

MSA length = 4709

Start crop Point



End crop Point



Start crop Point

End crop Point

0

10

0

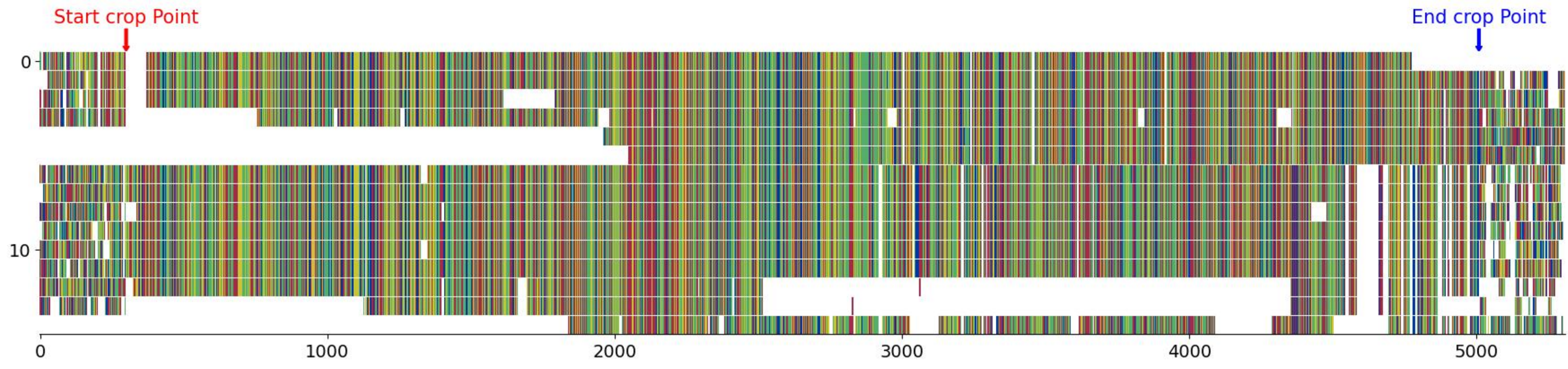
1000

2000

3000

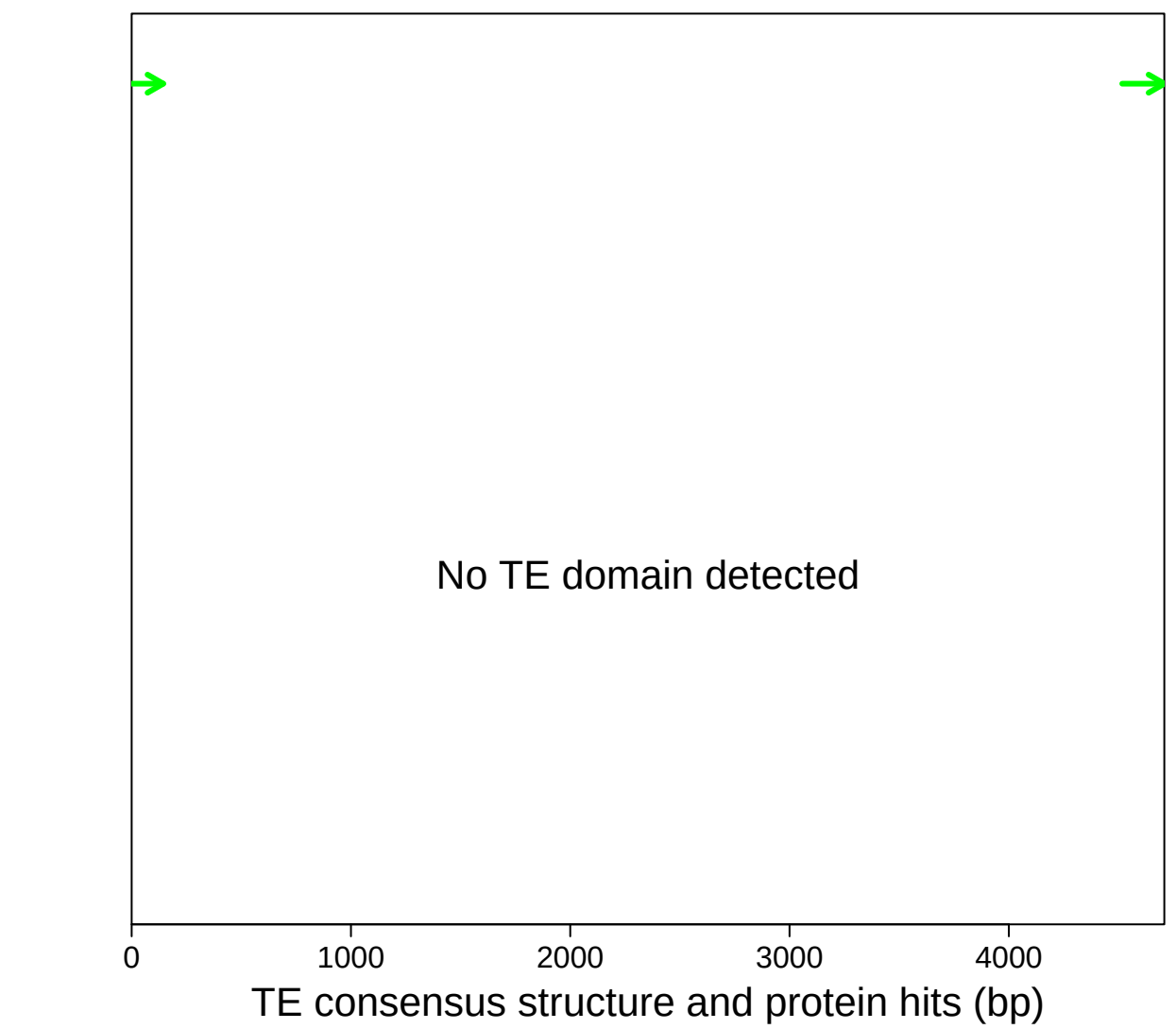
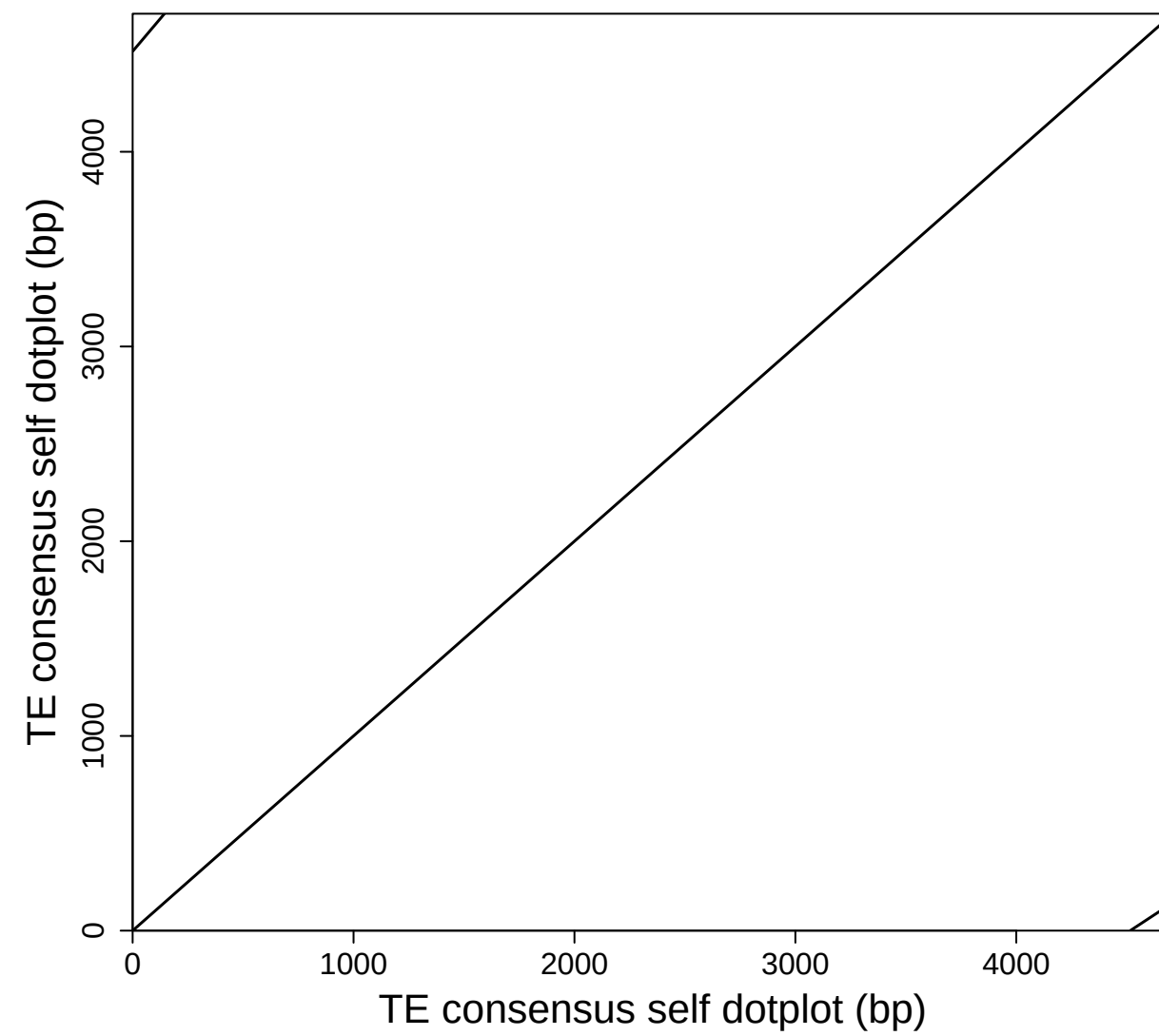
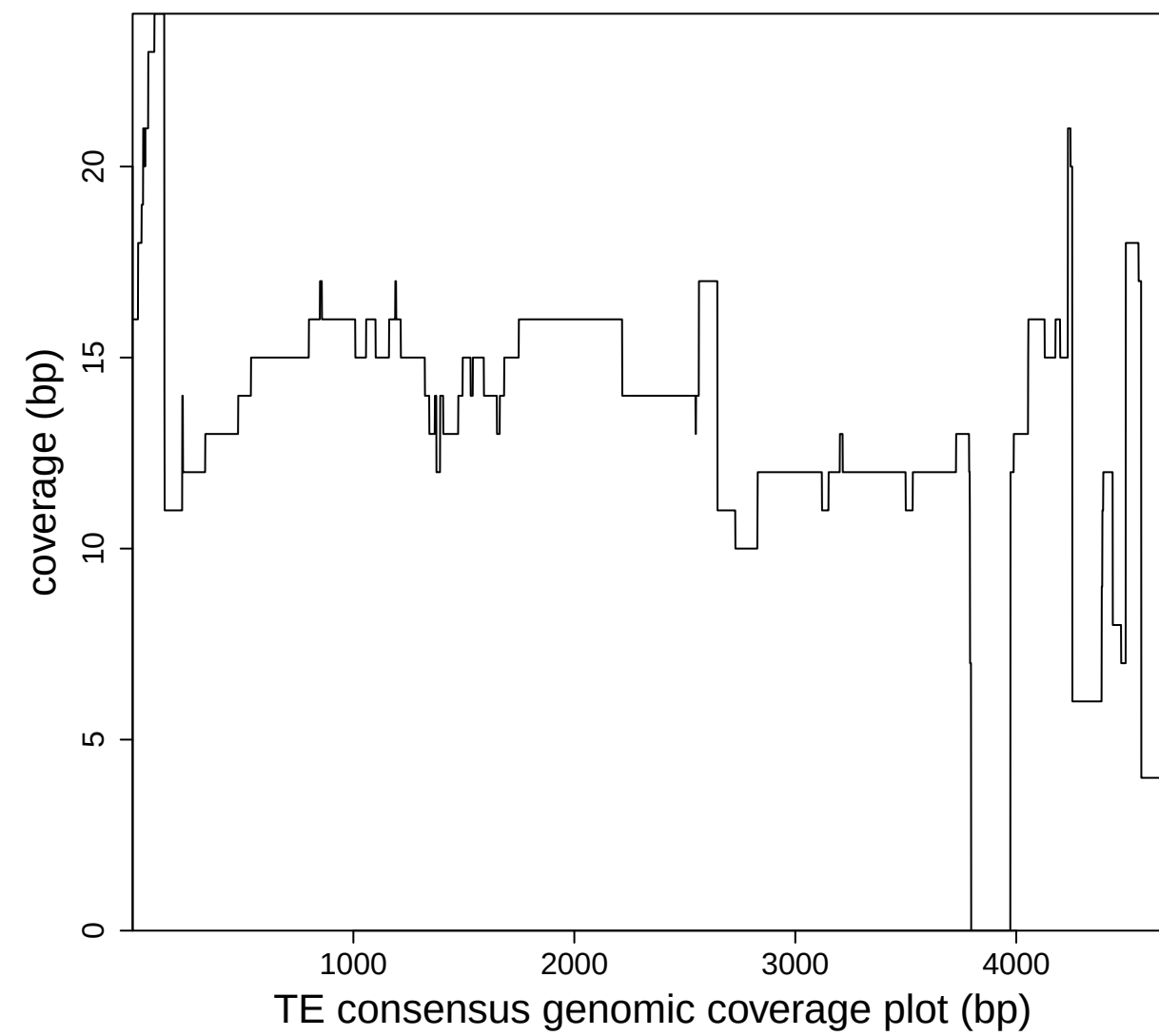
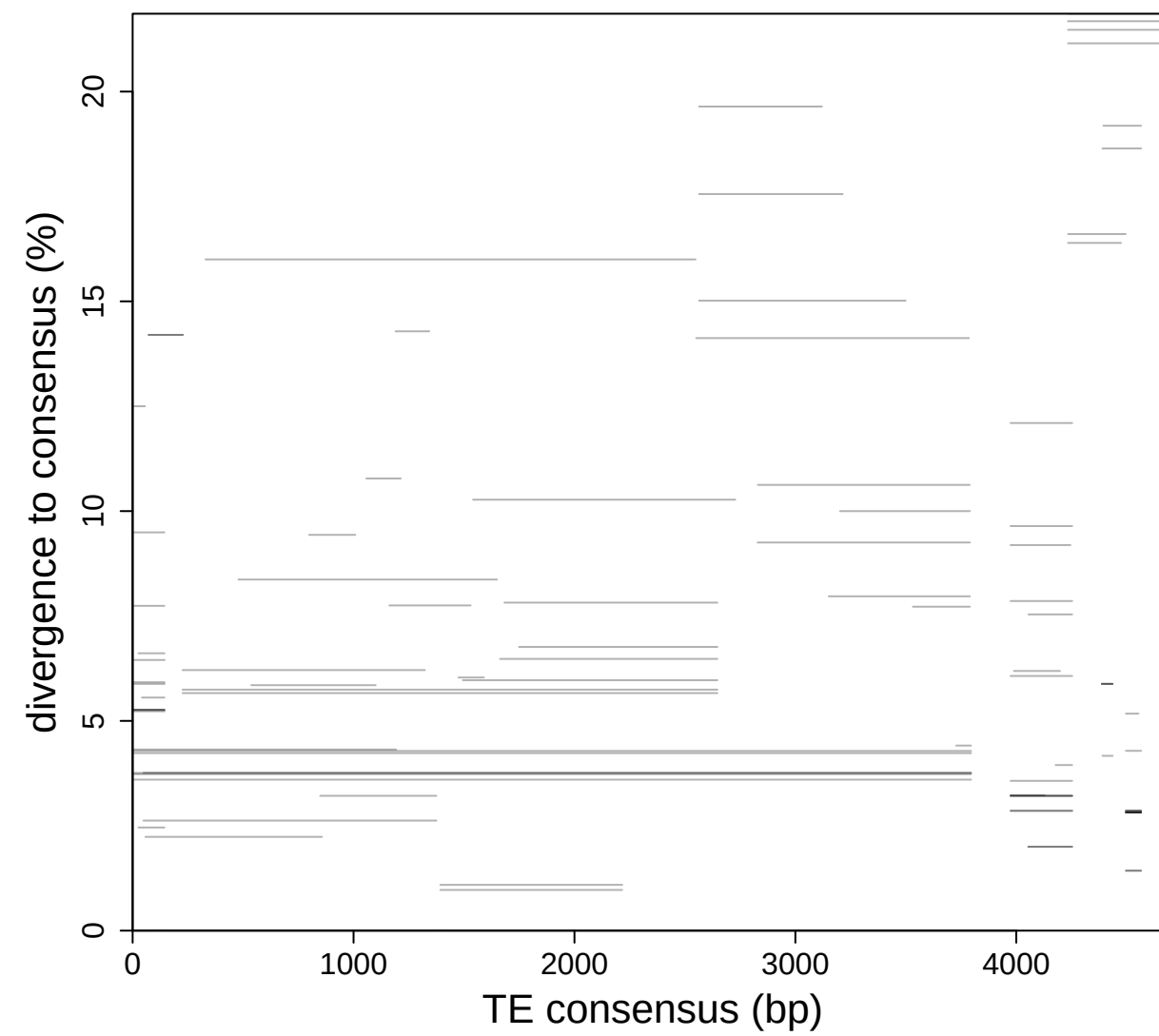
4000

5000



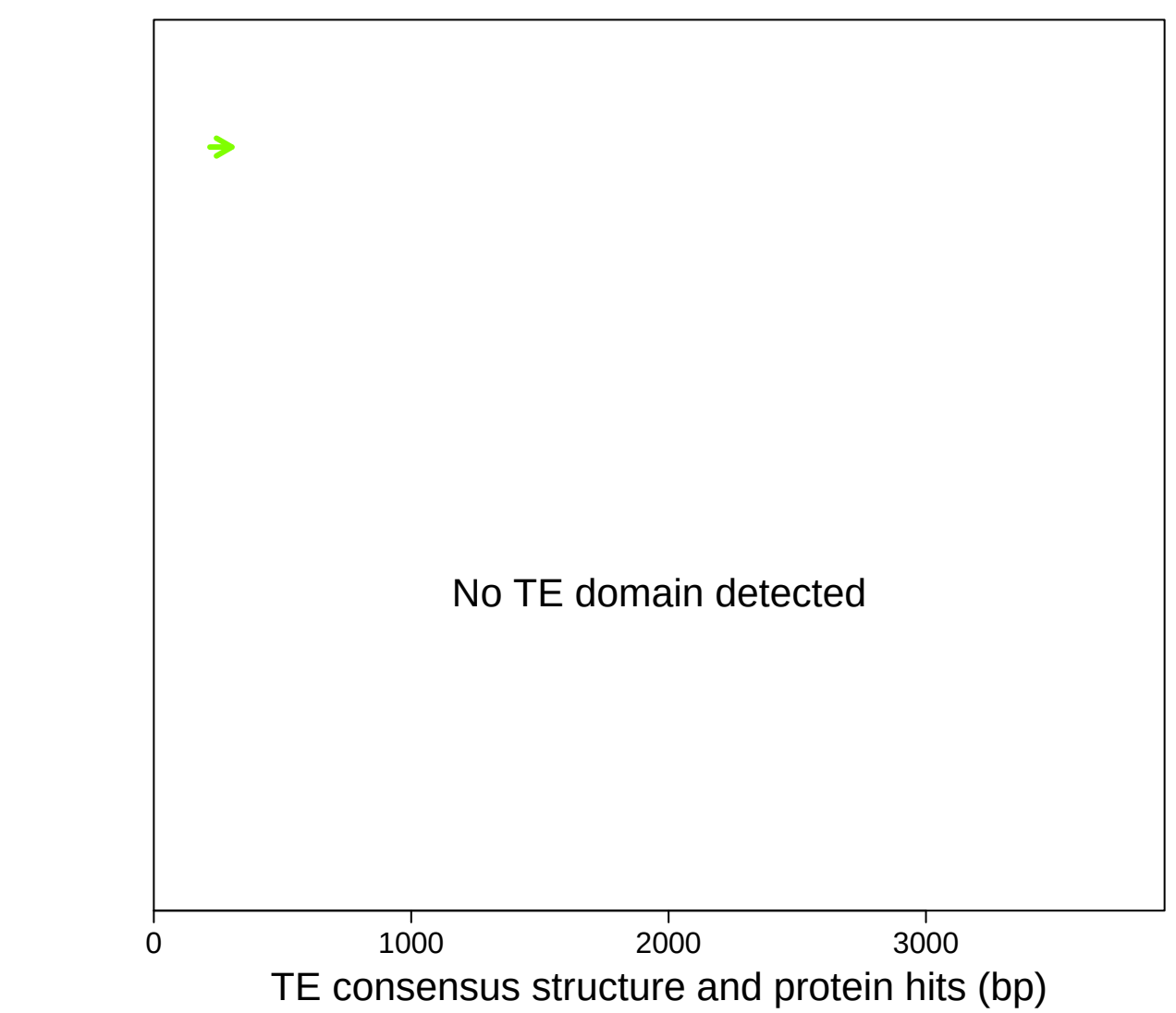
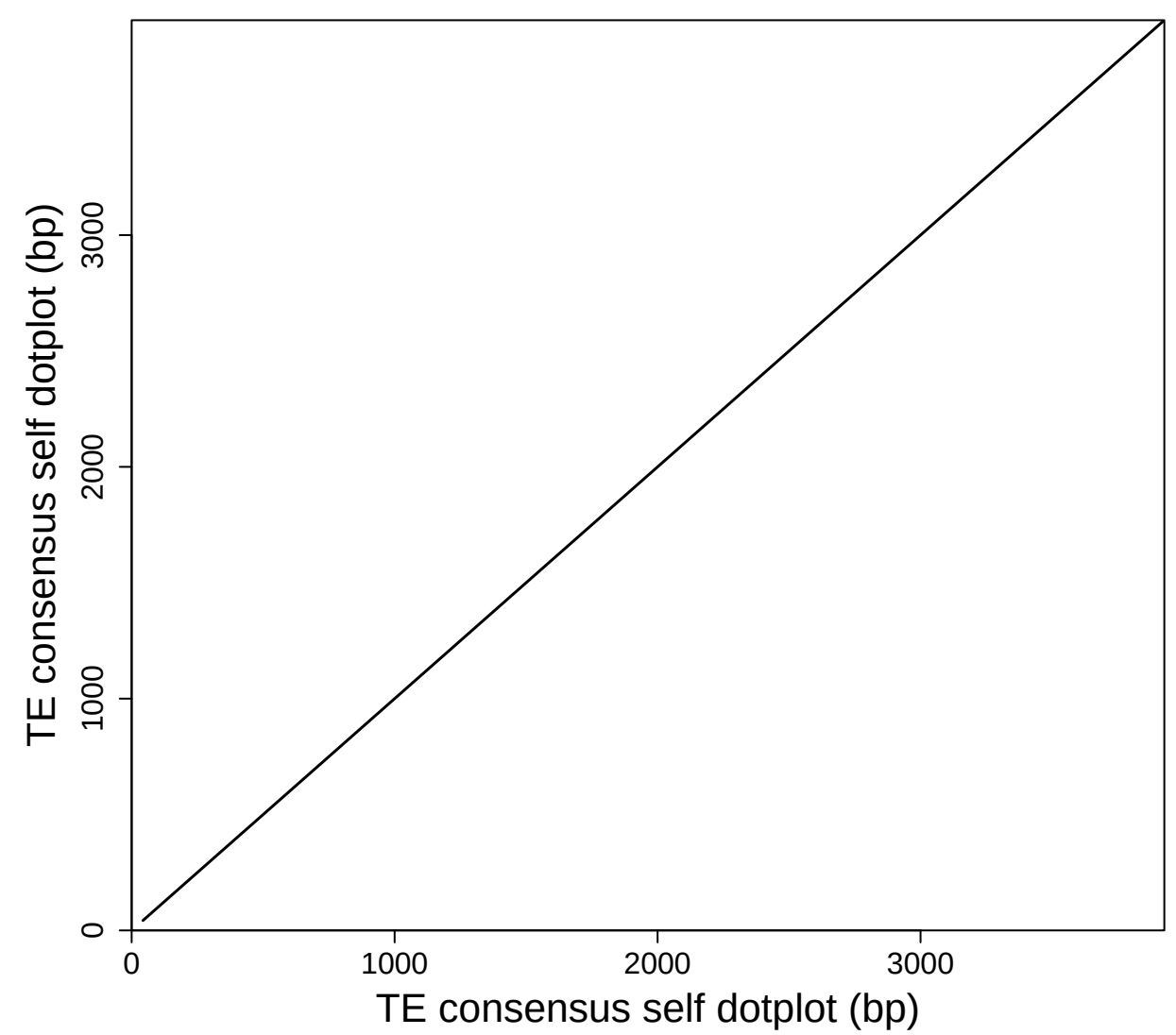
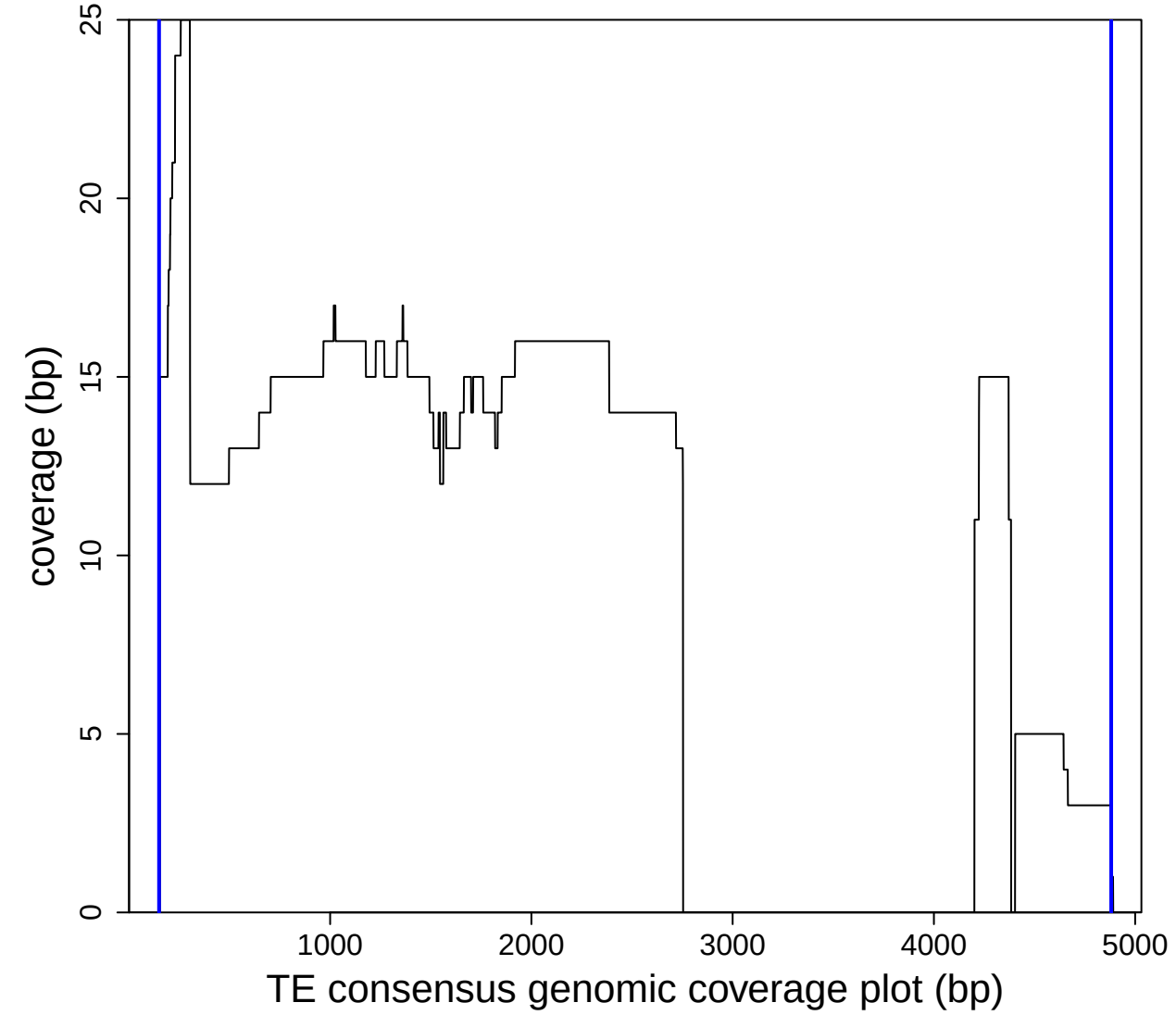
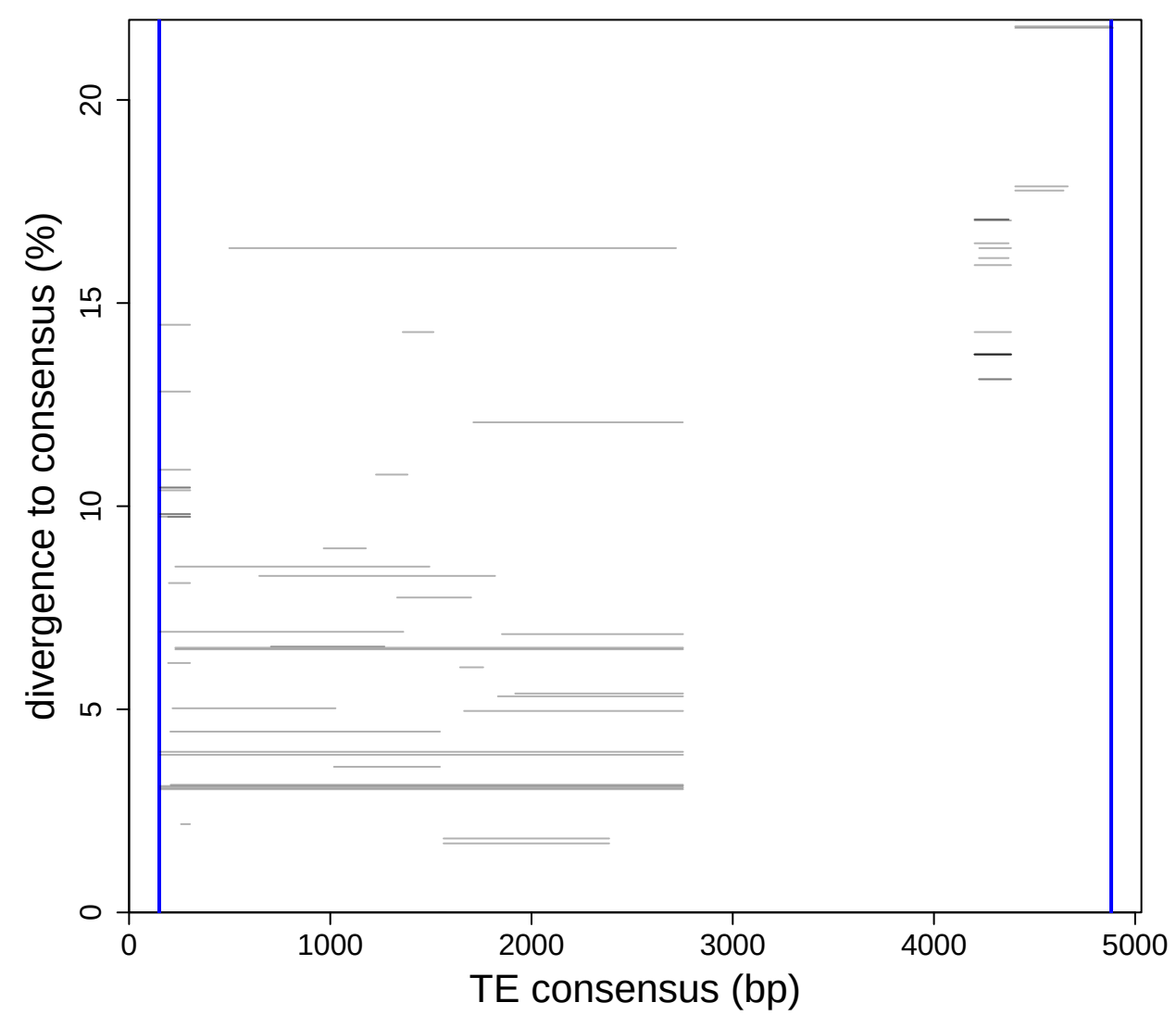
b.bed uf.bed g 1.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa
size: 4709bp; fragments: 96; full length: 0 (>=4238.1bp)

After TEtrimmer 4709 bp

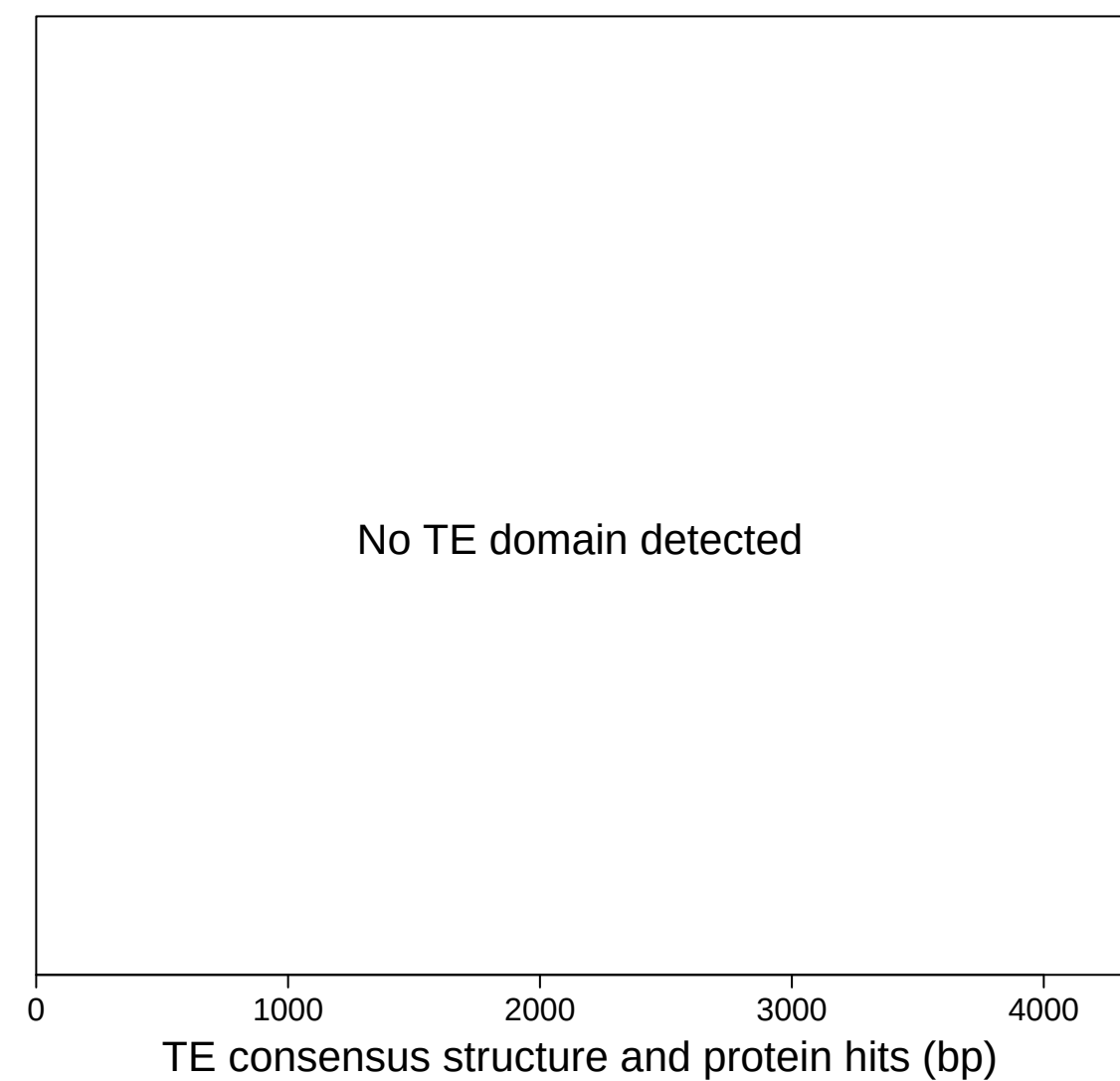
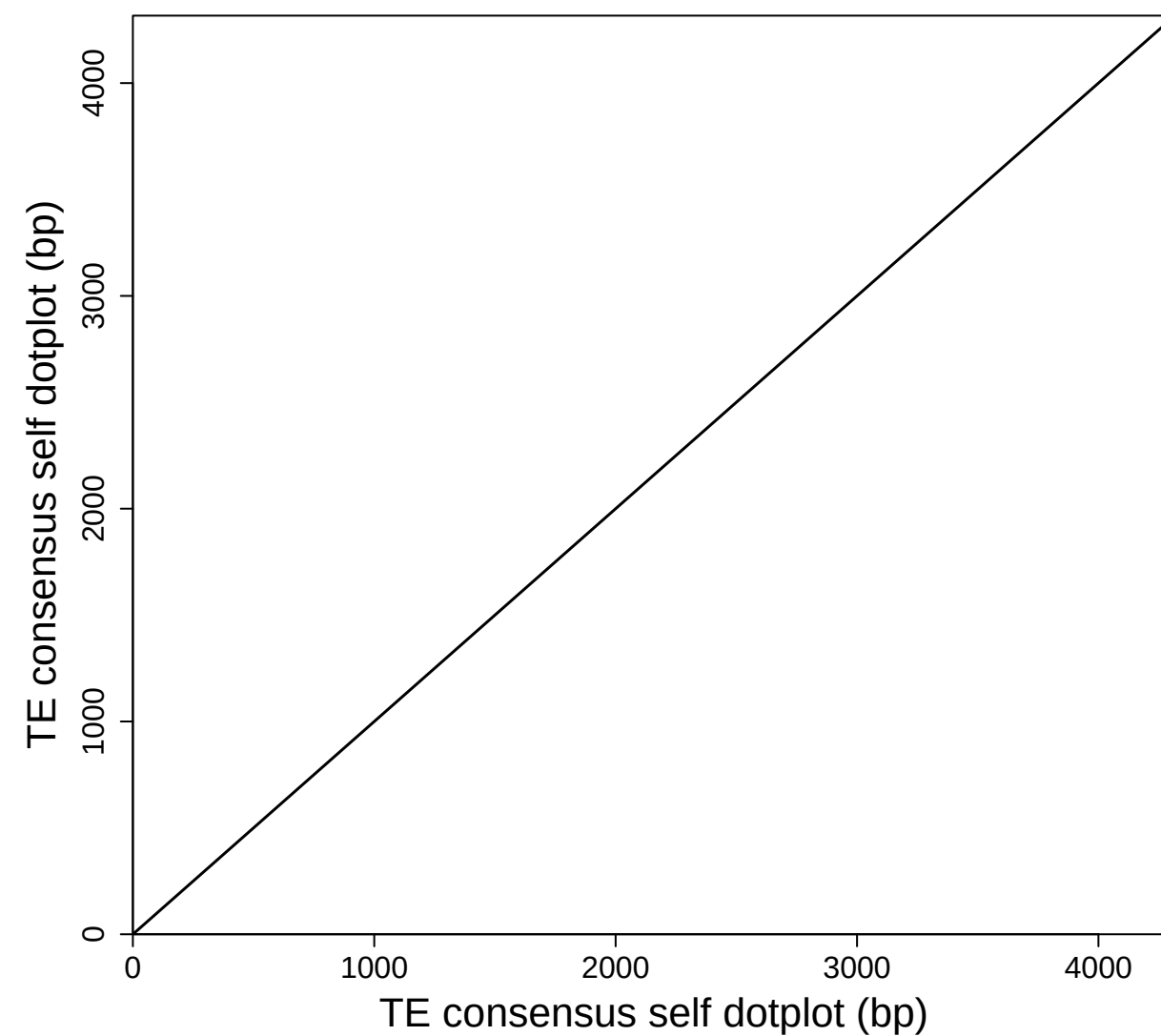
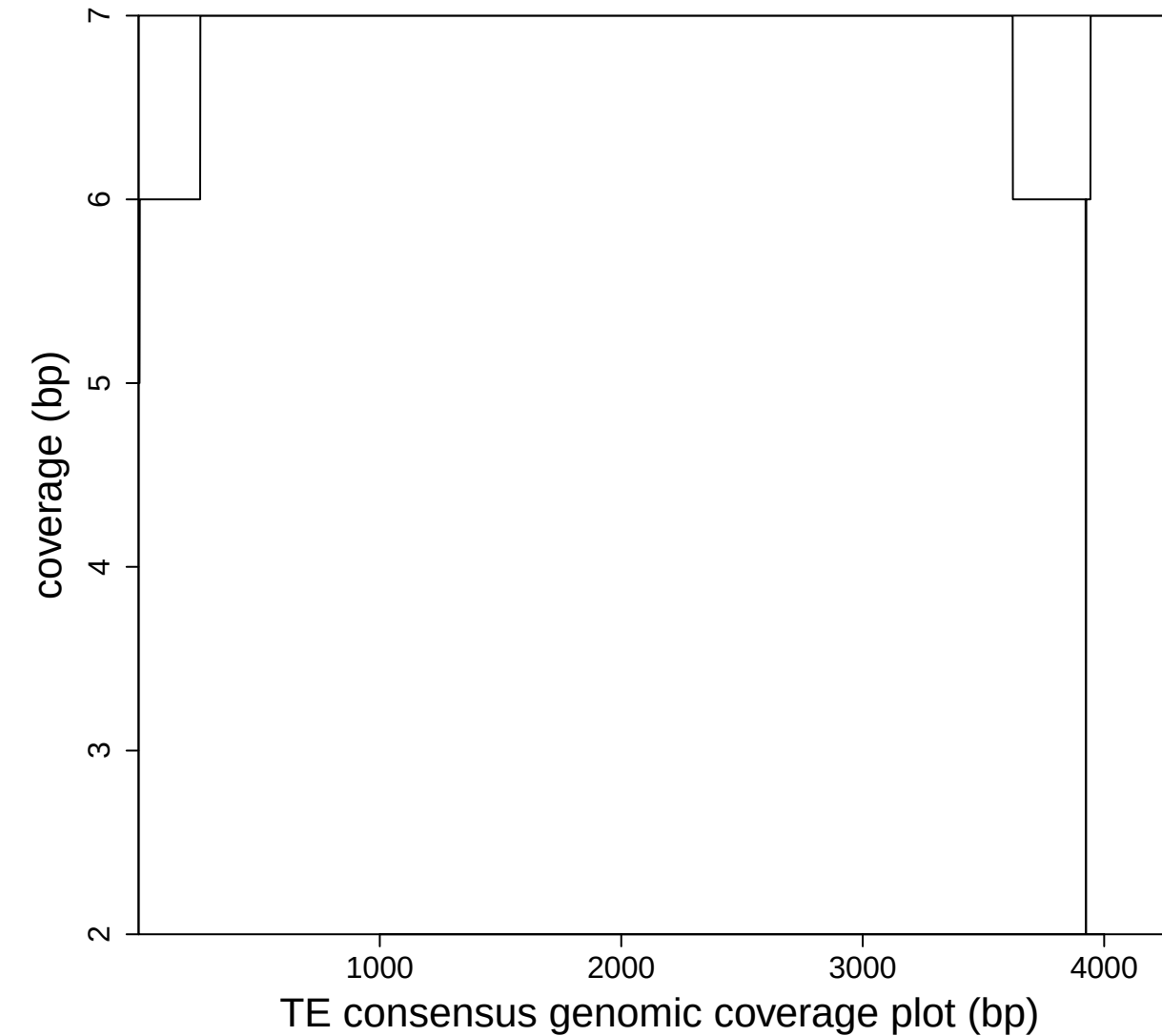
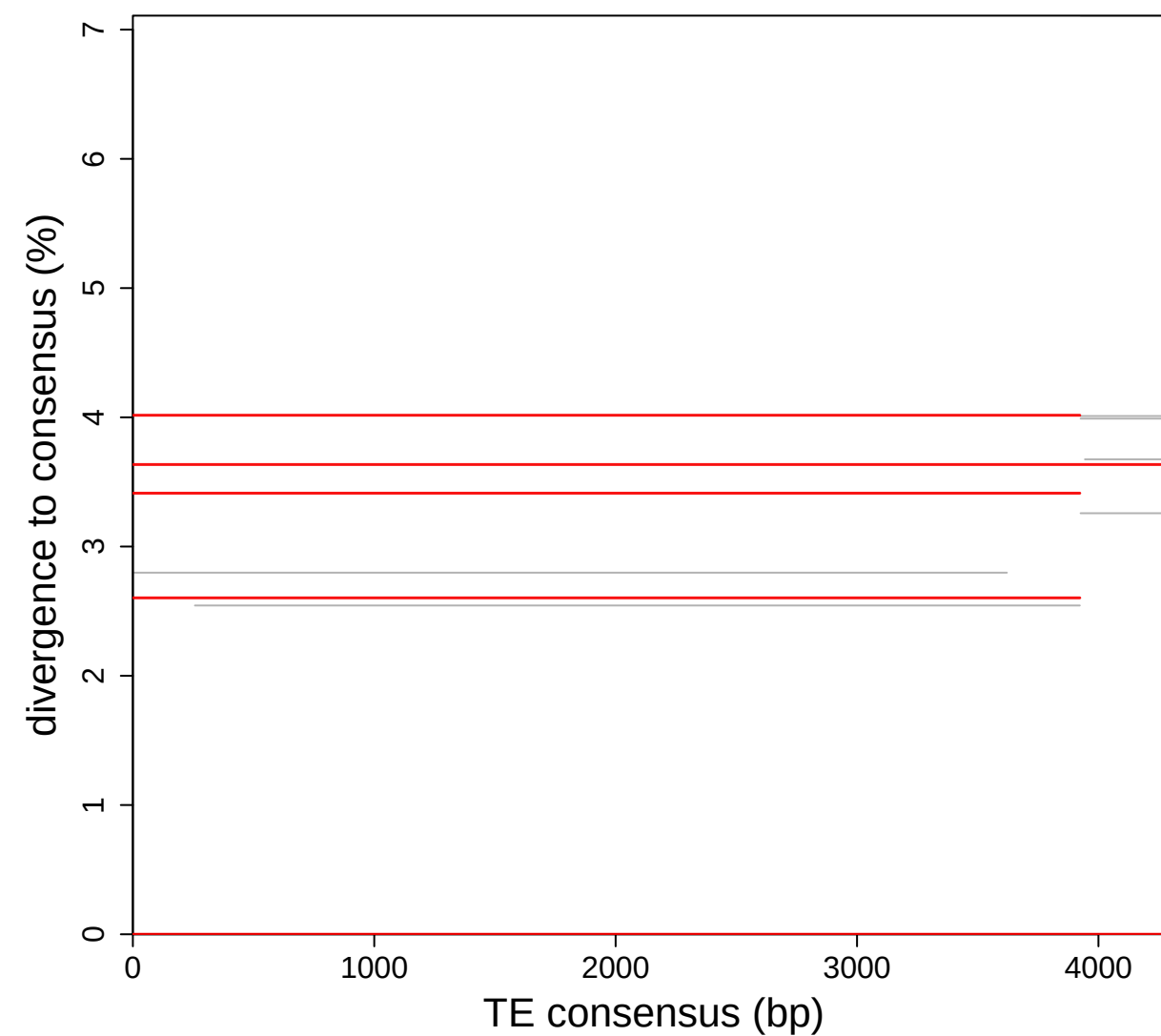


.fasta.b.bed_uf.bed_g_1.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa
size: 5031bp; fragments: 62; full length: 0 (>=4527.9bp)

After TEtrimmer Extended plot Blue lines are boundaries

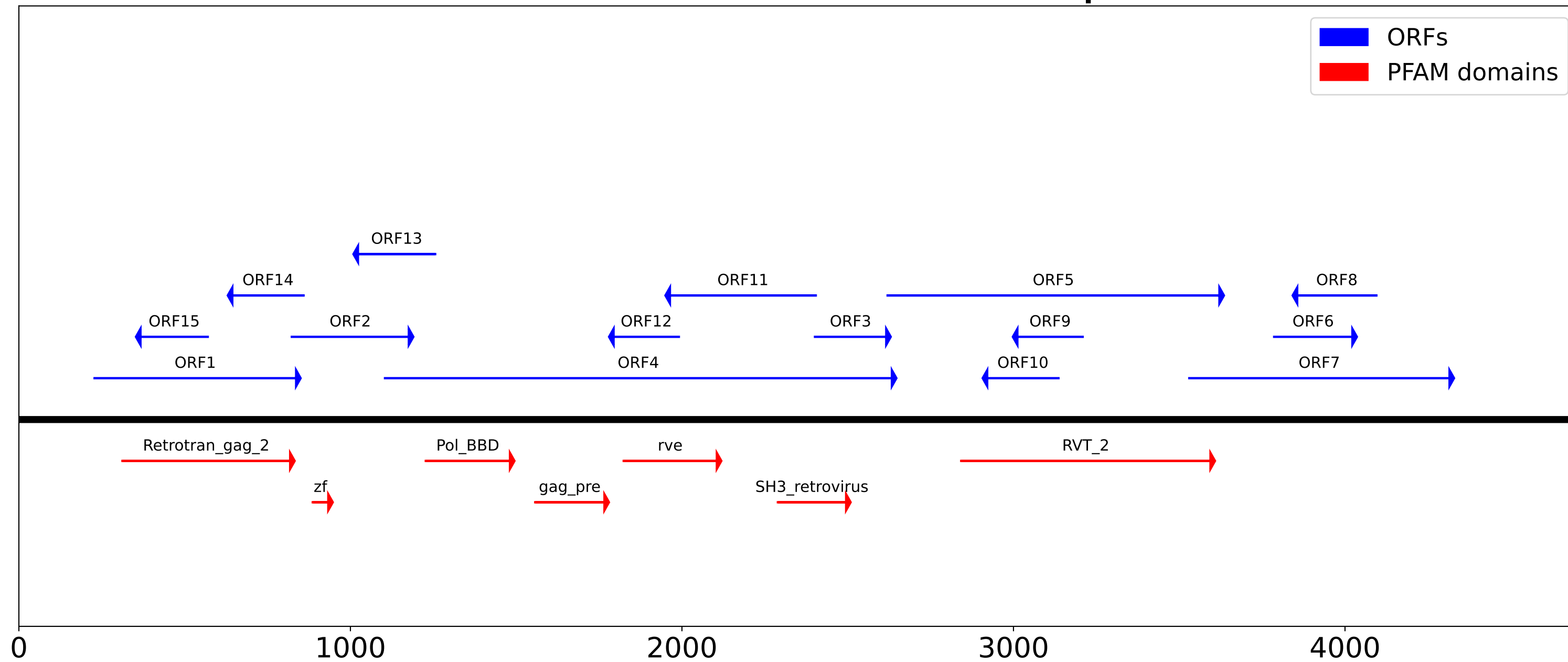


TE: ltr_1_family_801
size: 4317bp; fragments: 12; full length: 5 (≥ 3885.3 bp)

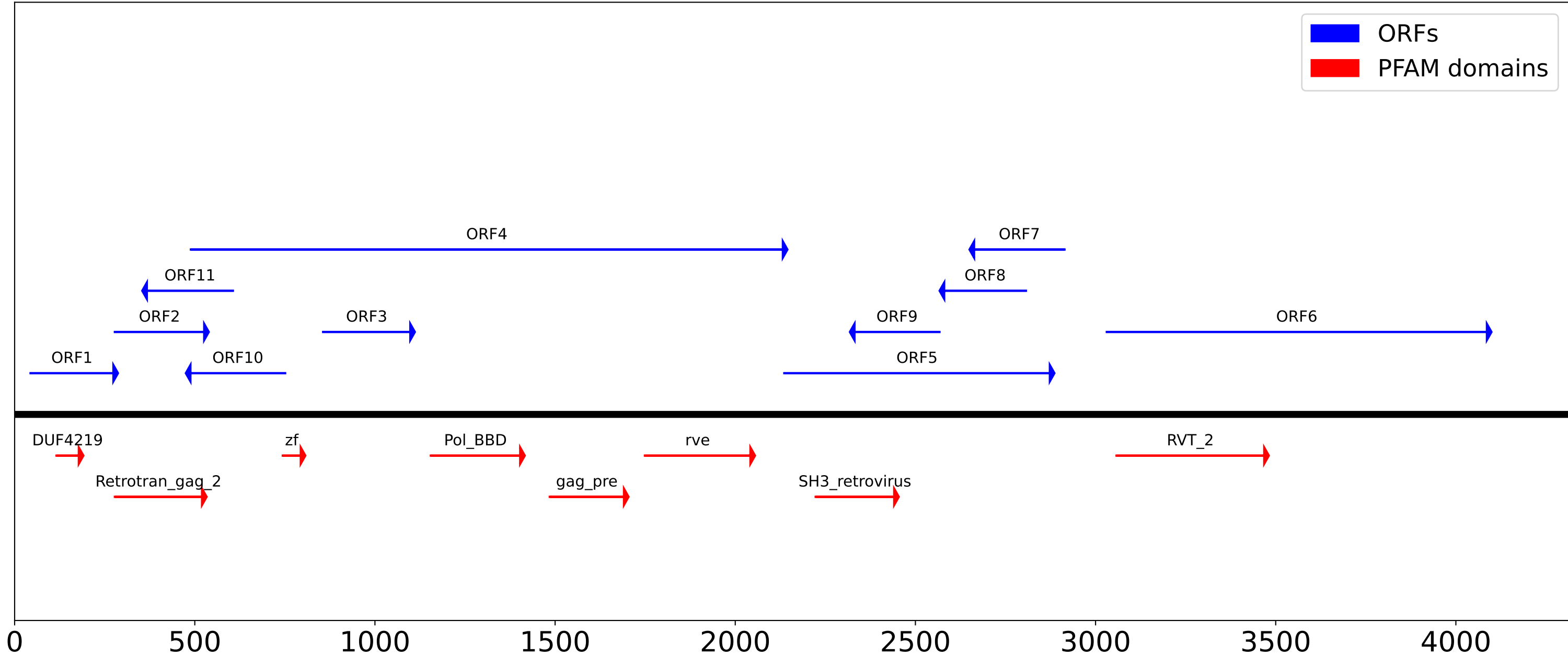


Before TEtrimmer 4317 bp

After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

