Title page for S2 Table
The title of : Transcriptomic comparison between beetle strains selected formanuscript short and long durations of death feigning.
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S2 Table. List of differentially expressed genes between the L and S strains.

#	LOC name	Region	Gene ID	Description	FPKM for L	FPKM for S	log2(Fold change+1)	P-value	FDR
1	LOC107398286	NC_007417.3:1379768-1380361	107398286	uncharacterized LOC107398286	52.2821	0.502158	5.148542473	0.00105	0.0470692
2	-	NW_015452025.1:2991-3878	-	-	25.5962	0.26362	4.39558555	0.0006	0.0297494
3	P41	NC_007418.3:10353706-10354992	661254	serine protease P41	85.9659	1.24604	5.274994294	5.00E-05	0.00352415
4	LOC657769	NW_015451510.1:1505-3305	657769	facilitated trehalose transporter Tret1	19.1283	0.688605	3.575321534	5.00E-05	0.00352415
5	LOC660420	NC_007423.3:9398892-9400590	660420	equilibrative nucleoside transporter 3	23.1626	1.15738	3.485423484	5.00E-05	0.00352415
6	LOC664395	NC_007417.3:8685030-8689026	664395	alpha-amylase-like	6.53327	0.42944	2.397826173	5.00E-05	0.00352415
7	LOC655017	NW_015450971.1:3368-5214	655017	moesin/ezrin/radixin homolog 1	7.75219	0.692362	2.370605861	5.00E-05	0.00352415
8	LOC655071	NC_007423.3:4594602-4595685	655071	uncharacterized LOC655071	2.7097	0.244532	1.575699196	0.0009	0.0416491
9	LOC103312472	NC_007418.3:25460046-25495251	103312472	uncharacterized LOC103312472	28.4757	2.9537	2.898250764	5.00E-05	0.00352415
10	H115	NC_007420.3:1471291-1478664	657133	serine protease H115	11.7177	1.23055	2.511366389	0.00085	0.0395751
11	-	NC_007423.3:54121-55236	-	-	12.8197	1.37677	2.539652092	5.00E-05	0.00352415
12	LOC103314782	NW_015450575.1:82793-86861	103314782	uncharacterized	109.221	13.0229	2.97454248	5.00E-05	0.00352415
13	LOC657849	NW_015451510.1:6335-7969	657849	facilitated trehalose transporter Tret1	10.8051	1.29803	2.360940725	5.00E-05	0.00352415
14	LOC100142014	NW_015452111.1:26-1007	100142014	uncharacterized LOC100142014	4.30895	0.552973	1.773393807	5.00E-05	0.00352415
15	LOC103314746	NC_007422.5:7413296-7414494	103314746	uncharacterized LOC103314746	6.57533	0.84491	2.037758298	5.00E-05	0.00352415
16	LOC103312957	NC_007420.3:5088956-5091766	103312957	adhesion G-protein coupled receptor G2	3.29397	0.450013	1.566246277	5.00E-05	0.00352415
17	LOC103312900	NC_007420.3:3289609-3290934	103312900	uncharacterized LOC103312900	10.0159	1.39886	2.1991665	5.00E-05	0.00352415
18	En	NC_007422.5:12546768-12551040	661645	engrailed	1.75671	0.246453	1.145119023	0.0001	0.00663971
19	-	NC_007417.3:5261973-5262712	-	-	6.67451	0.964678	1.965781759	0.00015	0.00949185
20	LOC103312546	NC_007419.2:733210-738581	103312546	uncharacterized LOC103312546	4.68397	0.709	1.733746543	0.00015	0.00949185
21	p98; p97	NC_007422.5:7350928-7355730	662682	serine protease P98	110.405	16.9	2.637782492	5.00E-05	0.00352415
22	LOC658555	NC_007416.3:1023768-1025032	658555	phospholipase A1	40.6537	6.27272	2.517877714	5.00E-05	0.00352415
23	LOC103314809	NC_007423.3:48118-53973	103314809	hypothetical protein	0.901306	0.148064	0.727787672	5.00E-05	0.00352415
24	P162	NC_007421.3:3491859-3492749	658877	serine protease P162	324.702	54.0901	2.563687592	5.00E-05	0.00352415
25	LOC657602	NC_007418.3:11094440-11095409	657602	glutathione S-transferase	92.1045	15.5342	2.493397656	5.00E-05	0.00352415
26	P167	NW_015451646.1:123355-125194	655811	brachyurin	133.333	22.6791	2.504127605	5.00E-05	0.00352415
27	LOC658800	NC_007421.3:215514-217461	658800	fatty acyl-CoA reductase 1	3.83549	0.721094	1.490336197	5.00E-05	0.00352415
28	-	NC_007420.3:3291809-3294329	-	-	8.07394	1.54969	1.83140727	0.00075	0.0357178
29	LOC103313637	NC_007422.5:8621702-8632850	103313637	uncharacterized LOC103313637	3.94685	0.779097	1.475364983	0.0002	0.0120247
30	LOC103312194	NC_007417.3:14780923-14782632	103312194	uncharacterized LOC103312194	279.889	56.7282	2.282651981	5.00E-05	0.00352415
31	LOC103314784	NC_007417.3:13814650-13958477	103314784	choline transporter-like protein 1	15.1393	3.08012	1.983894518	0.00105	0.0470692
32	-	NC_007422.5:15644810-15650547	-	-	1.55942	0.336451	0.937409969	5.00E-05	0.00352415
33	H106	NC_007420.3:1492710-1493841	657444	serine protease H106	36.19	7.84701	2.071652889	5.00E-05	0.00352415
34	LOC655001	NC_007422.5:1534305-1564073	655001	cytochrome P450 4C1	325.439	71.757	2.165655465	5.00E-05	0.00352415
35	LOC103314085	NC_007423.3:12238186-12238830	103314085	uncharacterized LOC103314085	41.5406	9.34823	2.039456357	5.00E-05	0.00352415
36	-	NC_007418.3:16224511-16225266	-	-	5.56382	1.25218	1.54321354	0.0003	0.0169681
37	LOC103314667	NW_015451779.1:18-981	103314667	RNA-directed DNA polymerase from mobile element jockey-like	75.816	17.1427	2.082017667	5.00E-05	0.00352415
38	-	NW_015450592.1:2313-2963	-	-	18.8732	4.35037	1.893113627	5.00E-05	0.00352415

39	-	NW_015451028.1:939-1324	-	-	52.9167	12.2117	2.028916083	5.00E-05	0.00352415
40	LOC661967	NC_007419.2:10352167-10455479	661967	UDP-glucuronosyltransferase 2B20	177.795	42.1197	2.051887346	5.00E-05	0.00352415
41	LOC100142031	NC_007423.3:6587154-6588963	100142031	sulfhydryl oxidase 2	8.20063	1.98056	1.626149235	5.00E-05	0.00352415
42	LOC659565	NC_007425.3:6902757-6908923	659565	cathepsin L precursor	1.93697	0.475683	0.992945688	0.00065	0.0319518
43	LOC660784	NC_007422.5:4982936-4984551	660784	translation initiation factor IF-2	4.01513	0.999779	1.326446525	0.00025	0.014684
44	LOC107397485	NC_007418.3:2823010-2827641	107397485	uncharacterized LOC107397485	2.77274	0.714714	1.137644713	0.00085	0.0395751
45	LOC664406	NC_007419.2:5876706-5879343	664406	double-stranded RNA-binding protein Staufen homolog 2	13.9026	3.62987	1.686520464	5.00E-05	0.00352415
46	LOC107399160	NW_015451916.1:2097-6354	107399160	uncharacterized LOC107399160	12.0641	3.16001	1.650948838	5.00E-05	0.00352415
47	LOC107397936	NC_007420.3:1468245-1469916	107397936	brachyurin-like	9.28293	2.43156	1.583314917	5.00E-05	0.00352415
48	LOC658629	NW_015451776.1:33994-49469	658629	excitatory amino acid transporter	38.19	10.2554	1.799868244	5.00E-05	0.00352415
49	LOC103314558	NW_015451937.1:352665-366702	103314558	uncharacterized LOC103314558	4.35173	1.1733	1.300117996	0.0001	0.00663971
50	-	NC_007420.3:12858-13232	-	-	16.973	4.59116	1.684611704	0.0002	0.0120247
51	LOC661353	NC_007416.3:4610333-4618961	661353	IQ motif and SEC7 domain-containing protein 1	9.46672	2.56825	1.552520807	0.00065	0.0319518
52	LOC103313572	NC_007422.5:6600363-6601159	103313572	uncharacterized LOC103313572	5.6366	1.53145	1.390480334	0.0004	0.0218162
53	LOC664571	NC_007422.5:9814138-9816152	664571	beta-hexosaminidase subunit alpha	28.4495	7.88636	1.728578646	5.00E-05	0.00352415
54	LOC103314151	NC_007418.3:31269917-31273035	103314151	caspase-1-like	124.418	35.081	1.79743319	5.00E-05	0.00352415
55	CYP6BK14	NC_007421.3:2191548-2200968	658048	cytochrome P450 6a9	30.1745	8.58782	1.701091692	5.00E-05	0.00352415
56	LOC107398944	NW_015450750.1:304-5356	107398944	uncharacterized LOC107398944	13.3049	3.79053	1.57825223	5.00E-05	0.00352415
57	LOC100141724	NC_007420.3:9455633-9460403	100141724	uncharacterized LOC100141724	13.3521	3.82245	1.573423662	5.00E-05	0.00352415
58	Cht11	NC_007422.5:3380907-3384466	661649	chitinase 11	160.253	46.7731	1.7550556	5.00E-05	0.00352415
59	LOC662574	NC_007420.3:4834999-4845524	662574	multidrug resistance-associated protein 4	16.9259	4.99384	1.580493076	5.00E-05	0.00352415
60	LOC654890	NC_007424.3:9-2543	654890	condensin complex subunit 2	1.89934	0.561078	0.893181901	0.00015	0.00949185
61	LOC103314327	NC_007424.3:13863233-13864178	103314327	uncharacterized LOC103314327	33.4387	9.8932	1.66060286	0.0001	0.00663971
62	LOC657270	NC_007421.3:3334661-3340656	657270	farnesol dehydrogenase	6.1236	1.86657	1.313281	5.00E-05	0.00352415
63	LOC107399097	NW_015451667.1:314-924	107399097	uncharacterized LOC107399097	32.5255	10.2772	1.571849941	0.0001	0.00663971
64	Ctlp-6a	NC_007423.3:9384852-9386634	660544	chymotrypsin-like proteinase 6A precursor	580.719	183.663	1.655427596	5.00E-05	0.00352415
65	H112	NC_007420.3:1445095-1446291	656795	serine protease H112	711.659	227.474	1.641181929	5.00E-05	0.00352415
66	LOC656564	NW_015450233.1:639257-647866	656564	alanine--glyoxylate aminotransferase 2-like	305.798	98.3532	1.626650738	5.00E-05	0.00352415
67	LOC100142621	NC_007424.3:5810259-5814549	100142621	uncharacterized LOC100142621	5.36544	1.72632	1.223305334	5.00E-05	0.00352415
68	LOC662738	NC_007422.5:491494-493570	662738	tenecin-3	3764.71	1211.94	1.634413714	5.00E-05	0.00352415
69	LOC103313776	NC_007423.3:2629468-2630331	103313776	39S ribosomal protein L34, mitochondrial	97.6414	31.5248	1.60065309	5.00E-05	0.00352415
70	LOC107397745	NC_007419.2:5039546-5040153	107397745	putative glycine-rich cell wall structural protein 1	8.79459	2.86334	1.342136453	0.0006	0.0297494
71	H110	NC_007420.3:1394616-1395757	656549	serine protease H110	71.2404	23.2313	1.575934074	5.00E-05	0.00352415
72	LOC655516	NC_007418.3:26705775-26718077	655516	CYCLE	4.22001	1.38464	1.130281086	5.00E-05	0.00352415
73	LOC103312887	NC_007420.3:28067-61231	103312887	uncharacterized LOC103312887	3.13478	1.03691	1.021428333	5.00E-05	0.00352415
74	Pmp5-a	NC_007418.3:628675-630154	662504	peritrophic matrix protein 5-A	1511.45	508.411	1.569985431	5.00E-05	0.00352415
75	LOC100141997	NC_007421.3:3075173-3079776	100141997	uncharacterized LOC100141997	19.0399	6.49399	1.419069352	5.00E-05	0.00352415
76	LOC103312772	NW_015451146.1:6-6203	103312772	uncharacterized LOC103312772	3.53287	1.22614	1.025880461	5.00E-05	0.00352415
77	LOC663233	NC_007422.5:13636232-13653424	663233	beta-mannosidase-like	50.9604	18.1518	1.439932545	5.00E-05	0.00352415
78	LOC662265	NC_007422.5:13799677-13816250	662265	40S ribosomal protein S20	3012.95	1073.82	1.487560411	5.00E-05	0.00352415
79	LOC657457	NW_015450689.1:72670-73558	657457	pathogenesis-related protein 5	967.362	355.99	1.439662805	5.00E-05	0.00352415
80	LOC662599	NC_007417.3:12004643-12007708	662599	protein Malvolio	25.8335	9.62938	1.335977795	5.00E-05	0.00352415
81	OBP02; TcOBP6E	NC_007421.3:4270904-4271453	103313402	uncharacterized LOC103313402	103.94	38.8519	1.396844281	5.00E-05	0.00352415
82	LOC661631	NC_007419.2:7874608-7876123	661631	lipase 1	272.785	102.308	1.406091429	5.00E-05	0.00352415

83	LOC663761	NC_007417.3:7304084-7351652	663761	neurotrimin	35.0154	13.1762	1.345143065	5.00E-05	0.00352415
84	LOC663779	NC_007422.5:11443752-11445913	663779	armadillo repeat-containing protein 6 homolog	16.9436	6.38819	1.280176492	5.00E-05	0.00352415
85	LOC103312285	NC_007418.3:2814876-2817198	103312285	hypothetical protein	21.085	7.98635	1.297259674	0.0003	0.0169681
86	LOC660599	NC_007420.3:9972389-9981631	660599	multidrug resistance-associated protein 4	10.7592	4.10827	1.202883228	0.00055	0.0281853
87	LOC103313234	NC_007420.3:14373667-14374332	103313234	uncharacterized LOC103313234	12.3884	4.79116	1.209059298	0.0008	0.037707
88	Lyz	NC_007418.3:24192177-24210829	658610	lysozyme	366.166	143.561	1.344754079	5.00E-05	0.00352415
89	LOC107398028	NC_007420.3:13176967-13177792	107398028	odorant binding protein 26	77.534	30.5099	1.317512204	5.00E-05	0.00352415
90	LOC655392	NC_007418.3:11409032-11418268	655392	protein henna	80.6237	31.9052	1.310672519	5.00E-05	0.00352415
91	LOC656754	NC_007418.3:27903750-28035531	656754	lysosomal alpha-mannosidase	122.125	48.332	1.319528042	0.0002	0.0120247
92	LOC655801	NC_007424.3:1353531-1382237	655801	high affinity cationic amino acid transporter 1	17.9432	7.1147	1.223070396	0.0002	0.0120247
93	LOC659891	NC_007422.5:3955419-3957350	659891	forkhead box protein D3	10.3091	4.10524	1.147433432	5.00E-05	0.00352415
94	-	NC_007418.3:16223589-16224312	-	-	9.77493	3.92195	1.13037659	0.00035	0.0194127
95	-	NW_015452251.1:11-762	-	-	81.3587	32.9418	1.278857982	5.00E-05	0.00352415
96	LOC103313070	NC_007420.3:9963200-9966670	103313070	multidrug resistance-associated protein 4	6.60952	2.67779	1.048966348	0.0003	0.0169681
97	LOC103313186	NC_007420.3:11563173-11563908	103313186	hypothetical protein	34.7562	14.0855	1.245030907	5.00E-05	0.00352415
98	Gpa2	NC_007424.3:11271960-11272443	659603	glycoprotein hormone alpha 2	16.3984	6.70151	1.175741397	0.0011	0.0486442
99	LOC661035	NC_007417.3:11485320-11487090	661035	sorbitol dehydrogenase	51.8167	21.1846	1.251435624	5.00E-05	0.00352415
100	LOC662228	NC_007422.5:12036815-12038954	662228	aromatic amino acid aminotransferase DDB_G0287711	125.95	52.1341	1.25655045	5.00E-05	0.00352415
101	LOC655628	NC_007424.3:14524749-14529705	655628	retinol dehydrogenase 11	99.6015	41.2924	1.250181479	5.00E-05	0.00352415
102	LOC661309	NC_007425.3:4272561-4275637	661309	double-stranded RNA-specific editase Adar	14.3085	5.9376	1.141824361	5.00E-05	0.00352415
103	LOC103313095	NC_007420.3:8434484-8435463	103313095	hypothetical protein	697.355	290.265	1.261628249	5.00E-05	0.00352415
104	LOC655554	NC_007423.3:630271-638678	655554	Niemann-Pick C1 protein	56.7915	23.7143	1.225511271	5.00E-05	0.00352415
105	LOC661924	NC_007420.3:4623499-4626668	661924	rhodopsin 1/6-like	1611.69	674.602	1.255223638	5.00E-05	0.00352415
106	LOC662513	NC_007420.3:13424740-13425890	662513	endocuticle structural glycoprotein SgAbd-8	95.3982	40.6846	1.209491717	5.00E-05	0.00352415
107	LOC656188	NC_007420.3:14740830-14742118	656188	regucalcin	46.2716	19.7615	1.187063015	5.00E-05	0.00352415
108	Cpap3-d2	NC_007417.3:14931519-14937394	662181	cuticular protein analogous to peritrophins 3-D2	25.2063	10.9014	1.138782385	5.00E-05	0.00352415
109	LOC103313294	NC_007418.3:19307486-19310005	103313294	uncharacterized LOC103313294	12.443	5.38244	1.074675157	5.00E-05	0.00352415
110	LOC661007	NC_007423.3:13829831-13837015	661007	sodium-independent sulfate anion transporter	21.4903	9.34143	1.120867212	5.00E-05	0.00352415
111	LOC655199	NC_007420.3:3549348-3550655	655199	putative thiosulfate sulfurtransferase, mitochondrial	16.0454	6.98422	1.094159076	5.00E-05	0.00352415
112	CYP301B1	NC_007419.2:8147128-8149464	662872	cytochrome P450 301B1	6.34127	2.78836	0.954456229	0.00035	0.0194127
113	LOC100142166	NC_007424.3:15004201-15015166	100142166	sortilin-related receptor	9.50901	4.18693	1.018673962	5.00E-05	0.00352415
114	Cda2	NC_007420.3:5690326-5696317	657879	chitin deacetylase 2	16.8791	7.48447	1.075377669	5.00E-05	0.00352415
115	-	NW_015451937.1:344610-351959	-	-	9.82392	4.37748	1.009220922	5.00E-05	0.00352415
116	LOC662282	NC_007416.3:5004669-5011572	662282	protein dispatched	10.8431	4.84512	1.018742216	0.0004	0.0218162
117	-	NC_007425.3:5090887-5094023	-	-	274.109	124.066	1.1373137	0.0003	0.0169681
118	LOC655432	NC_007418.3:26698761-26702399	655432	purine nucleoside phosphorylase	145.397	65.8867	1.130094716	5.00E-05	0.00352415
119	LOC103314416	NC_007425.3:4177500-4180560	103314416	major facilitator superfamily domain-containing protein 9	29.5831	13.4365	1.083013634	0.0005	0.0259129
120	LOC656943	NC_007421.3:100388-102720	656943	putative fatty acyl-CoA reductase CG5065	26.1632	11.921	1.071935719	0.00035	0.0194127
121	LOC660051	NC_007421.3:9329348-9338327	660051	facilitated trehalose transporter Tret1	62.3055	28.6112	1.09618789	0.0001	0.00663971
122	LOC662799	NC_007420.3:13454931-13455834	662799	cuticular protein	91.3492	41.9589	1.104142411	5.00E-05	0.00352415
123	-	NC_007422.5:3374943-3376651	-	-	38.266	17.5895	1.078792672	5.00E-05	0.00352415
124	LOC655457	NC_007424.3:19100-23233	655457	facilitated trehalose transporter Tret1	26.5642	12.3113	1.050144257	5.00E-05	0.00352415
125	LOC100124592	NC_007418.3:10621195-10631319	100124592	aspartate 1-decarboxylase	11.4935	5.3873	0.96789958	5.00E-05	0.00352415
126	LOC103313511	NC_007422.5:497209-497796	103313511	ctenidin-1	34.4555	16.3957	1.027278708	0.00045	0.0239168

127	LOC661923	NC_007419.2:7888979-7890342	661923	lipase 3-like	188.429	90.0108	1.057547551	5.00E-05	0.00352415
128	LOC657931	NW_015451510.1:9032-14230	657931	facilitated trehalose transporter Tret1-2 homolog	119.599	57.1615	1.052081562	5.00E-05	0.00352415
129	LOC658392	NC_007418.3:19715813-19736503	658392	proton-coupled amino acid transporter 1	73.4753	35.3597	1.034421734	5.00E-05	0.00352415
130	LOC661878	NC_007419.2:7884209-7887092	661878	lipase 3-like	354.717	171.129	1.047239743	5.00E-05	0.00352415
131	LOC661764	NC_007422.5:5957498-5967074	661764	ninjurin-2	120.025	58.0114	1.036239504	5.00E-05	0.00352415
132	P96	NC_007422.5:3177207-3178319	658137	brachyurin	265.291	128.431	1.040820471	5.00E-05	0.00352415
133	-	NW_015451163.1:58-971	-	-	11.1149	5.39036	0.922813384	0.00085	0.0395751
134	UV-opsin	NC_007418.3:10911917-10954172	658900	opsin, ultraviolet-sensitive	151.282	73.4773	1.031872745	5.00E-05	0.00352415
135	LOC664194	NC_007418.3:6596632-6599094	664194	probable ATP-dependent RNA helicase DDX52	8.08049	3.92701	0.88205775	0.0005	0.0259129
136	LOC662658	NC_007424.3:13443648-13448593	662658	4-hydroxyphenylpyruvate dioxygenase	517.829	254.711	1.020744899	5.00E-05	0.00352415
137	LOC656983	NC_007422.5:6833385-6834282	656983	hypothetical protein	691.433	340.564	1.019518556	5.00E-05	0.00352415
138	LOC659580	NC_007419.2:10032071-10033682	659580	venom acid phosphatase Acph-1	304.625	150.18	1.015495266	5.00E-05	0.00352415
139	LOC103313593	NC_007422.5:3615164-3616462	103313593	uncharacterized LOC103313593	79.2358	39.2097	0.996702517	5.00E-05	0.00352415
140	Cyp4g14	NC_007419.2:4413404-4415340	662217	cytochrome P450 monooxygenase	234.193	116.392	1.002511027	5.00E-05	0.00352415
141	LOC663325	NC_007417.3:9989620-9991074	663325	probable phosphoserine aminotransferase	152.021	75.7827	0.994876459	5.00E-05	0.00352415
142	LOC103314523	NC_007416.3:7718927-7720296	103314523	uncharacterized LOC103314523	23.0959	11.5492	0.941192291	5.00E-05	0.00352415
143	HEX1A	NC_007423.3:13938454-13940965	660335	arylphorin	5.66952	2.83945	0.796683275	0.00045	0.0239168
144	LOC659104	NC_007422.5:1194959-1197544	659104	vanin-like protein 2	149.815	75.4235	0.98069169	5.00E-05	0.00352415
145	LOC657162	NC_007417.3:4984251-4985436	657162	1,5-anhydro-D-fructose reductase	47.0419	23.8245	0.952528549	5.00E-05	0.00352415
146	LOC103312668	NC_007419.2:4994664-4995835	103312668	hypothetical protein	15.5251	7.86958	0.897721307	0.00045	0.0239168
147	LOC654861	NC_007418.3:20658743-20660124	654861	iodotyrosine deiodinase 1	41.2268	20.9708	0.94257152	5.00E-05	0.00352415
148	Ddc	NC_007420.3:9022378-9028416	662962	dopa decarboxylase	16.3908	8.35231	0.894929643	5.00E-05	0.00352415
149	LOC107398182	NC_007422.5:3052401-3054328	107398182	eukaryotic translation initiation factor 5B-like	10.7208	5.46701	0.857900298	0.0011	0.0486442
150	Chp	NC_007417.3:8576783-8595515	652931	cell surface protein chaoptin	28.493	14.546	0.923829158	5.00E-05	0.00352415
151	LOC659062	NC_007419.2:4066202-4071560	659062	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase	33.3892	17.0565	0.929437281	0.0003	0.0169681
152	LOC661515	NC_007422.5:8816451-8819563	661515	elongation factor Tu	143.833	74.13	0.946929349	0.0003	0.0169681
153	LOC103314151	NC_007418.3:31269917-31273035	103314151	caspase-1-like	59.0496	30.599	0.926275733	0.0007	0.0338289
154	ImpL2	NC_007421.3:8945769-8951756	657195	ecdysone-inducible gene L2	79.4786	41.3323	0.926846333	5.00E-05	0.00352415
155	LOC107398650	NC_007424.3:9686219-9686420	107398650	uncharacterized LOC107398650	2391.94	1250.67	0.934929974	5.00E-05	0.00352415
156	LOC659093	NC_007420.3:11252586-11253090	659093	endocuticle structural glycoprotein SgAbd-5	155.783	81.8622	0.919983107	5.00E-05	0.00352415
157	LOC660041	NC_007420.3:6044023-6045427	660041	Krueppel-like factor 11	94.9095	49.9855	0.911586713	5.00E-05	0.00352415
158	LOC658874	NC_007421.3:219042-220468	658874	alpha-tocopherol transfer protein-like	30.6796	16.3686	0.867072649	5.00E-05	0.00352415
159	LOC662648	NC_007422.5:3574137-3575741	662648	spermine oxidase	24.9704	13.3882	0.851982116	5.00E-05	0.00352415
160	LOC660047	NC_007421.3:2374864-2375715	660047	uncharacterized LOC660047	30.6459	16.4969	0.854919262	0.0006	0.0297494
161	Nag2	NC_007418.3:3684052-3691642	658249	beta-N-acetylglucosaminidase NAG2	32.9775	17.8294	0.851592677	0.0003	0.0169681
162	LOC662670	NC_007419.2:8123700-8129243	662670	aldose reductase	111.568	60.7089	0.867246284	0.00015	0.00949185
163	Pmp1-b	NC_007421.3:3525434-3526482	659324	peritrophic matrix protein 1-B	825.445	452.515	0.865768543	5.00E-05	0.00352415
164	LOC656561	NC_007422.5:4149292-4151763	656561	mannose-1-phosphate guanyltransferase alpha-A	62.6382	34.3436	0.848444034	5.00E-05	0.00352415
165	numb	NC_007424.3:6645097-6665968	661741	protein numb	24.382	13.3787	0.819872507	0.00105	0.0470692
166	LOC657451	NC_007425.3:5941152-5943554	657451	UDP-glucuronosyltransferase 2B9	8.19401	4.50222	0.74068041	0.00065	0.0319518
167	LOC661519	NC_007424.3:3821084-3827221	661519	facilitated trehalose transporter Tret1	45.4659	25.0317	0.835902822	0.00035	0.0194127
168	H111	NC_007420.3:1439218-1441500	656711	serine protease H111	40.6491	22.5145	0.824734665	5.00E-05	0.00352415
169	LOC103312286	NC_007418.3:2817643-2821512	103312286	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	168.014	93.2398	0.842734372	5.00E-05	0.00352415
170	LOC659054	NC_007420.3:1061308-1067260	659054	cytochrome P450 345B1	38.1201	21.2545	0.813812971	0.00095	0.0436105

171	LOC662035	NC_007417.3:6104312-6109694	662035	putative DNA helicase INO80	301.729	168.42	0.837422691	0.00015	0.00949185
172	LOC662543	NC_007420.3:6797945-6806048	662543	inter-alpha-trypsin inhibitor heavy chain H4	163.378	91.2198	0.833868783	0.0004	0.0218162
173	LOC658613	NC_007418.3:15582811-15592736	658613	glycine dehydrogenase (decarboxylating), mitochondrial	16.6143	9.27909	0.777034593	5.00E-05	0.00352415
174	-	NC_007418.3:15801610-15803677	-	-	30.29	16.997	0.797945221	5.00E-05	0.00352415
175	LOC656432	NC_007420.3:9468571-9470736	656432	beta-galactosidase-1-like protein 2	117.96	66.2797	0.822233375	5.00E-05	0.00352415
176	Pmp2-b	NC_007418.3:635588-636266	662632	peritrophic matrix protein 2-B	1670.46	941.89	0.825947453	0.0002	0.0120247
177	LOC100141952	NC_007421.3:5176885-5186355	100141952	uncharacterized LOC100141952	47.4934	26.836	0.800836496	0.00085	0.0395751
178	LOC664014	NC_007419.2:3203324-3204205	664014	uncharacterized LOC664014	269.934	153.219	0.812960933	5.00E-05	0.00352415
179	LOC662129	NC_007422.5:3466594-3468311	662129	alpha-N-acetylgalactosaminidase	68.5845	39.3028	0.787885908	5.00E-05	0.00352415
180	LOC655252	NW_015450233.1:23600-25618	655252	kynurenine--oxoglutarate transaminase 3	38.1793	21.9066	0.774328285	5.00E-05	0.00352415
181	LOC663674	NC_007418.3:1075965-1077185	663674	uncharacterized LOC663674	32.3425	18.5721	0.768563722	0.0001	0.00663971
182	Th	NC_007418.3:26517372-26538072	654918	tyrosine hydroxylase	50.4661	29.0366	0.776900946	5.00E-05	0.00352415
183	LOC103314048	NC_007423.3:10035093-10036045	103314048	uncharacterized LOC103314048	94.2427	54.3629	0.782689004	0.0007	0.0338289
184	LOC655368	NC_007423.3:9698633-9699893	655368	uncharacterized LOC655368	80.429	46.8678	0.766487184	5.00E-05	0.00352415
185	Csp12	NC_007422.5:13945713-13946306	661270	chemosensory protein 12	1471.04	859.881	0.773931142	5.00E-05	0.00352415
186	LOC663235	NC_007422.5:3641055-3642362	663235	hypothetical protein	93.6706	54.8118	0.76234629	5.00E-05	0.00352415
187	LOC656567	NC_007420.3:847715-857421	656567	glutamate--cysteine ligase catalytic subunit	42.3195	25.0197	0.735412263	5.00E-05	0.00352415
188	LOC103313530	NC_007422.5:179815-186554	103313530	uncharacterized LOC103313530	64.7618	38.423	0.738212222	0.00035	0.0194127
189	-	NC_007424.3:4463016-4463934	-	-	93.5573	55.5374	0.741983302	5.00E-05	0.00352415
190	LOC657720	NC_007419.2:3850272-3854338	657720	open rectifier potassium channel protein 1	19.0301	11.3343	0.699493782	5.00E-05	0.00352415
191	LOC100142298	NC_007419.2:4301445-4302896	100142298	uncharacterized LOC100142298	47.5589	28.4957	0.719231093	0.0002	0.0120247
192	LOC103313498	NC_007422.5:1065067-1067009	103313498	uncharacterized LOC103313498	202.179	122.301	0.720566797	0.0001	0.00663971
193	LOC661415	NC_007419.2:63447-66167	661415	nose resistant to fluoxetine protein 6-like	39.6411	24.1044	0.694999206	0.0001	0.00663971
194	LOC657080	NW_015450233.1:406664-408759	657080	venom carboxylesterase-6	93.183	57.0598	0.697927075	5.00E-05	0.00352415
195	LOC664567	NC_007422.5:9821196-9824417	664567	beta-hexosaminidase subunit alpha	104.754	64.2143	0.697451978	0.00015	0.00949185
196	-	NW_015450951.1:3564-4038	-	-	2114.46	1298.4	0.703125797	0.00075	0.0357178
197	LOC664439	NC_007422.5:10416132-10418741	664439	acyl-CoA synthetase family member 3, mitochondrial	50.4842	31.0425	0.684143038	0.0005	0.0259129
198	-	NW_015451782.1:48431-48717	-	-	2002.84	1234.33	0.697870831	5.00E-05	0.00352415
199	LOC656992	NC_007424.3:5204660-5208030	656992	4-aminobutyrate aminotransferase, mitochondrial-like	67.1836	41.4988	0.682002668	5.00E-05	0.00352415
200	-	NW_015451463.1:1816-2091	-	-	2040.91	1263.34	0.691534801	5.00E-05	0.00352415
201	Nat	NC_007419.2:6607412-6617811	664229	dopamine N acetyltransferase	213.457	133.072	0.677680435	0.00055	0.0281853
202	LOC655942	NC_007421.3:2045203-2047987	655942	protein GUCD1	53.3453	33.2693	0.665238548	0.0011	0.0486442
203	LOC655491	NC_007417.3:3288378-3296663	655491	tubulin alpha 1-like protein	77.6973	48.5684	0.666893448	0.00035	0.0194127
204	-	NW_015451371.1:7855-8898	-	-	752.714	472.036	0.672067208	0.0008	0.037707
205	LOC662761	NC_007418.3:687991-691412	662761	adenosine deaminase CECR1	89.3882	56.0948	0.662775088	0.0003	0.0169681
206	LOC664154	NC_007417.3:7763122-7780118	664154	uncharacterized LOC664154	89.2228	56.2431	0.656390256	0.0006	0.0297494
207	-	NC_007424.3:14489446-14491160	-	-	60.6251	38.6516	0.636139001	0.0006	0.0297494
208	LOC659321	NC_007420.3:12620445-12623447	659321	tyrosine aminotransferase	206.15	131.495	0.644737903	0.0005	0.0259129
209	LOC100142601	NC_007419.2:1397019-1402677	100142601	phosphoribosylformylglycinamidine synthase	42.277	27.1392	0.621019181	0.0011	0.0486442
210	LOC660688	NW_015451036.1:167479-175442	660688	proline-rich extensin-like protein EPR1	27.6115	17.7787	0.607497943	0.0007	0.0338289
211	Arr1	NC_007420.3:3790766-3798103	657618	arrestin 1	73.5273	47.3804	0.623346297	0.0005	0.0259129
212	LOC661336	NC_007422.5:3353677-3363322	661336	neuroendocrine convertase 2	58.8818	37.9922	0.618932032	0.0005	0.0259129
213	LOC103314006	NC_007423.3:11127895-11132433	103314006	prohormone-2	217.74	142.182	0.611366927	0.00075	0.0357178
214	LOC654884	NC_007422.5:7976218-7984456	654884	abhydrolase domain-containing protein 2	119.821	78.4816	0.604178412	0.00045	0.0239168

215	LOC655020	NC_007422.5:4256193-4265582	655020	protein phosphatase 1A	69.9566	104.739	-0.575498801	0.00065	0.0319518
216	Toll3	NC_007417.3:4930716-4940271	656158	toll-like receptor 3	16.4606	24.6816	-0.556631952	0.001	0.0455408
217	LOC663635	NC_007420.3:9273120-9279317	663635	sterol regulatory element-binding protein cleavage-activating protein	15.2285	23.1091	-0.571048138	0.0004	0.0218162
218	LOC660224	NC_007418.3:258591-259603	660224	rhythmically expressed gene 2 protein	96.9004	149.441	-0.619811142	0.0004	0.0218162
219	LOC657042	NC_007423.3:13439529-13441914	657042	nucleolar complex protein 2 homolog	14.6192	22.8659	-0.611630181	0.00055	0.0281853
220	LOC661892	NC_007422.5:12270478-12278083	661892	protein SOX-15	23.0709	36.1888	-0.627578112	0.00085	0.0395751
221	LOC658340	NC_007418.3:53870-59915	658340	UNC93-like protein MFSD11	58.2738	91.467	-0.641544032	0.00075	0.0357178
222	LOC663003	NC_007424.3:11843371-11846305	663003	uncharacterized LOC663003	12.6591	19.9564	-0.617528477	0.0006	0.0297494
223	LOC660215	NC_007416.3:4422796-4423566	660215	uncharacterized LOC660215	127.291	200.828	-0.653706372	0.0002	0.0120247
224	LOC659000	NC_007418.3:5146248-5148473	659000	protein SDA1 homolog	10.3984	16.4573	-0.614999118	0.001	0.0455408
225	LOC100142105	NC_007421.3:4278613-4281820	100142105	brain protein I3	99.6908	157.785	-0.657142759	0.0005	0.0259129
226	Cyp346a2	NC_007420.3:9730439-9732117	657412	cytochrome P450 346A2	30.9659	49.0199	-0.64596846	0.00025	0.014684
227	LOC661684	NC_007421.3:775511-777185	661684	short-chain specific acyl-CoA dehydrogenase, mitochondrial	24.5462	39.0937	-0.650266855	0.0003	0.0169681
228	LOC662326	NC_007417.3:14939348-14943419	662326	heat shock 70 kDa protein cognate 2	26.859	42.7952	-0.652629284	0.0002	0.0120247
229	Csp18	NC_007422.5:13932549-13933016	661601	chemosensory protein 18	465.515	741.726	-0.670906613	0.00025	0.014684
230	LOC660592	NC_007418.3:10096889-10113150	660592	N-acetylgalactosamine kinase	31.6173	50.5195	-0.659481229	5.00E-05	0.00352415
231	LOC658388	NW_015450712.1:76662-78322	658388	cytochrome P450 6BR1	16.0028	25.6226	-0.646879127	0.0005	0.0259129
232	LOC662079	NC_007419.2:2625995-2631595	662079	hypothetical protein	19.6107	31.4021	-0.652693814	0.00025	0.014684
233	LOC662383	NC_007423.3:4119857-4126194	662383	protein msta, isoform B	15.1998	24.5617	-0.658007785	0.00045	0.0239168
234	LOC659207	NC_007417.3:45734-68728	659207	transferrin	17.6007	28.4732	-0.664046792	0.00105	0.0470692
235	LOC655313	NC_007416.3:3756168-3765231	655313	semaphorin-5A	28.2365	45.6881	-0.675284267	0.00025	0.014684
236	LOC655245	NC_007423.3:167402-169487	655245	aldehyde dehydrogenase, dimeric NADP-preferring	36.2413	58.7413	-0.681825197	5.00E-05	0.00352415
237	LOC103313009	NC_007417.3:1760229-1763825	103313009	uncharacterized LOC103313009	154.96	251.789	-0.696757627	0.00055	0.0281853
238	LOC655423	NC_007418.3:1146005-1147378	655423	alpha-tocopherol transfer protein-like	38.3678	62.546	-0.690785223	0.0002	0.0120247
239	SA; stromalin	NC_007420.3:9385414-9389924	655276	cohesin subunit SA-1	8.52965	13.9946	-0.653947903	5.00E-05	0.00352415
240	LOC656104	NC_007421.3:63465-71878	656104	T-complex protein 1 subunit zeta	47.4364	77.8406	-0.702847114	0.0001	0.00663971
241	LOC659785	NC_007422.5:6522954-6527857	659785	probable cleavage and polyadenylation specificity factor subunit 2	10.3888	17.0823	-0.666962452	0.0002	0.0120247
242	LOC103314479	NC_007425.3:6234058-6237814	103314479	uncharacterized LOC103314479	7.33904	12.1694	-0.659236404	0.00035	0.0194127
243	LOC664562	NC_007422.5:9833967-9838122	664562	glucosylceramidase	41.8783	69.5296	-0.717981149	5.00E-05	0.00352415
244	LOC655815	NC_007418.3:3583259-3591506	655815	protein BTG1	64.3603	106.898	-0.723181613	0.0001	0.00663971
245	LOC656298	NC_007418.3:14512305-14528095	656298	annexin B9	71.0097	118.087	-0.72575277	0.0009	0.0416491
246	LOC103314187	NW_015450232.1:77786-80988	103314187	serine protease snake	29.4396	49.0301	-0.716846935	0.0008	0.037707
247	LOC103312942	NC_007420.3:4705674-4708861	103312942	uncharacterized LOC103312942	22.5772	37.6704	-0.713837292	0.0001	0.00663971
248	LOC659195	NC_007424.3:286609-287649	659195	troponin C, isoform 1	315.193	527.319	-0.740603866	5.00E-05	0.00352415
249	LOC657335	NC_007420.3:8152126-8155578	657335	sulfotransferase family cytosolic 1B member 1	61.3575	102.723	-0.734100845	5.00E-05	0.00352415
250	ML1	NC_007419.2:6588287-6589812	664531	MD2-like 1	278.172	465.905	-0.741974787	5.00E-05	0.00352415
251	LOC658084	NC_007418.3:3667009-3673954	658084	palmitoyl-protein thioesterase 1	14.1859	23.9438	-0.715948853	0.00015	0.00949185
252	LOC663261	NC_007424.3:12139213-12141584	663261	probable 28S rRNA (cytosine-C(5))-methyltransferase	8.46807	14.3689	-0.698871633	5.00E-05	0.00352415
253	LOC662530	NW_015450798.1:17423-18657	662530	transmembrane emp24 domain-containing protein bai	55.0696	93.5047	-0.753167303	5.00E-05	0.00352415
254	LOC661450	NC_007416.3:7275308-7297021	661450	solute carrier organic anion transporter family member 5A1	9.40076	16.0085	-0.709566961	0.0011	0.0486442
255	rad50	NC_007421.3:3442759-3447047	658288	rad50	2.10939	3.59625	-0.563825691	0.0011	0.0486442
256	LOC655289	NC_007422.5:1759507-1765805	655289	pentatricopeptide repeat-containing protein 2, mitochondrial	15.7703	26.9391	-0.736377051	0.00025	0.014684
257	Gr106	NC_007420.3:8958318-8966093	662798	glucose transporter	30.0719	51.4642	-0.755722844	0.0007	0.0338289
258	LOC100142097	NC_007423.3:11760941-11761714	100142097	uncharacterized LOC100142097	278.576	478.021	-0.776848385	5.00E-05	0.00352415

259	LOC655370	NC_007421.3:3124430-3133836	655370	uncharacterized LOC655370	14.7297	25.278	-0.740364322	5.00E-05	0.00352415
260	LOC107399196	NW_015452199.1:1353-2623	107399196	uncharacterized LOC107399196	46.882	80.7461	-0.771666489	5.00E-05	0.00352415
261	LOC656820	NC_007422.5:5375003-5382661	656820	C-1-tetrahydrofolate synthase, cytoplasmic	55.3313	95.3973	-0.775055972	5.00E-05	0.00352415
262	LOC662773	NC_007422.5:489656-490132	662773	tenecin-3	296.209	514.945	-0.795739478	5.00E-05	0.00352415
263	LOC103314922	NC_007420.3:7395440-7396587	103314922	uncharacterized LOC103314922	23.4531	40.9041	-0.777074036	0.00075	0.0357178
264	LOC103313789	NC_007423.3:3817639-3826196	103313789	uncharacterized LOC103313789	14.0284	24.5514	-0.76571092	5.00E-05	0.00352415
265	LOC655860	NC_007420.3:14729016-14731204	655860	nucleolar GTP-binding protein 2	9.25317	16.2081	-0.747017793	0.0001	0.00663971
266	LOC100142246	NC_007417.3:12105006-12111871	100142246	transmembrane protease serine 9	36.7111	64.7702	-0.802444824	0.00045	0.0239168
267	LOC659445	NC_007418.3:128530-136783	659445	importin-7	23.1932	40.9247	-0.793198855	0.0007	0.0338289
268	daw; Alp23B	NW_015451971.1:37267-41548	658911	dawdle	6.97833	12.3159	-0.738991239	0.0006	0.0297494
269	LOC663832	NC_007422.5:11420618-11426051	663832	aspartic proteinase A2	139.137	245.703	-0.815937342	5.00E-05	0.00352415
270	LOC659989	NC_007421.3:8060009-8076166	659989	zinc carboxypeptidase	50.6973	89.5994	-0.809412561	0.0003	0.0169681
271	LOC664209	NC_007423.3:9067215-9069530	664209	uncharacterized LOC664209	155.437	275.543	-0.821922049	5.00E-05	0.00352415
272	TcasZ9desA	NC_007425.3:6773285-6786677	658103	Z9 acyl-CoA desaturase A	156.491	277.739	-0.823645486	0.00075	0.0357178
273	serpin24	NC_007423.3:5884658-5886989	662831	serpin peptidase inhibitor 24	18.4766	32.9658	-0.802340984	5.00E-05	0.00352415
274	ML5	NC_007422.5:6846774-6848499	656806	MD2-like 5	129.41	231.391	-0.833499696	5.00E-05	0.00352415
275	LOC100142066	NC_007417.3:2909684-2920265	100142066	uncharacterized LOC100142066	9.68944	17.3362	-0.77850841	0.0008	0.037707
276	LOC658596	NC_007422.5:8324494-8335126	658596	nuclear pore membrane glycoprotein 210	3.43892	6.1997	-0.697728085	5.00E-05	0.00352415
277	LOC655281	NC_007423.3:9702093-9703508	655281	uncharacterized LOC655281	40.9712	73.9293	-0.836130262	5.00E-05	0.00352415
278	LOC663867	NC_007422.5:13157788-13158793	663867	proteasome subunit beta type-4	68.3952	123.59	-0.844280496	5.00E-05	0.00352415
279	LOC659791	NC_007421.3:5616218-5655473	659791	alpha-tocopherol transfer protein-like	30.1196	54.4762	-0.834045453	0.00025	0.014684
280	LOC658566	NC_007418.3:1393517-1395804	658566	4-coumarate--CoA ligase 1	43.6587	79.3134	-0.846699461	0.0008	0.037707
281	LOC103313132	NC_007422.5:5992519-6006521	103313132	uncharacterized LOC103313132	4.59717	8.36909	-0.743211362	0.00015	0.00949185
282	-	NC_007422.5:8836159-8837521	-	-	34.3424	62.6722	-0.849263601	5.00E-05	0.00352415
283	LOC658982	NW_015451959.1:3177-5999	658982	periodic tryptophan protein 2 homolog	4.2268	7.73082	-0.740189202	0.0006	0.0297494
284	LOC656402	NC_007416.3:105572-111276	656402	glycogenin-2	92.1874	168.819	-0.865791078	5.00E-05	0.00352415
285	LOC661235	NC_007418.3:18833724-18842456	661235	pre-rRNA-processing protein TSR1 homolog	8.42663	15.4628	-0.804395723	0.00045	0.0239168
286	LanA	NC_007418.3:5388902-5421238	661583	laminin subunit alpha	2.05359	3.7765	-0.645447498	0.00075	0.0357178
287	Y-1	NC_007423.3:13098920-13102773	662975	yellow-1	35.6633	65.5874	-0.860912563	5.00E-05	0.00352415
288	LOC663110	NC_007424.3:4101781-4102842	663110	protein BCCIP homolog	17.0472	31.4301	-0.84555845	0.0001	0.00663971
289	LOC655179	NC_007417.3:10821015-10824320	655179	WD repeat-containing protein 36	2.73119	5.0532	-0.698062192	0.0006	0.0297494
290	LOC658565	NC_007418.3:60561-75519	658565	arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein	16.2619	30.1676	-0.852455798	0.0007	0.0338289
291	LOC103313795	NC_007423.3:4191208-4197137	103313795	hypothetical protein	10.5553	19.876	-0.853290591	0.0003	0.0169681
292	P37	NC_007418.3:11916031-11923284	655840	serine protease P37	107.295	202.289	-0.908565518	5.00E-05	0.00352415
293	LOC657463	NC_007416.3:28041-32308	657463	sarcalumenin	68.0665	128.393	-0.905701551	5.00E-05	0.00352415
294	Cda8	NC_007420.3:6638235-6639855	662008	chitin deacetylase 8	102.165	192.787	-0.909518191	0.0004	0.0218162
295	Cyp4q1	NC_007424.3:9524439-9526264	659878	cytochrome P450 monooxigenase CYP4Q1	26.2928	49.7315	-0.894361408	5.00E-05	0.00352415
296	LOC663981	NC_007417.3:12412614-12414764	663981	epoxide hydrolase 4	5.29294	10.0192	-0.808213395	0.0002	0.0120247
297	LOC103314725	NW_015450989.1:282168-320687	103314725	eIF-2-alpha kinase activator GCN1	4.28045	8.13035	-0.790009284	0.00015	0.00949185
298	LOC103313111	NC_007420.3:9088174-9097602	103313111	collagen alpha-2(IV) chain	5.6274	10.691	-0.818883436	5.00E-05	0.00352415
299	LOC664288	NC_007419.2:9234736-9243034	664288	leucine--tRNA ligase, cytoplasmic	9.63733	18.3311	-0.861787658	0.0002	0.0120247
300	LOC103312937	NC_007420.3:4528636-4530444	103312937	sodium/potassium-transporting ATPase subunit beta-2	10.175	19.4098	-0.868987214	5.00E-05	0.00352415
301	LOC659823	NW_015452129.1:9-1304	659823	pescadillo homolog	10.3673	19.8592	-0.875794207	5.00E-05	0.00352415
302	LOC103312293	NC_007418.3:4255638-4262123	103312293	paramyosin	3.87539	7.4255	-0.789244674	0.0004	0.0218162

303	LOC655207	NC_007421.3:2015475-2022700	655207	carboxypeptidase D	87.7883	168.364	-0.931685764	0.0006	0.0297494
304	LOC664364	NC_007417.3:8617585-8620167	664364	SPARC	54.3415	104.505	-0.930877718	5.00E-05	0.00352415
305	MRP	NC_007421.3:188314-195426	658210	probable multidrug resistance-associated protein lethal(2)03659	4.32175	8.32368	-0.808998752	5.00E-05	0.00352415
306	LOC661092	NC_007417.3:13240881-13248493	661092	sodium/potassium-transporting ATPase subunit alpha	5.26452	10.1432	-0.830887715	5.00E-05	0.00352415
307	LOC662517	NC_007422.5:13780430-13781456	662517	deoxyuridine 5'-triphosphate nucleotidohydrolase	11.6912	22.5925	-0.894499815	0.0002	0.0120247
308	LOC656355	NC_007420.3:14744243-14746019	656355	regucalcin	32.7036	63.4655	-0.935624581	5.00E-05	0.00352415
309	P139; P138	NC_007422.5:6041473-6047386	661211	serine protease easter	9.55014	18.5341	-0.888732644	0.0002	0.0120247
310	LOC103313602	NC_007422.5:4646200-4647370	103313602	hypothetical protein	11.003	21.3714	-0.898260508	0.0001	0.00663971
311	LOC659125	NC_007420.3:1867701-1875585	659125	dual specificity protein phosphatase 14	12.5696	24.4162	-0.905370154	5.00E-05	0.00352415
312	LOC661261	NC_007420.3:10014458-10017089	661261	major facilitator superfamily domain-containing protein 1	10.259	20.0683	-0.903995212	5.00E-05	0.00352415
313	LOC663579	NC_007418.3:5980961-5982150	663579	zinc transporter ZIP1	20.6991	40.6013	-0.938993406	5.00E-05	0.00352415
314	LOC662498	NW_015450798.1:3368-13812	662498	senecionine N-oxygenase	61.9099	121.642	-0.963094155	5.00E-05	0.00352415
315	Z9desB	NW_015450728.1:196850-224677	657939	Z9 acyl-CoA desaturase B	73.9655	145.53	-0.966897359	0.00015	0.00949185
316	P92; P93	NC_007422.5:6573192-6575140	661472	serine protease P93	13.7271	27.1151	-0.93287181	5.00E-05	0.00352415
317	LOC656462	NC_007420.3:1368354-1389670	656462	pre-mRNA-splicing factor SYF1	4.82646	9.55406	-0.857106578	5.00E-05	0.00352415
318	LOC664474	NC_007422.5:10079316-10081020	664474	UDP-glucuronosyltransferase 2B20	12.8205	25.4082	-0.934176159	5.00E-05	0.00352415
319	LOC103313053	NC_007420.3:9479790-9480417	103313053	SH3 domain-binding glutamic acid-rich protein homolog	25.7716	51.1543	-0.962082841	0.00015	0.00949185
320	LOC654859	NC_007418.3:11533159-11608989	654859	muscle M-line assembly protein unc-89	36.3333	72.3594	-0.974518801	0.001	0.0455408
321	LOC656773	NC_007422.5:15123328-15125176	656773	3-ketoacyl-CoA thiolase, mitochondrial	164.065	327.018	-0.990740738	5.00E-05	0.00352415
322	LOC660518	NC_007419.2:4402949-4411547	660518	lipid storage droplets surface-binding protein 1	105.807	212.716	-1.000688718	5.00E-05	0.00352415
323	LOC659539	NC_007424.3:3531789-3552125	659539	uncharacterized LOC659539	31.3014	63.0919	-0.988545344	0.00105	0.0470692
324	LOC103314059	NC_007423.3:10651203-10704793	103314059	kielin/chordin-like protein	274.069	552.789	-1.009542839	5.00E-05	0.00352415
325	LOC657196	NC_007422.5:15087077-15087895	657196	protein lethal(2)essential for life	519.507	1050.88	-1.014980659	5.00E-05	0.00352415
326	LOC660270	NC_007420.3:7399862-7401745	660270	cytochrome P450-like protein	32.4981	65.783	-0.995401634	0.0002	0.0120247
327	LOC662842	NC_007419.2:738655-740578	662842	putative N-acetylglucosamine-6-phosphate deacetylase	7.08987	14.3685	-0.925787937	0.0005	0.0259129
328	-	NC_007418.3:27029845-27031125	-	-	23.2188	47.4103	-0.999186651	5.00E-05	0.00352415
329	H4	NC_007417.3:14188598-14191578	656917	tryptase alpha/beta-1	44.4942	91.0483	-1.016708448	5.00E-05	0.00352415
330	LOC654972	NC_007418.3:4222749-4228897	654972	ethanolamine-phosphate cytidylyltransferase	54.4605	111.825	-1.02455425	5.00E-05	0.00352415
331	LOC655556	NC_007418.3:11362444-11392799	655556	uncharacterized LOC655556	8.09174	16.6392	-0.956156799	5.00E-05	0.00352415
332	LOC100142446	NC_007423.3:13691816-13693879	100142446	kynurenine formamidase	24.5497	50.669	-1.015992611	5.00E-05	0.00352415
333	LOC657487	NC_007419.2:7211929-7212896	657487	uncharacterized LOC657487	8.07788	16.678	-0.961527742	0.00045	0.0239168
334	LOC103312884	NC_007421.3:4556300-4556688	103312884	putative uncharacterized protein DDB_G0287191	240.839	498.324	-1.045929333	5.00E-05	0.00352415
335	LOC659994	NC_007422.5:2209826-2213027	659994	RNA-binding protein pno1	39.9515	83.4204	-1.043675368	5.00E-05	0.00352415
336	LOC663195	NC_007418.3:793895-802728	663195	facilitated trehalose transporter Tret1	21.8349	45.7542	-1.033855498	5.00E-05	0.00352415
337	LOC658429	NC_007420.3:12101216-12111276	658429	transcription factor MafA	12.5793	26.3728	-1.011333905	5.00E-05	0.00352415
338	LOC659008	NC_007420.3:318605-330134	659008	protein takeout-like	15.3669	32.4941	-1.033125895	5.00E-05	0.00352415
339	LOC656237	NC_007416.3:1719129-1738731	656237	lipoyltransferase 1, mitochondrial	210.763	445.863	-1.077382057	0.0006	0.0297494
340	LOC103314203	NC_007424.3:6233088-6233823	103314203	ARL14 effector protein	9.9784	21.1327	-1.011511648	0.0002	0.0120247
341	Cyp4q2	NC_007424.3:9520015-9523792	659810	cytochrome P450 monooxigenase CYP4Q2	29.3936	62.3018	-1.058478957	0.00015	0.00949185
342	LOC659452	NC_007418.3:29326638-29443297	659452	FH1/FH2 domain-containing protein 3	55.2307	117.25	-1.072410272	0.0006	0.0297494
343	LOC663372	NC_007422.5:3665128-3686283	663372	dystroglycan	16.2427	34.5167	-1.04251184	5.00E-05	0.00352415
344	-	NW_015450261.1:0-2084	-	-	28.3137	60.468	-1.068260467	5.00E-05	0.00352415
345	LOC663877	NC_007419.2:8872422-8873190	663877	muscle-specific protein 20	1690.09	3620.88	-1.098785306	0.0001	0.00663971
346	LOC100141856	NC_007418.3:15539663-15540377	100141856	uncharacterized LOC100141856	121.382	260.053	-1.092951357	5.00E-05	0.00352415

347	LOC658250	NC_007416.3:505213-512474	658250	solute carrier family 41 member 1	4.43005	9.4958	-0.950774747	0.0003	0.0169681
348	LOC663650	NC_007418.3:6004785-6013734	663650	NFX1-type zinc finger-containing protein 1	11.8215	25.394	-1.041644953	5.00E-05	0.00352415
349	LOC103312157	NW_015452154.1:11769-15913	103312157	uncharacterized LOC103312157	14.2394	30.6539	-1.054577159	5.00E-05	0.00352415
350	LOC103312427	NC_007418.3:17580840-17588533	103312427	leucine-rich repeat-containing protein 15-like	26.5893	57.9561	-1.095532239	0.0011	0.0486442
351	-	NC_007423.3:12240617-12241207	-	-	33.8376	74.7594	-1.120779666	0.0001	0.00663971
352	LOC664529	NC_007422.5:9910444-9916586	664529	patj homolog	11.0615	24.5978	-1.085610488	5.00E-05	0.00352415
353	LOC655659	NW_015450233.1:53802-55347	655659	argininosuccinate synthase	16.9206	37.85	-1.116295658	5.00E-05	0.00352415
354	LOC662294	NC_007419.2:10755792-10761211	662294	ATP-binding cassette sub-family G member 1	71.9715	161.29	-1.153169091	5.00E-05	0.00352415
355	LOC656717	NC_007416.3:6224002-6240493	656717	Down syndrome cell adhesion molecule-like protein Dscam2	6.01681	13.4979	-1.04695674	5.00E-05	0.00352415
356	LOC660984	NC_007419.2:7653637-7656654	660984	leucine-rich repeat-containing protein 15	9.43468	21.1871	-1.088334752	5.00E-05	0.00352415
357	LOC103312995	NC_007420.3:6444194-6447050	103312995	cubilin	1.2824	2.92468	-0.782023376	0.0005	0.0259129
358	LOC103314029	NC_007423.3:11763948-11764598	103314029	uncharacterized LOC103314029	23.496	53.7601	-1.160578893	5.00E-05	0.00352415
359	Ypf1b; Irbp; Ku70	NC_007422.5:11080951-11082768	664190	inverted repeat-binding protein	7.37564	16.8851	-1.094486846	5.00E-05	0.00352415
360	LOC659631	NC_007417.3:11262009-11264896	659631	adhesive plaque matrix protein	19.8789	45.5555	-1.15690591	5.00E-05	0.00352415
361	LOC660368	NC_007422.5:1063298-1064687	660368	cathepsin L precursor	566.947	1307.57	-1.20416289	5.00E-05	0.00352415
362	LOC656478	NW_015450245.1:57584-72054	656478	acyl-CoA Delta(11) desaturase-like	9.9233	23.1562	-1.144984753	0.00095	0.0436105
363	LOC663738	NC_007417.3:12312221-12313397	663738	protein takeout	12.4889	29.3171	-1.168359055	5.00E-05	0.00352415
364	VTGl	NC_007425.3:2112481-2114171	656735	pancreatic triacylglycerol lipase	9.24748	22.022	-1.167743997	5.00E-05	0.00352415
365	LOC103314140	NC_007418.3:31227375-31227927	103314140	hypothetical protein	216.275	517.423	-1.25460754	5.00E-05	0.00352415
366	LOC660815	NC_007418.3:1970626-2018832	660815	tyrosine-protein kinase-like otk	1.99625	4.78198	-0.948405615	5.00E-05	0.00352415
367	LOC655472	NC_007425.3:1346023-1347021	655472	protein takeout	74.3584	179.316	-1.258687178	5.00E-05	0.00352415
368	LOC661444	NC_007418.3:10645058-10664332	661444	uncharacterized LOC661444	8.74035	21.248	-1.191630131	0.0006	0.0297494
369	LOC662582	NC_007422.5:13771747-13772726	662582	multiple organellar RNA editing factor 1, mitochondrial	3.76983	9.21205	-1.098262753	0.0009	0.0416491
370	LOC659061	NC_007417.3:14488131-14527717	659061	lipid storage droplets surface-binding protein 1	46.5878	115.724	-1.294437564	5.00E-05	0.00352415
371	LOC663816	NC_007424.3:13941478-13949379	663816	copper homeostasis protein cutC homolog	7.56796	18.8192	-1.20987508	0.0006	0.0297494
372	LOC663158	NC_007422.5:9227393-9230671	663158	vacuolar protein-sorting-associated protein 25	15.8657	39.5866	-1.266911291	5.00E-05	0.00352415
373	CYP6BQ13	NC_007417.3:2344028-2348733	655498	cytochrome P450 monooxygenase	19.9793	50.1742	-1.286450103	5.00E-05	0.00352415
374	LOC664132	NC_007417.3:7752330-7760165	664132	uncharacterized LOC664132	8.11401	20.4123	-1.232281912	5.00E-05	0.00352415
375	LOC100142054	NC_007424.3:12839739-12844719	100142054	carboxypeptidase D	7.49289	18.8606	-1.225581739	5.00E-05	0.00352415
376	LOC660437	NC_007423.3:12667945-12668741	660437	uncharacterized LOC660437	33.4953	84.4869	-1.309303551	5.00E-05	0.00352415
377	LOC103313299	NC_007421.3:102795-111634	103313299	uncharacterized LOC103313299	3.20777	8.12289	-1.116435074	5.00E-05	0.00352415
378	LOC100141741	NC_007422.5:10131306-10131850	100141741	endo-1,4-beta-xylanase A	326.63	829.259	-1.341493991	5.00E-05	0.00352415
379	LOC103312195	NC_007417.3:14784008-14786298	103312195	transient receptor potential cation channel protein painless	14.2272	36.1335	-1.286070621	5.00E-05	0.00352415
380	LOC663822	NC_007422.5:13195554-13225411	663822	papilin	0.503907	1.28181	-0.601463312	5.00E-05	0.00352415
381	ApoLI-II	NC_007421.3:4420485-4439966	663181	apolipophorins	192.196	492.282	-1.35234742	5.00E-05	0.00352415
382	LOC656825	NC_007417.3:4960193-4966514	656825	peroxiredoxin-6	37.713	97.5877	-1.348589553	5.00E-05	0.00352415
383	LOC659078	NC_007418.3:5148582-5158362	659078	major facilitator superfamily domain-containing protein 6	8.68528	22.7313	-1.292925471	0.00095	0.0436105
384	LOC656248	NC_007418.3:1193596-1206397	656248	glycerol kinase	10.22	26.834	-1.310775576	0.0006	0.0297494
385	LOC659396	NC_007422.5:14371132-14404279	659396	unc-112-related protein	12.0405	31.6773	-1.325289597	0.0005	0.0259129
386	LOC103314693	NC_007418.3:10852617-10887120	103314693	N-myc protein	8.51253	22.4566	-1.302092908	5.00E-05	0.00352415
387	H2	NC_007417.3:14191742-14196653	657085	serine protease H2	81.6972	216.999	-1.398411129	5.00E-05	0.00352415
388	LOC655021	NC_007425.3:121815-283364	655021	alpha-tocopherol transfer protein-like	9.95102	26.5315	-1.330017963	5.00E-05	0.00352415
389	LOC103313284	NC_007420.3:14473326-14486708	103313284	sperm-tail PG-rich repeat-containing protein 2-like	1.08398	2.89341	-0.901692845	0.00035	0.0194127
390	LOC103313185	NC_007420.3:11559385-11562424	103313185	transient receptor potential cation channel protein painless	3.05371	8.15128	-1.174730666	5.00E-05	0.00352415

391	LOC103314736	NC_007424.3:9708124-9710871	103314736	uncharacterized LOC103314736	6.94336	18.7103	-1.311128441	5.00E-05	0.00352415
392	LOC100141910	NC_007416.3:1031484-1032355	100141910	uncharacterized LOC100141910	8.01286	21.6362	-1.328574903	0.0003	0.0169681
393	Fz2	NC_007418.3:4400667-4448572	656499	frizzled 2	5.49526	14.8874	-1.290423863	0.00045	0.0239168
394	LOC103313518	NC_007422.5:485741-486808	103313518	uncharacterized LOC103313518	14.2983	38.871	-1.381968445	5.00E-05	0.00352415
395	LOC658706	NC_007418.3:19517182-19541777	658706	tolloid-like protein 1	9.82519	26.796	-1.360484939	5.00E-05	0.00352415
396	LOC660692	NC_007416.3:7235947-7240321	660692	transketolase-like protein 2	168.19	463.358	-1.45659319	5.00E-05	0.00352415
397	LOC664291	NC_007417.3:10691814-10694011	664291	protein spartin	3.00823	8.58332	-1.257560247	0.0007	0.0338289
398	LOC661102	NC_007423.3:7018361-7021997	661102	alpha-esterase like protein E1	1.1271	3.25283	-0.999535327	5.00E-05	0.00352415
399	LOC656039	NC_007424.3:12446086-12447094	656039	tetraspanin-8	66.5125	192.213	-1.516965618	5.00E-05	0.00352415
400	LOC654958	NC_007421.3:1029832-1041600	654958	cellular FABP-like protein	166.78	489.233	-1.546896851	0.00105	0.0470692
401	LOC659318	NC_007420.3:8350519-8364848	659318	uncharacterized LOC659318	35.3372	103.705	-1.526811177	5.00E-05	0.00352415
402	LOC656405	NC_007417.3:3308379-3309763	656405	venom protease	8.51499	25.1128	-1.456483117	0.00015	0.00949185
403	LOC103314028	NC_007423.3:11758818-11759722	103314028	hypothetical protein	3.59869	10.6778	-1.344473655	5.00E-05	0.00352415
404	LOC103312583	NC_007419.2:1728589-1756322	103312583	uncharacterized LOC103312583	18.8582	56.1503	-1.525026213	5.00E-05	0.00352415
405	LOC659265	NC_007424.3:7326977-7351458	659265	phosphoinositide 3-kinase regulatory subunit 4	3.65907	10.9193	-1.3551856	5.00E-05	0.00352415
406	LOC655389	NC_007425.3:4332332-4345941	655389	neutral alpha-glucosidase C	44.1687	132.022	-1.55826957	5.00E-05	0.00352415
407	CYP6BR2; CYP6BR3	NW_015450712.1:60752-76536	658247	uncharacterized LOC658247	8.60009	25.7238	-1.477005331	5.00E-05	0.00352415
408	LOC103313084	NC_007420.3:8150224-8151889	103313084	stromelysin-1-like	1.17838	3.59997	-1.07836881	0.00045	0.0239168
409	LOC107397720	NC_007419.2:9572226-9590168	107397720	4-coumarate--CoA ligase 2-like	19.8825	60.8507	-1.566495485	5.00E-05	0.00352415
410	GLEAN_12323	NC_007424.3:4850296-4851085	655079	uncharacterized protein LOC655079	5.38533	16.6719	-1.468624073	5.00E-05	0.00352415
411	LOC658487	NC_007417.3:13021892-13025659	658487	zinc finger protein GLIS2 homolog	27.8875	86.3857	-1.596951858	5.00E-05	0.00352415
412	LOC664182	NC_007422.5:11082944-11083973	664182	exosome complex component MTR3	4.11158	12.8908	-1.442288484	5.00E-05	0.00352415
413	LOC661049	NC_007420.3:10003666-10012997	661049	beta-lactamase-like protein 2 homolog	98.5079	309.884	-1.643493397	5.00E-05	0.00352415
414	LOC661756	NC_007419.2:2509618-2510608	661756	uncharacterized LOC661756	1559.75	4925.9	-1.658440724	5.00E-05	0.00352415
415	LOC107397480	NC_007418.3:4075263-4076325	107397480	uncharacterized LOC107397480	38.3833	123.176	-1.656730457	5.00E-05	0.00352415
416	LOC103315089	NC_007417.3:9904557-9905076	103315089	hypothetical protein	11.1065	35.9131	-1.608351061	5.00E-05	0.00352415
417	LOC661884	NC_007420.3:10074491-10080962	661884	cilia- and flagella-associated protein 47	0.320949	1.0423	-0.628620037	5.00E-05	0.00352415
418	LOC664253	NC_007423.3:9280816-9281998	664253	retinol dehydrogenase 11-like	4.08079	13.2653	-1.489385346	5.00E-05	0.00352415
419	LOC655889	NC_007418.3:19944068-19950826	655889	jouberin	12.3982	40.3232	-1.624912786	5.00E-05	0.00352415
420	P80	NC_007419.2:11668481-11669467	655599	serine protease P80	216.959	716.252	-1.718423309	5.00E-05	0.00352415
421	kinesin-5C	NC_007418.3:18199240-18204036	656336	kinesin 5C	0.957241	3.16133	-1.088223291	5.00E-05	0.00352415
422	sPLA2C	NC_007420.3:9902767-9903984	659784	phospholipase A2C	8.46914	28.2842	-1.628817173	5.00E-05	0.00352415
423	LOC103313391	NC_007421.3:3343020-3343468	103313391	uncharacterized LOC103313391	261.497	874.729	-1.738183553	5.00E-05	0.00352415
424	LOC654983	NC_007419.2:7071287-7072137	654983	cuticle protein 63	6.60227	22.3129	-1.61662631	5.00E-05	0.00352415
425	LOC657081	NC_007425.3:5474613-5478061	657081	innexin inx7	2.43559	8.57454	-1.478645299	5.00E-05	0.00352415
426	LOC103314603	NC_007418.3:15659344-15661900	103314603	putative nuclease HARBI1	3.9694	14.2416	-1.616870781	5.00E-05	0.00352415
427	LOC103313539	NC_007422.5:830025-860944	103313539	uncharacterized LOC103313539	18.7096	67.1462	-1.789734713	5.00E-05	0.00352415
428	LOC662944	NC_007422.5:7373905-7398504	662944	sodium/hydrogen exchanger 10	52.6121	190.67	-1.837993993	0.0001	0.00663971
429	serpin31	NC_007423.3:7024846-7026186	661214	serpin peptidase inhibitor 31	9.01205	32.8776	-1.758594272	5.00E-05	0.00352415
430	CYP346B1	NC_007420.3:9724498-9730156	657187	cytochrome P450 346B1	10.155	37.2619	-1.778218003	5.00E-05	0.00352415
431	LOC103313512	NC_007422.5:495848-496453	103313512	holotricin-3-like	4.43345	16.3598	-1.675809885	5.00E-05	0.00352415
432	LOC661699	NC_007424.3:15467402-15468942	661699	radical S-adenosyl methionine domain-containing protein 2	12.3567	45.6851	-1.805398564	5.00E-05	0.00352415
433	LOC657759	NW_015451620.1:66054-87805	657759	thymidylate synthase	3.5668	13.2108	-1.637732259	5.00E-05	0.00352415
434	-	NW_015451451.1:748-3157	-	-	2.7263	10.1745	-1.584394546	5.00E-05	0.00352415

435	-	NC_007417.3:170837-175251	-	-	9.42185	35.3481	-1.802268558	5.00E-05	0.00352415
436	LOC658244	NC_007420.3:970982-981609	658244	uncharacterized LOC658244	1.42336	5.45437	-1.413267544	5.00E-05	0.00352415
437	LOC657670	NC_007424.3:5685639-5714053	657670	patched domain-containing protein 3	16.2554	62.6441	-1.882978861	5.00E-05	0.00352415
438	LOC103312302	NC_007418.3:30184276-30184770	103312302	uncharacterized LOC103312302	118.485	467.497	-1.971210294	5.00E-05	0.00352415
439	LOC660178	NC_007421.3:367354-376893	660178	fatty acid synthase	0.167013	0.662965	-0.510937173	0.0002	0.0120247
440	ilr1; InR	NC_007416.3:5210343-5247750	661524	insulin-like receptor	2.38565	9.54539	-1.639107707	0.00095	0.0436105
441	Z9desB	NW_015450728.1:196850-224677	657939	Z9 acyl-CoA desaturase B	19.4274	77.8752	-1.949066169	5.00E-05	0.00352415
442	LOC655542	NC_007423.3:7118455-7124552	655542	ribosome biogenesis protein BMS1 homolog	1.54215	6.18561	-1.499061476	5.00E-05	0.00352415
443	Cda7	NC_007420.3:6635069-6636388	100126689	chitin deacetylase 7	5.10141	20.5562	-1.820888293	5.00E-05	0.00352415
444	LOC655598	NC_007419.2:9628012-9630052	655598	TBC1 domain family member 19	0.453191	1.86905	-0.981348775	0.0001	0.00663971
445	LOC103314558	NW_015451937.1:352665-366702	103314558	uncharacterized LOC103314558	0.590404	2.45871	-1.120840764	0.00015	0.00949185
446	LOC659172	NC_007420.3:5755461-5757901	659172	hypothetical protein	0.901662	3.86246	-1.354425537	0.0007	0.0338289
447	LOC656478	NW_015450245.1:57584-72054	656478	acyl-CoA Delta(11) desaturase-like	10.6022	45.7477	-2.010496992	5.00E-05	0.00352415
448	LOC658435	NC_007421.3:3462031-3465600	658435	cytosolic 10-formyltetrahydrofolate dehydrogenase	3.57965	15.4737	-1.846855372	5.00E-05	0.00352415
449	LOC103313827	NC_007422.5:14515184-14556050	103313827	monocarboxylate transporter 7	7.62668	33.5906	-2.003502692	0.00015	0.00949185
450	LOC662305	NC_007422.5:13796663-13799189	662305	protein DEK	5.00793	22.4606	-1.965300002	5.00E-05	0.00352415
451	LOC103315154	NC_007417.3:5901445-5903598	103315154	leucine-rich repeat-containing protein let-4-like	0.393696	1.78656	-0.99956931	0.0002	0.0120247
452	LOC660364	NC_007421.3:5683714-5691537	660364	band 7 protein AGAP004871	2.41607	11.268	-1.844490629	5.00E-05	0.00352415
453	LOC662610	NC_007421.3:1565076-1569411	662610	putative fatty acyl-CoA reductase CG5065	2.68057	12.5937	-1.884937074	0.00015	0.00949185
454	LOC103313579	NC_007422.5:3192754-3200292	103313579	receptor-type tyrosine-protein phosphatase kappa	0.510908	2.55092	-1.232777041	5.00E-05	0.00352415
455	gag	NW_015450678.1:10650-15931	100141955	ORF 1	0.547611	2.75826	-1.280021989	5.00E-05	0.00352415
456	LOC103314314	NC_007424.3:13079595-13137188	103314314	brachyurin	390.767	2020.48	-2.367344146	0.00045	0.0239168
457	LOC103312247	NC_007418.3:1081163-1087966	103312247	intraflagellar transport protein 43 homolog	1.0107	5.23447	-1.632569075	5.00E-05	0.00352415
458	LOC661074	NC_007424.3:15596693-15598718	661074	carboxylesterase 1E	1.62205	8.86383	-1.911452739	5.00E-05	0.00352415
459	Akh2	NC_007420.3:13480284-13480639	663044	adipokinetic hormone 2	6.95522	38.17	-2.299775395	5.00E-05	0.00352415
460	LOC107399289	NC_007417.3:9749344-9751437	107399289	sodium channel protein Nach-like	0.232501	1.30933	-0.90588553	0.00085	0.0395751
461	LOC107398763	NC_007425.3:4207123-4208204	107398763	uncharacterized LOC107398763	16.6393	104.424	-2.579338122	5.00E-05	0.00352415
462	LOC655322	NW_015452040.1:14345-15937	655322	venom carboxylesterase-6-like	0.315282	1.98004	-1.179959545	0.00015	0.00949185
463	LOC661561	NC_007423.3:3374630-3390831	661561	annexin A7	9.76415	61.6714	-2.541572821	0.0003	0.0169681
464	LOC656604	NC_007423.3:9636269-9638323	656604	venom carboxylesterase-6	1.57375	11.1145	-2.234791032	5.00E-05	0.00352415
465	LOC656826	NC_007425.3:2117796-2123085	656826	phospholipase A1-like	5.97957	42.2679	-2.632087039	5.00E-05	0.00352415
466	GLEAN_02953	NC_007418.3:5837554-5838654	663117	cathepsin B precursor	5.93956	42.8701	-2.660321898	5.00E-05	0.00352415
467	LOC107397872	NC_007419.2:12238272-12284334	107397872	uncharacterized LOC107397872	0.13632	1.05615	-0.855576345	0.0003	0.0169681
468	LOC660377	NC_007423.3:10431640-10433201	660377	putative protein TPRXL	21.7418	174.968	-2.951894745	5.00E-05	0.00352415
469	Cpap1-g	NC_007422.5:11276727-11280065	664005	cuticular protein analogous to peritrophins 1-G	0.47327	3.903	-1.73464291	5.00E-05	0.00352415
470	LOC662640	NC_007420.3:6930369-6932879	662640	facilitated trehalose transporter Tret1	2.65113	22.7008	-2.698520814	5.00E-05	0.00352415
471	LOC660146	NC_007420.3:7392974-7394114	660146	uncharacterized LOC660146	11.7103	102.602	-3.026981866	5.00E-05	0.00352415
472	LOC658176	NW_015450462.1:7116-21537	658176	phosphoribosylformylglycinamidine synthase	0.0669483	0.603053	-0.587331854	0.0002	0.0120247
473	OBP-C11; TcOBP10A	NC_007425.3:5617055-5726603	656161	odorant binding protein C11	1085.48	10247.1	-3.237622936	5.00E-05	0.00352415
474	-	NC_007419.2:12284404-12286440	-	-	0.168842	2.05763	-1.387333914	5.00E-05	0.00352415
475	P23; P24	NC_007417.3:12101023-12102083	662758	serine protease P23	1.09272	13.8693	-2.82888553	5.00E-05	0.00352415
476	LOC657170	NC_007417.3:14197609-14198889	657170	trypsin II-P29	2.25799	34.4754	-3.444764871	5.00E-05	0.00352415
477	LOC100141893	NC_007419.2:6662033-6671668	100141893	uncharacterized LOC100141893	0.169954	2.85942	-1.721932246	0.00025	0.014684
478	LOC103312301	NC_007418.3:30148152-30149679	103312301	salivary glue protein Sgs-3-like	4.55894	112.39	-4.350339792	5.00E-05	0.00352415

479	LOC657322	NC_007418.3:4131236-4149119	657322	venom carboxylesterase-6	2.1112	52.1333	-4.094073273	0.0001	0.00663971
480	LOC107397926	NC_007420.3:5233008-5233767	107397926	protein NPC2 homolog	1.24216	33.5822	-3.947068514	0.0001	0.00663971
481	-	NC_007417.3:551923-552167	-	-	0	6.69672	-2.944243764	5.00E-05	0.00352415
482	Nplp3	NC_007418.3:4125382-4126111	657788	cuticle protein 38	0	0.947354	-0.961515168	5.00E-05	0.00352415
483	LOC103313848	NC_007418.3:4126508-4126952	103313848	cuticle protein 63	0	1.45399	-1.29512937	5.00E-05	0.00352415
484	-	NC_007419.2:3198051-3198703	-	-	0	1.21861	-1.149656085	5.00E-05	0.00352415
485	LOC659176	NC_007420.3:11255780-11256299	659176	endocuticle structural glycoprotein SgAbd-5	0	0.822036	-0.865551464	0.001	0.0455408
486	LOC661258	NC_007420.3:6421267-6421839	661258	uncharacterized LOC661258	0	0.909295	-0.933040027	5.00E-05	0.00352415
487	LOC659862	NC_007421.3:9318737-9323082	659862	facilitated trehalose transporter Tret1	0	0.863507	-0.898020238	5.00E-05	0.00352415
488	-	NC_007421.3:9911374-9911849	-	-	0	0.995359	-0.996648336	5.00E-05	0.00352415
489	LOC107398740	NC_007425.3:1800702-1804977	107398740	uncharacterized LOC107398740	0	5.50343	-2.701200816	5.00E-05	0.00352415
490	LOC656244	NC_007425.3:6352529-6394030	656244	coiled-coil domain-containing protein 186	0	2.45839	-1.79010057	0.00105	0.0470692
491	-	NC_007425.3:17670-18339	-	-	0	0.986724	-0.990391464	5.00E-05	0.00352415
492	-	NC_007425.3:1799904-1800625	-	-	0	3.58448	-2.196758104	5.00E-05	0.00352415
493	-	NC_007425.3:1821835-1822113	-	-	0	5.02834	-2.591760788	5.00E-05	0.00352415
494	-	NW_015450315.1:75893-76156	-	-	0	2.64416	-1.865586303	5.00E-05	0.00352415
495	-	NW_015450524.1:3960-4092	-	-	0	52.6068	-5.744344112	5.00E-05	0.00352415
496	LOC100142598	NW_015450864.1:165-1246	100142598	uncharacterized LOC100142598	0	1.79018	-1.480358196	5.00E-05	0.00352415
497	-	NW_015451540.1:63-872	-	-	0	4.81272	-2.539213415	5.00E-05	0.00352415
498	-	NW_015451645.1:2730-3133	-	-	0	1.1935	-1.133234706	0.00025	0.014684
499	-	NW_015451645.1:3193-4113	-	-	0	0.637644	-0.71162177	5.00E-05	0.00352415
500	-	NW_015452269.1:21-416	-	-	0	36.036	-5.210856386	5.00E-05	0.00352415
501	-	NC_007416.3:8469639-8469930	-	-	2.33447	0	1.737457469	0.00055	0.0281853
502	LOC661960	NC_007417.3:13341079-13411736	661960	Kv channel-interacting protein 1	1.10321	0	1.072592907	0.00105	0.0470692
503	LOC107397543	NC_007418.3:11927693-11928397	107397543	uncharacterized LOC107397543	0.660694	0	0.731786266	5.00E-05	0.00352415
504	-	NC_007419.2:3699714-3700168	-	-	2.03159	0	1.600074653	5.00E-05	0.00352415
505	LOC103313177	NC_007420.3:11317219-11317627	103313177	carbonyl reductase [NADPH	3.22002	0	2.077249836	5.00E-05	0.00352415
506	LOC107398167	NC_007422.5:6049962-6051382	107398167	serine protease easter-like	0.675544	0	0.744629572	5.00E-05	0.00352415
507	LOC107398427	NC_007423.3:747341-747788	107398427	uncharacterized LOC107398427	1.91857	0	1.545261671	5.00E-05	0.00352415
508	LOC655293	NC_007423.3:2323500-2324587	655293	circumsporozoite protein	0.570097	0	0.650853691	5.00E-05	0.00352415
509	-	NC_007425.3:5237995-5238530	-	-	2.04683	0	1.607309006	5.00E-05	0.00352415
510	LOC103312403	NW_015450265.1:237-1091	103312403	uncharacterized LOC103312403	2.02857	0	1.598636757	5.00E-05	0.00352415
511	LOC103312400	NW_015450265.1:1399-4048	103312400	uncharacterized LOC103312400	0.728572	0	0.789580697	5.00E-05	0.00352415
512	-	NW_015450434.1:88-653	-	-	1.47712	0	1.308663759	5.00E-05	0.00352415
513	-	NW_015451025.1:44472-44704	-	-	13.879	0	3.895205663	5.00E-05	0.00352415
514	-	NW_015451646.1:102584-103025	-	-	2.75602	0	1.909204745	5.00E-05	0.00352415
515	-	NW_015451646.1:104058-104832	-	-	1.69542	0	1.430510091	5.00E-05	0.00352415
516	-	NW_015451723.1:7990-9393	-	-	0.721019	0	0.783263025	5.00E-05	0.00352415
517	-	NW_015451840.1:901-1036	-	-	54.374	0	5.791136835	5.00E-05	0.00352415
518	-	NW_015451896.1:48504-48829	-	-	3.55401	0	2.187137459	5.00E-05	0.00352415