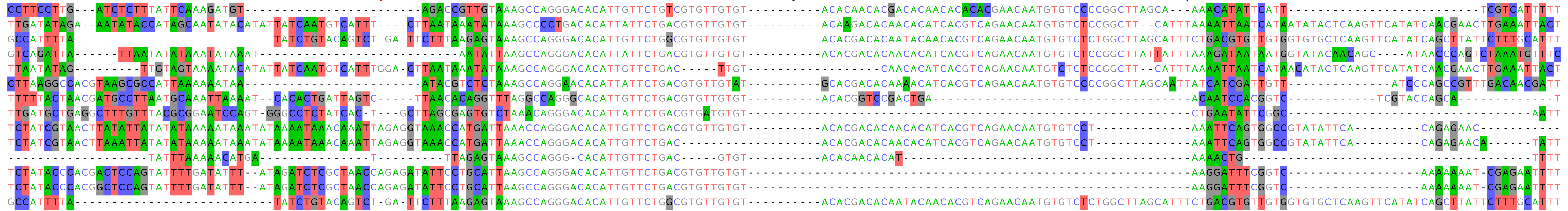
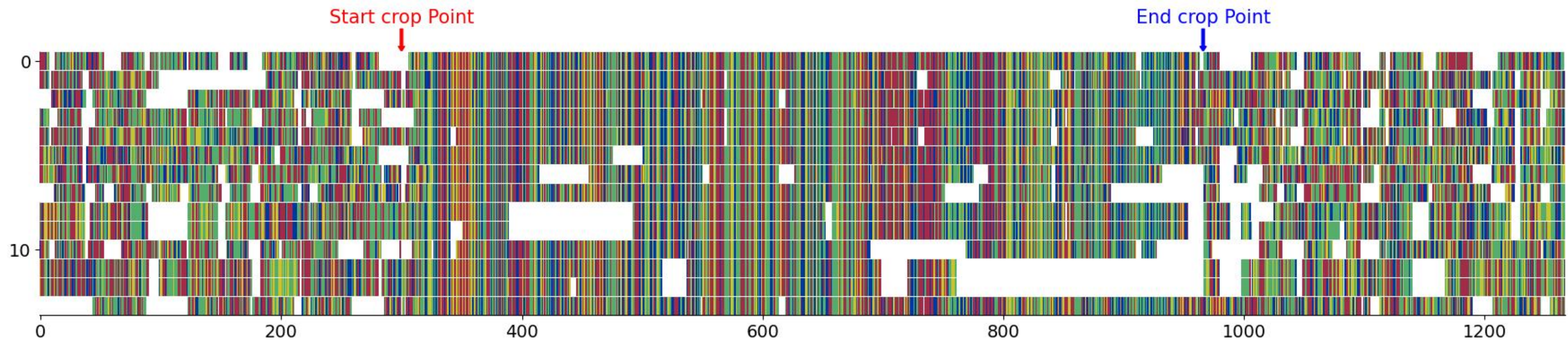




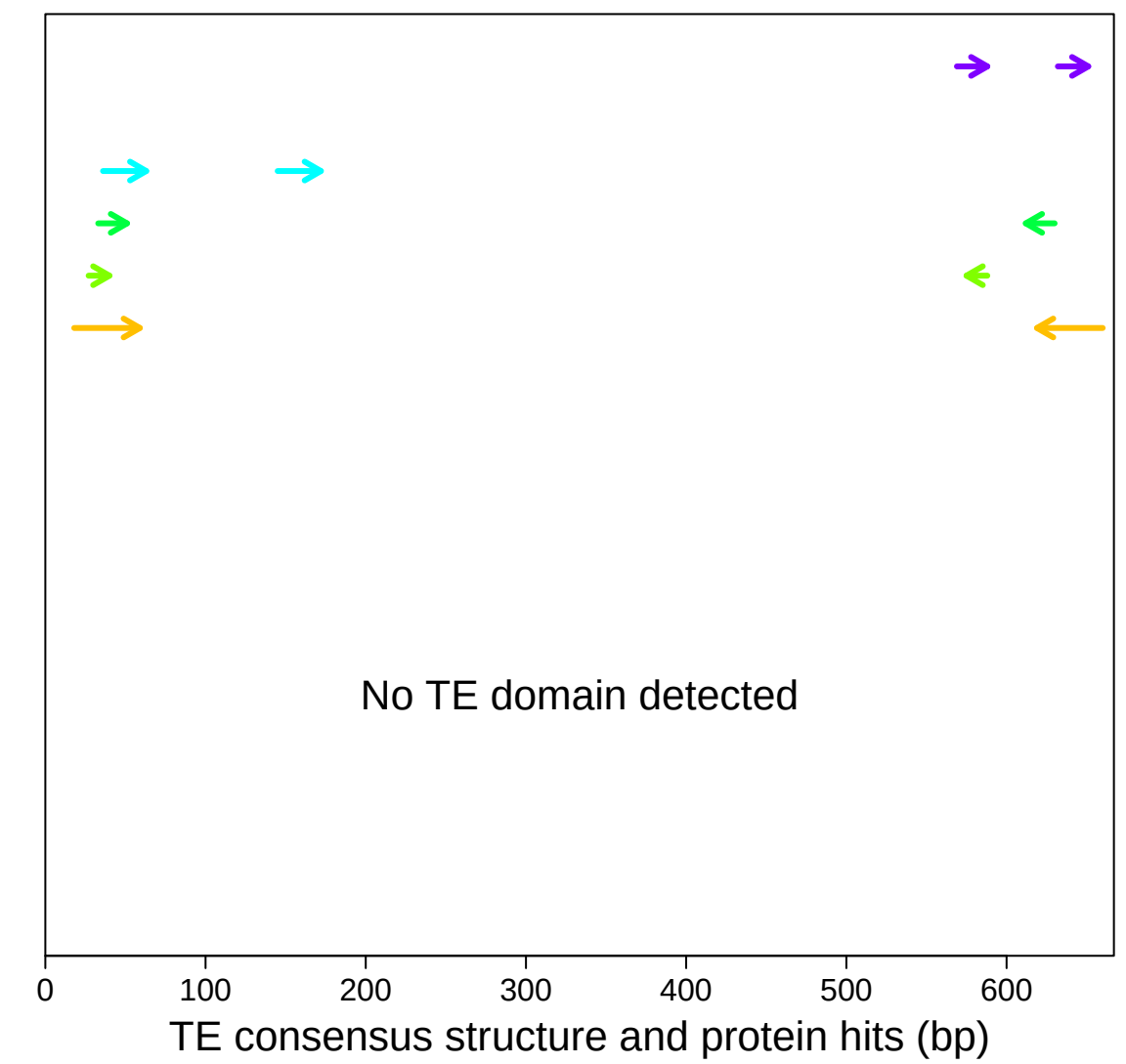
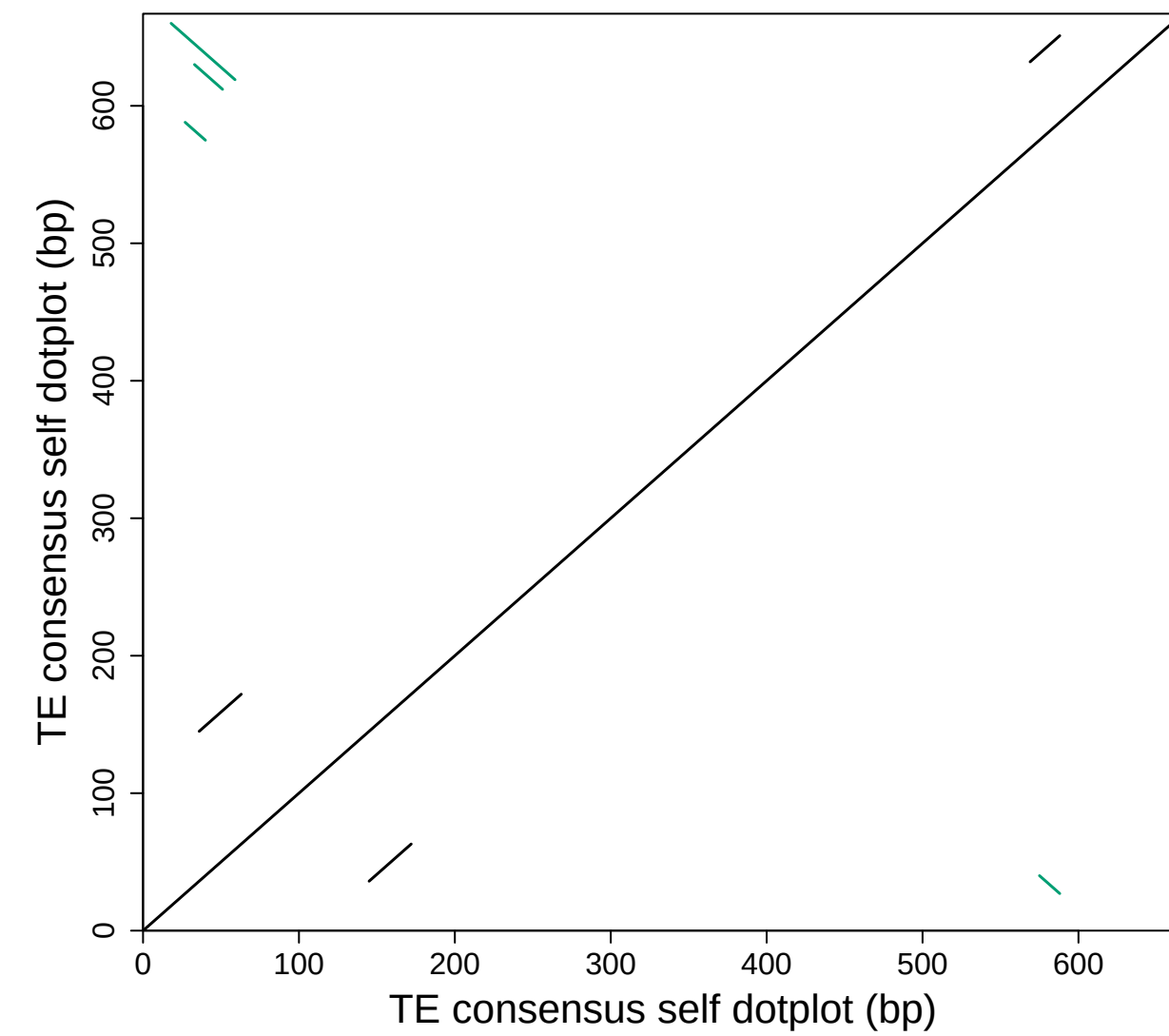
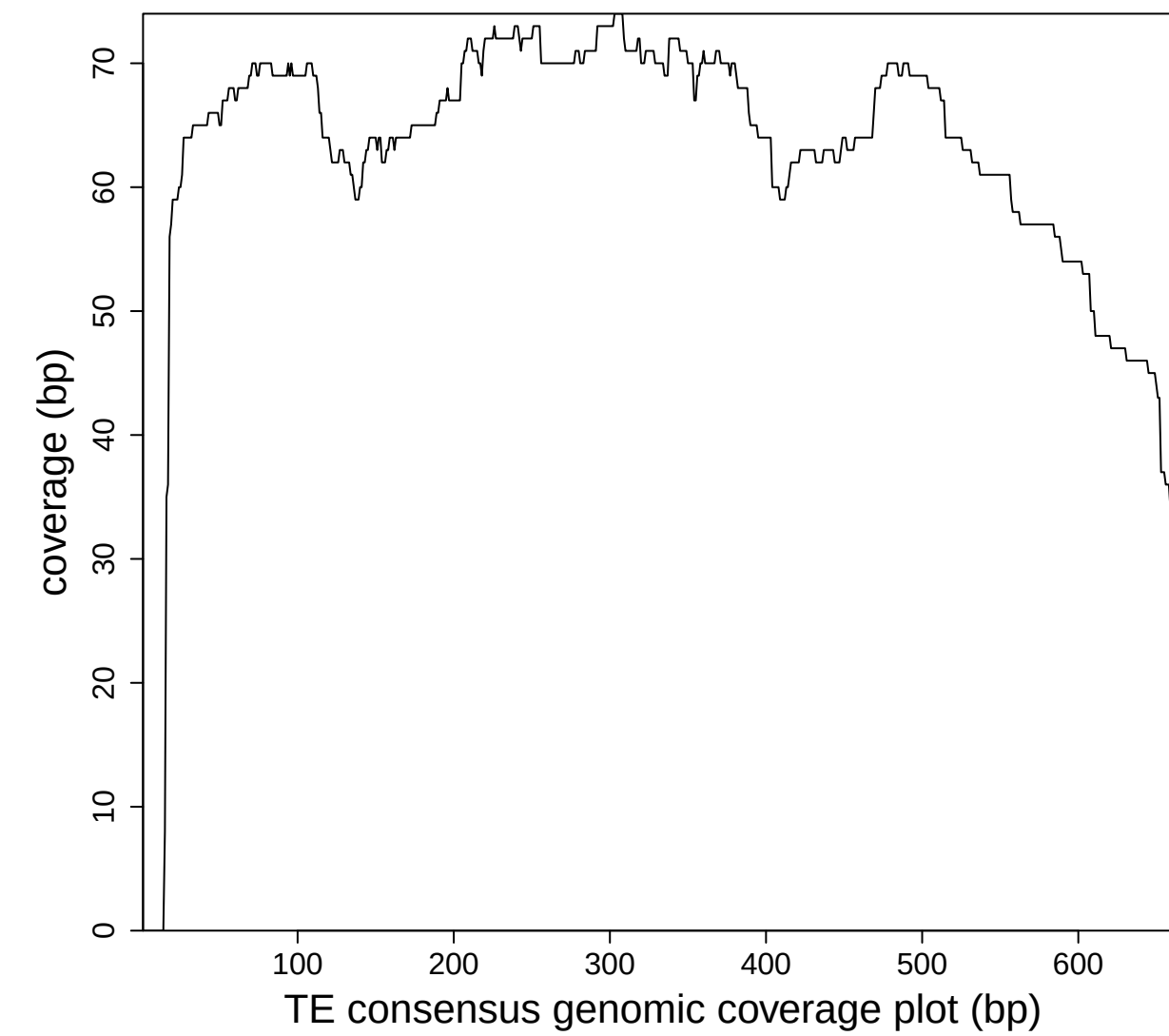
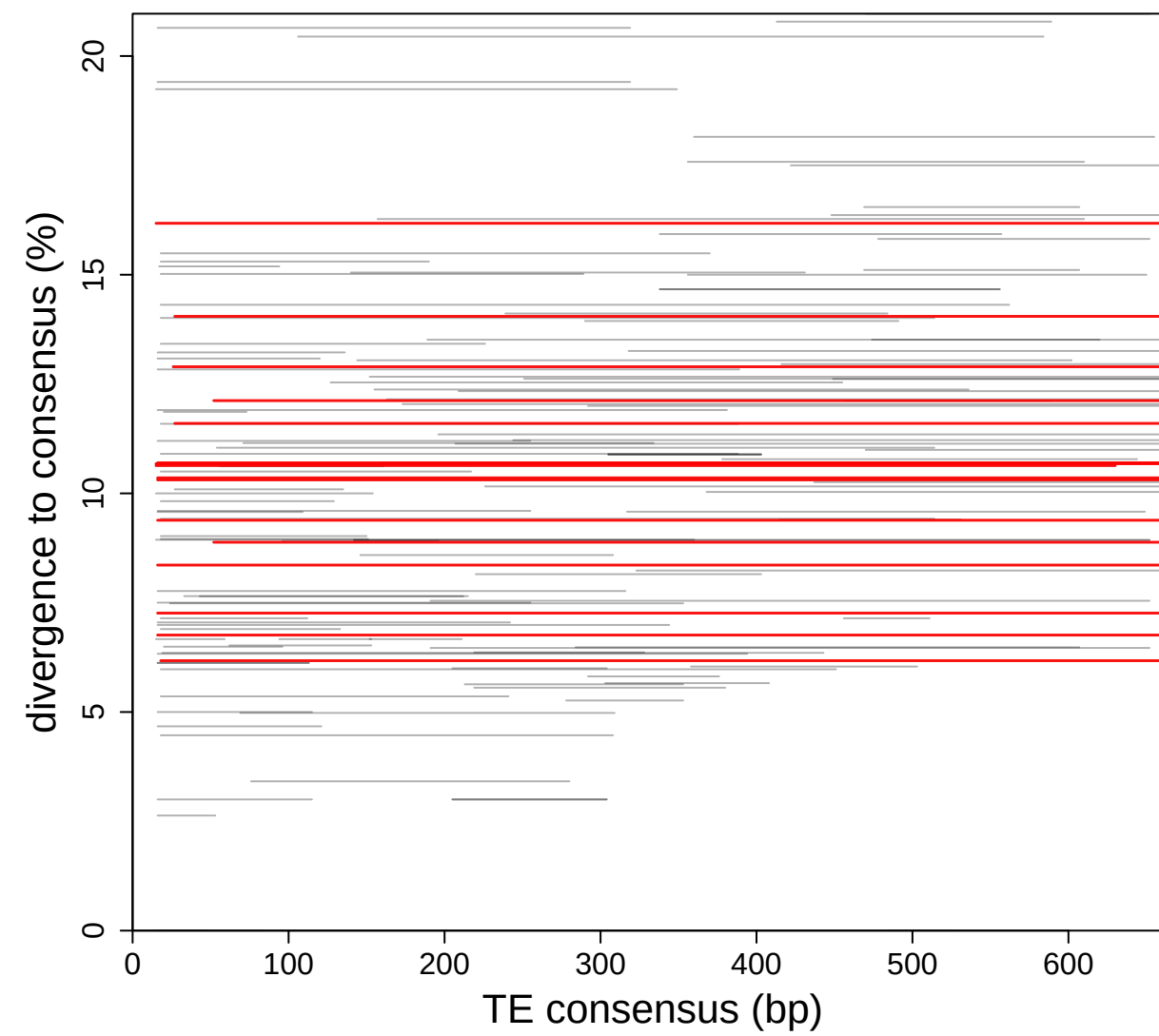
MSA length = 667





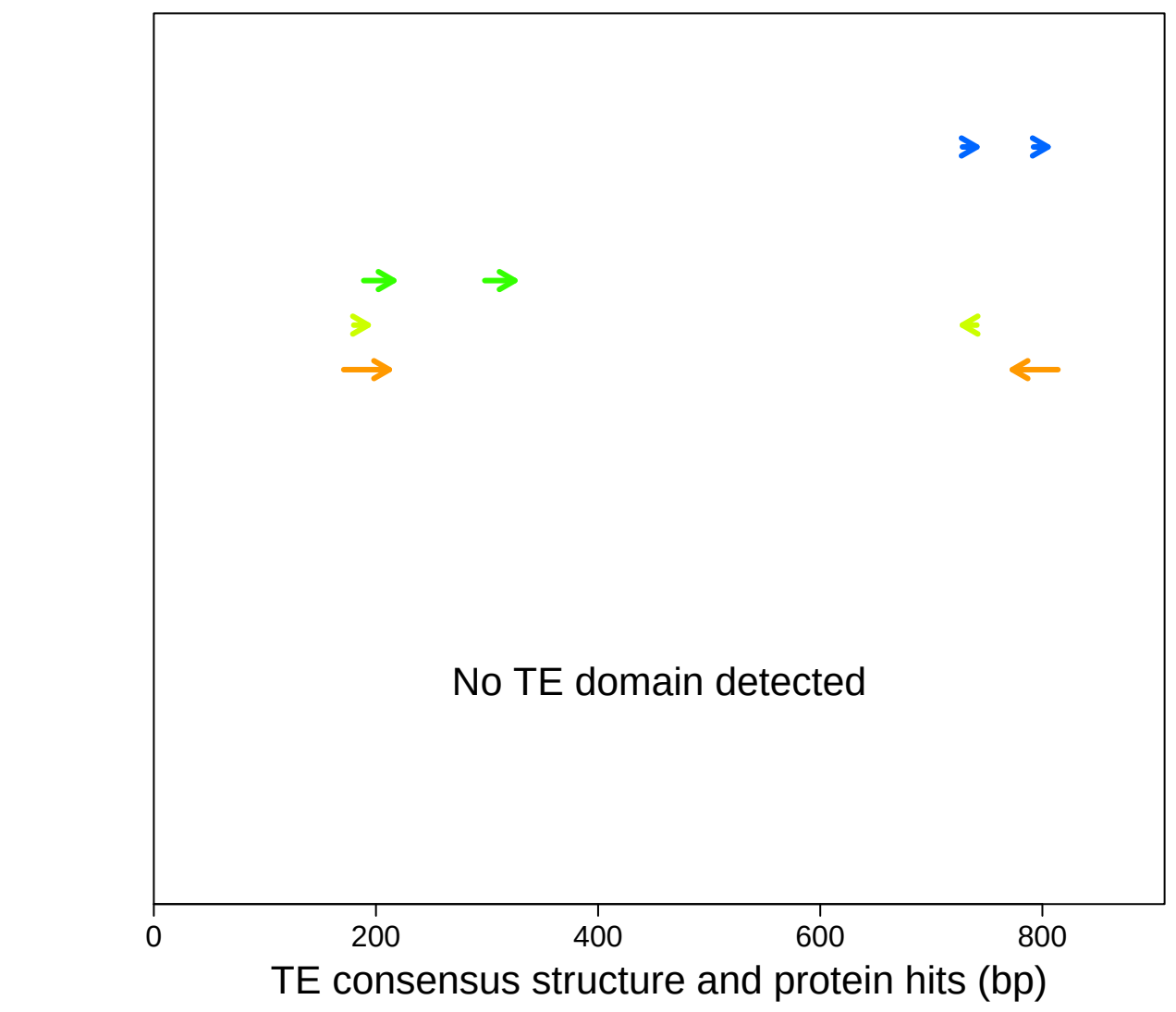
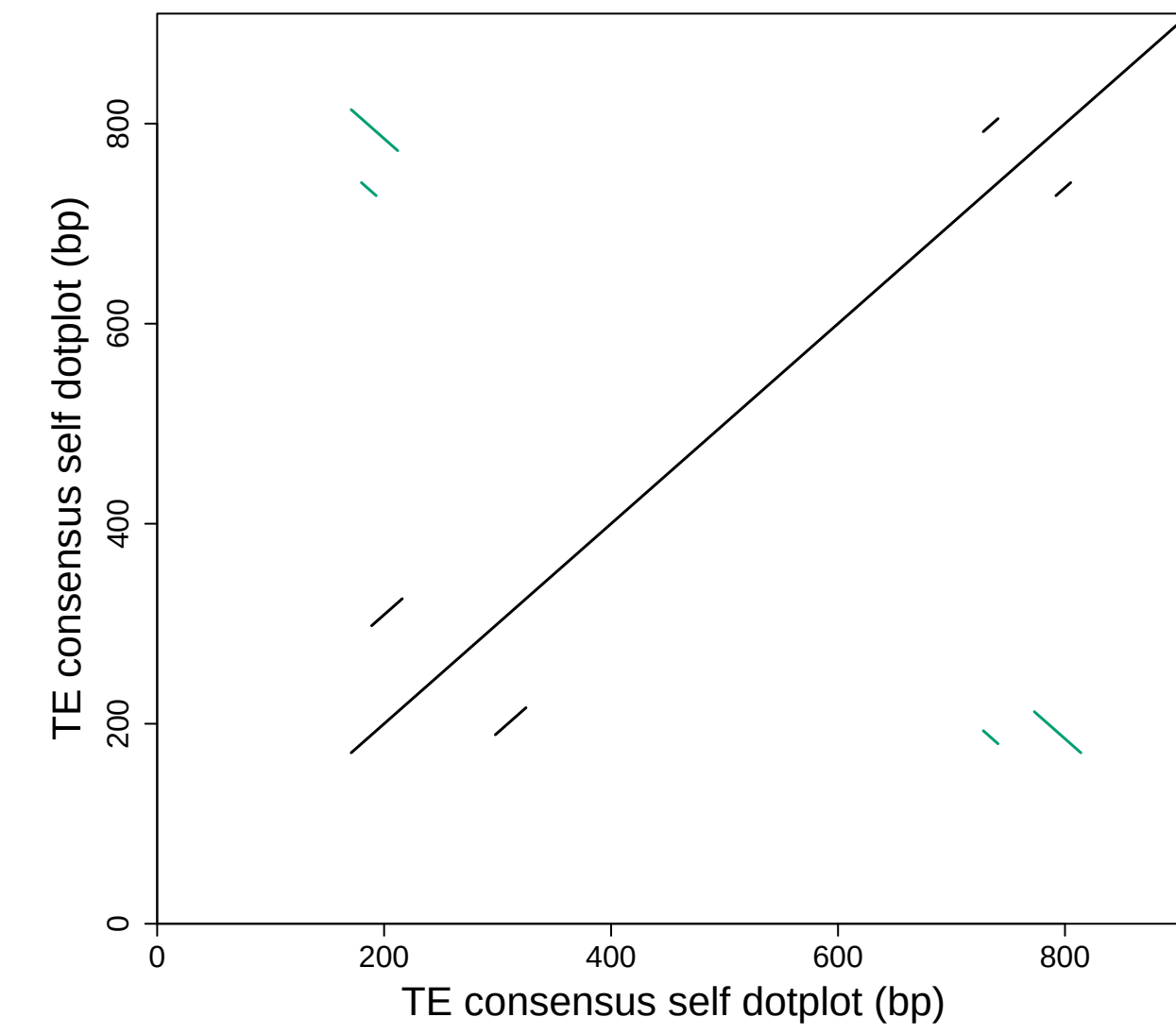
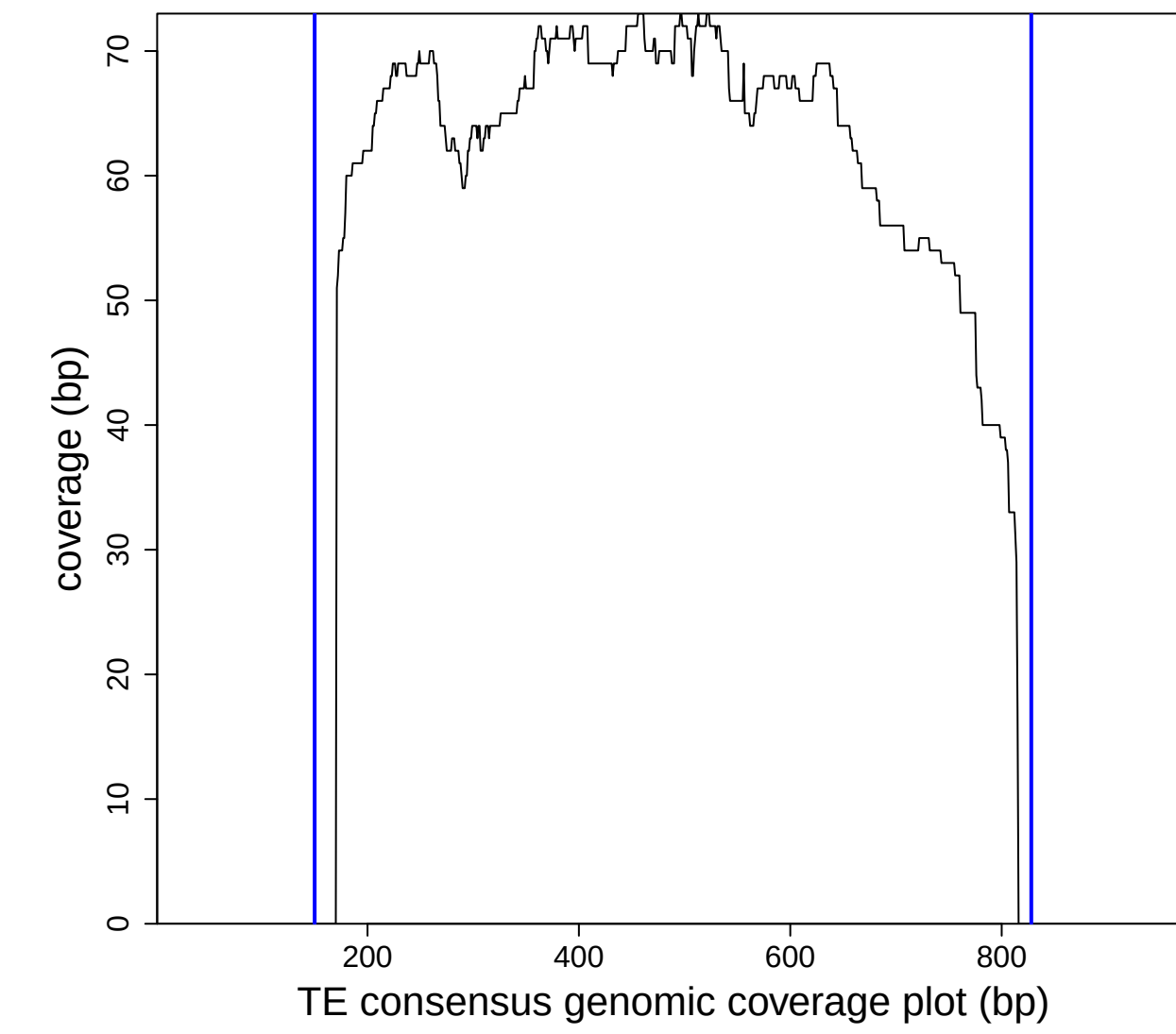
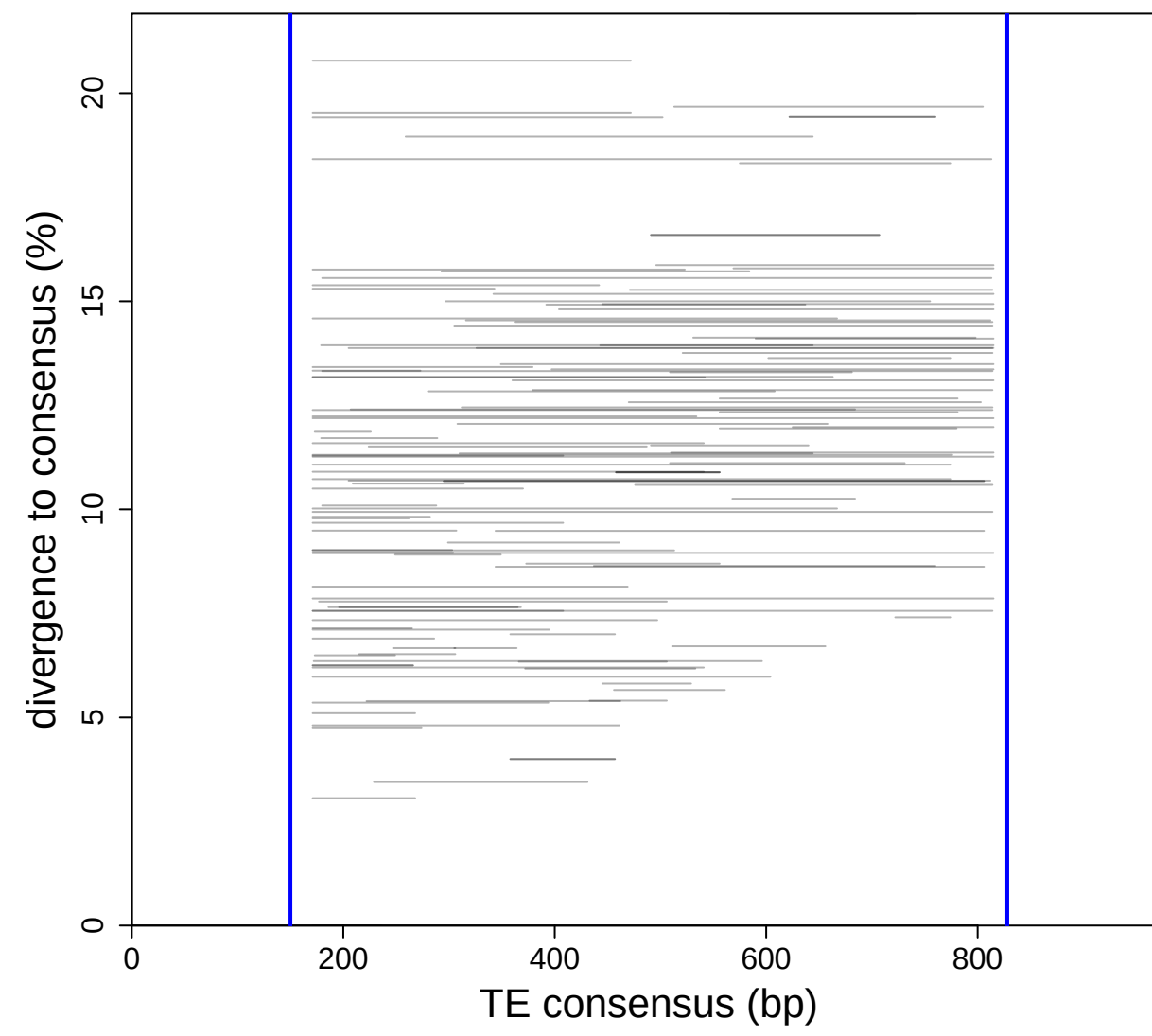
a.b.bed_uf.bed_g_1.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_gs.f
size: 667bp; fragments: 144; full length: 16 (≥ 600.3 bp)

After TEtrimmer 667 bp



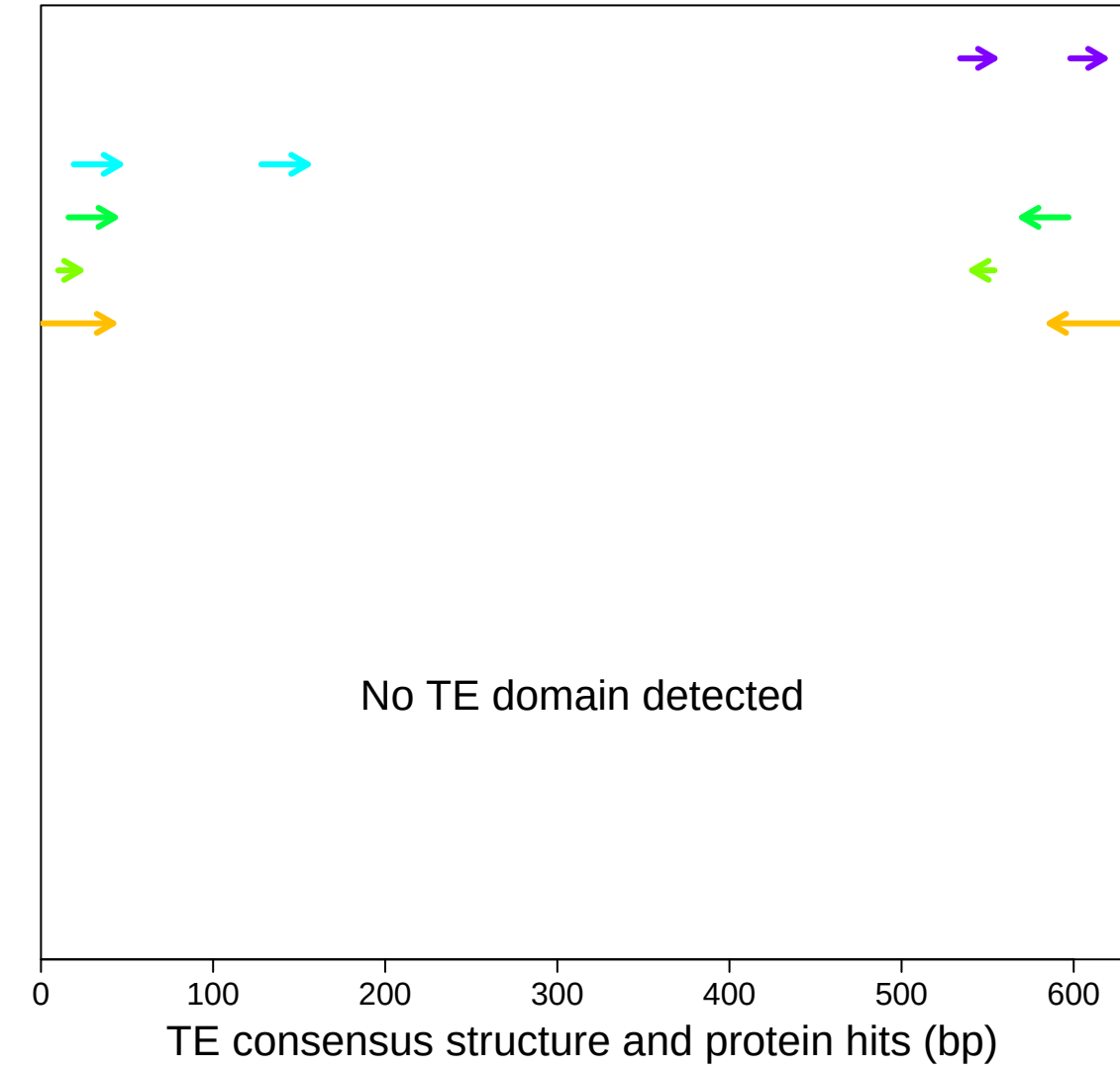
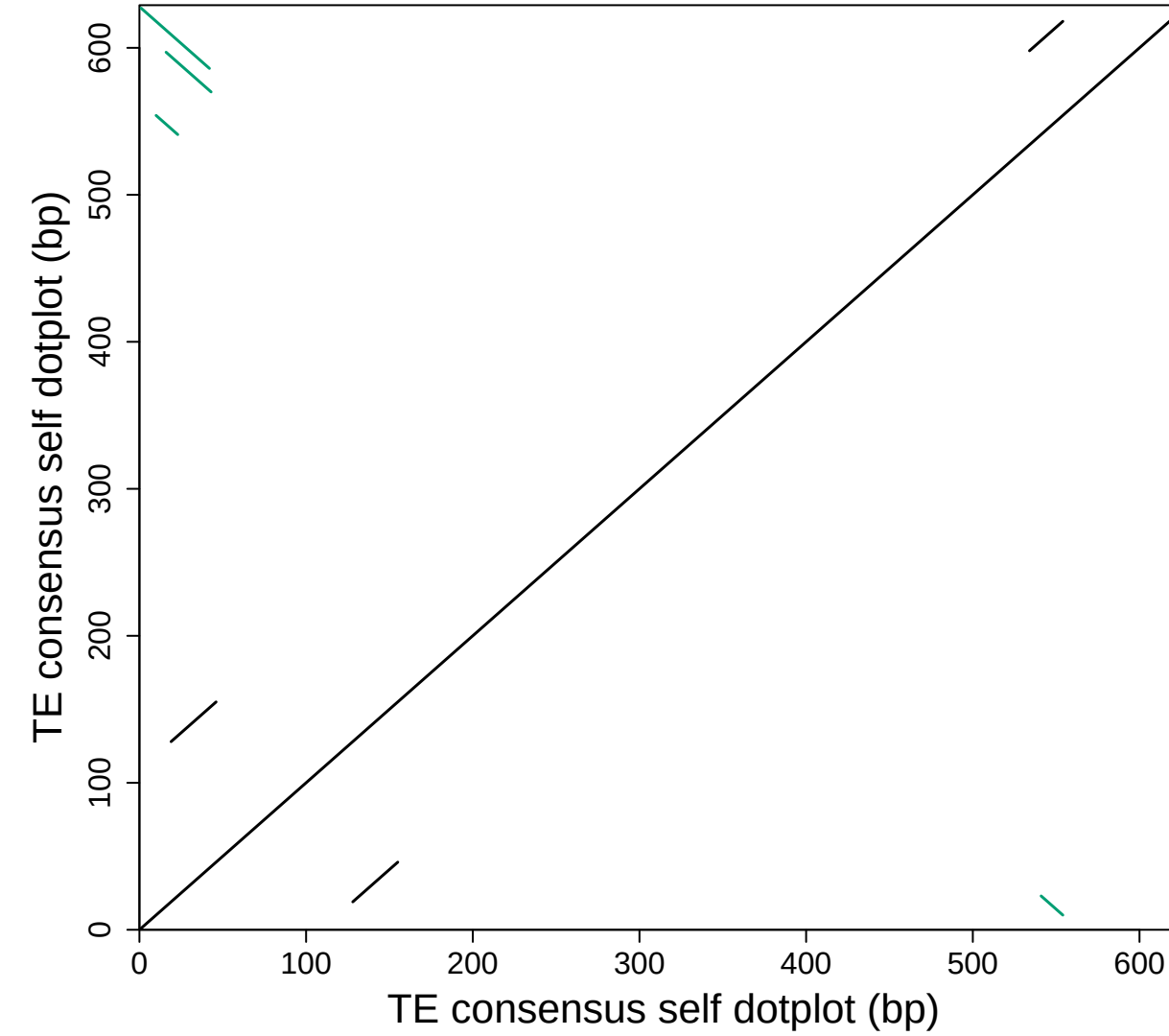
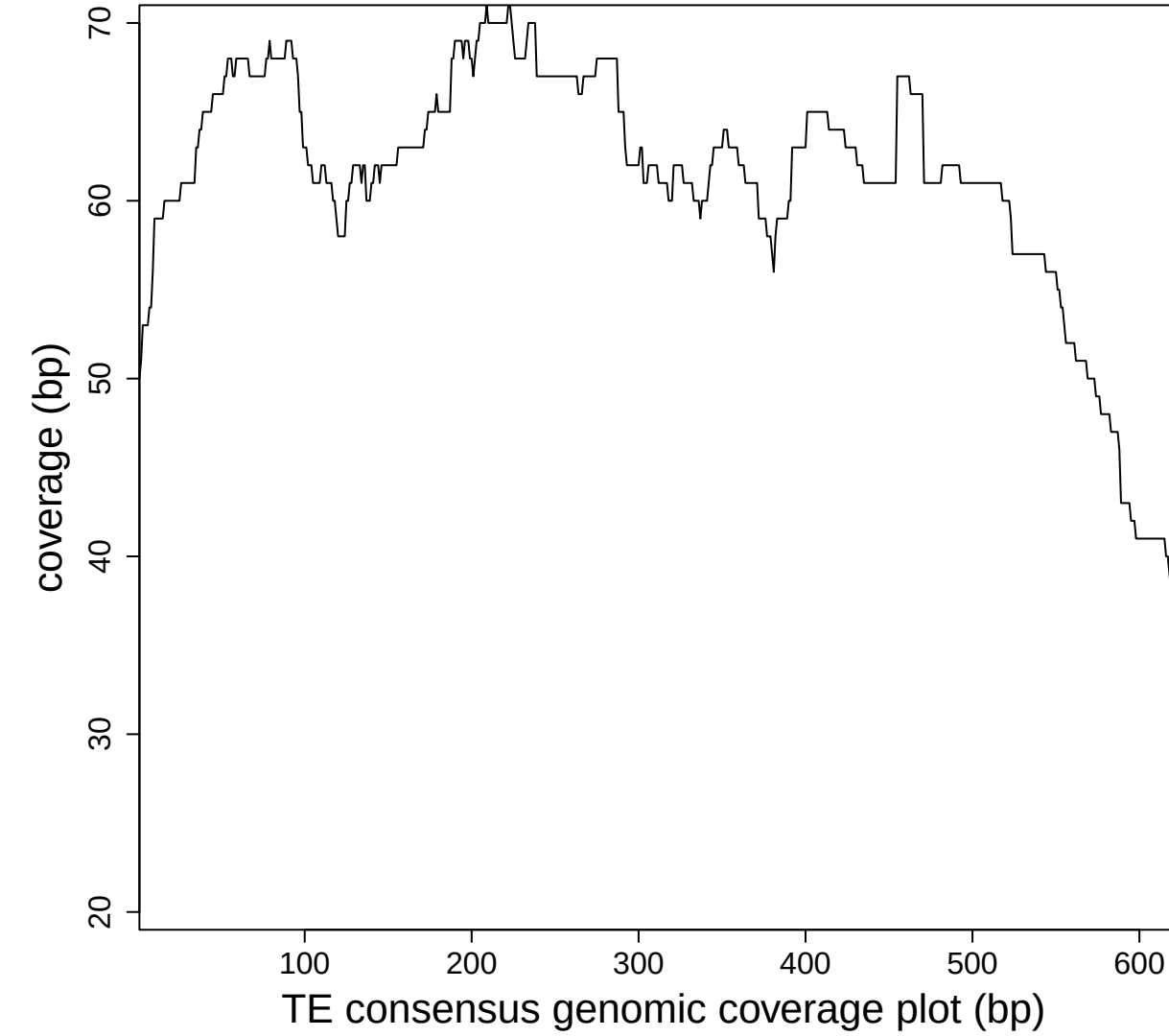
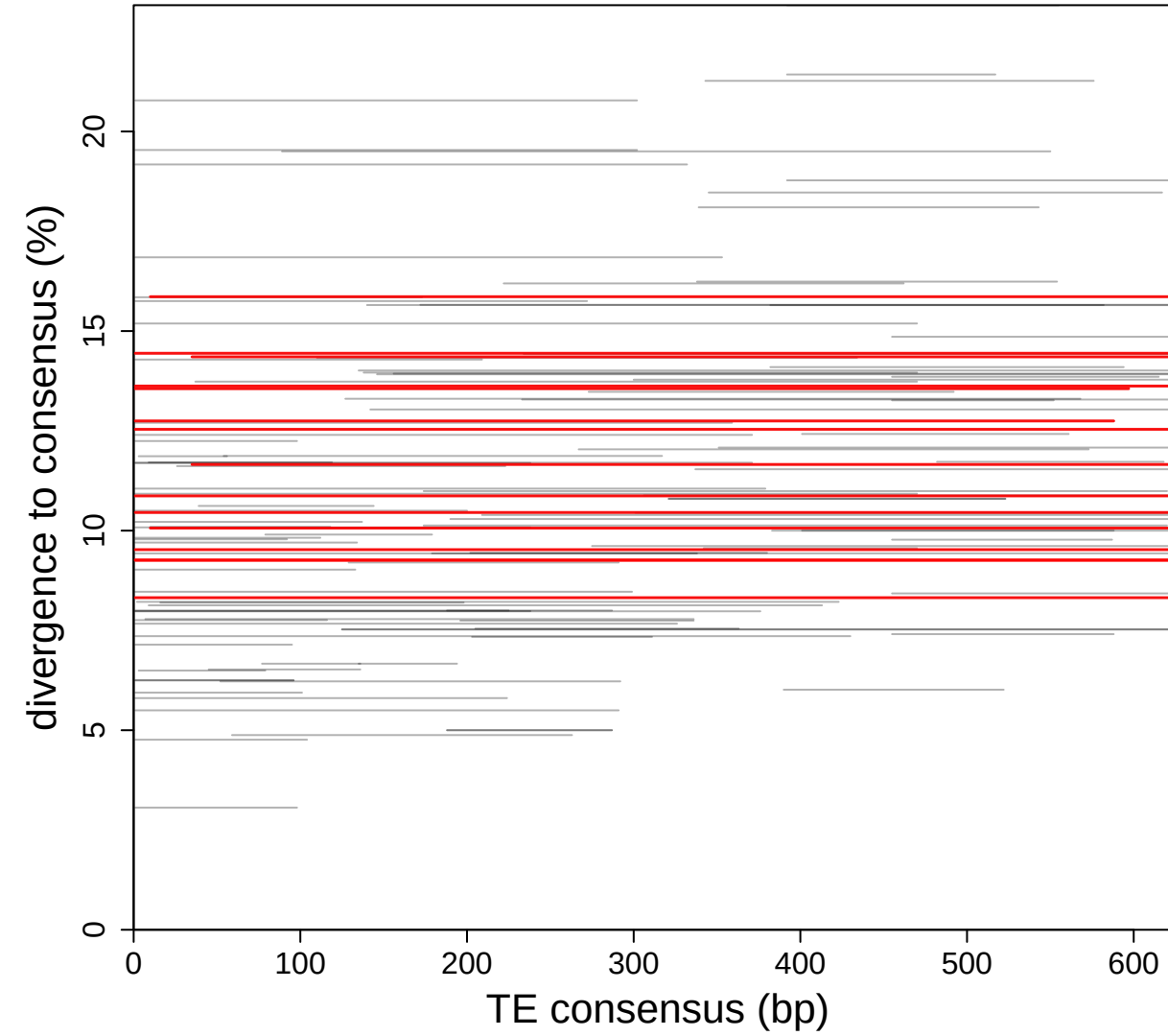
1.fasta.b.bed uf.bed g_1.bed fm_1.bed 0 0 bcIn.fa aln.fa cl.f
size: 978bp; fragments: 138; full length: 0 (>=880.2bp)

After TEtrimmer Extended plot Blue lines are boundaries

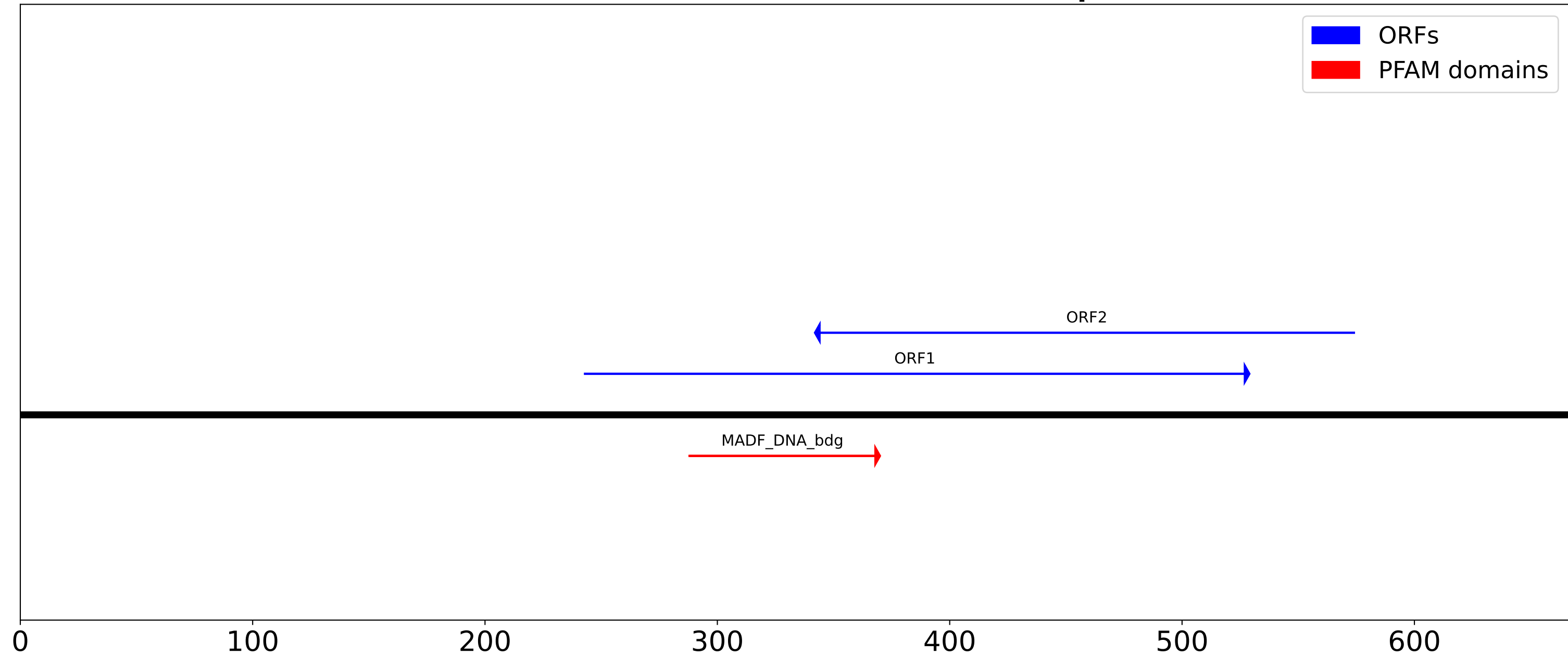


TE: rnd_5_family_2701
size: 629bp; fragments: 131; full length: 15 (≥ 566.1 bp)

Before TEtrimmer 629 bp



After TEtrimmer ORF and PFAM domain plot



Dotplot

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

