

NC_133778.1:67470104..67470166 Chelonoidis abingdonii isolate Lonesome George chromosome 10, CheloAbing 2.0, whole genome shotgun sequence

(U) Alignment for group templates, BLAST Results for: XM_032794021.1 PREDICTED: Chelonoidis abingdonii...
Query_7298787 <
(U) BLAST Results for: XM_032794021.1 PREDICTED: Chelonoidis abingdonii...

Genes, NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06

SCTR

XM_032794021.1

XP_032649912.1

GTA TGG TTT CCC AAC GTC TAT ATC AGG AAG GTG TTC TTC GGT TGA CAT CAA TCG GAC TTC

RNA-seq exon coverage, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06 - log 2 scaled

This figure displays four genomic tracks representing RNA-seq data from NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06. The tracks are arranged horizontally, corresponding to chromosomes 24, 24, 24, and 24. Each track shows a blue bar representing the total length of the chromosome. A red line indicates the position of intron-spanning reads, which are concentrated in specific regions along each chromosome. The y-axis on the left side of the first track is labeled "RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06 - log 2 scaled". The scale for the y-axis is indicated by two values: 24 at the top and 8 at the bottom.

RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_003597395.2-RS_2025_06