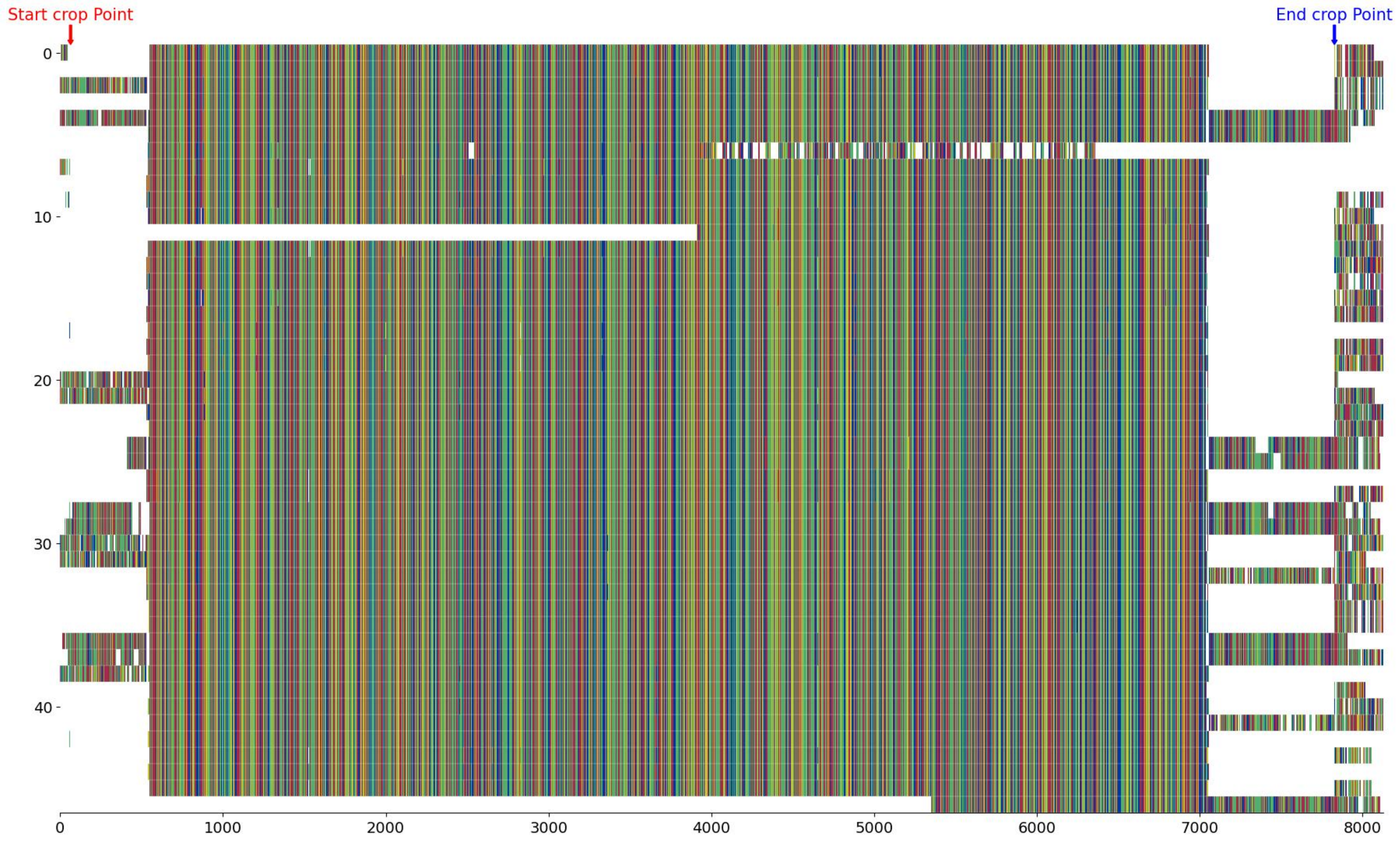


MSA length = 7765

Start crop Point

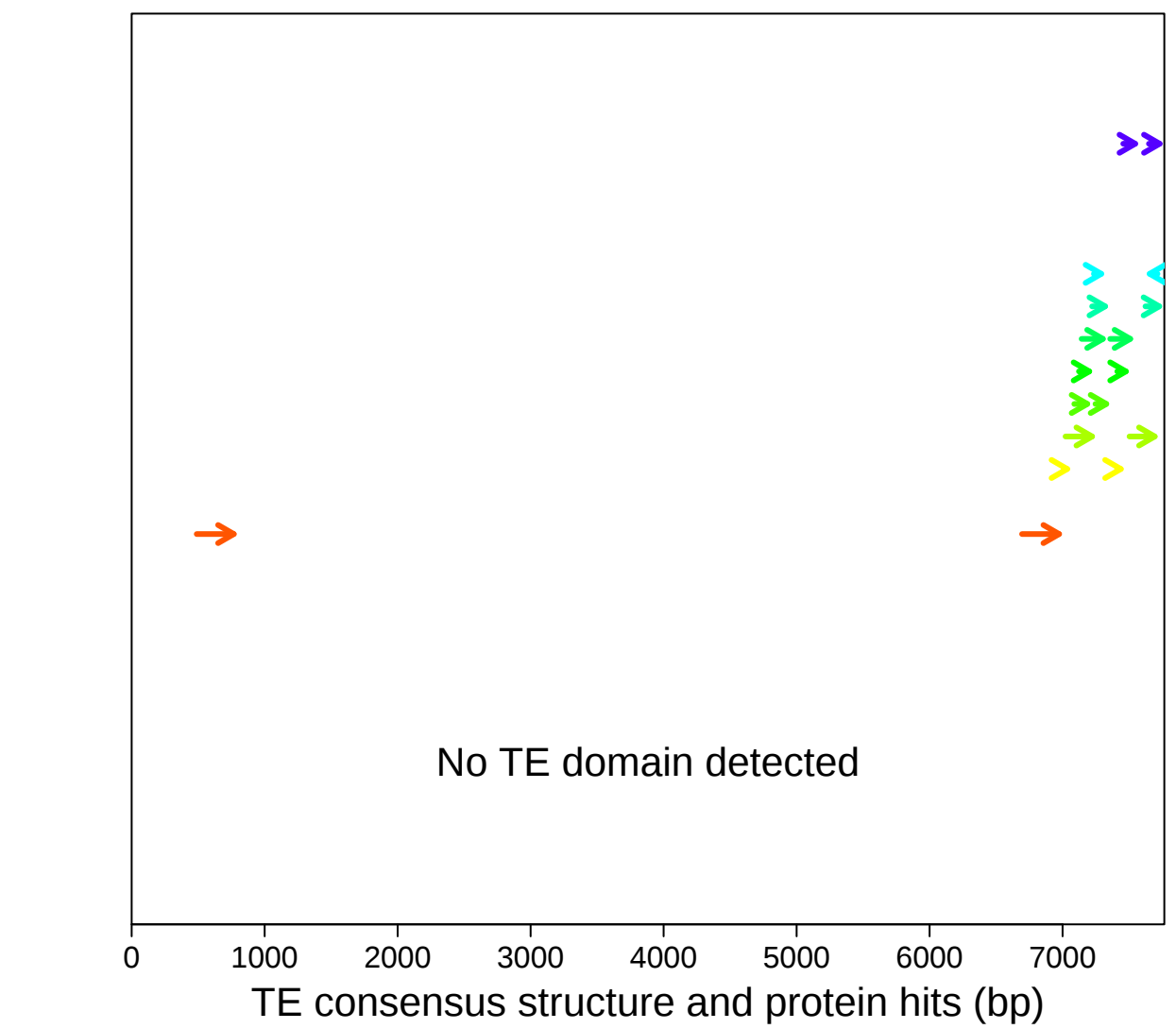
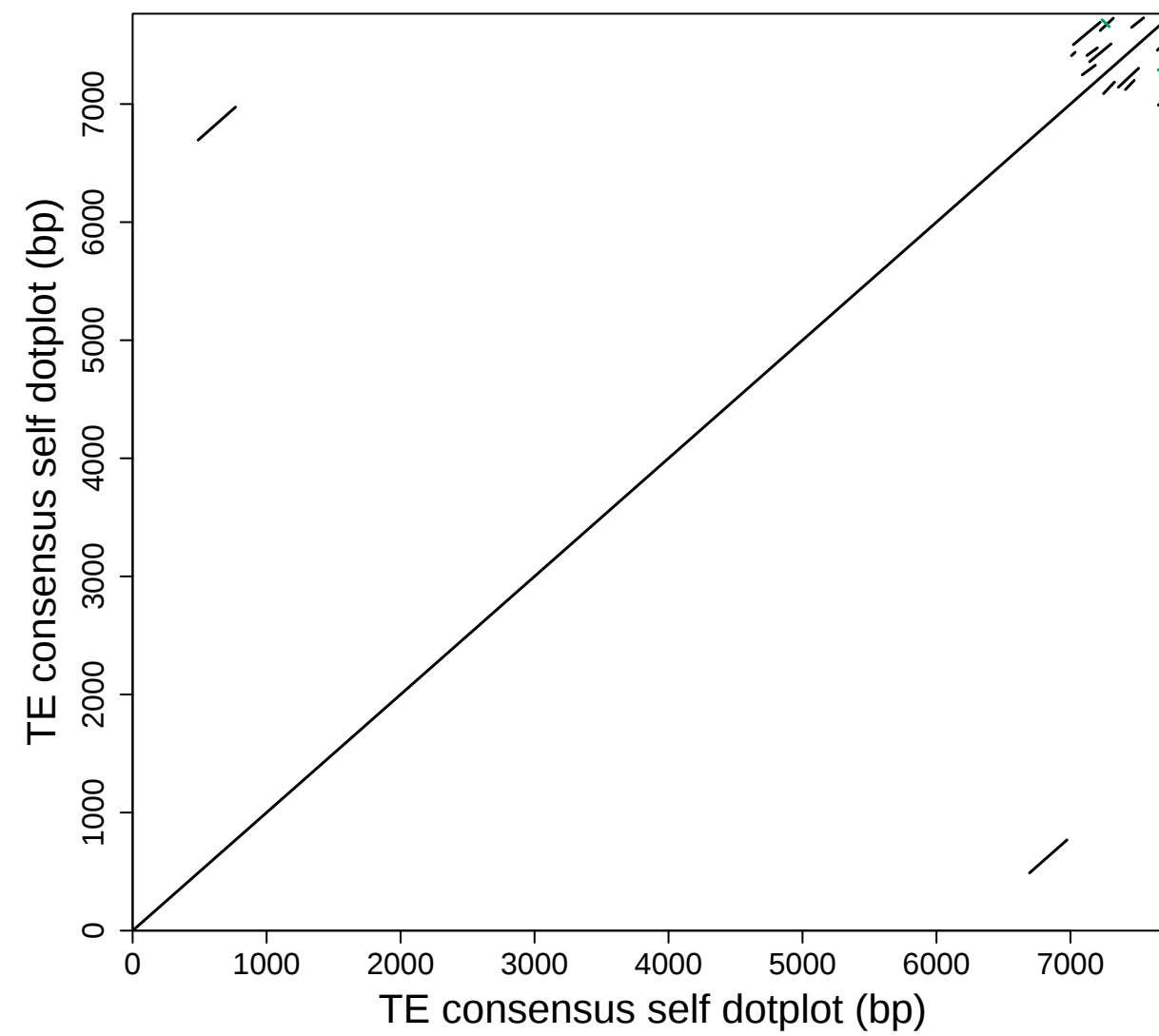
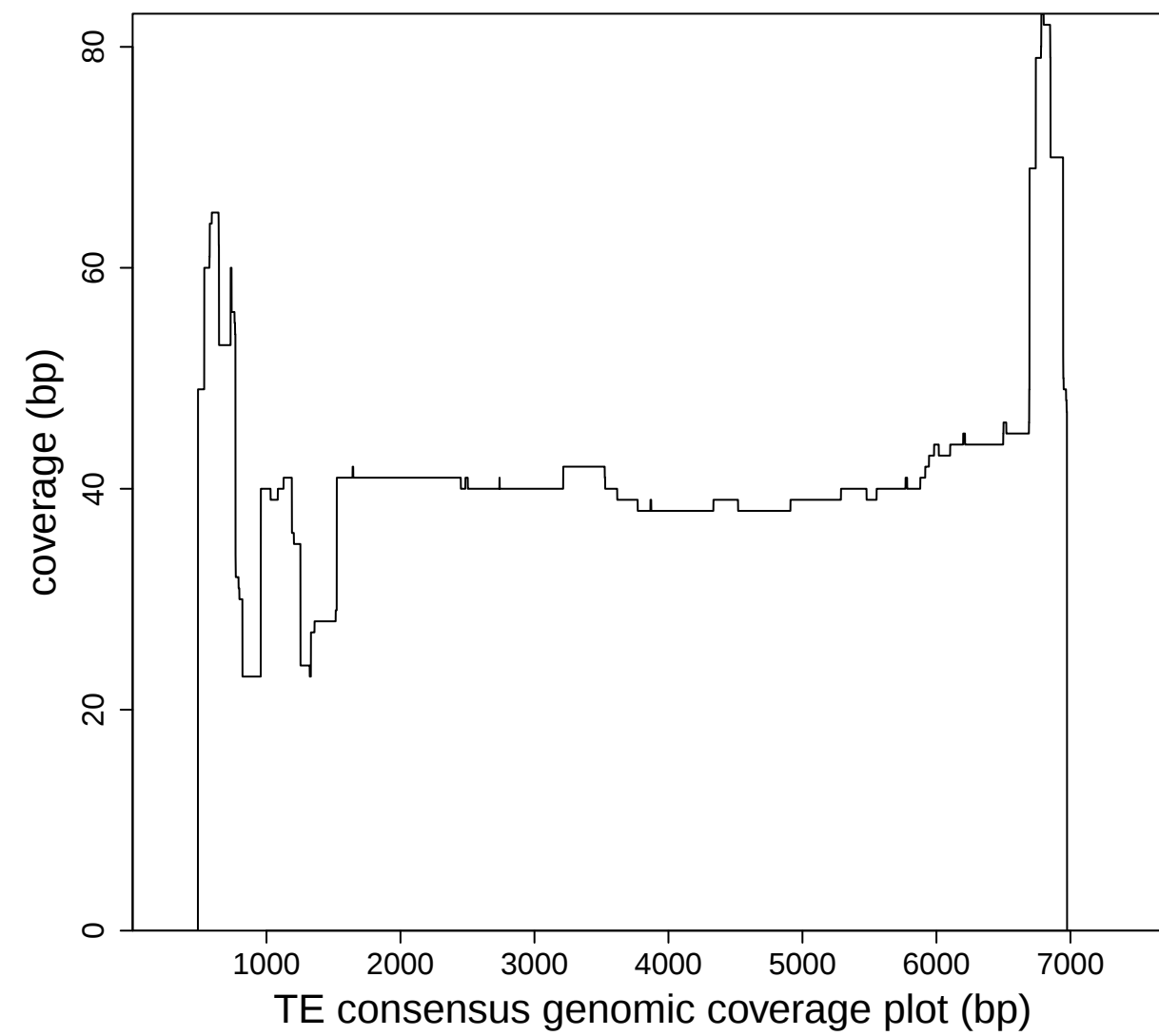
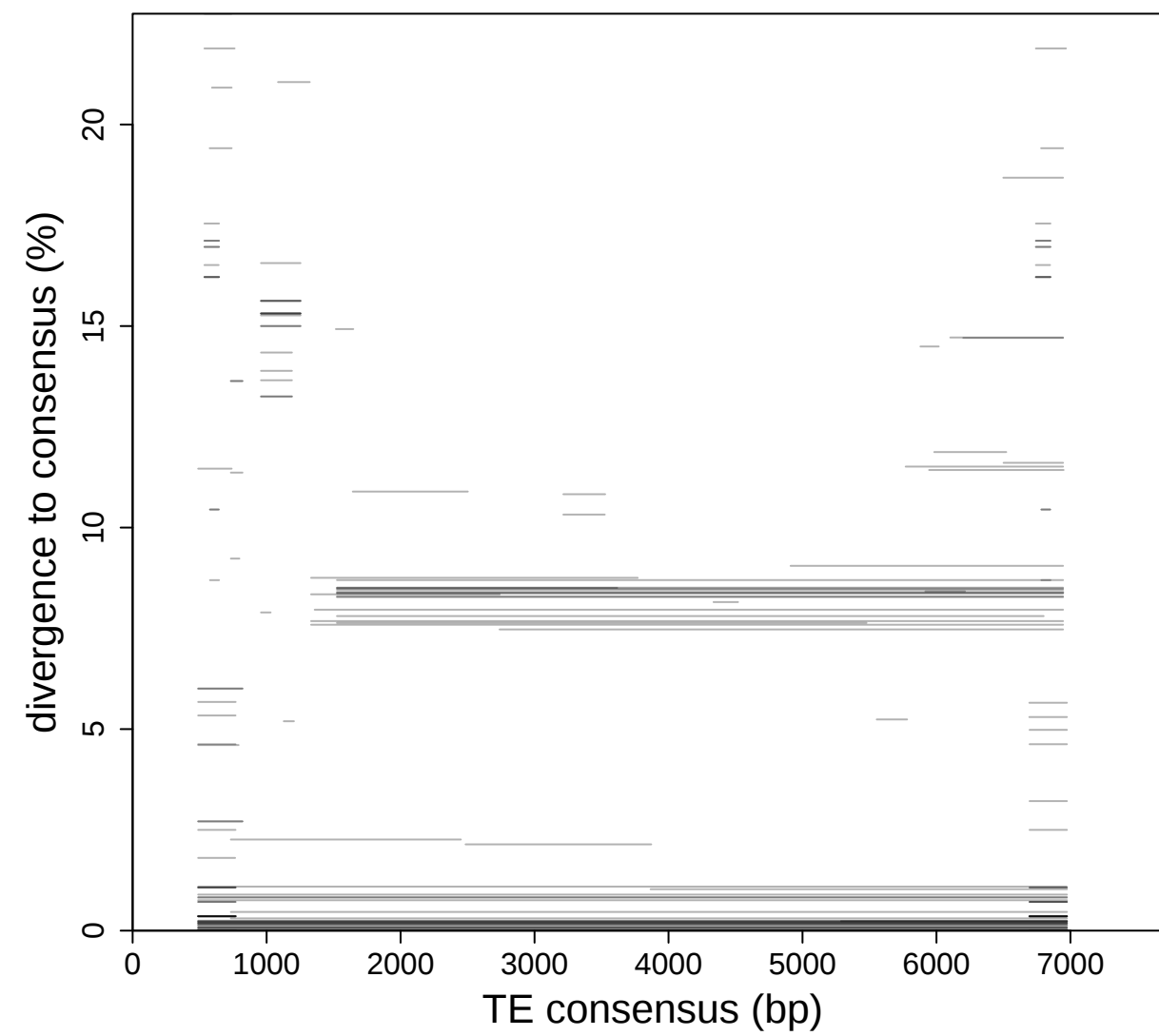
End crop Point

The figure displays a Multiple Sequence Alignment (MSA) of nucleotide sequences. The total length of the MSA is 7765. Two specific points are highlighted: the 'Start crop Point' indicated by a red arrow and the 'End crop Point' indicated by a blue arrow. The sequences are presented in multiple rows, with each row representing a different sequence. Nucleotides are color-coded: Adenine (A) is green, Cytosine (C) is blue, Guanine (G) is red, and Thymine (T) is black. Gaps are represented by dashes (-). The sequences are aligned such that homologous positions are in the same column.



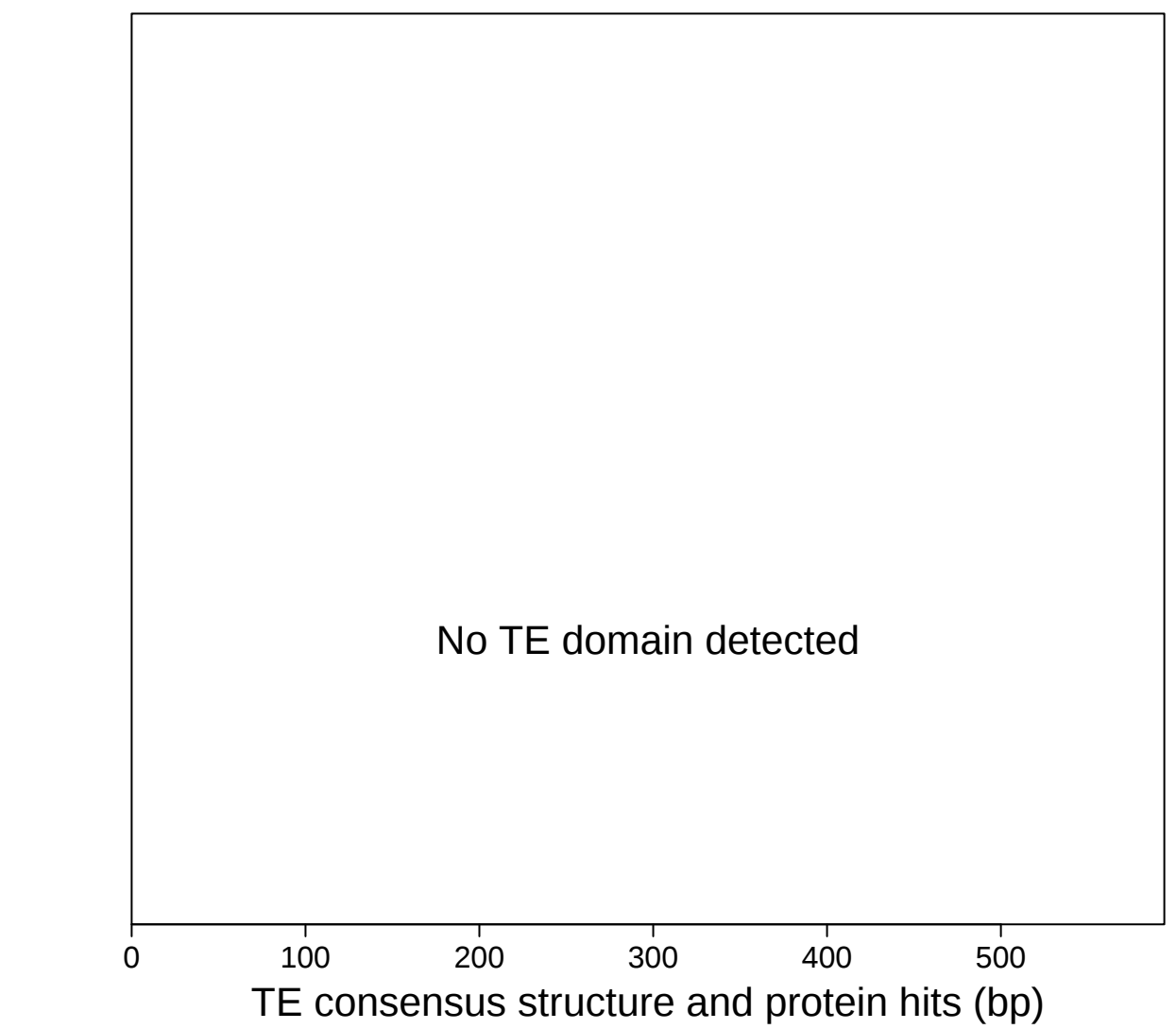
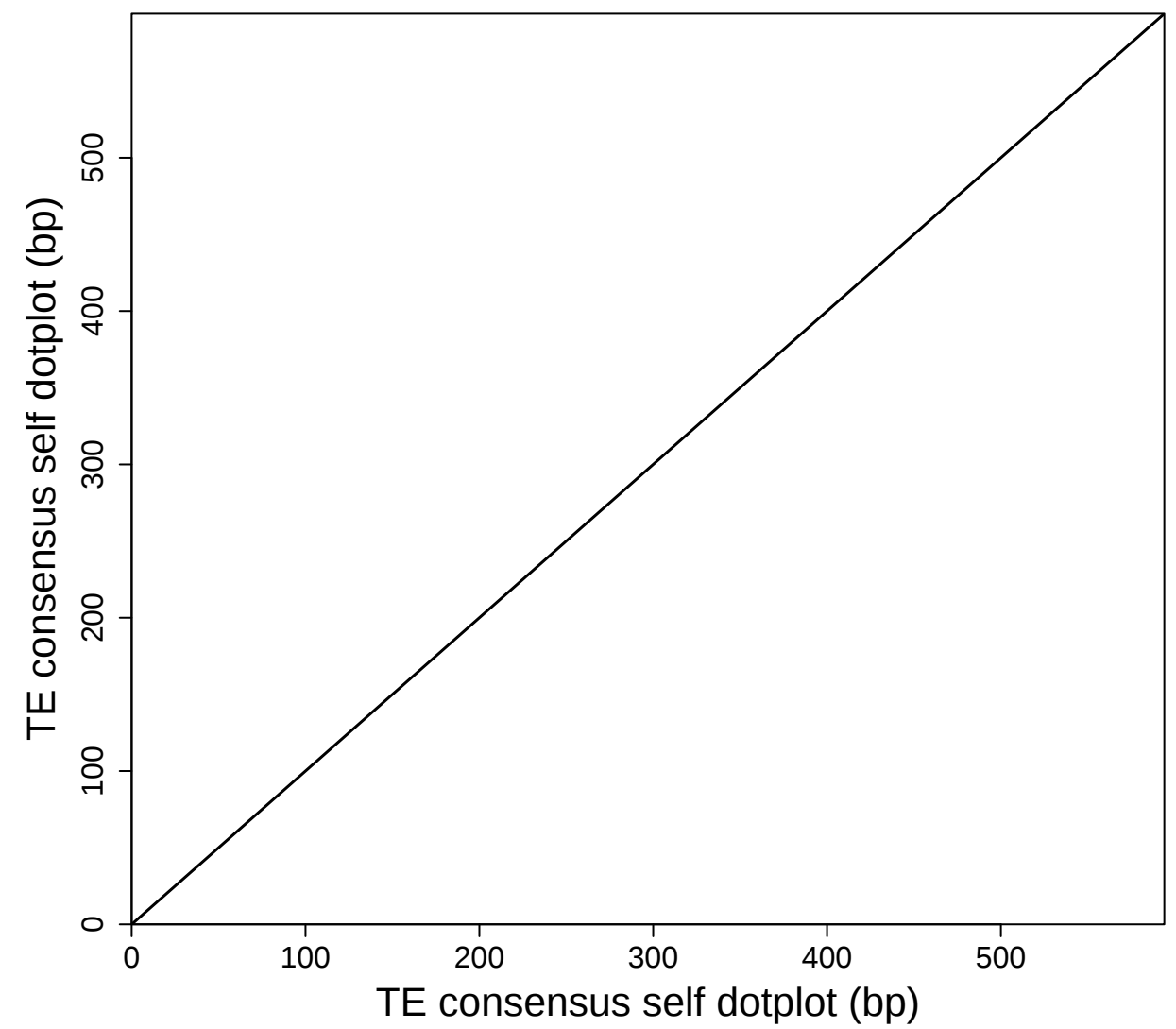
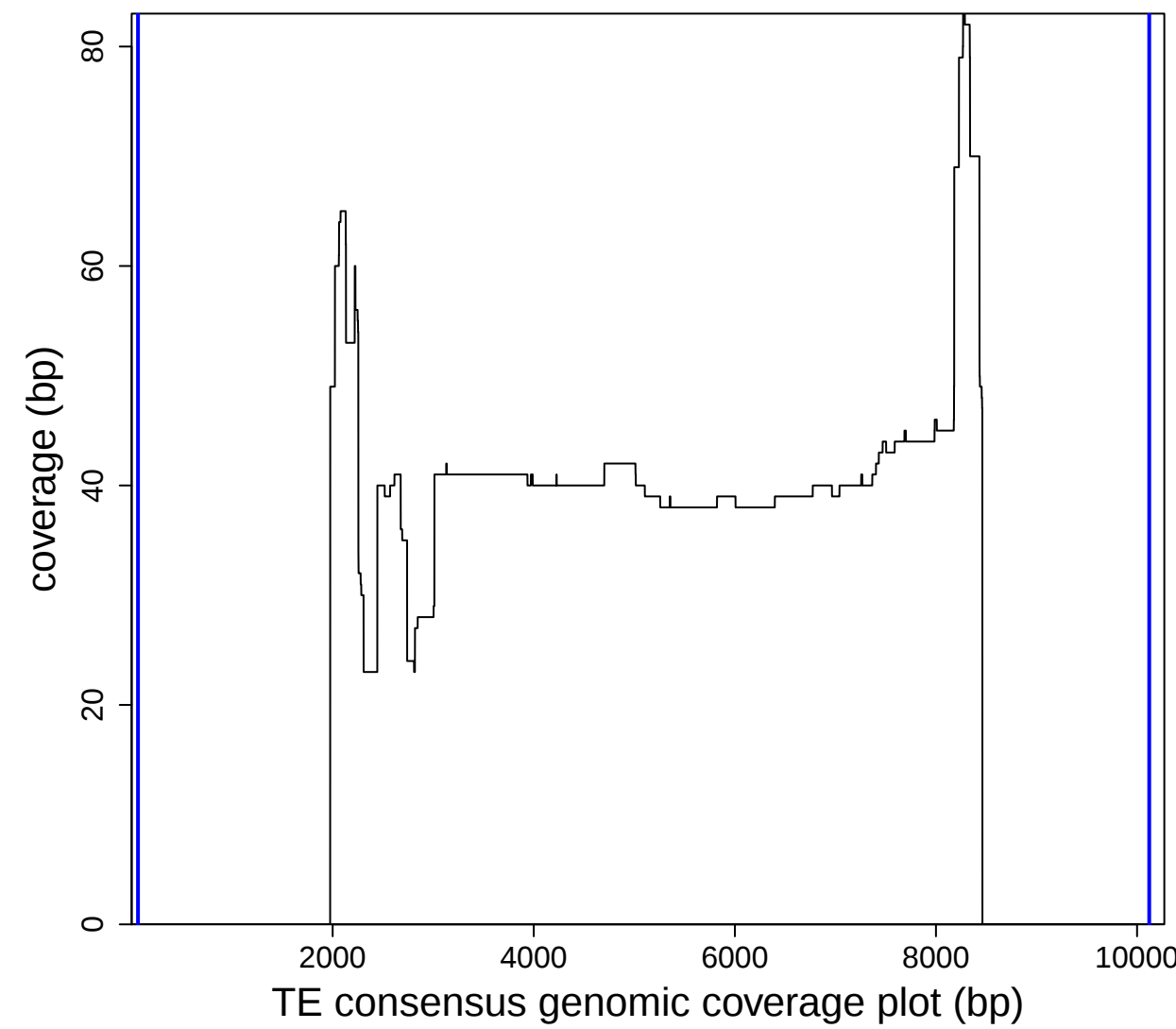
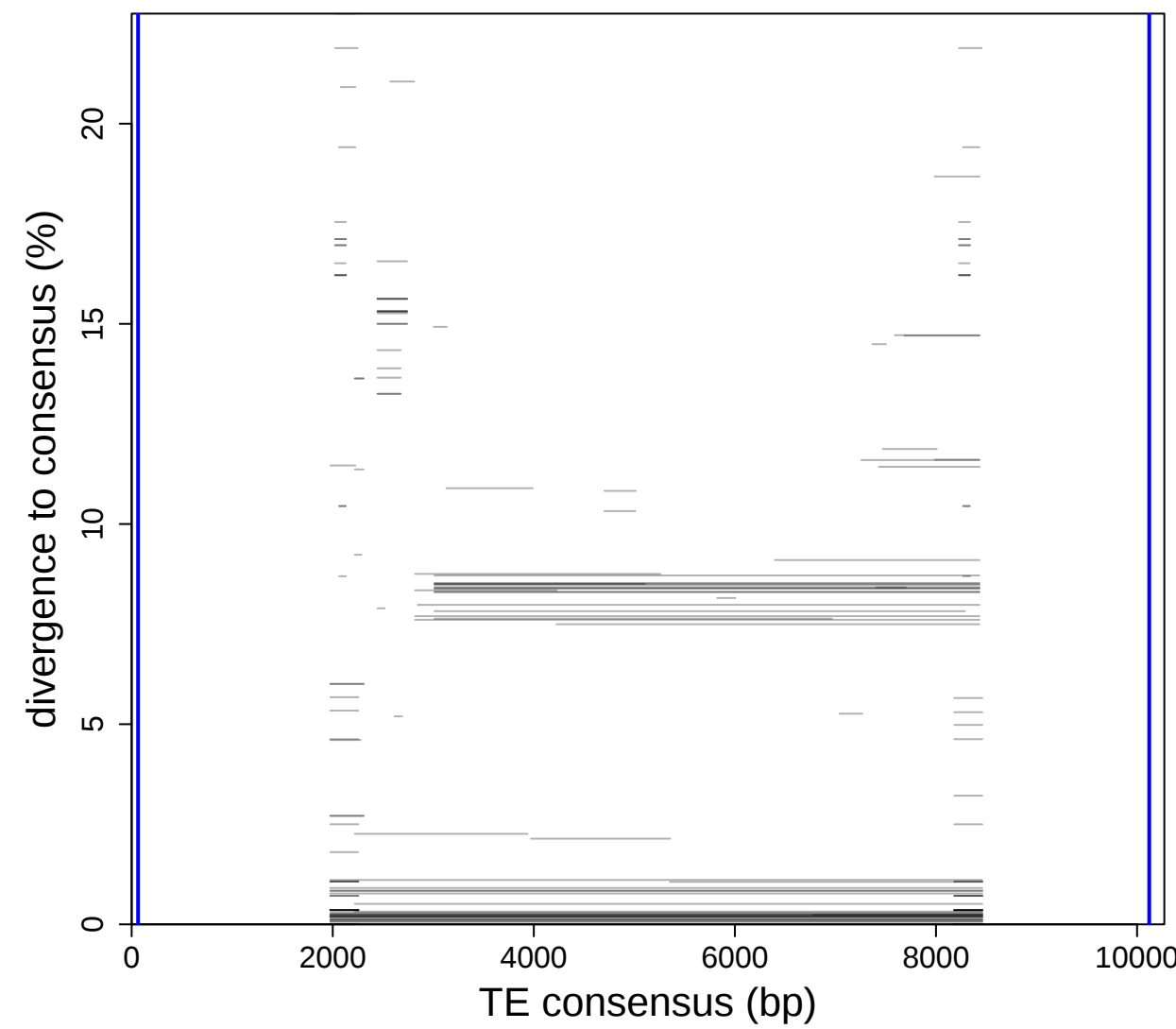
1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcIn.fa_alr
size: 7765bp; fragments: 166; full length: 0 (>=6988.5bp)

After TEtrimmer 7765 bp



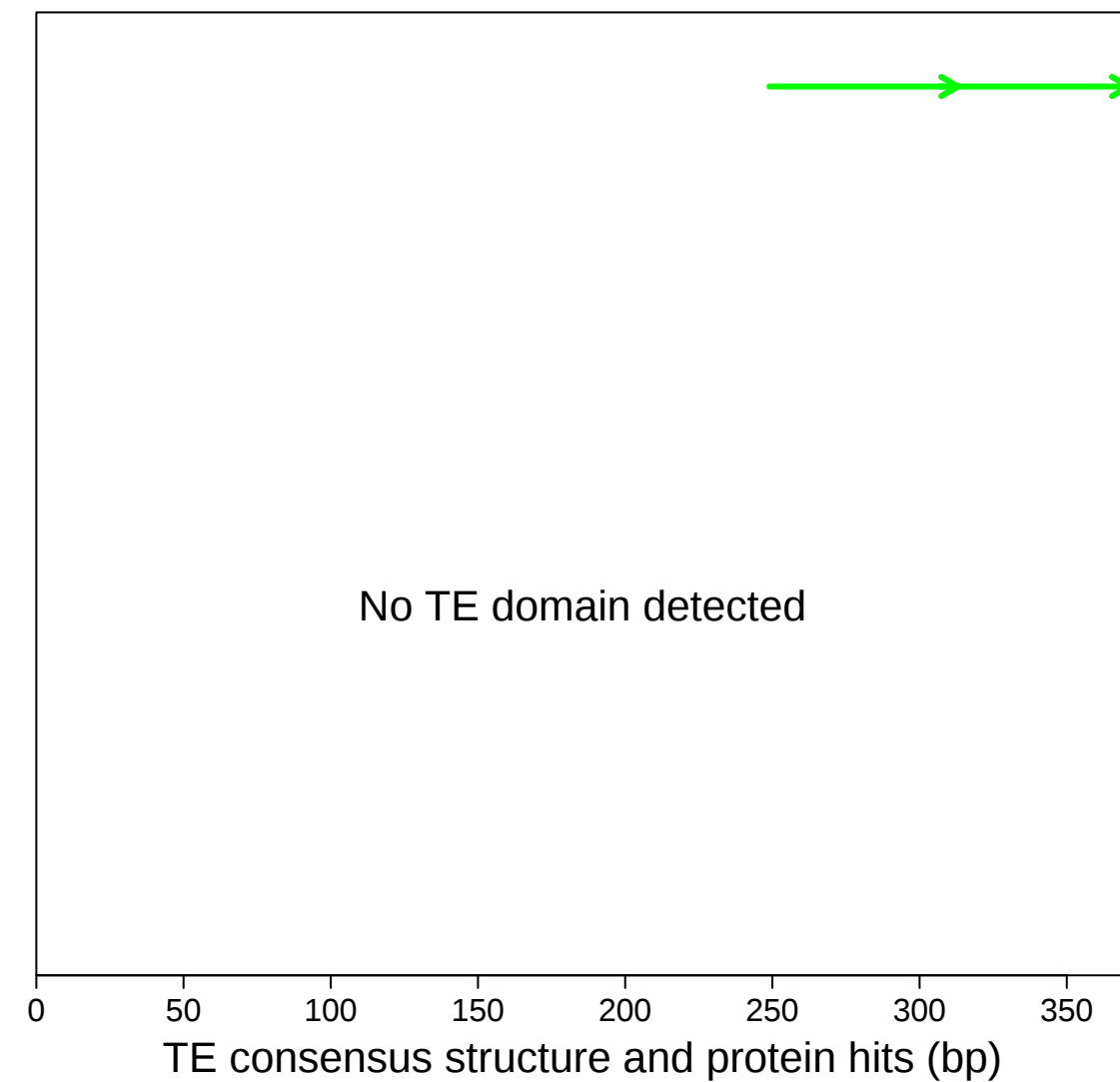
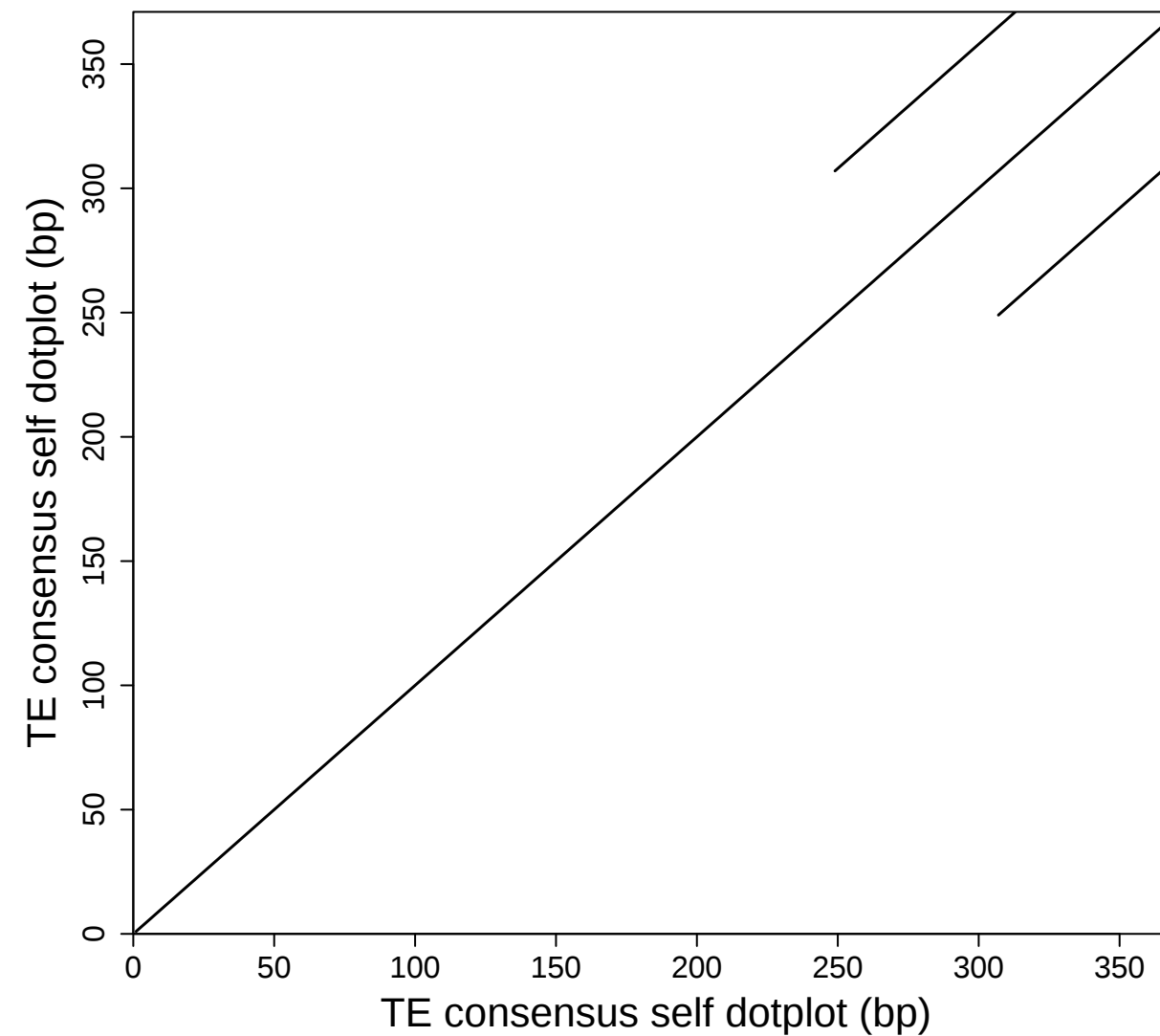
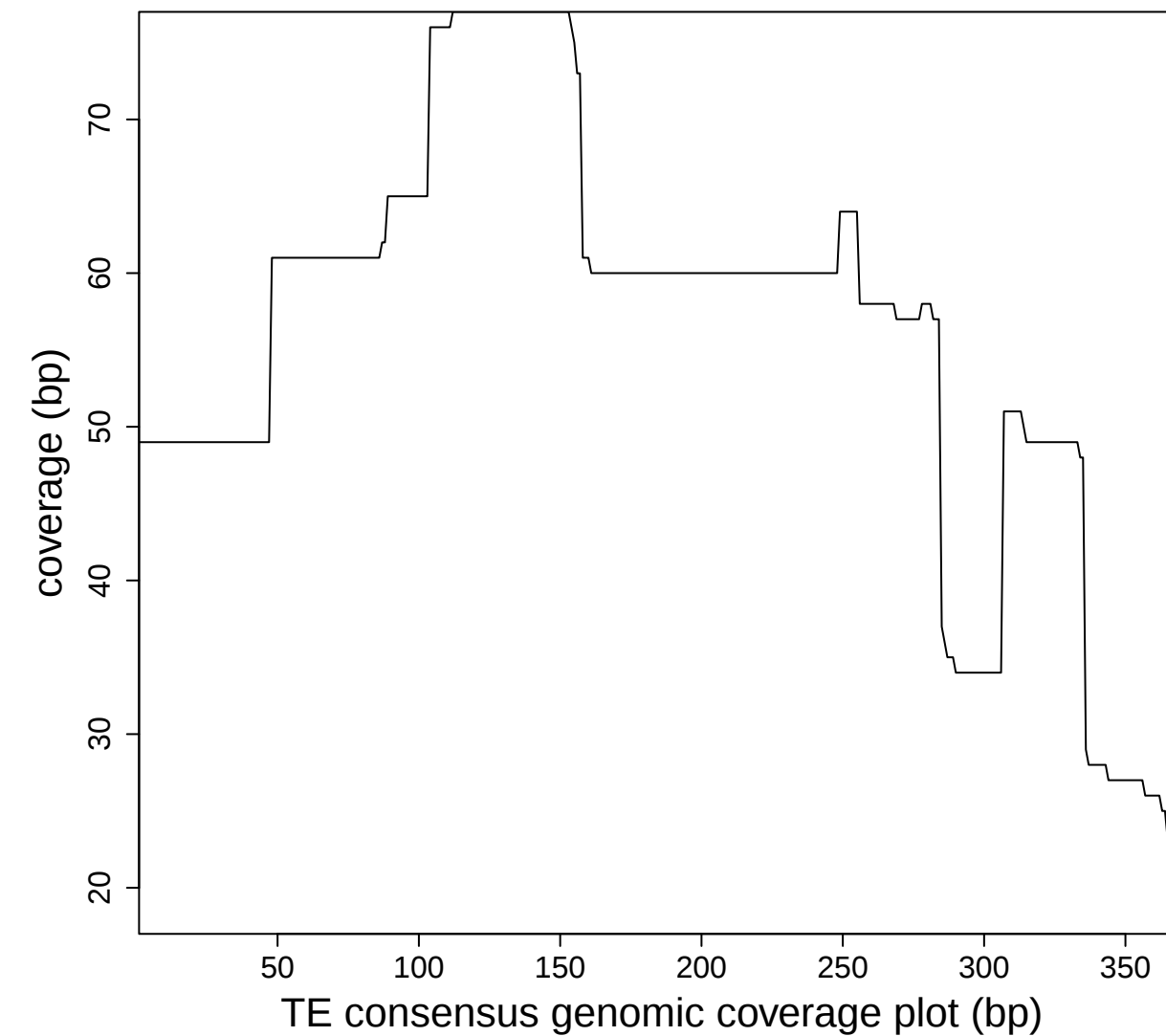
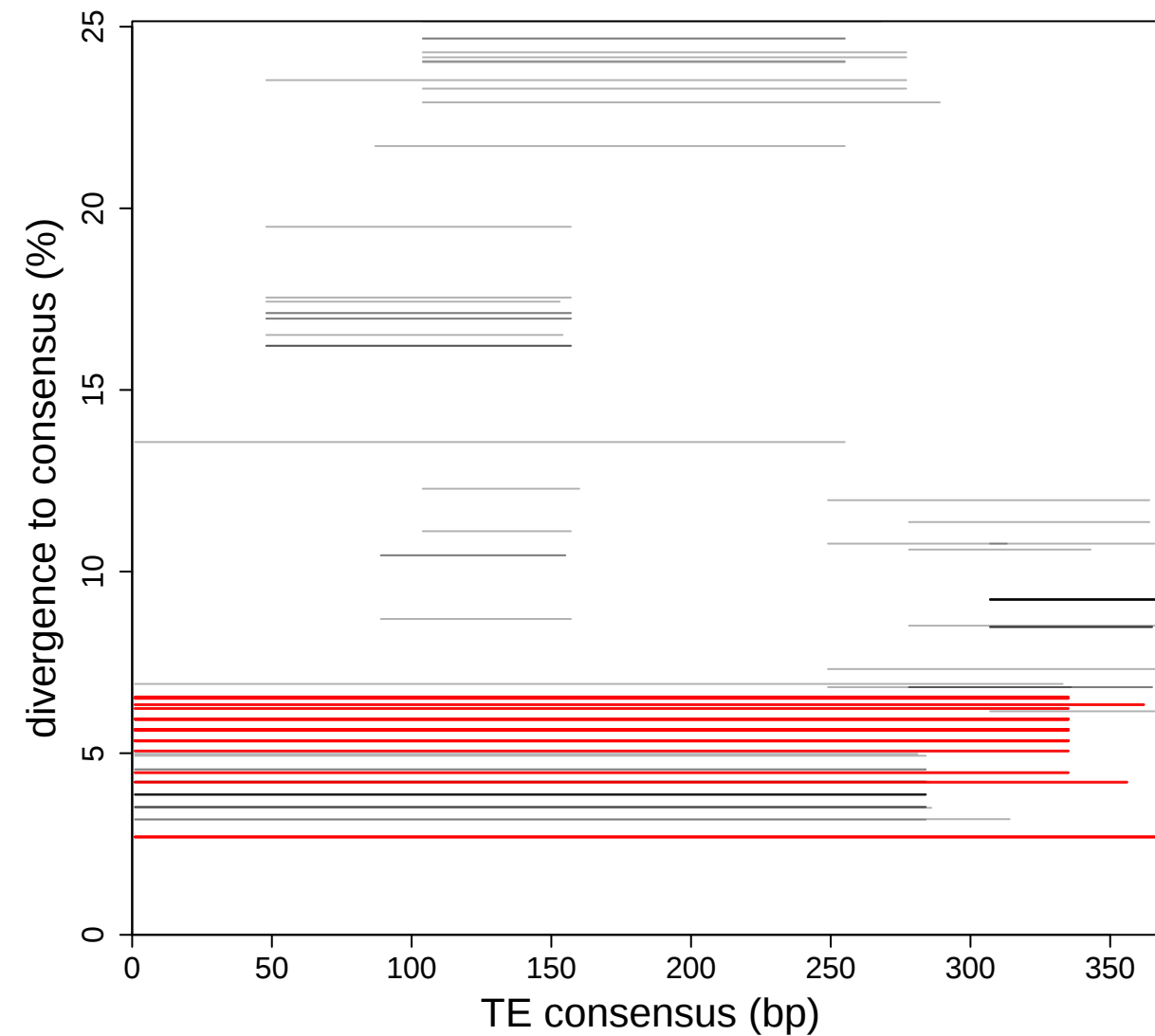
bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln
size: 10271bp; fragments: 166; full length: 0 (>=9243.9bp)

After TEtrimmer Extended plot Blue lines are boundaries

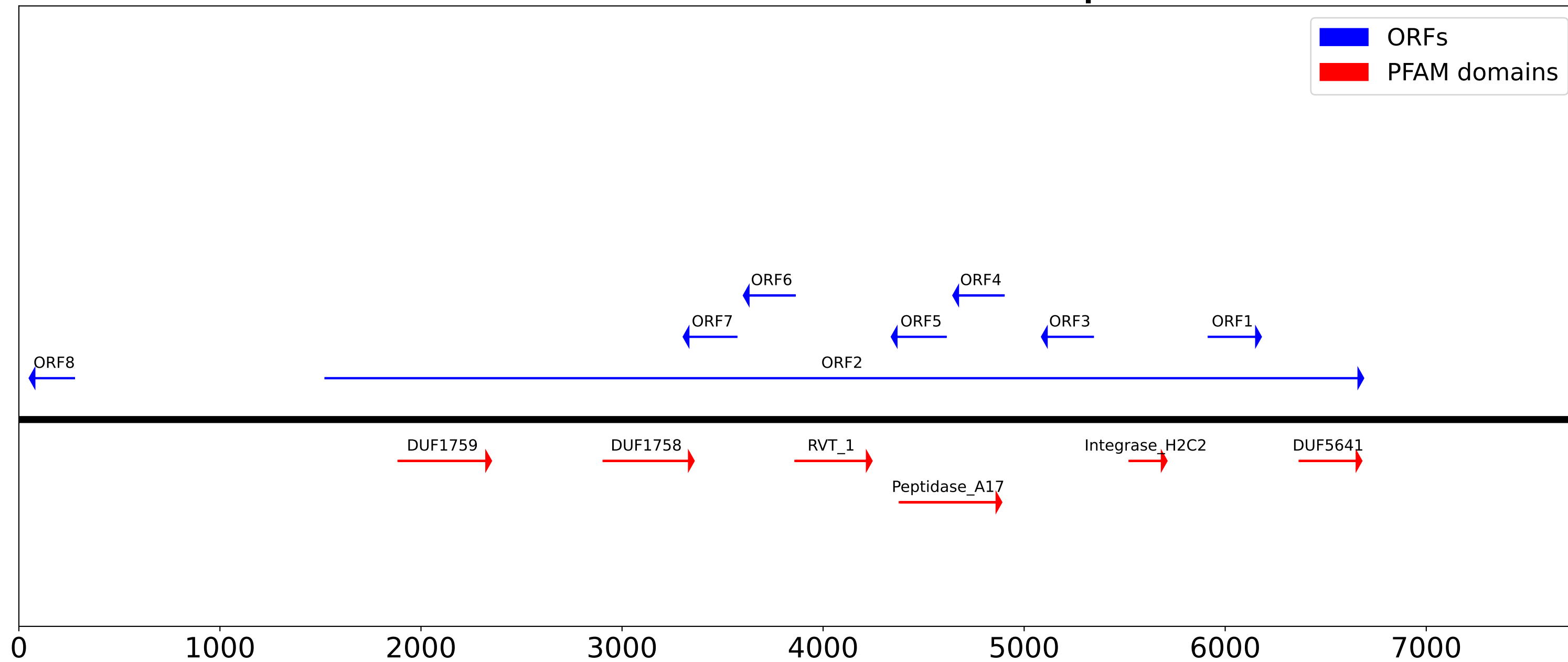


Before TEtrimmer 371 bp

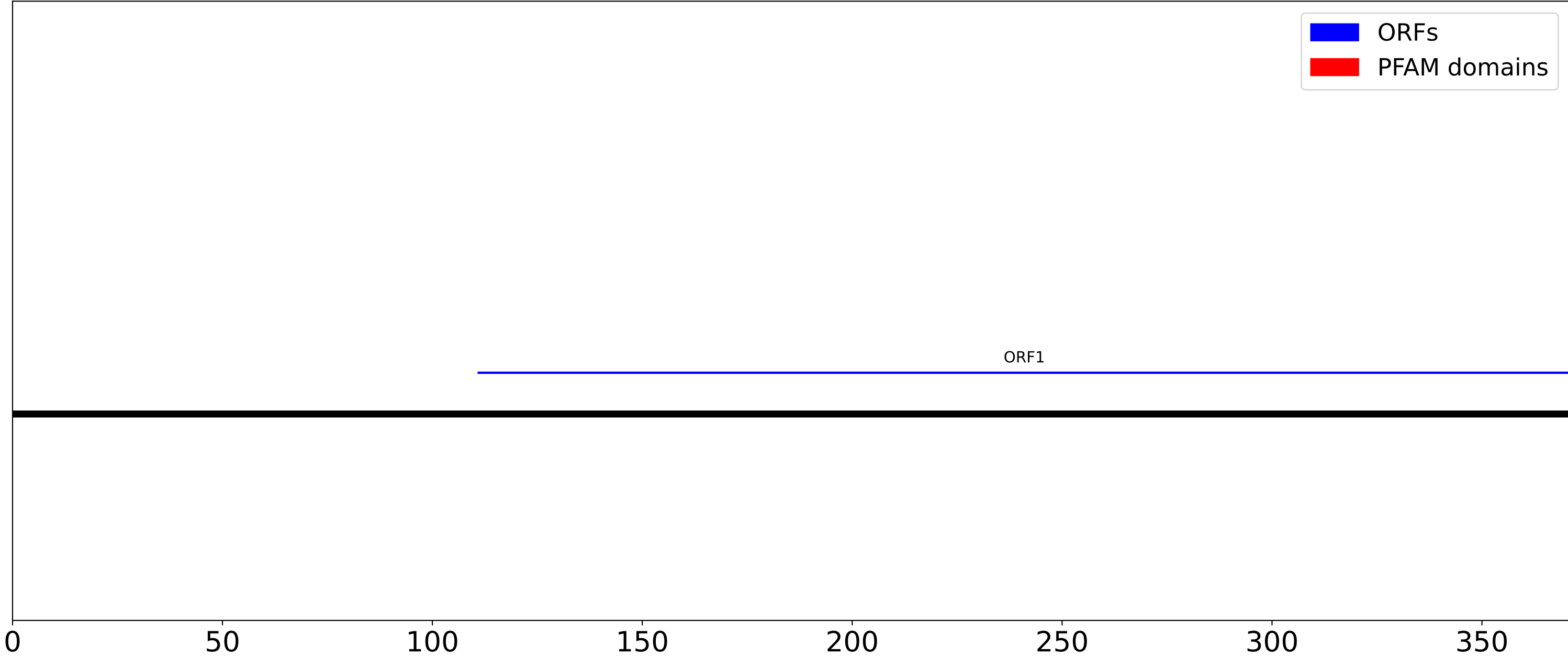
TE: ltr_1_family_95
size: 371bp; fragments: 103; full length: 23 (≥ 333.9 bp)



After TEtrimmer ORF and PFAM domain plot



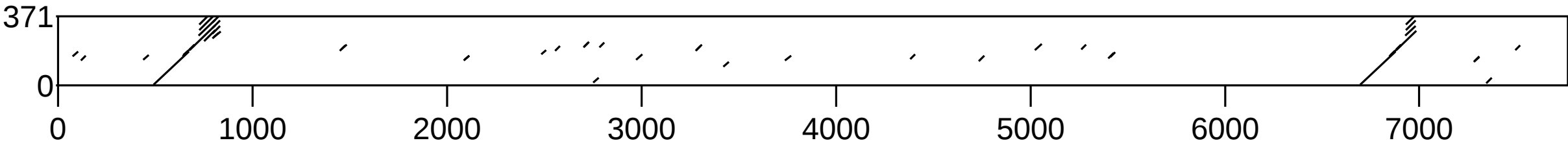
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

nsus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)