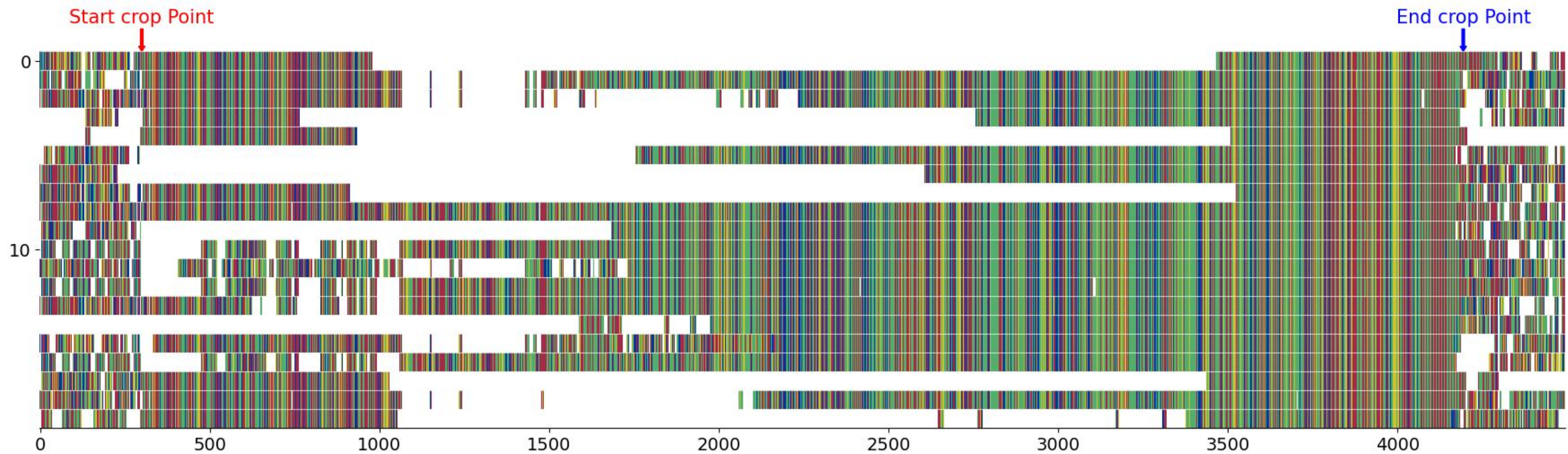


MSA length = 3895

[illegible]

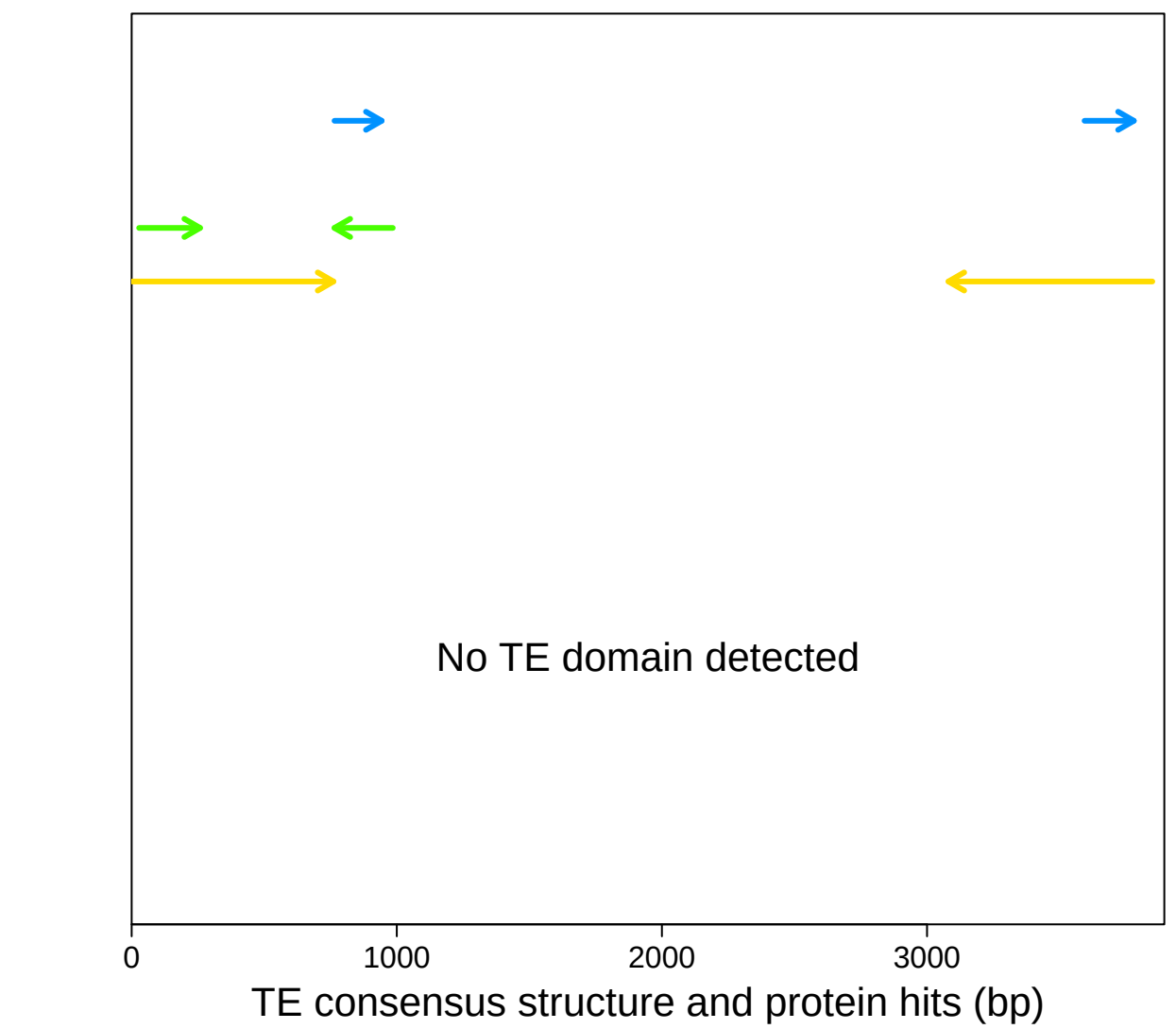
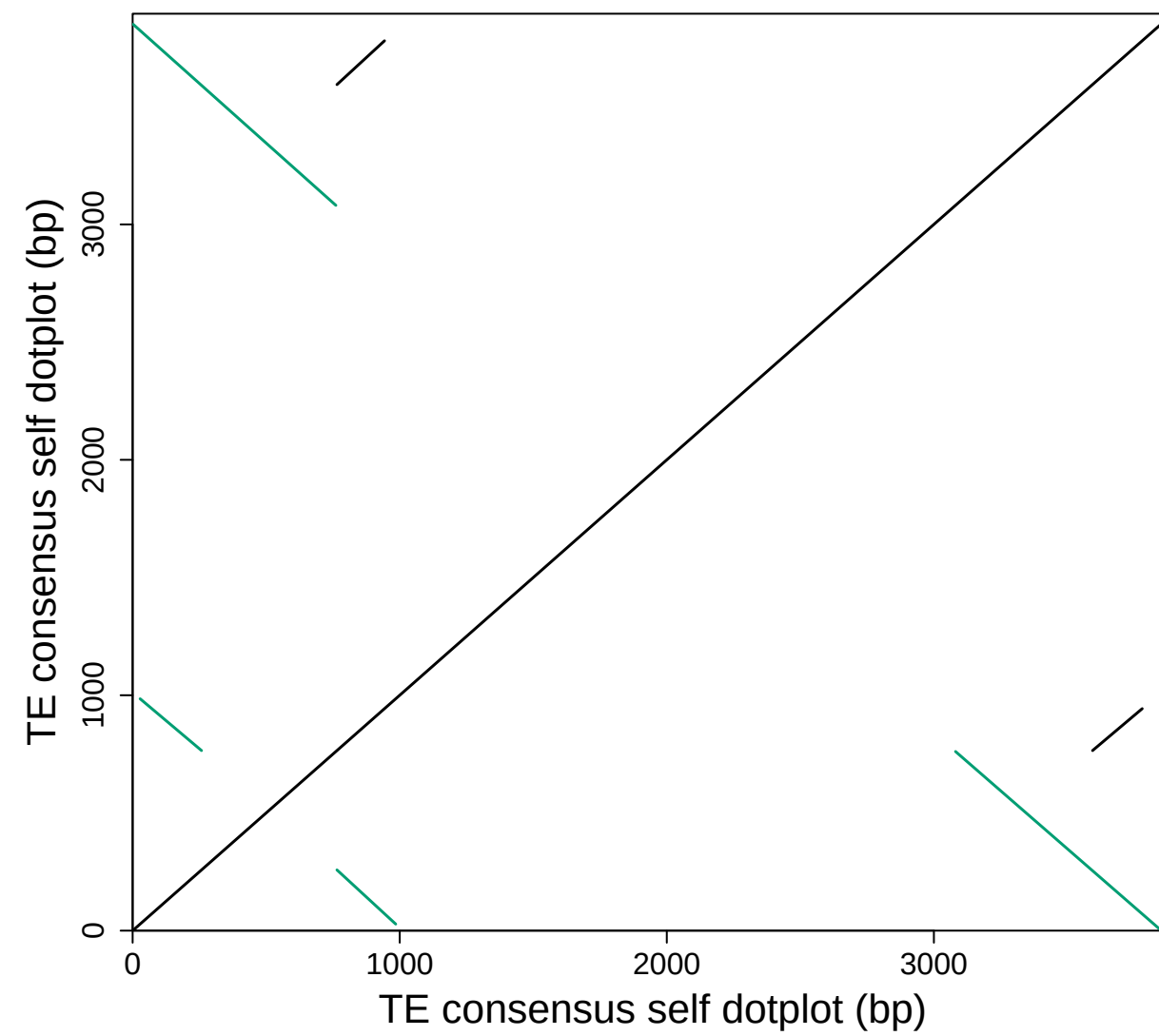
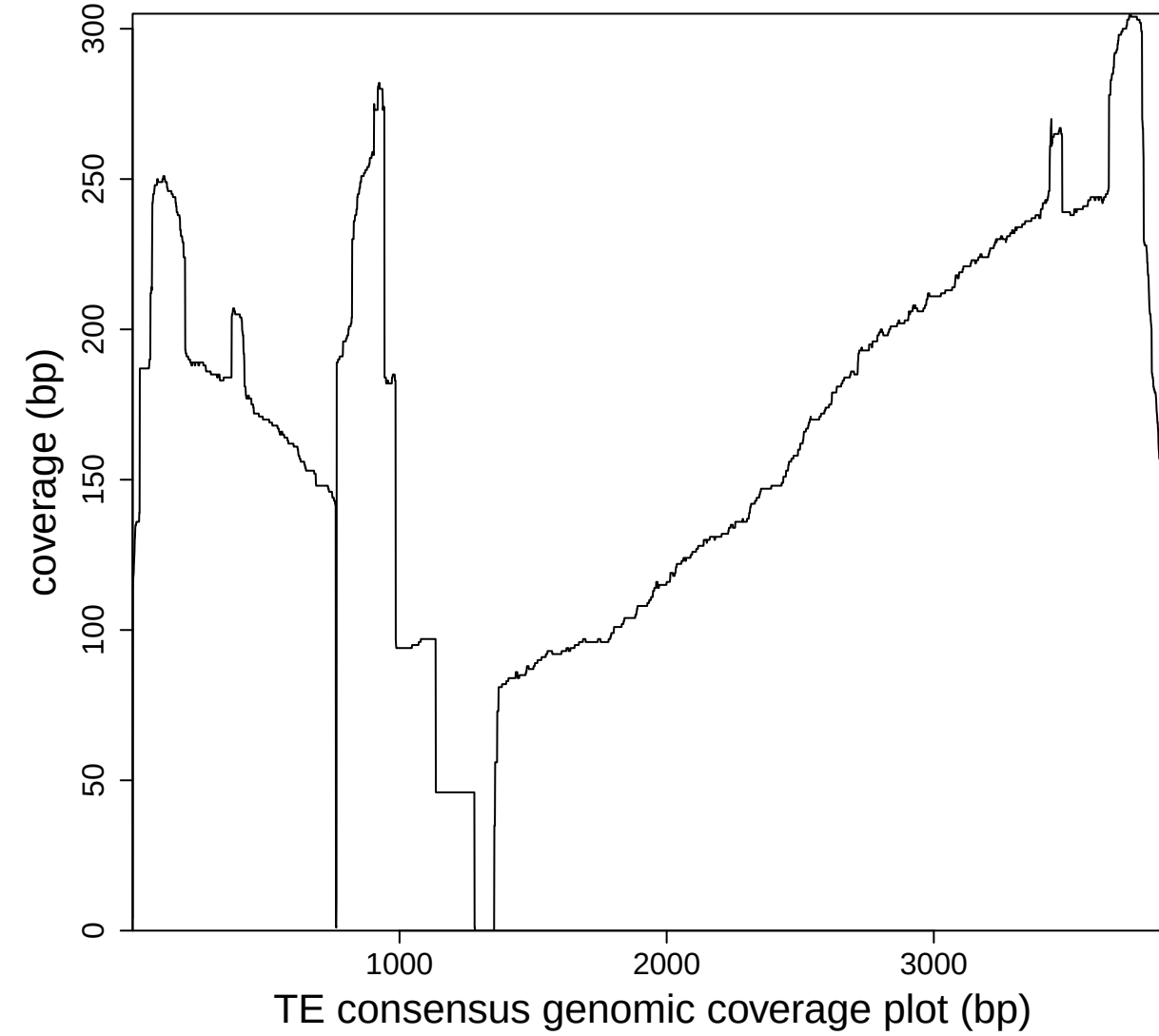
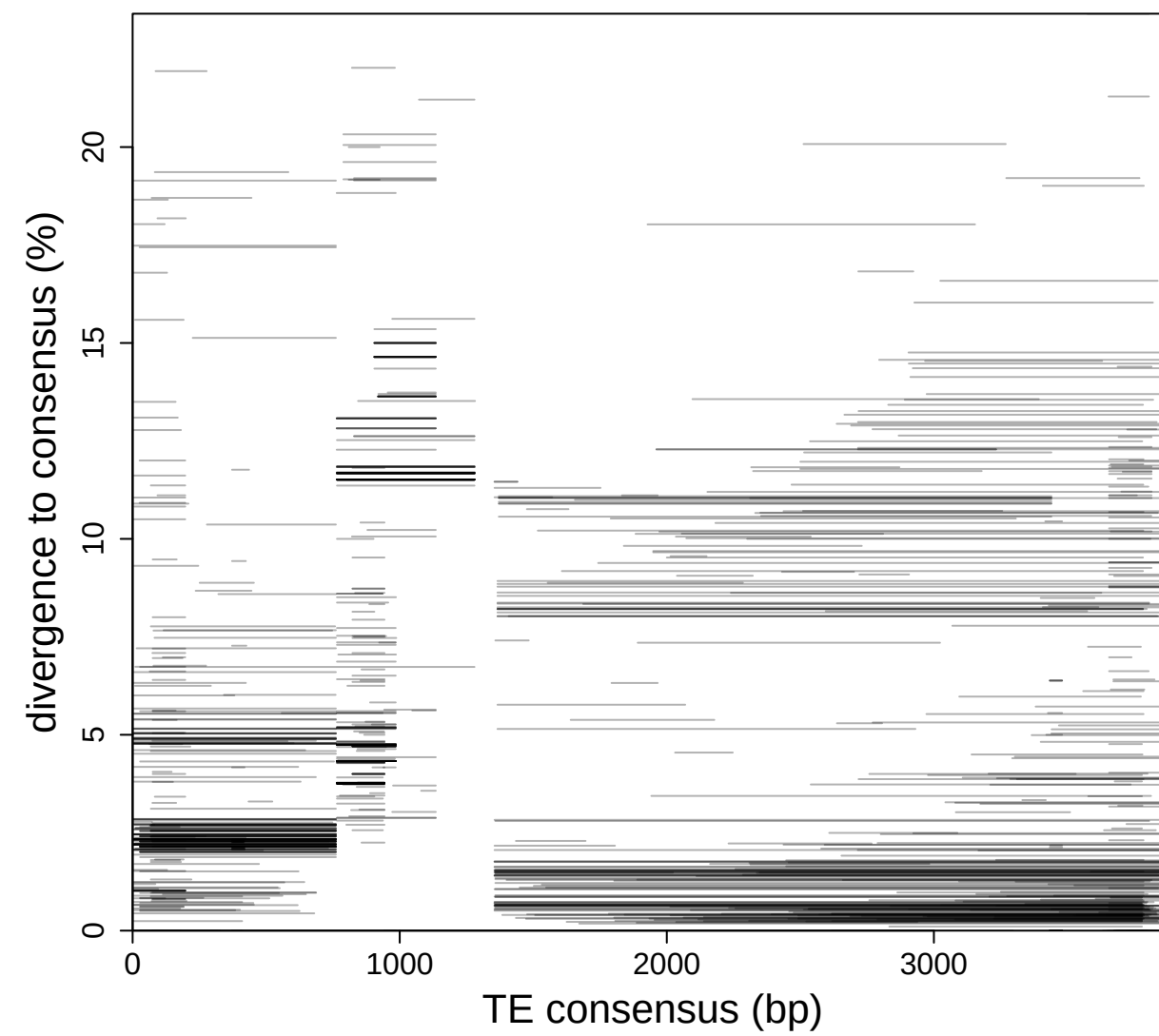
Start crop Point

End crop Point



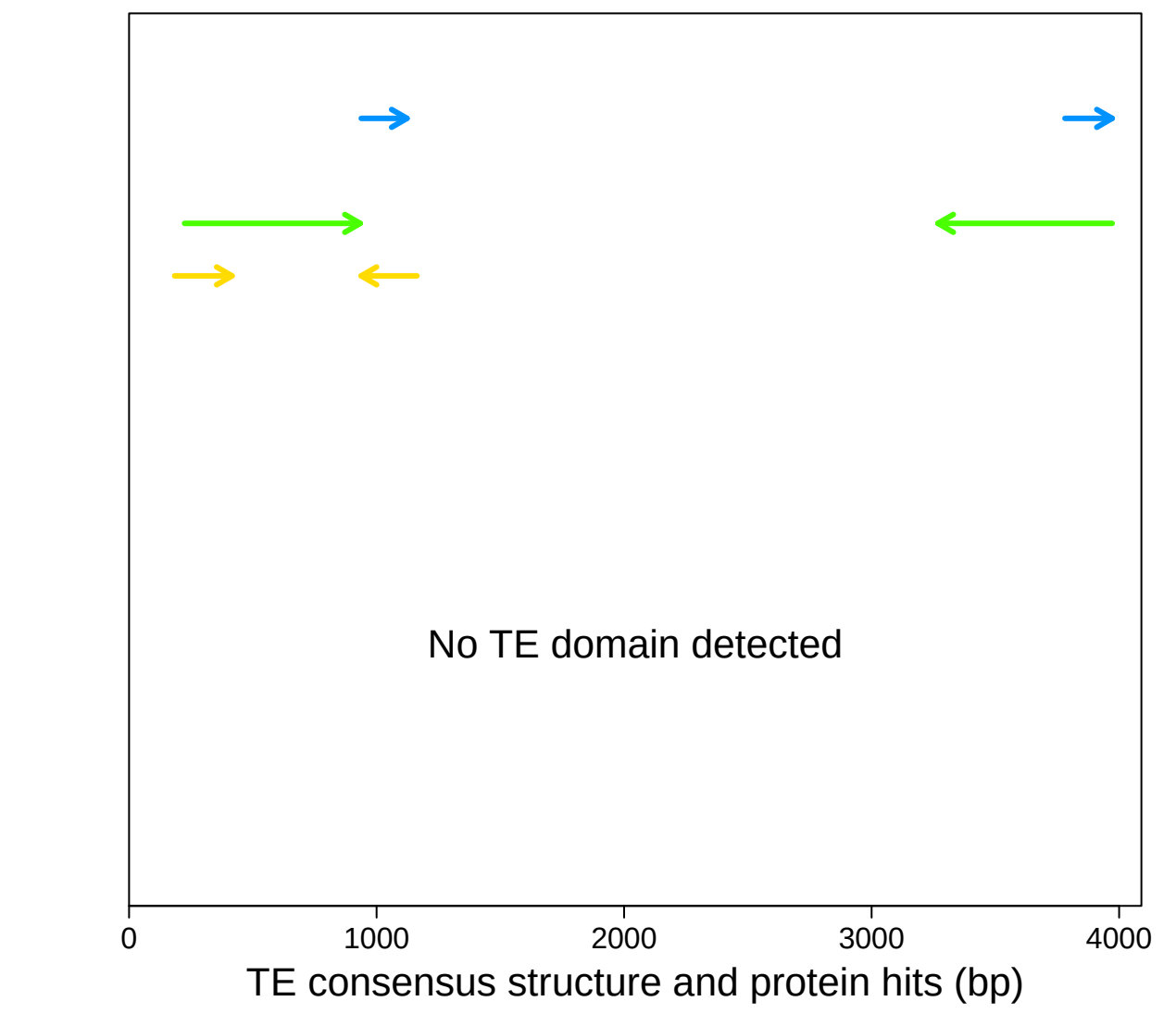
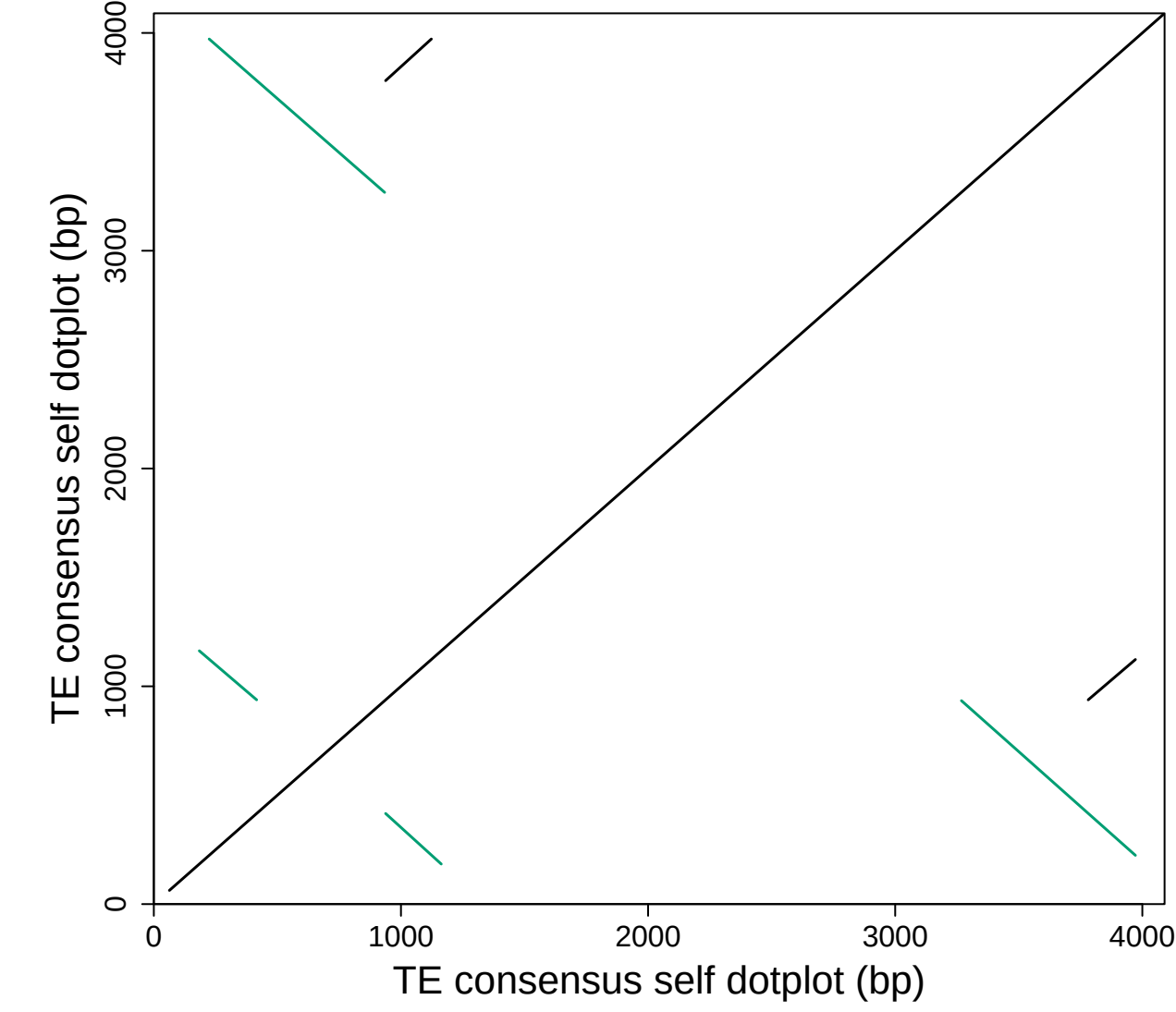
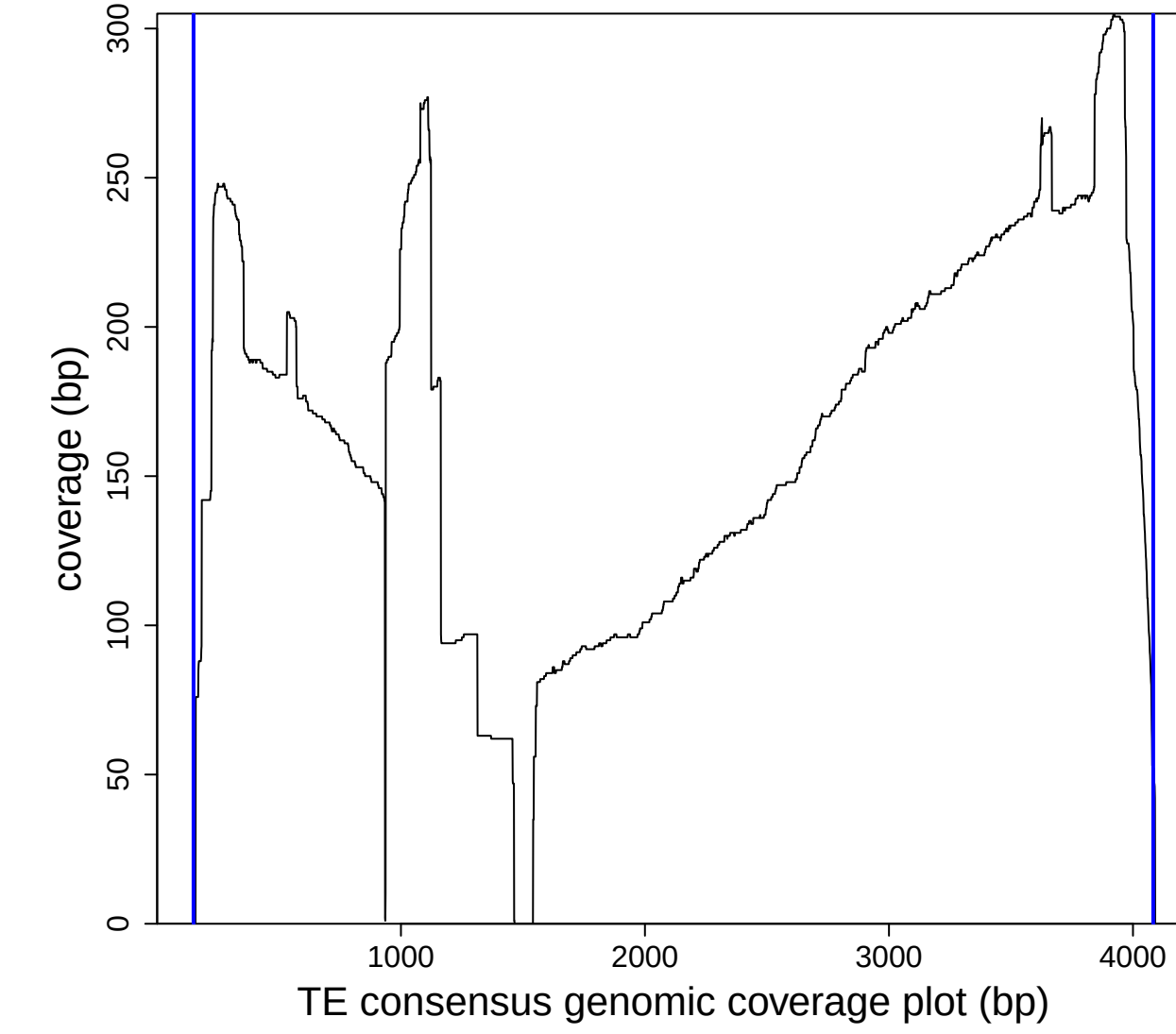
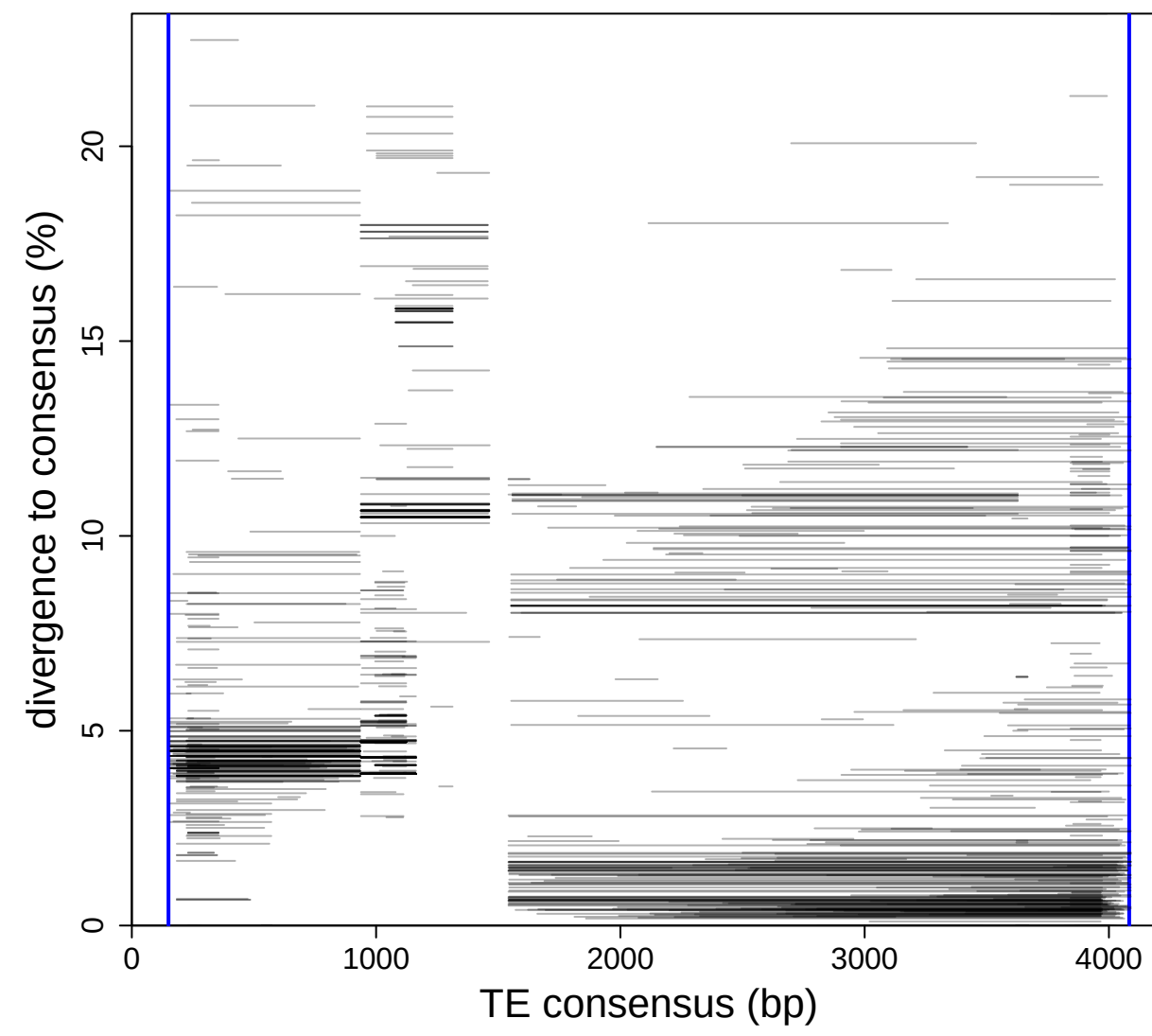
a.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.f
size: 3895bp; fragments: 974; full length: 0 (>=3505.5bp)

After TEtrimmer 3895 bp

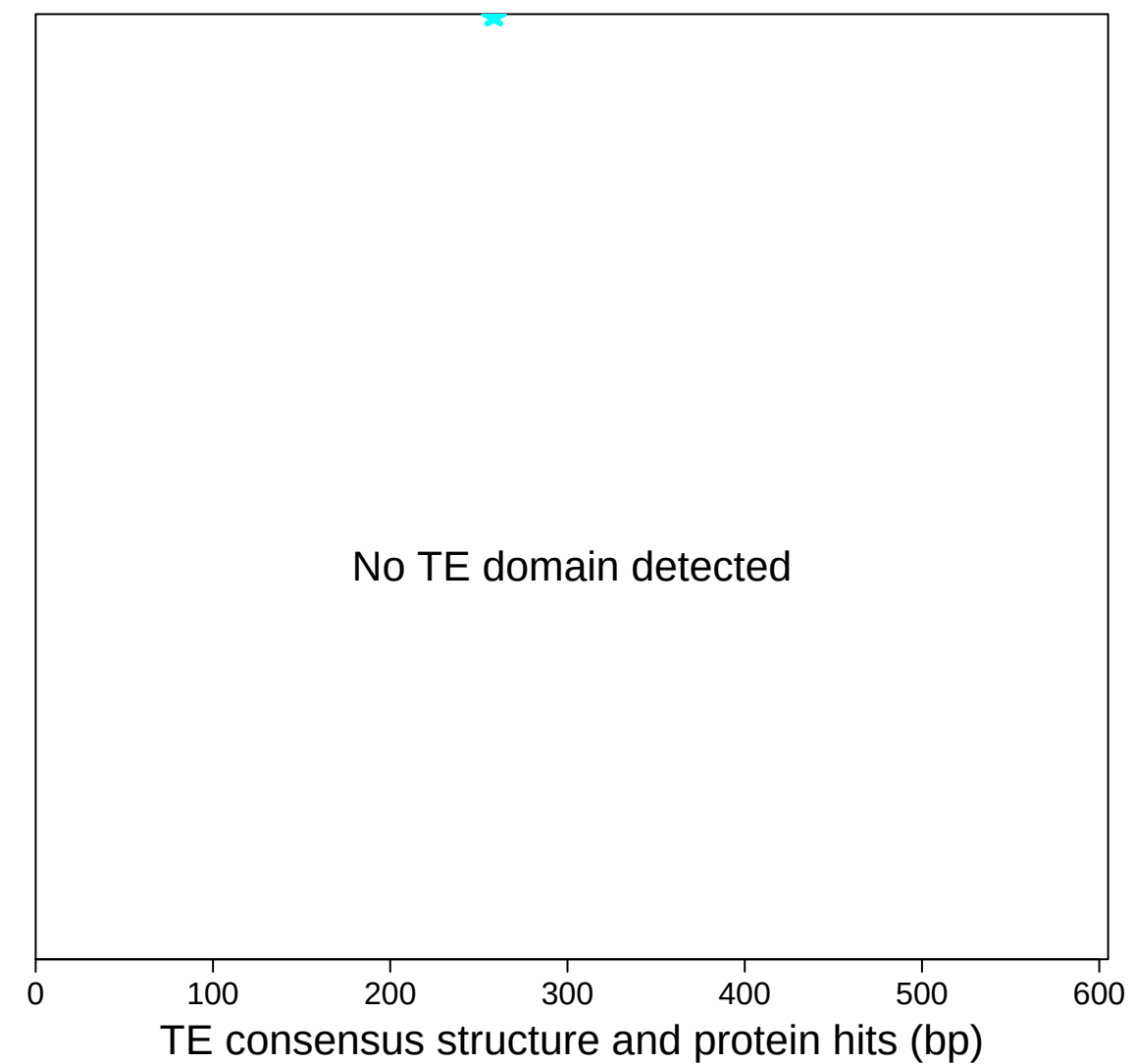
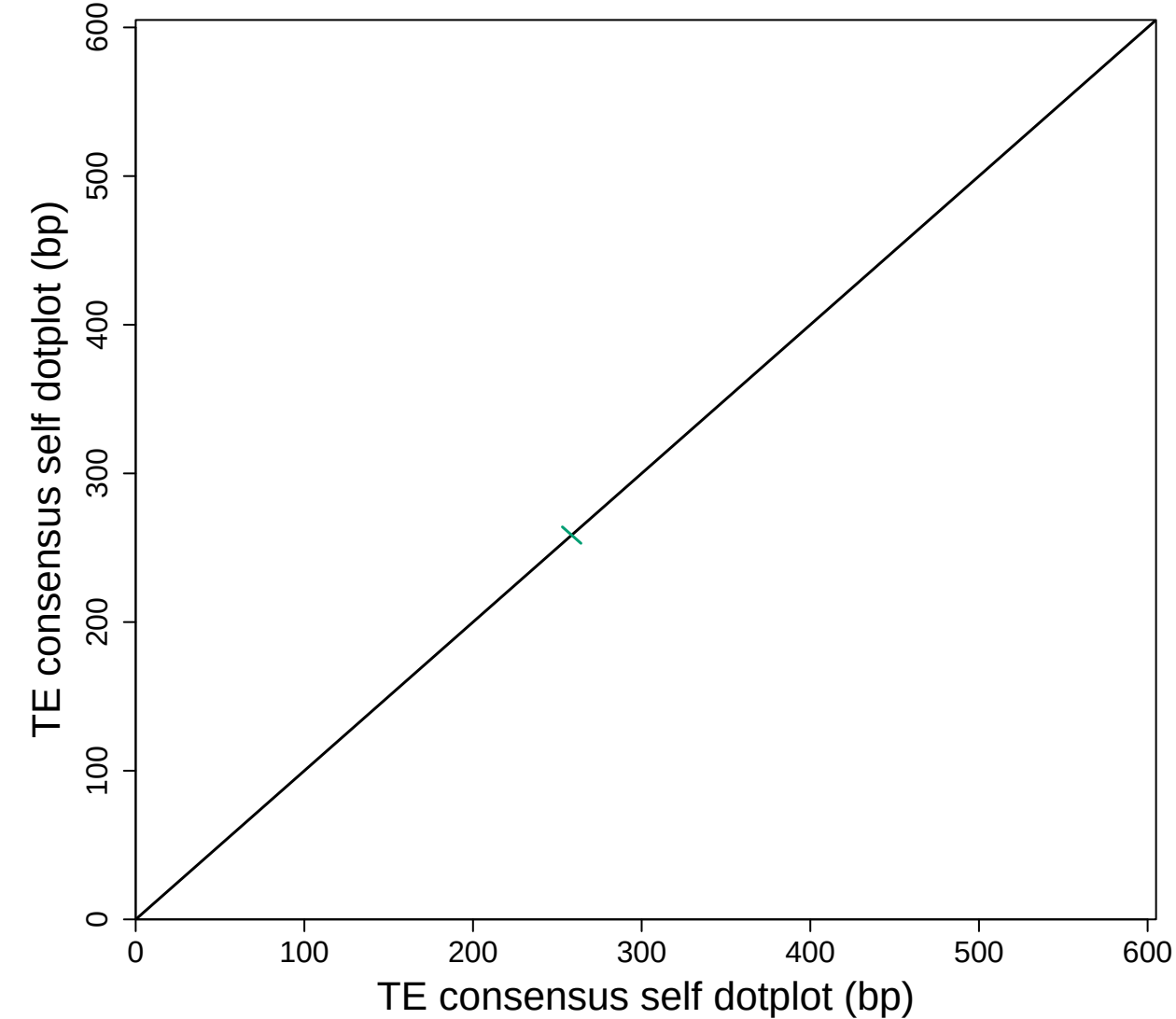
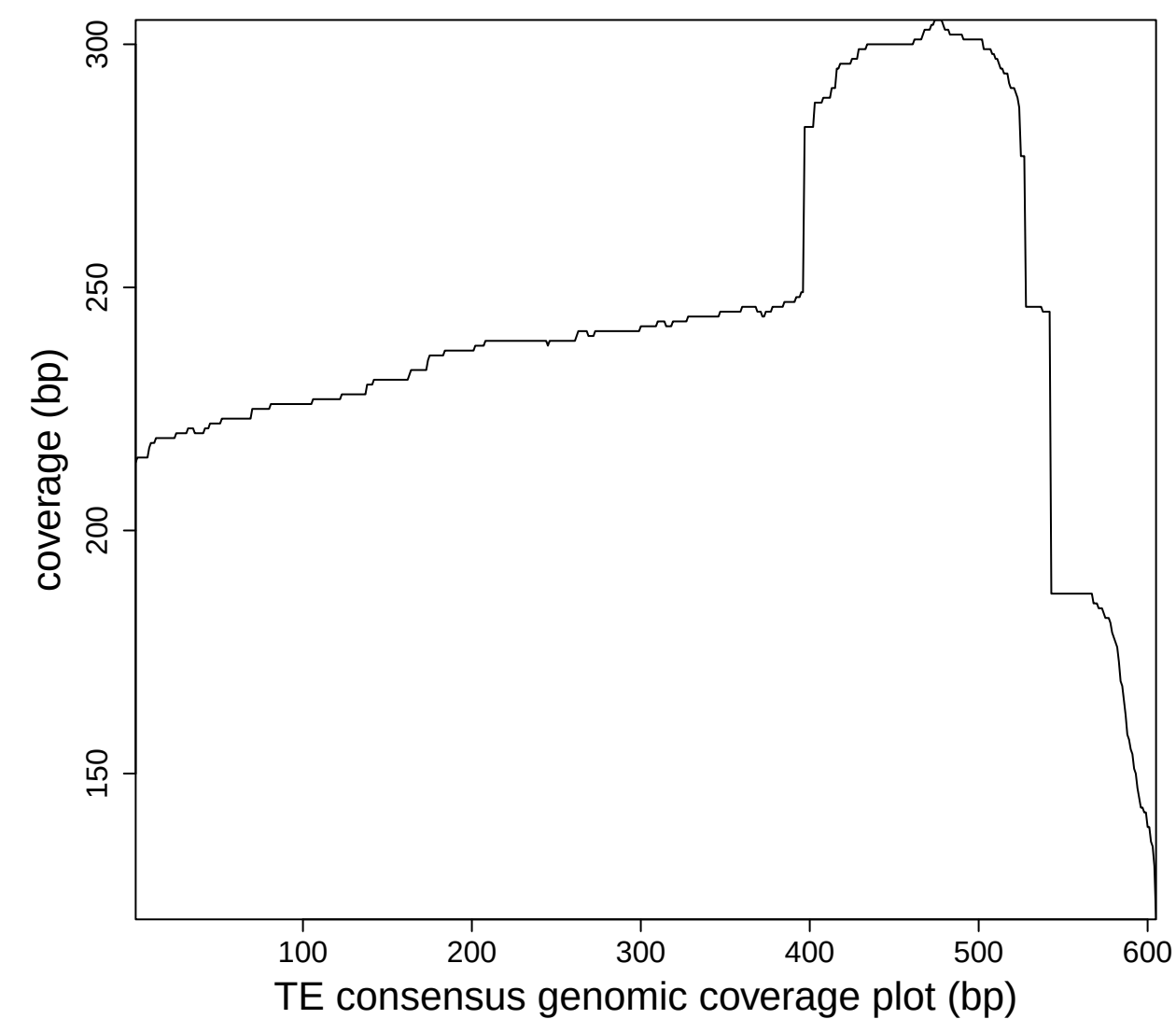
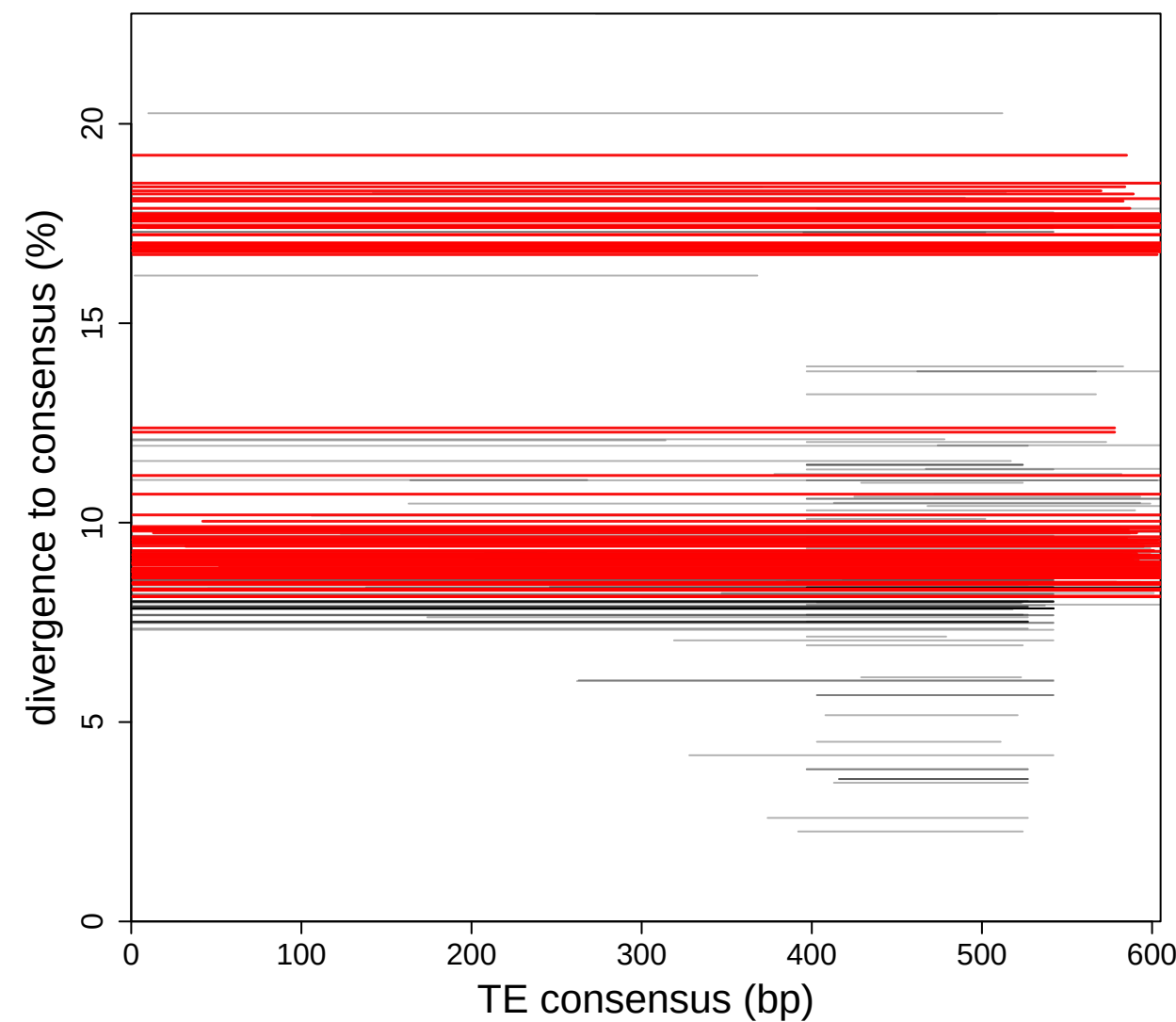


5.fasta.b.bed uf.bed g_3.bed fm_1.bed 0 0 bcln.fa aln.fa cl.f
size: 4233bp; fragments: 965; full length: 0 (>=3809.7bp)

After TEtrimmer Extended plot Blue lines are boundaries

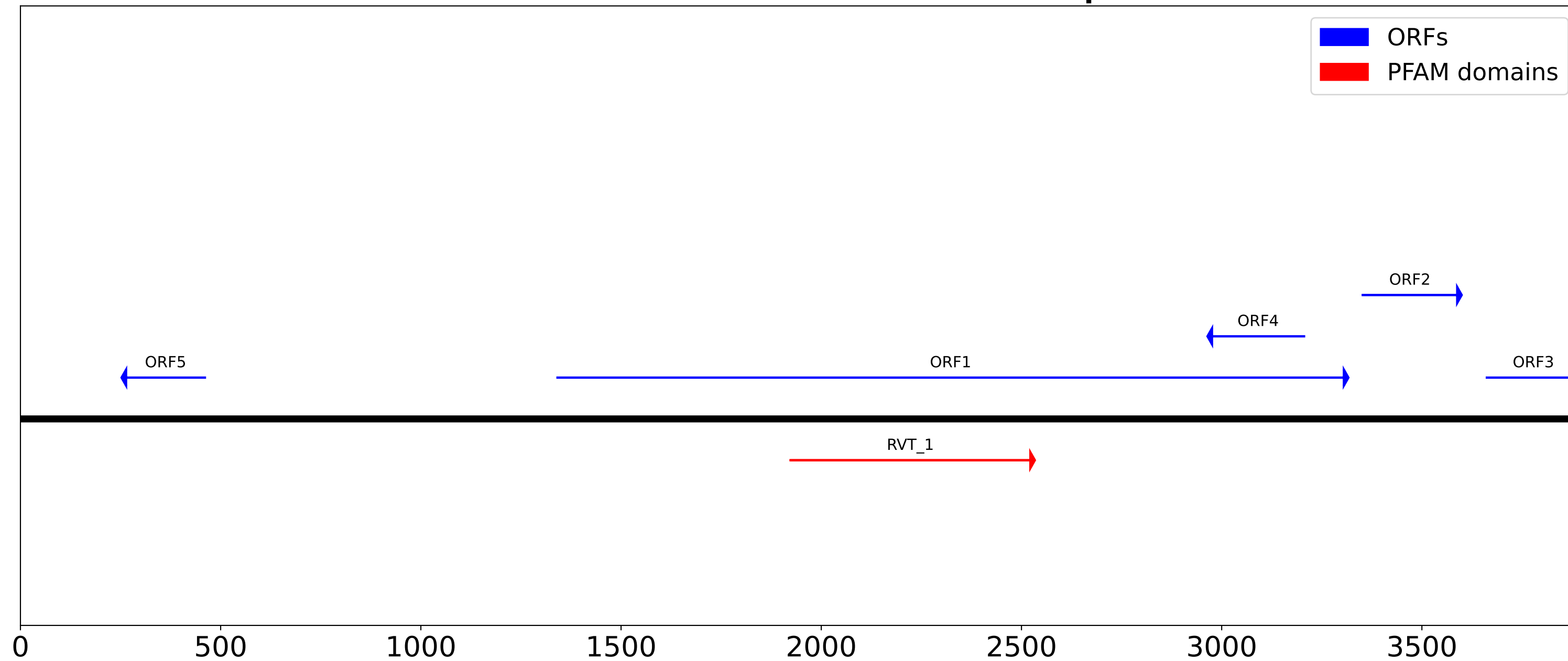


TE: rnd_4_family_1855
size: 605bp; fragments: 311; full length: 143 (≥ 544.5 bp)



Before TEtrimmer 605 bp

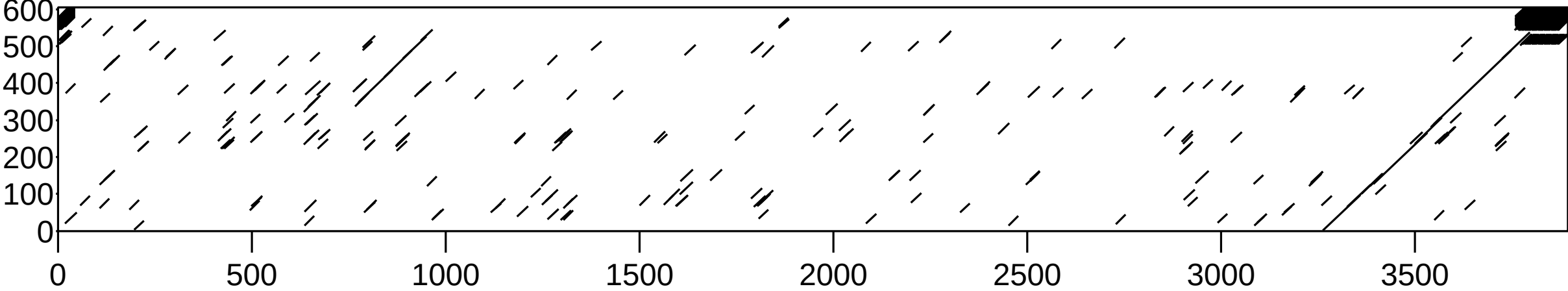
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

1sensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)