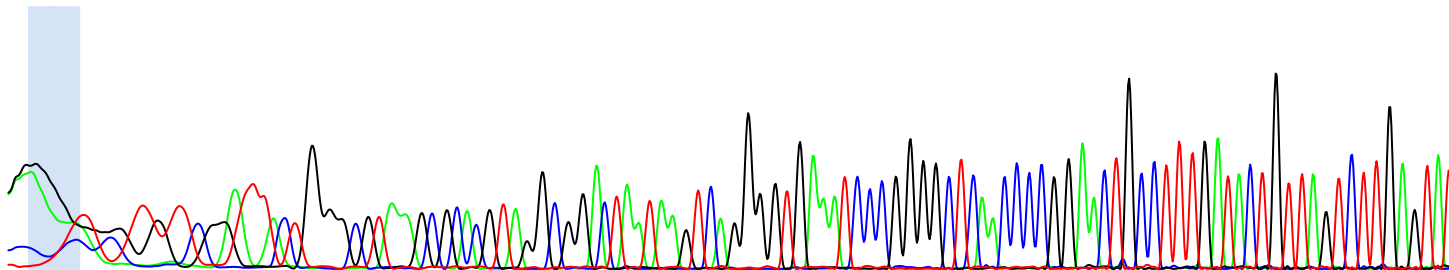


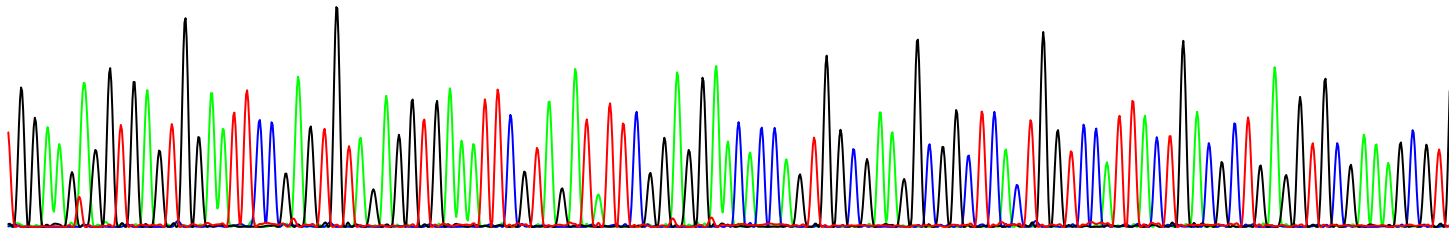
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1



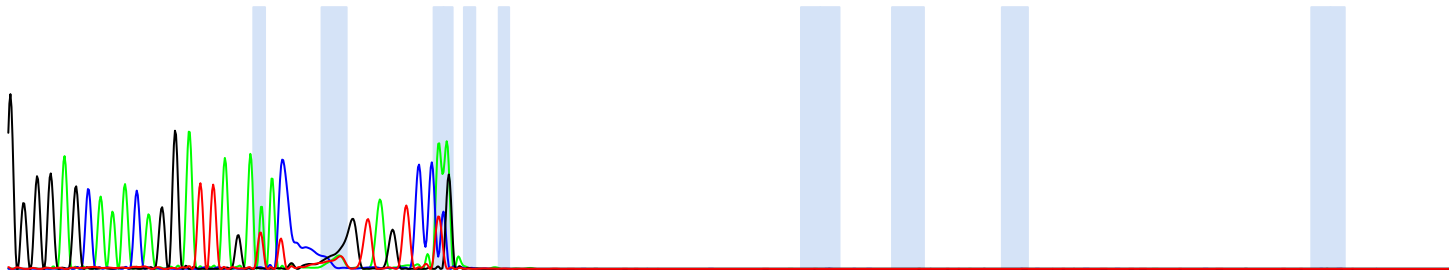
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114



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
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228



C TC
C TC

310
