

Start crop Point



End crop Point

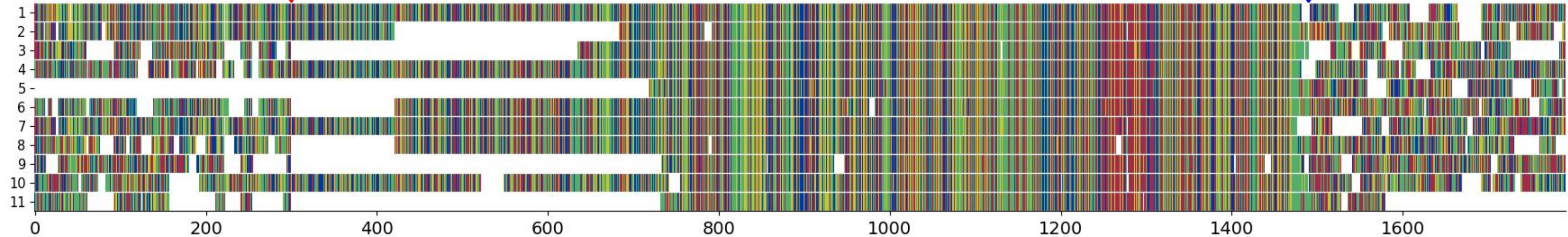


MSA length = 1191



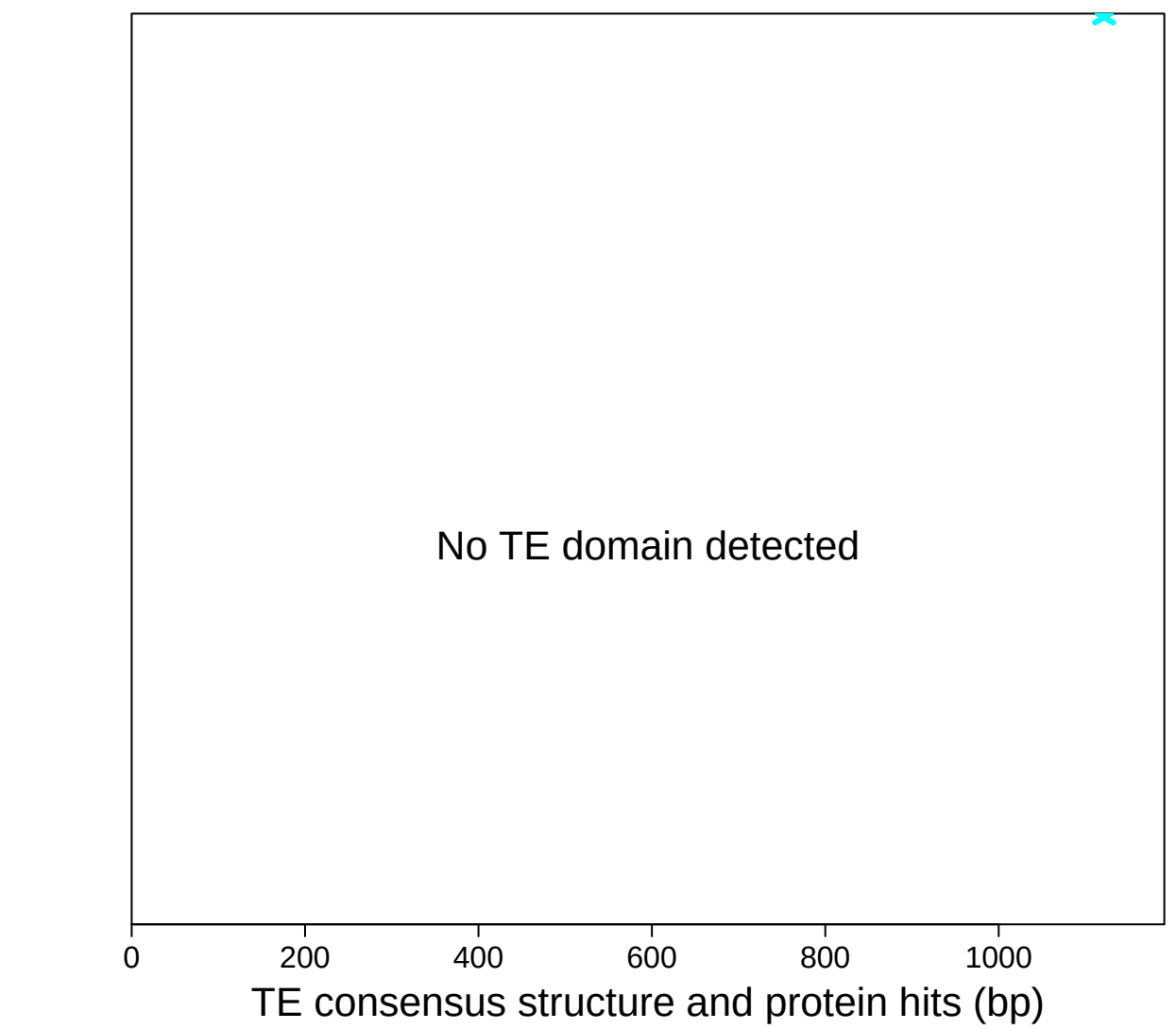
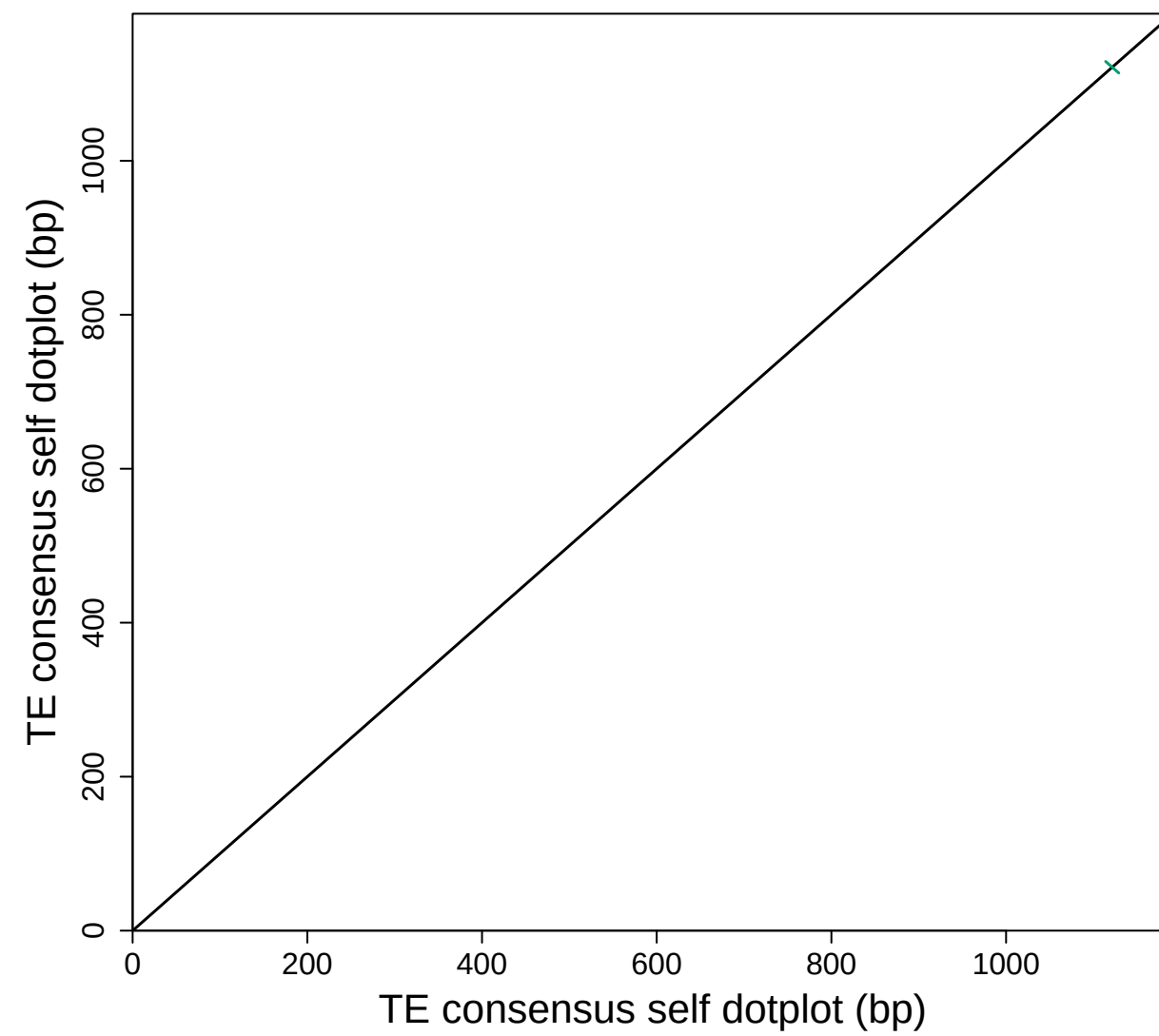
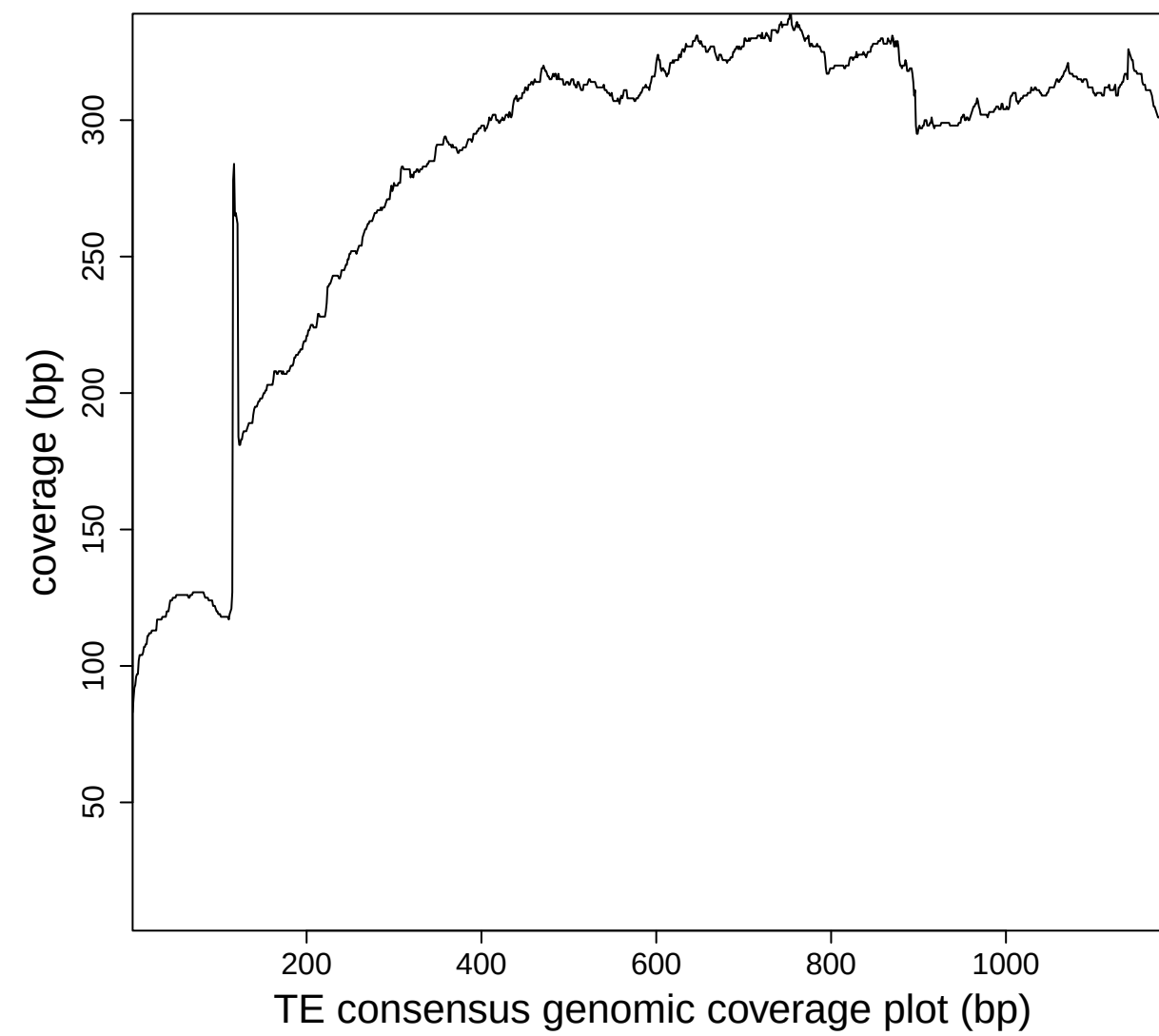
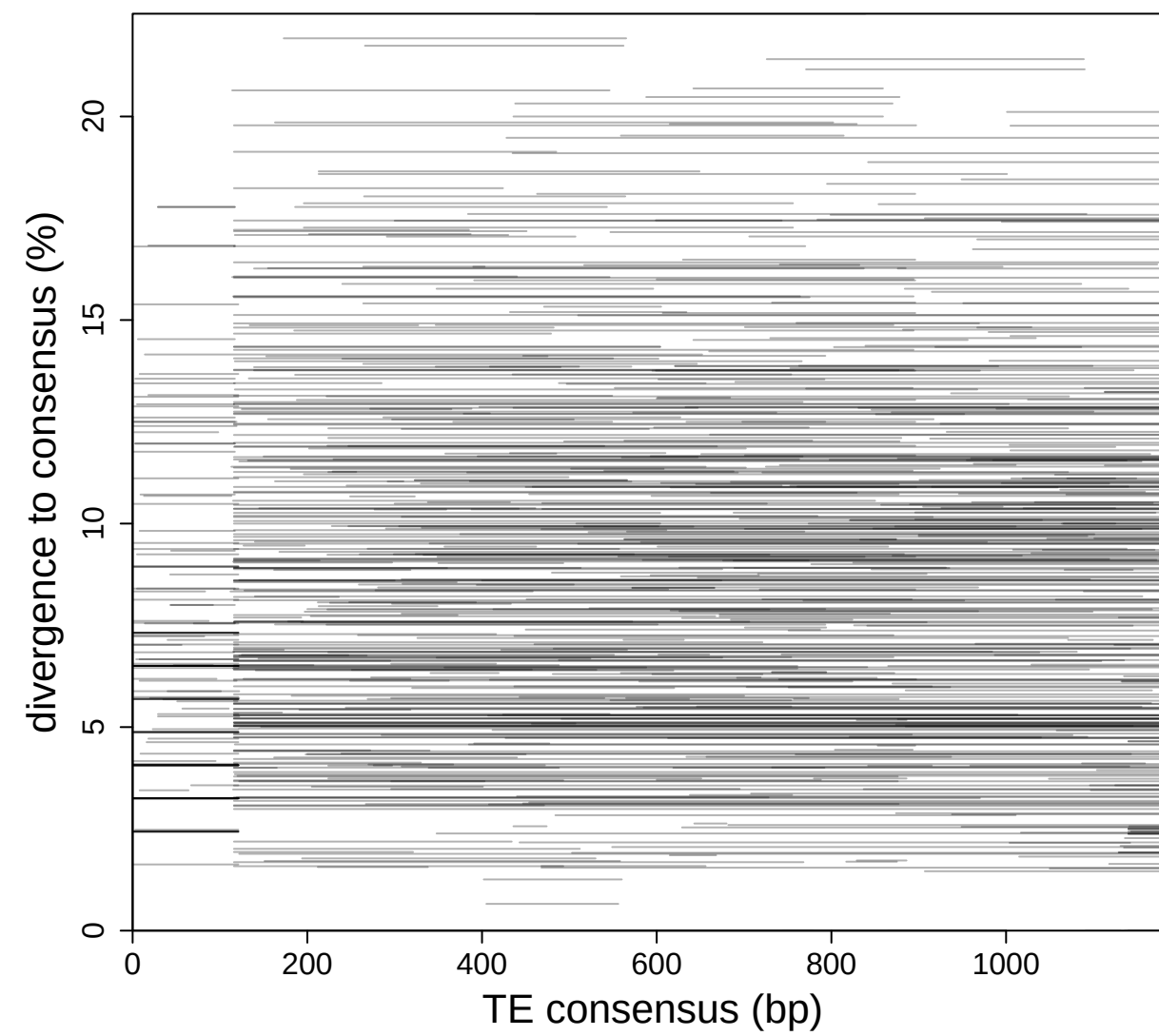
Start crop Point

End crop Point



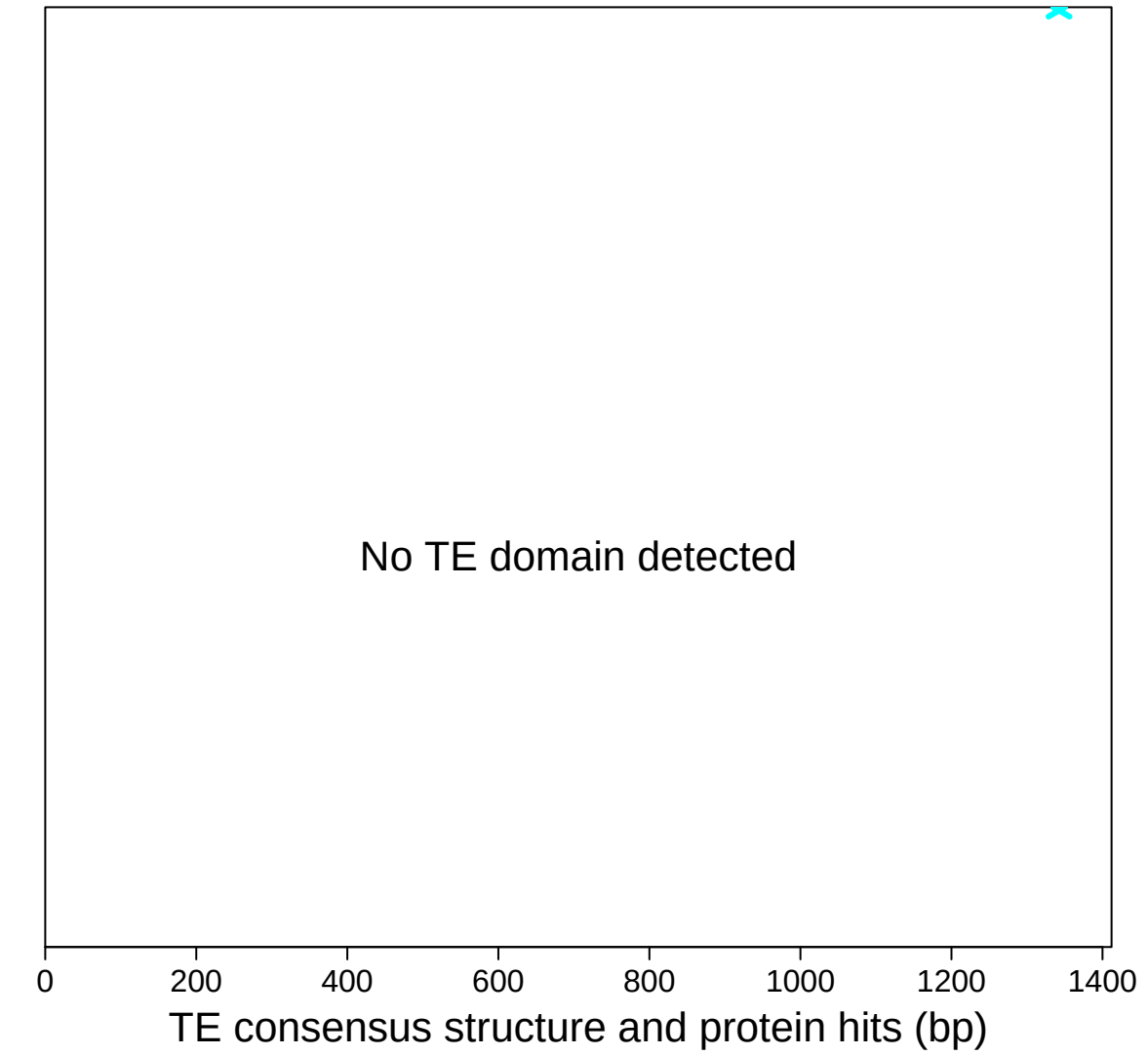
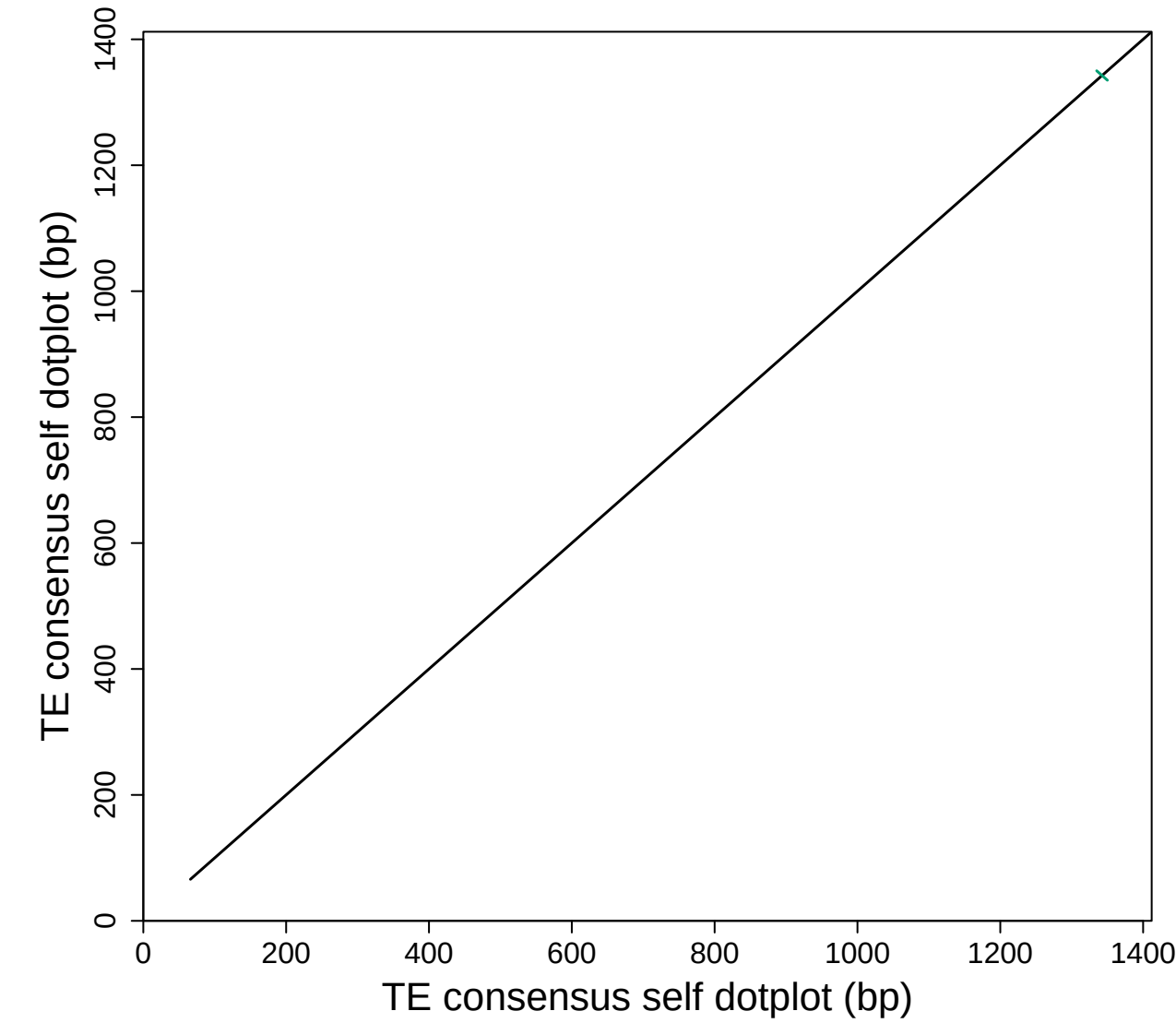
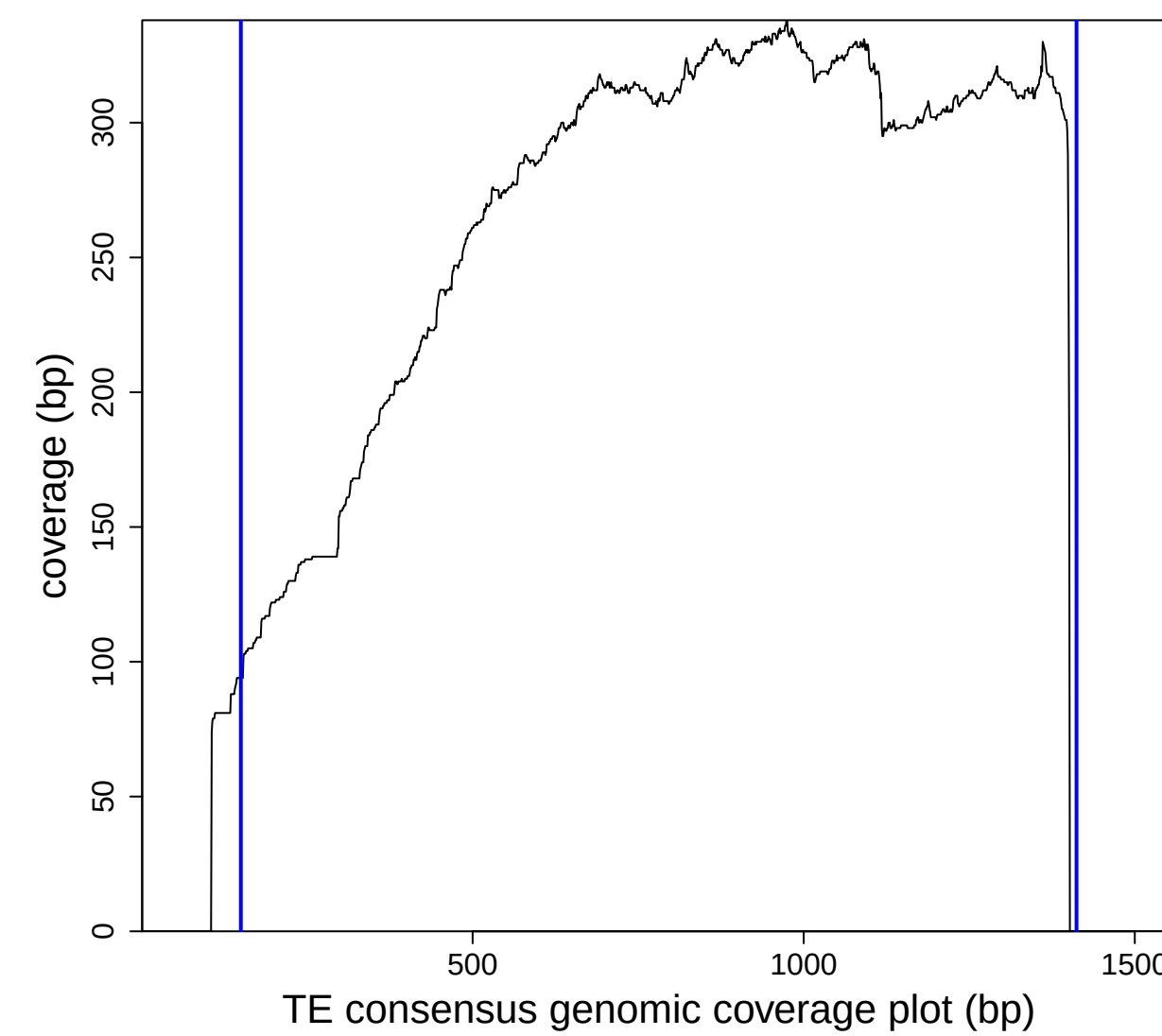
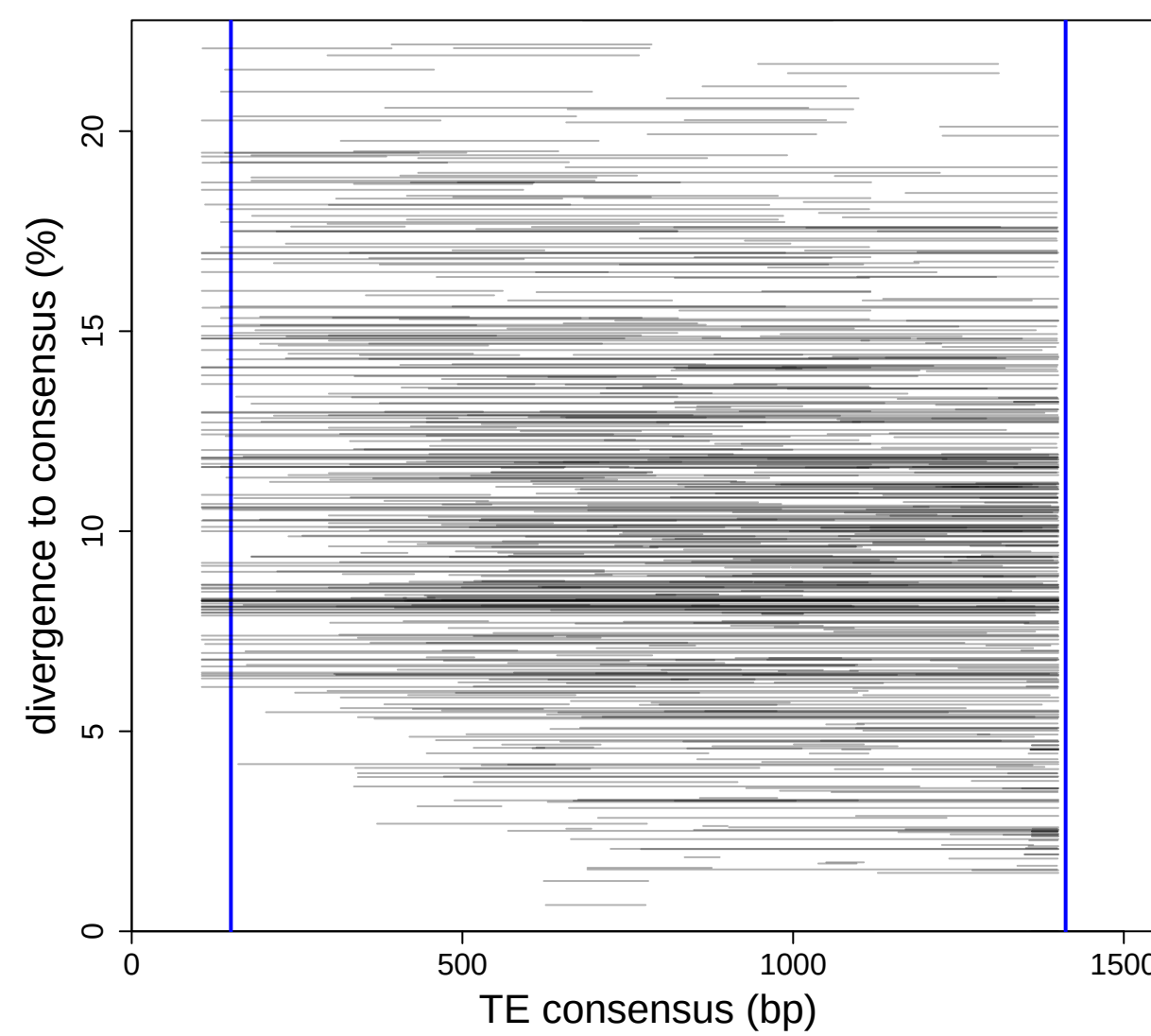
bed\_uf.bed g 4.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c  
size: 1191bp; fragments: 797; full length: 0 (>=1071.9bp)

# After TEtrimmer 1191 bp

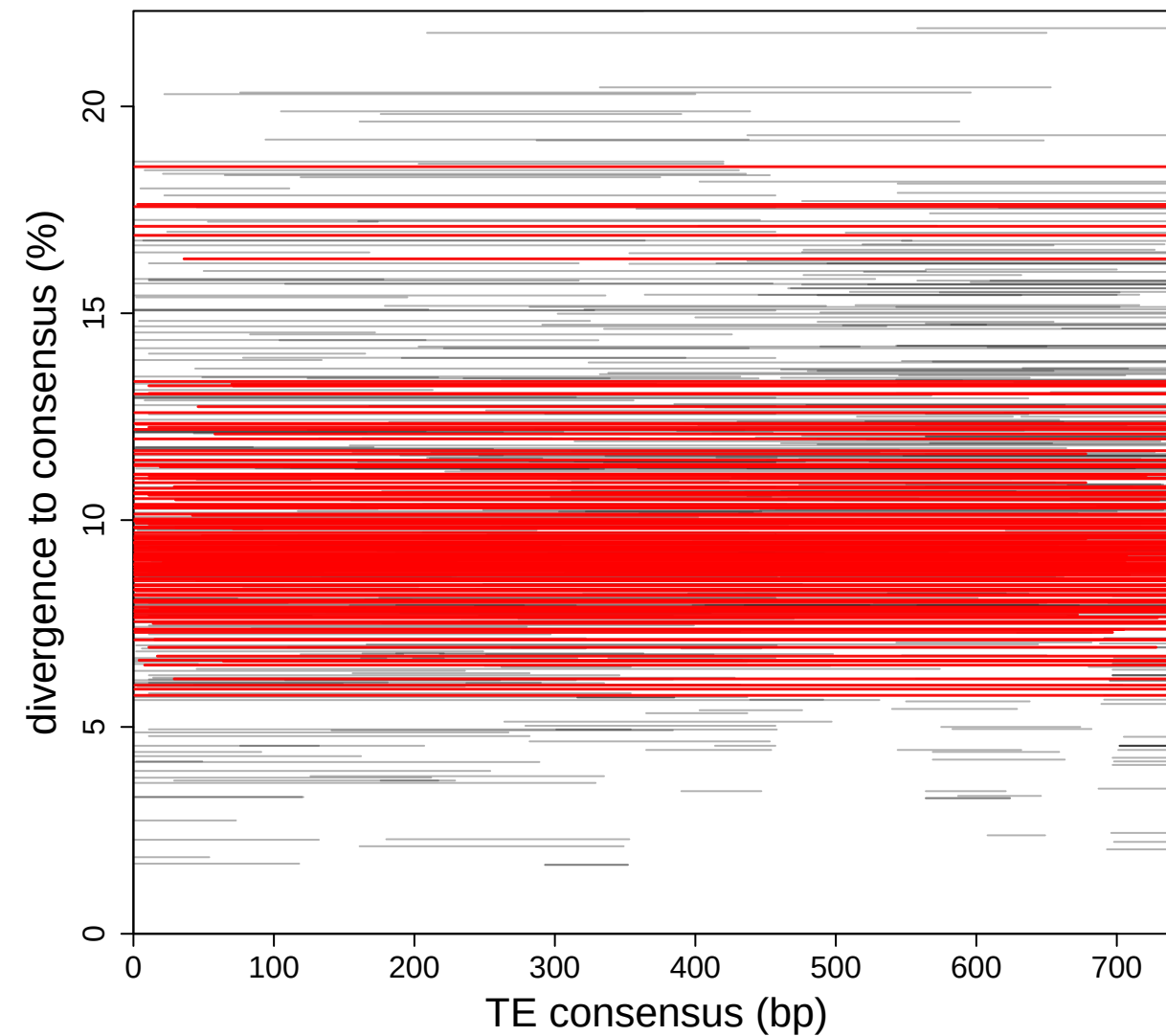


4.fasta.b.bed uf.bed g\_4.bed fm\_1.bed 0 0 bcIn.fa aln.fa cl.f  
size: 1562bp; fragments: 667; full length: 0 (>=1405.8bp)

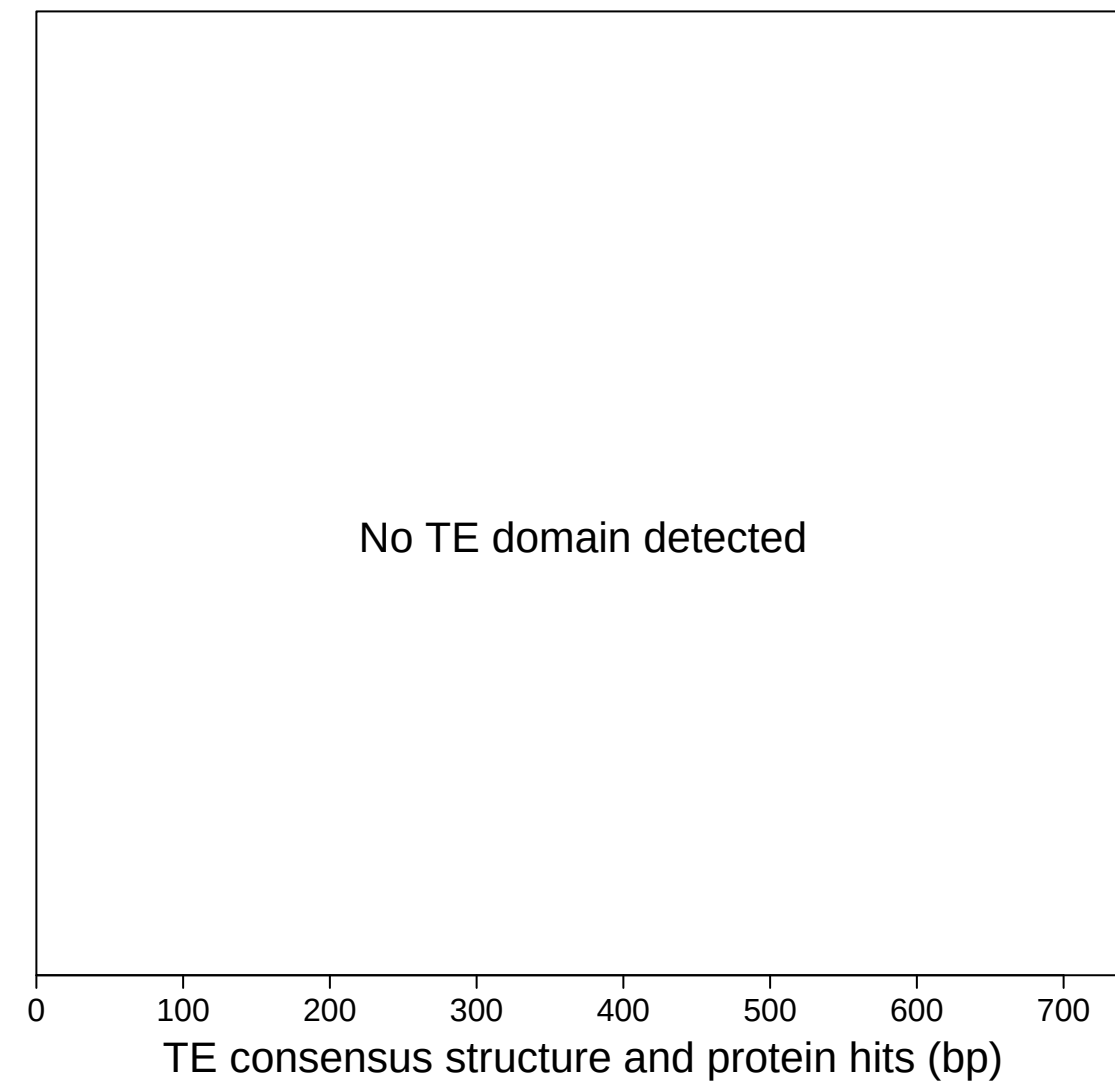
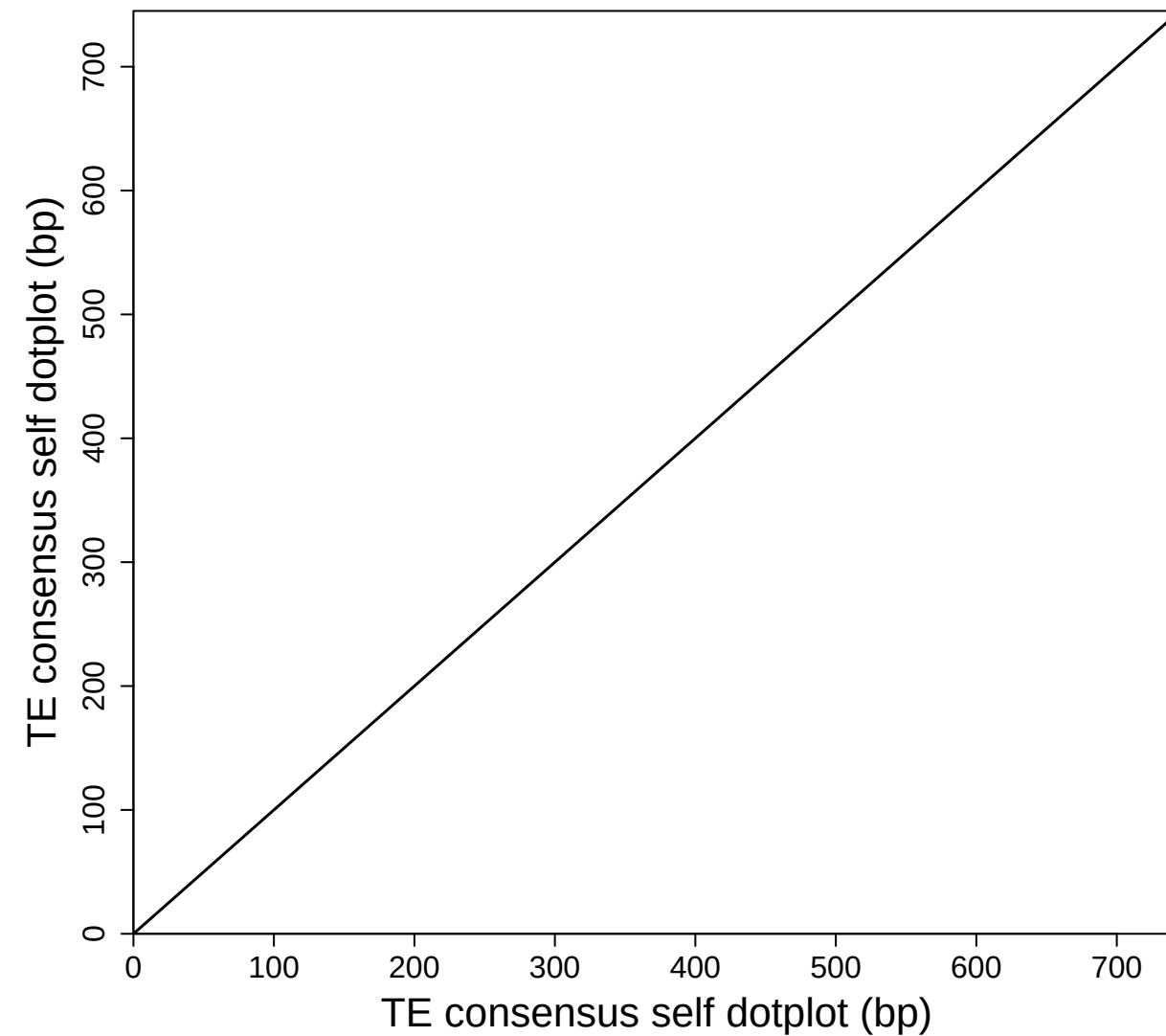
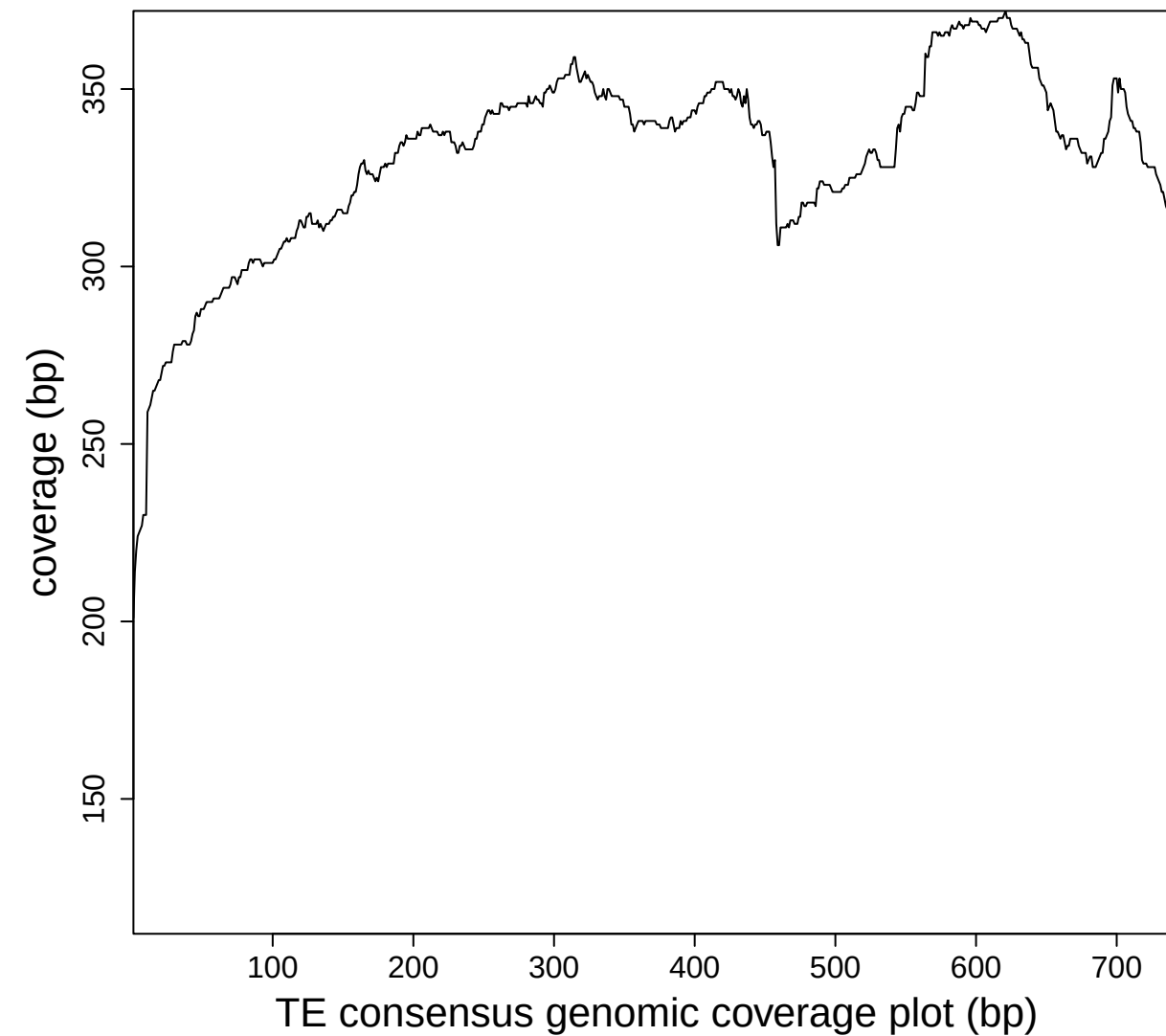
## After TEtrimmer Extended plot Blue lines are boundaries



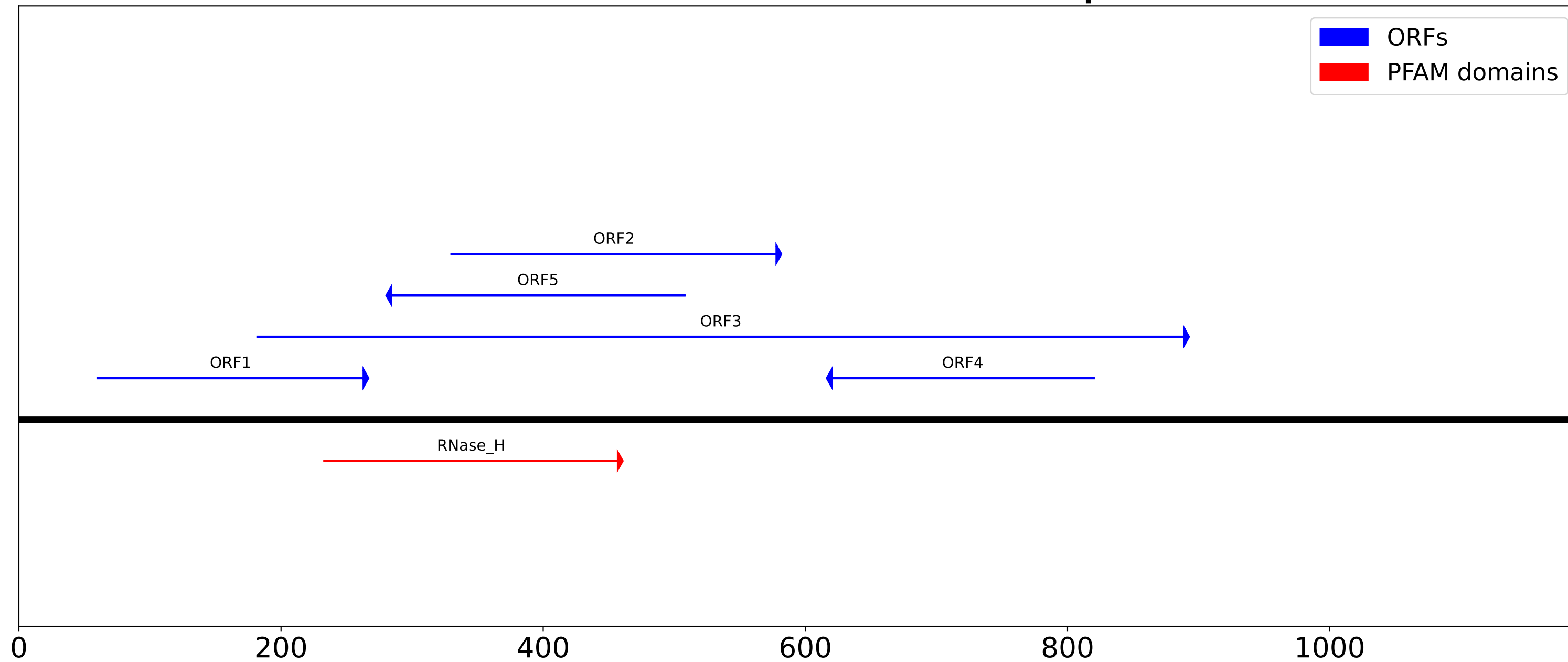
TE: rnd\_4\_family\_3624  
size: 745bp; fragments: 659; full length: 147 ( $\geq 670.5$ bp)



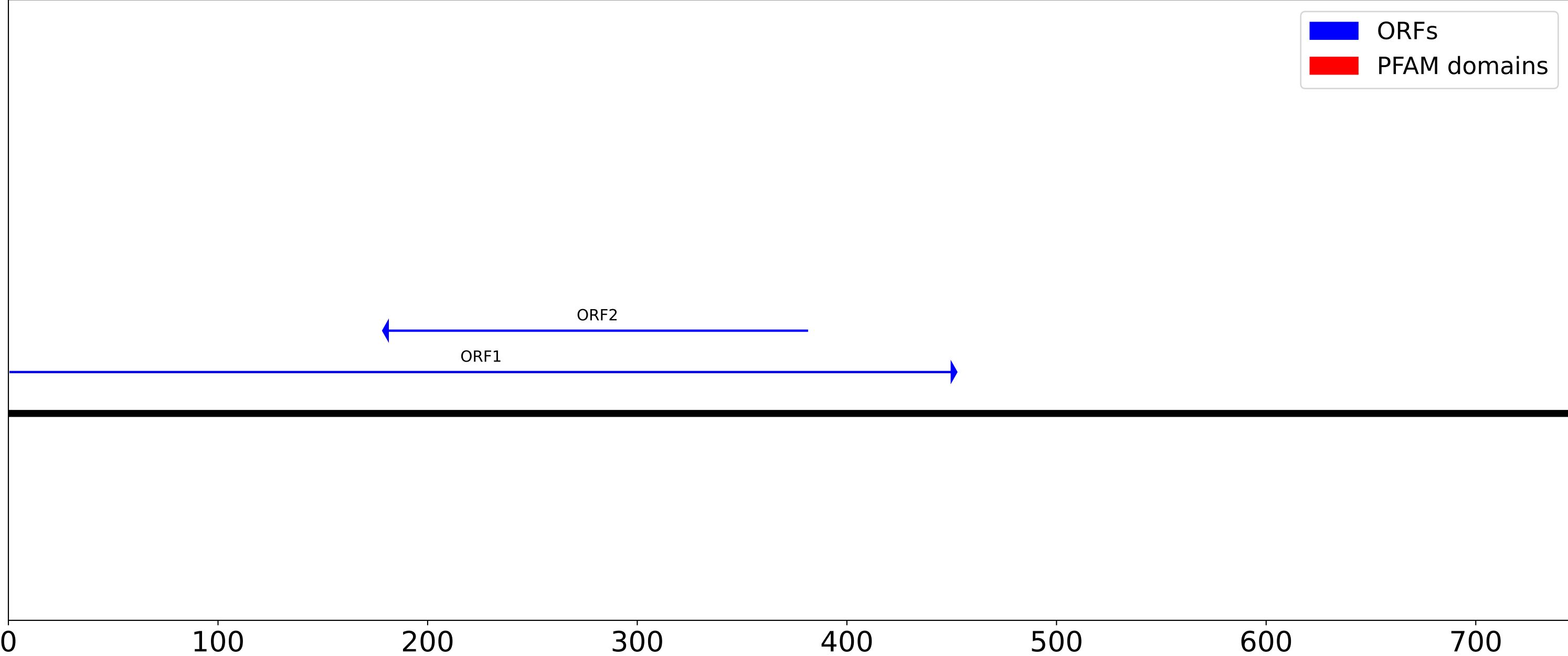
## Before TEtrimmer 745 bp



## After TEtrimmer ORF and PFAM domain plot



**Before TEtrimmer ORF and PFAM domain plot**

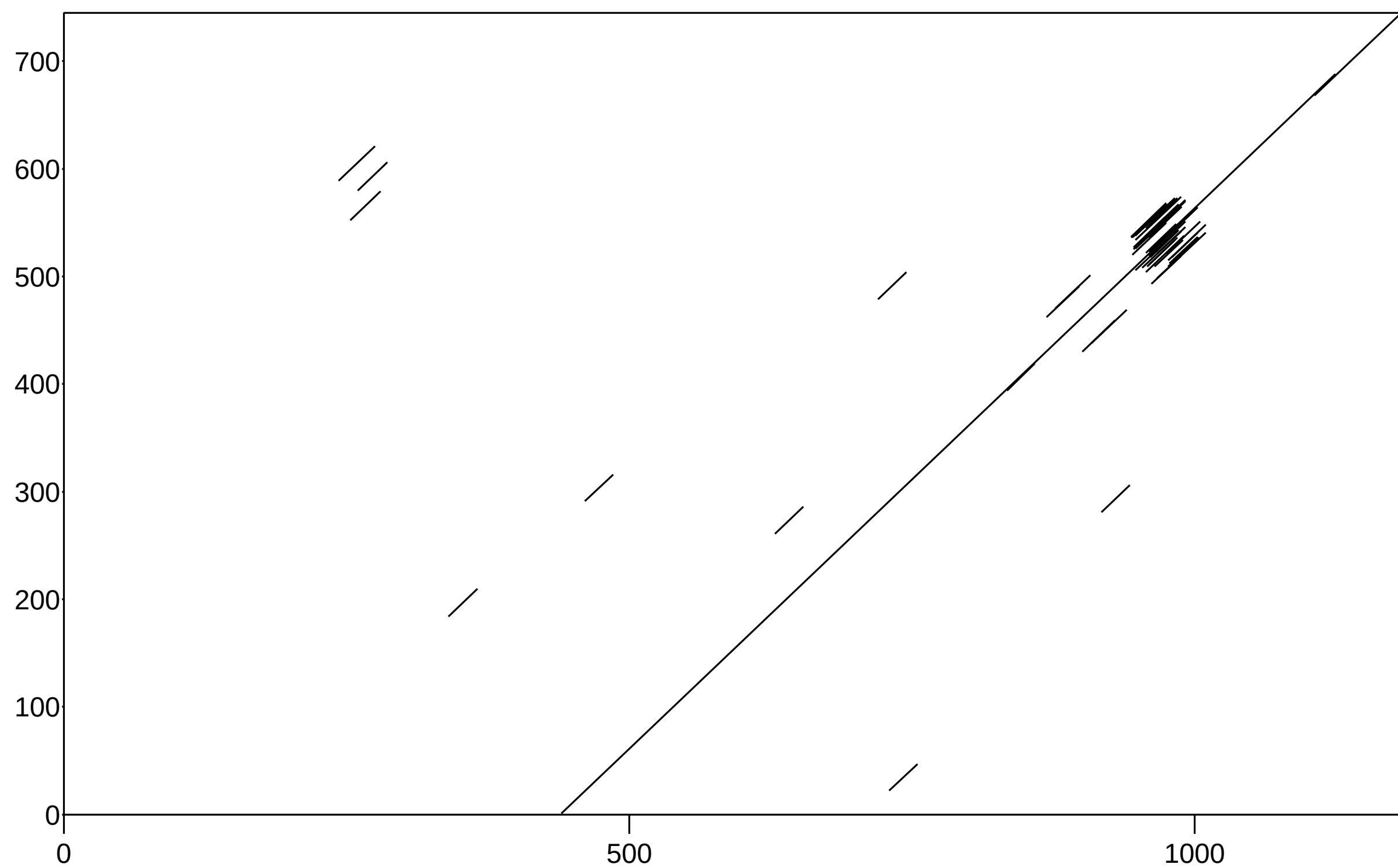




# Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)