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Comparative analysis of Hox downstream genes in *Drosophila*

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Functional diversification of body parts is dependent on the formation of specialized structures along the various body axes. In animals, region-specific morphogenesis along the anteroposterior axis is controlled by a group of conserved transcription factors encoded by the Hox genes. Although it has long been assumed that Hox proteins carry out their function by regulating distinct sets of downstream genes, only a small number of such genes have been found, with very few having direct roles in controlling cellular behavior. We have quantitatively identified hundreds of Hox downstream genes in *Drosophila* by microarray analysis, and validated many of them by in situ hybridizations on loss- and gain-of-function mutants. One important finding is that Hox proteins, despite their similar DNA-binding properties in vitro, have highly specific effects on the transcriptome in vivo, because expression of many downstream genes respond primarily to a single Hox protein. In addition, a large fraction of downstream genes encodes realizator functions, which directly affect morphogenetic processes, such as orientation and rate of cell divisions, cell-cell adhesion and communication, cell shape and migration, or cell death. Focusing on these realizators, we provide a framework for the morphogenesis of the maxillary segment. As the genomic organization of Hox genes and the interaction of Hox proteins with specific co-factors are conserved in vertebrates and invertebrates, and similar classes of downstream genes are regulated by Hox proteins across the metazoan phylogeny, our findings represent a first step toward a mechanistic understanding of morphological diversification within a species as well as between species.

KEY WORDS: *Drosophila*, Deformed, Morphogenesis, Realizators, Microarray, Hox downstream target genes

INTRODUCTION

In animals, morphology along the various body axes is very diverse, requiring both a system that confers positional identity and a means to respond to these positional cues. It has long been known that the system specifying positional identity along the anteroposterior (AP) axis is based on an evolutionarily conserved set of regulators, the Hox genes (Carroll, 1995; Mann and Morata, 2000; McGinnis and Krumlauf, 1992). In *Drosophila*, Hox genes are expressed in defined domains along the AP axis, and their activity assigns distinct morphologies to the various body segments (McGinnis and Krumlauf, 1992). In addition, Hox genes are very often expressed in overlapping domains and crossregulate each other (McGinnis and Krumlauf, 1992; Miller et al., 2001). Consequently, loss of function of one Hox gene frequently leads to the ectopic expression of neighboring Hox genes, which is one of the reasons for the drastic homeotic transformations of body segments initially identified by Ed Lewis (Lewis, 1978). Therefore, only a subset of Hox functions can be identified in loss-of-function mutants.

Hox genes code for transcription factors with a highly conserved DNA-binding domain, the homeodomain (McGinnis et al., 1984; Scott and Weiner, 1984), and it has been postulated that Hox proteins direct morphogenesis by regulating appropriate sets of downstream genes in a segment-specific manner (Graba et al., 1997; Hombria and Lovegrove, 2003). Although a wide range of strategies has been used to identify Hox downstream genes (Graba et al., 1997; Hombria and Lovegrove, 2003; Pradel and White, 1998), our knowledge of their nature is still limited. Initial attempts have focused on in vitro studies or on heterologous systems; however, Hox proteins acquire DNA-binding specificity mostly through interactions with various co-factors in vivo (Ebner et al., 2005; Gebelein et al., 2004; Mahaffey, 2005; Mann, 1995; Mann and Affolter, 1998). Therefore, most known Hox downstream genes have been identified by candidate gene approaches based on expression patterns or similar mutant phenotypes (Pearson et al., 2005), highlighting the power of in vivo strategies to identify Hox target genes. This notion is further supported by recent successful approaches combining loss- or gain-of-function alleles of Hox genes and microarray experiments to identify Hox downstream genes on a larger scale (Cobb and Duboule, 2005; Hedlund et al., 2004; Lei et al., 2005; Williams et al., 2005). Still, most previous efforts were biased toward the identification of direct Hox target genes, and, while knowledge of direct Hox targets is a prerequisite to understanding how Hox proteins acquire DNA-binding specificity in vivo, we need to know the entire Hox-dependent regulatory network with all its tiers of regulatory interactions to understand how Hox proteins control morphogenesis on a cellular level.

Most of the known Hox downstream genes code either for transcription factors or for signaling molecules (Hombria and Lovegrove, 2003; Pearson et al., 2005). These two classes represent the top tiers of regulatory cascades and are able to coordinate many downstream events. Hence, they are not informative for elucidating the role of Hox proteins in the specification of morphological properties on a cellular level per se. To this end, the functional analysis of the so-called realizators, which directly influence the morphology by regulating cytodifferentiation processes (Garcia-Bellido, 1975; Pradel and White, 1998), is required. Unfortunately, even though the concept of realizators was postulated more than 30 years ago, so far very few Hox realizator genes have been identified and studied mechanistically (Bello et al., 2003; Lohmann et al., 2002). One

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well-studied example of a realizator gene in *Drosophila* is the apoptosis-inducing gene *reaper* (*rpr*), which is expressed in the maxillary segment in *Drosophila* embryos and is directly controlled by the Hox protein Deformed (Dfd) (Lohmann et al., 2002). In addition, the Dfd-dependent expression of *rpr* and, consequently, the activation of apoptosis was shown to be necessary and sufficient for the maintenance of the boundary between the maxillary and mandibular segments of the embryonic head (Lohmann et al., 2002). This is one of the few examples demonstrating how a Hox protein can execute, via a single realizator gene, one specific aspect of segmental morphology on the cellular level. To understand and mechanistically link the many remaining Hox functions with morphogenetic outputs, we need to quantitatively identify Hox downstream genes. Functional analysis of this set will then allow us to elucidate all tiers of interactions within the Hox-regulatory network, and to establish links between Hox genes and realizator genes. This seems fundamental for a complete understanding of the role of Hox genes in development and evolution.

MATERIALS AND METHODS

Drosophila genetics

The wild-type strain used was Oregon-R. UAS-*lacZ*, UAS-*Dfd*, UAS-*Antp* and *arm*-GAL4 strains were from W. McGinnis, UAS-*Scr*, UAS-*Ubx* and UAS-*Abd-B* from F. Hirth (Hirth et al., 2001), UAS-*Abd-A* from A. M. Michelson (Michelson, 1994) and UAS-$hep^{act.}$ from M. Mlodzik (Weber et al., 2000). For trans-heterozygous mutants the following alleles were used: Dfd^{r11} and Dfd^{w21} from W. McGinnis; Scr^{1}, Scr^{4}, $Abd\text{-}B^{M2}$, $wg^{l\text{-}12}$ and $wg^{l\text{-}17}$ from the Bloomington Stock Center; and $Abd\text{-}B^{M5}$ from C. Nüsslein-Volhard (Tübingen *Drosophila* Stock Collection). *Dfd* mutant embryos for BrdU staining were Dfd^{w21}/TM3*Sb*[*twi*::GFP] crossed to Dfd^{r11}/TM3*Sb*[*twi*::GFP] and homozygous *Dfd* mutants (Dfd^{w21}/Dfd^{r11}) were identified by absence of GFP signal.

Plasmids

cDNAs were from the *Drosophila* Genomics Resource Center: *CG5080* (LD34147), *CG7447* (LD16414), *disco* (GH27656), *Dll* (LP01770), *ImpL2* (SD07266), *gt* (RE29225), *sage* (RE59356), *skl* (RE14076), *spz* (SD07354), *LysE* (LP07339), *CG8193* (GH07976), *CG3097* (RE43153), *Mp20* (RE55741), *CG17052* (LD43683), *Ance* (LD11258), *Hsp23* (LD06759), *sn* (RH62992), *mas* (LP06006), *pav* (RE22456), *wrapper* (GH03113), *wg* (RE02607) and *W* (AT13267). *prd* cDNA was from W. McGinnis, *Eip63E* cDNA and predicted Dfd response elements tested by EMSA were PCR amplified, cloned and sequenced. Expression plasmids for Dfd and Ubx were obtained from W. McGinnis and S. Carroll, respectively.

Histology and scanning electron microscopy

In situ hybridization and immunochemistry were performed as described (Bergson and McGinnis, 1990; Tautz and Pfeifle, 1989), and BrdU labeling and scanning electron microscopy were done as described (Dolbeare and Selden, 1994; Lohmann et al., 2002). Hox protein expression was measured by the fluorescent intensity of a standardized area of individual nuclei using the Zeiss LSM 510 META confocal microscope. Twenty nuclei of four independent embryos were analyzed for each expression domain and genotype. Antibodies were: anti-Dfd, W. McGinnis; anti-Scr, anti-Antp, anti-Abd-B and anti-wg, Developmental Studies Hybridoma Bank (Iowa, University), anti-Ubx, R. White (Cambridge); anti-Abd-A, I. W. Duncan (Washington, University); anti-GFP, Torrey Pines Biolabs (Houston); anti-BrdU, Roche; anti-mouse AlexaFluor 488, anti-guinea pig AlexaFluor 488 and anti-rabbit AlexaFluor 488, Molecular Probes.

Microarray experiments

Microarray hybridizations were carried out as described (Schmid et al., 2003) in biological triplicates with RNA from pools of stage 11 or stage 12 embryos. Raw data were quantile normalized and expression estimates were calculated using gcRMA (Wu et al., 2004) implemented in R. Statistical testing for differential expression was carried out using LogitT (Lemon et al., 2003). Microarray data discussed here have been deposited with ArrayExpress database at the EBI (http://www.ebi.ac.uk/arrayexpress-old/; Accession number E-MEXP-879). For analysis of gene ontology categories, GO lists from FlyBase were used. Genes were sorted using a combination of molecular and biological GO terms. Genes containing the following description in their GO annotations were classified as realizators: apoptosis, cell death, cell adhesion, cell shape, cell cycle, mitosis, cell proliferation, cytoskeleton, proteolysis, peptidolysis, cytoskeleton, structural constituent of larval cuticle or peritrophic membrane.

Quantitative real-time PCR

Quantitative real-time PCR (qRT-PCR) was carried out in triplicates from RNA of pooled tissue as described (Schmid et al., 2003) using SYBR-green QPCR Master Mix (Invitrogen). Expression of β-*Tubulin* was used for cross-experiment normalization. Primer and probe sequences are available upon request.

Bioinformatics

For cluster identification the Cis-Analyst algorithm (Berman et al., 2004) was used with a Position-Frequency-Matrix (PFM) based on DNaseI footprint data (Bergman et al., 2005) and consensus sequences from the literature. The PFM shown in Fig. S1B in the supplementary material was generated by PATSER. To define enhancer parameters, such as length of enhancer, number of Dfd-binding sites per enhancer, distance between binding sites, known Dfd-dependent enhancers were analyzed. The parameters identified, as shown in Fig. S1B in the supplementary material, were used to predict clusters of Dfd-binding sites in the regulatory regions of selected genes in *Drosophila melanogaster*. To this end, intergenic and intronic sequences of *D. melanogaster* were aligned to a multiple sequence file, sorted and separated to segment-files, which included annotation information. The PATSER program used these segment-files as a template to generate *P*-values for each Dfd-binding site identified according to the PFM. Using this binding site information, clusters of Dfd-binding sites were predicted using the standalone version of cis-Analyst-helper. To validate this approach statistically and to optimize the parameters chosen, Dfd downstream genes identified in the microarray experiment were used. The logic of this approach is based on the assumption that direct Dfd target genes should be enriched among the Dfd downstream genes identified in the microarray experiment when compared with randomly selected genes. To identify Dfd clusters in other *Drosophila* species (*D. simulans*, *D. yakuba*, *D. erecta*, *D. pseudoobscura*), a NCBI BLAST search was performed. To consider clusters as being conserved, the following conservation criteria had to be fulfilled: (1) conservation of the enhancer in at least two other *Drosophila* species; (2) the length of the homologues enhancer had to be ⩾50% of the enhancer length identified in *D. melanogaster*; (3) conservation of at least two Dfd-binding sites within the conserved enhancer elements; and (4) conserved enhancers with less then 50% of length conservation but more then two Dfd-binding sites conserved were treated as minor hits. Conserved enhancers were ranked according to the following parameters: (1) evolutionary distance of *Drosophila* species; (2) overall sequence similarity of conserved enhancers; (3) numbers of binding sites present in conserved clusters; and (4) degree of variation in enhancer length. Binding site matches for other transcription factors located in the Hox response elements were identified by using rVISTA, Transfac and Jasper databases.

Electrophoretic mobility shift assays

Electrophoretic mobility shift assays (EMSAs) were performed as described (Lohmann et al., 2002).

RESULTS

Identification of Hox responsive genes by microarray analysis

In order to systematically elucidate Hox-regulatory networks, we performed a comparative microarray screen using stage 11 and stage 12 embryos ubiquitously overexpressing six out of eight Hox genes – *Dfd*, *Sex combs reduced* (*Scr*), *Antennapedia* (*Antp*), *Ultrabithorax* (*Ubx*), *abdominal A* (*abd-A*) and *Abdominal B* (*Abd-B*) – by means of the UAS-GAL4 system (Brand and Perrimon, 1993) (Fig. 1A; for endogenous expression of Hox proteins see Fig. 1E). The Hox genes *labial* (*lab*) and *proboscipedia* (*pb*) were not included, as a similar study has been performed for *lab* (Leemans et al., 2001), and as *pb* mutant embryos do not exhibit any obvious defects (Wakimoto et al., 1984). We opted to use overexpression instead of a loss-of-function experiments for several reasons. First, the analysis of Hox mutants is complicated by the extensive crossregulatory interactions of Hox genes (Gould et al., 1997; Miller et al., 2001); loss of expression of one Hox gene often results in ectopic expression of other Hox genes, thereby obscuring the effects on downstream genes. Another important limitation of a loss-of-function approach in conjunction with microarray analysis is sensitivity; due to the small expression domains of many Hox genes (McGinnis and Krumlauf, 1992; Pearson et al., 2005), locally restricted differences in gene expression caused by Hox mutations will be diluted in RNA isolated from whole embryos, and therefore many downstream genes might not be detected. Isolation of cells expressing individual Hox genes by cell sorting (Wang et al., 2006) could provide a means to circumvent this problem; however, the required reporter genes that are expressed in specific Hox domains, although independent from Hox gene activity, currently do not exist. Conversely, although ectopic expression of one Hox gene affects the expression of other Hox genes, their ubiquitous overexpression should allow us to even detect genes whose expression is only weakly, or locally, affected, because the Hox expression domains are expanded manyfold and consequently their transcriptional output is amplified. To achieve ubiquitous Hox overexpression in the desired stages of development, we used an *armadillo* (*arm*)-GAL4 driver line (Sanson et al., 1996), which confers ubiquitous expression starting at stage 10, as judged from analyzing GFP activity in embryos carrying an additional UAS-*2xEGFP* transgene (Fig. 1A). Previous studies have shown that ubiquitous overexpression of Hox genes in UAS fly strains, which were also used in our study, is sufficient to induce ectopic differentiation of Hox-dependent structures without affecting the development of early embryonic stages in an unspecific manner (Li et al., 1999). Thus, a substantial part of Hox downstream genes seem to be responsive to Hox signaling even at ectopic locations and should be detectable by microarray analysis.

One concern with overexpression experiments, however, is that they might result in varying or even unphysiological concentrations of transcription factor proteins in the nucleus, which might unspecifically affect gene expression. Therefore, we confirmed similar RNA and protein expression levels in our overexpression lines by qRT-PCR and antibody stainings (Fig. 1B,E). In addition,

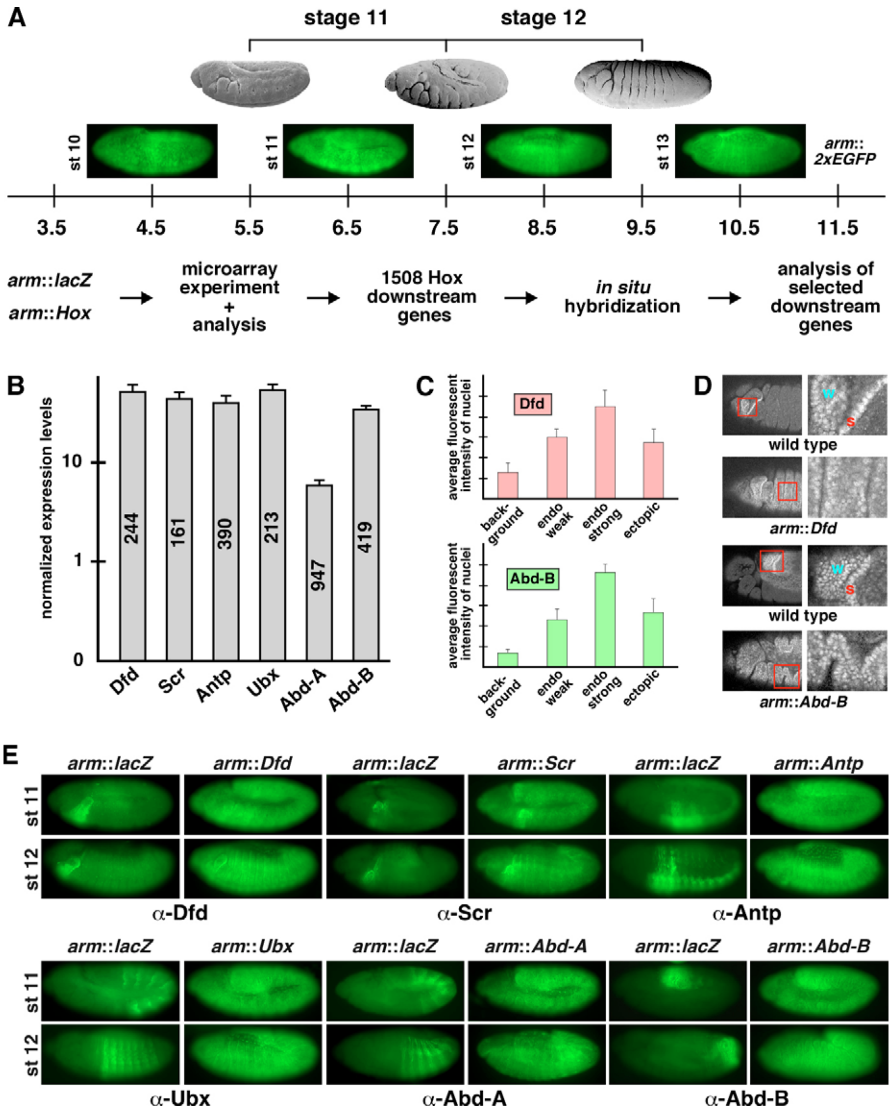

Fig. 1. Identification of Hox downstream genes during early embryogenesis. (**A**) Outline of microarray analysis. Scanning electron micrographs of embryos at late stage 10-early stage 11, late stage 11-early stage 12, and late stage 12-early stage 13. *arm*::*2xEGFP* embryos demonstrate ubiquitous transgene expression beginning at stage 10. Time scale shows hours of embryogenesis. (**B**) Quantitative real-time PCR shows similar levels of overexpression of Dfd, Scr, Antp, Ubx, Abd-A and Abd-B transgenes. Numbers of genes regulated by the different Hox proteins are indicated. (**C**) Average fluorescent intensity (in arbitrary units) of 20 independent nuclei at different locations in wild-type, *arm*::*Dfd* and *arm*::*Abd-B* embryos stained either with α-Dfd or α-Abd-B antibody. Due to variable expression levels of endogenous Hox proteins, fluorescence from nuclei in different expression domains was measured (marked as 'endo weak' and 'endo strong'). (**D**) Representative embryo used for measuring fluorescent intensity of nuclei is shown. The upper two rows show wild-type and *arm*::*Dfd* embryos stained with α-Dfd antibody, the lower two rows wild-type and *arm*::*Abd-B* embryos stained with α-Abd-B antibody. Red boxes mark the areas used for fluorescence analysis. s, strong endogenous expression domain; w, weak endogenous expression domain. (**E**) Ubiquitous overexpression of Hox proteins in stage 11 and 12 was confirmed by antibody staining on *arm*::*lacZ* and *arm*::*Hox* embryos.

we quantified Dfd and Abd-B protein levels in the nuclei of wild-type and the respective overexpression embryos and found that protein levels in transgenic embryos were on the lower end of the wild-type expression spectrum (Fig. 1C,D). Thus, non-physiological effects of Hox misexpression due to increased protein levels should not interfere with our experiment.

For the microarray experiment, total RNA from *arm*::*lacZ* (control), *arm*::*Dfd*, *arm*::*Scr*, *arm*::*Antp*, *arm*::*Ubx*, *arm*::*abd-A* and *arm*::*Abd-B* embryos collected separately at the different stages was prepared and hybridized in biological triplicates to Affymetrix *Drosophila* Genome 1 arrays, which contains probe sets interrogating more than 13,500 genes. A combination of per-gene (Lemon et al., 2003) and common variance (>1.5-fold change) filtering was used to identify 1508 Hox responsive genes (Table S1, Table S2, Table S3, Table S4, Table S5 and Table S6 in the supplementary material). This list contained six of the 18 genes previously shown to be under Hox control during stages 11 and 12 (Fig. 2A), and in situ hybridizations for three of these transcripts confirmed the microarray results (Fig. 2A). The fact that we were only able to recover one-third of the known Hox targets can be explained by a number of differences between our experimental setup and the ones used before, such as detection method (Capovilla et al., 2001; Mahaffey et al., 1993), timing and level of overexpression (Feinstein et al., 1995), and use of mutants instead of overexpression (Mahaffey et al., 1993; Ryoo and Mann, 1999). Based on this observation, it is conceivable that the actual number of all Hox downstream genes is two- to threefold the number we have discovered in our study, which is still significantly lower than previously suggested (Liang and Biggin, 1998). The microarray data also showed that anterior Hox genes were repressed by those normally expressed more posteriorly (data not shown), a crossregulatory interaction known as posterior suppression (Miller et al., 2001). Again, we could confirm the microarray data by performing antibody stainings for all Hox proteins on embryos ubiquitously misexpressing either Dfd or Abd-B (Fig. 2B).

Verification of Hox downstream genes identified in the microarray analysis

To verify differential expression of the newly identified genes at the cellular level, we carried out in situ hybridization on embryos misexpressing the various Hox genes (Fig. 3; see Fig. S1 in the supplementary material). Twenty-four of the 25 randomly selected genes that showed a specific in situ signal behaved as observed in the microarray experiment. In addition, for a selected subset of seven genes Hox-dependent regulation could also be shown in Hox mutants (Fig. 3), demonstrating the power of the initial microarray experiment. For example, three transcripts found to be induced by Dfd in the microarray experiment were *sickle* (*skl*), a known apoptosis activator (Wing et al., 2002), *CG5080*, a gene putatively involved in cytoskeletal regulation (Jasper et al., 2001), and CG7447, a gene of unknown function. In situ analysis confirmed strong and ectopic induction of all three genes in response to Dfd misexpression (Fig. 3B,F,J), and showed that their expression in the maxillary segment was lost in *Dfd* mutants (Fig. 3D,H,L). Similarly, mRNA levels of *salivary gland-expressed bHLH* (*sage*), a transcription factor gene exclusively expressed in the salivary gland primordium (Chandrasekaran and Beckendorf, 2003), were increased in response to ectopic Scr activity (Fig. 3N). By contrast, *sage* expression was abolished in *Scr* mutants (Fig. 3P), consistent with Scr being a master regulator of salivary gland morphogenesis (Panzer et al., 1992). Among the genes that were induced by Abd-B were *Ecdysone-inducible gene L2* (*ImpL2*), putatively involved in cell adhesion (Garbe et al., 1993), and *spätzle* (*spz*), which encodes a Toll receptor ligand involved in embryonic axis specification (DeLotto et al., 2001). Again, we observed strong ectopic expression of *ImpL2* and *spz* in *arm*::*Abd-B* embryos (Fig. 3R,V), whereas expression in the posterior end was lost in *Abd-B* mutants (Fig. 3T,X). In summary, in situ hybridization with probes for 24 randomly selected genes (Fig. 3; see Fig. S1 in the supplementary material) not only confirmed the microarray results, but also demonstrated that many of the identified Hox downstream genes responded in a converse manner in the respective Hox mutants.

Direct versus indirect Hox downstream genes

To understand the logic of Hox-dependent morphogenesis, it is important to place the newly identified downstream genes within the underlying regulatory hierarchy. To this end, we developed a bioinformatics tool to detect direct Hox target genes, based on the identification of evolutionarily conserved clusters of Hox consensus binding sites in the genome (see Materials and methods and Fig. S2 in the supplementary material for detail). Using this approach, we were able to identify a large number of putative direct targets of Dfd. From the 240 genes found to be significantly regulated by Dfd, 75 had clusters of Dfd-binding sites (31% of all identified Dfd responsive genes), which was significantly more than expected by chance ($P<0.001$). In addition, 46 of these clusters were well conserved in at least two other *Drosophila* species (19% of all identified Dfd responsive genes) (see Tables S7 and S8 in the supplementary material). Most of the predicted Dfd response elements also contained binding sites for other transcription factors (data not shown), a known prerequisite for functional enhancer elements (Berman et al., 2004). We randomly selected six of the 75 predicted Dfd response elements and performed EMSA to test whether Dfd protein could bind to these elements. All enhancer elements tested were bound by Dfd in vitro (Fig. 4), whereas Ubx, a Hox protein specifying trunk identity, was not able to interact with these enhancers (see Fig. S2C in the supplementary material). In addition, competition experiments showed that Dfd specifically bound some, but not all, of the predicted Dfd-binding sites in these enhancers (Fig. 4A-D), demonstrating that the simple presence of a consensus binding site is not sufficient for Dfd binding in the context of these enhancers in vitro and/or that some of the predicted sites are not functional in vivo. Based on our results with Dfd, it seems likely that about 20 to 30% of the identified downstream genes are direct Hox targets. In sum, the combination of microarray analysis with bioinformatics approaches will allow us in the future to not only identify direct Hox target genes, but also to construct complete Hox-regulatory networks.

Specificity of Hox-dependent regulation

To assess the specificity of Hox gene regulation, the 1508 responsive genes were classified according to the number of Hox proteins that influenced their expression and the influence of the developmental stage. Remarkably, most downstream genes (1039, 68.9%) were affected by only a single Hox protein, with Abd-A having a very high proportion of unique response genes (two-thirds of its downstream genes were unique), whereas the fraction of unique response genes was smaller (18 to 36%) for the other Hox genes (Fig. 5A). The use of various statistical cut-offs showed that this result is not an artifact of arbitrary thresholding (data not shown). In addition, we were able to confirm the specificity of the Hox response by analyzing the expression of some of the unique downstream genes by in situ hybridizations in embryos misexpressing any of the

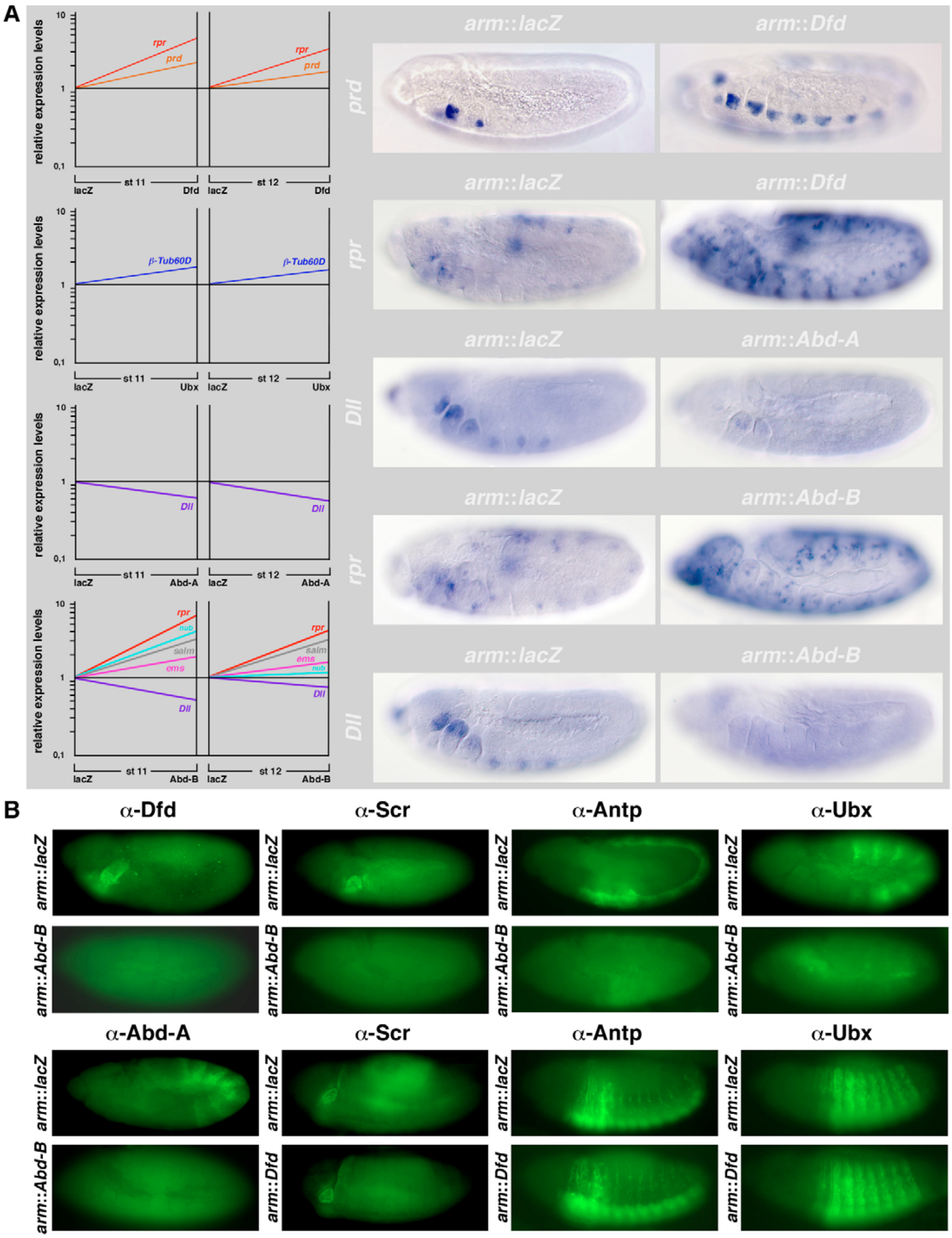

Fig. 2. Verification of known Hox downstream genes identified by microarray analysis. (**A**) Relative expression levels of seven known Hox downstream genes identified in a microarray screen are shown. For three of the seven genes, in situ hybridizations were performed. Genes shown are: *reaper* (*rpr*), *paired* (*prd*), *β-Tubulin at 60D* (*β-Tub60D*), *Distal-less* (*Dll*), *spalt major* (*salm*), *empty spiracles* (*ems*) and *nubbin* (*nub*). (**B**) α-Dfd and α-Abd-B antibody stainings on embryos misexpressing different *Hox* genes confirmed posterior suppression as seen in the microarray experiment. Antibody stainings for all (Abd-B misexpression) or for some (Dfd misexpression) Hox proteins are shown.

Hox genes (see Fig. S3 in the supplementary material). About one-third of the identified downstream genes (449, 29.8%) were affected by several Hox proteins, and only 20 genes (1, 3%) responded to all Hox proteins, representing the classes of regional and common downstream genes, respectively (Fig. 5A). Even when we excluded the Abd-A experiment, which was performed slightly differently from the rest of the set and therefore could interfere with this type of analysis, the result did not change: 63% of the genes were uniquely regulated by only one Hox protein, 34.5% of the genes by some and 2.5% by all Hox proteins (Fig. 5A). Remarkably, among the predicted direct Dfd target genes the distribution of unique and regional Hox downstream genes was similar to their distribution among all identified Hox downstream genes (Fig. 5B). Taken together, these results indicate that the specific effects of Hox proteins on morphology are largely mediated by regulatory interactions with uniquely regulated downstream genes, and that despite the very similar DNA-binding sequences for all Hox proteins observed in vitro (Ekker et al., 1994), the overlap of commonly regulated genes in vivo is relatively small.

To evaluate the influence of co-factors on the regulation of Hox downstream genes, we analyzed the Hox response at the two developmental stages. The idea was that overexpression of Hox genes remained the same, while the regulatory environment changed during the progression of embryogenesis. We found that most of the downstream genes were Hox responsive at either embryonic stage 11 or stage 12 (Fig. 5C,D), consistent with the hypothesis that Hox proteins strongly change their transcriptional output through the interaction with differentially expressed co-factors (Gebelein et al., 2004; Mahaffey, 2005; Merabet et al., 2005). To confirm stage-specific regulation of Hox downstream genes on a cellular level, we performed in situ hybridizations for some of the differentially expressed genes (Fig. 5D), and indeed found that most of these genes were Hox responsive primarily at one of the two stages (Fig. 5D).

Functional classification and comparative analysis of Hox downstream genes

To group the newly identified Hox downstream genes functionally, we used Gene Ontology (GO) annotations (Fig. 6A) and analyzed the distribution of GO categories within the Hox-responsive genes. We found that the two major groups of Hox downstream genes encoded metabolic and realizator functions, followed by the transcription or translation, signaling, transport, stress or defense response and DNA repair or replication classes (Fig. 6A). Supporting the significance of the realizator genes for the Hox response, we found that this group was the only class statistically over-represented among the Hox downstream genes by Fisher's exact test after Bonferoni correction ($P<0.001$). By contrast, the transcription or translation and transport classes were under-represented ($P<0.001$). Focusing on Dfd downstream genes, we also found that realizators were over-represented, whereas the transcription or translation functions were under-represented, albeit at weaker P-values. Intriguingly, even within the group of direct Dfd targets, the transcription or translation class was not over-represented. As sequence-specific transcription factors were never over-represented among any category tested, this suggests that the activation of regulatory proteins is not the preferred mode of Hox action. The fact that realizator processes at the same time are under direct as well as indirect Hox control demonstrates that Hox-dependent morphogenesis is indeed achieved by regulatory networks, rather than linear pathways. Furthermore, these results also argue against the idea that Hox genes mainly act on other transcription factors, a hypothesis that was based on the limited information on known direct Hox targets.

Since the realizator gene concept was postulated almost 30 years ago (Garcia-Bellido, 1975), but only a few such genes have previously been identified as Hox downstream genes in *Drosophila*, we decided to study this class of Hox response genes in more detail.

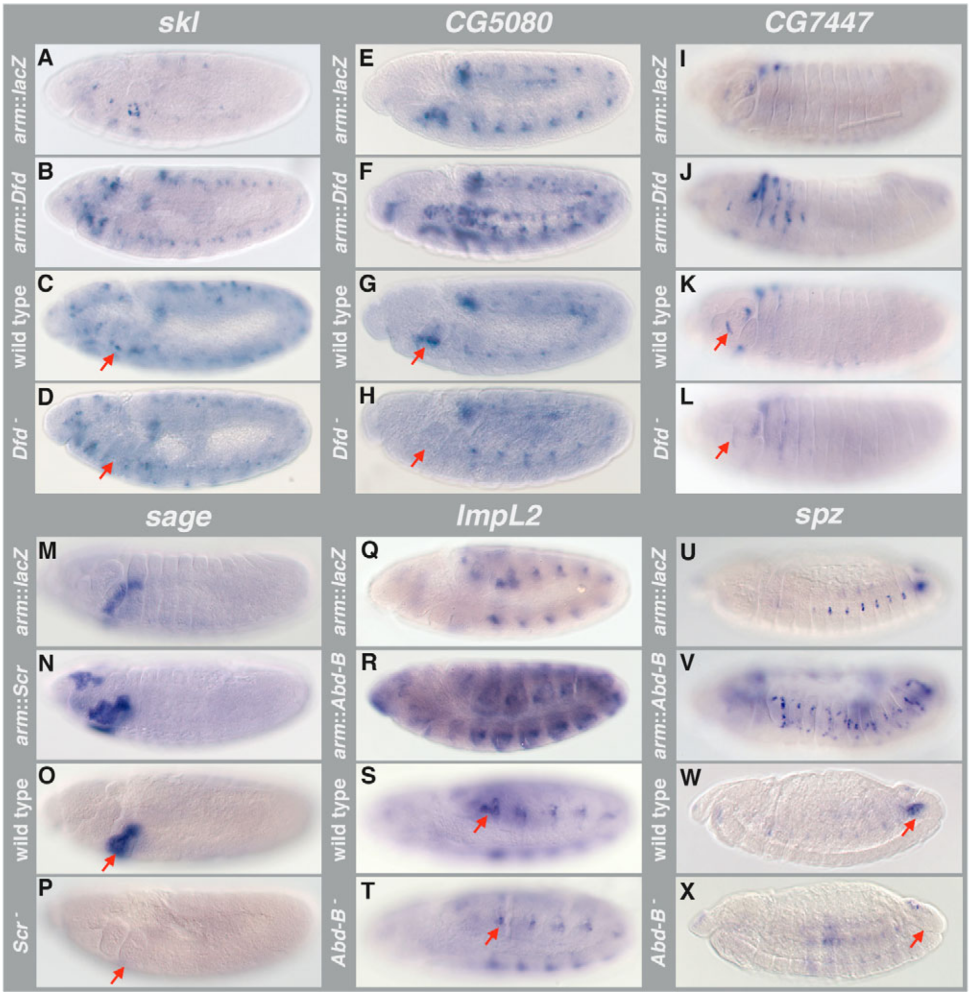

Fig. 3. Verification of newly identified Hox downstream genes by in situ hybridization. In situ hybridizations of the indicated genes in stage 11 and/or stage 12 *arm*::*lacZ*, *arm*::*Hox*, wild-type and *Hox* mutant embryos. Genes shown are: *skl* (**A-D**), *CG5080* (**E-H**), *CG7447* (**I-L**), *sage* (**M-P**), *ImpL2* (**Q-T**) and *spz* (**U-X**). Hybridizations on embryos misexpressing *Hox* genes and on *Hox* mutant embryos were performed independently (with the respective *arm*::*lacZ* and wild-type controls). Differences in staining intensities are due to differences in the in situ hybridization procedures. Pictures of *arm*::*lacZ* and wild-type embryos were taken at different focal planes and thus expression patterns in these embryos appear slightly different. Red arrows mark expression domains changed in wild-type and *Hox* mutant embryos.

Among the realizators, the largest subgroup comprises genes involved in proteolytic processes, followed by genes with cytoskeleton functions, a diverse group containing cuticle, chorion and peritrophic membrane genes, cell cycle or cell proliferation genes, apoptosis or cell death genes and cell adhesion genes (Fig. 6B). Genes within realizator subclasses are often coordinately regulated: most apoptotic (7/8) and cell cycle or proliferation genes (18/21) were activated, whereas almost all cell adhesion genes (12/14) and the majority of genes involved in proteolytic processes (56/75) were repressed by Hox proteins (Fig. 6C). Re-analyzing data from a more restricted microarray study, a similar trend can be identified for *lab*, another Hox gene (Leemans et al., 2001): one apoptotic gene and six cell cycle or cell proliferation genes were activated, whereas three cell adhesion genes were all repressed by *lab*. This suggests that a variety of cellular processes need to be regulated in a coordinated fashion in every segment in order to realize common aspects of segmental morphology. Support for this notion also comes from a previous analysis in *Drosophila*, showing that two Hox proteins, Dfd and Abd-B, locally activate the apoptosis gene *rpr* and thus the apoptotic machinery at segment boundaries for their maintenance (Lohmann et al., 2002).

Finally, we also wanted to analyze which role the identified Hox downstream genes play during the morphogenesis of segments. To this end, we first asked whether differences in morphology along the AP axis are reflected in the differential regulation of Hox responsive genes. One line of evidence supporting this idea is that many downstream genes responded only to a single Hox protein (Fig. 5A). In addition, we found that coordinated regulation of shared downstream genes was more frequent among Hox proteins specifying segments with similar morphologies than among those that specify diverse segmental morphologies (Fig. 6D). For example, both Dfd and Scr specify small lobe-shaped gnathal segments and only 4% (*n*=2) of their shared downstream genes are regulated in an opposite manner (Fig. 6D). One of the differentially regulated Dfd or Scr downstream genes is *PAPS synthetase*, which is repressed by Dfd and activated by Scr in our dataset (see Tables S1 and S2 in the supplementary material). Consistent with this observation, it had been shown that *PAPS synthetase* is specifically expressed in the salivary gland placodes in a Scr-dependent manner, while it is absent from Dfd-expressing cells in stage 11 and 12 embryos (Jullien et al., 1997). Another example for a strong correlation of differences in morphology and the differential regulation of shared downstream genes is the Scr-Abd-A pair. In this case, opposite regulation was found for 58% (*n*=55) of the targets shared by Scr and Abd-A, in line with the very different morphologies specified by these two Hox proteins (Fig. 6D). Again, two selected examples, *pipe* and *PH4αSG2*, both activated by Scr and repressed by Abd-A (see Table S2 and Table S5 in the supplementary material), are known to be expressed exclusively in the Scr-specified salivary glands at stages 11 and 12 (Abrams and Andrew, 2002; Zhu et al., 2005). Interestingly, it has been shown only recently that *pipe*, differentially regulated by Dfd and Abd-A, and *PAPS synthetase*, differentially regulated by Scr and Dfd in our microarray analysis, are both necessary for the production of sulfated macromolecules in the salivary glands of *Drosophila* embryos (Zhu et al., 2005). Thus, it seems that the diversification of segments is achieved, on the one hand, through the regulation of unique downstream genes, and, on the other hand, through the differential regulation of shared downstream genes.

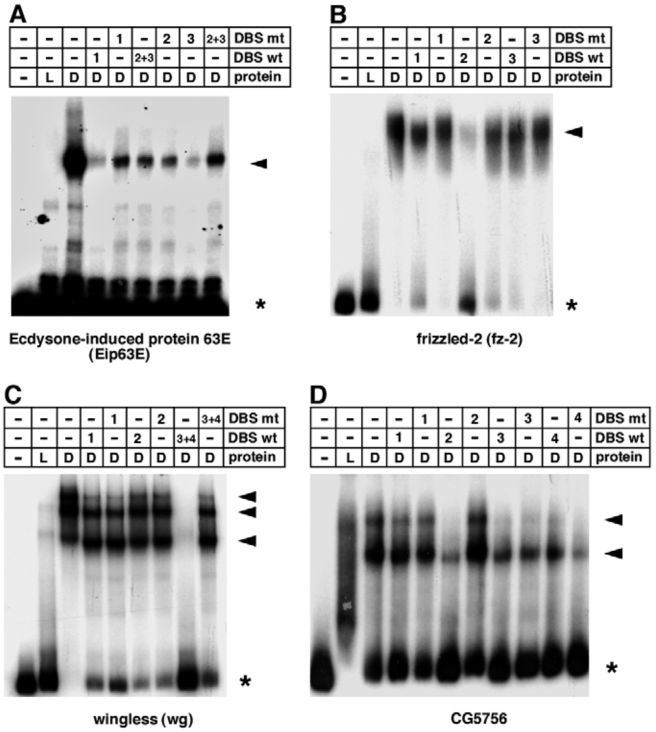

Fig. 4. Confirmation of predicted direct Dfd downstream genes by EMSA. (**A-D**) EMSA for four predicted direct Dfd downstream genes tested using no protein, translation lysate only (L) and lysate with Dfd protein (D). To test the specificity of binding of Dfd protein to the DNA fragments, competitor oligonucleotides for the individual Dfd-binding sites (DBS) were used either in their wild-type (wt) or mutant (mt) sequence versions. The black arrowhead indicates the specific DNA-protein complex containing Dfd protein. Asterisks indicate the unbound labeled probe. Predicted Dfd response enhancers of the following genes were used: *Eip63E* (A), *frizzled 2* (*fz2*) (B), *wg* (C) and *CG5756* (D).

A framework for the morphogenesis of the maxillary segment

To analyze the morphogenetic function of Hox responsive genes in more detail, we focused on the potential role of several newly identified Dfd downstream genes during the development of the maxillary segment. It has long been known that Dfd is expressed in the maxillary and mandibular segments, and is necessary for the morphological specializations (mouth hooks, cirri, ventral organ) of these head segments (McGinnis et al., 1990). However, only a single cellular event necessary for the morphogenesis of the maxillary segment and under the control of Dfd has been explained mechanistically so far: the maintenance of the boundary between the maxillary and mandibular segments, which is dependent on Dfd-mediated activation of *rpr* expression in the anterior part of the maxillary segment (Lohmann et al., 2002). Consistently, *rpr* was found among the activated Dfd downstream genes in our microarray analysis (see Table S1 in the supplementary material). Another prominent feature of *Dfd* mutants is the displacement of maxillary and mandibular segments to a more dorsal position, caused by the accumulation of supernumerary cells at the ventral side of both segments, which had been observed almost 20 years ago (Fig. 7B) (Regulski et al., 1987). There are two alternative explanations for this defect: loss of cell death and/or overactivation of cell proliferation. Consistent with the former explanation, we observed reduced local expression of the apoptosis activator *skl* (Fig. 7K,P), one of the newly identified genes activated by Dfd, and a concurrent

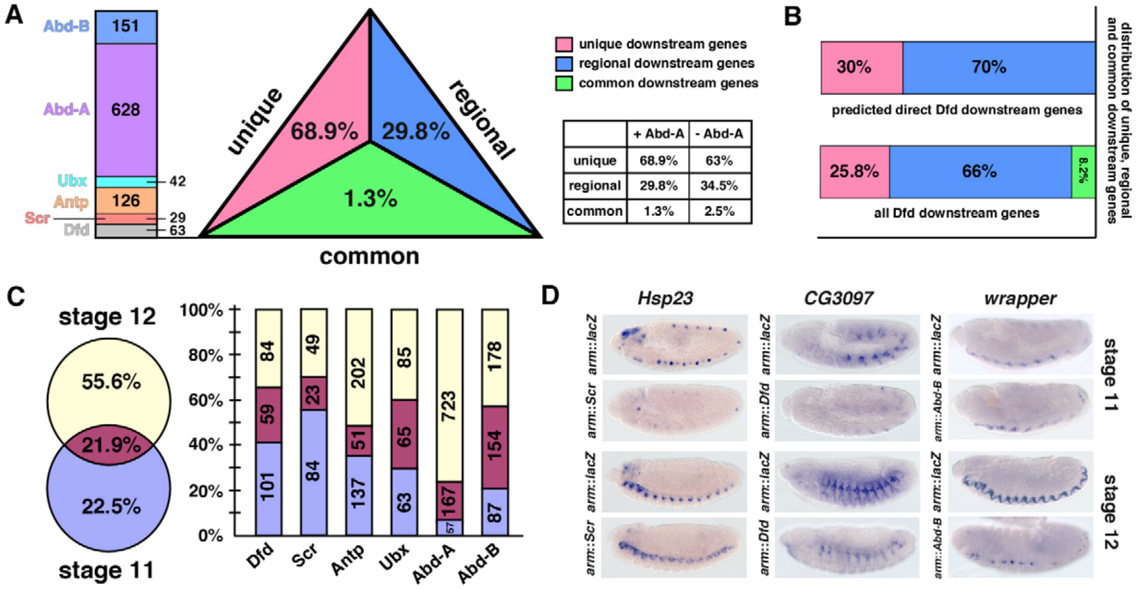

Fig. 5. Specificity of Hox downstream gene regulation. (**A**) Classification of Hox downstream genes according to their regulation by one (unique), several (regional) and all (common) Hox proteins. Numbers of unique downstream genes for each Hox protein are shown on the left. The distribution of classes does not change when the Abd-A experiment, which was performed independently, is excluded from the analysis (shown in the table). (**B**) Distribution of the regulatory classes among all identified Dfd downstream genes and predicted direct Dfd target genes is very similar. No commonly regulated downstream genes are found among the predicted direct Dfd target genes. (**C**) Distribution of Hox downstream genes regulated at the two different stages analyzed. On the left side, the percentage of all Hox downstream genes regulated at the two stages are shown; on the right side, the distribution for each individual Hox protein is indicated. Numbers of genes are shown within bars. (**D**) In situ hybridizations of selected examples of genes regulated at specific stages (early-specifc, early and late, late-specific). Expression patterns of the following genes are displayed: *Heat shock protein 23 (Hsp23), CG3097* and *wrapper.*

reduction in the number of apoptotic cells at the ventral side of the maxillary segment in *Dfd* mutants (data not shown) (Lohmann et al., 2002). Additionally, we were able to show that cell proliferation at the ventral region of the maxillary segment is increased in *Dfd* mutant embryos by performing BrdU labeling experiments (Fig. 7E,J). This might be attributed to the de-repression of two genes identified as repressed by Dfd in this study (see Table S1 in the supplementary material): *Ecdysone-induced protein 63E* (*Eip63E*), encoding a cyclin-dependent protein kinase (Stowers et al., 2000), and *wingless* (*wg*), encoding a signaling molecule known to play a role in cell proliferation (Giraldez and Cohen, 2003). In line with a role of these genes in shaping the maxillary segment, we found that both genes are ectopically expressed in the dorsal part of the maxillary segment in *Dfd* mutants (Fig. 7Q,R). Although the function of *Eip63E* during the morphogenesis of the maxillary segment could not be analyzed due to the lack of mutants, we could confirm that *wg* mutants have reduced gnathal lobes (Fig. 7D) (Rusch and Kaufman, 2000), suggesting an important role of *wg* in the regulation of cell proliferation in the maxillary segment. The third notable defect of *Dfd* mutants is the loss of the maxillary cirri primordium (Regulski et al., 1987). *paired* (*prd*), one of the transcription factor genes identified in our screen (see Table S1 in the supplementary material), is known to be important for development of cirri and the maxillary ventral organ (Vanario-Alonso et al., 1995). Because late *prd* expression is completely under the control of Dfd (Fig. 7N,S), we conclude that some aspects of ventral maxillary identity are specified by Dfd via *prd* regulation. Finally, we analyzed Dfd-dependent regulation of cell shape changes, because cells at ventral positions of wild-type maxillary segments are round (Fig. 7G), whereas in *Dfd* mutants many appeared elongated (Fig. 7H). The JNK pathway has been implicated in cell shape changes in *Drosophila*, for example during embryonic dorsal closure and adult thorax closure (Harden, 2002; Xia and Karin, 2004) and because we had identified several genes responsive to the JNK pathway (Jasper et al., 2001) [*Ras-related protein* (*Rala*), *Angiotensin converting enzyme* (*Ance*) and *CG5080*] (see Table S1 in the supplementary material) as Dfd downstream genes, we tested the contribution of the JNK pathway to the cell shape phenotype of *Dfd* mutants. After ubiquitous activation of the JNK pathway by overexpressing a constitutively active form of Hemipterous (Weber et al., 2000) using the *arm*-GAL4 driver, we observed elongated cells in the maxillary segment (Fig. 7I), as well as in other parts of the embryo (data not shown). As we could confirm for one of the JNK-responsive Dfd downstream genes, *CG5080*, implicated in the regulation of cytoskeletal dynamics (Jasper et al., 2001), strong upregulation by Dfd (Fig. 7T), we conclude that the JNK pathway plays a major role in organizing cell shapes in the maxillary segment.

DISCUSSION

More than 30 years ago Antonio Garcia-Bellido proposed that a hierarchy of three classes of genes, activators, selectors and realizators, accounts for cell differentiation during development, thereby providing a functional scheme for the control of morphogenetic processes. The key proposal was that, once activated in their appropriate territories by so-called activator genes, selector genes (he applied this name to homeotic genes) would not directly specify morphological differences between different segments, but would rather select a battery of subordinate downstream genes, the realizator genes, encoding cellular proteins directly required in cell

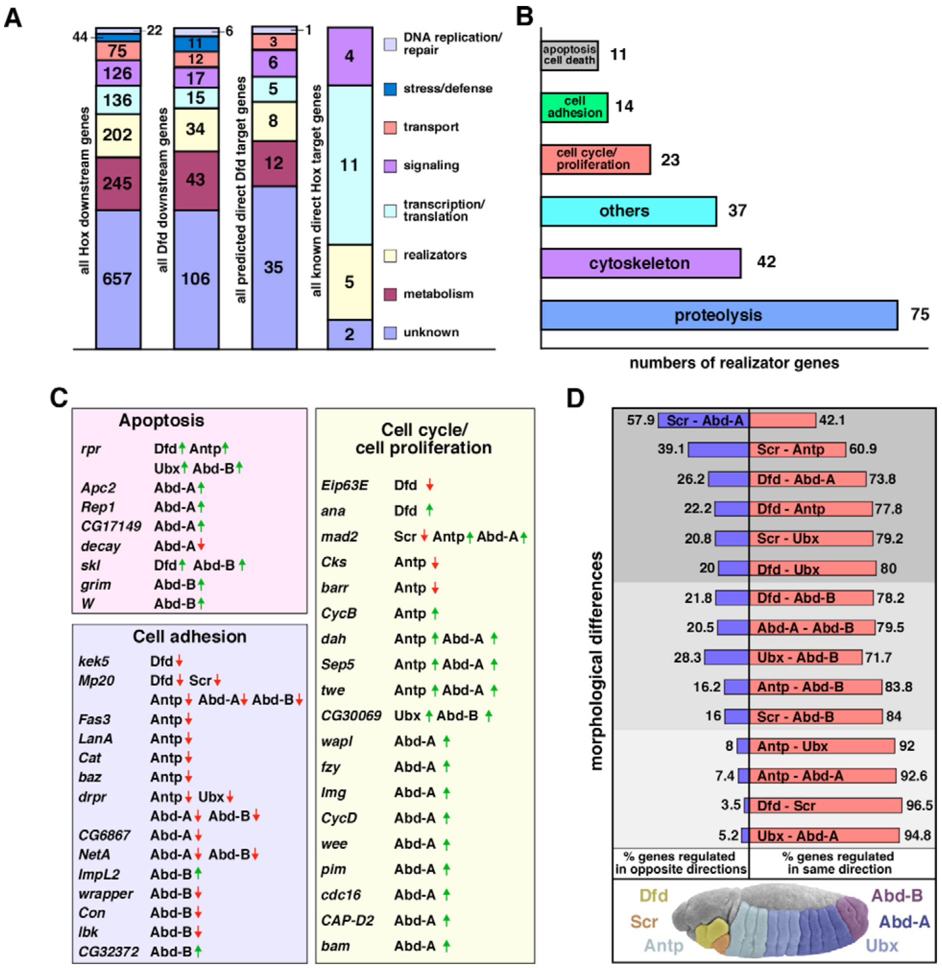

Fig. 6. Functional classification of Hox downstream genes using GO categories. (**A**) Functional categories of downstream genes are shown for all newly identified Hox downstream genes (first column), for all identified Dfd downstream genes (second column), for all predicted direct Dfd target genes (third column) and for all known direct Hox target genes (fourth column). Numbers of genes for each category are indicated within bars. (**B**) Diagram showing subclasses of realizator genes, with numbers of genes for each class indicated. (**C**) Subclasses of realizators are often coordinately regulated, as shown here by three examples (apoptosis, cell adhesion, cell cycle or cell proliferation). Green arrows, increased expression; red arrows, reduced expression. (**D**) Morphological differences along the AP axis are reflected in the percentage of shared downstream genes regulated oppositely by two different Hox proteins. Light gray indicates similar morphologies; medium gray and dark gray indicate increasing differences in morphologies directed by the *Hox* genes compared. The scanning electron micrograph shows the morphology of a stage 13 embryo, with the expression domains of the different Hox proteins highlighted.

differentiation processes (Garcia-Bellido, 1975). Until now much effort has gone into elucidating the nature and function of all three hierarchical levels, with a substantial amount of knowledge having accumulated at the activator and selector level. It is now well established that a genetic cascade comprising maternal and various classes of segmentation genes regulate the temporal and spatial expression of a unique combination of Hox genes in different segments, which subsequently specifies the identities of individual segments (McGinnis and Krumlauf, 1992; St Johnston and Nusslein-Volhard, 1992). Additionally, the discovery that Hox proteins act as transcriptional regulators established the general view that each segment will enter a specific morphogenetic program and develop unique shape and function depending on Hox downstream genes, in particular the realizator genes. Although the question of Hox downstream gene identity and function is not a novel problem, and although a considerable amount of progress has been made in recent years, our knowledge of their nature and function is still far from complete, especially with regard to the realizator genes in the sense of Garcia-Bellido.

Many of the known Hox downstream genes coded either for transcription factors or signaling molecules, and only very few of them were realizators (Hombria and Lovegrove, 2003; Pearson et al., 2005; Pradel and White, 1998). This was puzzling, as the primary function of Hox proteins is to specify the morphology of different segments, thus one would have expected to find a bias toward realizators. Moreover, this finding established the view that most of the cellular responses mediated by Hox proteins, including realizator functions, are indirectly influenced through the action of intermediate regulatory molecules. Our analysis of Hox downstream genes in *Drosophila*, which was designed to allow for a quantitative identification of Hox-regulatory networks (including most realizator genes), revealed that a major group of genes responsive to Hox input did indeed code for realizators. Therefore, our results constitute the first experimental support of the concept postulated by Garcia-Bellido more than three decades ago. We could furthermore show that a substantial part of the Hox output is directly transferred to the realizator level, suggesting that intermediate regulators might play a smaller role than previously thought. One possible explanation why so few Hox realizators had been identified before is that most realizators will be required for general functions in many cells. Consequently, mutations in realizator genes are likely to result either in early embryonic lethality or in pleiotropic effects, making it difficult to correlate their phenotypes to those found in Hox mutants. In addition, it seems likely that realizators act redundantly or have very subtle effects, making their identification in forward genetic screens extremely difficult. Similarly, individual mutations in all known guidance factors for border cell migration in *Drosophila* produce either no, or only mild, defects and thus they could be identified only by expression profiling studies (Wang et al., 2006). In this study we have quantitatively identified Hox realizator genes by a comparative microarray analysis, which now can serve as a resource to study the mechanisms of segmental morphogenesis. Focusing on the differentiation of the maxillary segment, we were able to functionally correlate all major morphological defects

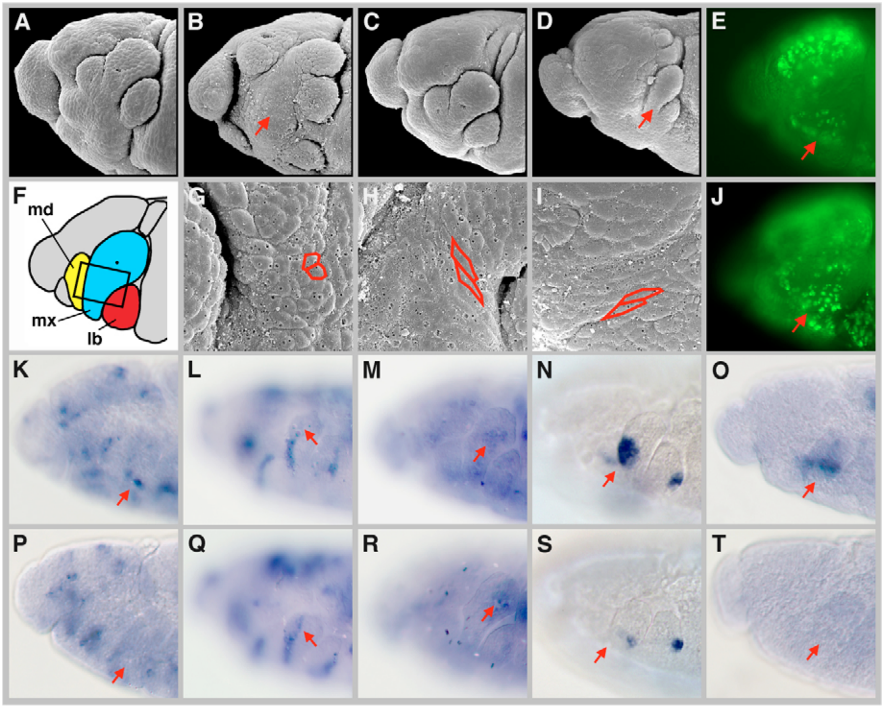

Fig. 7. A framework for the morphogenesis of the maxillary segment in *Drosophila*. (**A**,**C**) Scanning electron micrographs of heads of stage 12 wild-type embryos. (**B**) Head of a stage 12 *Dfd* mutant embryo. The red arrow marks additional cells at the ventral side of the maxillary segment. (**D**) Head of a *wg* mutant embryo. The red arrow marks the size-reduced maxillary segment. (**E**,**J**) BrdU labeling of stage 12 wild-type and *Dfd* mutant embryos, respectively. Red arrows mark proliferating BrdU-positive cells at the ventral side of the maxillary segment. (**F**) Diagram of a stage 12 wild-type embryo. Mandibular (md), maxillary (mx) and labial (lb) segments are indicated; the box marks the area shown in G,H,I. (**G**,**H**,**I**) In stage 12 wild-type embryos, cells in the ventral part of the maxillary segment are round (G), whereas in *Dfd* mutant (H) and *arm*::*hep*$^{act.}$ (I) embryos, cells are elongated (marked in red). (**K-T**) *skl* (K,P), *wg* (L,Q), *Eip63E* (M,R), *prd* (N,S) and *CG5080* (O,T) RNA expression in wild-type and *Dfd* mutant embryos, respectively. The red arrows indicate the expression of the respective genes that differs in wild-type and *Dfd* mutant embryos.

observed in *Dfd* mutants with newly identified Dfd downstream genes, many of which code for realizators, demonstrating the validity of this approach.

Another important discovery of our analysis is the enormous specificity of Hox protein action on the transcriptome in vivo, which sharply contrasts with the low DNA-binding specificity in vitro. Hox proteins have been shown to bind to very similar, relatively simple, DNA sequences containing a TAAT core sequence in vitro (Biggin and McGinnis, 1997; Carr and Biggin, 1999; Ekker et al., 1994; Walter and Biggin, 1996), whereas many of the identified Hox downstream genes are uniquely regulated by only a single Hox protein. This contrast may be explained by our observation that the majority of genes are primarily regulated at only one of the two stages, implicating that Hox proteins excessively interact with the regulatory environment in which they are embedded. Support for the notion that co-factor interactions have a major impact on Hox output also comes from a recent study, which has provided direct evidence that Hox proteins gain the ability to regulate their target genes in a context-specific manner by interaction with known cell- and/or tissue-specific transcription factors in vivo (Gebelein et al., 2004). In addition, this study also suggests that a large number of transcription factors might function as Hox co-factors, which could dictate the outcome of Hox gene action. Along these lines, we found that ubiquitous overexpression of Hox proteins never caused ubiquitous activation of downstream genes, but that ectopic expression was always locally restricted, suggesting that regional transcription factors are essential for Hox output. This is also reflected in our finding that conserved clusters of Hox binding sites in the regulatory regions of direct targets frequently contain binding sites for unrelated transcription factors. Taken together, these results support the hypothesis put forward by Michael Akam in 1998, that "we should think of the Hox genes with their short and relatively non-specific target sequences, as cofactors that modify the actions of other more specific transcription factors, rather than proteins in need of cofactors themselves" (Akam, 1998).

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Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/134/2/381/DC1

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Table S1. Genes responsive to Dfd induction

Up-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000459	143124_at	CG9908	disco	transcription factor activity	2,0	4,357	-	-
FBgn0001149	143184_at	CG10045	GstD1	glutathione transferase activity	-	-	1,6	4,5365
FBgn0001150	143185_at	CG7952	gt	transcription factor activity	3,1	5,5872	-	-
FBgn0001230	143197_at	CG5436	Hsp68	unfolded protein binding	2,0	3,3471	-	-
FBgn0003145	152870_at	CG6716	prd	DNA binding / specific RNA polymerase II transcription factor activity	2,2	3,6241	-	-
FBgn0003308	152200_at	CG7642	ry	xanthine dehydrogenase activity	-	-	2,5	3,0341
FBgn0004228	143441_at	CG7936	mex1	-	-	-	1,5	3,3205
FBgn0004898	143532_at	CG11922	fd96Cb	transcription factor activity	2,1	4,3416	2,2	3,6725
FBgn0010222	151767_at	CG18466	Nmdmc	magnesium ion binding	-	-	1,9	4,6204
FBgn0011706	143680_at	CG4319	rpr	-	3,8	8,8962	2,6	4,4461
FBgn0011722	143682_at	CG11527	Tig	binding	2,8	4,8534	1,9	4,3389
FBgn0011746	152113_at	CG8084	ana	-	-	-	3,3	4,199
FBgn0012037	153728_at	CG8827	Ance	peptidyl-dipeptidase A activity / zinc ion binding	2,6	7,0658	2,2	7,3712
FBgn0013772	142189_at	CG10248	Cyp6a8	electron transporter activity / oxidoreductase activity	2,6	5,9401	2,0	5,0729
FBgn0014011	153313_at	CG8556	Rac2	GTPase activity	1,6	3,0542	-	-
FBgn0025454	152900_at	CG8453	Cyp6g1	electron transporter activity / oxidoreductase activity	-	-	2,8	5,6701
FBgn0027610	151853_at	CG8790	-	carrier activity / dicarboxylic acid transporter activity	-	-	1,6	3,4751
FBgn0028469	154424_at	CG8062	-	monocarboxylic acid transporter activity	2,6	6,3211	-	-
FBgn0028519	154426_at	CG4500	-	long-chain-fatty-acid-CoA ligase activity	1,6	3,8268	-	-
FBgn0029531	144348_at	CG13362	-	-	-	-	2,1	5,9299
FBgn0030187	154819_at	CG2961	Ipod	-	-	-	2,6	3,1967
FBgn0030390	144937_at	CG15731	-	-	-	-	1,8	2,868
FBgn0030576	145075_at	CG15890	-	-	-	-	1,7	3,0235
FBgn0031000	145357_at	CG7876	-	-	-	-	2,3	2,9395
FBgn0031313	154669_at	CG5080	-	-	2,8	11,3649	3,2	6,472
FBgn0031908	153932_at	CG5177	-	trehalose-phosphatase activity	-	-	1,9	4,1808
FBgn0031938	145976_s_at	CG13796	-	glycine transporter activity / structural constituent of adult cuticle (sensu Insecta)	-	-	1,5	2,9116
FBgn0032213	146138_at	CG5390	-	NOT serine-type endopeptidase activity	-	-	2,9	3,4936
FBgn0032253	146162_at	CG5322	-	alpha-mannosidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds	-	-	2,2	3,4821
FBgn0032264	146165_at	CG6113	-	triacylglycerol lipase activity	1,6	3,651	1,9	3,244
FBgn0032283	146182_at	CG7296	-	-	1,6	2,972	1,9	6,39
FBgn0032284	146183_at	CG7294	-	-	2,1	2,9728	2,6	5,6124
FBgn0032681	141280_at	CG10283	-	-	1,6	3,3761	-	-
FBgn0032774	152759_at	CG17549	-	-	-	-	2,5	3,7858
FBgn0033204	146757_at	CG2065	-	oxidoreductase activity	-	-	2,2	2,8042
FBgn0033437	146898_at	CG12926	-	carrier activity / tocopherol binding	-	-	2,4	5,7145
FBgn0033456	153430_at	CG10536	cbx	-	-	-	1,5	3,0603
FBgn0033518	146946_s_at	CG11765	Prx2540-2	antioxidant activity / antioxidant activity / non-selenium glutathione peroxidase activity / peroxidase activity / peroxidase activity / peroxidase activity	-	-	2,2	7,4323
FBgn0033614	147010_at	CG13208	Obp47b	-	-	-	2,6	4,9623
FBgn0033788	147126_i_at	CG13323	-	-	2,1	5,9781	-	-
FBgn0034190	141536_at	CG8946	Sply	-	-	-	1,7	3,8374
FBgn0034200	152591_at	CG11395	-	-	-	-	1,6	3,663
FBgn0034227	147367_at	CG18431	-	-	-	-	1,5	4,2441
FBgn0034301	147413_at	CG5756	-	-	1,6	3,9247	3,0	4,5836
FBgn0034468	147514_at	CG11797	Obp56a	-	-	-	1,6	3,1572
FBgn0034736	147681_at	CG6018	-	carboxylesterase activity	-	-	2,0	5,1381
FBgn0035077	154985_at	CG9083	-	-	-	-	2,1	4,5431
FBgn0035089	147903_at	CG9358	Phk-3	-	-	-	1,6	2,8301
FBgn0035347	141711_at	CG33232	-	actin binding / structural constituent of cytoskeleton	-	-	1,7	4,3985
FBgn0035539	153881_at	CG7447	-	-	2,3	3,185	1,9	4,1811
FBgn0035638	148236_at	CG10541	Tektin-C	-	5,6	7,2903	8,0	10,754
FBgn0035717	152709_at	CG10078	Prat2	-	-	-	2,6	6,7826
FBgn0035736	148302_at	CG8638	-	structural constituent of cuticle (sensu Insecta)	-	-	3,4	5,7177
FBgn0035798	154595_at	CG7526	-	kinase activity / protein kinase activity / receptor activity / structural molecule activity / transmembrane receptor protein kinase activity / transmembrane receptor protein tyrosine kinase activity	-	-	1,7	3,4352
FBgn0035860	151948_at	CG8023	-	RNA cap binding / translation initiation factor activity	2,5	2,8568	6,1	4,5699
FBgn0035882	148396_f_at	CG13666	mam	-	1,6	3,0458	-	-
FBgn0036151	154125_at	CG7590	scyl	-	1,7	3,363	-	-
FBgn0036208	148605_at	CG10361	-	glycine C-acetyltransferase activity / transaminase activity	-	-	2,3	4,0423
FBgn0036572	154763_at	CG5165	Pgm	-	-	-	2,0	4,5099
FBgn0036663	153030_at	CG9674	-	-	1,7	3,4371	1,7	4,6458
FBgn0036678	142769_at	CG11905	-	-	-	-	1,5	4,1721
FBgn0036786	148994_at	CG13701	skl	-	1,6	2,8394	-	-
FBgn0037227	149271_at	CG14640	-	-	-	-	2,0	6,4728
FBgn0037513	153777_at	CG3027	pyd3	-	4,3	13,8516	3,1	6,1908
FBgn0037819	149633_at	CG14688	-	-	1,5	3,7441	-	-
FBgn0037913	151826_at	CG6783	-	carrier activity / fatty acid binding / tricarboxylate carrier activity	1,9	5,6727	2,7	9,4451
FBgn0037977	153367_at	CG3132	Ect3	beta-galactosidase activity	-	-	5,1	15,6732
FBgn0038027	149762_at	CG4421	GstD8	glutathione peroxidase activity / glutathione transferase activity	1,8	2,8607	-	-
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	2,3	5,2724	0,6	-
FBgn0038194	152120_at	CG3050	Cyp6d5	electron transporter activity / oxidoreductase activity	1,8	3,5325	-	-
FBgn0038198	149871_at	CG3153	-	receptor binding	-	-	2,5	4,7835
FBgn0038243	149906_i_at / 149907_r_at	CG8066	-	cysteine protease inhibitor activity	7,9	8,0656	12,6	13,4042
FBgn0038540	150095_at	CG14321	-	-	2,1	2,8534	-	-
FBgn0038645	150159_at	CG7714	-	-	3,7	9,0134	1,9	4,1558
FBgn0038661	141483_at	CG17836	-	protein dimerization activity	-	-	1,5	2,9145
FBgn0039102	153098_at	CG16705	-	monophenol monooxygenase activator activity / trypsin activity / trypsin activity	-	-	1,6	4,2179
FBgn0039176	141731_at	CG13610	-	organic cation transporter activity	1,5	3,0159	-	-
FBgn0039454	150684_at	CG14247	-	-	2,0	3,301	-	-
FBgn0039593	150780_at	CG9989	-	-	-	-	2,3	4,2849
FBgn0040716	151193_f_at	CG33516	dpr3	-	1,5	3,1399	-	-
FBgn0040736	151211_at	CG16844	IM3	-	3,7	4,5397	5,4	4,4152
FBgn0040769	151244_f_at	CG12431	-	-	1,5	3,0268	-	-
FBgn0040827	151301_at	CG13315	-	-	-	-	2,2	3,069

Downregulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st11	*t*-value st12
FBgn0000011	143051_at	CG4807	ab	specific RNA polymerase II transcription factor activity	-2,3	-6,5031	-	-
FBgn0000165	151955_at	CG5779	Bc	-	-	-	-3,4	-6,6184
FBgn0000180	155099_at	CG4722	bib	binding / carrier activity / water channel activity	-1,5	-2,9349	-	-
FBgn0000320	152004_at	CG9554	cli	-	-1,6	-3,0028	-1,8	-3,0166
FBgn0001145	143181_at	CG1743	Gs2	glutamate-ammonia ligase activity	-1,7	-4,5817	-	-
FBgn0001941	153842_at	CG9078	ifc	sphingolipid delta-4 desaturase activity / stearoyl-CoA 9-desaturase activity	-1,6	-3,435	-	-
FBgn0002561	143237_at	CG3839	l(1)sc	specific RNA polymerase II transcription factor activity / transcription factor activity	-1,5	-4,8136	-	-
FBgn0002789	143271_at	CG4696	Mp20	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	-1,7	-4,5238
FBgn0003057	143296_at	CG10598	-	-	-	-	-1,7	-3,4777
FBgn0003082	143303_at	CG11205	phr	nucleic acid binding / nucleic acid binding	-1,9	-4,7286	-1,7	-3,697
FBgn0003169	154591_at	CG7904	put	activin binding / activin receptor activity / hematopoietin/interferon-class (D200-domain) cytokine receptor activity / protein kinase activity / transforming growth factor beta receptor activity / type II activin receptor activity / type II transforming growth factor beta receptor activity	-1,9	-3,6256	-	-
FBgn0003326	143333_at	CG17579	sca	receptor binding / signal transducer activity	-1,7	-2,9038	-	-
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-14,6	-11,3715
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-15,3	-11,4934
FBgn0003411	143353_at	CG1641	sisA	protein heterodimerization activity / transcription factor activity	-1,6	-4,8064	-2,2	-4,1358
FBgn0003462	143358_at	CG11793	Sod	antioxidant activity / copper, zinc superoxide dismutase activity	-1,8	-4,9209	-	-
FBgn0003507	141687_at	CG3992	srp	DNA binding / general RNA polymerase II transcription factor activity / RNA polymerase II transcription factor activity / transcriptional activator activity	-	-	-2,2	-3,7314
FBgn0003655	151660_at	CG3429	swa	dynein binding / RNA binding	-2,1	-2,9477	-	-
FBgn0003995	143409_at	CG10037	vvl	DNA binding / protein binding / RNA polymerase II transcription factor activity / transcription factor activity	-2,2	-4,967	-1,6	-4,1734

FBgn0004009	143414_at	CG4889	wg	frizzled-2 binding / morphogen activity / Notch binding / receptor binding / signal transducer activity	-2,2	-5,6416	-	-
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-1,9	-5,3295	-	-
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,6	-7,9474	-	-
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,8	-5,7881	-1,9	-3,5723
FBgn0004606	141676_at	CG1322	zfh1	DNA binding / RNA polymerase II transcription factor activity	-1,9	-9,1395	-1,9	-5,9723
FBgn0005640	143565_at	CG10579	Eip63E	cyclin-dependent protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-1,6	-3,8357	-1,7	-3,2134
FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-	-	-5,7	-4,7816
FBgn0010425	143624_at	CG18681	epsilonTry	trypsin activity	-	-	-2,0	-3,6351
FBgn0011704	142872_at	CG8975	RnrS	ribonucleoside-diphosphate reductase activity	-1,7	-6,4233	-	-
FBgn0011761	154221_at	CG4193	dhd	thiol-disulfide exchange intermediate activity	-2,7	-7,6199	-1,9	-4,5365
FBgn0014141	141641_at	CG3937	cher	actin binding / structural constituent of cytoskeleton	-2,2	-4,7334	-	-
FBgn0015221	143784_at	CG1469	Fer2LCH	ferrous iron binding	-	-	-1,5	-4,4971
FBgn0015286	143790_at	CG2849	Rala	GTPase activity	-	-	-1,8	-4,076
FBgn0015321	154399_at	CG8284	UbcD4	ligase activity / ubiquitin conjugating enzyme activity	-1,7	-6,6779	-	-
FBgn0015800	143846_at	CG6920	mus309	ATP-dependent DNA helicase activity / ATP-dependent DNA helicase activity / DNA binding / DNA helicase activity / DNA-dependent protein kinase activity / helicase activity / nucleic acid binding	-1,6	-3,3066	-	-
FBgn0019686	154411_at	CG10895	lok	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-1,6	-2,9705	-	-
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-1,8	-4,0747	-2,4	-8,0161
FBgn0020637	143935_s_at	CG10534	Lcp65Ag2	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	-1,7	-4,7486	-	-
FBgn0024332	153592_at	CG4206	Mcm3	chromatin binding / DNA helicase activity / DNA replication origin binding	-1,7	-2,7777	-	-
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-3,1	-5,2097	-2,1	-2,97
FBgn0025627	154569_at	CG4194	-	-	-1,5	-4,8603	-	-
FBgn0025885	153296_at	CG11143	Inos	-	-2,3	-8,1773	-	-
FBgn0026415	144143_at	CG1780	Idgf4	imaginal disc growth factor activity	-1,8	-5,3384	-	-
FBgn0027348	153318_at	CG4501	bgm	-	-	-	-1,6	-2,9467
FBgn0027496	154510_at	CG9543	-	-	-1,6	-2,8224	-	-
FBgn0027560	152201_at	CG4104	Tps1	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity	-1,6	-3,6418	-	-
FBgn0027657	152233_at	CG9734	glob1	carrier activity / oxygen transporter activity	-1,6	-5,9619	-	-
FBgn0027842	154586_at	CG12891	CPTI	acetyltransferase activity / carnitine O-palmitoyltransferase activity	-1,7	-3,5423	-	-
FBgn0027945	141370_at	CG7758	ppl	hydrolase activity	-1,7	-3,1817	-	-
FBgn0028491	151495_at	CG2930	-	proton-dependent oligopeptide transporter activity	-2,6	-7,2922	-	-
FBgn0028855	144266_at	CG15282	-	-	-	-	-1,7	-3,1691
FBgn0028905	144302_at	CG32972	-	-	-2,3	-9,4381	-1,9	-5,6794
FBgn0029804	144549_at	CG3097	-	carboxypeptidase A activity	-1,8	-4,7854	-1,6	-3,7323
FBgn0030452	153453_at	CG4330	-	high affinity inorganic phosphate:sodium symporter activity	-1,6	-3,8435	-	-
FBgn0030653	153970_at	CG7860	-	asparaginase activity	-	-	-2,4	-4,7414
FBgn0030803	153983_at	CG4880	-	-	-1,5	-3,181	-	-
FBgn0030891	154246_at	CG7098	dik	-	-1,6	-4,7961	-	-
FBgn0031016	145366_at	CG12199	kek5	oxidoreductase activity / peroxidase activity	-	-	-2,5	-4,2562
FBgn0031097	151712_at / 142891_at	CG17052	-	structural constituent of peritrophic membrane (sensu Insecta)	-2,0	-4,6285	-1,7	-3,5272
FBgn0031316	141643_at	CG5105	Plap	phospholipase A2 activator activity	-1,5	-2,936	-	-
FBgn0031341	145584_at	CG5481	lea	axon guidance receptor activity / receptor activity	-1,6	-2,8561	-	-
FBgn0031356	145594_at	CG17660	-	-	-1,5	-3,3679	-	-
FBgn0031433	145648_at	CG18559	Cyp309a2	electron transporter activity / electron transporter activity / oxidoreductase activity / oxidoreductase activity	-	-	-1,9	-3,5301
FBgn0031599	145755_at	CG18013	-	transcriptional elongation regulator activity	-1,5	-3,0032	-	-
FBgn0031653	145795_at	CG8871	Jon25Biii	elastase activity / serine-type peptidase activity	-	-	-2,8	-7,4964
FBgn0031669	145804_at	CG31917	-	-	-1,7	-3,7768	-	-
FBgn0031706	145823_at	CG6634	nmr2	transcription factor activity	-1,8	-3,6911	-	-
FBgn0031914	153381_at	CG5973	-	carrier activity / retinal binding	-2,3	-4,2311	-2,0	-3,4906
FBgn0031936	145974_at	CG13794	-	-	-7,4	-9,4528	-5,6	-6,9459
FBgn0032014	154704_at	CG7840	-	-	-1,6	-5,8451	-	-
FBgn0032114	146084_at	CG3752	Aldh	aldehyde dehydrogenase (NAD) activity	-1,5	-3,559	-	-
FBgn0032136	153828_at	CG15828	-	lipid binding	-1,7	-3,8386	-1,6	-4,9562
FBgn0032246	154968_at	CG5168	-	-	-1,6	-3,6227	-	-
FBgn0032282	146181_at	CG7299	-	-	-	-	-2,2	-2,7929
FBgn0032287	151967_at	CG6415	-	-	-1,7	-4,277	-	-
FBgn0032295	155152_at	CG12299	-	transcription regulator activity	-1,6	-4,3079	-	-
FBgn0032489	146318_at	CG15480	-	-	-1,8	-4,1669	-	-
FBgn0032693	155069_at	CG10391	Cyp310a1	electron transporter activity / oxidoreductase activity	-	-	-1,5	-3,0347
FBgn0032706	146449_at	CG10369	Irk3	inward rectifier potassium channel activity	-1,5	-3,8264	-	-
FBgn0032985	146620_s_at / 146619_i_at	CG1742	Mgstl	glutathione transferase activity	-1,9	-5,9341	-	-
FBgn0033082	154155_at	CG3273	sced	-	-1,6	-3,9922	-	-
FBgn0033144	141404_at	CG12172	Spn43Aa	serine-type endopeptidase inhibitor activity	-3,1	-8,1274	-1,9	-4,8445
FBgn0033162	146732_at	CG1707	-	lactoylglutathione lyase activity	-1,7	-3,4917	-	-
FBgn0033275	146794_at	CG14756	-	-	-3,6	-5,2249	-8,3	-17,3377
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-4,4	-13,3764	-8,5	-13,2493
FBgn0033534	151592_at	CG12052	lola	RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity	-	-	-1,7	-4,2124
FBgn0033604	147002_at	CG9070	-	-	-3,5	-3,7283	-2,2	-5,6025
FBgn0033634	147022_at	CG7763	-	-	-1,8	-6,3439	-2,0	-3,8132
FBgn0033643	147029_s_at	CG30035	-	fructose transporter activity / glucose transporter activity / glucose transporter activity	-1,6	-4,5504	-	-
FBgn0033721	147084_at	CG13159	-	-	-11,6	-10,1467	-5,3	-12,0341
FBgn0033921	147193_at	CG8589	-	-	-2,0	-4,3502	-	-
FBgn0034158	154285_at	CG5522	-	guanyl-nucleotide exchange factor activity	-1,5	-5,9816	-1,5	-2,871
FBgn0034222	147364_at	CG14478	-	-	-1,6	-3,9799	-	-
FBgn0034312	155151_at	CG10916	-	-	-1,5	-3,4594	-	-
FBgn0034514	147549_at	CG13427	-	-	-	-	-1,7	-6,1262
FBgn0034698	141793_at	CG6698	NtR	-	-2,1	-4,1161	-1,6	-2,9455
FBgn0034934	154176_at	CG2827	Tal	-	-1,6	-4,1054	-	-
FBgn0035030	152422_at	CG3541	-	-	-1,8	-3,8074	-1,6	-3,4648
FBgn0035190	147960_at	CG13913	-	-	-7,7	-8,9485	-2,5	-5,9885
FBgn0035208	147969_at	CG9184	-	-	-1,8	-10,3863	-1,5	-3,7306
FBgn0035209	147970_at	CG13914	-	-	-1,7	-5,6441	-	-
FBgn0035315	152877_at	CG8960	-	-	-	-	-1,6	-4,1655
FBgn0035494	142340_at	CG14993	Faa	fumarylacetoacetase activity	-	-	-1,8	-2,8053
FBgn0035551	148182_at	CG7465	-	-	-3,4	-3,7869	-4,2	-8,7797
FBgn0035621	154354_at	CG10591	-	-	-1,8	-2,9702	-1,6	-5,4682
FBgn0035664	148253_at	CG6467	Jon65Aiv	chymotrypsin activity / serine-type endopeptidase activity	-	-	-1,7	-3,1501
FBgn0035706	148284_at	CG10125	zpg	innexin channel activity	-1,5	-2,8997	-	-
FBgn0035926	148422_at	CG5804	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,5	-5,469
FBgn0035961	153070_at	CG4821	Tequila	pancreatic elastase activity / serine-type endopeptidase activity / trypsin activity	-	-	-1,5	-4,2988
FBgn0035999	148467_at	CG3552	-	-	-2,1	-3,6543	-2,1	-3,9772
FBgn0036486	148795_at	CG7003	-	damaged DNA binding	-2,1	-3,3086	-	-
FBgn0036488	148796_at	CG6878	-	-	-1,7	-5,0372	-	-
FBgn0036533	148825_at	CG6151	-	-	-1,6	-3,2266	-	-
FBgn0036539	148828_at	CG32150	-	-	-1,7	-4,5548	-	-
FBgn0036787	148995_at	CG4306	-	-	-1,8	-3,0278	-2,1	-5,8814
FBgn0036802	142148_at	CG4144	GNBP2	glucosidase activity / Gram-negative bacterial binding / pattern recognition receptor activity	-1,6	-6,1791	-1,6	-3,1716
FBgn0036826	153914_at	CG3893	-	-	-1,6	-2,7762	-	-
FBgn0036852	149033_at	CG9739	fz2	G-protein coupled receptor activity / transmembrane receptor activity / Wnt receptor activity / Wnt-protein binding	-1,6	-3,3077	-1,9	-4,3575
FBgn0036863	154347_at	CG9670	fal	-	-1,8	-3,0516	-	-
FBgn0036875	149052_at	CG9449	-	acid phosphatase activity	-	-	-2,8	-6,607
FBgn0036898	151832_at	CG8782	Oat	ornithine-oxo-acid transaminase activity	-1,9	-3,2456	-	-
FBgn0036901	141311_at	CG8756	LCBP1	-	-2,2	-7,7939	-	-
FBgn0037083	141375_at	CG5656	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-1,8	-6,185
FBgn0037177	149244_at	CG14454	-	molecular_function unknown	-1,5	-3,5311	-	-
FBgn0037181	149248_at	CG11370	-	-	-	-	-1,5	-3,7342
FBgn0037353	155055_at	CG31549	-	oxidoreductase activity / structural constituent of cytoskeleton / structural molecule activity	-1,7	-3,8343	-	-
FBgn0037549	154657_at	CG7878	-	ATP-dependent RNA helicase activity / helicase activity / nucleic acid binding	-1,9	-4,0798	-	-
FBgn0037607	153373_at	CG8036	-	transketolase activity	-1,5	-6,8551	-	-
FBgn0037614	149520_at	CG8116	-	-	-1,6	-4,1849	-	-
FBgn0037699	154821_at	CG8147	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-2,0	-4,2542
FBgn0037844	153457_at	CG4570	-	-	-1,5	-5,7372	-	-

FBgn0037912	155150_at	CG6782	-	carrier activity / fatty acid binding / tricarboxylate carrier activity	-1,6	-3,1765	-	-
FBgn0038024	149759_at	CG12242	GstD5	glutathione transferase activity	-	-	-2,5	-5,5697
FBgn0038040	153596_at	CG5663	Dip-C	dipeptidyl-peptidase activity / X-Pro dipeptidase activity	-1,7	-3,6104	-	-
FBgn0038353	149968_at	CG5399	-	-	-2,8	-8,256	-	-
FBgn0038413	141589_at	CG6725	Sulf1	N-acetylglucosamine-6-sulfatase activity	-1,6	-3,3332	-	-
FBgn0038563	152336_at	CG7780	DNaseII	-	-2,2	-4,9595	-1,8	-3,5352
FBgn0038803	152563_at	CG5191	-	hydrolase activity	-1,5	-4,1467	-	-
FBgn0038971	150368_at	CG13845	-	-	-	-	-1,6	-3,4429
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-	-	-1,8	-4,6029
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-	-	-1,9	-3,526
FBgn0039098	142671_at	CG13822	-	-	-2,0	-3,8467	-1,8	-4,6726
FBgn0039114	152325_at	CG10374	Lsd-1	-	-	-	-3,4	-7,3861
FBgn0039251	150539_at	CG17462	-	nucleic acid binding / sigma DNA polymerase activity	-1,8	-2,7769	-	-
FBgn0039436	150665_s_at	CG6478	-	-	-2,2	-3,582	-	-
FBgn0039537	151807_at	CG5590	-	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	-1,6	-4,5367	-	-
FBgn0039539	154473_at	CG12880	-	-	-	-	-3,7	-3,1661
FBgn0039678	150831_at	CG18111	Obp99a	odorant binding	-2,2	-8,7211	-1,6	-5,2268
FBgn0039682	150834_at	CG7584	Obp99c	-	-	-	-1,8	-5,0039
FBgn0039686	150838_at	CG15506	-	-	-	-	-2,0	-4,3292
FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-6,9	-7,1207
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-8,4	-6,0641
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-	-	-2,1	-3,776
FBgn0039851	151691_at	CG12063	-	-	-	-	-1,9	-3,6417
FBgn0039873	150955_at	CG2191	-	cation transporter activity / sodium-dependent multivitamin transporter activity	-4,5	-5,2677	-	-
FBgn0039890	154488_at	CG2316	-	ATPase activity, coupled to transmembrane movement of substances / transporter activity	-1,5	-3,075	-	-
FBgn0039930	150994_at	CG11077	-	-	-1,8	-3,1431	-	-
FBgn0040609	151094_at	CG3348	-	-	-	-	-1,7	-5,9327
FBgn0040650	151134_at	CG15456	-	-	-2,4	-3,7144	-	-
FBgn0040796	151266_at	CG13064	-	-	-4,3	-3,6568	-1,6	-5,6827
FBgn0040942	151409_at	CG12643	-	-	-1,8	-3,691	-1,7	-2,8922
FBgn0040984	151444_at	CG4440	-	-	-1,6	-6,2295	-2,6	-9,0294

Table S2. Genes responsive to Scr induction

Up-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0001204	143189_at	CG9768	hkb	specific RNA polymerase II transcription factor activity	1,5	2,9421	-	-
FBgn0002570	143242_at	CG8696	LvpH	alpha-glucosidase activity	-	-	2,87	4,6416
FBgn0003089	143305_at	CG9614	pip	heparin-sulfate 2-sulfotransferase activity / sulfotransferase activity	1,9	3,1068	-	-
FBgn0012037	153728_at	CG8827	Ance	peptidyl-dipeptidase A activity / zinc ion binding	1,6	2,9181	-	-
FBgn0013772	142189_at	CG10248	Cyp6a8	electron transporter activity / oxidoreductase activity	1,8	3,7074	-	-
FBgn0014469	154078_at	CG2060	Cyp4e2	electron transporter activity / oxidoreductase activity	2,9	9,2143	2,795	9,1937
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-	-	1,672	4,2712
FBgn0023520	152934_at	CG3857	-	-	2,9	6,978	2,393	5,8163
FBgn0028922	144311_at	CG4182	yellow-c	-	-	-	2,249	3,7421
FBgn0029744	141469_at	CG11706	-	-	-	-	2,017	3,7502
FBgn0030498	145018_at	CG32632	-	protein-tyrosine sulfotransferase activity	-	-	1,722	3,4425
FBgn0031000	145357_at	CG7876	-	-	-	-	1,792	3,2698
FBgn0031313	154669_at	CG5080	-	-	-	-	1,774	2,8413
FBgn0031561	145731_at	CG16712	-	serine-type endopeptidase inhibitor activity	2,2	4,3382	2,99	5,2919
FBgn0031964	145995_at	CG33121	-	serine-type endopeptidase inhibitor activity / serine-type endopeptidase inhibitor activity	39,1	15,7134	41,3	9,2308
FBgn0033788	147126_i_at	CG13323	-	-	1,7	4,368	-	-
FBgn0034290	142954_at	CG5773	-	-	2,5	5,2975	2,26	3,4512
FBgn0034294	147409_at	CG5765	-	-	-	-	1,748	3,5225
FBgn0034352	147441_at	CG17669	-	-	1,5	-	2,032	3,5259
FBgn0034819	147740_at	CG9877	-	-	-	-	2,295	2,874
FBgn0035434	148103_at	CG10812	dro5	-	2,0	6,6404	1,926	6,217
FBgn0035880	152139_at	CG17352	-	-	-	-	1,515	3,3938
FBgn0036167	148580_f_at	CG33272	-	-	-	-	1,652	3,1667
FBgn0036390	148732_at	CG13738	-	-	-	-	1,835	3,2383
FBgn0036457	148772_at	CG3396	Ocho	-	2,5	4,6561	1,783	3,0176
FBgn0036786	148994_at	CG13701	skl	-	1,7	2,8069	-	-
FBgn0037179	149246_at	CG14453	-	-	-	-	1,683	3,5791
FBgn0037180	149247_s_at	CG14452	-	-	-	-	3,327	4,137
FBgn0037672	149545_at	CG12952	sage	transcription factor activity	1,8	4,2542	2,202	3,8284
FBgn0038009	149747_at	CG17738	-	-	-	-	3,76	5,6475
FBgn0039176	141731_at	CG13610	-	organic cation transporter activity	1,6	3,6383	-	-
FBgn0039441	150670_i_at / 150671_f_at	CG5476	-	-	-	-	3,617	4,875
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-	-	2,603	4,2357
FBgn0040736	151211_at	CG16844	IM3	-	2,6	4,2499	9,003	7,057
FBgn0040741	151217_at	CG14486	Uhg1	-	23,0	12,7921	17,87	9,2686

Downregulated genes:

FB code	Affy identifier	CG Numbers	Synonyms	Description / Molecular Function	Fold change st11	t-value st11	Fold change st12	t-value st12
FBgn0000166	142838_at	CG1034	bcd	morphogen activity / specific RNA polymerase II transcription factor activity / translation regulator activity	-1,8	-4,4284	-2,1	-3,6549
FBgn0000183	153897_at	CG6605	BicD	chromatin binding / dynein binding / NOT RNA binding	-1,5	-3,709	-	-
FBgn0001092	143175_at	CG8893	Gapdh2	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	-	-	-1,7	-3,6224
FBgn0001098	154218_at	CG5320	Gdh	glutamate dehydrogenase [NAD(P)+] activity	-1,7	-5,1886	-	-
FBgn0001224	153583_at	CG4463	Hsp23	actin binding	-2,3	-3,93	-	-
FBgn0002789	143271_at	CG4696	Mp20	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	-1,6	-3,0759
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-4,5	-7,1121
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-4,1	-4,9129
FBgn0003462	143358_at	CG11793	Sod	antioxidant activity / copper, zinc superoxide dismutase activity	-2,0	-5,5993	-	-
FBgn0003655	151660_at	CG3429	swa	dynein binding / RNA binding	-2,5	-3,6869	-	-
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-1,9	-4,3364	-	-
FBgn0004426	143465_f_at	CG9111	LysC	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-1,5	-3,0071	-	-
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,6	-6,3178	-	-
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,7	-8,008	-	-
FBgn0004606	141676_at	CG1322	zfh1	DNA binding / RNA polymerase II transcription factor activity	-1,6	-5,083	-1,6	-3,2994
FBgn0004834	154978_at	CG17998	Gprk2	G-protein coupled receptor kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity / regulator of G-protein signaling activity	-1,7	-3,111	-	-
FBgn0010019	152015_at	CG3972	Cyp4g1	electron transporter activity / oxidoreductase activity	-	-	-2,1	-3,3788
FBgn00102	153990_at	CG8938	GstS1	glutathione peroxidase activity / glutathione transferase activity	-1,6	-6,5369	-	-

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FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-	-	-5,1	-2,8246
FBgn0011761	154221_at	CG4193	dhd	thiol-disulfide exchange intermediate activity	-	-	-2,2	-5,723
FBgn0014032	151950_at	CG12117	Sptr	sepiapterin reductase activity	-1,7	-3,1071	-	-
FBgn0014141	141641_at	CG3937	cher	actin binding / structural constituent of cytoskeleton	-4,3	-8,575	-1,6	-3,6542
FBgn0015286	143790_at	CG2849	Rala	GTPase activity	-	-	-1,6	-3,3995
FBgn0015321	154399_at	CG8284	UbcD4	ligase activity / ubiquitin conjugating enzyme activity	-2,1	-6,1371	-	-
FBgn0015800	143846_at	CG6920	mus309	ATP-dependent DNA helicase activity / ATP-dependent DNA helicase activity / DNA binding / DNA helicase activity / DNA-dependent protein kinase activity / helicase activity / nucleic acid binding	-2,0	-2,9371	-	-
FBgn0024984	153908_at	CG3457	-	-	-1,6	-2,8049	-	-
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-3,1	-7,2971	-	-
FBgn0026077	153539_at	CG10287	Gasp	chitin binding / structural constituent of peritrophic membrane (sensu Insecta)	-	-	-1,9	-3,7994
FBgn0026150	153980_at	CG6291	ApepP	metallopeptidase activity	-1,6	-4,3423	-	-
FBgn0026415	144143_at	CG1780	Idgf4	imaginal disc growth factor activity	-1,7	-5,471	-	-
FBgn0027052	144169_at	CG5203	CHIP	ubiquitin-protein ligase activity	-1,9	-3,6669	-	-
FBgn0027547	152350_at	CG1927	-	-	-1,7	-4,9201	-	-
FBgn0027552	142257_at	CG10863	-	aldehyde reductase activity	-1,7	-4,6126	-	-
FBgn0027606	151864_at	CG12787	hoe1	cation transporter activity / L-tyrosine transporter activity / transporter activity	-2,0	-3,1918	-	-
FBgn0028905	144302_at	CG32972	-	-	-1,6	-6,2368	-	-
FBgn0029865	154623_at	CG15893	-	-	-1,8	-3,9968	-	-
FBgn0029899	151584_r_at	CG14438	-	-	-2,2	-3,3848	-	-
FBgn0030186	154400_at	CG2962	-	-	-	-	-1,9	-3,2645
FBgn0030472	153359_at	CG1633	Jafrac1	antioxidant activity / peroxidase activity / thioredoxin peroxidase activity	-	-	-1,6	-3,2793
FBgn0030557	154460_at	CG12047	mud	-	-1,9	-3,0921	-	-
FBgn0030803	153983_at	CG4880	-	-	-1,8	-6,4796	-	-
FBgn0031450	154536_at	CG2903	Hrs	protein binding	-1,6	-5,0312	-	-
FBgn0031737	151477_at	CG11142	-	structural constituent of peritrophic membrane (sensu Insecta)	-	-	-1,7	-3,5436
FBgn0031782	141393_at	CG9226	-	guanyl nucleotide binding	-1,6	-2,8655	-	-
FBgn0031936	145974_at	CG13794	-	-	-7,4	-5,7409	-5,6	-5,9005
FBgn0031990	153985_at	CG8552	-	phospholipase A1 activity	-1,8	-4,4156	-	-
FBgn0032014	154704_at	CG7840	-	-	-1,8	-4,9155	-	-
FBgn0032262	155142_at	CG7384	-	-	-1,8	-2,78	-	-
FBgn0032884	153490_at	CG9324	Pomp	-	-1,5	-2,7801	-	-
FBgn0032890	151641_at	CG31673	-	glyoxylate reductase (NADP) activity	-1,7	-3,2224	-	-
FBgn0032977	151479_at	CG6448	-	-	-	-	-1,7	-3,7154
FBgn0032985	146620_s_at / 146619_i_at	CG1742	Mgstl	glutathione transferase activity	-2,0	-5,9979	-2,3	-4,3739
FBgn0033082	154155_at	CG3273	sced	-	-1,9	-4,4074	-	-
FBgn0033144	141404_at	CG12172	Spn43Aa	serine-type endopeptidase inhibitor activity	-1,6	-4,5086	-	-
FBgn0033162	146732_at	CG1707	-	lactoylglutathione lyase activity	-1,6	-2,9196	-	-
FBgn0033205	141701_at	CG2064	-	oxidoreductase activity	-1,6	-4,7489	-1,5	-3,5809
FBgn0033236	154856_at	CG14764	-	-	-1,7	-4,0997	-	-
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-1,6	-3,0576	-	-
FBgn0033518	146946_s_at	CG11765	Prx2540-2	antioxidant activity / antioxidant activity / non-selenium glutathione peroxidase activity / peroxidase activity / peroxidase activity / peroxidase activity	-	-	-1,6	-5,8415
FBgn0033519	146947_at	CG11825	-	-	-2,1	-5,3767	-1,8	-4,6404
FBgn0033534	151592_at	CG12052	lola	RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity	-1,7	-3,2797	-	-
FBgn0033921	147193_at	CG8589	-	-	-2,1	-4,8515	-	-
FBgn0034079	154150_at	CG8430	Got1	-	-1,8	-5,4092	-1,6	-2,9654
FBgn0034171	153335_at	CG6657	veg	-	-1,5	-4,6969	-	-
FBgn0034201	147355_at	CG17290	-	-	-	-	-2,7	-2,9954
FBgn0034215	153128_at	CG4802	-	S-methyl-5-thioadenosine phosphorylase activity	-1,6	-5,5965	-	-
FBgn0034222	147364_at	CG14478	-	-	-1,6	-3,9422	-	-
FBgn0034250	141797_at	CG4924	icln	-	-1,6	-4,1044	-	-
FBgn0034345	155076_at	CG5174	-	-	-1,6	-4,3402	-	-
FBgn0035151	154989_at	CG17129	-	-	-1,8	-2,8859	-	-
FBgn0035190	147960_at	CG13913	-	-	-5,0	-10,4749	-2,0	-5,878
FBgn0035209	147970_at	CG13914	-	-	-1,8	-4,14	-	-
FBgn0035252	153945_at	CG7970	-	-	-1,6	-5,8803	-	-
FBgn0035420	152138_at	CG14967	-	-	-1,7	-2,7894	-	-
FBgn00354	154425_at	CG17746	-	protein serine/threonine phosphatase activity	-1,6	-3,1755	-	-

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FBgn0035471	141758_at	CG10849	Sc2	-	-1,6	-3,5032	-	-
FBgn0035513	148157_at	CG1259	-	structural constituent of larval cuticle (sensu Insecta)	-	-	-1,8	-3,4923
FBgn0035551	148182_at	CG7465	-	-	-2,5	-3,3454	-2,7	-9,9644
FBgn0035608	148223_at	CG10630	-	-	-1,9	-4,4117	-	-
FBgn0035640	148237_at	CG17498	mad2	-	-1,5	-4,6419	-	-
FBgn0035664	148253_at	CG6467	Jon65Aiv	chymotrypsin activity / serine-type endopeptidase activity	-	-	-1,6	-3,2976
FBgn0035735	148301_at	CG8640	-	structural constituent of cuticle (sensu Insecta)	-	-	-2,7	-7,112
FBgn0035811	154110_at	CG12262	-	acyl-CoA dehydrogenase activity	-1,5	-4,342	-	-
FBgn0035926	148422_at	CG5804	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,5	-3,3116
FBgn0035945	141294_at	CG5026	-	protein tyrosine/serine/threonine phosphatase activity	-1,6	-2,8947	-	-
FBgn0035999	148467_at	CG3552	-	-	-2,1	-3,3348	-2,4	-6,4687
FBgn0036030	148484_at	CG6767	-	nucleotide kinase activity / ribose-phosphate diphosphokinase activity	-1,7	-7,2292	-	-
FBgn0036182	153576_at	CG6084	-	aldehyde reductase activity	-	-	-1,8	-3,7437
FBgn0036272	148648_at	CG4300	-	-	-1,5	-2,8907	-	-
FBgn0036594	148867_at	CG13047	-	-	-	-	-1,8	-3,1834
FBgn0036600	148873_at	CG13043	-	-	-	-	-1,8	-3,0847
FBgn0036625	153654_at	CG4877	-	-	-1,5	-3,3666	-	-
FBgn0036689	154559_at	CG7730	-	-	-1,8	-4,0665	-	-
FBgn0036863	154347_at	CG9670	fal	-	-1,9	-3,1217	-	-
FBgn0036927	149085_at	CG7433	-	-	-1,8	-5,0221	-	-
FBgn0036980	154298_at	CG5701	RhoBTB	GTPase activity	-1,6	-3,4086	-	-
FBgn0037095	149186_at	CG7184	Mkrn1	-	-1,6	-2,8925	-	-
FBgn0037327	149333_at	CG2087	PEK	eukaryotic elongation factor-2 kinase activity / protein kinase activity / receptor signaling protein serine/threonine kinase activity / translation initiation factor activity	-1,6	-3,7676	-	-
FBgn0037353	155055_at	CG31549	-	oxidoreductase activity / structural constituent of cytoskeleton / structural molecule activity	-1,8	-3,7229	-	-
FBgn0037424	149389_at	CG1157	Osi15	-	-	-	-2,2	-6,4489
FBgn0037430	149395_at	CG15188	Osi20	-	-	-	-2,0	-3,5996
FBgn0037614	149520_at	CG8116	-	-	-1,7	-3,0106	-	-
FBgn0037696	141293_at	CG9362	-	glutathione transferase activity / maleylacetoacetate isomerase activity / transferase activity	-1,5	-3,3276	-	-
FBgn0037844	153457_at	CG4570	-	-	-1,5	-5,0737	-	-
FBgn0037930	142488_s_at	CG14715	-	FK506 binding / peptidyl-prolyl cis-trans isomerase activity / protein tyrosine phosphatase activity / receptor activity / transcription regulator activity	-1,6	-4,108	-1,7	-4,8033
FBgn0038013	153948_at	CG10038	-	-	-1,8	-4,2027	-	-
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	-	-	-2,9	-7,8376
FBgn0038256	155074_at	CG7530	-	-	-2,0	-3,5636	-	-
FBgn0038478	141516_at	CG5148	-	-	-1,5	-3,5919	-	-
FBgn0038771	151914_at	CG4390	-	hydrolase activity / hydrolase activity, acting on ester bonds	-1,7	-4,9434	-	-
FBgn0038772	154702_at	CG4973	-	-	-1,6	-3,1235	-	-
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-	-	-1,7	-4,6574
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-	-	-2,2	-3,135
FBgn0039251	150539_at	CG17462	-	nucleic acid binding / sigma DNA polymerase activity	-2,2	-3,8806	-	-
FBgn0039434	150663_r_at / 150662_i_at	CG5468	-	-	-	-	-1,6	-4,0992
FBgn0039436	150665_s_at	CG6478	-	-	-	-	-2,0	-7,282
FBgn0039658	154723_at	CG11956	SP1029	aminopeptidase activity / metallopeptidase activity / NOT aminoacylase activity / receptor activity	-1,5	-3,1247	-	-
FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-3,3	-4,6011
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-7,6	-5,2596
FBgn0039851	151691_at	CG12063	-	-	-	-	-2,3	-3,3317
FBgn0039888	150964_at	CG1487	krz	-	-1,6	-4,6981	-	-
FBgn0039930	150994_at	CG11077	-	-	-2,0	-3,1131	-	-
FBgn0040549	151036_f_at	CG5834	Hsp70Bbb	-	-1,5	-2,9472	-	-
FBgn0040874	151347_i_at	CG15600	-	-	-1,6	-3,4253	-	-
FBgn0040946	154370_at	CG14033	-	-	-1,7	-5,0616	-	-
FBgn0040981	151442_at	CG4482	mol	-	-1,9	-4,3917	-	-

Table S3. Genes responsive to Antp induction

Up-regulated genes:

FB code	Affy identifier	CG Numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000044	153531_at	CG10067	Act57B	glucuronosyltransferase activity / structural constituent of cytoskeleton	1,6	3,4052	-	-
FBgn0000055	151802_at	CG3481	Adh	-	2,1	7,288	-	-
FBgn0000116	152383_at	CG32031	Argk	-	1,9	3,1111	-	-
FBgn0000166	142838_at	CG1034	bcd	morphogen activity / specific RNA polymerase II transcription factor activity / translation regulator activity	-	-	1,6	3,1765
FBgn0000216	143088_at	CG3096	Brd	calmodulin inhibitor activity	-	-	3,0	11,0901
FBgn0000299	153378_at	CG4145	Cg25C	extracellular matrix structural constituent / structural molecule activity	1,6	2,8972	-	-

FBgn0000405	154177_at	CG3510	CycB	cyclin-dependent protein kinase regulator activity / kinase activator activity	-	-	1,7	4,3809
FBgn0000406	151932_at	CG13279	Cyt-b5-r	electron transporter activity / electron transporter activity / oxidoreductase activity	-	-	1,7	4,3044
FBgn0000448	143123_at	CG33183	Hr46	ligand-dependent nuclear receptor activity / transcription factor activity	2,0	3,0319	-	-
FBgn0001254	153951_at	CG1934	ImpE2	-	2,7	5,2104	-	-
FBgn0001256	141386_at	CG10717	ImpL1	-	2,5	4,8742	-	-
FBgn0002629	143251_at	CG6099	m4	-	-	-	2,3	6,1214
FBgn0002631	143252_at	CG6096	HLHm5	DNA binding / specific transcriptional repressor activity / transcription factor activity	-	-	3,4	8,3305
FBgn0002673	153947_at	CG4965	twe	protein tyrosine phosphatase activity / protein tyrosine/serine/threonine phosphatase activity	-	-	1,6	3,0993
FBgn0002772	143264_at	CG5596	Mlc1	ATPase activity, coupled / microfilament motor activity / NOT calcium ion binding	3,3	6,8014	-	-
FBgn0002773	143265_at	CG2184	Mlc2	ATPase activity, coupled / calcium ion binding / calmodulin binding / microfilament motor activity	3,0	6,3953	-	-
FBgn0002924	154464_at	CG7831	ncd	microtubule motor activity / minus-end-directed microtubule motor activity / structural constituent of cytoskeleton	-	-	1,6	4,4635
FBgn0003162	154812_at	CG9441	Pu	GTP cyclohydrolase I activity	1,8	3,5606	-	-
FBgn0004169	142555_at	CG7107	up	tropomyosin binding	3,0	4,7803	-	-
FBgn0005630	143561_at	CG12052	lola	RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity	-	-	1,6	3,8205
FBgn0005683	153746_at	CG5354	pie	-	-	-	1,8	2,9719
FBgn0010423	143622_at	CG9073	TpnC47D	calcium ion binding / calmodulin binding	2,9	4,4162	-	-
FBgn0010424	143623_at	CG7930	TpnC73F	calcium ion binding / calmodulin binding	2,9	3,5013	-	-
FBgn0010470	152208_at	CG9847	Fkbp13	FK506 binding / peptidyl-prolyl cis-trans isomerase activity	2,0	3,2205	-	-
FBgn0011653	141377_at	CG15002	mas	NOT peptidase activity / NOT serine-type endopeptidase activity	2,7	3,5384	-	-
FBgn0011706	143680_at	CG4319	rpr	-	2,3	4,3474	1,7	3,4519
FBgn0011823	141339_at	CG4799	Pen	protein carrier activity	-	-	1,5	3,0819
FBgn0012037	153728_at	CG8827	Ance	peptidyl-dipeptidase A activity / zinc ion binding	-	-	1,6	3,9146
FBgn0013772	142189_at	CG10248	Cyp6a8	electron transporter activity / oxidoreductase activity	-	-	2,0	3,9181
FBgn0014011	153313_at	CG8556	Rac2	GTPase activity	1,6	3,2321	-	-
FBgn0014032	151950_at	CG12117	Sptr	sepiapterin reductase activity	-	-	1,8	2,9455
FBgn0014469	154078_at	CG2060	Cyp4e2	electron transporter activity / oxidoreductase activity	2,3	5,4391	2,1	7,5308
FBgn0015391	154348_at	CG11397	glu	chromatin binding / DNA binding / nucleotide binding	-	-	1,6	3,3916
FBgn0015926	153153_at	CG6157	dah	-	-	-	1,8	4,6455
FBgn0016034	153959_at	CG11254	mael	-	-	-	1,8	3,2052
FBgn0016070	154516_at	CG5263	smg	mRNA 3'-UTR binding / protein binding / RNA binding / translation repressor activity / translation repressor activity, nucleic acid binding	-	-	1,9	5,1889
FBgn0020766	154396_at	CG13348	Aats-phe	phenylalanine-tRNA ligase activity	1,8	3,583	-	-
FBgn0021748	152922_at	CG6775	rg	protein kinase A binding	1,5	2,9172	-	-
FBgn0023023	153396_at	CG1411	-	-	2,1	3,8122	-	-
FBgn0023177	143976_at	CG32505	Pp4-19C	protein serine/threonine phosphatase activity	-	-	1,6	3,1145
FBgn0023513	143991_at	CG14803	-	-	-	-	1,5	3,13
FBgn0023520	152934_at	CG3857	-	-	5,2	8,7498	6,9	11,9386
FBgn0023528	153287_at	CG2924	-	transferase activity / ubiquitin conjugating enzyme activity	-	-	1,6	3,0625
FBgn0023546	144004_at	CG16902	Hr4	ligand-dependent nuclear receptor activity / molecular_function unknown / transcription regulator activity	2,7	3,7154	-	-
FBgn0024921	142581_at	CG7398	Trn	protein carrier activity / structural molecule activity	-	-	1,8	3,1014
FBgn0024984	153908_at	CG3457	-	-	-	-	1,6	3,1054
FBgn0025454	152900_at	CG8453	Cyp6g1	electron transporter activity / oxidoreductase activity	-	-	1,5	3,5612
FBgn0025885	153296_at	CG11143	Inos	-	-	-	2,1	4,5171
FBgn0026077	153539_at	CG10287	Gasp	chitin binding / structural constituent of peritrophic membrane (sensu Insecta)	3,1	5,0214	-	-
FBgn0026629	153839_at	CG6072	sra	receptor binding	-	-	1,8	3,7476
FBgn0026871	144162_at	CG14781	-	-	-	-	1,6	3,2601
FBgn0027521	154041_at	CG3679	-	-	-	-	1,8	2,9465
FBgn0027527	144185_at	CG1151	Osi6	-	2,2	5,2627	-	-
FBgn0027547	152350_at	CG1927	-	-	-	-	1,6	3,9127
FBgn0027570	152128_at	CG9761	Nep2	endothelin-converting enzyme activity / metalloendopeptidase activity / metallopeptidase activity	2,3	2,823	-	-
FBgn0027606	151864_at	CG12787	hoe1	cation transporter activity / L-tyrosine transporter activity / transporter activity	-	-	1,9	3,957
FBgn0027783	153548_at	CG10212	SMC2	chromatin binding / DNA binding	-	-	1,6	3,6068
FBgn0027889	153644_at	CG6386	ball	histone-threonine kinase activity / protein kinase activity / protein serine/threonine kinase activity	-	-	1,6	4,1681
FBgn0027890	153626_at	CG4584	dUTPase	-	-	-	1,5	3,2008
FBgn0027949	154597_at	CG10364	msb1l	molecular_function unknown	-	-	1,6	4,2379
FBgn0028420	154607_at	CG18783	Kr-h1	transcription factor activity	2,6	3,5812	-	-
FBgn0028469	154424_at	CG8062	-	monocarboxylic acid transporter activity	-	-	1,6	2,963
FBgn0029517	144338_at	CG13377	-	3-hydroxybutyrate dehydrogenase activity	2,1	3,6863	-	-
FBgn0029865	154623_at	CG15893	-	-	-	-	1,9	3,0276
FBgn0029876	151850_at	CG3960	-	actin binding / structural constituent of cytoskeleton	1,7	4,0152	-	-
FBgn0030079	144724_at	CG7267	-	-	1,9	3,1842	-	-
FBgn0030186	154400_at	CG2962	-	-	2,7	4,876	-	-
FBgn0030187	154819_at	CG2961	Ipod	-	2,3	5,253	-	-
FBgn0030336	154432_at	CG1578	-	-	-	-	1,6	2,9265
FBgn0030390	144937_at	CG15731	-	-	4,8	7,1126	-	-
FBgn0030436	144973_at	CG4396	fne	pre-mRNA splicing factor activity / RNA binding	2,2	3,7982	-	-
FBgn0030653	153970_at	CG7860	-	asparaginase activity	2,4	4,2801	-	-
FBgn0030803	153983_at	CG4880	-	-	-	-	1,9	3,8832
FBgn0030980	145340_at	CG7406	-	-	1,5	4,6851	-	-
FBgn0031097	151712_at / 142891_at	CG17052	-	structural constituent of peritrophic membrane (sensu Insecta)	2,3	4,1555	-	-
FBgn0031313	154669_at	CG5080	-	-	3,1	8,5617	-	-
FBgn0031434	145649_at	CG3227	insv	-	-	-	1,6	4,0844
FBgn0031629	145779_at	CG3244	-	-	2,7	2,872	-	-
FBgn0031878	145935_at	CG9188	sip2	-	-	-	1,9	4,6846
FBgn0031908	153932_at	CG5177	-	trehalose-phosphatase activity	2,9	3,4343	-	-
FBgn0031931	145970_at	CG7052	TepII	antibacterial humoral response (sensu Protostomia)	1,8	3,3383	-	-
FBgn0031964	145995_at	CG33121	-	serine-type endopeptidase inhibitor activity / serine-type endopeptidase inhibitor activity	47,4	8,3236	41,8	13,2306
FBgn0031970	152154_at	CG7227	-	scavenger receptor activity	2,0	3,2044	-	-
FBgn0032105	142833_at	CG4454	Borr	-	-	-	1,6	5,3035
FBgn0032262	155142_at	CG7384	-	-	-	-	1,8	3,7597
FBgn0032283	146182_at	CG7296	-	-	2,2	6,0908	-	-
FBgn0032400	142988_at	CG6770	-	-	3,0	4,3419	-	-
FBgn0032414	146274_at	CG17211	-	-	2,4	3,6556	-	-
FBgn0032489	146318_at	CG15480	-	-	-	-	1,8	3,5548
FBgn0032610	154661_at	CG31991	mdy	aspartate-tRNA ligase activity / diacylglycerol O-acyltransferase activity / RNA binding / sterol O-acyltransferase activity	1,6	2,9855	-	-
FBgn0032785	141465_at	CG10026	-	carrier activity / retinal binding / tocopherol binding	2,0	4,5707	-	-
FBgn0032803	146500_at	CG13082	-	-	2,9	5,5217	-	-
FBgn0032820	151797_at	CG31692	fbp	fructose-bisphosphatase activity	2,6	3,7275	-	-
FBgn0032897	146559_at	CG9336	-	-	4,0	7,3808	-	-
FBgn0032899	152155_at	CG9338	-	-	2,4	4,4162	-	-
FBgn0032962	146598_at	CG31612	-	nucleic acid binding	-	-	1,7	3,2455
FBgn0033033	146650_at	CG11066	scarface	NOT serine-type endopeptidase activity	1,5	3,5385	-	-
FBgn0033125	146708_at	CG12846	Tsp42Ed	-	2,8	4,0144	-	-
FBgn0033144	141404_at	CG12172	Spn43Aa	serine-type endopeptidase inhibitor activity	1,7	2,942	-	-
FBgn0033156	141608_at	CG12165	Incenp	-	-	-	1,7	3,3265
FBgn0033180	152970_at	CG11140	Aldh-III	aldehyde dehydrogenase activity	1,7	3,3525	-	-
FBgn0033242	146780_at	CG2916	Sep5	GTPase activity / structural constituent of cytoskeleton	-	-	1,9	3,3472
FBgn0033509	154737_at	CG12908	Ndg	structural molecule activity	1,6	3,8215	-	-
FBgn0033576	146978_s_at	CG30489	Cyp12d1-p	electron transporter activity / electron transporter activity / oxidoreductase activity / oxidoreductase activity	1,9	3,4056	1,5	2,9028
FBgn0033614	147010_at	CG13208	Obp47b	-	-	-	1,5	2,9576
FBgn0033631	142399_at	CG9027	-	-	-	-	3,1	4,9141
FBgn0033635	154391_at	CG7777	-	binding / carrier activity / water transporter activity	-	-	2,5	3,4188
FBgn0033757	147107_at	CG8811	muskelin	-	-	-	1,7	2,874
FBgn0033881	147175_at	CG13345	RacGAP50C	diacylglycerol binding / GTPase activator activity / Rho GTPase activator activity / signal transducer activity	-	-	1,6	6,101
FBgn0034016	147246_at	CG8171	dup	-	-	-	1,6	4,14
FBgn0034108	155081_at	CG3767	JhI-26	-	2,1	2,8323	-	-
FBgn0034145	147321_at	CG5065	-	oxidoreductase activity	3,2	5,0546	-	-
FBgn0034275	154837_at	CG5002	-	high affinity sulfate permease activity / transporter activity	-	-	1,5	2,9007
FBgn0034290	142954_at	CG5773	-	-	2,6	3,4785	2,1	3,4127
FBgn0034331	147433_at	CG15067	-	-	2,8	3,3706	-	-
FBgn0034343	142480_at	CG17534	GstE9	glutathione transferase activity	-	-	2,0	3,1661
FBgn0034398	147469_at	CG15098	-	-	-	-	1,8	4,5031

FBgn0034514	147549_at	CG13427	-	-	-	-	2,9	9,2434
FBgn0034736	147681_at	CG6018	-	carboxylesterase activity	1,7	3,1694	-	-
FBgn0035077	154985_at	CG9083	-	-	9,4	9,069	-	-
FBgn0035089	147903_at	CG9358	Phk-3	-	6,0	7,0235	-	-
FBgn0035103	142735_at	CG7047	-	-	1,6	3,3439	-	-
FBgn0035208	147969_at	CG9184	-	-	4,1	13,7014	-	-
FBgn0035252	153945_at	CG7970	-	-	-	-	1,5	3,0982
FBgn0035434	148103_at	CG10812	dro5	-	2,7	8,444	1,5	4,5917
FBgn0035547	148178_at	CG15022	-	-	1,5	4,5187	-	-
FBgn0035621	154354_at	CG10591	-	-	4,5	10,437	-	-
FBgn0035640	148237_at	CG17498	mad2	-	-	-	1,7	3,6125
FBgn0035717	152709_at	CG10078	Prat2	-	-	-	2,4	4,2194
FBgn0035735	148301_at	CG8640	-	structural constituent of cuticle (sensu Insecta)	2,5	4,2321	-	-
FBgn0035798	154595_at	CG7526	-	kinase activity / protein kinase activity / receptor activity / structural molecule activity / transmembrane receptor protein kinase activity / transmembrane receptor protein tyrosine kinase activity	1,6	3,2101	-	-
FBgn0035811	154110_at	CG12262	-	acyl-CoA dehydrogenase activity	-	-	1,7	4,2506
FBgn0035868	148390_at	CG7194	-	-	-	-	1,7	2,7814
FBgn0035881	151795_at	CG7176	Idh	-	2,3	6,3322	-	-
FBgn0036296	152168_at	CG10686	-	-	-	-	1,5	3,4641
FBgn0036352	148705_at	CG14110	-	-	7,9	9,3395	-	-
FBgn0036354	153557_at	CG10191	-	-	-	-	1,8	2,8556
FBgn0036381	148725_at	CG8745	-	-	1,9	3,7139	-	-
FBgn0036433	153786_at	CG9628	-	-	1,7	3,4094	-	-
FBgn0036458	148773_s_at	CG3396	Ocho	-	-	-	1,6	3,2335
FBgn0036572	154763_at	CG5165	Pgm	-	1,6	3,1431	-	-
FBgn0036616	148888_at	CG4893	-	molecular_function unknown	1,6	3,0594	-	-
FBgn0036689	154559_at	CG7730	-	-	-	-	1,9	3,1112
FBgn0036800	154409_at	CG6897	-	-	-	-	1,7	2,7988
FBgn0036824	152151_at	CG3902	-	short-branched-chain-acyl-CoA dehydrogenase activity	1,5	3,1798	-	-
FBgn0036901	141311_at	CG8756	LCBP1	-	2,7	5,7131	-	-
FBgn0036902	149070_at	CG32209	-	-	2,6	3,4492	-	-
FBgn0036980	154298_at	CG5701	RhoBTB	GTPase activity	-	-	1,8	3,5055
FBgn0037083	141375_at	CG5656	-	alkaline phosphatase activity / nucleotide phosphatase activity	3,5	6,846	-	-
FBgn0037128	149208_at	CG14572	-	-	2,5	5,2042	2,4	5,7206
FBgn0037211	142644_s_at	CG12414	nAcRalpha-80B	acetylcholine receptor activity / nicotinic acetylcholine-activated cation-selective channel activity	-	-	2,1	3,0786
FBgn0037224	153953_at	CG14639	-	-	3,9	5,2734	-	-
FBgn0037236	153298_at	CG9772	-	-	-	-	1,5	3,1441
FBgn0037414	149380_at	CG1153	Osi7	-	2,6	4,5321	-	-
FBgn0037424	149389_at	CG1157	Osi15	-	2,9	4,6513	-	-
FBgn0037447	154993_at	CG2330	-	extracellular matrix structural constituent / structural molecule activity	4,1	4,1761	-	-
FBgn0037624	155060_at	CG8223	-	-	-	-	1,5	3,0751
FBgn0037664	154972_at	CG8420	-	-	3,1	4,8138	-	-
FBgn0037844	153457_at	CG4570	-	-	-	-	1,8	4,1898
FBgn0037913	151826_at	CG6783	-	carrier activity / fatty acid binding / tricarboxylate carrier activity	2,0	4,6346	-	-
FBgn0037977	153367_at	CG3132	Ect3	beta-galactosidase activity	-	-	1,9	3,0429
FBgn0037992	155035_at	CG4702	-	-	2,9	4,2575	-	-
FBgn0038022	149757_at	CG4381	GstD3	glutathione transferase activity	1,8	2,9358	-	-
FBgn0038028	149763_at	CG10035	-	-	-	-	9,5	12,1424
FBgn0038151	149841_at	CG17044	yellow-e2	-	1,6	2,9186	-	-
FBgn0038256	155074_at	CG7530	-	-	-	-	1,8	4,3604
FBgn0038353	149968_at	CG5399	-	-	-	-	1,8	3,2691
FBgn0038610	153033_at	CG7675	-	oxidoreductase activity, acting on CH-OH group of donors	4,2	6,2163	-	-
FBgn0038613	142662_at	CG7678	-	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	2,5	3,3753
FBgn0038899	152554_at	CG31177	-	NOT membrane alanyl aminopeptidase activity / NOT membrane alanyl aminopeptidase activity / receptor activity / receptor activity	-	-	1,6	3,413
FBgn0038914	150335_at	CG17820	fit	-	2,2	4,0766	3,4	4,8255
FBgn0039021	151680_at	CG31139	-	-	-	-	1,8	4,0298
FBgn0039251	150539_at	CG17462	-	nucleic acid binding / sigma DNA polymerase activity	-	-	2,1	2,9762
FBgn0039444	150674_at	CG14243	-	-	2,6	3,7537	-	-
FBgn0039638	153804_at	CG11881	-	-	-	-	1,5	2,8603
FBgn0039728	154520_at	CG7896	-	receptor activity	1,9	2,9229	-	-
FBgn0040551	151038_at	CG11686	-	-	2,5	3,8999	-	-
FBgn0040718	151195_i_at / 151196_r_at	CG15353	-	-	2,6	5,0083	1,8	6,029
FBgn0040741	151217_at	CG14486	Uhg1	-	2-	8,383	16,4	10,7872
FBgn0040796	151266_at	CG13064	-	-	3,6	5,5516	-	-
FBgn0040808	151283_s_at	CG12487	BobA	-	-	-	2,3	5,3546
FBgn0040946	154370_at	CG14033	-	-	-	-	1,7	3,4912
FBgn0040981	151442_at	CG4482	mol	-	-	-	1,9	6,0578
FBgn0040984	151444_at	CG4440	-	-	-	-	1,9	5,4557

Downregulated genes:

FB code	Affy identifier	CG Numbers	Synonyms	Description / Molecular Function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000075	143066_at	CG10501	amd	aromatic-L-amino-acid decarboxylase activity / carboxy-lyase activity	-	-	-2,0	-3,1932
FBgn0000095	142814_at	CG1028	Antp	specific RNA polymerase II transcription factor activity	-	-	-1,9	-2,961
FBgn0000140	154866_at	CG6875	asp	microtubule binding / protein kinase activity	-1,8	-3,1329	-	-
FBgn0000163	143083_at	CG5055	baz	protein binding / protein kinase C binding / structural molecule activity	-1,9	-2,9753	-	-
FBgn0000165	151955_at	CG5779	Bc	-	-	-	-3,3	-8,1564
FBgn0000166	142838_at	CG1034	bcd	morphogen activity / specific RNA polymerase II transcription factor activity / translation regulator activity	-1,6	-3,0978	-	-
FBgn0000180	155099_at	CG4722	bib	binding / carrier activity / water channel activity	-1,9	-2,9311	-	-
FBgn0000261	143093_at	CG6871	Cat	antioxidant activity / catalase activity / heme binding / peroxidase activity	-	-	-1,5	-3,0994
FBgn0000337	143103_at	CG1555	cn	-	-2,6	-5,0028	-	-
FBgn0000411	143116_at	CG5893	D	DNA bending activity / transcription factor activity	-1,9	-3,7308	-	-
FBgn0000439	143122_at	CG2189	Dfd	RNA polymerase II transcription factor activity / transcription factor activity	-1,5	-2,8399	-	-
FBgn0000636	143157_at	CG5803	Fas3	-	-	-	-1,7	-3,9849
FBgn0001148	143183_at	CG3388	gsb	specific RNA polymerase II transcription factor activity	-1,6	-3,902	-	-
FBgn0001224	153583_at	CG4463	Hsp23	actin binding	-2,1	-2,8465	-	-
FBgn0001226	153307_at	CG4466	Hsp27	-	-	-	-2,0	-4,493
FBgn0001229	143196_at	CG4190	Hsp67Bc	-	-	-	-1,8	-5,0608
FBgn0001247	153407_at	CG5517	Ide	insulysin activity / zinc ion binding	-2,0	-3,046	-2,0	-3,2006
FBgn0002526	154252_at	CG10236	LanA	structural molecule activity	-	-	-1,7	-4,1368
FBgn0002561	143237_at	CG3839	l(1)sc	specific RNA polymerase II transcription factor activity / transcription factor activity	-2,0	-6,4033	-	-
FBgn0002578	143245_at	CG8342	m1	serine-type endopeptidase inhibitor activity	-	-	-1,7	-4,6109
FBgn0002629	143251_at	CG6099	m4	-	-1,6	-3,9084	-	-
FBgn0002631	143252_at	CG6096	HLHm5	DNA binding / specific transcriptional repressor activity / transcription factor activity	-1,8	-5,2045	-	-
FBgn0002632	143253_at	CG8354	m6	-	-	-	-1,5	-3,0828
FBgn0002734	143260_at	CG8328	HLHmdelta	DNA binding / specific transcriptional repressor activity / structural constituent of cuticle (sensu Insecta) / transcription factor activity	-1,6	-3,2187	-	-
FBgn0002789	143271_at	CG4696	Mp20	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	-1,8	-3,3277
FBgn0002868	143276_at	CG9470	MtnA	metal ion binding	-	-	-1,7	-4,6008
FBgn0003057	143296_at	CG10598	-	-	-	-	-2,3	-3,2484
FBgn0003082	143303_at	CG11205	phr	nucleic acid binding / nucleic acid binding	-2,4	-3,3605	-	-
FBgn0003189	142945_at	CG18572	r	aspartate carbamoyltransferase activity / carbamoyl-phosphate synthase (ammonia) activity / dihydroorotase activity / GDP binding / GTP binding / GTPase activity	-	-	-1,5	-2,8114
FBgn0003276	154098_at	CG3180	RpII140	DNA-directed RNA polymerase activity / nucleic acid binding	-1,5	-5,7452	-	-
FBgn0003326	143333_at	CG17579	sca	receptor binding / signal transducer activity	-2,0	-3,6049	-	-
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-18,3	-11,1439
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-14,9	-11,0599
FBgn0003411	143353_at	CG1641	sisA	protein heterodimerization activity / transcription factor activity	-1,6	-3,5437	-	-
FBgn0003430	151981_at	CG16738	slp1	RNA polymerase II transcription factor activity / transcription factor activity	-1,6	-2,8903	-	-
FBgn0003862	143384_at	CG8651	trx	contributes_to histone lysine N-methyltransferase activity (H3-K4 specific) / DNA binding / histone lysine N-methyltransferase activity (H3-K4 specific) / transcription regulator activity	-1,9	-4,5719	-2,0	-3,7689
FBgn0003867	143387_at	CG6705	tsl	torso binding	-	-	-1,6	-3,0733
FBgn0004009	143414_at	CG4889	wg	frizzled-2 binding / morphogen activity / Notch binding / receptor binding / signal transducer activity	-2,5	-3,0408	-	-
FBgn0004197	143438_at	CG6127	Ser	epidermal growth factor receptor binding / Notch binding / receptor binding / signal transducer activity	-	-	-1,5	-3,3234

FBgn0004243	154201_at	CG2092	scra	actin binding / microtubule binding / structural constituent of cytoskeleton	-1,6	-3,3318	-	-
FBgn0004378	153851_at	CG9191	Klp61F	microtubule motor activity / motor activity / plus-end-directed microtubule motor activity / structural constituent of cytoskeleton	-1,8	-4,8104	-	-
FBgn0004394	143457_at	CG12287	pdm2	DNA binding / specific RNA polymerase II transcription factor activity	-1,7	-3,6188	-	-
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-1,8	-3,6531	-	-
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,6	-3,9368	-1,7	-3,2124
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,7	-7,5174	-2,1	-2,878
FBgn0004777	143509_at	CG2342	Ccp84Ag	structural constituent of larval cuticle (sensu Insecta)	-	-	-1,6	-3,9788
FBgn0010228	143588_at	CG17921	HmgZ	chromatin binding / DNA binding / transcription regulator activity	-1,8	-4,1546	-2,1	-4,331
FBgn0010314	153961_at	CG3738	Cks30A	cyclin-dependent protein kinase activity / cyclin-dependent protein kinase regulator activity / protein serine/threonine kinase activity	-1,7	-3,2957	-	-
FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-	-	-5,6	-4,8985
FBgn0010383	143606_at	CG6816	Cyp18a1	electron transporter activity / oxidoreductase activity	-	-	-2,8	-4,2815
FBgn0010397	154588_at	CG10119	LamC	structural constituent of cytoskeleton	-	-	-2,2	-3,3692
FBgn0010425	143624_at	CG18681	epsilonTry	trypsin activity	-	-	-2,1	-3,0781
FBgn0011692	143677_at	CG1258	pav	microtubule motor activity / structural constituent of cytoskeleton	-2,0	-3,8184	-	-
FBgn0011704	142872_at	CG8975	RnrS	ribonucleoside-diphosphate reductase activity	-2,0	-5,3436	-	-
FBgn0011823	141339_at	CG4799	Pen	protein carrier activity	-1,6	-4,2439	-	-
FBgn0013263	142876_at	CG33261	Trl	DNA binding / RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity	-	-	-1,6	-3,3083
FBgn0013469	143712_at	CG12296	klu	transcription factor activity	-1,6	-3,4459	-	-
FBgn0014127	143751_at	CG10726	barr	-	-1,5	-3,0917	-	-
FBgn0015286	143790_at	CG2849	Rala	GTPase activity	-1,8	-2,8177	-1,7	-3,2916
FBgn0015766	155091_at	CG10596	Msr-110	-	-	-	-2,1	-3,1742
FBgn0015929	143860_at	CG1616	dpa	DNA binding / DNA helicase activity / DNA replication origin binding	-1,5	-3,4492	-	-
FBgn0016075	143868_at	CG16858	vkg	extracellular matrix structural constituent	-	-	-2,8	-3,613
FBgn0016724	151538_s_at	CG11064	RfaBp	fatty acid binding / heme binding / microtubule binding / retinoid binding / structural molecule activity	-	-	-1,5	-3,3124
FBgn0017551	152549_at	CG10800	Rca1	molecular_function unknown	-1,6	-3,3883	-	-
FBgn0019686	154411_at	CG10895	lok	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-2,0	-3,3316	-	-
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-	-	-2,0	-5,6063
FBgn0020637	143935_s_at	CG10534	Lcp65Ag2	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	-2,0	-4,3156	-1,8	-7,3651
FBgn0021748	152922_at	CG6775	rg	protein kinase A binding	-	-	-1,6	-2,7884
FBgn0022213	143953_at	CG13281	Cas	importin-alpha export receptor activity	-2,1	-3,131	-	-
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-2,8	-4,1375	-	-
FBgn0025618	141313_at	CG12311	Pomt2	dolichyl-phosphate-mannose-protein mannosyltransferase activity	-	-	-1,9	-2,8651
FBgn0026063	144112_at	CG17216	KP78b	protein kinase activity / protein kinase activity / protein serine/threonine kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-1,6	-2,9731	-	-
FBgn0026753	144156_at	CG6213	Vha13	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,5	-4,0642
FBgn0027500	142718_at	CG17286	-	-	-1,8	-3,9491	-	-
FBgn0027594	151918_s_at	CG2086	drpr	extracellular matrix structural constituent / receptor activity	-	-	-1,5	-3,1825
FBgn0027842	154586_at	CG12891	CPTI	acetyltransferase activity / carnitine O-palmitoyltransferase activity	-	-	-1,5	-3,055
FBgn0027948	152738_at	CG5000	msps	microtubule binding / protein binding / structural constituent of cytoskeleton	-1,6	-3,1346	-	-
FBgn0028504	151847_at	CG12182	-	-	-1,6	-2,8231	-	-
FBgn0028905	144302_at	CG32972	-	-	-	-	-1,9	-5,6682
FBgn0029531	144348_at	CG13362	-	-	-	-	-2,0	-5,4708
FBgn0029556	152743_at	CG14629	-	-	-	-	-1,6	-4,3489
FBgn0029576	151685_r_at	CG32813	-	-	-	-	-1,8	-2,9499
FBgn0029650	144430_at	CG3939	-	-	-	-	-1,6	-3,0217
FBgn0029804	144549_at	CG3097	-	carboxypeptidase A activity	-1,7	-2,8056	-	-
FBgn0029939	153744_at	CG9650	-	transcription regulator activity	-1,7	-4,1716	-	-
FBgn0030040	144700_at	CG15347	-	-	-	-	-2,9	-6,1432
FBgn0030183	152303_at	CG15309	-	molecular_function unknown	-	-	-2,0	-3,7397
FBgn0030241	153167_at	CG11207	feo	receptor binding	-1,5	-3,3173	-	-
FBgn0030242	141492_at	CG1655	sofe	receptor binding	-1,8	-2,8788	-	-
FBgn0030305	144879_at	CG1749	-	Mo-molybdopterin cofactor sulfurase activity	-	-	-1,5	-2,8029
FBgn0030436	144973_at	CG4396	fne	pre-mRNA splicing factor activity / RNA binding	-	-	-1,6	-4,4048
FBgn0030484	152675_at	CG1681	-	glutathione transferase activity	-	-	-1,6	-4,3081
FBgn0030557	154460_at	CG12047	mud	-	-2,0	-2,9859	-	-
FBgn0031221	145511_at	CG3164	-	ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	-1,7	-3,5694
FBgn0031316	141643_at	CG5105	Plap	phospholipase A2 activator activity	-1,8	-3,3179	-	-
FBgn0031433	145648_at	CG18559	Cyp309a2	electron transporter activity / electron transporter activity / oxidoreductase activity / oxidoreductase activity	-	-	-1,6	-3,4294
FBgn0031464	145670_at	CG3131	-	peroxidase activity / superoxide-generating NADPH oxidase activity	-	-	-1,6	-2,9805
FBgn0031538	142390_at	CG3246	-	-	-	-	-1,8	-4,8739
FBgn0031645	151989_at	CG3036	-	sodium:phosphate symporter activity	-1,7	-3,2152	-	-
FBgn0031653	145795_at	CG8871	Jon25Biii	elastase activity / serine-type peptidase activity	-	-	-2,9	-7,6679
FBgn0031706	145823_at	CG6634	nmr2	transcription factor activity	-	-	-1,6	-3,6882
FBgn0031832	145910_at	CG9596	-	nucleic acid binding / translation factor activity, nucleic acid binding / translation initiation factor activity	-1,6	-2,8177	-	-
FBgn0031897	152508_at	CG13784	-	-	-1,8	-3,3082	-	-
FBgn0031907	154061_at	CG5171	-	-	-	-	-1,9	-5,6136
FBgn0031936	145974_at	CG13794	-	-	-6,8	-9,5923	-5,6	-5,1974
FBgn0032036	141633_at	CG13384	-	-	-1,7	-3,1069	-	-
FBgn0032167	141658_at	CG5853	-	anion channel activity / ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	-2,0	-3,7223
FBgn0032284	146183_at	CG7294	-	-	-	-	-2,0	-3,788
FBgn0032287	151967_at	CG6415	-	-	-	-	-1,9	-3,2575
FBgn0032297	146190_at	CG17124	-	protein phosphatase inhibitor activity	-	-	-1,6	-2,8138
FBgn0032463	146305_at	CG3762	Vha68-2	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,5	-3,0764
FBgn0032726	146461_at	CG10621	-	-	-	-	-1,7	-4,5161
FBgn0032841	153191_at	CG10728	-	-	-1,7	-3,0963	-	-
FBgn0032844	146532_at	CG10746	fok	-	-	-	-1,8	-4,6414
FBgn0032885	146551_at	CG9326	-	guanylate kinase activity	-	-	-2,2	-3,6379
FBgn0033092	146687_at	CG9422	-	-	-	-	-1,5	-3,3972
FBgn0033205	141701_at	CG2064	-	oxidoreductase activity	-	-	-1,9	-4,8135
FBgn0033275	146794_at	CG14756	-	-	-2,5	-5,4302	-22,1	-19,7947
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-3,3	-7,1795	-6,5	-11,9779
FBgn0033446	152817_at	CG1648	-	-	-	-	-1,7	-3,8193
FBgn0033458	146908_at	CG18446	-	-	-1,7	-3,1467	-	-
FBgn0033529	153040_at	CG17765	-	calcium ion binding / calmodulin binding	-	-	-1,9	-5,4071
FBgn0033575	146977_at	CG33473	luna	-	-	-	-1,6	-2,955
FBgn0033604	147002_at	CG9070	-	-	-3,2	-3,7504	-1,9	-5,064
FBgn0033613	147009_at	CG13211	-	-	-	-	-2,1	-3,6262
FBgn0033624	152681_at	CG12384	-	enzyme activator activity / enzyme regulator activity	-	-	-1,6	-3,3684
FBgn0033634	147022_at	CG7763	-	-	-1,6	-3,0467	-1,9	-4,0521
FBgn0033643	147029_s_at	CG30035	-	fructose transporter activity / glucose transporter activity / glucose transporter activity	-2,0	-4,2071	-1,9	-3,491
FBgn0033721	147084_at	CG13159	-	-	-	-	-4,2	-10,1433
FBgn0033779	142416_at	CG3814	-	N-methyl-D-aspartate selective glutamate receptor activity	-	-	-2,1	-4,1871
FBgn0033913	151760_at / 143046_at	CG8468	-	monocarboxylate porter activity	-	-	-1,7	-3,3537
FBgn0034117	153785_at	CG7997	-	-	-	-	-1,7	-3,7933
FBgn0034212	142742_at	CG30101	-	-	-	-	-1,5	-3,2239
FBgn0034222	147364_at	CG14478	-	-	-1,7	-2,9621	-	-
FBgn0034294	147409_at	CG5765	-	-	-	-	-2,5	-4,1101
FBgn0034395	155162_at	CG15081	l(2)03709	-	-	-	-1,5	-2,9233
FBgn0034404	142196_at	CG15101	Jheh1	-	-	-	-2,4	-4,7715
FBgn0034438	147493_at	CG9416	-	-	-	-	-2,2	-4,8095
FBgn0034468	147514_at	CG11797	Obp56a	-	-	-	-3,3	-9,9265
FBgn0034501	141541_at	CG13868	-	-	-1,6	-3,0652	-	-
FBgn0034611	147615_at	CG10069	-	glycerol-3-phosphate transporter activity	-1,7	-4,132	-	-
FBgn0034613	151929_at	CG30390	-	-	-	-	-1,9	-2,8624
FBgn0034698	141793_at	CG6698	NtR	-	-	-	-2,5	-4,1793
FBgn0034702	152831_at	CG6741	a	-	-	-	-1,6	-3,7544
FBgn0034764	147701_at	CG9952	ppa	-	-2,5	-3,6951	-	-
FBgn0034798	141705_at	CG3820	Nup214	transporter activity	-2,0	-3,3053	-	-
FBgn0035083	142434_at	CG2803	Tina-1	structural constituent of muscle	-	-	-1,5	-3,6401
FBgn0035091	152752_at	CG3829	-	scavenger receptor activity	-	-	-1,6	-4,2392
FBgn0035147	154410_at	CG12030	-	UDP-glucose 4-epimerase activity	-	-	-1,7	-2,9555
FBgn0035181	153685_at	CG9205	-	-	-1,7	-3,0865	-	-

FBgn0035190	147960_at	CG13913	-	-	-3,2	-6,2912	-2,5	-7,3315
FBgn0035499	153092_at	CG14996	Chd64	actin binding / structural constituent of cytoskeleton	-	-	-1,9	-3,3101
FBgn0035551	148182_at	CG7465	-	-	-3,8	-5,4158	-5,1	-8,4003
FBgn0035583	148206_at	CG13704	-	-	-	-	-2,9	-2,9218
FBgn0035625	148232_at	CG5249	Blimp-1	transcription regulator activity	-	-	-1,8	-3,1713
FBgn0035664	148253_at	CG6467	Jon65Aiv	chymotrypsin activity / serine-type endopeptidase activity	-	-	-1,7	-3,6127
FBgn0035735	148301_at	CG8640	-	structural constituent of cuticle (sensu Insecta)	-	-	-2,4	-6,6415
FBgn0035926	148422_at	CG5804	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,0	-2,9148
FBgn0035968	148450_at	CG4484	-	sucrose:hydrogen symporter activity	-1,7	-3,0212	-	-
FBgn0035999	148467_at	CG3552	-	-	-2,2	-3,9158	-2,2	-6,0092
FBgn0036121	148546_at	CG6310	-	-	-	-	-2,3	-5,0054
FBgn0036147	154810_at	CG6199	-	procollagen-lysine 5-dioxygenase activity	-	-	-1,8	-4,3154
FBgn0036290	148662_at	CG10638	-	aldehyde reductase activity	-	-	-1,5	-3,1129
FBgn0036355	148706_at	CG32120	sens	RNA polymerase II transcription factor activity / transcription factor activity	-1,7	-3,4068	-	-
FBgn0036501	148804_at	CG7272	-	-	-	-	-1,8	-5,3433
FBgn0036594	148867_at	CG13047	-	-	-	-	-1,9	-2,938
FBgn0036600	148873_at	CG13043	-	-	-	-	-4,4	-6,634
FBgn0036622	142407_at	CG4753	-	1-acylglycerol-3-phosphate O-acyltransferase activity	-	-	-1,6	-2,8923
FBgn0036640	141733_at	CG4118	nxf2	-	-1,6	-3,0814	-	-
FBgn0036752	148973_at	CG5992	Adgf-A	adenosine deaminase activity / growth factor activity	-	-	-1,8	-3,3376
FBgn0036787	148995_at	CG4306	-	-	-	-	-3,2	-5,8082
FBgn0036815	153212_at	CG6874	l(3)neo26	-	-1,7	-2,9294	-	-
FBgn0036875	149052_at	CG9449	-	acid phosphatase activity	-	-	-3,2	-8,0341
FBgn0036901	141311_at	CG8756	LCBP1	-	-	-	-1,6	-2,7764
FBgn0036945	141349_at	CG6981	-	-	-	-	-1,9	-3,9313
FBgn0036983	149123_at	CG5408	trbl	NOT protein serine/threonine kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-1,5	-2,912	-	-
FBgn0037177	149244_at	CG14454	-	molecular_function unknown	-1,5	-3,5264	-1,7	-3,4797
FBgn0037271	149291_at	CG31530	-	polyspecific organic cation transporter activity	-	-	-1,8	-3,6537
FBgn0037424	149389_at	CG1157	Osi15	-	-	-	-1,6	-2,9966
FBgn0037549	154657_at	CG7878	-	ATP-dependent RNA helicase activity / helicase activity / nucleic acid binding	-2,0	-4,2984	-	-
FBgn0037598	149508_at	CG31258	-	-	-1,6	-2,8761	-	-
FBgn0037723	152178_at	CG8327	SpdS	spermidine synthase activity	-	-	-1,7	-3,47
FBgn0037779	149607_at	CG12811	-	-	-	-	-1,6	-2,7938
FBgn0038037	153031_at	CG11466	Cyp9f2	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-2,3	-3,3326
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	-2,1	-3,4367	-2,5	-7,3745
FBgn0038115	152571_at	CG7966	-	selenium binding	-	-	-1,9	-3,6924
FBgn0038222	151632_i_at	CG3307	pr-set7	-	-1,6	-3,3147	-	-
FBgn0038409	154554_at	CG6815	bor	-	-	-	-1,9	-3,0105
FBgn0038413	141589_at	CG6725	Sulf1	N-acetylglucosamine-6-sulfatase activity	-1,8	-3,5442	-	-
FBgn0038433	154549_at	CG14896	-	-	-1,8	-3,4898	-	-
FBgn0038563	152336_at	CG7780	DNaseII	-	-3,8	-6,5622	-1,8	-3,7394
FBgn0038647	150161_at	CG14302	-	-	-	-	-1,7	-3,4233
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-	-	-1,8	-4,612
FBgn0039008	150394_at	CG6972	-	-	-	-	-1,5	-2,9846
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-	-	-4,3	-5,0213
FBgn0039114	152325_at	CG10374	Lsd-1	-	-	-	-2,1	-3,8302
FBgn0039125	154986_at	CG5857	-	-	-1,6	-3,3772	-	-
FBgn0039227	154823_at	CG11375	baf180	transcription factor activity	-1,6	-3,7727	-	-
FBgn0039265	142237_at	CG11790	-	-	-	-	-1,7	-3,5835
FBgn0039434	150663_r_at / 150662_i_at	CG5468	-	-	-	-	-1,5	-3,5029
FBgn0039469	150698_at	CG14254	-	-	-	-	-1,6	-2,8255
FBgn0039539	154473_at	CG12880	-	-	-	-	-3,8	-3,252
FBgn0039566	154447_at	CG4849	-	pre-mRNA splicing factor activity / translation elongation factor activity / translation elongation factor activity	-1,6	-3,6016	-	-
FBgn0039567	150762_at	CG4869	betaTub97EF	structural constituent of cytoskeleton / tubulin binding	-	-	-1,9	-3,0844
FBgn0039586	142182_s_at	CG33103	Ppn	metallopeptidase activity / serine-type endopeptidase inhibitor activity	-	-	-1,9	-5,1982
FBgn0039643	153221_at	CG11886	Slbp	-	-1,8	-4,3623	-	-
FBgn0039682	150834_at	CG7584	Obp99c	-	-	-	-2,4	-6,47
FBgn0039686	150838_at	CG15506	-	-	-	-	-1,9	-4,457
FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-6,5	-6,0572
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-7,9	-7,9961
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-	-	-2,0	-3,6785
FBgn0039825	152434_at	CG31004	-	-	-	-	-2,8	-3,3203
FBgn0039873	150955_at	CG2191	-	cation transporter activity / sodium-dependent multivitamin transporter activity	-2,2	-4,2151	-	-
FBgn0040609	151094_at	CG3348	-	-	-	-	-2,9	-5,3924
FBgn0040764	151237_at	CG13230	-	-	-	-	-1,7	-3,0555
FBgn0040984	151444_at	CG4440	-	-	-1,6	-4,8492	-	-

Table S4. Genes responsive to Ubx induction

Up-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000406	151932_at	CG13279	Cyt-b5-r	electron transporter activity / electron transporter activity / oxidoreductase activity	2,2	4,9841	2,7	4,5879
FBgn0000566	154085_at	CG5345	Eip55E	cystathionine gamma-lyase activity	-	-	1,6	3,8921
FBgn0001228	142837_at	CG32041	Hsp22	-	1,7	3,0412	1,9	3,0387
FBgn0001254	153951_at	CG1934	ImpE2	-	1,7	3,0833	1,7	2,9952
FBgn0002570	143242_at	CG8696	LvpH	alpha-glucosidase activity	-	-	2,9	4,1184
FBgn0002772	143264_at	CG5596	Mlc1	ATPase activity, coupled / microfilament motor activity / NOT calcium ion binding	2,1	2,904	-	-
FBgn0002773	143265_at	CG2184	Mlc2	ATPase activity, coupled / calcium ion binding / calmodulin binding / microfilament motor activity	2,0	4,4881	-	-
FBgn0003430	151981_at	CG16738	slp1	RNA polymerase II transcription factor activity / transcription factor activity	-	-	2,1	4,6287
FBgn0003888	143391_i_at	CG3401	betaTub60D	GTP binding / structural constituent of cytoskeleton / tubulin binding	1,7	3,6205	-	-
FBgn0003944	143400_at	CG10388	Ubx	DNA binding / specific RNA polymerase II transcription factor activity / transcription factor activity	64,6	24,871	60,5	22,3302
FBgn0003996	143410_at	CG2759	w	anion channel activity / ATPase activity, coupled to transmembrane movement of substances / eye pigment precursor transporter activity / transmembrane receptor activity	2,0	3,7593	1,7	2,8481
FBgn0004898	143532_at	CG11922	fd96Cb	transcription factor activity	1,6	3,5172	-	-
FBgn0010423	143622_at	CG9073	TpnC47D	calcium ion binding / calmodulin binding	1,6	3,1354	-	-
FBgn0010470	152208_at	CG9847	Fkbp13	FK506 binding / peptidyl-prolyl cis-trans isomerase activity	1,7	3,7477	-	-
FBgn0011706	143680_at	CG4319	rpr	-	2,7	4,5438	-	-
FBgn0012034	153769_at	CG9390	AcCoAS	-	-	-	2,0	2,7983
FBgn0013953	142492_at	CG7005	Esp	sulfate porter activity	2,1	6,6478	2,1	4,6552
FBgn0014469	154078_at	CG2060	Cyp4e2	electron transporter activity / oxidoreductase activity	2,1	5,8635	1,7	3,0505
FBgn0016123	143872_at	CG1462	Aph-4	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	5,6	5,3963
FBgn0020637	143935_s_at	CG10534	Lcp65Ag2	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	2,3	6,6493	-	-
FBgn0022342	153679_at	CG4844	-	-	2,3	6,8089	1,8	4,4663
FBgn0023548	142987_at	CG33548	msta	molecular_function unknown	-	-	3,3	3,467
FBgn0024211	152375_at	CG3359	mfas	-	-	-	1,5	3,1181
FBgn0025627	154569_at	CG4194	-	-	-	-	2,1	4,8811
FBgn0029744	141469_at	CG11706	-	-	3,7	5,0701	6,6	5,2997
FBgn0030186	154400_at	CG2962	-	-	1,9	3,0225	-	-
FBgn0031097	151712_at / 142891_at	CG17052	-	structural constituent of peritrophic membrane (sensu Insecta)	2,2	4,1933	2,0	4,1654
FBgn0031530	145708_at	CG3254	pgant2	polypeptide N-acetylgalactosaminyltransferase activity	-	-	2,6	3,0291
FBgn0031913	145956_at	CG5958	-	carrier activity / retinal binding	1,5	2,9624	-	-
FBgn0032283	146182_at	CG7296	-	-	1,9	5,4856	1,9	4,2686
FBgn0033125	146708_at	CG12846	Tsp42Ed	-	5,0	7,5503	2,0	3,3204
FBgn0033234	153231_at	CG8791	-	high affinity inorganic phosphate:sodium symporter activity	3,1	2,9857	3,6	3,8616
FBgn0033518	146946_s_at	CG11765	Prx2540-2	antioxidant activity / antioxidant activity / non-selenium glutathione peroxidase activity / peroxidase activity / peroxidase activity / peroxidase activity	-	-	2,4	7,1914
FBgn0033910	141381_at	CG30069	-	-	-	-	2,6	4,3149
FBgn0033942	147207_at	CG10112	-	-	1,6	3,1487	-	-
FBgn0034227	147367_at	CG18431	-	-	2,0	3,2932	-	-
FBgn0034290	142954_at	CG5773	-	-	3,9	5,9188	3,5	5,6398
FBgn0034420	153286_at	CG10737	-	diacylglycerol binding	-	-	1,7	3,0604
FBgn0034437	147492_at	CG10051	-	-	-	-	5,0	4,2898
FBgn0034468	147514_at	CG11797	Obp56a	-	1,8	3,7645	-	-

FBgn0034514	147549_at	CG13427	-	-	2,1	5,0101	3,3	8,7284
FBgn0034985	152943_at	CG3328	-	-	4,3	4,9237	-	-
FBgn0035089	147903_at	CG9358	Phk-3	-	3,0	4,0764	-	-
FBgn0035131	147924_at	CG17084	mthl9	G-protein coupled receptor activity	-	-	2,7	3,244
FBgn0035189	152102_at	CG9119	-	-	2,0	4,3679	-	-
FBgn0035208	147969_at	CG9184	-	-	2,7	7,0256	1,5	3,8775
FBgn0035621	154354_at	CG10591	-	-	2,9	9,3854	2,2	6,3627
FBgn0035735	148301_at	CG8640	-	structural constituent of cuticle (sensu Insecta)	4,1	7,0762	-	-
FBgn0035880	152139_at	CG17352	-	-	1,9	5,5497	-	-
FBgn0035881	151795_at	CG7176	Idh	-	1,8	4,5525	2,1	5,4674
FBgn0035961	153070_at	CG4821	Tequila	pancreatic elastase activity / serine-type endopeptidase activity / trypsin activity	2,0	2,9974	2,3	6,5119
FBgn0036352	148705_at	CG14110	-	-	4,8	6,8724	3,2	8,3513
FBgn0036786	148994_at	CG13701	skl	-	2,1	3,6058	1,7	5,7467
FBgn0036898	151832_at	CG8782	Oat	ornithine-oxo-acid transaminase activity	-	-	1,8	2,8988
FBgn0037083	141375_at	CG5656	-	alkaline phosphatase activity / nucleotide phosphatase activity	2,2	3,6549	2,3	5,0533
FBgn0037356	152793_at	CG12170	-	3-oxoacyl-[acyl-carrier protein] synthase activity	-	-	1,9	3,1459
FBgn0037447	154993_at	CG2330	-	extracellular matrix structural constituent / structural molecule activity	-	-	1,6	2,9441
FBgn0037913	151826_at	CG6783	-	carrier activity / fatty acid binding / tricarboxylate carrier activity	1,8	3,0129	2,1	4,7814
FBgn0038366	149976_at	CG4576	-	-	-	-	2,0	3,1122
FBgn0038610	153033_at	CG7675	-	oxidoreductase activity, acting on CH-OH group of donors	2,7	4,0305	2,1	5,3415
FBgn0038681	150181_at	CG6042	Cyp12a4	electron transporter activity / oxidoreductase activity	2,1	4,3231	5,8	7,4163
FBgn0038733	152819_at	CG11407	-	ligase activity / long-chain fatty acid transporter activity	14,3	5,6995	6,1	5,8678
FBgn0038837	150283_at	CG3822	-	kainate selective glutamate receptor activity / ligand-gated ion channel activity	1,6	3,5237	-	-
FBgn0039434	150663_r_at / 150662_i_at	CG5468	-	-	2,2	4,6921	-	-
FBgn0039436	150665_s_at	CG6478	-	-	3,2	5,9211	-	-
FBgn0039437	154960_at	CG6447	-	-	1,8	3,1365	-	-
FBgn0039441	150670_i_at / 150671_f_at	CG5476	-	-	2,5	5,8994	-	-
FBgn0039444	150674_at	CG14243	-	-	2,1	2,8382	-	-
FBgn0039593	150780_at	CG9989	-	-	-	-	2,9	3,5719
FBgn0039690	154922_at	CG1969	-	-	2,1	2,7931	2,3	5,4819
FBgn0039795	141338_at	CG1342	-	serine-type endopeptidase inhibitor activity	-	-	3,9	7,5769
FBgn0040626	151112_s_at	CG15552	Sox100B	-	2,7	3,8143	4,1	3,2292
FBgn0040718	151195_i_at / 151196_r_at	CG15353	-	-	2,2	4,1762	1,7	9,9436
FBgn0040741	151217_at	CG14486	Uhg1	-	17,1	7,5556	15,1	5,784
FBgn0040796	151266_at	CG13064	-	-	2,2	3,6139	2,2	4,5389
FBgn0040843	151316_at	CG15213	-	-	2,1	4,3219	-	-

Down-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000165	151955_at	CG5779	Bc	-	-	-	-3,4	-4,4063
FBgn0000216	143088_at	CG3096	Brd	calmodulin inhibitor activity	-	-	-2,3	-4,2044
FBgn0000299	153378_at	CG4145	Cg25C	extracellular matrix structural constituent / structural molecule activity	-	-	-2,6	-6,3557
FBgn0000337	143103_at	CG1555	cn	-	-2,1	-4,4138	-	-
FBgn0000439	143122_at	CG2189	Dfd	RNA polymerase II transcription factor activity / transcription factor activity	-1,6	-3,7375	-	-
FBgn0000719	141493_at	CG9559	fog	-	-1,7	-3,0244	-	-
FBgn0001224	153583_at	CG4463	Hsp23	actin binding	-2,6	-4,1392	-	-
FBgn0001235	143199_at	CG17117	hth	specific RNA polymerase II transcription factor activity / transcription factor activity	-1,9	-5,1637	-1,5	-3,1856
FBgn0002561	143237_at	CG3839	l(1)sc	specific RNA polymerase II transcription factor activity / transcription factor activity	-1,6	-3,6828	-	-
FBgn0002578	143245_at	CG8342	m1	serine-type endopeptidase inhibitor activity	-3,3	-4,5634	-3,8	-7,8666
FBgn0002849	153515_at	CG1897	Dr	-	-1,5	-3,8132	-	-
FBgn0002868	143276_at	CG9470	MtnA	metal ion binding	-	-	-1,6	-3,6373
FBgn0003057	143296_at	CG10598	-	-	-	-	-2,5	-4,0513
FBgn0003067	143299_at	CG17725	Pepck	phosphoenolpyruvate carboxykinase (GTP) activity	-	-	-1,9	-5,0216
FBgn0003082	143303_at	CG11205	phr	nucleic acid binding / nucleic acid binding	-1,8	-2,9564	-	-
FBgn0003089	143305_at	CG9614	pip	heparin-sulfate 2-sulfotransferase activity / sulfotransferase activity	-	-	-1,9	-2,9694
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-	-	-25,8	-13,9133
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-1,6	-2,9701	-20,3	-13,5605
FBgn0003410	153438_at	CG9949	sina	ligase activity / protein binding	-1,7	-3,3617	-	-
FBgn0003411	143353_at	CG1641	sisA	protein heterodimerization activity / transcription factor activity	-1,8	-3,7862	-2,9	-5,304
FBgn0003862	143384_at	CG8651	trx	contributes_to histone lysine N-methyltransferase activity (H3-K4 specific) / DNA binding / histone lysine N-methyltransferase activity (H3-K4 specific) / transcription regulator activity	-1,8	-4,5967	-1,7	-4,2731
FBgn0004237	152021_at	CG12749	Hrb87F	RNA binding	-1,7	-3,769	-1,8	-2,8324
FBgn0004394	143457_at	CG12287	pdm2	DNA binding / specific RNA polymerase II transcription factor activity	-1,8	-3,8832	-	-
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-1,9	-4,8029	-1,5	-3,1279
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,7	-4,1387	-1,7	-5,0413
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,3	-4,9848	-	-
FBgn0004606	141676_at	CG1322	zfh1	DNA binding / RNA polymerase II transcription factor activity	-2,0	-3,1383	-1,9	-3,2193
FBgn0010105	143583_at	CG17943	comm	protein binding	-	-	-1,6	-3,0223
FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-	-	-5,5	-3,2476
FBgn0010387	143608_at	CG8627	Dbi	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,6	-3,4967
FBgn0010425	143624_at	CG18681	epsilonTry	trypsin activity	-	-	-2,3	-3,9854
FBgn0011202	143636_at	CG1768	dia	actin binding / structural constituent of cytoskeleton	-2,8	-3,276	-2,2	-3,1325
FBgn0011704	142872_at	CG8975	RnrS	ribonucleoside-diphosphate reductase activity	-	-	-1,5	-2,7863
FBgn0011828	152747_at	CG12002	Pxn	peroxidase activity	-	-	-2,5	-2,8741
FBgn0014141	141641_at	CG3937	cher	actin binding / structural constituent of cytoskeleton	-3,4	-7,7367	-	-
FBgn0014151	143753_at	CG5403	retn	DNA binding / transcription factor activity / transcriptional activator activity / transcriptional repressor activity	-1,6	-3,3945	-	-
FBgn0014343	143756_at	CG10601	mirr	protein binding / transcription factor activity / transcriptional activator activity	-2,0	-2,9534	-	-
FBgn0015321	154399_at	CG8284	UbcD4	ligase activity / ubiquitin conjugating enzyme activity	-1,5	-3,3015	-	-
FBgn0015550	143817_at	CG7659	tap	specific RNA polymerase II transcription factor activity	-1,7	-3,0738	-	-
FBgn0016075	143868_at	CG16858	vkg	extracellular matrix structural constituent	-	-	-3,5	-4,3661
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-2,0	-3,3177	-3,8	-7,1892
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-3,3	-4,3927	-	-
FBgn0027594	151918_s_at	CG2086	drpr	extracellular matrix structural constituent / receptor activity	-1,6	-4,3668	-	-
FBgn0028491	151495_at	CG2930	-	proton-dependent oligopeptide transporter activity	-2,8	-6,021	-	-
FBgn0028905	144302_at	CG32972	-	-	-2,6	-6,8388	-2,5	-7,0078
FBgn0029531	144348_at	CG13362	-	-	-	-	-2,1	-4,0554
FBgn0029804	144549_at	CG3097	-	carboxypeptidase A activity	-1,7	-3,2955	-	-
FBgn0029918	151557_i_at	CG33692	-	-	-2,3	-2,944	-	-
FBgn0030040	144700_at	CG15347	-	-	-	-	-3,2	-4,4889
FBgn0031653	145795_at	CG8871	Jon25Biii	elastase activity / serine-type peptidase activity	-	-	-3,0	-6,9789
FBgn0031839	145915_at	CG31634	Oatp26F	organic anion transporter activity	-	-	-1,7	-4,0354
FBgn0031936	145974_at	CG13794	-	-	-6,1	-7,0403	-	-
FBgn0031937	145975_at	CG13795	-	amino acid transporter activity / transporter activity	-2,3	-3,3437	-2,3	-3,9004
FBgn0032036	141633_at	CG13384	-	-	-1,9	-2,9209	-	-
FBgn0032082	146056_at	CG18088	-	-	-	-	-2,4	-4,1127
FBgn0032167	141658_at	CG5853	-	anion channel activity / ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	-2,7	-4,0902
FBgn0032192	146129_at	CG5731	-	-	-	-	-3,0	-3,8023
FBgn0032263	141619_at	CG7400	Fatp	long-chain fatty acid transporter activity	-1,5	-3,4487	-	-
FBgn0032282	146181_at	CG7299	-	-	-	-	-2,1	-3,5675
FBgn0032295	155152_at	CG12299	-	transcription regulator activity	-1,5	-3,4525	-	-
FBgn0032726	146461_at	CG10621	-	-	-1,6	-3,342	-1,9	-3,4576
FBgn0032803	146500_at	CG13082	-	-	-	-	-2,0	-3,7589
FBgn0032844	146532_at	CG10746	fok	-	-1,9	-3,6136	-2,0	-4,4548
FBgn0032899	152155_at	CG9338	-	-	-	-	-3,1	-4,0211
FBgn0032904	141458_at	CG9342	-	carrier activity / triglyceride binding	-2,0	-4,5311	-2,3	-3,0143
FBgn0033035	146652_at	CG17337	-	-	-	-	-1,7	-3,3994
FBgn0033068	146674_at	CG11212	Ptr	receptor activity	-1,5	-2,8605	-	-
FBgn0033144	141404_at	CG12172	Spn43Aa	serine-type endopeptidase inhibitor activity	-1,7	-3,6977	-1,7	-3,7247
FBgn0033205	141701_at	CG2064	-	oxidoreductase activity	-	-	-1,7	-3,0845
FBgn0033275	146794_at	CG14756	-	-	-4,4	-5,0137	-60,2	-17,2133
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-2,1	-4,7884	-5,0	-8,0326

FBgn0033604	147002_at	CG9070	-	-	-	-	-2,5	-4,642
FBgn0033613	147009_at	CG13211	-	-	-	-	-1,9	-3,1809
FBgn0033634	147022_at	CG7763	-	-	-2,0	-6,3539	-2,2	-5,465
FBgn0033643	147029_s_at	CG30035	-	fructose transporter activity / glucose transporter activity / glucose transporter activity	-2,1	-3,5807	-	-
FBgn0033721	147084_at	CG13159	-	-	-31,6	-8,6854	-67,1	-18,7729
FBgn0033724	153425_at	CG8501	-	-	-	-	-2,2	-3,3993
FBgn0033855	153848_at	CG13333	-	-	-	-	-1,8	-3,5898
FBgn0033921	147193_at	CG8589	-	-	-1,9	-3,1082	-	-
FBgn0034079	154150_at	CG8430	Got1	-	-1,6	-3,2624	-	-
FBgn0034108	155081_at	CG3767	Jhl-26	-	-	-	-8,1	-8,85
FBgn0034117	153785_at	CG7997	-	-	-1,7	-3,4281	-	-
FBgn0034203	147357_at	CG30457	-	-	-	-	-1,7	-3,3861
FBgn0034294	147409_at	CG5765	-	-	-	-	-3,1	-5,1884
FBgn0034356	147444_at	CG10924	-	-	-1,8	-4,6992	-	-
FBgn0034698	141793_at	CG6698	NtR	-	-2,0	-3,4155	-3,2	-3,701
FBgn0034716	142132_at	CG3380	Oatp58Dc	organic anion transporter activity / sodium-independent organic anion transporter activity	-1,8	-3,4856	-2,5	-3,2791
FBgn0035190	147960_at	CG13913	-	-	-4,5	-9,0967	-1,8	-3,0885
FBgn0035551	148182_at	CG7465	-	-	-	-	-6,4	-6,0362
FBgn0035717	152709_at	CG10078	Prat2	-	-2,4	-3,3659	-1,6	-3,3535
FBgn0035763	154884_at	CG8602	-	transporter activity	-1,5	-3,91	-1,7	-3,6002
FBgn0035926	148422_at	CG5804	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,8	-3,6054
FBgn0035968	148450_at	CG4484	-	sucrose:hydrogen symporter activity	-1,7	-3,4997	-	-
FBgn0035999	148467_at	CG3552	-	-	-	-	-2,0	-3,5132
FBgn0036182	153576_at	CG6084	-	aldehyde reductase activity	-	-	-1,8	-2,9273
FBgn0036381	148725_at	CG8745	-	-	-	-	-1,6	-2,9305
FBgn0036494	153641_at	CG7250	Toll-6	transmembrane receptor activity / transmembrane receptor protein serine/threonine kinase activity	-1,5	-3,6365	-	-
FBgn0036508	153226_at	CG7439	AGO2	-	-1,7	-3,7428	-1,8	-3,8357
FBgn0036600	148873_at	CG13043	-	-	-	-	-5,3	-6,1229
FBgn0036605	148878_s_at	CG13041	-	-	-	-	-1,8	-5,6174
FBgn0036875	149052_at	CG9449	-	acid phosphatase activity	-1,7	-3,3952	-3,7	-6,9339
FBgn0037177	149244_at	CG14454	-	molecular_function unknown	-1,5	-3,3418	-	-
FBgn0037372	151994_at	CG2091	-	-	-1,8	-3,9672	-1,9	-3,1675
FBgn0037549	154657_at	CG7878	-	ATP-dependent RNA helicase activity / helicase activity / nucleic acid binding	-1,7	-2,9874	-	-
FBgn0037672	149545_at	CG12952	sage	transcription factor activity	-	-	-1,5	-3,1526
FBgn0037930	142488_s_at	CG14715	-	FK506 binding / peptidyl-prolyl cis-trans isomerase activity / protein tyrosine phosphatase activity / receptor activity / transcription regulator activity	-1,5	-4,1997	-1,7	-3,5648
FBgn0038022	149757_at	CG4381	GstD3	glutathione transferase activity	-	-	-1,9	-3,0328
FBgn0038024	149759_at	CG12242	GstD5	glutathione transferase activity	-	-	-1,9	-2,8856
FBgn0038034	149768_s_at	CG17875	Cyp9f3Ψ	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-3,1	-5,2613
FBgn0038037	153031_at	CG11466	Cyp9f2	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-3,8	-4,6099
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	-	-	-2,7	-6,2164
FBgn0038077	142293_at	CG12286	kar	monocarboxylic acid transporter activity	-	-	-2,2	-2,8294
FBgn0038081	142746_at	CG10120	Men	carboxy-lyase activity / malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	-	-	-1,9	-3,8297
FBgn0038194	152120_at	CG3050	Cyp6d5	electron transporter activity / oxidoreductase activity	-5,6	-9,2367	-9,1	-10,5256
FBgn0038278	142158_at	CG7007	VhaPPA1-1	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,5	-3,1512
FBgn0038353	149968_at	CG5399	-	-	-2,1	-3,2389	-	-
FBgn0038563	152336_at	CG7780	DNaseII	-	-3,2	-5,2414	-3,4	-5,1751
FBgn0038647	150161_at	CG14302	-	-	-	-	-1,7	-3,4976
FBgn0038803	152563_at	CG5191	-	hydrolase activity	-	-	-1,6	-2,8992
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-	-	-1,8	-3,6371
FBgn0038982	142587_at	CG33093	-	gibberellin 20-oxidase activity	-1,6	-4,7419	-2,2	-5,5144
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-	-	-4,9	-7,4501
FBgn0039539	154473_at	CG12880	-	-	-	-	-3,3	-3,9831
FBgn0039567	150762_at	CG4869	betaTub97EF	structural constituent of cytoskeleton / tubulin binding	-	-	-1,7	-2,7953
FBgn0039586	142182_s_at	CG33103	Ppn	metallopeptidase activity / serine-type endopeptidase inhibitor activity	-2,3	-6,9391	-2,7	-6,6612
FBgn0039631	154649_at	CG11305	Sirt7	chromatin binding / deacetylase activity / hydrolase activity / nucleic acid binding / transcription regulator activity	-1,7	-3,0478	-	-
FBgn0039682	150834_at	CG7584	Obp99c	-	-	-	-3,0	-9,9305
FBgn0039686	150838_at	CG15506	-	-	-	-	-2,1	-4,3952
FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-6,8	-4,7892
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-8,0	-7,3744
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-	-	-2,2	-4,2621
FBgn0039800	142413_at	CG11314	-	-	-	-	-2,3	-3,5627
FBgn0039873	150955_at	CG2191	-	cation transporter activity / sodium-dependent multivitamin transporter activity	-3,4	-5,0807	-	-
FBgn0039922	153799_at	CG1793	MED26	RNA polymerase II transcription mediator activity / transcription factor activity	-1,5	-3,2789	-	-
FBgn0040813	151287_at	CG11051	Nplp2	-	-1,5	-3,9534	-1,6	-4,1908
FBgn0040865	151339_at	CG15758	-	-	-	-	-1,9	-3,2336
FBgn0040984	151444_at	CG4440	-	-	-	-	-2,0	-4,8177

Table S5. Genes responsive to Abd-A induction

Up-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000014	143052_at	CG10325	abd-A	specific RNA polymerase II transcription factor activity	9,8	10,0511	7,1	16,6262
FBgn0000139	154585_at	CG6677	ash2	transcription regulator activity	-	-	1,5	4,3546
FBgn0000158	143082_at	CG10422	bam	-	-	-	1,7	3,236
FBgn0000166	142838_at	CG1034	bcd	morphogen activity / specific RNA polymerase II transcription factor activity / translation regulator activity	1,5	3,7321	1,8	7,0277
FBgn0000228	143090_at	CG14025	Bsg25D	molecular_function unknown	-	-	1,7	4,1048
FBgn0000376	154489_at	CG2714	crm	DNA binding	-	-	1,5	3,4184
FBgn0000499	143133_at	CG18361	dsh	Notch binding	-	-	1,5	3,6127
FBgn0001078	154699_at	CG4059	ftz-f1	DNA binding / ligand-dependent nuclear receptor activity / transcription cofactor activity / transcription factor activity	-	-	1,5	4,8828
FBgn0001079	143170_at	CG6551	fu	protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,6	3,5523
FBgn0001086	155082_at	CG4274	fzy	-	-	-	1,5	4,5201
FBgn0001225	153731_at	CG4183	Hsp26	-	2,0	5,4787	-	-
FBgn0001974	143217_at	CG3688	l(2)35Bd	nucleic acid binding	-	-	1,6	4,6107
FBgn0002570	143242_at	CG8696	LvpH	alpha-glucosidase activity	-	-	3,1	7,9277
FBgn0002673	153947_at	CG4965	twe	protein tyrosine phosphatase activity / protein tyrosine/serine/threonine phosphatase activity	-	-	1,9	6,5679
FBgn0002715	154633_at	CG5303	mei-S332	molecular_function unknown	-	-	1,5	3,7778
FBgn0002775	143267_at	CG8631	msl-3	chromatin binding / protein binding / RNA binding / transcription regulator activity	-	-	2,0	2,8724
FBgn0002872	155050_at	CG1960	mu2	-	-	-	1,8	4,4071
FBgn0002924	154464_at	CG7831	ncd	microtubule motor activity / minus-end-directed microtubule motor activity / structural constituent of cytoskeleton	-	-	1,6	6,6883
FBgn0002962	151690_at	CG5637	nos	protein binding / RNA binding	2,1	3,2736	-	-
FBgn0003015	154312_at	CG10901	osk	-	1,8	3,4338	1,6	3,2952
FBgn0003087	153890_at	CG5052	pim	-	-	-	1,7	5,5487
FBgn0003114	143307_at	CG9183	plu	DNA binding	-	-	1,7	4,6624
FBgn0003138	141300_at	CG9181	Ptp61F	protein tyrosine phosphatase activity / receptor activity	-	-	1,5	6,6439
FBgn0003444	154678_at	CG11561	smo	G-protein coupled receptor activity / hedgehog receptor activity / transmembrane receptor activity	-	-	1,7	4,1672
FBgn0003655	151660_at	CG3429	swa	dynein binding / RNA binding	-	-	1,7	5,2166
FBgn0003701	141565_at	CG5785	thr	-	-	-	1,7	8,3845
FBgn0003733	143381_at	CG1389	tor	protein kinase activity / protein-tyrosine kinase activity / transmembrane receptor protein tyrosine kinase activity	-	-	1,9	6,6178
FBgn0004106	154844_at	CG5363	cdc2	protein binding / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,5	6,5855
FBgn0004377	143451_at	CG15844	Klp54D	microtubule motor activity / structural constituent of cytoskeleton	-	-	1,8	3,5021
FBgn0004554	143480_at	CG7539	Edg91	structural constituent of pupal cuticle (sensu Insecta)	2,2	4,0895	-	-
FBgn0004598	154521_at	CG18734	Fur2	furin activity	-	-	1,8	4,1055
FBgn0004611	153733_at	CG4574	Plc21C	phosphoinositide phospholipase C activity	-	-	1,5	3,7124
FBgn0004655	142777_at	CG3707	wapl	-	-	-	1,5	3,7589
FBgn0004698	141256_at	CG8153	mus210	damaged DNA binding	-	-	1,5	5,0127
FBgn0004924	143538_at	CG6146	Top1	nucleic acid binding	-	-	1,5	6,2242
FBgn0005617	143556_at	CG10385	msl-1	chromatin binding / DNA binding / protein binding	-	-	1,5	3,5543
FBgn0005694	151719_s_at	CG5683	Aef1	RNA polymerase II transcription factor activity / specific transcriptional repressor activity / transcription factor activity	1,6	3,7158	1,6	3,721
FBgn0010315	154137_at	CG9096	CycD	cyclin-dependent protein kinase regulator activity / kinase activator activity	-	-	1,6	7,017
FBgn0010441	142881_at	CG5974	pll	protein kinase activity / protein serine/threonine kinase activity / transmembrane receptor protein serine/threonine kinase activity	-	-	1,6	2,8446
FBgn0010550	154412_at	CG8068	Su(var)2-10	DEAD/H-box RNA helicase binding / DNA binding	-	-	1,6	3,1018

FBgn0011705	154129_at	CG9552	rost	-	-	-	1,6	3,1734
FBgn0011737	142924_at	CG4488	wee	non-membrane spanning protein tyrosine kinase activity / protein kinase activity / protein-tyrosine kinase activity	-	-	1,7	4,6435
FBgn0011761	154221_at	CG4193	dhd	thiol-disulfide exchange intermediate activity	3,0	5,358	-	-
FBgn0013746	141726_at	CG9556	alien	protein binding / signal transducer activity / transcription corepressor activity	-	-	1,5	4,8825
FBgn0013953	142492_at	CG7005	Esp	sulfate porter activity	1,5	4,51	2,1	10,5411
FBgn0014032	151950_at	CG12117	Sptr	sepiapterin reductase activity	-	-	1,9	6,279
FBgn0014931	151670_at	CG2678	-	transcription factor activity	-	-	1,9	5,9304
FBgn0015037	143782_at	CG10842	Cyp4p1	electron transporter activity / oxidoreductase activity	2,5	5,3164	3,6	6,122
FBgn0015321	154399_at	CG8284	UbcD4	ligase activity / ubiquitin conjugating enzyme activity	1,5	4,6147	-	-
FBgn0015391	154348_at	CG11397	glu	chromatin binding / DNA binding / nucleotide binding	-	-	1,6	7,212
FBgn0015573	152410_at	CG1089	alpha-Est5	carboxylesterase activity	-	-	1,6	3,683
FBgn0015800	143846_at	CG6920	mus309	ATP-dependent DNA helicase activity / ATP-dependent DNA helicase activity / DNA binding / DNA helicase activity / DNA-dependent protein kinase activity / helicase activity / nucleic acid binding	-	-	1,7	3,3192
FBgn0015926	153153_at	CG6157	dah	-	-	-	1,6	7,5231
FBgn0016034	153959_at	CG11254	mael	-	-	-	1,7	7,2831
FBgn0017448	143890_at	CG2187	-	cation transporter activity / sodium:iodide symporter activity	1,7	3,4138	-	-
FBgn0019637	154540_at	CG1433	Atu	molecular_function unknown	-	-	1,9	4,3352
FBgn0020018	154945_at	CG5796	Ppox	protoporphyrinogen oxidase activity	-	-	1,7	3,2891
FBgn0020360	153671_at	CG6219	cav	-	-	-	2,3	3,9551
FBgn0020911	154217_at	CG5595	Sce	protein binding	-	-	1,6	4,2711
FBgn0022772	153737_at	CG10667	Orc1	DNA binding / DNA replication origin binding	-	-	1,7	5,2674
FBgn0022981	153614_at	CG1058	rpk	amiloride-sensitive sodium channel activity / sodium channel activity	-	-	1,9	5,5308
FBgn0022987	143968_at	CG4816	qkr54B	RNA binding	-	-	1,8	5,0759
FBgn0023129	154184_at	CG3705	aay	phosphoserine phosphatase activity	-	-	1,5	3,077
FBgn0023177	143976_at	CG32505	Pp4-19C	protein serine/threonine phosphatase activity	-	-	1,5	5,8096
FBgn0023444	154250_at	CG4063	ebi	GTP binding / protein binding	-	-	1,6	6,6333
FBgn0023513	143991_at	CG14803	-	-	-	-	1,7	5,7545
FBgn0023522	154980_at	CG11596	-	-	-	-	1,5	5,5335
FBgn0024227	154863_at	CG6620	ial	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,6	3,7524
FBgn0024542	153420_at	CG8614	Neos	RNA binding	-	-	1,6	6,8124
FBgn0024732	144023_at	CG8357	Rep1	-	-	-	1,6	2,8396
FBgn0025458	144064_at	CG7838	Bub1	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,5	6,4085
FBgn0025615	154672_at	CG3024	torp4a	-	-	-	1,6	6,3412
FBgn0025626	152343_at	CG4281	-	-	-	-	1,5	3,9332
FBgn0025635	144078_at	CG17829	-	-	-	-	1,6	4,5283
FBgn0025743	144091_at	CG18582	mbt	protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,5	5,5244
FBgn0025781	144093_at	CG6759	cdc16	meprin A activity / ubiquitin-protein ligase activity	-	-	1,5	3,085
FBgn0025874	153556_at	CG8474	Meics	-	-	-	1,5	6,2103
FBgn0026150	153980_at	CG6291	ApepP	metallopeptidase activity	-	-	1,7	6,7532
FBgn0026317	154199_at	CG6147	Tsc1	kinase binding	-	-	1,5	2,8225
FBgn0026598	154309_at	CG6193	Apc2	microtubule binding / protein binding / structural constituent of cytoskeleton	-	-	1,9	5,1444
FBgn0026616	153670_at	CG4606	alpha-Man-IIb	alpha-mannosidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds / mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity	-	-	1,6	5,0267
FBgn0026629	153839_at	CG6072	sra	receptor binding	-	-	1,5	6,3994
FBgn0026751	153571_at	CG4208	XRCC1	nucleic acid binding	-	-	1,8	3,2126
FBgn0026871	144162_at	CG14781	-	-	-	-	1,8	7,6695
FBgn0027052	144169_at	CG5203	CHIP	ubiquitin-protein ligase activity	-	-	1,7	4,7111
FBgn0027055	144170_at	CG18332	CSN3	-	-	-	1,5	4,6261
FBgn0027511	154082_at	CG1619	-	-	-	-	1,6	3,291
FBgn0027521	154041_at	CG3679	-	-	-	-	2,0	3,5026
FBgn0027526	154017_at	CG6697	-	-	-	-	1,5	5,5686
FBgn0027606	151864_at	CG12787	hoe1	cation transporter activity / L-tyrosine transporter activity / transporter activity	-	-	1,8	6,0355
FBgn0027617	151768_at	CG5808	-	isomerase activity / mRNA 3′-UTR binding / mRNA binding / RNA binding / RNA binding	-	-	1,6	2,9189
FBgn0027783	153548_at	CG10212	SMC2	chromatin binding / DNA binding	-	-	1,6	3,7265
FBgn0027889	153644_at	CG6386	ball	histone-threonine kinase activity / protein kinase activity / protein serine/threonine kinase activity	-	-	1,6	6,9668
FBgn0027890	153626_at	CG4584	dUTPase	-	-	-	1,5	6,9801
FBgn0027914	153274_at	CG10670	Gen	damaged DNA binding / endonuclease activity / exodeoxyribonuclease activity / flap endonuclease activity / single-stranded DNA specific endodeoxyribonuclease activity	-	-	1,5	2,8563
FBgn0027949	154597_at	CG10364	msb1l	molecular_function unknown	-	-	1,6	6,1297
FBgn0028408	144208_at	CG1975	Rep2	-	-	-	1,6	5,3912
FBgn0028487	152215_at	CG9611	-	receptor binding / structural molecule activity	-	-	1,5	4,2904
FBgn0028528	154408_at	CG4482	mol	-	-	-	1,7	8,0834
FBgn0028708	144250_at	CG11993	Mst85C	-	-	-	1,7	6,2316
FBgn0028860	144271_at	CG15266	-	-	-	-	1,5	3,4807
FBgn0028967	144335_at	CG8947	26-29-p	-	2,0	5,3428	-	-
FBgn0029532	144349_at	CG13361	-	-	2,6	3,9913	-	-
FBgn0029546	154641_at	CG3704	-	purine nucleotide binding	-	-	1,5	4,0666
FBgn0029685	154104_at	CG2938	-	-	-	-	1,8	6,2064
FBgn0029744	141469_at	CG11706	-	-	3,4	5,7748	7,0	7,593
FBgn0029756	144516_at	CG3309	-	-	-	-	2,0	3,9094
FBgn0029824	154360_at	CG3726	-	DNA binding / transcription regulator activity	-	-	1,8	3,0521
FBgn0029865	154623_at	CG15893	-	-	1,5	3,1537	1,7	7,3329
FBgn0029891	152822_at	CG4523	-	protein kinase activity	-	-	1,6	6,636
FBgn0029899	151584_r_at	CG14438	-	-	-	-	1,6	3,06
FBgn0029924	154888_at	CG4586	-	acyl-CoA oxidase activity	-	-	1,6	3,9972
FBgn0029935	142921_at	CG4615	-	-	-	-	1,5	3,6013
FBgn0029970	153517_at	CG17256	Nek2	protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,7	2,9171
FBgn0029996	153913_at	CG2257	Ubc-E2H	ligase activity / ubiquitin conjugating enzyme activity	-	-	1,5	4,2273
FBgn0030003	153751_at	CG2116	-	-	-	-	1,7	3,634
FBgn0030048	153300_at	CG12112	-	-	-	-	1,6	3,4637
FBgn0030054	141513_at	CG12109	Caf1-180	chromatin binding	-	-	1,5	3,5348
FBgn0030057	144710_at	CG12108	Ppt1	palmitoyl-(protein) hydrolase activity	-	-	1,5	3,1873
FBgn0030100	151907_at	CG12106	-	-	-	-	1,5	3,1054
FBgn0030122	154992_at	CG16892	-	-	-	-	1,6	6,6823
FBgn0030147	144764_at	CG32697	l(1)G0232	-	-	-	1,5	3,362
FBgn0030228	144824_at	CG1826	-	actin binding / structural constituent of cytoskeleton	-	-	1,5	5,429
FBgn0030301	151708_s_at	CG1745	-	-	-	-	1,5	5,0475
FBgn0030312	144884_at	CG1558	l(1)G0237	-	-	-	1,5	2,8627
FBgn0030336	154432_at	CG1578	-	-	-	-	1,5	3,3576
FBgn0030353	153926_at	CG15737	-	polynucleotide adenylyltransferase activity	-	-	1,8	4,4908
FBgn0030373	144920_at	CG12721	-	-	-	-	2,0	4,3731
FBgn0030430	151663_at	CG32649	-	protein kinase activity	-	-	1,5	3,6409
FBgn0030432	144970_at	CG4404	-	-	-	-	1,9	4,2675
FBgn0030501	145019_at	CG11177	BthD	-	-	-	1,7	5,0459
FBgn0030557	154460_at	CG12047	mud	-	-	-	1,7	2,9859
FBgn0030603	141531_at	CG5541	-	-	1,5	2,8343	-	-
FBgn0030607	154001_at	CG5560	-	-	-	-	2,0	5,3752
FBgn0030709	142914_at	CG9126	Stim	carrier activity / nuclear export signal receptor activity / RAN protein binding	-	-	1,5	4,1628
FBgn0030710	153942_at	CG8924	-	DNA binding / transcription regulator activity	-	-	1,8	6,8247
FBgn0030711	145163_at	CG8928	-	-	-	-	1,5	4,0627
FBgn0030803	153983_at	CG4880	-	-	-	-	1,6	7,2147
FBgn0030855	145251_at	CG5800	-	nucleic acid binding / RNA helicase activity	-	-	1,5	2,8934
FBgn0030864	145258_at	CG8173	-	protein serine/threonine kinase activity	-	-	1,8	6,9568
FBgn0030874	154845_at	CG6506	-	-	-	-	1,8	3,2474
FBgn0030890	154547_at	CG7536	-	G-protein coupled receptor activity / receptor activity	-	-	1,6	4,2536
FBgn0030915	145297_at	CG6179	-	-	-	-	1,5	4,6737
FBgn0030973	154261_at	CG7332	-	-	-	-	1,6	3,8954
FBgn0031059	142464_at	CG14229	-	-	-	-	1,6	4,1227
FBgn0031062	154638_at	CG14230	-	RNA binding	-	-	1,5	3,8343
FBgn0031070	145396_at	CG12702	-	-	-	-	1,6	3,1704
FBgn0031090	154069_at	CG9575	Rab35	GTPase activity	-	-	1,6	3,9612
FBgn0031151	145455_at	CG32512	-	-	-	-	1,8	5,7355
FBgn0031152	145456_at	CG32512	-	-	-	-	1,6	3,9722
FBgn0031173	145473_at	CG1696	l(1)G0269	-	-	-	1,6	4,439

FBgn0031192	151481_s_at	CG14616	l(1)G0196	-	-	-	1,5	3,7308
FBgn0031360	154613_at	CG31937	-	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	-	-	1,5	4,1871
FBgn0031398	154325_at	CG10880	-	-	-	-	1,6	4,5516
FBgn0031434	145649_at	CG3227	insv	-	-	-	1,6	6,1095
FBgn0031435	153717_at	CG9883	-	-	-	-	1,7	4,7735
FBgn0031452	145663_at	CG2843	-	-	1,6	2,9301	-	-
FBgn0031498	155084_at	CG17260	-	-	-	-	2,1	3,2243
FBgn0031609	145763_at	CG15443	-	-	-	-	1,6	3,0559
FBgn0031610	154618_at	CG15436	-	transcription regulator activity	-	-	1,9	3,3247
FBgn0031739	154906_at	CG14005	-	-	-	-	1,7	3,7607
FBgn0031741	145847_at	CG11034	-	-	-	-	1,7	5,0193
FBgn0031773	145868_at	CG9144	-	-	-	-	1,6	4,5185
FBgn0031806	145894_at	CG9506	slam	-	-	-	1,7	5,8928
FBgn0031843	154616_at	CG31633	-	carrier activity / tocopherol binding	-	-	1,6	3,3151
FBgn0031871	153669_at	CG10158	-	-	-	-	1,6	4,2129
FBgn0031882	145938_at	CG9100	Rab30	GTPase activity	-	-	1,6	2,9816
FBgn0031886	141632_at	CG8902	-	-	-	-	1,6	4,313
FBgn0031893	155153_at	CG4495	-	-	-	-	1,6	3,831
FBgn0031895	142856_at	CG4497	-	-	-	-	1,6	4,5168
FBgn0031896	142056_at	CG4502	-	-	-	-	1,7	3,3399
FBgn0031996	153927_at	CG8460	-	-	-	-	1,7	6,167
FBgn0032022	146022_at	CG14275	-	-	1,9	3,2927	2,9	6,6405
FBgn0032040	151676_at	CG13386	-	molecular_function unknown	-	-	2,0	4,2727
FBgn0032043	146034_at	CG13399	Chrac-14	single-stranded DNA specific endodeoxyribonuclease activity	-	-	1,7	10,8253
FBgn0032056	146041_at	CG18042	lmg	-	-	-	1,5	4,232
FBgn0032059	146044_at	CG9296	-	cGMP-specific phosphodiesterase activity	-	-	1,6	3,0969
FBgn0032189	146128_at	CG18145	-	-	-	-	1,9	5,406
FBgn0032243	142536_at	CG5300	Klp31E	microtubule motor activity / motor activity / structural constituent of cytoskeleton	-	-	1,6	3,1028
FBgn0032250	152523_at	CG5198	-	molecular_function unknown	-	-	1,7	4,4499
FBgn0032251	146160_at	CG13142	-	-	-	-	1,7	3,7855
FBgn0032262	155142_at	CG7384	-	-	-	-	2,1	5,4795
FBgn0032354	146236_at	CG4788	-	-	-	-	1,5	6,1827
FBgn0032356	146238_at	CG33694	cana	-	-	-	1,7	3,4458
FBgn0032594	146370_at	CG4711	squ	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,7	5,2537
FBgn0032635	154299_at	CG15141	-	-	-	-	1,8	5,1322
FBgn0032714	154326_at	CG17322	-	2-hydroxyacylsphingosine 1-beta-galactosyltransferase activity	-	-	1,7	4,1539
FBgn0032725	146460_at	CG10679	Nedd8	protein binding	-	-	1,5	5,381
FBgn0032752	154745_at	CG10702	-	insulin-like growth factor receptor activity	-	-	2,0	3,6199
FBgn0032760	152500_at	CG10563	-	general RNA polymerase II transcription factor activity / transcription regulator activity	-	-	1,7	3,7512
FBgn0032789	146498_at	CG13083	-	-	-	-	1,6	5,0692
FBgn0032823	146514_at	CG10528	fs(2)ltoPP43	-	-	-	1,6	4,4647
FBgn0032882	153711_at	CG9320	-	GTP binding / hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding	-	-	1,7	5,5752
FBgn0032890	151641_at	CG31673	-	glyoxylate reductase (NADP) activity	-	-	1,7	4,7117
FBgn0032907	146565_at	CG9272	-	nucleic acid binding / pyrimidine-specific oxidized base lesion DNA N-glycosylase activity	-	-	1,6	3,0641
FBgn0032929	155063_at	CG9241	Mcm10	-	-	-	1,7	4,6482
FBgn0032998	153781_at	CG17478	-	-	-	-	2,1	3,829
FBgn0033082	154155_at	CG3273	sced	-	-	-	1,7	7,1376
FBgn0033109	146698_at	CG9446	coro	actin binding / structural constituent of cytoskeleton	-	-	1,6	5,6279
FBgn0033156	141608_at	CG12165	Incenp	-	-	-	1,6	4,8541
FBgn0033177	154461_at	CG11141	-	-	-	-	1,8	5,2185
FBgn0033233	142811_at	CG15835	-	transcription cofactor activity / transcription regulator activity	-	-	1,6	6,6376
FBgn0033234	153231_at	CG8791	-	high affinity inorganic phosphate:sodium symporter activity	2,1	3,4069	3,7	5,9369
FBgn0033236	154856_at	CG14764	-	-	-	-	1,8	4,3107
FBgn0033239	146778_at	CG14764	-	-	-	-	1,6	2,7809
FBgn0033242	146780_at	CG2916	Sep5	GTPase activity / structural constituent of cytoskeleton	-	-	1,8	4,126
FBgn0033316	154427_at	CG14749	-	-	-	-	1,7	8,4178
FBgn0033395	152833_at	CG1944	Cyp4p2	electron transporter activity / oxidoreductase activity	1,8	5,1058	2,6	8,603
FBgn0033414	146882_at	CG11804	ced-6	receptor binding	-	-	1,5	4,479
FBgn0033427	154357_at	CG1868	-	-	-	-	1,7	3,0679
FBgn0033453	154443_at	CG1667	-	-	-	-	1,8	6,1576
FBgn0033456	153430_at	CG10536	cbx	-	-	-	1,5	3,8341
FBgn0033458	146908_at	CG18446	-	-	1,6	2,8189	-	-
FBgn0033466	154695_at	CG12130	-	-	-	-	1,6	4,2828
FBgn0033475	154020_at	CG12129	-	-	-	-	1,7	5,5187
FBgn0033518	146946_s_at	CG11765	Prx2540-2	antioxidant activity / antioxidant activity / non-selenium glutathione peroxidase activity / peroxidase activity / peroxidase activity / peroxidase activity	-	-	1,7	9,5971
FBgn0033519	146947_at	CG11825	-	-	1,5	3,5679	2,5	7,8211
FBgn0033584	151723_at	CG7737	-	oxidoreductase activity	-	-	1,7	3,1369
FBgn0033607	147005_at	CG9062	-	-	-	-	1,7	5,0343
FBgn0033638	147023_at	CG9005	-	-	-	-	1,6	4,0919
FBgn0033656	147040_at	CG8988	S2P	metalloendopeptidase activity / sterol regulatory element-binding protein site 2 protease activity	-	-	2,0	5,7452
FBgn0033670	154801_at	CG8290	-	general RNA polymerase II transcription factor activity	-	-	1,5	3,6557
FBgn0033675	142664_at	CG8889	-	-	-	-	1,5	4,3315
FBgn0033683	147055_at	CG18343	-	-	-	-	1,6	5,2161
FBgn0033757	147107_at	CG8811	muskelin	-	-	-	1,8	3,4574
FBgn0033762	147110_at	CG8632	-	-	-	-	1,7	3,1888
FBgn0033827	147145_at	CG17047	-	-	-	-	1,5	3,0722
FBgn0033845	154035_at	CG17064	mars	-	-	-	1,7	4,2296
FBgn0033881	147175_at	CG13345	RacGAP50C	diacylglycerol binding / GTPase activator activity / Rho GTPase activator activity / signal transducer activity	-	-	1,5	5,8767
FBgn0033898	141695_at	CG8241	-	ATP-dependent RNA helicase activity / pre-mRNA splicing factor activity	-	-	1,5	4,4082
FBgn0033921	147193_at	CG8589	-	-	-	-	1,9	7,8243
FBgn0033941	154835_at	CG10110	cpsf	-	-	-	1,7	4,447
FBgn0033945	147210_at	CG12868	-	-	-	-	1,9	4,5401
FBgn0033986	147229_at	CG10261	aPKC	diacylglycerol binding / protein binding / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,6	4,7513
FBgn0034046	141221_at	CG8253	tun	-	-	-	1,8	3,1023
FBgn0034064	153183_at	CG8392	l(2)05070	endopeptidase activity	-	-	1,5	5,2234
FBgn0034080	142651_at	CG30094	-	-	-	-	1,7	3,6264
FBgn0034114	154012_at	CG4282	-	transcription regulator activity	-	-	1,5	3,3132
FBgn0034185	154614_at	CG8961	tef	-	-	-	1,7	5,1527
FBgn0034250	141797_at	CG4924	icln	-	-	-	1,8	5,8425
FBgn0034320	151659_at	CG5580	sbb	-	-	-	1,7	4,0385
FBgn0034366	147451_at	CG5489	Atg7	binding / carrier activity	-	-	1,6	5,0026
FBgn0034398	147469_at	CG15098	-	-	-	-	1,6	6,6121
FBgn0034470	147516_at	CG11218	Obp56d	-	3,2	5,7557	-	-
FBgn0034531	142991_at	CG30149	rig	ligand-dependent nuclear receptor transcription coactivator activity / protein binding	-	-	1,8	3,2821
FBgn0034594	141200_at	CG9418	-	DNA binding / transcription regulator activity	-	-	1,5	3,8368
FBgn0034640	154994_at	CG9858	clt	carboxylesterase activity	-	-	1,9	3,0203
FBgn0034703	152572_at	CG3045	-	-	-	-	1,7	4,7416
FBgn0034878	153852_at	CG3941	pita	transcription regulator activity	-	-	1,6	3,4341
FBgn0034933	154746_at	CG3735	-	-	-	-	1,6	3,5267
FBgn0034980	154372_at	CG4057	tamo	-	-	-	1,6	4,319
FBgn0035025	154497_at	CG11416	-	-	-	-	1,6	3,1148
FBgn0035061	154579_at	CG30422	-	-	-	-	1,6	5,3403
FBgn0035136	147928_at	CG6905	-	pre-mRNA splicing factor activity / transcription regulator activity	-	-	1,6	3,2824
FBgn0035151	154989_at	CG17129	-	-	-	-	1,8	4,5036
FBgn0035160	147938_at	CG13897	-	-	-	-	1,5	3,645
FBgn0035189	152102_at	CG9119	-	-	1,6	2,9688	-	-
FBgn0035208	147969_at	CG9184	-	-	1,9	6,5671	-	-
FBgn0035209	147970_at	CG13914	-	-	-	-	1,7	5,7922
FBgn0035350	155102_at	CG16757	Spn	-	-	-	1,7	3,5928
FBgn0035414	141266_at	CG14965	-	-	-	-	1,7	4,5611
FBgn0035425	154425_at	CG17746	-	protein serine/threonine phosphatase activity	-	-	1,7	6,4667

FBgn0035428	148099_at	CG14960	-	-	-	-	1,5	4,224
FBgn0035434	148103_at	CG10812	dro5	-	1,5	6,445	1,6	7,6576
FBgn0035461	153770_at	CG10855	-	-	-	-	1,9	3,9322
FBgn0035462	148124_at	CG1120	-	-	-	-	2,4	4,7733
FBgn0035511	148155_at	CG15007	-	structural constituent of larval cuticle (sensu Insecta)	-	-	1,9	2,8503
FBgn0035611	148226_at	CG13285	-	-	1,8	3,0002	-	-
FBgn0035617	155154_at	CG5146	-	-	-	-	1,5	3,4827
FBgn0035621	154354_at	CG10591	-	-	2,0	7,629	-	-
FBgn0035640	148237_at	CG17498	mad2	-	-	-	1,8	8,997
FBgn0035641	141286_at	CG5568	-	4-coumarate-CoA ligase activity / ligase activity	-	-	2,2	3,3533
FBgn0035705	154361_at	CG18769	-	-	-	-	1,6	4,2946
FBgn0035821	148362_at	CG32365	-	-	-	-	1,7	2,9865
FBgn0035822	148363_at	CG32365	-	-	-	-	1,5	3,4819
FBgn0035842	148373_at	CG7504	-	ATP-dependent RNA helicase activity / DNA helicase activity / nucleic acid binding	-	-	1,7	3,1418
FBgn0035876	141211_at	CG7081	-	-	-	-	1,5	2,7846
FBgn0035918	154316_at	CG5971	-	DNA clamp loader activity / DNA replication origin binding	-	-	1,6	5,4274
FBgn0035945	141294_at	CG5026	-	protein tyrosine/serine/threonine phosphatase activity	-	-	1,7	5,4477
FBgn0035959	148444_at	CG4911	-	-	-	-	1,5	5,9144
FBgn0035961	153070_at	CG4821	Tequila	pancreatic elastase activity / serine-type endopeptidase activity / trypsin activity	-	-	1,6	6,308
FBgn0036020	152064_at	CG8336	-	isomerase activity	-	-	1,6	3,2253
FBgn0036117	153845_at	CG6321	-	transaminase activity / transferase activity	-	-	1,6	4,1123
FBgn0036120	153797_at	CG7869	SuUR	-	-	-	1,6	3,7649
FBgn0036247	153973_at	CG6801	l(3)j2D3	-	-	-	1,5	3,0289
FBgn0036248	154560_at	CG17153	-	-	-	-	1,7	4,2551
FBgn0036272	148648_at	CG4300	-	-	-	-	1,5	8,8001
FBgn0036312	155126_at	CG17667	-	-	-	-	1,5	3,3955
FBgn0036330	148687_at	CG11263	-	-	-	-	2,1	4,6969
FBgn0036352	148705_at	CG14110	-	-	1,9	5,8211	-	-
FBgn0036354	153557_at	CG10191	-	-	-	-	1,6	4,5163
FBgn0036395	148737_at	CG17361	-	-	-	-	1,7	3,9605
FBgn0036402	154248_at	CG6650	-	-	-	-	1,6	3,7432
FBgn0036423	153907_at	CG3919	-	-	-	-	1,5	3,0932
FBgn0036565	148844_at	CG5235	-	dopamine beta-monooxygenase activity	-	-	1,6	3,226
FBgn0036612	148885_at	CG4998	-	NOT serine-type endopeptidase activity	-	-	1,8	3,341
FBgn0036625	153654_at	CG4877	-	-	-	-	1,6	4,5468
FBgn0036641	154173_at	CG16725	Smn	-	-	-	1,5	7,893
FBgn0036661	141237_at	CG9705	-	nucleic acid binding / RNA binding	-	-	1,5	5,089
FBgn0036689	154559_at	CG7730	-	-	1,5	4,3222	2,3	5,5655
FBgn0036777	153818_at	CG7341	-	molecular_function unknown	-	-	1,6	2,9063
FBgn0036800	154409_at	CG6897	-	-	-	-	1,5	5,8346
FBgn0036847	142238_at	CG11577	-	-	-	-	1,5	4,8313
FBgn0036850	141250_at	CG10419	-	-	-	-	1,6	4,3248
FBgn0036856	154328_at	CG9666	-	-	-	-	1,5	5,0335
FBgn0036863	154347_at	CG9670	fal	-	-	-	1,7	5,5112
FBgn0036955	155096_at	CG17149	-	oxidoreductase activity	-	-	1,5	4,4254
FBgn0036980	154298_at	CG5701	RhoBTB	GTPase activity	-	-	1,7	5,6916
FBgn0037006	153241_at	CG32425	-	-	1,6	3,266	1,7	5,5562
FBgn0037019	153962_at	CG3947	-	-	-	-	1,6	3,6519
FBgn0037082	141519_at	CG5664	-	-	-	-	1,9	4,4476
FBgn0037084	154189_at	CG7736	Syx6	-	-	-	1,5	4,8071
FBgn0037095	149186_at	CG7184	Mkrn1	-	-	-	1,6	6,5367
FBgn0037106	153689_at	CG11307	-	-	-	-	1,7	5,3032
FBgn0037156	153126_at	CG11523	-	-	-	-	1,5	3,9426
FBgn0037205	153555_at	CG11133	-	-	1,6	3,6776	2,3	3,9766
FBgn0037211	142644_s_at	CG12414	nAcRalpha-80B	acetylcholine receptor activity / nicotinic acetylcholine-activated cation-selective channel activity	-	-	1,9	7,0998
FBgn0037212	142645_r_at	CG12414	nAcR-80B	acetylcholine receptor activity / nicotinic acetylcholine-activated cation-selective channel activity	-	-	1,7	3,4079
FBgn0037327	149333_at	CG2087	PEK	eukaryotic elongation factor-2 kinase activity / protein kinase activity / receptor signaling protein serine/threonine kinase activity / translation initiation factor activity	-	-	1,6	6,3357
FBgn0037349	149342_at	CG14672	Spec2	-	-	-	1,6	3,8339
FBgn0037359	149346_at	CG1245	MED27	-	-	-	1,7	4,2105
FBgn0037376	149351_at	CG2051	-	histone acetyltransferase activity	-	-	1,5	5,6529
FBgn0037468	149420_at	CG1943	-	-	-	-	1,5	4,6401
FBgn0037479	154519_at	CG33546	gfzf	-	-	-	1,6	3,9661
FBgn0037487	149433_at	CG14608	-	-	5,8	3,4664	-	-
FBgn0037491	153896_at	CG1227	-	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,5	4,2732
FBgn0037595	154278_at	CG31453	-	transcription cofactor activity	-	-	1,6	2,9322
FBgn0037614	149520_at	CG8116	-	-	-	-	1,6	5,0364
FBgn0037620	142783_at	CG9793	-	transcription regulator activity	-	-	1,8	3,4407
FBgn0037624	155060_at	CG8223	-	-	-	-	1,6	7,3791
FBgn0037655	153500_at	CG11984	-	potassium channel regulator activity	-	-	1,7	5,8888
FBgn0037710	154154_at	CG9393	-	P-P-bond-hydrolysis-driven transporter activity	-	-	1,5	3,2269
FBgn0037717	154329_at	CG8301	-	transcription regulator activity	-	-	1,7	3,3275
FBgn0037746	154179_at	CG8478	-	-	-	-	1,6	5,8797
FBgn0037756	154479_at	CG8507	-	-	-	-	1,6	2,9228
FBgn0037792	154727_at	CG6241	-	-	-	-	1,6	3,6446
FBgn0037844	153457_at	CG4570	-	-	-	-	1,9	10,2238
FBgn0037878	153550_at	CG6693	-	-	-	-	1,5	5,0586
FBgn0037881	149678_at	CG10703	-	-	-	-	1,6	2,9121
FBgn0037894	141400_at	CG5252	Ranbp9	RAN protein binding	-	-	1,5	3,1432
FBgn0038047	149776_at	CG5245	-	transcription regulator activity	-	-	1,9	3,4653
FBgn0038058	141609_at	CG5608	-	-	-	-	1,8	4,3002
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	1,6	3,4138	0,4	-
FBgn0038169	153775_at	CG9351	flfl	-	-	-	1,6	4,612
FBgn0038251	154534_at	CG3508	-	-	-	-	1,5	5,9381
FBgn0038256	155074_at	CG7530	-	-	1,6	4,0375	2,1	5,4792
FBgn0038388	152212_at	CG4287	-	-	-	-	1,6	5,0605
FBgn0038428	150015_at	CG14894	-	-	-	-	1,6	3,5877
FBgn0038470	150044_at	CG18213	-	-	-	-	1,7	3,8414
FBgn0038487	154015_at	CG4060	-	-	-	-	1,8	4,868
FBgn0038489	150057_at	CG12265	-	-	-	-	1,5	4,8731
FBgn0038517	153862_at	CG5824	l(3)07882	-	-	-	1,5	4,2399
FBgn0038538	155012_at	CG7660	pxt	peroxidase activity	1,6	3,3127	-	-
FBgn0038551	142817_at	CG7357	-	-	-	-	1,6	4,3709
FBgn0038588	154268_at	CG7156	-	protein kinase activity	-	-	1,7	3,5558
FBgn0038650	154706_at	CG7719	gwl	protein kinase activity / protein serine/threonine kinase activity / receptor signaling protein serine/threonine kinase activity	-	-	1,7	5,3474
FBgn0038733	152819_at	CG11407	-	ligase activity / long-chain fatty acid transporter activity	3,7	4,9429	2,6	3,7286
FBgn0038767	150241_at	CG4413	-	transcription regulator activity	-	-	1,7	3,4222
FBgn0038772	154702_at	CG4973	-	-	-	-	1,9	4,9555
FBgn0038828	142610_at	CG17270	-	-	-	-	1,6	3,1286
FBgn0038857	142442_at	CG17282	-	-	1,6	3,0212	2,0	2,9843
FBgn0038962	150364_at	CG31285	-	molecular_function unknown	-	-	1,6	2,9411
FBgn0038992	153756_at	CG31156	-	chromatin binding / nucleic acid binding / RNA binding	-	-	1,6	3,3385
FBgn0039021	151680_at	CG31139	-	-	-	-	1,8	5,6574
FBgn0039066	154444_at	CG6755	EloA	transcription cofactor activity / transcriptional elongation regulator activity	-	-	1,7	2,9076
FBgn0039128	150472_at	CG13599	-	microtubule motor activity / plus-end-directed microtubule motor activity / structural constituent of cytoskeleton	-	-	1,6	4,9676
FBgn0039132	153802_at	CG5864	-	-	-	-	1,5	5,0592
FBgn0039206	153609_at	CG6631	-	-	-	-	1,5	4,0836
FBgn0039207	154494_at	CG5789	-	ATPase activity, coupled to transmembrane movement of substances / transporter activity / xenobiotic-transporting ATPase activity	1,5	3,1073	1,9	5,5436
FBgn0039240	150534_at	CG3744	-	serine-type peptidase activity	-	-	1,6	3,9368
FBgn0039251	150539_at	CG17462	-	nucleic acid binding / sigma DNA polymerase activity	1,7	4,2798	2,1	8,0085
FBgn0039252	141475_at	CG11771	-	-	-	-	1,5	5,0017
FBgn0039267	150548_at	CG31109	-	-	-	-	1,7	3,6647

FBgn0039352	142128_at	CG5053	-	-	-	-	1,6	4,079
FBgn0039355	150600_at	CG4730	-	transcription regulator activity	-	-	1,9	6,3547
FBgn0039449	150679_at	CG6425	-	-	-	-	1,9	4,9295
FBgn0039488	150713_at	CG6066	-	-	-	-	1,7	3,6257
FBgn0039543	141776_at	CG12428	-	-	-	-	1,6	5,4405
FBgn0039544	150748_at	CG12877	-	exoribonuclease activity / nuclease activity / nucleic acid binding	-	-	1,7	3,0813
FBgn0039558	142708_at	CG4980	-	-	-	-	1,5	4,6427
FBgn0039638	153804_at	CG11881	-	-	-	-	1,8	5,5091
FBgn0039644	153894_at	CG11897	-	multidrug transporter activity	-	-	1,6	4,7603
FBgn0039668	150823_at	CG2304	Trc8	-	-	-	1,5	3,6477
FBgn0039680	154905_at	CG1911	CAP-D2	nucleic acid binding	-	-	1,5	3,6903
FBgn0039705	141401_at	CG31033	-	-	-	-	1,6	3,7441
FBgn0039712	154243_at	CG15514	-	-	-	-	1,5	4,4088
FBgn0039740	153841_at	CG7928	-	transcription regulator activity	-	-	1,5	3,8827
FBgn0039861	154141_at	CG1800	pasha	double-stranded RNA binding	-	-	1,7	4,0169
FBgn0039870	154870_at	CG1896	-	-	-	-	1,6	3,6706
FBgn0039881	153510_at	CG1971	-	-	-	-	1,9	3,6419
FBgn0039888	150964_at	CG1487	krz	-	-	-	1,6	6,0859
FBgn0040626	151112_s_at	CG15552	Sox100B	-	-	-	2,8	5,5017
FBgn0040736	151211_at	CG16844	IM3	-	3,9	5,0704	4,8	6,7979
FBgn0040833	153602_at	CG7498	-	-	-	-	1,7	4,2813
FBgn0040835	151308_at	CG32365	-	-	-	-	1,6	3,1552
FBgn0040928	151397_at	CG15345	-	-	-	-	1,7	3,5601
FBgn0040929	151398_at	CG12659	-	-	-	-	1,6	4,5842
FBgn0040946	154370_at	CG14033	-	-	-	-	1,9	7,7195
FBgn0040981	151442_at	CG4482	mol	-	-	-	1,6	7,4564

Downregulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000055	151802_at	CG3481	Adh	-	-2,5	-8,2194	-8,0	-23,8077
FBgn0000061	143065_at	CG3935	al	specific RNA polymerase II transcription factor activity / transcription factor activity	-	-	-1,9	-5,4237
FBgn0000075	143066_at	CG10501	amd	aromatic-L-amino-acid decarboxylase activity / carboxy-lyase activity	-2,1	-5,1416	-1,5	-4,6981
FBgn0000095	142814_at	CG1028	Antp	specific RNA polymerase II transcription factor activity	-1,9	-3,3502	-1,7	-3,0894
FBgn0000150	142560_at	CG2210	awd	nucleoside-diphosphate kinase activity / nucleotide kinase activity	-	-	-1,7	-3,7198
FBgn0000157	143081_at	CG3629	Dll	specific RNA polymerase II transcription factor activity	-1,9	-2,9243	-1,7	-3,318
FBgn0000165	151955_at	CG5779	Bc	-	-1,6	-3,7614	-3,2	-9,6531
FBgn0000299	153378_at	CG4145	Cg25C	extracellular matrix structural constituent / structural molecule activity	-1,9	-5,1616	-4,3	-12,2501
FBgn0000337	143103_at	CG1555	cn	-	-3,7	-9,6807	-1,6	-4,43
FBgn0000439	143122_at	CG2189	Dfd	RNA polymerase II transcription factor activity / transcription factor activity	-2,1	-5,2306	-1,8	-5,1953
FBgn0000579	143150_at	CG17654	Eno	-	-	-	-1,6	-5,0686
FBgn0001091	154244_at	CG12055	Gapdh1	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	-	-	-3,4	-14,9483
FBgn0001092	143175_at	CG8893	Gapdh2	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity	-	-	-2,9	-9,2847
FBgn0001114	141472_at	CG9280	Glt	calcium ion binding	-1,9	-3,8028	-2,4	-6,9727
FBgn0001145	143181_at	CG1743	Gs2	glutamate-ammonia ligase activity	-	-	-2,4	-6,092
FBgn0001149	143184_at	CG10045	GstD1	glutathione transferase activity	-	-	-2,3	-7,9811
FBgn0001208	153434_at	CG7399	Hn	tryptophan 5-monooxygenase activity	-	-	-1,7	-6,9013
FBgn0001226	153307_at	CG4466	Hsp27	-	-	-	-1,7	-6,3693
FBgn0001229	143196_at	CG4190	Hsp67Bc	-	-	-	-1,9	-5,9677
FBgn0001230	143197_at	CG5436	Hsp68	unfolded protein binding	-	-	-2,2	-4,6316
FBgn0001233	143198_at	CG1242	Hsp83	ATPase activity, coupled	-	-	-1,8	-5,2296
FBgn0001235	143199_at	CG17117	hth	specific RNA polymerase II transcription factor activity / transcription factor activity	-2,0	-6,9188	-1,9	-5,7129
FBgn0001256	141386_at	CG10717	ImpL1	-	-	-	-1,5	-3,4666
FBgn0002031	152440_at	CG10691	l(2)37Cc	-	-	-	-1,8	-3,718
FBgn0002522	143230_at	CG1264	lab	specific RNA polymerase II transcription factor activity / transcription factor activity	-	-	-2,7	-5,2096
FBgn0002561	143237_at	CG3839	l(1)sc	specific RNA polymerase II transcription factor activity / transcription factor activity	-1,6	-3,6547	-	-
FBgn0002578	143245_at	CG8342	m1	serine-type endopeptidase inhibitor activity	-2,4	-5,1284	-2,7	-11,0232
FBgn0002741	143263_at	CG17927	Mhc	ATPase activity, coupled / cytoskeletal protein binding / microfilament motor activity / structural constituent of cytoskeleton / structural constituent of muscle	-	-	-2,0	-4,8243
FBgn0002772	143264_at	CG5596	Mlc1	ATPase activity, coupled / microfilament motor activity / NOT calcium ion binding	-	-	-2,1	-7,8301
FBgn0002773	143265_at	CG2184	Mlc2	ATPase activity, coupled / calcium ion binding / calmodulin binding / microfilament motor activity	-	-	-2,1	-5,7646
FBgn0002789	143271_at	CG4696	Mp20	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	-5,1	-18,2751
FBgn0002868	143276_at	CG9470	MtnA	metal ion binding	-1,9	-5,2107	-2,5	-10,2121
FBgn0002921	151602_at	CG5670	Atpalpha	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances / sodium:potassium-exchanging ATPase activity	-	-	-1,6	-2,8282
FBgn0003057	143296_at	CG10598	-	-	-	-	-7,2	-19,2688
FBgn0003067	143299_at	CG17725	Pepck	phosphoenolpyruvate carboxykinase (GTP) activity	-1,7	-3,6468	-2,0	-7,442
FBgn0003074	152515_at	CG8251	Pgi	phosphogluconate dehydrogenase (decarboxylating) activity	-	-	-1,7	-4,9858
FBgn0003075	143301_at	CG3127	Pgk	carbohydrate kinase activity / phosphoglycerate kinase activity	-	-	-2,2	-6,9739
FBgn0003089	143305_at	CG9614	pip	heparin-sulfate 2-sulfotransferase activity / sulfotransferase activity	-1,8	-6,5823	-2,9	-9,7353
FBgn0003149	152555_at	CG5939	Prm	cytoskeletal protein binding / motor activity / structural constituent of cytoskeleton / structural constituent of muscle	-	-	-2,1	-9,1374
FBgn0003178	141674_at	CG7070	PyK	carbohydrate kinase activity / pyruvate kinase activity	-	-	-2,3	-7,2221
FBgn0003187	143316_at	CG6433	qua	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	-1,6	-4,0332
FBgn0003308	152200_at	CG7642	ry	xanthine dehydrogenase activity	-	-	-2,1	-6,2458
FBgn0003326	143333_at	CG17579	sca	receptor binding / signal transducer activity	-1,6	-3,3097	-	-
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-11,6	-14,019	-47,6	-51,2387
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	-18,0	-23,073	-88,5	-37,7408
FBgn0003358	143341_at	CG31039	Jon99Ci	elastase activity / serine-type endopeptidase activity	-	-	-3,1	-9,772
FBgn0003411	143353_at	CG1641	sisA	protein heterodimerization activity / transcription factor activity	-1,9	-5,7123	-	-
FBgn0003507	141687_at	CG3992	srp	DNA binding / general RNA polymerase II transcription factor activity / RNA polymerase II transcription factor activity / transcriptional activator activity	-	-	-1,7	-3,8417
FBgn0003738	152334_at	CG2171	Tpi	intramolecular transferase activity / triose-phosphate isomerase activity	-	-	-1,7	-4,1505
FBgn0003863	143385_at	CG18444	epsilonTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity	-1,9	-4,5846	-8,1	-14,8921
FBgn0003944	143400_at	CG10388	Ubx	DNA binding / specific RNA polymerase II transcription factor activity / transcription factor activity	-7,8	-9,3768	-4,0	-5,968
FBgn0004028	143415_at	CG7178	wupA	actin binding / structural constituent of cytoskeleton / tropomyosin binding	-	-	-1,8	-6,1503
FBgn0004117	143427_at	CG4843	Tm2	actin binding / structural constituent of cytoskeleton	-	-	-1,8	-5,4259
FBgn0004169	142555_at	CG7107	up	tropomyosin binding	-	-	-1,7	-3,6698
FBgn0004396	143003_at	CG7450	CrebA	DNA binding / protein homodimerization activity / RNA polymerase II transcription factor activity / transcription factor activity	-	-	-1,5	-2,9694
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,8	-6,6445	-2,3	-9,8709
FBgn0004426	143465_f_at	CG9111	LysC	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,0	-7,715	-2,4	-8,2527
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-6,2	-11,8067	-5,6	-10,4875
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-4,1	-9,6155	-2,5	-10,4393
FBgn0004430	143469_at	CG1165	LysS	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-	-	-1,9	-4,1806
FBgn0004511	143475_at	CG9355	dy	structural constituent of cuticle (sensu Insecta)	-	-	-1,7	-4,3521
FBgn0004782	143514_s_at	CG1252	Ccp84Ab	structural constituent of larval cuticle (sensu Insecta)	-3,5	-7,116	-2,8	-5,5968
FBgn0005671	153041_at	CG17369	Vha55	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,9	-5,7867
FBgn0010019	152015_at	CG3972	Cyp4g1	electron transporter activity / oxidoreductase activity	-	-	-2,1	-5,6273
FBgn0010357	143602_at	CG18211	betaTry	trypsin activity	-	-	-46,3	-24,1431
FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-3,5	-7,577	-100,0	-23,6527
FBgn0010387	143608_at	CG8627	Dbi	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-1,7	-6,0713
FBgn0010423	143622_at	CG9073	TpnC47D	calcium ion binding / calmodulin binding	-1,5	-3,2612	-2,2	-8,6538
FBgn0010425	143624_at	CG18681	epsilonTry	trypsin activity	-2,8	-6,0566	-15,6	-21,1352
FBgn0011361	143658_at	CG9160	mtacp1	NADH dehydrogenase (ubiquinone) activity / NADH dehydrogenase activity	-	-	-1,5	-3,9743
FBgn0011555	143660_at	CG12385	thetaTry	trypsin activity	-	-	-1,5	-4,5503
FBgn0011556	143661_at	CG12387	betaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity / trypsin activity	-	-	-2,5	-4,8365
FBgn0011591	143664_at	CG10580	fng	acetylglucosaminyltransferase activity / receptor binding / transferase activity, transferring glycosyl groups / UDP-glycosyltransferase activity	-1,5	-3,8557	-1,9	-4,6555
FBgn0011603	153419_at	CG15444	ine	neurotransmitter:sodium symporter activity	-	-	-2,4	-6,7081
FBgn0011828	152747_at	CG12002	Pxn	peroxidase activity	-	-	-1,7	-6,8456
FBgn0012034	153769_at	CG9390	AcCoAS	-	-	-	-1,9	-6,4437
FBgn0014141	141641_at	CG3937	cher	actin binding / structural constituent of cytoskeleton	-2,1	-8,0145	-	-
FBgn0014343	143756_at	CG10601	mirr	protein binding / transcription factor activity / transcriptional activator activity	-	-	-1,7	-4,1197
FBgn0014388	143757_at	CG1921	sty	receptor binding	-1,6	-3,0585	-	-
FBgn0014455	153144_at	CG11654	Ahcy13	-	-	-	-1,5	-4,7591

FBgn0014863	143769_at	CG1019	Mlp84B	protein binding	-	-	-1,8	-7,226
FBgn0014869	152504_at	CG1721	Pglym78	phosphoglycerate mutase activity	-	-	-1,8	-9,1293
FBgn0014877	153163_at	CG6155	Roe1	unfolded protein binding	-	-	-1,8	-4,8517
FBgn0015245	141664_at	CG12101	Hsp60	ATPase activity, coupled / unfolded protein binding	-	-	-1,8	-6,9462
FBgn0015316	143796_at	CG9564	Try29F	peptidase activity / serine-type peptidase activity / trypsin activity	-3,0	-5,9168	-2,6	-3,3673
FBgn0015766	155091_at	CG10596	Msr-110	-	-2,0	-4,076	-1,6	-4,8614
FBgn0015774	151503_at	CG10521	NetB	structural molecule activity / structural molecule activity	-	-	-1,5	-3,212
FBgn0015904	143855_at	CG10571	ara	DNA binding / specific RNA polymerase II transcription factor activity / transcription factor activity / transcription regulator activity	-1,6	-4,2966	-1,8	-7,0689
FBgn0016075	143868_at	CG16858	vkg	extracellular matrix structural constituent	-1,9	-4,9525	-4,5	-12,311
FBgn0016694	153055_at	CG17888	Pdp1	DNA binding / protein homodimerization activity / transcription factor activity	-1,5	-3,4678	-1,8	-8,1595
FBgn0016718	151805_at	CG2194	Reg-3	-	-	-	-1,7	-4,8376
FBgn0016724	151538_s_at	CG11064	RfaBp	fatty acid binding / heme binding / microtubule binding / retinoid binding / structural molecule activity	-	-	-2,1	-4,311
FBgn0019643	152456_at	CG3318	Dat	aralkylamine N-acetyltransferase activity / arylamine N-acetyltransferase activity / cocaine binding / dopamine transporter activity / dopamine:sodium symporter activity	-	-	-1,5	-3,2529
FBgn0019650	152583_at	CG11186	toy	specific RNA polymerase II transcription factor activity	-1,8	-3,6756	-	-
FBgn0020235	143911_at	CG7610	ATPsyn-gamma	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,5	-4,8221
FBgn0020307	143919_at	CG5799	dve	AT DNA binding / transcription factor activity	-	-	-1,7	-4,1258
FBgn0020378	143922_at	CG1343	Sp1	RNA polymerase II transcription factor activity	-2,4	-3,9366	-1,6	-3,9632
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-2,3	-7,2436	-3,1	-12,2229
FBgn0020414	152116_at	CG4559	Idgf3	hydrolase activity, hydrolyzing N-glycosyl compounds / imaginal disc growth factor activity / NOT chitinase activity	-	-	-2,1	-6,9089
FBgn0020508	143929_at	CG9540	Ag5r2	-	-	-	-5,2	-8,1216
FBgn0020611	153422_at	CG8048	Vha44	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,7	-5,9893
FBgn0020637	143935_s_at	CG10534	Lcp65Ag2	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	-	-	-7,4	-32,1918
FBgn0020638	141314_at	CG10530	Lcp65Ag1	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	-	-	-7,9	-14,4544
FBgn0020642	143938_at	CG6956	Lcp65Ac	structural constituent of larval cuticle (sensu Insecta)	-2,0	-5,3089	-	-
FBgn0020653	154053_at	CG2151	Trxr-1	antioxidant activity	-	-	-2,0	-6,3777
FBgn0020906	143944_at	CG8867	Jon25Bi	elastase activity / pancreatic elastase activity / serine-type endopeptidase activity	-	-	-5,0	-12,8958
FBgn0020907	143945_at	CG14904	Scp2	calcium ion binding / GTPase activity	-	-	-1,6	-6,9152
FBgn0022341	143955_at	CG33521	-	-	-	-	-1,7	-3,9386
FBgn0022703	143961_at	CG17682	Cht1	chitinase activity	-	-	-1,6	-3,5522
FBgn0023417	143985_at	CG7807	AP-2	RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity	-	-	-1,7	-3,5163
FBgn0023496	143988_at	CG7279	Lip1	lipase activity / triacylglycerol lipase activity	-	-	-1,6	-3,1986
FBgn0023537	153323_at	CG17896	-	-	-	-	-2,9	-7,6408
FBgn0024315	142681_at	CG8098	Picot	high affinity inorganic phosphate:sodium symporter activity	-	-	-5,1	-10,9649
FBgn0024361	144018_at	CG11415	Tsp2A	-	-	-	-1,6	-4,4703
FBgn0024978	153536_at	CG2713	-	-	-	-	-1,5	-4,2554
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-1,7	-2,8639	-	-
FBgn0026210	153275_at	CG2520	lap	clathrin binding / phosphatidylinositol binding	-	-	-1,9	-3,3564
FBgn0026562	144147_at	CG6378	BM-40-SPARC	-	-1,8	-6,4566	-2,1	-7,9451
FBgn0026753	144156_at	CG6213	Vha13	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,7	-4,8235
FBgn0026761	155020_at	CG3152	Trap1	-	-	-	-1,5	-5,0896
FBgn0027107	144173_at	CG17063	inx6	gap-junction forming channel activity / gap-junction forming channel activity / innexin channel activity / innexin channel activity	-	-	-2,0	-3,9164
FBgn0027111	144176_at	CG1221	miple	-	-3,2	-7,8076	-2,1	-6,0085
FBgn0027348	153318_at	CG4501	bgm	-	-	-	-1,9	-6,526
FBgn0027527	144185_at	CG1151	Osi6	-	-2,2	-7,1157	-1,8	-5,1113
FBgn0027556	152286_at	CG4928	-	-	-1,9	-2,8439	-3,4	-7,9154
FBgn0027571	152126_at	CG3523	-	fatty-acid synthase activity	-	-	-4,3	-10,7826
FBgn0027573	152119_at	CG5518	sda	-	-	-	-2,7	-4,7862
FBgn0027580	152059_at	CG1516	-	-	-1,7	-3,8917	-2,1	-5,6933
FBgn0027594	151918_s_at	CG2086	drpr	extracellular matrix structural constituent / receptor activity	-1,6	-4,4208	-	-
FBgn0027596	151915_at	CG10249	-	-	-	-	-1,5	-3,7583
FBgn0027844	152261_at	CG7820	CAH1	carbonate dehydratase activity	-2,7	-4,1161	-3,0	-9,9222
FBgn0027945	141370_at	CG7758	ppl	hydrolase activity	-	-	-1,5	-4,1047
FBgn0028381	144201_at	CG14902	decay	caspase activity	-	-	-1,9	-3,5107
FBgn0028491	151495_at	CG2930	-	proton-dependent oligopeptide transporter activity	-1,6	-3,7713	-2,2	-7,075
FBgn0028510	144220_at	CG15261	-	-	-	-	-2,0	-4,7313
FBgn0028533	142950_at	CG7953	-	-	-	-	-1,5	-6,6359
FBgn0028536	144233_at	CG15281	-	-	-4,6	-9,9917	-10,0	-11,0219
FBgn0028544	153391_at	CG16884	-	-	-	-	-2,9	-8,4397
FBgn0028573	144238_at	CG5700	prc	-	-	-	-1,9	-5,6333
FBgn0028583	144239_at	CG12794	lcs	-	-	-	-1,6	-4,8891
FBgn0028789	144254_at	CG5133	Doc1	transcription factor activity	-1,5	-3,1091	-	-
FBgn0028876	144283_at	CG16876	-	-	-	-	-1,5	-4,6595
FBgn0028905	144302_at	CG32972	-	-	-2,4	-9,2896	-1,9	-4,4317
FBgn0028920	144310_at	CG8997	-	-	-	-	-1,6	-5,2814
FBgn0029531	144348_at	CG13362	-	-	-	-	-2,7	-11,5692
FBgn0029620	142467_at	CG7981	-	-	-	-	-2,1	-6,385
FBgn0029639	144419_at	CG14419	-	-	-1,5	-3,2095	-2,3	-7,5571
FBgn0029650	144430_at	CG3939	-	-	-	-	-1,7	-4,909
FBgn0029652	144432_at	CG14265	-	-	-2,4	-4,1318	-2,6	-11,5045
FBgn0029721	153790_at	CG7010	l(1)G0334	pyruvate dehydrogenase (acetyl-transferring) activity	-	-	-1,8	-5,4722
FBgn0029804	144549_at	CG3097	-	carboxypeptidase A activity	-1,9	-6,2935	-1,9	-5,5123
FBgn0029807	142938_at	CG3108	-	metallocarboxypeptidase activity	-1,6	-3,1342	-1,8	-4,2589
FBgn0029823	144561_at	CG3011	-	glycine hydroxymethyltransferase activity	-	-	-2,3	-7,0808
FBgn0029854	144586_at	CG3566	-	electron transporter activity	-	-	-1,5	-3,1736
FBgn0029889	155145_at	CG4094	l(1)G0255	fumarate hydratase activity / fumarate hydratase activity	-	-	-1,7	-5,7347
FBgn0029969	154229_at	CG10932	-	acetyl-CoA C-acetyltransferase activity	-	-	-1,6	-3,4687
FBgn0029990	152816_at	CG2233	-	-	-	-	-4,7	-8,5828
FBgn0029994	144675_at	CG2254	-	oxidoreductase activity	-	-	-1,9	-6,5915
FBgn0030040	144700_at	CG15347	-	-	-	-	-2,2	-9,048
FBgn0030041	144701_at	CG12116	-	sepiapterin reductase activity	-	-	-2,8	-6,0274
FBgn0030059	144712_at	CG1787	Hexo2	beta-N-acetylhexosaminidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds	-	-	-1,9	-4,3079
FBgn0030138	141481_at	CG32699	-	receptor activity	-	-	-1,7	-5,8333
FBgn0030183	152303_at	CG15309	-	molecular_function unknown	-	-	-1,7	-4,7525
FBgn0030187	154819_at	CG2961	Ipod	-	-2,4	-5,0215	-	-
FBgn0030251	152332_at	CG2145	-	serine-type peptidase activity	-	-	-1,8	-4,1102
FBgn0030263	142756_at	CG2076	-	-	-	-	-2,0	-5,4854
FBgn0030309	153527_at	CG1572	-	-	-	-	-1,5	-3,3512
FBgn0030362	141568_at	CG1803	regucalcin	-	-	-	-2,1	-6,8568
FBgn0030394	144941_at	CG2560	-	structural constituent of larval cuticle (sensu Insecta)	-	-	-2,1	-7,5504
FBgn0030465	144996_at	CG15743	-	nucleotide phosphatase activity	-	-	-1,6	-4,7213
FBgn0030472	153359_at	CG1633	Jafrac1	antioxidant activity / peroxidase activity / thioredoxin peroxidase activity	-	-	-5,0	-12,9174
FBgn0030478	141639_at	CG1640	-	-	-	-	-1,8	-5,1358
FBgn0030481	152076_at	CG1662	-	receptor signaling protein activity	-	-	-1,7	-4,3723
FBgn0030537	145043_at	CG12480	-	-	-1,9	-3,7377	-17,4	-17,0462
FBgn0030539	153732_at	CG1368	-	structural constituent of chorion (sensu Insecta)	-	-	-4,5	-16,5731
FBgn0030541	145047_at	CG11584	-	molecular_function unknown	-1,7	-2,9418	-12,4	-24,9284
FBgn0030569	155122_at	CG9411	-	-	-3,0	-4,2598	-1,7	-4,5488
FBgn0030593	152393_at	CG9512	-	choline dehydrogenase activity	-	-	-2,6	-3,4288
FBgn0030650	141692_at	CG33206	l(1)G0168	-	-1,6	-3,7621	-2,0	-7,8631
FBgn0030653	153970_at	CG7860	-	asparaginase activity	-	-	-1,8	-6,462
FBgn0030737	145178_at	CG9914	-	oxidoreductase activity / structural molecule activity	-	-	-1,5	-3,7204
FBgn0030775	145202_at	CG9673	-	NOT serine-type endopeptidase activity	-	-	-2,5	-4,5959
FBgn0030821	145230_at	CG5010	-	-	-	-	-1,5	-4,5602
FBgn0030825	155011_at	CG32563	-	-	-2,7	-7,5807	-16,4	-21,9345
FBgn0030837	145243_at	CG8661	-	-	-	-	-2,6	-3,6098
FBgn0030882	145269_at	CG6835	GS	catalytic activity / glutathione synthase activity / ligase activity	-1,6	-4,0629	-1,7	-6,7699
FBgn0030887	145273_at	CG6867	-	extracellular matrix structural constituent / structural molecule activity	-	-	-1,5	-2,9531
FBgn0030980	145340_at	CG7406	-	-	-	-	-2,1	-5,0583
FBgn0031000	145357_at	CG7876	-	-	-	-	-2,1	-4,456
FBgn0031021	145368_at	CG12203	-	NADH dehydrogenase (ubiquinone) activity / NADH dehydrogenase activity / oxidoreductase activity	-	-	-1,5	-3,2408
FBgn0031141	145450_at	CG1304	-	serine-type endopeptidase activity	-	-	-2,3	-5,4907

FBgn0031249	141435_at	CG11911	-	chymotrypsin activity / serine-type endopeptidase activity	-	-	-6,2	-12,2726
FBgn0031277	145547_r_at	CG13947	-	-	-	-	-2,2	-6,5392
FBgn0031294	153019_at	CG31795	ia2	protein tyrosine phosphatase activity / transmembrane receptor protein tyrosine phosphatase activity	-	-	-1,6	-3,6296
FBgn0031380	152801_at	CG4233	Got2	aspartate transaminase activity	-	-	-2,8	-8,6607
FBgn0031433	145648_at	CG18559	Cyp309a2	electron transporter activity / electron transporter activity / oxidoreductase activity / oxidoreductase activity	-	-	-4,1	-9,2889
FBgn0031561	145731_at	CG16712	-	serine-type endopeptidase inhibitor activity	-1,9	-6,0082	-3,9	-9,5336
FBgn0031579	145743_at	CG15422	-	-	-	-	-1,8	-3,2248
FBgn0031629	145779_at	CG3244	-	-	-	-	-2,2	-7,107
FBgn0031653	145795_at	CG8871	Jon25Biii	elastase activity / serine-type peptidase activity	-9,9	-9,5356	-58,8	-32,0902
FBgn0031654	145796_at	CG8869	Jon25Bii	chymotrypsin activity / serine-type endopeptidase activity	-	-	-33,8	-20,3352
FBgn0031688	145813_at	CG6081	Cyp28d2	electron transporter activity / oxidoreductase activity	-3,8	-5,1926	-5,2	-8,0957
FBgn0031702	152614_at	CG14021	-	-	-	-	-2,2	-6,5411
FBgn0031737	151477_at	CG11142	-	structural constituent of peritrophic membrane (sensu Insecta)	-	-	-2,7	-8,9442
FBgn0031816	145900_at	CG16947	-	-	-	-	-1,7	-4,2949
FBgn0031839	145915_at	CG31634	Oatp26F	organic anion transporter activity	-1,6	-5,1832	-	-
FBgn0031908	153932_at	CG5177	-	trehalose-phosphatase activity	-	-	-1,7	-5,2282
FBgn0031914	153381_at	CG5973	-	carrier activity / retinal binding	-	-	-1,5	-3,7957
FBgn0031936	145974_at	CG13794	-	-	-6,2	-10,4479	-3,0	-8,4854
FBgn0031937	145975_at	CG13795	-	amino acid transporter activity / transporter activity	-1,6	-3,771	-	-
FBgn0031938	145976_s_at	CG13796	-	glycine transporter activity / structural constituent of adult cuticle (sensu Insecta)	-	-	-1,5	-3,3866
FBgn0031939	145977_at	CG13796	-	glycine transporter activity / structural constituent of adult cuticle (sensu Insecta)	-	-	-1,6	-2,7962
FBgn0031948	152382_at	CG7149	-	-	-	-	-1,8	-5,1844
FBgn0032021	146021_at	CG7781	-	-	-	-	-1,6	-4,1508
FBgn0032068	142147_at	CG9466	-	alpha-mannosidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds	-	-	-2,5	-7,2059
FBgn0032069	146050_at	CG9468	-	alpha-mannosidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds	-2,2	-3,7299	-6,1	-8,4254
FBgn0032075	146053_at	CG9496	Tsp29Fb	-	-	-	-2,0	-4,4092
FBgn0032076	141703_at	CG9510	-	argininosuccinate lyase activity	-	-	-1,5	-3,3152
FBgn0032088	146061_at	CG13102	-	-	-	-	-2,0	-6,1659
FBgn0032114	146084_at	CG3752	Aldh	aldehyde dehydrogenase (NAD) activity	-	-	-7,4	-16,8193
FBgn0032136	153828_at	CG15828	-	lipid binding	-	-	-1,7	-5,6375
FBgn0032144	146103_at	CG17633	-	carboxypeptidase A activity	-	-	-3,8	-9,3587
FBgn0032152	141255_at	CG4535	FKBP59	FK506 binding / peptidyl-prolyl cis-trans isomerase activity	-	-	-1,6	-3,9093
FBgn0032167	141658_at	CG5853	-	anion channel activity / ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	-2,2	-7,7669
FBgn0032177	146118_at	CG33301	-	molecular_function unknown / structural constituent of cuticle (sensu Insecta)	-	-	-1,6	-5,2094
FBgn0032192	146129_at	CG5731	-	-	-2,1	-5,4013	-2,0	-4,2497
FBgn0032237	146151_at	CG5362	-	L-malate dehydrogenase activity	-	-	-1,6	-5,5648
FBgn0032264	146165_at	CG6113	-	triacylglycerol lipase activity	-	-	-1,5	-4,5853
FBgn0032282	146181_at	CG7299	-	-	-7,2	-8,7595	-22,4	-18,3639
FBgn0032287	151967_at	CG6415	-	-	-	-	-1,9	-5,8467
FBgn0032304	146197_at	CG17134	-	cathepsin D activity	-	-	-3,2	-6,3881
FBgn0032373	146249_at	CG12602	-	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-2,4	-6,5694
FBgn0032396	151733_at	CG5304	l(2)01810	transporter activity	-	-	-2,0	-5,2867
FBgn0032405	146269_at	CG14946	-	oxidoreductase activity	-	-	-2,7	-8,336
FBgn0032463	146305_at	CG3762	Vha68-2	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-1,8	-5,5828
FBgn0032511	142243_at	CG9306	-	NADH dehydrogenase (ubiquinone) activity / NADH dehydrogenase activity	-	-	-1,5	-2,8394
FBgn0032537	146350_s_at	CG16885	-	-	-	-	-2,7	-13,3271
FBgn0032606	146379_at	CG17932	Ugt36Bc	glucuronosyltransferase activity	-	-	-1,8	-4,3141
FBgn0032679	141807_at	CG10302	bsf	mRNA 3′-UTR binding / oxidoreductase activity	-	-	-1,6	-3,0186
FBgn0032693	155069_at	CG10391	Cyp310a1	electron transporter activity / oxidoreductase activity	-	-	-1,6	-5,174
FBgn0032721	154383_at	CG10602	-	metallopeptidase activity	-	-	-2,2	-6,1359
FBgn0032773	153365_at	CG15825	-	-	-1,6	-3,7069	-3,1	-7,2637
FBgn0032803	146500_at	CG13082	-	-	-	-	-2,4	-7,0825
FBgn0032806	146503_at	CG10363	TepIV	protease inhibitor activity	-	-	-1,7	-5,3094
FBgn0032844	146532_at	CG10746	fok	-	-2,2	-7,4202	-2,1	-6,6095
FBgn0032899	152155_at	CG9338	-	-	-1,6	-4,065	-2,6	-10,6606
FBgn0032946	146586_at	CG8663	nrv3	-	-	-	-2,2	-5,0678
FBgn0032993	141373_at	CG18117	-	-	-	-	-1,7	-4,1936
FBgn0033093	151882_at	CG3270	-	oxidoreductase activity	-	-	-1,8	-4,3555
FBgn0033173	146742_at	CG30502	-	-	-	-	-1,6	-4,2782
FBgn0033183	146745_at	CG1620	-	-	-	-	-1,7	-3,0673
FBgn0033205	141701_at	CG2064	-	oxidoreductase activity	-2,4	-5,0762	-1,6	-4,3174
FBgn0033221	146767_at	CG12825	-	-	-	-	-1,9	-3,8803
FBgn0033245	152407_at	CG11198	-	-	-	-	-1,6	-4,6551
FBgn0033268	146792_at	CG2297	Obp44a	-	-	-	-3,4	-10,5569
FBgn0033271	152726_at	CG8708	-	transferase activity / transferase activity, transferring glycosyl groups	-	-	-1,6	-3,257
FBgn0033275	146794_at	CG14756	-	-	-12,8	-16,1154	-100,0	-47,2649
FBgn0033319	146826_at	CG8579	Jon44E	chymotrypsin activity	-1,6	-3,5671	-10,6	-13,4573
FBgn0033359	155018_at	CG8213	-	serine-type endopeptidase activity / trypsin activity	-	-	-1,6	-4,4352
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-2,0	-6,9155	-2,4	-10,9751
FBgn0033423	151956_at	CG1809	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-2,7	-7,6072
FBgn0033446	152817_at	CG1648	-	-	-	-	-1,5	-6,0634
FBgn0033448	142262_at	CG1623	-	-	-	-	-1,5	-3,923
FBgn0033509	154737_at	CG12908	Ndg	structural molecule activity	-1,8	-4,2423	-1,5	-5,1768
FBgn0033541	146958_at	CG12934	-	-	-2,3	-5,0302	-6,2	-12,7578
FBgn0033590	146988_at	CG13217	-	-	-2,1	-4,5418	-1,5	-3,282
FBgn0033604	147002_at	CG9070	-	-	-	-	-9,5	-20,7797
FBgn0033613	147009_at	CG13211	-	-	-	-	-2,0	-4,1983
FBgn0033634	147022_at	CG7763	-	-	-2,5	-4,2105	-1,9	-5,6294
FBgn0033643	147029_s_at	CG30035	-	fructose transporter activity / glucose transporter activity / glucose transporter activity	-2,1	-7,5196	-	-
FBgn0033717	153538_at	CG8839	-	fatty acid amide hydrolase activity	-	-	-1,6	-3,9764
FBgn0033721	147084_at	CG13159	-	-	-8,8	-15,5485	-11,7	-19,612
FBgn0033724	153425_at	CG8501	-	-	-	-	-2,0	-6,5553
FBgn0033726	147087_at	CG8836	-	structural constituent of larval cuticle (sensu Insecta)	-	-	-3,2	-4,1423
FBgn0033765	152880_at	CG8772	nemy	glutaminase activity	-	-	-1,8	-3,6384
FBgn0033779	142416_at	CG3814	-	N-methyl-D-aspartate selective glutamate receptor activity	-1,6	-3,333	-2,0	-5,8007
FBgn0033787	147125_at	CG13321	-	-	-1,6	-4,6328	-3,1	-8,9716
FBgn0033788	147126_i_at	CG13323	-	-	-	-	-2,8	-5,6702
FBgn0033878	142709_s_at	CG6543	-	oxidoreductase activity	-	-	-2,0	-6,2334
FBgn0033913	151760_at / 143046_at	CG8468	-	monocarboxylate porter activity	-1,7	-2,8438	-1,5	-4,649
FBgn0033968	141323_at	CG10200	-	-	-	-	-1,6	-4,1015
FBgn0034010	147242_at	CG8157	-	-	-2,5	-6,4989	-8,7	-11,4505
FBgn0034011	147243_at	CG8160	-	-	-	-	-1,8	-4,9853
FBgn0034034	142370_at	CG8205	fus	RNA binding	-	-	-1,6	-3,3956
FBgn0034044	147264_at	CG12969	tun	actin binding / structural constituent of cytoskeleton	-	-	-1,5	-4,8793
FBgn0034048	152312_at	CG8256	l(2)k05713	glycerol-3-phosphate dehydrogenase activity	-	-	-2,1	-5,4681
FBgn0034108	155081_at	CG3767	JhI-26	-	-2,3	-5,013	-1,9	-7,7166
FBgn0034201	147355_at	CG17290	-	-	-	-	-7,3	-7,9886
FBgn0034203	147357_at	CG30457	-	-	-	-	-3,0	-5,5798
FBgn0034204	147358_at	CG10953	-	-	-	-	-2,1	-6,325
FBgn0034259	154495_at	CG6459	-	-	-	-	-2,0	-7,1972
FBgn0034288	147405_at	CG5084	-	-	-	-	-5,7	-9,8853
FBgn0034289	147406_at	CG10910	-	-	-	-	-7,0	-4,9793
FBgn0034292	147407_at	CG5767	-	-	-	-	-3,2	-7,3802
FBgn0034294	147409_at	CG5765	-	-	-1,8	-4,8159	-6,0	-18,3062
FBgn0034295	147410_at	CG10911	-	-	-	-	-2,1	-5,796
FBgn0034318	147422_at	CG14500	-	-	-	-	-1,8	-3,5902
FBgn0034364	147450_at	CG5493	-	-	-1,7	-5,8467	-	-
FBgn0034365	153187_at	CG5335	-	protein transporter activity	-	-	-2,4	-6,5707
FBgn0034390	152083_at	CG15093	-	-	-3,8	-6,3497	-22,7	-17,8495
FBgn0034394	153069_at	CG15096	-	high affinity inorganic phosphate:sodium symporter activity	-	-	-1,9	-8,424
FBgn0034395	155162_at	CG15081	l(2)03709	-	-	-	-1,6	-5,4739

FBgn0034406	154747_at	CG15106	Jheh3	epoxide hydrolase activity / juvenile hormone epoxide hydrolase activity	-	-	-1,6	-3,7982
FBgn0034428	147486_i_at	CG18606	-	-	-	-	-1,8	-2,9753
FBgn0034475	147521_at	CG13874	Obp56h	odorant binding	-	-	-1,5	-5,107
FBgn0034501	141541_at	CG13868	-	-	-	-	-1,7	-3,76
FBgn0034564	147588_at	CG9344	-	pre-mRNA splicing factor activity	-	-	-1,6	-3,1899
FBgn0034583	155148_at	CG10527	-	farnesoic acid O-methyltransferase activity	-	-	-2,5	-9,4385
FBgn0034584	152512_at	CG9364	Treh	-	-	-	-1,5	-4,1506
FBgn0034602	152886_at	CG15658	-	-	-	-	-1,7	-4,1315
FBgn0034698	141793_at	CG6698	NtR	-	-1,8	-3,9511	-2,2	-6,2329
FBgn0034712	147666_at	CG3264	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-2,8	-7,9348
FBgn0034819	147740_at	CG9877	-	-	-	-	-2,1	-7,32
FBgn0034885	147793_at	CG4019	-	carrier activity / water channel activity	-	-	-2,7	-9,273
FBgn0034900	147802_at	CG12491	-	-	-1,5	-4,2737	-16,4	-16,6263
FBgn0034901	142461_at	CG11300	-	-	-	-	-3,1	-8,9391
FBgn0034952	152806_at	CG33519	-	protein serine/threonine kinase activity / structural constituent of cytoskeleton	-	-	-1,8	-4,7387
FBgn0035030	152422_at	CG3541	-	-	-	-	-1,6	-6,0838
FBgn0035077	154985_at	CG9083	-	-	-8,5	-13,8321	-	-
FBgn0035095	147907_at	CG32475	mthl8	G-protein coupled receptor activity	-2,8	-3,0102	-2,5	-4,2689
FBgn0035154	152830_at	CG3344	-	carboxypeptidase C activity / serine carboxypeptidase activity	-	-	-1,6	-3,9571
FBgn0035190	147960_at	CG13913	-	-	-4,8	-10,3083	-	-
FBgn0035281	148008_at	CG1919	-	structural constituent of cuticle (sensu Insecta)	-3,4	-5,4757	-	-
FBgn0035289	141428_at	CG12026	-	-	-	-	-1,5	-3,7735
FBgn0035326	141439_at	CG32302	-	-	-	-	-3,9	-8,3249
FBgn0035482	148137_at	CG14985	-	-	-2,5	-5,2147	-1,6	-4,3785
FBgn0035495	152055_at	CG14989	-	-	-	-	-1,6	-4,6802
FBgn0035544	148175_at	CG15021	-	-	-1,7	-5,055	-	-
FBgn0035545	148176_at	CG12607	-	-	-1,5	-4,1417	-1,5	-5,938
FBgn0035548	148179_at	CG15023	-	-	-	-	-3,0	-5,8852
FBgn0035551	148182_at	CG7465	-	-	-2,1	-8,4916	-33,8	-38,4279
FBgn0035552	148183_at	CG11350	-	-	-	-	-7,0	-8,6022
FBgn0035558	151577_at	CG11357	-	transferase activity, transferring glycosyl groups / UDP-galactose beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity	-1,8	-2,9083	-2,9	-4,4692
FBgn0035579	148202_at	CG32237	-	-	-3,4	-5,1627	-	-
FBgn0035580	148203_at	CG32237	-	-	-3,9	-10,2694	-2,4	-4,6759
FBgn0035582	148205_at	CG13705	-	-	-1,7	-5,5497	-3,7	-17,3333
FBgn0035583	148206_at	CG13704	-	-	-	-	-1,6	-3,1565
FBgn0035588	141484_at	CG10672	-	oxidoreductase activity, acting on CH-OH group of donors	-	-	-1,9	-3,4536
FBgn0035608	148223_at	CG10630	-	-	-1,7	-2,9602	-2,0	-4,6957
FBgn0035612	154869_at	CG10625	-	-	-	-	-2,9	-9,0722
FBgn0035619	148228_at	CG10592	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-2,4	-5,7344
FBgn0035620	151980_at	CG5150	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-2,2	-6,3451
FBgn0035662	152176_at	CG6457	yip7	chymotrypsin activity / serine-type endopeptidase activity	-	-	-3,6	-5,6392
FBgn0035664	148253_at	CG6467	Jon65Aiv	chymotrypsin activity / serine-type endopeptidase activity	-2,3	-7,0935	-34,7	-23,3608
FBgn0035665	151793_at	CG6483	Jon65Aiii	elastase activity / serine-type endopeptidase activity	-2,0	-2,974	-5,1	-13,0282
FBgn0035667	148255_at	CG10475	Jon65Ai	serine-type endopeptidase activity	-	-	-3,8	-13,0152
FBgn0035670	152006_at	CG10472	-	serine-type endopeptidase activity	-	-	-3,1	-8,4391
FBgn0035717	152709_at	CG10078	Prat2	-	-2,4	-6,1853	-1,6	-2,817
FBgn0035742	148307_i_at / 148308_f_at	CG8629	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-2,5	-6,3069	-2,9	-8,8737
FBgn0035744	148310_i_at	CG8628	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-13,4	-12,9795
FBgn0035770	153088_at	CG8588	pst	-	-	-	-1,7	-3,1342
FBgn0035779	148332_at	CG8562	-	metallocarboxypeptidase activity	-3,4	-6,8414	-6,1	-11,765
FBgn0035781	152794_at	CG8560	-	NOT carboxypeptidase activity	-	-	-2,6	-6,5433
FBgn0035858	148382_f_at	CG13674	-	-	-	-	-1,9	-5,4698
FBgn0035859	148384_f_at	CG13678	-	-	-	-	-1,6	-5,315
FBgn0035904	148410_at	CG6776	-	glutathione transferase activity	-	-	-2,4	-5,3763
FBgn0035917	152762_at	CG6416	-	-	-	-	-4,5	-7,4994
FBgn0035926	148422_at	CG5804	-	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-1,9	-5,2182	-8,1	-13,0988
FBgn0035929	148424_at	CG13311	-	structural molecule activity	-	-	-1,5	-3,3118
FBgn0035956	148441_at	CG5187	Doc2	transcription factor activity	-1,8	-3,4897	-	-
FBgn0035963	148446_at	CG4821	Tequila	pancreatic elastase activity / serine-type endopeptidase activity / trypsin activity	-	-	-1,7	-5,3795
FBgn0035999	148467_at	CG3552	-	-	-2,5	-6,1793	-2,7	-8,1378
FBgn0036024	141418_at	CG18180	-	chymotrypsin activity	-	-	-14,0	-14,2728
FBgn0036041	148488_at	CG32046	-	-	-	-	-1,5	-3,5697
FBgn0036074	148513_at	CG6611	ect	-	-	-	-1,6	-4,6876
FBgn0036131	148554_at	CG12522	-	-	-	-	-2,1	-7,6438
FBgn0036144	154200_at	CG6207	GlcAT-P	asioloorosomucoid beta-1,3-glucuronosyltransferase activity / galactosyl beta-1,3 N-acetylgalactosamine beta-1,3-glucuronosyltransferase activity / galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity / glucuronosyltransferase activity / N-acetyllactosamine beta-1,3-glucuronosyltransferase activity	-	-	-2,3	-4,5328
FBgn0036167	148580_f_at	CG33272	-	-	-2,8	-4,646	-1,7	-3,4401
FBgn0036182	153576_at	CG6084	-	aldehyde reductase activity	-	-	-4,2	-14,5298
FBgn0036227	148620_at	CG17826	-	-	-	-	-2,1	-4,2322
FBgn0036233	148625_at	CG6947	-	structural constituent of peritrophic membrane (sensu Insecta)	-	-	-2,5	-9,5624
FBgn0036316	153366_at	CG10960	-	glucose transporter activity	-1,5	-4,7059	-	-
FBgn0036334	148689_at	CG11267	-	ATPase activity, coupled / unfolded protein binding	-1,6	-3,0261	-1,8	-4,3058
FBgn0036362	141395_at	CG10725	-	structural constituent of peritrophic membrane (sensu Insecta)	-	-	-3,6	-8,7635
FBgn0036381	148725_at	CG8745	-	-	-2,0	-4,3252	-3,4	-8,6181
FBgn0036390	148732_at	CG13738	-	-	-8,5	-8,8156	-2,3	-7,2616
FBgn0036422	152897_at	CG3868	-	-	-	-	-3,1	-9,77
FBgn0036424	148749_at	CG9598	-	-	-	-	-1,6	-5,636
FBgn0036436	141447_at	CG4914	-	serine-type endopeptidase activity / trypsin activity	-	-	-2,5	-4,787
FBgn0036444	154049_at	CG32145	ome	dipeptidyl-peptidase IV activity	-	-	-1,9	-3,3749
FBgn0036467	148781_at	CG12310	-	-	-1,9	-5,1659	-23,9	-22,7118
FBgn0036469	148783_at	CG18649	-	-	-6,7	-9,3138	-4,1	-8,4261
FBgn0036470	148784_at	CG13463	-	-	-4,4	-6,6968	-1,7	-2,9609
FBgn0036494	153641_at	CG7250	Toll-6	transmembrane receptor activity / transmembrane receptor protein serine/threonine kinase activity	-1,6	-5,2649	-	-
FBgn0036551	148837_at	CG17029	-	inositol-1(or 4)-monophosphatase activity	-	-	-1,6	-3,9928
FBgn0036599	148872_at	CG13044	-	-	-	-	-2,6	-5,6046
FBgn0036600	148873_at	CG13043	-	-	-2,6	-8,4903	-3,9	-14,6279
FBgn0036605	148878_s_at	CG13041	-	-	-3,6	-5,9729	-4,8	-5,8907
FBgn0036606	148880_r_at	CG13060	-	-	-3,7	-5,7984	-2,4	-4,9675
FBgn0036607	148881_at	CG13059	-	-	-1,8	-5,1438	-1,6	-7,0281
FBgn0036635	141806_at	CG32158	-	adenylate cyclase activity	-	-	-1,6	-3,3283
FBgn0036638	148900_at	CG13033	-	-	-1,6	-3,2442	-	-
FBgn0036639	155051_at	CG4229	-	-	-2,1	-4,1903	-	-
FBgn0036642	148901_at	CG4169	-	ubiquinol-cytochrome-c reductase activity	-	-	-1,5	-5,4909
FBgn0036675	148923_at	CG32171	Lmpt	-	-	-	-1,7	-4,2853
FBgn0036677	148925_at	CG13023	-	-	-	-	-1,7	-3,732
FBgn0036737	148963_at	CG6298	Jon74E	chymotrypsin activity	-2,1	-3,5989	-3,5	-9,3345
FBgn0036765	148979_at	CG7408	-	N-acetylgalactosamine-4-sulfatase activity	-	-	-1,9	-4,0359
FBgn0036779	148988_at	CG13695	gk	-	-1,6	-2,8991	-	-
FBgn0036787	148995_at	CG4306	-	-	-1,5	-2,9958	-2,1	-5,5291
FBgn0036806	152798_at	CG4120	Cyp12c1	electron transporter activity / oxidoreductase activity	-	-	-2,9	-9,1253
FBgn0036824	152151_at	CG3902	-	short-branched-chain-acyl-CoA dehydrogenase activity	-	-	-1,9	-8,3005
FBgn0036831	141416_at	CG6839	-	-	-	-	-1,6	-3,0605
FBgn0036833	149024_at	CG3819	-	-	-	-	-13,2	-9,186
FBgn0036837	155139_at	CG18135	-	RNA binding / RNA methyltransferase activity	-	-	-2,0	-5,4862
FBgn0036852	149033_at	CG9739	fz2	G-protein coupled receptor activity / transmembrane receptor activity / Wnt receptor activity / Wnt-protein binding	-	-	-1,6	-3,4852
FBgn0036871	149048_r_at	CG14096	-	molecular_function unknown / molecular_function unknown	-	-	-1,6	-4,7722
FBgn0036875	149052_at	CG9449	-	acid phosphatase activity	-2,3	-6,6777	-4,0	-14,1749
FBgn0036945	141349_at	CG6981	-	-	-	-	-1,9	-8,0072
FBgn0036948	142733_at	CG7298	-	structural constituent of peritrophic membrane (sensu Insecta)	-4,4	-8,7319	-9,7	-15,6126
FBgn0036949	149099_at	CG7290	-	structural constituent of peritrophic membrane (sensu Insecta)	-1,9	-4,2618	-25,7	-13,1711

FBgn0036951	149101_at	CG7017	-	structural constituent of peritrophic membrane (sensu Insecta)	-	-	-3,7	-6,0121
FBgn0036952	141330_at	CG6933	-	structural constituent of peritrophic membrane (sensu Insecta)	-3,3	-5,7873	-8,0	-9,9512
FBgn0036992	151899_at	CG11796	-	-	-	-	-3,2	-4,5731
FBgn0037057	152050_at	CG10512	-	oxidoreductase activity	-	-	-1,7	-4,6107
FBgn0037069	149172_at	CG7658	-	structural constituent of larval cuticle (sensu Insecta)	-	-	-3,9	-11,4871
FBgn0037099	142695_at	CG7173	-	-	-	-	-1,6	-3,4077
FBgn0037177	149244_at	CG14454	-	molecular_function unknown	-2,2	-6,3242	-	-
FBgn0037179	149246_at	CG14453	-	-	-6,3	-9,7564	-3,4	-7,1566
FBgn0037180	149247_s_at	CG14452	-	-	-19,2	-18,2423	-23,5	-24,4789
FBgn0037181	149248_at	CG11370	-	-	-	-	-1,9	-5,8362
FBgn0037204	149261_at	CG11131	-	-	-3,0	-5,2986	-7,1	-8,7553
FBgn0037224	153953_at	CG14639	-	-	-4,1	-9,7631	-	-
FBgn0037228	153398_at	CG1092	-	-	-	-	-1,8	-2,9295
FBgn0037290	149305_at	CG1124	-	-	-	-	-1,7	-4,8371
FBgn0037323	149329_at	CG2663	-	carrier activity / tocopherol binding	-	-	-1,7	-5,3564
FBgn0037414	149380_at	CG1153	Osi7	-	-2,0	-8,242	-1,9	-6,9851
FBgn0037420	149386_at	CG15597	-	-	-	-	-1,5	-4,6613
FBgn0037423	154231_at	CG1155	Osi14	-	-2,4	-6,4915	-1,7	-4,1792
FBgn0037424	149389_at	CG1157	Osi15	-	-1,7	-5,2887	-	-
FBgn0037429	149394_at	CG15189	Osi19	-	-1,7	-4,4652	-	-
FBgn0037430	149395_at	CG15188	Osi20	-	-2,2	-4,794	-	-
FBgn0037553	151894_at	CG18249	-	receptor activity	-	-	-1,7	-3,4796
FBgn0037575	149489_at	CG7459	Ctr1B	-	-	-	-7,7	-8,7768
FBgn0037607	153373_at	CG8036	-	transketolase activity	-1,5	-3,5776	-1,5	-3,1654
FBgn0037612	149518_at	CG8112	-	sterol O-acyltransferase activity	-	-	-1,6	-3,2128
FBgn0037643	152304_at	CG11963	-	-	-	-	-1,8	-5,5947
FBgn0037672	149545_at	CG12952	sage	transcription factor activity	-	-	-2,1	-5,4455
FBgn0037678	142402_at	CG16749	-	serine-type endopeptidase activity	-	-	-2,7	-6,9399
FBgn0037695	149559_at	CG8144	ps	pre-mRNA splicing factor activity / RNA binding	-	-	-1,5	-3,118
FBgn0037699	154821_at	CG8147	-	alkaline phosphatase activity / nucleotide phosphatase activity	-1,5	-3,3659	-2,0	-5,1465
FBgn0037709	152758_at	CG8199	-	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity	-	-	-1,6	-3,873
FBgn0037723	152178_at	CG8327	SpdS	spermidine synthase activity	-	-	-1,7	-6,0474
FBgn0037724	153941_at	CG9434	Fst	-	-	-	-6,1	-13,1075
FBgn0037801	149624_at	CG3999	-	-	-	-	-3,4	-6,6144
FBgn0037890	149681_at	CG17734	-	-	-	-	-2,4	-9,4575
FBgn0037891	153115_at	CG5214	-	acetyltransferase activity	-	-	-1,8	-5,8246
FBgn0037942	149705_at	CG14721	-	thiamin diphosphokinase activity	-	-	-1,5	-4,5609
FBgn0037992	155035_at	CG4702	-	-	-	-	-1,8	-7,8752
FBgn0037996	149737_at	CG4830	-	ligase activity / long-chain fatty acid transporter activity	-1,6	-3,0153	-2,9	-5,8123
FBgn0038010	149748_at	CG11502	svp	ligand-dependent nuclear receptor activity / receptor activity / transcription factor activity	-	-	-1,6	-3,2866
FBgn0038022	149757_at	CG4381	GstD3	glutathione transferase activity	-	-	-3,1	-8,2085
FBgn0038024	149759_at	CG12242	GstD5	glutathione transferase activity	-	-	-2,7	-7,0664
FBgn0038034	149768_s_at	CG17227	Cyp9f3Ψ	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-2,7	-9,2848
FBgn0038037	153031_at	CG11466	Cyp9f2	electron transporter activity / nucleic acid binding / oxidoreductase activity	-1,9	-3,997	-2,8	-8,9482
FBgn0038081	142746_at	CG10120	Men	carboxy-lyase activity / malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	-2,1	-5,4014	-2,1	-6,775
FBgn0038126	154850_at	CG8483	-	-	-1,6	-3,073	-2,3	-6,4805
FBgn0038135	141327_at	CG8773	-	glutamyl aminopeptidase activity	-	-	-2,3	-6,9124
FBgn0038148	149839_f_at	CG14377	-	-	-1,8	-4,3115	-	-
FBgn0038181	151605_at	CG9297	-	calcium ion binding / calmodulin binding	-	-	-3,3	-6,0701
FBgn0038184	154936_at	CG9285	Dip-B	cysteine-type endopeptidase activity / dipeptidyl-peptidase and tripeptidyl-peptidase activity / leucyl aminopeptidase activity	-	-	-2,1	-6,0831
FBgn0038194	152120_at	CG3050	Cyp6d5	electron transporter activity / oxidoreductase activity	-5,6	-9,1167	-11,6	-21,3116
FBgn0038222	151632_i_at	CG3307	pr-set7	-	-6,3	-16,3926	-6,6	-11,0143
FBgn0038255	149913_at	CG33967	-	-	-2,0	-3,5001	-	-
FBgn0038257	149914_at	CG7390	smp-30	calcium ion binding	-	-	-2,0	-3,8481
FBgn0038271	151769_at	CG3731	-	mitochondrial processing peptidase activity / ubiquinol-cytochrome-c reductase activity	-	-	-1,5	-3,0123
FBgn0038294	152565_at	CG6803	Zeelin1	-	-	-	-1,9	-4,5384
FBgn0038297	152602_at	CG4196	-	receptor signaling protein activity	-	-	-1,7	-4,653
FBgn0038353	149968_at	CG5399	-	-	-2,8	-10,7332	-	-
FBgn0038372	152020_at	CG31150	-	-	-1,6	-3,4857	-	-
FBgn0038400	153159_at	CG5903	-	-	-	-	-1,5	-4,0993
FBgn0038408	150002_at	CG6889	tara	-	-1,6	-2,9695	-	-
FBgn0038420	150008_at	CG10311	-	-	-	-	-2,1	-4,7398
FBgn0038524	141596_at	CG7623	sll	-	-	-	-1,7	-4,7976
FBgn0038555	150105_at	CG31247	tinc	-	-	-	-1,7	-3,4459
FBgn0038563	152336_at	CG7780	DNaseII	-	-3,6	-10,5195	-3,3	-7,0226
FBgn0038587	150121_at	CG7998	-	L-malate dehydrogenase activity	-	-	-2,7	-9,5782
FBgn0038613	142662_at	CG7678	-	hydrogen-exporting ATPase activity, phosphorylative mechanism	-	-	-2,8	-5,3989
FBgn0038643	150157_at	CG14300	-	-	-	-	-2,5	-7,3824
FBgn0038644	150158_at	CG7710	-	-	-	-	-3,0	-10,5113
FBgn0038645	150159_at	CG7714	-	-	-4,0	-10,5368	-10,1	-20,5657
FBgn0038646	150160_at	CG7715	-	-	-	-	-4,9	-10,3061
FBgn0038647	150161_at	CG14302	-	-	-12,0	-13,1545	-38,3	-20,6499
FBgn0038658	150168_at	CG14292	-	-	-	-	-2,0	-5,741
FBgn0038701	150192_at	CG18493	-	peptidase activity / serine-type peptidase activity	-	-	-1,6	-4,9049
FBgn0038740	150223_at	CG4562	-	ATPase activity, coupled to transmembrane movement of substances / transporter activity	-2,3	-2,9436	-2,1	-3,657
FBgn0038774	152841_at	CG5023	-	actin binding / structural constituent of cytoskeleton	-	-	-2,5	-5,3702
FBgn0038795	150261_at	CG4335	-	gamma-butyrobetaine dioxygenase activity	-	-	-1,9	-5,4495
FBgn0038803	152563_at	CG5191	-	hydrolase activity	-	-	-1,7	-4,342
FBgn0038845	141419_at	CG10827	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-1,9	-4,0058
FBgn0038898	152442_at	CG31233	-	membrane alanyl aminopeptidase activity / membrane alanyl aminopeptidase activity	-	-	-7,6	-12,4393
FBgn0038924	152903_at	CG6028	-	carboxy-lyase activity / isomerase activity / lyase activity	-1,5	-4,8825	-1,5	-3,9503
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-4,6	-10,8561	-9,0	-14,1491
FBgn0038982	142587_at	CG33093	-	gibberellin 20-oxidase activity	-1,8	-7,0297	-2,2	-8,4907
FBgn0038983	150375_at	CG5326	-	acyltransferase activity / transferase activity	-	-	-1,8	-2,9459
FBgn0038985	153820_at	CG6921	-	acyltransferase activity / transferase activity	-	-	-2,6	-5,0556
FBgn0038986	150376_at	CG5278	-	acyltransferase activity / transferase activity	-	-	-1,5	-3,2303
FBgn0039014	150396_at	CG6982	-	-	-1,6	-2,7895	-	-
FBgn0039049	150421_at	CG6726	-	NOT aminoacylase activity	-	-	-1,9	-3,9133
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-2,5	-5,9047	-14,8	-18,8476
FBgn0039053	150425_at	CG6738	-	NOT aminoacylase activity	-	-	-2,0	-3,6967
FBgn0039064	150434_at	CG4467	-	glutamyl aminopeptidase activity	-	-	-1,6	-3,0517
FBgn0039094	154671_at	CG10184	-	-	-	-	-2,1	-4,1787
FBgn0039098	142671_at	CG13822	-	-	-2,6	-5,236	-3,0	-5,6425
FBgn0039197	150509_at	CG17780	-	-	-	-	-1,8	-4,7271
FBgn0039200	150511_at	CG13616	-	-	-	-	-2,0	-5,8713
FBgn0039297	150565_at	CG11852	-	-	-2,3	-2,9337	-2,0	-5,6966
FBgn0039301	150568_at	CG11875	-	-	-1,5	-3,2059	-	-
FBgn0039317	150580_at	CG31102	-	-	-	-	-1,9	-3,5068
FBgn0039349	152837_at	CG4685	-	-	-	-	-1,9	-4,4315
FBgn0039416	150652_at	CG31323	-	-	-	-	-4,0	-6,0048
FBgn0039435	150664_at	CG14240	-	-	-	-	-1,9	-4,6942
FBgn0039436	150665_s_at	CG6478	-	-	-	-	-3,0	-11,9506
FBgn0039438	150666_at	CG6452	-	-	-	-	-7,5	-13,7133
FBgn0039441	150670_i_at / 150671_f_at	CG5476	-	-	-	-	-3,0	-7,6343
FBgn0039453	150683_at	CG6403	-	-	-	-	-1,7	-8,9675
FBgn0039468	150697_at	CG31075	-	aldehyde dehydrogenase (NAD) activity	-	-	-1,6	-6,2214
FBgn0039471	150699_at	CG6295	-	triacylglycerol lipase activity	-	-	-11,9	-12,8215
FBgn0039493	151522_at	CG5889	Mdh	carboxy-lyase activity / malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	-	-	-2,1	-5,5441
FBgn0039539	154473_at	CG12880	-	-	-	-	-2,3	-8,1883
FBgn0039567	150762_at	CG4869	betaTub97EF	structural constituent of cytoskeleton / tubulin binding	-	-	-2,1	-7,245

FBgn0039586	142182_s_at	CG33103	Ppn	metallopeptidase activity / serine-type endopeptidase inhibitor activity	-	-	-1,7	-3,5727
FBgn0039611	150791_at	CG14528	-	metalloendopeptidase activity	-	-	-1,6	-4,0791
FBgn0039670	150825_at	CG7567	-	-	-	-	-1,7	-3,2357
FBgn0039671	150826_at	CG11470	-	-	-	-	-1,7	-5,4398
FBgn0039682	150834_at	CG7584	Obp99c	-	-1,8	-4,039	-3,2	-13,2527
FBgn0039686	150838_at	CG15506	-	-	-	-	-2,0	-7,4177
FBgn0039737	153339_at	CG7920	-	4-hydroxybutyrate CoA-transferase activity	-1,9	-4,2499	-2,4	-8,0908
FBgn0039760	141310_at	CG9682	-	-	-	-	-5,2	-7,0514
FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-10,8	-12,3942	-58,5	-35,8775
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-10,7	-12,5847	-94,3	-43,8981
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-2,1	-3,2856	-3,6	-8,773
FBgn0039800	142413_at	CG11314	-	-	-	-	-1,7	-5,1293
FBgn0039825	152434_at	CG31004	-	-	-1,6	-3,3141	-2,5	-10,3848
FBgn0039851	151691_at	CG12063	-	-	-	-	-2,0	-6,2559
FBgn0039852	150946_at	CG1499	-	-	-	-	-1,6	-2,8878
FBgn0039915	150984_at	CG1732	-	gamma-aminobutyric acid:sodium symporter activity	-	-	-1,7	-3,7421
FBgn0040529	151016_at	CG9603	-	cytochrome-c oxidase activity	-	-	-1,5	-2,806
FBgn0040609	151094_at	CG3348	-	-	-	-	-1,7	-4,5751
FBgn0040764	151237_at	CG13230	-	-	-	-	-24,2	-15,9996
FBgn0040813	151287_at	CG11051	Nplp2	-	-1,5	-3,4168	-1,5	-2,9219
FBgn0040819	151293_f_at	CG33269	-	-	-4,0	-4,7333	-2,1	-4,3938
FBgn0040843	151316_at	CG15213	-	-	-	-	-3,0	-5,5837
FBgn0040941	151408_at	CG15308	-	-	-	-	-2,0	-5,2142
FBgn0040950	151415_at	CG13990	-	-	-2,6	-4,6508	-10,1	-14,3875
FBgn0040958	151421_at	CG31893	Peritrophin-15b	-	-	-	-1,8	-5,4577
FBgn0040959	151422_at	CG17814	Peritrophin-15a	-	-	-	-3,0	-7,8643
FBgn0040993	151452_at	CG17325	-	-	-	-	-2,3	-3,5688

Table S6. Genes responsive to Abd-B induction

Up-regulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000055	151802_at	CG3481	Adh	-	2,8	7,7156	2,5	8,1462
FBgn0000320	152004_at	CG9554	cli	-	2,0	4,2027	2,3	4,4066
FBgn0000368	153779_at	CG6383	crb	protein binding / receptor activity / receptor binding / spectrin binding / structural molecule activity	-	-	1,5	3,004
FBgn0000406	151932_at	CG13279	Cyt-b5-r	electron transporter activity / electron transporter activity / oxidoreductase activity	1,7	4,6848	-	-
FBgn0000576	143149_at	CG2988	ems	specific RNA polymerase II transcription factor activity	1,8	3,5047	-	-
FBgn0001138	143180_at	CG9656	grn	general RNA polymerase II transcription factor activity / RNA polymerase II transcription factor activity	2,5	4,3205	2,1	3,1375
FBgn0001208	153434_at	CG7399	Hn	tryptophan 5-monooxygenase activity	-	-	5,3	7,1862
FBgn0001256	141386_at	CG10717	ImpL1	-	2,2	4,9599	2,5	6,3303
FBgn0001257	141688_at	CG15009	ImpL2	-	1,6	3,857	1,9	5,99
FBgn0001991	151837_at	CG4894	Ca-alpha1D	voltage-gated calcium channel activity	4,5	6,7173	3,1	5,2713
FBgn0002570	143242_at	CG8696	LvpH	alpha-glucosidase activity	5,7	4,6659	8,0	8,3321
FBgn0002629	143251_at	CG6099	m4	-	-	-	1,6	4,0439
FBgn0002631	143252_at	CG6096	HLHm5	DNA binding / specific transcriptional repressor activity / transcription factor activity	-	-	1,9	3,2189
FBgn0002970	143285_at	CG6246	nub	RNA polymerase II transcription factor activity / transcription factor activity	3,0	7,102	-	-
FBgn0003130	143309_at	CG8246	Poxn	specific RNA polymerase II transcription factor activity / transcription regulator activity	2,1	2,8955	3,2	4,0166
FBgn0003162	154812_at	CG9441	Pu	GTP cyclohydrolase I activity	-	-	2,6	3,5458
FBgn0003187	143316_at	CG6433	qua	actin binding / calcium ion binding / structural constituent of cytoskeleton	-	-	3,2	3,2026
FBgn0003356	143338_f_at	CG31034	Jon99Cii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	10,4	8,808	-	-
FBgn0003357	143340_f_at / 143339_i_at	CG31362	Jon99Ciii	chymotrypsin activity / chymotrypsin activity / serine-type endopeptidase activity / serine-type endopeptidase activity / serine-type peptidase activity / serine-type peptidase activity	5,0	12,3251	-	-
FBgn0003495	141691_at	CG6134	spz	cytokine activity / morphogen activity / Toll binding	2,7	3,8469	11,4	8,9711
FBgn0003749	143382_at	CG6883	trh	protein heterodimerization activity / RNA polymerase II transcription factor activity / transcription factor activity	1,5	3,1364	2,4	3,0092
FBgn0003867	143387_at	CG6705	tsl	torso binding	1,6	3,8024	-	-
FBgn0003997	143411_at	CG5123	W	-	1,8	4,4774	-	-
FBgn0004509	154664_at	CG10772	Fur1	furin activity	1,5	4,1843	1,6	3,8826
FBgn0004554	143480_at	CG7539	Edg91	structural constituent of pupal cuticle (sensu Insecta)	-	-	2,5	4,7458
FBgn0004579	143487_at	CG6464	salm	specific RNA polymerase II transcription factor activity / transcription regulator activity	2,7	10,6083	2,8	4,6331
FBgn0004895	143530_at	CG1132	fd64A	transcription factor activity	2,4	4,9918	-	-
FBgn0010453	143629_at	CG4698	Wnt4	receptor binding / signal transducer activity	1,8	5,2958	1,7	5,1334
FBgn0011591	143664_at	CG10580	fng	acetylglucosaminyltransferase activity / receptor binding / transferase activity, transferring glycosyl groups / UDP-glycosyltransferase activity	4,1	10,9155	3,7	6,2899
FBgn0011653	141377_at	CG15002	mas	NOT peptidase activity / NOT serine-type endopeptidase activity	5,5	10,5078	-	-
FBgn0011706	143680_at	CG4319	rpr	-	5,4	9,7585	3,8	6,664
FBgn0012037	153728_at	CG8827	Ance	peptidyl-dipeptidase A activity / zinc ion binding	2,3	6,0432	2,3	5,4155
FBgn0013751	143717_at	CG1072	Awh	transcription factor activity	2,2	3,5092	3,1	4,0459
FBgn0014469	154078_at	CG2060	Cyp4e2	electron transporter activity / oxidoreductase activity	1,9	5,076	-	-
FBgn0015037	143782_at	CG10842	Cyp4p1	electron transporter activity / oxidoreductase activity	3,9	4,2119	2,9	3,7972
FBgn0015946	143862_at	CG4345	grim	-	2,3	4,1538	2,2	4,1172
FBgn0017448	143890_at	CG2187	-	cation transporter activity / sodium:iodide symporter activity	1,8	2,9258	-	-
FBgn0019952	152843_at	CG6331	Orct	cation transporter activity / organic cation transporter activity	-	-	1,9	4,7209
FBgn0020294	143918_at	CG10573	ko	-	-	-	3,3	3,6053
FBgn0023520	152934_at	CG3857	-	-	2,2	5,665	-	-
FBgn0024245	141525_at	CG17559	dnt	protein-tyrosine kinase activity / transmembrane receptor protein tyrosine kinase activity	-	-	1,8	3,7447
FBgn0024989	144042_at	CG3777	-	endopeptidase inhibitor activity	2,2	3,3891	2,5	3,6896
FBgn0025583	144068_at	CG18106	IM2	-	-	-	2,1	3,4482
FBgn0027348	153318_at	CG4501	bgm	-	2,8	5,248	2,1	3,6125
FBgn0027516	142661_at	CG18617	Vha100-2	-	1,5	3,4478	-	-
FBgn0027573	152119_at	CG5518	sda	-	-	-	2,9	3,8214
FBgn0027945	141370_at	CG7758	ppl	hydrolase activity	-	-	2,2	4,8937
FBgn0028536	144233_at	CG15281	-	-	2,6	6,085	7,1	4,4702
FBgn0028646	154731_at	CG2139	aralar1	calcium ion binding / carrier activity	2,5	4,8602	-	-
FBgn0028679	144243_at	CG5661	Sema-5c	receptor activity / receptor binding / serine-type endopeptidase inhibitor activity	1,7	3,2612	2,8	6,188
FBgn0028878	142688_at	CG15269	-	nucleic acid binding / RNA polymerase II transcription factor activity / single-stranded DNA binding / transcription regulator activity	-	-	2,8	4,1921
FBgn0028940	152734_at	CG8864	Cyp28a5	electron transporter activity / oxidoreductase activity	-	-	2,8	3,4468
FBgn0029823	144561_at	CG3011	-	glycine hydroxymethyltransferase activity	-	-	2,6	4,9893
FBgn0029830	144566_at	CG14447	Grip	-	3,3	5,0227	2,1	2,956
FBgn0029901	153038_at	CG3135	shf	receptor activity / receptor binding	1,9	3,0975	-	-
FBgn0029994	144675_at	CG2254	-	oxidoreductase activity	1,6	3,1552	2,5	4,0928
FBgn0030160	144771_at	CG9691	-	-	-	-	1,9	3,2648
FBgn0030218	144814_at	CG1628	-	carrier activity / L-ornithine transporter activity	2,4	4,6912	2,2	3,7635
FBgn0030362	141568_at	CG1803	regucalcin	-	3,3	5,8695	5,7	10,0001
FBgn0030478	141639_at	CG1640	-	-	-	-	2,4	4,37
FBgn0030766	145198_at	CG4521	mthl1	G-protein coupled receptor activity	2,0	3,2706	-	-
FBgn0030900	145282_at	CG15064	Him	-	1,8	3,7285	-	-
FBgn0031001	145358_at	CG7884	-	-	2,1	4,1058	-	-
FBgn0031010	145363_at	CG8028	-	monocarboxylic acid transporter activity	3,0	5,1833	1,6	4,2644
FBgn0031558	145728_at	CG16704	-	serine-type endopeptidase inhibitor activity	-	-	1,5	4,2933
FBgn0031561	145731_at	CG16712	-	serine-type endopeptidase inhibitor activity	2,3	5,463	3,3	5,1174
FBgn0031792	145882_at	CG13983	-	-	2,0	3,9521	5,2	5,8462
FBgn0031899	153385_at	CG4675	Ndae1	anion exchanger activity / bicarbonate transporter activity / cation transporter activity / high affinity inorganic phosphate:sodium symporter activity / sodium:bicarbonate symporter activity	1,5	3,1297	-	-
FBgn0031907	154061_at	CG5171	-	-	1,5	3,2707	-	-
FBgn0031931	145970_at	CG7052	TepII	antibacterial humoral response (sensu Protostomia)	5,9	16,9101	6,4	9,8844
FBgn0031949	141497_at	CG7144	-	saccharopine dehydrogenase (NAD+, L-lysine-forming) activity	1,6	4,1949	3,7	6,7556
FBgn0031970	152154_at	CG7227	-	scavenger receptor activity	-	-	3,2	5,0899
FBgn0032020	146020_at	CG7787	-	guanyl-nucleotide exchange factor activity / zinc ion binding	1,5	3,5049	-	-
FBgn0032253	146162_at	CG5322	-	alpha-mannosidase activity / hydrolase activity, hydrolyzing N-glycosyl compounds	1,8	3,1231	-	-
FBgn0032287	151967_at	CG6415	-	-	-	-	3,7	10,6637
FBgn0032387	146262_at	CG16965	-	-	4,3	6,24	5,2	4,5869
FBgn0032414	146274_at	CG17211	-	-	2,5	3,7337	3,3	6,9656
FBgn0032426	146285_at	CG31764	vir-1	-	-	-	2,2	4,2704
FBgn0032433	154627_at	CG5427	Oatp33Ea	-	-	-	1,8	3,8913

FBgn0032473	146312_at	CG5204	-	-	1,7	4,4246	-	-
FBgn0032601	155013_at	CG17914	yellow-b	-	1,8	3,9974	3,8	3,58
FBgn0032604	146377_at	CG13270	Ugt36Ba	glucuronosyltransferase activity	1,7	3,7032	-	-
FBgn0032806	146503_at	CG10363	TepIV	protease inhibitor activity	2,3	7,4785	3,1	7,2998
FBgn0032820	151797_at	CG31692	fbp	fructose-bisphosphatase activity	1,6	3,2149	-	-
FBgn0033234	153231_at	CG8791	-	high affinity inorganic phosphate:sodium symporter activity	5,9	6,1986	8,7	7,2399
FBgn0033295	142359_at	CG30359	-	glucosidase activity / glucosidase activity / hydrolase activity / hydrolase activity / transporter activity / transporter activity	-	-	1,8	3,1536
FBgn0033373	152258_at	CG8080	-	-	1,6	3,2685	-	-
FBgn0033395	152833_at	CG1944	Cyp4p2	electron transporter activity / oxidoreductase activity	2,0	5,651	2,2	5,2735
FBgn0033565	152569_at	CG18003	-	glycolate oxidase activity	2,1	2,8799	2,3	5,0009
FBgn0033642	147027_at	CG30035	-	fructose transporter activity / glucose transporter activity / glucose transporter activity	1,6	3,068	3,1	4,6642
FBgn0033674	142663_at	CG8964	-	kinase activity / non-membrane spanning protein tyrosine kinase activity / protein kinase activity / receptor activity / transmembrane receptor activity / transmembrane receptor protein kinase activity / transmembrane receptor protein tyrosine kinase activity	2,7	7,2423	-	-
FBgn0033799	142248_at	CG4604	GLaz	binding / carrier activity	1,5	3,3731	-	-
FBgn0033835	147151_at	CG18279	IM10	-	3,5	3,8661	7,2	9,4273
FBgn0033857	152245_at	CG13335	-	-	-	-	3,7	6,9476
FBgn0033910	141381_at	CG30069	-	-	-	-	3,1	5,0251
FBgn0033939	147205_at	CG17390	-	-	-	-	1,9	3,1207
FBgn0033945	147210_at	CG12868	-	-	-	-	2,4	3,5234
FBgn0033968	141323_at	CG10200	-	-	-	-	3,7	7,1777
FBgn0034190	141536_at	CG8946	Sply	-	-	-	2,0	2,8057
FBgn0034276	152764_at	CG6385	-	sarcosine dehydrogenase activity	-	-	1,8	5,0491
FBgn0034290	142954_at	CG5773	-	-	2,2	3,9721	1,9	3,6191
FBgn0034329	147431_at	CG18108	IM1	-	2,8	4,7792	9,7	6,5558
FBgn0034388	141242_at	CG15092	-	-	-	-	1,6	3,005
FBgn0034408	151924_at	CG12758	sano	-	2,9	8,2518	1,9	3,9568
FBgn0034436	153470_at	CG11961	-	-	1,6	3,2775	-	-
FBgn0034437	147492_at	CG10051	-	-	-	-	2,7	3,6624
FBgn0034468	147514_at	CG11797	Obp56a	-	2,0	4,9635	-	-
FBgn0034470	147516_at	CG11218	Obp56d	-	-	-	2,5	5,5537
FBgn0034501	141541_at	CG13868	-	-	-	-	1,8	2,8116
FBgn0034514	147549_at	CG13427	-	-	3,1	9,7604	6,4	13,7158
FBgn0034515	147550_at	CG13428	-	-	2,0	2,9203	1,5	4,317
FBgn0034736	147681_at	CG6018	-	carboxylesterase activity	-	-	2,2	3,7123
FBgn0035089	147903_at	CG9358	Phk-3	-	4,1	5,6126	3,1	9,3534
FBgn0035169	147946_at	CG13890	-	dodecenoyl-CoA delta-isomerase activity / hydro-lyase activity	1,6	2,8833	1,8	3,5448
FBgn0035325	148033_at	CG13806	-	-	-	-	2,0	5,5021
FBgn0035326	141439_at	CG32302	-	-	4,0	7,5581	14,4	13,348
FBgn0035347	141711_at	CG33232	-	actin binding / structural constituent of cytoskeleton	1,8	5,4056	-	-
FBgn0035434	148103_at	CG10812	dro5	-	2,4	5,7151	2,3	5,582
FBgn0035653	148245_at	CG33993	-	-	2,0	4,209	-	-
FBgn0035794	148343_at	CG32372	-	-	2,7	6,3721	2,3	5,3103
FBgn0035798	154595_at	CG7526	-	kinase activity / protein kinase activity / receptor activity / structural molecule activity / transmembrane receptor protein kinase activity / transmembrane receptor protein tyrosine kinase activity	-	-	1,9	3,2746
FBgn0035835	152824_at	CG7915	Ect4	-	1,6	2,8297	2,0	3,5069
FBgn0035927	141748_at	CG32030	-	actin binding	-	-	1,9	3,6288
FBgn0035961	153070_at	CG4821	Tequila	pancreatic elastase activity / serine-type endopeptidase activity / trypsin activity	2,0	6,9508	1,8	5,5227
FBgn0036073	148512_at	CG6611	ect	-	-	-	2,2	3,1102
FBgn0036262	148639_at	CG6910	-	oxidoreductase activity	2,3	4,1621	-	-
FBgn0036321	148678_at	CG14120	-	-	5,2	7,7527	15,1	11,087
FBgn0036352	148705_at	CG14110	-	-	18,7	20,4305	8,1	13,7666
FBgn0036436	141447_at	CG4914	-	serine-type endopeptidase activity / trypsin activity	-	-	4,7	5,7914
FBgn0036457	148772_at	CG3396	Ocho	-	1,9	4,3028	-	-
FBgn0036612	148885_at	CG4998	-	NOT serine-type endopeptidase activity	-	-	2,3	4,4504
FBgn0036632	148896_at	CG32159	-	-	-	-	2,8	5,2634
FBgn0036675	148923_at	CG32171	Lmpt	-	7,1	10,5315	5,9	6,8217
FBgn0036677	148925_at	CG13023	-	-	5,2	8,6691	10,1	10,106
FBgn0036678	142769_at	CG11905	-	-	-	-	1,7	3,1914
FBgn0036764	152169_at	CG5535	-	cationic amino acid transporter activity	1,6	3,0352	-	-
FBgn0036779	148988_at	CG13695	gk	-	4,1	5,0608	5,0	5,2677
FBgn0036786	148994_at	CG13701	skl	-	3,2	5,7301	2,8	4,2048
FBgn0036871	149048_r_at	CG14096	-	molecular_function unknown / molecular_function unknown	-	-	2,6	5,0745
FBgn0036891	149063_at	CG9372	-	serine-type peptidase activity / trypsin activity	1,9	5,1659	6,9	6,0175
FBgn0037000	149132_at	CG5130	-	zinc ion transporter activity	1,9	3,1592	-	-
FBgn0037140	149215_at	CG7442	-	carbohydrate transporter activity / organic cation porter activity	-	-	2,0	4,0343
FBgn0037181	149248_at	CG11370	-	-	-	-	4,8	6,5753
FBgn0037323	149329_at	CG2663	-	carrier activity / tocopherol binding	-	-	2,8	5,4215
FBgn0037414	149380_at	CG1153	Osi7	-	1,9	5,3799	-	-
FBgn0037423	154231_at	CG1155	Osi14	-	-	-	1,6	3,1121
FBgn0037513	153777_at	CG3027	pyd3	-	3,7	9,6209	4,6	8,6606
FBgn0037548	149474_at	CG7900	-	fatty acid amide hydrolase activity	2,8	3,7716	-	-
FBgn0037564	149479_at	CG31463	-	-	1,8	3,8726	13,6	9,2773
FBgn0037607	153373_at	CG8036	-	transketolase activity	-	-	1,6	3,8379
FBgn0037635	149528_at	CG9837	-	-	-	-	3,6	5,2766
FBgn0037664	154972_at	CG8420	-	-	1,7	3,8316	1,9	4,3071
FBgn0037699	154821_at	CG8147	-	alkaline phosphatase activity / nucleotide phosphatase activity	1,7	2,9635	-	-
FBgn0037739	149578_at	CG12948	-	-	-	-	2,0	2,9898
FBgn0037801	149624_at	CG3999	-	-	1,8	3,5737	5,9	4,1956
FBgn0037872	149672_at	CG31299	nocturnin	nucleic acid binding	-	-	2,2	3,0247
FBgn0037913	151826_at	CG6783	-	carrier activity / fatty acid binding / tricarboxylate carrier activity	2,2	6,5751	2,3	5,7998
FBgn0038009	149747_at	CG17738	-	-	2,1	3,2315	4,0	6,8051
FBgn0038010	149748_at	CG11502	svp	ligand-dependent nuclear receptor activity / receptor activity / transcription factor activity	1,8	4,3875	2,0	3,4815
FBgn0038027	149762_at	CG4421	GstD8	glutathione peroxidase activity / glutathione transferase activity	2,4	3,8825	2,0	2,8003
FBgn0038028	149763_at	CG10035	-	-	1,6	3,9142	4,0	4,9499
FBgn0038150	149840_at	CG17045	yellow-e3	-	1,7	5,14	1,6	4,1818
FBgn0038198	149871_at	CG3153	-	receptor binding	-	-	2,7	3,6431
FBgn0038353	149968_at	CG5399	-	-	1,7	3,3135	-	-
FBgn0038372	152020_at	CG31150	-	-	-	-	2,5	6,0886
FBgn0038465	152368_at	CG8913	-	peroxidase activity	2,7	6,6318	2,3	3,6015
FBgn0038511	150076_at	CG5873	-	peroxidase activity	-	-	4,6	4,9838
FBgn0038516	150080_at	CG5840	-	pyrroline-5-carboxylate reductase activity	1,7	3,2818	-	-
FBgn0038632	150152_at	CG14301	-	-	-	-	2,4	3,5499
FBgn0038661	141483_at	CG17836	-	protein dimerization activity	-	-	2,4	2,8662
FBgn0038799	152929_at	CG4288	-	high affinity inorganic phosphate:sodium symporter activity	7,3	6,3919	36,0	11,2103
FBgn0038914	150335_at	CG17820	fit	-	1,7	2,8099	9,7	8,4843
FBgn0038943	150352_at	CG5391	-	-	-	-	4,6	6,6219
FBgn0038958	150360_at	CG13857	-	-	4,3	3,9526	9,8	5,5551
FBgn0038959	150361_at	CG13856	-	-	11,9	13,6763	10,1	10,7859
FBgn0038969	150366_at	CG31160	-	protein binding / transcription regulator activity	-	-	2,2	4,1714
FBgn0038970	150367_at	CG31160	-	protein binding / transcription regulator activity	1,6	3,0531	-	-
FBgn0038971	150368_at	CG13845	-	-	2,0	3,6481	3,4	6,3525
FBgn0038981	142586_at	CG5346	-	-	-	-	2,2	3,4849
FBgn0039094	154671_at	CG10184	-	-	2,3	3,9316	3,9	4,6565
FBgn0039102	153098_at	CG16705	-	monophenol monooxygenase activator activity / trypsin activity / trypsin activity	-	-	4,8	7,1938
FBgn0039154	141409_at	CG6164	-	-	5,3	4,8391	6,6	8,4993
FBgn0039237	150531_at	CG13640	-	-	7,6	6,3097	15,9	11,7929
FBgn0039249	154181_at	CG11168	-	receptor binding / receptor signaling protein activity	-	-	2,8	3,1991
FBgn0039464	152255_at	CG6330	-	uridine phosphorylase activity	-	-	1,7	3,7996
FBgn0039593	150780_at	CG9989	-	-	1,6	3,1403	-	-
FBgn0039594	153864_at	CG9990	-	ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	2,0	3,4415
FBgn0039704	152879_at	CG7802	-	-	2,4	6,0705	1,7	3,4296
FBgn0039754	152137_at	CG9747	-	acyl-CoA delta11-desaturase activity	-	-	2,0	3,1638
FBgn0039800	142413_at	CG11314	-	-	2,3	5,0069	4,2	10,2432

FBgn0039882	142134_at	CG11576	-	-	1,7	3,5878	2,0	4,1742
FBgn0039884	153488_at	CG31000	heph	poly-pyrimidine tract binding / pre-mRNA splicing factor activity / RNA binding	1,6	2,8431	-	-
FBgn0040611	151096_i_at	CG31062	side	-	2,0	4,259	2,4	3,1797
FBgn0040653	151137_r_at	CG15231	IM4	-	-	-	3,1	9,6327
FBgn0040734	151209_at	CG15065	-	-	-	-	3,5	7,8238
FBgn0040736	151211_at	CG16844	IM3	-	29,8	20,5736	88,7	23,5371
FBgn0040790	151261_at	CG13695	gk	-	-	-	1,8	2,9548
FBgn0040796	151266_at	CG13064	-	-	4,2	6,7984	2,6	7,5521
FBgn0040984	151444_at	CG4440	-	-	-	-	1,5	3,1799
FBgn0040995	151453_at	CG12508	-	-	-	-	2,6	3,5406

Downregulated genes:

FB code	Affy identifier	CG numbers	Synonyms	Description / Molecular function	Fold Change st11	*t*-value st11	Fold change st12	*t*-value st12
FBgn0000014	143052_at	CG10325	abd-A	specific RNA polymerase II transcription factor activity	-1,7	-4,3296	-1,8	-3,0241
FBgn0000015	143053_at	CG11648	Abd-B	specific RNA polymerase II transcription factor activity	-2,4	-8,9175	-2,7	-7,0089
FBgn0000095	142814_at	CG1028	Antp	specific RNA polymerase II transcription factor activity	-1,7	-3,0237	-	-
FBgn0000114	151653_at	CG31762	aret	mRNA 3'-UTR binding / protein binding / RNA binding / RNA binding	-1,5	-3,1194	-	-
FBgn0000157	143081_at	CG3629	Dll	specific RNA polymerase II transcription factor activity	-1,8	-2,9039	-	-
FBgn0000299	153378_at	CG4145	Cg25C	extracellular matrix structural constituent / structural molecule activity	-	-	-2,2	-5,2844
FBgn0000337	143103_at	CG1555	cn	-	-3,2	-5,1073	-1,9	-3,5495
FBgn0000411	143116_at	CG5893	D	DNA bending activity / transcription factor activity	-2,3	-5,7145	-2,6	-4,8995
FBgn0000439	143122_at	CG2189	Dfd	RNA polymerase II transcription factor activity / transcription factor activity	-1,7	-4,5173	-	-
FBgn0000659	143160_at	CG10002	fkh	specific RNA polymerase II transcription factor activity / transcription regulator activity	-1,6	-2,8378	-	-
FBgn0001145	143181_at	CG1743	Gs2	glutamate-ammonia ligase activity	-2,4	-4,5524	-2,5	-4,9317
FBgn0001148	143183_at	CG3388	gsb	specific RNA polymerase II transcription factor activity	-2,2	-6,3702	-1,9	-4,2081
FBgn0001168	143186_at	CG6494	h	general transcriptional repressor activity / specific RNA polymerase II transcription factor activity / specific transcriptional repressor activity	-1,9	-4,2068	-	-
FBgn0001224	153583_at	CG4463	Hsp23	actin binding	-2,6	-4,3716	-	-
FBgn0001226	153307_at	CG4466	Hsp27	-	-1,5	-3,9231	-1,7	-3,0371
FBgn0001235	143199_at	CG17117	hth	specific RNA polymerase II transcription factor activity / transcription factor activity	-2,5	-7,4838	-4,3	-9,7778
FBgn0002561	143237_at	CG3839	l(1)sc	specific RNA polymerase II transcription factor activity / transcription factor activity	-2,1	-4,828	-	-
FBgn0002741	143263_at	CG17927	Mhc	ATPase activity, coupled / cytoskeletal protein binding / microfilament motor activity / structural constituent of cytoskeleton / structural constituent of muscle	-	-	-1,7	-3,3823
FBgn0002772	143264_at	CG5596	Mlc1	ATPase activity, coupled / microfilament motor activity / NOT calcium ion binding	-	-	-1,6	-3,9241
FBgn0002773	143265_at	CG2184	Mlc2	ATPase activity, coupled / calcium ion binding / calmodulin binding / microfilament motor activity	-1,6	-3,1784	-2,1	-7,2228
FBgn0002789	143271_at	CG4696	Mp20	actin binding / calcium ion binding / structural constituent of cytoskeleton	-1,7	-2,9359	-2,5	-5,9318
FBgn0002868	143276_at	CG9470	MtnA	metal ion binding	-	-	-2,6	-7,2343
FBgn0003057	143296_at	CG10598	-	-	-	-	-2,7	-6,0364
FBgn0003089	143305_at	CG9614	pip	heparin-sulfate 2-sulfotransferase activity / sulfotransferase activity	-	-	-1,6	-3,0734
FBgn0003149	152555_at	CG5939	Prm	cytoskeletal protein binding / motor activity / structural constituent of cytoskeleton / structural constituent of muscle	-	-	-2,0	-4,6613
FBgn0003326	143333_at	CG17579	sca	receptor binding / signal transducer activity	-2,3	-5,0606	-	-
FBgn0003411	143353_at	CG1641	sisA	protein heterodimerization activity / transcription factor activity	-	-	-2,1	-3,9704
FBgn0003430	151981_at	CG16738	slp1	RNA polymerase II transcription factor activity / transcription factor activity	-2,2	-4,7153	-3,2	-3,8437
FBgn0003447	143355_at	CG32858	sn	actin binding / structural constituent of cytoskeleton	-1,6	-2,8573	-2,1	-4,3152
FBgn0003448	143356_at	CG3956	sna	DNA binding / RNA polymerase II transcription factor activity / specific RNA polymerase II transcription factor activity / specific transcriptional repressor activity	-	-	-1,6	-3,4903
FBgn0003499	143365_at	CG7847	sr	RNA polymerase II transcription factor activity	-	-	-2,1	-3,0164
FBgn0003944	143400_at	CG10388	Ubx	DNA binding / specific RNA polymerase II transcription factor activity / transcription factor activity	-5,6	-10,4478	-2,7	-6,289
FBgn0004009	143414_at	CG4889	wg	frizzled-2 binding / morphogen activity / Notch binding / receptor binding / signal transducer activity	-2,5	-3,4453	-2,8	-3,5678
FBgn0004102	143425_at	CG12154	oc	transcription factor activity	-1,9	-2,9016	-	-
FBgn0004169	142555_at	CG7107	up	tropomyosin binding	-	-	-2,1	-4,3178
FBgn0004228	143441_at	CG7936	mex1	-	-	-	-2,1	-2,9119
FBgn0004425	143464_f_at	CG1179	LysB	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,0	-5,362	-	-
FBgn0004427	143466_f_at	CG9118	LysD	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-2,8	-6,3117	-1,8	-3,2188
FBgn0004428	143467_f_at	CG1180	LysE	chitinase activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity / lysozyme activity	-3,5	-7,4258	-	-
FBgn0004862	143523_at	CG7902	bap	DNA binding / specific RNA polymerase II transcription factor activity	-1,8	-4,8256	-	-
FBgn0004878	154755_at	CG2102	cas	DNA binding / RNA polymerase II transcription factor activity / transcription factor activity	-2,2	-6,9415	-1,6	-3,1797
FBgn0004898	143532_at	CG11922	fd96Cb	transcription factor activity	-2,1	-4,4938	-	-
FBgn0005775	152589_at	CG7503	Con	structural molecule activity	-2,4	-3,4427	-	-
FBgn0010359	143603_i_at	CG30028	gammaTry	NOT serine-type endopeptidase activity / trypsin activity / trypsin activity	-	-	-5,5	-5,5341
FBgn0010387	143608_at	CG8627	Dbi	acyl-CoA binding / carrier activity / diazepam binding / enzyme inhibitor activity	-	-	-2,2	-3,6361
FBgn0010423	143622_at	CG9073	TpnC47D	calcium ion binding / calmodulin binding	-2,1	-3,0901	-2,6	-6,3676
FBgn0010425	143624_at	CG18681	epsilonTry	trypsin activity	-	-	-2,0	-3,0029
FBgn0010433	143626_at	CG7508	ato	DNA binding / transcription factor activity	-2,8	-4,9364	-	-
FBgn0011828	152747_at	CG12002	Pxn	peroxidase activity	-	-	-2,8	-4,2375
FBgn0013772	142189_at	CG10248	Cyp6a8	electron transporter activity / oxidoreductase activity	-	-	-1,9	-4,3579
FBgn0014141	141641_at	CG3937	cher	actin binding / structural constituent of cytoskeleton	-3,2	-7,0108	-1,9	-3,7319
FBgn0014179	143754_at	CG12245	gcm	DNA binding / transcription factor activity	-1,9	-5,6151	-1,9	-3,6967
FBgn0014343	143756_at	CG10601	mirr	protein binding / transcription factor activity / transcriptional activator activity	-1,9	-2,9853	-	-
FBgn0014388	143757_at	CG1921	sty	receptor binding	-	-	-1,5	-3,0268
FBgn0014863	143769_at	CG1019	Mlp84B	protein binding	-	-	-1,9	-3,5437
FBgn0015286	143790_at	CG2849	Rala	GTPase activity	-	-	-1,8	-3,4566
FBgn0015766	155091_at	CG10596	Msr-110	-	-	-	-2,6	-4,2057
FBgn0015774	151503_at	CG10521	NetB	structural molecule activity / structural molecule activity	-2,0	-3,1125	-1,9	-3,2816
FBgn0016075	143868_at	CG16858	vkg	extracellular matrix structural constituent	-	-	-3,3	-2,8049
FBgn0019643	152456_at	CG3318	Dat	aralkylamine N-acetyltransferase activity / arylamine N-acetyltransferase activity / cocaine binding / dopamine transporter activity / dopamine:sodium symporter activity	-	-	-1,7	-3,6812
FBgn0019650	152583_at	CG11186	toy	specific RNA polymerase II transcription factor activity	-2,1	-4,027	-	-
FBgn0020299	142813_at	CG31317	stumps	-	-	-	-2,1	-4,1877
FBgn0020307	143919_at	CG5799	dve	AT DNA binding / transcription factor activity	-	-	-2,2	-4,2279
FBgn0020378	143922_at	CG1343	Sp1	RNA polymerase II transcription factor activity	-3,4	-4,0077	-2,2	-3,5998
FBgn0020389	154327_at	CG8363	Paps	nucleotide kinase activity	-1,6	-3,539	-3,2	-9,4085
FBgn0020637	143935_s_at	CG10534	Lcp65Ag2	structural constituent of larval cuticle (sensu Insecta) / structural constituent of larval cuticle (sensu Insecta)	-2,6	-6,893	-3,1	-11,4335
FBgn0022213	143953_at	CG13281	Cas	importin-alpha export receptor activity	-1,8	-3,0936	-	-
FBgn0023549	144005_at	CG3456	Mct1	monocarboxylic acid transporter activity	-	-	-1,8	-3,2462
FBgn0024988	141607_at	CG14801	-	exonuclease activity / exoribonuclease activity / nucleic acid binding	-2,8	-5,4705	-	-
FBgn0025878	151901_at	CG10382	wrapper	-	-	-	-2,3	-6,555
FBgn0025885	153296_at	CG11143	Inos	-	-1,9	-4,2801	-1,7	-4,2283
FBgn0027111	144176_at	CG1221	miple	-	-1,6	-3,7831	-	-
FBgn0027527	144185_at	CG1151	Osi6	-	-	-	-1,8	-3,2962
FBgn0027560	152201_at	CG4104	Tps1	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity	-1,9	-3,7442	-	-
FBgn0027570	152128_at	CG9761	Nep2	endothelin-converting enzyme activity / metalloendopeptidase activity / metallopeptidase activity	-	-	-1,7	-3,6473
FBgn0027594	151918_s_at	CG2086	drpr	extracellular matrix structural constituent / receptor activity	-	-	-1,6	-3,8814
FBgn0028516	144224_at	CG3994	-	metal ion transporter activity / zinc ion transporter activity	-	-	-2,3	-5,8786
FBgn0028855	144266_at	CG15282	-	-	-	-	-2,1	-3,3402
FBgn0028876	144283_at	CG16876	-	-	-	-	-1,8	-3,4049
FBgn0028905	144302_at	CG32972	-	-	-3,5	-12,8841	-4,9	-8,7308
FBgn0029576	151685_r_at	CG32813	-	-	-	-	-1,7	-2,8171
FBgn0029939	153744_at	CG9650	-	transcription regulator activity	-2,1	-5,4826	-1,6	-2,8373
FBgn0030040	144700_at	CG15347	-	-	-	-	-2,6	-4,4112
FBgn0030186	154400_at	CG2962	-	-	-	-	-2,2	-4,1689
FBgn0030237	144829_at	CG15209	-	-	-	-	-2,0	-6,0501
FBgn0030390	144937_at	CG15731	-	-	-	-	-3,0	-4,6124
FBgn0030650	141692_at	CG33206	l(1)G0168	-	-1,9	-4,825	-2,2	-5,0016
FBgn0030653	153970_at	CG7860	-	asparaginase activity	-	-	-2,9	-5,2277
FBgn0030818	145228_at	CG8936	Arpc3B	actin binding / structural constituent of cytoskeleton	-	-	-1,5	-3,1956
FBgn0030825	155011_at	CG32563	-	-	-	-	-2,5	-4,1591
FBgn0031489	145684_at	CG17224	-	-	-	-	-2,0	-4,4468
FBgn0031629	145779_at	CG3244	-	-	-	-	-1,7	-2,9361
FBgn0031645	151989_at	CG3036	-	sodium:phosphate symporter activity	-2,2	-5,6637	-	-
FBgn0031653	145795_at	CG8871	Jon25Biii	elastase activity / serine-type peptidase activity	-	-	-3,1	-6,5506
FBgn0031706	145823_at	CG6634	nmr2	transcription factor activity	-1,9	-3,239	-1,7	-3,5739
FBgn0031717	141443_at	CG6957	Oscillin	glucosamine-6-phosphate deaminase activity	-	-	-1,9	-3,4877
FBgn0031745	151809_at	CG8965	-	-	-2,6	-5,4222	-2,5	-2,9961

FBgn0031839	145915_at	CG31634	Oatp26F	organic anion transporter activity	-2,1	-3,1461	-1,6	-3,2466
FBgn0031936	145974_at	CG13794	-	-	-5,3	-4,637	-5,5	-3,5577
FBgn0032002	146014_at	CG8353	-	cytidine deaminase activity	-1,9	-4,8616	-2,0	-4,6351
FBgn0032070	151713_at	CG18024	SoxN	transcription factor activity	-	-	-2,7	-5,9445
FBgn0032167	141658_at	CG5853	-	anion channel activity / ATPase activity, coupled to transmembrane movement of substances / transporter activity	-	-	-3,2	-6,0142
FBgn0032263	141619_at	CG7400	Fatp	long-chain fatty acid transporter activity	-2,5	-3,0958	-1,9	-4,355
FBgn0032282	146181_at	CG7299	-	-	-	-	-2,3	-4,9494
FBgn0032283	146182_at	CG7296	-	-	-14,1	-12,6622	-17,7	-15,3051
FBgn0032284	146183_at	CG7294	-	-	-	-	-4,8	-8,1064
FBgn0032405	146269_at	CG14946	-	oxidoreductase activity	-	-	-1,5	-3,6922
FBgn0032683	154571_at	CG10275	-	-	-	-	-1,8	-3,043
FBgn0032774	152759_at	CG17549	-	-	-	-	-1,5	-3,2362
FBgn0032803	146500_at	CG13082	-	-	-	-	-2,6	-6,3409
FBgn0032842	146530_at	CG13969	bwa	ceramidase activity	-1,5	-3,6327	-	-
FBgn0032844	146532_at	CG10746	fok	-	-2,5	-4,731	-2,0	-4,9698
FBgn0033144	141404_at	CG12172	Spn43Aa	serine-type endopeptidase inhibitor activity	-2,1	-5,4925	-	-3,3041
FBgn0033188	152715_at	CG1600	-	-	-	-	-2,0	-6,2322
FBgn0033205	141701_at	CG2064	-	oxidoreductase activity	-1,6	-3,1039	-	-
FBgn0033275	146794_at	CG14756	-	-	-5,0	-7,4526	-57,1	-22,8808
FBgn0033367	142220_at	CG8193	-	monophenol monooxygenase activity	-3,7	-7,7169	-9,0	-11,9043
FBgn0033411	146880_at	CG8805	wun2	phosphatidate phosphatase activity	-	-	-2,0	-4,1909
FBgn0033446	152817_at	CG1648	-	-	-	-	-2,0	-3,9146
FBgn0033505	151736_at	CG18408	CAP	structural constituent of cytoskeleton / vinculin binding	-2,6	-3,9503	-3,0	-5,7005
FBgn0033518	146946_s_at	CG11765	Prx2540-2	antioxidant activity / antioxidant activity / non-selenium glutathione peroxidase activity / peroxidase activity / peroxidase activity / peroxidase activity	-2,0	-7,7505	-1,9	-4,7074
FBgn0033604	147002_at	CG9070	-	-	-5,7	-5,3912	-16,2	-13,8853
FBgn0033634	147022_at	CG7763	-	-	-1,9	-3,3099	-3,0	-7,7229
FBgn0033721	147084_at	CG13159	-	-	-25,8	-11,9103	-73,5	-17,6485
FBgn0033724	153425_at	CG8501	-	-	-	-	-2,8	-5,3942
FBgn0033764	152519_at	CG8776	-	carbon-monoxide oxygenase activity	-	-	-1,9	-3,3879
FBgn0033779	142416_at	CG3814	-	N-methyl-D-aspartate selective glutamate receptor activity	-	-	-2,4	-4,2181
FBgn0034083	153986_at	CG8434	lbk	-	-1,7	-3,0963	-	-
FBgn0034108	155081_at	CG3767	Jhl-26	-	-2,2	-3,3568	-2,3	-5,7929
FBgn0034117	153785_at	CG7997	-	-	-2,8	-7,4256	-4,9	-8,923
FBgn0034201	147355_at	CG17290	-	-	-	-	-2,9	-3,609
FBgn0034204	147358_at	CG10953	-	-	-1,6	-4,3121	-2,6	-4,2122
FBgn0034224	147366_at	CG6520	-	-	-1,7	-3,6365	-1,9	-4,2396
FBgn0034294	147409_at	CG5765	-	-	-	-	-4,2	-6,1543
FBgn0034337	147436_at	CG17524	GstE3	glutathione transferase activity	-	-	-1,5	-3,6401
FBgn0034404	142196_at	CG15101	Jheh1	-	-	-	-2,3	-3,187
FBgn0034406	154747_at	CG15106	Jheh3	epoxide hydrolase activity / juvenile hormone epoxide hydrolase activity	-	-	-2,1	-4,0471
FBgn0034589	151977_at	CG9398	king-tubby	-	-1,5	-2,9318	-	-
FBgn0034698	141793_at	CG6698	NtR	-	-2,9	-5,9085	-4,7	-5,2228
FBgn0034764	147701_at	CG9952	ppa	-	-2,0	-3,2038	-	-
FBgn0035030	152422_at	CG3541	-	-	-2,0	-4,4858	-	-
FBgn0035091	152752_at	CG3829	-	scavenger receptor activity	-	-	-1,8	-5,4566
FBgn0035147	154410_at	CG12030	-	UDP-glucose 4-epimerase activity	-1,6	-2,7781	-1,9	-3,5686
FBgn0035173	147949_at	CG13907	-	monocarboxylate porter activity	-1,6	-5,145	-1,7	-2,884
FBgn0035177	151651_at	CG13906	nerfin-1	RNA polymerase II transcription factor activity	-	-	-1,9	-3,2664
FBgn0035190	147960_at	CG13913	-	-	-7,4	-10,1993	-4,1	-9,144
FBgn0035208	147969_at	CG9184	-	-	-8,6	-18,7834	-7,5	-18,2179
FBgn0035289	141428_at	CG12026	-	-	-1,7	-3,7849	-	-
FBgn0035551	148182_at	CG7465	-	-	-3,1	-4,5903	-10,7	-11,1443
FBgn0035583	148206_at	CG13704	-	-	-	-	-2,8	-3,7252
FBgn0035621	154354_at	CG10591	-	-	-3,1	-4,9745	-2,9	-11,0251
FBgn0035664	148253_at	CG6467	Jon65Aiv	chymotrypsin activity / serine-type endopeptidase activity	-	-	-1,8	-3,9415
FBgn0035717	152709_at	CG10078	Prat2	-	-1,8	-3,4532	-	-
FBgn0035728	148296_at	CG18647	-	-	-2,4	-3,7537	-	-
FBgn0035735	148301_at	CG8640	-	structural constituent of cuticle (sensu Insecta)	-	-	-1,7	-3,3672
FBgn0035763	154884_at	CG8602	-	transporter activity	-	-	-1,5	-3,7418
FBgn0035767	152873_at	CG8596	-	transporter activity	-	-	-1,6	-3,5146
FBgn0035922	148419_at	CG6486	-	peroxisome targeting signal-2 receptor activity	-	-	-1,9	-3,0345
FBgn0035999	148467_at	CG3552	-	-	-2,1	-3,3358	-2,1	-4,0359
FBgn0036121	148546_at	CG6310	-	-	-	-	-2,6	-4,4219
FBgn0036182	153576_at	CG6084	-	aldehyde reductase activity	-	-	-1,7	-2,9959
FBgn0036194	153715_at	CG11652	-	-	-1,6	-2,9252	-	-
FBgn0036283	152957_at	CG32103	-	carrier activity	-1,7	-3,8811	-	-
FBgn0036355	148706_at	CG32120	sens	RNA polymerase II transcription factor activity / transcription factor activity	-1,6	-2,9459	-	-
FBgn0036378	154590_at	CG12478	bru-3	RNA binding	-	-	-2,2	-3,6358
FBgn0036433	153786_at	CG9628	-	-	-	-	-1,6	-3,1231
FBgn0036486	148795_at	CG7003	-	damaged DNA binding	-1,8	-3,158	-	-
FBgn0036494	153641_at	CG7250	Toll-6	transmembrane receptor activity / transmembrane receptor protein serine/threonine kinase activity	-1,6	-5,1553	-	-
FBgn0036501	148804_at	CG7272	-	-	-1,8	-5,7822	-1,8	-4,4057
FBgn0036539	148828_at	CG32150	-	-	-1,7	-3,2229	-	-
FBgn0036600	148873_at	CG13043	-	-	-	-	-1,6	-3,4811
FBgn0036787	148995_at	CG4306	-	-	-	-	-7,1	-12,0936
FBgn0036852	149033_at	CG9739	fz2	G-protein coupled receptor activity / transmembrane receptor activity / Wnt receptor activity / Wnt-protein binding	-	-	-2,5	-4,1061
FBgn0036875	149052_at	CG9449	-	acid phosphatase activity	-1,6	-3,5177	-4,8	-11,6635
FBgn0036898	151832_at	CG8782	Oat	ornithine-oxo-acid transaminase activity	-2,8	-3,8436	-3,2	-9,5971
FBgn0036945	141349_at	CG6981	-	-	-	-	-2,1	-4,2588
FBgn0037057	152050_at	CG10512	-	oxidoreductase activity	-	-	-1,6	-3,0581
FBgn0037083	141375_at	CG5656	-	alkaline phosphatase activity / nucleotide phosphatase activity	-	-	-3,7	-7,7569
FBgn0037177	149244_at	CG14454	-	molecular_function unknown	-1,5	-3,3269	-	-
FBgn0037224	153953_at	CG14639	-	-	-	-	-2,0	-3,8822
FBgn0037290	149305_at	CG1124	-	-	-	-	-3,6	-6,1115
FBgn0037723	152178_at	CG8327	SpdS	spermidine synthase activity	-1,7	-4,4261	-	-
FBgn0037902	149688_at	CG5281	-	-	-1,6	-2,8469	-	-
FBgn0038034	149768_s_at	CG17875	Cyp9f3Ψ	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-3,7	-5,9171
FBgn0038037	153031_at	CG11466	Cyp9f2	electron transporter activity / nucleic acid binding / oxidoreductase activity	-	-	-5,9	-7,3985
FBgn0038059	149782_at	CG6489	Hsp70Bc	-	-	-	-2,1	-4,9711
FBgn0038081	142746_at	CG10120	Men	carboxy-lyase activity / malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity	-	-	-1,8	-4,6088
FBgn0038126	154850_at	CG8483	-	-	-	-	-1,9	-4,6179
FBgn0038194	152120_at	CG3050	Cyp6d5	electron transporter activity / oxidoreductase activity	-3,0	-6,2175	-5,7	-7,9749
FBgn0038321	152123_at	CG6218	-	carbohydrate kinase activity / kinase activity	-1,8	-3,1728	-1,8	-3,0819
FBgn0038408	150002_at	CG6889	tara	-	-1,9	-3,6323	-1,7	-3,0337
FBgn0038413	141589_at	CG6725	Sulf1	N-acetylglucosamine-6-sulfatase activity	-1,6	-3,9648	-	-
FBgn0038563	152336_at	CG7780	DNaseII	-	-4,5	-12,3985	-3,1	-6,3489
FBgn0038647	150161_at	CG14302	-	-	-	-	-1,7	-4,1626
FBgn0038973	150369_at	CG18594	-	kinase inhibitor activity / kinase regulator activity	-	-	-1,9	-4,7751
FBgn0038982	142587_at	CG33093	-	gibberellin 20-oxidase activity	-	-	-1,6	-4,2697
FBgn0039052	150424_at	CG6733	-	NOT aminoacylase activity	-	-	-2,3	-4,3332
FBgn0039098	142671_at	CG13822	-	-	-2,2	-3,7166	-1,9	-3,0675
FBgn0039434	150663_r_at / 150662_i_at	CG5468	-	-	-	-	-1,8	-4,7636
FBgn0039436	150665_s_at	CG6478	-	-	-6,5	-6,4832	-4,0	-9,608
FBgn0039441	150670_i_at / 150671_f_at	CG5476	-	-	-2,2	-5,0894	-2,2	-6,5309
FBgn0039539	154473_at	CG12880	-	-	-	-	-4,3	-3,9017
FBgn0039559	150758_at	CG4976	Mes-4	histone methyltransferase activity / transcription cofactor activity / transcription factor binding	-1,7	-3,2565	-	-
FBgn0039586	142182_s_at	CG33103	Ppn	metallopeptidase activity / serine-type endopeptidase inhibitor activity	-3,2	-9,2947	-4,4	-9,7362
FBgn0039643	153221_at	CG11886	Slbp	-	-1,8	-3,9535	-	-
FBgn0039678	150831_at	CG18111	Obp99a	odorant binding	-2,6	-9,0152	-1,8	-5,1789
FBgn0039682	150834_at	CG7584	Obp99c	-	-	-	-1,9	-4,6964
FBgn0039686	150838_at	CG15506	-	-	-	-	-2,2	-6,7783

FBgn0039777	150893_f_at	CG2229	Jon99Fii	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-5,9	-7,4394
FBgn0039778	141369_at	CG18030	Jon99Fi	elastase activity / NOT serine-type endopeptidase activity / serine-type endopeptidase activity	-	-	-8,3	-10,9738
FBgn0039779	150894_at	CG1546	PH4alphaSG2	procollagen-proline 4-dioxygenase activity	-	-	-2,3	-3,9775
FBgn0039825	152434_at	CG31004	-	-	-	-	-2,9	-3,6157
FBgn0039873	150955_at	CG2191	-	cation transporter activity / sodium-dependent multivitamin transporter activity	-2,6	-5,6158	-	-
FBgn0040609	151094_at	CG3348	-	-	-	-	-2,1	-4,5843
FBgn0040715	151192_at	CG15386	-	-	-	-	-1,6	-3,2055
FBgn0040813	151287_at	CG11051	Nplp2	-	-1,8	-5,0897	-2,0	-4,7149
FBgn0040827	151301_at	CG13315	-	-	-	-	-1,6	-5,4826
FBgn0040865	151339_at	CG15758	-	-	-	-	-2,0	-4,1605
FBgn0040942	151409_at	CG12643	-	-	-	-	-1,7	-2,9807

Table S7. Predicted and conserved direct Dfd target genes

Affy identifier	FB code	CG numbers	Synonyms	Cluster length in bp	Conservation	# of species
154125_at	FBan0007590	CG7590	scyl	65	**Y**	5
148994_at	FBan0013701	CG13701	skl	201	Y	5
145823_at	FBan0006634	CG6634	nmr2	191	Y	5
154473_at	FBan0012880	CG12880	-	228	Y	5
148302_at	FBan0008638	CG8638	-	210	Y	5
147413_at	FBan0005756	CG5756	-	202	Y	4
143414_at	FBan0004889	CG4889	wg	182	Y	4
155150_at	FBan0031305	CG6783	-	470	Y	4
153828_at	FBan0015828	CG15828	-	190	Y	4
143409_at	FBan0010037	CG10037	vvl	219	Y	4
141280_at	FBan0010283	CG10283	-	267	Y	4
145584_at	FBan0005481	CG5481	lea	411	Y	4
150684_at	FBan0014247	CG14247	-	412	Y	4
145366_at	FBan0012199	CG12199	kek5	313	Y	4
148796_at	FBan0006878	CG6878	-	99	Y	4
149633_at	FBan0014688	CG14688	-	207	Y	4
147022_at	FBan0007763	CG7763	-	149	Y	4
149033_at	FBan0009739	CG9739	fz2	183	Y	4
151691_at	FBan0012063	CG12063	-	224	Y	4
142769_at	FBan0011905	CG11905	-	314	Y	4
143271_at	FBan0004696	CG4696	Mp20	347	Y	4
143680_at	FBan0004319	CG4319	rpr	517	Y	4
154586_at	FBan0012891	CG12891	CPTI	291	Y	4
151967_at	FBan0006415	CG6415	-	237	Y	4
147367_at	FBan0033006	CG18431	-	273	Y	4
141711_at	FBan0016764	CG33232	-	174	Y	4
144266_at	FBan0015282	CG15282	-	285	Y	4
153777_at	FBan0003027	CG3027	pyd3	290	Y	4
143565_at	FBan0010579	CG10579	Eip63E	247	Y	3
143051_at	FBan0004807	CG4807	ab	377	Y	3
152709_at	FBan0010078	CG10078	Prat2	301	Y	3
151193_f_at	FBan0015380	CG33516	dpr3	91	Y	3
144143_at	FBan0001780	CG1780	Idgf4	249	Y	3
149052_at	FBan0009449	CG9449	-	324	Y	3
147126_i_at	FBan0013324	CG13324	-	314	Y	3
146183_at	FBan0007294	CG7294	-	220	Y	3
146182_at	FBan0007296	CG7296	-	220	Y	3
143237_at	FBan0003839	CG3839	l(1)sc	298	Y	3
148236_at	FBan0010541	CG10541	Tektin-C	371	Y	3
147193_at	FBan0008589	CG8589	-	229	Y	3
153932_at	FBan0005177	CG5177	-	296	Y	3
146794_at	FBan0014756	CG14756	-	316	Y	3
154819_at	FBan0002961	CG2961	-	434	Y	3
143790_at	FBan0002849	CG2849	Rala	350	Y	3
154347_at	FBan0009670	CG9670	fal	119	Y	3
152120_at	FBan0003050	CG3050	Cyp6d5	197	Y	3

Table S8. **Identified Dfd enhancer elements in the *fz2*, *CG5657*, *wg*, and *Eip63E* genes**

Gene	Position enhancer	Chr	Binding site	Position Dfd-binding sites	Sequence Dfd-binding sites
fz2	***D. melanogaster:***				
	19192133… 19192319	3L	1	19192138… 19192145	T**TAAT**TAA
			2	19192272…19192279	T**TAAT**TAA
			3	19192306…19192313	T**TAAT**TAC
	D. simulans:				
	18527484…18527668	3L	1	18527487… 18527494	T**TAAT**TAA
			2	18527621…18527628	T**TAAT**TAA
			3	18527655…18527662	T**TAAT**TAC
	D. yakuba:				
	21897025… 21897204	3L	1	21897027… 21897034	T**TAAT**TAA
			2	21897161… 21897168	T**TAAT**TAA
			3	21897195… 21897202	T**TAAT**TAC
	D. erecta:				
	19033519… 19033698	scaffold	1	19033521… 19033528	T**TAAT**TAA
			2	19033655… 19033662	T**TAAT**TAA
			3	19033689… 19033696	T**TAAT**TAC
CG56575	***D. melanogaster:***				
	13621316… 13621527	2R	1	13621321… 13621328	TCA**ATTA**G
			2	13621423… 13621430	GCA**ATTA**T
			3	13621440… 13621447	GTA**ATTA**T
			4	13621506… 13621513	GCA**ATTA**G
			5	13621514… 13621521	ATA**ATTA**C
	D. simulans:				
	12728704… 12728916	2R	1	12728709… 12728716	TCA**ATTA**G
			2	12728812…12728819	GCA**ATTA**T
			3	12728829…12728836	GTA**ATTA**T
			4	12728895…12728902	GCA**ATTA**G
			5	12728903…12728910	ACA**ATTA**C
	D. yakuba:				
	15284603… 15284812	2R	1	15284608… 15284615	TCA**ATTA**G
			2	15284710… 15284717	GCA**ATTA**T
			3	15284727… 15284734	GTA**ATTA**T
			4	15284791… 15284798	GCA**ATTA**G
	D. erecta:				
	8215019… 8215228	scaffold	1	8215024… 8215031	TCA**ATTA**G
			2	8215126… 8215133	GCA**ATTA**T
			3	8215143… 8215150	GTA**ATTA**T
			4	8215207… 8215214	GCA**ATTA**G
			5	8215215… 8215222	ACA**ATTA**C
wg	***D. melanogaster:***				
	7288376… 7288484	2L	1	7288376… 7288383	TCA**ATTA**G
			2	7288457… 7288464	ATA**ATTA**G
			3/4	7288472… 7288483	C**TAAT**TA**ATTA**A
	D. simulans:				
	7083812… 7083920	2L	1	7083812… 7083819	TCA**ATTA**G
			2	7083893… 7083900	ATA**ATTA**G
			3/4	7083908… 7083919	C**TAAT**TA**ATTA**A
	D. erecta:				
	16209833… 16209941	scaffold	1	16209833… 16209840	TCA**ATTA**G
			2	16209914… 16209921	ATA**ATTA**G
			3/4	16209929… 16209940	C**TAAT**TA**ATTA**A
Eip63E	***D. melanogaster:***				
	3521487… 3521640	3L	1	3521492… 3521499	TTA**ATTA**A
			2	3521608… 3521615	GTA**ATTA**A
			3	3521627… 3521634	TTA**ATTA**A
	D. simulans:				
	3076069… 3076221	3L	1	3076073… 3076080	TTA**ATTA**A
			2	3076189… 3076196	GTA**ATTA**A
			3	3076208… 3076215	TTA**ATTA**A
	D. yakuba:				
	4165397… 4165508	3L	1	4165498… 4165505	TTA**ATTA**A
			2	4165479… 4165486	GTA**ATTA**A
	D. erecta:				
	6236768… 6236888	scaffold	1	6236879… 6236886	TTA**ATTA**A
			2	6236860… 6236867	GTA**ATTA**A

Bold sequences show ATTA core sequence within each Dfd binding site.