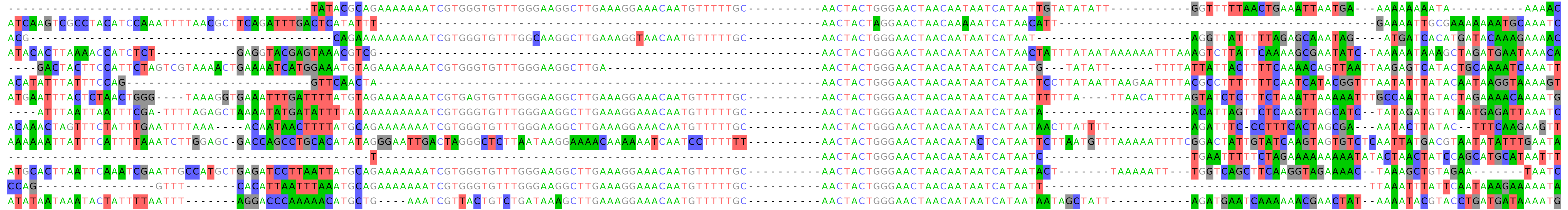
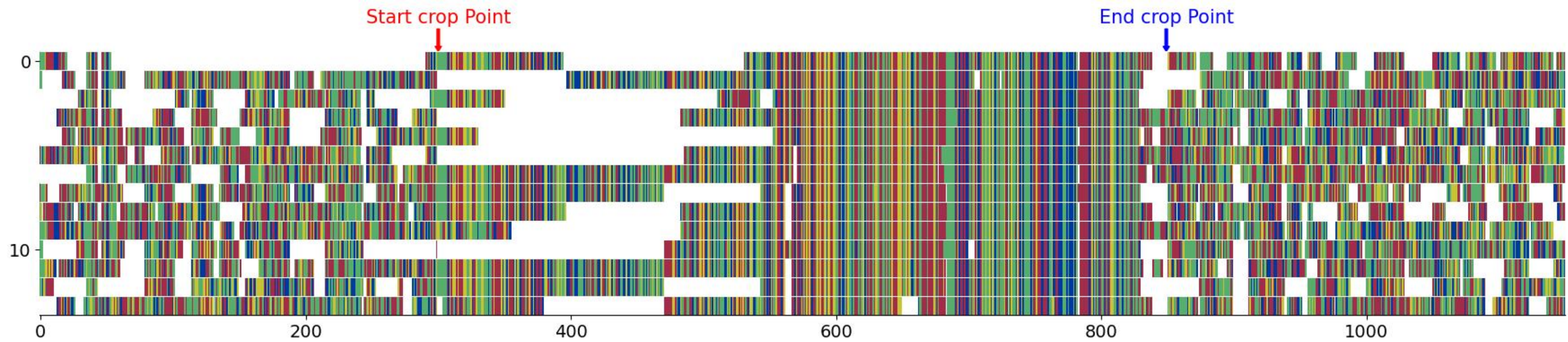


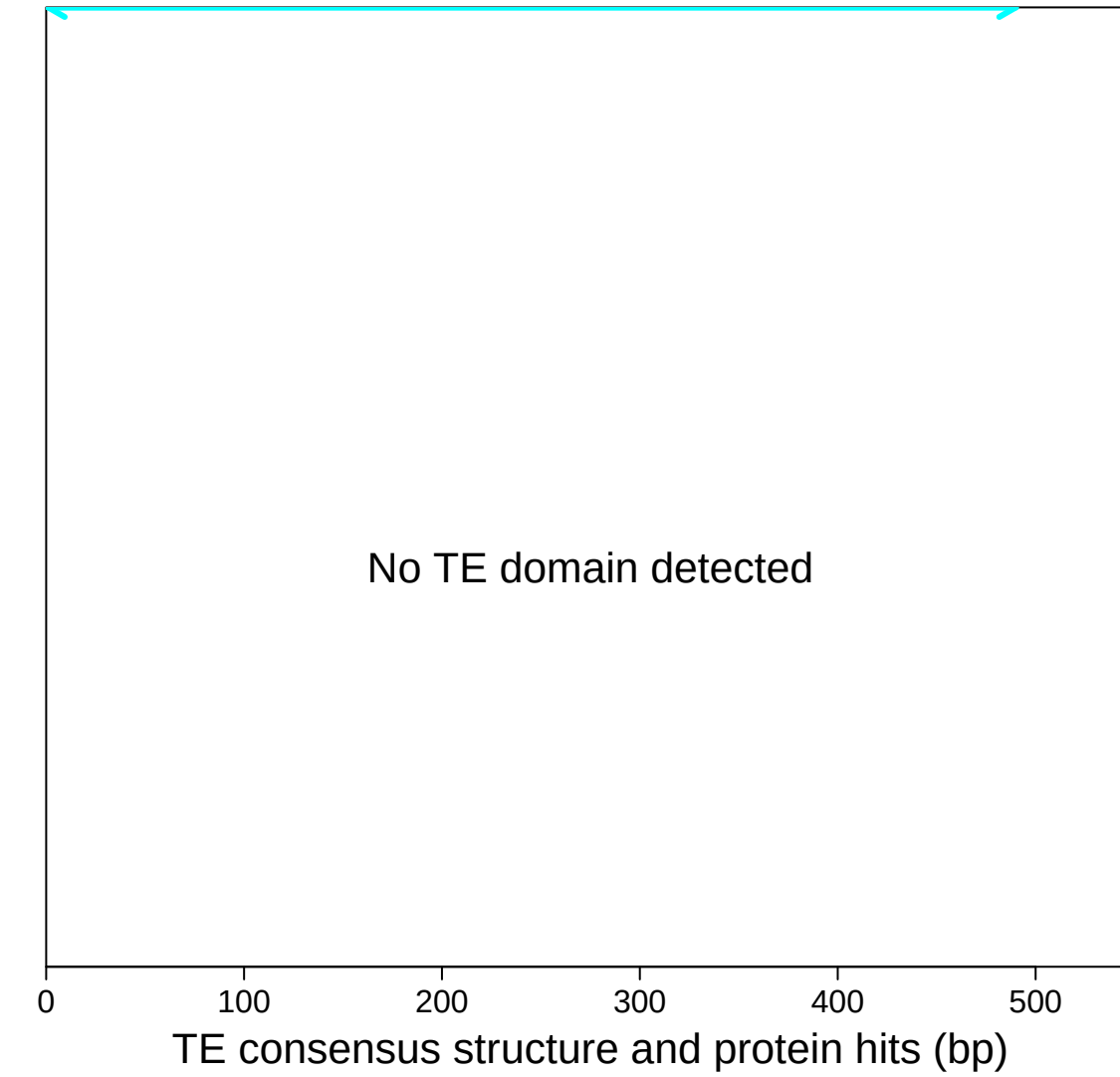
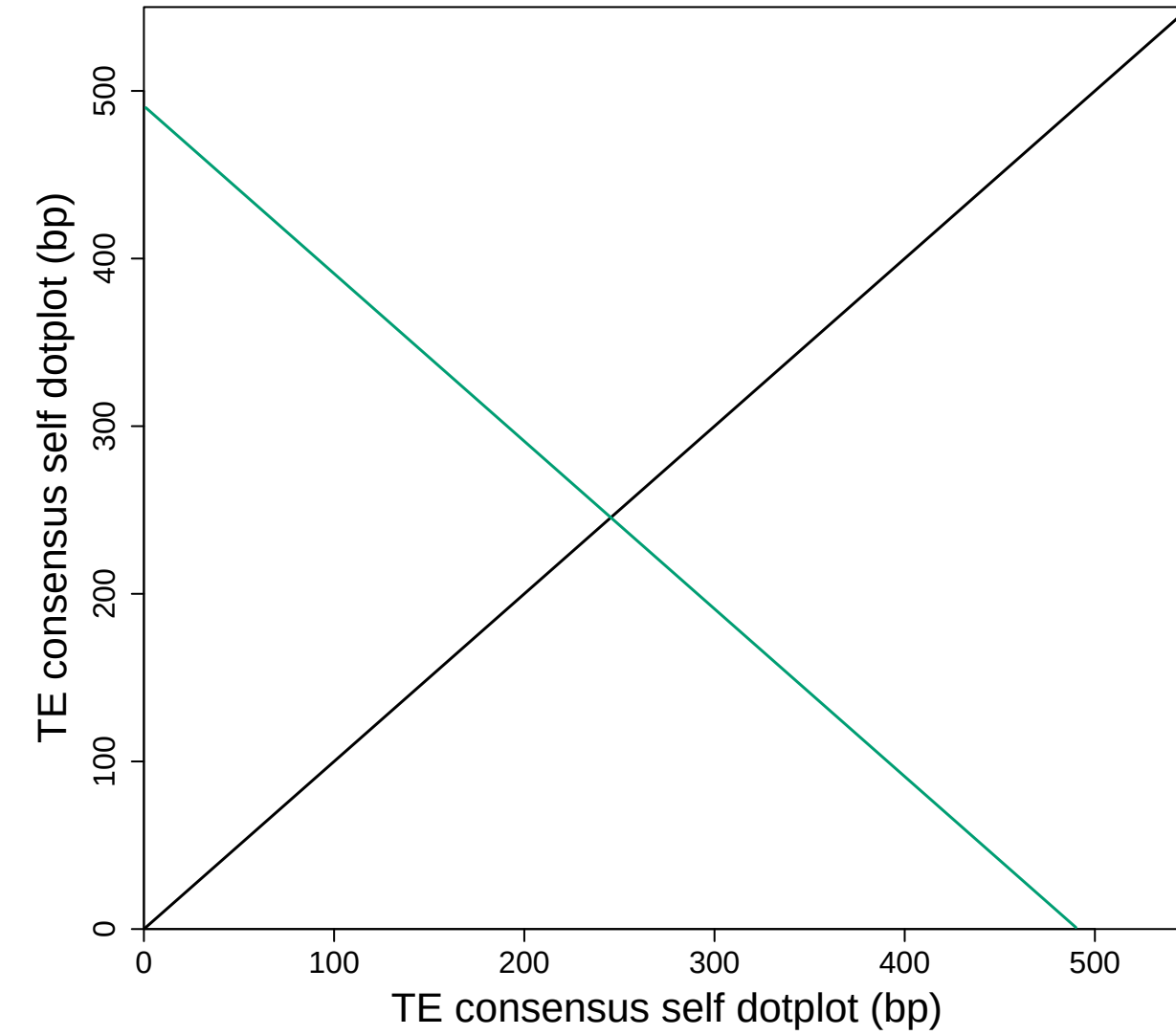
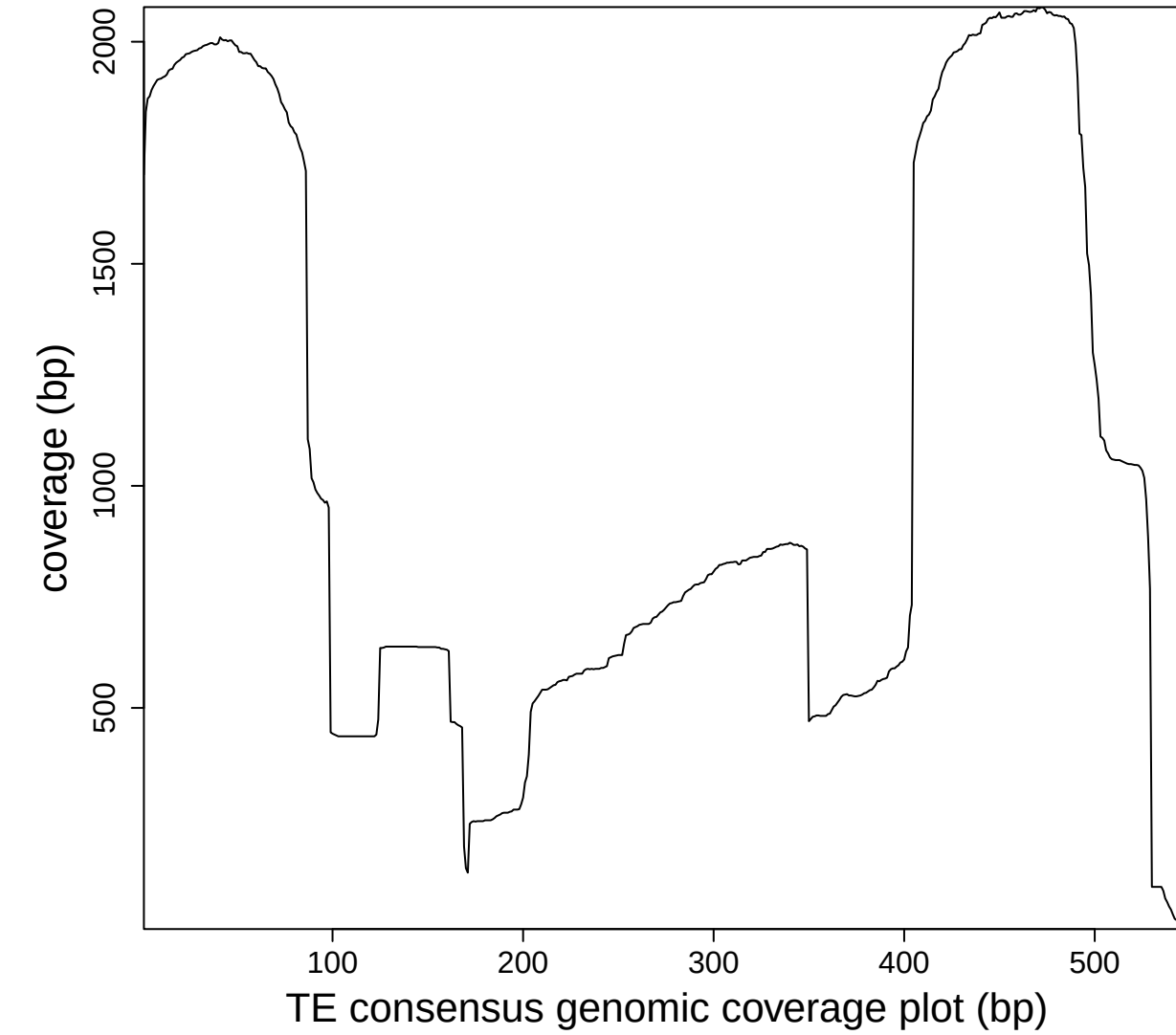
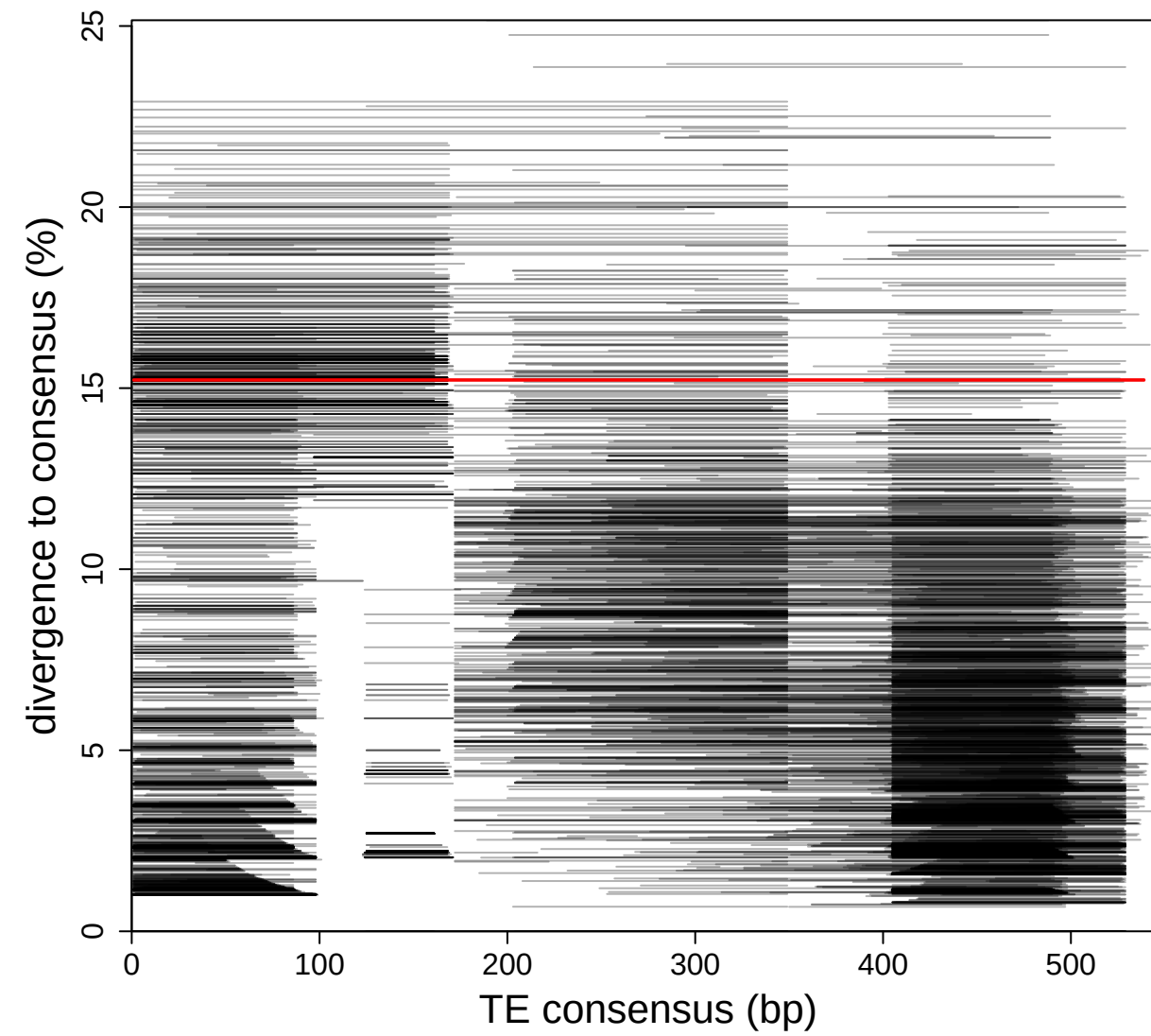
MSA length = 550





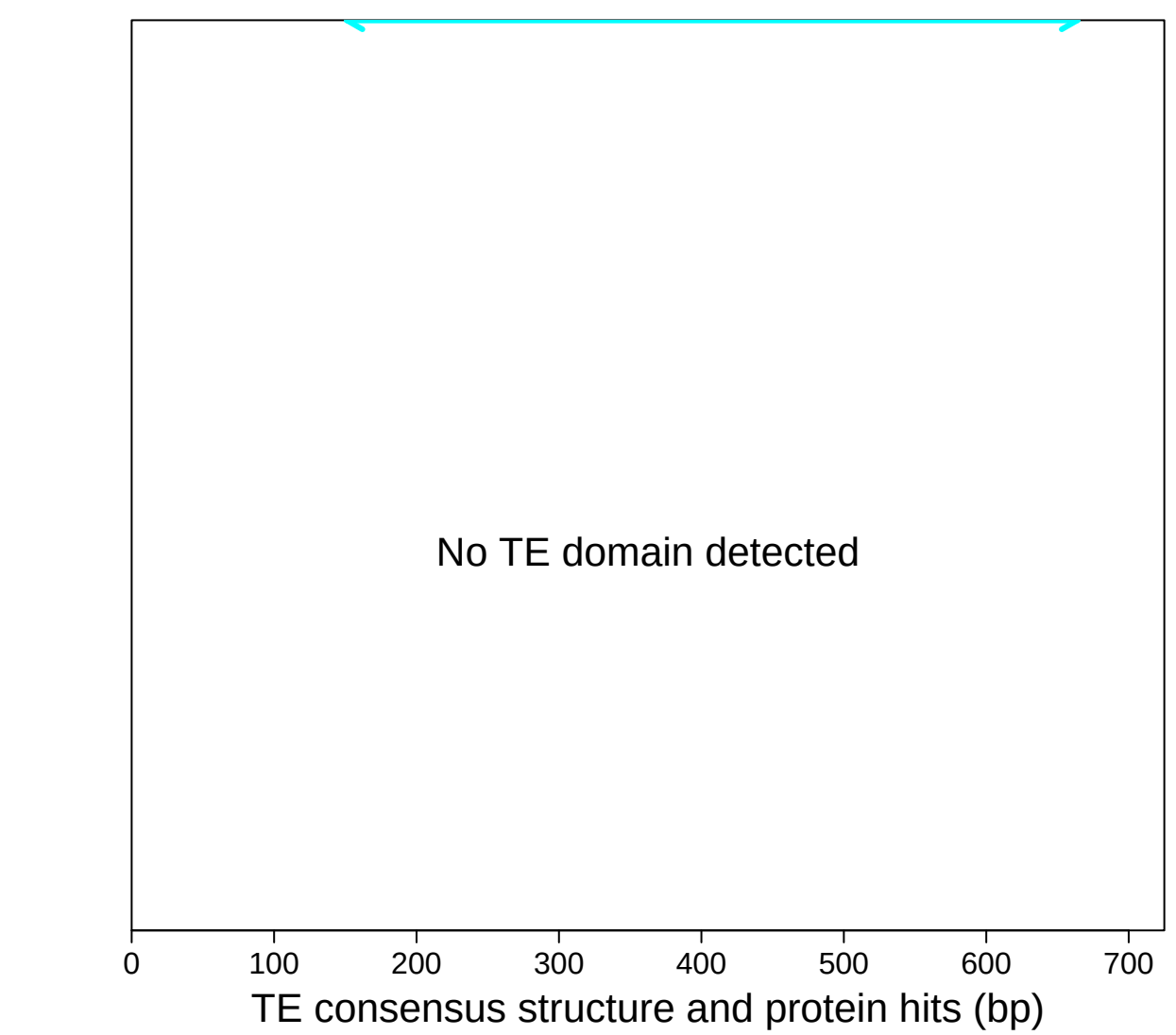
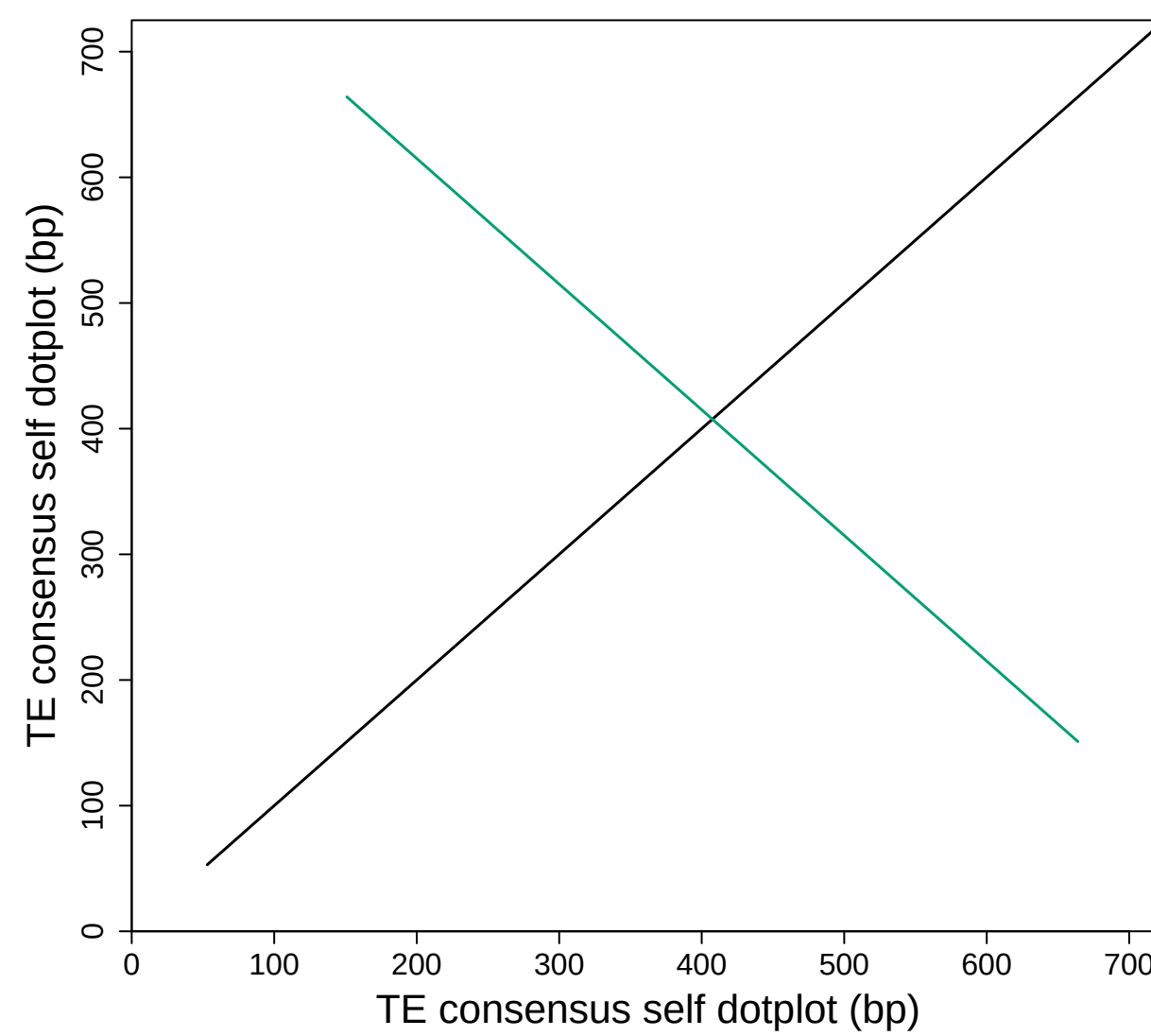
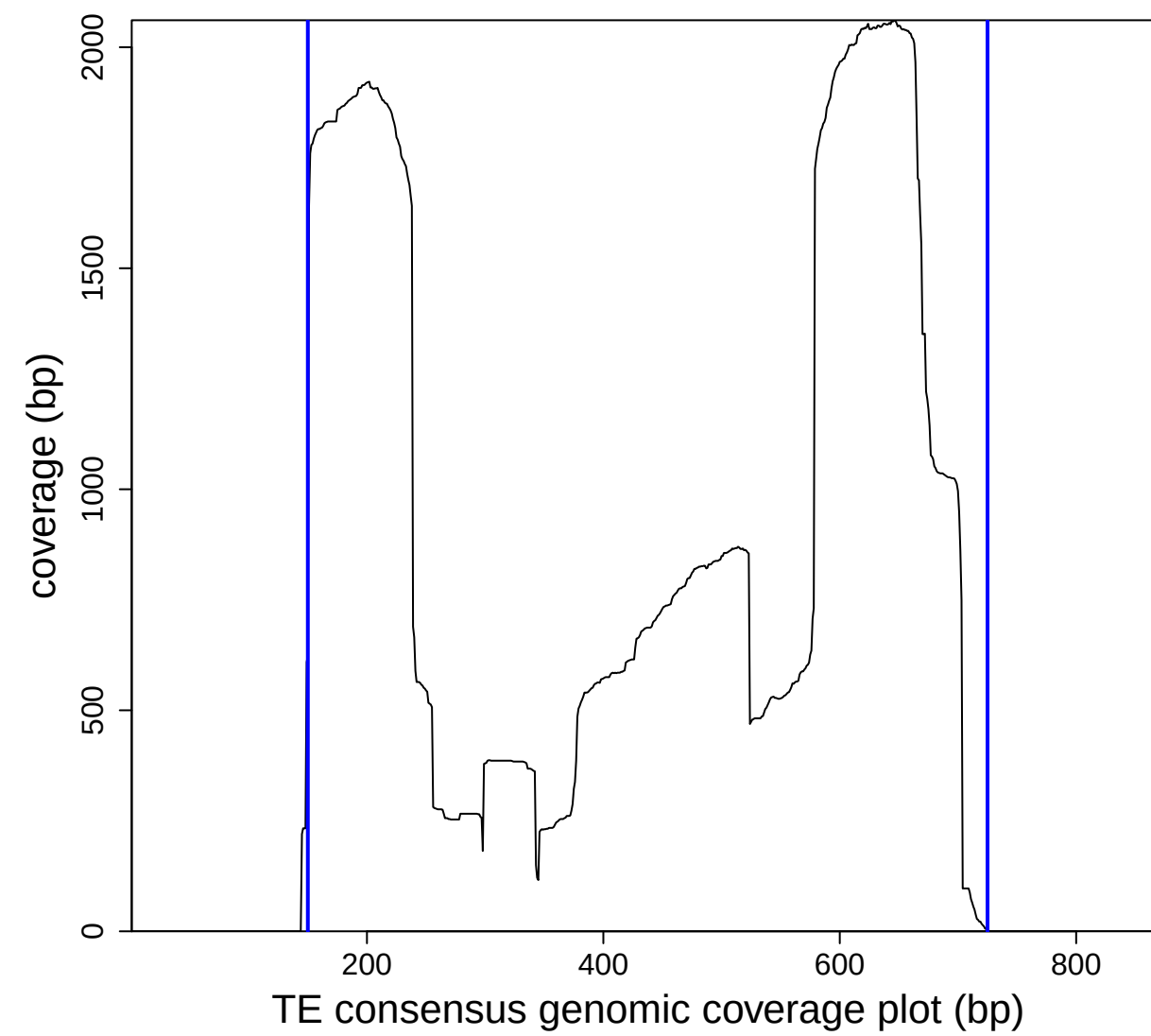
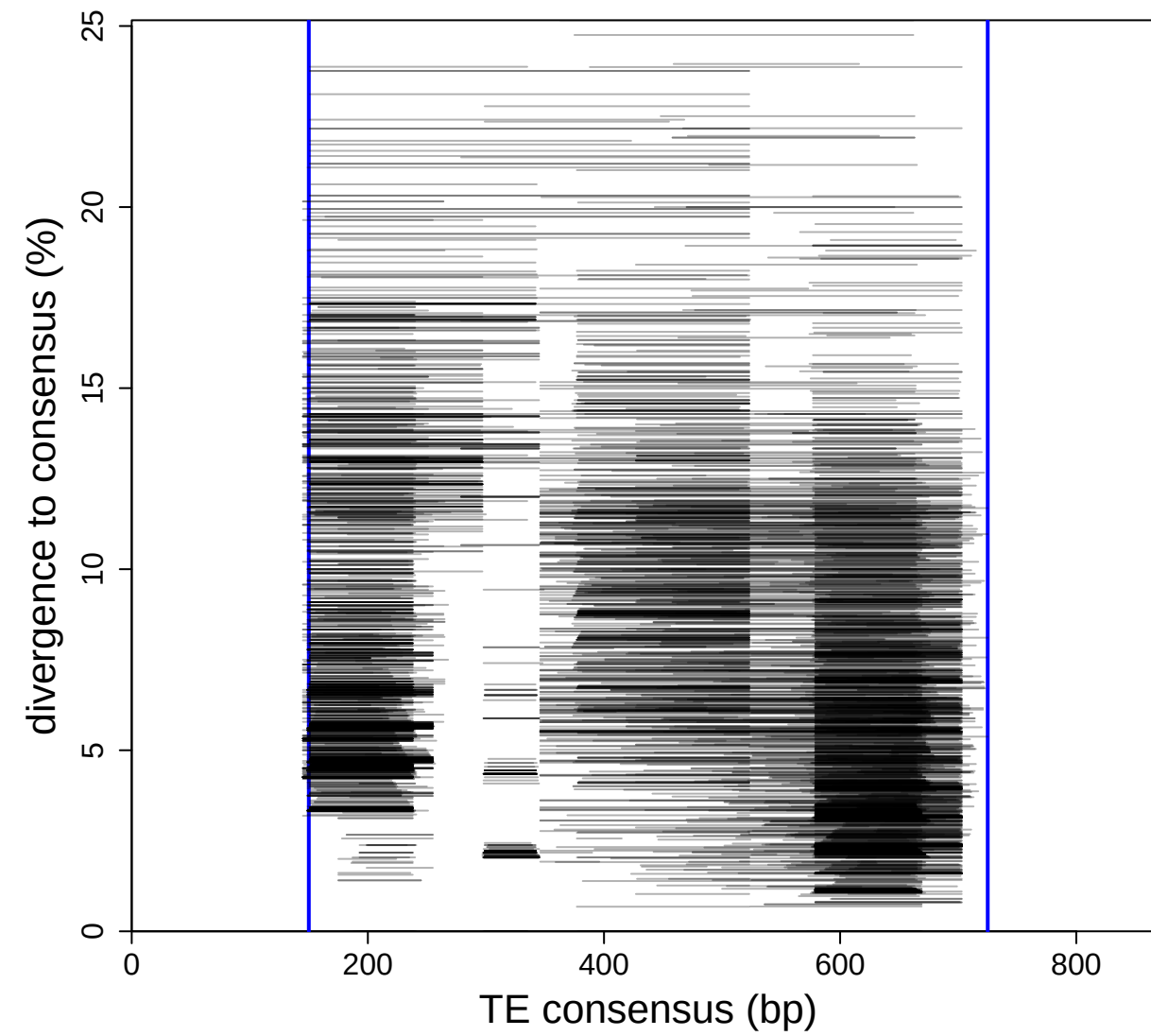
g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa_a
size: 550bp; fragments: 4853; full length: 2 (>=495bp)

After TEtrimmer 550 bp

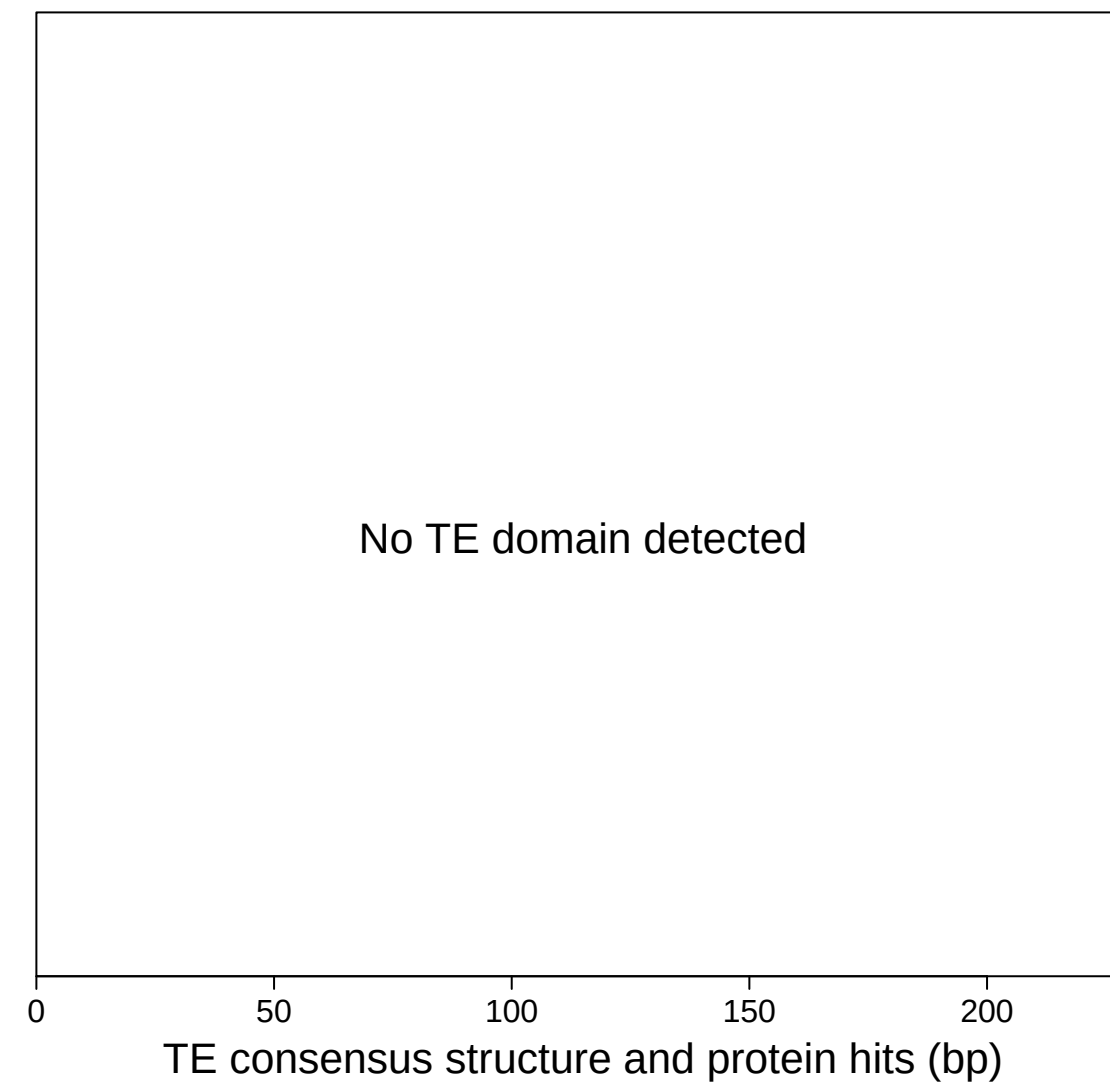
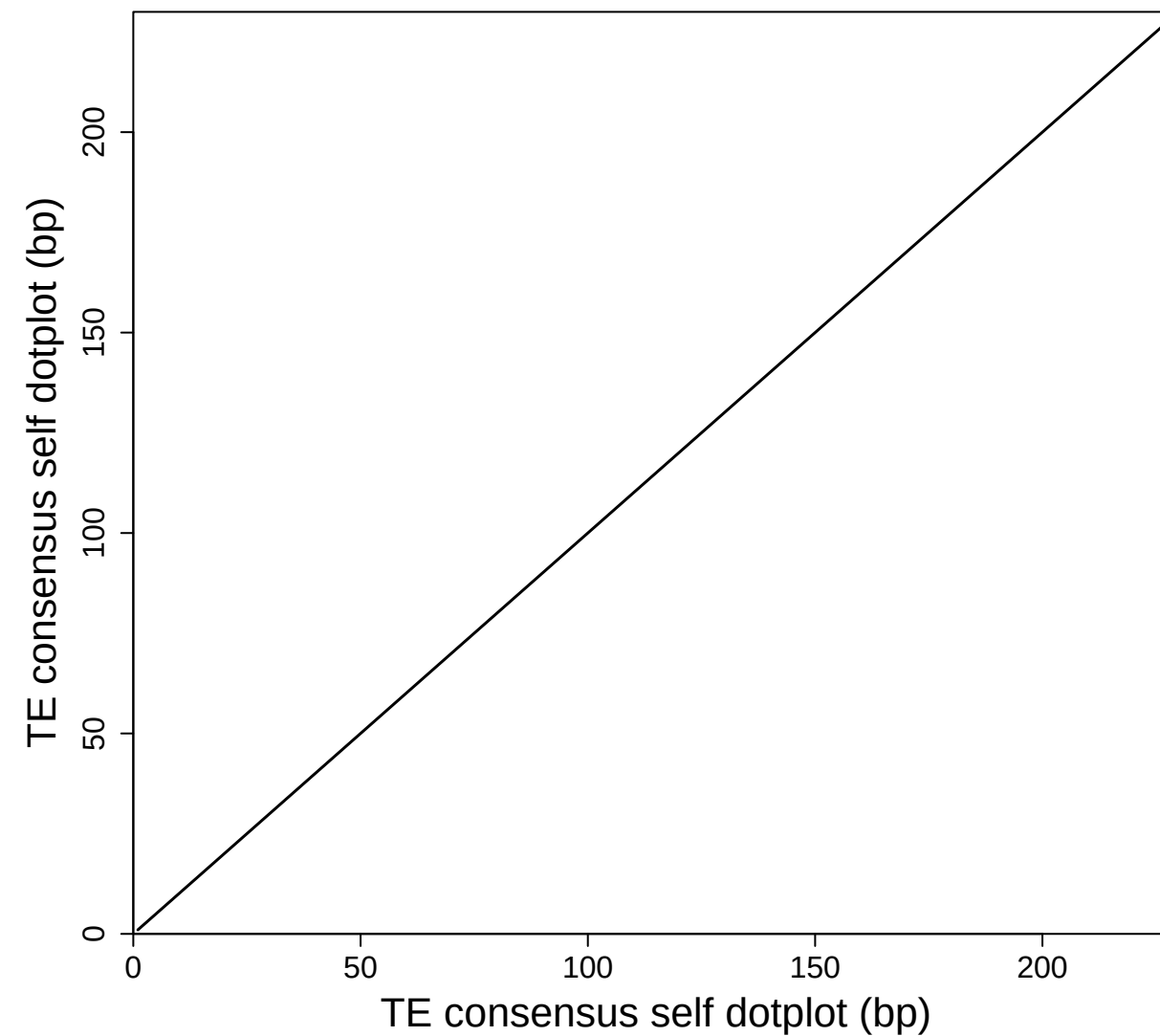
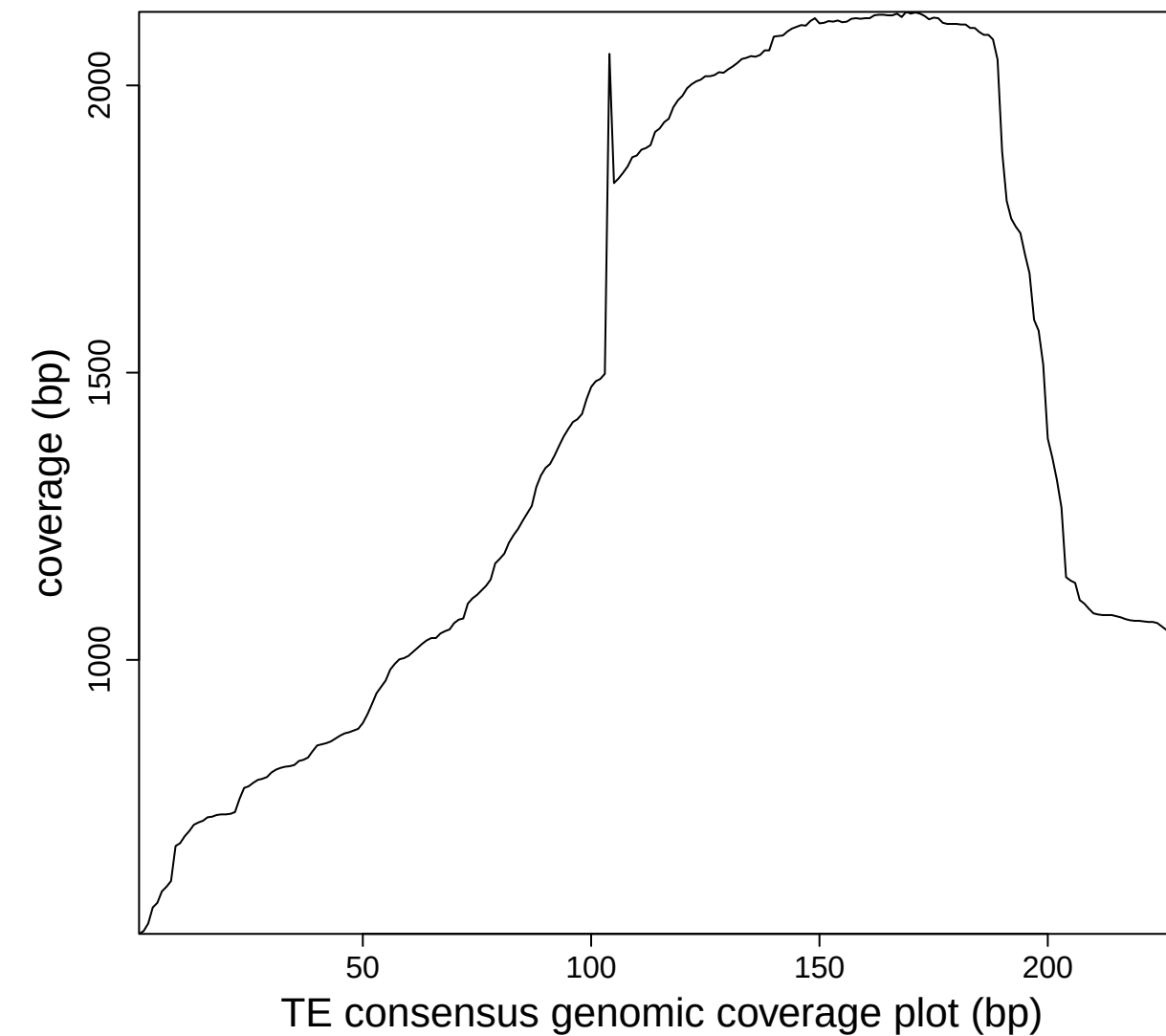
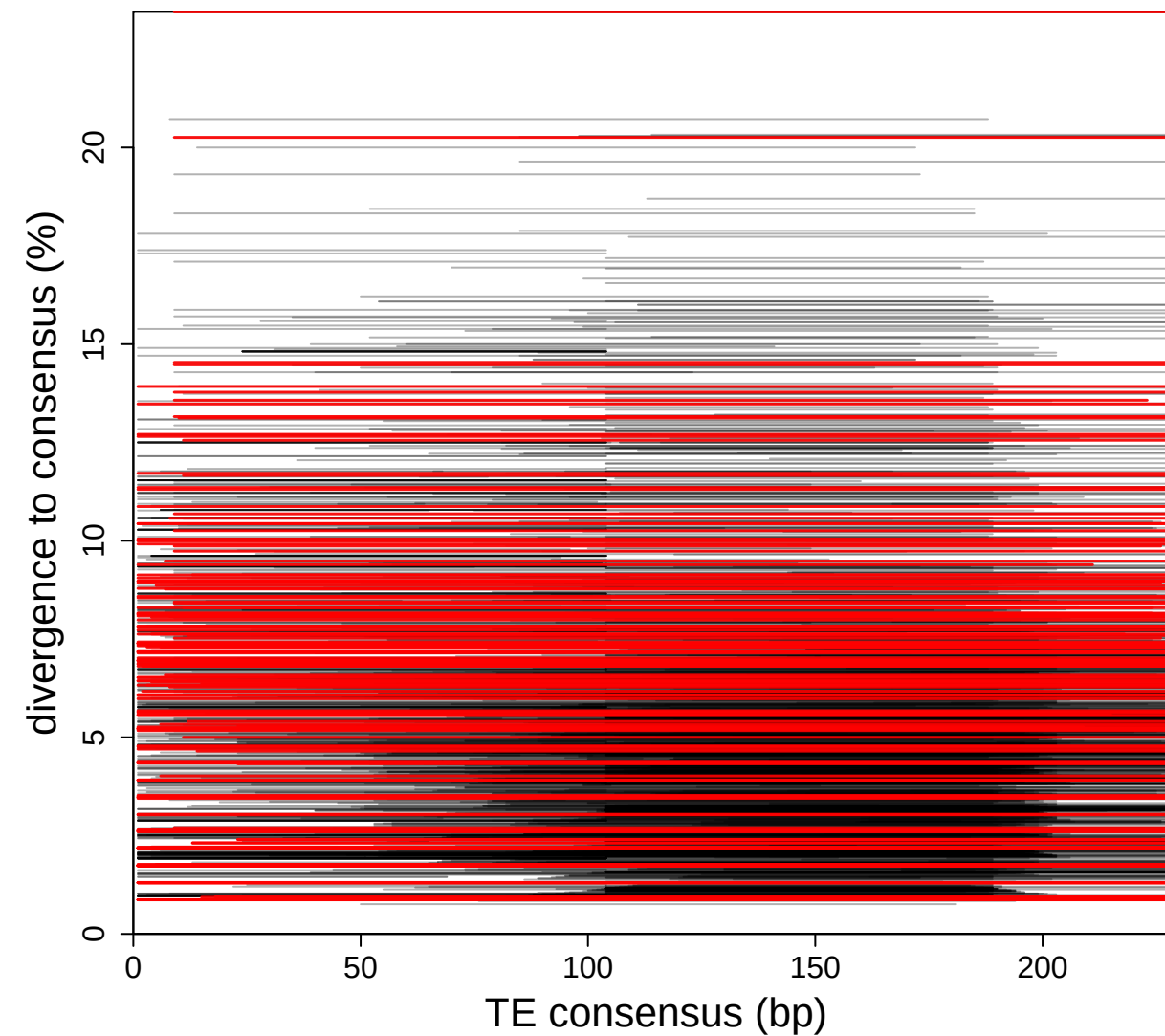


f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcl
size: 875bp; fragments: 4786; full length: 0 (>=787.5bp)

After TEtrimmer Extended plot Blue lines are boundaries

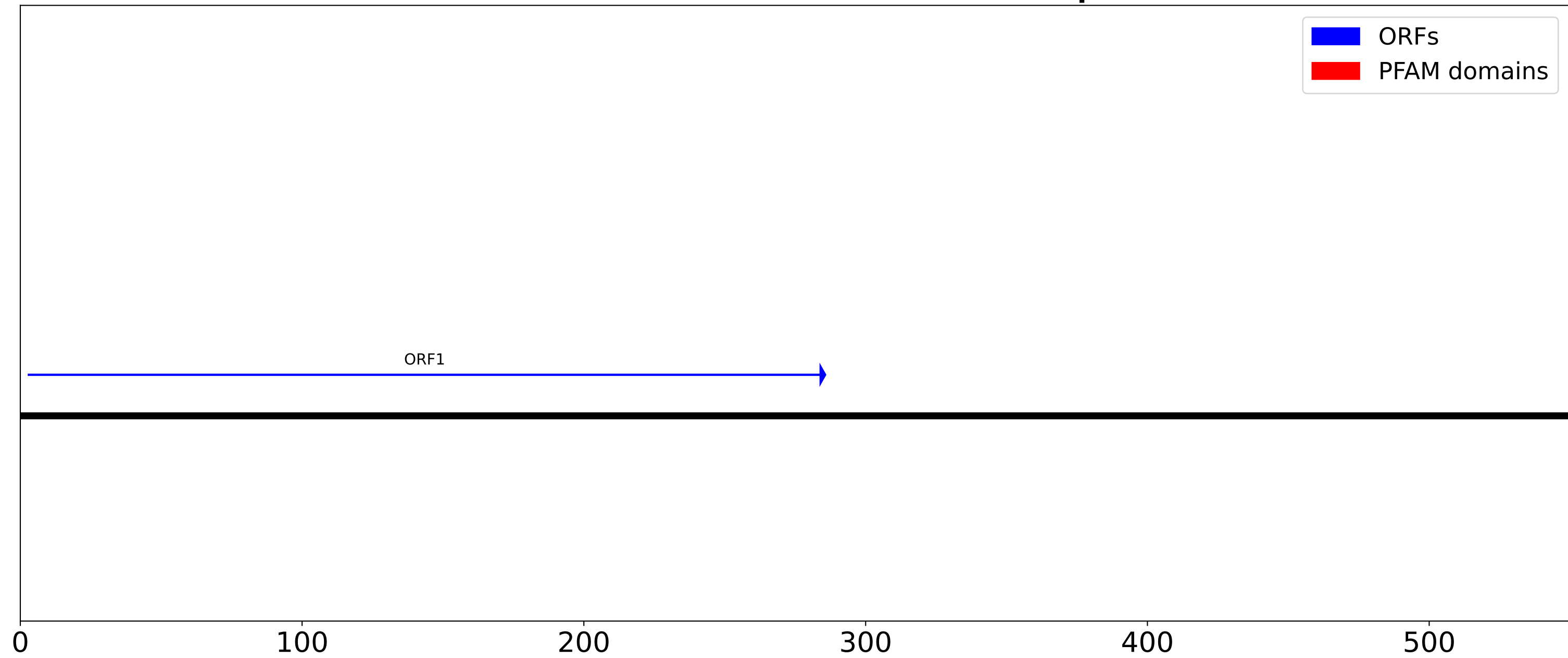


TE: rnd_1_family_195
size: 230bp; fragments: 2560; full length: 222 (≥ 207 bp)

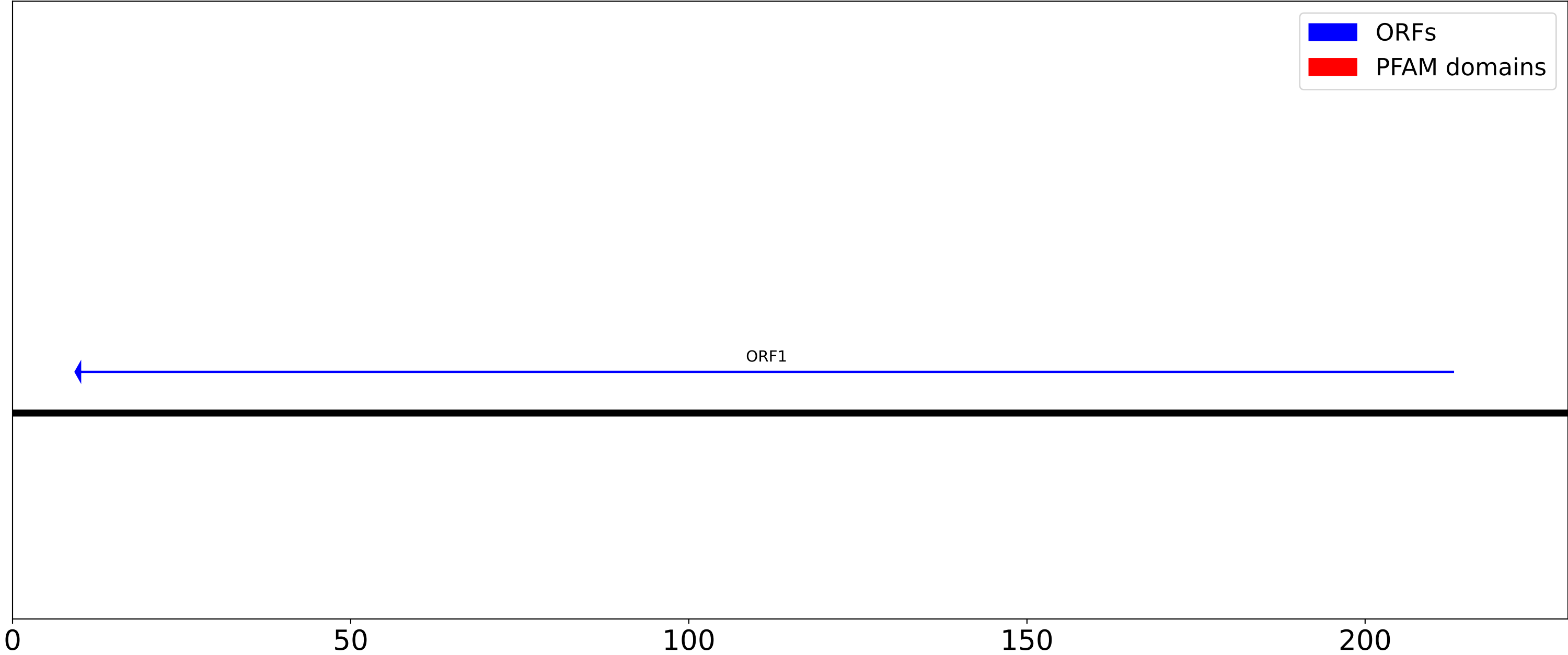


Before TEtrimmer 230 bp

After TEtrimmer ORF and PFAM domain plot



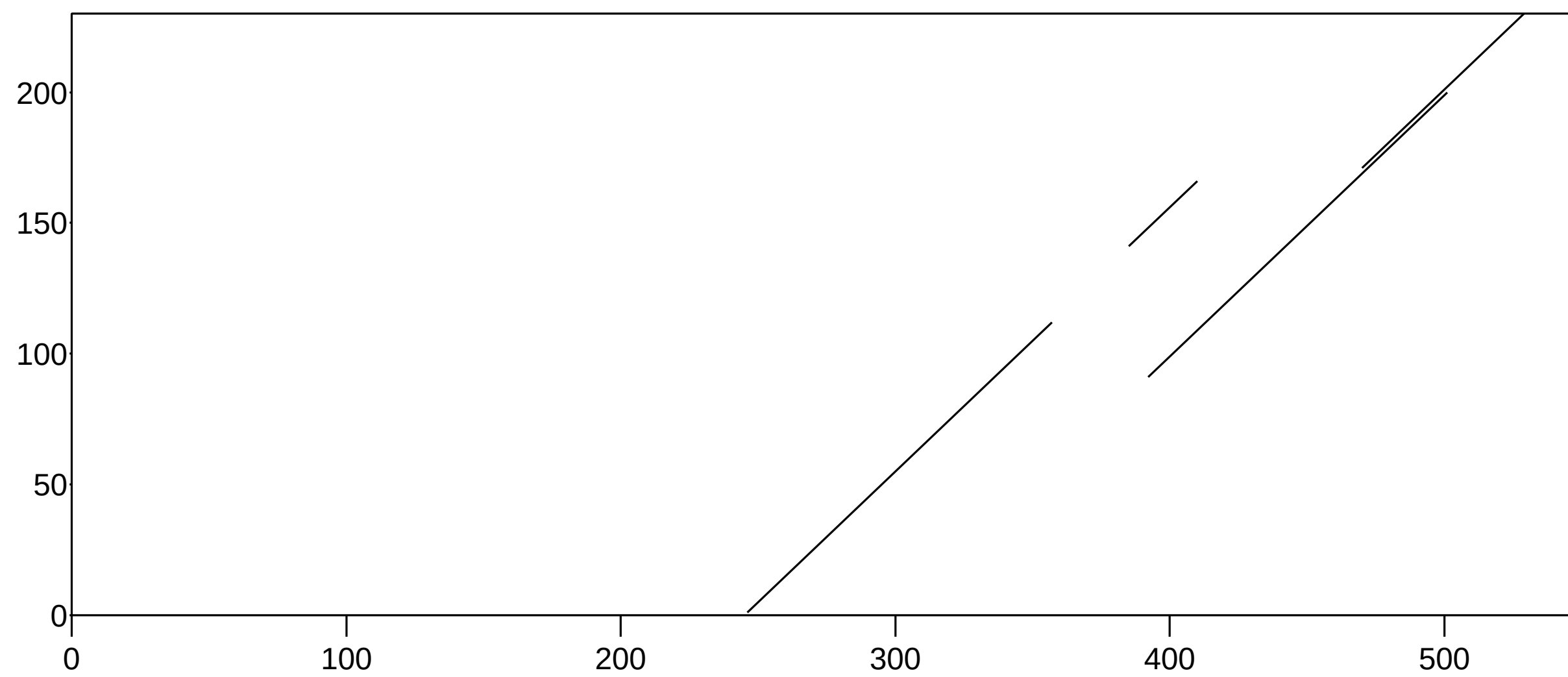
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)