

Start crop Point



End crop Point



MSA length = 2981



Start crop Point

End crop Point

0

10

0

500

1000

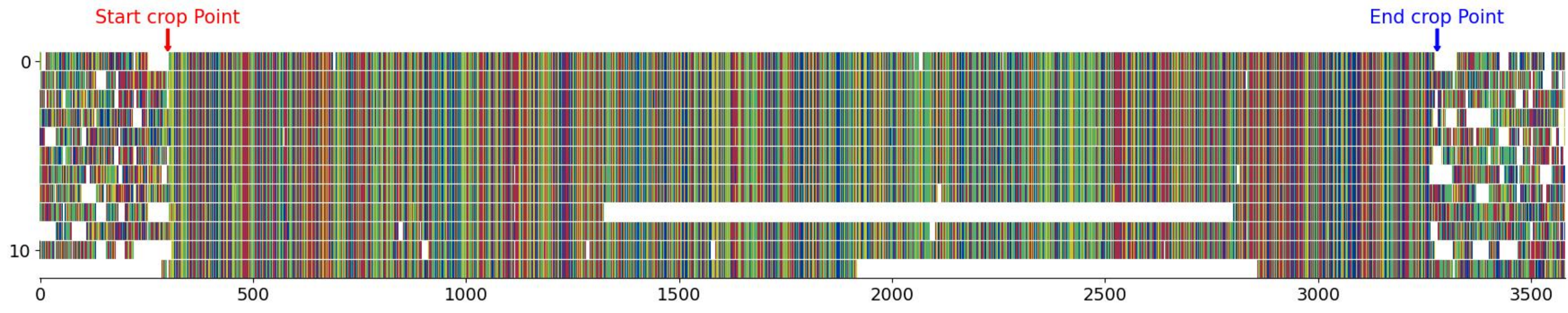
1500

2000

2500

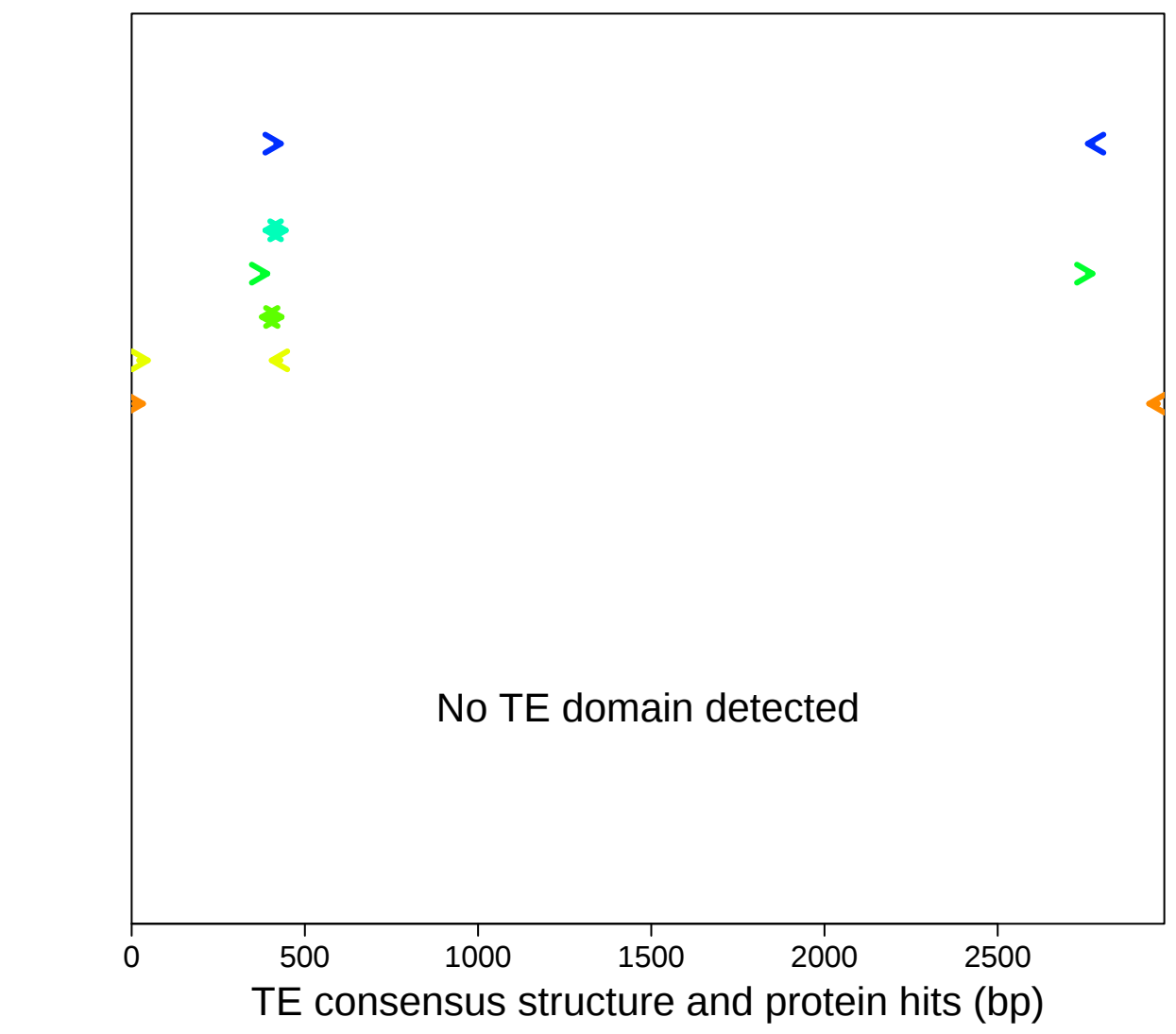
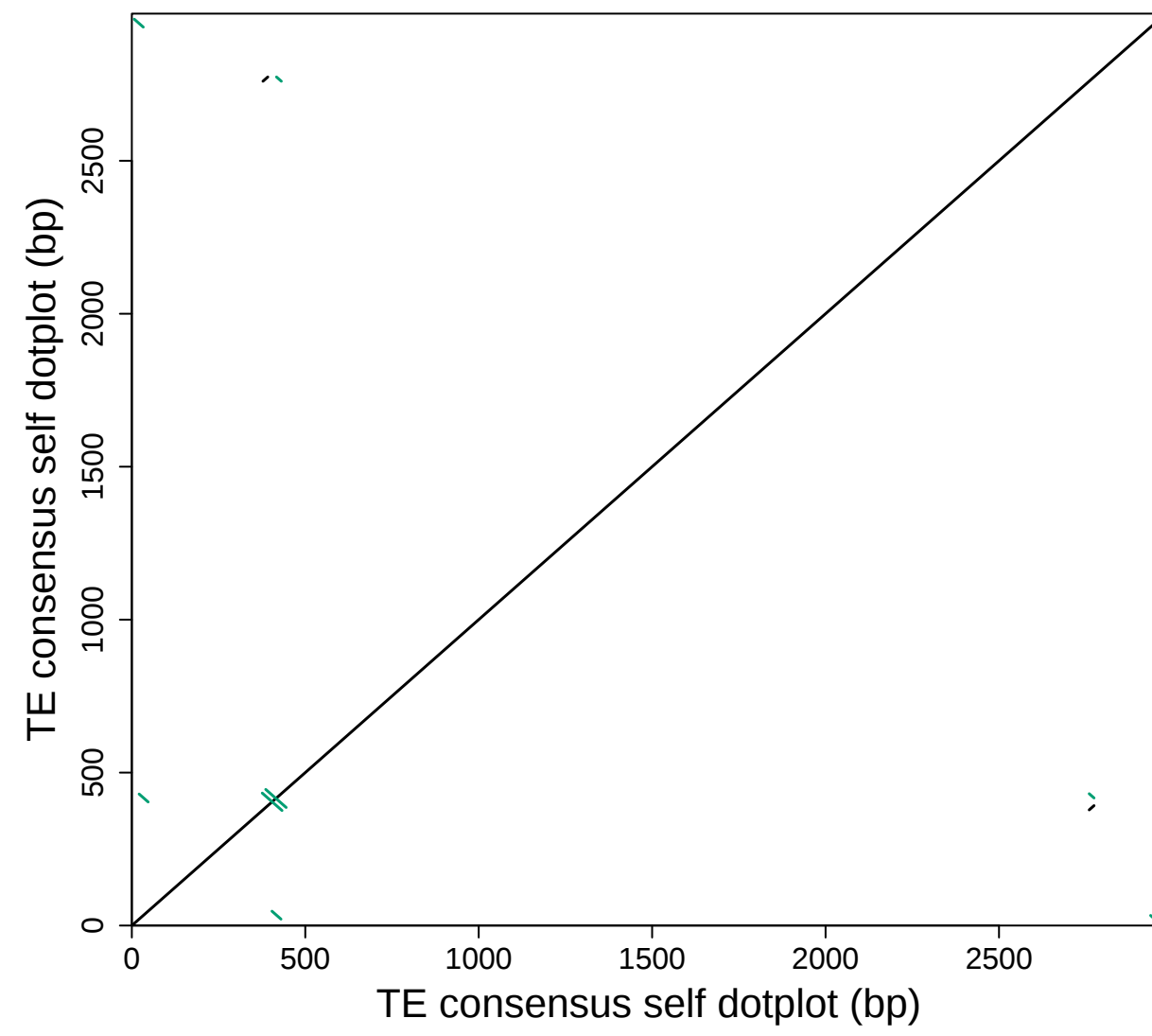
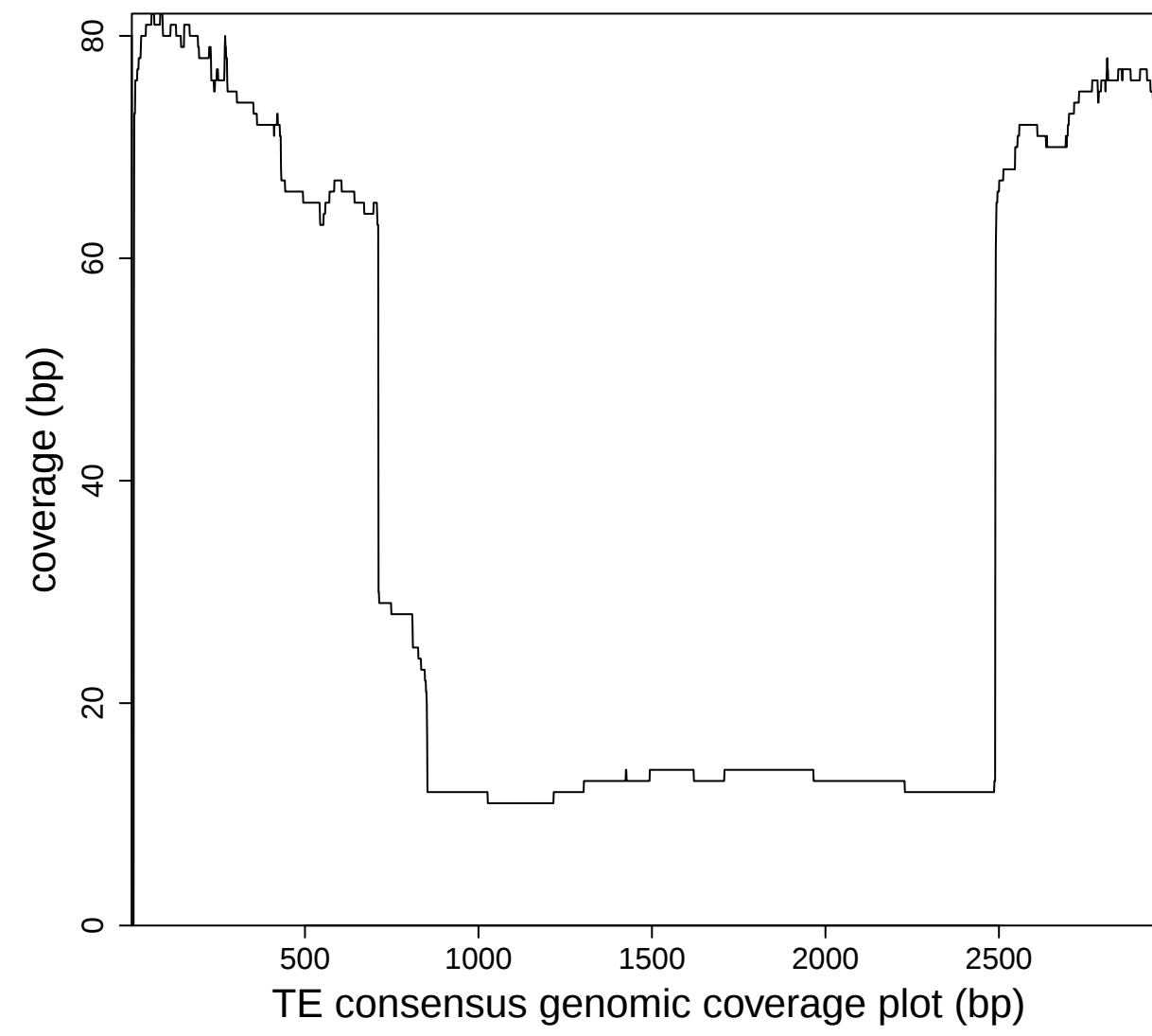
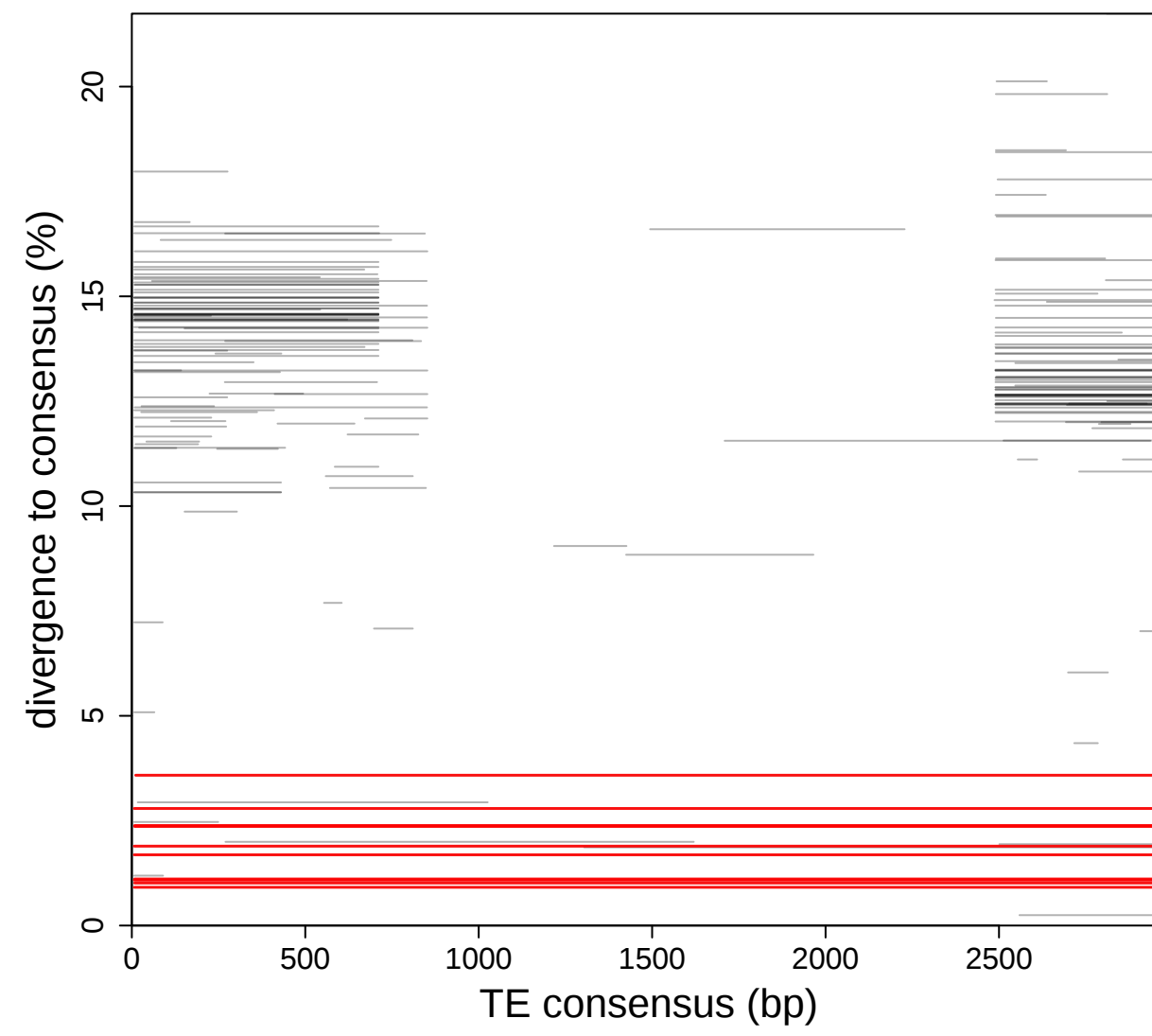
3000

3500



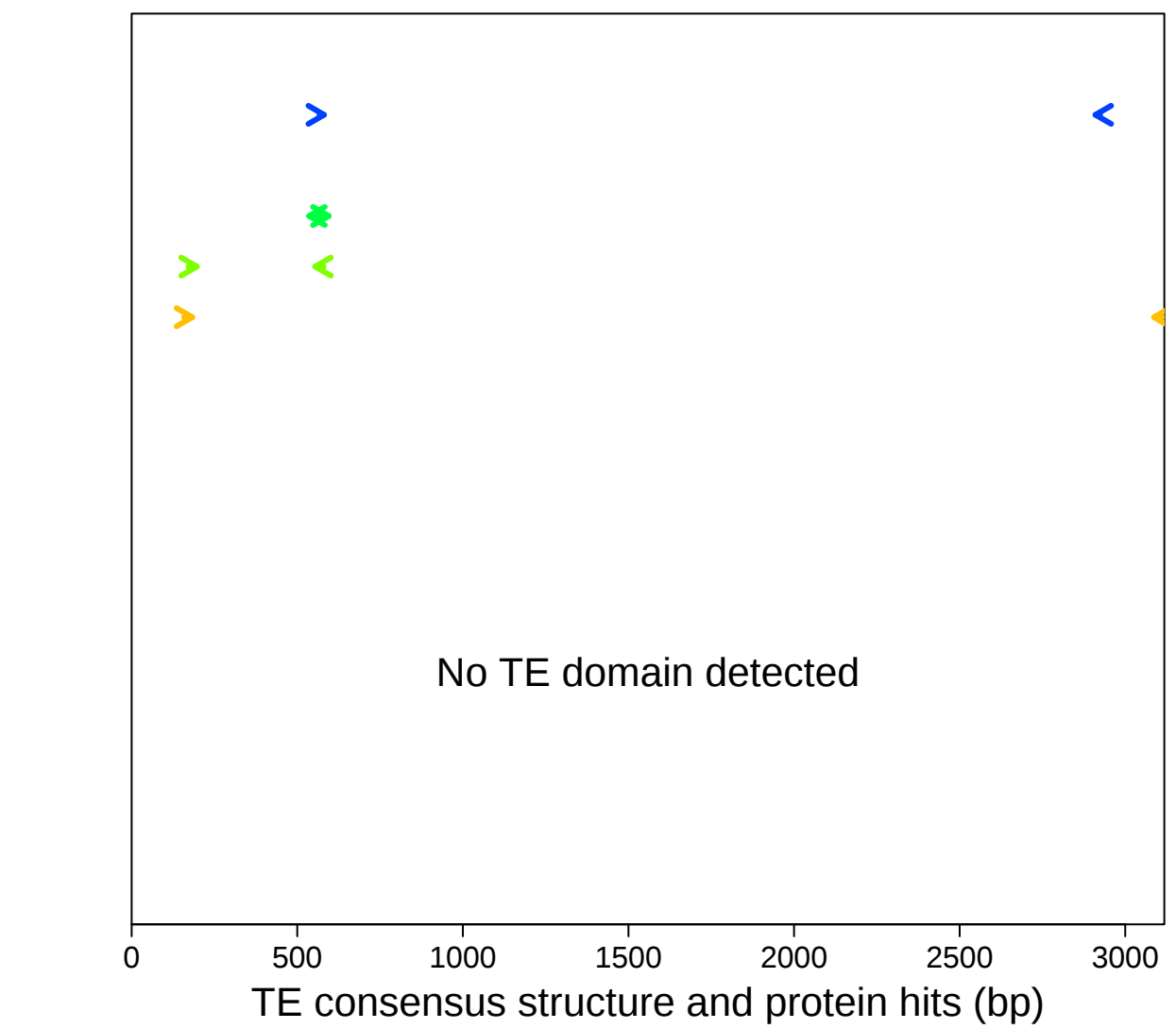
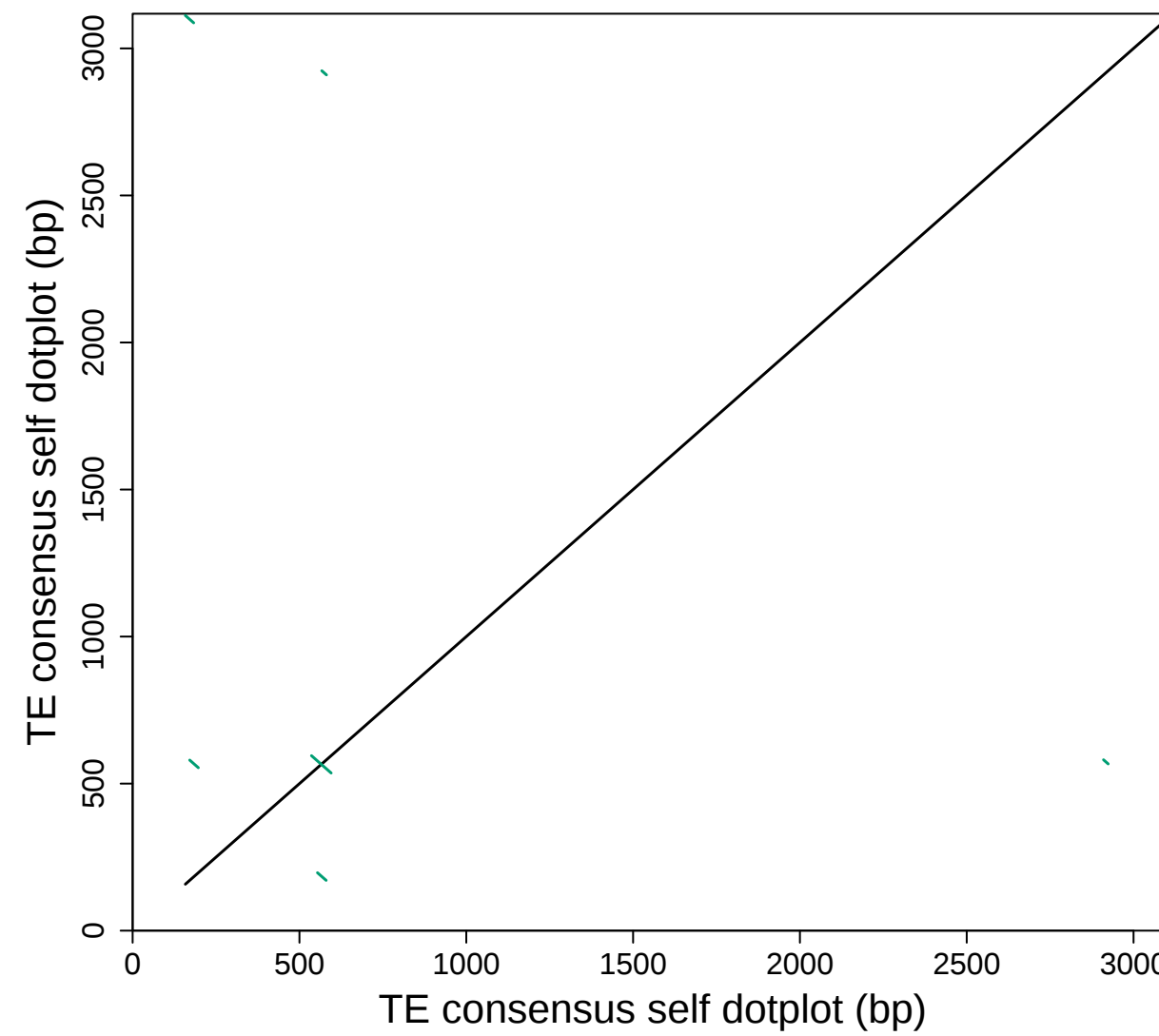
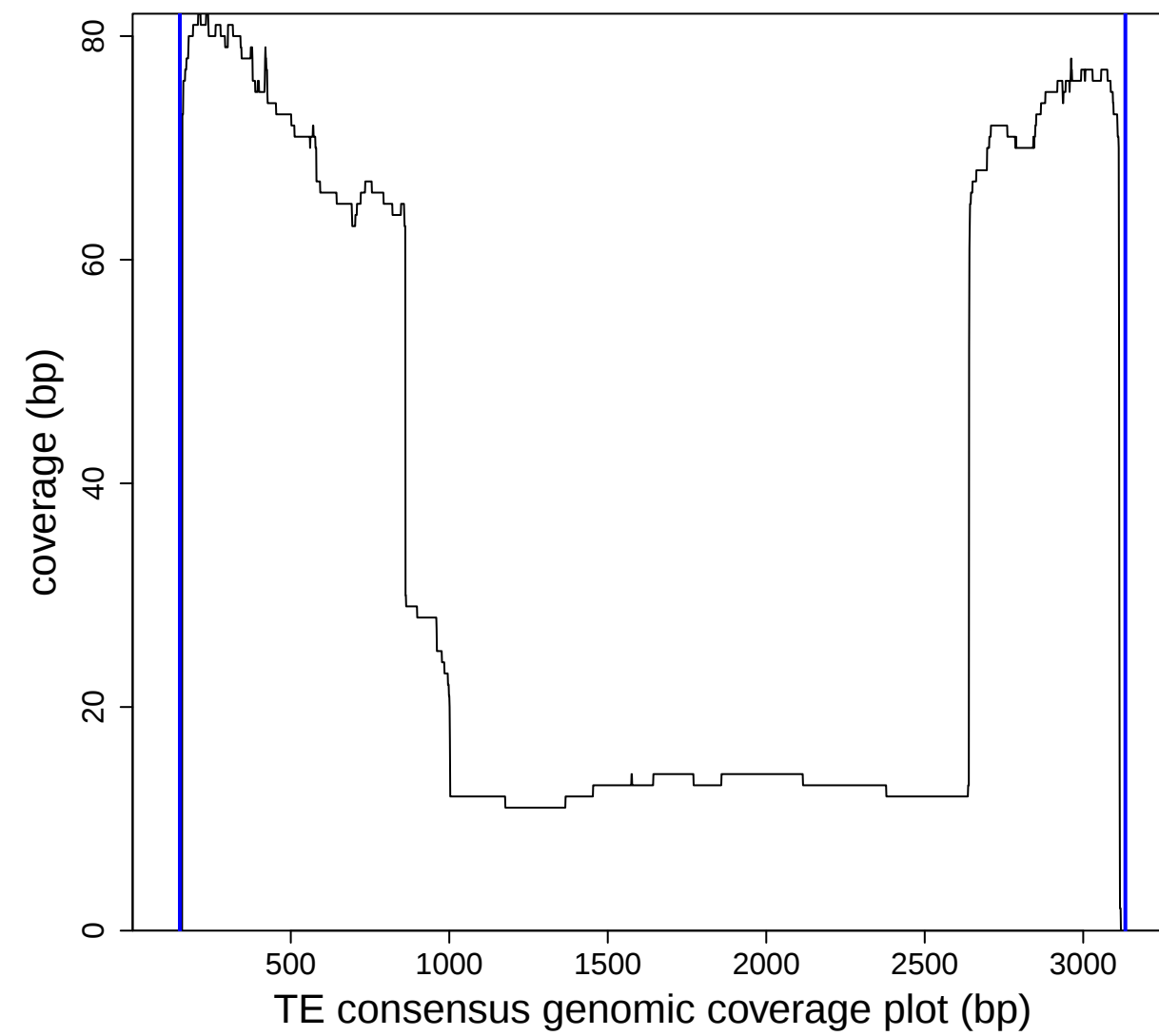
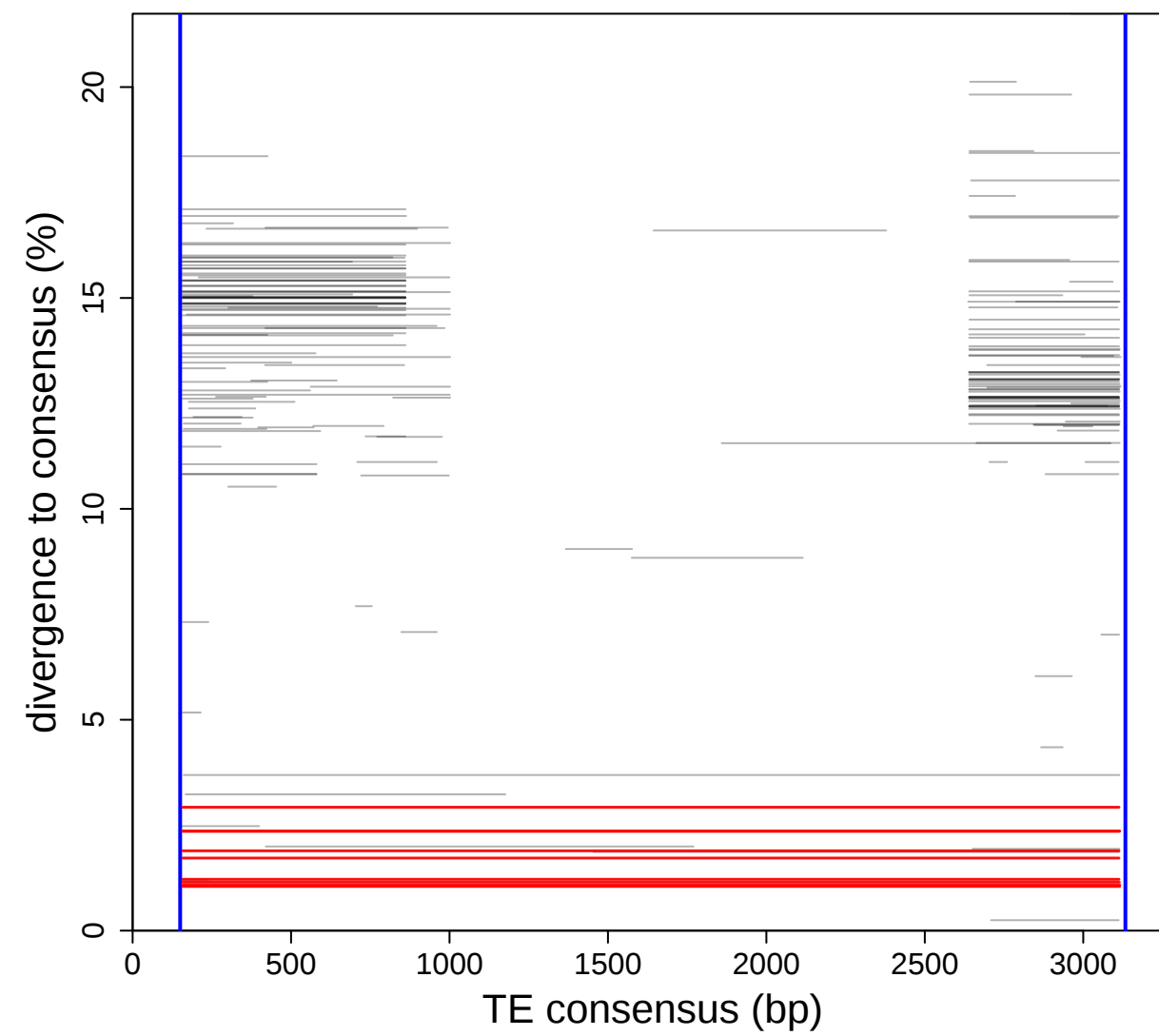
bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_c
size: 2981bp; fragments: 183; full length: 10 (≥ 2682.9 bp)

After TEtrimmer 2981 bp



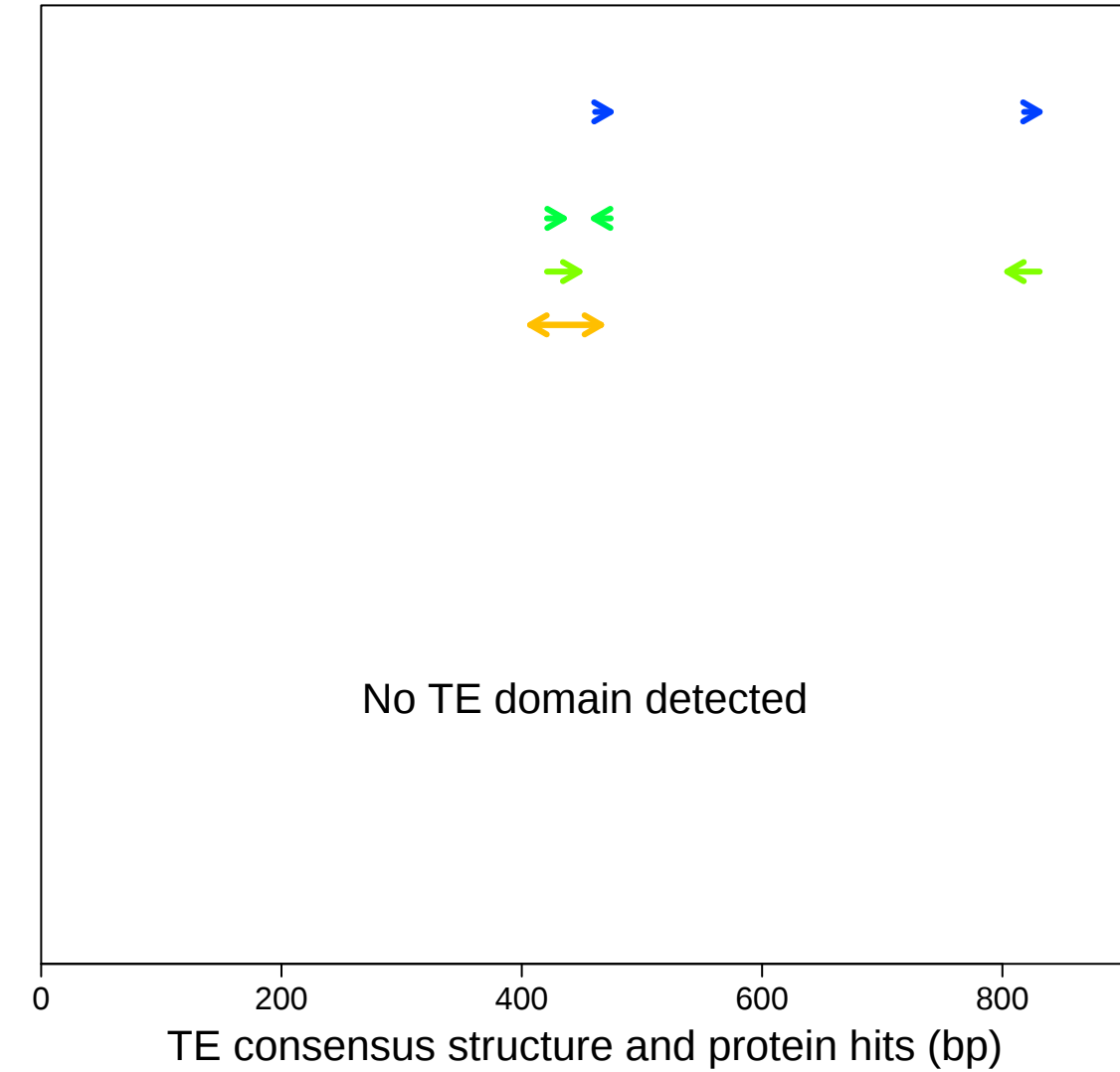
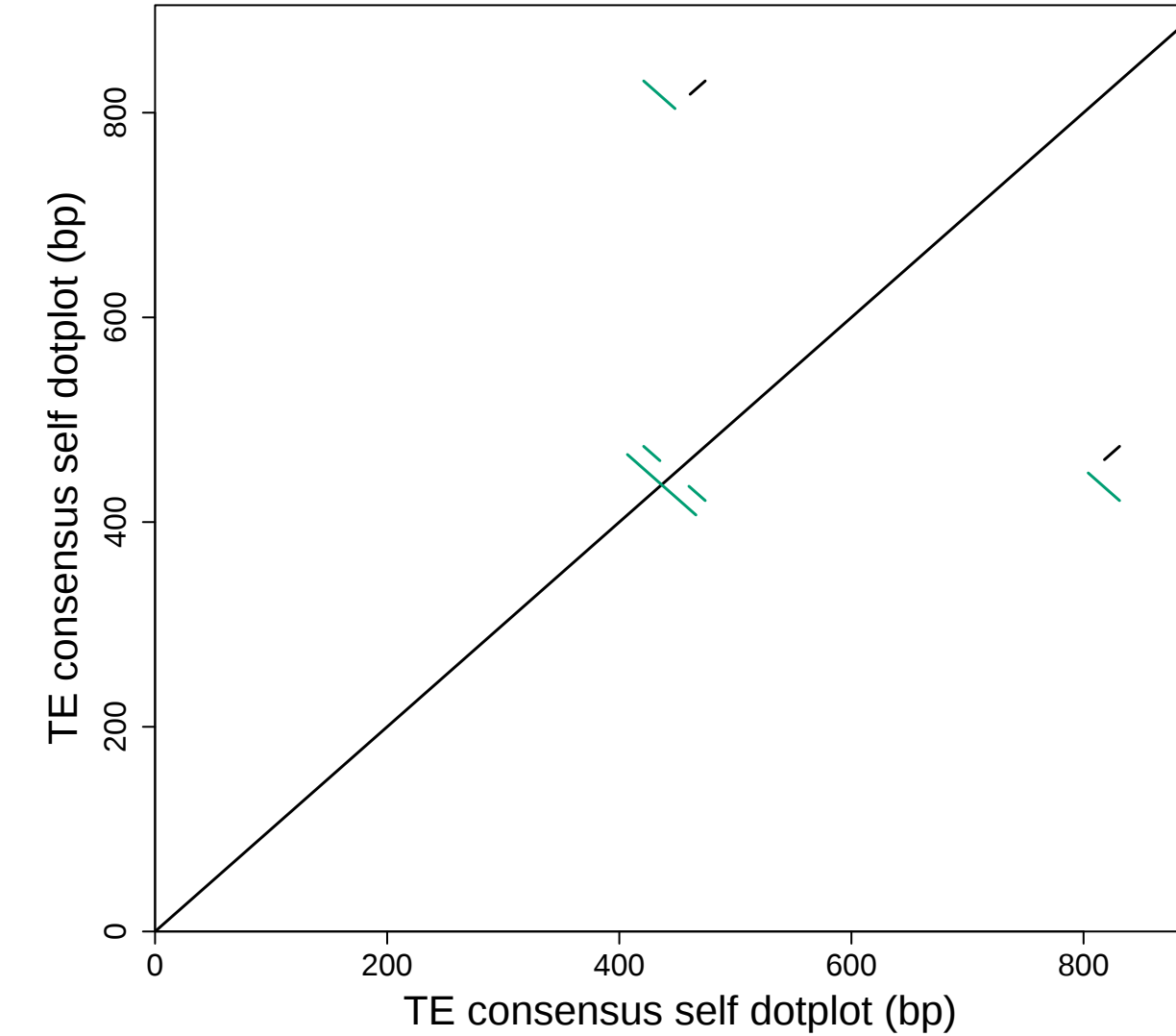
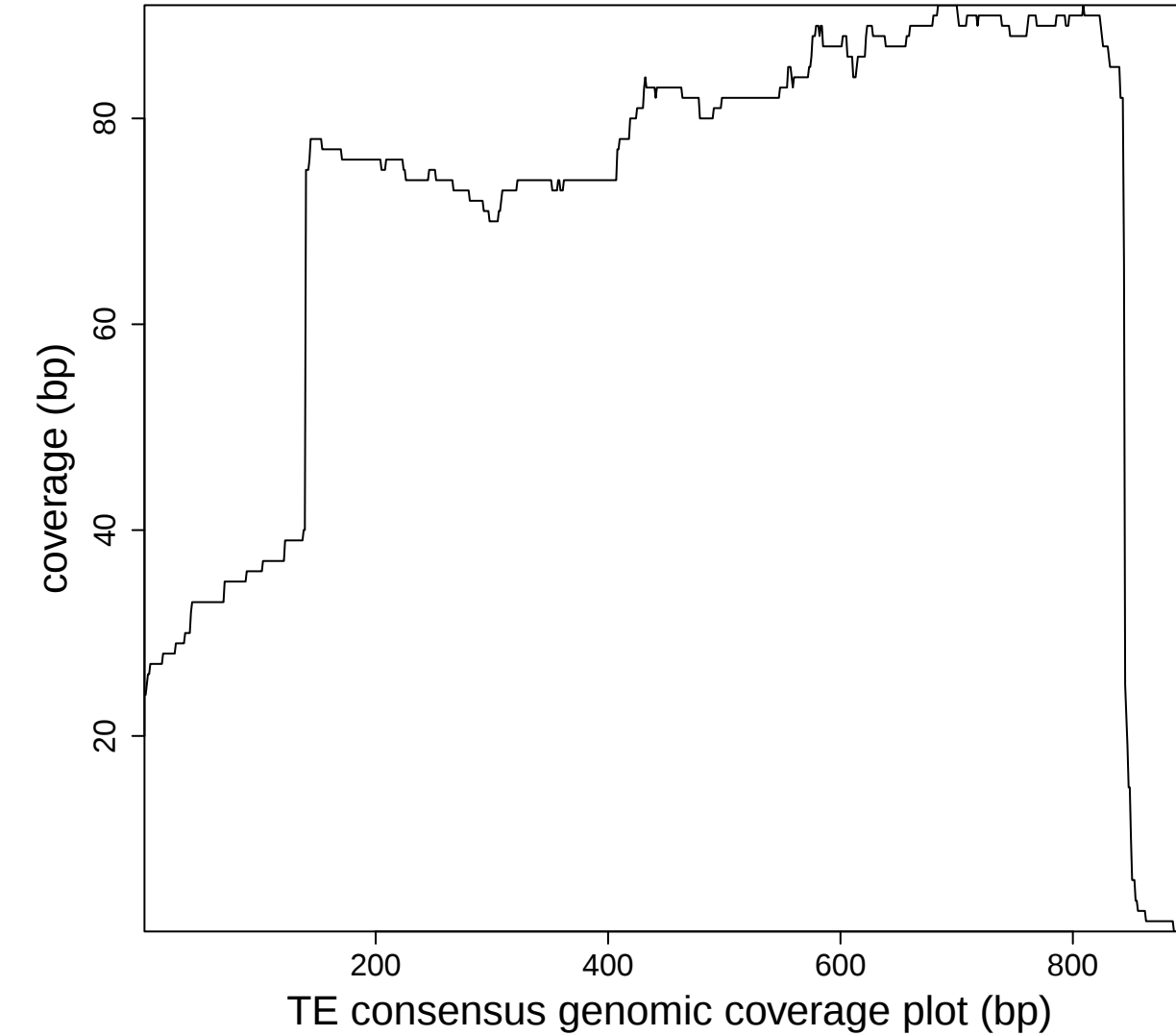
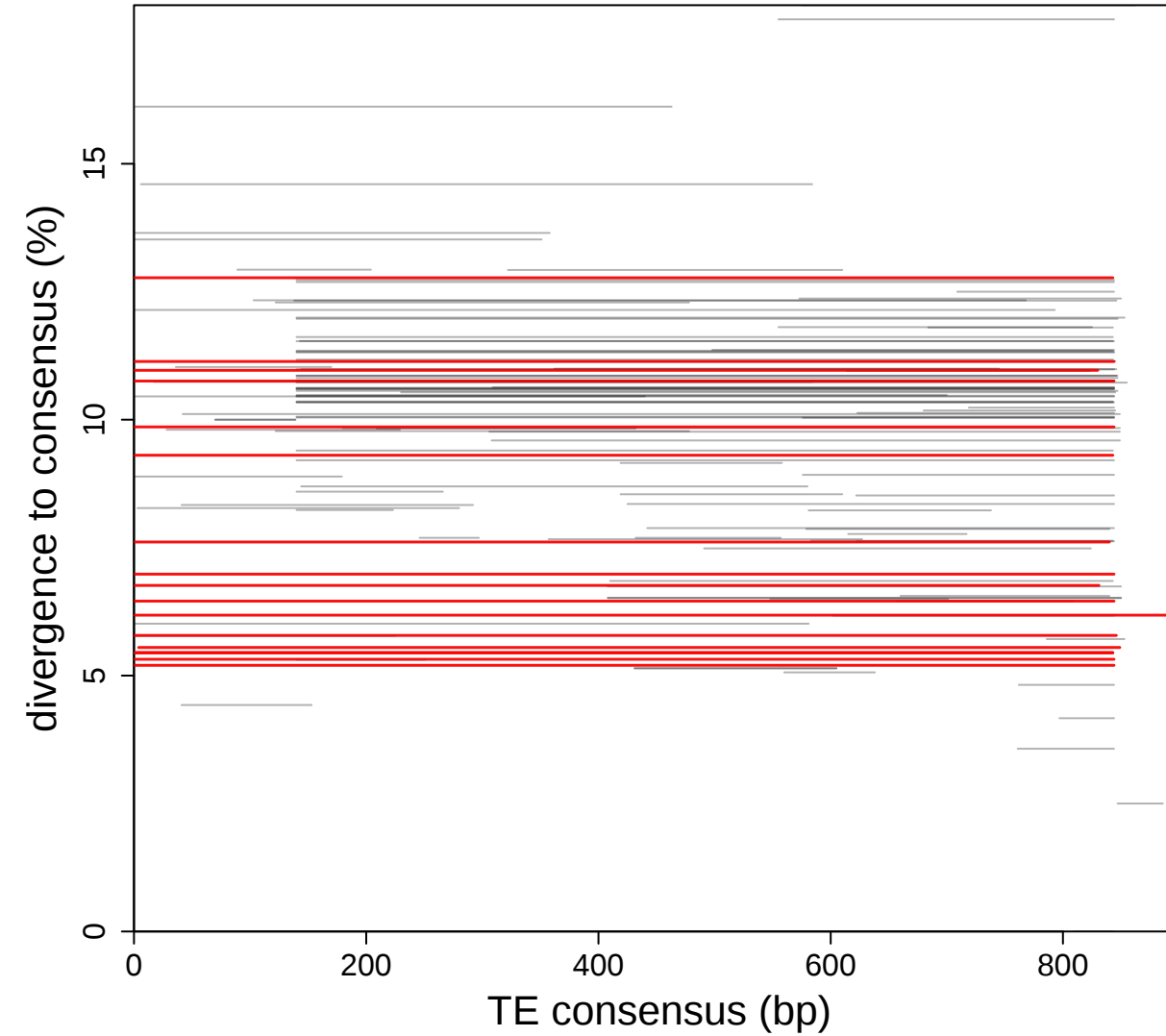
fasta.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_
size: 3283bp; fragments: 182; full length: 9 (>=2954.7bp)

After TEtrimmer Extended plot Blue lines are boundaries

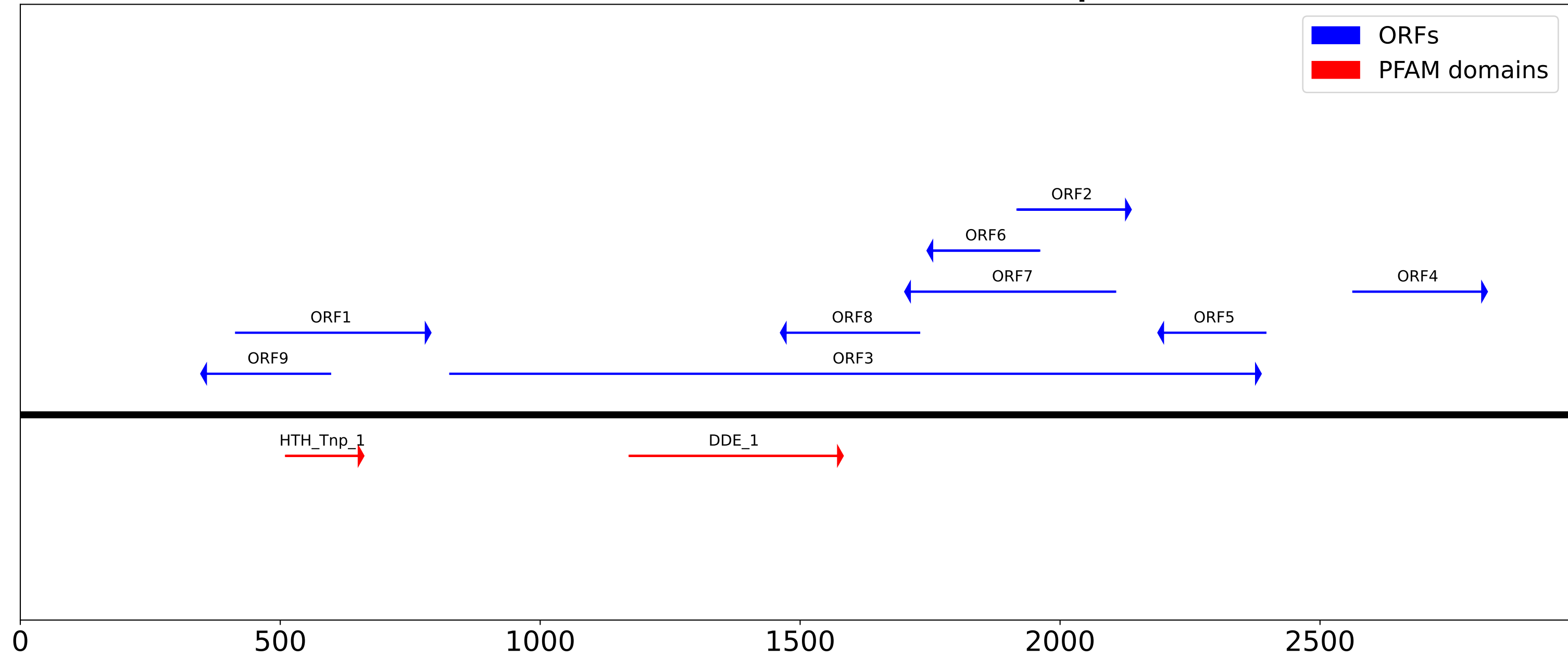


TE: rnd_5_family_10363
size: 905bp; fragments: 132; full length: 17 (≥ 814.5 bp)

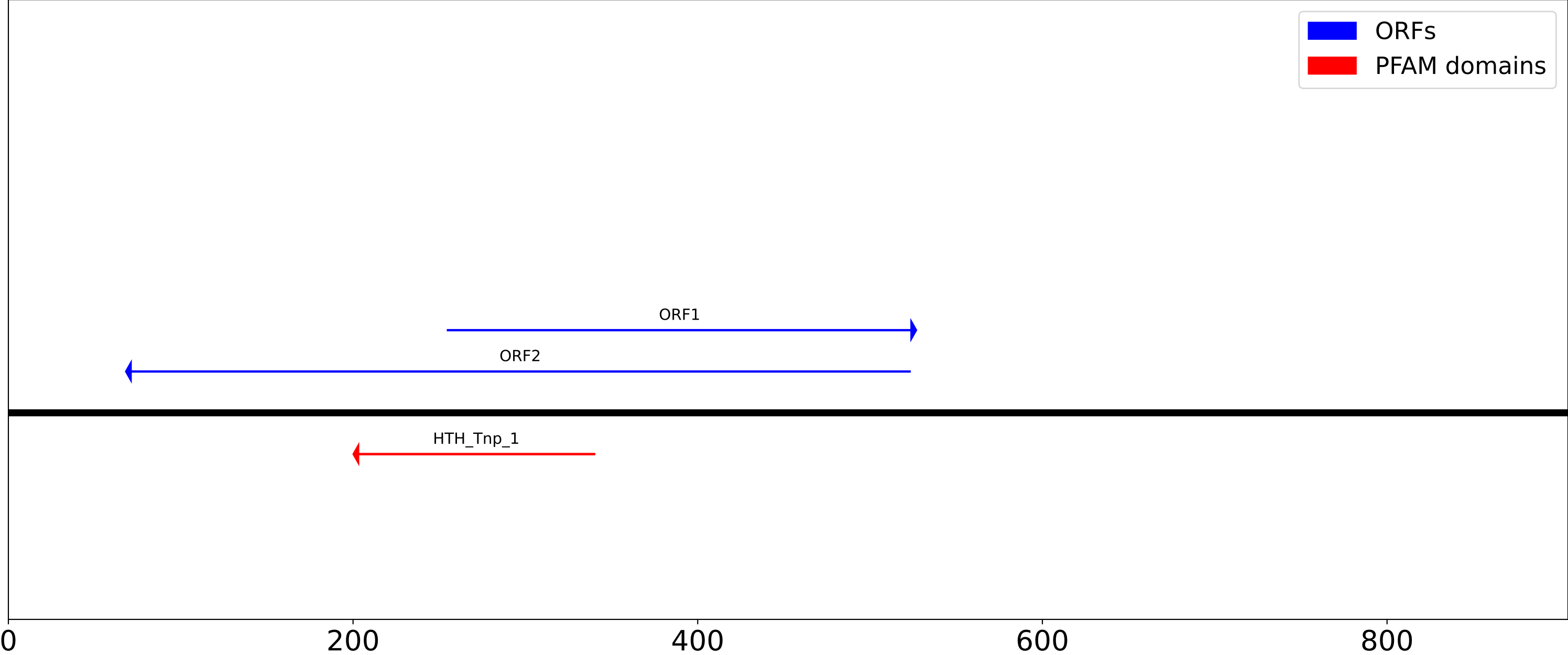
Before TEtrimmer 905 bp



After TEtrimmer ORF and PFAM domain plot



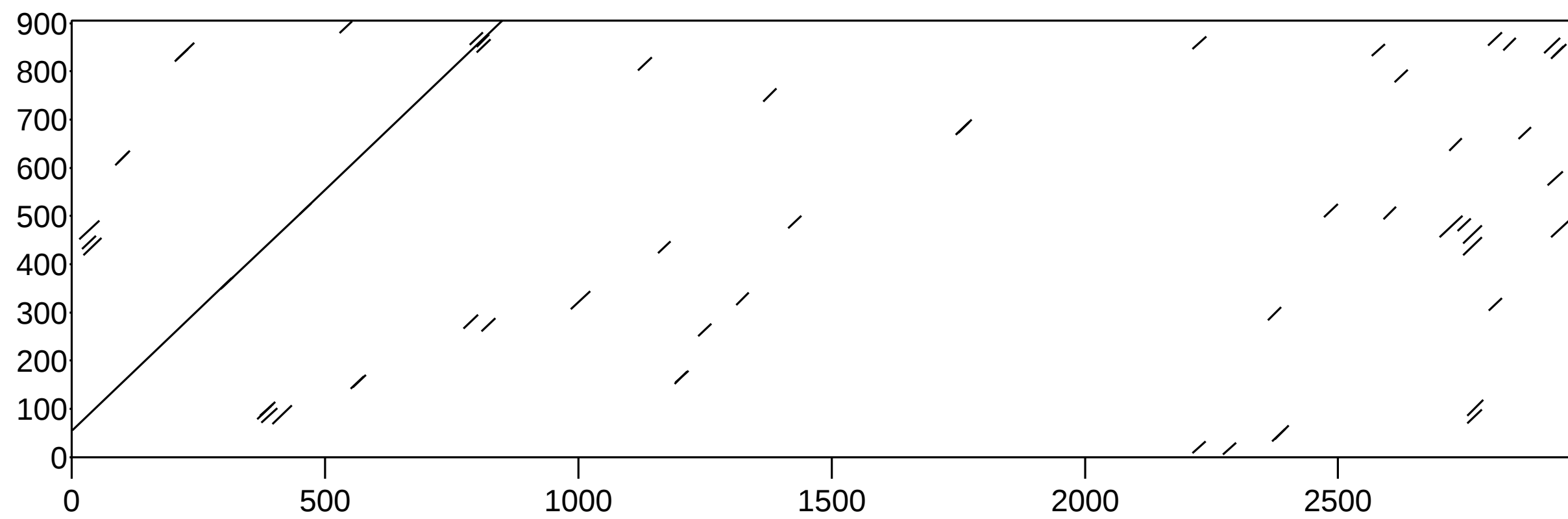
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

: consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)