

Drosophila kikkawai

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

Assembly: GCA_030179895.2_DkikHiC1v2_genomic

Dro_kik1 | CM058225.1:22493830-22495062 (+) | 1233 nt | lncRNA: noe consensus e-value: 5e-191

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.92

Sequence: 566C66TCCGCAATCCGACCAACACGGTTGGACACATCCCGTCTCATCCCGCACTCTCTCGAATTGTGTCCGTTGGTAGCCGAAGTTACGATTCGCAAAACCTTCGTCATCCCTCTCTCACTCTCTGAAGCAAAACAAA6CCA6GA

Dro_kik2 | CM058228.1:14802900-14803342 (+) | 443 nt | lncRNA: noe consensus e-value: 2.7e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.94

Sequence: 66C6GTCCGCGCTTCAGATTCACAGGGTTGGCCACGTCGCCACTAATGTGGTAAAAAAAATGATTCGAAAGTGTATGCAAAACCTTGAGAAAAACCTATGAAAAAAGGGTTATCTGAGACGCA

	Dro_kik1	Dro_kik2
Dro_kik1	-	20
Dro_kik2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

Dro_kik1	-----TggatagccgagtgactgtttgcactttgtgcacctTGCATTCCCAAGTCCGTGTTccgcgtggcgtttgcataaatagccgcatcgccaggaccttaatc-----
Dro_kik2	-----TggggctcttgaattttgctcaaaacagcggtttACGATTCCCAAGTCTTATTCagcngttgaatgcgaataaataaacactttatagccacgtatctc-----
Arthropod_7SK	-----TttaccctgacccdcacatttccatttctctcttGTGATTCCCAAGTACAGATTCCaccccaatatttataataatccacccctcaaacctcttctctc-----
RNAse_MRP	-----TaatctattttttatcacgcacggcactTATGATTCCCAAGTCGTTTTAccacagctgggttcgtataaataagcgctccggctgaacacataagcgctt-----
U6	-----CCGgaactcaggcagaagaacgaatgcaaggttctAATAATTCTCAAGTCCATTTTCcggttgagttcatataaataagagaattttccctttgaacttc-----
U6	-----TaatctcatalatttcacaactcccccgaatccctttATGATTCCTCAAGTCCGTTTTTCccctttgaattcatataaataaggaataaataccataaccttc-----
U6	-----ccccagagggcgctgtgtgacacactgtgtttATAATTCTCAAGTCCGTTTTTCcggttgagttcatataaataagagaattttcccatgaatttc-----
U6atac	-----TtcacaacatacataatctatttttagcttctgcgtTACAATTCCCAAGTCATTAATTCTgcctagctgcataataaaggcggaagcgagcctgaactt-----
tRNAsec	-----GataaaaaacaaatctctacgtcaacccctctTATAATTCCCAAGCTCTTAATTCTcdaacgtccatttaataaagaacccctttttcctctatctt-----
snoRNAme18SA1806	-----accaaagtgtgggaacttttatttttagctgcctTATGATTCCCAAGTCTGTTTCTgtctagttgggttttaataaggtgaacttgcgttaaaagcaa-----
U1	-----TaaacttcggggatgactgtgcacccactttcggaactTATAATTCCCAACC6TTTCTAGcggtctggttcattggaaccccttaggccgagcggaagaaagc-----
U1	-----atatctacggggtgtttttctgcaccaccagcgacatACGATTCCCAACTGGTTCGgcgttgctggcatggaaacccctggcccgagcagaggaagagc-----
U1	-----TtccaccccttaaaadaccctatttcadadccctctTGAATTCCCAACTGGTTCGgccttcttccatgaaacccctgcccggagcagaggaagagc-----
U1	-----gcattcttcagaggcaatttgagcacaattttgtTATGATTCCCAACTGGTTAAGcgactttcccgagggaagcctgcgccgagcagaggaagagc-----
U1	-----gtgtgtaataagaagaatttttctacccttgcgtgcctTATAATTCCCAACCAGTTATGAcgtttggcctcatcgagacccctcgcccgagcggaagaaagc-----
U1	-----tatcttaadotttaadttttacccaacacctttccctTATAATTCCCAACC6GTTATAGcaacacatcatgaaacccctctatccgaadadaaagaaagc-----
U2	-----ccaatgcacaactgaacttctatcccttggttacaaTTATAATTCCCAACC6GTTCTGcctcgacaacgatgaagtcctttaccagactccatctagtt-----
U2	-----actggccgcatactatgtttgcccgcacgtgcgtgaccACGATTCCCAACC6TTTCTAGaacatgtctctatggagacccctgcagcttccaagcagagtt-----
U2	-----gtatttgcataatacaacttttctactttcacatcTATAATTCCCAACTGGTTAAGcgactttttccatgaaacccctgatttttccctttccagtt-----
U2	-----gaacttccgaattgaattgtttctcccttttcaagagcaATAATTCCCAACTGCTTCTGAcctccgcagctcatgaagtccttaccctgaactctgcatagtt-----
U2	-----aacccaacttttgcagaccccttcgcttttggtttctTATAATTCTCAACTGCTTCTGgctgagcagcgcacgaaccccgagcctgggtctggttgagtt-----
U2	-----adacactccctgaadtatttttccccctctgcacaaTTATAATTCCCAACTGGTTATAGcggcttttccatgaaacccctgatttttccctttccagtt-----
U3	-----accgcgggctgttctattttttccagcgctgcgcctTGAATTCCCAACTGGTTCGgcctgcgcgcgacccaagagccacaggtcggttactcaatcttt-----
U3	-----accgcgggctgttctattttttccagcgctgcgcctGAAATTCCCAACTGGTTCGgcctgcgcgcgacccaagagccacaggtcggttactcaatcttt-----
U4	-----tcttttcttgaacttattttcttcttcttccatTACAATTCCCAACTGGTTCGgccttccacaaatgaaatgaaggttcccccgcacgaagagagtt-----
U4	-----acagtttctgttacttatttccgcatcgtgactttTATAATTCCCAACTGCTTCTAGcgaatccgactctagttaggaactcacttgggtttgaagtt-----
U4	-----attcttttatacatattccaggtcgaacactTATAATTCCCAACTGCTTCTATcatataattcagccttaggaacatgaagttttcacagtttgcatacc-----
U4atac	taagatctcaaaatttcaatttctccctcttcttgcacataTATAATTCCCAACTGCTACTGgaactttccatgaattacccctcaaatccctcactcc-----
U5	-----ctacttttaggtgtcttttgcatttcccttccgtgcacatTATAATTCCCAACTGCTTCTAGcttataaacggcttaggaagcccttagctgaaggttagcaaa-----
U5	-----caggttaacaaaaaaagtaaacacacatttgatctTATGATTCCCAACTGGTTAAGcccaacatgcattaggaacccagaggtttcggtttggttaaa-----
U5	-----ctaccttaadotttcttttttacccttctcttctcactTATAATTCCCAACTGCTTTTGGctgcacaaatagaagagcccttcttccggtttatata-----
U5	-----tttaaggttttagggacatttttgcacctcactttgcataTATAATTCCCAACTACTTCTAACTtgcacaatataagagagcccttgggttgaagtacaaa-----
U5	-----cagaacttttgcattttccctctcaacacacccctTATAATTCCCAACCAGTTGTGGcadcacccacatggaatagcccaagaaaaacatggaacaa-----
U7	-----ttatggggttaatttttcttcttcttcttctTATAATTCCCAACTCTATTGGctcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt-----
U11	-----ccccctttcattcaccataacccctcacttgcataTATAATTCCCAACCCTTCAAGcgaacacccacacacccctcacttcttcttcttcttcttcttctt-----
U12	-----tcttttgaacacattttatccccacacacacacacTACGATTCCCAACTGCTTCTGgccttcccttccatgaatttccacttcccttccacttccacttcc-----
OrCD1	-----gctgctatcacaaaaacaaaacccagcagcttcgtTACGATTCCCAACTGGTTCAgcccgtggcgactgggtagctctgcccgcgctggggcgagttg-----

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.