

| hemocyte-related | cell cycle | lipid metabolism | gene symbol | FlyBase ID | log ₂ (FC dsUsh-B/dsEGFP) | FC dsUsh-B/dsEGFP | -log ₁₀ (p-value) | p-value | FlyBase GO_Biological Function / additional references | expression pattern (BDGP) |
|------------------|------------|------------------|----------------|-------------|--------------------------------------|-------------------|------------------------------|----------|---|--|
| X | X | | N | FBgn0004647 | -0.652 | 0.64 | 1.65 | 2.26E-02 | regulation of crystal cell differentiation (GO:0042689); lamellocyte differentiation (GO:0035171); negative regulation of lamellocyte differentiation (GO:0035204); crystal cell differentiation (GO:0042688); larval lymph gland hemopoiesis (GO:0035167); embryonic crystal cell differentiation (GO:0035165); regulation of mitotic cell cycle (GO:0007346); positive regulation of G1/S transition of mitotic cell cycle (GO:1900087); hemocyte proliferation (GO:0035172); embryonic hemopoiesis (GO:0035162); positive regulation of cell population proliferation (GO:0008284); positive regulation of crystal cell differentiation (GO:0042691) | |
| X | X | | kay | FBgn0001297 | 0.331 | 1.26 | 1.35 | 4.50E-02 | positive regulation of biosynthetic processes of antibacterial peptides active against Gram-negative bacteria (GO:0006964); positive regulation of peptidoglycan recognition protein signaling pathway (GO:0061059); regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle (GO:0031660) | plasmatocytes A (stage 11-12) |
| X | | X | Cyt-b5-r | FBgn0000406 | 0.775 | 1.71 | 1.75 | 1.79E-02 | lipid metabolic process (GO:0006629) | procrystal cells (stage 11-12), crystal cells (stage 13-16) |
| X | | | Col4a1 / Cg25c | FBgn0000299 | -1.289 | 0.41 | 6.57 | 2.71E-07 | | plasmatocytes A (stage 11-12), plasmatocytes (stage 13-16) |
| X | | | vkg | FBgn0016075 | -1.114 | 0.46 | 4.19 | 6.52E-05 | | plasmatocytes A (stage 11-12), plasmatocytes (stage 13-16) |
| X | | | CG5397 | FBgn0031327 | -1.068 | 0.48 | 3.84 | 1.44E-04 | | plasmatocytes (stage 13-16) |
| X | | | Spn28Dc | FBgn0031973 | -0.876 | 0.54 | 3.60 | 2.48E-04 | negative regulation of melanization defense response (GO:0035009) | |
| X | | | Traf4 | FBgn0026319 | -0.681 | 0.62 | 1.73 | 1.86E-02 | defense response to Gram-negative bacterium (GO:0050829) | |
| X | | | CG8046 | FBgn0033388 | -0.646 | 0.64 | 1.33 | 4.64E-02 | positive regulation of peptidoglycan recognition protein signaling pathway (GO:0061059); positive regulation of antimicrobial humoral response (GO:0002760); peptidoglycan transport (GO:0015835) | |
| X | | | Tsp96F | FBgn0027865 | -0.541 | 0.69 | 1.79 | 1.64E-02 | | procrystal cells (stage 11-12) |
| X | | | CD98hc | FBgn0037533 | 0.489 | 1.40 | 1.55 | 2.83E-02 | | procrystal cells, plasmatocytes A (stage 11-12) |
| X | | | Rac1 | FBgn0010333 | 0.520 | 1.43 | 1.79 | 1.64E-02 | hemocyte development (GO:0007516); immune response-regulating cell surface receptor signaling pathway involved in phagocytosis (GO:0002433); hemocyte migration (GO:0035099); melanotic encapsulation of foreign target (GO:0035011) | |
| X | | | Phk-3 | FBgn0035089 | 0.616 | 1.53 | 1.56 | 2.74E-02 | response to bacterium (GO:0009617) | |
| X | | | p38c | FBgn0267339 | 0.690 | 1.61 | 1.33 | 4.64E-02 | response to bacterium (GO:0009617) | |
| X | | | Ugt36Bc | FBgn0040260 | 0.742 | 1.67 | 1.56 | 2.74E-02 | | crystal cell SA (stage 9-10), procrystal cells (stage 11-12), crystal cell (stage 13-16) |
| X | | | GILT3 | FBgn0039098 | 0.790 | 1.73 | 1.77 | 1.70E-02 | Involved in the immune response to bacterial infection (Kongton et al., 2014) | |
| X | | | Cyp310a1 | FBgn0032693 | 0.801 | 1.74 | 2.74 | 1.83E-03 | | plasmatocytes A (stage 11-12), plasmatocytes (stage 13-16) |
| X | | | pirk | FBgn0034647 | 0.847 | 1.80 | 2.29 | 5.07E-03 | negative regulation of peptidoglycan recognition protein signaling pathway (GO:0061060) | |
| | X | | mre11 | FBgn0020270 | -0.365 | 0.78 | 1.77 | 1.70E-02 | mitotic G2 DNA damage checkpoint (GO:0007059); intra-S DNA damage checkpoint (GO:0031573) | |
| | X | | 14-3-3epsilon | FBgn0020238 | 0.451 | 1.37 | 1.79 | 1.62E-02 | mitotic cell cycle checkpoint (GO:0007093); regulation of mitotic nuclear division (GO:0007088) | |
| | | X | Pmp70 | FBgn0031069 | 0.539 | 1.45 | 3.57 | 2.72E-04 | long-chain fatty acid import into peroxisome (GO:0015910) | |
| | | | CG5849 | FBgn0038897 | -0.975 | 0.51 | 3.33 | 4.65E-04 | | |
| | | | Tsp42Ed | FBgn0029507 | -0.889 | 0.54 | 2.53 | 2.97E-03 | | |
| | | | lncRNA:CR44458 | FBgn0265651 | -0.879 | 0.54 | 2.72 | 1.90E-03 | | |
| | | | kek1 | FBgn0015399 | -0.855 | 0.55 | 3.06 | 8.76E-04 | | |
| | | | ATP8B | FBgn0037989 | -0.854 | 0.55 | 2.26 | 5.55E-03 | | |
| | | | CG34034 | FBgn0054034 | -0.822 | 0.57 | 3.37 | 4.22E-04 | | |
| | | | CG8008 | FBgn0033387 | -0.729 | 0.60 | 1.55 | 2.83E-02 | | |

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|------------------|------------|------------------|-------------------|-------------|---------------------------------------|--------------------|------------------------------|----------|--|---------------------------|
| | | | mahe | FBgn0029979 | -0.722 | 0.61 | 3.15 | 7.07E-04 | | |
| | | | Pfdn5 / CG7048 | FBgn0038976 | -0.714 | 0.61 | 1.59 | 2.58E-02 | | |
| | | | Arc2 | FBgn0033928 | -0.668 | 0.63 | 1.75 | 1.79E-02 | | |
| | | | Pdfr | FBgn0260753 | -0.665 | 0.63 | 1.59 | 2.58E-02 | | |
| | | | CG3448 | FBgn0035996 | -0.640 | 0.64 | 1.53 | 2.94E-02 | | |
| | | | CG31777 | FBgn0051777 | -0.634 | 0.64 | 1.59 | 2.55E-02 | | |
| | | | CG18088 | FBgn0032082 | -0.627 | 0.65 | 2.84 | 1.44E-03 | | |
| | | | unc-13 | FBgn0025726 | -0.582 | 0.67 | 2.14 | 7.22E-03 | | |
| | | | Rab23 | FBgn0037364 | -0.574 | 0.67 | 1.55 | 2.84E-02 | | |
| | | | GstE2 | FBgn0063498 | -0.568 | 0.67 | 1.64 | 2.30E-02 | | |
| | | | CG12868 | FBgn0033945 | -0.534 | 0.69 | 3.06 | 8.76E-04 | | |
| | | | ver | FBgn0262524 | -0.471 | 0.72 | 3.71 | 1.94E-04 | | |
| | | | Bin1 | FBgn0024491 | -0.469 | 0.72 | 3.60 | 2.48E-04 | | |
| | | | Tsp42Ee | FBgn0029506 | -0.445 | 0.73 | 1.53 | 2.95E-02 | | |
| | | | Marc / CG1665 | FBgn0033451 | -0.415 | 0.75 | 1.35 | 4.46E-02 | | |
| | | | IscU | FBgn0037637 | -0.407 | 0.75 | 4.14 | 7.28E-05 | | |
| | | | Lst8 | FBgn0264691 | -0.397 | 0.76 | 1.58 | 2.64E-02 | | |
| | | | DNAIig4 / Lig4 | FBgn0030506 | -0.344 | 0.79 | 1.58 | 2.64E-02 | | |
| | | | CG33169 | FBgn0053169 | -0.342 | 0.79 | 1.35 | 4.46E-02 | | |
| | | | CG11436 | FBgn0029713 | -0.319 | 0.80 | 1.59 | 2.55E-02 | | |
| | | | CG4239 | FBgn0030745 | -0.313 | 0.80 | 1.79 | 1.64E-02 | | |
| | | | CG6171 | FBgn0026737 | -0.300 | 0.81 | 1.35 | 4.47E-02 | | |
| | | | muc | FBgn0283658 | 0.218 | 1.16 | 1.64 | 2.30E-02 | | |
| | | | TBCB | FBgn0034451 | 0.282 | 1.22 | 1.55 | 2.83E-02 | | |
| | | | CG1354 | FBgn0030151 | 0.293 | 1.23 | 2.51 | 3.09E-03 | | |
| | | | CysRS / Aats-cys | FBgn0027091 | 0.363 | 1.29 | 1.72 | 1.92E-02 | | |
| | | | eIF3d1 / eIF-3p66 | FBgn0040227 | 0.371 | 1.29 | 1.40 | 4.02E-02 | | |
| | | | CG17746 | FBgn0035425 | 0.376 | 1.30 | 1.56 | 2.74E-02 | | |
| | | | TyrRS /Aats-tyr | FBgn0027080 | 0.389 | 1.31 | 1.75 | 1.77E-02 | | |
| | | | bbc | FBgn0033844 | 0.390 | 1.31 | 1.64 | 2.30E-02 | | |
| | | | SCaMC | FBgn0052103 | 0.431 | 1.35 | 1.61 | 2.46E-02 | | |
| | | | ThrRS / Aats-thr | FBgn0027081 | 0.483 | 1.40 | 1.36 | 4.37E-02 | | |
| | | | AsnS | FBgn0270926 | 0.484 | 1.40 | 1.35 | 4.48E-02 | | |
| | | | CG3408 | FBgn0036008 | 0.520 | 1.43 | 1.36 | 4.34E-02 | | |
| | | | IP3K1 | FBgn0032147 | 0.541 | 1.45 | 3.29 | 5.11E-04 | | |
| | | | CG32280 | FBgn0052280 | 0.595 | 1.51 | 1.64 | 2.30E-02 | | |
| | | | CG30069 | FBgn0050069 | 0.605 | 1.52 | 2.14 | 7.22E-03 | | |
| | | | CG10737 | FBgn0034420 | 0.612 | 1.53 | 2.37 | 4.23E-03 | | |
| | | | ATPsyndelta | FBgn0028342 | 0.614 | 1.53 | 1.48 | 3.35E-02 | | |

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|------------------|------------|------------------|-----------------------|-------------|--------------------------------------|-------------------|------------------------------|----------|--|---------------------------|
| | | | CG8563 | FBgn0035777 | 0.665 | 1.59 | 1.75 | 1.77E-02 | | |
| | | | CG42458 | FBgn0259935 | 0.675 | 1.60 | 1.36 | 4.34E-02 | | |
| | | | CG4872 | FBgn0030799 | 0.691 | 1.61 | 2.26 | 5.55E-03 | | |
| | | | AdamTS-A | FBgn0286071 | 0.700 | 1.62 | 1.37 | 4.29E-02 | | |
| | | | nkd | FBgn0002945 | 0.727 | 1.66 | 1.53 | 2.96E-02 | | |
| | | | lncRNA:CR44138 | FBgn0264987 | 0.728 | 1.66 | 1.53 | 2.94E-02 | | |
| | | | CG3655 | FBgn0040397 | 0.729 | 1.66 | 1.55 | 2.83E-02 | | |
| | | | path | FBgn0036007 | 0.731 | 1.66 | 1.58 | 2.62E-02 | | |
| | | | CG42324 | FBgn0259224 | 0.738 | 1.67 | 1.58 | 2.64E-02 | | |
| | | | CG1077 | FBgn0037405 | 0.748 | 1.68 | 1.63 | 2.37E-02 | | |
| | | | CG4611 | FBgn0035591 | 0.774 | 1.71 | 3.37 | 4.22E-04 | | |
| | | | CG8312 | FBgn0037720 | 0.796 | 1.74 | 2.13 | 7.33E-03 | | |
| | | | RpL18 | FBgn0035753 | 0.860 | 1.82 | 3.46 | 3.44E-04 | | |
| | | | CG12075 | FBgn0030065 | 0.869 | 1.83 | 2.74 | 1.84E-03 | | |
| | | | CG14879 | FBgn0038419 | 0.908 | 1.88 | 2.72 | 1.92E-03 | | |
| | | | axo | FBgn0262870 | 0.978 | 1.97 | 3.37 | 4.22E-04 | | |
| | | | CG3246 | FBgn0031538 | 0.983 | 1.98 | 3.37 | 4.22E-04 | | |
| | | | comm2 | FBgn0041160 | 1.841 | 3.58 | 17.62 | 2.42E-18 | | |