Table S7.8. Sex-bias genes of stable expression during development.

GeneID	Eembryo 1	Eembryo 2	Larvae1	Larvae2	Pupae	Adult	CV	Gene_length	M-RPKM	F-RPKM	log2 Ratio(F/M)	Up-Down-Regulation(F/M)	P-value	FDR	Description	Pathway	GO Component	GO Function	GO Process
CCG027868.1	15.4797	17.49676	11.8427	13.5838	13.4373	18.6199	0.17283	1290	12.091483	25.1482797	1.056468461	Up	0	0	AAEL003248-PA OS=Aedes aegypti GN=AAEL003248 PE=4 SV=1	-	-	-	-
CCG027392.1	510.571	606.1046	634.122	473.069	553.867	436.542	0.14304	1728	589.93865	283.145857	-1.059019503	Down	0	0	AAEL002833-PA OS=Aedes aegypti GN=AAEL002833 PE=3 SV=1	ko04142//Lysosome;ko04145//Phagosome;ko04612//Antigen processing and presentation;ko05323//Rheumatoid	-	GO:0004197//cysteine-type endopeptidase activity;GO:0008234//cysteine-type peptidase activity	GO:0006508//proteolysis
CCG027327.1	10.574	9.001408	7.8957	7.19572	6.11269	9.56833	0.19501	8084	3.3699668	15.7666845	2.22607302	Up	######	######	AAEL005215-PA OS=Aedes aegypti GN=AAEL005215 PE=4 SV=1	-	-	-	-
CCG027323.1	14.0586	14.54251	10.6693	11.212	14.0046	18.2307	0.19676	2223	7.8091645	28.6522628	1.875408965	Up	######	######	AAEL006734-PA OS=Aedes aegypti GN=AAEL006734 PE=3 SV=1	ko03060//Protein export	GO:0016021//integral to membrane	-	GO:0051205//protein insertion into membrane

CCG026987.1	32.6826	31.92547	35.5349	28.5048	24.2537	35.5226	0.13914	2553	23.092235	47.9529515	1.054211806	Up	######	######	AAEL010359-PA OS=Aedes aegypti GN=AAEL010359 PE=3 SV=1	-	-	GO:0000166//nucleotide binding;GO:0005524//ATP binding;GO:0016887//ATPase activity;GO:0017111//nucleoside-triphosphata	-
CCG026883.1	13.3114	13.70704	11.4863	16.8222	17.0573	18.0557	0.1723	2490	11.078944	25.0323725	1.175974704	Up	0	0	AAEL006155-PA OS=Aedes aegypti GN=AAEL006155 PE=4 SV=1	-	-	-	-
CCG026744.1	8.36948	7.011122	5.34301	7.6484	8.24345	7.39901	0.15021	816	4.0020831	10.7959384	1.431665614	Up	0	0	AAEL000090-PA OS=Aedes aegypti GN=AAEL000090 PE=4 SV=1	-	GO:0016021//integral to membrane	-	GO:0015031//protein transport
CCG026342.2	63.4035	75.89128	60.6177	71.0767	86.625	75.7966	0.13096	3129	39.824938	111.768169	1.488765361	Up	0	0	Putative uncharacterized protein OS=Culex quinquefasciatus GN=CpipJ_CPIJ007196 PE=3 SV=1	ko04141//Protein processing in endoplasmic reticulum	-	GO:0005524//ATP binding	-
CCG025936.1	16.4685	21.09986	24.1471	29.8391	23.6693	26.4344	0.19352	1625	35.48639	17.3823309	-1.02964427	Down	######	######	AAEL006186-PA OS=Aedes aegypti GN=AAEL006186 PE=4 SV=1	-	-	-	-

CCG024937.1	7.93182	8.212841	9.10999	5.22466	6.32026	7.10955	0.1914	2190	3.7475887	10.4715203	1.48243638	Up	######	######	AAEL000965-PA OS=Aedes aegypti GN=AAEL000965 PE=4 SV=1	ko03013//RNA transport	-	GO:0005515//protein binding	-
CCG024781.1	1714.46	2159.377	2382.3	2573.08	1565.74	1865.07	0.19293	985	1124.0185	2606.11292	1.213233865	Up	######	######	60S ribosomal protein L31 OS=Culex quinquefasciatus GN=CpipJ_CPIJ010692 PE=3 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG024432.2	12.9459	12.47256	12.7774	10.7621	11.023	15.7305	0.14101	2394	9.0462599	22.4147681	1.309056221	Up	0	0	Uncharacterized protein OS=Anopheles darlingi GN=AND_12429 PE=3 SV=1	ko01100//Metabolic pathways;ko00790//Folate biosynthesis;ko04122//Sulfur relay system	GO:0019008//molybdopterin synthase complex	GO:0003824//catalytic activity;GO:0046872//metal ion binding;GO:0051536//iron-sulfur cluster binding;GO:0051539//4 iron, 4 sulfur cluster binding	GO:0006777//Mo-molybdopterin cofactor biosynthetic process
CCG024115.1	142.057	108.471	88.0886	104.534	93.2229	89.2249	0.19447	1488	53.769923	124.679822	1.21335668	Up	0	0	AAEL003634-PA OS=Aedes aegypti GN=AAEL003634 PE=2 SV=1	-	-	GO:0005515//protein binding	-
CCG024084.1	15.2345	12.47696	13.2749	9.65343	11.1553	11.3122	0.15916	402	4.2755955	18.3487473	2.101484298	Up	######	######	AAEL006551-PA OS=Aedes aegypti GN=AAEL006551 PE=4 SV=1	-	-	-	-

CCG023989.1	3.39417	3.005374	3.18954	3.95349	4.13388	2.37879	0.19241	678	1.4576754	3.29989633	1.178751248	Up	0.0005	0.0007	AAEL012676-PA OS=Aedes aegypti GN=AAEL012676 PE=4 SV=1	-	GO:0005622//intracellular	GO:0003676//nucleic acid binding;GO:0008408//3'-5' exonuclease activity	GO:0006139//nucleobase-containing compound metabolic process
CCG023798.1	12.1701	11.09828	10.9805	10.0235	6.48203	10.0827	0.19298	918	6.6467345	13.5187236	1.024241299	Up	######	######	AAEL015041-PA OS=Aedes aegypti GN=AAEL015041 PE=3 SV=1	-	-	-	-
CCG023581.1	30.0896	40.7704	34.4289	37.8724	26.2354	36.1372	0.1549	1162	14.421856	57.8526388	2.004125937	Up	######	######	Eukaryotic translation initiation factor 3 subunit G OS=Anopheles darlingi GN=AND_16989 PE=3 SV=1	ko03013//RNA transport	-	GO:0003676//nucleic acid binding	-
CCG023237.1	42.6813	51.19707	59.4757	65.3381	55.1634	67.2874	0.16185	2388	33.432901	101.141849	1.597039614	Up	0	0	AAEL012827-PA OS=Aedes aegypti GN=AAEL012827 PE=3 SV=1	ko05200//Pathways in cancer;ko04141//Protein processing in endoplasmic reticulum;ko05215//Prostate cancer;ko04621//NOD-like receptor signaling	-	GO:0005524//ATP binding;GO:0051082//unfolded protein binding	GO:0006457//protein folding;GO:0006950//response to stress

CCG023088.1	5.05262	4.392131	5.56389	3.66536	4.65097	4.6665	0.13665	3078	2.8478966	6.48511242	1.187234797	Up	######	######	AAEL014815-PA (Fragment) OS=Aedes aegypti GN=AAEL014815 PE=4 SV=1	-	-	-	-
CCG022489.1	15.5273	16.10361	17.1272	21.8795	15.3577	22.5519	0.18026	949	9.9613716	35.1424616	1.818798946	Up	######	######	AAEL011665-PA OS=Aedes aegypti GN=AAEL011665 PE=2 SV=1	-	-	-	-
CCG022381.1	46.6355	44.40605	59.4176	36.9522	49.7498	39.8072	0.17252	1899	55.075479	24.5389062	-1.166339184	Down	######	######	AAEL001770-PA OS=Aedes aegypti GN=AAEL001770 PE=4 SV=1	-	-	-	-
CCG022221.1	6.55003	8.865487	8.10164	10.7409	9.88563	10.5274	0.17628	663	6.0274288	15.0273135	1.317972502	Up	######	######	AAEL014296-PA OS=Aedes aegypti GN=AAEL014296 PE=4 SV=1	ko04530//Tight junction	-	GO:0005198//structural molecule activity	-
CCG022083.1	24.2474	15.43124	23.9736	17.2705	22.2941	24.729	0.18671	2613	12.399227	37.0587167	1.579562751	Up	0	0	AGAP005609-PB OS=Anopheles gambiae GN=AGAP005609 PE=4 SV=4	ko04144//Endocytosis	-	GO:0008060//ARF GTPase activator activity;GO:0008270//zinc ion binding	GO:0032312//regulation of ARF GTPase activity
CCG022026.1	25.7982	26.35676	35.0036	33.397	21.5708	31.5594	0.17906	1961	44.525498	18.5933109	-1.25984804	Down	######	######	AAEL014960-PA (Fragment) OS=Aedes aegypti GN=AAEL014960 PE=4 SV=1	-	-	GO:0005515//protein binding	-

CCG021835.1	145.205	132.1936	147.849	187.728	213.683	173.325	0.18399	6417	111.6664	234.983686	1.073365436	Up	0	0	AAEL017349-PA OS=Aedes aegypti PE=2 SV=1	ko04141//Protein processing in endoplasmic reticulum;ko04612//Antigen processing and presentation;ko05020//Prion diseases;ko03060//Prot	-	GO:0005524//ATP binding	-
CCG021738.1	1.53557	1.065325	0.8761	1.04037	1.19777	1.19005	0.19303	3384	1.739614	0.64048852	-1.441522569	Down	######	######	AAEL009813-PA OS=Aedes aegypti GN=AAEL009813 PE=4 SV=1	-	GO:0016020//membrane	GO:0004872//receptor activity;GO:0004970//ionotropic glutamate receptor activity;GO:0005216//ion channel activity;GO:0005234//extracellular-glutamate-gated ion channel activity;GO:0008080//N-acetyltransferase activity;GO:0016747//transferase activity, transferring acyl groups other than amino-acyl groups	GO:0006811//ion transport

CCG021101.1	13.2314	13.79872	12.0877	14.8817	10.6395	16.982	0.16208	1613	8.1517289	25.812342	1.662883059	Up	0	0	RING finger protein 121 OS=Culex quinquefasciatus GN=CpipJ_CPIJ006831 PE=4 SV=1	-	-	GO:0005515//protein binding;GO:0008270//zinc ion binding	-
CCG020519.1	16.0794	16.39716	14.5437	14.3789	20.4619	15.7783	0.13581	1355	9.2916105	22.2649394	1.260773099	Up	######	######	AAEL008561-PA OS=Aedes aegypti GN=AAEL008561 PE=4 SV=1	-	-	-	-
CCG019944.1	825.511	1237.726	1430.38	1330.65	1122.16	1130.04	0.17794	411	490.23135	1769.85845	1.852099324	Up	######	######	60S ribosomal protein L27 OS=Aedes aegypti GN=AAEL011587 PE=3 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG019892.1	10.45	9.888299	11.396	7.70382	6.95428	7.80206	0.19759	2877	3.9878064	11.6163061	1.54248408	Up	######	######	AAEL006466-PA (Fragment) OS=Aedes aegypti GN=AAEL006466 PE=4 SV=1	ko01100//Metabolic pathways;ko00532//Glycosaminoglycan biosynthesis - chondroitin sulfate	GO:0032580//Golgi cisterna membrane	GO:0005488//binding;GO:0016758//transferase activity, transferring hexosyl groups	-
CCG019426.1	2559.69	2772.395	3539.93	3722.73	2409.05	2607.47	0.18893	405	1360.8144	3854.12843	1.501934378	Up	0	0	60S ribosomal protein L32 OS=Culex quinquefasciatus GN=CpipJ_CPIJ001220 PE=4 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation

CCG019316.1	24.0824	22.21436	17.8682	20.08	23.5968	18.7168	0.12278	1831	9.6922449	27.7413305	1.51713422	Up	######	######	AAEL006663-PA OS=Aedes aegypti GN=AAEL006663 PE=4 SV=1	-	-	GO:0005515//protein binding	-
CCG018888.1	1.09018	0.891449	1.28952	0.89059	0.79024	0.93169	0.18363	40924	1.2799361	0.58343522	-1.133427439	Down	######	######	AAEL011412-PA OS=Aedes aegypti GN=AAEL011412 PE=4 SV=1	-	-	GO:0005515//protein binding;GO:0005543//phospholipid binding	-
CCG018659.2	4.39285	4.954161	4.09763	4.19743	4.32368	4.62435	0.07062	37887	2.8433269	6.40537275	1.171702573	Up	0	0	AAEL001869-PA OS=Aedes aegypti GN=AAEL001869 PE=4 SV=1	ko01100//Metabolic pathways;ko00230//Purine metabolism;ko00983//Drug metabolism - other enzyme	-	GO:0003922//GMP synthase (glutamine-hydrolyzing) activity;GO:0005524//ATP binding	GO:0006164//purine nucleotide biosynthetic process;GO:0006177//GMP biosynthetic process
CCG018559.2	12.1955	12.6653	12.544	7.60133	8.85491	11.3611	0.19631	2800	7.2281232	15.4940077	1.100017354	Up	0	0	AAEL002190-PA OS=Aedes aegypti GN=AAEL002190 PE=4 SV=1	-	-	-	-

CCG018260.1	4.38654	4.39352	3.54076	4.30378	3.07064	3.70273	0.14041	660	1.3672188	6.03824781	2.142885795	Up	######	######	AAEL009202-PA OS=Aedes aegypti GN=AAEL009202 PE=4 SV=1	ko01100//Metabolic pathways;ko00230//Purine metabolism;ko00240//Pyrimidine metabolism;ko03020//RNA polymerase;ko04623//Cytosolic DNA-	-	-	-
CCG017994.1	18.4797	27.23574	22.9207	19.695	20.689	20.4443	0.14513	24512	27.394258	13.4944197	-1.021510573	Down	0	0	AAEL003046-PA OS=Aedes aegypti GN=AAEL003046 PE=4 SV=1	ko04142//Lysosome	GO:0005764//lysosome	-	GO:0006629//lipid metabolic process;GO:0006665//sphingolipid metabolic process
CCG017810.1	6.79774	5.631188	6.01105	5.38182	5.84712	6.15375	0.08193	1851	2.6000056	9.70748474	1.900582831	Up	0	0	AAEL011465-PA OS=Aedes aegypti GN=AAEL011465 PE=4 SV=1	-	-	-	-
CCG017390.1	3.08964	2.991295	2.39676	2.52503	3.25229	2.96521	0.11672	15353	1.5085447	4.42187022	1.551499226	Up	######	######	AAEL010378-PA OS=Aedes aegypti GN=AAEL010378 PE=4 SV=1	-	-	GO:0005515//protein binding	-
CCG017294.1	36.7618	51.88637	29.3563	35.7555	39.9119	42.443	0.19237	941	58.769446	26.1165447	-1.170102255	Down	######	######	AAEL012023-PA OS=Aedes aegypti GN=AAEL012023 PE=4 SV=1	-	-	-	-

CCG017039.1	6.17312	4.757251	3.57358	4.23934	4.99279	4.25454	0.19007	1425	2.7440322	5.76504915	1.07103551	Up	######	######	AAEL006300-PA OS=Aedes aegypti GN=AAEL006300 PE=4 SV=1	ko04115//p53 signaling pathway	-	-	-
CCG016979.2	778.025	813.3981	900.419	773.521	695.232	813.55	0.0843	2286	458.30624	1168.79313	1.350635762	Up	######	######	AAEL010787-PA OS=Aedes aegypti GN=AAEL010787 PE=3 SV=1	ko03040//Spliceosome	-	GO:0003676//nucleic acid binding;GO:0004386//helicase activity;GO:0005524//ATP binding;GO:0008026//ATP-dependent	-
CCG016802.2	2.96238	2.57557	3.43879	2.06609	3.64391	3.00723	0.19452	213	5.8503395	0.16412337	-5.155667791	Down	######	######	-	-	-	-	-
CCG016700.1	38.1497	50.77071	43.1591	46.6864	46.1567	45.3005	0.09309	1150	27.463265	63.1376877	1.200998265	Up	######	######	AAEL009217-PA OS=Aedes aegypti GN=AAEL009217 PE=4 SV=1	-	-	-	-
CCG016699.1	12.2631	13.36915	14.191	13.6102	13.1895	18.538	0.15637	1020	9.5207451	27.5553476	1.533185933	Up	######	######	AAEL009225-PA OS=Aedes aegypti GN=AAEL009225 PE=4 SV=1	-	GO:0005739//mitochondrion	-	GO:0006412//translation
CCG016285.1	14.4105	11.18409	10.0648	11.1247	15.7909	12.9932	0.17476	953	7.7552931	18.2311265	1.233150491	Up	######	######	AAEL000701-PA OS=Aedes aegypti GN=AAEL000701 PE=4 SV=1	-	GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation

CCG016238.1	32.4067	36.73636	37.1494	25.4395	24.694	29.1269	0.17525	5792	16.143326	42.1104795	1.383241481	Up	0	0	AAEL004327-PA OS=Aedes aegypti GN=AAEL004327 PE=3 SV=1	ko00970//Aminoacyl-tRNA biosynthesis	GO:0005737//cytoplasm	GO:0000166//nucleotide binding;GO:0004812//aminoacyl-tRNA ligase activity;GO:0004832//valine-tRNA ligase activity;GO:0005524//A	GO:0006418//tRNA aminoacylation for protein translation;GO:0006438//valyl-tRNA aminoacylation
CCG014835.1	5.73652	5.499712	4.72049	4.24469	3.24207	5.2432	0.19403	1197	2.0461778	8.44021887	2.044348872	Up	0	0	AAEL011703-PA OS=Aedes aegypti GN=AAEL011703 PE=4 SV=1	ko01100//Metabolic pathways;ko00760//Nicotinate and nicotinamide metabolism	-	GO:0003951//NAD+ kinase activity	GO:0008152//metabolic process
CCG014810.1	19.6059	21.28283	15.2294	17.8519	15.3834	19.8246	0.13684	939	4.3930719	35.2561109	3.004571319	Up	0	0	AAEL006727-PA OS=Aedes aegypti GN=AAEL006727 PE=4 SV=1	-	-	-	-
CCG014302.1	26.2689	30.2943	33.5184	28.2459	22.3124	25.8712	0.13982	2922	17.190835	34.551507	1.007109016	Up	######	######	AAEL006519-PA OS=Aedes aegypti GN=AAEL006519 PE=4 SV=1	-	-	-	-
CCG014174.1	33.3993	62.16628	56.8901	54.454	53.6801	58.1383	0.19054	2556	26.309716	89.966958	1.773799555	Up	######	######	AAEL002834-PA OS=Aedes aegypti GN=AAEL002834 PE=4 SV=1	ko01100//Metabolic pathways;ko00562//Inositol phosphate metabolism	-	GO:0004512//inositol-3-phosphate synthase activity	GO:0006021//inositol biosynthetic process;GO:0008654//phospholipid biosynthetic process

CCG014051.1	1871.73	1974.567	2554.88	2546.1	1863.67	2109.24	0.14869	661	1138.6005	3079.87178	1.435608708	Up	0	0	60S ribosomal protein L17 OS=Culex quinquefasciatus GN=CpipJ_CPIJ015624 PE=3 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome;GO:0015934//large ribosomal subunit	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG013809.1	15.6377	11.68286	11.4218	13.453	13.3194	12.5085	0.11779	1023	5.8805111	19.1364956	1.702313204	Up	0	0	Putative arsenite-translocating ATpase OS=Glossina morsitans morsitans PE=2 SV=1	-	-	GO:0005524//ATP binding;GO:0016887//ATPase activity	GO:0071722//detoxification of arsenic-containing substance
CCG013430.1	643.224	575.8558	660.05	797.531	546.181	492.078	0.17308	276	3.4251238	980.731656	8.161558512	Up	######	######	Ribosomal protein L37 OS=Aedes aegypti PE=3 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG013234.1	207.068	228.3037	281.682	340.865	266.756	250.739	0.17788	869	111.30595	390.172988	1.809583155	Up	0	0	Ribosomal protein S19 OS=Aedes albopictus PE=2 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG012510.1	9.22208	8.874453	7.99122	12.0514	10.7704	9.65687	0.14835	2274	17.83792	1.47581116	-3.595367345	Down	######	######	AAEL010921-PA OS=Aedes aegypti GN=AAEL010921 PE=4 SV=1	-	GO:0016020//membrane	GO:0005215//transporter activity	GO:0006810//transport

CCG012397.1	33.0701	38.27269	35.0371	32.0729	28.0396	35.2272	0.1031	3091	20.657724	49.7966007	1.269365932	Up	######	######	Uridine kinase OS=Aedes aegypti GN=AAEL011273 PE=3 SV=1	ko01100//Metabolic pathways;ko00983//Drug metabolism - other enzymes;ko00240//Pyrimidine metabolism	-	GO:0005524//ATP binding;GO:0016301//kinase activity;GO:0016773//phosphotransferase activity, alcohol group as acceptor	GO:0008152//metabolic process
CCG012308.1	8.43324	10.29874	7.45281	8.26356	12.3462	9.50549	0.18773	1404	6.2128605	12.7981156	1.042601836	Up	######	######	AAEL010223-PA OS=Aedes aegypti GN=AAEL010223 PE=4 SV=1	ko01100//Metabolic pathways;ko00564//Glycerophospholipid metabolism	-	GO:0004609//phosphatidylserine decarboxylase activity	GO:0008654//phospholipid biosynthetic process
CCG011445.2	6.39854	5.858197	6.83611	5.75208	7.12491	4.71754	0.14203	1398	7.2845687	2.15050916	-1.76016529	Down	######	######	AAEL014355-PA OS=Aedes aegypti GN=AAEL014355 PE=4 SV=1	-	-	-	-
CCG010559.1	53.4576	33.51711	51.9897	51.2668	37.1533	48.8533	0.18467	636	30.538239	67.1682613	1.137162811	Up	######	######	AAEL012875-PA OS=Aedes aegypti GN=AAEL012875 PE=2 SV=1	ko04145//Phagosome;ko04130//SNARE interactions in vesicular transpor	GO:0016021//integral to membrane	-	GO:0016192//vesicle-mediated transport

CCG010206.1	0.79107	0.901967	0.71364	0.71624	0.66168	0.84689	0.11809	1173	0.2930587	1.40071527	2.256902055	Up	######	######	AAEL001724-PA (Fragment) OS=Aedes aegypti GN=GPRNNB3 PE=4 SV=2	-	GO:0016020//membrane	-	-
CCG009883.1	89.3897	71.88664	100.444	78.2518	63.396	97.8369	0.17707	840	46.6017	149.07208	1.677555582	Up	0	0	AAEL010954-PA OS=Aedes aegypti GN=AAEL010954 PE=4 SV=1	-	-	-	-
CCG009526.1	22.0016	22.4732	20.6588	23.0947	16.1825	24.7361	0.13655	2129	12.674962	36.7973219	1.537619388	Up	######	######	AAEL011442-PA OS=Aedes aegypti GN=AAEL011442 PE=4 SV=1	ko03013//RNA transport	-	GO:0016779//nucleotidyltransferase activity	GO:0009058//biosynthetic process
CCG009017.1	9.27921	10.96818	12.0158	11.8681	9.12938	13.6068	0.15498	836	4.2147347	22.9988663	2.448049008	Up	0	0	AAEL014657-PA OS=Aedes aegypti GN=AAEL014657 PE=4 SV=1	-	-	-	-

CCG008931.1	2.82337	3.586155	3.0013	2.39142	3.08539	2.77788	0.13442	26148	1.8471004	3.70866834	1.005638956	Up	######	######	UDP-glucose 6-dehydrogenase OS=Aedes aegypti GN=AAEL011242 PE=3 SV=1	ko01100//Metabolic pathways;ko00500//Starch and sucrose metabolism;ko00520//Amino sugar and nucleotide sugar metabolism;ko00040//Pentose and glucuronate interconversions;ko00053//Ascorbate and aldarate	-	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0051287//NAD binding	GO:0055114//oxidation-reduction process
CCG008569.1	222.701	177.9331	232.559	186.061	135.203	177.431	0.18653	1483	63.339069	291.52327	2.20244347	Up	0	0	Uncharacterized protein OS=Anopheles darlingi GN=AND_10459 PE=3 SV=1	ko03010//Ribosome	GO:0005622//intracellular;GO:0005840//ribosome;GO:0015935//small ribosomal subunit	GO:0003735//structural constituent of ribosome	GO:0006412//translation
CCG008270.1	1345.47	1281.778	1839.29	1470.97	1194.42	1065.24	0.19707	577	517.49859	1612.98822	1.640109068	Up	######	######	Ubiquitin OS=Anopheles stephensi GN=Ubi-p63E PE=2 SV=1	ko03010//Ribosome	GO:0005840//ribosome	GO:0003735//structural constituent of ribosome;GO:0005515//protein	GO:0006412//translation

CCG008208.1	18.2946	18.63321	19.9467	15.7058	11.41	16.0384	0.18238	1266	9.1302201	22.9465466	1.329555508	Up	0	0	AAEL006663-PA OS=Aedes aegypti GN=AAEL006663 PE=4 SV=1	-	-	-	-
CCG007928.1	15.722	14.54482	11.4741	12.4622	14.6242	18.1815	0.16427	687	9.444585	26.918382	1.511032377	Up	0	0	AAEL010931-PA OS=Aedes aegypti GN=AAEL010931 PE=2 SV=1	-	-	-	-
CCG007390.1	20.2019	19.23263	28.1189	22.5938	16.3184	23.2128	0.18684	2394	14.825815	31.5997122	1.091800016	Up	######	######	AGAP005404-PA OS=Anopheles gambiae GN=AGAP005404 PE=4 SV=3	ko04141//Protein processing in endoplasmic reticulum	GO:0016020//membrane	-	-
CCG006993.1	46.9801	50.20122	55.2212	34.6354	36.2446	39.3811	0.18896	715	26.202523	52.5596469	1.004249824	Up	######	######	AAEL007414-PA OS=Aedes aegypti GN=AAEL007414 PE=4 SV=1	-	-	-	-
CCG006570.1	22.1396	19.79788	23.3615	19.0759	21.592	19.8539	0.07888	2674	10.959371	28.7484109	1.391317164	Up	######	######	AAEL005728-PA OS=Aedes aegypti GN=AAEL005728 PE=3 SV=2	ko00970//Aminoacyl-tRNA biosynthesis	GO:0005737//cytoplasm	GO:0000166//nucleotide binding;GO:0004812//aminoacyl-tRNA ligase activity;GO:0004820//glycine-tRNA ligase activity;GO:0005524//A	GO:0006418//tRNA aminoacylation for protein translation;GO:0006426//glycyl-tRNA aminoacylation
CCG006321.1	7.16067	7.179526	6.50998	6.73634	5.21766	9.19185	0.18461	1752	4.3165943	14.0671148	1.704361032	Up	0	0	AAEL000426-PA OS=Aedes aegypti GN=AAEL000426 PE=4 SV=1	-	-	-	-

CCG006308.1	8.45106	6.250947	8.75042	9.98067	8.78754	8.26436	0.14468	1423	2.0835641	14.4451629	2.793461092	Up	0	0	CAAX prenyl protease 2 OS=Culex quinquefasciatus GN=CpipJ_CPIJ002690 PE=4	ko00900//Terpenoid backbone biosynthesis	GO:0016020//membrane	-	-
CCG006063.1	48.4494	52.68632	49.2411	46.8429	55.8018	32.6256	0.1684	357	54.283894	10.9673025	-2.307315497	Down	######	######	AAEL005948-PA OS=Aedes aegypti GN=AAEL005948 PE=4 SV=1	-	GO:0005634//nucleus	GO:0004861//cyclin-dependent protein kinase inhibitor activity	GO:0007050//cell cycle arrest
CCG005989.1	9.5741	12.61904	9.93908	7.64964	9.72931	10.8633	0.16247	1888	6.3953895	15.3312782	1.261373841	Up	0	0	AAEL009412-PA OS=Aedes aegypti GN=AAEL009412 PE=4 SV=1	-	-	GO:0003723//RNA binding	-
CCG005981.4	27.5232	21.33739	30.8937	23.2665	24.1932	28.721	0.13995	1269	17.607771	39.8342539	1.177797228	Up	######	######	AAEL005405-PA OS=Aedes aegypti GN=AAEL005405 PE=4 SV=1	-	-	-	-
CCG004532.1	8.12321	14.24925	11.0392	13.3357	12.631	10.2231	0.19427	297	5.4978112	14.9484887	1.443070377	Up	######	######	AAEL010223-PA OS=Aedes aegypti GN=AAEL010223 PE=4 SV=1	ko01100//Metabolic pathways;ko00564//Glycerophospholipid metabolism	-	GO:0004609//phosphatidylserine decarboxylase activity	GO:0008654//phospholipid biosynthetic process
CCG003530.1	58.8943	55.5866	36.6415	49.0885	59.2488	52.8763	0.16256	1326	32.988831	72.763834	1.141243909	Up	######	######	AAEL009345-PA OS=Aedes aegypti GN=AAEL009345 PE=2 SV=1	-	GO:0016020//membrane	-	-

CCG003296.1	23.689	20.69933	19.5132	17.5655	13.164	19.4246	0.1844	3364	8.9413835	29.9078242	1.741952969	Up	0	0	AAEL006415-PA OS=Aedes aegypti GN=AAEL006415 PE=3 SV=1	ko00970//Aminoacyl-tRNA biosynthesis	GO:0005737//cytoplasm	GO:0000166//nucleotide binding;GO:0004812//aminoacyl-tRNA ligase activity;GO:0005524//ATP binding	GO:0006418//tRNA aminoacylation for protein translation
CCG003277.1	10.3709	10.83362	6.95018	9.44283	8.62391	12.0557	0.18457	1360	5.6555754	18.4559138	1.70633746	Up	0	0	AAEL007895-PA OS=Aedes aegypti GN=AAEL007895 PE=4 SV=1	ko01100//Metabolic pathways;ko00532//Glycosaminoglycan biosynthesis - chondroitin sulfate;ko00534//Glycosaminoglycan biosynthesis - heparan sulfate	-	GO:0016757//transferase activity, transferring glycosyl groups	GO:0005975//carbohydrate metabolic process
CCG003063.1	7.01729	6.76908	4.94289	4.76091	6.63484	6.03935	0.1605	3126	9.8420761	2.236614	-2.137646384	Down	######	######	AAEL009547-PA OS=Aedes aegypti GN=AAEL009547 PE=3 SV=1	ko01100//Metabolic pathways;ko00260//Glycine, serine and threonine metaboli	GO:0005737//cytoplasm	GO:0004047//aminomethyltransferase activity;GO:0016491//oxidoreductase activity	GO:0006546//glycine catabolic process;GO:0055114//oxidation-reduction process

CCG002765.1	9.59617	11.2387	9.22305	14.7965	10.1323	12.5231	0.18766	1698	21.813846	3.23230239	-2.754610106	Down	######	######	AAEL012509-PA (Fragment) OS=Aedes aegypti GN=AAEL012509 PE=4 SV=1	ko01100//Metabolic pathways;ko00983//Drug metabolism - other enzyme	-	-	-
CCG002662.1	22.3007	35.6378	26.6771	24.2723	22.5357	24.8306	0.19074	1701	14.045369	35.6159281	1.34242807	Up	######	######	AAEL001206-PA OS=Aedes aegypti GN=AAEL001206 PE=3 SV=1	ko00970//Aminoacyl-tRNA biosynthesis	GO:0005737//cytoplasm	GO:0000166//nucleotide binding;GO:0004812//aminoacyl-tRNA ligase activity;GO:0004829//threonine-tRNA ligase activity;GO:0005524//ATP binding;GO:0016876//ligase activity, forming aminoacyl-tRNA and related	GO:0006418//tRNA aminoacylation for protein translation;GO:0006435//threonyl-tRNA aminoacylation;GO:0043039//tRNA aminoacylation
CCG002273.1	1.80671	1.13775	1.19143	1.29826	1.36245	1.40311	0.17402	2342	0.8806777	1.92554129	1.128577959	Up	######	######	Putative uncharacterized protein OS=Culex quinquefasciatus GN=CpipJ_CPIJ018868 PE=4 SV=1	ko04330//Notch signaling pathway	-	-	GO:0006355//regulation of transcription, DNA-dependent
CCG002188.1	857.08	785.6753	843.6	929.267	629.87	584.563	0.17637	558	349.61039	819.514728	1.229021836	Up	######	######	60S ribosomal protein L27a OS=Aedes albopictus PE=2 SV=1	ko03010//Ribosome	-	-	-

CCG002121.1	10.43	10.39614	6.29686	8.85555	9.95067	11.3761	0.18759	1911	6.7456412	16.006537	1.24663372	Up	######	######	AAEL001859-PA OS=Aedes aegypti GN=AAEL001859 PE=4 SV=1	ko04144//Endocytosis	-	-	GO:0006904//vesicle docking involved in exocytosis;GO:0016192//vesicle-mediated transport
CCG002118.1	168.258	156.5439	162.806	203.912	205.231	189.126	0.11772	5345	287.84497	90.4075322	-1.670777106	Down	0	0	Ubiquitin C variant (Fragment) OS=Homo sapiens PE=2 SV=1	ko03320//PPAR signaling pathway	-	GO:0005515//protein binding	-
CCG001876.1	17.454	17.63143	16.1617	12.8678	11.0358	18.4069	0.19036	2907	8.6619417	28.1518149	1.700465569	Up	0	0	AAEL014709-PA OS=Aedes aegypti GN=AAEL014709 PE=3 SV=1	ko00970//Aminoacyl-tRNA biosynthesis;ko00450//Selenocompound metabolism	GO:0005737//cytoplasm	GO:0000166//nucleotide binding;GO:0004812//aminoacyl-tRNA ligase activity;GO:0004825//methionine-tRNA ligase activity;GO:0005524//ATP binding	GO:0006418//tRNA aminoacylation for protein translation;GO:0006431//methionyl-tRNA aminoacylation
CCG001798.1	4.00088	3.271193	3.56556	3.42181	3.53646	5.29669	0.19489	3414	1.787259	8.80612713	2.300758934	Up	######	######	AAEL002465-PA (Fragment) OS=Aedes aegypti GN=AAEL002465 PE=4 SV=1	ko01100//Metabolic pathways;ko00563//Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	-	GO:0003824//catalytic activity	-
CCG001783.1	13.8437	16.22151	13.5916	13.0185	9.62334	15.4061	0.16856	1976	10.024822	20.7874368	1.052135305	Up	######	######	AAEL009394-PA OS=Aedes aegypti GN=AAEL009394 PE=4 SV=1	-	GO:0005622//intracellular	GO:0008270//zinc ion binding	-

CCG001753 .1	17.2161	16.48848	9.77097	14.928	14.0844	18.0994	0.1984	1742	11.174104	25.0246677	1.163191714	Up	######	######	AAEL004497-PA OS=Aedes aegypti GN=AAEL004497 PE=4 SV=1	-	-	-	-
CCG001451 .1	2.10592	1.667466	2.0408	2.4827	1.75842	2.46188	0.16376	564	1.1428121	3.78094837	1.726159946	Up	######	######	AAEL008356-PA OS=Aedes aegypti GN=AAEL008356 PE=4 SV=1	-	-	-	-
CCG000958 .1	7.29081	7.162047	8.39005	5.00088	5.52583	7.14529	0.18575	952	10.471616	3.81897141	-1.455228073	Down	######	######	-	-	-	-	-
CCG000705 .1	7.389	6.893737	5.32876	6.48262	7.9851	5.86853	0.14673	216	2.1882735	9.54878856	2.125524635	Up	######	######	Putative uncharacterized protein OS=Culex quinquefasciatus GN=CpipJ_CPIJ007491 PE=4 SV=1	-	-	-	-
CCG000461 .1	11.2602	17.31791	12.5408	12.2868	10.6588	15.1484	0.19235	267	22.048141	8.24858216	-1.418438956	Down	######	######	AAEL011100-PA OS=Aedes aegypti GN=AAEL011100 PE=4 SV=1	-	-	-	-
CCG000390 .1	11.7449	13.24728	12.6404	16.8251	16.0642	16.3766	0.15124	1479	5.2876888	27.4655291	2.376912917	Up	0	0	AAEL010378-PA OS=Aedes aegypti GN=AAEL010378 PE=4 SV=1	-	-	GO:0005515//protein binding	-