# Drosophila lutescens

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

Assembly: GCA\_040802685.1\_UNIL\_Dlut\_1.0\_genomic

### Dro\_lut1 | JAUZTH010000001.1:22028725-22029823 (-) | 1099 nt | IncRNA:noe consensus e-value: 9e-195

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

## Dro\_lut2 | JAUZTH010000002.1:12466263-12466788 (+) | 526 nt | IncRNA:noe consensus e-value: 5.9e-03

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

### Dro\_lut3 | JAUZTH010000002.1:1196009-1196256 (+) | 248 nt | IncRNA:noe consensus e-value: 2.8e-05

5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 3nt Trailing-T: 4nt PSE: 0.95

GGCGGTCGAGCGCCTCACAGTAATCAAGGGTTGGCCACTTTCCCGACTAATTGTGGCACCAAATTTAACTTAAAAGTTAAGCCAATACAAAAAACTTATTCCCAATGGGATAAACATACAAAACATACAAAACTTTACTTCACCCCTCGGGGTA
AATATTGAAAAACATTGTTCCTAAGTGGATCATTATCATTGCTGTGATGTGCGCTGGACGGGAGGACTCTTCCCTCCGTCCAGTTGACCGCTATTTT

## Dro\_lut4 | JAUZTH010000002.1:1190631-1190854 (+) | 224 nt | IncRNA:noe consensus e-value: 1.2e-05

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 4nt PSE: 0.90

	Dro_lut1	Dro_lut2	Dro_lut3	Dro_lut4
Dro_lut1	-	30	13	15
Dro_lut2		-	36	34
Dro_lut3			-	61
Dro_lut4				-

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

Dro lut1	aaagctctgcagttgcagtccccagtccttgcgct <b>TATAATTCCCAAGTTGGAATTC</b> tgcaggacgtcacttaaatagccccatcgcaaggacctcctcc
Dro lut2	cgtttattttatttttcctccgactcgggtcttTATAATTCCCAAGTGCCTTTTCcgcgcgtggtgtgtataaatagcgcttttgcagcagtgtttctc
Dro lut3	GacutcatuctetttececuccutegeateuteucTATAATTCCCAAGTGCTCATTCcucqtotoutucutataaataucuctgucacacaaacuauttte
Dro lut4	attaccaaaagcgcagtcgcagcgctctttggtcgcTATAATTCCCAAGTGCGAATTCgcaaagtgcttcgcataaatagagctttctcatagggcctttc
Arthropod 7SK	Octivituctivicuo octivicativici to ta
RNase_MRP	gettyttyttytgetyggetygetygetygetyttilaal techna is begaaagagtytettataatagetytettyttatogacagcattattactor
U6	ctctaccgcagaggtcgttaaatgtcacgattttTATAATTCTCAACTGCTTTTCcgcaaagagttcgtatatatacggccattttcaagattaactc
U6	
U6	<mark>uccacccuaaudtectteacateettutateetTATAATTEECCAAGTE</mark> TTTATTE <mark>eucaaudatucaatataaatauaauadaaaceeacttuaaette</mark>
U6	<mark>ccacc</mark> qata <mark>qaqqtcqqttqaqttqaqtctctq</mark> atttt <mark>TATAATTCCCAACT<mark>GC</mark>TTTTTT</mark> ttcaatttqtttqtatatata <mark>qqqcc</mark> ttttttcaa <mark>q</mark> cttacatc
U6atac	a <mark>ucq</mark> attatttacttatct <mark>tacqacacqqctccct<b>TAAAATTCCCAA</b></mark> gTGCTTATTCcqcaaa <mark>qcqqcq</mark> tataaaaq <mark>qcqqcqaacaattcaqqtcatt</mark>
tRNAsec	tcttaatttttcctaaaactacatagaactgct <b>TATAATTCCCAA<mark>GTGCTTITTC</mark>tgcacagcgtgcgtataaatagggaaattag</b> catgaaagttagt
snoRNAMe18SA1806	tca <mark>qttaaqqttttctattaataqcaacct<b>TACAATTCCCAAGTGCTTGTTC</b>aqqqatttqttc<mark>q</mark>tataaaataqqqqaatcttqattqcttacaatctct</mark>
U1	actat <mark>qq</mark> tttatacattctctc <mark>q</mark> tccttt <mark>q</mark> aatqcaa <b>TATAATTCCCAACTGATTCTAG</b> caqtttcctcatqqaaccctataatcqaqctqaqqaaa <mark>gc</mark>
U1	acagagectactuttctattugaautuatuaaatuct <b>TGTGATTCCCAACTAGTTCTAA</b> cacttttc <mark>ucaugugaatcc</mark> ttaaccctgagetgaggtgaggc
U1	ata <mark>qcataqqqqtqaqtttttacccq</mark> taaatctcact <b>TATAATTCCCAACTAATTCTAG</b> ccqc <mark>qcqctcatqtqaacctcqqqqqccqaqctqaqaaaaqc</mark>
U1	<mark>caatcaqqqtaqttttttqcctctcqqccacqctcac<b>TATAATTCCCAACTGGTTCTAA</b>caqtctactcaaqqaqaccctaqcttctaccqqaqataaqc</mark>
U1	actat <mark>qutttatacattctctcqtcctttqaatqcaaTATAATTCCCAACTGCTTCTAG</mark> cactttcctcaa <mark>qqaatcc</mark> ttaa <mark>qccaqaqqctqaq</mark> aaaa <mark>qc</mark>
ŬĪ	atacttacgggggtgcattatctcgccgcacgcacgt <b>TACAATTCCCAACTGCTTCTAG</b> ctgttctggcatggagaccctgctgccgagcatcgaaaagc
U1	gtagaaggctactaaggacacatttctcgataccagt <b>TACAATTCCCAACTGGTTCTAA</b> ctgctctggcatggaaaccctagagccgagctgagataagc
U1	actificqqqqtqqttfftctcccctatcqcataccTAGAATTCCCAACTGGTTCTGGccqctccctqqtqqaaaacccaacccaaqacqaaqaaqc
Ŭ1	actttcggggttagttttctccacgcaattgcataccTACAATTCCCAACTGGTTCTBGccgctccctggtggaaacccaacccccgagcggcaaagc
U1	ttggcttaggggtgagtttgtacccataactagcactTGTAATTCCCAACTAATTCTAGccgcgcctcatgtgaacctcgggggcgagctgagcagagc
U1	actific good to gottific tee active at a control of the control
U2	atgcaacgtagatttagtgttatgcatttgcaaacgtAATAATTCTCAACTGGTTCTAGctgcgtttgagggaagccccttcttcaaggtatcagtagtt
U2	- activance traduction to the control of the contro
U2 U2	
U2 U2	acade to the character to the control of the c
U2	
	tat <mark>q</mark> ctatqtaqattttqqtqttatqqcatttacaaactq <mark>AAAAATTCCCAACTGGTTCTAG</mark> ctqcqtttqaqqqaaqccccctttttttqqtttcaqtaqtt
U2	atoctatotagattioniditatocattiacaaactoAAAAATTCCCAACTGCTTCTAGctucottttganggaaucccccttcttcangtfocattatt
U2	tacaac <mark>qq</mark> tacatttatactttttccattttccaaaat <b>AATGATTCTCAACTGGTTCTAG</b> ctqcatttqaqtaaaccccctqctttttqqatqqaataqtt
U2	attcaqtcatqaacccctaaqataqqcacaatctttct <mark>TATAATTCCCAACTGG</mark> TTCTAGctqttttttatqqctaccctqctcttttcqtattttaaqtt
U3	<mark>ctctcututtcttaattttttctcatucucacaccct<b>TGTAATTCCC</b>AA<mark>GCAGTTCTGG</mark>cctctucaucaacaaagatccacaguttugacaucuaacagtt</mark>
Ú3	<mark>acattctatttttaggcacc</mark> gcacccttataaccct <b>TATAATTCTCAAGCAGTTCTAG</b> cccctggagcaccaaggttcacaaggttggacag <mark>c</mark> gaacagtt
U3	<mark>caqcatqcctqctqttttcqtcqctqtqtqqqcqccTATAATTCCCAACTGGTTCTGG</mark> ccqqcaqcqcaqcqaactattqctqqqqcaccqaacaatt
U4	<mark>caacacttacccau</mark> cttac <mark>gttucaccctucactctAATAATTCCCAACTAGTTATAG</mark> cttcttttgggtggaataggttctgattcgggttgaaagtt
U4	accattucttuauatattttcucttucututucucaTATAATTCCCAACTGTTTCTAGcaucucaucatuuaucauuutcuaatuccuututctautt
U4	aqttqaacactqtttcqqqtatatqtqtacc <b>TaGAATTCCCAAGCTGTTCAAG</b> ccctcttcatcaqqqqttttaaaaaaatttaattcaatttatcacc
U4atac	tta <mark>qatcatqqcaatqcqqattttqcqcacttqqtqcccc<b>TGTAATTCCCAACTAG</b>TACTAGccattttqqtatqaqqtqtqcttqcattccqtcactcq</mark>
U5	-gamancaattttcacmaaatntocccmanctmonoticaTATAATTCCCAACTGGTTCTAGcamttccmacatmactamcccmcamaaatamctmttcm
Ū5	ccatccccttttatatgcaattccaaacagttgtcccTATAATTCCCAAGTAGTTCTGGtcaatgctgcacctagaggcactatgtttggtggtgtaaag
U5	octttoggtttccaatccctactcaaaggtatcoctTGTAATTCTCAAATAGTTCTGGtcaatgcacctagaggctcaacatatggtggtgtaaaa
U5	GCCTTT GGGTTTCCCTacTcaagggtatcgctTGTAATTCTCAAATAGTTCTGGTCaataccccacctagggggCTcaacatffggtggtaaaa
U5	atatactttagggatggtaaaagtataagaattagttcTATGATTCCCAACAAGTTCTAGcttgttttgagtggaagggcagattaatttctatgccaaa
U5	-cccaccttaaggcaatacctttttccctttcttctccctTACAATTCCCAAGCAGTTCTAGcgcaaatcgggtgtagggcccttacctgggggtgaaagg
U5	-acaaaaaataattitaaamantamattaantaantataTATAATTCCCAATCAGTTTTAAGCatataataactamattaataataattaattaataattaat
U7	
U11	
U12	tottoaattuatuatuataattuataattuttotaanan isti istoituuttota josta ja
012 0rCD1	
OLCDI	grgetateaacgaaatttetacectegcagggtagchnihnii <mark>eeenneeng</mark> iiii <mark>ag</mark> ceeggaatgagtggddettegettegttetgtttttg

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.