

Table 3 Features of candidate noncoding transcripts

Curation			Data supporting expression			Likelihood of translation							
BDGP cDNA identifier ^a	Genomic coordinates	cDNA length	Predicted exons ^b	Overlapping ESTs, all ^c	Overlapping 5' ESTs ^d	ORF length ^e		Non-met. init. ORF length ^f	D.pse. seq. ortho- logous to cDNA ^g	Conservation of ORF > UTR ^h	Ka/Ks D.pseudo. ^k	Ka/Ks D.vir. ^m	QRNA ⁿ D.pseudo.
						88aa	148aa (F)						
AT08427	2R:620173-622359	1808nt	1	1	1	88aa	148aa (F)	81aa	+	-	No tblastn	No tblastn	O216
AT11392	2L:21925676-21924570	994	3	1	1	70	86 (E)	54	-	-	No tblastn	No tblastn	No nt align
AT13310	U:2638514-2637929	606	1	1	1	94	102 (S)	42	+	+	No tblastn	No tblastn	No nt align
AT14266	3R:23184952-23184092	781	1	1	1	56	103 (S)	56	+	-	No tblastn	No tblastn	P123 O381
AT21289	2L:6537649-6536219	1415	1	1	1	52	81 (V)	59	+	-	No tblastn	No tblastn	O685
AT22150	2L:19888725-19889711	1080	2	3	1	94	167 (O)	64	-	-	No tblastn	No tblastn	No nt align
AT24650	3L:6192910-6191994	578	3	1	1	77	99 (R)	37	-	-	No tblastn	No tblastn	No nt align
AT27057	3L:15558215-15559242	840	1	9	9	74	125 (A)	50	+	-	0.0667	0.0822	P522
AT28783	3L:593397-591836	1553	1	1	1	84	111 (T)	51	+	-	No tblastn	No tblastn	O199
AT31442	3L:17882911-17894999 ^b	1111	2	2	1	83	109 (C)	61	+	+	No tblastn	No tblastn	O368
GH03576	3L:11054189-11056091	931	2	6	5	38	81 (V)	50	+	-	No tblastn	No tblastn	O326
GH05108	3R:12165756-12164679	1094	1	2	1	33	83 (F)	62	+	-	No tblastn	No tblastn	O721
GH05710	2R:6692288-6691103	1211	1	1	1	80	163 (V)	59	+	+	0.3328	No tblastn	O231
GH06385	3L:17882887-17884453 ^b	1190	2	2	2	71	101 (A)	69	+	-	No tblastn	No tblastn	O380
GH08923	X:11174866-11172455	2462	1	3	1	44	70 (F)	56	+	-	No tblastn	No tblastn	O1221
GH14469	2L:20617275-20618592	695	4	1	1	40	67 (Q)	42	+	-	No tblastn	No tblastn	O518
GH22170	3R:4303330-4269856	743	2	1	1	36	88 (D)	59	+	-	No tblastn	No tblastn	O438
GH25188	2L:610799-610007	827	1	1	1	87	112 (A)	59	+	-	Failed [f]	Failed [f]	O638
GH25505	3R:5818318-5821108	2811	1	6	5	95	104 (L)	57	+	-	No tblastn	No tblastn	O2670
GH26692	3R:12272326-12270742	1674	1	1	1	64	74 (R)	46	+	-	No tblastn	No tblastn	O1030
GH26828	X:1206514-1208830	2335	1	3	1	66	147 (P)	51	+	-	No tblastn	No tblastn	O34 O1801
GH27201	2L:5154214-5150836	4554	1	7	7	84	152 (S)	88	+	-	No tblastn	No tblastn	O3629
GM01028	4:487255-488436	1157	2	1	1	70	71 (K)	47	-	-	0.1056	No tblastn	No nt align
GM01206	X:3867475-3868711 ^b	1214	2	6	3	39	50 (S)	49	+	-	No tblastn	No tblastn	O466
GM02923	2R:9126179-9125168	1035	1	1	1	44	91 (V)	46	+	-	No tblastn	No tblastn	Q77 O786
GM03003	X:3867701-3869573 ^b	1884	1	6	3	39	57 (N)	56	+	-	No tblastn	No tblastn	O759
GM03661	X:10535429-10534282	1159	1	1	1	78	80 (F)	40	+	-	No tblastn	No tblastn	O514
GM03914	3L:4571847-4570833	1046	1	1	1	72	76 (I)	59	+	-	No tblastn	No tblastn	O972
GM04921	X:7705291-7704128	1159	1	1	1	83	93 (L)	39	+	-	No tblastn	No tblastn	O488
GM07040	3R:19686405-19682860	3544	1	2	2	86	109 (K)	67	+	+	No tblastn	No tblastn	O705
GM07077	2L:20422321-20423687	1385	1	2	1	67	67 (L)	57	+	-	No tblastn	No tblastn	O766
GM07658	3R:7594207-7592110	2095	1	2	1	76	88 (F)	56	+	-	No tblastn	No tblastn	O1078
GM07660	X:16185157-16185994	853	1	1	1	19	62 (I)	27	+	-	No tblastn	No tblastn	O841
GM07702	2L:12532047-12533217	850	2	1	1	72	95 (K)	42	+	-	No tblastn	No tblastn	O574
GM09444	X:10533220-10532579	653	1	1	1	36	73 (F)	26	+	-	No tblastn	No tblastn	O570
GM09534	X:16293581-16292695	912	1	1	1	71	106 (N)	44	+	-	No tblastn	No tblastn	O446
GM09668	2L:4870261-4869463	834	1	1	1	24	52 (Q)	33	+	-	No tblastn	No tblastn	O716
GM10787	3R:3021116-3012764	1695	1	25	24	94	136 (F)	60	+	+	No tblastn	No tblastn	O1470
GM12657	3L:3415885-3417390	708	2	1	1	66	90 (S)	53	-	-	No tblastn	No tblastn	No nt align
GM24362	3L:8022988-8029926	450	2	1	1	55	95 (L)	49	-	+	No tblastn	No tblastn	No nt align
HL05775	X:4103626-4105491	1890	1	5	5	85	97 (F)	47	+	-	Failed [f]	No tblastn	O1118
LD11130	X:11174437-11173269	1187	1	2	1	44	70 (F)	44	+	-	No tblastn	No tblastn	O902
LD11162	3R:9638860-9640391	1549	1	13	11	49	163 (V)	64	+	-	0.1156	0.1393	O1040
LD13184	3L:13985612-13983409	2222	1	4	2	88	132 (T)	84	+	+	No tblastn	No tblastn	O992
LD16711	3R:14119833-14118160	1672	1	1	1	76	103 (K)	55	-	-	No tblastn	No tblastn	No nt align
LD23922	X:2619531-2658305	1721	6	1	1	82	96 (Y)	69	+	-	No tblastn	No tblastn	O163
LD28571	2R:19805458-19802173	3302	1	1	1	96	128 (V)	107	+	-	No tblastn	No tblastn	P189 O2070
LD30889	X:4137084-4136053	1069	1	1	1	49	76 (T)	63	+	-	No tblastn	No tblastn	O351
LD38553	2R:10858584-10915445	1317	2	16	14	42	110 (S)	68	+	+	No tblastn	No tblastn	O302
LP01161	3L:3754356-3754868	527	1	1	1	56	68 (Q)	43	+	-	No tblastn	No tblastn	O308
LP03188	3R:2525887-2525275	553	2	1	1	59	68 (I)	45	+	-	No tblastn	No tblastn	O475
LP06491	2L:14334311-14334773	403	2	1	1	67	67 (M)	29	-	-	No tblastn	No tblastn	O165
LP11739	3R:8981405-8985151	1222	3	4	4	35	90 (N)	59	+	-	No tblastn	No tblastn	O999
LP12023	3L:7365852-7366148	313	1	1	1	59	59 (L)	36	-	-	No tblastn	No tblastn	No nt align
RE21847	3R:5608431-5605255	3191	1	5	5	93	149 (L)	114	+	-	No tblastn	No tblastn	P108 O1680
RE28911	2L:16816677-16819971	1005	5	9	8	44	64 (A)	53	+	-	No tblastn	No tblastn	O856
RE45760	3R:21500275-21501180	758	2	2	1	35	97 (K)	44	+	-	0.1682	0.1284	P333 O159
RE54004	X:18905856-18902037	562	2	1	1	26	44 (S)	38	+	-	No tblastn	No tblastn	O406
RE63504	2R:19947503-19946983	331	3	77	77	38	38 (F)	40	+	-	No tblastn	No tblastn	O96
RE65113	3R:5354074-5355417	1062	2	9	3	67	67 (D)	45	+	-	No tblastn	No tblastn	O603
RE66017	3R:18597843-18593937	3461	2	2	1	69	102 (S)	57	+	-	No tblastn	No tblastn	O821
RH09485	2R:13775111-13775672	518	2	3	1	40	74 (V)	51	-	-	No tblastn	No tblastn	No nt align
RH45340	X:10201001-10201550	407	3	4	1	48	98 (T)	50	+	+	0.0488	No tblastn	P16 O129
RH57193	3L:19437267-19435625	981	4	6	6	33	101 (L)	65	+	-	0.2853	No tblastn	O684
RH62702	X:17891905-17889857	2049	1	1	1	95	114 (F)	52	+	-	No tblastn	No tblastn	O825
RH62830	3L:6180107-6180481	326	2	1	1	40	56 (V)	35	+	+	0.1831	0.0527	O259
RH63361	3R:22240192-22239779	424	1	1	1	62	66 (G)	40	+	+	Failed [f]	Failed [f]	Q72
SD03144	2L:11767980-11764057	3956	1	1	1	81	100 (V)	60	+	-	No tblastn	No tblastn	Q21 O2750
SD04448	2L:20718271-20720685	2301	2	3	1	71	84 (L)	58	+	-	No tblastn	No tblastn	O1618
SD05379	X:16070095-16071476	1391	1	1	1	83	83 (Q)	49	+	-	No tblastn	No tblastn	O197
SD10988	3R:27583061-27584522	1415	2	2	2	80	96 (R)	75	+	+	No tblastn	No tblastn	O1182
SD25037	2R:13839131-13840886	1560	2	2	1	90	205 (V)	56	+	-	error	Failed [f]	O1138
CR31400 (Hsr [I])	3R:17122362-17127386	5025	1	26	24	76	123 (S)	72	+	-	No tblastn	No tblastn	O2088
CR32777 (roX1)	X:3599512-3603303	3748	1	81	73	84	134 (V)	62	+	-	No tblastn	No tblastn	No nt align
CR32665 (roX2)	X:11320995-11322374	1285	1	2	2	45	79 (N)	45	+	-	No tblastn	No tblastn	O440
CG11296 (pcg)	2R:17373704-17376371	1197	2	9	8	112	113 (T)	65	+	+	0.2857	0.1677	No nt align

Curated candidate noncoding transcripts are listed alphanumerically. Horizontal lines separate clones from specific BDGP cDNA libraries indicated by clone identifiers.

^a cDNA identifiers for *pncr* gene transcripts are italicized.

^b Two pairs of cDNAs have overlapping genomic coordinates: AT31442 and GH06385; GM01206 and GM03003.

^c Exons predicted by automated genome alignment and subsequent manual inspection.

^d Number of ESTs overlapping any portion of transcript; total includes cDNA itself.

^e Number of ESTs overlapping 5' end of transcript; total includes cDNA itself.

^f Longest translation using methionine as an initiation codon.

^g Longest translation using any initiating codon.

^h Longest translation for randomized transcript sequence using met initiation codon (average translation length from six randomizations).

ⁱ '+' denotes BLASTN hsp with expectation score < 1e-5.

^j Transcript ORF is more conserved than transcript UTRs, as measured by BLASTN against *D. pseudoobscura*.

^k Values <0.5 signify conservation of codon structure; sequences that fail chi-square data fitness test or fail to produce a protein alignment are noted.

^l Non-parametric Ka/Ks value, possible codeml failure.

^m As in (k), with *D. virilis* used as comparative genome.

ⁿ P: protein-coding, O: known non-coding, O: Other. Number of nt for each; sequences that fail to yield a comparative nucleotide alignment are noted.