

Drosophila sordidapex

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > modified tarsi group > spoon tarsi subgroup

Assembly: GCA_035043295.1_ASM3504329v1_genomic

Dro_sor1 | JAWNNA010000753.1:1093650-1094617 (+) | 968 nt | lncRNA: noe consensus e-value: 2e-154

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.85

GGGGCGGTCTGTATTCGGCAGTAAAGACGGTGGACACATCCCGTTCCTACTACCAGCAAACTCAGAAATGTGTCCACTTTGGGTTACAACGCAGAAATTCAGATTGAAAAATAAAACAATATCACCTTTCGTATTCTCTGAAGC
AAAACTCCAAAGCAAATCAAGCAAGAAATTATGCAAAATATAAAACACAACTATATAAAAAAGAAATACAACAAAGATCTAAACAAAGAAATCACGAATCGCAAGATAAATATCAGACCAATAAATATATCCAATGCAAAACAAAAACT
AAAAAACAAAACTAAAAACACTAAAAAAAATGCAACTTAAATGTGAACCTAGGTTATAAAATCATCTGTGTTTATCAGGACGACAAAAAAATCTCTGAAAAATCTAAAAAAAACATTAAAACTACAAAACTGCATTGGTGTG
TGTGTCCGTTCTGAAAACTGCTGACBCGCCAAGCTCAGCCCTATCTAATCAGGTTGGCTTGGCTTACTAATAGAAAGGGGGTTCCCAATCATGGGACCGGCTTAAACCTCCCTCAGACAAAAGGCTCCAGGAAGCAAACTACTAGAAAGGAG
CAAAACAACAACATCTGCTCTCAGACAGGAGGAGACACCTCTCTCTGACCACTTTCACAGCAGTTGTGATTGGAGTCAACTGGTCAAGTTGACCCCAAGCTTTCGCGAAAAGGCTGGCTGGGCGCTCCACAAAAACTA
ACCATAGAGAGCTTTAAGGCAAAATCTAAATGAACAAAAGTATAAACCAAAACAAACAAAAACCAAGATATTCAAGAAAAGTCAAGCAACATTACTAATACTGGCAAAAAGAAAAATGCAAAATACBACACACACCTTCGAAAAA
TGACCTCAGTAAAAACAAACATATTTGCTGGGTGCTGCTGGAATGCTAGTTGTATCGCCCTTTTTT

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Dro_sor1      -----aaagctgctcctgcaaggattgcacttccatcgcatTGGAAATCCCAAAATGCAAAATCggcaagttgcaacataaataagccatagcatactcgttgggt-----  
Arthropod_7SK  ---tttcctaactotaactctatotttttcattccctTAAAAATCCCAAGTGCCTATTTCootoootototcatataaatadcaacacctgcacagtatgtt-----  
Arthropod_7SK  acccccatcttgtaactgtagctcatgtgtgttgctgcctgcattCAAAATCCCAAGTGCCTATACggcggaatgtgtcgtataaatagcagcaacctgcgca-----  
RNase_MRP      -----ggctgctgcttagttatagtaattgtTAAAAATCCCAACACGTTATTCggcgggcagcggtataaatagcggcgagcgaactgcgcatgttatgctgctt-----  
U6             -----taacaaaacttaaattttccacacacattgcctTGTAAATCCCAAGTGCCTGTTctctgcctaccatttaataacaaatttccacacatttctt-----  
U6             -----acagatgtcgtcttctctgtttgttgcgtgtgctTGTAAATCTCAACAAATTTATTTgactgatgcttatattatatacttaatttttggactacattc-----  
U6             -----acagatgtcgtcttctctgtttgttgcgtgtgctTGTAAATCTCAACAAATTTATTTggctgttgcctcatttaataacctcatttttggactacattc-----  
U6atac         -----tggtgggtgtgggacttgatctattttactctTATAATCCCAACGTTCTTTTccctgacattaaaggtataaacgatgactaagcccggaagtgtt-----  
tRNAsec       -----otaaaaatottttttattottttdaaaataacccTAGAATCCCAAGTCTTTTTCaaccattttotcttataaatatccttatottoaaadctcgtt-----  
snoRNAME18SA1806  agcttcgtgaatcaatctctattttgaacaacgtgctTAGAATCCCAAGTGCCTATTggcaccacgcttgataaatcagagatgaacggtcacgca-----  
U1             ---ttgctgtctataaaaacttttggtatgtcttgccatTACAATTCCAAATGGTTCTAGcagcgtggatagagtgccagttctcgagctgagcaagc-----  
U1             ---ancatacttttgcacacttttacattattacaaactTGTGATTCCAAGTGGTTCTGAcaccccccataatcccaaccccccagcaaaagc-----  
U1             ---tagctgtcgtgaatagttgttccttgcgtgtctactTGTGATTCCAAGTGGTTCTAGcaagccaggaatagtagtccattccagagcagcggaagc-----  
U1             ---tgccacttttcaagcgtacttgatgatactttctactTGTGATTCCAAGTGGTTATAAcaagtttggcgaatggttagtccagtcgcccgcgcgagaaaagc-----  
U1             ---atataaaattttcaatacccaaataaadatttcaacTACAATTCCAACGCTGTAGcaccacaatccactotaaaccaaaaadtaadctdaactfaac-----  
U2             ---gtaggcaaaaataaaaatatatacaacccccacgtgtGTAAATCCCAAGTGGTTCTAAcgttagctgggttagttagagttttcgcttgcaagtt-----  
U2             ---actatgcaatttttggcattgtacttataatagttctTATAATTCCAAATGGTTCTAAcgttagctgggttagttagagttttcgcttgcaagtt-----  
U2             ---ttaadtaaccaatttccaccccttaccacccatccctTAGAATTCGCAACTGATTTAGcttcttccctcatadattcaatottttaaacccttatttaagtt-----  
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U2             ---ttgccacccttaagtgattttatacacgcactgcctTAGAATTCGCAACTGCTTTTAGctgtggcattatagactactagattaaaccttgtttgagtt-----  
U3             ---aaccacttotothttttttttttcacotttaocttcccAATAATCCCAATGGGTTCTTgctootdaaocaaatatactottttcttccccttttadaaatt-----  
U3             ---tatgcaacatttaatttttggagccatgcagctgtTGAATTCGCAACTGATTTTGGcataltggttgtgtatattcgtggtttttcatttttaagtt-----  
U4             ---cacaagtaaacgttttaagttgactgtttagttgctTAGAATTCGCAACTGATTTATGcagcgtgcgcatgtagtadgcgaattcagcgtgtcctggt-----  
U4             ---ggaaccccttttattatcattaaaadaaattcaacAATAATCTCAATATGTTTAGc-caadctacatatacttcttcaatattcctcaatdaacaaagtac-----  
U4atac         ---ggcagtagttcttgcacatttttgcagctttttgcgtTAGAATTCGCAACGCTCTTgcaacggctgccttagtgcgcgcaactgtgcagcaatcg-----  
U5             ---acagcgaattttttcacttctttggcagcaagctgcattATAATTCGCAACGCTTCAAGcagcaactgccttagtaccgtctgaaattggtggtgtag-----  
U5             ---tccatactttaadodctccttaataattttttttccactATAATTCGCAATGGGTTTAAgcattotccaatototatctcaootdcttotootdatcat-----  
U5             ---tttgcaacttttagggcctccttaattgattttttccactATAATTCGCAACGATTTAAgcattgctgtgtgtagctcaggtttttagagtttccct-----  
U5             ---gcataccctaaggatgagctccttaataattttttccactATAATTCGCAATGGGTTTAAgcattgctgtgtgtagctcaggtttttagagtttccct-----  
U5             ---tgatacttcaadodctccttaataattttttttccactATAATTCGCAACGCTTAAgcattotccttctototatctcaootdcttotaotdatcttct-----  
U11            ---cagcgtatcaagcaaacgttttgccttcttcccagctAATAATTCGCAACTGGTTTAAgcagcagcgtgaccaatgcgaatttgttttgtctgcattt-----  
U12            ---ctgctgtgttaatttgtatgctatgcaacaacccTGGAAATTCGCAAGTGGTTTATGcagcgcacacataacatgtggcgtcctcaacagtgggcaattt-----  
OrCD1          ---gggtgctgtttaacaacttttcaacacatgttatgccaTATAATTCGCAAGCAGTTCTGcactctcaaatcaaaattacgcagagctcatgcactgtttt-----
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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.