

NC_085054.1:20459840..20459972 *Cinclus cinclus* chromosome 9, bCinCin1.1, whole genome shotgun sequence

|20 459 850 |20 459 860 |20 459 870 |20 459 880 |20 459 890 |20 459 900 |20 459 910 |20 459 920 |20 459 930 |20 459 940 |20 459 950

AGAGAAAAAAGCAAGGAGGGAAAATGATGAAGTGAAAGAGCTAGGAACCACGCTGGGGAGCATAACAAACAGCCTGCTGACCTCTGATGCCTGAGGGATGAAGAAAACAGACTGTGAGTGACTATGTGGACCTCTCTTTTCGTTCCCTCCCTTTACTACTTCACTTCTCGATCCTGGTGCGACCCCTCGTATGTTGTCGGACGACTGGAGACTACGCACCTCCCTACTTCTTTGTCTGACACTCACTGATAACACCTGG

(U) Alignment for group templates. BLAST Results for: XM_062498139.1 PREDICTED: Cinclus cinclus...

Query 478145

(U) BLAST Results for: XM_062498139.1 PREDICTED: *Cinclus cinclus*

Query_478145

Genes, NCBI RefSeq Annotation GCF_963662255.1-RS 2024_01

This diagram illustrates a genomic region with three distinct genes: SCTR, XM_062498139.1, and XP_062354123.1. The genes are represented by green arrows above the sequence, indicating their direction of transcription. Below the genes, the nucleotide sequence is shown as a series of letters (A, T, C, G) and amino acids (R, F, K, A, H, D, E, N, P, V, I, M, W, T). The genes overlap significantly, particularly SCTR and XM_062498139.1, which share many identical nucleotides. The sequence ends with a stop codon (TGA) followed by a poly-A tail (AAA).

RNA-seq exon coverage aggregate (filtered) NCBI RefSeq Annotation GCF_035898575 1-RS 2024-01 - log2 scale

RNA-seq intron-spanning reads, aggregate (filtered), NCBI RefSeq Annotation GCF_035898575.1-RS 2024_01 - log 2 scaled

RNA-seq intron features, aggregate (filtered), NCBI RefSeq Annotation GCF_035898575.1-RS_2024_01