



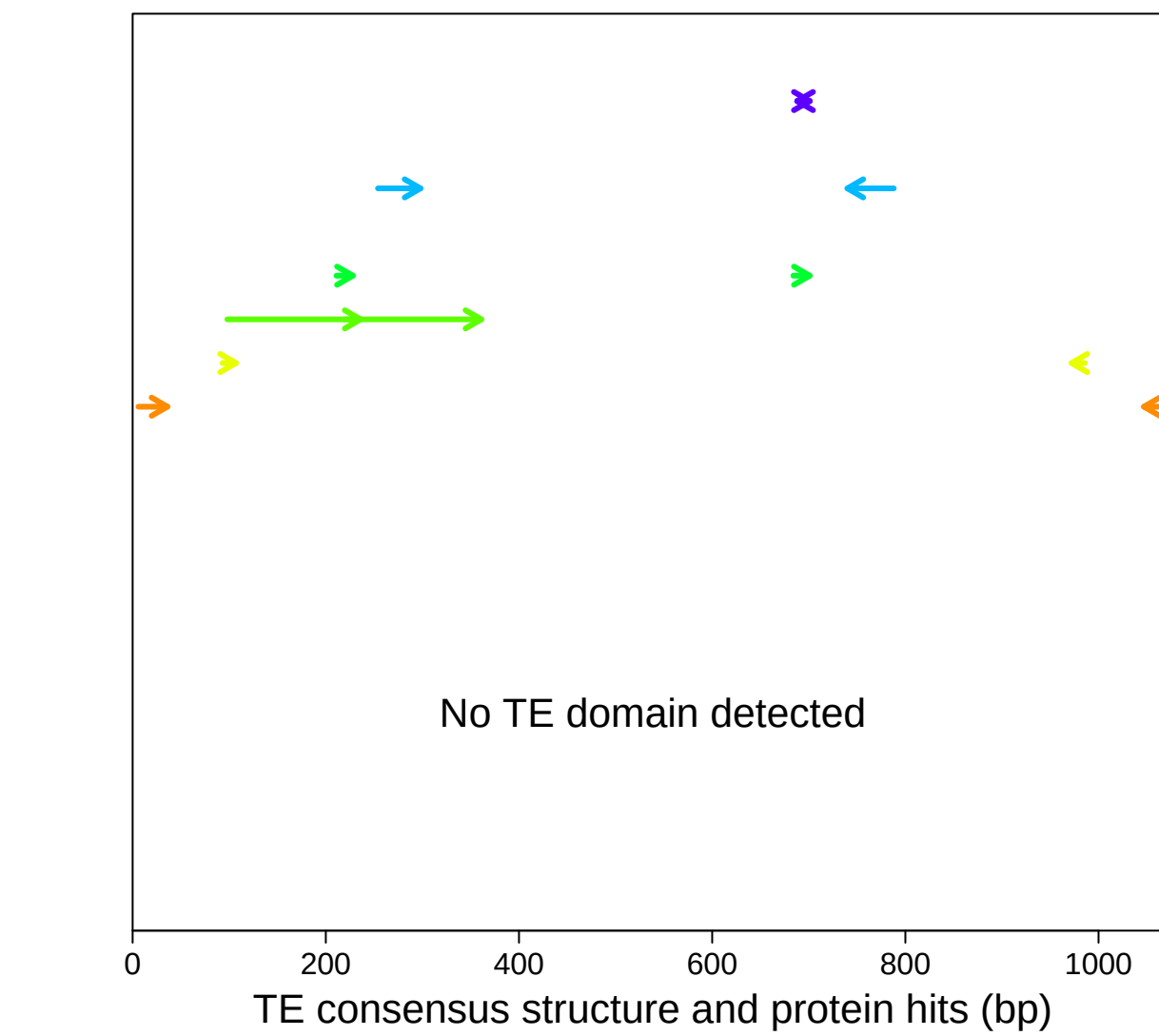
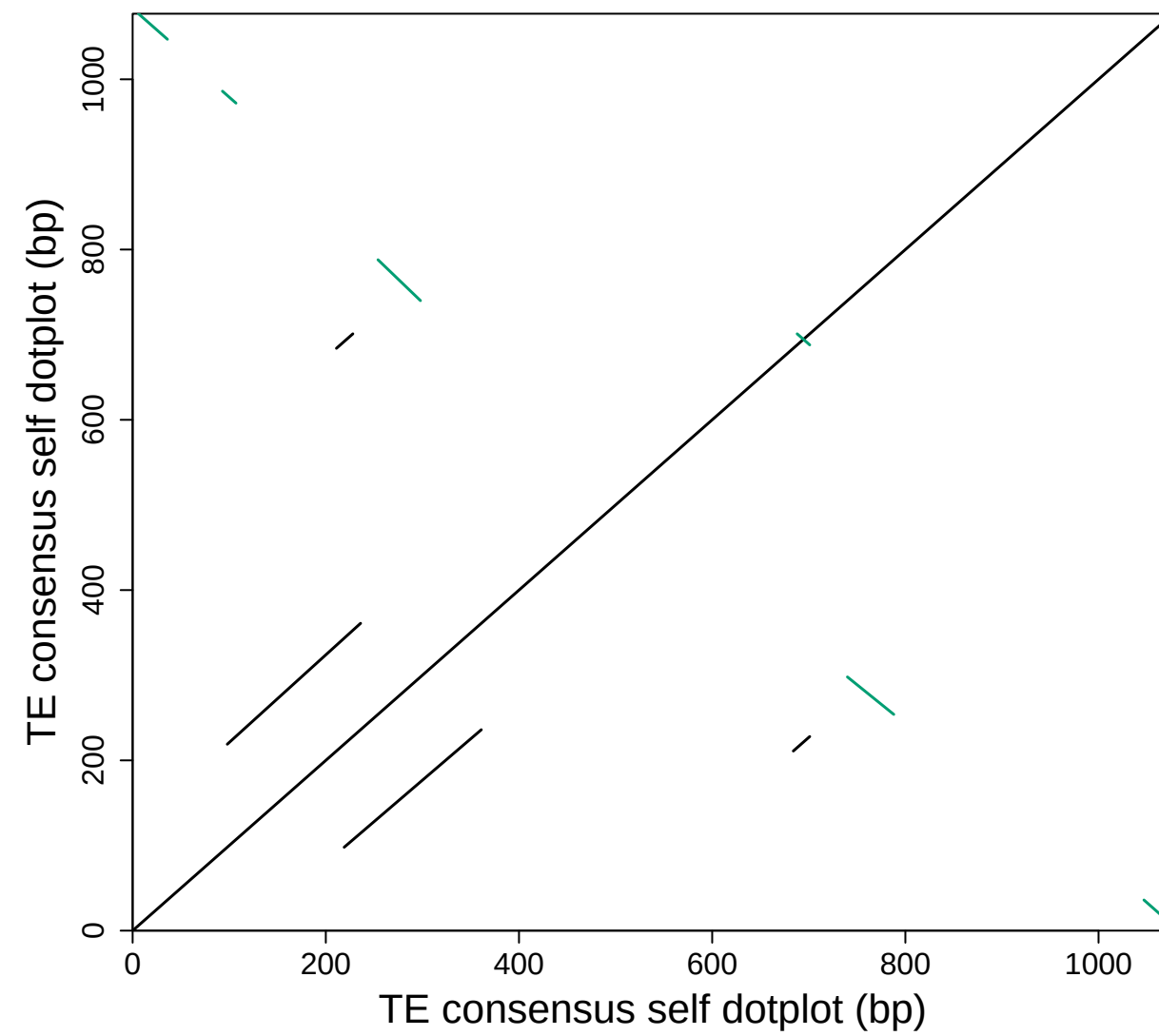
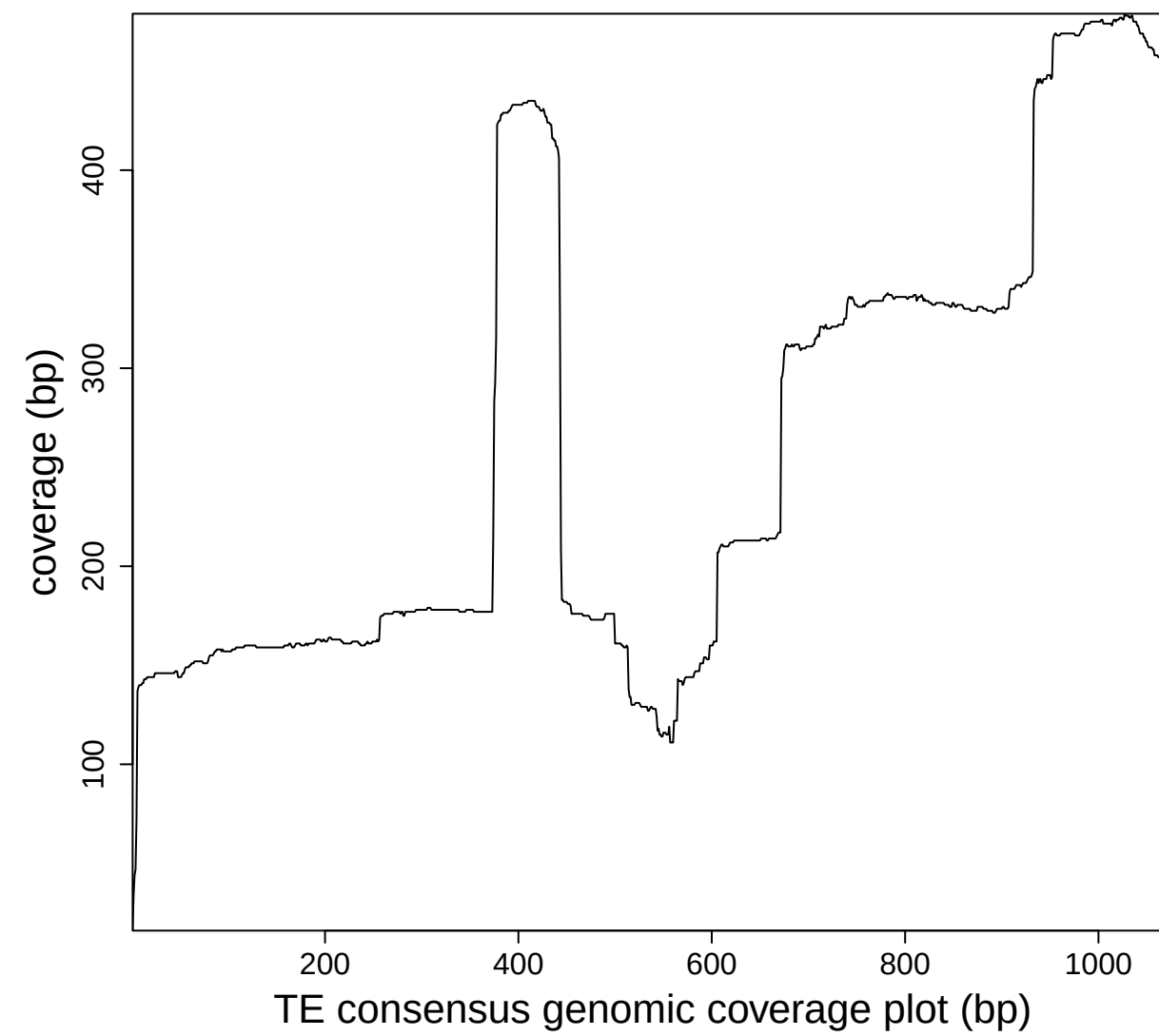
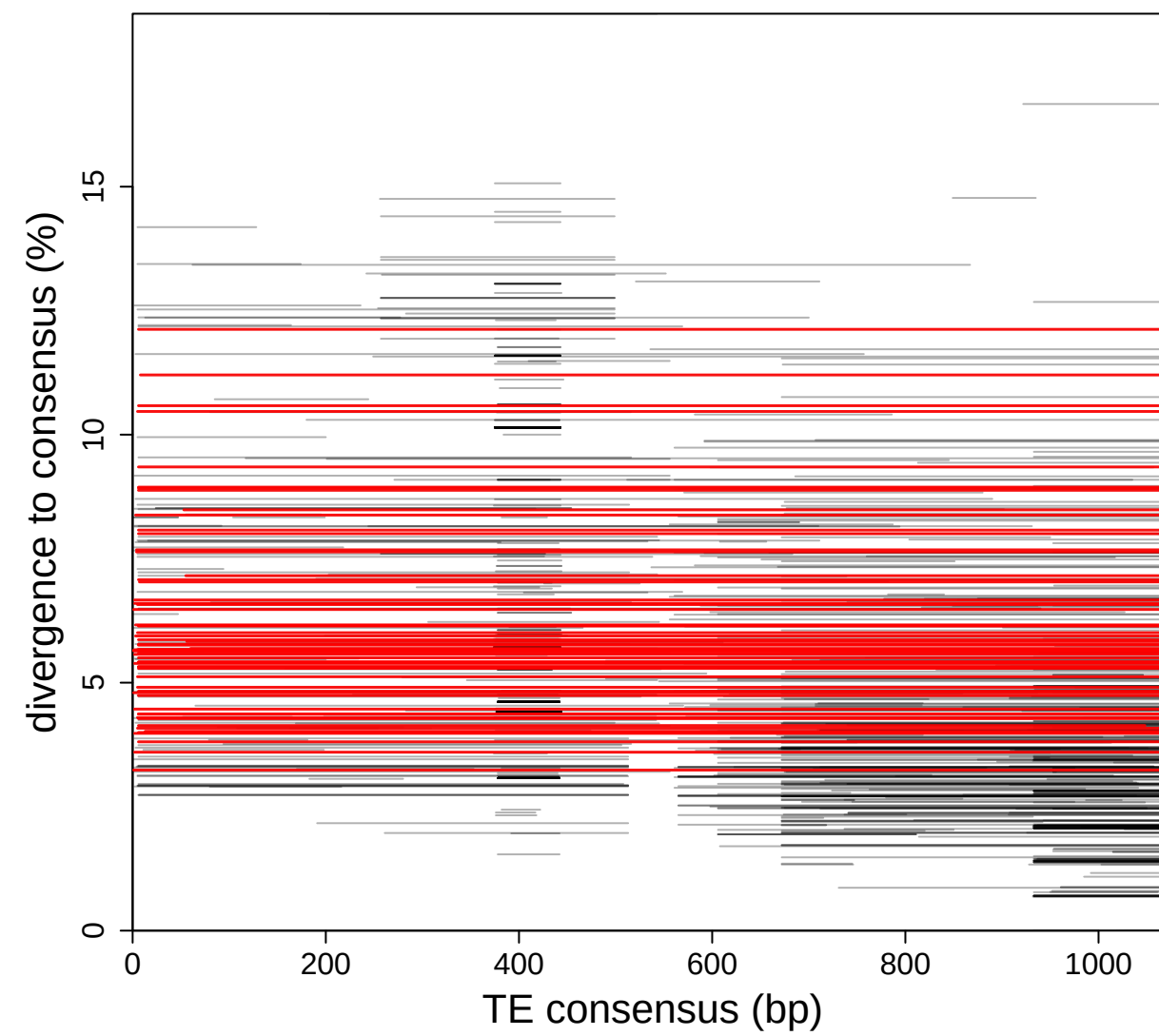
MSA length = 1077





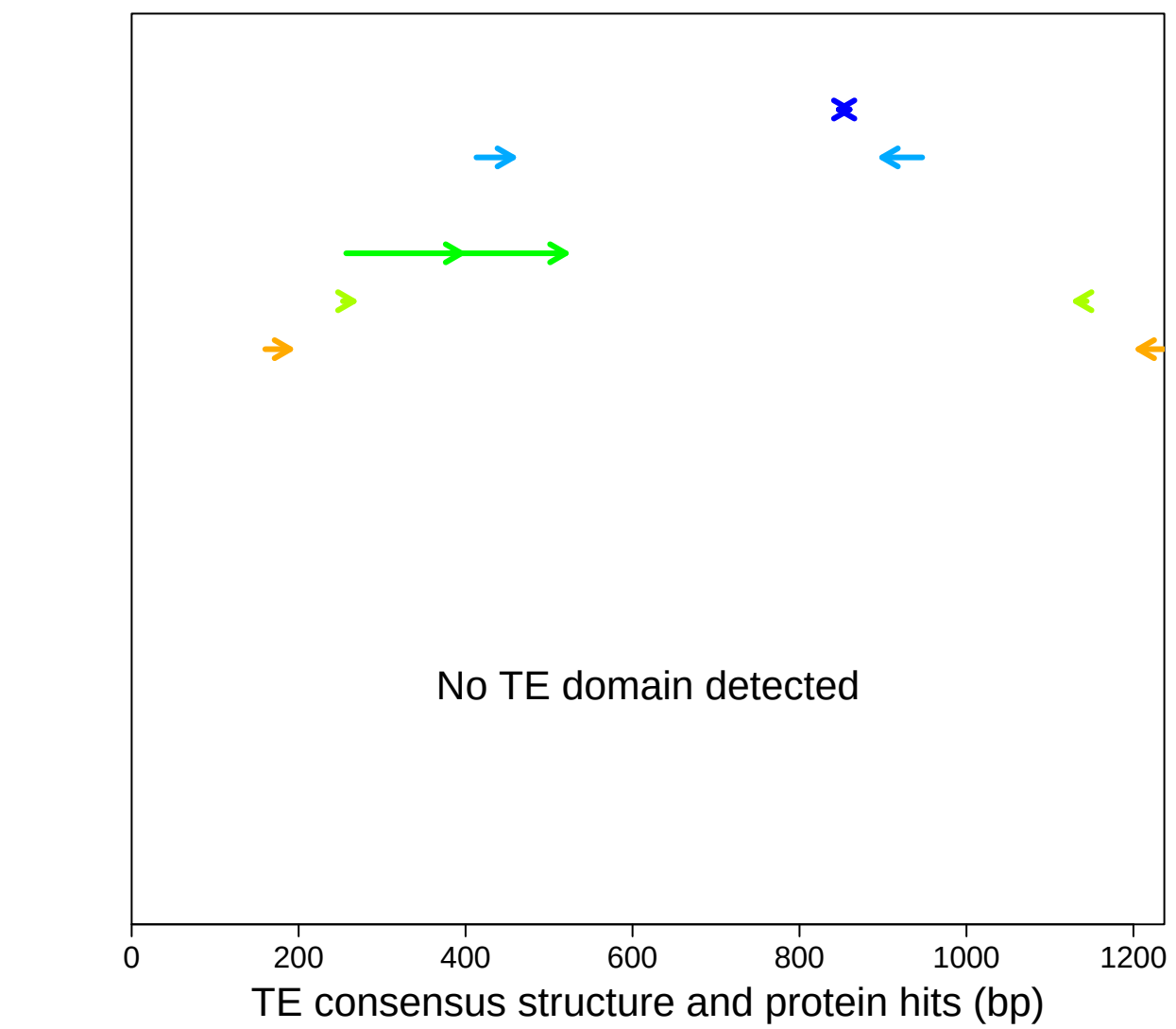
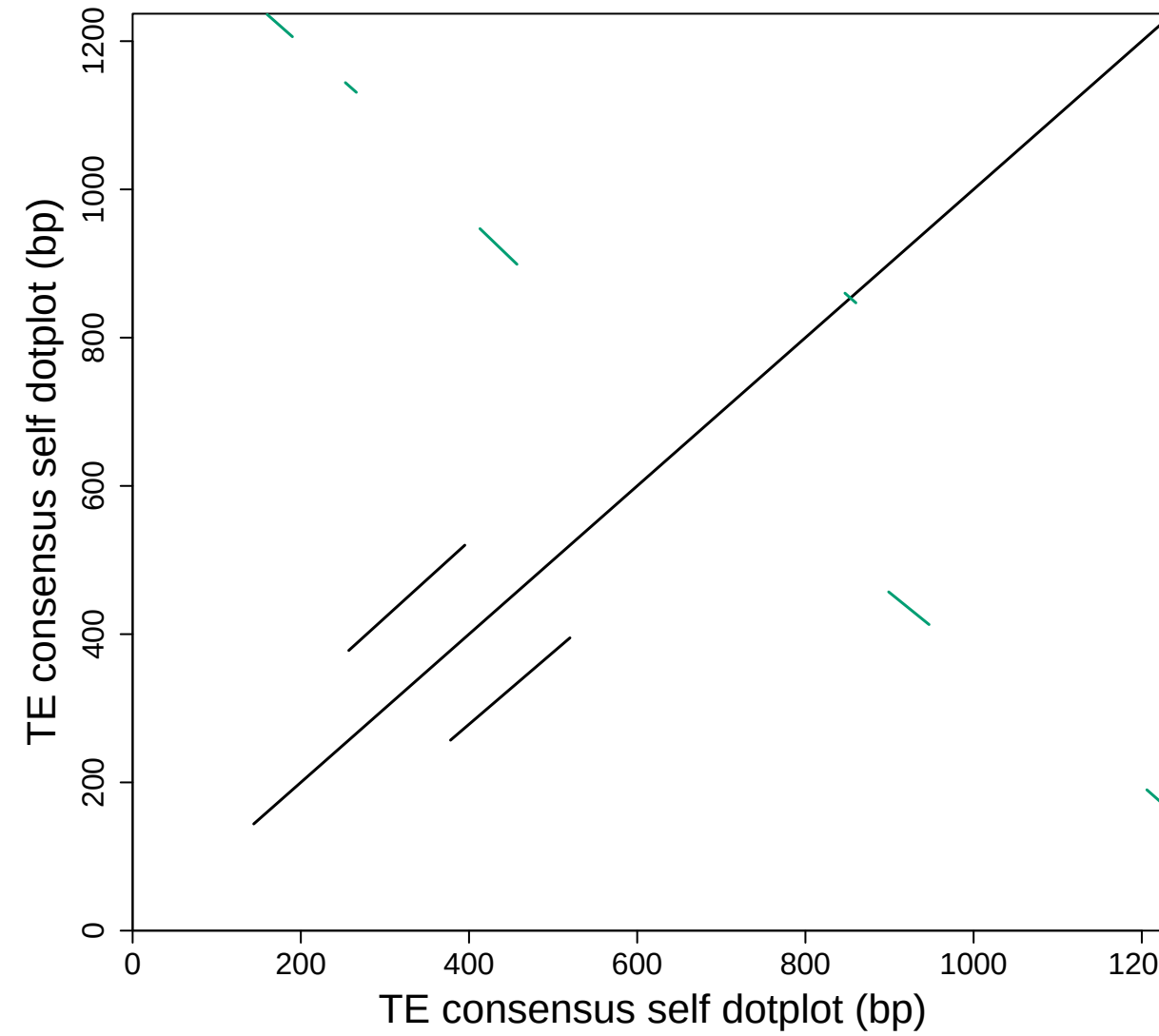
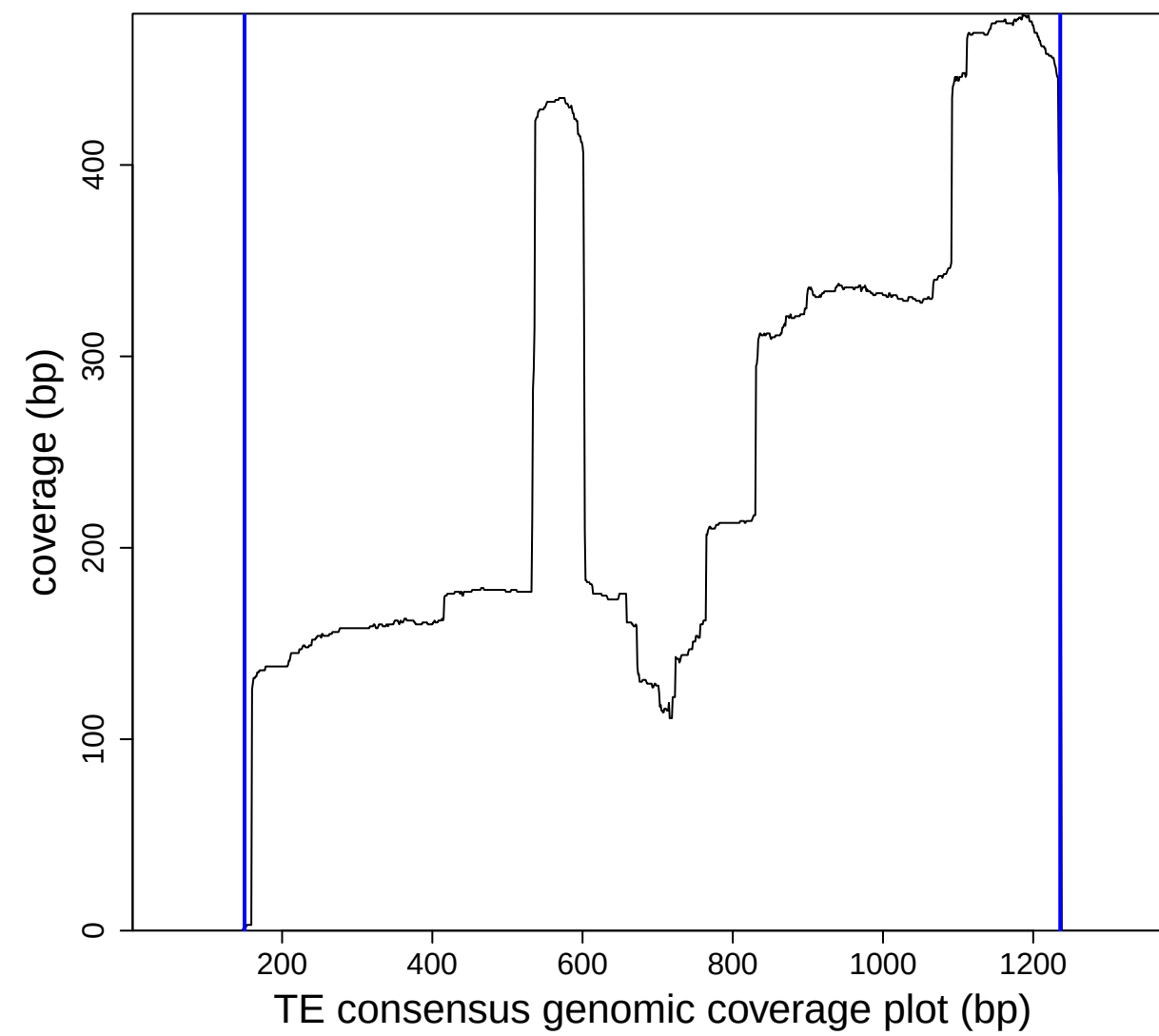
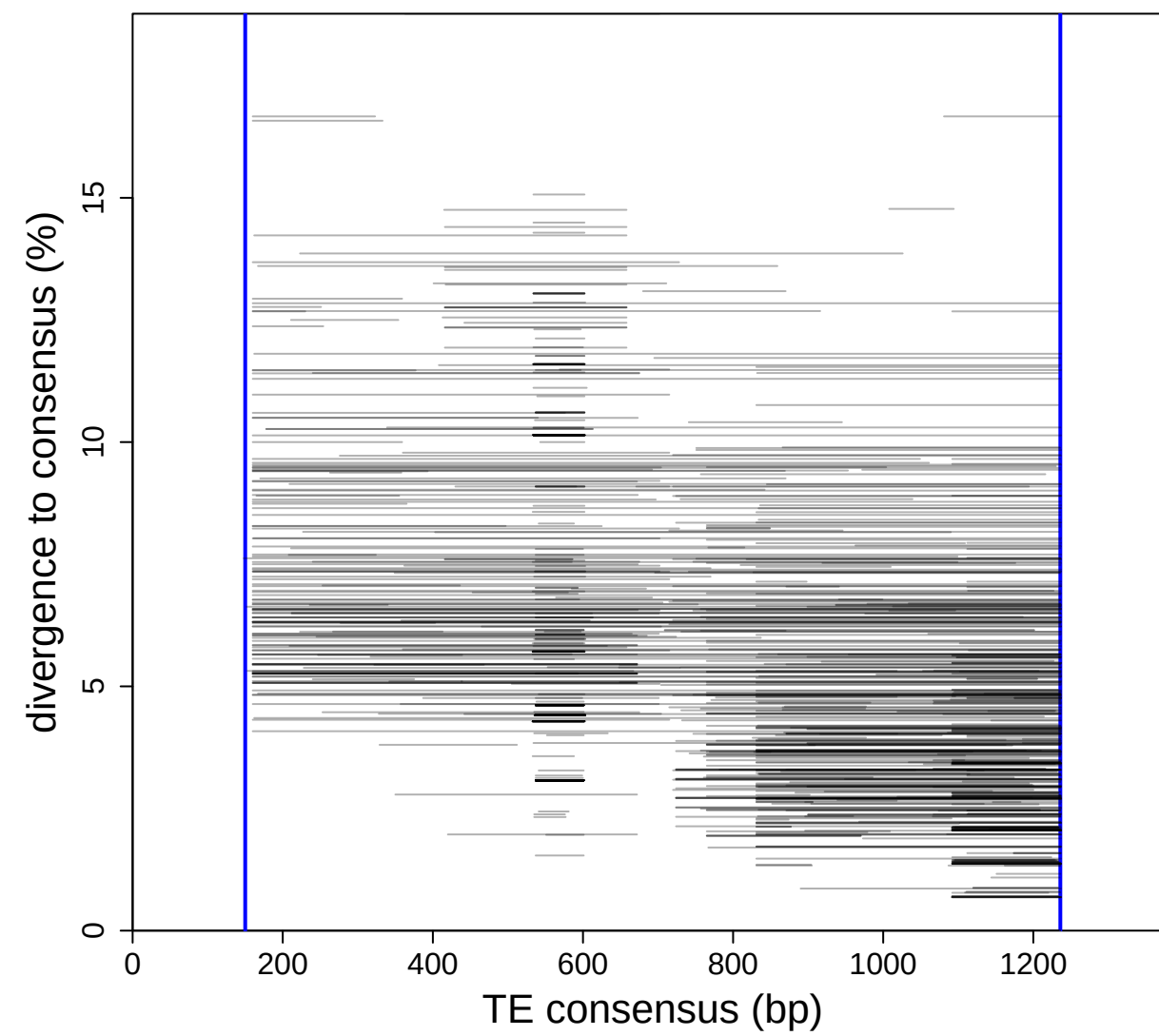
g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa_a
size: 1077bp; fragments: 928; full length: 66 (>=969.3bp)

After TEtrimmer 1077 bp

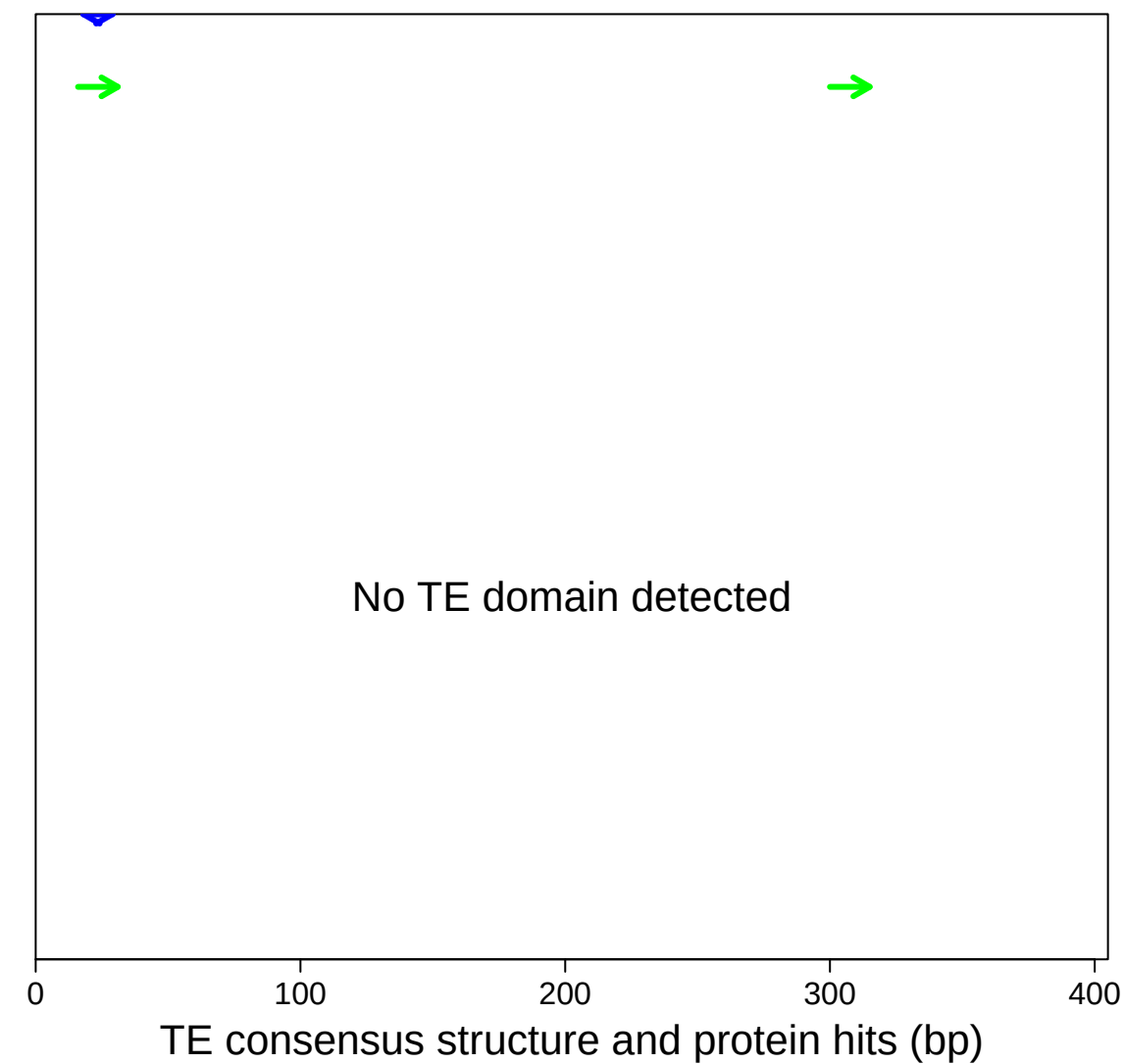
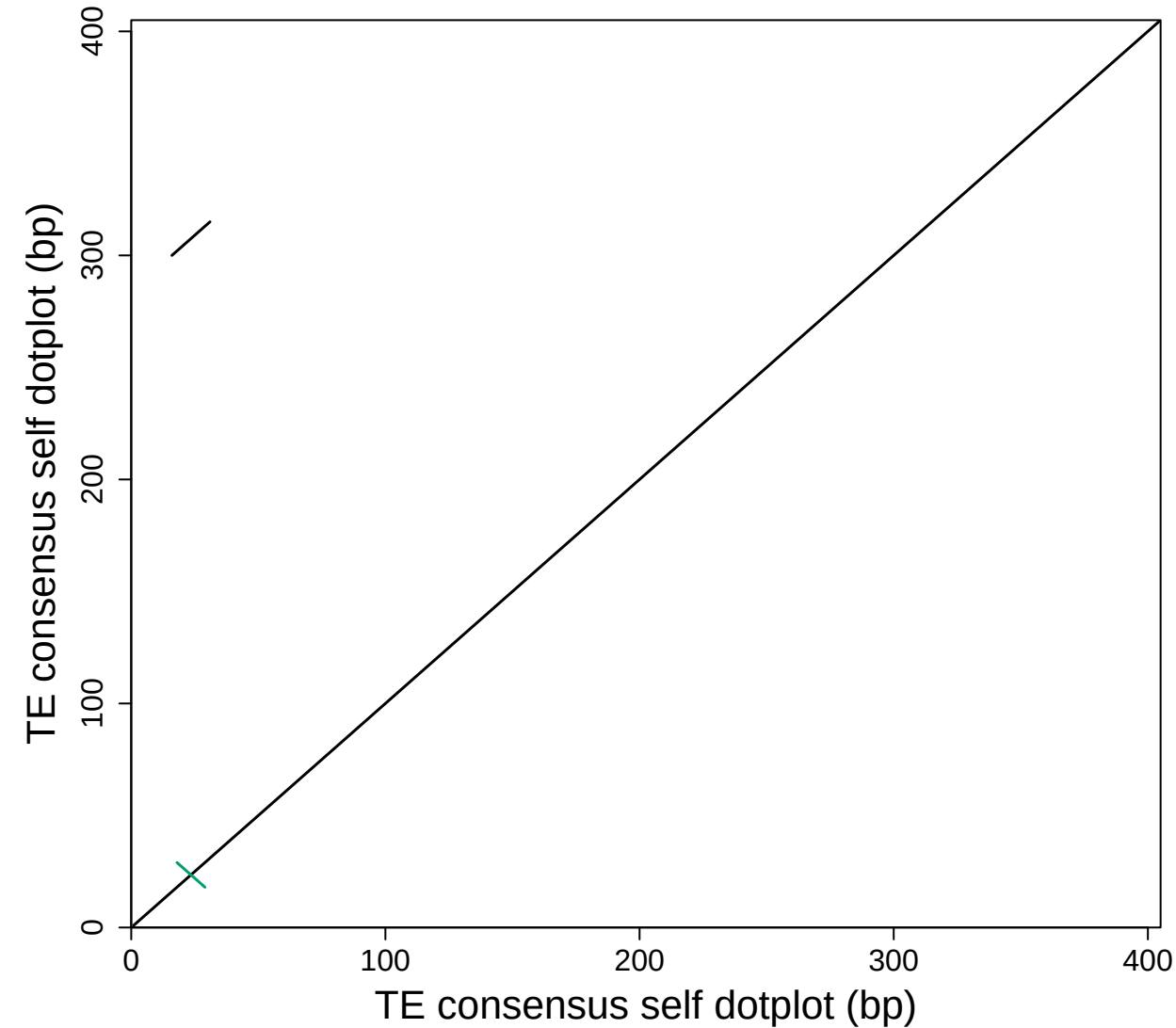
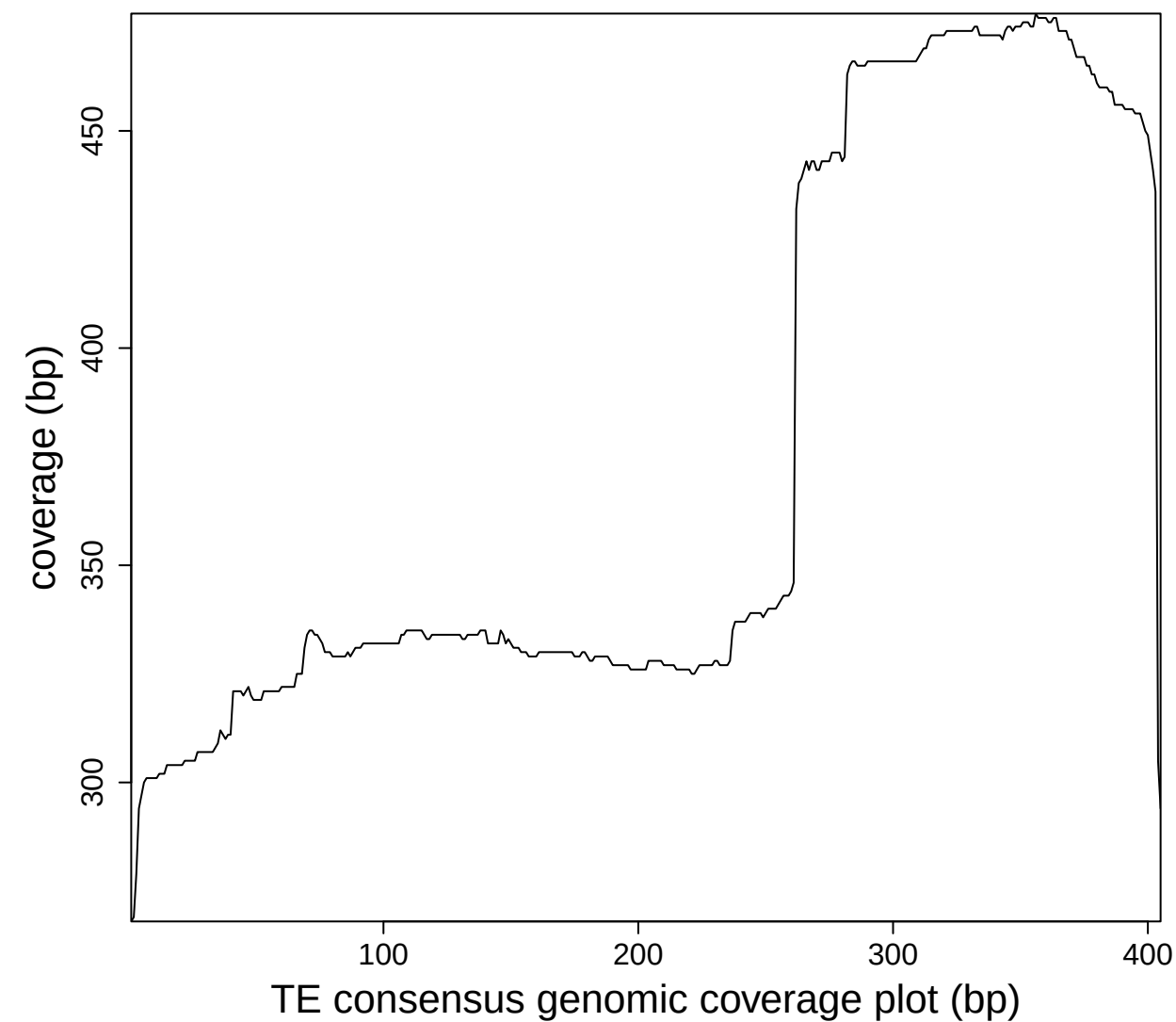
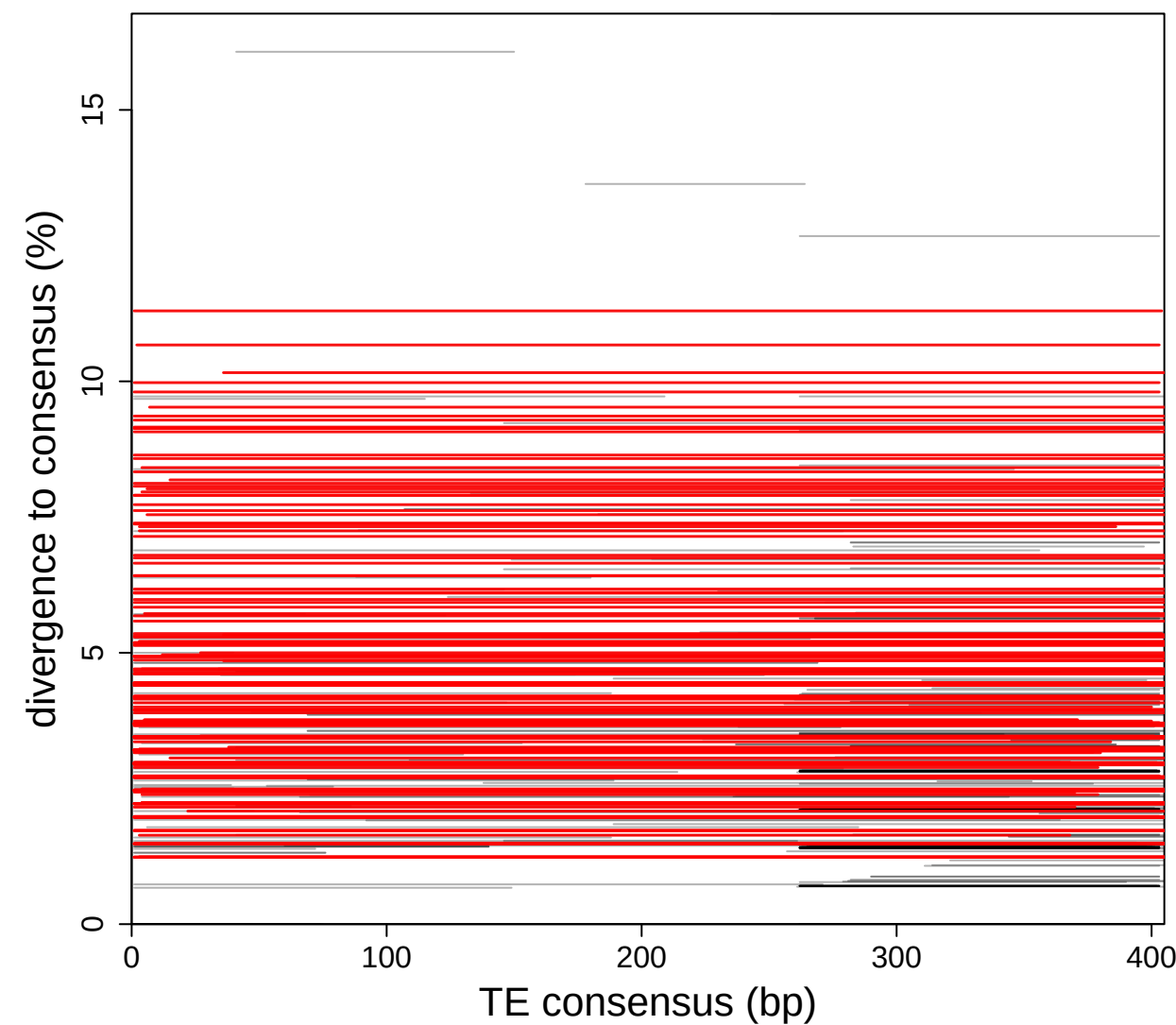


f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcl
size: 1386bp; fragments: 923; full length: 0 (>=1247.4bp)

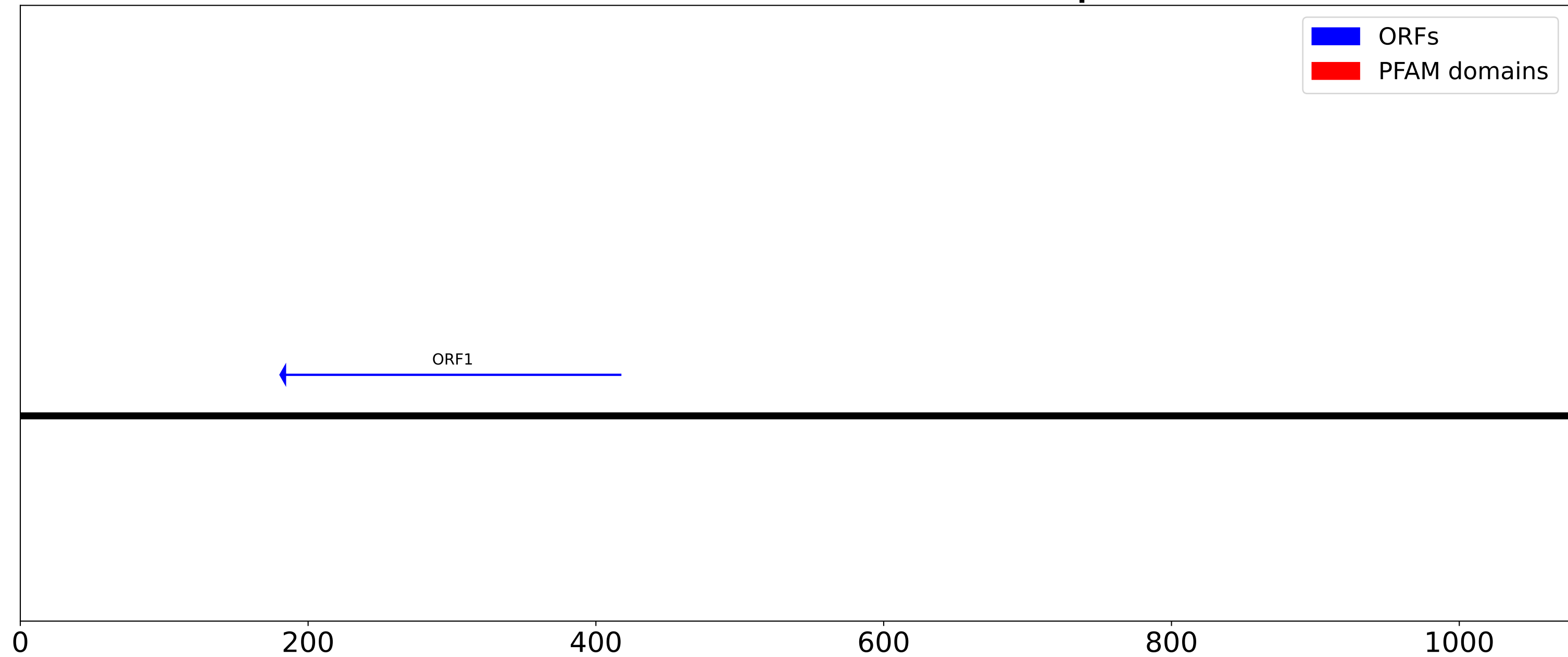
After TEtrimmer Extended plot Blue lines are boundaries



TE: rnd_1_family_997
size: 405bp; fragments: 544; full length: 250 (≥ 364.5 bp)



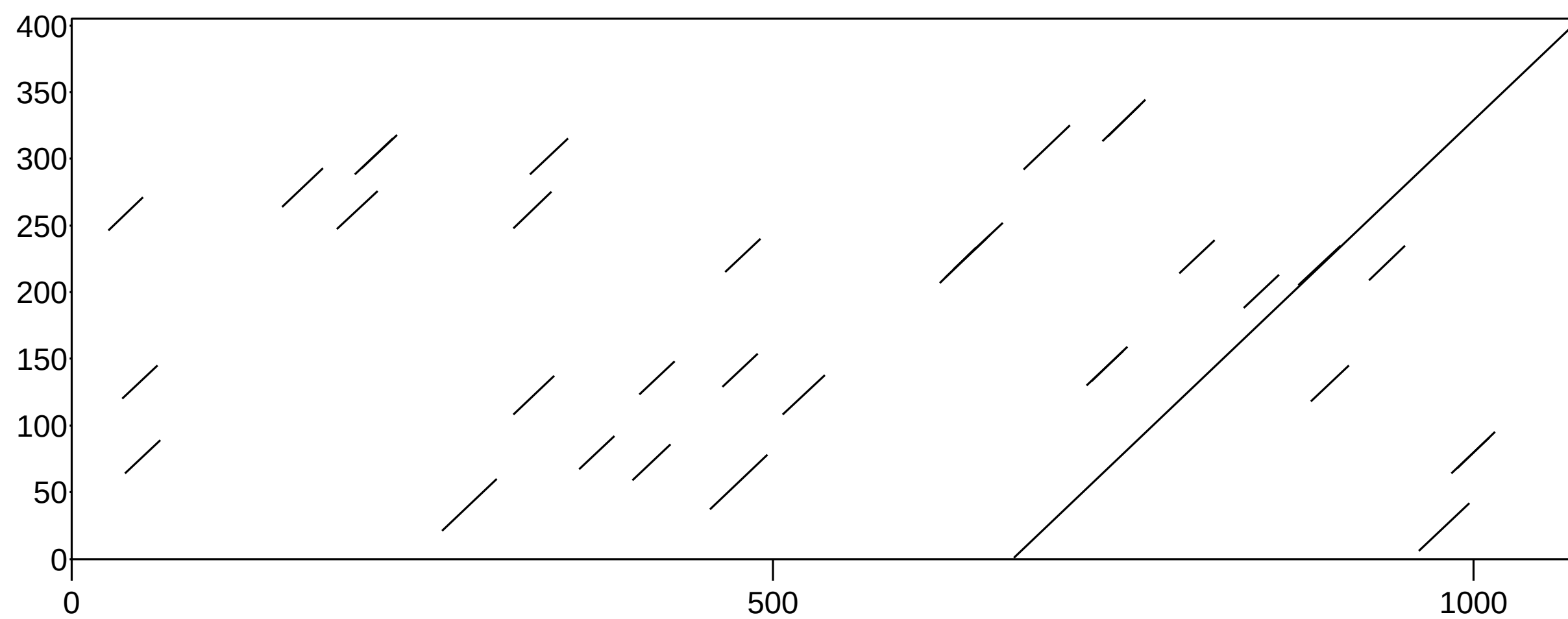
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)