Nephrocerus scutellatus

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Pipunculidae > Nephrocerus

Assembly: GCA_947095585.1_idNepScut1.1_genomic

Nep_scu1 | OX352763.1:4618992-4619298 (-) | 307 nt | IncRNA:noe consensus e-value: 3.4e-12

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

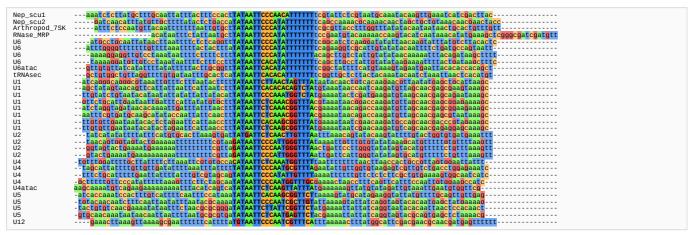
Nep_scu2 | OX352766.1:2557130-2557347 (+) | 218 nt | IncRNA:noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 1.00

GGCGGTTGGTCAACTCATAGCTGAAAGGTTGGTGGCATCCCTTAATTGCTGCAGCACACATACACAACATTGGATTTTCGTTTGGTAAGGGGCGGTTGGGAGGTAATAGGCGGGGTCCTAACCGTGTCATCCGCGCTCCTTCAAAGTCCC
TAATTGTGTCGGGAGGAGGAGAATTTCAACGGTGCTATGAGTGGTTGGATAGTGTAATCGCCTTTTTT

	Nep_scu1	Nep_scu2
Nep_scu1	-	49
Nep_scu2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.



Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAMe18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.