

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

Assembly: GCA_035045825.1_ASM3504582v1_genomic

Dro_eoh1 | JAWN0T010000070.1:6618286-6619216 (+) | 931 nt | lncRNA: noe consensus e-value: 1e-171

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

6GGGCGGGTCGGGATCCGCACTAAAGACGGTTGGACACAGCCGCTGAATCCGCACTCTGAATTTGTGTCCCTTCGGTTTCAGTTTGCAGAGCAATAAACGACGCAACTGCAAAACACACAAAGAAAAACCAAAACGCTGCGCAAACTTTC
GTCACTCTCTGTATGCAAAACACCAACTGCGCAAAATATATAAAGACACGAACATATATATATATACAACTGCTATATCTGAATAAAAATGCGCAAAAAAGCTGCAAACTGAAATCTACGATTCGCGCAAGATTAATGTAAGGAAGACAA
AGATACATCTCTGCAAAAAAGATATCAATGCAAAAAACAAAACATATAAAGACCACTAAAAACCACTAAAAAACAATGAAAGTAAAGCAACTTAATTAATGTGACCTATAGATTAAGATTAATCATCATGCTGTATCAGGACACAAAAA
ATCTCTGCAAAAATCTAAAAAAAATCTAAAACTGCAAAAATGCAATTTGGTGTGCTTCGCGCTCTGCTGTAATCTGCTGACACGCCAATTTGGCCACACACAGATGCTGGGCGCGGCTCTCCCTCTCTCCCTCTACACCGACCGGACATGCTAT
GGACACTATTTGGCCGCGCTGGGCGCTGCCAAAAATTAACCATAGAGACGATTTAGGCAAAATCTTAATGACAAAAAATTAATTAACCAAGAAAAACAAAAAGAAATTAATATGGAAGAAAAAGAAAAACAAAACCAAAAT
TTTAACCAAGAAAAACAAAACATTAATCAAAAATGAGCAATATGACCAACATCTAATAATGGCAAAAAAGCAAAAATGAAAAAATCTGCAAAATACGACACAACACCTCTCAAAAAAGACCTCAGTATATAACACATAATGCTGGGTCGTCGAAA
GGAAATCCGCTAGCTGATCGCCCTTTTTTTTT

Dro_eoh2 | JAWN0T010000036.1:5550839-5551625 (-) | 787 nt | lncRNA: noe consensus e-value: 5.8e-02

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

[illegible]

	Dro_eoh1	Dro_eoh2
Dro_eoh1	-	46
Dro_eoh2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

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.