Mycodrosophila poecilogastra

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

Assembly: GCA_040802665.1_ASM4080266v1_genomic

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

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

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GGGGCGGTCGCGCATTTGGCAGTACAGACGGTTGGACACAGCCCGTTTAACCCAATCTGAAATTGTGTCCGTTGGTTTTAATAGAGAAGCTATATAAAAGTTACGATTGCTGCGCAAACTTTCGTCATCTCTGAAGCAAAAACAAAATGA
AGAAAAATGCAGAAATGCAAAATATATGAAGAAGCACAAGAGCAAACTTAAATAAAAGCAAACAACAAAAAGTCTAAAACAAAAGTAATCACGAAACGCAAAGATAAAAAAAATATAAAGACAAAAAGAAAATCTATCAGACCAAAAGTA
TATCAATGCAAACAAAAAAAACTTATAAAACACATAAAATACACTAAAAAAATGAAAACTAACTTAAATGTGACCTAGTAGATAATGATCATCAGTAATTCACTTGGCAAGGCAACAAAAAAAAACATAAAGAAAATCAAATAAAAAATA
CAAAAAACTCTGAAAAATGTCTAAAAGCAACAAAAAAATATTAAAAACTGCAAAAACTGCATTGGTGTGTGTGTCCCGTTCGTGTAATCGCTGGCGCGTCAAAGGCCGTGGCTATGCGAGTCTTCCAGTATATAGATGCCACACTATC
CTCTCCACAGGCAGATAGCCGGCTGGCAGGAAATCAGGATGGAGAGAGGGACTACTACTGCAGCGGCGAACCAACATCTAACATCAGGCCGCGACGAAGATGAGAAGTGCATCAATCTGGGCGTAGAGATCGGGTTCCATATCTCCTCTA
TAAACAAGTTGGTATACCAATCATCGACGTCAATCCCTTGGAGAACGAACTCTCCACTTTCCGACCTGCGTGAACCCAGCCTTGCTGGCTTAGCGTTGCGGTATTGGTGTGCTGTGCGTGTGTGTGTGCTGCGGGGGCAAGAAGATGCCT
CTGGCCAGGCGCGTCCACAAAAAATAACCATAGAGACGTTTAAGGCAAATTCTAAATGAACAAAGTATAAACCAAAAATCAATTGTAACGAGGAAAACAAACAAACGATTCAAAAATATGAGCAATATGAGAGCAAACATACTAATAAT
GGCAAAAACGCAAAAATGAAAACTGCAAATTACGACACAACACCTTCGAAAAGACCTCAGTATAATACACATAATGCTGGGTGCTGCAAAGAAATGCCTCGGCTGTATCGCCCCTTTTTT
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Myc_poe2 | JBEQPP010010798.1:360-651 (+) | 292 nt | lncRNA:noe consensus e-value: 9.6e-10

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

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GGCGGTCGTACGTCTCACAGCTTAAAGGGTTGGCCACATCCCCGACTAATTGTGGCACAAAACGAATGACGGACCATGCTATATAAAAATCATCCTTCTTTATAATGGTATCCAGATTTTACAAATGAGCAAACAACGATCCCCATTGCT
GAAGTGGAGGACGTTTAAAGAATGAAAAAGTTATCCGAGGCCAGGGCCAACATAAAAAACATAAATTGAAACCATCAAAAATTTATAAATACCGCTGTGTAAGATAGTAATTCAGATTTATCTGATTTGATCGCCACTTTTT
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	Myc_poe1	Myc_poe2
Myc_poe1	-	16
Myc_poe2		-

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

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Myc_poe1          ------atcgctgctgcaccctggctatgtgaaaacatttTATAATTCTCAAGTTGCAATTCaaccgaacgcaacttaaatatccaaaaacttcagttgtctatt-------
Myc_poe2          ------cagccgtagacctttttgaatgtttgcgttttgctTATAATTCCCAAGTGCTTATTCcgcgcactattcgtttatataggccttgttaacagttgctatt-------
Arthropod_7SK     ------agccattgctgtgaacattgcaaacattgtgtgcatTATAATTCCCAAGTGGTTATTCagcacttgctacatttaaatacaagcagccacacaccgttagtt-------
RNase_MRP         -------------ctcgcgcactattgcttcgcttttgctTATAATTCTCAAGTTGTTTTTCtgccgtgagcgtgtataaatagcagcgagcgtttcttctactaagccattt
U6                -----actactacctgagatacatttgacactagtctgctTATAATTCCCAAGTTGTAGTTTgacagaacttccatttatatattacacccttctgtctacattc--------
U6                -----acagcagatggcgcccactattatttcaattatgctTATAATTCTCAAGTTGTTATTCcgcccacaattacatttaaataccagtgttcacagtctactttc--------
U6                -----acagtagatggcgcccactattatttcaattgtgctTATAATTCTCAAGTTCTTATTCcagaataaatacatttatataccagtgttaactgtctgcattc--------
U6atac            -------attgtatttgcacacgctgttgtgttttagcctTATAATTCTCAAGTTGTTATTCggcgagtgctgcgtataaaatgccgctgaaatgttgcgttcagtt------
tRNAsec           -----ttagtgcactgataacagatttcttaaaatttgctTATGATTCTCAAGTTGTTTTTCtgccaattctgcttataaaacaagctacttagtgtgttaaatt--------
snoRNAMe18SA1806  -----ccaatttttttcttgcacgttcaatttgctgcctTATAATTCTCAAGTGCTTATTCtggccgtcgacactttatatacgagctaaacgcgacttcgaac--------
U1                --tatttcaaaggaaatgtttcttgttgtaaatttattacTATAATTCCCAAATAGTTATAGtagcctggcagtagagacgcgtacgaatgttttcaaaatc----------
U1                ---gtttgttgcatacaataggcatttagcatttagaaccTATAATTCTCAAATAGTTATGAcagccctcagcatcgagcatgtgattaatgtgttgaatttagc----------
U2                ----actgcgcatgagtcaacaaaatatcttatagacgctTATAATTCTCAACCGGTTCTTGctgcttttaaatgagtattagcttagtttacagtttcaagtt---------
U2                ---gccgaaaagtaggctatagaatttctgttacattgctTAAAATTCTCAACTGGTTAAAGccaggatagaatagagttatgttcataattatggggtagtt----------
U2                ---cgttttacaacactaatgaatttgtactttatgttccTATAATTCTCAACCAGTTTTGGttgcatctcatagagttcattgggatgttgtgagtcaaagtt---------
U3                ----acatgcgtcgtagatttttttttctcgttggttgctTATAATTCTCAACTAGTTCTGGcgtatctggtatgtacagcgtttggttgagtgttggaaattt--------
U4                ------caaccccttttaaacatttagcaatttcaattaatTATAATTCTCAATTTGTTAAAGaagcgatcgcgtatttctctgcatatcgcgaaccatcttttaac-------
U4                ----gcagcattctgtgtactttttgtacttcttgtgctTATAATTCTCAACTGGTATTAGcagccgagacaagtagtgtgtaactacttgcgagtgaacggtt--------
U4                ---gacacctgaaagtatgcacttattttttcaatttcctTATAATTCTCAACTAGTTCTAGcacgttttgaatgagaagttgttgacttaggtgatgatgtt---------
U4atac            gggatatgcagcgatttctttattttttgcatgtttgcgcaTAAAATTCTCAAACGGTTAAAGcttgagcgcatagagaccaatcgaaatgccaacactca----------
U5                -ctttcagctttatatgatcctctactgatatccctcagtcCAAAATTCTCAAACAGTTAAAGcagatttcagtaagtgttgtgacaatcgtgtgcattcg----------
U11               -----taatgatcatatctaagtatttcacattttgcgctTATAATTCTCAACTGGTTTTAGatcgcccccaagaactatgcatctacgttgcaccattagacta--------
U12               -----gcctgtgtgcgaaactttttgccatttaaattctAAGAATTCTCAAACGGTTTTAGcccagcgcgcaactgttactcggtggcatgccacgtgcaaatt--------
OrCD1             ----tccgctcgcagcgcactgttattgacatgttaacacTATAATTCTCAACCAGTTCAAGcgctcacacattgggcactgtagtcaccccacattgatgttg--------
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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.