Table 1. Gene characteristics and dN/dS ratios of *Drosophila simulans* accessory gland ESTs

Acc. #	**EST**	**dN**	**dS**	**dN/dS**	**-2Dl**	**arm**	**Map**	**dbEST**	**(Gene) Function**	**CG #**	**AG En.**	**#AAs**	**S. Seq.**	**hits**
BG642142	02	NC	NC	-	-	3R	82D6	YES	translation factor	CG9769	NO	280	NO	1
BG642151	03	NC	NC	-	-	X	16F	YES	?	NONE	NO	?	NO	1
BG642154	04	0.0404	0.153	0.264	11.64	X	18B7	YES	?	CG7889	NO	319	NO	1
BG642155	05	0.0414	0.165	0.251	5.6	3R	96F3	YES	(MST57DA)	CG9074	YES	75	YES	17
BG642156	06	0.2073	0.271	0.764	0.34	2L	31F	YES	lipase/esterase	CG17093	YES	731	NO	6
BG642157	07	0.03	0.081	0.372	1.864	2L	28-29	YES	serpin protease inhib.	CG8137	YES	306	YES	2
BG642158	08	NC	NC	-	-	2R	60B2	YES	(eif-5A) translation factor	CG3186	YES	159	NO	1
BG642159	09	0.0469	0.023	2.039	0.444	2R	43A4	NO	?	CG12827	NO	99	NO	1
BG642132	10	?	?	-	-	X	3C-E	NO	no good prediction, AE003427	NONE	NO	?	?	1
BG642133	11	0.0195	0.26	0.075	33.71	2L	31F5	YES	?	CG18284	NO	356	NO	2
BG642134	12	0.0148	0.098	0.151	6.408	X	9E2	YES	?	CG1534	YES	121	NO	1
BG642135	13	?	?	-	-	2L	40B-40D	NO	no good prediction	NONE	NO	?	?	1
BG642137	14	0.0212	0.134	0.158	33.64	3R	84C1	YES	?	CG1965	NO	365	NO	1
BG642136	15	0.1349	0.066	2.05	3.012	3L	67B-C	YES	?	CG16707	YES	183	YES	1
BG642138	16	0.0938	0.047	1.996	20.42	2L	31F5	YES	esterase/lipase	CG17101	YES	355	NO	9
BG642139	17	NC	NC	-	-	3R	94C-D	NO	?	NONE	NO	?	?	1
BG642140	18	0.0037	0.232	0.016	27.43	3R	99D5	YES	(Sry-delta)	CG17958	YES	433	NO	1
BG642141	19	0.0001	0.121	8E-04	35.27	2R	48E2	YES	cell cycle regulator	CG8889	NO	323	NO	1
BG642160	1a11	?	?	-	-	2R	60D	NO	no good prediction AE003464	NONE	NO	?	?	1
BG642161	1a12	0.0043	0.069	0.062	9.364	2R	59F7	YES	?	CG5532	NO	112	NO	1
BG642162	1a2	0.0295	0.05	0.592	0.762	2L	26A5	NO	(DSF) hormone receptor	CG9019	NO	691	NO	1
BG642163	1a3	0.0784	0.05	1.559	0.176	2L	25A3	NO	?	CG11933	YES	91	NO	1
BG642164	1a4	0.1057	0.075	1.413	0.82	2L	32A	NO	?	NONE	YES	1087	YES	4
BG642165	1a5	?	?	-	-	3L	65A	NO	no good prediction AE003563	NONE	NO	?	?	1
BG642166	1a6	0.0469	0.033	1.421	0.39	3L	71B8	YES	transporter	CG7255	NO	880	NO	1
BG642167	1a8	0.1784	0.084	2.121	1.028	3	96F	NO	?	NONE	YES	50	YES	1
BG642169	1b12	0.0001	0.142	7E-04	24.28	3L	74D2	YES	ubiqitin ligase	CG7555	NO	1082	NO	1
BG642170	1b5	0.0114	0.064	0.18	2.026	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642172	1B8	NC	NC	-	-	2R	43B-C	NO	?	NONE	NO	479	NO	1
BG642173	1c1	0.003	0.151	0.02	25.5	2L	31F5	YES	esterase/lipase	CG17097	YES	318	NO	8
BG642174	1c10	0.0079	0.141	0.056	14.87	2L	31F5	YES	lipase	CG17097	YES	318	NO	8
BG642175	1c11	0.0026	0.134	0.019	15.12	3L	62A7	YES	cholinephosphate cytidylyltransferase	CG18330	NO	381	NO	1
BG642176	1C12	NC	NC	-	-	X	2A	YES	(EG:8D8.6) Acetyltransf	CG11412	NO	402	NO	1
BG642177	1c3	0.0001	0.057	0.002	2.056	3L	67D	YES	cell adhesion	CG6590	NO	1045	NO	1
BG642178	1c4	0.0589	0.137	0.431	6.356	2L	28E	YES	ligand binding/carrier	CG8552	NO	2016	NO	1
BG642180	1c5	0.006	0.149	0.04	12.99	3L	75D	NO	?	CG18231	NO	391	NO	2

BG642179	1c6	0.0383	0.2	0.191	7.378	3R	95E8	NO	(Acp95EF)	NONE	YES	52	YES	2
BG642181	1c8	0.051	0.199	0.256	2.628	3R	92E	YES	(ELONGIN-B)	CG4202	NO	118	NO	1
BG642182	1C9	NC	NC	-	-	2R	50E8	YES	kinase	CG8485	NO	860	NO	1
BG642183	1D1	NC	NC	-	-	2R	47C1	NO	(BCDNA:LD26050) FN3	CG12340	NO	1420	NO	1
BG642184	1D10	NC	NC	-	-	X	8B	YES	(MOE) actin binding	CG10701	NO	512	YES	1
BG642185	1d11	0.003	0.093	0.032	23.21	3R	100A1	YES	transporter	CG9702	NO	676	NO	1
BG642186	1d12	0.0047	0.071	0.066	15.61	2R	48f1	YES	(Cct5) chaperone	CG8439	NO	542	NO	1
BG642187	1D2	NC	NC	-	-	X	6E4	YES	(OGRE) ion channel	CG3039	NO	362	YES	1
BG642188	1d3	NC	NC	-	-	2L	25D	NO	?	NONE	NO	41	NO	1
BG642189	1D6	NC	NC	-	-	X	14A1	YES	(EXD) transcription factor	CG8933	NO	376	NO	2
BG642190	1d7	0.0232	0.106	0.218	7.298	2L	25C10	NO	enzyme-lipase	CG14034	YES	223	NO	3
BG642191	1D8	NC	NC	-	-	2R	45D5	YES	(PDK) kinase	CG8808	NO	413	NO	1
BG642192	1e11	0.0496	0.142	0.349	5.662	2	32A	NO	?	NONE	YES	1087	YES	4
BG642193	1e12	0.0089	0.237	0.038	27.96	2L	31F5	YES	lipase	CG17101	YES	355	NO	9
BG642194	1e3	NC	NC	-	-	2L	26A-B	NO	Kr-h no ecdysone response	NONE	NO	721	NO	1
BG642195	1e4	0.0076	0.076	0.1	7.012	2R	54C9	YES	endopeptidase	CG4847	YES	390	YES	1
BG642196	1e5	0	0	0	0	3L	69C	YES	(eIF-2beta)	CG4153	NO	312	NO	1
BG642197	1E9	NC	NC	-	-	3L	70B	YES	proline rich	CG10741	NO	535	NO	1
BG642198	1f12	0.0141	0.045	0.315	2.518	2L	62A11	YES	RPL23A) ribosomal protein	CG7977	NO	277	NO	1
BG642199	1f2	0.0095	0.091	0.104	14.06	3R	87A	YES	(mfas)	CG3359	NO	816	YES	4
BG642200	1f3	0.0143	0.103	0.139	2.628	2R	56D-E	NO	?	NONE	NO	635	NO	1
BG642201	1f5	0.0026	0.162	0.016	44.69	3L	79E2	YES	(Hem)	CG5837	NO	1126	NO	1
BG642203	1g10	0.0095	0.108	0.088	9.37	2L	31F5	NO	lipase	CG17097	YES	318	NO	8
BG642204	1g11	0.0002	0.195	0.001	9.166	2R	49D1	NO	?	CG17575	NO	291	YES	2
BG642205	1g12	?	?	-	-	X	19e	NO	no good prediction	NONE	NO	?	?	1
BG642206	1g2	0.0053	0.111	0.048	26.52	3R	0E6-90F1	YES	(BcDNA:GH04120)	CG7985	NO	752	NO	1
BG642207	1g4	0.0571	0.059	0.969	0.002	X	4A2	YES	?	CG6450	NO	2799	NO	1
BG642208	1g6	0.0153	0.041	0.372	0.428	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642209	1h3	0.0141	0.15	0.094	17.33	3L	76B	YES	(Taf60)	CG9348	NO	592	NO	1
BG642210	1h5	0.0533	0.063	0.847	0.086	2R	46B10	YES	ligand binding/carrier	CG1652	NO	322	YES	1
BG642211	1H7	?	?	-	-	X	19E	NO	no good prediction	NONE	NO	?	?	1
BG642143	20	NC	NC	-	-	3R	93F	NO	ecdysone response RNA	NONE	NO	-	NO	1
BG642144	21	0.1634	0.226	0.724	0.986	2L	38E9	YES	serpin protease inhib.	CG9334	NO	341	NO	1
BG642145	22	0.0258	0.138	0.188	19.04	2L	38F4	YES	DNA repair/nuclease	CG9272	NO	308	NO	1
BG642146	23	NC	NC	-	-	3L	64B	YES	?	CG11357	NO	401	NO	1
BG642147	24	0.003	0.15	0.02	34.51	3L	66A22	YES	(RNaseX25)	CG8194	NO	325	YES	1
BG642212	25	NC	NC	-	-	3L	62	NO	?	NONE	NO	?	?	1
BG642148	27	0.038	0.142	0.267	9.772	3L	66E1	NO	?	CG13309	NO	175	YES	1

BG642149	28	0.0038	0.039	0.099	4.712	2R	60B2	YES	ribosomal protein	CG3195	NO	165	NO	1
BG642150	29	0.0199	0.117	0.17	9.812	3L	36F6	YES	(ACP36DE)	CG7157	YES	912	YES	4
BG642213	2a10	0.0568	0.178	0.32	4.762	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642215	2a6	0.0001	0.147	7E-04	25.52	2	36C-36D	YES	?	NONE	NO	1263	NO	1
BG642216	2a7	0.0214	0.092	0.234	2.666	3L	68B3	NO	?	CG6168	NO	205	NO	3
BG642217	2a9	0.004	0.384	0.01	35.66	2L	31F	YES	enzyme lipase/esterase	CG17097	YES	318	NO	8
BG642218	2b10	0.0029	0.197	0.015	40.56	2R	47E5	YES	(FPPS_farnesyl pyrophosphate syn.	CG12389	NO	419	NO	1
BG642219	2b11	0.0743	0.094	0.791	0.216	2	32A	NO	?	NONE	YES	1087	YES	4
BG642220	2b7	0.0502	0.141	0.355	4.942	3L	68B3	NO	?	CG6168	NO	205	NO	3
BG642221	2c12	0.0175	2E-04	87.5	0.796	X	15A3	YES	(if) cell adhesion	CG9623	NO	1396	YES	1
BG642222	2c3	0.0074	0.13	0.057	14.18	X	3B6	YES	(EG:95B7.3)	CG2713	NO	415	NO	1
BG642223	2c4	?	?	-	-	3R	100C	NO	no good prediction	NONE	NO	?	?	1
BG642224	2c6	0.0223	0.167	0.134	21.78	3R	94D12	YES	dehydrogenase/reductase	CG17121	NO	361	NO	1
BG642225	2d10	0.0256	0.126	0.203	5.326	2L	33A2	YES	?	CG6488	NO	570	NO	1
BG642226	2d11	0.0107	0.039	0.278	0.76	3L	68C	NO	?	NONE	NO	172	NO	1
BG642227	2d12	0.011	0.213	0.052	30.87	3L	77E6	YES	hydroxyacylglutathione hydrolase	CG4365	NO	348	NO	1
BG642228	2d7	0.0277	0.162	0.171	2.38	3L	68B3	NO	?	CG6168	NO	205	NO	3
BG642229	2d8	NC	NC	-	-	2r	50	YES	?	NONE	NO	1835	YES	1
BG642230	2e10	0.0413	0.09	0.458	2.1	3R	98E2	NO	?	CG9997	NO	330	YES	1
BG642231	2e12	0.0256	0.099	0.26	3.144	2L	34B7	YES	?	CG7110	NO	740	NO	1
BG642232	2e2	0.0284	0.015	1.856	0.346	3R	83E6	YES	trypsin inhibitor	CG10284	NO	547	YES	1
BG642233	2e4	0.0483	0.2	0.242	5.932	3R	95E8	NO	(Acp95EF)	NONE	YES	52	YES	2
BG642234	2F1	NC	NC	-	-	3R	93B	YES	(RAB11)	CG5771	NO	214	NO	1
BG642235	2f11	0.0003	0.272	0.001	55.19	3R	94B6	YES	?	CG6921	NO	322	NO	1
BG642236	2f12	0.0229	0.159	0.144	5.818	3L	79C3	NO	(msopa) male-specific opa containing	CG14560	NO	83	YES	1
BG642237	2f3	0.0253	0.118	0.215	7.088	2L	36F6	YES	(ACP36DE)	CG7157	YES	912	YES	4
BG642238	2f4	0.0051	0.111	0.046	9.764	3L	64A10	YES	(RFC40)	CG14999	NO	331	NO	1
BG642239	2f9	0.0228	2E-04	114	1.264	3L	67A-B	YES	?	NONE	NO	348	NO	1
BG642240	2g2	0.0144	0.134	0.107	15.99	2L	36A7	YES	endopeptidase	CG17331	YES	201	NO	1
BG642241	2g4	0.0671	0.071	0.941	0.012	2L	26A5	YES	?	CG9029	NO	116	YES	3
BG642242	2h1	0.0103	0.109	0.094	16.33	X	17B4	YES	glutamyltranspeptidase	CG6461	NO	561	NO	1
BG642243	2h10	0.0115	0.076	0.151	2.4	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642244	2h3	0.0528	0.046	1.145	0.014	2L	32D1	NO	(ACP32CD)	CG4605	YES	249	YES	3
BG642245	2h4	0.057	0.199	0.286	4.52	3L	62A2	NO	?	CG9168	NO	574	NO	1
BG642247	2h7	0.026	0.157	0.165	10.27	X	1C4	NO	endopeptidase	CG11664	NO	254	YES	1
BG642248	2h8	0.0144	0.087	0.166	13.1	3R	93D1	YES	NLS_BP, PCI_DOMAIN	CG5862	NO	309	NO	1
BG642152	30	0.0001	0.105	9E-04	20.04	2L	31E1	YES	(KdelR) ER-lumen retain	CG5183	NO	212	YES	1
BG642153	32	0.0002	0.196	0.001	39.93	2R	57C	YES	(mago)	CG9401	NO	147	NO	1

BG642249	3a1	0.0138	0.151	0.091	15.08	3R	89B2	YES	?	CG5516	NO	176	NO	1
BG642250	3a11	0.0002	0.153	0.001	5.512	2L	31F5	YES	esterase/lipase	CG17101	YES	355	NO	9
BG642251	3a3	0.0609	6E-04	101.5	4.38	2L	26F	NO	?	NONE	NO	53	YES	1
BG642252	3a4	0.0001	0.052	0.002	5.85	2L	27F6	YES	?	CG5177	NO	276	NO	1
BG642253	3a5	0.0546	0.173	0.316	4.918	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642254	3a6	0.0142	0.04	0.356	0.468	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642255	3a8	0.0619	0.119	0.519	1.51	X	12B9	YES	(BcDNALD21129) structural	cg11092	NO	823	NO	1
BG642256	3b3	0.0137	0.233	0.059	41.35	3L	77C4	YES	transporter/dehydratase	CG17637	NO	504	NO	1
BG642257	3b5	0.0491	0.119	0.412	3.196	2R	54A1	NO	serpin	CG10956	NO	303	NO	1
BG642258	3B8	0.0075	0.045	0.166	5.308	2R	41E3	YES	?	CG8426	NO	948	NO	1
BG642259	3c1	0.0772	0.177	0.436	4.87	2L	31F	NO	?	NONE	YES	1087	YES	1
BG642260	3c4	0.007	0.19	0.037	28.52	3R	98F6	YES	kinase	CG1951	YES	835	NO	1
BG642261	3c8	0.0232	0.071	0.325	0.562	2L	31F4	YES	enzyme lipase/esterase	CG17093	YES	731	NO	6
BG642262	3d11	0.0614	0.094	0.65	0.654	3L	77B4	YES	serpin	CG6289	YES	94	YES	2
BG642263	3d3	0	0	-	0	3R	98D5	NO	?	CG9988	NO	598	NO	1
BG642264	3d6	0.0863	0.142	0.607	0.496	X	3A7	YES	N-acetyltransferase	CG13759	NO	205	NO	2
BG642264	3d6	0.0367	0.109	0.338	0.65	X	3A7	YES	N-acetyltransferase	CG13759	NO	205	NO	2
BG642265	3d7	0.0645	0.056	1.162	0.03	2L	28-29	YES	serpin	CG8137	YES	306	YES	2
BG642266	3e1	0.0233	0.162	0.144	14.29	3L	65F3	YES	(SRP19) signal recognition particle	CG4457	NO	160	NO	3
BG642267	3e4	0.0111	0.128	0.087	23.56	X	7C7	YES	vesicle docking protein	CG1422	NO	815	NO	1
BG642268	3e6	0.1072	0.044	2.436	0.614	2L	31F4	YES	esterase/lipase	CG17093	YES	654	NO	6
BG642269	3e9	0	0.04	0	2.384	3L	72B1	YES	(PKA-C3) kinase	CG6117)	NO	233	NO	1
BG642270	3f1	0.0106	0.133	0.079	20.28	2R	51E8	NO	lipase	CG8093	NO	398	YES	1
BG642271	3f7	?	?	-	-	3R	89AB	NO	no good prediction	NONE	NO	?	?	1
BG642272	3g11	?	?	-	-	2L	38A	NO	no good prediction AE003665	NONE	NO	?	?	2
BG642273	3g3	0.0339	0.201	0.168	14.5	?	UNKOWN	YES	RNA binding	CG17540	NO	384	NO	1
BG642274	3g6	0.0232	0.106	0.218	5.156	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642276	3H5	NC	NC	-	-	2L	26A	NO	?	CG9029	NO	116	YES	3
BG642277	3h7	0.0091	0.09	0.101	8.862	X	19f2	YES	(BBX) BOBBY SOX	CG1414	NO	769	NO	1
BG642278	3h8	0.033	0.171	0.193	2.292	X	19C1	YES	(ANNX) actin binding	CG9579	NO	320	NO	1
BG642279	4a10	0.0281	0.144	0.195	5.34	X	10B14	YES	diacylglycerol kinase	CG1747	NO	641	NO	1
BG642280	4a11	0.0568	0.178	0.32	4.762	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642281	4a5	0.0175	0.017	1.023	0.002	2L	31F	YES	enzyme lipase/esterase	CG17097	YES	318	NO	8
BG642282	4a6	0	0	-	0	3R	94A	YES	?	CG5382	NO	299	NO	1
BG642283	4a8	0.0001	0.079	0.001	21.71	3R	89B3	YES	(HEL89B) DNA binding	CG4261	NO	1861	NO	1
BG642284	4a9	0.0197	0.48	0.041	17.49	3L	75D1	YES	?	CG18231	NO	374	NO	2
BG642285	4b1	0.02	0.145	0.138	4.952	2L	21C5	YES	?	CG11840	NO	389	NO	1
BG642286	4b11	0.0003	0.291	0.001	31.63	X	11E6	YES	antioxidant enzyme	CG1633	NO	194	NO	1

BG642287	4b3	0.0114	0.122	0.093	19.54	3R	97A4	YES	endopeptidase	CG6069	NO	483	YES	1
BG642288	4b5	0.0965	0.086	1.125	0.008	2L	31F5	YES	enzyme lipase/esterase	CG17097	YES	318	NO	8
BG642289	4b9	?	?	-	-	2R	51B	NO	no good prediction AE003812	NONE	NO	?	?	1
BG642290	4c11	0.0275	0.124	0.222	5.528	X	7C9	YES	?	CG2206	NO	854	YES	1
BG642291	4c4	0.0078	0.203	0.038	32.32	2R	59C3	YES	[L(2)K09913)	CG3082	NO	389	NO	1
BG642292	4c9	0.0001	0.058	0.002	10.27	2L	21C2	YES	(RPP2) ribosomal	CG4087	NO	112	NO	1
BG642293	4d10	0.0001	0.067	0.001	2.254	3R	89B	NO	?	CG14879	NO	178	NO	1
BG642294	4d11	0.0499	0.033	1.503	0.134	2R	55B7	YES	?	CG16803	NO	42	NO	2
BG642295	4d7	0.0114	0.076	0.151	5.432	3R	93F10	YES	thioredoxin	CG17843	NO	552	YES	2
BG642296	4d9	0.0322	0.144	0.224	5.53	2L	26A5	NO	(ACP26Ab)	CG9024	YES	90	YES	1
BG642297	4e1	0.007	0.017	0.412	0.362	2R	55C	YES	?	CG5544	NO	404	NO	2
BG642298	4e10	0.0149	0.071	0.21	6.638	2L	37F1	NO	alpha-macroglobulin	CG10363	NO	1425	NO	1
BG642299	4E3	NC	NC	-	-	2L	33B	NO	(CROL)	CG14938	NO	934	NO	1
BG642300	4F12	NC	NC	-	-	3R	85E	YES	(SCM) transcription factor	CG9495	NO	877	NO	2
BG642300	4f12	0.0058	0.043	0.136	4.144	3R	85E2	YES	(SCM) transcription factor	CG9495	NO	877	NO	2
BG642301	4f2	0.127	0.082	1.549	0.154	3L	65F3	YES	(SRP19) signal recognition particle	CG4457	NO	160	NO	3
BG642302	4f5	0.0247	0.226	0.109	18.93	2L	31F5	YES	enzyme lipase/esterase	CG17101	YES	355	NO	9
BG642303	4f6	?	?	-	-	3R	93A	NO	no good prediction	NONE	NO	?	?	1
BG642304	4F7	NC	NC	-	-	2L	31B	YES	(SUR) receptor	CG5772	NO	2250	YES	1
BG642305	4F8	NC	NC	-	-	2R	55C	NO	?	CG16859	NO	109	NO	1
BG642306	4f9	NC	NC	-	-	3R	79D	NO	(msopa) male-specific opa containing	CG14560	NO	83	YES	1
BG642307	4g11	0.0053	0.084	0.063	6.534	2L	25B10	YES	?	CG8895	NO	234	NO	1
BG642308	4g2	0.0002	0.215	9E-04	22.18	2L	24C3	YES	tubulinyl--tyrosine ligase	CG3964	NO	989	NO	1
BG642309	4g3	0.039	0.2	0.195	10.06	3L	65F3	YES	(SRP19) signal recognition particle	CG4457	NO	160	NO	3
BG642310	4g4	NC	NC	-	-	3R	87A	YES	(mfas)	CG3359	NO	816	YES	4
BG642311	4g9	0.0152	0.198	0.077	22.11	3R	89B12	NO	sugar transporter	CG8925	NO	670	NO	1
BG642312	4h1	0.0616	0.361	0.17	3.322	3L	65A-B	NO	?	NONE	YES	71	NO	1
BG642313	4h10	0.004	0.144	0.028	19.23	2R	60A5	YES	(GBB) signal transduction TGF-beta	CG5562	NO	455	YES	1
BG642314	4h11	0.0179	0.114	0.157	11.79	X	19E7	NO	ABC transporters	CG1819	NO	1500	NO	1
BG642315	4h12	0.0146	0.136	0.108	12.87	2R	46B10	YES	C-type lectin	CG1656	NO	328	YES	2
BG642316	4h3	0.0361	0.115	0.314	3.944	2L	36F6	YES	(ACP36DE)	CG7157	YES	912	YES	4
BG642317	4h6	0.0331	3E-04	110.3	2.762	3R	87C1	YES	?	CG5333	NO	485	NO	1
BG642318	4h8	0.0277	0.11	0.251	7.224	2L	31F5	YES	esterase/lipase	CG17101	YES	388	NO	9
BG642319	5a2	0.0098	0.155	0.063	23.27	X	11B	YES	(SMR) defense/immune response	CG4013	NO	3469	NO	1
BG642320	5a3	0.0689	0.191	0.361	3.796	3R	100B4	YES	(Aph-4) alkaline phosphatase	CG1462	YES	596	YES	1
BG642321	5a5	0.011	0.064	0.172	2.122	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642322	5A7	NC	NC	-	-	2R	47C	NO	?	CG12341	NO	815	NO	1
BG642155	5a9	0.0142	0.04	0.356	0.468	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17

BG642323	5B1	NC	NC	-	-	2L	33B	YES	?	CG6770	NO	69	NO	1
BG642162	5b11	0.1268	0.106	1.201	0.158	2L	26A5	NO	(Acp26Aa)	CG8982	YES	264	YES	4
BG642324	5b2	?	?	-	-	3L	65	NO	no good prediction AE003562	NONE	NO	?	?	1
BG642326	5b7	0.0151	0.081	0.186	7.476	3R	95F10	YES	thioredoxin	CG6690	YES	562	YES	1
BG642327	5b8	0.0255	0.218	0.117	25.74	3R	87C5	NO	lipase	CG11598	NO	318	NO	1
BG642328	5c2	0.0139	0.038	0.363	1.454	2L	33B2	YES	kazal	CG14942	NO	582	YES	1
BG642329	5c3	0.034	0.045	0.759	0.218	2R	46B10	YES	C-type lectin	CG1656	NO	328	YES	2
BG642330	5c4	0.1237	0.217	0.57	2.524	2	32A	NO	?	NONE	YES	1087	YES	4
BG642331	5c6	0.0001	0.136	7E-04	31.58	3L	75E2	YES	(CH1-2) endopeptidase	CG3889	NO	525	NO	1
BG642332	5c7	0.0292	0.043	0.676	0.178	2L	25C10	NO	esterase/lipase	CG14034	YES	223	NO	3
BG642333	5c8	0.0072	0.202	0.036	32.06	2L	31F5	YES	lipase	CG17101	YES	355	NO	9
BG642334	5d2	0.0396	0.092	0.431	2.442	2R	46B	YES	?	CG1623	NO	456	NO	1
BG642335	5d3	0.0254	0.183	0.139	12.91	3R	84C4	YES	?	CG2640	NO	491	NO	1
BG642336	5d4	0.0001	0.071	0.001	8.71	3R	94F1	YES	(RPS3) ribosomal	CG6779	NO	246	NO	1
BG642337	5d6	0.0037	0.028	0.133	2.788	3L	79C2	YES	(BcDNA:LD21293)	CG7139	NO	969	NO	1
BG642339	5d7	0.0001	0.061	0.002	11.1	3R	85E	YES	?	CG9471	YES	204	NO	1
BG642340	5e1	?	?	-	-	3L	72	NO	no good prediction AE003529	NONE	NO	?	?	1
BG642341	5e3	0.0039	0	-	0.382	3L	68B1	YES	?	CG7590	YES	280	NO	1
BG642342	5E5	NC	NC	-	-	2R	46E	YES	(14-3-3ZETA) enzyme inhibitor	CG17870	NO	145	NO	1
BG642343	5e6	0.0001	0.123	8E-04	22.47	3R	94B-C	YES	(loco) reg. G-protein signaling	CG5248	YES	1175	NO	1
BG642344	5e7	0.061	0.035	1.743	0.57	2R	49E1	YES	(MDR49) ABC transporters	CG3879	NO	1279	NO	1
BG642346	5f2	0.0232	0.126	0.185	6.756	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642347	5f3	0.0502	0.033	1.521	0.14	2R	55B7	YES	?	CG16803	NO	42	NO	2
BG642348	5f5	0.0114	0.064	0.18	2.026	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642349	5g1	0.0002	0.159	0.001	20.78	3L	62F	YES	(RPL8) ribosomal	CG1263	NO	256	NO	1
BG642350	5g4	0.0002	0.237	8E-04	38.08	3R	94F	YES	(BcDNA:LD03471) transport vesicles	CG6773	NO	356	NO	1
BG642351	5g6	0.0032	0.131	0.024	23.84	3L	68D3	YES	nitrate reductase	CG5946	NO	313	YES	1
BG642352	5g7	0.0034	0.112	0.03	14.59	X	5A12	YES	ribosomal protein	CG4111	NO	121	NO	1
BG642190	5h10	0.0222	0.099	0.224	7.086	2L	25C10	NO	lipase	CG14034	YES	223	NO	3
BG642354	5h4	0.042	0.279	0.15	14.39	2L	31F5	YES	lipase	CG17101	YES	355	NO	9
BG642355	5h6	0.0211	0.045	0.469	0.966	2R	56D11	YES	(SM) RNA binding	CG9218	NO	475	NO	1
BG642356	6a1	0.0766	0.107	0.715	0.7	2L	26A5	YES	?	CG9029	NO	116	YES	3
BG642357	6A3	NC	NC	-	-	2R	55C	NO	?	CG5544	NO	404	NO	2
BG642358	6a4	0.0106	0.083	0.128	1.798	2L	31F5	YES	lipase	CG17101	YES	355	NO	9
BG642359	6a7	0.014	0.082	0.17	4.878	3R	93F10	YES	thioredoxin	CG17843	NO	552	YES	2
BG642360	6b1	0.0002	0.195	0.001	50.08	3R	87A	YES	(MFAS) signal transduction	CG3359	NO	816	YES	4
BG642156	6b2	0.0671	0.129	0.519	1.54	2L	31F	YES	lipase	CG17093	YES	654	NO	6
BG642361	6b3	0.0049	0.068	0.072	7.23	3L	73C1	YES	translation factor (Int6)	CG9677	NO	45	NO	1

BG642362	6b5	0.0067	0.039	0.17	2.212	2R	57F	YES	?	CG10433	NO	127	YES	1
BG642138	6b7	0.006	0.138	0.043	25.74	2L	31F5	YES	lipase	CG17101	YES	355	NO	9
BG642310	6b8	0.0092	0.165	0.056	26.26	3R	87A	YES	(mfas)	CG3359	NO	816	YES	4
BG642363	6c6	0.0001	0.068	0.001	13.2	3R	96B10	YES	(MAP-kinase-phosphatase)	CG6238	NO	319	NO	1
BG642364	6c7	0.068	0.131	0.52	1.626	2L	31F	YES	lipase	CG17093	YES	731	NO	6
BG642162	6d11	0.0943	0.289	0.326	1.478	2L	26A5	NO	(Acp26Aa)	CG8982	YES	264	YES	4
BG642366	6d6	0.005	0.09	0.055	11.99	2L	30C7	YES	?	CG4364	NO	627	NO	1
BG642367	6d7	0.08	8E-04	100	4.916	3L	77B4	YES	serpin	CG6289	YES	94	YES	2
BG642368	6e1	0.0085	0.234	0.036	42.8	3L	79B2	YES	DNA repair	CG7143	NO	885	NO	1
BG642369	6e4	0.0001	0.089	0.001	21.53	2L	34D	YES	(BG:DS00797.7) guan. Nucl. Exch.	CG7578	NO	1643	NO	1
BG642370	6e5	0.1433	0.117	1.227	0.266	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642156	6e5	0.1542	0.147	1.049	0.008	2L	31F	YES	lipase	CG17093	YES	731	NO	6
BG642371	6E7	NC	NC	-	-	2L	32B	YES	(DNZ1) transcription	CG6627	NO	276	YES	1
BG642373	6f2	0.0889	0.09	0.993	0	2L	36F	YES	(ACP36DE)	CG7157	YES	912	YES	4
BG642374	6f3	0.0133	0.015	0.864	0.012	2L	32D	NO	(Acp32CD)	CG4605	YES	249	YES	3
BG642375	6f4	0.0282	0.118	0.238	8.112	2L	35D	YES	(BG:BACR44L22.8) endopepidase	CG11864	NO	251	YES	1
BG642244	6f5	0.0472	0.041	1.146	0.028	2L	32D	NO	(Acp32CD)	CG4605	YES	249	YES	3
BG642162	6f9	0.1281	0.109	1.178	0.128	2L	26A5	NO	(Acp26Aa)	CG8982	YES	264	YES	4
BG642162	6g11	0.1228	0.1	1.232	0.206	2L	26A5	NO	(Acp26Aa)	CG8982	YES	264	YES	4
BG642377	6g2	0.0142	0.04	0.356	0.468	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642243	6g7	0.0115	0.084	0.137	2.608	3R	96F3	YES	(Mst57Da)	CG9074	YES	75	YES	17
BG642378	6h1	0.0717	0.126	0.571	1.68	3L	76	NO	?	NONE	YES	445	YES	1
BG642204	6h10	0.0002	0.159	0.001	17.23	2R	49D	NO	?	CG17575	NO	291	YES	2
BG642173	6h9	0.0241	0.131	0.184	6.532	2L	31F5	YES	lipase	CG17097	YES	318	NO	8
BG642389	7a1	0.0257	0.397	0.065	19.3	2L	31F	YES	lipase	CG17097	YES	318	NO	8
BG642379	7b1	0	0	-	0	2R	47AB	YES	(psq) transcription	CG2368	NO	136	NO	1
BG642380	7c1	0.0133	0.098	0.135	3.334	3R	99A	NO	(RPN2) endopeptidase	CG11888	NO	1020	NO	1
BG642381	7d1	0.0438	0.026	1.678	0.24	3L	61D3	YES	?	CG13887	NO	228	NO	1
BG642384	7d3	0.0729	7E-04	104.1	4.228	2L	31F	YES	?	CG18284	NO	356	NO	2
BG642387	7d7	0.0269	0.061	0.438	1.278	X	1E	YES	(SU9W[A]) RNA bindin	CG3019	NO	1041	NO	1
BG642382	7e1	0	0.038	0	1.792	3R	98E2	NO	?	CG9997	NO	330	YES	1
BG642390	7e3	0.0589	6E-04	98.17	1.4	4	102B	YES	(Bip-2)	CG2009	NO	1406	NO	1
BG642386	7e6	0.0452	0.045	1.011	0	2L	26D	YES	transport protein	CG9539	NO	423	NO	1
BG642385	7f5	0	0	-	0	3R	85D	YES	(methyl-CpG-bind-dom.-like-protein)	CG8208	NO	314	NO	1
BG642388	7f7	0.0001	0.058	0.002	8.864	2L	29D	YES	(ACER) peptidase	CG10593	NO	630	NO	1
BG642383	7h1	0.0154	0.105	0.147	2.444	3R	96F	YES	(MST57D)	CG9074	YES	75	YES	17

Supplementary material legend.

Acc. #: GenBank dbEST accession number.

EST: identification number of the EST clone.
dN: Maximum likelihood estimate nonsynonymous substitution per nonsynonymous site; NC indicates non-coding; ? indicates unknown
dS: : Maximum likelihood estimate of synonymous substitution per synonymous site; NC indicates non-coding; ? indicates unknown.
dN/dS: ratio of dN to dS as a measure of the selective force; - indicates no calculation (noncoding); infinite for divided by 0; ? indicates unknown.
-2Dl: negative of twice the log likelihood between null model and free estimates of dN and dS; - for no calculation (noncoding); ? indicates unknown.
Arm: Chromosome arm location of gene
Map: Map location of gene: ? indicates unknown.
dbEST: YES for gene being present in other EST databases, NO for not in other EST databases.
(Gene) Function: Gene name is parenthesis, function listed based on GadFly; ? indicates unknown.
CG #: Gene number from GadFly; NONE for no CG number
AG En.: YES if identified as Acp based on DTA-E/wild type differential hybridization screen; NO for non-differential
AAs: Length of the predicted amino acid sequence; ? indicates unknown
S. Seq: YES for predicted signal sequence, NO for no predicted signal sequence; ? indicates unknown
Hits: Number of times gene identified in our ESTs.