Platycheirus rosarum

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

Assembly: GCA 963971375.1 idPlaRosa1.1 genomic

Pla_ros1 | OZ020507.1:291982710-291983065 (+) | 356 nt | IncRNA:noe consensus e-value: 8.2e-09

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.97

Pla_ros2 | OZ020507.1:278966462-278966760 (-) | 299 nt | IncRNA:noe consensus e-value: 2.1e-08

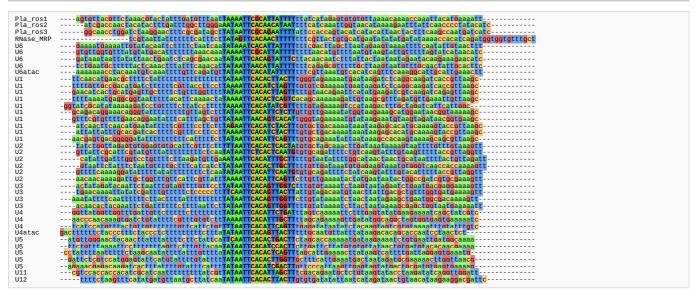
5' motif: GTGGT 3' motif: ATCAC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.81

Pla_ros3 | OZ020508.1:36367017-36367316 (-) | 300 nt | IncRNA:noe consensus e-value: 2.1e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.97

	Pla_ros1	Pla_ros2	Pla_ros3
Pla_ros1	-	44	47
Pla_ros2		-	46
Pla_ros3			-

Pairwise sequence identity matrix (%) showing similarity between IncRNA 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.