

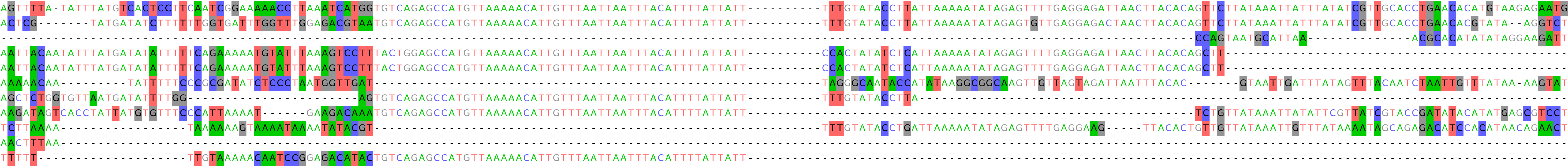
Start crop Point



End crop Point

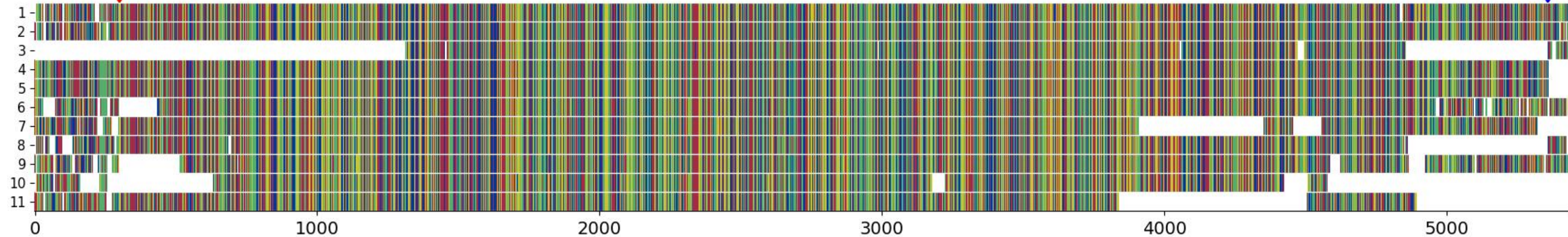


MSA length = 5059



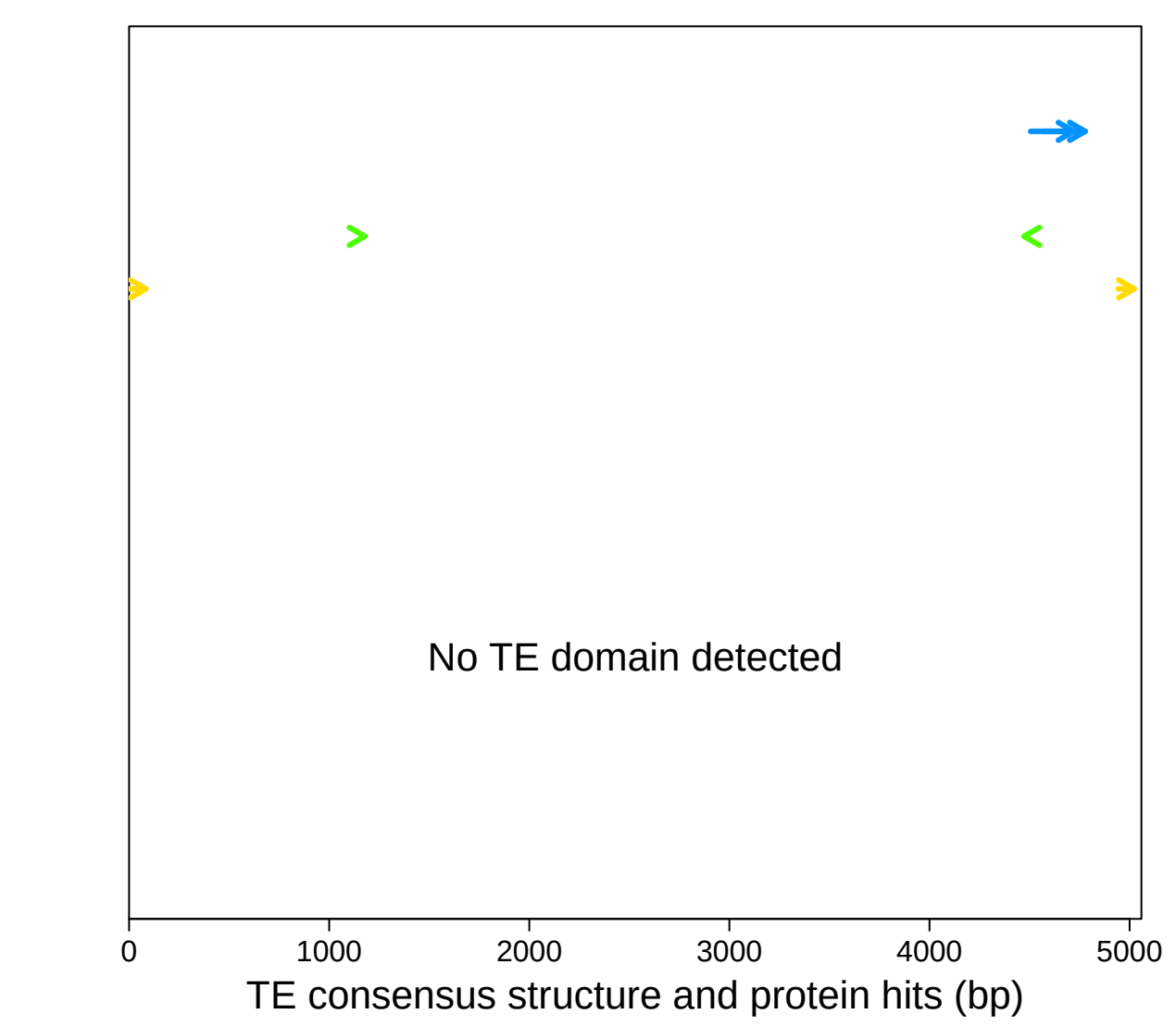
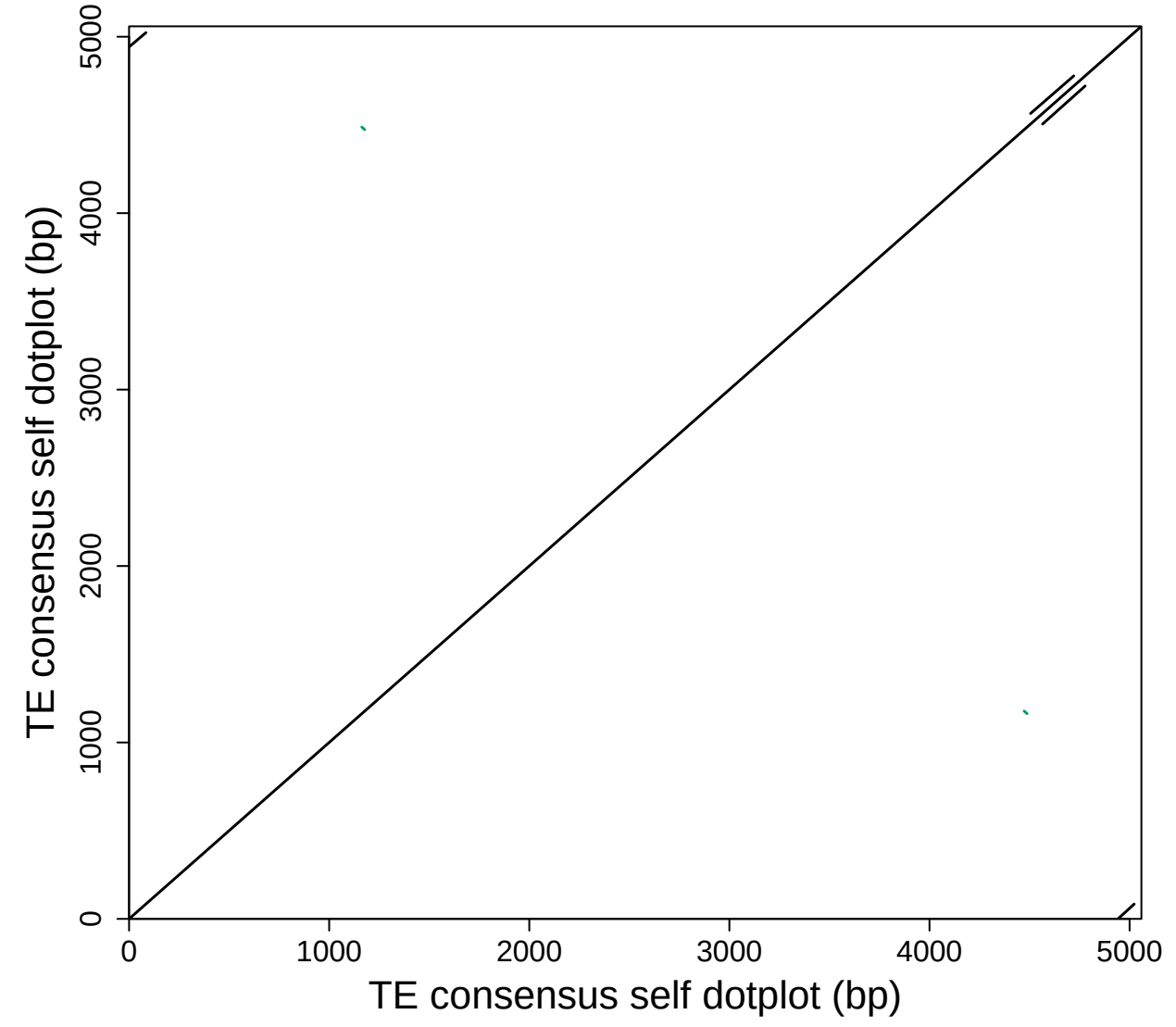
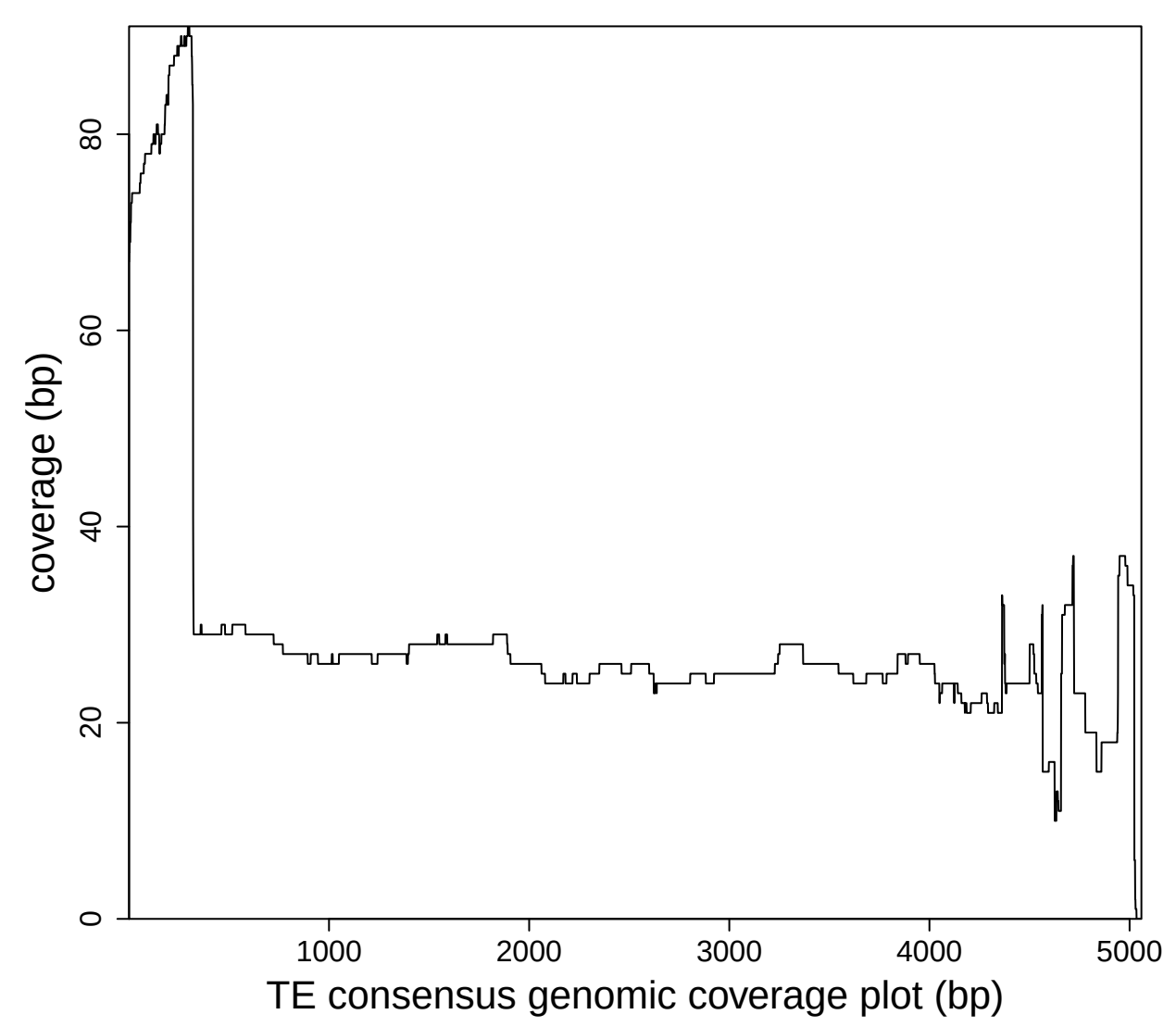
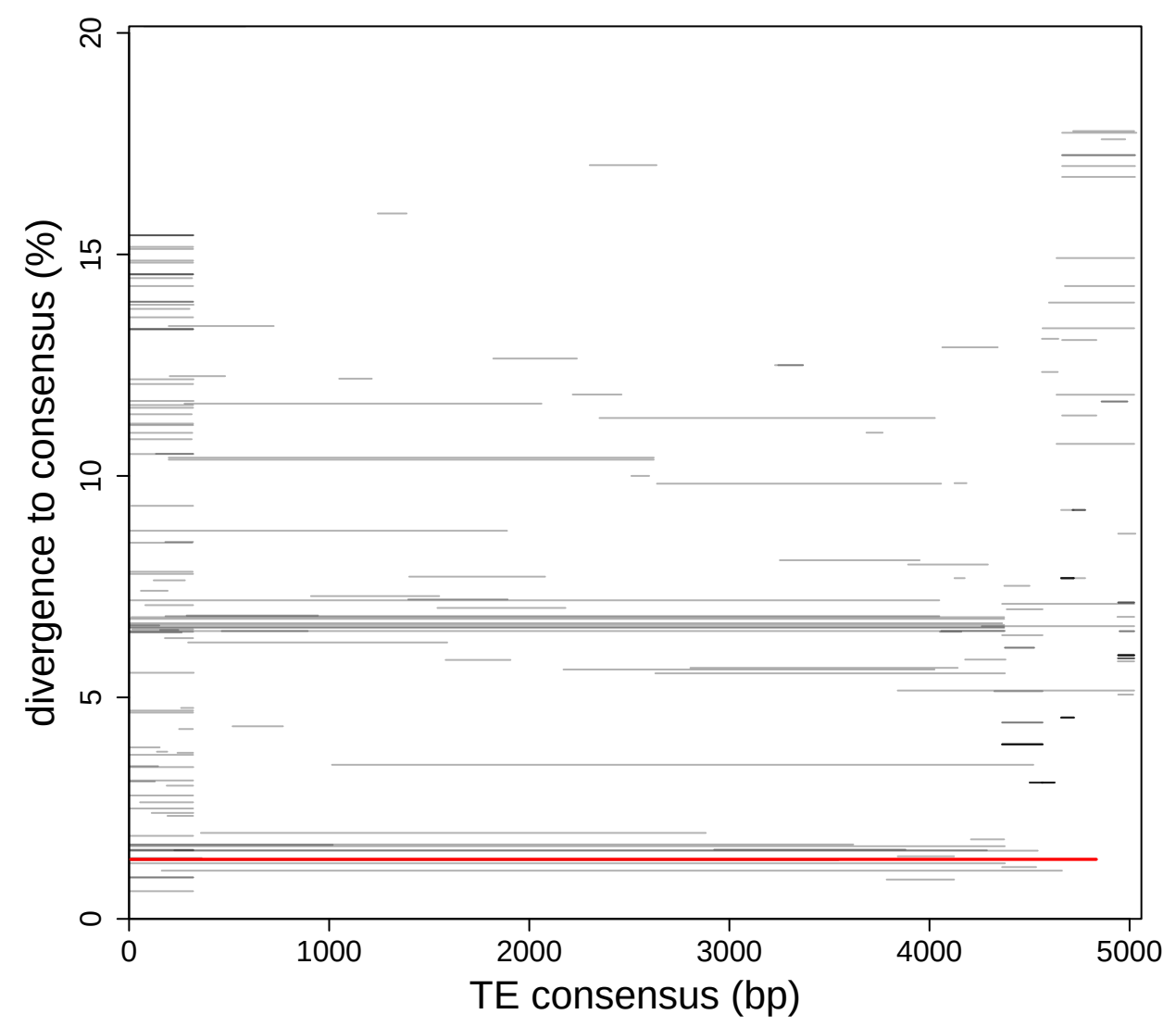
Start crop Point

End crop Point



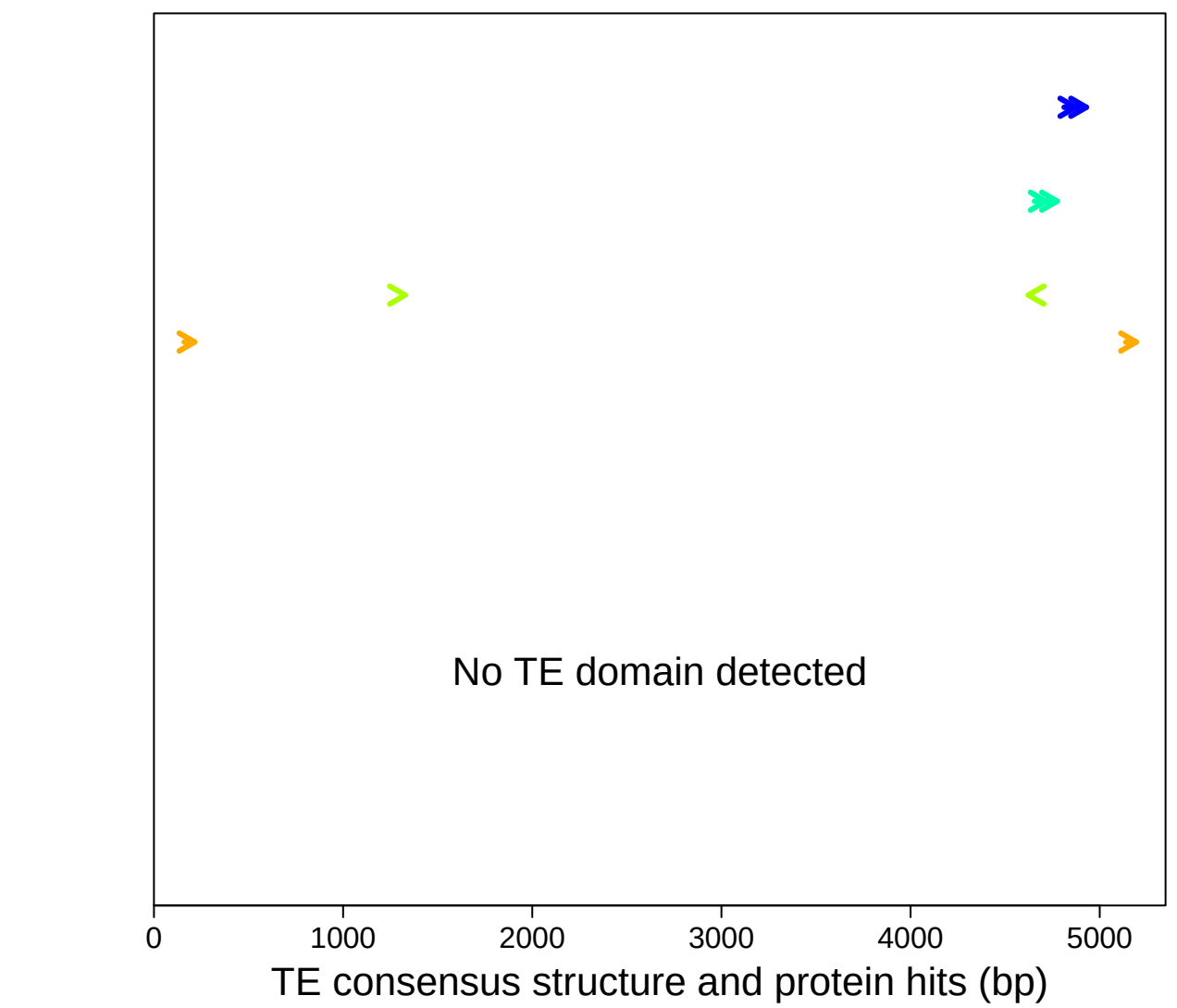
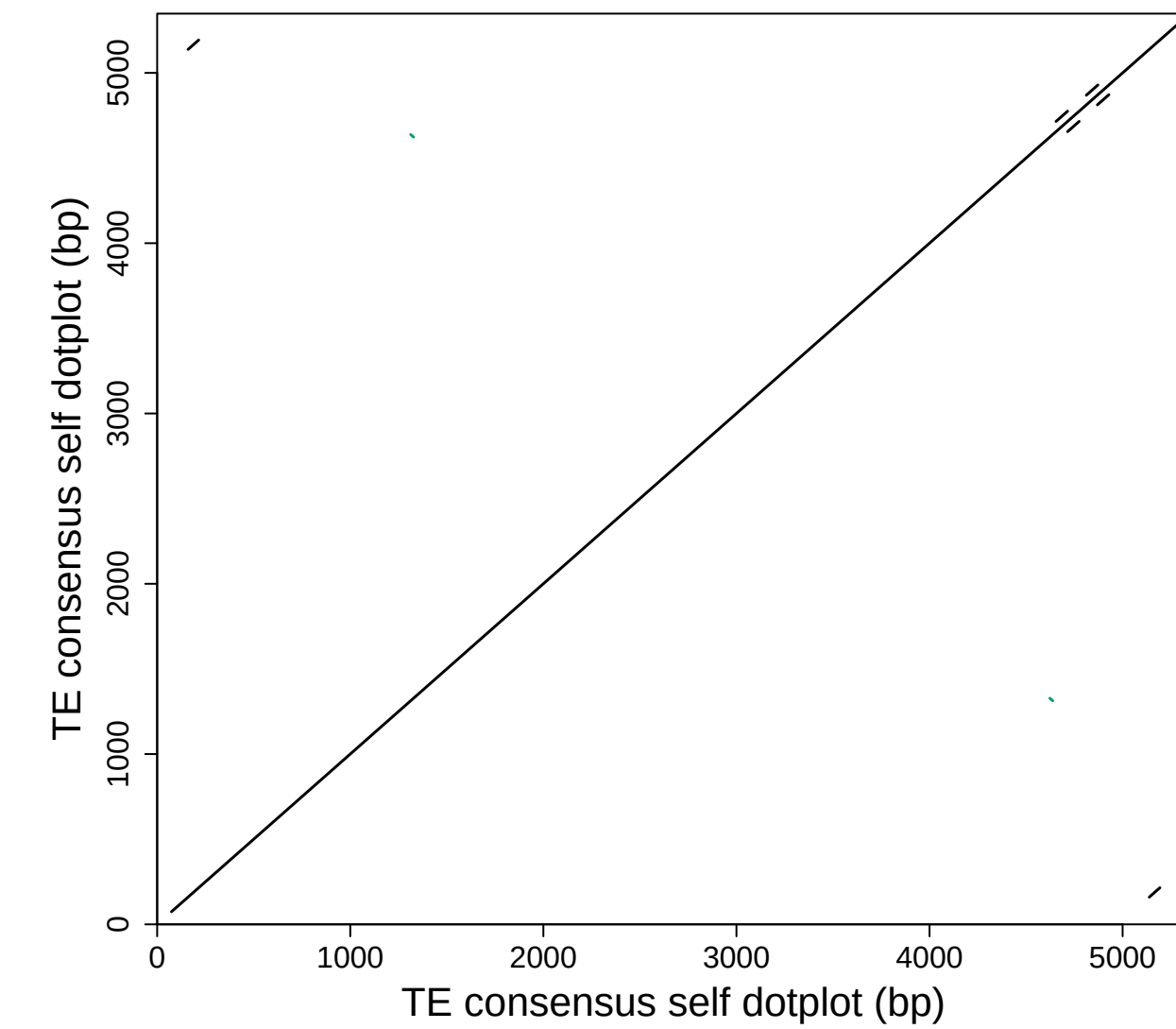
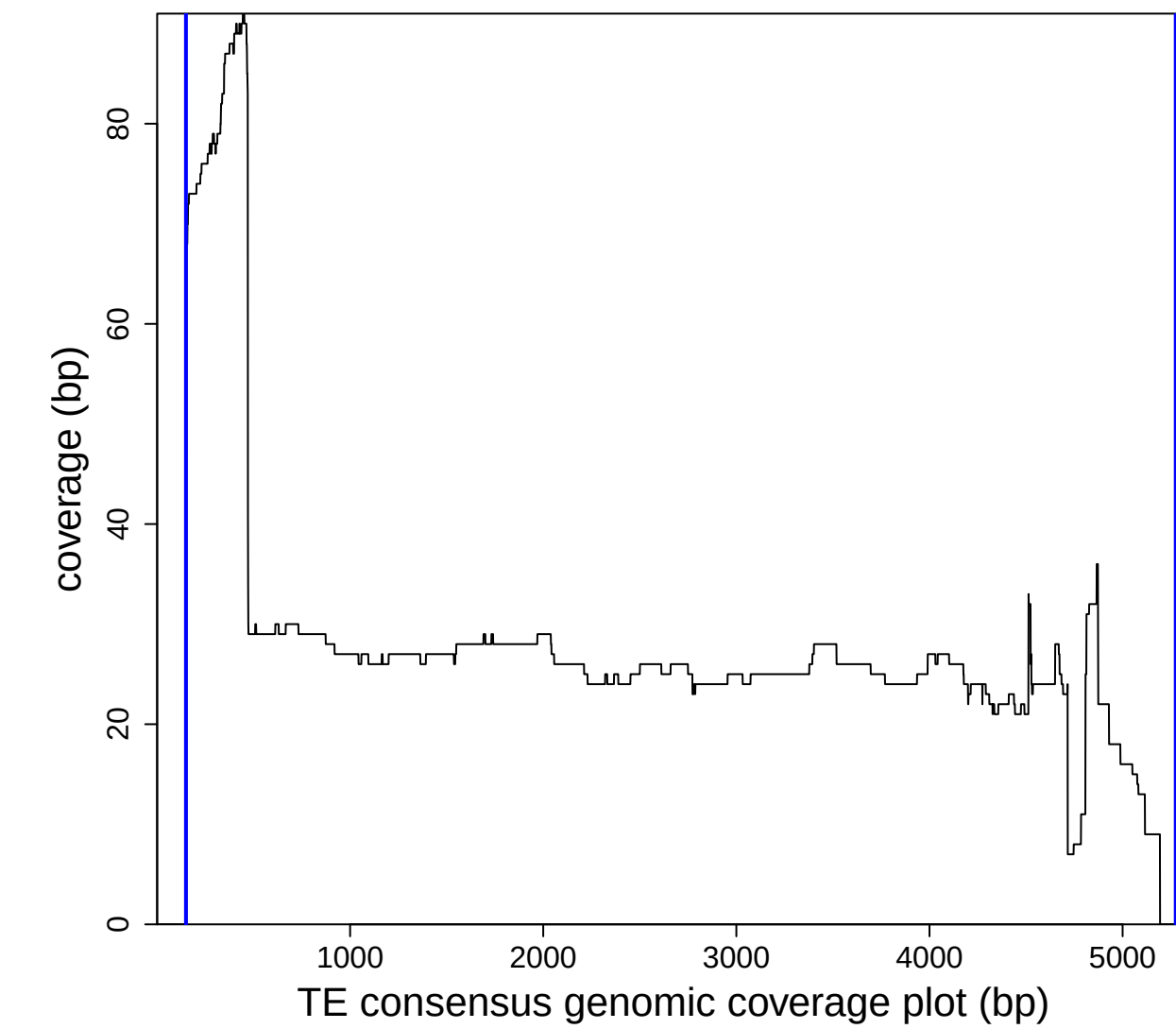
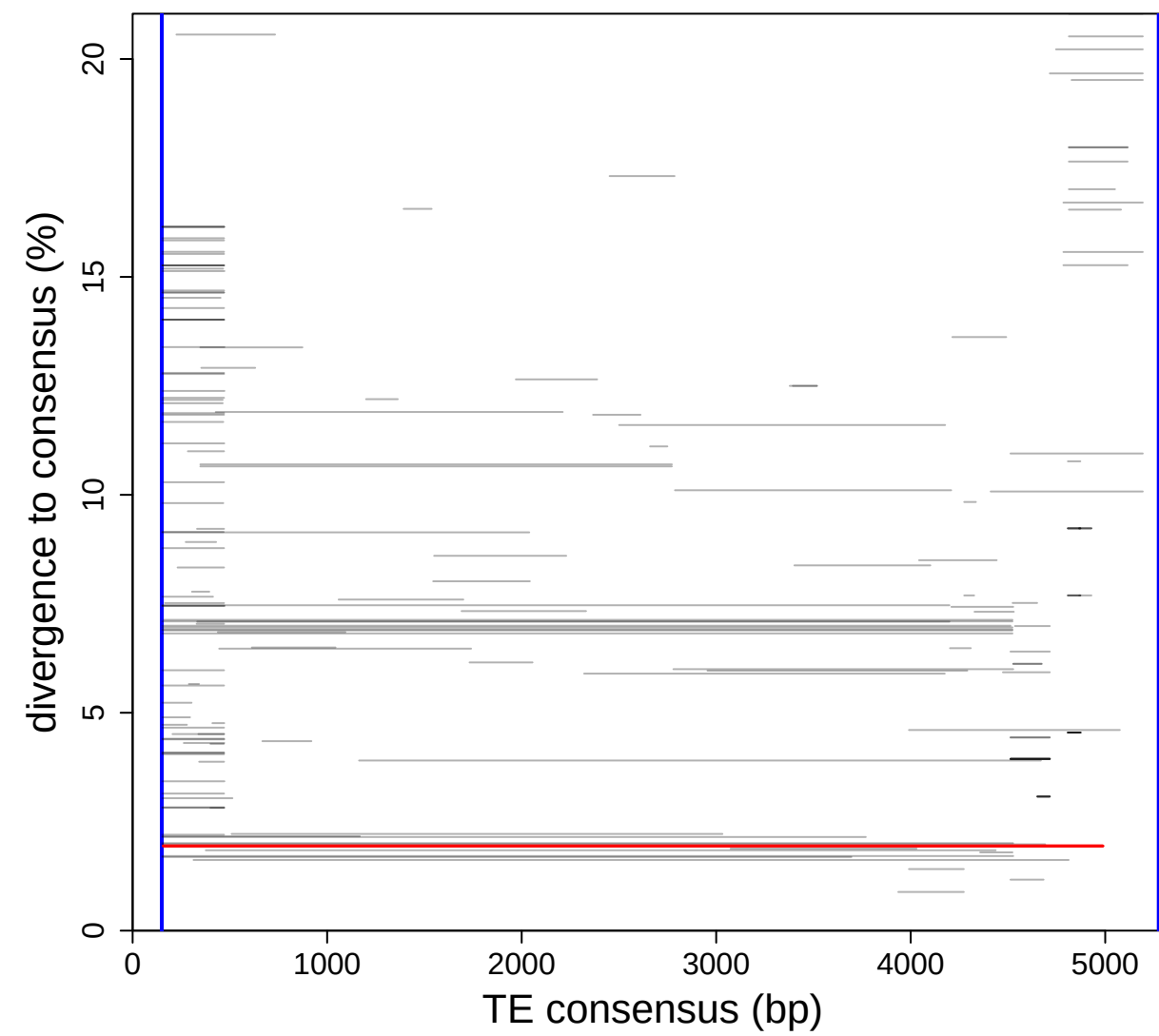
b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 5059bp; fragments: 221; full length: 2 (>=4553.1bp)

After TEtrimmer 5059 bp

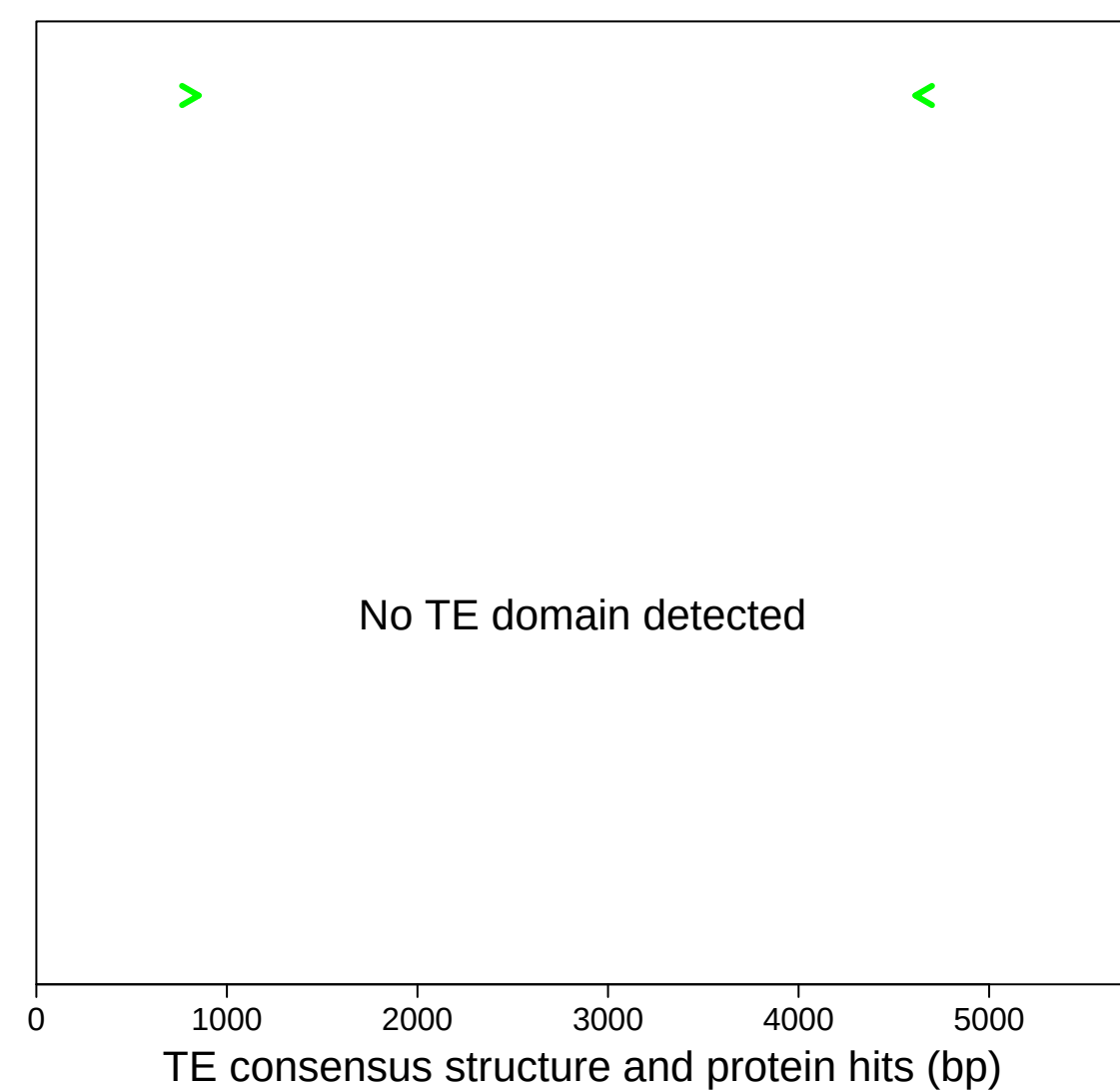
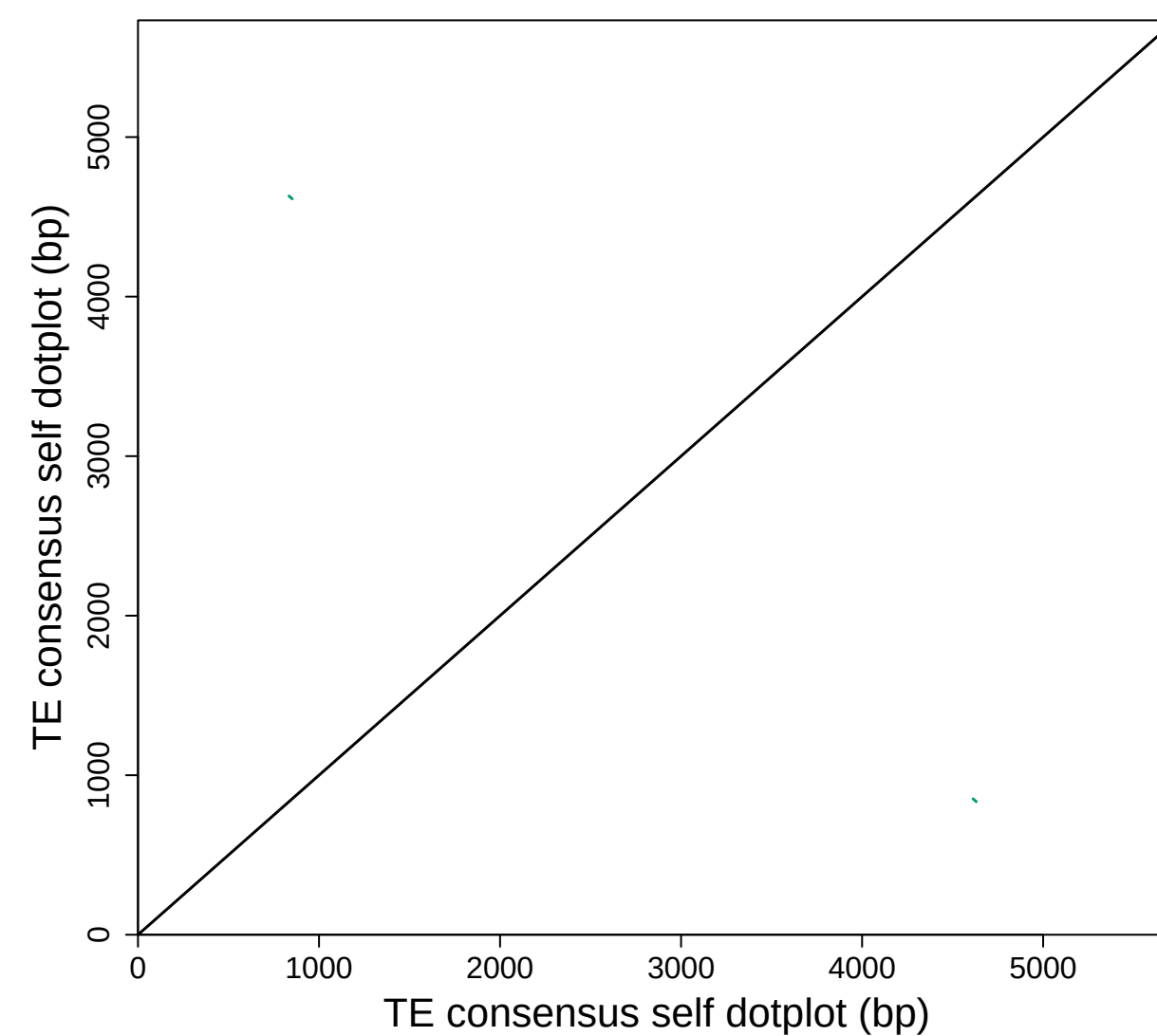
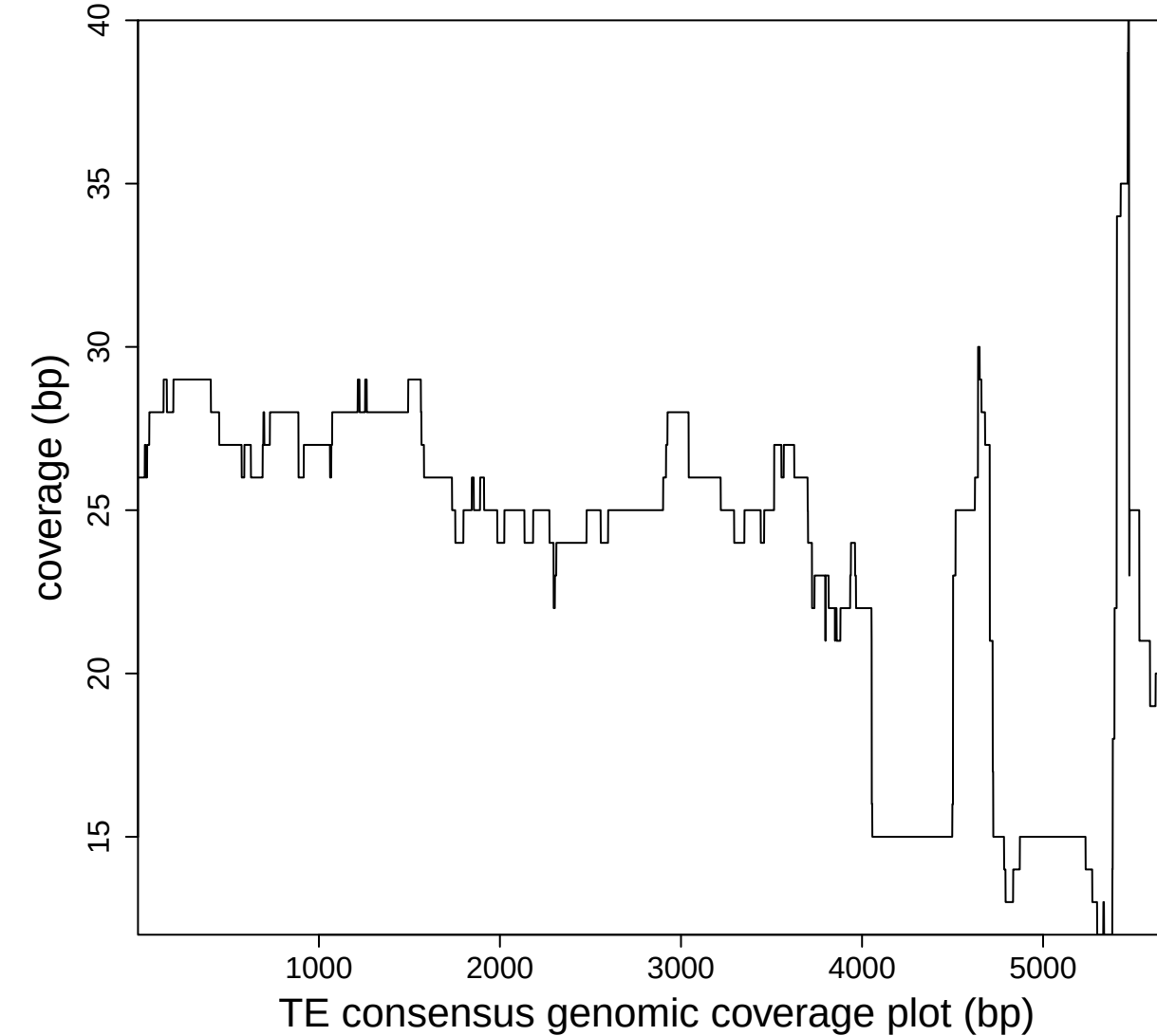
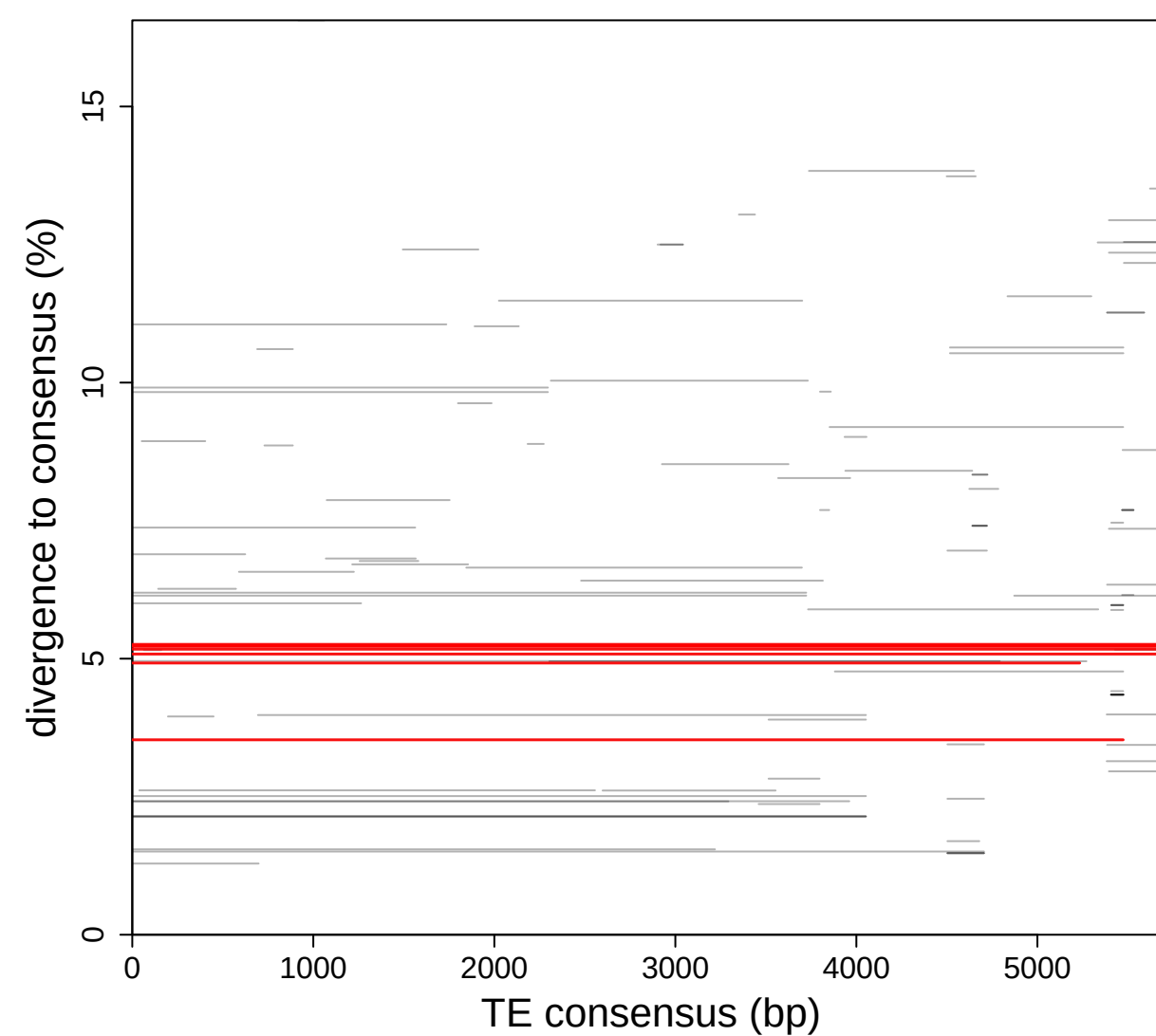


.fasta.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 5348bp; fragments: 187; full length: 2 (>=4813.2bp)

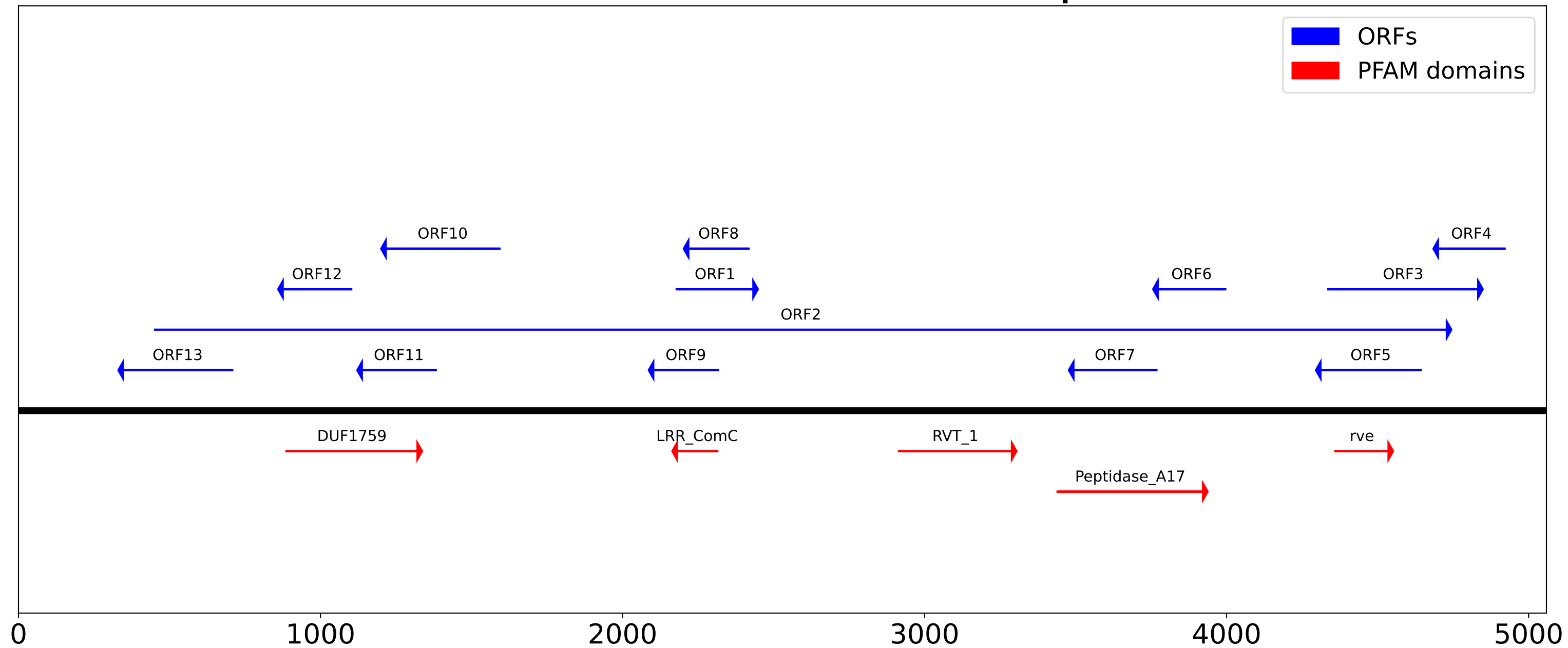
After TEtrimmer Extended plot Blue lines are boundaries



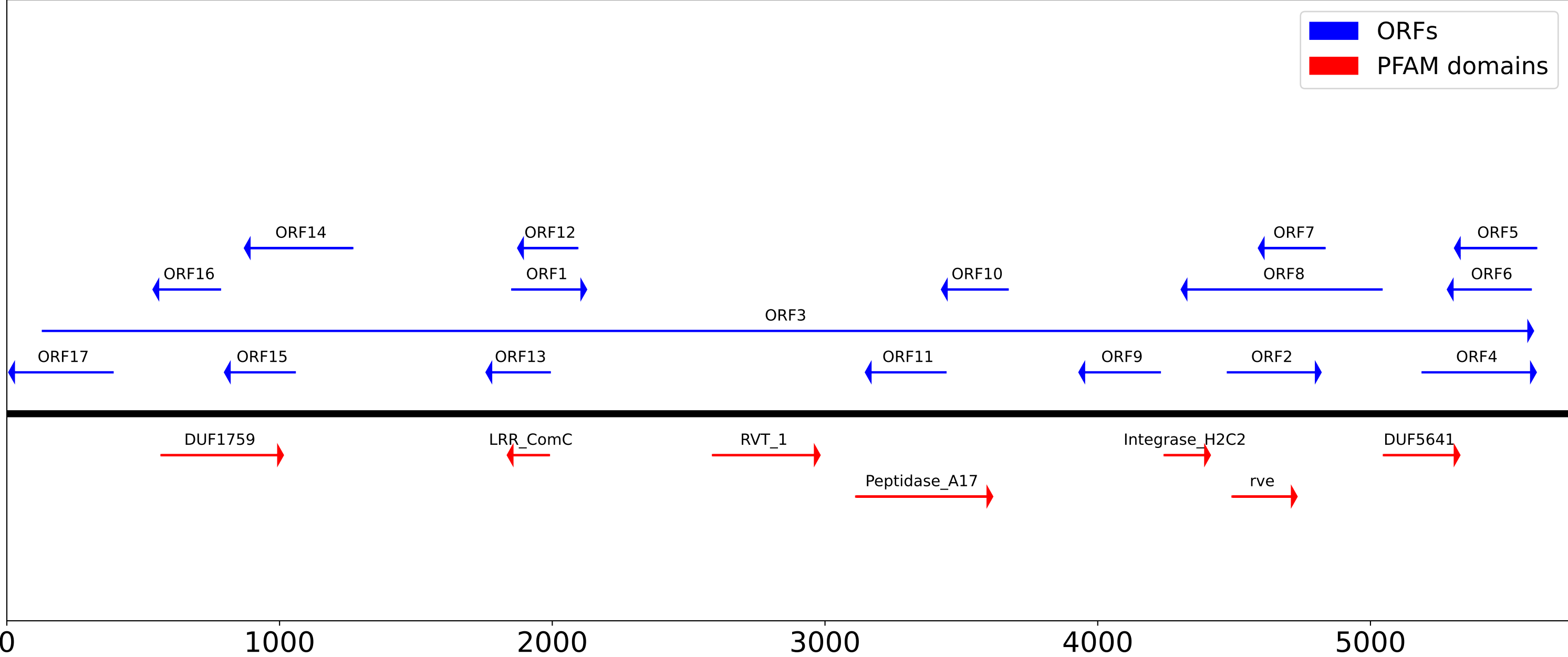
TE: ltr_1_family_506
size: 5732bp; fragments: 116; full length: 7 (≥ 5158.8 bp)



After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

