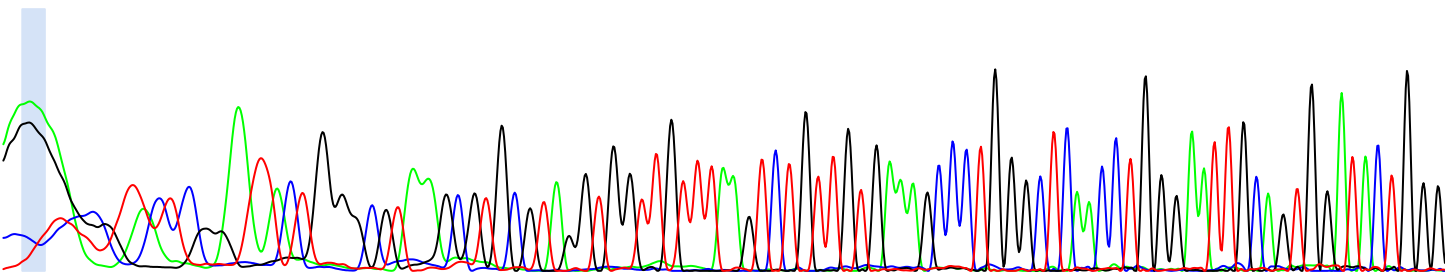


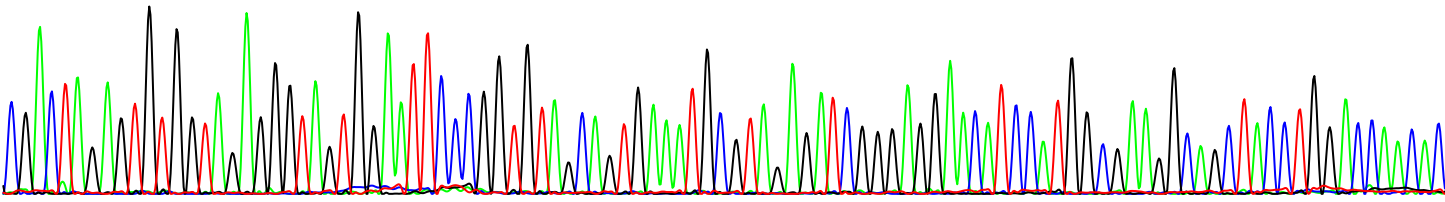
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1



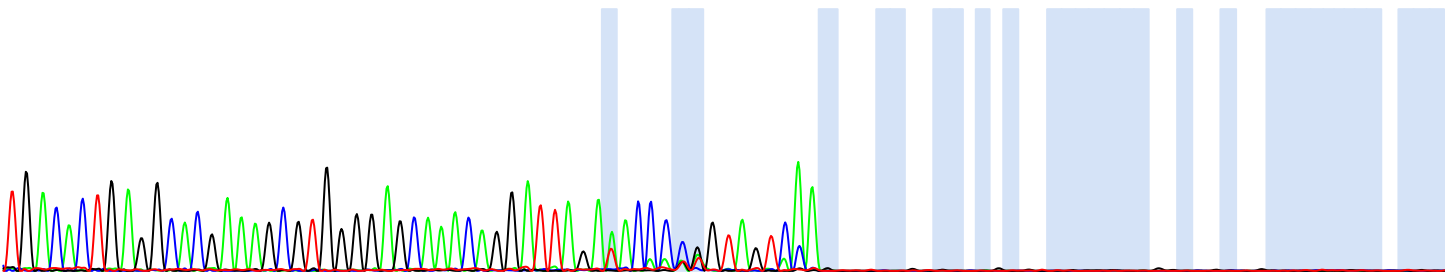
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98



TGACACTGAGGCACGAAAGCG TGGG GAGCAAACAG GATTAGAAACCC CGG TAGTCAAG T TCTGTG TC AGTG TTGGG GTA GGTCGC TGCCTTCCCTC TG T  
TGACACTGAGGCACGAAAGCG TGGG GAGCAAACAG GATTAGATACCC A WG TAGTCAAA T TTMGT C CK MG TCTCT CAK GG RC GG TGKKCCTTCTCC GT S

201



AT G G G G GN GGCNT CNCCCC GCC TCTCTT TG T CACACN GNAT CATACCC CCCC  
AT G G CM WN MCA NT GNGRA T GCT KMWCC GTS TYCTKN GNKT AT GKAGWR C WKR

301

