

Drosophila mojavensis

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

Assembly: GCA_018153725.1_ASM1815372v1_genomic

Dro_moj1 | JAECYD010000073.1:6667036-6667960 (+) | 925 nt | lncRNA: noe consensus e-value: 3e-170

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.82

GGGGCGGCTGCTGTTCCGCACTAAAGACGGTGGACACAGCCCGCTGAATCCGCACTCTGAATATGTCCTCTTTGGTTAAGCGTTGTGAAGAACACAAACAACAACACACAAACGACACAAACAATAATCAAAACGCTGCGCAAACTTTC
 TATCTTCTCTGTATGATCAACACGCAACTGCTAAATGTATTAAGGACACAGAACAAATATTAATATCATATCATGTATCTGAATTAAGTCAAAAAGTTGAACATAGAAATCAGCATAGACACAGAGATGAATTTGATGAGGACGACAAAGATAC
 TATCTGACCAAAAGATATATCAATGACCAAAACAAAAATATAAAACCGATAAAATACATCAAAAAATAGAACATGAAGTAAGCAATTAATGTGACGCTAGTAGATTAAGAGATATCATCTGTTGTTCAGGACGACAAAAAATATCT
 CTGCAAAAATCAAAAAAAAATATTTAAATCTGCAAAAATGCAATGGTGTGTTGTCCTGGCTGCTGATATGCTGATCAGCACTCAATCAGGACACACAGAGATCTCTGGCCGCGATCTCCCCCTCACCCTGACGACAGGATATGTACCTGGGA
 TAACGCTGTGGCCGCTGGGCGGTCCACAAAAATACCTAGACAGATATTAAGGCAATTTCTAAATGACAAAAATTTAAACCAAGAAAAATCAAGGAAAAATGAAAAATGAGAAAAACAAAAATGAAAAACAAAAACAAATTTGTAACG
 AAGAAACACACATATTTCAAAATGAGCAATATGAGCAACATACTAATATGGCAAAAAAGCAAAAAATGAAAAAAATCTCAAAATTCAGCAACAAACACCTTCGAAAAAGACCTCAGTATATACACATAATGCTGGGTGCTGACAGGGAATG
 CATACGCGTATCGCCCTTTTTTTTT

Dro_moj2 | JAECYD010000135.1:21299511-21300193 (+) | 683 nt | lncRNA: noe consensus e-value: NA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 17nt PSE: 0.95

[illegible]

	Dro_moj1	Dro_moj2
Dro_moj1	-	43
Dro_moj2		-

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

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Dro_moj1  -----acttgatttggctgcactttgacgacttcgtTACAATTCCCAATTTGGAAATCTgcgaagtgtttgtataaaggcattgcagccatcatgctgtt
Dro_moj2  -----acagcagcagtcaggccgtgtttacacgaataattTATAATTCCCAACTCATTAATCGccgtcattttgtataataacttcgacgttcaggcagcc
Rise_WRP  -----taagacagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
Arthropod_7SK  -----ttatgcagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
Rise_WRP  -----ttatgcagcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U6        -----tgcgttgcctgcacttactttacgaacatcgtGTAAATCCCAACGGTGGCTCctctacagcagcagcagcagcagcagcagcagcagcagcagc
U6        -----tccttcattacccttcacttcacttcctacgtcAGAAATCCCAAGTCCCAATCGctcacacatcatttataaagacacatttcactacatctt
U6        -----ggcgacgttcgactgtctgccttacttggtgtctGTAAATCCCAACTGCTATTTCgcaagtcacagcagcagcagcagcagcagcagcagcagcagc
U6atac    -----ttctgttttctctcagccacacatattctgtTATAATTCCCAACTGCTATTTCgcaagtcacagcagcagcagcagcagcagcagcagcagcagc
tRNAsec   -----ttatattcccttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
tRNAsec   -----tcaagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
tRNAsec   -----ttcagatatacgaaggaatttaattgcacacaaacGTAAATCCCAACGAGTTCGAAATcttaacatgaacacccagcagcagcagcagcagcagc
U1        -----gcatactttgaggaacttatatttcagaataattctTCCAATTCTCATGCACTTCAGcagccaaacacgttcgcaagatagaagatagaagaagac
U1        -----aadtattccctcatttcacattttatcaatcgaattTGTAAATCTCAACAGGGTTCAGcagccacagcagcagcagcagcagcagcagcagcagcagc
U1        -----tccttagtcagggccgacgttcttcacgaagtcgtTATAATTCTCAACAGGTTTAACTgtccgcaggaatgccctgaagtcgaagtgaaatagac
U1        -----gcctttctgacttcctcagtagaattttcacaagTCCAATTCTCAACAGGTTTCGAGcttcgcgtatggatgtgttccttcagagcaggaagaagac
U1        -----ttttctctctcagcaaaatttcacttcgccacaaacATAATTCCCAACGGTTCGAGcttcgcgtatggatgtgttccttcagagcaggaagaagac
U1        -----ttacatccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U2        -----tttaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U2        -----cttaagtcagcaaaaacttcctcaagataaattctTACAATTCTCAACGGTTCGAGcttcgcgtatggatgtgttccttcagagcaggaagaagac
U2        -----ataaagtccacatagggaattcaggtaaatgattTATAATTCTCAACGATTTAACTgtcagcagcagcagcagcagcagcagcagcagcagcagc
U2        -----tgccactgtataaataaagaatttcaccgtgcacACGAATTCAACAAGGTTCTAGctctgggcagcagcagcagcagcagcagcagcagcagcagc
U2        -----gtacacatagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
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U3        -----tccacttggaagcttttttttctctgtgtgcacATGAATTCTCAACGGGTTCTGgaagcagcagcagcagcagcagcagcagcagcagcagcagc
U3        -----accacacttccttccttttctctgtgtgcacATGAATTCTCAACGGGTTCTGgaagcagcagcagcagcagcagcagcagcagcagcagcagc
U4        -----tgtcacaatttcagatatttgatcatgtctgtTATAATTCCCAAGTGTAGGTTtcgtttggaagattctcgtgctgtgcgaagtgaaattt
U4        -----gttttgtctgtcagatattatttcgtgcagtgattTAGAATTCTCAACGGTTCATGctgggcagcagcagcagcagcagcagcagcagcagcagc
U4        -----caccctaaadaccccttaatttttcaattttctacAAAAATCTCAABTGTCTAAAGTccatcacacatataatcttaaaaattgcattctccacac
U4        -----tgcacacatttcgagatgaatttcctgttttgcacATGAATTCTCAACGGTTCATGctgggcagcagcagcagcagcagcagcagcagcagcagc
U5        -----ttgttcgttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt
U5        -----atctcacaataaattctctacttcacacttcgcgcgcctGTAAATCCCAACGGTTCGAGcagcagcagcagcagcagcagcagcagcagcagc
U5        -----tgcatacttttaggggtctcaggtaaatgagttgtTATAATTCTCAATTTGGAAATCTcaagtaagtagagcagcagcagcagcagcagcagcagc
U5        -----tcctcactcaggggtacttcctcaggtttgttaaaTGAATTCGCAATGGTTTAAGTgaacatttaagcagcagcagcagcagcagcagcagcagc
U5        -----tgcacacttttgggtttctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U5        -----tagcatactttaggggtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U5        -----tgcacacttttgggtttctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U11       -----tgcacacttttgggtttctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
U11       -----catcctctcttgggaatttcacactttctactaccctTATAATTCCCAACGGTTCGAGcagcagcagcagcagcagcagcagcagcagcagc
OrC01     -----ctgtcgtgtttatacaatttttctcagaagataATAATTCCCAACGGTTCGAGcagcagcagcagcagcagcagcagcagcagcagcagcagcagc

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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.