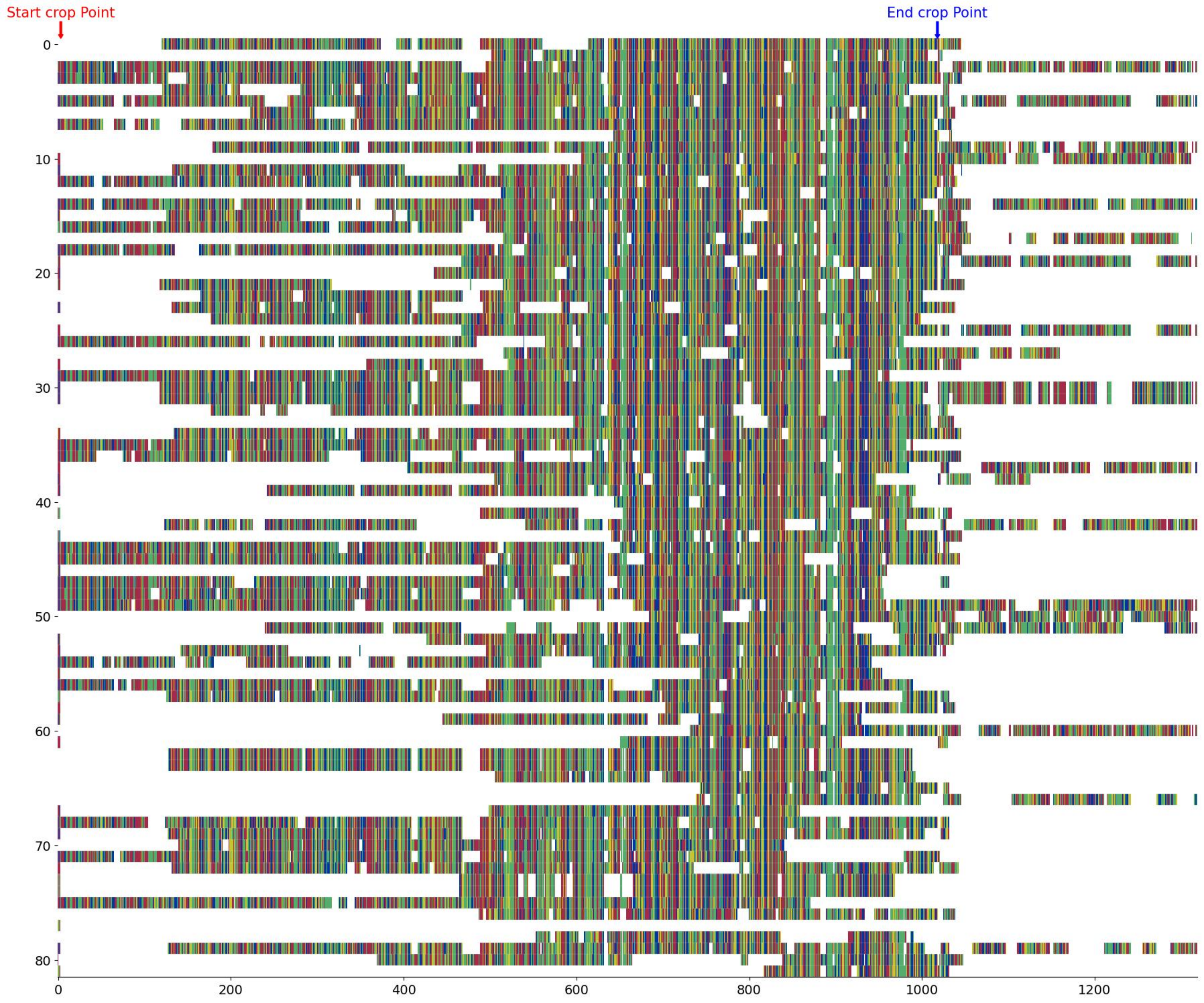
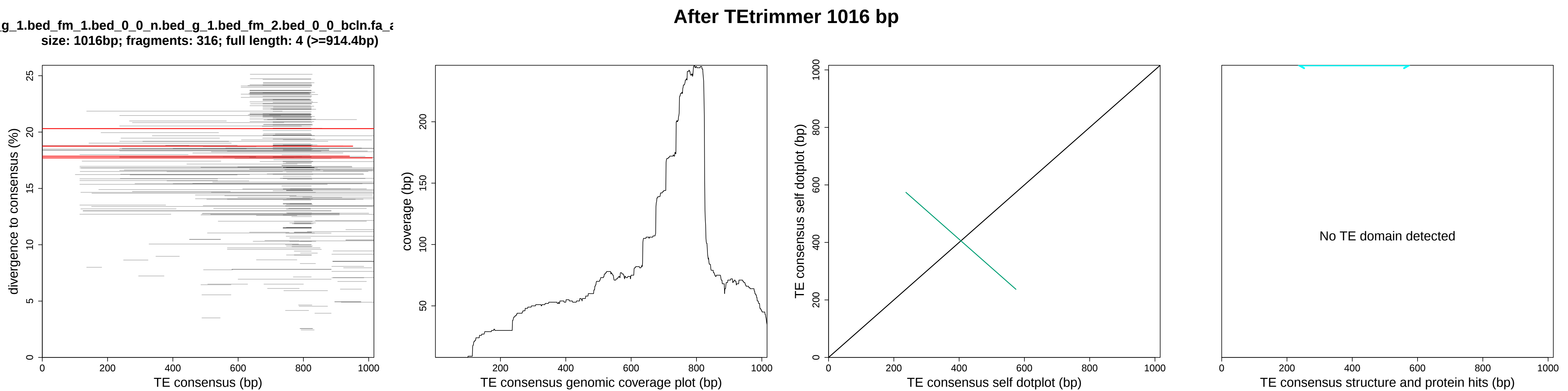


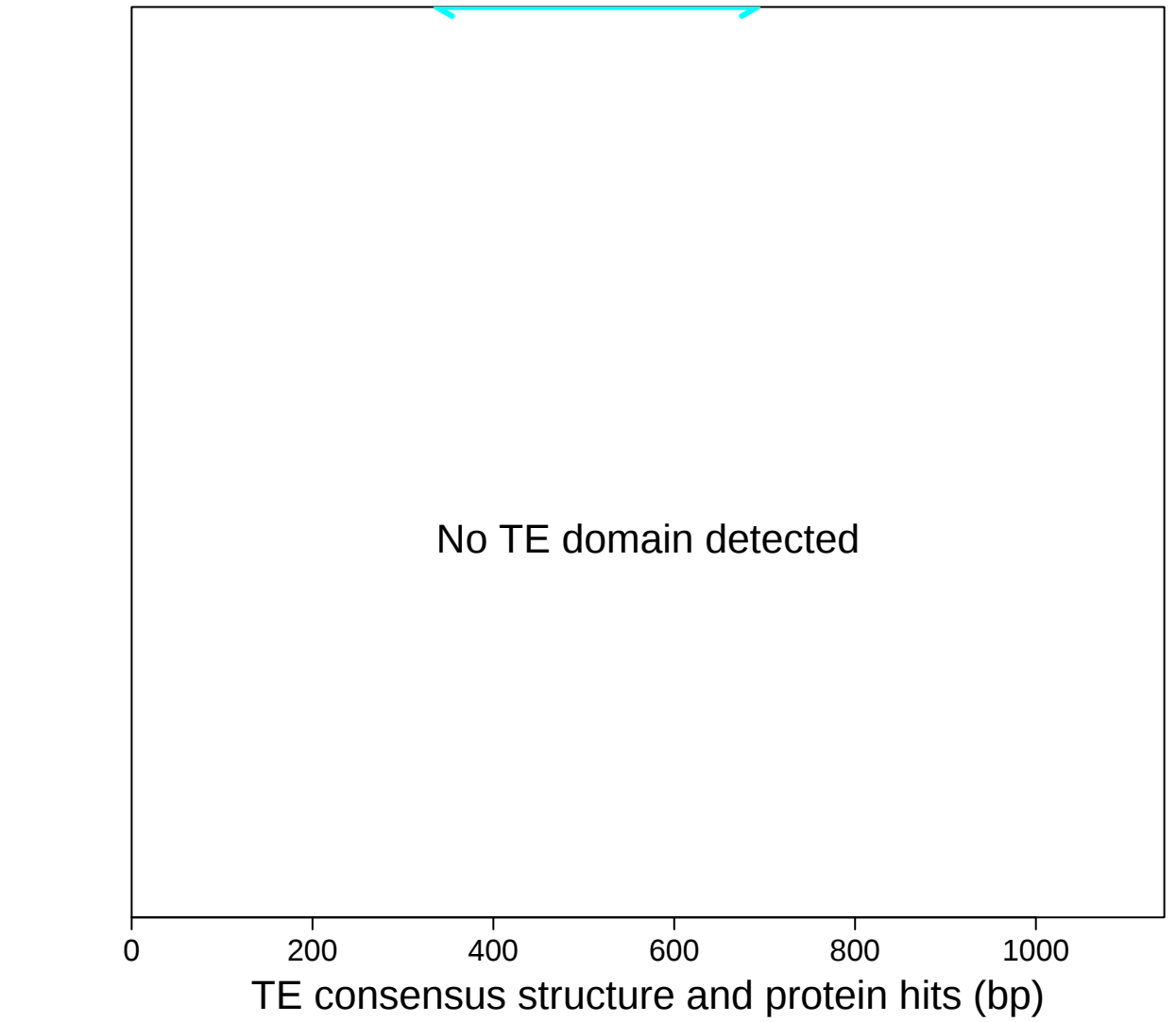
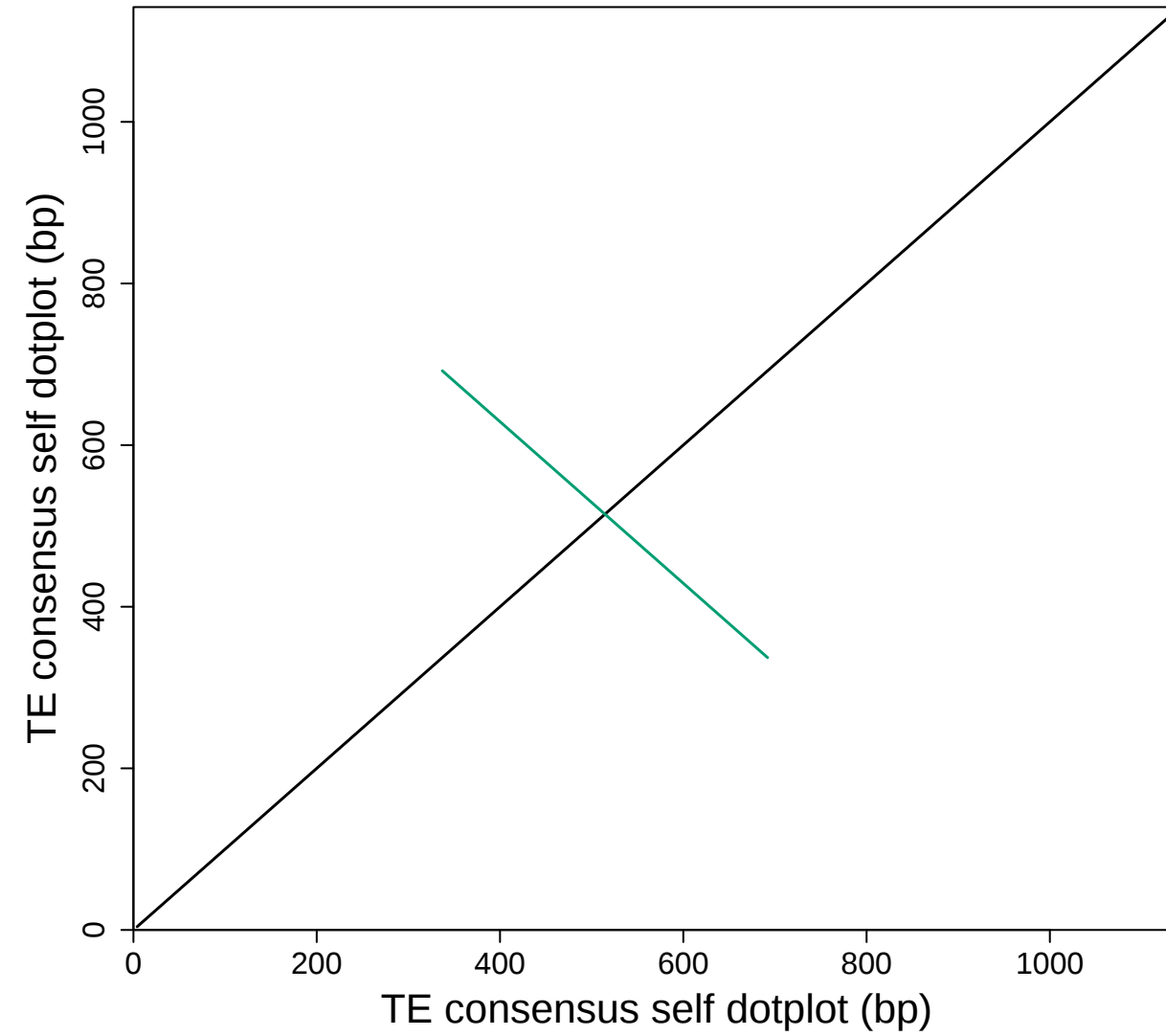
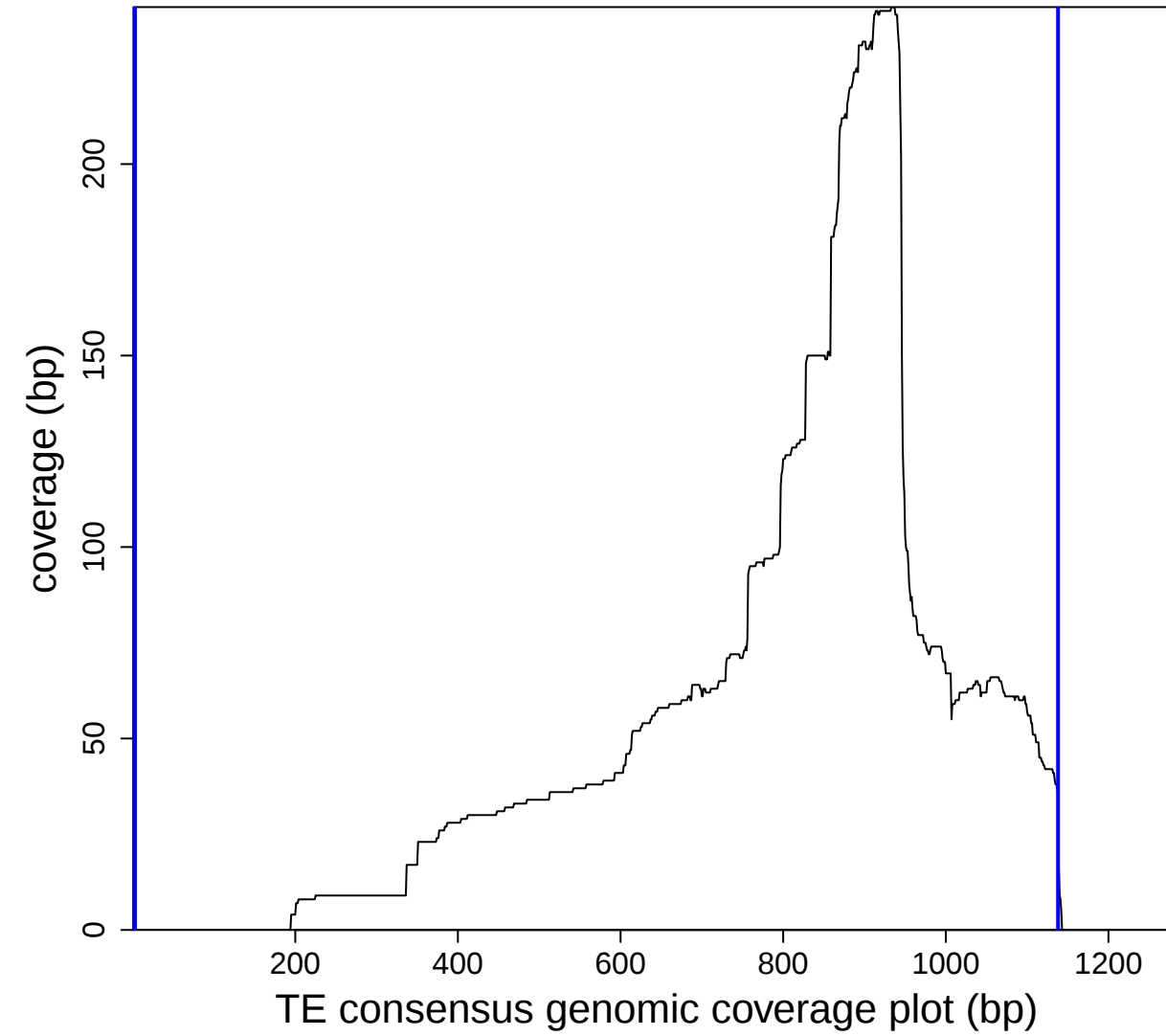
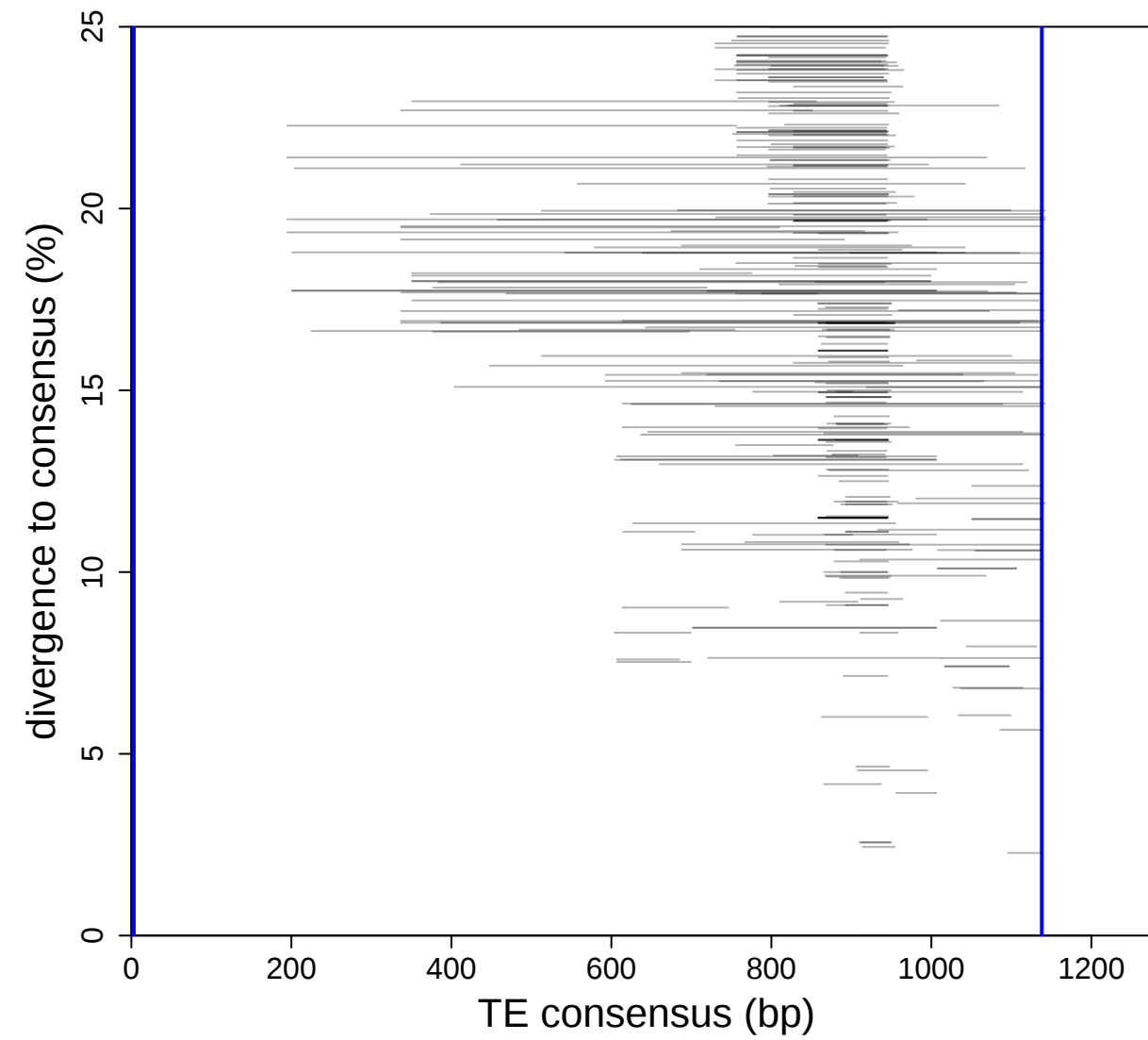
Figure 1: Comparison of the predicted and reference nucleotide sequences of the *hcr* gene. The figure displays two columns of DNA sequences. The left column represents the predicted sequence, and the right column represents the reference sequence. The sequences are aligned, with gaps indicated by dashes. The sequences are color-coded: Adenine (A) is green, Guanine (G) is blue, Cytosine (C) is red, and Thymine (T) is black. The alignment shows a high degree of similarity between the predicted and reference sequences, with some minor variations highlighted by the color coding.



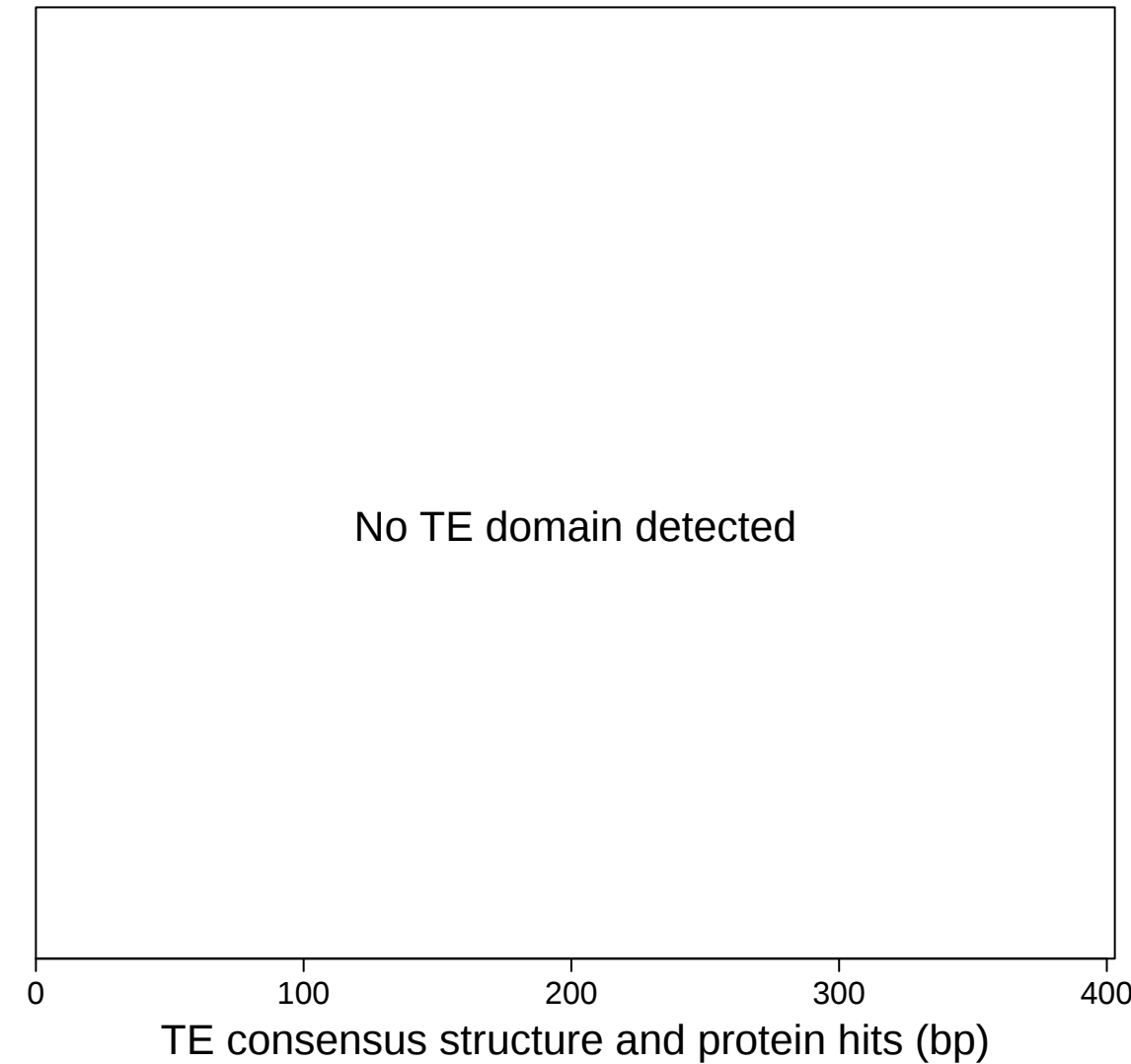
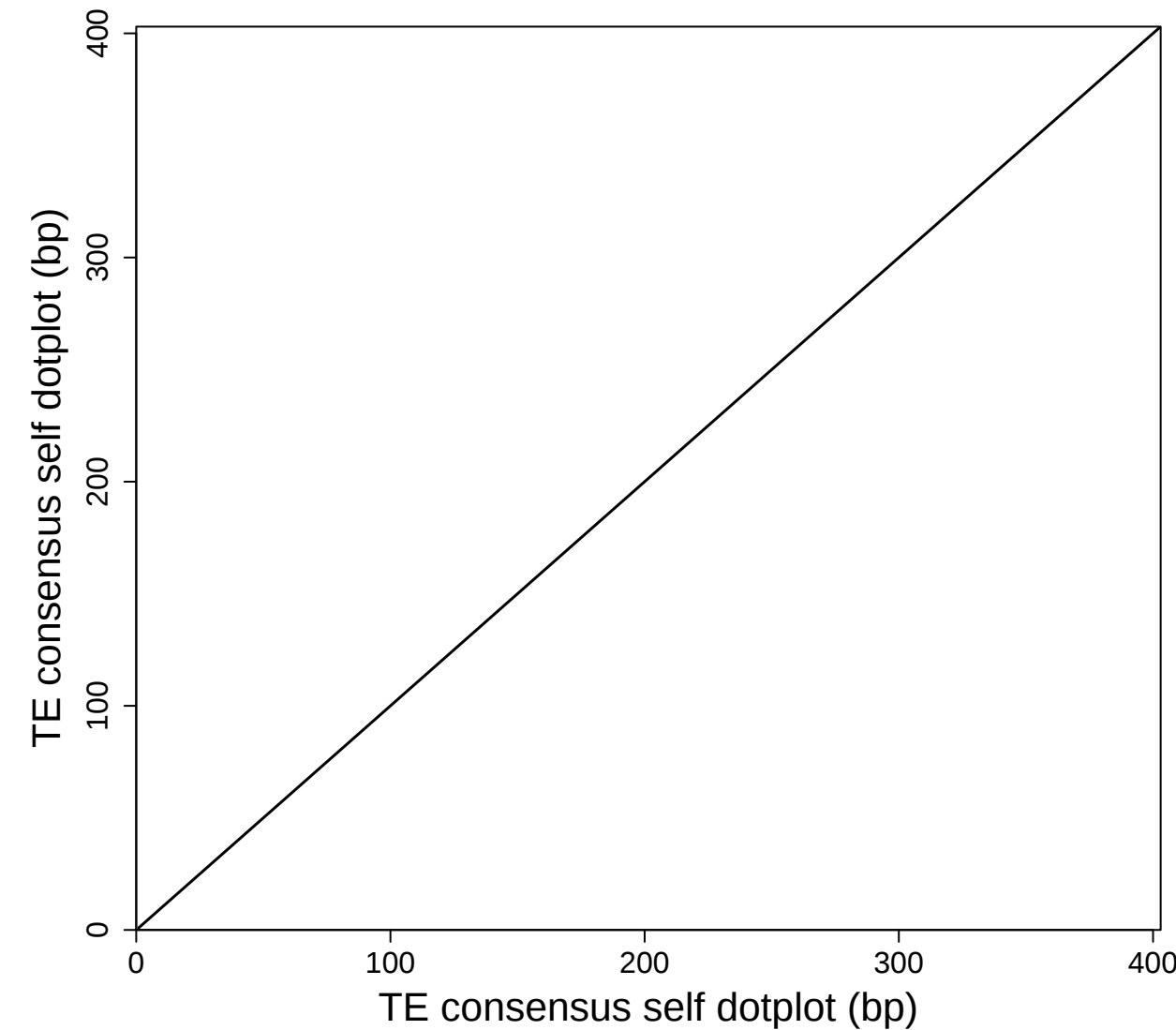
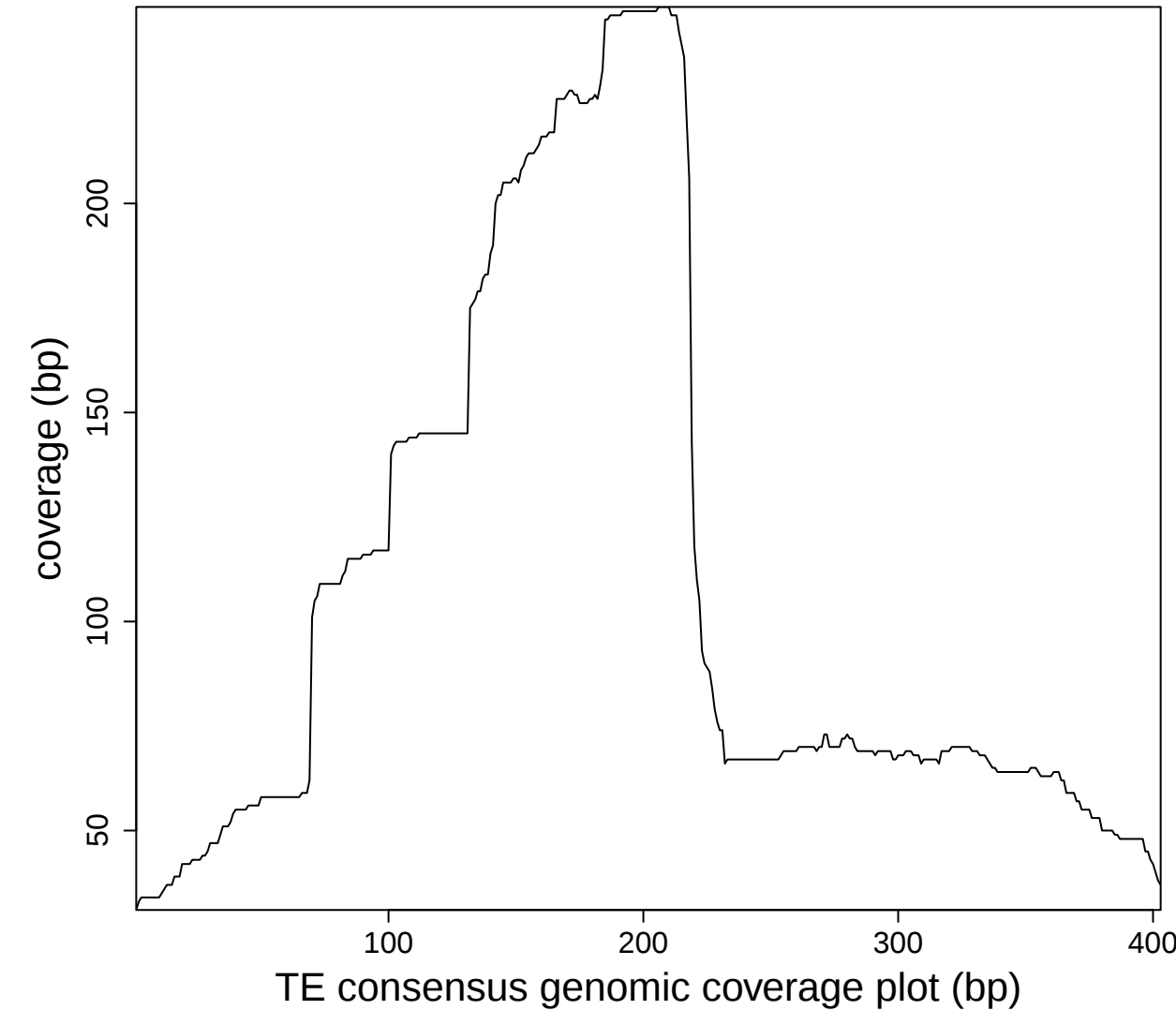
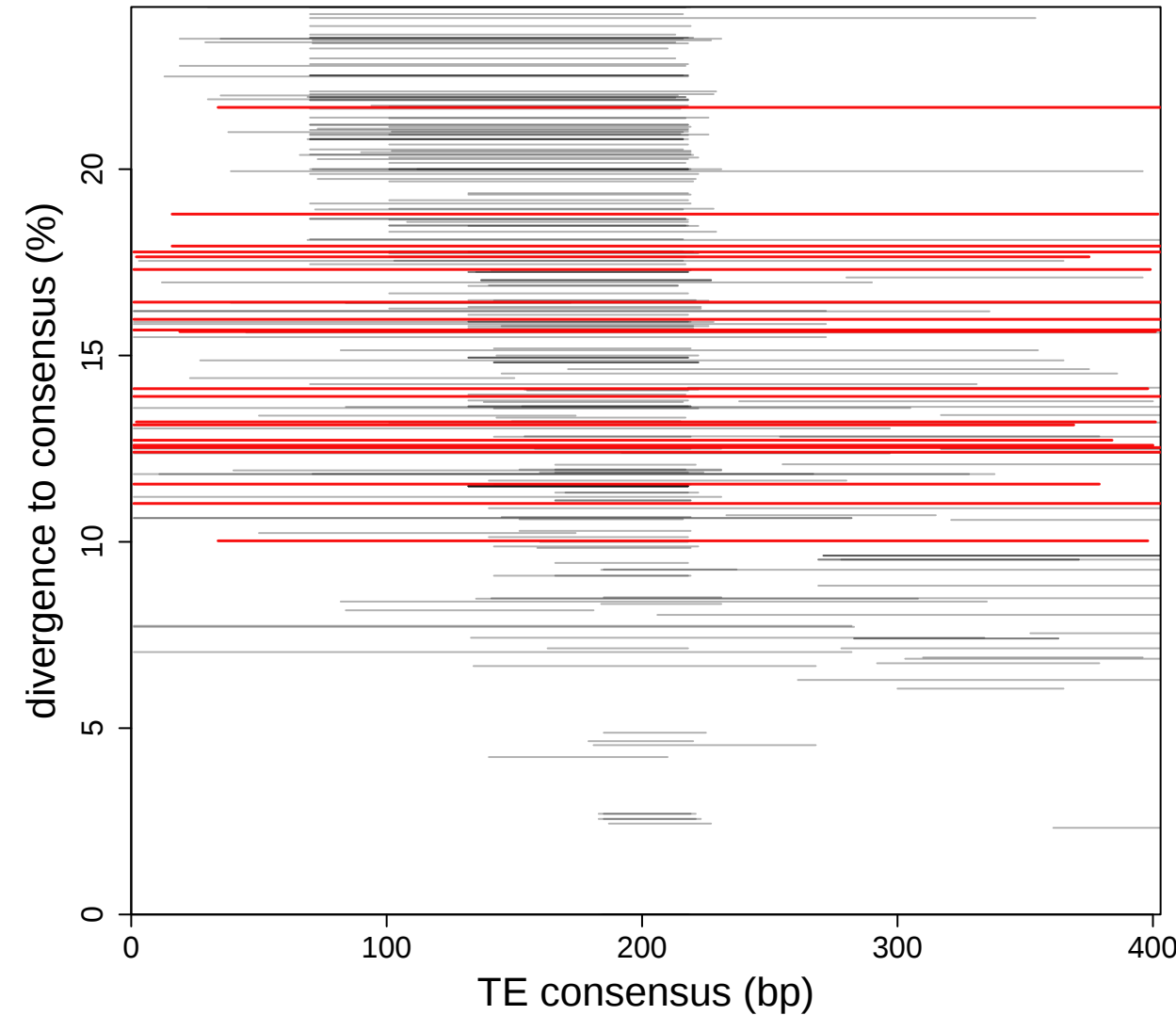


f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bc
size: 1288bp; fragments: 284; full length: 0 (>=1159.2bp)

After TEtrimmer Extended plot Blue lines are boundaries

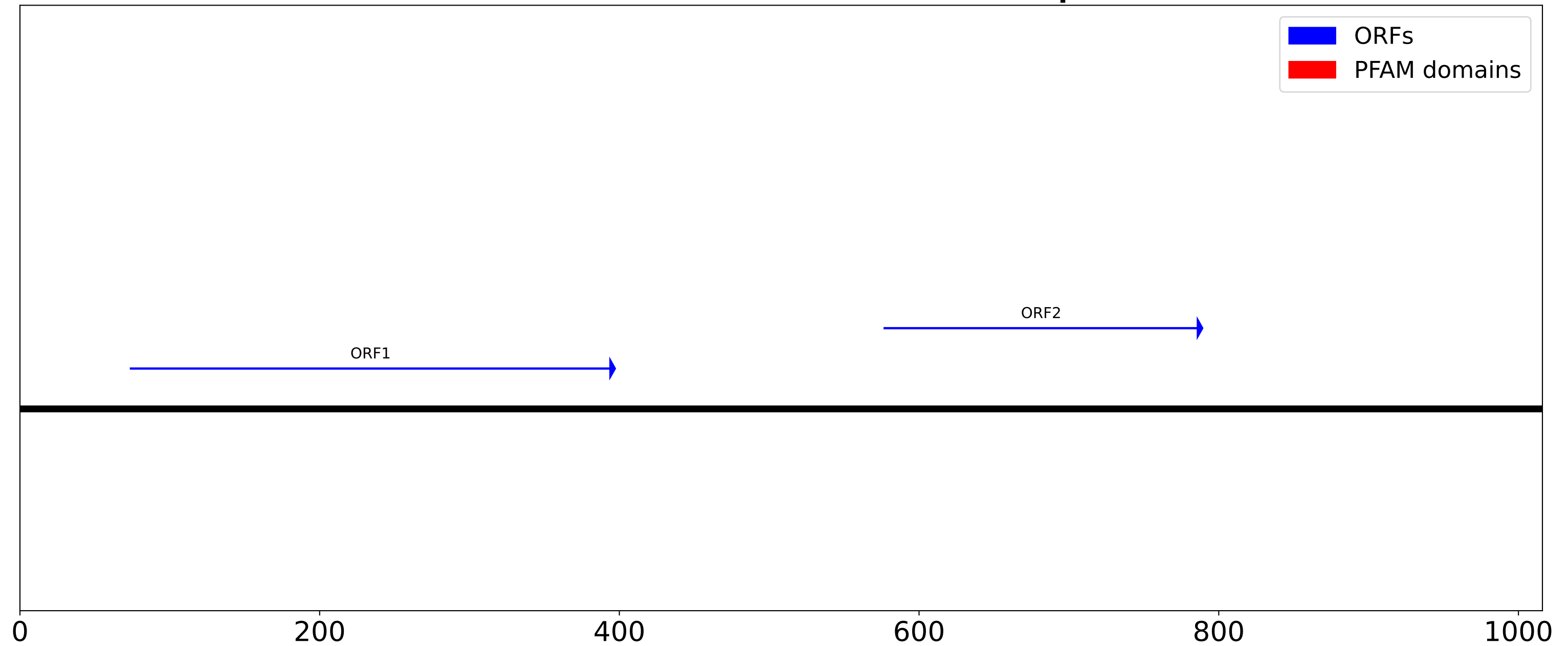


TE: rnd_5_family_6143
size: 403bp; fragments: 279; full length: 21 (≥ 362.7 bp)

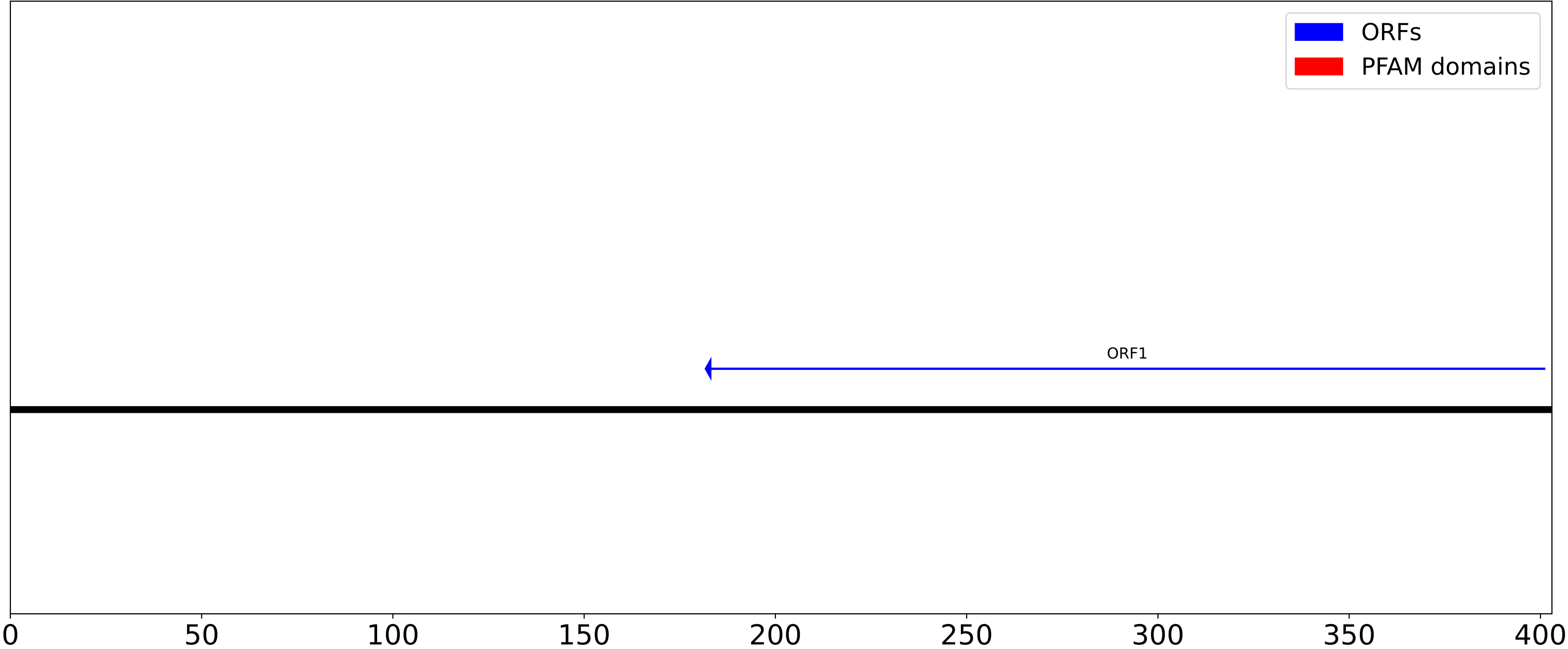


Before TEtrimmer 403 bp

After TEtrimmer ORF and PFAM domain plot



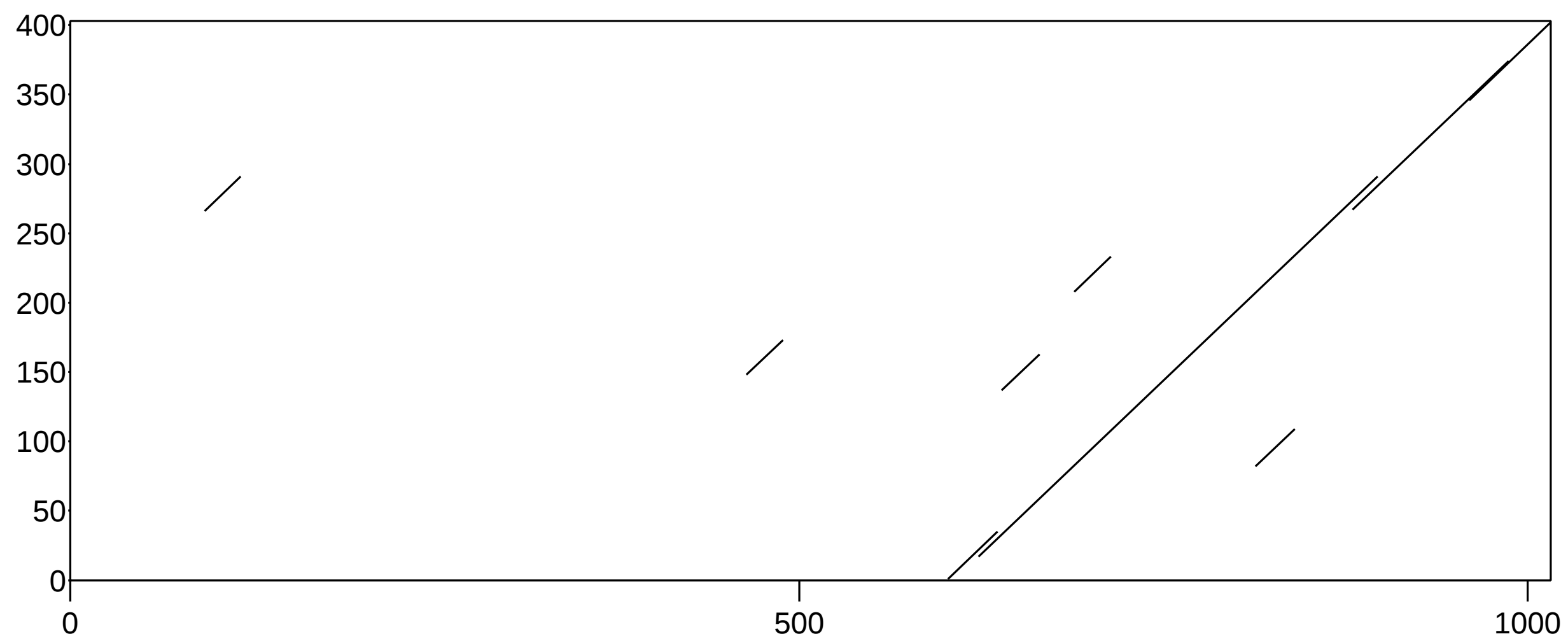
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)