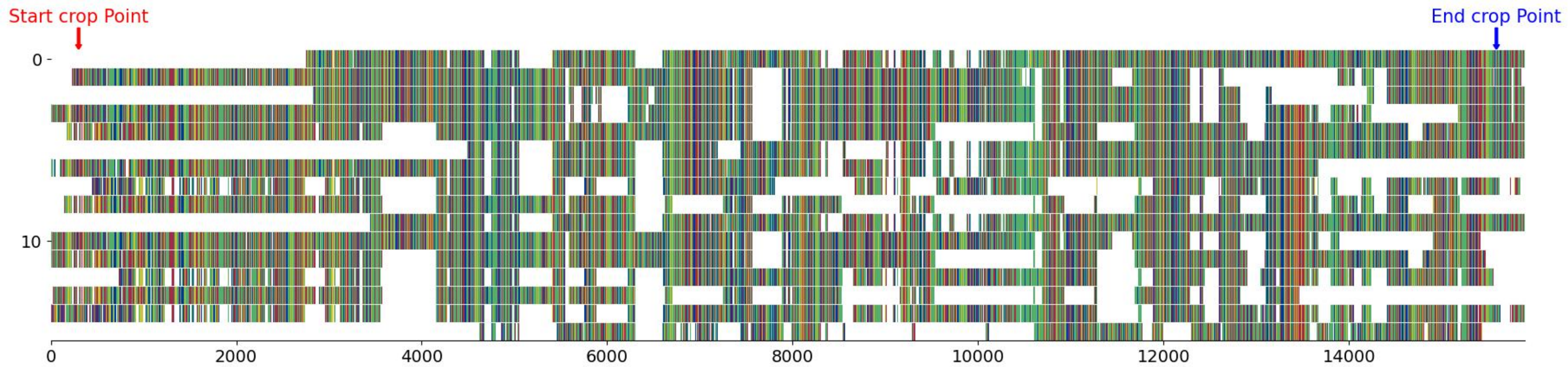


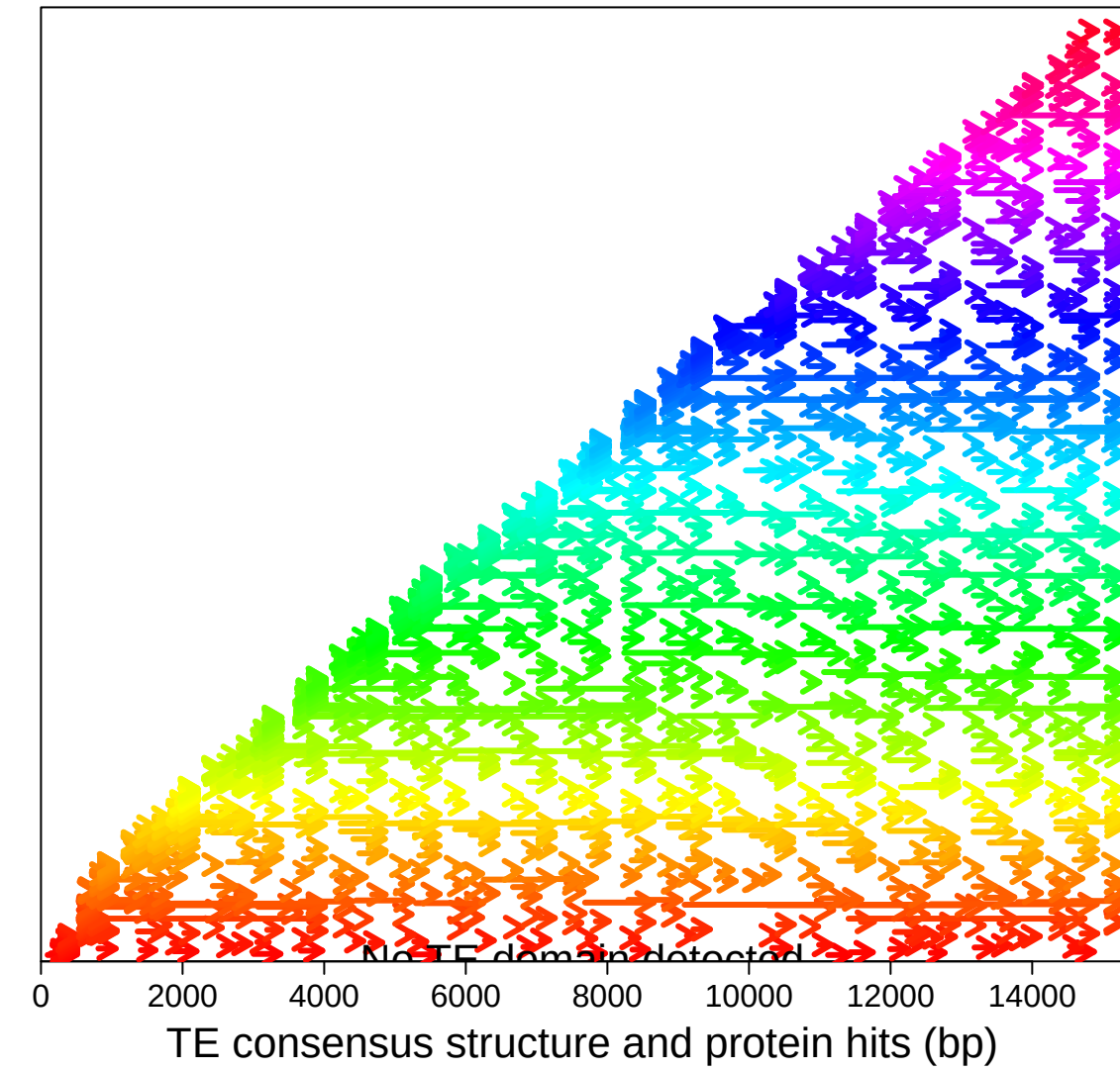
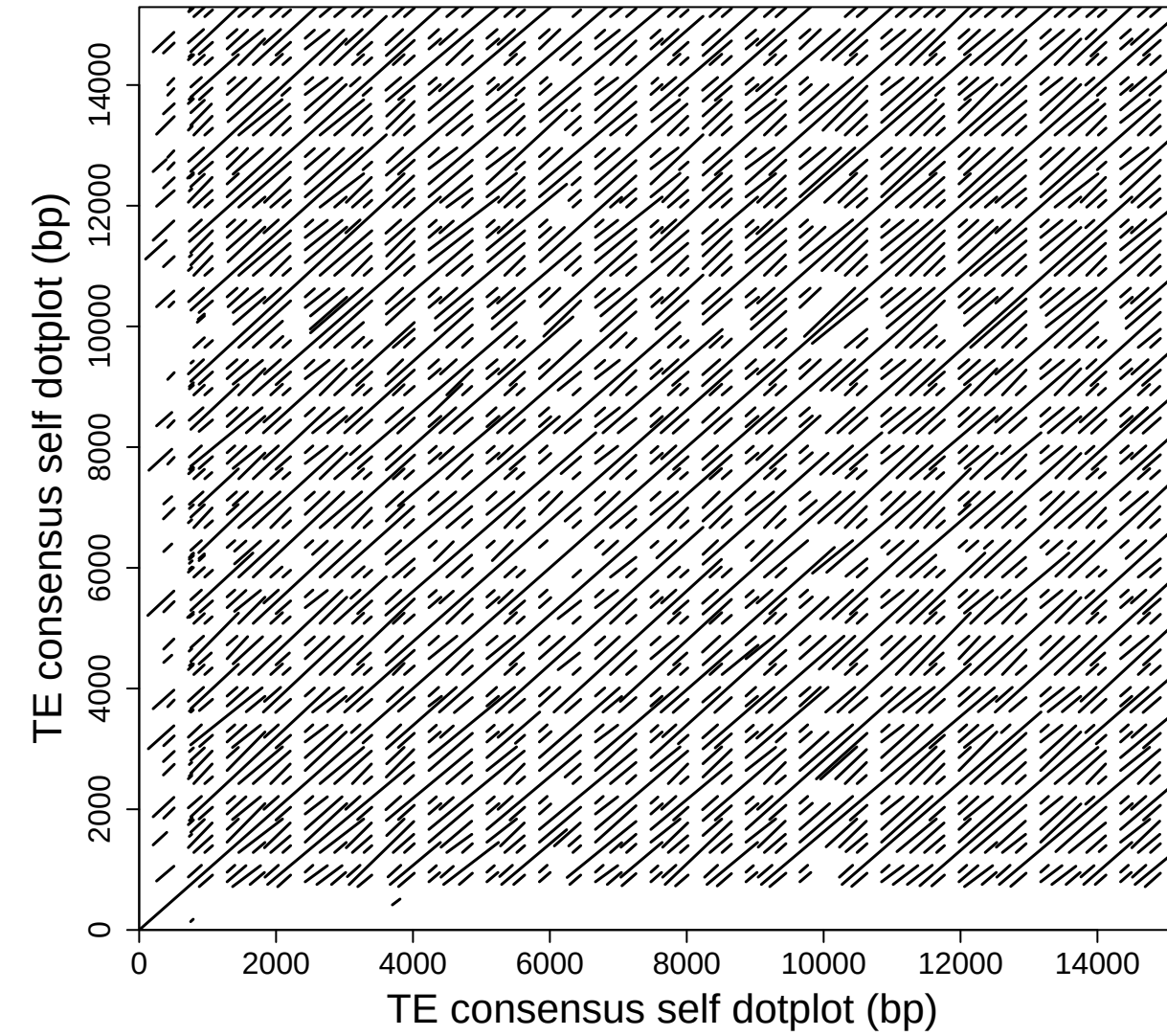
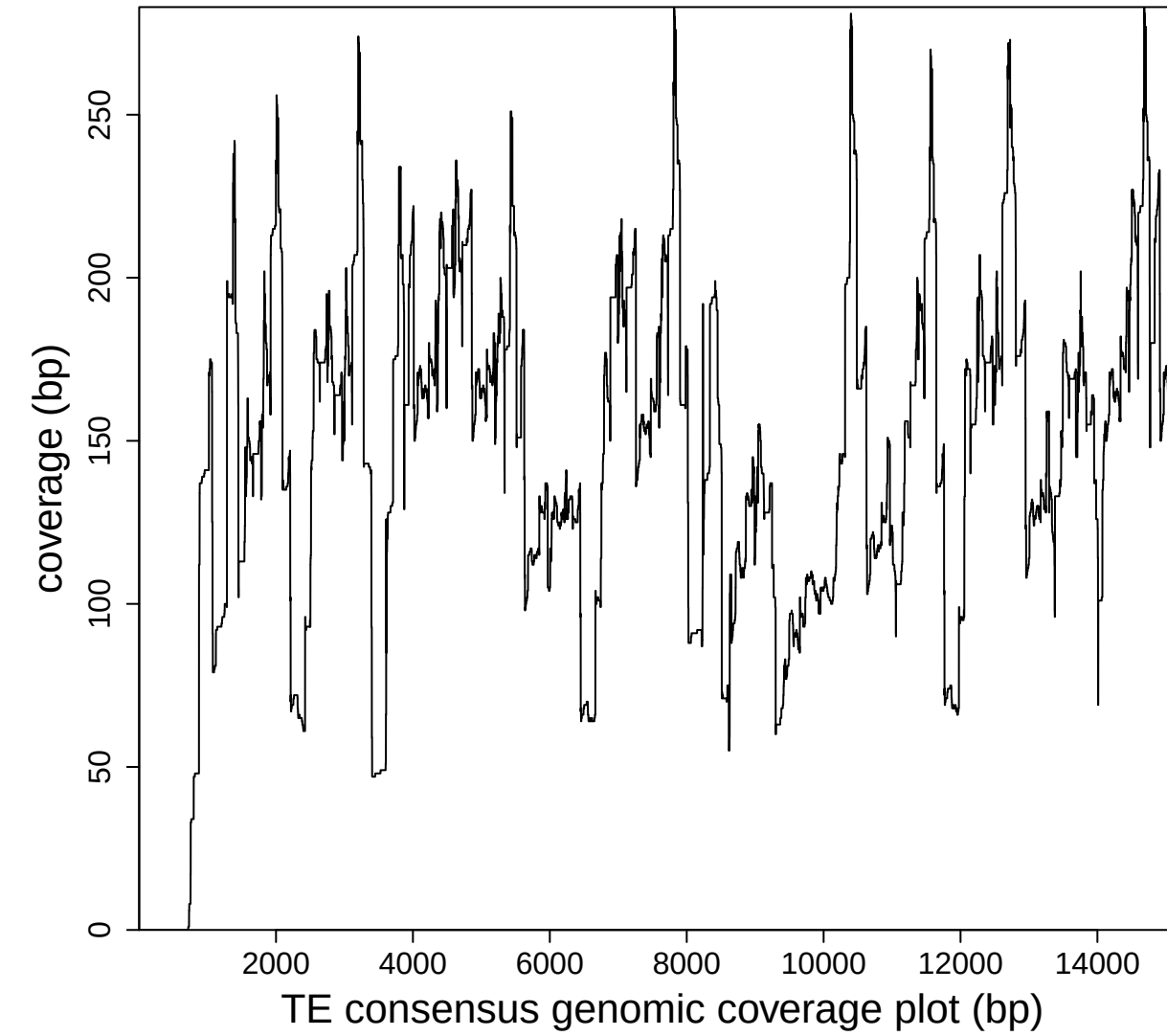
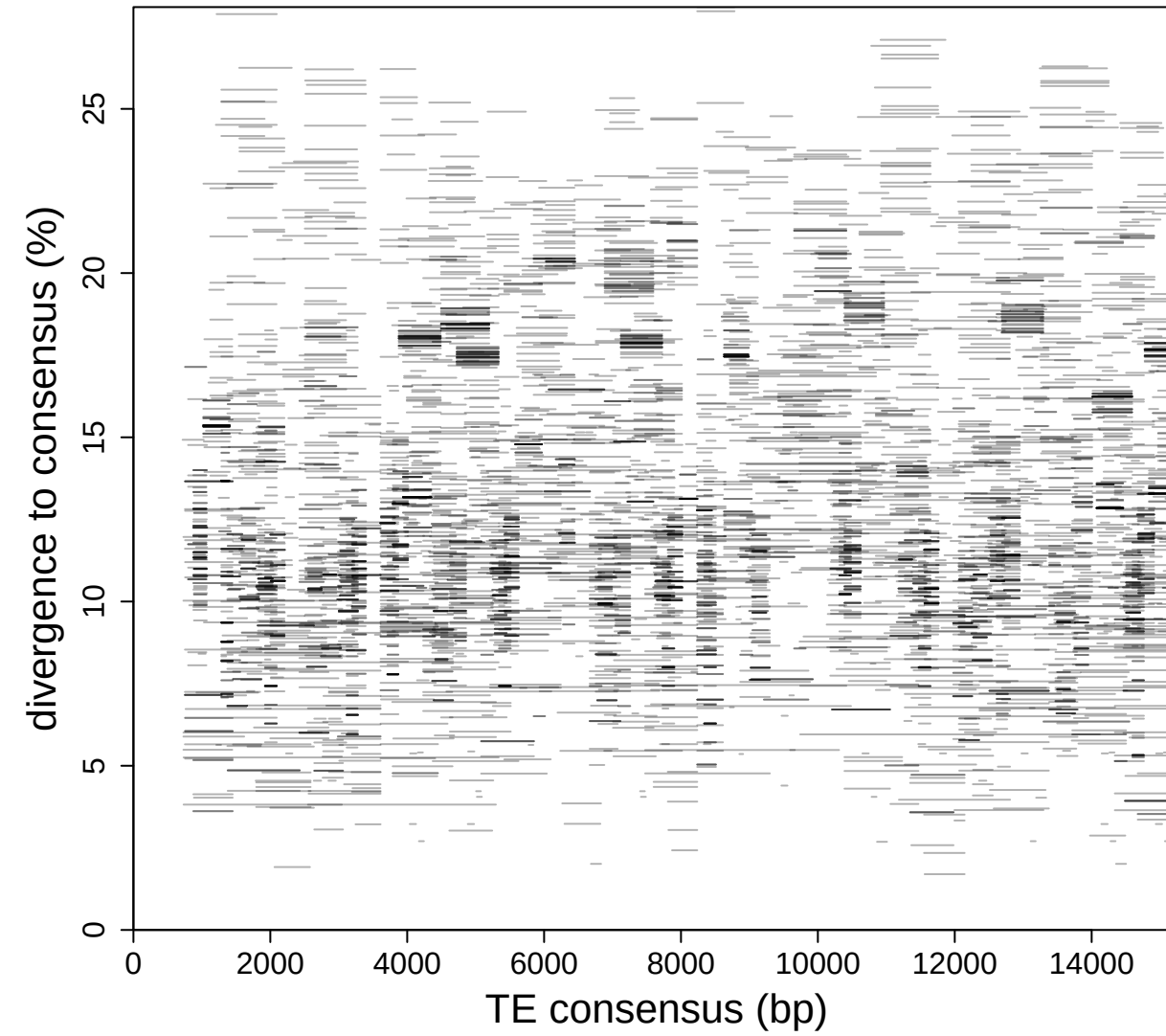
MSA length = 15291

[illegible]



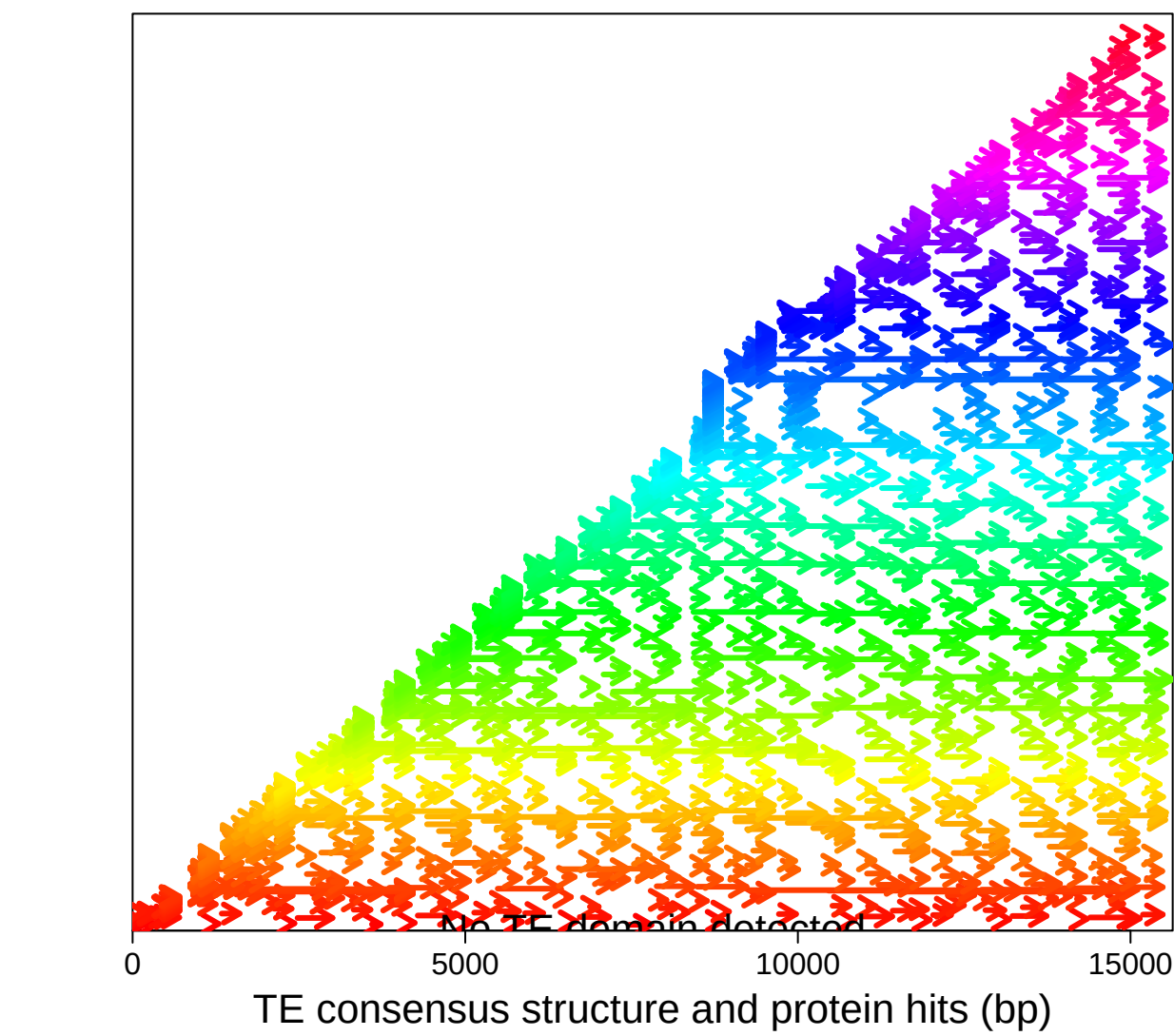
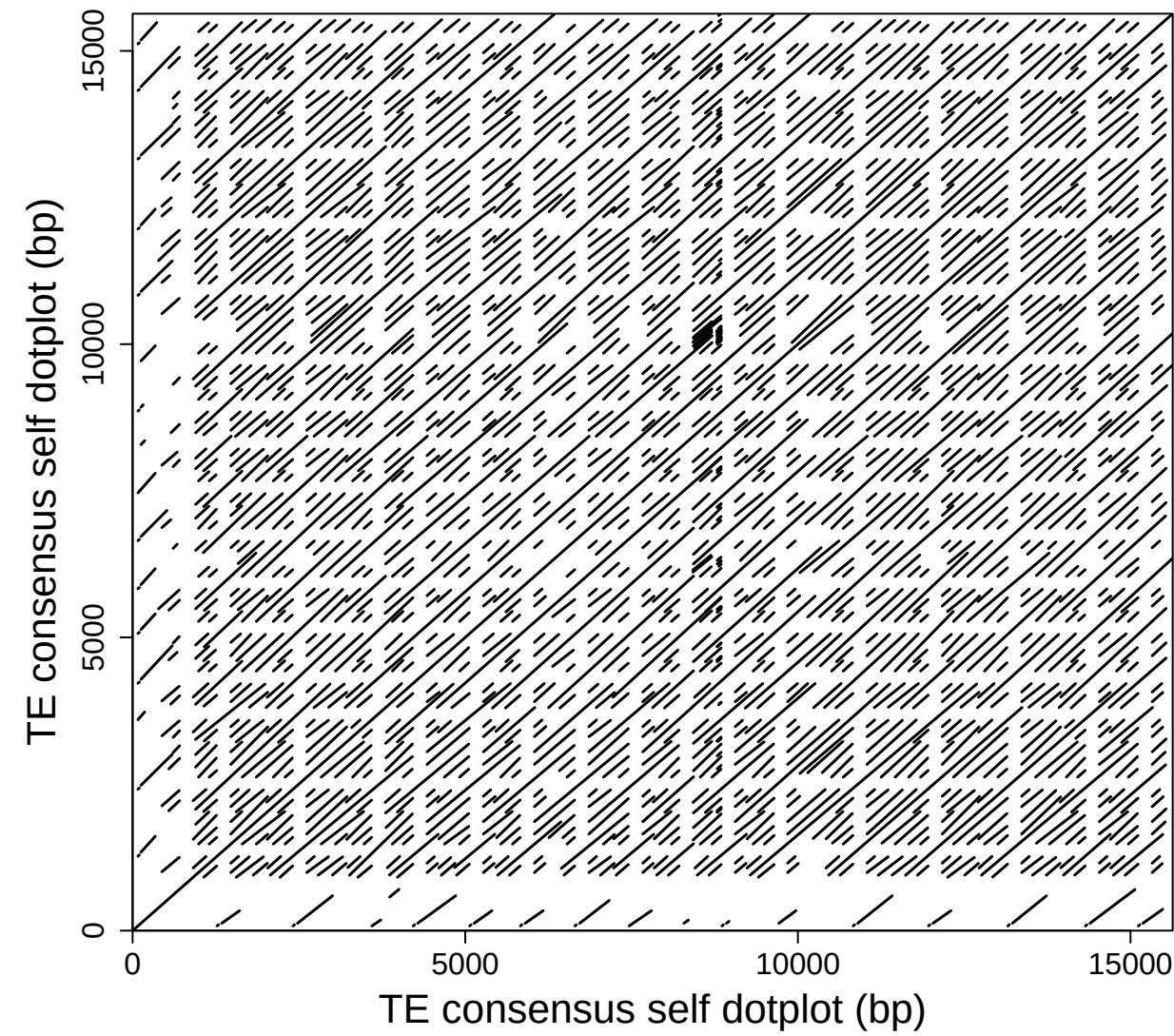
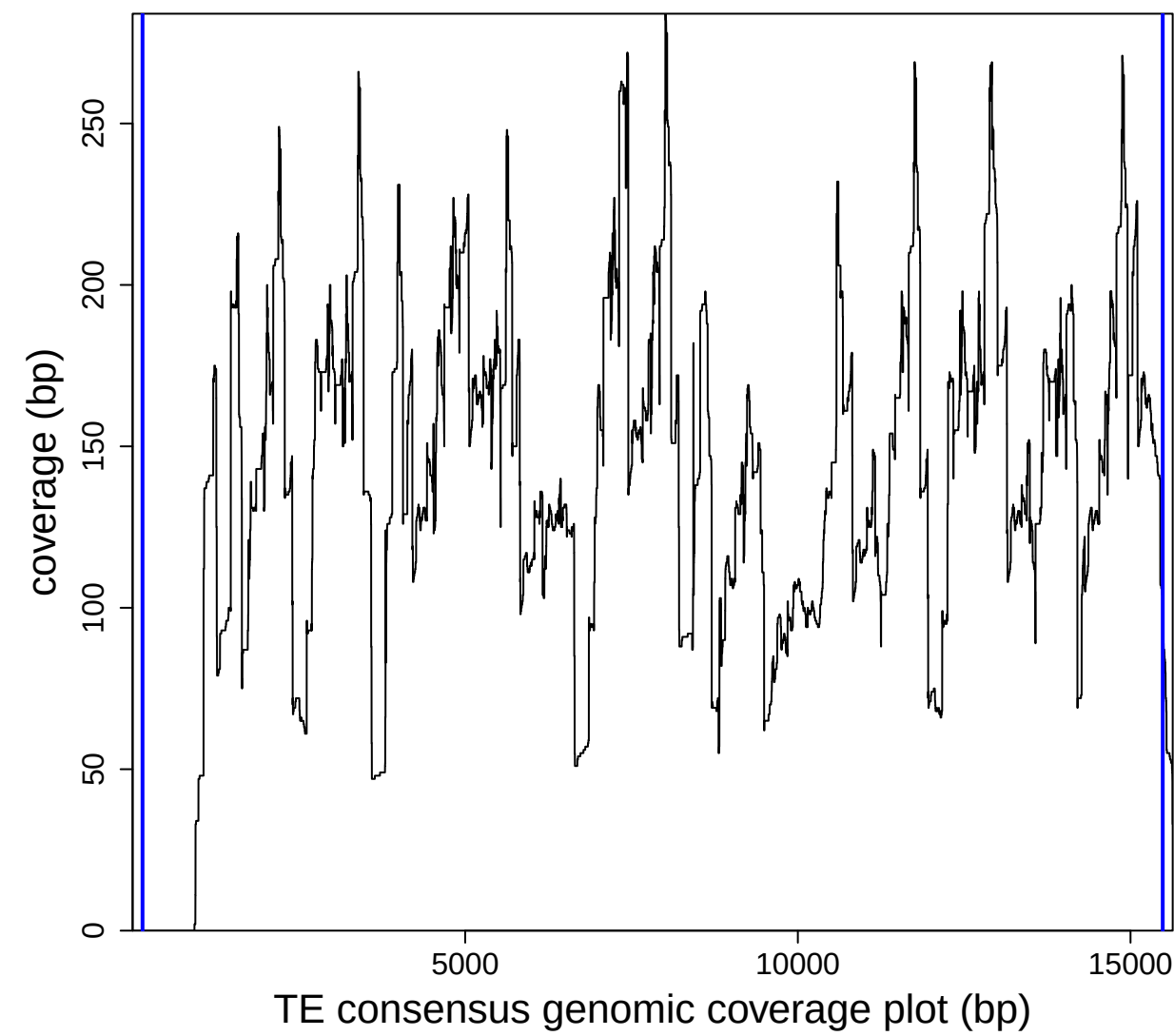
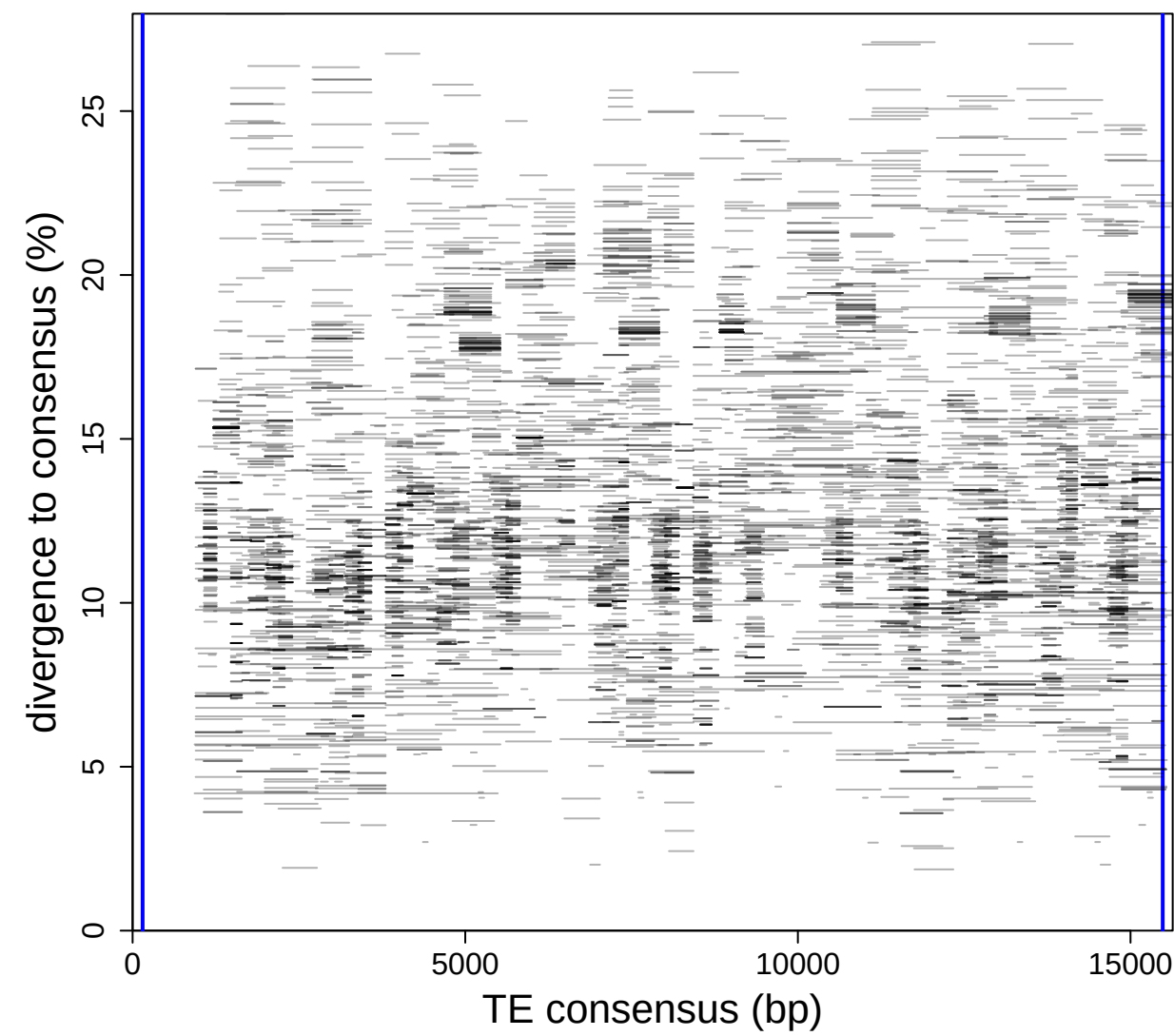
bed_uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c
size: 15291bp; fragments: 5347; full length: 0 (>=13761.9bp)

After TEtrimmer 15291 bp

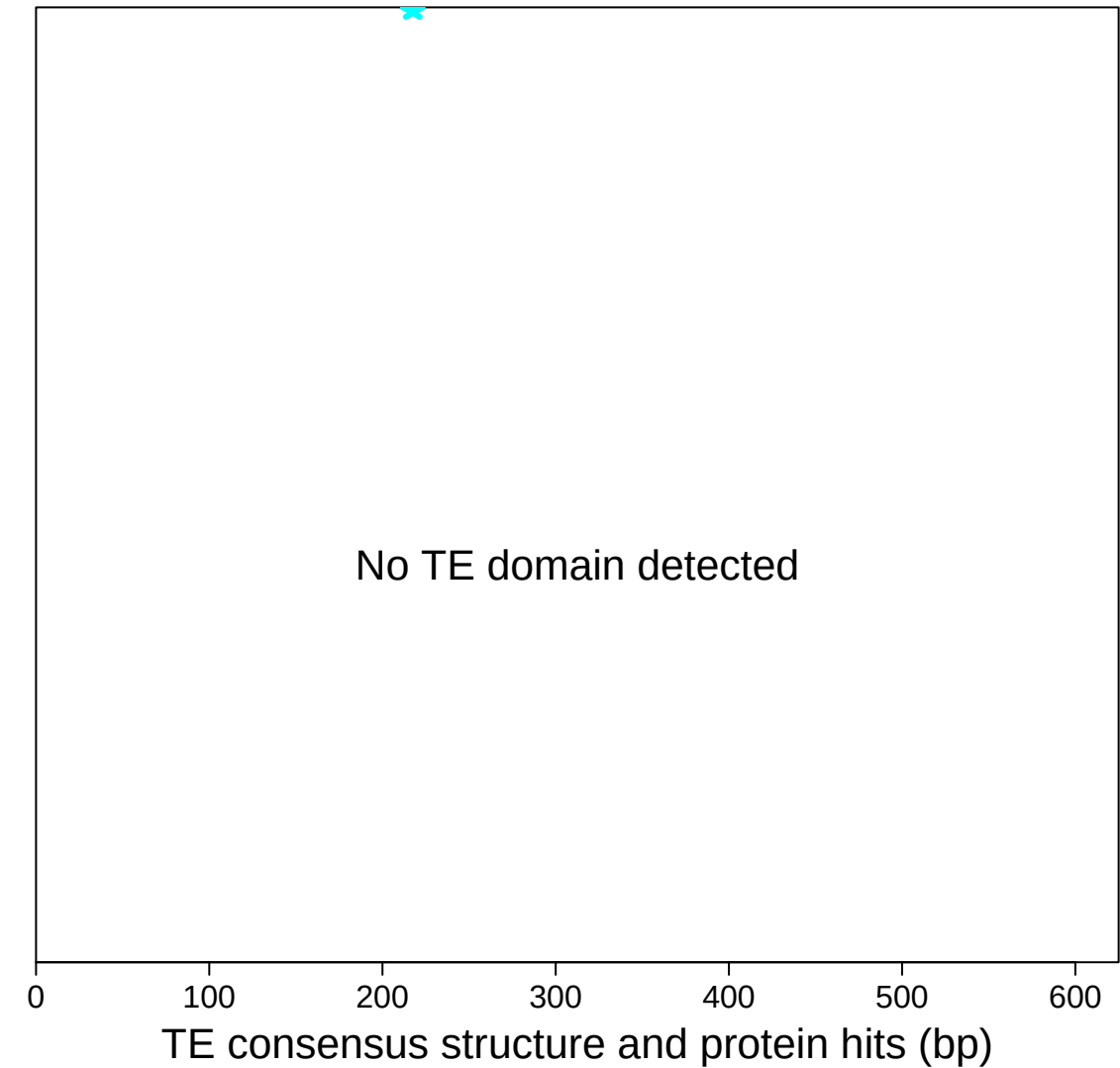
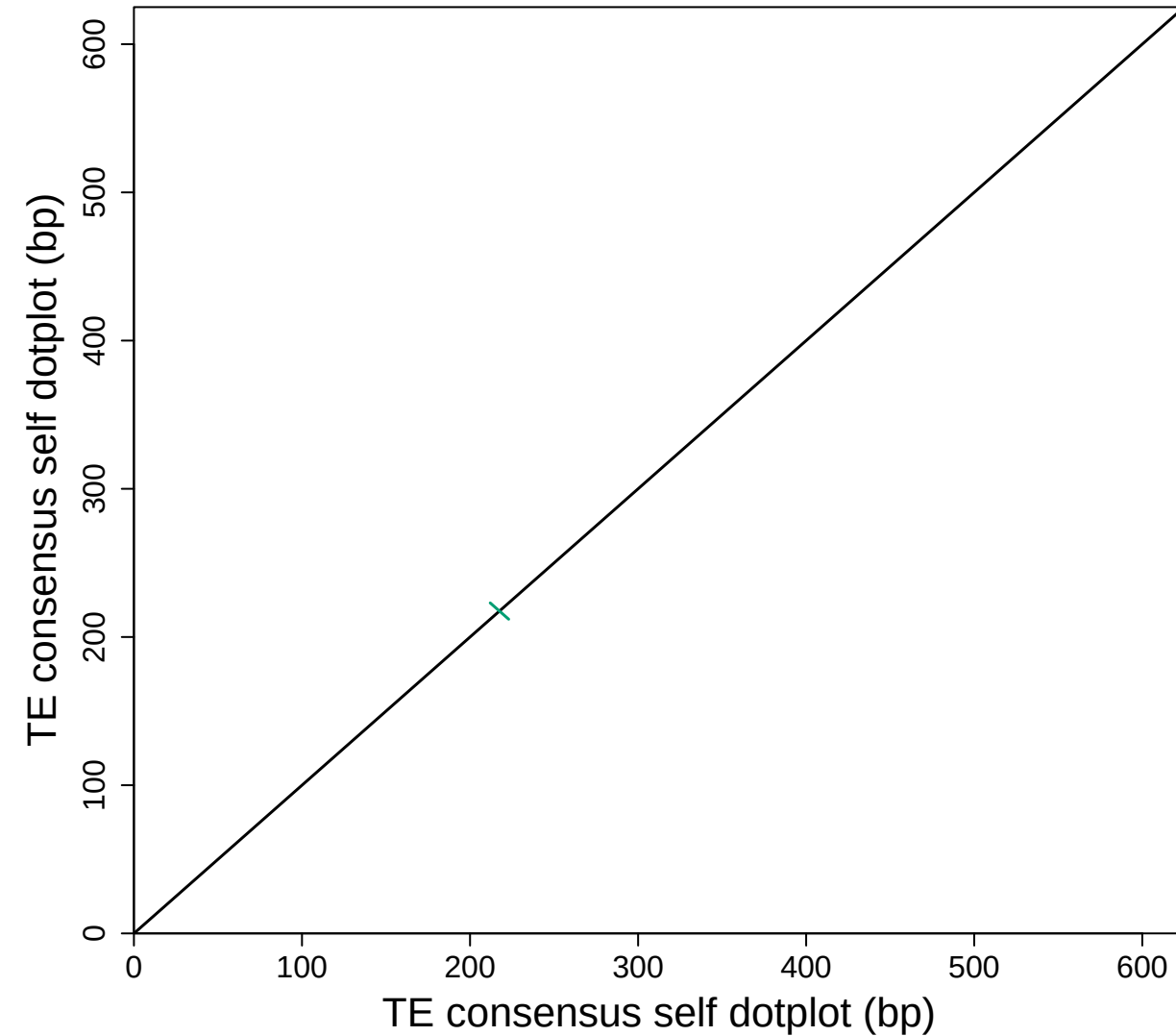
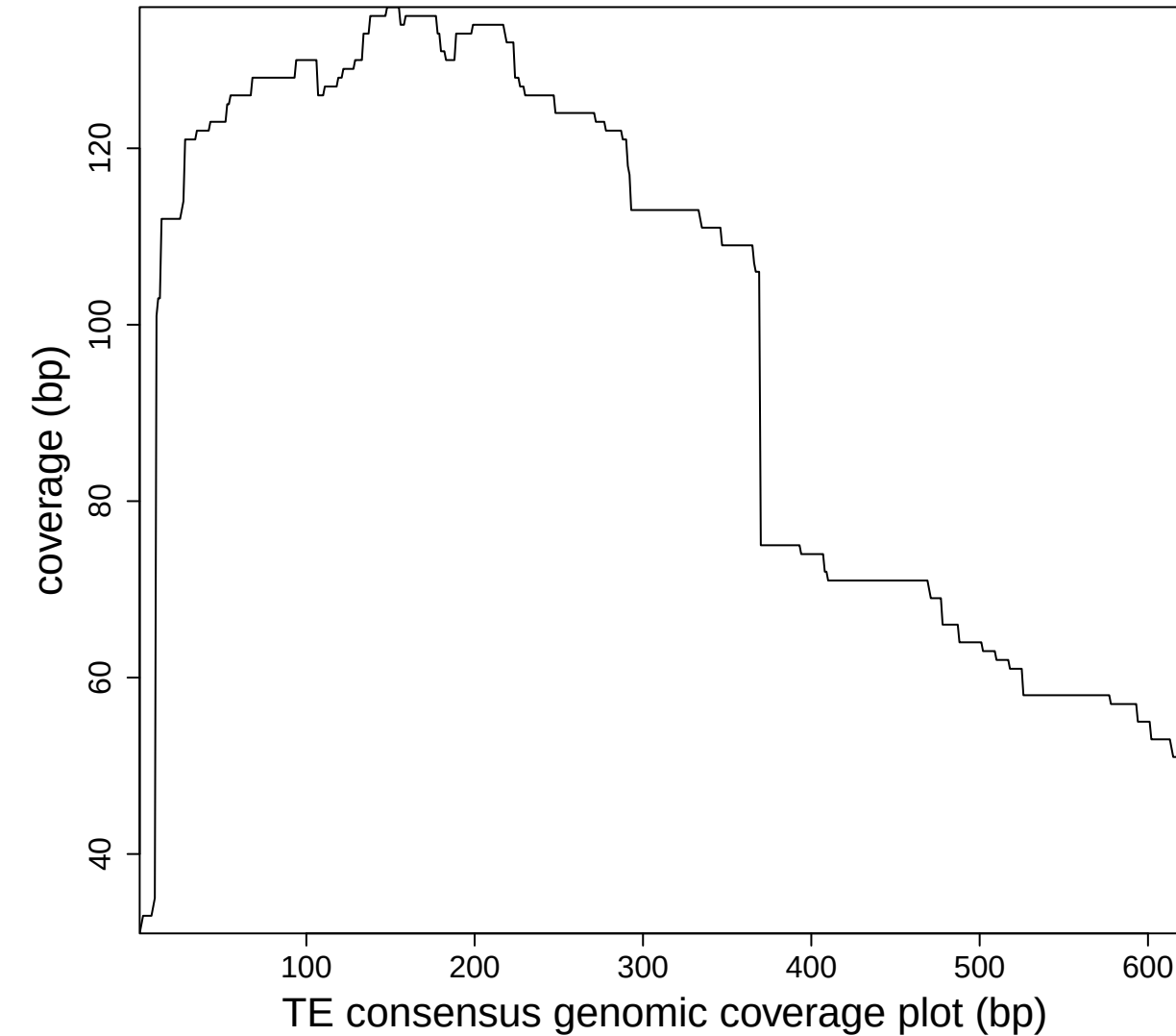
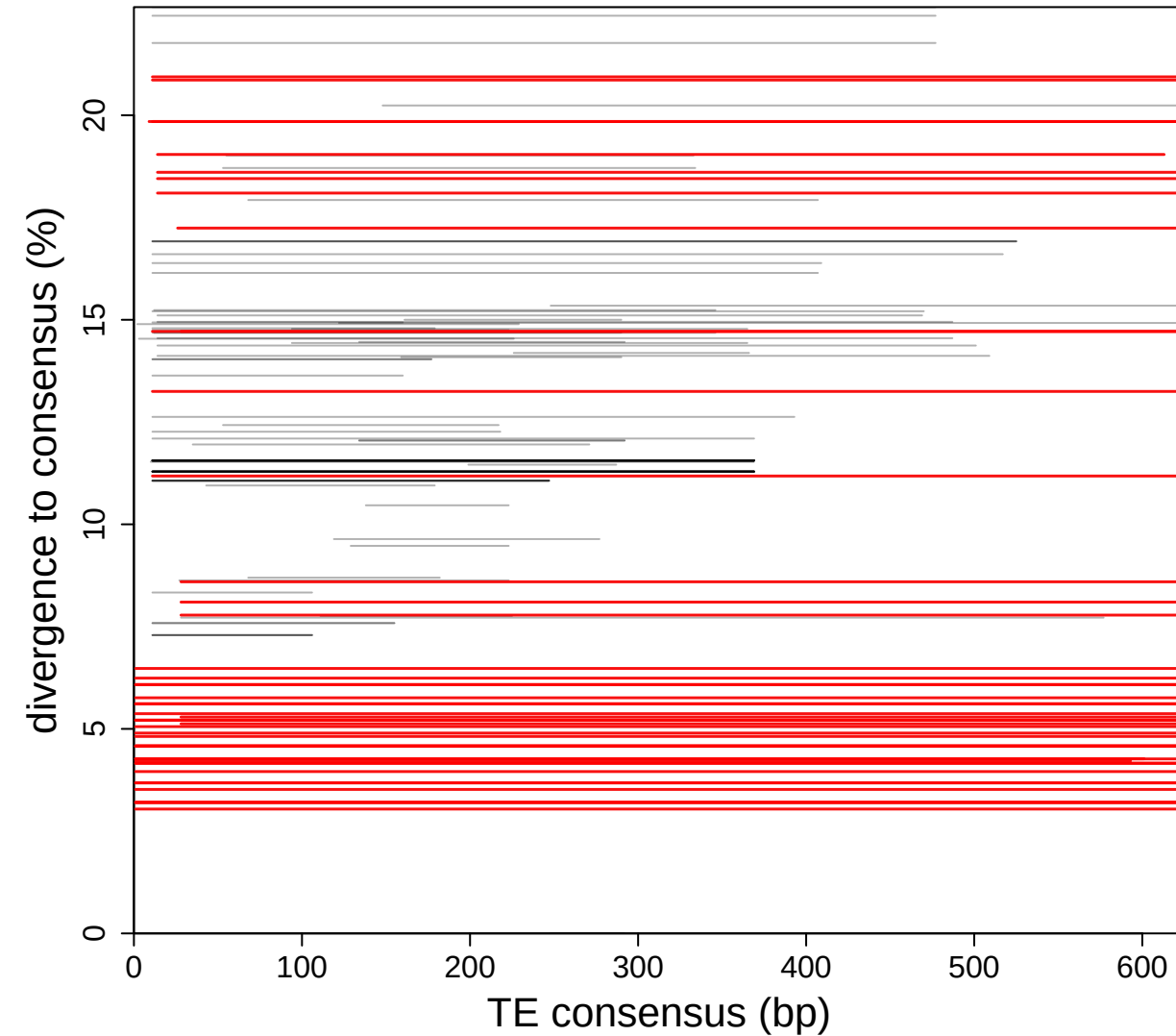


ly_1783.fasta.b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.f
size: 15634bp; fragments: 5297; full length: 0 (>=14070.6bp)

After TEtrimmer Extended plot Blue lines are boundaries

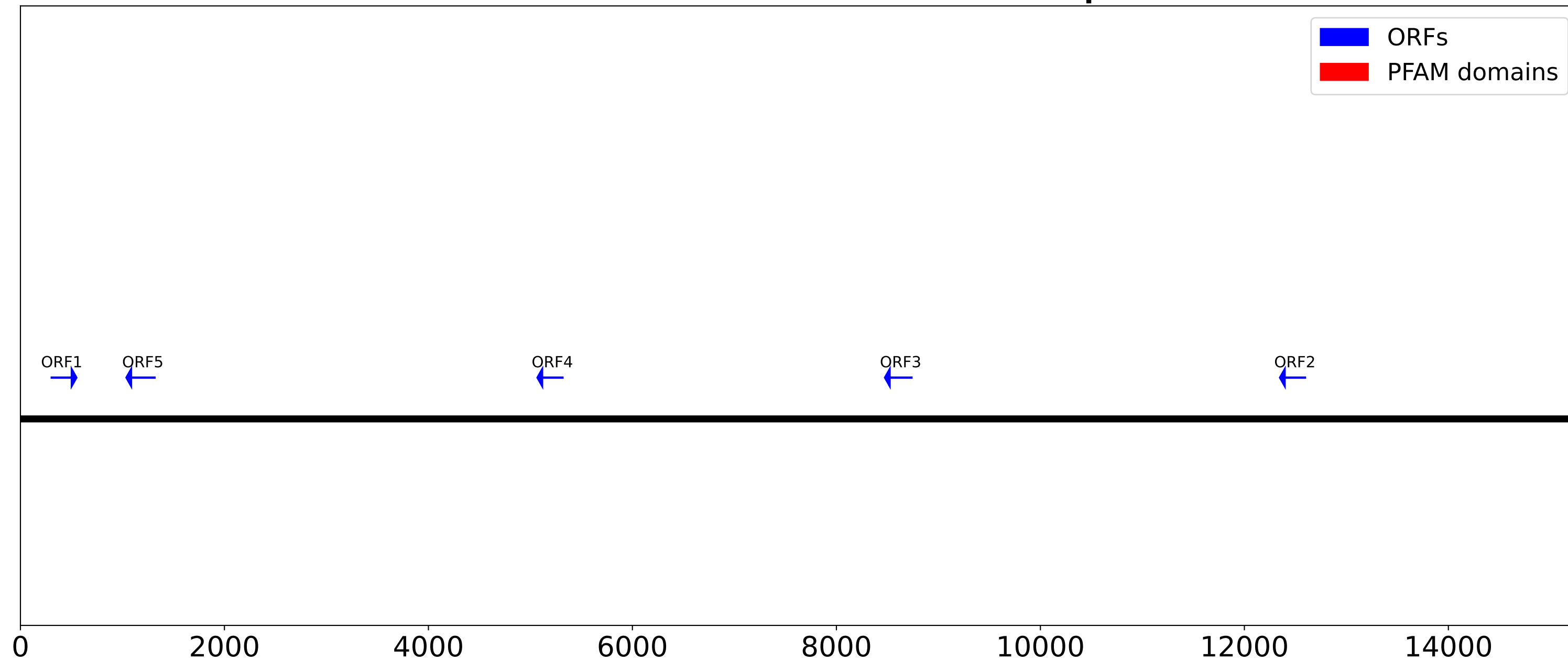


TE: rnd_4_family_1783
size: 625bp; fragments: 151; full length: 49 (≥ 562.5 bp)



Before TEtrimmer 625 bp

After TEtrimmer ORF and PFAM domain plot



Dotplot

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

nsus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)