Drosophila takahashii

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > takahashii subgroup

Assembly: GCA_030179915.2_DtakHiC1v2_genomic

Dro_tak1 | CM058219.1:16496855-16497976 (-) | 1122 nt | IncRNA:noe consensus e-value: 1e-196

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

Dro_tak2 | CM058222.1:20321720-20322233 (+) | 514 nt | IncRNA:noe consensus e-value: 5.1e-04

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

Dro_tak3 | CM058222.1:10541952-10542199 (+) | 248 nt | IncRNA:noe consensus e-value: 1.3e-04

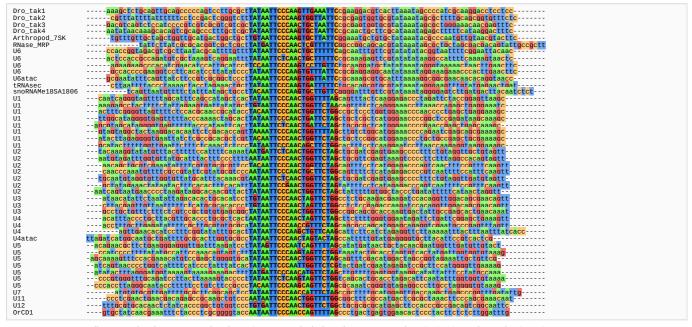
5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

Dro_tak4 | CM058222.1:10536868-10537086 (+) | 219 nt | IncRNA:noe consensus e-value: 2.2e-06

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

		Dro_tak1	Dro_tak2	Dro_tak3	Dro_tak4
	Dro_tak1	-	32	13	12
	Dro_tak2		-	38	34
	Dro_tak3			-	65
	Dro_tak4				-

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.