

MSA length = 3249



Start crop Point

End crop Point

0 -

10 -

0

500

1000

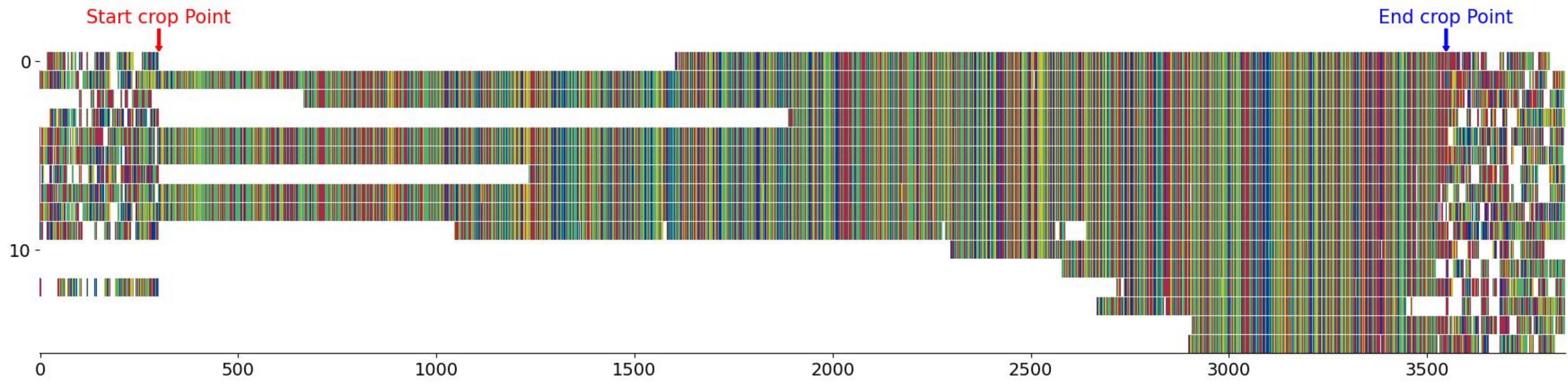
1500

2000

2500

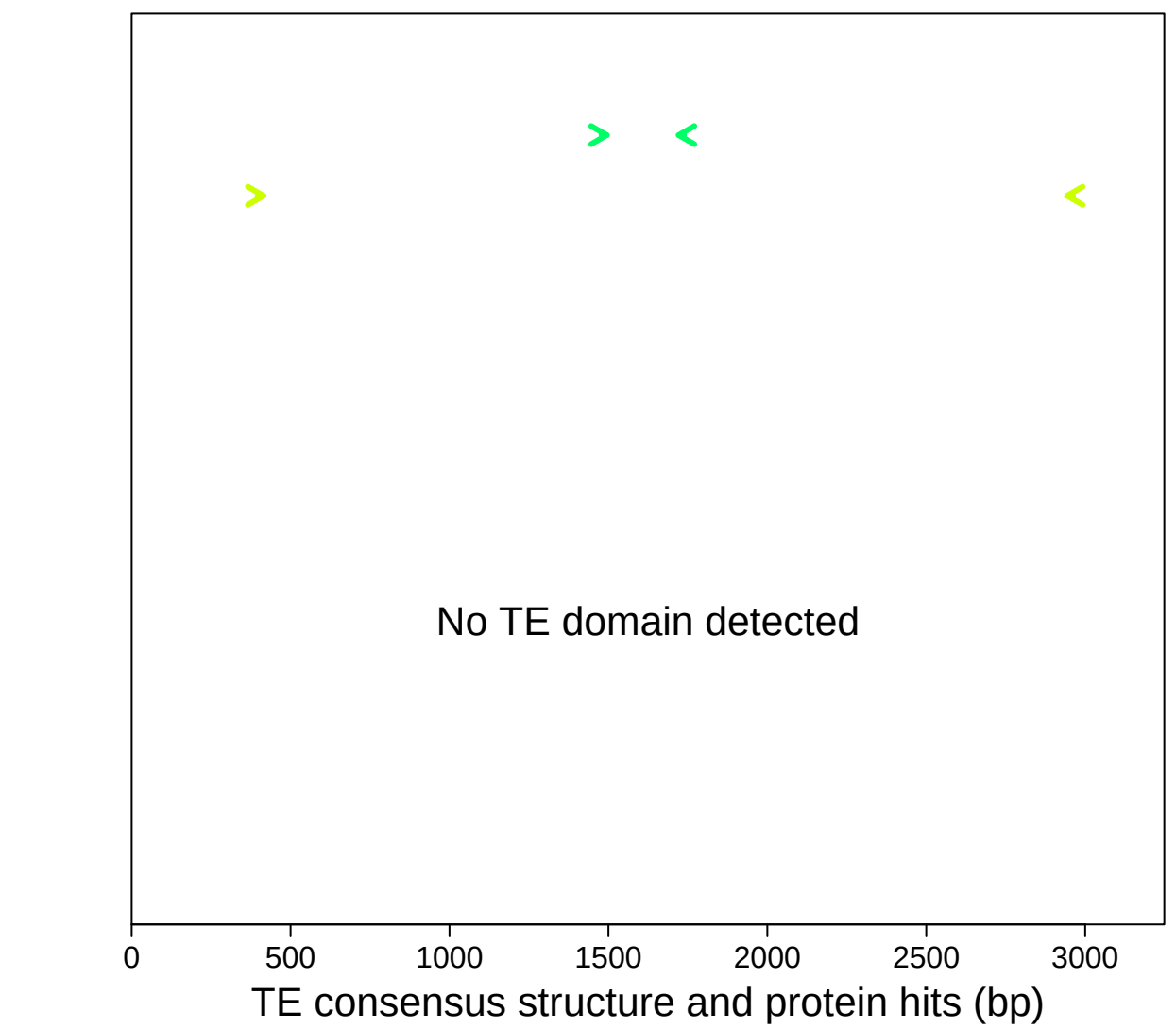
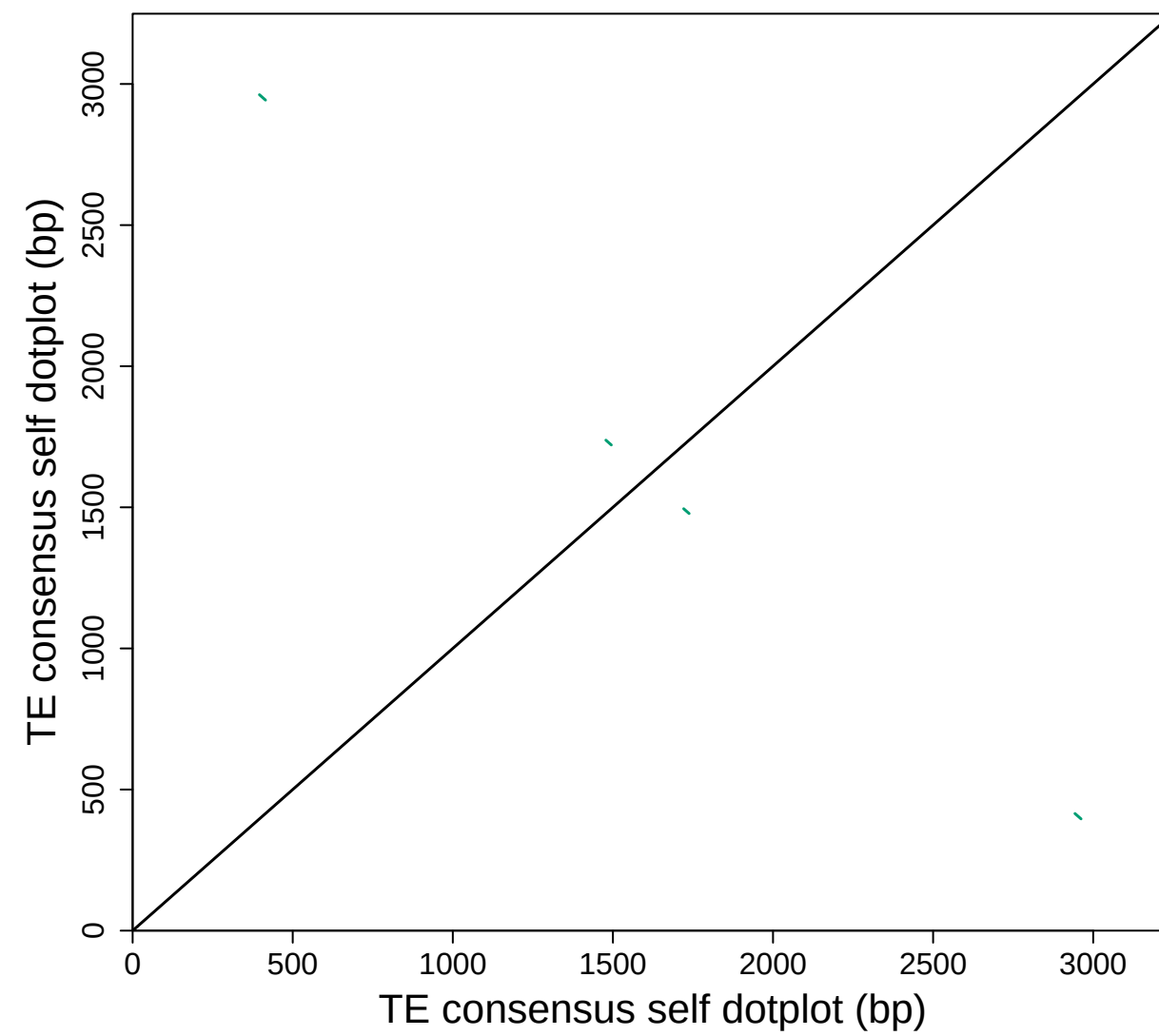
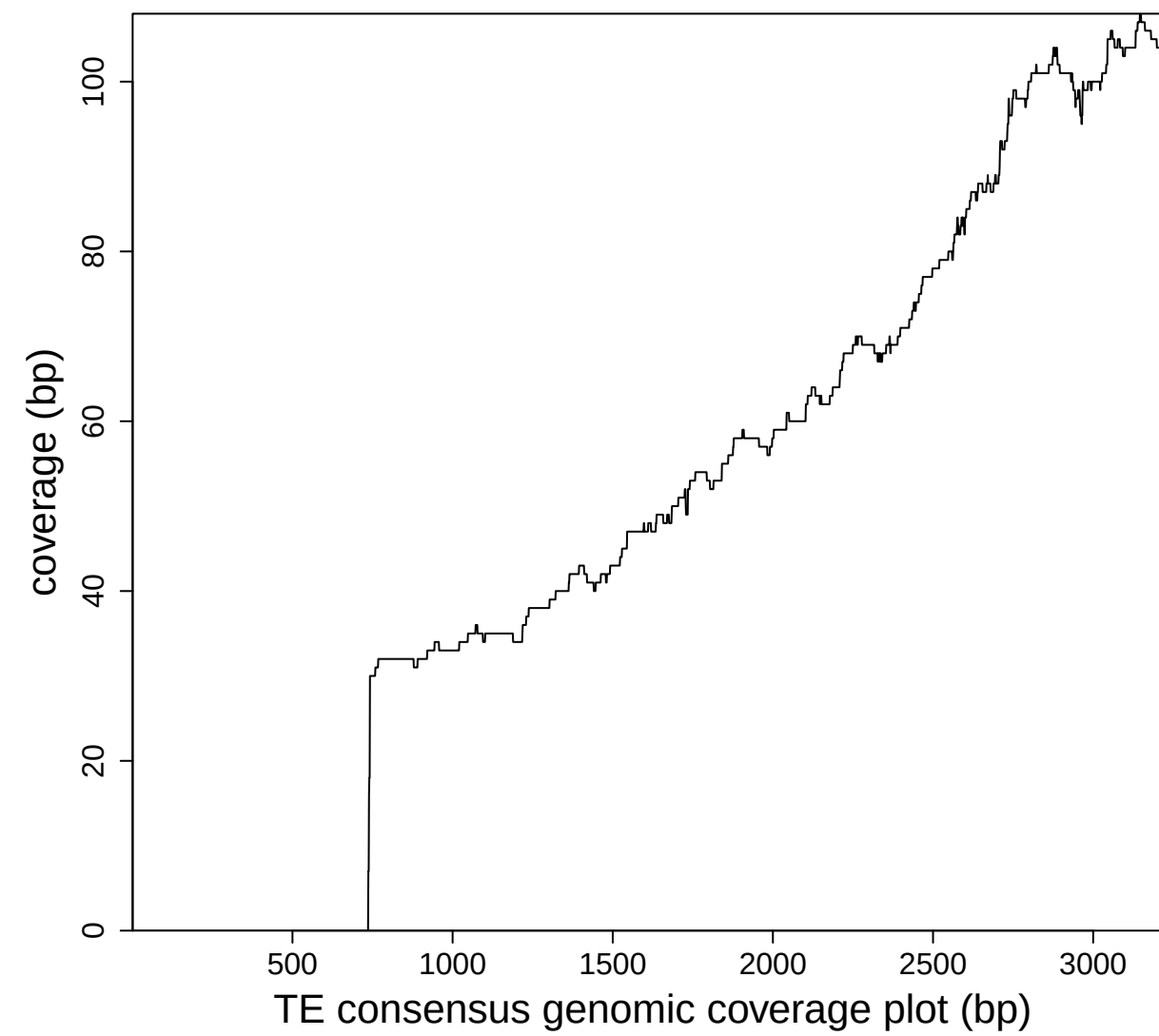
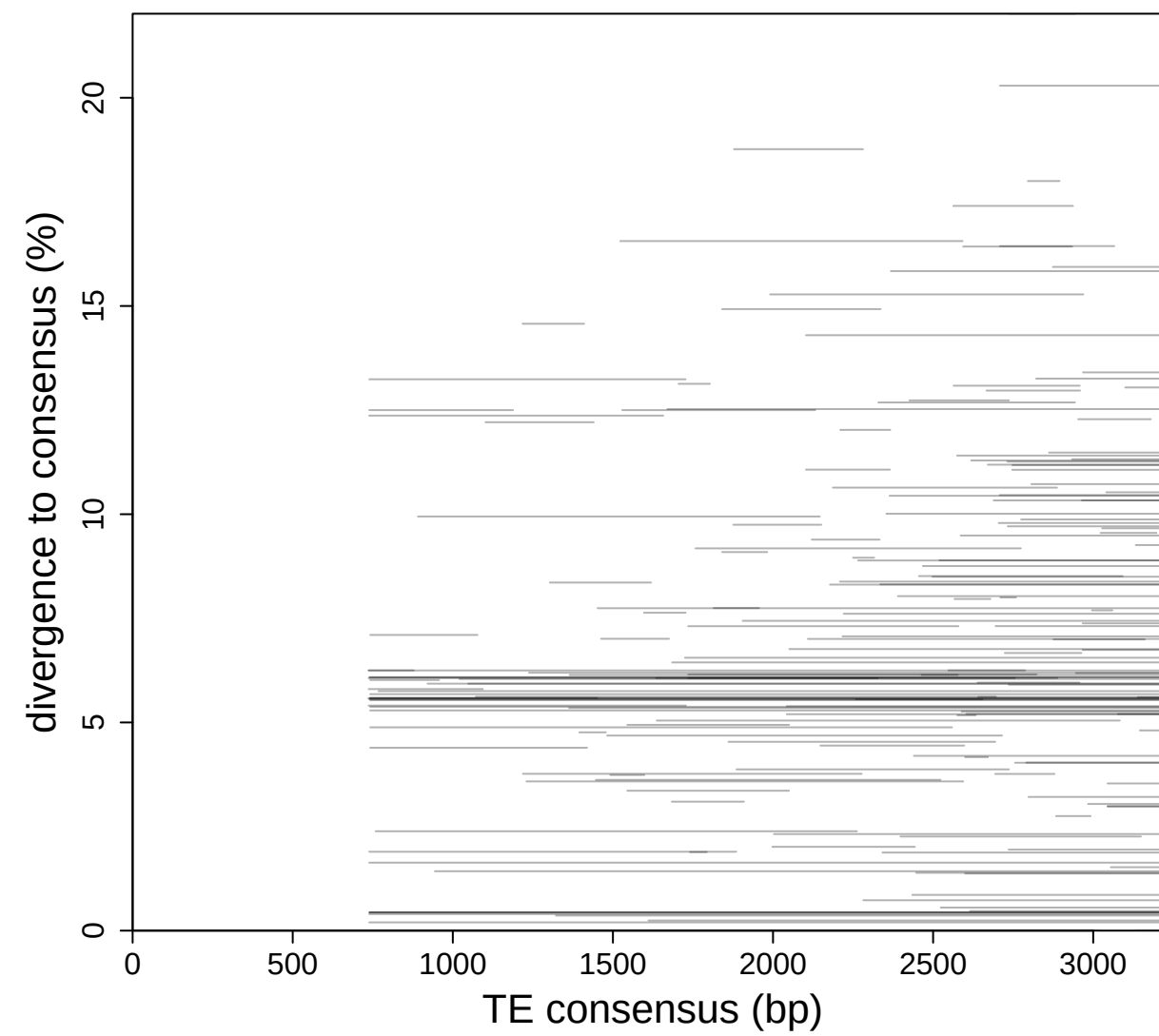
3000

3500



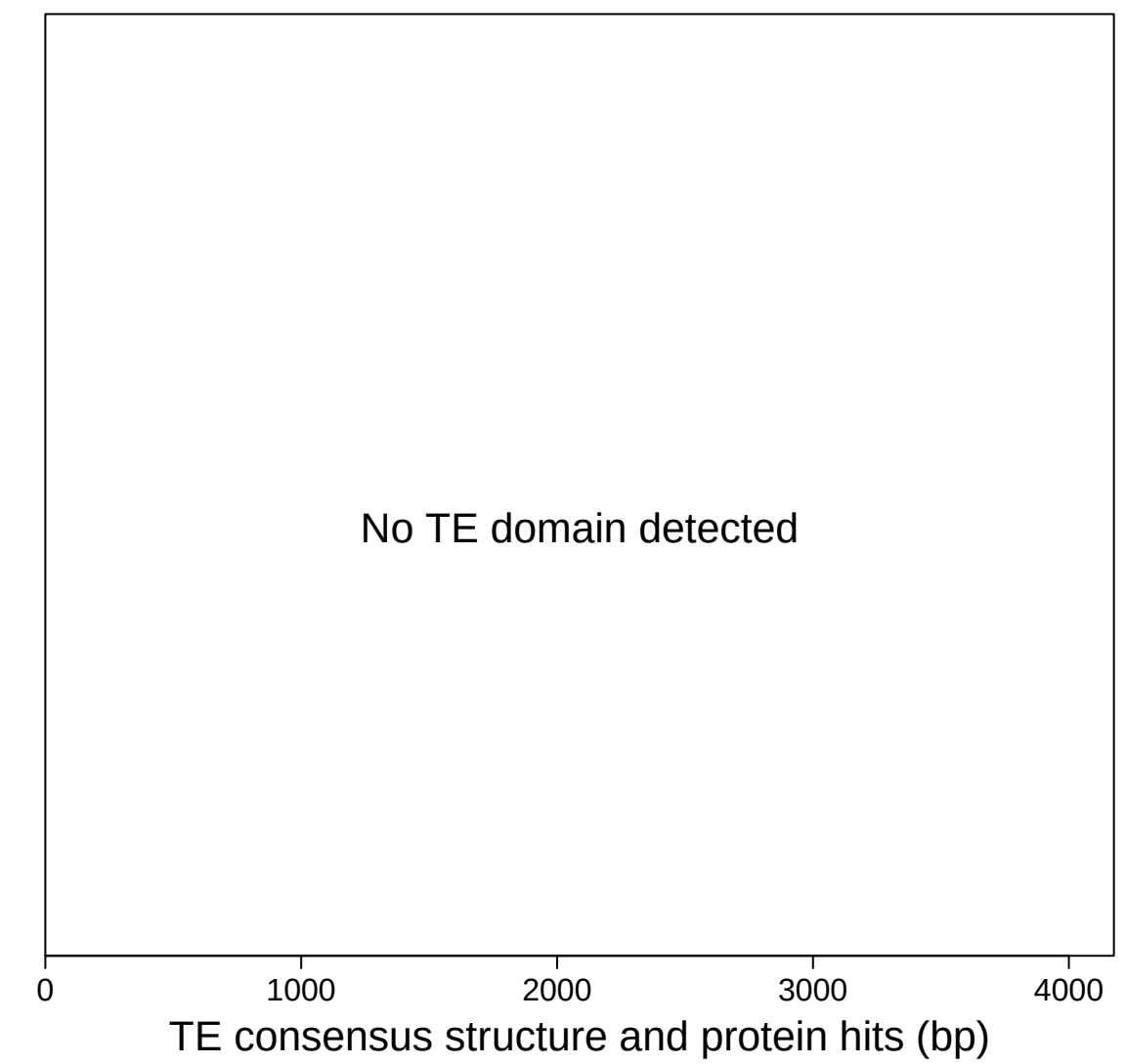
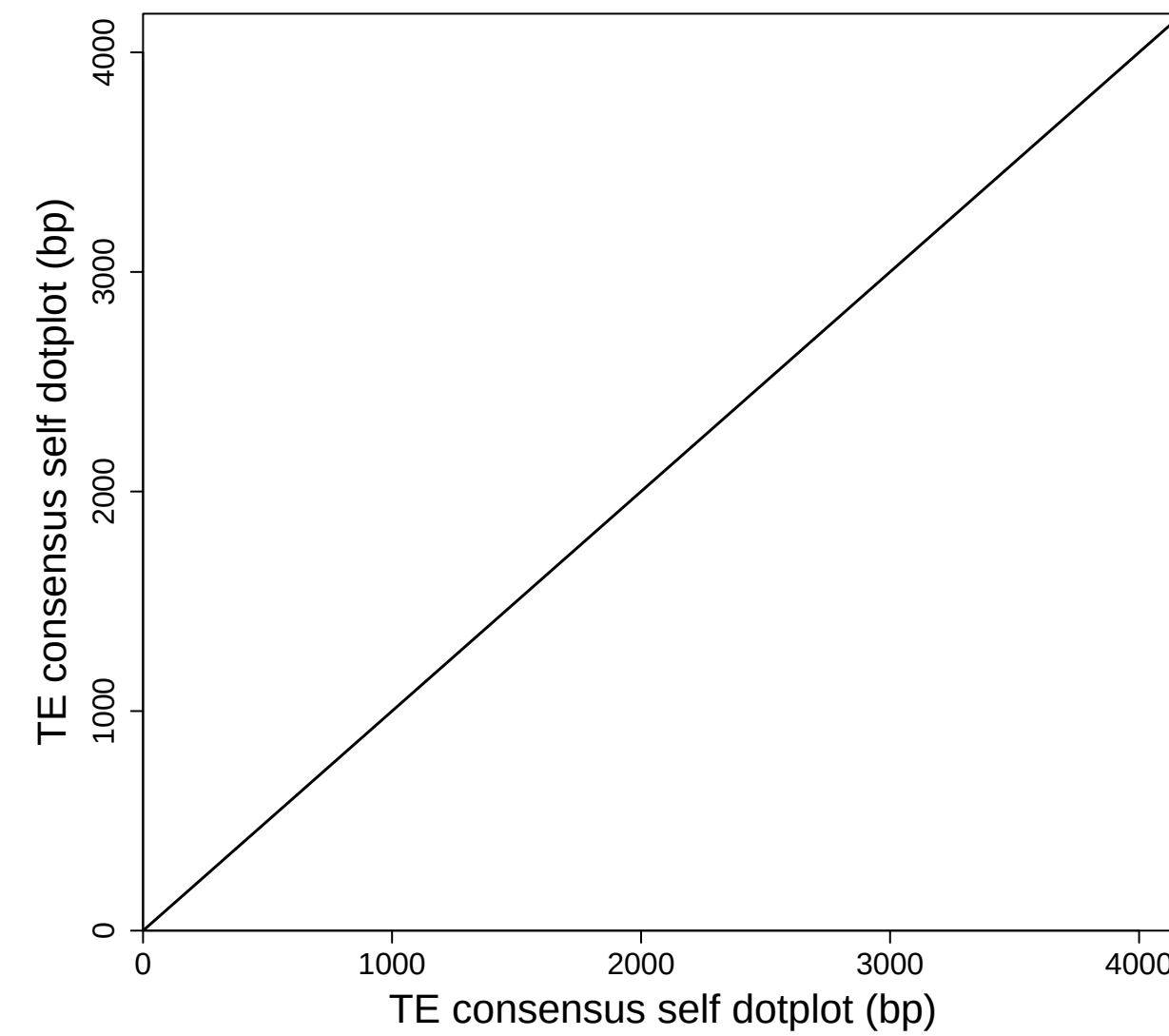
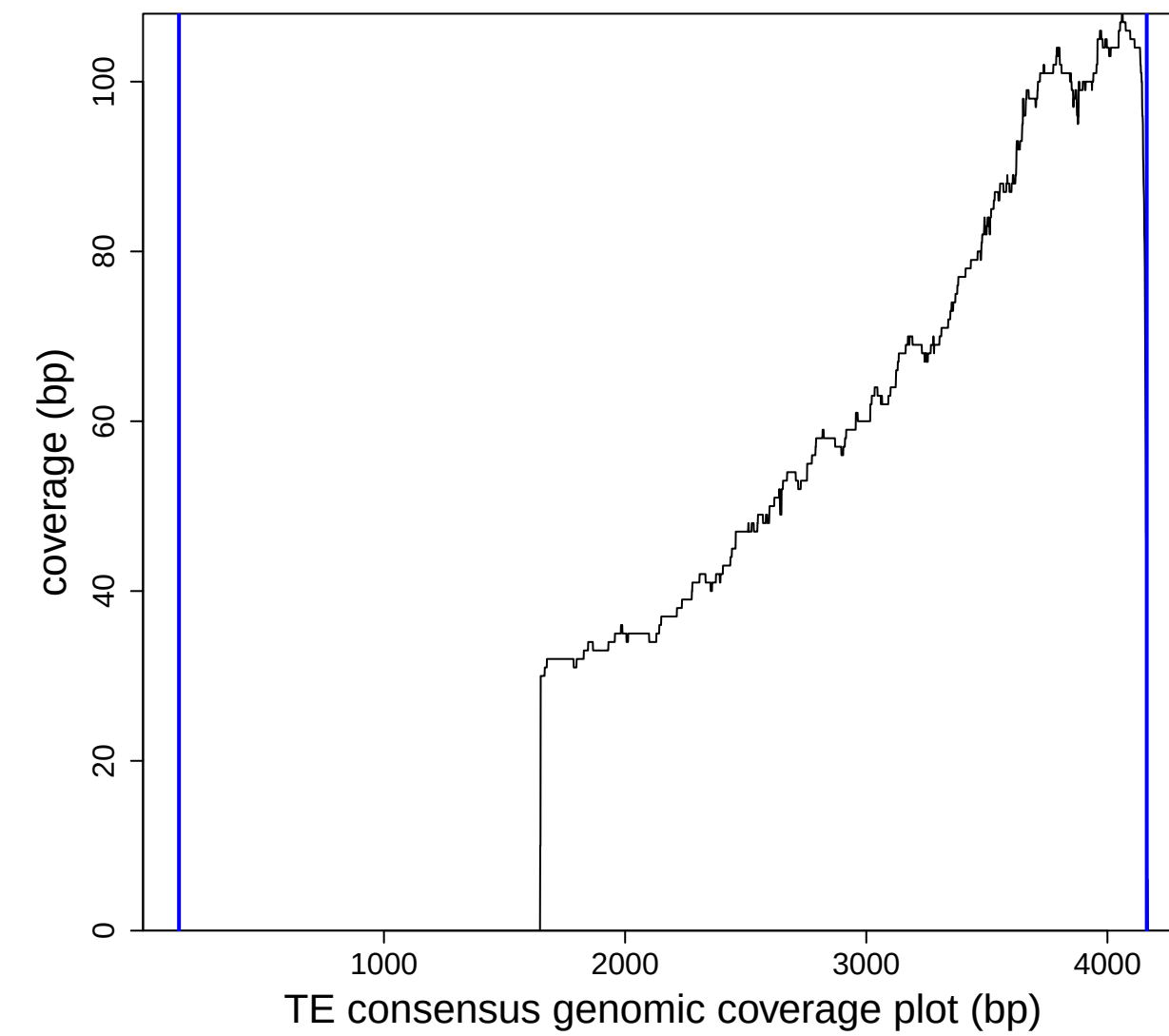
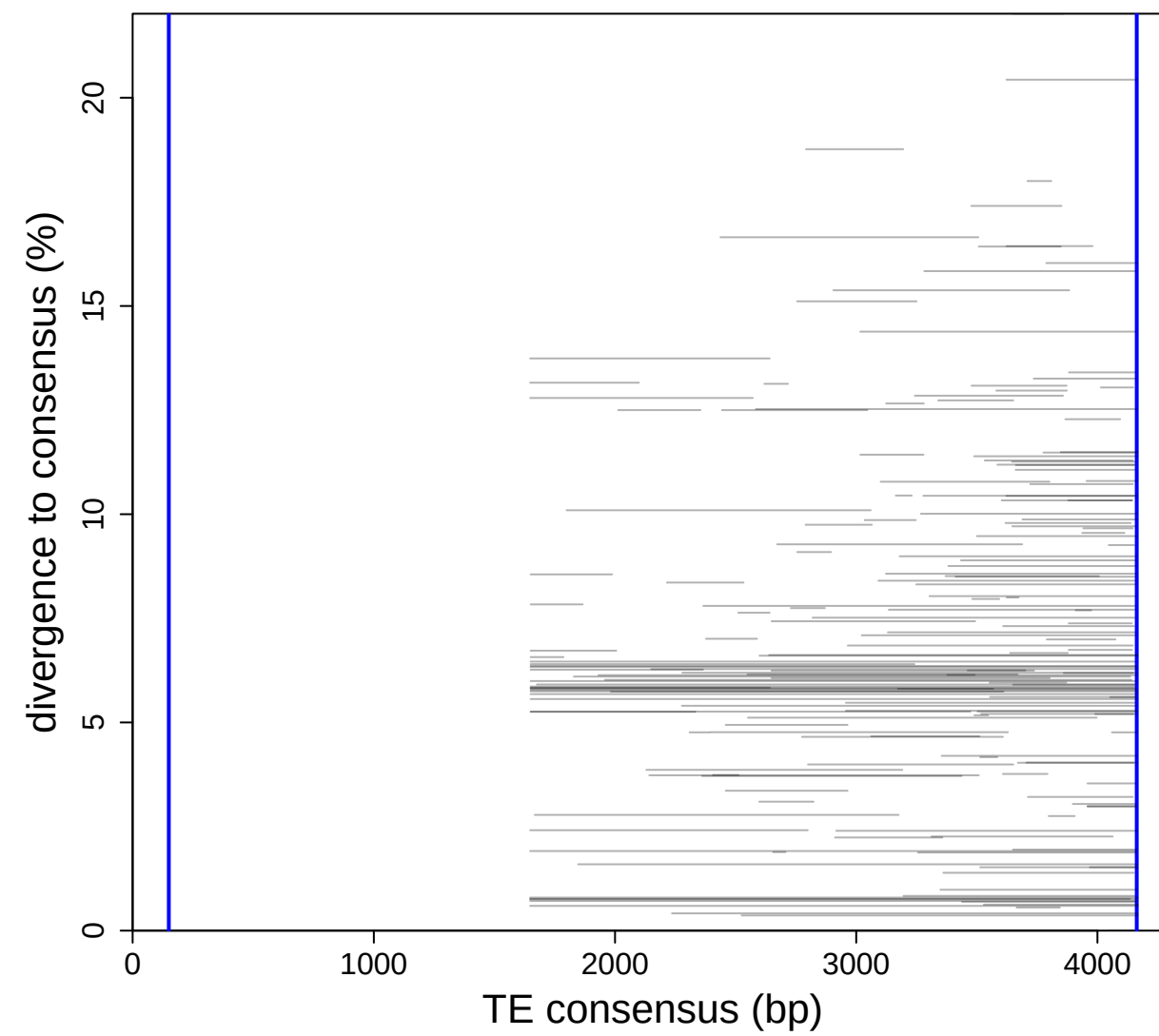
bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.fa_c
size: 3249bp; fragments: 187; full length: 0 (>=2924.1bp)

After TETrimmer 3249 bp

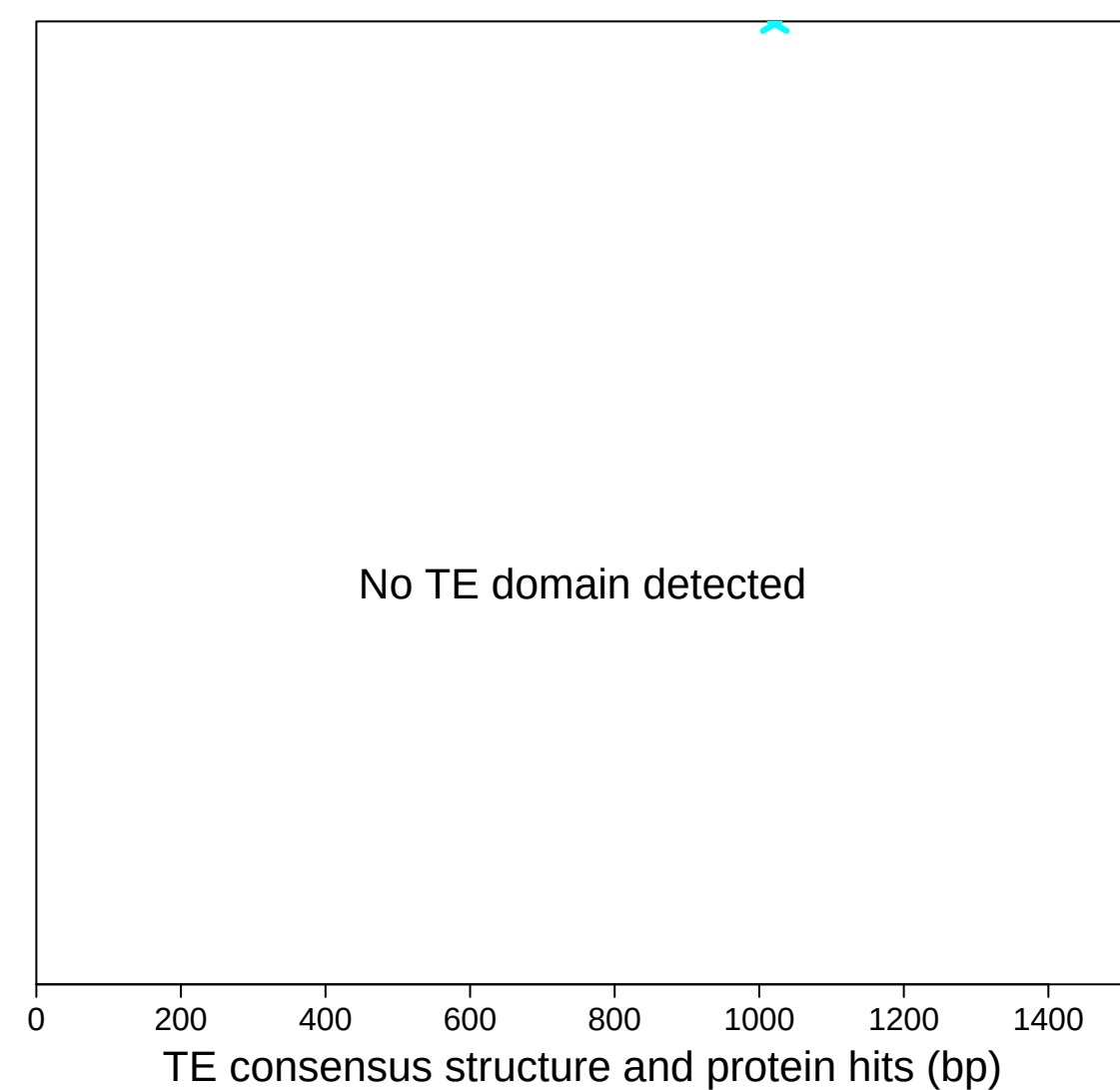
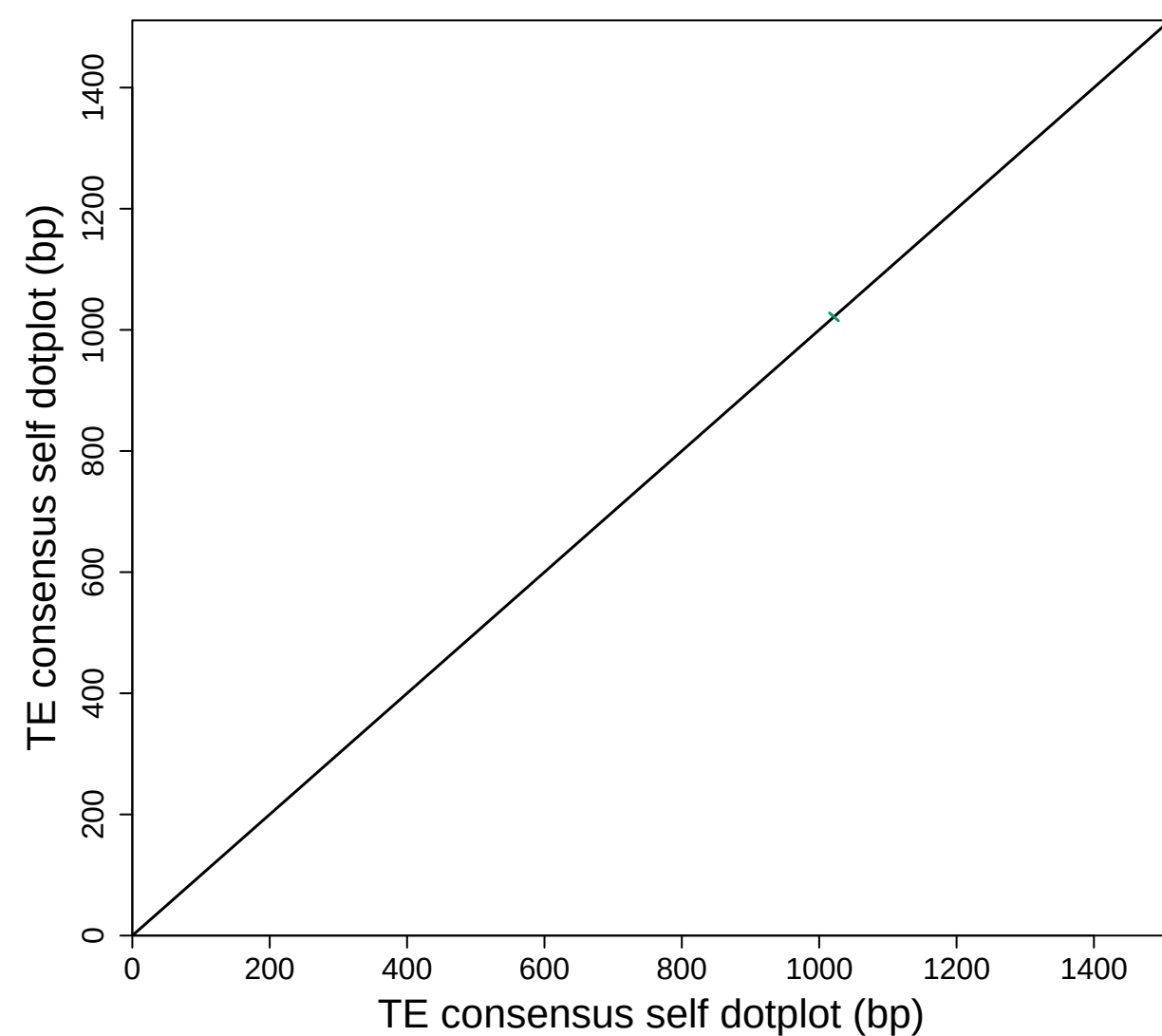
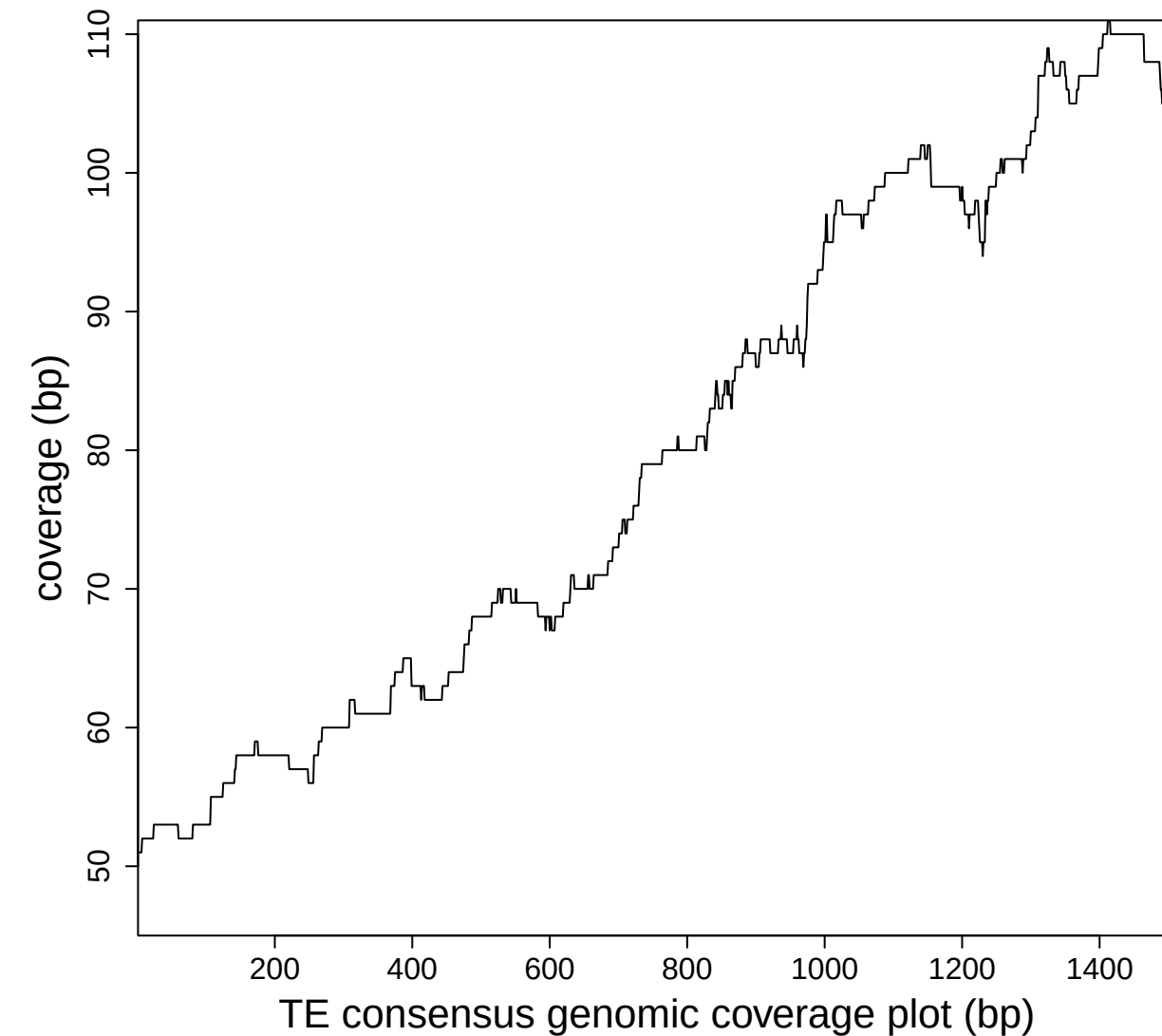
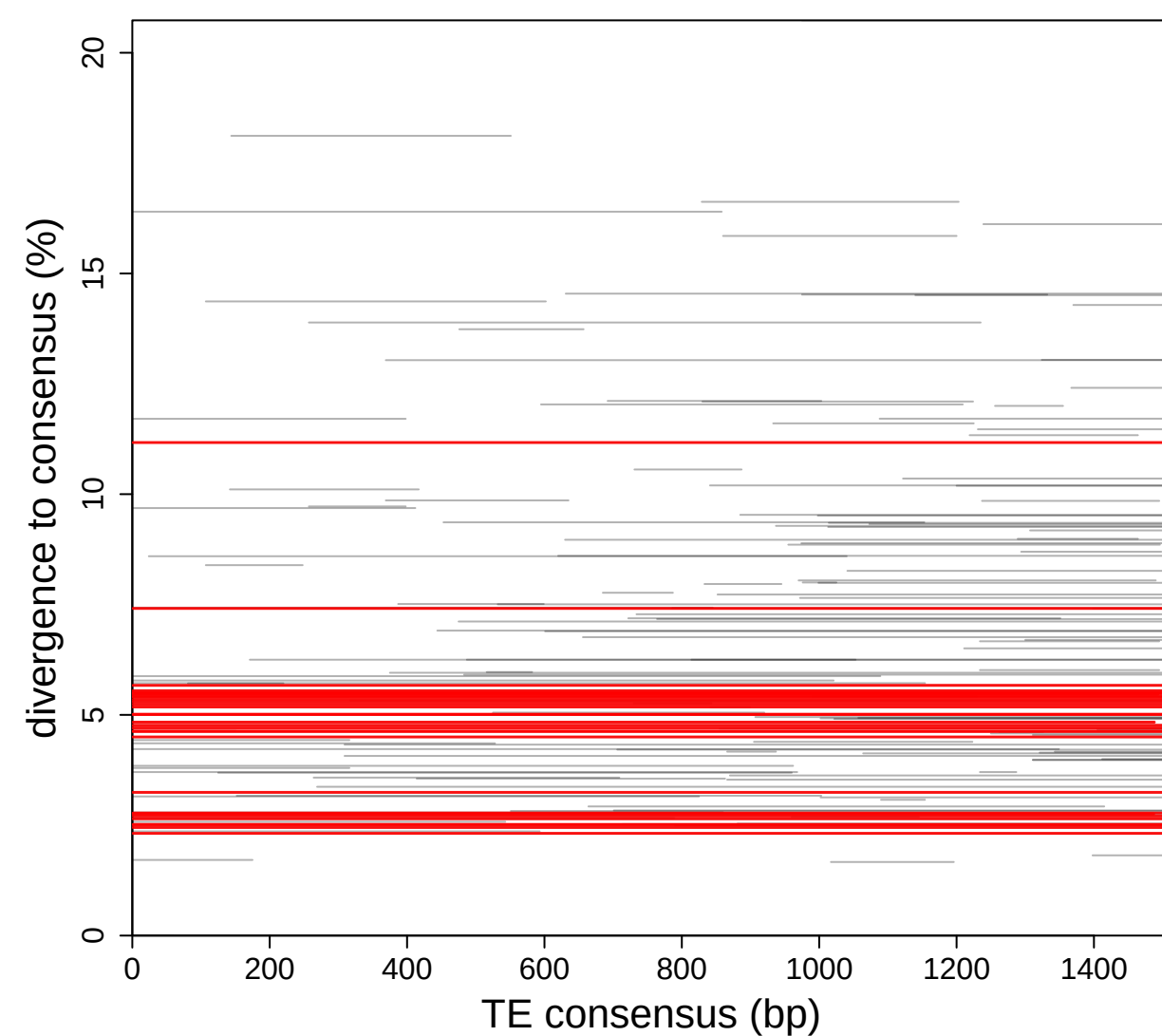


0.fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcIn.fa_aln.fa_cl.f
size: 4313bp; fragments: 186; full length: 0 (>=3881.7bp)

After TEtrimmer Extended plot Blue lines are boundaries

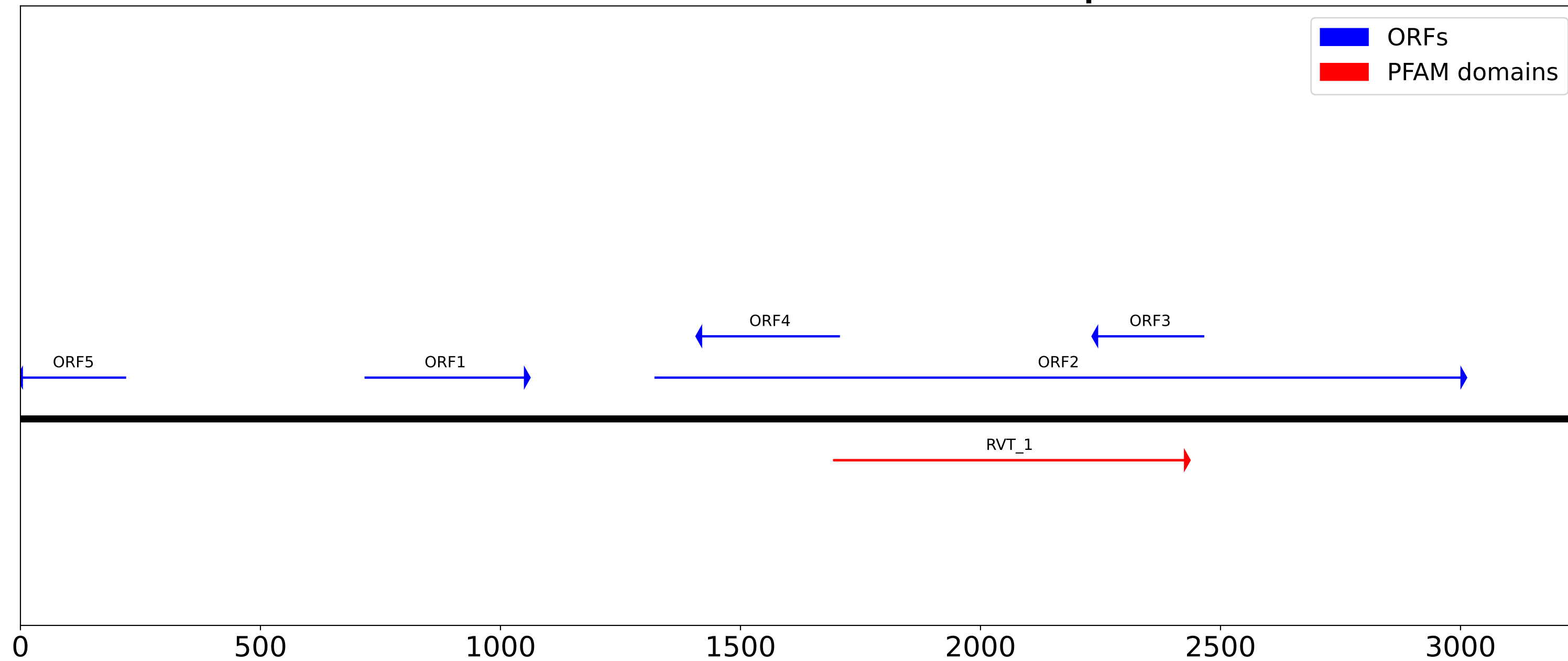


TE: rnd_5_family_1280
size: 1511bp; fragments: 175; full length: 31 (≥ 1359.9 bp)

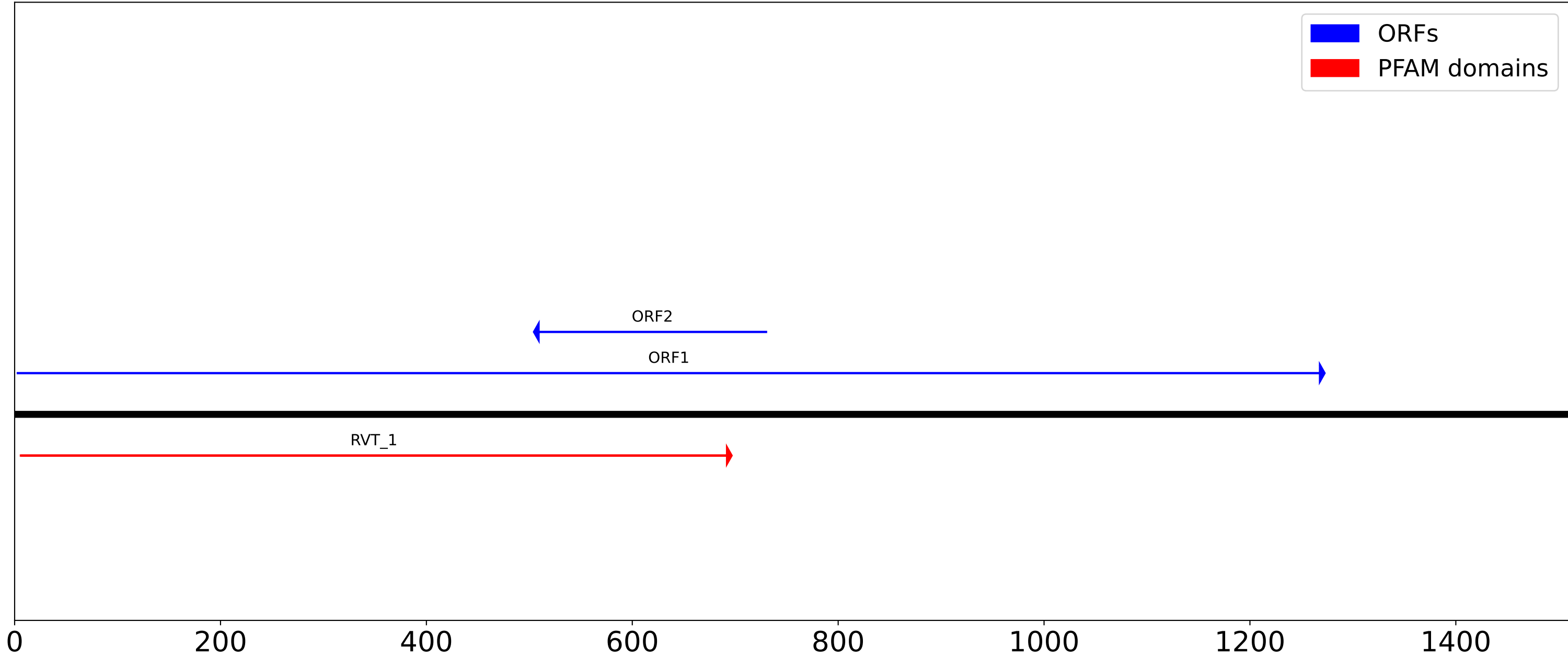


Before TEtrimmer 1511 bp

After TEtrimmer ORF and PFAM domain plot



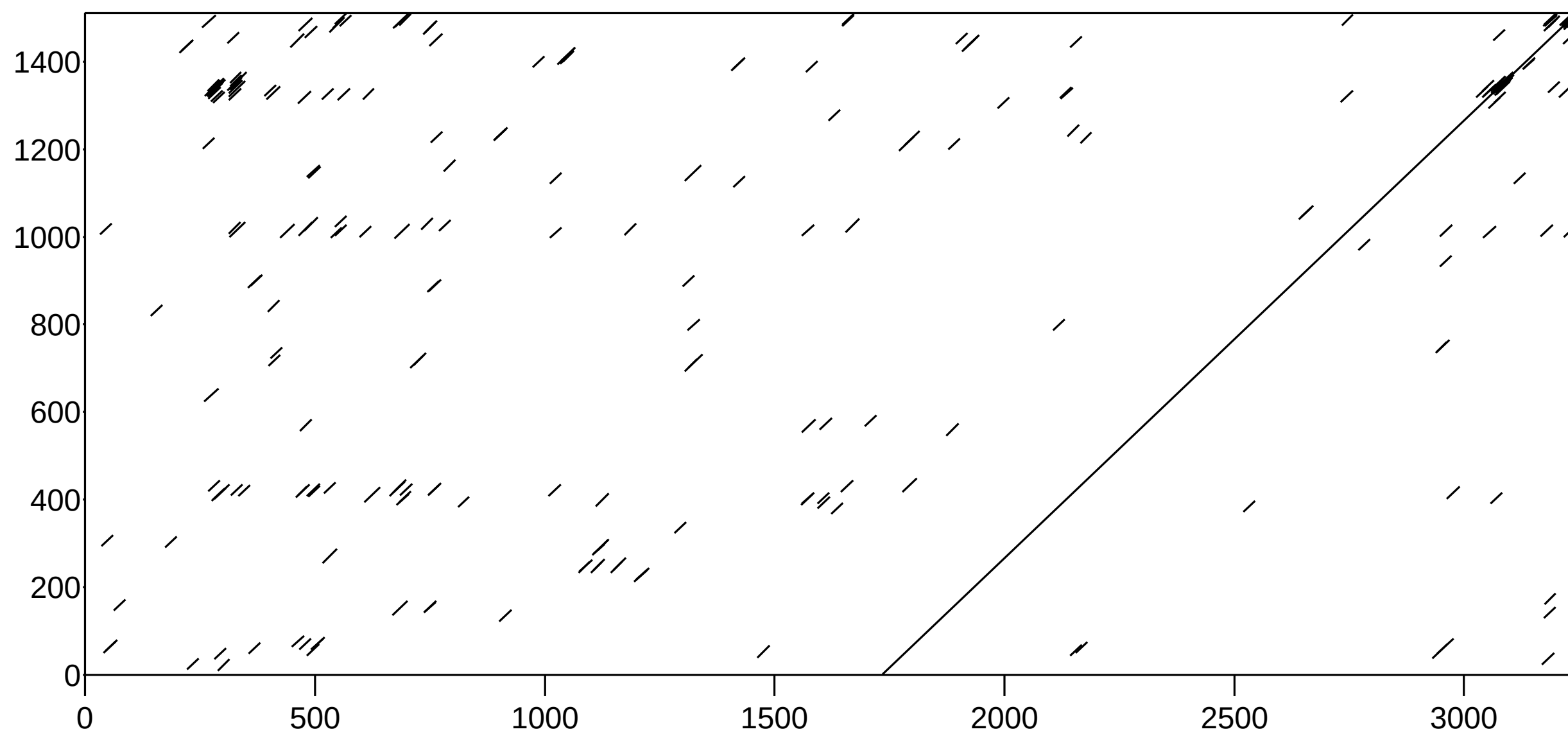
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)