

NC_080436.1:31908139..31908271 *Melospiza georgiana* isolate bMelGeo1 chromosome 7, bMelGeo1.pri, whole genome shotgun sequence

|31 908 150 |31 908 160 |31 908 170 |31 908 180 |31 908 190 |31 908 200 |31 908 210 |31 908 220 |31 908 230 |31 908 240 |31 908 250 |31 908 260

AGGGGAAAAGGCAAGGAGGGAAAAGGACGAAGTGAAAAGAGCTAGGAGCCACACTGGAGAGCATACAAACAGCCTGCTGACCTCTGATGCATGAGGCATGAAGAAAACAGACTGTGATTGACTATGTGGACCT
TCCCCCTTTCCGTTCCCTTCCCTGCTTCACTTTCTCGATCCTCGGTGTGACCTCTCGTATGTTGTCGGACGACTGGAGACTACGTACTCCGTACTTCTTTGTCGACACTAACTGATA
CACCTGG

(U) Alignment for group templates. BLAST Results for: XM_058028072.1 PREDICTED: Melospiza georgiana...

Query 2921411

(Li) BLAST Results for: XM_058028072.1 PREDICTED: Melospiza georgiana

Query 2021411

Genes NCBI RefSeq Annotation GCF_028018845.1_RS_2023_07

The figure displays a genomic track with three horizontal lines representing different reference sequences. The top line is green, the middle line is blue, and the bottom line is orange. Each line has a series of arrows pointing to the right, indicating the direction of transcription for genes. Above the green line, the label "SCTR" is positioned above the first arrow. Below the blue line, the identifier "XM_058028072.1" is shown. Below the orange line, the identifier "XP_057884055.1" is shown. The bottom line also features several amino acid sequence codons: AGG, GAA, AAG, GCA, AGG, AGG, GAA, AAG, GAC, GAA, GTG, AAA, AGA, GCT, AGG, AGC, CAC, ACT, GGA, GAG, CAT, AAA, CAG, CCT, GCT, GAC, CTC, TGA, TGC, ATG, AGG, CAT, GAA, GAA, AAC, AGA, CTG, TGA, TTG, ACT, ATG, TGG, ACC. These codons are color-coded to match the reference lines above them.

RNA-seq exon coverage aggregate (filtered) - NCBI RefSeq Annotation GCF_030389895.1_RS_2023-07_Img_2_scaled



RNA-seq intron-spanning reads aggregate (filtered) NCBI RefSeq Annotation GCF_030389895 1-RS 2023_07 - log 2 scaled



RNA-seq intron features aggregate (filtered) NCBI RefSeq Annotation GCF_030389895 1-RS 2023_07