

Drosophila stalkeri

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

Assembly: GCA_035047405.1_ASM3504740v1_genomic

Dro_sta1 | JAWNPR010000041.1:14011488-14012406 (-) | 919 nt | lncRNA: noe consensus e-value: 3e-172

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 7nt PSE: 0.85

GGGGCGGTCGTTGGATTCCGCAGTAAACGCGTTGGACACAGCCCGTTGAATCCGCACTCTGAAATTTGGTCCGTTTGGCTTAGCGCTTGTAGAGTAACATCAACTACAAACGAACAAAGAGAAAGCCAAACGCTGCACAACTTTTGGTCATTCTCTGATGCTAAACGCAACATGCTAAATATATGAAGCACAGAACAACTATATATATATACATATATATCTGAATTAATTCGAAATTAATTCGAAAGTCGAAACATAGAAATCAGGATACGCAAGATAAATTAAGAGAGACAAAGATATCTGA

Dro_sta1 -----acttgcatctggctgcacttttgcgactttcgtttTACAATCCCAAGTTGGAATTCgcgaggatgtcatataaatagcaatttgcagacgtatgctgtt-----
Arthropod_7SK -----tgtaaaatcaacatctctcaadtaaaaaacottTATAATCCCAAGTACATATTCgctctgctctcatataaaatcgaatttctcancottttaaot-----
RNase_MRP -----tcgagtttagtttgagcattttttatgctTAGAATTCCTCAACTCATTTTTGgcatgacgcacacitaaatagcggaagtgaataatcagttcagggcgttt-----
U6 -----aatttcgctgacttacttaagtgtcagcaatttgcTTGTAATCCCAACTAGAGATTcaccagctcatttgtataaatatatacattttatggcatgaacttc-----
U6 -----cgcctcttttcacttttattttaaactatgcctTATAATCCCAACTACCTATTTaccctatadcaacatataatadcaaaatttttaactactttc-----
U6 -----ttcaaacctgcctgcgcttacaggcaatgcacgctTGAATTCCTCAACTGTTTGGTTggttagactctacatttatatagcataattttgagctacgttc-----
U6atac -----ttactttatattcccggtttcatttttttgggtTGTAAATCCCAACTGCTTATTGccttacttctgtatataaaacgaggttttagccgcgctccattc-----
tRNAsec -----tdataatttcttgcataaacttcaatatttgaattTGAATTCCTCAACTGCTTTTgagcaatttattatataaatacaactttcttaaacacaaacc-----
snoRNAme18SA1806 -----cgctcaattggacatttgcctgctgctggttgcgctTGTAAATTCCTCAACTGCTTATTgacacacagctgtttataaacgagctgaaggaacaaatttg-----
U1 -----acttttcagattatgtcaattgtgtacatagggcttctGTAAATCCCAACTGGTTCTAGcagcttagcaatggaaattccctgccaaagctcgaattgagc-----
U1 -----atacttttaadoodatatttttcacaaaaattttctTATGATTCCTCAAGCGGTTCTGctadaaacaacatodaaccccaadaaadaacccgaatttaacc-----
U1 -----gcccttgcaacttttcacttgcatagaaaatttttcacaaTAAATTCCTCAATCAGTTCTCagttatcgatttggagtgactgtttcagagcaggagaagc-----
U1 -----ttctgcttgctatggaaaattttacttgcgtgcacacAATAATTCCTCAACCGGTTCTGGctctgcgctattggattgggtgttccagagcgaagcaaac-----
U2 -----adccatttcaadccactacatotttadaotctTATAATTCCTCAACTGGTTTtagttacactcccaatotaadcatadccatttttccatccattcaaac-----
U2 -----ttttacacactgaatttttatttaatttagagttcTATAATTCCTCAACCGTTCCAGcagctacagtgagttatgttgagttgagttgagcagcaaaattt-----
U2 -----pagtttctcagagatcattcatgcaacttcaatttatTATAATCCCAACCACTCCAGcagcagctggtatagttatgtgaatttagcagcgtaaatt-----
U2 -----tataatataacataacataacatacattattTAGAATTCCTCAACTGCTTTTACcttttaadacataadactaotatttaootttctaattott-----
U2 -----gcgcatgtgtaaaaatagaagtttttacgattcatACGAATTCACAAATGGTTTtagctgttaccagtgagcactaaatagaatgagagtggaagatt-----
U3 -----cataggtagacaaaaggttatcaaataaattcactTATAATTCCTCAACTGGTTTtagttgcaactcaatggaaactgaatgtttacctggggaagatt-----
U3 -----ttcttaacaaccactotattttctttaaotcgcctTAGAATTCCTCAACAGGTTTCTGcgcctadcaadtaadacttttttccatccatttcaaaatt-----
U3 -----catagcaaccacatgacgtttttttatcagcactTAGAATTCCTCAACAGGTTTCTGcgcgttagcaagtagagcgtttgttgggcatttgaaatt-----
U4 -----aaatgaatccttgagatattatttcttaoottcactTATAATTCCTCAACTGGTTTtagcttgggtgcacatggaaacttaacgttttttgggttttaggtt-----
U4 -----tgctacaacttttccaatttatcatcttttcttTACGATTCGCAACTGGTTTtaggaatttttttcatodaaactctcctcctcttctttaaataaatt-----
U4 -----cctcaaaatgcgctcaaaagttttcaattttcaactTATAATTCCTCAAGTTGTTAAGacaaatagaacatatataattgttgatttttctaatacaatcac-----
U4atac -----caacaatttgcattgaatttgcgtctttttctgcgctTACAATTCCTCAATGGTTATCctggcaaacgttaaggctctgtggcatttggcaacaatcg-----
U5 -----ggcactactttadoodttctcagotdaacccoodttctTGTAAATTCCTCAATAGTTAAGTcaaaaadnaadtaadttadccctttttcttatottttat-----
U5 -----tgccctaccccaaggggtctttgcatacattttgacataAAATTCCTCAATAGTTTAAgtagcagtaaaagcgaatgaagggtagttgtgctgttaaa-----
U5 -----tgctcaaaaattgcattactctcagaatgaacgcagctTATAATTCCTCAACCGGTTATGactgaagacacactcgtgctctgtgggttgtgtgggtttct-----
U5 -----agggtccttaadoodttttcttadaottttatttgaotctTATAATTCCTCAATAGTTCAAGcatctcttadaatcacatcdooodtttaattatccttttct-----
U7 -----ttctgtgcgctgttttttgacatttggccctTACAATTCCTCAACTGGTTTtagctgtgctcagctgagttatgcgaattttgcttccaattatttga-----
U11 -----ctatatactgtcataaatttgttttagcaaatgcgacAAAAATTCCTCAACCGGTTTtagcactgtgtatagctatatataaccccggttctcactcaaaattat-----
U12 -----tcttcaadttadnaatttcadacttttccaacccTACAATTCCTCAACCGGTTTGGccttccatcccttactccttcccttcccttccacttccaattc-----
OrCD1 -----ctgtgctgtttataacataatttctatttggcgtctTATAATTCACAAACCGTTCTATcactgctaagtaacagtggaactgtagttgccagctcggag-----

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.