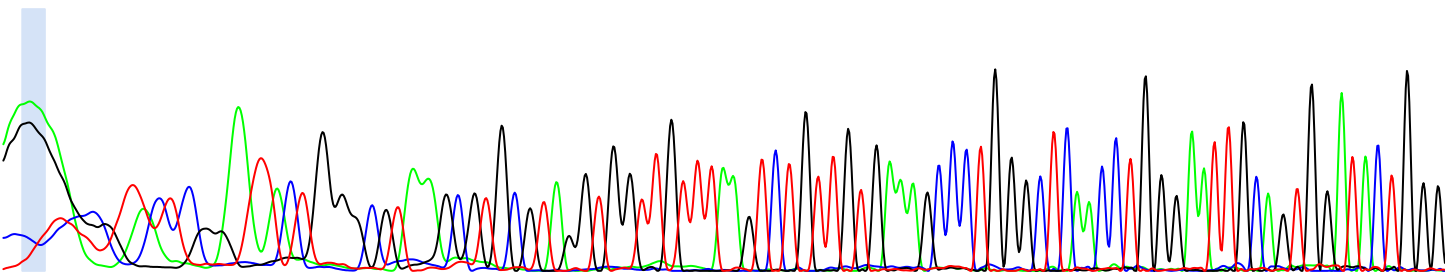


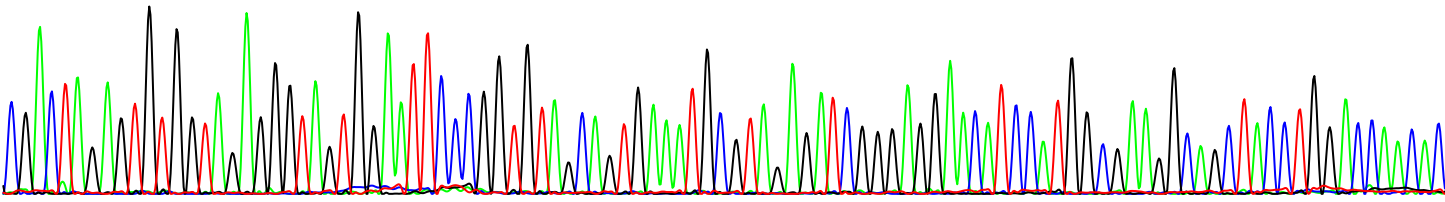
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1



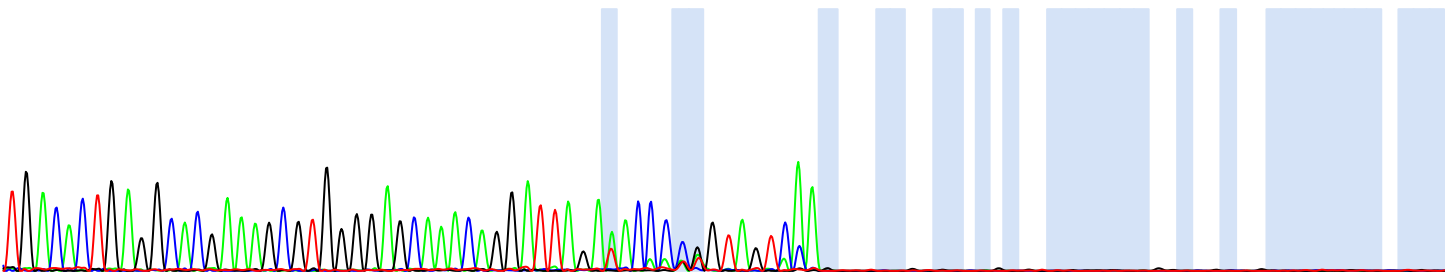
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98



TGACACTGAGGCACGAAAGCG TGGG GAGCAAACAG GATTAGAAACCC CGG TAGTCAAG T TCTGTG TCAGTG TTGGG GTA GGTCGC TGCCTTCCCTC TG T  
TGACACTGAGGCACGAAAGCG TGGG GAGCAAACAG GATTAGATACCC A WG TAGTCAAA T TTMGT C CKMG TCTCT CAKGG RCGG TGKKCCTTCTCC GT S

201



ATGGGG GN GGCNT CNCCCC GCC TCTCTT TG T CACACN GNAT CATACCC CCCC  
ATGG CM WNMCA NTGN GRAT GCT KMWCC GTS TYCTKN GNKT ATGKAGWR C WKR

301

