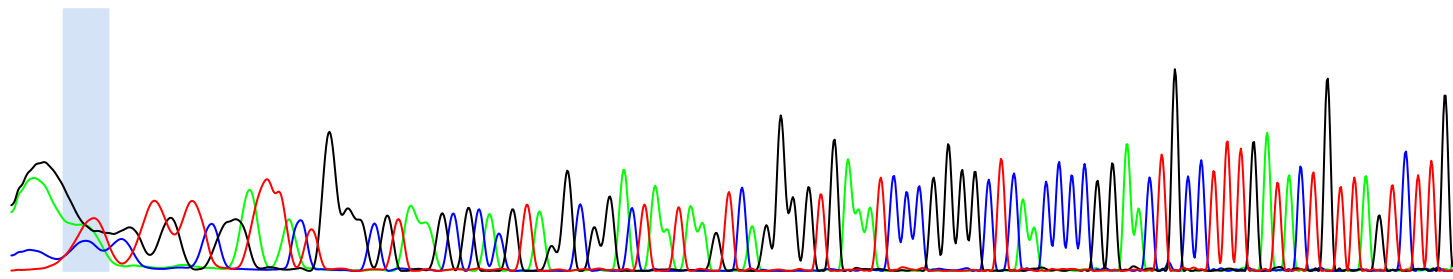


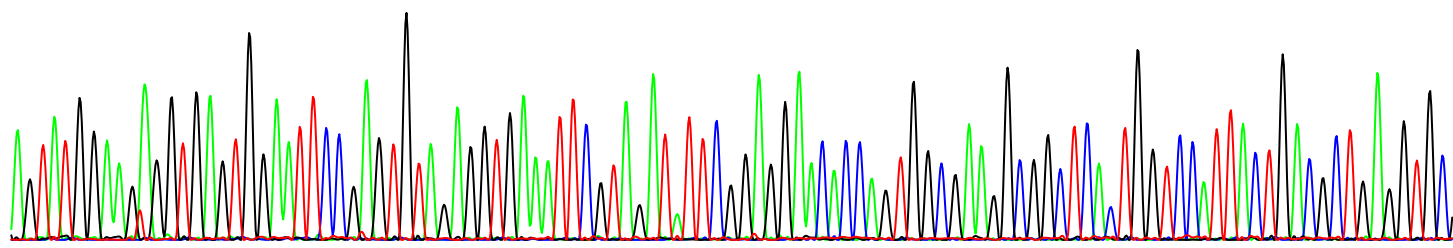
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1



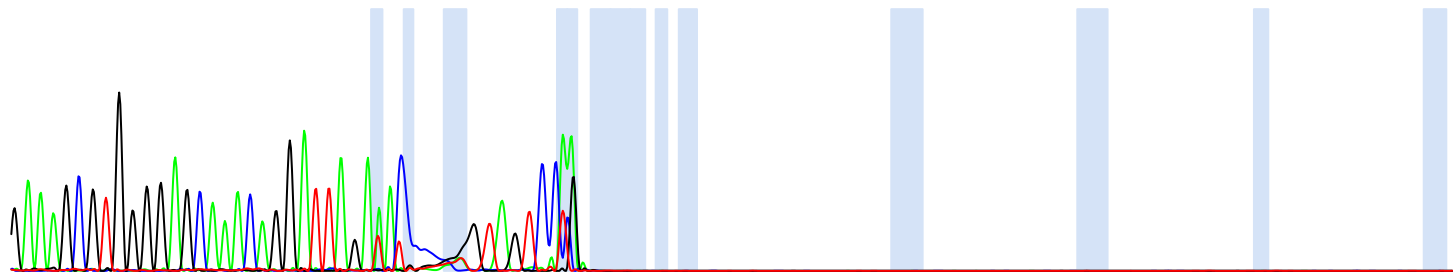
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A GTA TGG AAGAGG TGA GTGGAAT TCCGA GTGTA GAGG TGAAATTCG TAGATATTCG GAGG AACCCAG TGGCG AAGGCGGCTCACTGG TCCATTAC TGACGCTGAGGTGC

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GAAAGCG TGGGGAGCAAACAGGATTAGAAACGG AGTAGTCCAAA C TACA TC CT T C GC ATT A C A ACC AC GCG T C C C T T GTATTACC CC CT C  
GAAAGCG TGGGGAGCAAACAGGATTAGATACGCG TGTAGTCCCTGA W A GCTT CT T C GC ATT C C A ACC AC GCT T C C C T T GTTTACC CC CT T

218



TGG CAA C T  
TTG TAA C T

309

