

Start crop Point

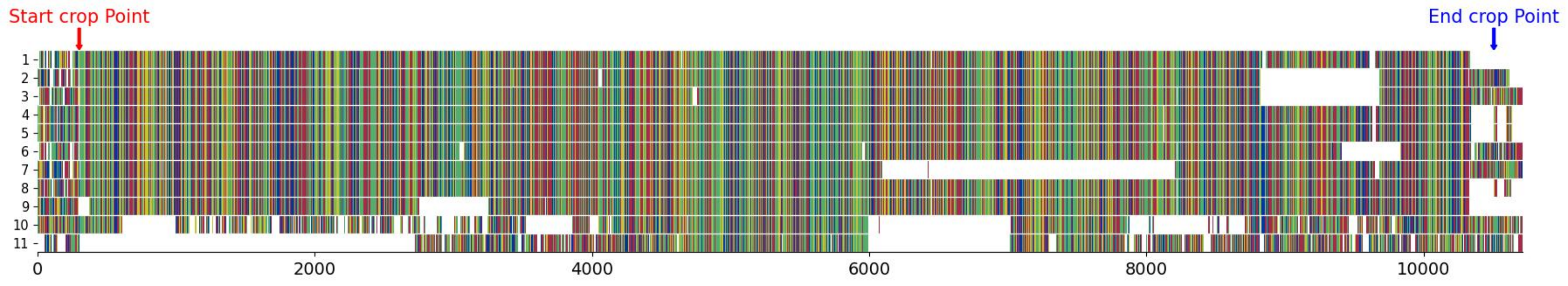


End crop Point



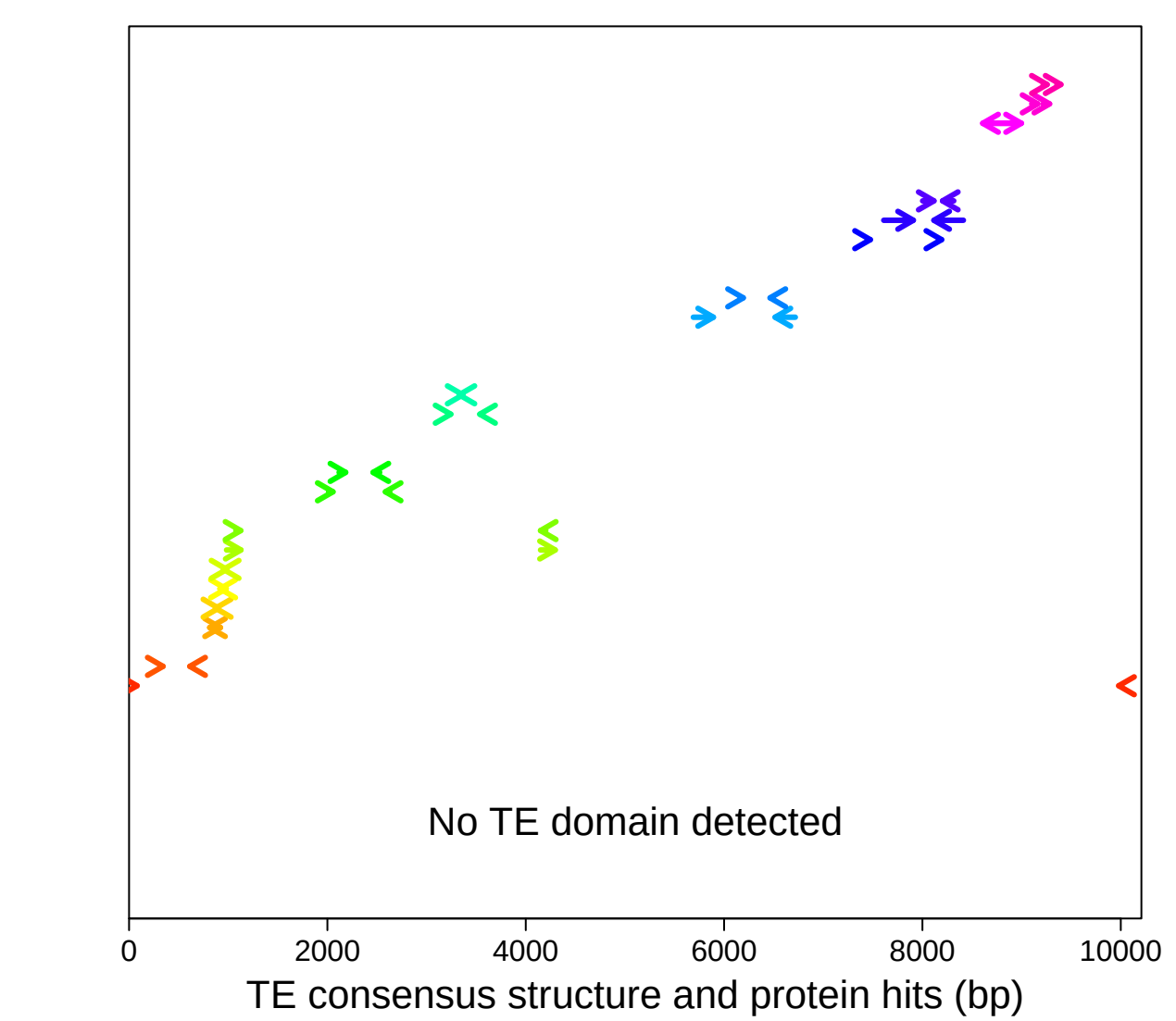
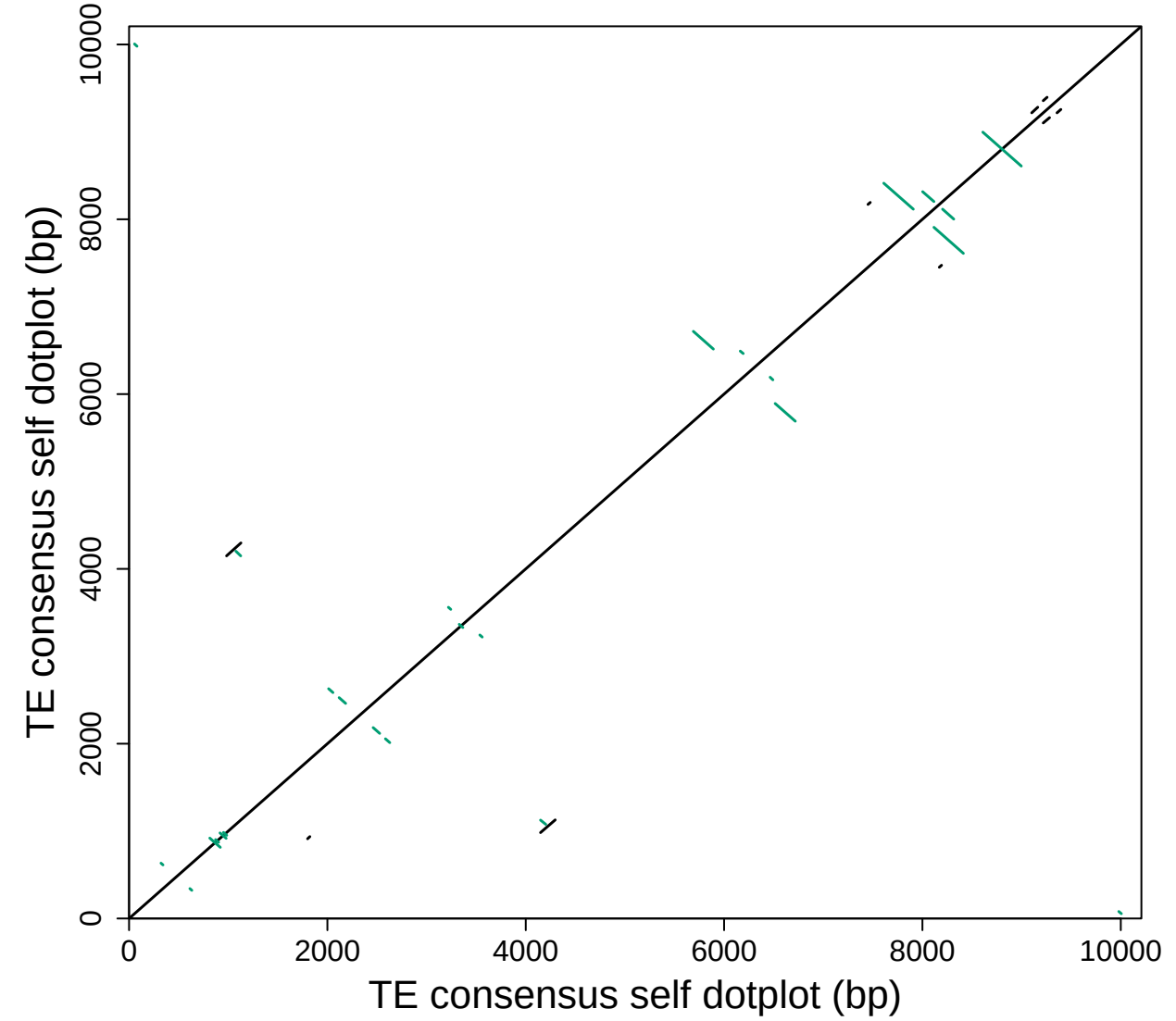
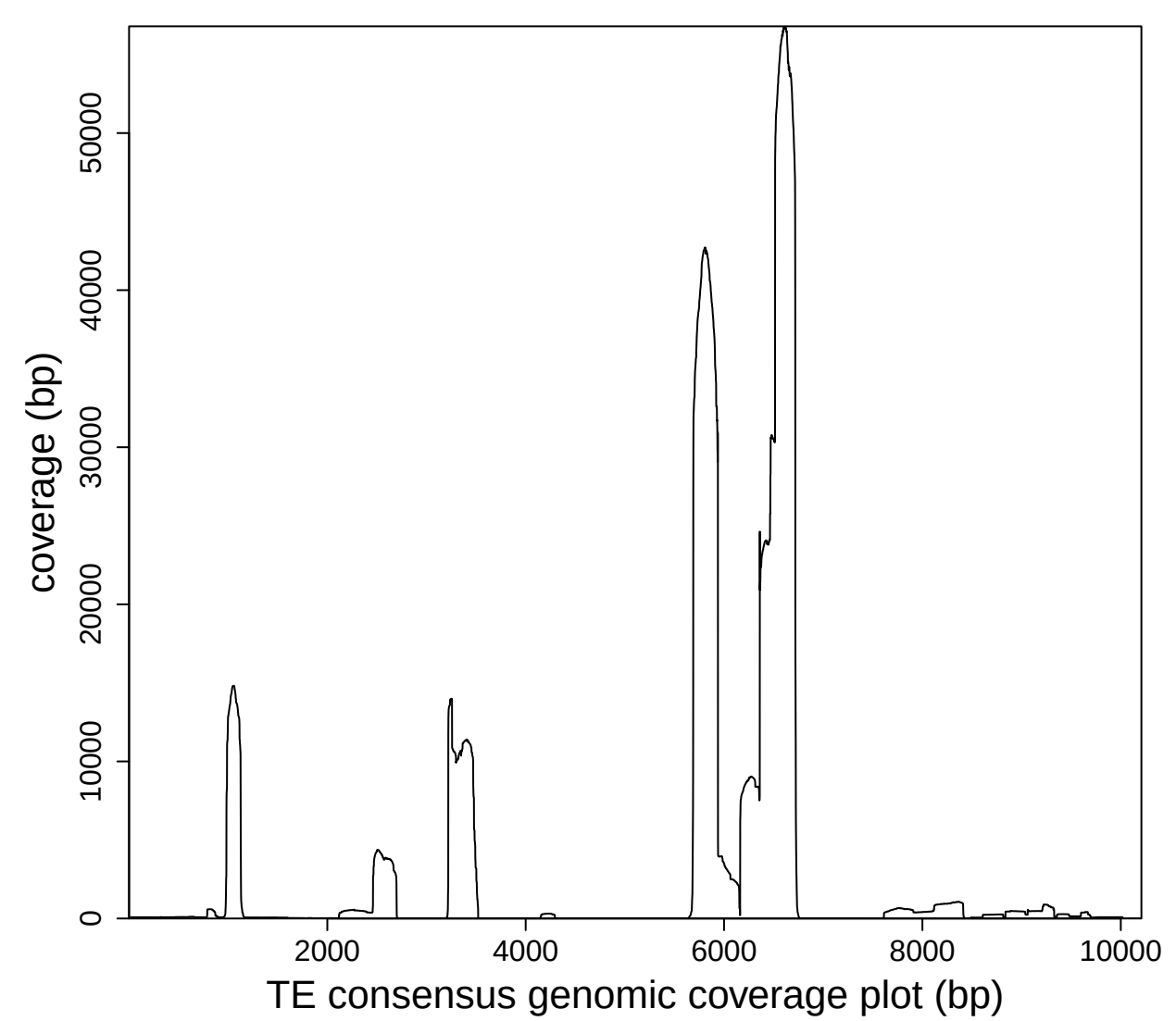
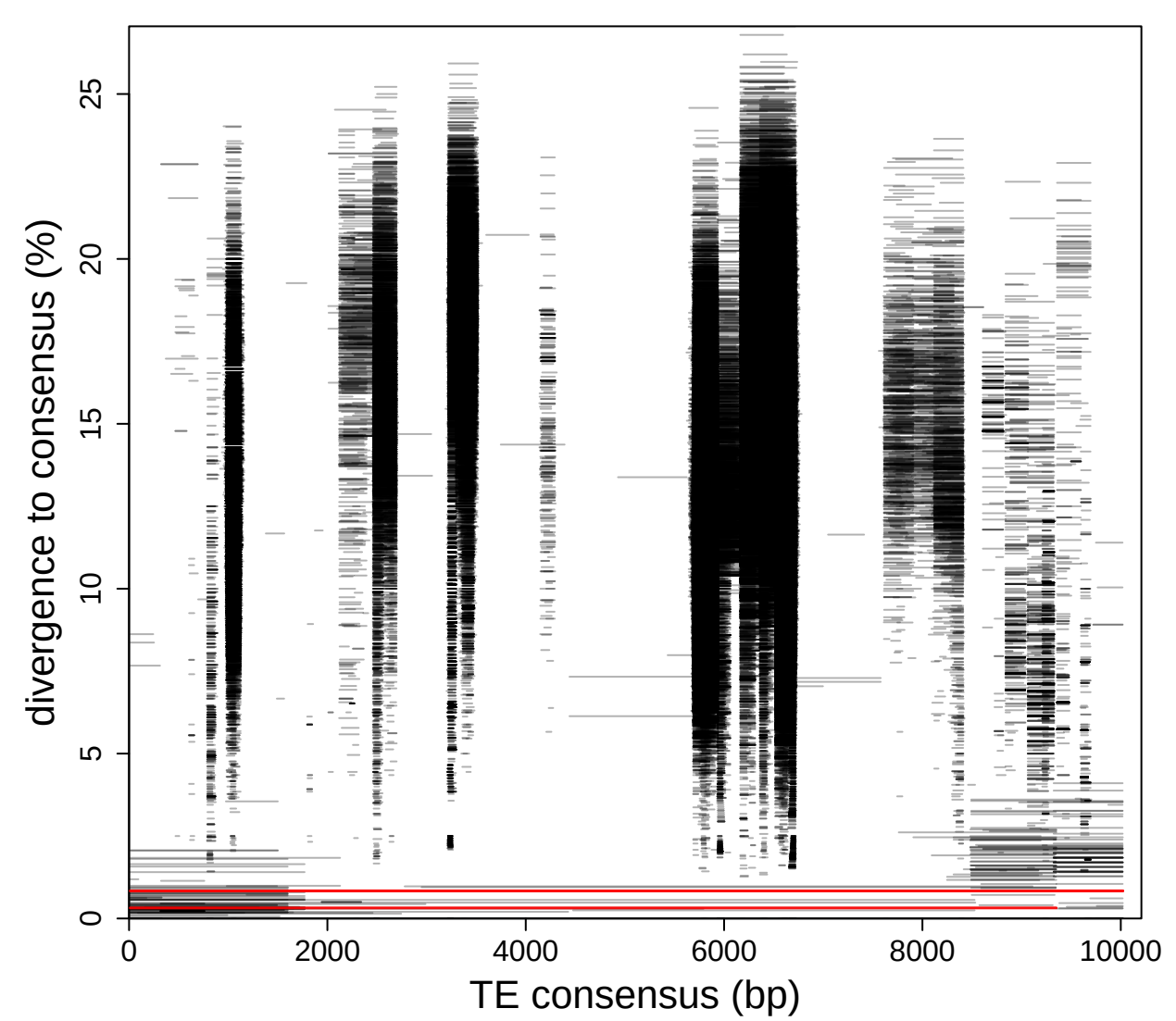
MSA length = 10208





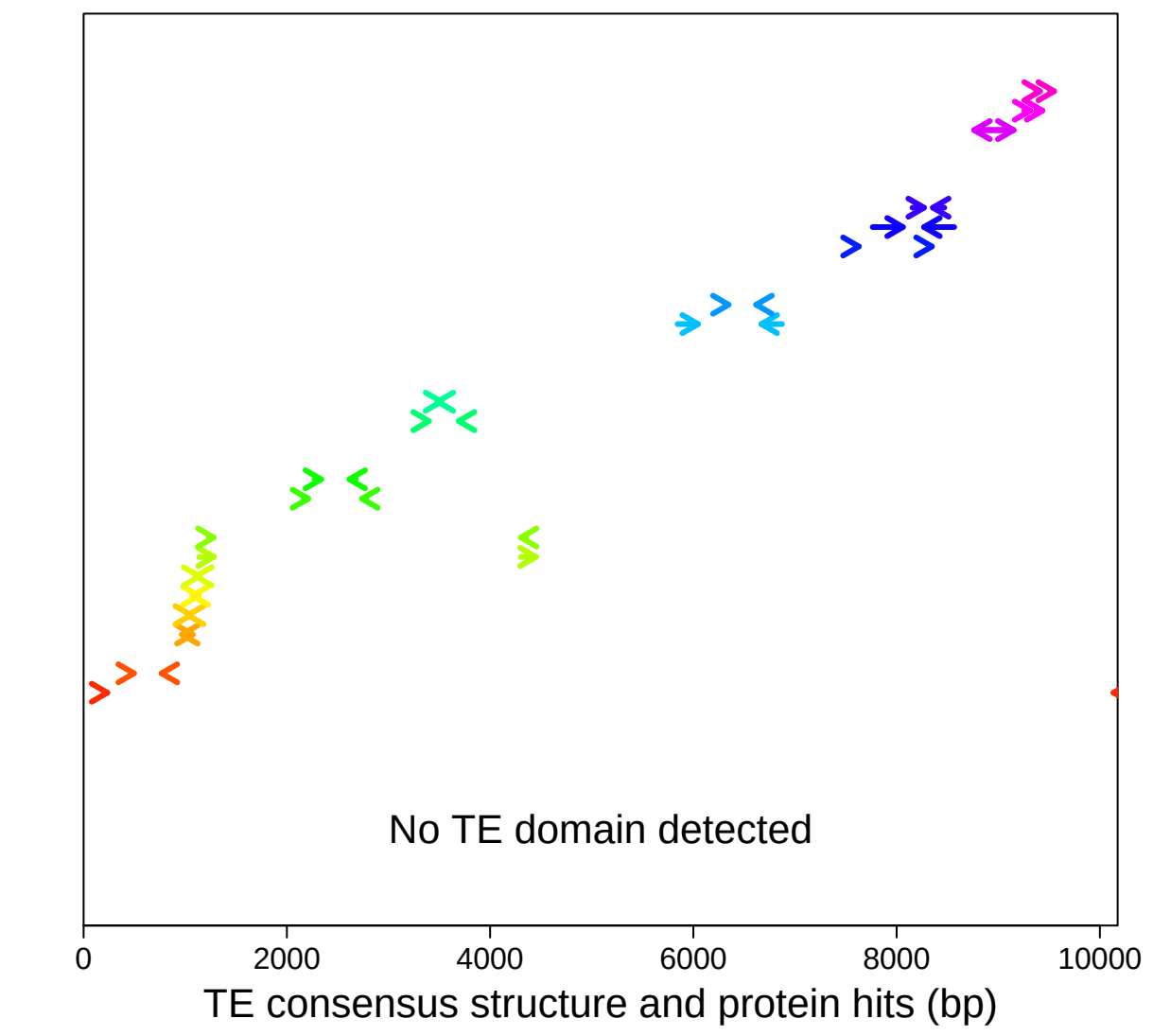
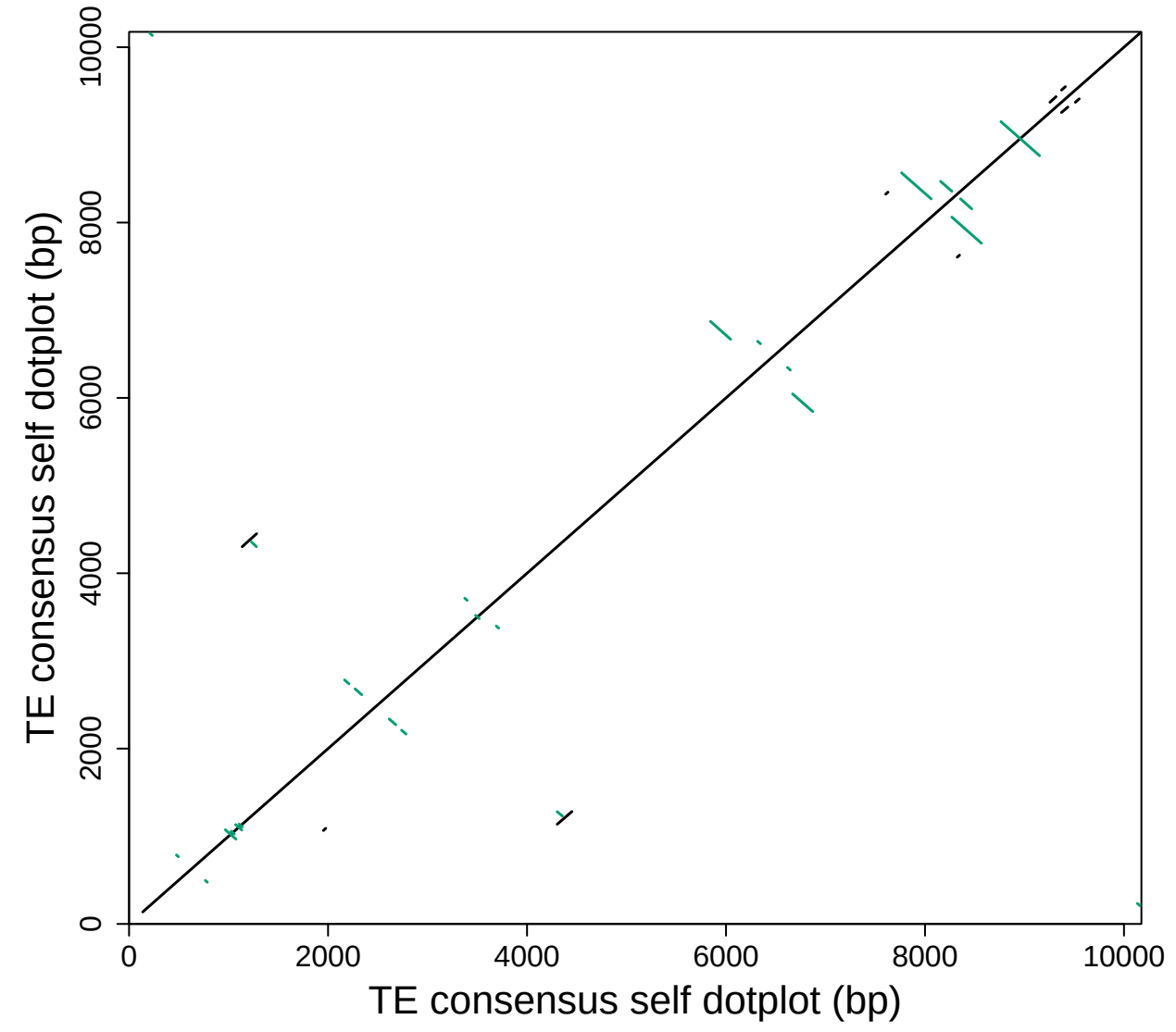
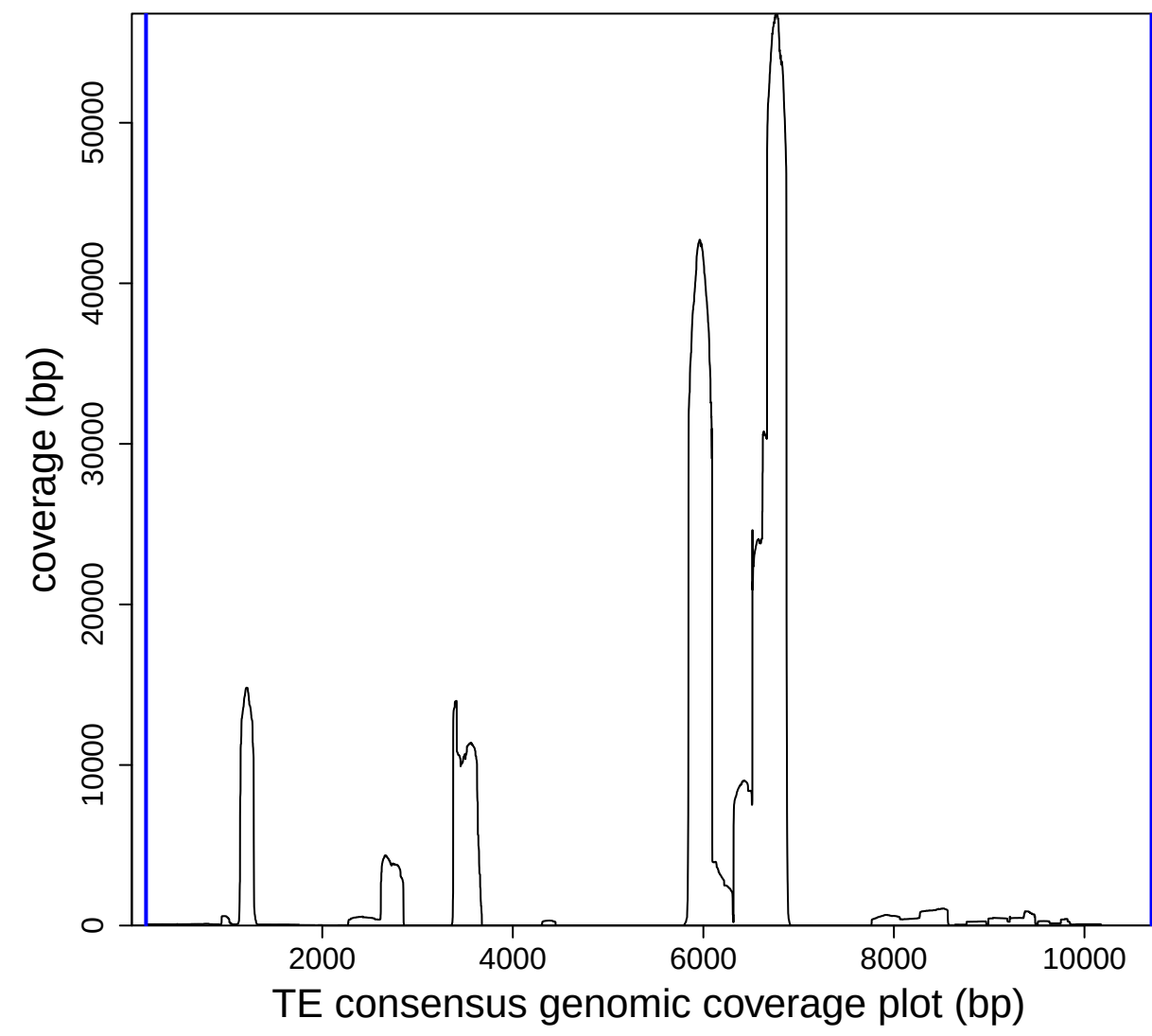
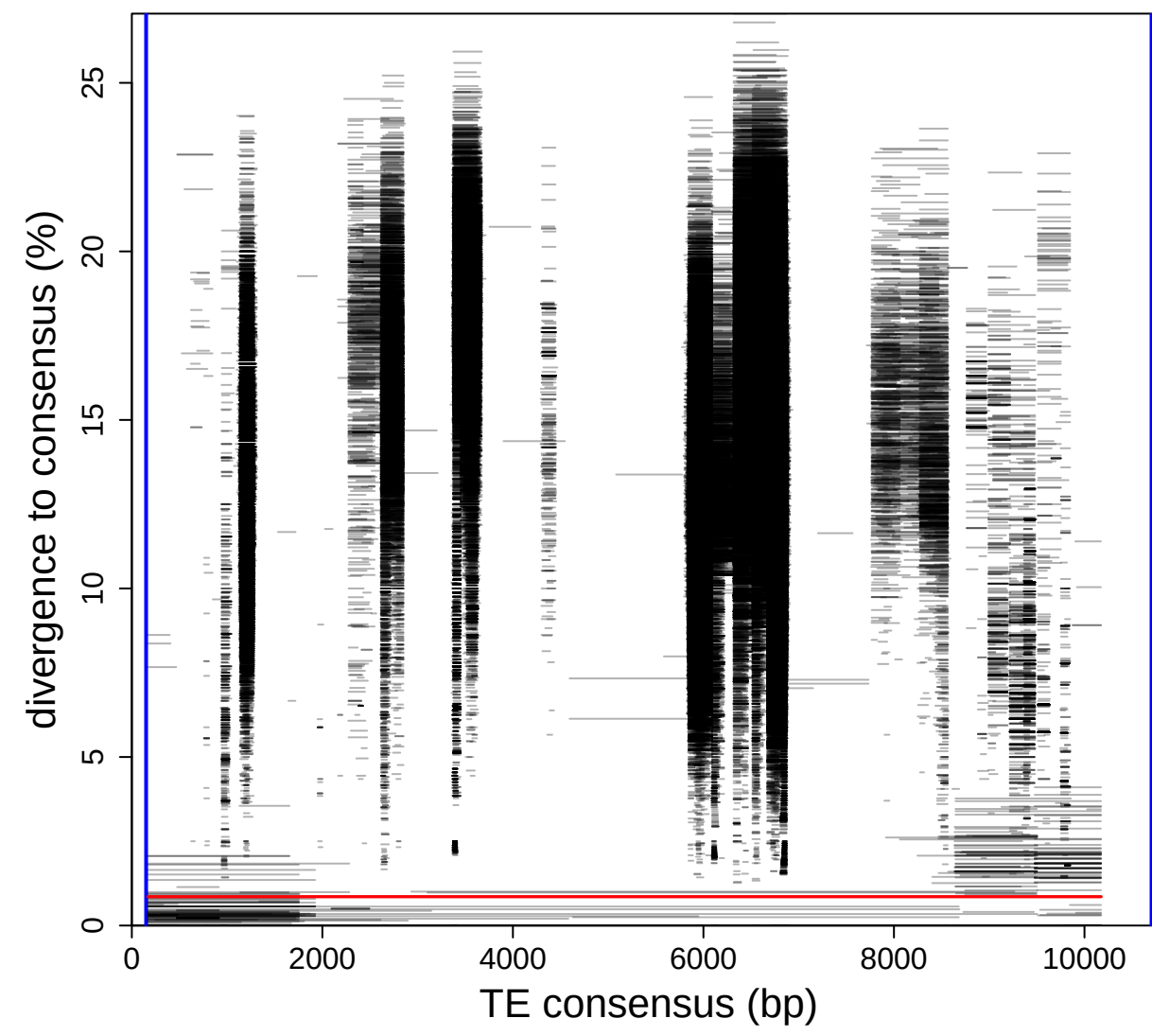
b.bed uf.bed g 1.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 10208bp; fragments: 159379; full length: 3 (>=9187.2bp)

After TEtrimmer 10208 bp

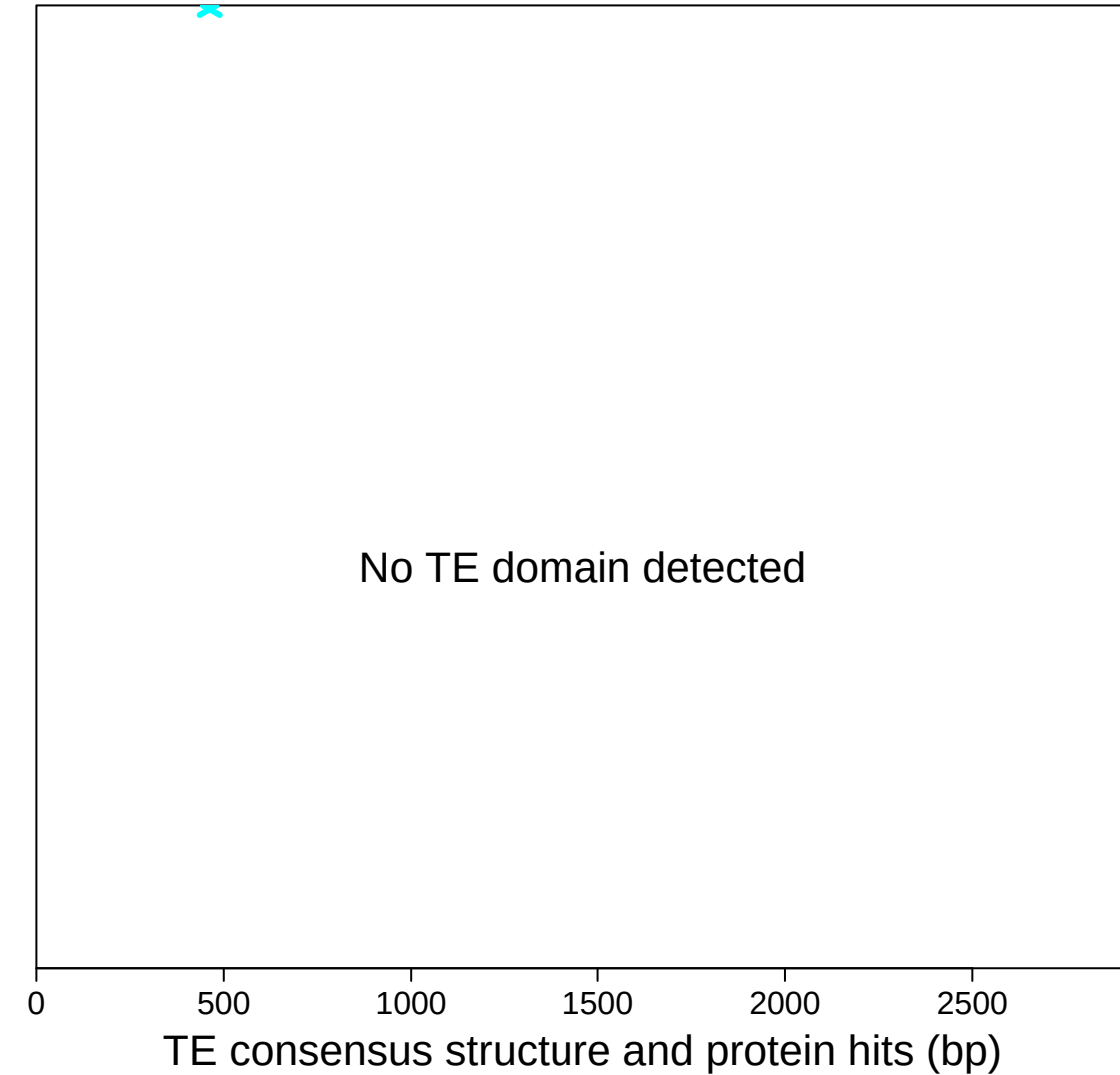
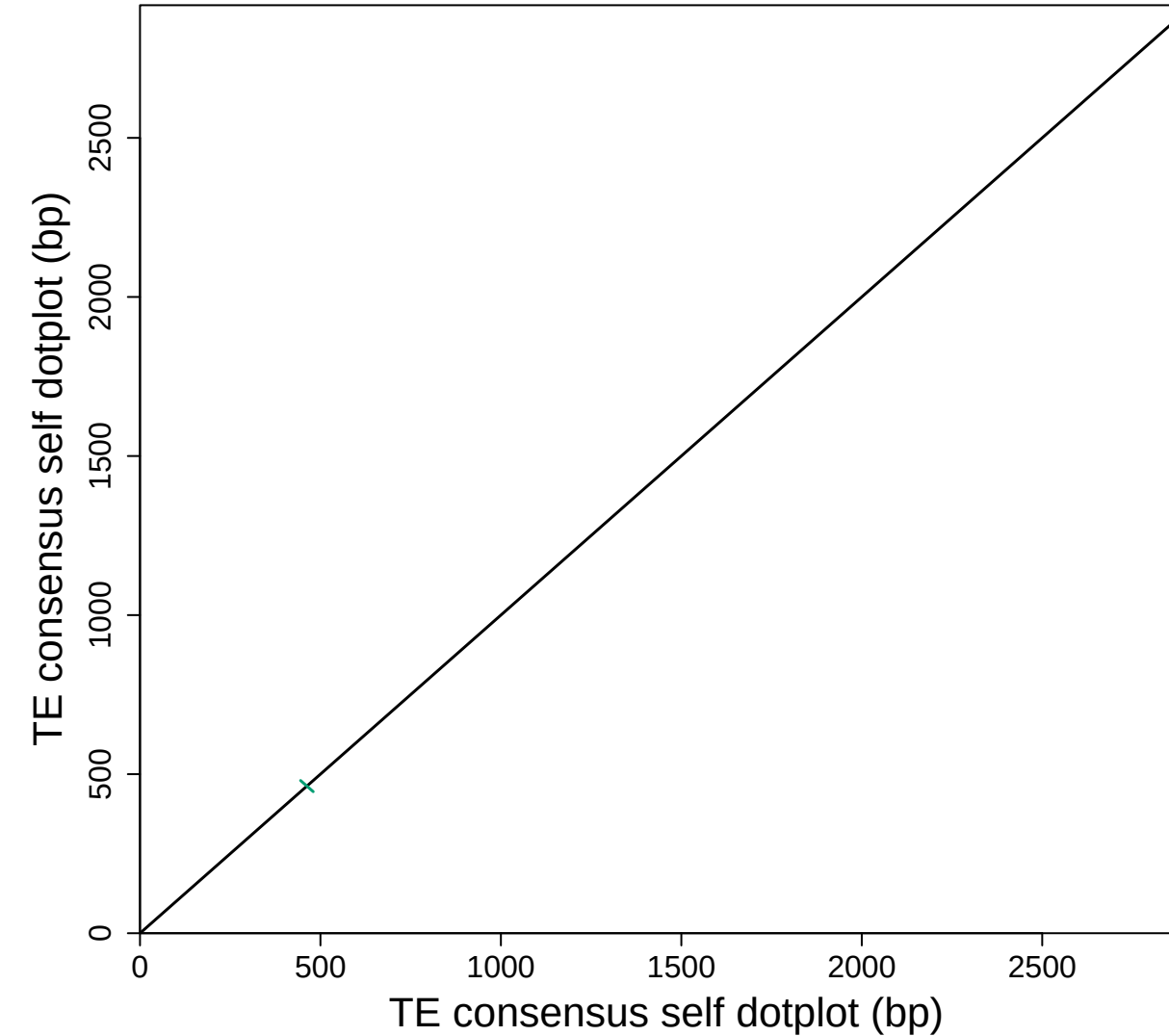
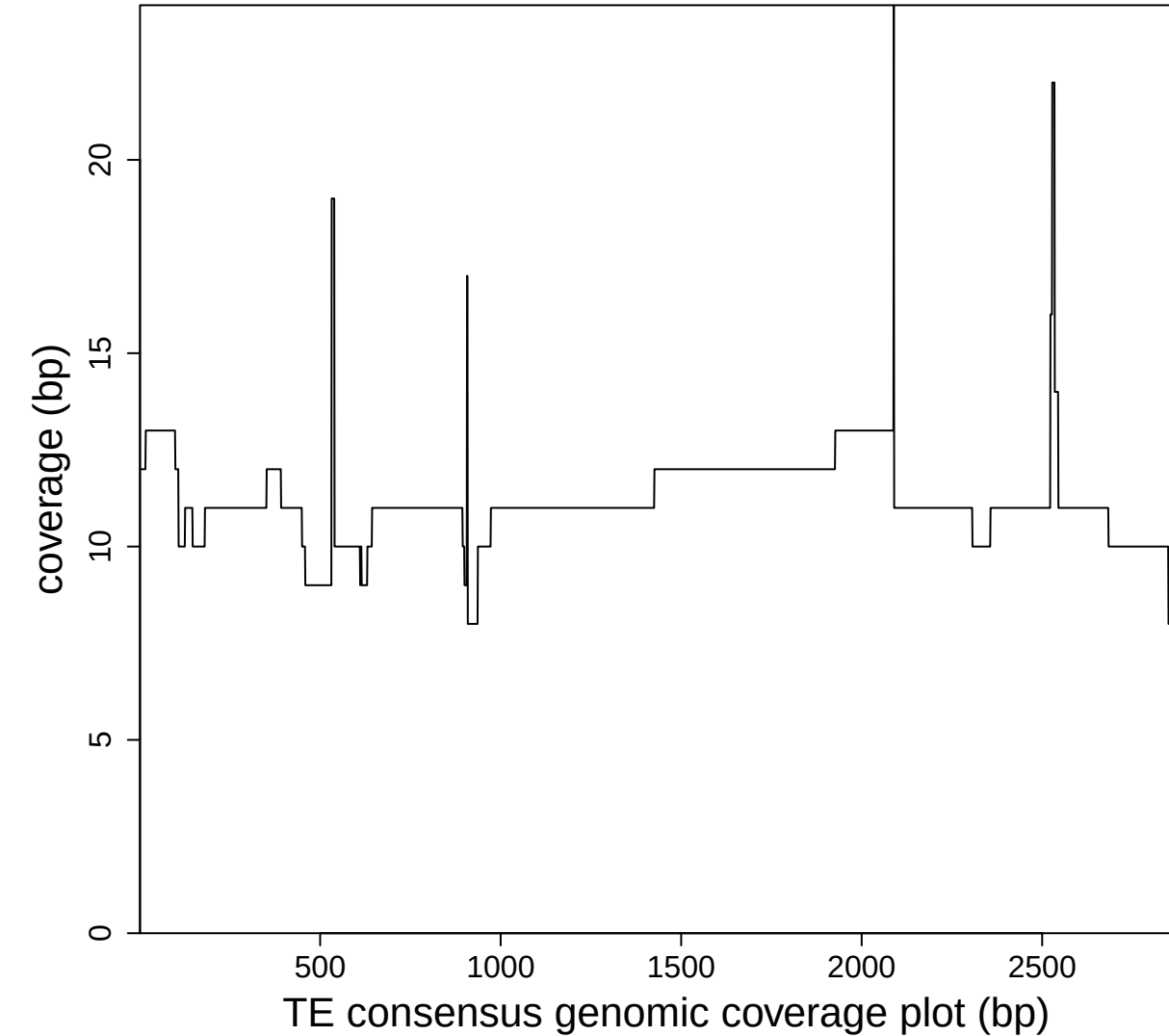
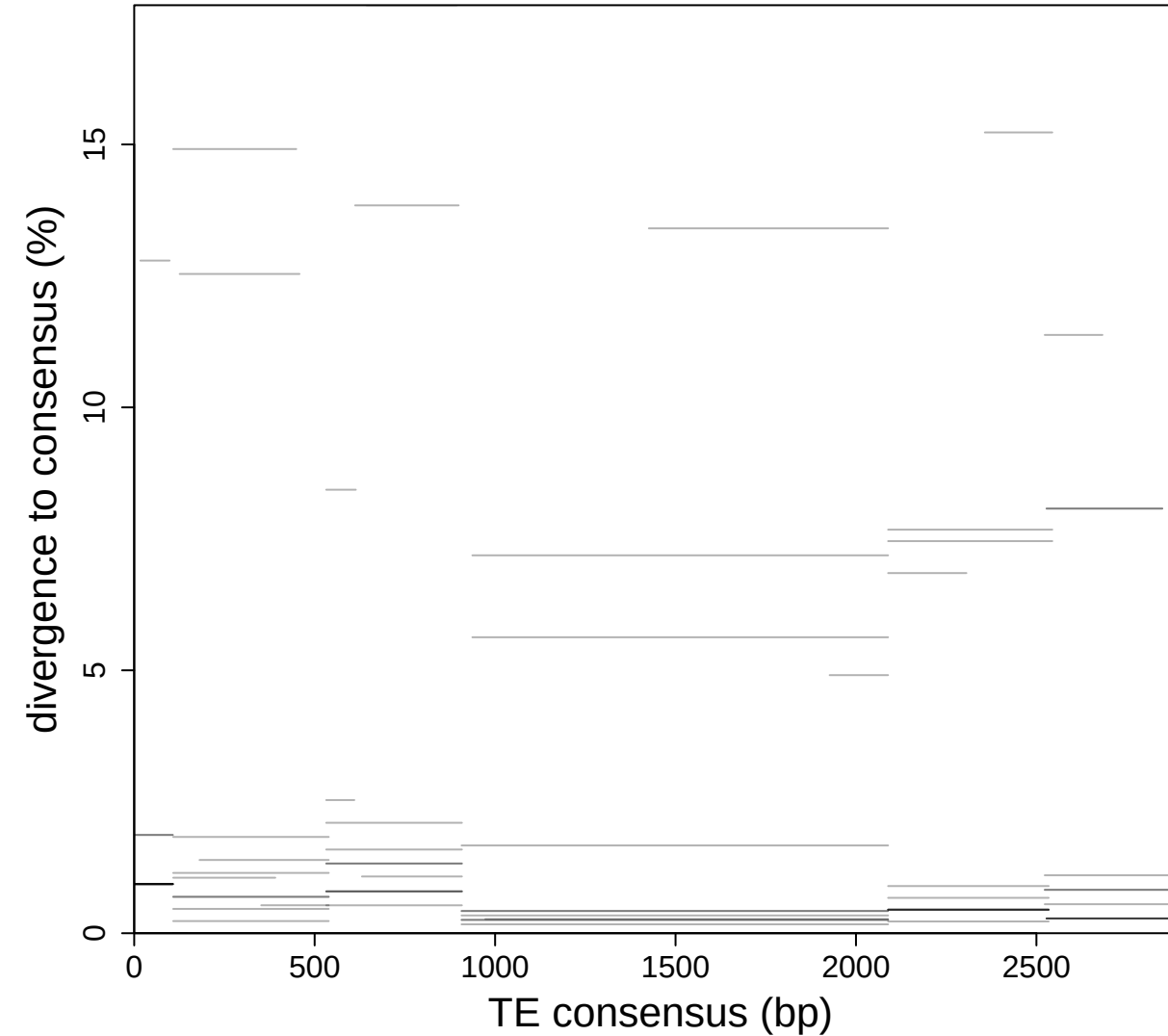


.fasta.b.bed_uf.bed_g_1.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 10854bp; fragments: 159379; full length: 2 (>=9768.6bp)

After TEtrimmer Extended plot Blue lines are boundaries

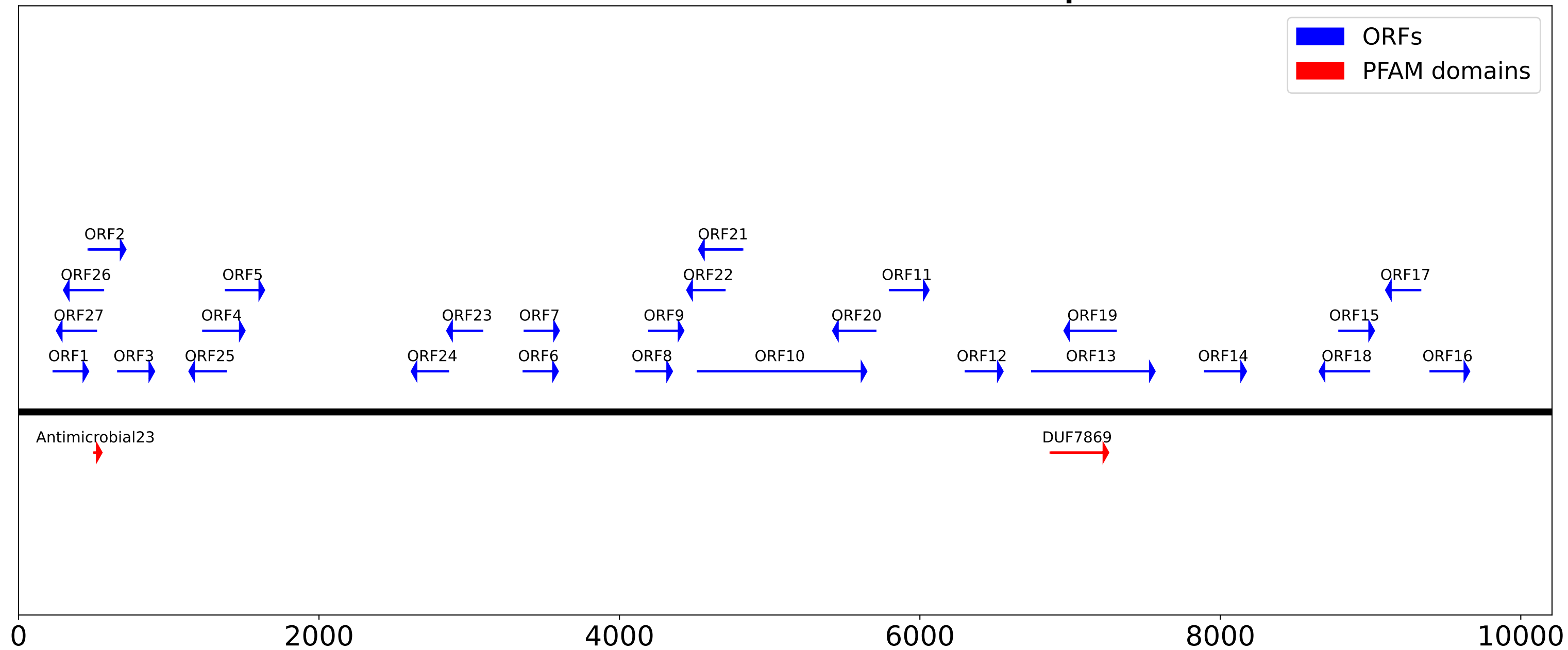


TE: ltr_1_family_936
size: 2917bp; fragments: 75; full length: 0 (≥ 2625.3 bp)

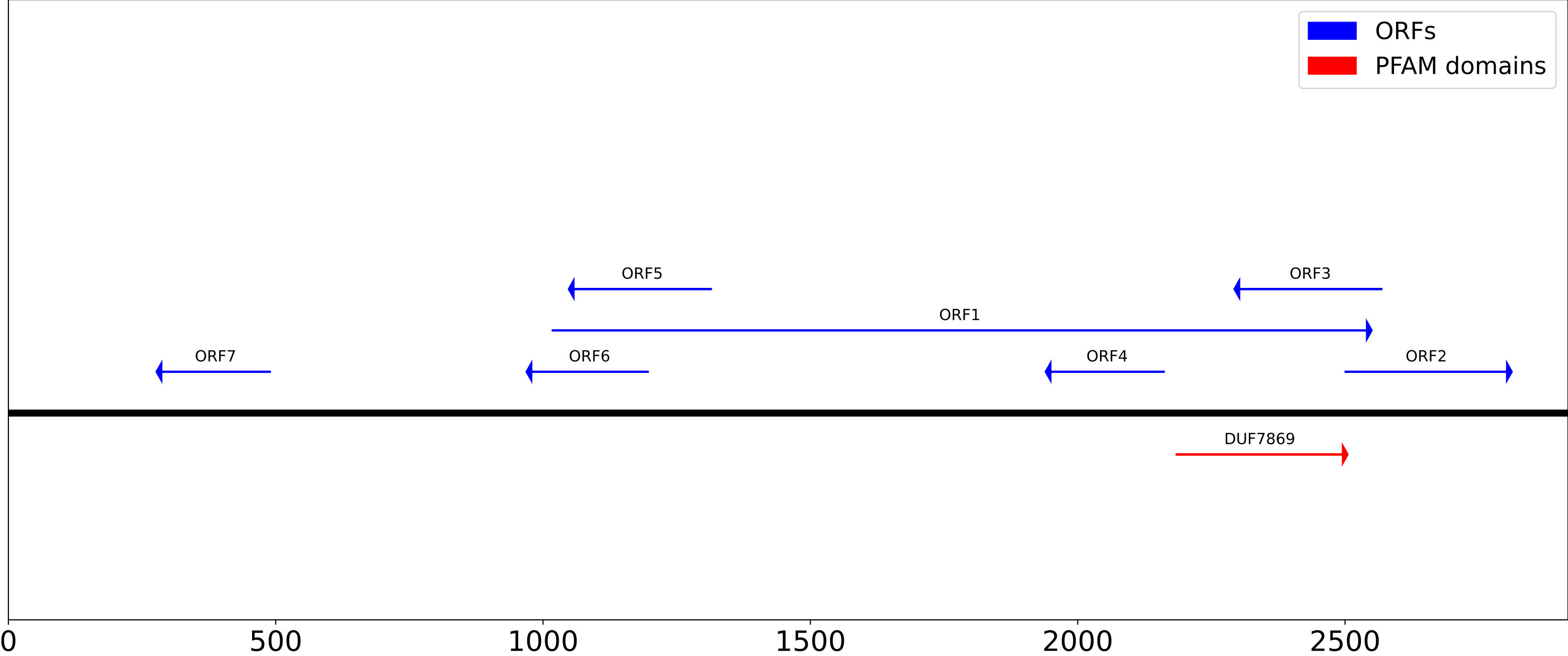


Before TEtrimmer 2917 bp

After TEtrimmer ORF and PFAM domain plot



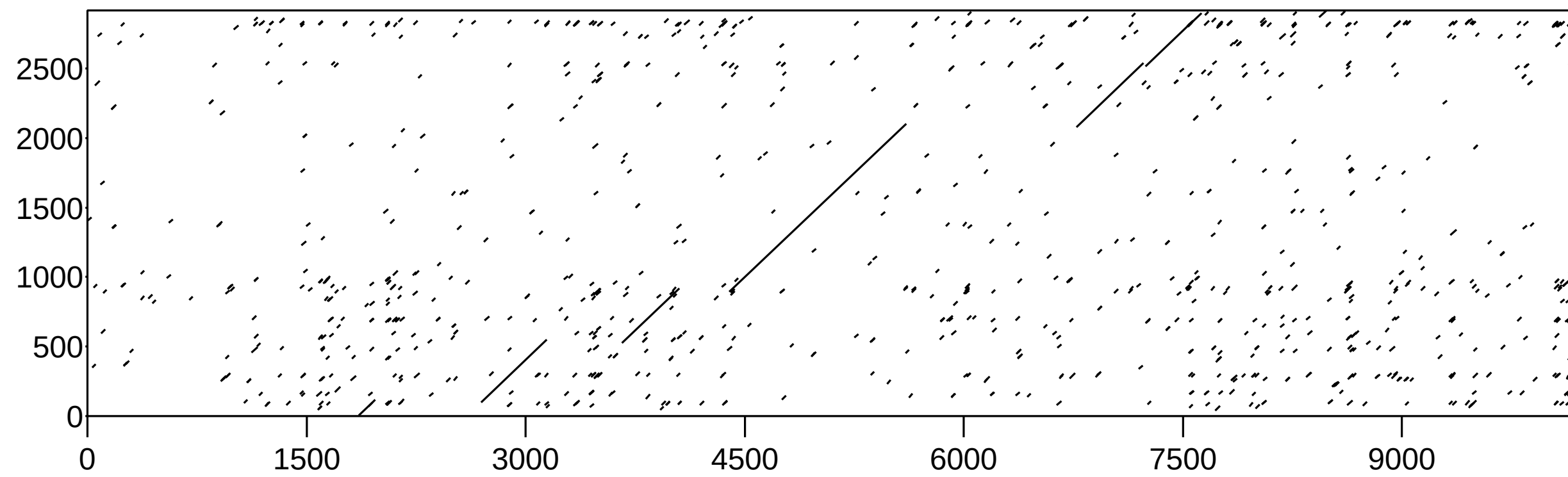
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)