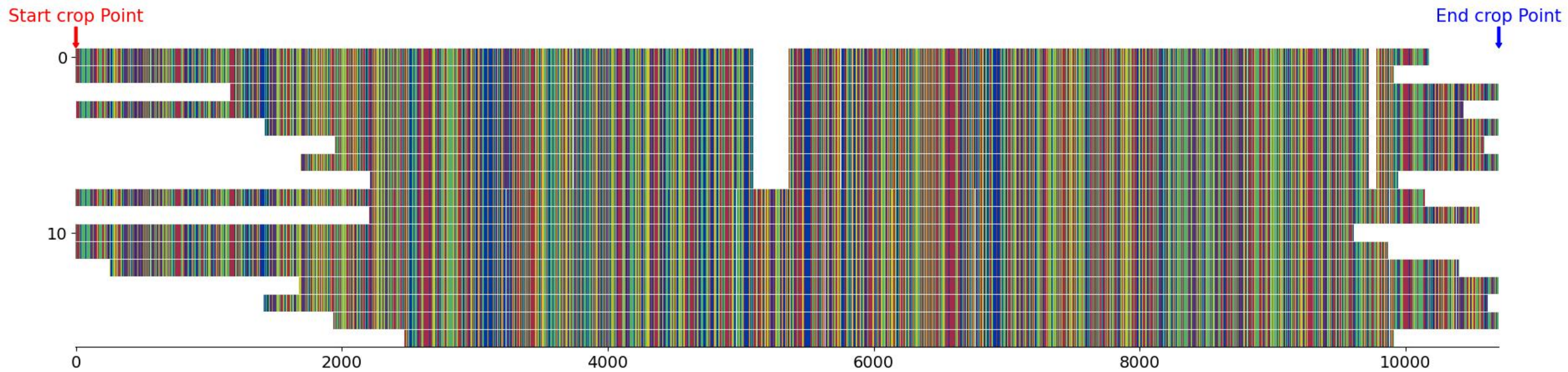




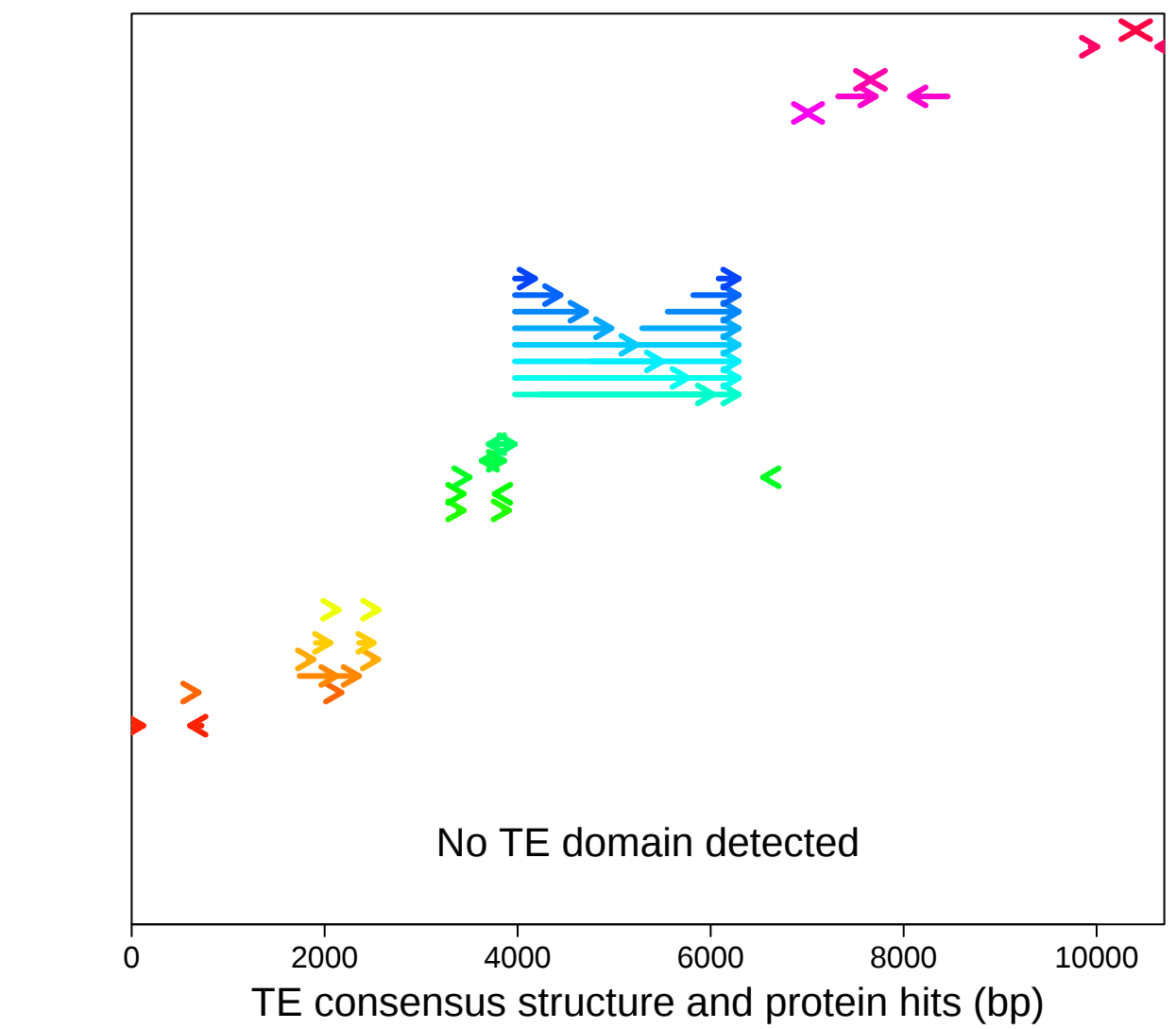
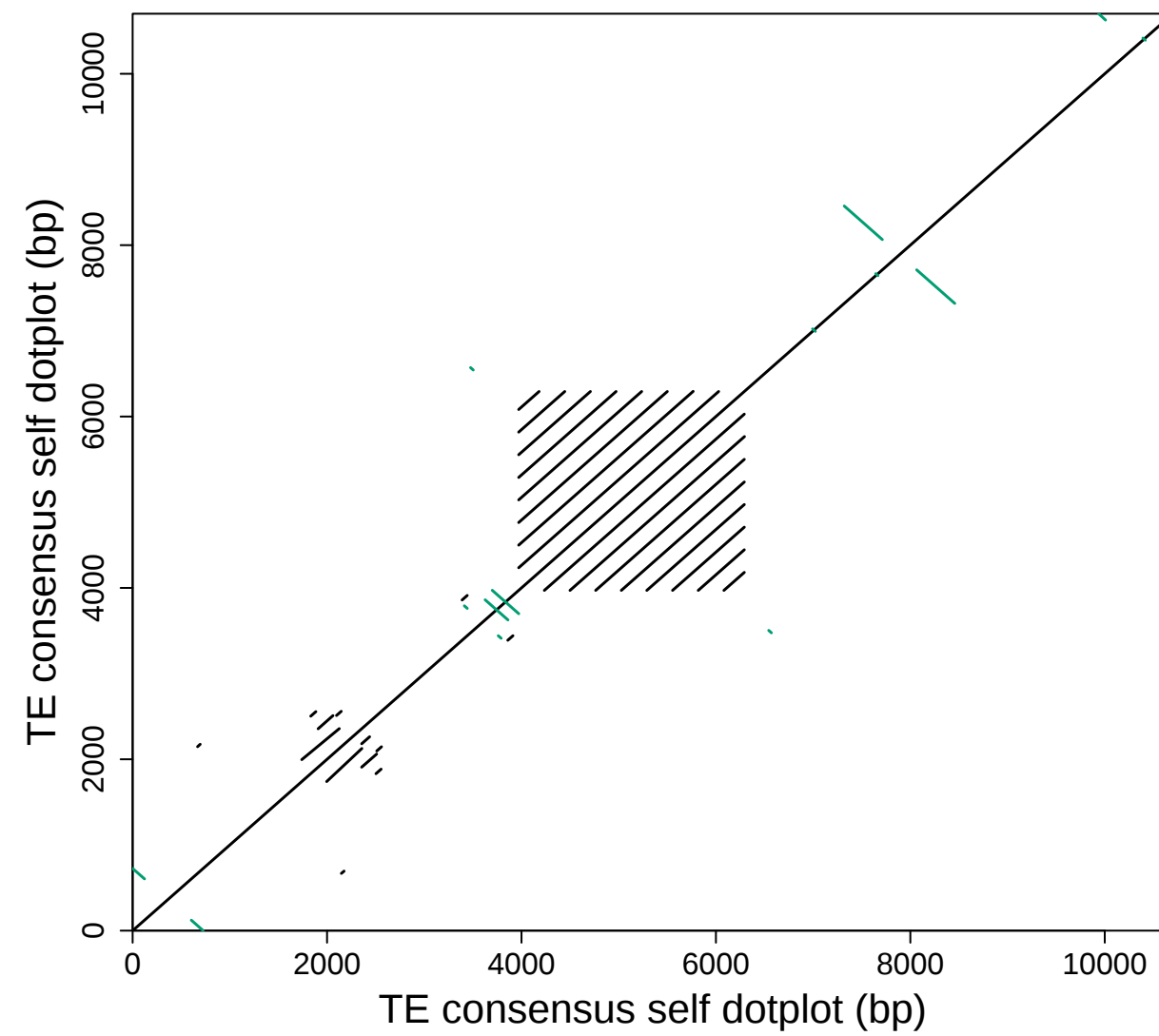
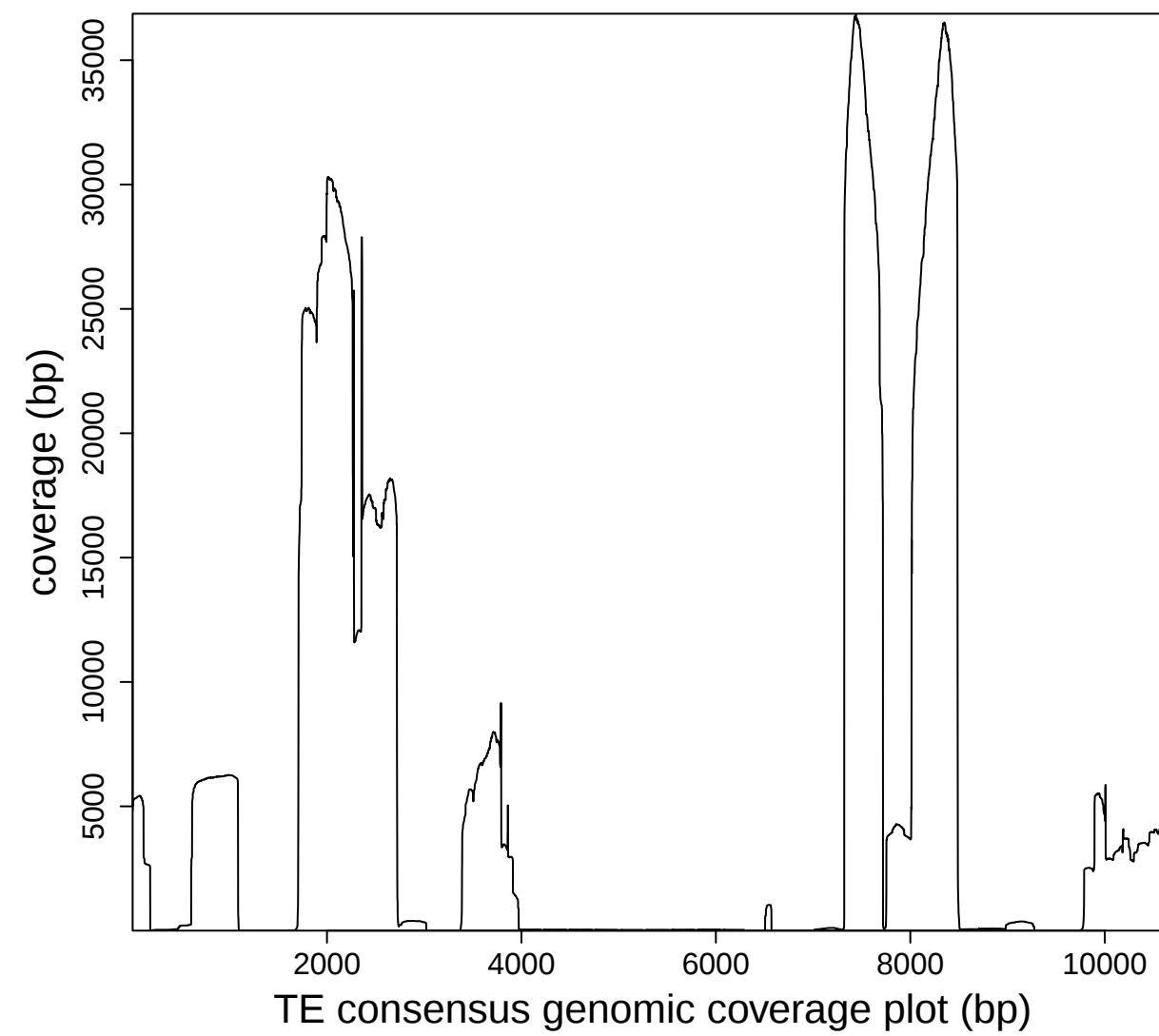
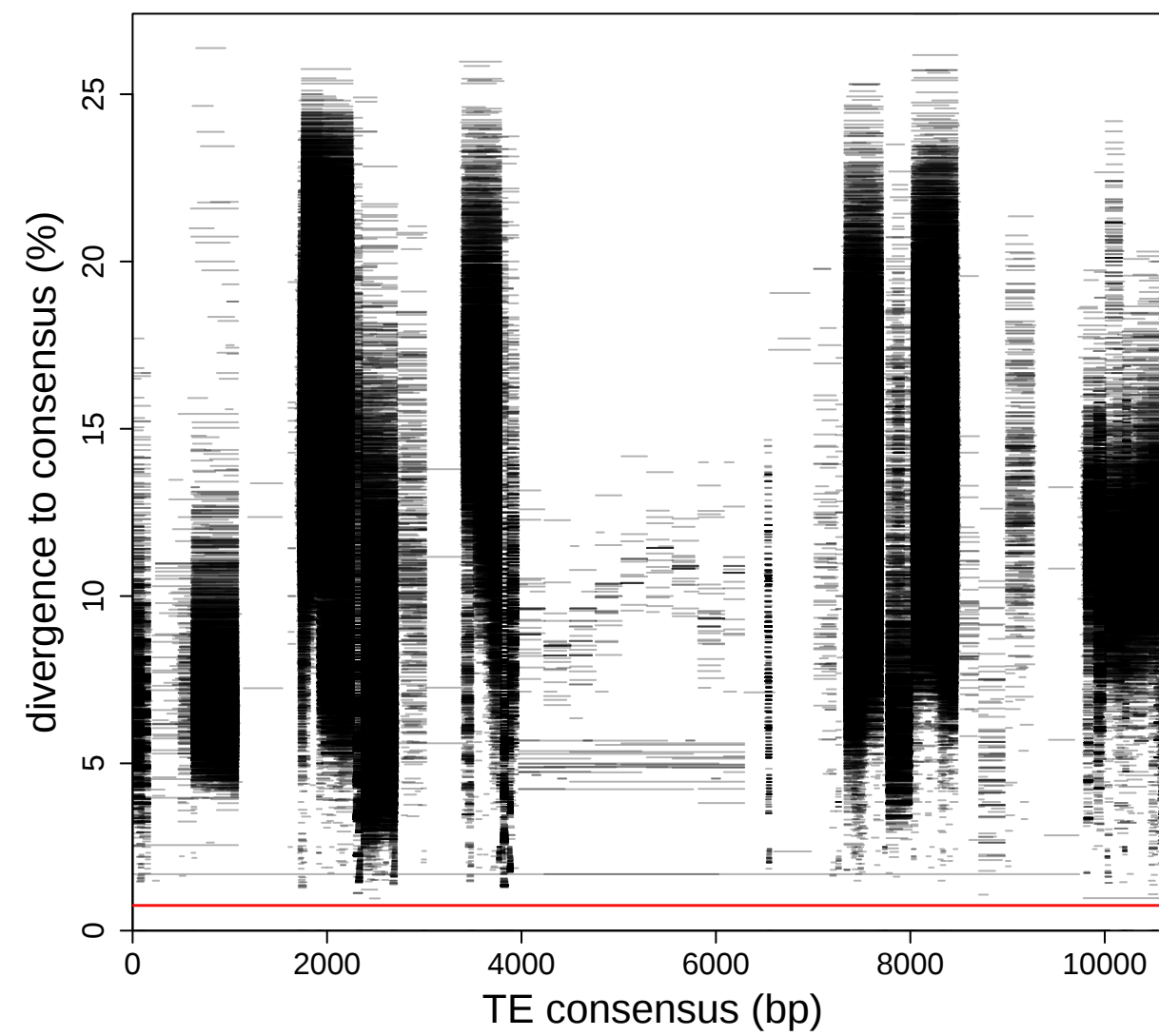
MSA length = 10701

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-----TGTATT TA AA ATATTTATTAAT GTGGTAT TAA TAG GTGA GT  
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GAAA TTTTAT T TTGTGTTTTTTTGATAAAA T A GATTAATTA-----  
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-----TGTATT TA AA ATATTTATTAAT GTGGTAT TAA TAG GTGA GT  
-----  
-----TGTATT TA AA ATATTTATTAAT GTGGTAT TAA TAG GTGA GT
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_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcIn.fa_al
size: 10701bp; fragments: 196042; full length: 1 (>=9630.9bp)

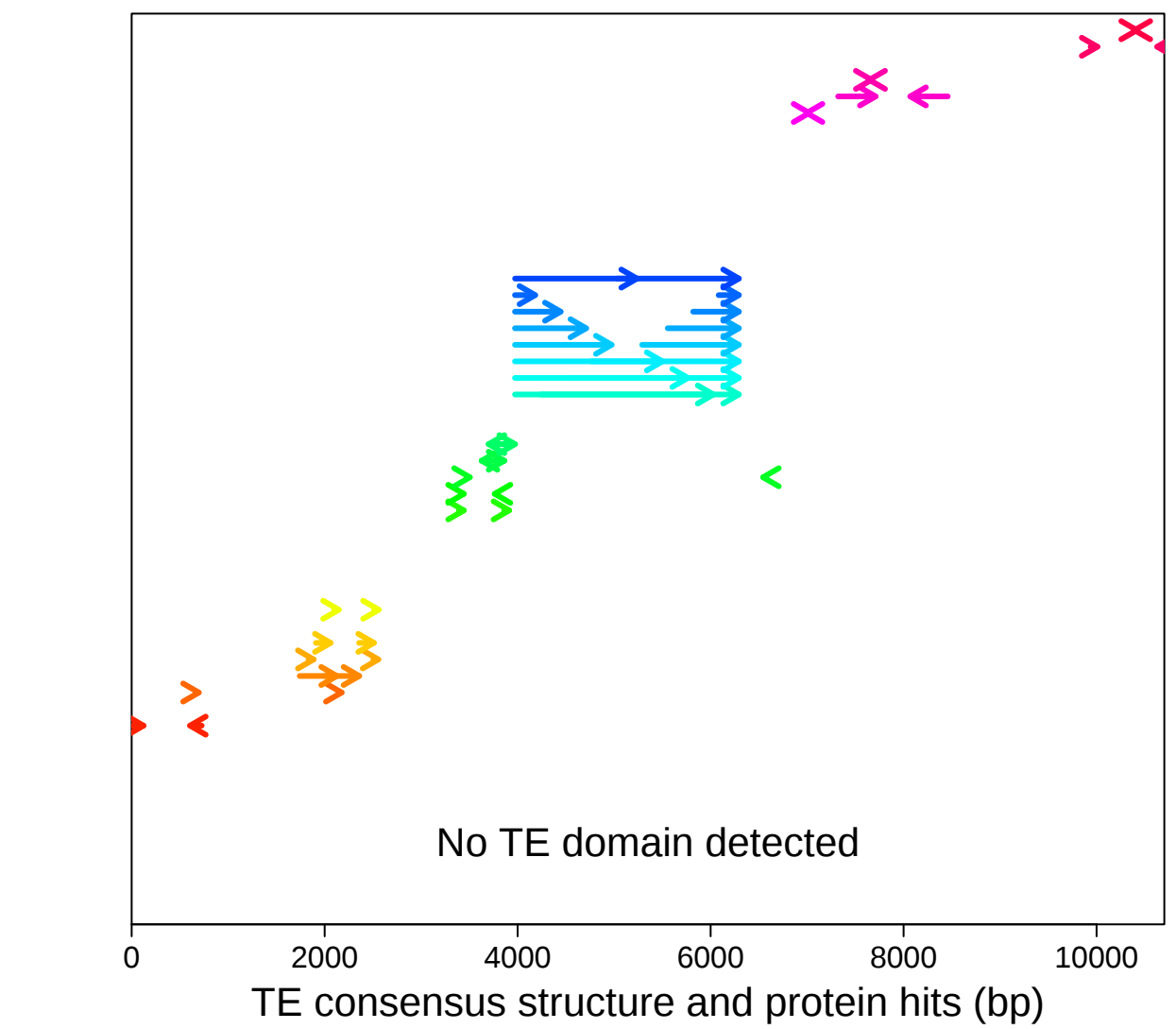
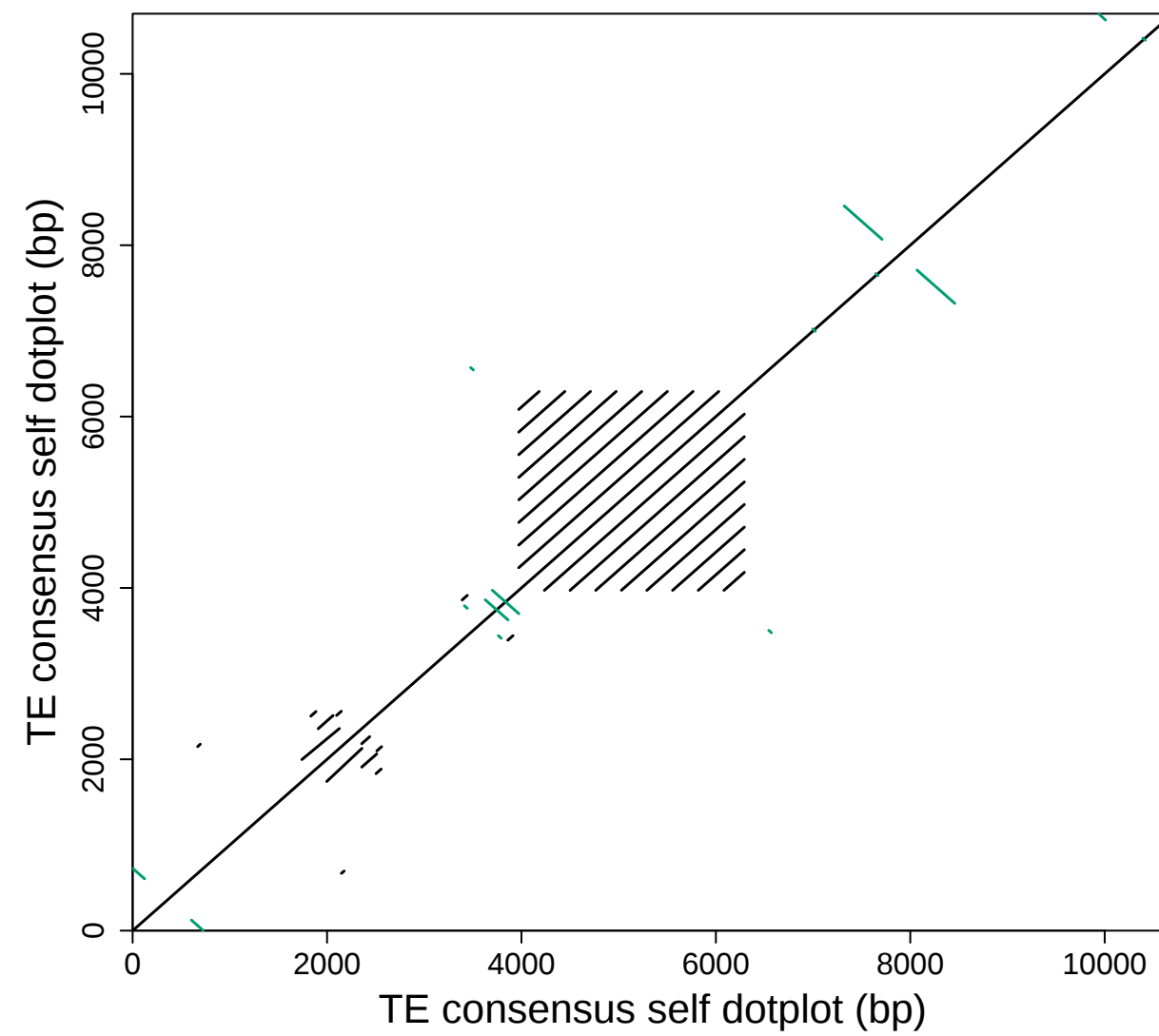
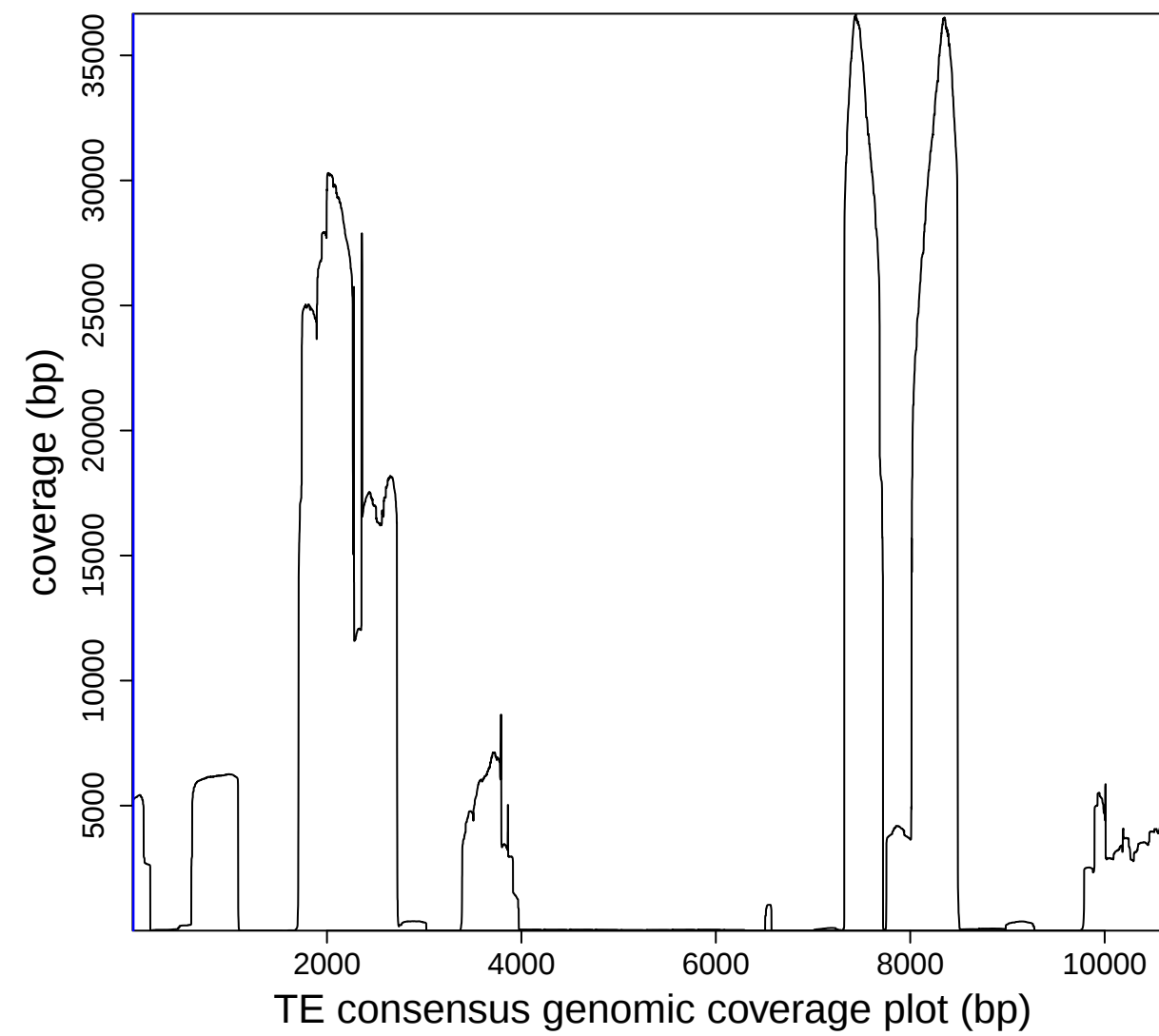
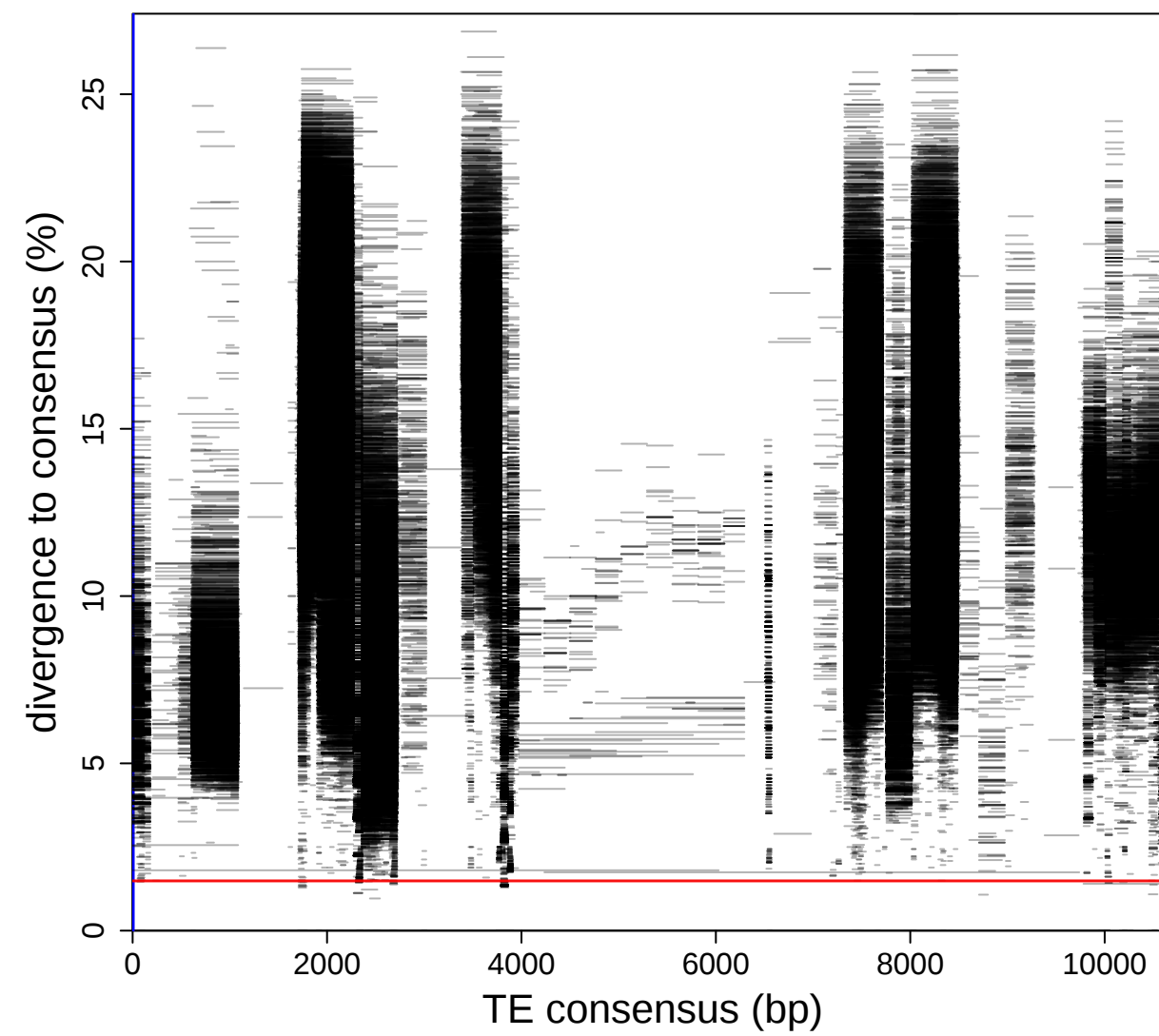
After TEtrimmer 10701 bp



bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bclr
size: 10702bp; fragments: 194369; full length: 1 (>=9631.8bp)

After TEtrimmer Extended plot

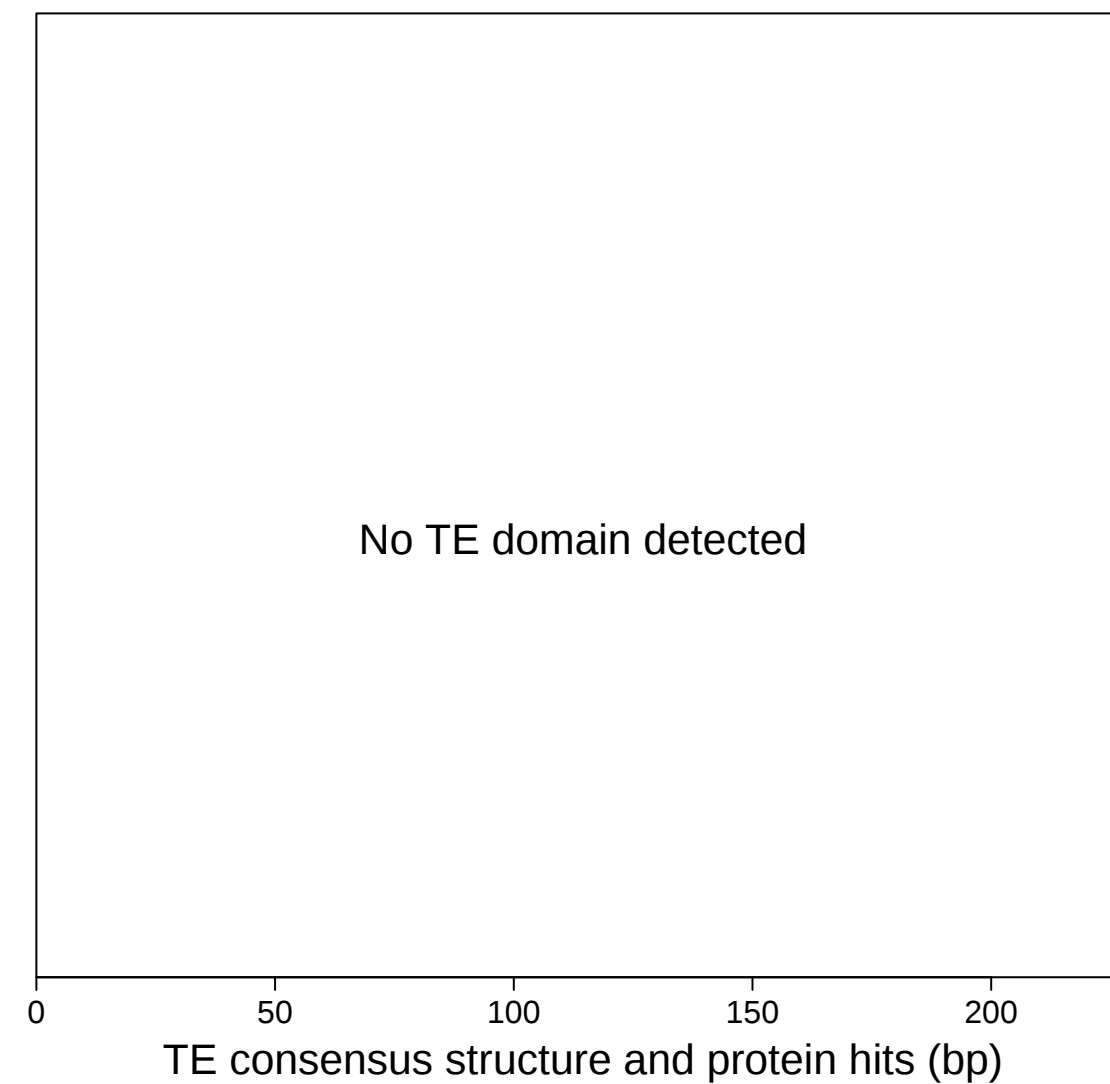
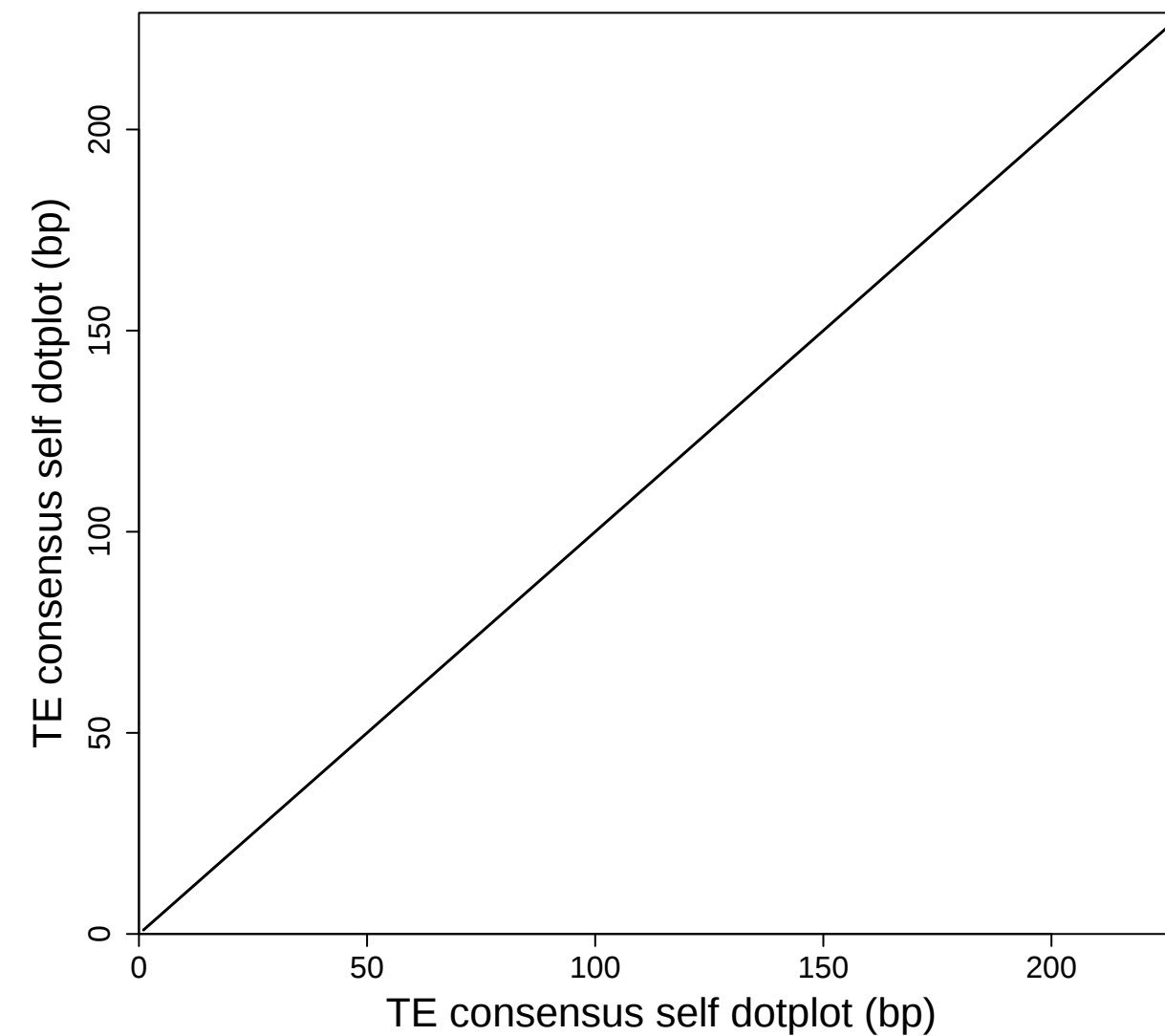
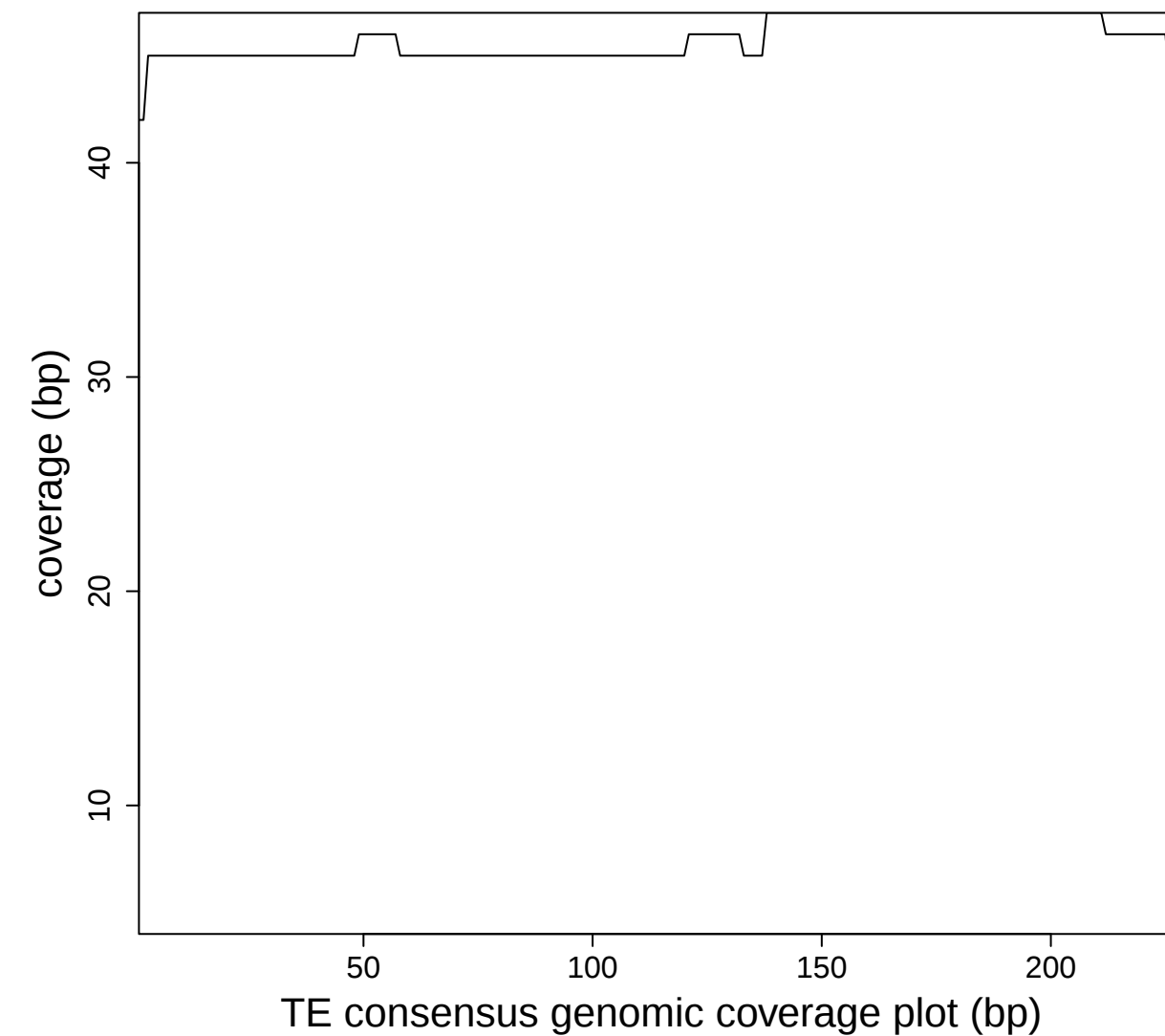
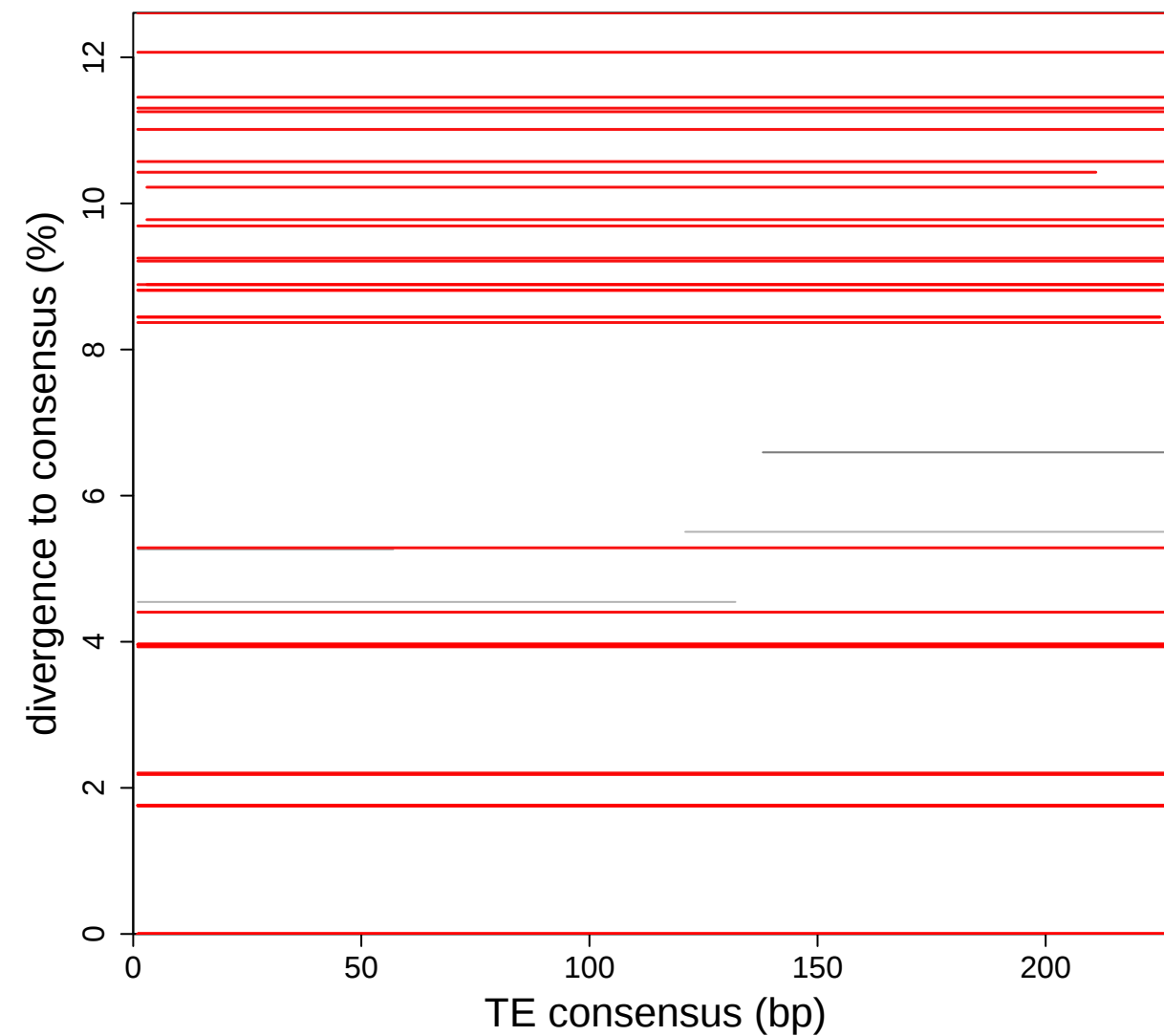
Blue lines are boundaries



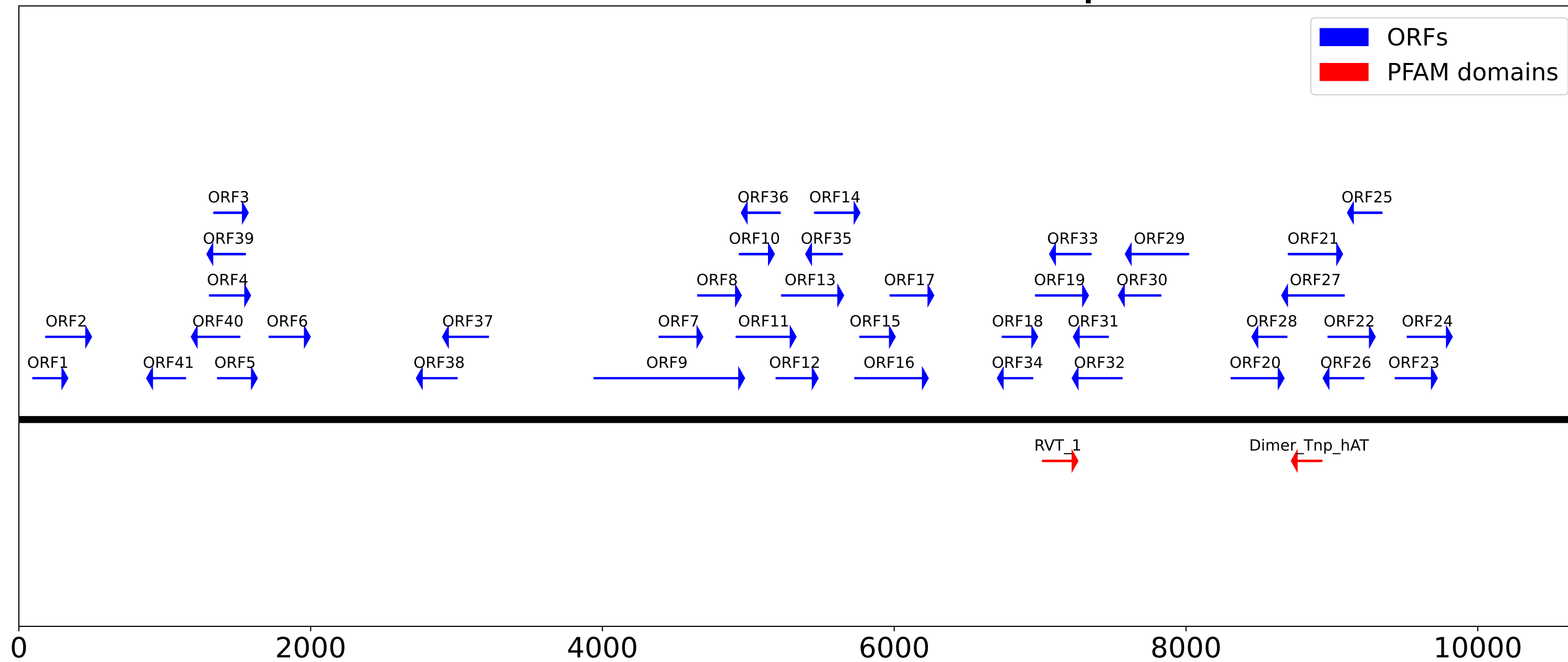
Before TEtrimmer 229 bp

TE: ltr_1_family_191

size: 229bp; fragments: 49; full length: 43 (≥ 206.1 bp)



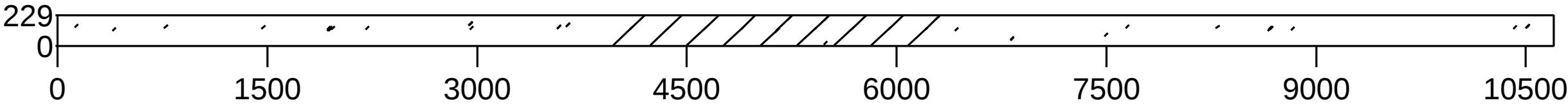
After TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)