**Supplementary Table S1:** Up-regulated components in the Systemic-1 population determined by a fold change of greater than 2 and a FDR of less than 0.059. Component Description is the reference gene associated with the blast hit from the reference database.

|  |  |  |  |
| --- | --- | --- | --- |
| Components | FDR | Fold Change | Component Description |
| comp100892\_c0 | 0.001 | 9.730 | ---NA--- |
| comp100923\_c0 | 0.001 | 2.674 | PREDICTED: similar to alpha-esterase |
| comp101093\_c0 | 0.006 | 11.940 | ---NA--- |
| comp101549\_c0 | 0.005 | 7.215 | caseinolytic peptidase b protein homolog (suppressor of potassium transport defect 3) |
| comp101816\_c0 | 0.001 | 2.364 | juvenile hormone-inducible |
| comp101841\_c0 | 0.040 | 2.525 | ---NA--- |
| comp101855\_c0 | 0.054 | 3.017 | ---NA--- |
| comp101939\_c0 | 0.001 | 2.443 | ---NA--- |
| comp102061\_c0 | 0.001 | 3.174 | cathepsin b-like like proteinase |
| comp102186\_c0 | 0.001 | 2.629 | AGAP009328-PA |
| comp102187\_c1 | 0.026 | 2.241 | Actin, muscle |
| comp102265\_c1 | 0.017 | 2.474 | ---NA--- |
| comp102305\_c0 | 0.041 | 2.263 | cg9090 cg9090-pa |
| comp102424\_c0 | 0.001 | 2.422 | translocator protein-like |
| comp102425\_c0 | 0.001 | 3.388 | ---NA--- |
| comp102476\_c0 | 0.001 | 21.655 | ---NA--- |
| comp102528\_c0 | 0.041 | 2.013 | ---NA--- |
| comp102657\_c0 | 0.011 | 2.389 | PREDICTED: similar to AGAP006424-PA |
| comp102690\_c0 | 0.001 | 4.905 | PREDICTED: hypothetical protein |
| comp102761\_c0 | 0.020 | 2.457 | 28 kda desiccation stress protein |
| comp102762\_c0 | 0.003 | 2.846 | ---NA--- |
| comp102853\_c0 | 0.001 | 2.304 | PREDICTED: similar to 3-oxoacyl- |
| comp102935\_c0 | 0.001 | 7.199 | ---NA--- |
| comp103119\_c0 | 0.001 | 3.230 | sodium-dependent phosphate transporter |
| comp103228\_c0 | 0.053 | 2.091 | PREDICTED: hypothetical protein LOC100570164 |
| comp103236\_c0 | 0.008 | 2.487 | AGAP007368-PA |
| comp103555\_c0 | 0.001 | 4.097 | ---NA--- |
| comp103556\_c0 | 0.057 | 4.272 | cg9427 cg9427-pa |
| comp103650\_c0 | 0.001 | 13.195 | defensin 1 |
| comp103658\_c0 | 0.001 | 2.373 | cytochrome p450 9z4 |
| comp103760\_c0 | 0.001 | 3.113 | beta- -glucan recognition protein 2 |
| comp103910\_c0 | 0.001 | 3.282 | ---NA--- |
| comp103967\_c0 | 0.001 | 2.168 | PREDICTED: similar to AGAP001449-PA |
| comp104160\_c0 | 0.015 | 2.940 | ---NA--- |
| comp104308\_c0 | 0.002 | 2.207 | PREDICTED: similar to GA15997-PA |
| comp104384\_c0 | 0.001 | 2.369 | ---NA--- |
| comp104411\_c0 | 0.001 | 2.528 | 29-kda galactose-binding lectin |
| comp104533\_c0 | 0.001 | 7.084 | acid phosphatase 1 |
| comp104646\_c0 | 0.001 | 2.164 | defensin 1 |
| comp104702\_c0 | 0.020 | 2.398 | ---NA--- |
| comp104711\_c0 | 0.022 | 2.206 | cg6870 cg6870-pa |
| comp104713\_c0 | 0.034 | 2.197 | niemann-pick type c-1b |
| comp104806\_c0 | 0.001 | 2.003 | PREDICTED: similar to conserved hypothetical protein |
| comp104861\_c0 | 0.003 | 2.326 | ---NA--- |
| comp104933\_c0 | 0.001 | 3.334 | glucose dehydrogenase |
| comp104970\_c0 | 0.001 | 2.164 | ---NA--- |
| comp104984\_c0 | 0.001 | 8.539 | allergen bla g |
| comp105039\_c1 | 0.032 | 2.567 | cathepsin l-like protein cysteine proteinase |
| comp105223\_c0 | 0.001 | 2.291 | serine protease 2 |
| comp105323\_c0 | 0.019 | 2.118 | ---NA--- |
| comp105434\_c0 | 0.001 | 2.130 | juvenile hormone-inducible |
| comp105457\_c0 | 0.058 | 2.066 | ---NA--- |
| comp105517\_c0 | 0.051 | 2.057 | ---NA--- |
| comp105537\_c2 | 0.001 | 3.163 | ---NA--- |
| comp105581\_c0 | 0.037 | 2.038 | purine biosynthesis protein pur6 isoform 1 |
| comp105731\_c1 | 0.001 | 2.325 | cg7675 cg7675-pb |
| comp105917\_c0 | 0.005 | 3.144 | ---NA--- |
| comp105956\_c0 | 0.013 | 2.012 | ---NA--- |
| comp105973\_c0 | 0.001 | 3.302 | PREDICTED: similar to AGAP005972-PA |
| comp105989\_c0 | 0.001 | 2.420 | AGAP011167-PA |
| comp106035\_c1 | 0.001 | 6.524 | tryptophan -dioxygenase |
| comp106072\_c0 | 0.001 | 2.504 | cytochrome p450 9z4 |
| comp106118\_c0 | 0.003 | 2.143 | PREDICTED: similar to conserved hypothetical protein |
| comp106220\_c0 | 0.001 | 2.867 | cg6870 cg6870-pa |
| comp106244\_c0 | 0.001 | 4.736 | 12 kda hemolymph protein b |
| comp106294\_c2 | 0.001 | 2.061 | atp-binding cassette transporter |
| comp106296\_c0 | 0.015 | 2.594 | ---NA--- |
| comp106421\_c0 | 0.026 | 2.346 | AGAP011167-PA |
| comp106543\_c1 | 0.001 | 2.747 | poils au dos |
| comp106548\_c0 | 0.001 | 2.517 | xanthine dehydrogenase |
| comp106668\_c0 | 0.001 | 2.061 | cg6084 cg6084-pa |
| comp106677\_c0 | 0.009 | 2.567 | AGAP011630-PA |
| comp106711\_c0 | 0.001 | 2.163 | acid phosphatase-1 |
| comp106832\_c0 | 0.006 | 2.289 | PREDICTED: similar to AGAP001553-PA |
| comp106834\_c0 | 0.001 | 2.182 | AGAP003206-PB |
| comp107125\_c0 | 0.001 | 2.385 | conserved hypothetical protein |
| comp107157\_c0 | 0.021 | 2.248 | pacifastin-related serine protease inhibitor isoform 2 |
| comp107172\_c0 | 0.001 | 2.076 | ---NA--- |
| comp107182\_c0 | 0.001 | 2.169 | zinc-containing alcohol dehydrogenase |
| comp107277\_c0 | 0.019 | 2.027 | variable lymphocyte receptor a |
| comp107290\_c0 | 0.001 | 3.318 | PREDICTED: hypothetical protein LOC100165870 |
| comp107322\_c0 | 0.001 | 2.375 | hemoglobin c1 polymer |
| comp107451\_c0 | 0.020 | 2.460 | ---NA--- |
| comp107507\_c0 | 0.001 | 2.123 | cg1673 cg1673-pa |
| comp107523\_c0 | 0.030 | 2.675 | hypothetical protein Phum\_PHXM454910 |
| comp107656\_c0 | 0.001 | 3.503 | ---NA--- |
| comp107703\_c0 | 0.001 | 5.077 | cg34115 cg34115-pa |
| comp107706\_c0 | 0.001 | 4.201 | PREDICTED: similar to AGAP005839-PA |
| comp107777\_c0 | 0.025 | 2.291 | ---NA--- |
| comp107842\_c0 | 0.001 | 2.050 | seven in absentia 1b |
| comp107865\_c0 | 0.006 | 2.013 | aldo-keto reductase |
| comp107875\_c0 | 0.018 | 3.357 | PREDICTED: similar to AGAP010241-PA |
| comp107926\_c0 | 0.001 | 3.099 | ---NA--- |
| comp108155\_c0 | 0.001 | 5.841 | PREDICTED: hypothetical protein LOC100574147 |
| comp108241\_c0 | 0.001 | 2.913 | PREDICTED: similar to AGAP003785-PA |
| comp108250\_c0 | 0.001 | 2.027 | cg15105 cg15105-pa |
| comp108251\_c0 | 0.001 | 5.033 | PREDICTED: hypothetical protein LOC100571634 |
| comp108262\_c0 | 0.001 | 2.930 | 3-hydroxy-3-methylglutaryl- reductase |
| comp108539\_c0 | 0.050 | 2.378 | cathepsin b-like cysteine proteinase-like |
| comp108541\_c1 | 0.001 | 2.178 | ---NA--- |
| comp108561\_c0 | 0.006 | 2.484 | cg3108 cg3108-pa |
| comp108640\_c0 | 0.001 | 2.469 | ---NA--- |
| comp108695\_c0 | 0.001 | 3.965 | ---NA--- |
| comp108705\_c0 | 0.020 | 2.044 | Xracil-DNA glycosylase, putative |
| comp108777\_c0 | 0.001 | 2.634 | acid phosphatase-1 |
| comp108826\_c0 | 0.006 | 2.470 | peritrophic matrix protein 3 precursor |
| comp108902\_c0 | 0.001 | 2.389 | PREDICTED: similar to AGAP001894-PA |
| comp108962\_c1 | 0.003 | 2.358 | ---NA--- |
| comp109050\_c0 | 0.001 | 3.063 | ---NA--- |
| comp109194\_c0 | 0.020 | 2.015 | isoform a |
| comp109331\_c0 | 0.010 | 2.519 | ---NA--- |
| comp109356\_c0 | 0.013 | 2.340 | eukaryotic translation initiation factor 4e binding protein |
| comp109435\_c0 | 0.001 | 2.349 | 29-kda galactose-binding lectin |
| comp109504\_c1 | 0.001 | 2.412 | chitinase 3 precursor |
| comp109529\_c0 | 0.001 | 2.328 | sodium-dependent phosphate transporter |
| comp109623\_c0 | 0.001 | 14.366 | PREDICTED: hypothetical protein |
| comp109630\_c0 | 0.001 | 2.468 | PREDICTED: hypothetical protein |
| comp109633\_c0 | 0.005 | 2.203 | PREDICTED: similar to putative esterase |
| comp109639\_c0 | 0.001 | 2.486 | sodium-dependent phosphate transporter |
| comp109647\_c0 | 0.001 | 2.064 | PREDICTED: similar to conserved hypothetical protein |
| comp109680\_c0 | 0.020 | 2.918 | juvenile hormone-inducible |
| comp109791\_c1 | 0.001 | 2.495 | uncharacterized protein LOC662961 |
| comp109815\_c1 | 0.033 | 2.313 | NA |
| comp109849\_c0 | 0.001 | 2.018 | cg14275 cg14275-pa |
| comp109878\_c0 | 0.001 | 3.644 | phosphodiesterase 9 cg32648-pa |
| comp109936\_c0 | 0.001 | 2.954 | NA |
| comp109941\_c0 | 0.010 | 2.597 | ---NA--- |
| comp110160\_c0 | 0.002 | 2.068 | cg17664 cg17664-pb |
| comp110161\_c0 | 0.001 | 3.175 | antennal-enriched xdp-glycosyltransferase |
| comp110172\_c0 | 0.012 | 2.056 | ---NA--- |
| comp110251\_c0 | 0.001 | 2.129 | cg9119 cg9119-pa |
| comp110258\_c0 | 0.039 | 2.370 | cg6084 cg6084-pa |
| comp110286\_c1 | 0.011 | 2.380 | equilibrative nucleoside |
| comp110308\_c0 | 0.001 | 2.375 | PREDICTED: hypothetical protein LOC100570299 |
| comp110336\_c0 | 0.002 | 2.103 | PREDICTED: similar to AGAP002198-PA |
| comp110381\_c0 | 0.001 | 7.377 | ---NA--- |
| comp110446\_c0 | 0.003 | 3.330 | peptidoglycan recognition protein short class (agap006343-pa) |
| comp110599\_c0 | 0.002 | 2.048 | propionyl- carboxylase alpha mitochondrial precursor (pccase subunit alpha) (propanoyl- :carbon dioxide ligase subunit alpha) |
| comp110691\_c0 | 0.024 | 2.247 | PREDICTED: similar to GA11424-PA |
| comp110698\_c2 | 0.001 | 2.174 | ---NA--- |
| comp110718\_c0 | 0.001 | 5.725 | alcohol dehydrogenase |
| comp110734\_c0 | 0.001 | 2.713 | alcohol dehydrogenase |
| comp110813\_c0 | 0.005 | 2.193 | glucosyl glucuronosyl transferases |
| comp110885\_c0 | 0.001 | 2.620 | amino acid transporter |
| comp110906\_c0 | 0.001 | 23.437 | PREDICTED: hypothetical protein |
| comp110935\_c0 | 0.001 | 3.993 | pancreatic lipase |
| comp110977\_c0 | 0.018 | 2.132 | lysosomal thiol reductase ip30 precursor |
| comp110997\_c1 | 0.001 | 2.505 | cg3106 cg3106-pa |
| comp111069\_c0 | 0.001 | 2.372 | peroxidasin homolog |
| comp111132\_c0 | 0.001 | 2.439 | PREDICTED: similar to GA12046-PA |
| comp111231\_c1 | 0.001 | 2.148 | ---NA--- |
| comp111255\_c0 | 0.007 | 2.465 | ---NA--- |
| comp111326\_c0 | 0.002 | 2.239 | transposable element p transposase (p-element transposase) |
| comp111372\_c0 | 0.001 | 2.447 | PREDICTED: similar to AGAP002559-PA |
| comp111513\_c0 | 0.038 | 2.254 | clip domain serine protease |
| comp111616\_c0 | 0.001 | 2.759 | PREDICTED: similar to predicted protein |
| comp111631\_c0 | 0.001 | 2.380 | ---NA--- |
| comp111641\_c0 | 0.006 | 3.581 | AGAP002387-PA |
| comp111653\_c0 | 0.001 | 3.354 | PREDICTED: similar to GA13362-PA |
| comp111660\_c0 | 0.004 | 2.378 | ---NA--- |
| comp111665\_c0 | 0.006 | 2.088 | AGAP002799-PA |
| comp111667\_c1 | 0.001 | 2.802 | cg1213 cg1213-pa |
| comp111672\_c0 | 0.001 | 2.971 | PREDICTED: similar to AGAP012156-PA |
| comp111691\_c1 | 0.001 | 2.775 | cytochrome p450 monooxygenase |
| comp111701\_c1 | 0.003 | 2.055 | cg5044 cg5044-pa |
| comp111719\_c0 | 0.001 | 2.280 | cationic amino acid transporter |
| comp111768\_c1 | 0.001 | 2.298 | juvenile hormone-inducible |
| comp111850\_c0 | 0.001 | 2.931 | isoform a |
| comp111874\_c0 | 0.001 | 2.042 | beta 1-like 2 |
| comp111910\_c0 | 0.025 | 2.027 | PREDICTED: similar to AGAP006427-PA |
| comp111916\_c1 | 0.051 | 2.048 | uncharacterized protein LOC662961 |
| comp111937\_c0 | 0.001 | 3.705 | ---NA--- |
| comp111971\_c0 | 0.001 | 2.037 | PREDICTED: similar to AGAP001553-PA |
| comp111980\_c0 | 0.011 | 2.095 | PREDICTED: hypothetical protein LOC100570299 |
| comp111987\_c1 | 0.001 | 2.145 | dimeric dihydrodiol dehydrogenase isoform 1 |
| comp112067\_c1 | 0.001 | 2.100 | cytochrome p450 monooxygenase |
| comp112077\_c0 | 0.001 | 2.031 | isoform a |
| comp112104\_c0 | 0.001 | 2.261 | ---NA--- |
| comp112120\_c0 | 0.002 | 2.009 | ---NA--- |
| comp112148\_c0 | 0.001 | 3.030 | PREDICTED: similar to cystathionine-beta-synthase |
| comp112200\_c0 | 0.018 | 2.113 | ---NA--- |
| comp112222\_c0 | 0.010 | 2.145 | juvenile hormone-inducible |
| comp112294\_c0 | 0.001 | 4.511 | ---NA--- |
| comp112295\_c0 | 0.001 | 2.069 | tpr repeat-containing protein c9orf52 |
| comp112376\_c0 | 0.002 | 2.017 | PREDICTED: hypothetical protein LOC100573156 |
| comp112427\_c1 | 0.001 | 2.031 | PREDICTED: similar to F28G4.5 |
| comp112459\_c0 | 0.001 | 2.906 | ventral nervous system defective |
| comp112482\_c0 | 0.005 | 2.831 | ---NA--- |
| comp112570\_c0 | 0.001 | 2.138 | PREDICTED: similar to chrysoptin |
| comp112604\_c0 | 0.001 | 3.249 | PREDICTED: similar to GA19585-PA |
| comp112608\_c0 | 0.001 | 2.056 | antennal-enriched xdp-glycosyltransferase |
| comp112638\_c0 | 0.001 | 3.741 | ---NA--- |
| comp112664\_c0 | 0.005 | 2.489 | ---NA--- |
| comp112685\_c0 | 0.001 | 6.499 | AGAP005332-PC |
| comp112752\_c0 | 0.001 | 2.116 | PREDICTED: similar to AGAP006569-PA |
| comp112759\_c0 | 0.001 | 2.492 | PREDICTED: similar to AGAP000973-PA |
| comp112816\_c0 | 0.001 | 5.786 | antennae-rich cytochrome p450 |
| comp112968\_c0 | 0.001 | 2.625 | glucosyl glucuronosyl transferases |
| comp113028\_c1 | 0.001 | 2.176 | aldo-keto reductase |
| comp113119\_c1 | 0.002 | 2.181 | PREDICTED: similar to chrysoptin |
| comp113204\_c0 | 0.009 | 2.061 | steroid dehydrogenase isoform 1 |
| comp113238\_c1 | 0.001 | 2.352 | cathepsin b |
| comp113270\_c0 | 0.001 | 2.655 | AGAP007074-PA |
| comp113283\_c0 | 0.005 | 2.058 | PREDICTED: hypothetical protein LOC100573212, partial |
| comp113360\_c0 | 0.001 | 3.071 | equilibrative nucleoside transporter 1 cg11907-pa |
| comp113424\_c0 | 0.001 | 2.794 | PREDICTED: hypothetical protein LOC100575395 |
| comp113436\_c1 | 0.001 | 2.040 | PREDICTED: hypothetical protein LOC100570299 |
| comp113475\_c0 | 0.001 | 2.435 | PREDICTED: hypothetical protein |
| comp113507\_c0 | 0.003 | 2.046 | lipase 3 |
| comp113542\_c1 | 0.001 | 2.676 | scavenger receptor acting in neural tissue and majority of rhodopsin is absent cg12789-pb |
| comp113584\_c0 | 0.002 | 2.057 | PREDICTED: similar to GA18316-PA |
| comp113592\_c0 | 0.001 | 2.974 | lysosomal acid lipase |
| comp113607\_c1 | 0.001 | 2.034 | inebriated protein |
| comp113625\_c1 | 0.001 | 3.771 | bifunctional protein fold |
| comp113636\_c0 | 0.001 | 3.098 | glucose dehydrogenase |
| comp113703\_c0 | 0.001 | 2.560 | ---NA--- |
| comp113704\_c0 | 0.001 | 2.140 | beta 1-like 2 |
| comp113764\_c0 | 0.001 | 2.434 | sodium-dependent phosphate transporter |
| comp113913\_c0 | 0.001 | 2.302 | ankyrin repeat |
| comp113948\_c0 | 0.001 | 6.193 | PREDICTED: similar to Luciferase |
| comp113982\_c0 | 0.005 | 2.046 | PREDICTED: hypothetical protein LOC100569635 |
| comp114026\_c0 | 0.001 | 2.089 | glutathione synthetase |
| comp114049\_c1 | 0.001 | 2.526 | ---NA--- |
| comp114076\_c0 | 0.001 | 2.530 | ornithine decarboxylase |
| comp114081\_c0 | 0.001 | 3.623 | PREDICTED: similar to alpha-esterase |
| comp114139\_c0 | 0.012 | 2.192 | ---NA--- |
| comp114166\_c0 | 0.005 | 2.234 | PREDICTED: similar to AGAP008487-PA |
| comp114174\_c0 | 0.001 | 2.211 | PREDICTED: similar to 4-nitrophenylphosphatase |
| comp114295\_c0 | 0.001 | 2.132 | cgmp-dependent protein kinase |
| comp114343\_c0 | 0.056 | 2.079 | PREDICTED: similar to carboxylesterase |
| comp114363\_c0 | 0.004 | 2.772 | ---NA--- |
| comp114539\_c1 | 0.055 | 2.171 | ---NA--- |
| comp114570\_c0 | 0.001 | 2.381 | cg12340 cg12340-pa |
| comp114596\_c0 | 0.020 | 3.412 | PREDICTED: similar to AGAP002559-PA |
| comp114629\_c0 | 0.012 | 2.416 | histone-lysine n-methyltransferase setmar-like |
| comp114643\_c0 | 0.001 | 2.891 | PREDICTED: similar to AGAP009114-PA |
| comp114658\_c0 | 0.001 | 7.200 | PREDICTED: hypothetical protein |
| comp114838\_c0 | 0.001 | 2.406 | cad88c cg3389-pa |
| comp114870\_c0 | 0.001 | 3.529 | PREDICTED: similar to beta-glucosidase |
| comp114950\_c0 | 0.052 | 2.003 | ---NA--- |
| comp114996\_c1 | 0.001 | 2.064 | cg4382 cg4382-pa |
| comp115030\_c0 | 0.001 | 3.015 | ---NA--- |
| comp115076\_c0 | 0.001 | 2.401 | PREDICTED: hypothetical protein |
| comp115119\_c0 | 0.001 | 2.290 | ---NA--- |
| comp115141\_c0 | 0.015 | 2.300 | PREDICTED: similar to AGAP012043-PA |
| comp115178\_c0 | 0.001 | 5.170 | sodium solute symporter |
| comp115194\_c0 | 0.001 | 4.482 | sodium solute symporter |
| comp115223\_c0 | 0.015 | 2.238 | ---NA--- |
| comp115261\_c0 | 0.001 | 2.075 | e3 ubiquitin-protein ligase siah2 (seven in absentia homolog 2-like) (siah-2) |
| comp115479\_c0 | 0.001 | 2.682 | ---NA--- |
| comp115507\_c0 | 0.001 | 3.920 | PREDICTED: similar to conserved hypothetical protein |
| comp115654\_c0 | 0.001 | 2.512 | matrix metalloproteinase |
| comp115666\_c0 | 0.003 | 2.328 | farnesyl pyrophosphate synthase |
| comp115689\_c0 | 0.001 | 2.472 | sodium solute symporter |
| comp115735\_c0 | 0.001 | 3.236 | kaz1-orfb cg1220-pe |
| comp115775\_c0 | 0.001 | 2.250 | sodium nucleoside cotransporter |
| comp115842\_c1 | 0.001 | 2.481 | chitinase 2 precursor |
| comp115848\_c0 | 0.001 | 2.882 | sodium-dependent phosphate transporter |
| comp115889\_c0 | 0.053 | 2.334 | rna-directed dna polymerase from mobile element jockey-like |
| comp115891\_c0 | 0.005 | 2.002 | ---NA--- |
| comp115908\_c0 | 0.001 | 2.165 | PREDICTED: similar to C25F9.2, partial |
| comp115954\_c0 | 0.001 | 2.277 | antennal-enriched xdp-glycosyltransferase |
| comp115994\_c0 | 0.053 | 2.609 | PREDICTED: similar to AGAP004918-PA |
| comp116046\_c1 | 0.001 | 2.926 | equilibrative nucleoside transporter 1 cg11907-pa |
| comp116113\_c0 | 0.001 | 2.397 | PREDICTED: similar to AGAP003785-PA |
| comp116205\_c0 | 0.001 | 2.036 | ankyrin unc44 |
| comp116246\_c0 | 0.001 | 2.020 | PREDICTED: similar to GA10859-PA |
| comp116262\_c0 | 0.001 | 3.195 | cg1213 cg1213-pa |
| comp116489\_c0 | 0.001 | 2.052 | chitin synthase 2 |
| comp116495\_c1 | 0.001 | 2.086 | sid-1-related a precursor |
| comp116505\_c0 | 0.001 | 2.069 | ---NA--- |
| comp116539\_c1 | 0.001 | 2.310 | probable galactose-1-phosphate uridylyltransferase-like |
| comp116612\_c0 | 0.018 | 2.058 | ---NA--- |
| comp116616\_c0 | 0.007 | 2.034 | PREDICTED: similar to AGAP012154-PA |
| comp116671\_c0 | 0.001 | 2.251 | ---NA--- |
| comp116743\_c1 | 0.001 | 2.284 | lysosomal alpha-mannosidase (mannosidase alpha class 2b member 1) |
| comp116803\_c0 | 0.001 | 3.867 | PREDICTED: similar to AGAP008487-PA |
| comp116806\_c2 | 0.015 | 2.054 | membrane alanyl aminopeptidase |
| comp116830\_c1 | 0.030 | 2.361 | ---NA--- |
| comp116900\_c0 | 0.001 | 2.120 | cgmp-dependent protein kinase |
| comp116927\_c1 | 0.038 | 3.190 | ---NA--- |
| comp116958\_c0 | 0.001 | 3.200 | labial |
| comp116970\_c0 | 0.016 | 2.002 | forked cg5424-pb |
| comp117027\_c0 | 0.007 | 2.044 | cg8709 cg8709-pb |
| comp117070\_c0 | 0.001 | 2.877 | transposable element p transposase (p-element transposase) |
| comp117074\_c0 | 0.001 | 2.526 | diphosphomevalonate decarboxylase |
| comp117076\_c0 | 0.001 | 9.178 | glucose dehydrogenase |
| comp117132\_c0 | 0.001 | 2.729 | PREDICTED: similar to phosphoribosylformylglycinamidine synthase, putative |
| comp117214\_c0 | 0.001 | 2.673 | reverse transcriptase homolog |
| comp117241\_c0 | 0.006 | 2.305 | ras-like gtp-binding protein rho1 |
| comp117263\_c0 | 0.050 | 2.208 | ---NA--- |
| comp117365\_c0 | 0.001 | 2.008 | npc1 protein |
| comp117371\_c0 | 0.001 | 2.433 | multi drug resistance 50 cg8523-pa |
| comp117423\_c1 | 0.001 | 2.479 | amp dependent ligase |
| comp117438\_c0 | 0.023 | 2.088 | isoform a |
| comp117469\_c0 | 0.001 | 2.356 | sugar transporter |
| comp117494\_c0 | 0.046 | 2.177 | laccase 1 |
| comp117534\_c0 | 0.001 | 2.082 | ---NA--- |
| comp117547\_c0 | 0.001 | 2.057 | PREDICTED: similar to conserved hypothetical protein |
| comp117554\_c0 | 0.027 | 2.037 | fatty acid synthase-like |
| comp117597\_c0 | 0.001 | 3.503 | elongation of very long chain fatty acids protein aael008004-like |
| comp117622\_c0 | 0.001 | 2.257 | cg7044 cg7044-pa |
| comp117771\_c0 | 0.001 | 7.446 | ---NA--- |
| comp117805\_c0 | 0.001 | 3.615 | ---NA--- |
| comp117812\_c0 | 0.034 | 2.272 | kynurenine alpha-aminoadipate aminotransferase mitochondrial precursor (kat ) (kynurenine--oxoglutarate transaminase ii) (kynurenine aminotransferase ii) (kynurenine--oxoglutarate aminotransferase ii) (2-aminoadipate transaminase) ( |
| comp117821\_c0 | 0.001 | 2.068 | atp-binding sub-family c (cftr mrp) member 4 |
| comp117866\_c0 | 0.001 | 2.046 | PREDICTED: similar to AGAP006427-PA |
| comp117882\_c0 | 0.001 | 2.695 | AGAP012173-PA |
| comp117934\_c0 | 0.001 | 4.610 | xanthine dehydrogenase oxidase |
| comp118021\_c0 | 0.001 | 2.119 | atp-binding cassette transporter |
| comp118072\_c0 | 0.001 | 2.649 | xanthine dehydrogenase |
| comp118086\_c0 | 0.001 | 2.762 | zinc finger bed domain-containing protein 5-like |
| comp118104\_c1 | 0.001 | 3.141 | 3-hydroxy-3-methylglutaryl coenzyme a synthase |
| comp118166\_c0 | 0.034 | 2.020 | cg41538 cg41538-pa |
| comp118239\_c0 | 0.001 | 2.222 | tripsin, putative |
| comp118287\_c1 | 0.012 | 2.221 | AGAP012074-PA |
| comp118327\_c0 | 0.016 | 2.268 | agap008849-pa isoform 1 |
| comp118337\_c0 | 0.035 | 2.481 | hemoglobin c1 polymer |
| comp118465\_c0 | 0.001 | 2.435 | PREDICTED: similar to beta-glucosidase |
| comp118468\_c0 | 0.001 | 2.200 | PREDICTED: similar to AGAP005839-PA |
| comp118479\_c0 | 0.001 | 2.256 | xanthine dehydrogenase |
| comp118549\_c0 | 0.002 | 2.165 | ---NA--- |
| comp118656\_c0 | 0.001 | 2.076 | cg31116 cg31116-pe |
| comp118737\_c0 | 0.021 | 2.392 | fatty acid |
| comp118743\_c0 | 0.001 | 2.331 | fatty acid synthase |
| comp118800\_c0 | 0.002 | 4.100 | agap002830-pa isoform 5 |
| comp118846\_c0 | 0.010 | 2.360 | glycosyltransferase 25 family member |
| comp118914\_c0 | 0.002 | 2.329 | PREDICTED: similar to polyprotein |
| comp118999\_c0 | 0.001 | 2.762 | PREDICTED: similar to AGAP006427-PA |
| comp119092\_c0 | 0.057 | 2.084 | oxidase peroxidase |
| comp119311\_c1 | 0.001 | 2.099 | PREDICTED: similar to AGAP012156-PA |
| comp119434\_c0 | 0.030 | 2.371 | PREDICTED: hypothetical protein LOC100573963 |
| comp119437\_c0 | 0.002 | 2.052 | AGAP004533-PA |
| comp119500\_c0 | 0.017 | 2.770 | ---NA--- |
| comp119526\_c0 | 0.009 | 2.040 | muscle-specific protein 300 cg33715-pd |
| comp119545\_c0 | 0.001 | 2.360 | glucosyl glucuronosyl transferases |
| comp119560\_c1 | 0.030 | 2.051 | sugar transporter |
| comp119617\_c1 | 0.032 | 2.053 | juvenile hormone-inducible |
| comp119690\_c0 | 0.001 | 2.915 | ---NA--- |
| comp119777\_c0 | 0.003 | 2.180 | cathepsin d isoform 1 |
| comp119857\_c0 | 0.051 | 3.065 | xbiquitin-conjugating enzyme e2-17 kda (xbiquitin-protein ligase) (xbiquitin carrier protein) (protein effete) |
| comp119907\_c0 | 0.016 | 3.255 | ---NA--- |
| comp119921\_c0 | 0.007 | 5.425 | ---NA--- |
| comp119922\_c0 | 0.031 | 3.110 | ---NA--- |
| comp119955\_c0 | 0.013 | 4.895 | ---NA--- |
| comp120081\_c0 | 0.032 | 4.448 | ---NA--- |
| comp120251\_c0 | 0.031 | 2.400 | ---NA--- |
| comp46473\_c0 | 0.046 | 2.375 | adenine nucleotide translocase isoform a |
| comp46590\_c0 | 0.001 | 2.235 | ---NA--- |
| comp57556\_c0 | 0.047 | 2.180 | ---NA--- |
| comp61890\_c0 | 0.042 | 3.395 | AGAP000462-PA |
| comp62119\_c0 | 0.059 | 2.690 | ---NA--- |
| comp62480\_c0 | 0.006 | 5.220 | ---NA--- |
| comp63542\_c0 | 0.032 | 3.640 | ---NA--- |
| comp63545\_c0 | 0.001 | 3.190 | elongation factor isoform a |
| comp65111\_c0 | 0.006 | 2.695 | PREDICTED: similar to putative esterase |
| comp65689\_c0 | 0.043 | 2.240 | ---NA--- |
| comp66456\_c0 | 0.006 | 2.845 | AGAP010885-PA |
| comp67283\_c0 | 0.031 | 4.580 | AGAP009623-PA |
| comp68119\_c0 | 0.058 | 2.100 | ---NA--- |
| comp68160\_c0 | 0.034 | 2.930 | cg6084 cg6084-pa |
| comp79274\_c0 | 0.010 | 3.955 | PREDICTED: similar to AGAP003584-PA |
| comp80300\_c0 | 0.051 | 3.210 | ---NA--- |
| comp80468\_c0 | 0.006 | 7.450 | tripartite motif-containing protein 2-like |
| comp81149\_c0 | 0.028 | 2.860 | cytochrome p450 isoform 1 |
| comp82505\_c0 | 0.041 | 2.020 | isoform a |
| comp82707\_c0 | 0.008 | 4.660 | ---NA--- |
| comp85114\_c0 | 0.048 | 3.030 | PREDICTED: hypothetical protein LOC100166108 isoform 3 |
| comp85230\_c0 | 0.001 | 14.250 | ---NA--- |
| comp87864\_c0 | 0.017 | 2.178 | calcium-transporting atpase type 2c |
| comp88149\_c0 | 0.006 | 5.040 | ---NA--- |
| comp88335\_c0 | 0.006 | 8.220 | small heat shock protein 21 isoform 1 |
| comp88374\_c0 | 0.048 | 3.567 | ---NA--- |
| comp89182\_c0 | 0.001 | 3.049 | ---NA--- |
| comp91024\_c0 | 0.025 | 3.530 | ---NA--- |
| comp92340\_c0 | 0.006 | 2.805 | 2-hydroxyphytanoyl-CoA lyase, putative |
| comp92480\_c0 | 0.031 | 3.950 | superoxide dismutase 2 |
| comp93486\_c0 | 0.009 | 3.695 | isoform e |
| comp93921\_c0 | 0.006 | 6.235 | lethal essential for life l2efl |
| comp94687\_c0 | 0.009 | 5.442 | ---NA--- |
| comp94693\_c0 | 0.006 | 5.155 | Catalase, putative |
| comp95046\_c0 | 0.006 | 3.810 | AGAP006958-PA |
| comp95711\_c0 | 0.001 | 4.987 | ---NA--- |
| comp95983\_c0 | 0.001 | 7.315 | PREDICTED: hypothetical protein |
| comp96315\_c0 | 0.039 | 3.531 | AGAP002599-PA |
| comp96596\_c0 | 0.050 | 2.425 | ---NA--- |
| comp97310\_c0 | 0.002 | 6.450 | heat shock 70 kda protein |
| comp97809\_c0 | 0.051 | 4.040 | ---NA--- |
| comp97937\_c0 | 0.011 | 2.535 | AGAP004936-PA |
| comp98499\_c0 | 0.059 | 2.045 | ---NA--- |
| comp99067\_c0 | 0.001 | 3.568 | ---NA--- |
| comp99795\_c0 | 0.023 | 2.030 | pro-phenol oxidase subunit 2 |
| comp99864\_c0 | 0.058 | 2.162 | 13 kda hemolymph protein a |
| comp99927\_c0 | 0.001 | 7.737 | ---NA--- |