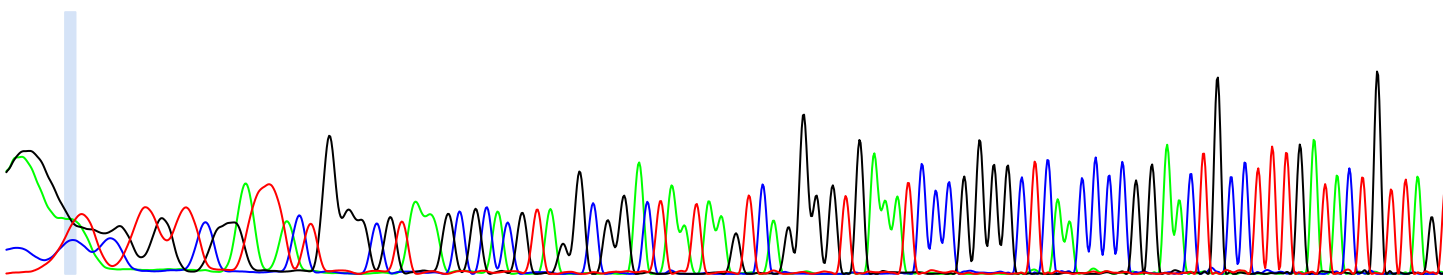


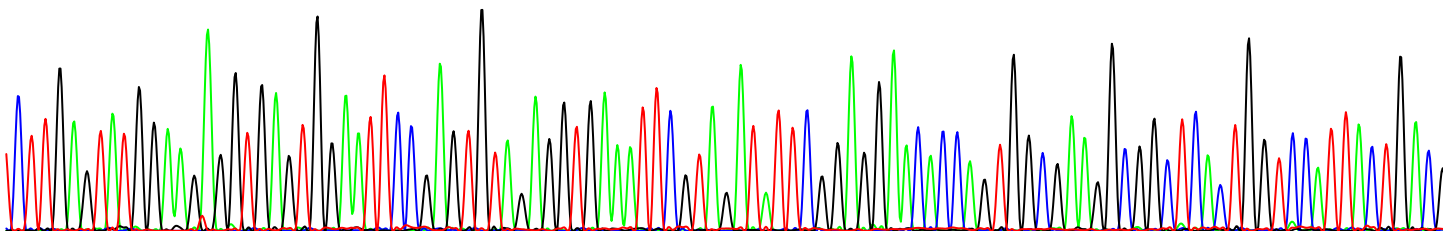
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AG ACT CG T GT C GA GT ACT G G G CG TAA GC GC ACG TA G G C G GACTAA TAA GT CAG G GG TGAAATCCC GG GG GCTCAACCCC GG AACTG C C T T TGATAC TG TTAG T

1



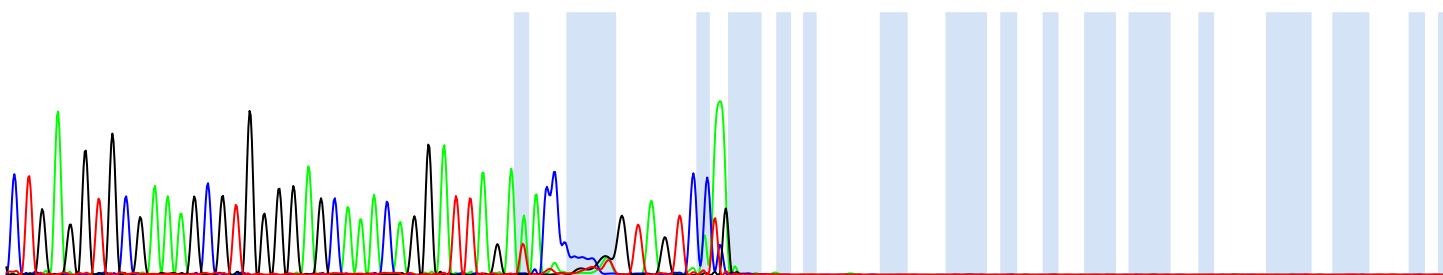
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CTGAGG TGC GAAA GCG TGGGG AGCAAACAGGA TTAGAAACC CCGGTAGTCCGAA AC GAC AAC GTTA CTGCCCGCG TGAC CCACCTTCGCTACTG TC TTCC TA
CTGAGG TGC GAAA GCG TGGGG AGCAAACAGGA TTAGATACC GTWGTAGTCATGC AKGTC AAC TGTA CCKCAGCTGTGTG CGGTCTACGCTTGS G CG TT CG TC

208



TTACCGTT CTGCTGGCAAC TCTAT A TTT TTTTCC
TTACTTCT GGGTTTTCAC TTTAT A TTT TTTTCC

311

