

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

Assembly: GCA_003285905.2_DhydRS2_genomic

Dro_hyd1 | QMEQ02000202.1:2676347-2677275 (-) | 929 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

GGGGCGGTCTGGGATTCGCAAGTAAGACGGTTGACACATGCCCGTTGAATCCGCACTCTGAATATGTCGGTTCCGGTTATATGTTTCAGACAGCAATACACACCAACTGCAAACACACAAAGAAAAAACAAACGCTGC8CAAACTTTC
GTCAATCTCTGATCGAAAACGCAATATGCAAAAATATATGAGACACATATATATATCAATCACTGTATATCGAATAAAAATGCAAAAAATGCAAAATGAAATACBATAACGACAAAGATATTGTAAGAGAGACAAAA
GATATCTATTGCAAAAAATATCAATGCAACAAAAAATATATCAATCAAAAACATATAAAATACATAAAAAACATGAATACAACTAAATGTACCTATAGATTAAGGATATCATCATCTGTGTATCATGAGACACAAAAAT
CTCTCAAAAAATCTAAAAAAAATATTAAAAAATCTGCAAAAATCTCTGGTGTGTGTGTCGGCTGTGTGATATGCAATGACACGCCAATTTGGCACAAGAGAGCTCTTGGGCGGAGCTCCCTCCCTCTCACTTCAAGGACGGACATCTATGG
ACATCTATTGGGCGAGGTGGCGCTGCCAAAAAATACCCATAGACAGCTTTAAGGACAACTTAATTAACGCAAAAAATGCAAAACAAAGAGAAAAATGAATCTGAAGAAAAACAAAAAGAAAAACAAACAAATGCTATGG
TAAACGAAGAAACAAACBATAATCAAAAATAGCAATATGACACATATCTAATAATTGGCAAAAAGCAAAAATGAAAAAATCGCAATTAACBACAACACACCTTCAAAAAAGACCTCAGTATATACACATTAATGCTGGGTGCTGCAAAAGG
ATACCATAGCTGATATGCCCGCTTTTTTTT

Dro_hyd2 | QMEQ02000048.1:1708233-1709024 (-) | 792 nt | lncRNA: no consensus e-value: 4.8e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.99

[illegible]

	Dro_hyd1	Dro_hyd2
Dro_hyd1	-	46
Dro_hyd2		-

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.