

Start crop Point

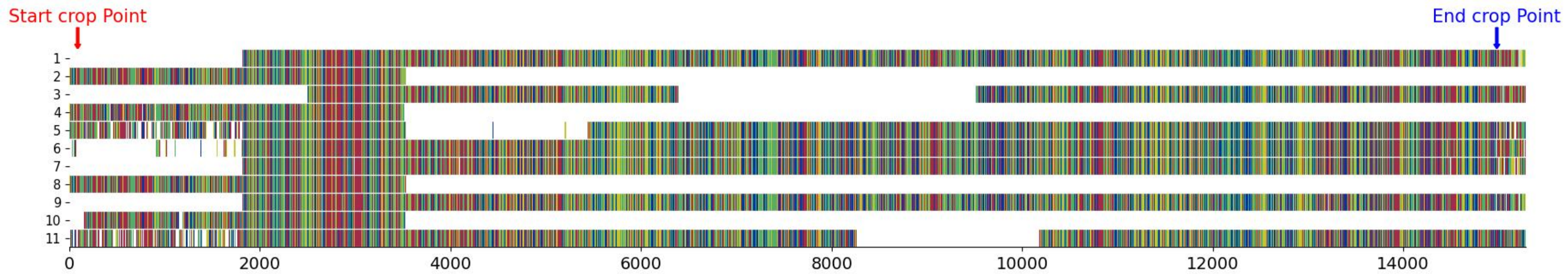


End crop Point



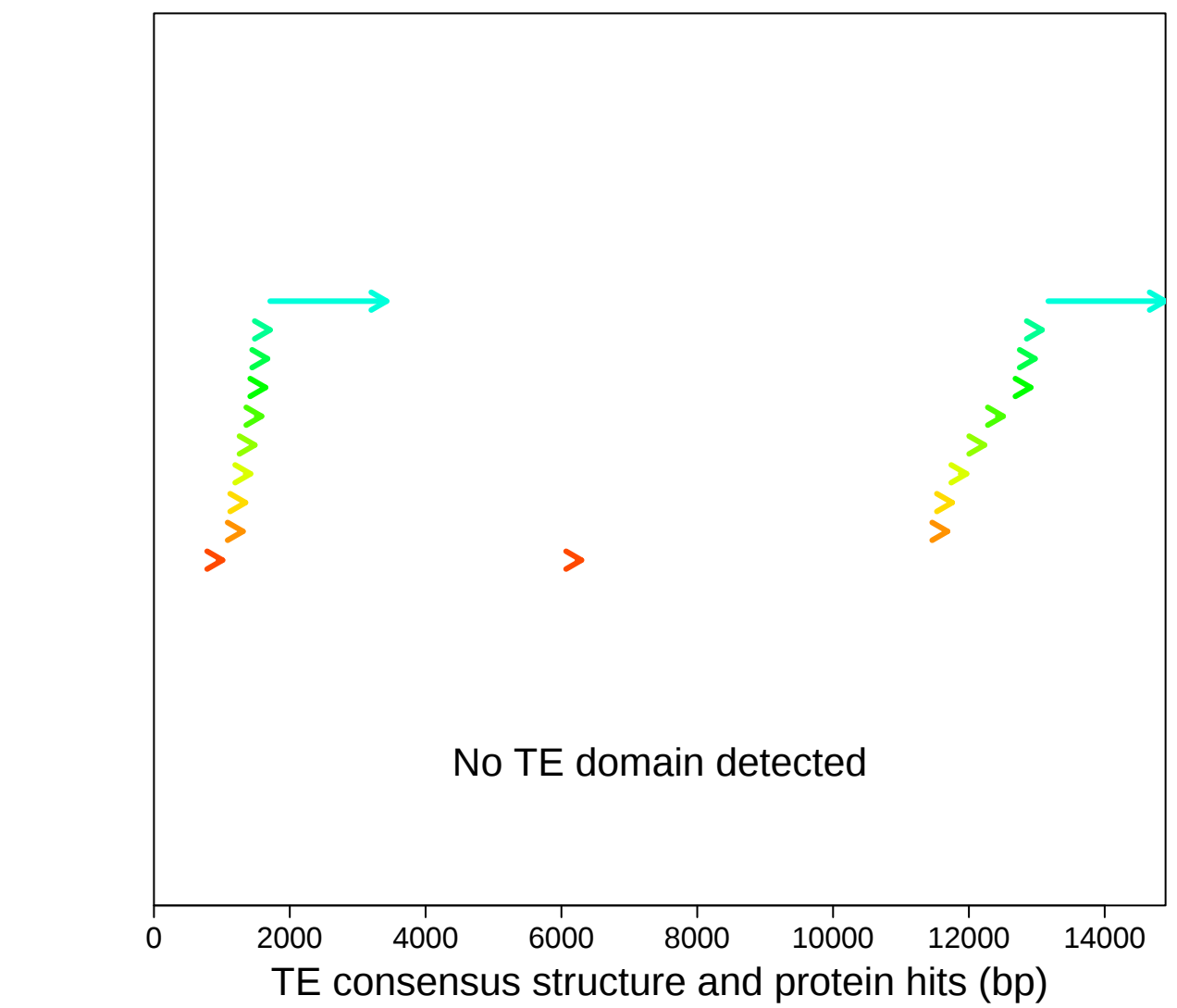
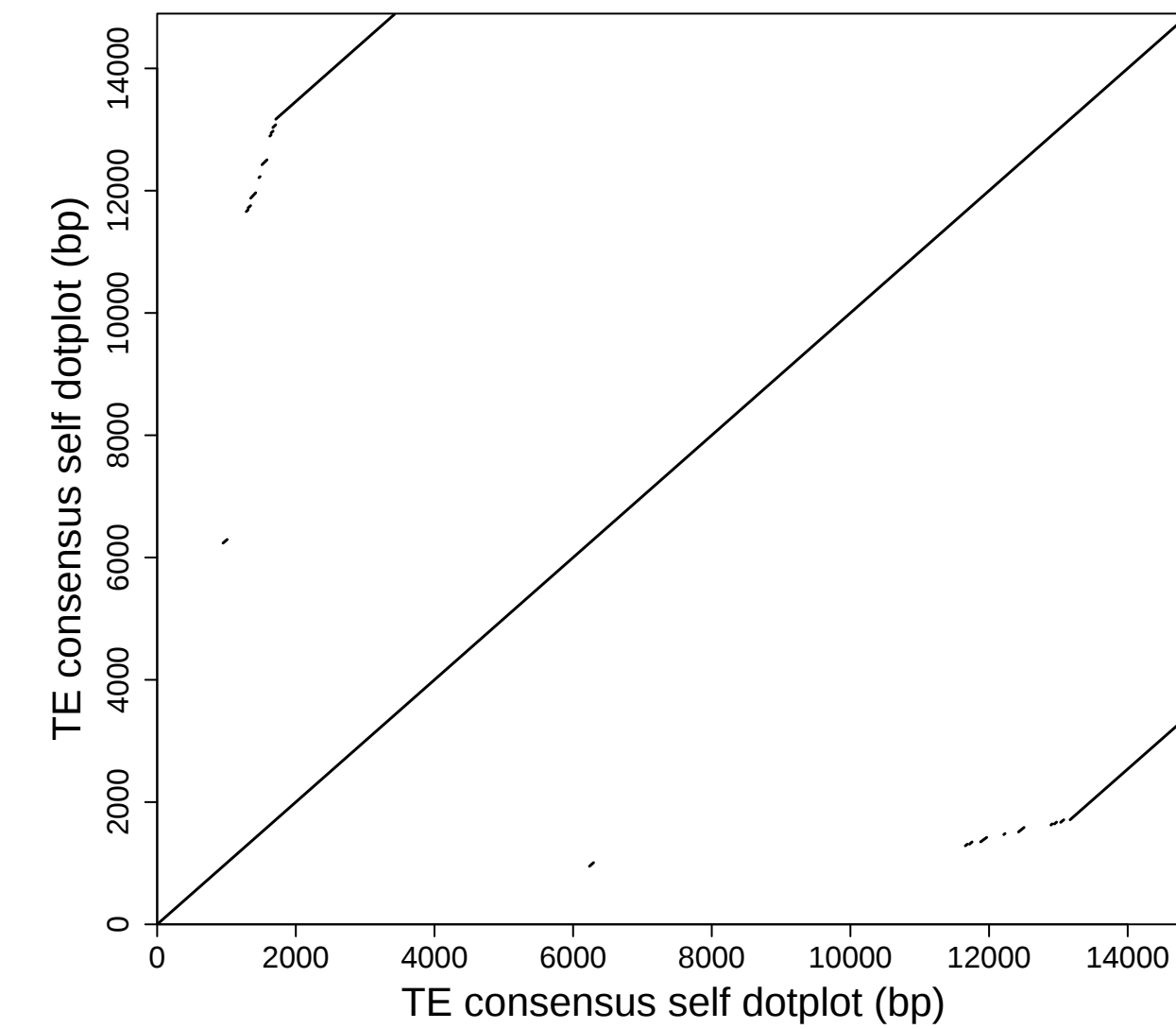
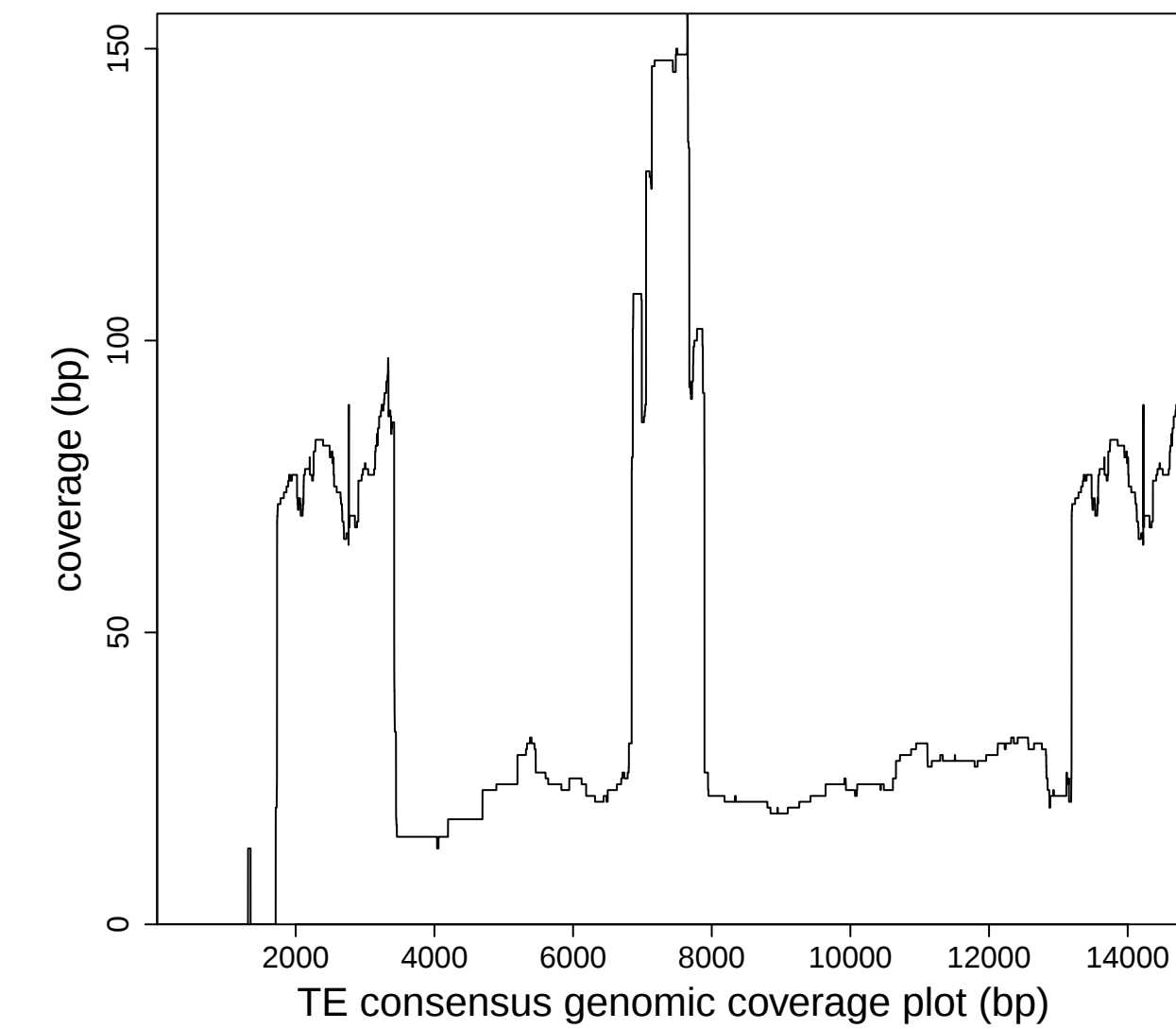
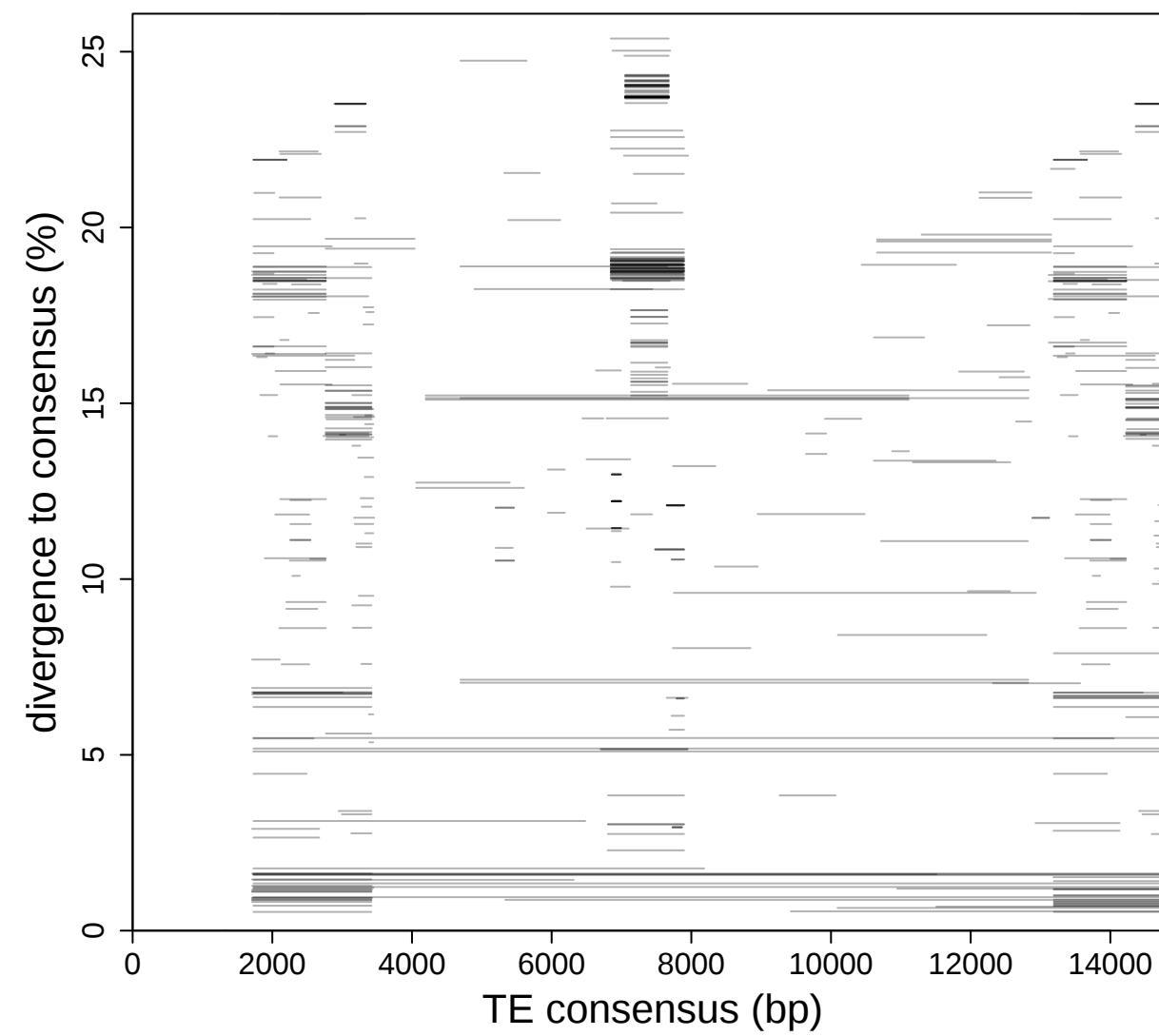
MSA length = 14896





g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa_3
size: 14896bp; fragments: 555; full length: 0 (>=13406.4bp)

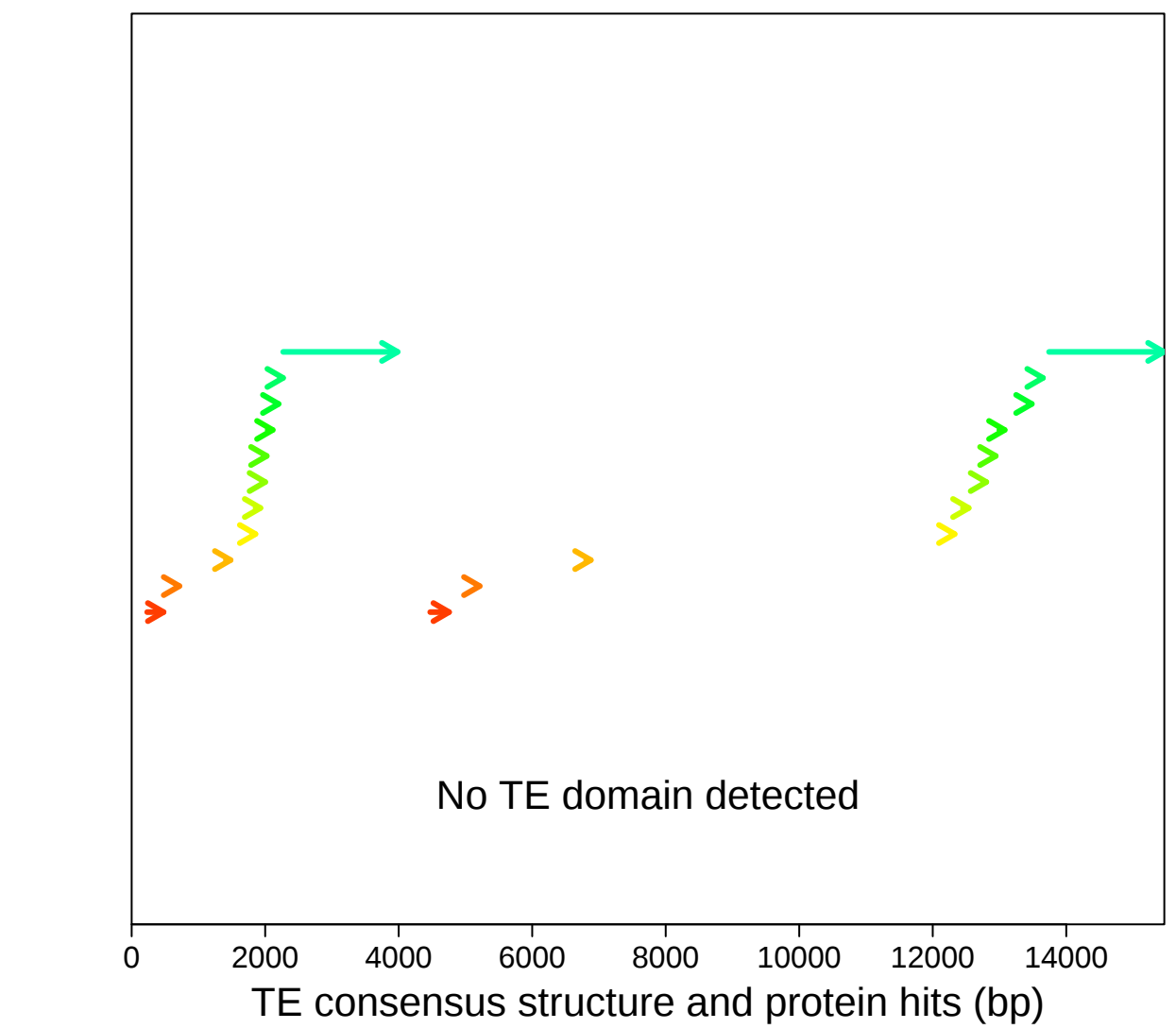
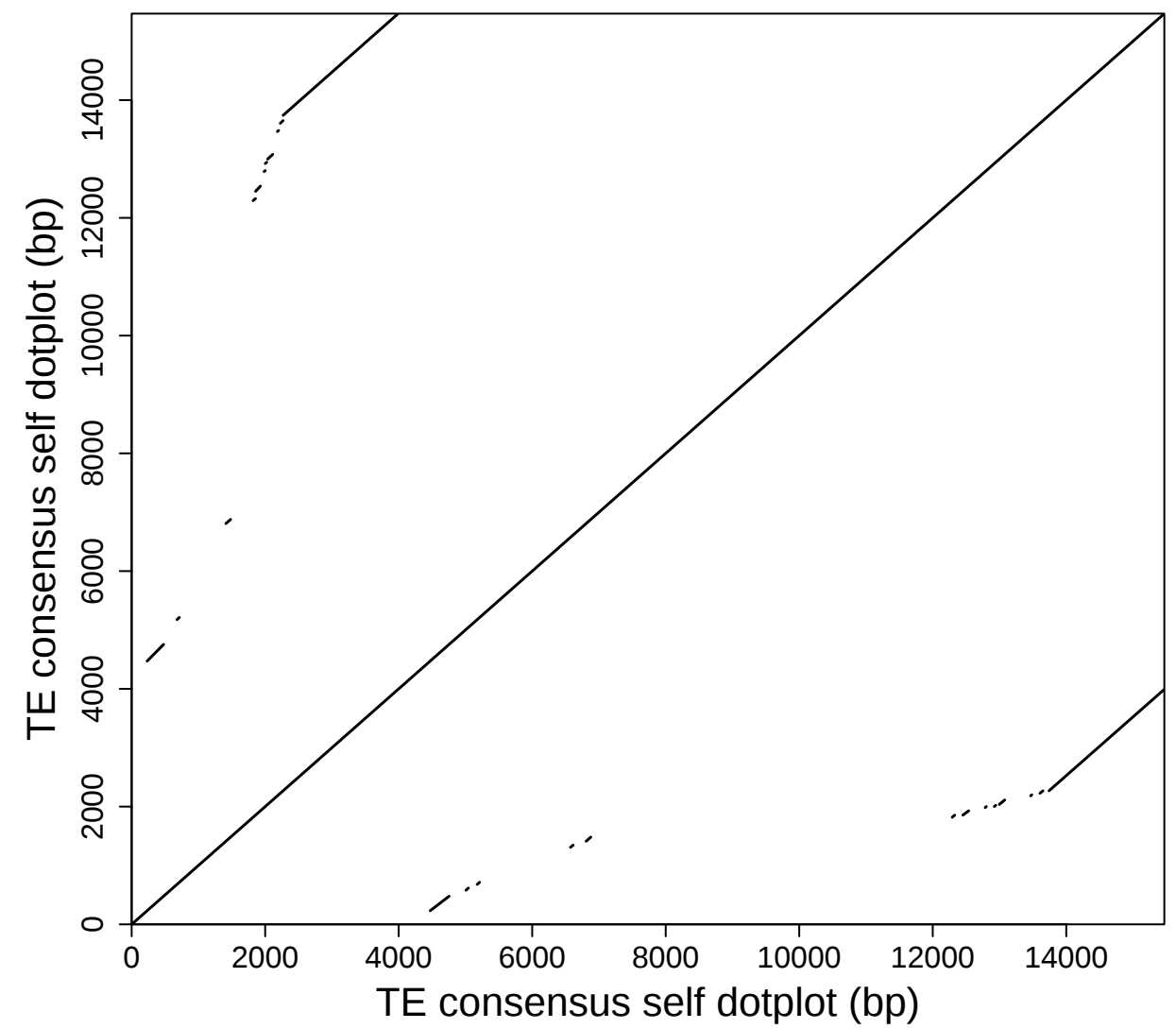
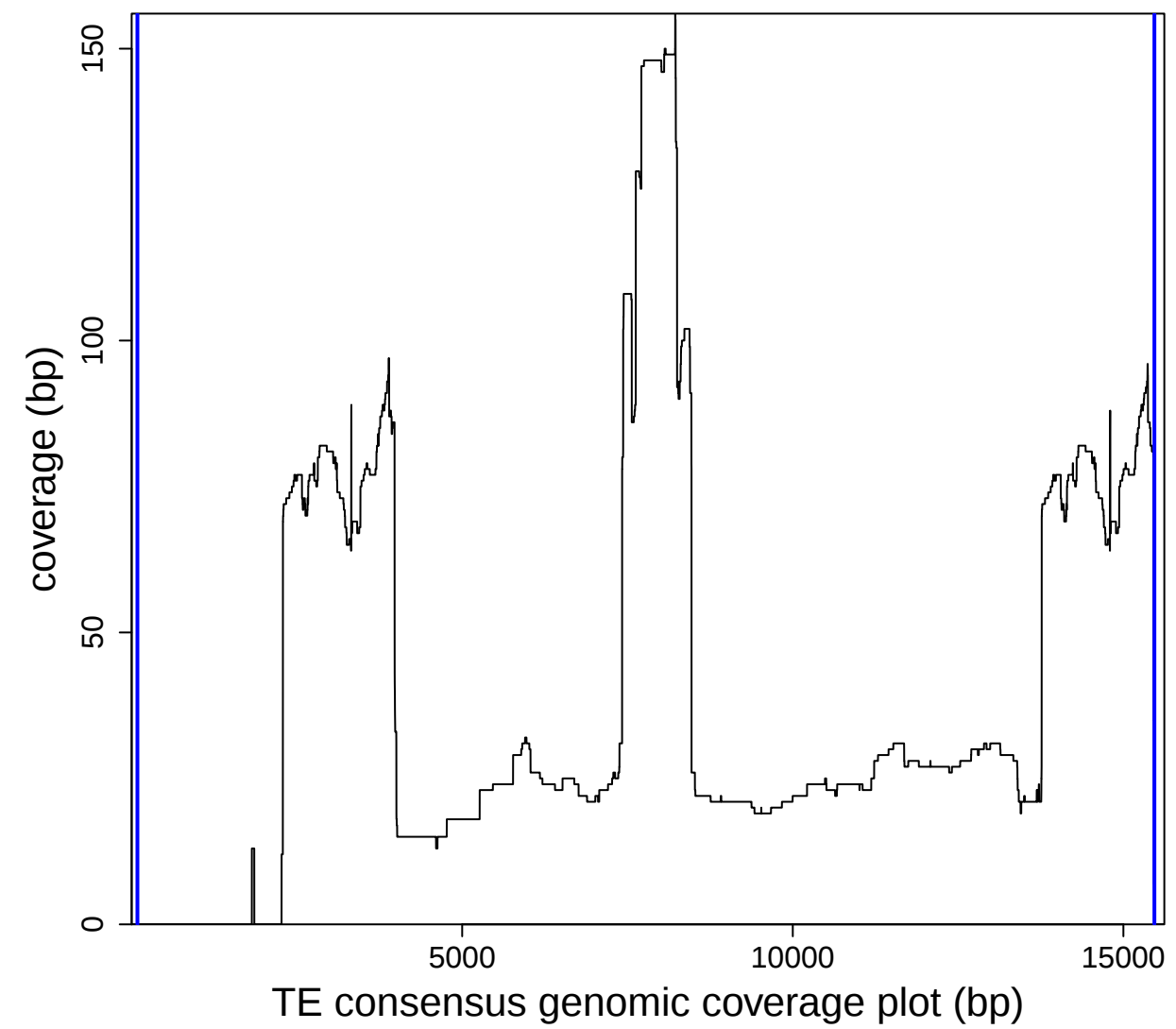
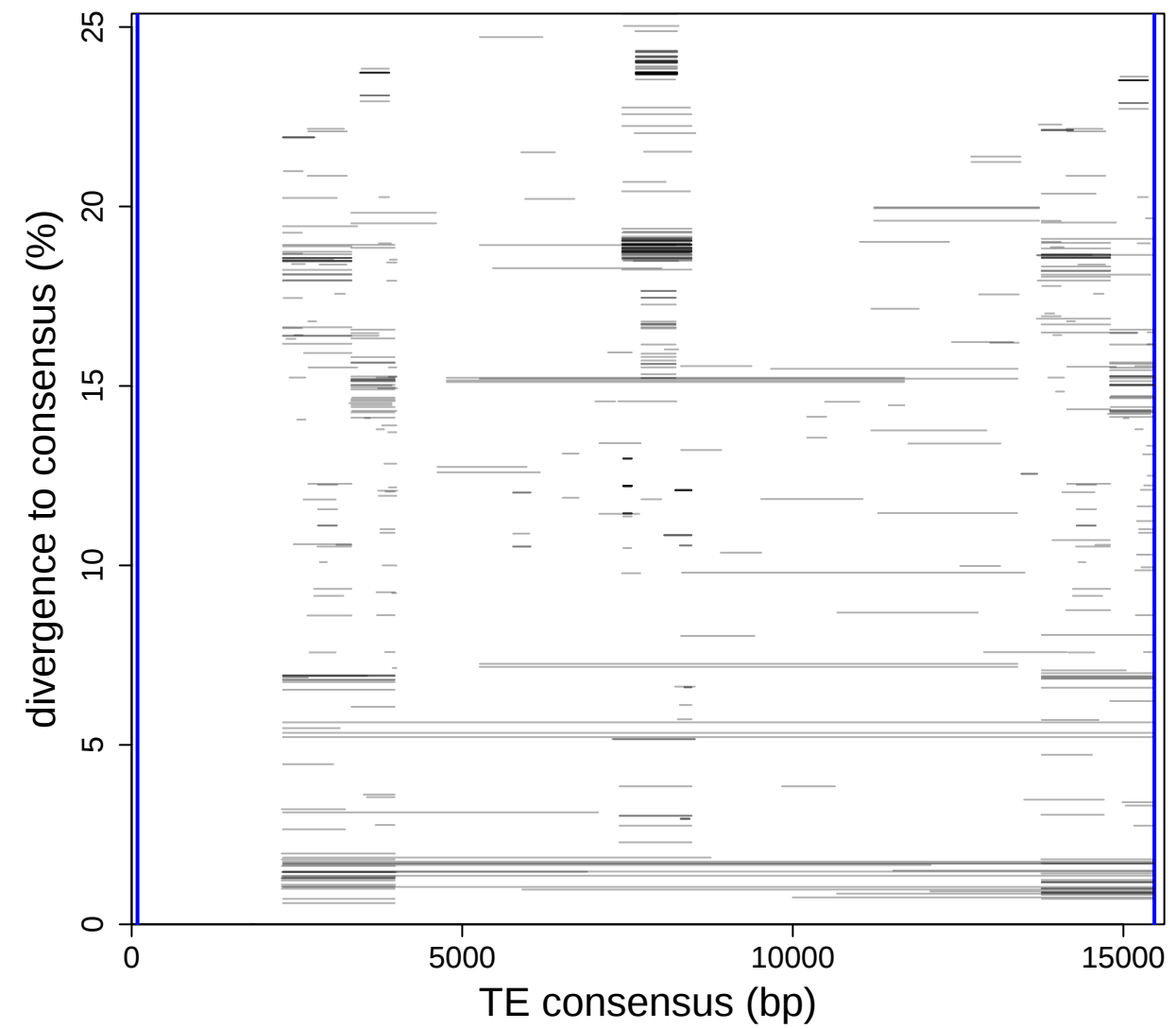
After TEtrimmer 14896 bp



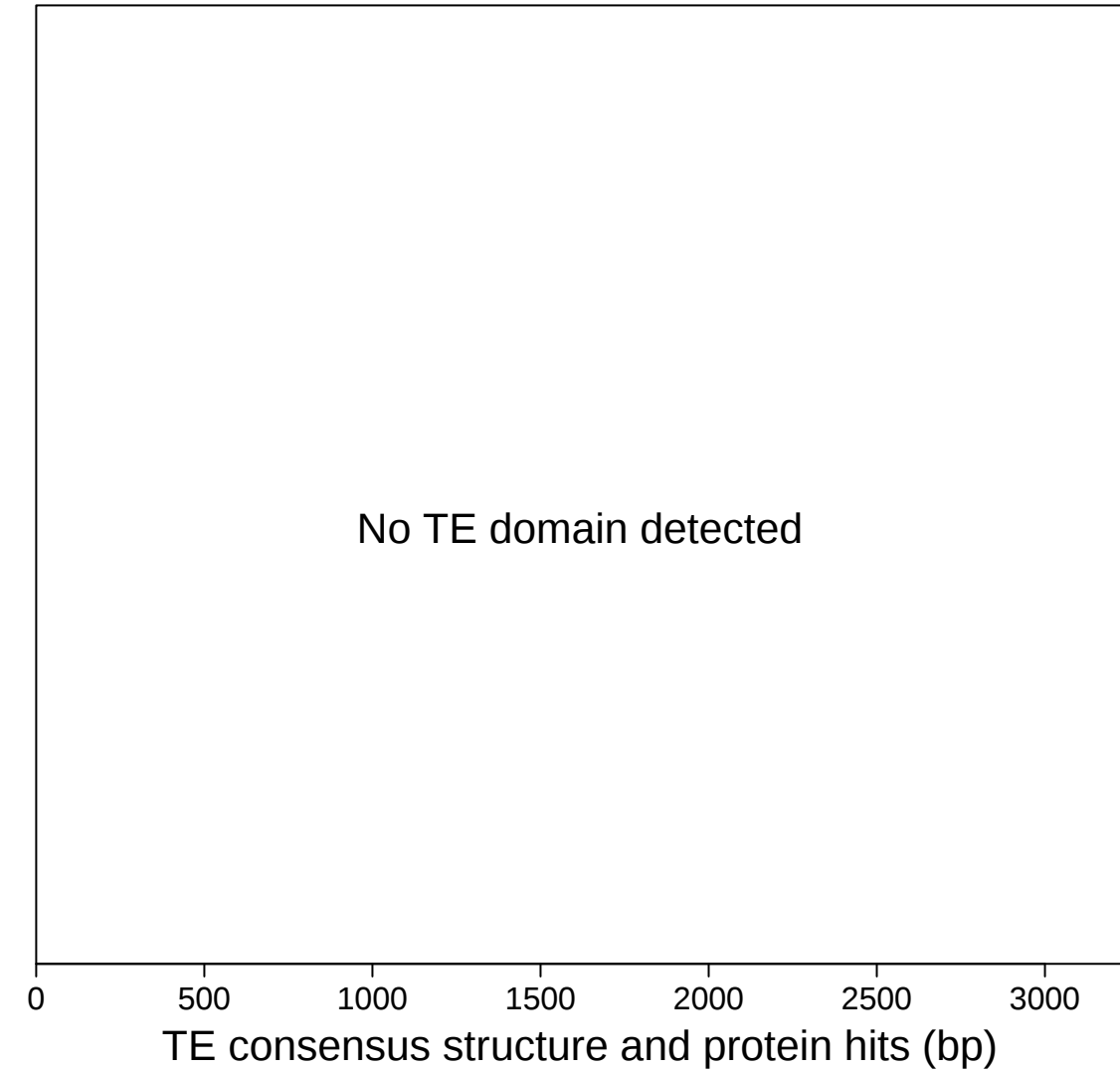
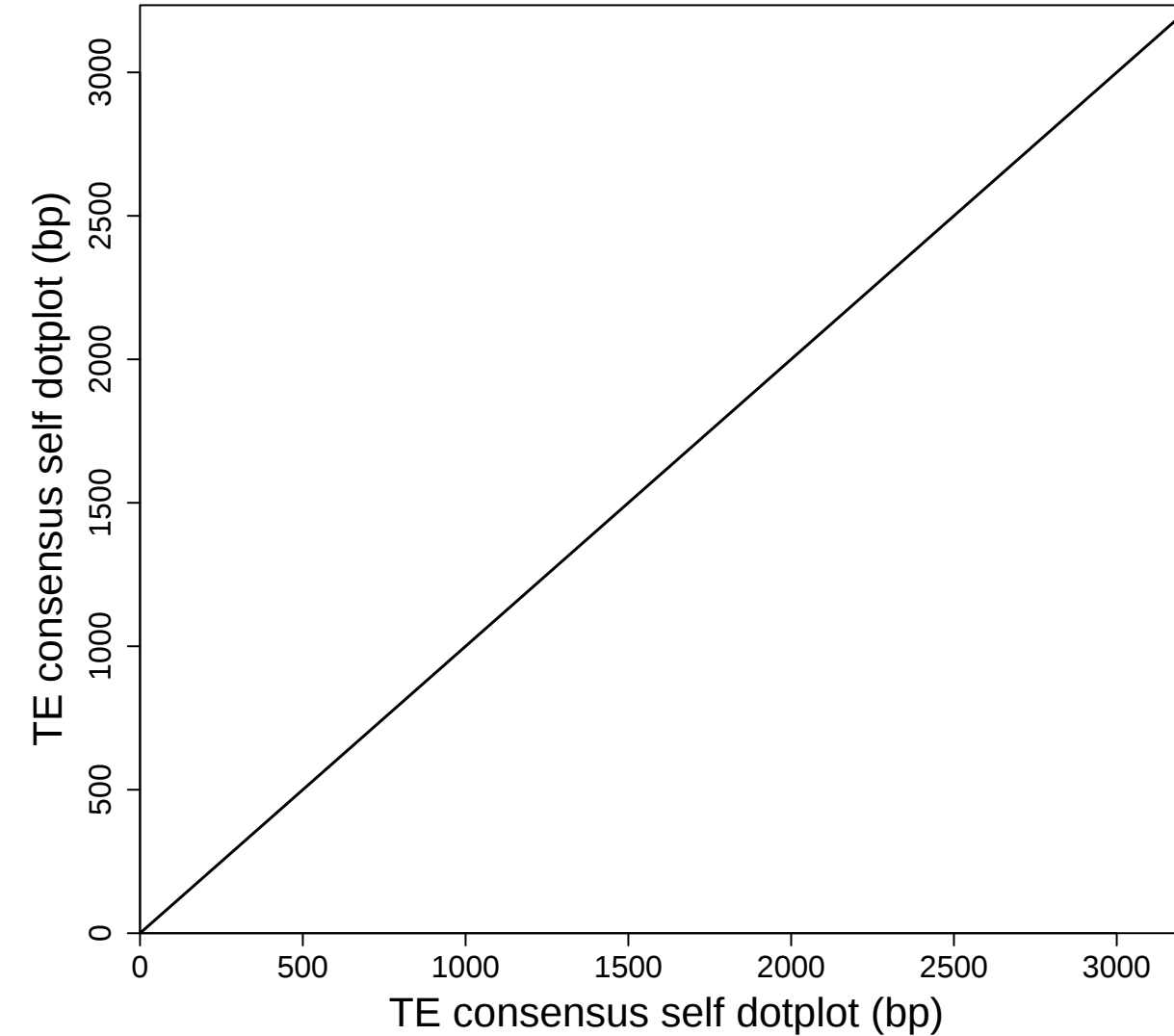
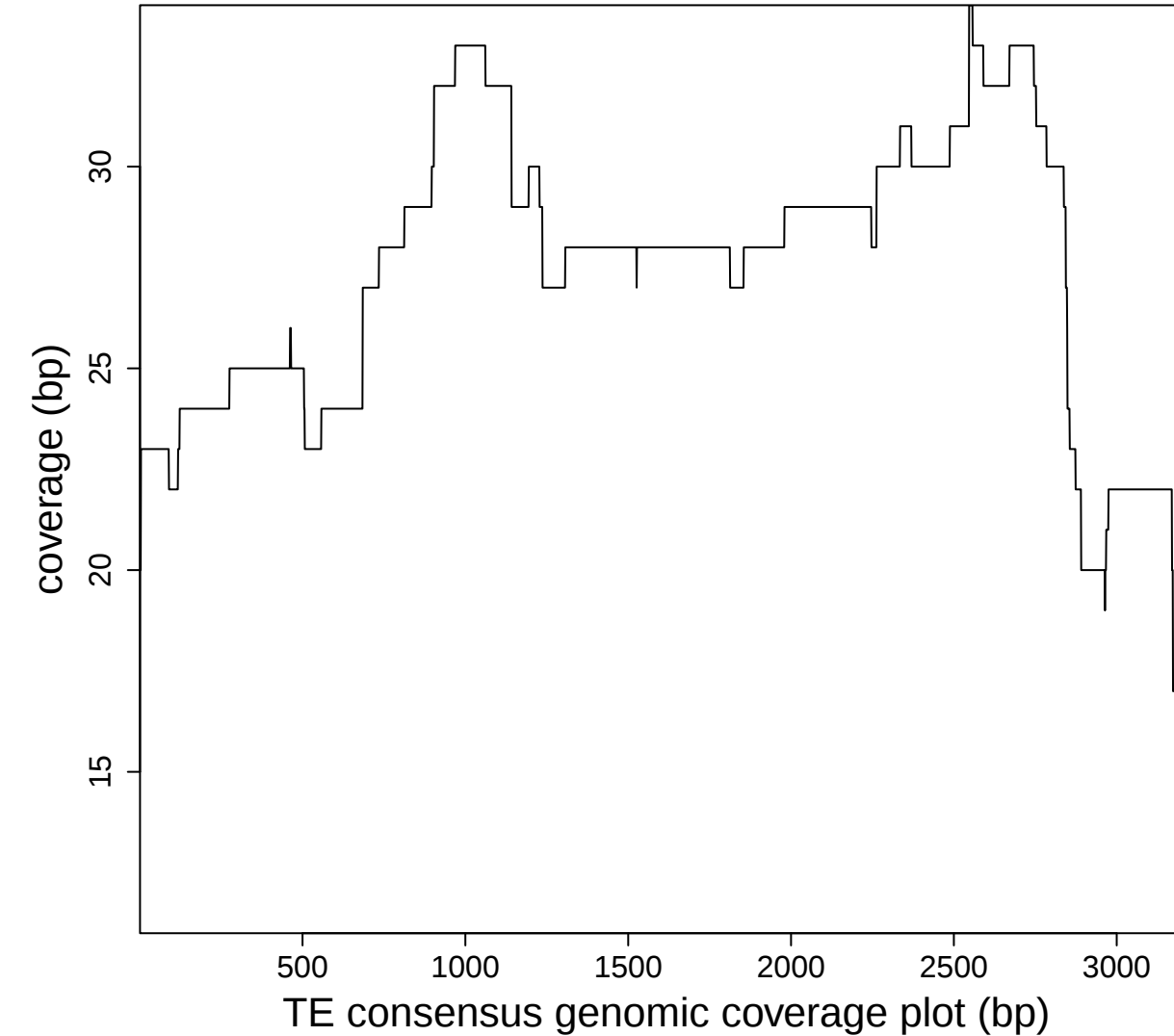
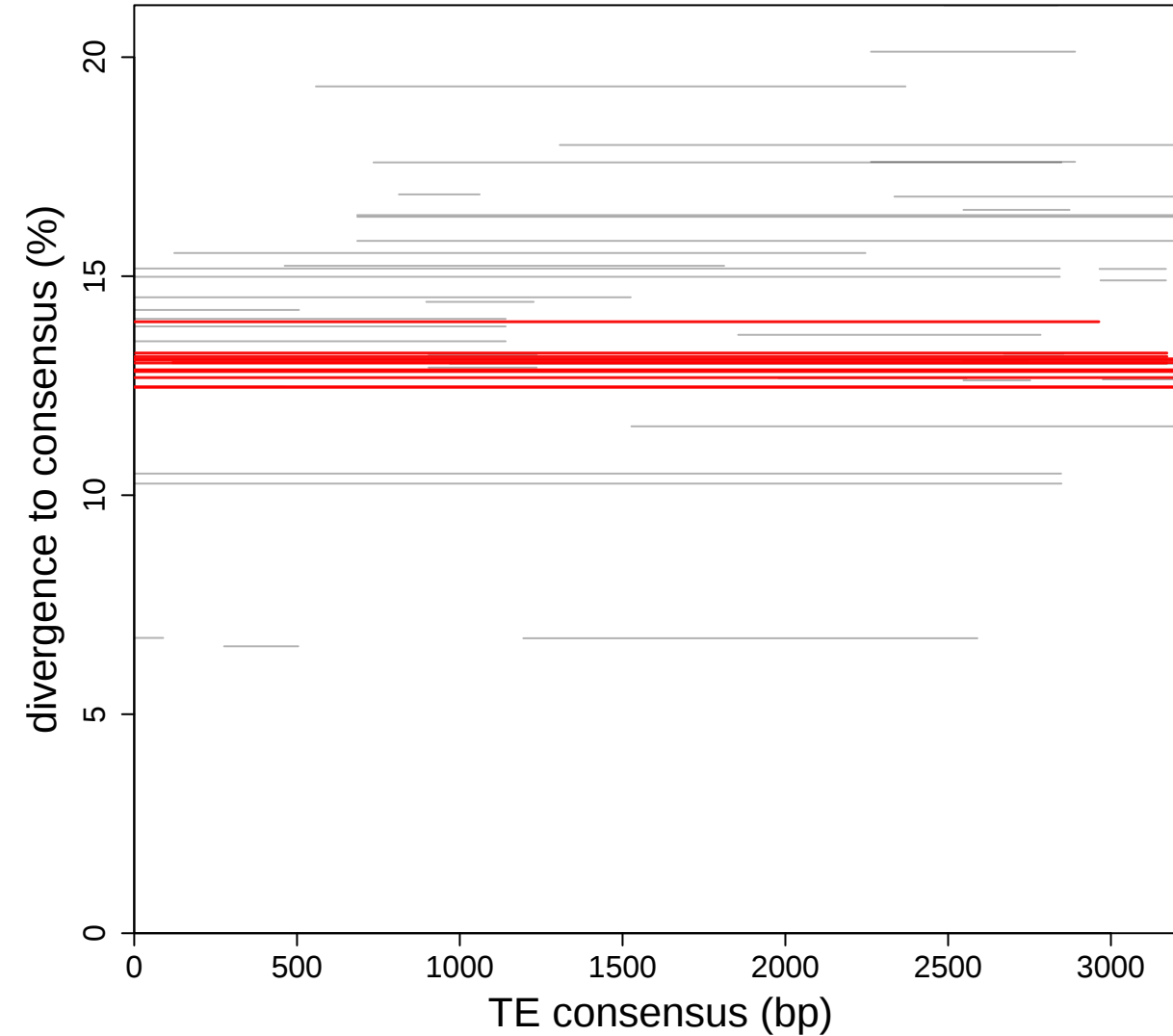
f.bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bc
size: 15619bp; fragments: 554; full length: 0 (>=14057.1bp)

After TEtrimmer Extended plot

Blue lines are boundaries



TE: rnd_5_family_1331
size: 3234bp; fragments: 53; full length: 13 (≥ 2910.6 bp)



The genomic map displays the distribution of Open Reading Frames (ORFs) and PFAM domains across a 12,800 bp contig. The x-axis represents the genomic position in base pairs, ranging from 0 to 14,000. The y-axis represents the ORF/Domain ID, with ORFs numbered 1 to 33 and PFAM domains labeled with their names.

Legend:

- ORFs:** Represented by blue arrows indicating the direction of the open reading frame.
- PFAM domains:** Represented by red arrows indicating the direction of the domain.

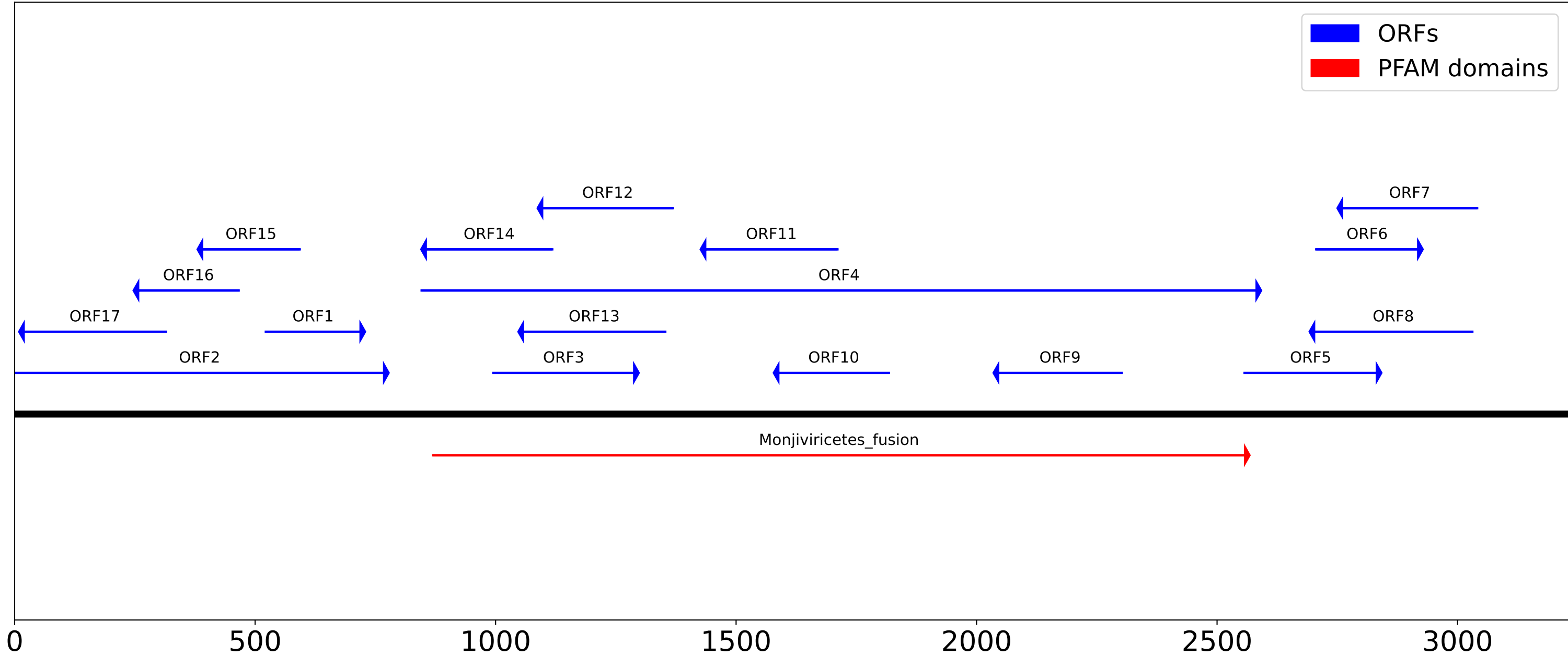
ORFs (Open Reading Frames):

- ORF1, ORF2, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11, ORF12, ORF13, ORF14, ORF15, ORF16, ORF17, ORF18, ORF19, ORF20, ORF21, ORF22, ORF23, ORF24, ORF25, ORF26, ORF27, ORF28, ORF29, ORF30, ORF31, ORF32, ORF33

PFAM domains:

- PNMA
- RVT_RT_NaseH
- RT_NaseH
- Integrase_H2C2
- Monjiviricetes_fusion
- RT_NaseH
- rve

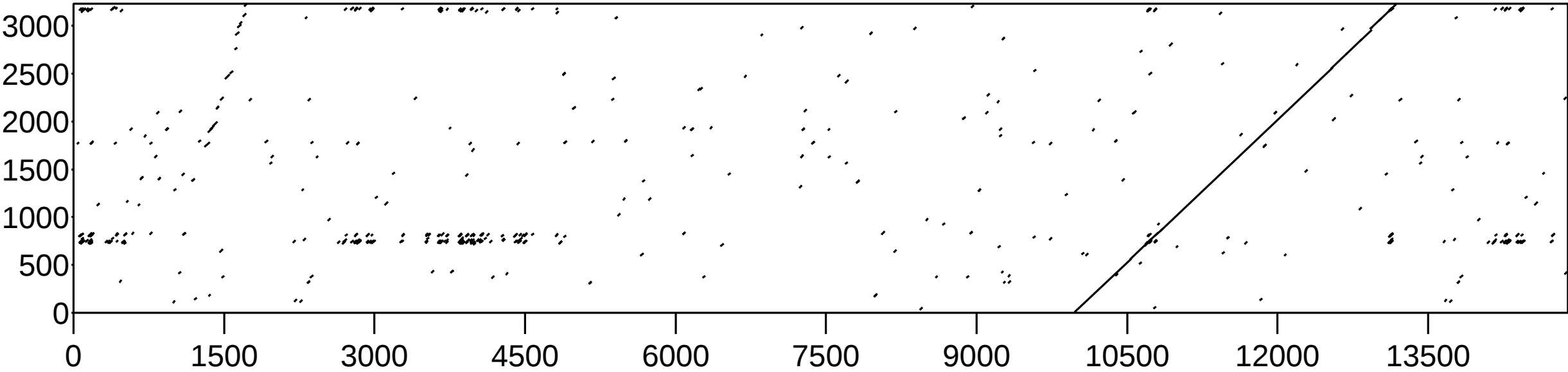
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

onsensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)