

Drosophila buzzatii

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

Assembly: GCA_035045845.1_ASM3504584v1_genomic

Dro_buz1 | JAWNOS010000505.1:6919972-6920889 (+) | 918 nt | lncRNA: noe consensus e-value: 4e-172

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.95

GGGGCGGTCTGGATTCCGCAGTAAGACGGTTGGACACACGCCGTGAATCCGCACCTCGAAATGTGTCCGTTTGGTTAGCTTTGTAGAGCAACATCCAACACAAGCGAGCAAAAGAAAGGCCAAACGCTGCGCAAACTTTCTCAT
TCTCTGATGCTAAACGCAACATGCTAAATATATGAAGCACAGAACAACTATATATATATACATATACAATGTATATCTGAATAAATTCAGAAAGTCBAAACTAGAAATCAGGATACGCAAAAGATAATTGAAGAAACAAAAAGATATCT
GACCAAAAGTATATCAATGCAAAACAAAAACATATAAACCCATATAAATACACATAAAAAAACAATGAAAGTAAACTAACTTAAATGTGACCTAGTATAGATTAAAGATATCATCATCTGTTATCAGGACAAACAAAAATCTCTCA
GAAATCTAAAAAATATATAAATCGCAAAAATGCAATGGGTGTGTGTCCCTCTGTGTATATCTGTACACGCACAAATGGCCAGACTAGAGTTCTAGGCGCAGTCTCCCTTCACCTCAAGCAGAGATATGCTATGGACTACACT
TGGCCGAGCTGGCGCTCCACAAAAATAACCATAGAGAGCTTTAAGGCAAAATCTAAATGAACAAAAAGTATAACCAAAAAACCAAGGAAATGAAACCTGAAGAAAAACAAAAAGAAAAACAAAAACAAATTTGTAATGAAGAA
CAACGATATTCAAAAATGAGCAATATGAGCAACATATAATATGGCAAAAGCAAAAATGAAAAATCTCAAAATACGACACAAACCTTCBAAAAAGACCTCAGTATAATACACATATATGCTGGGTGCTGCAAGGAATGCTCTTAGC
TGATCGCCCCTTTTTTT

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Dro_buz1      -----acttgcatcttggtgcacctttggcgcatttcgtttACAATCCCCAGTTGGAATTCgcgaggatgtcgtataaatagcaatttgcagacgtatgctgtt-----
Arthropod_7SK -----tgtaaaatccctcaatccctcaaatataaaacotTATAATCCCCACTAGATATTCcctctodtccacotataaaatcdaatttcttancaotutttaaot-----
RNase_MRP    -----tcgagtttgtctgcacattttttatgctTAGAATTCCTCAACTTGTATTTGgagctccacgtcttataataggagcgaacgtaaccatttcagggcgttt-----
U6           -----aatttcgctgcaccacttaagagtcagcagcttgctTGTAAATCCCCACTAAGGATTCTcactagtttgtataaataacattttatggtatgaatctc-----
U6           -----gatodacactctttccacatgatctccatcacotctTGTAAATCCCCACTACTTATTTaactctcacacacatttatataaagaatttttaactacattc-----
U6           -----ttcaaacctccttgccgtctaaaggcaatgcacgtctTACAATCCCCACTGTTTGTTTgtaggagtgatcatttatatagcagaatttttgagctacattc-----
U6atac       -----cattttatattggccagtttcattttcttggtgtTGTAAATCCCCACTGCTAATTCTcgtgagatctgcgtataaaacagaggttcagccgcaggtcaattt-----
tRNAsec      -----taattattottdccatagaattdaatatgatctTAGAATCCCCAGCATTTTGTaodcaattotttatataaatacaactattttadacatdacc-----
snoRNAme18SA1806 -----agctcaattggagcgtctcgtccgcgtcttgagctTATAATTCCTCAACTGCTTATTTGgagctccacgtcttataataggagtgaaaaataaaccttga-----
U1           -----gcatactttgagcgatgtattcgaaaaaaatctctTATGATTTCAAGCGGTTCTGcaacaacaacatgaaacctcagaacagagccgagtttaagc-----
U1           -----ttctcctactatadaaaatttcactctcccccacataATAATTTCAACCGGTTCAAGccctctcttattcdaatgottttccaaacccaaacaaac-----
U1           -----gcttttgctactttcactagcgtagaagaattttacaaTAAAAATCTCAACCAAGTTCTCAcgttatcgtgttgagtggtcgttccagagcaggagaaagc-----
U1           -----aaagtatatttaagggtataaggagttgaaacgcaatTGTAAATCTCAACCAAGTTTTCcgaatgccaaacttgaacccctgccaaagcctgagtttaagc-----
U1           -----adatttdcctacttttcadattatctcaatttctctTGTAAATTTCAAAATGGTTCTAGcaacctadcaatgaaatctcttctcdaadcccaatttaagc-----
U1           -----agctcaatggagcgtctcgtctcgtctagagctTATAATTCCTAACTGGTTTGTgagctccacgtctcgaaggtgaagccaaaggtcgaagcccaatgaagc-----
U2           -----gcgcatgtgaaaaatagaagaatttttacggtcacACGAATTCACAACCGGTTCTAGctgtttgccagtgagcagtagagaatgagagtgaaagtt-----
U2           -----ttttccaaacacadaattttattttaattadaattctTATAATTTCAACCAAGTTCTCAgcaatgcaatoottataatttgaatttadaatttadaatt-----
U2           -----tgaagctatgcaggatcatccacacacactcaatttatATAATTTCAACCAAGTTCTAGaagtgacatggtgtatgttgaattttaggactgtaaaatt-----
U2           -----cataggtagagaaaaggttttcaagtaagttcacTATAATTTCAACCAAGTTTATGttgctacacaaatggaatcgaatatttgccatggaataatt-----
U2           -----tdaactatctcaadattctccacacacactcaatttatATAATTTCAACCAAGTTCTAGaatttcacttoottatatttgaatttgaatttadaattt-----
U2           -----cccaaaaatagctacacattctgacctagattttTACAATTCCTCAACTGGTTTGTgagcttgagcaacatagagtgctgtatatattgacctctcaggt-----
U2           -----tgactctataaagatcatccatgcaattcaatttCACAAATTCACAACCAAGTTCTAGaagtgacatggtgtatgttgaattttaggattctaaagct-----
U3           -----accacatttctctttttttttttttttdttacacactTAGAATTTCAACTGGTTTGTcctccctatgactadagactttttattttdccattgtaaaact-----
U3           -----accaccagttctgttcaattttctcgtgagtgccgtctTAGAATTTCAACAGGTTTTTATctgctagcgactagagctttttatgggcattgtaaact-----
U4           -----gaaatgaactcgtgagtgatttatgttttaggtcactTAGAATTTCAACTGGTTTAAAGctgggtgcacatggagtaaatgttgccttgaggtgtttaggt-----
U4           -----gctaadaattatctcatttatataatcttaatttGTGATTCGCAACTGGTTTTGgaattttotttatodaaacccctcctcttccacactdaattt-----
U4           -----acccttgaagcgtcaaggtttcaattttcaacTACAATTTCAAGTTGTAAATGcacttagagcatatataatggtgatttctctgactgaatgcag-----
U4atac       caacaattccgcagtgaaatttgctgtcttttcacgcctTACAATTTCAAAATGGTTATCActggcagagcttaaggctctcggcatttggcaacaatcg-----
U5           tgcatactttadoodttctcdaotadaacodattctTGTAAATTCACAATTAGTTAACTcaaaoddaadadaactcaacttcttctctctctcc-----
U5           tgttcacagaattttgtactctcagcattaacgcgtctTATAATTTCAATAGGTTATAGccgagagcacactcctgtcctgtagttgtcagctggtttcg-----
U5           tttctcgttttagggctctttcgtgaattgcatttgacgtTATAATTTCAACAGTAGTTCAAGcatctgttagagtcactcggggttgattctcgtgtttat-----
U5           ttcctacactcaadoodttttttgaattcatttcttgaTAAAAATTCACAATAGTCTAAGtgaacadtaaaodtaaatatoodtaotttattctcttaaaa-----
U5           tggctacactcaaggtgtttttgaatgctgttgacaTAAAAATTCACAATAGTCTAAGtgaacagttaagtgaataatggggtagttgtagcttgaaa-----
U7           tctgtgtcgtgttttttgacacattttatcctTCAACTGGTTGTAGctgcgctcgaatttgtatataaagagttttgtcttgagagttattga-----
U11          tctatatatgctgtataaattgtctcagcaaatgcagAAAAATTTCAACCGGTTATAGcactgtgtgtgtatatatccagccctttctgttcgaatgtatg-----
U12          tctctcaadttaadaatttcaacactttttaacctttTACAATTTCAACCAAGGTTGTGgcttccctccatgaactcacctctccctccacactdaaatc-----
OrCD1        gtgttctgttatttaacattttttattttgtgcgtctTATAATTTCAACCAAGTTCTGTcgtcgttaagttaacagttgaaactgtagtgctcttgttctgag-----
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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.