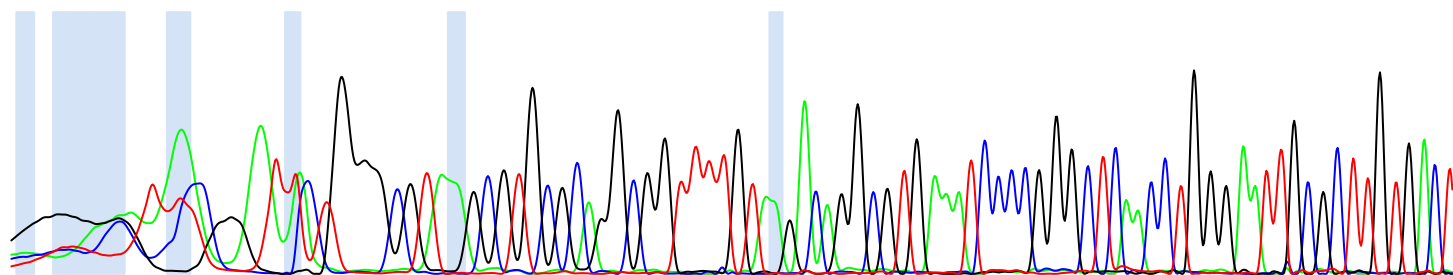


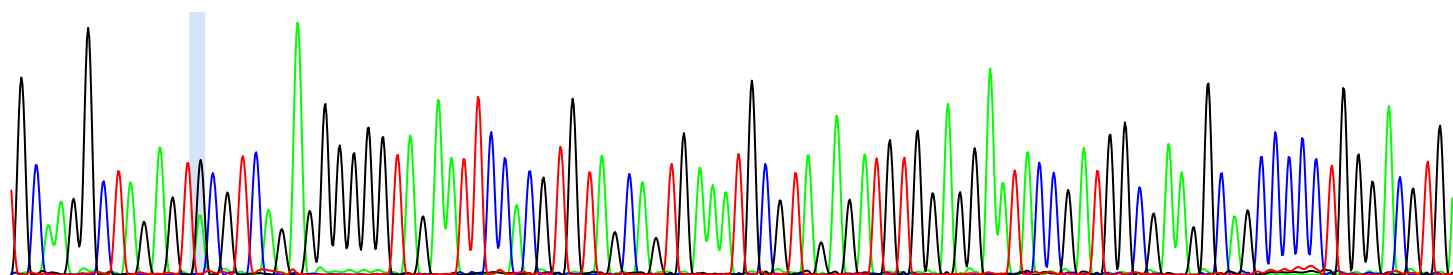
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1



GCAAGG CTAGAG TGC GT CAGA GGG GGG TAGAATTCC ACGTGTAGC AG TG A AATGCG TAGAGATGTGG AGG AATACCG ATGG C G AAGG CAGCC CCC TGGG ACGTG
 GCAAGG CTAGAG TAC GT CAGA GGG GGG TAGAATTCC ACGTGTAGC AG TG A AATGCG TAGAGATGTGG AGG AATACCG ATGG C G AAGG CAGCC CCC TGGG ACGTG

93



ACTGACGCTCATGCACGAAAGCGTGG G GAGCAAACAGG ATTAGAAACCC
 ACTGACGCTCATGCACGAAAGCGTGG G GAGCAAACAGG ATTAGATACCA

197

