Drosophila navojoa

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > repleta group > mulleri subgroup

Assembly: GCA_001654015.2_UFRJ_Dnav_4.2_genomic

Dro_nav1 | LSRL02000002.1:1202496-1203423 (+) | 928 nt | IncRNA:noe consensus e-value: 3e-170

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 8nt PSE: 0.82

Dro_nav2 | LSRL02001665.1:1095-1574 (+) | 480 nt | IncRNA:noe consensus e-value: 1.7e+00

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 10nt PSE: 0.95

Dro_nav3 | LSRL02001107.1:12613-13033 (+) | 421 nt | IncRNA:noe consensus e-value: 5.7e-04

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 25nt PSE: 0.95

	Dro_nav1	Dro_nav2	Dro_nav3
Dro_nav1	-	30	30
Dro_nav2		-	73
Dro_nav3			-

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.