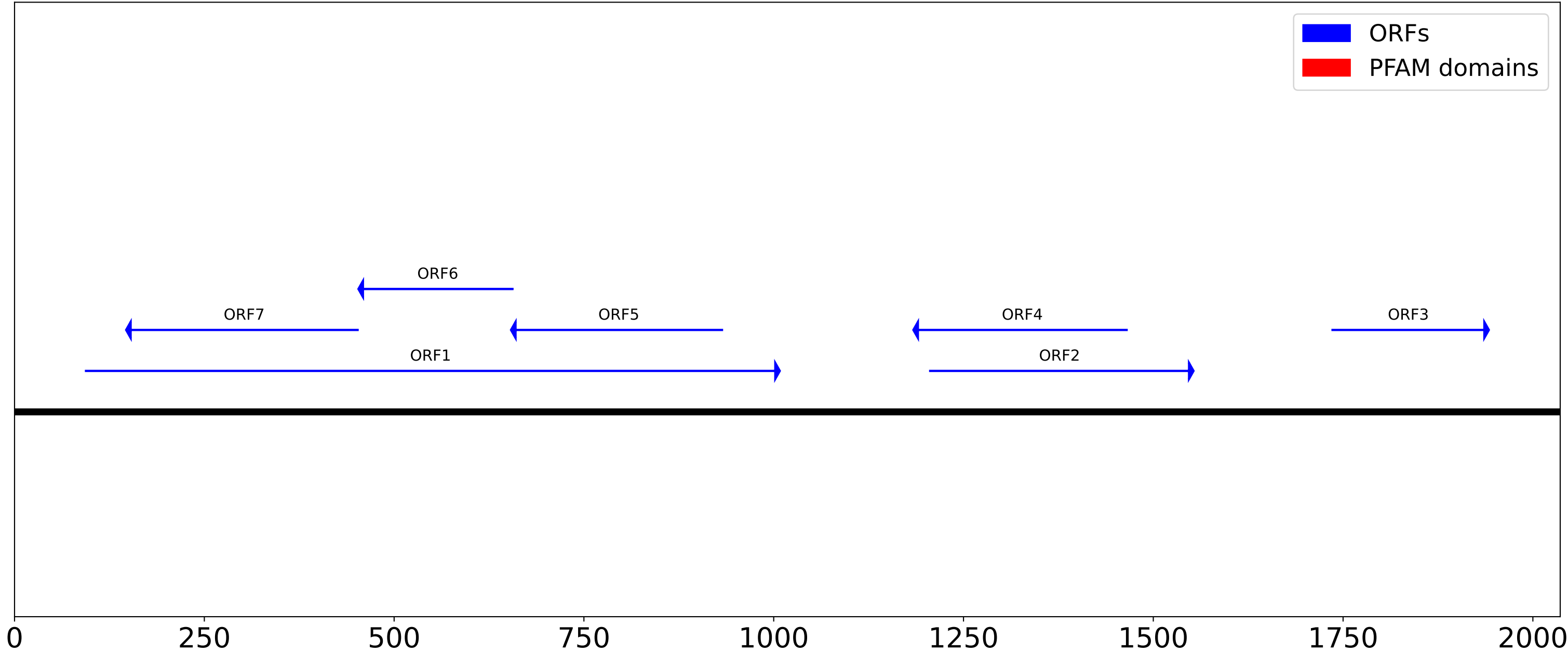
Before TEtrimmer 2036 bp



After TEtrimmer ORF and PFAM domain plot



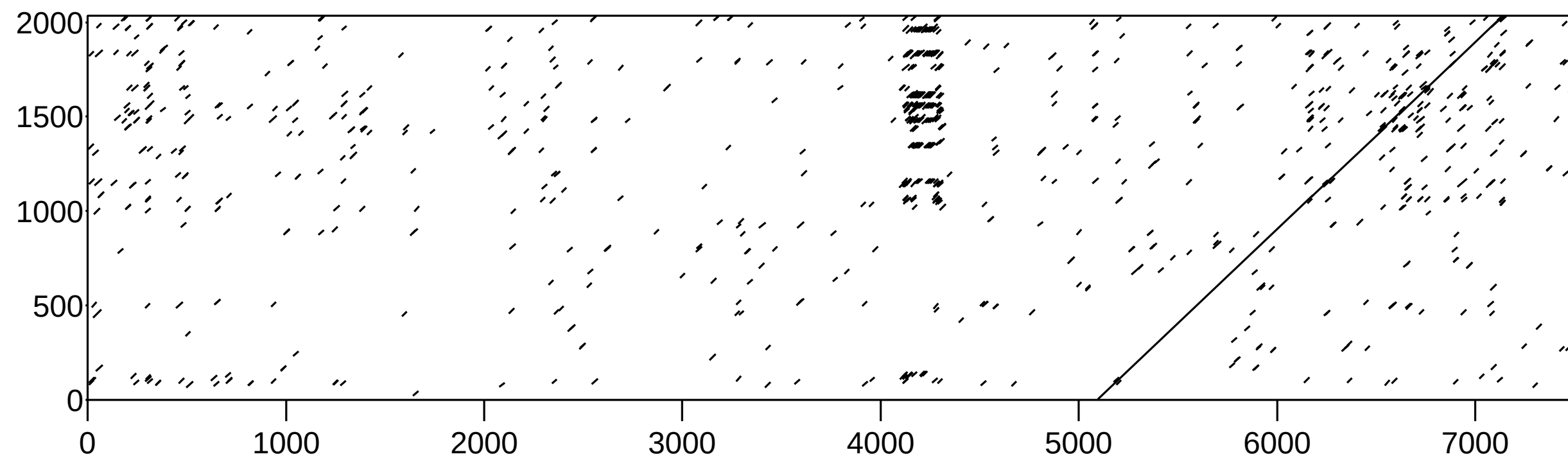
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)