

Drosophila littoralis

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group

Assembly: GCA_047116335.1_ASM4711633v1_genomic

Dro_lit1 | CM120399.1:7322141-7323252 (+) | 1112 nt | lncRNA: noe consensus e-value: 4e-189

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.90

GGGGCGGTGCTGCAATCCGCACTTAACGACGGTGGACACAGCCGTTTAAAGCCACACTCTGAAATTTGTTCCCGTTGGGTCGAGAGCAAAATTCGATTGAGGAGGAGAAAAAGACGCTCGCAAACTTTCTGTCATATCTCTGA
AGCAAAAGCAAAATACGCAAAATACGCAAAATACGCAAAATGCAAAATTAATGATGCACAGAGCAAAATCATATATATGGAATAACAAATATATATAAATGCAACAAAGCTTAACACAGAAATCACGAATCGCAA
TGATAAATCAAGCAAAATACTATCAGACCAAAATATATCAATGCAAAACAAAAAATCTATAAACAACATAAAAAATACATAAAAAAATATGAAAGCAAACTAACTTAAATGTACCTAGTATGTTTAAAGATATATCATCATC
GTGTTATCAGGACAAATGAAACTCTGAAAAAATCTAAAAAATATTAAGAACGCAAAATGCACTTGGTGTGTGTGTCGGCTTCGTGTAATCGCTGACGCGCCGAAAGCCAGCCAAATCCGGAATCTAGCACAGCTTTGGCTGGG
AAAAAGAGGGCCCCCGGGGGGGCTAGCTGTGTTGGCCAAAGCAATGCTGCTTATCAAAAAAACAACAAAAAATACAAAAAATACGCAATCTGATAGAGACCGGGGGGTGAGAGCTACCCCGAAGTCCCAACACCAAA
ACCAAGAGGCAAGCAGCAATTCGATGATCCCAATCAGCCCGGAGAAAGCCGTGTGGATACGACTGACGACTGGCCTCCCAAAAAAATAACCATAGABACGTTTAAAGCAAAATCTAAATGAACAAAAATATAAACCAAAATGA
AAAAAATACCAAGACAAATACGAATCAATTTGAACGTGAACCAACGATATTCAAAAATATAAGCAATATGAGCAACATACTAATAATGGCAAAAAGCAAAAATGAAAAATGCAAAATTCGACACACACCTTCGAAAAAGACCTCAG
TATAATCAACATATGCTGGGTGCTGCAAGGAATGCCCTAGCTGTATCGCCCCTTTTTTT

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Dro_lit1      -----GaaadcttcaccacactocacttttccadctccttTATAATCTCAAGTTGGAATTCccttgaattottdctttaaatacacaatccaccccatccttt-----
Arthropod_7SK -----ctgtttgtcggcgcccttgcctctatttgcgtctTATAATCCCAAGTGTCTATTtttgagtgctgagatataaatacaagcaatggttgggagagtttt-----
RNase_MRP     -----ttcgatatgtgtgtatttttcagcttTGAATCCCAACTCATTTTCggctacacacacataaatgcccgaacgatagcttcagcccgctt-----
U6            -----gacgctcactacctgaacatacaccatttgcgtTGAATCCCAACTGTAGTGTccttcaccccaataaacttataataaagctacacct-----
U6            -----bacagatgtccttttgtcaatttgcctccttgcctTATAATCCCAACTGCGTATTtggcatcagctgcatattatagttgatttttttggtctacattc-----
U6            -----gtcgaactactgagctgacagcgcctgcgtTGAATCCCAAGTGTCTTtggcctcagctgatttatagttgatttttttggtctacattc-----
U6atac        -----cttggtcgaatgaatgctagcaccctttgcgtTGAATCCCAAGTGTCTGctgtgcctcagcttatataacgggggttgaccgcgctttggtt-----
tRNAsec       -----hdaadcccttaacataaadaadaatttttcctTGAATCCCAAGTGTCTTTTaaccaacttcttacaatacacaattttataatctatctct-----
snoRNAme18SA1806 -----tctttaaagtttaagatttggccttccgcattctggtTGAATCCCAACTGCTTAATCgcccgccttgcgtgataaataagctagacgaataagaatt-----
U1            -----tgcatactcgaagggcgtttttcatgtgtatgagctTGAATCCCAATGGTTTACgagttgtcccatggtatgccaaactcagacagagaaagc-----
U1            -----ttccatatttaagccctactcttttacaacatcacTGAATCCCAATGGTTTATAGcaatgdaatatodaaccccttaacccaaacadaaaaaac-----
U1            -----gcttaacgtttaggtgcagctttacgcagcattttctTATGATCCCAAGCGGTTCTAGcagctgcccgtatggtaacccaaggcctgagctggtttaagc-----
U1            -----ttttgtcgtctgtaggaattttcacatgtcgcgctctTATAATCTCAAACGGTCTGActcggcagccatgggtgtccctgtccagagcgaagaaaaagc-----
U1            -----aaadoodttccctacttttadctdaadtcacacccaTATAATCCCAACAGTCCAGcccaacccaatodaacccaaccccttadaatodaadaaac-----
U1            -----gaattttgcttctcgcctggaattgaatttttcacctTATAATCTCAAAACAGTCTGAcgcccctggaatggagtgccgtttccagagcagagaaaaagc-----
U2            -----aagttagccaccactagctttcacacacgtgtcgtTATAATCCCAACTGGTTTCAgctgtggctacatagagtgctgggattttatccattggaagct-----
U2            -----tctcacaattcaatttcacacacatctccctccctTATAATCCCAACTGGTTTCAgctgttgcctacataaatactodaattttatctatttcaagtt-----
U2            -----aatgtcacgattcagtttcaaacacgtgtcgtTATAATCCCAACTGGTTTAGttgtggctatagagtgctgggattttatctattggaagtt-----
U2            -----aacgtgcgactgagctgtcttcacgtcgtgtcgcactTGAATCCCAAAATGGTTTGGctagctggcaatgagtaggggctggcataacggtaactagtt-----
U2            -----aatotacacdaatttaotttcacacacatccctcctTATAATCCCAACTGGTTTAAActotocctacataadaatctodaattttatccattodaatt-----
U2            -----tttcacaacactgtacgtattttcatttgaaatctTATAATCTCAAAAGGTTCTATcctggcggtgtgtagtactgcgagcatagcatttggagtt-----
U2            -----ggcacacaataatttgcacttgcataaacacgataaTATAATCTCAAAAGGTTCTATcctggcggtgtgtagtactgcgagcatagcatttggagtt-----
U2            -----caatatgaattttatattatatacacacacatctcctTGAATCCCAACTGGTTTATAGctacacacaaatodaaccccttaaaadaaacactttodaattt-----
U3            -----ccctgtacgaattgtttgttttttcattcgtcttctGCAATCCCAATCGGTTCTTgctcgaatggcgtatagagcattttggtgggcatagaaaaatt-----
U3            -----ccctcgaacgatttgattatttttttcttgcctttctTATAATCTCAATCGGTTCTTgctcgaatggcgtatagagcattttggtgggcatgaaaaatt-----
U4            -----cgcttctcactttotattattatottatattcactTGAATCTCAACTGGTTTGAActotocctacataadaatctccttcttctctotodaadott-----
U4            -----gccaagcaacccltaagctttttgatttttcaacATAATCCCAACAGTTCAGctacacgcccgtgcattctgtaagcattttcctgtatcaagcac-----
U4            -----gcttttaatttggaacttcttcgcacacccgttgcTGAATCCCAACAGTTCAGctacacgcccgtgcattctgtaagcattttcctgtgtttgagct-----
U4atac        -----aggcaatcttttcccccattccctactttttacccTGAATCTCAAAATGGTTTGGctaccccacattgaatttcccccacttccaacactc-----
U5            -----gctttaaacgcgctgttttgcgttaactgttcaggcgctTGAATCCCAAAATGGTTTGGcgccgagtgcatgggtgtgctgctttgagtggttcga-----
U5            -----gttgccctaccctcaggagcttttgaagcaatgccctcTATAATCTCAAAACAGTCTAAGcatacattgaaaactagaagcagggtgatttattgttga-----
U5            -----tccctactttadoodttcttcaadtdcaacotcaatcTATAATCCCAACTAGTTCAGGaatcttccaotadoodtcaadotttttadattadatt-----
U5            -----ccctactttaagggtgtttcgaattgtttccttgaagcTGAATCCCAACAGTTCAGGaatcttccaotadoodtcaadotttttadattadatt-----
U5            -----tttaagggtgtgttcgagtgcaactgcataataataATAATCCCAACTAGTTCAGGaatcttccaotadoodtcaadotttttadattadatt-----
U5            -----attttagggttttccaatccactcctataataataATAATCCCAACTAGTTCAGGaatcttccaotadoodtcaadotttttadattadatt-----
U7            -----ttgtgcgctacttgcgcacatttttccctctGCAATCTCAAAATGGTTTGAccgctgttgcagtgagtgctgcgctgtttgaagagataaactgaattga-----
U11           -----tcaaaattctcgggacaataatttcattagtagccccaATAATCCCAACCGGTTTAGcactgagcagatgaattgcgtctcatgtccagatgtgatt-----
U12           -----cctcctcttcttodaatttttaacottttcaacctTAAATTCACAAACGGTTCGAcaccccccacaaactccccccttcccacactacacaactc-----
OrCD1        -----ttgtcttgattataacattttaccacttgttatgctATAATCCCAACAGTTCGGcgtgccaaagtgttaactgtcacagcctcactttaacaattg-----
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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.