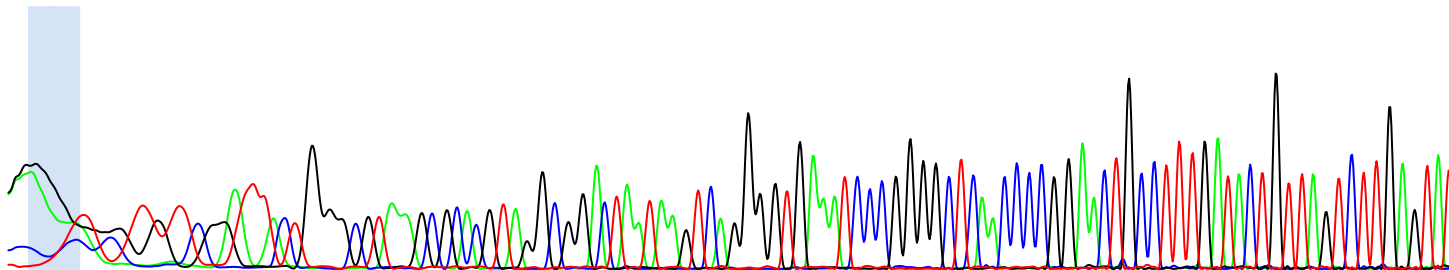


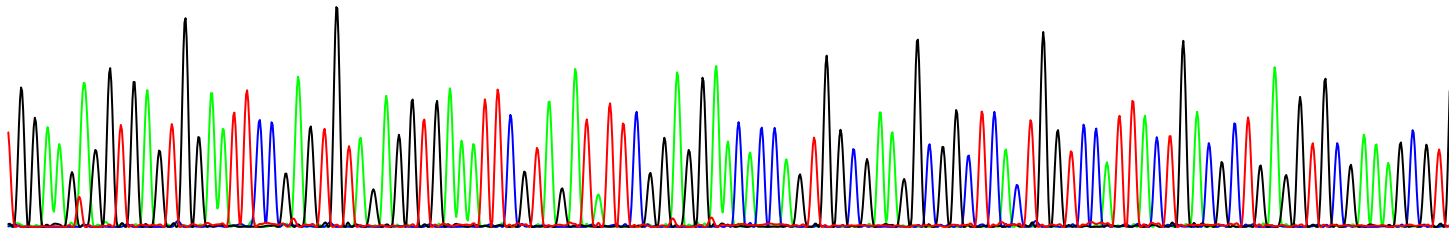
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TGA CT GG T GT CTGA TTA CT GG GCGTA A GCGAC GTA GC GGACTAATAAGTCAG GG GTGAAATCCC GG GCCTCAACCCCGGAAC TGCC TTTGATAC TG TTAGTCTT GAGTAT

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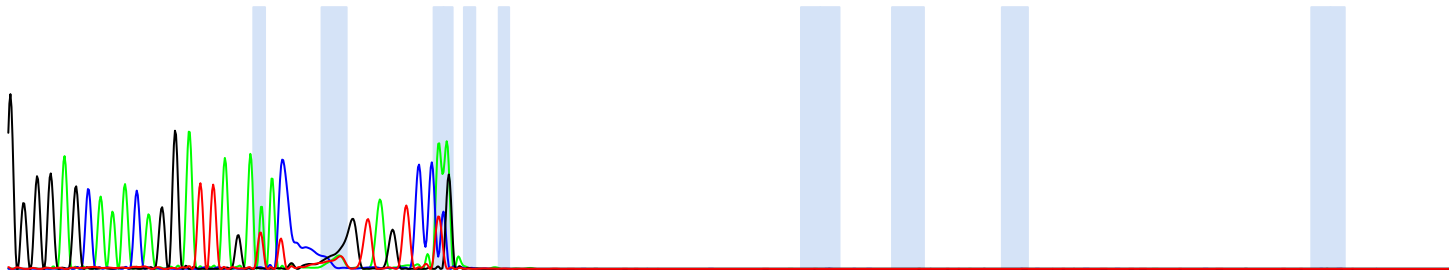
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114



GG GAGCAAACAGGA TTAGAAAC C AG TAGTCCAA GATAA TTCG TTCT C T A AC CC AGTTAG CC TTGC TCTTA T CT G T T CCT C  
GG GAGCAAACAGGA TTAGATAC C TG TAGTCCAA GATCAA TTCG TTCT C T A TG CC TGTTAG TC TTGC TCTTA T CT G T T GTT C

228



C TC  
C TC

310

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