

Start Crop Point

End Crop Point

MSA length = 765

Sequence alignment visualization showing 10 rows of nucleotide sequences (A, C, G, T) with gaps (-). The alignment is color-coded: A (green), C (blue), G (red), and T (grey). The sequences are aligned across 765 positions. A red arrow points to the Start Crop Point at position 285, and a blue arrow points to the End Crop Point at position 685.

Sequence 1: GCTGATCTTTAATAACATCTATT - - - - - AATTTTCCCTTTACTCTACCT - - - - - TCTGTTATAGTCCCATCCTCATTTTAATT - - - - - TTTTATTTAAGTATGAAGAAAATAGAACAAATTAAAGATTAAATAAAAATACGTCCAATTAAATGGA - - - - - AATAAATAATTGT - - - - - AACAAAA

Sequence 2: ATTAGCTCCTTGACACGTCAACATATCTCAAAAAATTTGTTTATGTAGTT - - - - - GTTTT - - - - - ATATATGTGTTATAATCCCATCCTCATTTTAATT - - - - - TTTTATTTAAGTATGAAGAAAATAGAACAAATTAAAGATTAAATAAAAATACGTCCAATTAAATGGA - - - - - AATAAATAACTGT - - - - - AACAAAA

Sequence 3: - - - - - AACACTATAAATGGGTCTTTGTGAGGTAGTAAACCATTTAGCTGAAGAGTGTATAATCCCATCCTCATTTTAATT - - - - - TATTGCTGTACTATAT - - - - - GACGTACAAATATAAGATACCTCGCACAAAA

Sequence 4: GCTTCGTATTTGCTTAATTATATATCTCACACTTTTTCTTT - - - - - AAAAAACCTTTAAGAAATAAACCATGTTATAATCTCATCCTCATTTTAATT - - - - - TTTTATTTAAGTATGAAGAAAATAGAACAAATTAAAGATTAAATAAAAATACATCCACGTGATGCCCGTG - - - - - GTAAATTTCCCGCGTAA

Sequence 5: GCTTCGTATTTGCTTAATTATATATCTCACACTTTTTCTTT - - - - - AAAAAACCTTTAAGAAATAAACCATGTTATAATCCCATCCTCATTTTAATT - - - - - TTTTATTTAAGTATGAAGAAAATAGAACAAATTAAAGATTAAATAAAAATACATCCACGTGATGCCCGTG - - - - - GTAAATTTCCCGCGTAA

Sequence 6: GCTTCGTATTTGCTTAATTATATATCTCACACTTTTTCTTTA - - - - - AAAAAACCTTTAAGAAATAAACCATGTTATAATCCCATCCTCATTTTAATT - - - - - TTTTATTTAAGTATGAAGAAAATAGAACAAATTAAAGATTAAATAAAAATACATCCACGTGATGCCCGTG - - - - - CTAAATTTCCCGCGTAA

Sequence 7: - - - - - CAATTTTTTTTATATTTTGA AAA AAA - AATTCCTTAGGGGGGAGGTTGTTATAGTCCCATCCTCATTTTAATT - - - - - TTTTCTCTCAGTGCAGAGTG - - - - - TAGGTGATTTTAGCAATGTT - - - - - CTCTCGA

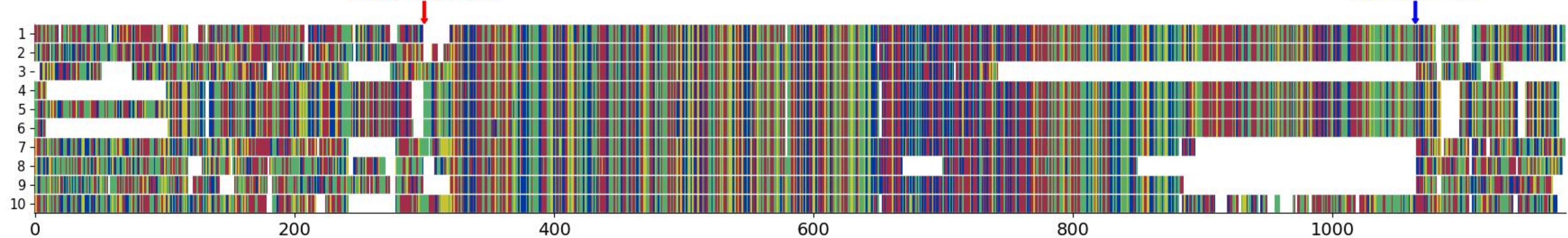
Sequence 8: ATCACGTTTTTTACCTGAAAAA - - - - - GAAAAATTAGATCAAATTAAC - - - - - TCAAACCATAGAAATTTGTTAAATCCCATTCCTCATTTTAATT - - - - - CCTCCAAGTTTAAACAGTGATTATTTACTTATAGAAAGTTT - - - - - CTTGAAA

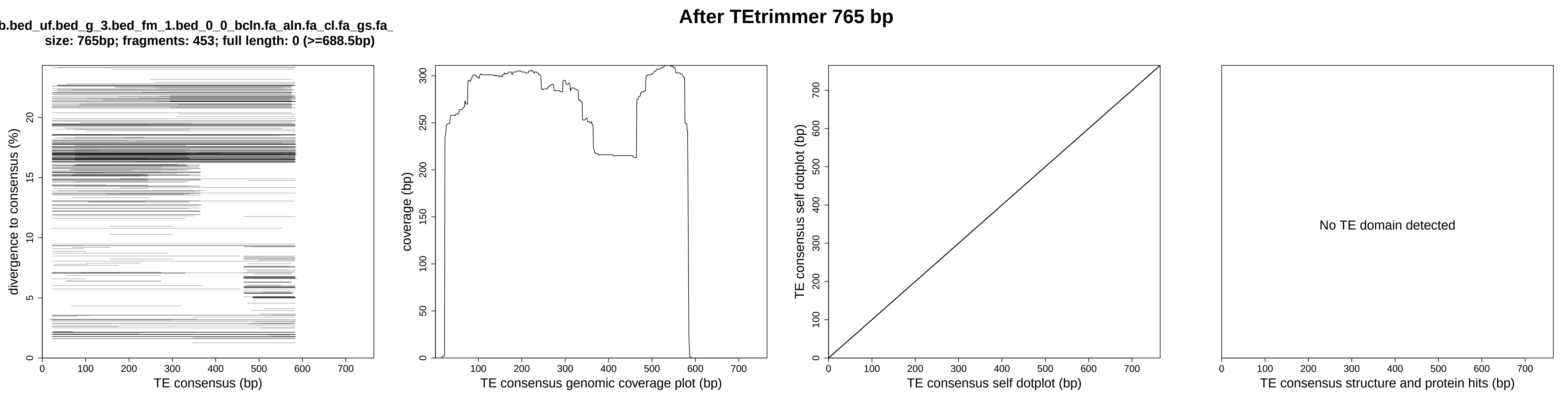
Sequence 9: GCTATATT - TTGACTTA AAAAATAT - - - - - TAAACTAAGTTTCTTCTAATT - - - - - GTTGTATAATCCCATCCTCATTTTAATT - - - - - TCTTTGCGAAATGAAT - - - - - AATAAATAAATATGACAAATGTACACAATA

Sequence 10: - - - - - CAAATTTTTTTTATTAATGA AAA AAAATTTTTCCTTAGGGGGGAGGTTGTTATAATCCCATCCTCATTTTAATT - - - - - ATT - - - - - TTTTGTCCGCTGGAAAAATTAAAAATAAAAAATACAAACGGACTTTTTTTCTCAATGATTGTGAATTAAATAATTTTAACAAATTT - - - - - CACGAAA

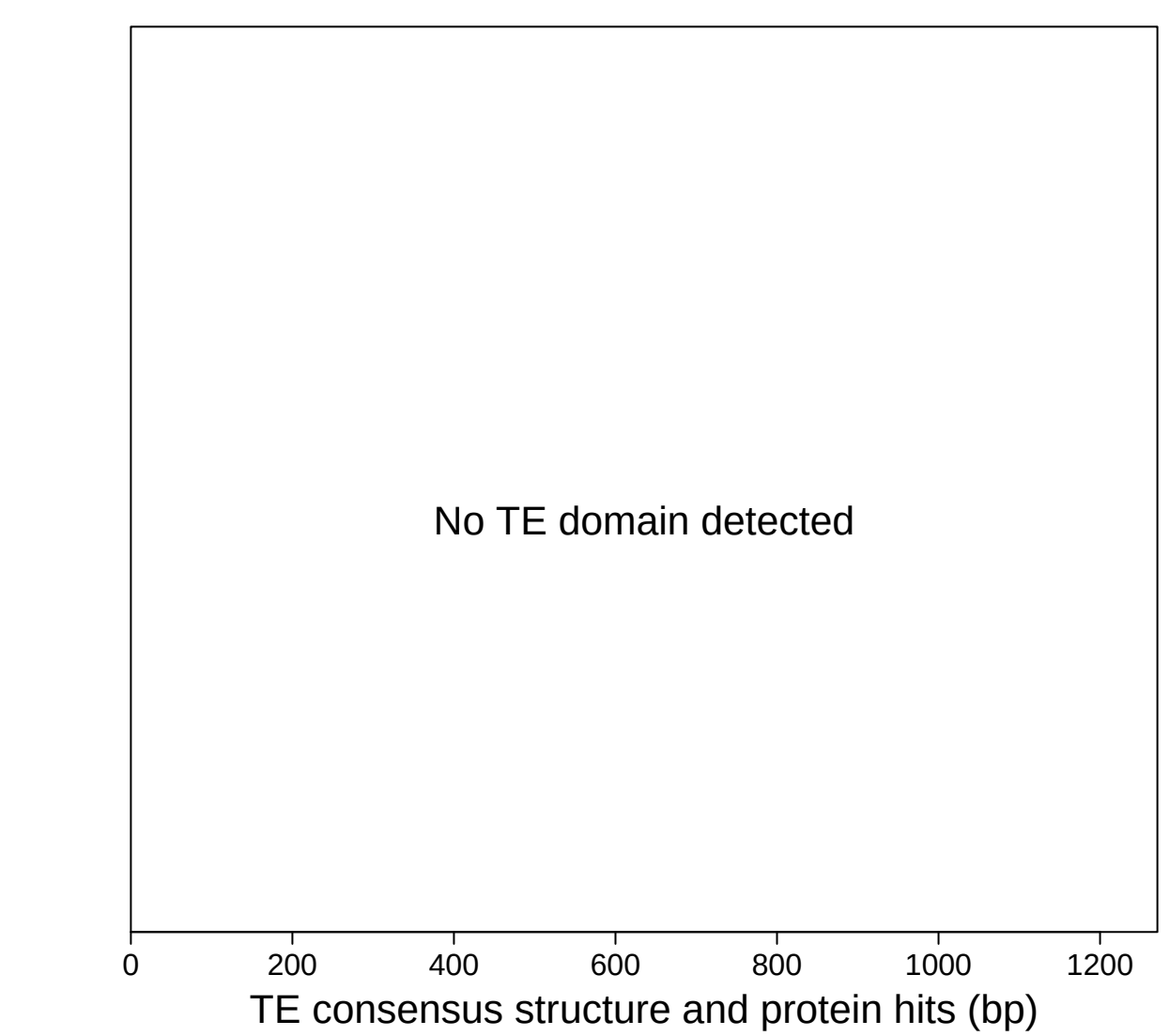
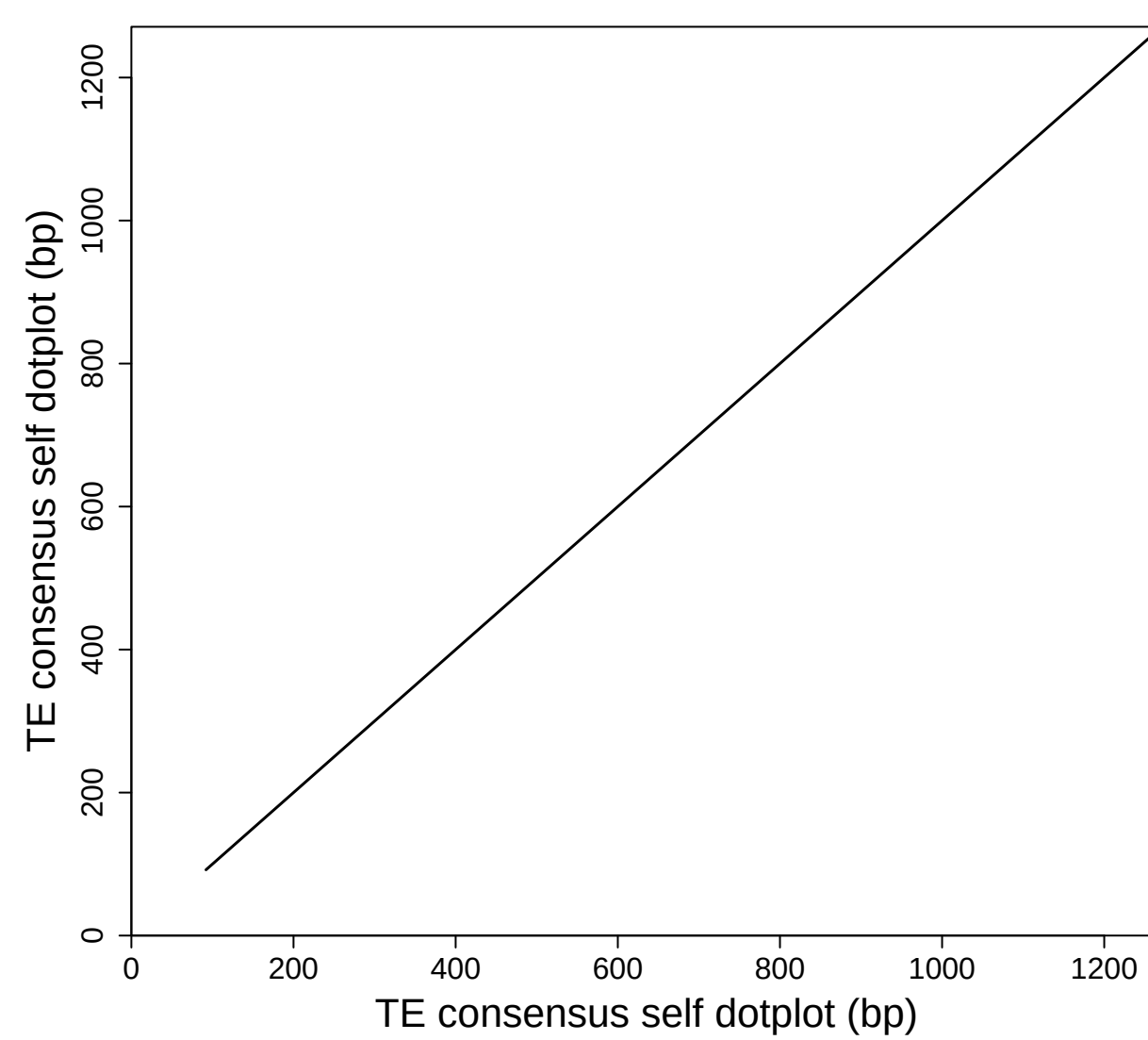
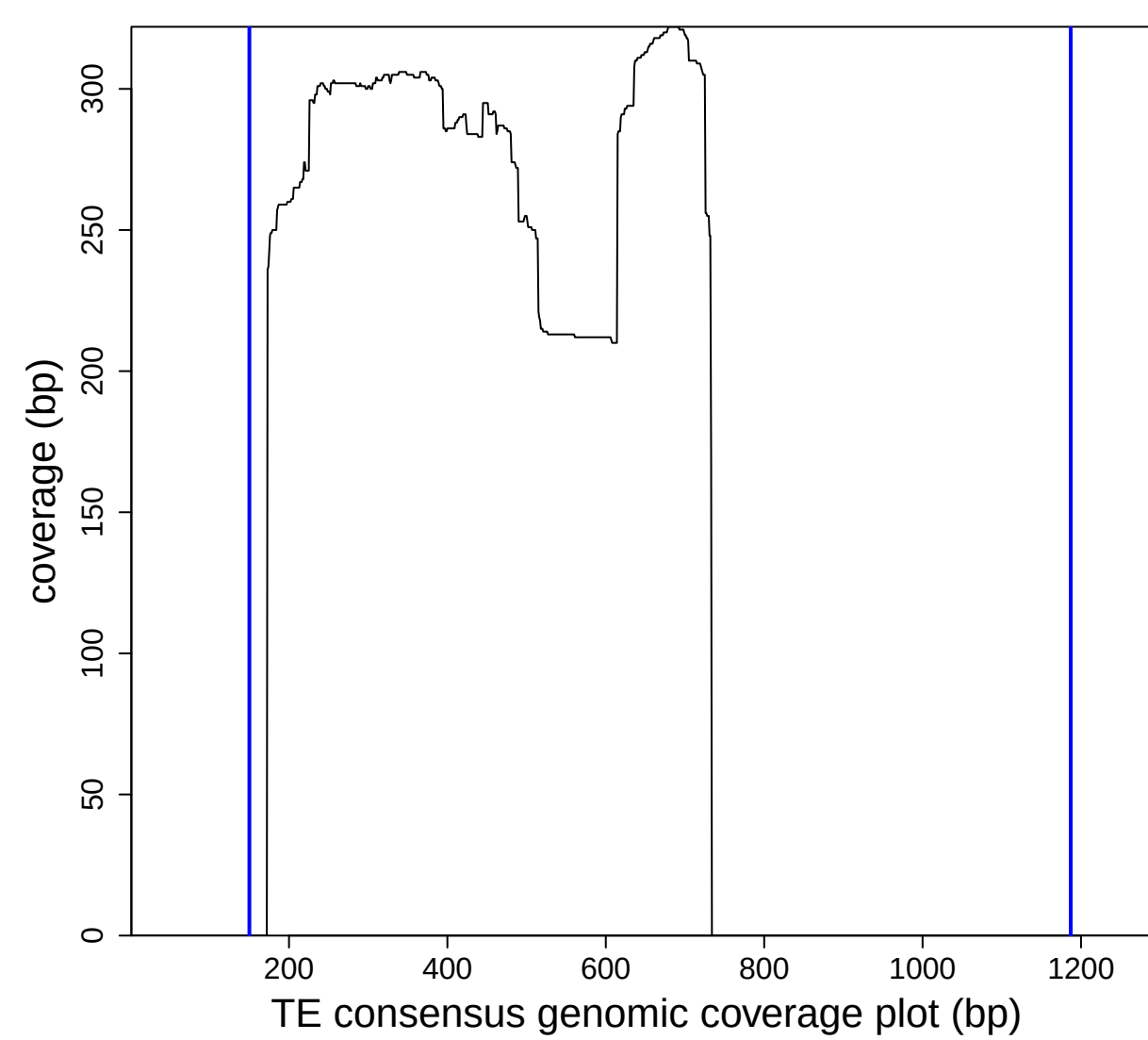
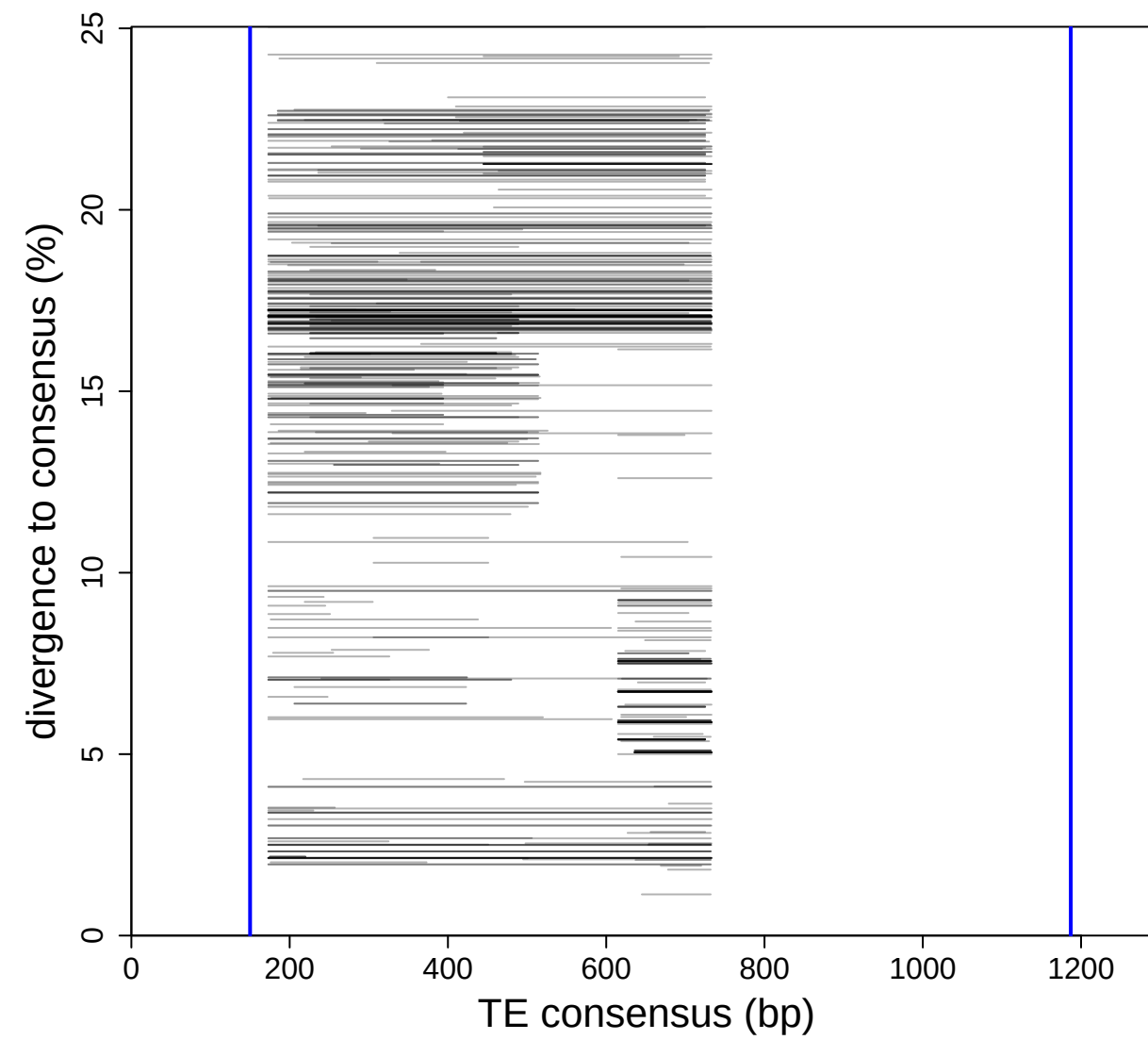
Start crop Point

End crop Point

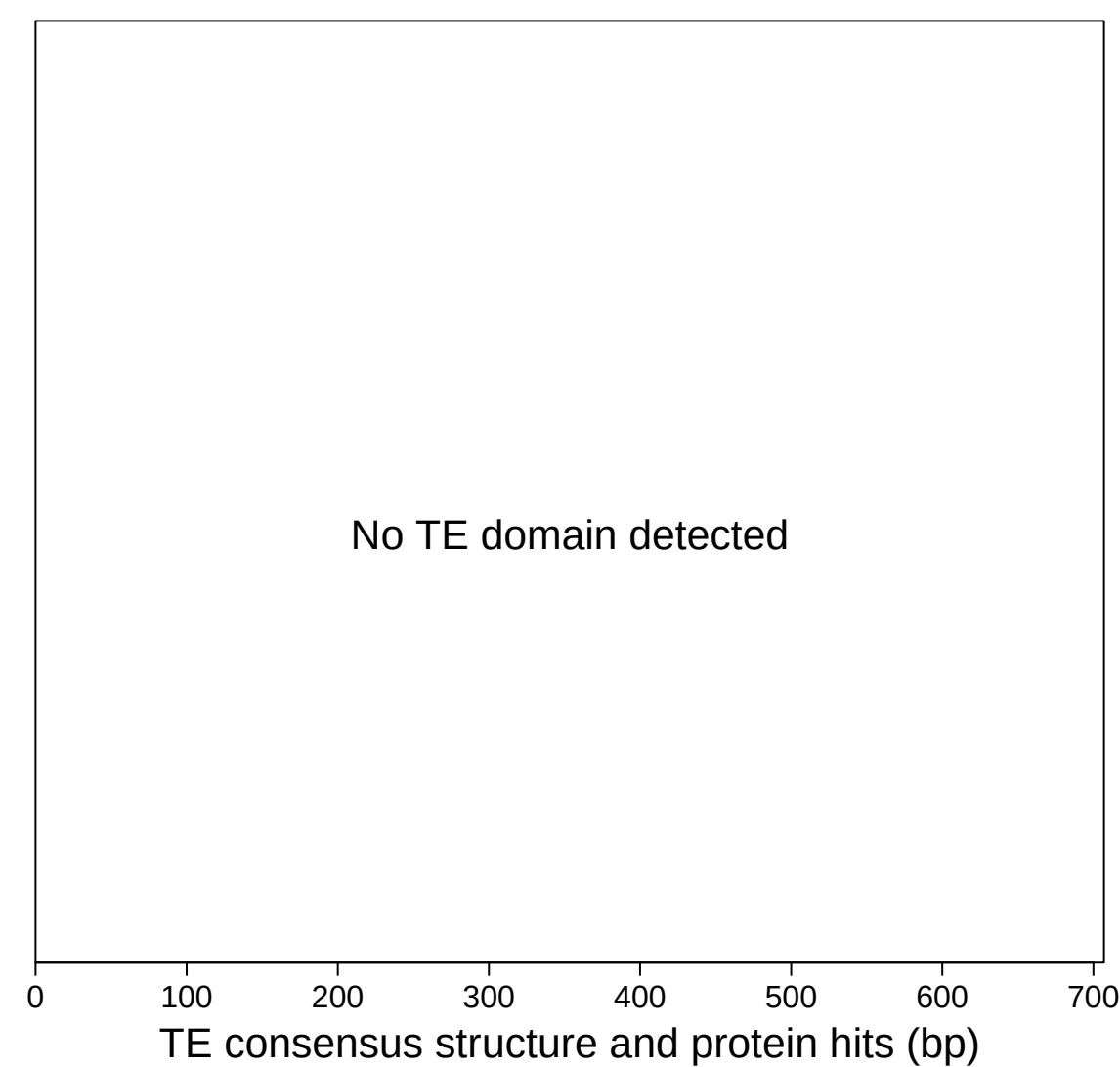
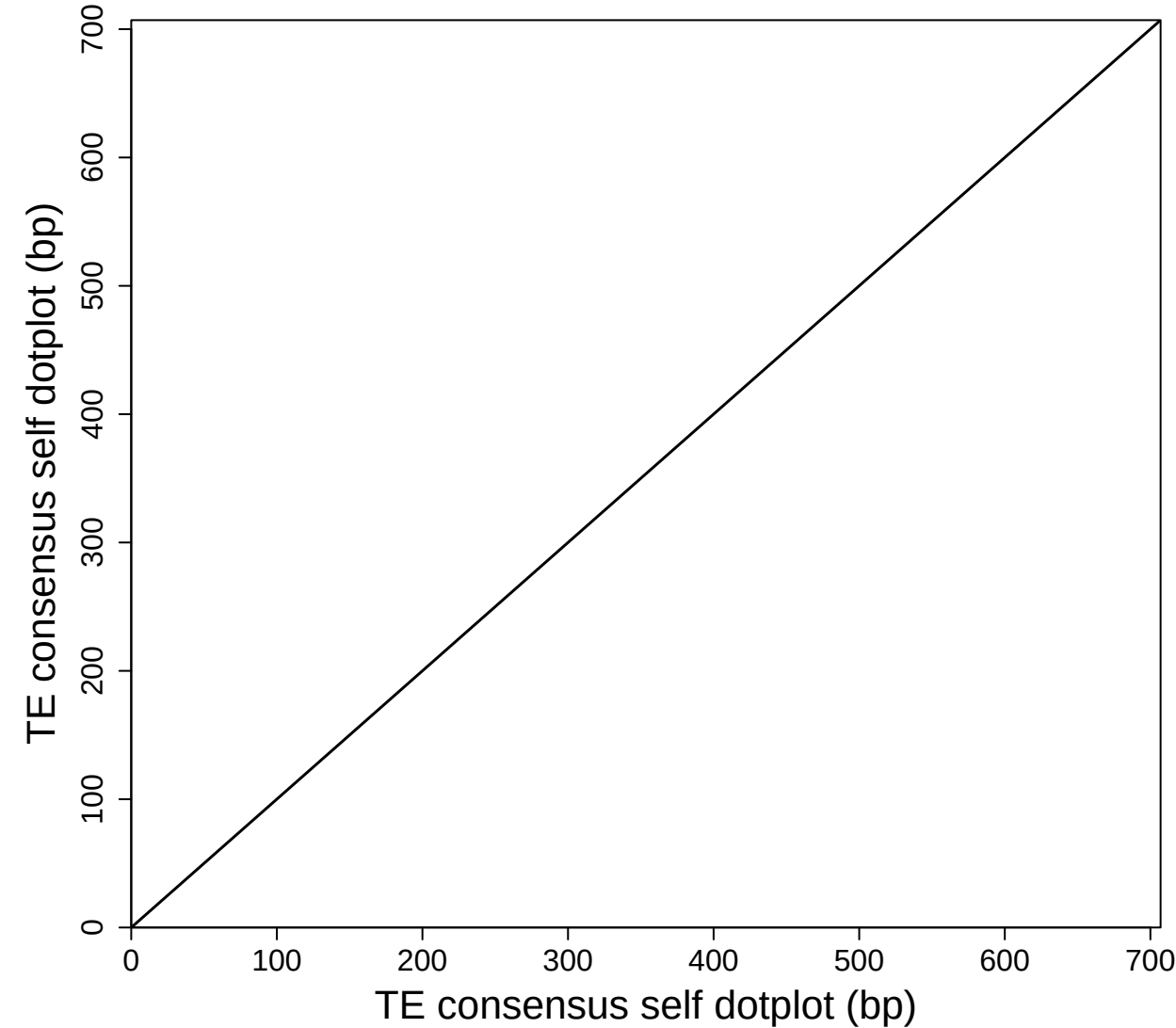
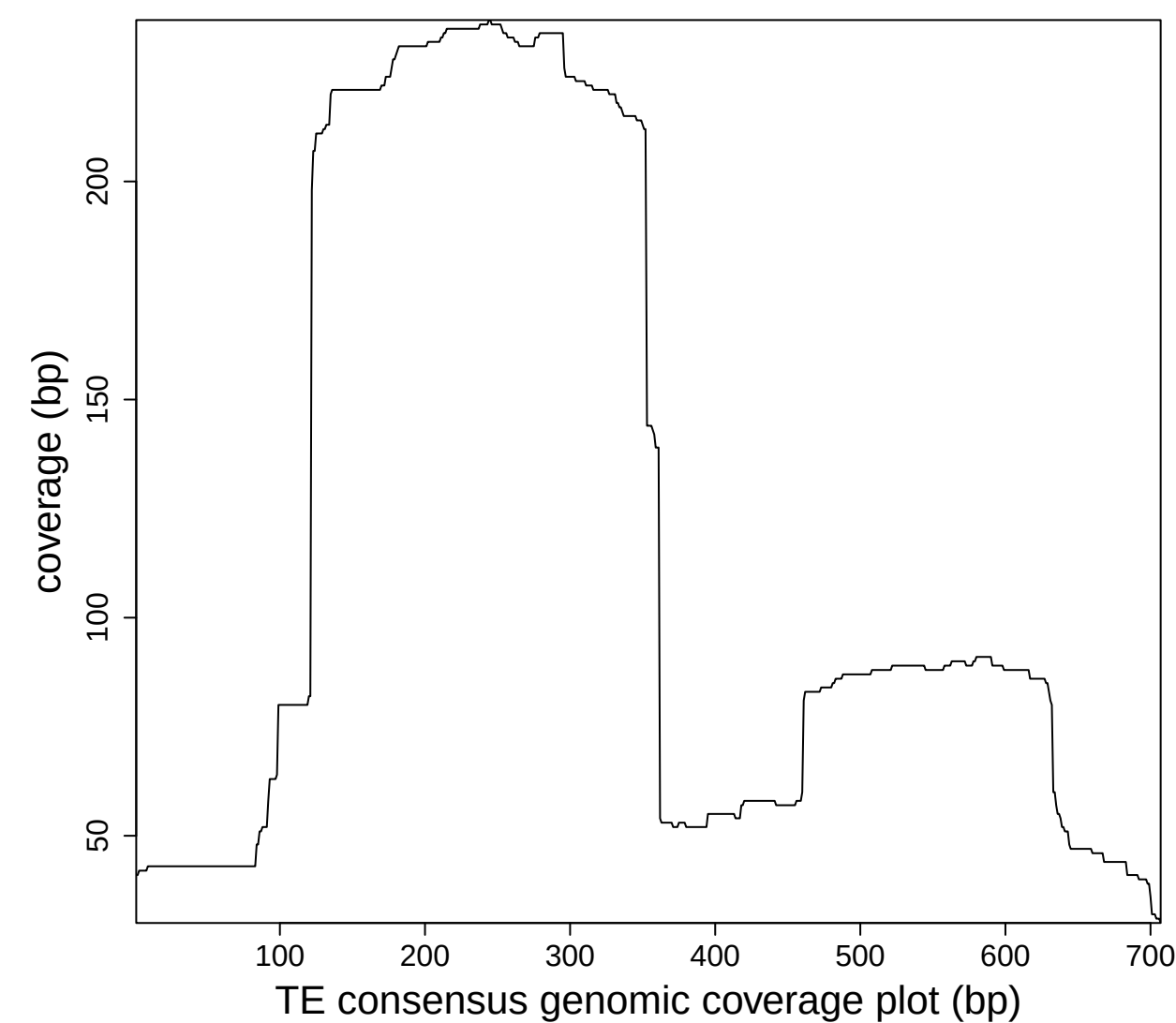
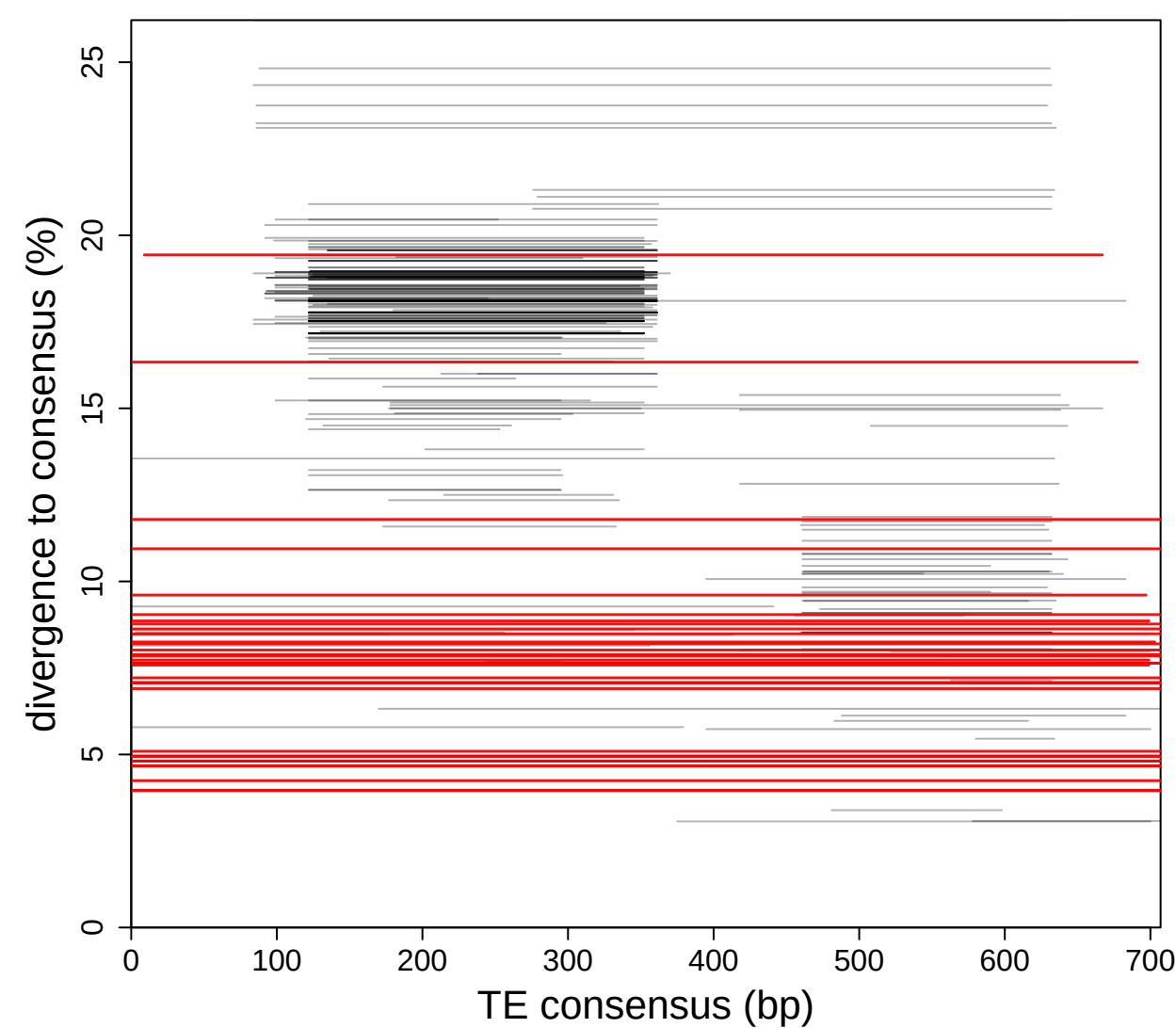




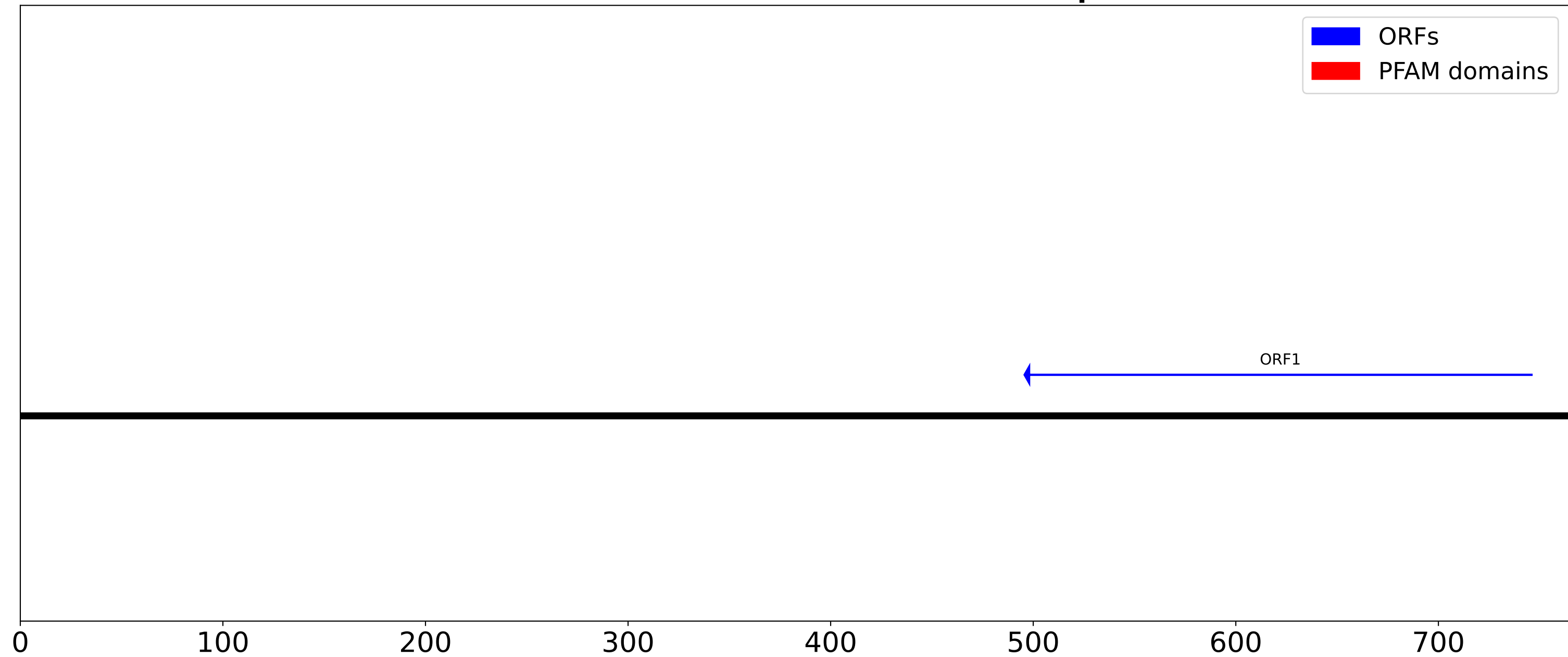
fasta.b.bed_uf.bed_g_3.bed_fm_1.bed_0_0_bcln.fa_aln.fa_cl.fa_
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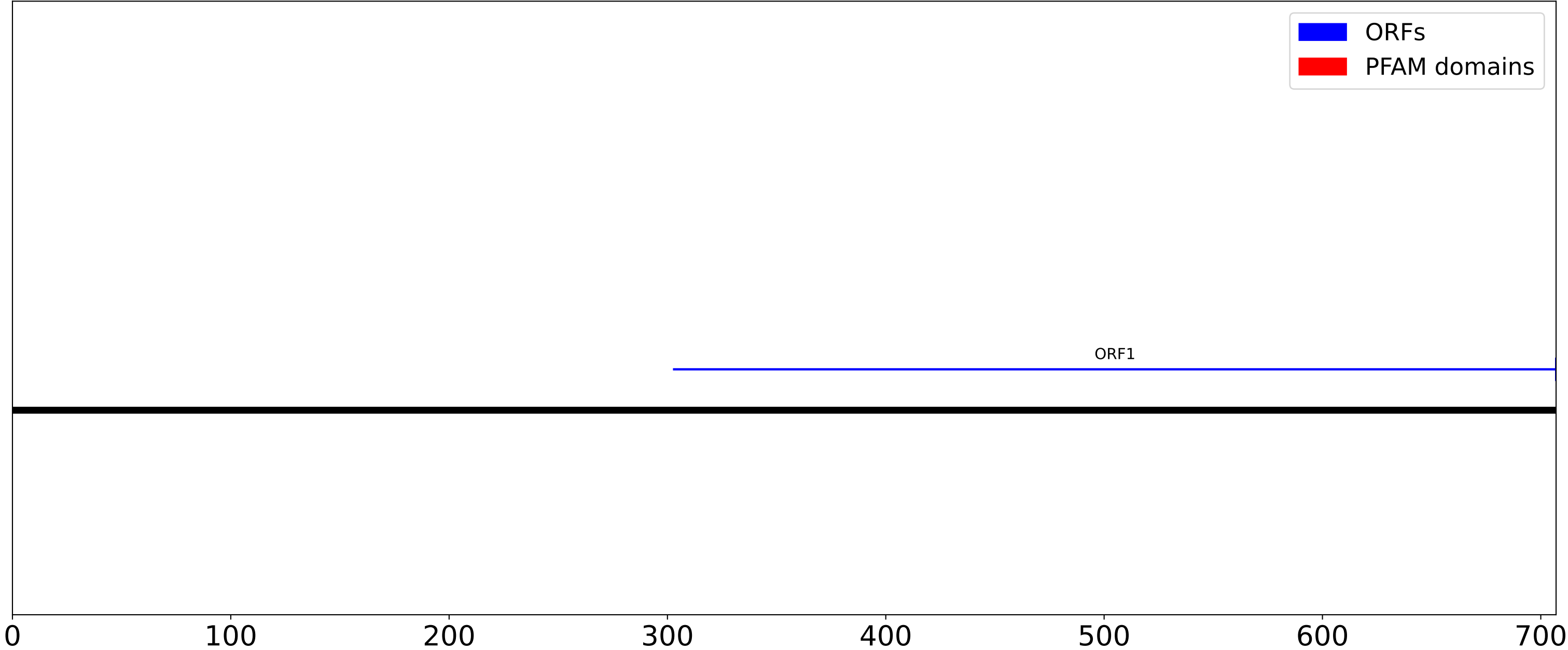
TE: ltr_1_family_96
size: 707bp; fragments: 285; full length: 35 (≥ 636.3 bp)



After TEtrimmer ORF and PFAM domain plot



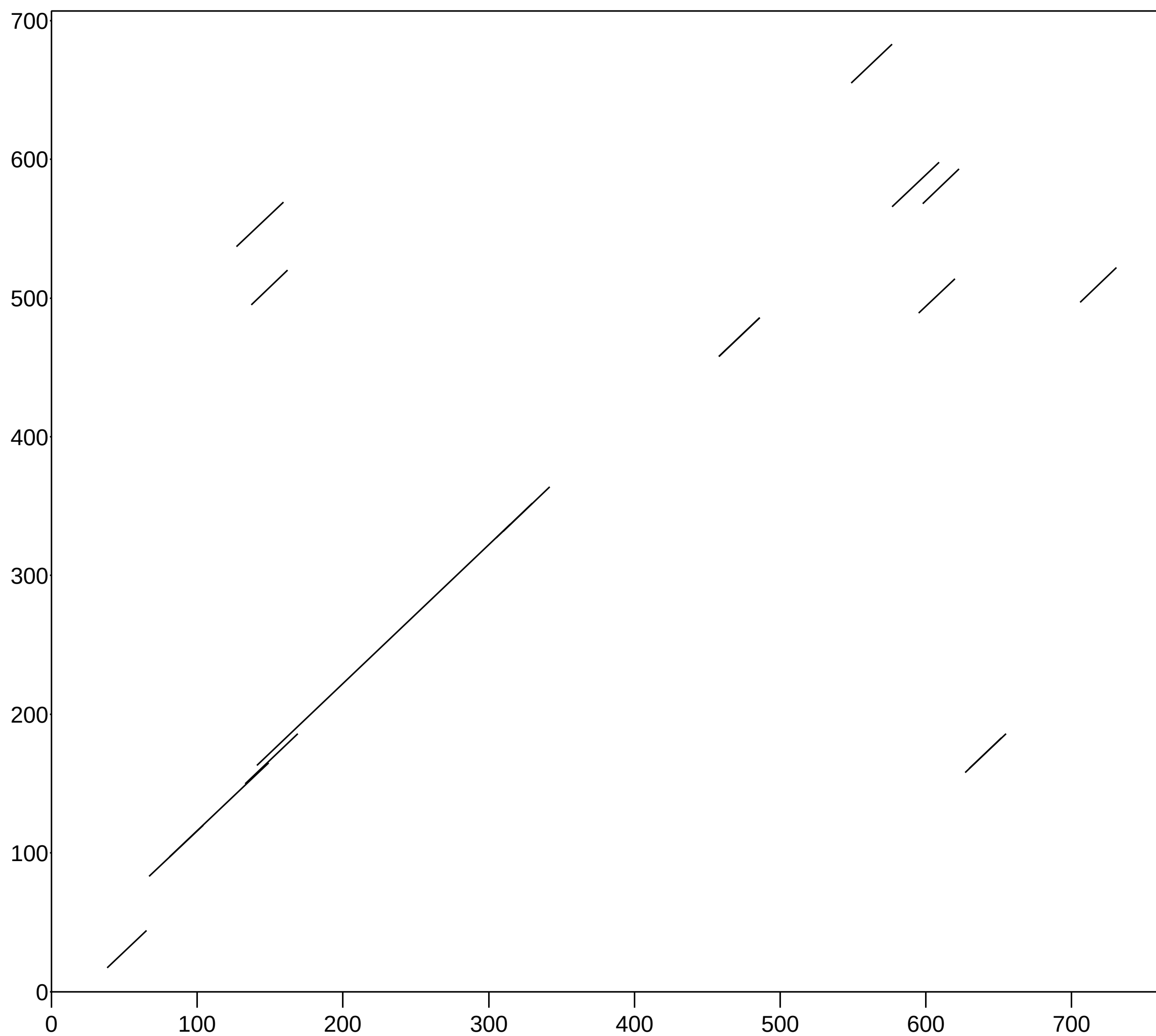
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)