

Start crop Point



MSA length = 6630

End crop Point



Start crop Point

End crop Point

0 -

10 -

0

1000

2000

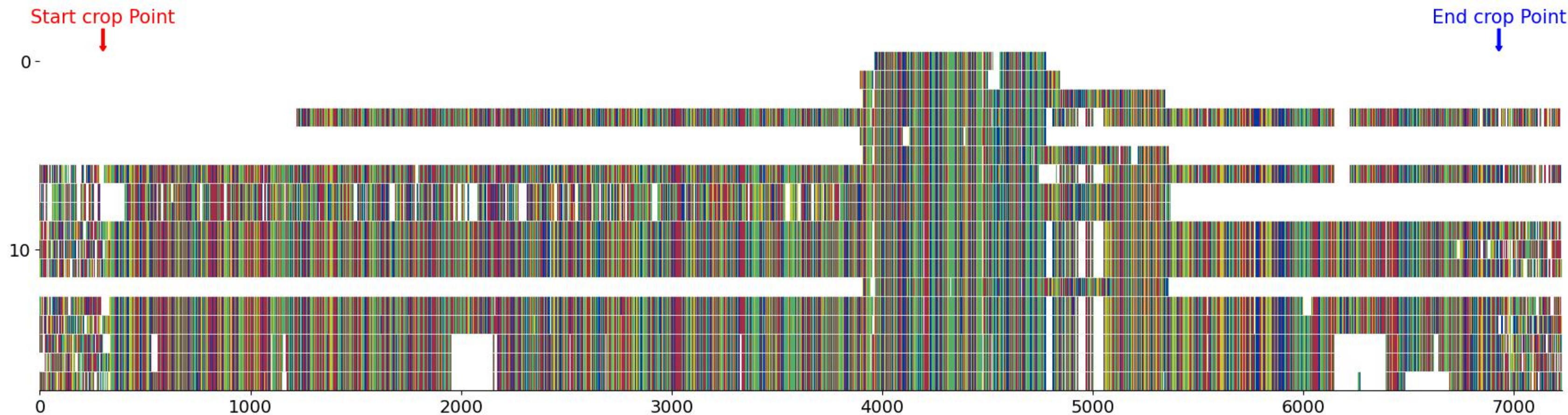
3000

4000

5000

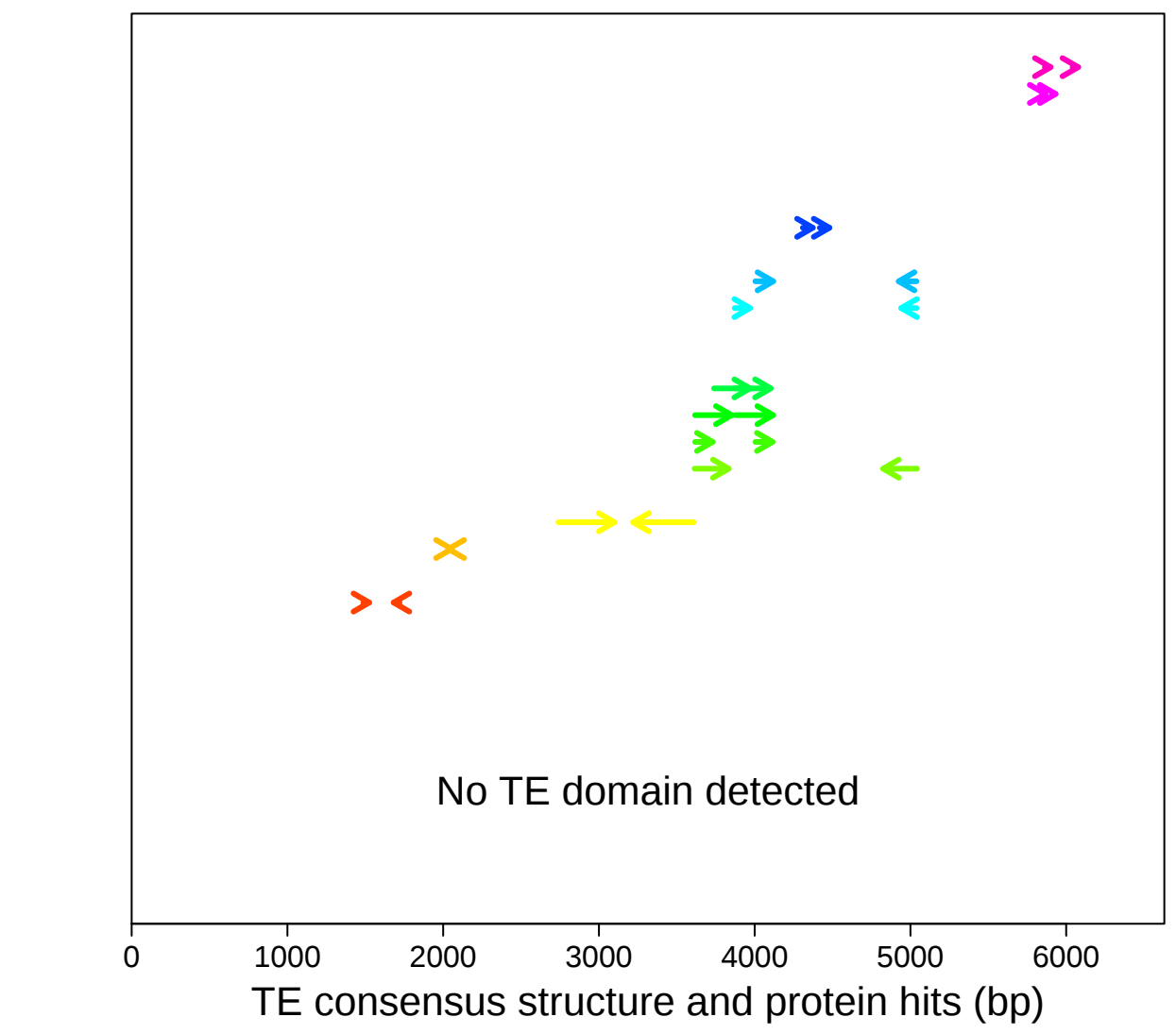
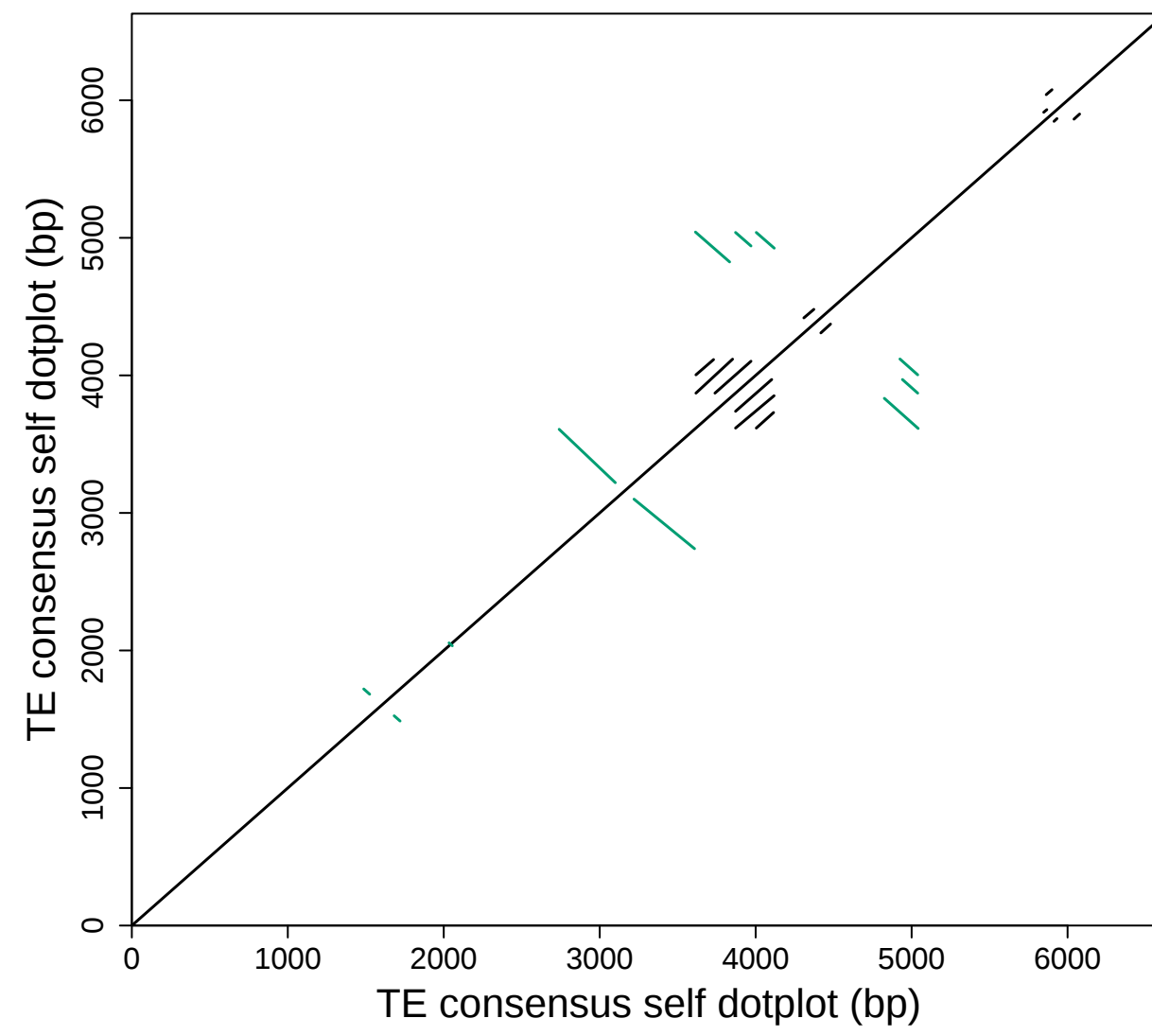
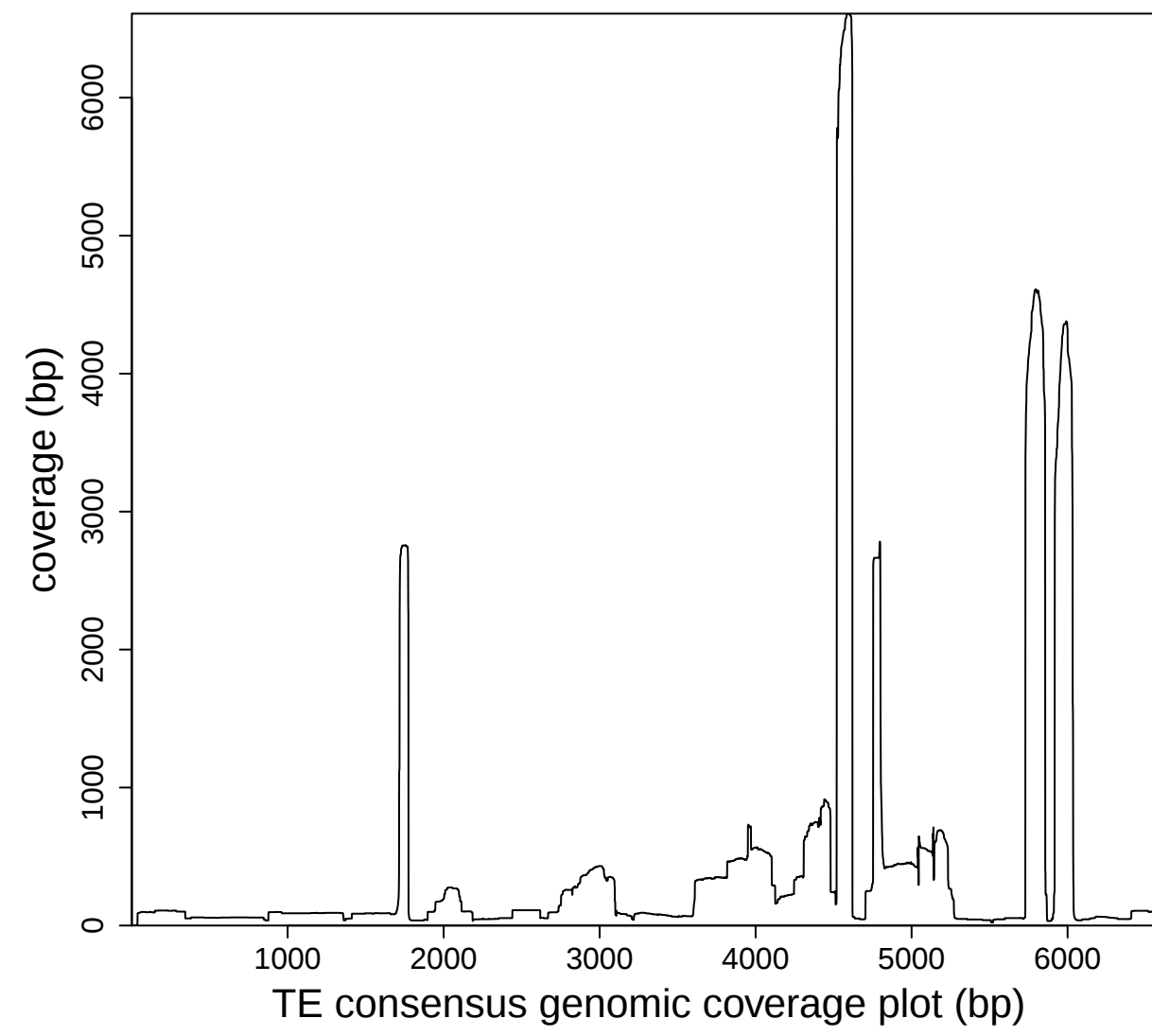
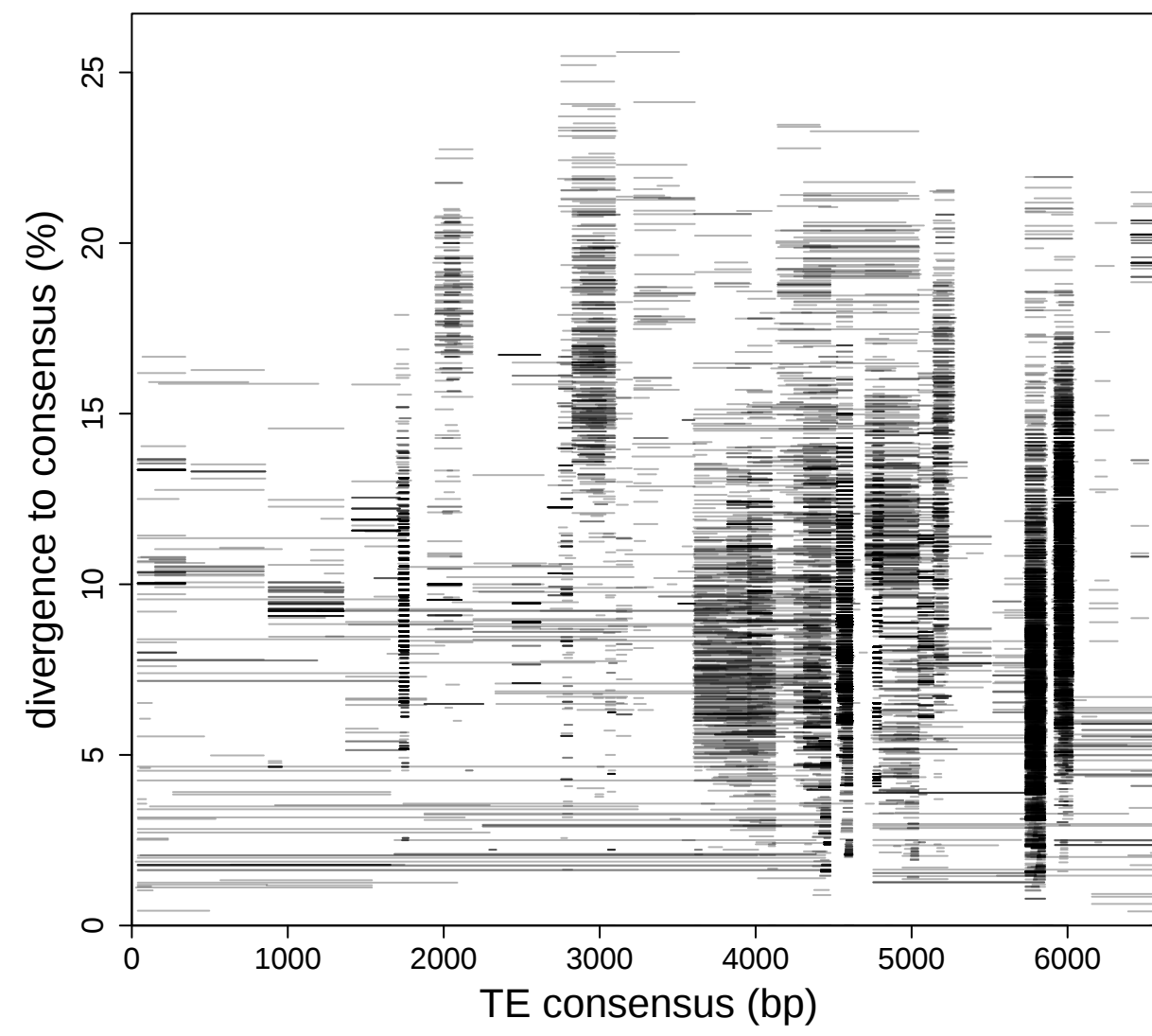
6000

7000



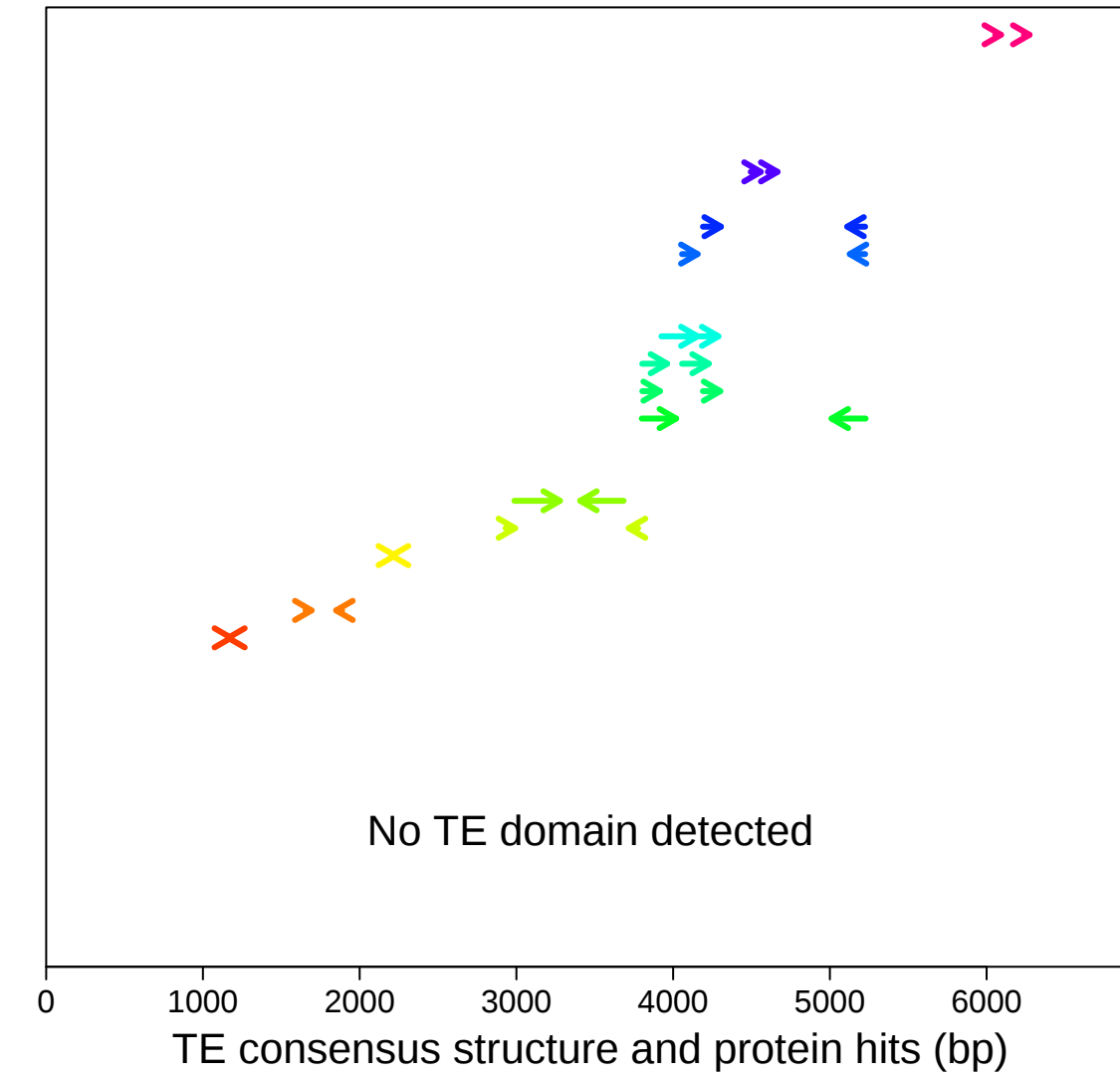
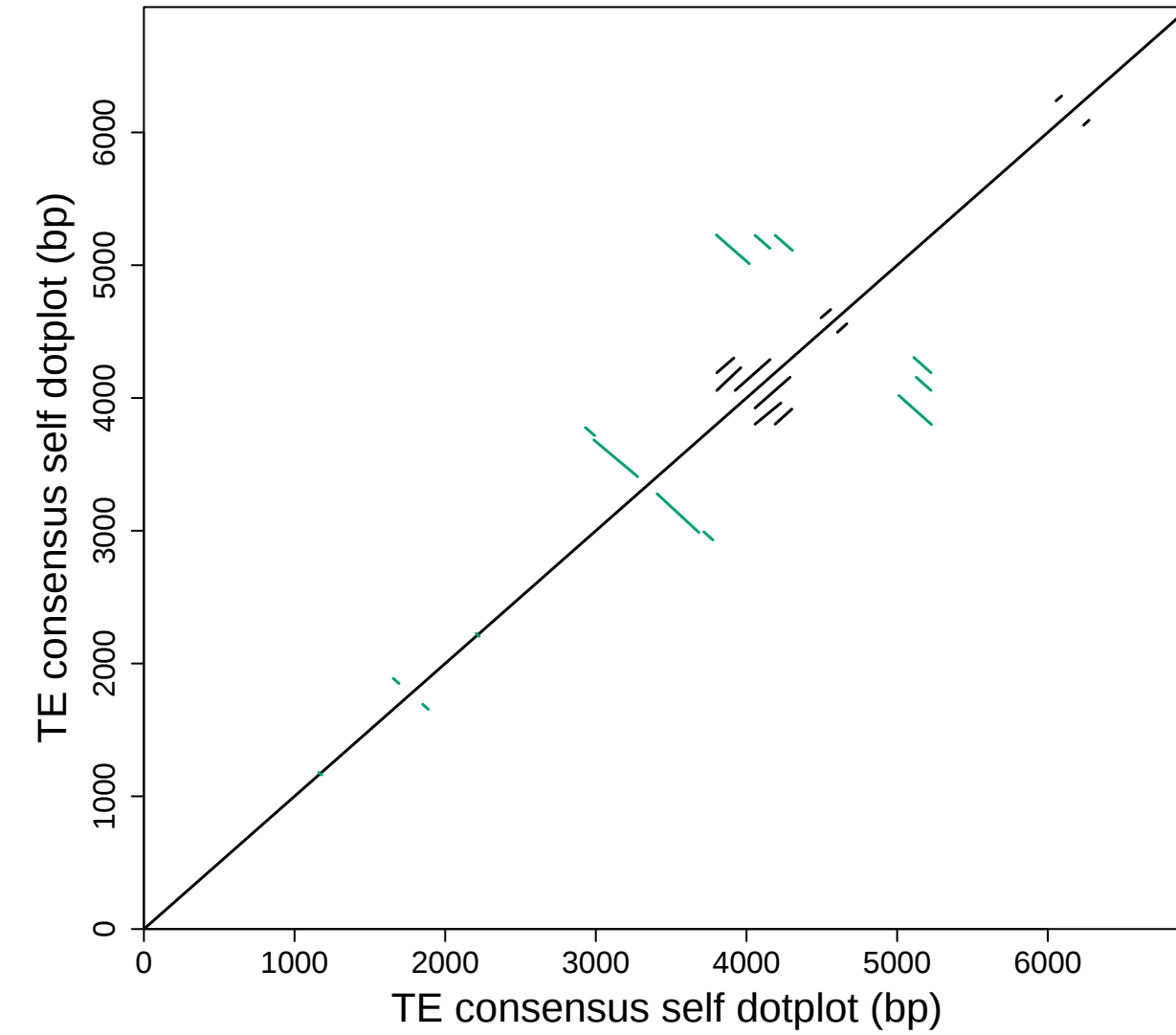
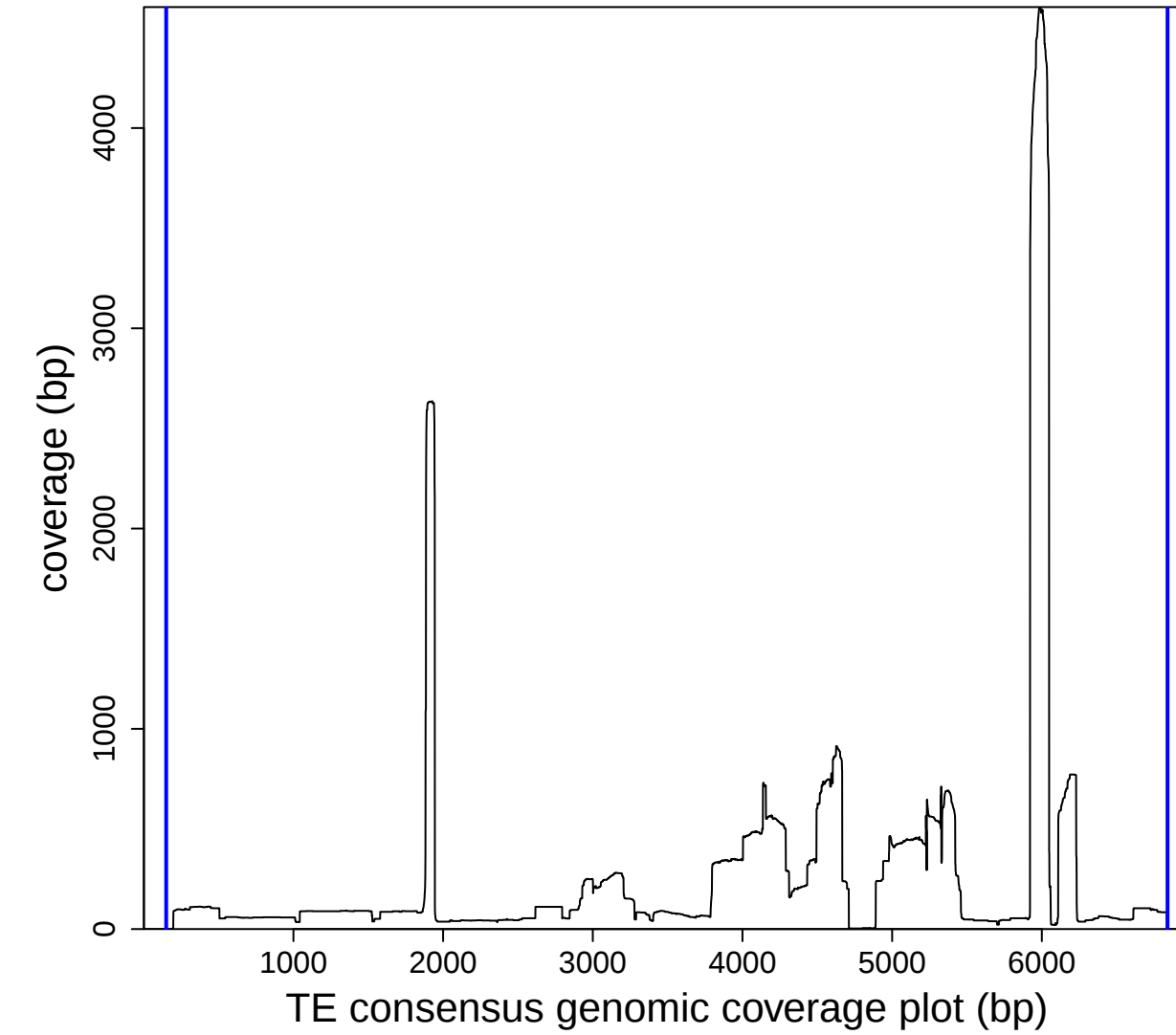
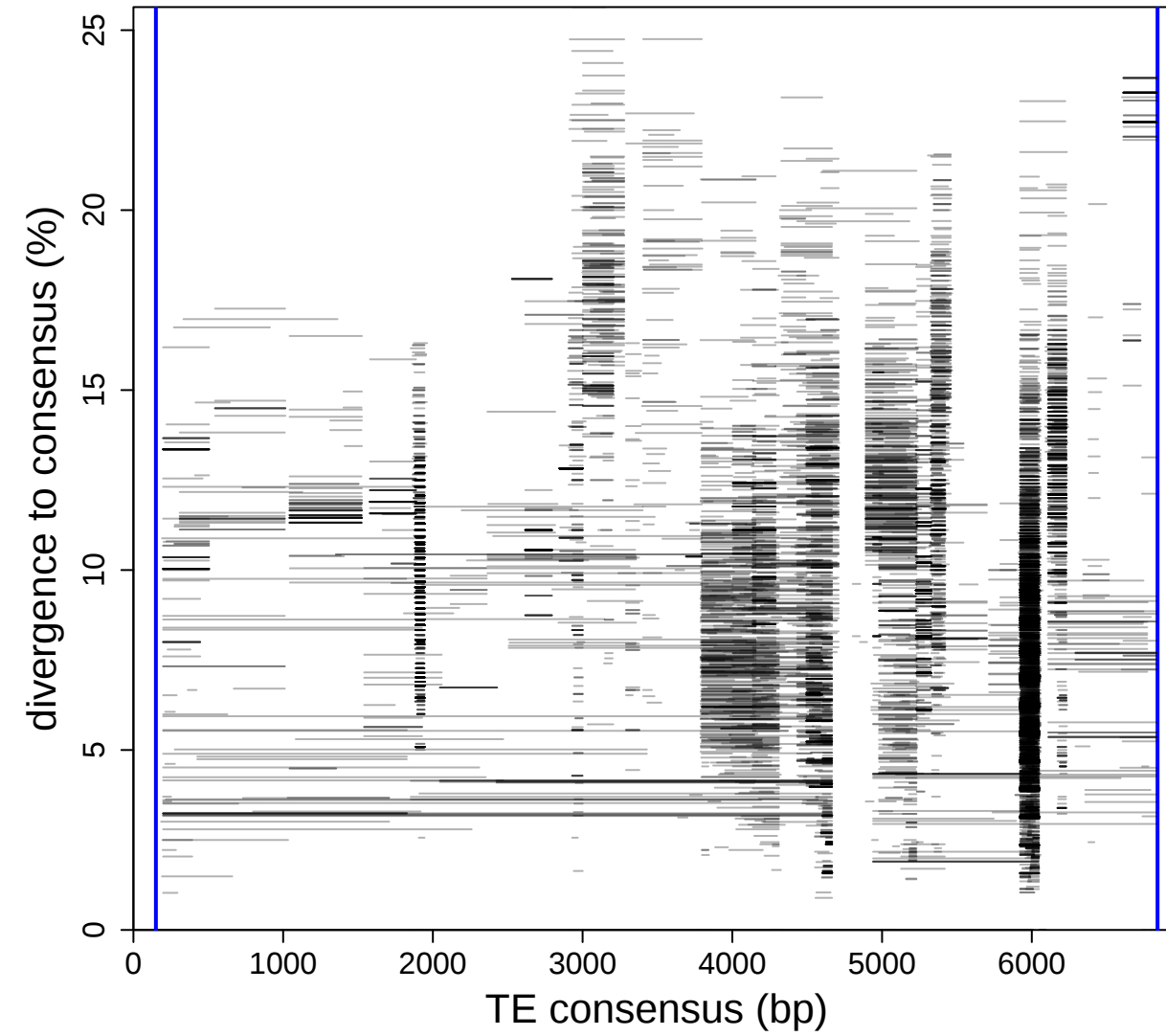
a.b.bed\_uf.bed\_g\_2.bed\_fm\_1.bed\_0\_0\_bcln.fa\_aln.fa\_cl.fa\_gs.f  
size: 6630bp; fragments: 25717; full length: 0 (>=5967bp)

# After TEtrimmer 6630 bp



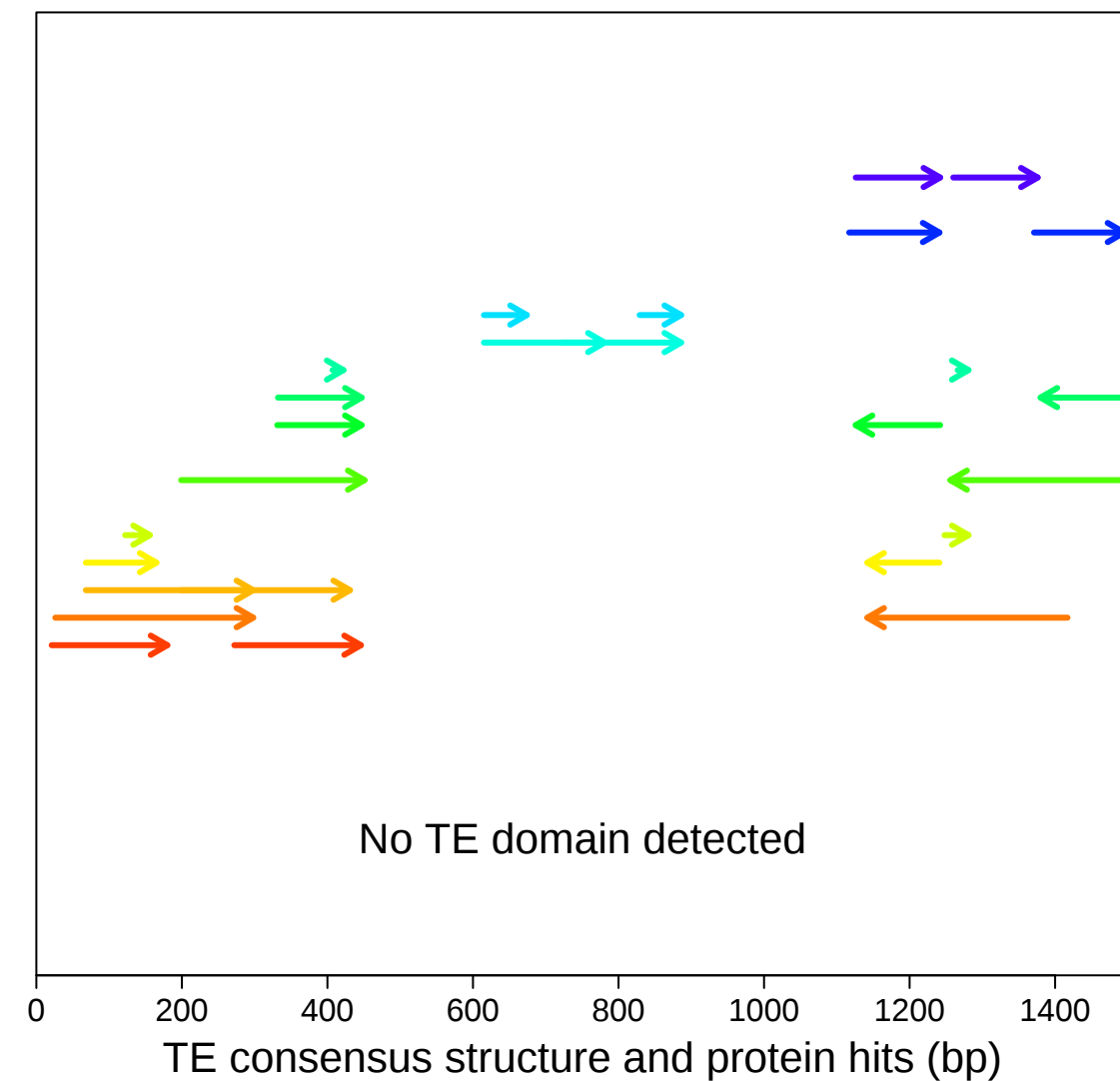
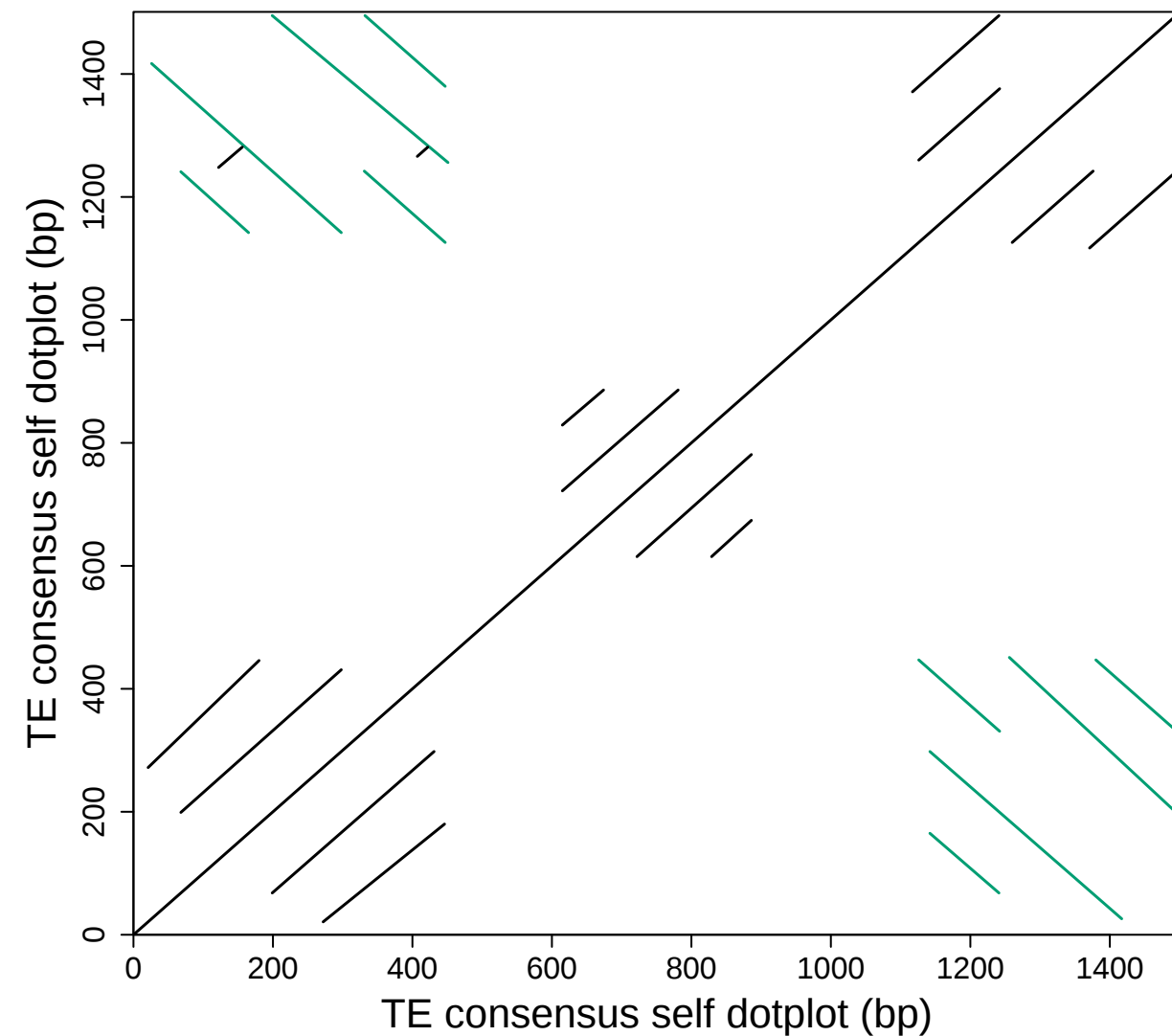
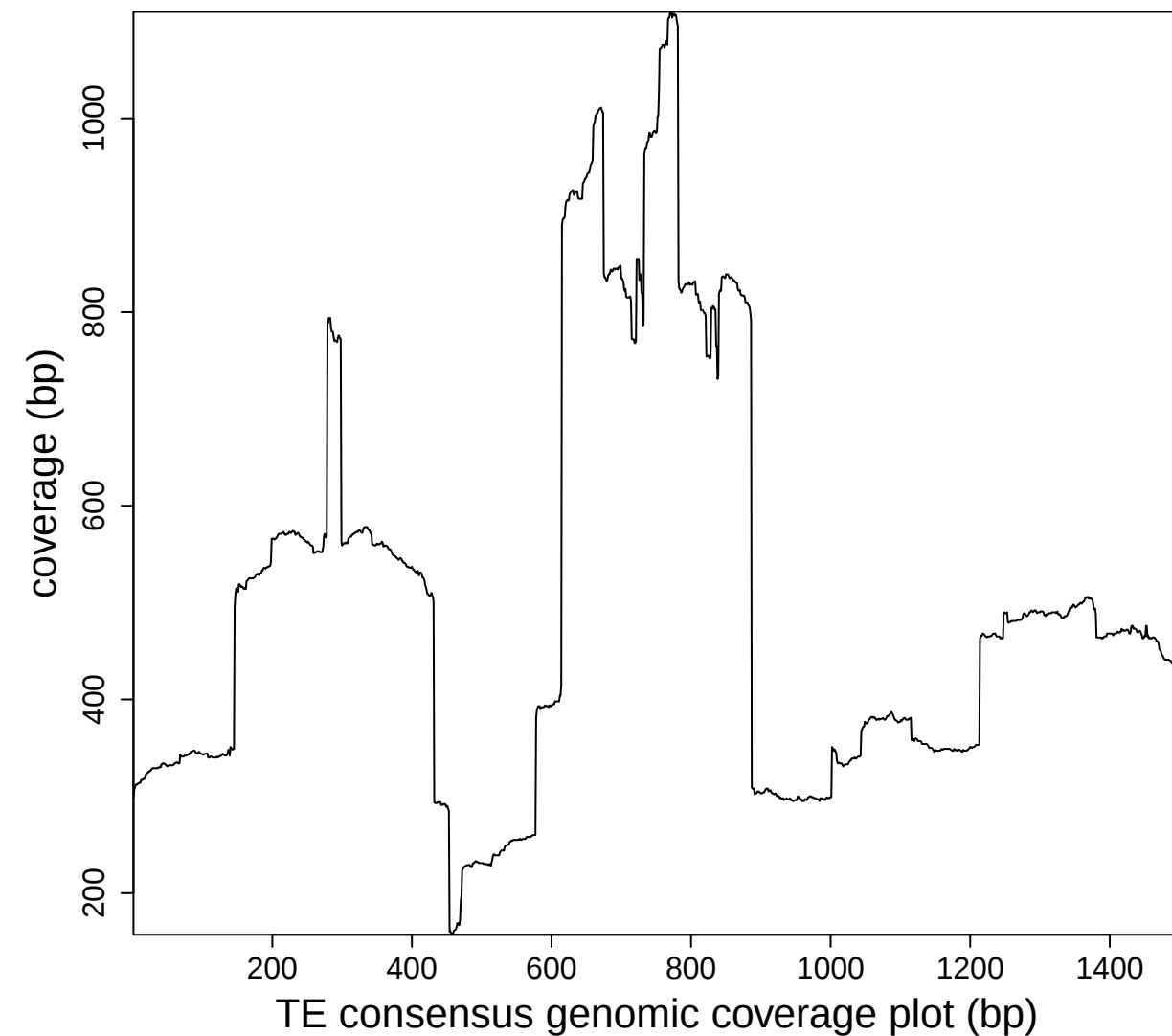
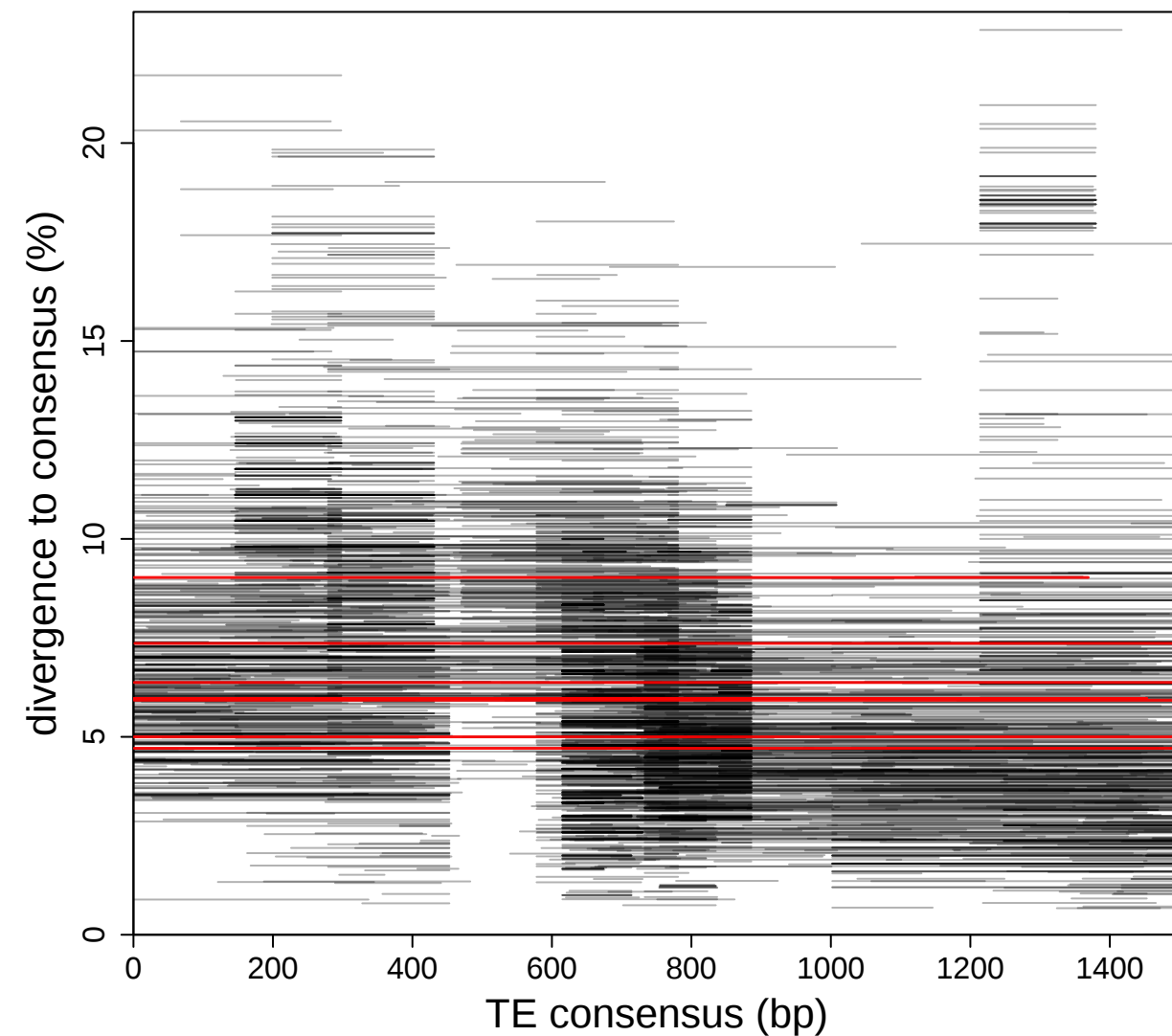
0.fasta.b.bed\_uf.bed\_g\_2.bed\_fm\_1.bed\_0\_0\_bcln.fa\_aln.fa\_cl.f  
size: 6990bp; fragments: 12680; full length: 0 (>=6291bp)

## After TEtrimmer Extended plot Blue lines are boundaries

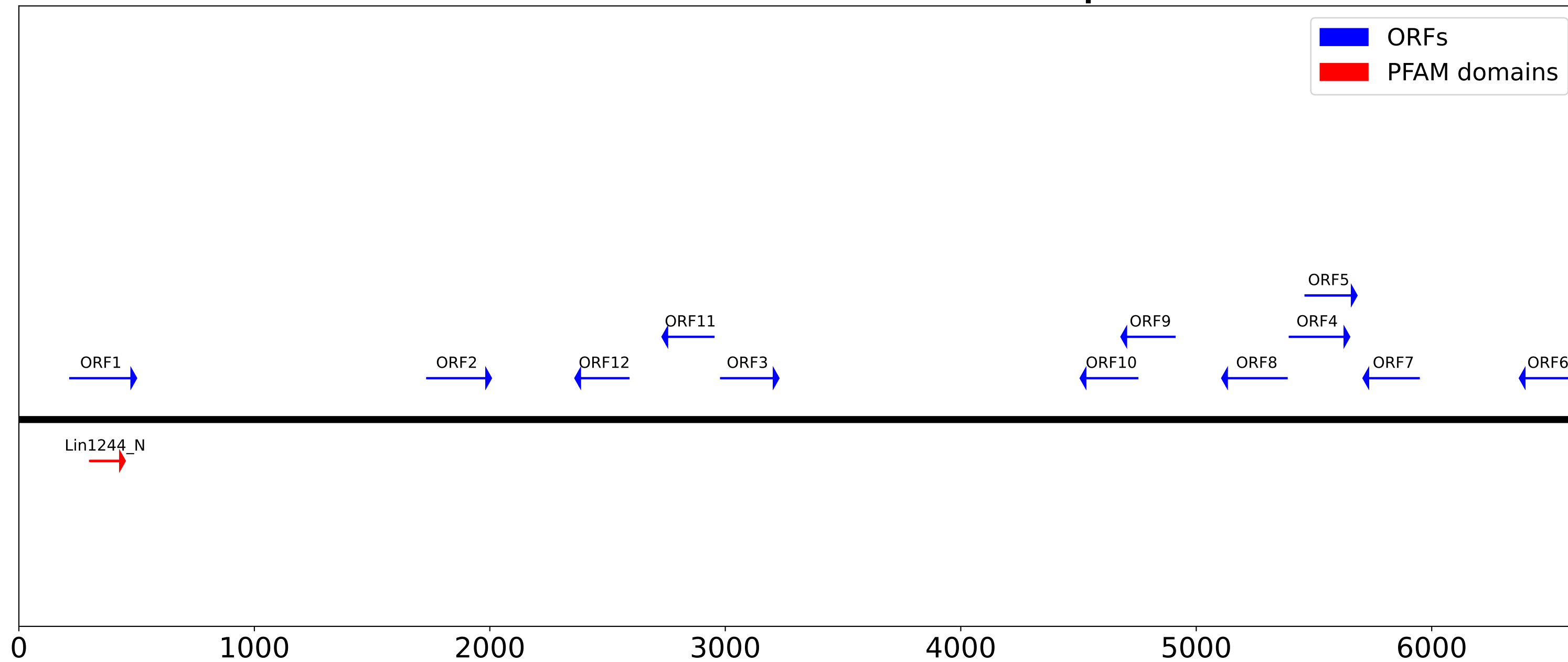


TE: rnd\_5\_family\_1220  
size: 1501bp; fragments: 3138; full length: 8 ( $\geq 1350.9$ bp)

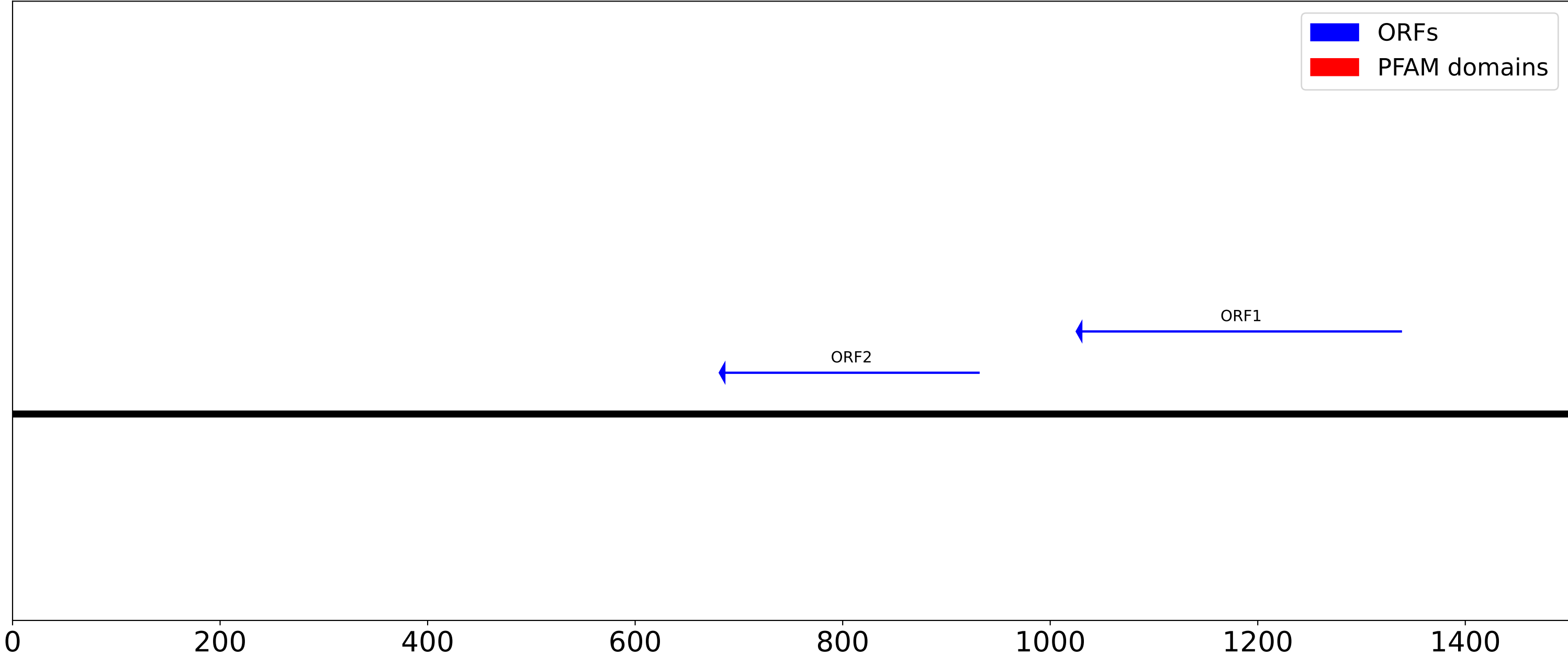
## Before TEtrimmer 1501 bp



## After TEtrimmer ORF and PFAM domain plot



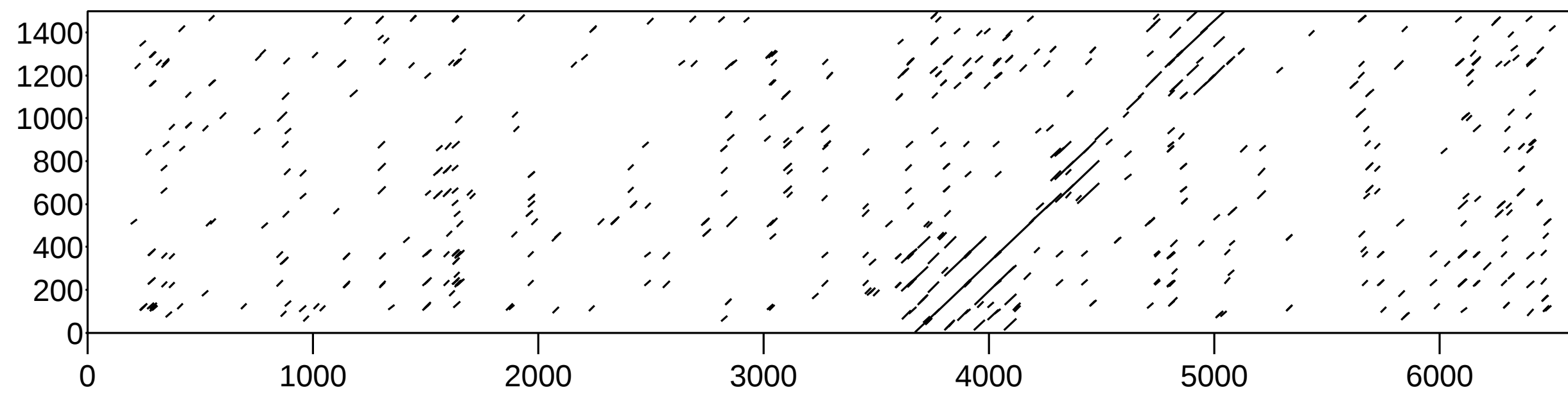
**Before TEtrimmer ORF and PFAM domain plot**



# Dotplot

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

onsensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)