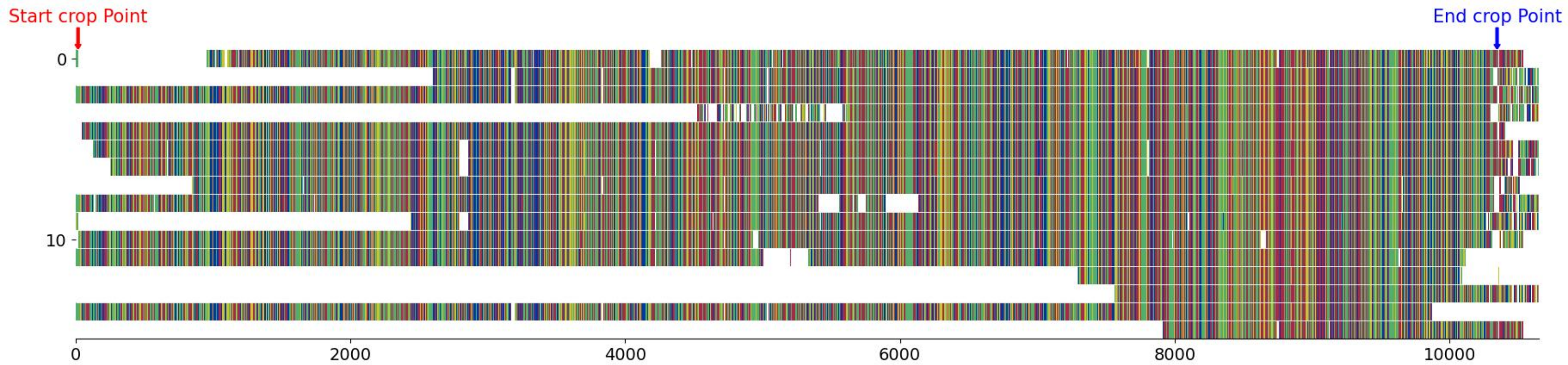


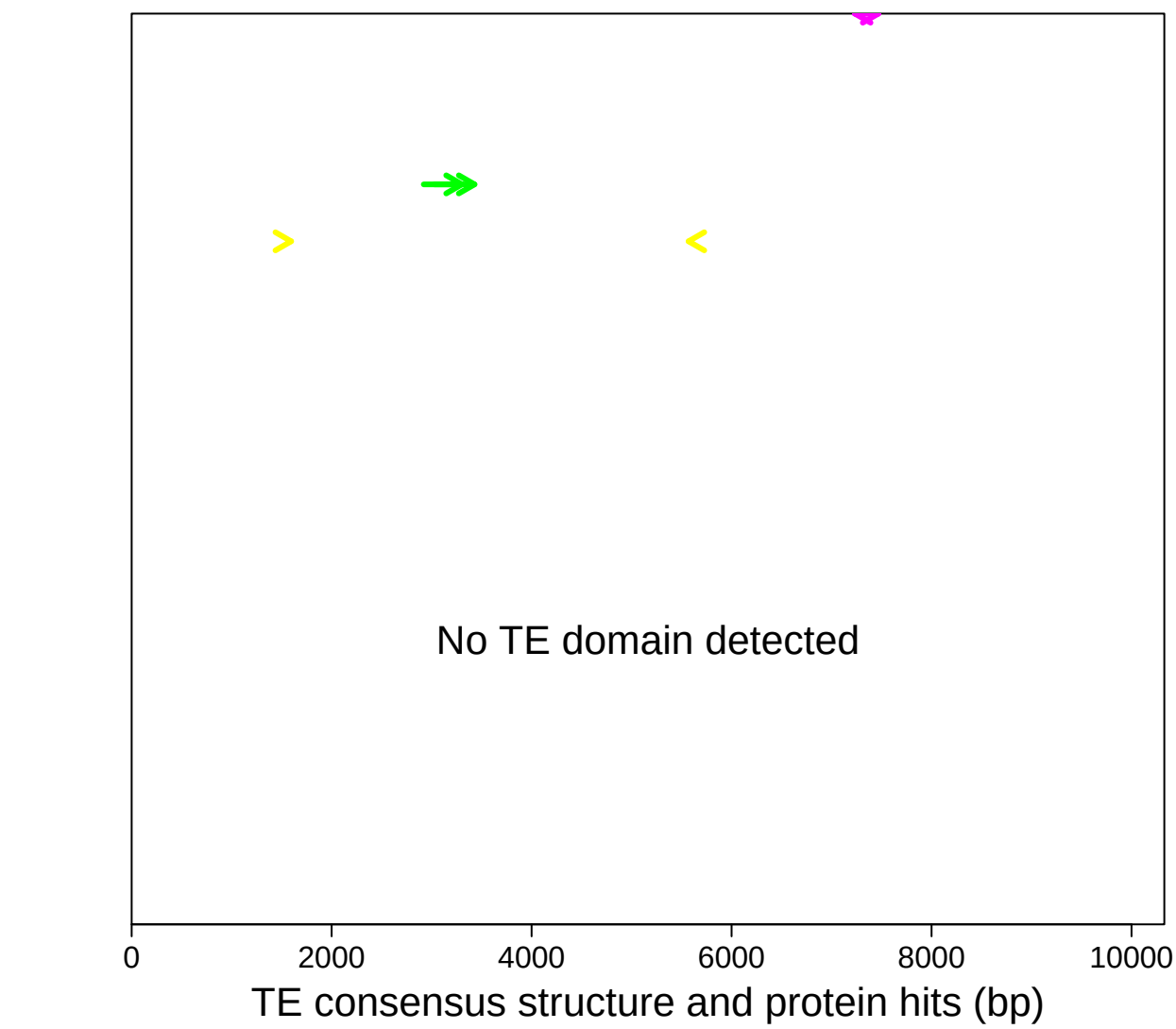
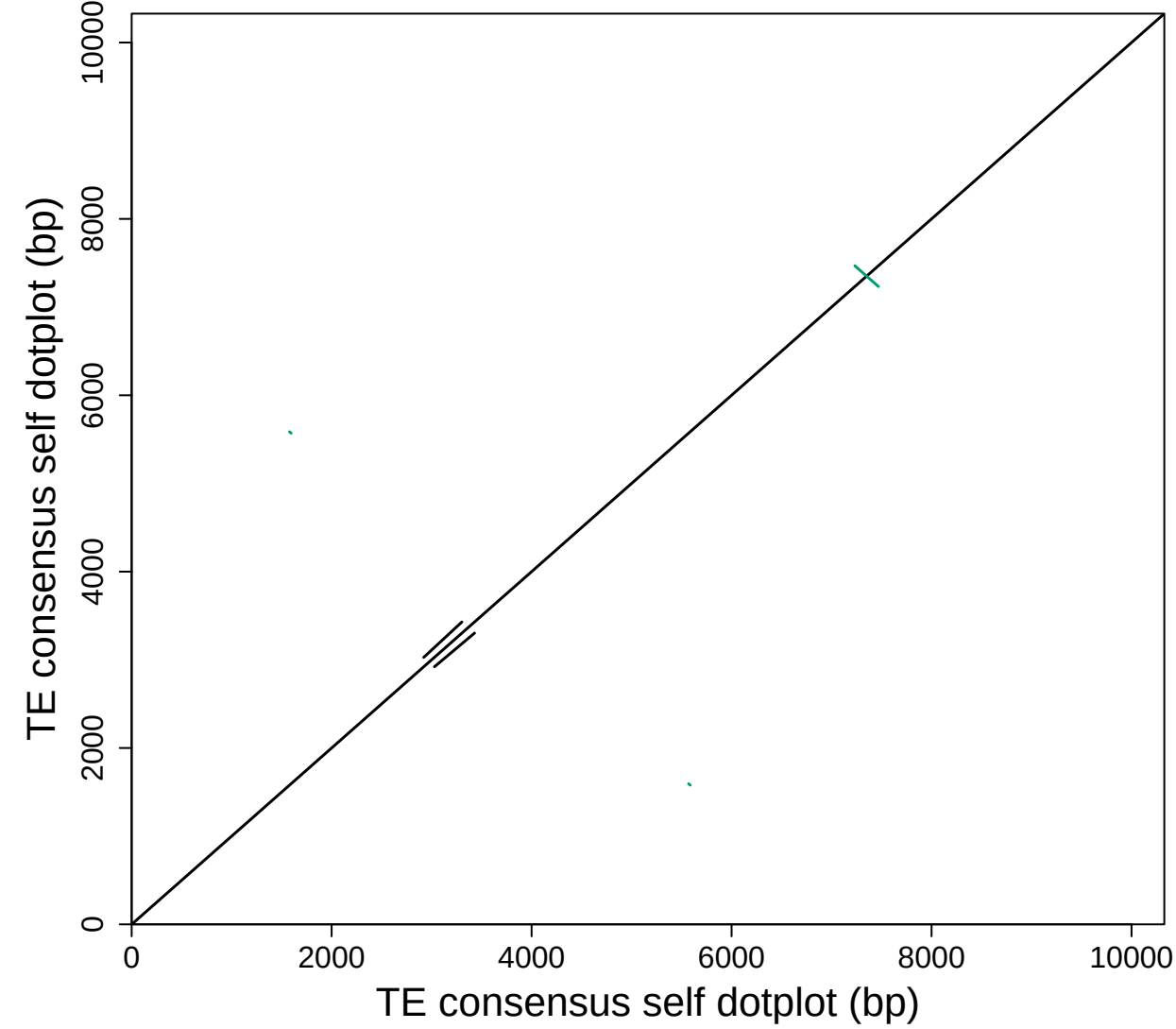
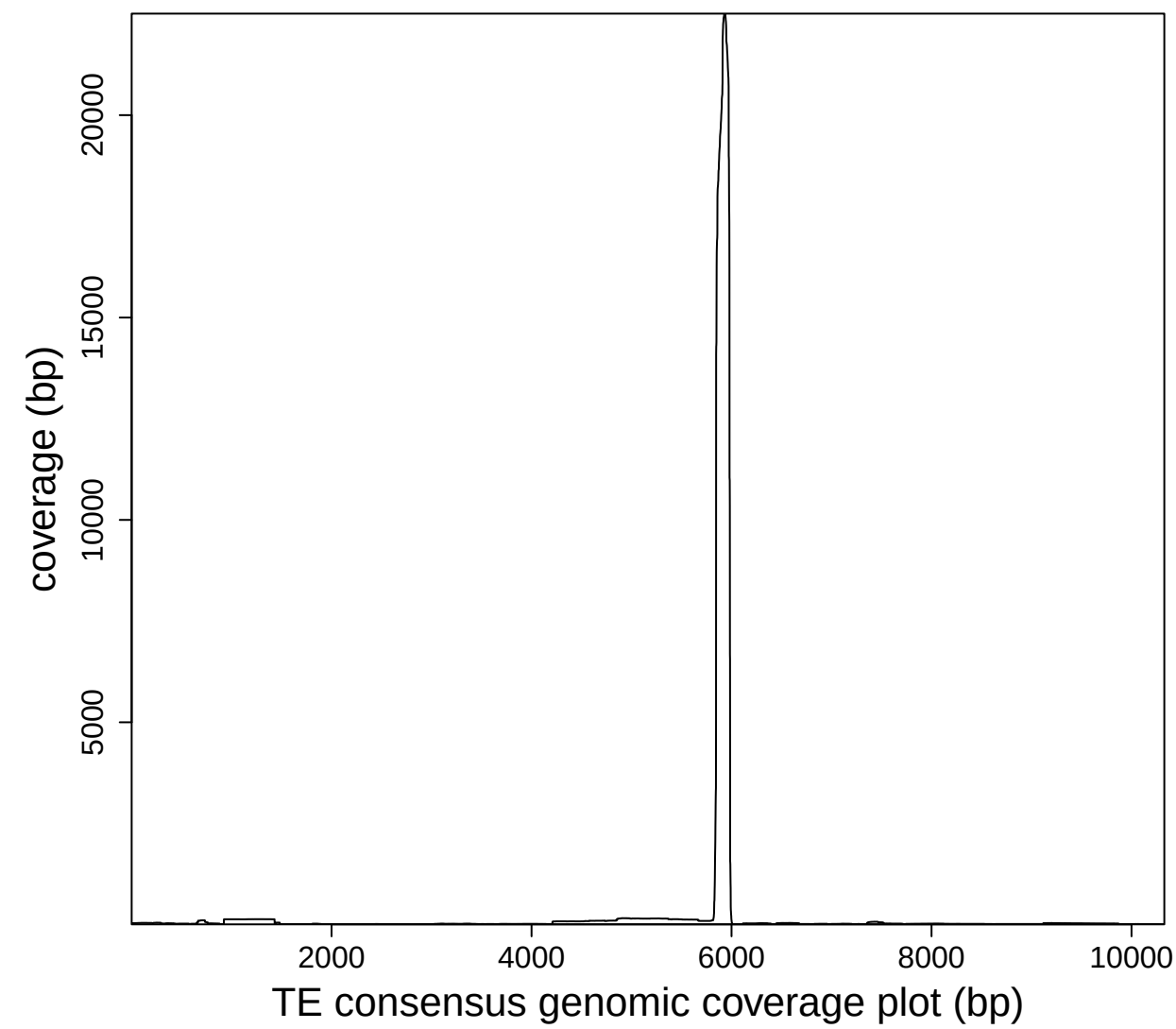
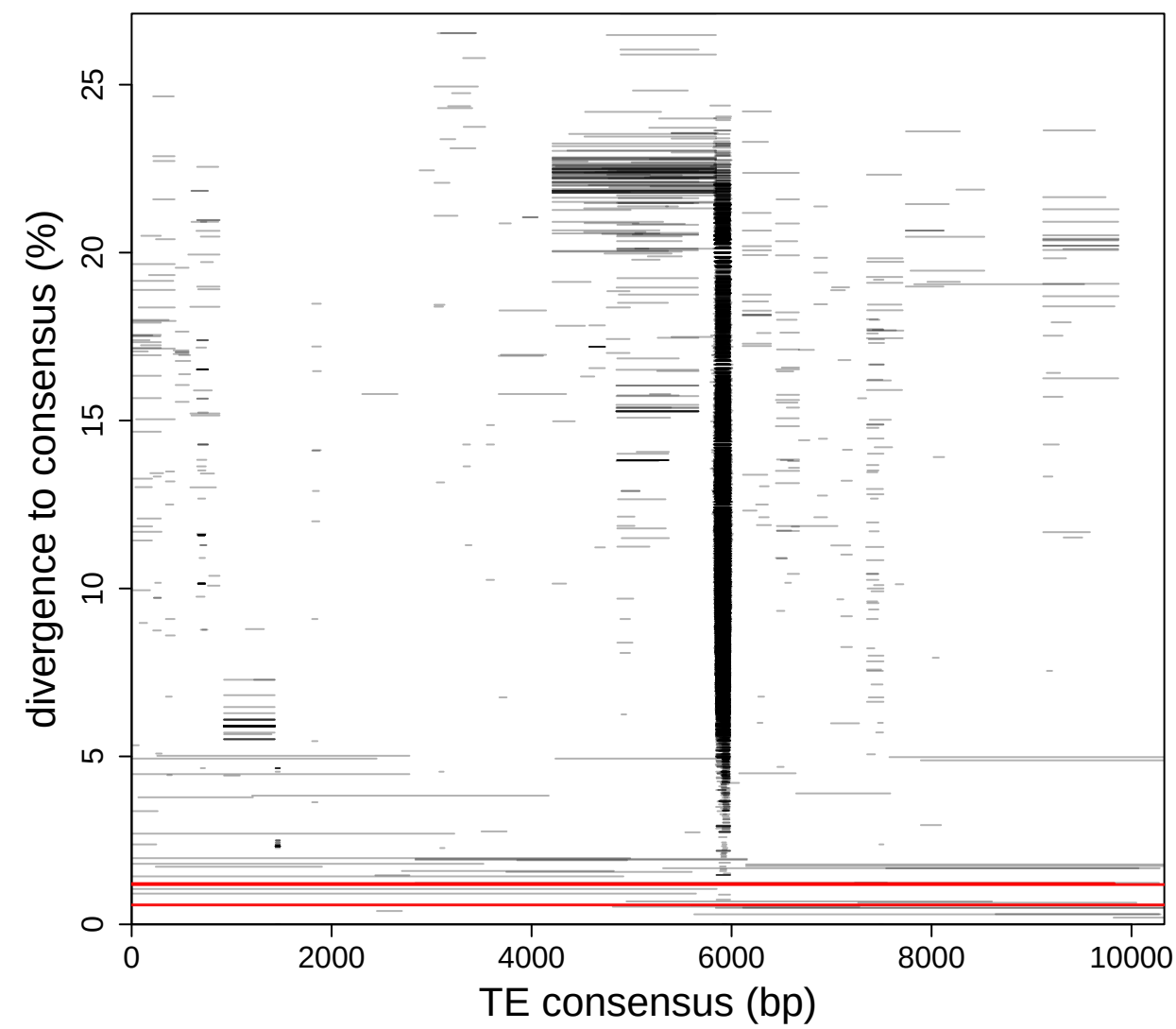
MSA length = 10328

[illegible]



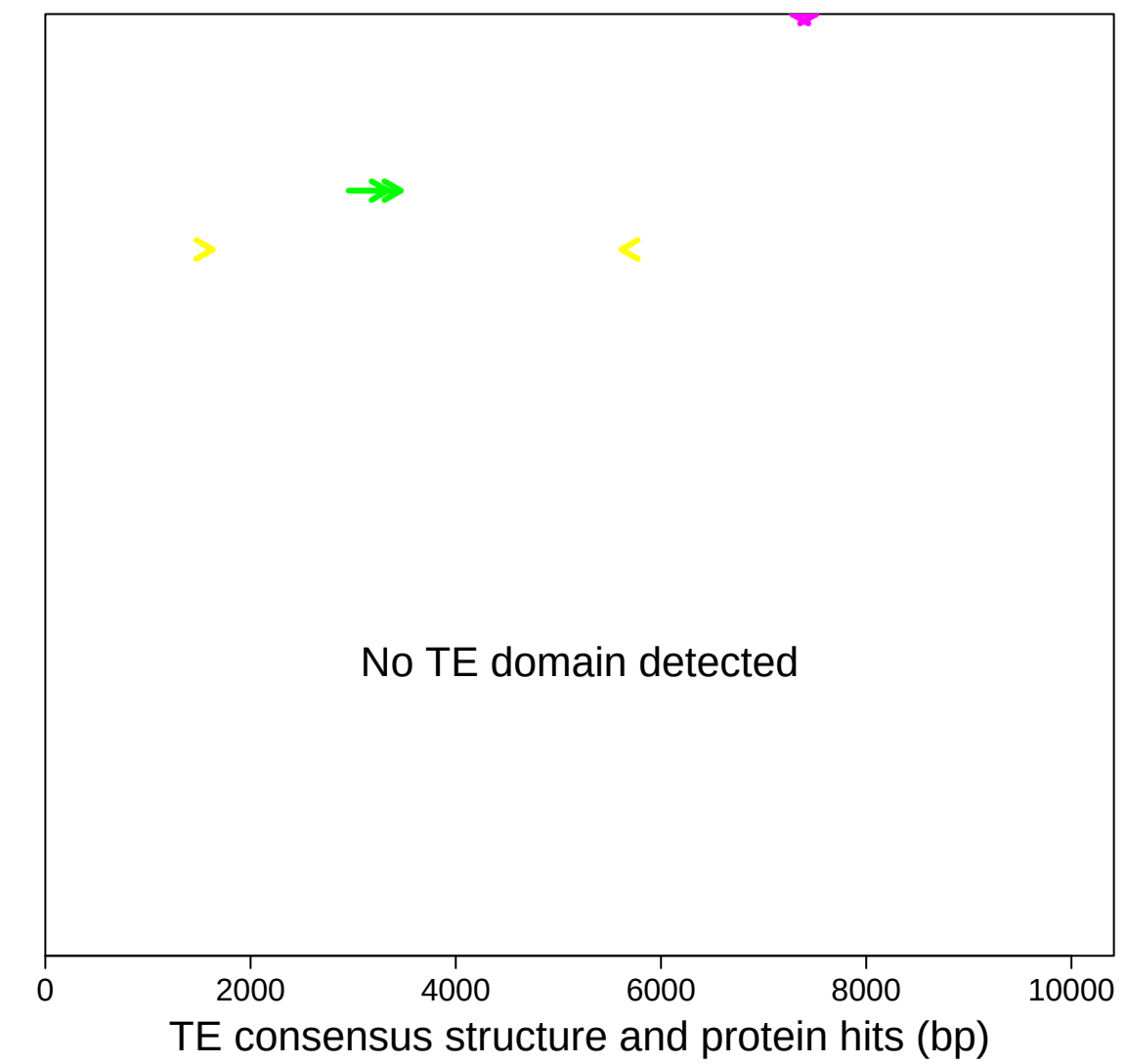
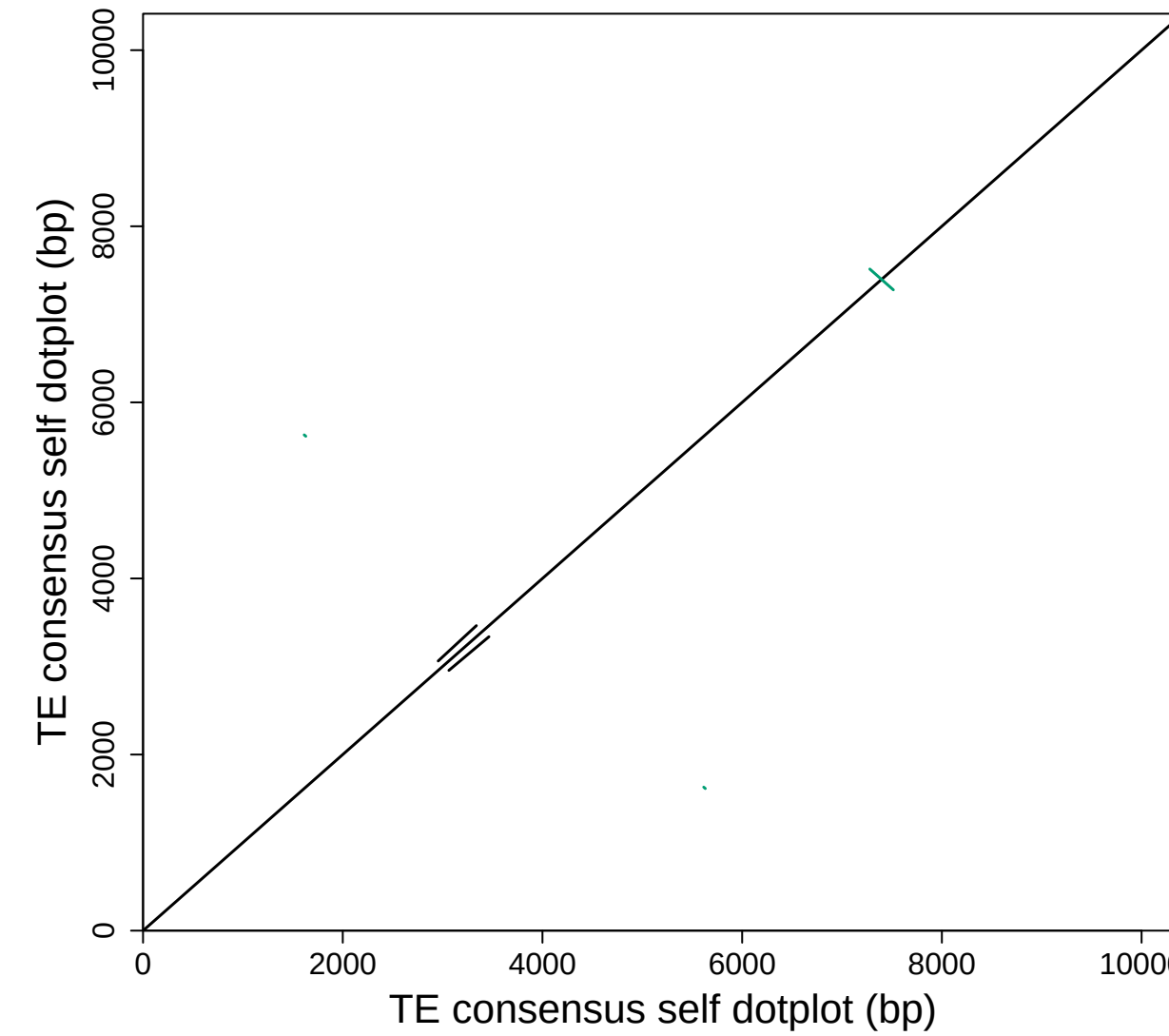
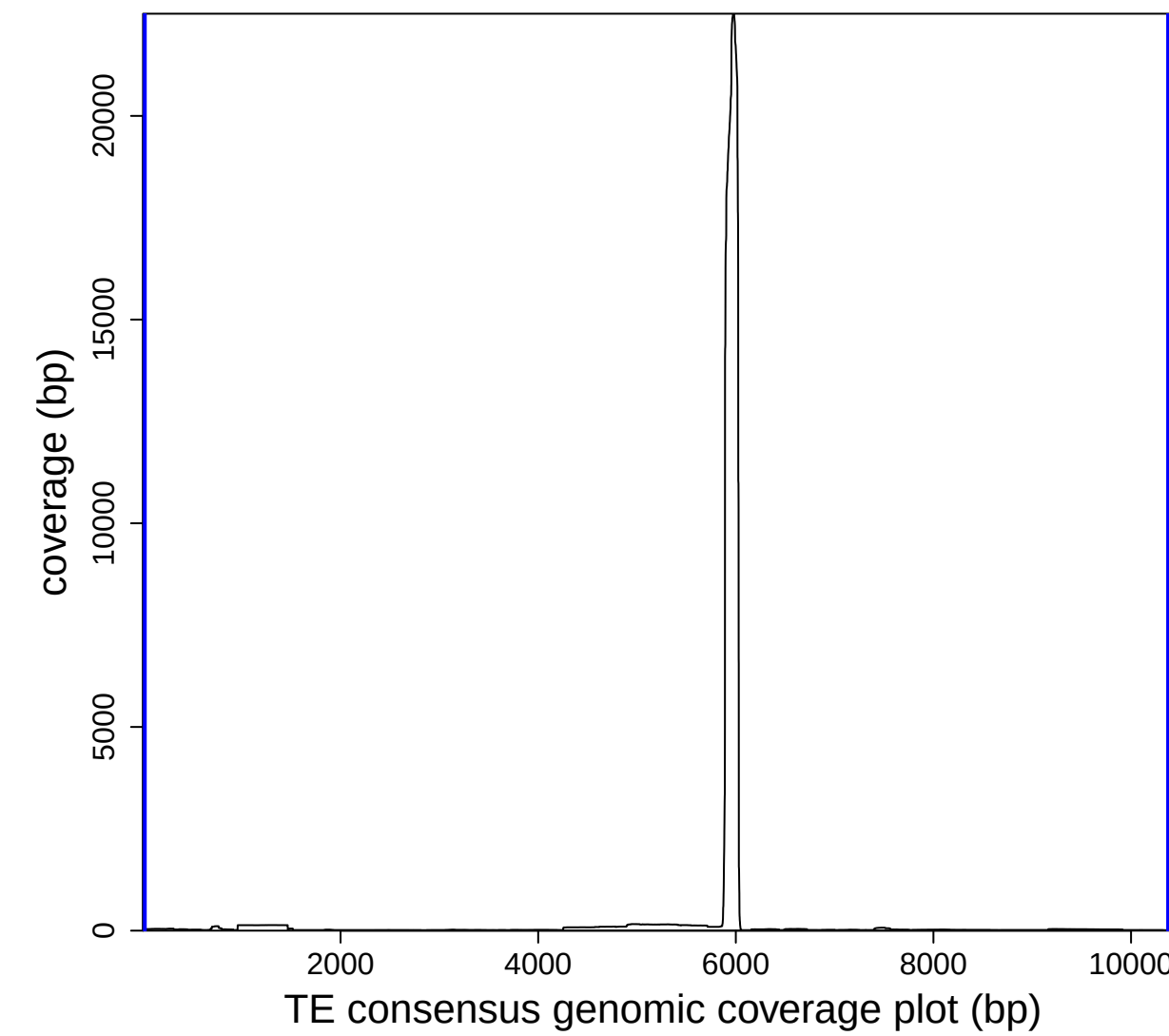
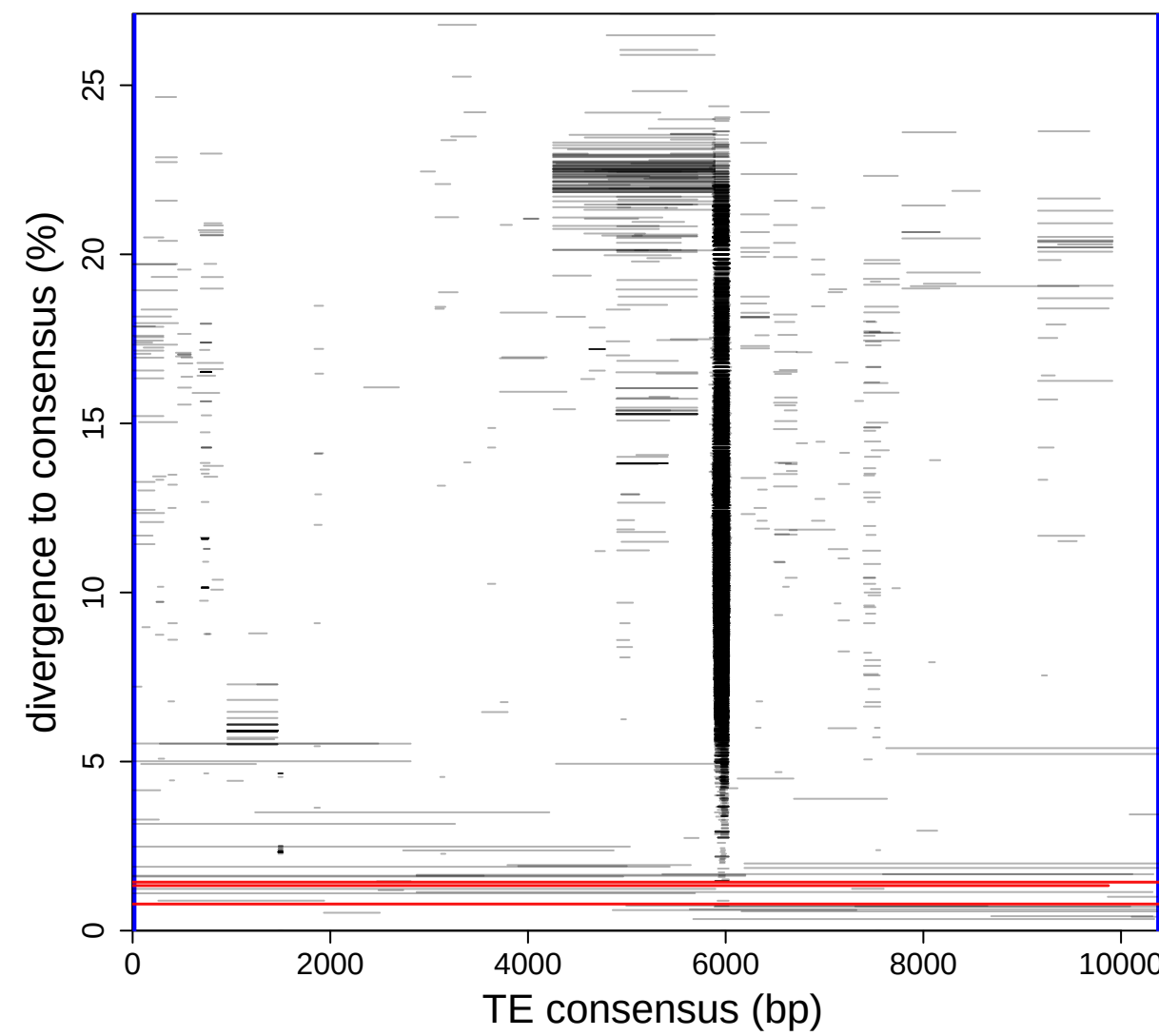
ta.b.bed uf.bed g_3.bed fm_1.bed 0_0 bcln.fa aln.fa cl.fa gs.f
size: 10328bp; fragments: 23314; full length: 3 (>=9295.2bp)

After TEtrimmer 10328 bp



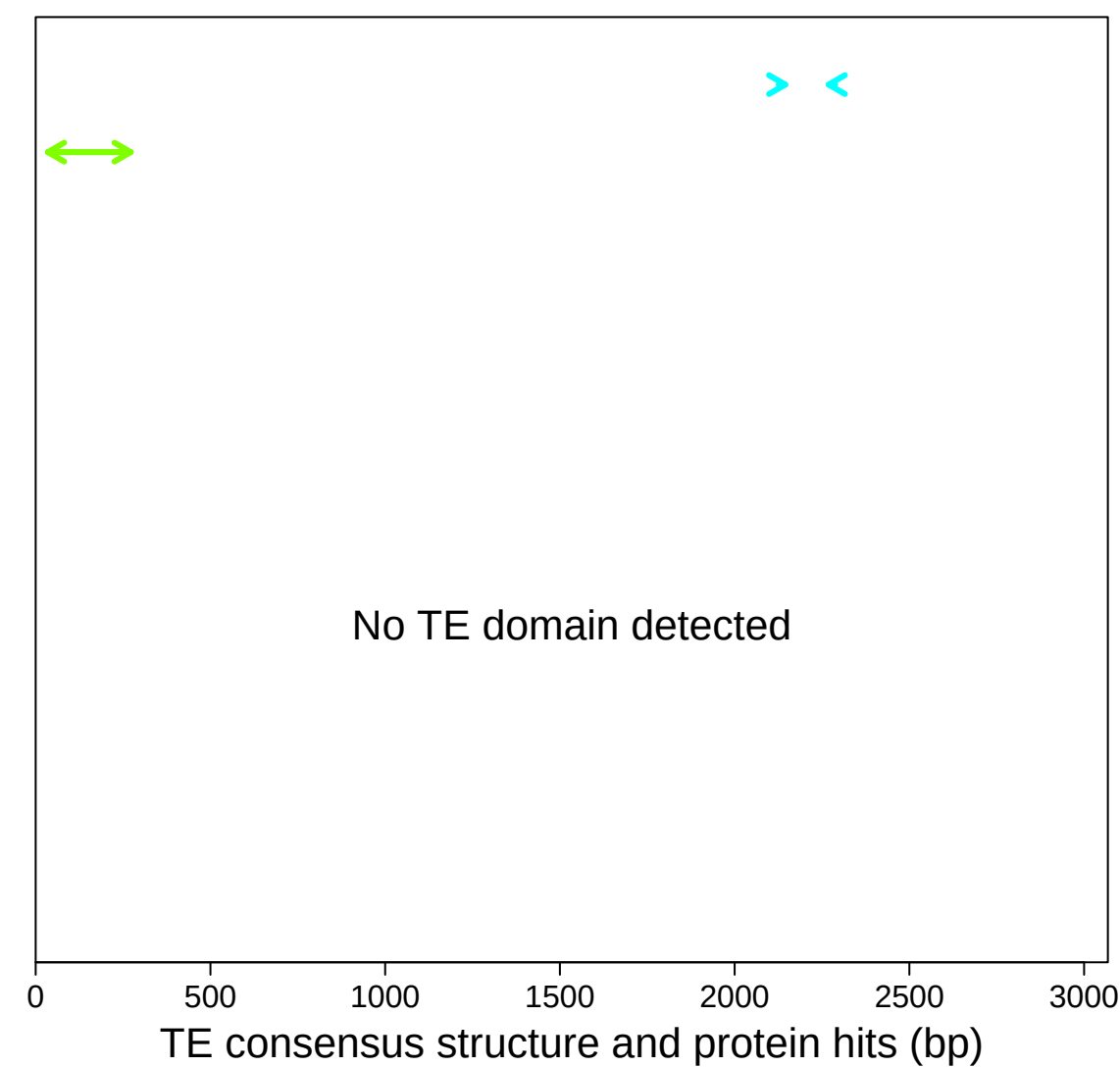
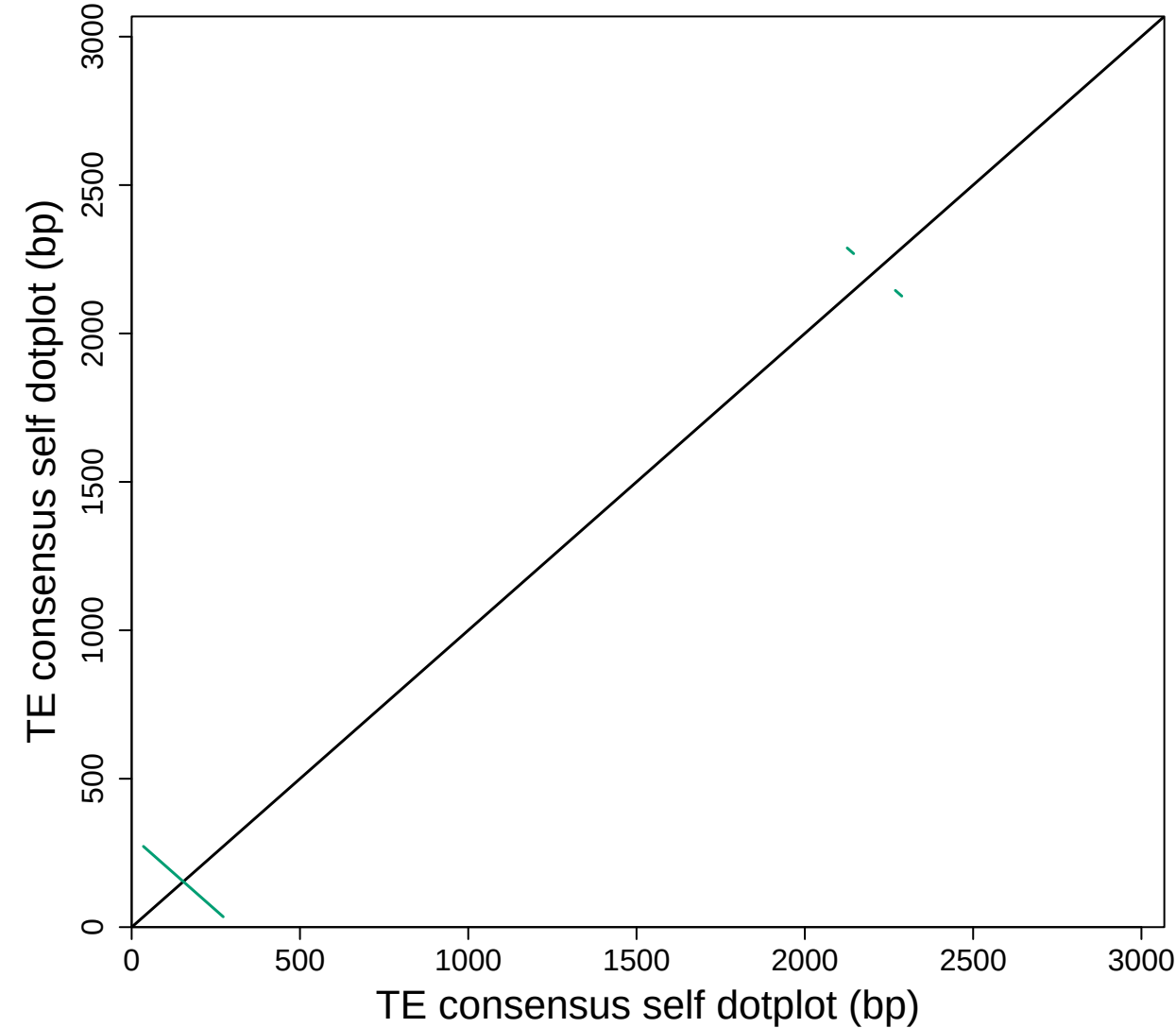
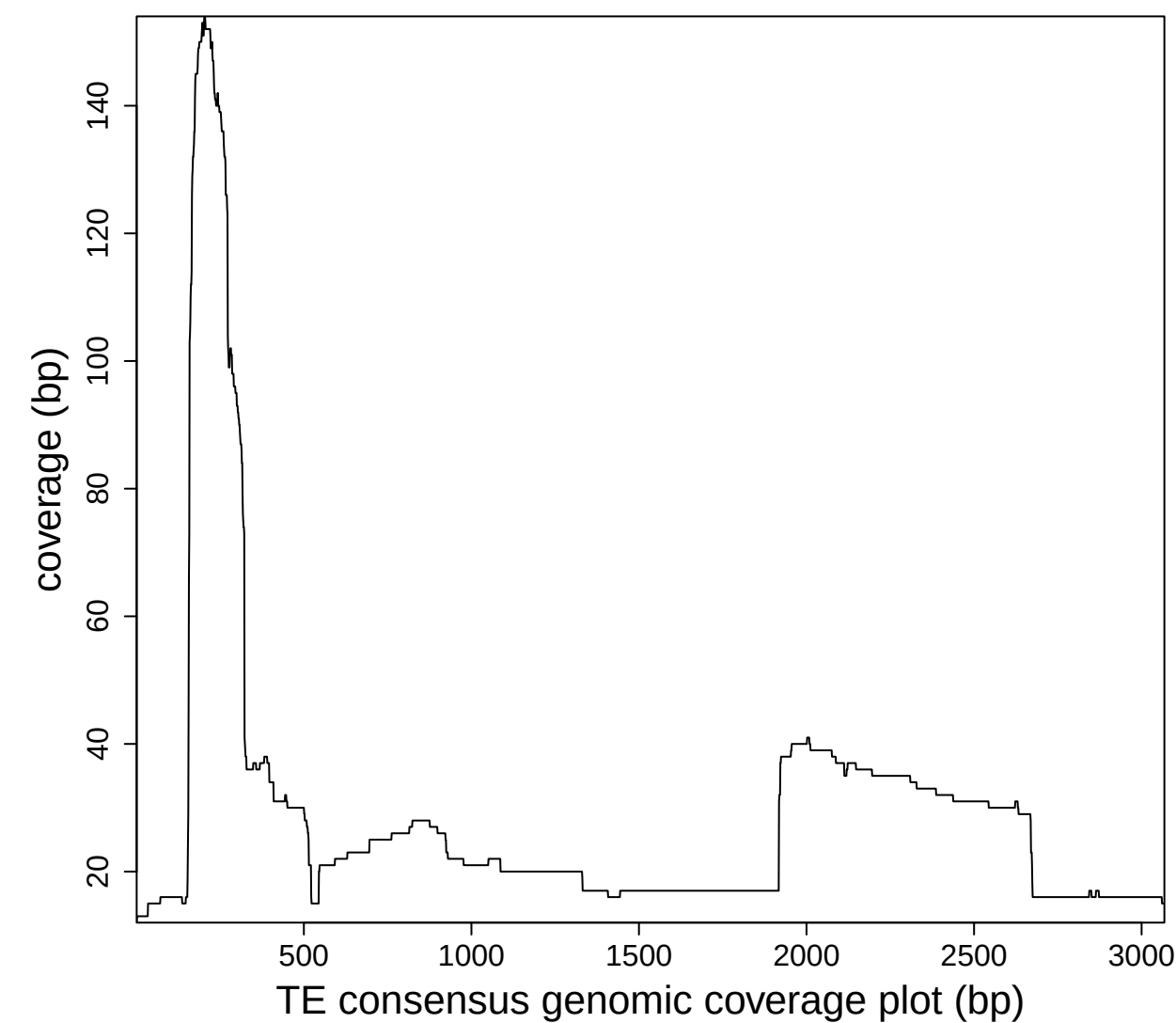
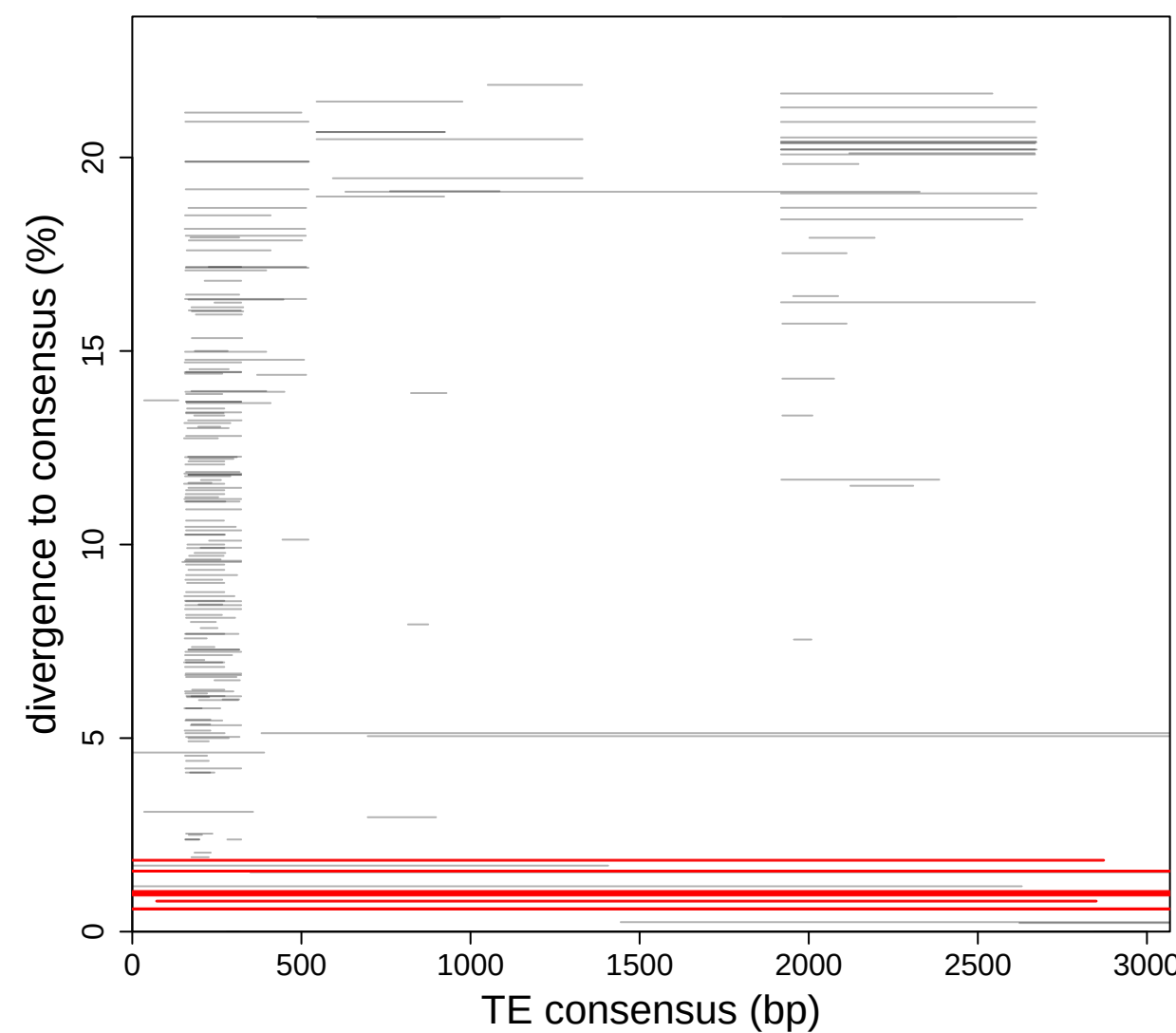
39.fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.1
size: 10525bp; fragments: 23307; full length: 3 (>=9472.5bp)

After TEtrimmer Extended plot Blue lines are boundaries

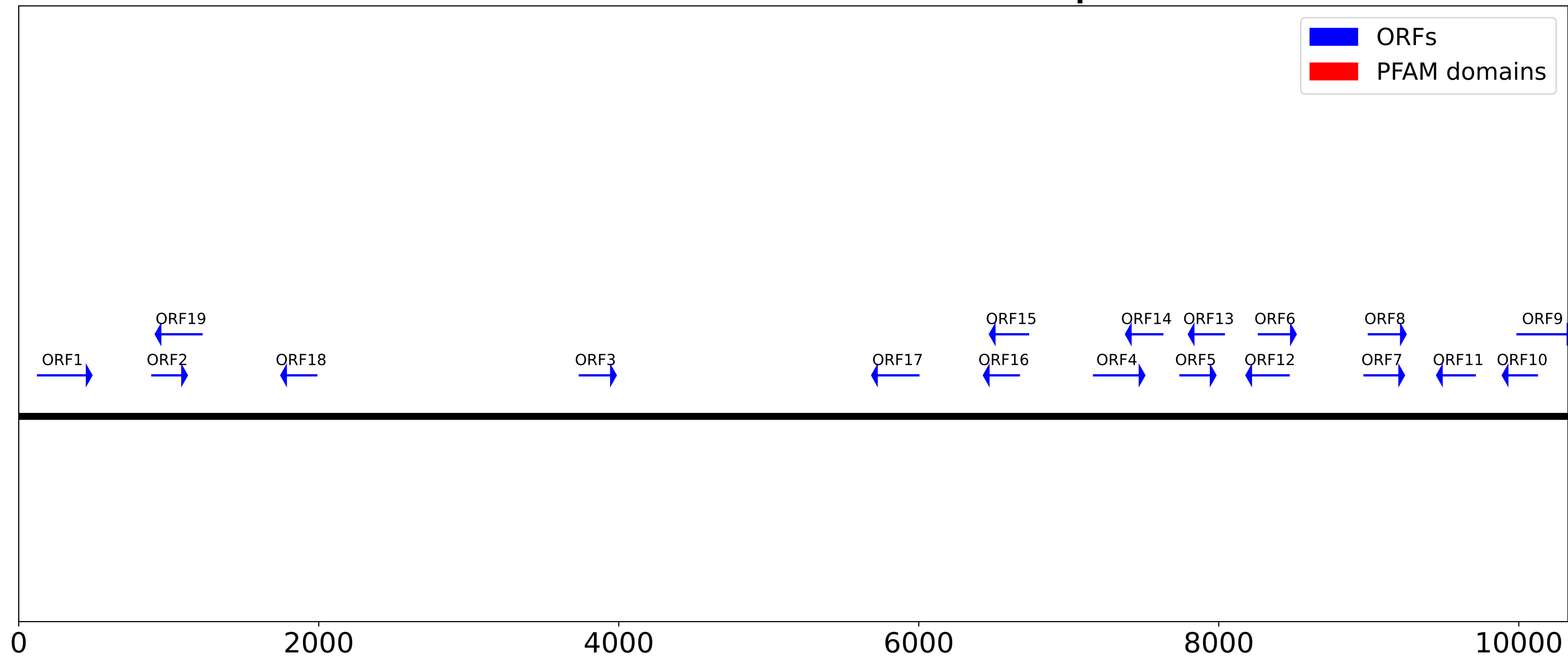


TE: rnd_5_family_13939
size: 3068bp; fragments: 214; full length: 11 (≥ 2761.2 bp)

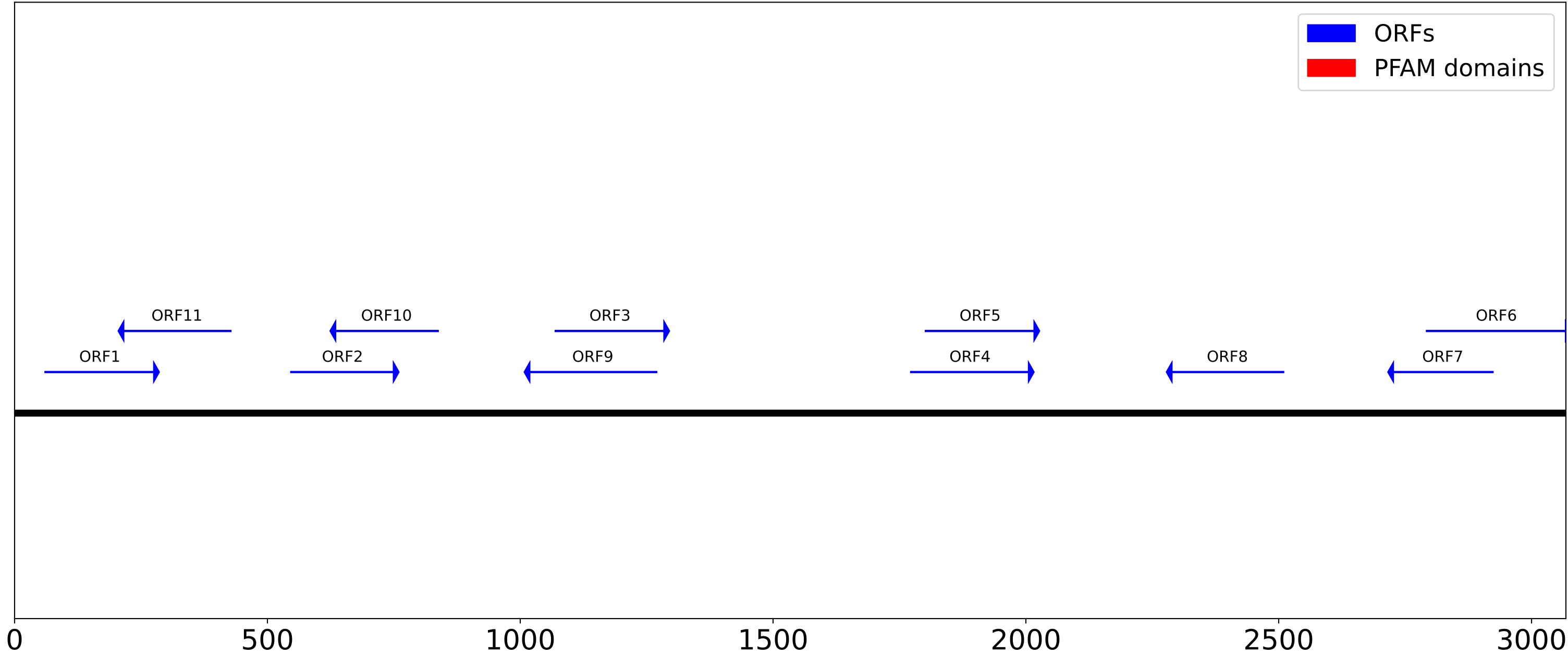
Before TEtrimmer 3068 bp



After TEtrimmer ORF and PFAM domain plot



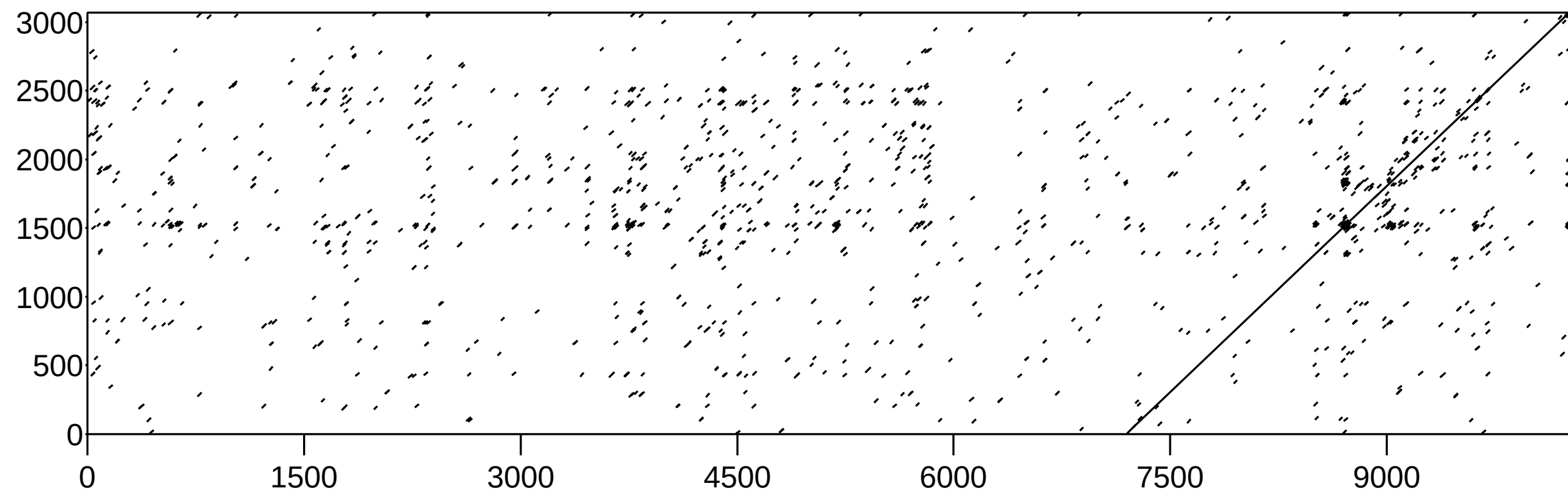
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)