

Sericomylia silentis

Taxonomic lineage: Brachycera > Muscomorpha > Syrphoidea > Syrphidae > Sericomylia

Assembly: GCA\_964264485.1\_idSerSile2.1\_genomic

Ser\_sil1 | OZ183052.1:40121342-40121610 (+) | 269 nt | lncRNA: noe consensus e-value: 1.3e-14

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 14nt PSE: 0.99

666C66TCTGATGCTCAGATGTTGACGGTGGGTACATTCCGTTTCCCAATTTGATGATCTAAATCGTATGCTTTGACATCCATCTACAATAAACTTCAAAAAAGTGTGTTTGAAAAAGTCTCACCACCAACGACTAAAAAACAAATCTTTCTCTCTATCATAGATATATAGAAATAGCAATTCATAAAAATGAGAAAAACAAGTTTCAAAACGGTTTCTGCTGAGGTAGATGTGATCGCCTTTTTTTTTTTTTT

Ser\_sil2 | OZ183050.1:122687615-122687813 (+) | 199 nt | lncRNA: noe consensus e-value: 2.3e-04

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.91

666C66TCTGATTTCTGACATGATATAGGTTGGCCACATTCCTTTGATTTGACGATATGAGAGTGGTACGGGAGTATAGTAACGTATTTCATCTCTTGAAGCACCAACAACGCAACTACAAACATTTAAATTTATTTATACACAGCAATAGCTCTTAATTTTAAATGTCAGGTGTTGGGGAGACCGTGATCGCCTTTTTT

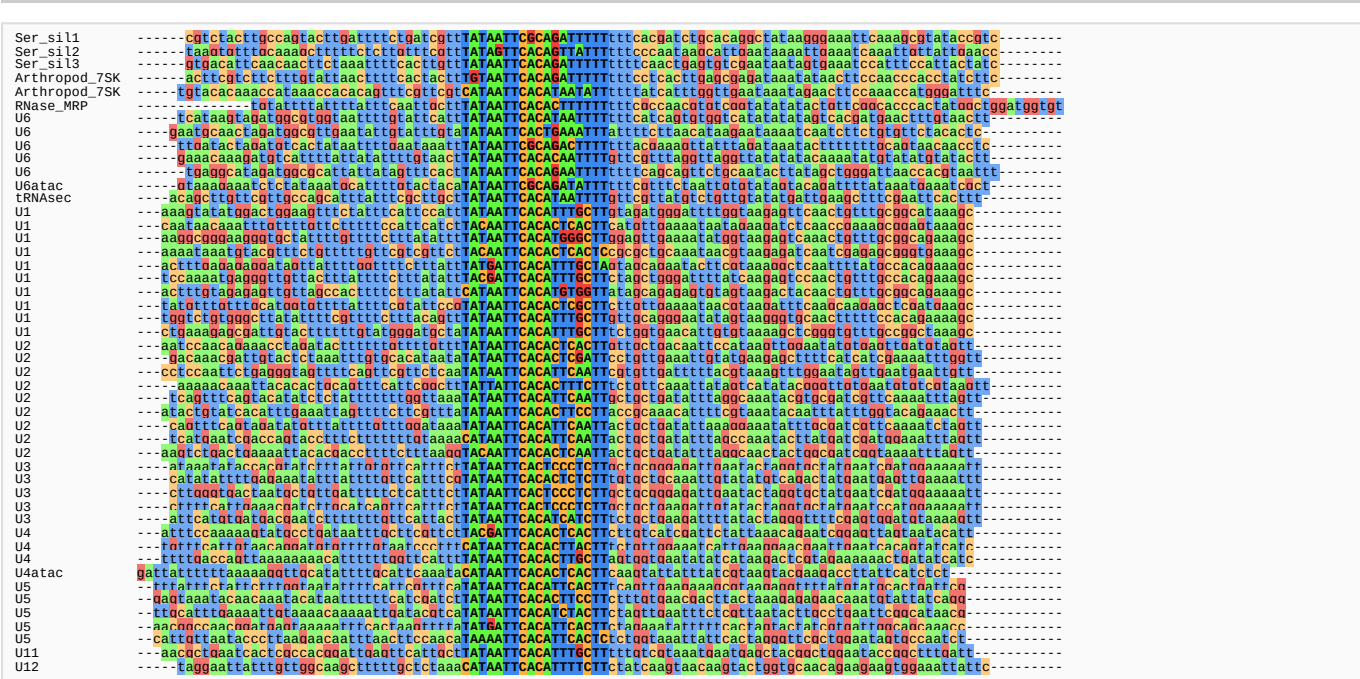
Ser\_sil3 | OZ183050.1:122686957-122687126 (-) | 170 nt | lncRNA: noe consensus e-value: 5.0e-05

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

666C66TCTGATGCTCAGACTCAGAAAGGTTGACCGCATCCCTTAATTTGGACGATATAGTGTTGTAACCTTAAAAAGGGAAAAACACAGAAATATAAAAAGAAATAAAAAAACCAATTTGTATGCACTCAAATTAAGGTTGATGAGATGATTTGATCGCCTTTTTT

	Ser_sil1	Ser_sil2	Ser_sil3
Ser_sil1	-	49	47
Ser_sil2		-	58
Ser_sil3			-

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, snoRNA18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.