

27,114,640 | 27,114,650 | 27,114,660 | 27,114,670 | 27,114,680 | 27,114,690 | 27,114,700 | 27,114,710 | 27,114,720 | 27,114,730 | 27,114,740 | 27,114,750 | 27,114,760

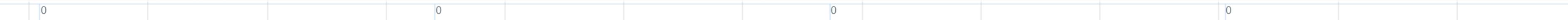
AGAAACATTGGCTAAGGATGGTCAAAGCTGGGAAGGGAAAAAGGCAAGGAGGGAAAAGGATGAAGTGAAAAGAGCTAGGAGCCACGCTGGAGAGCATAACACAGCATGCTGACTTCTGATGCATGAGGCAT
TCTTGTAACCGATT CCTACCAGTT CGACCC TTCCCTTCCGTTCCCTCCCTTCCACTTCAC TTTCTCGATCCTCGGTGCGACCTCTCGTATGTT CGTACGACTGAAAGACTACGTACTCCGTA
(U) Alignment for group templates, BLAST Results for: XM_071434261.1 PREDICTED: Agelaius tricolor...

(U) BLAST Results for: XM_071434261.1 PREDICTED: Agelaius tricolor...

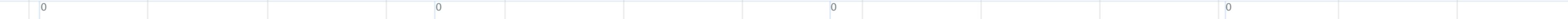
Genes, NCBI RefSeq Annotation GCF_023055355.1-RS_2025_02



RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_023055355.1-RS_2025_02 - log 2 scaled



RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_023055355.1-RS_2025_02 - log 2 scaled



RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_023055355.1-RS_2025_02