

Start crop Point

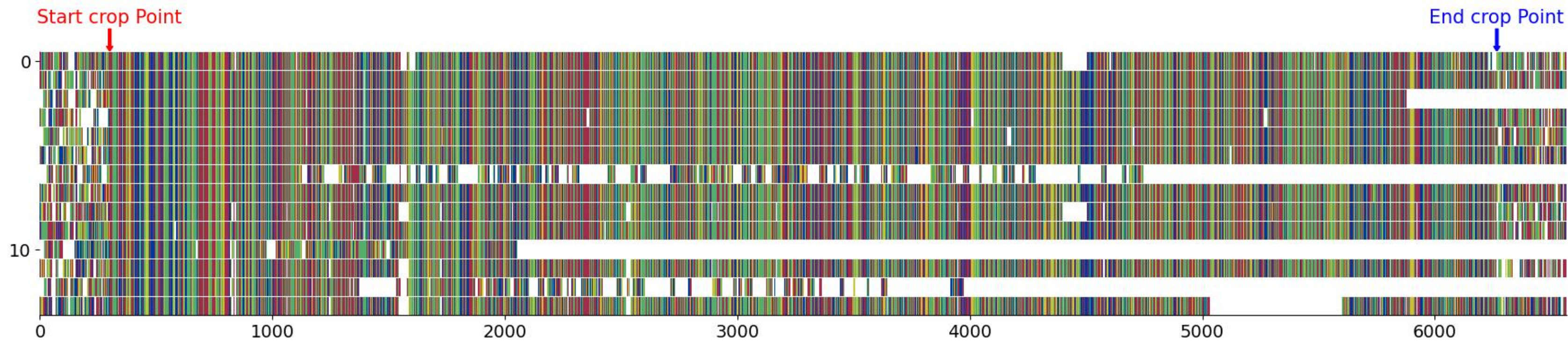
End crop Point

MSA length = 5968



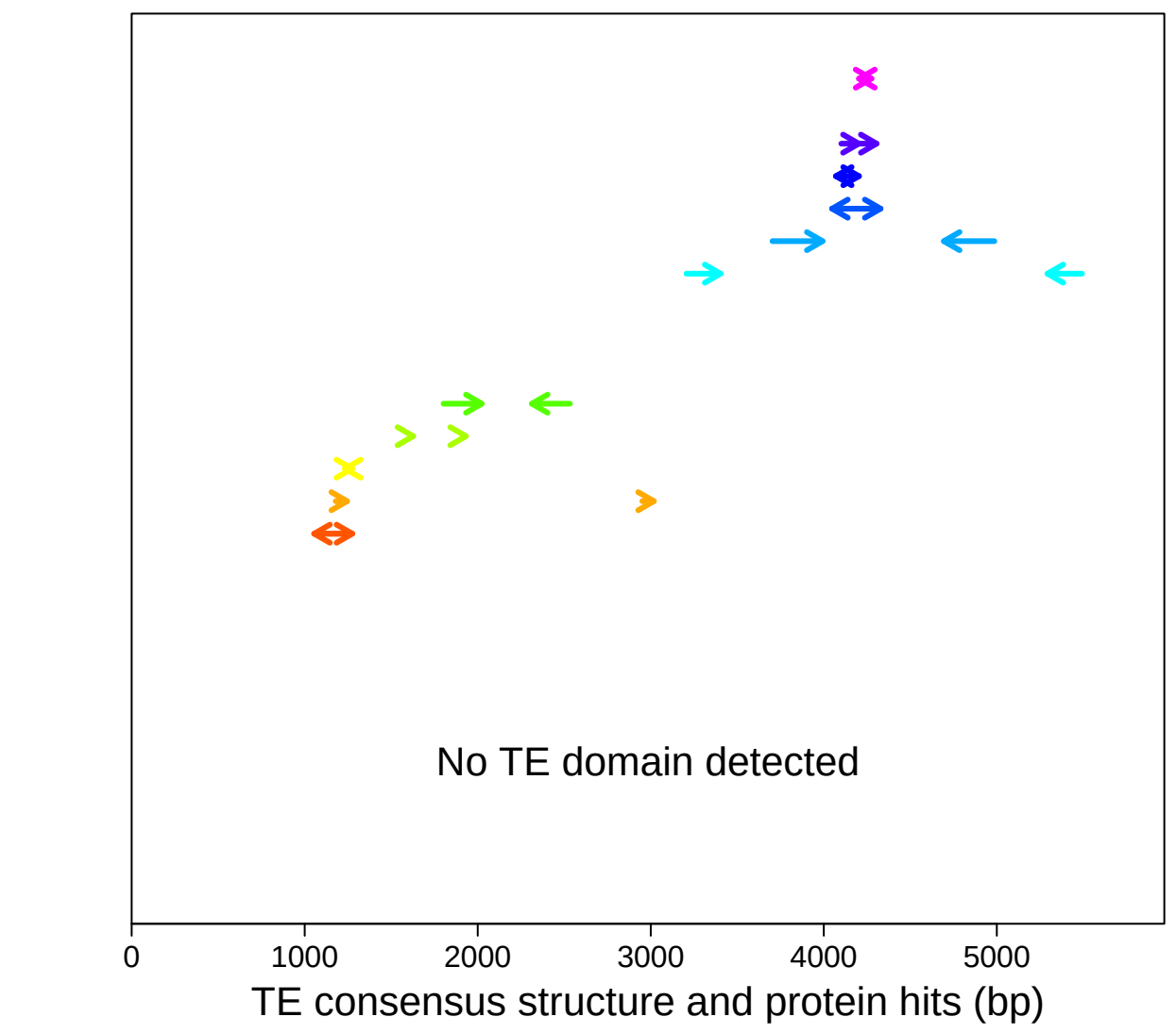
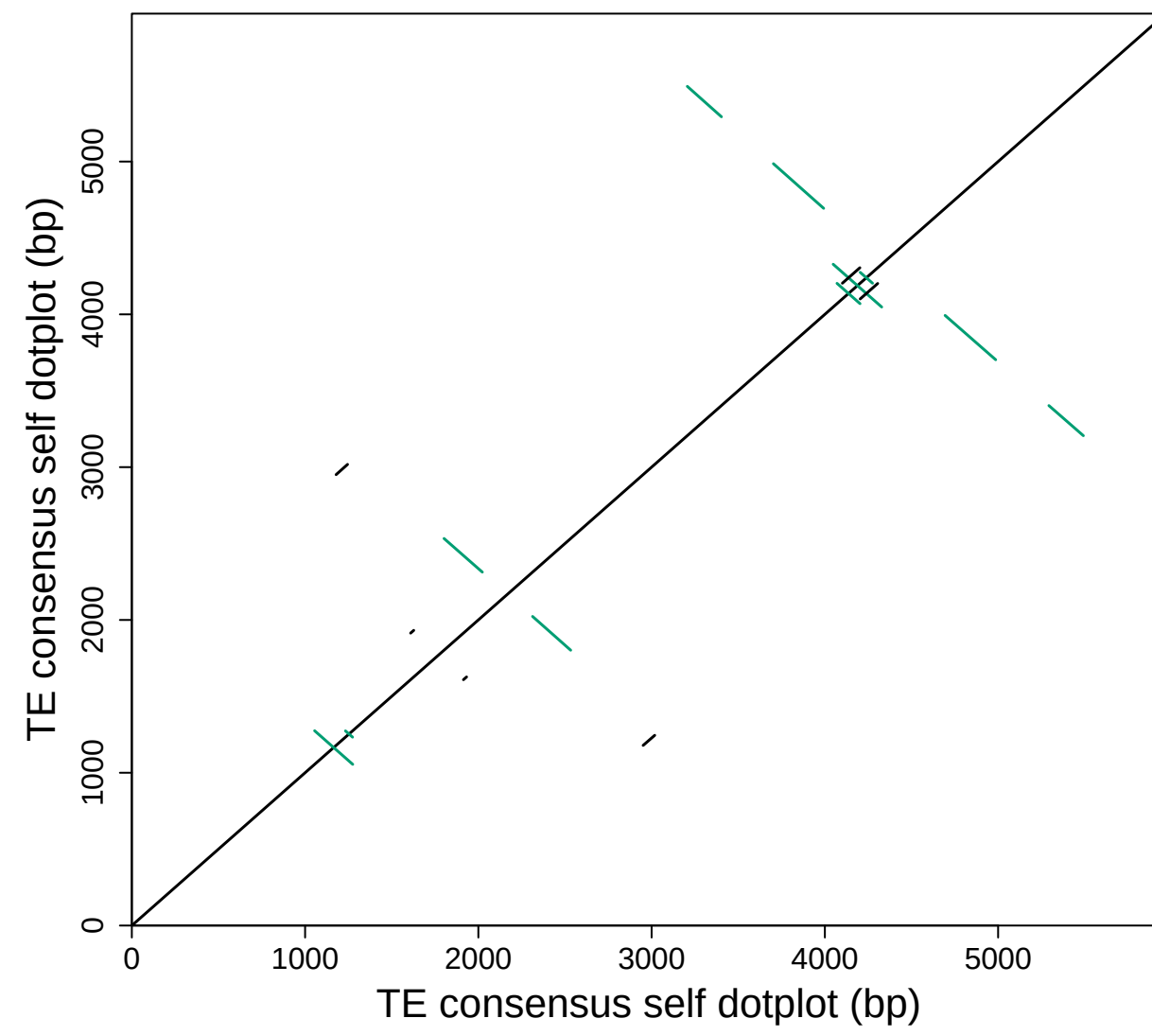
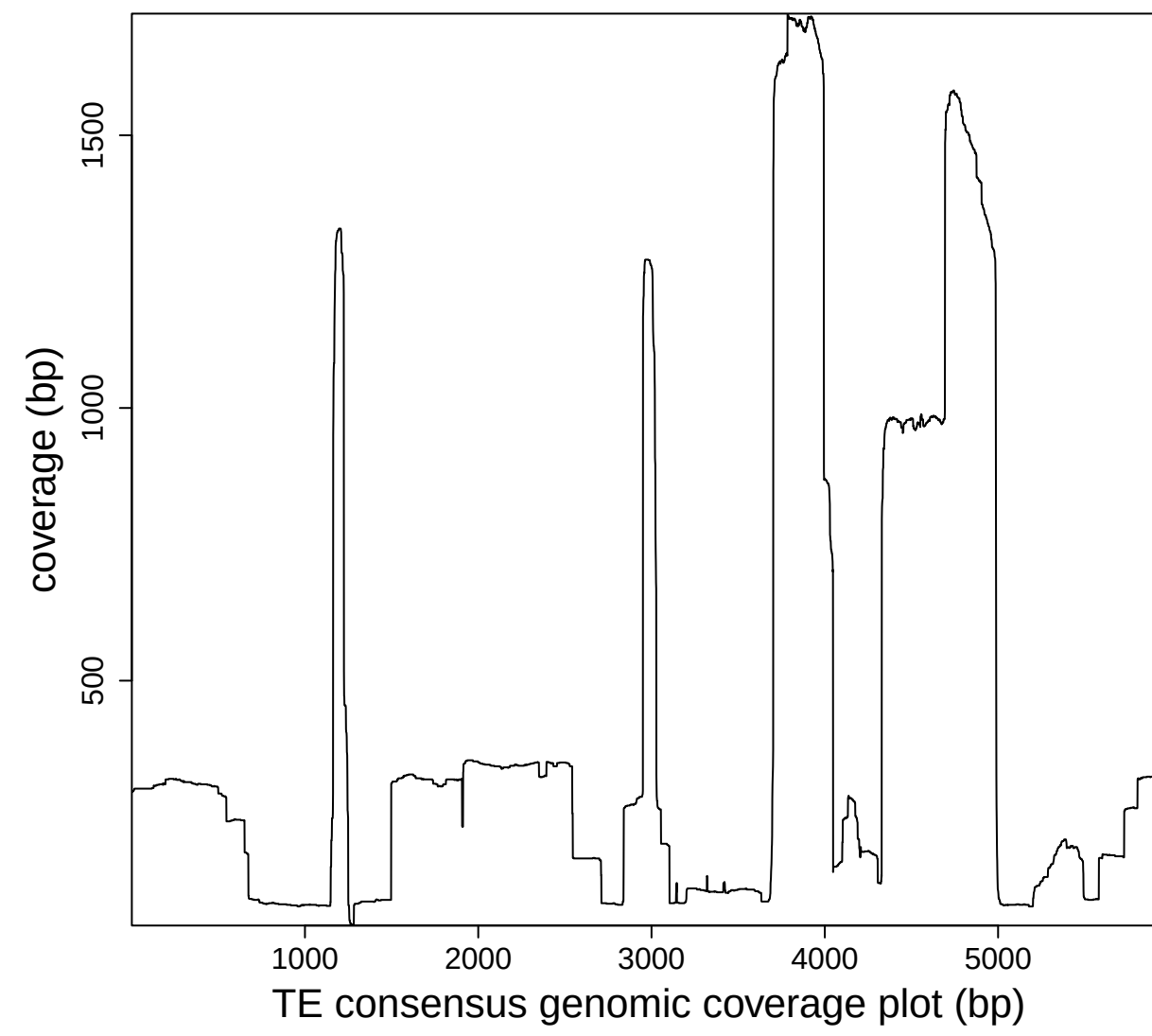
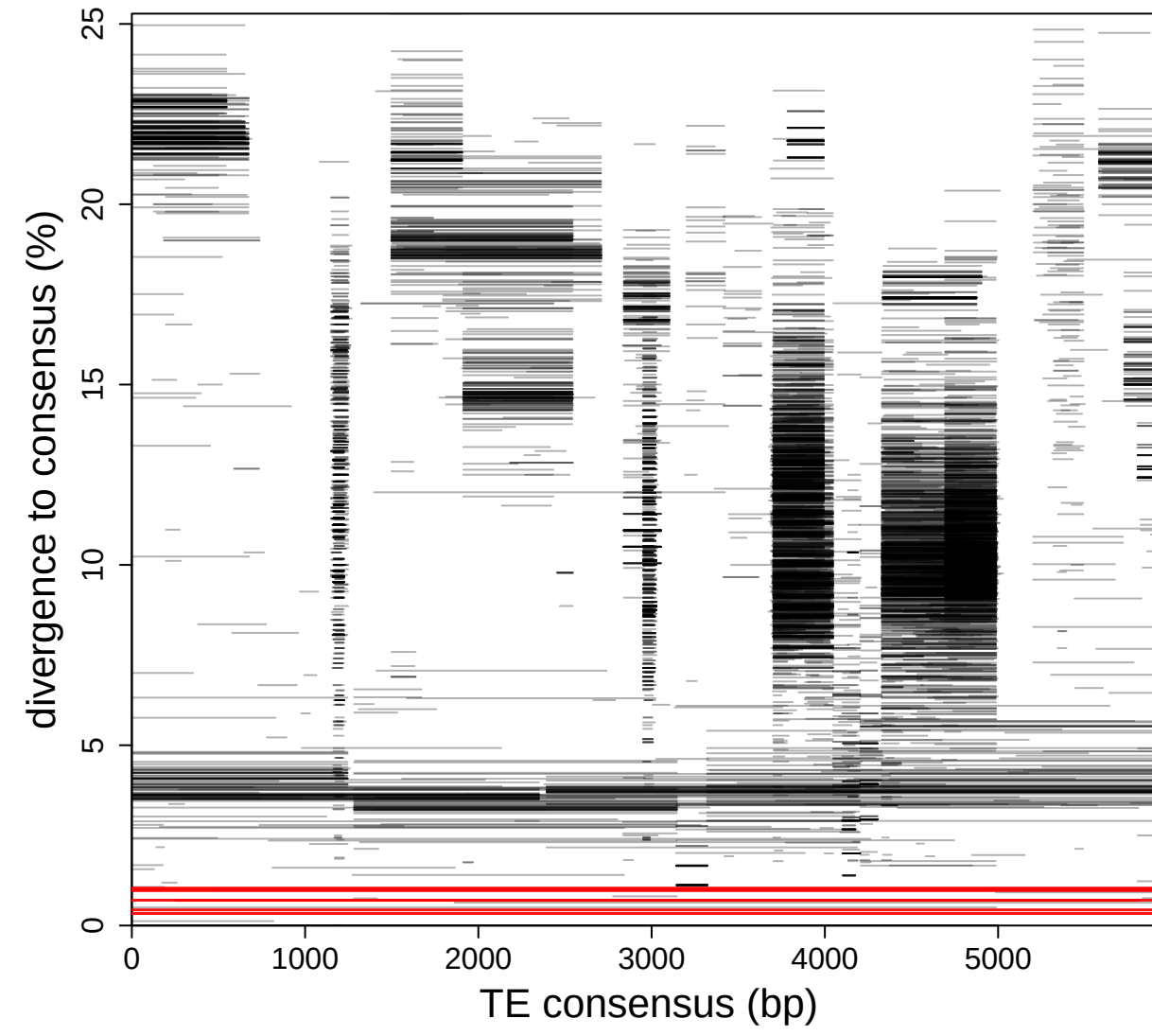
Start crop Point

End crop Point



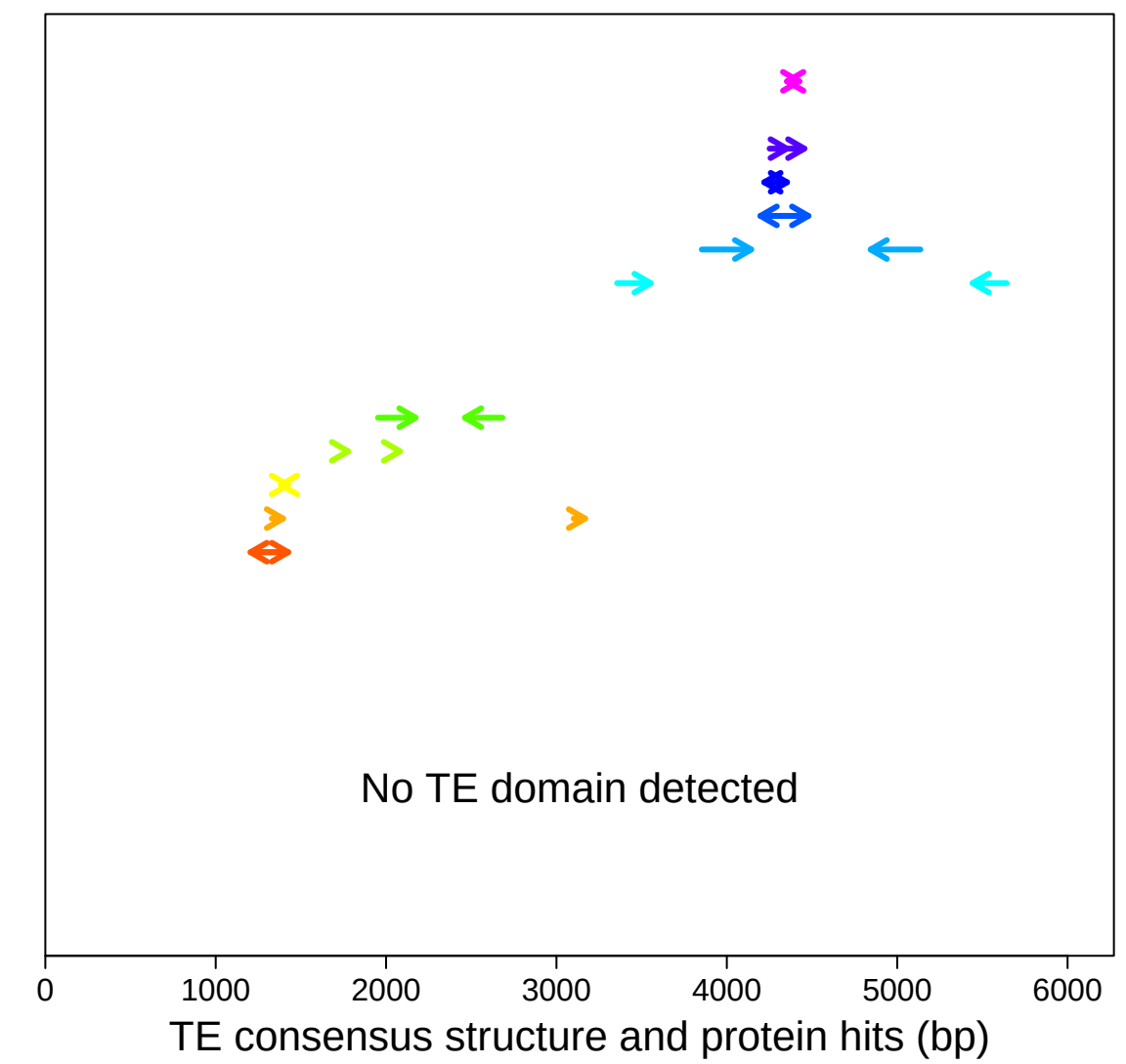
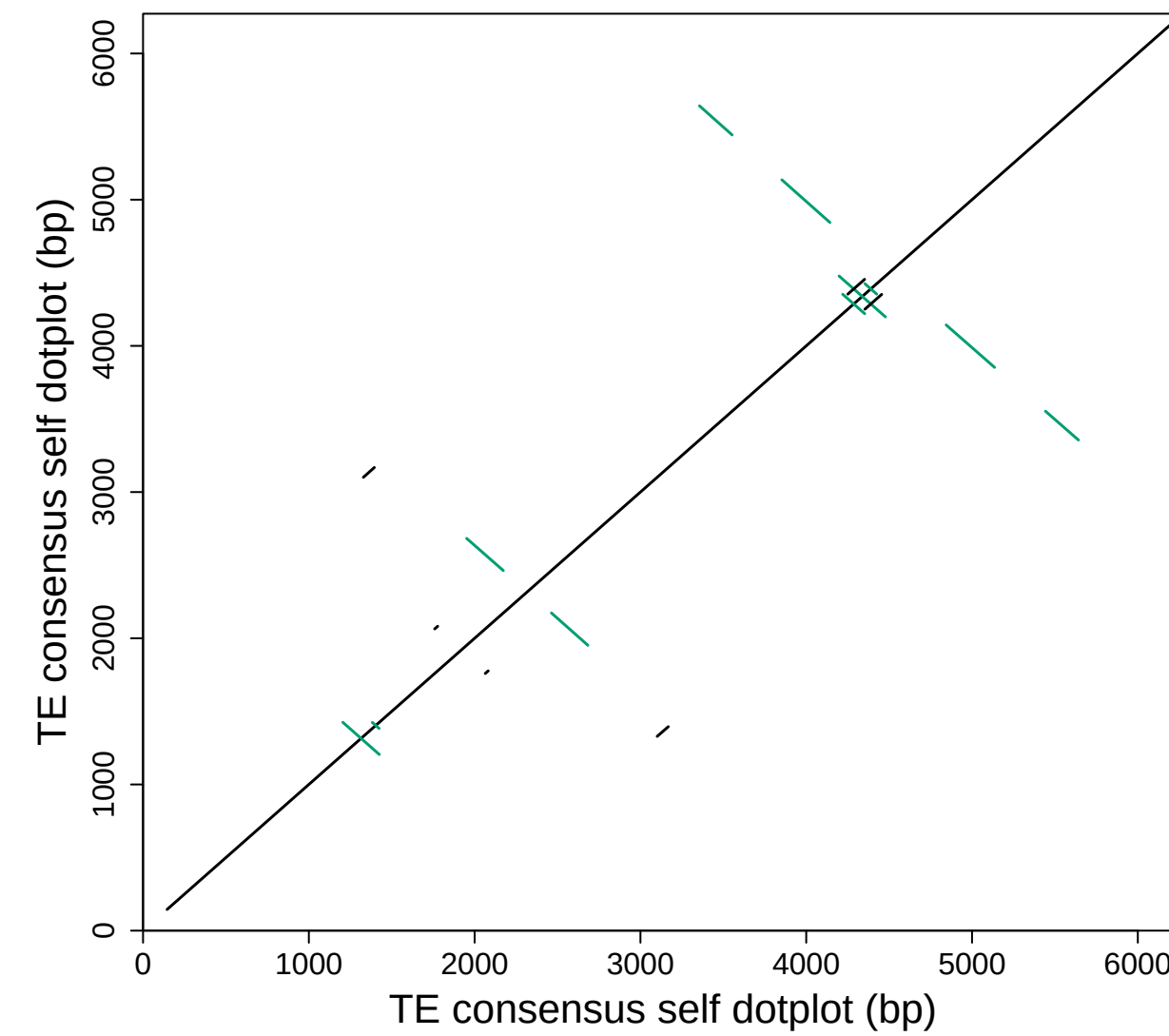
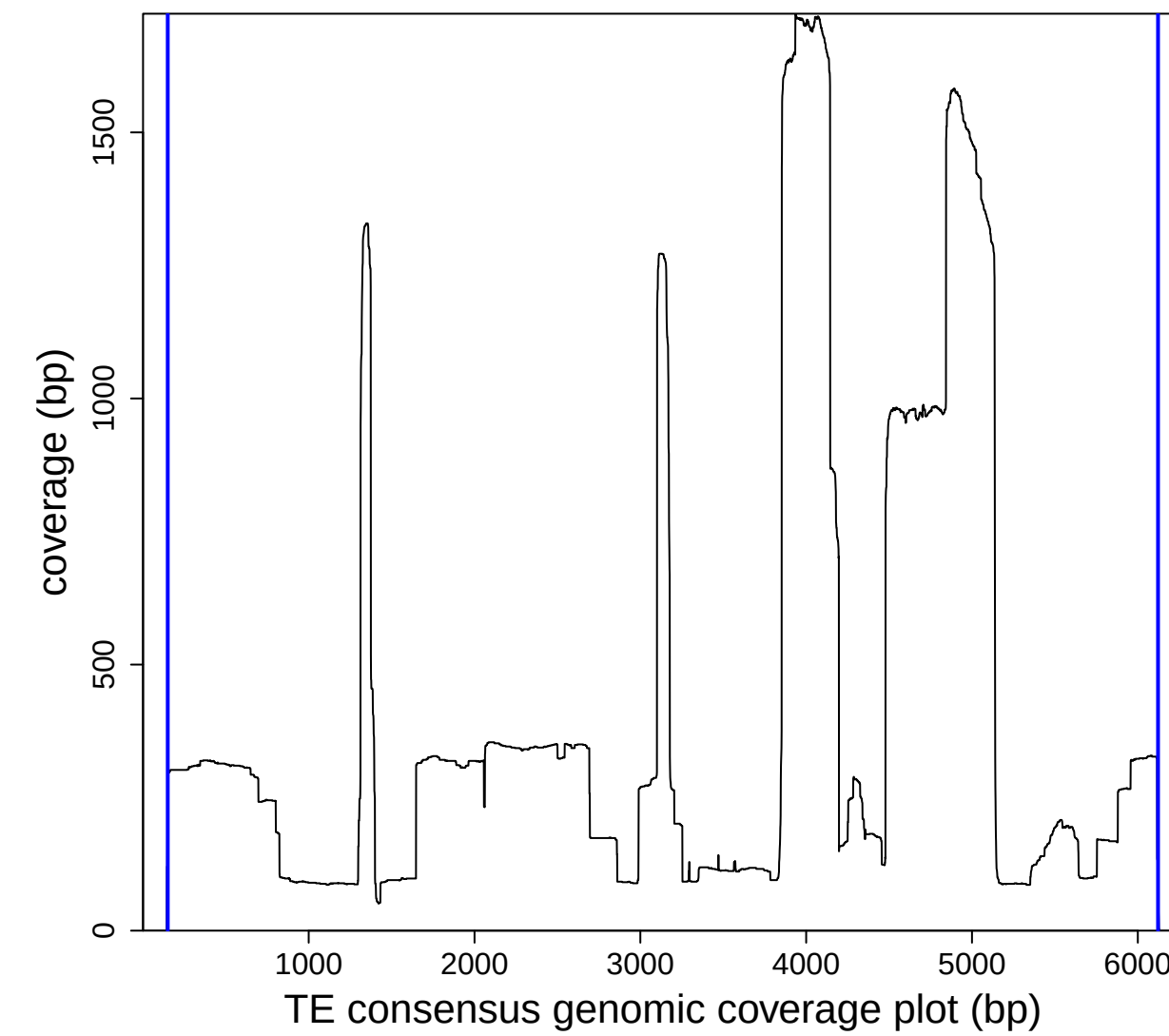
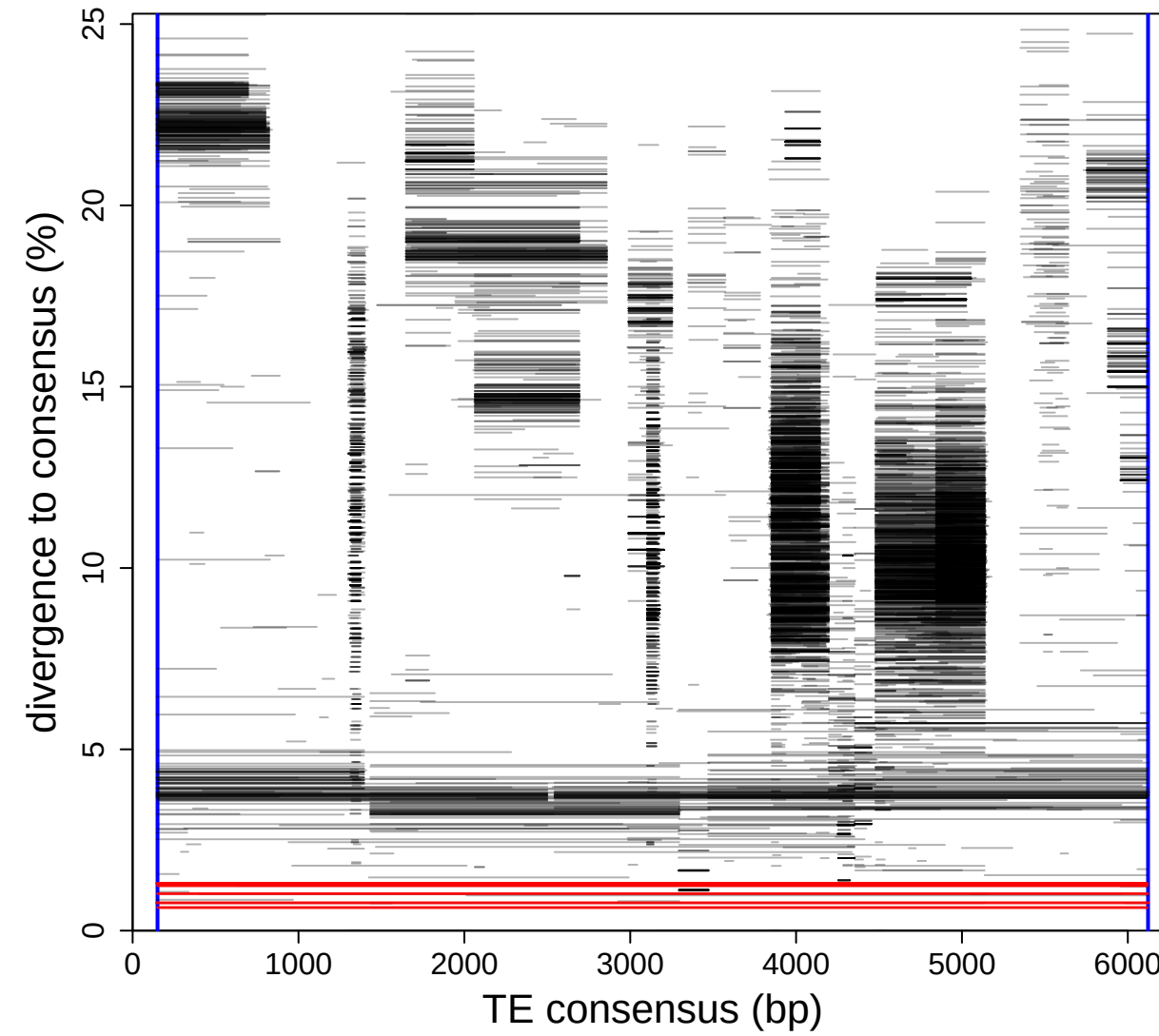
g\_2.bed\_fm\_1.bed\_0\_0\_n.bed\_g\_1.bed\_fm\_2.bed\_0\_0\_bcln.fa\_a  
size: 5968bp; fragments: 7565; full length: 8 (>=5371.2bp)

# After TEtrimmer 5968 bp

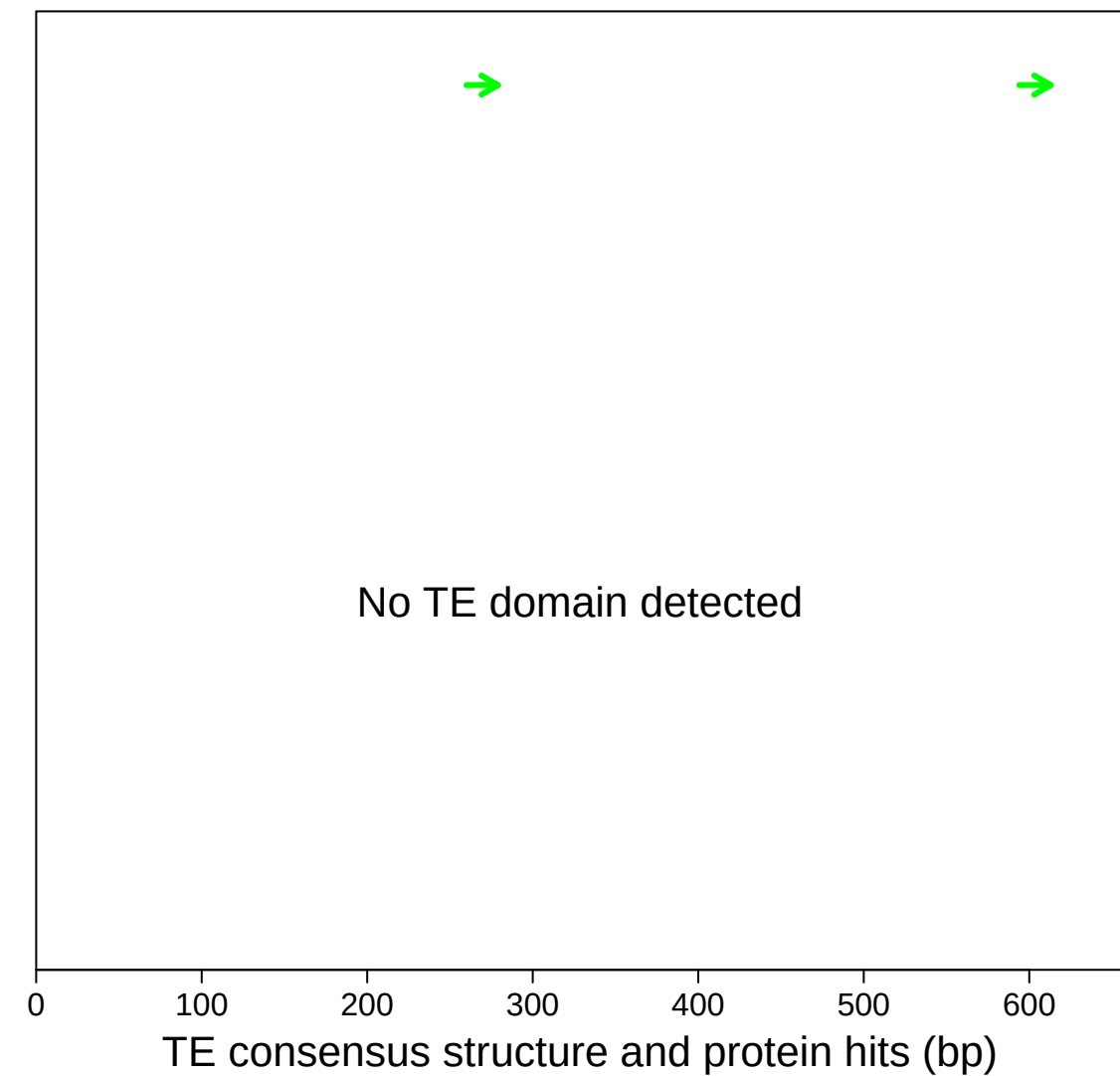
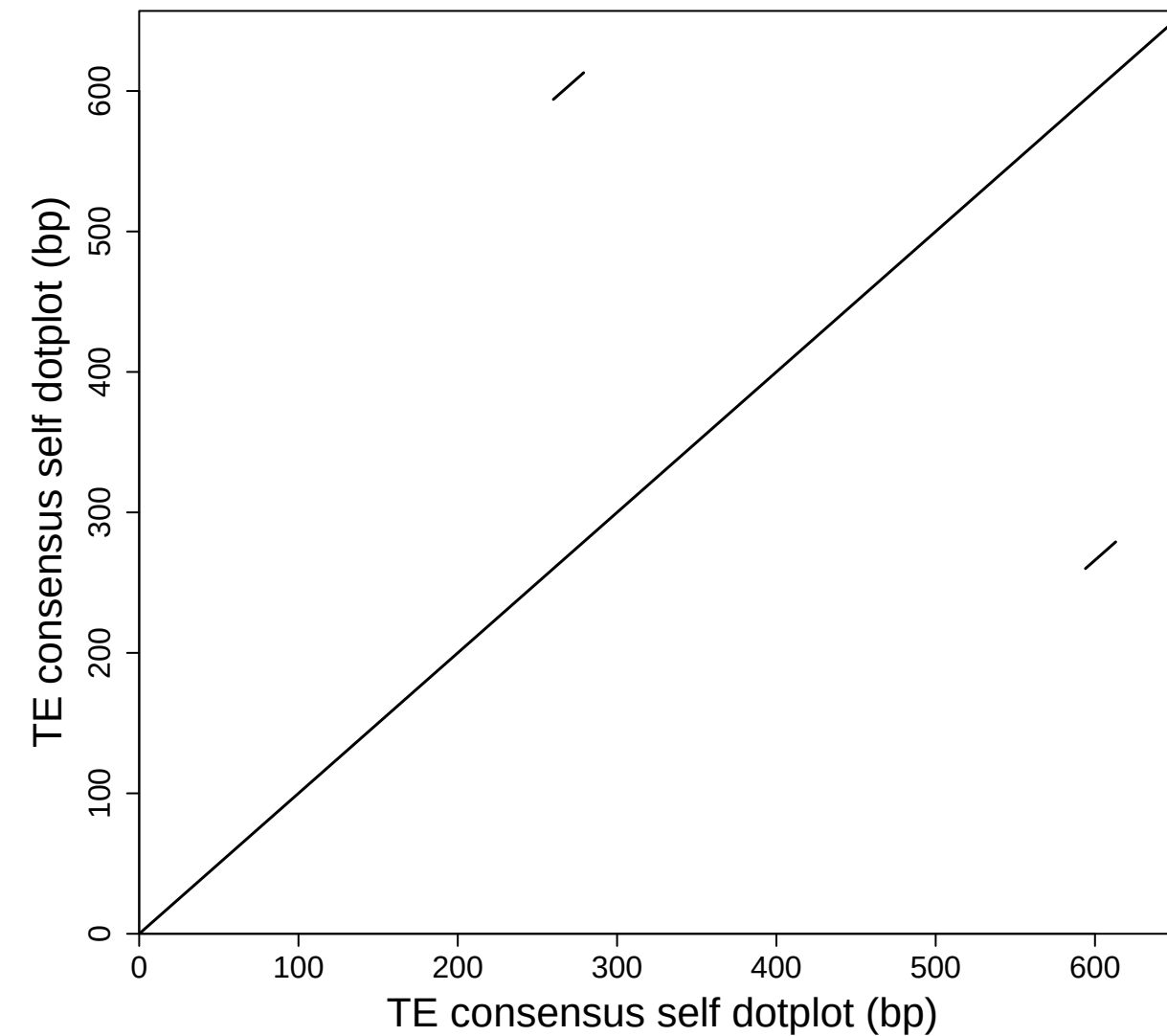
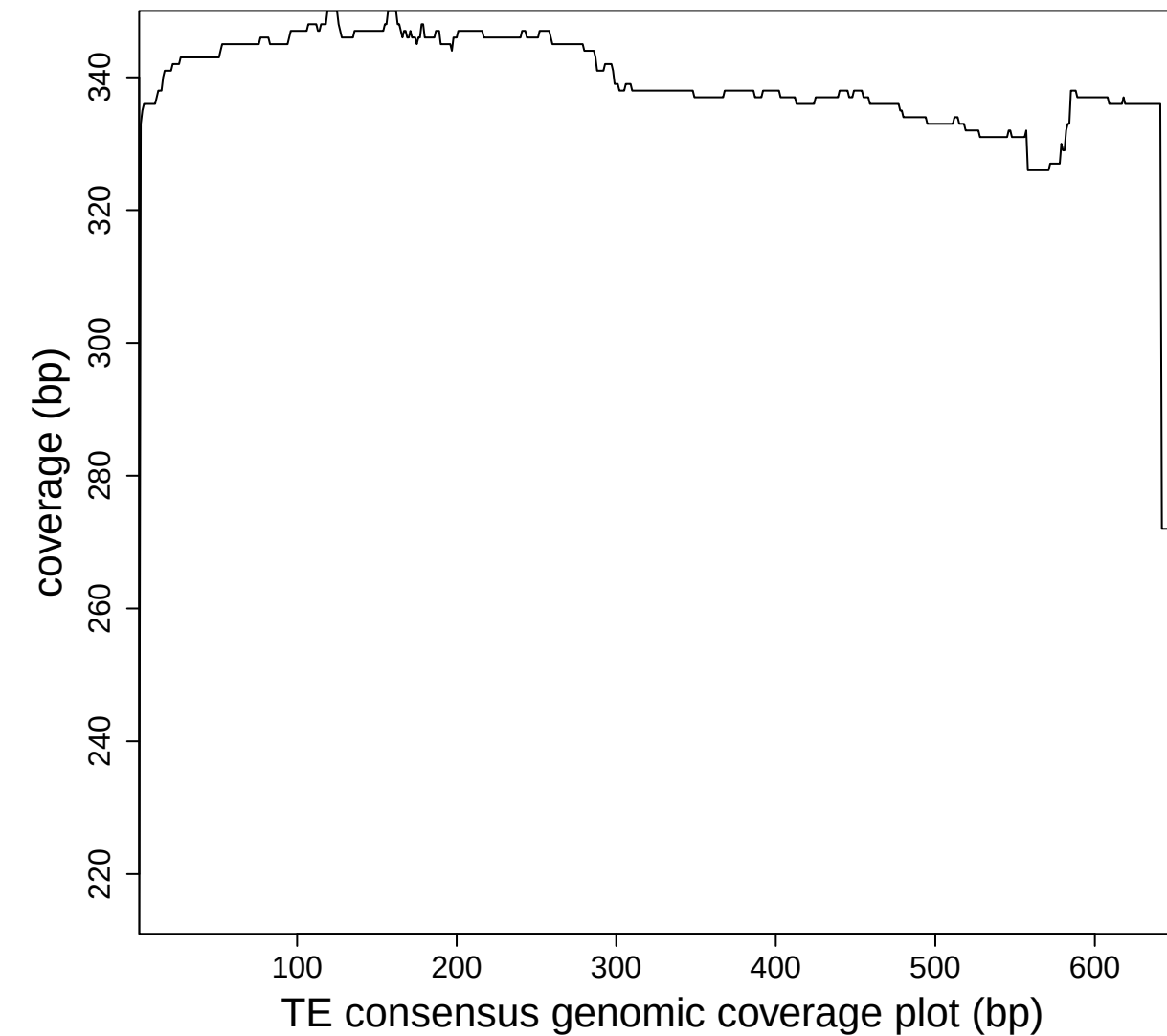
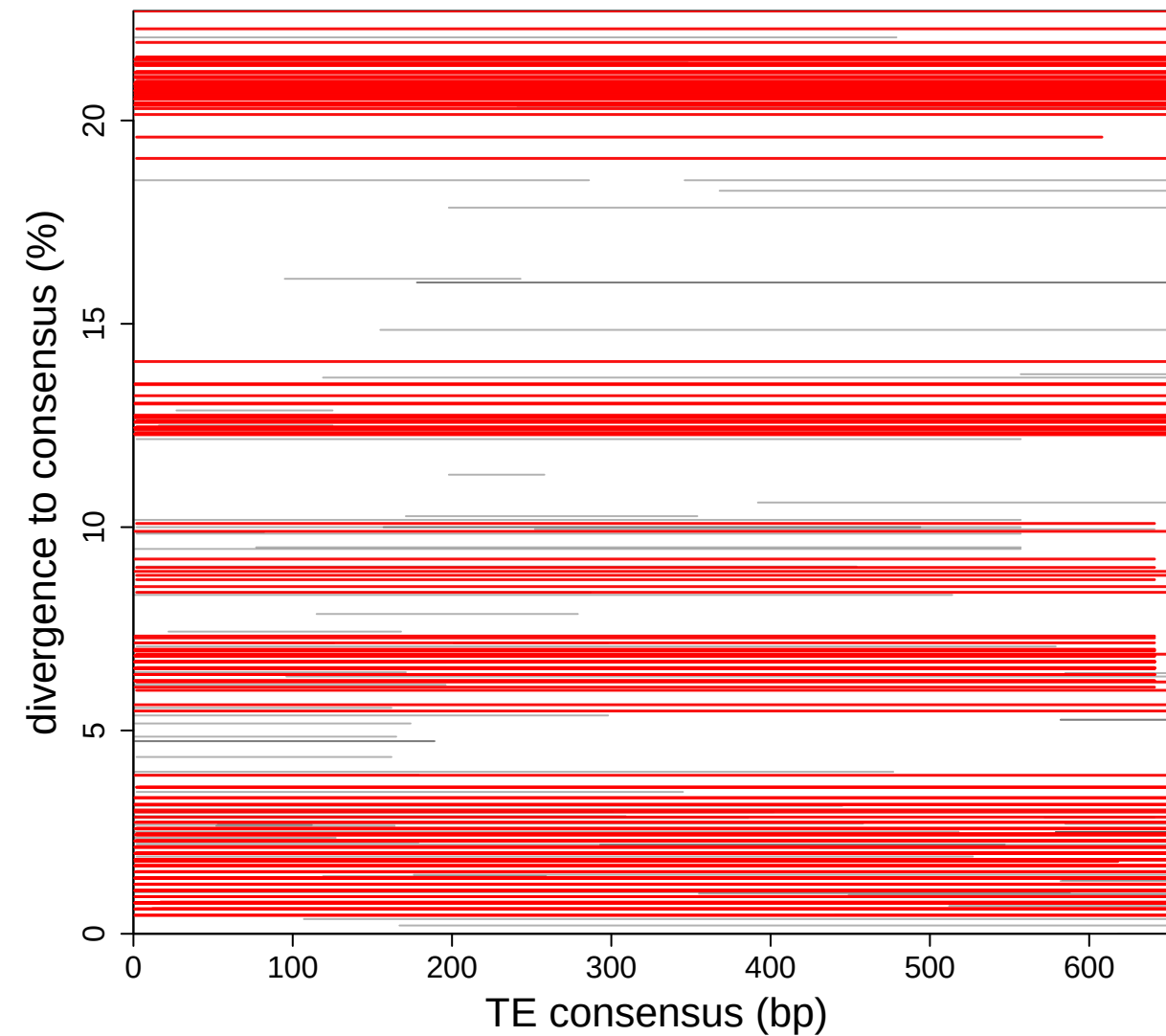


f.bed\_g\_2.bed\_fm\_1.bed\_0\_0\_n.bed\_g\_1.bed\_fm\_2.bed\_0\_0\_bcl  
size: 6272bp; fragments: 7557; full length: 6 (>=5644.8bp)

## After TEtrimmer Extended plot Blue lines are boundaries

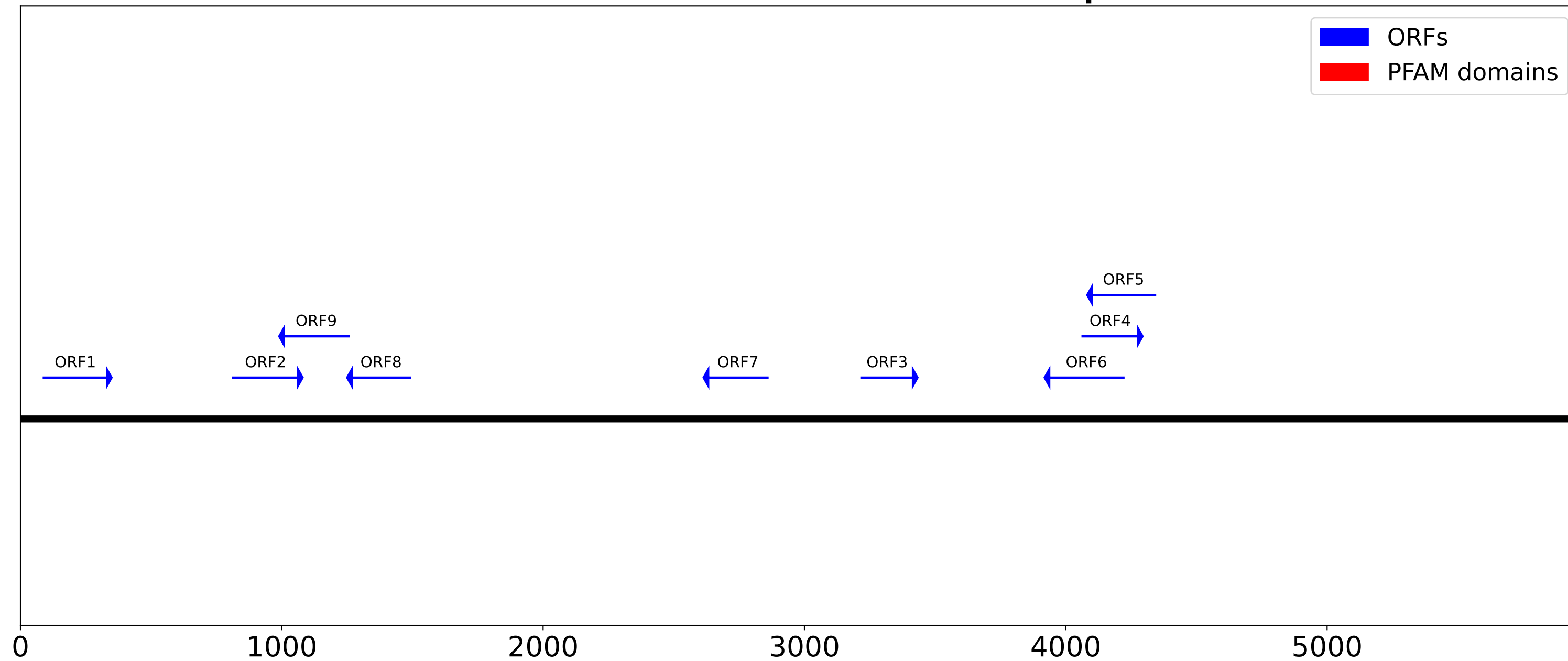


TE: rnd\_1\_family\_772  
size: 657bp; fragments: 393; full length: 300 ( $\geq 591.3$ bp)

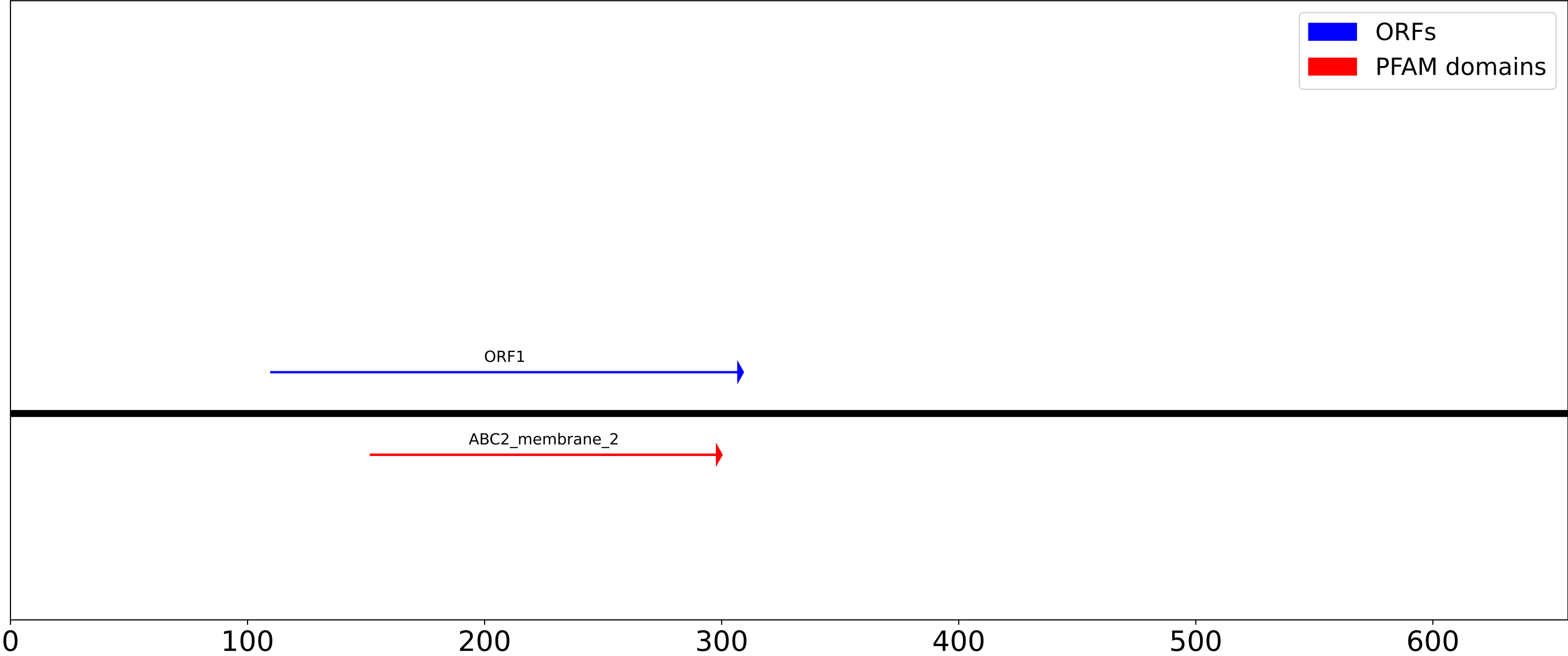


Before TEtrimmer 657 bp

## After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot

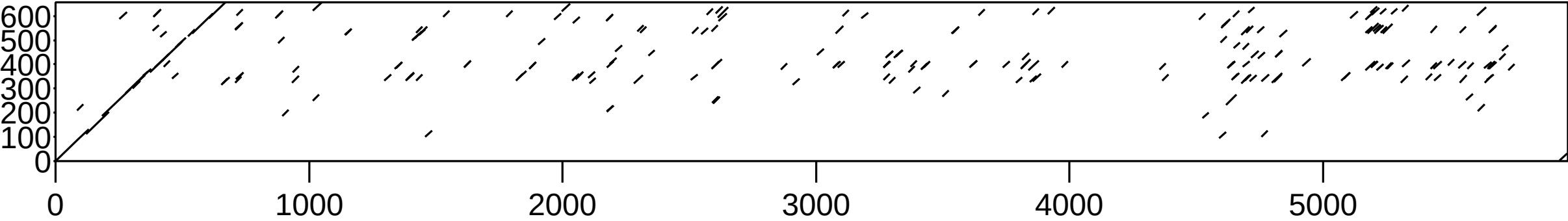




Dotplot

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

consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)