

Start crop Point



End crop Point



MSA length = 1363



Start crop Point

End crop Point

0

10

0

250

500

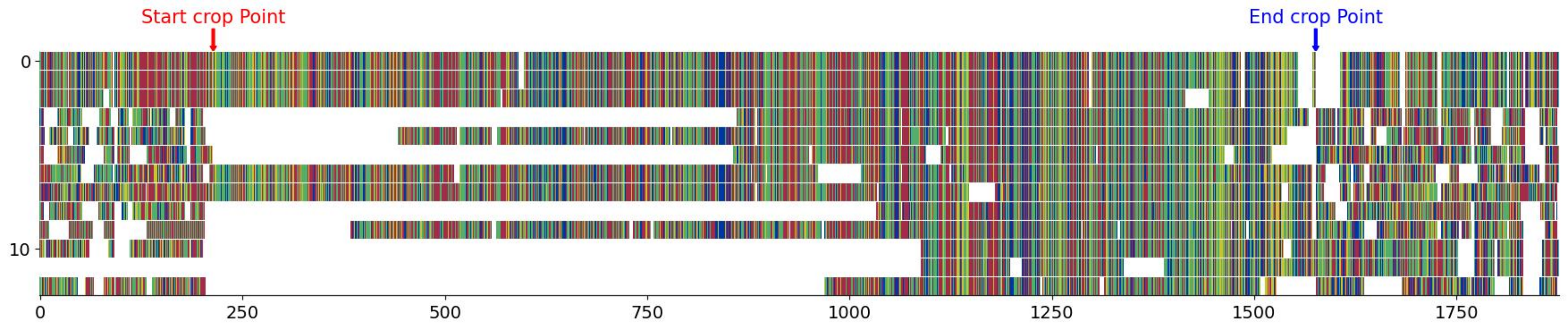
750

1000

1250

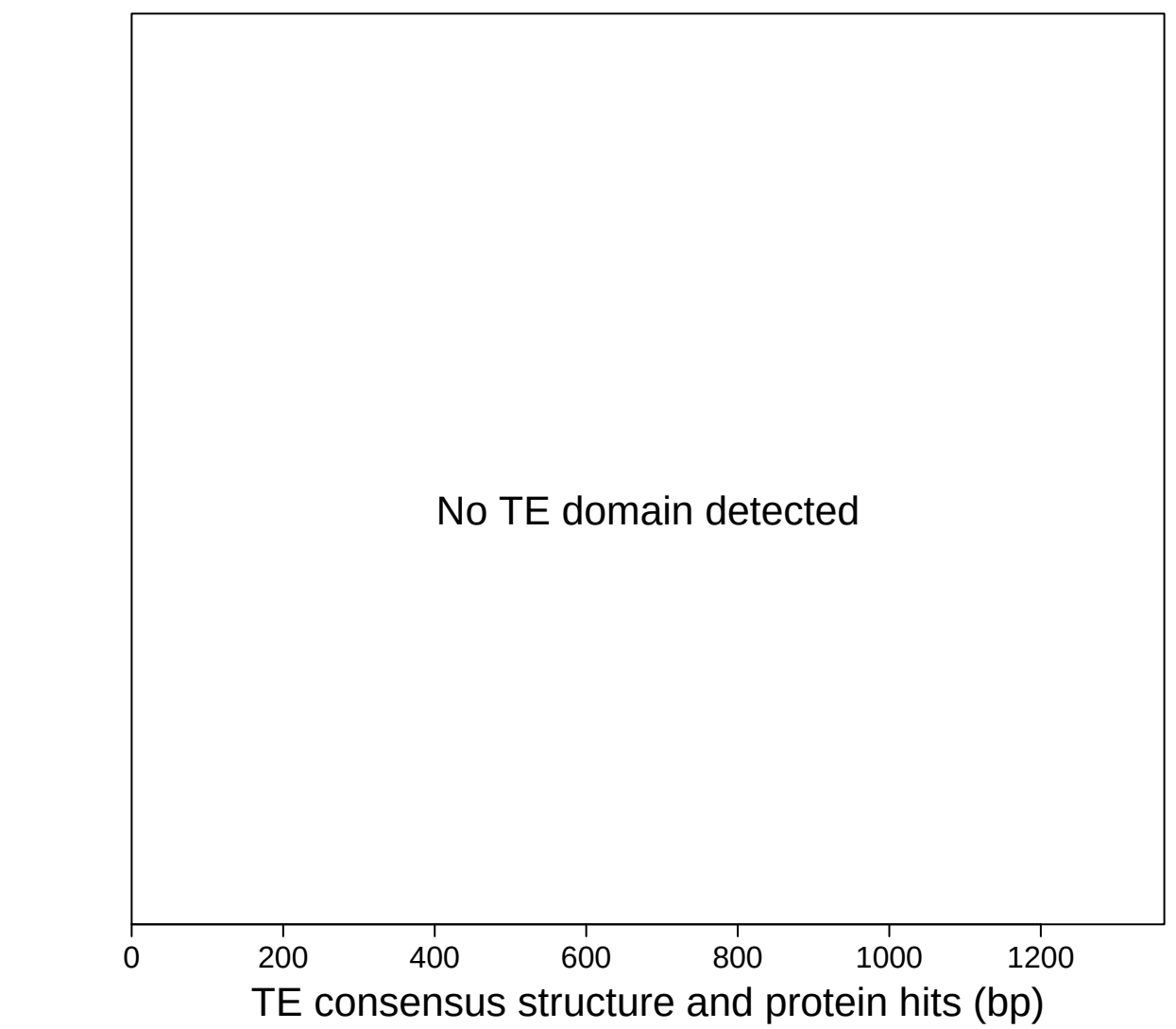
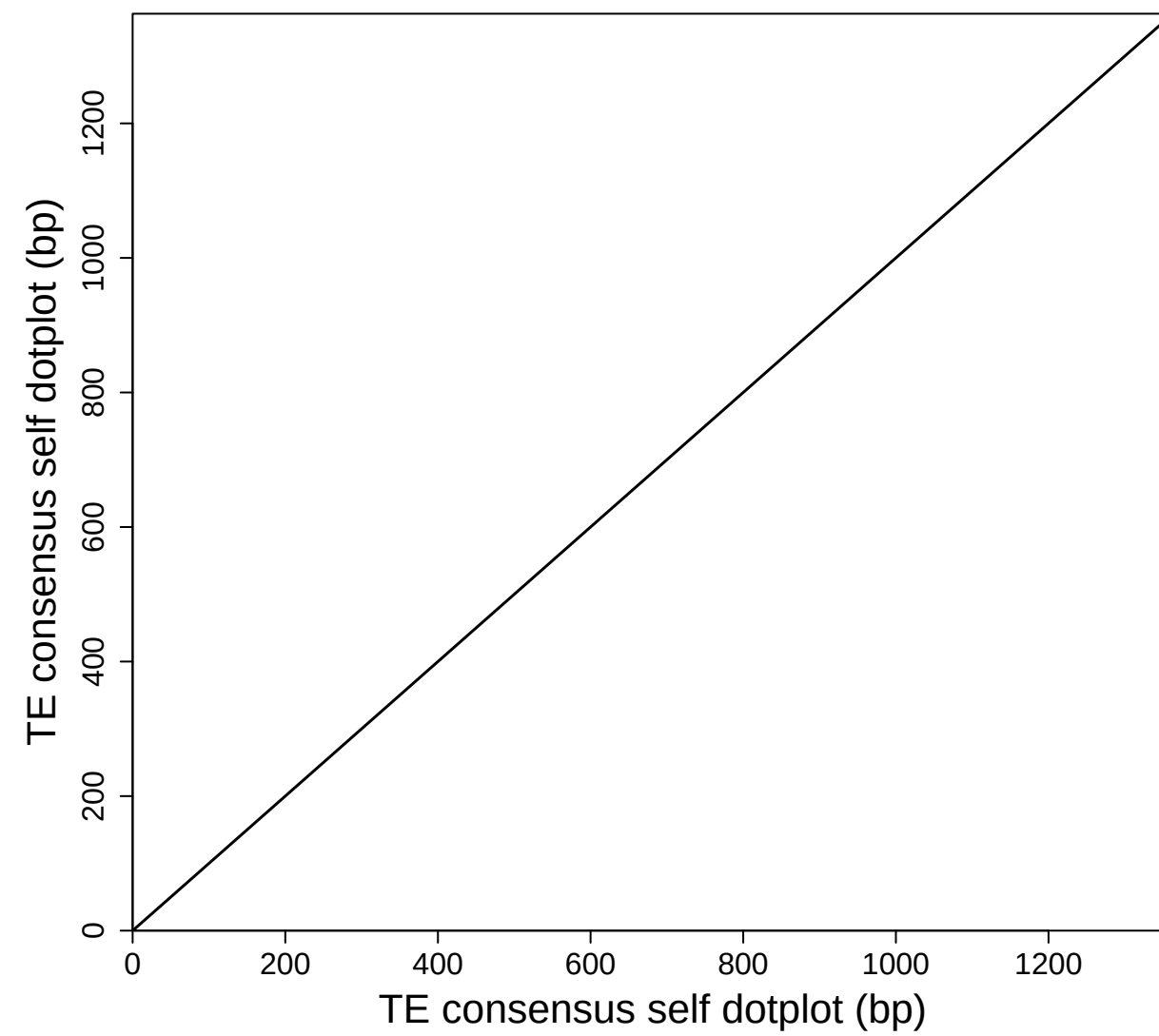
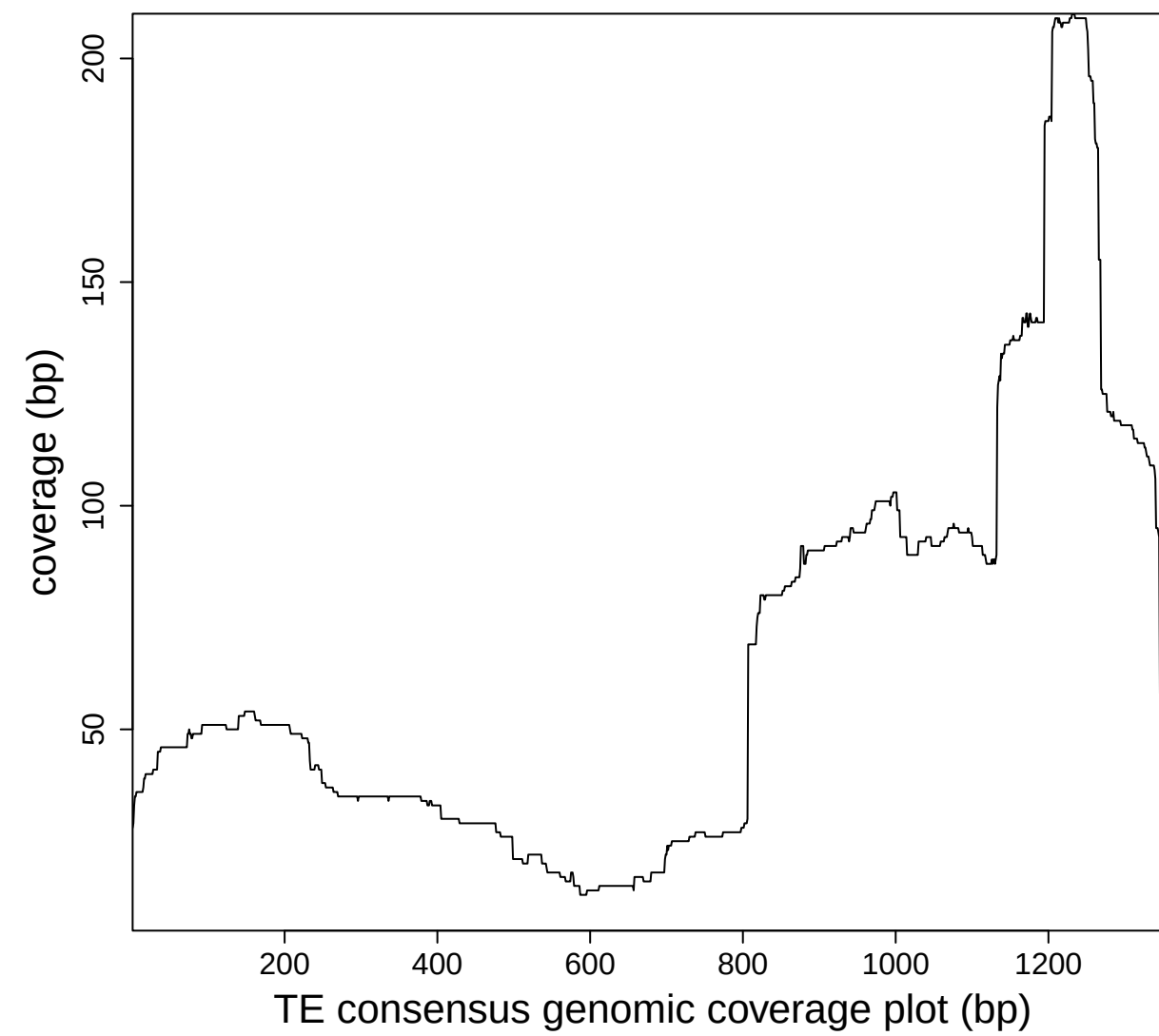
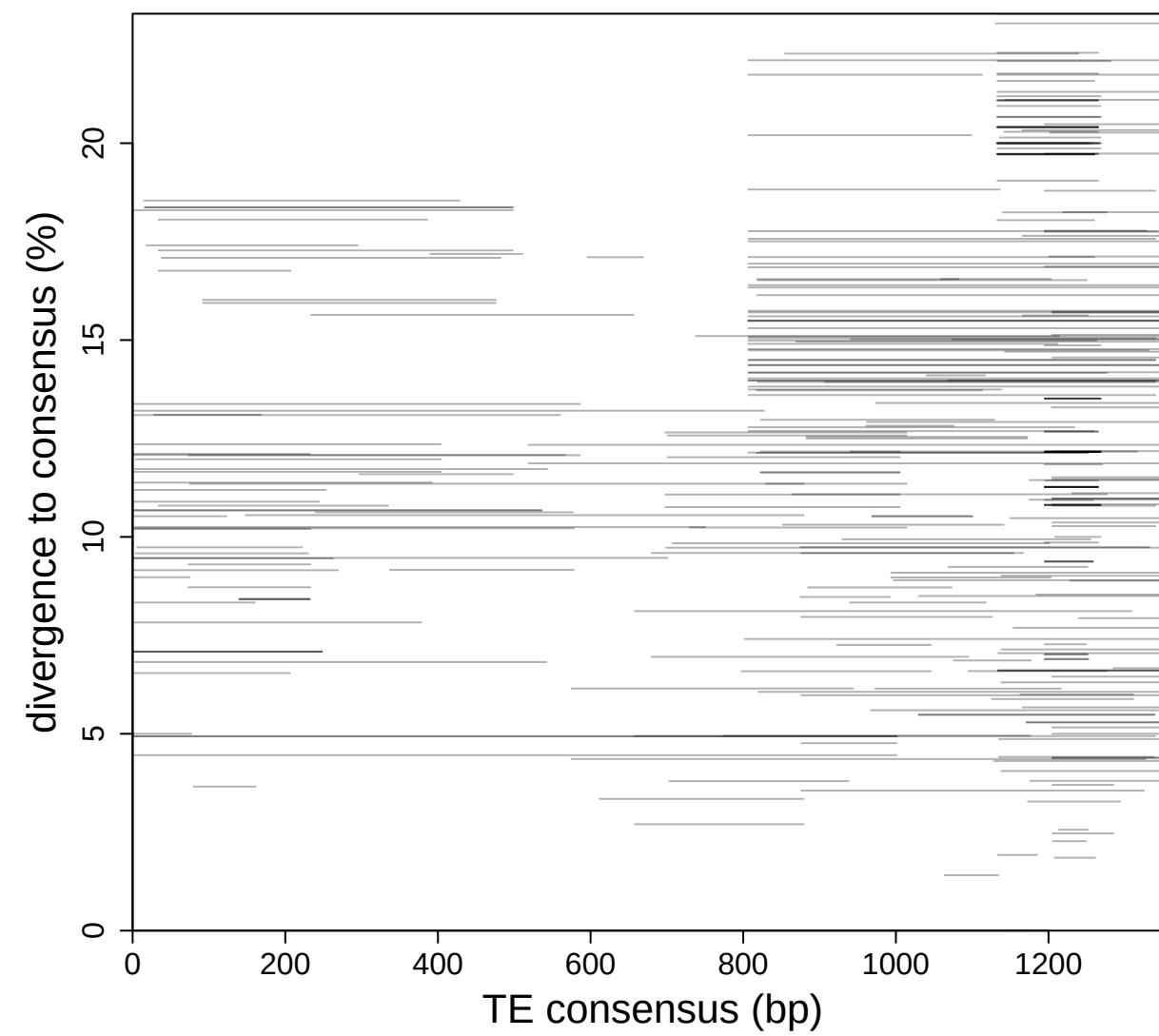
1500

1750



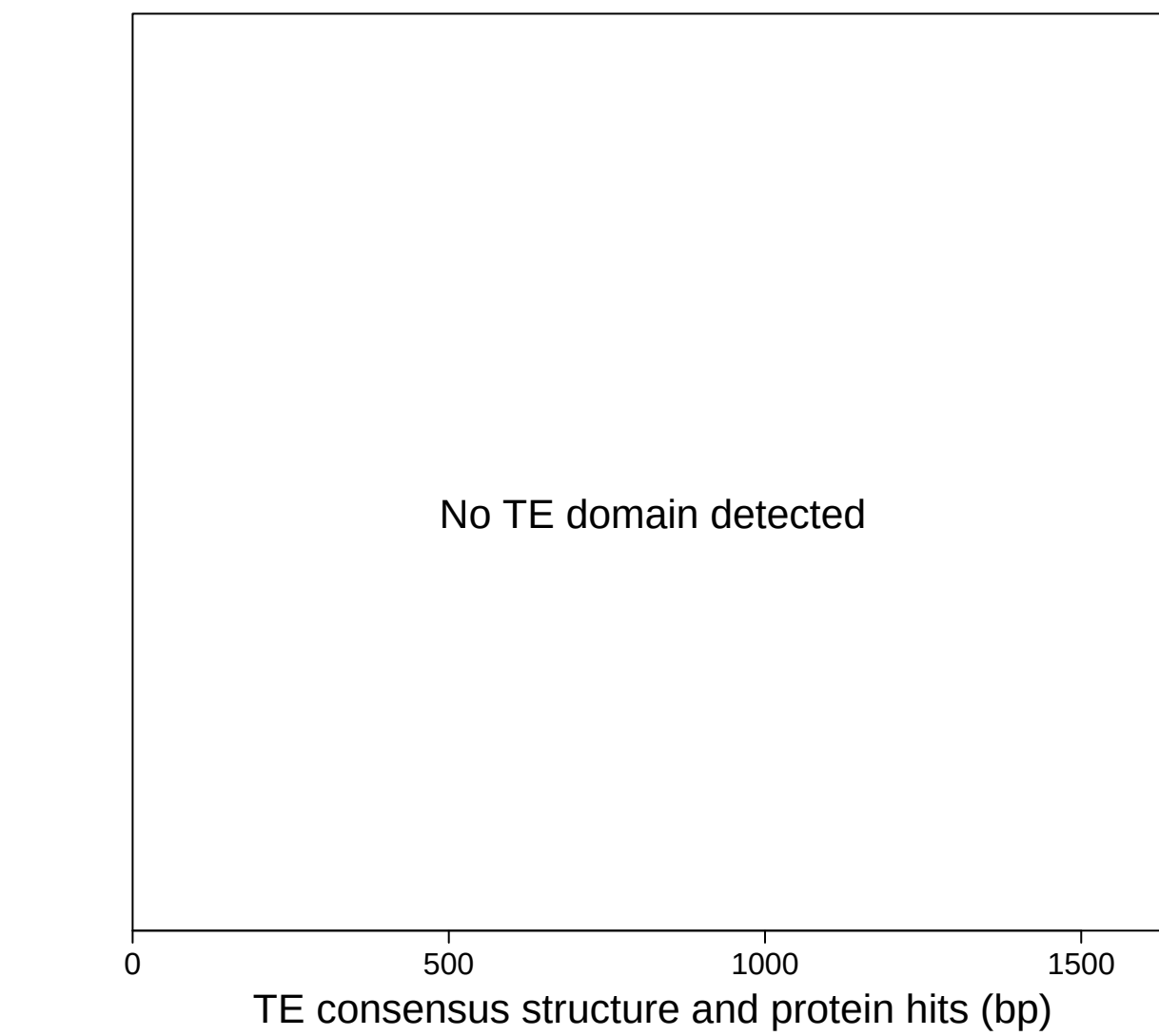
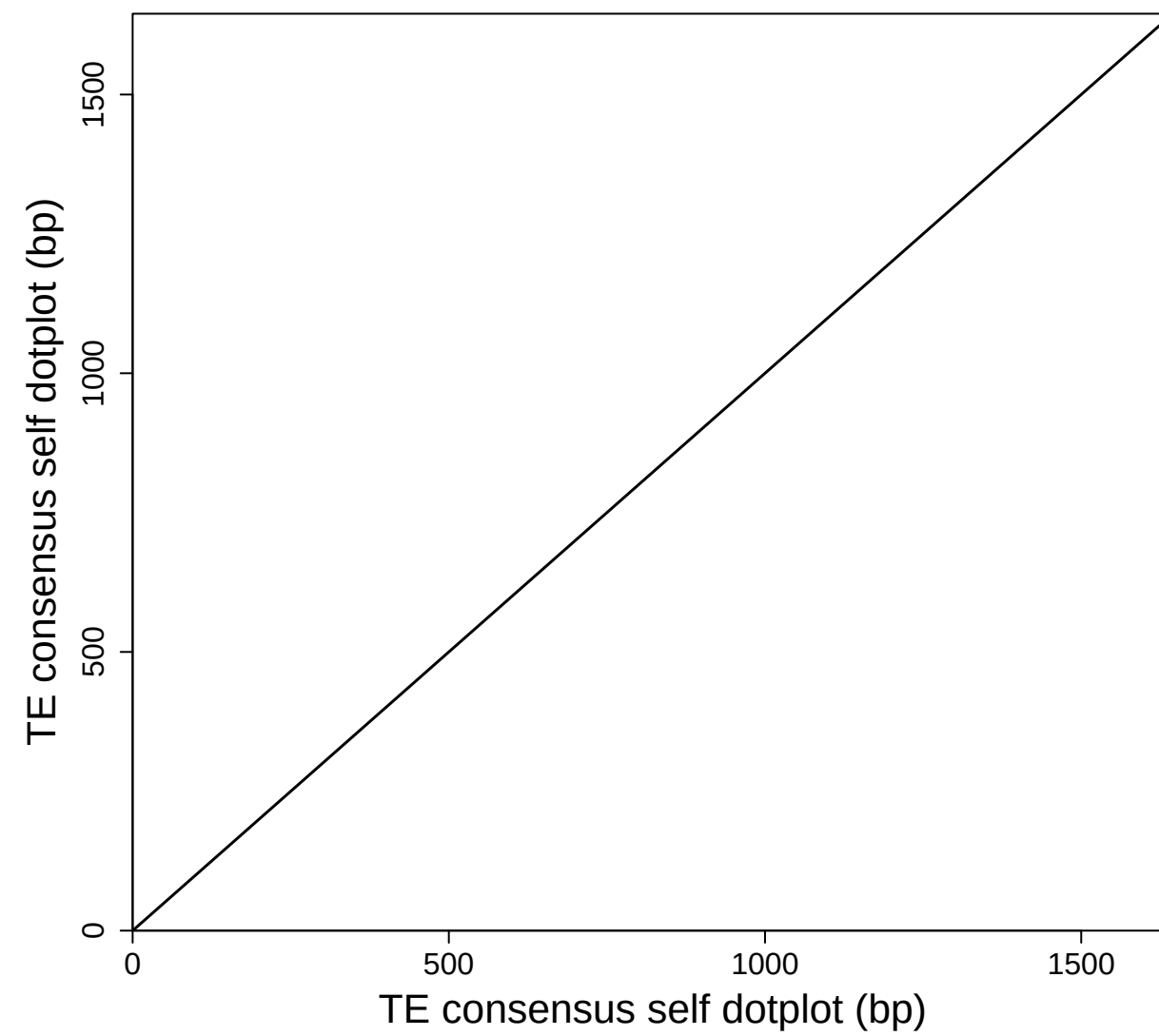
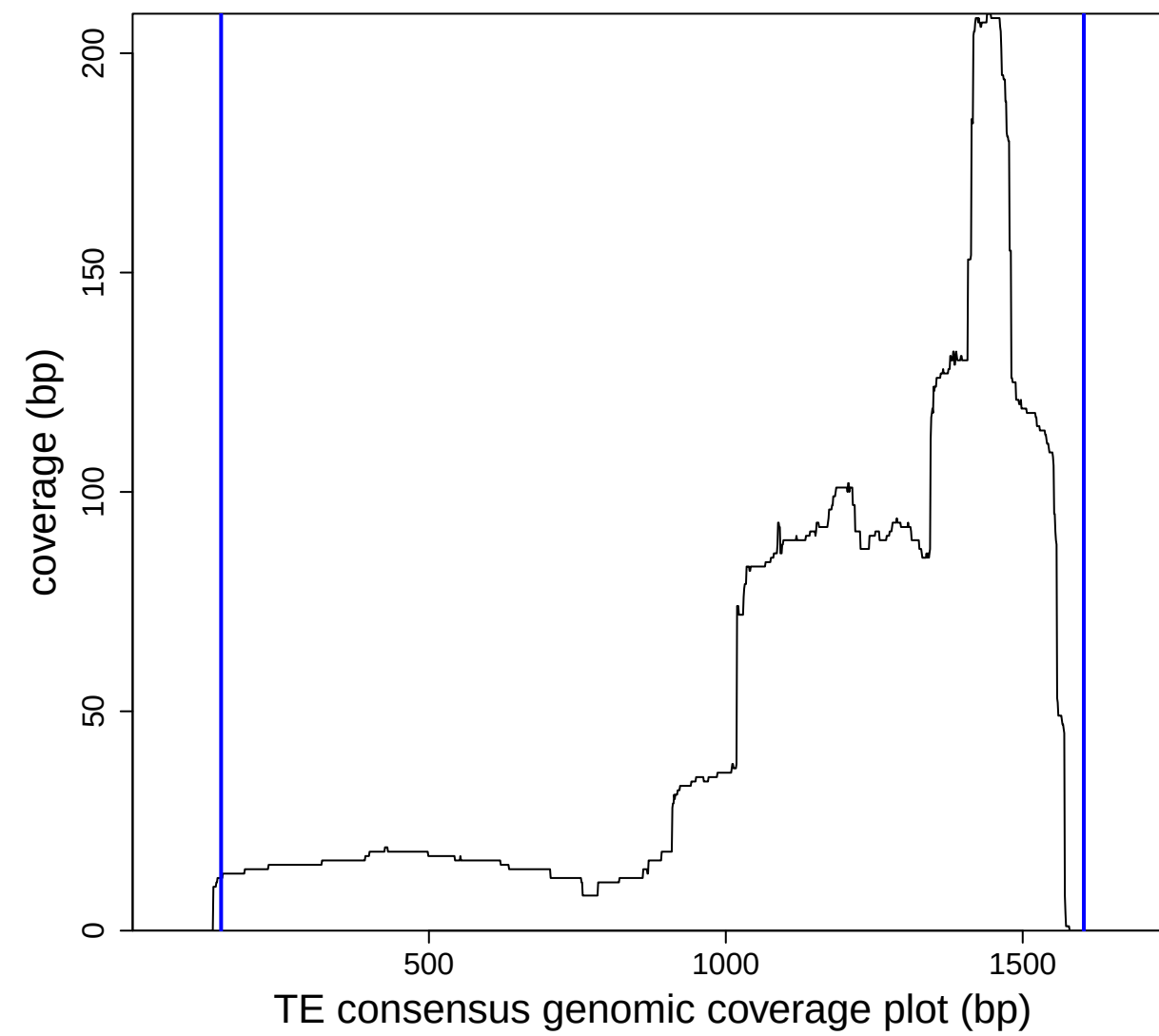
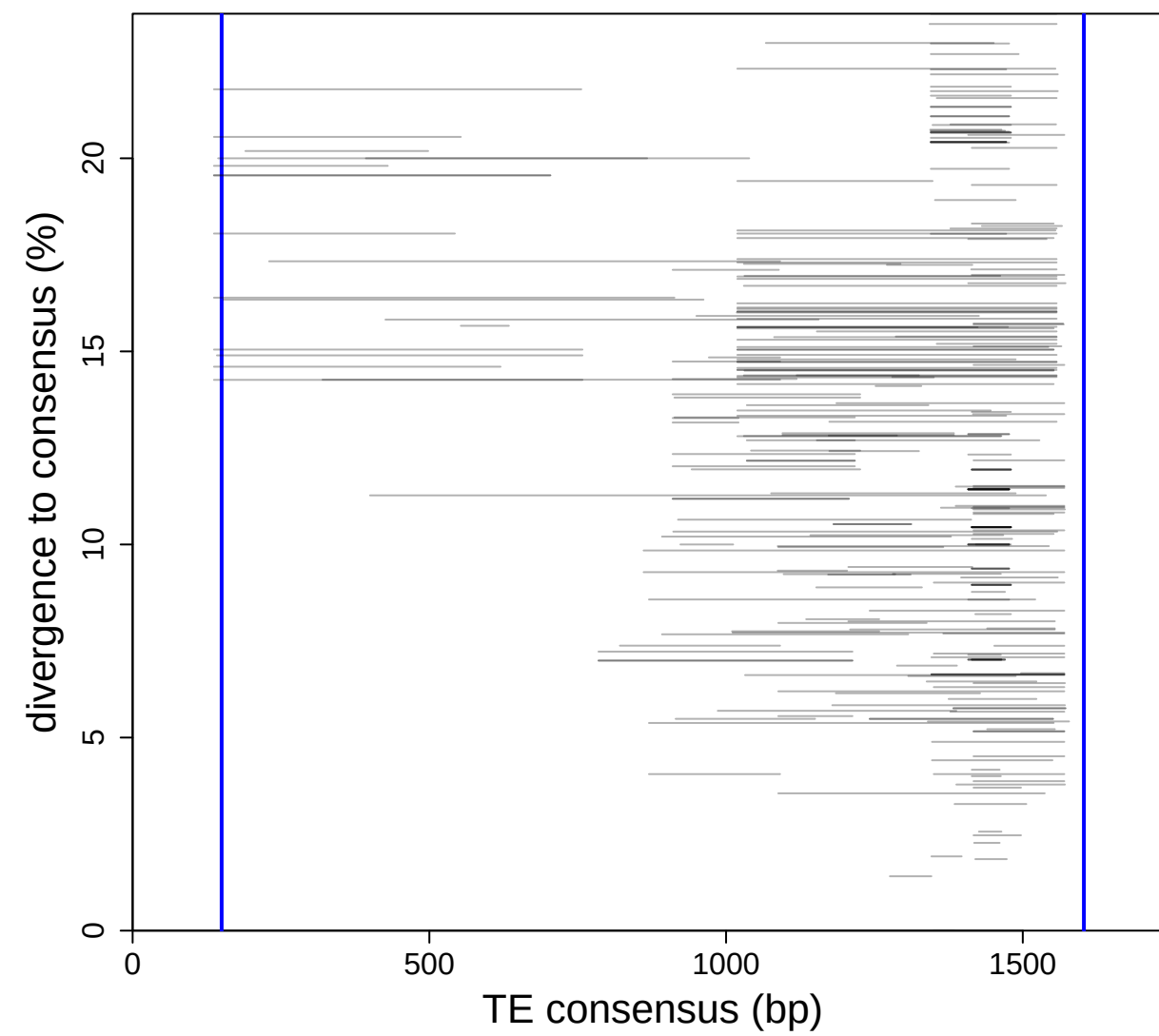
a.b.bed_uf.bed_g_2.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.f
size: 1363bp; fragments: 325; full length: 0 (>=1226.7bp)

After TEtrimmer 1363 bp

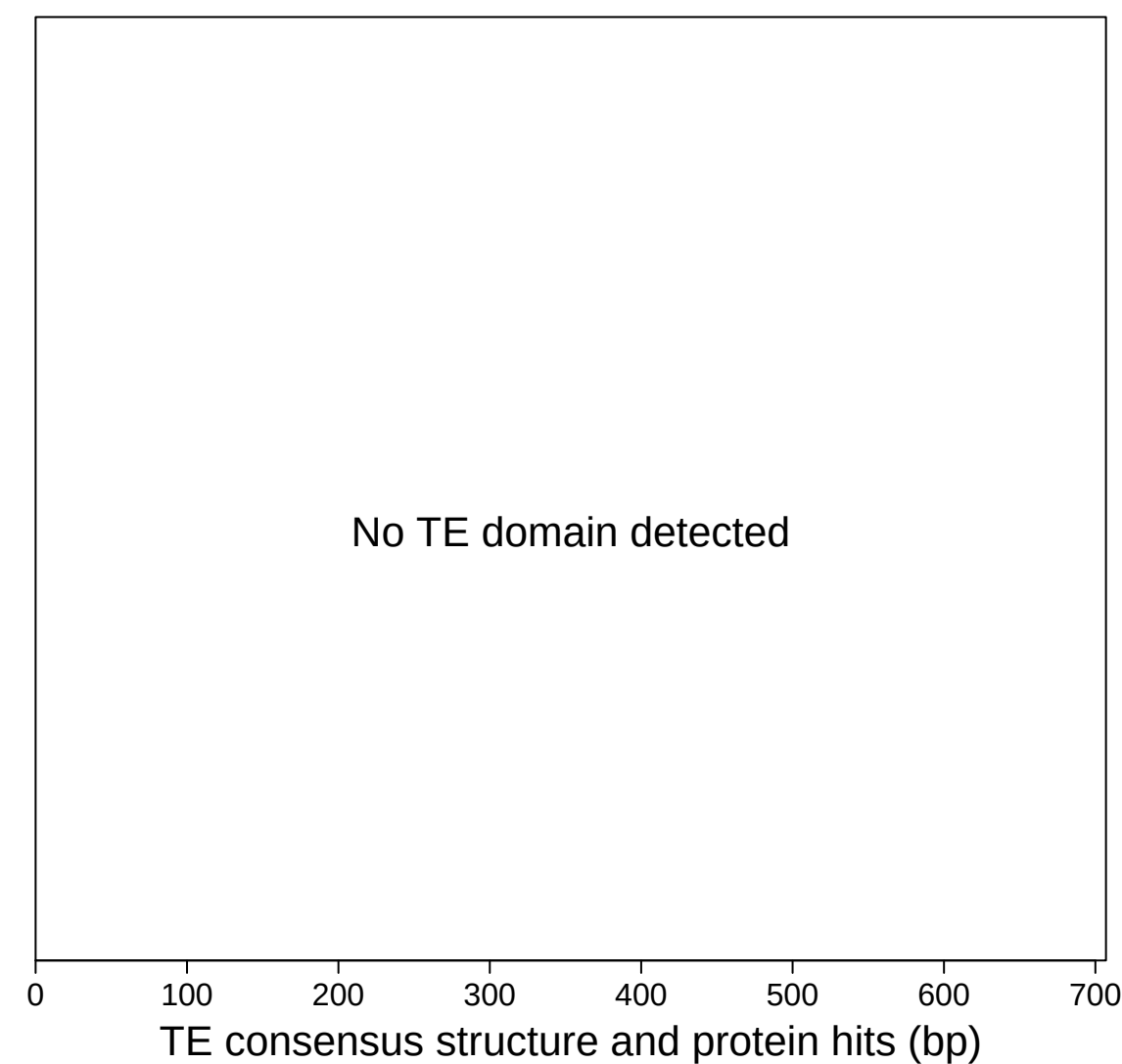
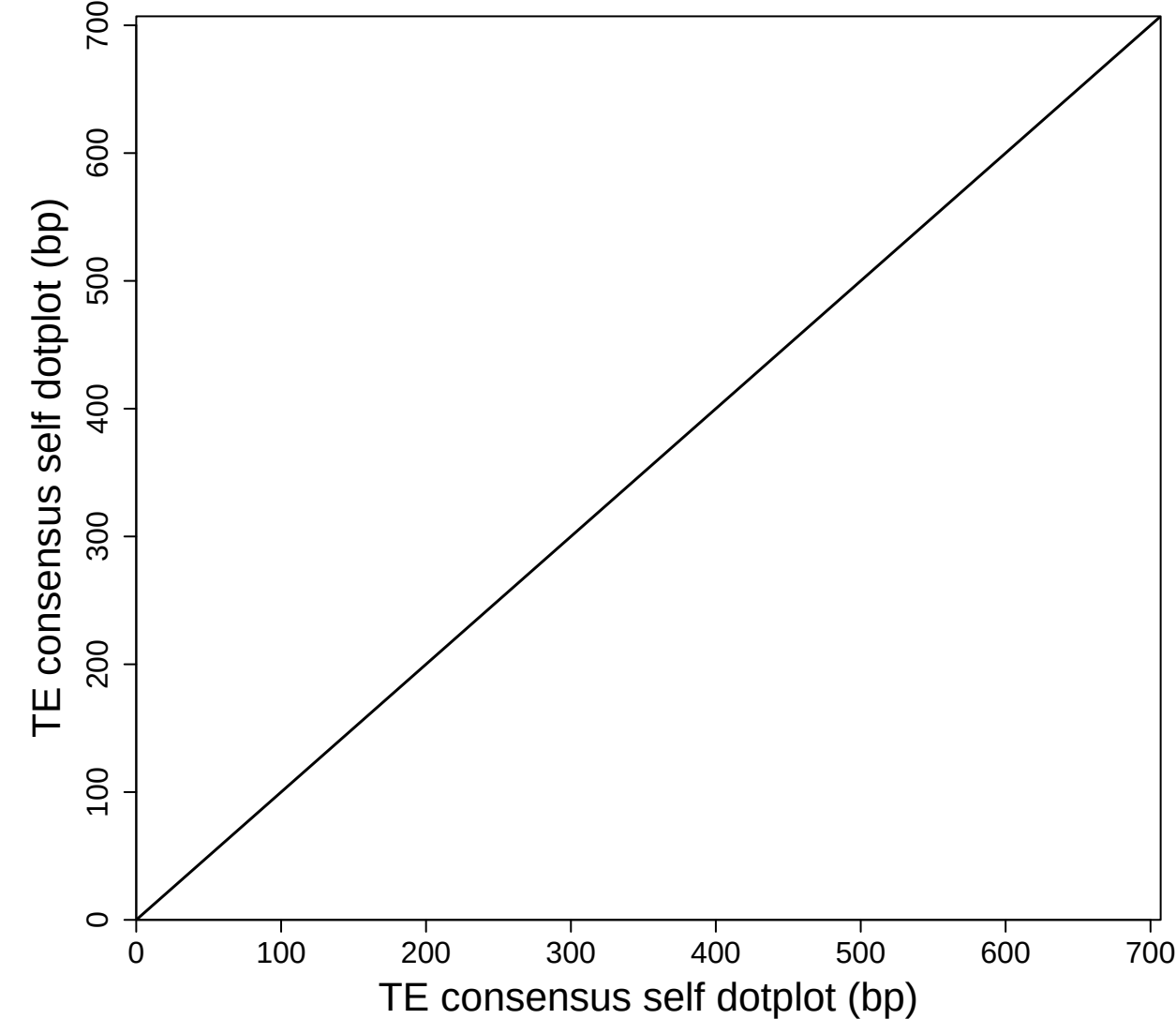
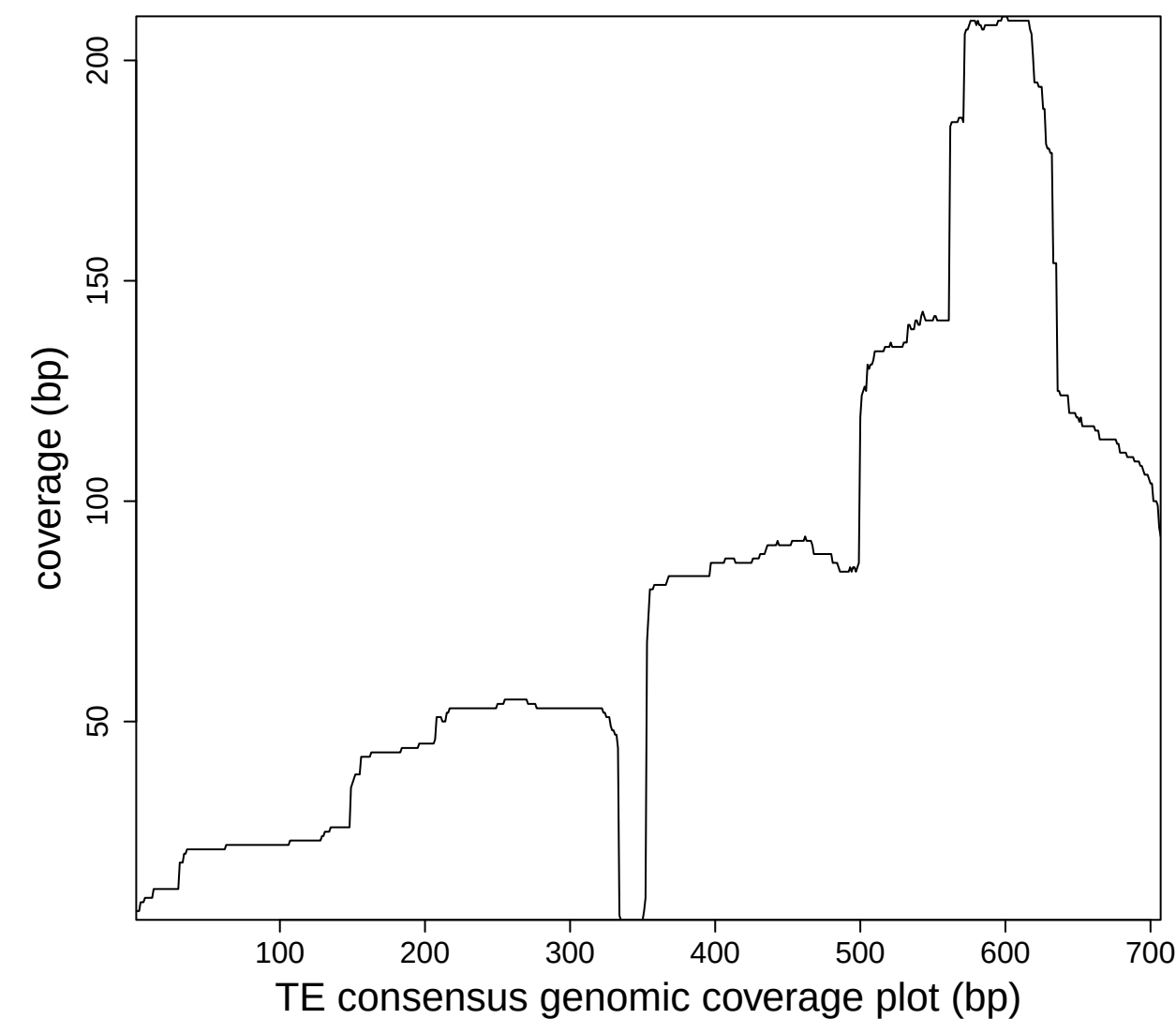
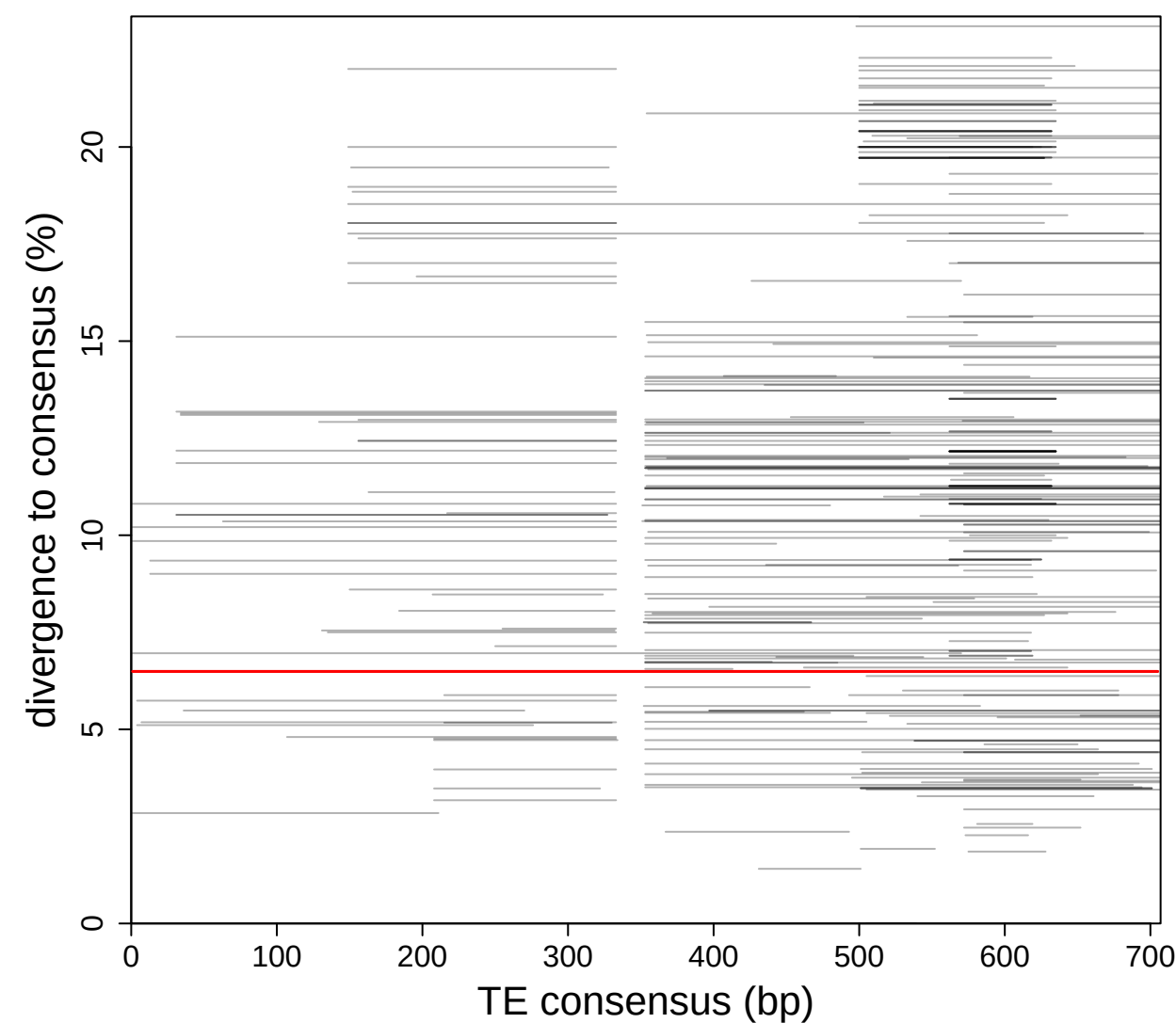


5.fasta.b.bed uf.bed g_2.bed fm_1.bed 0_0_bcln.fa aln.fa cl.f
size: 1753bp; fragments: 290; full length: 0 (>=1577.7bp)

After TEtrimmer Extended plot Blue lines are boundaries

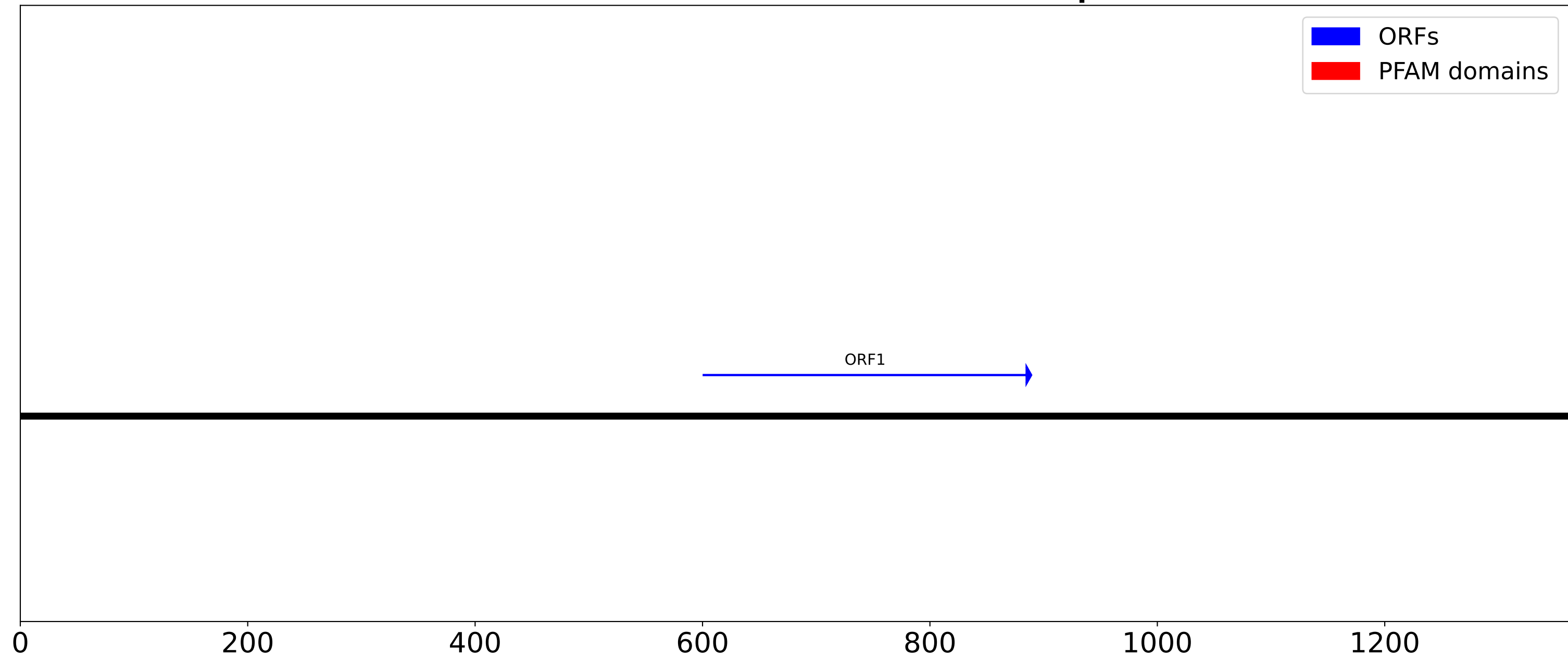


TE: rnd_5_family_1395
size: 707bp; fragments: 292; full length: 2 (≥ 636.3 bp)

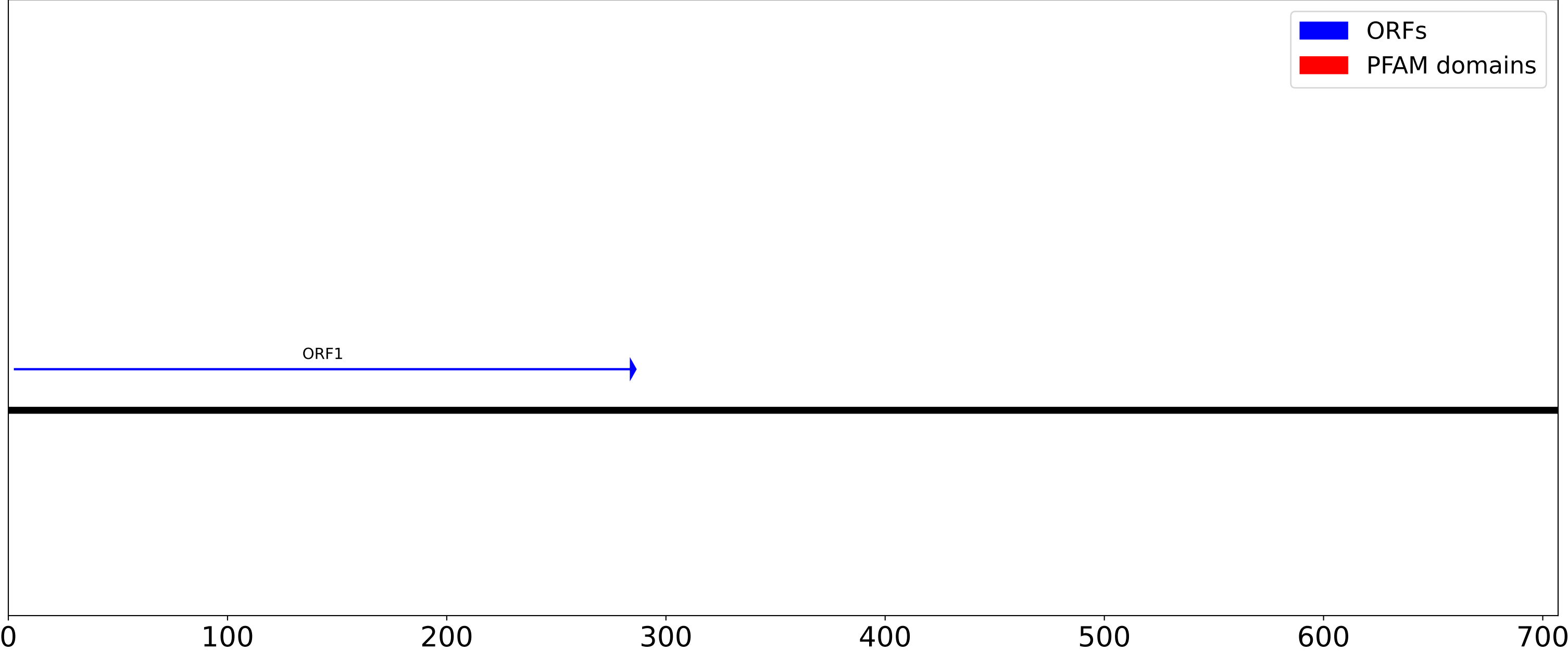


Before TEtrimmer 707 bp

After TEtrimmer ORF and PFAM domain plot



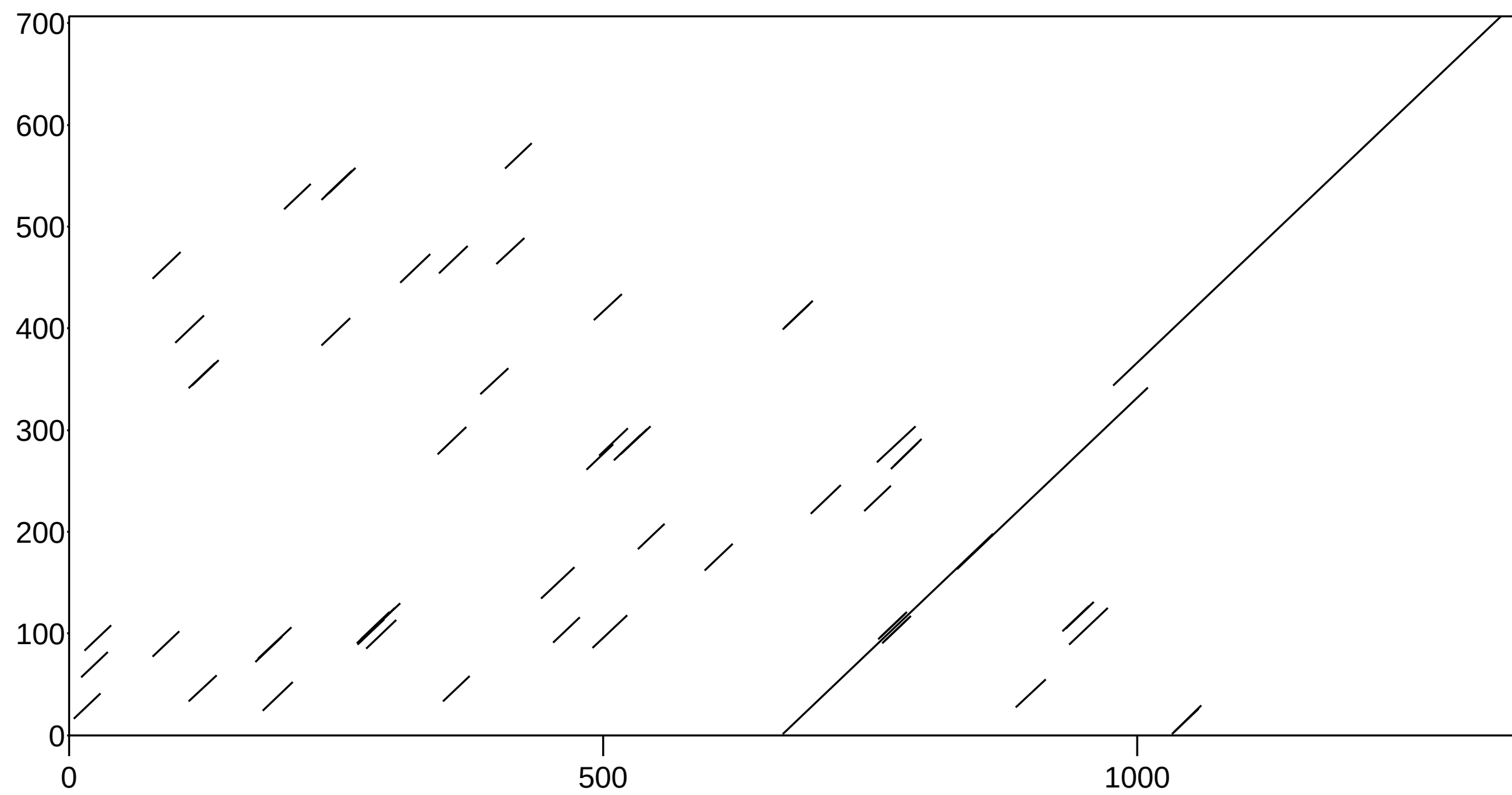
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)