Mycodrosophila poecilogastra

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Mycodrosophila

Assembly: GCA_040802665.1_ASM4080266v1_genomic

Myc_poe1 | JBEQPP010007031.1:884-2054 (+) | 1171 nt | IncRNA:noe consensus e-value: 8e-173

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.94

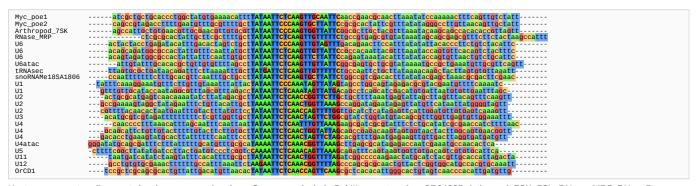
Myc_poe2 | JBEQPP010010798.1:360-651 (+) | 292 nt | IncRNA:noe consensus e-value: 9.6e-10

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.98

GGCGGT_GTACGTCTCACAGCTTAAAGGGTTAGCACACTCCCGACTAATTGTGGCACAAAACACGAATGAAGCCCATGCTATATAAAAATCATCCTTCTTTAAATGGTATCCAGATTTACAAATGAGCATGAAACACGAAACACGAATGAAGCCATTACTAAATGAATCATCCTTCTTTAAATGCTTCTCTTTAAATGCTATCCAGATTTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTTACCAGATTACAGATTACAGATTACAGATTACAGATTACAGATTACAGATTACAGATTACCAGATTACCAGATTACA

	Myc_poe1	Myc_poe2
Myc_poe1	-	16
Myc_poe2		-

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.