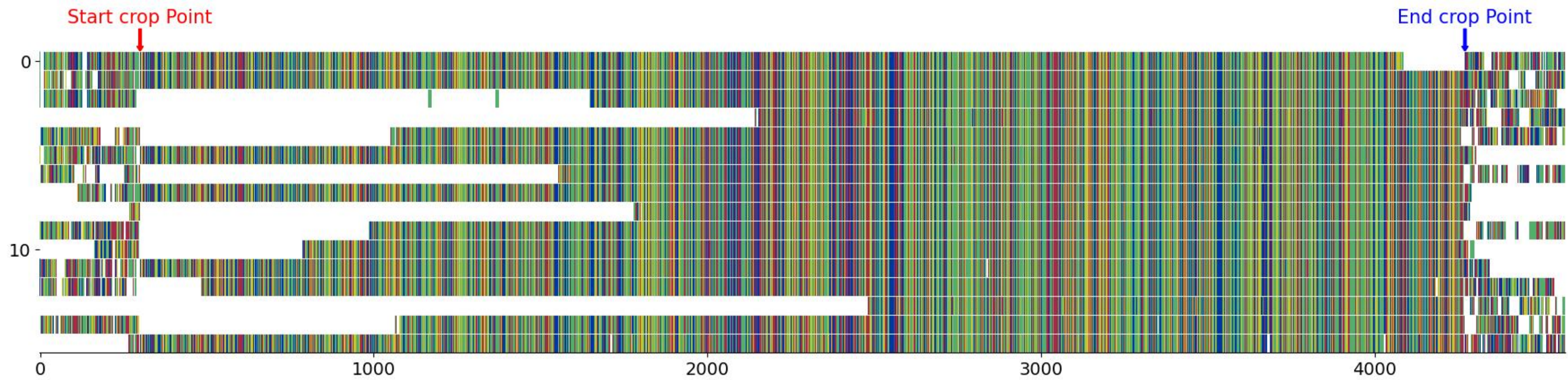


MSA length = 3971



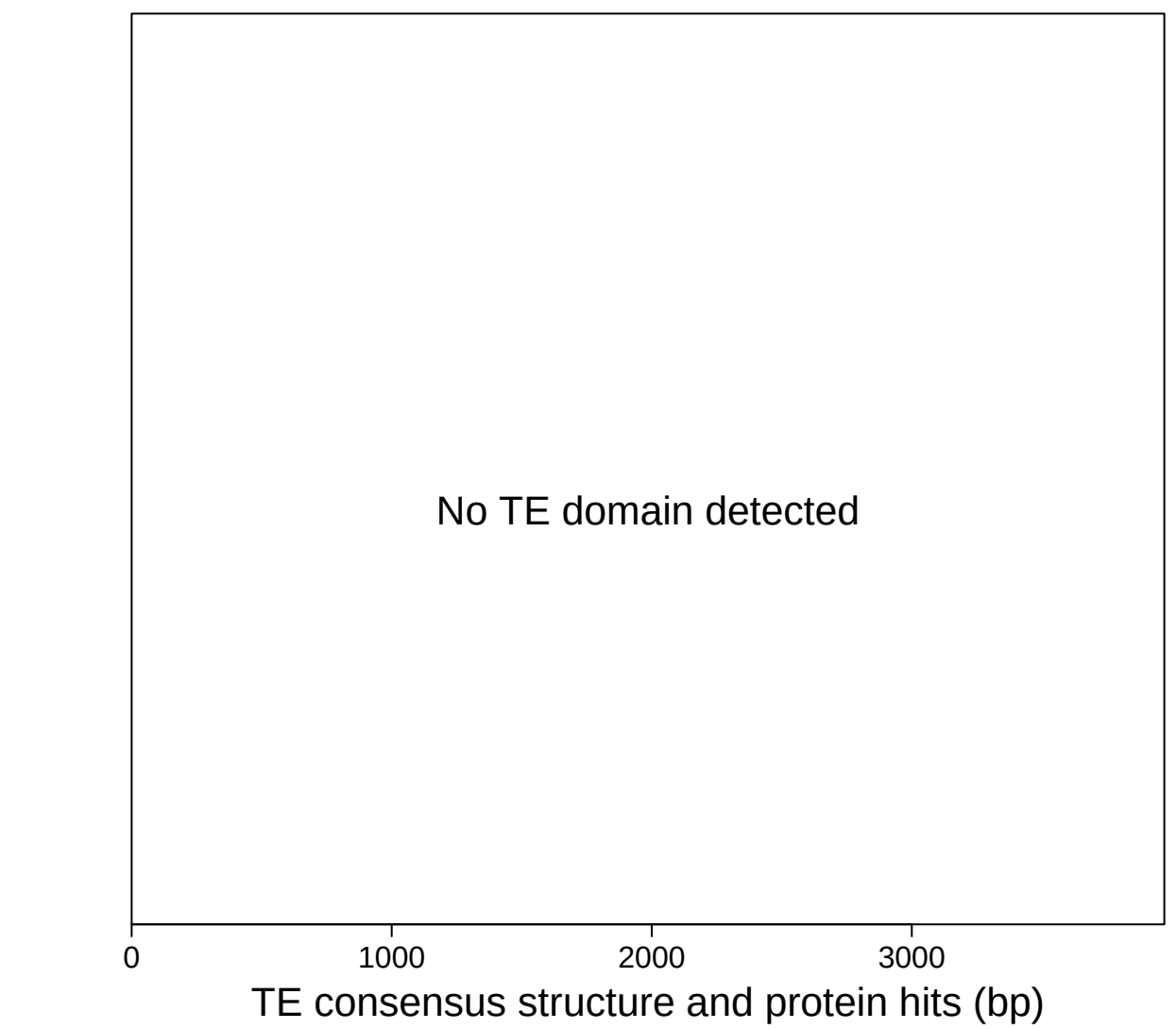
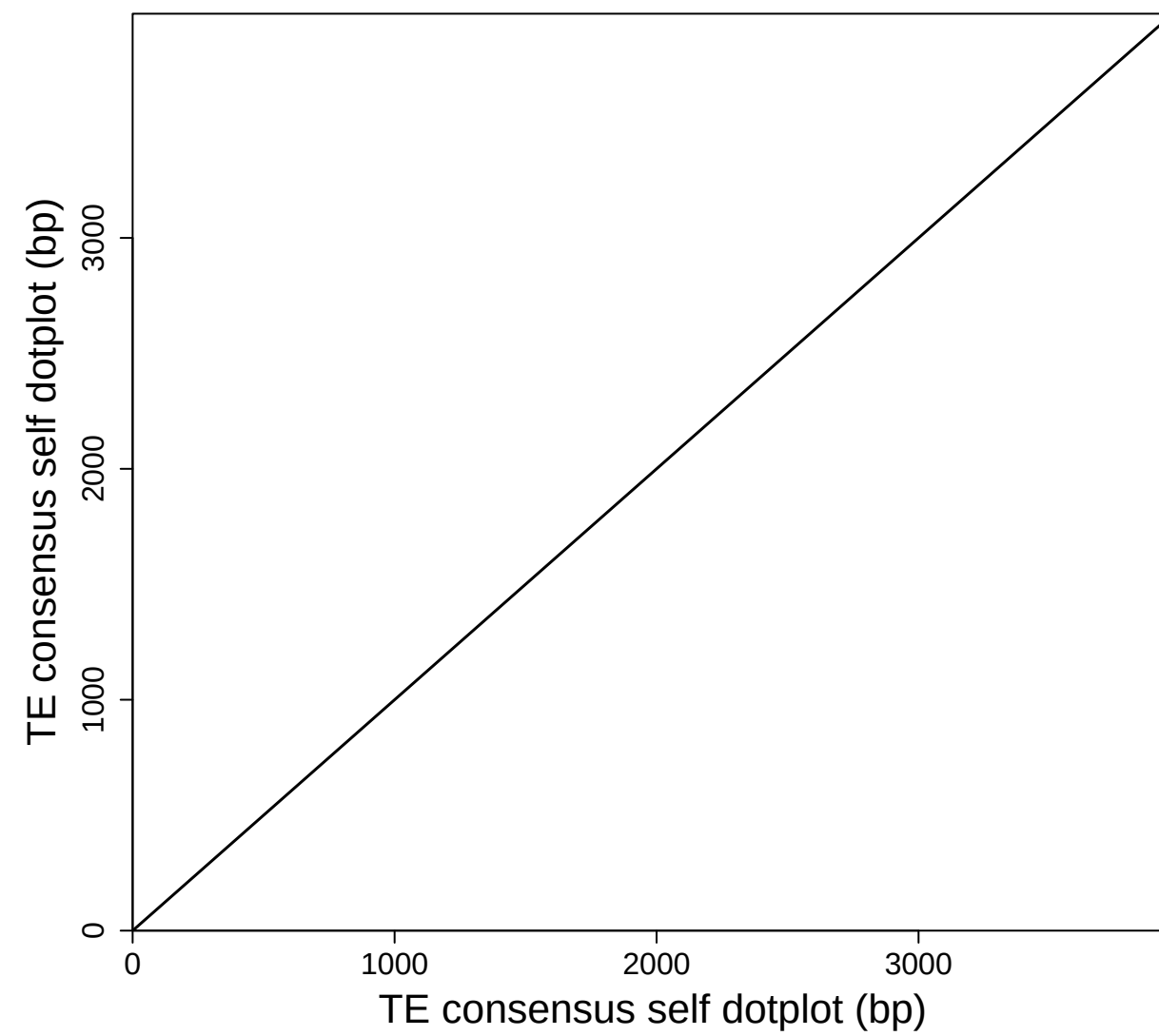
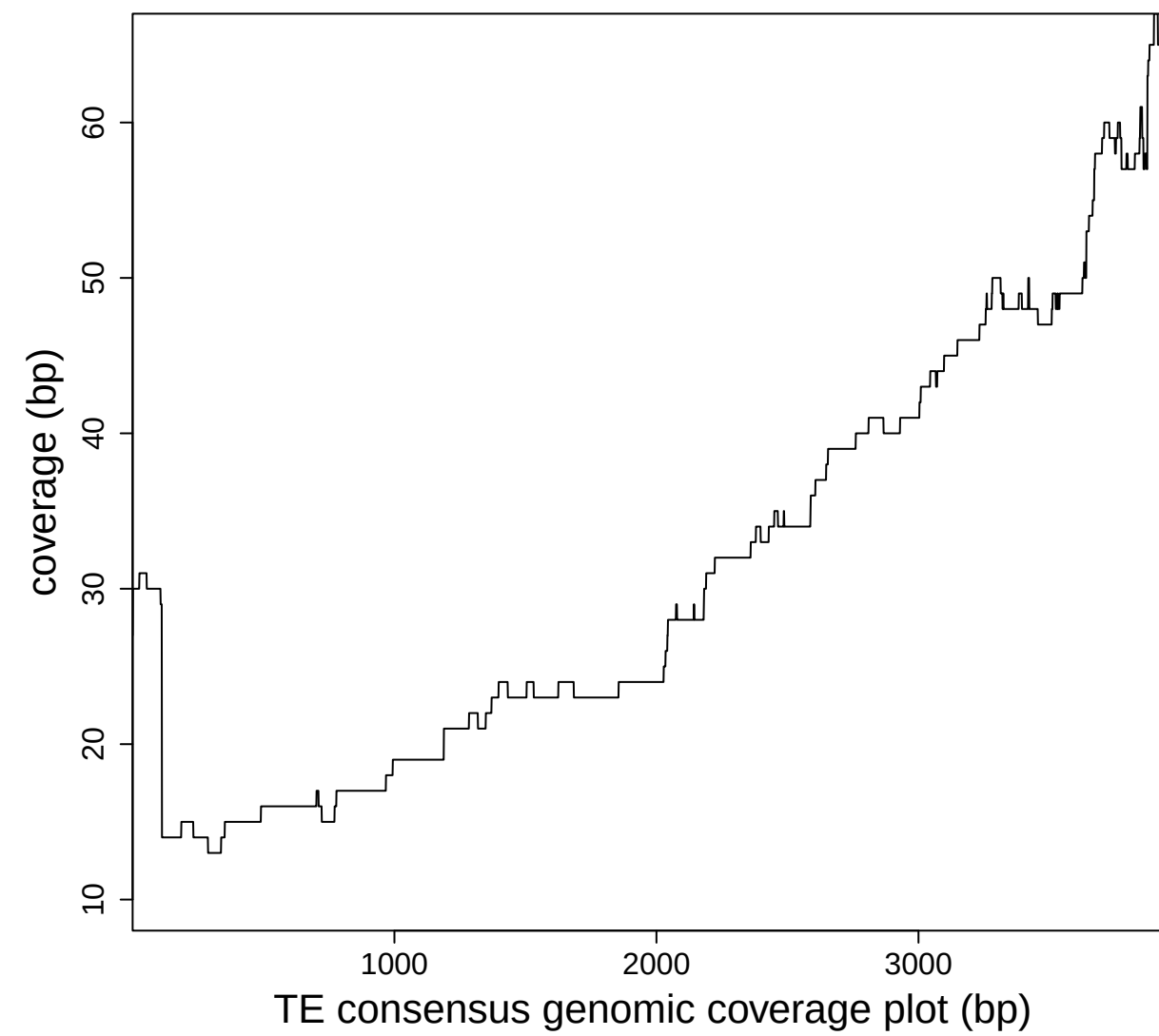
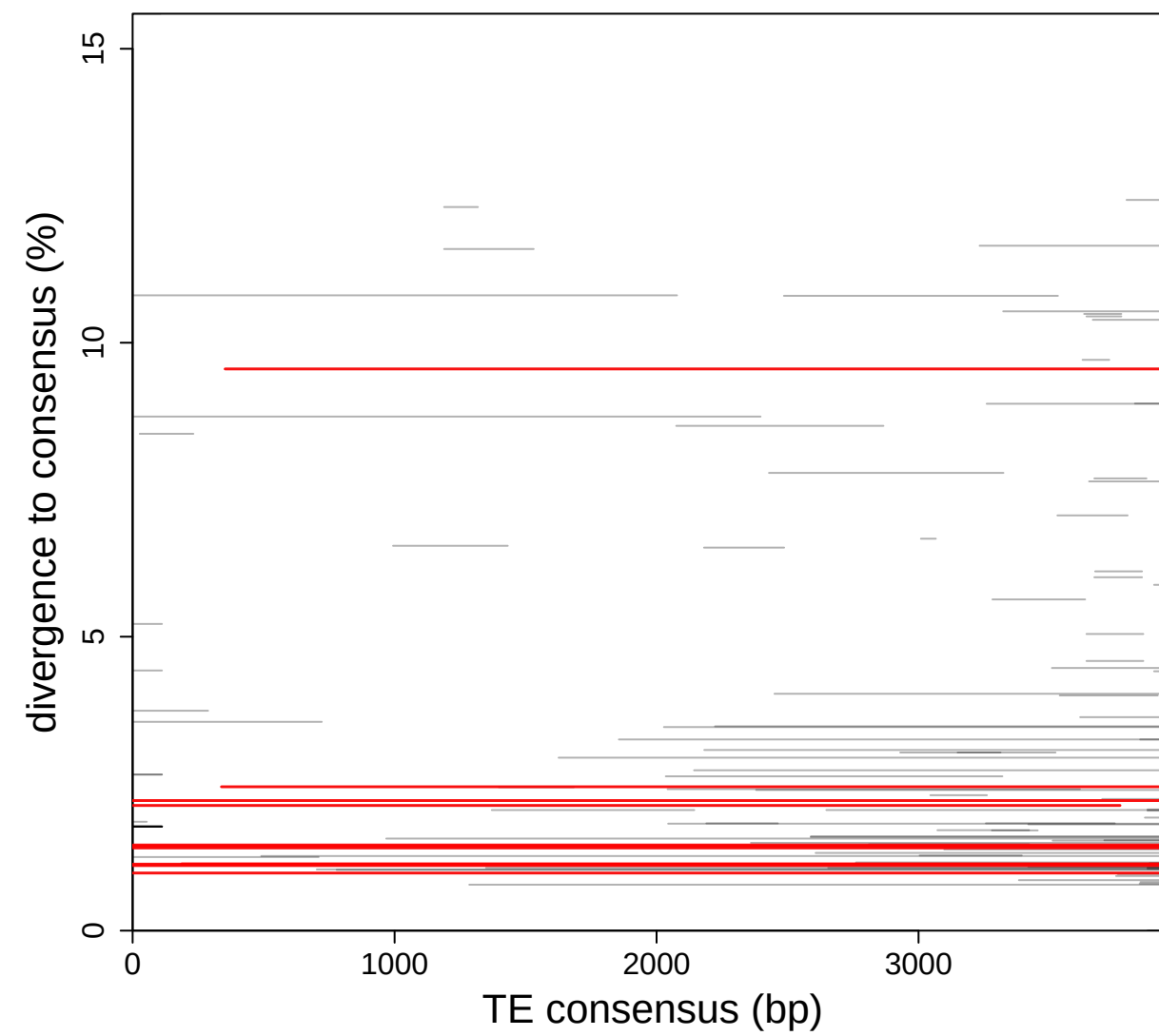
Start crop Point

End crop Point



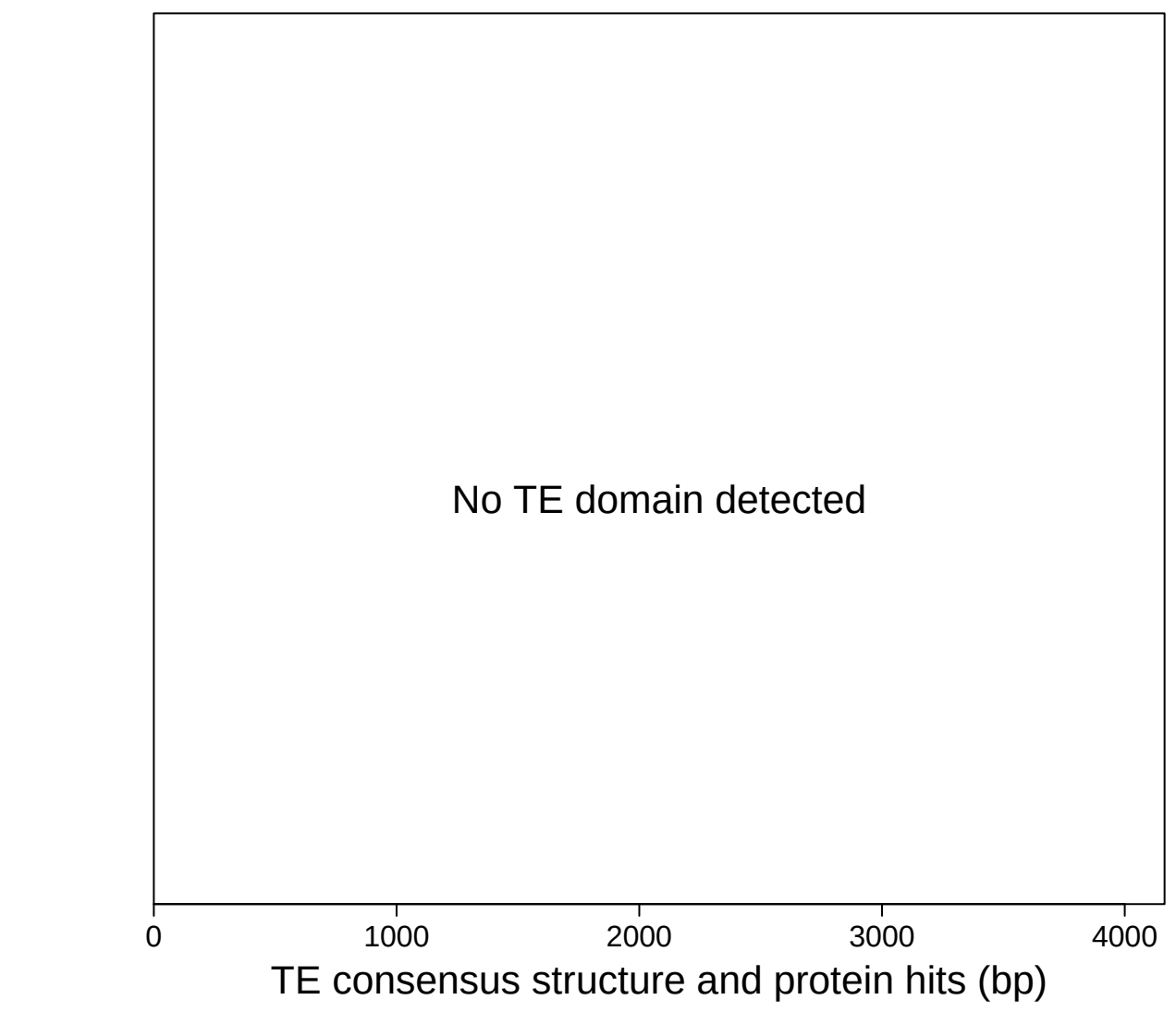
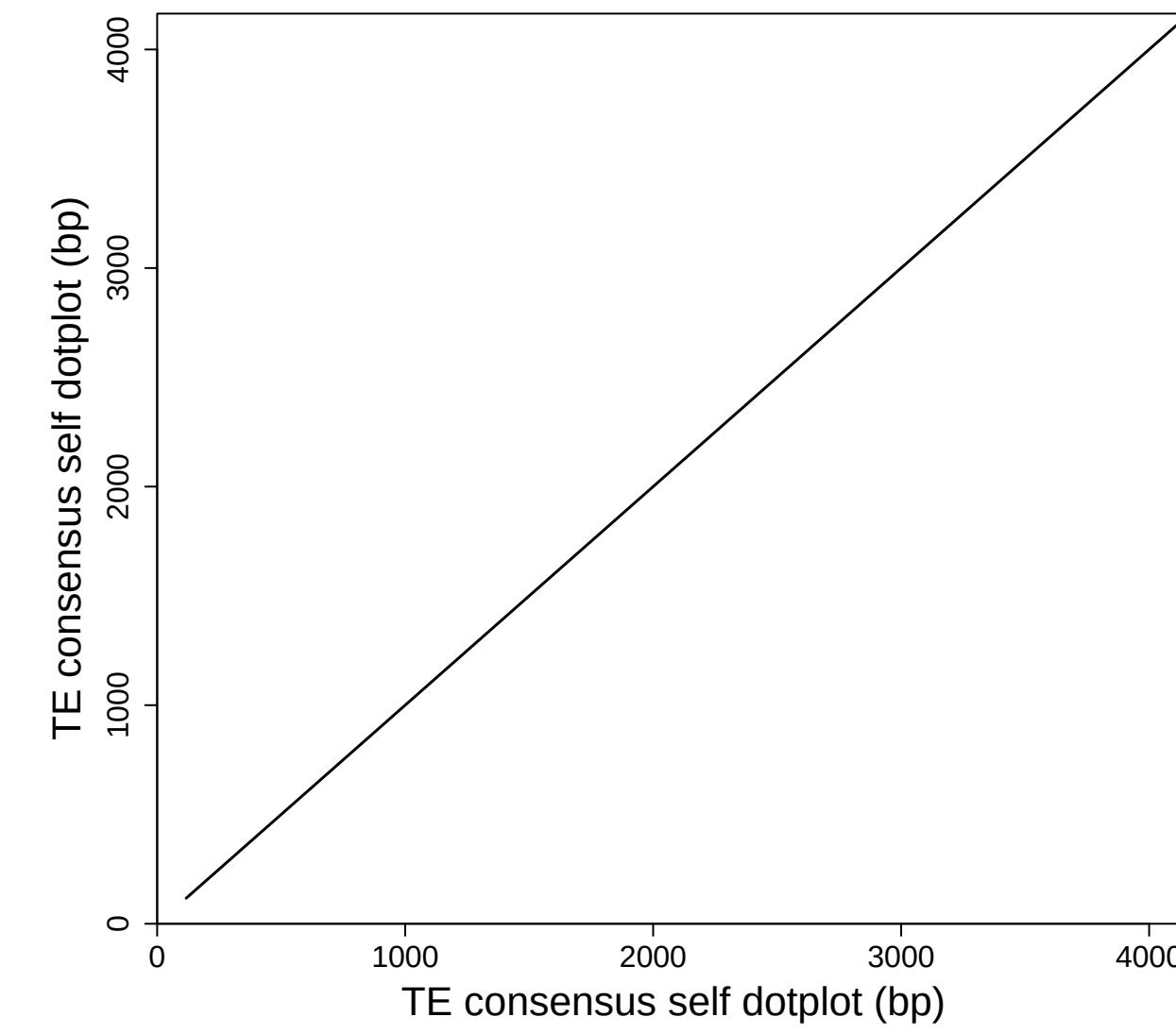
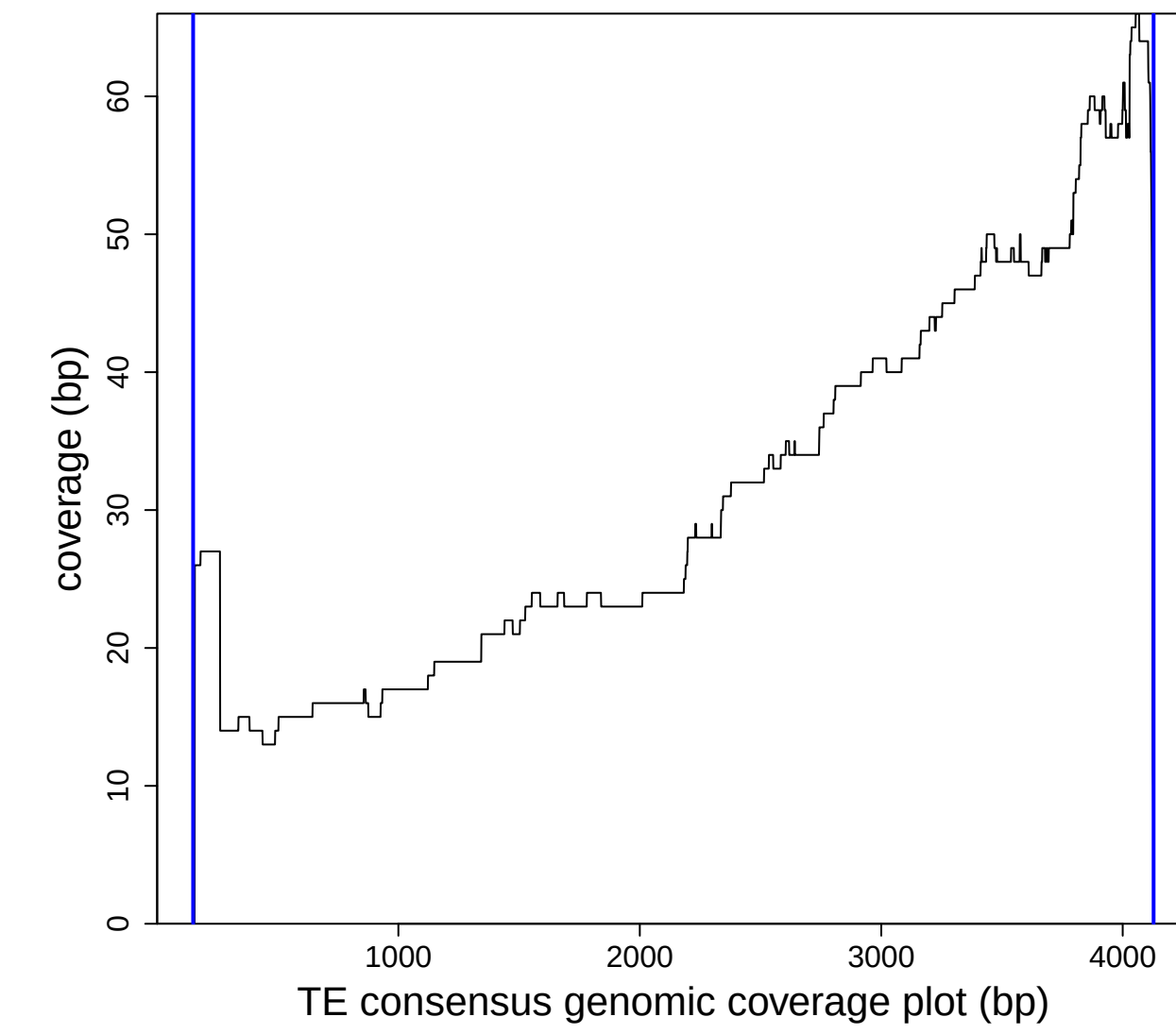
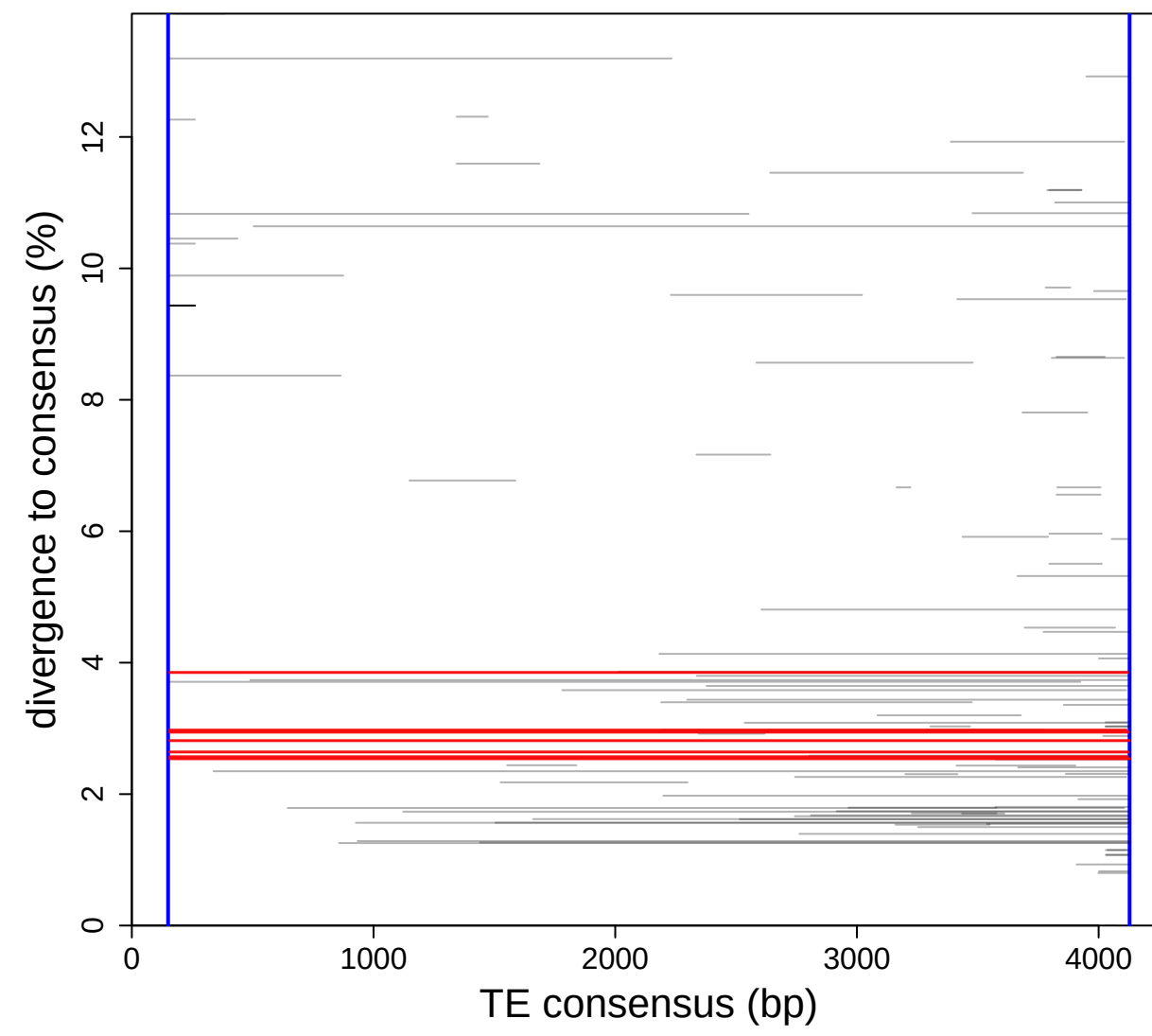
bed_uf.bed g_3.bed fm_1.bed 0_0 bcln.fa aln.fa cl.fa gs.fa c
size: 3971bp; fragments: 122; full length: 11 (>=3573.9bp)

After TETrimmer 3971 bp

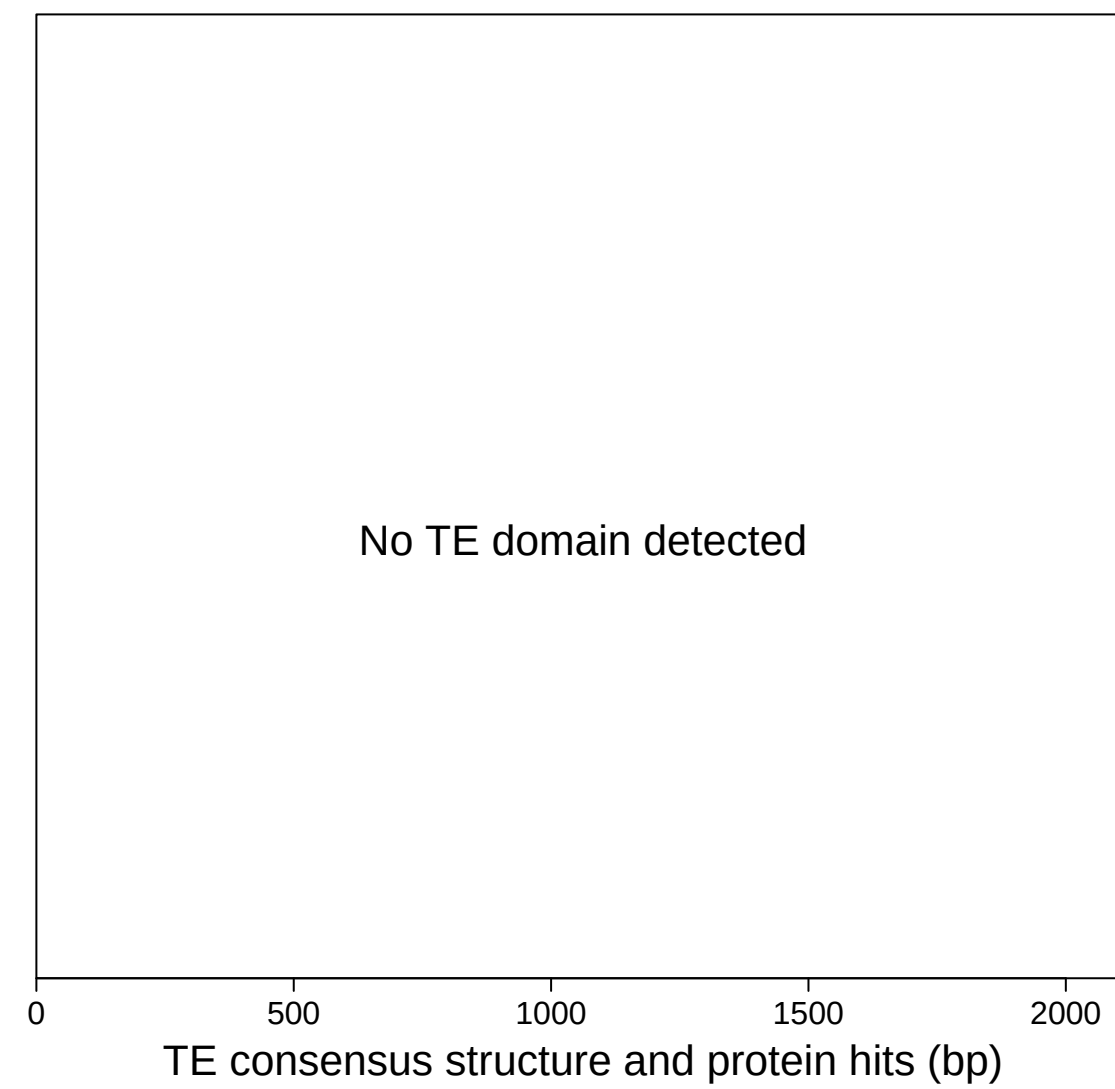
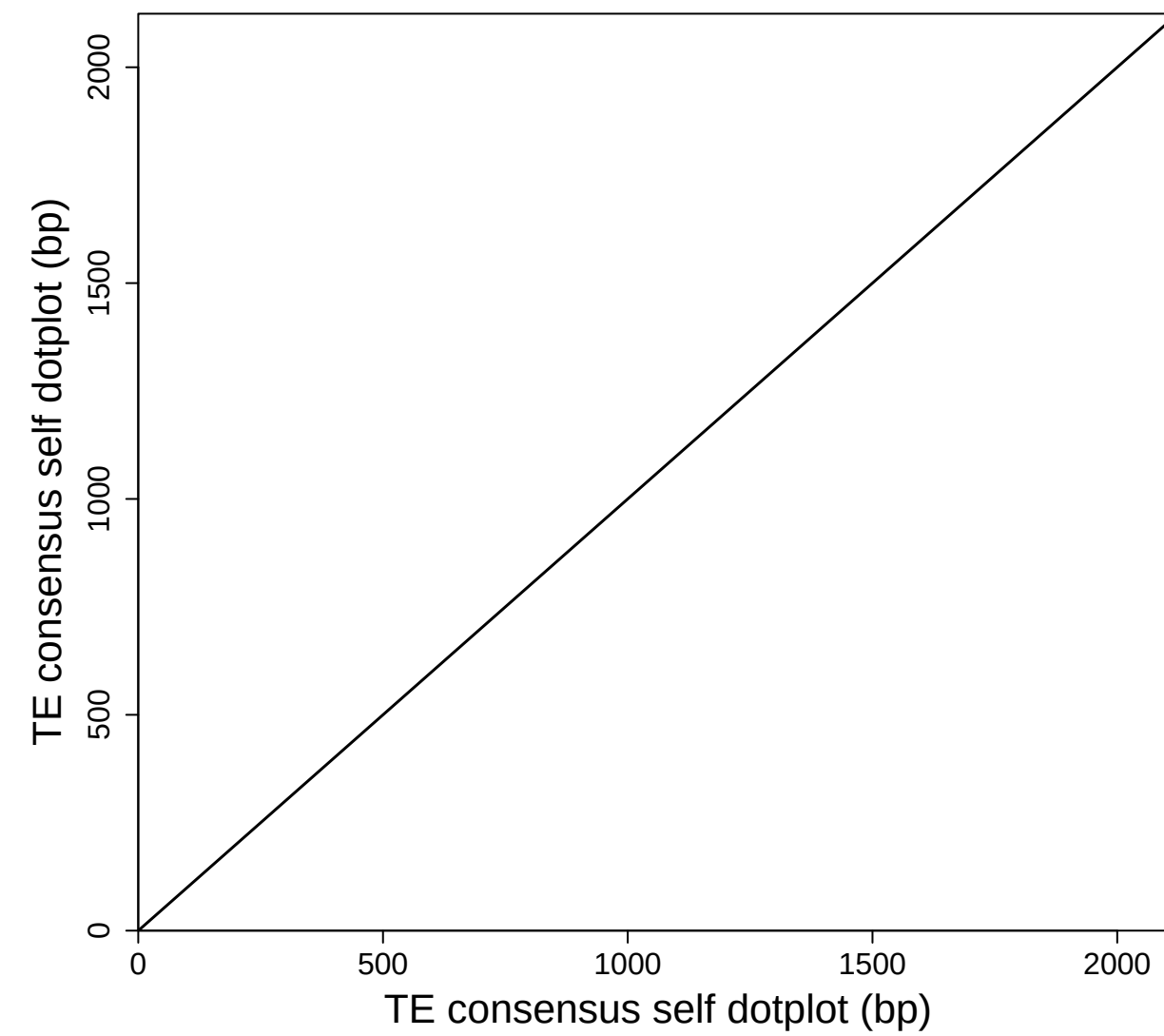
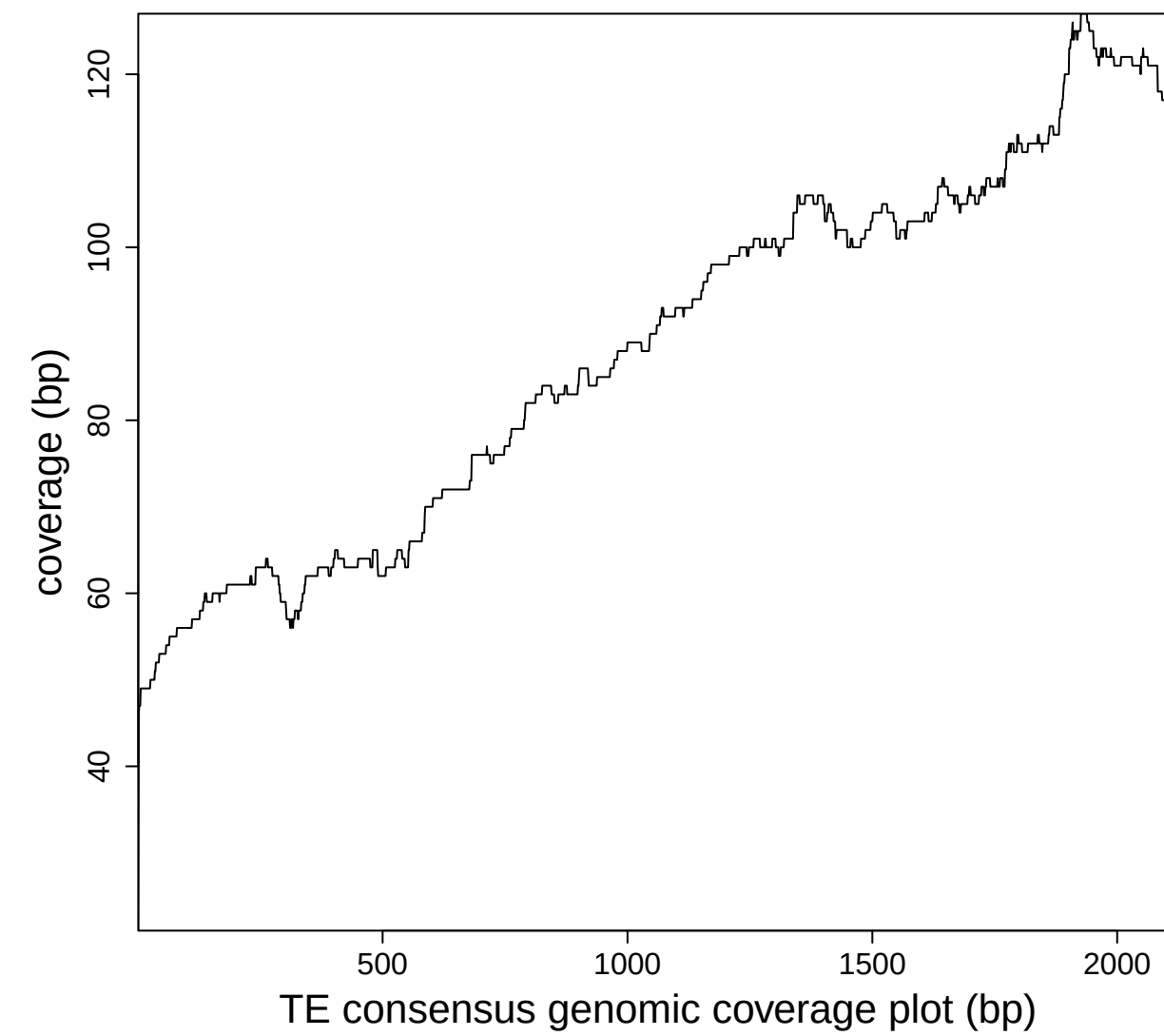
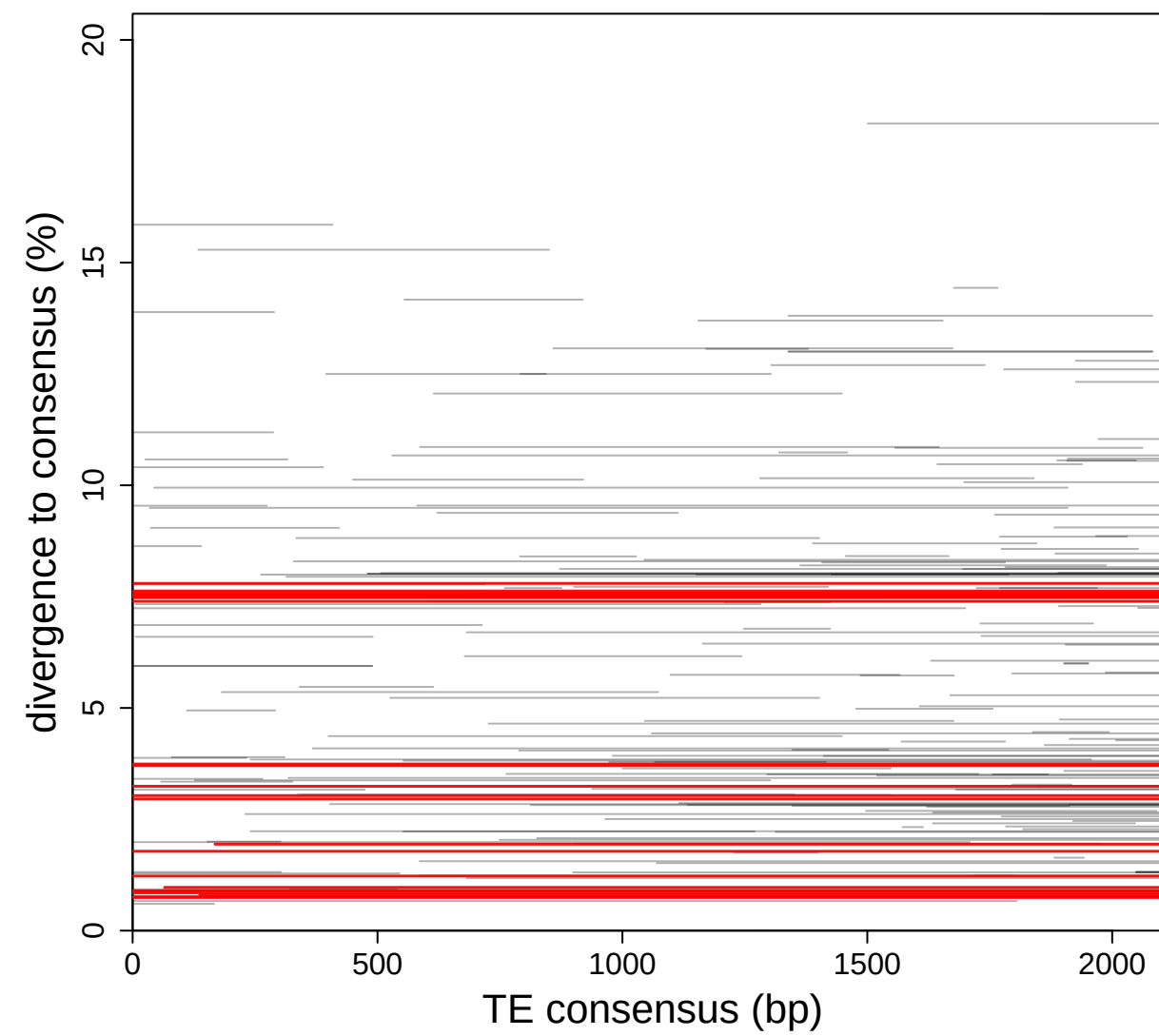


2.fasta.b.bed uf.bed g_3.bed fm_1.bed 0_0_bcln.fa aln.fa cl.f
size: 4278bp; fragments: 117; full length: 7 (>=3850.2bp)

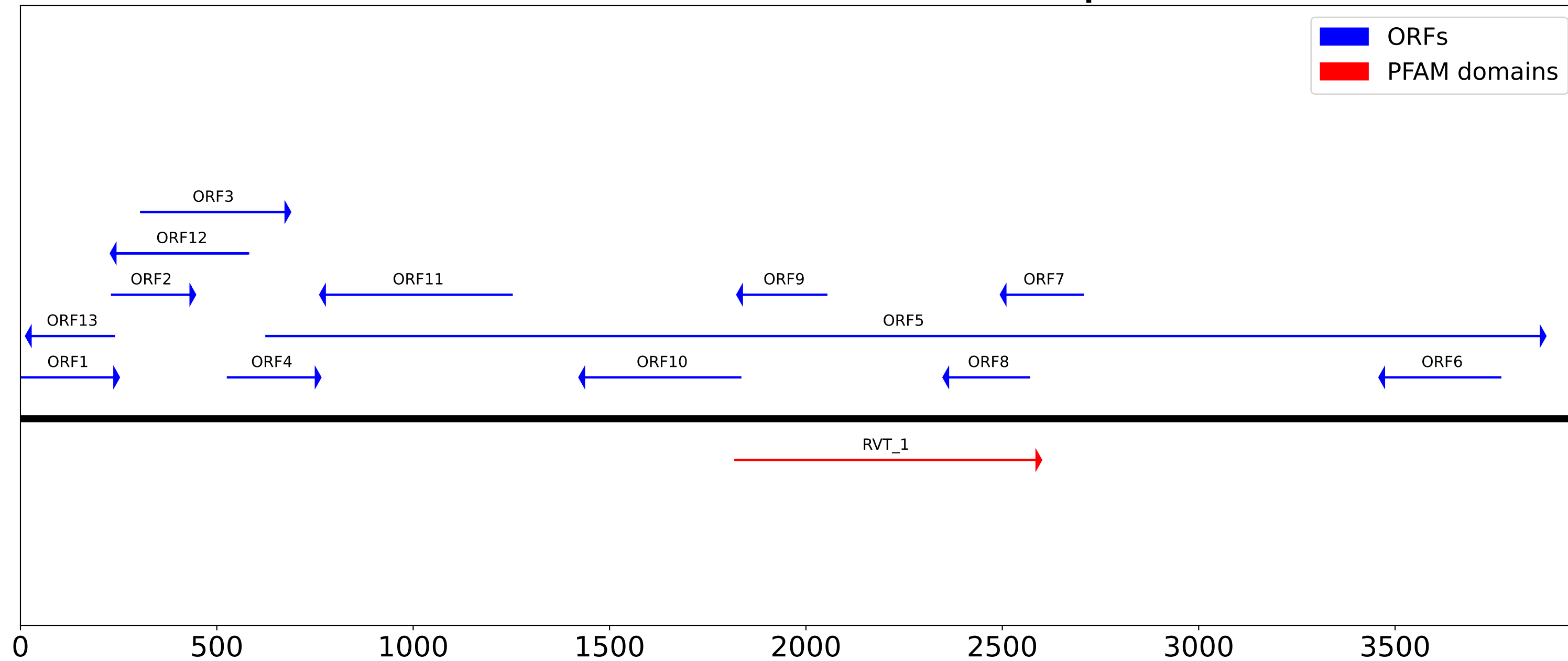
After TEtrimmer Extended plot Blue lines are boundaries



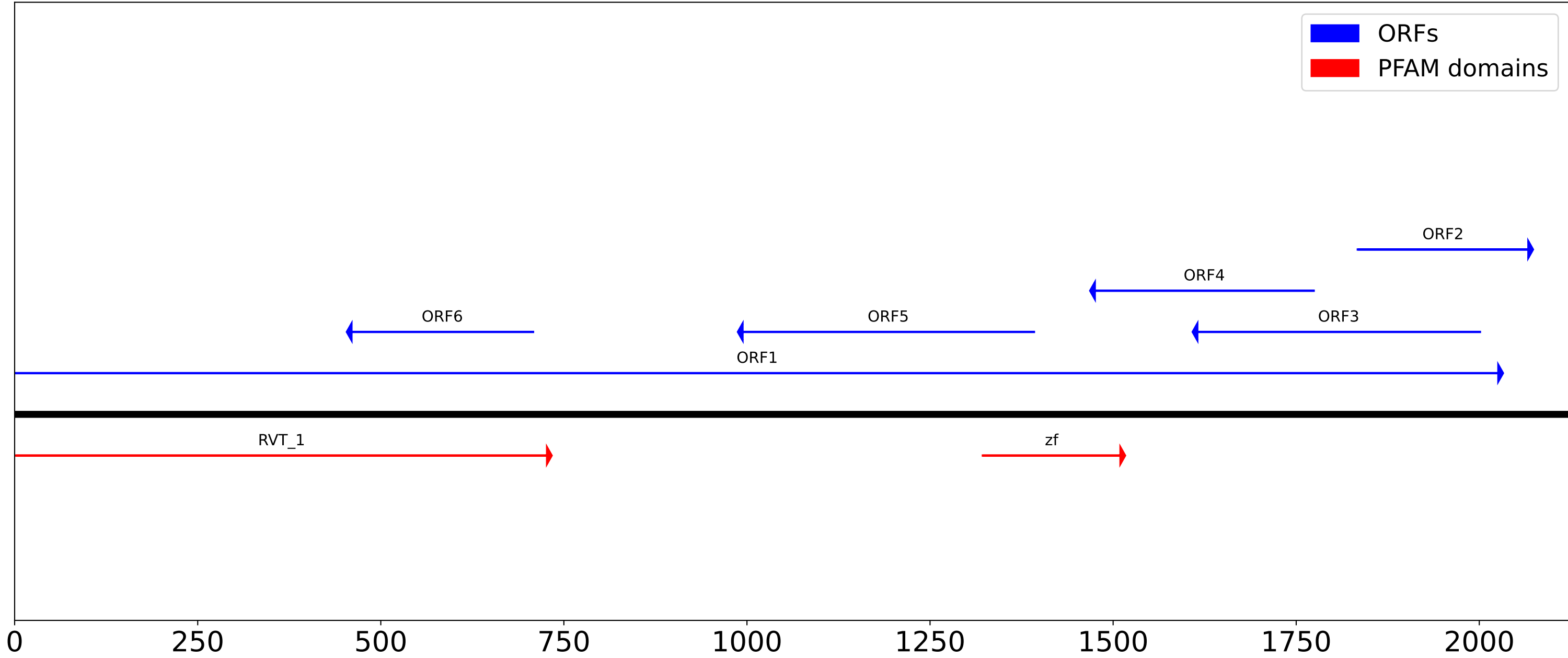
TE: rnd_5_family_5022
size: 2124bp; fragments: 217; full length: 30 (≥ 1911.6 bp)



After TEtrimmer ORF and PFAM domain plot



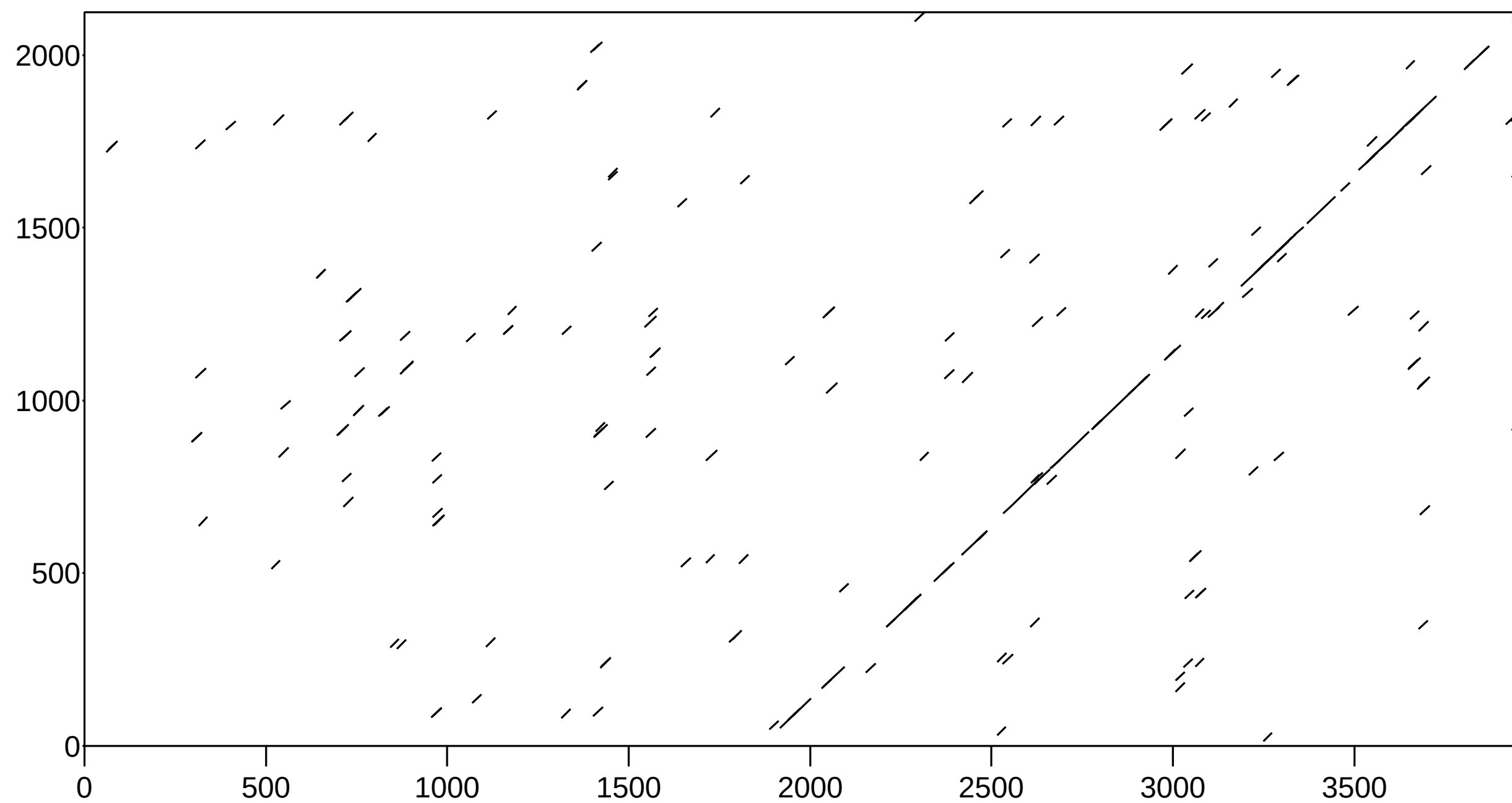
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)