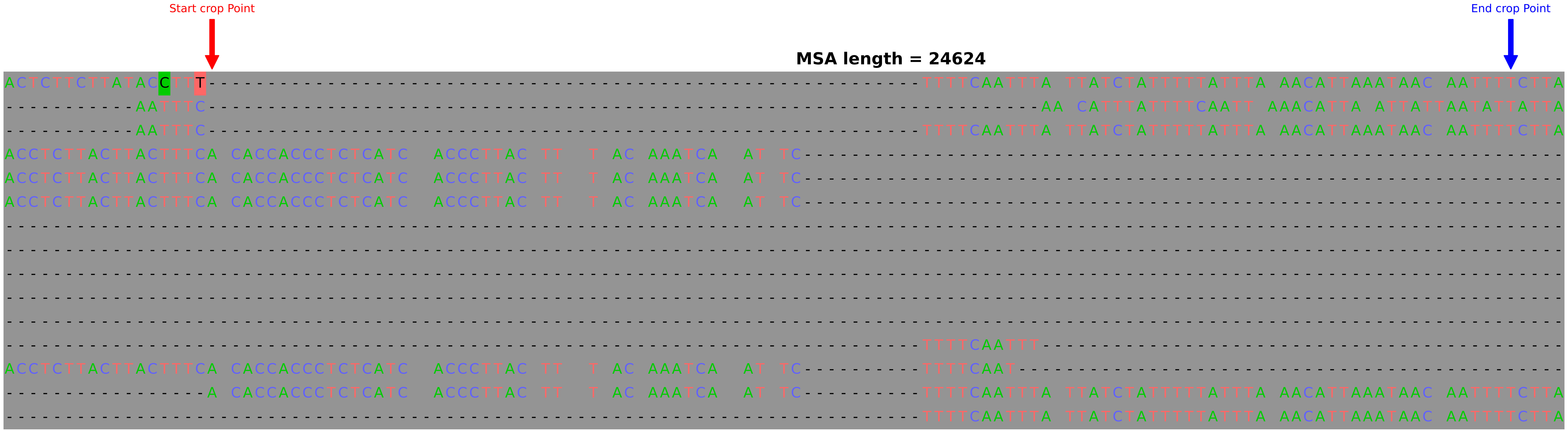
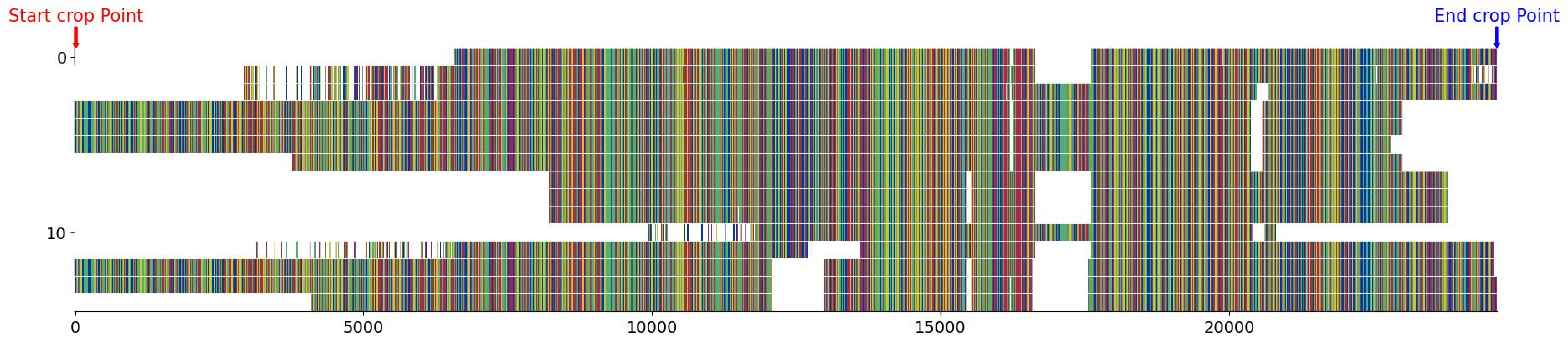

Start crop Point
End crop Point
MSA length = 24624
ACTCTTCTTATACCTTT TTTTCAATTTA TTATCTATTTTTATTTA AACATTAAATAAC AATTTTCTTA
AATTTC AA CATTTATTTTCAATT AAACATTA ATTATTAATATTATTA
AATTTC TTTTCAATTTA TTATCTATTTTTATTTA AACATTAAATAAC AATTTTCTTA
ACCTCTTACTTACTTTCA CACCACCCTCTCATC ACCCTTAC TT T AC AAATCA AT TC
ACCTCTTACTTACTTTCA CACCACCCTCTCATC ACCCTTAC TT T AC AAATCA AT TC
ACCTCTTACTTACTTTCA CACCACCCTCTCATC ACCCTTAC TT T AC AAATCA AT TC
TTTTCAATTT
ACCTCTTACTTACTTTCA CACCACCCTCTCATC ACCCTTAC TT T AC AAATCA AT TC TTTTCAAT
A CACCACCCTCTCATC ACCCTTAC TT T AC AAATCA AT TC TTTTCAATTTA TTATCTATTTTTATTTA AACATTAAATAAC AATTTTCTTA
TTTTCAATTTA TTATCTATTTTTATTTA AACATTAAATAAC AATTTTCTTA

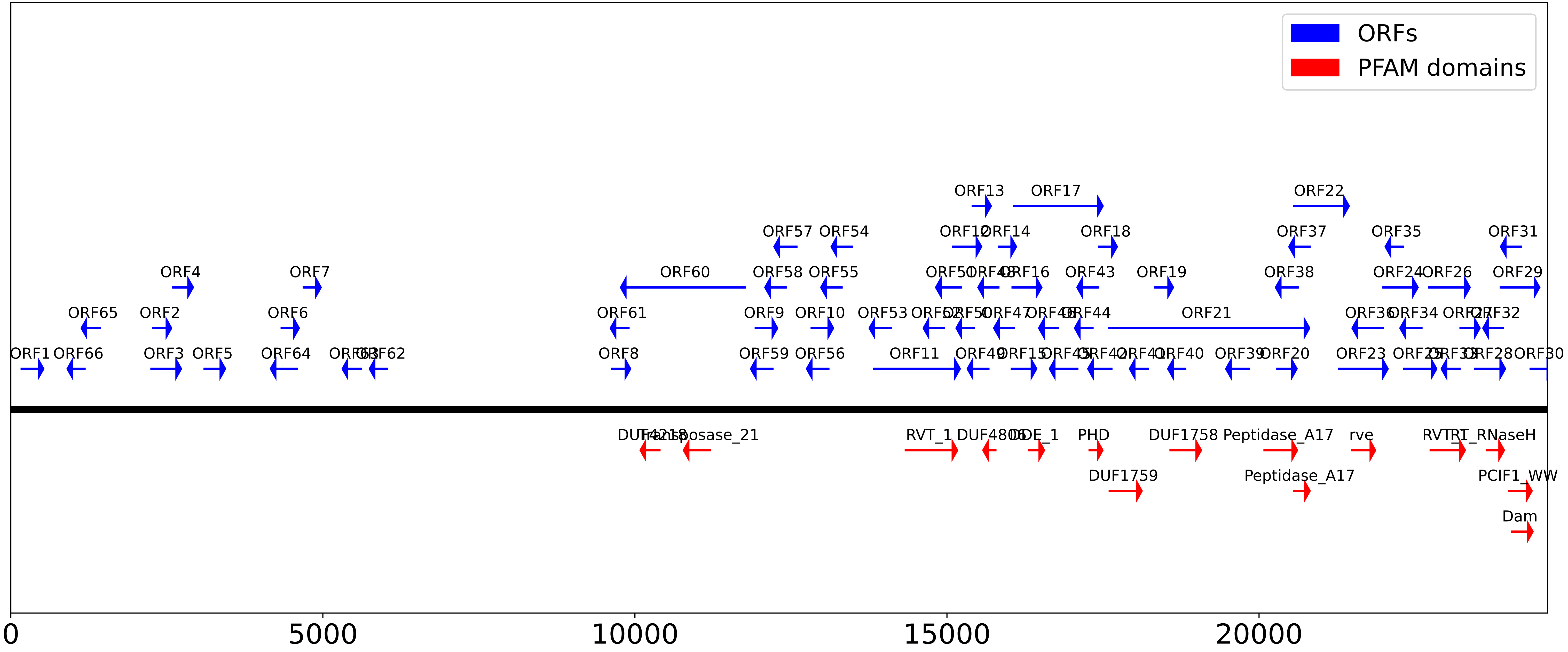

Start crop Point
End crop Point
0
10
0
5000
10000
15000
20000


After TEtrimmer 24624 bp
2.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcln.fa_aln.
size: 24624bp; fragments: 109733; full length: 0 (>=22161.6bp
divergence to consensus (%)
0
5
10
15
20
0
5000
10000
15000
20000
TE consensus (bp)
coverage (bp)
0
5000
10000
15000
20000
25000
5000
10000
15000
20000
TE consensus genomic coverage plot (bp)
TE consensus self dotplot (bp)
0
5000
10000
15000
20000
0
5000
10000
15000
20000
TE consensus self dotplot (bp)
No TE domain detected
0
5000
10000
15000
20000
TE consensus structure and protein hits (bp)

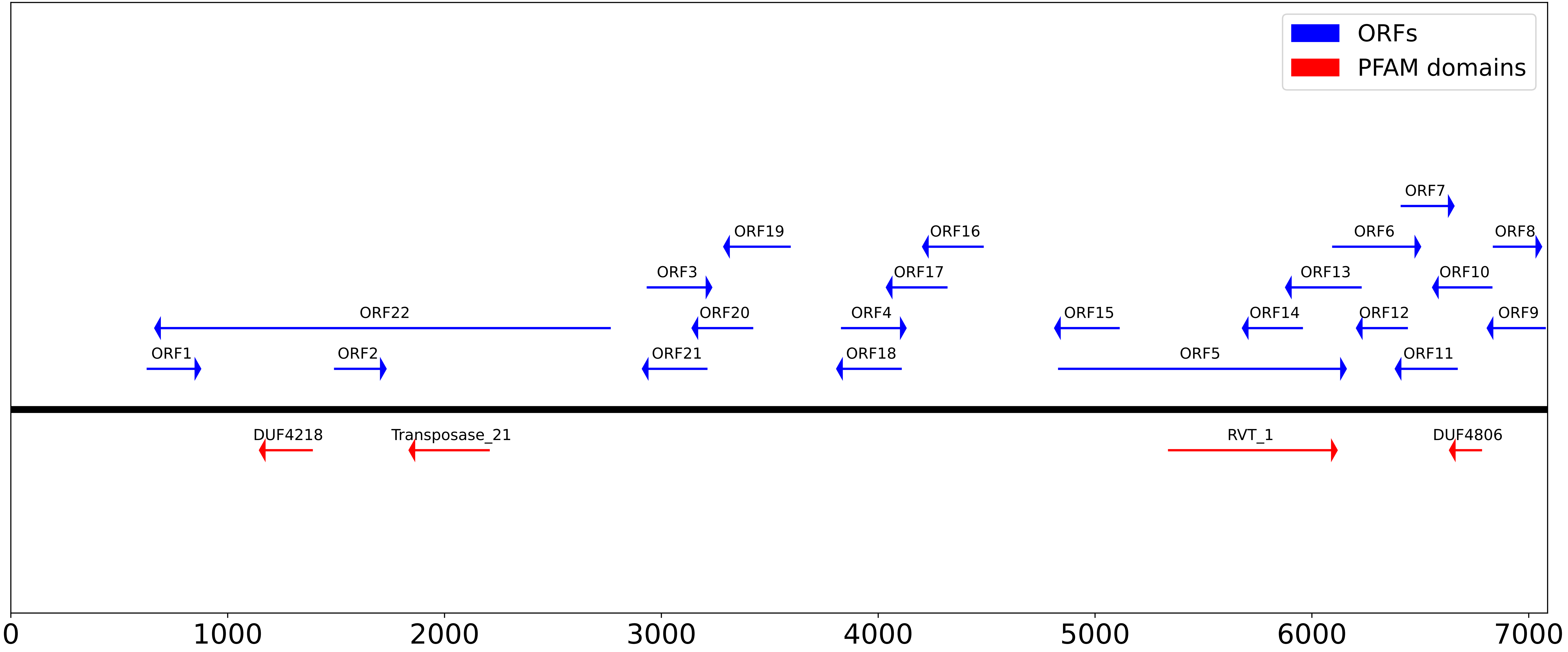

After TEtrimmer Extended plot Blue lines are boundaries
.bed_uf.bed_g_2.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_(
size: 24666bp; fragments: 109733; full length: 0 (>=22199.4bp
divergence to consensus (%)
0
5
10
15
20
0
5000
10000
15000
20000
TE consensus (bp)
coverage (bp)
0
5000
10000
15000
20000
25000
5000
10000
15000
20000
TE consensus genomic coverage plot (bp)
TE consensus self dotplot (bp)
0
5000
10000
15000
20000
0
5000
10000
15000
20000
TE consensus self dotplot (bp)
No TE domain detected
0
5000
10000
15000
20000
TE consensus structure and protein hits (bp)

Before TEtrimmer 7087 bp

After TEtrimmer ORF and PFAM domain plot



Before TEtrimmer ORF and PFAM domain plot



Dotplot

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