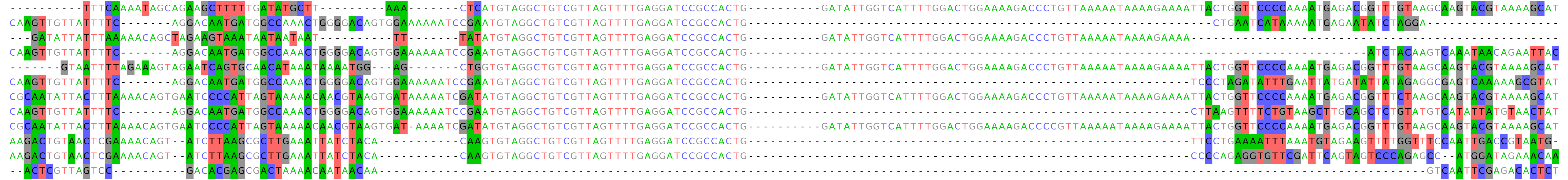


Start crop Point

End crop Point

MSA length = 3398



Start crop Point

End crop Point

0

10

0

500

1000

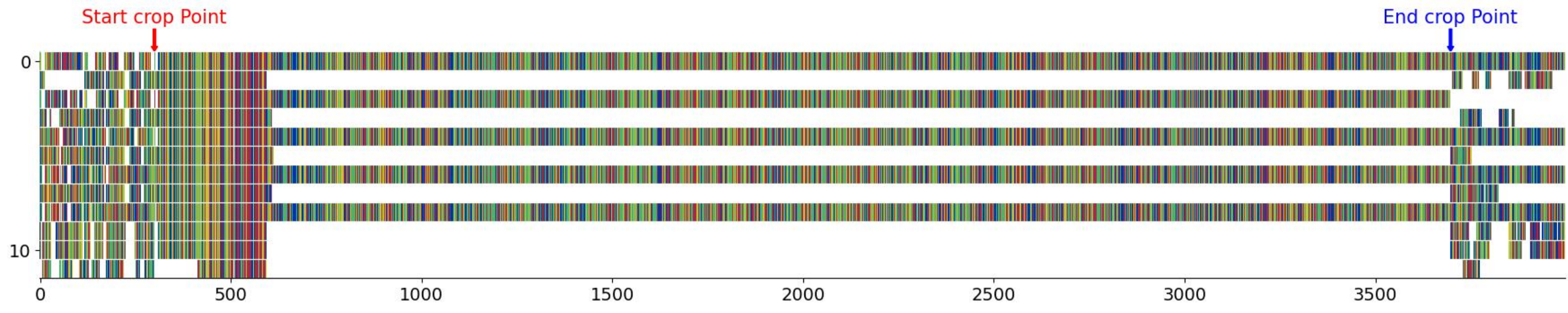
1500

2000

2500

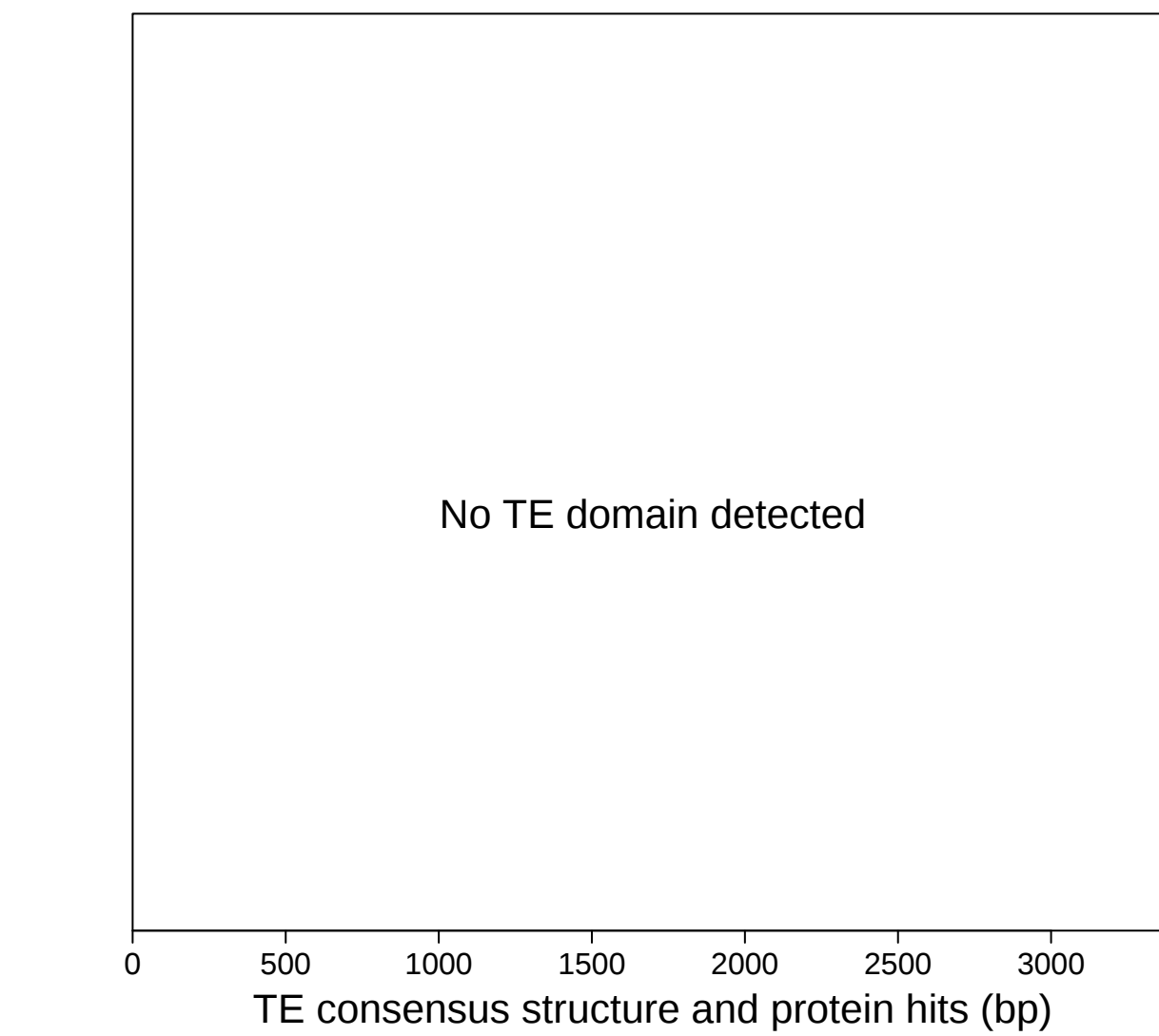
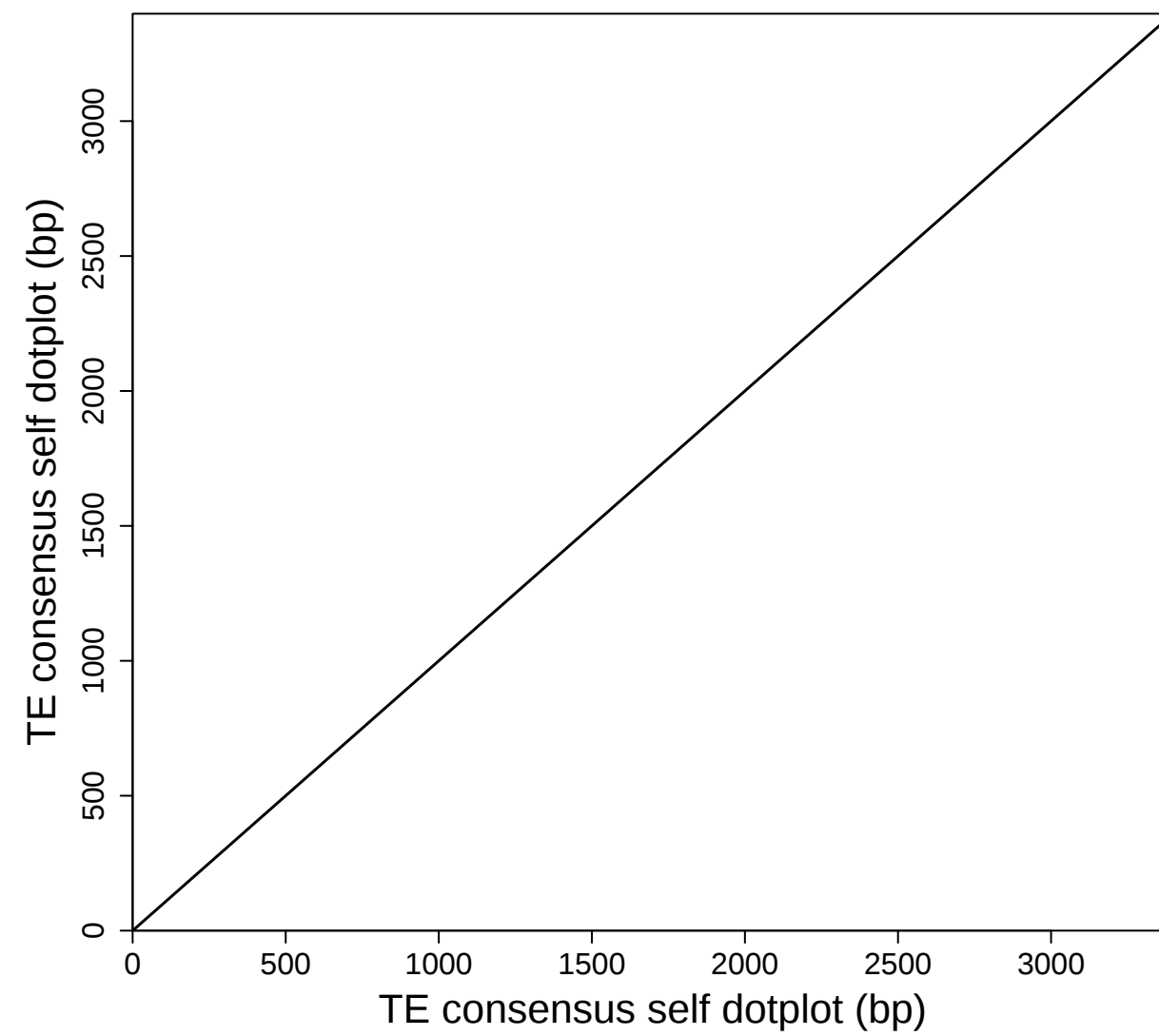
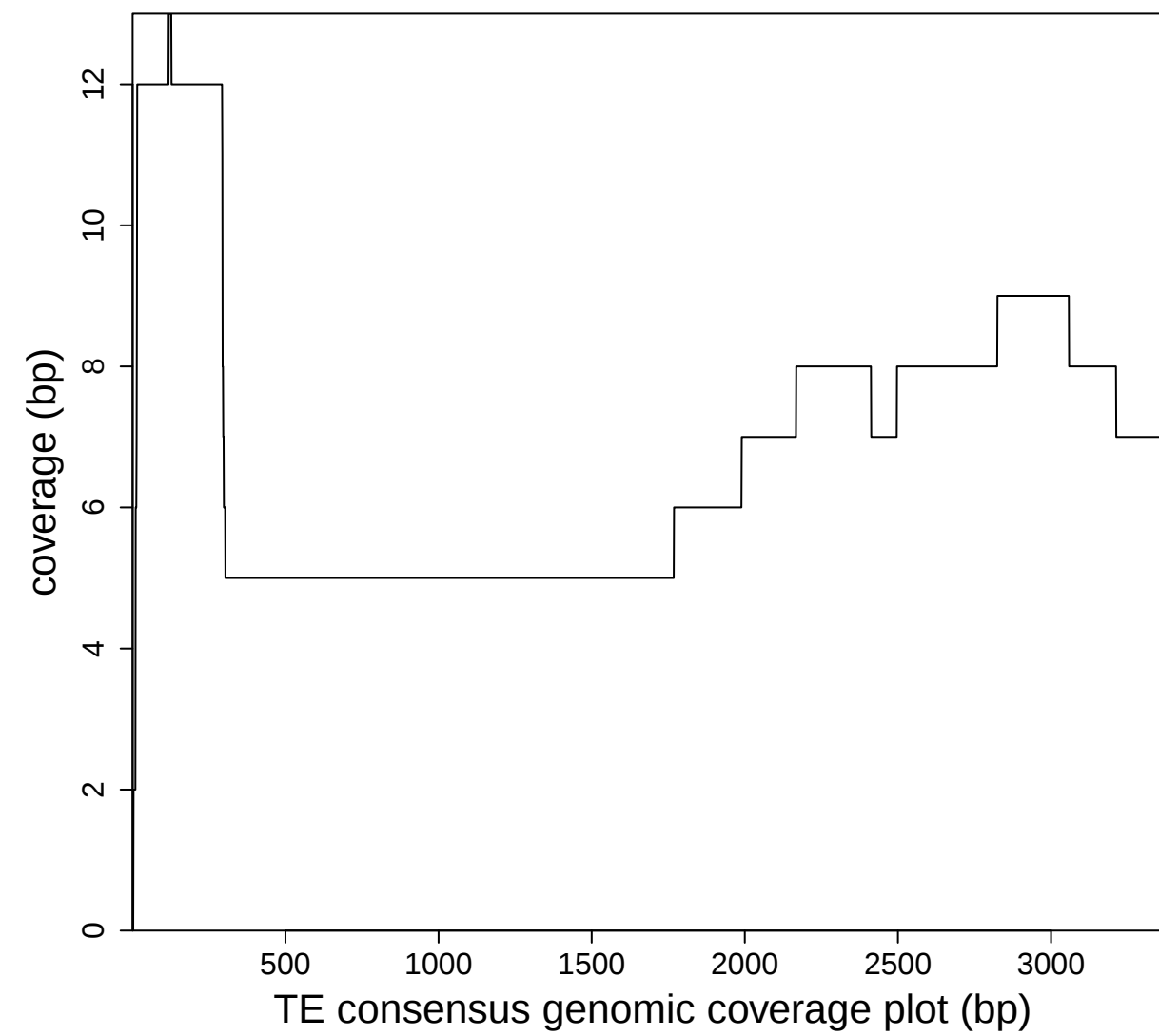
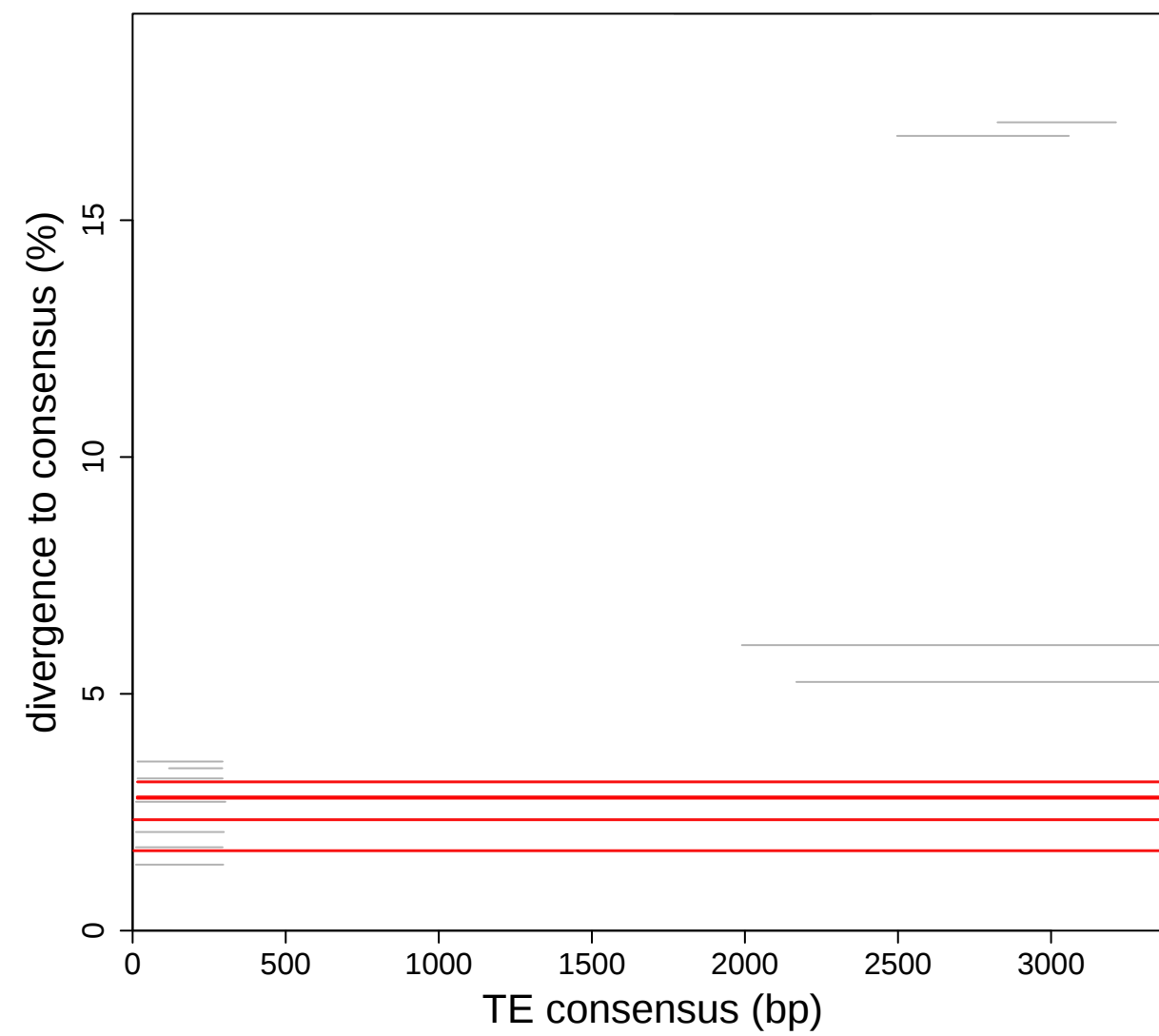
3000

3500



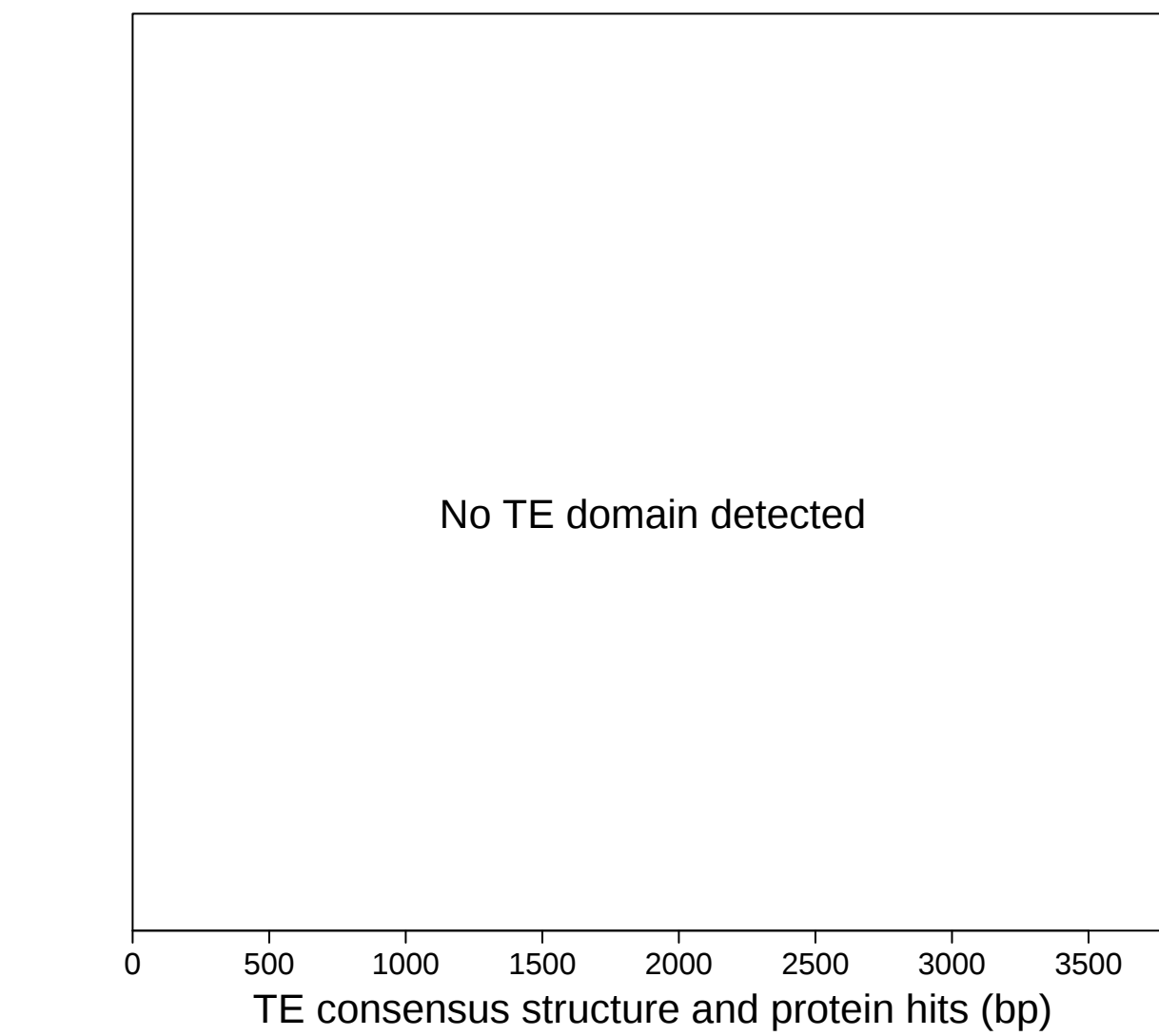
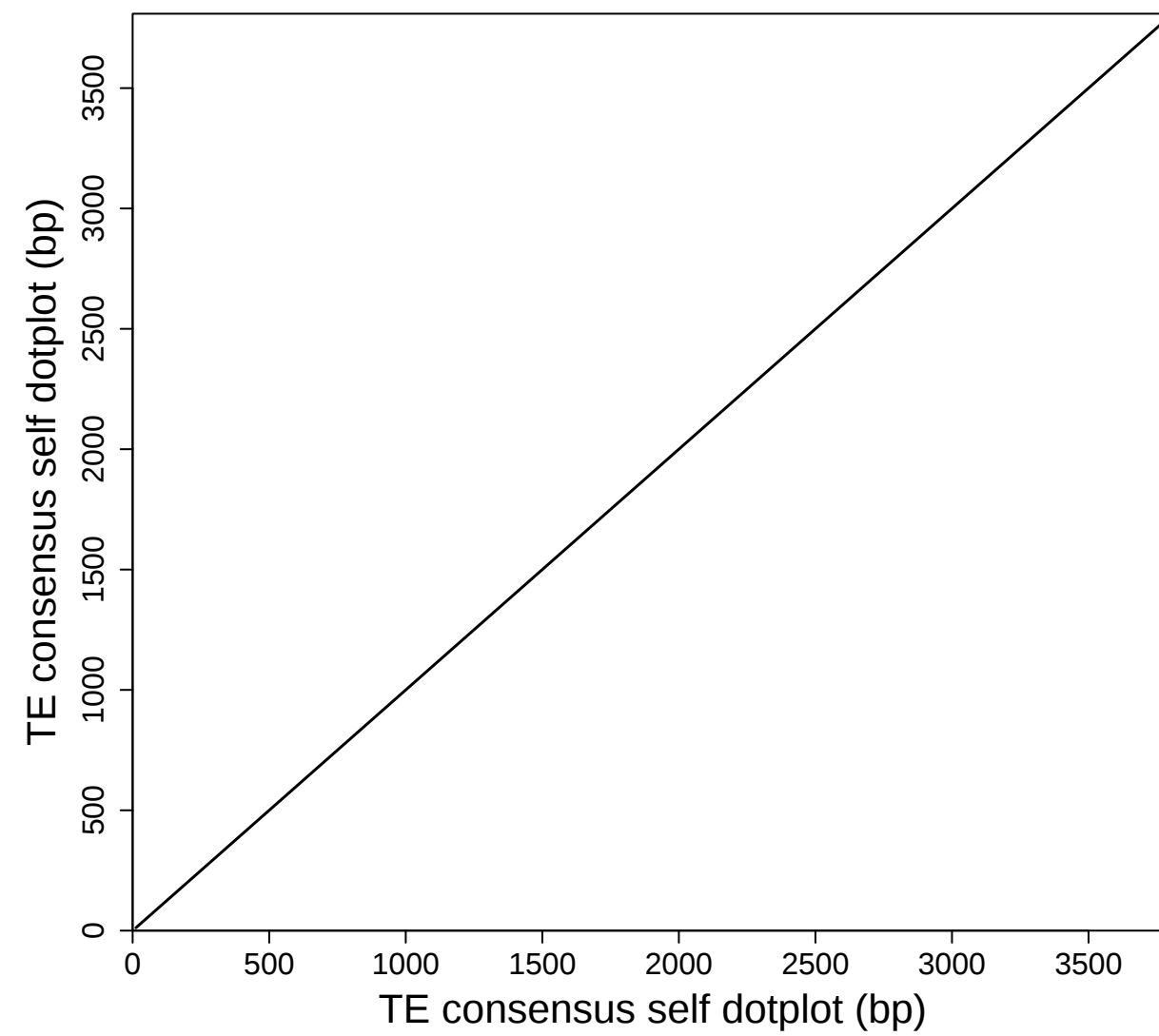
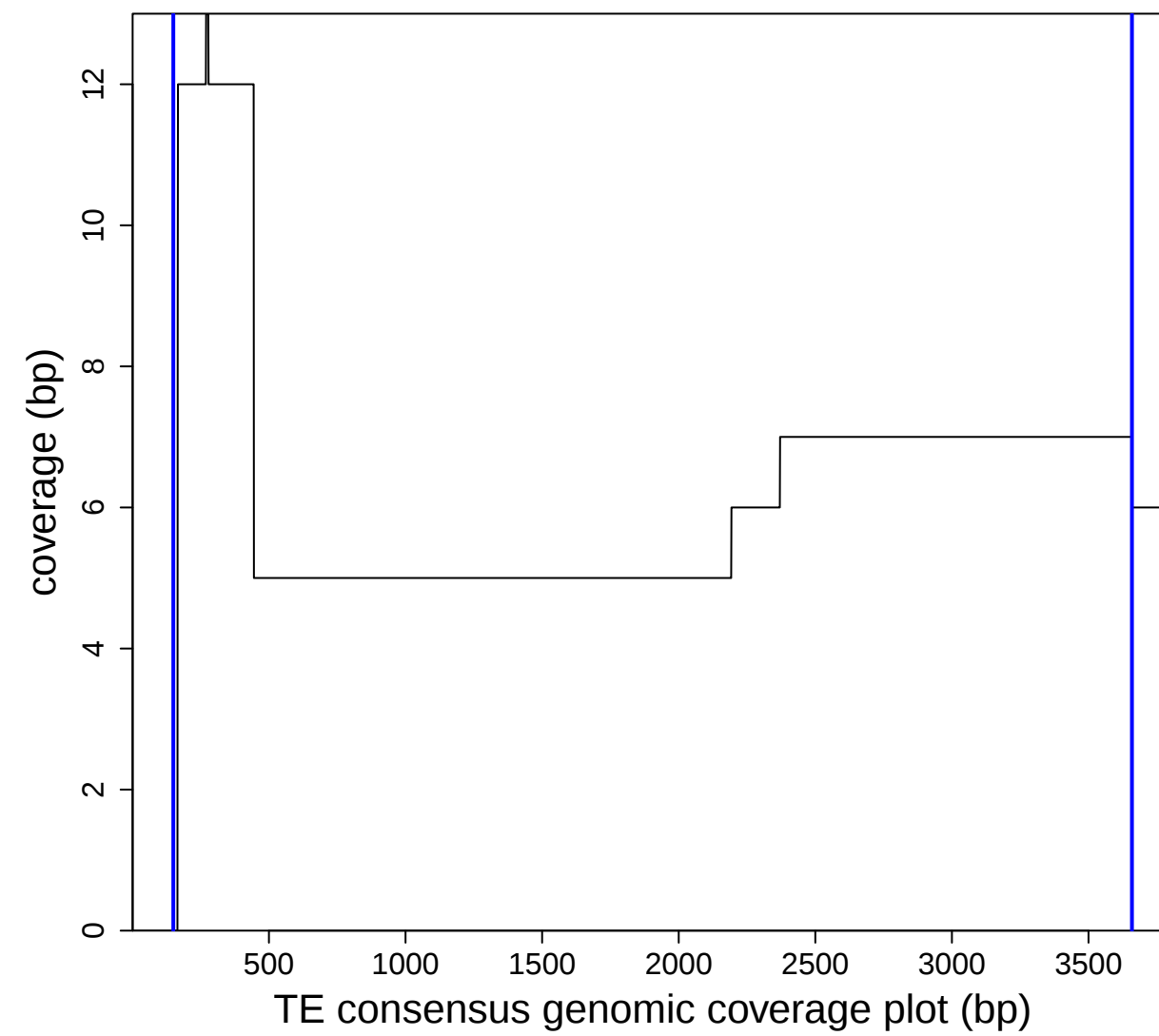
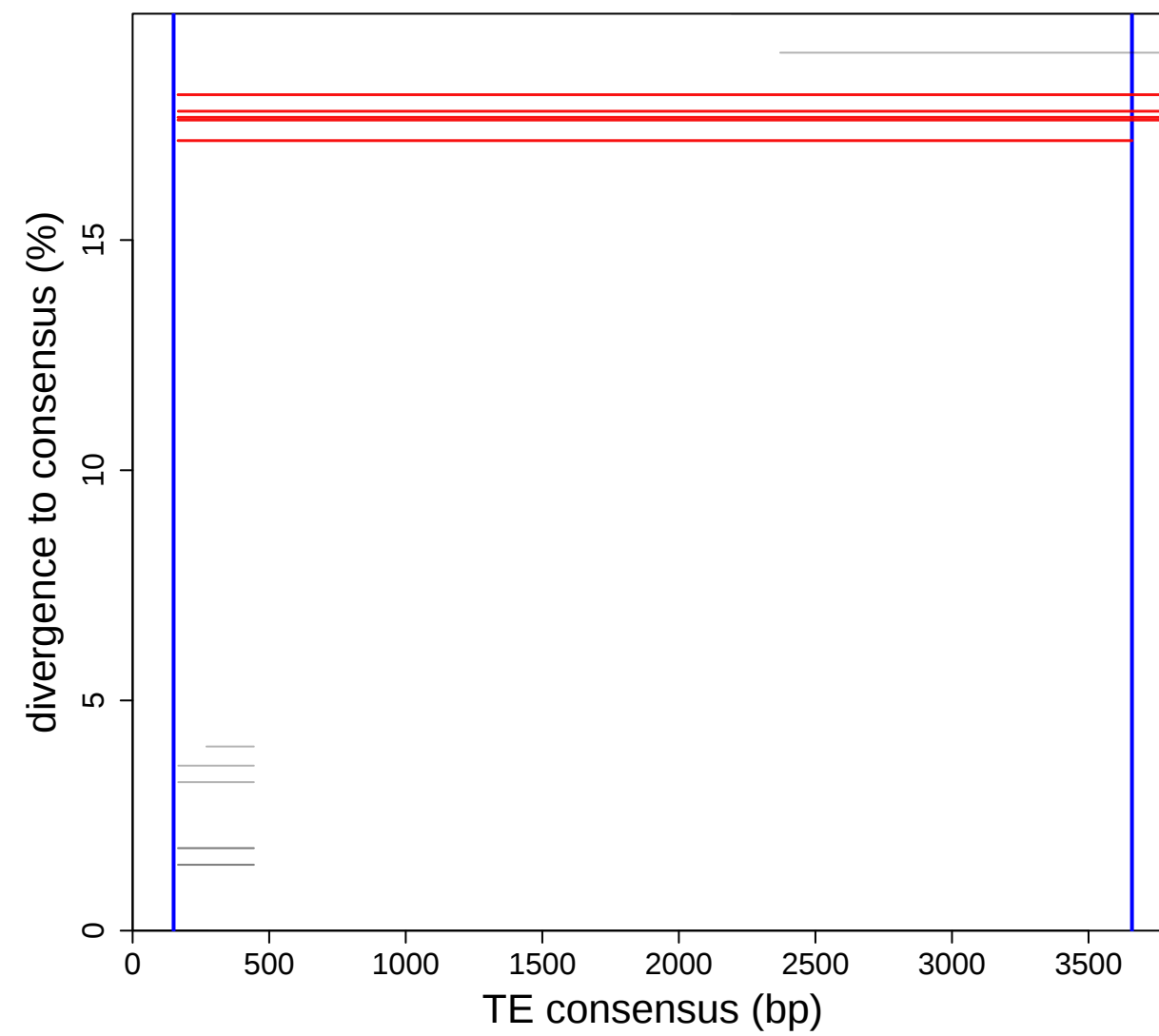
b.bed uf.bed g\_1.bed fm\_1.bed 0\_0\_bcln.fa aln.fa cl.fa gs.fa  
size: 3398bp; fragments: 18; full length: 5 ( $\geq 3058.2$ bp)

# After TEtrimmer 3398 bp

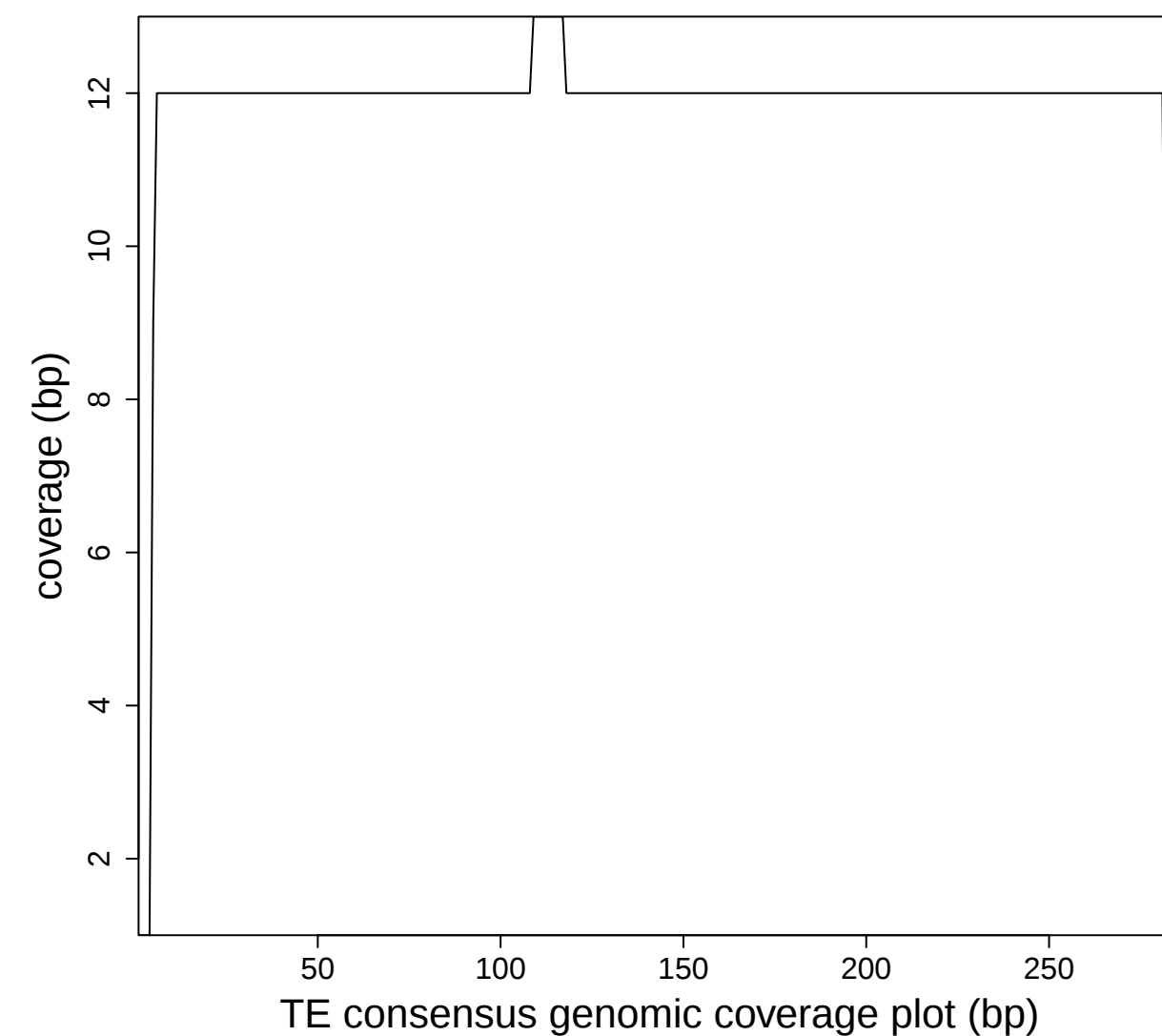
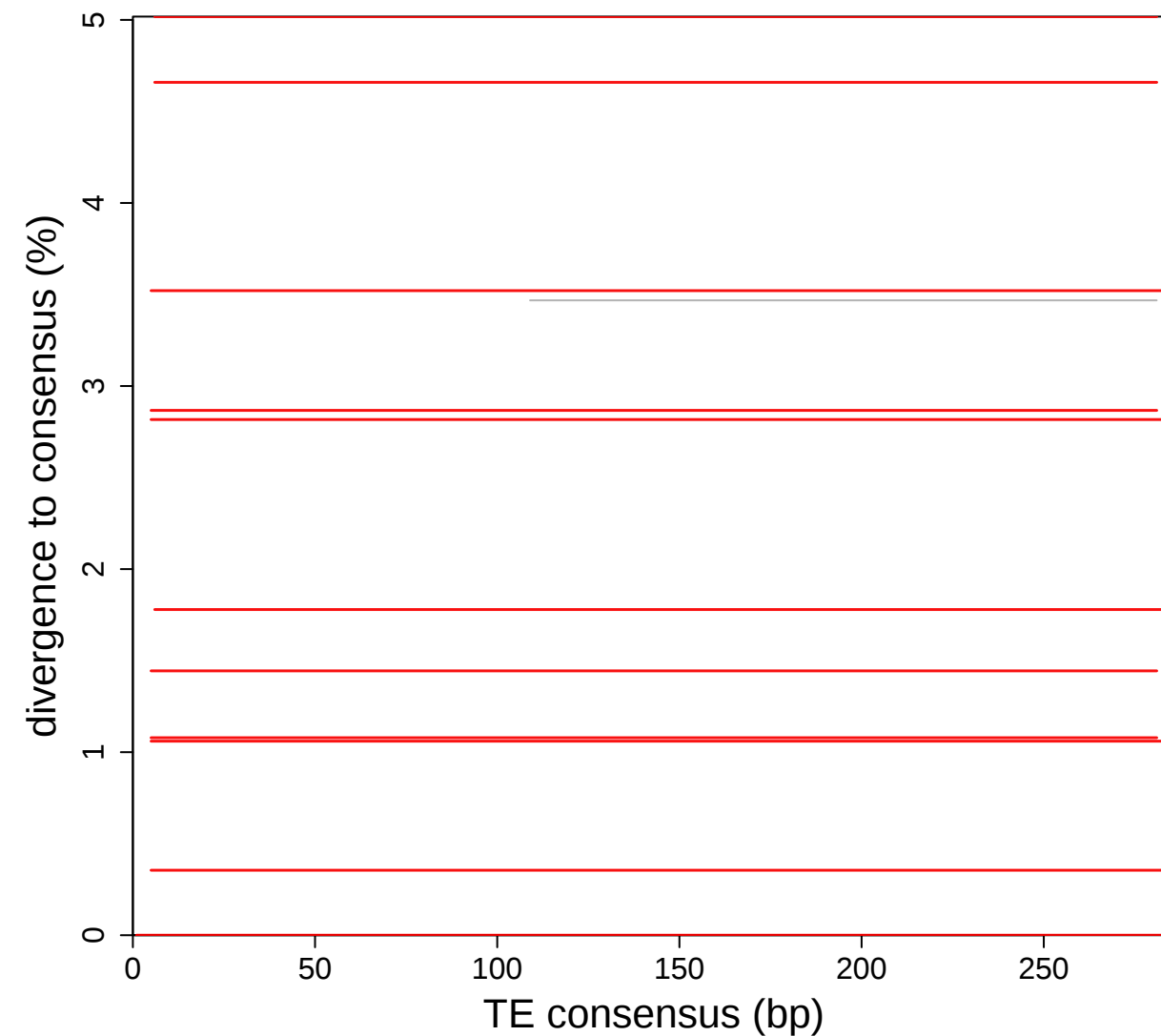


.fasta.b.bed\_uf.bed\_g\_1.bed\_fm\_1.bed\_0\_0\_bcln.fa\_aln.fa\_cl.fa  
size: 3809bp; fragments: 15; full length: 5 ( $\geq 3428.1$ bp)

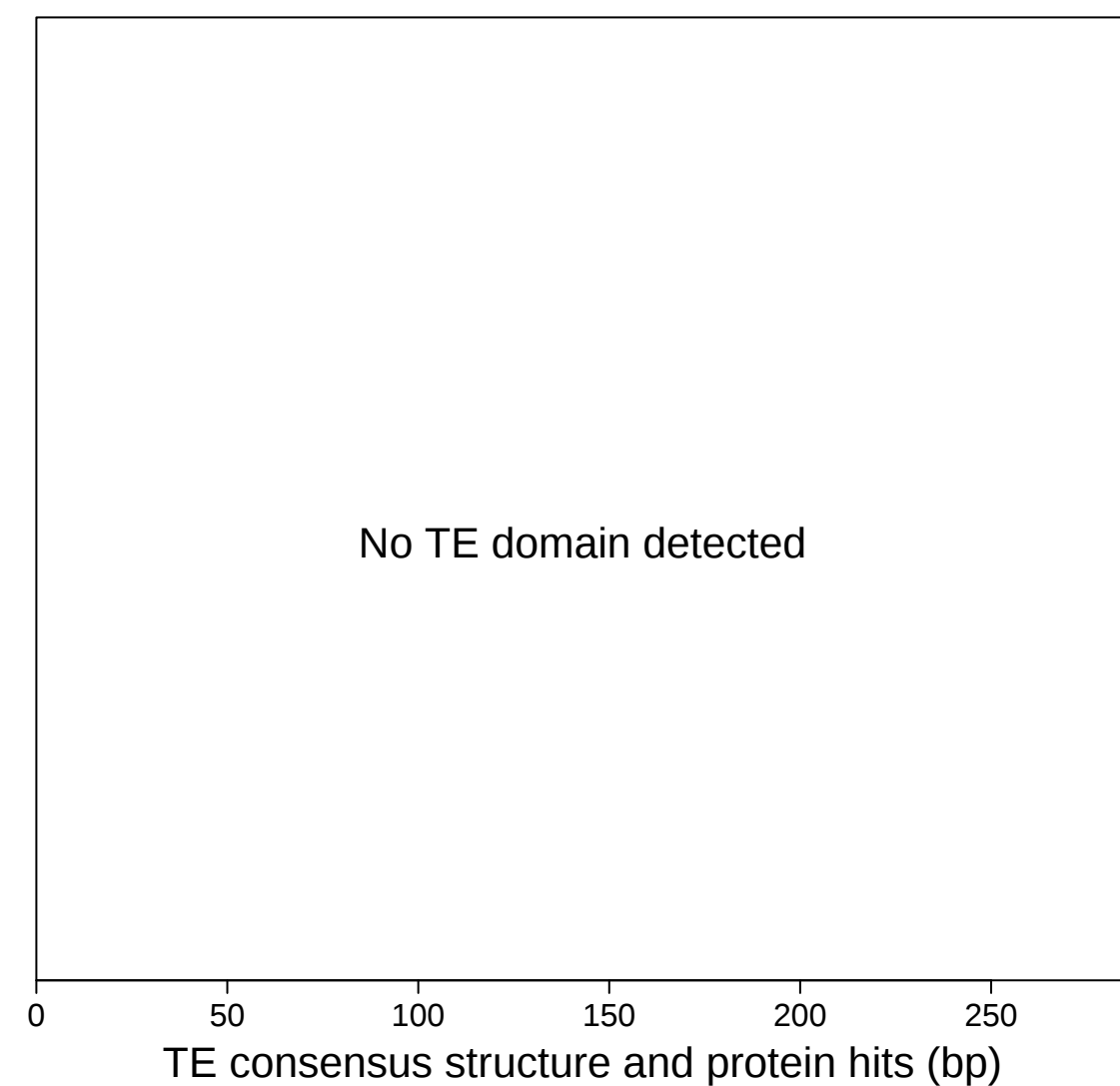
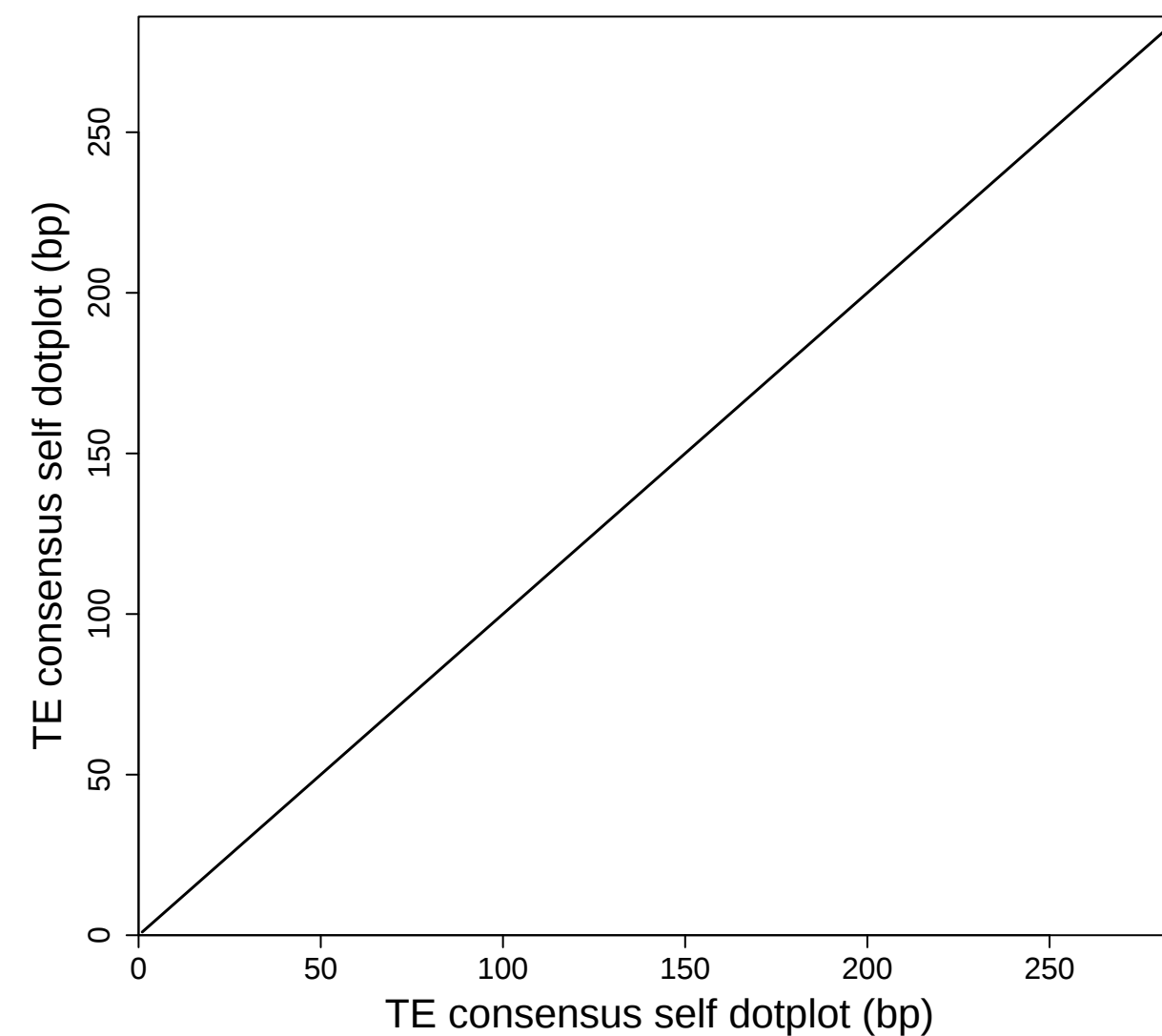
# After TEtrimmer Extended plot Blue lines are boundaries



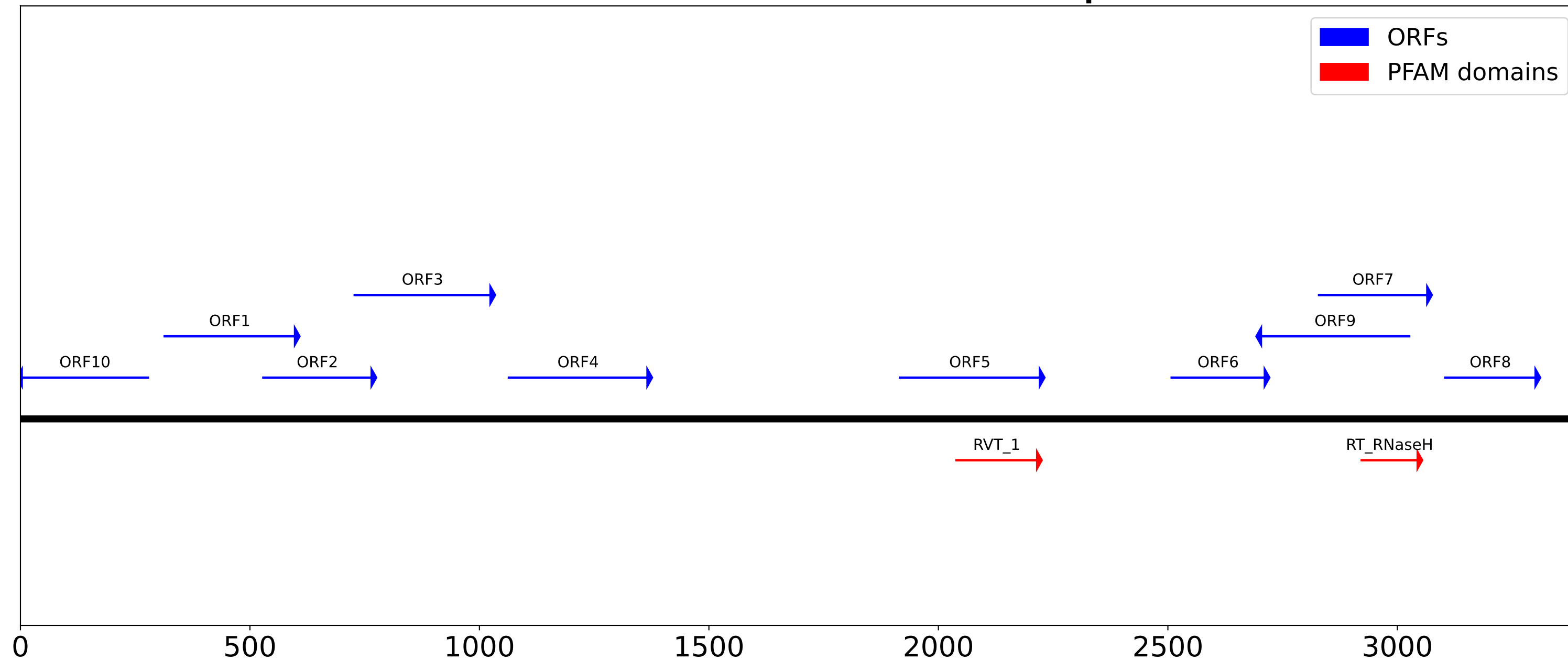
TE: ltr\_1\_family\_129  
size: 286bp; fragments: 13; full length: 11 ( $\geq 257.4$ bp)



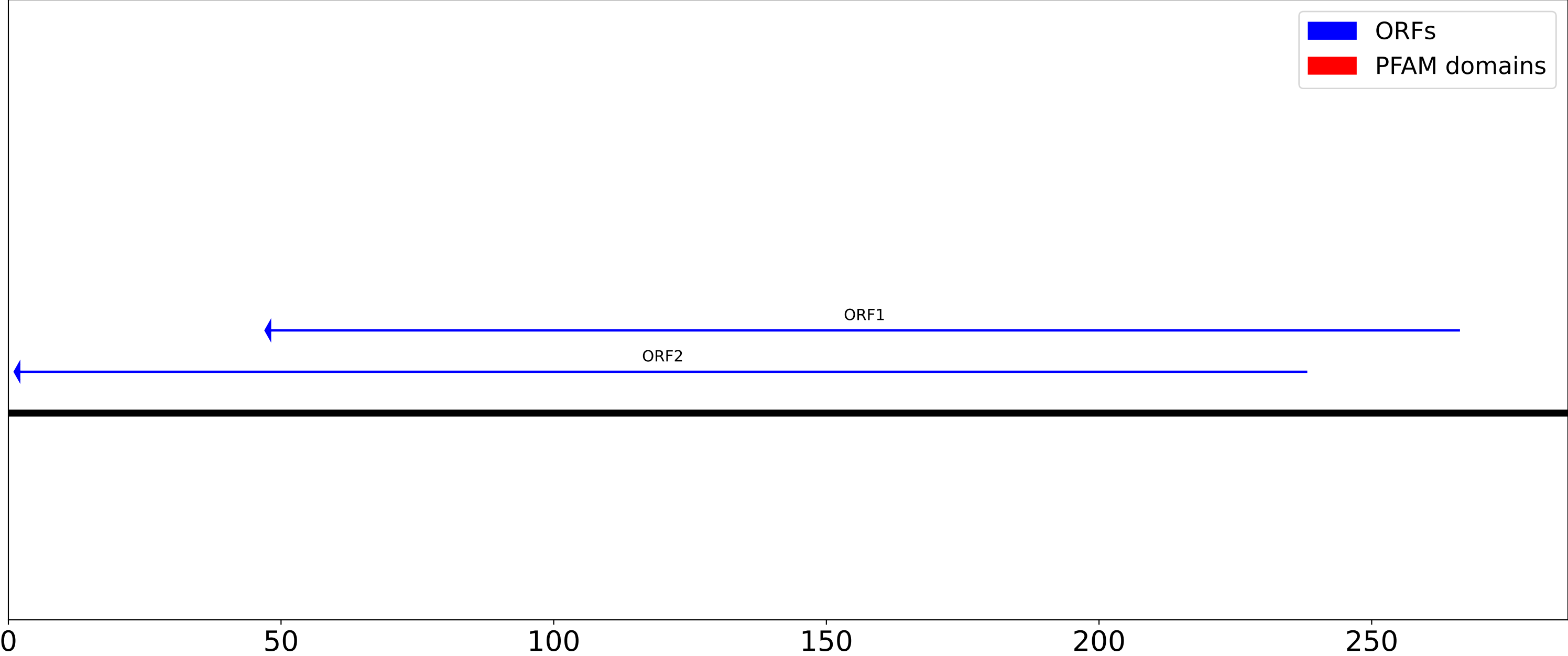
## Before TEtrimmer 286 bp



## After TEtrimmer ORF and PFAM domain plot



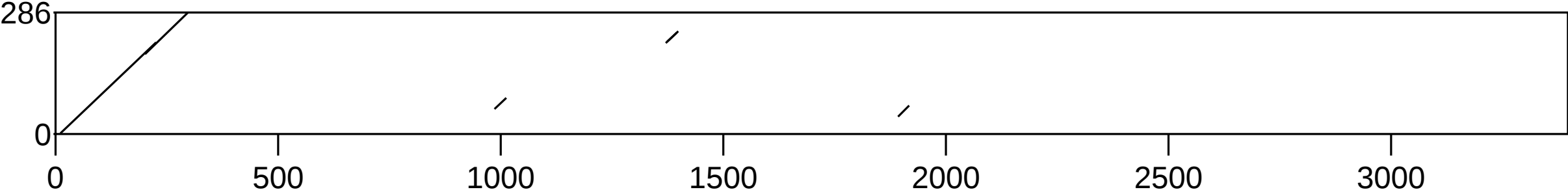
**Before TEtrimmer ORF and PFAM domain plot**



Dotplot

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

ensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)