Drosophila pseudotakahashii

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

Assembly: GCA_035046095.1_ASM3504609v1_genomic

Dro_pseud1 | JAWNOE010000218.1:1513807-1514939 (+) | 1133 nt | IncRNA:noe consensus e-value: 8e-196

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 6nt PSE: 0.88

Dro_pseud2 | JAWNOE010000105.1:3035943-3036475 (+) | 533 nt | IncRNA:noe consensus e-value: 7.7e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 1.00

Dro_pseud3 | JAWNOE010000105.1:15702694-15702942 (-) | 249 nt | IncRNA:noe consensus e-value: 8.2e-06

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.92

GGCGGTCGAGCGCCTCACAGTTATCAAGGGTTGGCCACTTTCCCGACTAATTGTGGCACCAAATTTAACTTTAAACAGTTAAAGCTAATGCAAAAAACTTTTCCCCAATGGGATAAACATACAAAACCTTACTTCACCCCCTCGGGG TACATATTGAAATCAACTTATCCAAAGTGATAAACATTAAGCTGTGGGGGGGATGCACTGGATGGGGAGGACTCTTCCCTCCATTCCAGTTGACCGCTATTTT

Dro_pseud4 | JAWNOE010000105.1:15707483-15707693 (-) | 211 nt | IncRNA:noe consensus e-value: 9.8e-07

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.93

TEAGGIGGCIGGACGGGIGGIAAAIGGAGGIACACCCCCCAIICCAGIGAICGCIAIIII

	Dro_pseud1	Dro_pseud2	Dro_pseud3	Dro_pseud4
Dro_pseud1	-	33	15	10
Dro_pseud2		-	36	32
Dro_pseud3			-	63
Dro_pseud4				-

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

Dro_pseud1	aaa <mark>getetgeegetgeagteecagteettgegetTATAATTCCCAAG</mark> TT <mark>GGAATTC</mark> egetegaegteacttaaata <mark>geeccategeaaggaceteetee</mark>
Dro_pseud2	cgattattttatattttccttcgactggggtctt TATAATTCCCAAGTGCTTATTC ggcgaatggtgcgtataaatagcgcttttgcagcagcgtttctc
Dro_pseud3	otgacotcatottctatccccoccotcoacotcoc TATAATTCTCAAGTGCGAATTCOGCGaatootcoctataaatagcocttocacataacoaotttc
Dro_pseud4	cccactdtgcagtaggcaaccagccctdtgcgcacTATAATTCCCAACTGCGAATTCgcaaatggttcgcataaatagagctttctcataaggactttc
Arthropod_7SK	gctggtcgcttagttggctgcatgactgctgtfgTAATTCCCAA6CGCTTATTCcgaattgtcgtgctataaatacgaccaatattgtaacgtttctc
RNase_MRP	tattcttatcgcgcacggtcgcttat6ATTCCCAACTCGTTTTTCcgcagaaggcacgtataaatagcgctgcaacagcacgtattgccgctt
U6	caccggtagaggtcgctccgagtcactctgattttATAATTCCCAACTGCTTTTCtctgttttgttcgtatatatacggcctttttcgaaacaacatc
U6	acting and the content of the c
	gccacccttadujtctteacatctalattctalanarit_ctaasisiinii Cccaasisiitattaatatagaatagaattaatataatatagaattactta
U6 U6	
	<mark>ctctaccuccauaqutcuttaaatutaacu</mark> atttt TATAATTCTCAACT<mark>GCETTTTG</mark>Cucu aa <mark>uaqttcu</mark> tatatataa <mark>aaccatttttcaaaataaactc</mark>
U6atac	<mark>accaacatttcacttatctcccqactct<mark>q</mark>ctccct<mark>TAAAATTCCCAAGTGCTTATTC</mark>cqcaaa<mark>qcq</mark>aqcatataaaaq<mark>qcqqcaaacatttcaqqtcatc</mark></mark>
tRNAsec	tettaattttttgetaaaaetgetetataaaetget <mark>IATAATTCCCAA</mark> GTGCTT <u>ITTC</u> tgeteagegtgegtgegtgegtgeggaaatttgtatggaaaetagt
snoRNAMe18SA1806	<mark></mark>
U1	a <mark>u</mark> catactttttggttgcattctttctcaaactctccc <mark>TATAATTCCCAACTGCTTCTAG</mark> cactttactcaaggataccttttgccaagagctgaggaaagc
U1	<mark>caatcannotantttttocctctcnoccannoctcacTATAATTCCCAACTGGTTCTAG</mark> cantttttctcaannanaccccanattctcccancuataa <mark>nc</mark>
Ü1	<mark>catac</mark> tac <mark>qattcatq</mark> attttttccttttqaaatcaa TATAATTCCCAACT<mark>G</mark>TTTCTAG caqttttctaatqqaaaccctaqqqtcqaaqataqc
U1	<mark>cataqcataqqqqtqaqttttacacataattaqcacqTATAATTCCCAACTGATTCTAG</mark> ctq <mark>cqcattqatcqqaqccccqqttqccqaq</mark> caaa <mark>qc</mark>
U1	<mark>cattoucatagugutuautttatacccaactaucacaTATAATTCCCAACTGATTCTAG</mark> Ctococcactcatougaaccccgutuccgaguctgaucaaagc
U1	atacttagaggggtgcattatctcgccgcacgctcgt TATAATTCCCAACTGCTTCTAG ctggtctggcatggaaaccctgctgccgagcgaaaagc
U1	atactttc <mark>qqqqtqaq</mark> ttttttac <mark>q</mark> caatc <mark>q</mark> catacc TATAATTCCGAACTGGTTCTGG ccqcttcccqatqqaaacccaacccctqaq <mark>cqqcqaaaaqc</mark>
U1	dtataagtagtagtagtagtagaga <mark>ctcAtttctcAATACAATTCCC</mark> aactgcttctagctgggagaccctacagccaaactgagaaaagc
ŬĪ	actttttggggtgagtttccttcacgcaatcgcatacc TATAATTCCGAACTGGTTCTGG ccgcttcccgatggaaacccaaccgctgagcggcgaaaagc
U1	acagagcctacttttctgtaagacgtgatgatatgct TGTGATTCCCAACTGGTTCTAA cagttttctcagggaaaccttaacccagagctgaggaaagc
U2	gcaatgtagatttfgttgttgtgcatttgcatttgcaagcatAATAATTCTCAACTGGTTCTAGctgcgttcgagtgaagccctctttattaggttgcagatagtt
U2	aaataggctatagaaatactttcacactttcacactt TATAATTCCAAACTGGTTCTAG cagttttatcatggagacccagttaatattcccattatagtt
U2	acagatgcgtcaaaatatgtgccatgtgcgcgtcccAATAATTCCCAACTGCTTCTABcagttttctcatggaggcccagttaatattcagtttctagtt
U2	tucaatucaattttuuttttatucacttaaaaacaaAAAATTCTCAACTGGTTCTAGCtucauttcaacaaautctccttttcauctcacautautt
U2	tocaatgcacattttggtgtttttgcgtttataaacatAATGATTCTCAACTGCTTCTAGctgcagttgagtaaagtcccctcttttaggtcccagtagtt
U2	tatttcttacctaccctottttcgcctotacotcccAATAATTCCCAACTGCTTCTAGcaotttcctcatogagacccaottaatattcagattctagtt
U2	acacontacatttttantttttccatttccaaaaatAATGATTCTCAACTGGTTCTAACTGGTTCTGattgacccctttctttantttanttttcatttttc
U2 U2	attcautcctgaacccctaggagaggcacaaactttctTATAATTCCCAACTGGTTCTAGctgtttttatggctaccctgttatttttcctaattatgtt
U3	acacatcctatttttagacacacacacacacatAAAATTCCAACTAGTTCTAGCCattagacacaaaattttttagacaacaacattt
	atacaticaticaticaticaticaticaticaticatic
U3 U3	
	<mark>gcctgctgtttcaatttcgtccgctgtgtgagcgcttGTAATTCCCAACTGGTTCTGGccagcaagtgtctgttt<u>ccgggcacc</u>gaacattt</mark>
U4	<mark>acatttcccctac</mark> ctac <mark>qttqcaccctqcactaccAATAATTCCCAACTAG</mark> TTCTAG <mark>cttctqatqqqtqqaataqqttctqattcqqttc</mark> qtqaaaqtt
U4	<mark>accg</mark> tt <mark>q</mark> cttcagatattttc <mark>q</mark> ctt q cqtqtqcaca TATAATTCCCAA<mark>CCGC</mark>TTCTAG cagcqccagcatqqagaqqtcqaatqcctqtgactqqtt
U4	auttmaamacaccocttcontatatutmcacc <mark>TATAATTCCCAAGCTG</mark> TTCAGGcactcttcatctamanuttcttaaaaatttaattttattatcacc
U4atac	tta <mark>gatcatggcaatgctgattttgcacacttggtgcgccTATAATTCCCAACTAG</mark> TACTAG
U5	atatactttaq <mark>qq</mark> att <mark>qq</mark> ttaaaqtaaaaqaaaqtcttt TATGATTCCCAA<mark>C</mark>AAGTTCTAG cttqttttqaqtqqtaaqqcaqattatttcctqttcaaaa
U5	<mark>ccaccttagggcaatacctttttccctttcttctgcccTAAAATICCCAAG</mark> CAGTTTTAGcgcaagtcgggttaagaggccgttgtcggggggtgaaaag
U5	<mark>-catccccttttcatqtqcaattccaaacaqttqtcccTATAATTCCCAAGTAGTTCTGGtcaatact<mark>q</mark>cattcaqaqqcactatqtttqqqtqqtqtaaag</mark>
U5	-tgcaqaqcaqttttcacqaaactaccqaqctqqtqtqcc <mark>tACAATTCCCAACTGGTTCTAG</mark> ctqtttcqacatqqactaqccqqtaqaaattqctqttcq
U5	aactucatttuuutttteeetaeteaaaautaee <mark>uetTATAATTETEAAGTAGTTETAGfeaataetueaeetauauueaetatutttuueeuttutaaag</mark>
Ú5	-cataaqtaacccctqqtaactttcatccctttatatqac TATAATTCTCAA<u>T</u>TGGTTTTCG tactqqtcqaataqaqaqqcccttccttqqqttqcattq
U5	<mark>cctttgggttttgcagatccctactcaaaagtaccgctTATAATTCTCAAGTAGTTCTGG</mark> tcagtact <mark>gcacg</mark> tagaggctcaatacttggtggtgtaaaa
U5	acaaaacatatetoaagggagggttgaggttgaggateetTATAGTTCCCAATCAGTTTAAC
Ū7	tqtqtqcqtttqqtttttcqcttcqqctqccca TATAATTCCCAACCTTTTCTAG tcqcctttqcatqqaqttqaccatqctqaqtctqqtttqatattqa
U11	cctcqaactqaacqaacqcaaqctqtcccAATAATTCCCAACTGGTTTTGGcqqcttttqccatqactcccqctaaacttccatacqcaqcaat
U12	tructtucacaactctatcauccuuccutuutcccTGTGATTCCCAACTGGTTCTGGCTucucuccatcaucttttacccuccuaacautcuucaattc
OrCD1	qtqctatcaacqaaatttctaccctcqcqcqqtaccAAAAATTCCCAACCAGTTTAAGacctqaatqaqtqqaaqtctcctcacttctcactctqqtttq

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.