

MSA length = 10238

TTT TAG TT CCGAAT TAAAT AAAAAGAA TTT AA - - - - - GAG AACACACC CTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCACTAAAC - - - - - GGAACCACTAAAAAATATCATATT - - - - - TTA - - - - -

ATAAAA TA - - - - - AAATCGGAC TTT AAAAAAAT TTT CAGAAACTGTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTACTTTGGGTAAACGACAGAAAAGTCGTCAACAAC TGT TTG - - - - - GAGTTCTCCAAAAAT TGT TTTTATATCTATTATAATA TTA

TTT TAAAGT AAGGCT AAAAAAT ATATATT - - - - - ATTAATACATA TTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATT TTTT TTTTTCATTCTACTTTGGGTAAACGACAGAAAAGTCGTCACAATATGTCT - - - - - AAAACTATCGAAATATATTTACTCCTATCTTATTATAATA

CCGTGATATCGATATAGTTTATACAAATTTAATTAGA - ATTTGGCAACAGTTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCAACAGTGTCCAAAAGGATTTTCAGAGGATTTTAAAGTCAGTTTC - TTCTAA - -

- - - - - CGTCAGTCGGA TTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCAAGGATCTTT - - - - - GAGAGCGCCAGCAATTTTTTCGCTGCC TTAATTAAAG - -

CTACACAATTTTGA TCTCAAAAGAAAA - - - - - AAAGTCAGT - CTGAAAAATA TTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCACAATAT - - - - - ACCATGCCCTGATGAAATTTATCGACACTTTT - TTA - - - -

CCACACTATCAGCC TGGCGAAATAGGA - - - - - TG TAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCACAAGG - - - - - AAACGCTTATCAGGAAGATTCCTATT - - - - - TAATG

- - - - - TAAATAAATTTGCACATAAAAC - - - - - AGATTTAAAAACCTACTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCAACAACAGTGTGCG - - - - - TTTGTAATCGTATTCTCTG - - - -

TCGTATTATT CGAAGGGCATCAAAAAATTAGAATCGTT - - - - - ACAAAAGTGTTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTACTTTGGGTAAACGACAGAAAAGTCGTCAAGTGTATAGAAAGTTTGGCGAAAAAAGTTGTGTTTTCTTAC - CTATAATA

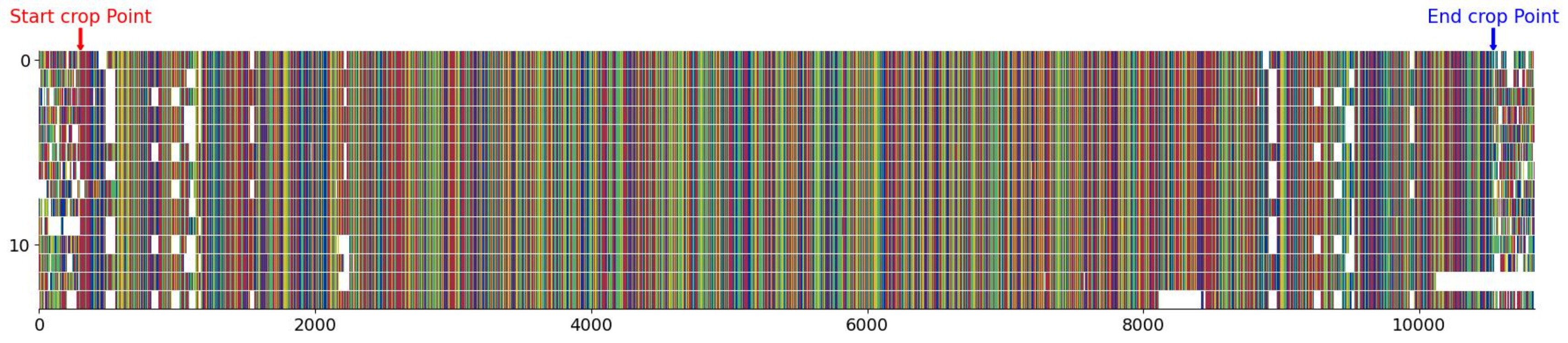
- - - - - TTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCACA - - - - - AA - - - - - TAAATAAATTTTCTTCGT TTTT - TTATAA - -

CTATACTAGCTAAC TTTGAGTGTGACAGCGCGCATAAACCGCCAACCTTAGTTGTAGCATTTT TTTTCTTTGATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTACTTTGGGTAAACGACAGAAAAGTCGTCACATTAGTTTCGATAGTATATCGATAACTCATAGTTCTAA TTTGTATAGAAA - -

TCGCAGATTGCGACTAAAAATTTCTTACTTAGTTAAT - CTGCCGCAAACTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTACTTTGGGTAAACGACAGAAAAGTCGTCACAAACCGTTT - - - - -

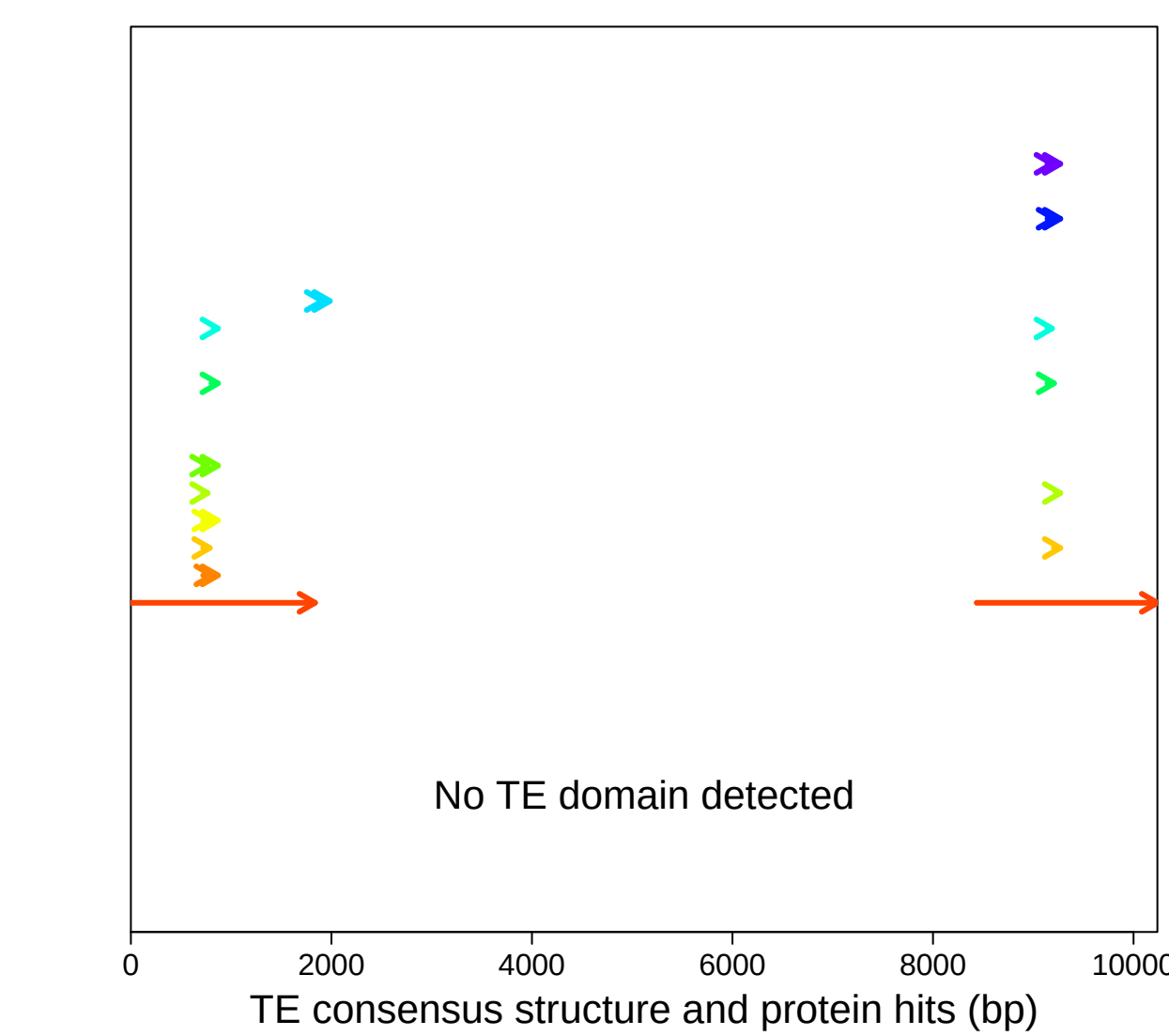
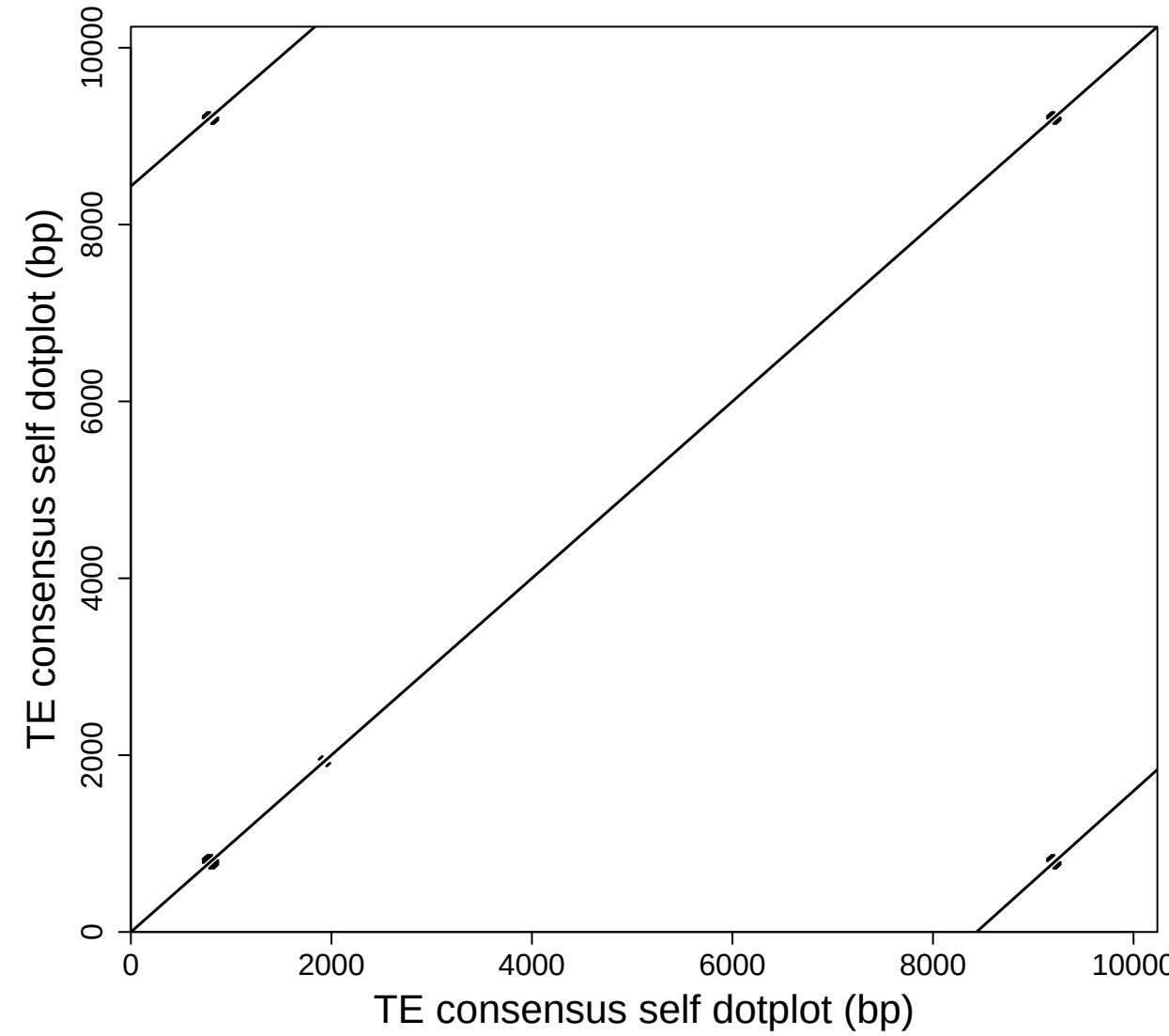
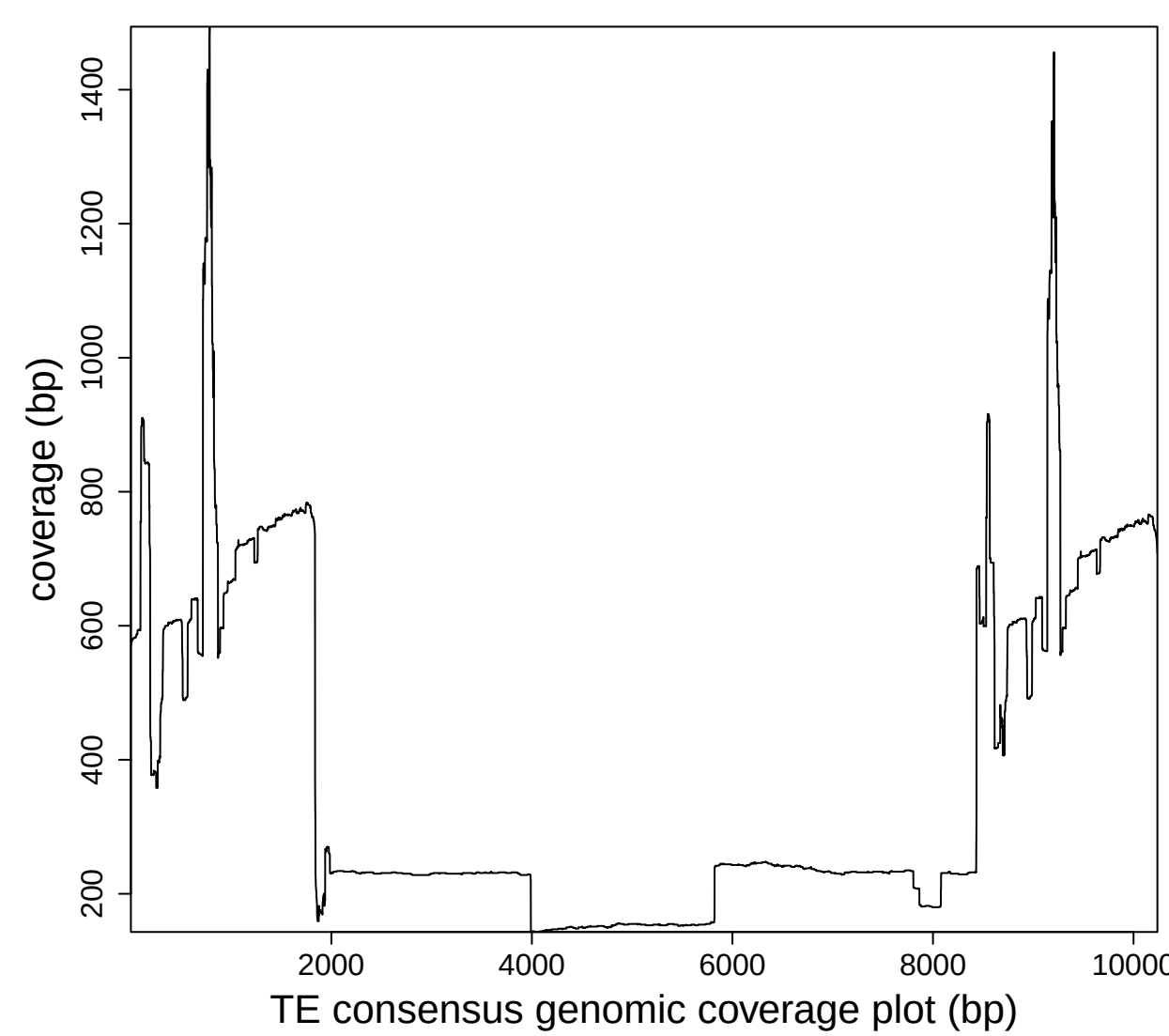
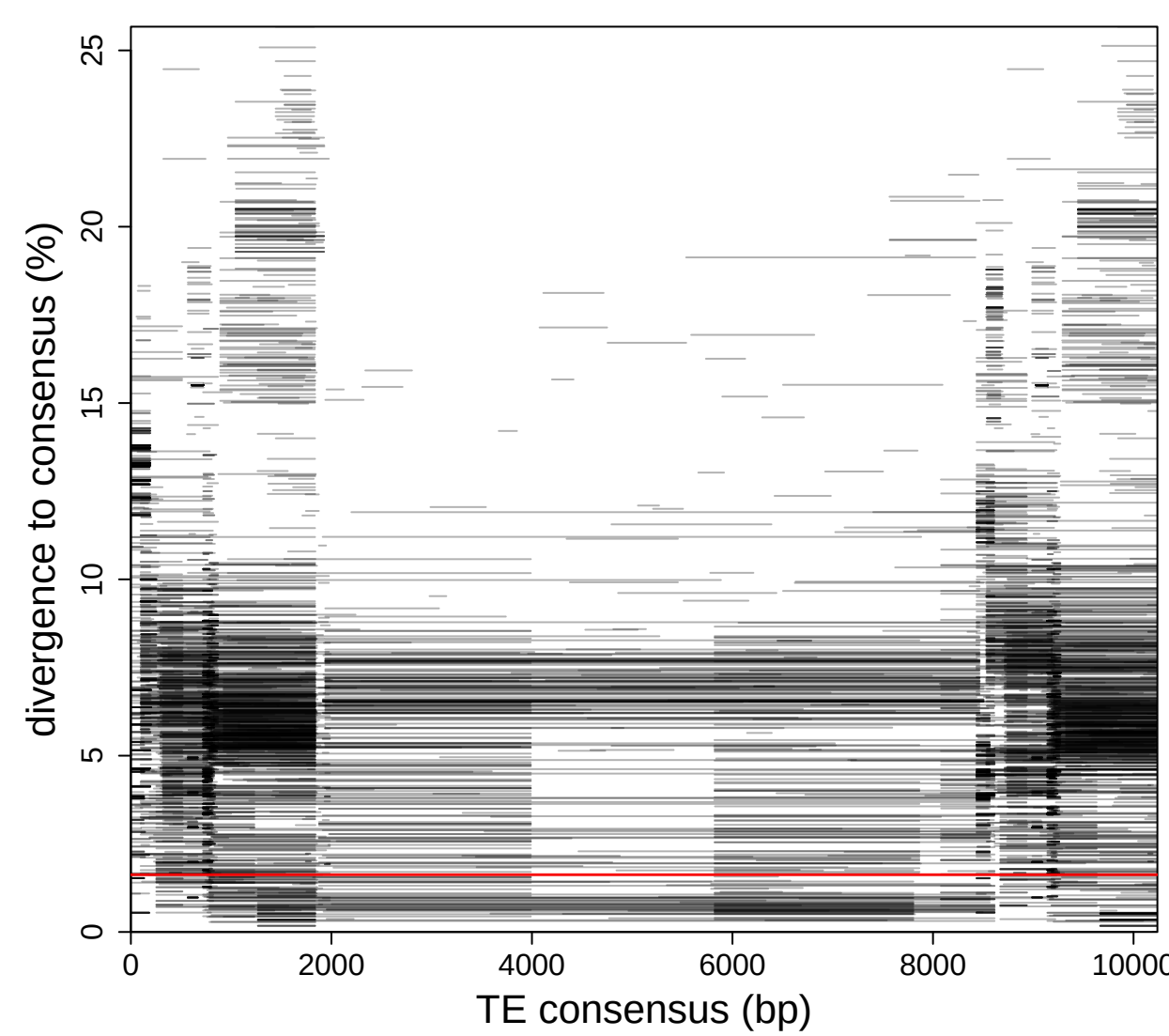
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- - - - - TTAGTATGAAC TGT TATATAAATTTGTAGCATTTT TTTTCTTTAATAAATTTGAATTTAAAAATCTATTTT - - - - - AACGGATTCTTTTTCATTCTATTTGGGTAAACGACAGAAAAGTCGTCACAA AATA TAC - - - - - AGGGTGTCACAAAATTTCA TGGAC - - - - - TA



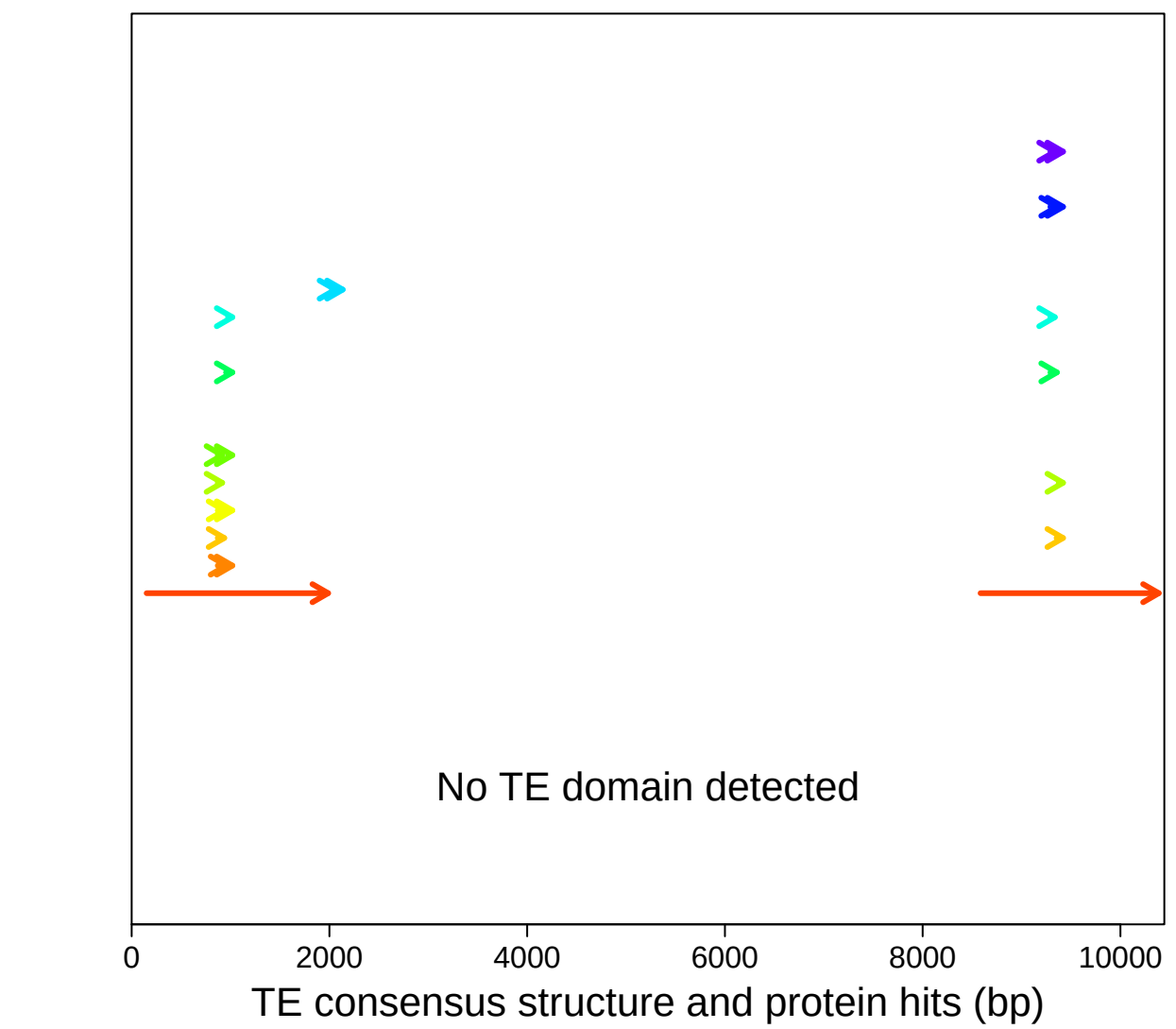
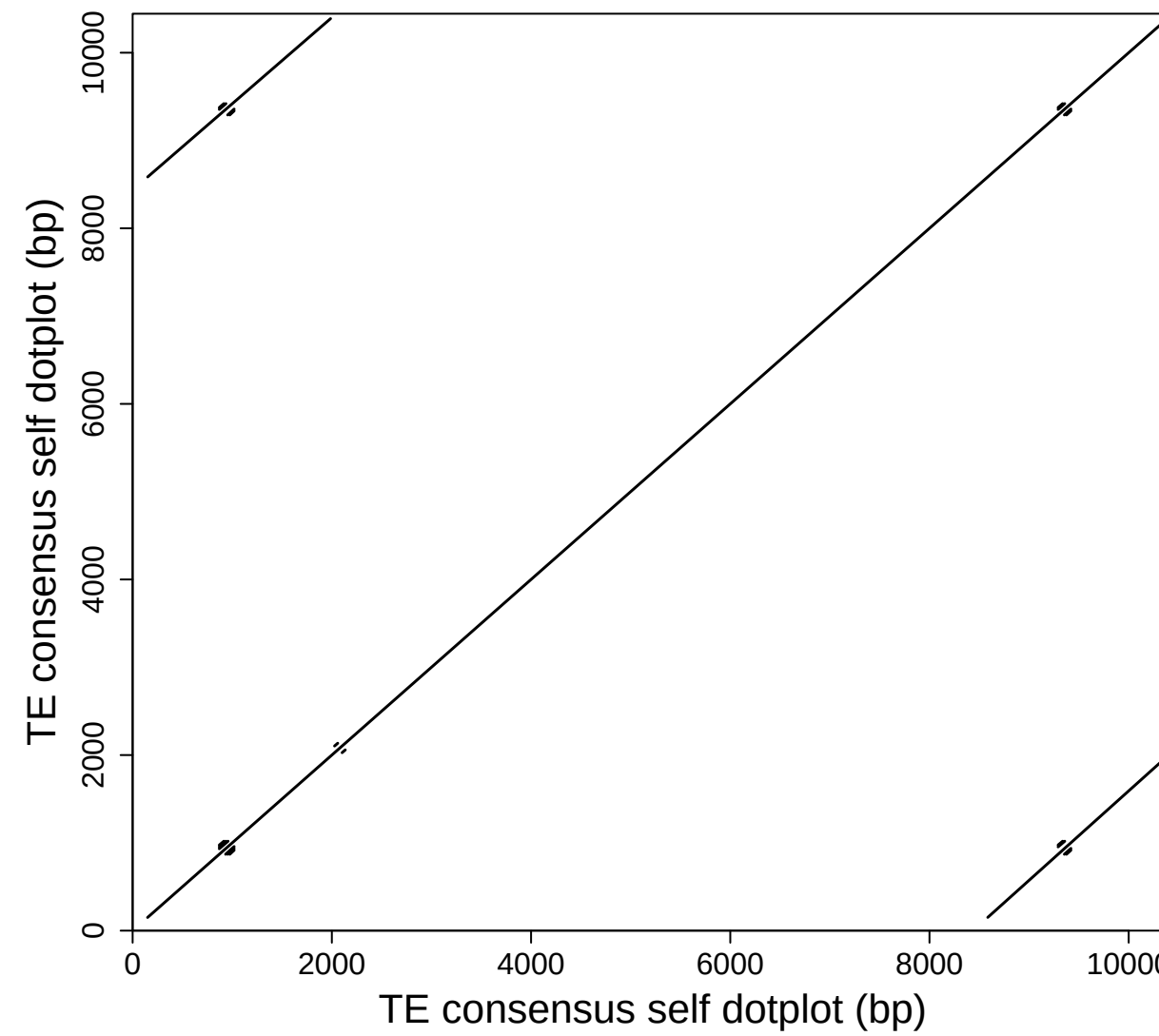
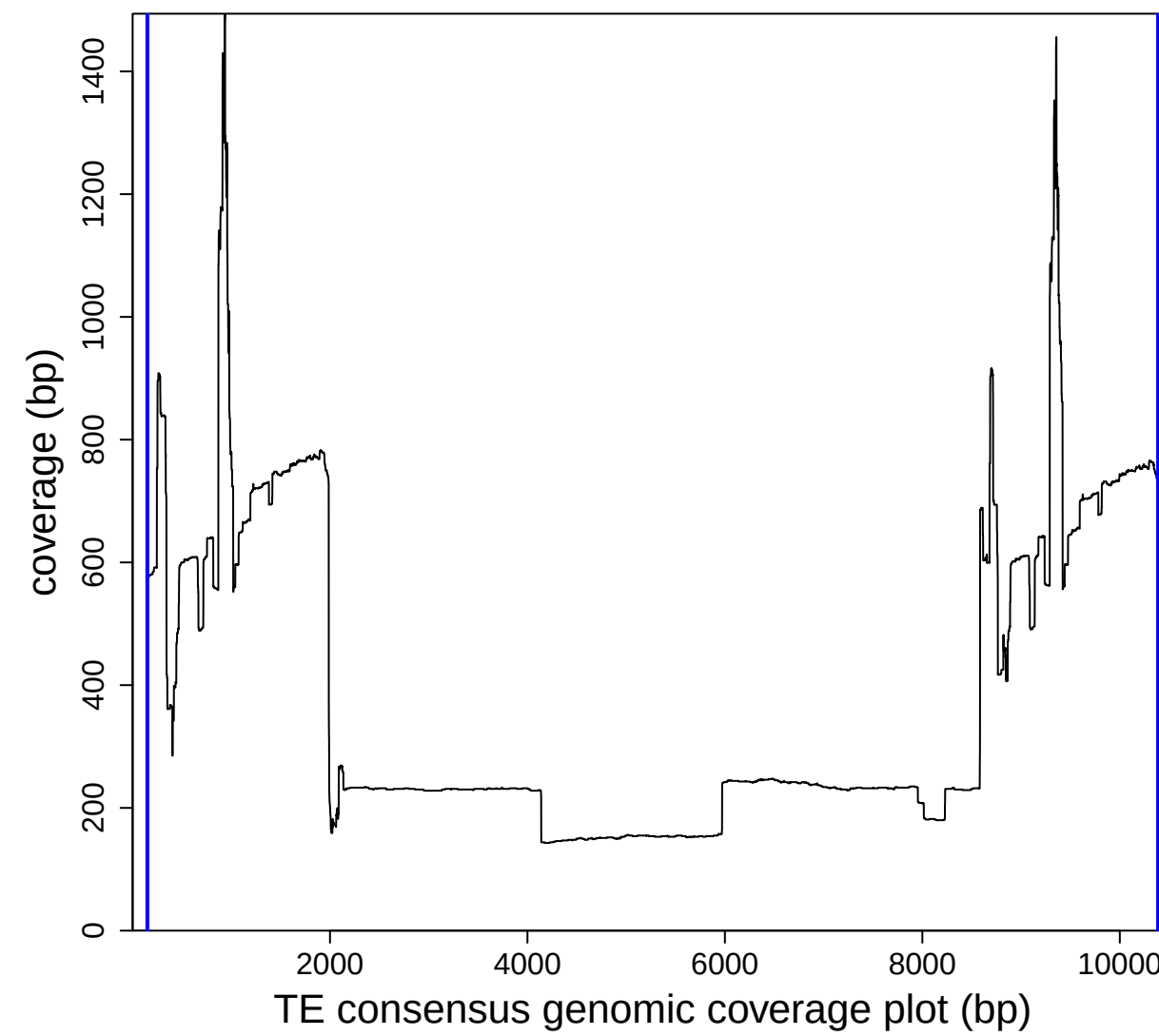
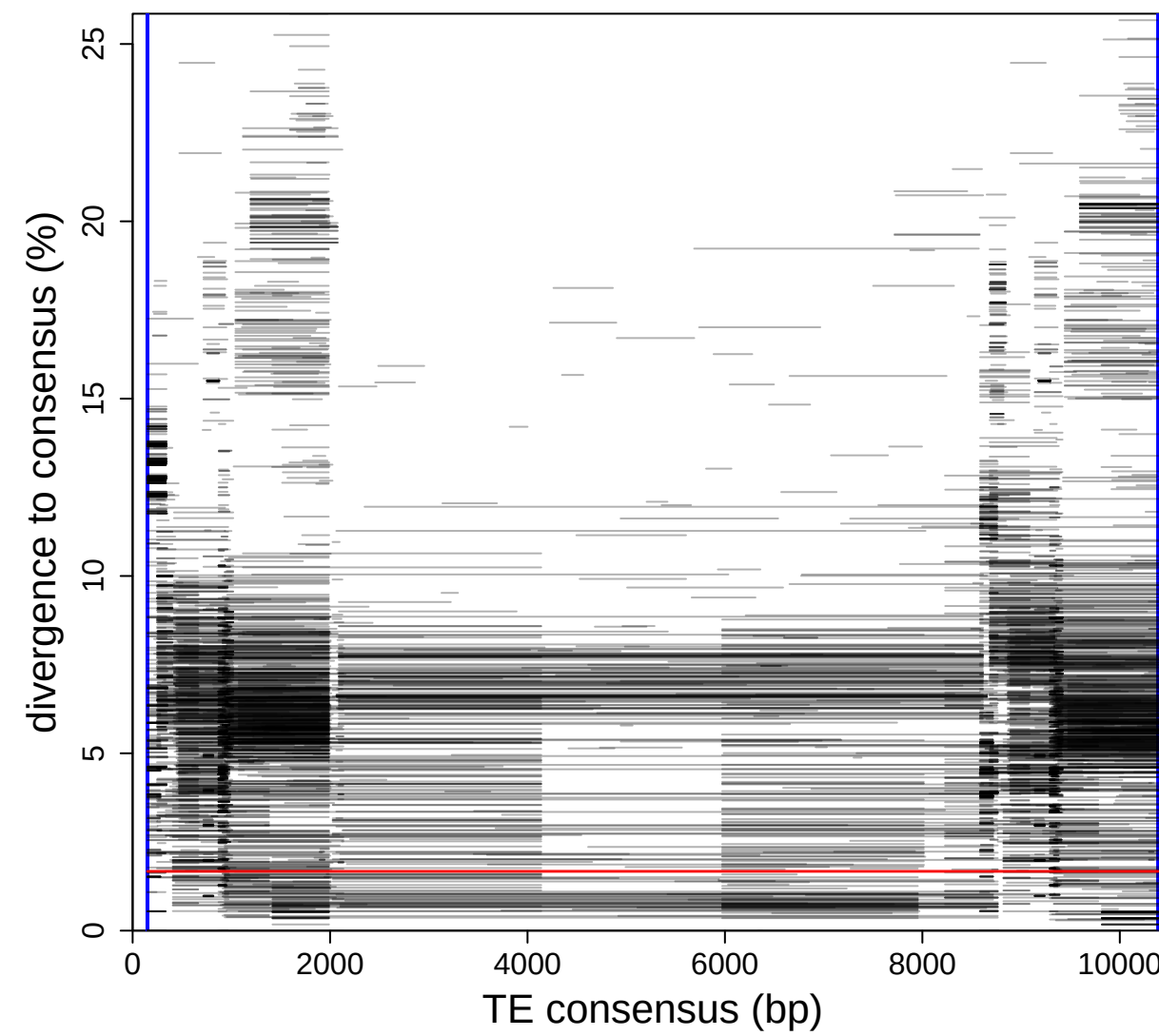
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size: 10238bp; fragments: 6427; full length: 1 (>=9214.2bp)

After TEtrimmer 10238 bp



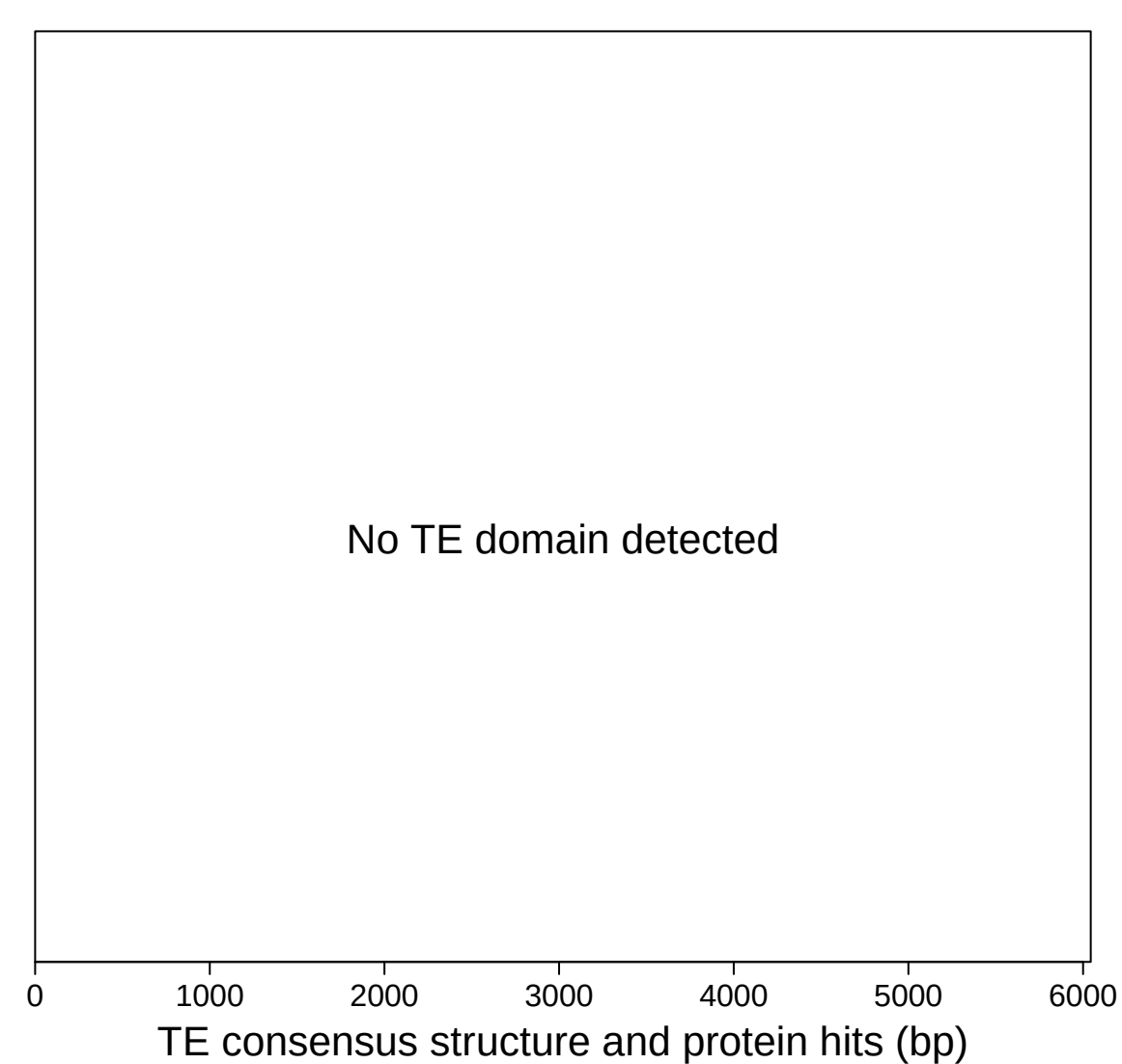
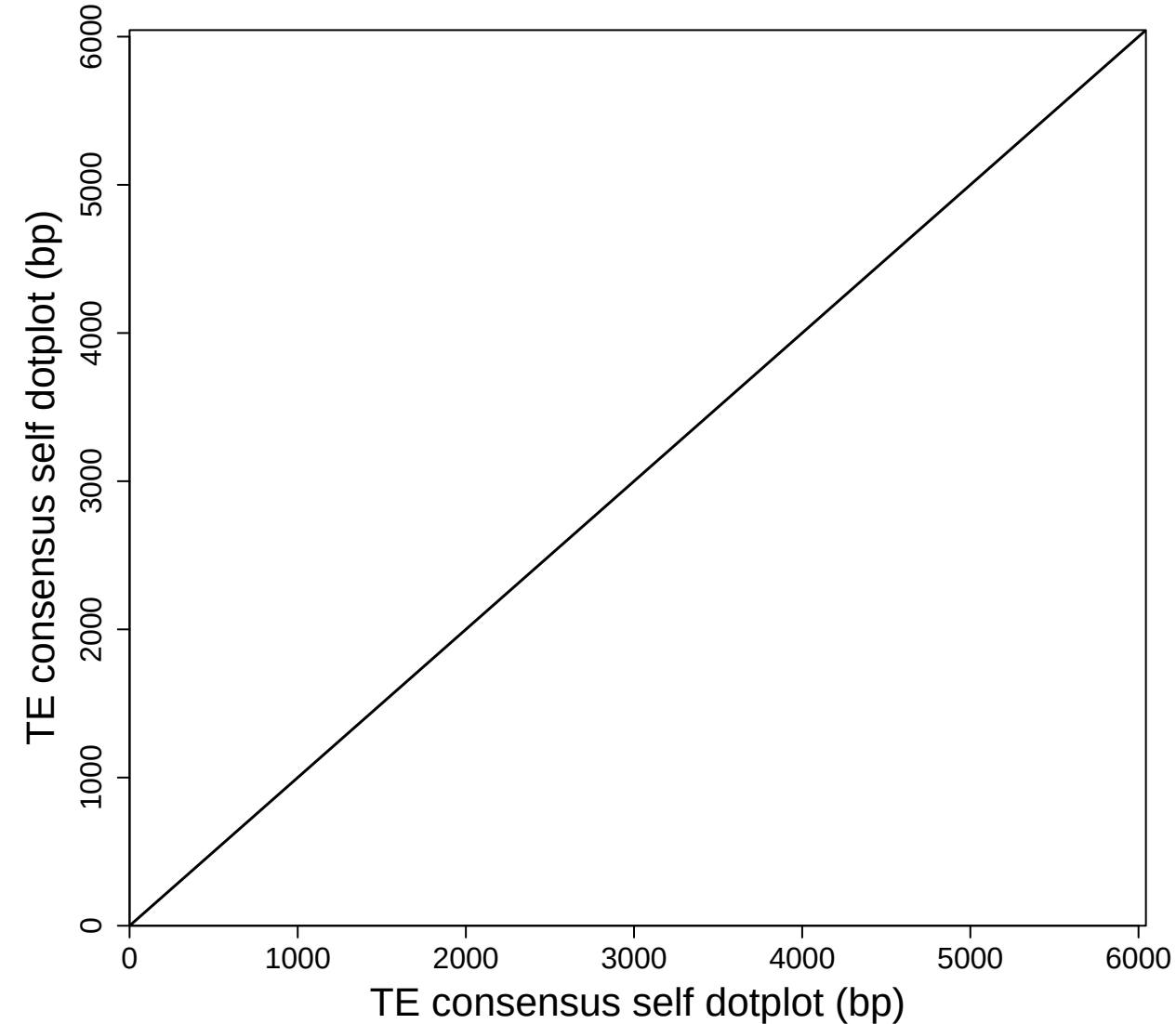
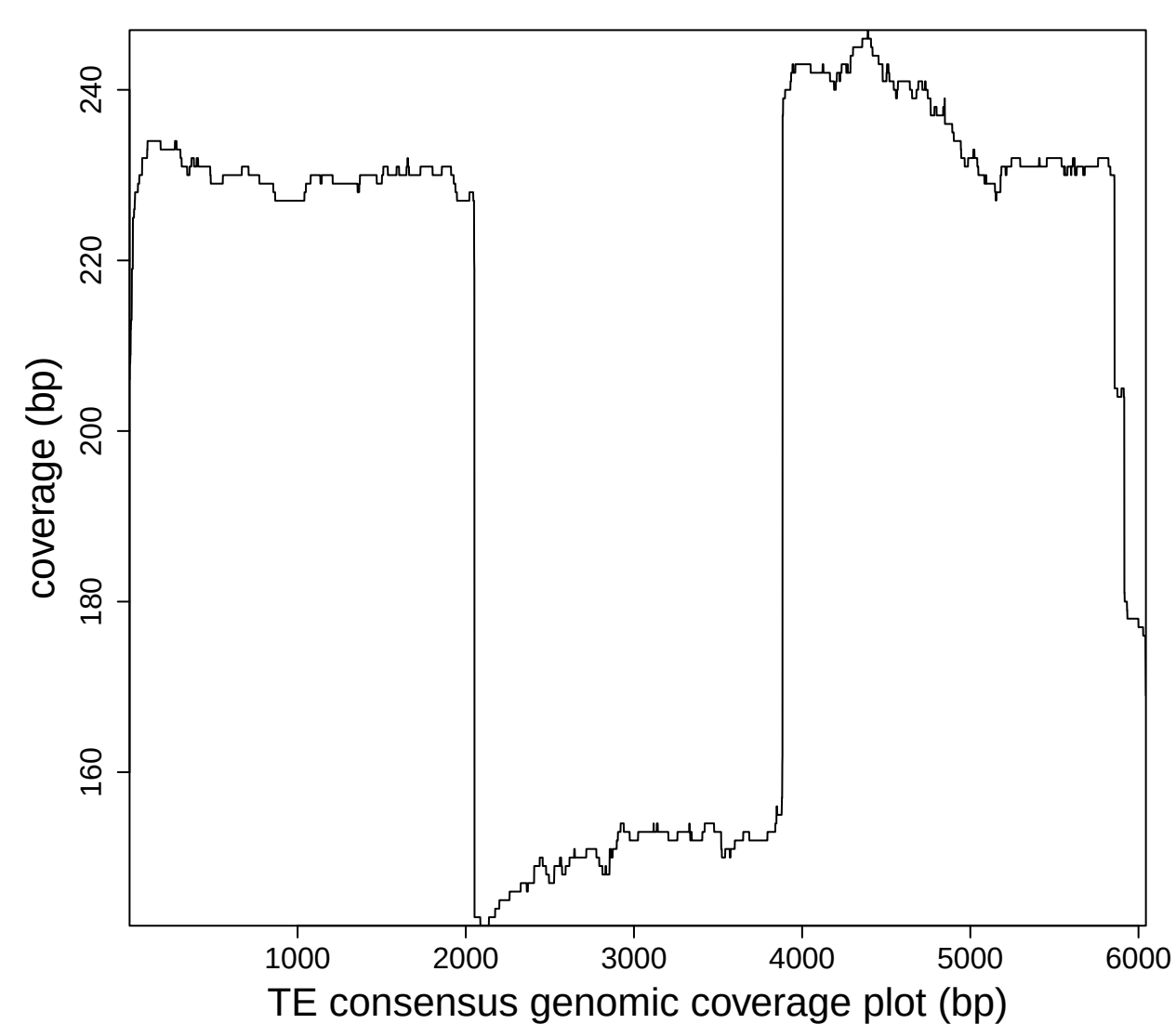
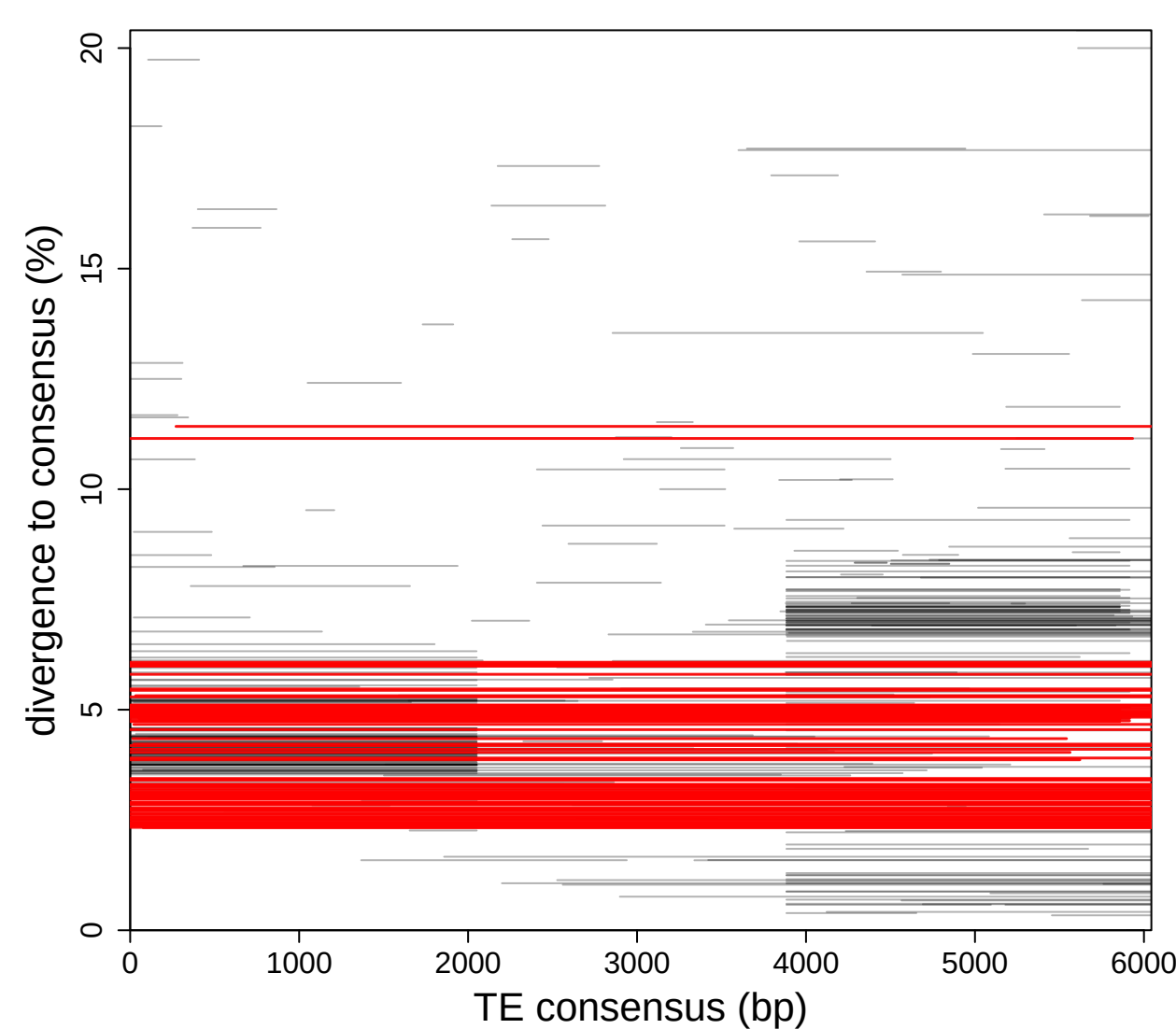
bed uf.bed g 2.bed fm 1.bed 0 0 n.bed g 1.bed fm 2.bed 0
size: 10538bp; fragments: 6438; full length: 1 (>=9484.2bp)

After TEtrimmer Extended plot Blue lines are boundaries

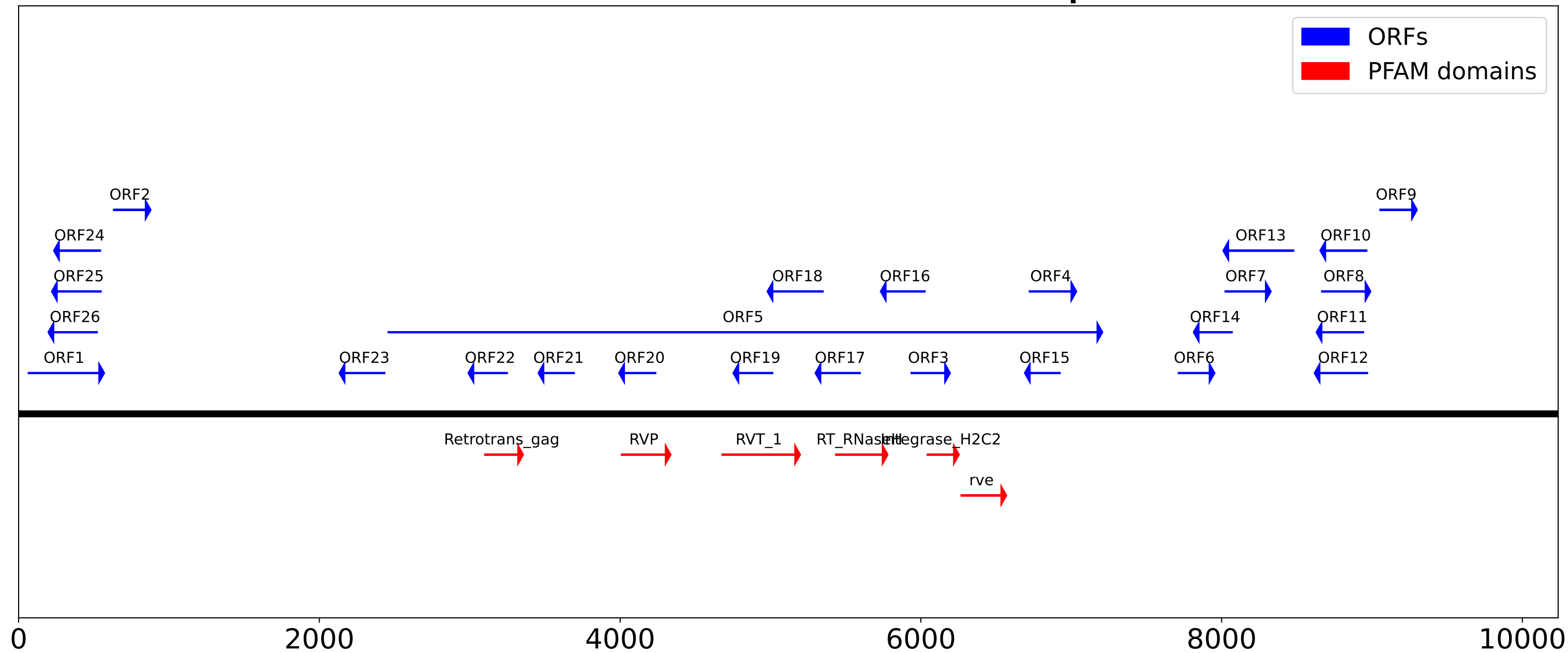


TE: rnd_1_family_284
size: 6044bp; fragments: 426; full length: 111 (≥ 5439.6 bp)

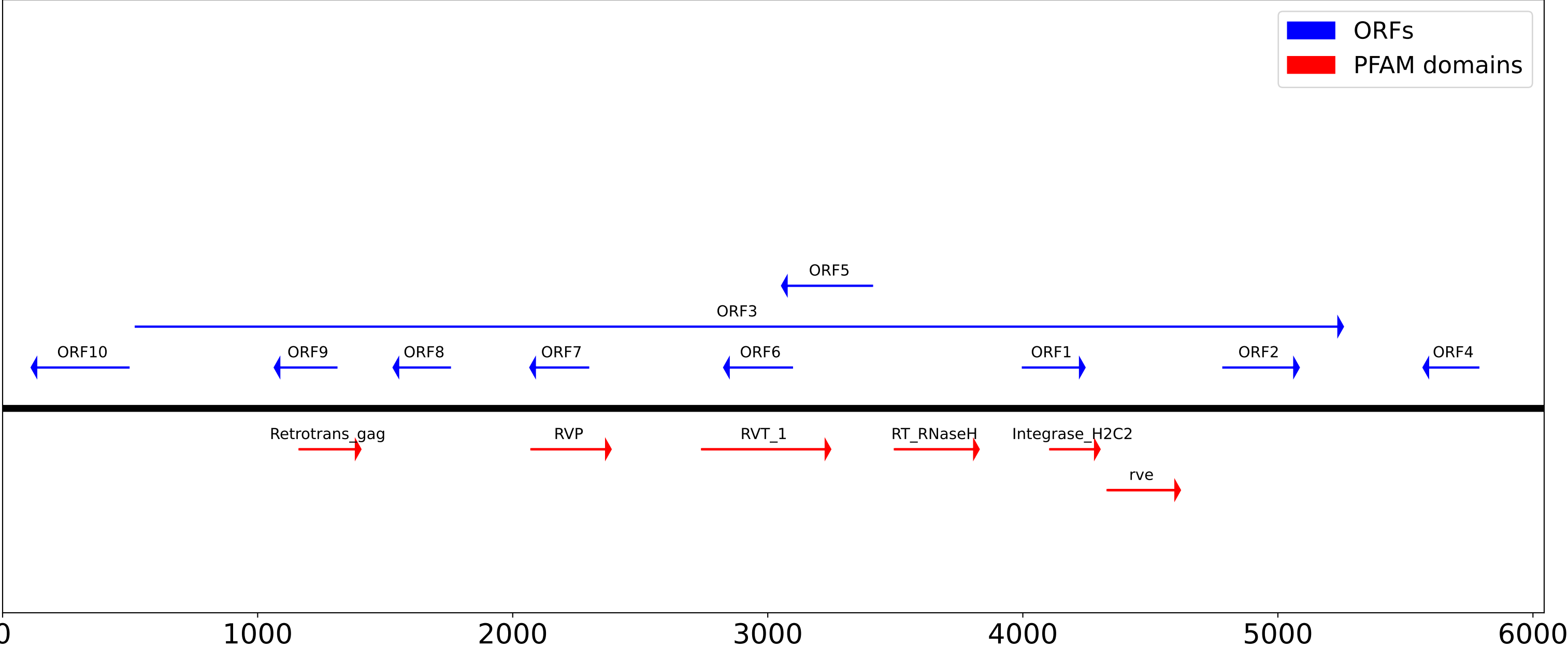
Before TEtrimmer 6044 bp



After TEtrimmer ORF and PFAM domain plot



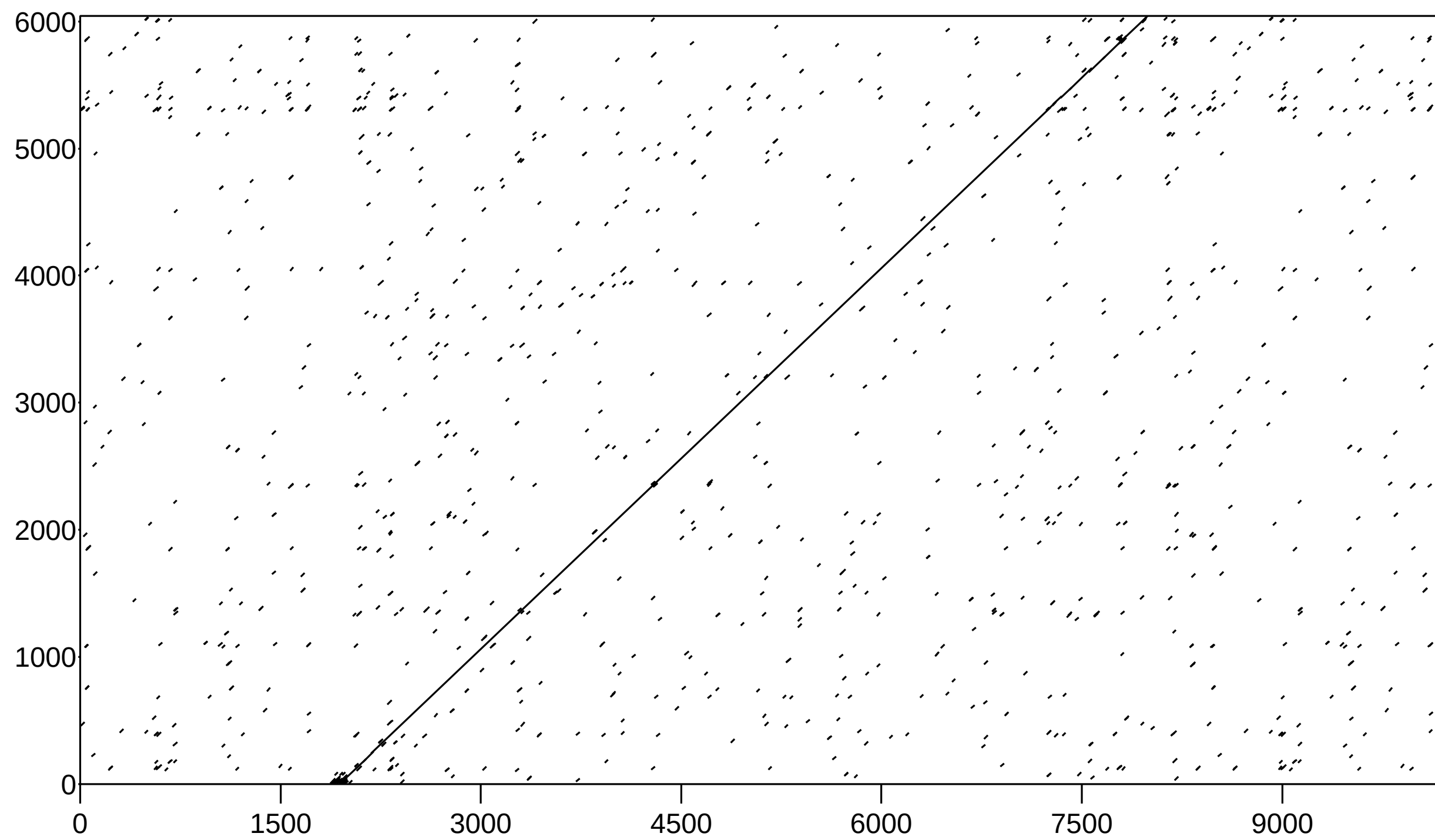
Before TEtrimmer ORF and PFAM domain plot



Dotplot

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

TE consensus before TEtrimmer (bp)



TE consensus after TEtrimmer (bp)