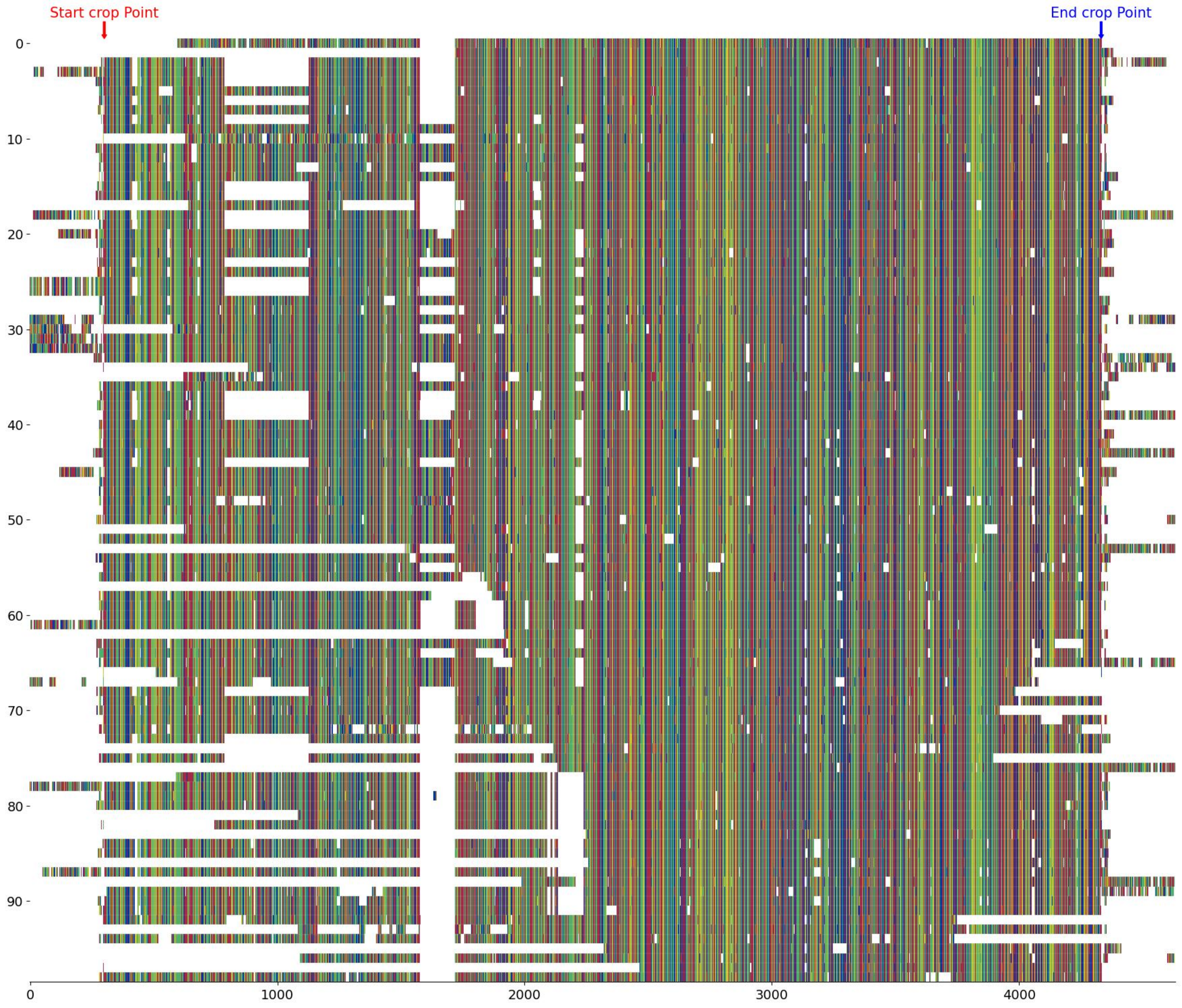


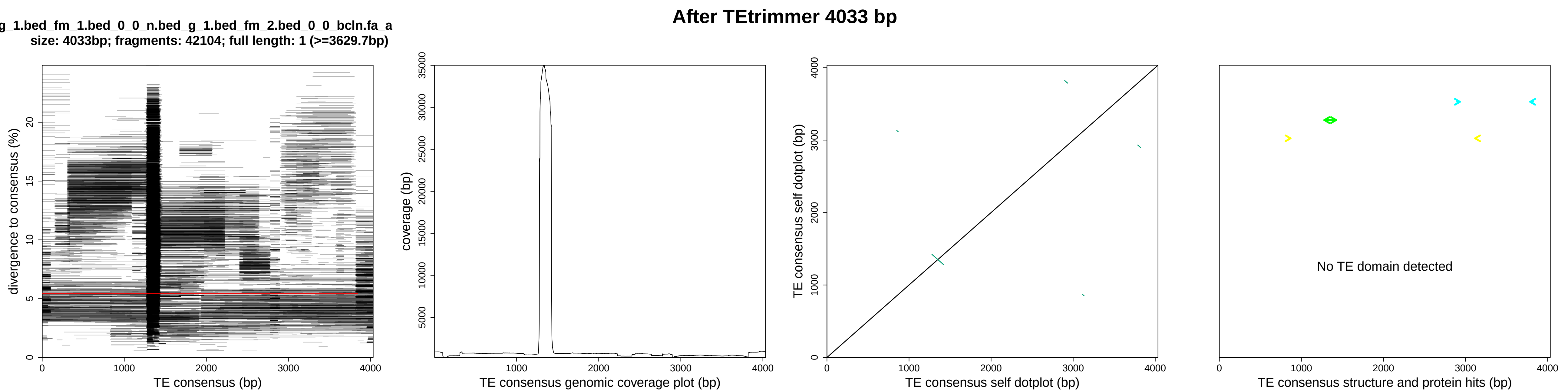
MSA length = 4033

Start crop Point

End crop Point

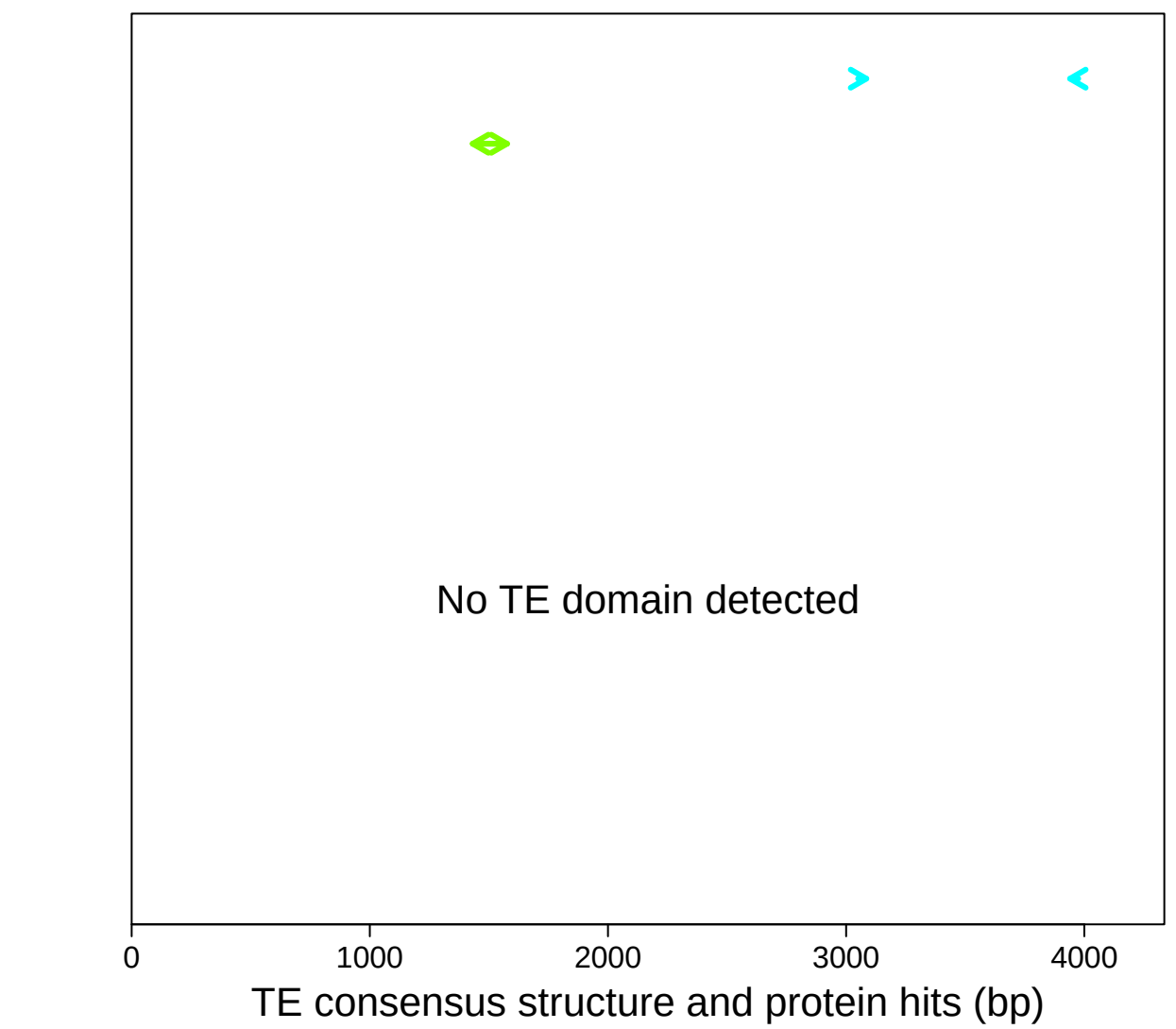
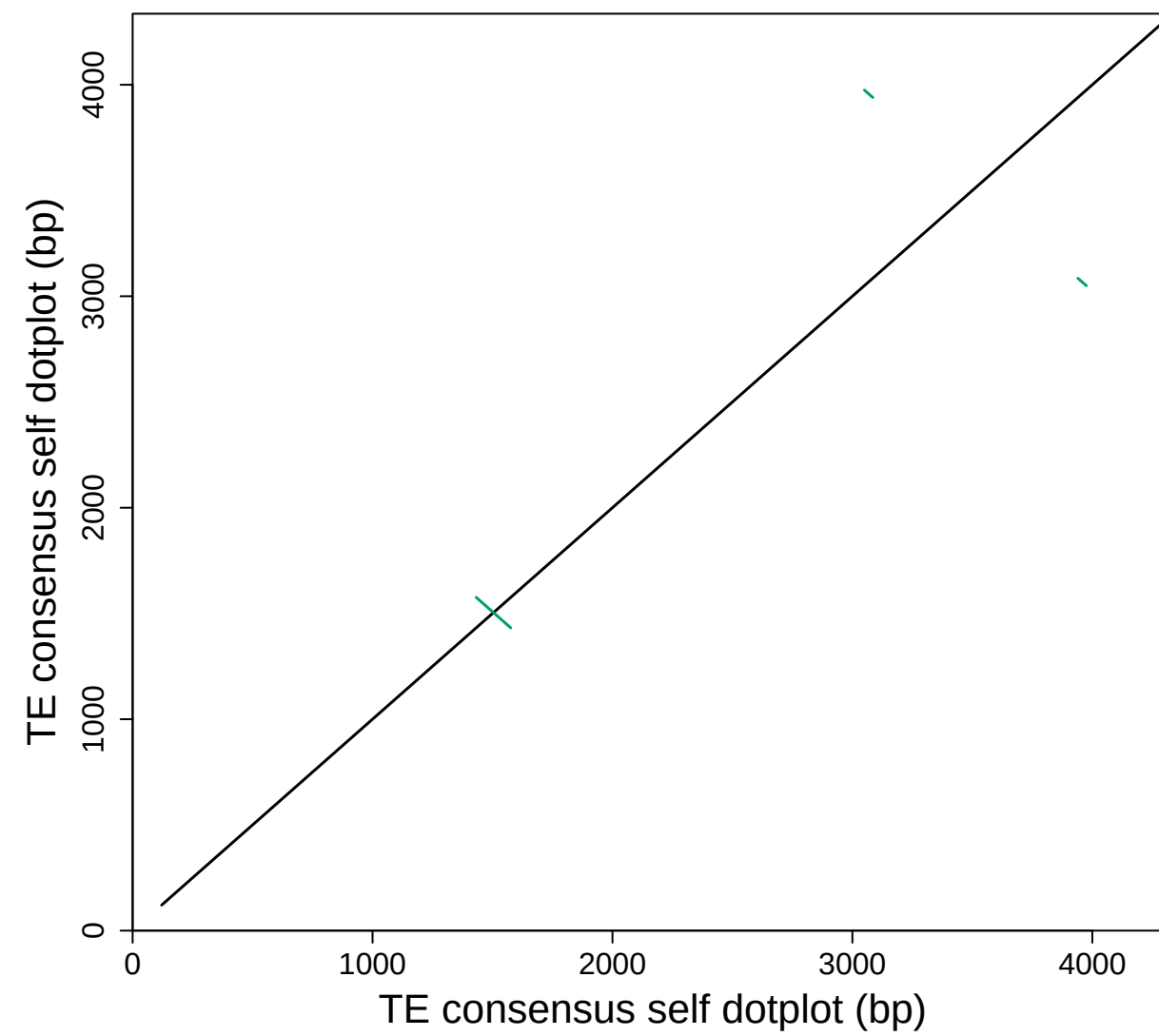
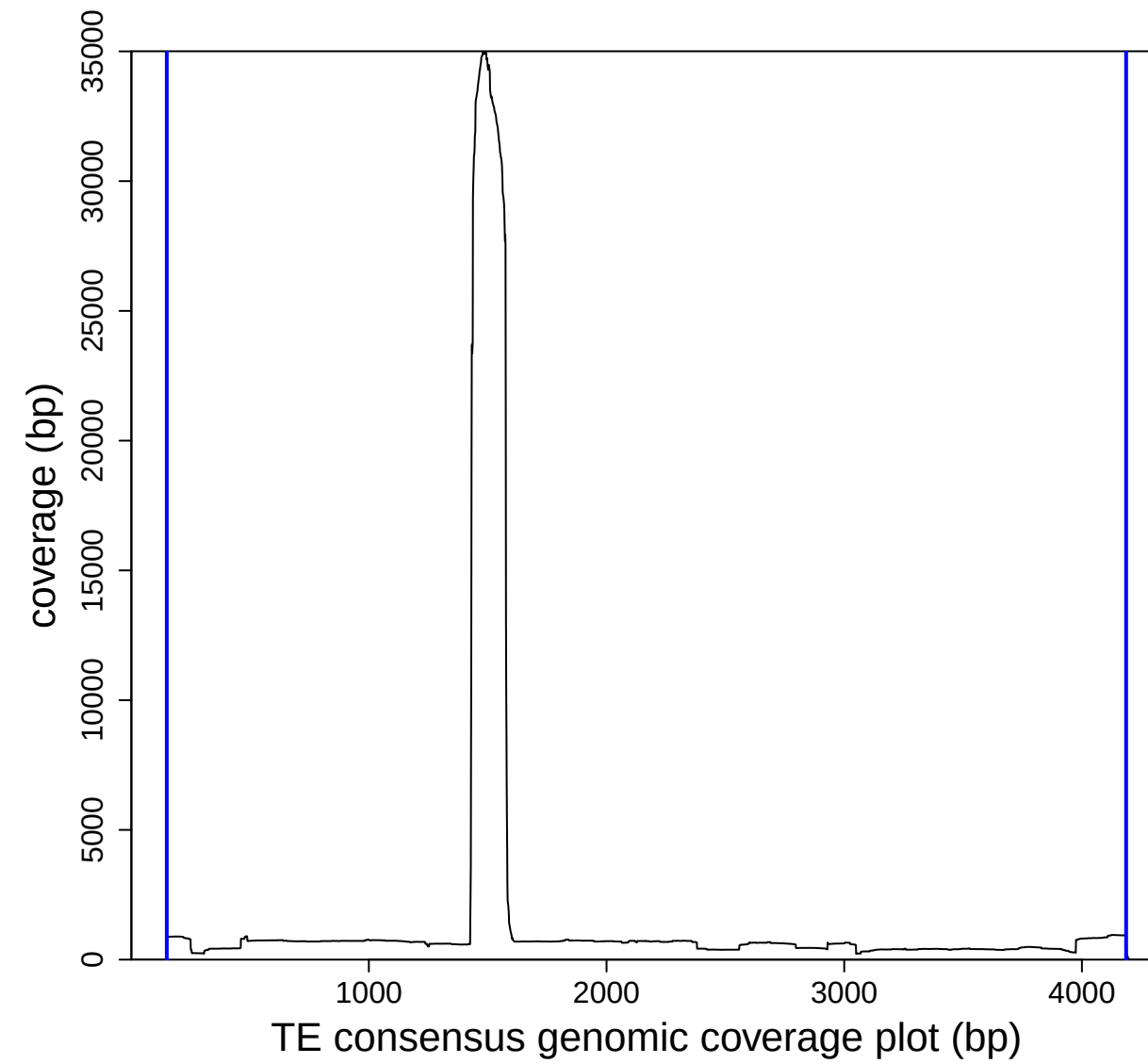
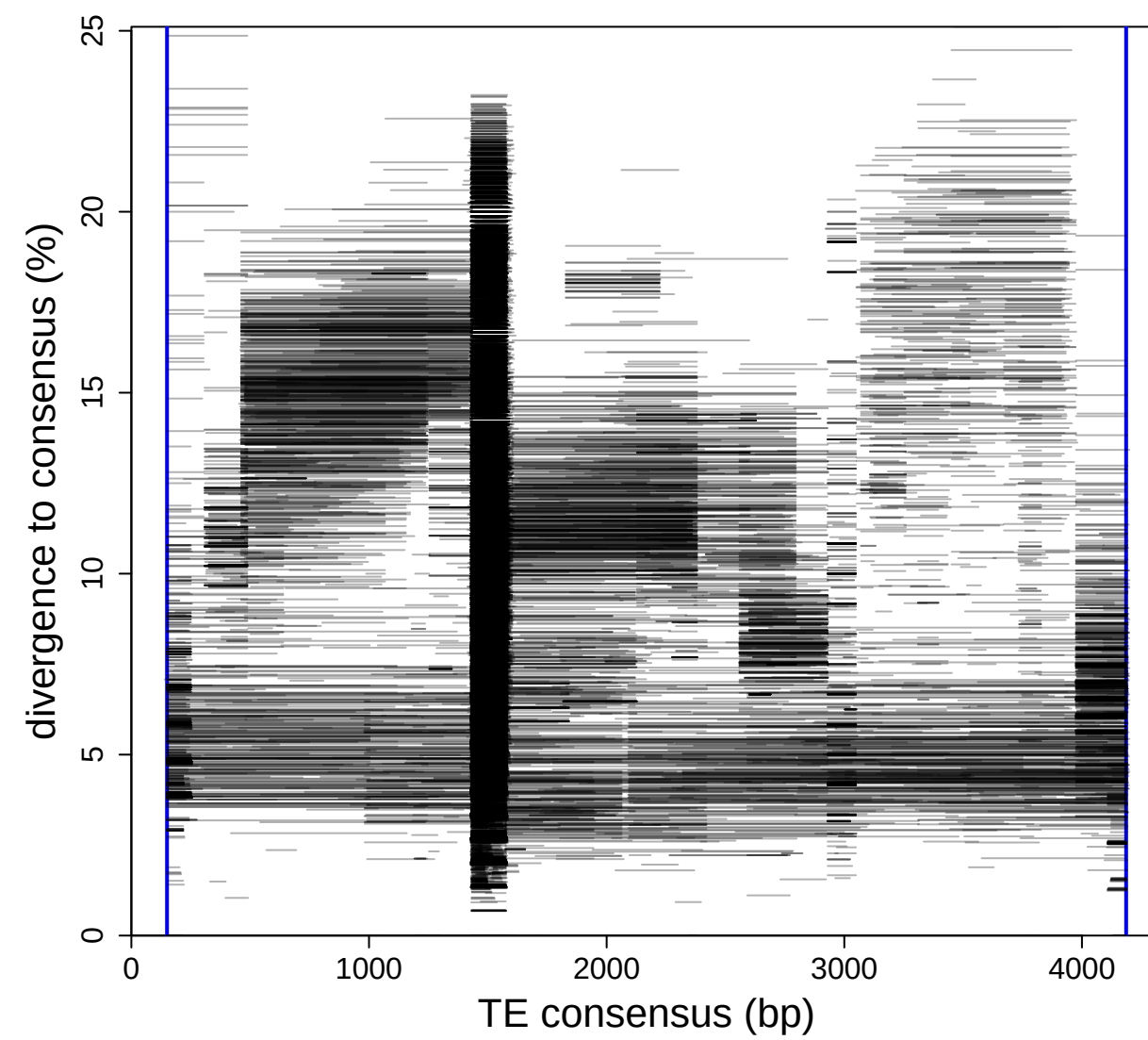
MSA visualization showing sequence alignment across multiple rows. The alignment is displayed as a grid of colored blocks representing different amino acid residues. The sequence is flanked by "Start crop Point" (red arrow) and "End crop Point" (blue arrow). The MSA length is 4033. The alignment shows a high degree of conservation across the sequences, with many identical residues highlighted in the same color. The sequence is presented in a standard 3-letter amino acid code, with some residues highlighted in bold or italicized font. The alignment is organized into columns, with each column representing a specific position in the sequence. The rows represent individual sequences, with some sequences being truncated at the ends. The overall structure of the alignment suggests a conserved protein structure with a high degree of sequence identity across the different sequences.



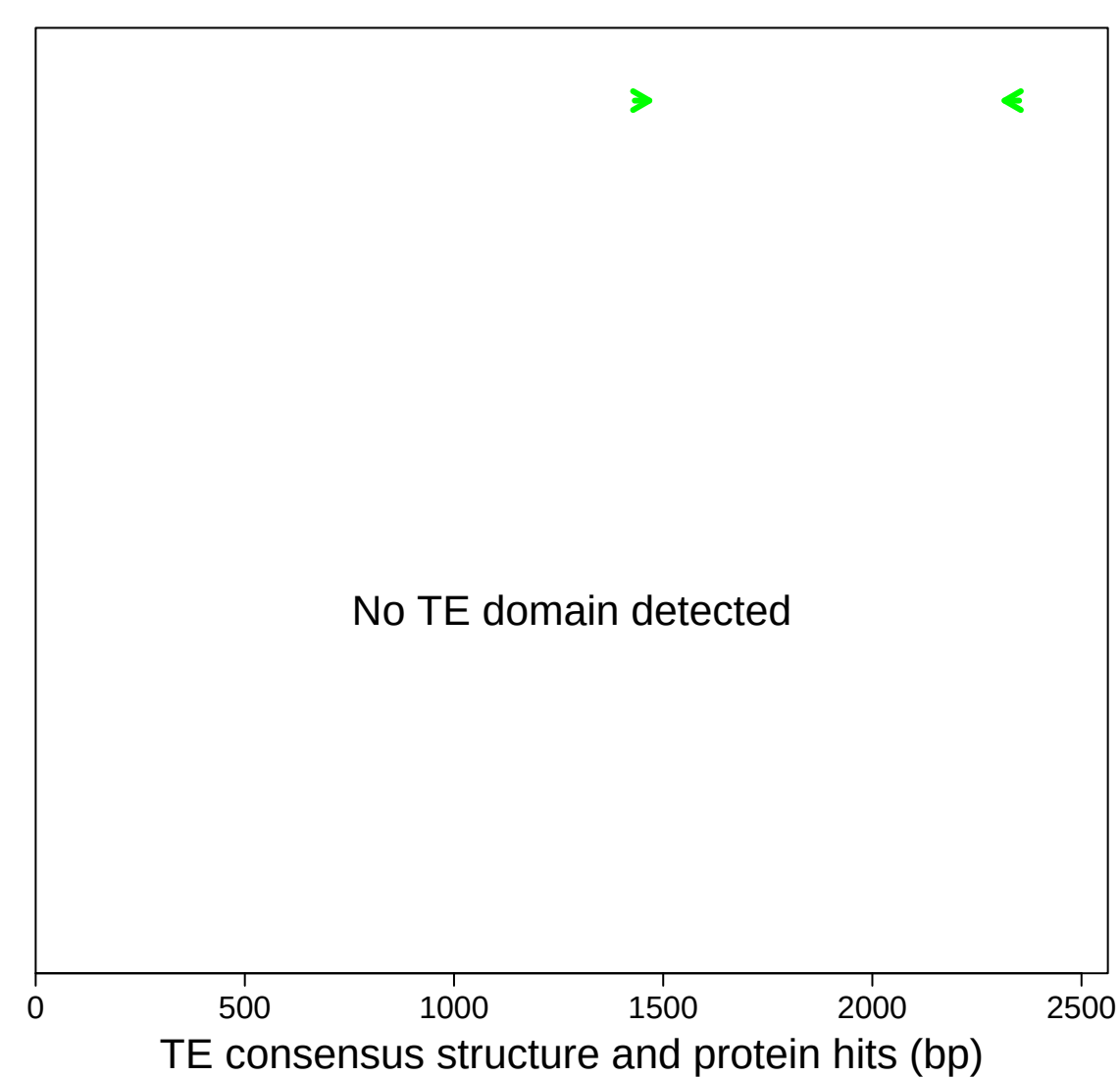
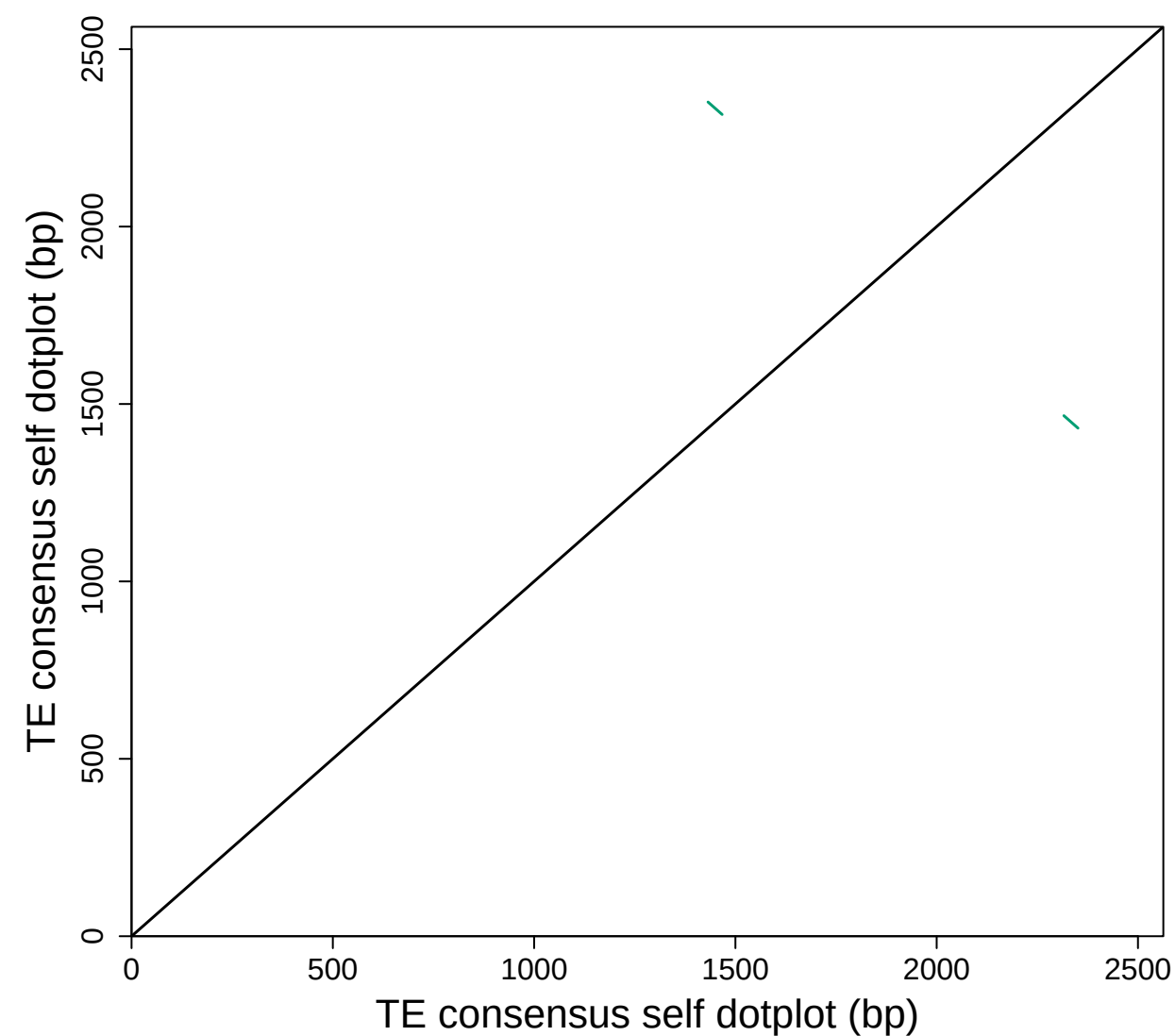
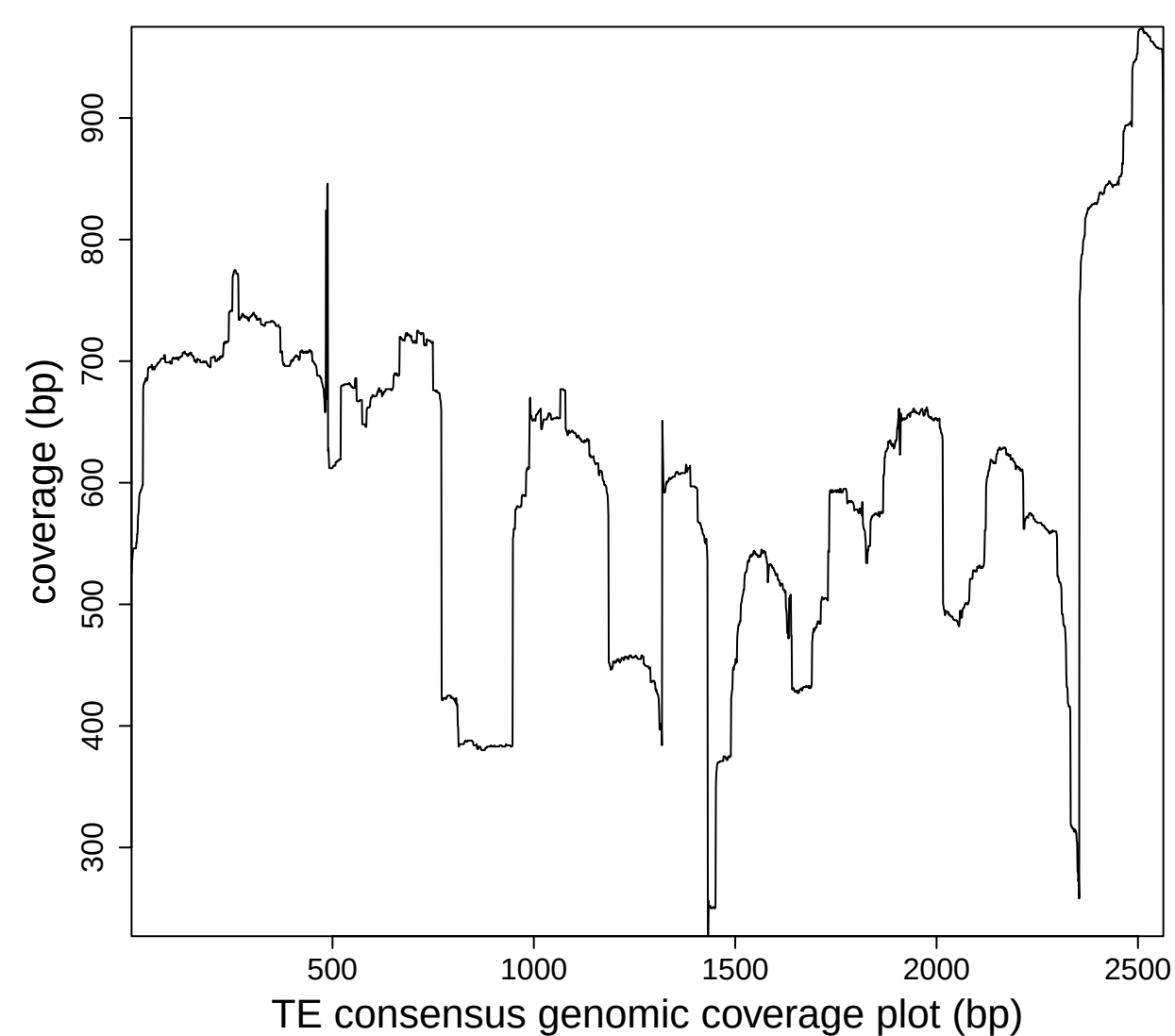
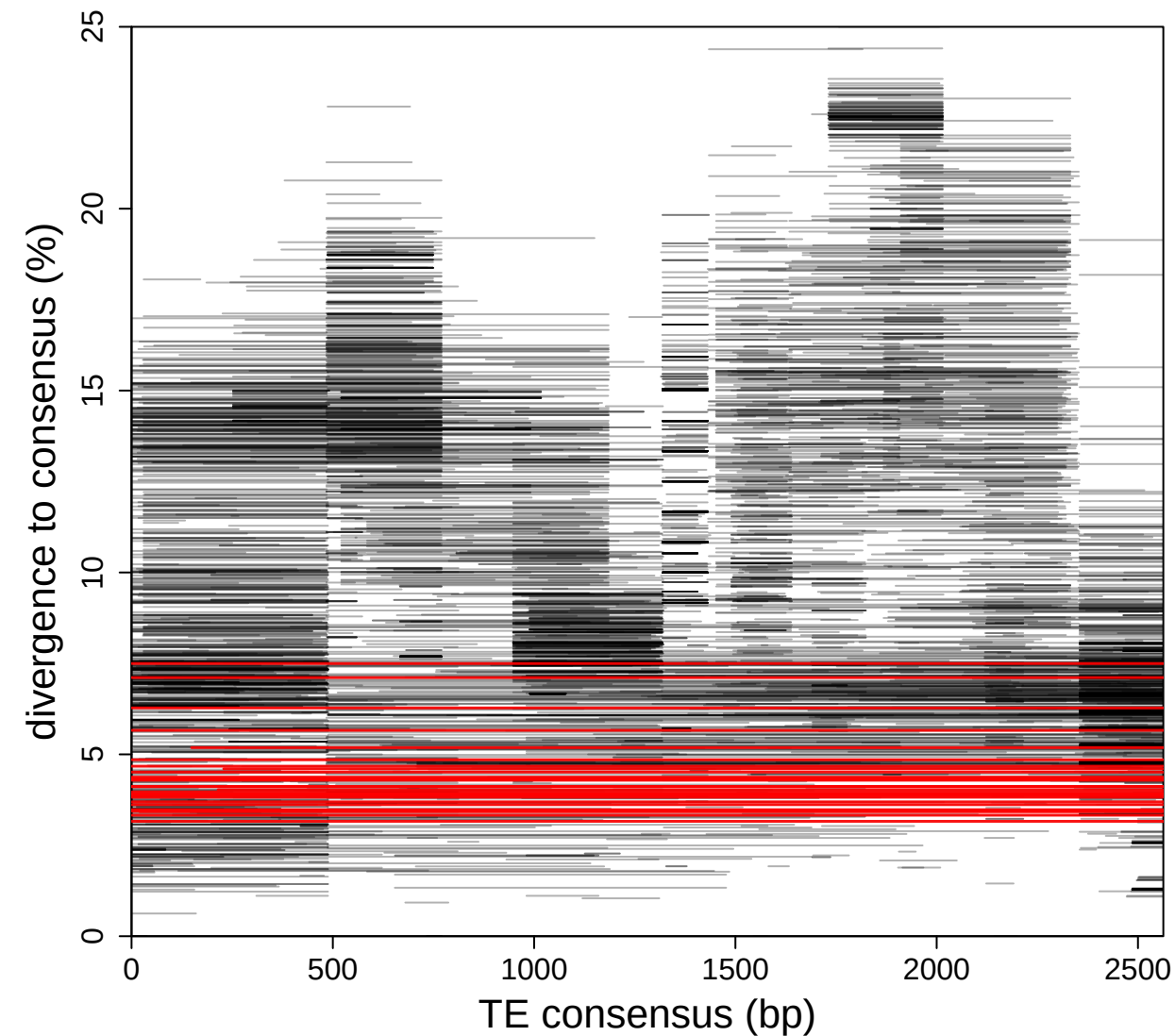


f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcl
size: 4336bp; fragments: 41877; full length: 0 (>=3902.4bp)

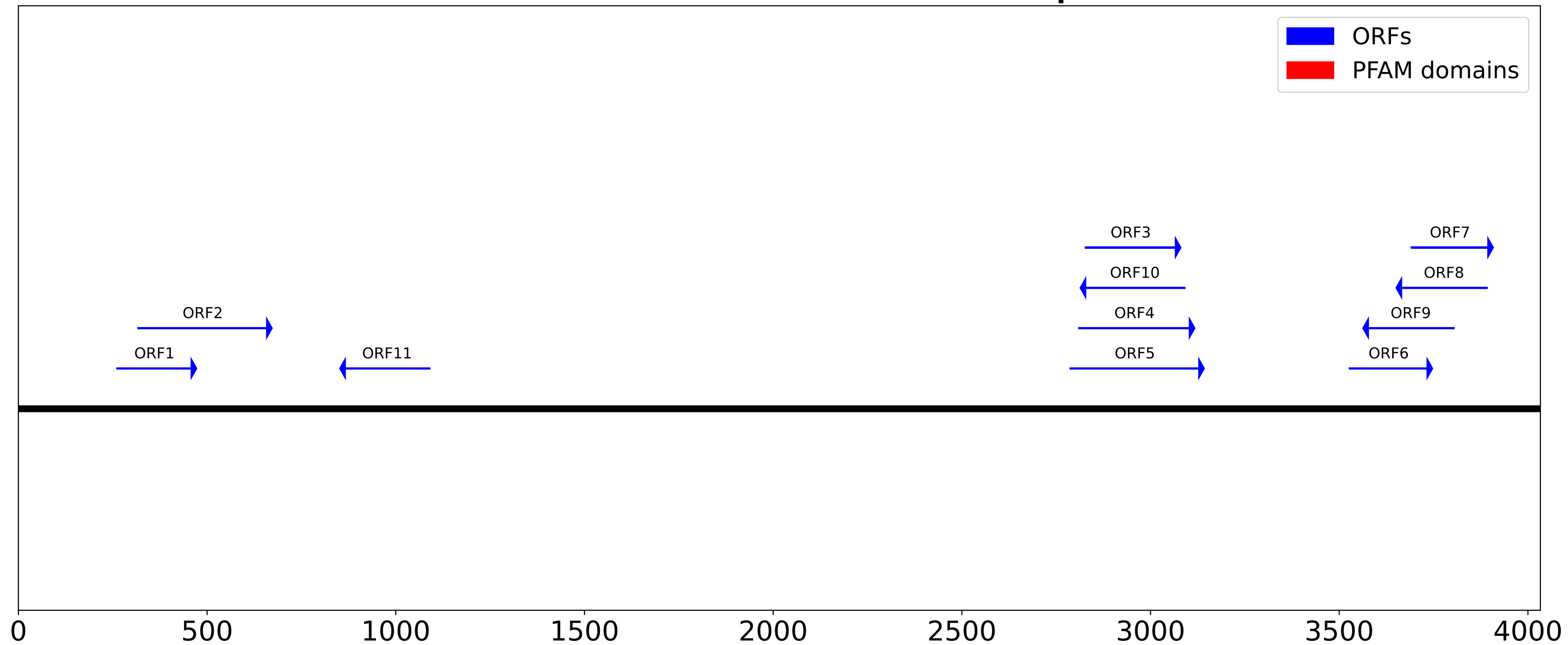
After TEtrimmer Extended plot Blue lines are boundaries



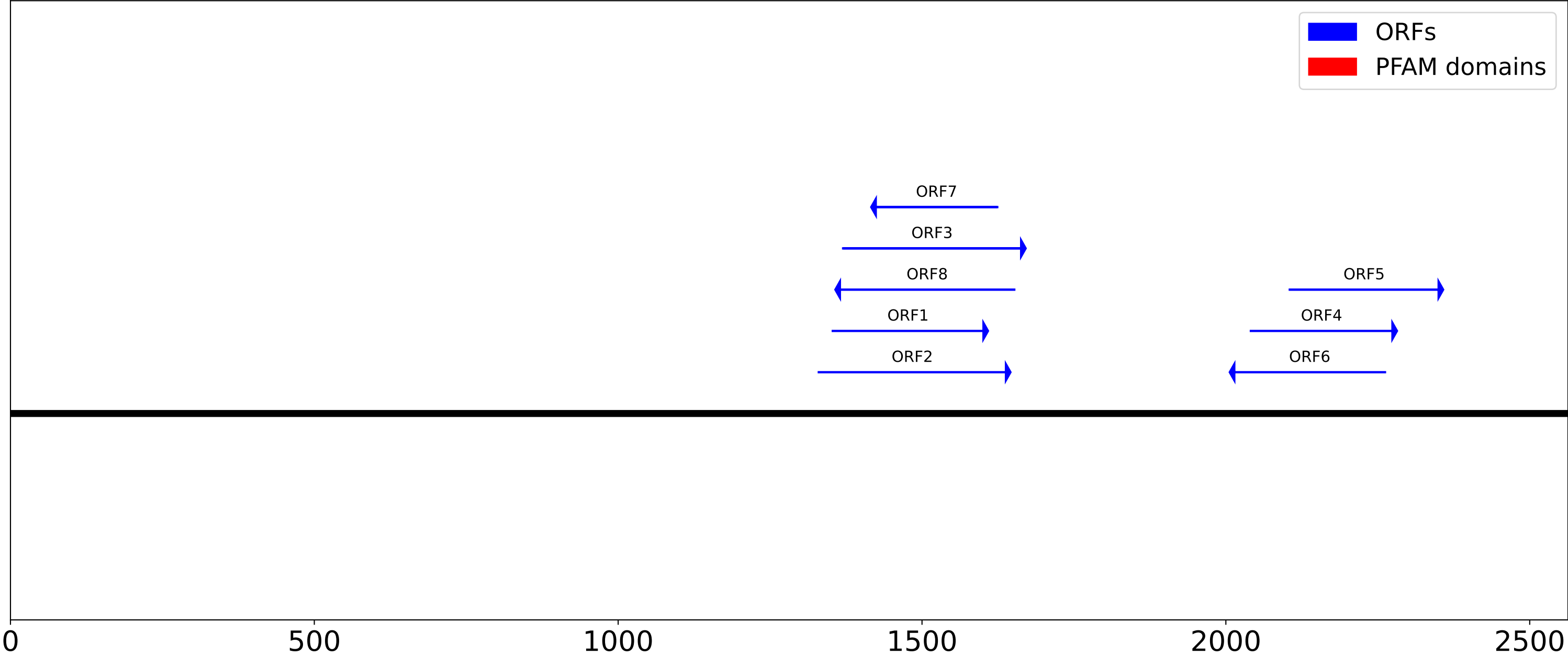
TE: rnd_4_family_559
size: 2563bp; fragments: 4315; full length: 31 (≥ 2306.7 bp)



After TEtrimmer ORF and PFAM domain plot



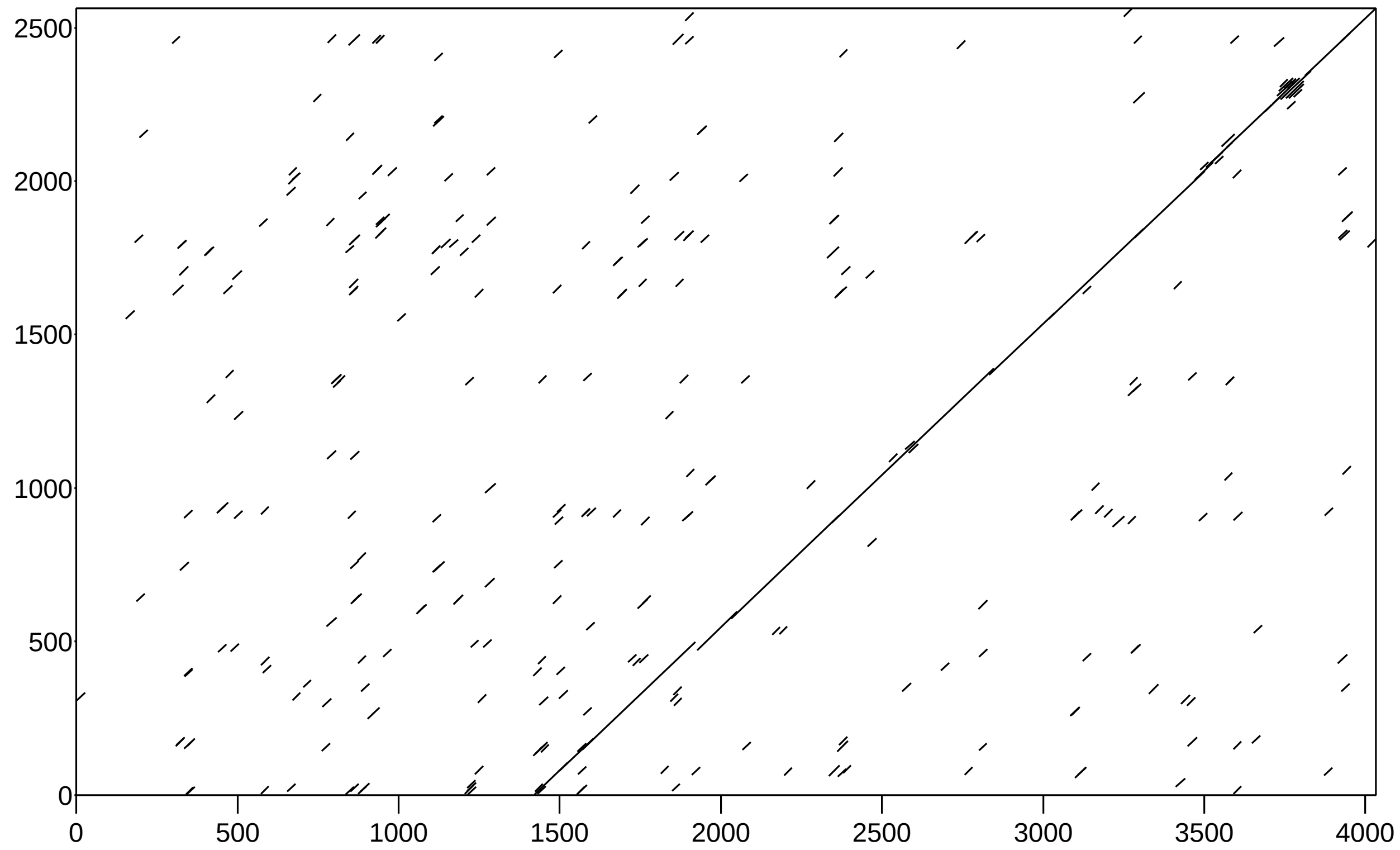
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)