

NC_059477.1:33613142..33613273 *Gymnogyps californianus* isolate 813 chromosome 7, ASM1813914v2, whole genome shotgun sequen

|33 613 150 |33 613 160 |33 613 170 |33 613 180 |33 613 190 |33 613 200 |33 613 210 |33 613 220 |33 613 230 |33 613 240 |33 613 250 |33 613 260

AGGAAAATAAGCAAGGAGGGAAAGGGGTGAAGTGAAAGGAGCTAGGAGCCACACTGGAGAGCATACAGACAGCCCCGGTGACCTCTGGTGCACGAGGGATGAAGGAAACAGACTGTGATTGACTATGTGGAC
TCCTTTATTCGTTCCCTCCCTTCCCCACTTCACTTCCCTCGATCCTCGGTGTGACCTCTCGTATGTCTGGAGACCGACGTGCTCCCTACTTCCTTGTCTGACACTAAGTACACCTG

(U) Alignment for group templates. BLAST Results for: XM_050900053.1 PREDICTED: Gymnogyps californianus...

Query 5754321

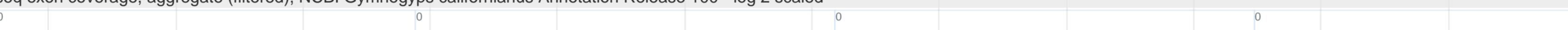
(1) BLAST Results for: XM_050900053.1 PREDICTED: Gymnogyps californianus

Query 5754321

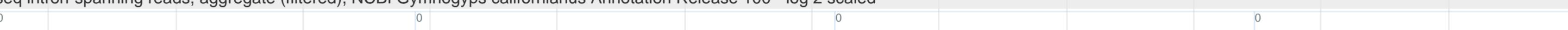
NCBI RefSeq Annotation GCF_018139145.2-RS 2023_02

This figure displays a genomic track diagram across a sequence of bases (AGG, AAA, ATA, GCA, AGG, AGG, GAA, AGG, GGT, GAA, GTG, AAA, GGA, GCT, AGG, AGC, CAC, ACT, GGA, GAG, CAT, AGA, CAG, CCC, GGT, GAC, CTC, TGG, TGC, ACG, AGG, GAT, GAA, GGA, AAC, AGA, CTG, TGA, TTG, ACT, ATG, TGG, AC). The tracks are color-coded: green for SCTR, purple for XM_05990053.1, and orange for XP_050756010.1. Arrows indicate the direction of transcription for each gene.

RNA-seq exon coverage aggregate (filtered) - NCBI Gymnogyps californianus Annotation Release 100 - Log 2 scaled



RNA-seq intron spanning reads, aggregate (filtered), NCBI Gymnopgys californianus Annotation Release 100, Jig 3 scaled



RNA-seq intron features_aggregate (filtered)_NCBI_Gymnopyps_californianus.Annotation.Release.100