

Start crop Point

End crop Point

MSA length = 5623



Start crop Point

End crop Point

0

10

0

1000

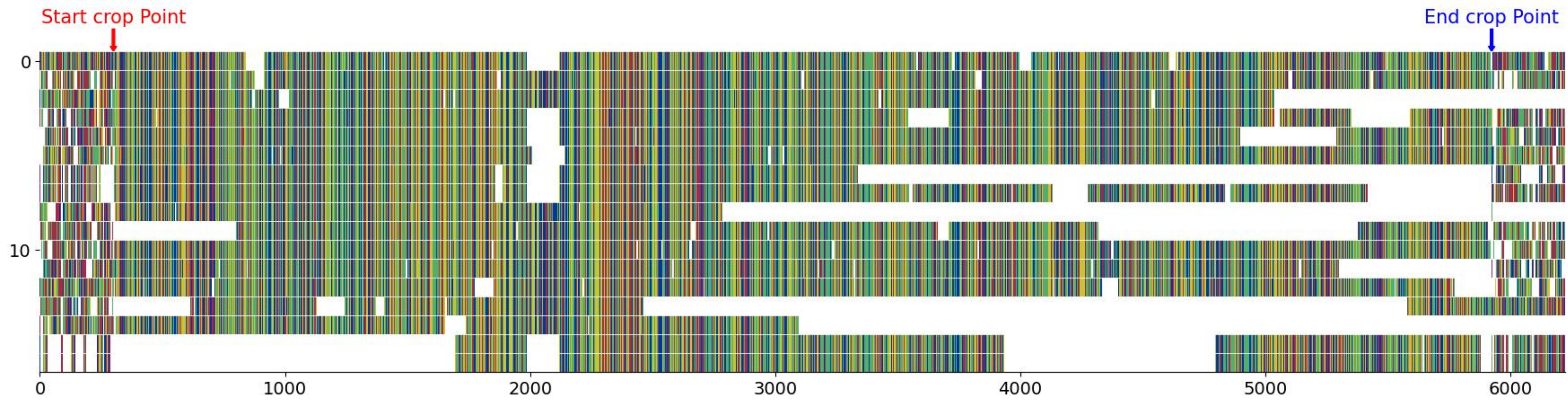
2000

3000

4000

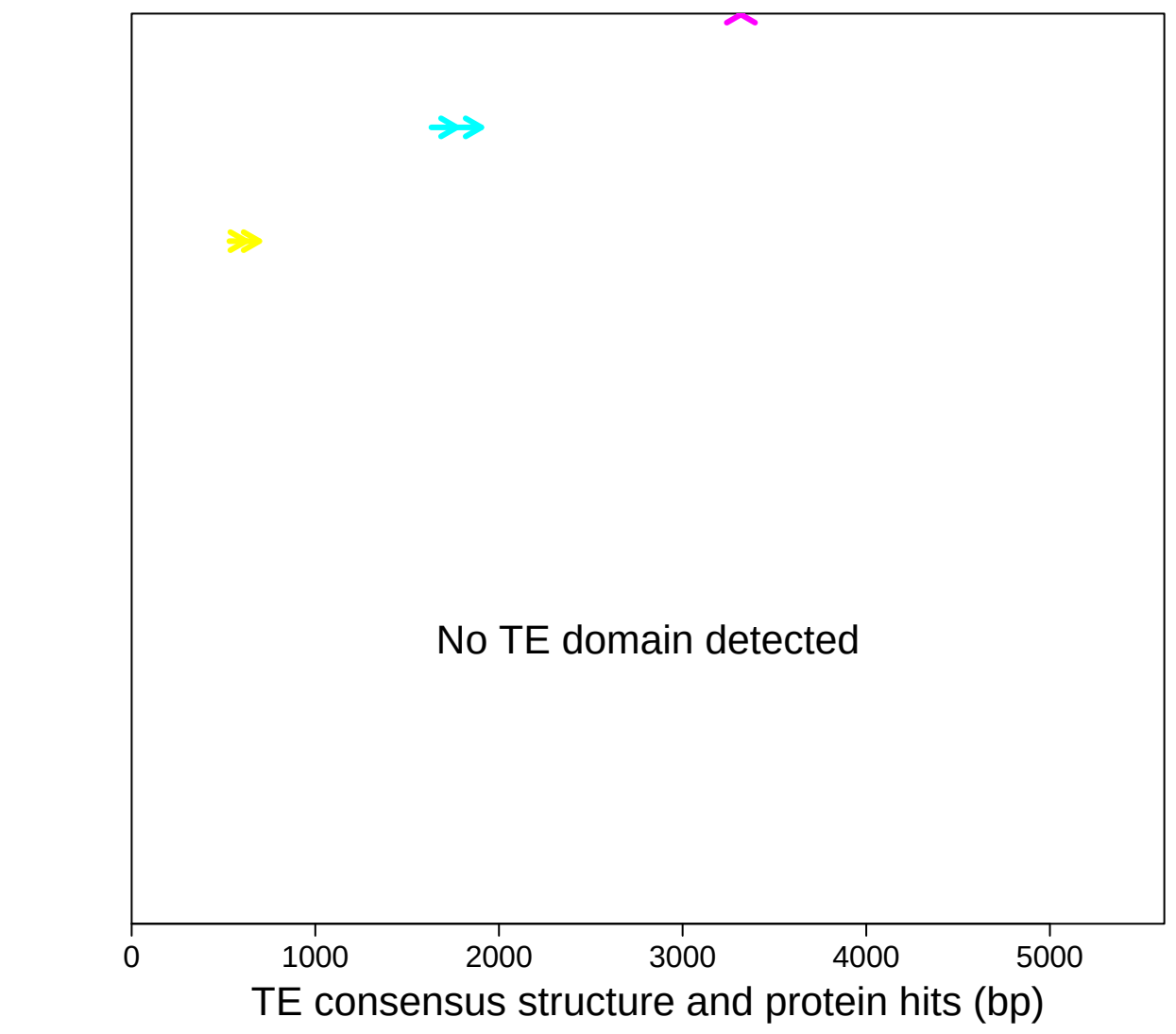
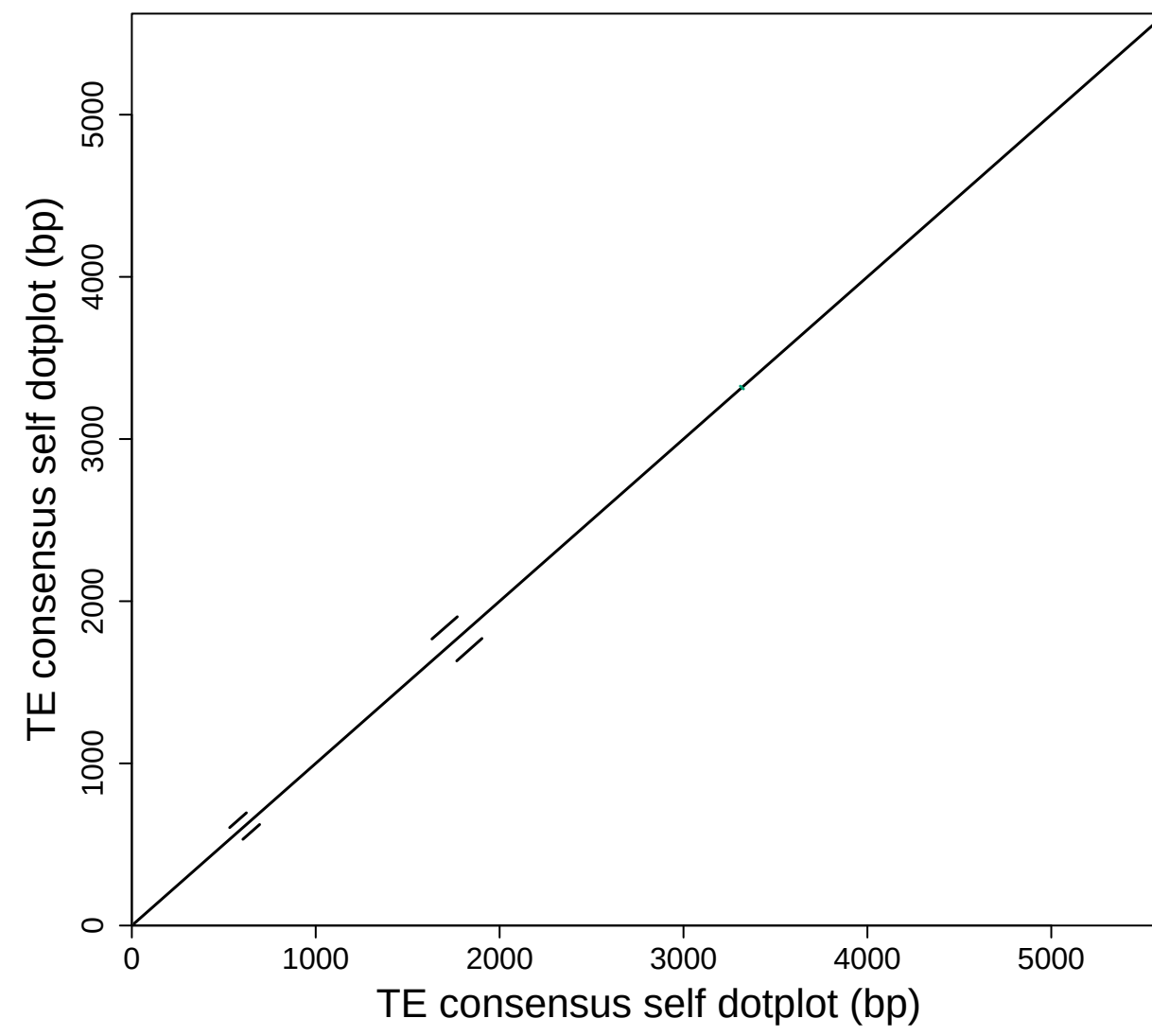
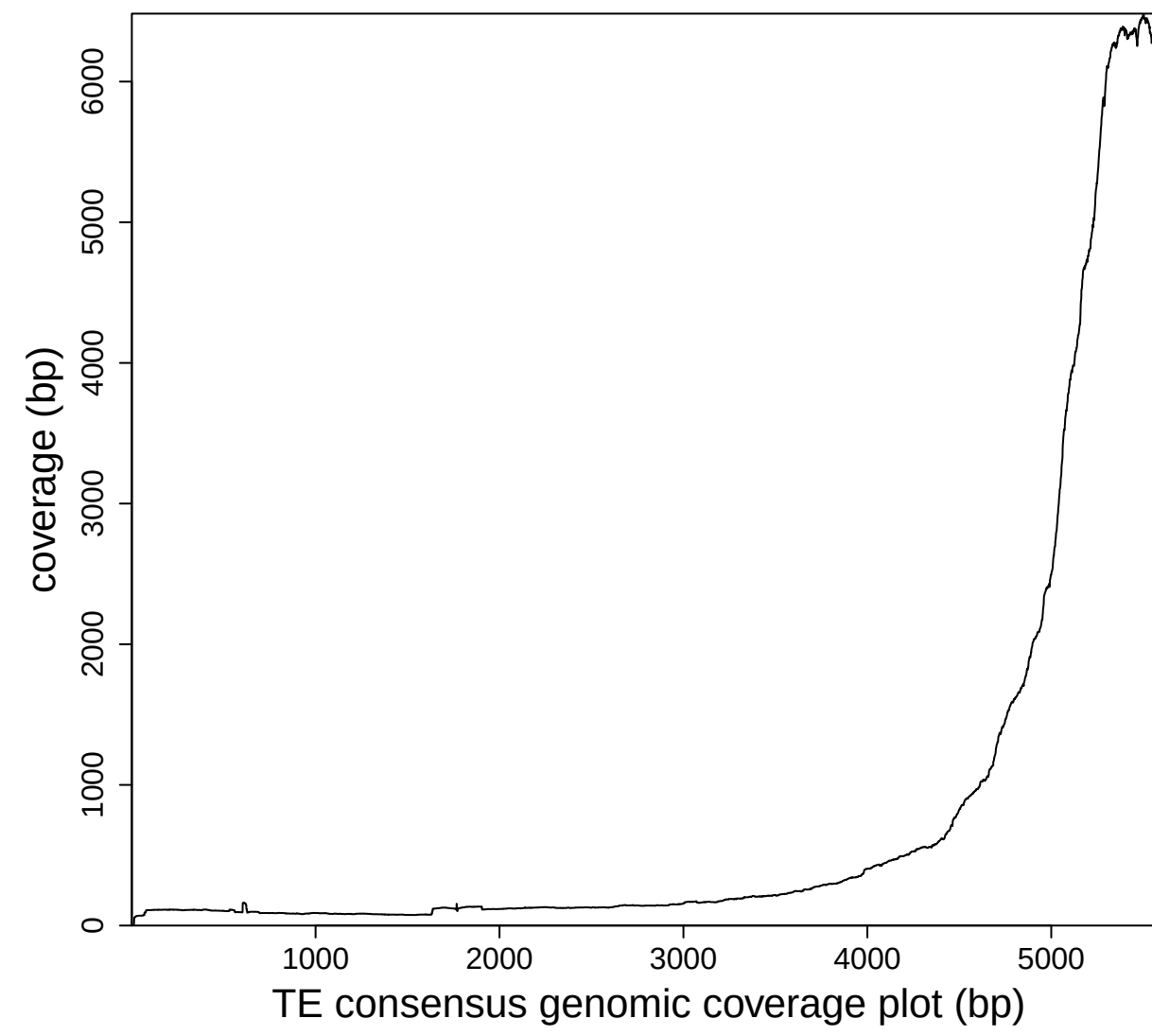
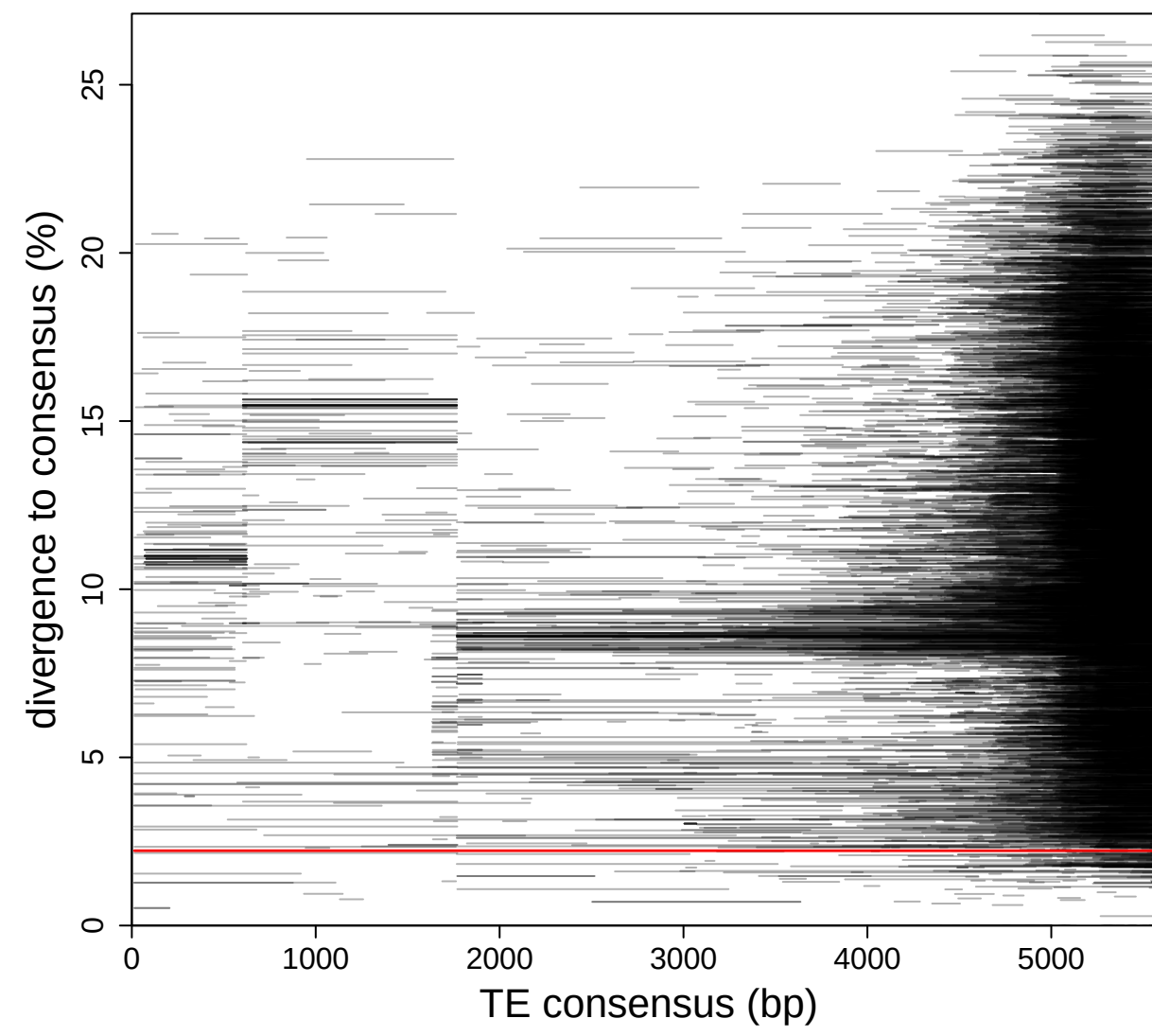
5000

6000



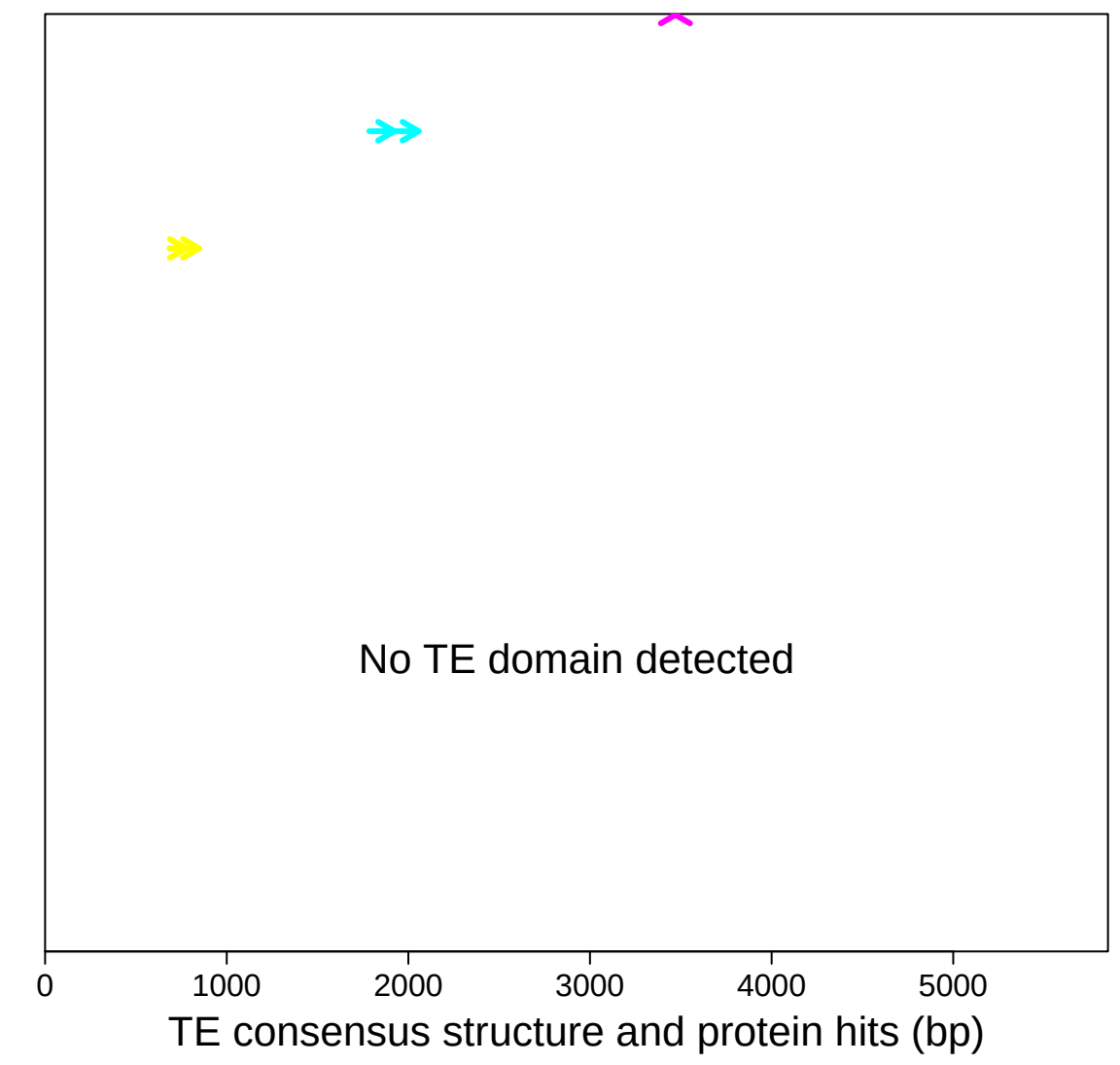
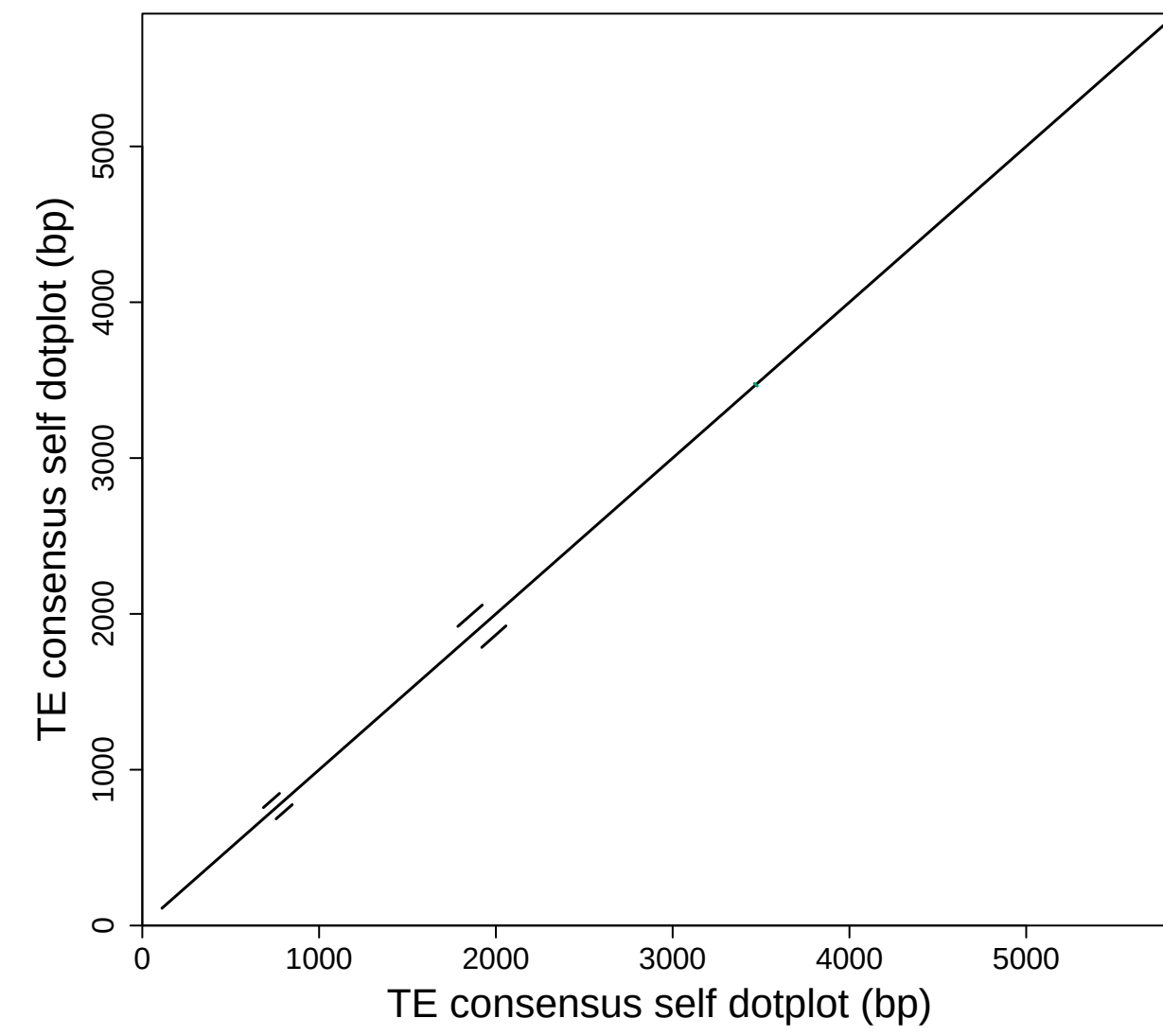
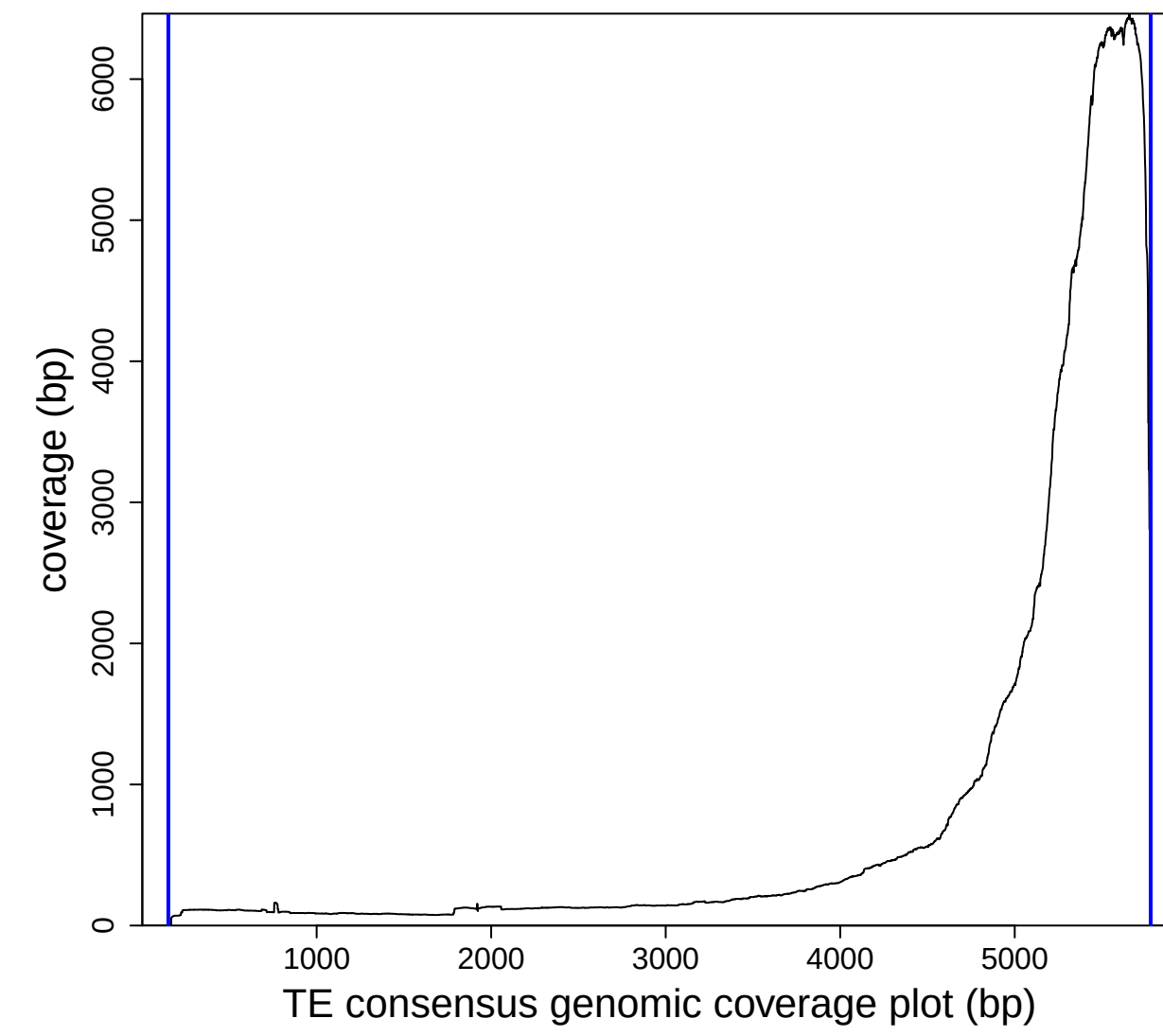
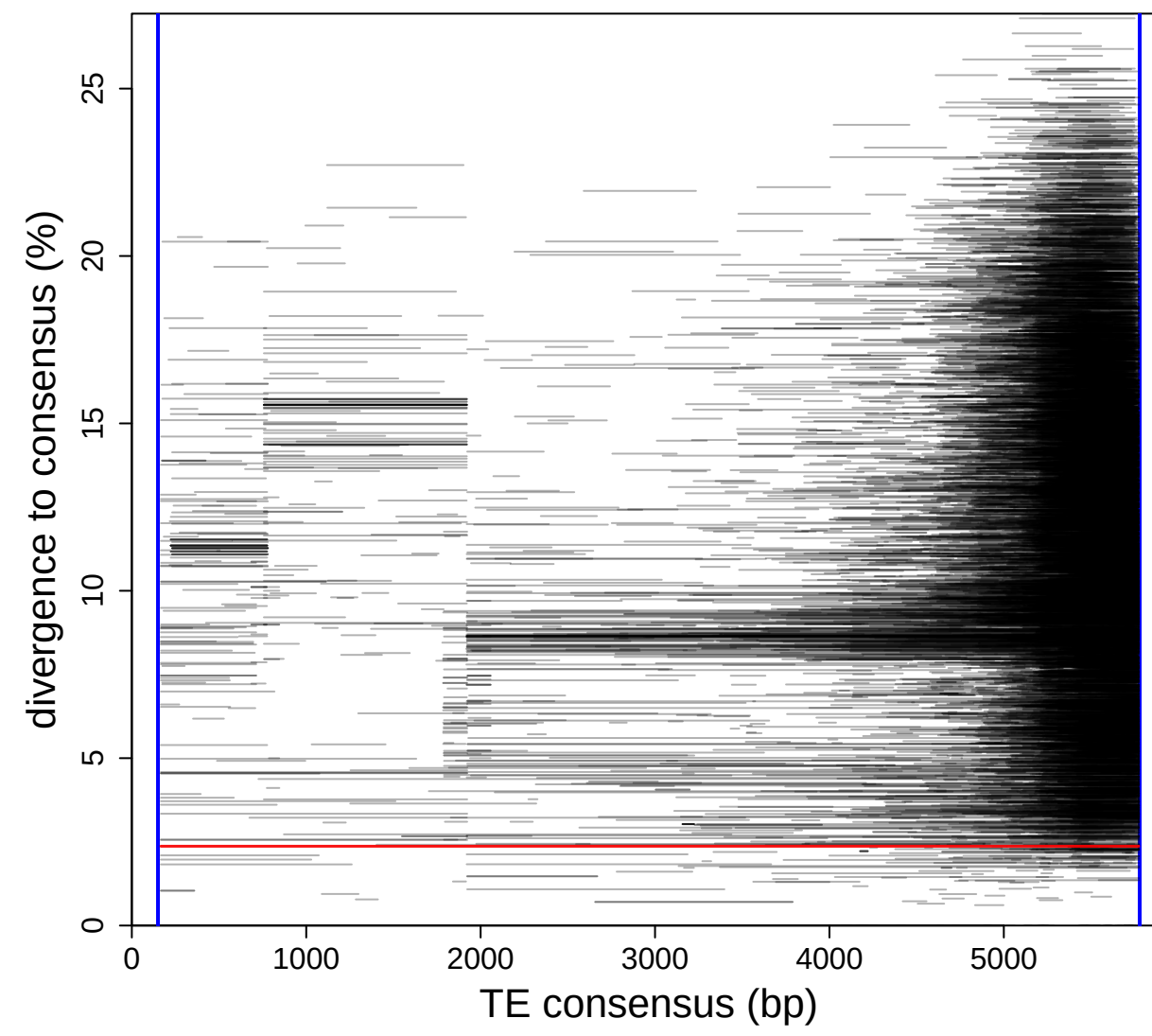
bed uf.bed g 3.bed fm 1.bed 0 0 bcln.fa aln.fa cl.fa gs.fa c
size: 5623bp; fragments: 11463; full length: 1 (>=5060.7bp)

After TEtrimmer 5623 bp

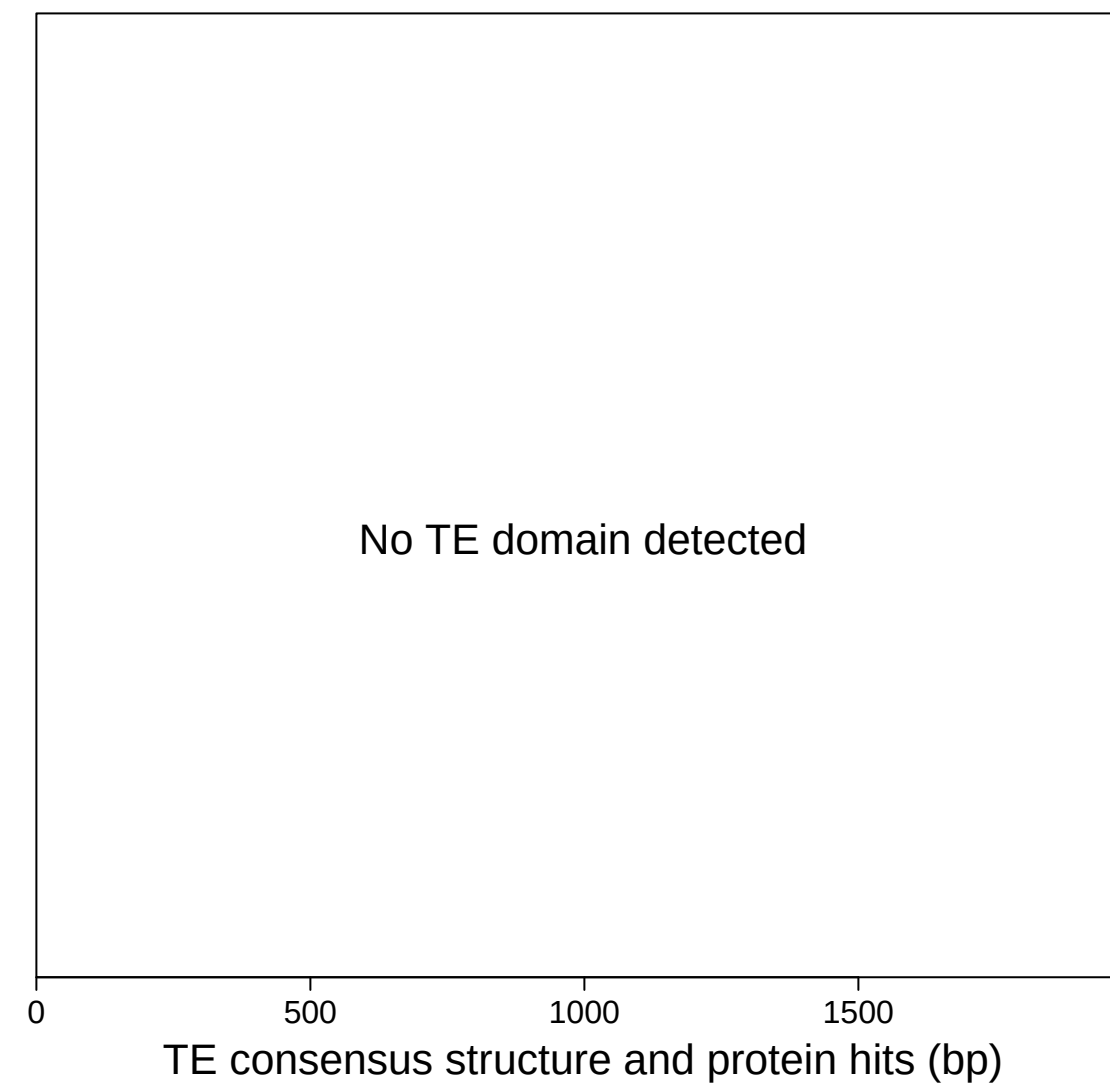
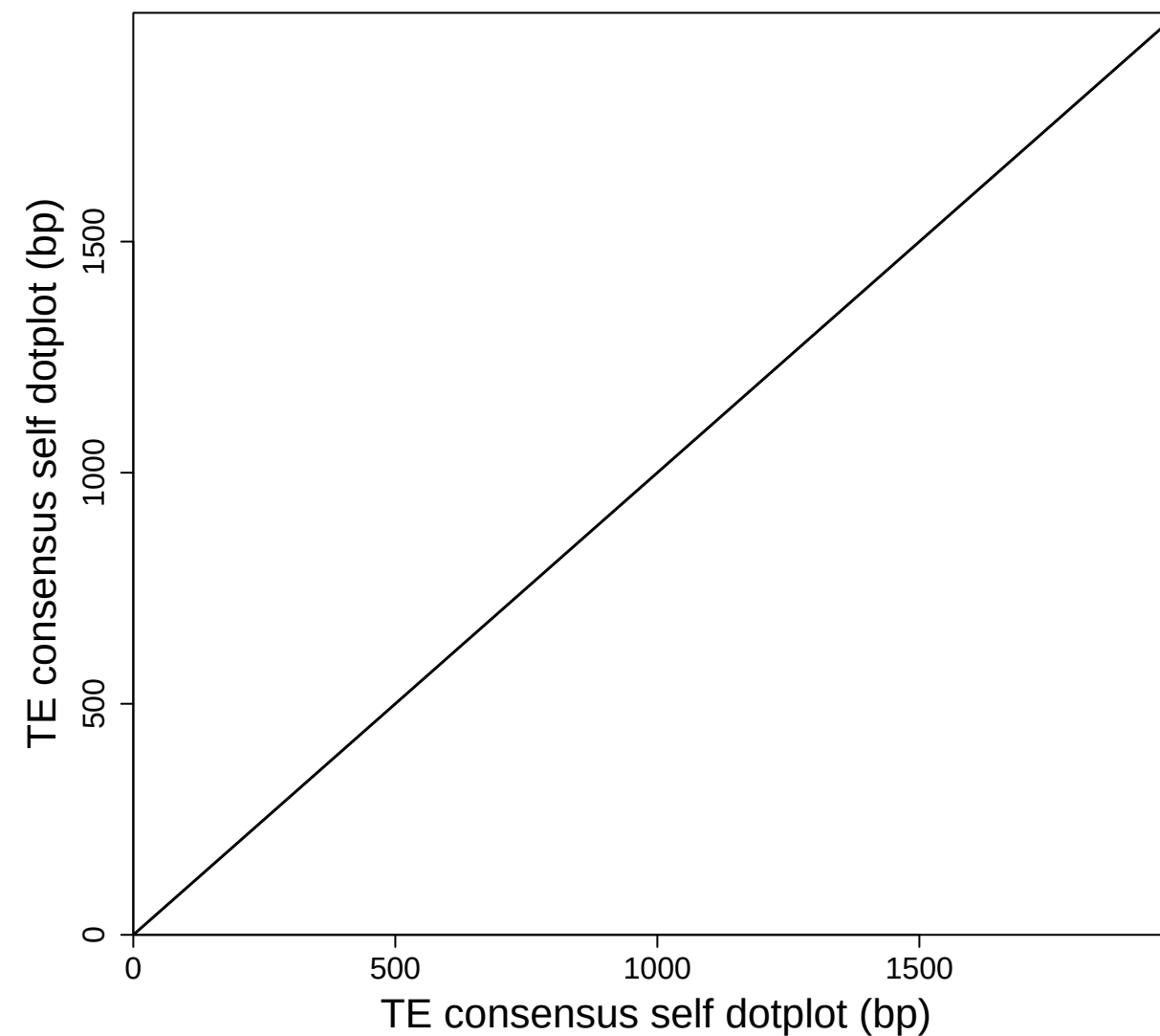
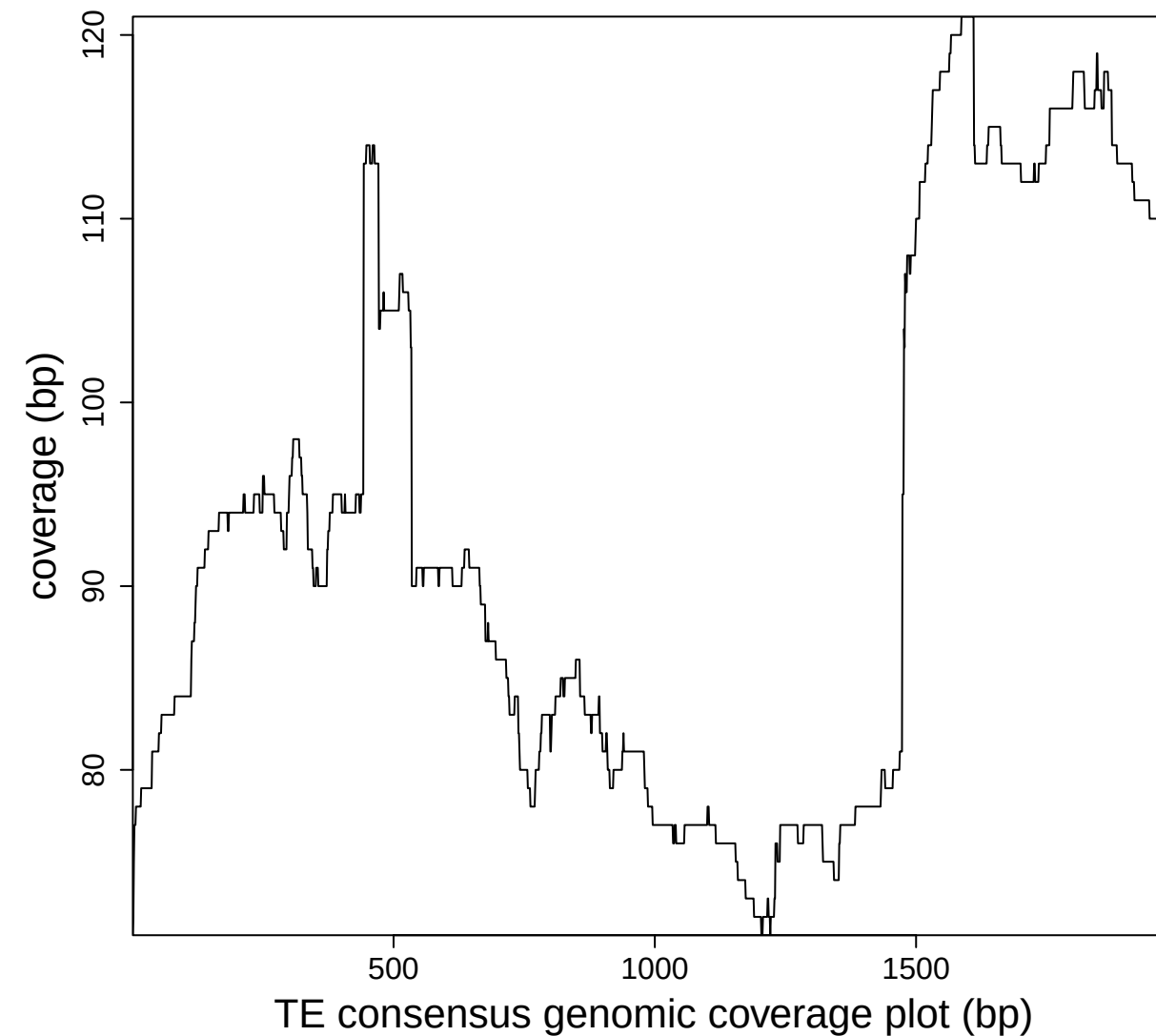
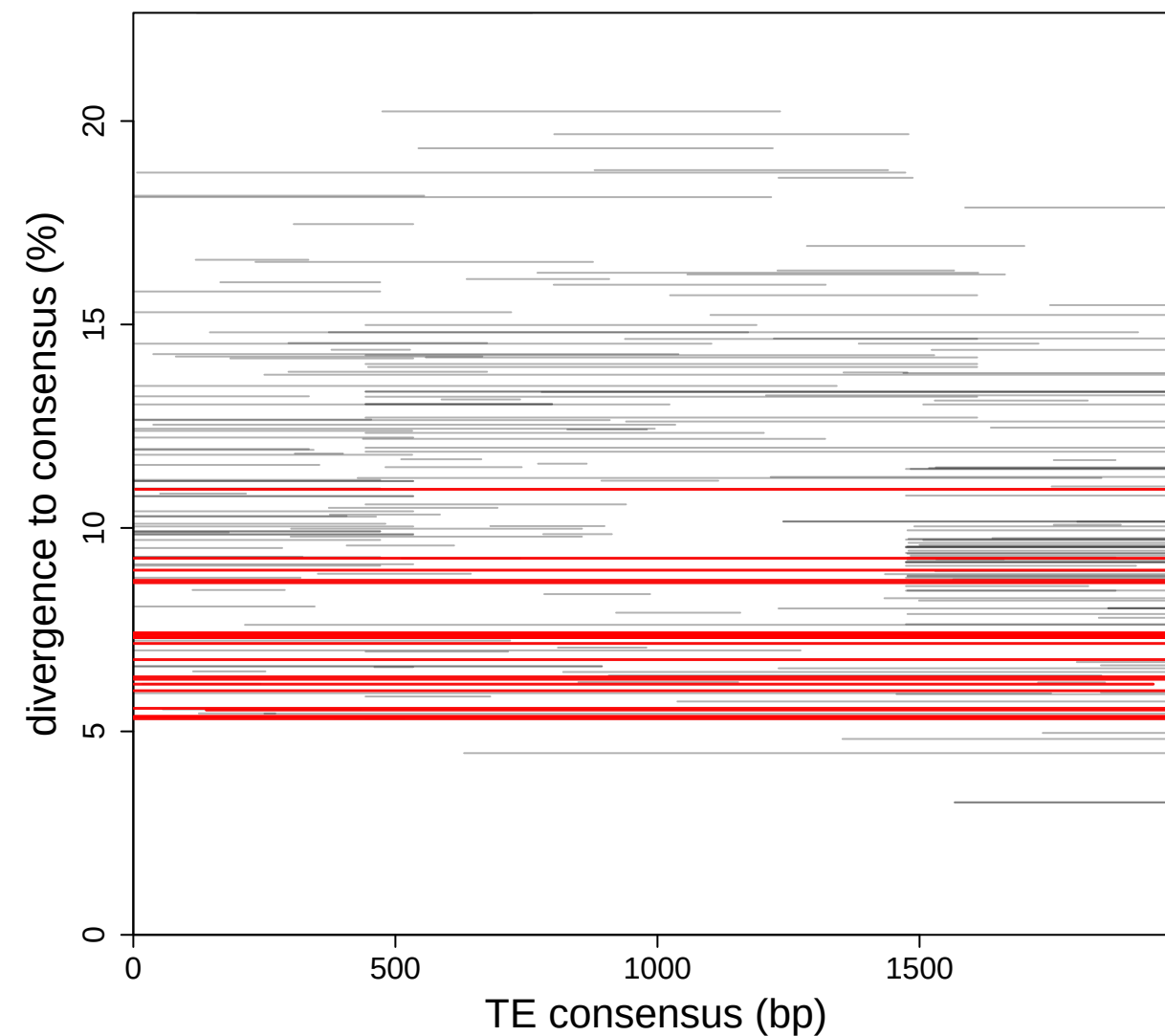


3.fasta.b.bed uf.bed g_3.bed fm_1.bed 0 0 bcln.fa aln.fa cl.f
size: 5929bp; fragments: 11417; full length: 1 (>=5336.1bp)

After TEtrimmer Extended plot Blue lines are boundaries

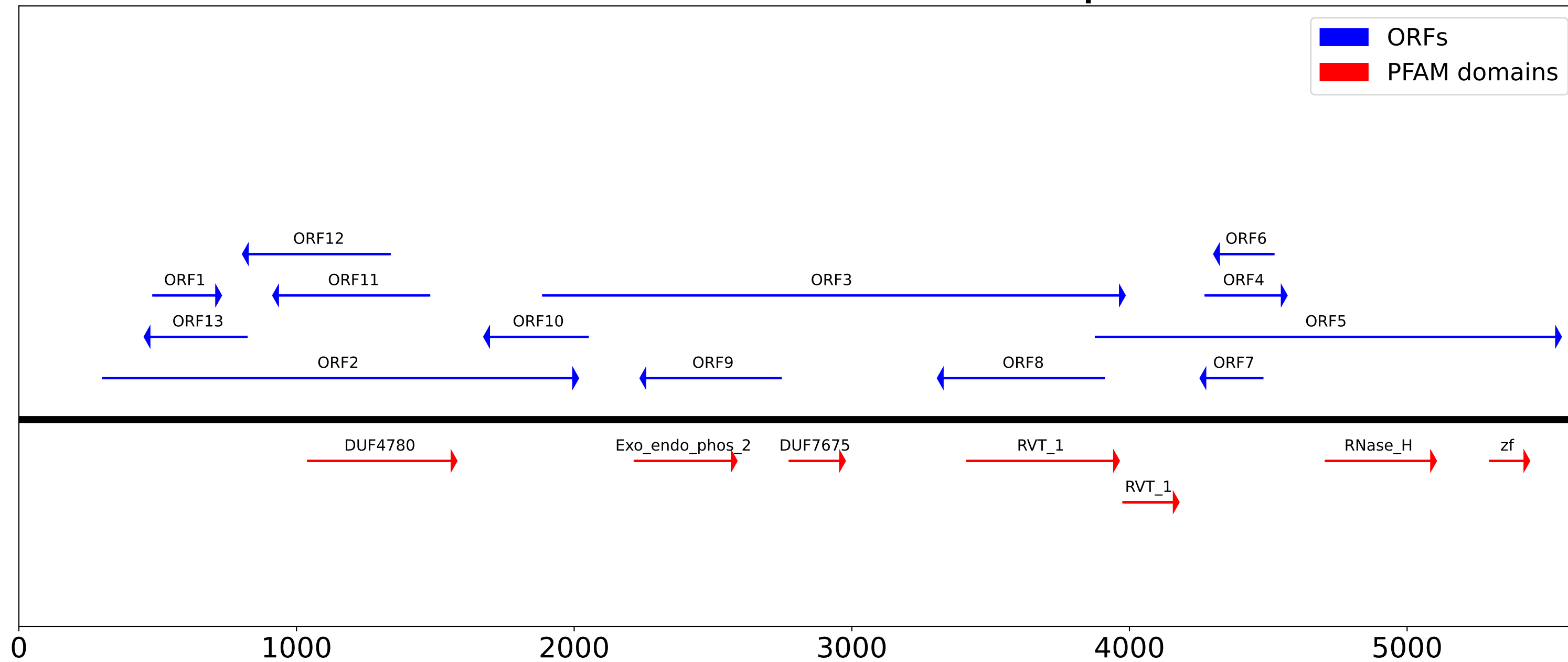


TE: rnd_5_family_2193
size: 1995bp; fragments: 245; full length: 33 (≥ 1795.5 bp)

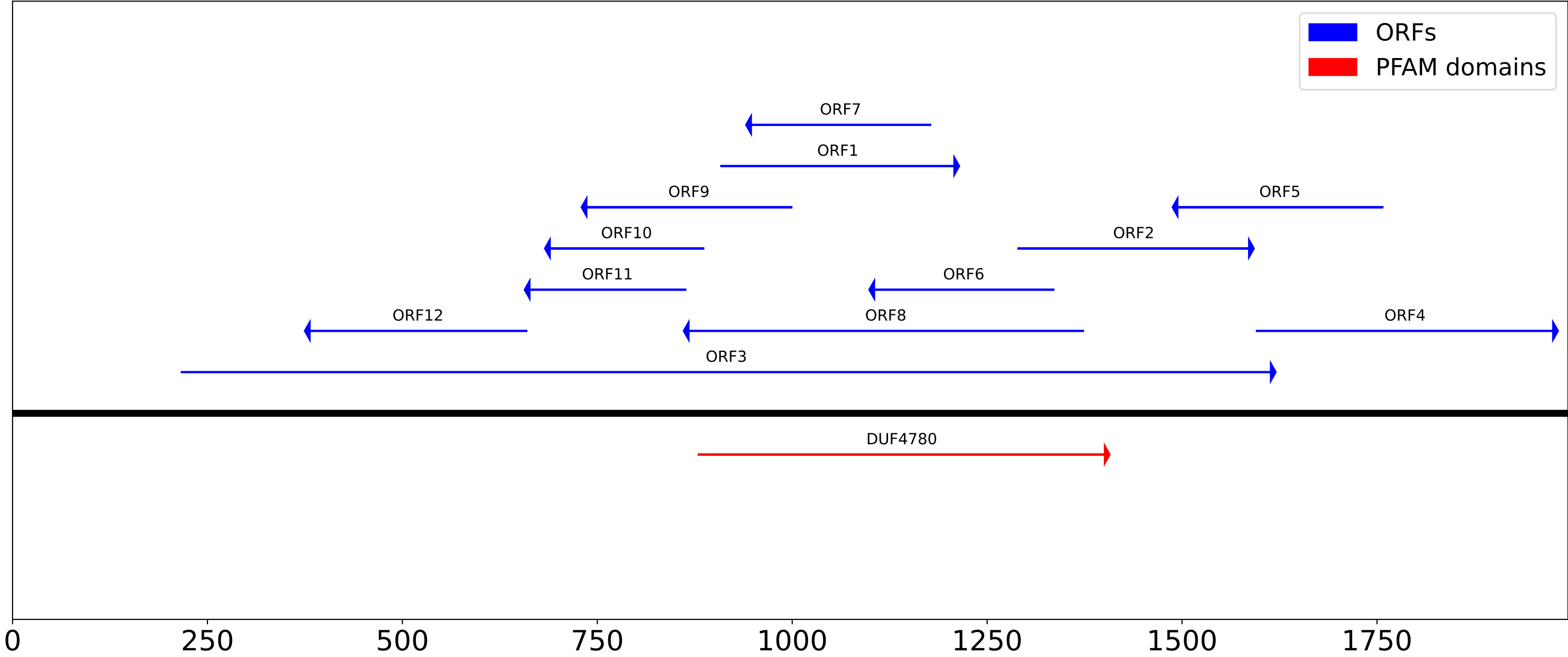


Before TEtrimmer 1995 bp

After TEtrimmer ORF and PFAM domain plot



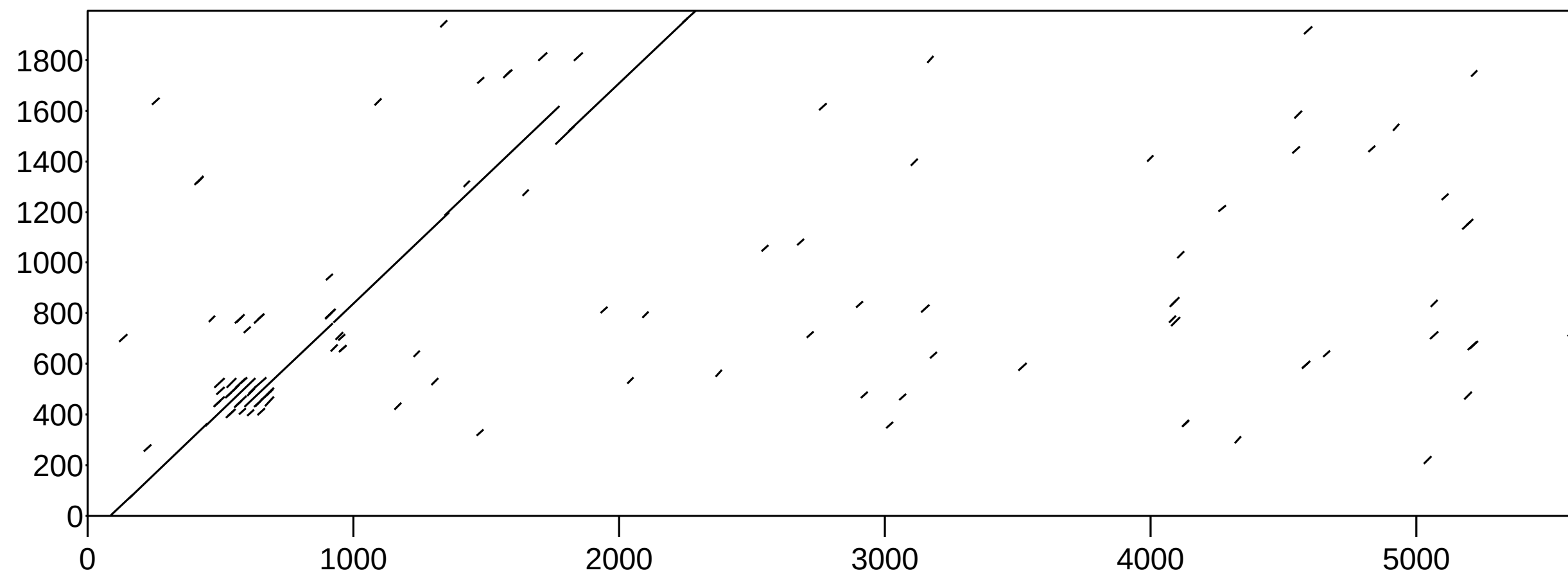
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)