

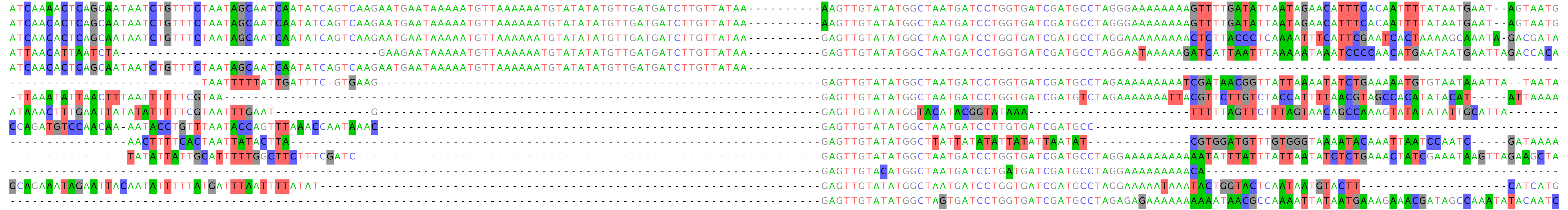
Start crop Point



End crop Point



MSA length = 1928



Start crop Point

End crop Point

0

10

0

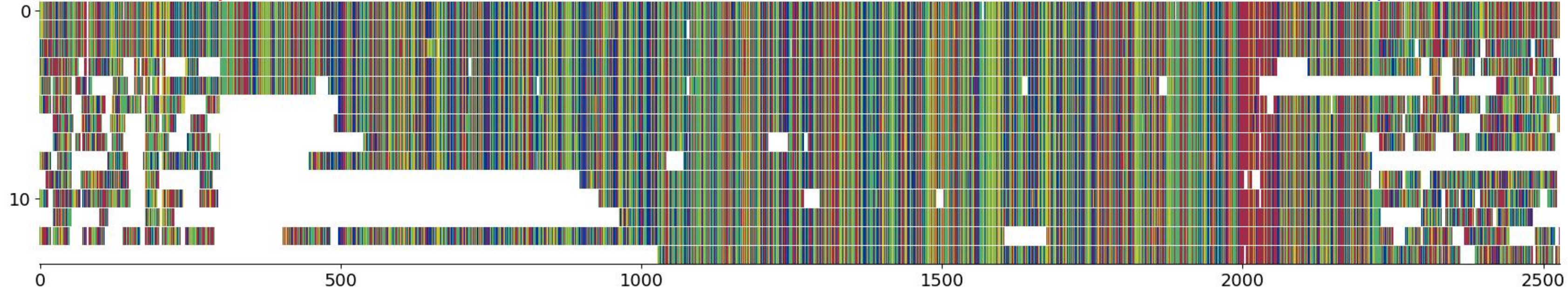
500

1000

1500

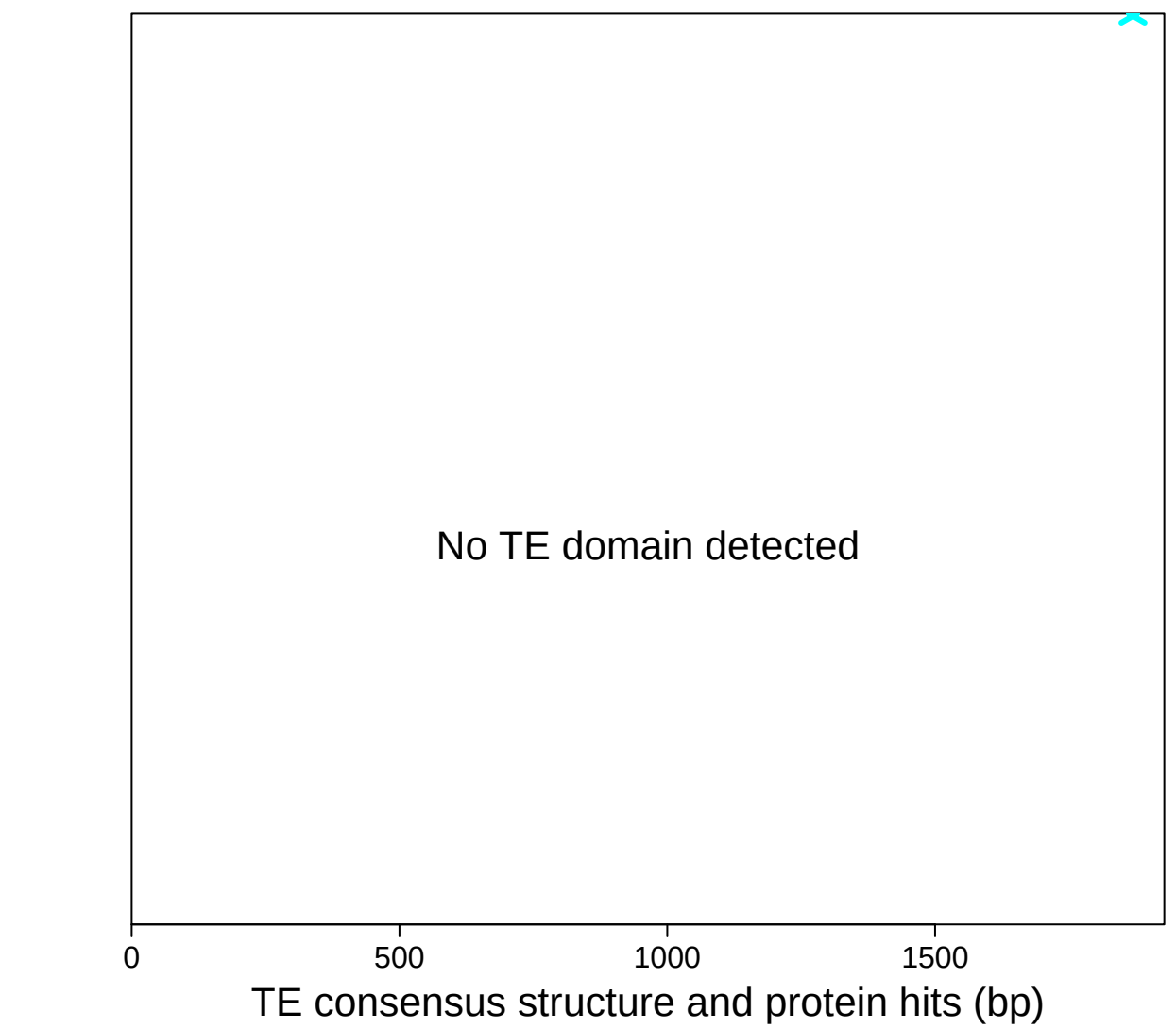
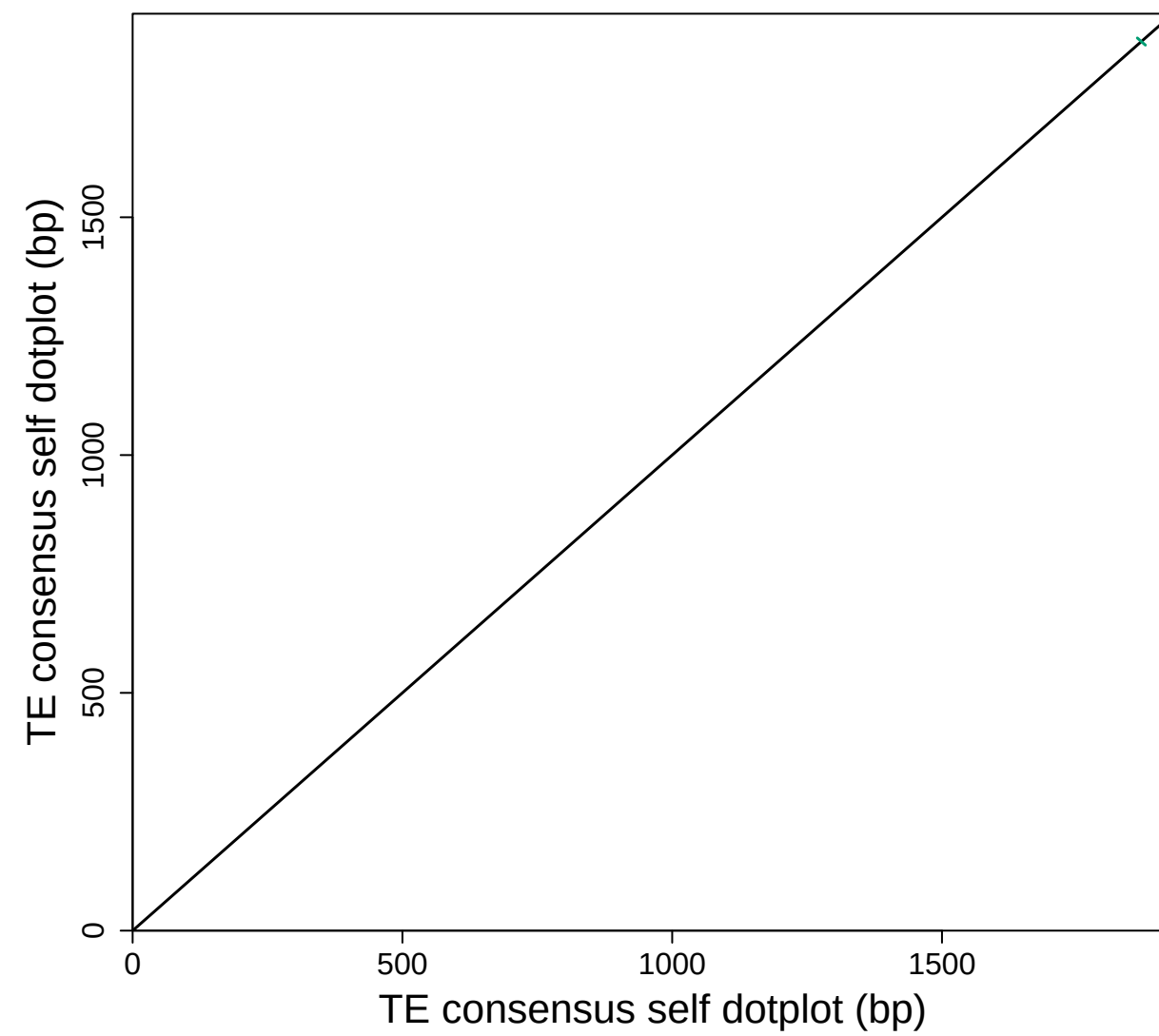
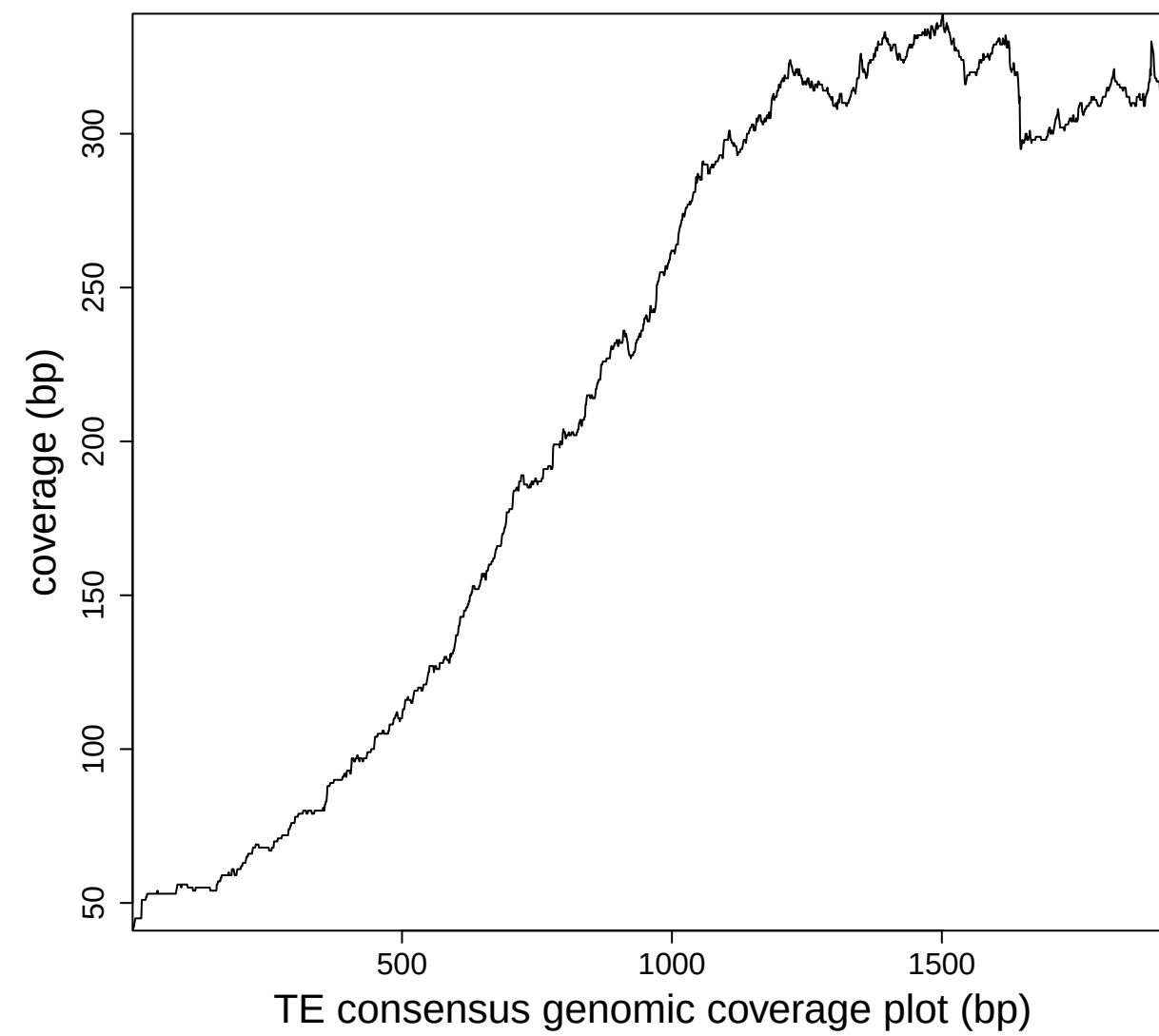
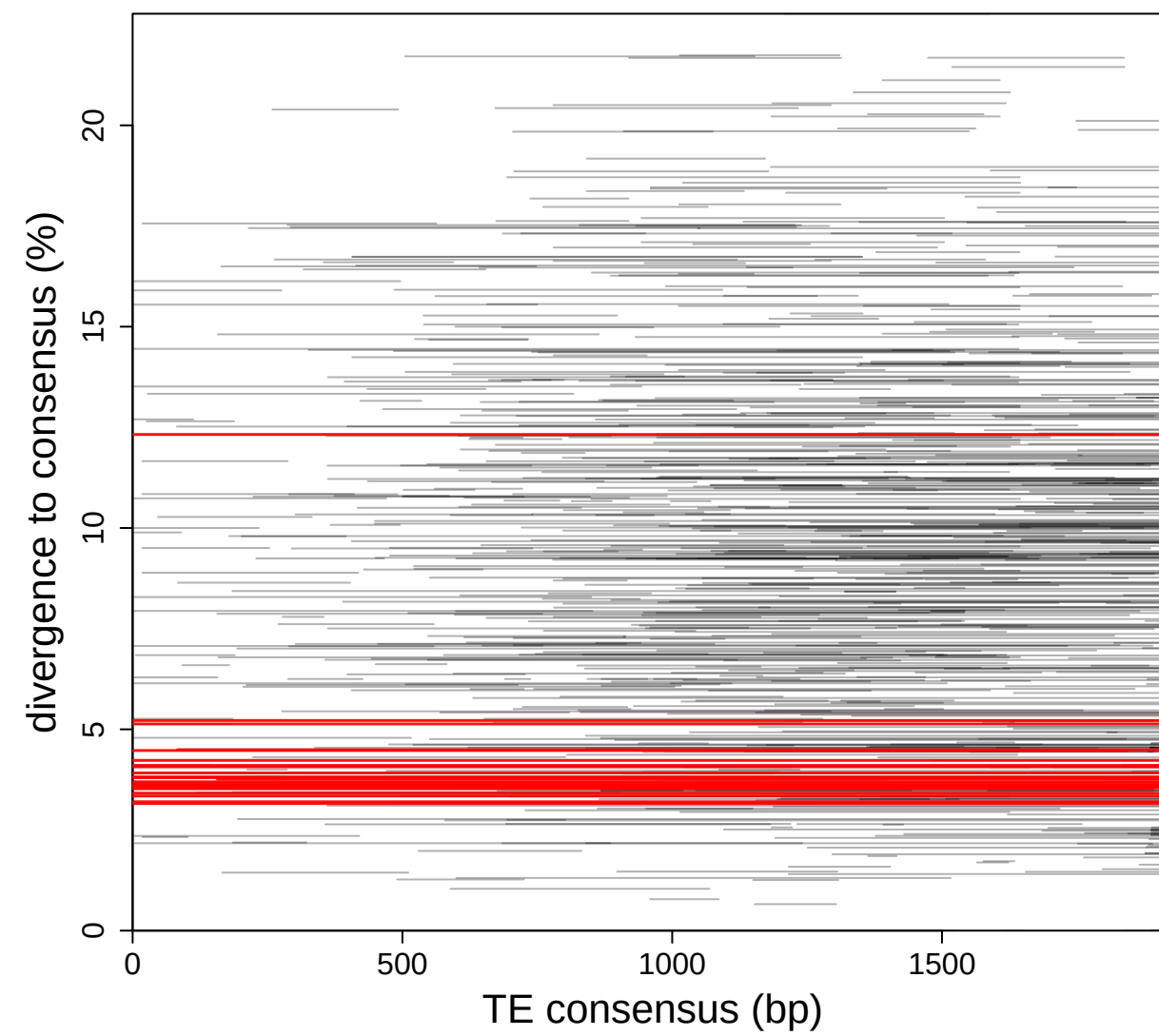
2000

2500



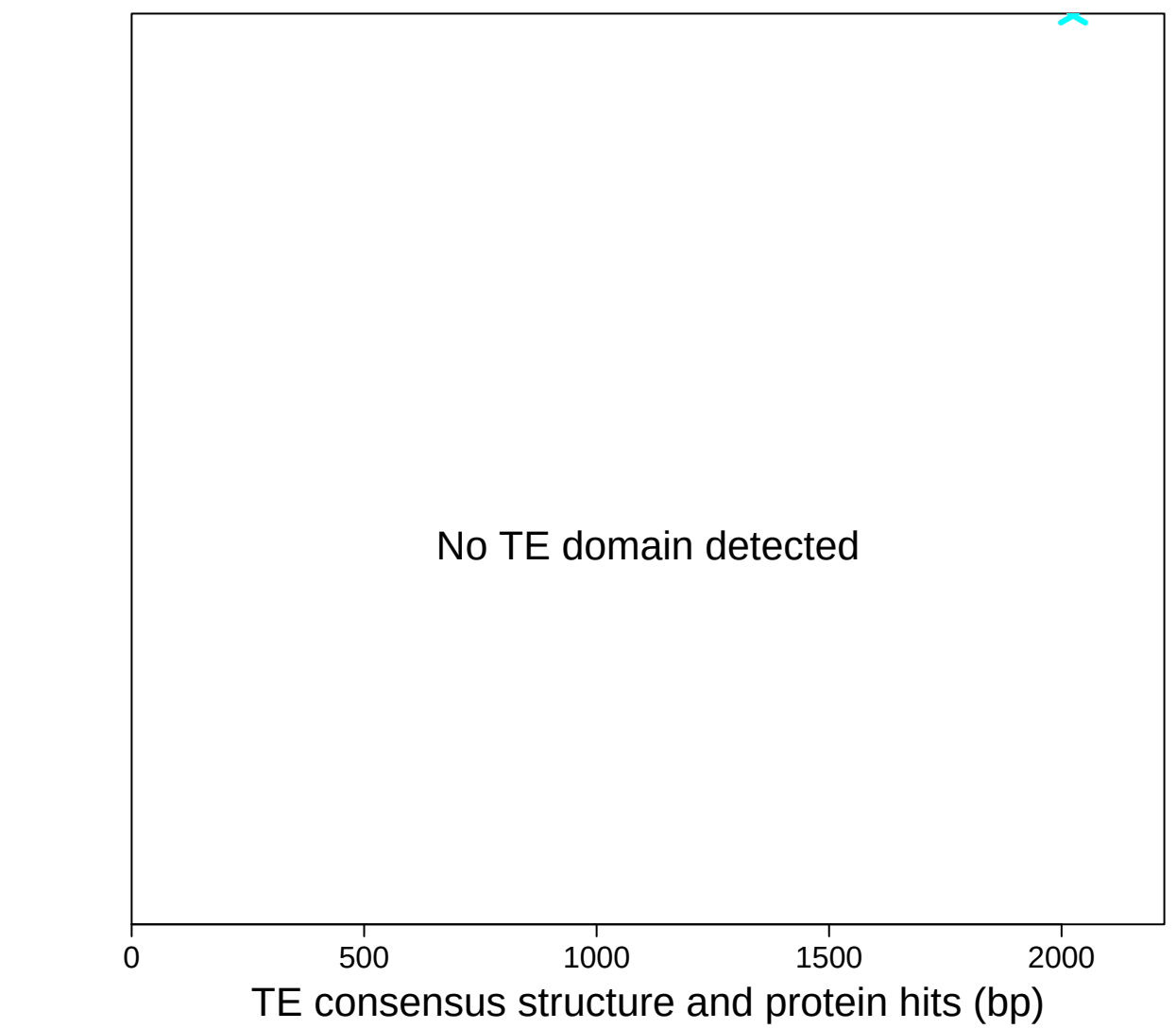
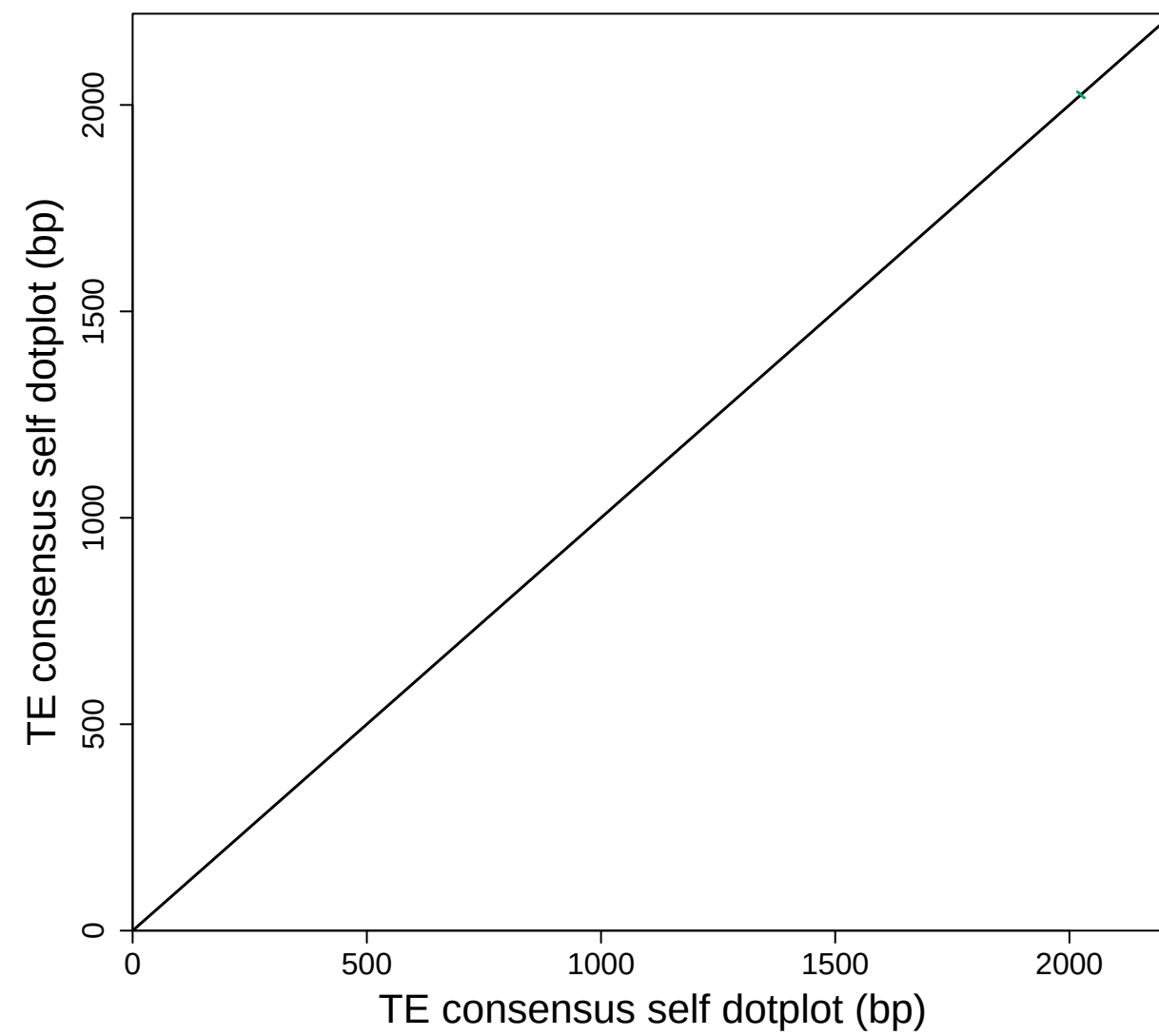
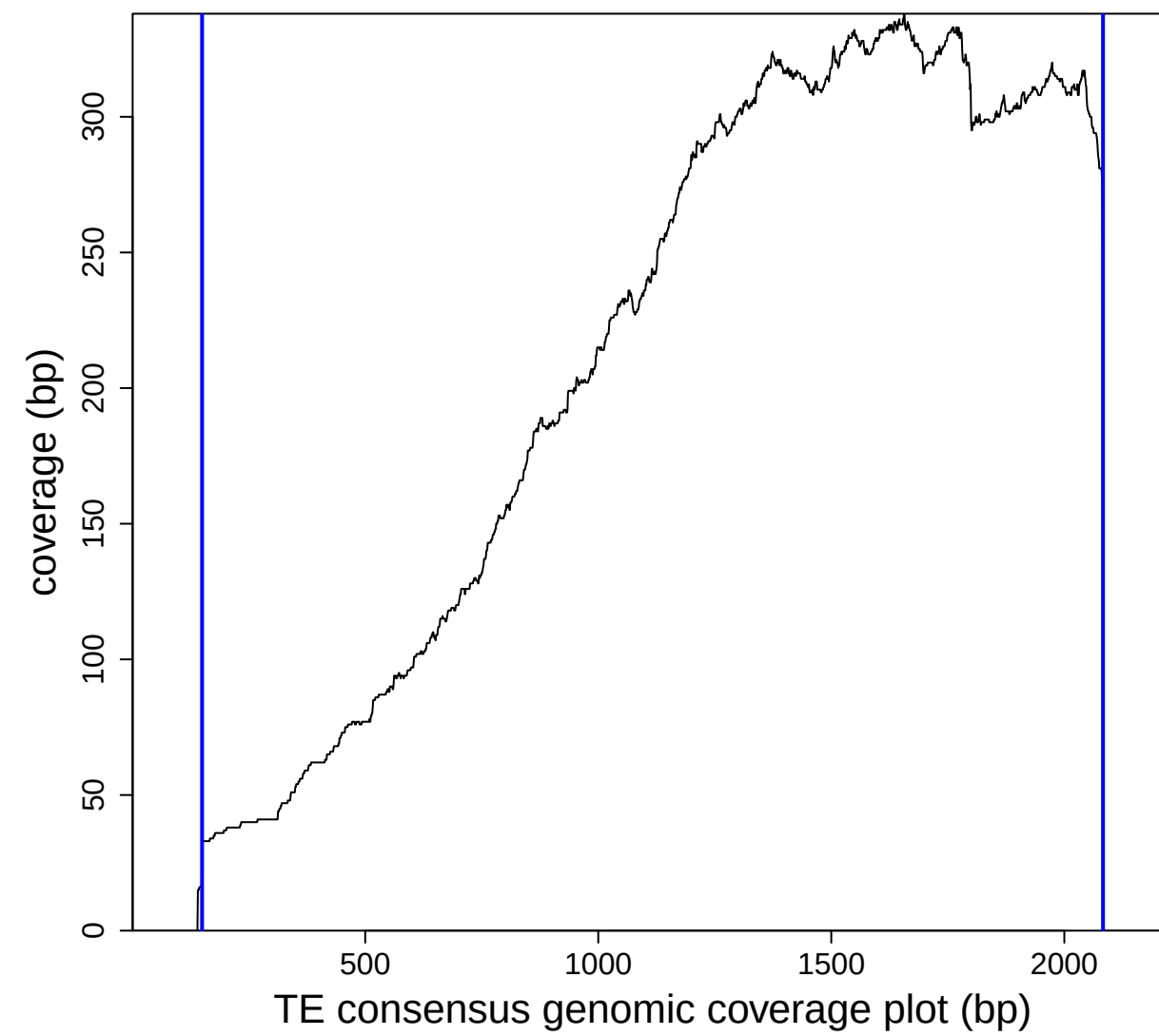
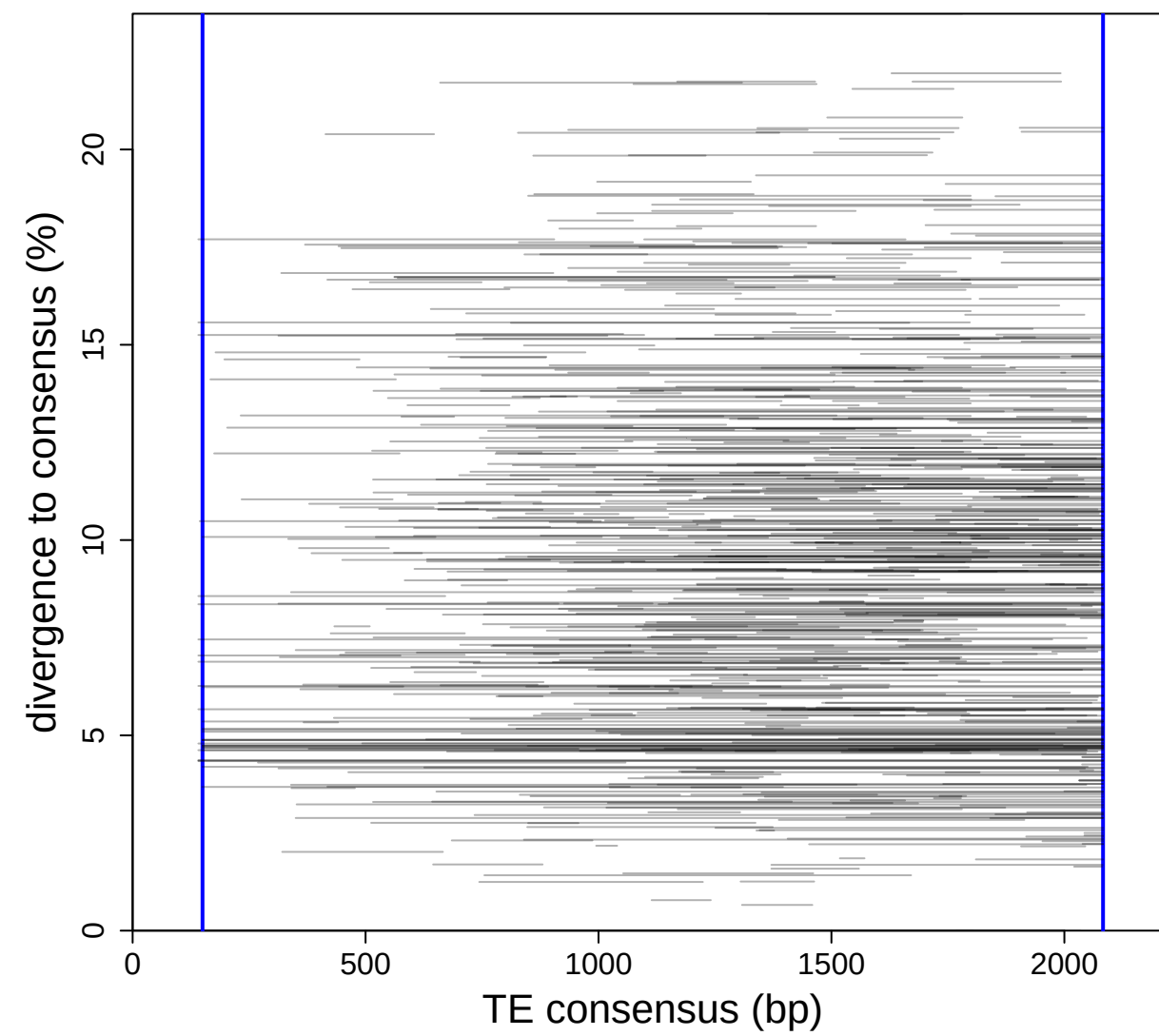
bed_uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c
size: 1928bp; fragments: 786; full length: 25 (≥ 1735.2 bp)

After TEtrimmer 1928 bp



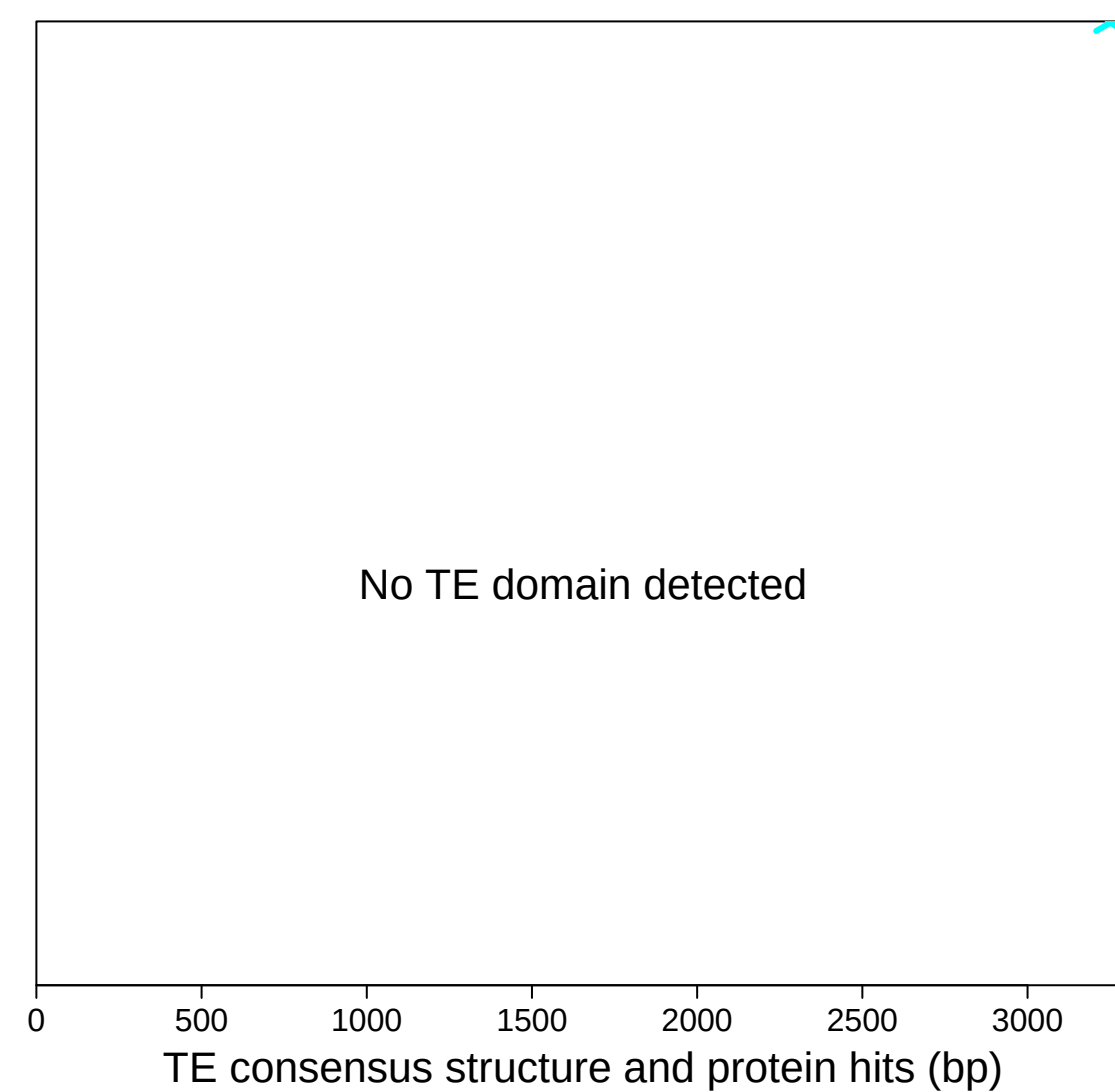
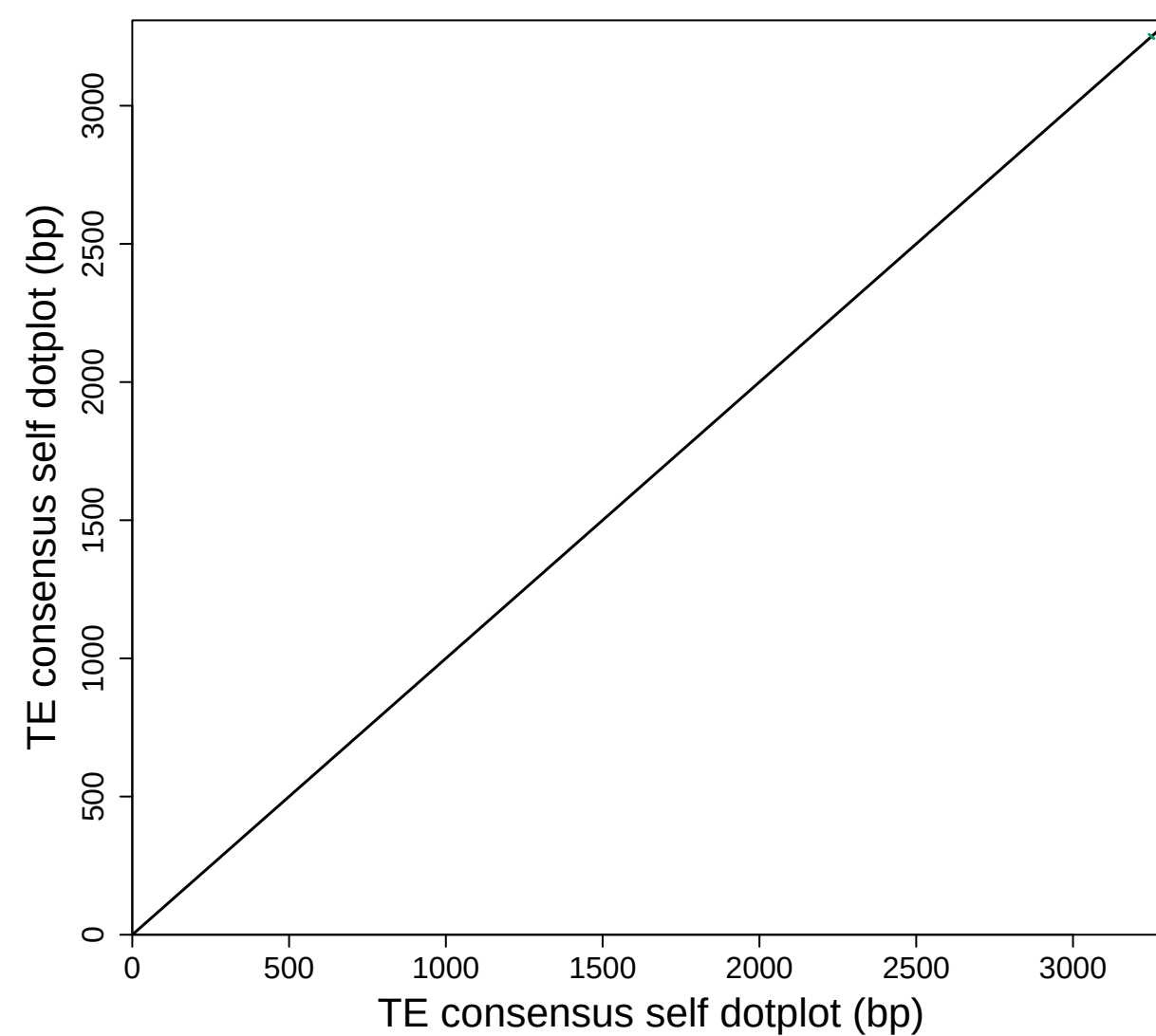
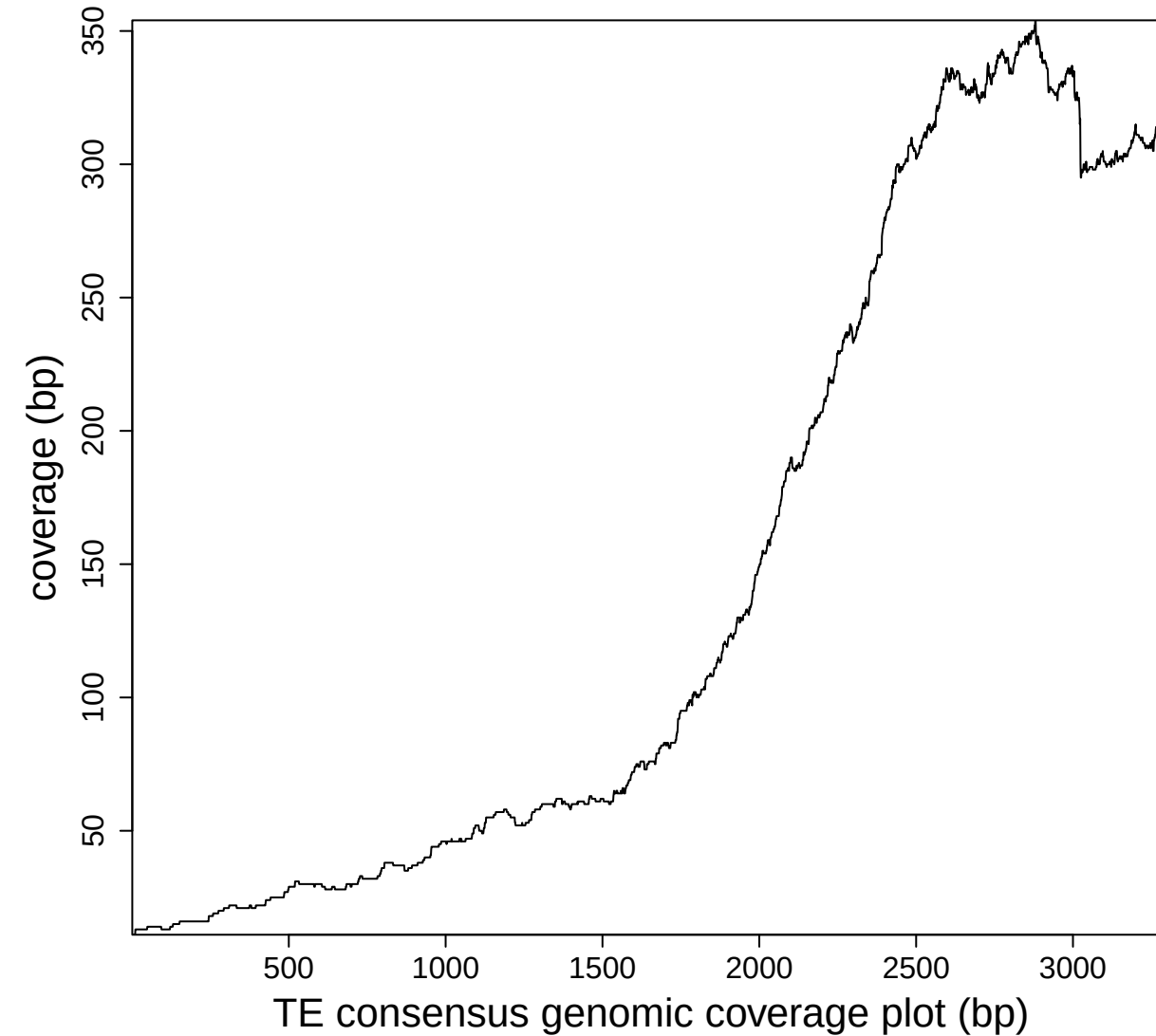
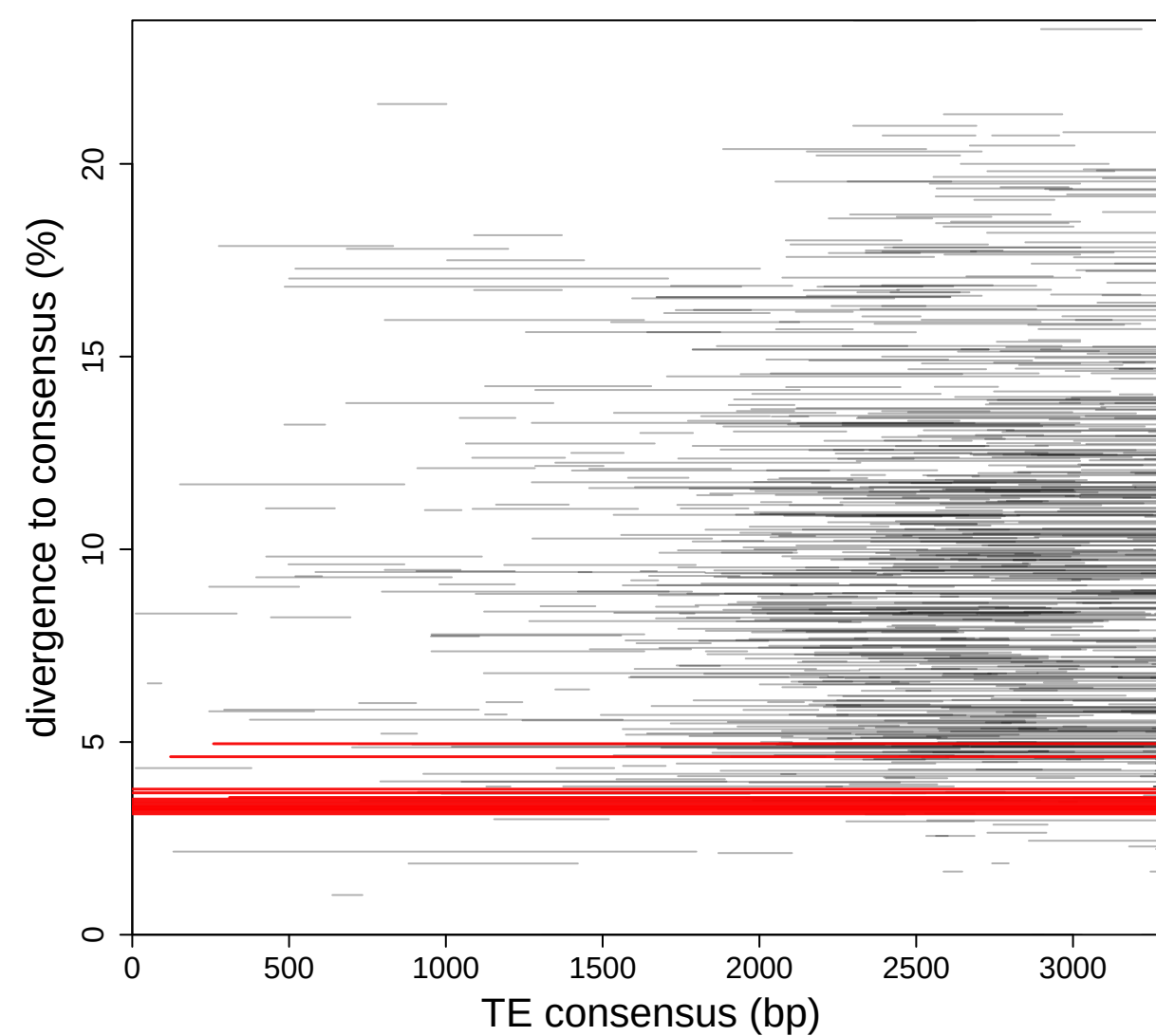
6.fasta.b.bed uf.bed g_2.bed fm_1.bed 0 0 bcln.fa aln.fa cl.f
size: 2233bp; fragments: 752; full length: 0 (>=2009.7bp)

After TEtrimmer Extended plot Blue lines are boundaries

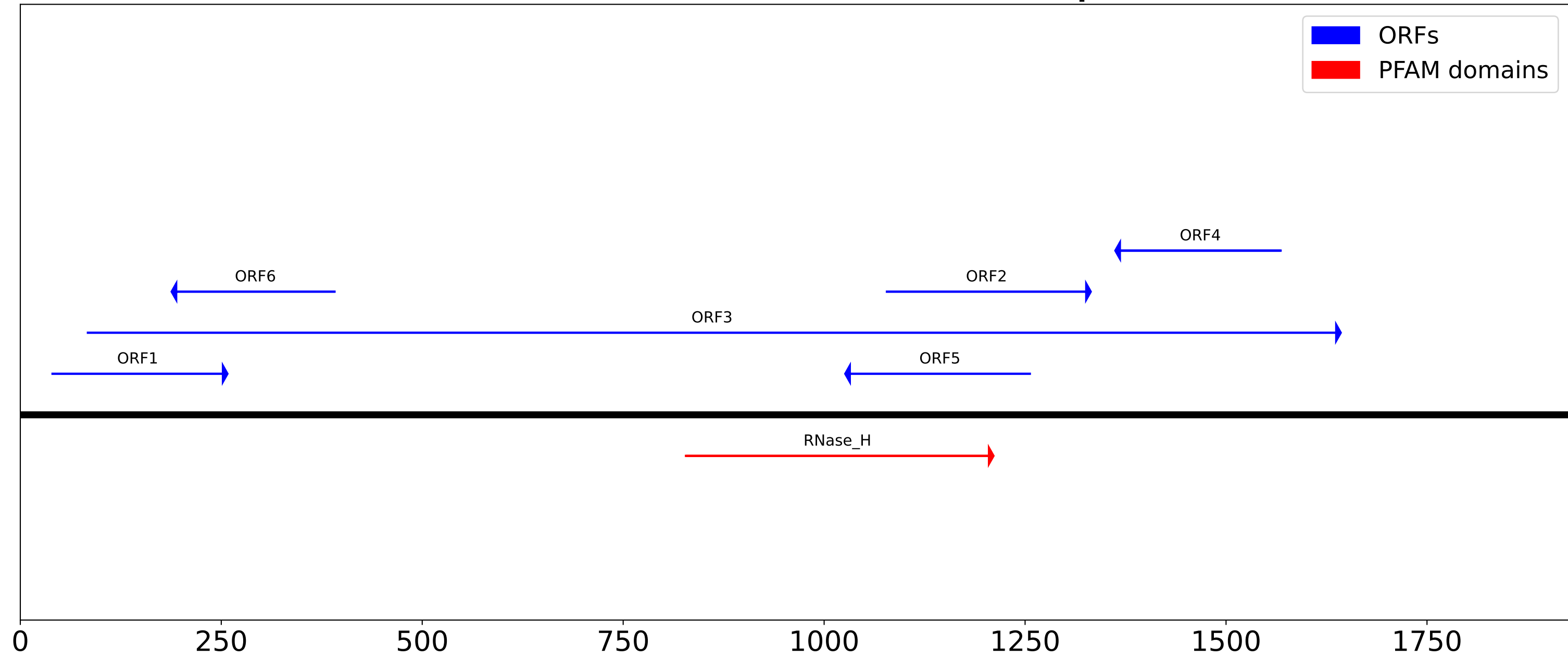


TE: rnd_5_family_3116
size: 3309bp; fragments: 836; full length: 14 (≥ 2978.1 bp)

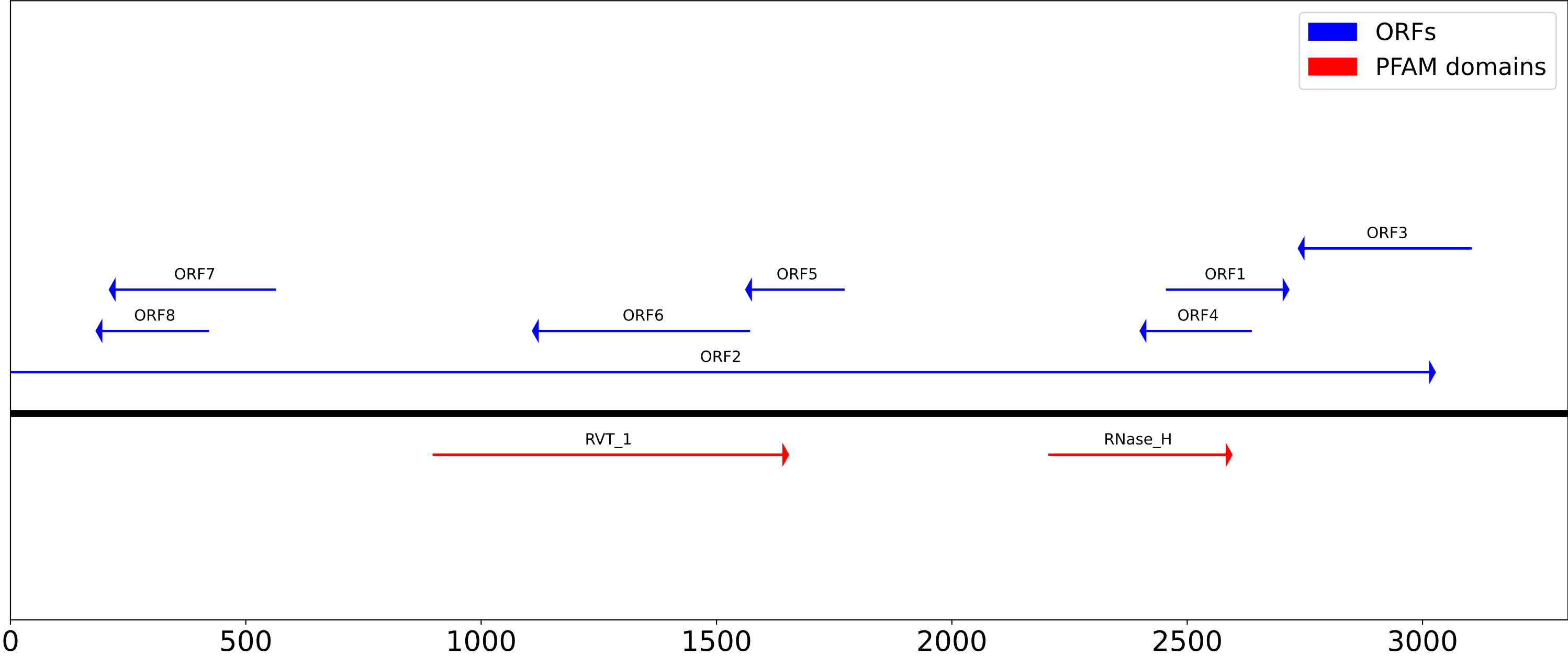
Before TEtrimmer 3309 bp



After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

