# Drosophila prostipennis

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

Assembly: GCA\_037075205.1\_ASM3707520v1\_genomic

## Dro\_prost1 | JBAMCJ010007287.1:464348-465448 (-) | 1101 nt | IncRNA:noe consensus e-value: 3e-195

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

### Dro\_prost2 | JBAMCJ010000012.1:192455-192970 (-) | 516 nt | IncRNA:noe consensus e-value: 6.7e-04

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

### Dro\_prost3 | JBAMCJ010001283.1:372693-372939 (-) | 247 nt | IncRNA:noe consensus e-value: 7.6e-05

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

### Dro\_prost4 | JBAMCJ010001283.1:378329-378554 (-) | 226 nt | IncRNA:noe consensus e-value: 9.2e-06

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

	Dro_prost1	Dro_prost2	Dro_prost3	Dro_prost4
Dro_prost1	-	33	16	12
Dro_prost2		-	36	34
Dro_prost3			-	60
Dro_prost4				-

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

Dro_prost1	aaagetet <mark>geagttgeagteeceagteettgegetTATAATTCCCAAGTTGGAATTC</mark> cgeeggaegteaettaaatageegeategeaaggaeeteetee
Dro_prost2	togtttttttttttttctccagactagagtcttTATAATTCCCAAGTGCTTATTCcactagtagtagtacdtataataagcactttagcagaagcatttctc
Dro_prost3	atgacutcatottctatacucuccuccutcutcuccutariaat Toccaa Grant Toccaa Grant Gr
Dro_prost4	quactitudate to attacked to the transfer and the state of the st
Arthropod 7SK	
RNase_MRP	tattettate <mark>gegeactotedegetTATAATTCCCAACTCGTTTTTC</mark> egeagaeg <mark>geac</mark> gtatagata <mark>gegettoetagegaeggettoetagegettoet</mark>
U6	<mark>caceggtagaggtegeteegagteactetgattttTATAATTCCCCAACTETTTTTTC</mark> ttttaattgttegtatatata <mark>ggg</mark> ttttttteggtattacate
U6	<mark>ctctaccuttau</mark> atutc <mark>u</mark> ttaaatutcac <mark>u</mark> tttet <b>TATAATTCCCAA<mark>CTGCTTTTTC</mark>cu</b> caatcautteutatatac <mark>uaccattttcaaacataactc</mark>
U6	<mark>auatuacucceac</mark> at <mark>cuaacateetttueateet<b>TCTAATTCCCAA</b></mark> GTGCTTATTCtueaauuatueaatataaatauuutuaaaaaeteuuttuaaette
U6	<mark>-qc</mark> cacccttaaqqtcctttacatccttatatccc <b>TATAATTCCCAAGT<mark>G</mark>TTTATTC</b> cqcaatqaqqccatataaataqqaaatctcctttqaacttc
U6atac	gaqaatatttcatqtatctttc <mark>qacqcqqctccct<b>TAAAATTCCCAAGTGCTTATTC</b>cq</mark> caaaqcqtacatataaaaqq <mark>cqqcqaacaattcaqqtcatc</mark>
tRNAsec	<mark>tcttc</mark> atattt <mark>cctaaaaccacctau</mark> aaact <mark>u</mark> ct <b>TATAATTCCCAAGTGCTTITTC</b> tucacaucutucutaaaatauuaaaatttutatuuaauuctaut
snoRNAMe18SA1806	<mark>tcaq</mark> tta <mark>qqq</mark> ctttctatttata <mark>q</mark> ctacct <b>TACAATTCCCAAGTGCTTGTTC</b> qqqqatttqttcqtataaataqaqqaatattqttatcttacaatctct
U1	<mark>caatqaqqqtaqtttttqcctctcatccacaqctcacTATAATTCCCAACTGCTTCTAG</mark> caqttcactcaaqqaqaccctaqattctacccaaqttaa <mark>qc</mark>
U1	<mark>acagagoctacttttctataagaagtgatgatgcaatgct<b>TGTGATTCCCAACTGGTTCTAG</b>cagttttctcagggaaaccttaacccagag<mark>octgaggaaagc</mark></mark>
ŬĪ	<mark>cctactacqattcattcttttttcctttttaaaaq</mark> taa <b>TATAATTCCCAACTGCTTCAAG</b> caqttttctaatqqaaacccttqqqqtcqaqctaaqaaaqc
U1	ctautatauguutgautttuaacccatauctaccactTATAATTCCCAACCGATTCTAGctucuctctcatuugaaccccuctuccuauctgaucaaauc
Ü1	ucautoucatagoggitaatttataataactagcactTATAATTCCCAACCCATTCTAGctgcgctcfcatgggaaccccgggtgccgaagctgagcaaagc
Ŭ1	atacttagaggggtgcattatctcgccgcacgctcgt <b>TATAATTCCCAACTGCTTCTAG</b> ctgctccggcatggaaaccctgctgccgagcagcgaaaagc
Ü1	catactttttauttuattuttttctcaaacccttccTAAAATTCCCAACTGCTTCTAGcacttttcccauguaaaccttaacccauauctgcuagaaauc
U1	actif congressed and tittitic acacaat cocat occ TATAATTCCCAACTGGTTCTGGccuctf cctout on an acceptance of occupancy of the construction of the co
U1	actttcggggtgagttttctccacacacaattgcttaccTATAATTCCCAACTGGTTCTGGccgcttcctggtggaaacccaacccctgagcgggaaagc
U2	actatagaaattataatactttcacactttcacattTATAATTCCGAACTGGTTCTAGcagtttcatcacagagaccccgtcaatttcacattgcaagtt
U2	
U2 U2	tctuagcaagcaaatuttttcgcctutgcutcccAATAATTCCCAACTACTTCTAGcagattctcatggagacccagutgaatattccttttctagut
U2	tucaatotaguatetagutttuguttatucattacaactaAATAATTCCAACTGGTCTCAGttucguttaguttcagttatattttuguttaattagutt
	atycaatytagattttyytyttatycattacaaactaaataattoivaacigoittagettyottotaatytaactooottottoayottacattagti incaatotaaattiinnotottatacaattacaaraataataattottoaatogattoaattaaataaatooottottitaanottaattiaantt
U2	
U2	atcca <mark>qtcatqaacccctaqq</mark> ata <mark>qq</mark> caaaatccctct <b>TATAATTCCCAACTTGTTCTAG</b> ctqttttttatqqctaccctqttctttttcctaactaaqtt
U2	<mark>acaacqqtacatttttactttttccattttcctaaaatAATGATTCTCAACTGGTTCTAG</mark> ttt <mark>qcqtttqaqtcqacccactttctqtaaqq</mark> ttq <mark>c</mark> atta <mark>q</mark> tt
U2	acateccettaaatatucaatutataauta <mark>aacatAATACCCAACTGGTTCTAG</mark> etucutteuautuaauccetettetetauuttacattautt
U3	<mark>dtattattattettettataatettitetettaaaacaetaaaaaaateetaaaaaaaaaa</mark>
U3	<mark>acacattctatttttaqattccttatcqcacaccct<b>TATAATTCCCAAGCAGTTCTGG</b>cccqcqqcqcacaqqqtcacaqqqttqqacaqctaaaaqtt</mark>
U3	<mark>ncctnctntttanttttcatccnccntncncncncactATAATTCCCAACTGGTTCTGG</mark> ctnncancnaccaantnactattnccnnncaccnaacattt
U4	<mark>acctttqcttqaqatattttcqcttqcqtqtqcqcatATAATTCCCAACCGCTTCTAG</mark> caqcqccaqcatqqaqcaqaqqtcqaqtqcctqtqqacqqtt
U4	<mark>aacattttcccctqcctacttqcaccctqcactcactAATAATTCCCAAC</mark> TA <mark>GTTCTAG</mark> Cttcttttqqqtqqaataqqttttqattcqatqtttaaaqtt
U4	a <mark>qttqaacacccucttcqq</mark> taaat <mark>qttcact<b>TATAATTCCCAAG</b>TT<b>GTTCAAG</b>cactcttcaacta<mark>qaqqttc</mark>ttaaaaatttaatttaatttatcacc</mark>
U4atac	ttanateatoncaatoctnattttococacttootococcTATAATTCCCAACTAGCcatttttotatoaootoccacattccotcactco
U5	gagagcagtgttcacgaaatatgcccgagctggggtgca <b>TATAATTCCCAACTGGTTCTAG</b> cagtttcgacatcgactggccggtagaaattgctgttcg
U5	tccaccccttttaactucaattccaaacauctutcccTATAATTCCCAAGTAGTTCTGGaccatactucacctacaugcactatutttuatuutuatuutuaaaa
U5	ccaccttagggcaataccttattcccttccctccccTACAATTCCCAAGCACTTCTAGcgcaagtcgagtgtagaggccgttgtctgggggttggaaag
Ü5	atatactttagggatggtaaaagtaaaagaagttt <b>TATGATTCCCAACCAGTTCTAG</b> cttgttttgagtggtagtggtttattttccatgccaaa
U5	cctctgggtttgcagatccctactcaaaagaacccctTATAATTCTCAAGTAGTTCTGGtcaatactgcacctagaggctcaatatttggcggtgtaaaa
U5	
U5	-aaccagtaacccctcgtaattttcatccctttatttcacTATAATTCCCAATTAGTTTTCCtacttatcgaatagagggcccttccatatggtgatatg
U5	acaaaacataactgaagggagggttgagttaaaatcctTATAGTTCCCAAACAGTTTTAGcatatgataaatggcacaatgaatagtttaatgttgttct
U7	-adadadatadat ugayuwayunt ugartadadat CETTATATI TECAACCATI TAGATATUGA Adaduya Cadatuad Agut Lada utu Litet
U11	of the control
U12	
OrCD1	gugctatcaacgaaatttctaccccgcggggtaccaafaaff <mark>ccc</mark> aaccagifffagctctgagtcgagtcgagtcacttctcattctgttttg

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.