

Drosophila aldrichi

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

Assembly: GCA_035045965.1_ASM3504596v1_genomic

Dro_ald1 | JAWNOM010000501.1:8382466-8383396 (-) | 931 nt | lncRNA: noe consensus e-value: 8e-168

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.89

GGGGCGGTCSTGGATCCGCAGTAAAGACCGTTGGACACCGCCGTTGAATCCGCACCTCTGAAATGTGTCCGTTTGGTTAAAGCCTTGTAGAACAAACAAACAGCAACTACAAACGCACAAACAAAAATCAAACGCTGCGCAAACTTTC
GTCAATCTCTGATGCTAAACGCAACATGCTAAAGGTATAAGGCACAGAACAACTATTAAATACTATACATGTATATCTGAATAAAATGCAAAAAGTTGAAACTAGAAATCACGATACBCAAAGATAAATGATGAAGAAACAAAAAGATA
CTATCTGACAAAAAGTATATCAATGCAAAAAAATAATATAAACACCATAAAAATACACAAAAAATGAAACATGAAAGTAAACCACTTAAATGTGACCTAGTAAATTAAGATATCATCATCTGTATCAAGGACACACAAAA
TCTCTCABAAAAATCAAAAAAATATATAAAATGCAAAAAATGCAATTTGGTGTGTGTGTCCGTTTCTGTATATGCTGACACGTCATTCGCGCACACAGAGTCTGGAGCGCAGTCTCCCTTCACCTCAAGCGAGATATGCTATG
GATAACGCTTGGCCGAGCTGGCGCATCCACAAAAATACCATAGACGCTTTAAGGCAAAATCTAAATGAAACAAAAATATAAACCAAGAAAAACAAAGGCAATGAACTGAAGAAAAACAAAAATGAAAAACAAAAACAAATTTGTAA
CGAAAGAAACAAACATATTTCAAAATGAGCAATATGAGCAACATACTAATAATGGCAAAAAGCAAAAAATGAAAAAATAAACTGCAAAATTACGACACCAACCTTCGAAAAAGACCTCAGTATATACACATAATGCTGGGTCTGCAA
AGGAATGCCATAGCCBTATCGCCCCTTTTTTT

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Dro_ald1      -----acttgcatctggctgcacttttgcgcatttcgtttATAATCCCAAGTTGGAATTCgcaaggatgtagtatataaagcgaattgccagtggcatgctgtt-----
Arthropod_7SK -----tgtattttccctcacttctttaaactttaaaccctTATAATCCCAAGTGGCGTTTCccttcttctctctataaatacgaactcgaatccttcttctt-----
RNase_MRP    -----tataattggccgtgatttttttggctTATAATCCCAACTCATTTTCggcgtgtgcacacattaaatagcggcaagcgaatactgttttagggcgttt-----
U6           -----tcccttaactggccctctaacctgcttgcattgtctTATAATCCCAACTGCCATTTCggctacagctacatttaaatagtagaatttttggctatattc-----
U6           -----ggccaccattcccttttctacttcttctcatctctTGTAAATCCCAACTGGTCAATTcacaadotatacgtataaataacacattttttctactacattc-----
U6           -----agttgtgtgccttaccataaattgcaggaaatggctTGTAAATCCCAACTGGTGTGGcctgcgtgcacagataaataatgagttttgttgaggagagcttc-----
U6atac       -----ttgtgtttacccttcaagtcagcacacattctgtTATAATCCCAACTGCTTATTGccggaatatcgcatataaaaggaggggtctgctgcgcttccattt-----
tRNAsec      -----ttdatattctctctadagaadaaattttaaatttccTAGAATCCCAAGTGGCTTTTGTaacaatttcttctataaatacaatttaattttaaadaaaaaact-----
snoRNAme18SA1806 -----tctctgctagtagagactctcacacagtttgcgtTGTAAATCCCAACTGTTTATTCggcaaacacttggcttataaagagttgaatgctcggaatttcca-----
U1           -----tctgtataactaaaggagtttctctgacacataaacTACAATCCCAACCACTTTGACaatgtttaaactggaaccccgagccgagccaggttaagc-----
U1           -----aaotatttccctacttttataactcttatcaattaaactTGTAAATCCCAACCACTTTTGAcaattttaaacatgaaccccccaccccaactgaatttaagc-----
U1           -----gcatacttttgggagctataatttcatgaaatgctttTATAATCTCATACGGTACTAGcaacaataacatggttatgccaagttagagcgaggttaaagc-----
U1           -----tggcctatctgtaggcgccttttgcatacaagattctTATAATCTCTAAACGGTTTGGTtgcctcacacatggtaacccctagaccctcagctggttttaagc-----
U1           -----gttttcttcttctataaataatttcaacttcccccacTATAATCTCAACCGTTCTGACTctgaactatcttgaatttgcacattcccaaccccaaaaaac-----
U1           -----tctttgctacttctcacttcagtagaattcttacaataTATAATCTCAACCGTTCTGACTctgaactatcttgaatttgcacattcccaaccccaaaaaac-----
U2           -----gtatgccacataaacggtattcaattgaattcattTATAATCTCAACTGGTTTTAACTgtagcccaatggagtagtgaattttgactgattgaagtt-----
U2           -----cttaadtaagtdaaadotattcaadotaaattcattTATAATCTCAACTGGTTTTAACTgtatgcccaatgaadactgaattttgactgtgtaagtt-----
U2           -----cttaggtaggtaaaaggttttcaaggtaaatttaattTATAATCTCAACTGGTTTTAACTgtatgcccaatggagtagtgaattttgactgtgtaagtt-----
U2           -----tgaactctgttttaggatattttccaaactccaccttAATAATCTCAACCACTTTGAGcagtgaaatgggtgtagtggtgtgagtttaggagtttaaagtt-----
U2           -----cttgcacactgaatttcttfaatttttgaacccaAATAATCTCAACCACTTTGAGcagtdaaatgaatttgaatttgaatttgaatttgaatttgaattt-----
U2           -----gtatgccacataaacggtattcaattgaattcattTATAATCTCAACTGGTTTTAACTgtagcccaatggagtagtgaattttgactgattgaagtt-----
U2           -----tgcgcattgttcaaaaatagaagtttgcgcacCGAATCTCAACCGTTTAACTgtgtagcgaatgagtaggaaactgggaatgacgttgaagtt-----
U3           -----caaccattctcccttttctttttctctgtctcactTAGAATCTCAACCACTTCTTAAagacacagaatttgaadcccttgaatttgaatttgaattt-----
U3           -----gcccctgtctacgttttcttttttctgtgtgtgcgtTAGAATCTCAACAGGTTCTTAAagacacagaggttagagcgcttcgtagggcattgaaattt-----
U3           -----accattgtctacgttttcttttttctgtgtgtgcgtTAGAATCTCAACAGGTTCTTAAagacacagaggttagagcgcttcgtagggcattgaaattt-----
U4           -----gtttcattcttgaatataattttgaatttgaattcattTAGAATCTCAACTGGTTATAGcttgccttgaatttgaatttgaatttgaatttgaattt-----
U4           -----tgcacaaatttaattttatttttagcatattgtgtTATAATCCCAACTGGTTTAAggtttcatttgaaggaaacctgcttctgcgcagaaagtt-----
U4           -----tcttaagcgttcaaaaatttttcaattttcccaAATAATCTCAAGTGTAAAGTcaatcagagcatatataattgttagagtttcttgatccaatcac-----
U4atac       -----ccaacaaatttcccatgaattttacacttttttgaactTACAATCTCAAAATGGTTATCAccttgaacatagaadctcttgaacttttcccaacttcc-----
U5           -----atgcaacaaaatttgcgtctattgttgcatttgcgcacacTATAATCCCAACCGGTTGAGcagtggaatcacatggaatttgcgcgctgtgaccttattcc-----
U5           -----cgcatcacttttaggggttggccagataggacaggtgtttGTAAATCTCAACTGGTTAACTcggaatgaaggtaaaatcagcgtgttagcttgtgttttct-----
U5           -----tgccttccctcaatttttcttcaactttadcttcatTAGAATCCCAAGGAGTTCAAGcatcttctgaattacatcgaatttgaatttgaatttgaattt-----
U5           -----tggcatcacttttaggggttgcctcagtaggacagatattttGTAAATCTCAACTGGTTAACTcggaatcaggtggaatttgaatttgaatttgaatttgaattt-----
U5           -----tggcatcacttttaggggttgcctcagtaggacagatattttGTAAATCTCAACTGGTTAACTcggaatcaggtggaatttgaatttgaatttgaatttgaattt-----
U5           -----tgccttaccctcaagggtgtcttttcatgcattgttgaatTAGAATCGCAAAATGGTTTAAAGTgaacatttgggacaaatgtaggacatttgcacagacaaa-----
U7           -----tctoddccttttttttcaacattttctcactTACAATCTCAACTGGTTGTGGctctcgaatttgaatttgaatttgaatttgaatttgaatttgaattt-----
U11          -----tggcaccggaattgtagcaaaagcaaatgcgcAAAAATCTCAACCGGTTTAACTccttgcctgactatgcaactaattttctcagtcgaatttatt-----
U12          -----tttctgtgttgggaatttcaacacatttactacctTATAATCCCAACCGGTTGTGGcggccctgcactcacttcaactatggcggccacatggcaatc-----
OrCD1        -----tgtcgtgttatataaacttttcttctcaggaatctTATAATCCCAACCGGTTCTGACgctactgagtaggagctgcacagctgctgccaatgtttattg-----
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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.