

Start crop Point



End crop Point



MSA length = 1612



Start crop Point

End crop Point

0 -

10

0

250

500

750

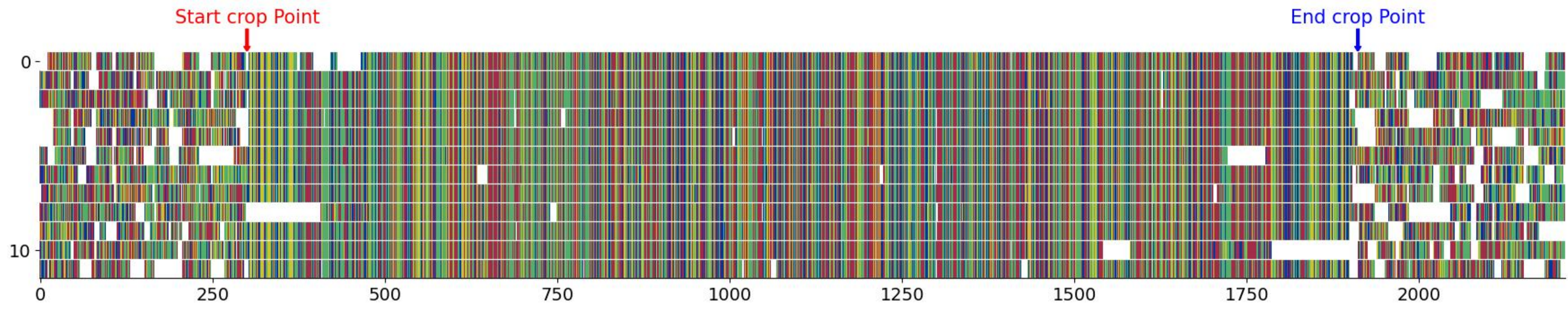
1000

1250

1500

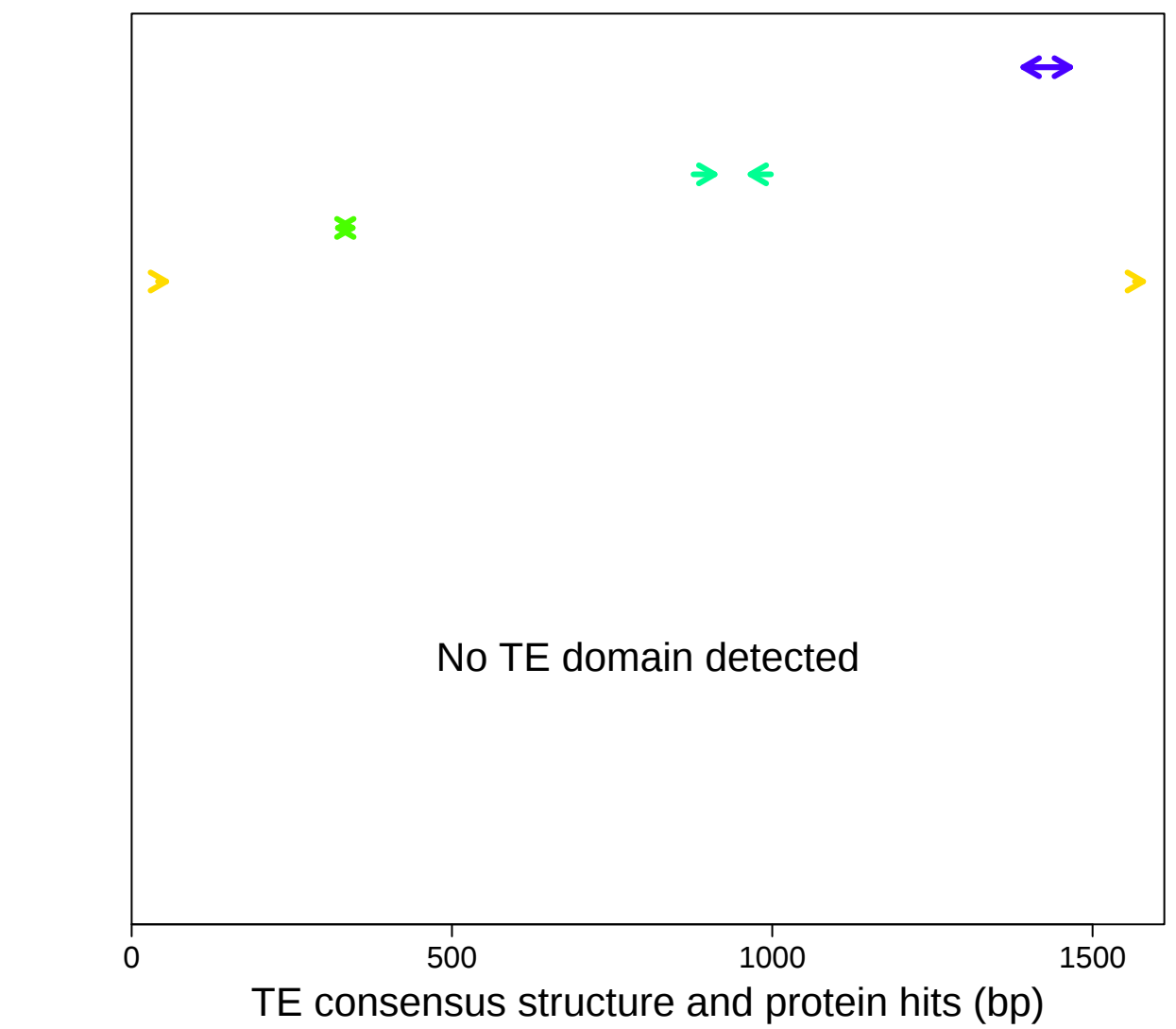
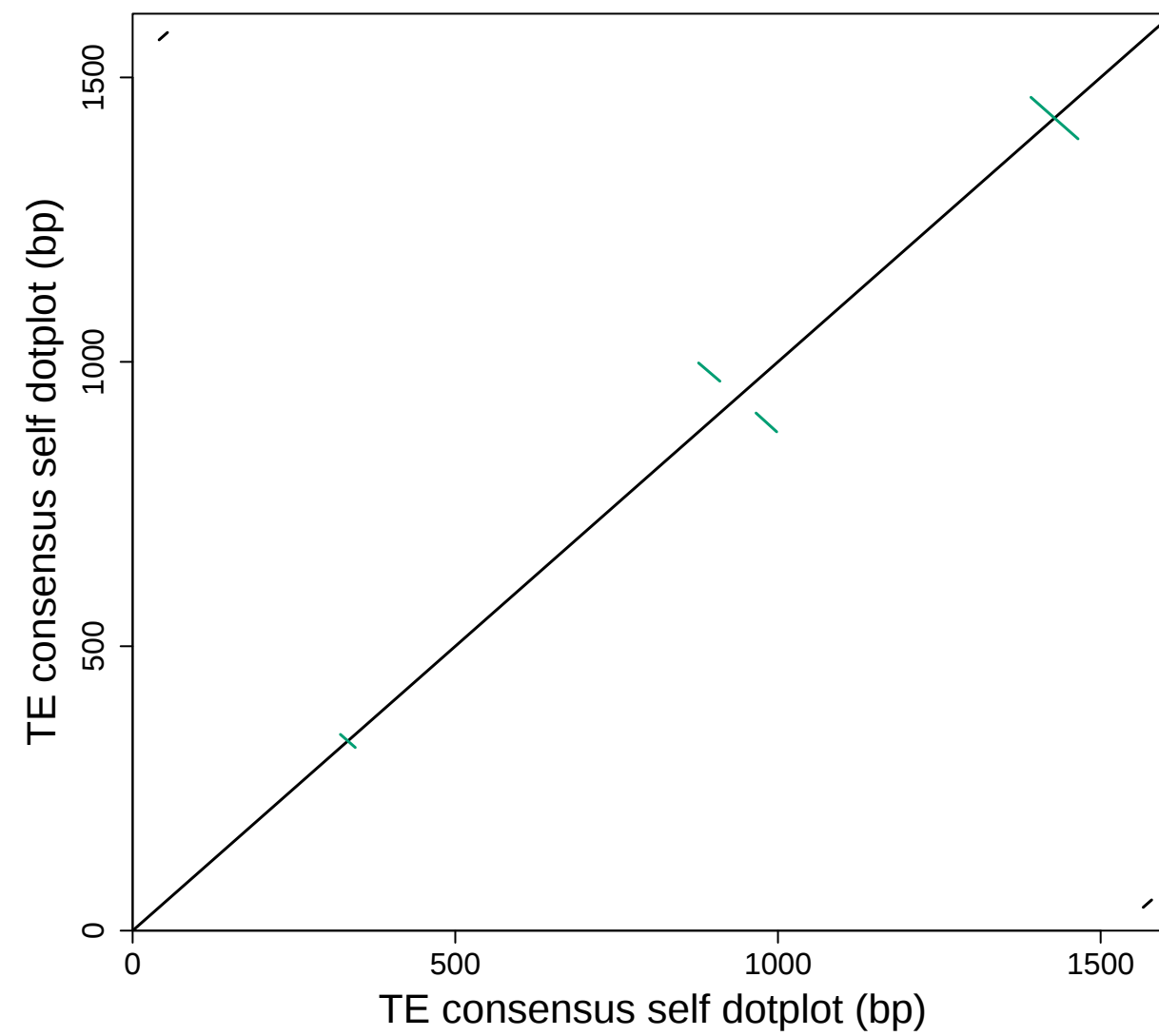
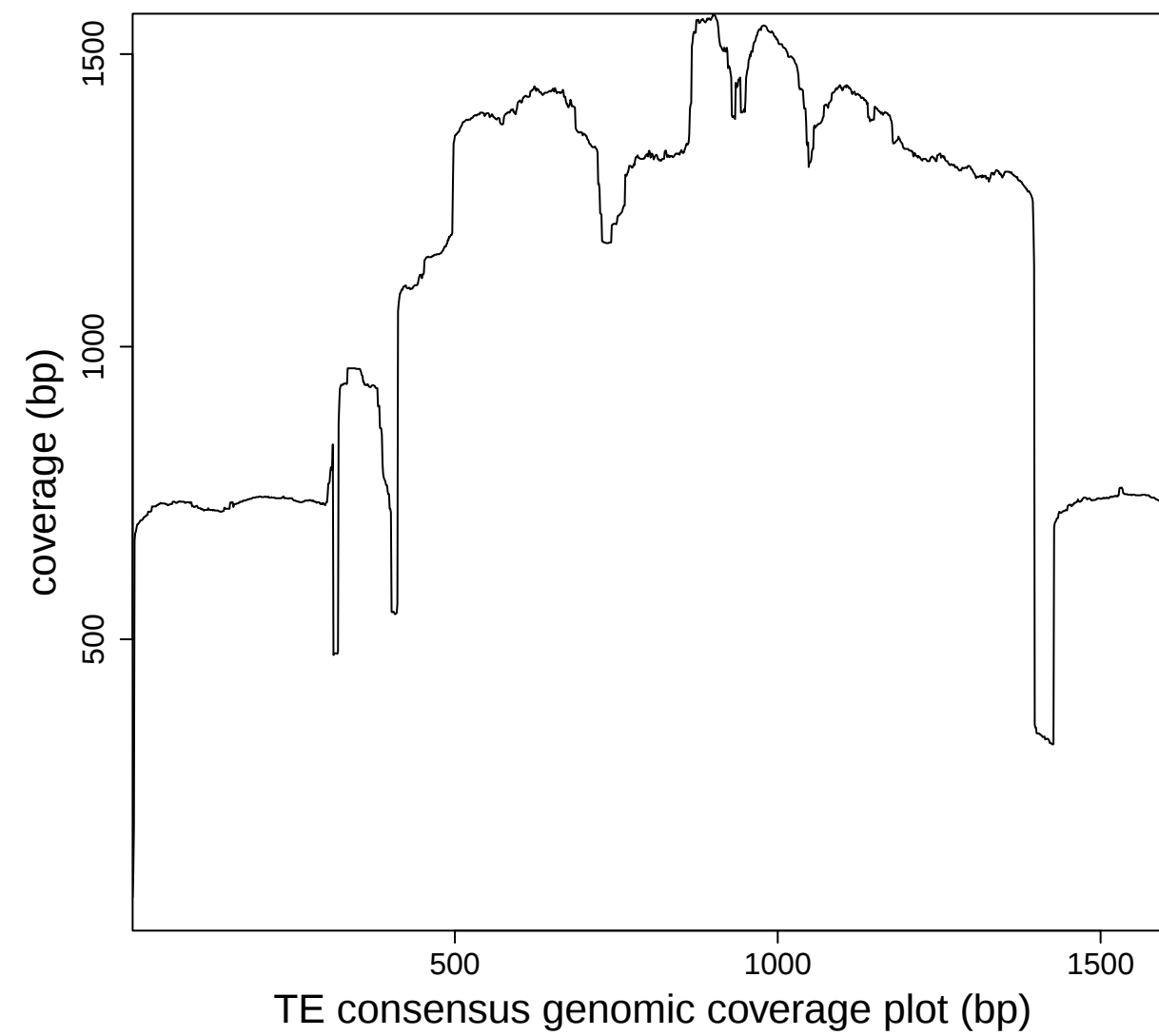
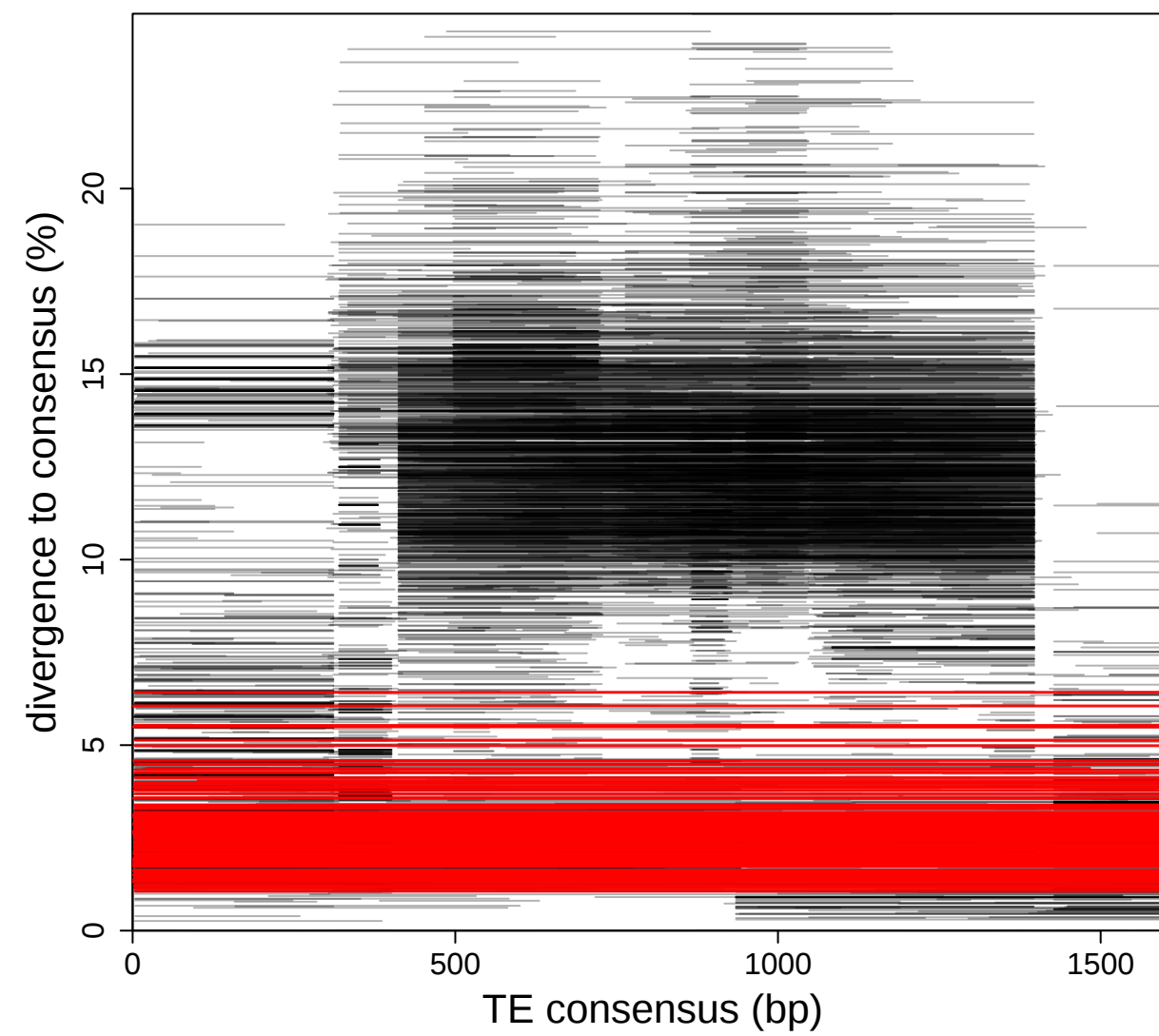
1750

2000



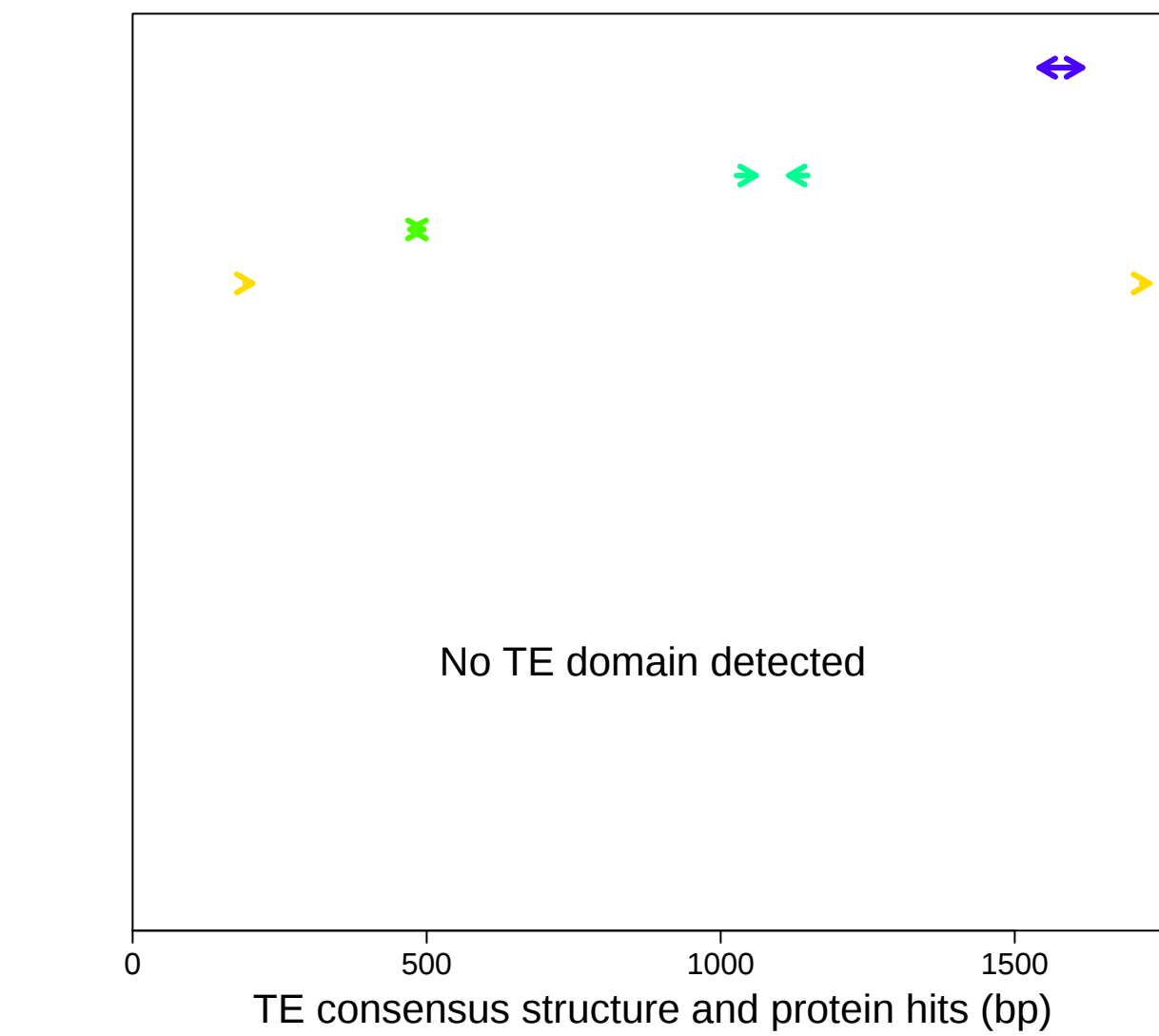
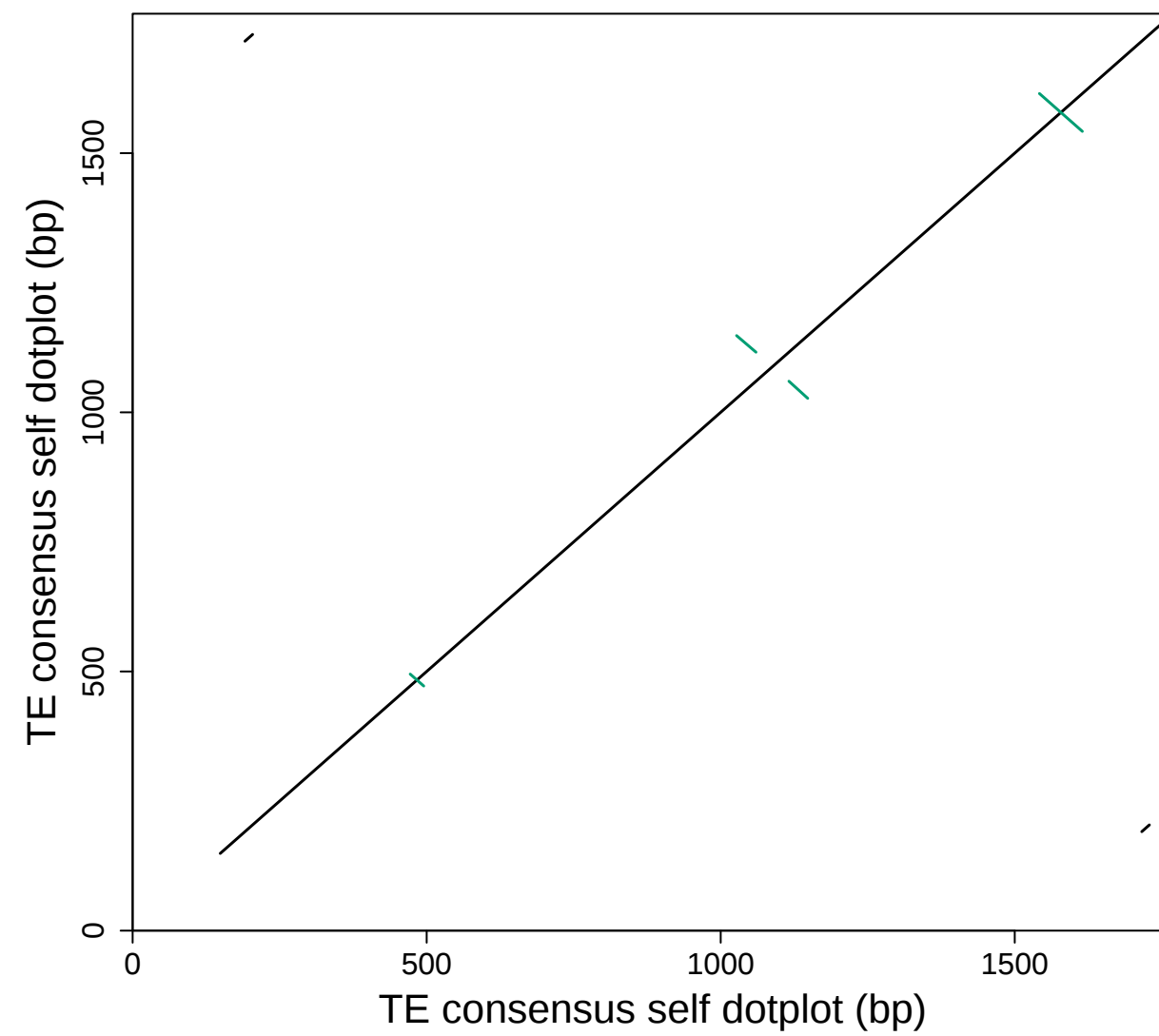
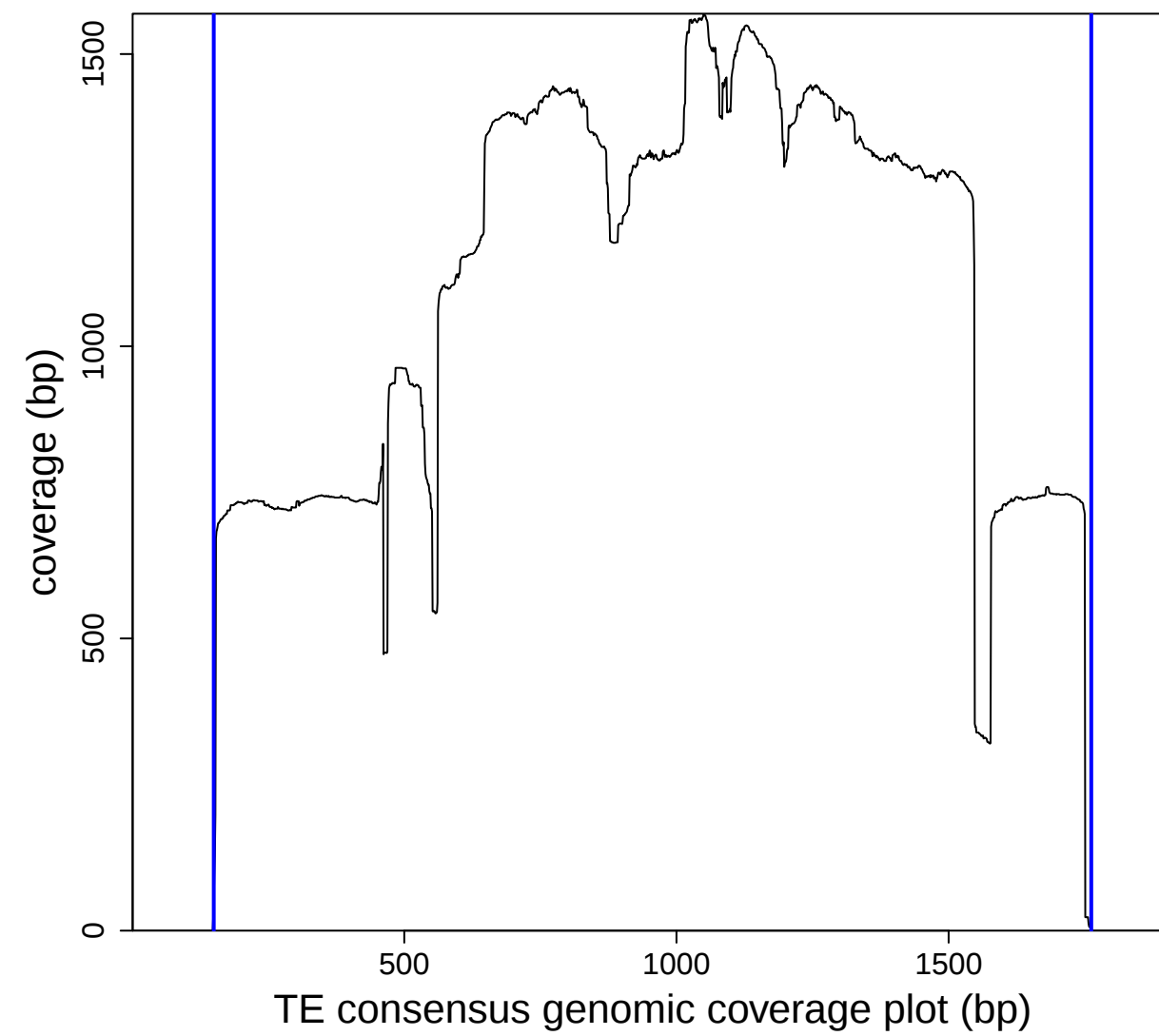
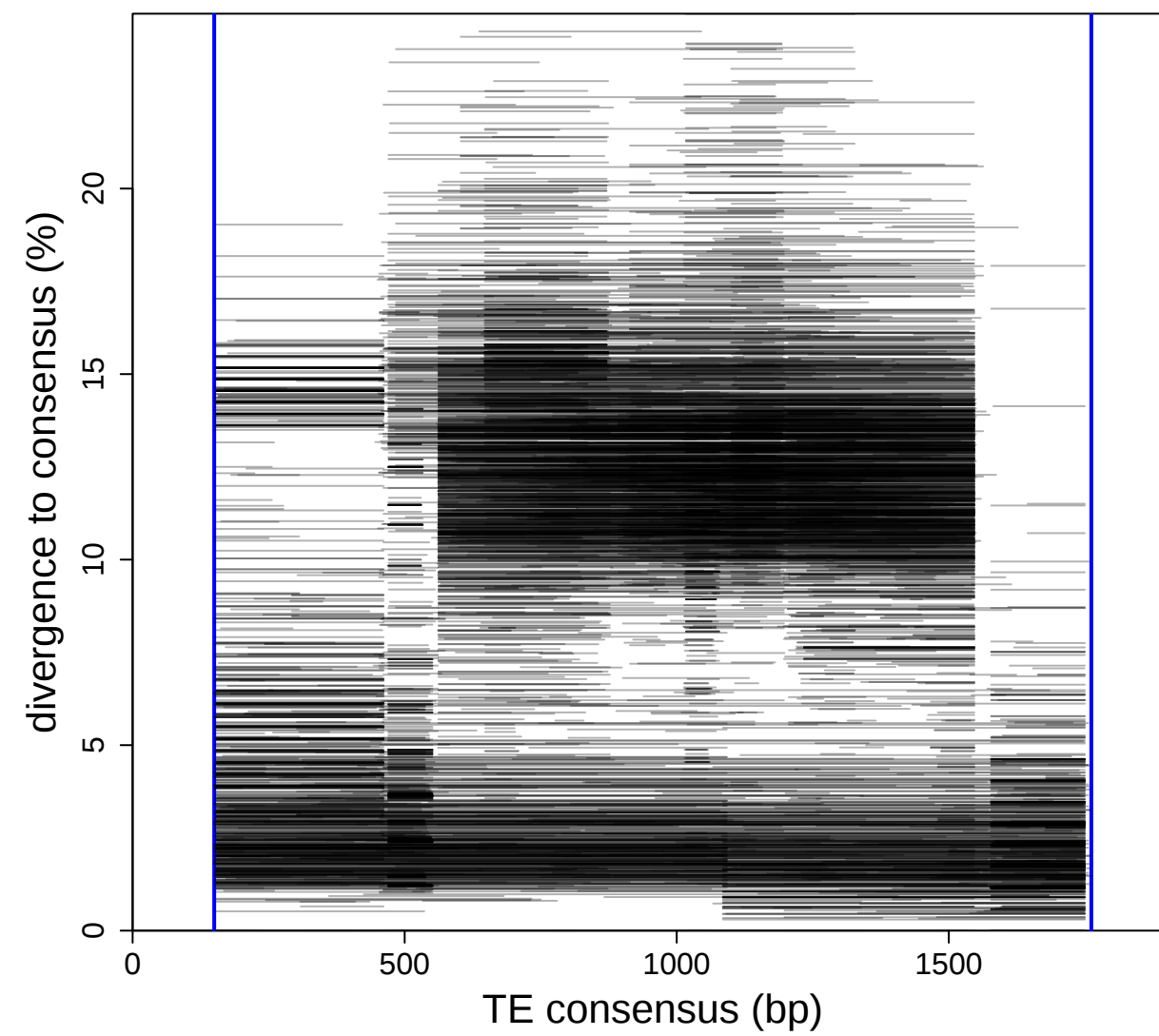
g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa_a
size: 1612bp; fragments: 4477; full length: 152 (>=1450.8bp)

After TEtrimmer 1612 bp

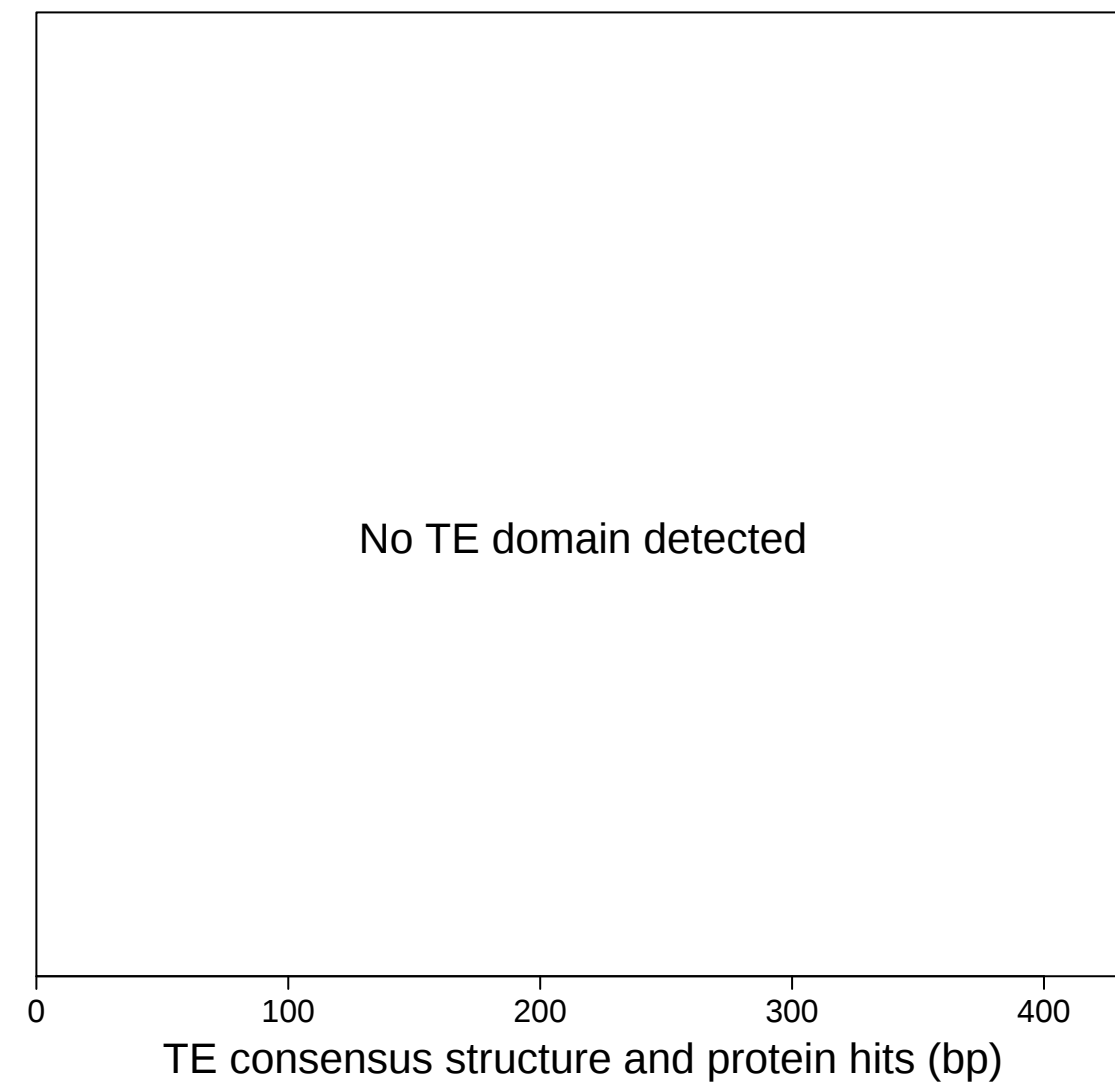
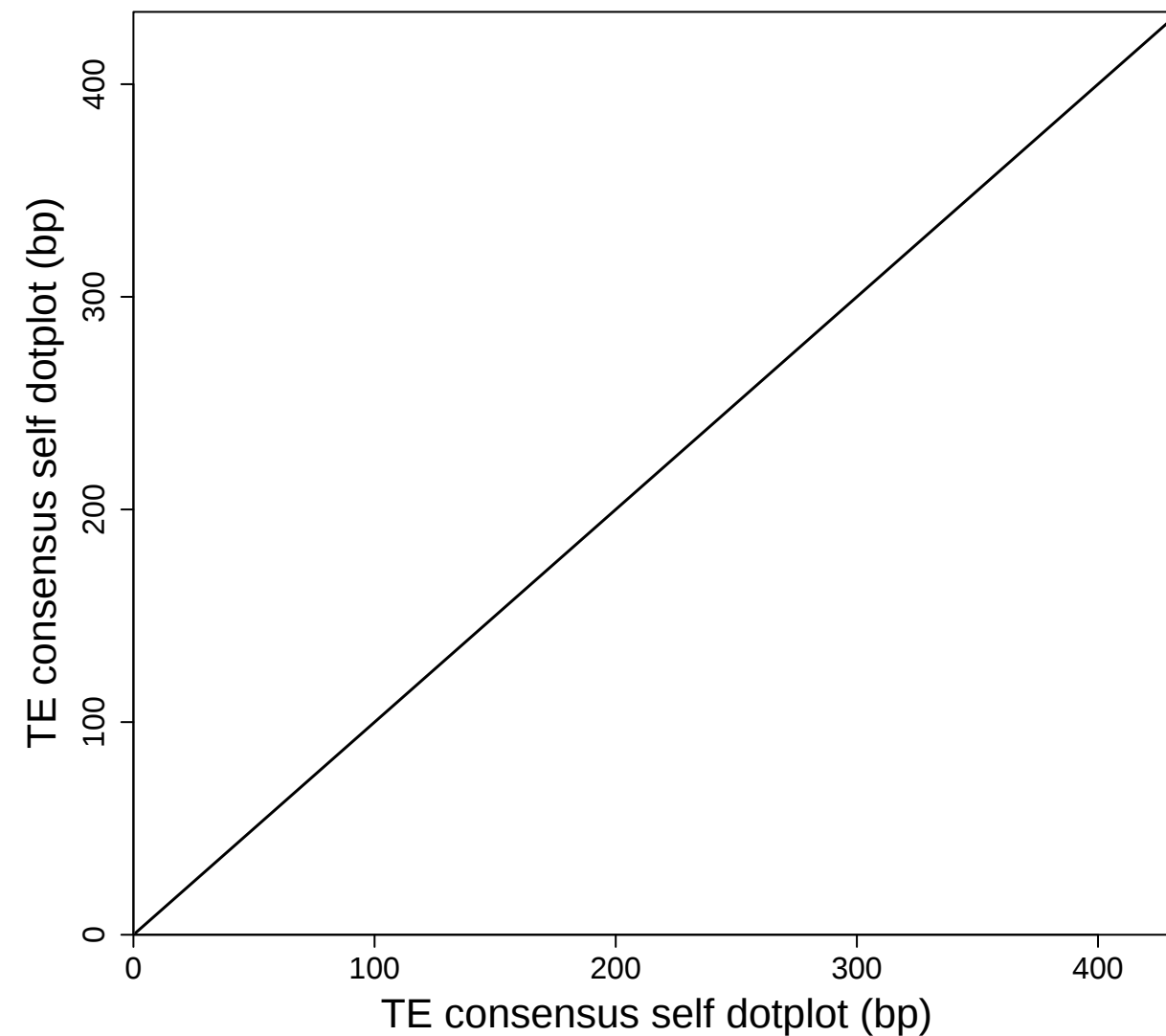
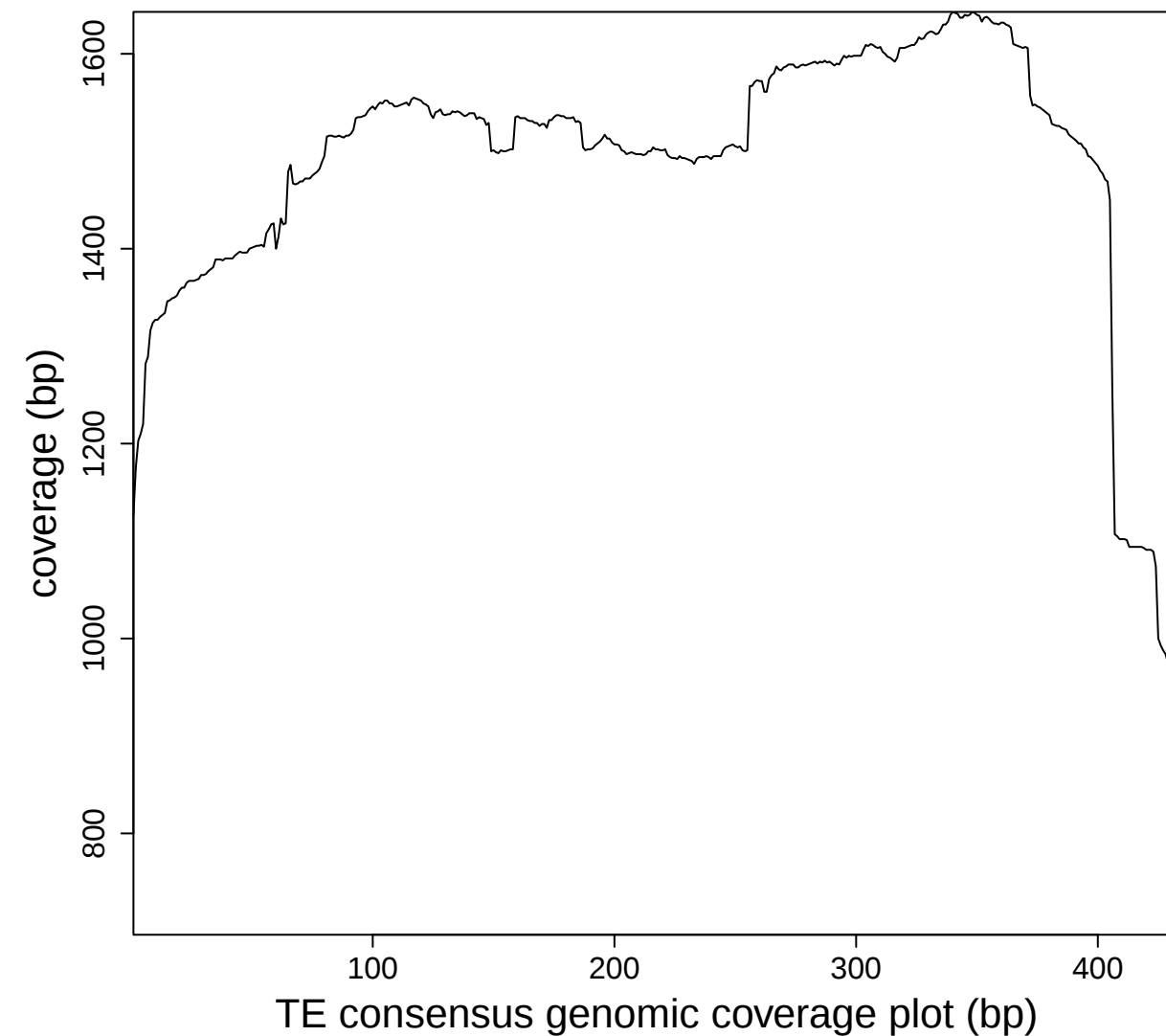
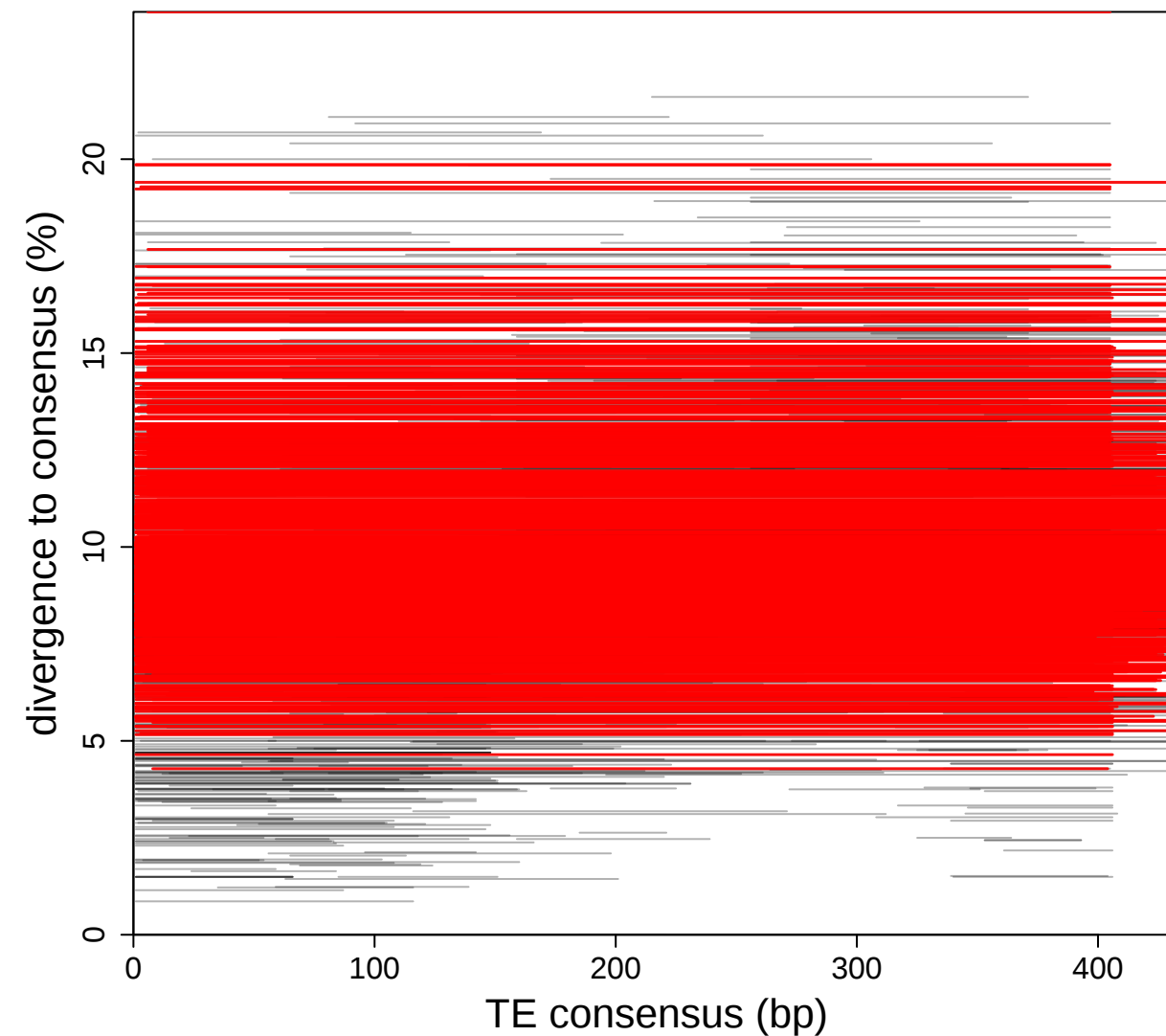


f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcl
size: 1912bp; fragments: 4478; full length: 0 (>=1720.8bp)

After TEtrimmer Extended plot Blue lines are boundaries

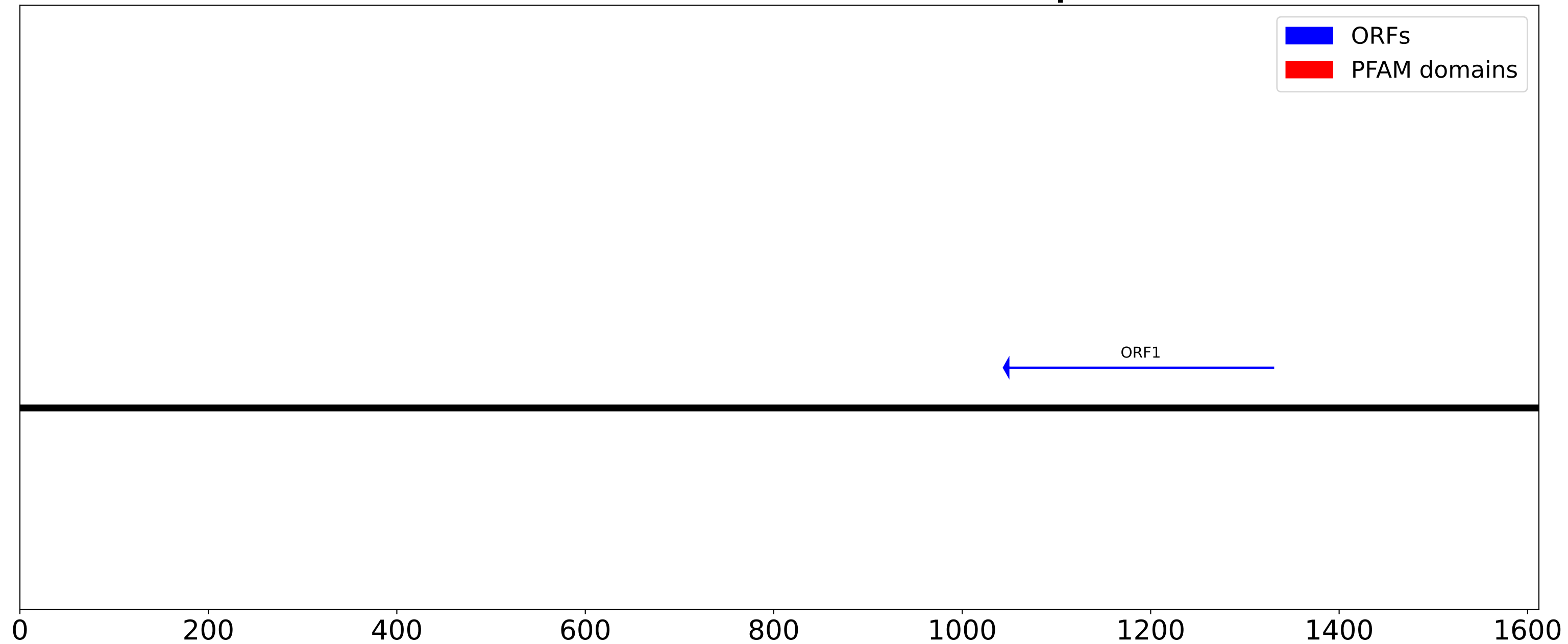


TE: rnd_1_family_417
size: 434bp; fragments: 2195; full length: 969 (≥ 390.6 bp)

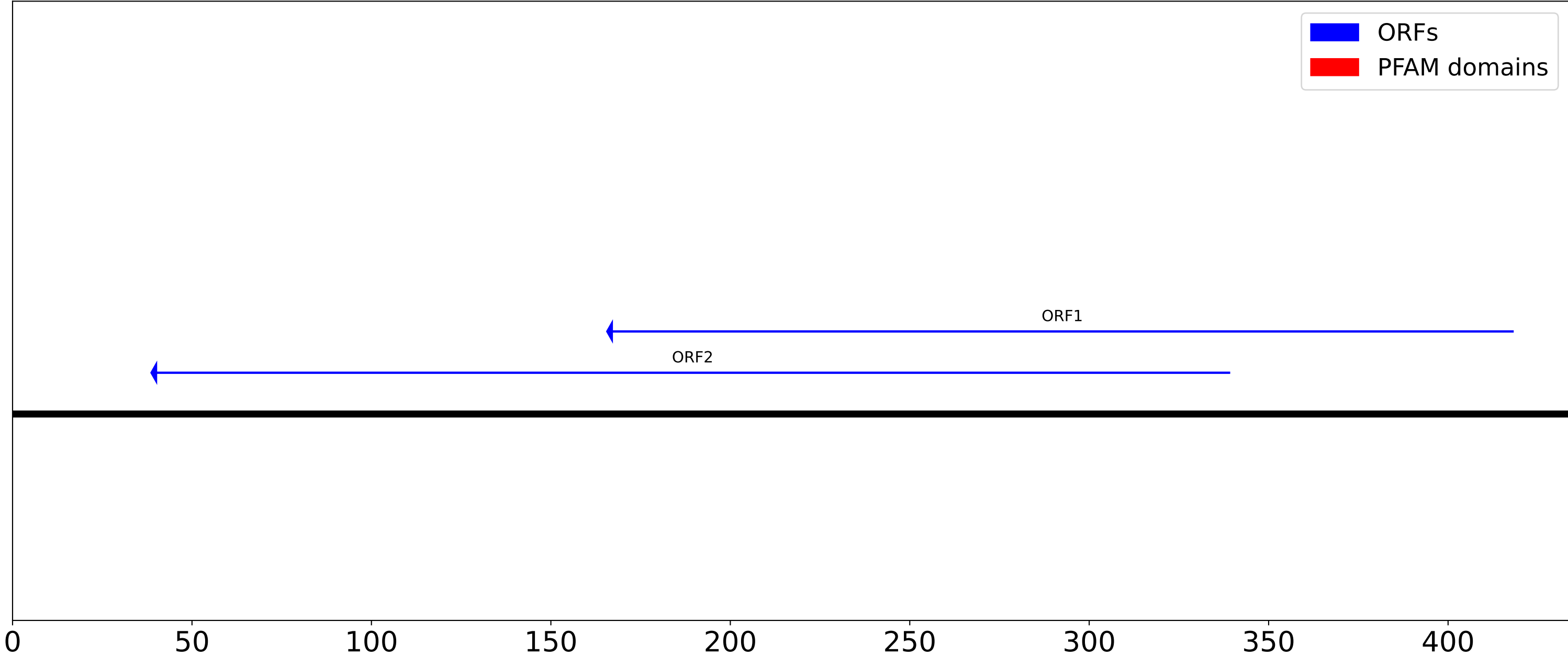


Before TEtrimmer 434 bp

After TEtrimmer ORF and PFAM domain plot



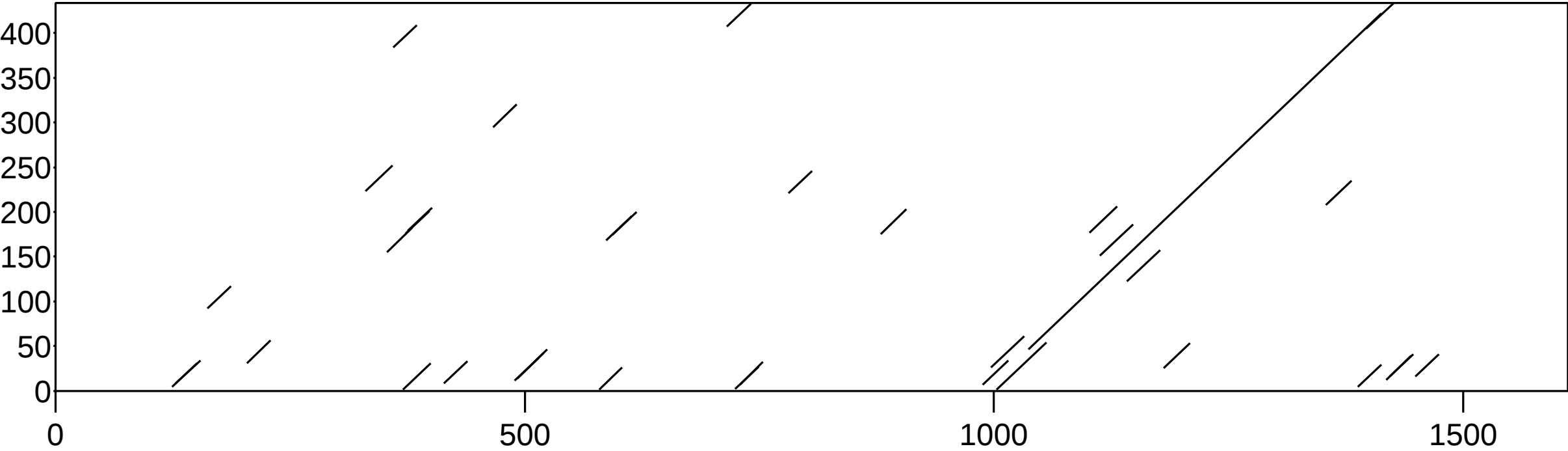
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)