

Supplementary Table 3: Differential expression and protein group identification of significant proteins associated with LTM formation.

<i>Lymanaea</i> transcript ID	Putative protein name	Top mouse BLASTp hit UniProt accession	LTM vs. no LTM		LTM vs. yoke control		No LTM vs. yoke control	
			Log ₂ -fold change	Adjusted p-value (FDR)	Log ₂ -fold change	Adjusted p-value (FDR)	Log ₂ -fold change	Adjusted p-value (FDR)
evgLocus_FX_24424	Partitioning defective 6 homolog gamma	Q9JK84	10.338	1.29E-03	13.743	2.94E-14	3.406	0.0769
evgLocus_strawberry_AH_33731	NA	NA	13.356	3.39E-13	13.356	2.94E-14	0.000	0.4926
evgLocus_Trinity_GG_DRR_462 7	Spermatogenesis-associated protein 13	Q5DU57	12.575	3.39E-13	12.575	2.94E-14	0.000	0.4926
evgLocus_FX_25648	Leucine-rich repeat- containing protein 59	Q922Q8	5.012	7.83E-01	11.448	2.83E-03	6.437	0.0796
evgLocus_FX_27227	Mitochondrial ribosome- associated GTPase 1	Q8R2R6	8.649	6.60E-04	11.369	2.94E-14	2.720	0.0783
evgLocus_Trinity_AE_62019	XK-related protein 6	E9Q6C8	8.441	1.08E-03	11.095	2.94E-14	2.654	0.0841
evgLocus_FX_50942	NA	NA	5.098	7.64E-01	11.029	2.73E-03	5.931	0.0879
evgLocus_Trinity_RF_Nov18_94 87	Glutathione hydrolase 1 proenzyme	Q60928	6.120	5.54E-01	10.285	4.69E-04	4.166	0.1156
evgLocus_FX_30900	Spliceosome-associated protein CWC15 homolog	Q9JHS9	7.551	3.87E-01	9.913	5.73E-04	2.362	0.2488
evgLocus_stringtie_AE_51001	NA	NA	6.477	3.99E-01	9.842	6.83E-05	3.365	0.1278
evgLocus_FX_48384	GTPase, IMAP family member 7	Q8R379	10.021	5.85E-02	9.784	8.36E-05	-0.236	0.4699
evgLocus_Trinity_AG_6231	1-phosphatidylinositol 3- phosphate 5-kinase	Q9Z1T6	6.364	3.23E-01	9.773	1.17E-05	3.409	0.1062
evgLocus_FX_23535	Protein Hikeshi	Q9DD02	9.363	1.06E-01	9.659	2.34E-04	0.296	0.4652
evgLocus_FX_28006	Zinc finger FYVE domain- containing protein 21	Q8VCM3	6.570	4.76E-01	9.562	5.64E-04	2.993	0.1785
evgLocus_scallop_AF_16710	Oligoribonuclease, mitochondrial	Q9D8S4	10.191	8.25E-02	9.552	4.03E-04	-0.639	0.4319
evgLocus_strawberry_AG_14684	Dystonin (Fragment)	S4R1Y6	9.385	5.76E-02	9.420	4.68E-05	0.036	0.4891
evgLocus_FX_17339	Clathrin interactor 1	Q5SUH6	6.245	5.11E-01	9.410	6.83E-04	3.166	0.1655
evgLocus_FX_28816	NA	NA	6.867	5.66E-01	9.383	7.09E-03	2.516	0.2738
evgLocus_FX_21884	Heat shock factor 1	Q52L52	6.573	4.69E-01	9.210	8.16E-04	2.636	0.2064
evgLocus_Trinity_UM_DRR_74 05	GTPase IMAP family member 4	Q99JY3	8.974	9.04E-02	9.070	1.69E-04	0.096	0.4832
evgLocus_Trinity_AH_113193	CTD small phosphatase-like protein 2	Q8BG15	4.010	7.14E-01	9.052	3.68E-04	5.042	0.0525

evgLocus_FX_21779	Aurora kinase A	P97477	6.355	3.86E-01	9.008	1.93E-04	2.653	0.1751
evgLocus_scallop_AH_22207	NA	NA	3.532	8.45E-01	8.964	1.42E-02	5.432	0.0996
evgLocus_strawberry_AG_41478	Copper-transporting ATPase 1	Q64430	3.970	7.98E-01	8.923	5.90E-03	4.953	0.0961
evgLocus_Trinity_AE_55449	E3 ubiquitin-protein ligase RNF115	Q9D0C1	10.910	3.59E-01	8.822	3.15E-02	-2.088	0.3478
evgLocus_Trinity_AE_94168	Family with sequence similarity 102, member B	E9Q4R1	8.217	2.40E-01	8.731	1.56E-03	0.515	0.4455
evgLocus_Scallop_AE_27698	Cystathionine gamma-lyase	Q8VCN5	3.148	8.23E-01	8.485	2.66E-03	5.337	0.0589
evgLocus_FX_34502	Aldo-keto reductase family 1 member A1	Q9JII6	5.723	4.77E-01	8.475	4.68E-04	2.751	0.1667
evgLocus_FX_20709	Tudor and KH domain-containing protein	Q80VL1	8.415	9.25E-02	8.352	2.45E-04	-0.063	0.4861
evgLocus_Trinity_AE_66075	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	Q922H2	10.035	3.54E-01	8.328	2.76E-02	-1.707	0.3654
evgLocus_FPS_64	Cytochrome b-c1 complex subunit 7	Q9CQB4	10.741	6.04E-02	8.193	2.83E-03	-2.548	0.2109
evgLocus_strawberry_AG_31434	Leucine-rich repeats and immunoglobulin-like domains protein 3	Q6P1C6	3.593	8.39E-01	8.076	2.34E-02	4.482	0.1369
evgLocus_FX_28769	Putative peptidyl-tRNA hydrolase PTRHD1	D3Z4S3	5.213	5.34E-01	7.866	1.14E-03	2.653	0.1739
evgLocus_scallop_AG_1191	Arylsulfatase B	A0A0R4J138	6.554	4.97E-01	7.713	8.58E-03	1.159	0.3819
evgLocus_FX_17754	NA	NA	7.784	4.62E-01	7.547	2.30E-02	-0.238	0.4749
evgLocus_FX_19487	Coiled-coil-helix-coiled-coil-helix domain containing 2-like	B2RPU8	10.238	9.22E-02	7.360	1.02E-02	-2.879	0.1873
evgLocus_FX_16702	Phosphatidylinositol 4-kinase alpha	E9Q3L2	7.055	5.18E-01	7.320	2.44E-02	0.265	0.4725
evgLocus_FX_17041	Hemicentin-1	D3YXG0	9.477	1.07E-01	7.316	7.78E-03	-2.161	0.2522
evgLocus_Scallop_DRR_36504	Glutaminyl-peptide cyclotransferase-like protein	Q8BH73	3.657	8.12E-01	7.305	2.12E-02	3.649	0.1564
evgLocus_FX_22624	NA	NA	3.063	8.36E-01	7.264	1.58E-02	4.201	0.1118

evgLocus_FX_54901	PHD finger-like domain-containing protein 5A		4.117	8.02E-01	7.244	3.12E-02	3.127	0.2110
		P83870						
evgLocus_FX_18507	Cyclic AMP-responsive element-binding protein 3-like protein 3	Q91XE9	3.933	8.15E-01	7.242	3.29E-02	3.308	0.1995
evgLocus_Trinity_AG_107445	Carcinoembryonic antigen-related cell adhesion molecule 1	Q3LFS5	4.678	6.48E-01	7.142	8.55E-03	2.463	0.2130
evgLocus_FX_34864	COMM domain-containing protein 9	Q8K2Q0	3.910	7.63E-01	7.141	1.31E-02	3.231	0.1613
evgLocus_FX_16749	Integrin beta-1	P09055	3.195	8.32E-01	7.092	2.02E-02	3.897	0.1324
evgLocus_Scallop_AE_689	Serine/threonine-protein phosphatase 4 catalytic subunit	P97470	3.655	8.01E-01	7.081	1.98E-02	3.426	0.1609
evgLocus_FX_28130	Protein ABHD13	Q80UX8	10.315	1.07E-01	7.072	1.86E-02	-3.243	0.1706
evgLocus_FX_18228	Glycylpeptide N-tetradecanoyltransferase 1	O70310	4.258	7.13E-01	7.069	1.10E-02	2.811	0.1854
evgLocus_FX_30398	Prostaglandin reductase 1	Q91YR9	3.346	8.04E-01	7.049	1.24E-02	3.703	0.1252
evgLocus_FX_21593	Ubiquitin-like modifier-activating enzyme 5	Q8VE47	3.816	8.05E-01	7.044	2.71E-02	3.228	0.1881
evgLocus_FX_37268	CDC42 small effector protein 2	Q8BGH7	7.694	4.61E-01	6.944	3.14E-02	-0.751	0.4323
evgLocus_FX_28362	D-aspartate oxidase	Q922Z0	6.691	4.85E-01	6.887	1.99E-02	0.196	0.4762
evgLocus_FX_21345	Nuclear transcription factor Y subunit gamma	P70353	9.744	1.00E-01	6.826	1.47E-02	-2.918	0.1778
evgLocus_FX_27207	Lactoylglutathione lyase	Q9CPU0	2.738	8.63E-01	6.742	3.37E-02	4.004	0.1401
evgLocus_strawberry_AG_34998	D-amino acid oxidase	A0A0R4J203	3.831	7.61E-01	6.712	1.69E-02	2.880	0.1819
evgLocus_Trinity_AG_113184	Calponin-2	Q08093	9.165	1.72E-01	6.673	2.28E-02	-2.491	0.2312
evgLocus_FX_53228	D-dopachrome decarboxylase	O35215	3.385	7.88E-01	6.651	1.37E-02	3.266	0.1432
evgLocus_FX_16960	Tricarboxylate transport protein, mitochondrial	Q8JZU2	2.957	8.56E-01	6.649	3.80E-02	3.692	0.1624
evgLocus_Trinity_GG_DRR_25954	Histone deacetylase	A0A1B0GSQ5	5.369	6.16E-01	6.640	2.49E-02	1.271	0.3718
evgLocus_Trinity_AG_109189	Serine palmitoyltransferase 2	P97363	11.420	2.76E-02	6.621	1.59E-02	-4.799	0.0682
evgLocus_FX_36449	Thioredoxin domain-containing protein 9	Q9CQ79	5.479	5.68E-01	6.591	1.91E-02	1.111	0.3813

evgLocus_FPS_3754	Tetraspanin-31	Q9CQ88	3.836	8.06E-01	6.590	3.71E-02	2.754	0.2306
evgLocus_FX_21592	Proton-coupled zinc antiporter SLC30A5	Q8R4H9	3.011	8.33E-01	6.573	2.29E-02	3.562	0.1410
evgLocus_FX_22547	Myotubularin-related protein 10	Q7TPM9	6.618	5.47E-01	6.563	3.71E-02	-0.054	0.4885
evgLocus_stringtie_AF_9179	Carboxylic ester hydrolase	E9PV38	2.555	8.48E-01	6.536	1.56E-02	3.981	0.1014
evgLocus_Scallop_AE_28246	U4/U6.U5 tri-snRNP- associated protein 2	Q3TIX9	9.443	1.36E-01	6.526	2.34E-02	-2.917	0.1865
evgLocus_FX_18903	Lipopolysaccharide-binding protein	Q61805	3.322	8.11E-01	6.506	2.29E-02	3.184	0.1648
evgLocus_Scallop_AE_36784	U5 small nuclear ribonucleoprotein 40 kDa protein	Q6PE01	6.372	5.38E-01	6.490	3.09E-02	0.118	0.4832
evgLocus_FX_23729	Flavin-containing monooxygenase 3	P97501	6.740	4.30E-01	6.479	1.99E-02	-0.261	0.4692
evgLocus_Trinity_AG_105748	Tyrosine-protein kinase	Q3U436	3.392	8.27E-01	6.473	3.61E-02	3.081	0.1949
evgLocus_FX_27805	Synaptic vesicle membrane protein VAT-1 homolog-like	Q80TB8	3.264	8.23E-01	6.472	2.76E-02	3.208	0.1715
evgLocus_Strawberry_DRR_228	Cytoplasmic polyadenylation element binding protein 2	E9Q5X2	6.438	5.76E-01	6.461	4.51E-02	0.023	0.4909
evgLocus_FX_19014	Exocyst complex component 8	Q6PGF7	4.360	7.07E-01	6.456	2.14E-02	2.095	0.2648
evgLocus_FX_16621	Cation-independent mannose- 6-phosphate receptor	Q07113	9.305	6.11E-02	6.449	7.62E-03	-2.857	0.1507
evgLocus_FX_21860	HHIP-like protein 2	Q9D2G9	9.951	1.33E-01	6.448	3.04E-02	-3.503	0.1556
evgLocus_FX_28914	Adenylyltransferase and sulfurtransferase MOCS3	A2BDX3	3.688	7.80E-01	6.365	2.43E-02	2.677	0.2028
evgLocus_scallop_AF_22694	Serine/threonine-protein kinase 3	Q9J110	0.889	9.15E-01	6.342	2.77E-02	5.453	0.0576
evgLocus_scallop_AH_27557	Spectrin beta chain, non- erythrocytic 1	Q62261	3.694	7.72E-01	6.341	2.24E-02	2.647	0.2004
evgLocus_stringtie_AF_25807	Spermatogenesis-associated serine-rich protein 2	Q8K1N4	3.483	8.18E-01	6.340	3.62E-02	2.858	0.2084

evgLocus_FX_25165	Regulator of chromosome condensation		3.887	7.37E-01	6.323	1.82E-02	2.435	0.2109
		Q8VE37						
evgLocus_FX_16744	Unconventional myosin-IXb	Q9QY06	3.317	8.02E-01	6.322	2.21E-02	3.005	0.1698
evgLocus_FX_23826	Hsp70-binding protein 1	Q99P31	9.425	1.27E-01	6.271	2.61E-02	-3.154	0.1650
evgLocus_FX_19530	Papillary Renal Cell carcinoma (Translocation-associated)	Q9EQC8	6.302	5.64E-01	6.249	4.26E-02	-0.053	0.4886
evgLocus_FX_20302	Growth hormone secretagogue receptor type 1	Q99P50	5.800	5.93E-01	6.187	4.11E-02	0.387	0.4613
evgLocus_Trinity_AH_121246	Ankyrin repeat and zinc finger domain-containing protein 1	Q80UU1	5.769	5.35E-01	6.179	2.40E-02	0.410	0.4545
evgLocus_FX_24042	E3 ubiquitin-protein ligase HERC2	Q4U2R1	5.330	5.83E-01	6.155	2.77E-02	0.825	0.4137
evgLocus_strawberry_AE_25323	Tetratricopeptide repeat protein 5	Q99LG4	9.243	9.73E-02	6.141	1.93E-02	-3.102	0.1495
evgLocus_FX_30625	Cancer-related nucleoside-triphosphatase homolog	Q9CQA9	8.626	1.04E-01	6.123	1.43E-02	-2.503	0.1871
evgLocus_FX_29369	Peptidyl-tRNA hydrolase ICT1, mitochondrial	Q8R035	6.303	5.50E-01	6.119	4.12E-02	-0.184	0.4780
evgLocus_Trinity_AE_131571	Electroneutral sodium bicarbonate exchanger 1	Q8JZR6	8.811	1.03E-01	6.114	1.62E-02	-2.696	0.1743
evgLocus_Scallop_AE_23883	BRISC and BRCA1-A complex member 2	Q8K3W0	5.574	6.36E-01	6.108	4.56E-02	0.534	0.4494
evgLocus_Trinity_AE_125033	Probable serine carboxypeptidase CPVL	Q9D3S9	5.911	5.29E-01	6.099	2.72E-02	0.188	0.4760
evgLocus_FX_24720	D-ribitol-5-phosphate cytidyltransferase	Q5RJG7	8.106	1.00E-01	6.068	8.66E-03	-2.038	0.2206
evgLocus_FX_21063	Neuronal cell adhesion molecule	A0A1W2P7Y9	3.638	7.42E-01	6.064	1.70E-02	2.425	0.1985
evgLocus_Scallop_AE_38455	NA	NA	9.252	9.72E-02	6.052	2.09E-02	-3.200	0.1423
evgLocus_FX_20478	Threonine synthase-like 2	Q80W22	3.277	8.12E-01	6.018	3.11E-02	2.741	0.1973
evgLocus_FX_29539	Pre-mRNA-splicing factor 38A	Q4FK66	5.365	6.28E-01	6.009	4.08E-02	0.643	0.4369

evgLocus_Trinity_RF_Nov18_21 983	Protein mono-ADP- ribosyltransferase PARP11		5.478	5.78E-01	5.996	3.32E-02	0.519	0.4459
evgLocus_Trinity_AG_112948	Telomerase protein component 1	Q8CFF0	8.962	1.37E-01	5.977	2.77E-02	-2.985	0.1700
evgLocus_FX_22113	Serine/threonine-protein kinase Chk2	P97499	8.243	2.36E-01	5.903	3.33E-02	-2.340	0.2382
evgLocus_FX_19141	Regulation of nuclear pre- mRNA domain containing 2	Q9Z265	6.728	4.00E-01	5.868	2.71E-02	-0.860	0.4050
evgLocus_Scallop_AE_3482	NA	A0A0G2JFN1	3.747	7.78E-01	5.857	3.68E-02	2.111	0.2691
evgLocus_Trinity_AF_50472	Ceramide kinase	NA	3.345	7.87E-01	5.811	2.63E-02	2.466	0.2048
evgLocus_FPS_2840	Transmembrane protein 263	Q8K4Q7	2.656	8.52E-01	5.787	3.82E-02	3.132	0.1687
evgLocus_FX_17871	NPC intracellular cholesterol transporter 2	Q9DAM7	3.125	8.28E-01	5.775	4.17E-02	2.650	0.2135
evgLocus_Scallop_AE_1633	Receptor-type tyrosine- protein phosphatase alpha	Q9Z0J0	6.218	5.31E-01	5.773	4.23E-02	-0.445	0.4540
evgLocus_strawberry_AG_49481	Anamorsin	Q91V35	6.141	5.37E-01	5.741	4.31E-02	-0.400	0.4581
evgLocus_scallop_AG_12589	4- trimethylaminobutyraldehyde dehydrogenase	Q8WTY4	3.754	7.75E-01	5.701	3.96E-02	1.947	0.2864
evgLocus_Strawberry_DRR_452 32	Methionine synthase	Q9JLJ2	8.432	2.16E-01	5.696	3.93E-02	-2.736	0.1978
evgLocus_FX_18824	Vacuolar protein sorting- associated protein 41 homolog	A6H5Y3	5.500	6.01E-01	5.695	4.69E-02	0.195	0.4765
evgLocus_FX_37125	Mitochondrial peptide methionine sulfoxide reductase	Q5KU39	0.742	9.16E-01	5.677	2.65E-02	4.935	0.0537
evgLocus_scallop_AF_8451	Eukaryotic translation initiation factor 2D	Q9D6Y7	8.704	9.92E-02	5.631	2.27E-02	-3.073	0.1391
evgLocus_scallop_AH_42089	von Willebrand factor A domain-containing protein 8	Q61211	3.669	7.94E-01	5.629	4.73E-02	1.960	0.2940
evgLocus_FX_20583	Mediator of RNA polymerase II transcription subunit 15	Q8CC88	8.389	1.19E-01	5.595	2.45E-02	-2.794	0.1635
evgLocus_Trinity_AF_125460	Probable E3 ubiquitin-protein ligase HERC4	Q924H2	6.166	5.21E-01	5.588	4.33E-02	-0.579	0.4399
evgLocus_FX_30076	NA	Q6PAV2	3.567	7.63E-01	5.582	3.00E-02	2.014	0.2568
		NA						

evgLocus_Trinity_AF_1950	Ral GTPase-activating protein subunit alpha-2		5.995	5.10E-01	5.543	3.79E-02	-0.452	0.4502
		A3KGS3						
evgLocus_Scallop_AE_19166	WD repeat-containing protein 44		5.131	5.84E-01	5.531	3.77E-02	0.400	0.4553
		Q6NVE8						
evgLocus_FX_23448	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase		5.676	5.62E-01	5.513	4.50E-02	-0.163	0.4786
		Q9JI78						
evgLocus_FX_36321	Proteasome assembly chaperone 2		2.382	8.66E-01	5.459	4.72E-02	3.077	0.1734
		Q9EST4						
evgLocus_Trinity_AF_43207	Protein PTHB1		8.517	1.04E-01	5.437	2.58E-02	-3.080	0.1369
		Q811G0						
evgLocus_FX_25261	Family with sequence similarity 151, member B		2.733	8.24E-01	5.345	3.00E-02	2.612	0.1789
		D3YUE4						
evgLocus_strawberry_AH_15947	Glycosyltransferase 8 domain-containing protein 1		8.855	8.96E-02	5.318	2.84E-02	-3.538	0.1071
		Q6NSU3						
evgLocus_FX_28997	39S ribosomal protein L40, mitochondrial		1.469	8.95E-01	5.292	3.87E-02	3.824	0.1052
		Q9Z2Q5						
evgLocus_FX_18266	DENN domain-containing protein 5B		3.224	7.67E-01	5.264	2.62E-02	2.040	0.2292
		A2RSQ0						
evgLocus_FX_18540	Macrophage-expressed gene 1 protein		1.566	8.94E-01	5.201	4.68E-02	3.635	0.1232
		E9QN37						
evgLocus_FX_28631	Mitochondrial ribosomal protein S35		8.410	1.39E-01	5.072	4.23E-02	-3.338	0.1302
		A0A0R4J0L6						
evgLocus_FPS_3061	Cytochrome c, somatic		0.249	9.27E-01	4.998	4.39E-02	4.749	0.0602
		P62897						
evgLocus_Trinity_AE_28460	Flavin-containing monooxygenase 5		0.619	9.18E-01	4.957	3.55E-02	4.338	0.0644
		P97872						
evgLocus_scallop_AF_31778	Histone-lysine N-methyltransferase SETD2		0.490	9.21E-01	4.914	2.98E-02	4.425	0.0524
		E9Q5F9						
evgLocus_FX_20242	Dual oxidase maturation factor 1		0.475	9.22E-01	4.788	4.59E-02	4.313	0.0710
		Q8VE49						
evgLocus_Trinity_AE_3911	Calcipressin-3		1.654	8.75E-01	4.678	3.05E-02	3.024	0.1155
		Q9JKK0						
evgLocus_FX_20879	Glutathione S-transferase theta-3		0.384	9.23E-01	4.645	3.56E-02	4.261	0.0563
		Q99L20						

evgLocus_FX_26577	Phytanoyl-CoA dioxygenase domain containing 1		0.503	9.20E-01	4.623	3.46E-02	4.120	0.0602
evgLocus_FPS_3926	Calcineurin B homologous protein 1	A2AQZ7	0.598	9.17E-01	4.617	3.18E-02	4.019	0.0610
evgLocus_FX_19326	Dihydropyrimidine dehydrogenase [NADP(+)]	P61022	0.106	9.30E-01	4.519	4.02E-02	4.413	0.0507
evgLocus_FX_16882	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	Q8CHR6	0.523	9.21E-01	4.507	4.87E-02	3.984	0.0783
evgLocus_Trinity_RF_Nov18_36711	Cytotoxic granule associated RNA binding protein TIA1	G3X8Y3	0.734	9.12E-01	4.501	2.87E-02	3.767	0.0636
evgLocus_FX_26819	Replication factor C subunit 4	P52912	1.633	8.53E-01	4.486	1.23E-02	2.853	0.0859
evgLocus_Scallop_AE_35822	Casein kinase II subunit alpha	Q99J62	0.727	9.15E-01	4.476	4.75E-02	3.749	0.0876
evgLocus_FX_18132	Angiotensin-converting enzyme (Fragment)	Q60737	1.113	9.01E-01	4.465	3.91E-02	3.352	0.0981
evgLocus_FX_27480	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	F6QCP8	0.923	9.05E-01	4.460	2.78E-02	3.537	0.0711
evgLocus_Trinity_AE_48334	E3 ubiquitin-protein ligase HERC2	P36552	1.918	8.49E-01	4.402	2.79E-02	2.484	0.1418
evgLocus_FX_16636	NA	Q4U2R1	0.910	9.02E-01	4.385	2.12E-02	3.475	0.0616
evgLocus_FX_21493	Armadillo repeat-containing protein 10	NA	0.298	9.25E-01	4.360	3.52E-02	4.062	0.0531
evgLocus_FX_35389	Riboflavin kinase	Q9D0L7	0.823	9.09E-01	4.331	3.47E-02	3.508	0.0770
evgLocus_FX_23456	Dehydrogenase/reductase SDR family member 6	Q8CFV9	0.112	9.29E-01	4.269	4.29E-02	4.157	0.0546
evgLocus_FX_20982	Conserved oligomeric Golgi complex subunit 2	Q8JZV9	0.720	9.10E-01	4.258	2.52E-02	3.538	0.0598
evgLocus_FX_18336	RNA-binding protein Ro60	Q921L5	0.663	9.15E-01	4.241	4.09E-02	3.578	0.0772
evgLocus_FX_18331	Mannose-1-phosphate guanyltransferase alpha	O08848	0.649	9.16E-01	4.238	4.57E-02	3.589	0.0828
evgLocus_FX_27252	Sorbitol dehydrogenase	Q922H4	0.311	9.25E-01	4.228	4.76E-02	3.916	0.0684
		Q64442						

evgLocus_FX_17209	Inositol polyphosphate 5-phosphatase OCRL		0.448	9.20E-01	4.218	3.45E-02	3.770	0.0596
evgLocus_FPS_9099	6-phosphogluconolactonase	Q6NVF0	0.196	9.27E-01	4.213	4.24E-02	4.017	0.0577
evgLocus_FX_25350	Cytochrome P450 3A11	Q9CQ60	-0.017	9.31E-01	4.200	4.82E-02	4.217	0.0554
evgLocus_Scallop_DRR_66432	NA	Q64459	0.807	9.09E-01	4.194	3.87E-02	3.387	0.0828
evgLocus_FX_24663	Bifunctional coenzyme A synthase	NA	0.814	9.07E-01	4.191	2.98E-02	3.377	0.0712
evgLocus_FX_21430	Ubiquitin-conjugating enzyme E2D 3	Q9DBL7	0.863	9.09E-01	4.188	4.63E-02	3.325	0.0967
evgLocus_scallop_AG_39902	Proteasome adapter and scaffold protein ECM29	A0A0G2JGL0	0.259	9.26E-01	4.142	3.95E-02	3.882	0.0572
evgLocus_FX_17233	WASH complex subunit 5	Q6PDI5	0.892	9.04E-01	4.141	3.05E-02	3.249	0.0774
evgLocus_FX_21373	Nuclear cap-binding protein subunit 1	Q8C2E7	0.654	9.13E-01	4.128	3.34E-02	3.474	0.0684
evgLocus_FX_19041	Charged multivesicular body protein 3	Q3UYV9	0.568	9.18E-01	4.127	4.83E-02	3.559	0.0827
evgLocus_strawberry_AH_53198	TBC1 domain family, member 25	Q9CQ10	0.701	9.10E-01	4.103	2.57E-02	3.402	0.0608
evgLocus_FX_22663	Docking protein 3	A0A6I8MX15	0.422	9.21E-01	4.036	4.14E-02	3.614	0.0671
evgLocus_FX_26005	Protein RCC2	Q9QZK7	0.785	9.11E-01	4.019	4.80E-02	3.233	0.0963
evgLocus_FX_21170	Opioid growth factor receptor-like protein 1	Q8BK67	0.389	9.22E-01	4.014	3.86E-02	3.625	0.0625
evgLocus_FX_18907	NA	Q8VE52	0.811	9.06E-01	4.014	2.79E-02	3.202	0.0704
evgLocus_scallop_AF_38586	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	NA	0.478	9.19E-01	3.966	3.58E-02	3.489	0.0638
evgLocus_FX_26359	Retinol dehydrogenase 14	Q9DBB8	0.194	9.27E-01	3.963	4.72E-02	3.769	0.0637
evgLocus_FX_17126	NFX1-type zinc finger-containing protein 1	Q9ERI6	0.869	9.04E-01	3.919	3.60E-02	3.050	0.0867
evgLocus_FX_19021	GPI inositol-deacylase	Q8R151	0.671	9.12E-01	3.908	3.65E-02	3.237	0.0748
evgLocus_FX_16839	Alpha-mannosidase 2x	Q3UUQ7	1.060	8.99E-01	3.900	4.58E-02	2.840	0.1127
evgLocus_FX_16691	Cullin-5	Q8BRK9	0.755	9.09E-01	3.879	3.98E-02	3.124	0.0850
evgLocus_FX_29709	NA	Q9D5V5	0.617	9.15E-01	3.856	4.83E-02	3.239	0.0881
		NA						

evgLocus_strawberry_AE_51715	Rho guanine nucleotide exchange factor (GEF) 26		0.106	9.29E-01	3.849	4.17E-02	3.743	0.0533
evgLocus_stringtie_AG_35236	Protocadherin 9	D3YYY8	0.349	9.23E-01	3.825	3.99E-02	3.476	0.0631
evgLocus_FX_31416	Trafficking protein particle complex subunit 4	A0A0A6YY09	0.012	9.31E-01	3.785	4.32E-02	3.774	0.0508
evgLocus_strawberry_AF_32608	NA	Q9ES56	0.290	9.25E-01	3.759	4.60E-02	3.469	0.0673
evgLocus_FX_22532	V-type proton ATPase subunit S1	NA	0.876	9.04E-01	3.758	4.09E-02	2.882	0.0962
evgLocus_FX_19284	Vacuolar protein sorting-associated protein 33A	Q9R1Q9	1.020	8.99E-01	3.757	4.79E-02	2.736	0.1153
evgLocus_Trinity_AE_35232	NA	Q9D2N9	0.566	9.17E-01	3.750	4.83E-02	3.184	0.0858
evgLocus_Scallop_DRR_67004	Myoferlin	NA	0.855	9.04E-01	3.743	3.74E-02	2.888	0.0903
evgLocus_FX_28378	Retinol dehydrogenase 14	Q69ZN7	0.239	9.26E-01	3.730	4.45E-02	3.492	0.0633
evgLocus_FX_17292	Protein PAT1 homolog 1	Q9ERI6	0.283	9.25E-01	3.715	4.52E-02	3.432	0.0663
evgLocus_Trinity_AF_3700	Heterogeneous nuclear ribonucleoprotein C (Fragment)	Q3TC46	0.459	9.20E-01	3.711	4.89E-02	3.251	0.0803
evgLocus_FX_21189	39S ribosomal protein L4, mitochondrial	A0A2I3BRM6	0.645	9.13E-01	3.673	4.72E-02	3.028	0.0904
evgLocus_FX_40657	Protein archease	Q9DCU6	0.383	9.22E-01	3.610	4.78E-02	3.226	0.0750
evgLocus_Trinity_AH_45644	Paired amphipathic helix protein Sin3a	B2KGA7	0.193	9.27E-01	3.551	4.52E-02	3.358	0.0624
evgLocus_FX_26252	Estradiol 17-beta-dehydrogenase 2	Q60520	0.463	9.19E-01	3.421	5.00E-02	2.958	0.0845
evgLocus_FX_16457	Proto-oncogene tyrosine-protein kinase R	P51658	1.071	8.92E-01	3.391	4.90E-02	2.321	0.1315
evgLocus_FPS_6493	Tropomyosin 3, gamma	Q78DX7	2.388	1.50E-01	3.091	1.13E-05	0.704	0.2022
evgLocus_FX_39302	NA	E9Q7Q3	1.226	7.64E-01	2.813	1.35E-03	1.587	0.0678
evgLocus_Scallop_DRR_7627	60S ribosomal protein L11	NA	2.351	1.14E-01	2.491	2.00E-04	0.140	0.4396
evgLocus_FX_19125	Thymidine phosphorylase	Q9CXW4	1.268	6.55E-01	2.206	2.59E-03	0.938	0.1361
evgLocus_Trinity_AF_88729	GTPase, IMAP family member 7	Q99N42	0.442	9.03E-01	2.199	1.93E-02	1.758	0.0570
evgLocus_FX_17361	Protein disulfide-isomerase A4	Q8R379	1.828	4.94E-01	2.171	7.66E-03	0.343	0.3735
		P08003						

evgLocus_FX_17689	Collagen alpha-1(XXIV) chain	Q30D77	2.354	3.42E-01	2.116	1.76E-02	-0.237	0.4209
evgLocus_strawberry_AG_9469	Tropomyosin 1, alpha	Q8BSH3	1.036	5.95E-01	2.062	1.33E-04	1.026	0.0611
evgLocus_Strawberry_DRR_32069	Kinesin-1 heavy chain	Q61768	1.193	5.61E-01	2.007	5.64E-04	0.813	0.1190
evgLocus_FX_18602	Endoplasmin	P08113	1.210	4.40E-01	2.004	2.87E-05	0.794	0.0891
evgLocus_Scallop_AE_33496	Synaptic vesicle membrane protein VAT-1 homolog-like	Q80TB8	0.741	8.22E-01	1.929	3.63E-03	1.188	0.0672
evgLocus_FX_21744	IgLON family member 5	Q8HW98	1.792	5.33E-01	1.917	2.38E-02	0.125	0.4550
evgLocus_FX_18671	V-type proton ATPase catalytic subunit A	P50516	1.691	6.19E-01	1.834	4.35E-02	0.143	0.4537
evgLocus_FX_22185	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Q99MR8	1.986	4.32E-01	1.760	2.93E-02	-0.226	0.4184
evgLocus_FX_23556	Carboxylic ester hydrolase	E9PV38	1.821	1.89E-01	1.753	2.81E-03	-0.067	0.4642
evgLocus_FX_28857	Signal peptidase complex subunit 3	Q6ZWQ7	0.931	7.70E-01	1.746	1.26E-02	0.815	0.1527
evgLocus_FX_29802	Ras-related protein R-Ras2	P62071	1.381	5.48E-01	1.629	1.64E-02	0.247	0.3909
evgLocus_FX_17883	Methenyltetrahydrofolate synthase domain-containing protein	P62071	1.330	5.74E-01	1.560	2.33E-02	0.230	0.4010
evgLocus_FPS_3026	Galectin	Q3URQ7	1.831	1.59E-01	1.540	7.51E-03	-0.291	0.3465
evgLocus_FX_16466	Vimentin	A0A140LHI8	0.373	9.00E-01	1.531	3.19E-02	1.159	0.0868
evgLocus_FX_22748	T-complex protein 11-like protein 1	P20152	1.945	7.80E-02	1.498	3.90E-03	-0.448	0.2301
evgLocus_FX_18785	Spectrin beta chain, non- erythrocytic 1	Q8BTG3	0.804	5.81E-01	1.393	7.25E-04	0.589	0.1141
evgLocus_FX_19353	Citrate synthase, mitochondrial	Q62261	1.250	6.26E-01	1.356	4.50E-02	0.106	0.4542
evgLocus_FX_24972	26S proteasome regulatory subunit 7	Q9CZU6	1.756	1.97E-01	1.352	2.04E-02	-0.404	0.2827
evgLocus_FX_16806	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	Q8BVQ9	0.568	7.64E-01	1.294	1.46E-03	0.727	0.0695
evgLocus_FX_20864	Cytochrome P450 2C44	O55143 E9Q5K4	0.614	8.50E-01	1.287	4.22E-02	0.672	0.1829

evgLocus_Scallop_AE_15376	ATP-dependent 6-phosphofructokinase, muscle type		0.418	8.81E-01	1.284	2.89E-02	0.866	0.1052
evgLocus_FX_19254	Phenazine biosynthesis-like domain-containing protein 1	P47857	1.277	7.67E-02	1.254	1.61E-04	-0.023	0.4758
evgLocus_FPS_604	SH3 domain-binding glutamic acid-rich-like protein 3	Q9DCG6	0.751	5.94E-01	1.244	1.66E-03	0.493	0.1432
evgLocus_FPS_5134	Proteasome subunit beta type-6	Q91VW3	1.146	5.22E-01	1.242	2.04E-02	0.096	0.4461
evgLocus_FX_22750	STE20/SPS1-related proline-alanine-rich protein kinase	Q60692	0.521	8.53E-01	1.219	2.93E-02	0.698	0.1410
evgLocus_Scallop_AE_35598	Tripeptidyl-peptidase 2	Q9Z1W9	0.530	8.36E-01	1.191	2.12E-02	0.661	0.1322
evgLocus_FX_16976	Sialin	Q64514	0.371	8.75E-01	1.191	1.64E-02	0.819	0.0786
evgLocus_Trinity_AF_3627	Septin	Q8BN82	0.136	9.20E-01	1.186	4.49E-02	1.050	0.0731
evgLocus_FX_18734	Vimentin	E9Q1G8	0.608	8.08E-01	1.137	2.71E-02	0.529	0.1847
evgLocus_FX_29452	UDP-glucose 4-epimerase	A0A0A6YWC8	1.517	1.61E-01	1.132	1.87E-02	-0.385	0.2461
evgLocus_Scallop_AE_3938	Cysteine desulfurase	Q8R059	0.543	8.18E-01	1.089	2.35E-02	0.547	0.1603
evgLocus_FX_19274	Propionyl-CoA carboxylase alpha chain, mitochondrial	Q9Z1J3	0.586	7.93E-01	1.080	2.21E-02	0.493	0.1785
evgLocus_FX_29592	60S ribosomal protein L21	Q91ZA3	0.789	7.00E-01	1.075	2.92E-02	0.287	0.3236
evgLocus_FX_19151	26S proteasome non-ATPase regulatory subunit 11	O09167	0.738	6.99E-01	1.073	2.17E-02	0.334	0.2755
evgLocus_FX_32998	Hematopoietic prostaglandin D synthase	Q8BG32	0.217	9.08E-01	1.058	4.21E-02	0.842	0.0907
evgLocus_scallop_AF_41460	Nucleoside diphosphate kinase B	Q9JHF7	0.145	9.17E-01	1.037	4.32E-02	0.891	0.0766
evgLocus_FX_18571	Annexin	Q01768	0.372	8.81E-01	1.028	4.41E-02	0.656	0.1398
evgLocus_FX_45797	Cytochrome c oxidase subunit 6C	A0A2C9F2D2	0.052	9.27E-01	1.015	4.79E-02	0.963	0.0648
evgLocus_FX_23258	non-specific serine/threonine protein kinase	Q9CPQ1	0.885	5.84E-01	1.010	2.96E-02	0.126	0.4211
evgLocus_FX_17706	Programmed cell death protein 6	G5E884	0.542	7.91E-01	0.974	2.41E-02	0.432	0.1895
		P12815						

evgLocus_FX_17012	NA	NA	0.708	7.55E-01	0.967	4.67E-02	0.259	0.3448
evgLocus_FX_31919	Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase subunit DAD1		0.567	8.14E-01	0.962	4.40E-02	0.395	0.2483
evgLocus_FX_17087	Apoptosis regulator BAX	P61804	0.607	6.16E-01	0.959	4.01E-03	0.352	0.1791
evgLocus_FX_18832	Exocyst complex component 2	Q07813	0.937	4.02E-01	0.946	1.18E-02	0.009	0.4866
evgLocus_FX_21233	Ubiquitin carboxyl-terminal hydrolase isozyme L3	Q9D4H1	0.309	8.76E-01	0.946	2.25E-02	0.636	0.0943
evgLocus_FPS_7252	Ferritin heavy chain	Q9JKB1	0.635	7.15E-01	0.941	2.31E-02	0.306	0.2679
evgLocus_FX_22272	Ankyrin repeat domain- containing protein 13D	P09528	0.208	9.02E-01	0.925	2.96E-02	0.717	0.0783
evgLocus_FX_22317	NA	Q6PD24	0.462	8.07E-01	0.922	1.92E-02	0.460	0.1522
evgLocus_Scallop_AE_36510	Tubulin alpha-1A chain	NA	0.558	7.34E-01	0.894	1.91E-02	0.335	0.2201
evgLocus_FX_40735	NA	P68369	0.747	5.89E-01	0.893	2.49E-02	0.145	0.3919
evgLocus_FX_24999	Thioredoxin	NA	0.383	8.41E-01	0.880	2.22E-02	0.497	0.1304
evgLocus_FX_26032	DnaJ homolog subfamily C member 3	P10639	0.136	9.12E-01	0.863	2.36E-02	0.727	0.0547
evgLocus_FX_23045	Translationally-controlled tumor protein	Q91YW3	0.844	4.28E-01	0.862	1.34E-02	0.018	0.4799
evgLocus_FX_19733	Proliferation-associated protein 2G4	P63028	0.314	8.77E-01	0.861	3.80E-02	0.546	0.1317
evgLocus_FX_21486	Importin subunit alpha-4	P50580	0.554	7.10E-01	0.837	1.99E-02	0.282	0.2510
evgLocus_FX_20164	Glyoxylate reductase/hydroxypyruvate reductase	O35344	0.346	8.39E-01	0.825	1.73E-02	0.478	0.1137
evgLocus_FPS_6925	Cystatin-B	Q91Z53	0.230	8.81E-01	0.822	1.28E-02	0.592	0.0641
evgLocus_scallop_AG_36507	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	Q62426	0.552	7.70E-01	0.813	4.18E-02	0.262	0.3032
evgLocus_Trinity_AF_10786	Tubulin alpha-3 chain	A0A1W2P7Q9	0.701	5.30E-01	0.813	1.49E-02	0.111	0.4006
		P05214						

evgLocus_FX_33052	Hydroxysteroid (17-beta) dehydrogenase 14		0.482	7.98E-01	0.806	3.69E-02	0.325	0.2404
evgLocus_strawberry_AH_57745	Alpha-galactosidase	E9Q3D4	0.143	9.08E-01	0.800	2.09E-02	0.657	0.0549
evgLocus_FX_20443	Peroxisomal sarcosine oxidase	Q8BGZ6	0.202	8.88E-01	0.799	1.31E-02	0.597	0.0583
evgLocus_FX_35553	Superoxide dismutase [Mn], mitochondrial	Q9D826	0.514	7.68E-01	0.798	3.33E-02	0.284	0.2666
evgLocus_FX_17232	Dedicator of cytokinesis protein 1	P09671	0.401	8.35E-01	0.793	3.65E-02	0.393	0.1864
evgLocus_FX_18065	NA	Q8BUR4	0.674	5.79E-01	0.781	2.61E-02	0.107	0.4107
evgLocus_Stringtie_DRR_5207	Glutathione S-transferase omega-1	NA	0.207	8.93E-01	0.776	2.72E-02	0.569	0.0856
evgLocus_FX_30835	Sodium/potassium-transporting ATPase subunit beta-1	O09131	0.381	7.76E-01	0.762	8.48E-03	0.382	0.1257
evgLocus_FX_19464	Eukaryotic peptide chain release factor subunit 1	P14094	0.347	8.56E-01	0.762	4.22E-02	0.415	0.1738
evgLocus_FX_22739	26S proteasome regulatory subunit 6B	Q8BWY3	0.433	7.61E-01	0.761	1.66E-02	0.327	0.1806
evgLocus_FX_17603	Rab GTPase-binding effector protein 1	P54775	0.644	6.25E-01	0.759	3.26E-02	0.115	0.4061
evgLocus_FX_18184	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	O35551	0.197	8.93E-01	0.754	2.37E-02	0.557	0.0782
evgLocus_FX_23164	T-complex protein 1 subunit alpha	Q6PD03	0.776	5.27E-01	0.754	3.48E-02	-0.022	0.4779
evgLocus_FX_43554	60S ribosomal protein L12	P11983	0.391	8.44E-01	0.753	4.87E-02	0.362	0.2140
evgLocus_strawberry_AH_41597	Prolyl endopeptidase	P35979	0.331	8.60E-01	0.750	4.19E-02	0.418	0.1676
evgLocus_scallop_AG_20031	Neprilysin	Q9QUR6	0.210	8.82E-01	0.749	1.46E-02	0.539	0.0672
evgLocus_FX_20386	Phenylalanine--tRNA ligase beta subunit	Q61391	0.243	8.87E-01	0.742	4.08E-02	0.500	0.1225
evgLocus_Trinity_RF_Nov18_10052	N-alpha-acetyltransferase 10	Q9WUA2	0.776	5.47E-01	0.728	4.54E-02	-0.048	0.4608
		Q9QY36						

evgLocus_FX_27735	Peptidyl-prolyl cis-trans isomerase B		0.196	8.93E-01	0.665	3.98E-02	0.469	0.1111
		P24369						
evgLocus_FX_23564	Tubulin alpha-3 chain	P05214	0.332	8.45E-01	0.655	4.60E-02	0.323	0.2025
evgLocus_FX_30032	U1 small nuclear ribonucleoprotein A		0.868	3.91E-01	0.650	4.73E-02	-0.218	0.3026
		Q62189						
evgLocus_FX_24902	Pyrroline-5-carboxylate reductase 1, mitochondrial		0.385	8.04E-01	0.631	4.30E-02	0.246	0.2604
		Q922W5						
evgLocus_FX_25038	Eukaryotic translation initiation factor 2 subunit 3, Y-linked		0.277	8.49E-01	0.629	2.95E-02	0.352	0.1468
		Q9Z0N2						
evgLocus_FX_22228	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1		0.102	9.12E-01	0.607	3.48E-02	0.505	0.0718
		Q60967						
evgLocus_FX_19012	Signal recognition particle subunit SRP68		-0.047	9.25E-01	-0.655	3.56E-02	-0.608	0.0541
		Q8BMA6						
evgLocus_strawberry_AF_8915	Trifunctional purine biosynthetic protein adenosine-3		-0.191	8.96E-01	-0.680	4.28E-02	-0.489	0.1115
		Q64737						
evgLocus_FX_23464	DnaJ homolog subfamily C member 2		-0.910	4.14E-01	-0.738	3.91E-02	0.172	0.3589
		P54103						
evgLocus_FPS_4858	Proteasome subunit alpha type-3		-0.482	8.17E-01	-0.828	4.40E-02	-0.346	0.2435
		O70435						
evgLocus_scallop_AG_1247	Extracellular superoxide dismutase [Cu-Zn]		0.000	9.32E-01	-0.837	4.39E-02	-0.837	0.0510
		O09164						
evgLocus_FX_19991	NA	NA	-1.353	1.01E-01	-0.881	2.27E-02	0.472	0.1429
evgLocus_Trinity_AE_116888	Dedicator of cytokinesis 9	E9QMR2	-0.348	8.63E-01	-0.893	2.80E-02	-0.545	0.1241
evgLocus_strawberry_AE_59408	Transcription elongation factor A protein 1		-0.867	6.14E-01	-0.914	4.67E-02	-0.047	0.4679
		P10711						
evgLocus_FX_20158	Copine-7		-0.411	8.46E-01	-0.932	2.75E-02	-0.521	0.1430
		Q0VE82						
evgLocus_FX_18203	Methionine--tRNA ligase, cytoplasmic		-0.363	8.34E-01	-0.973	5.26E-03	-0.610	0.0700
		E9QB02						
evgLocus_Trinity_AF_39799	L-fucose kinase	Q7TMC8	-1.247	2.70E-01	-0.990	2.41E-02	0.257	0.3203
evgLocus_FX_35206	NHP2-like protein 1	Q9D0T1	-0.341	8.87E-01	-0.991	4.96E-02	-0.650	0.1418

evgLocus_FX_27886	Cytochrome b-c1 complex subunit Rieske, mitochondrial		-1.829	9.26E-02	-1.015	4.07E-02	0.814	0.0869
		Q9CR68						
evgLocus_FX_19090	Ubiquitin conjugation factor E4 B		-0.409	8.62E-01	-1.071	2.49E-02	-0.662	0.1152
		Q9ES00						
evgLocus_FX_39332	Glutaredoxin-1		-0.904	6.37E-01	-1.071	3.42E-02	-0.168	0.4037
		Q9QUH0						
evgLocus_FX_22088	26S proteasome non-ATPase regulatory subunit 3		-0.358	8.83E-01	-1.084	3.36E-02	-0.727	0.1128
		P14685						
evgLocus_FX_19688	Small nuclear ribonucleoprotein Sm D3		-1.085	2.05E-01	-1.101	1.91E-03	-0.016	0.4818
		P62320						
evgLocus_FX_17420	5'-3' exoribonuclease 2		-0.284	8.97E-01	-1.118	3.02E-02	-0.835	0.0869
		Q9DBR1						
evgLocus_Scallop_AE_23752	Ppf1a1 protein		-0.038	9.29E-01	-1.175	4.01E-02	-1.137	0.0522
		B2RXW8						
evgLocus_FX_38432	Cytochrome c oxidase subunit 6B1		-0.297	9.01E-01	-1.212	3.73E-02	-0.915	0.0944
		P56391						
evgLocus_Trinity_AE_39975	Thrombospondin type-1 domain-containing protein 4		-0.691	7.68E-01	-1.218	1.82E-02	-0.527	0.1828
		Q3UTY6						
evgLocus_scallop_AG_36364	Ran-binding protein 3		-0.509	8.46E-01	-1.236	1.94E-02	-0.727	0.1149
		Q9CT10						
evgLocus_FPS_8367	ADP-ribosylation factor 5		-0.232	9.12E-01	-1.272	4.37E-02	-1.040	0.0874
		P84084						
evgLocus_FX_19485	Piwi-like protein 1		-0.611	7.84E-01	-1.280	7.11E-03	-0.669	0.1118
		Q9JMB7						
evgLocus_Trinity_AE_131040	MAP7 domain-containing protein 2		-0.589	8.65E-01	-1.320	4.94E-02	-0.730	0.1808
		A2AG50						
evgLocus_Trinity_AE_135383	Adenylate cyclase type 9		-0.474	8.75E-01	-1.331	3.08E-02	-0.858	0.1167
		P51830						
evgLocus_FX_30958	Carbonyl reductase (NADPH)		-0.627	8.10E-01	-1.422	8.23E-03	-0.796	0.1021
		A0A1B0GRG8						
evgLocus_scallop_AG_6257	Calcium uptake protein 3, mitochondrial		-0.772	7.80E-01	-1.444	1.59E-02	-0.672	0.1613
		Q9CTY5						
evgLocus_Scallop_AE_26410	Tudor domain-containing protein 1		-0.529	8.80E-01	-1.450	4.33E-02	-0.921	0.1398
		Q99MV1						
evgLocus_Trinity_GG_DRR_45918	Receptor-type tyrosine-protein phosphatase alpha		-0.266	9.08E-01	-1.468	2.54E-02	-1.202	0.0627
		Q91V35						
evgLocus_FX_20236	Galectin		-0.994	5.75E-01	-1.477	3.75E-03	-0.483	0.2046
		A0A140LHI8						
evgLocus_FX_16703	Coronin-7		-1.004	4.93E-01	-1.524	4.50E-04	-0.520	0.1545
		Q9D2V7						
evgLocus_FX_17351	Acyl-CoA 6-desaturase		-0.794	8.11E-01	-1.580	2.13E-02	-0.786	0.1576
		Q9Z0R9						

evgLocus_FX_22423	Serpine1 mRNA binding protein 1		-1.098	7.34E-01	-1.612	2.89E-02	-0.515	0.2848
evgLocus_strawberry_AG_52091	Dual specificity mitogen-activated protein kinase kinase 3	Q3UMP4	-0.369	9.02E-01	-1.632	2.85E-02	-1.263	0.0769
evgLocus_FX_24432	Ran GTPase-activating protein 1	O09110	-0.305	9.05E-01	-1.633	1.82E-02	-1.328	0.0521
evgLocus_FX_19551	Myelin expression factor 2	P46061	-1.431	4.01E-01	-1.697	2.48E-03	-0.266	0.3590
evgLocus_Trinity_RF_Nov18_5762	Stathmin	Q8C854	-0.598	8.76E-01	-1.704	3.11E-02	-1.106	0.1157
evgLocus_Scallop_AE_38624	Oxysterol-binding protein	P54227	-2.766	2.09E-01	-1.729	4.99E-02	1.037	0.1633
evgLocus_FPS_4461	Guanine nucleotide-binding protein subunit gamma	E9PXZ2	-0.131	9.25E-01	-1.761	4.83E-02	-1.630	0.0692
evgLocus_FX_28123	Eukaryotic translation initiation factor 3 subunit M	G3X9Q2	-0.871	8.11E-01	-1.782	1.86E-02	-0.911	0.1449
evgLocus_FX_20958	E3 UFM1-protein ligase 1	Q99JX4	-2.718	2.62E-01	-1.846	4.45E-02	0.872	0.2109
evgLocus_Trinity_AE_101245	Triple functional domain protein	Q8CCJ3	-0.136	9.25E-01	-1.892	4.28E-02	-1.756	0.0629
evgLocus_FX_32862	SUMO-activating enzyme subunit 1	Q0KL02	-1.140	8.15E-01	-1.986	4.09E-02	-0.845	0.2326
evgLocus_FX_22992	Thyroglobulin	Q9R1T2	-0.657	8.82E-01	-2.031	2.98E-02	-1.373	0.1061
evgLocus_FX_23171	GTP-binding protein Rheb	O08710	-0.909	8.39E-01	-2.044	2.34E-02	-1.135	0.1366
evgLocus_FX_19280	Dynamin 1-like	Q921J2	-2.488	4.21E-02	-2.046	6.52E-04	0.442	0.2760
evgLocus_Scallop_AE_7234	Proline-rich coiled-coil 2C (Fragment)	E9PUD2	-2.440	5.19E-01	-2.176	4.53E-02	0.265	0.4308
evgLocus_Trinity_AE_48479	Tudor domain-containing protein 3	S4R2E2	-1.223	8.21E-01	-2.392	2.84E-02	-1.169	0.1761
evgLocus_FX_16753	Macoilin	Q91W18	-2.258	8.23E-01	-3.857	4.94E-02	-1.598	0.2552
evgLocus_FX_23152	WASH complex subunit 1	Q7TQE6	-2.582	7.76E-01	-3.890	4.13E-02	-1.308	0.2927
evgLocus_FX_26388	Protoporphyrinogen oxidase	Q8VDD8	-2.920	7.55E-01	-4.060	4.42E-02	-1.139	0.3334
evgLocus_Trinity_AG_86028	Carnitine O-acetyltransferase	P51175	-3.208	7.11E-01	-4.161	3.96E-02	-0.953	0.3616
evgLocus_FX_17491	Importin subunit beta-1	P47934	-2.406	7.54E-01	-4.248	1.41E-02	-1.842	0.1734
evgLocus_Trinity_AF_92785	Transforming acidic coiled-coil-containing protein 1	P70168	-3.749	6.07E-01	-4.289	3.33E-02	-0.540	0.4224
		Q6Y685						

evgLocus_FX_20015	Choline dehydrogenase, mitochondrial		-3.182	6.74E-01	-4.446	2.11E-02	-1.264	0.2955
evgLocus_Scallop_AE_554	Polypeptide N-acetylgalactosaminyltransferase 13	Q8BJ64	-3.439	7.00E-01	-4.686	2.93E-02	-1.247	0.3240
evgLocus_FX_39105	39S ribosomal protein L50, mitochondrial	Q8CF93	-4.349	6.26E-01	-4.855	4.07E-02	-0.506	0.4385
evgLocus_FX_17562	Peroxidase homolog	Q8VDT9	-3.363	6.83E-01	-4.894	1.86E-02	-1.531	0.2673
evgLocus_FX_22878	NA	Q3UQ28	-5.018	4.26E-01	-5.116	1.33E-02	-0.098	0.4809
evgLocus_FX_19775	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	NA	-4.682	5.45E-01	-5.259	2.11E-02	-0.577	0.4251
evgLocus_FX_20148	Late secretory pathway protein AVL9 homolog	Q61466	-6.828	1.53E-01	-5.325	1.31E-02	1.503	0.2794
evgLocus_FX_33855	Neuferricin	Q80U56	-0.652	9.20E-01	-5.340	4.96E-02	-4.688	0.0808
evgLocus_FX_32864	L-amino acid oxidase semialdehyde dehydrogenase-phosphopantetheinyl transferase	Q5SSH8	-0.975	9.13E-01	-5.431	4.93E-02	-4.456	0.0940
evgLocus_Stringtie_DRR_8722	Serine and arginine-rich splicing factor 4	Q9CQF6	-4.740	5.27E-01	-5.566	1.30E-02	-0.826	0.3896
evgLocus_FX_26894	Charged multivesicular body protein 1B2	Q542V3	-5.577	4.74E-01	-5.751	1.81E-02	-0.174	0.4749
evgLocus_scallop_AG_408	ADP-ribosylation factor GTPase-activating protein 1	Q9CQD4	-0.484	9.24E-01	-5.820	4.19E-02	-5.335	0.0639
evgLocus_FX_16802	Transmembrane protein 131	Q9EPJ9	-8.504	1.38E-01	-5.884	2.37E-02	2.621	0.1878
evgLocus_FX_22455	Vitamin K-dependent gamma-carboxylase	O70472	-8.689	2.25E-01	-6.025	3.67E-02	2.664	0.2142
evgLocus_FX_35889	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase MESH1	Q9QYC7	-4.350	5.11E-01	-6.173	1.47E-03	-1.822	0.2104
		Q9D114						

evgLocus_FX_23214	Acidic leucine-rich nuclear phosphoprotein 32 family member B		-3.432	8.05E-01	-6.198	2.98E-02	-2.766	0.1997
evgLocus_Trinity_AG_87255	Guanine nucleotide-binding protein subunit beta-5	Q9EST5	-3.724	8.08E-01	-6.424	3.79E-02	-2.700	0.2304
evgLocus_FX_24175	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	P62881	-10.553	3.34E-02	-6.488	1.19E-02	4.065	0.0880
evgLocus_FX_21197	NA	J3QMM7	-0.025	9.31E-01	-6.673	4.32E-02	-6.648	0.0508
evgLocus_Trinity_GG_DRR_44399	C2 calcium-dependent domain containing 5	NA	-9.051	1.98E-01	-6.853	2.23E-02	2.199	0.2698
evgLocus_Trinity_AG_82051	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	E9Q026	-2.725	8.54E-01	-6.904	2.12E-02	-4.179	0.1126
evgLocus_FX_53844	Splicing factor 3B subunit 6	Q80VJ3	-3.171	8.47E-01	-6.997	3.20E-02	-3.826	0.1568
evgLocus_Scallop_AE_14271	Kyphoscoliosis peptidase	P59708	-0.279	9.28E-01	-7.041	4.13E-02	-6.762	0.0550
evgLocus_FX_18096	Thrombospondin-3	Q8C8H8	-3.796	8.15E-01	-7.434	2.48E-02	-3.638	0.1688
evgLocus_FX_27375	Meiosis regulator and mRNA stability 1	Q05895	-2.989	8.49E-01	-7.527	1.79E-02	-4.538	0.1078
evgLocus_FX_23268	Plasminogen receptor (KT)	A0A2R8VH96	-7.588	1.74E-01	-7.731	1.12E-03	-0.143	0.4782
evgLocus_strawberry_AG_2355	Actin, cytoplasmic 1	Q9D3P8	-3.609	8.59E-01	-8.221	4.00E-02	-4.612	0.1631
evgLocus_strawberry_AG_19301	NA	P60710	-4.147	8.44E-01	-8.421	4.05E-02	-4.274	0.1868
evgLocus_FX_25705	General transcription factor 3C polypeptide 5	NA	-6.534	4.86E-01	-8.461	2.84E-03	-1.927	0.2913
evgLocus_FPS_4905	VIP36-like protein	Q8R2T8	-7.457	1.17E-01	-9.082	1.48E-05	-1.625	0.2690
evgLocus_FX_19457	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	P59481	-7.230	3.55E-01	-9.302	5.05E-04	-2.072	0.2633
evgLocus_FX_32908	Trafficking protein particle complex subunit 1	A0A087WRF2	-5.664	5.56E-01	-10.710	7.20E-05	-5.046	0.0649
evgLocus_FX_41427	ATP synthase subunit delta, mitochondrial	Q5NCF2	-7.538	4.51E-01	-12.680	2.75E-05	-5.142	0.0838
		Q9D3D9						