

Supplementary Data 1. Details of differential expressed genes (DEGs) between antennae of uncontaminated and contaminated female houseflies collected in spring.

Readcount is the average read count of each gen, log2FoldChange is calculated by formular $\log_2(\text{readcount_CFA}/\text{readcount_UFA})$, pval is the *p* value, padj is the *fdr* corrected *p* value using Benjamini/Hochberg method. All *p*-values are based on two-sided tests. CFA: contaminated female antennae, UFA: uncontaminated female antennae.

Gene_id	readcount_CFA	readcount_UFA	log2FoldChange	pval	padj	gene_name	description
Novel00014	7537.245	4769.258	0.66027	1.94E-08	6.13E-06	-	-
Novel00064	210.219	343.5999	-0.70884	6.26E-05	0.005288	-	-
Novel00120	84.47008	38.82137	1.1216	0.000242	0.015504	-	-
Novel00123	43.26445	99.21784	-1.1974	7.38E-05	0.005952	-	-
Novel00124	1693.019	2551.585	-0.5918	3.32E-06	0.000439	-	-
Novel00191	715.562	1079.466	-0.59317	1.01E-05	0.001142	-	-
Novel00414	390.315	224.1678	0.80006	2.25E-06	0.000324	-	-
Novel00526	38.79558	11.96498	1.6971	0.000608	0.031147	-	-
Novel00590	356.6062	541.6666	-0.60307	0.000112	0.008572	-	-
Novel00703	442.1205	795.0391	-0.84659	8.24E-05	0.006547	-	-
Novel00963	37.27293	12.54994	1.5704	0.001131	0.047385	-	-
Novel00983	292.9741	528.807	-0.85197	0.000671	0.032795	-	-
Novel01056	150.749	239.6613	-0.66885	0.000558	0.02915	-	-
Novel01163	62.62001	27.09577	1.2086	0.000916	0.041098	-	-
Novel01302	124.211	206.6684	-0.73453	0.000903	0.041098	-	-
Novel01333	119.1503	221.7139	-0.89592	0.000723	0.0345	-	-
Novel01520	278.175	141.1361	0.97891	3.84E-07	7.65E-05	-	-
Novel01536	1280.825	1811.356	-0.5	0.000127	0.009388	-	-
Novel01619	52.90038	112.7257	-1.0915	7.13E-05	0.005868	-	-
Novel01700	251.6967	449.7512	-0.83744	0.000114	0.008595	-	-
Novel01713	221.93	343.6948	-0.63102	0.000284	0.017643	-	-
Novel01728	65.76915	149.6639	-1.1862	3.00E-06	0.000406	-	-
Novel01775	56.19449	20.72571	1.439	0.000221	0.01458	-	-
Novel01777	97.28813	44.03301	1.1437	0.00018	0.012371	-	-

Novel01799	103.7958	49.80543	1.0594	0.000225	0.014751	-	-
gene-CYP6G4	112931.7	167468.3	-0.56844	6.91E-07	0.000122	CYP6G4	cytochrome P450 6g1-like
gene-Gr2	3107.626	4132.36	-0.41115	0.000675	0.032895	Gr2	gustatory and odorant receptor 63a-like
gene-LOC101887389	710.1956	1045.074	-0.55732	3.12E-05	0.003051	LOC101887389	acyl-CoA desaturase
gene-LOC101887437	380.0691	557.031	-0.5515	0.001196	0.048974	LOC101887437	serine/arginine repetitive matrix protein 2
gene-LOC101887456	430.2276	296.0369	0.53932	0.00091	0.041098	LOC101887456	saccharopine dehydrogenase-like oxidoreductase
gene-LOC101887458	9089.886	15796.14	-0.79724	6.40E-12	3.69E-09	LOC101887458	heat shock 70 kDa protein cognate 3%2C transcript variant X2
gene-LOC101887475	219.3885	54.02036	2.0219	1.03E-05	0.001158	LOC101887475	farnesyl pyrophosphate synthase-like
gene-LOC101887499	241.7068	107.8003	1.1649	0.001142	0.0476	LOC101887499	venom carboxylesterase-6
gene-LOC101887559	1971.519	1444.666	0.44857	0.000367	0.02162	LOC101887559	uncharacterized protein LOC101887559 uncharacterized LOC101887559%2C transcript variant X2
gene-LOC101887573	107.1639	56.00358	0.93623	0.000653	0.032234	LOC101887573	formin-like protein 3
gene-LOC101887634	114.7579	57.69821	0.99199	0.000286	0.017652	LOC101887634	saccharopine dehydrogenase-like oxidoreductase%2C transcript variant X2 saccharopine dehydrogenase-like oxidoreductase isoform X2
gene-LOC101887665	1075.914	1595.97	-0.56887	1.54E-05	0.001654	LOC101887665	calcium-binding mitochondrial carrier protein SCaMC-2 isoform X3 calcium-binding mitochondrial carrier protein SCaMC-2%2C transcript variant X3
gene-LOC101887677	45.27347	13.00262	1.7999	7.95E-05	0.006346	LOC101887677	uncharacterized protein LOC101887677 uncharacterized LOC101887677
gene-LOC101887709	359.4128	86.62324	2.0528	0.000403	0.023294	LOC101887709	phormicin
gene-LOC101887828	327.1154	564.0233	-0.78595	4.35E-07	8.45E-05	LOC101887828	F-box only protein 28%2C transcript variant X3 F-box only protein 28 isoform X3
gene-LOC101887974	570.8843	841.9188	-0.56048	0.000104	0.00797	LOC101887974	rhophilin-2-A
gene-LOC101887978	124.4807	298.581	-1.2622	5.15E-11	2.77E-08	LOC101887978	protein OPI10 homolog
gene-LOC101888002	36.19956	10.92336	1.7286	0.000573	0.02963	LOC101888002	lipoprotein lipase

gene-LOC101888004	11070.34	16621.7	-0.58637	5.30E-07	0.000101	LOC101888004	pyruvate carboxylase%2C mitochondrial isoform X2 pyruvate carboxylase%2C mitochondrial%2C transcript variant X2
gene-LOC101888064	20.333	56.9739	-1.4865	0.000154	0.010978	LOC101888064	tyrosine aminotransferase isoform X1 tyrosine aminotransferase%2C transcript variant X1
gene-LOC101888130	156.9747	249.8967	-0.6708	0.000717	0.034309	LOC101888130	proteoglycan 4%2C transcript variant X2 proteoglycan 4
gene-LOC101888166	73.43389	131.2942	-0.83829	0.001024	0.043928	LOC101888166	H/ACA ribonucleoprotein complex subunit 2-like protein
gene-LOC101888171	1707.94	2402.02	-0.49199	7.31E-05	0.005936	LOC101888171	tubulin beta chain
gene-LOC101888337	198.602	328.9904	-0.72817	0.000714	0.034255	LOC101888337	10 kDa heat shock protein%2C mitochondrial
gene-LOC101888348	1411.717	2184	-0.62952	3.67E-07	7.40E-05	LOC101888348	hypothetical protein%2C transcript variant X2 uncharacterized protein LOC101888348 isoform X2
gene-LOC101888428	264.9164	144.4425	0.87504	2.75E-05	0.002742	LOC101888428	aquaporin AQPcic
gene-LOC101888470	432.6642	639.2775	-0.56319	0.000242	0.015504	LOC101888470	protein CREBRF homolog%2C transcript variant X2
gene-LOC101888515	15.68618	45.13604	-1.5248	0.000622	0.031392	LOC101888515	uncharacterized LOC101888515 uncharacterized protein LOC101888515
gene-LOC101888550	327.1	198.1683	0.72301	5.17E-05	0.004533	LOC101888550	protein roadkill
gene-LOC101888609	150.2448	69.30597	1.1163	2.67E-06	0.000374	LOC101888609	uncharacterized LOC101888609 uncharacterized protein LOC101888609
gene-LOC101888662	3746.433	2440.994	0.61805	3.54E-07	7.22E-05	LOC101888662	uncharacterized protein LOC101888662 uncharacterized LOC101888662
gene-LOC101888673	21.85006	2.808729	2.9596	6.47E-05	0.005407	LOC101888673	ctenidin-1-like
gene-LOC101888696	683.5997	1085.877	-0.66764	0.000735	0.034767	LOC101888696	probable trehalose-phosphate phosphatase C
gene-LOC101888736	10207.88	7218.924	0.49983	1.30E-05	0.001431	LOC101888736	bacchus
gene-LOC101888799	88.86402	193.1538	-1.1201	7.28E-05	0.005936	LOC101888799	phosphoenolpyruvate carboxykinase [GTP]
gene-LOC101888842	1207.782	837.6626	0.52792	8.96E-05	0.007	LOC101888842	protein takeout

gene-LOC101888926	146.2219	59.61412	1.2944	1.60E-05	0.001708	LOC101888926	sodium/potassium/calcium exchanger 4
gene-LOC101889000	213.9776	102.243	1.0655	4.75E-05	0.004237	LOC101889000	Membrane-associated protein protein snakeskin
gene-LOC101889021	1498.105	2045.987	-0.44966	0.000418	0.023751	LOC101889021	dnaJ homolog shv
gene-LOC101889074	1902.606	2751.688	-0.53234	2.59E-05	0.002599	LOC101889074	putative uncharacterized protein DDB_G0271606%2C transcript variant X2 putative uncharacterized protein DDB_G0271606
gene-LOC101889145	1503.629	2145.207	-0.51267	3.63E-05	0.003449	LOC101889145	uncharacterized LOC101889145%2C transcript variant X2
gene-LOC101889157	383.12	558.8548	-0.54468	0.000418	0.023751	LOC101889157	putative inorganic phosphate cotransporter
gene-LOC101889191	749.1975	539.404	0.47398	0.000929	0.041531	LOC101889191	serine/threonine-protein kinase nek1-2
gene-LOC101889260	184.4605	107.6882	0.77645	0.000543	0.028599	LOC101889260	protein valois
gene-LOC101889269	48.1086	15.92787	1.5947	0.000185	0.012616	LOC101889269	cytochrome P450 6g1
gene-LOC101889292	184.2648	79.68313	1.2094	1.49E-07	3.42E-05	LOC101889292	probable G-protein coupled receptor Mth-like 10
gene-LOC101889378	572.3521	813.0534	-0.50645	0.000292	0.018002	LOC101889378	glycogenin-1 isoform X1 glycogenin-1%2C transcript variant X1
gene-LOC101889471	89.17651	155.1207	-0.79866	0.000453	0.025418	LOC101889471	facilitated trehalose transporter Tret1-2 homolog
gene-LOC101889476	853.4075	1197.179	-0.48833	0.000348	0.020616	LOC101889476	putative uncharacterized protein DDB_G0277255%2C transcript variant X8
gene-LOC101889495	116.9633	192.0257	-0.71524	0.000967	0.042739	LOC101889495	elongation of very long chain fatty acids protein AAEL008004
gene-LOC101889504	1399.512	1884.86	-0.42953	0.000731	0.034767	LOC101889504	dnaJ homolog subfamily C member 3
gene-LOC101889542	168.2186	88.98506	0.9187	6.91E-05	0.005747	LOC101889542	EGF domain-specific O-linked N-acetylglucosamine transferase
gene-LOC101889565	192.5205	46.03433	2.0642	5.99E-17	6.44E-14	LOC101889565	alpha-tocopherol transfer protein-like
gene-LOC101889696	90.49382	43.23474	1.0656	0.000467	0.025998	LOC101889696	uncharacterized protein LOC101889696 uncharacterized LOC101889696
gene-LOC101889724	83.30894	39.0282	1.094	0.000472	0.026149	LOC101889724	peptide chain release factor 1-like%2C mitochondrial
gene-LOC101889838	3924.783	2521.955	0.63807	2.87E-07	6.01E-05	LOC101889838	murinoglobulin-2%2C transcript variant

gene-LOC101889957	105.3506	41.60814	1.3403	0.000901	0.041098	LOC101889957	X3 murinoglobulin-2 isoform X3
gene-LOC101889961	11.9847	37.78462	-1.6566	0.000766	0.036031	LOC101889961	attacin-A-like
gene-LOC101890035	131.0036	219.4716	-0.74443	0.000417	0.023751	LOC101890035	chaoptin isoform X1 chaoptin%2C transcript variant X1
gene-LOC101890125	2210.114	3978.217	-0.848	3.03E-12	1.88E-09	LOC101890125	whirlin%2C transcript variant X7
gene-LOC101890139	461.5995	657.2489	-0.5098	0.000627	0.03141	LOC101890139	elongation of very long chain fatty acids protein 7
gene-LOC101890180	1700.71	1231.451	0.46578	0.000235	0.015183	LOC101890180	dual oxidase maturation factor 1
gene-LOC101890185	1304.674	2094.421	-0.68286	8.04E-08	2.20E-05	LOC101890185	period circadian protein%2C transcript variant X1
gene-LOC101890283	1599.993	2419.52	-0.59666	2.18E-06	0.000317	LOC101890283	uncharacterized protein LOC101890185 isoform X1 uncharacterized LOC101890185%2C transcript variant X1
gene-LOC101890440	73.76893	18.34609	2.0075	6.13E-08	1.77E-05	LOC101890440	protein EFR3 homolog cmp44E
gene-LOC101890446	859.6634	619.4085	0.47288	0.000945	0.041985	LOC101890446	lipase 3-like
gene-LOC101890474	13.62086	0.306549	5.4736	6.02E-05	0.005137	LOC101890474	probable galactose-1-phosphate uridylyltransferase
gene-LOC101890546	307.6552	192.3775	0.67737	0.000207	0.013828	LOC101890546	uncharacterized LOC101890474 uncharacterized protein LOC101890474
gene-LOC101890607	1123.705	501.6322	1.1636	3.23E-07	6.67E-05	LOC101890607	rho GTPase-activating protein 28%2C transcript variant X2 rho GTPase-activating protein 28 isoform X2
gene-LOC101890610	72.08193	149.7501	-1.0548	0.000272	0.017049	LOC101890610	lipase 3-like
gene-LOC101890630	1808.812	1321.752	0.45259	0.000317	0.019225	LOC101890630	SH3 domain-containing protein C23A1.17
gene-LOC101890655	1074.412	1434.823	-0.41733	0.001173	0.048378	LOC101890655	ATP-binding cassette sub-family G member 4%2C transcript variant X2
gene-LOC101890677	872.1874	1405.461	-0.68833	1.86E-07	4.23E-05	LOC101890677	uncharacterized LOC101890655
gene-LOC101890728	653.5245	1822.599	-1.4797	2.22E-28	8.95E-25	LOC101890728	non-lysosomal glucosylceramidase%2C transcript variant X1 non-lysosomal glucosylceramidase isoform X1
							probable cytochrome P450 313a4

gene-LOC101890854	2305.01	1309.478	0.81578	8.57E-11	4.32E-08	LOC101890854	glucose dehydrogenase [FAD%2C quinone]
gene-LOC101890896	101.8514	8.688401	3.5512	9.42E-06	0.001092	LOC101890896	peptidoglycan-recognition protein SA-like
gene-LOC101890942	702.5819	1087.242	-0.62993	3.84E-06	0.000499	LOC101890942	uncharacterized oxidoreductase YoxD isoform X2 estradiol 17-beta-dehydrogenase 11%2C transcript variant X2
gene-LOC101890961	1243.858	644.2372	0.94916	6.12E-12	3.66E-09	LOC101890961	putative nuclease HARBI1%2C transcript variant X2 putative nuclease HARBI1 isoform X2
gene-LOC101890997	157.7735	286.4865	-0.86061	7.56E-06	0.00091	LOC101890997	Kv channel-interacting protein 1
gene-LOC101891012	60.90093	140.0928	-1.2018	0.000211	0.014049	LOC101891012	uncharacterized LOC101891012
gene-LOC101891023	345.7416	505.7248	-0.54866	0.000363	0.021454	LOC101891023	serine/threonine-protein phosphatase 2B catalytic subunit 3
gene-LOC101891055	252.2193	446.3724	-0.82357	5.99E-07	0.00011	LOC101891055	tRNA-splicing ligase RtcB homolog
gene-LOC101891295	1633.855	894.0816	0.8698	1.92E-08	6.13E-06	LOC101891295	putative inorganic phosphate cotransporter
gene-LOC101891392	3306.771	4316.788	-0.38454	0.001107	0.046607	LOC101891392	ATP-dependent 6-phosphofructokinase%2C transcript variant X3 ATP-dependent 6-phosphofructokinase isoform X3
gene-LOC101891408	398.4515	254.6489	0.64589	0.000526	0.028001	LOC101891408	probable cytochrome P450 6a21
gene-LOC101891418	1487.113	2033.027	-0.45112	0.000406	0.023365	LOC101891418	protein transport protein Sec23A isoform X2 protein transport protein Sec23A%2C transcript variant X2
gene-LOC101891430	10.44192	34.66978	-1.7313	0.000917	0.041098	LOC101891430	heat shock protein 70
gene-LOC101891440	1036.63	1658.151	-0.67767	2.48E-07	5.40E-05	LOC101891440	solute carrier family 26 member 6
gene-LOC101891486	1431.115	3826.005	-1.4187	1.81E-30	9.76E-27	LOC101891486	uncharacterized protein LOC101891486 uncharacterized LOC101891486
gene-LOC101891523	270.1301	408.5681	-0.59692	0.000333	0.01999	LOC101891523	organic cation transporter protein
gene-LOC101891572	762.684	1079.505	-0.50121	0.000232	0.015019	LOC101891572	membrane alanyl aminopeptidase
gene-LOC101891646	2399.222	3296.501	-0.45837	0.000232	0.015019	LOC101891646	transcription factor Sp9
gene-LOC101891654	82.20984	160.8504	-0.96834	3.69E-05	0.003456	LOC101891654	probable H/ACA ribonucleoprotein complex subunit 1
gene-LOC101891657	29.19914	173.583	-2.5716	1.83E-20	2.69E-17	LOC101891657	basic-leucine zipper transcription factor A

gene-LOC101891680	38.00248	4.592047	3.0489	1.32E-07	3.14E-05	LOC101891680	lactase-like protein
gene-LOC101891684	4151.497	12206.19	-1.5559	8.65E-39	1.40E-34	LOC101891684	proton-coupled amino acid transporter 2
gene-LOC101891702	1026.724	622.3026	0.72236	3.99E-05	0.003675	LOC101891702	estradiol 17-beta-dehydrogenase 11
gene-LOC101891715	808.2839	1165.58	-0.52811	0.000519	0.027754	LOC101891715	apoptosis-stimulating of p53 protein 1 isoform X1 apoptosis-stimulating of p53 protein 1%2C transcript variant X1
gene-LOC101891733	434.0621	666.4553	-0.61861	2.94E-05	0.002908	LOC101891733	facilitated trehalose transporter Tret1%2C transcript variant X3 facilitated trehalose transporter Tret1 isoform X2
gene-LOC101891759	1015.691	395.8768	1.3593	1.84E-21	3.29E-18	LOC101891759	probable cytochrome P450 4d14
gene-LOC101891842	1582.732	2114.581	-0.41795	0.000744	0.035092	LOC101891842	cyclin-dependent kinase-like 1
gene-LOC101891912	2733.064	1419.475	0.94516	6.31E-14	4.85E-11	LOC101891912	chymotrypsin inhibitor
gene-LOC101891996	113.6828	280.685	-1.3039	7.32E-11	3.81E-08	LOC101891996	venom acid phosphatase Acph-1
gene-LOC101891997	977.3662	471.4439	1.0518	1.68E-13	1.23E-10	LOC101891997	general odorant-binding protein 56h
gene-LOC101892036	102.3069	38.78425	1.3994	2.80E-06	0.000387	LOC101892036	uncharacterized protein LOC101892036 uncharacterized LOC101892036
gene-LOC101892041	449.0468	293.7768	0.61215	0.000188	0.012763	LOC101892041	vanin-like protein 2
gene-LOC101892046	366.5215	534.9617	-0.54554	0.000454	0.025418	LOC101892046	SRSF protein kinase 1 isoform X4 SRSF protein kinase 1%2C transcript variant X5
gene-LOC101892072	6006.194	4024.318	0.57771	7.33E-07	0.000129	LOC101892072	cytochrome P450 6A1-like
gene-LOC101892091	6533.359	8686.865	-0.41101	0.000569	0.029513	LOC101892091	gamma-glutamyltranspeptidase 1
gene-LOC101892168	672.6099	924.6824	-0.45919	0.001058	0.045014	LOC101892168	eukaryotic translation initiation factor 2-alpha kinase
gene-LOC101892221	1294.522	910.1054	0.50831	0.00015	0.010788	LOC101892221	dynein light chain Tctex-type
gene-LOC101892248	317.7541	460.0499	-0.53388	0.000916	0.041098	LOC101892248	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform X2 brain-specific angiogenesis inhibitor 1-associated protein 2%2C transcript variant X2
gene-LOC101892265	142.7452	278.4476	-0.96396	6.46E-07	0.000117	LOC101892265	transcription factor Adf-1

gene-LOC101892292	354.272	526.5669	-0.57176	0.000994	0.04312	LOC101892292	uncharacterized LOC101892292 uncharacterized protein LOC101892292
gene-LOC101892311	2746.36	4470.892	-0.70304	5.26E-09	1.77E-06	LOC101892311	trehalase
gene-LOC101892323	113.7063	201.8008	-0.82762	5.53E-05	0.004745	LOC101892323	nucleoside diphosphate kinase 7
gene-LOC101892399	4443.94	6575.538	-0.56527	1.52E-06	0.000236	LOC101892399	facilitated trehalose transporter Tret1
gene-LOC101892443	130.5512	236.2617	-0.85577	2.50E-05	0.002524	LOC101892443	gamma-glutamyl hydrolase%2C transcript variant X1 gamma-glutamyl hydrolase isoform X1
gene-LOC101892510	2794.449	2025.627	0.4642	0.00015	0.010788	LOC101892510	GTP cyclohydrolase 1 isoform X1 GTP cyclohydrolase 1%2C transcript variant X1
gene-LOC101892606	7667.792	4599.486	0.73734	0.000513	0.027648	LOC101892606	uncharacterized LOC101892606 uncharacterized protein LOC101892606
gene-LOC101892627	251.5728	156.6974	0.68299	0.000476	0.026293	LOC101892627	uncharacterized protein LOC101892627 uncharacterized LOC101892627
gene-LOC101892719	1565.983	2355.535	-0.58899	2.16E-05	0.002208	LOC101892719	uncharacterized LOC101892719%2C transcript variant X1
gene-LOC101892728	558.5919	1804.695	-1.6919	1.53E-23	4.10E-20	LOC101892728	phytanoyl-CoA dioxygenase domain-containing protein 1
gene-LOC101892729	892.2125	1220.049	-0.45148	0.000822	0.038221	LOC101892729	phosphoserine phosphatase
gene-LOC101892804	2546.118	1675.751	0.60349	1.30E-06	0.000206	LOC101892804	SEC14-like protein 2
gene-LOC101892808	3495.964	2568.233	0.44491	0.000204	0.013725	LOC101892808	organic cation transporter protein
gene-LOC101892812	455.1261	653.673	-0.5223	0.000554	0.029111	LOC101892812	mannose-1-phosphate guanyltransferase beta%2C transcript variant X2
gene-LOC101892829	414.1331	156.0446	1.4081	4.30E-15	3.47E-12	LOC101892829	peptide methionine sulfoxide reductase LOW QUALITY PROTEIN: peptide methionine sulfoxide reductase
gene-LOC101893003	2019.156	892.4939	1.1778	2.33E-19	3.13E-16	LOC101893003	protein takeout Hemolymph juvenile hormone binding protein (JHBP)
gene-LOC101893008	508.7614	809.1696	-0.66945	3.22E-06	0.000429	LOC101893008	protein grindelwald

gene-LOC101893009	31.93605	72.13679	-1.1755	0.000668	0.032767	LOC101893009	uncharacterized LOC101893009
gene-LOC101893013	179.3659	89.99281	0.99502	1.90E-05	0.001997	LOC101893013	uncharacterized LOC101893013%2C transcript variant X2
gene-LOC101893017	2192.853	3847.379	-0.81107	3.35E-11	1.86E-08	LOC101893017	glutamyl aminopeptidase isoform X2 glutamyl aminopeptidase%2C transcript variant X2
gene-LOC101893080	798.6332	556.9961	0.51987	0.000258	0.016369	LOC101893080	ubiquitin-conjugating enzyme E2-22 kDa
gene-LOC101893156	409.5759	247.0709	0.72921	1.52E-05	0.001647	LOC101893156	probable serine hydrolase
gene-LOC101893236	66.19271	145.5771	-1.137	7.17E-06	0.000876	LOC101893236	odorant receptor 67d-like
gene-LOC101893282	1553.848	2472.842	-0.67033	1.16E-07	2.93E-05	LOC101893282	integral membrane protein GPR155
gene-LOC101893379	137.4445	227.6914	-0.72823	0.000408	0.023423	LOC101893379	ribosome biogenesis regulatory protein homolog
gene-LOC101893387	1702.668	2575.597	-0.59711	3.55E-06	0.000465	LOC101893387	pancreatic triacylglycerol lipase
gene-LOC101893442	102.4785	305.4611	-1.5757	0.001094	0.046211	LOC101893442	cuticle protein 1
gene-LOC101893496	78.47295	164.0974	-1.0643	1.11E-05	0.001248	LOC101893496	uncharacterized LOC101893496 uncharacterized protein LOC101893496
gene-LOC101893618	6611.321	4754.896	0.47552	4.30E-05	0.003898	LOC101893618	nose resistant to fluoxetine protein 6
gene-LOC101893628	105.9087	31.03539	1.7708	8.80E-09	2.90E-06	LOC101893628	pancreatic lipase-related protein 2
gene-LOC101893655	941.5058	663.5723	0.50472	0.000231	0.015019	LOC101893655	Major Facilitator Superfamily protein uncharacterized protein LOC101893655
gene-LOC101893676	938.1976	1404.715	-0.58231	1.52E-05	0.001647	LOC101893676	(11Z)-hexadec-11-enoyl-CoA conjugase
gene-LOC101893715	55.72991	21.6788	1.3622	0.00052	0.027754	LOC101893715	nuclear RNA export factor 2
gene-LOC101893720	2927.805	4313.645	-0.55909	0.000638	0.031662	LOC101893720	twitchin isoform X2 twitchin%2C transcript variant X2
gene-LOC101893723	807.92	1251.749	-0.63166	0.000615	0.031215	LOC101893723	titin%2C transcript variant X2
gene-LOC101893737	6915.048	4802.908	0.52583	9.48E-06	0.001092	LOC101893737	RNA-binding protein Rsf1
gene-LOC101893815	4523.301	6037.611	-0.4166	0.000529	0.028053	LOC101893815	organic cation transporter-like protein
gene-LOC101893835	158.6143	249.722	-0.6548	0.000911	0.041098	LOC101893835	zinc finger protein 704
gene-LOC101893875	108.4337	34.63664	1.6464	2.92E-08	8.72E-06	LOC101893875	lipase 3-like
gene-LOC101893978	658.6186	1006.375	-0.61165	1.29E-05	0.001431	LOC101893978	uncharacterized LOC101893978

gene-LOC101894001	805.4858	294.5292	1.4514	2.17E-08	6.74E-06	LOC101894001	probable asparagine synthetase [glutamine-hydrolyzing]
gene-LOC101894016	324.9383	145.1134	1.163	3.28E-05	0.003188	LOC101894016	chymotrypsin-elastase inhibitor ixodidin
gene-LOC101894050	2259.007	1649.711	0.45348	0.000625	0.03141	LOC101894050	lipase 3-like
gene-LOC101894072	8544.43	5121.904	0.7383	2.01E-10	9.24E-08	LOC101894072	protein timeless
gene-LOC101894109	68.1639	142.6342	-1.0652	1.76E-05	0.001869	LOC101894109	uncharacterized protein LOC101894109 isoform X1 uncharacterized LOC101894109%2C transcript variant X1
gene-LOC101894137	801.7999	494.9585	0.69593	1.17E-06	0.000189	LOC101894137	translocating chain-associated membrane protein 1
gene-LOC101894154	3413.757	4485.101	-0.39378	0.001037	0.044357	LOC101894154	actin-binding LIM protein 2 isoform X3 actin-binding LIM protein 2%2C transcript variant X3
gene-LOC101894182	335.6416	556.2589	-0.72884	4.13E-06	0.000529	LOC101894182	band 7 protein AGAP004871%2C transcript variant X2
gene-LOC101894192	371.3254	604.569	-0.70322	5.45E-06	0.000682	LOC101894192	tetratricopeptide repeat protein 28
gene-LOC101894235	31.54638	110.5915	-1.8097	1.63E-09	6.10E-07	LOC101894235	uncharacterized protein LOC101894235 Chitin binding protein
gene-LOC101894362	469.7294	657.9193	-0.48608	0.001078	0.045639	LOC101894362	pescadillo homolog
gene-LOC101894368	173.1312	345.8232	-0.99817	6.91E-08	1.95E-05	LOC101894368	uncharacterized protein LOC101894368 isoform X3 serine-rich adhesin for platelets%2C transcript variant X3
gene-LOC101894398	13175.57	17911.88	-0.44305	0.000153	0.010932	LOC101894398	sialin LOW QUALITY PROTEIN: sialin
gene-LOC101894425	564.9513	391.1608	0.53036	0.000376	0.022044	LOC101894425	cytochrome P450 4d8%2C transcript variant X2 cytochrome P450 4d8 isoform X2
gene-LOC101894436	1087.526	718.3025	0.59839	9.99E-06	0.001142	LOC101894436	small ubiquitin-related modifier 3
gene-LOC101894440	279.1889	176.892	0.65837	0.000486	0.026685	LOC101894440	wee1-like protein kinase
gene-LOC101894472	347.0333	600.8109	-0.79184	8.62E-05	0.006813	LOC101894472	tyrosine-protein kinase Btk29A
gene-LOC101894477	731.5177	503.972	0.53755	0.000193	0.013054	LOC101894477	protein NASP homolog
gene-LOC101894480	1934.794	2557.517	-0.40256	0.001072	0.045494	LOC101894480	protein ABHD4

gene-LOC101894546	1242.272	839.1659	0.56595	3.36E-05	0.003246	LOC101894546	uncharacterized LOC101894546 uncharacterized protein LOC101894546
gene-LOC101894606	2097.241	3351.17	-0.67617	8.61E-07	0.000146	LOC101894606	uncharacterized protein LOC101894606 uncharacterized LOC101894606
gene-LOC101894736	1884.427	1359.743	0.47079	0.00017	0.011789	LOC101894736	acidic leucine-rich nuclear phosphoprotein 32 family member A%2C transcript variant X1
gene-LOC101894790	193.2051	315.6082	-0.708	0.000391	0.022747	LOC101894790	putative mediator of RNA polymerase II transcription subunit 26
gene-LOC101894797	1501.072	888.4737	0.75659	0.000713	0.034255	LOC101894797	uncharacterized LOC101894797 uncharacterized protein LOC101894797
gene-LOC101895135	96.34431	40.36561	1.2551	0.00014	0.010265	LOC101895135	uncharacterized LOC101895135 uncharacterized protein LOC101895135
gene-LOC101895287	147.5345	85.83015	0.7815	0.001021	0.043928	LOC101895287	putative folylpolyglutamate synthase
gene-LOC101895322	616.6082	327.1276	0.9145	3.44E-09	1.21E-06	LOC101895322	protein cutoff
gene-LOC101895356	6937.518	9315.819	-0.42526	0.000311	0.019014	LOC101895356	UTP--glucose-1-phosphate uridylyltransferase isoform X2 UTP--glucose-1-phosphate uridylyltransferase%2C transcript variant X2
gene-LOC101895417	1247.1	803.3974	0.63439	2.27E-05	0.002305	LOC101895417	uncharacterized protein LOC101895417 isoform X1 uncharacterized LOC101895417%2C transcript variant X1
gene-LOC101895580	184.9411	296.2455	-0.67973	0.000222	0.014636	LOC101895580	WD repeat-containing protein 43
gene-LOC101895609	406.6086	256.6605	0.66378	6.23E-05	0.005287	LOC101895609	twinkle protein%2C mitochondrial
gene-LOC101895657	501.8876	846.7654	-0.7546	1.35E-07	3.16E-05	LOC101895657	clusterin-associated protein 1 homolog
gene-LOC101895658	1434.347	2168.862	-0.59654	4.21E-05	0.003856	LOC101895658	muscle M-line assembly protein unc-89%2C transcript variant X2
gene-LOC101895698	1700.881	1025.946	0.72933	0.000679	0.033002	LOC101895698	acyl-CoA-binding protein homolog
gene-LOC101895722	453.567	308.6443	0.55537	0.000514	0.027648	LOC101895722	probable peroxisomal acyl-coenzyme A oxidase 1
gene-LOC101895857	202.1227	113.6904	0.83012	0.000989	0.043013	LOC101895857	protein PFC0760c-like

gene-LOC101895876	111.3519	217.1926	-0.96385	3.14E-06	0.000422	LOC101895876	phospholipase B1%2C membrane-associated
gene-LOC101895892	514.7954	797.3144	-0.63115	8.91E-06	0.001057	LOC101895892	uncharacterized LOC101895892
gene-LOC101895908	4.17256	22.81558	-2.451	0.000514	0.027648	LOC101895908	pupal cuticle protein Edg-78E
gene-LOC101895911	3488.092	5171.415	-0.56812	2.34E-06	0.000334	LOC101895911	zinc finger matrin-type protein CG9776
gene-LOC101895918	16468.58	11158.34	0.56159	1.21E-06	0.000194	LOC101895918	circadian clock-controlled protein-like
gene-LOC101895958	842.3405	1411.906	-0.74517	2.73E-08	8.31E-06	LOC101895958	dual 3'%2C5'-cyclic-AMP and -GMP phosphodiesterase 11%2C transcript variant X2 dual 3'%2C5'-cyclic-AMP and -GMP phosphodiesterase 11 isoform X2
gene-LOC101895965	436.0345	1448.162	-1.7317	2.26E-33	1.82E-29	LOC101895965	partner of bursicon
gene-LOC101895976	1014.724	747.8871	0.44019	0.00111	0.046629	LOC101895976	uncharacterized protein LOC101895976 uncharacterized LOC101895976
gene-LOC101895994	115.5437	188.2736	-0.70439	0.001192	0.04891	LOC101895994	ribosomal RNA small subunit methyltransferase NEP1
gene-LOC101895996	5003.797	3719.615	0.42787	0.000314	0.019118	LOC101895996	protein scylla
gene-LOC101896013	276.0219	159.6516	0.78986	5.20E-05	0.004538	LOC101896013	LIRP isoform X1 LIRP%2C transcript variant X1
gene-LOC101896067	962.2358	1700.394	-0.82141	0.000166	0.011694	LOC101896067	neurogenic locus notch homolog protein 1%2C transcript variant X1 neurogenic locus notch homolog protein 1 isoform X1
gene-LOC101896081	1201.041	717.8651	0.7425	3.54E-08	1.04E-05	LOC101896081	cytochrome P450 4e2
gene-LOC101896165	498.2901	799.9541	-0.68293	2.18E-06	0.000317	LOC101896165	Sporozoite P67 surface antigen
gene-LOC101896233	4132.301	2932.437	0.49485	3.71E-05	0.003456	LOC101896233	glucose-6-phosphate 1-dehydrogenase%2C transcript variant X2 glucose-6-phosphate 1-dehydrogenase isoform X2
gene-LOC101896294	850.6662	1242.793	-0.54692	3.63E-05	0.003449	LOC101896294	uncharacterized LOC101896294%2C transcript variant X2 uncharacterized protein LOC101896294 isoform X2
gene-LOC101896306	155.2637	260.6507	-0.7474	0.00014	0.010265	LOC101896306	LON peptidase N-terminal domain and RING finger protein 2

gene-LOC101896362	256.6881	387.8166	-0.59536	0.000489	0.026746	LOC101896362	neurochondrin homolog
gene-LOC101896384	936.8249	2031.612	-1.1168	8.56E-18	1.06E-14	LOC101896384	histone-lysine N-methyltransferase%2C H3 lysine-79 specific%2C transcript variant X4 histone-lysine N-methyltransferase%2C H3 lysine-79 specific isoform X3
gene-LOC101896415	439.7547	284.0998	0.6303	0.000121	0.009042	LOC101896415	lysoplasmalogenase-like protein TMEM86A
gene-LOC101896442	23643.72	31234.83	-0.4017	0.000973	0.04287	LOC101896442	farnesol dehydrogenase
gene-LOC101896469	7946.924	3867.156	1.0391	1.09E-07	2.79E-05	LOC101896469	probable cytochrome P450 313a4%2C transcript variant X2 probable cytochrome P450 313a4 isoform X2
gene-LOC101896501	10261.42	16717.92	-0.70416	1.29E-09	4.97E-07	LOC101896501	heat shock protein 83
gene-LOC101896517	349.0468	208.5273	0.74318	3.66E-05	0.003452	LOC101896517	chitooligosaccharidolytic beta-N-acetylglucosaminidase%2C transcript variant X5 chitooligosaccharidolytic beta-N-acetylglucosaminidase
gene-LOC101896544	1594.423	2094.768	-0.39376	0.001204	0.049167	LOC101896544	pyruvate dehydrogenase (acetyl-transferring) kinase%2C mitochondrial
gene-LOC101896559	295.7255	574.3182	-0.95759	1.07E-09	4.22E-07	LOC101896559	phospholipase D2
gene-LOC101896673	6263.983	8199.088	-0.38838	0.00087	0.040077	LOC101896673	2-oxoglutarate dehydrogenase-like%2C mitochondrial
gene-LOC101896690	240.8474	114.677	1.0705	1.32E-07	3.14E-05	LOC101896690	alkaline phosphatase 4%2C transcript variant X1 alkaline phosphatase 4 isoform X1
gene-LOC101896715	4188.998	5499.509	-0.3927	0.000988	0.043013	LOC101896715	adenylosuccinate synthetase
gene-LOC101896755	258.3671	398.0083	-0.62338	0.000115	0.008659	LOC101896755	glutamic acid-rich protein%2C transcript variant X7 glutamic acid-rich protein isoform X1
gene-LOC101896765	195.1811	423.5162	-1.1176	1.26E-10	6.15E-08	LOC101896765	zinc finger protein jing isoform X2 zinc finger protein jing%2C transcript variant X3
gene-LOC101896814	387.9107	234.0699	0.72879	1.91E-05	0.001997	LOC101896814	frizzled-3
gene-LOC101896822	1404.103	2243.453	-0.67607	8.43E-08	2.27E-05	LOC101896822	calcium-binding mitochondrial carrier protein

							Aralar1%2C transcript variant X3 calcium-binding mitochondrial carrier protein Aralar1 isoform X3
gene-LOC101896861	227.7644	130.3204	0.80548	4.88E-05	0.004299	LOC101896861	T-cell activation inhibitor%2C mitochondrial
gene-LOC101896936	402.8271	613.4745	-0.60684	4.86E-05	0.004299	LOC101896936	mesencephalic astrocyte-derived neurotrophic factor homolog
gene-LOC101896986	1492.827	1047.373	0.51127	9.10E-05	0.007061	LOC101896986	RNA-binding protein lark
gene-LOC101897025	1266.988	1948.11	-0.62067	1.00E-06	0.000167	LOC101897025	GTP-binding protein 1
gene-LOC101897046	4526.298	5983.471	-0.40265	0.000664	0.032644	LOC101897046	protein ref(2)P
gene-LOC101897148	620.4747	866.0529	-0.48108	0.00059	0.030429	LOC101897148	sulfide:quinone oxidoreductase%2C mitochondrial
gene-LOC101897194	180.9764	58.47305	1.63	8.49E-07	0.000146	LOC101897194	double-headed protease inhibitor%2C submandibular gland
gene-LOC101897216	684.2629	374.237	0.8706	0.000273	0.017049	LOC101897216	uncharacterized protein
							LOC101897216 uncharacterized LOC101897216
gene-LOC101897223	188.5153	55.30769	1.7691	7.48E-10	3.02E-07	LOC101897223	uncharacterized LOC101897223 uncharacterized protein LOC101897223
gene-LOC101897275	722.7501	452.9094	0.67427	4.43E-06	0.000562	LOC101897275	uncharacterized family 31 glucosidase KIAA1161
gene-LOC101897317	347.4204	191.864	0.8566	1.57E-06	0.000241	LOC101897317	uncharacterized LOC101897317%2C transcript variant X1
gene-LOC101897343	608.8687	848.2875	-0.47842	0.000632	0.031571	LOC101897343	intraflagellar transport protein 56
gene-LOC101897347	1361.795	2339.616	-0.78076	4.98E-10	2.11E-07	LOC101897347	dnaJ protein homolog 1%2C transcript variant X2 dnaJ protein homolog 1
gene-LOC101897406	552.9218	313.4962	0.81863	1.89E-07	4.24E-05	LOC101897406	cytochrome b561 domain-containing protein 2-like cytochrome b561 domain-containing protein 2-like%2C transcript variant X2
gene-LOC101897428	328.6245	177.6572	0.88734	3.89E-06	0.000502	LOC101897428	phosphatidylserine decarboxylase proenzyme%2C mitochondrial%2C transcript variant X2
gene-LOC101897522	3288.92	4578.692	-0.47732	7.32E-05	0.005936	LOC101897522	scavenger receptor class B member 1
gene-LOC101897587	923.4515	608.3073	0.60224	0.000883	0.040591	LOC101897587	cytochrome P450 4e2-like

gene-LOC101897649	308.6232	444.9637	-0.52784	0.001042	0.044453	LOC101897649	uncharacterized LOC101897649 uncharacterized protein LOC101897649
gene-LOC101897660	612.2523	86.03284	2.8312	8.26E-07	0.000143	LOC101897660	vasotab
gene-LOC101897674	130.7774	256.6116	-0.97247	5.96E-07	0.00011	LOC101897674	zinc metalloproteinase nas-14
gene-LOC101897717	215.3297	344.8227	-0.67931	0.000114	0.008595	LOC101897717	uncharacterized protein LOC101897717 uncharacterized LOC101897717
gene-LOC101897719	540.7451	744.368	-0.46107	0.001162	0.048291	LOC101897719	band 7 protein AGAP004871-like
gene-LOC101897739	619.6305	426.4899	0.5389	0.000339	0.020246	LOC101897739	FACT complex subunit Ssrp1
gene-LOC101897767	919.0306	1438.865	-0.64675	9.47E-07	0.000159	LOC101897767	protein disulfide-isomerase A6 homolog%2C transcript variant X2
gene-LOC101897863	505.8201	842.0786	-0.73533	2.59E-07	5.58E-05	LOC101897863	microsomal glutathione S-transferase 1
gene-LOC101897926	4251.663	5745.101	-0.43431	0.000219	0.014539	LOC101897926	multiple inositol polyphosphate phosphatase 1
gene-LOC101897978	1678.138	2259.535	-0.42916	0.000697	0.033775	LOC101897978	serine/threonine-protein kinase PITSLRE%2C transcript variant X2 serine/threonine-protein kinase PITSLRE isoform X1
gene-LOC101897984	558.7945	829.1539	-0.56932	5.27E-05	0.004569	LOC101897984	zinc transporter 2%2C transcript variant X4
gene-LOC101898011	932.2134	1269.526	-0.44556	0.00101	0.043665	LOC101898011	probable cytochrome P450 28c1
gene-LOC101898055	59.03929	126.4071	-1.0983	3.05E-05	0.003003	LOC101898055	adenylate cyclase type 8%2C transcript variant X1
gene-LOC101898132	1433.244	2486.682	-0.79494	2.55E-10	1.11E-07	LOC101898132	fatty acyl-CoA reductase wat
gene-LOC101898153	1974.975	2904.973	-0.55669	6.87E-06	0.000846	LOC101898153	carboxypeptidase B
gene-LOC101898193	968.8011	670.1101	0.5318	0.000146	0.010622	LOC101898193	selenocysteine methyltransferase%2C transcript variant X1 selenocysteine methyltransferase isoform X1
gene-LOC101898279	127.7306	264.382	-1.0495	1.32E-07	3.14E-05	LOC101898279	putative inorganic phosphate cotransporter
gene-LOC101898280	7.644622	54.24338	-2.8269	6.67E-07	0.000119	LOC101898280	major heat shock 70 kDa protein Ba-like
gene-LOC101898324	9346.033	6422.666	0.54118	2.82E-06	0.000387	LOC101898324	very long-chain-fatty-acid--CoA ligase bubblegum
gene-LOC101898389	1149.976	766.2601	0.5857	1.48E-05	0.001625	LOC101898389	L-galactose dehydrogenase
gene-LOC101898439	270.1745	411.7971	-0.60804	0.000278	0.017306	LOC101898439	probable ATP-dependent RNA helicase pitchoune

gene-LOC101898458	2368.101	3199.916	-0.4343	0.000449	0.025298	LOC101898458	ethanolamine kinase
gene-LOC101898467	1251.693	1751.689	-0.48487	0.000173	0.01195	LOC101898467	mesocentin mesocentin%2C transcript variant X3
gene-LOC101898520	4023.918	5813.822	-0.53089	7.53E-06	0.00091	LOC101898520	putative phospholipase B-like lamina ancestor
gene-LOC101898526	3217.972	6471.198	-1.0079	3.35E-17	3.87E-14	LOC101898526	esterase B1%2C transcript variant X2 esterase B1
gene-LOC101898545	169.4513	100.872	0.74835	0.000947	0.041985	LOC101898545	double-strand break repair protein MRE11
gene-LOC101898640	2703.83	1614.437	0.74397	3.32E-09	1.19E-06	LOC101898640	ecdysteroid-regulated 16 kDa protein
gene-LOC101898644	323.9984	852.3196	-1.3954	1.63E-20	2.63E-17	LOC101898644	purine nucleoside phosphorylase%2C transcript variant X3 purine nucleoside phosphorylase isoform X3
gene-LOC101898663	3511.534	7855.968	-1.1617	2.46E-22	5.67E-19	LOC101898663	carnitine O-palmitoyltransferase 1%2C liver isoform%2C transcript variant X2
gene-LOC101898711	1539.98	2230.798	-0.53465	0.000457	0.025489	LOC101898711	elongation of very long chain fatty acids protein AAEL008004%2C transcript variant X1
gene-LOC101898731	16.91496	70.03648	-2.0498	8.80E-08	2.33E-05	LOC101898731	uncharacterized protein LOC101898731 isoform X5 uncharacterized LOC101898731%2C transcript variant X5
gene-LOC101898770	2.922895	48.98139	-4.0668	2.38E-12	1.54E-09	LOC101898770	venom allergen 5
gene-LOC101899102	173.4493	94.68767	0.87327	0.00016	0.011326	LOC101899102	parkin coregulated gene protein homolog
gene-LOC101899135	212.703	78.00159	1.4473	1.46E-10	6.94E-08	LOC101899135	cytochrome P450 6d1-like
gene-LOC101899158	298.5451	499.6956	-0.7431	2.60E-06	0.000368	LOC101899158	ATP-binding cassette sub-family G member 5
gene-LOC101899169	2859.425	4074.931	-0.51105	2.13E-05	0.002207	LOC101899169	endoplasmic homolog
gene-LOC101899230	8898.635	6410.903	0.47306	0.00089	0.0408	LOC101899230	ATP-binding cassette sub-family A member 12%2C transcript variant X2 ATP-binding cassette sub-family A member 12
gene-LOC101899240	333.3438	483.5544	-0.53667	0.000623	0.031392	LOC101899240	carbohydrate sulfotransferase 13 isoform X1 carbohydrate sulfotransferase 13%2C transcript variant X1
gene-LOC101899314	487.6764	294.3821	0.72823	8.18E-06	0.000977	LOC101899314	integumentary mucin A.1

gene-LOC101899329	923.4752	571.5986	0.69207	9.33E-06	0.001091	LOC101899329	tissue factor pathway inhibitor%2C transcript variant X2 tissue factor pathway inhibitor
gene-LOC101899370	688.8	1029.809	-0.58022	2.16E-05	0.002208	LOC101899370	stress-induced-phosphoprotein 1
gene-LOC101899381	1042.704	1590.407	-0.60907	8.87E-05	0.006983	LOC101899381	uncharacterized protein LOC101899381 uncharacterized LOC101899381
gene-LOC101899427	198.7078	309.0061	-0.63699	0.000614	0.031215	LOC101899427	uncharacterized protein LOC101899427 Zona pellucida-like domain protein
gene-LOC101899434	273.8865	439.5219	-0.68236	4.27E-05	0.003893	LOC101899434	probable cytochrome P450 6t3
gene-LOC101899573	215.5315	349.188	-0.69611	0.000272	0.017049	LOC101899573	ionotropic receptor 21a
gene-LOC101899613	296.2084	448.1939	-0.59751	0.000331	0.019938	LOC101899613	GTP-binding protein 1 GTP-binding protein 1%2C transcript variant X2
gene-LOC101899617	3107.041	4740.197	-0.60941	4.09E-07	8.05E-05	LOC101899617	choline/ethanolamine kinase isoform X2 choline/ethanolamine kinase%2C transcript variant X2
gene-LOC101899620	4762.629	6346.698	-0.41425	0.00053	0.028053	LOC101899620	protein krasavietz%2C transcript variant X1 protein krasavietz
gene-LOC101899666	179.8418	65.14333	1.465	5.95E-10	2.46E-07	LOC101899666	maltase A3-like
gene-LOC101899684	597.4224	377.374	0.66276	4.64E-05	0.004154	LOC101899684	vitellogenin-1-like
gene-LOC101899700	440.4461	652.0529	-0.56602	0.00017	0.011789	LOC101899700	L-lactate dehydrogenase
gene-LOC101899715	215.1249	109.9778	0.96796	6.33E-05	0.005314	LOC101899715	ribosome-recycling factor%2C mitochondrial
gene-LOC101899769	115.4302	200.9915	-0.80011	0.00119	0.04891	LOC101899769	protocadherin-15%2C transcript variant X2
gene-LOC101899804	1787.886	2909.623	-0.70258	0.000568	0.029513	LOC101899804	farnesol dehydrogenase
gene-LOC101899870	56.00684	23.20093	1.2714	0.001169	0.048342	LOC101899870	uncharacterized protein LOC101899870 pseudouridine kinase
gene-LOC101899878	1790.085	3045.876	-0.76683	1.06E-06	0.000174	LOC101899878	titin%2C transcript variant X1
gene-LOC101899903	5231.045	3428.189	0.60965	2.34E-07	5.17E-05	LOC101899903	flagellar radial spoke protein 2
gene-LOC101899963	601.4574	929.8041	-0.62846	6.38E-06	0.000791	LOC101899963	protein late bloomer
gene-LOC101899983	13.87206	39.54599	-1.5113	0.000863	0.039872	LOC101899983	pancreatic triacylglycerol lipase%2C transcript variant

gene-LOC101900065	124.7529	39.10539	1.6736	2.83E-06	0.000387	LOC101900065	X1 pancreatic triacylglycerol lipase isoform X1 probable cytochrome P450 6a14 LOW QUALITY PROTEIN: probable cytochrome P450 6a14
gene-LOC101900080	838.2519	566.7877	0.56458	5.41E-05	0.00467	LOC101900080	hyccin
gene-LOC101900132	101.4236	53.34525	0.92696	0.001014	0.043732	LOC101900132	uncharacterized protein LOC101900132 uncharacterized LOC101900132
gene-LOC101900224	3891.822	5300.357	-0.44564	0.000167	0.011694	LOC101900224	uncharacterized LOC101900224%2C transcript variant X5
gene-LOC101900234	207.7389	317.0643	-0.61	0.000814	0.037928	LOC101900234	kinesin-like protein Nod
gene-LOC101900252	9099.015	13593.66	-0.57915	5.33E-07	0.000101	LOC101900252	tensin
gene-LOC101900253	395.9838	255.3459	0.63299	0.000184	0.012573	LOC101900253	UNC93-like protein%2C transcript variant X2
gene-LOC101900256	1404.424	2017.976	-0.52293	0.000913	0.041098	LOC101900256	protein tyrosine phosphatase type IVA 1
gene-LOC101900259	994.9222	1360.153	-0.45111	0.00098	0.043013	LOC101900259	UPF0389 protein CG9231
gene-LOC101900280	70.81532	167.0299	-1.238	0.000168	0.011749	LOC101900280	adult cuticle protein 1
gene-LOC101900422	109.6964	224.183	-1.0312	9.22E-06	0.001086	LOC101900422	serine/threonine-protein phosphatase 2B catalytic subunit 1 isoform X2 serine/threonine-protein phosphatase 2B catalytic subunit 1%2C transcript variant X2
gene-LOC101900442	114.786	56.8232	1.0144	0.000634	0.031584	LOC101900442	probable proline--tRNA ligase%2C mitochondrial%2C transcript variant X1
gene-LOC101900472	304.7244	515.8309	-0.75939	2.09E-06	0.00031	LOC101900472	chloride channel protein 2 isoform X4 chloride channel protein 2%2C transcript variant X5
gene-LOC101900502	1147.3	805.8862	0.50959	0.000125	0.009263	LOC101900502	uncharacterized protein LOC101900502 uncharacterized LOC101900502
gene-LOC101900674	349.6545	230.5631	0.60077	0.000597	0.030677	LOC101900674	neuferricin homolog
gene-LOC101900692	357.8147	238.4199	0.58571	0.000947	0.041985	LOC101900692	alpha-tocopherol transfer protein-like
gene-LOC101900724	27.5026	4.230256	2.7008	3.75E-05	0.003479	LOC101900724	cytochrome P450 4d1-like
gene-LOC101900736	193.7904	302.1371	-0.64071	0.000479	0.026369	LOC101900736	serine palmitoyltransferase 2 isoform X1 serine

gene-LOC101900747	237.9504	137.2756	0.79359	0.000798	0.037302	LOC101900747	palmitoyltransferase 2%2C transcript variant X1
gene-LOC101900815	173.1071	378.4447	-1.1284	2.53E-10	1.11E-07	LOC101900815	alpha-tocopherol transfer protein
gene-LOC101900874	156.9321	294.8715	-0.90995	1.47E-06	0.000231	LOC101900874	F-box only protein 32
gene-LOC101901071	835.4228	1193.124	-0.51417	0.000143	0.010463	LOC101901071	uncharacterized protein LOC101900874 uncharacterized LOC101900874
gene-LOC101901086	2347.498	1688.215	0.47563	0.000113	0.008572	LOC101901086	ELMO domain-containing protein 2%2C transcript variant X4
gene-LOC101901112	394.0875	561.3483	-0.51038	0.000984	0.043013	LOC101901112	uncharacterized LOC101901086 uncharacterized protein LOC101901086
gene-LOC101901151	35.64721	2.362974	3.9151	3.96E-09	1.36E-06	LOC101901151	lipase member H-B
gene-LOC101901231	805.163	1554.768	-0.94935	0.000149	0.010788	LOC101901231	nose resistant to fluoxetine protein 6
gene-LOC101901237	1626.186	2209.662	-0.44233	0.0005	0.027224	LOC101901237	hypothetical protein uncharacterized protein LOC101901231
gene-LOC101901243	939.7371	1357.942	-0.53109	7.00E-05	0.005792	LOC101901243	heat shock factor protein isoform X1 heat shock factor protein%2C transcript variant X5
gene-LOC101901262	1611.998	2214.844	-0.45836	0.000257	0.016369	LOC101901262	ubiquitin-conjugating enzyme E2 Q2%2C transcript variant X3
gene-LOC101901296	3199.036	4495.367	-0.4908	4.44E-05	0.004001	LOC101901296	sialin
gene-LOC101901311	2489.964	4578.449	-0.87873	5.04E-13	3.53E-10	LOC101901311	aminopeptidase N-like
gene-LOC101901393	494.7502	192.4486	1.3622	9.43E-16	8.45E-13	LOC101901393	proline dehydrogenase 1%2C mitochondrial
gene-LOC101901407	1998.122	3163.346	-0.66281	7.19E-08	2.00E-05	LOC101901407	uncharacterized LOC101901393%2C transcript variant X1
gene-LOC101901572	1996.433	1228.128	0.70096	0.00039	0.022747	LOC101901572	hypoxia up-regulated protein 1
gene-LOC101901600	3898.504	2459.915	0.66431	1.32E-07	3.14E-05	LOC101901600	uncharacterized threonine-rich GPI-anchored glycoprotein PJ4664.02
gene-LOC101901705	1642.443	2659.691	-0.69541	2.03E-06	0.000307	LOC101901705	dynein light chain 2%2C cytoplasmic%2C transcript variant X1
							excitatory amino acid transporter isoform

							X1 excitatory amino acid transporter%2C transcript variant X1
gene-LOC101901767	37.45815	87.70893	-1.2274	7.92E-05	0.006346	LOC101901767	proton-associated sugar transporter A
gene-LOC101901806	220.2785	352.6367	-0.67885	8.98E-05	0.007	LOC101901806	putative sodium-dependent multivitamin transporter
gene-LOC101901815	127.3102	68.81574	0.88754	0.000796	0.037302	LOC101901815	uncharacterized LOC101901815 uncharacterized protein LOC101901815
gene-LOC101901820	1.234381	15.19148	-3.6214	0.000703	0.033952	LOC101901820	larval cuticle protein 5-like isoform X1 larval cuticle protein 5-like%2C transcript variant X1
gene-LOC101901826	1296.319	1981.833	-0.61241	1.94E-06	0.000295	LOC101901826	uncharacterized LOC101901826 uncharacterized protein LOC101901826
gene-LOC105261419	3661.995	2385.893	0.6181	2.63E-07	5.59E-05	LOC105261419	high mobility group protein D%2C transcript variant X1
gene-LOC105261447	1071.04	1487.058	-0.47345	0.000326	0.019667	LOC105261447	helicase domino
gene-LOC105261583	1255.848	331.7024	1.9207	1.17E-21	2.37E-18	LOC105261583	uncharacterized LOC105261583%2C transcript variant X2 uncharacterized protein LOC105261583 isoform X2
gene-LOC105261589	245.5875	155.0461	0.66354	0.00065	0.032165	LOC105261589	uncharacterized protein LOC105261589 uncharacterized LOC105261589
gene-LOC105261744	3342.229	4415.892	-0.40189	0.000734	0.034767	LOC105261744	hexokinase type 2
gene-LOC105261803	11206.99	8095.03	0.46929	0.000989	0.043013	LOC105261803	uncharacterized LOC105261803 uncharacterized protein LOC105261803
gene-LOC105261829	2317.701	1254.226	0.8859	1.50E-12	1.01E-09	LOC105261829	cytochrome P450 6A1-like
gene-LOC105261914	322.0876	110.603	1.5421	2.81E-15	2.39E-12	LOC105261914	general odorant-binding protein 56h-like
gene-LOC105261927	404.0688	94.30716	2.0992	7.75E-28	2.50E-24	LOC105261927	farnesyl pyrophosphate synthase
gene-LOC105262082	16.08477	0	Inf	1.10E-06	0.000179	LOC105262082	LOW QUALITY PROTEIN: uncharacterized protein LOC105262082 uncharacterized LOC105262082
gene-LOC105262153	48.78821	19.38903	1.3313	0.001134	0.047385	LOC105262153	putative protein tag-52
gene-LOC105262272	85.27771	7.975278	3.4186	9.29E-17	8.82E-14	LOC105262272	lectin subunit alpha-like

gene-LOC105262305	3188.717	5146.448	-0.6906	2.08E-06	0.00031	LOC105262305	uncharacterized protein LOC105262305 isoform X2 uncharacterized LOC105262305%2C transcript variant X2
gene-LOC105262391	221.5931	42.48375	2.3829	6.61E-17	6.66E-14	LOC105262391	turriptide Pal9.2-like
gene-LOC105262393	32.35719	2.56361	3.6578	1.04E-07	2.70E-05	LOC105262393	uncharacterized protein LOC105262393 uncharacterized LOC105262393
gene-LOC105262450	240.9986	383.0837	-0.66863	9.18E-05	0.007088	LOC105262450	uncharacterized protein LOC105262450 uncharacterized LOC105262450%2C transcript variant X1
gene-LOC105262478	1906.695	2762.892	-0.53511	0.000557	0.02915	LOC105262478	nucleic-acid-binding protein from mobile element jockey uncharacterized protein LOC105262478
gene-LOC109611735	6.184764	28.31136	-2.1946	0.000297	0.0182	LOC109611735	uncharacterized LOC109611735 uncharacterized protein LOC109611735
gene-LOC109611747	123.7585	56.67854	1.1267	2.07E-05	0.002153	LOC109611747	protein spaetzle 5-like protein spaetzle 5-like%2C transcript variant X2
gene-LOC109612301	213.1578	330.0458	-0.63074	0.000611	0.031205	LOC109612301	max-binding protein MNT-like
gene-LOC109613297	218.2967	121.2905	0.84782	3.45E-05	0.00331	LOC109613297	hexokinase type 2-like
gene-LOC109613447	397.5786	227.839	0.80323	0.00042	0.023789	LOC109613447	uncharacterized protein LOC109613447 uncharacterized LOC109613447
gene-LOC109613802	572.3346	798.067	-0.47965	0.000842	0.03905	LOC109613802	uncharacterized LOC109613802
gene-LOC109613852	140.0823	276.9291	-0.98324	5.43E-07	0.000102	LOC109613852	von Willebrand factor D and EGF domain-containing protein
gene-LOC109613860	126.5936	227.7347	-0.84715	0.00027	0.017049	LOC109613860	uncharacterized LOC109613860 uncharacterized protein LOC109613860
gene-LOC109613986	1105.57	791.2175	0.48264	0.000347	0.020616	LOC109613986	uncharacterized LOC109613986
gene-LOC109614129	41.32639	86.20918	-1.0608	0.000509	0.027648	LOC109614129	uncharacterized LOC109614129
gene-LOC109614175	521.8618	153.9478	1.7612	2.59E-09	9.51E-07	LOC109614175	uncharacterized LOC109614175 uncharacterized protein LOC109614175

gene-LOC109614213	44.56404	16.892	1.3995	0.001168	0.048342	LOC109614213	uncharacterized LOC109614213
gene-LOC109614258	53.33515	125.1758	-1.2308	5.28E-06	0.000665	LOC109614258	uncharacterized LOC109614258
gene-defensin-1	590.9002	120.1658	2.2979	0.000393	0.022784	defensin-1	phormicin-like uncharacterized protein LOC101887540