

Drosophila baimaii

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Sophophora > melanogaster group > montium subgroup

Assembly: GCA_018874675.1_ASM1887467v1_genomic

Dro_bai2 | JAEIU010047996.1:4311-4659 (+) | 349 nt | lncRNA: noe consensus e-value: 1.6e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 2nt Trailing-T: 6nt PSE: 0.90

66C6GT6A6C6CCTCAC6TTCTCAA66GTT6TCC6TTCC6ACAAATT6T66AA6CATT6C6CT6C6CATATCAT6AACCTAC6AA6AAATTAACAGAA6ATTATAAGATTAAGAAAC66TCAGAAAAATGAAT6CAATAAAGT6CCAAAACAAACAAACACGGTC6TCBAAAGATAAAATATACAAACACACAAATCATGAAAAACAT6AACAATAAGAAAGGAAAACTTAAAAAACCAAGCAAAACAAACAAACAAACAAAGAAAAACGTACATATTGTACATACA

TAAAAACTGTAG6GT6C6AT66GAGGAAATTC6A6TGA6TCCCTTTTTT

Dro_bai2	---gctgcgtctctggttttgcctccgtctgcgcacTGAAATTC6AAGTCATTATTCcgtgagaattctttttaaatagcgtgtgccagcttaattcttc-----
Arthropod_7SK	--laccgactggcgcgctgcacatgctgcgttcttGTGATTCCCAAGTC6TATTCcgcgcagggtacgtataaatagcgcgcagcactccattc-----
RNAse_MRP	-----tatcttattcccccaccccgccttGTGATTCCCAAGTTGTTTTACccacacccctacgtataaatagcgcacccctaacattaatcgtgccgctt
U6	---caccagaggcgctttaccgtcccccactgattctTATGATTCCCAAGTC6TTTTCCgcgaaggagttcatataaatagagacattttcccttgtacttc-----
U6atac	---caccttctgagttttctcactctgcagtgccgtACAAATCCCAAGTCITTTATTCcgcacagcgtacgtataaatagcgcgaagcaagccacgaacact-----
tRNAsec	-----caagtttaictadcaatdaactcccaaacccctctTATAATTCCCAAGTTCTTATTCctcaaacccctotttaaatadocaaatttcttactadtatt-----
snoRNAme18SA1806	-----actcttgggtgttctattatagccaccTAC6ATTCCCAAGTC6TTCCgcgtgggtgtgtgataaaatagggaacctgcagcatatatacTaaaca
U1	-gtcttaggggttgatttttcttcacacccccagaattATAATTCTCAACTGGTTATAGcagtgccgtcatggaaacctctgacgaagcagaggaaagc-----
U2	---dotaatttaacottacdaaatttcttccctttacattTATAATTCCCAACTGGTTCTACccbattdttatdaaatccctactttdcccaactaaatt-----
U4	--gcttgaattgtttttttgttttgcgtgcgttgcccatAGAAATCCCAACC6TCTTAAcgttctggcatggagtggaggtcgccagccagtaattggtt-----
U4	--acagccttgaacgttttactttatgcaacctcacttttTATAATTCCCAACTGGTTCTAGcgcacgcaactgtagtagtgaccgatttggggtggaaggtt-----
U4	-----ctaccccccdaactttacttcttcttcttTATAATTCCCAAGC6ATTCTAAcattattcaotcfaaadaccttgaattattttcatatdcatcacc-----
U5	gctcaagtaaacagggaagaaatcaccaattgttgctTAA6ATTCCCAACTGGTTCAAGcacaactgtctatggagcgtgcgtgctcgggttgataat-----
U5	taccttaggggtgtcttcttttcttcttcttttgcctTATAATTCCCAACC6CTTTAGctcgcatcagtagagagttccctgtttcagggttgtaa-----
U5	ctattttadodttctcttttaccctcccttttcttTATAATTCCCAACC6CTTCTAGctcaaaacaadtaadadcccttcaadadottadadaad-----
U5	catggcgtcgctcgctcacttgctcgagccgagctgctTAGAATTCCCAACCAGTTCAAGcagcggcgcatggagtacccgcggaaacagttgtcaaa-----
U5	ctattttaaggggcattcttctccacttgccttgcctTATAATTCCCAATCGCTTCTAGctcgcaacacatcagaggcccttgccttggggttgtttaa-----
U7	-----tctgcacatttaadctcctcacttcccttcactTATAATTCCCAACT6CTTCTAGctctctctccatgggttacgcataacaaadctacttgggtattga-----
U11	-acccttgcctactcagcgtataaccgctgttgcctT66AATTCCCAACCACTTCTAGctgcctggccatgactctgtagatattgaatgcaaaagctt-----
U12	--ttgcttgcaacaattgataccccccagcagccctTGTGATTCCCAACT6CTTCTGGatgccagcgcattgaattgctctgcggcagtcagcaattc-----
OrCD1	--gctgctatcaagaattctccaccaacagtgagccctACAATTCCCAACTGGTTCTGGctgtgaacgcgaggtagtcgcgtcgtcgtgggcttgggtg-----

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.