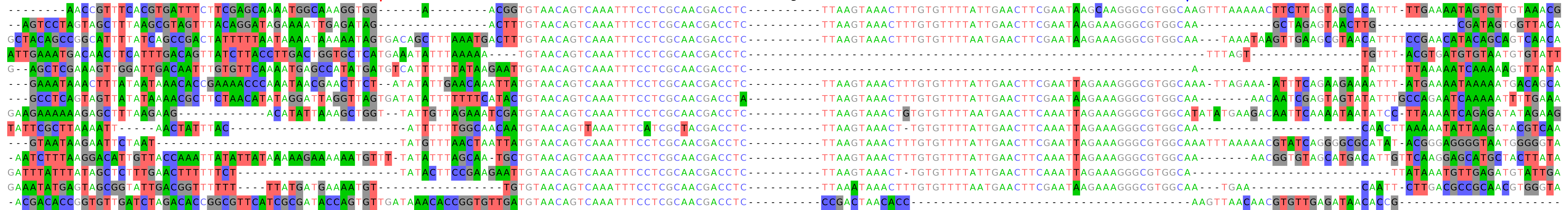


Start crop Point

End crop Point

MSA length = 1964



Start crop Point

End crop Point

0

10

0

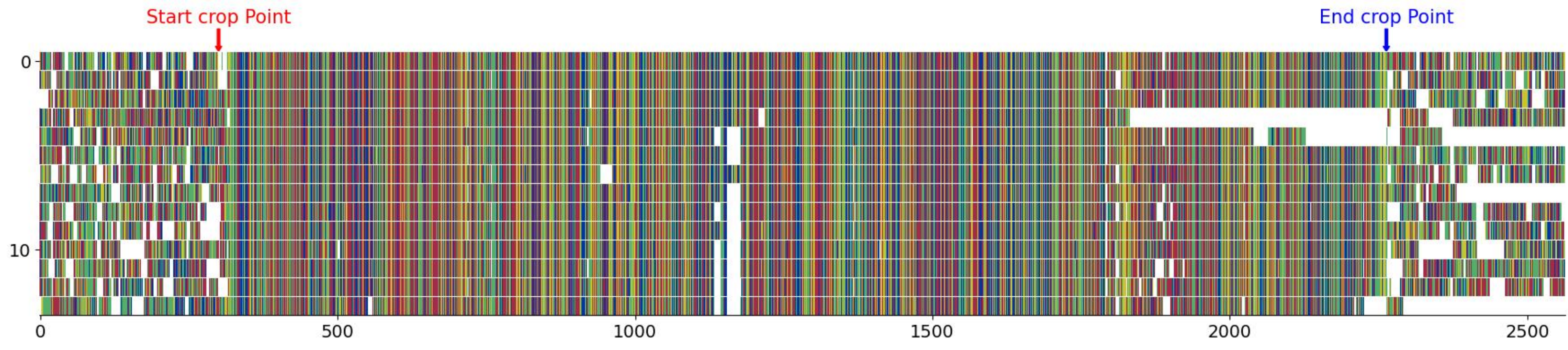
500

1000

1500

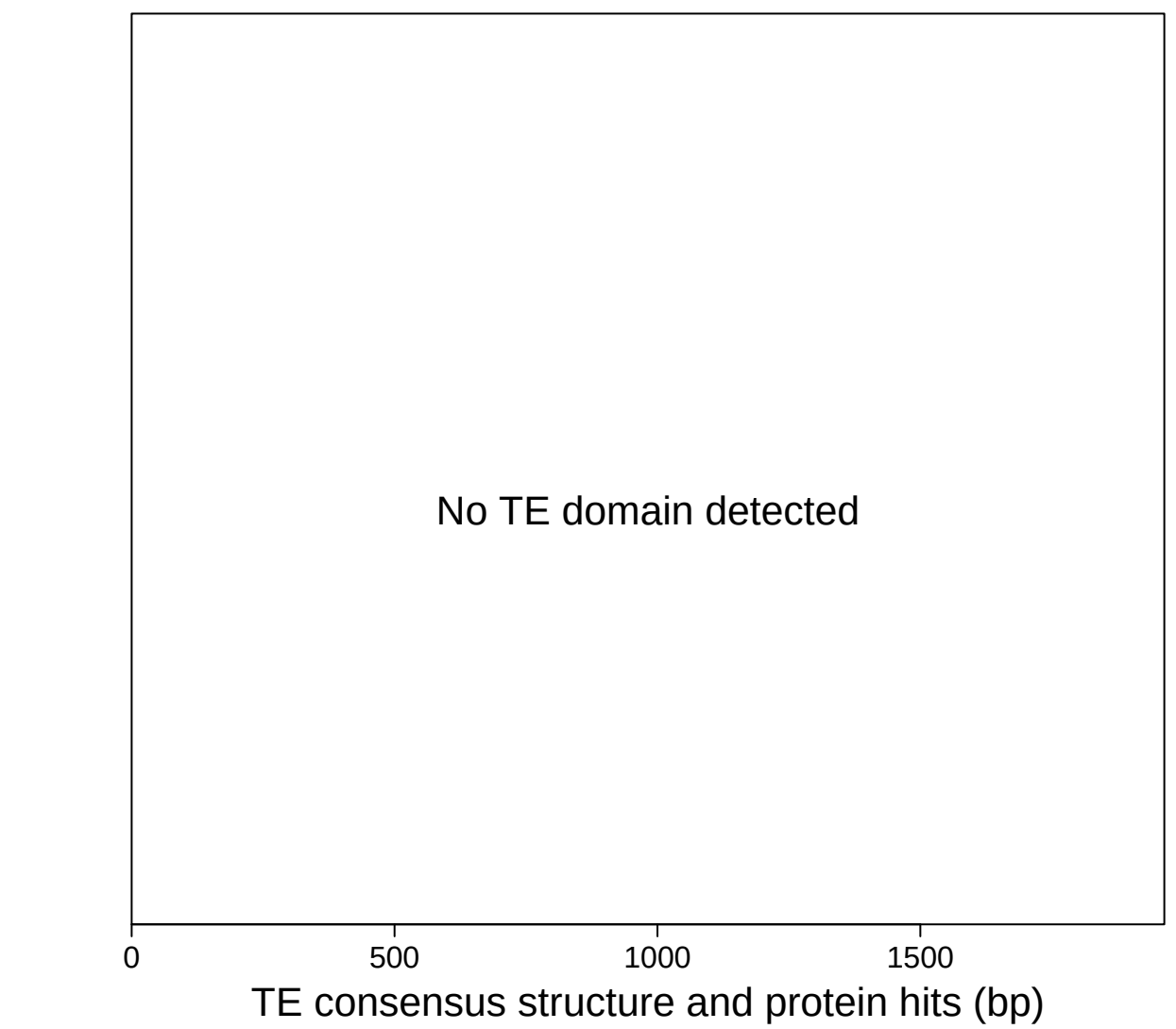
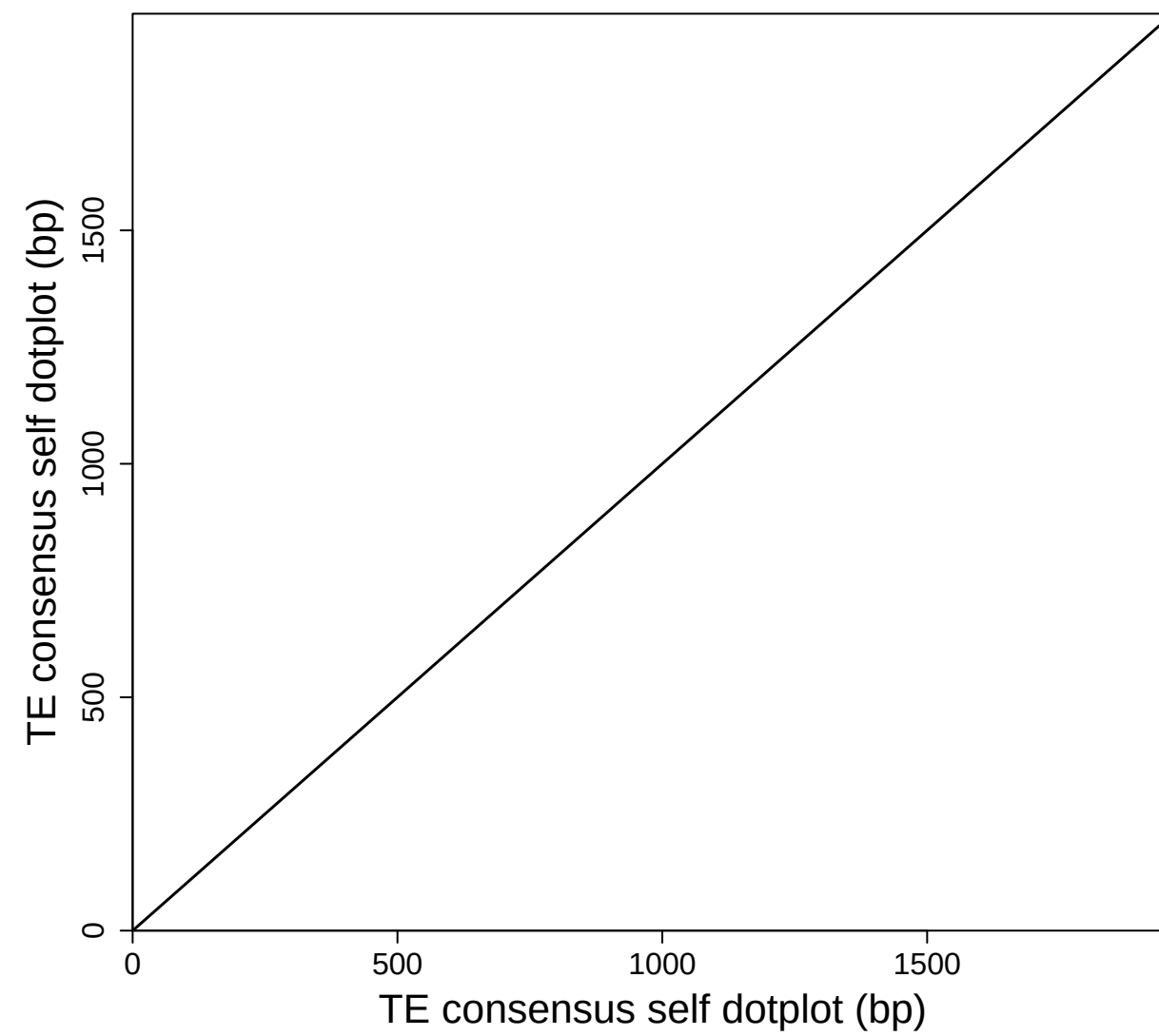
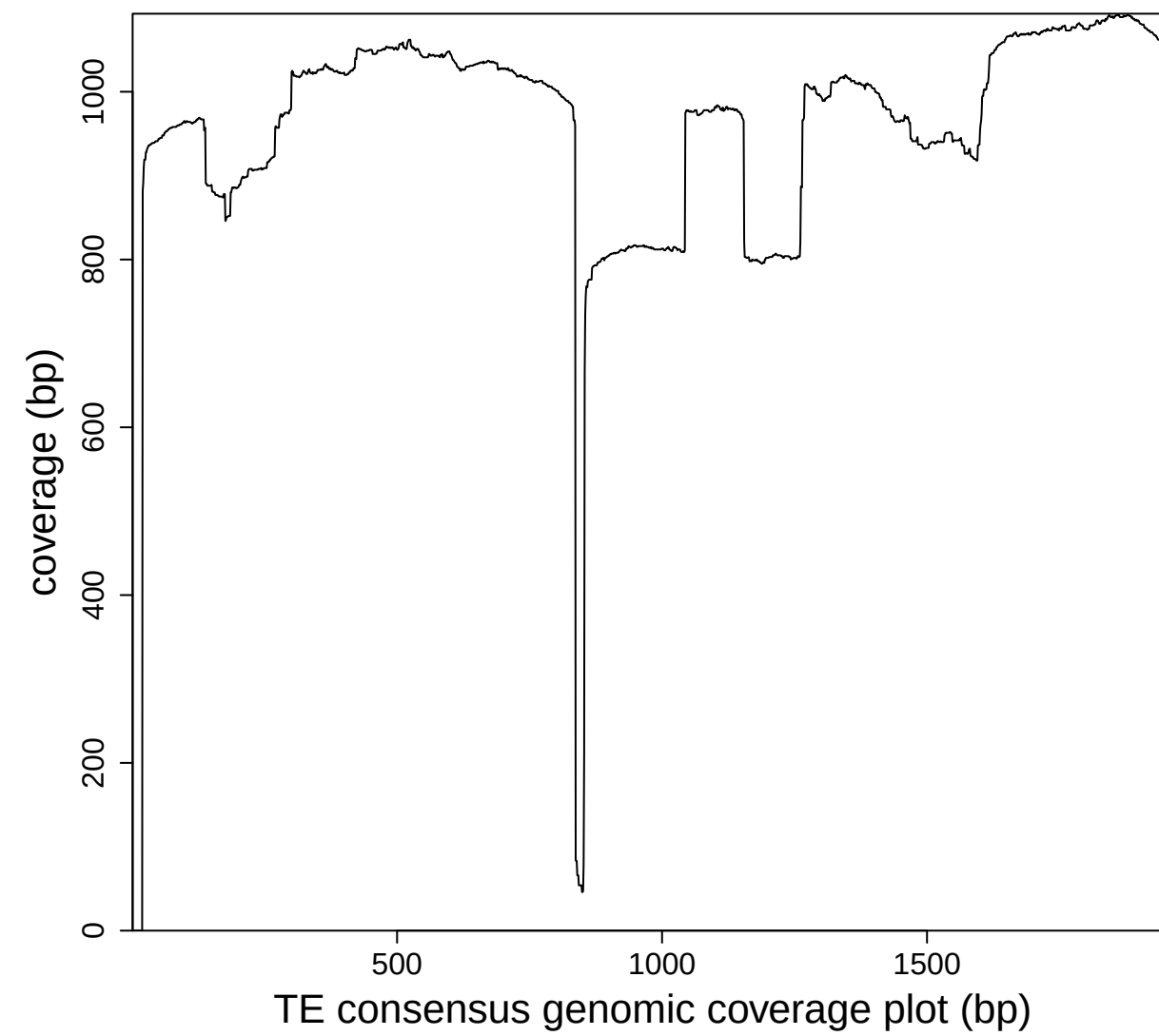
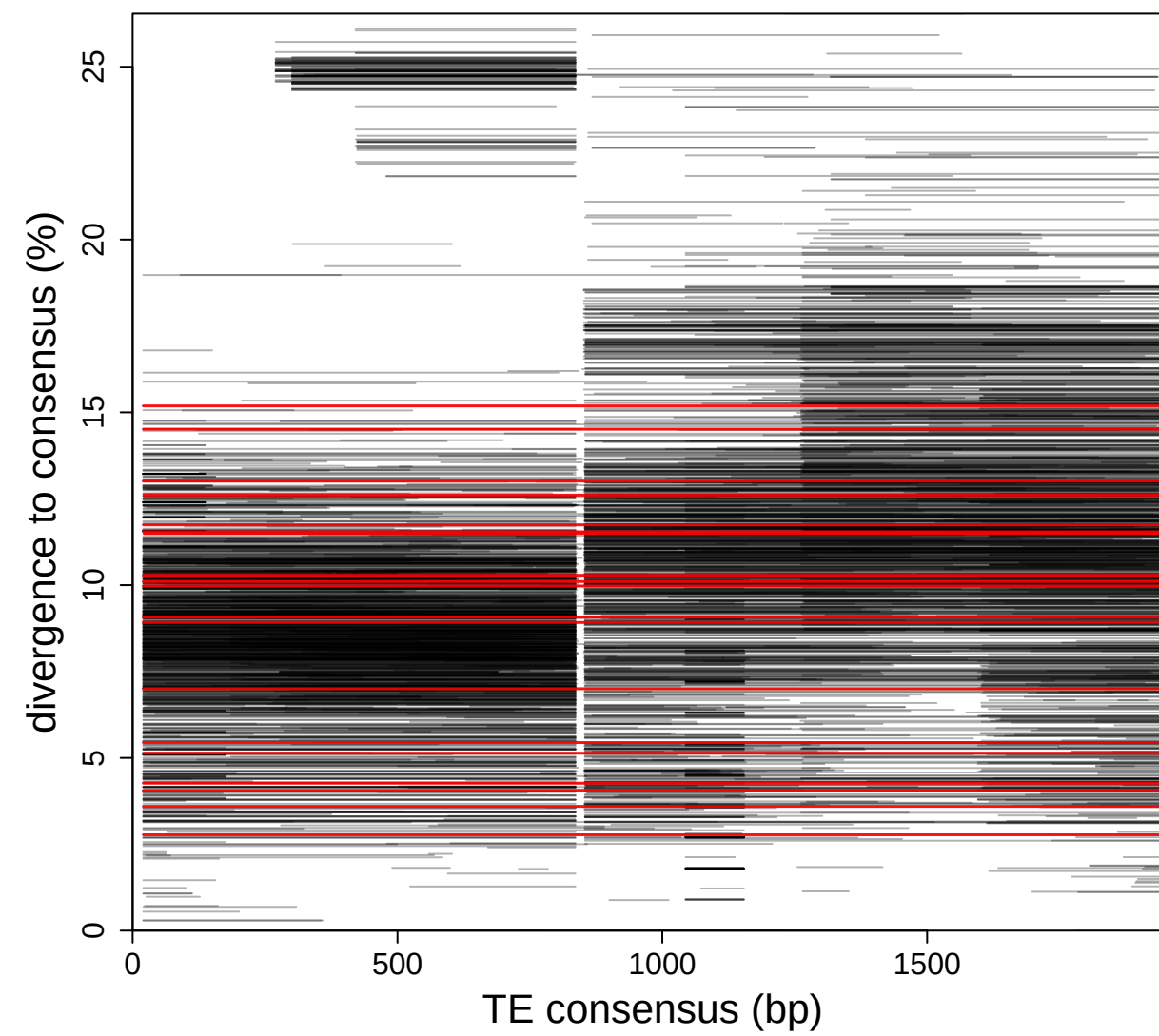
2000

2500



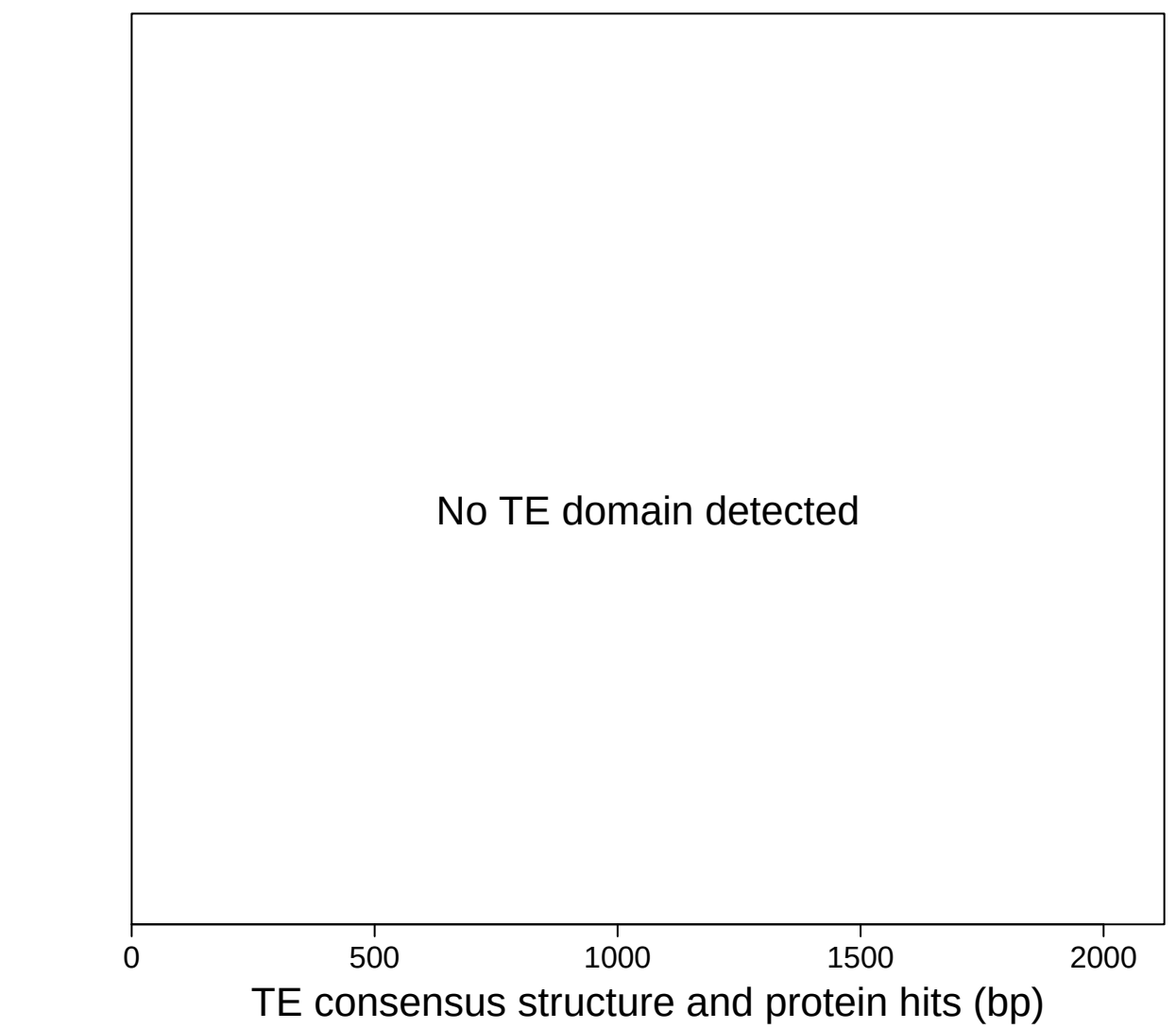
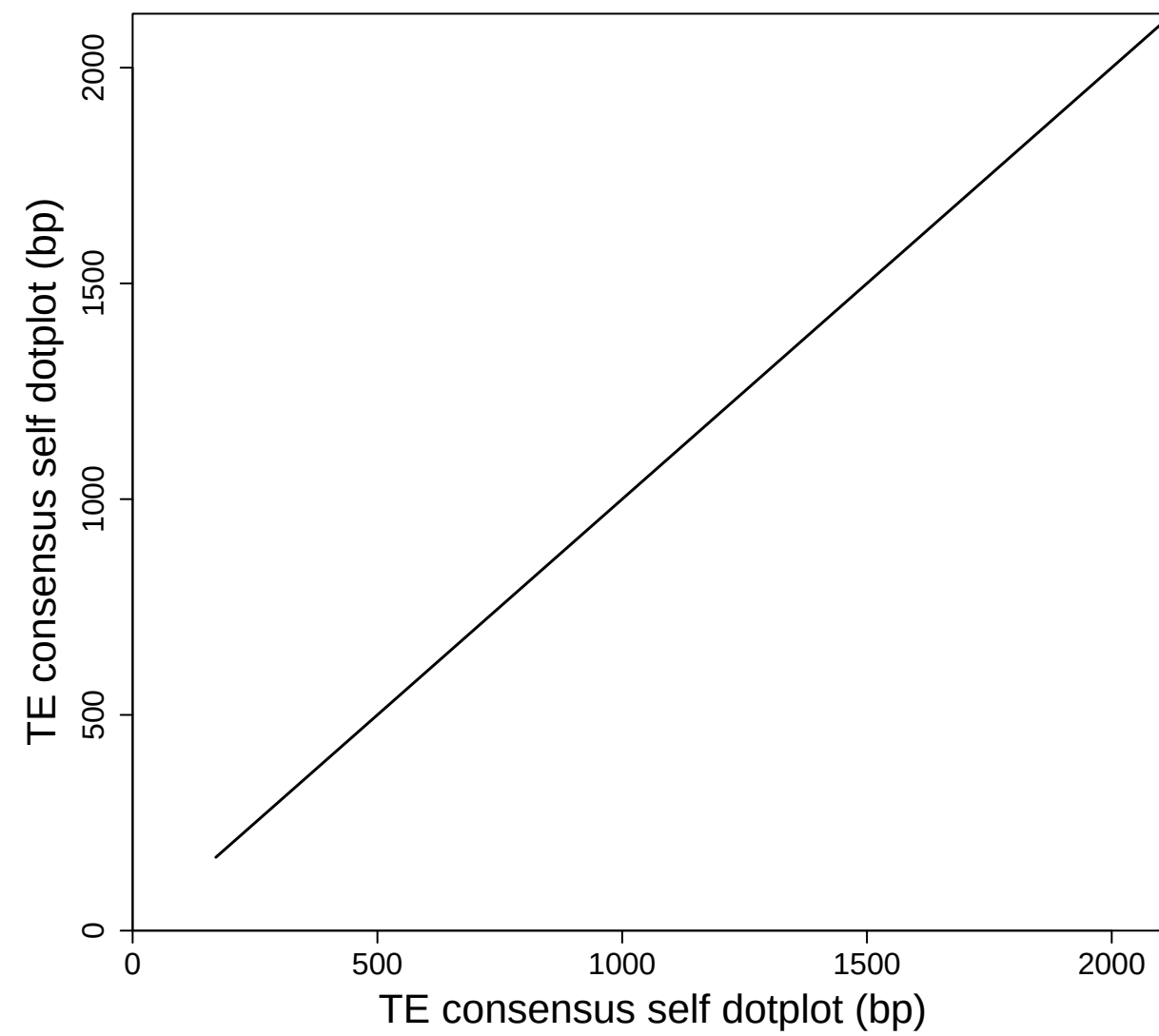
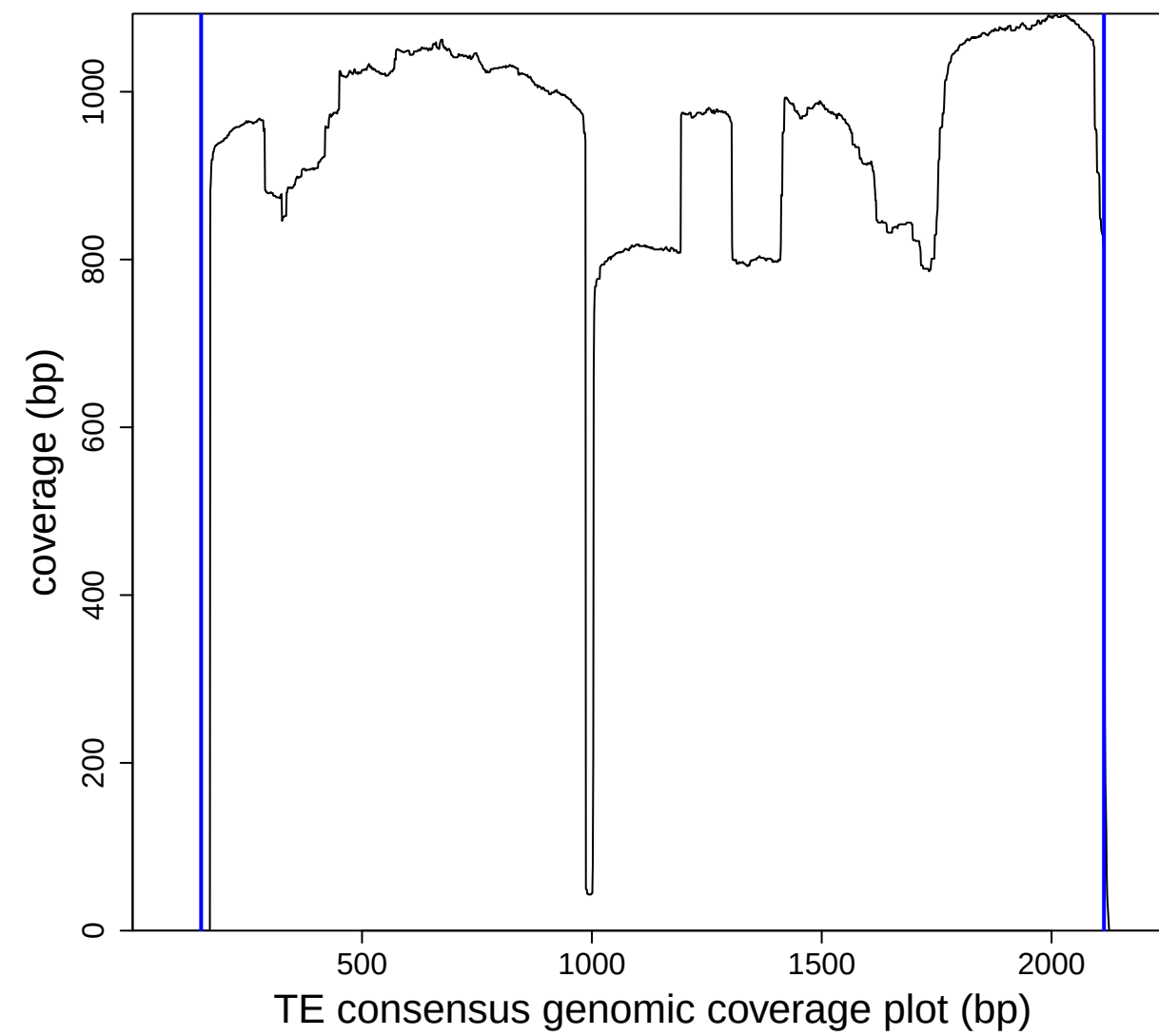
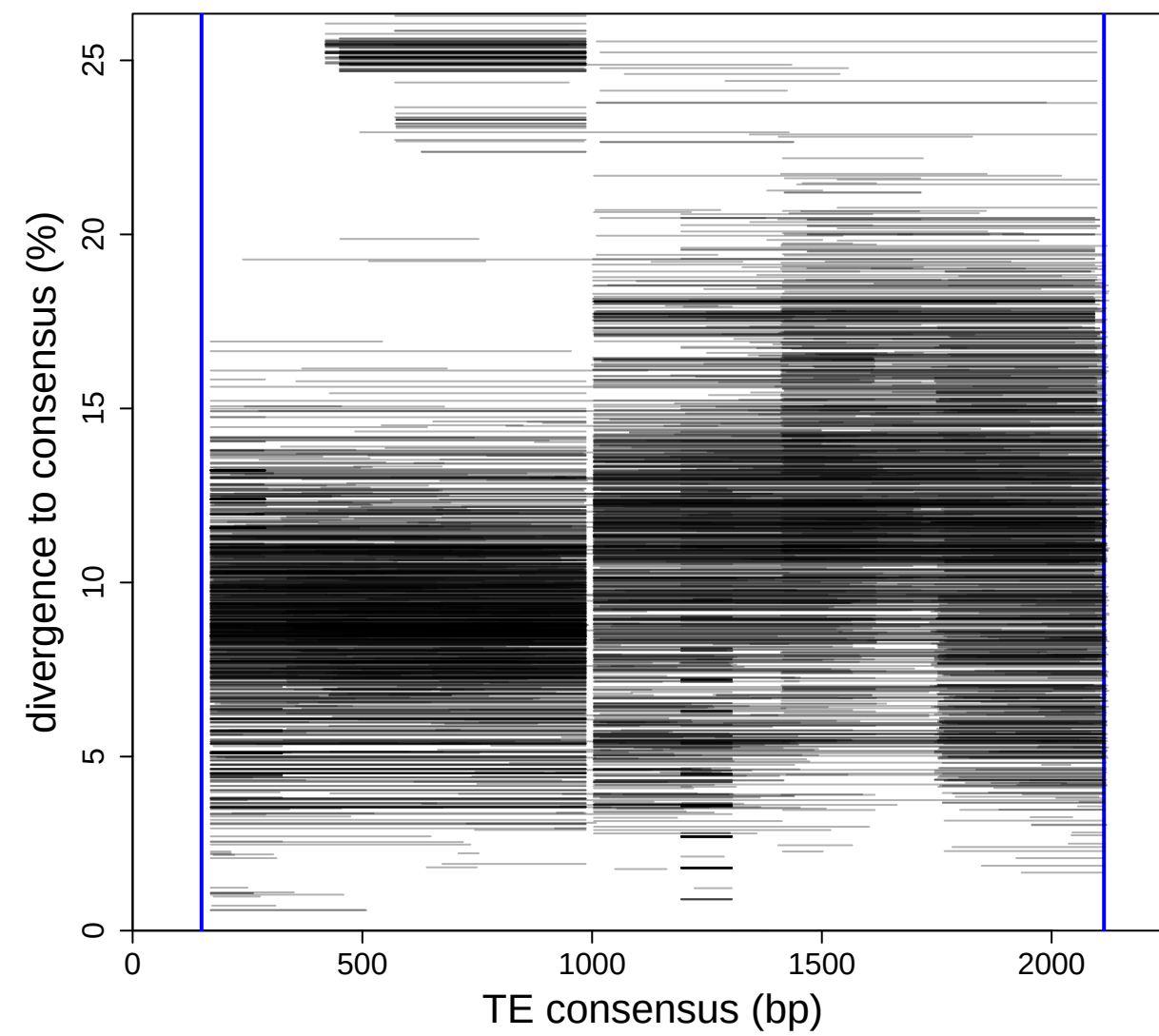
l.b.bed uf.bed g\_2.bed fm\_1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa  
size: 1964bp; fragments: 3039; full length: 19 (>=1767.6bp)

# After TEtrimmer 1964 bp



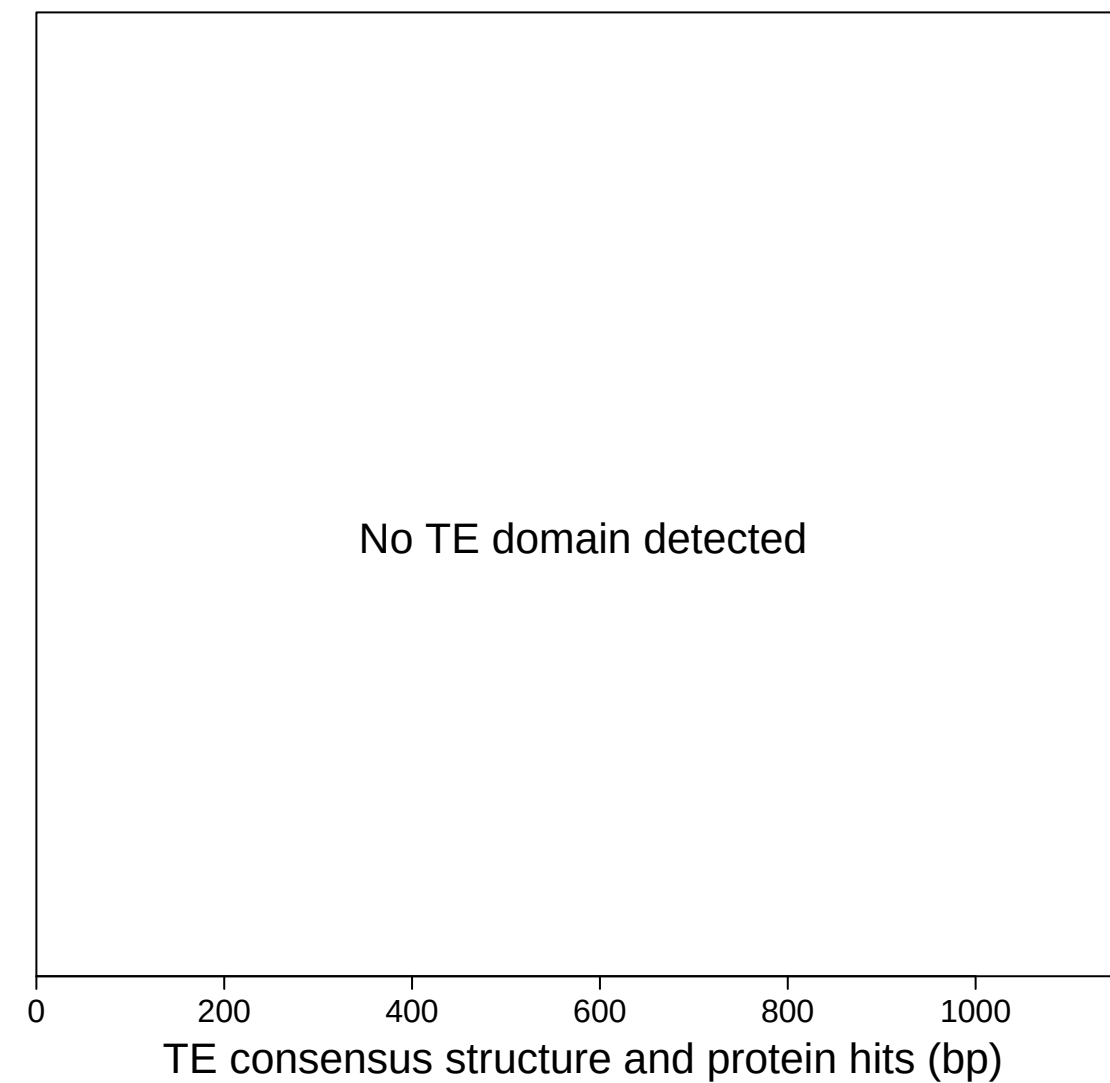
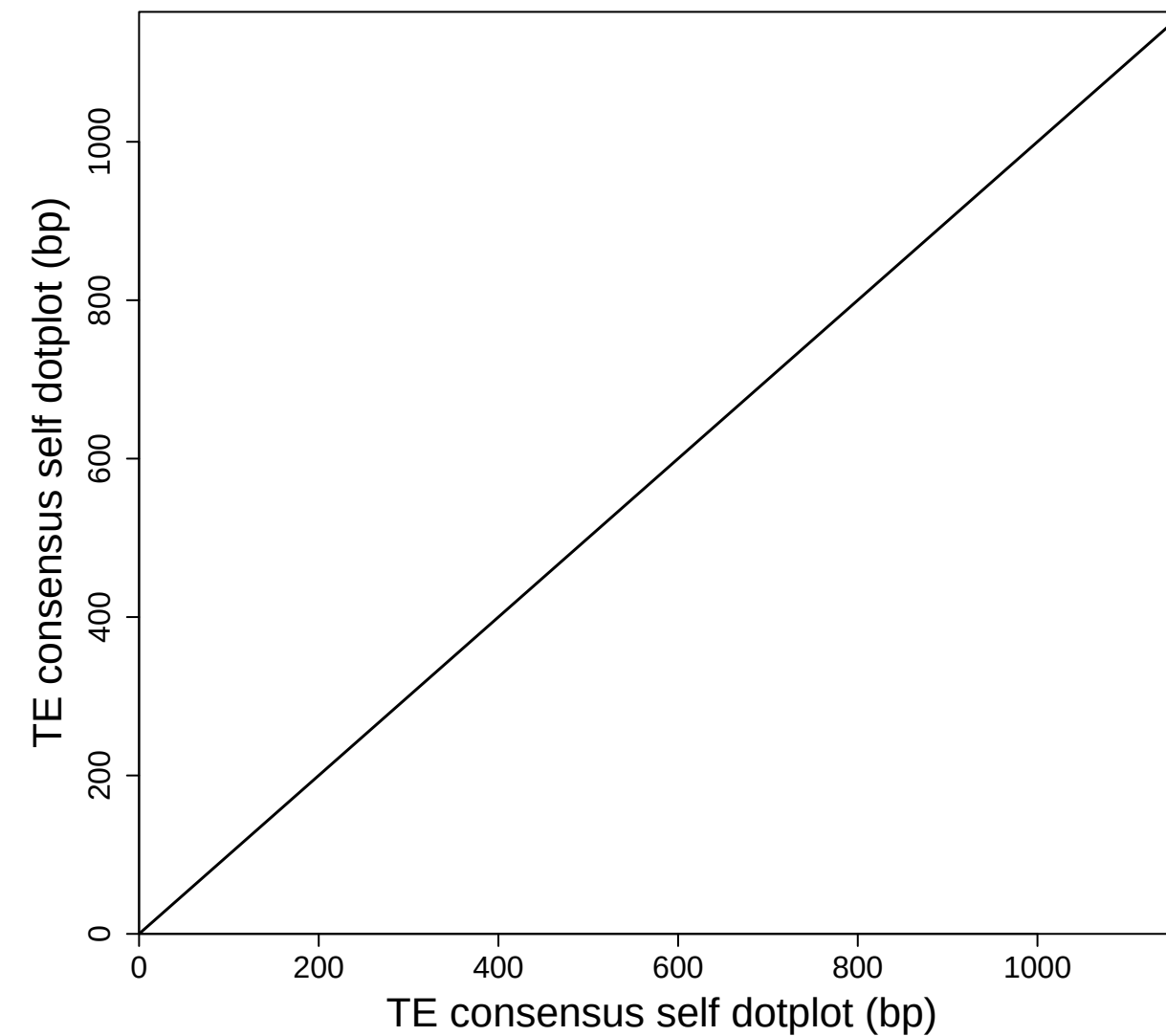
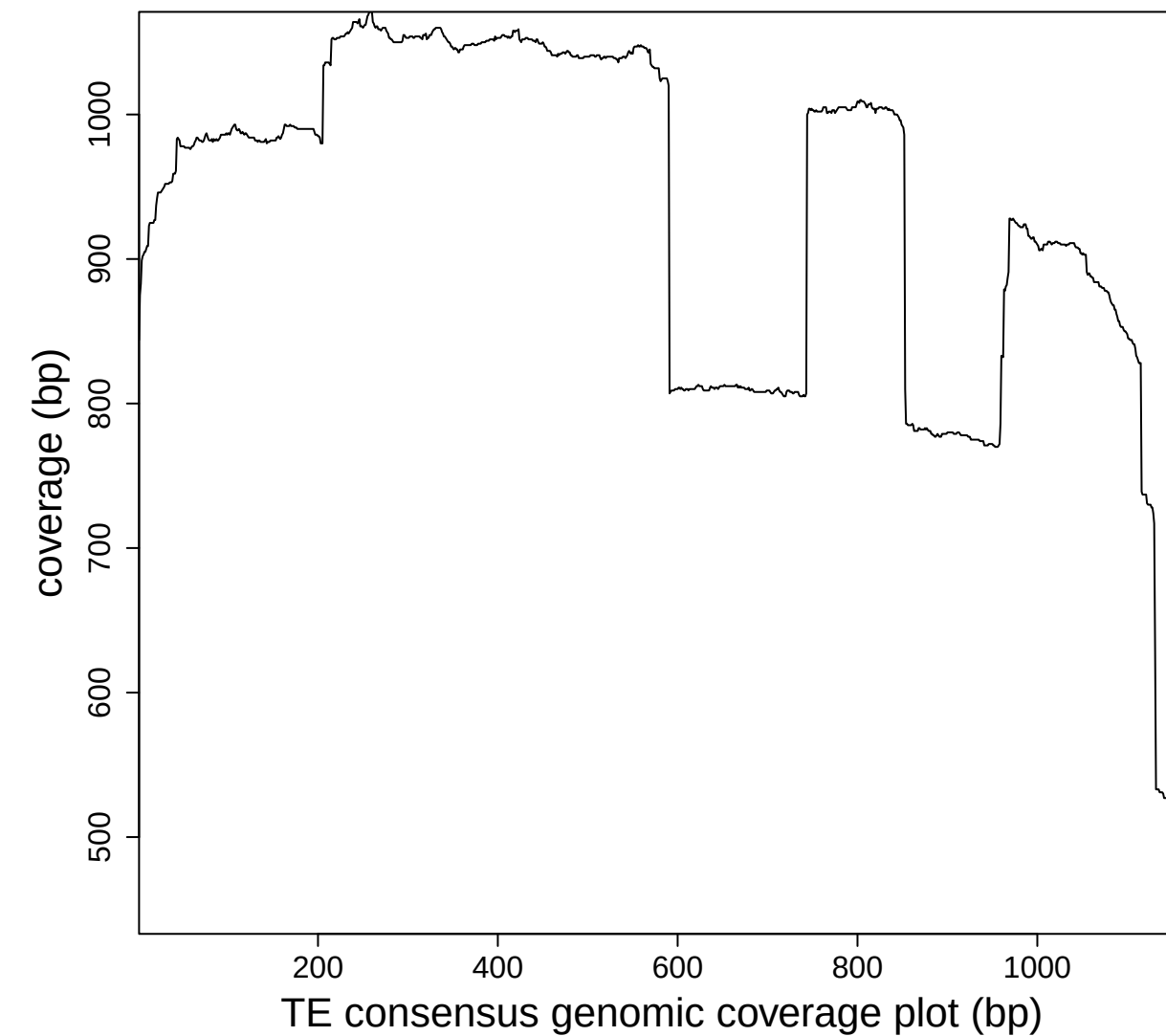
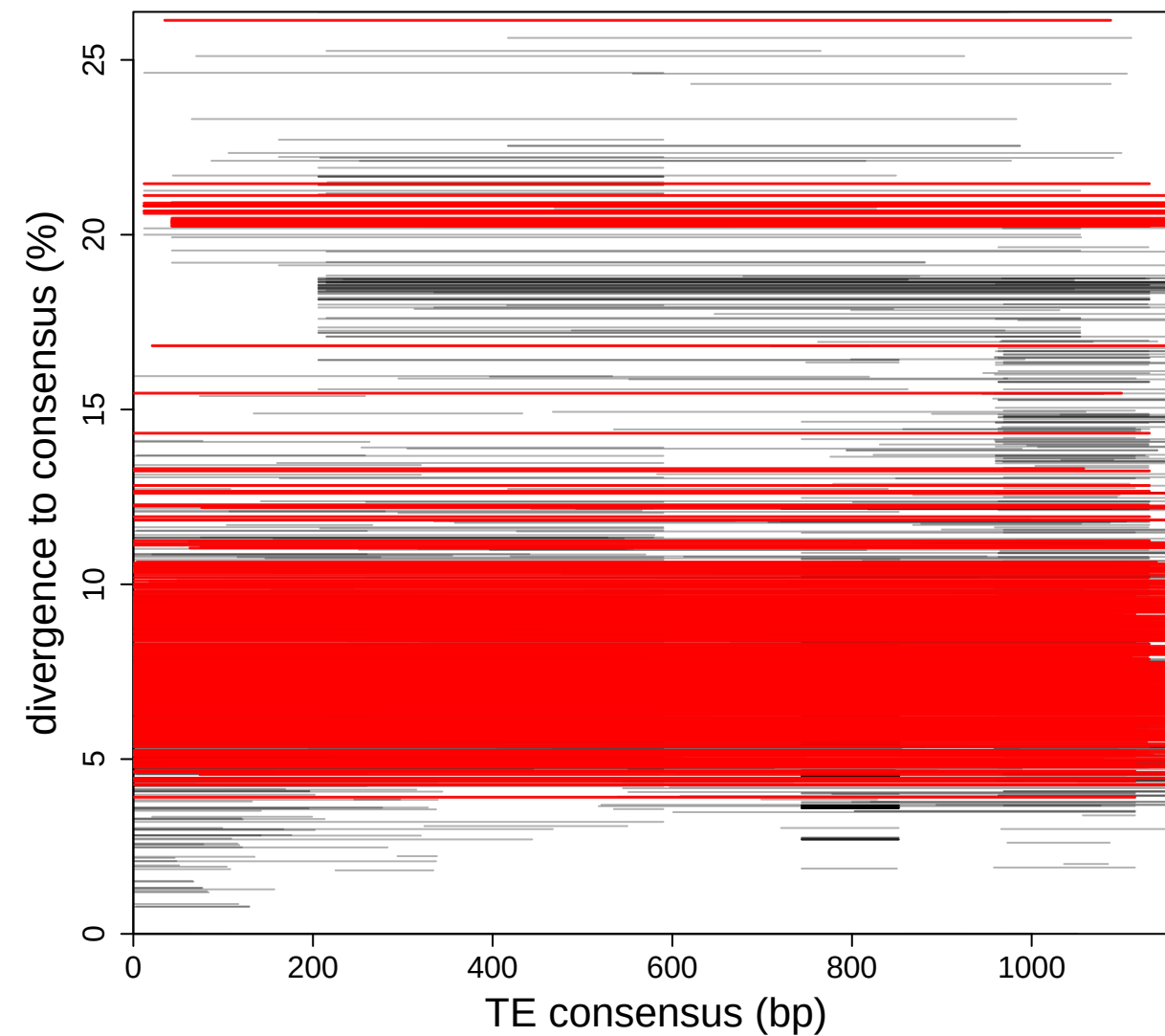
5.fasta.b.bed uf.bed g 2.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa  
size: 2264bp; fragments: 3083; full length: 0 (>=2037.6bp)

# After TEtrimmer Extended plot Blue lines are boundaries

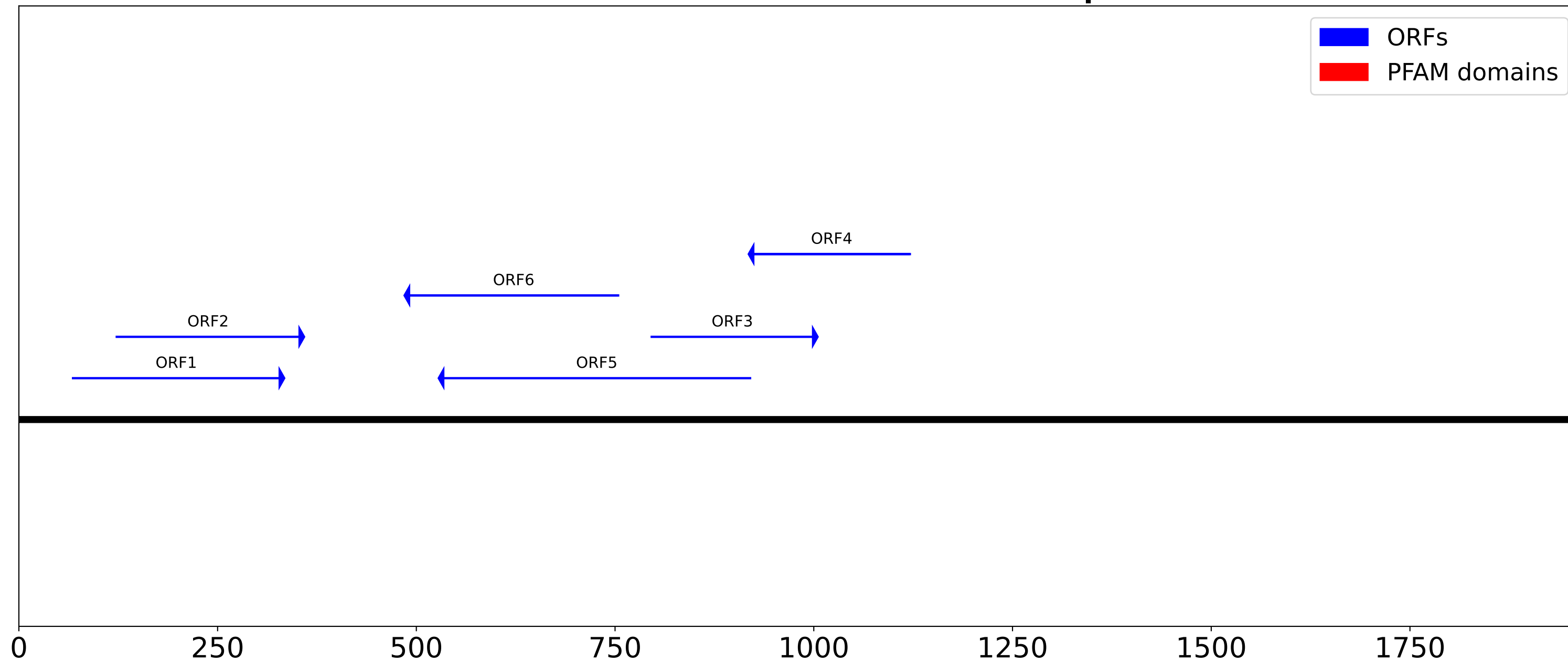


TE: rnd\_1\_family\_625  
size: 1164bp; fragments: 1742; full length: 470 ( $\geq 1047.6$ bp)

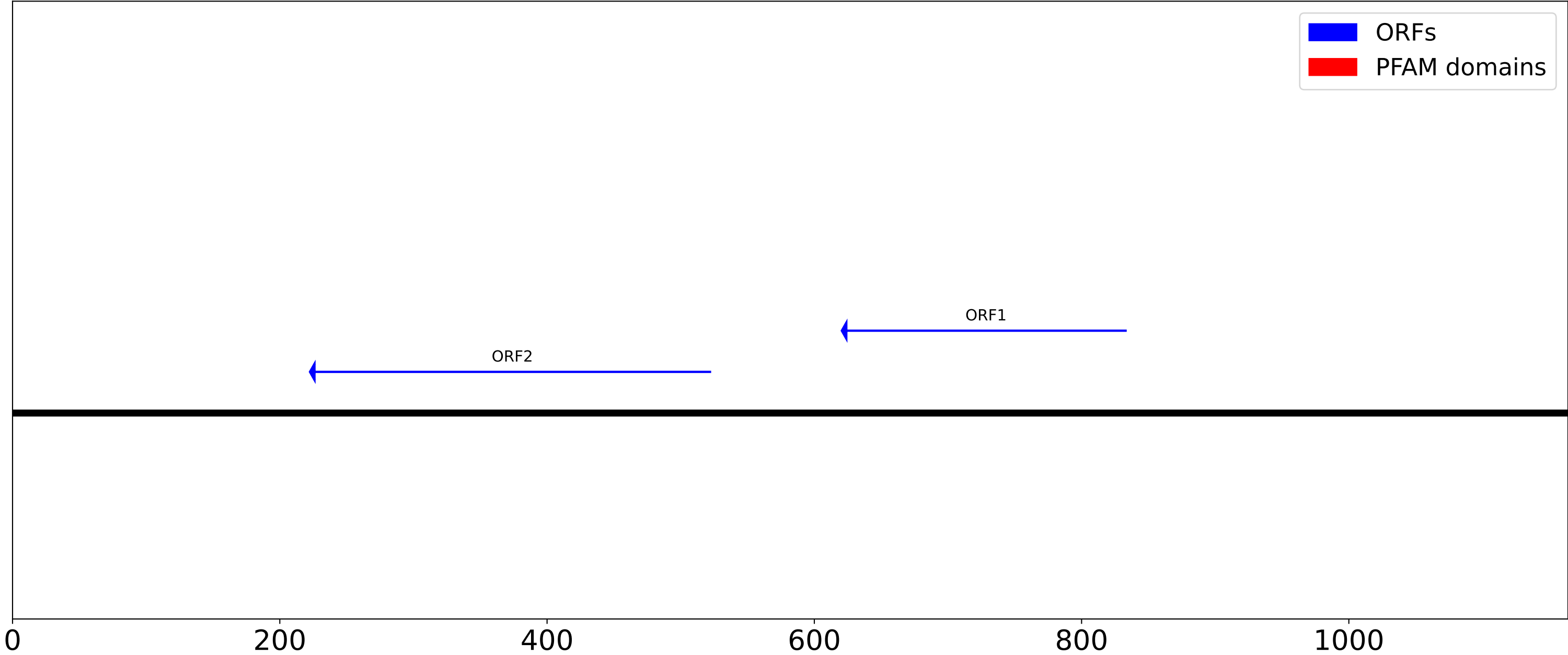
## Before TEtrimmer 1164 bp



## After TEtrimmer ORF and PFAM domain plot



**Before TEtrimmer ORF and PFAM domain plot**

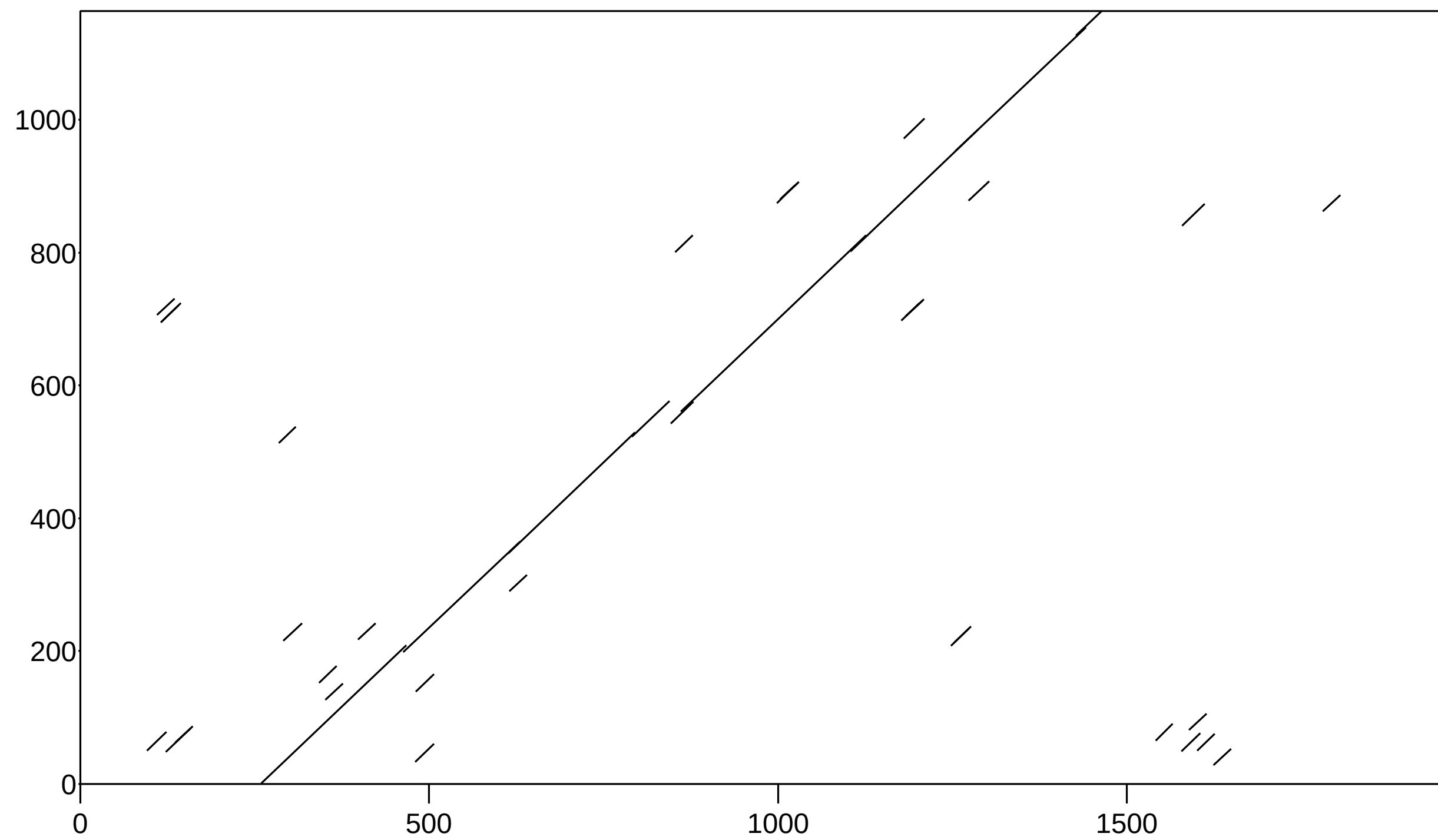




# Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)