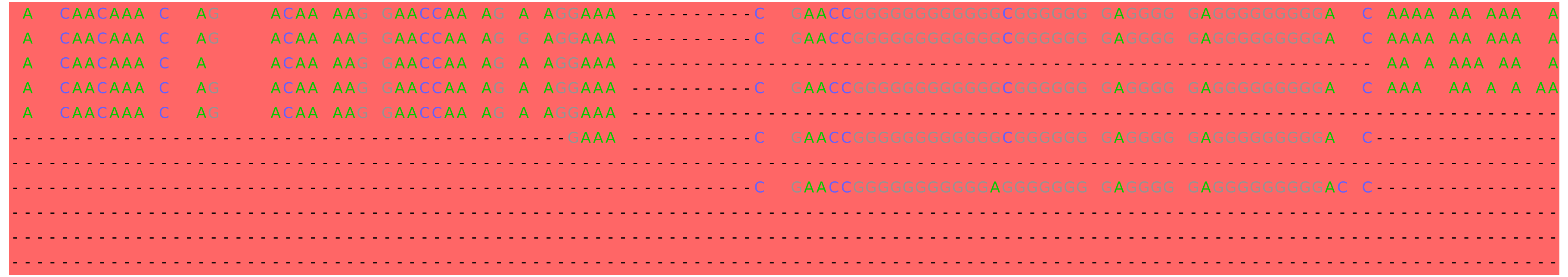
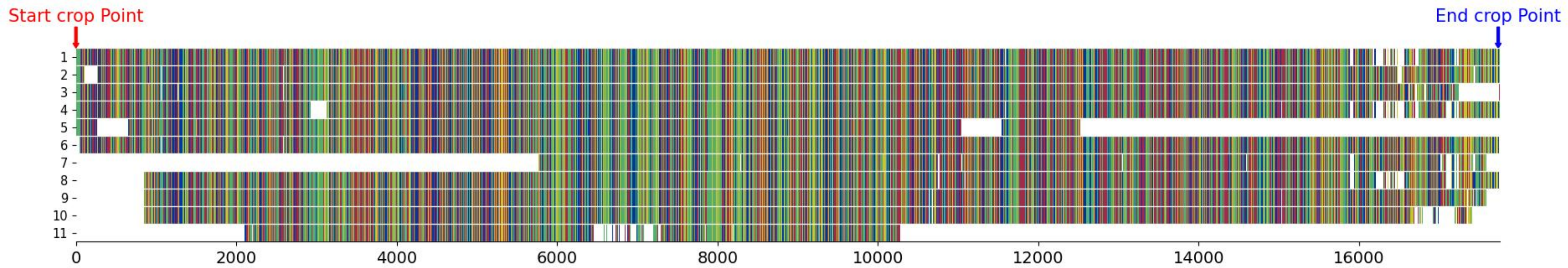


Start crop Point

End crop Point

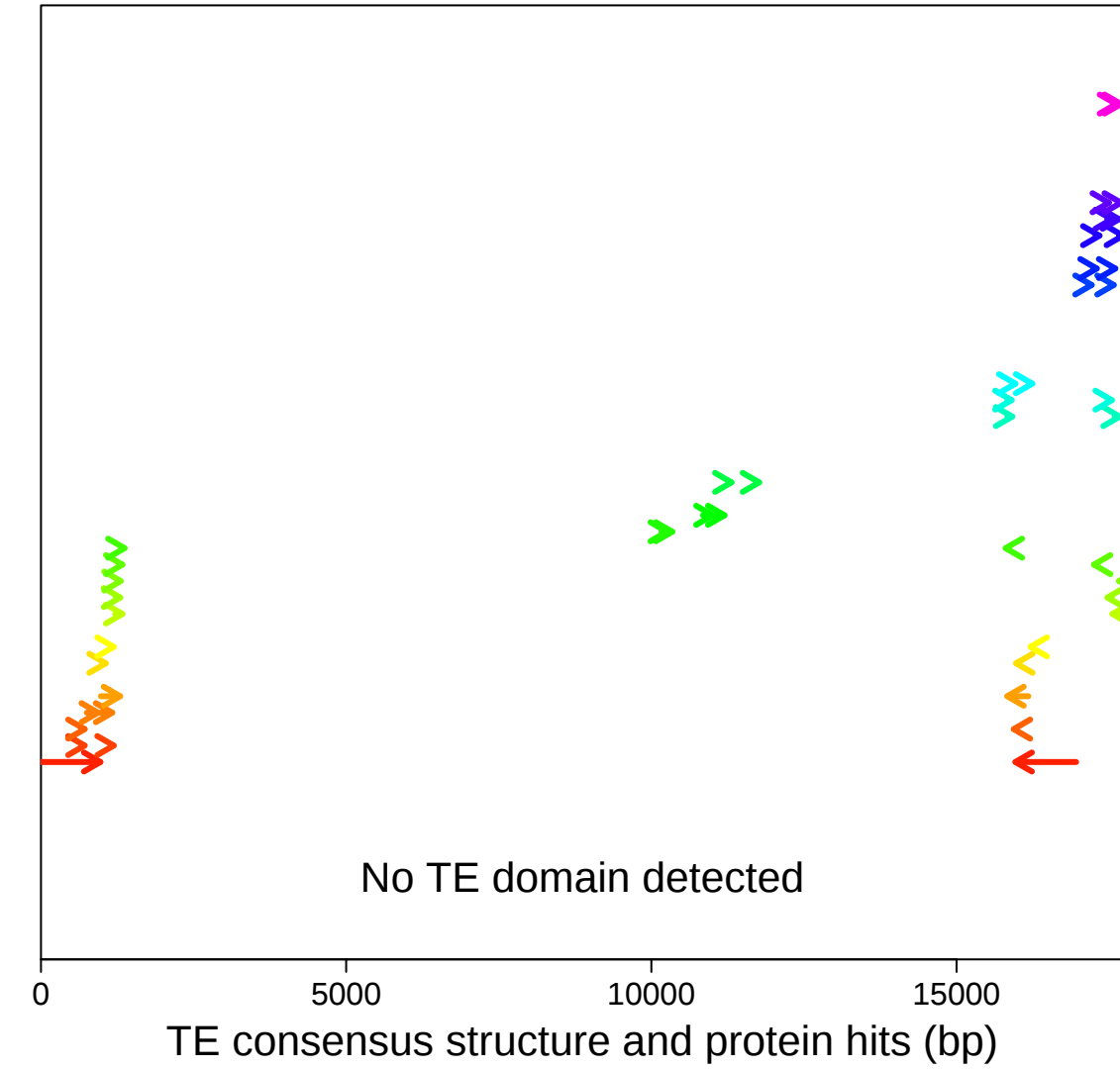
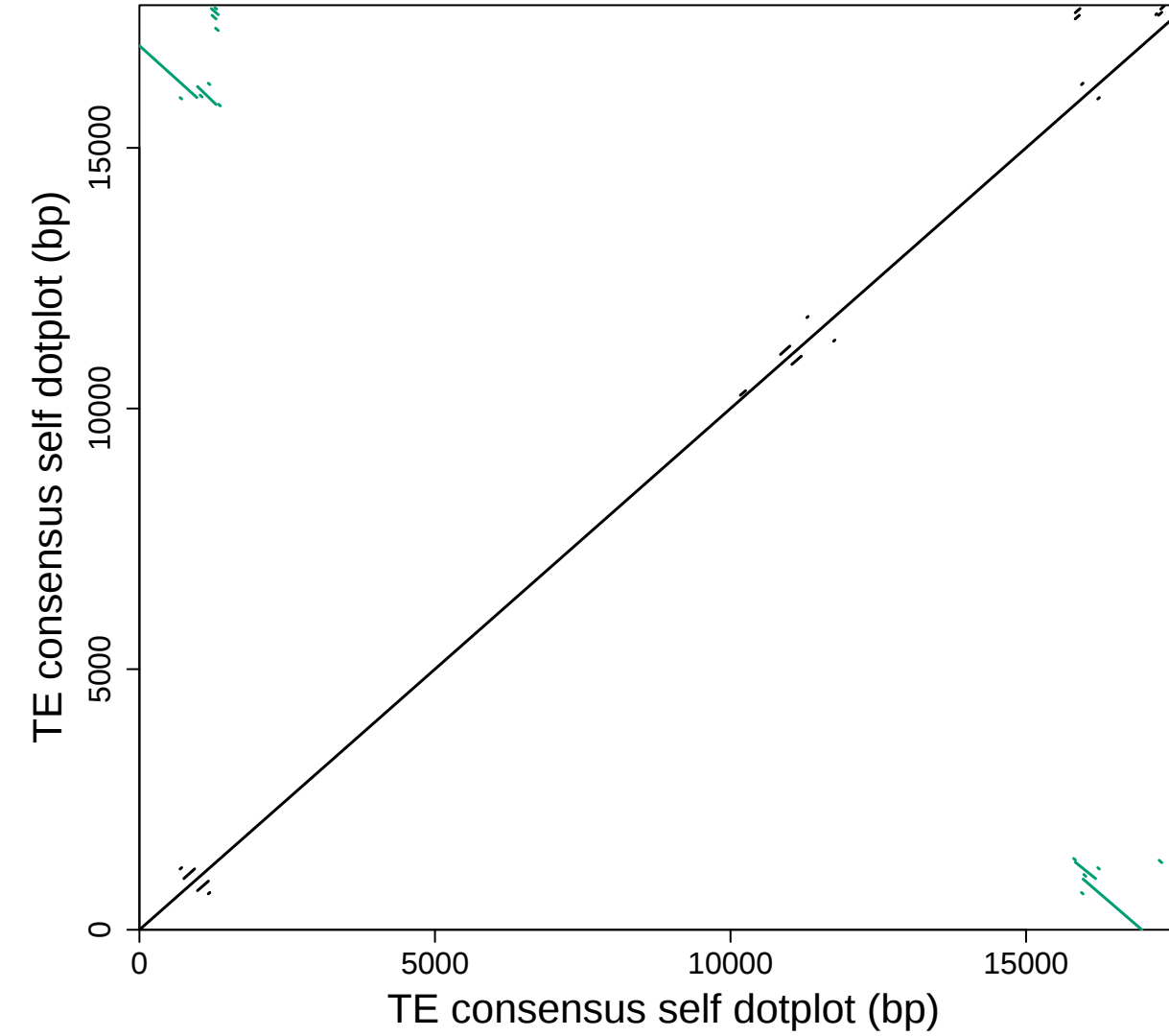
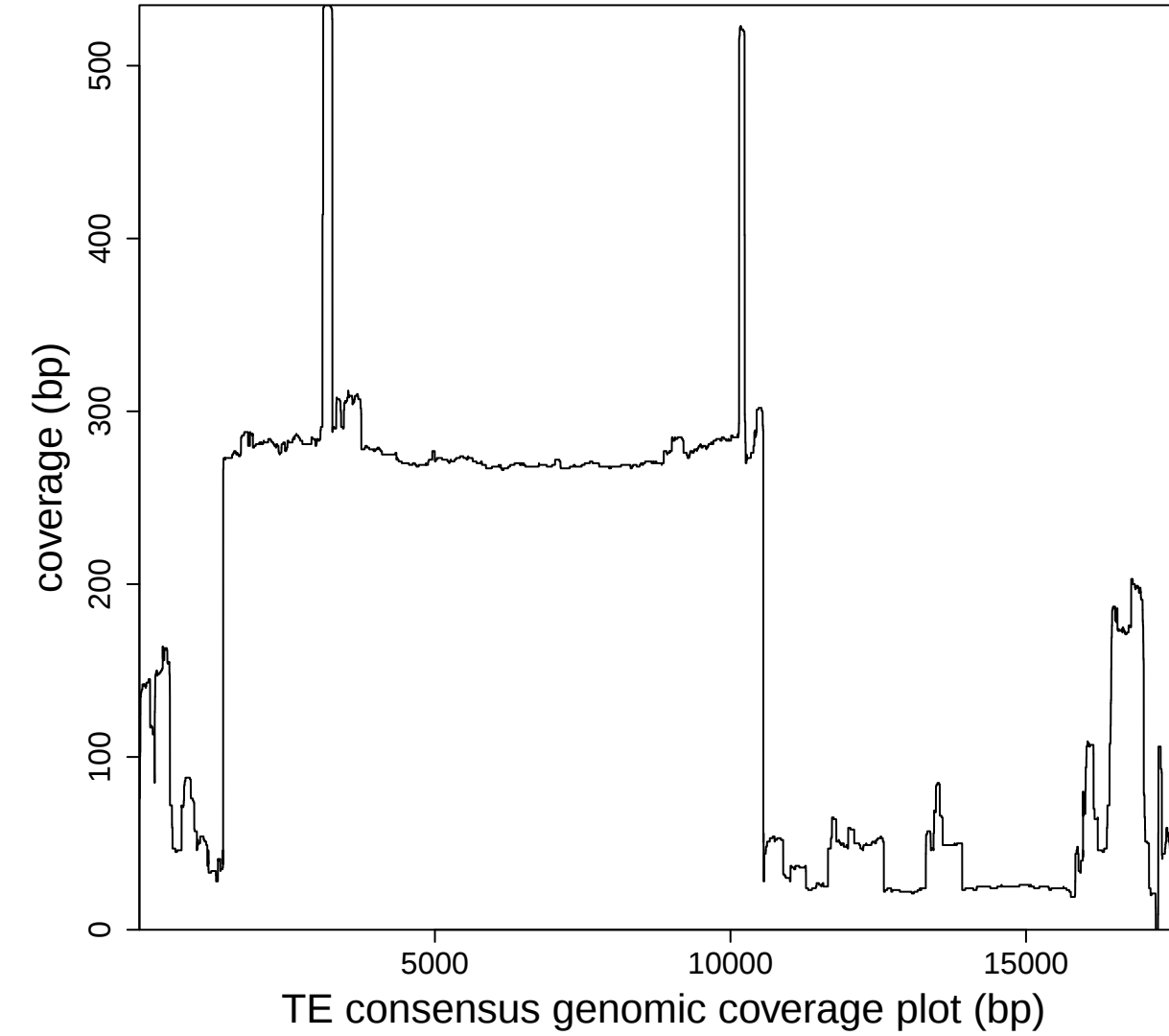
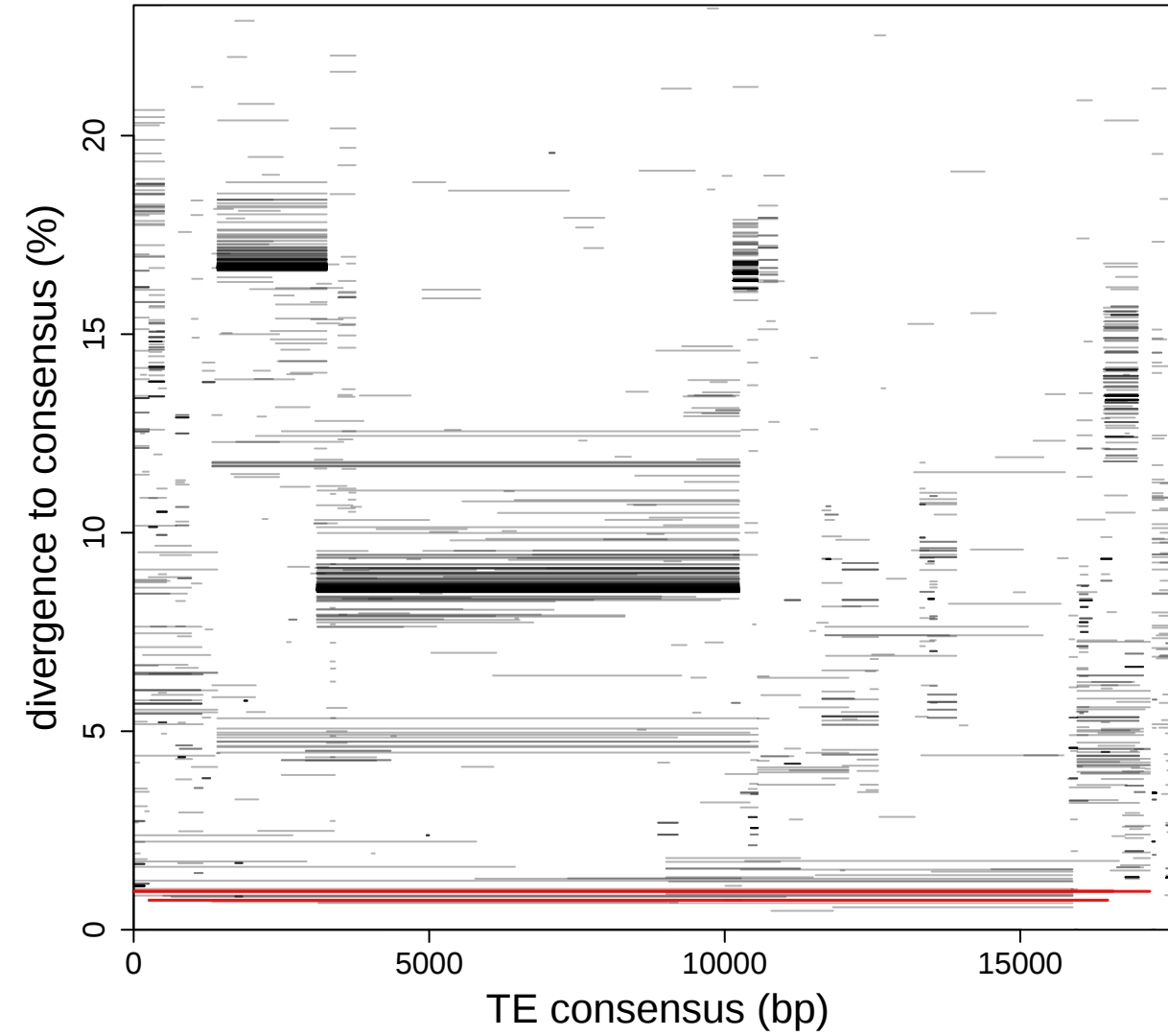
MSA length = 17737





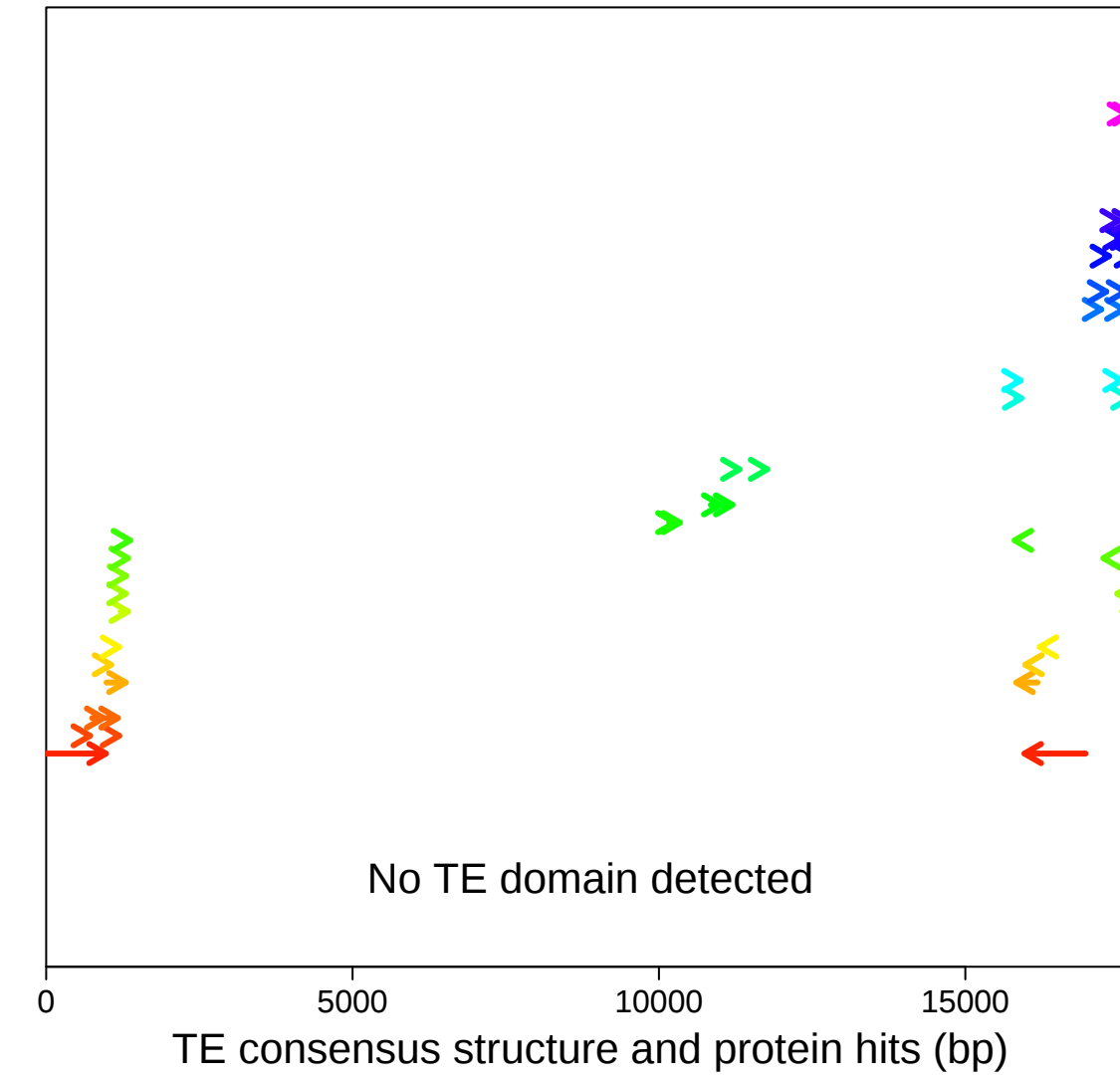
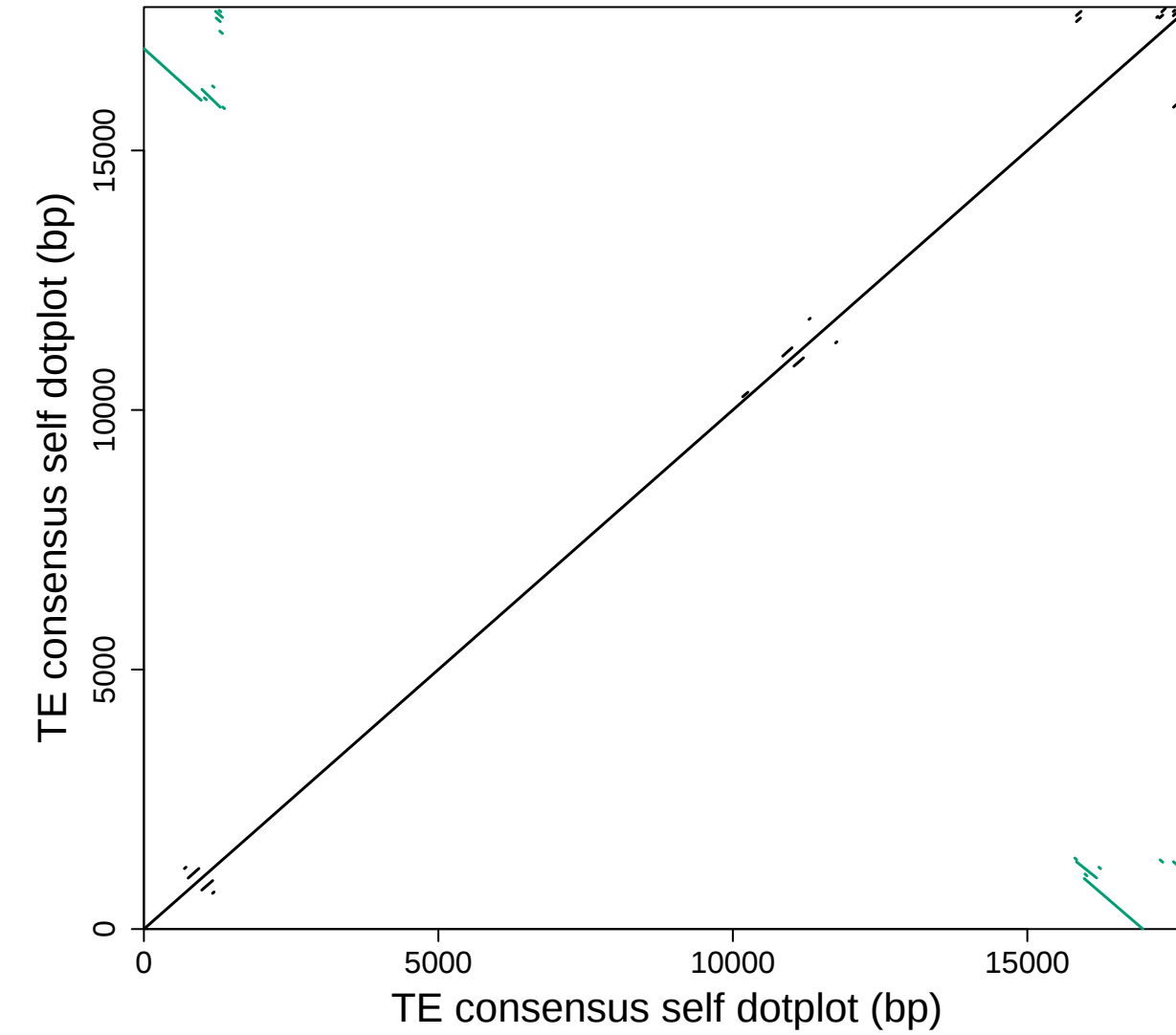
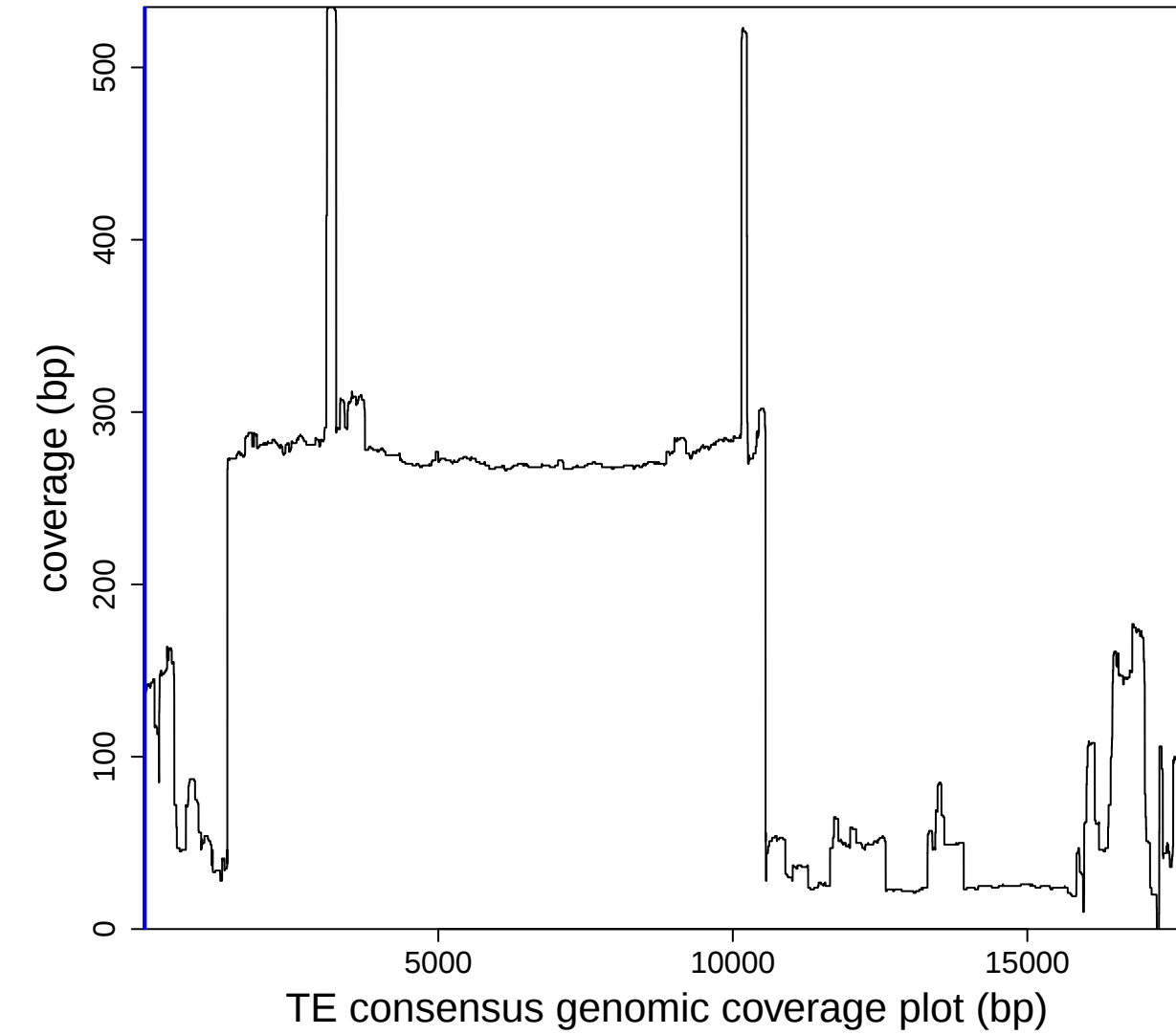
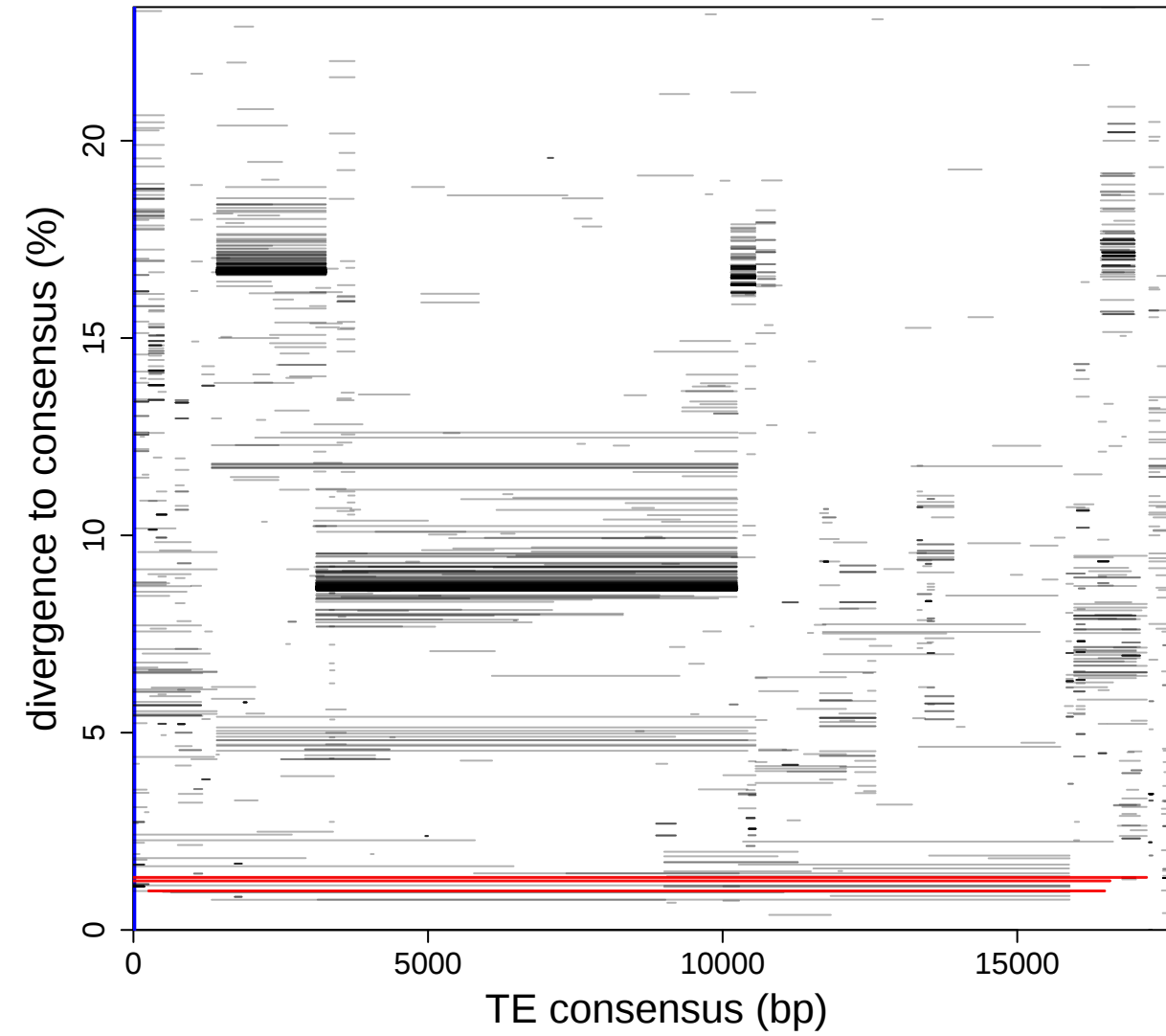
_2.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcIn.fa_al
size: 17737bp; fragments: 2185; full length: 3 (>=15963.3bp)

After TEtrimmer 17737 bp



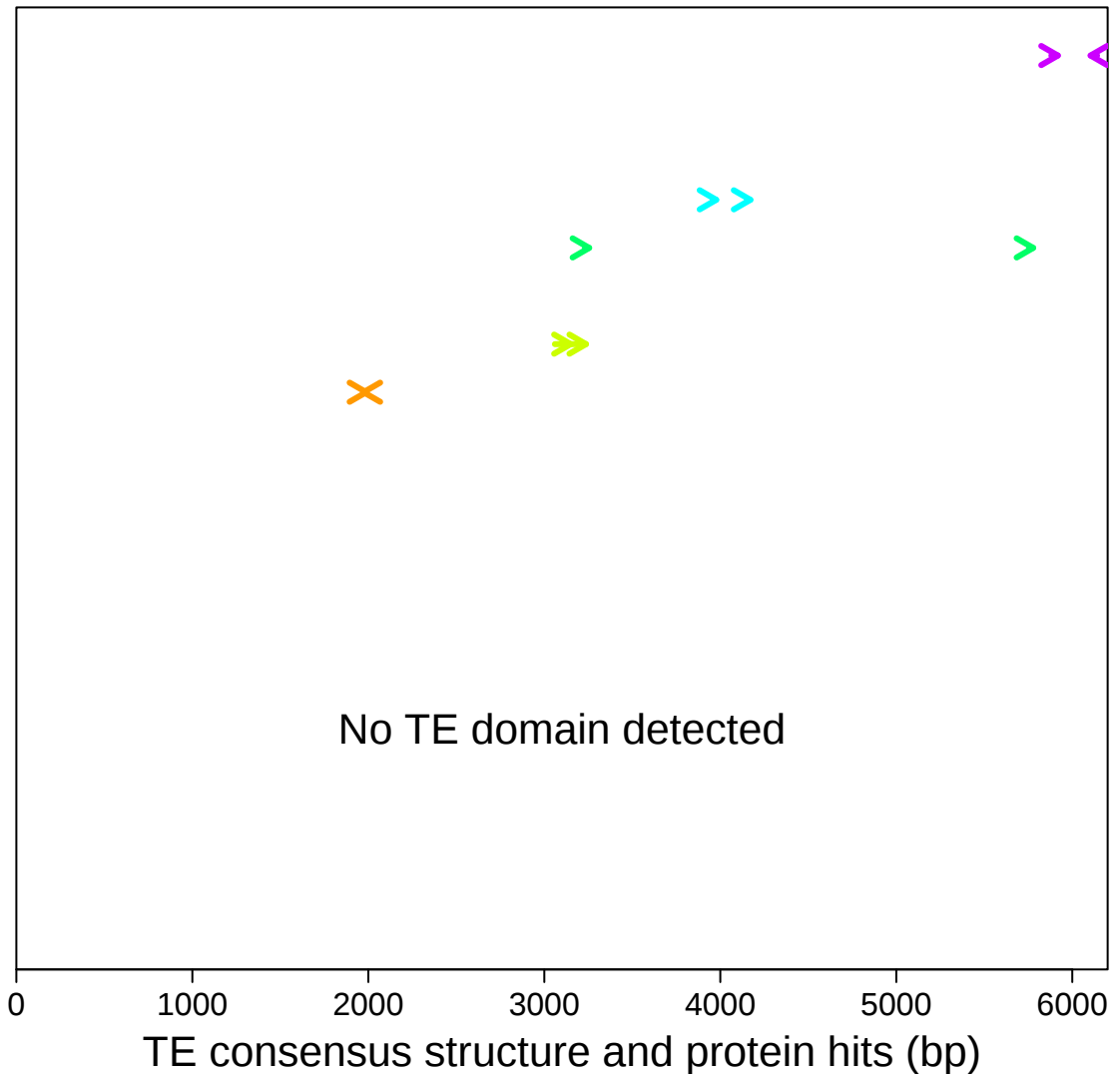
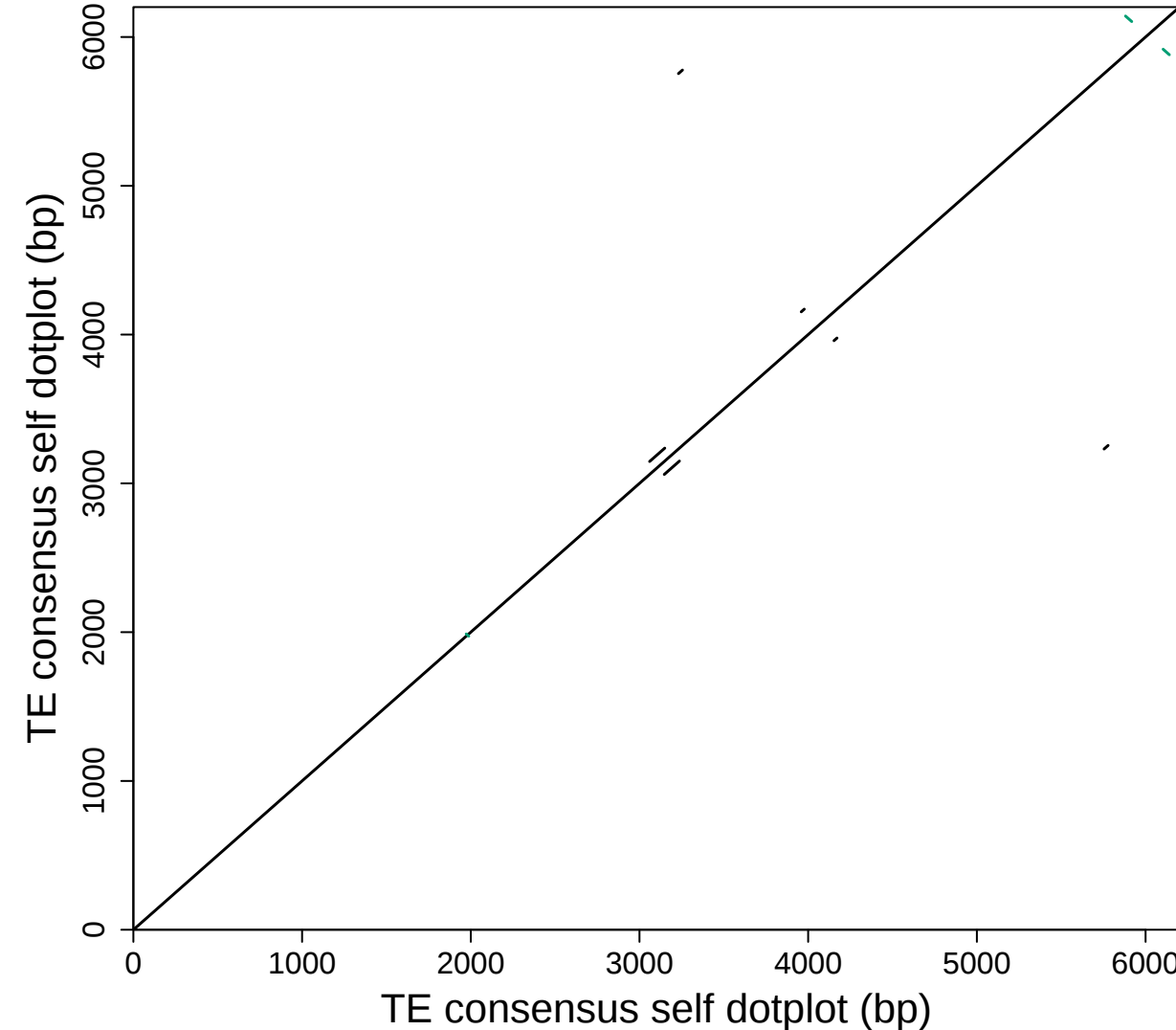
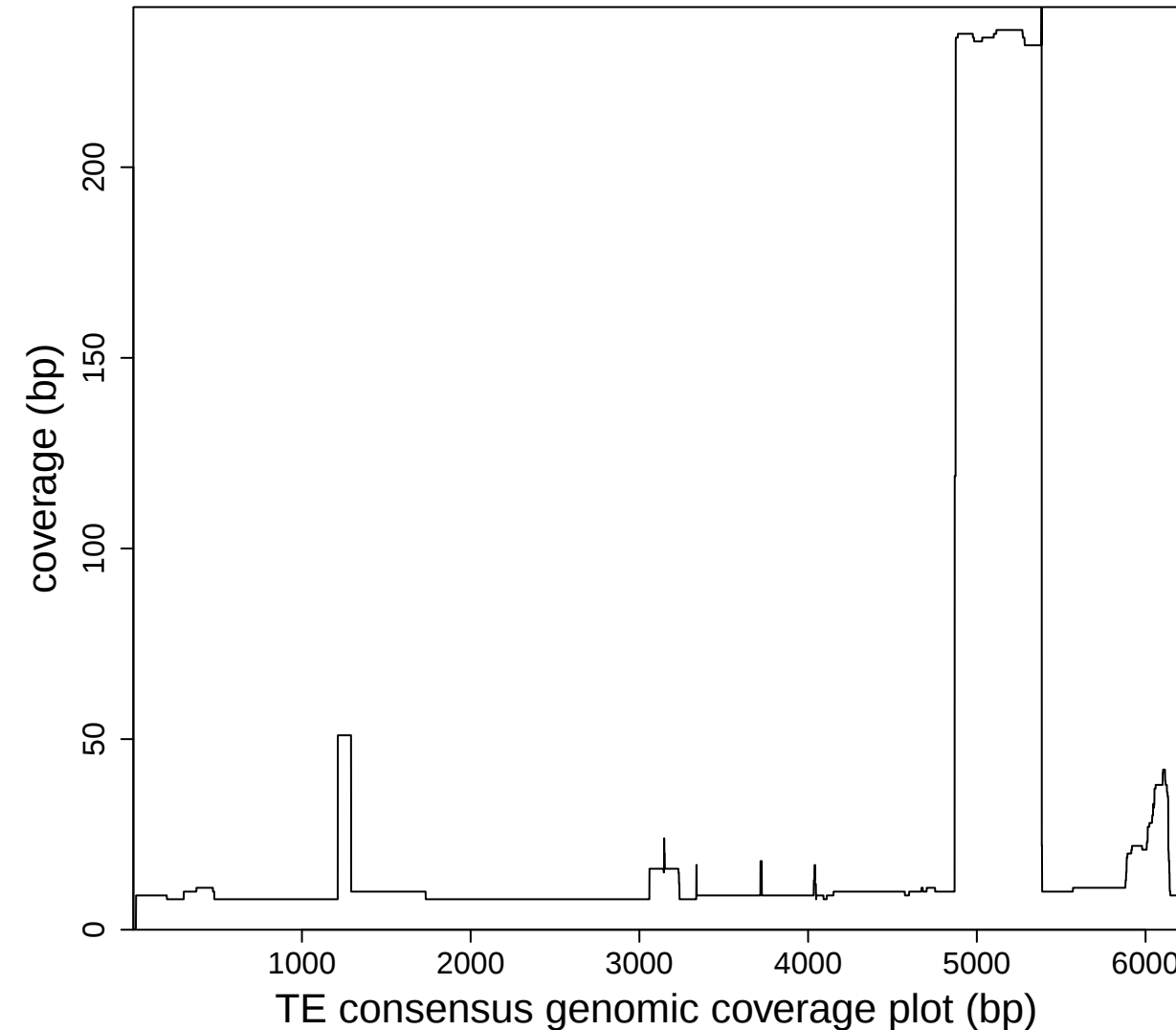
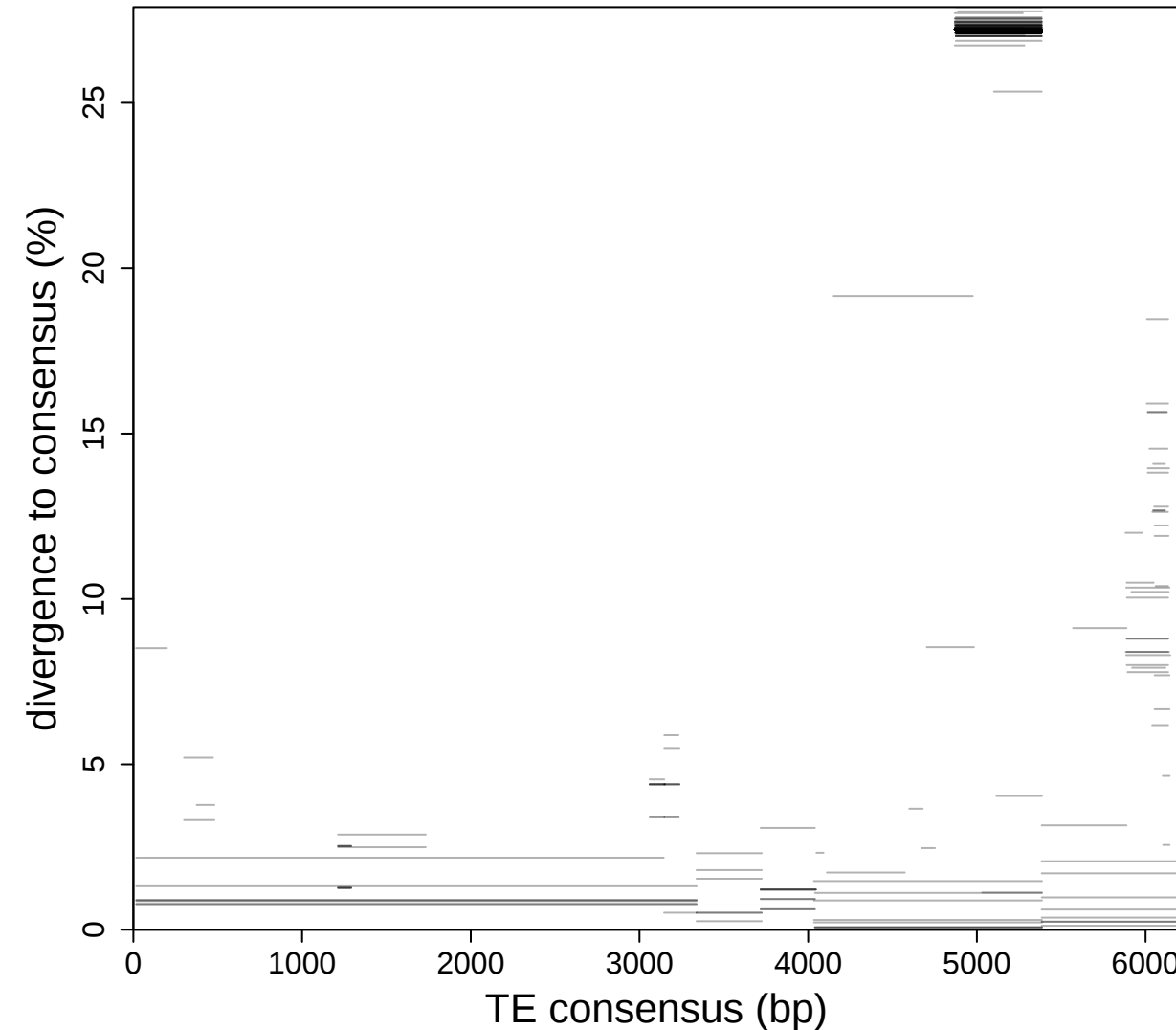
d_g_2.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa
size: 17762bp; fragments: 2148; full length: 3 (>=15985.8bp)

After TEtrimmer Extended plot Blue lines are boundaries



TE: ltr_1_family_748
size: 6201bp; fragments: 378; full length: 0 (>=5580.9bp)

Before TEtrimmer 6201 bp



This genomic map displays the distribution of Open Reading Frames (ORFs) and PFAM domains across a 16,000 bp contig. The x-axis represents the genomic position in base pairs, ranging from 0 to 16,000. The y-axis indicates the relative frequency or density of features, with a prominent peak around 7,000 bp.

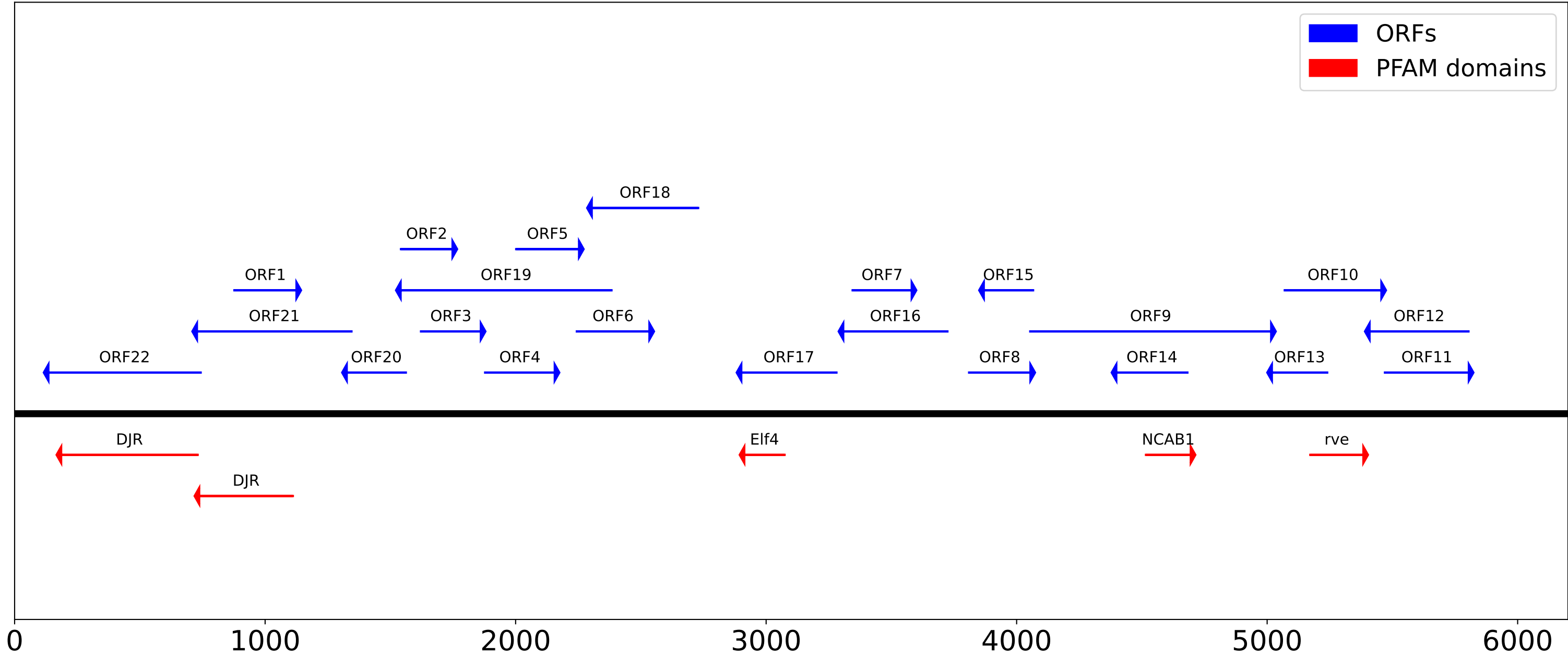
Legend:

- ORFs (Open Reading Frames):** Represented by blue arrows indicating the direction of translation.
- PFAM domains:** Represented by red arrows indicating the direction of the domain.

Key Features and Annotations:

- ORFs:** Numerous ORFs are identified and labeled, including ORF1 through ORF44. ORF14 is notably long, spanning from approximately 9,000 to 10,500 bp. Other significant ORFs include ORF29 (approx. 12,000 to 15,000 bp) and ORF35 (approx. 7,000 to 7,500 bp).
- PFAM Domains:** Several domains are identified and labeled, including Phage_T4_tail (approx. 2,500 to 3,500 bp), Phage_T4_tail_2 (approx. 3,500 to 4,500 bp), Phage_T4_tail_3 (approx. 4,500 to 5,500 bp), Phage_T4_tail_4 (approx. 5,500 to 6,500 bp), Phage_T4_tail_5 (approx. 6,500 to 7,500 bp), Phage_T4_tail_6 (approx. 7,500 to 8,500 bp), Phage_T4_tail_7 (approx. 8,500 to 9,500 bp), Phage_T4_tail_8 (approx. 9,500 to 10,500 bp), Phage_T4_tail_9 (approx. 10,500 to 11,500 bp), Phage_T4_tail_10 (approx. 11,500 to 12,500 bp), Phage_T4_tail_11 (approx. 12,500 to 13,500 bp), Phage_T4_tail_12 (approx. 13,500 to 14,500 bp), Phage_T4_tail_13 (approx. 14,500 to 15,500 bp), Phage_T4_tail_14 (approx. 15,500 to 16,000 bp), and Phage_T4_tail_15 (approx. 16,000 to 16,500 bp).
- Other Annotations:** The map also includes labels for 'egyptin_C' (approx. 1,000 bp), 'Phage_T4_tail_1' (approx. 1,500 bp), 'Phage_T4_tail_2' (approx. 2,000 bp), 'Phage_T4_tail_3' (approx. 2,500 bp), 'Phage_T4_tail_4' (approx. 3,000 bp), 'Phage_T4_tail_5' (approx. 3,500 bp), 'Phage_T4_tail_6' (approx. 4,000 bp), 'Phage_T4_tail_7' (approx. 4,500 bp), 'Phage_T4_tail_8' (approx. 5,000 bp), 'Phage_T4_tail_9' (approx. 5,500 bp), 'Phage_T4_tail_10' (approx. 6,000 bp), 'Phage_T4_tail_11' (approx. 6,500 bp), 'Phage_T4_tail_12' (approx. 7,000 bp), 'Phage_T4_tail_13' (approx. 7,500 bp), 'Phage_T4_tail_14' (approx. 8,000 bp), 'Phage_T4_tail_15' (approx. 8,500 bp), 'Phage_T4_tail_16' (approx. 9,000 bp), 'Phage_T4_tail_17' (approx. 9,500 bp), 'Phage_T4_tail_18' (approx. 10,000 bp), 'Phage_T4_tail_19' (approx. 10,500 bp), 'Phage_T4_tail_20' (approx. 11,000 bp), 'Phage_T4_tail_21' (approx. 11,500 bp), 'Phage_T4_tail_22' (approx. 12,000 bp), 'Phage_T4_tail_23' (approx. 12,500 bp), 'Phage_T4_tail_24' (approx. 13,000 bp), 'Phage_T4_tail_25' (approx. 13,500 bp), 'Phage_T4_tail_26' (approx. 14,000 bp), 'Phage_T4_tail_27' (approx. 14,500 bp), 'Phage_T4_tail_28' (approx. 15,000 bp), 'Phage_T4_tail_29' (approx. 15,500 bp), and 'Phage_T4_tail_30' (approx. 16,000 bp).

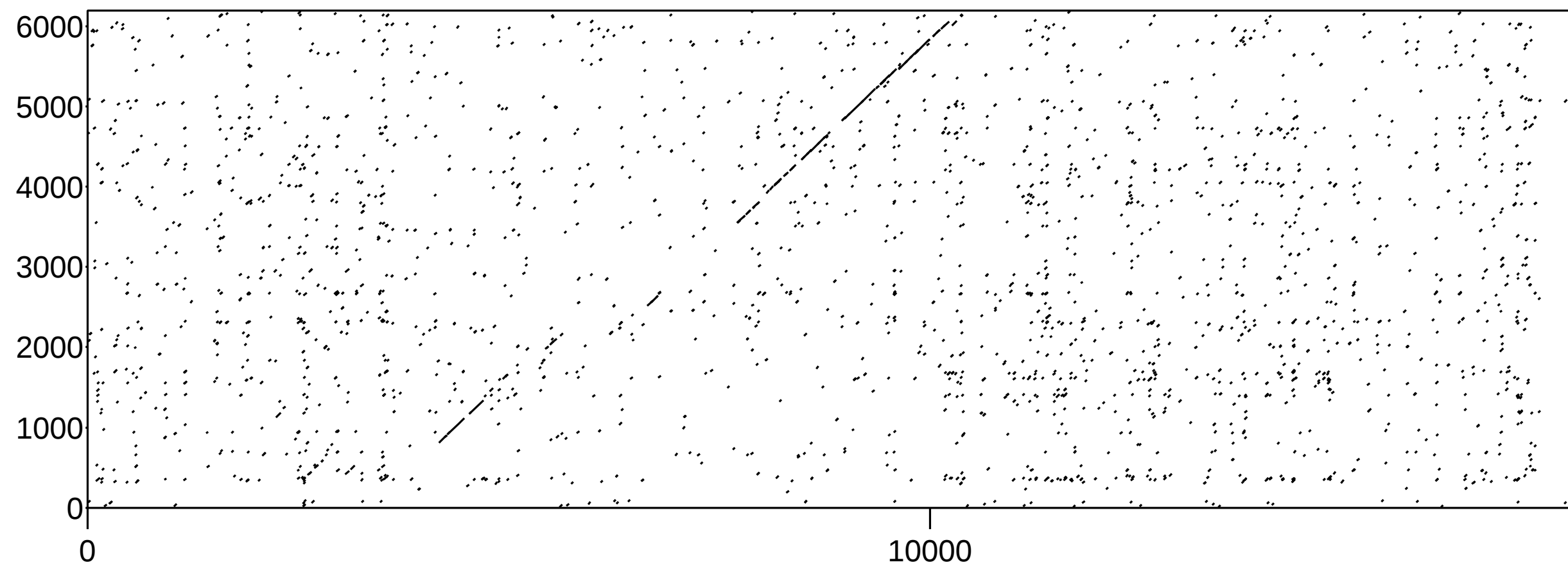
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

E consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)