

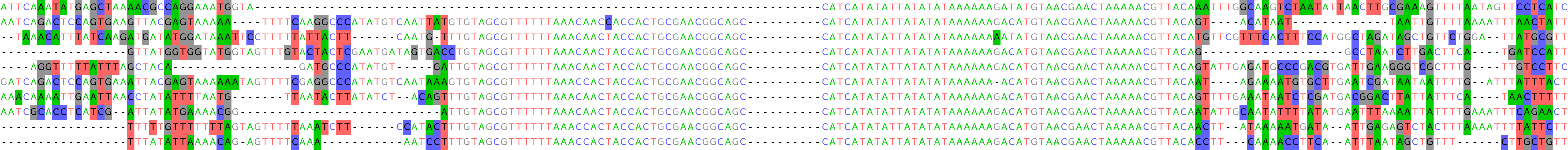
Start Crop Point



End Crop Point



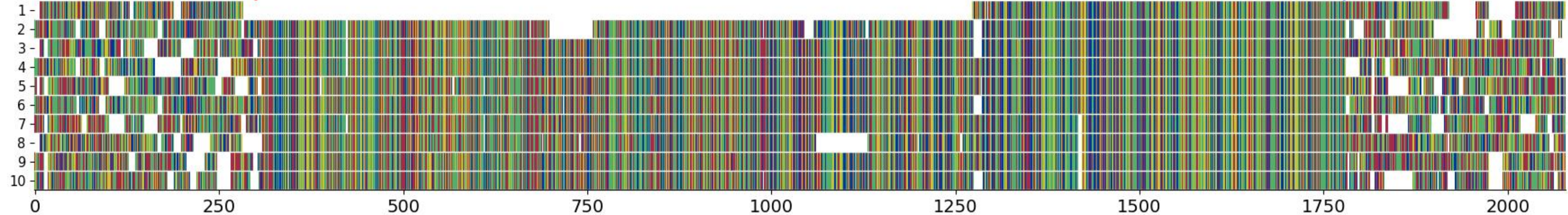
MSA length = 1479



Start crop Point

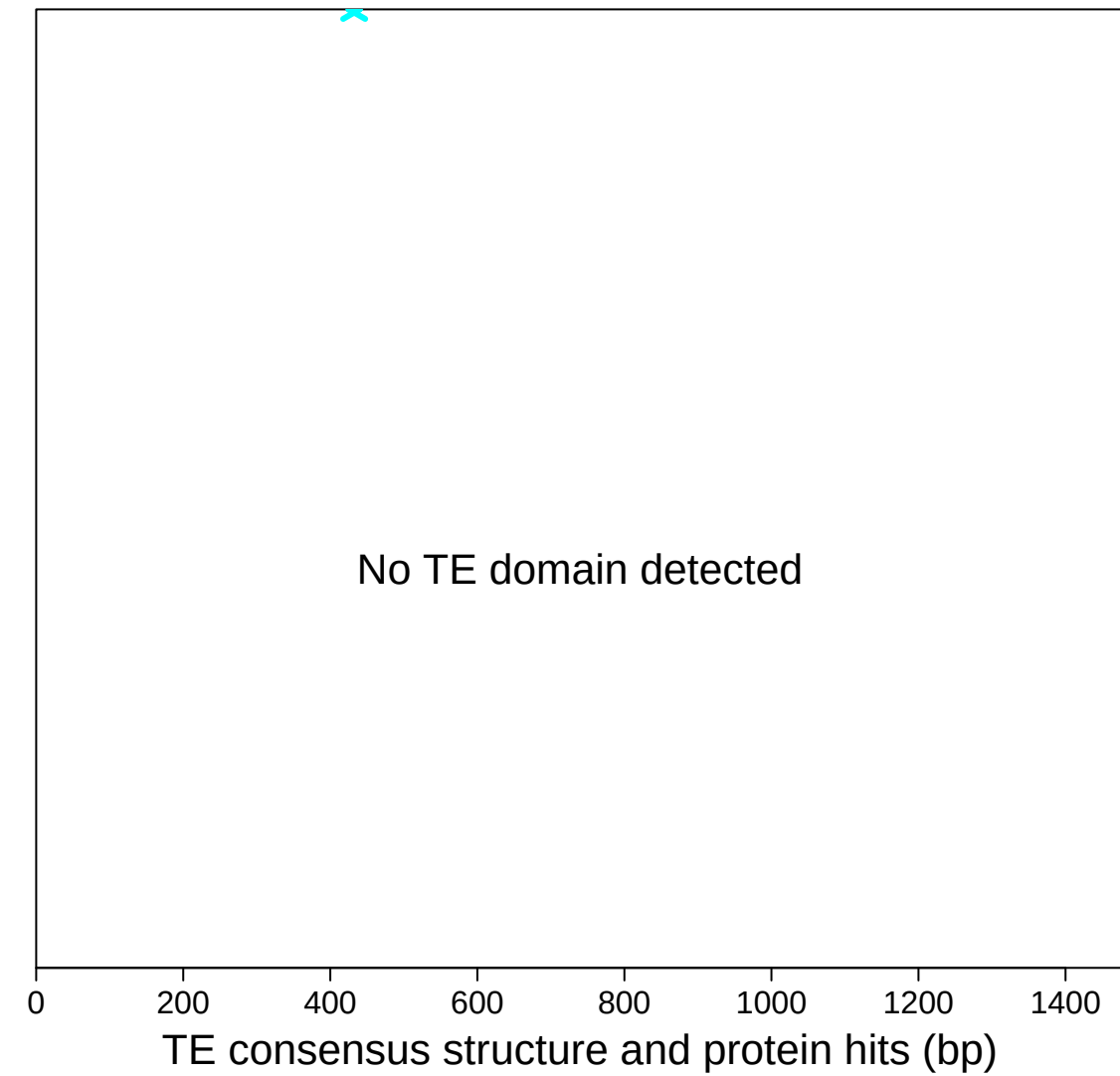
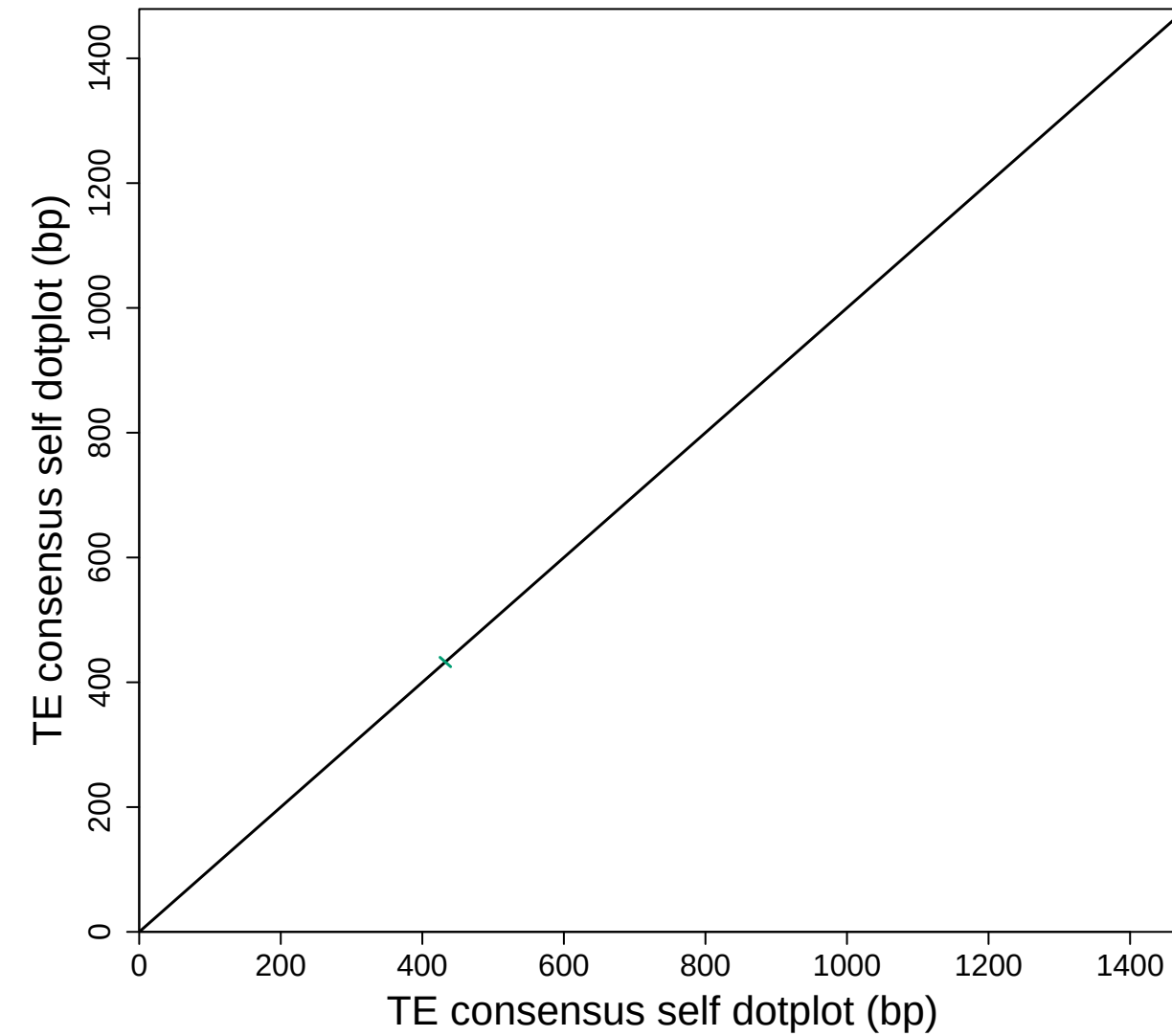
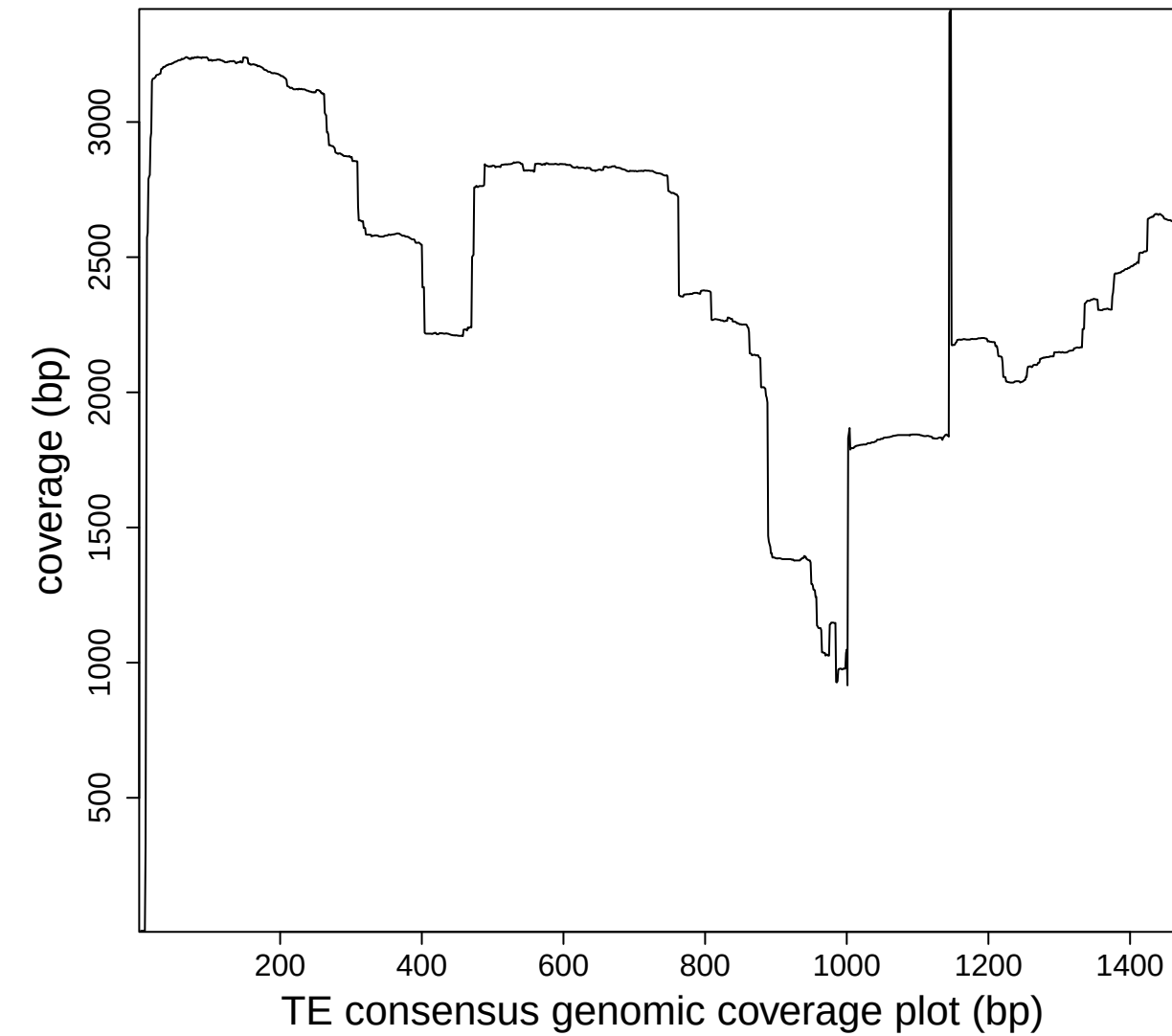
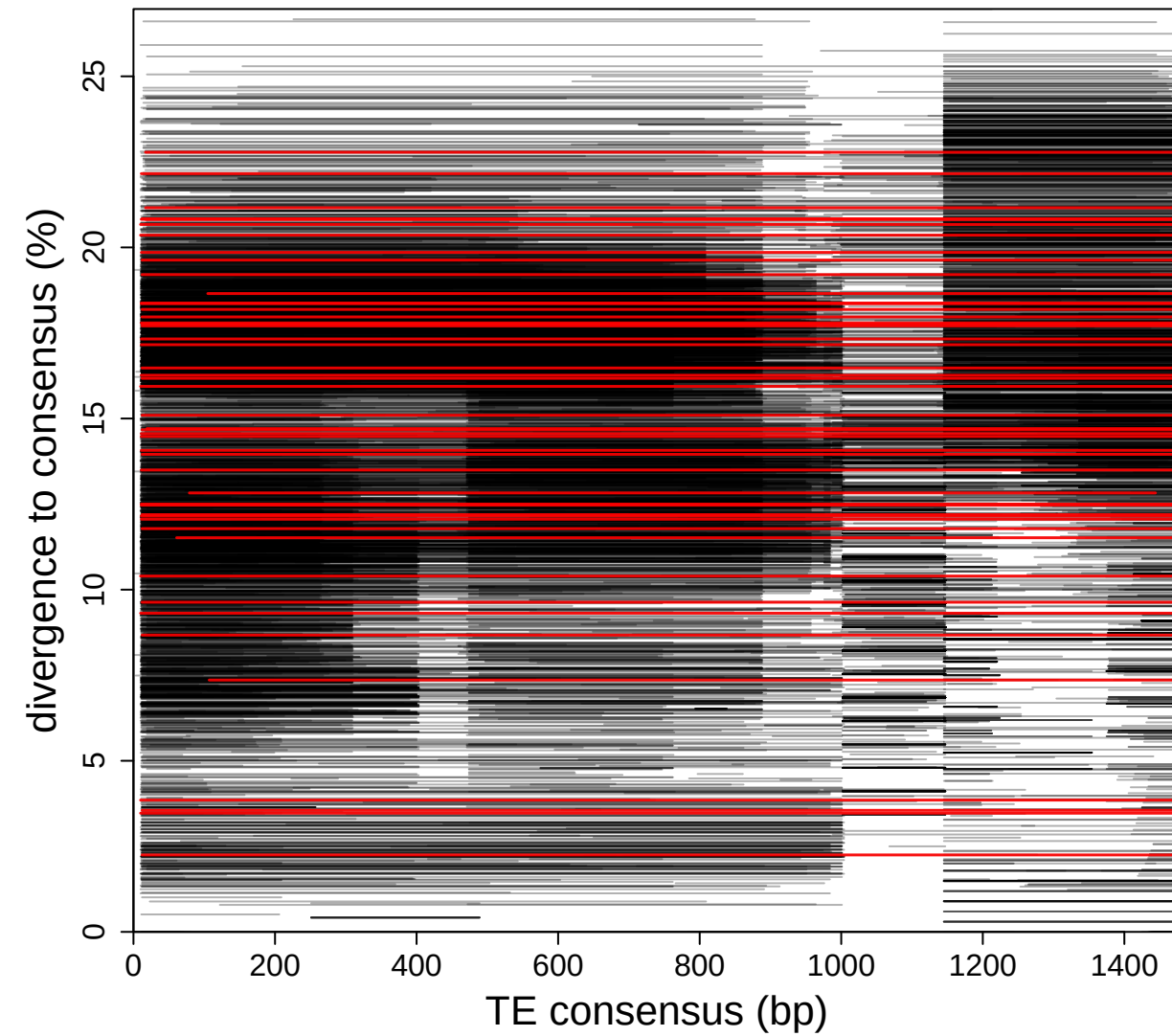


End crop Point



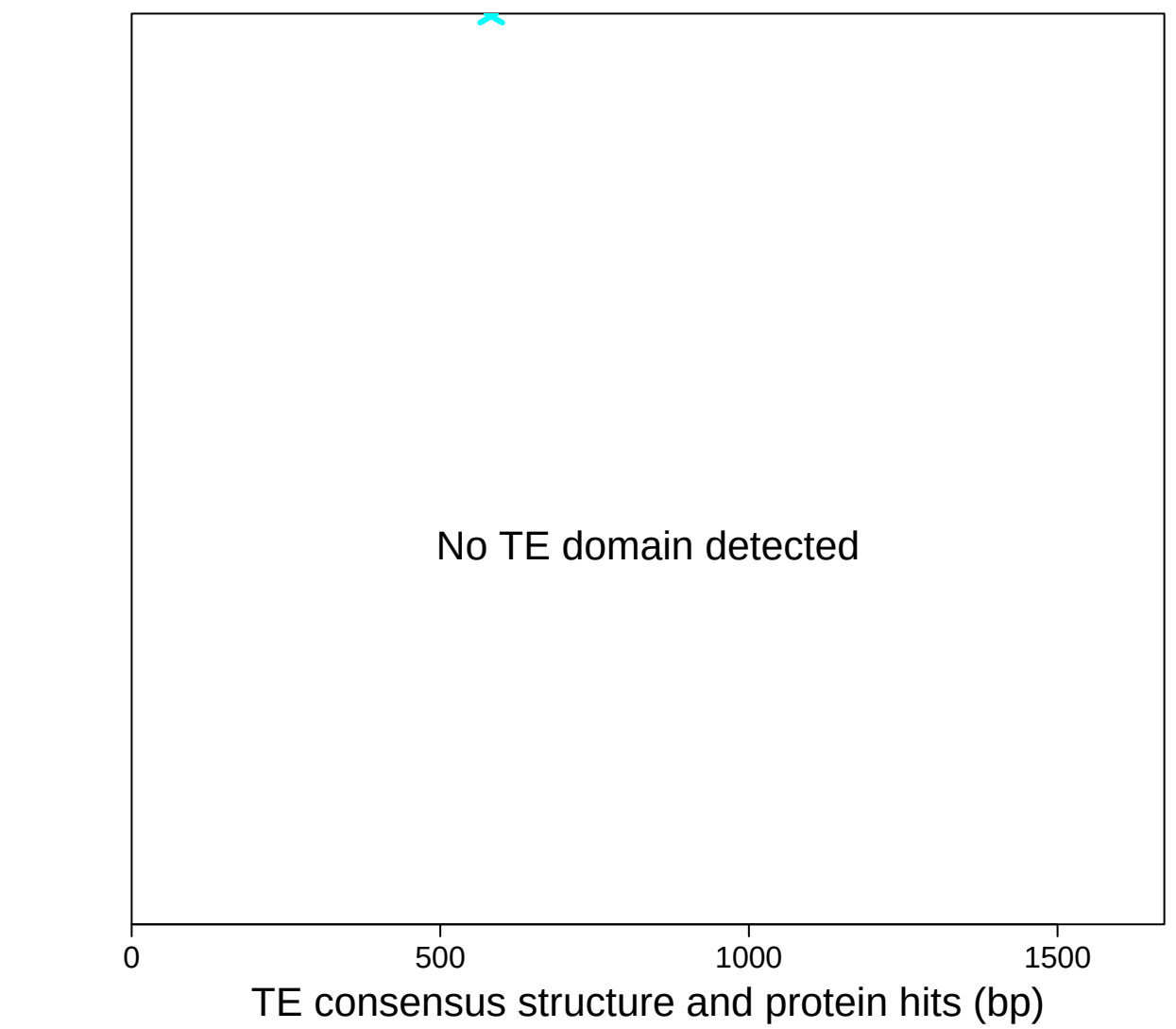
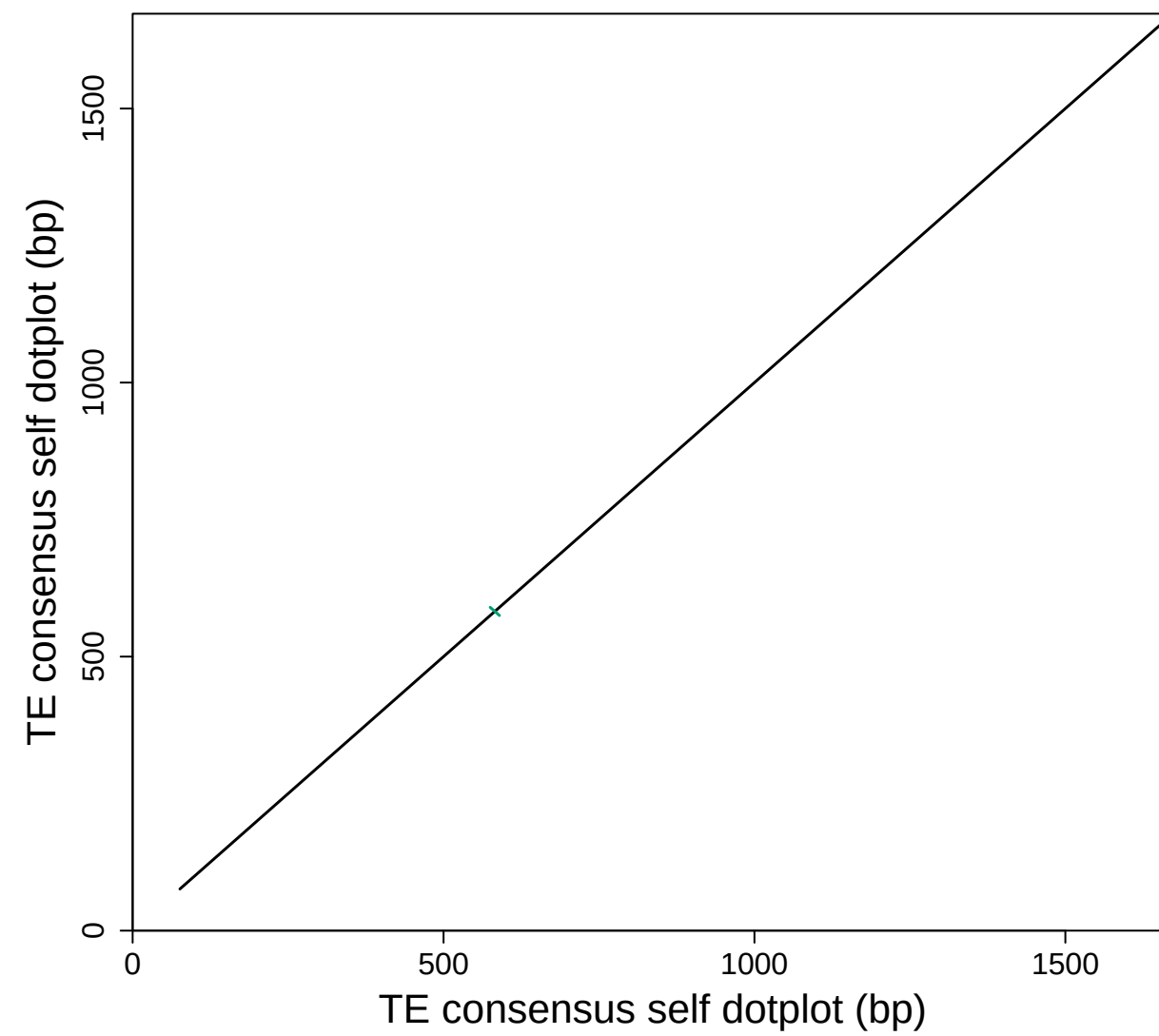
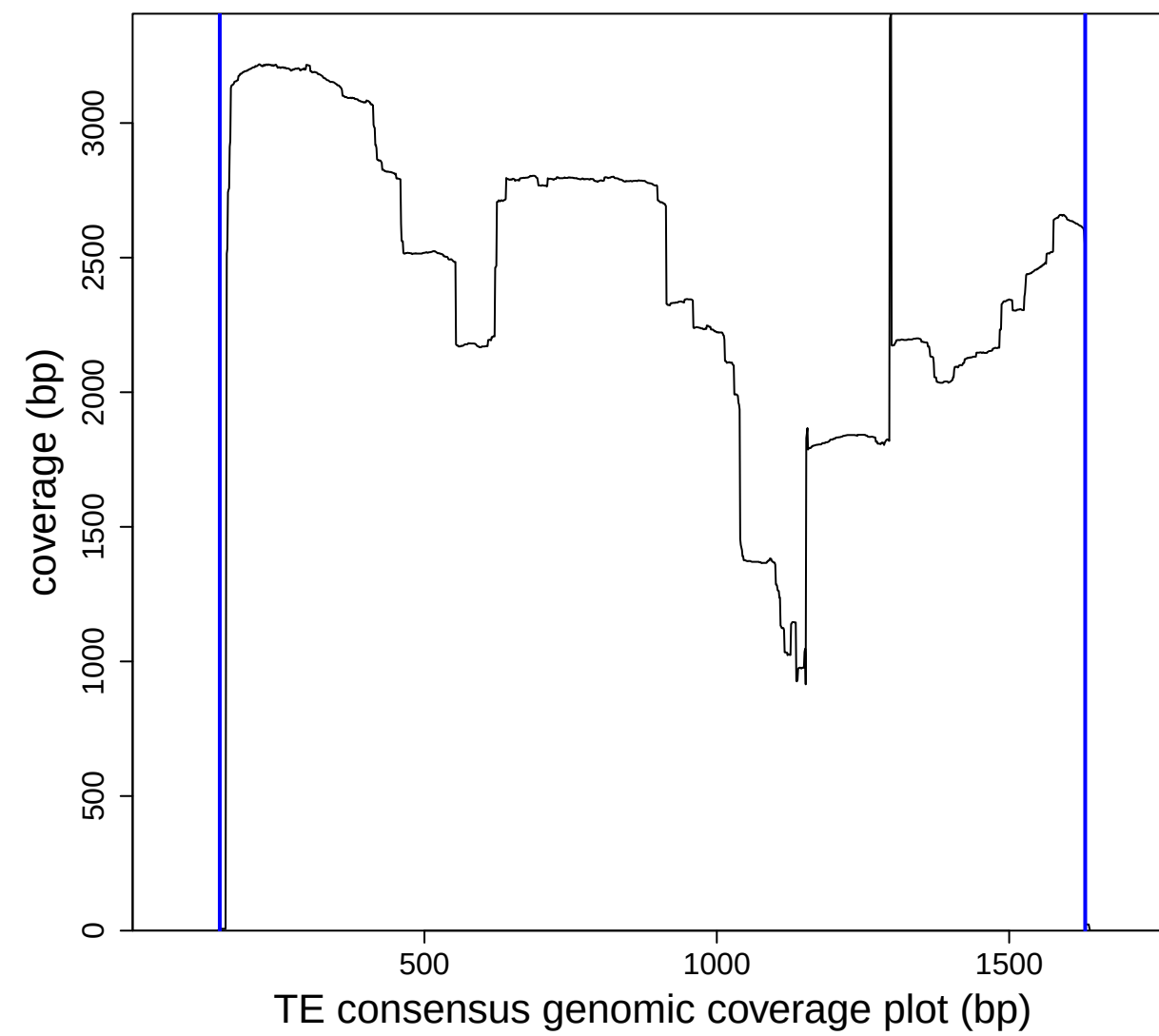
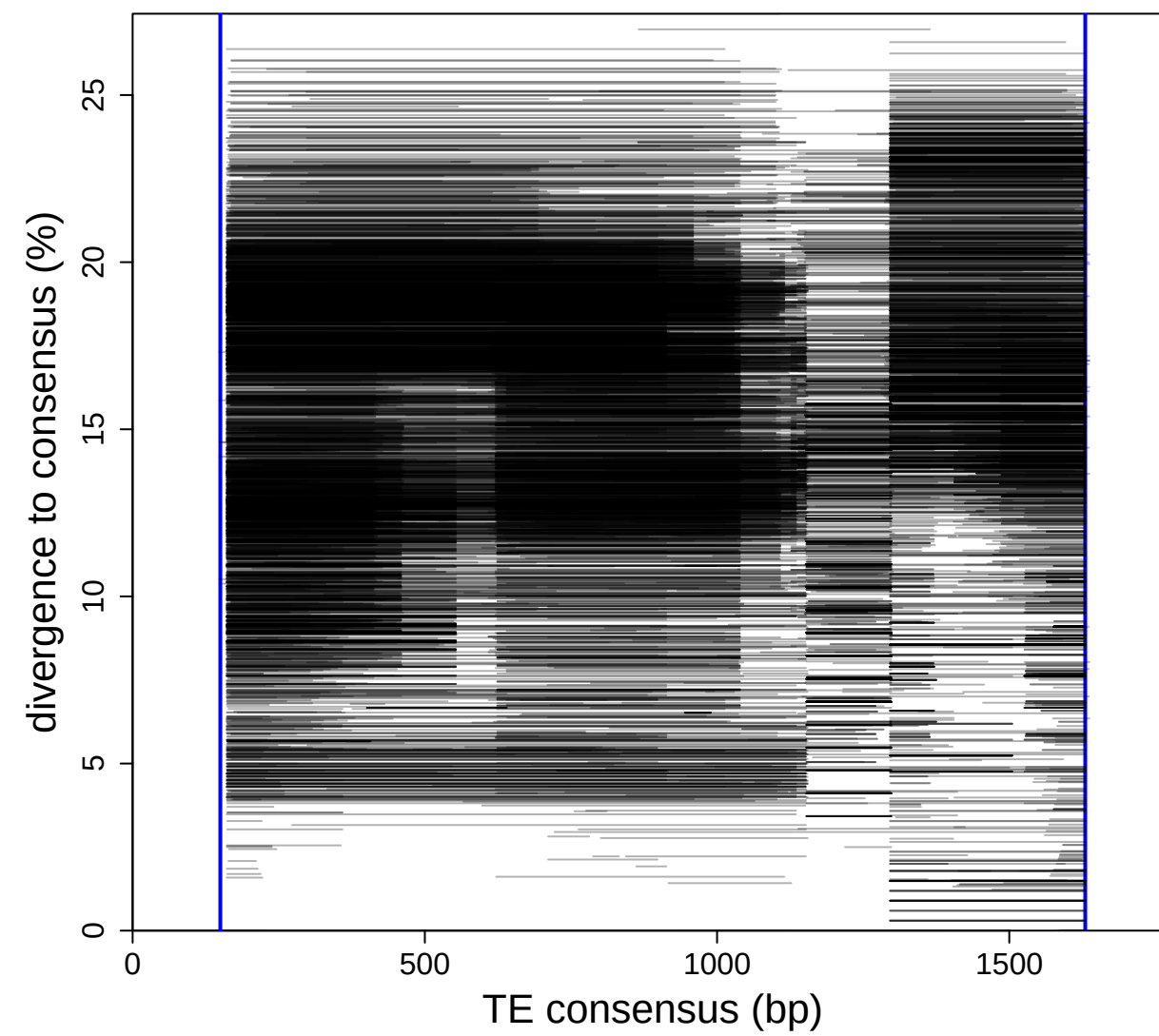
b.bed uf.bed g 4.bed fm\_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa  
size: 1479bp; fragments: 8587; full length: 50 ( $\geq 1331.1$ bp)

# After TETrimmer 1479 bp

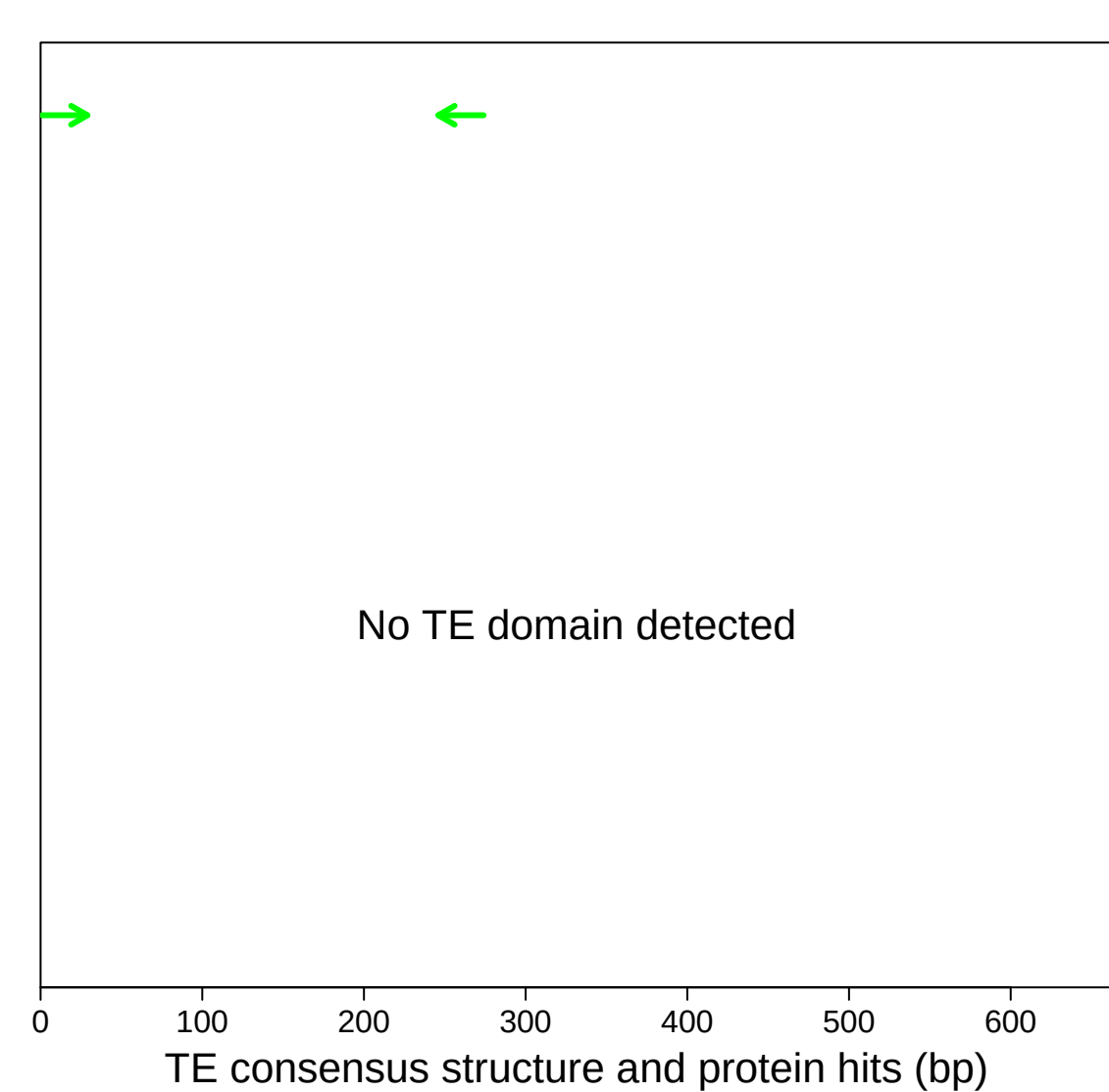
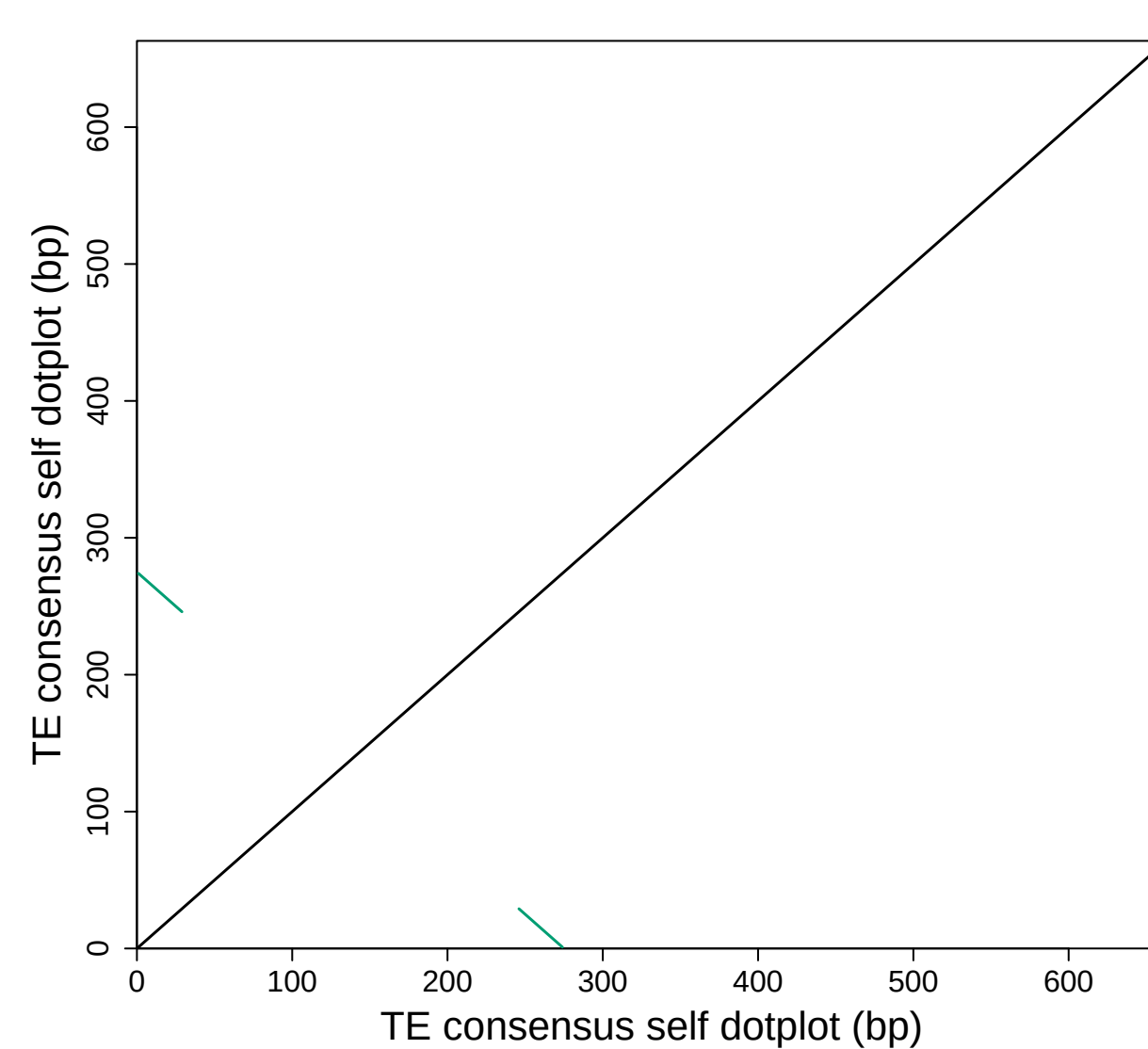
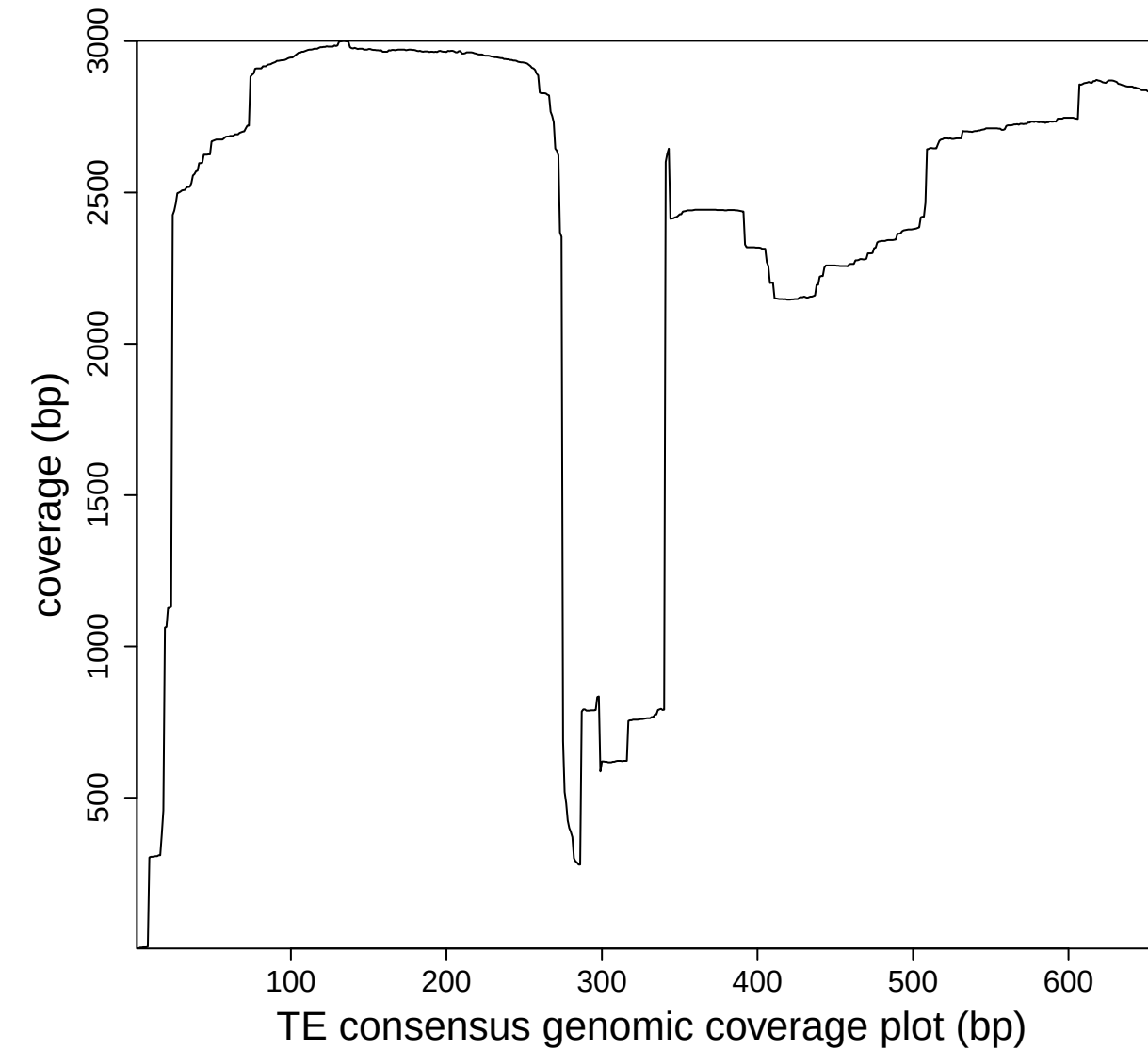
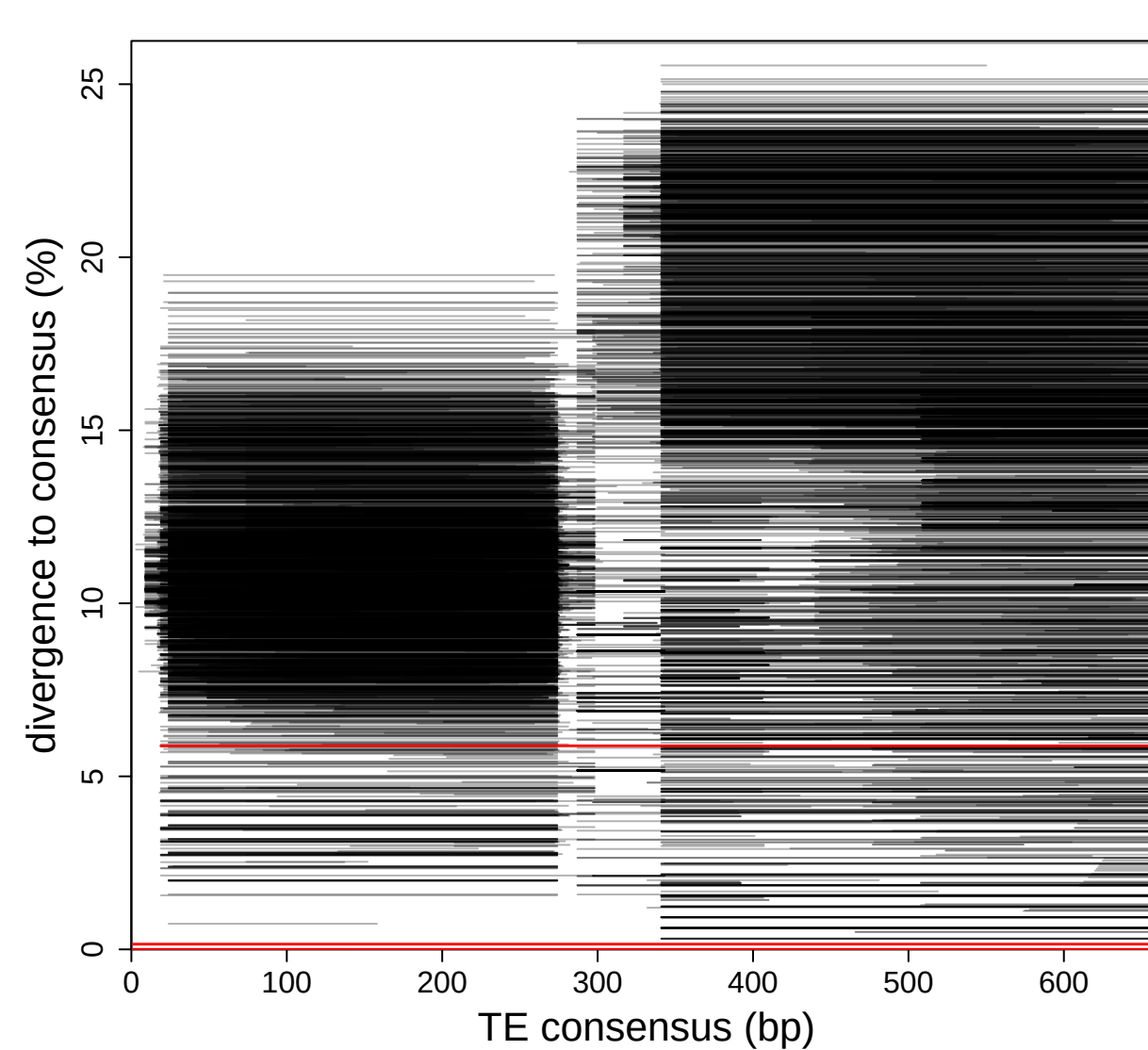


.fasta.b.bed\_uf.bed\_g\_4.bed\_fm\_1.bed\_0\_0\_bcln.fa\_aln.fa\_cl.fa  
size: 1780bp; fragments: 8522; full length: 0 (>=1602bp)

# After TEtrimmer Extended plot Blue lines are boundaries

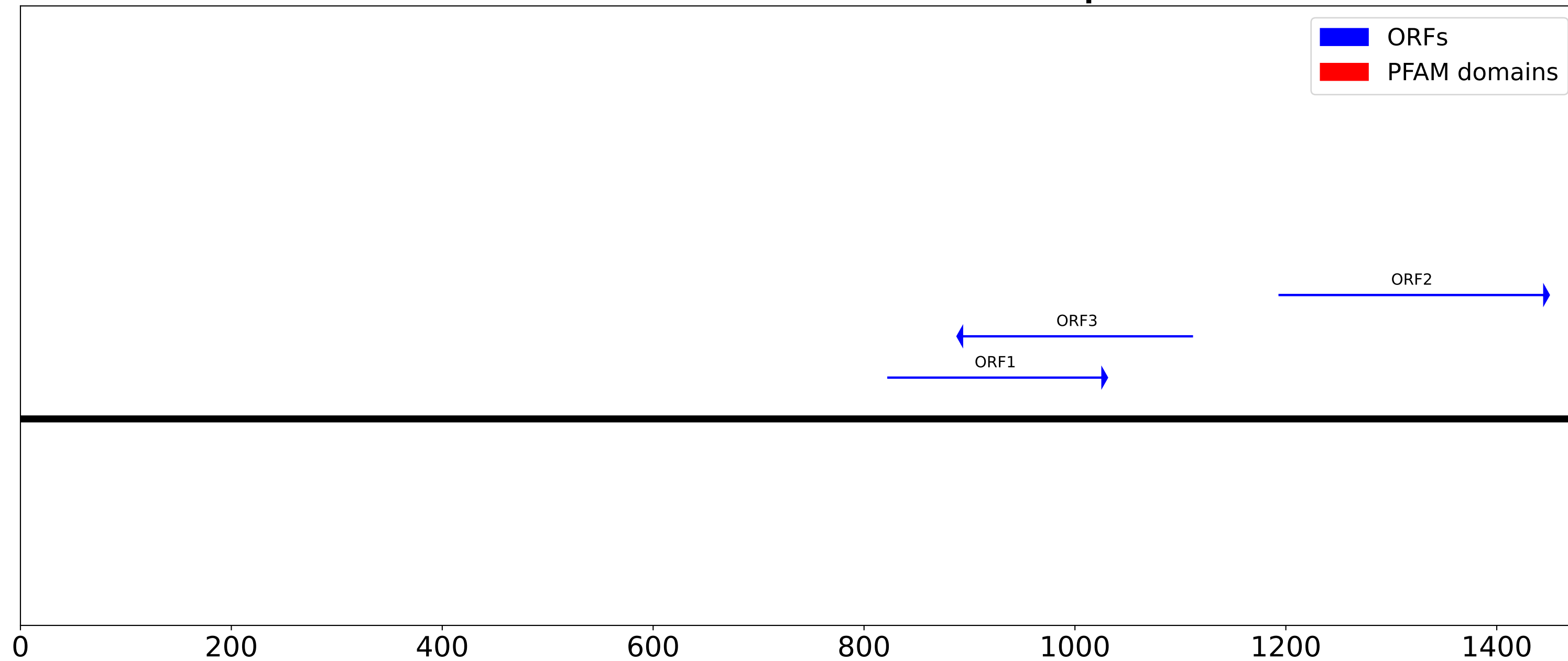


TE: ltr\_1\_family\_257  
size: 663bp; fragments: 6624; full length: 3 ( $\geq 596.7$ bp)

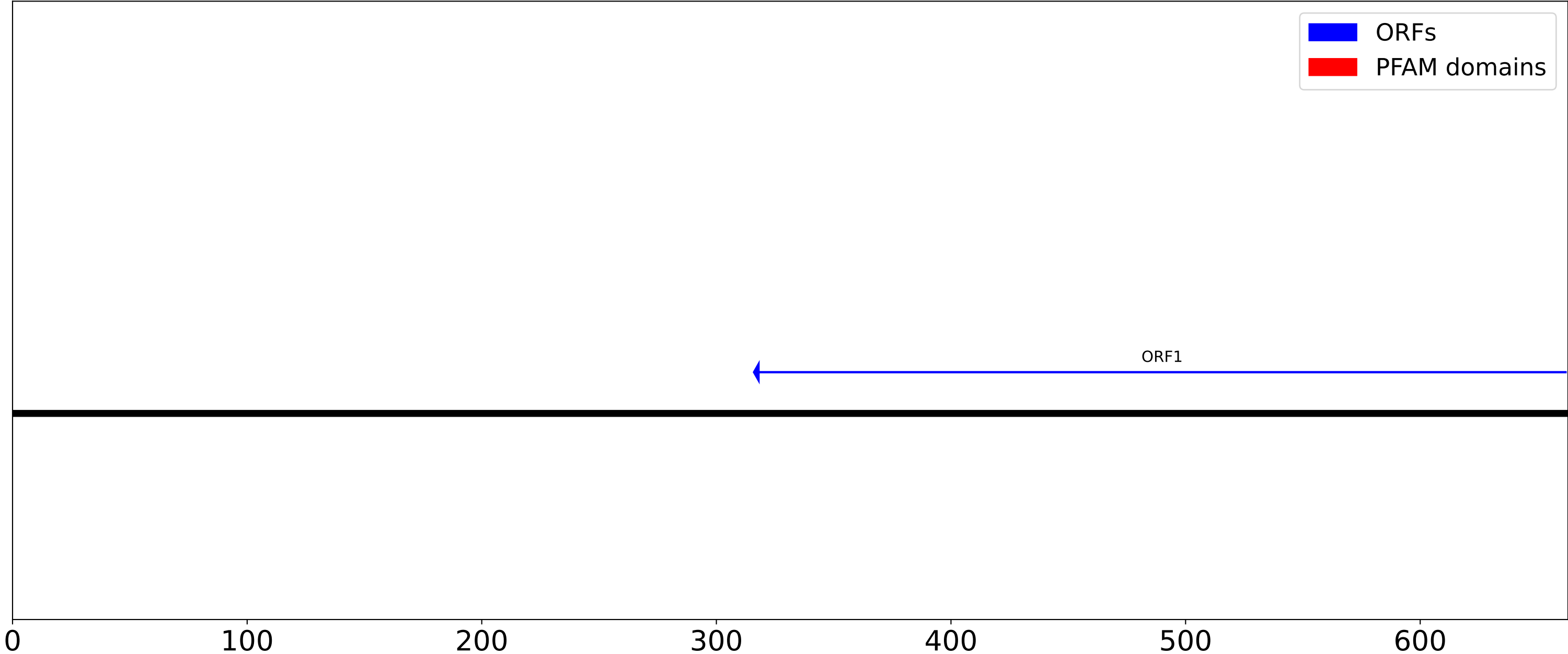


Before TEtrimmer 663 bp

## After TEtrimmer ORF and PFAM domain plot



**Before TEtrimmer ORF and PFAM domain plot**

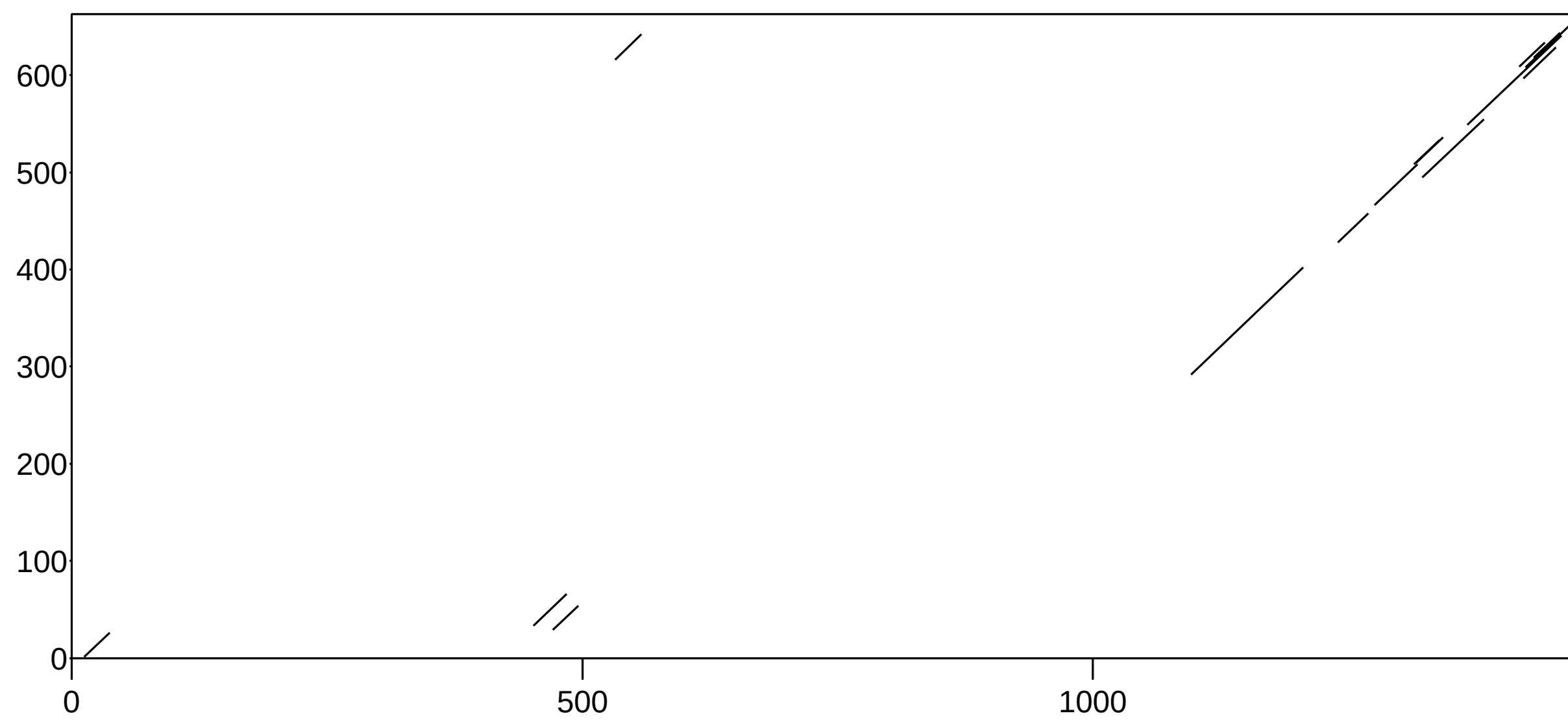




# Dotplot

(window size = 25, threshold = 50.00 09/10/25)

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)