

Start Crop Point

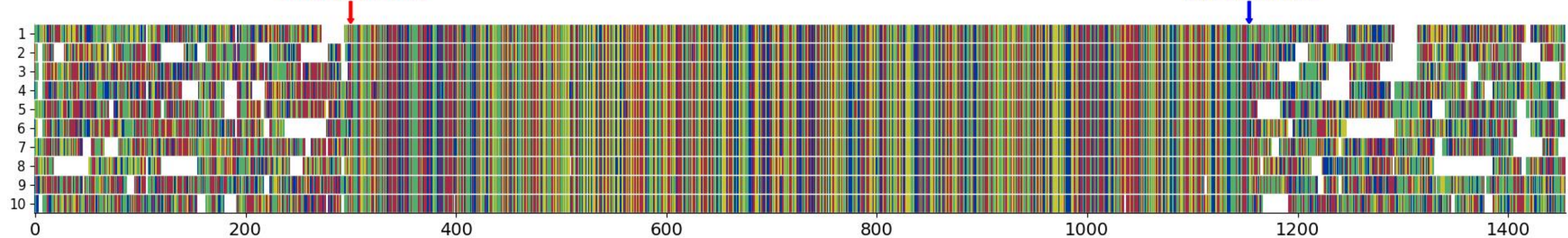
End Crop Point

MSA length = 855



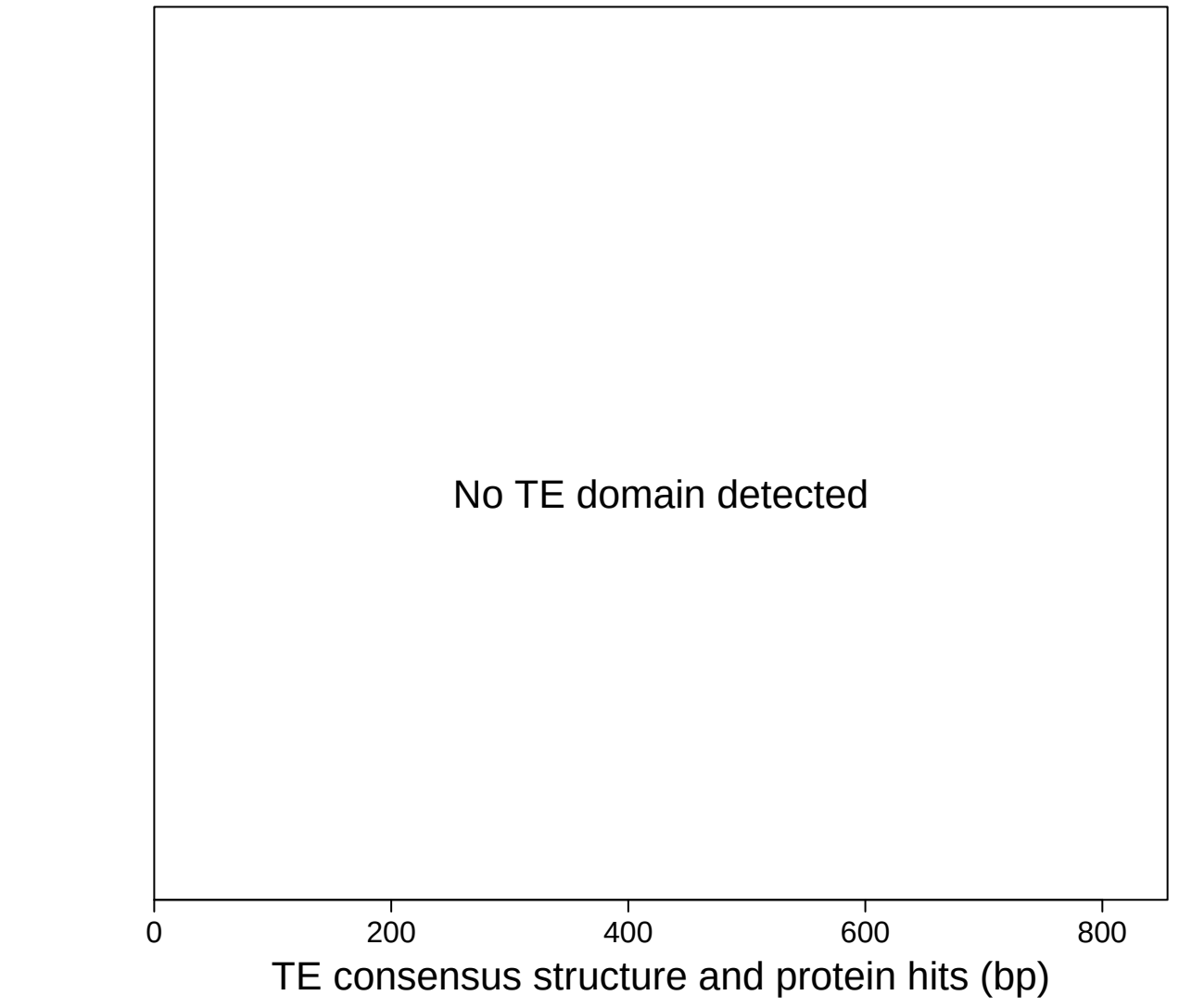
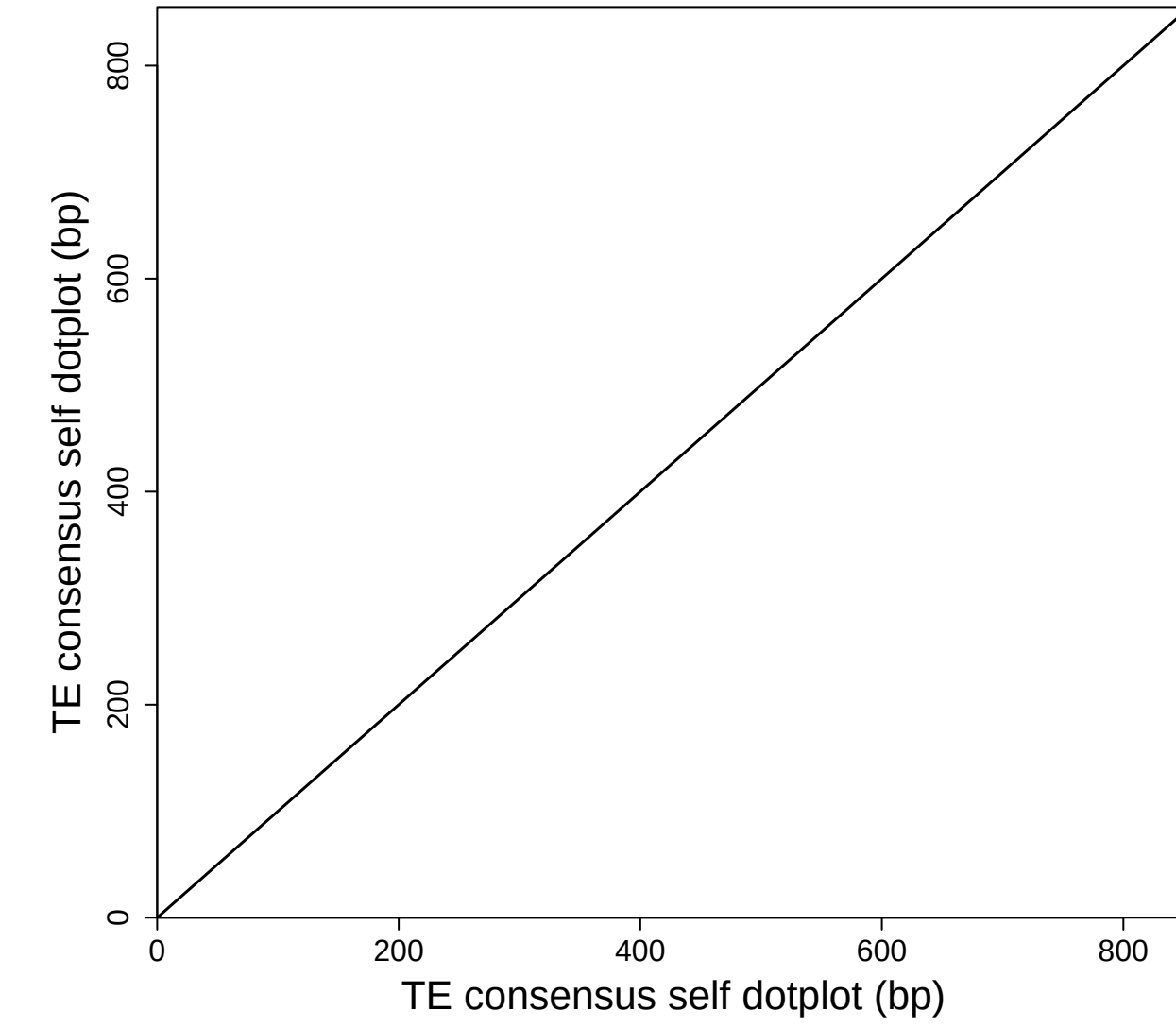
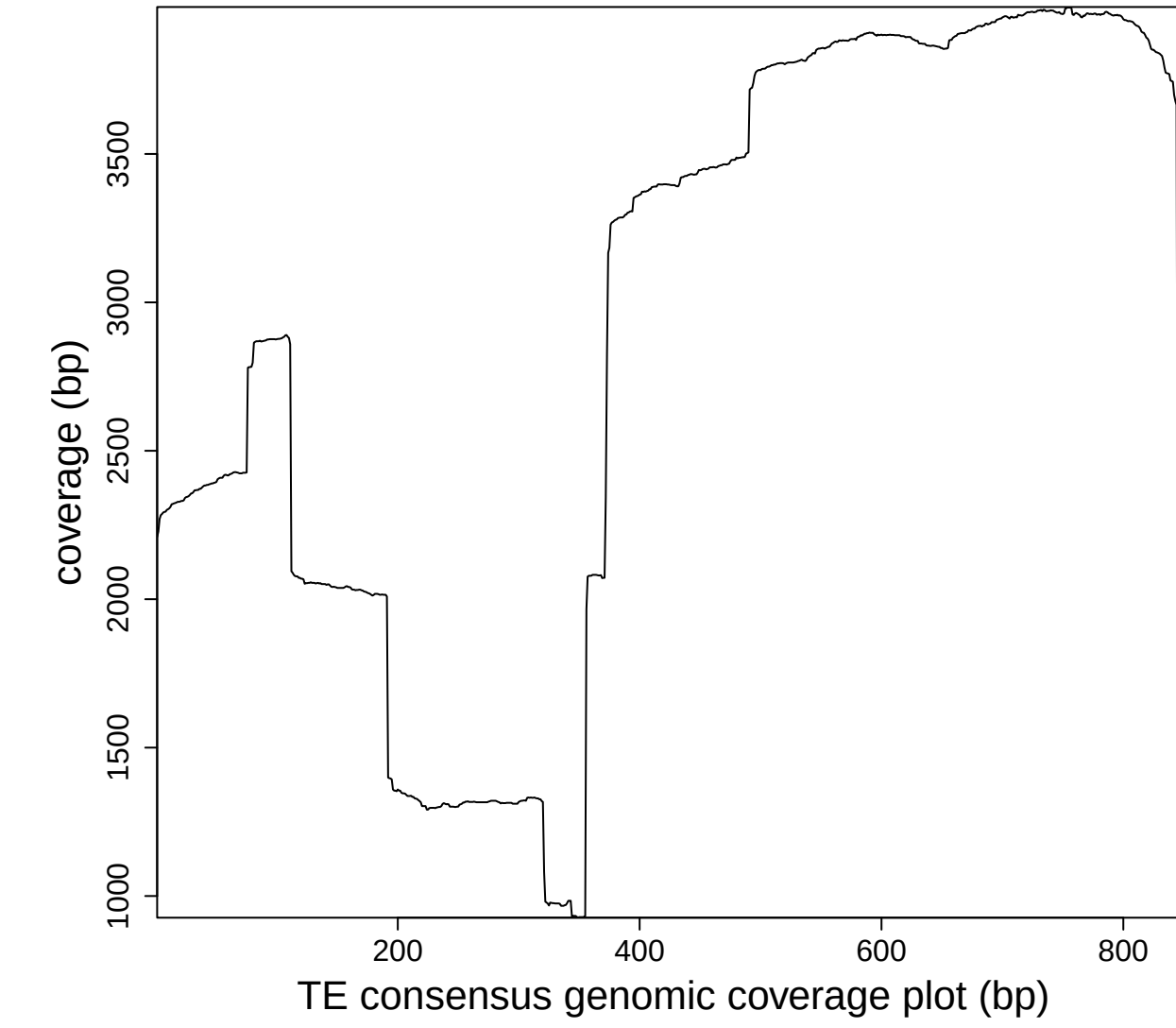
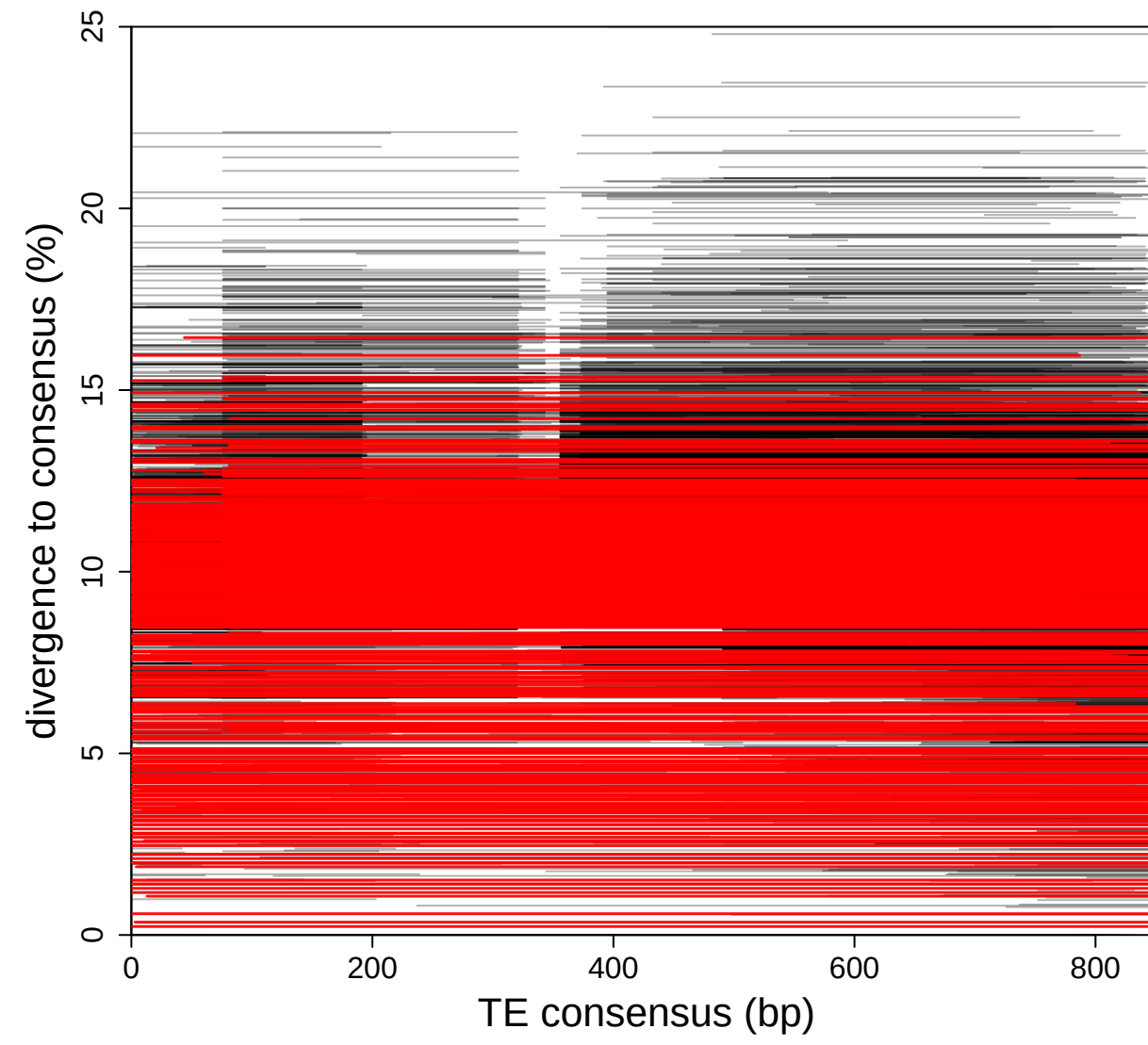
Start crop Point

End crop Point



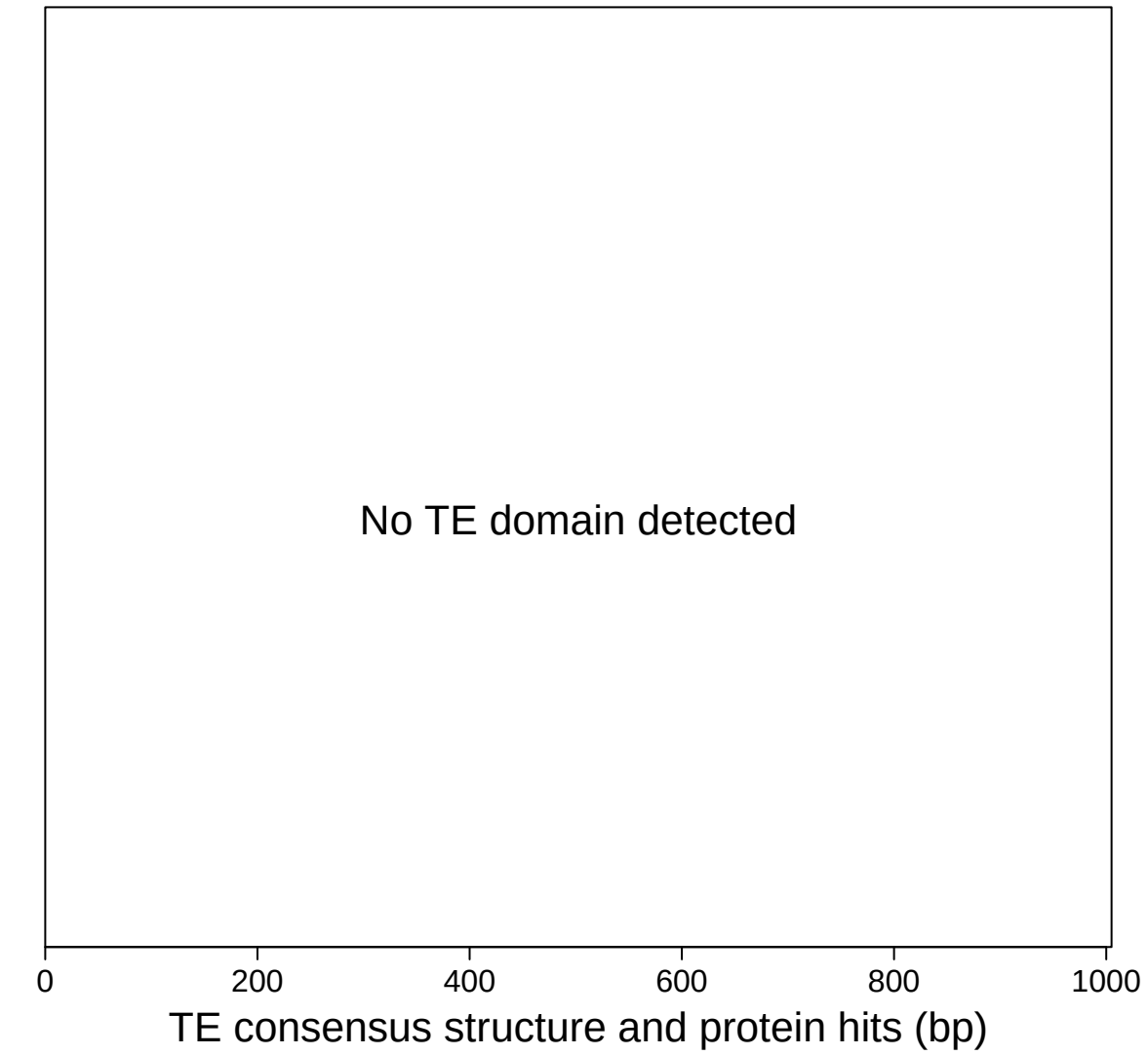
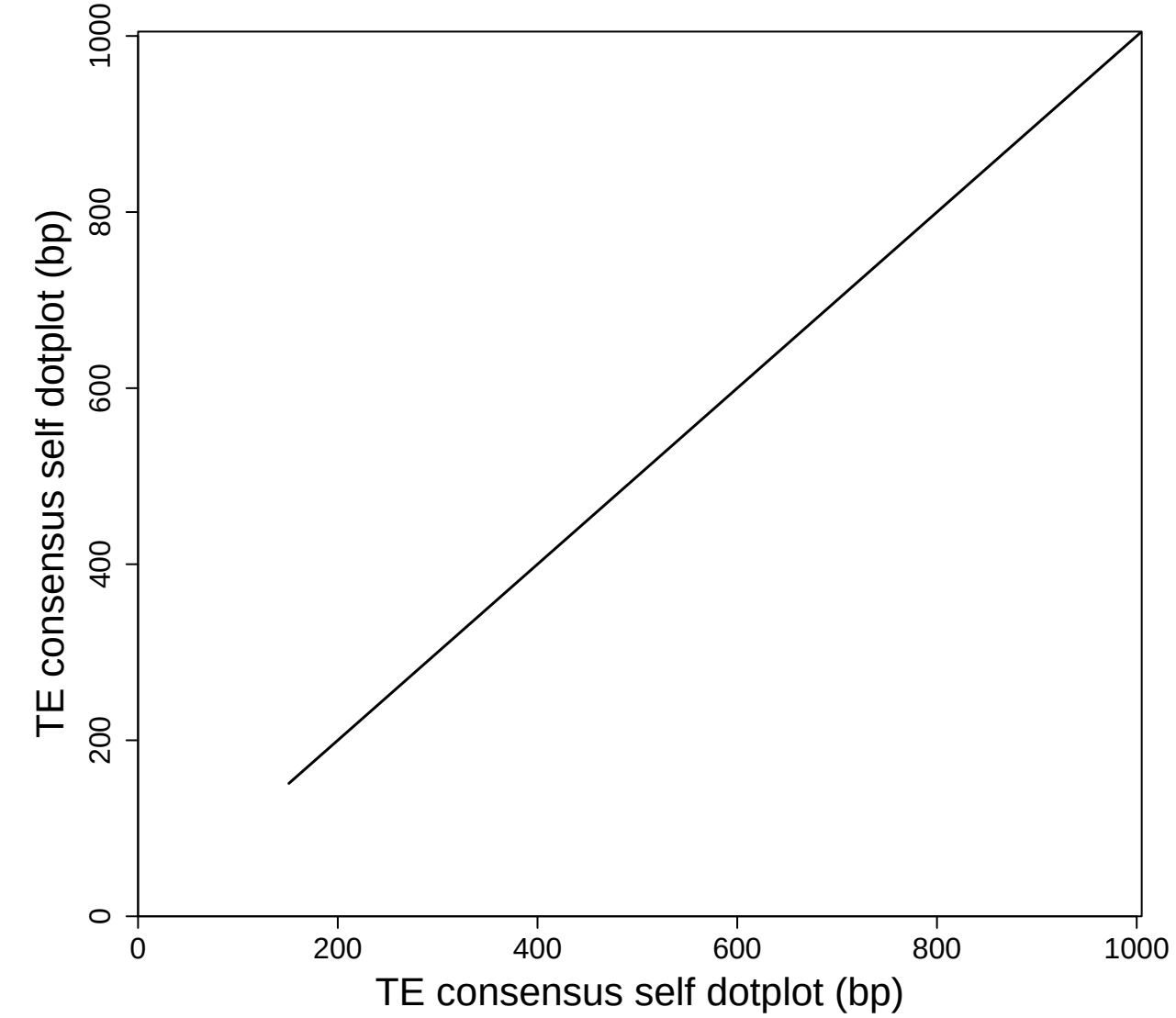
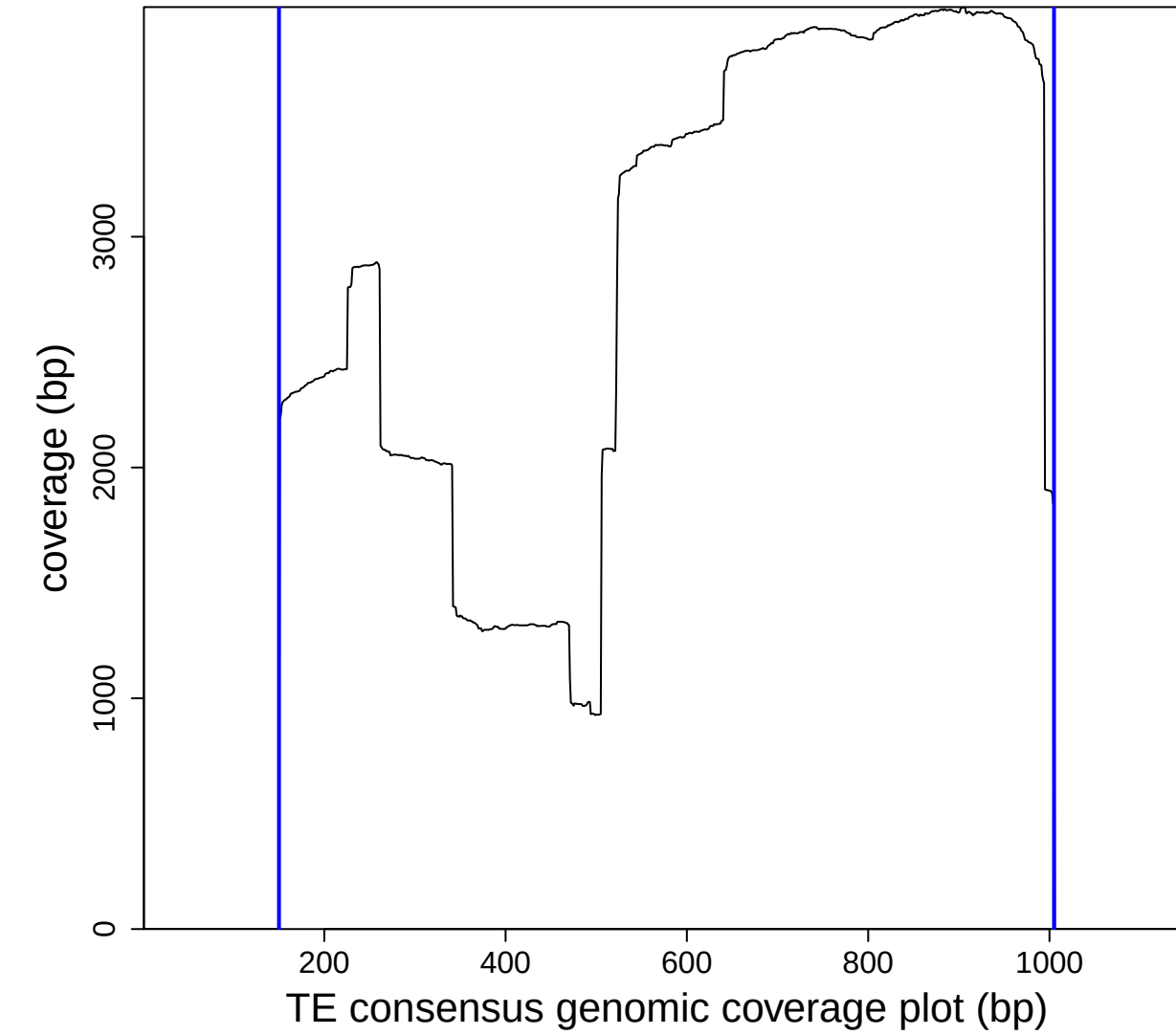
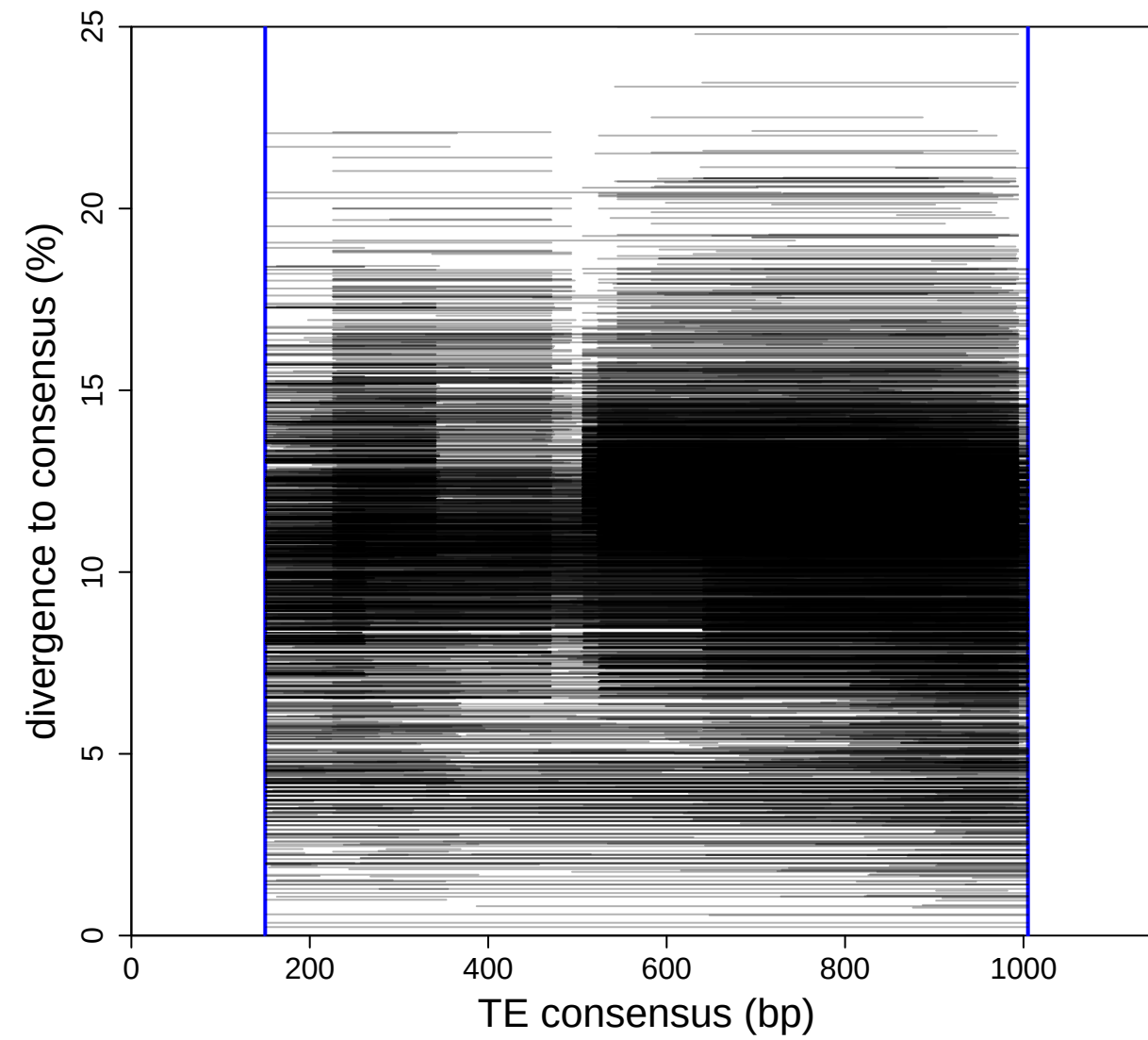
b.bed uf.bed g 4.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa  
size: 855bp; fragments: 6595; full length: 607 ( $\geq 769.5$ bp)

# After TEtrimmer 855 bp

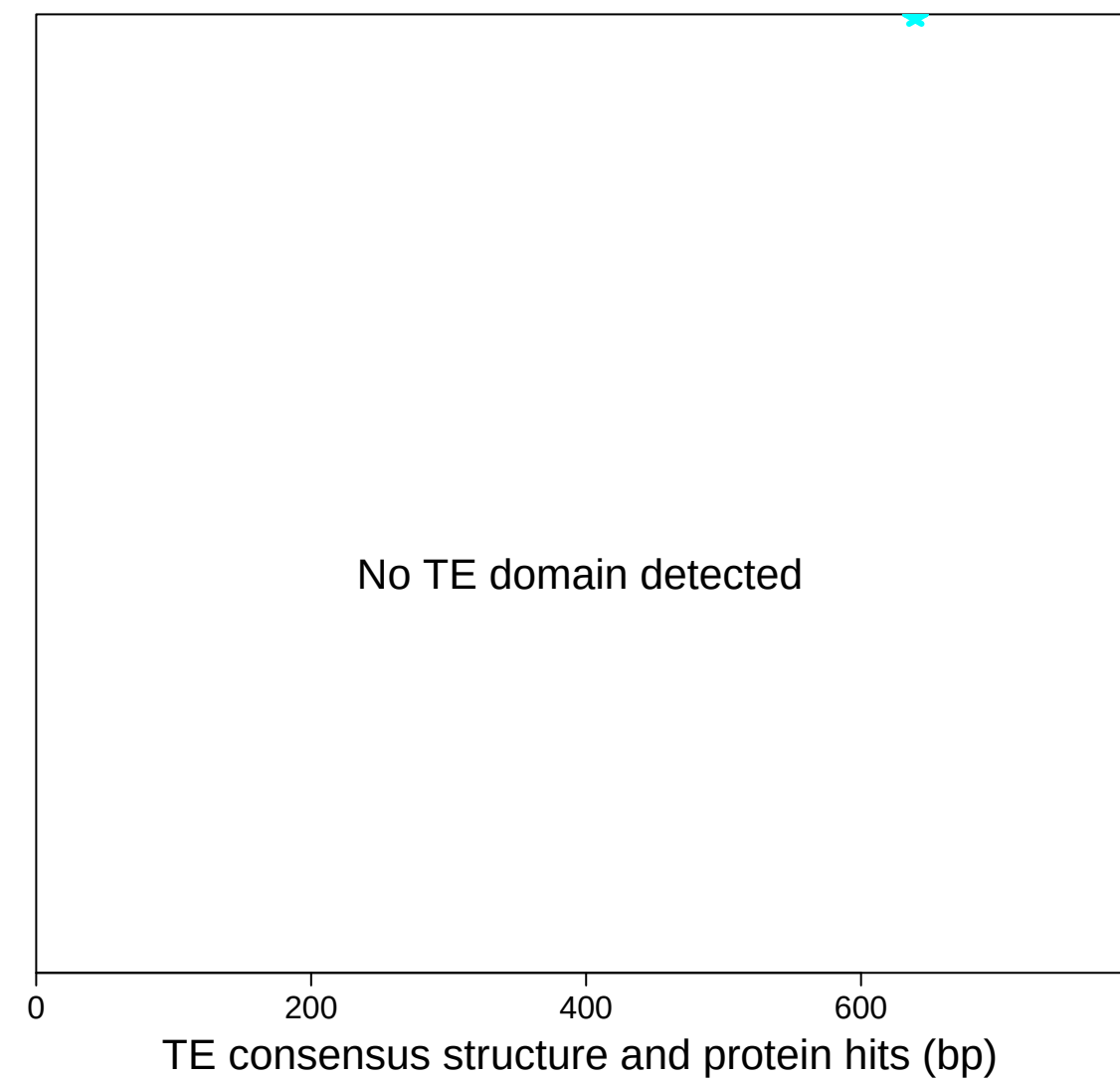
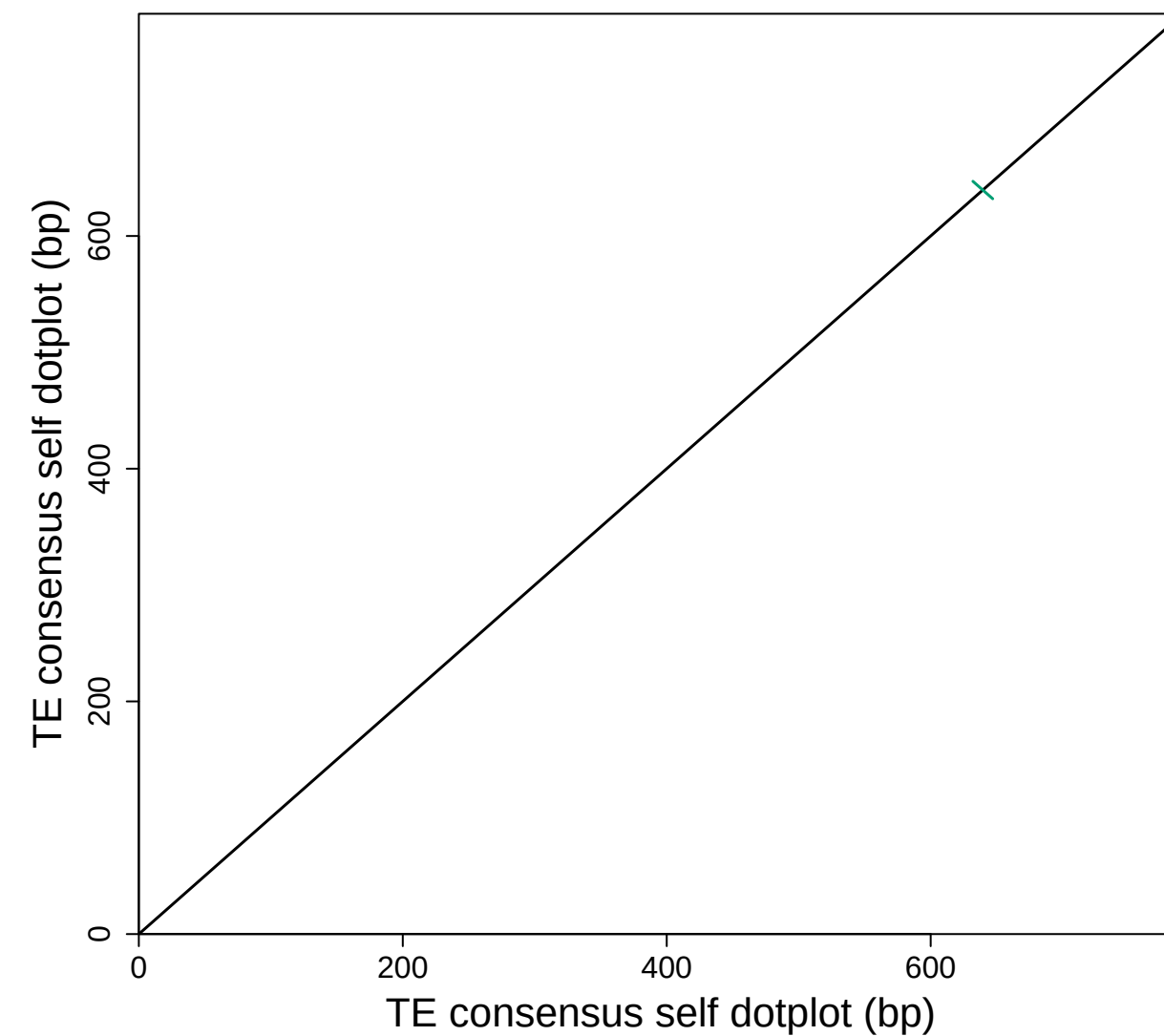
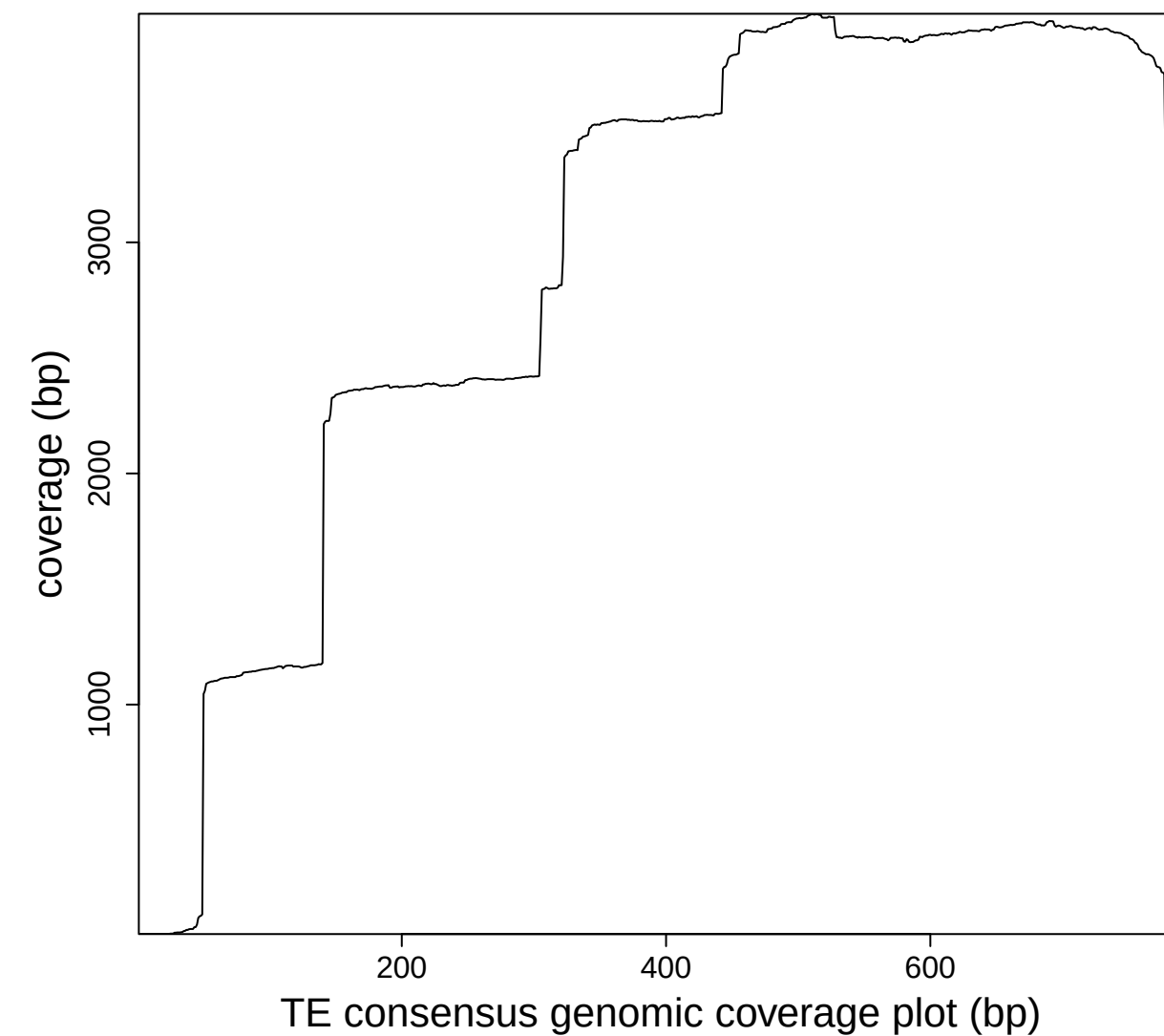
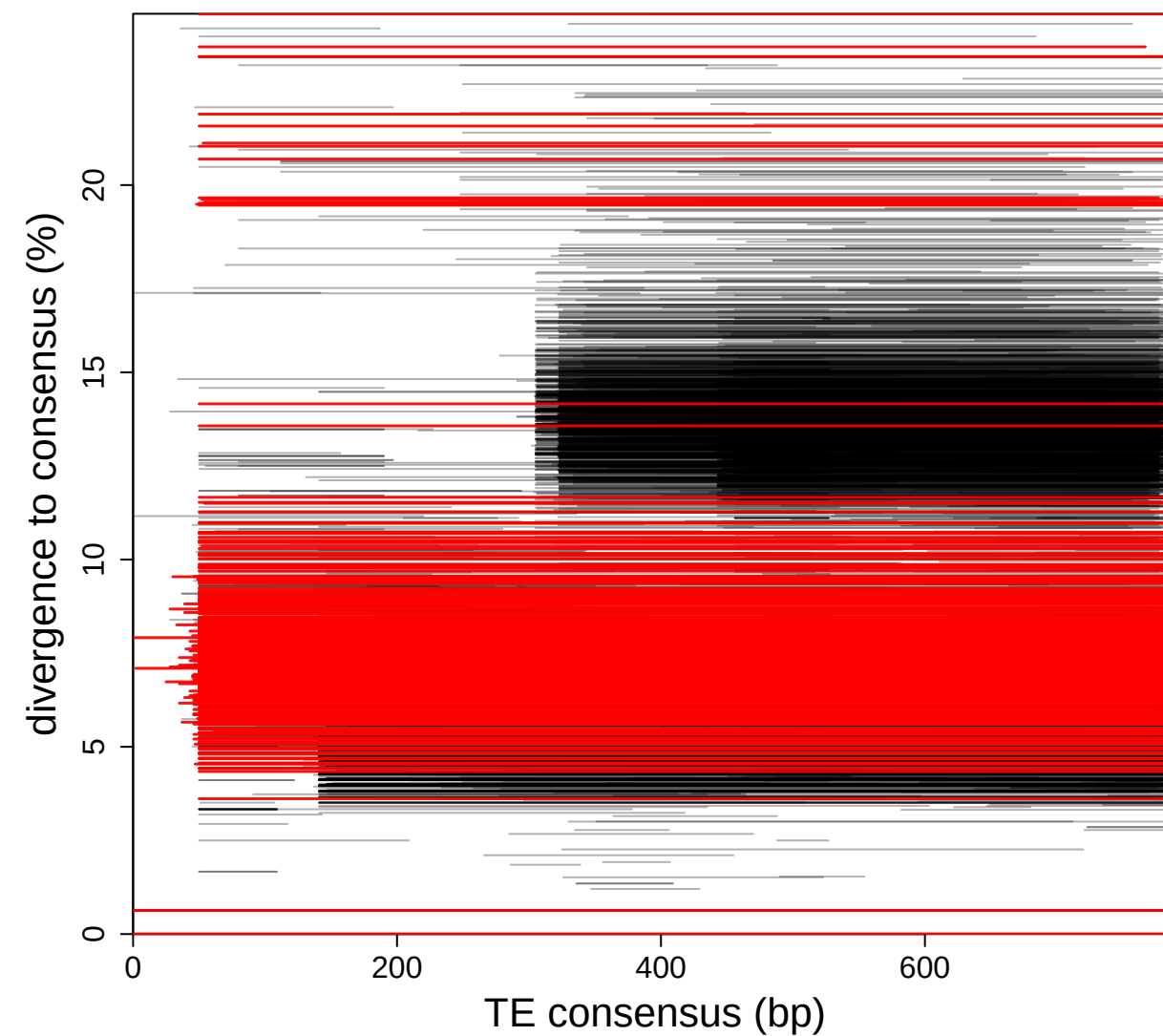


.fasta.b.bed\_uf.bed\_g\_4.bed\_fm\_1.bed\_0\_0\_bcln.fa\_aln.fa\_cl.fa  
size: 1155bp; fragments: 6595; full length: 0 (>=1039.5bp)

## After TEtrimmer Extended plot Blue lines are boundaries

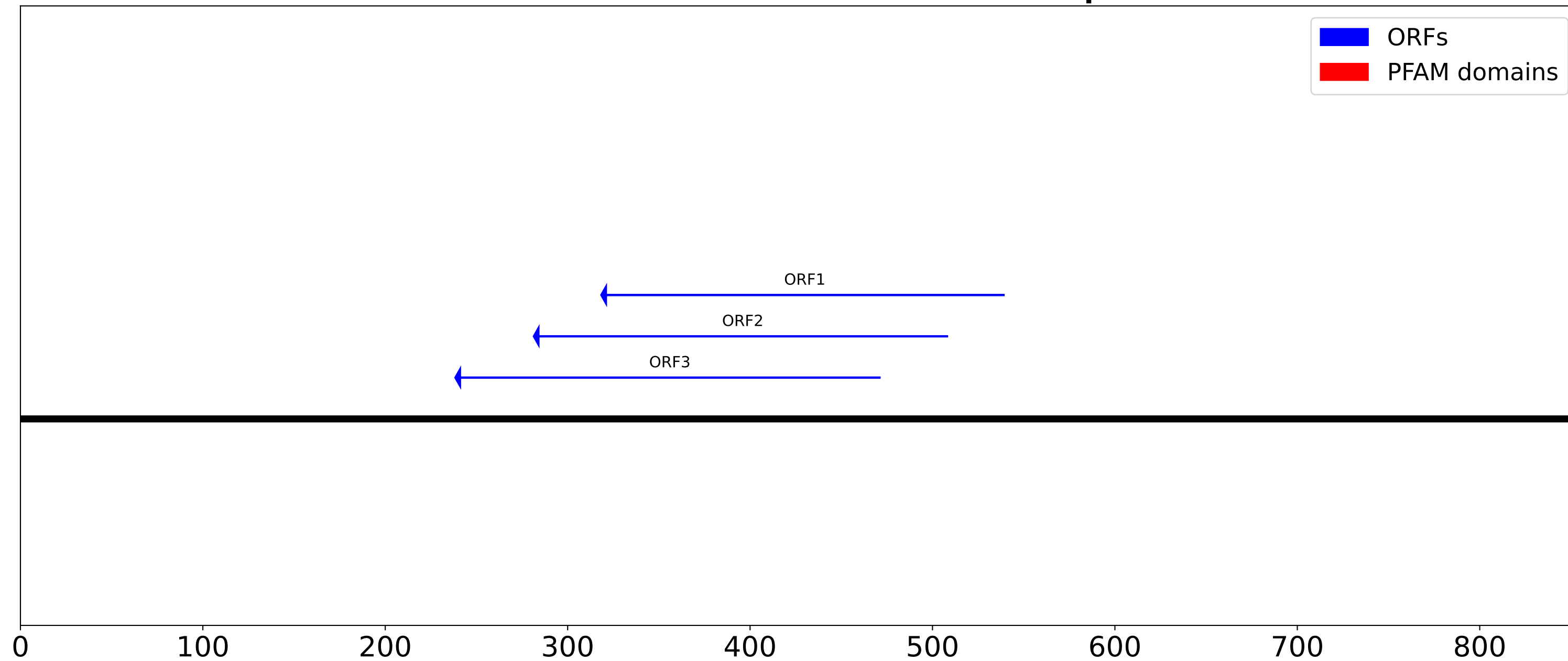


TE: ltr\_1\_family\_290  
size: 791bp; fragments: 4736; full length: 813 ( $\geq 711.9$ bp)

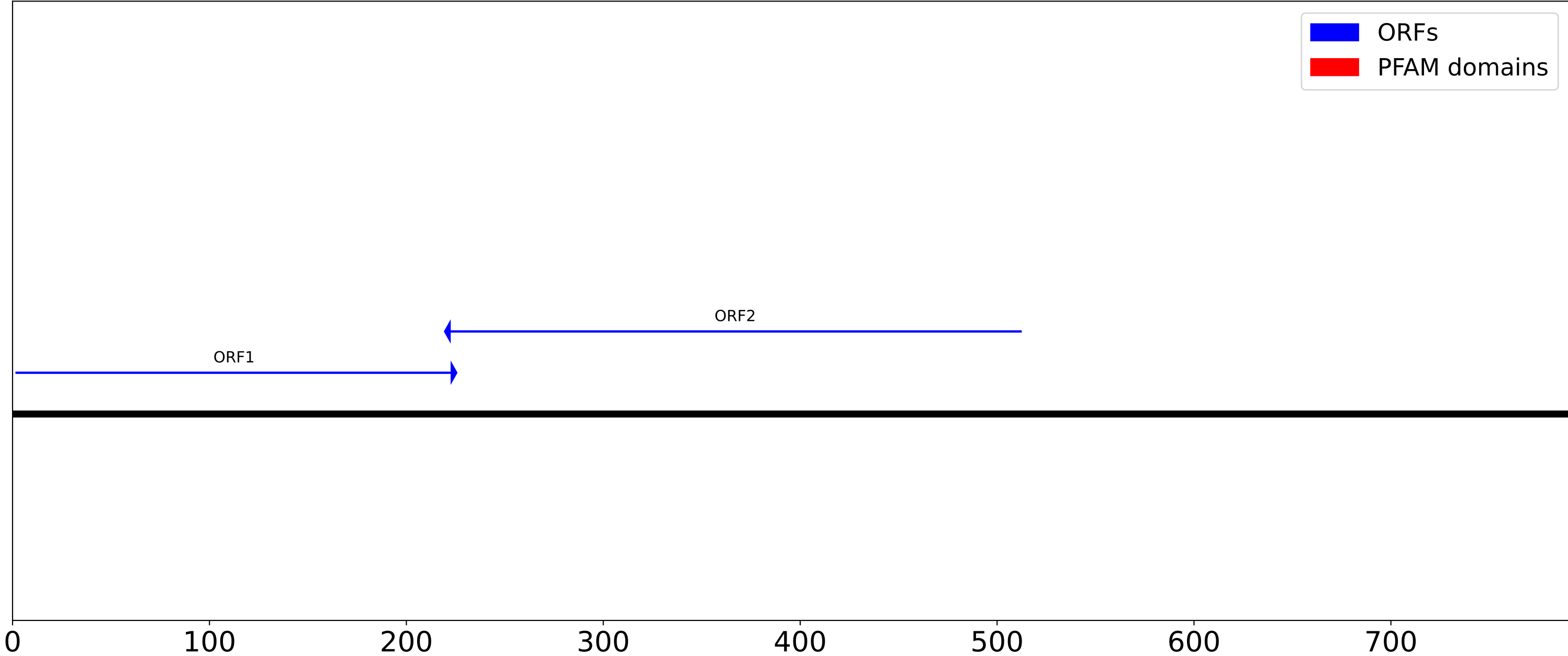


## Before TEtrimmer 791 bp

## After TEtrimmer ORF and PFAM domain plot



**Before TEtrimmer ORF and PFAM domain plot**





# Dotplot

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

