

**A cigarette smoke induced *Drosophila* model  
identifies molecular mechanisms underlying  
COPD development**

**Dissertation**

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## Abbreviations

AMP	Antimicrobial Peptide
ARE	Antioxidant Response Element
Att	Attacin
BSO	Buthionine Sulfoximine
CD8 <sup>+</sup>	Cluster of Differentiation 8 positive
cDNA	complementary DNA
CDS	Coding Sequence
Cec	Cecropin
cnc	Cap'n'collar
COPD	Chronic Obstructive Pulmonary Disease
CRISPR/Cas9	Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR associated endonuclease 9
CS	Cigarette Smoke
CT	Cycle Threshold
Ctrl	Control
CXCL8	C-X-C motif Ligand 8
d	Day
DEG	Differentially Expressed Gene
Dipt	Diptericin
DNA	Deoxyribonucleic Acid
dNTPs	Deoxyribonucleoside Triphosphates
Dredd	Death related ced-3/Nedd2-like caspase
Drs	Drosomycin
ERK	Extracellular-signal Regulated Kinase
Fadd	FAS-associated death domain orthologue
FEV <sub>1</sub>	Forced Expiratory Volume in 1 second
Fig.	Figure
FVC	Forced Vital Capacity
GAL4	Yeast transcription activator protein 4
Gclc	Glutamate-cysteine ligase catalytic subunit c



Gclm	Glutamate-cysteine ligase modifier subunit
GFP	Green Fluorescent Protein
Ggt	$\gamma$ -glutamyl transpeptidase
GO	Gene Ontology
GPx	Glutathione peroxidase
Gr	Glutathione reductase
GSH	Reduced form of glutathione
GSS	Glutathione synthetase
GSSG	Oxidized form of glutathione
GstD	Glutathione S-transferase class D
GstE	Glutathione S-transferase class E
h	Hour
IL-1/6	Interleukin 1/6
Imd	Immune deficiency
JAK	Janus Kinase
JNK	Jun N-terminal Kinase
Keap1	Kelch associated protein 1
KO	Knock Out
LABA	Long-Acting $\beta_2$ Agonist
LAMA	Long-Acting Muscarinic Antagonist
max	maximum
$\mu$ g	microgram
mg	milligram
min	Minute
MMP-9	Matrix Metalloprotease 9
MRP	Multidrug Resistance Protein
Mtk	Metchnikowin
Nrf2	Nuclear factor erythroid 2-related factor 2
ns	Not significant
OTU	Operational Taxonomic Unit
PAMP	Pathogen Associated Molecular Pattern
PC	Protein to Carbohydrate ratio

PCR	Polymerase Chain Reaction
Pep	cysteinyl-glycine dipeptidase
PI3K	Phosphoinositide-3-Kinase
Prx	Peroxiredoxin
qPCR	Quantitative PCR
RNA	Ribonucleic acid
RNAi	RNA interference
RNaseq	RNA sequencing
ROS	Reactive Oxygen Species
Rpl32	Ribosomal protein l 32
s	Second
SD	Standard Deviation
SEM	Standard Error of the Mean
sMaf	Small Musculoaponeutronic fibrosarcoma
STAT	Signal Transducers and Activators of Transcription
Tab.	Table
TAG	Triacylglyceride
Tak1	TGF- $\beta$ activated kinase 1
TGF- $\beta$	Tumor Growth Factor $\beta$
TNF $\alpha$	Tumor Necrosis Factor $\alpha$
Trabid	Orthologue of the mammalian A20
Trxr	Thioredoxin reductase
TSS	Transcription Start Site
UAS	Upstream Activated Sequence
Upd	Unpaired

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## Summary

Chronic Obstructive Pulmonary Disease (COPD) serves as an umbrella term that encompasses a group of chronic lung diseases, which collectively cause obstructive and irreversible airflow limitation and finally lead to premature death. The main cause of COPD is undoubtedly cigarette smoking but with rising air pollution and aging populations COPD is suggested to even increase in incidences. However, detailed cellular mechanisms involved in the development of this disease still remain unclear. This thesis introduces a novel cigarette smoke (CS) induced *Drosophila* model to elucidate underlying causes of disease development. Exposure of flies to CS reproduced major hallmarks of COPD, such as reduced lifespan, impaired activity or increased antioxidant responses. Detailed transcriptomic analyses revealed crucial processes that were induced by the airway epithelium upon CS exposure. Short-term responses were characterized by the activation of antioxidant responses. The Nrf2 pathway was identified as a crucial mediator of these responses by regulating the glutathione metabolism, which in turn plays a pivotal role in detoxification. Ectopic activation of the Nrf2 pathway during CS exposure resulted in an increased lifespan of the fruit fly. Besides these short-term responses, transcriptomic analyses revealed the immune system to be involved in the chronic response to CS. Long-term CS exposure involved the immune system, which was found to decrease the lifespan of CS exposed flies by a genetic manipulation of the immune response. The immune system responses changed in an age dependent manner and transcriptomic analyses proved the relevance of aging for the development of COPD. These results suggest an abnormal aging of CS exposed airways and provided evidence that COPD can be considered as premature aging of the lung. However, CS cessation could reverse the effects of CS exposure to a certain extent but could not fully rescue the reduced lifespan. Transcriptomic analyses elucidated the immune system and an induction of age-related factors that might underlie this chronic response. Moreover, the influence of nutrition on the lifespan of CS exposed flies, suggested the relevance of dietary intervention in COPD patients. Finally, this thesis provides a pioneer data set for the characterization of adult tracheal epithelial cells.

In summary, this thesis proves that *Drosophila melanogaster* can serve as an effective model for studying CS induced effects, pinpoint potential treatment strategies and relate findings in the invertebrate system to human COPD development.

## Zusammenfassung

Die chronisch obstruktive Lungenerkrankung (*Chronic Obstructive Pulmonary Disease*, COPD) beschreibt einen Sammelbegriff für Atemwegserkrankungen, welche kollektiv zu einer Limitierung des Atemflusses und damit zu vorzeitigem Tod führen. Obwohl das Rauchen die Hauptursache für die Entwicklung von COPD ist, führen eine anhaltende Luftverschmutzung und alternde Populationen zu zunehmender Inzidenz dieser Krankheit. Allerdings sind zugrunde liegende zelluläre Mechanismen weitestgehend unbekannt. Daher wird in dieser Arbeit ein neues *Drosophila* Modell für Zigarettenrauch (ZR) vorgestellt, um diese Mechanismen aufzuklären. ZR exponierte Fliegen zeigten COPD typische Symptome wie reduzierte Lebensspanne, reduzierte Aktivität oder eine erhöhte antioxidative Antwort. Detaillierte Transkriptomanalysen des Atemwegepithels zeigten Prozesse, welche entscheidend an der Antwort auf ZR beteiligt waren. Kurzfristige Antworten waren charakterisiert durch aktivierte antioxidative Signalwege wie Nrf2, welcher wiederum eine Detoxifizierung über die Regulation des Glutathion Metabolismus auslöste. Eine ektopische Aktivierung des Nrf2 Signalwegs führte zu einer Verlängerung der Lebensspanne von ZR exponierten Fliegen. Transkriptomanalysen zeigten außerdem, dass eine langfristige Antwort auf ZR durch das Immunsystem definiert war, dessen Inhibierung zu einer verlängerten Lebensspanne führte. Eine altersbedingte Immunantwort sowie zusätzliche Transkriptomanalysen zeigten die Relevanz des Alterungsprozesses für die Entwicklung von COPD. Anhand dieser Ergebnisse ließ sich ein beschleunigtes Altern der Atemwege erkennen, was auf ein vorzeitiges Altern der Lunge in COPD Patienten hinweist. Eine Entwöhnung von ZR konnte observierte Effekte in Teilen umkehren, allerdings konnte die Lebensspanne nicht gänzlich wiederhergestellt werden. Basierend auf Transkriptom Daten wurden Alterungsprozesse und das Immunsystem als potentielle Faktoren für diese Veränderungen gefunden. Zusätzlich wurde gezeigt, dass die Ernährung einen Einfluss auf die Lebensspanne von ZR exponierten Fliegen hatte, was auf die Relevanz der Ernährungsweise von COPD Patienten hinweist. Des Weiteren stellt diese Arbeit erstmalig einen Datensatz zur Charakterisierung adulter Tracheenzellen zur Verfügung.

Das in dieser Arbeit vorgestellte *Drosophila* Modell dient als effektives Instrument, um ZR induzierte Effekte zu identifizieren, potentielle Behandlungsansätze zu finden und diese Erkenntnisse schließlich auf den Menschen zu übertragen.

# 1 Introduction

## 1.1 Chronic Obstructive Pulmonary Disease

Chronic Obstructive Pulmonary Disease (COPD) serves as an umbrella term that encompasses a group of chronic lung diseases, which collectively cause obstructive and irreversible airflow limitation and finally lead to premature death. The term COPD does not describe a fixed disease pattern. It is rather defined by a decline in lung function that is measured by the ratio of Forced Expiratory Volume in one second (FEV<sub>1</sub>) to Forced Vital Capacity (FVC). The lung obstructions are characterized by a chronic inflammation, which in turn causes small airway narrowing and destruction of lung parenchyma<sup>1</sup>.

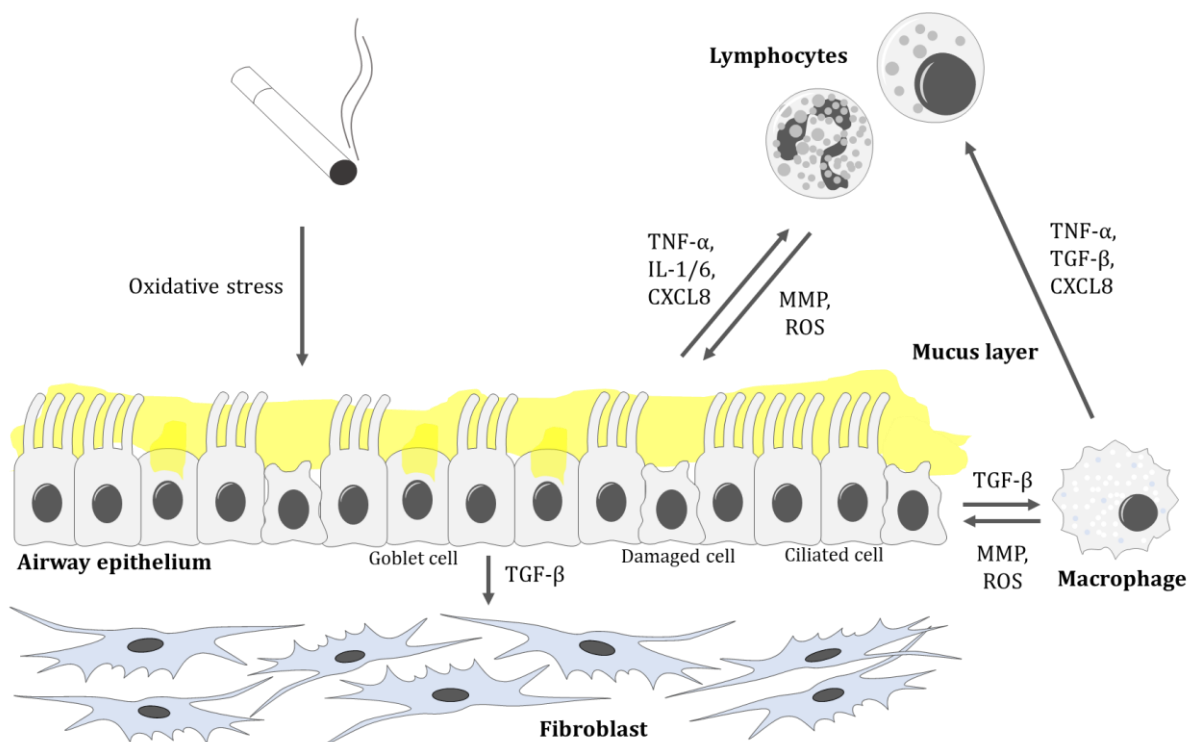
COPD is ranked the third leading cause of death worldwide and is considered to even increase in incidence in future due to aging populations and rising air pollution<sup>2-9</sup>. Although tobacco smoke still is the main risk factor for the development of COPD, a variety of different other factors are causes of COPD<sup>8</sup>.

Genetic factors such as  $\alpha$ 1-antitrypsin deficiency lead to alveolar wall destruction but only account for approximately 1-5 % of all COPD cases<sup>10,11</sup>. Nowadays a large proportion of COPD patients suffer from this disease due to exposure to noxious particles originating from different sources such as air pollution, second-hand smoke or biomass smoke<sup>12-15</sup>. Especially in developing countries indoor cooking is an important risk factor for the development of COPD even in non-smokers<sup>16</sup>. The constant inhalation of noxious particles induces a persistent immune response and finally leads to chronic inflammation of the lung<sup>17</sup>. This inflammation involves both the innate and adaptive immune response and is characterized by an increase of neutrophils, macrophages and T-lymphocytes entering the lung<sup>17,18</sup>. Together with the airway epithelium, these cells respond to inhaled irritants to induce protective mechanisms<sup>19</sup>. Especially the epithelial cells play a critical role for the development of the obstructive phenotype observed in COPD patients<sup>20</sup>. As the first line of defense and acting as a physical barrier against invasive particles, epithelial cells furthermore initiate an immune response in the airways. Activated by cigarette smoke or other inhaled irritants, they drive the release of pro-inflammatory cytokines like Tumor Necrosis Factor  $\alpha$  (TNF $\alpha$ ), Interleukin 1 $\beta$  and 6 (IL-1/6) and C-X-C motif Ligand 8 (CXCL8)<sup>21</sup>. Release of these mediators results in the activation and recruitment of immune cells to the site of inflammation<sup>20</sup>. Although being effectors of inflammation, epithelial



cells at the same time are the target in remodeling of small airways and destruction of lung parenchyma, potentially leading to emphysema<sup>21</sup>.

Oxidative stress originating from inhaled irritants and an exaggerated immune response cause injury of ciliated cells, which in turn impairs the mucociliary clearance<sup>22</sup>. Transforming Growth Factor  $\beta$  (TGF- $\beta$ ) activation stimulates fibroblasts in order to repair the damaged lung tissue<sup>23</sup>. However, the chronic induction of fibroblasts in turn promotes fibrosis and therefore causes an abnormal narrowing of airways. Combined with an excessive production of mucus from increased numbers of goblet cells, the luminal diameter of airways is substantially reduced in COPD<sup>24</sup> (Fig. 1). COPD patients try to compensate for these morphologic changes in the airway epithelium with severe cough, trying to clear excess mucus from the airways. Moreover, they show an increased work of breathing to overcome narrowed and clogged airways in order to fill the lungs with fresh air<sup>25</sup>.



**Fig. 1 The effects of cigarette smoke on the airway epithelium.** Mainly caused by oxidative stress originating from cigarette smoke, the airway epithelium reacts to irritants by releasing the pro-inflammatory cytokines Transforming Growth Factor  $\beta$  (TGF- $\beta$ ), Tumor Necrosis Factor  $\alpha$  (TNF $\alpha$ ), Interleukin 1 $\beta$  and 6 (IL-1/6) and C-X-C motif Ligand 8 (CXCL8) and recruits T-lymphocytes and macrophages. Macrophages and neutrophils secrete Reactive Oxygen Species (ROS) and Matrix Metalloproteases (MMP) that damage ciliated cells and rupture alveolar cell walls. The airway epithelium tries to compensate for these alterations by inducing a chronic wound response of fibroblasts that lead to a narrowing of airways. Combined with an excess mucus production from goblet cells to clear airways from irritants, the airway flow is substantially decreased.

Epithelial cells are not the sole drivers of COPD phenotypes. Mediated by the airway epithelium, recruited inflammatory cells of both the innate and adaptive immune system, release various mediators affecting the airways<sup>26-28</sup>. Especially macrophages play a key role in the response to airborne particles<sup>29</sup>. Next to orchestrating the recruitment of lymphocytes by releasing TGF- $\beta$ , TNF- $\alpha$  or CXCL8 they additionally secrete Matrix Metalloprotease 9 (MMP-9)<sup>30</sup>. The release of this elastolytic enzymes results in an imbalance between proteases and antiproteases and a subsequent rupture of alveolar walls and elastic recoil<sup>31</sup>. Rupture of epithelial integrity is further driven by an abnormal release of Reactive Oxygen Species (ROS), that damage the airway epithelium<sup>32</sup>. Activated neutrophils amplify the inflammation response and further contribute to the protease/antiprotease imbalance via the secretion of MMPs in the alveolar airways<sup>33</sup> (Fig. 1). The additional release of ROS elevates the oxidative stress level in the lung even further<sup>34</sup>. Together, these mechanisms disrupt alveolar walls, which appear to trap old, oxygen poor air and have a heavily reduced respiratory surface<sup>35</sup>. COPD patients with emphysema cannot exhale air from the lung completely and therefore also are not able to refill the lung with fresh, oxygen rich air<sup>36</sup>. Combined with the aforementioned airflow limitations from narrowed airways, these phenotypes express in overall shortness of breath and in exercise intolerance<sup>37</sup>.

There are strategies available to slow down the progression of COPD. Nevertheless, there is still no treatment option available to stop the progression or even to fully cure the disease<sup>6</sup>. The simplest and most effective strategy to prevent COPD development is smoking cessation or equivalently the reduction of indoor cooking with open fires<sup>38,39</sup>. Also an increase in physical activities has been shown to correlate with reduced symptoms and mortality of COPD patients, similar to the effects of smoking cessation<sup>6,40,41</sup>. Besides to lifestyle changes, there are pharmacological interventions available to treat emerging symptoms in COPD patients<sup>6</sup>. The treatment with corticosteroids reduces inflammation and mildens symptoms especially during acute worsening of symptoms, called exacerbations<sup>42</sup>. Inhaled Long-Acting  $\beta_2$  Agonists (LABA) and Long-Actin Muscarinic Antagonists (LAMA) are widely used for the treatment of COPD patients<sup>6,43</sup>. A combination of both LABA and LAMA seems to be most beneficial for COPD patients<sup>44</sup>.

As a complex and multifactorial disease, COPD usually shows variances in manifestation of distinct disease features, from patient to patient<sup>45,46</sup>. This makes the understanding of

underlying mechanisms difficult, which is essential for the finding of novel, sustainable and personalized treatment strategies. Such strategies aim to improve not only personal burden but also economic burden, appearing from high health care costs<sup>47</sup>. An improved understanding of COPD pathology is therefore essential for the development of novel and effective intervention strategies in order to milden both social and economic burden<sup>47</sup>.

COPD is a chronic disease that worsens over time and is associated with an abnormal aging of the lung that results in an overall decline in lung function<sup>16</sup>. The normal aging lung is characterized by several features similar to those observed in COPD patients, like chronic inflammation, increased oxidative stress and genomic instability<sup>16</sup>. The aging phenotype in the lung is inclined to develop an emphysema-like phenotype. However, COPD related phenotypes generally occur at earlier stages of life than in the normal aging lung<sup>16</sup>. The risk for developing COPD correlates with increasing age and therefore older people are more prone to develop this disease<sup>6</sup>. COPD might therefore be considered as a premature aging of the lung. Understanding age related effects in COPD may contribute to better understanding of disease pathophysiology.

## **1.2 Aging**

During the life of most multicellular organisms, a progressive decline in organ and tissue function over time is observed<sup>48</sup>. This natural and irreversible process is called aging and consequently causes biological death of the organism. As a highly complex, multifactorial and time dependent process, aging expresses in diverse physiologic parameters and ultimately determines lifespan<sup>49</sup>. These parameters share common criteria that define them as aging-related processes<sup>49</sup>. Firstly, they have to manifest during normal aging and secondly, experimental manipulation should either accelerate or retard the aging process<sup>49</sup>. All of these hallmarks collectively cause time-dependent cellular damage and finally lead to corruption of according tissues<sup>50-52</sup>.

In the course of life, an organism accumulates a number of genetic alterations<sup>53</sup>. Arising from exogenous physical, chemical or biological agents and from endogenous sources such as DNA replication errors or ROS, these alterations lead to genomic instability<sup>54</sup>. Next to point mutations, translocations and chromosomal gains or losses, the shortening of telomeres substantially contributes to the aging phenotype<sup>55</sup>. Telomeres are structures that cap chromosomes and preserve the DNA<sup>56,57</sup>. Since DNA polymerases cannot

replicate a DNA molecule completely, each cell replication cycle shortens the genomic DNA<sup>58-60</sup>. To protect the genome from shortening, telomeres are necessary to maintain the original length of a chromosome. Telomeres are elongated by telomerases that add repetitive sequence to the end of a chromosome in order to protect coding sequences from getting shortened. This repetitive sequence is synthesized from an RNA template contained in the telomere itself<sup>61</sup>. However, some organisms like *Drosophila melanogaster* maintain their telomere lengths by a telomerase independent mechanism. In this functionally similar mechanism, the retrotransposable elements Het-A and TART are reverse transcribed onto the telomere ends<sup>62,63</sup>. A decline either in telomerase activity or in retrotransposition is correlating with age and adds up to genomic instability<sup>64,65</sup>.

Cellular damage in aging organisms appears not only on genomic but also on epigenetic and protein levels<sup>49,66,67</sup>. Epigenetic alterations like DNA methylation, histone modification or transcriptional regulation are correlating with age and affect the physiology and lifespan of an organism<sup>68-70</sup>. In contrast to genomic damage, these epigenetic changes theoretically can be reversed and might serve as potential targets for anti-aging interventions<sup>71-73</sup>. Moreover, in age there is an accumulation of misfolded proteins that have to be degraded in order to assure for correct folding and biological activity<sup>49</sup>. This so called Unfolded Protein Response alters proteostasis in age and is a contributor to age-related diseases such as Alzheimer's disease, Parkinson's disease or cataract<sup>66,74</sup>.

The aforementioned processes collectively damage cells and lead to subsequent manifestations of tissue dysfunction. Especially genomic damage can potentially be an underlying cause of cellular senescence<sup>75</sup>. Cellular senescence is defined as a non-dividing state of cells, that is caused by age-related telomere shortening and nontelomeric DNA damage<sup>48,76,77</sup>. This mechanism is supposed to be a necessary step to control tissue homeostasis and clear from damaged and potentially oncogenic cells<sup>49</sup>. Removal of these damaged cells is necessary in order to maintain tissue function and to prevent from premature aging. The origin of increased senescent cells in aging organisms is not fully resolved. It is possible that cell senescence is a consequence of an inefficient turnover system, where stem cells do not divide anymore in age<sup>49</sup>. This age-related stem cell exhaustion indicates a decline in tissue function, contributes to aging and possibly leads to an accumulation of senescent cells<sup>78-80</sup>. However, it is unclear whether the generation

of senescent cell drives this increase or if it is a matter of reduced clearance by the immune system<sup>49</sup>.

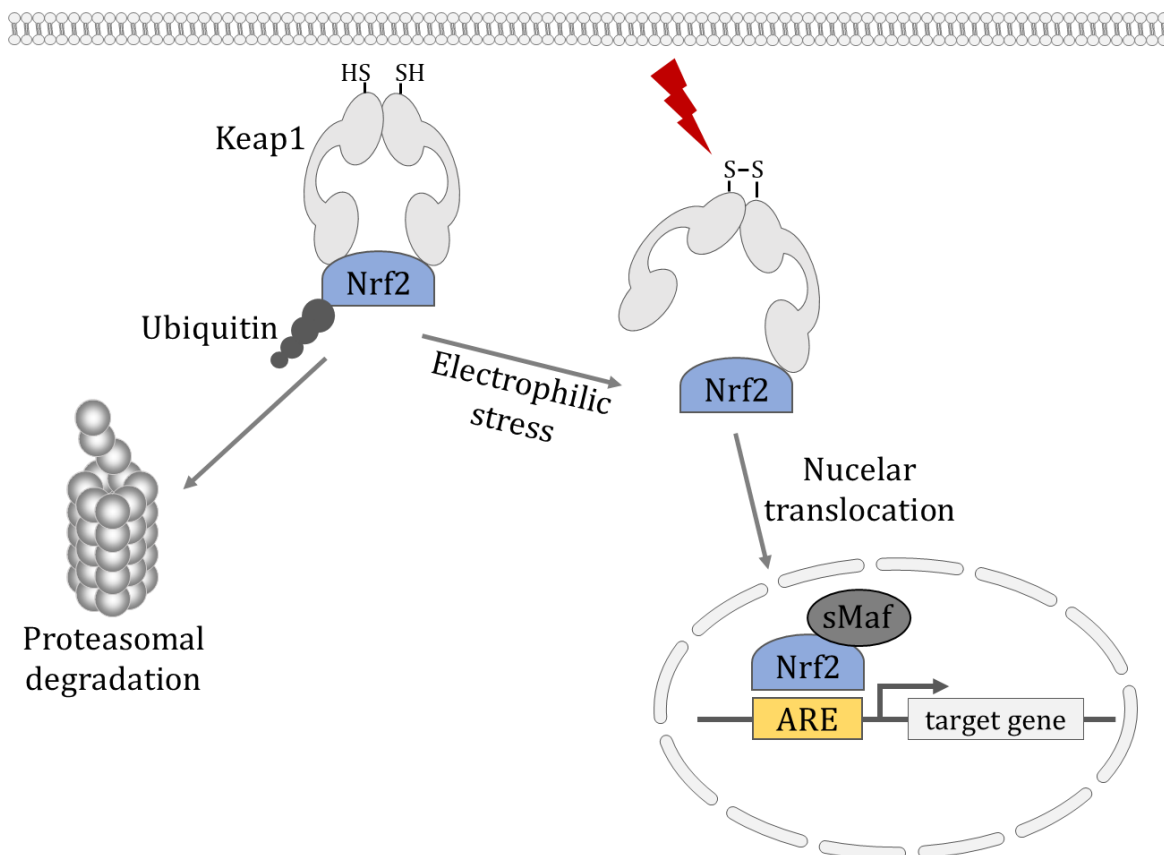
In aging organisms an increase in inflammation is observed, that leads to attenuated immunity and is referred to as “Inflammaging”<sup>81</sup>. This process has several causes and might be a of central importance in mediating other age-related symptoms<sup>81</sup>. Accumulating stress, originating from diverse sources such viral and bacterial infections, oxidative stress or an imbalance in proteostasis lead to an increased release of proinflammatory cytokines<sup>49,82</sup>. These cytokines activate the immune system, which in turn enhances this inflammatory response even further, resulting in a chronic low-grade inflammation. Central players in this response are macrophages, that are stimulated by these stressors and contribute to a chronic activation of NF-κB signaling<sup>83-85</sup>. The inflammaging phenotype is a crucial risk factor for the development of several diseases and accelerates their development. Age-related diseases such as cancer, type 2 diabetes mellitus or cardiovascular diseases were previously identified to correlate with a chronic inflammation in older people<sup>86-88</sup>.

Inflammaging is tightly related to other aging phenotypes such as mitochondrial dysfunction, proteasomal dysregulation or defective autophagy<sup>89</sup>. Especially mitochondrial dysfunction results in increase of intracellular ROS, which long has been considered to be a detrimental byproduct of aging<sup>90</sup>. Nowadays it is supposed that production of ROS rather is a mechanism to trigger proliferation and may prolong lifespan<sup>91,92</sup>. Reconsideration for the role of ROS therefore has to be made and evaluated towards a signaling function to ensure for survival upon stress induction<sup>49,93</sup>. However, ROS levels need to be in homeostatic balance in order to be have protective roles rather than damaging the tissue<sup>94</sup>.

For many diseases like cancer, Alzheimer’s disease or COPD, aging is considered as the main risk factor for the development of the disease<sup>16,49,95</sup>. Hence, knowledge about aging might contribute to the understanding of disease progression and potentially can drive the development of new treatment strategies.

### 1.3 The Nrf2 antioxidant pathway

Organisms are constantly exposed to various endogenous and exogenous stressors. Noxious particles that originate from exogenous sources are referred to as xenobiotics. These particles often cause the formation of ROS, which in turn potentially might lead to oxidative damage of the cells. Therefore, an appropriate protection from ROS is essential for redox homeostasis and survival of cells<sup>96</sup>. Eukaryotic cells possess a broad range of mechanisms to protect from oxidative damage, coming from endogenous and exogenous sources.



**Fig. 2 The Nrf2 antioxidant pathway.** Under normal conditions the Nuclear factor erythroid 2-related factor 2 (Nrf2) transcription factor is bound by Kelch-like ECH-associated protein 1 (Keap1) that ubiquitinates Nrf2 and promotes its proteasomal degradation. Electrophilic stress induces a conformational change of Keap1 and Nrf2 dissociates, forms a heterodimer with small Musculoaponeurotic fibrosarcoma (sMaf) and translocates into the nucleus. The dimer binds the antioxidant response element (ARE) and induces the transcription of target genes.

One of the main antioxidant response regulating mechanisms is the Nuclear factor erythroid 2-related factor 2 (Nrf2) pathway<sup>97</sup>. The Nrf2 pathway is a simple signaling cascade that is activated by ROS stress (Fig. 2). Under reducing conditions, the Kelch-like ECH-associated protein 1 (Keap1) binds the cap'n'collar (Cnc) basic-region leucine zipper transcription factor Nrf2 and thereby ubiquitinates Nrf2 and promotes its proteasomal

degradation. Under oxidative conditions cysteine residues of Keap1 are modified and Keap1 alters its conformation leading to the dissociation and subsequent nuclear translocation of Nrf2<sup>98</sup>. When Nrf2 migrates to the nucleus it forms a heterodimer with small Musculoaponeurotic fibrosarcoma (sMaf) and binds a regulatory region of target genes, called the antioxidant response element (ARE)<sup>99-101</sup>. The subsequently driven expression of target genes comprises a number of genes coding for cytoprotective proteins such as Glutamate-cysteine ligase (Gcl)<sup>102,103</sup>, Glutathione S-transferases (Gst) or Thioredoxin reductases (Trxr)<sup>98,102-105</sup>.

Besides to acting as a master regulator of redox homeostasis, Nrf2 is involved in several other cellular processes by interacting with diverse partners and pathways such as p62, Extracellular-signal Regulated Kinase (ERK) or Phosphoinositide-3-Kinase/Protein Kinase B (PI3K/AKT)<sup>106-108</sup>. A few of Nrf2 associated processes are proliferation<sup>109,110</sup>, differentiation<sup>111,112</sup> and inflammation<sup>113</sup>. These processes especially play a critical role in tumor growth and are known to have an impact on cancer development.

Nrf2 therefore is a complex player in cellular signaling, making it a promising but at the same time vulnerable target for treatment strategies for human diseases, that easily can be brought out of balance<sup>114,115</sup>. Interference with the Nrf2 signaling pathway will also affect downstream pathways like the glutathione metabolism<sup>116</sup>.

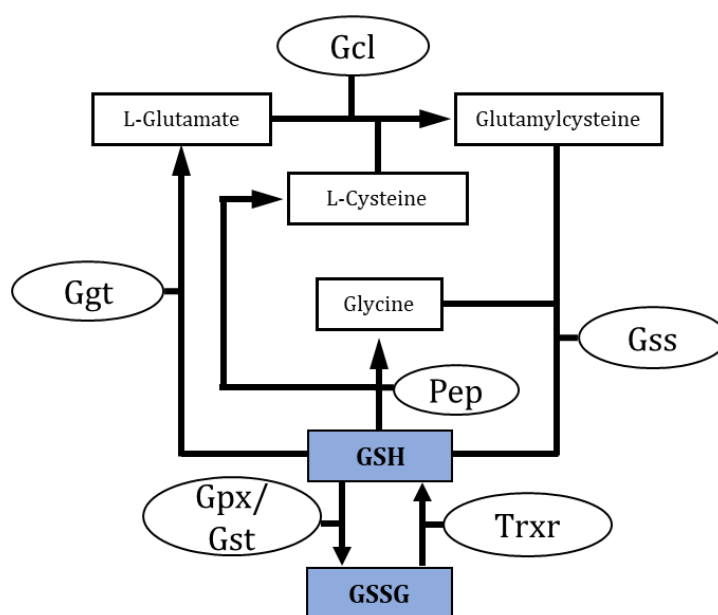
#### **1.4 The glutathione metabolism**

The peptide glutathione (GSH) is a very abundant molecule in the cytosol of cells and is synthesized from the three amino acids L-glutamate, L-cysteine and L-glycine<sup>117</sup>. The bipartite synthesis step is catalyzed by two enzymes. In the first and rate limiting step L-glutamyl-cysteine is synthesized by the glutamate-cysteine ligase (Gcl) from L-glutamate and L-cysteine. The Gcl is composed of a catalytic subunit (Gclc) and a modifier subunit (Gclm). In a second enzymatic step, L-glycine is added by the glutathione synthetase (GSS) to form GSH. Although all cell types are capable of synthesizing GSH, the liver is the main producer and exporter of GSH<sup>118</sup>.

GSH serves a thiol source and is involved in many processes such as signal transduction, gene expression and apoptosis<sup>119-121</sup>. However, the most important function of glutathione (GSH) is its ability to effectively scavenge xenobiotics and ROS in order to maintain cellular redox homeostasis<sup>122</sup>. Therefore, GSH is conjugated to noxious particles

and eliminates them either by reduction or by secretion. These detoxification processes are catalyzed by a number of different enzymes, which accelerate the elimination of various toxic molecules.

Glutathione peroxidases (Gpx) catalyze the conjugation of GSH to hydrogenperoxide ( $H_2O_2$ ), leading to the reduction of  $H_2O_2$ <sup>123</sup>. In this reduction process, the thiol group of GSH acts as an electron donor and eliminates the oxidative potential of  $H_2O_2$ . When GSH is oxidized it changes its monomeric form to a dimeric form, called GSSG. In mammals the potential toxic GSSG is rapidly reduced back to GSH by the glutathione reductase (GR), whereas *Drosophila* relies on the thioredoxin reductase (Trxr) system<sup>124</sup>. The ratio of GSH to GSSG indirectly indicates the redox state of cells. Under reducing conditions this ratio tends towards GSH, while oxidative conditions will shift it towards GSSG<sup>125</sup>. High cellular GSH/GSSG ratios therefore are beneficial for protection from oxidants<sup>126</sup>.



**Fig. 3 Glutathione metabolism in *Drosophila melanogaster*.** Glutathione (GSH) is synthesized from the amino acid L-glutamate, L-cysteine and glycine. The glutamate-cysteine ligase (Gcl) catalyzes the conjugation of glutamate and cysteine to glutamylcysteine, that is further conjugated with glycine by the glutathione synthetase (Gss) to form glutathione (GSH). Conjugation of xenobiotics to GSH is catalyzed by glutathione peroxidase (Gpx) and glutathione S-transferases and results in oxidation of GSH. The formed GSSG is reduced to GSH by thioredoxin (Trxr). GSH is degraded to its constituents by  $\gamma$ -glutamyl transpeptidase (Ggt) and cysteinyl-glycine dipeptidase (Pep).

Moreover, the detoxifying ability of GSH is further characterized by disposing xenobiotics and transporting them out of the cells. Many members of the superfamily of glutathione S-transferases (Gst) conjugate GSH to various hydrophobic and electrophilic agents. Toxic molecules such as aflatoxin B1, 4-hydroxynoneal (4-HNE) or acrolein can potentially act as carcinogens or damage membranes and proteins<sup>127-129</sup>. When Gsts conjugate these



molecules to the thiol group of GSH, the obtained mercapturate or GS-HNE adducts can then be neutralized by removing the molecule from the cell via multidrug-resistance proteins (MRP)<sup>129</sup>. The degradation of GSH in its constituents is accomplished via  $\gamma$ -glutamyl transpeptidase (Ggt) and cysteinyl-glycine dipeptidase (Pep)<sup>130,131</sup>.

Defects in GSH metabolism contribute to increased oxidative stress and hence might play a crucial role in aging and many human diseases<sup>117</sup>. Neurodegenerative diseases like Alzheimer's disease and Parkinson's disease are correlated to a reduction of GSH levels and a change of Gst activity<sup>132,133</sup>. Also in different kinds of cancer high Gst activity is involved in tumor resistance to anticancer drugs<sup>127,134</sup>. Finally, an increase in GSH levels correlates with cigarette smoking and the GSH:GSSG ratio is shifted towards GSSG<sup>135,136</sup>. These facts suggest a protective role of GSH to adapt to increasing oxidative stress and prevent from cellular damage in COPD patients<sup>137</sup>.

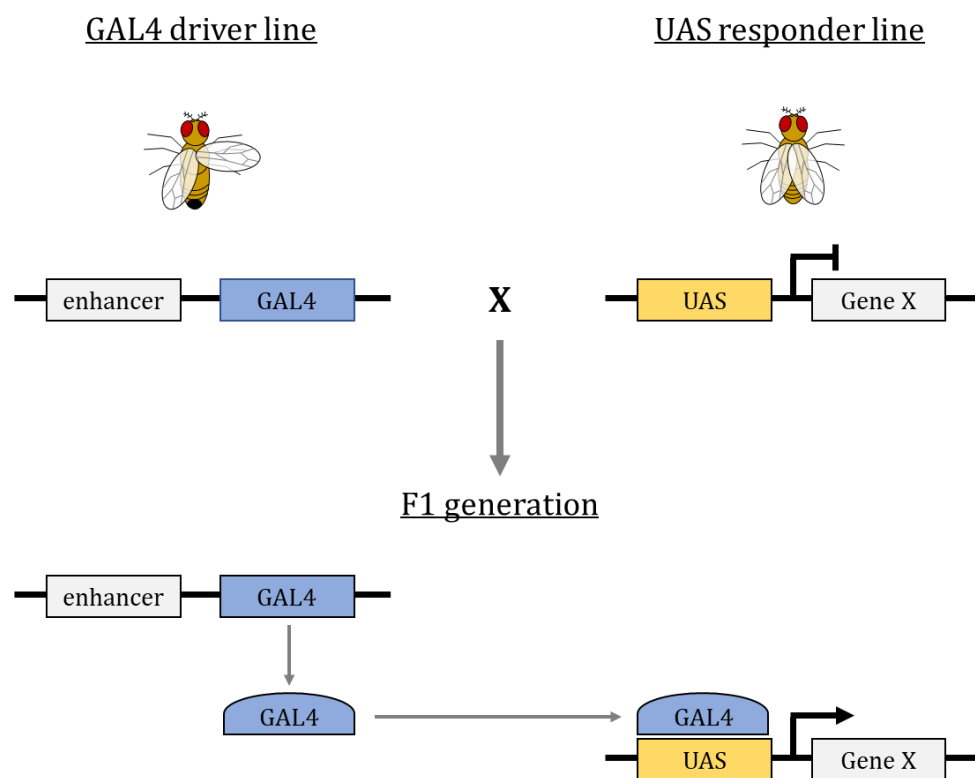
### **1.5 *Drosophila* as a model organism to study human diseases**

To better understand mechanisms and principles of human diseases, animal models are ideally suited. Findings in these models are transferred to the human system and should add to the knowledge about diseases and finally drive the development of novel and specific therapeutic strategies. These model organisms however have to match certain requirements to make them suitable for studying human diseases. Evolutionary conserved pathways, a well characterized genome, easiness of handling and a short generation cycle are a few of the main demanding factors for model organisms.

As a common model organism in many fields of biological research, the fruit fly *Drosophila melanogaster* offers all these advantages. It has a short life cycle of approximately 10 days (at 25 °C). *Drosophila* is a holometabolic insect, which means that after hatching it passes three larval stages before pupating and finally developing to an imago. With a completely sequenced genome and homologies in over 60 % of all human disease related genes, *Drosophila* delivers a solid base for biomedical research<sup>138,139</sup>. Combined with a broad range of available tools and techniques to manipulate the fly, both genetically and pharmaceutically, it makes *Drosophila* a very powerful model to study human diseases.

In 1993, Brand and Perrimon set the basis for modern *Drosophila* research by developing the GAL4/UAS binary expression system, which allows for a specific expression of a desired transgene simply by crossing two distinct fly lines<sup>140</sup>. One of the parental lines

drives the expression of the yeast transcription factor GAL4 under control of a specific enhancer. This so-called driver line is then crossed to a responder line, which carries a transgene whose expression in turn is controlled by the UAS (Upstream Activated Sequence) element. This element is bound by GAL4 and transgene expression can be induced in a very specific manner (Fig. 4). With this tool, *Drosophila* researchers are able to express transgenes specifically in certain tissues of interest. It is very well applicable to many different experimental approaches such as overexpression studies, RNAi or CRISPR/Cas9 experiments<sup>141-143</sup>.



**Fig. 4 The binary GAL4/UAS expression system.** The GAL4/UAS system allows for a tissue specific activation of target genes. The driver line expresses the GAL4 transcription factor, that is controlled by an enhancer. In case the enhancer is active, GAL4 will be expressed. In the responder line, transcription of a target gene (Gene X) is controlled by the Upstream Activated Sequence (UAS). In the F1 generation of a crossing of both lines, the enhancer specific expression of GAL4 activates the transcription of Gene X by binding the UAS.

There are not only alternatives to this system like the LexA/LexAop<sup>144</sup> and the Q-System<sup>145</sup> but also expansions. Besides a spatial expression of transgenes, these expansions further allow for a spatiotemporal control of gene expression. Both, the gene switch and the temporal and regional gene expression targeting (TARGET) system are generally based on the repression of GAL4<sup>146</sup>. In the TARGET system, the temperature sensitive GAL4 repressor GALI80 is utilized. At 18 °C this repressor is active and blocks

the transcriptional activation domain of GAL4. Whereas at 29 °C or higher temperatures GAL80 is inactive and GAL4 can bind the UAS element and induce target gene expression. With this system *Drosophila* researchers can induce potentially harmful or even lethal transgenes at any point of development that usually would lead to an altered physiology or even death before the start of the experiment.

In summary, all these aspects and a broad availability of tools make the fruit fly a very powerful and effective model to study human diseases.

### **1.6 The respiratory system of *Drosophila melanogaster***

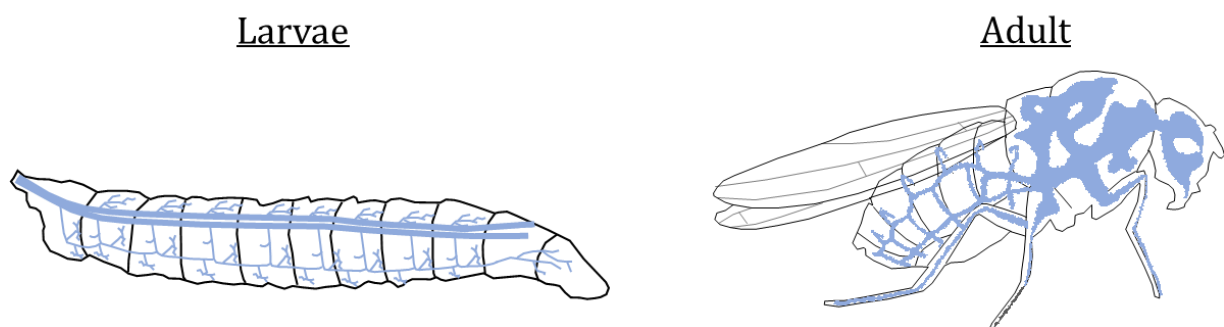
Throughout the animal kingdom, most metabolic processes are dependent on a constant oxygen supply. The uptake of oxygen in almost all animals is encompassed through specialized organs, which deliver oxygen either directly or indirectly to the tissue. As in all other insects, the tracheal system fulfils this task in *Drosophila*. The tracheal system is a formation of interconnected tubes that are built from a monolayer of epithelial cells, wrapping around a lumen<sup>147</sup>. In order to maintain the tubular shape and prevent the trachea from collapsing, the luminal side is scaffolded by a chitin layer<sup>148</sup>. Air enters the trachea through spiracles and diffuses into a network of interconnected tubes<sup>149</sup>.

The larval tracheal system is organized in a very simple and bilateral structure (Fig. 5). The air enters through two pairs of spiracles in the anterior and posterior end of the larvae and diffuses into the dorsal trunks. From the dorsal trunks it passes primary, secondary and tertiary branches until it is delivered to the tissue by terminal cells. These cells sit in the end of the tertiary branches and spread over the tissue for a maximum of respiratory surface. Terminal cells have a very high plasticity and hence are able to adapt to higher oxygen demands by increasing respiratory surface. Beyond an oxygen supplying function, terminal cells previously have been reported to further interact with other tissues like the gut or brain<sup>150,151</sup>. These studies show that the terminal cells not only can react to nutritive signals but also affect the intestinal homeostasis.

The morphologic branching program of the invertebrate trachea shows high similarities to tube formation and growth in the vertebrate vascular system<sup>152</sup>. These similarities make the *Drosophila* trachea system a suitable model to study angiogenesis<sup>152</sup>. Tracheal outgrowth is realized by cell migration and cell elongation that is mediated by fibroblast growth factor (FGF) signaling. Recognized by the FGF receptor Breathless (Btl), cell

migration is directed by the ligand Branchless (Bnl)<sup>153,154</sup>. As tracheal cells were yet not identified to divide, structural remodeling of the trachea is solely achieved by cell growth and migration<sup>152</sup>.

During metamorphosis, the tracheal system changes both in structure and physiology. The simple structure of the larval trachea develops into a more branched and complex system (Fig. 5). In the head and thorax, the adult trachea are organized in air sacs that surround attached tissues like the brain and flight muscles. In the abdomen this bilateral structure spreads into a tubular system and branches out to all organs.



**Fig. 5 The respiratory system of *Drosophila melanogaster*.** Tracheal system of larvae and adult flies is shown in blue.

Tracheal epithelial cells possess a broad range of molecular signaling mechanisms, including Immune deficiency (Imd) regulated immune responses or other stress response signaling pathways such as Janus Kinase/Signal Transducers and Activators of Transcription (JAK/STAT) or Jun N-terminal Kinase (JNK) and antioxidant pathways like the Nuclear factor erythroid 2-related factor 2 (Nrf2) pathway<sup>155,156</sup>.

Hence, the respiratory cells of *Drosophila* are able to induce an appropriate response to airborne and toxic particles, in order to prevent from damage. Additionally, a proper innate immune response guarantees for protection from invading pathogens.

### 1.7 Immunity in *Drosophila melanogaster*

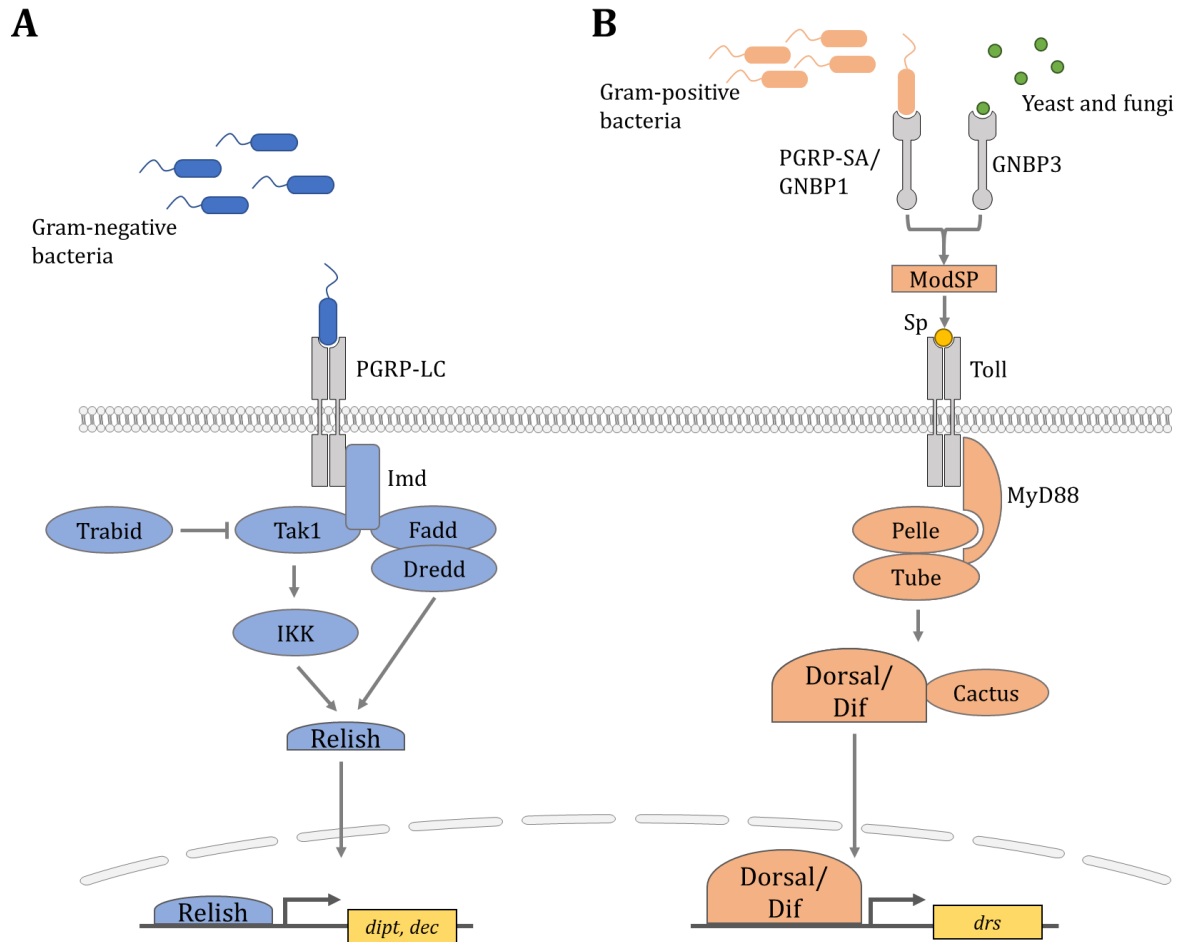
As an invertebrate organism, *Drosophila* solely relies on an innate immune system to protect from pathogen induced damage or to clear from apoptotic or aberrant cells. Being more than a physical epithelial barrier to protect from invading pathogens, the innate immune system possesses effective functions to ensure integrity of the host's tissues. To fulfil this task, the innate immune system consists of two distinct parts that operate

synergistically. Namely, the humoral and the cellular response complement each other in order to keep a homeostatic physiology.

The activation of innate immunity is driven by the microbial recognition via the immune deficiency pathway (Imd) and Toll pathway (Fig. 6). Both pathways are activated by different Pathogen Associated Molecular Patterns (PAMPs) and independently induce the activation of appropriate immune responses.

The cell membrane compartment peptidoglycan from gram-negative bacteria is recognized by the peptidoglycan recognition protein (PGRP)<sup>157</sup>. This receptor transduces the signal by recruiting a complex, consisting of Imd, TGF- $\beta$  activating kinase 1 (Tak1), FAS-associated death domain orthologue (Fadd) and Death related ced-3/Nedd2-like caspase (Dredd)<sup>158,159</sup>. The resulting cleavage of Imd subsequently activates Tak1, which in turn activates the I $\kappa$ B Kinase (IKK) complex<sup>160,161</sup>. Tak1 activation is regulated by Trabid<sup>162</sup>. When bound to Tak1, Trabid (orthologue of the mammalian A20) inhibits the activation of the IKK complex. In the absence of Trabid, the NF- $\kappa$ B transcription factor relish is phosphorylated by IKK or cleaved in an alternative way by Dredd, which allows for translocation to the nucleus and transcription of AMPs such as Diptericin (Dipt) or Cecropin(Cec) to protect from invading gram-negative bacteria<sup>161,163-165</sup>.

In contrast to the recognition of gram-negative bacteria by the Imd pathway, gram-positive bacteria and fungi are recognized by systems assigned to the Toll pathway<sup>166,167</sup>. The lysine type of gram-positive bacteria is recognized by PGRP-SA and the gram-negative binding protein 1 (GNBP1)<sup>168</sup>. Fungal components are recognized by GNBP3<sup>167</sup>. The association with microbial cell wall components to these molecules initiates the activation of the Toll receptor ligand Spätzle (Sp) via the induction of modular serine protease (modSP). When Sp binds the Toll receptor, it recruits the adaptor protein MyD88, which forms a complex with Tube and Pelle<sup>169-171</sup>. This complex transmits the signal to Cactus, that is bound to the NF- $\kappa$ B transcription factors Dorsal or Dif. Phosphorylation of cactus leads to dissociation with Dorsal/Dif and a subsequent nuclear translocation of the corresponding transcription factor<sup>172,173</sup>. The translocation of Dorsal and Dif to the nucleus leads to an activated transcription of AMPs like Drosomycin (Drs)<sup>174</sup>.



**Fig. 6 Microbial recognition in *Drosophila melanogaster*.** The immune deficiency (Imd) and Toll pathways recognize microbial compartments and induce an immune response. **A** The Imd signaling receptor peptidoglycan recognition protein (PGRP-LC) recognizes gram-negative bacteria and transduces the signaling into the cell where the NF- $\kappa$ B transcription factor Relish is activated and induces the transcription of AMP genes like *dipterucin* (*dipt*) and *cecropin* (*dec*). **B** Gram-positive bacteria and fungi are recognized by PGRP-SA, gram-negative binding protein 1 (GNBP1) and GNBP3. Modular serine protease (modSP) cleaves Spätzle (Sp), which binds the toll receptor. The signal is transduced to the cell and activates the NF- $\kappa$ B transcription factors Dorsal and Dif, which induce the transcription of AMP genes like *drosomycin* (*drs*). TGF- $\beta$  activating kinase 1 (Tak1), FAS-associated death domain orthologue (Fadd), death related ced-3/Nedd2-like caspase (Dredd), I $\kappa$ B Kinase (IKK).

Besides the induction of AMPs in response to microbial confrontation, the humoral part of the innate immune system additionally involves the release of ROS<sup>175</sup>. ROS are generated by the two conserved NADPH dependent enzymes dual oxidase (Duox) and NADPH oxidase (Nox)<sup>176,177</sup>. Duox induces the release of hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) and hypochlorous acid. Nox activity results in a release of H<sub>2</sub>O<sub>2</sub>. Especially at epithelial barriers like the gut an appropriate ROS balance is not only important for protection from pathogens but also to maintain the commensal bacteria for a healthy microbiota<sup>178</sup>.

Next to a humoral immune response, the innate immune system of *Drosophila* is capable of launching cellular defense mechanisms. These mechanisms are mediated by specialized

immune cells that circulate through the hemolymph and therefore are referred to as hemocytes. The fruit fly possesses three kinds of hemocytes that are responsible for different functions in innate immunity<sup>179</sup>. Plasmatocytes are the most abundant hemocytes in *Drosophila* and share many similarities to mammalian macrophages<sup>180,181</sup>. These cells not only phagocytose microbes and apoptotic particles but further are also involved in humoral immune responses by secreting AMPs and clotting factors<sup>182-186</sup>. Crystal cells are responsible for melanization reactions by releasing the enzyme prophenol oxidase in order to catalyze the production of melanin<sup>187</sup>. Lamellocytes are specialized encapsulation cells that contain parasitic damage from invading wasp infections by arresting them and marking them for melanization<sup>188,189</sup>.

These two parts of innate immunity do not act independently from each other but rather communicate and crosstalk<sup>190</sup>. It has been demonstrated, that activated Toll and JAK/STAT signaling in the fat body cells and muscle cells led to the induction of cellular immune responses in *Drosophila*<sup>191,192</sup>. This kind of communication between both parts of the immune system is mediated by cytokines. There have been several cytokines identified in *Drosophila* yet, that are linked to immune regulation<sup>179</sup>. The JAK/STAT ligands Unpaired 2, 3 (Upd, Upd2/3) are related in inducing a cellular immune response upon injury or infection<sup>193,194</sup>. The Toll ligand Sp transduces PAMPs in order to drive the expression of AMPs, additionally has been linked to cellular immunity and is secreted by activated hemocytes<sup>173,195</sup>. Moreover, the TNF homologue Eiger (Egr) is involved in cellular immunity upon pathogenic confrontation or by mediating the melanization reaction of crystal cells<sup>196,197</sup>.

### **1.8 *Drosophila* as a model to study COPD**

The majority of human lung diseases such as COPD, lung cancer or asthma involve the immune system of the host. Both the innate and the adaptive immune system interact with each other and are responsible for the development of these diseases<sup>198-200</sup>. Even though, *Drosophila* lacks a mammalian lung, it displays an effective model organism to study human lung diseases. However, with the tracheal system it possesses a proper oxygen supplying tissue, that is made from epithelial cells. As mentioned before (chapter 1.6), these cells are capable of launching a diversity of defense mechanisms in order to protect from cellular damage that share homologies in human disease related genes.

It is obvious that *Drosophila* does not possess an adaptive immune system. However, this aspect is not necessarily a limiting factor for studying human lung diseases in the fruit fly. As a very complex disease, that is uniquely different from patient to patient, COPD involves various players and factors (chapter 1.1). This complexity hampers the research on basal understandings of the underlying factors that drive this disease. The fact that *Drosophila* lacks an adaptive immune system allows for the focused examination on innate immunity of airway epithelial responses upon exogenous stress factors like cigarette smoke. To exclusively consider the responses of the innate immune system in cigarette smoking, so far is not possible in any other model organism. The innate immune system of *Drosophila* is evolutionary highly conserved and shows striking similarities to the human innate immune system<sup>201</sup>. These aspects allow for identification of triggers for cigarette smoke responses. Hence, findings in this rather simple system can later be transferred to the more complex mammalian system in order to understand the crosstalk between both parts of the immune system.

COPD is a chronic disease that is tightly connected to age and usually manifests in late stages of life<sup>16</sup>. The examination of cigarette smoke induced murine models therefore consumes a lot of time and effort for phenotypic changes to arise. With a short lifecycle, *Drosophila* offers a very satisfying base to study long term and chronic effects of cigarette smoke exposure. The most meaningful phenotype of cigarette smoke exposure, namely lifespan, can be assessed satisfactorily in the fruit fly. Unlike murine systems, the fruit fly model is more flexible according to lifespan analyses as well as for sufficient screening of intervention effects. Combined with the convenient experimental approaches, the interference with specific targets or even whole pathways is conceivably useful to study their effects during cigarette smoke exposure.

## **1.9 Aim of the thesis**

COPD is the third leading cause of death worldwide, that is mainly caused by cigarette smoking and with aging populations it is thought to increase in incidences. Due to lacking knowledge about underlying molecular mechanisms, there are still no therapeutic approaches available to stop the progression of the disease or to even to fully cure it. The aim of this thesis is to establish a novel *Drosophila* model for studying the effects of cigarette smoke on the airway epithelium. By utilizing aforementioned advantages that *Drosophila* offers, molecular players mediating the response to cigarette smoke exposure



should conveniently be identified. Acquired knowledge about these mediators should then be translated to a functional role for interventional studies during cigarette smoke exposure. Therefore, the short lifecycle of flies should be exploited in order to screen for effects of certain interventions for the lifespan during exposure to cigarette smoke. These analyses will pinpoint key mediators to further lead to better understanding of cigarette smoke induced effects on the airway epithelium.

Incomplete knowledge about the tracheal system of the fruit fly hampers research on the airway epithelium. In order to resolve characteristics of the respiratory system in *Drosophila*, both, larval and adult tracheal cells should be investigated and compared by transcriptomic analyses. Obtained results should be useful for future research on development of the tracheal system and might give further explanation for alterations of the airway epithelium in response to stimuli like cigarette smoke.

## 2 Material & Methods

### 2.1 Material

Consumables and plastic labware were acquired either from Nerbe Plus (Winsen an der Luhe, Germany) or Sarstedt AG & Co. KG (Nümbrecht, Germany). Fly vials and plugs were acquired from Nerbe Plus and from VWR International (Radnor, PA, USA).

#### 2.1.1 Fly Lines

Following list shows all fly lines that were either directly used for experimental approaches or used for crossings (Tab. 1).

**Tab. 1** Used fly lines.

Name	Genotype	Source
w <sup>1118</sup>	w[1118]	BDSC #5905
yw	y[1] w[1118]	BDSC #6598
UAS-Keap1-RNAi	P{VSH330323}attP40	VDRC #330323
GstD1-GFP	;GstD1-GAL4, UAS-GFP;	Dirk Bohmann, Rochester, NY, USA
ARE-GFP	;P{y[+t7.7]w[+mC]=ARE-EGFP}attP16	Dirk Bohmann, Rochester, NY, USA
Nplp4-GFP	PBac{fTRG00897.sfGFP-TVPTBF}VK00033	VDRC #v318254
Btl-GAL4	y[1] w[1118], hsflp;+/CyO;btl-GAL4,UAS-GFP/btl-GAL4,UAS-GFP	Benedikt Best, Heidelberg, Germany
STAT92E-GFP	w[1118]; P{w[+mC]=10XStat92E-GFP	Erika A. Bach, New York City, NY, USA
Ppk4-GAL4	y[1] w[1118];ppk4-gal4	Mike Welsh, IA, USA
Prx2540-2 GAL4	;y[1] w[67c23]; Prx2540-GAL4	BestGene Inc., Chino Hills, CA, USA
Btl-GAL4, UAS-GFP; GAL80ts	w[1118]; Btl-GAL4, UAS-GFP/CyO; Gal80/TM6B	Thomas Roeder, Kiel, Germany

UAS-Trxr2	y[1] w[1118];UAS-Trxr2	Andrew Pickering, San Antonio, TX, USA
UAS-Gpx	; ; UAS-Gpx	
UAS-Prx	; y[1] w[67c23], UAS-prxr2540-1	BestGene Inc., Chino Hills, CA, USA
UAS-GstD5	; y[1] w[67c23], UAS-GstD5	BestGene Inc., Chino Hills, CA, USA
AMP KO	; iso w[1118], Def <sup>Sk3</sup> , AttC <sup>Mi</sup> , ΔDro, ΔAttA, ΔAttB, Mtk <sup>R1</sup> , ΔDptA, ΔDptB; Drs <sup>R1</sup> , AttD <sup>SK1</sup>	Mark Hanson, Lausanne, Switzerland
AMP KO Ctrl	iso w[1118]	Mark Hanson, Lausanne, Switzerland
FoxO KO	y[1]w[1118];+ / +;dfoxo24/dfoxo24	Marc Tatar, Providence, RI, USA
UAS-GFP	y1 w*; wgSp-1/CyO, P{Wee-P.ph0}BaccWee-P20; P{20XUAS-6XGFP}attP2	BDSC #52262
Timeless reporter	yw;;Clock <sup>TIM</sup>	Norbert Perrimon, Harvard, MA, USA

### 2.1.2 Crossings

Tab. 2 shows the nomenclature for used crossings and the corresponding lines that were crossed with each other.

**Tab. 2 Used crossings.**

Name	Crossing
Prx2540 Reporter	Prx2540-GAL4 > UAS-GFP
Trachea Reporter	Btl-GAL4 > UAS-GFP
Keap1-RNAi	Btl-GAL4,UAS-GFP, Gal80ts > UAS-Keap1-RNAi
Keap1-RNAi control	yw > UAS-Keap1-RNAi
Gpx OE	Btl-GAL4 > UAS-Gpx
Gpx OE control	yw > UAS-Gpx

Prx2540 OE	Btl-GAL4 > UAS-Prx2540
Prx2540 control	yw > UAS-Prx250
GstD5 OE	Btl-GAL4 > UAS-GstD5
GstD5 control	yw > UAS-GstD5
Trxr2 OE	Btl-GAL4 > UAS-Trxr2
Trxr2 Ctrl	yw > UAS-Trxr2

### 2.1.3 Kits and Reagents

Kits and reagents that were used for experimental approaches are shown in Tab. 3.

**Tab. 3 Kits and reagents.**

<b>Kit / Reagent</b>	<b>Source of supply</b>
Ambion Purelink RNA Mini Kit	ThermoFisher Scientific, Waltham, MA, USA
SureClean Plus	Biocat, Heidelberg, Germany
Nextera DNA Flex Library Prep Kit	Illumina, San Diego, CA, USA
RNA Magic	Bio Budget, Krefeld, Germany
Qubit dsDNA HS Assay Kit	ThermoFisher Scientific, Waltham, MA, USA
NucleoBond Xtra Maxi Kit	Macherey-Nagel, Düren, Germany
qPCRBIO SyGreen	PCR Biosystems, London, UK
MasterPure DNA purification Kit	Epicentre, Madison, WI, USA
DNeasy Blood & Tissue Kit	Qiagen, Hilden, Germany
Infinity triglyceride solution	ThermoFisher Scientific, Waltham, MA, USA
Rotimount	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Advantage 10x cDNA PCR buffer	Takara Bio Europe, St-Germain-en-Laye, France

### 2.1.4 Chemicals and minerals

Tab. 4 shows all used chemicals and minerals with the according source of supply.

**Tab. 4 Chemicals and minerals.**

<b>Chemical</b>	<b>Source of supply</b>
L-Buthionine-(S,R)-Sulfoximine	Cayman Chemicals, Ann Arbor, MI, USA
Oltipraz	Cayman Chemicals, Ann Arbor, MI, USA
Reduced L-Glutathione	Carl Roth GmbH + Co KG, Karlsruhe, Germany
2-vinylpyridine	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Triethanolamine	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Chloroform	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Isopropanol	Carl Roth GmbH + Co KG, Karlsruhe, Germany
DTT	ThermoFisher Scientific, Waltham, MA, USA
MnCl <sub>2</sub>	ThermoFisher Scientific, Waltham, MA, USA
BSA	Carl Roth GmbH + Co KG, Karlsruhe, Germany
dNTPs	ThermoFisher Scientific, Waltham, MA, USA
MgCl <sub>2</sub>	ThermoFisher Scientific, Waltham, MA, USA
NGS	Sigma-Aldrich, St. Louis, MI, USA
Tween-20	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Triton-X-100	Carl Roth GmbH + Co KG, Karlsruhe, Germany

Paraformaldehyd powder EM grade	Polysciences Inc., Hirschberg and der Bergstraße, Germany
Trioleate standard	Sigma-Aldrich, St. Louis, MI, USA
Soda lime	Carl Roth GmbH + Co KG, Karlsruhe, Germany
DTNB	Carl Roth GmbH + Co KG, Karlsruhe, Germany
NADPH	Sigma-Aldrich, St. Louis, MI, USA
Agarose	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Glycerol	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Ethanol	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Molasses	Biohof Heidelicht, Gerdau, Germany
Sugar bead syrup	Kanne Brottrunk GmbH, Selm-Bork, Germany
Cornmeal	Davert GmbH, Ascheberg, Germany
Brewer's yeast	Leiber GmbH, Bramsche, Germany
D-Glucose monohydrate	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Agar-Agar	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Sucrose	Carl Roth GmbH + Co KG, Karlsruhe, Germany
EDTA sodium salt	Carl Roth GmbH + Co KG, Karlsruhe, Germany
5-Sulfosalicylic acid dihydrate	Carl Roth GmbH + Co KG, Karlsruhe, Germany
Na <sub>2</sub> HPO <sub>4</sub>	Carl Roth GmbH + Co KG, Karlsruhe, Germany
KCl	Merck

NaCl	Carl Roth GmbH + Co KG, Karlsruhe, Germany
KH <sub>2</sub> PO <sub>4</sub>	Carl Roth GmbH + Co KG, Karlsruhe, Germany
K <sub>2</sub> HPO <sub>4</sub>	Applichem

### 2.1.5 Enzymes

Following list shows all used enzymes with the corresponding source of supply (Tab. 5).

**Tab. 5 Enzymes.**

<b>Enzyme</b>	<b>Source of supply</b>
Superscript IV reverse transcriptase	ThermoFisher Scientific, Waltham, MA, USA
RiboLock RNase inhibitor	ThermoFisher Scientific, Waltham, MA, USA
T4 DNA Ligase	ThermoFisher Scientific, Waltham, MA, USA
LA Taq polymerase	Takara Bio Europe, St-Germain-en-Laye, France
DreamTaq polymerase	ThermoFisher Scientific, Waltham, MA, USA
Gateway BP Clonase Enzyme Mix	ThermoFisher Scientific, Waltham, MA, USA
Gateway LR Clonase Enzyme Mix	ThermoFisher Scientific, Waltham, MA, USA
FastDigest restriction enzymes NotI, EcoRI	ThermoFisher Scientific, Waltham, MA, USA
Glutathione Reductase from baker's yeast	Merck, Darmstadt, Germany
RNase A	ThermoFisher Scientific, Waltham, MA, USA

### 2.1.6 Primers and oligonucleotides

Following primers and oligonucleotides were used for standard PCR, qPCR, cDNA synthesis and amplification of RNA experiments (Tab. 6).

**Tab. 6 Primers and oligonucleotides.**

<b>Primer</b>	<b>Sequence</b>
<i>gstd5</i>	F: GACCTCAACAAGTACCCGAATG R: CCTGACGGGCATCAAATACTC
<i>gstd5</i> CDS (including Kozak sequence and restriction sites)	F:GAGAGAATTCCAAAATGGATTTCTATTACTCGCCCCG R: GAGAGCGGCCGAGGCGGCCGGAAGCAATAA
<i>Het-A</i>	F: ACAGATGCCAAGGTTTCAGG R: GCCAGCGCATTTTCATGC
<i>prx2540</i> promoter region	F: GGGACAAGTTTGTACAAAAAAG CAGGCTCGCTTCATTTGCGACAGACC R: GGGGACCACTTTGTACAAGAAAGCTGG GTCTTGCTGTTTGTATTTTGTAGTTTCACTTGG
<i>prx2540</i> CDS (including Kozak sequence and restriction sites)	F: GAGAGAATTCCAAAATGCGTTTGGGACAGACCGT R: GAGAGCGGCCGCTCAGTAGTTGTCAGTGGTGC
<i>gclc</i>	F: CGCTTTATCCAGAAGCGTGC R: GATGCGCTTCAGCAAATCGT
<i>V2</i>	F: AGAGTTTGATCCTGGCTCAG R: TGCTGCCTCCCGTAGGAGT
<i>rpl32</i>	F: CCGCTTCAAGGGACAGTATC R: GACAATCTCCTTGCGCTTCT
oligo dT	GAGAGAGGATCCAAGTACTAATACGACTCACTA TAGGGAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
cap finder primer with amplification tag	AAGCAGTGGTATCAACGCAGAGTACATrGrG+G
oligo dT with amplification tag	AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTVN
Primer for cDNA amplification	AAGCAGTGGTATCAACGCAGAGT



### 2.1.7 Fly Media

All fly media and according recipes that were used in this study either for fly husbandry or experiments are listed in Tab. 7 - Tab. 9.

**Tab. 7 Recipe for standard fly medium.**

<b>Component</b>	<b>Amount</b>
Corn meal	31.25 g
Brewer's yeast	31.25 g
D-Glucose monohydrate	10 g
Agar-Agar	5 g
Mollasses	15 g
Sugar bead syrup	15 g
Added 500 ml dH <sub>2</sub> O	
Cooked for 15 min in a beaker and autoclaved	
Cooled down to 60 °C	
Propionic acid (10 % in dH <sub>2</sub> O)	5 ml
Nipagin (10 % in 70 % EtOH)	15 ml

**Tab. 8 Recipe for concentrated fly medium.**

<b>Component</b>	<b>Amount</b>
Yeast extract	25 g
Corn meal	43 g
Sucrose	25 g
Agar-Agar	2.5 g
<i>Ad</i> 500 ml dH <sub>2</sub> O	
Cooked for 15 min in a beaker and autoclaved	
Cooled down to 60 °C	
Propionic acid (10 % in dH <sub>2</sub> O)	5 ml
Nipagin (10 % in 70 % EtOH)	15 ml

The recurrent diet was based on the concentrated medium. Dietary restriction phases were implemented by reducing the yeast extract to 1.25 g (0.25 %).

Tab. 9 Recipe for the control holidic diet (PC 1:2)

Component/Stock	Stock ingredients	Amount/L
L-isoleucin	-	3.64 g
L-leucin	-	2.42 g
L-tyrosine	-	0.84 g
Glucose	-	75 g
Agar-Agar	-	20 g
CaCl <sub>2</sub>	250 g/l	1 ml
CuSO <sub>4</sub>	2.5 g/l	1 ml
FeSO <sub>4</sub>	25 g/l	1 ml
MgSO <sub>4</sub>	250 g/l	1 ml
MnCl <sub>2</sub>	1 g/l	1 ml
ZnSO <sub>4</sub>	25 g/l	1 ml
Buffer	10x: 30 m/l glacial acetic acid 30 g/l KH <sub>2</sub> PO <sub>4</sub> 10 g/l NaHCO <sub>3</sub>	100 ml
Autoclaved and subsequent components were added after media cooled down to 60 °C:		
Cholesterol stock	20 mg cholesterol in 100 % ethanol	15 ml
Essential amino acid stock	8 g/l L-arginine 10 g/l L-histidine 19 g/l L-lysine (HCl) 8 g/l L-methionine 13 g/l L-phenylalanine 20 g/l L-threonine 5 g/l L-tryptophan 28 g/l L-valin	121,02 ml
Non-essential amino acid stock	35 g/l L-alanine 17 g/l L-asparagine 17 g/l L-aspartic acid 1 g/l L-cysteine HCl 25 g/l L-glutamine	121,02 ml

	32 g/l glycine	
	15 g/ L-prolin	
	19 g/l L-serine	
Sodium glutamate stock	100 g/l	30,26 ml
Vitamine stock	0.1 g/l thiamine (aneurin)	10 ml
	0.05 g/l riboflavin	
	0.6 g/l nicotinic acid	
	0.775 g/l Ca pantothenate	
	0.125 g/l pyridoxine (HCl)	
	0.01 g/l biotin	
Sodium folate stock	0.5 g/l	10 ml
Other nutrients stock	6.25 g/l choline chloride	24 ml
	0.63 g/l myo-inositol	
	8.13 g/l inosine	
	7.5 g/l uridine	
10 % Propionic acid	-	6 ml
Nipagin	-	15 ml

To prepare dietary restriction (PC 1:16) and protein energy malnutrition (PC 1:50) holidic media, all amino acids (or according stocks) were diluted 1:16 and 1:50 respectively. The missing volume was then refilled with ddH<sub>2</sub>O in order to not change the concentration of components.

### 2.1.7.1 Ingredients for holidic diet

All ingredients for the holidic diets are listed in Tab. 10.

**Tab. 10** Ingredients for holidic diet.

Ingredient	Company
Cholesterol	Sigma-Aldrich, St. Louis, MI, USA (C8667)
Ergosterol	Sigma-Aldrich, St. Louis, MI, USA (45480)
KH <sub>2</sub> PO <sub>4</sub>	Carl Roth GmbH + Co KG, Karlsruhe, Germany (P018.2)
NaHCO <sub>3</sub>	Sigma-Aldrich, St. Louis, MI, USA (S5761)

Glacial acid	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3738.2)
Agar-agar	Carl Roth GmbH + Co KG, Karlsruhe, Germany (5210.2)
L-alanine	Sigma-Aldrich, St. Louis, MI, USA (A7627)
L-aspartic acid	Sigma-Aldrich, St. Louis, MI, USA (A6683)
L-asparagin	Sigma-Aldrich, St. Louis, MI, USA (A0884)
Glycin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (0079.1)
L-prolin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (T205.2)
L-glutamin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3772.2)
L-serin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (1714.2)
L-cystein HCl	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3468.2)
L-arginine monohydrochloride	Sigma-Aldrich, St. Louis, MI, USA (A5131)
L-threonin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (T206.2)
L-methionine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (9359.1)
L-tryptophan	Carl Roth GmbH + Co KG, Karlsruhe, Germany (4858.2)
L-phenylalanine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (4491.1)
L-histidine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3852.3)
L-lysin HCl	Carl Roth GmbH + Co KG, Karlsruhe, Germany (9357.1)
L-valin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (4879.4)

L-isoleucine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3922.2)
L-leucine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3984.3)
L-tyrosine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (T207.2)
Cholin chloride	Sigma-Aldrich, St. Louis, MI, USA (C1879)
Myo-inositol	Sigma-Aldrich, St. Louis, MI, USA (I7508)
Inosine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (6770.1)
Uridine	Carl Roth GmbH + Co KG, Karlsruhe, Germany (0714.3)
Folic acid	Carl Roth GmbH + Co KG, Karlsruhe, Germany (T912.1)
Riboflavin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (9607.1)
D(+)-biotin	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3822.1)
Nicotinic acid	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3815.2)
Calcium-D(+)-pantothenat	Carl Roth GmbH + Co KG, Karlsruhe, Germany (3812.2)
Thiamine	Sigma-Aldrich, St. Louis, MI, USA (T4625)
Pyridoxine HCl	Carl Roth GmbH + Co KG, Karlsruhe, Germany (T914.1)
L-glutamic acid monosodium salt hydrate	Sigma-Aldrich, St. Louis, MI, USA (G5889)
Copper(II) sulfate pentahydrate	Sigma-Aldrich, St. Louis, MI, USA (C7631)
Zinc sulfate heptahydrate	Sigma-Aldrich, St. Louis, MI, USA (Z0251)
Iron(II) sulfate heptahydrate	Sigma-Aldrich, St. Louis, MI, USA (F7002)
Manganese(II) chlorid tetrahydrate	Sigma-Aldrich, St. Louis, MI, USA (M3634)
CaCl • 6H <sub>2</sub> O	Carl Roth GmbH + Co KG, Karlsruhe, Germany (5239.2)

MgSO <sub>4</sub>	Carl Roth GmbH + Co KG, Karlsruhe, Germany (P027.2)
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### 2.1.8 Vectors

Following table lists all used vectors for cloning experiments (Tab. 11).

**Tab. 11 Vectors.**

Vectors	Source
pBPGAL4.2::VP16Uw	Addgene, Teddington, UK
pBID-UASC	Addgene, Teddington, UK
pDONR221	Addgene, Teddington, UK

### 2.1.9 Solutions and Buffers

All used buffers and according recipes are listed in Tab. 12.

**Tab. 12 Solutions and buffers with according ingredients.**

Solution/Buffer	Ingredients
10 x Phosphate buffered saline (PBS)	1.37 M NaCl 0.027 M KCl 0.018 M KH <sub>2</sub> PO <sub>4</sub> 0.1 M Na <sub>2</sub> HPO <sub>4</sub> pH 7.4
PBST	0.3 % Triton-X-100 in 1 x PBS (v/v)
PFA fixation solution	4 % PFA in 1 x PBS (w/v)
Blocking buffer	5 % normal goat serum (NGS) in PBST
Potassium phosphate buffer with EDTA (KPE)	16 ml of solution A (6.8 g KH <sub>2</sub> PO <sub>4</sub> <i>ad</i> 500 µl H <sub>2</sub> O), 84 ml of solution B (8.5 g K <sub>2</sub> HPO <sub>4</sub> <i>ad</i> 500 ml H <sub>2</sub> O), pH 7.5, 0.327 g EDTA sodium salt
GSH extraction buffer	20 µl Triton-X-100 and 120 mg sulfosalicylic acid to 20 ml KPE, pH 7.5

### 2.1.10 Antibodies and probes

Primary and secondary antibodies as well as probes used for immunohistochemistry experiments are listed in Tab. 13.

**Tab. 13 Antibodies and probes.**

<b>Antibody</b>	<b>Dilution</b>	<b>Source of supply</b>
$\alpha$ -GFP from mouse	1:250	Developmental Studies Hybridoma Bank, University of Iowa, Iowa city,
$\alpha$ -mouse IGG AF488 conjugated	1:300	Jackson ImmunoResearch, West Grove, PA, USA
GFP booster AF488 conjugated	1:200	Chromotek, Planegg-Martinsried, Germany

### 2.1.11 Devices and equipment

All devices and equipment used in this study are listed in Tab. 14.

**Tab. 14 Devices and equipment.**

<b>Device/equipment</b>	<b>Source of supply</b>
Vacuum Pump ME 1C	Vacuubrand, Wertheim, Germany
LAM25 System	TriKinetics, Waltham, MA, USA
Bead mill homogenizer, Bead Ruptor	Omni International, Kennesaw, GA, USA
Labcycler	Sensoquest, Göttingen, Germany
StepOne Real Time PCR System	ThermoFisher Scientific, Waltham, MA, USA
DeNovix DS-11 Spectrometer	Biolabproducts, Bebensee, Germany
Qubit 3	ThermoFisher Scientific, Waltham, MA, USA
Microplate Reader Synergy H1	BioTek Instruments GmbH, Bad Friedrichshall, Germany
Vibratome	Leica Biosystems, Nußloch, Germany
Axiolmager Z1	Carl Zeiss AG, Oberkochen, Germany
Apotome	Carl Zeiss AG, Oberkochen, Germany

Axiocam MRm camera	Carl Zeiss AG, Oberkochen, Germany
Forceps Dumont Nr. 9	Biolabproducts GmbH, Bebensee
Thermomixer comfort	Eppendorf, Hamburg, Germany
Cooling centrifuge Heraeus Fresco 17	ThermoFisher Scientific, Waltham, MA, USA
Benchtop centrifuge 5424	Eppendorf, Hamburg, Germany
Vortex Genie 2	Scientific Industries, Bohemia, NY, USA
Cleanbench Labguard ES ClassII	Nuaire, Plymouth, MN, USA
Mediaclave 9	INTEGRA Biosciences AG, Zizers, Switzerland
HiSeq4000/HiSeq2500	Illumina, San Diego, CA, USA
MiSeq	Illumina, San Diego, CA, USA
Zirconia beads	Biolabproducts, Bebensee, Germany

### 2.1.12 Software

Following table lists all software that were used for data analysis in this work (Tab. 15).

**Tab. 15 Software**

<b>Software</b>	<b>Source of supply</b>
StepOne	ThermoFisher Scientific, Waltham, MA, USA
Prism 7	Graphpad, San Diego, CA, USA
DAM FileScan ImageJ	Trikinetics Inc., Waltham, NIH, Bethesda, MD, USA
CLC Genomic workbench including Microbial Genomics Module	Qiagen, Hilden, Germany
Axiovision SE64 rel.4.9	Zeiss, Oberkochen, Germany
Zen black	Zeiss, Oberkochen, Germany
R Studio	
DESeq2	Bioconductor R package
TopHat	CCB, John Hopkins University, Baltimore, MD, USA
HTSeq	Anders <i>et al.</i> <sup>202</sup>



## **2.2 Methods**

### **2.2.1 Fly husbandry**

If not mentioned differently, fly stocks were raised and cultured on standard medium at 25 °C with 50 – 60 % relative humidity in a 12:12 h day and night rhythm.

### **2.2.2 Smoke exposure experiments**

Cigarette smoking exposures were performed in a smoking chamber attached to a diaphragm pump. Common research 3R4F cigarettes (CTRP, Kentucky University) were used for all experiments. For all larvae experiments, young 3<sup>rd</sup> instar larvae were exposed to cigarette smoke three times a day for 30 min each, on two consecutive days. Subsequent experiments were performed 30 min after the last smoking exposure step. For adult smoke exposure experiments, 5-7 d old, age-matched, female flies were transferred to empty vials to prevent them from sticking to the media. Smoking exposures for adults were applied once a day for 30 min each on 5 d a week. Subsequent experiments were performed 2 h after the last smoke exposure step. Vials containing larvae or adult flies were capped with a monitoring grid to allow the cigarette smoke to diffuse into the vial.

### **2.2.3 Lifespan experiments**

For lifespan analyses 5-7 days old, age-matched and mated female flies were exposed to cigarette smoke as previously described (chapter 2.2.2) and compared to non-smoke exposed flies. For each replicate 10 flies were put in one vial. Every other day the surviving flies were counted and transferred to fresh media vials. Lifespan analyses with oltipraz treatment were carried out by supplying normal medium with a final concentration of 400 µM oltipraz. For lifespan experiments with BSO treatment, 100 µl of 100 mM BSO were dribbled on 25 ml standard medium and it was air dried before transferring flies to it. GSH supplementation was carried out by adding 10 mM reduced GSH to standard media.

### **2.2.4 Locomotor Activity**

To monitor the locomotor activity of smoke exposed, age-matched and mated female flies a Locomotor Activity Monitoring (LAM) system <sup>203</sup> was used. One fly each was put into vials containing media made of 1.5 % Agarose and 5 % sucrose. The LAM system was

placed upright and the activity was monitored for 2 d in a climate chamber set to a 25/20 °C and 12:12 h day and night rhythm. Activity counts were binned to 30 min for analysis using the DAM File Scan software.

### **2.2.5 DNA extraction**

The extraction of genomic DNA was performed by using the epicenter MasterPure DNA Purification Kit. Therefore, whole animals were homogenized in 300 µl Cell lysis solution supplied with 1 µl Proteinase K using a bead mill homogenizer. To lyse cells, homogenates were incubated at 54 °C for 15 min and mixed every 5 min. Subsequently, homogenates were cooled to 37 °C and 1 µl of RNase A (5 µg/µl) was added to the sample. The mixture was incubated at 37 °C for 30 min and placed on ice for 5 min. To precipitate DNA, 175 µl of Protein Precipitation Reagent was added to the lysed samples and vortexed for 10 s. Cell debris were removed by centrifugation for 10 min at 14.000 x g and 4 °C. The supernatant was transferred to a new tube, supplied with 500 µl isopropanol and inverted 30 times. DNA was pelleted by centrifugation for 10 min at 14.000 x g and 4 °C. Supernatant was removed carefully and the remaining DNA pellet was washed twice with 70 % ethanol. Excessive ethanol was aspirated carefully and the pellet was resuspended in 35 µl TE Buffer.

For metagenomic analyses of the gut, 16S rDNA was extracted using the Qiagen DNeasy Blood & Tissue Kit. In short, intestines were homogenized in 180 µl ATL buffer and 20 µl proteinase K in a bead mill homogenizer. Subsequently 200 µl AL buffer were added and incubated at 56 °C for 10 min. 200 µl 100 % ethanol was added and vortexed. The mixture was transferred to a DNeasy Mini spin column and centrifuged at 6000 x g for 1 min. The flow through was discarded and 500 µl AW1 buffer were added to the spin column and centrifuged at 6000 x g for 1 min. The flow through was discarded and 500 µl AW2 buffer were added to the spin column. Then the DNA was eluted by adding 200 µl AE buffer directly on to the center of the column, incubated for 1 min and centrifuged at 6000 x g for 1 min.

### **2.2.6 16S rDNA analysis**

Bacterial variable regions 1 and 2 of 16S DNA genes were amplified according to Rausch *et al*, 2019<sup>204</sup>. Amplicons were sequenced using Illumina MiSeq with 2x 300 bp paired-end reads. The analysis of 16S metagenomic sequencing data was performed by using the

Qiagen CLC Genomics Workbench 12 Microbial Genomic module. Prior to analysis, Illumina sequencing adapters were trimmed from paired end reads. OTU clustering was done based on the SILVA 16S v132 97 % database with a similarity score of 80 % and best match finding option, using following settings: minimum occurrences: 2, chimera cross over costs 3, Kmer size 6, Mismatch costs 1, Minimum score 40, Gap costs 4, maximum unaligned end mismatches 5. Differential abundance of OTUs was calculated by comparing intestines from 10 d CS exposed *w*<sup>1118</sup> female flies to untreated control *w*<sup>1118</sup> female flies.

### **2.2.7 RNA Extraction**

For RNA extraction, tissues were dissected in cold PBS and transferred to RNA Magic. The tissue was homogenized in a bead mill homogenizer and 200 µl chloroform per ml RNA Magic were added. Samples were inverted 20 times and incubated for 10 min on ice. After centrifugation for 15 min at 12.000 x g and 4 °C the upper aqueous phase was transferred to a new tube and an equal volume of 70 % ethanol was added. The sample was inverted and loaded onto an Ambion PureLink RNA Mini Kit column and further extraction was done by following the manufacturer's protocol.

To extract RNA from adult trachea samples, 60 µl of chloroform were added to 300 µl RNA Magic and vortexed for 10 s. After an incubation time of 7 min on ice the samples were centrifuged for 5 min at 12.000 x g and 4 °C. The aqueous phase was transferred to a new tube and an equal volume of ice-cold isopropanol was added. Samples were incubated for 15 min at 4 °C and centrifuged at 14.000 x g and 4 °C for 10 min. The supernatant was removed by aspiration and the pellet was washed twice with 70 % ethanol with a following centrifugation step for 10 min at 14.000 x g and 4 °C. The supernatant was aspirated and the pellet was air dried and dissolved in 10 µl RNase free water.

### **2.2.8 cDNA synthesis**

Prior to cDNA synthesis, the oligo dT primer was initially bound to RNA. Therefore, the following reaction mix was set up:

0.5 µl oligo dT primer (10 pM)

0.5 µl dNTPs (10 mM)

X µl RNA

*ad* 6.5 µl RNase free water

This mix was then incubated at 65 °C for 5 min and for 1 min on ice. The actual synthesis was performed by adding following reagents to the mix:

2 µl 5 x Superscript IV buffer

0.5 µl DTT (0.1 M)

0.5 µl RiboLock RNase Inhibitor (10 U)

0.5 µl Superscript IV reverse transcriptase (100 U)

The final reaction mix was then incubated for 5 min at 25 °C, 20 min at 55 °C and was stopped at 80 °C for 10 min.

### 2.2.9 Standard PCR

For the standard amplification of DNA fragments, a PCR reaction mix was set up in the following way:

0.5 µl forward Primer (10 µM)

0.5 µl reverse Primer (10 µM)

0.5 µl dNTPs (10 mM)

2.5 µl Advantage 10x cDNA PCR buffer

50 ng DNA (or picked colony)

1 µl DreamTaq polymerase

*ad* 25 µl H<sub>2</sub>O

Cycling conditions, such as annealing and elongation times were adjusted individually to the needs of specific primers and fragments based on conditions from Tab. 16.

**Tab. 16 Standard cycling conditions for PCR.**

95 °C	1:00	
95 °C	0:30	30 cycles
55 °C	0:45	
72 °C	1:00	
72 °C	5:00	

### 2.2.10 Amplification of RNA from adult trachea

Due to low amounts of RNA from dissected adult trachea, samples had to be amplified prior to subsequent transcriptomic analyses. The RNA was transcribed to cDNA by using an oligo dt primer and a cap finder primer that binds the 5' cap of the RNA. Both primers carried a tag, allowing the amplification primer to bind this tag in the subsequent amplification.

5  $\mu$ l RNA

0.5  $\mu$ l oligo dt primer (10  $\mu$ M)

0.5  $\mu$ l cap finder primer (100  $\mu$ M)

4  $\mu$ l 5x Superscript IV buffer

2  $\mu$ l DTT

4  $\mu$ l dNTPs (10 mM)

1  $\mu$ l MnCl<sub>2</sub>

1  $\mu$ l BSA (0.1 %)

0.25  $\mu$ l RiboLock RNase inhibitor

1  $\mu$ l Superscript reverse transcriptase

0.75  $\mu$ l RNase-free H<sub>2</sub>O

The reaction mix was incubated for 1 h at 42 °C and 15 min at 30 °C. With this modified cDNA synthesis each single transcript carried a tag and could be amplified with one universal primer, independently on the sequence or length of the fragment. The amplification mix was set up as follows:

56.5  $\mu$ l H<sub>2</sub>O

10  $\mu$ l 10x LA buffer

10  $\mu$ l MgCl<sub>2</sub> (2.5  $\mu$ M)

16  $\mu$ l dNTPs (2.5  $\mu$ M)

2  $\mu$ l amplification primer (10  $\mu$ M)

5  $\mu$ l cDNA

0.5  $\mu$ l LA Taq polymerase

The reaction mix was split in two tubes containing 70  $\mu$ l and 30  $\mu$ l, respectively. The tube with 30  $\mu$ l was used to optimize for cycle numbers in order to prevent an overamplification bias. The tube containing 70  $\mu$ l reaction mix was stored on ice until

appropriate cycle numbers were determined and later used for the final amplification. The optimization tube was cycled for 10 cycles and 5  $\mu$ l were removed and transferred to a new tube. Every 3 additional cycles, another 5  $\mu$ l were removed until a total number of 22 cycles was reached (Tab. 17). The amplification mixes for each cycle number were analyzed by gel electrophoresis and an appropriate cycle number was determined. The tube on ice was then run for the corresponding number of cycles. Excessive primers and nucleotides were removed with SureClean Plus by following the manufacturer's protocol. DNA concentrations were determined in a Qubit using the high sensitivity dsDNA kit.

**Tab. 17 PCR cycling conditions for amplification of cDNA.**

94 °C	1:00	
98 °C	0:30	x- cycles
68 °C	5:00	
72 °C	10:00	
72 °C	5:00	

### 2.2.11 Quantitative PCR

For the quantification of relative transcript levels, RNA was transcribed to cDNA as previously described in chapter 2.2.8. The concentration of cDNA samples was adjusted to 5 ng/ $\mu$ l and 4  $\mu$ l of samples were mixed with 5  $\mu$ l qPCRBIO SyGreen and 0.5  $\mu$ l of each forward and reverse primer (5  $\mu$ M). The reaction mix was loaded into wells of 48-well plates and subsequently sealed with adhesive film. For all analyses, *rpl32* was used as reference gene. Cycling conditions for quantitative PCR (qPCR) were set up as shown in Tab. 18.

**Tab. 18 Cycling conditions for qPCR.**

95 °C	1:00	
95 °C	0:30	30 cycles
55 °C	0:45	
72 °C	1:00	
72 °C	5:00	

Differential gene expression levels between treatments were analyzed by the  $\Delta\Delta$ CT method. With this method, not only the treatment was compared to the control but also each gene was normalized to the corresponding reference gene *rpl32*. Following equation was used for calculation of relative transcript levels:

$$\Delta CT = CT_{\text{target gene}} - CT_{\text{reference gene}}$$

$$\Delta\Delta CT = \Delta CT_{\text{treatment}} - \Delta CT_{\text{control}}$$

$$\text{Relative transcript levels} = 2^{-\Delta\Delta CT}$$

### 2.2.12 RNA sequencing

cDNA libraries were created either with the Nextera DNA flex Library Prep kit. The sequencing runs were performed on the HiSeq2500 and HiSeq4000, respectively. Sequencing data of airway epithelial cells from 3<sup>rd</sup> instar larvae and from adult CS recovered flies was trimmed for adapter sequences and quality by using Cutadapt and prinseq respectively. Mappings were done with Tophat based on the BDGP6 reference and subsequent calculation of read counts was done with HTSeq. Differential expression of read counts was performed with DESeq2 from the R Bioconductor package. For recovery data, an outlier replacement was additionally conducted. Visualization of data was done in R by using the ggplot2 package based on z-score of normalized rlog values. Differential expression of sequencing data of airways from 5 d and 15 CS exposed flies as well as young and old flies were processed with the CLC genomic workbench software. In brief, adapter sequences were trimmed and reads were normalized and mapped to the BDGP6 reference by the RNA-Seq Analysis tool. Differential expression was calculated with the Differential Expression for RNA-Seq tool.

Distance matrices for the comparison of adult CS exposed airways to young and old airways were created by calculating euclidean distances based on PCoA plots. Distances from CS exposed airways and corresponding controls were projected into the calculated distances from young and old profiles.

### 2.2.13 Triglyceride measurements

Prior to body fat measurements, 5 flies or 5 larvae were weighed with a microscale in 2 ml screw cap tubes. Subsequently 3 zirconia beads (2,6 – 2,8 mm) were added and the samples were homogenized in 500  $\mu$ l 0.05 % PBS/Tween-20 using a bead mill homogenizer. Homogenates were heated to 70 °C for 5 min to inactivate enzymatic activity. Cell debris were centrifuged at 3000 x g for 3 min and the supernatant was transferred to a new tube. A trioleate standard was treated the same way and was serially diluted, starting from 100  $\mu$ g/50 $\mu$ l to 3.12  $\mu$ g/50 $\mu$ l. 50  $\mu$ l duplicates of samples and standards were loaded into wells of a 96-well plate. Absorbance at 540 nm was measured

using a plate reader and 200  $\mu\text{l}$  infinity triglyceride solution pre-warmed to 37  $^{\circ}\text{C}$  was added to each well. After 30 min incubation at 37  $^{\circ}\text{C}$  the absorbance at 540 nm was measured again. The amount of triglycerides was calculated and normalized to the weight of the respective sample.

#### 2.2.14 Metabolic rate measurements

Measurements of metabolic rates were performed as previously described<sup>205</sup>. Briefly,  $\text{CO}_2$  consumption of 10 d CS exposed flies was measured as a mean for energy expenditure. For this respirometer-based assay, three pieces of soda lime were soaked with  $\text{H}_2\text{O}$  and put into the respirometer. After the addition of a foam plug, 3 flies were added to each respirometer and it was then sealed with putty. The respirometers were hung into dyed water and the difference in height of liquid sucked into the capillaries before and after 2 h was measured, using ImageJ and converted to  $\text{CO}_2$  consumption by following equation:

$$\frac{\text{CO}_2 \mu\text{l}}{\text{hr} * \text{fly}} = \frac{(\pi \times R^2) \times (\Delta d - \Delta c) \times 1000}{n \times \text{hr}}$$

#### 2.2.15 Glutathione measurements

The measurements of total GSH and GSSG levels were carried out as previously described by Vandeputte *et al.* and Rahman *et al.* with slight modifications<sup>206,207</sup>. In summary, 5 larvae or 5 flies were homogenized in 200  $\mu\text{l}$  extraction buffer together with 3 zirconia beads in a bead mill homogenizer. Total GSH (GSH + GSSG) was measured by adding 5  $\mu\text{l}$  sample homogenate or GSH standards to wells of a 96-well plate. Equal volumes of DTNB and glutathione reductase solutions were mixed and 30  $\mu\text{l}$  of this mixture was added to each well. After an incubation of 30 s to allow for the conversion from GSSG to GSH, 15  $\mu\text{l}$  of  $\beta$ -NADPH was added to each well and absorbance was read immediately at 412 nm in a microplate reader. In total, 5 readings were made with a pause of 30 s between each read.

For the measurement of GSSG, 2  $\mu\text{l}$  2-vinylpyridine were added to 100  $\mu\text{l}$  sample homogenates and GSSG standards to avoid oxidation of GSH to GSSG. The reaction was incubated for 1 h at RT and excessive 2-vinylpyridine was neutralized by addition of 6  $\mu\text{l}$  triethanolamine. After an incubation of 10 min, GSSG was measured as described above for the GSH measurement.



Values for reduced GSH were calculated by subtracting the amounts of GSSG from total GSH amounts. The GSSG:GSH ratio was calculated for each sample separately.

### 2.2.16 Generation of fly lines

For the generation of the prx2540-GAL4 line the presumptive promoter region, a 1260 bp fragment located upstream of the transcription start site, was amplified by PCR (chapter 2.2.9). For the generation of UAS overexpression lines, coding sequences were amplified by PCR. Prior to cloning, PCR fragments were purified with SureClean Plus. Tab. 19 shows vectors, fragments and methods used for cloning experiments.

**Tab. 19 Overview of used vectors and cloning methods for the generation of fly lines.**

<b>Fly line</b>	<b>Fragment</b>	<b>Vector</b>	<b>Cloning method</b>
Prx2540-2-GAL4	1260 bp, upstream of TSS	pBPGAL4.2::VP16Uw	Gateway cloning
Prx2540-2 Overexpression	663 b, CDS	pBID-UASC	Restriction (EcoRI, NotI)
GstD5 Overexpression	655 bp, CDS	pBID-UASC	Restriction (EcoRI, NotI)

The promoter region for prx2540 was cloned by using the gateway recombination cloning method. Therefore, a mix consisting of 100 ng of fragment, flanked with attB sites and 100 ng donor vector pDONR221 were filled up to 8 µl with TE buffer (pH 8.0) and 2 µl of BP Clonase reaction mix was added. The mix was incubated for 1 h at 25 °C and 1 µl proteinase K was added to stop the reaction for 10 min at 37 °C. Cloned plasmids were then transformed into chemically competent DH5α cells by adding 5 µl reaction mix to 50 µl bacteria and incubated on ice for 30 min. The solution was heat shocked for 30 s at 42 °C and diluted in 250 µl SOC media. After an incubation of 30 min at 37 °C and shaking (500 rpm), the cells were plated onto kanamycin positive LB-Agar (Lennox) selection plates. To check for positive clones, colonies were picked with a pipette tip and used as a template for PCR (chapter 2.2.9). Positive clones were raised in kanamycin containing LB-Medium (Lennox) in overnight cultures and plasmids were extracted using the NucleoBond Xtra Maxi Kit. To clone the promoter region of prx2540 into the destination vector pBPGAL4.2::VP16Uw, a LR Clonase reaction mix was set up by adding 150 ng

pDONR221 vector to 150 ng pBPGAL4.2::VP16Uw and filling it up to 8  $\mu$ l TE buffer. To this mix 2  $\mu$ l of LR Clonase mix was added and incubated at 15 °C for 1 h. To stop the reaction 1  $\mu$ l proteinase K was added and incubated for 10 min at 37 °C. The transformation process, selection of positive clones and plasmid extraction was conducted as described above. Purified pBPGAL4.2::VP16Uw plasmid, carrying the 1260 bp long fragment was sequenced for injected into the  $w^{1118}$  strain by BestGene (Chino Hills, USA).

The CDS for Prx2540-2 and GstD5 was amplified from RNA transcribed to cDNA and by using primers containing two restriction sites for EcoRI and NotI, respectively. After PCR amplification of fragments, they were purified with SureClean Plus by following the manufacturer's protocols. Both, the purified fragments and the pBID-UASC vector were digested with EcoRI and NotI FastDigest enzymes. Double digestions were performed by following the manufacturer's protocol. Digested fragments and plasmids were ligated by T4 DNA Ligase at 4 °C over night and inactivated for 10 min at 65 °C. The ligated plasmid was incubated at 65 °C for 10 min to stop the ligation reaction and transformed into chemically competent DH5 $\alpha$  cells after selection of positive clones. Purified pBDID-UASC carrying the cloned fragments were injected into the  $w^{1118}$  strain by BestGene.

### **2.2.17 Recurrent dietary restriction**

For the alternating dieting of recurrent phases of dietary restriction and the corresponding control diet, flies were kept on the control diet (concentrated medium) for 4 d and were then transferred for 3 d to the dietary restriction diet. The CS exposure lifespan of  $w^{1118}$  flies was started on the control diet and after 4 d of CS exposure they were transferred to the dietary restriction media.

### **2.2.18 Immunohistochemistry**

For immunohistochemistry, tissues were dissected in PBS and fixed with 4 % PFA for 30 min at RT. Tissues were washed three times for 10 min each with PBST and subsequently epitopes were blocked with 5 % NGS in PBST for 1 h. Primary antibodies were diluted in 5% NGS and incubated over night at 4 °C. Next day remaining primary antibodies were washed three times for 15 min each and the secondary antibodies, diluted in 5 % NGS, were incubated at 4 °C over night. Tissues were washed three times for 15 min each and mounted on a slide in Rotimount and covered with a cover slip.

### **2.2.19 Longitudinal sections from adult flies**

Adult flies were anaesthetized using CO<sub>2</sub>, legs and wings were cut with spring scissors and pricked with needles, to allow subsequent fixation solution to enter the body. Whole flies were transferred to 4 % PFA and incubated at 4 °C over night. Fixed flies were washed three times for 15 min with 0.05 % PBST and embedded in 7.5 % agarose. The embedded tissue was cut with a Vibratome into 200 µm thick sections. For visualization, sections were either mounted directly in 80 % glycerol on slides or further treated for immunohistochemistry.

### **2.2.20 Fluorescence microscopy**

The visualization for microscopic pictures was done using the Zeiss AxioImager Z1 equipped with an Apotome. Pictures of trachea from 3<sup>rd</sup> instar larvae were acquired by applying a z-projection of 10 slices and maximum projection images were created.

Longitudinal sections from whole flies were visualized using the Zeiss LSM880 confocal microscope. Therefore, sections from a *btl-gal4, UAS-GFP* line were stained with a GFP booster probe to enhance the GFP signal in the specimen.

### **2.2.21 Statistical analysis**

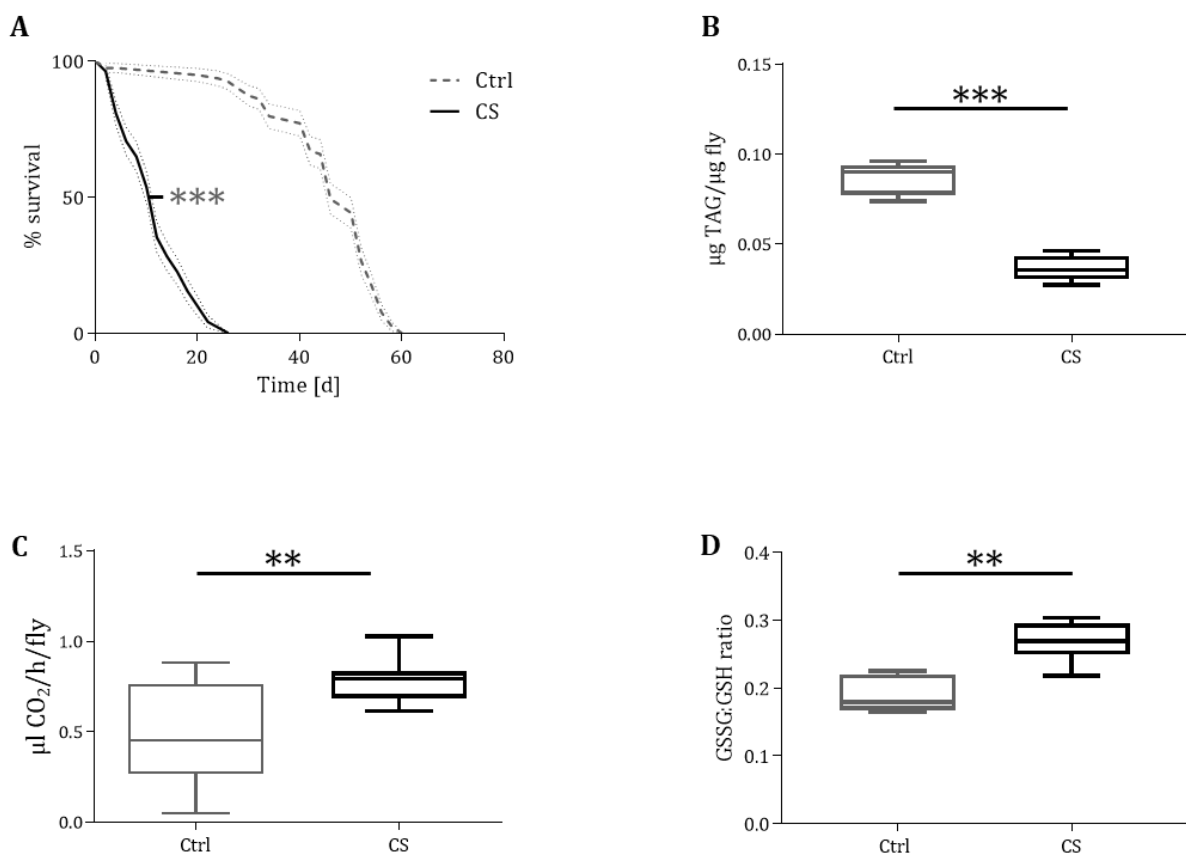
Statistical analyses were performed using the Graph Pad Prism 7 software. Data was tested for distribution prior to statistical test. Parametric data was analyzed with students t-test. For nonparametric data either the Kolmogorov-Smirnov or Mann-Whitney test were used. Lifespan experiments were tested with the Log-rank test.

### 3 Results

#### 3.1 Cigarette smoke exposure reduces the fly's lifespan and alters physiologic parameters

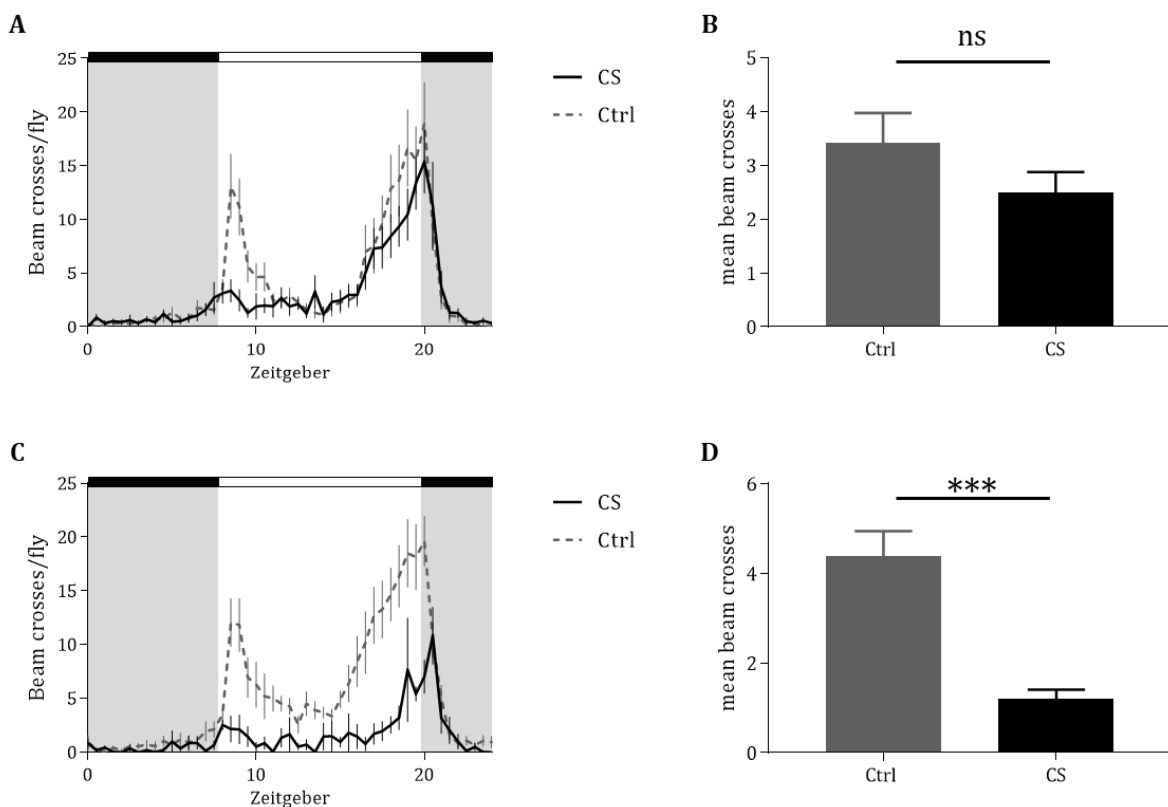
COPD patients suffer from multifactorial symptoms caused by the chronic exposure to cigarette smoke (CS) or other inhaled irritants. In order to model these phenotypic observations, a novel *Drosophila* model was established.

To initially assess the effects of cigarette smoke (CS) on the fly's physiology, a comprehensive phenotyping was conducted and several physiologic parameters were analyzed in *w*<sup>1118</sup> female flies (Fig. 7, Fig. 8). Therefore, symptomatic parameters that are observed in COPD patients were selected and tested for changes in *Drosophila*.



**Fig. 7 CS exposure reduces lifespan and affects the physiology of *Drosophila*.** **A** Lifespan analysis of cigarette smoke (CS) exposed, female *w*<sup>1118</sup> flies compared to untreated flies (Ctrl). Error indicators are shown in dotted lines and represent standard deviation. *n* = 80. **B** Body fat content of CS exposed flies compared to untreated flies. Shown are the amounts of triglycerides (TAG) in relation to the body weight per fly. *n* = 5. **C** Metabolic rate measurement of CS exposed flies compared to untreated flies. The volume of produced CO<sub>2</sub> was measured per hour and fly. *n* = 11. **D** Ratio of oxidized glutathione (GSSG) to reduced glutathione (GSH) in CS exposed flies compared to untreated control flies. *n* = 6. Whiskers represent min to max range. \*\* = *p* < 0.01, \*\*\* = *p* < 0.001.

The most obvious and consequential physiologic parameter in COPD patients undoubtedly is the lifespan. In the fruit fly, daily CS exposure for 30 min significantly reduced the lifespan by about 70 %, with a median lifespan of 12 d compared to 46 d of control flies (Fig. 7 A). Additionally, CS exposure for 10 d significantly decreased the body fat content in flies by approximately 68 % (Fig. 7 B). In contrast to that an increased metabolic rate was observed after 10 d CS exposure. The metabolic rate is significantly increased by 75 % (Fig. 7 C). Moreover, the fly's redox homeostatic balance was influenced by the exposure to CS. When exposed to CS for 10 d, the GSSG:GSH ratio is significantly shifted towards the oxidized form of glutathione, indicating an increased electrophilic stress level (Fig. 7 D).



**Fig. 8 CS exposure reduces locomotor activity of *Drosophila*.** **A** Locomotor activity pattern of 10 d cigarette smoke (CS) exposed *w<sup>1118</sup>* female flies compared to untreated flies (Ctrl). Day- and night-time activities are emphasized in light and dark areas respectively. Mean beam crosses were binned to 30 min. **B** Overall mean activity of 10 d CS exposed flies compared to untreated flies. **C** Locomotor activity pattern of 14 d cigarette smoke exposed *w<sup>1118</sup>* female flies compared to untreated flies. Day- and night-time activities are emphasized in light and dark areas respectively. **D** Overall mean activity of 10 d CS exposed flies compared to untreated flies. Error indicators represent SEM. ns = not significant, \*\*\* =  $p < 0.001$ ,  $n = 16$ .

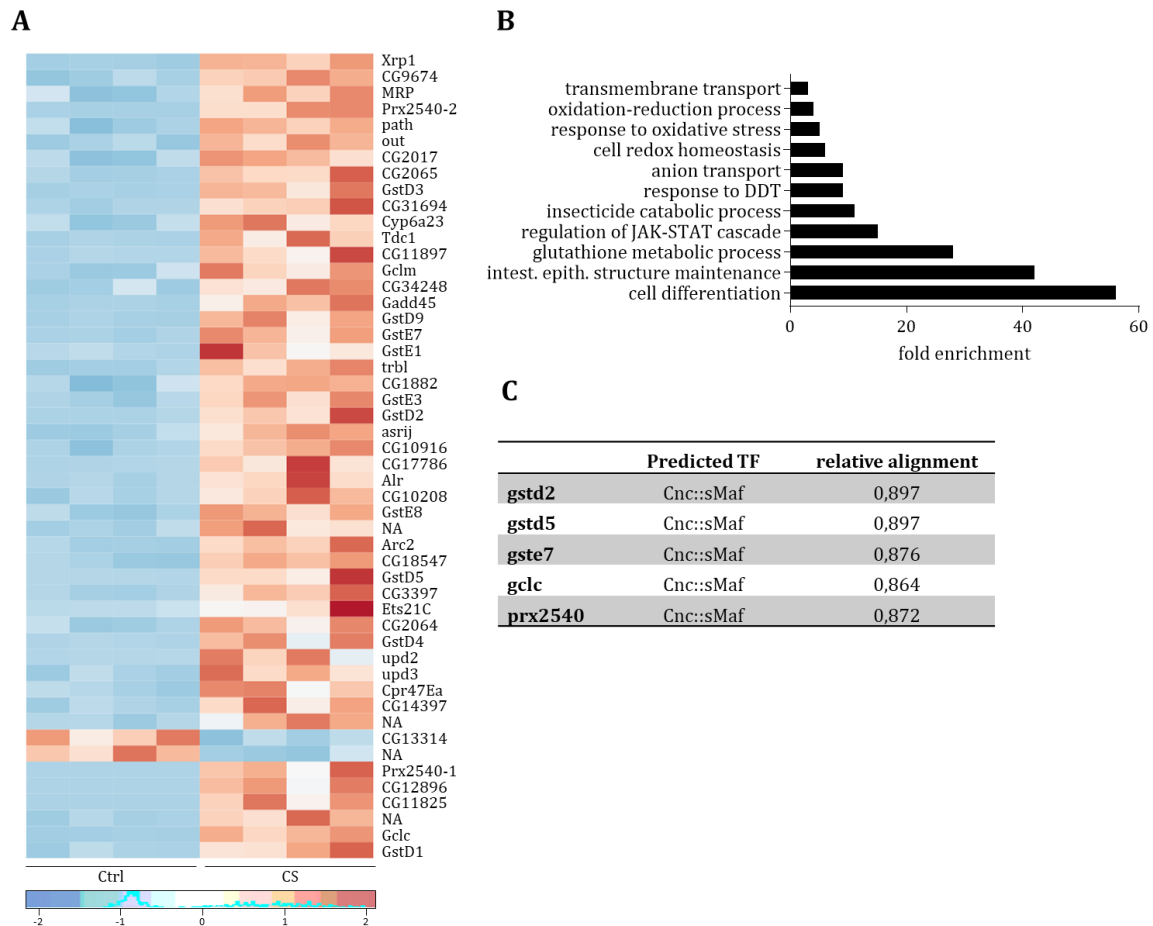
Another important physiologic parameter that is altered in COPD patients is the physical activity. A locomotor activity monitor was used to assess the fly's ability to move after the exposure to CS. The locomotor activity of CS exposed flies was impaired in an age-related

manner (Fig. 8). When exposed to CS for seven days, the morning activity peak is almost completely diminished but the overall locomotor activity is not significantly altered (Fig. 8, A, B). However, when flies were exposed to CS for 14 days instead, both morning and evening activity peaks were decreased, resulting in a significantly reduced overall activity (Fig. 8 C, D).

### 3.2 The airway epithelial response to acute CS exposure is characterized by the induction of stress related pathways

To identify underlying mechanisms that drive the observed phenotypic changes (chapter 3.1), in response to CS exposure, transcriptomic analyses were performed. Therefore, the response of the airway epithelial cells to a short and acute exposure to CS was analyzed in 3<sup>rd</sup> instar larvae. After CS exposure for 30 min and 3 times each day, on two consecutive days, tracheal cells were dissected from the animals and an RNA sequencing experiment was performed. As shown in Fig. 9 the transcriptomic profile of tracheal epithelial cells was modulated upon CS exposure, with a total number of 179 differentially expressed genes (DEGs). In Fig. 9 A, the 50 strongest regulated genes are displayed in a heatmap and many of them could be associated with antioxidative properties, such as *glutathione s-transferases* from different classes (*gstd* and *gste*), *peroxiredoxins* (*prx2540*) or *cytochrome p450* (*Cyp6a23*). Moreover, general stress response related genes such as *unpaired 2* and *3* (*upd2/3*) were upregulated. A gene ontology (GO) enrichment analysis based on all DEGs identified biological processes involved in the response to acute CS exposure (Fig. 9 B). Next to redox homeostasis processes like oxidation-reduction, response to oxidative stress or anion transport, there are also distinct pathways involved in the response to CS. The ligands of the JAK/STAT pathway *upd2/3* and its negative regulator *socs36E* were transcriptionally regulated and therefore the GO term *regulation of JAK/STAT cascade* is enriched by a factor of 15. Markedly the GO term *glutathione metabolic process* is enriched 28-fold and includes a broad range of *gsts* and other glutathione metabolism associated genes such as the *glutamate-cysteine ligase catalytic subunit* (*gclc*) and its modifier subunit (*gclm*). To check for upstream regulating mechanisms of the GSH response, a transcription factor binding site analysis was performed (Fig. 9 C). Therefore, the presumptive promoter regions of selected genes were analyzed for binding motifs of the Nrf2 pathway transcription factor Cnc::sMaf heterodimer. All of the selected genes showed a high similarity score of above 0.85 for the

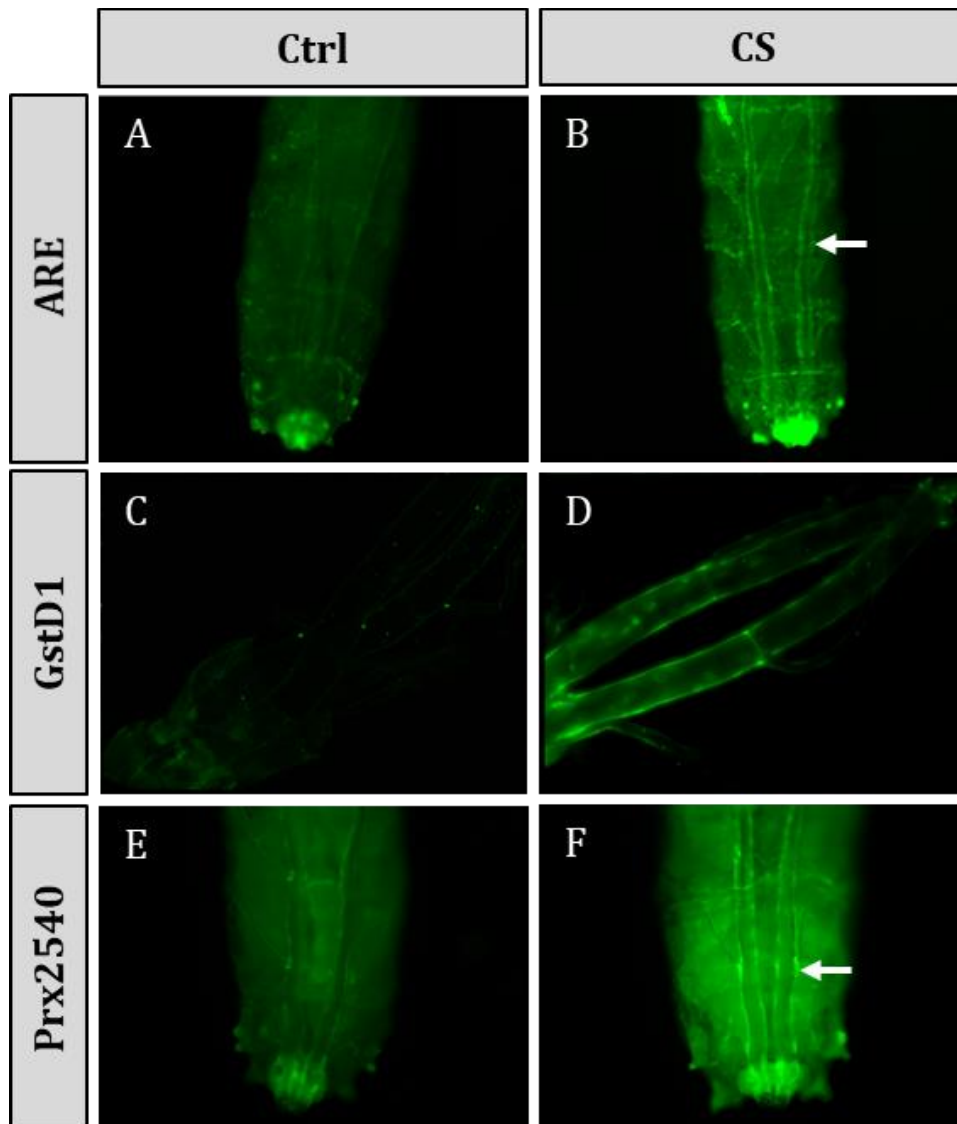
predicted Nrf2 binding motif called the antioxidant response element (ARE). The core consensus sequence of all genes is located in a range 1000 to 2000 bp upstream of the transcription start site.



**Fig. 9 Transcriptomic profiling of airway epithelial cells from 3<sup>rd</sup> instar larvae in response to acute CS exposure.** *w*<sup>1118</sup> 3<sup>rd</sup> instar larvae were exposed to cigarette smoke (CS) for 30 min, three times a day on two consecutive days. **A** Heatmap of the 50 most regulated genes with a cutoff value of  $p < 0.05$ . **B** GO enrichment analysis of biological processes for all DEGs with a  $p$ -value  $< 0.05$ . **C** Transcription factor binding site analysis for selected glutathione metabolism related DEGs for the Nrf2 pathway transcription factor Cnc::sMaf heterodimer.

Based on the transcriptomic analyses, further approval to strengthen the assumed involvement of Nrf2 and JAK/STAT pathways in the response to CS was required. Accordingly, a set of fluorescence microscopy experiments was performed in 3<sup>rd</sup> instar larvae in order to resolve the mode of action of both identified pathways (Fig. 10, Fig. 11). Visualized by a reporter line that is monitoring the transcriptional regulation of ARE binding activity, CS exposure led to an activation of the ARE promoter (Fig. 10 A, B). Also downstream of ARE, CS exposure induced the expression of Gstd1 and Prx2540 (Fig. 10

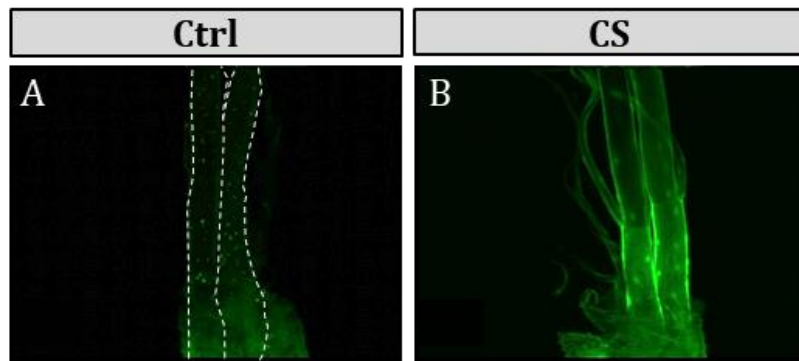
C-F). Notably the GFP fluorescence of all reporter lines was stronger towards the posterior spiracles of CS exposed trachea and decreased gradually towards the anterior end.



**Fig. 10 Activation of the Nrf2 pathway and downstream target genes upon acute CS exposure.** 3<sup>rd</sup> instar larvae were exposed to cigarette smoke (CS) and compared to untreated larvae (Ctrl). **A, B** Posterior end of 3<sup>rd</sup> instar Larvae of an ARE-GFP reporter line. Arrow indicates GFP expression in trachea **C, D** Posterior end of dissected trachea from 3<sup>rd</sup> instar larvae of a GstD1-GFP reporter line. An additional antibody staining with an  $\alpha$ -GFP antibody was applied to enhance GFP signal intensity **D, E** Posterior end of 3<sup>rd</sup> instar larvae from a prx2540-GAL4 >UAS-GFP crossing. Arrow indicates GFP expression in trachea.

Moreover, the exposure to CS resulted in an activation of the STAT92E transcription factor in the fly's airway epithelium (Fig. 11 A, B). In a reporter line, in which the expression of GFP is controlled by the STAT92E promoter, a strong increase in GFP signal was observed upon CS exposure. Also, this signal was stronger towards the posterior spiracles.





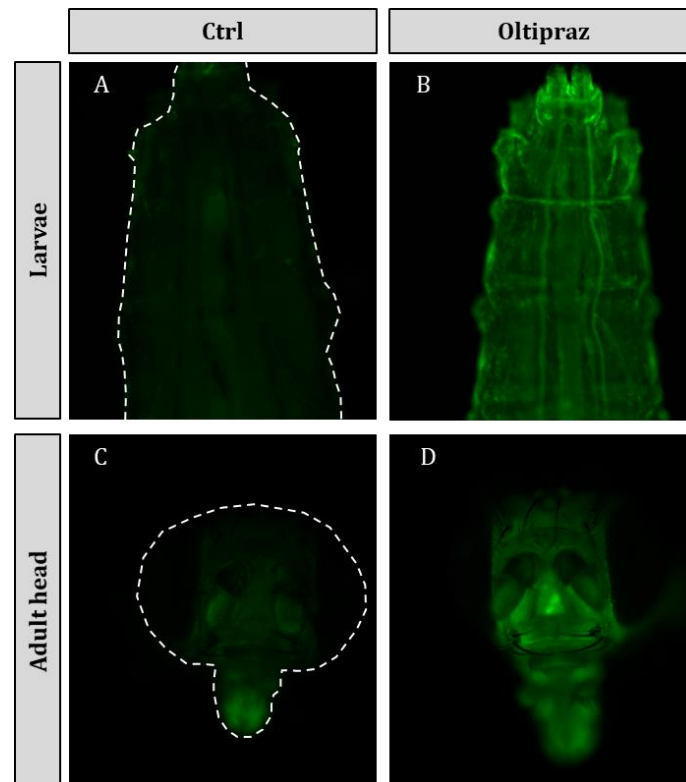
**Fig. 11 CS exposure induces the activation of the transcription factor STAT92E.** A reporter line that expresses GFP under the control of the STAT92E promoter was used to monitor the activity of JAK/STAT signaling. An additional antibody staining with an  $\alpha$ -GFP antibody was applied to enhance GFP signal intensity. **A** Posterior end of trachea from untreated 3<sup>rd</sup> instar larvae (Ctrl). **B** Posterior end of trachea from cigarette smoke (CS) exposed 3<sup>rd</sup> instar larvae.

Regarding the combined outputs from the transcriptomic and microscopic analyses, it can be concluded that acute CS exposure induces a variety of stress responses in the airway epithelial cells. Defined by the activation of JAK/STAT and Nrf2 these pathways seem to play a central role in the response to short and acute phases of CS exposure.

### 3.3 Ectopic activation of the Nrf2 pathway increases lifespan in CS exposed flies

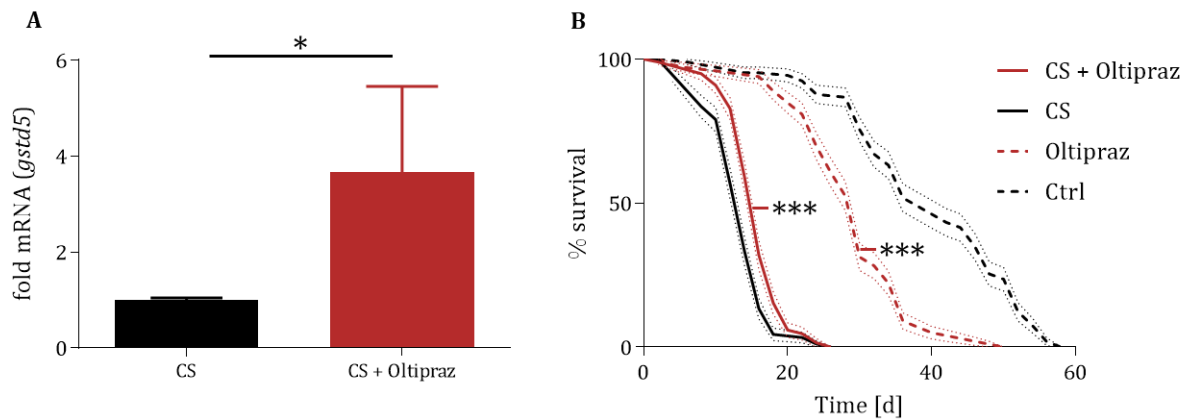
Concerning the aforementioned results from chapter 3.2, the Nrf2 pathway was assumed to play a role in the response to CS. However, it is uncertain what that role is in detail. To elucidate the potential effects of an activated Nrf2 signaling on the airway epithelium, the pathway was ectopically activated by both a pharmacologic and a genetic approach.

To activate Nrf2 pharmacologically, the agonist oltipraz was used. Oltipraz inhibits the negative regulator of Nrf2 signaling Keap1<sup>208</sup>. The subsequent translocation of Nrf2 into the nucleus induces the transcription of target genes<sup>209,210</sup>. As shown in Fig. 12, treatment of the ARE-GFP reporter line with the Nrf2 activator oltipraz (400  $\mu$ M, supplied with media) resulted in an activated ARE binding motif in both larvae (Fig. 12 A, B) and adult flies. To further validate the expression of downstream target genes, a qPCR experiment was performed and the transcription of *gstd5* in airway epithelial cells from 3<sup>rd</sup> instar larvae was measured. After feeding with oltipraz, an activated Nrf2 pathway induced an overexpression of *gstd5* in the trachea of w<sup>1118</sup> larvae (Fig. 13 A).



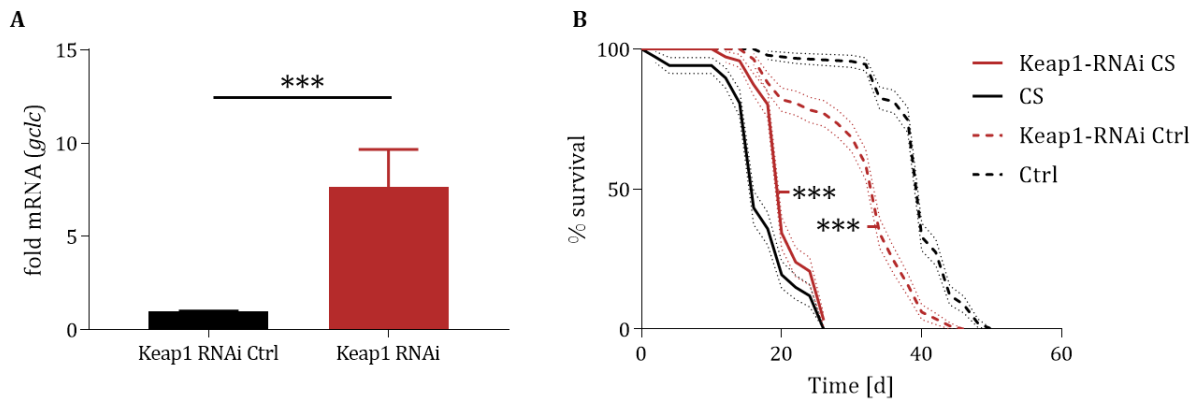
**Fig. 12 Oltipraz ectopically activates Nrf2 signaling in larvae and adults.** ARE-GFP reporter lines were fed with oltipraz, supplemented to the media. **A, B** 3<sup>rd</sup> instar larvae raised on control media (0.5 % DMSO solvent control) or media containing 400  $\mu$ M oltipraz respectively. **C, D** Heads from adult flies, fed for 5 d with control media (0.5 % DMSO solvent control) or media containing 400  $\mu$ M oltipraz.

To evaluate the effects of an ectopically activated Nrf2 pathway, a series of lifespan assays was performed. Therefore, *w*<sup>1118</sup> flies were constantly fed with 400  $\mu$ M oltipraz, exposed to CS and compared to flies fed on a solvent control diet (0.5 % DMSO). As shown in Fig. 13 B the application of oltipraz was beneficial for the survival of flies during CS exposure. The median lifespan of oltipraz treated flies was 16 d and thus 14 % higher compared to untreated flies with a median lifespan of 14 d. However, under control conditions without CS exposure, oltipraz treatment had dramatic side effects regarding the lifespan of flies. The median lifespan of oltipraz treated control flies was significantly decreased by 26 % compared to untreated control flies.



**Fig. 13 Pharmacologic activation of Nrf2 signaling by oltipraz enhances lifespan during CS exposure.** **A** qPCR analysis for *gst5* comparing trachea of untreated  $w^{1118}$  3<sup>rd</sup> instar larvae (0.5 % DMSO solvent control) with larvae raised on a diet containing 400  $\mu$ M oltipraz. Shown are mean values and error bars represent standard deviation,  $n = 5$  **B** Lifespan analysis of cigarette smoke exposed  $w^{1118}$  flies fed with 400  $\mu$ M oltipraz (CS + Oltipraz) compared to CS exposed flies fed on a solvent control diet (CS). Non-CS exposed control flies either fed with 400  $\mu$ M oltipraz (Oltipraz) or with the solvent control diet (Ctrl).  $n = 100 - 115$ . Error indicators are shown in dotted lines and represent standard deviation. \* =  $p < 0.05$ , \*\*\* =  $p < 0.001$ .

To potentially bypass the side effects of an unspecific and ectopic Nrf2 activation in the whole animal by oltipraz, a tissue specific, genetic approach was carried out. Therefore, an RNA interference (RNAi) against Keap1 was expressed specifically in adult trachea. The Keap1-RNAi was driven in Breathless (Btl) positive cells and time dependently controlled by using the TARGET system. This *btl-GAL4*, *GAL80 > UAS-Keap1-RNAi* crossing induced the transcription of the Nrf2 target gene *gclc* in trachea from 3<sup>rd</sup> instar larvae (Fig. 14 A). The constitutive activation of Nrf2 in the adult trachea via the Keap1-RNAi was beneficial for the survival during CS exposure. With a median lifespan of 20 d compared to 16 d of the corresponding responder control, the constitutive and trachea specific expression of Keap1-RNAi reversed the effects of CS exposure by 25 % (Fig. 14 B). However, this specific activation of Nrf2 still had side effects under control conditions. The lifespan of the untreated Keap1-RNAi crossing was significantly reduced by 18 % with a median lifespan of 36 d compared to 40 d of the control crossing.



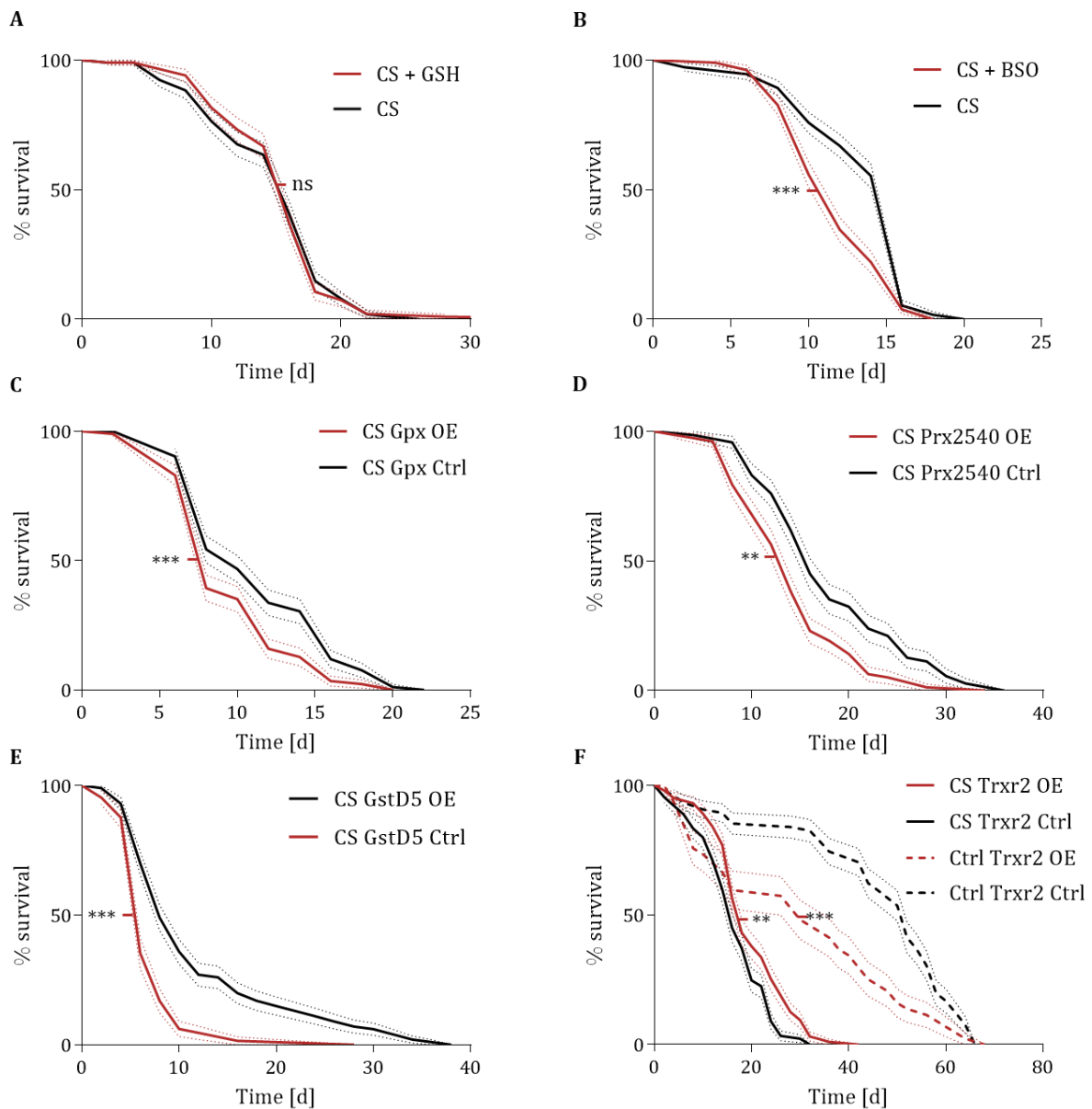
**Fig. 14 Genetic activation of Nrf2 signaling by Keap1-RNAi enhances lifespan during CS exposure.** **A** qPCR analysis of *gclc* comparing flies from a Btl-GAL4; GAL80 > Keap1-RNAi crossing (Keap1-RNAi) with flies from the corresponding responder control crossing  $w^{1118}$  > Keap1-RNA (Ctrl). Error bars represent standard deviation,  $n = 5$ . **B** Lifespan analysis of CS exposed Btl-Gal4; Gal80 > Keap1-RNAi crossing (Keap1-RNAi CS) compared with the corresponding responder control crossing  $w^{1118}$  > Keap1-RNA (CS). Untreated flies from the Btl-Gal4; Gal80 > keap1-RNAi crossing (Keap1-RNAi Ctrl) compared to untreated flies from the  $w^{1118}$  > Keap1-RNA corresponding responder control crossing,  $n = 86$  -97. Error indicators are shown in dotted lines and represent standard deviation. \*\*\* =  $p < 0.001$ .

Nevertheless, activation of Nrf2 signaling is beneficial during chronic CS exposure and significantly extended lifespan in *Drosophila*. Both a tissue unspecific and an airway specific approach shared these beneficial properties. The specific inhibition of Keap1 in tracheal cells was more powerful than the treatment with oltipraz. Also, side effects in control flies could be reduced using an airway specific, genetic approach via Keap1-RNAi.

### 3.4 The GSH metabolism influences lifespan during CS exposure

Based on the lifespan prolonging effects of an activated Nrf2 signaling, it remained unclear what exactly the mode of action in this response was defined by. As already mentioned before, the Nrf2 signaling pathway is one of the main antioxidant response mechanisms of the cell<sup>97</sup>. Characterized by the release of various antioxidants, Nrf2 induces the transcription of several glutathione associated target genes. Furthermore, the complementing transcriptomic data from CS exposed larval trachea suggested the GSH metabolism to lie downstream of Nrf2 signaling (Fig. 9). Moreover, it was shown that the exposure to CS led to a shift from the reduced GSH form towards oxidized GSSG form of glutathione (Fig. 7 D). Hence, GSH metabolism might act as a gate keeper and potentially mediate the responses to CS exposure in the airway epithelium. To examine the role of GSH metabolism for lifespan determination and thus identify crucial players, an extensive analysis of GSH metabolism intervention was conducted (Fig. 15). Therefore, the GSH

metabolism was manipulated either genetically or pharmacologically in CS exposed flies, while the lifespan was analyzed for effects on the fly.



**Fig. 15 Manipulation of the GSH metabolism affects the lifespan during CS exposure.** **A** Lifespan of reduced GSH supplemented and cigarette smoke exposed (CS + GSH)  $w^{1118}$  flies compared to untreated, CS exposed flies.  $n = 104 - 108$ . **B** Buthionine Sulfoximine (BSO, 100 mM) supplemented  $w^{1118}$  flies (CS + BSO) compared to untreated CS exposed flies.  $n = 105 - 112$ . **C** CS exposed female flies from a Btl-Gal4 > UAS-Gpx crossing (Gpx OE) compared to corresponding responder control crossing (Gpx Ctrl).  $n = 96 - 100$ . **D** CS exposed female flies from a Btl-GAL4 > UAS-Peroxiredoxin 2540 crossing (Prx2540 OE) compared to the corresponding responder control crossing (Prx2540 Ctrl).  $n = 71 - 78$ . **E** CS exposed flies from a Btl-GAL4 > UAS-GstD5 crossing (GstD5 OE) compared to the corresponding responder control (GstD5 Ctrl).  $n = 65 - 100$ . **F** CS exposed female flies from a Btl-GAL4 > UAS-Trxr2 crossing (Trxr2 OE) compared to the corresponding responder control crossing (Trxr2 Ctrl).  $n = 90 - 104$ . Error indicators are shown in dotted lines and represent SD. ns = not significant, \*\* =  $p < 0.01$ , \*\*\* =  $p < 0.001$ .

Initially, CS exposed  $w^{1118}$  flies were constantly fed with the reduced form of glutathione (GSH). The nutritive addition of GSH had no effects on the lifespan of CS exposed flies

compared to CS exposed flies without GSH supplementation (Fig. 15 A). In contrast, the depletion of GSH negatively affected the lifespan of CS exposed *w<sup>1118</sup>* flies. By inhibiting the GSH rate limiting enzyme glutamate-cysteine ligase (Gcl), by application of the compound Buthionine Sulfoximine (BSO), a significant reduction of lifespan was observed (Fig. 15 B)<sup>211</sup>. With 12 d median lifespan, BSO treated flies lived 33 % shorter, compared to 16 d of the corresponding solvent control (H<sub>2</sub>O).

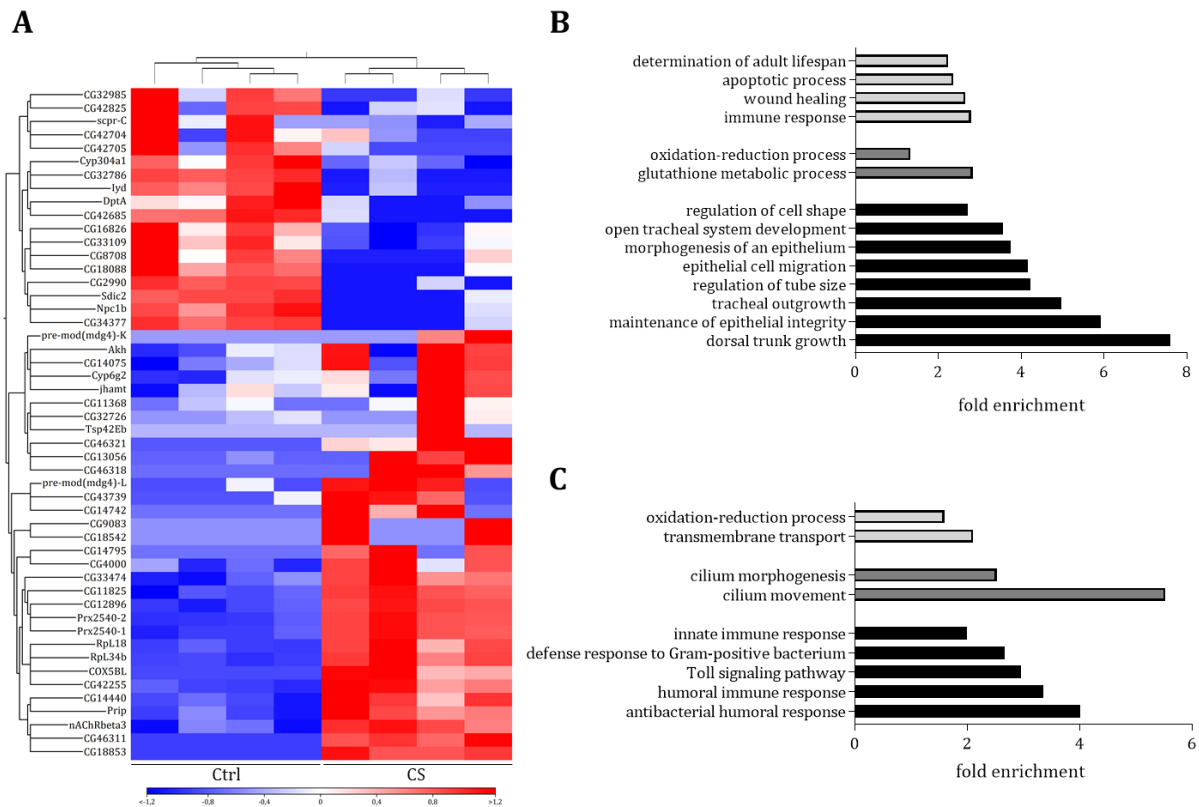
Furthermore, a set of genetic and trachea specific manipulations of the enzymatic control of GSH metabolism were conducted. First, the effect of an overexpressed Gpx specifically in airway epithelial cells during CS exposure was analyzed. Gpx catalyzes the conjugation of GSH to H<sub>2</sub>O<sub>2</sub> and enzyme activity results in the formation of GSSG. The lifespan of this *Btl-GAL4 > UAS-Gpx* crossing was substantially reduced by 20 % with a median lifespan of 8 d compared to 10 d in the responder control crossing (Fig. 15 C). Complementing that result, an overexpression of the two GSH to xenobiotic conjugation catalyzing enzymes Prx2540 and GstD5 led to significantly reduced lifespan of CS exposed flies (Fig. 15 D, E). With a median lifespan of 14 d, the *Btl-GAL4 > UAS Prx2540* crossing reduced lifespan by 22 %, compared to 16 d of the corresponding responder control crossing. Also, the *Btl-GAL4 > UAS-GstD5* overexpression led to a reduction of lifespan. With a median lifespan of 6 d, GstD5 overexpressing flies lived 25 % shorter than responder control flies with a median lifespan of 8 d.

Since all overexpressed enzymes, which are responsible for the conversion of GSH to GSSG, led to reduced lifespan of CS exposed flies, it remained uncertain what the effects of a shifted ratio towards GSH look like. To elucidate these effects, Trxr2 was specifically overexpressed in tracheal cells (*Btl-GAL4 > UAS-Trxr2*) and flies were exposed to CS. An overexpressed Trxr2 in the respiratory system increased the median lifespan in flies of 18 d by 13 % compared to 16 d median lifespan of the responder control crossing flies (Fig. 15 F). However, the untreated flies lived significantly shorter, compared to the responder control.

### 3.5 The airway epithelium differentially reacts to CS in a time-dependent manner

As a chronic disease, COPD usually manifests after a long time of exposure to CS or other irritants. To further explain the observed phenotypic changes in response to long-term CS exposure (chapter 3.1), a set of RNAseq analyses were performed. Two different periods of CS exposure were chosen in order to check for differential transcriptomic profiles in a time and age dependent manner. Trachea from 5 d and 15 d CS exposed w<sup>1118</sup> female flies were dissected and isolated RNA were pre-amplified due to low yields during dissection. Accordingly, RNA was transcribed to cDNA and PCR amplified prior to RNAseq experiments.

The exposure to CS for 5 d resulted in a total number of 2881 differentially expressed genes, compared to the age matched and untreated controls. Expression patterns of CS exposed and untreated samples showed clear differentiation between these treatments (Fig. 16 A). The 50 most regulated genes are displayed in Fig. 16 A. Amongst many uncharacterized genes, both *prx2540* splice variants were strongly upregulated by 85 and 72-fold, respectively. Notably, many immune response associated genes, such as several AMPs (*dpt*, *att*, *mtk*, *listericin* etc.), the Imd pathway receptor *peptidoglycan recognition protein* (*pgrp*) or *kenny* (*key*) were downregulated upon 5d CS exposure. A GO enrichment analysis revealed the involvement of a broad spectrum of biological processes in the response to CS exposure (Fig. 16 B, C). Enrichment analyses were performed for upregulated and downregulated DEGs separately. Upregulated DEGs were mainly characterized by morphologic processes, that regulate tracheal structure (Fig. 16 B). Processes like *open tracheal development*, *regulation of tube size* or *dorsal trunk growth* are enriched by 4 to 8-fold. Besides structure giving processes, general stress responses such as wound healing, apoptotic processes, determination of lifespan or immune response were also enriched but at lower enrichment scores with 2 to 4-fold. Furthermore, redox homeostatic processes like oxidation-reduction or glutathione metabolism processes were also overrepresented.



**Fig. 16 Transcriptomic analyses of airway epithelial cells from 5 d CS exposed flies.** **A** Heatmap for the 50 most regulated genes upon CS exposure w<sup>1118</sup> female flies with an FDR corrected p-value of < 0.05. **B** GO enrichment analysis of all 1576 upregulated DEGs. Shown are selected biological processes with a p-value of < 0.05. **C** GO enrichment analysis of all 1314 downregulated DEGs. Shown are selected biological processes with a p-value of < 0.05.

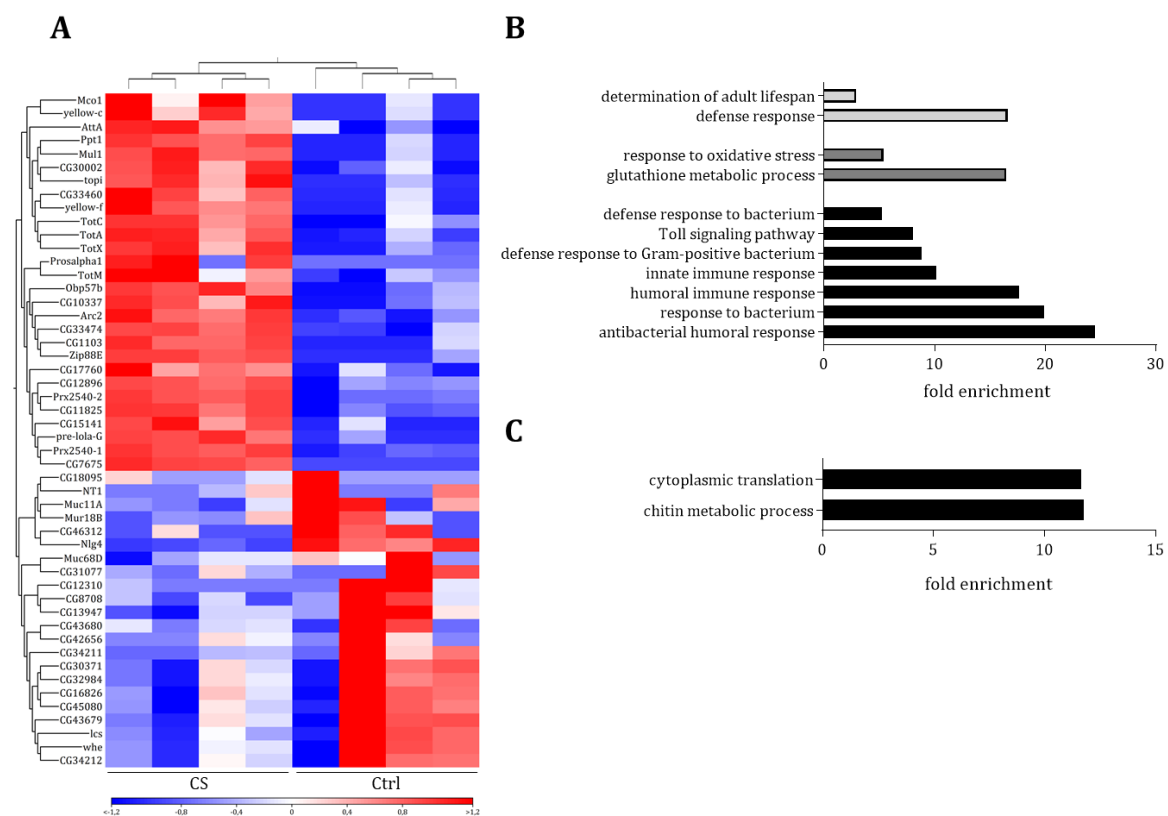
Downregulated biological processes were characterized by the enrichment of immune system related biological processes like *defense response to Gram-positive bacterium*, *Toll signaling pathway* or *antibacterial humoral response* (Fig. 16 C). These processes were enriched 2 to 4-fold. Next to detoxification processes like *oxidation-reduction process* and *transmembrane transport*, cilium related processes were overrepresented. *Cilium movement* was the most overrepresented biological process with an approximately 6-fold enrichment score.

Compared to untreated control flies, the transcriptome of airway epithelial cells from 15 d CS exposed w<sup>1118</sup> flies was characterized by the differential expression of 284 genes in total. As already observed for 5 d CS exposed flies, the expression patterns of 15 d exposed flies clustered well (Fig. 17 A). Among the most upregulated genes were *prx2540*, *turandot (tot)* and a variety of AMP coding genes. A GO ontology analysis revealed involved processes that were significantly enriched in response to a chronic exposure to CS for 15 d (Fig. 17 B, C). Upregulated DEGs were analyzed independently from



downregulated genes. Based on 192 upregulated DEGs, GO terms *defense response* and *determination of adult lifespan* were enriched by 16 and 3-fold respectively (Fig. 17 B). Moreover, many oxidative stress related genes like *gst*, *gclm* or *cyp9b2* were upregulated upon CS exposure. Hence, biological processes *response to oxidative stress* and *glutathione metabolic process* were strongly enriched by 5 and 16 times. Interestingly, diverse immune related GOs were enriched upon 15 d CS exposure. Biological processes such as *humoral immune response*, *response to bacterium* or *antibacterial immune response* were strongly enriched up to 24 times.

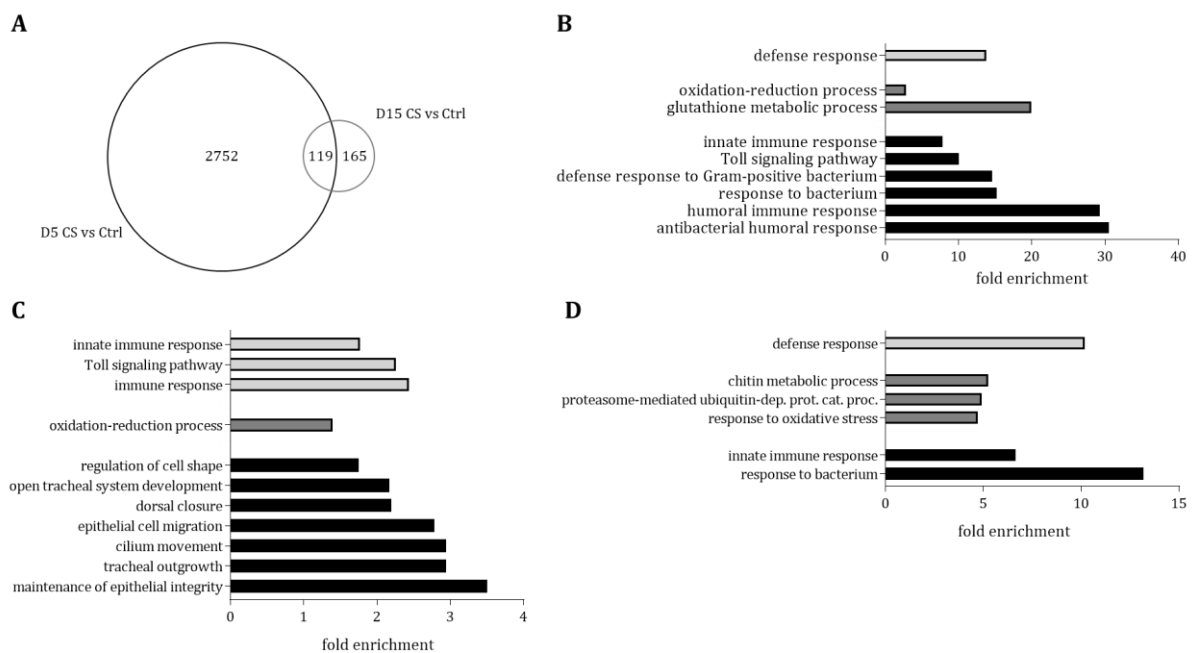
From 92 downregulated DEGs, only two biological processes could be assigned. *Cytoplasmic translation* and *chitin metabolic process* were both enriched 12-fold.



**Fig. 17 Transcriptomic analyses of airway epithelial cells from 15 d CS exposed flies.** A Heatmap of the 50 most differentially expressed genes upon CS exposure in  $w^{1118}$  female flies with an FDR corrected p-value of  $< 0.05$ . B GO enrichment analysis of all 284 upregulated DEGs. Shown are selected biological processes with a p-value of  $< 0.05$ . C GO enrichment analysis of all 92 downregulated DEGs. Shown are selected biological processes with a p-value of  $< 0.05$ .

To further evaluate the effects of CS exposure over different periods of time, in relation to each other, DEGs of both comparisons were analyzed for overlapping transcriptomic patterns (Fig. 18). Using a venn diagram analysis, an overlap of 119 DEGs was observed (Fig. 18 A). These commonly regulated DEGs were analyzed for biological process GO

terms. As shown in Fig. 18 B, both CS exposure periods shared various immune response GO terms and redox homeostasis processes like *oxidation-reduction process* and *glutathione metabolic process*. Interestingly, GO terms for DEGs that were exclusively expressed in 5d CS exposed airways, revealed involved morphology related processes like *open tracheal system development*, *tracheal outgrowth* or *maintenance of epithelial integrity* (Fig. 18 C). The observed immune related biological processes *innate immune response*, *Toll signaling pathway* and *immune response* originated from downregulated DEGs after 5d of CS exposure.

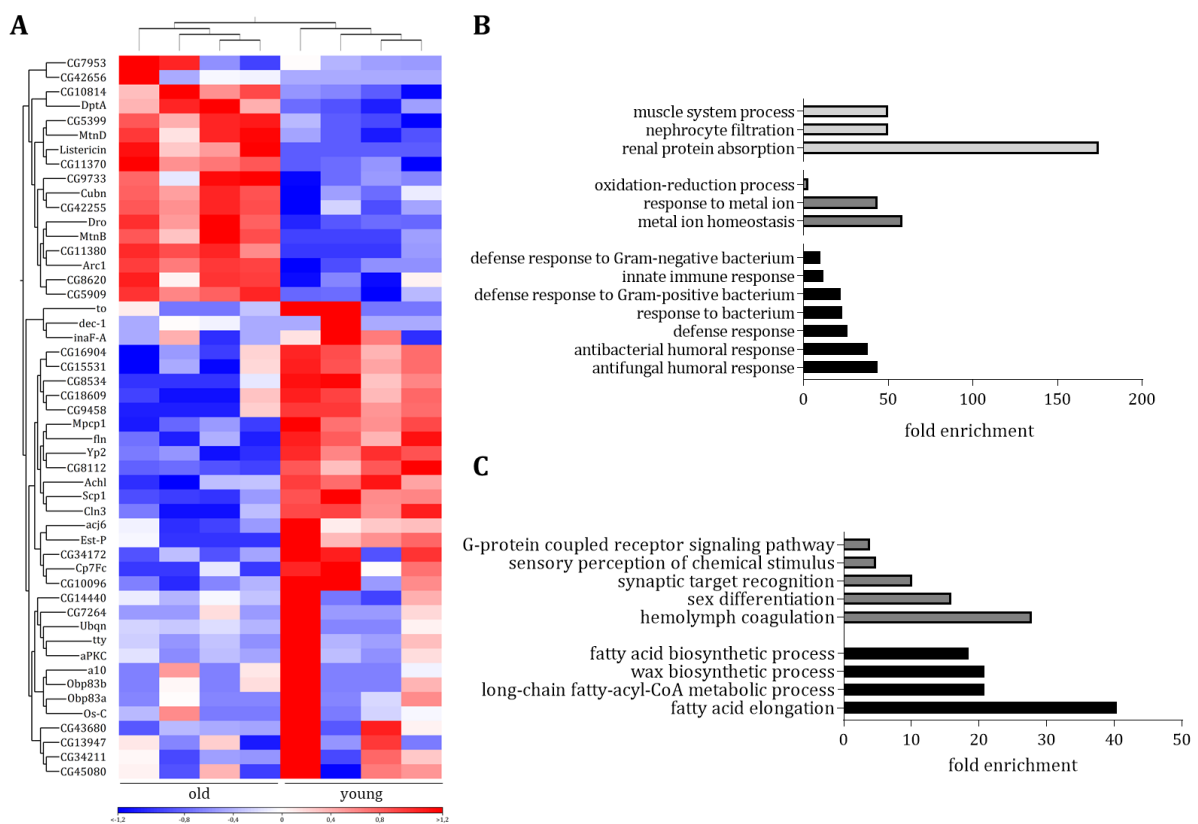


**Fig. 18 Overlapping and exclusive transcriptomic patterns of 5 d and 15 d CS exposed airway epithelia.** **A** Venn diagram analysis of DEGs from 5 and 15 d CS exposed airways. **B** GO enrichment analysis of biological processes for all 119 commonly shared DEGs.  $p > 0.05$  **C** Enriched GO terms for biological processes from 2752 DEGs, which were exclusively expressed in 5 d CS exposed tracheal cells.  $p > 0.05$ . **D** Enriched GO terms for biological processes from 165 genes exclusively expressed in 15 d CS exposed flies.  $p > 0.05$ .

The enrichment analysis for 15 d CS exposed exclusive DEGs revealed the biological processes *defense response*, *chitin metabolic process*, *response to oxidative stress* and *proteasome-mediated ubiquitin dependent protein catabolic process*. Moreover, the GO terms *innate immune response* and *response to bacterium* were enrichment by 5 and 13 times respectively. Notably, these terms were enriched due to upregulated immune-related DEGs. These results were in contrast to immune related GO terms from 5 d exclusive patterns, that were mainly defined by downregulated immune-related DEGs.

### 3.6 The transcriptome from aging airway epithelial cells is characterized by an activated immune system

The effects of cigarette smoke exposure differed in a time and age dependent manner, when flies were exposed for different periods (chapter 3.5). Nonetheless, it was uncertain how the effects of cigarette smoke exposure and the effects of an aging airway epithelium could be distinguished or if they accumulate. To assess the effects of an aging airway epithelium, the tracheal transcriptome from 52 days old female  $w^{1118}$  flies were compared to the tracheal transcriptome from seven days old flies.



**Fig. 19** Transcriptomic analyses of airway epithelial cells from 7d and 52 d old flies. **A** Heatmap of the 50 most differentially expressed genes of 52 d old  $w^{1118}$  female flies (old) compared to 7 d old flies (young) with an FDR corrected p-value of < 0.05. **B** GO enrichment analysis of all 127 upregulated DEGs. Shown are selected biological processes with a p-value of < 0.05. **C** GO enrichment analysis of all 88 downregulated DEGs. Shown are selected biological processes with a p-value of < 0.05.

The transcriptomic analysis revealed a total number of 219 differentially expressed genes between the airway epithelium of aged and young flies. The profile from aged flies showed a strong increase in many immune related DEGs. As shown in the heatmap from the 50 most regulated DEGs, antimicrobial peptides were among the most upregulated genes, such as *listericin*, *dro* and *dpt*. An enrichment analysis revealed a broad range of involved immune responses in old flies compared to young flies. Moreover, a set of xenobiotic

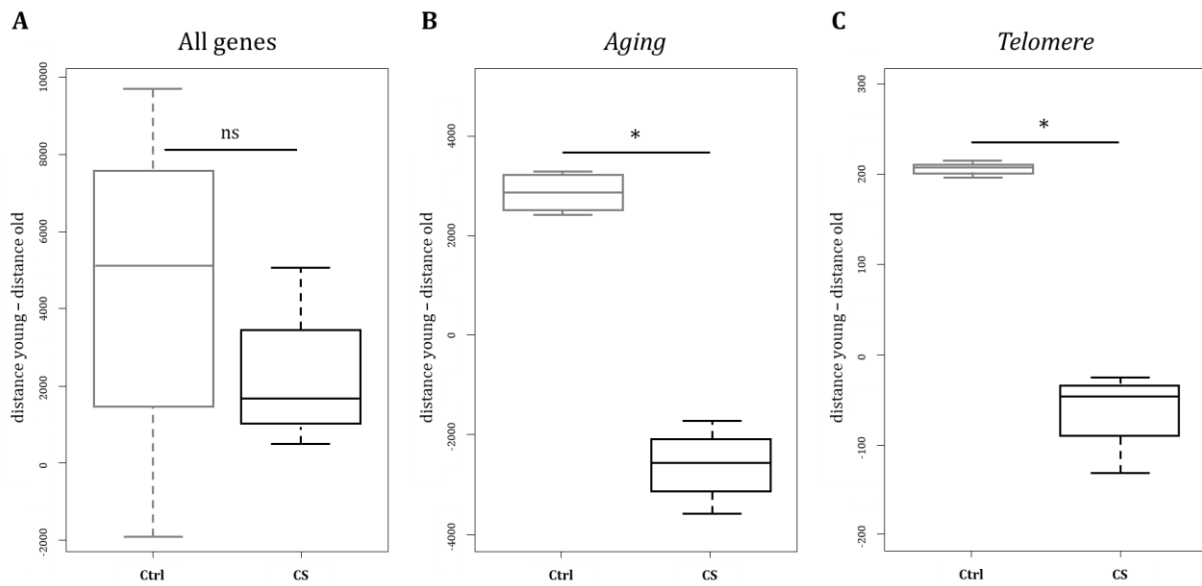
response related genes like *metallothionin* were upregulated in trachea from 52 d old flies. These genes led to an enrichment of redox homeostatic GO terms *oxidation reduction process* and *metal ion homeostasis*. Downregulated DEGs were defined by fat metabolism processes like *fatty acid elongation*, *fatty acid biosynthetic process* or *long-chain fatty-acyl-CoA metabolic process*.

### 3.7 CS exposure induces age-related transcriptomic responses

To evaluate the hypothesis that COPD might be considered as premature aging of the lung, the transcriptomic profiles of CS exposed and aged airways were compared for overlapping patterns<sup>212</sup>. These patterns should pinpoint similarities or differences of the airway epithelium between both conditions. With these findings, the hypothesis of an accelerated lung aging in COPD patients should further be investigated to improve the knowledge about the pathology of COPD.

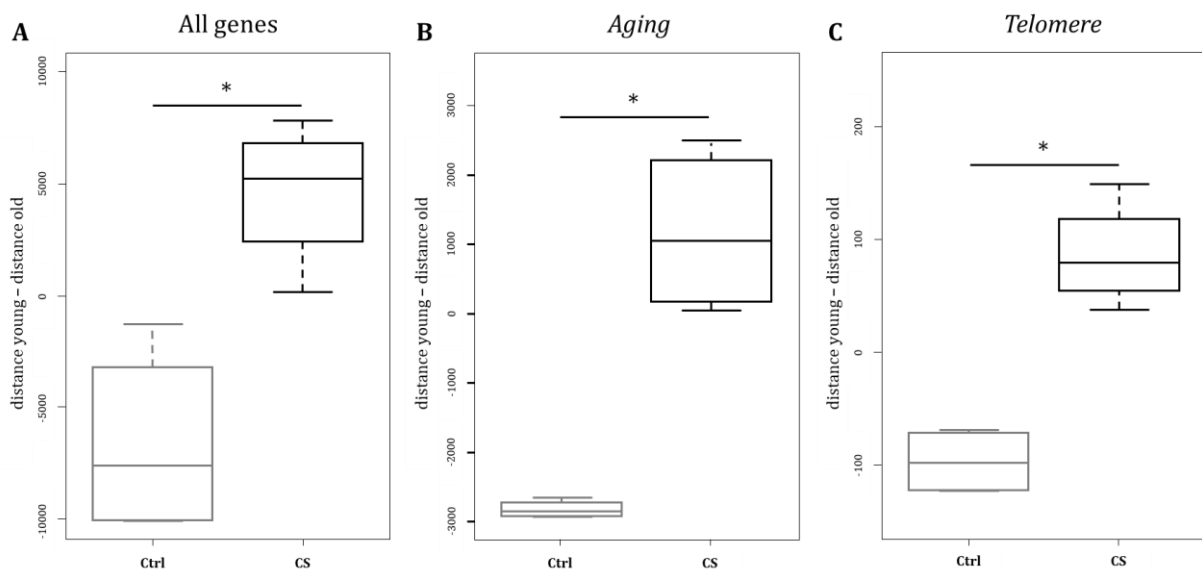
Because the transcriptomic profiles from 5 d and 15 d CS exposed airway epithelial cells showed substantially differences, both datasets were analyzed for potential similarities to aging. Therefore, euclidean distances were calculated for genes of young and old airways. The transcriptomic patterns of according genes from 5 d or 15 d CS exposed airways and corresponding controls were then projected into the distances of young and old airways.

As shown in Fig. 20 A, airways from 5 d CS exposed flies do not show a shift towards the profiles of young or old airways, when comparing all genes to the age matched control flies. However, the comparison of all genes which are assigned to the GO term *Aging*, revealed a significant shift towards profiles from young flies (Fig. 20 B). This result was concomitant with a likewise shift towards young airways, regarding genes from the *Telomere* associated GO terms (Fig. 20 C).



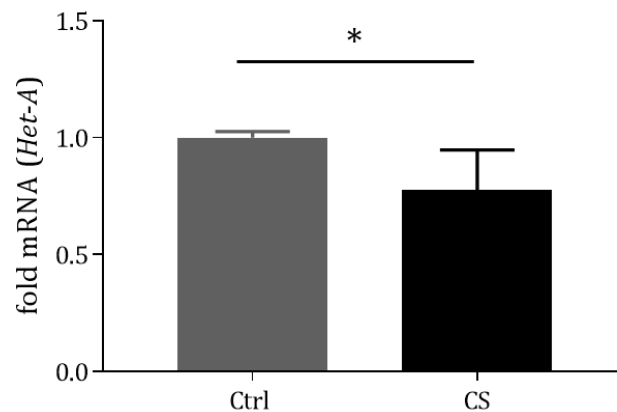
**Fig. 20 Comparison of transcriptomic profiles from 5 d CS exposed and old airways.** Euclidean distances for young and old flies were calculated and according distances from 5 d CS exposed airways and corresponding controls were projected into this matrix. **A** Comparison of profiles for all genes. **B** Genes that are assigned to the GO term *Aging* are shown. **C** All *Telomere* GO term associated genes are displayed. Whiskers show min to max range. ns = not significant, \* =  $p < 0.05$ .

To further evaluate the observations in 5 d CS exposed flies, also 15 d CS exposed airways were analyzed for alignment towards aging profiles (Fig. 21). For all analyzed gene categories, there was a significant shift towards transcriptomic profiles of old airways observed.



**Fig. 21 Comparison of transcriptomic profiles from 15 d CS exposed and old airways.** Euclidean distances for young and old flies were calculated and according distances from 5 d CS exposed airways and corresponding controls were projected into this matrix. **A** Comparison of profiles for all genes. **B** Genes that are assigned to the GO term *Aging* are shown. **C** All *Telomere* GO term associated genes are displayed. Whiskers show min to max range. \* =  $p < 0.05$ .

Based on the observed shifts towards profiles from 15 d CS exposed airways towards old airways, it remained unclear if that shift also expresses phenotypically. To assess an age-related effect of CS exposure on the fly, the telomere composition was analyzed by qPCR. Therefore, genomic DNA was extracted from CS exposed flies and relative expression of the retrotransposable element *Het-A* was measured.



**Fig. 22 *Het-A* expression of CS exposed flies.** Genomic DNA from 10 d CS exposed flies was extracted and analyzed for *Het-A* expression by qPCR. \* =  $p < 0.05$ .

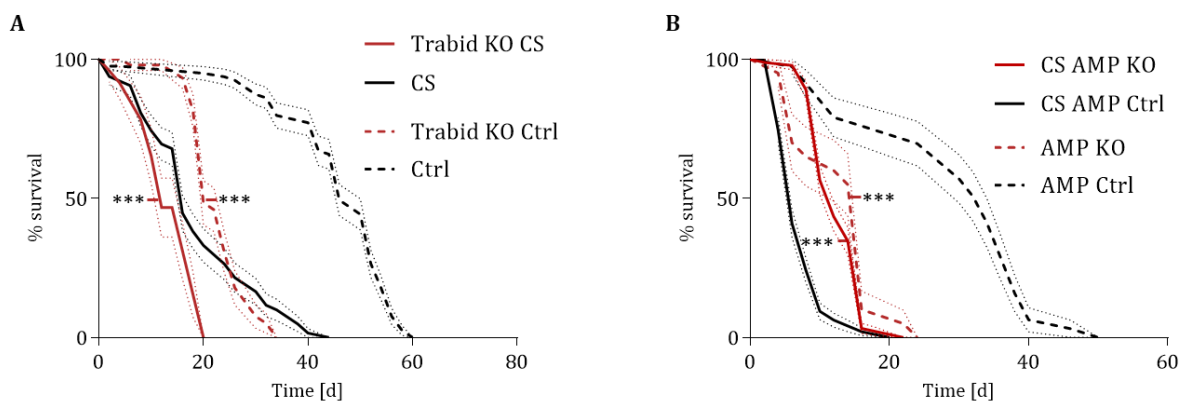
As shown in Fig. 22, the relative expression of the *Het-A* retrotransposon was significantly reduced upon CS exposure, compared to the expression of corresponding age matched control flies.

### 3.8 The immune system modulates lifespan during CS exposure

As shown in previous transcriptomic analyses (Fig. 16, Fig. 17), the innate immune system seems to be involved in a response to chronic CS exposure. However, the exact mode of response still remained unclear. To further elucidate the role of the innate immune system on the lifespan of CS exposed flies, the immune response was manipulated in those flies. To unravel the effects of immune responses on lifespan determination, survival analyses of genetically modified flies were performed. Therefore, fly lines with modulated immune responses were used. Since exposure to CS for different periods led to contradictory statements about the involvement of immune responses, an activated immune system was compared to an attenuated immune response.

First, a fly line that harbors a KO for *Trabid* was exposed to CS and analyzed for lifespan. *Trabid* is the negative regulator of IMD signaling and the absence of this regulator leads to a constant activation of the NF- $\kappa$ B transcription factor Relish and a subsequent

induction of IMD target genes<sup>162</sup>. Characterized by the regulation of diverse immune related genes, IMD mediates the immune system response in *Drosophila*<sup>161</sup>. When exposed to CS, Trabid KO flies live significantly shorter than corresponding control flies (Fig. 23 A). With a median lifespan of 12 d compared to 20 d of the control, Trabid KO flies live 25 % shorter. Also, untreated Trabid KO flies live significantly shorter by 57 % than the corresponding, untreated control flies with a median lifespan of 12 d compared to 20 d.



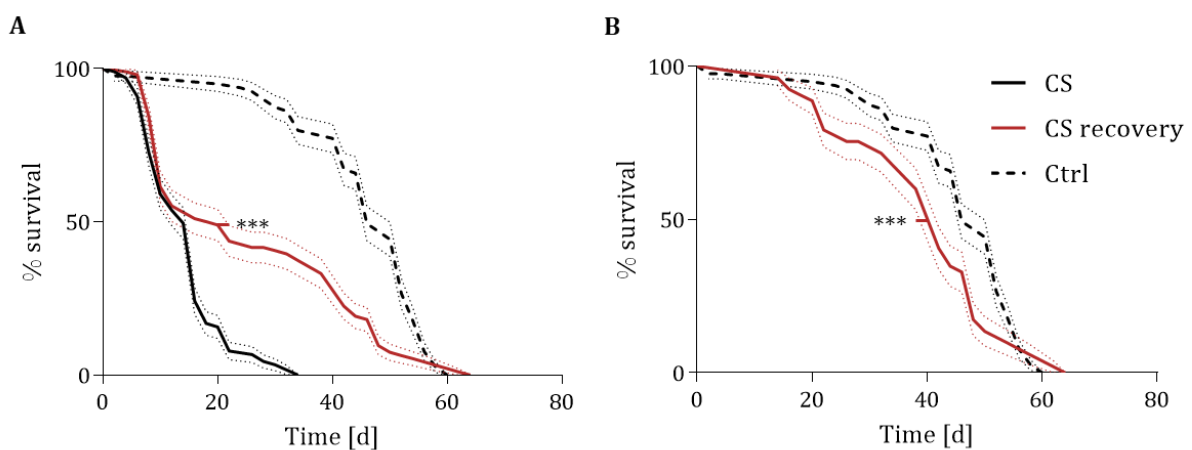
**Fig. 23 A modulated immune system affects the lifespan of CS exposed flies.** Manipulation of the immune system in cigarette smoke (CS) exposed flies. **A** Lifespan of CS exposed Trabid KO flies compared to corresponding CS exposed control flies ( $w^{1118}$ ) and untreated control flies both, from the KO and the control (Ctrl) **B** Lifespan of CS exposed flies that harbor a KO for all AMPs in the fly compared to the corresponding control and untreated control flies from the KO and the control. Error indicators are shown in dotted lines and represent SD. \*\*\* =  $p < 0.001$ ,  $n = 54 - 96$ .

In order to additionally evaluate the obtained results from an activated immune system, the opposite effects of an attenuated immune system were assessed. Based on the observed differential expression of diverse AMPs in response to CS, a fly line that harbors a CRISPR/Cas9 mediated knock-out for 10 of the 14 known AMPs in *Drosophila* was exposed to CS and compared to the corresponding genetic control<sup>213</sup>. As shown in Fig. 23 B, the absence of AMPs significantly increased the lifespan of CS exposed flies by 50 % compared to the corresponding genetic control. The median lifespan of AMP KO flies was 12 d compared to the median lifespan of 6 d of the corresponding control. In contrast, untreated AMP KO flies lived significantly shorter than corresponding control flies (Fig. 23 B).

### 3.9 CS cessation does not completely rescue CS induced effects in *Drosophila*

As a chronic and irreversible disease, COPD causes long lasting phenotypic changes that persist even after smoking cessation<sup>214</sup>. In human patients, smoking cessation has positive effects on the deceleration of the progression of the disease<sup>215</sup>. To evaluate long-term effects of CS on *Drosophila*, several physiologic parameters were analyzed after 10 d of CS exposure and a subsequent recovery phase for 14 d of w<sup>1118</sup> flies.

The CS cessation after 10 d CS exposure led to a substantially increased lifespan by 260 % with a median lifespan of 42 d compared to 16 d from constantly CS exposed flies (Fig. 24 A). However, this cessation did not fully rescue the lifespan to the extent of untreated control flies. When comparing the lifespan after CS cessation to untreated flies, CS recovered flies lived 10 % shorter with a median lifespan of 42 d compared to 46 d (Fig. 24 B).

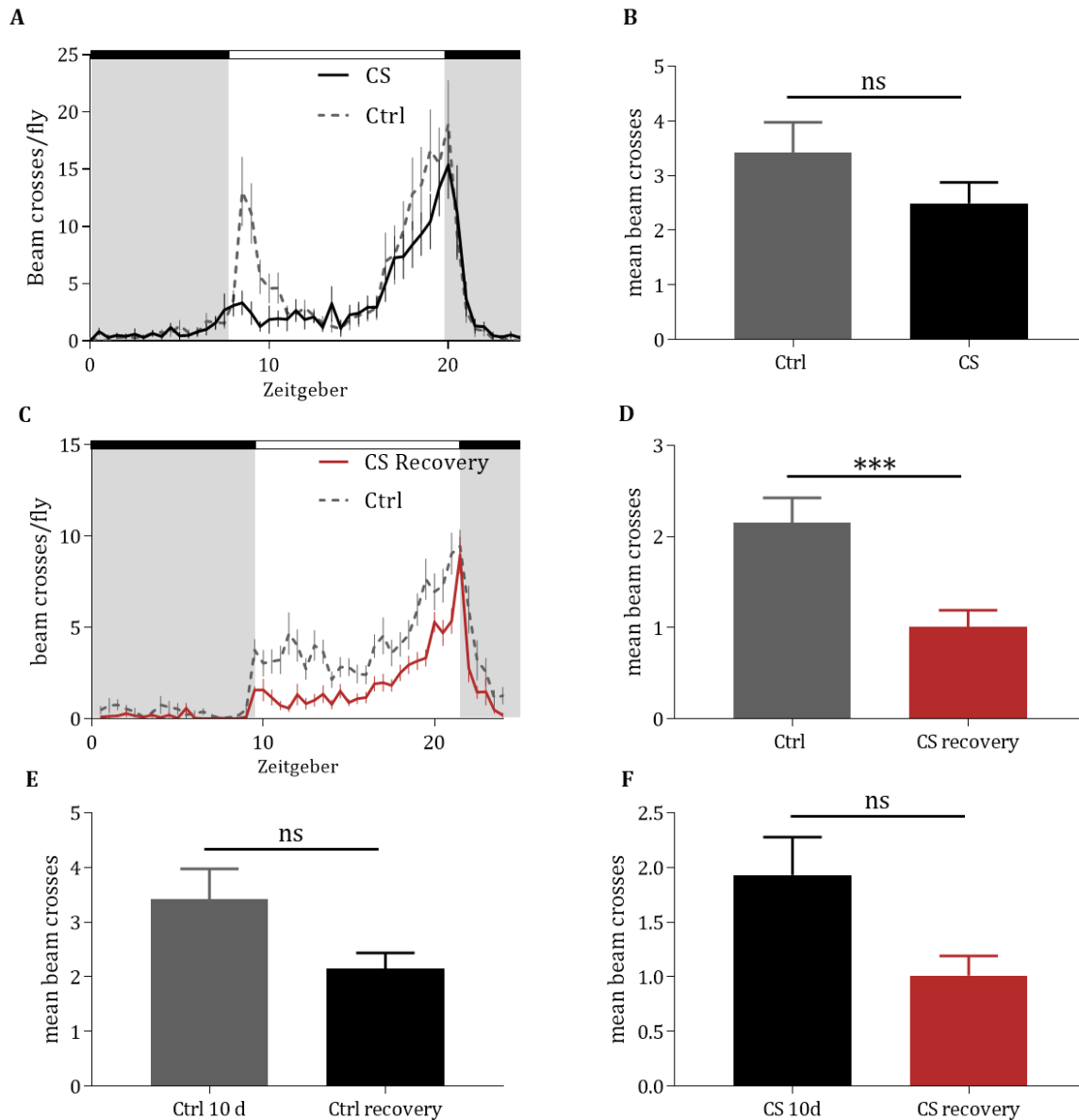


**Fig. 24 CS exposure has long-lasting and chronic effects on the lifespan of *Drosophila*.** **A** Lifespan of CS exposed (CS), recovered flies after 10 d CS exposure (CS recovery) and untreated w<sup>1118</sup> flies (Ctrl). **B** Comparison of lifespan from CS recovered flies and Ctrl flies after an initial phase of 10 d CS exposure. Error indicators are shown in dotted lines and represent standard deviation. \*\*\* =  $p < 0.001$ ,  $n = 80 - 101$ .

Besides to an altered lifespan after CS cessation, also the locomotor activity was impaired after the recovery phase (Fig. 25). After 10 d of CS exposure the locomotor activity of CS exposed flies was not significantly reduced. However, after a cessation phase of 14 d CS recovered flies showed a significantly reduced locomotor activity with approximately one beam crossing in 30 min compared to two beam crosses of corresponding control flies (Fig. 25 C, D). To evaluate the effects of an aging organism, additional comparisons for the locomotor activity between 10 d and 24 d old control flies were made. As shown in Fig. 25 E, the overall activity of 24 d old flies is not significantly decreased compared to 10 d



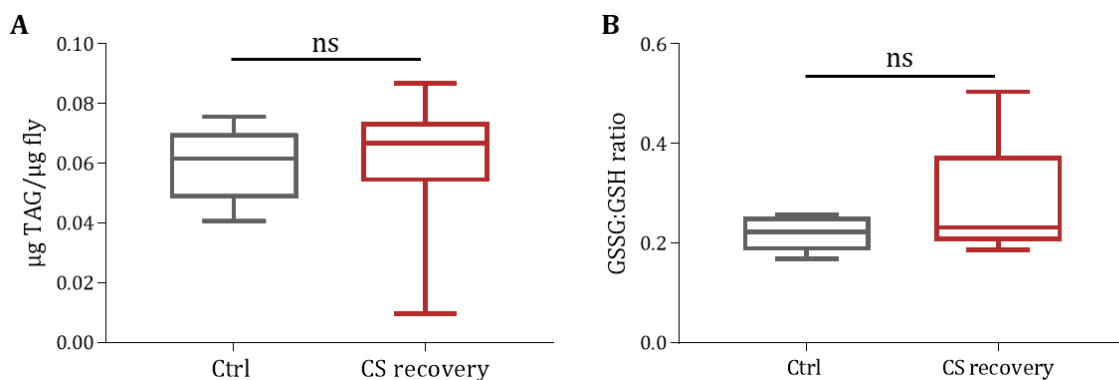
old flies. To assess whether there are long-term effects of CS exposure on the locomotor activity, CS recovered flies were compared to flies exposed for 10 d to CS. Similar to untreated control flies, the locomotor activity of CS recovered flies is reduced but without significant differences.



**Fig. 25 CS exposure has long lasting effects on locomotor activity that can be inhibited by cessation.**

Locomotor activity measurements were performed with female  $w^{1118}$  flies and the activity was monitored using a locomotor activity monitor system (LAM). **A** Locomotor activity pattern of 10 d CS exposed flies (CS) and age-matched, untreated control flies (Ctrl). **B** Overall activity of 10 d CS exposed flies compared to control flies. **C** Locomotor activity pattern flies after a recovery phase of 14 d after an initial CS exposure period for 10 d (CS recovery). **D** Overall activity of CS recovered flies compared to untreated control flies. **E** Overall activity of 10 d old untreated control flies compared to untreated control flies after a time period of 14 d. **F** Overall activity of 10 d CS exposed compared to CS recovered flies. Overall activities shown in corresponding bar plots display mean beam crosses per fly in 30 min. Error bars represent SEM. ns = not significant, \*\*\* =  $p < 0.001$ ,  $n = 32$ .

Based on the observed impairments of CS on body fat content and GSH metabolism (Fig. 7 B, D), the effects of CS cessation should be examined for these parameters. The reduced body fat content after 10 d CS exposure (Fig. 7 B), could be rescued by a recovery phase of 14 d after CS cessation. The body fat content of recovered flies was not significantly different compared to control flies (Fig. 26 A). Moreover, the increased ratio of GSSG to GSH after 10 d CS exposure (Fig. 7 D) was reduced to the extent of the control flies after the 14 d recovery phase (Fig. 26 B).



**Fig. 26 Cessation of CS exposure rescues impaired body fat content and redox levels.** **A** Body fat content of 14 d CS recovered female  $w^{1118}$  flies compared to untreated and age matched flies. Shown are the amounts of triglycerides (TAG) in relation to the body weight per fly.  $n = 10$ . **B** Ratio of oxidized glutathione (GSSG) to reduced glutathione (GSH) of 14 d CS recovered flies compared to untreated and age matched control flies.  $n = 5-7$ . Whiskers show min to max range. ns = not significant

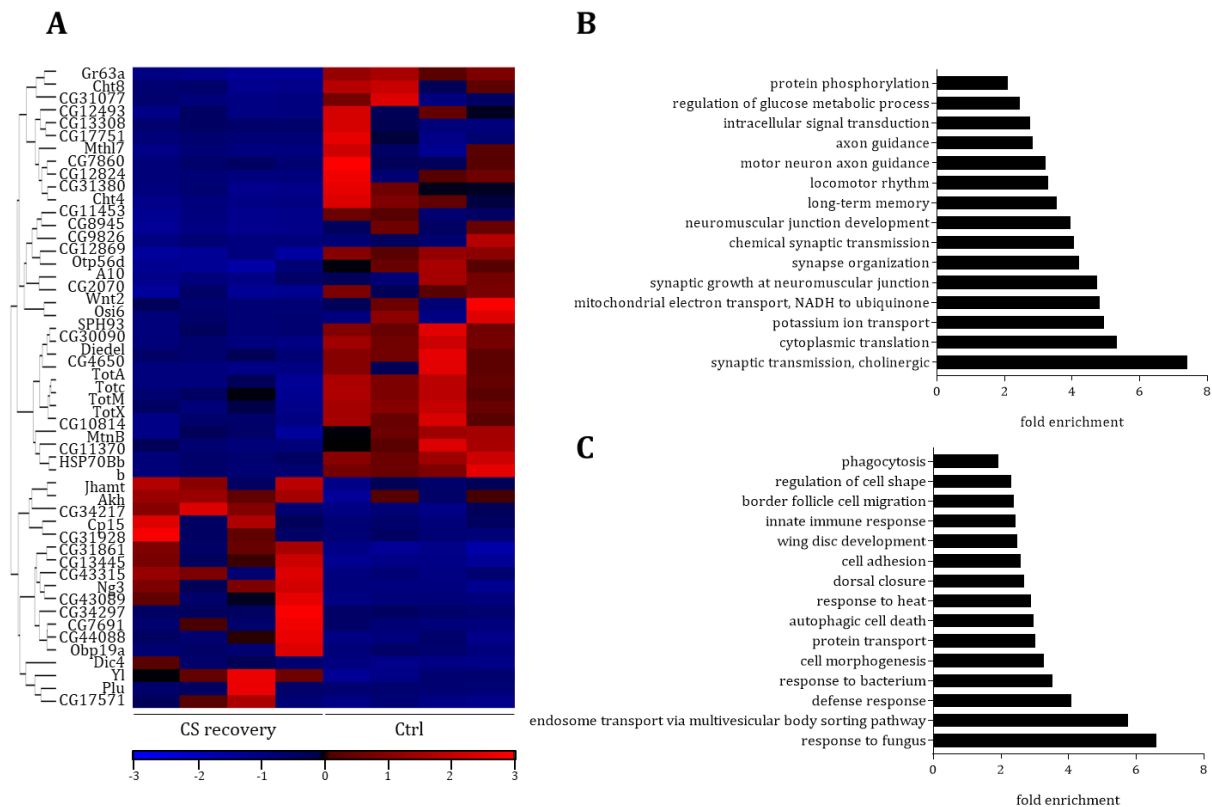
It was shown that the cessation of CS exposure has beneficial effects on the physiology of *Drosophila* and could partly reverse CS induced effects (Fig. 24-Fig. 26). However, the exposure to CS has long-lasting and chronic effects on the lifespan of *Drosophila*, that could not be conveniently explained by examined physiologic parameters.

### 3.10 CS exposure induces a long-lasting transcriptomic alteration after cessation

Even though the cessation of CS exposure had beneficial effects on the survival of flies, this intervention could not fully compensate negative effects of CS treated flies compared to untreated ones (Fig. 24). This could not be explained by the examined physiologic parameters (Fig. 25, Fig. 26), the underlying causes of this chronic impairment remained unclear. To further elucidate potential mediators in this long-lasting response, an RNA sequencing experiment was performed. Therefore, airways from 14 d CS recovered, female  $w^{1118}$  flies and age matched control flies were analyzed.

A total number of 2461 DEGs resulted from the transcriptomic comparison of CS recovered airways and untreated control airways. As shown in the heatmap of Fig. 27,

the 50 strongest regulated DEGs are displayed. The most downregulated genes are the turandot coding genes *totX* and *totM*. Besides to *tot* genes there was a broad range of immune related genes, such as various AMP coding genes like *listericin*, *dipt*, *dro* or *att* that were downregulated in CS recovered airways. Moreover, the gene *diedel* was highly downregulated. *Diedel* is involved in the determination of lifespan<sup>216</sup>.



**Fig. 27 Transcriptomic analysis of airway epithelial cells after CS cessation.** **A** Heatmap of the 50 most differentially expressed genes of  $w^{1118}$  female flies that were initially exposed to CS for 10 d with a subsequent recovery phase of 14 d, compared to age matched and untreated control flies. Genes with an FDR corrected p-value of  $< 0.05$  are shown. **B** GO enrichment analysis of all 1254 upregulated DEGs. Shown are selected biological processes with a p-value of  $< 0.05$ . **C** GO enrichment analysis of all 1207 downregulated DEGs. Shown are selected biological processes with a p-value of  $< 0.05$ .

To further investigate the biological meaning of these regulated genes, a GO analysis was performed. Upregulated and downregulated genes were separately analyzed for enriched biological processes and the 15 most significant terms were plotted in Fig. 27. As shown in Fig. 27, B, downregulated genes were strongly characterized by diverse immune related GO terms like *phagocytosis*, *innate immune response*, *response to bacterium* or *response to fungus*. Moreover, there were morphology related GO terms enriched in downregulated DEGs such as *regulation of cell shape*, *dorsal closure* or *cell morphogenesis*.

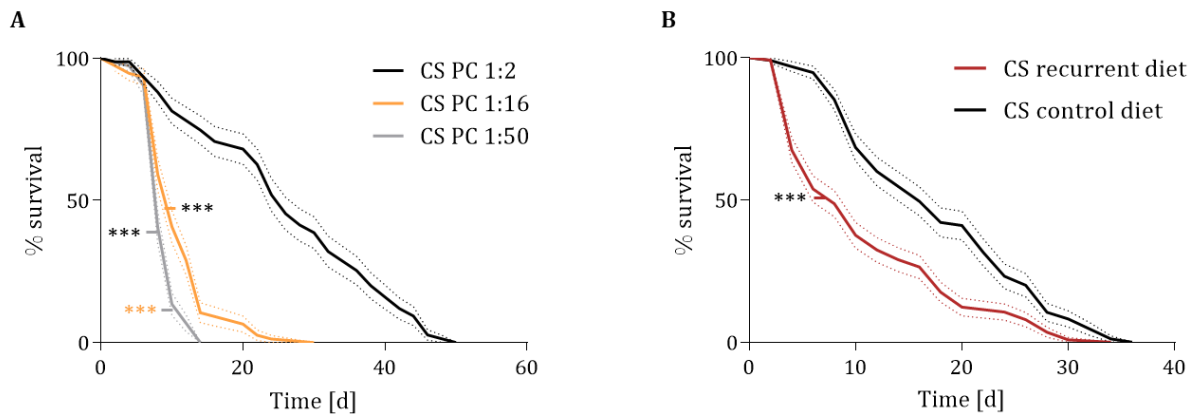
In contrast to that, upregulated DEGs were mainly defined by neural related GO terms such as *axon guidance*, *synapse organization* or *synaptic transmission, cholinergic* (Fig. 27 B).

### 3.11 Protein restricted diets decrease lifespan during CS exposure

Based on symptoms of undernutrition in COPD patients, it was suggested that nutritional uptake has an influence on the pathophysiology of the development of COPD<sup>217</sup>. The application of nutritional interventions was shown to have beneficial effects on the lung function of COPD patients and improved disease burden<sup>218</sup>.

To examine the effects of protein availability during CS exposure on the lifespan of *Drosophila*, a chemically defined holidic diet was used<sup>219</sup>. This diet allows for a targeted manipulation of every single component of this diet. Based on previously reported benefits of a dietary restricted (DR) media for lifespan<sup>>220</sup><sup>>220</sup>, the effects of a limited amino acid content were investigated in CS exposed flies<sup>220</sup>. Additionally, as a further prove of importance of a dietary intervention, an amino acid diminished diet was chosen. CS exposed, female w<sup>1118</sup> were cultured on the corresponding diets and were then compared to flies cultured on a control diet.</sup></sup>

As shown in Fig. 28, on DR media cultured flies with a protein to carbohydrate ratio of 1:16 (PC 1:16) lived significantly shorter than flies cultured on the control diet (PC 1:2). With a median lifespan of 10 d compared to 26 d of flies on the control diet, the dietary restricted media decreased lifespan by 62 %. Concomitant to the effects of a protein restricted diet, flies cultured on a protein diminished diet (PC 1:50) lived even shorter when exposed to CS. The median lifespan of 8 d is significantly shorter compared to both PC 1:16 and PC 1:2 diets.



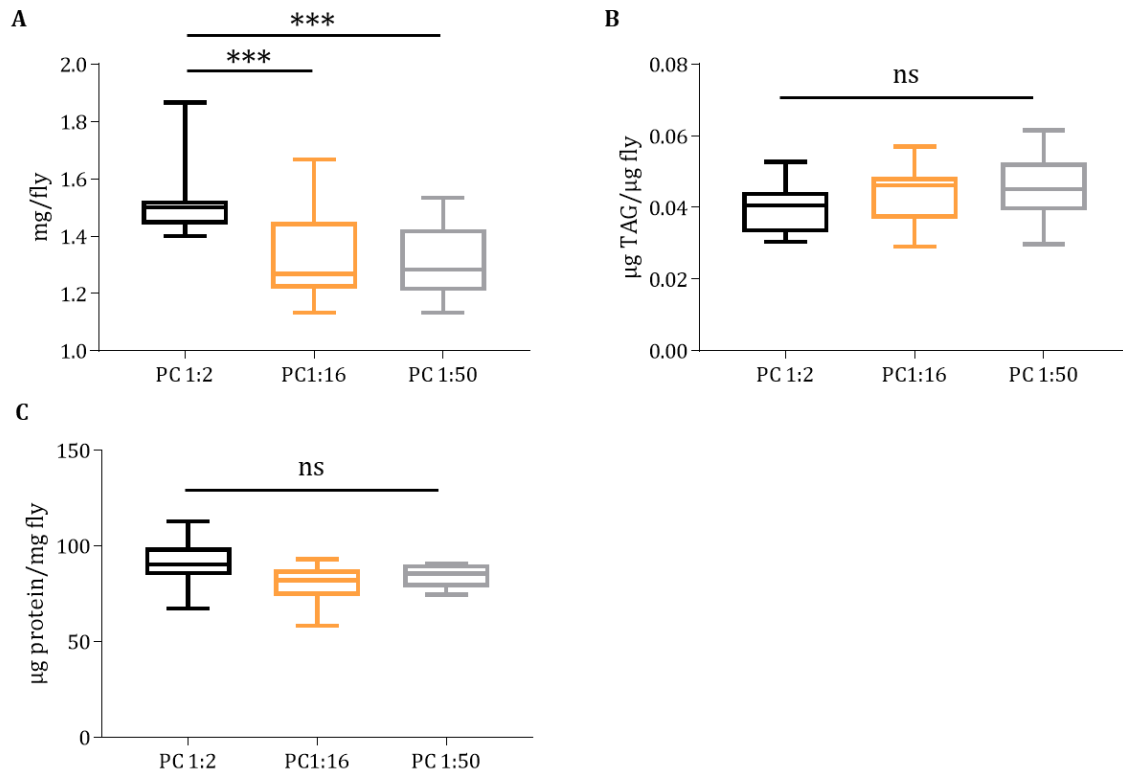
**Fig. 28 Protein availability affects the lifespan of CS exposed flies.** **A** Cigarette smoke (CS) exposed female  $w^{1118}$  flies cultured on media with restricted protein to carbohydrate ratios (PC). Lifespans of flies on dietary restriction (PC 1:16) diet and protein diminished diet (PC 1:50) were compared to the control diet (PC 1:2) during CS exposure.  $n = 75$ . **B** CS exposed female  $w^{1118}$  flies cultured on alternating phases of dietary restriction and control media (recurrent diet), compared to flies kept on control medium.  $n = 101 - 117$ . Error indicators are shown in dotted lines and represent standard deviation. \*\*\* =  $p < 0.001$ .

As there were no beneficial effects of a DR intervention on the lifespan of CS exposed flies, another approach was carried out to mimic molecular effects of DR intervention without constitutively restricting the calorie intake. The lifespan prolonging effect of DR media relies on reduced insulin and Target of Rapamycin (TOR) signaling, which in turn increases stress resistance<sup>221-223</sup>. In order to sustain these positive effects of DR signaling but simultaneously bypass negative effects of a calorie restricted diet, flies were kept on alternating DR medium and control medium. Female  $w^{1118}$  flies were cultured on this recurrent diet during CS exposure and lifespan was compared to flies kept constantly on the control diet. As shown in Fig. 28 B the lifespan of flies kept on the recurrent diet was significantly reduced compared to kept flies on the control diet. The median lifespan of 8 d was reduced by 50 % compared to 16 d of flies on the corresponding control medium.

### 3.12 Nutrition regulates body composition and GSH metabolism of CS exposed flies

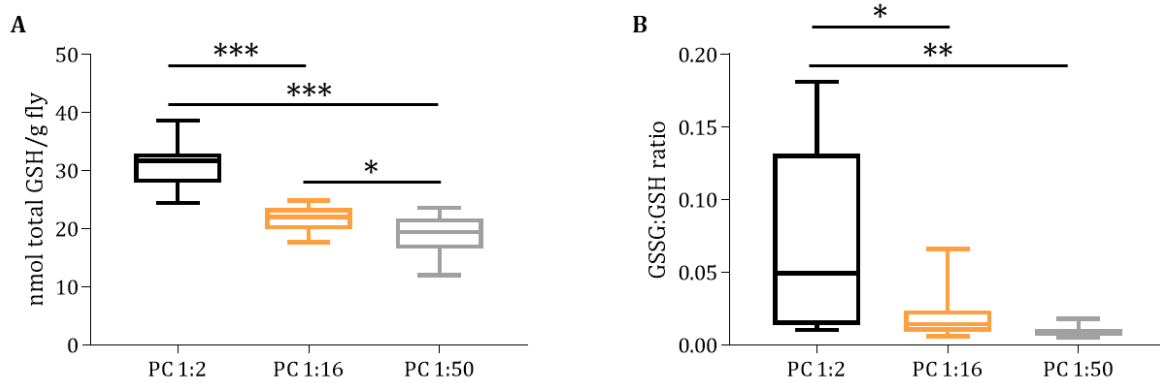
The underlying causes for a reduced lifespan in the different dietary interventions were not clear, so the body composition of CS exposed flies cultured on PC 1:2, PC 1:16 and PC 1:50 diets was analyzed.

Flies cultured on the PC 1:2 control diet had a significantly higher body weight than flies on the protein restricted diets (Fig. 29 A). To further examine this influence on the body composition, body fat content and protein levels were measured. As shown in Fig. 29 B, C, both, protein and body fat contents were not significantly altered in CS exposed flies, cultured on the three different diets.



**Fig. 29 Effects of nutritive intervention on body composition during CS exposure.** Female  $w^{1118}$  flies cultured on diets with different protein to carbohydrate ratios (PC) and cigarette smoke (CS) exposed for 10 d. Flies on the control diet (PC 1:2) were compared to a dietary restriction diet (PC 1:16) and an amino acid diminished diet (1:50). **A** Body weight of CS exposed flies on the three different diets.  $n = 10$ . **B** Body fat measurement of CS exposed flies cultured on the diets. The amounts of triglycerides were related to the corresponding body weight per fly.  $n = 8-10$ . **C** Protein content of CS exposed flies cultured on the diets, related to the corresponding body weight per fly.  $n = 6-10$ . Whiskers represent min to max range. ns = not significant.

Due to the lack of differences in relative body composition, it still remained unclear what led to a reduced lifespan of flies on the protein restricted diets during CS exposure. To further explain the nutritive effects on lifespan, the GSH metabolism was analyzed in  $w^{1118}$  flies on the three different diets. As shown in Fig. 30 A 10 d CS exposed flies on the control diet had significantly more total GSH (GSH + GSSG) than flies on PC 1:16 and PC 1:50 diets. The amount of total GSH in flies on the PC 1:50 diet was significantly lower than flies on the PC 1:16. However, the ratio from GSSG to GSH was significantly higher in control diets, compared to both protein restricted diets (Fig. 30 B).

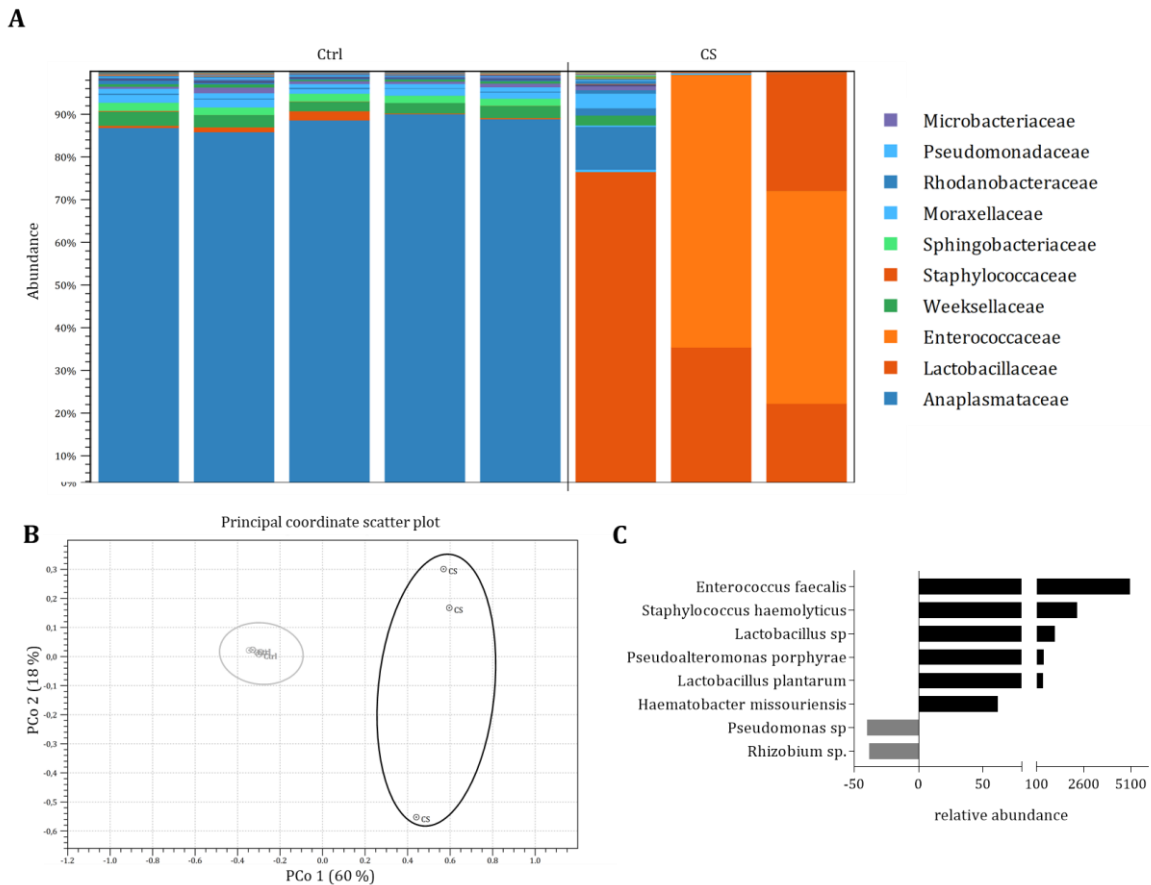


**Fig. 30 The GSH metabolism is affected during nutritive intervention of CS exposed flies.** 10 d cigarette smoke (CS) exposed, female  $w^{1118}$  flies cultured on diets with different protein to carbohydrate ratios (PC). Flies on the control diet (PC 1:2) were compared to a dietary restriction diet (PC 1:16) and an amino acid diminished diet (1:50). **A** Total glutathione (GSH) levels, calculated by the addition of oxidized (GSSG) and reduced glutathione (GSH) related to the according body weight. **B** Ratio of GSSG to GSH.  $n = 9-10$ . Whiskers represent min to max range. \* =  $p < 0.05$ , \*\* =  $p < 0.01$ , \*\*\* =  $p < 0.001$ .

### 3.13 CS exposure affects the intestinal microbial composition

As previously shown, CS exposure had an effect not only on the transcriptome of airway epithelial cells but also on other physiologic parameters of *Drosophila* such as lifespan, locomotor activity or body fat content (Fig. 7, Fig. 8). In order to investigate if there is a direct crosstalk between the airway epithelium and other tissues, the microbial composition of the intestine was examined. The gut and the respiratory system are directly connected via the oxygen supplying terminal cells of the tracheal system.

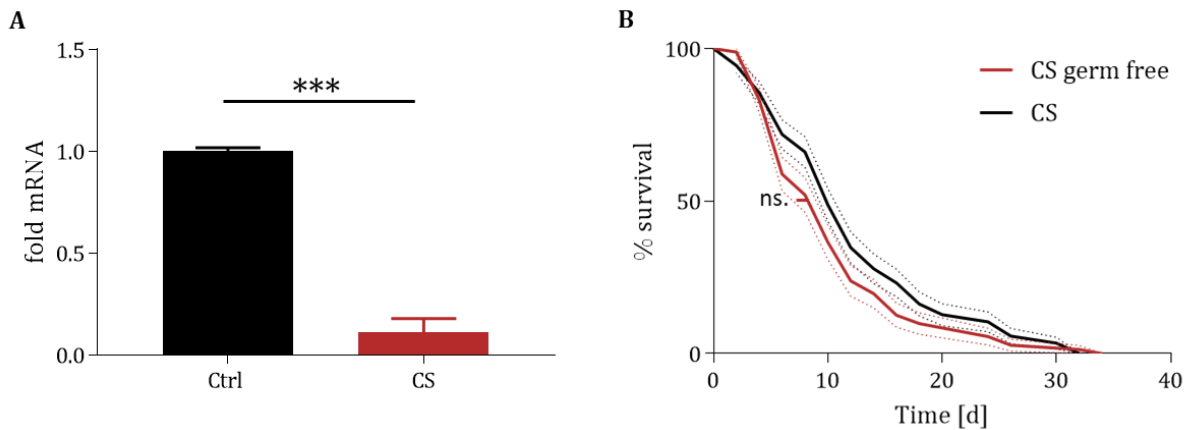
Female  $w^{1118}$  flies were exposed to CS for 10 d, DNA was isolated from intestines and subsequently a 16S rDNA sequencing experiment was performed (Fig. 31). A principal component analysis (PCoA) showed a distinct clustering between intestines from control flies and CS exposed flies (Fig. 31 B). As shown in Fig. 31 A, the abundances of operational taxonomic units (OTUs) on the family level are composed differently between both treatment groups. In control flies, the majority of all annotated bacterial families were *Anaplasmataceae*, whereas in CS exposed flies the most abundant families were *Lactobactillaceae*, *Staphylococcaceae* and *Enterococcaceae*. From these families, a total number of 8 annotated OTUs were differentially abundant between both groups. Except for *Pseudomonas sp.* and *Rhizobium sp.* all other OTUs like *Lactobacillus plantarum*, *Staphylococcus haemolyticus*, or *Enterococcus faecalis* were heavily enriched in intestines from CS exposed flies compared to untreated flies.



**Fig. 31 16S rDNA analysis of intestinal microbial composition from CS exposed flies.** For the microbiome analysis of intestines, conventional  $w^{1118}$  female flies were exposed to CS for 10 d. **A** Abundance analysis for annotated OTUs on family level. **B** Principle component analysis (PCoA) of cigarette smoke exposed (CS) and control flies (Ctrl). **C** Differentially abundant OTUs between CS exposed intestines and untreated control intestines with an FDR corrected p-value of  $< 0.05$ .

To further assess whether CS exposure not only has an effect on the microbial composition but also on bacterial load, a qPCR experiment was performed. As shown in Fig. 32 A, the intestinal bacterial load was significantly reduced after CS exposure for 10 d by approximately 90 %. Based on the observed effects of CS exposure on the gut microbiota, it was still unknown whether there also is communication from the microbiota towards the host during CS exposure. To elucidate effects of the intestinal microbiota on the hosts physiology during CS exposure, female  $w^{1118}$  were initially made germ-free. These germ-free flies were then exposed to CS and analyzed for lifespan. As shown in Fig. 32 the lifespan of CS exposed and untreated flies did not significantly differ.





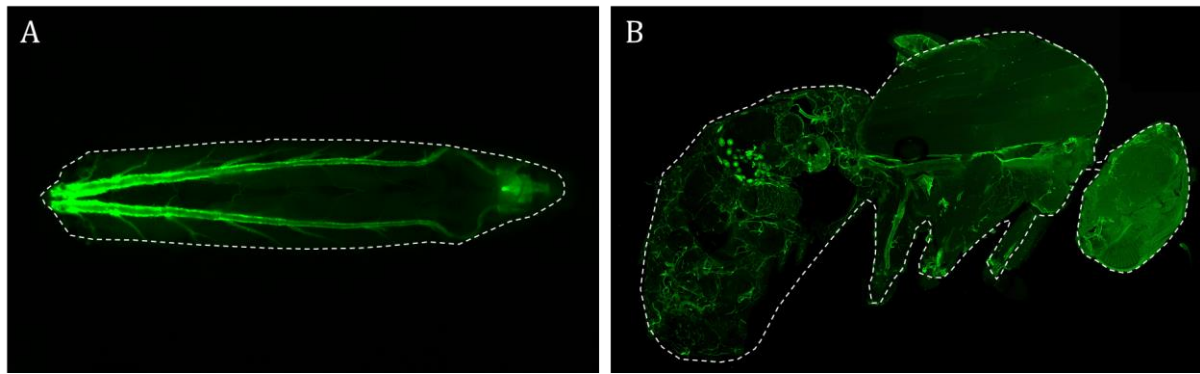
**Fig. 32 CS exposure reduces bacterial load, which has no effect on the lifespan determination. A** Female  $w^{1118}$  flies were exposed to cigarette smoke (CS) for 10d, DNA from the gut was extracted and the intestinal bacterial load was measured by qPCR with a V2 primer.  $n = 5$ . Shown are mean values with error bars that indicate standard deviation. **B** Conventional female  $w^{1118}$  flies were initially made germ-free by culturing them on media containing ampicillin (100 mg/ml), kanamycin (50 mg/ml) and tetracyclin (5 mg/ml). These germ-free flies were kept on the antibiotics medium, exposed to cigarette smoke (CS) and lifespan was compared to conventional CS exposed flies. ns = not significant,  $n = 87 - 90$ .

### 3.14 The tracheal system changes during metamorphosis from larvae to adult flies

Due to the complex structure of the adult tracheal system, lacking experimental approaches limit the accessibility to this tissue. A novel experimental approach to extract RNA from adult tracheal cells by dissection and the subsequent amplification of transcribed cDNA was used to further characterize the transcriptome of adult trachea. This dataset was compared with the transcriptome from 3<sup>rd</sup> instar larvae.

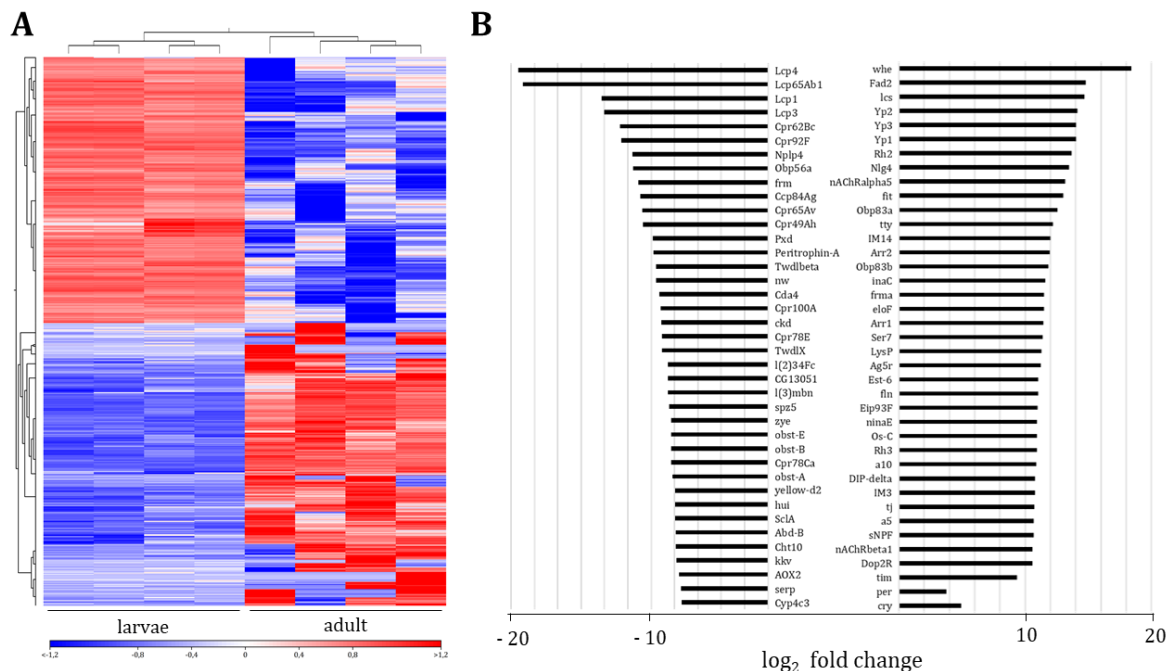
#### 3.14.1 The larval and adult tracheal systems have a distinct morphology and transcriptome

During metamorphosis from larvae to imago the structure and physiology of the animal drastically changes. Due to the remodeling of whole tissues like muscle, fat body or ovaries, the respiratory system must adopt to these structural changes in order to guarantee for oxygen supply of all organs in *Drosophila*. As shown in Fig. 33 the rather simple structure of the larval tracheal system changes in structure after metamorphosis to an adult fly.



**Fig. 33 Structural differences between the larval and adult respiratory system.** **A** Specific GFP expression in larval tracheal cells of a *Nplp4* reporter line. **B** Tracheal specific GFP expression of a longitudinal section from a *Btl-GAL4 > UAS-GFP* crossing. The GFP signal was enhanced by using a GFP booster probe.

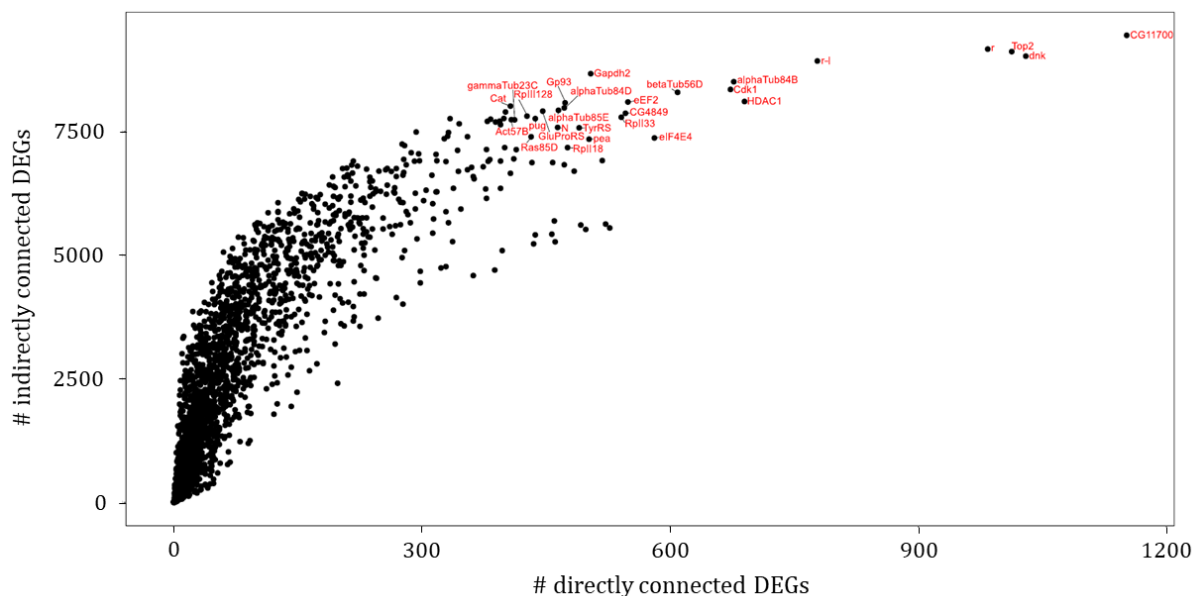
Based on the structural changes of the respiratory system, it was supposed that there are also physiologic changes of the tracheal system between both developmental stages of the fruit fly. However, these differences were largely unknown and it was not clear which molecular patterns defined larval and adult trachea. To address this question, an RNA sequencing experiment was performed with larval and adult airway epithelial cells and transcriptomic profiles were compared.



**Fig. 34 Transcriptomic profiles from adult and larval airway epithelial cells.** **A** Heatmap of DEGs from adult *w<sup>1118</sup>* airway epithelial cells compared to airway epithelial cells from *w<sup>1118</sup>* 3<sup>rd</sup> instar larvae. **B** Shown are the 39 most up- and downregulated DEGs with an FDR corrected p-value of < 0.05. Positive  $\log_2$  fold change values represent DEGs upregulated in adult trachea, whereas negative values indicate DEGs upregulated in larval trachea.

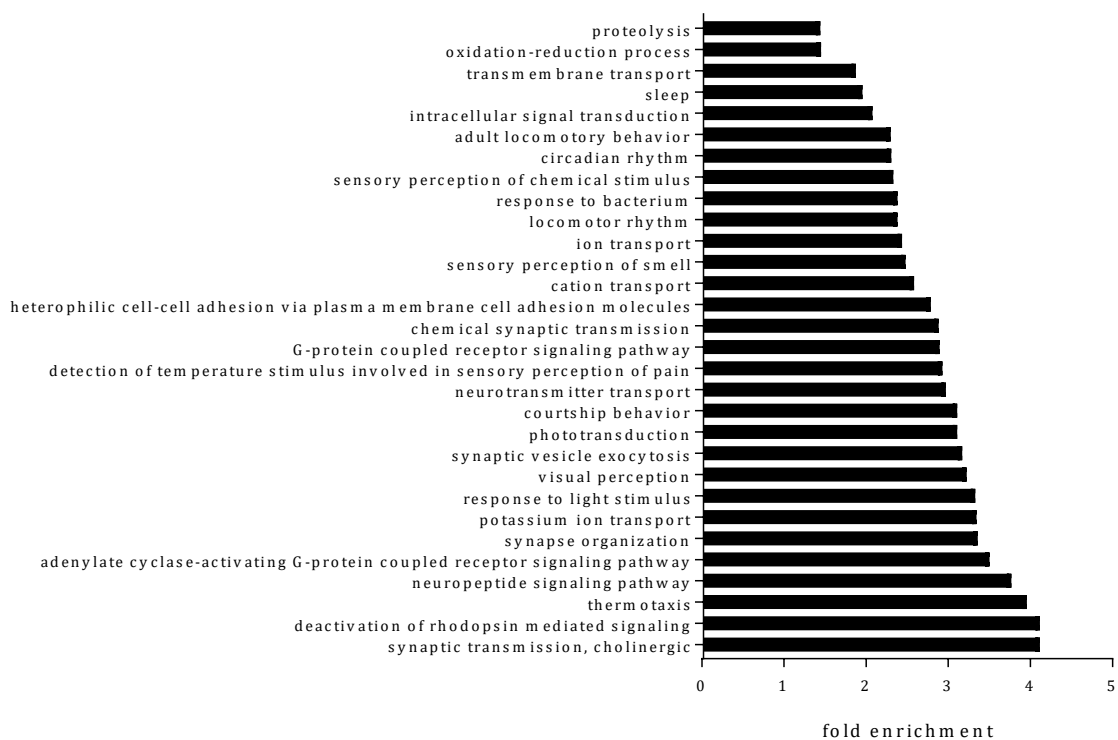
Airway epithelial transcriptomes of both developmental stages clustered well from each other and a total number of 6464 genes were differentially expressed and the most regulated genes are displayed in Fig. 34 B. The most upregulated genes in larval airway epithelial cells compared to the adult trachea are *larval cuticle proteins (Lcp)* from different classes. Amongst these genes also cell morphology related genes like *obstructor (obst)* were identified. In the adult system are various receptors such as the *nicotinic acetylcholine receptor (nAChR)* or the *dopamine receptor (Dop2R)* upregulated. Interestingly, compartments of the circadian clock were upregulated in the adult tracheal system as well. The three upregulated genes *timeless (tim)*, *period (per)* and *cryptochrome (cry)*, indicate the presence of a circadian clock in the adult respiratory epithelial cells.

Due to the high number of DEGs a complex network of connected genes resulted from a network analysis. For visualization purposes this network was converted to a dot plot, that plots the number of direct connections to indirect connection for each DEG. As shown in Fig. 35 the DEGs with the highest number of direct and indirect connections are displayed with red gene names. These genes were located in the center of the network and seem to be central mediators in the remodeling of the tracheal system during metamorphosis. Interestingly, a majority of these genes were structure giving genes like *gapdh2*, *alphaTub56D*, *betaTub56D* or *Act57B*.



**Fig. 35 Simplified network analysis from the transcriptomic comparison between adult and 3<sup>rd</sup> instar larval tracheal cells.** Complex network analysis simplified in a scatter plot that displays all DEGs. Each dot represents one DEG and is plotted against its number of direct and indirect connections to other DEGs within the network. Red names display the 30 DEGs with the most connections. Displayed DEGs have an FDR corrected p-value of < 0.05.

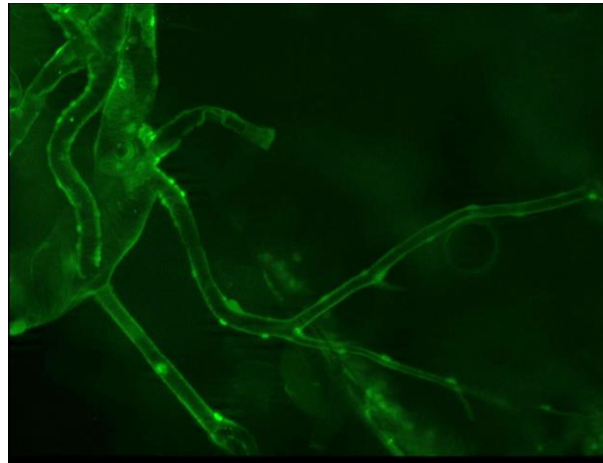
Based on these genes, a GO analysis was conducted to identify involved biological processes. A total number of 146 GO terms were significantly enriched in adult trachea, compared to larval 3<sup>rd</sup> instar trachea. In Fig. 36 the 30 most significant GO terms are displayed and reveal a broad array of involved biological process during the remodeling of the respiratory system between larvae and adult. The majority of enriched GO terms were signaling related processes. These terms are involved in various general responses such as *intracellular signal transduction*, *G-protein coupled receptor signaling pathway* or *adenylate cyclase-activating G-protein coupled receptor signaling pathway*. Also, more specific signaling processes like *neuropeptide signaling pathway* or *deactivation of rhodopsin mediated signaling* were enriched. Next to signaling GO terms there were behavior-related processes such as *adult locomotor activity* or *courtship behavior* enriched during remodeling of the trachea.



**Fig. 36 GO enrichment analysis of adult vs. 3<sup>rd</sup> instar larval airway epithelial cells.** Shown are the 30 most significant GO terms for biological processes. p-value < 0.05.

### 3.14.2 The adult airway epithelium expresses components of the circadian clock

Interestingly, transcriptomic analyses revealed genes related to the circadian rhythm that were upregulated in adult tracheal cells. Timeless (Tim), Period (Per) and Cryptochrome (Cry) are involved in mediating the circadian clock in *Drosophila*<sup>224,225</sup>. This observation was further approved by the GO analysis of biological processes, where circadian clock processes such as *circadian rhythm* and *sleep* were significantly enriched (Fig. 36). To visualize the location of *tim* expression in the trachea of adult flies, a reporter-line was used. As shown in Fig. 37 expression of *tim* was observed in the dorsal branches between abdominal segments one and two, where the dorsal branch starts to sprout out into the abdomen in order to properly supply organs with oxygen.



**Fig. 37 Expression of *tim* in the abdominal trachea.** Filet dissection of a GFP reporter line that visualizes timeless (*tim*) expression. Dorsal branches between the first two abdominal segments were analyzed for expression.

## 4 Discussion

### 4.1 *Drosophila melanogaster* as a novel model system to study CS induced effects

The major cause for the development of COPD is cigarette smoking<sup>19</sup>. Although there is much known about the symptoms that cigarette smoking causes, it is still not resolved in detail what drives these symptoms and how they interact with each other in further disease progression<sup>33</sup>. In order to improve our knowledge about this disease, functional research that aims to understand the underlying mechanisms is required. COPD is a chronic disease that usually manifests after very long periods of time. That makes research in the human system not only very time consuming but at the same time very difficult to obtain reproducible results, enabling to draw robust conclusions about disease development. Hence, animal models are highly demanded for studying disease pathophysiology<sup>226</sup>. In this study a novel invertebrate model was introduced for the research on CS induced effects on the airway system and its consequences on the physiology of the organism. Findings in this *Drosophila* model might later be transferred to the human system and contribute to our knowledge about the disease and finally drive the development of new treatment strategies.

Surprisingly, chronic exposure to CS resulted in the reproduction of major COPD hallmarks in *Drosophila*. Flies exposed to CS have a strongly reduced lifespan, impaired activity, decreased body fat content, an increased metabolic rate and an increased oxidative stress. All of these physiologic parameters are typically represented in COPD patients<sup>9,227-229</sup>. Combined with transcriptomic analyses of respiratory cells, it is obvious that CS induces a variety of response mechanisms that subsequently cause systemic physiologic alterations of the fly. Interference with these responses is seemingly easy by using pharmacological or genetic approaches. Intervention results in the fly can be uniquely screened with lifespan analyses and yield a powerful statement for the relevance during CS exposure. The utilization of *Drosophila* therefore seems reasonable to study the effects of CS on the airway epithelium. As previously described, *Drosophila* offers several advantages for the research on CS induced effects and proves to be an effective and useful tool to potentially study COPD underlying mechanisms.

#### 4.2 Nrf2 signaling mediates the detoxification response and extends lifespan during CS exposure by enhancing GSH metabolism

As described in 3.3, the activation of the Nrf2 binding motif ARE in the airways was induced by exposure to CS (Fig. 10). In turn, activation of the Nrf2 pathway induced the transcription of various target genes, that are related to an antioxidant response. A transcription factor binding site analysis revealed a potential regulation of *gstd2/5*, *gste7*, *gclc* and *prx2540* by Nrf2 in response to CS (Fig. 8). Moreover, the ectopic activation of Nrf2 either by the application with oltipraz or by introduction of a Keap1-RNAi resulted in an activated transcription of *gstd5* and *gclc* respectively. These molecules are known components of the glutathione metabolism and are involved in maintaining the cellular redox homeostasis. That implies the Nrf2 pathway to be an important regulator of glutathione metabolism, assuming a corporate detoxification role of these pathways in response to CS exposure in airway epithelial cells.

The cellular detoxification response is characterized by three distinct phases, that collectively assure for protection from xenobiotics. In phase I xenobiotics and electrophilic stressors are rapidly reduced by antioxidants like cytochrome P450 or peroxiredoxins. In phase II xenobiotics are scavenged by GSH in order to be disposed from the cell by transmembrane transporters in phase III. When looking at transcriptomic analyses from CS exposed airway epithelial cells, this detoxification response is represented at all phases in *Drosophila*. Phase I proteins like Cyp6a and Prx2540 are strongly overexpressed upon CS exposure both in larval and adult trachea. Moreover, the relevance of the GSH metabolism for survival during CS exposure was shown in chapter 3.4. This phase II response seems to be a central mediator of the response to CS in airway epithelial cells. Defined by the activation of several glutathione S-transferases from different classes (GstD, GstE), the conjugation of xenobiotics to GSH presumably is a major mechanism to maintain the redox balance of the cells. These conjugates can then be excreted from the cell via multidrug resistance proteins (MRP). The transcriptomic analyses from 3<sup>rd</sup> instar larval airway epithelial cells revealed an overexpression of the *mrp* gene upon CS exposure, indicating a relevance presumably to enhance clearing from scavenged xenobiotics that originate from CS.

As described in 3.3 an ectopic activation of the Nrf2 pathway was beneficial for survival of flies and increased the lifespan after CS exposure. This constitutive activation could be

achieved by an unspecific, pharmacological approach that had severe side effects in control flies that were not exposed to CS. Application of oltipraz presumably not only activated Nrf2 signaling in the trachea, via diffusion through the body, but also in other tissues and therefore induced artificial side effects. These side effects could slightly be attenuated from a decrease in survival by using a Keap1-RNAi. Nevertheless, the observed increase in lifespan by the activation of Nrf2 signaling during CS exposure probably relies on a subsequent activation of GSH related genes (Fig. 13, Fig. 14). The screening of involved GSH metabolism players revealed not only the importance of this pathway but also the complication in interfering with it. The availability of GSH is crucial for survival during CS but does not solely rely on total amounts of the peptide. As shown in Fig. 15, A-B, addition of GSH had no effects on the lifespan of CS exposed flies. However, depletion of GSH led to reduced lifespan. As GSH is crucially required for the survival of CS exposed flies, it is rather equally important to keep the ratio of GSSG to GSH as low as possible. As described in 3.4, overexpression of enzymes that catalyze the conjugation of xenobiotics to GSH led to a reduced lifespan upon CS exposure. Apparently, this decrease is caused by an artificial and unspecific shift of the GSSG:GSH ratio towards GSSG, preventing GSH to be an effective scavenger of xenobiotics. This assumption is further proved by an overexpression of the opposite enzymatic step of GSSG reduction by Trxr2. Since the ectopic overexpression of Trxr2 led to an increased lifespan upon CS exposure, it can be concluded that an shifted GSSG:GSH ratio is beneficial for cellular survival. Presumably a rapid reduction of GSSG to GSH increases GSH availability and therefore also enhances the detoxification capacity and finally helps for survival during CS exposure.

Both pathways have been shown to be involved in COPD pathology before. Nrf2 signaling was shown to be impaired in COPD patients and the reduced GSH form was identified to be depleted upon CS exposure in human lungs<sup>230,231</sup>. Thus, these pathways display potential targets to milden the burden of an increased oxidative stress in order to protect from cellular damage and maintain proper tissue function. Intervention with these pathways therefore could be a conceivable treatment option for COPD patients. This might give a short and rapid solution to decrease oxidative stress and prevent from consequences that subsequently might arise. Genetic damages or chronic inflammation that result in a vicious circle might be interrupted by interference with the Nrf2 and GSH pathways. However, these pathways appear to be extremely pleiotropic and are sensitive to ectopic activation that can cause severe side effects when brought out of balance.



Therefore, an appropriate manipulation of these pathways is required to assure for beneficial effects upon CS exposure. The targeted and lung specific intervention is required to be tightly controlled for strength and time of application.

### 4.3 Airway epithelium responses to CS exposure are dose and age dependent

COPD is a progressive disease that is not only dependent on the dose and time of cigarette smoking but also on the age of the patient. These multifactorial causes result in distinct stages of the disease that are uniquely characterized and correlate with severity of the disease. Defined by the Global Initiative of Chronic Obstructive Lung Disease (GOLD) these four stages are categorized by measurements of FEV<sub>1</sub><sup>232</sup>.

However, these are only functional classifications of the airflow limitations and do not provide information about the underlying mechanisms that drive these obstructions. The understanding of disease progression requires the consideration of basic knowledge for distinct phases of COPD. In this study three phases of CS exposure were analyzed that can be compared to each other. The transcriptomic responses of the airway epithelium of 2 d exposed larvae, 5 d and 15 d exposed adult flies share crucial similarities. The antioxidant response in all three situations is commonly enriched to defend from oxidative stress originating from CS. This aspect additionally proves the importance for an appropriate defense from oxidative stress in the airway epithelium and can be considered as a central mediator of the defense response.

Besides the shared antioxidant response, there are substantial differences between the phases of CS exposure. The responses to acute exposure to CS in 3<sup>rd</sup> instar larvae express not only in an activated antioxidant response but also initiate structural changes. As shown in the GO analysis from CS exposed airway epithelial cells, the most upregulated GO terms are *intestinal epithelial structure maintenance* and *cell proliferation* (Fig. 9, B). These biological functions might be involved in remodeling of the tracheal system which thereby adapts to potential damage caused by CS. These responses are eventually involved in repairing the damaged tissue and expanding the respiratory system to compensate for these ruptures. Notably, this response is even stronger represented in 5 d CS exposed adult flies. Upregulation of protease coding genes like *mmp1* in 5 d CS exposed airways presumably disturb the protease/antiprotease balance and might damage the tissue. The GO analysis from 5 d CS exposed airways revealed numerous

biological processes related to structural remodeling that were enriched in upregulated DEGs (Fig. 17 C). Surprisingly, these processes were not observed in airways from 15 d CS exposed flies anymore (Fig. 17). It seems plausible that the remodeling of airways appears rather early in the course of CS exposure and potentially is already completed in flies exposed for longer periods. This would also implicate an obstructive effect of CS exposure in the fly's respiratory system that is not reversible once it has fully established. These presumable obstructions could finally be a determinant of lifespan in CS exposed flies. The airflow obstruction in fruit flies might therefore mimic the situation observed in COPD patients. Understanding why these morphologic alterations appear and what causes the remodeling can be key for understanding the detrimental effects of CS.

Interestingly, the immune system is differentially involved in the response to CS in different periods of exposure. In 5 d CS exposed airway epithelial cells a variety of immune related genes are significantly downregulated. A GO analysis further proved the involvement of the immune system by revealing immune related biological processes that are enriched among downregulated DEGs (Fig. 16 C). This observation is contradictory to the situation observed in 15 d CS exposed airway epithelial cells. As seen in Fig. 17, many immune related genes are strongly overexpressed in response to 15 d CS exposure. The activation of the immune system indicates a chronically activated immune system in older flies.

Concludingly, the comparison of different periods of CS exposure also indicates a progressive regulation of response mechanisms in the respiratory system. This structural and physiologic regulation presumably is not only dependent on the dose of CS exposure but also on the age of exposed flies. These results emphasize the importance of early diagnosis for COPD in order to prevent the establishment of chronic phenotypes like lung obstructions and inflammation to cause irreversible damage. An early diagnosis in COPD development could effectively slow down disease progression<sup>233</sup>.

#### **4.4 The immune system is a central mediator for lifespan determination in CS exposed flies**

Based on contradictory results from transcriptomic analyses of CS exposed airway epithelial cells with different exposure times, it remained unclear what role the inflammation response plays. Triggered by exposure to CS, the immune system in the

respiratory cells of *Drosophila* react by releasing a variety of AMPs and induction of other immune related genes. This mirrors the situation of COPD patients, where a chronic inflammation is one of the major hallmarks of the disease, which is defined by an increased AMP secretion of the airway epithelium<sup>22,234</sup>.

To evaluate whether this response is protective or detrimental, manipulations of the immune system during CS exposure provided information of its role (Fig. 23). As observed from lifespan analyses, an attenuated immune system is beneficial for survival and its activation leads to premature death. These results strongly suggest a damaging role of chronically activated AMPs in CS responses rather than protective roles. It is not known which mechanisms underlie the observed lifespan extension of AMP diminished flies during CS exposure. However, these results indicate a role beyond an antibiotic function of AMPs, which rather might act as signaling mediators upon chronic inflammation induced by CS exposure. As previously described, AMPs are additionally involved in releasing pro-inflammatory mediators, epithelial wound repair, epithelial remodeling via mucin synthesis or chemotactic attraction<sup>235-237</sup>. The increased release of AMPs potentially is an overexaggerated response to compensate for CS induced damages in the airway epithelium. Accordingly, the non-antimicrobial functions might further contribute to the chronic and persistent damage of the airway epithelium caused by CS exposure. It seems plausible that the chronic inflammation and airway obstruction observed in COPD patients are at least partly regulated by the increased release of AMPs and other immune effectors. Hence, depletion of AMPs might interrupt the vicious circle of chronic inflammation caused by the exposure to CS and thereby might contribute to increased survival. Interference with AMP release has already been considered as a treatment option of symptoms in COPD but effective strategies to beneficially modulate AMPs are still missing<sup>238</sup>.

The assumption of the immune system as a major determinant of lifespan during CS exposure in *Drosophila* is supported by a recent observation of an association between immune cells and the tracheal cells. It was shown that hemocytes reservoirs are tightly connected to the respiratory surface in adult flies<sup>239</sup>. With attached hemocytes, especially the *Drosophila* macrophage-like plasmatocytes, it is possible that these cells further increase the immune response in the airway epithelium upon CS exposure. Plasmatocytes are involved in relaying inflammatory signals to other tissues by releasing the JAK/STAT ligand upd3<sup>239</sup>. JAK/STAT signaling is a known inducer of immune responses both in

humans and *Drosophila*<sup>240,241</sup>. As mentioned in chapter 3.2 the JAK/STAT signaling pathway is activated in CS exposed airway epithelial cells. Secretion of upd2 and upd3 therefore might be mediated not only by the airway epithelium itself but also by colocalized hemocytes.

In summary, the persistent activation of the immune system in the airway epithelium by exposure to CS results in a chronic inflammation of the airways. This inflammation presumably is even enhanced by the immune system itself via the activation of JAK/STAT signaling. It is uniquely shown in the novel CS induced *Drosophila* model, that a chronic activation of the immune system significantly reduces lifespan of CS exposed flies whereas an attenuated immune response increases lifespan. Hence, the immune system represents a critical player in lifespan determination and needs to be considered for intervention studies in COPD. Appropriate treatment of the immune response seems to be essential in order to adjust this abnormal reaction to a more physiologic level that go beyond LABA, LAMA or corticosteroid therapies. These pharmacotherapy options target the inhibition of inflammation but are quite unspecific, often accompanied by corticosteroid resistance and outcomes in old COPD patients have yet not been completely clarified<sup>6,242</sup>.

The chronic immune system impairment seems to establish in a late phase rather than in an early phase of CS exposure. Therefore, it is even more important to diagnose symptoms before they have established and could cause irreversible damage. Early diagnosis of COPD and consequential treatment to prevent establishing symptoms originating from early life events may serve to effectively milden disease burden.

#### **4.5 CS exposure induces chronic and persistent effects that can partly be rescued by CS cessation**

As a chronic and irreversible disease, COPD and its phenotypes persist as soon as they have once established even after smoking cessation. Though, smoking cessation is proven to be beneficial for restoring lung function and slowing down disease progression<sup>215</sup>. However, it is still not much known about underlying mechanisms of long-term effects on the airway epithelium, induced by cigarette smoking. By evaluating the effects of CS cessation in *Drosophila*, underlying causes that determine the outcome of these effects were evaluated.

An increased GSSG:GSH ratio after CS exposure could be rescued by CS cessation (Fig. 26), indicating a short-term and acute role for the antioxidant response. Hence, the GSH metabolism is a fast-acting process to effectively protect the cell from oxidative damage. Regulation of GSH metabolism is a dynamic feedback mechanism and will be shut down when no further GSH is required. Thus, CS cessation could neutralize the oxidative stress caused by prior CS exposure. Moreover, the body composition of flies was affected by CS cessation.

However, there still were CS induced effects detected even after CS cessation for 14 d. The physical activity of initially CS exposed flies was significantly reduced and even more important, so was the lifespan. These two results suggest a long-term effect of CS exposure, which is not reversible and cannot be rescued by CS cessation. As body fat content and oxidative stress levels could not explain these persistent impairments of the flies, transcriptomic analyses should reveal the mode of action in these impairments. When looking at the transcriptomic analyses after 14 d of CS cessation in airway epithelial cells it is obvious that processes like immune responses or structural alterations were substantially downregulated (Fig. 27). Interestingly, these processes were initially upregulated either after 5 d or 15 d of CS exposure. These results indicate that CS cessation leads to a compensation response that tries to reverse the previous impairments arising from CS exposure. Notably, the inflammation in airway epithelial cells is obviously reversible, which might be an underlying cause for the rescued oxidative stress by CS cessation due to reduced ROS secretion of the immune response. Besides a reduced inflammation level, the transcriptomic analyses additionally revealed an underrepresentation of morphogenesis associated GO terms (Fig. 27). This response might also be a reaction to compensate for initial remodeling in order to assure no further progressing structural alterations. Combined with the so far unexplained chronic effects of CS both, on the lifespan and physical activity, it can be hypothesized that structural impairments of the airway epithelium might be responsible for these effects. As already shown for COPD patients, early life events often directly determine the outcome of COPD development in later stages<sup>243,244</sup>. With results obtained from the *Drosophila* model, this observation can be supported and it even gives hints for its underlying causes. Since inflammation, body composition and oxidative stress could be reversed, it is assumed that the chronic effects of CS exposure rely on the remodeling of the respiratory system. Premature death of CS exposed flies, even after CS cessation therefore might be a

consequence of tracheal obstructions. This remodeling process is presumably not reversible and is already completed in the early phase of CS exposure.

Moreover, the transcriptomic analyses revealed the gene *diedel* as one of the most regulated DEG obtained from the RNAseq experiment. The cytokine Diedel has an immunomodulatory function and is a known repressor of IMD signaling<sup>245,246</sup>. As already mentioned, a downregulation of many immune related genes is observed after CS cessation, that is surprisingly accompanied by a downregulation of the Diedel coding gene. A lack of Imd inhibition normally should lead to an activated Imd induced immune response. Thus, it is unclear why the immune response is attenuated after CS cessation. A plausible explanation for this might be that this attenuation is Imd independent and driven by other pathways. The most regulated DEGs after CS cessation are the *totX* and *totM* genes. These genes are known targets of the JAK/STAT signaling pathway and inducers of bacterial responses in the fruit fly<sup>247,248</sup>. The downregulation of these genes might be a potential cause of an attenuated immune response, indicating a crucial role of the JAK/STAT signaling pathway for chronic responses to CS.

Diedel has recently been tightly associated with governing tissue aging and lifespan in *Drosophila*<sup>216</sup>. This study assumes Diedel to promote longevity via attenuation of the apoptosis machinery, which may be a driving force of tissue aging. Increasing Diedel levels were observed with age and are shown to be an effective counter mechanism against age-related apoptosis and consequential loss of proliferative capacity. Hence, an increase in Diedel acts as a gatekeeper of premature aging in *Drosophila*. The strongly reduced transcription of the Diedel coding gene in airways after CS cessation, suggests an altered lifespan determination. The observed decrease in lifespan even after CS cessation might be at least partially explained by an increase in apoptosis that is potentially driven by the downregulation of Diedel.

The involvement of Diedel in the chronic response to CS exposure implies a direct connection between CS induced effects and premature aging in the airway epithelium.

#### **4.6 CS exposure induced effects are age-related**

COPD and aging share distinct mechanisms and the disease development is crucially dependent on the aging process<sup>16</sup>. Emerging theories propose that COPD might be considered as premature ageing of the lung<sup>212,249</sup>. The aforementioned advantages that

*Drosophila* offers (chapter 1.8), were utilized in this study in order to evaluate the relation between CS induced effects and aging. The transcriptomic analyses of CS exposed airways were performed for two different time periods. This allows for an age dependent analysis of a potential alignment of CS exposed and aging airways.

The exposure to CS for 5 d showed no shift in transcriptomic profiles regarding the expression for all genes (Fig. 20, A). Surprisingly, when looking at aging and telomere associated genes, transcriptomic profiles from CS exposed airways shift towards profiles of young airways (Fig. 20, B, C). This result is contradictory to the assumption of CS induced accelerated aging of the airways. A reasonable explanation for this observation might be an early induced response to compensate for CS induced effects. The shift towards young profiles, might be characterized by repair mechanisms, such as the remodeling of airways to prevent damage. As seen in Fig. 16, the transcriptomic response to CS is defined by several enriched remodeling biological processes. These observations are concomitant with a decreased immune response in 5 d CS exposed airways. As shown in transcriptomic analyses from aging airways, the involved biological processes are mainly defined by an upregulation of immune responses (Fig. 18). When looking at distinct processes such as the immune response, the CS induced response leads to a shift towards transcriptomic profiles of young flies. Nevertheless, these mechanisms seem to be aging independent, since the transcriptomic analysis across all genes shows no significant shift neither to profiles from young airways nor to profiles of from old airways.

However, short-term repair mechanisms are not persistent and break down after continuous CS exposure. The transcriptomic profiles of 15 d CS exposed airway epithelial cells show a significant alignment with the profiles from old airways. Analysis across all genes as well as aging and telomere associated genes revealed a consistent shift towards profiles from old airways. This damage presumably impairs repair mechanisms in a time and age dependent manner and hence leads to an aging like transcriptomic pattern. Processes like an activated immune system in 15 d CS exposed airway epithelial cells might be an underlying factor for the shift towards old airways. An activated immune system is a hallmark of aging and contributes to the aging process<sup>49</sup>. Hence, the observed immune activation of 15 d CS exposed airways potentially is an initiator of an aging related response of the airway epithelium.

As the alignment of transcriptomic profiles from CS exposed airways towards old airways suggests, there might be age-related features commonly regulated. To examine if there are aging related effects, induced by CS exposure, telomere lengths were analyzed. As a hallmark of aging, telomere attrition contributes to genomic instability<sup>49</sup>. Transcriptomic analysis of Het-A by qPCR, revealed significantly less expression of Het-A elements in genomic DNA from CS exposed flies. The Het-A retrotransposon is the most abundant sequence in *Drosophila* telomeres<sup>250</sup>. Hence, a reduction in expression levels of this element implies a shortened telomeric sequence. The observed telomere shortening, induced by CS exposure, strongly suggests age associated effects on genomic stability. Impairment of genomic stability could be an explanation for observed phenotypic alterations of physiologic parameters like reduced lifespan or reduced activity (chapter 3.1). As an underlying cause for this effect, accumulating oxidative stress probably drives these impairments. The time dependent accumulation of oxidative stress would also explain the differences between 5 d and 15 d CS exposed airway epithelial cells. Potentially, a certain amount of oxidative stress is eliminated by the host until it exceeds a certain threshold. When this threshold is exceeded, the epithelial capacity of eliminating the increasing oxidative stress presumably is too poor to protect from damage. These oxidative stress induced effects might cause age-related changes in a time dependent manner and drive the shift of CS exposed airways towards profiles of old airways.

Combined with previously described results of an impaired immune system (chapter 4.4), these transcriptomic datasets suggest that there are striking similarities between aging and CS exposure. Impaired immunity as well as transcriptional alterations and telomere shortening are hallmarks of aging and occurrence of these hallmarks contributes to the aging process<sup>49</sup>. However, the exact mechanisms that underlie these age-related responses of the airway epithelium is not clear. It is reasonable that these mechanisms are highly complex and additionally affect each other in a yet unpredicted way. Thus, gaining a deeper insight into other hallmarks of aging such as proteostasis, stem cell exhaustion or cellular senescence is essential to further understand the observed age-related effects of CS exposure in the airway epithelium of *Drosophila*.

However, the results from this study show that the responses of CS induced effects have significant similarities to age-related effects. These observations might be an initial hint to prove the hypothesis of COPD as an accelerated form of lung ageing.



#### 4.7 Nutrition is a crucial mediator of CS induced effects

From an evolutionary point of view, nutrient deprivation is one of the most challenging factors for an organism's survival<sup>251</sup>. Especially for COPD development, the nutritional status of the patient is of crucial relevance and undernutrition causes specific symptoms like reduced body mass, dry mouth, stomach ache or impaired muscle function<sup>252,253</sup>. The assessment of nutritional status in human patients is only estimative and does partly rely on subjective perception<sup>254</sup>. The lack of unbiased and standardized methods complicates the reliable examination of nutritive effects on COPD development<sup>255</sup>.

The possibility of manipulating the nutritive uptake by using different media makes the research on dietary effects during CS exposure very effective and highly reproducible in *Drosophila*. As shown in chapter 3.11, a reduction in dietary protein concentration resulted in significantly reduced lifespan of CS exposed flies. Surprisingly, flies fed with the DR medium (PC 1:16) died significantly earlier than flies on the control diet (PC 1:2). As already mentioned, DR was shown to have lifespan extending properties by reducing insulin and TOR signaling, thus increasing stress resistance<sup>221-223</sup>. Moreover, it has been associated with enhanced phase II detoxification activity<sup>256</sup>. The approach to maintain these molecular effects of a DR diet without limiting protein availability could not reverse the effects on lifespan (Fig. 28). Supported by the result of a decreased lifespan of flies fed on a protein diminished diet (PC 1:50, Fig. 28), it is obvious that reduced protein uptake is detrimental for survival during CS exposure. Albeit these nutritive interventions did not alter the relative body composition, it resulted in weight loss (Fig. 29), which is similar to studies on malnourished COPD patients<sup>217</sup>. However, it remained unclear which mechanisms connect the observed reduction in lifespan and the loss of body weight. The tripeptide GSH is synthesized from the three amino acids glutamate, cysteine and glycine, and its production is dependent on availability of these components. As shown in Fig. 30, the total levels of GSH are substantially reduced in flies raised on both protein diminished diets. This observation might explain the reduction in lifespan, as the cell cannot rely on a reservoir of GSH to effectively protect from oxidative stress. With decreasing GSH amounts also the GSSG:GSH ratio decreased in protein diminished flies. This finding might be the consequence of impaired GSH availability and the existing GSSG rapidly is reduced back to GSH by compensating enzymatic activity of Trxr. Even though, the GSSG:GSH ratio indicates less cellular oxidative stress, the overall amounts of GSH presumably limit the elimination of ROS. The resulting increase in oxidative stress potentially causes damage

to the tissue which consequently disrupts tissue function and ultimately might lead to reduced survival of the organism.

These results underpin the previously assumed high relevance of nutrition on COPD disease management<sup>217</sup>. Nutritional supplementation for COPD patients has already been shown to be beneficial for reducing the risk of COPD development and on the progression of the disease<sup>257,258</sup>. Understanding the molecular underlying mechanisms of nutritional impact on CS induced effects in *Drosophila* potentially may help to improve dietary therapies for COPD patients. Thus, prospective screening of the nutritional status of COPD patients should be considered as a standard method for monitoring the development of disease. Tailored and individual approaches to regulate nutritional uptake would be a simple but effective method to milden disease burden by attenuating symptoms<sup>259,260</sup>.

#### **4.8 The relation of the intestinal microbiome and CS exposure**

Several factors like nutritional uptake, drugs or infection influence the microbial composition that is habiting the intestinal tract<sup>261-263</sup>. The intestinal microbiome has been associated with numerous physiologic processes that impact health of the host. Various disease like obesity, diabetes mellitus or cancer are influenced by the microbiota<sup>264-266</sup>.

To understand the influence of the microbiota on the physiology of the host, germ-free models are used to further elucidate these associations<sup>267</sup>. Germ-free models serve to unravel microbial effects on disease development<sup>268</sup>. The *Drosophila* model for CS induced effects, described in this study, should clarify the influence of the intestinal microbiota on the survival during CS exposure. As shown in Fig. 32, the depletion of microbes by introducing antibiotics to the food had no effects on the lifespan of CS exposed flies. This result implies that there are no direct influences of the microbiota on the survival of CS exposed flies.

However, there was a *vice versa* effect of CS exposure on the intestinal microbiota. Based on the alterations in bacterial composition, CS exposure seems to cause conditions that favor a remodeling of the intestinal microbiota. The exposure to CS did not only affect the relative abundance of bacteria but also the total bacterial load (chapter 3.13). This result is concomitant with observations made in COPD patients where microbial dysbiosis is a feature especially during acute exacerbations<sup>269</sup>. Since intestinal dysbiosis plays a pivotal role in the pathogenesis of intestinal bowel diseases (IBD) including Crohn's disease and

ulcerative colitis. It may be assumed that CS induced dysbiosis is a potential driver of comorbidities in COPD patients. This assumption is strengthened by previous studies that reveal COPD patients of having a higher risk of suffering from IBD<sup>270,271</sup>. The occurring dysbiosis in COPD patients can potentially be used as biomarkers for disease management and might serve as targets for future therapies<sup>269</sup>. However, mechanisms that modulate the intestinal/respiratory axis during CS exposure are yet unknown. A conceivable explanation for effects of CS may be the systemic increase of oxidative stress and an activated immune system during CS exposure, as previously reported in this thesis. These aspects might be mediators of the observed dysbiosis in the gut. This assumption implies a transduction of CS responses from the respiratory system to the gut. The mode of this communication is unclear and it remains unsolved whether it is of direct or indirect origin. This transduction might be mediated by increased levels of circulating cytokines that were also reported in COPD patients<sup>272,273</sup>. The chronically released cytokines of COPD patients transit through the plasma, affect other tissues and cause systemic inflammation<sup>25</sup>. Therefore, it is considerable that these cytokines also drive an inflammatory response of intestinal epithelial cells and indirectly influence the microbial composition in the gut. In *Drosophila* the situation might be very similar due to immune cells sitting at the tracheal system<sup>239</sup>. These cells potentially relay this signal by secreting cytokines into the hemolymph which transmits the CS induced signal also to the gut and promotes an inflammation in the epithelial cells. Additionally, the tracheal system might also relay the CS induced signal in a direct manner through the terminal cells. Previous studies have demonstrated that the terminal cells interact with other tissues and also influence the intestinal homeostasis by releasing the TGF- $\beta$  signaling ligand Decapentaplegic<sup>150,151</sup>. Therefore, it seems reasonable that terminal cells might also release mediators upon CS exposure and directly impact the microbial composition of the gut.

However, it is yet unknown how broad the capacity of terminal cells is to directly interact with other tissues. Due to insufficient data about the exact characteristics of tracheal cells in *Drosophila*, it remains ambiguous what exactly defines the intersection between CS exposure and dysbiosis observed in the *Drosophila* model.

#### 4.9 The transcriptome of adult airway epithelial cells reveals striking differences to larval trachea and identifies circadian clock components

The lack of knowledge about the nature of tracheal epithelial cells, especially in adult *Drosophila* limits not only research on development but also on responses of the tracheal cells to endogenous factors like CS exposure. Hence, further understanding of the tracheal system might be beneficial for driving relevant research in this field. In this thesis, a pioneering characterization of the adult tracheal transcriptome was performed. Providing this novel dataset for research should improve research on it trachea in *Drosophila*.

When comparing this dataset with transcriptomic data from larval trachea, it becomes obvious that the tracheal system undergoes a dramatic change during metamorphosis. Based on DEGs of this comparison, numerous receptors such as nAChR, Dop2R, Glutamate receptor IB (GluRIB) or Pyrokinin 1 receptor (PK1-R) were differentially expressed, only to name a few. The variety of differentially expressed receptors between both developmental stages indicate a strong alteration in cellular signaling mechanisms. This suggestion is further supported by a GO analysis for involved biological processes. Several signaling related GO terms were enriched in the comparisons of adult and larval trachea (Fig. 36).

As the network analysis revealed, the central components in the remodeling of the tracheal system during metamorphosis are structure giving genes (Fig. 35). This observation is further strengthened by various *obstructor* genes that are highly overrepresented in larval trachea. The *obst* gene family has chitin binding domains and is involved in chitin bundle assembly<sup>274</sup>. Therefore, it seems obvious that a differential expression of structural genes might be orchestrating the remodeling process.

Interestingly, this novel dataset already could help identifying new findings about so far undescribed mechanisms in the adult trachea. The DEG analysis and the GO enrichment analysis revealed the expression of circadian clock components in the adult trachea (Fig. 34, Fig. 36). Tracheal cells have yet not been known to possess a circadian rhythm. Additional evidence from a reporter line in abdominal trachea strongly suggest the existence of such components. The *tim* gene is a core component of the circadian clock in *Drosophila* and its expression was associated with regulating cellular rhythm<sup>224</sup>. To ultimately prove that these cells are rhythmically cycling, more research has to be done

in deciphering the role of circadian rhythm in tracheal cells and further knowledge about distinct cell types will be helpful.

It is necessary to further elucidate cell identities to better understand the tracheal system. Until now, it is not known if there are different types of tracheal cells and if so, how many of them and what distinguishes them. With rising applications of single cells analysis, it is getting more reasonable to screen for cell identities with these approaches.

#### **4.10 Future perspective of *Drosophila* to study CS induced effects**

Results from this thesis prove that *Drosophila* can be used to study CS induced effects, that not only mimic those seen in COPD patients. It can rather be used to elucidate underlying mechanisms, which show striking similarities to those observed in the human system. This novel model helped to understand the relation between CS exposure and processes like the immune system, antioxidant responses, aging and other processes. Intervention studies revealed targets that increase lifespan during CS exposure. These findings might be transferred to the human system in order to pinpoint prospective approaches for the treatment of COPD patients to eventually slow down or even stop disease progression. For the perception of CS induced effects, it will be important to screen the airway epithelium of *Drosophila* for structural changes. In relation to other results, structural analyses might give a hint for the biological relevance.

However, there are limitations for the use of *Drosophila* for CS induced effects. The lack of adaptive immunity undoubtedly simplifies research of the airway epithelium but does not fully mimic the human system. Conclusions in the *Drosophila* model therefore need to be validated and eventually adjusted for the human system. Moreover, the respiratory system of the fruit fly is not fully characterized and knowledge about cell identities are still not resolved. In the human lung there are different types of lung epithelial cells such as ciliated cells, goblet cells or neuroendocrine cells. In order to better understand the mechanics of the response to CS, it will be essential to have a fully characterized airway epithelium. Single cell sequencing approaches of a CS exposed airway epithelium might provide additional information about the pathophysiology of COPD.

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## 6 Appendix

### 6.1 DEGs of 2 d CS exposed airways from 3<sup>rd</sup> instar larvae

Gene name	Max group mean	Fold change	FDR p-value
Prx2540-2	13411.76	100.79	4.8E-204
CG11825	5932.64	67.75	5.2E-128
CG12896	3855.83	50.57	1.3E-104
Prx2540-1	4726.40	44.97	1.3E-96
GstD5	260.90	12.92	6.4E-41
GstD3	1425.99	9.92	3.1E-68
GstD2	814.47	9.49	9.5E-34
Gclc	3244.07	8.90	5.8E-129
Tdc1	1741.65	7.82	9.0E-39
GstE7	458.56	6.76	1.5E-29
GstD4	62.54	6.02	4.9E-18
upd2	48.06	5.31	1.6E-14
CG3397	92.90	4.67	9.0E-18
CG2065	1594.56	4.32	4.7E-27
GstD9	577.40	4.21	4.9E-28
NA	227.04	4.17	6.8E-13
GstE8	157.19	3.97	2.7E-14
GstE1	572.07	3.87	6.6E-12
upd3	43.33	3.82	6.3E-11
Arc2	412.74	3.60	2.3E-23
GstE2	1053.12	3.54	1.4E-16
CG14397	12.99	3.52	5.1E-08
out	1243.88	3.50	4.5E-21
Gadd45	668.54	3.48	1.4E-20
NA	4486.59	3.38	3.0E-22
Cpr47Ea	18.72	3.34	7.6E-08
Ets21C	75.96	3.22	2.9E-07
NA	53.11	3.07	1.7E-06
NA	24.74	3.01	1.5E-06
path	1467.86	2.98	2.7E-13
GstE6	1682.86	2.79	3.4E-06
CG18547	379.33	2.76	2.1E-25
CG3348	282.73	2.76	2.0E-05
CG14695	52.25	2.70	3.6E-05
CG34248	671.06	2.62	1.3E-07
CG11897	741.44	2.62	2.9E-10
Cyp6a23	2159.05	2.58	7.6E-08
CG6830	654.30	2.56	5.2E-06
MRP	13866.16	2.47	8.3E-08
GstE5	37.50	2.45	1.3E-04
Alr	290.98	2.43	2.4E-10
Ugt36Ba	43.07	2.40	1.4E-05
trbl	1076.61	2.36	2.2E-22
CG34281	20.65	2.35	1.4E-03
CG15096	836.57	2.35	4.1E-05
Gclm	677.75	2.34	8.9E-09
CG2064	71.93	2.32	3.5E-08
CG10208	178.64	2.31	1.0E-09
l(2)08717	534.67	2.30	7.1E-06
Cyp6a2	203.80	2.28	8.2E-04
GstD10	329.28	2.24	3.0E-03
Xrp1	12037.79	2.22	4.9E-47
CG12224	43.03	2.19	3.7E-04
CG1882	883.95	2.17	3.7E-09
Arc1	62524.54	2.14	8.2E-03
GstD6	37.49	2.14	9.2E-03
CG13157	103.60	2.10	5.0E-04
CG17786	399.83	2.09	1.3E-07
GstD1	34367.16	2.08	8.2E-10
Cyp28d1	52.74	2.04	1.5E-03
Jhl-26	1102.37	2.03	1.4E-02
CG2017	1316.48	2.00	1.5E-10
CG14866	11.84	1.99	2.8E-02
CG42365	182.12	1.98	1.5E-03
CG13894	18.81	1.97	1.6E-02
asparagine-synthetase	668.44	1.97	2.0E-02
tnc	341.66	1.96	8.2E-03
CG11893	14.13	1.96	2.8E-02
CG31288	37.77	1.96	3.6E-02
CG13223	14.90	1.94	2.6E-02
CG7130	84.96	1.92	1.5E-03
NA	44.17	1.92	6.1E-03
CG9674	9617.47	1.91	1.2E-17
Cyp6d2	71.33	1.91	1.4E-02
Cpr64Ad	324.59	1.87	2.7E-02
CG14907	264.39	1.85	3.7E-04
Keap1	580.45	1.82	2.1E-02
Socs36E	763.86	1.81	1.3E-03
CG13068	6711.30	1.79	4.2E-02
CG12868	177.96	1.79	4.9E-02
CG5010	980.25	1.79	1.9E-04
CG10916	364.92	1.78	8.7E-11
CG2076	1175.64	1.78	1.6E-03
GstE11	467.29	1.76	4.2E-06
Swim	4189.68	1.75	4.9E-03
CG7841	82.81	1.75	4.3E-03
NimB2	691.51	1.74	1.3E-04
CG3008	707.96	1.73	2.1E-04
CG3842	435.45	1.73	3.1E-03
CG31694	2275.75	1.72	5.1E-08
CG34409	38.00	1.72	4.8E-02
Mrp4	1344.89	1.71	8.7E-04
ver	44.50	1.68	1.7E-02
CG5646	145.02	1.66	1.6E-04

Dgp-1	737.71	1.66	3.2E-04
CG17278	367.17	1.66	2.5E-02
CG12171	805.47	1.65	9.1E-03
CG6512	1834.63	1.65	1.4E-02
CG42553	180.65	1.65	1.6E-04
CG32549	445.59	1.64	3.4E-02
Esp	110.61	1.63	8.8E-03
CG14906	107.10	1.58	8.2E-03
asrij	418.98	1.58	6.4E-07
CG2909	100.94	1.57	3.2E-03
B4	1302.75	1.55	2.9E-06
Gcn5	696.37	1.54	2.1E-02
eIF6	823.14	1.54	7.6E-03
Hmgs	851.04	1.53	1.4E-02
mal	400.37	1.52	8.8E-03
Trxr-1	5277.57	1.51	3.3E-04
CG3609	897.26	1.51	8.4E-04
Ugt86Da	1278.91	1.50	3.1E-05
Hsc70-5	3444.99	1.48	6.8E-03
Atg1	949.08	1.47	5.4E-04
CG10019	538.65	1.47	8.2E-03
Tpc1	286.65	1.47	3.1E-05
MFS3	2858.26	1.46	1.0E-02
l(3)02640	1115.58	1.45	6.2E-03
CG17260	142.01	1.44	2.7E-02
CG10802	260.84	1.44	7.3E-03
Irpb	227.38	1.42	4.0E-02
Hmgcr	1577.52	1.42	3.6E-04
CG12264	481.65	1.42	3.1E-02
Aats-trp	516.03	1.42	4.1E-03
CG6171	130.43	1.41	1.5E-02
CG9008	449.19	1.41	1.2E-04
NA	662.12	1.41	1.4E-05
CG8778	490.99	1.40	5.2E-03
CG7632	171.52	1.40	4.8E-02
CG5577	165.21	1.40	1.3E-02
Cpr	3024.63	1.39	8.4E-04
wdp	2031.33	1.39	9.7E-04
sda	3770.56	1.39	1.0E-02
CG3608	146.13	1.39	3.1E-02
Aats-val	2009.25	1.38	1.7E-02
CG31793	311.47	1.37	3.1E-02
mus205	544.16	1.34	2.8E-04
CG8531	963.64	1.33	4.3E-03
Gadd34	766.11	1.29	3.5E-02
PEK	1624.80	1.27	1.8E-02
cher	38833.18	1.27	6.7E-03
Aats-asp	2620.89	1.26	1.9E-02
CG9372	5434.49	1.21	1.1E-04
Z6-29-p	3893.61	1.16	2.8E-02
AGO1	3327.88	1.20	4.7E-02
bun	4139.28	1.22	3.7E-02
Snoo	1410.23	1.24	1.7E-02
CG32428	579.51	1.27	3.2E-02
CG4658	1436.85	1.27	1.6E-04
CG16947	529.64	1.32	2.7E-02
NA	850.99	1.32	3.0E-03
CBP	2462.87	1.39	9.2E-03
Sod3	1846.55	1.41	1.7E-02
CG18549	705.49	1.46	9.8E-03
NA	186.85	1.48	1.4E-02
Osi24	256.43	1.48	4.8E-03
GV1	1516.70	1.53	4.4E-05
CG9664	102.22	1.58	2.4E-02
NA	651.07	1.60	7.4E-06
CG6770	12151.49	1.69	2.7E-02
CG11550	669.08	1.73	5.9E-03
CG9896	114.51	1.75	1.6E-03
NA	429.51	1.76	3.6E-04
Blimp-1	233.46	1.77	2.1E-04
CG32365	115.20	1.84	3.4E-02
ju	1486.74	1.86	1.3E-02
sxe2	253.96	1.86	4.2E-04
sro	80.50	1.89	2.8E-02
CG42249	55.22	1.91	4.3E-02
Cpr78E	3077.86	1.99	1.4E-02
vri	551.27	1.99	2.0E-04
CG13314	515.16	2.03	3.1E-07
NA	547.93	2.05	1.4E-02
CG32213	83.03	2.09	1.0E-02
Cyp313a5	209.60	2.13	4.3E-05
Cpr56F	107.37	2.18	6.9E-03
NA	289.45	2.21	1.2E-08
CREG	934.58	2.66	1.6E-06
CG15068	29.05	2.89	1.4E-05

### 6.2 DEGs of airways from 5d CS exposed flies

Gene name	Max group mean	Fold change	FDR p-value
CG46311	1.06	748.07	7.8E-07
CG18853	2.01	469.93	4.8E-06
CG18542	1.17	311.04	2.4E-04
CG32726	10.60	197.81	3.3E-07
pre-modf(mdg4)-K	0.22	194.08	1.7E-03
CG12896	283.73	125.34	0.0E+00
CG46318	0.17	114.94	1.8E-03
CG11825	77.84	112.23	0.0E+00
Prx2540-2	479.84	85.23	0.0E+00
Prx2540-1	482.91	72.39	0.0E+00
CG14075	104.04	68.75	7.0E-13
Akh	184.17	63.46	4.8E-10
CG46321	0.05	62.19	7.2E-03

CG11368	5.33	47.23	3.1E-05
COX5BL	0.33	46.70	1.1E-02
pre-mod(mdg4)-L	0.70	39.75	3.3E-09
Tsp42Eb	0.23	38.63	4.9E-02
CG14742	0.31	37.65	2.0E-02
jhamt	12.44	35.46	1.7E-06
CG43739	0.18	34.49	1.7E-05
CG9083	0.14	34.48	3.2E-02
RpL34b	37.71	32.57	0.0E+00
CG14795	0.27	28.37	4.0E-02
CG33474	5.27	26.36	0.0E+00
CG4000	0.56	24.41	2.2E-05
CG14440	14.72	22.48	0.0E+00
RpL18	76.57	20.62	0.0E+00
CG42255	2.68	20.54	0.0E+00
Prip	6.61	20.50	0.0E+00
nAChRbeta3	3.00	20.32	0.0E+00
Cyp6g2	11.24	19.20	4.4E-07
CG13056	0.48	18.21	4.9E-03
RpL24	52.06	18.17	0.0E+00
Hand	7.15	17.65	0.0E+00
CG11699	2.86	16.83	0.0E+00
lectin-33A	5.70	16.28	7.3E-12
Tsp42Eo	0.20	16.24	8.2E-03
SmD1	0.24	16.24	8.2E-03
CG11370	2.97	15.87	0.0E+00
Pkg21D	0.67	14.91	5.9E-06
MtnD	8.79	14.60	1.3E-11
CG13678	1.18	14.38	4.5E-04
CG42656	4.66	14.23	4.7E-03
Ing3	0.59	13.27	3.8E-13
CG9572	1.12	13.25	1.2E-11
RpL4	85.05	13.11	0.0E+00
met-217	0.03	12.92	3.6E-02
MtnE	4.15	12.54	7.4E-11
regucalcin	26.65	12.31	0.0E+00
CG13679	0.41	11.61	4.2E-03
up	6.35	11.60	0.0E+00
CG13068	3.15	11.48	1.8E-09
Hml	7.44	11.21	0.0E+00
CG13606	1.00	11.21	1.7E-10
SmB	0.78	10.78	2.2E-06
MtnB	1.80	10.54	6.4E-07
Amnionless	4.05	10.51	6.5E-14
ScIB	1.79	10.46	4.5E-06
Rab9D	0.41	10.45	3.9E-02
RpLP1	111.50	10.42	0.0E+00
TpnC47D	0.49	10.38	3.3E-05
UQR-CZ	7.29	10.23	0.0E+00
NC2beta	1.26	9.92	6.3E-10
CG7834	9.65	9.50	0.0E+00
pre-mod(mdg4)-Y	0.44	9.38	1.9E-05
Mp20	26.16	9.25	8.7E-12
CG45078	1.80	9.20	1.9E-05
Fuca	2.65	9.14	0.0E+00
CG8888	0.83	9.10	6.7E-07
RpL13	61.35	9.03	0.0E+00
Ppn	11.71	8.95	0.0E+00
Vinc	3.36	8.90	0.0E+00
Twdlbeta	0.69	8.81	2.3E-06
CG15021	0.47	8.69	9.7E-05
Thiolase	4.77	8.68	0.0E+00
CG4038	0.34	8.58	3.1E-04
CG46317	1.01	8.39	3.4E-08
CypI	1.27	8.33	2.7E-10
CG10527	16.24	8.22	0.0E+00
CG11852	7.69	8.08	0.0E+00
betaTub60D	5.62	7.93	0.0E+00
Ccp84Ae	0.17	7.84	3.2E-02
PPO1	4.90	7.77	4.4E-14
TpnC73F	8.65	7.59	1.5E-05
sta	60.39	7.45	0.0E+00
Nacalpa	28.96	7.44	0.0E+00
ImpL2	30.41	7.42	1.4E-11
Mhc	8.24	7.35	6.8E-12
Cpr64Ad	2.25	7.32	2.2E-09
Mur18B	0.75	7.30	1.3E-03
CG9205	2.73	7.27	4.4E-14
CG5612	2.83	7.26	2.7E-04
Hsp70Bbb	0.44	7.24	4.4E-02
ATPsynF	19.55	7.17	0.0E+00
CG2076	10.65	7.15	0.0E+00
Ets21C	1.47	7.13	0.0E+00
CG13044	0.55	7.07	8.8E-03
Arc1	240.84	7.05	0.0E+00
LanA	3.61	7.01	0.0E+00
RFeSP	14.05	6.92	0.0E+00
Cubn	3.86	6.91	0.0E+00
CG3348	27.90	6.83	0.0E+00
CG43236	2.94	6.77	6.5E-08
verm	2.98	6.76	0.0E+00
Nmdmc	7.26	6.75	1.0E-13
Tm2	5.23	6.70	4.1E-09
Sr-CI	3.99	6.66	0.0E+00
Pex19	2.25	6.62	0.0E+00
CG46307	0.26	6.61	6.3E-03
mthl2	4.06	6.57	0.0E+00
CG11752	4.51	6.50	5.6E-11
TwdIE	0.39	6.47	1.5E-04
Pxn	4.06	6.37	8.4E-08
serp	1.74	6.33	0.0E+00
Tpi	14.84	6.32	0.0E+00
CG3740	1.04	6.19	1.1E-05
CG13674	0.31	6.17	5.6E-03
CG4950	2.55	6.12	0.0E+00
Rpi	4.10	6.02	0.0E+00
PPO2	4.09	6.01	0.0E+00
CG43326	0.15	6.00	1.6E-02
SPARC	17.50	5.98	0.0E+00
CG5532	6.97	5.97	0.0E+00
CG6891	3.91	5.96	1.0E-11

LanB1	2.28	5.94	0.0E+00
RpL13A	71.65	5.93	6.4E-13
CG1943	12.14	5.93	0.0E+00
NtR	4.24	5.89	2.3E-14
CG17002	0.46	5.89	4.1E-07
eIF3g1	14.40	5.89	0.0E+00
CG15353	19.29	5.81	2.0E-05
Alr	1.88	5.75	4.3E-13
RpLP2	30.57	5.66	0.0E+00
lectin-24Db	4.22	5.65	0.0E+00
fau	8.07	5.65	4.3E-09
scu	7.34	5.61	2.3E-14
CG6617	2.96	5.56	2.3E-14
CG9815	1.13	5.52	4.1E-09
CG5397	10.91	5.50	1.2E-13
CG31038	4.76	5.47	0.0E+00
CG13807	1.61	5.46	2.3E-07
CG14095	0.76	5.41	2.2E-04
Klf15	0.39	5.38	1.6E-04
GstD5	2.28	5.37	8.7E-05
CG1907	4.14	5.32	4.8E-13
CG5399	3.50	5.29	5.6E-08
CG34446	1.63	5.28	1.7E-03
CG14132	3.25	5.27	1.3E-07
Antp	1.52	5.24	3.1E-13
CG32512	5.14	5.21	0.0E+00
Act87E	3.24	5.21	1.9E-06
Alas	11.54	5.18	1.4E-10
CG6847	3.34	5.13	0.0E+00
AnxB9	35.25	5.10	2.9E-13
CG15068	62.12	5.09	2.4E-10
so	0.35	5.06	3.1E-03
CCt3	3.72	5.06	0.0E+00
Hsp70Ba	2.30	5.05	3.7E-06
drd	7.33	5.04	0.0E+00
CG14879	1.20	5.03	1.4E-04
a6	1.17	4.99	4.9E-12
Pglym78	21.91	4.96	0.0E+00
CG4250	38.25	4.95	4.4E-14
dj-1beta	4.88	4.92	0.0E+00
NimC1	2.53	4.91	0.0E+00
Fer2LCH	112.02	4.90	9.9E-11
Muc30E	1.23	4.89	9.9E-12
sktI	4.16	4.88	0.0E+00
Ptp52F	0.40	4.87	6.4E-10
Rab9Fb	1.00	4.86	1.2E-05
CG16786	0.55	4.83	3.1E-08
inaF-A	0.66	4.79	1.7E-02
Msr-110	87.82	4.79	2.9E-09
CecB	2.02	4.72	2.9E-04
cher	9.47	4.72	2.4E-10
CG14327	2.38	4.71	3.2E-07
CG45076	1.56	4.71	5.0E-08
CG8642	0.13	4.71	2.8E-02
CG1942	2.53	4.69	2.4E-08
betaTub56D	45.40	4.68	4.6E-12
CG2157	5.92	4.67	1.3E-11
CG42598	0.99	4.66	2.2E-05
Myo10A	1.49	4.66	2.3E-14
Gapdh1	32.20	4.65	1.8E-13
wgn	8.08	4.63	0.0E+00
CG13069	1.16	4.60	6.9E-05
Chi	1.15	4.60	1.1E-09
CG13051	0.56	4.58	1.3E-02
Spx	0.88	4.57	3.0E-08
Cyp318a1	1.18	4.56	1.2E-09
CG8501	0.55	4.55	7.2E-05
GV1	6.27	4.55	2.1E-10
CG17065	1.71	4.54	1.2E-11
Pgd	5.46	4.54	0.0E+00
RhoGAP5A	0.66	4.54	2.3E-07
CG42516	1.09	4.53	2.2E-08
CG31826	1.19	4.52	6.1E-05
CG4115	1.99	4.48	9.7E-08
CG11876	6.73	4.47	0.0E+00
CG43646	0.54	4.45	9.6E-03
CG8483	0.71	4.41	2.3E-06
kraken	6.25	4.37	1.5E-09
AIMP1	1.10	4.37	4.6E-07
CG13639	2.38	4.36	1.3E-05
SdhB	6.85	4.33	2.3E-13
CG7049	0.67	4.31	1.5E-05
eater	0.94	4.31	1.4E-12
CG13516	1.19	4.30	7.1E-07
CG13482	3.03	4.30	7.3E-06
Kal1	1.32	4.27	3.1E-04
Cyp6a8	81.02	4.27	1.0E-08
Act57B	24.35	4.26	1.8E-07
gom	0.32	4.24	4.4E-04
CG6830	2.80	4.22	1.6E-11
Ubqn	12.68	4.21	4.6E-12
CG9626	0.98	4.21	1.1E-02
Pym	0.83	4.18	4.8E-05
Neurochondrin	2.73	4.17	6.3E-04
CG9577	1.57	4.17	3.5E-07
kdn	5.73	4.14	2.3E-14
Dat	16.43	4.13	4.6E-09
abd-A	0.88	4.11	4.3E-08
Scamp	8.16	4.10	0.0E+00
CG44085	2.55	4.10	2.6E-05
Cyp313a4	3.11	4.09	8.5E-14
CG7322	4.13	4.08	3.3E-09
vkg	3.03	4.08	0.0E+00
hemo	0.71	4.08	1.0E-04
CG10131	2.04	4.07	1.2E-07
CG5862	2.08	4.06	7.0E-10
CG13367	0.93	4.06	2.1E-06
zhf1	2.42	4.05	0.0E+00
Mlc2	23.87	4.05	4.1E-07
CG8740	9.93	4.04	7.2E-11
ND-B17	4.87	4.04	8.5E-14

CG18107	21.06	4.03	1.5E-06
LanB2	2.32	4.03	0.0E+00
Atu	0.80	4.02	4.2E-09
Cpr62Bb	7.51	4.02	1.1E-07
Capa	11.62	4.01	6.2E-03
RpS19a	51.92	4.01	2.5E-09
Gadd45	6.50	4.00	2.6E-12
Rab40	4.29	4.00	0.0E+00
eIF2alpha	3.50	3.99	1.6E-13
Epps	4.24	3.97	2.0E-03
ninaD	0.44	3.96	7.0E-05
mRplL48	1.23	3.96	1.2E-04
CG2841	10.50	3.95	2.3E-09
CG13067	20.63	3.95	2.6E-06
dpp	1.47	3.94	2.2E-11
Hsp70Bb	7.15	3.93	2.1E-09
obst-E	0.63	3.93	4.0E-05
Snap24	2.84	3.92	0.0E+00
CG10383	8.94	3.89	3.0E-06
CG11073	4.85	3.88	1.6E-10
llp8	0.37	3.87	5.9E-03
pre-mod(mdg4)-X	0.19	3.86	1.6E-02
dar1	5.52	3.86	3.8E-12
Pgk	7.98	3.85	1.2E-13
CG8312	4.33	3.85	7.0E-13
Brms1	1.61	3.85	3.0E-09
Rpn10	4.72	3.85	5.2E-11
edl	2.20	3.84	2.7E-12
CG6287	14.21	3.83	5.9E-12
Hsp26	18.18	3.81	1.9E-07
Sod2	5.53	3.80	2.3E-14
CG2065	10.08	3.79	3.2E-12
mirr	2.08	3.79	2.6E-11
CG15065	7.02	3.78	1.2E-04
geko	1.33	3.78	2.1E-05
Xrp1	39.96	3.77	1.7E-08
nahoda	4.63	3.77	1.2E-12
ND-B14.5A	4.87	3.75	1.5E-08
Traf-like	0.57	3.75	2.8E-04
CG15186	0.39	3.75	4.7E-03
GstD10	1.45	3.73	7.1E-05
CG1882	3.61	3.73	2.3E-11
CG9372	10.41	3.72	2.3E-10
Prm	4.47	3.72	4.0E-07
CG42488	0.34	3.72	8.2E-03
sona	1.76	3.70	1.7E-10
CG5191	2.65	3.70	1.3E-11
Hr38	2.72	3.69	1.7E-05
Osbp	1.32	3.68	2.7E-12
trh	5.93	3.68	2.2E-12
eEF1gamma	50.49	3.67	5.6E-08
wmd	1.24	3.67	1.9E-08
Cyp6a2	9.29	3.66	1.2E-06
fig	0.94	3.65	3.5E-06
AdamTS-A	4.33	3.64	1.2E-11
Tspo	18.98	3.64	7.7E-12
ND-75	5.86	3.64	0.0E+00
CG7512	0.33	3.62	9.4E-03
Rpn13	4.75	3.62	1.7E-10
Sec13	2.26	3.59	7.9E-12
boi	0.42	3.59	4.0E-02
CG5913	0.75	3.58	3.3E-05
CG9119	4.19	3.58	3.5E-08
CG34179	0.35	3.57	1.7E-02
arg	1.74	3.56	2.0E-02
MF	8.57	3.55	7.4E-06
CG32170	5.65	3.55	2.2E-09
Gp93	13.62	3.54	6.1E-09
CG12065	5.24	3.54	2.9E-11
awd	59.92	3.53	2.2E-10
Hsp60A	9.62	3.53	2.9E-11
CG6175	1.49	3.53	1.7E-08
CG42246	20.20	3.52	8.3E-07
Trxr-1	8.71	3.52	2.9E-11
Act42A	13.90	3.52	6.3E-11
CG30281	3.77	3.52	1.9E-10
topi	0.78	3.51	8.2E-04
snRNP-U1-C	1.29	3.51	3.9E-04
CG43351	3.90	3.51	2.5E-03
CG13551	3.73	3.50	1.2E-05
DCTN3-p24	1.93	3.50	2.3E-06
mfas	55.53	3.49	5.7E-07
CG11413	0.75	3.49	8.6E-03
CG43448	0.58	3.49	2.5E-02
CG4998	0.85	3.47	4.7E-05
Tapdelta	10.36	3.47	2.0E-09
RnpS1	1.15	3.46	4.3E-05
cv-2	3.35	3.46	1.2E-11
Vps29	2.61	3.45	8.2E-09
ImpL3	1.83	3.45	1.8E-07
per	0.71	3.45	6.0E-11
CG43897	7.25	3.45	3.6E-07
Tango14	1.41	3.45	7.9E-07
tn	1.32	3.44	6.4E-07
Hrs	2.92	3.43	1.1E-11
ush	1.86	3.43	0.0E+00
cwo	9.32	3.42	2.7E-11
alphaTub84B	57.30	3.42	1.3E-07
mfrn	5.24	3.41	2.3E-14
pot	10.32	3.41	3.4E-09
GstD4	0.91	3.41	5.0E-04
CG7272	87.99	3.41	1.1E-05
Tep3	5.36	3.40	7.6E-08
uif	1.41	3.39	1.0E-10
CG34171	1.12	3.39	2.5E-06
Cisd2	8.20	3.38	4.9E-09
CG15673	4.19	3.37	1.0E-08
Ref1	2.35	3.37	5.3E-09
CG42245	0.63	3.36	1.9E-04
Trpgamma	0.36	3.35	4.7E-02
Nf-YC	1.25	3.35	3.3E-09

RabX1	1.74	3.35	5.2E-11
CstF64	0.58	3.34	9.5E-05
CG42837	8.66	3.34	6.7E-11
CG8927	0.64	3.34	1.3E-02
RpS2	71.89	3.33	4.2E-06
CG17127	0.55	3.33	2.2E-02
I(1)G0004	0.28	3.33	2.2E-02
CG8012	240.83	3.33	4.2E-05
Shroom	6.03	3.33	4.7E-10
PSR	1.48	3.33	1.6E-07
I(2)tid	0.35	3.31	8.1E-04
CG10359	1.21	3.31	9.0E-07
ham	0.44	3.31	3.9E-04
MrgBP	1.60	3.31	2.5E-04
CG43630	4.53	3.30	1.6E-02
Vti1b	1.78	3.30	2.3E-06
colt	4.46	3.29	1.1E-07
tgo	2.53	3.29	1.8E-09
Muc96D	0.75	3.27	2.1E-07
ox	16.85	3.27	3.7E-09
Col4a1	5.21	3.27	8.2E-09
RhoGAP16F	0.52	3.25	2.9E-05
PGRP-LB	0.66	3.25	8.6E-05
dod	1.97	3.24	2.2E-06
vri	7.81	3.24	1.2E-08
Hsp70Bc	1.83	3.24	2.6E-07
rush	4.65	3.23	5.2E-12
CG9095	1.99	3.22	7.1E-08
cib	38.90	3.22	7.7E-07
CG5180	0.82	3.22	3.2E-05
CG5554	2.74	3.21	4.3E-07
e(Y)1	0.60	3.20	1.7E-04
CG9692	0.48	3.20	4.6E-04
betaTub97EF	3.88	3.20	5.5E-10
vig2	4.33	3.19	1.1E-08
CG17190	5.82	3.19	1.9E-07
Grasp65	2.90	3.19	2.1E-10
Hakai	0.21	3.19	6.2E-03
CG31908	2.00	3.19	1.8E-09
CG17187	0.56	3.18	3.4E-03
Rrp4	0.54	3.18	1.2E-03
Hmg-2	1.17	3.18	8.1E-06
CG7365	0.66	3.17	3.1E-04
CG4927	1.36	3.17	3.1E-05
CG8046	0.72	3.16	4.0E-06
Cpr97Eb	0.91	3.16	1.6E-02
Vta1	3.12	3.15	2.5E-09
CG12991	3.97	3.15	2.1E-12
Diap1	19.24	3.14	1.2E-07
CG12279	1.86	3.13	2.0E-04
CG13117	10.33	3.13	1.4E-08
CG43210	0.69	3.13	4.0E-03
UQCR-C1	13.50	3.13	8.2E-09
CG13204	0.81	3.12	2.5E-04
TRAM	1.99	3.12	8.0E-10
CG42327	5.22	3.11	6.2E-08
bic	20.70	3.10	7.0E-10
insc	2.68	3.10	6.2E-08
CG3760	2.28	3.09	9.9E-09
Mlp84B	4.38	3.09	9.6E-08
spz3	1.43	3.09	5.8E-09
CG4119	1.15	3.09	2.7E-10
Is(1)Ya	0.12	3.09	3.1E-02
CG7470	6.55	3.09	7.3E-08
CG34398	2.53	3.08	1.4E-07
Karl	3.22	3.07	7.2E-08
GstD3	12.19	3.07	1.9E-06
CG10103	6.80	3.07	2.5E-11
Sec61beta	3.44	3.06	8.9E-05
trbl	4.18	3.06	9.0E-08
RYBP	1.90	3.06	7.0E-11
CG5023	3.15	3.04	4.0E-02
CG5162	50.99	3.04	1.7E-05
Traf4	1.44	3.04	1.6E-09
grsm	2.90	3.04	1.0E-07
pck	4.39	3.03	1.0E-07
CG11122	0.86	3.03	1.9E-09
Adeff-A	1.71	3.02	5.7E-08
TpnC25D	2.01	3.02	1.1E-02
Fas3	4.74	3.02	6.5E-09
out	6.85	3.02	4.0E-07
CG12075	0.66	3.02	2.5E-08
CG18659	3.40	3.02	1.2E-10
CG12056	1.01	3.01	1.2E-03
CG2781	3.40	3.00	1.8E-06
pio	4.31	3.00	2.0E-07
DOR	8.02	3.00	1.7E-08
CG2310	1.19	3.00	1.6E-04
Acp36DE	1.29	2.98	3.4E-08
LamC	6.63	2.98	2.9E-08
CG10970	1.28	2.98	1.5E-03
CG17108	6.45	2.98	5.1E-06
GstD2	3.21	2.97	8.2E-05
CG17189	2.04	2.97	1.2E-03
cora	15.87	2.97	1.9E-06
CG40006	1.84	2.96	2.9E-09
eIF2beta	1.05	2.96	1.9E-06
CG30273	1.79	2.96	6.9E-06
CG13082	7.76	2.96	3.8E-05
CG32091	6.40	2.95	4.2E-09
CG6908	6.53	2.94	6.3E-05
laccase2	1.51	2.94	3.0E-07
CG16820	12.30	2.94	2.5E-04
levy	25.17	2.94	2.6E-09
CG3777	2.12	2.93	5.4E-05
CG9536	2.61	2.93	1.1E-09
firl	0.79	2.93	2.0E-04
CG42496	1.58	2.92	8.2E-06
CG11802	0.43	2.92	3.6E-03
CG11147	21.15	2.91	1.5E-05
CG5854	4.55	2.91	1.3E-06

CG5999	0.48	2.91	3.2E-02
mth9	0.62	2.90	1.6E-05
ibug	10.37	2.90	9.3E-05
CG11444	3.55	2.90	5.2E-08
Pura	5.94	2.89	3.4E-08
CG30411	1.65	2.88	6.2E-05
form3	5.20	2.88	1.0E-06
Nlpn3	1.27	2.87	6.0E-03
CG8112	2.13	2.87	3.3E-05
CG32816	0.59	2.87	7.1E-04
Prx5	13.19	2.87	3.3E-09
CG13003	1.54	2.87	9.6E-06
Myo31DF	9.85	2.86	2.2E-07
bru2	2.59	2.86	1.2E-09
ana	1.37	2.85	2.3E-02
srp	3.42	2.85	3.3E-08
CG15611	6.23	2.84	9.9E-08
CG5080	6.10	2.84	7.7E-08
Tsp42Eg	6.91	2.84	6.8E-05
Mrp4	3.52	2.84	2.7E-08
Dbi	32.69	2.83	6.0E-06
Moe	13.26	2.83	3.3E-06
Lasp	3.63	2.83	4.8E-09
Atg3	2.66	2.83	2.9E-07
grass	3.17	2.82	3.0E-06
CG32396	0.38	2.82	2.9E-03
Vrp1	6.93	2.81	2.4E-08
yellow-g	0.32	2.81	1.7E-02
stv	15.35	2.81	7.0E-06
CG6310	3.95	2.81	3.5E-04
tty	4.46	2.81	4.8E-05
btz	0.93	2.81	9.4E-08
Nup93-1	1.65	2.80	2.0E-07
CG14777	1.23	2.80	3.6E-05
CG4511	3.04	2.80	5.2E-08
yki	3.05	2.80	2.1E-06
CG5151	2.90	2.80	4.9E-08
wupA	10.97	2.79	1.7E-03
RplL39	126.76	2.79	7.4E-06
Hmgcr	1.70	2.79	2.4E-06
CG12171	4.11	2.79	1.8E-07
CG42711	3.82	2.78	2.2E-04
Hmgs	6.42	2.78	2.7E-04
alpha-Est10	2.67	2.78	2.4E-07
chas	1.72	2.77	6.3E-08
Cpr67B	0.97	2.77	2.1E-02
sol	1.00	2.76	6.4E-07
NimC2	0.53	2.76	7.3E-04
Rpl35A	96.19	2.76	7.7E-05
Mct1	1.72	2.75	1.9E-05
CG8788	1.66	2.75	2.5E-06
Sf3b5	3.36	2.75	7.0E-05
Samuel	2.00	2.74	2.9E-09
rgn	15.56	2.74	1.9E-05
Tollo	3.86	2.74	3.1E-06
Cpr57A	0.20	2.74	4.2E-02
Ppcdc	1.28	2.74	6.8E-05
CG6163	0.79	2.74	3.0E-04
FK506-hp1	1.65	2.73	1.4E-05
CG11686	9.03	2.73	3.2E-05
peb	0.97	2.73	9.5E-07
gbb	3.23	2.73	4.9E-06
Hsp70Ab	20.06	2.73	1.3E-04
CG42237	0.30	2.73	3.6E-02
CG33260	2.43	2.73	1.7E-04
how	4.24	2.72	9.0E-08
CG11737	2.08	2.72	1.2E-07
CG1208	8.67	2.72	2.3E-05
CG30377	0.46	2.71	3.1E-05
CG42240	4.73	2.71	1.3E-07
dome	1.42	2.71	5.0E-06
ZnT63C	9.15	2.70	1.2E-06
CG34330	1.00	2.70	4.6E-02
CG33672	0.48	2.70	2.1E-02
CG43114	5.88	2.70	2.4E-04
IM14	22.58	2.69	7.3E-05
CG7185	1.22	2.69	4.4E-07
CG10232	0.86	2.69	7.7E-04
CG17111	4.76	2.69	2.4E-06
CG12814	6.87	2.69	3.2E-06
COX4	18.93	2.69	3.7E-07
CG11999	2.45	2.69	1.3E-05
stac	4.10	2.68	2.9E-07
TotM	4.55	2.67	3.7E-02
CG43163	1.54	2.67	6.8E-07
p47	2.95	2.67	1.1E-06
l(2)41Ab	5.54	2.66	7.3E-08
tamo	3.43	2.66	5.5E-08
CG7556	1.00	2.66	6.2E-06
Mmp1	4.80	2.66	2.2E-06
GstE3	23.37	2.66	1.8E-05
Ets98B	4.40	2.66	7.7E-07
Pvf2	0.54	2.66	7.7E-03
CG17202	1.67	2.66	7.2E-05
SmydA-9	0.32	2.66	9.1E-03
lvr	2.33	2.65	3.8E-06
mRpl4	1.07	2.64	2.1E-02
Pep	4.52	2.64	5.2E-09
prage	1.97	2.64	4.3E-06
CG15766	0.31	2.63	4.4E-02
Debel	1.87	2.63	1.5E-06
aop	5.98	2.63	7.3E-08
NimC4	0.91	2.63	2.9E-03
SRm160	0.80	2.63	2.8E-05
CG14613	1.53	2.63	1.9E-07
sa	1.05	2.63	5.4E-03
CG4404	4.56	2.63	4.2E-06
CG2034	0.99	2.62	7.2E-05
CrebB	2.19	2.62	1.1E-09
CG3328	1.00	2.62	9.4E-05
RpS10b	4.58	2.62	1.0E-06

Roe1	3.39	2.61	7.7E-07
eIF6	2.05	2.61	4.8E-04
CG8170	0.21	2.61	3.1E-02
wb	1.32	2.61	2.4E-04
Sap30	1.52	2.60	3.5E-07
l(3)02640	6.77	2.60	2.1E-07
CG5500	1.06	2.60	2.7E-03
Pvf1	2.35	2.60	2.6E-05
CG10341	2.36	2.59	1.4E-07
mRpS35	1.29	2.59	5.0E-04
CG3306	0.36	2.59	3.6E-02
IRSp53	5.33	2.59	3.3E-05
CG7379	1.25	2.58	3.9E-05
Spn31A	0.76	2.58	2.5E-02
mthl3	1.55	2.58	3.6E-04
CG2765	16.99	2.58	3.3E-03
Tdrd3	1.10	2.58	2.8E-05
aru	2.39	2.58	1.4E-05
CG1737	2.10	2.57	1.2E-06
bark	2.14	2.57	5.2E-06
CG10337	1.12	2.57	4.8E-04
bel	2.27	2.57	1.3E-06
CG12912	0.35	2.57	2.7E-03
raw	8.54	2.57	7.6E-07
CG1299	6.86	2.56	3.5E-04
Cyp4g15	5.33	2.56	4.9E-07
CG17919	4.92	2.56	1.3E-04
wat	28.07	2.56	2.4E-04
Akap200	14.68	2.56	7.2E-05
dmGlut	0.40	2.56	7.9E-03
pk	0.38	2.56	1.1E-06
CG17834	2.49	2.55	8.4E-06
CG18507	2.15	2.55	2.9E-04
CG17746	2.01	2.55	7.4E-07
CG32544	2.02	2.55	1.5E-03
DCP1	0.72	2.55	2.3E-03
CG31157	0.94	2.54	2.1E-02
ttm50	1.16	2.54	2.0E-05
ND-MLRQ	33.57	2.54	2.8E-07
CG7358	0.42	2.54	2.2E-04
CG6543	7.57	2.54	4.3E-05
Pvr	4.50	2.54	1.2E-06
CG5346	5.64	2.54	1.7E-06
CG9416	1.09	2.53	2.3E-05
Hil	1.68	2.53	1.7E-04
RpS8	110.24	2.53	6.1E-04
Non2	2.67	2.53	7.7E-07
MTF-1	2.36	2.53	1.6E-08
CG30269	2.02	2.53	1.9E-04
Hsp27	2.88	2.52	1.3E-04
DCTN2-p50	3.47	2.52	1.8E-06
zormin	4.34	2.52	1.7E-04
CG9451	8.02	2.52	3.4E-07
CG8399	8.58	2.52	1.0E-05
Hsc70-4	35.72	2.52	1.0E-04
RpL6	70.63	2.52	3.7E-04
CG34172	0.94	2.52	1.5E-02
CG4607	11.60	2.51	1.0E-05
POLDIP2	1.14	2.51	1.6E-05
AnxB10	6.81	2.51	1.1E-04
bocks	2.80	2.51	1.2E-05
bigmax	2.82	2.51	1.5E-05
Rab32	2.13	2.51	2.2E-05
Esy2	8.01	2.51	8.2E-06
Rpl41	318.79	2.50	5.5E-04
wuho	0.94	2.50	1.0E-03
CG32280	4.66	2.50	4.2E-06
CG31871	0.46	2.50	8.7E-03
CG8635	1.50	2.50	2.1E-05
COX5A	19.11	2.50	1.7E-04
CG34424	5.41	2.50	4.2E-04
Hmu	9.82	2.50	3.3E-07
CG7675	2.46	2.49	4.6E-04
CG14830	2.62	2.49	9.8E-04
Ctl1	9.15	2.49	9.5E-06
CG12237	2.77	2.49	6.6E-07
CG42709	4.23	2.49	1.1E-06
CG32982	2.89	2.49	1.8E-06
trol	15.65	2.49	6.2E-04
T48	3.61	2.48	1.2E-04
CG6040	2.74	2.48	1.4E-07
sut1	1.14	2.48	9.5E-05
CG8630	12.73	2.48	2.4E-04
Glc	9.01	2.48	3.7E-06
MFS14	14.39	2.47	1.4E-04
CG34166	78.45	2.47	1.0E-02
CG4585	2.57	2.47	4.2E-05
usp	1.78	2.47	2.8E-05
sav	0.74	2.46	1.6E-03
Cyp4p1	14.36	2.46	2.1E-05
Est-6	327.66	2.46	1.1E-02
ken	1.79	2.46	7.7E-05
Sep1	2.13	2.46	3.7E-07
CG31522	5.19	2.45	1.2E-05
AdoR	1.68	2.45	2.5E-04
CG10737	8.62	2.44	6.0E-06
Dpy-30L1	1.48	2.44	1.1E-02
NC2alpha	1.10	2.44	5.3E-03
CG6695	1.04	2.44	2.6E-05
CG7903	1.05	2.44	1.1E-03
CG32640	7.97	2.44	6.6E-04
Pcvt1	6.05	2.44	3.4E-07
CoproX	1.18	2.43	7.3E-04
phyl	1.48	2.43	2.2E-03
tna	5.75	2.43	4.8E-07
FeCH	8.75	2.43	3.9E-07
tzx	1.67	2.43	2.6E-04
CG42808	7.15	2.43	1.1E-03
sima	12.11	2.43	1.7E-04
Cdc7	2.64	2.43	7.9E-04
CG45085	3.08	2.42	2.1E-05

GstD1	150,35	2,42	1,7E-03
CG4752	4,18	2,42	6,9E-07
CG5810	2,27	2,42	3,8E-05
Inos	18,92	2,41	5,6E-05
Cht10	0,80	2,41	2,1E-02
pnut	2,10	2,41	1,9E-05
CG1673	9,07	2,40	2,8E-04
gless	2,53	2,40	2,7E-05
CSN7	2,27	2,40	1,1E-04
caix	68,07	2,40	7,7E-03
CG8010	1,15	2,40	2,4E-03
htk	1,18	2,40	6,9E-06
dwg	0,40	2,40	2,3E-02
dia	1,71	2,40	7,9E-08
CG6051	4,71	2,40	8,5E-06
Cyp310a1	1,22	2,39	1,2E-03
phu	5,34	2,39	1,2E-03
CG33785	0,66	2,39	3,8E-02
Sobp	0,48	2,38	1,1E-02
RhoGAP15B	2,64	2,38	1,1E-05
h	13,21	2,38	4,3E-06
CG9990	8,60	2,38	1,5E-05
Bgb	0,90	2,38	4,1E-03
CG7650	1,13	2,38	8,7E-05
Mgstl	14,17	2,37	1,9E-06
howl	1,24	2,37	4,7E-04
dnr1	3,14	2,37	1,1E-05
l[2]37Cc	2,96	2,37	2,5E-06
mys	9,47	2,37	2,5E-05
CG8239	1,28	2,36	3,7E-03
Syx16	0,90	2,36	3,3E-03
CG17121	8,08	2,36	1,8E-04
Pp1-87B	13,19	2,36	3,7E-06
MED19	2,11	2,36	4,7E-05
tx	0,44	2,36	6,5E-03
Lac	9,98	2,36	9,1E-06
emp	14,95	2,36	6,5E-04
l[1]G0320	9,04	2,36	1,6E-06
CG1146	5,68	2,35	1,8E-05
CG7789	0,75	2,35	1,6E-02
SH3PX1	3,17	2,35	2,9E-05
Pbgs	2,51	2,35	6,6E-04
CG9485	6,26	2,35	1,1E-04
Mpcp1	2,18	2,35	3,2E-04
Shmt	6,06	2,35	2,4E-05
cer	18,78	2,35	2,8E-04
vvl	7,62	2,35	3,5E-05
Rcd6	1,13	2,35	7,5E-04
Sodh-1	15,21	2,35	7,0E-03
CG3918	1,12	2,34	2,1E-04
CG1307	2,44	2,34	5,0E-06
Shark	1,11	2,34	2,6E-05
Act5C	83,88	2,34	1,2E-03
CG5001	2,84	2,34	1,9E-05
CG32645	0,52	2,34	1,1E-02
CG8180	1,28	2,34	2,9E-05
Bap111	0,35	2,34	1,0E-02
ND-B18	4,49	2,33	6,3E-05
CG5953	1,92	2,33	1,0E-03
Gs1l	5,69	2,33	8,3E-05
CG8547	14,74	2,33	9,8E-05
CG7694	2,99	2,33	3,9E-05
CG41520	2,02	2,32	1,8E-05
ptc	0,86	2,32	6,9E-05
pnt	0,98	2,32	1,3E-05
Rac2	3,87	2,32	3,6E-04
CG17265	0,28	2,32	4,1E-02
CecC	7,90	2,32	1,3E-02
Pka-C3	2,01	2,31	2,8E-02
CG9512	225,86	2,31	9,7E-03
CG5613	0,69	2,31	5,0E-03
Spn88Ea	8,32	2,31	1,5E-05
ovo	2,54	2,31	1,4E-05
Arp3	5,81	2,31	1,2E-06
Cyp313b1	1,63	2,31	4,4E-04
Shawn	0,80	2,30	7,4E-06
gukh	1,07	2,30	3,5E-05
ed	8,44	2,30	2,6E-04
tj	0,59	2,30	3,7E-02
dpy	3,09	2,30	2,3E-03
crb	3,64	2,29	5,4E-05
FrI	4,95	2,29	1,9E-05
CG13559	0,74	2,29	3,4E-02
GstE7	5,84	2,29	6,4E-04
Ugt36Bc	9,17	2,29	4,3E-05
CG8281	0,63	2,29	3,5E-02
Mhcl	6,33	2,29	1,4E-03
eIF3a	4,20	2,29	3,9E-06
wash	0,68	2,29	1,9E-03
Mlp60A	3,00	2,29	2,1E-03
kav	6,48	2,29	2,4E-04
CG2701	1,92	2,29	3,0E-06
GstE1	9,89	2,29	6,3E-04
CCT2	6,31	2,28	1,5E-06
CG16885	0,34	2,28	3,6E-02
nirk	2,52	2,28	1,9E-03
wapl	1,24	2,28	4,5E-05
galla-1	1,66	2,28	9,5E-05
Drat	9,51	2,28	1,2E-05
p24-2	3,00	2,28	2,8E-04
ubi	1,99	2,27	3,7E-02
Vdup1	2,49	2,27	1,7E-03
SsRbeta	9,46	2,27	7,6E-05
Reg-5	5,55	2,27	5,4E-05
ATP7	2,84	2,27	1,6E-05
CG5381	5,34	2,27	1,3E-05
CG11178	0,62	2,26	2,7E-04
CG3529	3,15	2,26	7,2E-05
msk	10,27	2,26	2,4E-05
Spn43Aa	0,39	2,26	4,9E-02
Spn55B	2,63	2,25	1,0E-03

CG12581	2,50	2,25	2,9E-04
apt	2,80	2,25	4,0E-06
Swim	3,07	2,25	1,6E-02
CG15771	5,55	2,25	5,5E-05
HisRS	2,15	2,25	8,5E-05
kst	3,82	2,25	3,0E-04
l[2]eff	5,64	2,25	4,8E-04
MFSR3	6,66	2,24	4,9E-05
Mvb12	1,74	2,24	3,5E-05
IP3K2	3,27	2,24	1,3E-06
crim	6,41	2,24	7,4E-05
tsr	45,97	2,24	6,9E-04
CG9812	10,85	2,24	1,7E-03
TrR99D	1,15	2,24	4,5E-04
kni	0,77	2,24	7,1E-04
CG30499	3,90	2,24	3,5E-05
CycY	1,63	2,24	3,0E-05
Zw	3,68	2,24	1,5E-04
Khc	3,86	2,23	6,9E-06
z	1,01	2,23	3,8E-05
ex	3,16	2,23	4,6E-05
Gli	2,66	2,23	4,6E-06
CG1486	1,40	2,22	3,3E-04
sea	4,34	2,22	2,1E-04
Usp16-45	0,89	2,22	3,0E-05
CG3815	0,52	2,22	3,6E-03
CG31904	0,43	2,22	5,5E-03
GlyP	21,47	2,22	1,3E-03
CG30280	1,48	2,22	8,3E-03
AIMP3	2,16	2,22	5,3E-03
RpLP0	71,05	2,21	3,3E-03
pnr	0,26	2,21	1,3E-02
meso18E	0,63	2,21	5,8E-03
CG10321	1,62	2,21	2,8E-04
CG8303	1,42	2,21	9,4E-03
Lkb1	0,68	2,21	6,1E-04
da	2,61	2,21	3,9E-05
Tsp42Ee	69,24	2,21	4,1E-03
Mrtf	1,67	2,21	5,5E-05
CG8745	17,11	2,21	7,0E-04
GlcT-1	1,89	2,21	3,7E-04
CG6294	0,19	2,21	4,5E-02
Cdc37	2,40	2,21	3,8E-05
mthl5	2,69	2,21	1,2E-03
pwn	0,35	2,20	2,4E-03
CG5639	0,28	2,20	6,9E-03
slz	5,36	2,19	1,2E-05
PRAS40	3,43	2,19	2,9E-04
CG8854	1,03	2,19	6,4E-03
Usp12-46	3,59	2,19	5,5E-05
CheB42c	3,11	2,19	3,8E-04
CG2200	1,04	2,18	2,8E-02
CG1632	0,23	2,18	3,5E-02
AhcyL1	4,53	2,18	1,5E-05
Msr1	4,10	2,18	1,6E-03
Scalpa	10,83	2,18	2,6E-05
CG3308	11,75	2,18	3,9E-05
CG1105	2,95	2,18	8,5E-04
sas	4,00	2,18	4,0E-04
CG2006	0,37	2,18	3,8E-02
CG30456	0,59	2,18	6,1E-03
CG1236	1,42	2,18	2,4E-03
CG5778	6,81	2,18	1,4E-03
CG12219	0,94	2,18	1,5E-03
PIG-V	1,56	2,17	9,7E-05
MED18	1,09	2,16	2,0E-02
Rpb10	3,62	2,16	2,1E-02
CG15394	8,97	2,16	7,3E-03
Fdh	8,65	2,16	5,6E-05
Hexim	0,79	2,16	4,8E-03
Sec22	5,83	2,16	3,3E-05
sni	4,59	2,16	5,4E-04
Cad86C	1,14	2,15	1,4E-03
Saf-B	2,87	2,15	3,0E-05
CG4239	1,69	2,15	2,1E-04
CG13919	1,32	2,15	3,9E-02
ytr	2,71	2,15	2,5E-04
CG5458	1,25	2,15	5,9E-03
CG1136	1,17	2,15	1,5E-03
Rpn1	4,88	2,15	7,2E-06
CG12576	5,86	2,15	2,6E-05
Ctr1B	0,98	2,15	2,9E-02
CG42673	2,74	2,15	2,0E-05
HP1b	0,98	2,15	5,8E-03
sw	6,06	2,14	9,5E-05
pzg	1,68	2,14	1,3E-04
CG31955	0,58	2,14	3,1E-02
Arpc1	4,53	2,14	2,7E-04
CG6084	17,50	2,13	5,4E-04
l[1]G0007	0,69	2,13	1,5E-04
CG32638	7,69	2,13	6,3E-05
c12.1	1,27	2,13	2,5E-02
Cyp6a9	12,22	2,13	4,6E-04
sano	2,42	2,13	1,0E-04
CG5597	4,54	2,13	8,9E-03
SERCA	14,38	2,13	3,1E-03
Fit1	7,84	2,12	7,9E-05
Mnt	4,41	2,12	8,6E-05
mRp521	3,30	2,12	7,8E-03
Cle	7,81	2,12	7,0E-05
CG5789	3,61	2,12	3,1E-05
CG4645	2,61	2,12	9,6E-05
RasGAP1	4,08	2,12	8,7E-05
ci	3,08	2,11	3,1E-05
CG5002	1,29	2,11	4,9E-03
scramb2	4,93	2,11	3,5E-04
ect	0,39	2,11	8,1E-03
CG10211	0,43	2,11	1,2E-02
CG2218	1,57	2,11	1,5E-04
Sesn	5,61	2,11	9,7E-04
CG3773	1,14	2,11	4,3E-02

CG33229	30,61	2,11	8,4E-04
Ras64B	7,83	2,10	1,8E-04
CG17278	6,03	2,10	4,2E-05
l(3)05822	3,75	2,10	9,1E-05
Pyk	19,86	2,10	7,1E-04
RhoU	0,72	2,10	3,4E-03
pyd	6,21	2,10	3,8E-03
CG1662	1,60	2,10	1,2E-02
Sox14	3,11	2,09	1,4E-05
nuc	6,86	2,09	2,8E-04
CG3655	5,30	2,09	3,4E-03
CG4266	1,00	2,09	8,7E-05
CG46306	0,74	2,09	5,4E-03
CG6479	1,07	2,09	3,6E-03
Sas10	0,88	2,08	8,2E-03
CHKov2	5,16	2,08	5,8E-04
CCT7	5,12	2,08	8,1E-06
AMPKalpa	3,62	2,08	2,1E-05
CG11089	8,31	2,08	2,8E-03
Prosbeta7	9,43	2,08	9,8E-05
luna	2,45	2,08	2,1E-04
CG1648	6,27	2,08	1,0E-02
CG15083	10,70	2,08	1,9E-03
CG5986	1,26	2,08	1,1E-02
CG34325	8,08	2,08	3,5E-04
Zasp66	8,32	2,07	3,1E-03
CG12024	3,02	2,07	1,5E-03
nec	15,24	2,07	2,5E-04
CG12947	2,18	2,07	2,1E-03
CG7239	0,77	2,07	1,4E-02
mbt	1,38	2,07	1,4E-04
mRpS17	1,12	2,07	4,2E-02
CG1572	23,14	2,07	2,0E-03
CG13384	7,23	2,07	2,0E-04
Igbn	1,04	2,07	3,4E-04
CG3558	2,90	2,07	3,1E-05
UOCR-6.4	7,96	2,07	4,5E-04
kermi	0,39	2,07	4,1E-02
vito	0,77	2,07	4,4E-02
Jhl-26	5,67	2,07	2,3E-03
Sec61alpha	18,80	2,07	5,6E-04
scb	3,26	2,07	1,1E-04
kibra	2,47	2,06	1,2E-04
sog	9,47	2,06	5,0E-03
CG42855	1,52	2,06	3,0E-02
mod(mdq4)	1,22	2,06	1,7E-04
Pgam5	1,06	2,06	2,0E-02
Oat	2,45	2,06	7,6E-03
CG31550	2,22	2,05	1,9E-04
CG12384	13,80	2,05	2,2E-03
CG4101	5,13	2,05	9,5E-03
eEF1beta	28,83	2,05	3,0E-03
Lint-1	1,18	2,05	1,6E-03
CG34056	1,66	2,05	3,9E-03
nocte	2,14	2,05	8,9E-05
Kcmf1	2,66	2,05	5,0E-04
ATPsvnCF6	19,77	2,05	2,1E-04
CG9436	1,22	2,05	2,4E-02
Cat	184,62	2,04	1,6E-02
Eno	21,30	2,04	3,8E-03
Su(z)12	1,22	2,04	1,4E-03
mgl	7,00	2,04	6,6E-03
CG9215	0,68	2,04	9,7E-03
e(v)3	1,75	2,04	7,0E-05
mRpl33	3,10	2,04	1,4E-02
Cortactin	2,81	2,04	6,6E-04
CG8468	2,91	2,04	3,0E-03
CG5903	4,02	2,04	1,8E-04
Pez	1,69	2,04	4,4E-04
chic	18,32	2,04	4,3E-03
Vps26	3,22	2,04	8,3E-04
CG8728	3,40	2,03	2,2E-04
Ten-m	9,18	2,03	6,0E-03
Synj	2,44	2,03	2,4E-04
salm	1,28	2,03	1,0E-02
CG45086	2,87	2,03	1,5E-03
Tpc1	1,88	2,03	1,4E-03
RplL24-like	10,78	2,02	2,2E-03
CG11367	0,62	2,02	1,7E-02
CG3732	0,85	2,02	1,6E-02
CG3295	2,88	2,02	2,4E-03
Prat2	12,00	2,02	3,3E-03
CG6398	6,79	2,02	3,3E-03
CG4733	1,14	2,02	3,3E-03
CHKov1	7,36	2,02	2,6E-05
Sema5c	1,23	2,01	2,7E-03
mor	1,24	2,01	1,7E-03
CG18304	0,37	2,01	1,7E-02
ValRS	2,05	2,01	4,4E-04
mam	2,02	2,01	1,0E-04
rho-7	1,39	2,01	8,2E-03
CG10939	6,97	2,01	4,5E-03
CG4603	1,02	2,01	2,2E-02
Sirt4	1,39	2,01	4,3E-02
Pdi	34,59	2,01	5,5E-03
CG5885	8,70	2,00	4,9E-04
CG10657	2,62	2,00	6,1E-04
sals	0,82	2,00	8,9E-04
CG7518	1,76	2,00	9,9E-05
S	2,17	2,00	1,1E-04
CG5292	0,86	2,00	7,2E-03
CG3634	0,95	2,00	1,2E-03
CG16886	0,88	1,99	4,8E-02
CG8929	3,25	1,99	1,1E-04
CG31195	3,15	1,99	2,1E-04
loco	1,65	1,99	8,3E-05
rols	0,75	1,99	6,0E-04
CG14414	1,35	1,99	1,2E-02
CG7497	13,09	1,99	4,5E-03
CG42741	3,13	1,98	7,7E-04
SoxN	2,40	1,98	1,1E-04

CG9149	3,88	1,98	4,9E-03
spict	5,93	1,98	1,4E-03
CG30159	4,63	1,98	5,5E-04
Ask1	2,48	1,98	5,7E-03
Sirup	16,12	1,97	9,0E-03
ATPsynE	15,79	1,97	4,9E-04
vialf	5,62	1,97	7,6E-04
CG1092	3,77	1,97	1,5E-03
Pgl	24,86	1,97	8,4E-03
Npc2b	20,29	1,97	5,4E-03
elB	2,63	1,97	2,0E-03
vir-1	71,27	1,97	2,5E-02
CG32687	3,86	1,97	8,7E-03
CG3699	7,48	1,97	1,1E-02
CG11334	1,50	1,97	3,6E-03
Rox8	3,56	1,96	1,2E-04
PheRS-m	3,18	1,96	5,7E-03
sra	3,13	1,96	6,0E-04
Ira	4,25	1,96	9,4E-04
Cyp6a21	1,16	1,96	2,7E-02
Tre1	2,41	1,96	5,5E-03
Lrpprc2	0,64	1,96	3,9E-03
CG43954	2,08	1,96	2,3E-03
ens	7,81	1,96	2,4E-03
Dmtn	4,94	1,96	1,4E-04
EndoGl	5,10	1,96	5,4E-03
noc	2,96	1,96	3,3E-03
Uch	4,91	1,96	1,2E-03
Mur2B	2,32	1,96	9,6E-05
baz	8,35	1,95	1,7E-02
CGT6	5,20	1,95	4,0E-05
CG42336	1,54	1,95	9,0E-04
CG8306	3,16	1,95	4,0E-03
c12.2	1,17	1,95	4,1E-03
bab2	1,33	1,95	2,2E-02
CG31997	29,73	1,95	1,1E-02
CG11893	0,98	1,95	2,1E-02
tim	5,23	1,95	2,9E-02
egr	1,97	1,95	9,1E-04
CG42319	1,09	1,95	1,2E-03
CG11779	1,19	1,95	2,5E-03
ND-18	2,33	1,95	5,2E-03
Pino	16,86	1,94	5,4E-03
vsg	34,60	1,94	9,6E-03
CG7054	3,47	1,94	3,4E-03
Sema2a	2,11	1,94	1,1E-03
CG7655	1,58	1,94	1,3E-02
Bx42	1,26	1,94	1,1E-02
Rr-h1	4,64	1,94	8,7E-03
Lnk	1,09	1,94	4,4E-04
CG9932	12,69	1,94	1,2E-02
Cyp305a1	13,69	1,94	1,8E-02
for	5,85	1,94	3,3E-03
Hexo2	4,00	1,93	3,1E-03
CG11448	5,42	1,93	1,2E-03
CG42374	0,50	1,93	4,3E-02
fus	3,48	1,93	6,0E-03
CG33080	2,45	1,93	2,9E-03
CG32649	1,25	1,93	2,0E-03
Tm1	3,78	1,93	5,5E-03
pyr	0,93	1,93	4,0E-03
red	2,38	1,93	1,5E-03
Capr	2,50	1,93	5,3E-04
CG6959	6,94	1,93	7,3E-03
CG12236	1,24	1,93	1,5E-03
DCTN4-p62	1,54	1,93	5,0E-03
SNF4Agamma	3,47	1,93	1,7E-03
CG34293	2,14	1,93	5,0E-03
glec	8,91	1,93	1,4E-04
IntS4	0,60	1,93	1,4E-02
if	3,98	1,92	8,1E-04
CG3077	2,19	1,92	5,8E-04
Timp	19,52	1,92	2,7E-03
sinu	2,95	1,92	1,0E-03
sowah	1,82	1,92	1,7E-03
HP1c	1,21	1,92	3,2E-02
Hel89B	3,49	1,92	8,2E-04
beta-Spec	11,11	1,92	9,3E-03
Srp54	2,40	1,92	4,6E-03
Tab2	1,84	1,92	5,3E-04
Vps37B	1,70	1,92	9,9E-03
CG42684	1,56	1,92	4,0E-04
His3.3A	5,93	1,92	7,6E-03
CG3999	1,24	1,91	1,1E-02
Ack	1,85	1,91	2,2E-03
InR	4,48	1,91	1,3E-02
stumps	5,16	1,91	1,7E-03
CG10492	1,32	1,91	1,9E-03
mRpl27	1,67	1,91	3,0E-02
mth10	2,18	1,91	1,1E-02
phol	1,60	1,91	3,8E-03
Rab10	3,57	1,91	2,7E-03
Ndfip	5,04	1,91	1,6E-04
Madm	1,15	1,91	4,4E-03
Cyt-c1	15,05	1,91	7,8E-04
woc	1,78	1,91	3,7E-04
CG43736	2,56	1,91	9,0E-04
CG11951	2,45	1,91	8,8E-03
Cyp6d4	3,04	1,91	2,2E-03
Pcl	1,17	1,91	4,2E-03
Cht5	4,96	1,91	5,4E-03
Sema1b	5,76	1,91	2,3E-03
CG31869	0,94	1,90	3,5E-03
CG17574	3,72	1,90	1,7E-03
Ppat-Dpck	1,53	1,90	6,9E-03
CG5445	3,54	1,90	2,0E-03
coro	3,98	1,90	1,0E-03
Pax	3,01	1,90	6,6E-04
Spt6	2,26	1,89	2,6E-04
ZnT77C	3,40	1,89	4,0E-02
GstE11	1,70	1,89	4,4E-02

moody	4,46	1,89	1,9E-04
Cyp4d20	2,32	1,89	4,5E-03
blw	53,50	1,89	1,8E-02
Unc-115b	3,01	1,89	1,9E-02
CG9065	6,68	1,89	7,0E-03
CG11050	5,08	1,89	3,7E-04
blp	1,69	1,89	1,2E-02
qsm	1,00	1,89	4,4E-02
CG3609	18,57	1,89	7,0E-03
Cont	6,54	1,89	3,2E-03
CG32267	5,25	1,89	1,6E-03
Uba1	9,85	1,89	3,9E-03
Atg13	4,61	1,89	8,2E-04
CG3548	0,50	1,88	2,0E-02
CG33978	0,79	1,88	2,1E-03
Acn	4,22	1,88	5,6E-04
CG32137	2,26	1,88	3,0E-03
Rpb7	1,42	1,88	3,9E-02
alc	5,99	1,88	2,1E-03
Rpb12	4,93	1,88	8,9E-03
Atf3	4,68	1,88	2,8E-03
Dip-C	1,63	1,88	8,3E-03
YhaPPA1-1	11,59	1,88	7,7E-04
CG13124	18,26	1,88	2,0E-02
Rpt5	6,45	1,88	2,9E-04
Ns3	1,06	1,88	1,4E-03
SP1173	5,25	1,88	6,9E-03
Cul5	1,49	1,88	5,0E-03
CSN1b	2,36	1,87	9,1E-04
arm	5,74	1,87	1,6E-03
cv-c	4,72	1,87	8,5E-03
Svil	3,80	1,87	1,9E-02
Pak3	5,90	1,87	2,4E-03
Dif	3,94	1,87	3,7E-03
tk	2,46	1,87	1,2E-03
CG8735	3,19	1,87	3,1E-03
drongo	6,66	1,87	2,4E-03
CG4552	2,33	1,87	1,7E-03
Med	0,72	1,87	8,1E-03
CG14207	16,88	1,87	1,1E-02
hid	0,88	1,87	9,4E-04
Tsp29Fb	9,05	1,87	1,8E-02
conv	0,51	1,87	2,7E-02
alph	5,23	1,87	8,1E-04
Brd8	0,61	1,87	1,1E-02
CG6907	0,91	1,86	2,6E-02
Taf6	1,72	1,86	9,6E-04
Pip1	0,99	1,86	2,4E-03
Nrd1	1,44	1,86	1,8E-03
fax	25,11	1,86	3,7E-02
alpha-Est7	25,93	1,86	2,3E-02
CG13607	5,63	1,86	1,1E-03
CG6843	1,69	1,86	4,6E-02
SerRS	3,91	1,86	3,5E-03
MRP	7,30	1,86	6,9E-03
dl	2,98	1,86	2,8E-03
yellow-b	2,20	1,85	5,8E-03
Rip11	2,21	1,85	3,2E-03
Pomp	6,60	1,85	1,9E-03
CG30022	5,46	1,85	7,1E-03
CG33774	4,47	1,85	4,6E-02
CG11695	0,65	1,85	4,0E-02
CG12268	0,94	1,85	1,0E-02
CG3847	1,59	1,85	2,5E-03
hay	1,00	1,85	5,7E-03
btsz	2,76	1,85	1,7E-02
CAP	2,16	1,85	3,7E-03
CG17600	0,41	1,84	3,7E-02
Jupiter	8,45	1,84	3,3E-03
CG5273	9,03	1,84	6,1E-03
Tie	0,69	1,84	4,5E-03
CG18809	1,00	1,84	1,0E-02
Tsp42Ef	12,74	1,84	8,2E-04
c11.1	4,44	1,84	2,9E-03
CG4825	2,52	1,84	2,5E-02
CG32579	1,56	1,84	1,2E-02
CG3902	8,78	1,84	1,8E-03
AOX3	5,58	1,84	4,2E-03
Bet1	1,46	1,84	4,6E-02
aay	26,84	1,84	7,7E-03
RapGAP1	3,55	1,84	1,8E-03
MED15	0,96	1,84	6,6E-03
CG30122	2,87	1,84	1,2E-03
Meltrin	2,86	1,84	2,4E-03
dip	1,44	1,83	2,4E-02
Nxt1	2,98	1,83	2,1E-02
CG4936	0,89	1,83	1,8E-02
CG6420	1,08	1,83	8,9E-03
18w	2,96	1,83	8,6E-04
CG17593	3,04	1,83	2,7E-03
Galphai	4,05	1,83	1,0E-02
CG7763	2,63	1,83	5,9E-03
CG8738	1,17	1,83	3,8E-02
Tsp42El	8,99	1,83	7,6E-03
SNRPG	3,62	1,82	2,1E-02
COX8	23,82	1,82	3,3E-03
Best2	2,27	1,82	2,1E-02
CG10126	6,58	1,82	2,8E-02
CHMP2B	4,18	1,82	1,9E-02
CG34133	2,66	1,82	1,2E-03
shg	3,07	1,82	6,0E-03
Acon	24,41	1,82	2,1E-02
CG12393	0,94	1,82	2,9E-02
Glycogenin	2,62	1,82	1,4E-03
ckn	2,66	1,82	1,3E-03
CG16903	0,78	1,82	1,9E-02
BTBD9	1,07	1,82	1,2E-02
Ance	4,94	1,82	2,7E-03
Tango1	3,55	1,82	1,1E-03
CG10209	1,14	1,82	2,1E-03
Piezo	5,46	1,82	2,1E-02

Gpo-1	7,53	1,82	2,7E-03
ACC	24,82	1,82	3,7E-02
CG16711	1,48	1,82	4,4E-03
RpS21	68,27	1,82	2,9E-02
CG8993	6,45	1,81	1,2E-03
tank	1,76	1,81	1,1E-02
Mfe2	4,48	1,81	9,5E-04
NK71	3,23	1,81	1,1E-03
CG2918	5,51	1,81	6,1E-03
Ssrp	2,35	1,81	1,1E-02
l(C)C0289	8,16	1,81	2,5E-03
CG8008	1,09	1,81	1,9E-02
koi	2,49	1,81	1,6E-03
Lpin	6,06	1,80	4,8E-03
B52	6,05	1,80	2,7E-03
D19A	0,79	1,80	6,6E-03
Zif	1,31	1,80	2,3E-02
ASPP	1,15	1,80	7,1E-03
Prosalpha6	6,52	1,80	3,2E-03
Csk	9,30	1,80	2,5E-02
Set2	1,12	1,79	7,5E-03
CG42271	0,80	1,79	3,2E-03
RpL38	68,63	1,79	4,3E-02
sina	1,37	1,79	8,0E-03
RpII215	3,51	1,79	2,6E-03
Rga	2,07	1,79	5,2E-03
Cyp6a20	12,85	1,79	1,2E-02
caet	8,74	1,79	3,6E-03
THHalpha	1,09	1,79	2,2E-02
RanBPM	3,74	1,79	7,8E-04
alpha-Est3	1,29	1,79	7,2E-03
sick	3,69	1,79	1,7E-02
sdt	4,35	1,78	2,2E-02
CG7457	0,89	1,78	4,8E-03
Myo61F	1,26	1,78	2,4E-02
GstE6	18,05	1,78	4,6E-02
CG5004	1,84	1,78	1,3E-03
CG13116	18,08	1,78	4,8E-03
rhea	8,49	1,78	3,7E-02
CG1703	2,52	1,78	1,7E-02
CG9581	0,85	1,78	3,1E-02
CG7632	3,85	1,78	1,0E-02
SF1	1,37	1,78	2,7E-03
PEK	1,56	1,78	7,5E-03
ine	2,53	1,78	8,4E-04
CG43394	2,01	1,77	3,9E-03
CG30344	4,03	1,77	1,1E-02
PDCD-5	3,49	1,77	6,3E-03
ATPsvnB	7,72	1,77	4,2E-03
GluProRS	3,27	1,77	2,1E-03
GC52beta	2,77	1,76	8,5E-03
CG6495	1,18	1,76	1,1E-02
kek5	2,48	1,76	3,8E-03
CG9775	3,97	1,76	1,1E-03
Flo1	2,62	1,76	2,4E-02
CG6227	0,61	1,76	2,2E-02
CG14995	1,64	1,76	8,5E-03
axed	1,05	1,76	1,5E-02
flr	1,98	1,76	2,9E-02
CG9674	17,42	1,76	4,7E-02
kume	7,49	1,76	3,0E-02
Clic	5,68	1,76	9,3E-03
RhoGAP92B	2,34	1,75	5,1E-03
bif	2,10	1,75	5,4E-03
lJeh2	12,39	1,75	1,1E-02
CG44195	1,80	1,75	3,4E-02
CenG1A	2,91	1,75	1,7E-03
ND-MWFE	6,11	1,75	2,2E-02
egl	3,79	1,75	4,4E-03
CG32694	0,72	1,75	2,0E-02
CG3842	1,98	1,75	7,5E-03
caz	1,25	1,75	2,1E-02
Drxg	0,88	1,75	4,0E-02
by	3,94	1,75	1,1E-02
Rhp	1,27	1,75	1,0E-02
Sp7	3,18	1,75	2,0E-02
Prosheta1	12,63	1,75	5,1E-03
MED14	1,80	1,75	8,0E-04
CG34253	6,58	1,75	1,3E-02
TSG101	4,97	1,75	5,8E-03
CG5262	2,75	1,74	7,7E-03
CG1824	1,19	1,74	1,3E-02
Mcr	4,77	1,74	8,5E-03
Dad	4,91	1,74	5,9E-03
Ptip	1,32	1,74	1,5E-03
CG31103	6,92	1,74	2,3E-02
CG8026	4,02	1,74	2,3E-03
Indy	15,89	1,74	3,1E-02
CG5446	4,81	1,74	1,9E-02
be	2,23	1,74	2,7E-03
CG12773	1,40	1,74	8,7E-03
Vha26	26,66	1,74	4,4E-02
kar	2,57	1,74	1,3E-02
CG15093	6,25	1,74	2,3E-02
CG2604	3,68	1,74	1,6E-02
Mdh2	24,77	1,74	1,9E-02
Nrs	6,42	1,73	4,7E-02
CG10916	2,90	1,73	3,6E-02
SREBP	11,39	1,73	3,0E-02
pll	1,23	1,73	4,8E-02
Df31	5,24	1,73	1,0E-02
Fbxl7	0,53	1,73	3,7E-02
CG10932	2,93	1,73	2,4E-02
Prosheta6	10,75	1,73	1,9E-03
beta4GalNacTA	2,61	1,73	3,2E-02
mew	1,93	1,73	5,3E-03
GekIII	1,79	1,73	1,0E-02
Ppox	1,25	1,73	2,6E-02
Mipp1	6,76	1,73	1,2E-02
CG14411	1,30	1,73	1,7E-02
AsnS	3,54	1,73	8,9E-03



CG33144	3.49	1.73	9.7E-03
Drip	11.47	1.73	3.0E-02
Myd88	3.05	1.72	3.5E-03
POSH	1.33	1.72	1.1E-02
RhoL	3.91	1.72	1.4E-02
SdhD	7.37	1.72	1.5E-02
kto	0.90	1.72	7.5E-03
mxt	3.85	1.72	4.5E-03
egb	7.30	1.72	1.3E-02
hop	1.47	1.72	1.3E-02
CG3402	2.02	1.72	5.0E-02
pod1	3.76	1.71	8.2E-03
eIF3c	6.64	1.71	7.1E-03
spz	3.67	1.71	3.0E-02
nuf	5.63	1.71	1.0E-02
CG31710	1.63	1.71	3.8E-02
Rs1	0.93	1.71	3.1E-02
CG34310	0.52	1.71	1.9E-02
CG43781	2.19	1.71	2.6E-02
CG31121	0.74	1.71	1.5E-02
Subc	1.49	1.71	4.0E-02
CG7656	1.30	1.71	1.3E-02
lig	2.52	1.71	6.2E-03
eIF1	19.92	1.71	8.0E-03
Ublcp1	1.93	1.71	9.8E-03
DI	0.52	1.71	3.0E-02
Djp-B	16.16	1.71	2.7E-02
Dcr-2	3.27	1.71	1.6E-02
unc-45	1.02	1.71	3.5E-02
p38a	1.98	1.70	2.0E-02
Ugr86Da	8.03	1.70	4.5E-02
LRR	4.74	1.70	1.1E-02
Idh	23.07	1.70	4.7E-02
CG43143	1.42	1.70	1.3E-02
TrpRS	1.79	1.70	1.4E-02
cnk	1.24	1.70	1.4E-02
CG4797	5.95	1.70	1.9E-02
CG30460	3.89	1.70	2.5E-02
Sh3beta	3.82	1.70	8.5E-03
Stam	4.43	1.70	5.7E-03
mRNA-cap	1.30	1.70	1.7E-02
I(2)gl	4.87	1.70	1.2E-02
Rpl115	2.01	1.69	3.2E-02
lute	3.18	1.69	1.1E-02
fz2	4.31	1.69	1.3E-02
Exn	1.76	1.69	1.3E-02
bnl	0.69	1.69	4.5E-02
Shc	2.60	1.69	1.2E-02
PIG-M	0.83	1.69	4.1E-02
mEFTu2	1.23	1.69	2.2E-02
CG8860	7.24	1.69	4.7E-02
Eb1	7.48	1.69	1.0E-02
Hexo1	2.31	1.69	3.5E-02
CG6903	3.23	1.69	2.8E-02
CG1275	19.44	1.68	4.9E-02
Sf3b2	1.45	1.68	8.8E-03
CG32066	2.43	1.68	3.0E-02
CG13364	9.14	1.68	4.0E-02
Cad99C	0.42	1.68	3.5E-02
CG8188	2.70	1.68	5.5E-03
Hydr2	5.71	1.68	4.0E-03
Top3beta	0.70	1.68	1.2E-02
CG42813	2.58	1.68	1.8E-02
Asap	3.92	1.68	1.2E-02
drpr	5.24	1.68	2.1E-02
cl	8.56	1.68	3.3E-02
ste24a	4.75	1.68	2.1E-02
lig3	1.91	1.68	3.4E-02
CG17233	1.76	1.67	4.8E-03
mRps22	2.05	1.67	3.0E-02
CG3008	3.76	1.67	2.3E-02
seq	0.93	1.67	2.9E-02
Mitofillin	2.93	1.67	9.0E-03
lqf	3.87	1.67	1.3E-02
btl	1.40	1.67	3.3E-02
Yps24	1.92	1.67	4.3E-02
sun	14.54	1.67	3.2E-02
CG4080	1.80	1.66	2.1E-02
Sec15	1.47	1.66	1.2E-02
CG13698	4.59	1.66	1.9E-02
CG8009	2.82	1.66	1.5E-02
CG14153	3.61	1.66	3.5E-02
tmod	2.85	1.66	3.2E-02
GM130	2.00	1.66	1.5E-02
HERC2	1.55	1.66	2.5E-02
grh	0.80	1.66	3.9E-02
MED10	3.64	1.66	3.7E-02
CG4557	1.02	1.66	2.1E-02
CG10026	1.13	1.66	4.3E-02
Atg1	4.06	1.66	7.1E-03
CG14650	2.10	1.66	2.6E-02
CG40228	5.23	1.65	1.0E-02
su(Hw)	0.95	1.65	1.3E-02
CG5323	2.64	1.65	4.8E-02
CG16817	15.50	1.65	9.3E-03
CG17754	0.74	1.65	3.3E-02
pins	1.34	1.65	3.6E-02
ena	1.99	1.65	1.1E-02
r-i	2.07	1.65	3.6E-02
Faf2	2.47	1.65	2.0E-02
Tom7	6.68	1.65	1.8E-02
TBCB	3.35	1.65	1.6E-02
goe	1.48	1.64	4.2E-02
CG8405	2.32	1.64	5.3E-03
CG6701	5.45	1.64	2.9E-02
SC35	1.67	1.64	3.1E-02
Ced-12	1.92	1.64	3.9E-02
Sf3b6	3.69	1.64	2.5E-02
CG8243	1.21	1.64	3.3E-02
CG4751	0.99	1.64	4.4E-02
CG42674	1.84	1.64	1.9E-02

CG43780	2.04	1.64	5.0E-02
Map205	5.14	1.64	3.9E-02
dap	1.30	1.64	3.9E-02
CG32549	11.04	1.64	4.7E-02
Cyp12a5	1.26	1.64	4.9E-02
Naa20A	3.07	1.63	1.1E-02
Smd2	2.82	1.63	2.8E-02
Pfrx	6.50	1.63	2.1E-02
Usp47	4.20	1.63	4.0E-02
CG43759	1.17	1.63	3.0E-02
Red-1	4.61	1.63	3.7E-02
Rbf	1.47	1.63	3.1E-02
CG8034	2.73	1.63	9.7E-03
neur	0.85	1.63	2.2E-02
Unc-89	1.65	1.63	2.6E-02
CG11284	1.28	1.62	1.9E-02
ATPsvnD	16.06	1.62	1.3E-02
Vps20	4.73	1.62	4.9E-02
ALIX	7.18	1.62	2.4E-02
Mlc-c	12.26	1.62	1.9E-02
mol	1.26	1.62	4.4E-02
CG10435	1.27	1.62	4.8E-02
zip	4.76	1.62	4.1E-02
numb	2.37	1.62	2.0E-02
mth11	1.90	1.62	6.2E-03
Ire1	4.06	1.62	1.4E-02
spri	1.64	1.62	2.7E-02
Gcn5	1.99	1.61	4.1E-02
CG13887	18.87	1.61	3.6E-02
CG40160	1.91	1.61	1.1E-02
Jht-1	0.94	1.61	3.1E-02
Prx3	11.59	1.61	2.2E-02
I(1)G0156	5.91	1.61	1.2E-02
HDAC6	1.92	1.61	4.5E-02
Hrb98DE	7.89	1.61	2.6E-02
CG10376	2.05	1.61	4.8E-02
GEFmeso	1.48	1.60	1.5E-02
Ptp10D	2.96	1.60	3.3E-02
CG42390	3.66	1.60	4.4E-02
BRWD3	1.70	1.60	1.0E-02
ZnT41F	1.05	1.60	3.3E-02
dsh	0.95	1.60	2.3E-02
mts	9.17	1.60	3.4E-02
Kdm2	2.16	1.60	2.4E-02
cbt	6.48	1.60	2.2E-02
CG34394	4.20	1.60	3.0E-02
Tre8	1.71	1.60	4.9E-02
CG1317	3.81	1.59	2.1E-02
CG11897	3.10	1.59	1.6E-02
emc	10.85	1.59	2.7E-02
CG9135	1.07	1.59	4.6E-02
CG7378	4.03	1.59	4.2E-02
Mer	1.13	1.59	3.9E-02
fl(2)d	3.05	1.59	1.0E-02
Usp5	1.17	1.59	3.5E-02
ND-AGGG	18.93	1.58	3.4E-02
swm	2.33	1.58	1.7E-02
Rab6	3.36	1.58	4.0E-02
CG4631	1.54	1.58	3.7E-02
RhoGAP18B	2.37	1.58	4.7E-02
Snp	3.94	1.58	3.7E-02
E2f1	2.23	1.58	1.9E-02
CG14200	1.89	1.58	2.1E-02
Toll-7	2.01	1.58	3.4E-02
ssp2	2.58	1.57	2.5E-02
CHES-1-like	3.26	1.57	3.3E-02
ZnT86D	1.64	1.57	3.5E-02
velo	2.02	1.57	2.3E-02
sns	1.03	1.57	1.8E-02
yata	1.85	1.57	1.7E-02
CG5726	1.61	1.56	4.7E-02
CG5484	2.32	1.56	4.8E-02
CG42511	0.75	1.56	3.7E-02
rudhira	2.88	1.56	4.8E-02
Ucp4A	1.82	1.55	3.8E-02
Parp	5.41	1.55	3.0E-02
Patj	1.15	1.55	3.1E-02
Phb2	5.69	1.55	2.2E-02
capr	2.87	1.55	3.7E-02
Rpl34a	14.13	1.55	4.6E-02
CG13907	4.15	1.54	4.8E-02
raptor	1.21	1.54	3.7E-02
tara	2.44	1.54	3.6E-02
Rok	1.92	1.54	3.4E-02
UQCR-11	6.50	1.54	2.8E-02
Hnf4	2.77	1.54	3.2E-02
Mmp2	2.35	1.54	4.7E-02
lic	2.03	1.54	3.7E-02
sclank	3.49	1.53	3.4E-02
CG32425	2.97	1.53	3.7E-02
Abl	1.11	1.53	3.5E-02
Eip74EF	1.09	1.53	4.4E-02
I(2)01289	1.06	1.53	5.0E-02
slim	5.36	1.53	3.2E-02
ApapP	0.98	1.53	4.4E-02
Opn1	3.67	1.53	2.7E-02
Su(ds)	3.13	1.52	3.4E-02
Pt3K92E	2.62	1.52	3.8E-02
CG7430	6.25	1.52	3.5E-02
CalpB	3.24	1.52	4.3E-02
CG42353	2.53	1.51	2.4E-02
CG31694	5.68	1.51	4.0E-02
mld	2.02	1.51	4.1E-02
CCT4	4.59	1.50	3.6E-02
Atx2	2.65	1.49	3.4E-02
CG16979	1.81	1.49	4.6E-02
CG12004	3.87	1.48	4.2E-02
Sec31	2.41	1.48	4.1E-02
CG42524	3.98	1.48	4.9E-02
Smurf	2.68	1.48	4.5E-02
CG42588	1.10	1.47	4.9E-02

frj	4,90	-1,50	5,0E-02
conu	5,04	-1,50	4,6E-02
corn	1,69	-1,50	4,8E-02
CanB2	7,28	-1,52	3,9E-02
Tango9	3,40	-1,52	4,1E-02
CG3198	3,18	-1,53	4,9E-02
CG1427	2,40	-1,53	4,9E-02
CG17883	6,77	-1,54	4,6E-02
Rab4	8,71	-1,54	3,6E-02
Ctr9	3,01	-1,55	2,8E-02
Dic1	5,09	-1,55	2,4E-02
Pli	3,52	-1,55	2,8E-02
CG17493	2,49	-1,56	3,4E-02
dsb	2,88	-1,56	3,2E-02
gus	7,84	-1,57	2,6E-02
olf413	2,06	-1,57	4,6E-02
cal1	1,42	-1,57	4,9E-02
CG8671	2,94	-1,58	1,9E-02
CG11388	2,31	-1,58	4,1E-02
ewg	1,98	-1,58	2,2E-02
dtn	3,49	-1,59	4,8E-02
ATP8B	1,62	-1,59	3,3E-02
CG1888	0,63	-1,60	4,2E-02
CG1636	2,28	-1,60	3,9E-02
CG12484	1,76	-1,60	4,6E-02
Iscll	35,43	-1,60	4,6E-02
Rpt6	9,05	-1,60	1,6E-02
fru	0,96	-1,60	3,5E-02
IP3K1	12,59	-1,61	2,5E-02
CG2736	20,58	-1,61	2,2E-02
CG17715	3,42	-1,61	2,9E-02
Sema2b	1,80	-1,61	3,9E-02
SrpRbeta	3,38	-1,61	3,9E-02
cyc	1,83	-1,61	4,6E-02
Gbp3	12,06	-1,61	4,8E-02
CG5021	3,86	-1,61	4,7E-02
S1P	1,20	-1,62	3,2E-02
toy	3,24	-1,62	3,1E-02
CG3689	2,60	-1,62	3,7E-02
CG40191	8,17	-1,62	2,7E-02
CG4050	1,63	-1,62	3,8E-02
M6	2,15	-1,62	3,9E-02
GlcAT-P	3,97	-1,63	4,1E-02
eIF3i	17,09	-1,63	3,6E-02
CG3940	4,23	-1,63	4,9E-02
CG10068	2,03	-1,63	4,1E-02
CG3436	2,01	-1,64	4,5E-02
p24-1	4,15	-1,64	3,9E-02
CG8132	3,01	-1,64	4,4E-02
Iml1	3,89	-1,64	4,6E-02
sno	2,15	-1,64	2,5E-02
CG14868	1,31	-1,64	4,4E-02
CG9837	2,84	-1,64	2,8E-02
COQ7	4,65	-1,65	3,3E-02
CG17724	0,95	-1,65	3,4E-02
SrpK79D	1,34	-1,65	4,7E-02
Pur-alpha	12,08	-1,65	2,3E-02
g	2,78	-1,65	8,1E-03
Syn2	2,48	-1,66	4,0E-02
CG11456	1,39	-1,66	4,3E-02
DIP-theta	0,97	-1,66	4,9E-02
Nab2	1,77	-1,66	2,6E-02
CG13397	1,15	-1,67	3,2E-02
Den1	2,20	-1,67	3,5E-02
CG15431	1,44	-1,67	4,7E-02
Ssadh	6,77	-1,67	2,1E-02
jpg	7,09	-1,67	1,7E-02
CG12605	3,07	-1,67	3,7E-02
Ca-alpha1D	2,96	-1,67	4,6E-02
CG33203	1,93	-1,68	3,9E-02
Calx	2,15	-1,68	5,0E-02
CG42265	1,37	-1,68	3,8E-02
CG42806	4,12	-1,68	3,8E-02
Tnpo-SR	0,64	-1,68	4,0E-02
CG2217	2,38	-1,68	4,5E-02
Eaat2	3,38	-1,68	3,2E-02
stnA	4,30	-1,69	4,6E-02
CG4822	4,96	-1,69	4,0E-02
CG9902	0,44	-1,69	4,8E-02
esc	1,30	-1,69	4,2E-02
Cyp28d1	23,84	-1,69	3,2E-02
mth4	1,21	-1,69	4,8E-02
CG31213	0,51	-1,69	3,0E-02
Rhau	0,98	-1,69	2,9E-02
Gk1	5,68	-1,70	1,6E-02
CG45263	2,04	-1,70	4,9E-02
CG11400	14,80	-1,70	1,3E-02
CG6836	4,05	-1,70	4,5E-02
HIPP1	2,04	-1,70	1,2E-02
barc	3,28	-1,70	1,9E-02
Ars2	3,03	-1,71	6,0E-03
stnB	4,30	-1,71	4,3E-02
PTP-ER	1,78	-1,71	9,3E-03
lol	3,31	-1,71	9,3E-03
Rbfox1	4,79	-1,71	1,2E-02
veli	2,29	-1,71	2,4E-02
dati	2,59	-1,71	4,1E-02
Nep4	3,59	-1,71	2,6E-02
F-cup	1,44	-1,71	2,9E-02
smog	2,30	-1,71	1,8E-02
pgant2	0,81	-1,71	4,1E-02
CG17778	1,80	-1,72	4,0E-02
Dap160	3,07	-1,72	1,5E-02
pigeon	0,81	-1,72	2,0E-02
CG42541	1,77	-1,72	2,9E-02
CG15602	1,56	-1,72	2,3E-02
Toll-6	1,44	-1,72	2,8E-02
Aplip1	3,50	-1,72	4,8E-02
RagC-D	2,51	-1,72	2,9E-02
RpLP0-like	2,40	-1,72	2,2E-02
Nmdar2	1,36	-1,73	3,9E-02

CG17075	1,29	-1,73	1,5E-02
CG6805	4,14	-1,73	8,3E-03
Ent3	2,50	-1,73	3,4E-02
CG8525	2,55	-1,73	4,4E-02
beat-VI	1,65	-1,74	2,4E-02
Rbp1-like	6,44	-1,74	2,7E-02
fand	1,18	-1,74	2,5E-02
CG15270	1,78	-1,74	2,8E-02
Octheta3R	1,05	-1,74	4,9E-02
dysc	3,85	-1,74	3,0E-02
Pde6	2,71	-1,74	9,9E-03
urp	3,81	-1,74	1,8E-02
SPE	7,21	-1,74	2,9E-02
SCCRO	1,81	-1,74	1,5E-02
Gs1	9,60	-1,74	1,8E-02
DopEcR	4,59	-1,74	4,8E-02
Ect3	3,10	-1,75	3,9E-02
r2d2	1,78	-1,75	3,3E-02
Gfri	2,34	-1,75	3,6E-02
Drep4	1,88	-1,75	1,4E-02
Gasz	1,32	-1,75	2,5E-02
AkhR	4,20	-1,75	2,3E-02
CG8331	12,42	-1,75	9,6E-03
smal	1,57	-1,75	4,6E-02
Vps16A	1,22	-1,75	1,4E-02
CG3556	4,17	-1,76	2,1E-02
CG14182	2,15	-1,76	1,7E-02
JHDM2	0,96	-1,76	2,0E-02
Cyp4ac3	1,38	-1,76	1,9E-02
Seld	1,19	-1,76	4,8E-02
CG6654	3,50	-1,76	2,9E-02
CG11523	2,13	-1,76	4,6E-02
CG17816	4,32	-1,76	2,1E-02
ND-20	11,48	-1,77	4,4E-03
CG32165	1,19	-1,77	2,9E-02
Mys45A	1,25	-1,77	3,9E-02
anne	10,03	-1,77	3,6E-02
Ctr1A	2,93	-1,77	7,2E-03
CG1463	1,85	-1,77	1,5E-02
PlexB	5,44	-1,77	1,1E-02
Cyp6u1	1,12	-1,77	1,5E-02
klg	2,99	-1,77	2,4E-02
Eip63F-1	2,34	-1,77	4,0E-02
Nhe3	5,12	-1,77	3,4E-03
Rab21	2,24	-1,77	1,0E-02
CG3262	2,04	-1,78	1,7E-03
dpr1	1,99	-1,78	3,7E-02
sPLA2	9,73	-1,78	3,5E-02
CG5618	5,39	-1,78	3,1E-03
CG31115	2,30	-1,78	2,6E-02
dpr2	0,75	-1,78	4,6E-02
Mat1	1,38	-1,79	5,0E-02
CG17163	1,65	-1,79	1,9E-02
CG32681	0,93	-1,79	1,6E-02
stj	3,48	-1,79	1,9E-02
Dbp45A	1,32	-1,79	2,4E-02
CG6044	7,71	-1,79	3,0E-02
KiF3C	1,58	-1,79	8,5E-03
Fbxl4	1,00	-1,79	1,3E-02
Ac3	3,48	-1,80	3,6E-02
CG4686	4,34	-1,80	2,3E-02
Pkc98E	5,04	-1,80	4,5E-03
nAChRbeta2	1,97	-1,80	3,8E-02
CG15760	1,78	-1,80	3,8E-02
CG32850	6,08	-1,80	4,9E-03
Dh44-R2	1,10	-1,80	2,2E-02
prel	4,74	-1,80	6,6E-03
gprs	1,61	-1,80	1,5E-02
Sfxn2	2,40	-1,81	1,8E-02
Nca	13,79	-1,81	1,6E-03
CG43778	2,72	-1,81	1,7E-02
GNBP-like3	6,04	-1,81	5,0E-02
5-HT1B	0,66	-1,82	1,6E-02
CG46309	1,64	-1,82	3,9E-02
mRpS18A	2,78	-1,82	4,7E-02
CG11426	2,43	-1,82	1,3E-02
CG13086	3,08	-1,82	2,9E-02
CG10702	1,31	-1,82	2,2E-02
Fcp1	0,70	-1,82	1,6E-02
EndoA	6,08	-1,83	1,5E-02
stai	4,82	-1,83	7,2E-03
CG8586	8,10	-1,83	1,5E-02
CG6067	14,74	-1,83	9,2E-03
rad	1,57	-1,83	2,4E-02
Asator	5,19	-1,83	2,8E-02
Sdr	1,35	-1,83	4,3E-02
Dscam4	2,45	-1,83	4,0E-02
Gbeta76C	5,57	-1,83	2,9E-02
CG14015	0,71	-1,84	4,5E-02
CG17018	0,38	-1,84	2,3E-02
na	1,30	-1,84	9,7E-03
CG6329	10,05	-1,84	2,4E-02
ldgf5	6,14	-1,84	4,0E-02
Nep1	0,47	-1,84	2,0E-02
Rgk2	0,81	-1,84	2,6E-03
Sxl	8,26	-1,85	2,4E-02
CG11158	1,77	-1,85	1,4E-02
CG45782	2,05	-1,85	5,8E-03
CG6282	1,63	-1,85	4,0E-02
CG17321	1,44	-1,85	5,1E-03
GluRIB	1,31	-1,85	4,9E-03
SP2637	5,69	-1,85	1,4E-03
unc-104	15,22	-1,85	4,8E-02
KP78a	0,63	-1,85	3,3E-02
CG7997	5,01	-1,85	5,1E-03
Teh3	1,80	-1,85	1,8E-02
Ubi-p5E	35,82	-1,85	1,9E-02
Epac	2,14	-1,86	5,6E-03
Gyc88E	0,60	-1,86	2,9E-02
CG14535	0,65	-1,86	1,5E-02
Vps11	2,04	-1,86	3,9E-03

CG9380	0.43	-1.86	1.7E-02
CG4230	3.81	-1.87	5.6E-03
CG13293	1.35	-1.87	1.2E-02
dpr9	2.58	-1.87	9.0E-03
CG3857	0.67	-1.87	3.5E-02
CG9631	2.52	-1.87	1.2E-02
CREG	9.90	-1.87	8.5E-03
dpr13	1.97	-1.87	4.3E-02
SmydA-8	0.63	-1.87	5.0E-02
MP1	8.03	-1.88	3.8E-03
CG14688	4.62	-1.88	2.3E-02
CG32191	3.07	-1.88	2.8E-03
CG9609	1.11	-1.88	2.7E-02
CG45002	2.18	-1.88	2.5E-02
Cvt-b5-r	111.37	-1.88	3.0E-02
CG31937	9.29	-1.88	2.4E-03
CG43092	2.11	-1.88	3.7E-02
mmd	5.21	-1.88	1.6E-02
CG9265	0.96	-1.88	2.3E-02
CG9279	1.68	-1.88	8.7E-03
CG9590	1.34	-1.89	3.1E-02
kcc	7.19	-1.89	1.3E-02
CG6123	1.13	-1.89	2.5E-02
CG5071	1.19	-1.89	2.1E-03
nAchRalpha4	4.22	-1.89	2.8E-02
CaMKII	21.57	-1.89	3.5E-02
Nrk	0.63	-1.90	3.4E-02
Ddc	5.99	-1.90	2.1E-02
GABPI	2.28	-1.90	3.6E-03
CG17027	1.07	-1.90	3.2E-02
Nlg3	1.63	-1.90	1.6E-03
Rab26	0.87	-1.91	2.9E-02
jus	4.61	-1.91	5.1E-03
CDase	2.29	-1.91	5.9E-03
beat-IIIa	0.50	-1.91	4.5E-02
CG7668	3.72	-1.91	9.7E-03
Trax	1.25	-1.91	3.6E-02
sr	2.46	-1.91	1.8E-02
CG6972	1.94	-1.91	5.7E-03
RpL5	75.04	-1.91	2.3E-02
RpS6	156.37	-1.91	2.3E-02
CG42700	0.60	-1.91	3.0E-02
CG4753	1.96	-1.91	4.6E-02
Octbeta1R	1.80	-1.92	3.7E-03
GXIVsPLA2	2.20	-1.92	1.1E-02
CG6218	2.56	-1.92	6.3E-03
Vha16-1	41.97	-1.93	1.5E-02
Ufd1-like	3.59	-1.93	1.4E-03
Ekar	0.92	-1.93	1.1E-02
CG9649	3.22	-1.93	1.4E-02
Ser7	3.34	-1.93	1.4E-02
sei	1.65	-1.94	1.2E-02
CG9596	0.63	-1.94	3.4E-02
Cht6	0.23	-1.94	3.7E-03
CG4766	0.91	-1.94	1.0E-02
bma	1.53	-1.94	1.8E-03
Galphao	7.22	-1.94	9.5E-03
CG10513	5.82	-1.94	4.4E-02
CG44098	1.26	-1.94	1.8E-02
Rph	0.65	-1.94	9.7E-03
hlg	6.54	-1.94	1.1E-02
CG6912	9.72	-1.94	1.2E-03
ZnT33D	0.68	-1.95	4.1E-02
elav	4.70	-1.95	1.1E-02
CG10384	0.93	-1.95	1.1E-02
Sp1	0.31	-1.95	4.3E-02
amon	8.19	-1.95	1.3E-02
CG4725	2.38	-1.95	9.5E-03
Cyp9h1	2.09	-1.95	2.6E-02
Dlip3	0.97	-1.95	4.5E-02
Nfl	6.21	-1.95	3.4E-03
CG33470	26.05	-1.95	5.0E-03
CG15765	6.87	-1.95	1.1E-02
Su(H)	0.66	-1.96	2.1E-02
CG6426	39.09	-1.96	1.4E-03
Dhit	1.56	-1.96	7.5E-03
fat-spondin	13.16	-1.96	2.2E-03
beat-1c	1.29	-1.96	2.0E-02
SPR	3.15	-1.96	5.2E-03
eIF5	6.58	-1.96	6.4E-04
Est-Q	3.26	-1.96	6.0E-03
Rab3-GEF	2.59	-1.96	4.3E-03
psh	2.80	-1.96	6.4E-03
CG16716	0.60	-1.97	3.6E-02
Rdl	8.24	-1.97	3.2E-02
CG18476	0.79	-1.97	3.8E-03
CG4562	1.24	-1.97	3.2E-03
nrv3	36.74	-1.97	3.3E-02
Schip1	1.80	-1.97	8.2E-03
CG9467	3.79	-1.97	4.1E-04
ds	0.15	-1.97	3.9E-02
CG43707	1.72	-1.98	9.6E-03
Gr47a	0.87	-1.98	4.9E-02
CG32700	2.14	-1.98	7.7E-03
Ir56a	1.21	-1.98	8.0E-03
GILT2	7.72	-1.98	3.4E-02
yellow-f	1.10	-1.98	1.8E-02
P5cr-2	2.68	-1.98	8.8E-03
CG42399	0.71	-1.98	1.4E-02
isoQC	2.67	-1.99	3.0E-03
Dri-2	0.95	-1.99	1.3E-02
CG9008	2.99	-1.99	1.9E-02
CAH1	9.34	-2.00	3.6E-03
CG13315	58.09	-2.00	1.3E-03
chinmo	2.28	-2.00	1.1E-02
CaMKI	22.42	-2.00	8.8E-03
EndoB	3.07	-2.00	2.0E-03
CG6752	0.43	-2.00	1.9E-02
CG14234	0.40	-2.00	3.9E-02
mus308	0.39	-2.00	8.1E-03
dob	2.73	-2.00	7.2E-03

CG2993	4.92	-2.00	1.0E-02
sca	0.98	-2.00	5.1E-03
CG5835	3.00	-2.00	8.1E-03
GatA	0.63	-2.00	4.7E-02
unc-13	10.00	-2.00	2.1E-02
CG1695	1.60	-2.00	2.5E-03
CG3822	1.46	-2.00	9.4E-03
CG1418	1.77	-2.01	3.9E-02
PVRAP	1.44	-2.01	6.4E-03
CG9410	1.44	-2.01	3.7E-02
CG31817	0.24	-2.01	3.3E-02
Non3	1.49	-2.01	1.7E-02
CadN	3.95	-2.01	2.6E-02
cac	6.29	-2.01	2.4E-02
CG5281	1.59	-2.01	8.7E-03
CG6685	1.66	-2.01	2.6E-03
CG42402	3.92	-2.02	8.4E-03
vers	1.26	-2.02	1.9E-02
CG32052	1.55	-2.02	6.3E-03
igl	6.89	-2.02	9.3E-03
CG9368	1.15	-2.02	6.9E-03
CG44014	6.23	-2.02	1.2E-02
CG42369	14.45	-2.02	1.2E-02
heph	5.13	-2.02	1.5E-02
Syx18	1.69	-2.02	3.0E-03
Zfp88E	1.15	-2.02	2.0E-02
gb	0.92	-2.02	1.5E-03
CG7795	1.18	-2.03	1.5E-02
CG32698	1.31	-2.03	3.7E-03
CG31897	0.30	-2.03	4.1E-02
Wee1	2.63	-2.03	1.6E-03
CG6723	1.17	-2.03	2.4E-02
jeb	4.33	-2.03	1.2E-02
SmydA-7	0.97	-2.03	2.6E-02
CG4461	5.48	-2.03	1.9E-02
CG3987	1.52	-2.03	6.1E-03
CG6209	0.49	-2.03	4.9E-02
gogo	0.57	-2.04	1.5E-02
comt	4.88	-2.04	8.9E-03
CG3618	1.93	-2.04	1.3E-02
CG3078	1.46	-2.04	3.2E-03
CG12256	2.84	-2.04	3.9E-02
MetRS-m	0.52	-2.04	5.3E-03
Reg-2	4.29	-2.05	1.0E-02
CG13409	1.31	-2.06	5.7E-03
CG14230	0.55	-2.06	4.2E-02
CG5895	4.80	-2.06	6.6E-03
CG16743	6.20	-2.06	2.0E-03
dao	1.01	-2.06	2.8E-03
SIFaR	0.25	-2.06	3.7E-02
CG7720	2.35	-2.07	3.2E-02
dpr19	2.20	-2.07	9.1E-04
unc-5	0.94	-2.07	8.4E-03
Nplp2	752.83	-2.07	2.4E-02
Proc	11.26	-2.07	4.3E-02
AstC-R1	2.02	-2.07	1.4E-02
CG6674	1.38	-2.07	3.9E-02
nAchRalpha1	2.11	-2.07	8.0E-03
CG18749	0.37	-2.08	4.1E-02
5-HT2B	0.64	-2.08	1.1E-03
Sap47	10.95	-2.08	9.0E-03
rdgBbeta	1.52	-2.08	3.9E-03
CG15312	2.87	-2.08	1.1E-03
CG13373	1.28	-2.08	2.5E-02
Fite	2.81	-2.08	1.1E-02
BCAS2	0.99	-2.08	4.7E-02
Ccn	1.27	-2.08	5.7E-03
mei-41	0.36	-2.08	3.9E-03
Fmo-1	1.02	-2.08	3.9E-02
CG3345	0.52	-2.09	3.7E-02
CG42342	2.04	-2.09	3.2E-04
CG2233	747.11	-2.09	2.7E-02
jef	5.88	-2.09	5.1E-03
GstE2	4.32	-2.09	1.7E-03
CG32262	1.70	-2.09	1.3E-02
Syt7	8.09	-2.09	4.8E-03
CG15814	3.69	-2.10	1.0E-03
eag	1.85	-2.10	2.6E-03
mth8	3.54	-2.10	1.4E-04
CG2972	0.92	-2.10	1.4E-02
CG8908	0.72	-2.11	1.1E-02
CG9396	7.04	-2.11	2.6E-03
CG7560	3.81	-2.11	2.1E-03
CG11360	6.06	-2.11	7.7E-04
CG31156	0.87	-2.11	2.6E-03
mei-9	0.53	-2.11	1.1E-02
Nnp-1	1.07	-2.11	2.0E-03
CG15537	1.26	-2.11	2.5E-02
Spat	11.61	-2.11	3.5E-03
CG4627	1.10	-2.12	4.2E-02
CG40485	1.20	-2.12	8.2E-03
CG9813	12.62	-2.12	2.8E-03
CG7084	1.12	-2.12	1.0E-02
CG8665	1.64	-2.12	2.7E-02
CG14502	0.98	-2.12	1.5E-03
Snm1	0.58	-2.12	3.1E-02
Ank2	7.16	-2.12	1.8E-02
CG42346	1.12	-2.13	1.1E-04
Gvc32E	0.40	-2.13	1.2E-02
Amy-d	2.69	-2.13	1.4E-02
CG8861	4.82	-2.13	2.3E-03
CG16790	1.11	-2.13	3.4E-02
CG6293	0.92	-2.14	2.0E-02
nAchRalpha6	5.74	-2.14	3.5E-03
Fie	8.90	-2.14	1.3E-04
CG1646	3.24	-2.14	8.9E-05
ppk25	1.49	-2.15	1.9E-02
klu	0.53	-2.15	1.0E-02
CG8419	0.28	-2.15	4.6E-02
Con	2.13	-2.15	1.3E-03
Hsc70-1	1.27	-2.15	7.0E-03

CG2316	7.73	-2.15	1.4E-04
CG30083	3.18	-2.15	1.2E-03
CG42817	1.66	-2.15	1.9E-04
CG42507	0.64	-2.15	3.7E-02
SP2353	2.05	-2.15	1.2E-03
nAchRalpha3	1.53	-2.15	3.2E-03
CG42502	2.67	-2.15	1.3E-02
CG6191	18.82	-2.15	2.0E-03
CG12224	1.66	-2.15	3.9E-03
Shaw	3.38	-2.16	4.6E-04
Tob	5.05	-2.16	4.0E-04
CG4587	4.73	-2.16	1.8E-03
CG32485	3.87	-2.16	3.0E-04
dpr14	1.98	-2.16	1.1E-03
CG15201	69.37	-2.16	1.1E-03
DIP-beta	0.89	-2.16	3.8E-03
CG10214	3.25	-2.17	3.3E-03
CG14797	0.66	-2.17	5.8E-03
GLaz	3.35	-2.17	5.2E-04
alrm	3.08	-2.17	2.5E-02
Ir51b	0.55	-2.17	3.6E-02
CG3491	0.26	-2.17	9.1E-03
CG9890	0.85	-2.17	3.0E-02
CG14529	1.18	-2.17	2.1E-03
CG1847	1.22	-2.17	3.7E-03
CG13300	0.51	-2.17	5.7E-03
CG1461	1.40	-2.17	1.3E-02
Hk	3.12	-2.18	4.1E-04
CG3955	2.47	-2.18	2.4E-03
CG9098	0.38	-2.18	1.9E-02
GIIIspla2	7.76	-2.18	8.8E-03
ND-23	19.09	-2.18	5.9E-05
IA-2	40.14	-2.18	1.8E-02
CG14141	4.69	-2.18	1.0E-02
FoxP	3.10	-2.18	1.6E-03
l(2)k09848	0.78	-2.18	1.7E-02
TAF1B	0.41	-2.18	2.4E-02
Cyp4ac1	4.92	-2.19	1.2E-03
CG15881	0.90	-2.19	4.8E-02
Lfg	0.80	-2.19	4.3E-02
Ir76a	1.30	-2.19	1.3E-03
Adgf-D	7.83	-2.19	6.7E-03
stan	1.17	-2.19	6.8E-04
CG9121	1.86	-2.19	1.7E-03
CG10362	1.21	-2.19	1.8E-03
brat	2.46	-2.20	1.3E-04
rn	0.55	-2.20	1.6E-02
CG15098	89.60	-2.20	2.4E-03
Smu1	0.83	-2.20	6.4E-03
CG6765	1.45	-2.20	5.1E-03
CG10804	2.74	-2.20	4.3E-04
CG9123	0.87	-2.20	1.9E-02
CG44437	1.26	-2.20	1.6E-02
2mit	2.26	-2.21	1.0E-03
rdhB	2.94	-2.21	4.6E-02
nAchRalpha7	6.35	-2.21	5.7E-03
mbl	4.93	-2.21	4.0E-03
CG13404	1.20	-2.21	3.2E-02
Syt12	1.11	-2.22	1.9E-02
PCNA2	0.86	-2.22	5.0E-02
CG14439	1.17	-2.22	1.2E-02
Teh1	1.76	-2.22	2.0E-03
IMPPP	27.95	-2.22	1.1E-03
Dscam3	1.24	-2.22	2.7E-03
CG14183	0.51	-2.23	1.9E-02
Sh	6.99	-2.23	6.1E-03
Alk	4.88	-2.23	3.4E-03
Pask	0.97	-2.23	5.9E-03
S6kII	1.45	-2.23	3.7E-04
CG33493	17.27	-2.23	3.0E-03
l(3)72Dp	1.57	-2.24	4.3E-04
trv	3.19	-2.24	7.1E-04
Grik	0.40	-2.24	1.7E-02
CG4408	5.02	-2.24	3.9E-03
CG13375	2.73	-2.24	1.7E-03
CG12851	1.82	-2.24	1.7E-03
Cap-D3	0.40	-2.24	1.9E-02
CG31068	0.46	-2.25	2.5E-02
nclb	1.16	-2.25	4.5E-03
Tret1-2	2.46	-2.25	6.2E-04
Odc1	5.50	-2.25	4.2E-03
CG3184	0.85	-2.25	2.5E-02
Xport-A	1.76	-2.26	7.2E-03
miple1	22.62	-2.26	5.4E-03
btv	0.21	-2.26	9.3E-04
orb2	5.03	-2.26	2.1E-04
Oaz	0.24	-2.27	1.4E-02
CG6024	3.19	-2.27	2.2E-04
beat-Ila	2.10	-2.27	5.3E-04
CG43091	1.86	-2.27	1.3E-02
CG13685	1.54	-2.27	1.1E-03
GluRIA	1.35	-2.27	5.3E-03
CG14082	0.63	-2.28	3.9E-03
CG6154	1.37	-2.28	1.3E-02
Tdc2	0.54	-2.28	2.7E-02
CG5348	0.75	-2.28	1.4E-02
CG15890	0.34	-2.29	3.9E-02
mtt	0.92	-2.29	2.1E-03
CG7888	8.41	-2.30	2.5E-04
beat-Ia	1.25	-2.30	1.1E-02
CG14400	5.88	-2.30	1.7E-03
CG16965	1.19	-2.30	4.2E-03
CG11436	0.94	-2.30	3.9E-03
Dh44	2.42	-2.30	3.9E-03
TkR86C	0.47	-2.30	3.5E-02
CG33234	1.00	-2.30	1.3E-02
DNAPol-eta	0.41	-2.30	1.5E-02
List	1.43	-2.31	1.6E-03
CG5707	2.60	-2.31	5.6E-05
Ext2	1.85	-2.31	6.5E-04
temp	2.18	-2.31	1.4E-04

PIG-H	1.25	-2.31	1.5E-02
CG40498	8.99	-2.31	3.1E-04
dpr15	1.20	-2.32	9.4E-04
CG10793	0.87	-2.32	2.6E-02
CG9164	0.94	-2.32	8.9E-05
CG30172	6.47	-2.32	3.8E-03
Myo81F	1.05	-2.32	5.6E-03
beat-Vc	0.53	-2.32	2.0E-02
CG10570	2.58	-2.32	3.6E-03
CG5038	0.51	-2.32	1.4E-02
CG1628	2.76	-2.32	6.8E-04
sff	1.95	-2.33	7.4E-04
SvngR	5.29	-2.33	1.6E-04
CG32174	0.98	-2.34	1.4E-04
CG31814	1.52	-2.34	4.6E-04
CG1764	1.90	-2.34	1.4E-04
Vhl	2.05	-2.34	6.0E-04
slo	8.17	-2.34	9.2E-04
ninaE	109.60	-2.34	3.3E-03
Elk	1.70	-2.34	8.9E-04
Ets65A	0.43	-2.35	2.0E-02
CG14434	0.51	-2.35	4.9E-02
VhaM9.7-a	9.26	-2.35	5.3E-04
CG7058	0.91	-2.35	1.0E-03
kek3	0.92	-2.35	3.0E-05
CG12402	0.87	-2.35	1.7E-03
CG10680	21.96	-2.36	2.0E-03
It	0.19	-2.36	5.1E-04
CG16896	0.63	-2.37	1.7E-03
SpdS	4.12	-2.37	8.1E-05
mRpS31	1.66	-2.37	1.8E-03
wcd	0.57	-2.37	3.0E-02
onecut	6.04	-2.37	1.1E-03
CG12913	0.84	-2.38	4.4E-03
Muc14A	0.16	-2.38	4.5E-05
CDC45L	0.39	-2.38	4.5E-02
hbs	0.54	-2.38	1.0E-03
CG43095	1.87	-2.38	1.1E-02
CG4847	8.54	-2.38	4.6E-06
pHCl-1	2.42	-2.38	7.4E-06
Dh44-R1	1.01	-2.39	3.4E-04
CG15199	3.37	-2.39	7.1E-04
CG9760	0.44	-2.39	3.4E-02
Gpb5	3.22	-2.39	6.9E-04
mACHR-B	0.86	-2.39	9.6E-04
CG32655	1.06	-2.39	1.4E-02
CG6201	0.99	-2.39	5.4E-04
CG12950	3.44	-2.39	1.2E-04
Obp99c	165.23	-2.39	2.7E-03
fred	1.18	-2.40	9.8E-04
Ppt2	4.83	-2.40	1.1E-03
CG2269	19.12	-2.40	4.5E-03
Pms2	0.33	-2.40	2.2E-02
CG8353	1.44	-2.40	2.4E-02
CG9509	1.01	-2.40	3.1E-04
CG34134	6.28	-2.40	9.3E-05
RSg7	1.79	-2.41	1.0E-04
CG17364	1.28	-2.41	1.1E-04
scrt	5.77	-2.41	2.1E-03
CG14252	0.71	-2.41	3.3E-02
CG33310	0.48	-2.41	1.2E-02
etp	0.43	-2.41	1.9E-02
CG43324	8.48	-2.41	1.0E-04
CG46308	1.44	-2.42	6.2E-04
CG9395	1.83	-2.42	4.3E-05
dpr7	8.66	-2.42	1.4E-03
CG43402	4.40	-2.43	8.8E-03
CG6808	0.31	-2.43	2.4E-02
HDAC11	1.38	-2.43	9.3E-05
CG12822	4.13	-2.43	2.3E-05
CG8641	0.96	-2.43	5.1E-04
iav	0.26	-2.44	2.6E-02
CG7646	8.71	-2.44	2.6E-05
Tsp39D	4.24	-2.44	1.4E-06
Vps16B	0.62	-2.44	2.6E-02
CG9503	0.29	-2.44	5.0E-02
CG17026	1.57	-2.45	3.0E-03
met-P26	7.61	-2.45	7.2E-04
PK2-R1	0.34	-2.46	3.0E-02
sced	0.89	-2.46	1.3E-04
dpr18	2.41	-2.46	5.8E-04
CG33181	1.87	-2.46	7.6E-05
CG3812	1.82	-2.47	1.1E-04
CG4984	0.40	-2.48	1.6E-02
hubl	0.62	-2.48	1.1E-02
Nep3	3.23	-2.48	1.9E-05
moi	0.39	-2.48	3.7E-02
GABA-B-R3	1.89	-2.48	6.0E-06
rha	0.23	-2.48	2.2E-02
CG14882	0.65	-2.48	1.2E-02
Cyp4a2	0.39	-2.49	5.0E-02
CG14864	0.48	-2.49	3.7E-02
CG6985	0.68	-2.49	1.1E-02
CG32333	0.93	-2.49	1.3E-05
key	4.68	-2.49	2.5E-05
CG4374	0.16	-2.49	2.9E-02
sv	0.47	-2.50	1.0E-03
CG8958	0.67	-2.50	5.7E-03
EndoG	0.70	-2.50	3.4E-02
CG12398	0.54	-2.50	2.0E-02
bru3	6.49	-2.51	1.1E-03
Ir68a	0.50	-2.51	2.1E-02
Lkr	0.67	-2.51	2.8E-02
fs(1)M3	0.22	-2.51	3.1E-02
Gad1	11.49	-2.52	2.0E-02
CG33226	2.09	-2.52	1.2E-03
CG34135	0.49	-2.53	5.4E-05
DCTNS-p25	2.79	-2.53	1.8E-03
CG17159	0.71	-2.53	4.5E-03
CG9657	0.91	-2.53	8.7E-05
CG18368	0.26	-2.53	1.8E-02

Or63a	0.56	-2.53	2.0E-02
mwh	0.21	-2.53	1.4E-02
Atg10	0.99	-2.53	3.3E-03
CG7300	0.43	-2.53	8.1E-03
santa-maria	2.70	-2.54	2.7E-05
Hf	19.26	-2.54	7.9E-05
CG7368	0.54	-2.54	3.2E-03
qin	0.15	-2.55	1.6E-02
CG11407	1.23	-2.55	1.1E-03
CG7339	2.04	-2.55	6.6E-05
CG9919	3.81	-2.55	5.2E-05
AstA-R1	1.20	-2.55	3.7E-04
CG6574	1.51	-2.56	3.9E-05
CG4269	5.39	-2.57	1.7E-02
CG42740	2.19	-2.57	6.0E-05
DIP-delta	1.99	-2.57	3.2E-04
CG31249	1.40	-2.57	1.0E-03
CG11317	1.75	-2.58	3.2E-04
CG13283	2.03	-2.58	1.3E-05
yellow-h	1.16	-2.58	7.2E-03
CG3568	0.57	-2.59	2.9E-02
CG16789	0.67	-2.59	1.6E-03
Syt14	1.45	-2.59	4.4E-04
APP-BP1	1.13	-2.59	1.2E-03
Cyp4ac2	4.31	-2.60	6.2E-06
VGAT	2.37	-2.61	2.3E-05
Fer1	0.68	-2.61	1.5E-02
Drep3	1.05	-2.62	1.9E-03
CC32225	5.28	-2.62	7.7E-05
CAHbeta	2.28	-2.62	2.2E-04
CG6867	0.69	-2.63	2.2E-04
beat-VII	4.02	-2.63	3.2E-04
DIP-epsilon	1.04	-2.63	7.4E-05
twit	2.58	-2.63	1.2E-05
pdm2	0.38	-2.64	7.9E-03
dpr21	3.83	-2.64	2.2E-05
CG13999	1.93	-2.64	1.8E-03
wtrw	3.72	-2.64	3.1E-06
Lcch3	2.97	-2.64	7.5E-05
Gas41	0.92	-2.66	3.1E-02
cep290	0.15	-2.66	1.5E-02
Lip2	0.50	-2.66	7.1E-03
CG43343	0.41	-2.67	1.0E-03
CG16898	1.55	-2.68	2.7E-02
CG18622	1.37	-2.68	1.8E-03
CCHa1-R	0.59	-2.69	3.4E-03
park	0.88	-2.69	2.5E-03
t	2.40	-2.69	2.2E-04
lov	0.60	-2.69	7.0E-05
Pkc53E	4.81	-2.70	3.2E-06
Spc105R	0.12	-2.70	3.6E-02
Dhc62B	0.20	-2.70	1.3E-04
CG10960	11.83	-2.70	1.6E-05
Cyp28c1	0.47	-2.70	2.3E-02
Ddr	1.04	-2.70	2.9E-04
CG15293	83.70	-2.70	3.9E-04
CG7342	0.32	-2.71	3.1E-02
CG6429	1.89	-2.71	3.6E-02
Hr4	1.49	-2.71	2.1E-08
CG13708	0.16	-2.71	4.8E-02
unc-13-4A	1.71	-2.71	1.6E-05
CG10151	0.60	-2.71	2.9E-03
nAChRalpha5	6.71	-2.72	4.9E-04
Irk3	0.86	-2.73	6.9E-04
Gfat1	1.20	-2.73	1.7E-04
Spn88Eb	22.83	-2.73	1.5E-02
Dop1R1	2.10	-2.74	8.0E-06
CG42361	2.09	-2.74	3.5E-04
CG5282	2.05	-2.74	7.7E-06
CG12239	30.05	-2.74	4.0E-02
AstC-R2	0.62	-2.74	1.8E-03
Pcyt2	10.68	-2.75	1.1E-06
CG1137	0.71	-2.75	1.6E-02
Gld2	0.27	-2.75	4.0E-03
CarT	0.91	-2.76	1.8E-04
Klp54D	0.21	-2.76	4.9E-02
CG6220	0.61	-2.76	1.6E-02
CG15803	0.94	-2.76	6.2E-04
CG8492	0.21	-2.76	2.3E-02
CG12147	0.39	-2.76	3.0E-02
pre-mod(mdg4)-Z	0.89	-2.77	2.9E-03
Ret	0.24	-2.77	1.2E-02
Actbeta	5.02	-2.78	3.5E-08
twz	0.47	-2.78	5.7E-03
CG9701	1.10	-2.78	3.0E-02
Root	0.59	-2.79	6.3E-06
cmet	0.12	-2.79	2.0E-02
CG43968	1.15	-2.79	5.1E-03
st	0.37	-2.80	3.9E-02
CG34402	0.58	-2.80	3.3E-03
CG9254	0.53	-2.80	1.7E-02
rnh1	0.80	-2.80	1.4E-02
Chp53E	7.60	-2.80	1.9E-05
mGluR	4.06	-2.80	2.6E-04
boil	0.71	-2.80	4.7E-03
Ykt6	2.86	-2.81	1.3E-06
beat-lb	1.80	-2.81	9.1E-05
CG5890	2.34	-2.81	6.3E-06
7FAP-2	0.46	-2.82	4.5E-03
CG31097	0.56	-2.82	2.4E-02
CG12309	0.76	-2.82	1.8E-03
frm	0.12	-2.82	4.0E-02
pre-mod(mdg4)-W	0.34	-2.83	2.4E-02
CG7166	3.60	-2.83	3.9E-06
CG3257	1.43	-2.83	1.2E-05
CG15651	1.56	-2.83	7.0E-05
CG11619	0.95	-2.84	6.8E-05
CG5022	0.79	-2.85	1.7E-03
CanB	9.12	-2.85	1.7E-07
CG7708	4.15	-2.86	1.1E-06
CG15332	0.32	-2.86	4.1E-02

CG12768	0.72	-2.87	3.4E-04
PICK1	1.00	-2.87	1.1E-04
CG12355	3.47	-2.87	1.7E-05
pre-mod(mdg4)-T	0.80	-2.88	4.4E-03
CG10257	1.46	-2.89	2.4E-03
CG1239	0.98	-2.89	3.5E-03
CG17977	1.04	-2.89	1.1E-02
CG17141	0.90	-2.90	5.4E-03
fne	8.31	-2.91	7.2E-05
Kr	0.54	-2.91	5.6E-05
euc	11.98	-2.91	2.7E-03
Lsp1beta	3.92	-2.93	7.3E-03
CG14274	2.61	-2.94	1.4E-04
AstC	7.43	-2.94	8.2E-03
CG8925	0.22	-2.94	4.6E-02
CG9270	0.17	-2.94	2.7E-02
CG17270	2.35	-2.94	4.0E-05
CG4842	0.84	-2.94	2.0E-02
CG42339	0.88	-2.96	2.1E-04
CG4907	0.19	-2.96	3.1E-02
CG1143	0.36	-2.96	4.4E-02
GNBP2	2.79	-2.97	1.2E-04
Pbp49	0.80	-2.97	8.1E-03
CG18539	0.78	-2.98	4.2E-02
CG8100	0.19	-2.98	4.1E-02
CG32939	8.87	-2.98	4.7E-06
CG34106	0.58	-2.99	2.1E-05
CG31832	0.91	-2.99	2.9E-02
CG15909	0.51	-3.00	3.0E-02
Trxr-2	0.34	-3.00	3.6E-02
CG30158	1.77	-3.01	9.5E-07
Sry-alpha	0.16	-3.02	4.6E-02
shd	0.17	-3.02	4.1E-02
CG5897	0.54	-3.03	1.7E-02
CG34256	1.39	-3.03	5.6E-03
CG4653	0.83	-3.03	1.7E-02
CG18467	2.10	-3.04	1.1E-06
DIP-alpha	0.79	-3.04	3.6E-07
mnd	2.80	-3.04	1.0E-05
CG3253	0.73	-3.04	2.4E-03
PGRP-SD	30.29	-3.04	3.5E-09
CG31664	1.14	-3.05	2.6E-04
pip	0.12	-3.05	2.5E-03
CG13694	0.96	-3.05	7.2E-03
CG5493	2.98	-3.06	1.0E-06
Sytbeta	1.45	-3.06	1.5E-06
CCKLR-17D1	0.37	-3.06	2.2E-03
slv	1.15	-3.07	5.4E-04
CG4301	0.38	-3.07	3.7E-05
Cyp4s3	1.44	-3.07	1.1E-06
CG10799	51.81	-3.08	1.8E-06
Xport-B	1.97	-3.08	7.5E-04
stum	0.17	-3.08	2.9E-03
CG7191	0.88	-3.08	1.5E-03
CG5961	0.89	-3.09	9.6E-04
CG6125	0.39	-3.09	2.2E-02
Obp57c	3.16	-3.10	7.9E-03
Cycl	0.61	-3.10	1.2E-02
fest	0.28	-3.10	8.9E-03
CG34354	2.22	-3.11	5.5E-07
CG4596	0.65	-3.11	1.5E-03
CG1545	2.24	-3.11	2.4E-03
CG16756	19.58	-3.12	1.5E-04
alphaKap4	0.54	-3.12	9.3E-03
rost	9.35	-3.13	3.5E-09
Tehao	0.68	-3.13	8.9E-04
ms(3)76Ba	0.51	-3.14	6.7E-03
nompA	0.18	-3.14	2.0E-02
CG11034	0.35	-3.15	1.0E-02
Rrp46	1.09	-3.16	1.5E-02
Muc68E	0.19	-3.17	2.5E-03
tombboy40	0.62	-3.17	1.2E-02
CG13088	0.38	-3.17	3.4E-02
TTL3A	0.16	-3.18	4.2E-02
Listericin	3.41	-3.18	4.6E-02
CG10924	0.44	-3.18	1.6E-02
CG18003	5.42	-3.20	1.0E-05
CG8245	3.64	-3.21	2.2E-07
CG9449	2.52	-3.21	1.2E-04
cmpy	1.21	-3.21	4.0E-06
Cyp28d2	1.42	-3.21	3.3E-05
OS9	1.62	-3.21	9.7E-03
Mur29B	0.87	-3.21	1.8E-03
CG9413	4.96	-3.22	1.6E-05
Mdr50	0.37	-3.22	4.8E-03
ninaA	2.65	-3.23	1.1E-04
CG2750	0.12	-3.24	2.1E-02
Dhc16F	0.13	-3.24	4.5E-04
frac	0.13	-3.24	2.0E-02
Sytalpha	3.24	-3.24	1.3E-07
CG12594	1.84	-3.24	3.7E-07
Pdh	19.65	-3.25	1.0E-04
CG5096	0.34	-3.25	3.1E-02
CG13965	1.15	-3.26	2.8E-02
CG15522	1.23	-3.26	4.5E-04
CG6602	0.43	-3.27	4.1E-02
CG9531	1.12	-3.28	3.0E-04
beat-Vb	1.45	-3.28	4.4E-05
oc	0.41	-3.29	8.3E-05
CG31221	27.83	-3.29	6.7E-05
CG14567	9.29	-3.29	2.4E-08
CG3270	1.91	-3.29	1.8E-05
CG11425	2.03	-3.29	3.7E-03
CG1552	8.01	-3.29	1.6E-05
CG7742	0.54	-3.30	1.1E-03
CG18155	0.88	-3.30	5.4E-05
Cyp303a1	0.30	-3.32	1.1E-02
CG42235	0.81	-3.32	1.2E-05
dtr	0.15	-3.33	1.6E-02
Marcal1	0.31	-3.33	1.8E-02
CG2680	1.41	-3.34	2.5E-04

CG13895	2.19	-3.35	1.8E-08
CG5285	0.89	-3.35	8.1E-03
CG31161	0.30	-3.36	3.2E-02
CG14301	0.29	-3.36	3.0E-02
Gbeta5	2.09	-3.37	5.2E-07
CG30484	0.16	-3.37	5.0E-02
CG32373	0.39	-3.37	8.6E-03
Igr3	0.38	-3.37	1.1E-03
CG8219	0.22	-3.38	2.2E-02
CG34109	0.41	-3.39	1.9E-03
CG1909	7.21	-3.39	5.9E-09
CG2121	0.35	-3.39	2.5E-02
inaD	1.42	-3.39	2.1E-06
GC	1.87	-3.40	8.6E-07
zyd	2.65	-3.40	1.7E-07
NPFR	0.29	-3.41	6.2E-03
CG30419	0.86	-3.43	2.1E-07
CG10185	0.37	-3.43	8.2E-03
CG5773	8.79	-3.43	6.0E-10
tyn	0.49	-3.44	5.1E-07
Cyp309a1	1.98	-3.44	1.2E-03
CG10650	0.85	-3.44	2.8E-02
CG18213	0.37	-3.45	1.9E-03
CG6071	0.24	-3.45	2.8E-02
CG4329	0.18	-3.45	2.8E-02
CG32647	6.30	-3.45	1.3E-10
Adk3	1.62	-3.45	1.1E-06
CG7460	0.30	-3.45	2.0E-02
CG13436	0.36	-3.45	2.0E-02
CG31872	0.16	-3.46	4.0E-02
Dro	2.23	-3.46	1.8E-02
CG17803	1.03	-3.47	5.8E-06
CG31036	0.25	-3.48	6.7E-03
CG10494	0.42	-3.48	7.8E-03
CG14321	1.31	-3.49	7.3E-03
skl	0.46	-3.50	2.2E-02
Or98a	0.44	-3.50	3.1E-02
CG32591	0.30	-3.50	2.6E-02
CG1402	1.31	-3.50	3.7E-07
CG14857	0.21	-3.51	4.1E-02
CG15358	1.82	-3.51	1.8E-03
CG33233	1.03	-3.52	5.5E-05
Sse	0.54	-3.53	2.5E-03
CG33307	6.70	-3.54	2.0E-08
Damm	0.39	-3.55	8.2E-03
CG32301	0.13	-3.56	3.8E-02
Trh	1.09	-3.58	2.6E-04
Abd-B	0.08	-3.58	4.8E-03
CG4836	0.13	-3.59	4.0E-02
CG32017	16.30	-3.59	9.9E-07
CG13539	0.40	-3.62	3.4E-02
CG13978	0.16	-3.62	4.1E-02
Psf3	7.39	-3.64	1.3E-11
nompB	0.20	-3.64	2.2E-02
CG14937	0.36	-3.64	2.4E-02
Dhc98D	0.19	-3.65	2.7E-06
CG1924	0.40	-3.65	3.9E-03
Cyp6a14	0.77	-3.66	6.4E-06
DNaseII	11.88	-3.66	2.2E-06
CG3339	0.12	-3.69	1.3E-04
CG7607	17.57	-3.69	7.4E-08
CG32683	0.90	-3.70	4.8E-09
CG10654	1.93	-3.72	4.9E-08
CG14989	28.93	-3.72	3.1E-04
CG7884	0.14	-3.73	1.8E-02
CG46244	1.07	-3.73	1.4E-07
CG2656	3.74	-3.77	1.1E-07
Ppil1	0.23	-3.77	1.0E-02
CG12662	1.37	-3.77	7.0E-03
Cpr66D	0.82	-3.77	1.1E-02
CG30110	0.35	-3.80	1.3E-02
SP555	0.95	-3.81	1.8E-07
CG13991	0.09	-3.84	3.9E-02
Oatp33Ea	0.35	-3.84	9.3E-04
CG32845	0.26	-3.84	3.3E-02
CG3277	0.30	-3.87	9.8E-04
CG18302	0.27	-3.87	2.7E-02
Ist	16.70	-3.89	6.3E-06
CG7896	0.10	-3.89	2.4E-02
CG43085	2.12	-3.90	5.3E-05
CG6083	1.05	-3.90	1.7E-04
CG5342	0.20	-3.90	3.9E-02
CG14312	0.79	-3.93	4.6E-02
CG34425	0.41	-3.93	1.9E-02
UQCR-11L	1.61	-3.94	1.0E-02
CG14495	0.73	-3.94	1.9E-02
beat-Va	1.34	-3.94	6.9E-08
CG32368	32.29	-3.94	3.8E-06
CG31706	2.23	-3.96	1.8E-07
Menl-1	0.09	-3.99	4.7E-02
Crz	11.18	-4.00	3.7E-04
CG9673	0.90	-4.00	7.6E-03
CBP	0.16	-4.00	4.9E-02
lbl	0.18	-4.00	2.5E-02
CG12715	0.23	-4.00	2.0E-02
Rpn13R	0.45	-4.00	2.1E-02
CG43291	0.32	-4.01	1.3E-02
CG7589	1.82	-4.01	8.1E-04
e(r)	2.86	-4.02	3.5E-10
zye	0.12	-4.04	2.6E-03
CG17224	13.97	-4.04	4.3E-08
Hsc70-2	0.25	-4.06	1.8E-02
kmg	0.17	-4.06	4.2E-02
CG5142	0.69	-4.07	1.6E-04
CG2104	0.39	-4.08	2.1E-03
CG34215	7.19	-4.09	3.0E-06
CG14406	0.95	-4.10	1.1E-02
CG7227	2.36	-4.10	6.3E-07
MFS9	1.77	-4.14	7.0E-08
CG12038	1.73	-4.16	1.4E-07
CG17167	0.95	-4.16	9.1E-07

Cht2	0.92	-4.18	7.6E-07
CG1801	0.07	-4.19	3.8E-02
CG3014	0.16	-4.20	3.3E-02
ND-51L1	0.93	-4.20	3.8E-06
CG31343	0.24	-4.20	2.3E-02
CG9507	1.46	-4.21	1.8E-07
CG5160	0.28	-4.21	1.8E-02
CG11788	0.47	-4.24	1.1E-02
CG45067	0.25	-4.24	1.1E-02
Rh4	5.13	-4.25	3.3E-09
CG14118	0.27	-4.26	4.5E-02
CG1979	0.94	-4.27	7.2E-06
CG9928	77.10	-4.27	2.2E-12
CG14331	0.45	-4.27	1.4E-02
CG8654	3.25	-4.28	2.3E-07
CG16959	0.29	-4.28	7.8E-03
Dh31	13.30	-4.28	1.8E-06
CG12699	0.75	-4.28	1.8E-02
CG6052	0.31	-4.28	5.9E-05
Lsp1alpha	0.28	-4.32	1.6E-02
CG31780	0.39	-4.34	1.4E-02
Dhc93AB	0.19	-4.37	6.0E-04
CG34025	0.55	-4.38	8.6E-03
CG11044	0.60	-4.38	1.1E-04
Vha100-3	0.20	-4.39	2.1E-02
nompC	0.13	-4.40	2.0E-03
G6P	0.62	-4.40	4.5E-03
CG1667	9.94	-4.41	9.8E-11
Dfd	0.25	-4.43	6.1E-03
CG5882	0.18	-4.46	4.8E-02
Obp99a	44.65	-4.46	4.5E-06
CG32447	0.11	-4.48	3.0E-02
CG4839	0.44	-4.49	2.8E-05
CG15599	0.17	-4.50	1.1E-02
CG31528	0.47	-4.50	1.1E-02
mey	0.15	-4.52	3.1E-02
CG10505	0.16	-4.53	1.2E-02
CG5756	0.11	-4.53	3.2E-02
CG5909	1.68	-4.54	1.7E-05
CG15143	0.14	-4.54	2.9E-02
Odc2	1.37	-4.59	3.1E-05
Ilp2	8.41	-4.61	1.9E-02
wrapper	2.86	-4.65	2.6E-06
CG32106	0.13	-4.66	9.0E-03
CG13609	0.31	-4.67	1.8E-02
CG30438	0.48	-4.68	1.8E-05
CG16825	0.26	-4.69	2.6E-03
pre-mod(mdg4)-G	0.83	-4.70	4.7E-06
CG12817	0.76	-4.72	1.6E-03
Oatp33Eb	0.18	-4.73	4.1E-02
CG11404	0.59	-4.74	2.3E-02
r-cup	0.22	-4.74	1.9E-02
Cc2d2a	0.17	-4.75	5.1E-03
CG14838	0.17	-4.75	2.0E-02
CG10969	0.15	-4.78	4.3E-02
CG40470	4.78	-4.80	7.5E-13
Ihe	0.21	-4.80	1.7E-02
CG14692	0.15	-4.83	7.2E-04
AttB	6.81	-4.85	2.4E-04
nerfin-2	0.15	-4.87	4.5E-02
CG43691	0.13	-4.88	1.6E-02
CG33791	0.09	-4.88	1.5E-02
ImpE1	0.14	-4.89	1.5E-03
CG15382	0.56	-4.93	8.6E-03
CG9733	0.98	-4.94	1.2E-03
ndl	0.11	-4.96	2.6E-03
CG1537	0.45	-4.96	3.7E-02
TwdlG	1.57	-4.97	7.1E-10
CG32793	0.14	-5.05	3.4E-02
CG32719	0.10	-5.05	4.0E-02
SmydA-6	0.21	-5.05	4.3E-02
CG34459	0.28	-5.05	4.7E-02
CG6041	1.18	-5.12	9.9E-05
CG9981	0.09	-5.14	3.5E-02
CG34002	0.76	-5.16	1.6E-03
Sid	0.80	-5.16	6.4E-03
CG9689	3.42	-5.16	2.2E-07
Or43b	0.75	-5.17	5.5E-04
CG11898	0.13	-5.20	6.4E-03
alpha-Man-1c	0.91	-5.20	4.4E-03
Dhc36C	0.14	-5.22	5.5E-06
CG4714	0.17	-5.23	3.1E-02
CG31198	0.22	-5.28	3.9E-02
Oseg2	0.18	-5.28	9.2E-04
tld	1.64	-5.31	2.7E-06
CG8157	0.54	-5.32	3.4E-02
CG18480	0.11	-5.36	1.8E-02
CG11671	1.21	-5.40	1.7E-03
CG42816	0.15	-5.54	4.4E-03
BubR1	0.31	-5.54	4.6E-05
Mtk	9.48	-5.55	2.1E-03
CG17264	0.79	-5.55	7.4E-07
Muc26B	0.34	-5.56	9.3E-03
I(2)03659	0.13	-5.56	7.9E-03
Cyp309a2	0.24	-5.58	2.4E-02
CG31551	0.11	-5.59	2.2E-02
prs-mod(mdg4)-B	0.45	-5.73	2.7E-03
CG18170	0.07	-5.75	2.5E-02
sad	0.25	-5.76	1.9E-02
ACXC	0.12	-5.76	1.9E-02
CG31467	0.36	-5.76	7.7E-03
CG15539	0.27	-5.77	4.0E-02
Cyp4d1	0.53	-5.77	1.0E-04
CG4676	0.92	-5.79	4.4E-04
CG5681	0.20	-5.84	2.2E-02
Cpr50Ca	0.13	-5.85	1.7E-02
CG5235	0.18	-5.85	1.7E-02
CG15209	46.08	-5.85	0.0E+00
Rh5	4.97	-5.98	7.7E-12
CG5966	6.98	-6.00	5.6E-07
fit	151.85	-6.02	4.2E-11

CG13634	0.27	-6.12	1.6E-02
betaTub85D	0.26	-6.21	1.3E-02
grim	0.29	-6.21	1.3E-02
Cad74A	0.11	-6.24	2.6E-03
mfr	0.11	-6.24	7.0E-03
Trissin	3.71	-6.25	5.4E-04
Efhc1.2	0.12	-6.27	4.7E-02
CNT1	0.11	-6.27	4.7E-02
CG4459	0.16	-6.27	4.6E-02
spm-B	0.23	-6.27	4.7E-02
CG13699	0.09	-6.27	4.7E-02
CNMa	0.17	-6.27	4.8E-02
CG14086	0.22	-6.27	4.6E-02
CG15740	0.16	-6.32	1.8E-02
CG31205	10.80	-6.38	1.5E-04
CG5404	0.49	-6.40	1.3E-05
MCO3	0.16	-6.41	4.8E-02
CG6296	0.16	-6.41	4.4E-02
CG17387	0.12	-6.41	4.5E-02
CG43896	0.11	-6.41	2.0E-03
CG9316	0.14	-6.44	4.9E-02
CG33235	0.19	-6.45	4.9E-04
CG42296	0.16	-6.47	1.1E-02
His4:CG33875	1.00	-6.47	1.2E-02
Vago	51.47	-6.50	1.4E-09
CG33017	0.12	-6.51	3.6E-03
unc	0.10	-6.55	1.0E-02
Sep5	0.29	-6.56	1.3E-02
Vha100-5	0.17	-6.56	2.0E-02
CG30371	3.79	-6.60	7.6E-04
CG3942	0.21	-6.64	1.3E-02
ord	0.09	-6.66	3.9E-02
lobo	0.13	-6.66	4.2E-02
e(y)2b	0.58	-6.67	4.2E-02
CG14142	0.38	-6.68	5.5E-03
Cpr76Bd	0.12	-6.74	8.5E-03
S-Lap3	0.12	-6.78	3.9E-02
Cp7Fb	0.17	-6.79	3.6E-02
SA-2	0.11	-6.79	3.6E-02
CG9826	0.17	-6.79	4.3E-02
CG13617	0.14	-6.79	3.8E-02
CG30480	0.23	-6.79	9.4E-04
ChLD3	0.24	-6.91	9.1E-03
CG34027	0.12	-6.92	9.1E-03
CG42876	0.25	-6.92	3.4E-02
CG34193	0.23	-6.92	7.4E-03
CG7953	0.48	-7.00	9.1E-03
CG1314	0.37	-7.00	6.9E-03
Tb	0.39	-7.05	3.7E-02
CG7140	0.19	-7.05	3.1E-02
CG9864	0.68	-7.08	9.9E-04
ppk8	0.18	-7.15	3.9E-02
RabX2	0.48	-7.17	3.5E-02
CG13391	0.33	-7.18	7.8E-03
CG18109	0.13	-7.22	3.2E-03
CG17717	0.37	-7.24	4.9E-02
CG12866	0.26	-7.26	2.6E-03
CG7059	0.63	-7.27	1.0E-04
Ost17	0.10	-7.31	3.5E-02
CG33137	0.66	-7.31	3.0E-02
ATPsynbetaL	0.20	-7.32	4.1E-02
ms(3)76Cc	0.15	-7.36	5.5E-03
GstE14	0.34	-7.42	2.8E-02
CG30043	0.13	-7.43	2.6E-02
CG7311	0.33	-7.47	1.9E-03
CG7882	0.18	-7.56	2.4E-02
Dsk	6.43	-7.56	3.8E-09
Ir60e	0.24	-7.56	2.5E-02
swi2	1.20	-7.60	7.1E-10
CS-2	0.17	-7.66	1.5E-03
CG9686	37.90	-7.68	0.0E+00
CG6324	0.11	-7.68	2.4E-02
CG43338	0.14	-7.68	2.4E-02
CG18477	0.38	-7.71	4.5E-03
CG42662	0.14	-7.81	2.3E-02
ssp5	0.18	-7.81	2.4E-02
Gr32a	0.25	-7.82	2.2E-02
CG31016	0.11	-7.84	3.7E-02
CG4793	0.34	-7.84	2.1E-04
CG15930	0.43	-7.93	1.7E-03
LysX	1.07	-7.94	2.6E-02
Rh6	5.11	-7.94	9.7E-12
CG10051	0.15	-8.02	3.5E-02
CG6927	0.24	-8.08	2.4E-02
CG13842	0.27	-8.17	4.3E-03
CG43064	3.35	-8.21	2.1E-10
Cyp6d2	0.48	-8.23	3.1E-03
CG13326	0.17	-8.33	2.2E-02
CG32107	0.16	-8.33	3.0E-03
CG14120	0.11	-8.34	1.9E-02
Dnah3	0.10	-8.38	5.8E-06
CG9492	0.16	-8.39	3.3E-06
CG13362	0.24	-8.42	2.2E-02
CCDC151	0.35	-8.42	3.6E-03
CG3964	0.12	-8.46	1.6E-02
CG34290	0.68	-8.56	1.3E-02
Dic61B	0.17	-8.58	1.7E-02
CG14651	0.14	-8.59	1.8E-02
CG16734	0.34	-8.60	1.5E-02
Orco	0.26	-8.60	2.4E-02
Ugt86D1	0.42	-8.67	8.7E-05
CG13641	7.07	-8.68	6.9E-07
fs(1)Yb	0.13	-8.71	1.4E-02
DJ-1alpha	1.48	-8.78	9.7E-05
CG34124	0.21	-8.80	4.5E-05
CG13177	0.41	-8.84	1.5E-02
CG33287	0.14	-8.85	1.3E-02
CG30048	0.12	-8.89	1.7E-02
CG15497	0.41	-9.11	1.1E-02
Mal-B1	16.00	-9.11	7.0E-06
CG33655	0.87	-9.15	4.1E-06

Cad89D	0.14	-9.16	3.5E-04
CG2528	0.09	-9.24	1.1E-02
AttC	78.80	-9.25	6.5E-11
gt	0.83	-9.29	1.3E-05
LysP	30.79	-9.47	8.4E-03
NT1	0.13	-9.48	1.1E-02
Ohp56a	1.94	-9.62	5.7E-03
CG15475	0.56	-9.64	1.1E-02
CG34219	1.10	-9.72	1.9E-05
CG15144	0.15	-9.87	9.8E-03
sage	0.88	-10.00	1.8E-05
Cyp308a1	0.33	-10.01	8.1E-03
CG13131	0.14	-10.01	9.7E-03
CG31636	0.48	-10.03	2.0E-03
CG4409	4.44	-10.09	1.2E-13
CG17687	0.11	-10.25	7.8E-03
pre-mod(mdg4)-U	0.28	-10.43	2.0E-04
CG15711	0.25	-10.44	9.0E-03
f	0.09	-10.57	8.2E-04
CG15548	0.32	-10.65	1.4E-03
CG45080	286.08	-10.92	2.7E-05
AttA	3.25	-11.01	3.3E-06
PGRP-SB1	38.74	-11.09	0.0E+00
CG33012	0.12	-11.34	4.8E-02
CG8664	0.22	-11.34	4.8E-02
CG3544	0.15	-11.56	4.4E-03
Vha100-4	0.12	-11.56	4.6E-02
CG14085	0.11	-11.56	4.6E-02
Ir52b	0.20	-11.57	4.8E-02
CG33125	0.09	-11.57	4.6E-02
Galphaf	0.36	-11.93	5.0E-03
Oatp58Da	0.16	-12.03	4.2E-02
CG11164	0.23	-12.03	4.2E-02
CG4161	0.19	-12.04	4.2E-02
CG13492	0.16	-12.18	4.5E-06
CG31533	0.13	-12.26	4.0E-02
dec-1	0.11	-12.32	3.2E-03
CG46313	0.21	-12.33	4.4E-02
S-Lap1	0.18	-12.34	4.7E-02
CG30289	0.59	-12.45	3.3E-03
CG14205	0.15	-12.72	3.7E-02
Pxd	0.15	-12.88	4.6E-02
EACHm	0.49	-13.17	4.2E-02
CG9068	0.11	-13.19	3.4E-02
sha	0.11	-13.45	2.4E-03
CG15614	0.28	-13.48	3.7E-02
sens	0.18	-13.59	3.4E-02
CG33286	0.12	-13.65	3.0E-02
His4:CG33873	0.72	-13.98	3.2E-02
CG6337	0.28	-14.13	3.0E-02
DptB	17.11	-14.30	3.4E-06
CG45062	0.15	-14.36	2.6E-02
CG9377	5.62	-14.43	0.0E+00
CG10814	4.81	-14.75	7.6E-07
CG15570	0.10	-14.81	2.4E-02
Tsp29Fa	0.55	-14.83	6.1E-03
Adgf-E	0.27	-14.84	2.6E-02
CG10170	0.26	-15.05	2.5E-02
CG11760	0.97	-15.24	3.7E-07
CG10472	0.52	-15.31	2.3E-02
CG5122	0.11	-15.51	2.1E-02
S-Lap2	0.23	-15.52	2.3E-02
CG12637	0.46	-15.53	2.2E-02
Cyp4e3	1.62	-15.66	5.1E-07
CG6709	0.69	-15.75	1.2E-03
Spn100A	0.24	-15.99	1.9E-02
CG9313	0.15	-16.20	2.2E-02
CG32984	5.02	-16.68	6.6E-06
His4:CG33871	0.99	-16.77	2.0E-02
CG12184	0.16	-16.87	1.9E-02
CG5379	0.32	-17.11	1.7E-02
SdhBL	0.27	-17.15	1.5E-02
CG32236	0.37	-17.40	1.5E-02
CG32436	0.10	-17.57	1.7E-02
Ag5r	87.12	-17.72	3.5E-06
CG42825	1.03	-18.88	1.2E-04
CG42685	0.10	-18.94	1.2E-02
lyd	0.23	-19.44	1.2E-02
CG2990	0.16	-20.40	9.1E-03
Npc1b	0.16	-21.31	9.0E-03
CG16826	691.86	-21.64	5.8E-09
CG18088	0.46	-22.49	3.1E-04
CG34377	0.13	-22.96	6.7E-03
CG32786	0.21	-22.96	6.5E-03
Sdic2	0.59	-26.61	4.8E-05
CG32985	0.41	-27.81	8.0E-03
CG8708	3.16	-28.05	1.9E-07
Cyp304a1	8.52	-49.47	1.2E-13
CG42704	22.87	-50.08	3.3E-06
scpr-C	3.56	-54.66	3.9E-06
CG42705	2.10	-55.06	1.1E-03
DptA	15.27	-65.02	4.1E-08
CG33109	198.15	-67.81	2.7E-12

### 6.3 DEGs of airways from 15 d CS exposed flies

Gene name	Max group mean	Fold change	FDR p-value
CG7675	4.45	356.73	2.6E-02
Prosalpha1	5.97	334.28	4.0E-02
CG11825	133.80	329.14	0.0E+00

Prx2540-1	661,34	104,05	0,0E+00
Prx2540-2	612,93	87,13	0,0E+00
CG12896	393,00	84,23	0,0E+00
TotC	373,10	69,65	2,2E-12
TotX	22,55	62,62	8,9E-09
TotA	729,26	54,91	0,0E+00
CG33474	17,72	46,16	0,0E+00
TotM	170,34	34,63	3,9E-11
pre-lola-G	0,57	31,97	4,3E-02
Zfp88E	1,19	30,64	5,0E-02
topi	1,06	28,37	1,1E-02
Arc2	11,06	27,89	2,5E-07
yellow-c	2,25	26,52	8,3E-03
CG30002	6,30	25,14	6,4E-06
Mco1	0,93	22,63	1,8E-02
CG1103	1,59	21,81	2,3E-02
Obp57b	3,83	21,54	7,1E-03
CG10337	2,30	21,06	9,1E-03
Mul1	1,85	21,04	9,1E-03
CG17760	2,36	19,51	8,3E-03
CG15141	1,17	19,10	4,5E-02
AttA	8,95	19,09	2,0E-04
CG33460	2,71	18,65	2,2E-02
Ppt1	2,04	18,54	1,3E-02
yellow-f	2,21	17,79	1,5E-02
CG8578	3,36	17,58	9,4E-05
Skeletor	0,56	16,41	2,0E-02
GstE8	8,27	15,98	3,9E-05
Nmdmc	29,34	15,82	2,1E-10
Sid	3,08	13,39	1,7E-02
CktIalpha-13	1,56	13,33	2,5E-02
GstD3	46,24	11,68	2,2E-12
CG14969	3,73	11,46	1,5E-03
AttB	21,82	11,01	5,0E-07
CG14442	15,61	10,64	4,4E-08
CG6830	2,61	10,53	2,8E-04
CG34330	5,89	10,47	3,9E-02
STUB1	3,91	10,20	7,1E-03
CG5861	4,57	9,85	5,5E-03
GstE1	39,63	9,82	2,2E-09
CG6310	11,28	9,82	7,8E-03
Amy-d	5,58	9,14	6,5E-03
CG13796	1,68	8,96	3,1E-02
Scp	1,52	8,94	4,4E-02
ttv	40,65	8,92	1,6E-06
GstE7	19,38	8,86	5,3E-04
GstD2	25,81	8,50	1,2E-05
CG18547	9,28	8,35	2,0E-04
IMPPP	117,43	8,25	1,8E-09
Hsp23	30,03	8,24	8,0E-08
Cdk5	1,82	8,19	4,9E-02
CG2846	5,09	8,17	8,4E-03
Pa1	2,62	8,10	1,6E-02
CG17919	9,81	8,07	1,4E-03
Ho	5,36	7,94	1,1E-02
GIIIspla2	16,26	7,88	5,3E-05
Gnmt	57,04	7,84	8,2E-07
Pdf	18,72	7,79	6,0E-03
CG4269	20,96	7,78	4,2E-06
CG32485	4,24	7,78	2,2E-02
RhoGAP16F	1,23	7,78	4,1E-02
CG15117	3,03	7,72	1,1E-04
CG33470	126,21	7,43	2,8E-10
Ubc4	4,83	7,42	4,9E-03
caz	5,93	7,35	3,7E-04
Karl	13,10	7,02	1,1E-05
DptB	45,89	6,98	5,3E-04
GstD5	15,68	6,95	4,5E-03
IM1	63,29	6,93	1,4E-05
GstE6	41,30	6,66	8,9E-06
Cbs	2,21	6,57	3,9E-02
Sep2	8,95	6,57	4,4E-04
CG10814	10,20	6,51	1,6E-03
Hr38	4,24	6,50	3,4E-03
Obp56d	9,79	6,30	1,9E-02
Cyp12c1	2,51	6,28	4,3E-02
CG15347	32,30	6,27	1,8E-04
GstE3	42,10	6,16	1,6E-07
GNBP-like3	17,49	6,16	3,6E-03
Obp19d	14,13	6,11	1,8E-03
ImpL3	4,63	6,08	1,2E-02
lwr	3,34	5,95	2,5E-02
AttC	134,35	5,95	4,8E-06
sPLA2	15,77	5,84	2,6E-03
Ms	28,87	5,69	1,8E-02
Pbgs	3,66	5,57	1,9E-02
CG1890	8,40	5,55	3,1E-02
CG42807	7,30	5,54	3,0E-02
Spm88Ea	21,18	5,53	6,9E-07
Hsp22	27,72	5,53	7,8E-07
Spt-I	4,64	5,49	8,4E-03
CG3348	52,22	5,45	3,9E-05
tra	6,26	5,43	2,4E-02
Drs	805,41	5,25	7,2E-04
lectin-28C	25,40	5,23	7,1E-05
aPKC	24,45	5,14	1,7E-06
CG8735	4,32	5,11	9,1E-03
cv	3,84	5,08	1,6E-02
CG15394	21,10	5,04	2,6E-03
Rab2	13,36	4,99	3,7E-04
GstT4	10,33	4,88	6,5E-03
CG9360	7,06	4,86	4,1E-02
CG9391	12,79	4,79	3,5E-03
verm	4,26	4,78	2,6E-02
CG11686	31,19	4,72	2,6E-03
CG10916	4,88	4,71	9,2E-03
CG2065	23,49	4,70	5,5E-03
CG42246	27,59	4,57	6,3E-03
CG14440	71,58	4,54	1,2E-02
PGRP-SA	14,13	4,52	9,1E-03
Dro	31,72	4,51	4,2E-02

Bl-1	38,28	4,49	6,5E-04
CG8300	9,29	4,40	4,7E-02
CG4757	56,92	4,32	2,2E-04
CG31997	61,53	4,31	2,7E-04
Ubqn	119,02	4,29	1,4E-03
IM2	232,18	4,26	7,8E-05
CG34424	9,71	4,25	2,6E-02
CG6767	39,40	4,20	6,0E-04
CG2004	15,61	4,16	1,1E-03
CG17834	3,95	4,16	2,5E-02
Tsp42E1	13,15	4,13	5,5E-03
CG2767	9,27	4,06	3,0E-02
ade5	49,52	4,04	1,3E-04
RNaseX25	9,62	4,01	3,2E-02
Gie	5,37	4,01	2,7E-02
Mp20	19,02	3,98	1,8E-02
CG12814	9,68	3,97	1,1E-02
Spm88Eb	33,62	3,95	5,9E-04
Lsd-1	15,78	3,95	5,8E-04
CG33129	6,17	3,86	7,9E-03
rg	10,58	3,81	5,3E-04
CG15098	126,77	3,80	3,0E-04
Prosalph4	15,59	3,76	7,6E-03
Tsp66E	6,43	3,73	3,9E-02
CG5867	103,29	3,73	2,1E-04
stck	8,59	3,71	2,5E-02
Cyp4p1	20,16	3,69	1,3E-03
CG13887	40,94	3,66	2,2E-04
CG33494	39,11	3,66	1,6E-03
EbpIII	98,06	3,64	2,0E-04
LspZ	80,39	3,58	2,6E-02
ade3	14,76	3,53	5,8E-03
CG8012	270,87	3,46	4,6E-03
Tsp42E2	45,66	3,45	8,1E-04
RhoGAP92B	3,15	3,45	4,9E-02
Tsp42E3	15,44	3,43	2,3E-02
Gelm	17,28	3,43	2,2E-02
CG5953	3,26	3,41	1,3E-02
aay	60,06	3,36	2,6E-03
CG16758	81,89	3,32	1,1E-02
CG6409	67,53	3,29	1,8E-02
drk	7,40	3,27	1,4E-02
CG6357	41,46	3,21	1,5E-03
CG44325	61,27	3,19	7,3E-03
Chd64	46,44	3,11	1,1E-02
Chmp1	15,85	3,09	4,3E-02
CG11899	17,83	3,06	4,5E-02
CG13315	69,46	3,05	4,0E-03
MsR1	4,88	3,04	4,3E-02
CG32032	25,83	3,04	1,1E-02
CG18067	193,28	3,03	1,8E-02
CG31689	28,42	3,02	4,3E-03
CG8026	6,01	3,01	4,2E-02
mfas	81,99	3,00	1,2E-02
GstD1	318,17	2,97	2,4E-02
Npc2b	29,82	2,92	1,7E-02
CG31676	56,47	2,84	1,7E-02
CG15067	111,81	2,79	2,8E-02
GstE9	49,54	2,79	2,1E-02
AOX1	10,36	2,75	3,1E-02
MSBP	28,81	2,75	2,9E-02
Tsp42Ea	41,73	2,74	2,0E-02
IM3	103,63	2,72	2,9E-02
CG14933	29,92	2,71	1,9E-02
NimB2	22,54	2,69	1,6E-02
Got1	25,34	2,64	2,6E-02
CG16779	4,30	2,63	3,6E-02
CG5390	20,05	2,60	1,9E-02
Mlc-c	20,54	2,59	1,9E-02
CG3609	28,64	2,56	4,3E-02
sqh	23,18	2,56	2,9E-02
Rab1	23,39	2,53	3,0E-02
CG8331	17,11	2,51	4,9E-02
glob1	68,72	2,51	4,0E-02
Cyp9b2	16,42	2,47	4,7E-02
Xbp1	40,47	2,39	4,3E-02
Tsp42Ee	77,01	2,39	4,9E-02
Cys	244,07	2,32	4,3E-02
RpL13A	57,88	2,38	4,3E-02
Strn-Mlck	1,05	-2,49	3,7E-02
Pp2C1	3,10	-2,55	2,0E-02
Liprin-gamma	3,02	-2,69	3,4E-02
RpLP1	158,74	-2,75	2,6E-02
Gbs-76A	2,80	-2,80	4,1E-02
Herc4	8,77	-2,81	1,5E-02
Lmpt	2,47	-2,82	1,4E-02
RpL13	39,17	-2,89	6,4E-03
RpL34b	22,88	-2,90	4,9E-03
RpS10b	10,17	-2,97	1,9E-02
bt	6,16	-3,00	3,1E-02
CG42795	1,71	-3,02	3,3E-02
kdn	3,88	-3,04	5,0E-02
CG7518	1,98	-3,10	1,8E-02
CG43078	2,39	-3,13	4,2E-03
Yp1	961,74	-3,22	1,0E-02
CG12728	7,35	-3,25	5,8E-03
Yp2	753,68	-3,35	1,6E-02
Zasp52	3,43	-3,54	3,4E-03
Set2	1,49	-3,56	2,3E-02
RpL18	63,59	-3,58	6,8E-04
CG5991	4,65	-3,62	3,6E-02
CG1674	2,28	-3,70	1,5E-02
Unc-89	1,48	-3,80	1,7E-02
mnd	2,24	-3,95	4,9E-02
Ndg	1,97	-4,15	1,2E-02
ATPsynF	16,16	-4,22	1,8E-03
Cubn	1,27	-4,28	2,5E-02
Npl4	8,39	-4,38	6,7E-06
tea	1,08	-4,71	1,3E-02
RpL24	41,66	-4,78	8,8E-07
CG32681	0,93	-5,10	2,5E-02



CG10097	3.21	-5.46	4.3E-02
Adar	67.79	-5.49	1.9E-05
CG33120	7.24	-5.52	8.9E-06
LUBEL	0.78	-5.61	7.3E-04
CG4461	4.43	-5.73	1.9E-02
Irk1	1.74	-5.78	3.0E-02
not	3.16	-7.24	3.2E-05
Nlg1	1.54	-8.17	3.9E-05
aub	1.19	-8.23	3.9E-02
Sox21b	1.07	-8.39	3.8E-02
Hsc70-1	1.57	-8.46	1.3E-03
Root	0.55	-8.51	3.7E-03
CG6752	0.82	-9.22	8.6E-03
Mal-B1	27.13	-9.43	2.5E-03
asp	0.32	-9.65	5.0E-02
CG34220	8.09	-9.73	1.7E-02
CG4928	8.93	-10.32	1.0E-04
CG7589	4.37	-10.35	1.3E-03
CG34231	1.32	-10.37	2.1E-02
Cyp6g2	5.67	-10.73	8.8E-03
pgc	7.30	-10.76	3.8E-02
CG42255	0.88	-11.40	6.0E-04
Ntl	1.75	-11.45	1.5E-03
CG34324	6.15	-11.64	2.8E-02
Ag5r	91.65	-11.94	2.2E-02
CG14645	22.72	-12.15	9.9E-03
gnu	4.78	-13.22	2.3E-02
LysP	114.10	-13.53	2.3E-02
fln	1.09	-13.74	3.5E-02
yellow-d	11.31	-14.11	3.4E-03
Hr4	10.63	-14.70	0.0E+00
CG33109	202.72	-14.78	2.0E-02
CG15515	4.21	-14.98	3.0E-02
WRNexo	1.52	-15.08	4.1E-02
CG9377	1.84	-15.42	6.2E-03
cort	1.39	-15.58	1.8E-02
alpha-Man-Ic	2.29	-15.94	1.7E-03
CG16826	1245.94	-19.46	1.2E-03
CG46312	0.90	-20.98	1.9E-02
CG30371	14.48	-24.24	2.5E-04
CG31077	1.29	-25.47	1.1E-02
CG32984	10.74	-26.41	2.5E-04
Mur18B	3.19	-26.85	5.5E-03
NT1	0.68	-27.59	2.6E-02
CG18095	1.16	-34.51	3.6E-02
CG42656	11.79	-35.22	1.2E-02
CG8708	4.47	-36.74	1.4E-05
CG43679	178.61	-39.35	1.5E-05
Muc68D	3.97	-41.30	2.8E-05
Ics	645.55	-50.17	1.9E-07
CG12310	2.68	-52.17	2.7E-02
Muc11A	1.62	-54.90	4.8E-06
whe	7644.73	-59.93	3.7E-07
CG45080	5435.25	-61.44	2.1E-06
CG34212	1488.89	-61.51	7.5E-07
CG13947	103.96	-94.88	8.9E-10
CG43680	216.43	-134.22	2.0E-07
CG34211	56.54	-183.26	3.0E-07
Nlg4	380.93	-275.26	0.0E+00

## 6.4 DEGs of airways from old flies

Gene name	Max mean	group	Fold change	FDR p-value
CG42656	15.358		229.353	4.2E-02
Listericin	5.859		149.793	4.9E-02
Dro	17.153		110.653	1.3E-10
DptA	35.148		97.541	8.7E-11
MtnB	4.413		50.579	4.3E-03
CG11380	0.795		45.736	5.3E-03
CG10814	4.893		37.736	2.9E-07
CG42255	2.451		23.773	0.0E+00
CG7953	4.669		21.625	3.2E-03
CG5399	4.095		14.941	6.2E-07
Cubn	3.742		13.827	7.3E-10
CG9733	0.940		11.804	4.8E-02
CG8620	4.137		11.589	2.0E-03
MtnD	12.975		11.161	4.0E-04
CG11370	8.603		10.694	2.9E-09
CG5909	1.513		10.628	3.6E-03
Arc1	677.031		9.616	6.5E-06
CG12268	1.357		9.451	2.5E-03
TotM	10.936		9.296	3.0E-02
Mco1	0.811		9.110	1.2E-02
Amnionless	2.784		9.082	3.1E-04
CG17018	0.971		7.995	1.0E-04
CG13741	0.846		7.922	3.9E-02
Attc	55.258		7.398	5.7E-07
CAH2	3.227		7.355	1.2E-02
E[sp]mbeta-HLH	2.080		6.978	3.9E-02
yellow-c	1.297		6.818	3.5E-02
CG14906	3.192		6.673	1.6E-03
Mtk	22.927		6.585	9.9E-03
grass	7.810		6.364	3.9E-06
RnrL	0.888		6.240	1.4E-02
CG6409	43.788		6.219	2.1E-05
CG12868	3.914		6.175	1.2E-02
tut	1.877		6.147	4.1E-02
hdly	15.532		6.045	4.9E-02
Drs	343.701		5.852	2.8E-02
Hsp22	4.258		5.640	4.5E-05
Fuca	1.514		5.640	3.7E-03
gammaTub23C	1.001		5.499	4.1E-02

DptB	14.685	5.392	2.6E-02
Arc2	3.418	5.285	2.3E-02
CG4269	5.440	5.140	5.3E-05
CG4757	60.546	5.079	8.3E-03
Traf4	2.103	4.857	2.4E-04
Neurochondrin	1.948	4.682	4.3E-02
Srp54	3.312	4.453	1.1E-03
Lig4	0.956	4.426	4.0E-02
CG14907	3.185	4.333	2.4E-02
Cyp12a5	1.588	4.204	4.0E-02
NAAT1	7.103	4.052	6.4E-03
CG14291	2.250	4.048	3.5E-02
CG2157	6.355	3.849	5.0E-03
CG33057	1.139	3.696	4.0E-02
CG15784	27.814	3.603	1.3E-02
CG1582	2.674	3.581	4.0E-04
CG14401	3.089	3.535	2.9E-02
CG16886	1.708	3.527	3.9E-02
CG34347	2.548	3.512	2.1E-04
Ssrp	3.869	3.454	9.0E-03
AOX1	12.731	3.447	1.8E-03
vir	1.271	3.401	1.9E-02
CCT8	4.814	3.295	4.9E-03
betaTub60D	10.764	3.269	1.2E-02
CG12239	7.340	3.243	4.3E-02
CCT3	3.322	3.225	1.2E-02
CG10527	14.985	3.222	7.0E-03
nAChRbeta3	4.852	3.208	2.1E-02
CCT2	5.395	3.064	1.8E-03
CG13117	10.208	3.030	3.9E-03
Tsp42Ed	21.092	2.979	1.7E-02
cv-2	3.701	2.951	2.4E-03
sas	5.636	2.931	2.5E-02
wb	1.281	2.895	5.6E-03
CG8399	10.073	2.875	1.4E-03
Ance-3	16.287	2.810	2.0E-02
Ada2b	2.882	2.755	1.9E-02
obe	2.174	2.733	8.1E-03
CG5397	10.451	2.723	2.4E-02
CCT5	5.241	2.641	2.6E-02
CalpB	3.800	2.613	1.7E-02
Mmp1	5.207	2.569	1.9E-02
CG2076	7.742	2.537	3.9E-02
dos	1.679	2.536	4.5E-02
CG5346	6.817	2.495	2.6E-02
CG33978	1.101	2.458	4.5E-02
CG11897	4.434	2.392	2.2E-02
alpha-Est8	9.213	2.391	2.3E-02
CG42673	2.432	2.308	3.9E-02
Zasp66	4.123	-2.434	4.5E-02
Unc-89	1.661	-2.442	2.9E-02
ND-49	7.611	-2.443	4.3E-02
CG2736	13.527	-2.472	4.0E-02
Eaat2	2.163	-2.521	4.3E-02
nrm	0.896	-2.569	3.9E-02
CG15096	15.601	-2.571	4.0E-02
CG42795	1.007	-2.572	2.9E-02
LpR1	2.621	-2.656	1.9E-02
nutl	1.803	-2.672	7.5E-03
CG6912	4.966	-2.673	2.3E-02
CG5973	3.214	-2.673	3.4E-02
CG42492	1.497	-2.705	2.0E-02
unc80	1.533	-2.732	2.9E-02
CG32647	2.453	-2.745	1.3E-02
Elai	3.369	-2.774	2.9E-02
CG16820	8.869	-2.776	1.0E-02
Zasp52	3.703	-2.799	1.7E-02
jheh2	10.498	-2.815	8.7E-04
para	2.376	-2.816	1.3E-02
Rab3-GEF	1.107	-2.842	1.3E-02
Npl4	5.882	-2.866	2.1E-03
nrv3	10.740	-2.882	2.0E-02
Zmit	0.700	-2.889	2.6E-02
Ance-4	3.065	-2.894	1.2E-02
l[2]01289	1.107	-2.938	4.5E-02
Iris	6.791	-2.977	8.8E-03
nwk	1.462	-3.006	5.1E-03
CG42541	0.796	-3.019	2.0E-02
Sc2	9.539	-3.091	2.0E-02
CG3940	1.799	-3.123	4.2E-02
plx	1.206	-3.127	8.3E-03
CG43066	2.098	-3.150	1.8E-03
TM45F	2.685	-3.168	1.9E-02
nAChRbeta1	3.241	-3.258	3.2E-03
Dop2R	2.904	-3.323	1.0E-03
CG6908	3.430	-3.338	1.2E-02
FoxP	0.900	-3.349	2.4E-02
CG2765	16.514	-3.413	5.9E-03
ZnT77C	3.120	-3.415	3.5E-02
CG44195	2.634	-3.424	1.0E-02
Ugt35b	13.742	-3.585	1.1E-03
CG6746	8.716	-3.658	1.3E-02
CG44098	0.865	-3.727	2.0E-02
Npc2g	11.169	-3.737	1.8E-03
GABA-B-R3	1.163	-3.751	3.2E-03
CG6329	2.587	-3.760	1.8E-03
ND-MLRQ	35.299	-3.805	1.9E-02
spidev	6.733	-3.826	1.6E-03
CG31523	13.802	-3.851	3.2E-03
CG9297	4.392	-3.883	3.2E-03
Mid1	0.767	-3.904	1.2E-02
inaF-B	4.063	-4.023	3.0E-02
Zw	4.762	-4.025	2.0E-02
Obp99a	32.532	-4.038	1.9E-03
CG13995	0.711	-4.243	4.0E-02
CG8861	0.854	-4.246	2.9E-02
Lsp1beta	3.008	-4.270	4.9E-02
Pka-C3	1.085	-4.319	1.3E-02
inaC	2.794	-4.332	1.2E-02
CG5065	3.092	-4.577	3.9E-03
CG34166	98.580	-4.605	2.7E-03

CG16779	2.345	-4.671	4.3E-03
Yp1	1152.966	-4.700	7.5E-03
dpr4	0.649	-4.735	4.0E-02
Ndg	2.549	-4.849	2.6E-04
Dbi	59.210	-4.886	2.2E-02
GlyT	0.408	-5.068	1.9E-02
CG15353	12.538	-5.100	3.2E-02
Elp17CD	6.530	-5.134	1.6E-05
PP01	3.007	-5.169	6.4E-04
CG6484	1.148	-5.327	4.8E-02
MF	7.035	-5.360	3.4E-05
CrzR	1.063	-5.533	1.9E-02
PP02	2.336	-5.727	2.7E-03
CG10479	2.144	-5.758	2.1E-02
CG12605	2.240	-6.119	1.1E-03
cpv	14.486	-6.147	1.2E-02
CG13284	2.395	-6.291	4.7E-03
CG42450	4.552	-6.457	4.3E-03
14-3-3epsilon	45.420	-6.733	4.0E-02
Npc2h	3.836	-6.780	1.5E-03
CG6660	8.484	-6.903	5.0E-03
CG14688	3.198	-7.076	4.4E-04
CG17323	1.928	-7.095	1.8E-04
FASN2	10.199	-7.465	1.3E-02
Yp3	692.263	-7.601	7.2E-05
CG17562	3.378	-7.643	2.2E-02
CG7910	12.115	-7.846	1.7E-02
CG6432	4.458	-7.927	1.2E-02
Fad2	65.070	-7.928	4.6E-02
CG32816	0.705	-7.994	1.3E-02
CG13607	19.933	-8.022	2.0E-02
CG30008	27.998	-8.166	5.3E-03
BTBD9	4.242	-8.291	1.4E-02
CG4666	5.367	-8.701	1.6E-03
CG43630	11.649	-8.855	1.8E-02
CG9459	4.722	-9.439	2.1E-02
Achl	0.438	-9.610	1.9E-03
inaF-A	2.643	-9.697	5.0E-02
Yp2	1022.010	-9.789	3.9E-06
CG45080	884.635	-9.847	3.2E-02
acj6	0.964	-10.190	1.8E-03
CG15531	11.236	-10.204	3.4E-05
Cln3	0.545	-12.203	3.7E-02
CG8112	1.614	-12.814	1.8E-05
Est-P	0.505	-13.701	4.7E-02
CG16904	30.664	-14.043	3.4E-05
Mcp1	2.883	-14.707	4.0E-07
CG9458	8.464	-15.594	3.0E-05
aPKC	18.893	-15.976	1.2E-03
CG18609	14.252	-16.232	1.1E-04
CG8534	1.301	-17.045	1.5E-02
CG34211	8.650	-17.332	1.9E-02
Ubnq	99.103	-17.816	2.0E-03
CG10096	0.343	-18.024	5.6E-03
to	1.405	-18.063	4.0E-02
Cp7Fc	0.933	-18.409	4.2E-02
Os-C	5.185	-19.292	3.4E-02
a10	7.440	-20.447	3.2E-02
CG13947	32.537	-21.429	2.3E-03
CG34172	1.497	-25.505	1.3E-02
Obp83b	5.375	-26.718	1.3E-02
fln	1.569	-27.430	4.4E-04
tty	31.910	-29.812	5.2E-05
CG7264	0.917	-38.378	2.9E-02
CG14440	144.860	-42.210	1.3E-04
dec-1	0.840	-59.890	5.0E-03
Scp1	17.335	-82.073	0.0E+00
Obp83a	4.675	-99.617	3.1E-04
CG43680	62.206	-204.687	3.8E-09

## 6.5 DEGs of airways from CS recovered flies

Gene name	Max group mean	Fold change	FDR p-value
Cp15	41.6368061	96.6156191	0.00327526
CG31928	3.91360394	47.3036188	0.00923295
ng3	3.84996277	27.7570129	0.0008054
CG7691	2.92446506	27.6196955	0.02378917
CG13445	4.67719328	26.3507559	0.0029059
CG43315	4.7940973	25.7540695	0.0043658
jhamt	179.251021	20.4004527	0.00411296
CG43089	4.31562979	17.5040312	0.00413049
CG33775	3.23179408	14.1756613	0.00379793
CG34217	5.57969978	14.0680765	0.00886584
Akh	765.604245	13.938323	0.00944661
yl	26.3188445	13.9128231	3.40E-06
CG31861	6.62388147	13.6348017	5.11E-05
CG15047	6.80125993	12.8296491	0.0025798
CG44088	3.18324326	12.316718	0.01917329
CG15563	2.54179551	11.7708543	0.03278265
osk	40.1197125	11.5571409	0.00023481
Gr68a	13.9284922	11.2853174	2.73E-05
CG17329	2.88805983	11.1702014	0.01959393
nos	7.16325628	10.4279726	0.01749852
CG9672	7.75677418	9.94063681	0.00277782
GstE4	6.88179006	9.82586296	0.03153989
CG14075	386.163928	9.3874173	0.01225636
mtm	17.80663	9.13772249	0.00671857
CG13557	3.79346338	9.12695211	0.00520612
CG13641	54.0959761	9.02192502	4.26E-05
plh	35.6915339	8.98077757	8.90E-09

otu	17.256055	8.93876291	0.00921632
CG12725	5.11251838	8.84363658	0.04468375
run	4.72082576	8.7638733	0.02774672
mir-2491	5.77162608	8.54443751	0.00191646
CG14579	4.01754628	8.43308684	0.01475714
swa	7.09228771	8.30915217	0.02524672
CG33463	5.12980464	8.29069296	0.01154492
alphaKap4	14.392143	8.05786328	0.00013116
CG15071	5.86470329	7.94308894	0.0013507
CG43919	11.1917494	7.93598435	5.75E-06
CG10993	6.95276706	7.76732932	9.13E-05
CG12347	7.04018556	7.70856172	0.00510629
CG11425	64.7530633	7.69295682	0.00018555
Rp55b	36.3472859	7.66501974	0.00032795
CG4375	14.7097009	7.6045477	1.26E-06
Gr47a	23.0743759	7.49608728	8.38E-05
stil	4.51964493	7.48080002	0.04308156
Obp51a	4.27324118	7.31218205	0.0352183
CG31642	20.9212731	7.30218455	0.00242032
Muc11A	14.7872109	7.13610274	0.04378334
CG2209	6.83346022	7.09923098	0.01305907
CG11912	16.5618941	7.06202643	2.29E-07
Cyp303a1	13.9126956	7.04569607	3.91E-07
CG18472	3.49377114	6.96715118	0.0067703
CG5906	7.03231386	6.95276814	0.04167033
CG11437	7.45083929	6.93701737	0.00294031
CG44437	24.7234221	6.83997342	2.40E-06
CG7856	5.14831836	6.5888167	0.00528557
CG32259	8.67023355	6.56864759	0.00028702
Gr97a	4.68212908	6.4740317	0.03955962
CG43386	3.17829934	6.35804926	0.02954268
CG33752	3.6409426	6.1692459	0.03003438
CG14545	12.5813178	5.96578433	0.0059422
CG1988	6.02589013	5.96380857	0.0129214
CG8850	4.71894646	5.89810701	0.04706234
Ir56a	44.7033824	5.88495478	2.14E-06
ToTF	5.45432119	5.8844846	0.03920013
CG15403	4.88167377	5.85349549	0.01334551
CG16853	8.85681951	5.81889426	0.00463438
BigH1	12.1714397	5.81811319	0.02284076
CG8072	9.91535762	5.70745646	0.01530088
CG7730	7.62722548	5.6638105	0.00919359
CG31627	7.90587424	5.65866256	0.00238693
hog	8.57580853	5.65839516	0.00081165
Gr59d	5.11298381	5.62694524	0.02030414
Tb	9.45018038	5.60233899	0.02468946
CG34261	4.65217096	5.5997248	0.01110548
RpL23A	610.333072	5.57229136	2.48E-30
Ilp8	3.95228197	5.53890642	0.01135745
TpmC4	16.2381985	5.4374713	0.0001803
Elp17CD	918.431748	5.41359205	3.27E-06
CG18063	19.2720053	5.41174604	5.31E-05
CG15333	8.67125339	5.41034553	0.00902274
CG14556	8.29146366	5.40207079	0.01388994
CG34330	28.0044003	5.29759736	0.00626662
CG43396	11.2110793	5.26824915	1.33E-05
boil	25.5942576	5.26230986	0.00015895
CG9570	4.79305209	5.20883771	0.03493492
cln3	36.4407152	5.20088371	2.15E-06
CG42564	6.29570971	5.19470357	0.04282871
CG16852	6.96180298	5.16085732	0.03142083
CG6441	16.4784694	5.14457641	0.00115382
CG45428	3.93383476	5.12340142	0.04168097
CG42733	5.01273497	5.09786768	0.027151
Poxn	4.70300467	5.01856251	0.04960541
CG2336	12.1559272	5.01444315	0.01000289
wds	43.1386946	5.01253317	0.00080343
CG31407	7.32011105	5.00399165	0.02984942
tup	40.1923773	5.0032632	2.44E-05
SmD3	41.2337308	4.98749525	7.19E-14
CG42264	8.74169456	4.96661369	0.00556504
CG18467	85.2537514	4.94823269	3.72E-06
CG11113	5.6269758	4.91602059	0.02193273
titB	7.62987204	4.89251214	0.01118327
CG11997	24.4475347	4.88158116	1.13E-05
CG1314	12.4509249	4.83103807	0.0046973
CG43799	11.1951523	4.7896254	0.02000457
Mst36Fb	6.62896658	4.7846645	0.02892729
CG31826	13.3666378	4.78028301	0.0048376
CG16825	8.9715723	4.74130263	0.00098065
CG13436	17.4269599	4.72417967	0.00092012
CG17199	7.89252361	4.6888521	0.00358946
CG13442	6.42945803	4.63455167	0.01311071
CG32232	14.074152	4.63348433	0.00030423
CG2104	21.1696125	4.62176654	0.00291746
Obp73a	4.9845682	4.61392625	0.01237336
Ir48c	8.66170884	4.60329212	0.0014116
Rcd7	20.4902719	4.58393155	0.00123074
DNApol-alpha73	8.24111144	4.56425685	0.00347473
ATPsynCF6L	7.22590977	4.49860408	0.01976683
CG32814	9.69536503	4.4715707	0.00074475
CG6209	14.9628034	4.455796	0.00540681
bt	4350.68309	4.42924135	6.24E-07
CG43647	6.94481896	4.38514396	0.02335789
CG32845	8.49042724	4.38181311	0.03490965
CG33127	11.8279531	4.27733471	0.01028203
CG32141	6.987415	4.25754771	0.01069855
ZnT33D	26.0630645	4.25507428	5.37E-07
tor	13.8856808	4.2427846	0.03581549
CG3257	76.8171285	4.2288248	2.70E-05
Zasp67	21.4250808	4.15895068	1.69E-05
CG7708	202.656797	4.15615499	1.44E-07
Cdc6	25.9938301	4.14472064	0.00135437
CG9072	20.2233182	4.13336853	3.79E-05
CG42266	7.40795413	4.09232433	0.01704309
Hsp60D	26.2988703	4.0791977	0.00010171
CG11741	35.3609172	4.04598444	0.00019107
CG14082	42.0001021	4.02670253	5.78E-05
CG31759	14.6144723	3.99661858	0.02271673
Trim9	54.967437	3.9959245	4.93E-11
CG12309	26.7460009	3.99212357	1.92E-05

CG12147	16,1675236	3,98769303	0,00108964
Shal	135,965029	3,9799361	9,96E-15
CG43155	7,03727579	3,97787447	0,03235817
CG5882	6,71501088	3,97359808	0,03493472
CG34172	8,01635787	3,97313406	0,01453923
SdhAL	11,0473383	3,97120691	0,00125763
CG6123	136,172088	3,92409956	9,90E-05
CG6527	53,3783559	3,9223839	1,03E-07
CG8617	23,2238452	3,9171077	3,46E-05
CG12985	11,0238301	3,89430638	0,01498212
CG14340	14,1566895	3,89027623	0,03235817
Acp33A	5,51739005	3,88994431	0,02615639
CG33301	14,94802	3,87797627	0,00067477
Cyp6E2Psi	9,29802449	3,86984428	0,00995202
Scr	20,4934675	3,8628603	0,00023481
Nlg1	60,8141379	3,82260227	0,00123914
CG15642	6,35880591	3,81452752	0,01388994
CG13607	158,937989	3,79393113	4,24E-17
CG34155	32,0224108	3,78381657	1,59E-06
CG4415	12,6547493	3,7723197	0,00226597
AAANATL2	20,9270803	3,74818039	0,00013583
CG14186	128,477767	3,74027754	3,11E-07
CG17707	15,4073498	3,72407829	0,03946988
Ir47a	43,2223025	3,72154023	2,07E-06
CG15233	9,42751374	3,68253959	0,01015701
ND-51L1	37,0928967	3,66705717	0,00011868
dpr5	34,2830719	3,65003268	0,0345201
Rpl22	64,115183	3,64633526	5,31E-11
CG3964	8,53947509	3,62411601	0,03300676
Tig	273,037651	3,6233882	2,01E-10
CG30065	8,51621339	3,61048062	0,034773
CG10132	104,186857	3,60078203	0,0002136
Dscam3	178,460186	3,59986745	1,53E-11
CG9503	13,7599037	3,58478008	0,01131783
nAChRalpha3	301,401427	3,56169009	2,37E-06
CG13995	100,931534	3,54714862	1,23E-05
CG32323	40,0888241	3,51407239	4,10E-06
Alk	834,421945	3,47731855	2,77E-10
CG8958	40,4782387	3,46415606	6,67E-05
Ork1	54,2755566	3,43862281	3,70E-08
CG12426	7,35076974	3,43036981	0,02271805
CG43861	19,237735	3,40925324	0,00261919
Mf	427,902026	3,40679886	3,28E-06
CG32681	77,9924982	3,39937346	4,12E-09
CG9471	119,192905	3,36943419	0,00024842
CG42339	41,2945408	3,36799423	0,00012753
CG5235	11,9186497	3,34619206	0,04237447
CG33645	9,49551605	3,34167717	0,00905771
CG31068	23,767714	3,33606571	0,0009503
CG13693	24,1290777	3,32537371	0,01116642
CG14814	32,1839829	3,32335759	0,01867239
CG10384	65,8252265	3,32076815	3,89E-05
CG13001	6,37768536	3,31759947	0,03585022
CG11068	9,24179289	3,30854828	0,01515489
CG3982	9,65257603	3,30346853	0,04887362
CG2111	21,5210573	3,30054565	3,18E-05
CG7460	11,30401	3,29354082	0,0410725
CG6738	28,118469	3,2865665	0,00025546
CG11449	20,0172941	3,28117855	0,00100982
CG33640	10,7925767	3,2745568	0,0151515
CG9377	93,910233	3,27349155	0,01693667
CG5071	87,4937552	3,27322115	8,07E-09
CG12229	16,9048912	3,26860058	0,03881797
Ir51b	16,3050693	3,25515253	0,00158565
Tace	37,6638784	3,25160952	0,00318839
CG34025	16,3270872	3,21234141	0,00059169
Shawl	115,859939	3,21101854	0,00019921
Mid1	274,460747	3,19216958	1,02E-11
mof	24,1522706	3,18538859	8,21E-05
CG15803	94,1965089	3,18328191	3,05E-06
CG43755	50,6455505	3,17095168	3,63E-08
CG13737	16,6991707	3,16150653	0,01618601
dpr9	228,428464	3,14323528	4,92E-05
CG12116	833,019411	3,14299658	3,84E-10
CG13594	35,8615644	3,14276446	0,00077295
rn	61,520779	3,14101484	8,68E-05
CanA1	27,1504206	3,14063365	0,00367112
CG18171	40,2803767	3,13993326	0,000191
CG15894	153,013771	3,12917794	0,00019318
CG6867	50,6023506	3,12413641	0,02182317
RumxA	12,5202164	3,12278181	0,01805952
kek3	80,6879528	3,11661785	0,0001946
CG34117	31,1280451	3,11595475	0,000989
CG42523	9,02561155	3,11032688	0,01768945
ND-18	19,5456845	3,09788056	9,83E-05
CG30158	103,23087	3,08349357	0,00021841
Rab3-GEF	403,009113	3,08166811	4,21E-08
CG11911	10,2062009	3,06174965	0,02403129
CG17075	180,584151	3,05925941	8,02E-09
CG34450	8,59097185	3,05628814	0,01048837
CG5773	170,071744	3,05519263	3,62E-08
Blos3	6,20667894	3,04842992	0,02549459
CG13108	25,1202165	3,03359293	0,0221857
CG43347	166,119613	3,03100235	2,18E-09
CG45002	317,577896	3,02772094	3,40E-07
mRRF1	22,9555137	3,02242884	0,0112238
hbs	52,9969821	3,0214635	0,01308767
RSG7	199,365898	3,01941198	0,0004387
CG3517	17,8134845	3,01808389	0,01482077
exd	266,962406	3,0130849	1,70E-09
futsch	1961,01401	3,00932572	2,18E-09
CG6746	334,084097	3,00658196	0,01158027
Oct-TyrR	40,1622124	3,00582834	0,00018031
w-cup	19,1480666	3,00429095	0,00155819
CG43091	27,8600041	2,98876521	0,0308823
CG43312	12,4136312	2,97034578	0,04223586
dmrt11E	8,77380982	2,96836476	0,04395575
nvy	18,7148514	2,96320901	0,01768945
sff	217,009456	2,96059831	3,41E-05
CG43788	11,6096907	2,95567213	0,03076495
Spred	305,633215	2,95481604	2,92E-15

CG9650	69,9131646	2,94631528	0,00025322
CG3597	315,009773	2,94589203	0,00045623
CheB42b	8,25434469	2,94418238	0,02642588
fid	59,3618908	2,93968216	2,38E-08
CG43094	111,179624	2,93470674	0,00024806
Gad1	13,1216962	2,93365068	0,00468083
beat-1la	931,272401	2,91593889	6,97E-05
unc80	136,010979	2,913478	1,23E-05
nAChRalpha1	557,519785	2,90322246	7,80E-08
Dop2R	430,336286	2,90181041	4,67E-06
Dhit	321,272107	2,88857186	1,48E-07
twz	138,282318	2,88496475	1,24E-05
CG14234	25,8866061	2,86793311	0,00085149
Apoltp	21,2210223	2,86046284	0,00190014
CG30076	3498,69935	2,85294602	1,97E-05
Cyp28D2	18,0719021	2,848085	0,00026169
CG2192	51,6949823	2,83053777	0,00361419
CG32192	11,4438409	2,8273822	0,01154492
CG10874	15,7569011	2,80946328	0,00839929
pb	20,325049	2,80366336	0,02623931
CG42561	13,3625489	2,80122201	0,00797273
CG9395	146,125398	2,78233994	0,00079012
Nlg4	108,166847	2,78103212	8,41E-05
orb2	795,909907	2,78092805	2,20E-08
CG42818	12,7830012	2,77911984	0,00948887
daw	238,069337	2,77863275	1,65E-05
yellow-d2	15,0646589	2,76566085	0,00821491
CDK2AP1	23,0339094	2,7625255	0,00197544
Sse	27,500935	2,76006932	0,00540681
Shn	55,584456	2,75946433	0,00317343
CG42450	571,725802	2,75763598	5,21E-07
sp4d	10,1367904	2,75570754	0,03786639
CG42265	202,25915	2,75155546	4,83E-06
CG13631	136,500258	2,74678303	1,37E-06
mAChR-A	154,326189	2,73809896	0,00026582
Zmit	298,967452	2,73661477	3,01E-06
VGAT	129,12392	2,72871067	0,01075776
CG1494	15,214401	2,71738731	0,00932395
CG5214	180,701077	2,71674336	1,78E-09
CG31345	64,5378353	2,71211593	0,00042898
mei-W68	28,8403451	2,70629558	0,00136006
Hr3	79,8148152	2,70284696	2,07E-05
dpr14	148,178555	2,69879461	3,95E-06
ief	471,475029	2,69818656	6,23E-05
CG10483	30,1491199	2,69752438	0,02258885
CG31053	18,8470373	2,69004765	0,04896924
CG32206	193,227356	2,68752114	1,64E-06
CG14440	44,6866897	2,6817336	0,00071716
Epac	356,282262	2,67207436	5,45E-08
elav	911,87673	2,67022999	3,25E-07
Eip78C	80,649307	2,666594686	7,32E-05
CadN	1014,99315	2,6636567	3,41E-08
Mp20	127,67699	2,6636128	0,0151515
Scp1	199,599582	2,65960571	0,00466653
Tpc2	8,69929363	2,65422181	0,03766022
zld	114,46295	2,65358098	6,41E-05
CG9760	26,3508823	2,65108427	0,008566
CG43329	23,0648863	2,65091355	0,03121243
svp	151,252215	2,63975404	1,86E-07
CG9902	53,7610478	2,63912075	0,00274529
Sap47	1384,38171	2,63660231	9,37E-09
Gluc1alpha	696,806589	2,63041613	7,85E-08
CG33644	10,2517841	2,62815154	0,03880466
HERC2	293,067371	2,62761378	0,00012143
Cyp12d1-p	10,8749002	2,62561789	0,03265914
Grip163	74,5304002	2,61954876	2,18E-06
RyR	475,558784	2,61346673	6,46E-08
CG34189	11,5093652	2,61282087	0,02643233
dco	169,885611	2,60555888	1,86E-09
CG13685	101,353714	2,60326893	0,00569484
CG42288	18,6361329	2,59915583	0,01584719
CG30325	12,9729621	2,59531584	0,01749598
CG14817	41,1635591	2,5901173	4,51E-06
Hsc70-1	56,0426639	2,57450222	0,02319632
Nmdar1	97,1178155	2,56382412	0,01466407
esc	58,2153682	2,5617735	5,74E-07
DIP-alpha	119,359873	2,56097582	0,00083793
LBR	26,2216323	2,56055164	0,01142245
CG43778	328,533129	2,560455	5,28E-05
Aven	16,7785943	2,55686706	0,04244974
CG34300	11,9763483	2,55659072	0,019443
Octbeta3R	127,566868	2,55588868	1,07E-06
CG16779	586,679677	2,55560439	1,05E-06
mspo	38,4251824	2,55532452	0,00932277
Tdc2	27,9780287	2,55263847	0,02549478
alpha-Man-1Ib	118,315914	2,55176929	0,00017945
Ten-a	1008,50827	2,54967567	1,16E-06
Actbeta	417,287261	2,5391901	2,73E-09
CG4213	39,0421938	2,53608142	0,0462043
ymp	42,0583963	2,53484259	0,00012138
CG42287	12,209219	2,53283902	0,0404601
rg	29,6881119	2,53111537	7,84E-05
CG12693	13,378953	2,52887213	0,03065131
whip	29,3934304	2,52777597	0,00123513
CG4238	131,36318	2,52641141	1,50E-06
CG18449	25,1941569	2,52627936	0,00103045
mclur	465,522209	2,52485331	7,70E-06
Teh1	166,961664	2,52458694	0,0007929
CG30116	306,874332	2,5217258	1,34E-06
CG33199	37,4702551	2,51912221	0,0027287
CG42346			

CG34384	461.560511	2.48102589	4.97E-05
mRpS28	45.3781531	2.47820742	3.14E-05
Fred	148,884342	2.4754614	0.00143497
TrpA1	22.2235564	2.47428819	0.03258162
PIP5K59B	170.162424	2.47314444	0.00370317
ND-23	360.690251	2.47190576	1.29E-13
CG42492	582.093609	2.47114789	7.01E-07
CG6908	155.803678	2.47073582	0.01123627
pip	22.6024122	2.47023298	0.02998414
RhoGAP100F	668.254508	2.46827477	6.77E-05
Cyp4ac1	174.557888	2.46472454	0.0006967
fru	352.518552	2.46418704	9.97E-05
CG46301	44.9523887	2.4565943	0.00019987
CG31921	46.7068863	2.4560894	0.00024785
Sytralpa	197.605933	2.45595131	0.00428649
l(3)72Dn	30.10066	2.45019129	0.00713242
EndoA	456.325359	2.44870881	0.00016506
trv	516.265618	2.44739752	3.80E-05
Mhc	314.447633	2.44677559	0.00995202
Dop1R1	446.550099	2.44546743	0.00019318
CG7742	24.872575	2.44519068	0.02072531
CG31122	76.259769	2.44377052	0.00015432
CG12662	14.1612265	2.44318084	0.01360678
Tango10	84.6808434	2.43519978	0.00053718
Spn	535.778006	2.43213754	7.47E-08
Myo81F	100.828652	2.43117163	0.00112813
hiw	525.82938	2.4309104	1.07E-06
orb	263.774541	2.42994661	5.96E-06
DIP-delta	159.393325	2.42678533	0.00011084
CG42322	187.278082	2.42276468	0.00071257
leb	726.944746	2.42028491	0.00072273
CG12605	445.462242	2.41906976	1.88E-05
CG8539	79.8420078	2.41892672	0.00434128
CG11319	508.848274	2.41569514	1.45E-07
retn	18.5842847	2.41540479	0.01142754
Yp3	38923.8146	2.41173139	0.00798537
MagR	94.6217763	2.41143207	6.98E-06
unc-13-4A	224.40693	2.41109646	0.00177341
Ndg	213.689165	2.40387327	0.00092639
CG12502	41.1570537	2.40072684	0.0045482
Syn	723.062354	2.39927051	9.30E-06
Dscam2	720.103434	2.39887821	0.00017293
CG6024	313.590713	2.39709987	0.00012683
CG14535	64.5773457	2.3956875	0.00247679
osa	429.938999	2.39011458	3.17E-15
CG4341	166.996833	2.38770122	0.00057358
kek2	171.377964	2.38583919	0.00256515
CG9090	71.3762357	2.3849699	0.01156301
alrm	138.51573	2.38451309	0.04332788
CG42340	94.3475842	2.38199512	0.01247922
na	197.245325	2.37933561	6.39E-06
AstC-R2	41.2815477	2.37818683	0.0072607
CG10804	277.89203	2.37682177	3.13E-06
bru3	1447.69273	2.37529917	0.00033304
side	254.553606	2.37470577	3.67E-08
CG1402	86.7739881	2.37335281	0.04479594
Ets65A	44.7028712	2.37330258	4.44E-05
sei	113.43196	2.37015299	0.03504015
CG13743	188.052486	2.3696506	0.00046633
CG43901	344.827002	2.36682884	0.00141724
Glo1	90.0060544	2.36636965	0.00032241
CG9360	140.205056	2.36613916	1.29E-07
scrt	1011.14768	2.36608134	0.00035269
CG1674	200.859257	2.36303475	0.00206706
mRpS6	23.342014	2.3626086	0.04914846
onecut	870.964427	2.35979274	4.07E-05
CG44245	164.753688	2.3518899	0.019443
Nlg3	209.878474	2.34937915	4.79E-06
CG9314	13.6539627	2.34932711	0.04308156
5-HT1A	85.9555349	2.34876811	3.20E-06
tomboy40	22.3137174	2.34633412	0.00269852
CG8910	43.2044739	2.3450031	0.01034853
CG42594	56.8096083	2.34057879	0.022597
CG8679	67.2462984	2.33654821	0.0296295
Myo10A	107.253582	2.33381268	0.00166469
CG7466	214.539318	2.33367495	6.32E-07
DIP-zeta	41.029	2.33094815	0.01679443
CG30419	48.7175755	2.32713675	0.00574547
mRpL52	31.9680329	2.32576814	0.00248712
Pde1c	328.519411	2.31475668	3.41E-05
CG17724	38.4783552	2.31382338	0.00224848
VACH7	952.058586	2.30922636	5.35E-06
CG5890	194.52826	2.30621818	0.00013199
CG32523	22.7630889	2.30621634	0.00132106
CG32655	23.5298546	2.30400903	0.01100421
Obp83cd	66.2189513	2.30285609	0.02467938
CG12290	143.807189	2.302206	5.94E-06
Nhe2	253.035063	2.30074043	1.03E-06
Gycbeta100B	208.35792	2.30025126	7.15E-06
pHCl-1	370.969093	2.29812582	1.41E-05
CG43795	68.2891865	2.2977574	0.00312355
Pde6	324.092379	2.29646365	1.25E-06
Med	22.9808619	2.2931974	0.04065833
CG42700	37.9022913	2.28806829	0.02323092
rad	260.088611	2.27980577	0.00216811
CG13528	11.2961363	2.27620427	0.03366073
CG17364	128.069329	2.27541347	0.00014904
Impl2	683.230122	2.27498101	0.00327229
lov	57.890991	2.27473486	0.00364168
ZnT77C	116.045946	2.27167151	0.04235475
Nos	75.8882976	2.27028409	0.01564596
PsGEF	363.353129	2.26976731	0.00051341
CG14372	29.4760804	2.26955277	0.02259986
Obp99a	573.47959	2.26922066	0.04881773
Calx	368.090417	2.26852444	0.00082638
CG42313	145.539738	2.26381947	0.00479063
CG44422	188.16266	2.2593942	0.00124251
CG12769	93.1533265	2.25735298	4.74E-05
Yps25	52.2896539	2.25402198	6.82E-05
CG32568	17.5405137	2.25235776	0.03854082
mRpS18A	34.5950882	2.24899734	0.00028296

mir-967	17.9514986	2.24652712	0.0092465
mei-41	48.3385699	2.24105812	0.00974413
GABA-B-R3	122.88051	2.2399461	0.01319544
ND-24	273.228026	2.23844536	4.28E-05
Gbeta5	70.2801184	2.23773179	0.01466407
sm	1905.07479	2.23732357	4.97E-05
GatB	43.8354396	2.23301151	0.03501938
CG43737	571.915221	2.23193556	0.00022769
CG5937	207.1822	2.22778482	0.00069621
eag	346.789453	2.22461788	0.0016675
Rpn13R	10.7766107	2.22446954	0.04734484
Pkc53E	524.694516	2.22316419	6.32E-05
CG31817	28.222292	2.2229751	0.00424134
CG6752	34.465353	2.22075688	0.00995202
apolpp	68083.5726	2.22015176	0.00644308
amon	589.681921	2.20702161	0.00375592
RpL41	1161.03512	2.20475284	0.00016853
CG2046	88.1622355	2.20186728	0.04308156
IA-2	7552.64727	2.20097423	0.00203165
CG11029	21.2800804	2.20002916	0.0214342
DENR	27.6236394	2.19874245	0.00176382
Rbfox1	769.348862	2.19773159	3.52E-16
CG32683	72.1803079	2.19698318	0.01214712
Con	226.54197	2.19434998	0.00279491
CG1698	21.3264937	2.19317528	0.01855413
wisp	23.5753306	2.19168049	0.01439625
CG2065	145.860935	2.19015149	1.26E-05
Octbeta1R	171.093474	2.18942537	0.00028196
pros	4774.58151	2.18742412	0.00263678
CG12123	41.2310766	2.18709004	0.00027223
tj	27.8737113	2.18485678	0.01749852
	2158.20173	2.18392671	1.19E-05
Vhl	40.6521407	2.18176964	0.0226006
CG17816	538.853414	2.18061748	7.21E-06
CG9766	21.5193059	2.17422673	0.00823532
CG11138	213.769864	2.16909929	5.45E-08
CG31760	240.772258	2.16853574	0.00149865
Cyp6w1	2986.91913	2.1680608	0.00947907
CG8909	754.683259	2.16654569	0.00215612
dsh	37.9123824	2.16348392	0.00115382
CG17778	60.1789033	2.16286768	0.00043461
sws	407.769263	2.16187607	1.71E-07
dpr13	142.299547	2.16147055	0.03066861
CG41378	158.133635	2.15943031	3.72E-06
CG3800	271.040171	2.15542118	8.25E-08
Nrk	43.2381534	2.15364457	0.02498347
NacP60E	1558.2181	2.15186897	1.83E-05
CG2202	47.5348035	2.15167363	0.02376794
CG34371	99.491704	2.1512828	0.02308223
CG5023	30.3682426	2.14802989	0.04862329
Hus1-like	39.6625438	2.14328983	0.00347023
enc	450.704389	2.1430826	5.52E-09
RpL36A	1312.81229	2.14102607	1.54E-05
Sec71	143.805969	2.14067043	1.37E-06
	351.217776	2.13733834	1.44E-05
nwk	206.423746	2.13441837	0.01140788
Cyp313a4	62.3341322	2.1335044	0.01724873
salm	80.1097706	2.1286343	0.01054
sced	62.4486671	2.12784103	0.00058387
lectin-46Ca	16.4357907	2.12649186	0.04565201
CG32647	783.95578	2.12573414	1.00E-09
Cyp4ac2	129.605707	2.1239289	0.00314014
CG14982	96.3879841	2.12356429	0.00795222
Cpr73D	55.3665836	2.12154606	0.00051554
CG34188	35.0917978	2.12114326	0.02363492
CG18809	32.6865999	2.12106941	0.00166469
CG9132	58.938331	2.12082365	0.00099381
CG8132	87.7563318	2.11524801	0.00213831
CG14509	353.486051	2.11504601	4.27E-05
CG4587	675.69065	2.11482423	0.00428649
CG43192	28.7900687	2.11348081	0.04409163
Rab26	86.9888697	2.11262055	0.01850494
nAchRalpha4	487.791766	2.11176777	0.00034555
CG15203	70.2120126	2.10618016	0.03473206
CG42260	289.803132	2.10477548	0.00134688
CG32000	1439.26677	2.10353009	1.67E-09
CG17776	19.2372724	2.10259997	0.01057796
CG31213	67.9760258	2.10197382	0.00278689
nocte	279.445119	2.09558601	4.34E-05
RpS14a	1836.04309	2.08867583	0.000748
Als2	134.576896	2.0879743	0.01428582
hwt	289.85757	2.08706695	0.01234449
CG33639	90.0063049	2.0861655	0.00333704
RpS28b	1781.99335	2.08380561	3.77E-06
ND-B14	113.190847	2.08371967	3.20E-08
CG11438	20.0262141	2.08193045	0.03484204
CG3191	60.0960791	2.0815644	0.0006967
Bacc	568.814204	2.08094515	2.01E-13
CG43066	407.741983	2.08092293	0.0006311
Nckx30C	1563.94742	2.0788846	0.00010932
Syn1	70.2067166	2.07848227	0.02954268
CG18622	61.3645835	2.07738515	0.03919105
CG14688	147.922683	2.07458455	0.00963006
ATPsmD	660.756678	2.07208413	1.99E-09
CG4168	139.537657	2.07123416	0.0185997
bru1	255.188922	2.07115786	0.00062464
ChuR1A	76.5753408	2.06969977	0.00997377
CG43056	14.3853145	2.06812513	0.04558875
CG14459	153.599066	2.06779897	0.0067703
CG34357	167.78219	2.06694571	0.00089294

plx	240,650159	2,04738111	7,41E-06
beat-Vb	56,5901035	2,04696126	0,02370256
east	447,108263	2,04651778	7,40E-10
RpL14	3295,10732	2,0450042	5,31E-07
CG30172	80,0761226	2,04423261	0,00619861
wry	576,275633	2,04416986	8,77E-05
CG5549	93,3499077	2,04216462	0,00377682
ATPsynG	440,713706	2,04209713	1,13E-05
Rbp6	1467,87293	2,04203359	1,60E-05
Dap160	418,077399	2,04181982	0,00013403
Sod1	1245,36879	2,04024542	0,000109
Nrmt	47,3787295	2,04018314	0,01886928
CG43103	56,7867222	2,03865409	0,0105132
Mlc1	162,078666	2,03754768	0,02516244
CG31248	143,029291	2,03716617	0,00030423
CG13375	256,988098	2,03707019	0,00097107
SdhC	249,439506	2,03662971	6,98E-06
RpS9	1622,61509	2,03613127	1,65E-05
bma	107,062365	2,03582854	0,04022829
muskelin	58,8576803	2,03256018	0,0012753
CG5644	27,9967894	2,02988408	0,03825271
CG14141	67,6667222	2,02952037	0,0309429
Yglut	899,11576	2,02778214	0,00376584
fus	302,375996	2,02769238	0,01548436
trr	124,165188	2,02509473	0,00973297
CG8861	258,435607	2,0244811	3,76E-05
dpr11	167,002397	2,02364372	0,01716114
biv	54,185024	2,0234367	0,00195327
CG12594	107,554467	2,02334537	0,01071129
Asator	901,01989	2,02231863	2,14E-06
Ca-alpha1T	774,174931	2,02169528	0,00197544
CG14757	64,4644811	2,01443453	0,01724567
Nmdar2	192,162255	2,01430096	0,00253611
chinmo	568,246965	2,01343393	0,00021826
Nrx-1	858,139452	2,01225376	7,45E-05
kug	728,771359	2,01033684	1,20E-08
CG42238	154,322784	2,00965461	4,72E-07
RpS27A	3106,6664	2,00952871	7,96E-06
CG3812	171,3526206	2,00948197	0,00425448
CG32506	83,9732838	2,0094747	0,04187571
CG7166	233,615475	2,00896887	0,02740367
Tob	826,62789	2,00826462	1,82E-06
beat-Va	76,5049461	2,00618632	0,00400763
RpL36	2653,80895	2,00518676	2,42E-05
larp	1062,81092	2,00358616	4,44E-07
CG4467	808,25434	2,00314613	0,00074487
CG9509	68,0794063	2,00259584	0,01515489
CG14270	24,6735222	2,00250213	0,02549459
CG15201	622,300239	2,00202368	0,00781056
Neb-cGP	218,688283	2,00033057	0,00032879
CG31805	22,6489574	1,9991043	0,04394656
Pcv2	430,730949	1,99875495	0,02349379
CG11679	29,073127	1,99793202	0,03113024
CG34401	453,626096	1,9968036	0,00056796
Bap170	93,2940034	1,99659567	0,02844746
CG42795	400,282837	1,99630818	5,37E-07
CG42540	812,610284	1,99566958	0,00646215
5-HT2B	76,2204542	1,99271913	0,00427408
Elk	160,290571	1,99169439	0,01309462
sqa	46,5857196	1,99142297	0,01058635
ksh	19,7732302	1,9912899	0,01346784
mura	759,540168	1,99053538	9,51E-06
RpL10Ab	3630,57165	1,99048054	7,90E-06
CG14431	74,8368861	1,98996127	0,00048638
oIf413	279,889075	1,98574096	7,95E-06
RpS18	2720,51445	1,98475862	3,91E-07
Rim	934,056605	1,98285113	0,00013102
RpL27	2171,49194	1,98270163	1,97E-05
mRpL23	29,200103	1,98251146	0,02168898
smal	149,74043	1,98187211	0,0002327
Octbeta2R	325,208186	1,98092446	0,00016217
nrV3	334,474396	1,98092003	9,69E-05
CG32333	102,248604	1,9794191	0,00371851
CG13890	56,2228317	1,97548125	0,03312126
sno	289,133731	1,9752489	3,41E-05
Rm62	463,59555	1,97355961	5,21E-14
PGRP-SD	433,832962	1,97169962	6,53E-06
RpL10	4951,47731	1,97060897	1,23E-05
fas	144,819255	1,97046934	0,01518602
CG1090	329,880312	1,96936837	0,00010747
Tim9a	22,271225	1,96886456	0,02738903
Sam-S	1523,02035	1,96794501	2,51E-06
mACHR-B	73,0713106	1,96785327	0,04068018
VhaM9.7-a	124,586452	1,96777091	0,0085707
tou	460,349017	1,96594985	1,44E-05
CG12950	253,361132	1,9650257	0,00225439
Adar	750,328419	1,9647986	6,11E-05
raptor	82,948794	1,96350922	0,00765039
Hsc70-4	831,926056	1,9634001	2,61E-05
CG3626	123,84979	1,95977633	0,00043461
ND-19	134,281278	1,95782174	9,61E-05
CG9515	21,2199669	1,95710582	0,01638705
Rab35	165,230142	1,95563252	0,00105019
Corin	342,098068	1,95517083	0,00533359
tutl	827,75604	1,9545819	0,00033368
NetB	339,266831	1,94980531	0,00121749
Prosbeta3	205,449169	1,9497067	0,00345608
CG33234	43,1106672	1,94918312	0,04859284
CG43902	206,879972	1,94862773	0,00059413
CG34355	195,57401	1,94388553	0,00019987
mtt	123,168075	1,94357467	0,02422081
br	360,930165	1,94349943	0,0068804
CG5991	320,872908	1,94078124	0,00621624
SrpK79D	166,561561	1,93894076	0,00430301
CG14882	29,0469276	1,93818852	0,01988535
CG31140	377,848838	1,93813501	0,01746389
Art1	103,929806	1,93611371	0,00145787
stai	421,390911	1,93502199	8,69E-05
rost	313,238371	1,93454391	0,00445323
CG32816	18,5017041	1,93433668	0,03583341
ND-30	302,32662	1,93373496	0,0016868

Nxf3	49,0328642	1,93336309	0,00149865
GluRIB	154,518542	1,93287159	0,00013545
CG15760	154,490795	1,93212141	0,00459051
eIF5	31,9307004	1,93204575	0,01181711
Comp-C	43,0259737	1,9289177	0,03536381
CG32772	64,0859351	1,9284217	0,03945142
Nep3	301,853699	1,92836835	0,00261284
mRpS25	30,0311916	1,92741314	0,01305643
Vmat	865,821705	1,9257677	0,04760121
RpL11	3737,26227	1,92569263	1,93E-06
CG7368	28,4442254	1,9250122	0,04487399
CG2258	203,128392	1,92456648	0,00395732
Fire	492,676245	1,9243768	0,00719128
kek6	206,698538	1,92273451	0,01995628
CG34114	283,341475	1,92107952	0,00166328
	1861,49131	1,92087019	3,14E-05
CG15312	212,086728	1,92041196	0,00422669
CadN2	133,306061	1,91991028	0,01888372
Asx	238,917698	1,91936404	4,14E-07
RpS15Aa	2146,88375	1,91768037	5,25E-06
Rhp1-like	351,038762	1,9170971	0,00115337
RpS14b	586,603248	1,91610305	0,00043825
CG14408	104,467292	1,91461368	0,01362297
RpS5a	4135,81267	1,91436441	3,31E-06
mei-P26	3226,87824	1,91287649	2,47E-05
CG15908	15,5715	1,91209813	0,04294307
CG4408	206,720785	1,910118	0,00954743
RpL28	2619,54327	1,90981674	0,00014675
Yp2	32586,661	1,90910788	0,04290804
Cngl	798,239822	1,90847495	0,00210228
kek1	233,456143	1,90812339	1,71E-05
CG31323	33,3580833	1,90729572	0,03792052
robo3	143,743275	1,90592037	0,02831177
UQR-Q	223,817066	1,90560545	4,20E-05
Tango13	360,555497	1,90557286	3,46E-05
CG10793	25,475821	1,90461811	0,0351604
CG34449	250,681106	1,9027002	5,50E-07
Hr4	59,2560907	1,90161734	0,00358674
kcc	741,468369	1,90082007	0,0005435
Rbp	315,009927	1,90077807	0,00074487
CG10555	52,7672333	1,89977896	0,00261027
COX6B	542,124629	1,89870968	3,22E-05
chn	344,386906	1,89854443	0,00028556
tok	616,753255	1,89553008	0,00804164
Hk	575,677731	1,89530367	7,37E-05
Shab	712,784577	1,89497547	0,01033868
CG3775	379,115201	1,8944572	0,00042497
Tnks	109,751599	1,89393173	0,00086498
CG33181	164,147692	1,8932995	0,00036473
CG43707	289,377938	1,89161114	0,00107634
SCAP	336,522243	1,88915864	1,69E-06
CG5270	168,60107	1,8891225	1,21E-05
CG15096	1007,33756	1,88881835	0,00342602
Irps-1B	525,486566	1,88773952	0,02818676
Sik2	91,3059176	1,88762223	0,02937175
ND-B22	232,501049	1,88672522	8,66E-06
CG17786	69,3398626	1,88485994	0,00527896
chrb	719,677308	1,8848263	0,00050109
5-HT7	69,6984288	1,88418349	0,0339859
CG13300	43,114762	1,883946	0,02870301
sty	327,686028	1,88359499	0,00038407
CG2852	1299,70523	1,88353573	0,00048054
CG13623	34,7624242	1,88311341	0,012862
Rab21	65,9748412	1,88242951	0,04316832
Cpsf160	83,1351796	1,88040871	0,00657184
CG13928	220,520673	1,88010219	0,03215505
drosna	80,7705548	1,87572769	0,01871848
eIF3k	341,566064	1,87561733	0,00020759
Toll-6	195,800454	1,87416773	0,03298887
PTP-ER	163,377767	1,87409209	0,00314344
Dim1	19,9646558	1,87365575	0,03258162
Sep 04	128,699128	1,87356174	0,00039612
RpS23	2225,61829	1,86940081	0,00055314
jheh1	741,930492	1,8687767	0,00179134
SF2	125,085104	1,8685224	0,000664
Ca-beta	314,386673	1,86744695	0,00053346
Odc2	38,0900101	1,86660544	0,00716487
Ephrin	574,067818	1,8665947	5,09E-07
JHDM2	78,4611546	1,86457661	0,03440162
nmo	568,730477	1,86454089	7,45E-05
AP-2sigma	130,639629	1,86305627	2,01E-05
ZAP3	250,407916	1,8624885	6,54E-08
Cbp53E	427,611924	1,86044766	0,00149474
pico	321,628511	1,86033598	6,58E-06
ksr	68,6243248	1,85919312	0,00222128
Orct	100,671077	1,85918768	0,01491689
CG10960	1006,49559	1,85538258	0,04233938
Sh	2903,23744	1,85532111	0,00050483
ftz	40,9606597	1,85445695	0,00675741
CG3527	33,9452482	1,85373149	0,02193733
CG6329	798,093494	1,85270907	0,00161422
CG44098	96,3082908	1,84849117	0,04891533
amn	127,558871	1,84716905	0,00320995
Tlk	409,551965	1,84569097	2,13E-07
Ars2	246,92962	1,84553086	1,39E-05
CG1578	215,294067	1,84546226	0,00085124
Ubr1	619,819646	1,844496	3,74E-07
unc-104	2515,44295	1,84372762	0,00075385
unc-5	90,4032642	1,84300568	0,02732167
aPK	494,155948	1,84056647	0,00012526
CG34354	154,739737	1,84042211	0,00476368
Shaw	332,041731	1,83980654	

CG11374	45,691567	1,8306193	0,03103029
CG16789	30,5087962	1,83053701	0,0463053
B52	321,584346	1,83019688	7,19E-06
mor	61,1203756	1,82998404	0,00501942
ND-20	378,952291	1,82833834	2,42E-07
tipE	104,082065	1,82814024	0,02826368
CG14232	42,3244124	1,82776164	0,04980819
CG4661	25,0167163	1,82730933	0,04786134
inaE	264,508193	1,82679945	0,00134912
slo	179,11351	1,82659729	0,00044958
CG32017	1226,84629	1,82560958	0,00235091
Kat60	76,125446	1,82366343	0,02990005
eIF4EHP	527,087647	1,82326785	0,00062233
CG45263	514,09534	1,82134852	0,00056788
	3270,17963	1,81915752	0,00024413
Pvf3	343,518319	1,81855795	0,00546468
sl	110,313916	1,81855698	0,02296064
tty	247,228997	1,81768461	0,01054
RpL12	2810,67142	1,81635117	8,57E-05
GABA-B-R1	248,787041	1,81585053	0,00243127
Ddr	94,6312046	1,81521123	0,03316981
Pfdn4	34,7882998	1,8119516	0,02583322
Frq2	234,23776	1,81100072	0,02290593
Gbs-76A	385,434161	1,80360237	0,00600624
I(1)G0469	65,0674147	1,80296315	0,00484229
Prosheta4	176,935826	1,80224986	0,01818075
CG31108	106,914993	1,80161539	0,02046009
tai	518,299258	1,8004852	2,46E-06
RpS11	2421,29514	1,79832179	0,00018349
Psf3	308,105339	1,79763932	2,47E-05
E(bx)	763,000155	1,79377885	7,05E-11
thoc7	76,4993462	1,79188091	0,00402067
unc-13	3639,03293	1,78995606	0,00048331
CG33226	57,2619381	1,78612141	0,02750048
ND-B12	113,808145	1,78505403	0,00084144
RpS17	2165,21648	1,78484399	0,00069621
mRpL49	44,0561532	1,78334071	0,00576542
Or71a	27,4927111	1,78197463	0,0364795
MetRS-m	41,8881833	1,77955878	0,04384477
arr	259,703336	1,77603241	1,07E-07
pdm3	126,258925	1,7720332	0,04960541
Ca-alpha1D	616,024849	1,77221581	0,00256248
mmd	779,151796	1,77188994	0,00055116
RpL15	6075,25286	1,77181617	0,00013403
CG8331	427,082314	1,76992317	0,00309466
nAChRalpha5	986,037631	1,76737949	0,0021461
CG15270	202,005215	1,76736201	0,03066671
DCTN6-p27	33,9413189	1,7668171	0,0477262
CG18731	20,5128764	1,76656218	0,04637631
pgant2	67,184159	1,76613148	0,01699931
klg	236,777998	1,76578135	0,00978382
RpS29	3329,05211	1,7652903	0,00028085
ND-B15	76,378311	1,76501987	0,01131486
tos	31,7087596	1,76471636	0,04548436
CaDps	1224,91228	1,76329585	0,00197344
CG1722	46,5532172	1,76261841	0,01943986
phf	174,738719	1,76240273	0,00348812
dac	56,2363757	1,76154592	0,04479594
CG12851	212,454274	1,7615401	0,04788816
CG6044	233,227066	1,76151215	0,01340212
Socs16D	161,984827	1,76130679	0,00206706
caps	300,768829	1,76060289	2,78E-05
Gug	488,04909	1,75810516	8,66E-06
trn	74,5476804	1,75622306	0,00223418
kto	99,1701394	1,7562218	0,02080269
Np4	282,60541	1,75560987	0,00899956
PDZ-GEF	264,464641	1,7541684	0,00069053
CG4725	116,839358	1,75348569	0,00562836
Pkc98E	591,418412	1,75294132	0,00085511
sgg	629,145985	1,74842234	1,10E-05
CG34351	142,655466	1,74841598	0,00209848
brat	544,937229	1,7461489	0,00045283
CG9657	50,184544	1,74604434	0,04902087
CG18208	427,535584	1,74577014	0,00444313
DCTN5-p25	37,0220798	1,74574096	0,03317416
htt	212,871654	1,74521764	0,00025102
nrm	450,370492	1,74520627	0,00180837
Cfrl	371,515832	1,74502283	0,00206706
Ac3	360,205027	1,74465998	0,01766937
eIF3a	191,564643	1,74229638	0,00258548
CanA-14F	595,292218	1,74177201	0,00033883
Rdl	1282,90427	1,74003753	0,00275971
jim	2107,70581	1,73995115	0,00152223
BtbVII	211,380477	1,73866669	4,98E-06
CG32698	238,193094	1,73760607	0,00786115
mago	64,2948971	1,73727968	0,01688515
Vps13B	142,762526	1,73684346	0,0105903
CG32686	98,8554299	1,73675882	0,02498347
fne	1489,67732	1,73565832	0,01389868
dpr12	420,594503	1,73493985	0,03850973
CG12531	428,681465	1,73420355	0,01901724
CG14502	56,3403648	1,73408401	0,00189214
CG13293	113,413532	1,73083986	0,019443
Lrrk	155,95675	1,72690013	0,0003003
CG9034	64,1417042	1,72663739	0,01422829
Art4	108,910984	1,72648626	0,00072465
ling	223,208619	1,72646344	0,00696339
net	56,4125677	1,7259422	0,04963593
haf	69,0701161	1,72563603	0,0216694
Galphao	956,207055	1,72445976	0,00065872
CG3711	137,259118	1,7244045	0,00480516
X11Lbeta	293,771701	1,72328409	0,02046009
ftz-f1	269,982741	1,72292498	9,36E-06
RpL39	313,049992	1,7229129	0,00218407
CG34134	66,0284602	1,72163367	0,01402919
CG17684	372,513884	1,71746196	0,01028203
Rhc-73	740,846965	1,71669696	7,41E-06
lbk	198,408187	1,71644976	4,26E-05
I(3)87Df	36,5594815	1,71565329	0,0419763
Rbcn-3A	818,880918	1,7147249	6,24E-07
BIm	38,8525201	1,71405008	0,04002505

Pex11	69,7160086	1,714045	0,01647242
Obp83ef	37,9204786	1,71242664	0,04731826
CG12375	79,3682006	1,71134168	0,00059884
Scgalpha	59,9629151	1,71082516	0,02844881
Cyp49a1	78,0074592	1,71059082	0,0151515
CG9775	159,776117	1,70968519	0,00035272
gry	122,991182	1,70951167	0,00545936
dsx	163,56659	1,70820821	0,00351381
Kaz1-ORFB	113,392482	1,70703796	0,02321484
Ac13E	152,082562	1,70675276	0,01803535
CG6812	105,58295	1,70603653	0,00020723
CG44242	56,3924101	1,70513728	0,03783188
RpS25	2362,19535	1,70395599	0,00050187
CG10077	2267,64659	1,70349967	0,00074319
Smr	582,432442	1,70303173	1,67E-05
eys	285,744377	1,70206656	0,03022993
sr	80,7687686	1,70184211	0,03502916
CG42337	95,9546701	1,7017377	0,02209943
RpL30	1125,9213	1,70082941	0,00646215
wech	276,227233	1,69810709	0,00042996
	715,640998	1,69700065	1,68E-05
Gprk2	272,758697	1,69538134	0,00302292
CG8586	552,861994	1,69535793	0,00427784
Sxl	1522,20454	1,69379021	5,87E-05
PlexA	1786,89582	1,69232346	4,61E-06
EMCI	310,623473	1,69214083	0,00584928
Roc1a	238,315055	1,69201225	4,54E-05
ND-ASH1	178,200291	1,69120955	6,80E-05
ATPyngamma	932,675648	1,69018288	1,73E-05
vig	281,563531	1,68894181	0,00200903
wcy	162,581552	1,68844997	0,00050109
NH	587,53793	1,68815091	0,00088533
fs(1)h	833,715651	1,68745945	8,90E-09
CG2186	112,981065	1,68582496	0,00107717
CG11050	175,523414	1,68573129	0,04740201
Nc73EF	1963,54785	1,685366	7,47E-05
DAAM	129,844453	1,68511956	0,01336618
ND-B17.2	167,899807	1,68479491	0,00025887
RpL9	2719,32327	1,68294544	0,00045935
CG6145	338,209021	1,68175814	0,04502545
qvr	1116,12173	1,68066395	0,00190577
CG14438	393,065203	1,6791549	0,00183854
nonA	585,152903	1,67792467	6,57E-05
RpL18A	3901,09624	1,67643766	0,00074088
MFS17	574,446576	1,67616898	2,47E-05
CG5850	109,974969	1,67430834	0,00651871
ago	159,119318	1,67372352	0,00361419
ttv	317,874158	1,67368483	0,00102777
slgA	702,120913	1,6732657	0,04760121
	4445,42617	1,67314431	0,00194881
Pde9	469,074231	1,66997506	0,03112929
CG7646	339,817493	1,66902926	0,01268368
ltp-r3A	578,581043	1,66784834	6,97E-05
Hers	416,856975	1,66753399	0,00039286
ssp3	134,529666	1,66578792	0,00579144
Liprin-alpha	219,046256	1,66531836	0,00044922
Cfz2	288,1482	1,66384491	6,55E-05
CG43736	306,758924	1,66226771	0,01547574
CG8184	908,688863	1,66106934	1,79E-12
RpL5	7844,65768	1,65835438	5,78E-05
unc79	867,27625	1,65708402	0,00908701
CG17839	612,399049	1,65698084	0,00097107
Cyp6d5	4148,32758	1,65688829	0,02750781
vvl	426,842021	1,65666384	0,01665092
Cul4	116,0649	1,65540224	0,03309618
Gpo-1	381,345054	1,65526833	0,00077667
CG14669	125,064625	1,6540672	0,01598688
clo	47,2786276	1,6523086	0,03391425
sns	132,913499	1,6493785	0,00308669
dtn	609,980105	1,64850913	0,00161076
CG42342	285,762683	1,64720888	0,0044114
trc	79,5654496	1,64618355	0,01117908
CG32264	1095,10408	1,6434927	0,00129895
Atx2	238,65852	1,64317075	2,21E-05
FoxP	254,068068	1,64219986	0,01679443
AGO1	1449,28436	1,64096414	1,17E-05
Appl	1729,98018	1,63982614	0,02011445
bel	101,78126	1,63726967	0,01488711
CG9005	356,973816	1,637207	0,00107598
tweek	1149,33228	1,63653788	1,45E-05
RpS4	5831,32441	1,63506285	0,00056861
cert	145,276679	1,63499553	0,00351806
CG5789	265,940485	1,63486198	0,02266952
CG42541	332,182156	1,63410423	0,03440628
	2350,89508	1,63409194	0,00837319
nAChRalpha7	737,183652	1,63403605	0,0186493
Sptr	71,5019365	1,63344393	0,04224714
Atg1	285,674077	1,63033341	0,01933932
Trf4-1	204,692401	1,62961675	0,00948887
CG7530	413,278299	1,62811559	0,00860357
CG3262	319,833283	1,62684735	4,33E-08
Tango1	264,643195	1,62612101	0,00486252
COQ7	111,130125	1,62496044	0,0281575
Stk	165,679418	1,62462537	0,04452412
RpS20	1830,15845	1,62271952	0,00562513
Pfrx	520,462756	1,6225058	0,02446779
dpr15	68,3480353	1,62143399	0,04365219
nAChRbeta2	160,157695	1,62035952	0,04095596
dlidm	228,773512	1,61862274	0,00011465
gus	432,537168	1,61707602	0,00412219
stj	440,778142	1,61703478	0,01534646
CG12338	225,948015	1,	

ND-15	158.23969	1.6051503	0.00128993
eIF3i	566.655973	1.60496959	0.00026705
ctrip	862.816332	1.6040981	2.64E-05
Cka	303.961808	1.60243911	3.78E-06
RpL7	5167.72753	1.60118373	0.00035903
ND-13B	106.665591	1.59986445	0.00254034
Frq1	518.321021	1.59920036	0.00898467
CG13907	335.109807	1.59732006	0.0003316
heph	1234.09107	1.59661323	0.02131043
mub	1613.46318	1.59633785	0.01527713
RhoGEF3	444.13508	1.59596193	0.02569461
CG34394	474.681584	1.59554247	0.00014457
jp	231.725141	1.59542765	0.01351961
CG2747	585.623818	1.59285285	0.00263678
mRpL47	53.3819528	1.59222124	0.02080826
CG4847	271.122565	1.59159196	0.03375843
Ptr	135.65057	1.59006892	0.03431779
mamo	1560.36379	1.58911346	0.00050629
RpS15Ab	98.2011722	1.58868089	0.02068878
Ulp1	260.827613	1.58865833	2.10E-05
Hmt-1	225.328695	1.58820897	0.0184546
CG10326	150.797531	1.58808127	0.02013591
ssh	91.7344287	1.58784979	0.04572708
BEAF-32	81.6269852	1.587831	0.04655461
CG7339	65.6315101	1.58767449	0.01630711
tl	339.757819	1.58646047	0.00889595
CG31793	190.13281	1.58585284	0.03258286
RpS13	2747.46461	1.58552964	0.0015328
Max	81.4343392	1.58513416	0.0451188
nChRalpha6	743.73862	1.58466256	0.04407665
CG4752	188.837285	1.58334737	0.00921101
CG11537	298.413112	1.58245957	0.01915707
brm	254.361927	1.58159511	0.00487625
CaMKII	2046.57225	1.58001481	0.0034494
Nlg2	239.324124	1.57988851	0.04374058
tth	74.93479	1.57861114	0.02265166
Reph	293.76784	1.57430789	0.01534646
fra	147.423402	1.57352795	0.01255135
lute	198.360077	1.57161951	0.02631039
dysc	735.120695	1.57005444	0.01382092
CG11360	773.442007	1.56693387	0.00087175
wts	160.934964	1.56033142	0.004117
cac	1470.16487	1.56011896	0.03209102
puf	500.720424	1.55936888	0.00211264
Moca-cyp	99.434969	1.55872265	0.02954268
Ranbp16	245.704995	1.55781572	0.00247283
simj	269.506426	1.55533111	0.00068368
lap	641.316903	1.55450875	0.00430301
CG5861	85.7529267	1.55372455	0.01186574
Torsin	112.925218	1.55303509	0.03527408
SoxN	119.610798	1.55003235	0.02252896
Syt7	563.80639	1.5498083	0.0295121
CG14441	269.720434	1.54939645	0.00156502
cpx	3708.6002	1.54877076	0.01087075
Sur-8	276.052496	1.54836625	0.0126264
CG8034	197.961218	1.54772709	0.00682882
SpOck	730.958909	1.54769091	0.00166015
Yav	170.993176	1.54747352	0.0044114
RpS3	3597.95491	1.54694955	0.00306769
CaMKI	1788.39542	1.54376076	0.00250601
CG16756	179.039105	1.54280728	0.02589917
chb	366.390656	1.54189904	0.00079471
Ubi-p5E	329.056317	1.53946717	0.0010148
capt	144.522212	1.53840111	0.00331969
CG3961	401.957942	1.53732084	0.02683361
muc	270.901386	1.53633298	0.00317619
LpR1	536.715093	1.53536991	0.04647585
uex	650.834998	1.53474585	8.65E-06
Ufc1	57.2244352	1.53361331	0.04551297
PI4KIIIalpha	435.808703	1.53214862	0.0027131
l3)neo38	396.671228	1.53065459	0.04359187
eIF4G2	486.600969	1.53000878	0.00024806
Est-Q	168.603165	1.5296216	0.02086842
RpL40	2378.71564	1.52747772	0.01429873
mlt	519.719686	1.52724778	0.00019321
riCTOR	193.904258	1.52115754	0.00383809
LRP1	1629.49921	1.52114751	0.00010007
CG1718	344.224466	1.51958231	0.01382315
Nipped-A	768.084329	1.51950394	9.01E-07
CG31145	356.304537	1.51908655	0.00136692
lh	918.432145	1.51143466	0.03725348
Ptpmeg2	589.47356	1.51078616	4.31E-05
CG32767	591.261036	1.50985118	0.0006305
hang	282.171233	1.50885701	0.0012616
CG1909	346.738656	1.50786802	0.04997343
Plc21C	885.332947	1.50781294	0.00650994
CG14200	238.090544	1.50730473	0.01556203
toc	580.583398	1.50692322	0.015538
RpS27	1734.67564	1.50517677	0.01313041
stx	284.824226	1.50406761	0.00015895
RpS15	2666.05891	1.50382593	0.01118327
CG1910	113.760915	1.50230226	0.03903263
CG14805	76.8320511	1.49902782	0.02801207
CG9934	183.177719	1.49900276	0.00997867
mbl	1351.66533	1.49712664	0.04235475
Usp32	355.087238	1.49696877	0.00956221
Evis	421.552083	1.49456105	0.00997377
Pmp70	386.06097	1.49381231	0.03880466
Fur2	364.222368	1.49354925	0.00206706
Syt1	2612.49966	1.49341488	0.04785946
Vps11	111.642388	1.49265874	0.03583341
COX5B	333.259396	1.4924156	0.03564339
alpha-Man-Ia	423.358254	1.49130833	0.01599311
CG12084	151.9287	1.49118327	0.01366841
Snap25	1087.59383	1.48743661	0.04972656
CG32278	68.7493717	1.48614865	0.0463053
CG14073	334.850587	1.48411422	0.01433748
mask	1104.32309	1.48222831	0.00123074
ND-51	678.133595	1.48187438	0.00450108
frj	249.782429	1.48044244	0.00700184
Su(var)3-7	100.85067	1.48002949	0.01935097

RpS6	4641.06598	1.47994172	0.00365227
Plp	584.751578	1.47660007	0.00111281
fog	310.034793	1.47574891	0.00548741
Eip75B	683.061512	1.47521254	0.00096698
msi	668.825865	1.47412094	0.00327229
fln	392.368963	1.47338407	0.00024458
shep	2470.76326	1.4705787	0.00948887
CG1463	72.2495879	1.4700755	0.03726341
e(r)	129.51592	1.46992166	0.02411156
nej	635.096687	1.46955274	0.00048331
dlg1	661.052949	1.46802358	0.00052828
Zir	343.404752	1.46702462	0.00775528
Hsromega	21158.7345	1.46588479	0.03721522
Eip63E	398.331556	1.46254183	0.02738903
Eps-15	245.792448	1.46143087	0.01935097
Hipk	1360.74582	1.4610287	0.01186574
Atg17	534.884265	1.45910402	0.00227078
Pka-C1	877.515799	1.45910096	0.00828726
shi	1129.6698	1.4575928	0.04022829
Tao	366.005483	1.45538578	0.00824233
SekII	141.624169	1.45508867	0.02098838
HDAC4	293.351225	1.45451287	0.02953027
CG9425	489.453134	1.45426742	0.03525208
beta-Spec	1130.30582	1.45425627	2.48E-05
CG9776	208.259229	1.45307034	0.01378963
cpo	755.210986	1.45295928	0.03507973
RpS3A	5244.50258	1.45224402	0.0322772
Psi	135.707903	1.45222071	0.01239239
RhoGAP19D	414.044539	1.45213274	0.00454971
psq	536.135887	1.45038479	6.98E-06
gek	170.367156	1.44917817	0.01665315
Sik3	266.788036	1.44698223	0.0417398
cdi	361.927064	1.44673722	0.02749804
CG7149	126.359319	1.44647239	0.03720076
bchs	509.146185	1.4461379	0.03380709
RpL29	646.042568	1.4460838	0.04841235
Tomosyn	695.077518	1.44489565	0.02894287
kis	2670.66609	1.44468628	1.25E-07
Cul1	354.232284	1.44266972	0.00027916
Sema1a	835.021014	1.43946968	0.0226006
RpL23	1512.19801	1.43866489	0.04760121
Gp210	184.319724	1.43807819	0.00368322
JIL-1	212.845736	1.4367305	0.01227342
E(Pc)	433.564622	1.43527437	0.00028929
Trf2	634.9148	1.43357982	0.00039269
Pp2C1	269.174136	1.43318884	0.00682882
skd	670.646058	1.42806821	0.0034494
Dhc64C	1424.32033	1.4245637	8.89E-05
Spp43Ab	1273.22906	1.42183037	0.03581803
frv	514.889932	1.42066122	0.00242384
Mnn1	411.07785	1.41961236	0.04052219
Mbs	414.623896	1.41889212	0.02061072
Csk	788.666919	1.41651099	0.03310931
ND-13A	119.024769	1.41479691	0.04388914
CG15012	242.661315	1.41352159	0.01855413
Ptp4E	298.048293	1.41045262	0.00328402
rno	399.092822	1.40880478	0.00116153
Rich	132.248239	1.40853878	0.00871855
PI3K21B	208.840025	1.40670605	0.01963359
Rim2	168.916135	1.40518111	0.02952882
alpha-Spec	1354.58128	1.40426195	0.00055314
Prosap	466.977016	1.40033435	0.00057577
Jarid2	374.154166	1.39983281	0.00801033
Maf1	545.215872	1.39895483	0.00932395
Atg2	304.959246	1.39645755	0.00706141
CG12054	591.052155	1.39639372	0.03786025
chif	274.050438	1.39490814	0.01749852
msn	320.832324	1.39176829	0.0203993
spb	332.796372	1.39169797	0.0387855
mng	281.663909	1.39068253	0.01440847
Ptp10D	391.984651	1.38857641	0.04379809
Ecr	471.838511	1.38323045	0.03501663
minv	785.667819	1.38258276	7.56E-05
Sin3A	345.99972	1.38077193	0.04271517
nsl1	387.408423	1.37710748	0.01397155
Pdk1	810.338358	1.37290065	0.01053474
CG11486	557.653769	1.37136992	0.02648556
rdgA	914.29067	1.36995922	0.03766022
Dys	1365.44978	1.36842564	0.00075936
Cam	4103.78363	1.36810184	0.01769455
Pde8	312.770762	1.36789772	0.0211097
Tim17b	354.71587	1.36776079	0.02249756
Dsp1	501.342379	1.3650411	0.04330466
G9a	256.601317	1.36306484	0.01209969
Not1	2362.74283	1.36257776	0.00139636
B4	732.65321	1.36192875	0.01915707
CG4300	134.341687	1.35947715	0.0280826
shg	298.293443	1.35926038	0.0498472
CG6966	375.486948	1.35455401	0.03066935
gw	1166.17661	1.34982023	0.00997377
eph	663.031064	1.34656853	0.02940407
rdgB	487.330613	1.34545752	0.02512681
Dlg5	306.503933	1.34317727	0.01529249
Mef2	471.837256	1.34017402	0.02750488
Axud1	179.301515	1.33876006	0.022533
Eaat1	1487.12503	1.33694743	0.0112238
svd	262.67123	1.33542449	0.0339859
sdk	421.414684	1.33358072	0.00804783
CG17698	481.812462	1.32907607	0.00700528
CG10289	534.003784	1.32419866	0.00867694
bin3	185.417017	1.31868859	0.0387116
Hcf	620.259116	1.31027103	0.01156301
emb			

Glut4EF	2039.48725	1.2636393	0.02299733
l(1)G0196	1159.24888	1.24703091	0.02037489
Ufd4	1214.47475	1.24220856	0.01975307
Pur-alpha	881.731317	1.23624648	0.01888939
Gyf	673.038113	1.21655538	0.02968042
ps	3509.56061	1.18329981	0.02616092
Su(z)2	249.31619	1.25593205	0.0447665
CG42724	287.386162	1.28423225	0.04157874
cathD	1708.89506	1.29000992	0.0316621
CklIbeta	427.524734	1.29514525	0.03066671
bves	260.299691	1.29971298	0.03695892
XNP	201.480633	1.30553053	0.0477262
Men-b	393.21783	1.31847658	0.03176339
Lk6	4444.94904	1.32021489	0.04574369
CG2991	246.003721	1.32429869	0.0309429
Pink1	398.270613	1.32777961	0.0336841
CG6439	236.458003	1.33452618	0.01627829
Mob4	156.986989	1.33453268	0.04109115
Unc-76	566.829439	1.34162561	0.00140212
mRps5	121.717352	1.34476935	0.03927126
CAP	612.407047	1.3451152	0.0047747
sima	1158.73566	1.34797748	0.03501663
mts	643.174805	1.34835572	0.03306794
CG45049	269.505465	1.35174051	0.0248806
Khc	212.121476	1.3544591	0.03144154
godzilla	418.136437	1.35594833	0.01064639
l(2)k09913	443.902475	1.35820499	0.01571181
Dhpr	117.388119	1.36355144	0.04974376
CG3061	313.283758	1.3639498	0.03651451
Ate1	147.783407	1.36723923	0.01585377
tna	387.509385	1.36727584	0.03596639
Dyb	284.921081	1.36877278	0.04456023
eRF2	8898.97154	1.36919801	0.02501932
NTase	346.999973	1.36979312	0.0151515
Arf79F	598.283693	1.37156304	0.03825271
Wnk	565.262326	1.37220114	0.00178174
CG9821	3852.37024	1.37380196	0.00069571
Usp47	364.889167	1.37633285	0.0387116
Kap-alpha1	195.684431	1.37739519	0.04779902
Atg8a	1474.79255	1.37799692	0.02713401
mop	454.570817	1.38984874	0.03706429
CG7083	213.032182	1.3946475	0.03842734
CG7430	345.758487	1.39706377	0.01969096
Hlc	328.5313	1.39956875	0.02894227
ll(2)d	188.358913	1.40183437	0.03436812
rhea	1590.34646	1.4046514	0.00014991
pix	749.998818	1.4087979	0.00698849
CalpA	285.214177	1.40924295	0.04587203
CG3164	140.85015	1.40978608	0.03766441
jar	574.220786	1.41225307	0.02549459
CG6364	119.872324	1.41311841	0.02154172
Synd	288.957495	1.41537729	0.02411156
CG12576	255.215441	1.41597487	0.03706429
Fbl6	155.506888	1.41725605	0.00729798
casp	138.592322	1.41833014	0.04891533
fws	110.107872	1.42048563	0.02467754
CG9636	142.071399	1.42832708	0.03850973
CG5734	124.303272	1.4290637	0.04894344
Rheb	193.722415	1.42957828	0.04543316
sau	252.771696	1.42979661	0.02038142
Srp54k	160.116507	1.43017301	0.03451616
Fim	548.670368	1.4322727	0.01784431
Hsl	163.946444	1.4342097	0.0245816
CG13124	1019.18381	1.43618013	0.01305683
raw	526.816006	1.43661566	0.04379809
CG32473	174.108385	1.43752403	0.03758381
GluProRS	210.663423	1.43974615	0.02084958
CG6707	363.577445	1.43987735	0.00020603
CG11791	304.145088	1.44235534	0.03216616
lost	1192.29229	1.44327299	0.00263678
Cyt-c1	405.424762	1.44377772	0.00588702
CG12012	157.309558	1.44463405	0.04566706
Ptip	147.347853	1.44697417	0.01658932
AGO2	928.524177	1.44835208	0.00103818
Ect4	1556.74002	1.45205059	0.0004306
Tailor	100.375547	1.45516302	0.02934593
CCT8	223.06105	1.45566234	0.02825062
CG12099	339.483051	1.45920593	0.00200835
lig3	91.4593115	1.46192403	0.02750781
Marf	509.729065	1.46253087	0.00644558
Not3	342.479344	1.46423368	0.00050988
Exo84	81.8732415	1.46423529	0.02178698
Surf4	316.689846	1.46568111	0.02007843
Dip-C	81.3315467	1.46659677	0.02542011
Pdkk	192.246953	1.47022055	0.04909934
cbt	340.056414	1.47051352	0.02384616
Fer1HCH	3685.07884	1.47108245	0.04023568
Got1	758.89733	1.47113962	0.03872221
Rtnl1	1286.75437	1.47275457	2.08E-05
eIF3l	578.702505	1.47282423	0.01368199
Pdk	1157.83763	1.47395718	0.0404379
ex	267.470978	1.47632961	0.01745899
Gdi	634.968381	1.48139056	0.00013199
Edc3	257.929435	1.48184269	0.02333591
Myb	156.968325	1.48296878	0.00881616
CG7414	531.82044	1.48519335	0.00605874
CG30015	730.549572	1.48563352	0.00529334
CG30069	942.471343	1.48615238	0.03202941
CG31445	301.871489	1.48658673	0.03799345
slim	330.565068	1.48678958	0.00689899
parvin	140.106856	1.48745716	0.01587054
CG33080	138.909746	1.48756544	0.02271673
CG18067	2757.17061	1.4886701	0.00122952
Phm	538.001891	1.48993465	0.00226866
Rox8	230.15019	1.49263889	0.00689899
Dis3l2	131.745314	1.49318484	0.01551333
CG10311	179.331261	1.49404557	0.01179329
CG7332	183.916763	1.49440448	0.00709109
CG4502	130.191218	1.49545729	0.01911513
Tfb1	87.6272501	1.49629488	0.04365217
Ptp61F	180.450705	1.49643012	0.00101924

MBD-R2	149.242503	1.49941438	0.0061248
CG31705	1431.18229	1.50035611	0.0019066
CG4658	141.231903	1.50130492	0.02512681
Rab8	272.581182	1.50221658	0.00208781
egl	275.888867	1.50248851	0.00997377
CG11412	98.5707867	1.50536338	0.02029176
P13K92E	225.181831	1.50874831	0.01467523
l(1)G0156	315.853141	1.50970807	0.02598628
CG12004	277.118242	1.5103298	0.00113187
CG8032	108.054242	1.51046188	0.02411156
Calr	1227.57815	1.51186509	0.01234773
bv	299.24506	1.51280581	0.00997377
CG5080	335.180208	1.51343677	0.02954268
Sherpa	378.984741	1.51465959	0.00266175
CG2182	260.379923	1.51467454	0.01389868
GCs2alpha	934.514472	1.51486922	1.49E-05
Ankle2	205.120786	1.51500692	0.02760675
YME1L	102.676628	1.52000727	0.03032465
CG5028	385.550725	1.5207297	0.01543321
CG1951	99.1277857	1.52514829	0.03425557
dbr	139.13513	1.52529346	0.00181157
CG5390	518.831059	1.52605029	0.00032241
KdelR	360.556542	1.527225	0.03850973
CG7461	396.725857	1.52757616	0.03549875
CG14712	83.226975	1.52805441	0.01897944
RhoGAP15B	204.585044	1.52993405	0.04957987
alphaTub84B	1477.32528	1.53099322	0.01105303
	47.1585473	1.5311139	0.03430773
Dhx15	135.83286	1.53162583	0.00930622
NufFhit	76.2171567	1.53187109	0.04568419
CG5830	427.723266	1.53229468	0.02478269
CycG	2362.9744	1.53395065	2.10E-05
SP1173	283.071861	1.53444551	0.01795776
MDI19	60.756616	1.53460207	0.02037489
ced-6	814.217381	1.53466889	0.00430925
stumps	421.494373	1.54372804	0.04230365
par-6	226.554826	1.54421495	0.00562836
Nop17l	299.43408	1.54633938	0.03500306
SCAR	171.208188	1.54740331	0.01207148
SREBP	947.631111	1.54877253	0.00170255
dl	304.753959	1.54894735	0.00471042
GlcT-1	77.677912	1.54900096	0.0382108
CG31650	84.1825587	1.55021003	0.04088649
vimar	84.9339923	1.55190624	0.0387116
Spu77Ba	276.681611	1.55240758	0.03130383
Pis	313.094855	1.55428577	0.0082898
Desat1	7729.97572	1.55646577	0.01817111
mim	451.260527	1.55730063	0.00439042
Rcd1	195.061697	1.55807683	0.00107717
CG5004	177.785309	1.55834786	0.01983684
nuf	584.422354	1.55903853	1.35E-05
BOD1	90.8064935	1.56179094	0.02104725
GlyRS	133.638568	1.56215353	0.01627677
CG10863	365.7972	1.56259489	0.00028984
CG14650	118.007291	1.56297161	0.04046636
drongo	430.949563	1.56324669	0.01006597
Rpa-70	173.083244	1.56373917	0.014677
CtsB1	1046.89991	1.56389741	0.00042497
isoQC	60.1161789	1.56468883	0.02147118
Mocs1	57.2782325	1.5671763	0.03902272
MFS16	145.677302	1.56746154	0.04182047
Dok	88.5162835	1.56861981	0.00954168
Mgat1	48.9123302	1.57316551	0.03298887
CG15661	359.740225	1.57411294	0.00384611
Hexo1	92.7496303	1.57975586	0.03066671
FAM21	70.8946516	1.58013146	0.03105413
CG8188	187.019856	1.58071181	0.00213831
CG8531	98.296712	1.58237598	0.01365557
ArtGAP3	172.22327	1.58298021	0.02825062
Hsc70C	489.408878	1.58327262	0.01779249
CG31689	956.727937	1.58413295	0.01026731
chico	177.168197	1.58455661	0.00046633
CG6903	163.988098	1.58530545	0.00120977
CG5903	173.58419	1.58637739	0.00275971
CG9784	116.654962	1.58702851	0.0227356
prel	201.200102	1.58706833	0.00040284
Nif-2	160.357412	1.59149102	0.0005066
CG8578	108.432409	1.59489489	0.0245816
GEFmeso	171.085356	1.59648968	0.01934393
CG17549	716.931586	1.59650261	0.04615959
CG8300	90.2978364	1.59810977	0.04908386
koi	201.21623	1.5982314	0.003659
OstDelta	239.720962	1.59988186	0.0346662
Pura	462.863507	1.60089975	0.01110548
Rho1	1013.82225	1.60092941	0.00121414
CG1927	268.943381	1.60219084	0.00313132
CG3907	257.256606	1.60220862	0.00814604
Eb1	408.008272	1.60382793	0.02586708
modf(mdg4)	264.434176	1.60475041	0.00187254
Cand1	190.984381	1.60792912	0.03828654
piic	331.914939	1.61137475	0.04931118
beta-Man	306.616833	1.61195635	0.00411296
wfs1	64.0547363	1.61496867	0.03770806
CG9917	390.072489	1.61537917	0.00400763
cora	1246.47439	1.6192051	0.00076658
CSN7	46.4812632	1.62119683	0.02077283
scf	260.425217	1.62144877	0.03066671
Egm	56.9389408	1.62296532	0.03255962
PheRS-m	77.4468047	1.62300491	0.0066058
CG3662	1856.22262	1.62499173	2.03E-09
Rab39	125.863655	1.625565	0.00605874



CG9947	204.270263	1.63786471	0.00427418
CG15118	150.150303	1.63834859	0.02026705
Srp68	107.998492	1.64027637	0.03074882
MetR8	99.589741	1.64174675	0.00168019
CG8397	156.163915	1.64320413	0.00374553
Dref	97.7628058	1.64530556	0.03505636
sqh	486.122742	1.64594435	0.00094637
Klc	298.387839	1.64955358	1.32E-06
GstD1	1760.60216	1.65080058	0.00322301
CG8547	568.720015	1.65132813	0.01212451
kay	689.051766	1.65226684	0.00107056
Mapmodulin	225.545604	1.65331664	0.01427761
CG6923	129.714554	1.65343197	0.00451956
CG3793	48.5573361	1.65352619	0.04740201
Droj2	688.290127	1.65594377	3.74E-07
Oscillin	72.1193673	1.6560497	0.03725866
CG16721	178.470863	1.6570343	0.00657184
CG6565	55.4368539	1.65735851	0.02948378
Clc	250.338178	1.65946934	0.00322134
CG11137	60.2184264	1.65993216	0.01389868
CG3529	95.0560637	1.66131034	0.04316832
Gbp2	711.045138	1.66220496	0.00387515
pont	39.2792988	1.66321109	0.04010416
CHKov1	179.235558	1.66732313	0.00161422
cpb	121.313627	1.66768171	0.01711611
CG7656	65.5205138	1.66787693	0.01076085
GstO2	122.639453	1.66840651	0.01122156
spi	288.401078	1.66932944	0.00070879
glec	312.156242	1.66947359	8.90E-06
Phkgamma	423.583702	1.66980517	0.01397155
Snx3	247.53645	1.67006874	0.00070879
CG31694	312.874612	1.67180525	0.00053435
Dkpepsilon	81.1064114	1.67183878	0.02485089
Irbp18	44.7237271	1.67208613	0.02929443
CG2162	141.18135	1.67462707	0.01152885
NimB2	618.929618	1.67528384	0.02569461
CG8765	82.9610193	1.67611798	0.01734243
Cyp28a5	1118.86483	1.67725507	0.01367861
CG32195	45.9711577	1.67750397	0.04032459
CG3792	73.5374132	1.67801174	0.00469603
CTPsyn	97.3787603	1.67902237	0.01499514
mfrn	129.177642	1.67975985	0.00213949
CG8818	94.5550435	1.68236252	0.015291
CG6171	31.1010511	1.68406677	0.03519321
ZnT86D	72.7579866	1.68479233	0.01429561
CG13671	57.1080923	1.68940213	0.02042191
CG11247	157.949286	1.69030396	0.00379226
eIF2Bbeta	74.3307391	1.69039295	0.03805328
CG8412	87.1572783	1.69409182	0.03251595
Svx13	113.71353	1.69513892	0.02197946
Sra-1	250.737289	1.69643042	0.02080826
Pgk	360.367549	1.69670556	0.02150761
dar1	146.002539	1.69682512	0.0077267
lwr	99.1139459	1.69716826	0.01693569
CG6766	292.599023	1.6974466	9.64E-05
alphaTub84D	96.3517391	1.69800529	0.00231528
ens	702.518922	1.69831378	5.23E-07
iPLA2-VIA	270.223874	1.69833736	0.00131427
MED1	115.792683	1.69955942	0.0024276
CG13116	329.537434	1.70112553	0.01805083
Rpt4	243.284459	1.70170782	0.04888503
Sox14	173.886627	1.70217979	0.00014772
dmpd	94.952471	1.70258374	0.00077201
CG3376	383.176224	1.70422585	0.01123111
EloB	138.168203	1.70674058	0.02227608
I(I)G0320	235.349314	1.70921384	0.00316927
CG15629	336.941853	1.71019466	0.04407665
lhm	68.1655065	1.71080257	0.02873965
Vha26	1460.24058	1.71080385	0.03275169
CG15117	112.763024	1.7118247	0.04118762
Hsp60A	246.439588	1.71313331	0.00297005
RtcB	34.9340951	1.71386523	0.04953226
GM130	103.444025	1.71390684	0.00093274
UbeE2M	57.8000896	1.71544548	0.03027157
CG7453	83.8388675	1.71779981	0.00117656
Sh3beta	297.087987	1.71790688	0.00119036
CG5098	154.634663	1.71805918	0.00038471
ALIX	391.993271	1.71834708	6.91E-05
CG7600	117.740339	1.71942402	0.02333591
CG32066	155.072885	1.71953361	0.01611072
GallNac-T1	91.0278175	1.72077612	0.04896276
Vamp7	240.713454	1.72115101	0.01939392
Rag-C-D	102.272749	1.72158402	0.04400937
CG17834	97.6272876	1.72308084	0.0162888
Atg18b	177.330423	1.72339836	0.03066935
CalpB	151.289343	1.72458603	0.00420426
CCT1	146.287103	1.72523522	0.01186574
Patj	66.9354705	1.72537397	0.01053514
Ku80	36.9888755	1.72705112	0.0339757
CG44085	179.501175	1.72786403	0.00101492
bdg	110.926608	1.73196392	0.00042996
CG9338	169.318707	1.73333567	0.00932395
CG1572	542.944459	1.73351478	0.00842878
Ahp1	80.653299	1.73630858	0.00342602
cact	528.924698	1.73903917	1.67E-06
CG7115	151.47037	1.73938864	0.04010313
CG3558	201.809469	1.74177404	0.01155985
Ist2)ltoPP43	56.9029712	1.74184097	0.01482077
Rab14	201.396782	1.74295994	0.00316927
Rpn10	92.2507918	1.74455358	0.01028208
NAA20	57.9849755	1.74481028	0.00348495
CG1662	59.1893663	1.74487321	0.03577852
CG31038	167.366919	1.74692529	0.00178337
Lnk	70.4302183	1.74711323	0.01263384
alc	189.992285	1.74859239	0.00086787
VhaAC45	723.665836	1.74971797	0.01563358
rngo	78.2710339	1.75334187	0.00877748
nec	533.891708	1.7540863	0.00804684
CG32649	47.9108681	1.75637423	0.04662565
Rint1	60.8446842	1.75768263	0.01797314
Scsalpha	418.205097	1.75836947	0.00665423

TBC1D5	112.670784	1.7589973	0.03676996
Uba1	796.099233	1.75922703	6.96E-11
TyrRS	141.22906	1.75925385	0.01740175
drl	92.908865	1.75967911	0.01247922
CG3168	568.200216	1.75970414	0.00342602
Elp2	31.8868	1.76183512	0.01749852
NUCB1	606.796537	1.76189515	0.02013591
stac	250.5126	1.76232316	0.00341422
CG7943	58.2370236	1.76292315	0.01102791
Jupiter	497.861323	1.76429492	0.00271111
14-3-3epsilon	1893.45583	1.76544951	1.94E-07
NKAIN	585.156627	1.7657079	4.18E-11
Dif	324.708267	1.76582677	0.00250944
srp	201.646058	1.76849623	0.00861375
CG3860	192.222713	1.77060186	0.00538765
lic	87.8683218	1.77064869	0.00191646
msl-3	49.7389811	1.7712337	0.02880908
MED31	37.2365521	1.77126771	0.03911045
dpv	2487.71874	1.77152584	0.00731363
Exn	243.677486	1.7722932	0.00346083
CG9186	114.137576	1.77343073	0.00035903
Lap1	263.263908	1.77458162	0.00713242
Rh50	487.783877	1.77486069	0.0034494
sinu	79.1918351	1.77517139	0.0048532
ahf186-M	142.14908	1.77569507	0.02150761
CG6770	2471.80983	1.77914743	0.01268654
Dhp80	439.254144	1.78008021	6.47E-05
Pax	225.286943	1.78252885	0.00713242
Hop	197.678302	1.78284128	0.01498212
Pten	164.556908	1.78440913	0.0027131
CG9684	47.6479644	1.78585046	0.04440238
CG8399	227.257742	1.78946399	0.00119572
FeCh	175.425127	1.79028267	0.00943961
CG4848	109.41679	1.79119233	4.24E-05
Xbp1	1242.56773	1.79139034	0.00021894
Gli	149.626095	1.79457951	0.00013756
vsg	1300.30237	1.79507446	3.46E-05
CG6664	98.1194427	1.79604765	0.00176803
moody	287.929621	1.79606643	0.00078481
phol	109.525482	1.79623336	0.04157874
Ero1L	103.925200	1.79805747	0.01537631
Arp2	263.175392	1.79836816	6.80E-06
ash2	99.3026916	1.80029399	0.0226006
PGRP-LF	44.8355652	1.80063145	0.02378917
Vrn1	349.370139	1.80264038	0.00011359
Las	49.2996519	1.80362828	0.0051457
CG8630	313.46298	1.8038737	0.01069855
CG2017	95.6038871	1.80720611	0.01675816
CG5196	87.6914267	1.80757444	0.01839168
CG3011	325.479661	1.80858055	0.01927576
Mvb12	59.3343666	1.81090027	0.00621624
CG33978	160.089362	1.81102577	0.00805169
CG17593	143.482039	1.81217897	0.00024256
CG2889	32.3065964	1.81295783	0.01945108
Meltrin	310.811184	1.81298074	3.72E-06
CG14629	854.58207	1.81464794	0.00139636
Rab5	697.706358	1.81476136	9.89E-07
Cyp12c1	65.6424107	1.81485637	0.02104725
CG4282	30.3363449	1.81626323	0.0301843
CG14969	154.196602	1.81724915	0.000109
Vps29	30.9810149	1.82400489	0.0306917
	563.145518	1.82507439	0.00219054
Cyp12a4	288.398191	1.82552866	0.00966528
twr	96.3791575	1.82742178	0.00647348
Chchd3	120.158815	1.82775171	0.00031892
NK7.1	237.046673	1.82936673	0.00103716
CG1882	127.044863	1.82944874	0.00649121
Sec13	71.7018798	1.82973101	0.00187254
CG5541	185.371421	1.83064552	0.00995202
CG12236	69.5519238	1.8311773	0.00362361
CG31751	209.659567	1.83137396	0.00641088
QC	132.519888	1.8344601	0.03708281
CG1806	25.1085486	1.83638357	0.0451597
Nmd3	68.0898676	1.83788193	0.00026277
CG2211	33.9251845	1.83822117	0.02507734
betaTub56D	798.958347	1.84170486	2.03E-07
Tapdelta	141.992436	1.84209432	0.00161422
CG8735	98.3065846	1.84228903	0.01156301
mmy	237.763956	1.84266617	0.00523076
Ctp-bp	122.018861	1.84289848	0.01335338
Arc2	63.2149737	1.84379922	0.04786134
pck	96.9924637	1.84502736	0.00032241
CG17574	188.073313	1.84581028	0.00036874
Fas3	371.449368	1.8464928	0.00049693
CG17746	86.9023487	1.84884187	0.00486286
Fgop2	36.7930077	1.84957704	0.03402552
qkr58E-1	80.5206644	1.84977695	0.00055314
CG2218	77.9220715	1.85060941	0.02736187
CG3847	64.5265071	1.85283276	0.00085511
Galphai	181.320092	1.85164716	0.00016682
Vps36	30.707461	1.85728355	0.0245816
CG5823	49.1663053	1.85907296	0.04148547
CG11426	125.026346	1.85931614	0.00089988
Best1	245.459873	1.8594039	6.30E-06
Hrb98DE	451.887582	1.86034585	2.63E-08
GstE7	60.8160016	1.86115846	0.02648556
subdued	209.474611	1.86190314	0.01181637
CG7054	50.0087984	1.86277493	0.04397335
TORIP	57.7782161	1.86363841	0.02776544
CG13698	199.366333	1.86484794	0.

Sce	22,8572503	1,88196663	0,02799725
CG5174	393,094952	1,88865305	0,00013444
CG14401	120,210304	1,89090166	0,00443354
CG30349	52,7119914	1,8929255	0,03766022
Snap24	39,5865318	1,89641166	0,00370899
CG3223	38,1611209	1,8964471	0,0256366
CG8064	35,7934311	1,89697421	0,04468375
Cyp6a23	282,900819	1,8969897	0,04961202
SH3PX1	98,6531766	1,89932899	0,03568178
Ns3	44,3633309	1,90020589	0,00559787
Jabba	461,833288	1,90062237	0,03610587
emc	411,247238	1,90184231	0,00284276
Hsc70-3	1890,95053	1,90201035	0,00098675
scramb2	138,173854	1,90229033	0,00152786
CG17260	33,1298254	1,90276601	0,01255135
chnp	298,650648	1,90380635	0,04330547
TNIB	66,2271226	1,90474395	0,00298294
CG5885	142,838985	1,90758052	0,0018229
CG4615	73,8586781	1,90961574	0,0021528
shv	113,896932	1,91093337	0,00302751
Pex13	73,6568348	1,91272335	0,00066883
Cog3	67,0511788	1,91651975	0,04870266
CG12071	133,150554	1,91704366	0,0081774
eIF3c	469,043631	1,91767197	7,15E-06
CG13850	45,4492484	1,91834784	0,04316832
CG3008	150,338074	1,91923015	3,07E-05
CG1311	267,700682	1,92058916	0,00149865
CG2200	26,4360747	1,92078874	0,04667476
CG5292	33,2625189	1,92234728	0,02229724
CG31301	52,027688	1,92544383	0,00864223
CG31849	31,0389569	1,92738091	0,04891533
sprt	97,8831245	1,92819466	0,00169366
CG15067	430,385591	1,9294786	0,03593206
vih	35,0736655	1,92951883	0,00910307
ref(2)P	1152,73842	1,92994613	0,0001333
RhoL	142,793987	1,93100302	0,01308924
I-2	82,2628568	1,93148203	0,00041998
RYBP	56,5986032	1,9350493	0,00590138
CLS	52,1537099	1,93539703	0,03430773
CG18507	122,026286	1,93580087	0,02323092
Ocrl	113,964134	1,93663103	0,00624587
deltaCOP	159,152256	1,93691997	0,00138649
Trxr-1	269,500309	1,93706872	7,95E-06
CG18858	23,4493902	1,94093861	0,01261335
nsidm	67,4511924	1,94100801	0,01850494
CG17271	179,032654	1,94135969	0,00427301
gnv	29,9959381	1,9426855	0,03786639
bmm	532,401621	1,94342855	0,0490506
azz	22,5396524	1,94507929	0,03792052
CG10338	55,4859216	1,94575811	0,00739561
Nmda1	933,418562	1,94584168	0,00154677
Rab7	679,194841	1,94585963	1,33E-05
Vha55	1394,42017	1,94721806	0,00298304
egr	130,314176	1,94909453	0,022597
GstT2	28,9787208	1,95072004	0,0067703
CG14526	423,745053	1,954944	0,0224299
CG30460	482,230932	1,95628233	8,84E-06
IP3K1	50,0340846	1,95901418	0,03996974
Tsfl	3405,67197	1,96869589	0,01988535
CG14613	36,3440999	1,96952329	0,04067578
inc	164,918959	1,96985742	5,31E-07
kuk	169,209251	1,97052416	0,00469659
CG42240	133,300603	1,97134864	0,01630956
CG31633	29,5841741	1,97176554	0,01983965
Pp1-87B	434,70793	1,97325719	1,19E-10
mys	709,166573	1,97541291	4,97E-05
RFesp	193,350191	1,97661271	0,00581341
CG33494	355,173009	1,9766999	0,00348495
CG11577	99,4616519	1,97679546	0,00112188
CG6495	61,5737678	1,97846863	0,00902114
CG7016	31,0226128	1,98303582	0,03144236
CG8312	190,756735	1,98311104	0,00210097
CG32280	104,106007	1,98363186	0,00429068
Elp3	37,3069727	1,98455486	0,00443354
SerRS	137,100984	1,99144001	0,0008391
Hr96	67,4591737	1,99156959	0,00010588
IP3K2	229,094776	1,99510113	0,03504015
I(3)04053	44,7946451	1,99652591	0,00192985
mRpl37	33,9444806	1,99687468	0,03248038
CG7997	184,152613	1,99780937	0,00604314
mRpl12	25,6854023	2,00247873	0,03996974
CC2	246,059465	2,00360383	0,00427748
su(f)	105,478893	2,00400196	0,01322011
Pal2	233,590349	2,00576704	0,02375165
cv-2	128,044604	2,00683557	0,01238642
CG7650	17,6023032	2,00719344	0,04235475
Vps35	198,241973	2,00822541	5,09E-07
CG10352	32,5477551	2,01075771	0,01779249
nudE	367,133571	2,01076299	2,18E-05
Spps	34,2601029	2,01079862	0,00968609
Vha16-1	4245,01427	2,01091552	0,00272069
CG6225	57,071867	2,01207881	0,04794181
Nmdmc	87,9299123	2,013112	0,04888503
Flo1	107,754924	2,01396866	3,02E-06
MRE16	1643,53828	2,01679482	6,48E-09
nll	47,0500623	2,01693136	0,0015113
unc-45	55,8959339	2,01750552	0,00149817
CG11307	28,0264541	2,01799385	0,04794592
Tollo	308,905085	2,01916411	0,01177975
Rcd2	79,281132	2,02092495	0,00355725
CG12024	68,0125719	2,02128439	0,00155885
CG3021	17,7567299	2,02150986	0,04837584
CG6357	831,606556	2,02192003	1,13E-08
CG1523	44,1669957	2,02448004	0,0133501
CG6543	161,791657	2,02568932	7,21E-06
Atg3	64,0212573	2,02757536	0,0229334
RhoGAP68F	240,10269	2,02819364	0,00074171
CG7523	100,916983	2,02988555	0,0006898
CG15743	23,7828231	2,03179678	0,04296857
chic	936,761607	2,03281154	8,21E-08
dgt1	59,8232143	2,03649527	0,01675816

MESR3	296,792318	2,03750888	0,00100023
ast	28,775263	2,03896298	0,03941707
CG12007	85,96322	2,04314808	0,00601574
CG16812	32,4256777	2,04317613	0,03599282
ZIFPC	26,181295	2,04412384	0,01785021
CG7130	25,3451584	2,04802112	0,02109696
Sp212	27,5899405	2,04838966	0,02894227
TNIEbeta	31,2232687	2,04927824	0,03485943
CG18659	157,157307	2,05008581	0,00025464
DnaI-1	948,907211	2,05196406	0,0001495
pio	155,680645	2,05236706	0,02015592
yuri	106,752592	2,05275801	0,0140211
Bmcp	92,5652246	2,05637385	0,00291804
CG31769	370,678959	2,05748618	0,00031642
CG7379	35,9683692	2,05764281	0,0368325
CG11444	78,9500166	2,05840505	0,00506726
qm	178,25562	2,05951227	1,64E-07
lrpb	48,9938099	2,06258234	0,00091614
Snx1	157,185181	2,06265308	0,00057425
drd	186,898595	2,06421018	0,01209969
CG5446	70,313761	2,06588044	0,00030575
CG12237	79,4127912	2,06725532	0,04330466
emp	871,805123	2,06792241	0,00276256
CG4080	108,699331	2,07024833	0,00183218
CG8963	184,555237	2,07043669	0,00487547
CG14995	133,320688	2,07490595	0,00052828
CaBP1	303,37368	2,07558726	0,0039137
Mtl	150,52021	2,07818924	3,78E-06
	139,609719	2,07869885	0,000109
kri	55,8134526	2,07909591	0,01435217
CG17660	96,7245536	2,08194337	0,00039108
PS8IPK	327,688198	2,0830752	0,00180762
llp6	295,166964	2,08343823	0,00294672
defl	38,2585611	2,08366673	0,00235008
qkr5E-3	153,879493	2,08386275	3,18E-05
p115	80,4721591	2,08452771	0,00019507
bigmax	45,6900023	2,08514298	0,00804783
Phb2	221,713252	2,08603211	0,01585377
tapas	368,724663	2,08729	0,0046973
CG31997	316,7171311	2,08739415	0,00922823
Arp3	189,076797	2,0889428	0,0011137
Sirup	181,705417	2,08912799	9,67E-05
CG5532	55,5315156	2,08959577	0,00518425
CG5484	89,6624572	2,09335761	0,00012698
CHMP2B	45,1291048	2,09490704	0,01533611
CG17565	41,4135161	2,09653819	0,00101492
Gs2	4439,39724	2,09690145	0,00154162
Ance-5	214,852914	2,09716817	0,01378963
Esvt2	394,590991	2,0985351	5,54E-09
rtet	42,1922873	2,09917741	0,00048331
Zif	51,3673514	2,09970976	0,00048331
CG10576	233,699925	2,10097756	9,67E-06
CG11089	377,66178	2,10099653	0,01740226
CG10527	42,700107	2,10608668	0,04479594
CG17726	20,6088246	2,1062295	0,034773
CG18870	56,2048893	2,11339557	0,00997377
Past1	353,720934	2,11389609	0,00156139
CG3270	49,0023982	2,11618718	0,00478829
Vps60	92,0804062	2,11658717	0,00041998
Dlip3	26,4330354	2,11777091	0,03706429
CG2909	37,6782111	2,1178264	0,00261027
ATP5vNF	114,195485	2,11789573	0,00279491
Cyp420	72,0780617	2,11800552	0,01482077
CG32170	129,483936	2,11998456	0,00682204
CG4557	58,2610988	2,12034064	0,03253157
CG9664	123,763957	2,12116031	0,01170614
Best2	126,837191	2,12129331	0,00932395
Gasp	92,5162482	2,12190895	0,0067459
GlnR5	115,592813	2,12471957	2,76E-06
CG1129	125,333703	2,12516179	0,00135097
Uvrsg	35,2122482	2,12599012	0,00193192
CG14907	51,4824436	2,12729135	0,03915602
bbg	195,185535	2,12798459	0,00107598
CG4404	143,323931	2,13811806	0,00038471
CG7872	48,761636	2,13827243	0,01467236
CG5445	145,725225	2,13843364	3,85E-08
IM3	198,266115	2,1410361	0,01533611
CG8839	338,747468	2,14141815	1,76E-06
AOX1	498,981176	2,14583781	0,00371351
CG5641	38,4770102	2,14762379	0,0022059
Ance	238,149748	2,1476813	0,00824297
grh	106,704078	2,14901551	0,00028085
CG15611	144,069479	2,15185812	0,0002229
AdenoK	228,2805	2,15355961	0,00700583
Scamp	215,481429	2,15636668	0,00025102
Alp4	71,4979834	2,16126906	0,00011346
CAH1	40,1332649	2,1614986	0,01547574
CG10324	18,2905828	2,16346349	0,0245816
Dat	299,589241	2,16413357	0,00243255
gbb	103,5601	2,16878342	8,66E-06
pnt	105,235781	2,16906796	0,03786025
kraken	67,6855422	2,16942702	0,00587763
Diap1	843,623214	2,17217416	5,31E-11
fok	453,03621	2,17262257	9,13E-05
NiPp1	27,5477786	2,17354358	0,03737076
CG4927	56,2177546	2,17709137	0,00605874
he	182,277185	2,18062797	1,10E-06
cib	956,716863	2,18140791	1,73E-05
CG5554	68,5251676	2,1814485	0,00157808
PpV	103,529016	2,18179525	0,00450108
CG13204	21,3038699		

grnd	37.2543558	2.19745074	0.03199887
MoE	918.546261	2.19818355	5.37E-07
Syz5	168.688339	2.19885643	4.10E-06
CG2145	547.980462	2.19968471	0.00125366
Cyp6d4	88.6290656	2.19995586	0.0207958
CG5704	42.3468693	2.20061561	0.00263678
Ptpa	36.7559915	2.20080634	0.0051269
Hn	1039.25166	2.20185348	1.21E-05
CG1468	415.11899	2.20253608	0.00284276
rho-4	105.001368	2.21811741	0.01257397
eEF1gamma	1060.91427	2.22074091	2.35E-07
sip3	204.137338	2.22121094	4.56E-06
Cyp6a9	284.011308	2.22170825	1.90E-05
CG4291	16.125322	2.22266208	0.02549478
MFS15	104.869361	2.226979	0.00639741
CG8303	45.2735876	2.22753865	0.01158027
ft	39.5874324	2.22919588	0.00922823
CSN3	59.7594459	2.23187002	0.03142083
lrk2	295.609948	2.23510991	0.01022255
Non2	52.8977814	2.23743418	0.00858591
NF-YC	34.7358429	2.23870022	0.00173887
CG11073	126.945704	2.24725902	0.00211888
Herp	202.502485	2.24974323	2.47E-07
CG7903	21.9471436	2.25110564	0.01484654
Tsp42Eg	105.754888	2.25156129	0.03234243
Tab2	156.639002	2.25614017	0.0006778
CG17754	53.4319675	2.25629349	0.00718439
l1lG0289	178.8686	2.25911871	2.48E-08
CG4078	76.6952292	2.25922864	0.00137487
Cyp9h1	85.3970804	2.26414762	0.00932395
Tsp42Ed	456.703117	2.26534487	0.00476253
pn	76.482239	2.26564355	0.00548741
CG8950	23.5789216	2.26635836	0.02266952
CG11686	69.4495862	2.26723847	0.00555562
CG11737	55.5532258	2.27431274	0.02442434
eIF2alpha	80.0806357	2.2757624	0.02091743
Pex19	32.1736019	2.27655044	0.01587054
CysRS	62.4417668	2.27801515	0.00033408
scb	349.922588	2.27824928	5.09E-05
CG8785	242.522127	2.28102064	0.0155092
Rab32	134.04785	2.28146904	0.00137969
AhcyL1	226.434109	2.28687235	3.07E-05
Grasp65	105.685864	2.28769992	0.00029425
CG3386	39.0170782	2.28878393	0.01730421
lch	125.337746	2.28985994	0.00032795
TSG101	166.297077	2.29593061	1.45E-05
CG4645	76.1211036	2.29945244	2.80E-06
SeIg	39.6099038	2.30534388	0.00469659
Msr-110	1793.22747	2.30659643	0.00018042
l1J237Cc	127.7272011	2.30711297	0.00027935
vig2	121.197079	2.31098482	0.00010498
Tsf3	64.9982743	2.31208508	0.0046973
Pvf1	74.7748623	2.31209719	0.00244233
CG31522	254.290309	2.31296358	0.00023737
CG16935	87.9905845	2.31834724	4.26E-05
CG14971	75.2386585	2.32031053	0.04028347
Jra	130.119878	2.3230305	3.37E-05
ERp60	866.880701	2.33079964	1.98E-08
YL-1	34.1649514	2.33400074	0.00487421
CG14194	84.6279798	2.33473007	0.0022059
CG6617	35.1745952	2.33912698	0.00948887
CG5110	46.5722627	2.33957296	0.00061071
trem	14.0243321	2.3404288	0.0296781
Pez	111.815389	2.34050235	2.47E-05
GV1	61.5667962	2.34123898	0.00017967
Traf4	75.2425459	2.34125019	8.41E-06
Arfp1	32.6743395	2.34431054	0.0205096
Hsp83	4249.78369	2.34644926	2.73E-09
MED25	37.2237904	2.34824932	0.00161422
CG14450	28.2998646	2.34977796	0.01763809
Cortactin	150.712935	2.35212211	2.64E-05
ninaE	5004.5902	2.35290991	0.0397184
cactin	49.9252647	2.35314064	3.84E-05
CG15211	49.7291043	2.36055053	0.00231897
VhaSFD	666.960883	2.36123475	9.13E-05
Ndfip	175.199776	2.36281675	4.67E-11
galla-2	19.1639884	2.37138232	0.02894303
PPP1R15	188.730897	2.3749369	0.01267565
TRAM	82.2272443	2.37880611	0.00129833
CCT7	167.86957	2.37883686	1.33E-06
mbf1	205.813067	2.37948609	2.73E-09
CG10209	39.5225541	2.38112522	0.04384477
CG9215	20.4975076	2.38230453	0.01795906
Sap30	41.4979613	2.38242776	0.00127317
Taf6	57.1868658	2.38454773	0.03611909
Ras64B	213.843758	2.38543464	1.34E-06
Vha100-2	667.927879	2.3866329	0.03292368
sgl	127.453671	2.3877207	0.03834952
spz	169.786376	2.38828005	0.00013199
AnxB9	694.430689	2.39151129	1.10E-07
CG30022	112.801313	2.39227697	0.00032529
Timp	589.101909	2.39265555	9.35E-05
Vha68-2	996.991665	2.39637993	0.01337797
CG7685	21.8541182	2.40034657	0.01697382
Sec22	197.110068	2.40275592	3.45E-09
CG14646	45.1099012	2.40481769	0.0006311
PCGRP-LA	84.2494455	2.41296625	0.00121885
loco	219.371632	2.41630852	1.32E-08
bip1	28.367931	2.41732039	0.01447092
CG1208	286.153692	2.41787763	0.00145417
CG12581	178.669153	2.42259796	0.00024633
wcd	19.3062729	2.42647972	0.03351534
pain	65.5871174	2.4357139	3.09E-05
CG11876	209.612515	2.43732436	8.99E-05
Hmu	325.450817	2.43768579	4.03E-07
Arpc1	187.0905	2.44032061	6.46E-08
Drs	748.464064	2.44130399	0.04504443
Act5C	4562.78768	2.44286096	3.15E-07
Sply	220.808322	2.44722653	1.47E-07
CG18812	1219.84513	2.44786863	0.00468083
nemy	65.3585449	2.44866974	0.02037489

Sin1	26.5520978	2.44867343	0.01945108
bc10	124.094709	2.44894336	4.48E-07
CG9630	24.2956324	2.45367411	0.02284076
Ssrp	101.433008	2.4560736	6.80E-05
CG3760	45.3016459	2.45680254	0.00115636
CG33158	81.6050403	2.45857324	0.00657581
PIG-V	50.434432	2.46054235	7.72E-05
lglr36Bc	248.078306	2.46782943	0.00721371
CG8042	89.1985085	2.48069358	2.39E-07
mEFTu2	41.7367464	2.48813315	3.32E-05
IM14	40.1408283	2.49261828	0.00185473
CG17121	179.265259	2.49328571	1.05E-05
CG10103	170.483553	2.50032468	1.84E-06
CG40485	57.4295814	2.50073454	0.02819007
ldgf3	1318.02216	2.51291652	0.00050109
Sl3a2	26.0148155	2.51487701	0.01842845
CG11975	80.8293261	2.51796085	4.51E-06
	478.713375	2.51801361	0.00032743
CG15068	80.8017103	2.52050543	0.00037353
wuh0	19.2939249	2.52134786	0.01354213
CG8009	30.3943356	2.52173008	0.00682204
CG16713	64.4937603	2.52357921	0.01913023
CG7655	20.6415749	2.52489864	0.00681256
Cyp6a20	457.928631	2.52908586	1.49E-06
VhaPPA1-1	344.872214	2.53098747	0.00010028
CG42675	41.5539137	2.53182273	0.02332547
spag	33.2985788	2.53934959	0.00318839
NAAT1	102.006657	2.54106112	0.04290804
CG5500	20.2478308	2.5423649	0.00634326
Spn27A	281.507157	2.54380614	5.10E-05
Cmx99A	371.414213	2.54667941	1.28E-12
CG3918	20.7946268	2.54675609	0.00301836
CG3902	404.49826	2.55001923	6.13E-19
Rcd6	43.8158643	2.55112807	0.00120375
Thiolase	50.7290905	2.55573623	0.02826368
CG5167	312.427561	2.55732298	3.14E-05
slp1	29.7926134	2.56188203	0.00064029
Liprin-beta	139.247701	2.56311234	0.03258162
Srp54	103.250074	2.56441775	6.84E-07
Alr	24.2750854	2.56893199	0.00532189
Cyp9b1	41.5918228	2.57008056	0.01170614
p47	63.9839554	2.57255117	3.31E-06
CCT3	83.3181548	2.57383027	0.00019835
vn	33.8352351	2.57595171	0.02143883
CG30154	38.5819999	2.57801036	0.00671696
wir-1	2816.99353	2.5795258	4.24E-06
cpa	147.008461	2.58166327	0.00190655
CG6650	69.1670274	2.58320139	7.44E-07
CG6287	409.86809	2.58731316	0.00183218
CG31549	61.4272173	2.58771234	3.18E-05
CG7110	47.5791147	2.58902415	0.0315893
CG5001	71.8670615	2.58913173	0.00468083
CG10562	89.0265764	2.59017779	0.012863
lok	35.545452	2.59135731	0.00570261
CG1299	160.919189	2.60427156	0.01713411
ergic53	346.113765	2.60610735	0.00894736
CG6724	38.0543856	2.60742326	0.04437753
CG7834	57.6960031	2.61267333	0.00780971
Tsp3A	32.2381338	2.62072368	0.00047025
CG31370	38.9630791	2.62148937	0.01571713
CG4293	42.0452282	2.62172189	0.03380299
CG9147	27.2766017	2.62381384	0.00387279
Clic	226.92705	2.62811959	1.21E-05
CG15347	355.140724	2.63045325	0.02511297
Itgbn	55.9870359	2.63320431	0.01455313
CG15065	13.8826487	2.63445137	0.02143883
Cyp6a21	26.6335723	2.64392932	0.0046973
RabX1	43.5008379	2.64473462	4.25E-05
Cyp6a22	67.0097074	2.64495647	0.00394086
Eaf6	21.7959233	2.65145087	0.04742841
Ntr	197.154348	2.65152922	0.0108079
kermitt	22.6731646	2.66162608	0.03534535
Tap4	163.295118	2.66166259	0.00756884
CG3520	30.1246814	2.66234937	0.00657668
Ppp38	17.4403877	2.66288534	0.00522951
CG4269	171.103734	2.66357318	0.00247471
CG5862	30.5615561	2.66588309	0.0068141
CG10341	68.4908393	2.6729612	0.0033335
AnxB11	248.446318	2.6747818	1.20E-08
CG5321	56.9725076	2.67830129	0.00429495
Thp	14.9045813	2.67893809	0.04014437
DNApol-lota	57.7232091	2.6804867	2.56E-05
CG17896	604.531798	2.68653909	0.00100982
CG17600	20.4411264	2.68717033	0.0045482
Fmo-2	221.61405	2.68744821	0.00990676
edl	37.1832785	2.68771061	0.04088649
CG32638	181.323163	2.68888618	1.55E-05
CG2004	281.746694	2.69538846	0.00348823
pvr	35.16089	2.69793069	0.00468083
MrgBP	17.479616	2.69961132	0.02134745
CG31674	13.5089138	2.70069614	0.03721522
Brms1	35.8012744	2.70703967	0.00024806
CG8207	31.3454288	2.70771665	0.00111745
CG30281	37.1499867	2.70928793	0.000485
CG1792	23.4273829	2.71487791	0.0012753
Pdi	1645.92391	2.71830344	1.91E-08
Cyp12a5	36.8388484	2.71931324	0.00129995
Faa	20.5956333	2.72444476	0.02442434
CG1529	33.6151457	2.72479922	0.01073303
CG11723	32.6974282	2.73016665	0.00124573
CG10516	102.077287	2.7319	

Nacalpa	346,618497	2,76425193	4,96E-09
CG16898	41,9690293	2,77111849	0,01488302
CG6907	31,9897063	2,77208521	3,07E-05
Ance-3	516,055276	2,77219295	2,70E-05
Akap200	839,211243	2,78325828	3,80E-07
Vta1	45,247983	2,78731333	0,00042268
CG12065	276,458763	2,78765725	8,89E-11
Mfap1	19,4113702	2,78794355	0,01414009
sav	17,2081712	2,79444578	0,02510999
CG3163	22,8733956	2,79826216	0,01163786
betaggt-II	113,088438	2,80281656	2,47E-05
CG4872	23,7078567	2,80596107	0,00107634
betaggt-I	122,24572	2,80910645	0,00048761
et	34,7661999	2,80975923	0,0005638
CChA2	196,099023	2,81010627	3,85E-05
Spn55B	51,6511452	2,81087401	0,00027037
CG4511	59,5089352	2,81201718	3,05E-06
CG32512	135,005903	2,81214392	0,0010469
CG8306	106,224622	2,82404725	5,57E-05
CG13902	31,1761283	2,82837187	0,00893399
CG12104	50,9835897	2,82958995	0,00197408
CG8620	29,6087505	2,83016318	0,00101815
CG7556	45,8028553	2,83479745	6,47E-05
Hsp26	356,431276	2,83791842	0,03686137
Vinc	62,2179946	2,83993864	6,67E-05
CG2310	21,4584973	2,84256862	0,0092618
CG10939	192,620648	2,85175518	0,00027223
Cdc37	53,1673875	2,85464348	9,06E-05
CG9372	198,054835	2,85660477	1,42E-09
CG8837	112,738477	2,86100839	0,02490013
Lac	314,609319	2,86765687	6,52E-08
CkIIalpha-I1	16,1320919	2,8744843	0,0076014
Shc	104,65834	2,87737926	0,0001555
hgo	17,455561	2,88137898	0,04536172
MTPAP	14,6533232	2,88316272	0,01331123
CG10435	35,5218121	2,88349237	0,00275688
CG9689	124,739398	2,88457883	0,00079946
shf	78,7064167	2,89267834	0,00072465
Golgin84	39,1218275	2,89267965	0,00022479
CTC6	196,445669	2,89455857	4,53E-09
alph	232,927001	2,91111697	9,90E-05
CG1146	252,039539	2,92094382	1,50E-07
CG4820	13,6452299	2,92185796	0,01179329
CG4159	17,5044739	2,93057903	0,01123111
DCTN4-p62	42,808922	2,93668894	3,13E-06
bocks	53,905902	2,93768201	0,00106131
Sac1	140,268982	2,94156823	1,03E-06
MTF-1	134,736126	2,94691803	1,20E-08
Hydr2	293,380505	2,95092041	2,45E-14
CG5621	26,1934459	2,95545216	0,04567622
CG30026	86,6458282	2,9561788	0,00420893
grau	52,3419485	2,96468376	8,15E-06
rgn	950,475974	2,96617638	1,18E-13
Rh4	188,221949	2,96693629	0,02143883
Sep 01	84,7688254	2,97003298	2,72E-05
CG10916	90,3640189	2,97179614	1,64E-06
CG7632	89,7797379	2,97245532	5,15E-08
Sid	25,1779573	2,97989775	0,00339617
CG15824	19,1275929	2,9824629	0,01547574
CG17129	11,162343	2,98378295	0,03412994
CG31955	9,59843358	2,98492666	0,02757685
CG7718	20,9308419	2,98705888	0,00163988
T48	99,4441827	3,01177019	0,00028571
CG5791	39,4937138	3,03202434	0,0110089
sw	49,6057004	3,03405445	1,44E-08
CG5346	158,28986	3,0441838	5,30E-05
Upf3	14,669397	3,04694384	0,00522692
rush	129,226256	3,05040868	0,00030591
Wnt6	10,1468696	3,05770694	0,03431779
CG16947	98,8903318	3,07320222	0,00194348
Srp72	108,003917	3,07736648	1,93E-06
stv	705,87191	3,08295383	9,67E-06
Rab40	78,9604852	3,0839121	3,04E-12
CG15673	55,2803292	3,08485232	7,41E-05
Arp5	23,3996499	3,0849615	0,00178762
CG5147	20,4436562	3,09065314	0,0051237
dwg	15,3431061	3,10248849	0,01427424
CG3339	19,7957634	3,10931473	0,03239181
meigo	117,291018	3,12236542	9,43E-05
CG42615	20,1948474	3,12456575	0,00638225
CG5382	108,2684	3,15040804	2,37E-10
Cyp311a1	68,9521358	3,15637254	0,00362171
Skeleton	19,1263407	3,16188118	0,01360678
CG1622	15,2086717	3,16730605	0,00409076
CG43897	524,152136	3,19781731	0,00213493
GstE1	105,385659	3,20352032	1,89E-05
Strica	23,9330076	3,20888624	0,03620589
Gp93	451,869713	3,21550832	6,00E-05
	152,05666	3,22533375	6,52E-08
CG10347	41,0912619	3,25358848	0,00540393
Xrp1	2240,35189	3,2541743	8,04E-17
Clect27	41,2396958	3,25868786	0,00661598
Hrs	68,1280501	3,25890821	2,18E-09
CG1907	86,2645757	3,27099148	2,50E-09
CG8321	52,4532572	3,27868965	4,12E-09
RIOK2	19,7836899	3,29251952	0,00241963
Roel	53,3880583	3,29824983	6,85E-07
Nep5	20,6130972	3,31434117	0,00398714
CG10660	46,0953988	3,32101694	0,00035269
Nsf2	114,337611	3,33340803	1,40E-11
CG3309	27,2093973	3,33792092	0,0012343
CG6695	47,9591576	3,339432	0,0011511
Mmp1	326,815724	3,34637083	1,71E-07
CG15879	13,9195686	3,35762079	0,01179677
AspRS	63,6069974	3,36289018	3,86E-05
Amy-d	68,2320141	3,37632789	0,00195245
CG11334	42,8721598	3,3777963	0,00169684
MtnD	18,0328841	3,38097195	0,03780466
Ptp52F	20,1211524	3,38527509	0,02384616
Gfat2	91,1813296	3,3865404	0,0001557
CG8326	11,3722763	3,40561638	0,0229511

CG13482	16,1845589	3,4107025	0,03737076
	38,4508546	3,41243444	0,02562503
CG2641	15,1071052	3,43157128	0,00374523
CG33110	24,2197754	3,43445618	0,0112238
CG3295	107,98431	3,43833914	7,55E-13
He	18,3229115	3,47039671	0,0346157
e(y)1	6,41899257	3,47394862	0,04572708
sta	1158,32938	3,48546802	5,17E-06
trbl	166,922538	3,49549539	4,21E-06
CG17249	9,25190086	3,50509894	0,00566165
CG30456	31,3465859	3,51105466	0,00521816
Obp57b	25,1652764	3,52116086	0,00889595
CG2034	18,1202967	3,54119927	0,00025902
CG5397	261,101345	3,55239349	0,0004306
Rpl18	285,120074	3,57795447	0,00517261
phu	84,7350567	3,57859453	0,01294117
Tpi	192,845636	3,59326297	2,63E-05
Pglym78	338,896263	3,59771975	4,76E-15
Rh3	252,205544	3,60241539	0,01020917
CG13067	143,878845	3,60545658	0,01484944
SsRbeta	138,793517	3,61274989	3,96E-11
Fs	19,9697222	3,61709987	0,02450521
CG1943	204,176054	3,61746338	4,00E-07
CG15440	19,5951054	3,63793665	6,05E-05
CG31636	13,2413429	3,64062111	0,0387116
ArfGAP1	61,4181319	3,67470508	6,62E-11
CG9205	24,6002686	3,72580053	1,17E-05
CG13741	12,2438643	3,73503715	0,01498212
Tango14	14,5937607	3,7357525	0,00147477
Ammonless	18,5178423	3,74095614	0,04971515
CG14286	8,694375	3,74810648	0,02680638
CG42331	12,0194928	3,76841241	0,02171328
CG12333	39,5753764	3,77046227	3,12E-06
CG13807	9,29555125	3,77521332	0,00403736
CG11407	42,8373911	3,79273503	5,65E-05
Ugt35a	34,6763835	3,80050659	0,00021537
Act42A	736,915706	3,81038303	7,51E-06
Adgf-A	114,480133	3,83736387	0,00032511
AhcyL2	42,8295265	3,83837301	0,0001015
AnxB10	44,2200522	3,86427654	0,00065995
CG17186	17,2948076	3,87377886	0,00308973
Rpl4	1078,09661	3,88053942	0,00039886
CG3077	71,5651805	3,88695303	2,55E-12
CG11825	14,7541577	3,89127842	0,04157874
DCTN3-p24	23,5058269	3,89383041	3,23E-05
Cdc2rk	13,1676779	3,92360532	0,00297066
mfas	2351,09719	3,92783232	1,15E-11
ninaD	10,020532	3,93101073	0,01907747
Cpr67B	10,3244339	3,93535638	0,01367677
mthl2	233,579055	3,93684273	5,72E-05
CG9577	17,6508785	3,94528328	0,00256134
Kua	31,028267	4,01054642	0,03850973
CG10126	143,216266	4,01207818	1,82E-05
Gadd45	107,865604	4,02162887	4,10E-06
CG15082	12,791363	4,02887194	0,03430773
GNBP-like3	62,1591136	4,03475909	0,00052531
Ets21C	24,909763	4,04530078	0,01228663
CG3281	28,9563923	4,07120697	7,04E-05
verm	51,3652551	4,07831277	0,00226597
CG43062	6,60626037	4,10979363	0,04525669
CG30427	11,0589586	4,1384472	0,03719754
CG14636	20,0676873	4,14958564	0,0226006
CG13367	17,3621593	4,19306841	4,14E-05
Fnta	65,8351356	4,20200045	0,00286646
Osbp	54,0335729	4,28374243	5,41E-07
grass	86,4727106	4,30736512	0,00031331
Spn47C	20,1757158	4,31331139	0,01147124
CecB	18,7250666	4,33028368	0,01797314
FMRFa	127,562667	4,33124727	0,0407598
Vps37B	29,2481276	4,33375821	2,09E-07
CG30002	100,841267	4,35257509	0,00129304
Oga	19,0440894	4,37704047	0,00038471
CG15784	918,759423	4,38884148	8,37E-10
CG17843	11,4553893	4,41366302	0,00700184
DCP1	10,274344	4,41394997	0,01028203
Cad88C	9,76533491	4,41694361	0,04235475
CG34056	27,439822	4,42727532	0,00017967
hebe	92,9002536	4,44618884	6,85E-07
Tsp29Fb	333,014021	4,46820813	0,02349379
CG15556	20,4626708	4,47471986	0,04088649
Edg91	63,5884155	4,48687384	0,01730421
Cpn	101,708963	4,4876693	6,37E-06
CG41520	88,6765515	4,4920299	2,69E-07
CG2121	19,313719	4,49885438	0,00878042
CG5854	98,9253826	4,50263871	5,21E-09
Tsp2A	10,1490295	4,5304782	0,01945108
CG6749	20,5397945	4,53606904	0,00051554
CG7675	40,0313378	4,54132063	0,00187341
CG9150	14,5235418	4,57287518	0,00233582
SPARC	372,843389	4,5995464	8,21E-14
CG14253	8,7258024	4,62658618	0,00415498
Prip	73,1147184	4,6287828	1,00E-06
CG3448	17,2477207	4,63980383	0,00023481
hng3	6,9490876	4,67497042	0,02749934
CG5180	17,3428672	4,6866055	9,97E-05
meft	24,3131407	4,72820872	0,00353205
AttC	1053,62073	4,74844611	0,03780466
RhoGAP16F	38,8792172	4,74941595	5,58E-05
CG34220	75,356103	4,76566508	0,00050197
obst-E	12,6723	4,81214378	0,00078036
CG6891	131,911908	4,84867054	0,00011933

Galphaf	11,9582097	5,33292827	0,01945108
Spm42Dc	14,8092605	5,39266479	0,02137093
CG13748	6,13474469	5,45269706	0,03282312
RpL34b	208,6858286	5,50491768	0,00014006
upd3	9,9590846	5,53426999	0,01290001
hdly	313,531533	5,55802264	0,00797134
CG8292	9,37645451	5,59798006	0,02601037
CG14109	25,7680716	5,724163	0,02046009
CG43672	10,3223193	5,85663864	0,02107815
CG15546	21,3485522	5,88706363	0,0339859
NC2beta	6,02725871	5,94691438	0,00598962
CG2157	78,0481403	5,99273093	1,31E-11
Zfp48c	184,466117	5,99505358	0,00038865
CG16772	107,160057	6,08583305	8,35E-05
CG10062	21,8757799	6,13944168	0,00045623
Atf-2	40,2364839	6,21609615	3,67E-09
CG33474	5,90974963	6,23531871	0,0263571
CG5909	43,1984935	6,25881594	9,89E-05
Arc1	1852,54864	6,32414343	5,25E-33
Traf-like	15,6848803	6,38998393	0,00877963
Tap1	19,1357081	6,51173657	0,00328402
betaTub60D	313,248669	6,63699058	1,15E-14
CG30289	14,0218969	6,66425396	0,00140212
hll	11,9092974	6,73715108	0,03881398
Muc30E	11,9260811	6,74262723	0,00075713
odd	11,0523354	6,84819376	0,01658311
Cyp309a2	11,7834113	6,92250817	0,00291992
CG8281	10,7694232	7,00075256	0,00051549
CG17108	97,8536714	7,04394986	3,03E-09
Cpr49Ae	7,55361265	7,0460462	0,00928636
CG9452	6,31303829	7,18210841	0,00869546
prc	7,77601265	7,22321215	0,01778879
Dro	69,359479	7,23319009	0,04351421
CG42876	4,91498941	7,40548497	0,04723601
CG5002	62,4284517	7,49390507	7,04E-05
a6	14,8862832	7,59760894	4,97E-05
CG13321	7,67528242	7,62881154	0,00411568
CCAP	6,46898874	7,6488252	0,02973421
CG5096	26,2642467	8,06017123	0,04379809
Damm	14,3562916	8,1204845	0,00997377
rho-7	14,2371303	8,14674932	4,26E-05
spirit	4,26274796	8,17426026	0,03391425
MFS3	33,34978	8,24499468	1,40E-07
Hsp70Ab	7,53096589	8,30084646	0,00314744
Obp99b	16,1252986	8,30342589	0,00274708
CG6409	681,540533	8,48820514	5,45E-08
Lsp1alpha	12,7856206	8,5682208	0,00605874
Pvr2	24,5118022	8,75737412	1,88E-05
CG14327	17,3258664	8,79498445	0,00016285
CG13950	5,20720126	8,80395323	0,03258162
CG31207	15,1392115	8,88871342	0,00086764
CG18869	4,62339798	8,90815753	0,03511786
CG5399	122,975241	9,13385298	0,01097998
Oatp58Db	11,6884991	9,18130973	0,03291728
CG12262	9,11947166	9,31213212	0,00055314
CG31055	3,49413399	9,47578927	0,03563468
CG14195	6,20969268	9,55948024	0,04753931
yellow-g	10,8241299	9,82135896	0,00107429
Listericin	18,1653427	10,1040818	0,01563358
sea	3,50365839	10,1333732	0,0443164
CG12268	28,8380724	10,4565334	4,57E-06
sad	7,1931229	10,5907133	0,01070151
CG13919	6,66088375	10,770388	0,00263678
Hsp70Bb	6,51726109	10,9750645	0,0072298
CG14625	2,40122523	11,0844803	0,03309618
Cpr49Ac	3,32970415	11,2289903	0,0322702
CG10182	3,09377957	11,3183578	0,0469753
HgaP55	5,88497949	11,637214	0,019443
Hsp70Bc	21,9375789	11,7046324	1,41E-05
CG12869	8,28819576	11,9565206	0,00164068
CG2070	5,01394449	12,2343313	0,01447092
Rpt6R	2,79622733	12,2993178	0,03539414
CG11453	4,41546956	12,5222958	0,0129214
CG11380	9,00731385	12,652109	0,00144185
CG10814	133,459919	12,7085234	0,03092921
ChT8	6,72898015	12,9480734	0,004117
CG13285	7,89849798	13,2499192	0,02090132
CG6347	4,82607564	13,3311539	0,01096026
Obp56d	96,7776144	13,4750285	2,91E-06
SPH93	11,6533135	15,0555609	0,00062866
a10	9,70435184	15,4571685	0,01720973
Gr63a	4,14709189	15,6857256	0,00523192
CG15570	6,4826687	17,1507242	0,00415498
CG9826	4,52779337	17,449298	0,01699931
CG8945	5,56688176	18,4548065	0,00327229
CG7860	3,91118366	18,5902428	0,02266952
Wnt2	8,16982909	19,027024	0,01489204
CG11370	49,8776782	19,5122208	5,15E-09
CG17751	3,67492742	20,5641441	0,03098847
CG12493	6,05659099	22,2143663	0,00671108
CG31380	12,4199495	22,2327366	0,00071257
CG31077	9,30693598	23,0552798	0,00687842
CG4650	6,58871299	29,5670492	0,00127142
TotC	1084,05585	30,6537484	0,00028662
TotA	2556,39499	33,2720868	2,00E-06
Os16	4,9125522	34,2955205	0,01839168
Hsp70Bbb	3,54975576	34,8590313	0,00173039
CG12824	9,10022014	41,6426876	0,00074171
ChT4	6,12988113	43,9387405	0,00024138
CG30090	15,9773577	55,7499972	1,00E-05
Diedel	79,5544449	57,2448435	0,00135097
TotM	537,445342	58,1123165	3,10E-05
TotX	213,760492	101,807755	1,64E-06

## 6.6 DEGs of the comparison from adult and larval airways

Gene name	Max mean group	Fold change	FDR p-value
whe	2170,01	346218,98	0,0E+00
CG16826	768,39	157010,54	0,0E+00
CG34212	325,05	152810,45	0,0E+00
CG45080	884,64	36581,42	0,0E+00
CG43679	48,69	32311,98	0,0E+00
CG16904	30,66	30856,11	0,0E+00
CG43680	62,21	29954,16	0,0E+00
Fad2	65,07	28833,28	0,0E+00
lcs	247,93	26214,86	0,0E+00
Yp2	1022,01	18090,01	0,0E+00
Yp3	692,26	16817,10	0,0E+00
Yp1	1152,97	16563,58	0,0E+00
Rh2	45,44	13134,26	0,0E+00
CG13947	32,54	11373,94	0,0E+00
Nlg4	40,99	11304,65	0,0E+00
nAChRalpha5	0,99	9131,57	0,0E+00
fit	42,86	8382,55	0,0E+00
CG33109	57,22	7142,85	0,0E+00
Obp83a	4,67	6091,18	1,9E-11
CG32984	6,73	5301,01	0,0E+00
CG44195	2,63	5300,38	0,0E+00
CG6503	80,85	5248,37	0,0E+00
ttv	31,91	4676,50	0,0E+00
CG4716	105,44	4534,87	0,0E+00
CG17560	19,30	4454,22	0,0E+00
IM14	33,88	4072,64	0,0E+00
Arr2	76,27	3978,14	0,0E+00
Obp83b	5,37	3750,03	9,5E-10
inaC	2,79	3109,21	0,0E+00
frma	3,51	2879,45	0,0E+00
CG16836	13,50	2869,70	0,0E+00
elof	24,36	2854,52	0,0E+00
Arr1	11,02	2793,01	0,0E+00
Ser7	1,83	2689,53	1,3E-12
LysP	29,12	2515,19	0,0E+00
CG42265	0,59	2495,94	0,0E+00
Ag5r	59,88	2405,38	0,0E+00
CG34211	8,65	2274,35	2,2E-09
CG14989	3,09	2244,10	0,0E+00
Est-6	175,71	2129,24	0,0E+00
fln	1,57	2075,96	3,7E-11
CG15067	16,73	2048,63	0,0E+00
Eip93F	4,25	2037,11	0,0E+00
ninaE	37,76	1975,62	0,0E+00
CG14459	0,67	1948,87	0,0E+00
CG10680	7,57	1946,78	0,0E+00
Os-C	5,18	1943,66	2,2E-12
Rh3	2,27	1929,84	0,0E+00
a10	7,44	1876,89	1,1E-13
DIP-delta	0,37	1773,13	1,1E-10
IM3	12,74	1740,88	0,0E+00
tj	0,43	1709,97	2,1E-10
CG8708	3,23	1692,13	0,0E+00
a5	1,58	1638,03	2,6E-07
sNPF	2,70	1624,77	0,0E+00
nAChRbeta1	3,24	1535,14	0,0E+00
Dop2R	2,90	1505,06	0,0E+00
trp	2,60	1411,28	0,0E+00
wrv	1,47	1378,25	0,0E+00
Obp19a	1,61	1377,82	3,1E-07
trpl	1,92	1314,30	0,0E+00
IM2	26,79	1295,92	0,0E+00
ninaB	1,29	1288,84	0,0E+00
CG15065	6,46	1280,36	6,6E-09
Iris	6,79	1279,02	0,0E+00
Obp19d	9,66	1248,51	0,0E+00
Hasp	2,24	1238,54	0,0E+00
beat-Va	0,39	1217,70	1,7E-09
CG10384	0,29	1205,83	2,2E-09
euc	2,66	1205,39	2,2E-09
CG8861	0,85	1166,63	0,0E+00
CG1504	0,41	1165,86	8,4E-14
CG12605	2,24	1128,57	0,0E+00
CG18609	14,25	1101,45	0,0E+00
CG16854	0,31	1049,29	6,8E-09
CG10562	1,89	1030,04	0,0E+00
nAChRalpha6	1,52	1016,88	0,0E+00
Muc30E	0,89	1010,82	0,0E+00
CG1138	0,54	1006,33	1,8E-06
Pdf	6,58	969,94	0,0E+00
VGlut	1,95	963,99	0,0E+00
Cngl	0,99	956,92	0,0E+00
CG33310	0,39	932,90	1,6E-08
Lrp4	1,59	921,06	0,0E+00
Gad1	1,65	914,97	0,0E+00
Cpr72Ec	0,57	910,42	1,3E-08
nAChRbeta2	0,47	905,72	2,1E-15
CG1942	1,19	897,16	1,0E-14
Sfp84E	0,89	816,68	4,1E-06
GluClalpha	1,65	796,71	0,0E+00
AstC-R1	0,43	789,15	5,3E-13
Orco	0,32	781,30	1,1E-07
nAChRalpha2	0,29	758,77	3,9E-08
CG13026	0,50	748,07	1,8E-08
CG16772	2,38	743,43	0,0E+00
nhl	0,78	723,08	2,1E-09
CG34172	1,50	713,79	2,9E-12
CG12239	2,05	707,20	0,0E+00
beat-1c	0,29	678,19	2,5E-13
Dscam3	0,38	674,71	0,0E+00
CG30158	0,40	666,87	6,6E-12

CG4744	0.15	660.57	2.5E-07
CG18107	17.43	657.83	0.0E+00
GlurIB	0.38	652.74	0.0E+00
tim	2.42	648.10	0.0E+00
CG14645	3.73	634.06	0.0E+00
Dh31	1.07	632.93	1.7E-12
CG9459	4.72	616.54	0.0E+00
CG33639	0.24	601.37	1.6E-13
Task7	0.32	598.88	6.6E-08
CG12502	0.29	595.67	1.2E-12
DIP-zeta	0.14	585.97	1.3E-07
dpr13	0.52	581.37	0.0E+00
nAChRalpha1	0.46	579.97	0.0E+00
CG6067	5.82	579.24	0.0E+00
Eaat1	14.42	575.54	0.0E+00
rdhB	0.47	573.69	9.1E-08
CG11391	0.46	566.36	2.1E-08
CG33470	8.95	565.63	0.0E+00
beat-IIIb	0.56	558.34	0.0E+00
CG43329	0.70	546.93	1.7E-07
CG10097	3.55	541.69	0.0E+00
CG43732	0.44	541.40	0.0E+00
CG31300	5.34	536.57	0.0E+00
CG9394	0.63	529.18	5.0E-12
CG14853	1.65	522.20	0.0E+00
CG42613	3.52	521.61	0.0E+00
minaG	0.25	518.96	3.2E-07
CG15765	1.82	515.99	0.0E+00
CG7443	0.72	507.34	4.6E-07
CG42750	0.64	506.13	0.0E+00
CG6432	4.46	502.79	0.0E+00
CG12912	0.42	500.80	0.0E+00
inaF-A	2.64	495.78	0.0E+00
IM4	10.66	485.20	0.0E+00
CG1552	0.96	483.35	8.7E-12
CG34220	7.35	476.90	0.0E+00
CG43202	0.99	476.21	8.8E-06
Ugt86De	0.58	471.13	1.5E-11
beat-la	0.39	469.43	5.6E-10
Obp28a	3.49	466.39	2.5E-11
CG3822	0.47	466.32	0.0E+00
Act79B	3.12	464.12	0.0E+00
CG32532	0.11	463.55	1.2E-06
Cpr49Ab	1.31	460.28	4.2E-08
CG10177	1.02	459.92	0.0E+00
Xport-B	0.95	456.62	6.5E-11
CG16978	2.23	453.66	6.2E-12
Cpn	0.65	449.95	0.0E+00
Capa	1.50	441.90	1.2E-10
unc80	1.53	440.11	0.0E+00
CG9458	8.46	437.57	0.0E+00
SPR	1.34	433.99	0.0E+00
CG44837	0.23	429.23	0.0E+00
Clk	1.48	426.89	0.0E+00
CG17005	0.36	422.88	2.3E-11
CG14309	0.61	422.85	8.1E-12
CG31199	0.75	420.12	1.7E-11
Cyp4g15	2.95	419.43	0.0E+00
Cyp4g1	477.18	419.40	0.0E+00
DIP-theta	0.30	411.62	6.6E-11
kek3	0.30	409.90	0.0E+00
CG43402	1.80	397.18	0.0E+00
CG34392	0.50	392.18	0.0E+00
DIP-gamma	0.60	390.19	0.0E+00
FoxP	0.90	388.54	0.0E+00
CG44140	1.66	383.97	5.1E-10
Nep4	1.95	381.72	0.0E+00
acj6	0.96	379.37	0.0E+00
CG14440	144.86	374.81	2.1E-15
Csas	1.09	372.53	1.3E-10
CG32641	0.77	368.14	5.0E-06
CG34290	0.94	365.78	2.3E-10
Sprn	0.15	364.59	5.0E-06
Cp7Fb	0.87	363.14	8.1E-10
Mip	0.55	362.46	2.5E-10
Zasp67	0.11	360.30	2.7E-06
dany	0.38	359.18	3.3E-05
PVRAP	0.24	356.24	1.6E-11
DopEcR	1.98	356.11	0.0E+00
CG43066	2.10	353.44	0.0E+00
CG2839	0.90	349.98	0.0E+00
Mst33A	0.29	341.64	9.3E-06
CG12147	0.21	341.64	9.3E-06
Muc68D	0.52	336.57	0.0E+00
CG11319	1.31	336.30	0.0E+00
CG4587	1.22	335.72	0.0E+00
dpr20	0.30	333.58	8.8E-13
CG42450	4.55	327.38	0.0E+00
CG16756	4.06	324.85	0.0E+00
TotC	2.58	324.80	0.0E+00
OS9	2.10	324.15	6.8E-12
CCKLR-17D1	0.09	323.01	6.0E-06
GlyT	0.41	322.03	0.0E+00
5-HT1A	0.32	321.15	0.0E+00
CG2233	332.18	320.89	0.0E+00
CG9377	0.47	320.53	4.8E-10
inaF-B	4.06	319.55	0.0E+00
nAChRalpha7	1.34	315.63	0.0E+00
CG14982	0.41	311.97	0.0E+00
mmd	1.82	311.31	0.0E+00
Mal-A7	0.12	308.72	7.1E-06
CG13091	0.50	308.40	9.4E-14
CG44141	1.43	307.90	1.6E-09
CG34370	0.42	306.92	0.0E+00
CG43351	4.53	306.39	3.1E-12
Gr47a	0.24	305.13	4.7E-06
CG33234	0.41	305.08	7.5E-10
CG32985	0.25	304.64	7.9E-09
CG32371	0.22	304.47	9.8E-06
Cyp6d5	83.49	302.42	0.0E+00
dpr9	0.88	301.60	0.0E+00

hig	1.39	299.36	0.0E+00
rd102C	0.10	298.67	2.7E-05
Pdh	6.83	298.04	0.0E+00
Vsx1	0.06	296.77	1.9E-05
Sodh-1	17.92	296.19	0.0E+00
ZnT33D	0.11	294.37	2.6E-05
CG14591	1.61	291.93	0.0E+00
Rab26	0.64	287.58	0.0E+00
boss	0.82	287.43	0.0E+00
hbn	0.13	286.20	1.4E-05
TotX	0.58	285.98	2.7E-05
Ugt35b	13.74	285.07	0.0E+00
TotM	1.03	284.76	1.1E-09
CG13527	0.42	284.39	4.9E-09
Ir47a	0.29	283.42	5.0E-12
cpx	14.49	283.02	0.0E+00
Rdl	2.30	282.89	0.0E+00
CG43630	11.65	282.26	0.0E+00
Pph13	0.30	278.50	2.1E-09
Or85b	0.18	278.09	1.7E-04
CG30002	1.05	277.33	0.0E+00
beat-1b	1.30	275.06	0.0E+00
CG33233	0.28	274.90	1.9E-09
CG31760	0.86	274.02	0.0E+00
IM1	7.17	271.83	0.0E+00
CG32647	2.45	271.31	0.0E+00
retinin	0.50	271.18	1.7E-08
CG18367	0.91	268.24	8.9E-05
Shawl	0.20	267.75	0.0E+00
CG31933	0.14	266.81	1.6E-05
sif	2.36	263.34	0.0E+00
CG31419	0.27	261.93	4.9E-05
CG4467	1.68	258.58	0.0E+00
dpr4	0.65	256.90	0.0E+00
AstC	0.82	256.82	8.3E-15
CG6484	1.15	253.85	0.0E+00
CG14669	0.55	253.52	0.0E+00
CG43396	0.43	248.67	1.7E-05
Drsl5	2.80	248.54	2.6E-08
Ir60d	0.11	246.22	2.4E-04
CG32053	0.12	246.22	2.4E-04
Ir75a	0.10	246.22	2.4E-04
CG6140	0.16	246.22	6.3E-05
CG34353	1.09	245.65	0.0E+00
Fife	0.81	244.51	0.0E+00
SLO2	0.95	243.06	0.0E+00
wa-cup	0.10	240.77	1.3E-04
CG30083	0.53	240.23	1.4E-07
dec-1	0.84	239.58	1.3E-08
CG44259	0.33	237.30	9.9E-05
tobi	15.55	235.38	0.0E+00
Mtk	2.77	235.38	3.2E-12
CG13579	0.16	234.31	2.0E-11
CG31205	0.22	234.18	4.2E-05
Npc2h	3.84	232.52	0.0E+00
TpnC4	1.05	232.27	3.5E-13
CG43332	0.18	232.24	1.4E-06
Prat2	6.90	232.02	0.0E+00
lobo	0.07	229.43	7.3E-05
CG32052	0.24	229.20	2.1E-11
Dscam2	1.16	227.91	0.0E+00
Grik	0.16	227.56	4.5E-11
glob2	0.10	226.82	4.4E-05
CG15449	0.55	225.74	5.2E-07
CG31797	0.08	225.01	1.7E-05
CG31861	0.36	224.76	8.2E-05
CG9570	0.18	223.10	3.0E-05
IMPPP	7.91	222.79	0.0E+00
pros	3.15	222.64	0.0E+00
CG12448	0.20	221.57	5.3E-05
CG15293	30.06	221.08	0.0E+00
CG13607	19.93	220.38	0.0E+00
hb	0.17	220.14	2.0E-12
thrd-3	0.28	220.08	6.9E-05
LManIV	0.08	220.03	2.5E-04
Cyp6t1	0.77	219.33	0.0E+00
Obp69a	1.31	218.69	2.4E-08
CG14400	2.17	218.54	0.0E+00
Vsx2	0.09	216.78	4.0E-05
CG14823	1.99	216.19	0.0E+00
CG34324	2.88	215.21	0.0E+00
Or83a	0.17	213.97	9.4E-05
CG30008	28.00	213.31	0.0E+00
CG30395	0.25	211.57	1.1E-10
Ir56a	0.22	210.92	1.4E-07
CG31517	0.13	208.49	1.8E-04
Mal-B1	11.62	205.33	0.0E+00
CG9631	1.08	205.07	0.0E+00
Or47a	0.12	204.28	1.8E-04
Mst36Fb	7.27	203.94	0.0E+00
CG7910	12.11	201.83	0.0E+00
klg	1.25	201.04	0.0E+00
CG42740	0.55	200.93	0.0E+00
CG8757	0.10	200.05	3.7E-05
CG15236	0.94	200.03	0.0E+00
CG43074	0.27	200.03	4.0E-05
Tps1	30.40	199.58	0.0E+00
CG34045	0.43	195.82	2.6E-04
CG32457	0.40	195.82	2.6E-04
CG42741	1.56	195.50	0.0E+00
nAChRalpha3	0.43	195.47	0.0E+00
Rh4	1.38	195.04	0.0E+00
CG33926	19.87	194.82	0.0E+00
CG5897	0.08	194.76	2.0E-04
Sox21b	0.49	193.73	0.0E+00
Eaat2	2.16	192.70	0.0E+00
CG11236	1.90	192.42	0.0E+00
Ir48c	0.10	192.05	1.1E-04
beat-VI	0.42	191.37	0.0E+00
Obp59a	0.30	187.73	1.6E-05
Hdc	0.21	186.71	4.0E-12

CG4577	4.39	186.57	0.0E+00
CG11842	0.97	186.35	0.0E+00
CG3955	0.57	185.93	1.8E-10
CG6154	0.29	185.59	0.0E+00
scrt	1.30	185.38	0.0E+00
CG12594	0.22	185.29	7.3E-13
Sytalpha	0.41	184.96	0.0E+00
CG10479	2.14	184.81	0.0E+00
CG43347	0.25	182.93	0.0E+00
CG9686	3.16	182.40	0.0E+00
CG13002	0.22	182.29	4.6E-04
CG5556	0.13	182.29	4.6E-04
CG13801	0.07	182.29	4.6E-04
CG12950	0.85	181.69	0.0E+00
CG34351	0.78	181.61	0.0E+00
CG9072	0.63	181.47	2.1E-07
Xport-A	0.89	180.81	1.6E-11
Trissin	0.31	179.78	1.7E-04
Tk	0.31	178.06	8.3E-10
toy	0.79	177.42	0.0E+00
CG1979	0.61	177.29	0.0E+00
Obp99a	32.53	176.08	0.0E+00
CG11898	0.08	175.95	1.1E-06
Or63a	0.09	175.17	5.7E-05
Dhx	0.06	175.13	7.4E-05
ms(3)76Ba	0.17	174.51	1.8E-07
CG8401	0.17	174.24	1.2E-04
Drpx	0.50	173.79	0.0E+00
qvr	4.26	173.77	0.0E+00
GstE4	0.79	173.14	4.9E-07
Ir75c	0.08	172.08	2.6E-04
CG32391	0.15	171.82	5.1E-04
CG4476	0.23	170.93	1.2E-09
CG45676	0.41	170.57	9.6E-05
Or98a	0.14	170.57	9.7E-05
CG3491	0.14	170.41	0.0E+00
CG9497	3.86	169.83	0.0E+00
mtt	0.28	169.39	0.0E+00
CG12484	0.84	169.33	0.0E+00
gprs	0.62	168.78	0.0E+00
CG9813	3.44	168.72	0.0E+00
Drl-2	0.38	167.73	0.0E+00
Gba1a	0.08	167.30	2.7E-04
CG9512	246.34	167.27	0.0E+00
CG15358	1.54	166.98	3.1E-12
CG9780	3.12	166.96	0.0E+00
dysc	0.96	166.17	0.0E+00
dhd	2.15	165.24	0.0E+00
CG7560	2.01	165.23	0.0E+00
CG32206	0.59	163.96	0.0E+00
beat-IIa	0.49	163.87	0.0E+00
rad	0.49	162.66	0.0E+00
Jon44E	0.25	160.66	4.6E-07
CG6282	0.40	160.22	0.0E+00
eag	0.73	159.89	0.0E+00
CG11741	0.57	159.80	1.1E-05
kek2	0.47	159.34	0.0E+00
CG10553	19.10	158.69	0.0E+00
rd59A	0.21	158.23	5.5E-10
Rbp6	1.87	156.03	0.0E+00
NimC4	0.56	154.18	1.9E-10
CG11891	7.38	153.99	0.0E+00
CG13127	0.07	153.90	2.8E-04
sphinx2	0.46	153.70	1.4E-07
CG10799	13.21	153.23	0.0E+00
5-HT7	0.35	152.03	0.0E+00
Asta	0.53	151.68	5.3E-11
CG34114	0.80	151.48	0.0E+00
CG8916	0.07	151.38	1.4E-04
CG17048	0.19	150.23	1.2E-04
sut4	0.09	150.22	1.1E-04
CG31007	0.19	150.22	6.7E-05
Sfp24Ba	0.26	150.21	1.1E-04
Acp24A4	0.18	150.15	6.3E-04
CG4815	0.11	150.15	6.2E-04
CG4461	2.04	149.65	0.0E+00
Pdfr	0.80	149.65	0.0E+00
Ir60b	0.09	149.64	1.6E-04
HP1c	0.26	149.64	1.6E-04
Nlg2	0.75	149.55	0.0E+00
CG1402	0.27	149.34	0.0E+00
dpr6	0.34	148.94	0.0E+00
unc79	2.43	148.52	0.0E+00
Cyt-b5-r	46.95	148.42	0.0E+00
nwk	1.46	148.31	0.0E+00
polyph	0.10	147.91	6.5E-04
CG31002	0.09	147.91	6.6E-04
Hr3	0.37	147.50	0.0E+00
CG46301	0.08	147.39	1.1E-09
ninaD	0.23	146.38	1.3E-08
CG12071	0.85	146.10	0.0E+00
CG14762	5.27	145.94	0.0E+00
gl	0.29	145.48	1.5E-13
CG34113	0.55	144.82	0.0E+00
CG15040	0.17	144.69	6.3E-15
CG42322	0.66	144.44	0.0E+00
Hsp60D	0.19	143.91	9.6E-09
Vago	6.03	143.60	0.0E+00
CG43707	0.50	142.93	0.0E+00
CG1358	1.30	142.50	0.0E+00
beat-VII	0.96	142.36	0.0E+00
Pif2	0.20	141.87	6.9E-04
CG11694	0.19	141.87	6.9E-04
CG5111	0.09	141.87	7.0E-04
CG32432	1.02	141.76	0.0E+00
Tkr86C	0.13	140.82	1.8E-09
jeb	0.90	140.69	0.0E+00
Cbp53E	1.81	140.35	0.0E+00
Obp57a	0.69	139.85	6.8E-09
CG7653	0.04	139.70	3.7E-04
CG31465	0.66	139.22	0.0E+00

bru3	1.99	138.02	0.0E+00
CG14760	0.08	137.69	3.3E-04
Acp33A	0.42	137.69	3.3E-04
CG46320	0.05	136.80	6.2E-10
CG43778	0.86	136.62	0.0E+00
jef	1.72	136.27	0.0E+00
CG31221	4.39	136.06	0.0E+00
CG8358	0.64	135.74	0.0E+00
Dop1R1	0.48	134.42	0.0E+00
CG43850	0.52	134.21	1.6E-11
chp	2.69	133.80	0.0E+00
CG6723	0.53	133.66	0.0E+00
Mid1	0.77	132.79	0.0E+00
CG5778	6.29	132.78	0.0E+00
CG4341	0.51	132.58	0.0E+00
Actbeta	1.70	132.18	0.0E+00
CG32700	0.97	132.07	0.0E+00
phyl	0.63	132.04	0.0E+00
CG1468	20.18	130.94	0.0E+00
Trxr-2	0.11	130.92	2.1E-05
brp	1.95	130.67	0.0E+00
Sfp53D	0.36	129.58	1.7E-06
CG31445	2.74	129.12	0.0E+00
SIFaR	0.07	129.02	9.6E-09
Cp19	0.71	128.60	3.0E-09
dpr2	0.17	128.12	7.4E-12
CG43331	0.14	127.96	3.0E-04
Dh44	0.62	127.27	0.0E+00
prom	0.09	126.54	6.9E-10
CG2993	1.27	125.92	0.0E+00
CCDC151	0.06	125.31	2.2E-04
CG33669	0.20	125.29	1.2E-04
CG17030	0.16	125.29	2.8E-04
Ipod	0.07	125.28	2.6E-04
ATPsynCF6L	0.20	125.28	1.8E-04
stnB	1.54	125.06	0.0E+00
CG15617	0.26	124.71	1.2E-08
CG4020	6.38	124.41	0.0E+00
Muc68E	0.22	124.12	4.2E-15
Pp1-13C	0.07	123.83	9.0E-04
Tsp42Eb	0.15	123.83	9.0E-04
CG10950	0.07	123.83	9.0E-04
Gr98c	0.11	123.83	9.0E-04
S-Lap4	0.11	123.12	5.6E-07
hec	0.09	123.10	3.1E-07
CG15548	0.09	123.08	6.0E-07
CG1545	0.33	123.08	3.1E-07
CG18265	0.21	122.71	0.0E+00
lambdaTry	0.14	122.67	4.3E-04
CG18088	0.61	122.26	3.0E-11
CG42540	2.12	122.16	0.0E+00
Gfri	0.81	121.18	0.0E+00
CG33203	0.75	121.01	0.0E+00
Snap25	6.25	120.99	0.0E+00
Oatp26F	0.17	120.93	2.3E-07
Gr64d	0.04	120.00	3.7E-04
CG8419	0.22	119.47	2.1E-13
CG1213	17.97	119.36	0.0E+00
mGluR	0.75	118.86	0.0E+00
GABA-B-R3	1.16	118.71	0.0E+00
CG1208	4.87	118.51	0.0E+00
Scp1	17.33	118.07	0.0E+00
CG34028	0.17	117.81	1.0E-03
CG12126	0.16	117.81	1.0E-03
Gr22b	0.08	117.81	1.0E-03
CG31644	0.19	117.81	1.0E-03
aly	0.04	117.81	1.0E-03
Ir75b	0.05	117.81	1.0E-03
Or88a	0.08	117.81	1.0E-03
Hug	0.27	117.08	2.1E-05
Syt1	4.33	117.02	0.0E+00
CG6295	0.39	116.82	3.8E-08
CG43219	0.31	115.75	1.4E-05
ninaC	4.88	115.70	0.0E+00
CG12531	0.86	115.66	0.0E+00
CG15721	0.08	113.95	4.7E-06
CecC	1.95	113.64	4.9E-12
CG42492	1.50	113.16	0.0E+00
nSvb	4.64	112.57	0.0E+00
CG4328	0.04	112.17	1.2E-03
Crys	0.16	111.91	6.9E-07
rd3F	0.18	111.87	4.6E-08
CG33322	0.14	110.79	1.2E-06
Nckx30C	3.12	110.79	0.0E+00
mth13	0.33	109.87	2.0E-10
CG30275	0.05	109.60	1.2E-05
CG12355	0.45	109.50	1.3E-13
CG32368	12.49	109.36	0.0E+00
CG15661	3.38	109.27	0.0E+00
Gbp2	11.41	109.22	0.0E+00
Drs14	0.76	109.22	1.6E-05
CG16965	1.10	109.14	0.0E+00
CG6052	0.08	109.10	1.7E-07
Drep3	0.19	108.43	2.1E-08
stnA	1.50	108.33	0.0E+00
Sfp24Bb	0.18	107.72	6.6E-04
VAcHt	2.35	107.50	0.0E+00
fine	1.32	107.37	0.0E+00
Nmdar1	0.30	106.86	0.0E+00
CG2269	3.38	106.20	0.0E+00
dan	0.08	106.09	3.2E-08
CG15531	11.24	106.00	0.0E+00
CG43737	0.85	105.59	0.0E+00
CG14070	0.07	104.66	6.6E-04
CG3078	0.39	104.45	0.0E+00
CG17321	0.85	103.94	0.0E+00
CG5103	0.12	103.80	1.2E-04
Vha36-2	0.07	103.77	6.6E-04
CG31191	0.24	103.60	4.2E-15
CG5966	2.20	103.19	0.0E+00
CG1695	0.56	102.49	0.0E+00

CG18223	0.10	101.89	6.4E-04
Cyp28d1	10.27	101.67	0.0E+00
CheB74a	0.16	101.46	6.5E-04
Muc12Ea	0.20	101.08	0.0E+00
Syn2	0.63	101.03	0.0E+00
CG42260	0.46	100.50	0.0E+00
Gr64c	0.03	100.40	5.7E-04
CG1690	0.05	100.39	3.7E-04
CG17821	0.09	100.39	3.5E-04
CG31677	0.14	100.39	3.4E-04
CG44434	0.02	100.38	4.8E-04
CG7025	0.08	100.37	3.9E-04
Or82a	0.09	100.37	3.9E-04
CG43056	0.32	100.37	5.4E-04
grim	0.06	100.37	5.3E-04
CG43277	0.23	100.37	5.2E-04
obst-1	0.14	100.36	5.0E-04
CG12637	0.10	100.01	6.0E-04
Hs3st-A	0.75	99.68	0.0E+00
CG3492	0.07	99.68	1.4E-03
rho-6	0.11	99.68	1.4E-03
CG33700	0.09	99.68	1.4E-03
ppk5	0.07	99.68	1.4E-03
CG9395	0.27	99.65	0.0E+00
CG17716	0.63	99.48	0.0E+00
CG44836	0.17	99.18	3.3E-09
Obp18a	7.22	98.72	0.0E+00
Hs3st-B	0.08	98.56	1.4E-06
CG13137	0.13	98.54	4.8E-06
Prosalpha4T1	0.22	98.52	5.3E-06
Toll-6	0.46	98.28	0.0E+00
CG1137	0.21	97.92	5.7E-08
CG31200	1.19	97.41	8.3E-15
Cp36	1.55	97.36	6.8E-08
dpr21	0.66	97.28	1.8E-14
Syngt	1.35	96.82	0.0E+00
PGRP-SB1	5.68	96.54	0.0E+00
Mal-A1	0.49	96.48	7.7E-10
ACXC	0.05	96.45	8.0E-05
Amy-d	1.07	96.31	0.0E+00
Prosheta5R2	0.09	96.30	2.8E-04
CG2336	0.10	96.30	2.8E-04
lManV	0.06	96.13	5.2E-05
CG6660	8.48	96.09	2.1E-15
CG30026	2.28	96.00	0.0E+00
Oli	0.33	95.60	2.5E-13
CG6209	0.25	94.89	8.4E-07
CG17193	0.22	94.51	7.1E-11
clumsv	0.30	93.74	2.9E-11
CG42541	0.80	93.73	0.0E+00
CG5819	2.56	93.47	0.0E+00
Gbeta76C	3.96	93.24	0.0E+00
CG30419	0.11	93.00	2.7E-10
Vml	0.28	92.83	2.6E-07
CG14528	2.22	92.55	0.0E+00
CG13284	2.40	92.21	0.0E+00
CG4415	0.24	92.00	9.5E-08
Ugt86Dg	0.13	91.86	2.1E-04
CG2217	0.93	91.75	0.0E+00
CG34334	0.07	91.22	9.1E-05
jhedup	1.78	90.13	1.3E-08
Odc1	3.00	89.98	0.0E+00
CG13978	0.09	89.96	6.1E-06
CG13148	0.17	89.79	3.0E-07
Attc	5.59	89.61	0.0E+00
fs(1)M3	0.13	89.56	4.4E-09
CG43800	1.92	89.46	0.0E+00
CG10362	0.35	89.31	0.0E+00
CG32301	0.08	89.28	2.8E-07
CG8500	1.14	89.16	0.0E+00
Cpr30B	0.20	89.01	2.9E-04
dpr15	0.23	89.00	4.2E-15
CG14529	0.48	88.76	0.0E+00
CG14743	0.05	88.47	1.8E-03
Send1	0.11	88.47	1.8E-03
CG13243	0.07	88.47	1.8E-03
CG33339	0.10	88.47	1.8E-03
CG42809	0.35	88.40	7.2E-05
PsGEF	0.61	88.30	0.0E+00
CG14120	0.04	87.99	4.1E-05
Gycbeta100B	0.85	87.20	0.0E+00
CG16779	2.34	87.15	0.0E+00
CG16713	10.34	87.14	0.0E+00
CG16926	18.76	86.71	0.0E+00
CG14024	0.31	86.62	1.1E-13
CG32444	20.19	86.47	0.0E+00
v	3.24	85.70	0.0E+00
Ggamma30A	4.30	85.61	0.0E+00
CG44153	0.27	85.51	0.0E+00
betaNActes4	0.07	85.18	2.3E-03
CG43996	0.07	85.18	2.3E-03
CG12780	0.16	85.18	2.3E-03
CG44341	0.07	85.18	2.4E-03
CG15880	0.08	85.18	2.4E-03
CG10943	0.06	85.18	2.4E-03
CG18581	0.11	85.18	2.4E-03
gdl-ORF39	0.07	85.18	2.4E-03
TrR99D	0.18	85.16	3.9E-12
dpr11	0.66	85.09	0.0E+00
CG5910	3.66	85.07	0.0E+00
fid	0.28	85.05	0.0E+00
CG42878	1.37	84.65	2.1E-08
cac	1.82	84.35	0.0E+00
CG7907	0.06	84.12	1.0E-04
CG7058	0.27	84.08	0.0E+00
CG1773	0.64	84.07	1.2E-12
Ekar	0.54	84.03	0.0E+00
Mal-A3	0.12	83.75	2.0E-04
phu	0.36	83.69	8.8E-12
Ktl	1.58	83.57	0.0E+00
CG2111	0.19	83.26	3.5E-12

CG31077	0.15	83.16	4.0E-07
eIF3d2	0.08	82.82	4.1E-05
CG14042	0.25	82.80	2.7E-13
fusl	0.99	82.47	0.0E+00
CG6910	29.89	82.38	0.0E+00
Con	0.42	82.34	0.0E+00
Amy-p	0.57	82.14	4.2E-15
CG33477	0.10	82.01	2.7E-03
CG9010	0.05	82.01	2.7E-03
CG13501	0.03	82.01	2.7E-03
CG31741	0.03	82.01	2.7E-03
CG15475	0.06	82.01	2.7E-03
EACHm	0.07	82.01	2.7E-03
CG31706	0.31	81.94	1.1E-08
Rkh	0.91	81.79	0.0E+00
erm	0.07	81.67	2.3E-07
CG13315	13.88	81.65	0.0E+00
Nos	0.29	81.65	0.0E+00
CG13872	0.20	81.55	5.0E-06
Ccn	0.33	80.98	2.1E-15
Apoltp	9.69	80.82	0.0E+00
dpr7	1.10	79.31	0.0E+00
CG43373	0.45	79.21	0.0E+00
CG42784	0.66	79.12	0.0E+00
CG5895	1.26	79.07	0.0E+00
Sybeta	0.29	79.06	0.0E+00
CG44422	0.37	78.99	0.0E+00
CG1688	0.22	78.94	2.1E-15
CG5890	0.28	78.64	0.0E+00
CG14053	0.14	78.53	1.9E-06
Rph	0.32	78.36	1.1E-12
scro	0.95	78.05	0.0E+00
CG3906	0.48	77.92	3.1E-09
5-HT2B	0.25	77.85	0.0E+00
robo3	0.34	77.82	0.0E+00
CG42825	0.18	77.73	2.7E-07
CG7589	1.61	77.08	0.0E+00
dpr12	1.50	77.01	0.0E+00
CG15373	0.10	76.64	8.8E-07
Pxt	0.20	76.44	1.5E-11
CG11566	0.04	76.42	4.7E-05
Adef-D	3.04	76.38	0.0E+00
CG17562	3.38	76.34	6.8E-12
CG46298	0.29	76.10	1.1E-05
CG3597	5.47	75.79	0.0E+00
CG15478	0.11	75.77	1.5E-06
HF	5.90	75.74	0.0E+00
ACXA	0.02	75.48	1.8E-03
ppk20	0.04	75.48	1.8E-03
CG5755	0.04	75.48	1.8E-03
CG14113	0.12	75.48	1.8E-03
CG15337	0.05	75.48	1.6E-03
CG1387	0.02	75.48	1.6E-03
CG42867	0.17	75.48	1.6E-03
Ir67b	0.03	75.48	1.6E-03
CG17732	0.03	75.48	1.6E-03
Bsg25A	0.05	75.48	1.0E-03
fa2h	0.05	75.48	1.6E-03
prim	0.14	75.48	1.6E-03
CG43168	0.06	75.48	1.6E-03
CG7906	0.05	75.48	1.6E-03
stg1	0.02	75.47	1.5E-03
CG7179	0.03	75.47	1.5E-03
CG18577	0.09	75.47	1.5E-03
CG13984	0.11	75.47	1.5E-03
CG4650	0.07	75.47	1.5E-03
CG16998	0.09	75.47	1.5E-03
CG11698	0.08	75.47	1.4E-03
CG31220	0.05	75.47	1.4E-03
CG15719	0.08	75.47	1.4E-03
Ir7a	0.04	75.47	9.6E-04
CG9016	0.10	75.47	9.6E-04
CG34162	0.04	75.47	9.6E-04
CG32232	0.03	75.46	1.2E-03
CG17625	0.14	75.46	1.2E-03
CG34429	0.10	75.46	1.2E-03
tombboy20	0.10	75.46	1.2E-03
CG30177	0.05	75.46	1.1E-03
AstCC	0.06	75.46	1.1E-03
laf	0.03	75.46	1.1E-03
CG12994	0.07	75.36	2.9E-03
Acp26Aa	0.08	75.36	2.9E-03
CG18420	0.04	75.36	2.9E-03
CG31806	0.12	75.36	2.9E-03
CG34259	0.06	75.36	2.9E-03
CG32024	0.11	75.36	2.9E-03
ind	0.07	75.36	2.9E-03
CG13723	0.14	75.36	2.9E-03
CG31275	0.13	75.36	2.9E-03
CG14316	0.05	75.36	2.9E-03
CG10183	0.04	75.36	2.9E-03
CG13972	0.06	75.36	2.9E-03
Ork1	0.67	75.30	0.0E+00
CG15760	0.36	75.26	0.0E+00
CG31551	0.09	75.21	1.1E-06
Sox21a	0.07	75.16	1.1E-04
CG9657	0.48	74.31	3.0E-12
CG1889	0.18	74.25	6.7E-07
dpr19	0.53	74.12	0.0E+00
CG18208	0.79	73.92	0.0E+00
CG43678	0.59	73.73	2.4E-04
Gycalpa99B	1.39	73.53	0.0E+00
Lmx1a	0.08	73.50	1.2E-06
Sh	1.78	73.40	0.0E+00
CG13288	0.07	73.32	6.4E-05
beat-Vb	0.15	73.27	2.7E-08
CG6332	0.22	73.26	5.4E-08
CG15403	0.14	73.24	4.6E-04
CG31016	0.03	73.24	4.6E-04
CG44014	2.11	73.16	0.0E+00
TyrR	0.20	72.99	0.0E+00



CG42313	0.45	72.94	0.0E+00
beat-IIIa	0.13	72.91	3.7E-12
CG15270	0.45	72.85	0.0E+00
GC2	0.14	72.33	7.6E-05
Spn88Eb	6.06	72.19	0.0E+00
CG7166	0.58	71.94	0.0E+00
dpr8	0.44	71.91	0.0E+00
CG12158	0.50	71.78	7.5E-05
ldgf5	3.35	71.47	0.0E+00
CG4660	0.28	71.38	3.8E-08
CG14274	0.20	71.09	7.4E-09
CG18063	0.06	70.87	2.8E-03
CG31802	0.09	70.87	2.8E-03
CG13810	0.05	70.87	2.8E-03
CG8750	0.12	70.87	2.8E-03
CG13700	0.04	70.87	2.8E-03
CG34260	0.14	70.87	2.8E-03
CG11404	0.09	70.87	2.8E-03
CG14370	0.10	70.87	2.8E-03
CG14244	0.15	70.87	2.8E-03
CG10912	0.32	70.78	1.9E-06
Obp99c	58.51	70.76	0.0E+00
nolo	1.10	70.48	0.0E+00
lov	0.13	70.40	2.6E-14
ort	0.15	70.33	1.1E-07
GluRIA	0.16	70.16	2.7E-13
CG6329	2.59	69.95	0.0E+00
CG31769	4.61	69.90	0.0E+00
CG31326	5.98	69.89	0.0E+00
CG8197	0.11	69.59	1.3E-04
CG13325	0.04	69.50	4.7E-04
CG6123	0.41	69.42	0.0E+00
CG13739	0.61	69.41	0.0E+00
Frg1	1.13	69.39	0.0E+00
CG4835	0.05	69.31	8.4E-06
Aplp1	0.82	69.27	0.0E+00
Teh2	1.28	68.93	0.0E+00
CG33120	3.00	68.30	0.0E+00
CG34384	0.74	68.11	0.0E+00
Or45a	0.43	68.00	0.0E+00
Toll-9	0.06	67.88	7.8E-06
CS-2	0.04	67.56	5.8E-06
CG42404	0.36	67.41	0.0E+00
Rx	0.08	67.32	1.2E-05
Syt7	1.48	67.28	0.0E+00
CG14499	0.20	67.01	4.6E-04
dpr1	0.54	66.92	0.0E+00
CG10096	0.34	66.84	1.5E-13
CG16898	0.52	66.44	5.8E-12
sff	0.53	66.24	0.0E+00
CG31089	0.09	66.10	1.4E-04
CG44098	0.87	65.73	0.0E+00
CG33143	0.53	65.70	0.0E+00
CG11700	0.39	65.62	1.4E-08
CG17364	0.18	65.60	0.0E+00
CG30371	8.01	65.14	3.7E-12
CG15631	0.07	65.01	5.7E-04
CG4161	0.10	64.54	1.2E-05
Rab3-GEF	1.11	64.49	0.0E+00
CG13794	1.15	64.32	2.1E-15
Drs	43.87	64.29	0.0E+00
aqrs	0.10	64.28	1.4E-04
lush	1.62	64.25	7.9E-07
Dh44-R1	0.20	63.97	7.3E-09
DNaseII	7.70	63.96	0.0E+00
CG7990	1.03	63.91	0.0E+00
teq	7.76	63.79	0.0E+00
CG45002	0.63	63.64	0.0E+00
CG14579	0.49	63.64	2.4E-07
trv	0.81	63.37	0.0E+00
CG15651	0.24	63.13	1.9E-12
Npc1b	0.06	63.12	5.7E-05
alpha-Catr	0.49	62.90	0.0E+00
IA-2	7.50	62.74	0.0E+00
CG11099	0.89	62.66	0.0E+00
CG3775	2.36	62.47	0.0E+00
Tbh	0.53	62.27	1.4E-14
CG45782	1.58	62.05	0.0E+00
dpr18	0.89	61.92	0.0E+00
CG31659	0.17	61.84	1.0E-04
CG18585	0.09	61.73	6.5E-05
CG43330	0.21	61.73	4.2E-05
CG6435	0.15	61.72	3.8E-05
Toll-4	0.04	61.72	7.6E-05
Orcokinin	0.53	61.62	6.9E-08
Ir8a	0.08	61.57	6.7E-06
CG33493	5.58	61.50	0.0E+00
IM33	46.36	61.30	0.0E+00
kek4	0.60	61.23	2.1E-12
BigH1	0.16	61.21	5.2E-06
Mdr50	0.15	61.11	3.1E-11
Rbp	0.67	61.10	0.0E+00
CG14196	2.18	61.10	0.0E+00
CG13912	1.76	61.05	0.0E+00
CG33458	0.51	60.74	5.7E-07
CG6429	0.51	60.53	5.3E-07
P5CDh2	0.57	60.52	0.0E+00
CG3515	0.15	60.30	4.1E-05
CG32683	0.24	60.11	0.0E+00
alpha-Man-Ic	1.91	59.81	0.0E+00
santa-maria	0.69	59.76	0.0E+00
Cow	3.56	59.09	0.0E+00
Uch-L5R	0.12	58.96	6.4E-04
CG12438	0.16	58.80	6.5E-04
sm	2.10	58.70	0.0E+00
CG7708	0.91	58.68	0.0E+00
CG31207	0.34	58.53	4.0E-09
CG14118	0.20	58.37	6.5E-07
5-HT2A	0.77	58.35	0.0E+00
CG4706	0.03	58.28	8.1E-04
CG2736	13.53	58.14	0.0E+00

D	0.56	58.08	0.0E+00
dpr16	0.34	58.02	6.1E-09
CG14082	0.19	57.85	6.3E-15
CG18368	0.05	57.85	4.2E-05
CG13360	24.30	57.77	0.0E+00
CG15068	71.20	57.77	0.0E+00
Appl	5.24	57.43	0.0E+00
eEF1alpha2	4.34	57.30	0.0E+00
CG7888	2.63	57.16	0.0E+00
Cyp309a1	0.68	56.85	4.2E-15
CG34106	0.07	56.50	4.8E-08
CG8539	1.04	56.01	1.0E-11
yellow-f2	2.01	55.99	0.0E+00
CanB	1.22	55.89	0.0E+00
BicC	0.16	55.67	1.1E-08
DIP-beta	0.23	55.25	8.3E-15
Fie	2.31	55.25	0.0E+00
CG1090	1.23	55.24	0.0E+00
ssp6	0.24	55.22	0.0E+00
CG42810	0.43	55.01	5.8E-07
Cp38	0.57	54.82	1.1E-08
Ugt86Dc	0.23	54.54	1.1E-07
CG15522	0.17	54.44	1.4E-07
Rim	0.94	54.39	0.0E+00
Dscam4	0.61	54.32	0.0E+00
Cp7Fc	0.93	54.15	6.5E-13
Sep4	0.83	54.09	0.0E+00
apolpp	140.48	54.07	0.0E+00
CG42346	0.40	53.77	0.0E+00
Crg-1	0.22	53.67	1.6E-07
CG34188	0.53	53.57	2.4E-10
Syn	1.90	53.42	0.0E+00
Prosalpha1	2.85	53.32	3.9E-05
slo	2.07	53.25	0.0E+00
CG4168	0.53	53.06	0.0E+00
Syt4	2.50	53.01	0.0E+00
CG13634	0.04	52.89	1.0E-03
CG31872	0.10	52.79	1.1E-07
CG12817	0.29	52.66	2.2E-06
Myo81F	0.27	52.60	0.0E+00
RunxA	0.10	52.58	3.7E-07
pre-mod(mdg4)-K	0.41	52.39	1.9E-06
stl	0.19	52.36	3.6E-11
ppk3	0.11	52.31	7.6E-05
FASN2	10.20	52.29	0.0E+00
CG14736	0.09	52.29	3.7E-04
CG14052	0.05	52.25	6.2E-03
CG8117	0.06	52.25	6.2E-03
Cyp308a1	0.03	52.25	6.2E-03
CG30265	0.03	52.25	6.2E-03
CG3748	0.02	52.25	6.2E-03
CG4218	0.04	52.25	6.3E-03
CG42357	0.03	52.25	6.3E-03
CG7304	0.03	52.25	6.3E-03
CG33769	0.09	52.25	6.4E-03
CG33770	0.08	52.25	6.4E-03
CG34309	0.08	52.25	6.4E-03
CG42446	0.04	52.25	6.4E-03
Indy-2	0.01	52.25	6.3E-03
CG34432	0.07	52.25	6.3E-03
Teh3	0.71	52.09	0.0E+00
Nplp1	1.09	52.03	0.0E+00
CG31104	0.21	51.93	7.7E-07
CG42704	0.86	51.83	5.7E-07
CG8072	0.09	51.68	1.0E-03
CG31664	0.38	51.61	2.6E-12
rtp	1.71	51.61	0.0E+00
nimaA	0.80	51.60	8.4E-08
Gr59e	0.03	51.51	6.5E-03
CG15425	0.05	51.51	6.5E-03
CG34181	0.05	51.51	6.5E-03
Or33a	0.03	51.51	6.5E-03
CG15140	0.03	51.51	6.5E-03
CG5592	0.02	51.51	6.5E-03
CG6885	0.03	51.51	6.5E-03
CG15177	0.04	51.51	6.5E-03
CG31446	0.04	51.51	6.5E-03
CG11951	1.53	51.30	0.0E+00
CG8343	0.23	51.25	1.8E-04
meth7	0.17	51.08	1.4E-04
CG4009	0.11	51.08	1.4E-04
CG3246	6.68	50.83	0.0E+00
Ilp4	0.15	50.78	9.1E-04
CG9928	18.32	50.58	0.0E+00
CG43997	0.08	50.56	5.4E-03
CG6290	0.06	50.56	5.4E-03
CG10081	0.02	50.56	5.4E-03
CG15172	0.06	50.56	5.4E-03
His2B:CG33872	0.07	50.56	5.4E-03
CG5768	0.04	50.56	5.4E-03
CG3687	0.07	50.56	5.4E-03
CG3215	0.04	50.56	5.4E-03
CG42383	0.04	50.56	5.4E-03
Gr23a	0.02	50.56	5.4E-03
CG44521	0.07	50.56	5.4E-03
CG13455	0.04	50.56	5.4E-03
CG31418	0.07	50.56	5.4E-03
CG13614	0.05	50.56	5.4E-03
CG34433	0.06	50.56	5.4E-03
Sr-CII	0.02	50.56	5.4E-03
Hr51	0.02	50.56	5.4E-03
CG3347	0.02	50.56	5.4E-03
CG18109	0.01	50.56	5.4E-03
CG10168	0.02	50.56	5.4E-03
CG18672	0.04	50.56	5.4E-03
CG6048	0.05	50.55	5.5E-03
CG10920	0.03	50.55	5.5E-03
Ir11a	0.03	50.55	5.5E-03
CG32651	0.01	50.55	5.6E-03
CG12986	0.10	50.55	5.6E-03
Ser6	0.06	50.55	5.6E-03

CG1946	0.04	50.55	5.6E-03
SkpF	0.08	50.55	5.6E-03
CG3640	0.05	50.55	5.6E-03
CG12511	0.06	50.55	5.7E-03
COX5BL	0.08	50.55	5.7E-03
CG45307	0.13	50.55	5.7E-03
CG9582	0.04	50.55	5.7E-03
CG18302	0.02	50.55	5.7E-03
CG31867	0.06	50.55	5.7E-03
CG31862	0.08	50.55	5.8E-03
wor	0.02	50.55	5.8E-03
CG32388	0.05	50.55	5.8E-03
CG43885	0.12	50.55	5.8E-03
CG32228	0.02	50.55	5.8E-03
Osi11	0.04	50.55	5.9E-03
CG3809	0.04	50.55	5.9E-03
CG5265	0.02	50.55	5.9E-03
Dup99B	0.17	50.55	5.9E-03
CG34025	0.04	50.55	5.4E-03
CG14625	0.02	50.55	5.4E-03
CG4892	0.05	50.55	5.4E-03
Gr10b	0.04	50.55	5.4E-03
Ir52a	0.03	50.55	5.4E-03
CG9068	0.01	50.55	5.4E-03
Nrf-2r	0.07	50.55	5.4E-03
CG5906	0.06	50.55	5.4E-03
CG18231	0.03	50.55	5.4E-03
TengI4	0.04	50.55	5.4E-03
CG43288	0.15	50.55	5.4E-03
CG5662	0.05	50.55	5.4E-03
Gr59a	0.05	50.55	5.4E-03
Gr59b	0.05	50.55	5.4E-03
Or22c	0.04	50.55	5.4E-03
CG43760	0.12	50.55	5.4E-03
CG43083	0.12	50.55	5.4E-03
Adgf-B	0.03	50.55	5.4E-03
CG33647	0.09	50.55	5.4E-03
CG43392	0.16	50.55	5.4E-03
Osi4	0.03	50.55	5.4E-03
CG33325	0.05	50.55	5.4E-03
CCha2	2.15	50.47	4.2E-15
CG10352	0.37	50.08	2.5E-10
CG45084	0.11	50.01	5.5E-09
Hmx	0.02	49.99	4.3E-04
GABA-B-R1	0.69	49.88	0.0E+00
CG32395	0.09	49.78	4.2E-04
CG43064	0.85	49.76	0.0E+00
kat-60L1	0.23	49.67	1.1E-10
CG16716	0.18	49.66	6.7E-11
CG34190	0.13	49.65	5.4E-05
CG12116	7.98	49.58	0.0E+00
ana	0.29	49.46	1.3E-12
Or67d	0.08	49.46	2.1E-04
CG10014	0.07	49.46	1.3E-04
nerfin-2	0.04	49.46	2.3E-04
CG34217	0.13	49.46	3.6E-04
CG43789	0.42	49.46	1.1E-04
CG5968	0.24	49.45	1.7E-04
Muc91C	0.03	49.45	9.9E-05
SA-2	0.03	49.45	9.7E-05
CG10713	0.04	49.45	1.8E-04
RabX2	0.12	49.45	2.5E-04
CG34377	0.02	49.45	2.3E-04
CG31189	0.11	49.45	1.1E-04
CG13871	0.06	49.44	1.9E-04
Gr33a	0.06	49.44	3.1E-04
CG6628	0.09	49.44	3.0E-04
Mur82C	0.05	49.42	3.9E-04
CG13299	0.44	49.38	4.2E-05
gnu	0.16	49.10	1.3E-05
BG642163	0.10	49.08	2.1E-05
CG46318	0.08	49.04	5.7E-04
CG4409	0.57	49.03	3.5E-08
CG45603	0.38	48.91	2.7E-06
CG10508	0.56	48.85	0.0E+00
PGRP-SD	9.25	48.79	0.0E+00
Cdk5alpha	1.87	48.66	0.0E+00
CG30431	0.43	48.65	4.1E-08
AlkR	1.15	48.60	0.0E+00
Rh7	0.32	48.45	2.1E-15
CG13423	0.10	48.43	8.6E-05
PGRP-SB2	0.28	48.40	7.5E-06
X11Lbeta	0.52	48.28	0.0E+00
Ca-alpha1T	1.30	47.78	0.0E+00
Bace	0.28	47.78	8.9E-06
CG15394	3.85	47.56	1.0E-14
CG9507	0.43	47.52	9.8E-14
CG13999	0.44	47.40	1.3E-08
CG30048	0.03	47.38	1.3E-03
ACXE	0.03	47.38	1.3E-03
para	2.38	47.38	0.0E+00
Cyp311a1	0.62	47.36	2.0E-14
Gyc32E	0.04	47.30	7.0E-05
CG10804	0.59	46.67	0.0E+00
Igt86Dh	0.08	46.65	5.6E-04
CG15169	0.13	46.62	5.4E-05
CecA2	0.72	46.47	3.5E-06
beat-IV	0.52	46.31	0.0E+00
amon	1.68	46.22	0.0E+00
CG6220	0.31	46.17	6.6E-11
pHCl-1	0.41	46.13	0.0E+00
CG15570	0.08	45.98	8.9E-07
CG7582	0.93	45.95	1.2E-14
CG32695	1.55	45.93	0.0E+00
beat-Vc	0.08	45.87	2.1E-05
Tsp42EJ	2.23	45.85	0.0E+00
Lcch3	0.67	45.83	0.0E+00
CG34109	0.12	45.82	1.6E-05
CG1315	1.07	45.81	3.5E-10
PK2-R1	0.06	45.39	1.7E-04
ase	0.05	45.22	7.6E-04

CG11052	0.14	45.22	7.6E-04
CG34253	3.36	45.22	3.4E-11
stj	1.09	45.19	0.0E+00
Tusp	0.38	44.94	0.0E+00
Shab	1.69	44.85	0.0E+00
ms(2)34Fe	0.05	44.78	3.5E-05
Fer2	0.20	44.68	1.3E-07
CG13458	0.30	44.67	2.5E-06
YhaM9.7-a	1.56	44.55	1.0E-14
Task6	0.28	44.54	0.0E+00
CG5937	0.48	44.48	0.0E+00
CG32488	0.09	44.48	4.4E-04
wech	11.55	44.47	0.0E+00
dpr14	0.33	44.24	4.2E-15
TTL3A	0.04	44.14	4.0E-04
Epac	0.90	44.01	0.0E+00
orb	0.47	43.99	0.0E+00
Dic4	0.05	43.83	1.3E-03
smog	0.60	43.64	0.0E+00
CG42367	0.14	43.47	2.0E-03
Gr64a	0.05	43.47	2.0E-03
hmw	0.11	43.28	5.1E-06
CG3513	0.96	43.06	5.9E-08
CG32506	0.24	42.85	8.1E-13
CG13337	0.06	42.83	2.1E-05
eIF4E4	0.16	42.82	9.1E-06
CG7295	0.13	42.81	1.5E-05
onecut	1.42	42.74	0.0E+00
CG15894	0.37	42.74	2.1E-15
PH4alphaPV	0.12	42.69	5.3E-05
Cp16	0.23	42.56	1.3E-03
Tehao	0.13	42.51	1.7E-08
miple1	5.36	42.38	0.0E+00
CG10357	0.36	42.30	2.7E-05
CG31343	0.15	42.08	1.3E-06
nrv3	10.74	42.05	0.0E+00
CG6356	2.11	42.01	0.0E+00
CG17778	0.66	41.91	1.5E-09
CG10911	0.24	41.68	1.4E-05
anthd	0.89	41.66	9.3E-06
CG10560	34.01	41.54	2.2E-09
stet	0.13	41.22	1.6E-07
CG6280	0.04	41.14	9.0E-04
jus	1.13	41.11	0.0E+00
CG44247	1.81	40.97	0.0E+00
CG13305	0.09	40.96	1.1E-04
kappaTry	0.13	40.95	2.4E-04
Erk7	0.03	40.95	6.4E-05
CG31235	0.05	40.94	1.3E-04
CG7135	1.55	40.72	2.1E-15
CG8245	0.98	40.57	4.5E-11
Teh1	0.26	40.47	8.3E-15
CG17375	0.06	40.32	2.3E-03
DrsI3	0.20	40.32	2.3E-03
mAChr-B	0.39	39.95	2.1E-15
CG42392	1.71	39.94	1.8E-14
pgc	0.27	39.70	3.7E-06
NPF	0.34	39.64	1.2E-05
Gnmt	10.84	39.17	0.0E+00
CG7264	0.92	39.03	8.3E-06
CG33017	0.05	39.03	8.9E-06
CG8129	1.52	38.88	0.0E+00
Gat	0.78	38.82	0.0E+00
Muc96D	0.49	38.79	0.0E+00
CG11298	0.40	38.74	2.0E-05
Rab3	2.14	38.62	0.0E+00
betaNActes3	0.08	38.41	2.5E-03
CG14605	0.06	38.36	1.1E-03
CG8641	0.21	38.32	5.7E-13
CheB42c	3.31	38.22	0.0E+00
FASN3	17.23	38.11	1.4E-12
CG14125	0.19	37.98	3.9E-05
igl	1.20	37.91	0.0E+00
Adar	22.58	37.90	1.0E-14
CG32750	0.08	37.83	1.6E-03
CG15306	0.08	37.83	1.6E-03
CG17378	0.59	37.77	0.0E+00
Gba1b	0.95	37.73	0.0E+00
CG30172	0.89	37.71	1.4E-12
CG31204	0.20	37.69	3.0E-05
Obp84a	0.32	37.49	2.4E-04
tutI	1.80	37.36	0.0E+00
CG42284	0.12	37.35	2.7E-04
ND-B8	0.43	37.31	2.8E-05
CG17264	0.28	37.31	4.7E-10
Hr4	1.89	37.24	0.0E+00
CG10887	0.03	37.19	1.3E-03
Or43a	0.05	37.19	1.2E-03
CG45063	0.08	37.18	1.5E-03
Or59b	0.04	37.18	1.5E-03
CG42705	0.08	37.18	1.4E-03
CG13055	0.02	37.18	7.1E-04
Mal-A4	0.04	37.18	1.3E-03
CG11369	0.03	37.18	1.2E-03
Zip42C1	0.06	37.18	1.2E-03
Or85a	0.06	37.18	1.2E-03
Vmi32E	0.14	37.18	5.8E-04
CG15056	0.05	37.17	9.4E-04
CG8642	0.04	37.17	9.8E-04
Ser12	0.09	37.17	8.5E-04
CG11449	0.12	37.02	1.2E-05
Optix	0.22	36.91	6.7E-08
CG9164	0.20	36.88	3.4E-10
CG5342	0.06	36.84	2.0E-04
CG4404	2.14	36.84	0.0E+00
Irk2	2.39	36.77	0.0E+00
CG32106	0.03	36.73	8.5E-05
Cycj	0.09	36.73	1.1E-04
CrzR	1.06	36.72	0.0E+00
CG43710	0.15	36.72	1.0E-04
CG6738	0.40	36.72	7.0E-09

CG43218	0.21	36.72	4.4E-05
Ugt37a1	0.14	36.58	4.5E-07
CG9109	0.12	36.58	2.7E-07
dpr5	0.12	36.57	5.8E-07
CG12699	0.12	36.54	1.2E-03
CG6304	0.06	36.54	1.2E-03
Tace	0.26	36.41	4.0E-12
Nrx-1	1.32	36.24	0.0E+00
CadN2	0.30	36.22	0.0E+00
CG4781	0.05	36.20	2.2E-03
inaF-D	0.04	36.09	1.7E-03
Npc2e	0.49	35.95	1.1E-06
CG9555	0.15	35.72	1.2E-05
CG4335	1.73	35.57	6.3E-15
CG9368	0.24	35.54	2.2E-10
CG6495	0.57	35.51	4.2E-15
Gvc88E	0.18	35.47	2.8E-11
dpr3	0.31	35.46	2.0E-13
CecA1	0.82	35.45	1.7E-05
Nep5	0.29	35.12	4.8E-10
CG32834	0.28	35.11	1.8E-08
Mur2B	1.38	35.06	0.0E+00
ssp7	24.56	34.99	0.0E+00
CG14877	0.11	34.95	1.6E-05
CG2528	0.01	34.70	2.7E-03
HHEX	0.17	34.62	1.1E-05
dmrt99B	0.03	34.59	2.7E-03
dsb	1.30	34.54	0.0E+00
CG34021	0.16	34.53	1.2E-03
CG5538	0.29	34.30	3.7E-06
CG42759	0.45	34.16	1.2E-04
CG32115	0.45	34.02	9.5E-10
CG11000	0.89	33.96	0.0E+00
Patsas	0.34	33.94	1.1E-12
CG16743	2.65	33.93	0.0E+00
Dhc98D	0.06	33.42	4.6E-14
CG34180	1.68	33.29	5.2E-10
CG30259	0.08	33.15	7.6E-04
Gbp3	5.59	33.15	0.0E+00
TotA	10.84	33.08	0.0E+00
Igr4	0.15	33.03	3.0E-09
Oct-TyrR	0.15	32.95	3.8E-11
CG46321	0.08	32.92	1.3E-04
His4-CG33871	0.19	32.81	5.1E-04
CG9173	0.04	32.80	4.8E-04
exex	0.04	32.80	3.6E-04
CG8907	0.31	32.80	1.8E-09
Cvp12d1-p	0.84	32.71	0.0E+00
pb	0.05	32.64	1.2E-05
hiw	0.84	32.62	0.0E+00
CG6765	0.58	32.57	0.0E+00
Ir40a	0.09	32.56	2.2E-05
Hex-C	3.34	32.53	0.0E+00
osk	0.16	32.51	7.4E-07
CG43902	0.42	32.49	0.0E+00
CG9541	0.11	32.47	6.3E-07
CG34354	0.46	32.47	0.0E+00
CG9766	0.55	32.39	9.9E-10
iav	0.11	32.38	1.5E-09
Cyp309a2	0.27	32.37	2.9E-05
Lim3	0.11	32.36	2.8E-10
CG8910	0.19	32.28	6.3E-09
inaD	1.01	32.25	0.0E+00
dj	0.12	31.93	4.5E-04
CG42594	0.32	31.88	0.0E+00
CG13868	7.38	31.83	0.0E+00
CG32547	0.17	31.73	2.9E-10
CG7079	0.26	31.59	8.2E-08
Cpr47Ee	0.19	31.55	6.0E-07
shakB	0.88	31.50	0.0E+00
CG7781	2.59	31.42	0.0E+00
dao	0.53	31.37	0.0E+00
CG14312	0.45	31.37	8.4E-06
DIP-eta	0.25	31.30	2.2E-12
Lip4	0.85	31.20	0.0E+00
SK	0.98	31.19	0.0E+00
lhbq	99.10	31.15	5.2E-07
CheB98a	0.17	31.10	1.4E-03
CG33340	0.09	31.03	2.4E-03
CG17324	0.20	30.90	5.4E-06
CG7384	0.57	30.84	0.0E+00
Kr	0.21	30.84	1.2E-07
sPLA2	2.80	30.76	0.0E+00
Cyp6w1	22.98	30.67	0.0E+00
CG46026	0.06	30.64	1.3E-04
CG13511	0.05	30.63	7.9E-05
dmrt93B	0.12	30.63	1.3E-04
CG18765	0.17	30.55	1.5E-05
CG17666	0.09	30.41	1.9E-06
beat-IIB	0.13	30.40	8.4E-08
nerfin-1	0.04	30.37	1.9E-04
CG11294	0.10	30.36	3.4E-04
CG7607	2.45	30.27	1.1E-12
CG43071	0.47	30.15	2.0E-05
CG3257	0.24	30.12	4.0E-09
crv	5.23	30.09	0.0E+00
CG17739	3.21	29.97	0.0E+00
CG16704	8.79	29.93	1.9E-12
CG14545	0.20	29.81	4.7E-04
CHAT	0.48	29.79	0.0E+00
CG13795	2.52	29.77	0.0E+00
S-HT1B	0.13	29.71	4.8E-06
CG1561	0.77	29.55	0.0E+00
CG14339	0.13	29.50	1.4E-09
swa	0.07	29.34	1.6E-04
CG5493	1.04	29.33	4.6E-13
CG31690	0.19	29.12	2.1E-10
Sln	0.18	29.09	8.9E-12
CG43795	0.26	29.05	1.0E-14
CG43693	2.50	28.95	0.0E+00
Ance-4	3.06	28.67	0.0E+00

Spat	7.85	28.63	0.0E+00
CG5080	2.70	28.54	0.0E+00
Ion74E	0.42	28.51	1.6E-06
danr	0.09	28.48	1.5E-05
CG12866	0.05	28.48	4.0E-05
CG13995	0.71	28.36	0.0E+00
CG6024	0.71	28.36	0.0E+00
slp1	0.24	28.34	1.7E-07
Cyp6a20	5.10	28.32	0.0E+00
NPR	0.10	28.28	9.9E-07
CG10116	0.35	28.19	4.6E-06
CG46308	0.27	28.17	4.6E-07
CG6168	0.12	28.12	3.1E-04
dati	0.86	28.07	0.0E+00
CG10226	1.83	28.05	0.0E+00
disco	0.71	28.02	0.0E+00
CG42366	0.17	27.99	3.1E-06
repo	0.61	27.98	0.0E+00
CG9875	0.16	27.98	2.7E-03
CG11381	0.25	27.94	3.3E-07
CG5892	0.08	27.93	8.7E-06
Corin	0.88	27.91	0.0E+00
Vmat	1.35	27.90	0.0E+00
CG43448	0.36	27.87	1.8E-05
nos	0.09	27.77	4.1E-06
Cyp6a22	0.53	27.72	1.3E-13
CG14535	0.17	27.70	1.4E-10
Mur29B	0.21	27.65	6.2E-08
CG4271	0.15	27.63	1.6E-03
CG12885	0.11	27.62	2.5E-06
CG13532	0.24	27.52	4.1E-08
Dop1R2	0.17	27.52	1.6E-09
CG31528	0.12	27.52	2.3E-04
CG31704	0.83	27.50	3.6E-08
CG31157	0.71	27.39	3.5E-09
CG32032	5.25	27.34	0.0E+00
CG12541	0.17	27.30	1.4E-09
bru1	0.75	27.28	0.0E+00
CecB	0.72	27.27	9.4E-06
CG13650	0.83	27.27	2.6E-14
CCHa1-R	0.09	27.25	4.7E-05
Rdh	1.86	27.19	2.8E-10
CG9396	4.03	27.19	1.8E-14
CG14153	1.60	27.18	1.2E-12
CG12374	0.20	27.07	9.9E-06
pgant4	0.10	27.04	3.5E-06
CG31974	1.20	26.99	0.0E+00
CG14717	0.07	26.85	6.5E-04
Hk	1.00	26.77	0.0E+00
Dsk	1.64	26.68	8.4E-09
bma	0.29	26.64	0.0E+00
CG13155	0.13	26.57	4.0E-03
mACHR-A	0.53	26.52	0.0E+00
GILT2	3.09	26.43	4.0E-14
Diedel3	0.03	26.41	4.1E-03
Obp44a	3.42	26.40	0.0E+00
CG13806	0.12	26.33	5.8E-04
CG14106	0.06	26.32	4.6E-03
Cyp28c1	0.10	26.19	3.2E-05
arg	1.91	26.18	2.1E-13
Cyp304a1	0.70	26.13	3.6E-09
Nlg3	0.43	26.09	0.0E+00
Crz	1.90	26.07	3.3E-09
slp2	0.15	26.02	1.8E-08
CG15537	0.22	26.02	5.4E-07
CG13594	0.13	25.99	7.0E-08
CG31886	0.71	25.96	0.0E+00
CG6785	0.40	25.92	6.2E-08
CG13086	1.05	25.81	3.5E-09
Octbeta3R	0.22	25.80	2.4E-11
CG11671	0.44	25.79	5.1E-05
AttD	0.18	25.79	2.2E-03
CG9837	1.01	25.73	0.0E+00
CG4269	0.83	25.61	3.4E-12
CG15199	1.53	25.56	2.2E-09
CG12725	0.58	25.45	1.6E-07
fest	0.05	25.42	2.6E-04
CG9649	2.31	25.42	0.0E+00
Ion99Ciii	0.15	25.41	2.6E-04
CG8701	0.98	25.37	3.2E-13
ilp3	0.35	25.36	4.3E-05
na	0.33	25.35	0.0E+00
gudu	0.02	25.30	9.5E-03
I-t	0.05	25.30	9.5E-03
CG14380	0.05	25.30	9.5E-03
Or92a	0.04	25.30	9.5E-03
CG7470	3.55	25.30	0.0E+00
CG43777	0.02	25.27	9.3E-03
CG4302	3.72	25.26	0.0E+00
Bili	0.35	25.21	4.2E-15
CG34357	0.72	25.21	0.0E+00
CG43673	0.20	25.20	2.9E-04
CG15468	0.12	25.14	2.0E-04
CG43114	10.76	25.13	1.1E-08
CG18649	0.22	25.11	7.2E-04
CG5171	2.57	25.10	0.0E+00
CG6262	0.02	25.09	1.4E-03
Rgk1	0.27	25.09	0.0E+00
CG5327	0.10	25.07	1.5E-03
CG13577	0.02	25.07	9.6E-03
TwdlQ	0.04	25.07	9.6E-03
CG10587	0.05	25.03	9.7E-03
CG1894	0.03	25.03	9.7E-03
Ac3	0.74	24.92	0.0E+00
Or42b	0.03	24.91	9.5E-03
CG33125	0.01	24.91	9.5E-03
CG16732	0.03	24.91	5.5E-03
CG5614	0.04	24.91	5.4E-03
Ir56c	0.03	24.91	8.7E-03
CG33965	0.05	24.91	8.7E-03
CG8093	0.03	24.91	6.1E-03

Or42a	0.03	24,91	6,2E-03
CG30270	0.08	24,91	5,0E-03
CG32642	0.03	24,91	5,5E-03
sowi	0.06	24,90	5,0E-03
CG43397	0.05	24,90	8,8E-03
nht	0.06	24,90	8,8E-03
CG15219	0.10	24,90	8,8E-03
CG42536	0.07	24,90	8,8E-03
Dnai2	0.03	24,90	8,8E-03
intr	0.06	24,90	8,7E-03
CG1999	0.05	24,90	9,0E-03
CG12376	0.03	24,90	9,0E-03
Mur11Da	0.03	24,90	9,3E-03
CG5565	0.06	24,90	9,3E-03
Osi13	0.03	24,90	9,3E-03
CG12674	0.04	24,90	5,4E-03
CG13526	0.07	24,90	5,3E-03
CG9988	0.02	24,90	5,0E-03
CG5883	0.04	24,90	5,2E-03
CG45011	0.12	24,90	7,5E-03
CG34266	0.12	24,90	7,5E-03
snky	0.02	24,90	7,5E-03
CG44954	0.06	24,90	7,5E-03
CG32751	0.03	24,90	7,9E-03
CG14515	0.08	24,90	8,1E-03
Diedel	0.12	24,90	8,1E-03
CG13685	0.57	24,88	5,2E-14
CG13949	0.07	24,83	3,2E-03
CG15533	0.03	24,82	2,7E-03
side	0.34	24,77	0,0E+00
CG5282	0.41	24,76	1,6E-07
CG10433	14,97	24,76	0,0E+00
alphaTry	1,27	24,70	1,5E-06
CG3942	0.03	24,67	2,3E-03
CG43788	0.20	24,67	1,2E-03
ord	0.02	24,67	1,6E-03
CG33934	0.02	24,67	1,5E-03
Or94a	0.06	24,67	1,5E-03
CG12970	0.06	24,67	2,3E-03
CG10202	0.03	24,67	1,4E-03
Osi23	0.08	24,67	1,4E-03
spag4	0.06	24,67	1,5E-03
Ag5r2	0.09	24,66	1,8E-03
CG5379	0.05	24,66	2,3E-03
CG42493	0.12	24,66	6,9E-04
wrapper	0.27	24,66	8,3E-10
Dat	9,75	24,63	0,0E+00
CG8586	3,05	24,61	0,0E+00
eIF3g2	0.09	24,55	9,2E-04
CG14540	0.04	24,54	5,8E-04
CG15930	0.05	24,54	7,6E-04
CG14327	0.88	24,50	1,4E-06
CG14905	0.04	24,50	2,6E-03
CG30472	0.13	24,48	3,7E-04
Hsc70-1	0.57	24,48	1,3E-12
cola	0.35	24,44	3,6E-10
CG14838	0.04	24,43	8,8E-05
Sidpn	0.07	24,39	1,0E-05
CG34002	0.21	24,33	3,1E-07
Shaw	0.48	24,32	0,0E+00
CG9616	0.70	24,27	1,2E-05
CG14314	0.24	24,27	4,3E-08
ST6Gal	0.22	24,26	7,6E-11
Odc2	0.44	24,25	2,9E-10
TrissinR	0.18	24,24	6,0E-11
fred	0.25	24,23	0,0E+00
CG43729	1,53	24,23	0,0E+00
CG32797	0.08	24,20	3,5E-03
S-Lap3	0.07	24,13	1,1E-03
Lapsyn	0.75	24,12	2,5E-12
Sox102F	1,73	24,05	0,0E+00
CG11191	0.47	24,02	4,6E-07
CG14247	0.10	23,98	1,4E-03
Dltp3	0.71	23,97	9,2E-09
Ugt36Bb	0.05	23,77	3,9E-03
CG11693	0.04	23,77	3,9E-03
CG32846	0.18	23,69	9,2E-06
CG12194	1,15	23,57	0,0E+00
CG34457	0.07	23,43	2,8E-03
CG14022	1,09	23,28	1,8E-09
spaw	0.64	23,25	9,9E-13
CG3397	2,47	23,24	0,0E+00
CG13404	0.19	23,23	8,1E-05
CG43843	0.06	23,17	6,2E-03
CG15628	1,02	23,16	0,0E+00
HisCl1	0.21	23,00	5,1E-07
CG34425	0.22	22,92	3,9E-06
RhoGAP100F	0.89	22,88	0,0E+00
CG30036	0.08	22,85	1,0E-03
CG42489	1,00	22,79	2,6E-07
CG2082	1,15	22,74	0,0E+00
tipE	0.59	22,55	0,0E+00
TM4SF	2,68	22,41	0,0E+00
CG31810	0.32	22,39	2,0E-04
CG13928	2,01	22,37	0,0E+00
Prf3	0.71	22,35	0,0E+00
CG33992	0.29	22,32	9,6E-06
CG31259	0.11	22,28	4,8E-05
CG12402	0.16	22,22	2,2E-09
CG15870	0.40	22,21	2,6E-04
UK114	13,51	22,18	8,3E-15
CG17684	0.91	22,17	0,0E+00
GC	0.28	22,17	6,6E-09
CG7342	0.33	22,10	1,2E-07
CG30484	0.06	22,06	7,0E-04
Tsp5D	0.54	22,00	1,9E-10
NLaz	17,41	21,95	0,0E+00
CG43689	0.13	21,90	1,3E-09
MsR2	0.34	21,87	6,3E-12
tok	3,07	21,81	0,0E+00
CG14742	0.31	21,79	1,3E-03

AOX4	0.07	21,70	1,9E-05
Sdr	0.60	21,66	2,1E-15
CG10289	30,08	21,64	6,6E-11
CG3517	0.16	21,63	9,5E-04
CG6938	0.03	21,62	1,3E-03
CG4546	0.21	21,60	4,0E-07
Obp57c	0.79	21,56	6,5E-06
Cyp408	0.57	21,53	7,0E-11
Npc2g	11,17	21,44	0,0E+00
CG18598	0.48	21,34	1,1E-05
Spm85F	0.07	21,33	1,3E-04
boil	0.10	21,32	1,6E-04
NAATI	1,06	21,24	3,9E-13
Ets96B	0.23	21,23	7,7E-05
CG7370	0.12	21,22	4,3E-04
CG13877	3,52	21,07	3,6E-14
CG12344	0.20	21,01	1,8E-08
CG44102	0.20	20,93	3,3E-03
CG43109	0.57	20,92	1,0E-04
CCAP	0.12	20,91	1,6E-04
CG43165	0.23	20,89	1,1E-03
CG13229	0.39	20,82	1,7E-07
CG15772	0.24	20,79	4,2E-06
MsR1	2,22	20,74	0,0E+00
Muc14A	0.06	20,73	3,0E-13
CG43349	0.14	20,68	4,0E-03
CG32320	0.12	20,66	2,1E-06
bgm	2,83	20,60	0,0E+00
CG15120	0.26	20,59	1,3E-05
CG43324	1,19	20,57	2,4E-09
Rgk2	0.46	20,49	5,9E-10
dpr10	0.31	20,43	4,8E-12
CG5506	0.19	20,40	1,1E-03
CG13075	0.11	20,38	5,3E-04
CG42339	0.10	20,23	3,9E-06
Gyc89Db	0.13	20,22	1,9E-07
Ank2	2,51	20,19	0,0E+00
ICA69	0.26	20,14	1,7E-08
CG15385	0.87	20,12	0,0E+00
CG14757	1,15	20,10	1,7E-09
CG6614	0.03	20,09	3,2E-03
CG1909	0.86	20,04	0,0E+00
DAT	0.34	20,03	8,8E-11
Eip78C	0.24	19,95	3,0E-13
CG34166	98,58	19,92	0,0E+00
CG11425	0.52	19,91	3,2E-06
Ace	2,44	19,86	0,0E+00
Cyp6a8	50,15	19,85	4,1E-07
FucTA	0.56	19,83	1,1E-09
sim	0.03	19,78	5,6E-03
ths	0.32	19,76	1,1E-10
CG14526	5,52	19,70	0,0E+00
CG42324	1,36	19,63	0,0E+00
vas	0.04	19,61	1,1E-03
Cp7Fa	0.09	19,61	1,1E-03
CG13021	0.15	19,61	1,5E-03
Trf4-2	0.05	19,61	1,9E-03
CG1924	0.04	19,61	1,0E-03
CG14662	0.05	19,60	1,5E-03
CG31676	20,95	19,60	0,0E+00
Akh	4,08	19,55	9,1E-05
Cyp9b1	0.55	19,50	3,4E-09
CG5790	0.05	19,49	1,6E-03
h-cup	0.05	19,36	4,4E-03
Cyp9h1	1,08	19,35	0,0E+00
CG34136	2,20	19,33	1,6E-11
Ddr	0.40	19,28	0,0E+00
CG40498	1,36	19,25	0,0E+00
futsch	2,63	19,19	0,0E+00
CG4393	0.95	19,19	0,0E+00
w-cup	0.39	19,14	3,1E-07
CG34189	0.50	19,10	4,9E-06
CG30049	0.03	19,10	5,4E-03
CG3556	1,06	19,00	0,0E+00
CG10035	0.03	18,99	4,6E-03
CG8745	4,47	18,98	0,0E+00
CG33490	0.06	18,95	3,9E-03
Schip1	0.49	18,92	1,6E-08
Pal2	2,17	18,90	0,0E+00
CG4721	6,46	18,86	0,0E+00
CG5849	0.62	18,76	4,2E-15
nAchRalpha4	1,04	18,74	0,0E+00
CarT	0.41	18,70	3,5E-10
rho-5	0.50	18,63	1,3E-12
bmm	7,47	18,61	0,0E+00
Ir68a	0.10	18,61	2,4E-04
CG33296	0.27	18,60	8,2E-05
Vm26Aa	0.47	18,58	1,6E-03
List	0.47	18,54	6,0E-10
CG13654	0.84	18,53	0,0E+00
atc	1,39	18,51	0,0E+00
CG16775	0.25	18,51	3,7E-03
CG31827	0.20	18,50	6,6E-04
CG3819	0.05	18,46	3,0E-03
CG43235	0.11	18,45	2,4E-03
CG34178	0.08	18,45	3,4E-03
CG6576	0.06	18,45	2,7E-03
CG44314	0.04	18,45	1,7E-03
til	0.04	18,45	3,0E-03
Alk	1,33	18,44	0,0E+00
CG5281	0.59	18,40	8,3E-12
Rhs	0.54	18,38	8,0E-09
CG1231	0.10	18,37	4,0E-04
Vha68-3	0.03	18,35	3,5E-03
CG34345	0.04	18,30	5,0E-03
Andorra	0.15	18,29	7,5E-05
Sid	0.18	18,26	4,5E-05
CG15312	0.77	18,25	0,0E+00
CG18478	0.31	18,17	1,5E-03
dob	0.86	18,14	1,0E-11
CG17323	1,93	18,09	0,0E+00

CG14945	1.10	18.06	0.0E+00
CG8534	1.30	18.03	4.7E-05
alpha-Est6	0.07	18.01	4.7E-03
CG5687	3.02	17.99	0.0E+00
CG16825	0.04	17.91	8.5E-03
CG34315	0.04	17.82	5.0E-03
CG12446	0.07	17.81	5.1E-05
Scgalpha	0.57	17.79	2.4E-10
GNBP-like3	1.78	17.74	2.8E-07
swif	0.29	17.72	3.6E-08
CG42370	0.64	17.67	1.4E-09
CG17167	0.14	17.64	7.8E-07
CG8550	0.75	17.64	1.2E-09
CG17687	0.02	17.63	8.4E-03
Jon99Cii	0.18	17.59	1.9E-03
blanks	0.12	17.58	6.8E-04
yellow-g2	0.09	17.52	1.3E-03
CG31743	3.20	17.52	0.0E+00
CG31286	0.07	17.51	4.1E-03
Trh	0.05	17.46	6.9E-04
CG13114	0.08	17.45	5.8E-04
CG42486	10.49	17.45	6.3E-15
Amt	0.11	17.42	5.9E-05
Mct1	1.29	17.40	0.0E+00
CG5107	0.14	17.34	6.8E-03
Mal-A6	0.11	17.34	3.5E-05
SP555	0.11	17.32	3.8E-05
CG14868	0.45	17.28	2.4E-08
CG32500	2.71	17.26	6.1E-04
TBC1D16	0.59	17.25	3.9E-13
Tsp42Ed	5.72	17.20	0.0E+00
CG7231	1.03	17.19	0.0E+00
CG13749	0.22	17.10	8.3E-04
bw	0.20	17.10	3.7E-06
Tret1-1	11.79	17.06	0.0E+00
CG15450	0.10	17.05	9.9E-05
CG5791	0.33	16.98	8.7E-07
CG46244	0.24	16.96	7.5E-08
CG1314	0.08	16.94	1.8E-03
stops	0.79	16.94	1.9E-13
Lkr	0.34	16.90	4.2E-06
Act88F	0.47	16.88	6.2E-07
RTBD9	4.24	16.84	7.0E-07
Fmo-1	0.52	16.83	6.6E-08
CG4995	0.28	16.83	4.8E-07
CG17097	0.04	16.82	8.0E-03
CG31279	0.13	16.81	1.5E-03
sunm	0.02	16.80	2.0E-02
CG9925	0.03	16.70	3.5E-03
CG14238	0.05	16.68	3.8E-03
CG17207	0.09	16.67	6.9E-03
CG1571	0.06	16.65	1.5E-03
erg-1	0.09	16.65	8.1E-05
piwi	0.31	16.63	4.8E-09
CG11407	0.56	16.55	9.5E-06
hlp6	1.09	16.54	0.0E+00
Ir56d	0.03	16.53	1.4E-02
Jon99Ci	0.05	16.53	1.4E-02
lin-28	0.04	16.52	1.4E-02
rob162A	0.05	16.52	1.6E-02
CG42685	0.01	16.52	1.3E-02
CG11037	0.05	16.52	1.3E-02
CG43776	0.02	16.52	1.0E-02
zpg	0.03	16.52	1.0E-02
CG14323	0.05	16.52	1.0E-02
CG3483	0.03	16.52	1.7E-02
CG31253	0.03	16.52	1.7E-02
CG10051	0.02	16.52	1.1E-02
CG13084	0.03	16.52	1.7E-02
CG3565	0.06	16.52	1.1E-02
CG31459	0.05	16.52	1.1E-02
CG16723	0.02	16.52	1.8E-02
alphaKap4	0.03	16.52	1.0E-02
CG34177	0.04	16.52	1.8E-02
CG42764	0.05	16.52	9.3E-03
CG9806	0.02	16.52	1.6E-02
ovm	0.02	16.52	1.6E-02
His2A:CG33826	0.10	16.52	1.5E-02
CG10459	0.04	16.52	9.7E-03
Ir52b	0.03	16.52	1.7E-02
CG4704	0.02	16.52	1.6E-02
CG33003	0.03	16.52	1.7E-02
CG18233	0.03	16.52	1.7E-02
CG34040	0.05	16.52	1.4E-02
CG30432	0.06	16.52	1.4E-02
LysX	0.09	16.52	1.4E-02
CG15357	0.09	16.52	1.0E-02
mfr	0.01	16.52	1.6E-02
CG13251	0.01	16.52	1.5E-02
tey	0.38	16.44	2.4E-08
CG30480	0.07	16.42	2.3E-04
CG40813	0.24	16.42	4.9E-04
Ca-beta	0.97	16.39	0.0E+00
CG18003	1.93	16.39	1.0E-10
CG12362	0.05	16.33	2.3E-03
gsc	0.03	16.33	2.9E-03
CG6927	0.05	16.32	1.8E-03
CG43338	0.05	16.26	1.7E-04
primo-2	0.10	16.26	4.3E-04
CG43896	0.02	16.17	4.6E-03
Rh6	0.36	16.17	8.1E-06
Far0	1.95	16.16	3.5E-06
Fmr1	35.18	16.15	6.0E-13
CheB42a	0.76	16.09	2.3E-06
aPKC	18.89	16.08	1.3E-05
CG45263	0.68	16.04	0.0E+00
CG30268	0.10	16.04	4.7E-05
CG13409	0.55	16.02	8.6E-11
gol	1.68	16.02	0.0E+00
CG32085	0.39	15.98	1.1E-06
Vm34Ca	0.20	15.90	9.6E-03

CG30103	0.03	15.90	2.5E-02
CG14826	0.04	15.90	2.5E-02
Lip3	0.04	15.85	2.7E-02
RpS10a	0.09	15.85	2.7E-02
CG13081	0.18	15.80	1.9E-03
CG18249	1.09	15.79	1.0E-11
Nplp3	1.13	15.68	4.7E-07
Elal	3.37	15.60	0.0E+00
rdcC	0.71	15.60	2.1E-15
Or22a	0.17	15.56	1.1E-03
CG43076	0.06	15.51	2.6E-02
CG15201	18.52	15.50	1.4E-14
CG34355	0.89	15.46	0.0E+00
Hsp60B	0.03	15.44	9.3E-03
CG5011	0.13	15.44	9.1E-03
Ect3	1.90	15.41	0.0E+00
Muc4B	0.13	15.41	9.4E-05
CG13482	0.66	15.39	9.2E-06
Ms	1.76	15.39	2.4E-08
mah	0.05	15.35	4.7E-03
GABA-B-R2	0.89	15.35	0.0E+00
ktub	0.11	15.34	8.3E-07
loopin-1	0.06	15.33	9.8E-04
Cpr76Bd	0.02	15.29	5.9E-03
CG43740	0.20	15.28	9.6E-05
CG6357	8.28	15.28	0.0E+00
CG33223	0.11	15.27	1.4E-03
CG44296	0.30	15.26	1.2E-03
CG42654	0.24	15.26	6.8E-04
CG15347	2.32	15.24	7.5E-08
CG13707	0.19	15.24	5.7E-05
aay	12.20	15.22	0.0E+00
Dgk	0.72	15.21	0.0E+00
CG43060	0.07	15.21	1.1E-02
CG43755	0.59	15.14	1.5E-12
CG31814	0.27	15.13	1.2E-11
CG30116	0.84	15.13	0.0E+00
CG13743	0.86	15.13	4.7E-11
CG14418	0.08	15.11	1.3E-02
CG43111	0.10	15.10	9.6E-03
CG32225	0.69	15.10	4.6E-09
CG43192	1.56	15.09	3.6E-10
CG8837	0.58	15.02	6.5E-06
Sardh	0.77	15.01	2.5E-10
CG13954	0.35	14.92	0.0E+00
CG10654	0.16	14.92	4.5E-05
CG43139	0.10	14.80	8.7E-03
CG10591	0.07	14.76	8.0E-03
Obp73a	0.07	14.74	8.0E-03
CG9287	0.04	14.74	5.4E-03
CG8568	0.02	14.74	7.6E-03
CG44435	0.01	14.74	6.7E-03
solo	0.02	14.74	8.7E-03
Tango8	0.44	14.74	4.4E-03
Eig71Ee	0.05	14.74	6.6E-03
CG12698	0.04	14.74	2.5E-03
ap	2.21	14.74	0.0E+00
CG8476	0.08	14.74	4.7E-03
Drep2	0.44	14.73	2.1E-15
Scgbeta	0.35	14.72	3.0E-07
Cyp4aa1	0.38	14.66	4.2E-04
CG12851	0.66	14.66	0.0E+00
CG17279	0.28	14.65	4.9E-04
CG32107	0.04	14.63	1.6E-04
CG14036	0.33	14.63	3.6E-04
CG4629	0.59	14.62	9.5E-13
CG16758	14.84	14.62	0.0E+00
Cyp6a2	5.50	14.61	0.0E+00
CG40470	0.64	14.59	2.1E-15
CG31088	0.31	14.58	1.5E-05
Mdr65	1.88	14.55	0.0E+00
CG9084	0.05	14.55	1.0E-02
CG10947	0.29	14.55	2.3E-06
betaTry	0.41	14.46	1.9E-04
CG33543	0.81	14.45	0.0E+00
CG32655	0.39	14.40	3.4E-06
CG4714	0.04	14.39	6.6E-03
CG13492	0.05	14.39	2.1E-05
tor	0.09	14.33	2.3E-04
CG13510	0.53	14.28	1.3E-05
cmpy	0.07	14.26	3.5E-04
beat-IIIc	0.53	14.25	2.1E-15
dsx	0.64	14.24	0.0E+00
CG17224	3.59	14.20	0.0E+00
TpnC41C	0.34	14.19	1.6E-06
CG10029	0.06	14.17	1.8E-02
tadr	0.28	14.13	2.2E-07
ppk16	0.03	14.13	5.0E-03
CG5079	0.51	14.07	5.3E-07
CG9170	0.89	14.07	0.0E+00
CG9919	0.56	14.06	1.9E-09
Root	0.29	14.06	4.1E-09
CG3216	0.03	13.98	2.7E-03
CG13442	0.06	13.98	1.8E-03
CG43935	0.24	13.98	4.2E-03
CG30110	0.19	13.96	9.4E-03
Chs-70E	9.54	13.94	0.0E+00
disco-r	0.48	13.90	1.8E-12
CG31823	0.07	13.90	1.7E-02
hll	0.29	13.86	5.9E-05
CG1988	0.29	13.86	3.0E-06
ppk10	0.04	13.81	1.9E-02
CG11384	0.05	13.80	1.8E-03
CG12310	1.24	13.79	3.3E-03
E(spl)m6-BFM	0.09	13.75	9.8E-03
PIP5K59B	1.01	13.72	0.0E+00
eIF4H2	0.04	13.71	2.0E-02
CG11400	5.98	13.70	0.0E+00
CG32121	0.18	13.67	1.9E-05
Pask	0.19	13.62	8.3E-07
CG32698	0.45	13.59	0.0E+00

run	0.04	13.56	1.2E-03
RpS5b	0.26	13.56	2.1E-05
per	0.27	13.53	3.4E-08
CG32944	0.20	13.48	7.8E-07
wisp	0.12	13.47	9.1E-07
HDAC11	0.77	13.44	2.1E-07
Ir75d	0.04	13.43	9.1E-03
Nrt	1.37	13.41	0.0E+00
pug	8.07	13.39	0.0E+00
CG15824	0.03	13.35	4.0E-04
CG12498	0.05	13.35	3.1E-02
CheA29a	0.18	13.35	1.3E-02
comit	1.14	13.21	0.0E+00
CG15096	15.60	13.20	0.0E+00
pirk	0.95	13.20	8.8E-13
CG31140	1.26	13.12	0.0E+00
Cpr73D	0.61	13.12	4.8E-12
sibo	0.04	13.09	2.9E-03
CG32549	7.71	13.08	0.0E+00
CG33510	0.11	13.05	1.4E-03
CG12590	0.03	13.05	3.5E-02
AcCoAS	16.27	13.04	0.0E+00
NH	1.73	13.02	0.0E+00
Timp	7.36	12.97	0.0E+00
Gabat	4.74	12.97	2.1E-15
l(3)72Dr	0.34	12.91	1.5E-05
CG32040	0.69	12.89	4.6E-09
Ir85a	0.43	12.84	6.8E-08
CG12983	0.02	12.79	6.6E-03
CG4753	1.46	12.78	0.0E+00
GstE9	11.81	12.77	0.0E+00
CG34291	13.38	12.72	4.2E-06
CG3699	8.22	12.70	2.4E-09
CG8051	1.43	12.69	0.0E+00
Prosbeta2R2	0.06	12.61	2.4E-02
Prx2540-2	7.49	12.60	0.0E+00
fon	17.97	12.57	0.0E+00
sug	1.20	12.56	1.2E-09
CG17199	0.03	12.56	2.5E-02
CG41242	0.10	12.56	2.8E-02
CG6409	4.97	12.52	7.0E-09
yellow-d	4.57	12.51	1.2E-07
cDIP	2.67	12.50	0.0E+00
bol	1.46	12.47	0.0E+00
Spn28Db	0.15	12.45	2.4E-03
CG6912	4.97	12.43	0.0E+00
CG5048	0.17	12.41	2.3E-03
CG3999	1.33	12.40	5.5E-13
CG33307	1.54	12.39	1.1E-10
Svt14	0.28	12.38	2.7E-09
godddard	0.08	12.36	2.6E-02
epsilonTry	0.06	12.36	2.5E-02
LysD	0.09	12.36	1.8E-02
CG13617	0.02	12.36	1.8E-02
SmydA-6	0.03	12.36	1.8E-02
CG17570	0.05	12.36	2.5E-02
dil	0.04	12.36	2.2E-02
CG43925	0.16	12.36	1.5E-02
Cpr92A	0.03	12.36	2.2E-02
CG34205	0.05	12.36	1.4E-02
CG10317	0.04	12.36	2.1E-02
CG17571	0.04	12.36	2.2E-02
CG9083	0.04	12.36	1.7E-02
Nmdar2	0.44	12.35	0.0E+00
Ir60e	0.13	12.30	8.3E-04
prt	0.13	12.30	1.9E-04
CG4950	1.64	12.28	1.5E-11
CG11211	0.11	12.27	1.0E-02
CG33673	0.10	12.27	1.4E-02
CG6138	0.09	12.27	1.2E-02
Ppm1	0.05	12.27	8.2E-03
Obp19c	0.08	12.27	1.0E-02
CG31327	0.02	12.24	1.4E-02
hlp5	0.44	12.24	7.8E-03
CG43049	0.05	12.23	3.2E-02
SerT	0.16	12.21	4.4E-07
CG14431	0.36	12.20	1.0E-14
yellow-g	0.09	12.20	9.7E-04
CG32483	0.08	12.20	1.2E-03
CG3726	0.59	12.20	2.5E-10
CG43775	0.02	12.19	3.0E-02
CG34256	0.29	12.15	7.2E-05
Adhr	2.37	12.13	1.6E-11
CG30203	0.25	12.13	4.2E-07
CG33468	0.09	12.04	3.2E-02
PGRP-SC2	0.24	12.04	1.1E-03
CG18128	0.39	12.03	3.4E-06
CG10031	3.66	12.03	0.0E+00
CG12256	0.33	12.00	3.4E-05
CG10513	6.23	12.00	8.7E-05
Ror	0.36	11.90	3.0E-07
CG18467	1.05	11.90	2.0E-12
slam	0.19	11.87	9.6E-05
CG5160	0.15	11.84	2.9E-04
dve	0.24	11.83	4.9E-07
CG31921	0.41	11.82	4.5E-10
CG3790	0.48	11.77	8.9E-07
Obp83ef	0.57	11.75	8.6E-06
VepD	0.46	11.74	1.8E-05
Dhc93AB	0.02	11.74	1.4E-04
CG14615	1.68	11.72	2.6E-13
Slob	1.22	11.71	0.0E+00
CG3014	0.13	11.70	3.6E-03
CG15047	0.06	11.65	2.2E-02
CG34258	0.23	11.62	2.2E-03
CG31663	0.53	11.62	2.5E-06
Trpgamma	0.05	11.60	2.7E-04
CG44008	1.95	11.54	4.2E-11
Kua	0.19	11.50	2.6E-06
Nplp2	322.74	11.48	6.9E-07
Nep3	0.81	11.47	4.0E-13

pes	1.97	11.45	0.0E+00
Liprin-gamma	1.37	11.43	0.0E+00
Pk53E	1.03	11.43	0.0E+00
CG15739	0.65	11.40	2.3E-08
CG42855	0.90	11.40	4.3E-08
PICK1	0.33	11.38	2.6E-06
Or46a	0.08	11.36	2.6E-03
CG12309	0.10	11.36	3.1E-04
CG5781	0.20	11.35	5.6E-04
CG31778	2.04	11.35	2.3E-09
Myo28B1	0.06	11.32	1.9E-05
CG43085	1.18	11.24	1.2E-06
Mal-B2	4.76	11.22	0.0E+00
NimC2	0.23	11.20	1.2E-06
orb2	1.27	11.18	0.0E+00
nec	9.74	11.12	0.0E+00
Cad89D	0.02	11.09	2.2E-03
CG14417	0.11	11.08	4.9E-03
CG12038	0.24	11.05	4.0E-05
CG9510	2.26	11.00	2.1E-15
DIP-epsilon	0.34	10.99	8.1E-06
lab	0.07	10.98	5.0E-04
CG32354	0.28	10.97	1.3E-07
CG13539	0.21	10.93	3.1E-04
2mit	0.70	10.93	0.0E+00
CcHa2-R	0.07	10.93	3.6E-04
scpr-C	0.50	10.90	2.4E-05
CG31689	5.97	10.86	0.0E+00
pdm2	0.09	10.84	1.1E-05
CG6044	1.08	10.83	7.4E-11
Cyp305a1	8.86	10.83	0.0E+00
CG7368	0.06	10.80	1.5E-03
CG31773	0.02	10.80	4.2E-02
CG30325	0.15	10.79	1.3E-04
CG3339	0.02	10.78	5.0E-04
CG30222	0.04	10.74	2.4E-02
CG14141	0.68	10.73	3.0E-05
CG8248	0.42	10.73	4.2E-06
SfA	0.52	10.71	2.2E-03
Dh31-R	0.27	10.70	5.5E-05
CG11768	0.13	10.70	1.0E-08
CG34155	0.41	10.68	4.4E-05
CG42319	0.52	10.66	1.0E-11
CG9961	0.09	10.65	1.4E-02
CG34328	0.40	10.65	8.6E-04
CG42516	0.51	10.62	4.0E-07
gammaSnap2	0.33	10.62	2.9E-05
Ugr86Dd	6.05	10.61	2.8E-07
Sesn	3.43	10.60	0.0E+00
Pcvt2	1.71	10.56	8.1E-12
betaTub85D	0.07	10.55	1.5E-02
CG4250	19.23	10.54	1.7E-10
Ance-3	4.38	10.54	0.0E+00
CG13326	0.03	10.53	2.4E-02
CG11786	0.23	10.52	2.4E-03
CG31752	0.04	10.51	2.2E-02
Gr5a	0.05	10.51	1.5E-02
CG5550	0.08	10.51	1.4E-02
can	0.02	10.51	1.3E-02
Idl	3.50	10.51	4.6E-10
CG34402	0.04	10.49	9.8E-03
CG13937	2.48	10.49	0.0E+00
CG15564	0.07	10.45	5.1E-03
CG43062	0.51	10.43	7.6E-05
NT5E-2	1.14	10.43	5.9E-11
unc-104	5.38	10.42	0.0E+00
CG6675	0.15	10.42	2.8E-04
CG14234	0.08	10.40	5.8E-05
boly	0.30	10.39	3.0E-05
CG18449	0.37	10.39	4.8E-04
CG13116	7.24	10.36	0.0E+00
ey	0.16	10.33	3.0E-05
Or65c	0.10	10.33	4.6E-03
laza	0.83	10.30	4.1E-07
mtsh	0.06	10.24	9.6E-03
CG6184	0.18	10.23	7.6E-05
CG6908	3.43	10.23	2.7E-12
bdl	1.74	10.21	2.1E-15
CG12768	0.33	10.21	9.6E-06
CG6761	0.05	10.20	2.6E-03
tau	0.90	10.18	6.3E-15
CG7191	0.12	10.16	4.2E-03
CG42369	6.21	10.14	5.5E-11
Frq2	0.82	10.13	0.0E+00
CG13488	0.27	10.12	1.2E-04
Tsp42Ec	0.13	10.11	4.6E-03
CG12520	0.06	10.11	2.2E-02
CG3526	0.09	10.10	1.4E-02
CG8292	0.25	10.09	2.6E-04
Ptp36E	0.82	10.07	1.3E-09
Vha68-1	3.23	10.06	0.0E+00
Pk34A	0.10	10.03	1.3E-02
CG16749	0.20	10.02	1.4E-03
glec	4.67	10.00	0.0E+00
Idgf1	8.87	10.00	0.0E+00
CG7509	0.62	9.99	9.8E-06
CG46307	0.07	9.95	5.7E-03
CG17127	0.48	9.94	1.6E-04
CheB42b	0.29	9.93	1.5E-03
Obp57b	0.54	9.92	1.1E-03
Est-Q	2.25	9.91	1.0E-13
Or71a	0.47	9.89	2.0E-05
CG32631	0.04	9.88	3.4E-02
CG13965	0.08	9.88	3.4E-02
bin	0.02	9.88	4.8E-02
Ir67c	0.03	9.87	3.6E-02
gammaTub37C	0.03	9.87	2.8E-02
Or45b	0.04	9.87	3.7E-02
CG13474	0.09	9.87	3.7E-02
CG13898	0.07	9.87	3.3E-02
Spn38F	0.04	9.87	3.3E-02

CG33463	0.11	9.87	3.3E-02
CG14321	0.07	9.87	4.1E-02
CG13004	0.54	9.87	5.6E-08
CG1774	0.92	9.83	8.2E-11
whip	0.29	9.82	6.5E-04
CG42819	0.16	9.81	1.6E-02
Galk	5.36	9.81	0.0E+00
CG10621	3.03	9.80	6.8E-09
CG10257	0.29	9.78	2.7E-05
CG32687	1.72	9.77	0.0E+00
CG5062	0.61	9.76	1.2E-07
Thor	29.27	9.76	0.0E+00
CG13538	0.05	9.74	4.8E-02
CG7381	0.07	9.73	1.2E-03
Cpr47Ef	0.02	9.72	4.8E-02
CG10827	0.09	9.70	8.0E-03
AttB	0.98	9.70	1.6E-05
fend	1.10	9.69	2.0E-14
CG42263	0.43	9.67	1.5E-04
Jon25Biii	0.14	9.66	1.3E-02
CCKLR-17D3	0.10	9.62	8.1E-04
sage	0.34	9.61	6.6E-06
CG32187	0.08	9.60	1.2E-02
TfAP-2	0.19	9.58	8.2E-05
DntB	1.88	9.58	6.4E-05
CG5458	0.55	9.57	1.4E-05
CG4661	0.29	9.54	4.8E-06
CG42514	1.49	9.51	0.0E+00
CG15803	0.20	9.50	7.2E-07
CG15530	0.04	9.46	1.7E-02
Teh4	0.16	9.43	1.3E-04
CG7763	2.01	9.41	3.1E-07
CG14397	0.19	9.41	2.1E-02
CG6421	0.17	9.39	3.2E-02
CG9121	0.36	9.38	1.1E-06
Pfrx	4.52	9.37	0.0E+00
CG42337	0.57	9.36	8.4E-14
sens	0.36	9.36	2.4E-04
CG31808	3.03	9.33	0.0E+00
CG46306	0.50	9.32	1.3E-06
CG9498	4.29	9.29	0.0E+00
CG3829	3.54	9.29	0.0E+00
HP1D3csd	0.33	9.29	1.8E-03
CG11668	0.72	9.26	3.2E-05
CG7335	0.28	9.22	4.5E-03
CG14694	0.05	9.20	2.5E-02
CG43116	0.09	9.19	2.8E-02
Gr61a	0.04	9.19	2.1E-02
CG31288	0.42	9.18	8.8E-04
CG15465	0.57	9.17	0.0E+00
CG5804	0.51	9.16	3.4E-03
Cda9	0.12	9.15	2.6E-03
pdm3	0.64	9.15	2.2E-07
CG18675	0.08	9.13	2.3E-03
kek6	0.61	9.11	0.0E+00
CG11841	0.54	9.10	3.8E-04
daw	1.61	9.08	6.9E-14
Dhit	0.48	9.07	1.0E-09
Oamb	0.31	9.07	1.2E-09
CG42655	0.14	9.02	3.2E-02
CG32809	1.11	8.99	0.0E+00
CG11317	0.38	8.99	9.6E-06
cep290	0.03	8.96	1.3E-03
CG1850	0.15	8.95	9.8E-04
CG14421	0.08	8.94	3.4E-02
CG5348	0.24	8.93	5.2E-06
CG1544	1.75	8.92	0.0E+00
CG44006	0.16	8.91	3.1E-03
sinah	0.07	8.88	8.5E-03
hoe1	1.39	8.87	9.1E-10
ss	0.07	8.86	3.1E-03
Prx2540-1	6.28	8.81	2.1E-15
CG12769	0.32	8.81	3.0E-11
spidey	6.73	8.77	0.0E+00
CG42331	0.11	8.74	1.6E-05
CG34287	0.13	8.71	4.5E-03
CG18135	9.10	8.70	0.0E+00
mtl115	0.09	8.70	9.6E-04
DIP-jota	0.16	8.70	2.7E-03
CG42458	0.06	8.68	6.3E-04
CG4757	9.02	8.66	0.0E+00
CG7149	0.81	8.64	8.3E-15
Octbeta1R	0.37	8.61	5.5E-14
CG17764	0.50	8.59	2.4E-04
FMRFa	0.11	8.57	6.0E-03
LpR2	7.26	8.57	3.2E-14
Cyp313a1	0.17	8.56	2.5E-04
Ndae1	2.90	8.55	8.8E-14
path	10.28	8.52	0.0E+00
CG13578	0.20	8.51	3.0E-03
CG4133	0.20	8.50	3.2E-04
Rab32	1.45	8.50	0.0E+00
Kif3C	0.29	8.50	2.3E-08
Grd	0.16	8.50	1.5E-06
Ca-alpha1D	1.08	8.46	3.1E-12
CG42507	0.27	8.45	2.9E-03
fax	13.76	8.43	2.6E-14
CG13203	0.05	8.43	3.7E-02
CG6465	0.20	8.42	6.0E-03
CG31145	2.27	8.41	0.0E+00
CG3306	0.22	8.41	8.7E-04
Acer	3.77	8.39	0.0E+00
CG7742	0.22	8.38	4.1E-05
CG14606	0.09	8.38	2.4E-02
CG6870	0.52	8.37	1.5E-04
Ets21C	0.23	8.30	6.5E-07
Blimp-1	1.90	8.28	0.0E+00
VGAT	0.49	8.27	3.0E-09
jotaTry	0.18	8.26	1.0E-02
Calx	0.64	8.24	1.1E-13
7B2	4.55	8.23	3.2E-14

CG14402	0.03	8.22	5.0E-02
Spn53F	0.04	8.22	4.7E-02
eas	5.07	8.21	0.0E+00
Tb	0.10	8.17	2.0E-02
CG12913	0.03	8.14	1.2E-02
CG4408	3.11	8.14	4.6E-04
CG6931	0.10	8.14	1.3E-02
CG8918	0.11	8.10	1.8E-03
CG5002	0.69	8.10	1.2E-08
Fmo-2	2.85	8.10	5.9E-13
CG13083	0.07	8.10	2.2E-02
Is(1)N	0.08	8.10	1.5E-04
CG14933	8.35	8.08	1.1E-11
CG17991	0.46	8.08	4.1E-05
kcc	2.70	8.08	0.0E+00
Lsp2	116.49	8.08	6.4E-05
CG10702	0.49	8.00	2.6E-06
CG30271	0.06	7.98	6.7E-03
Cyp9b2	8.75	7.96	0.0E+00
Kah	0.14	7.93	3.3E-04
Adh	74.38	7.93	1.6E-06
AstC-R2	0.07	7.93	1.2E-03
topi	0.10	7.91	1.3E-03
CG32573	0.19	7.91	2.9E-04
CG6059	0.05	7.91	8.9E-03
CG11635	0.34	7.87	1.3E-03
CG32815	0.32	7.85	1.7E-06
stum	0.02	7.84	7.0E-03
CG15666	0.07	7.81	1.9E-03
yl	0.14	7.80	6.5E-05
azot	0.35	7.80	1.0E-03
CG15233	0.83	7.79	1.4E-05
CG6834	1.57	7.79	2.2E-08
CG10970	0.55	7.76	1.4E-06
SP2353	0.75	7.76	0.0E+00
GlcAT-P	1.96	7.76	3.1E-10
CG33914	0.09	7.74	8.1E-03
gogo	0.10	7.71	4.0E-05
eys	0.95	7.69	1.2E-13
CG11638	0.33	7.67	1.8E-04
CG32686	1.06	7.66	5.0E-14
CG40472	2.81	7.64	7.7E-05
CG5267	0.34	7.63	5.1E-04
CG8834	0.07	7.62	1.1E-02
CG13408	0.32	7.60	1.3E-04
Galk	6.54	7.57	0.0E+00
CG4797	4.81	7.56	0.0E+00
CG1667	5.37	7.55	2.1E-15
CG8958	0.16	7.54	4.7E-04
CG12057	0.17	7.53	1.6E-02
MtnE	0.75	7.52	9.6E-04
CG6661	0.05	7.51	2.5E-02
spab	0.47	7.50	3.6E-03
CG31627	0.28	7.50	6.2E-03
CG18095	0.23	7.47	1.1E-02
CG4607	5.16	7.43	0.0E+00
CG16739	0.21	7.43	2.1E-02
CG13708	0.13	7.43	7.0E-05
CG15202	0.54	7.40	9.2E-05
CG31809	0.13	7.38	4.4E-03
SdhBL	0.08	7.38	1.4E-02
CG13077	0.55	7.37	5.8E-05
CG14015	0.03	7.35	3.5E-02
ppk11	0.02	7.35	4.5E-02
CG8945	0.02	7.35	3.9E-02
CG11619	0.20	7.33	3.7E-04
CG13907	2.41	7.33	0.0E+00
CG17816	1.19	7.33	2.1E-15
CG31115	1.09	7.31	2.8E-05
RYa-R	0.09	7.30	3.9E-03
CG7916	0.23	7.29	1.6E-03
CG14629	23.51	7.28	5.0E-12
CG44251	0.13	7.28	3.8E-03
P5cr-2	1.42	7.27	1.3E-06
MFS14	4.72	7.27	0.0E+00
CG34138	0.31	7.27	9.4E-03
CG34376	2.90	7.27	0.0E+00
CG3812	0.41	7.25	1.3E-05
vis	0.20	7.24	1.9E-02
CG12105	0.35	7.23	7.4E-07
CG43901	0.59	7.20	6.2E-12
CG17177	0.04	7.20	1.7E-02
CG9447	0.11	7.19	2.7E-03
Nhe2	1.21	7.17	8.3E-15
sr	0.35	7.17	2.4E-07
CG14044	0.09	7.17	9.0E-03
sens-2	0.13	7.16	4.3E-04
Cyp6a19	0.12	7.14	9.9E-04
cpo	1.27	7.11	2.1E-15
CG32811	0.19	7.11	4.8E-02
CG8785	3.53	7.10	1.6E-09
CG4306	1.68	7.10	1.1E-07
smP-30	2.98	7.09	1.6E-06
CG14990	0.80	7.08	6.5E-04
Hn	13.97	7.07	8.2E-10
Wnt4	0.11	7.07	7.1E-04
CG14340	0.21	7.06	2.8E-03
CG13405	0.14	7.05	1.6E-02
CG14000	0.15	7.05	3.6E-03
TrpA1	0.05	7.05	1.1E-03
Sema1a	1.35	7.04	0.0E+00
CG18067	21.83	7.03	1.9E-11
CG34051	0.18	6.99	1.4E-02
Snmpl	1.59	6.98	2.6E-09
CG32204	0.49	6.98	4.1E-07
CG13870	0.05	6.98	1.9E-02
Spn28Da	0.08	6.97	1.7E-02
Cpr50Ca	0.03	6.97	2.7E-02
otu	0.05	6.97	5.5E-03
CG4725	1.02	6.97	2.1E-11
CG15431	0.33	6.94	1.4E-09

Rbp9	1.89	6.89	4.2E-10
CG1628	1.15	6.86	1.3E-08
CG5527	0.36	6.86	8.7E-05
CG9270	0.22	6.86	1.6E-04
ppk25	0.50	6.84	1.2E-04
CG14834	0.25	6.83	5.8E-03
CG9760	0.11	6.83	3.3E-03
vg	0.30	6.83	6.5E-06
Ntl	0.75	6.81	4.8E-08
alpha-Est7	14.06	6.81	0.0E+00
oc	0.06	6.81	1.2E-03
Gbeta5	0.25	6.80	6.5E-04
NaCP60E	2.27	6.79	4.2E-14
CG14797	0.16	6.78	3.5E-04
elav	1.29	6.78	0.0E+00
AstA-R1	0.25	6.77	1.3E-03
CG15890	0.21	6.76	3.0E-05
CG34374	0.11	6.74	2.6E-02
CG33494	3.67	6.73	1.9E-08
CG7848	0.08	6.72	6.0E-03
amn	0.78	6.72	0.0E+00
rdo	0.47	6.69	1.2E-09
CG5432	0.04	6.68	4.5E-02
CG33723	0.14	6.68	4.6E-02
CG15599	0.02	6.68	4.5E-02
CG45066	0.07	6.68	4.5E-02
Pdp1	3.58	6.67	1.4E-14
hwt	0.63	6.66	2.7E-10
CG13658	0.20	6.65	2.4E-03
CG12914	0.33	6.65	1.5E-03
CG6405	0.23	6.62	1.3E-03
CG1537	0.13	6.61	2.8E-02
NK7.1	1.58	6.59	0.0E+00
Shal	0.53	6.58	4.0E-07
CG14937	0.22	6.58	1.9E-03
CG42523	0.07	6.57	4.8E-02
CG3655	5.13	6.56	1.9E-10
CG6191	8.22	6.56	6.5E-10
Tsp29Fa	0.52	6.55	3.2E-03
tow	0.26	6.55	6.5E-04
CG34423	2.49	6.55	8.4E-07
Tsp68C	0.11	6.54	7.6E-03
Cyp4p1	4.98	6.54	5.6E-10
gsb-n	0.04	6.54	2.4E-02
sNPF-R	0.41	6.54	5.7E-08
CG31454	0.05	6.51	2.2E-02
CG7378	2.23	6.49	4.2E-12
lms	0.17	6.49	5.8E-03
p38c	0.26	6.48	9.8E-04
CG3104	0.16	6.48	3.4E-04
CG43175	0.26	6.47	9.9E-03
mtrm	0.20	6.47	3.5E-03
Cyp4ac2	1.09	6.47	2.6E-07
ACXD	0.07	6.46	7.9E-03
CG4723	1.08	6.45	3.8E-09
CG14372	0.42	6.43	9.0E-07
Obp83cd	1.12	6.42	2.4E-05
Nha2	1.15	6.41	4.2E-09
dy	0.05	6.41	1.3E-02
CG17669	0.06	6.41	3.2E-02
CG18477	0.14	6.38	6.7E-03
RSG7	0.57	6.37	1.2E-10
CG12766	0.15	6.36	1.1E-02
CG8128	1.89	6.36	1.3E-08
alpha-Est2	1.04	6.36	6.5E-07
ymp	0.28	6.36	2.1E-04
CG14630	1.29	6.35	4.2E-05
Rbp1-like	2.59	6.34	8.2E-11
CG32544	0.59	6.34	5.9E-03
CG15771	2.77	6.33	0.0E+00
CG6974	0.16	6.32	3.0E-02
CG34054	0.41	6.32	7.1E-03
CG2678	0.12	6.31	2.4E-03
Dh44-R2	0.27	6.30	2.6E-04
LpR1	2.62	6.30	0.0E+00
CG2127	0.28	6.29	9.7E-04
Ptp99A	2.06	6.28	2.2E-14
CG2898	0.82	6.27	6.3E-06
nvv	0.22	6.23	3.0E-04
atk	0.15	6.21	2.9E-04
unc-13	2.43	6.19	1.2E-11
CG13733	0.20	6.18	8.5E-03
CCAP-R	0.30	6.16	3.3E-04
MtnA	66.26	6.15	2.9E-05
Gagr	0.23	6.15	5.5E-04
Cyp6g1	14.90	6.14	1.3E-03
Lsd-1	6.23	6.14	7.9E-09
CG2254	2.85	6.14	6.0E-07
CG14448	0.09	6.12	3.7E-02
retn	0.12	6.12	4.2E-04
CG12016	1.96	6.12	0.0E+00
CG14406	0.87	6.11	2.1E-04
CG12896	3.66	6.10	2.5E-05
CG3868	0.08	6.10	2.9E-02
CG13375	0.73	6.10	1.2E-10
CG32681	0.65	6.08	1.2E-13
Gr43a	0.14	6.08	7.5E-03
CG16886	0.36	6.07	1.6E-04
Cpr62Bb	4.41	6.07	3.2E-08
CG44838	0.91	6.07	1.0E-11
Spn43Ad	1.20	6.06	4.1E-07
nki	0.10	6.06	1.5E-02
CG2533	0.43	6.06	1.5E-03
CG4325	0.48	6.06	1.5E-03
CG14183	0.28	6.05	1.1E-03
CG32333	0.21	6.04	1.7E-05
CG12224	0.58	6.04	7.8E-05
dpr17	0.29	6.04	9.3E-06
CG12338	2.75	6.03	7.1E-07
mdy	1.72	6.01	1.0E-14
CG13982	0.07	6.01	1.1E-02

fs(1)h	9.81	5.97	1.3E-03
Gyc89Da	0.06	5.94	2.2E-02
Ten-a	1.07	5.93	1.0E-11
Itgbn	0.61	5.91	2.1E-06
cuff	0.15	5.89	5.7E-03
Galphao	1.77	5.88	4.2E-15
Scp2	4.94	5.86	4.5E-04
CG31248	1.52	5.86	1.9E-05
GstE2	0.74	5.86	4.5E-03
Sp1	0.28	5.85	3.7E-03
svp	0.88	5.85	2.1E-10
pre-mod(mdg4)-Y	0.20	5.85	3.4E-03
cv-d	3.06	5.84	3.1E-10
CG32091	5.75	5.82	4.3E-09
unc-13-4A	0.44	5.81	2.4E-08
CG31323	0.23	5.80	1.9E-04
Tep5	0.08	5.80	1.8E-02
CG13437	0.34	5.80	2.8E-03
PIP82	1.18	5.80	1.7E-11
fuss	0.42	5.80	2.2E-07
CG8301	0.40	5.80	4.0E-06
Gr77a	0.91	5.79	3.9E-04
CG43845	0.76	5.79	5.9E-04
Cadps	4.10	5.78	0.0E+00
CG40485	0.31	5.77	3.9E-04
tlid	0.19	5.75	9.9E-03
CG17189	1.15	5.75	1.8E-04
CG32719	0.03	5.75	4.6E-02
Arl6	0.14	5.74	3.5E-02
CG11269	0.24	5.74	3.3E-02
CG8407	0.13	5.74	3.7E-02
Cpr	30.24	5.73	1.0E-07
Tsp29Fb	4.58	5.71	2.9E-08
CG31030	1.74	5.70	3.3E-09
Cyp4e2	15.71	5.68	7.1E-11
CG43236	1.83	5.67	2.1E-03
CG30046	1.25	5.63	1.7E-06
CG13074	0.10	5.62	1.4E-02
CG6424	2.78	5.61	1.3E-13
Pde9	0.93	5.58	1.2E-13
mspo	0.60	5.56	3.4E-06
CG7220	5.25	5.55	0.0E+00
GNBP2	0.96	5.54	2.2E-05
CG3984	3.00	5.54	3.9E-13
normA	3.44	5.54	4.1E-13
CG34424	2.97	5.52	8.9E-04
CG46315	2.66	5.51	3.6E-11
lectin-33A	0.38	5.49	7.1E-03
CG30378	0.26	5.49	2.9E-03
CG34193	0.06	5.49	3.3E-02
twz	0.29	5.48	1.1E-03
CG9279	0.62	5.47	1.1E-09
CG31097	0.34	5.47	2.9E-02
CG33643	0.72	5.47	1.0E-02
lh	1.70	5.47	1.6E-14
CG7084	0.37	5.45	7.6E-03
ade3	6.06	5.42	2.0E-11
aop	2.91	5.42	7.7E-13
Achl	0.53	5.41	4.8E-07
CG34134	2.51	5.41	4.5E-05
mith2	2.27	5.41	1.0E-05
CG32392	0.11	5.40	6.4E-03
CG3253	0.12	5.40	8.5E-03
PpD6	0.40	5.40	9.4E-03
CG6688	0.40	5.38	5.7E-03
CG15630	0.99	5.37	5.1E-07
ACC	27.39	5.34	3.4E-06
Spn43Ab	15.97	5.33	7.0E-12
CG40178	3.80	5.33	3.1E-13
CG11459	0.60	5.32	1.4E-04
CG15186	0.10	5.32	3.8E-03
CG4238	0.72	5.32	4.3E-09
Ubc84D	0.31	5.32	2.1E-02
mei-W68	0.77	5.31	4.9E-07
CG2854	0.13	5.31	1.3E-02
CG3987	0.80	5.31	2.8E-05
CG5958	6.98	5.31	8.8E-08
CG14186	0.49	5.30	1.1E-04
alpha-Est4	0.21	5.30	5.4E-03
CG30334	0.95	5.30	3.6E-03
CG32305	0.11	5.30	2.6E-03
Ppcs	1.43	5.30	4.6E-14
rib	0.03	5.30	3.0E-02
CG6225	0.47	5.28	4.4E-04
Cyp12e1	0.42	5.27	6.3E-04
CG11893	0.41	5.26	1.0E-03
CG4666	5.85	5.26	4.6E-08
Bx	0.69	5.24	9.5E-10
bab2	1.12	5.24	2.8E-11
Acox57D-p	1.78	5.23	1.3E-09
CG5991	3.98	5.23	2.8E-10
Neto	0.20	5.22	1.5E-04
CG11313	0.13	5.22	2.5E-02
Tob	1.21	5.21	2.7E-12
CG6415	1.69	5.20	4.0E-04
msi	1.45	5.20	1.1E-12
CG17841	7.99	5.20	5.9E-13
CG11594	2.85	5.19	1.0E-07
t	1.87	5.18	4.0E-06
Glut4EF	3.54	5.17	4.5E-10
Cyp12a4	4.20	5.16	3.3E-07
tio	0.23	5.16	2.1E-05
axed	0.62	5.16	2.1E-05
Gpb5	0.64	5.16	2.4E-03
mei-P26	2.28	5.16	2.6E-09
CadN	1.35	5.16	5.6E-10
Asator	1.90	5.16	3.1E-12
CG30273	0.87	5.14	2.8E-03
CG7841	1.27	5.14	3.4E-08
ttm2	0.07	5.14	4.4E-02
CG3376	3.57	5.13	2.1E-15



CG30357	1.04	5.12	6.1E-06
twit	0.35	5.11	1.4E-02
Gr39a	0.79	5.10	2.7E-08
CG42846	3.87	5.10	5.8E-05
rdgA	2.11	5.09	4.9E-11
CG42751	0.38	5.09	4.4E-02
jtb	1.09	5.08	4.6E-03
CG4565	0.42	5.08	5.5E-03
srp	1.71	5.07	1.5E-07
Glut1	1.74	5.07	2.0E-14
AdipoR	17.62	5.03	1.9E-11
CCHa1	0.77	5.02	1.4E-03
CG4842	0.36	5.01	1.0E-02
CG14516	0.44	5.01	3.7E-06
CNMaR	0.42	5.00	5.1E-05
dtr	0.10	5.00	6.6E-03
Lgr1	0.23	5.00	4.5E-03
GlT	21.90	4.99	3.0E-06
CG4822	2.60	4.95	6.4E-08
CG17124	5.23	4.94	2.8E-12
Mtp	4.55	4.94	3.5E-12
moody	4.35	4.93	8.6E-13
dar1	3.41	4.93	1.8E-11
Pzl	0.03	4.93	2.5E-02
vip7	0.52	4.92	2.8E-02
CG10801	0.19	4.92	9.1E-03
bwa	1.07	4.92	8.8E-07
CG5071	0.65	4.89	7.4E-08
Culd	1.17	4.88	2.8E-05
lrk3	0.33	4.88	4.7E-02
Gctc	5.46	4.87	4.8E-12
Lsd-2	12.80	4.87	1.8E-08
CG43291	0.07	4.87	4.0E-02
CG7387	0.32	4.87	1.4E-02
Gale	7.74	4.87	1.5E-08
Gbp1	3.88	4.87	1.3E-05
Tmc	0.21	4.86	3.2E-04
CG42763	0.55	4.85	9.9E-03
Rh50	2.51	4.85	2.6E-06
CG11664	0.38	4.85	5.6E-03
Cyp4ac1	2.34	4.84	1.5E-08
CG30345	1.13	4.83	2.5E-06
Tsp42Ea	13.33	4.83	2.5E-08
Tpc2	0.10	4.82	3.8E-02
CG7646	1.73	4.82	4.8E-06
Proc	1.77	4.81	3.6E-08
smal	0.48	4.81	2.7E-05
slow	1.07	4.80	2.0E-06
CG43340	2.21	4.79	2.6E-08
ine	3.49	4.78	3.6E-08
CG10550	17.42	4.77	1.4E-10
CG10694	0.24	4.77	4.2E-02
Cyp4d2	1.57	4.76	8.9E-10
Lectin-galC1	4.86	4.75	1.5E-03
Ent3	0.48	4.74	1.4E-05
ppl	6.87	4.74	5.7E-07
CG4741	0.12	4.73	2.5E-02
CG7272	23.31	4.72	2.9E-11
CG32219	0.29	4.71	2.2E-02
CG15203	1.69	4.70	5.6E-04
CG30269	0.82	4.69	2.3E-03
CG31161	0.09	4.69	4.4E-02
CG17118	0.15	4.68	4.7E-02
CG5793	3.50	4.68	1.4E-07
lds	0.21	4.68	1.4E-02
zhf1	1.38	4.68	7.1E-07
CG14687	3.23	4.67	2.2E-04
Tim17b1	1.43	4.67	7.9E-04
Srpk79D	0.87	4.66	7.6E-07
Mctp	1.01	4.66	3.8E-10
CG32006	0.15	4.65	3.2E-02
CG31777	5.62	4.65	5.9E-04
pre-mod(mdg4)-N	0.27	4.64	8.8E-03
CG6006	1.67	4.63	3.7E-07
CG12926	1.18	4.62	1.6E-04
trk	0.29	4.62	2.0E-02
UGP	20.10	4.59	3.5E-08
lrk1	2.10	4.58	1.4E-05
CG33947	0.51	4.58	2.0E-03
pn	1.51	4.57	5.0E-05
NimB2	14.17	4.57	1.4E-13
CG9628	25.26	4.56	2.9E-09
CG10063	0.22	4.56	2.6E-02
CG8136	0.18	4.55	2.2E-02
CG4669	0.80	4.54	5.0E-06
CG3961	3.21	4.53	4.2E-08
Spn31A	0.64	4.51	2.3E-02
CG42795	1.36	4.51	2.5E-11
Reph	1.43	4.50	6.6E-12
CG44385	0.79	4.50	8.7E-04
cnn	1.44	4.49	1.3E-08
CG9123	0.35	4.48	2.3E-03
FASN1	85.19	4.47	2.0E-04
Tango13	3.21	4.47	1.1E-10
seq	0.62	4.44	1.2E-03
Gpo-1	7.44	4.44	4.4E-11
ND-49L	0.40	4.42	5.5E-03
NimB3	1.25	4.42	8.0E-03
CG30485	0.08	4.42	1.9E-02
CG30283	1.96	4.41	3.4E-05
CG4297	1.77	4.40	6.6E-12
CG42340	0.19	4.39	5.1E-04
CG43093	1.33	4.38	2.9E-03
nmo	1.75	4.37	1.2E-10
CG15117	0.85	4.37	2.2E-05
MESR3	3.85	4.36	3.5E-08
nord	0.11	4.36	2.6E-02
hli	1.18	4.36	5.3E-06
CG5466	0.42	4.35	3.7E-03
CG11899	6.51	4.35	4.0E-08
CG18754	0.17	4.34	1.7E-02

stas	3.25	4.33	5.1E-10
Cyp12b2	2.37	4.33	1.5E-06
CG44405	0.31	4.32	3.1E-03
Lgr3	0.10	4.32	2.1E-02
hoe2	0.64	4.32	3.3E-03
CG12990	0.34	4.28	1.5E-03
CG13618	0.98	4.28	4.3E-02
CG13894	0.17	4.27	2.3E-02
CG11353	0.10	4.27	1.8E-02
suf1	2.30	4.27	5.7E-06
CG12728	3.58	4.25	3.1E-05
hub1	0.11	4.25	3.3E-02
CG30287	2.05	4.24	2.3E-05
CG31780	0.16	4.24	2.7E-02
CG7510	5.86	4.23	1.4E-08
Ugt36Bc	6.09	4.21	3.2E-08
CG42402	1.38	4.21	5.0E-07
CG42456	1.90	4.20	1.9E-06
Ac13E	1.10	4.20	2.6E-07
ebd1	0.70	4.20	2.2E-04
LManII	12.68	4.20	1.1E-09
CG18336	0.40	4.17	3.1E-02
olf186-M	3.66	4.16	1.4E-06
MtnD	1.15	4.16	3.4E-02
evg	0.28	4.15	1.1E-02
Adef-A	1.80	4.15	2.5E-03
CG4615	1.72	4.14	5.9E-04
CG13606	0.93	4.14	2.7E-03
CG11825	0.75	4.14	3.3E-02
CG16852	0.29	4.13	4.3E-02
CG13293	0.15	4.13	5.4E-03
CG43110	0.25	4.13	8.0E-05
CG5577	2.28	4.12	5.8E-07
CG10383	5.95	4.12	6.8E-10
NKCC	1.84	4.11	3.1E-04
CG11089	10.64	4.10	2.5E-09
Cyp49a1	0.60	4.10	2.7E-04
CG30148	0.79	4.10	7.6E-03
dnc	2.49	4.09	4.1E-08
CG13430	0.80	4.09	2.3E-03
Cyp4s3	0.65	4.08	6.4E-04
CG10960	6.09	4.08	1.2E-09
Gpdh	18.23	4.07	9.2E-08
CG11883	1.62	4.06	5.4E-09
CG30503	0.46	4.06	5.5E-03
obst-1	0.17	4.06	4.4E-02
CG34371	0.78	4.06	4.6E-05
CG17075	0.59	4.05	1.9E-07
Atta	0.37	4.05	3.9E-02
Lap1	2.91	4.03	5.5E-07
CG30054	2.06	4.02	5.0E-05
CG42240	2.89	4.02	1.5E-08
fat-spondin	10.31	4.02	2.6E-06
egh	5.14	4.02	3.1E-10
CG31805	0.40	4.02	5.9E-03
CG5955	1.00	4.01	1.7E-02
Cnx14D	0.28	4.00	3.8E-03
scw	0.24	4.00	4.2E-02
CG6026	0.10	4.00	7.5E-03
insc	1.46	3.99	3.5E-10
mim	2.62	3.97	1.5E-08
CG13641	1.24	3.97	1.7E-02
CG33293	1.04	3.97	8.5E-03
pre-mod(mdg4)-E	0.45	3.97	3.0E-02
CG10472	0.39	3.96	3.2E-02
Mos	0.19	3.96	5.0E-02
Ehfc1.1	0.10	3.96	3.9E-02
CG5245	0.33	3.96	1.8E-02
mino	8.35	3.95	6.1E-08
CG17270	0.58	3.95	3.5E-03
DAAM	1.00	3.94	2.6E-06
Hex-A	10.17	3.93	3.6E-10
CG9821	16.86	3.93	2.2E-06
Spn42Dd	5.17	3.92	1.4E-11
CG10793	0.73	3.92	2.4E-03
CG4259	2.89	3.92	2.2E-04
Dif	3.91	3.90	4.6E-10
CG43646	0.85	3.89	3.3E-02
rha	0.07	3.89	3.5E-02
Phos	2.61	3.89	9.9E-11
sei	0.68	3.89	2.7E-05
CG13397	0.86	3.88	3.8E-05
CG33235	0.05	3.87	4.0E-02
CG13843	0.22	3.86	3.9E-02
CG14441	1.72	3.85	1.2E-09
wtrw	1.83	3.84	2.1E-05
[(3)72Dp	0.77	3.83	3.7E-04
spdo	0.20	3.83	2.7E-02
shf	1.05	3.83	4.9E-04
Sik2	0.56	3.82	6.7E-04
Dhc16F	0.03	3.82	2.9E-02
mirr	1.66	3.81	4.4E-07
bab1	0.19	3.80	7.4E-03
Trim9	0.58	3.80	1.0E-04
CG45075	0.40	3.78	3.5E-04
SoxN	1.57	3.78	5.1E-09
CG16799	6.00	3.78	4.1E-06
CG14443	0.53	3.77	1.8E-02
CG43867	1.51	3.77	6.6E-09
CG4301	0.15	3.76	2.7E-02
Cln3	0.86	3.76	1.0E-02
CG13085	0.24	3.76	4.5E-02
lectin-28C	3.28	3.75	1.9E-03
CG10863	21.99	3.74	1.6E-07
pxb	0.55	3.74	4.7E-04
CG1971	0.24	3.74	4.1E-02
Dnah3	0.02	3.74	4.7E-02
CG12992	0.88	3.74	7.2E-04
Plk-C3	1.93	3.74	9.3E-05
Octbeta2R	2.02	3.73	1.9E-06
5PPhaseI	2.04	3.73	1.3E-08

Zw	8.70	3.72	5.1E-04
Mes2	1.00	3.71	3.6E-04
Desat1	155.81	3.70	3.6E-04
CG16771	0.91	3.69	8.2E-05
CG8854	1.19	3.69	4.9E-06
CG5707	1.39	3.68	2.8E-03
CG5522	1.85	3.68	1.2E-07
dac	0.25	3.68	4.8E-02
CG31183	1.18	3.68	3.3E-06
Glaz	2.11	3.68	1.0E-03
CG7120	1.32	3.67	1.8E-03
ade2	4.77	3.67	2.1E-07
psh	1.58	3.66	1.7E-04
CG14164	0.41	3.65	4.3E-02
inaE	0.87	3.65	4.1E-08
CG8249	1.48	3.65	3.6E-04
spir	2.26	3.64	1.1E-06
CG34431	0.34	3.63	1.1E-02
CG11760	0.35	3.63	2.8E-02
CG13784	6.39	3.62	7.0E-09
mid	0.29	3.61	2.8E-02
Mmp2	1.61	3.61	2.0E-06
flw	4.97	3.59	8.6E-10
CG3638	3.95	3.58	2.1E-07
pre-mod(mdg4)-C	0.51	3.58	1.7E-02
Fs	0.25	3.58	1.3E-02
RhoGEF3	0.90	3.57	7.7E-07
dnd	0.60	3.57	4.8E-02
Atg101	3.83	3.57	8.8E-09
Lerp	1.89	3.56	5.5E-05
Npc2a	10.18	3.56	3.2E-05
InR	2.74	3.56	3.5E-08
CG14523	2.42	3.56	7.8E-04
CG32486	5.67	3.55	4.5E-06
pre-mod(mdg4)-G	0.52	3.55	1.6E-02
CG7530	6.97	3.55	7.1E-10
Drak	5.85	3.53	7.4E-10
CG42568	0.62	3.53	1.0E-02
Syt12	0.22	3.53	1.6E-02
CG8475	7.62	3.52	2.8E-09
alrm	0.72	3.52	3.5E-02
CG6793	0.44	3.51	4.4E-02
HPS4	2.65	3.50	4.7E-06
CG18327	0.42	3.50	4.2E-02
Gsl	5.47	3.48	5.8E-05
rdgBbeta	1.61	3.48	2.4E-04
CG9743	2.08	3.47	1.8E-03
DIP-alpha	0.21	3.45	4.2E-04
CG4752	5.78	3.45	1.5E-06
metro	1.03	3.44	3.4E-03
Hus1-like	2.76	3.43	2.6E-05
Atpalpha	53.03	3.42	7.6E-04
CG31759	1.48	3.42	2.1E-04
Fas1	18.91	3.42	1.7E-05
CG32191	1.34	3.42	3.0E-03
lama	3.13	3.42	1.3E-05
CG34394	4.10	3.41	6.8E-08
sosie	0.45	3.41	1.5E-02
Tap2	13.61	3.41	1.6E-06
rn	0.16	3.40	4.4E-02
CG8360	12.44	3.39	5.7E-05
CG43102	1.37	3.36	4.3E-06
Fer1HCH	55.04	3.36	6.1E-05
cdi	3.40	3.35	2.3E-07
CG11426	0.91	3.35	3.7E-02
Rgk3	0.35	3.34	5.4E-03
CG15080	0.20	3.34	4.3E-02
GstE5	0.91	3.34	3.2E-02
rgr	0.85	3.33	1.6E-03
CG31793	2.38	3.33	5.1E-06
csw	9.79	3.33	8.3E-06
Tret1-2	0.72	3.33	7.7E-03
out	5.58	3.32	1.7E-07
CG17928	3.22	3.32	1.9E-03
hid	0.92	3.31	2.8E-04
CG8654	2.87	3.31	1.1E-05
klu	0.68	3.31	2.7E-03
ry	4.00	3.29	9.7E-06
retm	3.59	3.29	2.5E-07
CG5810	2.91	3.28	2.5E-03
Sap47	5.58	3.28	4.1E-07
CG7997	2.53	3.28	3.9E-04
Rcd2	1.11	3.27	9.0E-04
sns	0.63	3.27	2.1E-03
AMPdeam	8.26	3.27	3.0E-06
CG2543	0.82	3.27	9.8E-03
CG44243	12.85	3.26	2.1E-07
Ziz	2.37	3.26	1.2E-07
Cyp4ae1	0.99	3.26	2.5E-03
CG3703	0.81	3.26	1.5E-02
Mal-A5	5.30	3.24	1.7E-04
CG8924	0.75	3.24	3.4E-03
CHKov2	7.15	3.24	1.8E-06
Indy	23.57	3.23	3.4E-06
Hydr1	2.73	3.23	4.0E-07
htl	0.74	3.23	9.0E-03
CG3609	19.64	3.22	1.4E-04
CG30411	1.28	3.22	7.6E-03
CG42399	0.70	3.22	1.8E-03
CG31051	0.58	3.22	4.9E-02
CG9664	1.51	3.21	8.4E-05
Nlg1	0.90	3.21	5.1E-03
CG10361	1.64	3.21	5.5E-03
Pdk	14.23	3.21	2.3E-07
CG10307	0.92	3.21	2.5E-02
pigs	4.73	3.20	7.6E-07
CASK	4.83	3.20	5.8E-06
vir-1	53.63	3.19	4.0E-04
KP78b	0.91	3.19	2.6E-03
CG44249	0.94	3.18	1.3E-02
Ndg	4.98	3.18	7.6E-04

Cyp6a9	13.16	3.17	4.4E-06
CG13283	1.19	3.17	1.9E-02
LRP1	7.10	3.16	5.8E-05
Gel	39.74	3.16	2.7E-04
CG9636	3.21	3.15	6.2E-06
CG6428	1.64	3.14	2.9E-04
CG31523	26.29	3.14	7.5E-05
CG18661	0.78	3.13	3.7E-02
CG43092	1.49	3.13	1.6E-02
kar	2.32	3.13	2.6E-03
lhex1	32.67	3.12	2.8E-07
CG3860	4.03	3.12	1.2E-06
NetB	1.08	3.12	6.9E-06
CG13248	1.36	3.11	1.4E-02
babos	16.52	3.09	1.2E-04
Pect	14.16	3.08	1.5E-06
magu	11.60	3.07	4.0E-06
ade5	17.30	3.07	2.7E-06
Mob2	4.80	3.07	1.6E-06
olf413	1.41	3.06	2.4E-04
aralar1	10.37	3.05	1.7E-06
rost	7.65	3.04	5.7E-04
CG14688	6.48	3.03	1.2E-03
CG33995	0.65	3.02	9.7E-03
Rfx	1.02	3.02	2.5E-03
CG46310	2.06	3.02	7.5E-03
Cyp9f3	1.49	3.00	6.9E-04
rogdi	3.77	3.00	3.1E-05
CG32017	4.07	3.00	3.4E-06
CG13841	1.63	2.99	2.1E-02
EDTP	5.57	2.99	1.5E-05
Cat	239.48	2.99	5.0E-03
CG42807	2.36	2.98	5.7E-03
CG13506	5.25	2.97	1.4E-06
CG8229	3.42	2.96	6.7E-05
CG11897	2.87	2.96	1.3E-05
CG2278	0.91	2.96	2.5E-03
zyd	1.37	2.95	5.5E-04
CG9485	7.69	2.95	4.7E-05
CG9413	2.43	2.94	3.0E-03
CG4462	1.25	2.94	3.4E-02
CG32425	3.56	2.93	2.6E-06
CG10165	1.78	2.92	2.2E-03
lrc	15.16	2.92	3.6E-06
Dr	0.63	2.92	3.3E-02
baz	8.69	2.92	8.4E-05
pan	4.76	2.91	1.1E-05
MTF-1	2.55	2.90	6.3E-05
CG3168	4.72	2.90	1.3E-03
CG8177	4.19	2.90	4.9E-06
Ir76a	0.75	2.90	3.3E-02
Tsp96F	5.15	2.89	5.1E-06
Mdr49	1.59	2.89	9.1E-04
CG6767	18.57	2.89	8.6E-06
CG3198	3.29	2.89	4.0E-06
HEATR2	1.40	2.88	1.7E-05
CG42711	2.53	2.88	2.6E-02
Zasp52	7.82	2.88	6.4E-04
CG2765	34.50	2.87	2.4E-04
CG5262	4.11	2.87	4.1E-05
ps	17.78	2.86	2.9E-03
sws	4.83	2.85	1.9E-06
nonA	3.44	2.84	1.5E-05
glob1	48.30	2.84	1.4E-04
CG3164	50.53	2.84	1.4E-03
SeIR	3.68	2.84	3.3E-05
CG33229	39.53	2.84	1.9E-05
Fer2LCH	83.25	2.83	3.9E-04
CG33090	1.42	2.82	1.8E-04
CG33260	2.62	2.81	2.5E-03
Pgm	34.15	2.78	4.7E-04
CG7458	1.03	2.78	3.4E-02
bchs	2.90	2.77	2.7E-06
IP3K2	4.73	2.77	3.3E-06
CG34135	0.29	2.77	6.8E-03
Pkcdelta	0.85	2.76	2.9E-03
CG14505	2.13	2.76	9.3E-03
Invadylsin	3.75	2.76	1.0E-04
CG18812	9.44	2.75	1.1E-05
Sdc	15.68	2.74	2.7E-05
whd	20.74	2.72	2.1E-05
Bsg	8.68	2.71	2.1E-04
CG6746	19.38	2.71	5.2E-05
Npl4	13.33	2.70	1.5E-06
Csk	12.12	2.69	5.4E-05
lawc	2.56	2.69	3.4E-05
CdsA	10.88	2.68	1.7E-05
CG3534	10.28	2.68	6.4E-04
KrT95D	4.78	2.68	9.6E-05
CG3618	0.81	2.68	1.3E-02
CG32512	5.22	2.68	3.7E-04
CG12947	1.99	2.67	1.1E-02
CG9416	1.17	2.67	6.5E-03
Ir62a	1.69	2.65	2.9E-03
bhc	10.32	2.64	2.6E-05
CG5938	5.12	2.64	1.8E-05
lhm	1.99	2.63	1.2E-02
CG18853	1.54	2.63	3.1E-02
CG5916	1.23	2.63	2.9E-02
tun	1.65	2.62	6.8E-05
CG9663	2.66	2.62	3.0E-06
CanA-14F	4.06	2.61	9.6E-06
Grip	0.56	2.61	8.3E-03
CG8679	1.72	2.61	9.6E-03
Nna1	1.79	2.61	1.3E-03
CG17278	5.24	2.61	7.5E-05
Spn	2.11	2.60	2.5E-04
CG11155	3.48	2.60	2.2E-04
CG6330	6.07	2.60	6.3E-03
oys	10.89	2.60	3.5E-05
CaMKII	10.31	2.60	4.9E-05

smg	3.37	2.60	4.4E-05
CG5098	1.86	2.60	4.8E-04
ImpL2	19.02	2.60	8.3E-04
PH4alphaEFB	7.45	2.59	2.2E-04
CG1146	4.96	2.59	1.7E-04
CG30281	3.56	2.59	2.4E-02
CG7565	2.80	2.59	2.1E-04
CG33199	11.30	2.58	1.2E-04
ksr	4.10	2.58	2.3E-02
CG17108	11.09	2.58	1.5E-02
CG10444	5.12	2.57	3.0E-04
Cyp9f2	28.97	2.57	1.2E-04
CG7362	1.85	2.57	1.5E-03
GlcT-1	2.31	2.57	4.8E-06
Plc21C	5.23	2.56	7.6E-05
CG45092	2.54	2.55	2.4E-04
CG42353	4.36	2.55	4.1E-05
CG11722	2.67	2.55	3.7E-02
CG3409	2.47	2.55	3.9E-04
Rab39	5.66	2.54	4.9E-03
CG8012	112.57	2.54	5.6E-03
CG11247	3.13	2.54	2.9E-04
CG4945	1.22	2.53	1.4E-02
chrB	5.71	2.53	1.0E-05
Cyp313a4	3.95	2.52	1.1E-03
puc	7.77	2.52	1.4E-05
dtn	2.64	2.52	1.5E-04
SLC5A11	5.07	2.51	8.2E-04
CG3662	23.56	2.51	2.4E-04
vri	6.11	2.50	1.2E-04
mnb	3.14	2.50	1.3E-04
CG15210	8.99	2.50	2.8E-02
pyx	0.48	2.50	3.6E-02
Mef2	3.56	2.50	1.6E-05
CG2258	1.99	2.49	1.2E-03
CG5445	5.68	2.49	1.5E-04
Mnt	6.81	2.49	6.5E-05
Tsp97E	5.21	2.49	6.3E-04
HDAC6	3.05	2.49	1.8E-03
CG15547	1.24	2.48	4.7E-02
CG1722	2.21	2.48	1.7E-02
CG4502	3.42	2.47	5.7E-03
Atg8a	62.18	2.47	9.7E-04
CG42806	5.61	2.47	6.0E-03
luna	2.01	2.46	6.6E-05
Syx1A	12.22	2.46	2.0E-04
rdgB	2.72	2.46	5.7E-04
sfl	4.70	2.46	5.4E-05
temp	1.62	2.46	1.2E-02
CG9003	3.35	2.45	1.3E-03
GlcAT-S	2.55	2.45	1.1E-03
otk	0.62	2.45	3.0E-02
Fitm	5.34	2.44	8.8E-05
CG10516	3.73	2.44	1.7E-02
CG14502	1.09	2.44	2.0E-02
CycT	5.68	2.44	3.0E-05
CG18547	6.30	2.43	1.1E-02
Treh	15.46	2.43	2.7E-04
CG13082	10.53	2.43	2.6E-03
mub	5.03	2.43	1.2E-04
fhp	25.79	2.43	1.7E-03
CG10089	0.73	2.43	4.4E-02
B4	4.79	2.42	8.7E-05
CG12428	1.53	2.42	4.7E-02
CG3630	3.33	2.42	8.3E-03
Lar	4.49	2.41	5.2E-04
CG6218	2.13	2.40	1.6E-02
bun	15.03	2.40	9.4E-03
fok	14.67	2.40	1.9E-03
Plp	4.73	2.40	6.6E-04
CHES-1-like	4.69	2.40	6.3E-05
cyc	3.23	2.39	1.6E-03
Ttd14	9.16	2.39	4.0E-05
CG6836	4.42	2.39	1.8E-03
CG10011	2.26	2.39	1.8E-04
Atg17	6.94	2.38	4.0E-04
CG17111	5.06	2.38	6.4E-04
CG17646	41.62	2.38	3.2E-03
gce	7.40	2.38	2.8E-04
sigmar	3.84	2.38	2.4E-04
CG10082	10.38	2.38	3.7E-04
Fsf3	2.75	2.38	8.7E-03
sni	4.70	2.37	4.1E-05
Syx8	5.34	2.37	6.9E-03
Dcp-1	1.50	2.37	3.2E-02
CG9896	3.19	2.37	2.4E-03
Sulf1	2.36	2.35	1.2E-03
Scamp	8.64	2.33	1.7E-04
Cdep	7.00	2.33	4.4E-03
S	2.79	2.33	6.3E-04
CG30280	2.51	2.32	3.6E-02
Deaf1	2.56	2.32	2.4E-03
CG42709	4.54	2.32	5.1E-03
fzo	2.68	2.32	2.7E-02
CG10365	7.85	2.32	2.6E-03
Tet	2.80	2.31	1.4E-03
CG6287	18.59	2.31	6.5E-03
sqa	0.96	2.30	1.8E-02
E23	0.76	2.30	1.8E-02
Gbs-76A	5.30	2.30	2.5E-03
Sfxn1-3	8.26	2.30	1.2E-03
Ric	8.31	2.29	1.5E-03
wgn	7.03	2.29	3.8E-04
CG13384	7.51	2.29	3.7E-03
tamo	3.26	2.28	9.6E-04
CG17508	20.71	2.28	2.0E-03
Rim2	5.25	2.28	2.8E-03
Cbl	2.83	2.28	1.6E-03
Pp1alpha-96A	8.84	2.28	4.8E-04
CG5867	81.20	2.27	9.6E-03
I(1)G0196	7.92	2.27	8.2E-04

bc10	6.15	2.27	7.3E-04
Trpm	3.29	2.26	1.7E-03
CG4630	1.26	2.26	4.9E-02
CG14661	30.44	2.26	1.9E-02
stmA	8.48	2.25	4.1E-04
CG5853	3.78	2.25	2.2E-03
Pde6	2.11	2.24	3.8E-02
CG3348	12.07	2.24	1.6E-02
CG7115	5.19	2.24	1.2E-03
GstE3	20.09	2.23	1.3E-02
CenG1A	3.32	2.23	4.9E-03
Mondo	6.32	2.23	8.6E-04
bves	1.76	2.23	4.1E-03
Jupiter	8.49	2.22	1.0E-02
CG30493	2.10	2.22	1.9E-02
Baldspot	15.68	2.21	1.5E-03
mamo	2.82	2.21	2.6E-03
CG11147	21.59	2.21	9.7E-04
CG6145	9.61	2.20	3.2E-03
Mhcl	7.85	2.20	2.8E-03
RhoGAPp190	6.82	2.20	1.9E-03
CG8009	5.10	2.20	3.2E-02
CG31712	6.55	2.19	7.5E-04
CG5946	15.97	2.19	7.5E-04
Ssadh	8.09	2.18	2.7E-03
Lrch	1.85	2.18	1.0E-02
ttv	2.45	2.18	4.3E-03
tnc	0.87	2.17	6.6E-03
CG5381	10.10	2.17	3.8E-04
CG8188	3.65	2.16	4.1E-03
rho	2.55	2.16	1.1E-02
ewg	2.58	2.16	1.8E-03
Usf	2.86	2.16	1.8E-03
ush	2.04	2.16	7.1E-03
IscU	22.03	2.15	1.3E-02
cu	3.31	2.15	3.6E-02
Ndfip	5.51	2.15	1.5E-03
MESK2	9.03	2.15	8.3E-04
hfp	8.84	2.15	1.5E-03
CG42837	13.02	2.15	2.5E-04
CG6178	7.36	2.14	4.8E-03
CG9674	30.72	2.14	4.3E-02
Lk6	55.44	2.14	4.8E-02
Nc73EF	33.69	2.14	1.8E-02
CG4991	5.13	2.13	4.0E-02
ab	1.30	2.13	3.9E-03
spin	15.36	2.13	2.2E-03
HPS1	2.07	2.12	3.6E-02
SNF4Agamma	4.89	2.12	1.8E-03
Mnn1	4.42	2.11	1.2E-02
CG5789	6.43	2.11	3.8E-03
CG14408	2.43	2.11	2.2E-02
CG18858	8.95	2.11	3.5E-03
CG6084	31.82	2.10	6.1E-03
St1	3.09	2.10	4.5E-02
CG10600	4.90	2.10	4.5E-03
rl	12.20	2.09	3.7E-03
Ect4	15.19	2.09	1.7E-02
Mul1	3.48	2.09	1.5E-02
egr	3.24	2.09	2.2E-02
Oat	7.58	2.09	7.7E-03
CG6903	5.70	2.09	8.0E-03
CG5027	4.39	2.09	2.2E-02
Drip	16.89	2.08	3.5E-03
sgg	6.68	2.08	3.8E-03
CG18809	2.59	2.08	1.2E-02
Dhap-at	2.21	2.08	1.0E-02
F-cup	2.18	2.08	1.7E-02
CG42390	4.39	2.07	1.5E-02
Cln7	5.37	2.07	1.2E-02
Pis	10.65	2.07	1.4E-02
Thd1	8.82	2.06	1.0E-02
Dyrk2	5.40	2.05	4.0E-03
CG1636	2.20	2.05	1.8E-02
Pdk1	8.75	2.05	5.2E-03
CG8034	5.51	2.05	1.3E-02
oaf	3.11	2.04	8.6E-03
MFS17	8.77	2.04	1.7E-03
CG16791	6.50	2.04	3.9E-03
toc	4.30	2.04	5.8E-03
CG11658	2.52	2.03	4.1E-02
isoQC	4.22	2.03	2.4E-03
Diap1	25.41	2.02	5.9E-03
CG5455	11.35	2.02	3.7E-03
CG7766	14.24	2.02	3.7E-03
PGRP-LF	4.63	2.02	1.2E-02
CG4294	4.99	2.02	4.1E-03
CG32850	3.38	2.02	1.9E-02
Gk1	9.04	2.02	6.9E-03
bru2	3.37	2.01	3.4E-03
TBC1D5	5.22	2.01	2.3E-03
cav	1.79	2.01	3.9E-02
Atg13	7.93	2.01	6.6E-03
hth	8.17	2.01	1.0E-02
CG8206	11.55	2.01	1.1E-02
Taz	2.29	2.00	3.7E-02
CG11309	7.29	2.00	1.0E-02
CG4619	2.34	2.00	2.0E-02
RasGAP1	4.88	2.00	7.9E-03
I(3)O2640	14.58	2.00	1.2E-02
CG3097	5.45	2.00	3.9E-02
CG31436	4.69	2.00	1.1E-02
Kap3	3.38	1.99	1.6E-02
D2hgdh	17.84	1.99	9.6E-03
CG4407	6.41	1.99	5.2E-03
mnd	4.09	1.99	2.0E-02
ZnT77C	9.70	1.99	4.9E-02
CG3714	9.74	1.98	2.6E-03
Sxl	6.67	1.98	6.9E-03
Ggamma1	31.81	1.98	8.5E-03
gem	9.76	1.98	7.6E-03

ERR	4.92	1.97	6.8E-03
Pif1A	10.28	1.97	2.7E-02
sli	2.79	1.97	1.9E-02
CG4562	1.11	1.97	2.7E-02
CG45781	2.74	1.96	2.9E-02
CG31635	5.88	1.96	5.6E-03
Cyp18a1	23.23	1.96	6.7E-03
Pitslr	9.78	1.96	3.8E-03
Fatp	13.45	1.96	1.2E-02
CG10669	1.27	1.95	3.6E-02
CG15309	1.84	1.94	2.4E-02
CG12512	5.33	1.94	3.8E-02
sev	3.55	1.94	2.8E-02
Pmp70	8.80	1.93	1.7E-02
CG1607	13.01	1.93	6.3E-03
CG1657	4.69	1.93	1.1E-02
capu	1.54	1.93	1.6E-02
Pif1B	10.87	1.92	3.5E-02
Kdm4B	2.37	1.92	1.4E-02
Mkp3	3.79	1.92	1.3E-02
CG46319	9.71	1.92	1.2E-02
slim	9.25	1.92	8.9E-03
Dic1	10.16	1.92	3.3E-02
CG6928	2.34	1.92	3.9E-02
Pde11	5.44	1.92	3.2E-03
Galphaq	6.21	1.91	5.6E-03
AsnS	7.09	1.91	3.1E-02
SP2637	5.45	1.91	1.6E-02
Stat92E	23.11	1.91	2.0E-02
Rab14	6.96	1.90	2.0E-02
Jing	2.36	1.90	5.9E-03
CG9328	3.43	1.90	3.8E-02
CG11275	7.73	1.90	3.9E-02
CG17360	3.61	1.90	1.9E-02
RhoGAP18B	4.12	1.90	6.5E-03
fz-1	5.00	1.90	5.0E-03
Parp	10.12	1.89	1.4E-02
CG5151	4.72	1.89	8.6E-03
Pino	38.01	1.88	1.8E-02
Adk1	8.07	1.88	4.9E-02
Ugt86Da	19.18	1.88	6.9E-03
CG31324	2.92	1.87	3.8E-02
Hsepi	3.60	1.87	2.1E-02
CG14478	6.36	1.87	2.9E-02
RN-tre	2.87	1.87	2.4E-02
Cyt-b5	96.15	1.87	3.8E-02
Fur1	6.30	1.86	7.0E-03
Ext2	2.11	1.86	3.7E-02
CG10543	4.18	1.86	1.4E-02
CG1637	8.09	1.84	1.5E-02
CG1718	4.47	1.84	8.8E-03
Kr-h1	8.81	1.84	2.9E-02
sog	12.85	1.84	1.4E-02
Xe7	7.95	1.83	1.3E-02
CG5830	10.97	1.83	1.0E-02
Nmda1	18.51	1.83	1.2E-02
CG30344	7.77	1.83	4.5E-02
Usp12-46	5.69	1.82	2.9E-02
CG6700	8.30	1.82	3.1E-02
foi	12.25	1.82	2.7E-02
Atg1	6.86	1.82	1.8E-02
CG2865	3.52	1.82	3.1E-02
Tollo	7.35	1.82	3.0E-02
mlt	9.24	1.81	3.0E-02
RtGEF	2.52	1.81	2.8E-02
CG11873	4.80	1.81	4.3E-02
FeCH	13.60	1.81	1.4E-02
spg	4.54	1.80	1.6E-02
CG5287	6.44	1.80	8.3E-03
CG42524	8.38	1.80	2.8E-02
Ent1	7.91	1.80	3.3E-02
Cals	17.13	1.80	2.7E-02
EndoA	4.98	1.80	3.7E-02
CG31102	4.13	1.80	4.8E-02
CG32767	3.56	1.80	1.1E-02
Sox14	6.57	1.80	3.4E-02
fus	9.98	1.80	1.4E-02
Clc-a	4.00	1.79	1.8E-02
Lpin	14.10	1.79	1.7E-02
I(3)L1231	9.48	1.78	2.0E-02
dl	6.29	1.78	1.6E-02
CG4911	8.03	1.78	1.6E-02
CG3625	18.60	1.77	2.3E-02
ari-1	5.06	1.77	2.2E-02
Pvfl	3.66	1.77	3.2E-02
CtsB1	50.09	1.77	1.7E-02
trbl	9.70	1.77	1.8E-02
mura	7.29	1.77	3.1E-02
mth8	3.51	1.77	2.4E-02
Shroom	9.48	1.77	3.1E-02
alc	13.68	1.76	1.9E-02
AdenoK	8.93	1.76	3.5E-02
CG42672	4.05	1.76	1.6E-02
Camta	2.84	1.76	4.5E-02
C1GalTA	4.65	1.75	2.4E-02
tay	6.28	1.75	2.9E-02
wb	1.11	1.75	4.2E-02
app	2.88	1.75	4.8E-02
CG9005	7.45	1.74	3.1E-02
Pur-alpha	13.59	1.74	2.0E-02
DIP1	12.92	1.74	1.7E-02
CG45085	4.50	1.74	4.5E-02
Tomosyn	7.42	1.73	3.3E-02
CG16711	3.42	1.73	4.8E-02
foxo	9.44	1.72	3.8E-02
Sec22	12.81	1.71	3.1E-02
CG5316	4.31	1.71	4.1E-02
Unc-76	8.15	1.71	4.3E-02
tma	11.13	1.71	2.4E-02
Dip-B	32.24	1.71	4.1E-02
CG6923	1.99	1.70	4.2E-02

CG3907	12.23	1.70	4.6E-02
CG11360	4.59	1.69	3.6E-02
Ptpmeg2	3.68	1.69	4.0E-02
Gprk2	6.75	1.69	1.8E-02
CG13917	11.09	1.68	5.0E-02
siz	8.31	1.68	4.5E-02
mRps5	20.84	1.67	4.0E-02
CG43658	3.66	1.67	2.8E-02
CYLD	5.73	1.67	4.7E-02
cindr	11.39	1.65	4.3E-02
Reep1	10.29	1.65	2.7E-02
BuGZ	5.44	1.61	3.9E-02
psq	17.48	-1.64	4.9E-02
CG7461	35.47	-1.64	3.4E-02
CG12099	29.71	-1.65	3.6E-02
Tpr2	29.23	-1.66	4.4E-02
Sec71	15.07	-1.67	4.2E-02
CG5009	24.59	-1.67	3.6E-02
sktl	18.29	-1.68	3.5E-02
Ulp1	12.67	-1.69	4.5E-02
dor	5.07	-1.69	4.5E-02
elB	12.33	-1.69	3.5E-02
CG11857	30.17	-1.70	2.7E-02
Cand1	15.11	-1.70	3.3E-02
Etl1	6.54	-1.70	4.9E-02
Sema1b	29.31	-1.70	3.2E-02
ovo	12.09	-1.70	3.3E-02
Rbfox1	14.40	-1.70	4.1E-02
CG8858	10.31	-1.71	3.5E-02
robo1	7.09	-1.71	4.5E-02
CG11306	17.85	-1.71	4.1E-02
Uhl	14.48	-1.71	4.2E-02
AP-2alpha	20.45	-1.72	4.3E-02
Klp10A	12.94	-1.72	3.2E-02
CG7518	9.66	-1.72	2.7E-02
Z6-29-p	109.81	-1.72	4.5E-02
Mitofillin	21.06	-1.72	3.0E-02
stx	12.46	-1.72	3.4E-02
CG11876	36.16	-1.73	4.7E-02
CG8230	13.71	-1.73	3.9E-02
Klc	29.30	-1.74	3.2E-02
Nipped-A	13.67	-1.74	3.9E-02
SppL	5.98	-1.74	4.7E-02
CG8202	5.17	-1.74	3.4E-02
Lac	39.52	-1.74	3.3E-02
CG16974	19.72	-1.75	2.6E-02
mts	44.72	-1.75	2.6E-02
Fsn	11.55	-1.75	3.2E-02
Clc-c	14.51	-1.75	2.9E-02
Rab10	22.05	-1.75	3.3E-02
Pdc44	33.22	-1.76	2.6E-02
uzip	16.31	-1.76	4.0E-02
CG9095	11.57	-1.76	3.2E-02
Dcr-2	17.36	-1.76	2.8E-02
Tom20	29.03	-1.76	4.4E-02
CG8814	21.19	-1.76	3.0E-02
CG7987	10.34	-1.77	3.6E-02
CG3107	13.71	-1.77	2.0E-02
Arf79F	84.74	-1.77	3.3E-02
Fs(2)Ket	21.97	-1.77	2.5E-02
rush	17.58	-1.77	2.4E-02
CG13605	7.51	-1.77	3.2E-02
Vha44	27.13	-1.78	2.7E-02
CG17931	12.92	-1.78	4.1E-02
CG17271	29.48	-1.78	4.5E-02
tou	10.72	-1.78	4.2E-02
Not3	21.52	-1.78	1.0E-02
Dscam1	7.58	-1.78	3.7E-02
how	23.37	-1.78	3.6E-02
mbf1	21.41	-1.78	4.1E-02
Mer	5.23	-1.79	4.5E-02
cv-c	26.39	-1.79	4.7E-02
caps	17.73	-1.79	2.1E-02
alpha-Cat	23.22	-1.79	7.9E-03
CG8778	13.73	-1.80	3.9E-02
Droj2	45.50	-1.80	2.1E-02
Rop	24.98	-1.80	2.4E-02
ND-24	25.76	-1.80	4.6E-02
alpha-Est9	21.12	-1.80	2.1E-02
CG13746	9.38	-1.80	2.8E-02
P58IPK	31.14	-1.80	2.2E-02
pita	7.08	-1.80	2.4E-02
ste24a	26.27	-1.81	1.8E-02
Ras64B	29.85	-1.81	3.8E-02
Ddc	19.41	-1.81	4.3E-02
CG5214	43.39	-1.81	1.1E-02
sinu	15.98	-1.81	3.9E-02
Rgl	11.92	-1.81	1.6E-02
Nrd1	7.59	-1.81	3.1E-02
tank	7.58	-1.81	4.0E-02
Tor	9.55	-1.82	1.7E-02
Exo84	7.54	-1.82	2.1E-02
Mfe2	28.72	-1.82	1.8E-02
CG33096	6.00	-1.82	4.8E-02
Kr-h2	31.01	-1.82	2.5E-02
CG12262	78.43	-1.82	2.9E-02
CG7927	12.96	-1.82	3.2E-02
Dlic	33.00	-1.82	1.5E-02
sch	17.01	-1.82	1.4E-02
CG42389	14.94	-1.82	2.6E-02
Mtnalpha	49.78	-1.83	1.0E-02
CG6512	15.38	-1.83	2.5E-02
Prosbeta5	63.95	-1.83	3.5E-02
CG7523	17.73	-1.83	2.7E-02
Cul2	11.66	-1.83	3.7E-02
CG8728	10.44	-1.83	3.1E-02
gcl	6.94	-1.84	2.9E-02
Surf4	60.26	-1.84	2.1E-02
Pop2	13.59	-1.84	2.0E-02
CG10413	16.68	-1.84	2.0E-02
Chf5	27.56	-1.84	4.7E-02

Spf45	14.10	-1.84	1.6E-02
NAT1	53.72	-1.85	4.4E-02
eco	8.34	-1.85	2.7E-02
Ugt	28.11	-1.85	1.3E-02
CG31195	20.99	-1.85	1.5E-02
Past1	22.52	-1.85	1.1E-02
l[2]k09913	28.90	-1.85	1.4E-02
Bsg25D	9.26	-1.85	2.4E-02
Hem	11.97	-1.85	3.4E-02
Toll-7	12.06	-1.85	1.2E-02
Pp2A-29B	52.70	-1.85	8.1E-03
nocte	14.60	-1.86	2.9E-02
SMC1	10.40	-1.86	1.3E-02
Patr-1	9.09	-1.86	2.6E-02
dome	7.90	-1.86	3.3E-02
Pgd	55.96	-1.86	3.5E-02
qkr58E-3	10.24	-1.87	3.3E-02
Trap1	10.38	-1.87	4.3E-02
Smap	13.25	-1.87	1.5E-02
Gnf1	5.95	-1.87	4.1E-02
ZAP3	13.93	-1.87	1.4E-02
CG7453	10.89	-1.87	2.8E-02
Rab6	20.89	-1.88	1.2E-02
Ckl1alpha	25.21	-1.88	1.1E-02
mRps30	10.34	-1.88	3.8E-02
CG31368	5.46	-1.88	3.3E-02
Ythdf	10.32	-1.88	2.7E-02
mbt	9.03	-1.88	4.6E-02
CG42813	14.40	-1.88	2.7E-02
CG7065	4.49	-1.88	3.6E-02
cl	18.69	-1.89	1.1E-02
MRP	36.25	-1.89	4.0E-02
CG2004	33.45	-1.89	4.8E-02
SdhB	35.09	-1.90	1.6E-02
CG7265	10.80	-1.90	2.6E-02
CG15445	6.74	-1.90	2.1E-02
CG12321	21.51	-1.90	4.8E-02
CG1646	11.01	-1.90	3.9E-02
CG42306	6.45	-1.90	1.4E-02
CG33523	11.93	-1.90	1.9E-02
CG1129	8.12	-1.90	2.5E-02
CG17691	40.15	-1.91	6.5E-03
Start1	8.33	-1.91	2.4E-02
Sfmbt	6.61	-1.91	3.8E-02
CG5033	8.94	-1.91	3.0E-02
CG17593	19.52	-1.91	2.0E-02
CG13252	7.16	-1.91	2.1E-02
osa	16.76	-1.91	3.2E-02
sl	4.99	-1.91	4.9E-02
Scalpa	62.73	-1.91	2.6E-02
CG12093	13.44	-1.91	1.7E-02
CG31751	18.85	-1.92	1.3E-02
alt	39.13	-1.92	1.4E-02
CG10638	14.37	-1.92	4.0E-02
pr	14.50	-1.92	3.4E-02
Sps2	10.02	-1.92	3.4E-02
AnxB11	19.05	-1.92	6.4E-03
tai	9.98	-1.92	9.9E-03
CG4050	7.20	-1.92	3.5E-02
Shark	6.79	-1.92	1.6E-02
Syx5	19.97	-1.93	1.2E-02
Ggt-1	7.82	-1.93	2.0E-02
Mtr4	5.66	-1.93	4.5E-02
yrt	7.67	-1.93	3.0E-02
CG32280	24.93	-1.93	1.0E-02
Clbn	10.01	-1.93	3.1E-02
alpha-Man-IIa	6.46	-1.93	2.1E-02
CG8481	13.17	-1.93	1.6E-02
Mapmodulin	20.35	-1.93	1.3E-02
AP-1-2beta	25.86	-1.93	5.9E-03
Upf1	9.18	-1.94	1.0E-02
Txl	32.56	-1.94	2.6E-02
PGRP-LE	6.28	-1.94	4.2E-02
mxt	17.03	-1.94	8.4E-03
CG4239	10.45	-1.94	4.5E-02
CG42637	6.17	-1.94	1.6E-02
Cnx99A	44.99	-1.94	6.6E-03
CG7879	3.80	-1.94	4.6E-02
CG7456	9.78	-1.94	3.4E-02
CG5273	41.93	-1.94	2.0E-02
Traf4	3.77	-1.94	4.4E-02
CG16989	10.69	-1.94	9.0E-03
mRpl22	10.78	-1.94	3.2E-02
mri	12.29	-1.95	1.6E-02
CG9799	6.90	-1.95	3.1E-02
CSN1b	11.89	-1.95	3.8E-02
pasi2	13.74	-1.95	2.7E-02
vlc	16.28	-1.95	1.1E-02
CG11168	7.45	-1.95	2.5E-02
CG1161	28.86	-1.95	1.7E-02
Taf6	7.39	-1.95	3.5E-02
CG14641	14.79	-1.95	1.1E-02
row	10.68	-1.95	1.3E-02
CG6650	6.88	-1.95	1.6E-02
CG5149	8.44	-1.95	1.2E-02
usp	10.46	-1.96	1.7E-02
CG32276	124.55	-1.96	9.7E-03
Mo25	15.96	-1.96	1.5E-02
CG31108	5.44	-1.96	2.6E-02
IntS2	6.45	-1.96	4.5E-02
Rich	7.81	-1.96	1.5E-02
Smr	15.78	-1.96	1.4E-02
Liprin-beta	13.27	-1.96	1.6E-02
Prosalpa3	60.78	-1.96	2.6E-02
egl	22.45	-1.96	7.0E-03
Acf	7.09	-1.96	1.8E-02
CG7379	7.36	-1.96	4.4E-02
Flo2	11.92	-1.97	1.8E-02
CG8060	2.65	-1.97	3.8E-02
Zip102B	15.39	-1.97	9.1E-03
lace	12.53	-1.97	1.5E-02

CG1824	8.85	-1.97	9.6E-03
Sara	16.89	-1.97	5.0E-03
CG10657	20.68	-1.97	2.6E-02
kel	8.70	-1.97	2.9E-02
MetRS	12.75	-1.97	7.5E-03
DUBAI	9.82	-1.97	5.0E-03
CG6907	9.81	-1.97	1.1E-02
RpA-70	14.65	-1.97	1.6E-02
CG33111	11.61	-1.97	1.7E-02
DCTN1-p150	18.24	-1.98	2.2E-03
stai	14.15	-1.98	1.3E-02
NSD	6.46	-1.98	2.9E-02
CG6231	7.81	-1.98	3.5E-02
Mpcp2	187.55	-1.98	3.4E-02
SF1	13.02	-1.98	1.5E-02
Psc	2.83	-1.98	1.9E-02
tinc	5.72	-1.98	1.5E-02
Vps13B	5.20	-1.99	3.4E-03
CG11377	8.27	-1.99	4.2E-02
Fur2	25.09	-1.99	4.4E-03
Vps35	18.11	-1.99	6.7E-03
Sf3b6	22.84	-1.99	2.0E-02
l[2]gd1	9.69	-2.00	1.0E-02
dally	42.07	-2.00	9.5E-03
CG10747	9.55	-2.00	2.6E-02
CG8207	6.75	-2.00	3.6E-02
dmt	4.91	-2.00	3.5E-02
CG8578	9.34	-2.01	1.1E-02
CG30349	10.98	-2.01	3.8E-02
Adsl	14.60	-2.01	1.3E-02
vih	9.21	-2.01	4.1E-02
brm	14.72	-2.01	4.6E-03
Spt5	15.75	-2.01	5.8E-03
Rox8	21.97	-2.01	4.0E-03
Amun	18.11	-2.01	2.1E-03
CG3967	5.16	-2.01	8.5E-03
CG17168	7.16	-2.01	2.5E-02
Der-1	34.50	-2.01	1.6E-02
CG17565	6.93	-2.01	2.8E-02
CG3702	24.55	-2.02	3.7E-03
CG9304	8.46	-2.02	8.5E-03
dom	21.27	-2.02	2.4E-02
UQCR-C2	55.63	-2.02	2.8E-02
Sec10	6.44	-2.02	2.8E-02
CG10321	10.03	-2.02	4.7E-02
Ube3a	6.52	-2.02	2.9E-02
Bet1	8.99	-2.02	4.5E-02
Cp190	15.72	-2.02	2.8E-03
Pex14	13.80	-2.03	1.4E-02
CG32428	10.07	-2.03	1.5E-02
ago	11.78	-2.03	5.3E-03
CG9248	14.05	-2.03	1.3E-02
Mon1	6.29	-2.03	4.7E-02
thoc7	11.44	-2.03	4.1E-02
CG4585	10.16	-2.03	1.5E-02
MED15	6.73	-2.04	6.5E-03
CG13887	82.40	-2.04	7.1E-03
CG16979	9.88	-2.04	3.7E-02
COX5A	107.83	-2.04	3.4E-02
Rme-8	12.58	-2.04	2.7E-03
ldgff6	259.00	-2.04	3.8E-02
CG8237	9.32	-2.04	3.4E-02
CG1407	5.94	-2.04	9.7E-03
CG10932	21.14	-2.05	3.5E-02
CG8498	39.09	-2.05	4.5E-02
mRpl46	10.19	-2.05	4.7E-02
p24-1	25.06	-2.05	3.5E-02
COX4	92.98	-2.05	3.1E-02
Pfdn6	21.33	-2.05	2.2E-02
slmb	15.46	-2.05	4.9E-03
CG8369	153.56	-2.05	4.4E-02
FER	9.95	-2.05	1.5E-02
CG7206	7.40	-2.06	4.0E-02
noc	29.22	-2.06	2.7E-03
CG11210	16.06	-2.06	5.7E-03
CG10184	12.41	-2.07	1.6E-02
dap	6.00	-2.07	2.8E-02
Elp1	6.53	-2.07	4.6E-02
ric8a	3.54	-2.07	2.0E-02
RpS14a	346.66	-2.07	3.3E-02
Cdc27	6.01	-2.07	2.9E-03
TER94	88.10	-2.07	9.8E-03
mRps22	12.37	-2.07	4.2E-03
CG17272	15.85	-2.07	3.1E-02
CSN3	9.97	-2.07	1.6E-02
key	14.97	-2.07	4.3E-03
klar	17.71	-2.07	5.4E-03
CG3505	35.62	-2.07	3.3E-02
Oatp74D	25.36	-2.07	2.7E-03
GluProRS	22.37	-2.08	3.4E-03
kto	6.98	-2.08	4.1E-03
CG16817	94.47	-2.08	6.6E-03
Ctr9	16.41	-2.08	1.5E-03
mei-41	1.59	-2.08	3.2E-02
CG7028	6.42	-2.08	8.6E-03
Cog7	6.78	-2.08	9.3E-03
CC5346	26.04	-2.09	4.0E-03
RpS24	639.88	-2.09	2.3E-02
CG13865	5.55	-2.09	2.6E-02
tub	10.15	-2.09	7.8E-03
Sbf	9.28	-2.09	5.3E-03
RpS14b	242.96	-2.09	1.3E-02
SF2	21.84	-2.09	4.0E-03
PIG-K	13.70	-2.09	5.2E-03
Uba3	8.67	-2.09	2.9E-02
goe	10.90	-2.10	6.6E-03
cold	22.04	-2.10	9.0E-03
CG12241	5.94	-2.10	4.3E-03
AMPKalpha	22.39	-2.10	1.6E-02
AP-2sigma	21.58	-2.10	2.1E-02
Capr	19.05	-2.10	2.5E-03

Rpn9	35.11	-2.10	2.5E-03
IntS11	8.84	-2.10	6.2E-03
CG11982	7.99	-2.10	2.8E-02
stc	10.04	-2.10	5.8E-03
CG12333	4.69	-2.11	2.5E-02
csul	5.26	-2.11	2.6E-02
betaGlu	6.07	-2.11	2.3E-02
Nop60B	17.81	-2.11	1.3E-02
CG17385	11.01	-2.11	9.7E-03
EbpIII	188.12	-2.11	5.0E-02
GEFmeso	7.24	-2.11	1.0E-02
CG30122	17.89	-2.11	3.5E-03
PhI1D1	6.22	-2.12	8.2E-03
Cap-G	5.84	-2.12	3.1E-02
cnk	7.19	-2.12	2.2E-03
CG14883	4.88	-2.12	3.0E-02
CG11241	4.55	-2.12	1.5E-02
CG3902	77.24	-2.12	1.4E-03
CG6805	18.91	-2.12	9.1E-03
htk	9.55	-2.12	7.4E-03
mRpl44	8.82	-2.12	2.5E-02
Psi	7.12	-2.12	5.7E-03
hyx	6.79	-2.13	4.5E-03
sona	18.41	-2.13	3.1E-02
beta4GalNAcTB	10.64	-2.13	2.8E-02
mge	14.97	-2.13	7.6E-03
CG17556	12.15	-2.13	1.4E-02
Glg1	26.39	-2.13	3.3E-03
GCS2alpha	89.37	-2.13	2.1E-02
CG17896	62.17	-2.13	1.3E-03
Aldh-III	37.85	-2.13	6.0E-03
Arp3	33.00	-2.13	2.6E-03
phr	11.43	-2.13	2.8E-03
tst	5.10	-2.13	5.0E-03
IKKbeta	7.29	-2.14	6.5E-03
Sec3	5.61	-2.14	2.8E-03
CG45099	4.48	-2.14	2.9E-02
Naa35	5.28	-2.14	2.5E-02
CG33181	5.67	-2.14	2.2E-02
Nup153	16.12	-2.14	2.0E-03
Prosbeta1	55.75	-2.14	1.1E-02
Rpl37A	365.05	-2.15	3.8E-02
Nup358	23.54	-2.15	3.5E-03
CG15784	73.18	-2.15	7.5E-03
jagn	24.69	-2.15	1.9E-03
Art4	8.71	-2.15	9.6E-03
Ars2	15.95	-2.15	1.0E-03
CG9990	53.09	-2.15	3.5E-03
vari	26.90	-2.15	5.2E-03
kug	12.58	-2.15	8.8E-03
CG13827	9.65	-2.15	3.8E-02
Zw10	8.45	-2.15	6.9E-03
CTPsvn	9.55	-2.15	1.5E-02
CG7255	3.30	-2.16	1.0E-02
CG2982	7.46	-2.16	7.8E-03
Dhx15	16.80	-2.16	3.7E-03
GABPI	8.16	-2.16	1.7E-02
Sema5c	13.50	-2.16	8.9E-03
yki	18.86	-2.16	2.0E-02
CG3548	5.30	-2.16	2.7E-02
CG4557	5.46	-2.16	3.0E-03
CG34125	14.62	-2.16	3.5E-02
sdk	20.57	-2.16	4.3E-03
PpD3	10.91	-2.16	9.7E-03
plx	89.78	-2.16	4.9E-03
Prosbeta3	62.50	-2.17	8.7E-03
Mob3	9.08	-2.17	4.0E-02
Mocs1	7.28	-2.17	8.9E-03
CG18273	4.91	-2.17	6.8E-03
CG8331	55.99	-2.17	6.0E-03
ocm	4.29	-2.17	2.2E-02
hdc	13.22	-2.17	5.5E-03
Ptp4E	16.59	-2.17	1.2E-03
BicD	12.01	-2.17	1.5E-03
Rbp1	15.96	-2.17	4.6E-03
Edem1	5.91	-2.17	1.8E-02
CG6276	8.44	-2.17	4.6E-02
kraken	23.32	-2.17	2.9E-02
Cyp4d20	20.15	-2.18	3.3E-02
PIG-B	14.62	-2.18	5.8E-03
CG5745	8.59	-2.18	2.1E-02
Sap30	6.36	-2.18	1.8E-02
wol	16.84	-2.18	3.1E-03
CG4360	8.27	-2.18	7.0E-03
kra	87.40	-2.18	3.7E-03
Trpml	4.90	-2.18	1.9E-02
RpS6	531.56	-2.18	4.8E-02
crb	25.98	-2.18	4.4E-03
CG12128	3.14	-2.18	4.0E-02
CG9992	11.54	-2.19	6.2E-03
CG17065	6.66	-2.19	4.8E-02
CG8108	18.22	-2.19	3.1E-03
CG7099	2.13	-2.19	1.8E-02
p115	13.78	-2.19	4.8E-03
CG8042	11.78	-2.19	6.4E-03
CG1907	22.29	-2.19	9.2E-03
CG40045	49.74	-2.19	8.9E-03
Sec31	25.31	-2.19	9.1E-03
CG5439	7.22	-2.20	1.9E-02
mri	13.64	-2.20	1.1E-03
CG11474	5.63	-2.20	3.4E-02
ssp	6.61	-2.20	2.5E-02
CG3224	13.54	-2.20	2.5E-02
Eip63E	13.88	-2.20	1.3E-03
nito	7.91	-2.20	1.2E-02
porin	93.75	-2.20	4.0E-03
SA	6.63	-2.21	1.6E-02
Usp47	29.93	-2.21	1.7E-03
CG5597	11.73	-2.21	4.9E-02
CG7878	11.16	-2.21	1.0E-02
mr	5.41	-2.21	3.1E-02

Sym	6.09	-2.21	7.5E-03
CG17765	37.40	-2.21	6.3E-03
CG5861	16.60	-2.21	4.9E-03
Tsr1	12.27	-2.21	2.6E-02
CG8312	41.79	-2.21	1.2E-03
Br140	4.03	-2.21	3.0E-03
CG6163	4.10	-2.21	4.8E-02
Rpi	24.91	-2.21	2.1E-02
Chro	11.15	-2.22	8.3E-03
CG32147	11.80	-2.22	1.9E-02
Dgp-1	6.83	-2.22	4.3E-03
CG5902	9.99	-2.22	4.8E-03
mRps9	16.89	-2.22	3.7E-03
Rpn2	36.71	-2.22	1.0E-03
Phb2	36.87	-2.22	5.4E-04
CG14253	8.52	-2.22	9.7E-03
CG42307	3.42	-2.22	2.3E-02
CG7275	6.55	-2.22	2.4E-02
CG10803	4.69	-2.23	3.7E-03
CG9281	31.86	-2.23	1.6E-03
Esyt2	47.40	-2.23	4.5E-03
Clic	54.97	-2.23	6.8E-04
CG3191	7.08	-2.23	2.9E-02
CG10347	6.07	-2.23	1.5E-02
CG2930	8.50	-2.23	2.3E-03
CG1418	8.92	-2.23	1.3E-02
Abp1	11.34	-2.24	7.3E-03
CG11151	48.38	-2.24	8.0E-03
MED8	8.44	-2.24	3.9E-02
eIF3h	91.52	-2.24	1.4E-03
mRpl3	7.35	-2.24	3.3E-02
CG7280	5.88	-2.24	2.2E-02
Nap1	97.79	-2.24	6.8E-04
bnl	7.75	-2.24	2.2E-02
Vinc	20.36	-2.24	1.0E-02
mmps	29.49	-2.24	1.5E-03
CG14407	16.90	-2.25	3.7E-02
Usp30	9.47	-2.25	3.1E-03
mRps35	7.15	-2.25	3.2E-02
CTCF	7.28	-2.25	5.1E-03
boca	23.28	-2.25	7.3E-03
GalNAc-T1	20.57	-2.25	1.3E-02
CG42638	4.75	-2.25	1.5E-02
Manf	62.62	-2.25	2.6E-03
Madm	10.78	-2.25	1.5E-02
DCTN4-p62	9.24	-2.25	3.7E-03
PIG-U	9.33	-2.25	4.8E-02
hpo	11.39	-2.26	2.2E-03
Sf3b2	12.42	-2.26	8.3E-03
su(f)	6.32	-2.26	4.0E-03
Cortactin	18.80	-2.26	9.4E-03
heph	17.63	-2.26	2.3E-03
Max	10.52	-2.26	1.0E-02
eIF3h	110.04	-2.26	5.5E-03
CG6426	120.77	-2.26	1.6E-02
Rcd6	7.52	-2.26	2.5E-03
Tailor	16.98	-2.27	2.3E-03
peb	9.94	-2.27	2.0E-03
Rhf	8.28	-2.27	1.3E-02
Prosalph6	54.19	-2.27	1.2E-03
CG10274	3.28	-2.27	1.4E-02
Tim17b	51.14	-2.27	2.7E-03
CG1910	17.61	-2.27	1.5E-03
drl	7.47	-2.27	2.0E-02
CG9186	34.22	-2.27	1.3E-03
SMC3	6.51	-2.27	2.8E-03
Galphas	27.44	-2.28	1.6E-03
Fkbp14	41.48	-2.28	1.4E-03
Rok	11.99	-2.28	2.9E-04
Spn28Dc	28.87	-2.28	7.5E-03
Tango1	29.39	-2.28	2.2E-03
CG17322	17.55	-2.28	2.2E-03
CG14818	36.72	-2.28	7.0E-03
SRm160	7.67	-2.28	2.6E-03
exd	22.03	-2.28	8.0E-04
RpL26	425.09	-2.28	4.8E-02
nrv1	61.63	-2.28	8.7E-04
CG42246	40.26	-2.28	4.2E-03
CG5708	11.56	-2.29	2.5E-02
CG6959	40.85	-2.29	6.0E-04
Rpl37a	375.95	-2.29	2.9E-02
HSPC300	14.36	-2.29	2.7E-02
Arfp	7.83	-2.29	6.7E-03
Rpl1140	17.16	-2.29	1.4E-03
msn	23.20	-2.29	2.0E-03
HmgZ	41.82	-2.29	1.9E-03
tud	68.62	-2.29	2.0E-02
P5CDh1	47.21	-2.29	2.6E-04
Karybeta3	87.24	-2.29	6.3E-03
Fas3	23.77	-2.30	4.0E-04
CG14817	10.23	-2.30	2.9E-02
lf2(tid)	6.79	-2.30	1.0E-02
CG3740	10.61	-2.30	4.4E-02
Vha100-2	159.22	-2.30	3.2E-02
E2f1	14.55	-2.30	7.7E-04
Vps28	14.65	-2.30	1.9E-03
CG2701	8.35	-2.30	4.7E-03
Ccdc56	9.06	-2.30	2.6E-02
emp	99.26	-2.30	5.6E-03
CG10939	50.64	-2.30	1.9E-04
Dis3	6.04	-2.31	5.1E-03
Dref	9.98	-2.31	4.0E-03
Adk2	64.98	-2.31	4.1E-03
Gcn2	5.42	-2.31	2.4E-03
Atg14	6.36	-2.31	1.4E-02
GCC185	6.53	-2.31	4.2E-03
CG1582	7.80	-2.31	3.5E-03
CG8891	12.25	-2.31	2.4E-02
CG46280	14.51	-2.31	8.9E-04
CG14043	6.31	-2.32	1.3E-02
CG4038	8.56	-2.32	4.6E-02

Ubc4	15,30	-2,32	3,9E-03
CG10623	6,22	-2,32	3,1E-02
TfIIA-L	19,36	-2,32	5,3E-03
CG9300	5,71	-2,32	2,0E-02
CG15611	28,99	-2,32	1,4E-03
CG33095	5,42	-2,32	7,1E-03
Rpn1	40,74	-2,32	4,0E-04
lrp-1A	10,71	-2,32	2,2E-03
Arf102F	51,11	-2,33	2,4E-03
CG6015	4,71	-2,33	1,9E-02
Ubi-p5E	135,72	-2,33	3,1E-03
CG5903	27,04	-2,33	8,7E-04
14-3-3zeta	169,65	-2,33	1,9E-02
CG17985	6,86	-2,33	1,2E-02
Rpl34a	92,02	-2,34	4,2E-03
RAF2	4,74	-2,34	3,7E-03
CG1665	13,62	-2,34	1,2E-02
SmE	29,15	-2,34	1,3E-02
GstO2	27,79	-2,34	2,2E-03
Med	5,51	-2,34	1,6E-03
CG31365	4,67	-2,34	2,0E-02
loco	6,78	-2,34	1,1E-03
CG12325	3,37	-2,34	3,4E-02
grv	12,17	-2,35	2,0E-02
eEF2	988,44	-2,35	3,5E-02
Vha36-1	79,13	-2,35	6,3E-04
stck	30,92	-2,35	1,3E-03
ecd	6,50	-2,35	9,9E-03
CG8735	16,30	-2,35	2,3E-03
CG12096	3,13	-2,35	1,2E-02
Cyp1	418,85	-2,35	2,9E-02
Syx13	10,32	-2,35	1,2E-03
sol	6,25	-2,35	1,8E-02
AlaRS-m	4,47	-2,35	5,8E-03
Sec24CD	32,08	-2,35	6,0E-04
imd	8,37	-2,35	4,9E-02
Ecr	19,05	-2,35	4,4E-04
CG8311	7,83	-2,35	9,2E-03
CG4266	9,84	-2,36	1,8E-03
CG9630	4,00	-2,36	4,6E-02
CG7430	47,18	-2,36	5,7E-04
scramb1	11,86	-2,36	8,3E-03
ana1	3,19	-2,36	1,3E-03
Taf2	4,65	-2,36	3,9E-03
tefu	3,64	-2,36	3,0E-03
mRp57	15,77	-2,36	7,7E-03
CG2091	5,39	-2,36	3,6E-02
Sh	7,21	-2,37	1,2E-03
Rab2	29,99	-2,37	2,3E-03
Hrb87F	14,09	-2,37	2,4E-03
CG9330	20,05	-2,37	1,5E-03
mib1	10,79	-2,37	4,8E-04
CG6749	5,44	-2,37	2,4E-02
CG14411	6,21	-2,37	4,7E-03
CG14969	8,69	-2,37	1,6E-02
be	14,71	-2,37	2,9E-04
btz	7,62	-2,37	3,0E-02
slv	3,33	-2,37	4,8E-02
Buffy	22,94	-2,38	1,8E-03
sowah	10,04	-2,38	2,0E-03
CG42359	7,55	-2,38	3,1E-02
snRNP-U1-70K	7,29	-2,38	1,1E-02
bonsai	10,29	-2,38	9,2E-03
CG11454	11,19	-2,38	1,6E-02
galactin	20,22	-2,38	3,0E-03
polybromo	8,80	-2,38	5,1E-04
CG5045	12,79	-2,38	1,1E-02
CG31075	37,87	-2,38	1,7E-03
sqh	64,50	-2,39	3,2E-04
Claspin	2,47	-2,39	3,2E-02
mRpL17	5,71	-2,39	3,8E-02
CG12499	6,41	-2,39	1,3E-03
pAbp	516,39	-2,39	2,6E-02
Lst8	8,31	-2,39	1,6E-02
CG2023	2,42	-2,39	3,4E-02
Prosalpha2	73,80	-2,39	1,3E-03
hav	3,84	-2,39	2,1E-02
Nsun2	8,10	-2,39	3,5E-03
Neur4	3,92	-2,39	1,0E-03
prominin-like	18,14	-2,40	4,7E-04
PpV	16,10	-2,40	2,5E-03
Nsf2	10,26	-2,40	2,1E-03
CG8298	2,34	-2,40	4,3E-02
Vps36	5,21	-2,40	4,2E-02
Rtf1	9,42	-2,40	5,6E-03
CG17834	15,92	-2,40	2,4E-03
CG12170	5,96	-2,40	3,2E-02
CG17121	40,85	-2,40	6,2E-04
CG31522	42,04	-2,40	9,3E-04
endos	25,69	-2,41	8,7E-04
CG3430	3,00	-2,41	4,2E-02
Sec61gamma	52,45	-2,41	1,5E-03
Snn27A	29,32	-2,41	3,6E-04
Dip-C	14,47	-2,41	1,9E-03
CG34398	17,05	-2,41	1,3E-04
CG7372	5,23	-2,41	2,9E-03
Hr39	8,85	-2,41	3,1E-04
mtm	9,35	-2,41	1,5E-03
beta4Gall7	6,39	-2,41	4,7E-02
lic	10,48	-2,41	1,2E-02
CG7639	6,51	-2,41	7,5E-03
Vps33B	6,09	-2,42	1,0E-02
Bx42	11,32	-2,42	1,6E-03
CalpB	16,03	-2,42	4,3E-04
swm	13,72	-2,42	2,6E-04
CG3689	9,44	-2,42	5,9E-04
salm	12,36	-2,42	5,3E-04
CG8777	4,20	-2,42	9,2E-03
CG2794	5,49	-2,42	1,7E-02
Dgkepsilon	10,91	-2,42	1,5E-03
SCCRO	7,08	-2,42	1,9E-02

sls	28,82	-2,42	4,8E-02
mbo	6,23	-2,42	3,7E-03
Dhpr	35,31	-2,42	7,2E-04
KdelR	53,47	-2,42	4,3E-04
Suf(var)3-3	3,46	-2,42	1,4E-02
CG4554	4,39	-2,43	3,6E-03
Bet3	10,73	-2,43	2,1E-02
PNPase	4,00	-2,43	9,0E-03
Bes2	16,73	-2,43	2,4E-04
Nup154	6,13	-2,43	4,7E-03
XNP	15,72	-2,43	1,7E-04
Rpn5	45,03	-2,43	2,5E-04
CG10979	4,61	-2,43	1,7E-02
CG5934	7,72	-2,43	3,5E-02
CG8031	12,49	-2,43	8,2E-03
HIPP1	11,19	-2,43	9,0E-04
rad50	4,95	-2,43	1,4E-03
CG9175	6,32	-2,43	9,4E-03
vimar	6,25	-2,44	1,4E-03
CG18766	7,60	-2,44	9,5E-03
CG42374	3,26	-2,44	4,0E-02
CG2224	4,02	-2,44	1,6E-02
Mcrr	34,62	-2,44	5,2E-04
RpS18	936,77	-2,44	4,1E-02
blow	6,99	-2,44	1,8E-03
CG5174	37,24	-2,44	2,3E-04
TyrRS	29,72	-2,45	9,3E-04
Ppn	92,09	-2,45	3,4E-02
mRpL18	7,20	-2,45	4,6E-02
Arc2	7,11	-2,45	4,3E-02
Acph-1	10,13	-2,45	5,0E-03
Zn72D	7,31	-2,45	3,7E-03
CG7945	10,91	-2,45	2,5E-03
CG5734	11,02	-2,45	1,8E-03
mRpL53	7,78	-2,45	4,7E-02
Nct	16,02	-2,45	3,1E-04
CG5727	6,07	-2,46	4,5E-02
Gp93	136,28	-2,46	2,9E-03
Vps20	17,60	-2,46	4,0E-03
CG8320	12,04	-2,46	5,9E-03
CG4866	8,82	-2,46	4,5E-02
CG4278	7,39	-2,46	2,8E-02
CG11790	42,54	-2,46	8,4E-04
CG6398	45,00	-2,46	6,8E-04
Cle	58,11	-2,46	4,2E-04
CG11076	14,45	-2,46	1,1E-03
CG18178	8,08	-2,46	7,1E-03
Prosalpha4	53,06	-2,47	9,1E-04
sqd	56,86	-2,47	3,9E-03
CG33298	9,49	-2,47	1,9E-04
RpS26	253,53	-2,47	1,5E-02
Cys	616,34	-2,47	2,2E-02
CG4598	19,23	-2,47	2,2E-03
Vha13	177,07	-2,47	1,9E-04
PyK	189,84	-2,47	4,0E-03
pkaap	12,47	-2,47	1,9E-03
CG8441	6,51	-2,47	3,4E-02
Gga	10,24	-2,47	6,0E-04
vig	24,08	-2,47	1,8E-04
mRpL32	7,21	-2,48	4,1E-02
mRpL38	7,50	-2,48	4,2E-03
CG13185	9,12	-2,48	8,0E-04
CG9941	9,33	-2,48	9,3E-04
Fdh	62,24	-2,48	9,6E-05
Khc	31,38	-2,48	1,3E-04
CG5037	8,91	-2,48	5,8E-03
CG7466	11,21	-2,48	1,8E-04
kune	30,12	-2,48	2,2E-03
[(2)37Cb	4,16	-2,49	1,7E-02
mRpL27	7,78	-2,49	3,7E-02
Ccs	7,10	-2,49	3,8E-02
GstZ1	7,98	-2,49	2,8E-02
mRpS11	14,94	-2,49	5,9E-03
YME1L	10,72	-2,49	9,5E-04
CG5114	9,95	-2,49	2,9E-02
CG1344	8,86	-2,50	6,8E-04
Arp6	11,55	-2,50	8,8E-03
trh	43,30	-2,50	1,7E-03
CG17209	3,45	-2,50	9,6E-03
CG31908	12,14	-2,50	9,1E-04
CG8611	3,37	-2,50	7,2E-03
Prp8	23,39	-2,50	1,5E-04
Zpr1	6,61	-2,50	1,1E-02
Vps37B	15,82	-2,50	2,1E-03
CG42239	20,22	-2,50	4,2E-02
CG13097	4,77	-2,50	2,0E-02
CG9914	61,19	-2,50	2,0E-03
Hsc70Cb	44,68	-2,51	5,1E-05
Fip1	8,00	-2,51	7,2E-03
LBR	4,23	-2,51	1,2E-02
Gp150	320,75	-2,51	1,7E-02
Dcr-1	5,80	-2,51	4,9E-04
CG3797	11,76	-2,51	5,1E-04
CG2010	3,53	-2,51	4,7E-02
Pex13	10,33	-2,52	8,7E-04
scramb2	29,02	-2,52	2,3E-04
Nmd3	10,16	-2,52	6,9E-04
Pex11	11,18	-2,52	3,7E-03
CG13663	9,57	-2,52	4,3E-02
eff	68,34	-2,53	3,8E-05
Prosap	18,58	-2,53	6,4E-05
CG9240	11,59	-2,53	4,1E-03
wat	185,42	-2,53	3,2E-03
shams	4,66	-2,53	4,2E-02
CG11771	9,60	-2,53	2,4E-03
Dhfr	11,25	-2,53	4,4E-02
SelG	30,05	-2,53	2,1E-03
Gli	17,02	-2,53	2,7E-04
eIF3g1	87,28	-2,53	2,5E-03
CG6418	5,42	-2,53	5,6E-03
CG2918	57,63	-2,54	6,1E-04

Eip74EF	8.56	-2.54	2.8E-04
CG2970	14.47	-2.54	1.3E-03
Tdrd3	7.83	-2.54	1.9E-03
ATPsynB	115.47	-2.54	1.7E-03
Sh3beta	21.98	-2.54	8.9E-05
cin	13.09	-2.54	1.2E-03
dia	17.32	-2.54	6.1E-05
CG11180	4.27	-2.54	1.2E-02
Ino80	4.74	-2.54	2.7E-03
CngB	19.62	-2.54	1.8E-03
narvin	28.70	-2.55	1.5E-04
ATPsyngamma	105.15	-2.55	1.3E-04
Rpt2	49.38	-2.55	1.6E-04
Rm62	71.91	-2.55	3.2E-03
I(1)10Bb	8.80	-2.55	1.7E-02
CG5110	13.34	-2.55	9.3E-03
CG6693	8.17	-2.55	3.8E-03
CG2658	7.00	-2.56	7.5E-04
CG7246	3.25	-2.56	3.8E-02
CG32640	27.31	-2.56	1.5E-02
CG8963	21.01	-2.56	5.2E-04
mRpl20	11.74	-2.56	3.3E-02
Cep135	2.53	-2.56	8.7E-03
CG1902	20.89	-2.56	2.0E-04
mEFTu2	6.36	-2.56	6.4E-03
CG44000	22.57	-2.56	1.8E-04
CG13516	8.43	-2.56	7.8E-03
Arp8	2.93	-2.56	1.7E-02
CstF64	4.45	-2.56	2.8E-02
Nprl2	4.80	-2.56	2.6E-02
Adat1	3.92	-2.57	1.1E-02
CG6878	15.59	-2.57	2.0E-02
CG2063	9.41	-2.57	3.7E-03
CG12107	18.82	-2.57	6.5E-03
Hsp68	28.14	-2.57	3.0E-04
CG12773	14.69	-2.57	2.0E-03
Gmd	7.92	-2.57	4.7E-03
Ufc1	31.03	-2.58	1.4E-03
Sem1	82.44	-2.58	2.3E-02
CG43163	8.35	-2.58	2.2E-04
Sod2	37.20	-2.58	1.7E-03
REG	24.60	-2.58	4.2E-04
Rpb10	25.01	-2.58	4.9E-03
CG12204	4.40	-2.58	3.7E-02
woc	17.33	-2.58	1.9E-04
alpha-Spec	85.25	-2.58	8.6E-03
I(3)7ZAb	15.13	-2.59	7.9E-05
CG5800	4.46	-2.59	2.2E-02
CG14232	4.15	-2.59	2.8E-02
Arc1	805.02	-2.59	2.5E-02
gro	12.30	-2.59	6.9E-04
CG5862	18.32	-2.59	2.4E-03
CG7655	10.13	-2.60	2.8E-03
Trx-2	94.47	-2.60	9.4E-04
mRpl28	20.51	-2.60	9.4E-04
SMC5	3.16	-2.60	6.2E-03
Snx1	18.16	-2.60	3.8E-04
Wdr24	2.82	-2.60	2.6E-02
Bre1	6.26	-2.60	3.9E-03
Fhl6	7.70	-2.60	4.7E-04
ArfGAP3	25.66	-2.60	5.9E-04
Atg16	4.48	-2.61	4.0E-03
bark	12.68	-2.61	3.6E-05
GC1	14.10	-2.61	3.4E-04
mRps23	8.03	-2.61	3.1E-02
SmD3	17.90	-2.61	4.3E-03
janA	16.48	-2.61	1.4E-02
CG3792	17.46	-2.61	2.2E-03
Vha14-1	76.43	-2.61	1.1E-03
Swip-1	35.13	-2.61	8.9E-04
CG13220	19.15	-2.62	2.4E-03
Dok	12.05	-2.62	5.8E-04
ast	3.44	-2.62	9.4E-03
CycH	6.44	-2.62	2.4E-02
ct	9.38	-2.62	2.9E-04
mRpl45	10.91	-2.62	4.7E-03
Hira	3.59	-2.62	7.8E-03
Arpc2	22.99	-2.62	4.5E-04
numb	14.63	-2.63	3.7E-05
eIF3m	86.88	-2.63	7.8E-05
ND-18	32.00	-2.63	1.4E-03
fu	3.54	-2.63	3.1E-03
CG6179	3.95	-2.63	2.4E-02
CG4452	12.47	-2.63	5.6E-04
CG3071	7.16	-2.63	4.7E-03
CG9776	11.11	-2.63	6.3E-05
CG14657	4.72	-2.63	6.5E-03
CG15881	5.44	-2.63	3.1E-02
Der-2	13.89	-2.64	2.4E-04
CG7970	21.59	-2.64	1.6E-03
Roc2	13.25	-2.64	5.2E-03
Dek	18.29	-2.64	4.6E-05
Rac1	23.46	-2.64	8.1E-05
uri	3.99	-2.64	1.2E-02
eIF4A	363.20	-2.65	7.8E-03
CG10628	3.67	-2.65	4.5E-02
AP-2mu	21.19	-2.65	4.6E-05
CG6984	5.30	-2.65	3.1E-02
Egm	6.74	-2.65	8.5E-03
eIF3e	78.96	-2.65	2.0E-04
HBS1	8.45	-2.65	1.2E-03
PIG-G	5.32	-2.65	6.4E-03
dgo	4.38	-2.66	2.3E-03
CG13390	3.76	-2.66	3.2E-02
CG6388	7.69	-2.66	3.9E-03
Smyd4-1	2.06	-2.66	4.5E-02
CG13365	9.39	-2.66	3.5E-02
Nup93-2	5.26	-2.66	3.9E-03
CG6664	12.83	-2.66	3.0E-04
cyp33	7.07	-2.66	2.8E-02
ISm1	13.17	-2.66	2.9E-02

eIF3k	77.87	-2.66	6.4E-05
mew	16.19	-2.66	6.1E-05
noi	9.18	-2.66	1.2E-03
Cklalpha-i3	9.26	-2.66	3.6E-03
CG14567	26.38	-2.66	1.9E-03
GlnRS	21.39	-2.66	1.8E-04
Mekk1	13.25	-2.66	1.3E-04
CG14215	6.53	-2.66	2.5E-04
CG13850	5.45	-2.66	5.1E-03
DCAF12	3.28	-2.67	2.8E-02
Alg-2	24.00	-2.67	8.7E-03
Alg10	5.63	-2.67	1.1E-02
I(1)G0156	46.94	-2.67	5.3E-05
CG4968	18.19	-2.67	1.8E-03
Fbxl7	5.79	-2.67	1.9E-04
CG6891	18.05	-2.67	1.1E-03
DNApol-delta	3.14	-2.68	6.7E-03
CG6583	14.61	-2.68	2.7E-03
Hlc	21.59	-2.68	8.1E-05
pll	8.08	-2.68	1.8E-03
IleRS	21.78	-2.68	2.1E-05
CG6073	6.08	-2.68	2.4E-02
mst	3.38	-2.68	1.1E-02
CG15386	9.72	-2.68	1.6E-02
Hip1	5.57	-2.68	1.6E-03
CG2218	12.97	-2.68	1.0E-03
Php95	1.77	-2.68	2.7E-02
CG3645	3.83	-2.68	2.6E-02
CG13796	6.46	-2.69	1.2E-03
rngo	16.57	-2.69	5.2E-04
Patj	8.69	-2.69	5.8E-04
elg1	3.46	-2.69	3.1E-03
mRps17	9.86	-2.69	2.4E-02
CG4293	5.71	-2.69	1.4E-02
RpL3	552.38	-2.69	8.1E-03
me31B	36.97	-2.69	4.2E-05
I(2)01289	16.41	-2.70	3.6E-03
eIF5B	24.33	-2.70	2.1E-05
kz	2.25	-2.70	2.0E-02
Uev1A	48.54	-2.70	5.2E-05
LanA	31.68	-2.70	6.4E-03
Usp16-45	8.89	-2.70	1.4E-04
CG11208	18.33	-2.70	4.9E-04
Brd8	3.94	-2.71	3.4E-03
CG1307	12.92	-2.71	1.5E-03
Prp31	6.79	-2.71	3.2E-03
snf	21.30	-2.71	3.4E-04
CG5844	13.03	-2.71	3.0E-04
pk	3.99	-2.71	2.6E-04
CG5382	21.09	-2.71	5.8E-04
galla-2	8.78	-2.71	3.8E-02
Smg6	17.65	-2.71	9.5E-05
Arp5	3.50	-2.71	4.7E-02
CG10139	5.83	-2.71	2.5E-02
CG12288	3.72	-2.72	4.2E-02
tyr	1.55	-2.72	3.6E-02
CG44001	22.46	-2.72	2.4E-05
CycD	6.67	-2.72	3.2E-03
drd	56.60	-2.72	2.0E-04
Arc42	15.97	-2.72	6.5E-04
bsf	16.06	-2.72	2.4E-05
CG5676	37.78	-2.73	2.5E-03
Ssrp	13.47	-2.73	2.0E-03
CG6724	8.88	-2.73	4.1E-02
CG5885	77.91	-2.73	7.6E-05
AspRS	38.83	-2.73	4.1E-05
CG4849	7.25	-2.74	2.2E-04
RpL23	1070.78	-2.74	1.7E-02
spn-A	4.17	-2.74	2.2E-02
CG31717	11.47	-2.74	4.4E-03
Sirup	91.92	-2.74	1.3E-04
Vps16A	6.59	-2.74	3.4E-04
CG16717	5.89	-2.75	8.0E-03
escl	2.44	-2.75	4.3E-02
mor	16.87	-2.75	7.1E-05
zetaCOP	29.39	-2.75	3.8E-04
kri	15.84	-2.75	1.2E-04
CG6843	5.62	-2.75	1.6E-02
Gyc76C	6.36	-2.75	1.3E-04
M6	11.21	-2.75	3.3E-04
CG4813	3.16	-2.75	3.2E-02
PEK	11.28	-2.75	5.9E-05
CG6695	8.08	-2.75	2.4E-04
CG13807	8.26	-2.75	1.8E-02
His3.3A	43.43	-2.75	7.8E-05
Samuel	20.11	-2.75	3.9E-05
sw	38.70	-2.75	9.8E-06
prod	7.26	-2.75	3.4E-03
Cont	40.98	-2.76	6.5E-05
Cul4	8.96	-2.76	1.9E-04
Rpt4	46.82	-2.76	6.1E-06
RpL7A	555.84	-2.76	5.8E-03
Attn7	4.44	-2.76	3.8E-04
APC10	5.58	-2.76	2.4E-02
CG6180	49.98	-2.76	1.1E-04
E(var)3-9	5.30	-2.76	7.5E-03
CG12814	41.45	-2.76	1.9E-05
SNRPG	31.89	-2.76	3.2E-03
cnl	19.84	-2.76	2.5E-04
VhaPPA1-1	96.85	-2.76	1.2E-04
CG5026	8.82	-2.76	5.9E-04
Tnks	8.13	-2.77	2.0E-05
DppIII	36.75	-2.77	2.4E-06
eIF5	34.53	-2.77	1.5E-04
atms	8.38	-2.77	1.6E-04
defl	3.64	-2.77	3.8E-03
CG3402	12.82	-2.77	2.2E-03
CG9344	25.57	-2.77	4.2E-03
APC4	2.47	-2.77	1.6E-02
CG34348	10.32	-2.77	2.1E-03
SkpA	57.76	-2.77	9.0E-05



Rpn13	32.29	-2.77	1.7E-04
CG12173	8.87	-2.78	1.4E-02
sav	5.45	-2.78	2.4E-03
CG8939	8.06	-2.78	2.6E-03
CG9588	13.62	-2.78	1.0E-03
CG3887	25.82	-2.78	5.0E-04
CG1291	6.65	-2.78	1.3E-02
RhoGAP5A	4.22	-2.78	1.7E-02
Usp39	4.31	-2.78	1.6E-02
CngA	2.55	-2.78	1.5E-02
Act42A	123.92	-2.78	4.9E-04
Msr-110	453.47	-2.78	6.5E-03
CG7724	5.93	-2.79	1.8E-02
CG11980	14.32	-2.79	1.7E-04
Nrg	52.30	-2.79	2.5E-03
CG9864	4.80	-2.79	1.9E-02
jumu	4.36	-2.79	2.4E-03
CG11077	8.65	-2.79	3.7E-02
CG9509	7.43	-2.79	2.9E-03
strat	10.17	-2.80	7.1E-03
trem	2.15	-2.80	5.0E-02
CG15717	6.05	-2.80	2.3E-04
CG6762	6.85	-2.80	2.4E-02
Prp3	7.97	-2.80	7.8E-05
Nup214	8.15	-2.80	4.8E-04
CG30373	9.14	-2.80	1.2E-02
Wdr33	6.89	-2.80	1.5E-03
CG3704	5.92	-2.80	5.8E-03
Tcs3	4.50	-2.80	2.2E-02
CG32537	2.17	-2.81	2.4E-02
CG5521	12.30	-2.81	1.8E-05
RpS7	710.37	-2.81	6.4E-03
Ubi-p63E	131.27	-2.81	3.0E-04
mRpl42	13.87	-2.81	1.5E-02
TBCB	15.76	-2.81	2.3E-04
CG2685	4.00	-2.82	1.8E-02
CG6638	10.53	-2.82	4.3E-03
Rab11	58.29	-2.82	1.9E-06
Klp64D	10.43	-2.82	8.9E-05
PIG-T	9.78	-2.82	6.0E-05
gammaSnap1	8.84	-2.82	4.2E-03
Mat89Ba	4.74	-2.82	6.1E-04
Ns3	8.41	-2.82	3.7E-04
eca	67.95	-2.82	9.8E-06
CG7556	13.68	-2.82	1.2E-03
CG3781	5.19	-2.82	1.9E-02
Rhp	6.99	-2.82	2.8E-04
GNBP1	9.37	-2.83	9.8E-04
Vps4	26.47	-2.83	5.5E-06
Tim23	37.85	-2.83	1.8E-04
CG8435	5.41	-2.83	1.3E-02
CG33722	4.86	-2.83	2.0E-03
AhcyL2	7.01	-2.83	7.8E-03
CG11927	4.77	-2.83	1.6E-02
CG6758	3.84	-2.84	1.2E-02
Srp68	26.21	-2.84	1.7E-05
Xpd	4.19	-2.84	2.8E-03
Trs31	10.66	-2.84	2.1E-02
CG31301	10.66	-2.84	1.1E-03
mrt	11.76	-2.84	9.9E-04
CG10194	3.79	-2.84	3.0E-02
eIF2Bgamma	11.02	-2.84	9.8E-04
CG5013	5.14	-2.84	3.1E-02
ksh	16.30	-2.84	2.4E-02
rin	30.38	-2.84	1.1E-05
Cerk	21.79	-2.84	2.7E-05
Pa1	6.88	-2.85	1.5E-03
Rpl23A	436.96	-2.85	8.4E-03
Ac78C	2.45	-2.85	6.7E-03
CG11284	15.75	-2.85	6.7E-05
CG4603	9.08	-2.85	1.7E-03
CG8289	13.65	-2.85	1.7E-04
Rchy1	12.19	-2.85	8.7E-04
CG9911	36.85	-2.86	2.1E-06
eIF1	154.96	-2.86	5.7E-04
Spase25	54.92	-2.86	2.5E-05
coro	25.65	-2.86	1.1E-04
CG7011	12.75	-2.86	3.0E-04
CG11560	4.14	-2.87	2.4E-02
Pdi	392.14	-2.87	3.9E-03
CG13369	10.01	-2.87	1.5E-03
Eno	192.95	-2.87	8.3E-03
arm	53.11	-2.87	3.3E-05
CG1575	4.32	-2.87	1.0E-02
CG17712	4.66	-2.87	2.3E-02
RpS4	634.55	-2.88	5.7E-03
CG33303	40.49	-2.88	1.3E-06
Lint-1	6.80	-2.88	3.6E-04
CG31103	52.33	-2.88	9.5E-06
ttm50	9.39	-2.88	1.7E-03
CG1434	2.27	-2.89	2.5E-02
CG1529	3.64	-2.89	4.5E-03
Rpn11	42.60	-2.89	1.5E-04
Dp	16.24	-2.89	3.6E-05
CG9205	17.54	-2.89	4.0E-04
CG14210	8.90	-2.89	1.6E-02
CG10068	6.40	-2.89	1.6E-03
Reg-5	33.58	-2.89	6.4E-04
eIF3f1	69.25	-2.89	1.5E-06
TFAM	11.24	-2.90	1.9E-03
mus101	2.67	-2.90	1.0E-02
Rpt6	41.67	-2.90	1.3E-05
lig	28.10	-2.90	1.5E-05
Grip128	3.18	-2.90	2.8E-03
Sas-4	2.58	-2.90	1.6E-02
Tsp42El	34.47	-2.90	3.4E-03
CG17265	4.62	-2.90	1.1E-02
alien	10.32	-2.90	9.1E-05
Sep1	18.50	-2.91	2.2E-04
CG11456	3.05	-2.91	1.5E-02
Gstd1	944.38	-2.91	4.9E-03

Est-P	9.80	-2.91	1.4E-02
CG5611	3.70	-2.91	1.9E-02
sxe2	7.42	-2.91	5.2E-03
CG17327	8.00	-2.91	1.2E-02
Rp11	9.30	-2.92	2.0E-04
CG3420	10.71	-2.92	1.1E-02
CG15715	16.32	-2.92	2.6E-03
vito	4.91	-2.92	2.4E-02
CG2116	10.96	-2.92	3.8E-04
Spase22-23	32.61	-2.92	3.6E-05
Iswi	9.19	-2.92	2.5E-03
SH3PX1	20.53	-2.92	3.1E-05
Nnp-1	8.36	-2.92	8.8E-03
I(2)05287	7.28	-2.92	2.0E-04
CG2100	4.81	-2.92	1.6E-02
CG2972	5.60	-2.93	1.1E-02
CG8010	4.42	-2.93	4.7E-02
CG31342	11.14	-2.93	9.7E-04
VhaM8.9	119.85	-2.93	1.2E-06
Rpt3	39.62	-2.93	7.5E-05
Ndc1	5.83	-2.93	2.3E-03
prel	15.97	-2.93	4.9E-05
Spm55B	8.63	-2.93	2.0E-03
CG2371	3.48	-2.93	4.2E-02
Atac2	3.16	-2.93	1.3E-02
Ns1	14.75	-2.93	5.4E-04
Cse1	17.24	-2.94	3.0E-05
CG4036	6.41	-2.94	2.3E-02
CG10481	2.50	-2.94	2.2E-02
Tst2	26.33	-2.94	3.6E-06
colt	33.41	-2.94	1.1E-04
mRpl113	8.99	-2.94	1.9E-02
CRAT	19.04	-2.94	3.6E-05
CG8239	2.70	-2.94	2.2E-02
CG6523	28.77	-2.94	9.2E-05
CG3719	25.02	-2.94	5.1E-04
Orc2	7.91	-2.94	2.6E-04
CG33172	1.47	-2.94	2.2E-02
CG1265	16.61	-2.94	1.5E-02
eIF4E1	49.83	-2.94	2.4E-06
mTFB1	9.40	-2.94	5.3E-03
CG8003	10.52	-2.94	4.2E-03
CG7744	3.63	-2.94	9.2E-03
CG4119	7.91	-2.95	5.0E-04
betaCOP	40.10	-2.95	7.8E-05
CG8372	15.49	-2.95	1.7E-03
CG3520	2.80	-2.95	6.9E-04
RpS5a	523.96	-2.95	5.2E-03
CG17807	3.22	-2.95	3.5E-02
Sec8	10.90	-2.95	1.6E-04
Reps	9.10	-2.95	2.2E-05
MED28	7.00	-2.95	1.7E-02
CG17598	7.46	-2.95	2.8E-04
Rat1	8.35	-2.95	4.5E-04
Oga	7.82	-2.95	1.6E-04
DCP1	8.53	-2.95	9.2E-03
CG3021	4.59	-2.96	1.1E-02
CG15093	78.07	-2.96	1.5E-06
I(1)G0007	8.73	-2.96	8.9E-05
e	12.07	-2.96	1.3E-03
CG15237	8.00	-2.96	2.3E-02
sel	26.85	-2.96	3.5E-04
CG7519	10.33	-2.96	1.1E-02
GSS	9.18	-2.97	5.6E-05
Stu3B	51.63	-2.97	2.8E-05
CG34132	17.81	-2.97	3.2E-03
AIF	6.78	-2.97	5.7E-04
CG2691	9.56	-2.97	6.6E-05
CG11837	4.74	-2.97	2.2E-02
Vang	7.73	-2.97	1.0E-03
Cps160	5.48	-2.97	3.0E-04
alphaCOP	44.00	-2.97	2.5E-06
CG10731	4.87	-2.97	2.0E-02
CG11334	12.48	-2.98	8.1E-05
CG9855	11.15	-2.98	5.0E-05
fdipdime	6.58	-2.98	1.6E-03
CG15877	3.87	-2.98	4.0E-02
CG3267	14.90	-2.98	8.8E-04
Taf5	4.44	-2.98	3.6E-03
CG31612	1.15	-2.98	4.8E-02
CSN7	14.68	-2.99	3.8E-05
Vps25	14.17	-2.99	6.8E-03
eRF1	30.41	-2.99	4.6E-07
mRps10	8.42	-2.99	1.1E-02
CG7358	9.31	-2.99	2.0E-03
Mob4	23.07	-2.99	3.0E-04
nahoda	44.12	-2.99	3.5E-05
HP1b	8.11	-2.99	1.7E-03
CG4511	22.46	-2.99	2.9E-03
CG3436	11.36	-3.00	7.4E-03
CG5001	26.00	-3.00	6.9E-04
eIF2Bbeta	13.83	-3.00	6.6E-05
CG2021	10.82	-3.00	3.1E-02
Cisd2	65.52	-3.00	7.9E-04
I(2)k09848	6.57	-3.00	1.6E-02
Pfdn5	25.00	-3.00	2.9E-04
Red4	5.36	-3.00	3.4E-02
Ns2	18.40	-3.00	3.1E-05
tz4	4.24	-3.00	2.4E-04
gammaCOP	24.95	-3.01	2.8E-05
CG10019	2.33	-3.01	6.6E-03
SC35	15.53	-3.01	1.9E-04
CG13117	45.88	-3.01	1.1E-05
zld	4.07	-3.01	3.5E-04
I(3)07882	4.09	-3.01	2.2E-04
THIS	7.92	-3.01	8.6E-04
achi	2.59	-3.01	8.4E-03
CG1461	10.20	-3.01	1.2E-02
Kul	20.67	-3.02	2.5E-06
tho2	12.74	-3.02	3.2E-07
CG4747	30.87	-3.03	4.5E-05

Dp1	91.42	-3.03	1.2E-03
eIF1A	93.17	-3.03	6.5E-06
c12.1	9.24	-3.03	9.0E-04
CG9666	3.25	-3.03	1.4E-02
His3.3B	203.55	-3.03	6.2E-04
awd	502.47	-3.03	4.7E-03
CG15891	9.70	-3.03	9.0E-03
mre11	11.27	-3.04	4.8E-04
R1OK1	3.62	-3.04	1.2E-02
CG34417	43.32	-3.04	1.9E-03
mRpl37	6.19	-3.04	4.0E-03
pms	10.30	-3.04	9.2E-05
FK506-bp2	209.42	-3.04	3.0E-05
CG13630	14.31	-3.04	8.0E-05
VhaAC45	135.96	-3.04	3.7E-05
Eip55E	30.49	-3.04	7.1E-06
Cpr49Ae	4.72	-3.04	4.8E-02
Vps13	42.23	-3.04	1.2E-04
Spt6	20.71	-3.05	2.2E-05
Glo1	74.00	-3.05	2.1E-04
CG2118	11.74	-3.05	2.6E-05
CG11417	6.30	-3.05	5.6E-03
xmas-2	3.68	-3.05	6.5E-04
CG1532	32.47	-3.05	2.0E-04
sut1	13.44	-3.05	8.7E-05
Nup98-96	13.68	-3.05	4.0E-07
CG32473	21.75	-3.05	7.6E-07
Hml	68.05	-3.05	1.1E-02
Trxr-1	56.70	-3.06	9.0E-07
Impbeta11	9.19	-3.06	2.2E-04
CG3589	3.55	-3.06	1.1E-02
Coprox	5.20	-3.06	1.1E-02
CG15514	7.79	-3.06	2.7E-03
CG32694	9.63	-3.06	5.6E-04
if	36.38	-3.06	3.9E-06
CG9689	7.50	-3.06	5.5E-03
CG7006	9.43	-3.06	1.0E-02
CG10343	7.94	-3.06	6.9E-03
CG5112	27.62	-3.06	3.8E-06
P32	22.24	-3.07	3.7E-04
Pabp2	12.33	-3.07	2.7E-05
CG32069	18.96	-3.07	1.0E-02
CG11920	4.91	-3.07	1.5E-02
CG5641	10.12	-3.07	5.4E-03
CG2875	5.52	-3.07	2.5E-03
CG3527	5.63	-3.08	2.9E-02
Hpr1	5.04	-3.08	1.0E-03
ebo	9.93	-3.08	1.4E-04
CG8209	23.23	-3.08	6.6E-04
Asph	8.82	-3.08	4.8E-04
TfllFalpba	9.75	-3.08	1.8E-05
Meics	2.55	-3.08	1.2E-02
Rrp45	4.35	-3.08	2.7E-02
CG18507	18.35	-3.09	2.4E-06
CG4558	4.89	-3.09	1.9E-03
CG6745	4.12	-3.09	7.0E-03
Suf(var)205	46.94	-3.09	2.8E-05
Sf3b3	32.54	-3.09	2.3E-06
MARG15	7.45	-3.09	5.0E-04
CG32129	2.01	-3.09	3.0E-02
Msh6	2.04	-3.09	8.2E-03
mRpl40	6.97	-3.10	1.4E-02
CG1523	6.09	-3.10	2.7E-03
CalpA	32.00	-3.10	3.1E-06
CG3223	7.01	-3.10	6.6E-04
Ostgamma	53.56	-3.10	1.1E-04
mRpl43	9.24	-3.10	8.8E-03
CG1550	10.40	-3.10	4.8E-05
Sgt	26.50	-3.10	5.4E-05
Stip1	37.51	-3.10	8.8E-07
CG11885	13.06	-3.11	1.4E-02
mthl10	16.46	-3.11	5.9E-06
SrpRbeta	21.63	-3.11	1.0E-05
Ugt35a	11.56	-3.11	8.5E-05
eIF3j	45.98	-3.11	3.2E-05
CG30382	105.34	-3.11	4.3E-06
Gfat2	17.62	-3.11	4.9E-04
CG2656	5.39	-3.11	1.5E-02
CG9915	7.86	-3.11	1.1E-03
pnut	17.02	-3.11	3.9E-05
D19B	6.28	-3.12	1.4E-04
trsn	11.08	-3.12	3.4E-03
CG11403	1.76	-3.12	1.3E-02
CG14803	2.93	-3.12	2.3E-02
pcm	5.81	-3.12	8.9E-05
CG40160	28.04	-3.12	1.4E-05
CG46317	10.09	-3.13	1.1E-02
CG7414	93.06	-3.13	7.1E-06
mRpl9	14.45	-3.13	4.1E-04
CG11655	10.95	-3.13	2.0E-05
CREG	59.19	-3.13	3.7E-04
p38b	12.58	-3.13	4.9E-05
brn	3.49	-3.13	1.6E-02
CG3408	5.62	-3.13	1.5E-03
Ptp10D	34.97	-3.13	1.6E-05
dwg	4.25	-3.14	4.3E-02
Gmer	4.89	-3.14	9.7E-03
NHP2	23.71	-3.14	2.2E-04
Cdc37	23.32	-3.14	9.4E-05
CG14683	10.32	-3.14	4.1E-04
CG1416	27.03	-3.14	4.4E-06
PDCD-5	31.18	-3.14	1.9E-04
Mau2	3.10	-3.15	1.6E-02
Dhc64C	65.43	-3.15	2.0E-03
CG6726	6.00	-3.15	1.9E-02
CG2931	4.54	-3.15	9.9E-03
CG41520	11.43	-3.15	2.6E-04
Hel25E	29.13	-3.15	4.2E-06
CG12608	8.87	-3.15	6.2E-04
Vps29	12.47	-3.15	6.3E-04
tzn	13.41	-3.15	8.1E-04

Pcmt	23.96	-3.16	9.9E-05
CG12034	9.59	-3.16	5.3E-04
CG10559	3.37	-3.16	2.2E-02
CG33785	2.58	-3.16	3.9E-02
CG11583	9.02	-3.16	4.6E-03
apt	28.54	-3.16	5.6E-06
AsnRS	29.22	-3.17	5.4E-05
mRps18B	7.47	-3.17	9.9E-03
rumi	6.01	-3.17	3.2E-03
eEF1gamma	462.34	-3.17	2.1E-03
Ykt6	8.18	-3.17	1.1E-03
ics	29.88	-3.17	8.2E-06
mRpl49	11.36	-3.17	5.2E-03
Proc-R	10.61	-3.17	1.4E-04
CG11811	11.75	-3.17	2.6E-05
Rpn10	45.43	-3.18	5.7E-07
CG5003	6.70	-3.18	2.4E-04
abo	4.41	-3.18	6.6E-03
chic	96.39	-3.19	5.2E-06
AP-Imu	17.96	-3.19	2.2E-04
Gal	8.61	-3.19	1.6E-04
CG7137	4.08	-3.19	1.5E-02
Ciao1	24.43	-3.19	2.1E-05
CG12643	24.15	-3.19	5.3E-04
RhoGDI	105.06	-3.19	1.2E-07
Bka	5.57	-3.19	3.4E-02
Gdi	86.83	-3.19	1.5E-06
CG5773	50.18	-3.20	2.5E-03
rig	7.10	-3.20	1.3E-04
Roc1a	43.24	-3.20	1.1E-04
Chp80	11.71	-3.20	2.6E-05
CG16753	5.55	-3.20	3.9E-02
rod	2.72	-3.20	4.8E-04
Hsp83	522.92	-3.20	2.0E-03
CG3678	14.27	-3.20	4.7E-03
Mi-2	28.55	-3.20	7.3E-07
CG1674	23.59	-3.20	5.3E-05
srl	8.10	-3.20	6.0E-04
CG34057	3.27	-3.20	3.4E-02
ldlCp	5.75	-3.21	1.0E-04
CG17568	1.78	-3.21	3.6E-02
CG12393	4.34	-3.21	5.9E-03
CG12384	142.85	-3.21	9.0E-05
TBPH	8.00	-3.21	1.2E-04
ECSIT	2.46	-3.21	3.3E-02
CG7834	57.14	-3.21	2.0E-04
CG6707	20.48	-3.22	5.3E-06
ZnT86D	13.14	-3.22	1.9E-05
LeuRS	14.30	-3.22	1.2E-04
dbe	6.99	-3.22	1.2E-02
Sec23	47.81	-3.22	2.0E-07
CG9667	7.51	-3.23	1.3E-02
san	17.49	-3.23	1.4E-03
CG4045	8.69	-3.24	5.8E-03
Pfdn4	26.13	-3.24	2.1E-03
GILT3	5.10	-3.24	4.7E-02
Det	5.06	-3.24	3.3E-02
shg	26.23	-3.24	6.9E-07
CG10463	3.20	-3.24	7.2E-03
Dysb	2.41	-3.24	3.8E-02
Spt-I	12.16	-3.24	1.9E-05
CG13901	4.33	-3.24	2.8E-02
loqs	6.43	-3.25	1.5E-03
CG17768	5.09	-3.25	7.6E-03
mRpl21	3.69	-3.26	2.0E-02
rump	22.02	-3.26	2.6E-05
metI	7.26	-3.26	3.3E-03
Hr38	6.10	-3.26	1.2E-04
Tapdelta	74.97	-3.26	4.5E-07
Sf3b1	12.77	-3.26	4.3E-06
Ski6	4.88	-3.26	1.7E-02
Pep	42.91	-3.27	6.5E-06
CG2182	19.55	-3.27	6.7E-07
btsz	29.01	-3.27	1.5E-04
Pms2	1.73	-3.27	1.0E-02
beag	5.33	-3.27	1.2E-03
Tom40	10.67	-3.28	1.5E-04
GV1	54.89	-3.28	3.7E-07
CG8191	2.58	-3.28	3.1E-02
Rpl135	4.38	-3.28	1.4E-03
Pcp	18.06	-3.28	1.7E-02
wds	6.57	-3.29	7.7E-04
CG6125	3.57	-3.29	5.2E-03
D19A	5.82	-3.29	4.3E-05
Tango2	4.14	-3.29	5.6E-03
lpk2	6.62	-3.29	5.1E-03
CG1105	30.32	-3.29	4.0E-06
eIF2D	9.18	-3.29	1.2E-04
gwl	1.25	-3.30	3.1E-02
ScpX	33.42	-3.30	6.1E-06
Prosalp7	64.15	-3.30	1.7E-05
CG43781	16.61	-3.30	5.0E-05
barr	3.81	-3.30	4.0E-04
ck	8.93	-3.30	4.0E-07
Smu1	3.98	-3.31	5.5E-03
CG14356	7.70	-3.31	4.9E-02
Prip	24.70	-3.31	1.2E-04
CG4901	5.83	-3.31	8.2E-04
Inos	145.62	-3.31	2.1E-05
mrm	4.83	-3.31	7.8E-03
CG33964	1.72	-3.31	4.2E-02
Hsp60A	68.47	-3.32	3.6E-07
Rs1	8.82	-3.32	1.4E-04
Arfrp1	4.39	-3.32	1.1E-02
pck	25.38	-3.32	3.8E-05
CG9246	9.88	-3.32	3.7E-04
CG5290	5.09	-3.32	3.7E-03
CG1969	23.92	-3.32	4.5E-04
Spp	48.87	-3.32	1.8E-05
Csn5	15.02	-3.32	1.1E-05
CG15822	4.38	-3.32	5.9E-03

mRpl14	8.15	-3.33	9.4E-03
Sp212	9.62	-3.34	3.7E-02
CG1234	5.48	-3.34	4.4E-03
Rpn7	46.70	-3.34	1.1E-07
CG6236	10.71	-3.34	4.0E-06
Noa36	12.86	-3.34	4.7E-04
CG33051	5.40	-3.35	2.3E-02
CG6686	11.60	-3.35	8.1E-06
Tie	15.66	-3.35	3.8E-06
PIG-L	10.31	-3.35	1.1E-05
bt	97.82	-3.35	4.9E-03
wcd	5.39	-3.35	4.4E-03
smid	14.25	-3.35	2.0E-05
Zip88E	2.24	-3.35	3.7E-02
RpIII128	6.36	-3.35	9.8E-05
CG3281	3.14	-3.35	2.0E-02
CG31869	12.90	-3.36	2.2E-06
hdly	37.89	-3.36	6.8E-06
Mettl14	6.61	-3.36	1.9E-03
Int54	5.61	-3.36	4.8E-05
r2d2	9.16	-3.37	6.5E-05
Cyp6u1	7.99	-3.37	1.6E-04
I(2)k10201	3.64	-3.37	5.0E-02
eIF2Bdelta	8.61	-3.37	1.2E-05
CG11555	8.45	-3.37	7.7E-03
Ice1	3.16	-3.37	5.9E-04
CG13101	18.73	-3.37	4.1E-04
CG8243	11.47	-3.37	8.4E-05
Npc2b	206.27	-3.37	2.7E-05
Usp5	13.05	-3.38	1.2E-05
CG43780	16.40	-3.38	6.2E-05
Rbbp5	4.02	-3.38	5.3E-03
Vps60	31.64	-3.38	6.9E-05
dre4	16.50	-3.38	2.8E-06
CG5969	6.78	-3.38	8.7E-03
Spase12	52.39	-3.39	1.9E-04
CG10147	2.27	-3.39	6.9E-03
CG11563	8.56	-3.39	1.4E-02
Updo	16.79	-3.39	6.5E-06
FRG1	10.37	-3.39	7.5E-03
APP-BP1	5.09	-3.40	2.5E-03
papi	15.13	-3.40	5.7E-06
CG7839	6.24	-3.40	1.4E-05
Cad87A	13.72	-3.40	3.1E-08
Ranbp21	6.95	-3.40	5.1E-05
AIMP2	24.19	-3.40	9.3E-06
Atac3	3.16	-3.41	4.9E-03
asrj1	12.17	-3.41	9.7E-04
P13K21B	12.50	-3.41	2.1E-06
ome	29.19	-3.41	8.4E-08
Hsp70Ab	190.23	-3.41	1.5E-04
CG11109	5.33	-3.41	4.0E-03
CG8569	3.44	-3.41	5.5E-03
Cnb	2.04	-3.41	1.5E-02
DCTN3-p24	19.81	-3.41	7.5E-05
Art7	4.47	-3.41	1.3E-03
cib	266.90	-3.41	1.8E-04
Nmt	18.19	-3.41	9.0E-06
pea	5.52	-3.42	1.1E-05
Zfrp8	4.98	-3.42	6.2E-03
Slc45-1	2.62	-3.42	9.2E-03
angel	5.33	-3.42	8.3E-03
Pgk	73.10	-3.42	5.7E-07
bbg	10.65	-3.42	8.0E-07
Fancd2	2.09	-3.42	3.0E-03
ppan	5.62	-3.42	1.1E-02
CG1572	159.70	-3.42	1.7E-06
CG13773	3.28	-3.42	3.5E-02
Tbp	5.06	-3.42	6.2E-03
Mys45A	8.13	-3.43	6.0E-05
bel	31.82	-3.43	4.7E-07
nom	2.41	-3.43	1.6E-02
CSN6	12.08	-3.43	8.8E-04
Rpn3	36.62	-3.43	2.6E-07
rst	4.37	-3.43	1.2E-05
Cyp301a1	15.44	-3.43	1.7E-03
Blos2	4.70	-3.43	4.8E-02
Such	15.32	-3.43	3.7E-05
CG4951	3.66	-3.43	7.5E-03
mfas	458.86	-3.43	1.7E-03
Cad86C	17.65	-3.44	1.8E-06
SsRbeta	108.05	-3.44	3.0E-08
CG4291	3.83	-3.44	9.9E-03
CG17549	275.02	-3.44	1.1E-05
lark	19.37	-3.45	9.9E-06
CG32495	9.27	-3.45	3.6E-06
MrgBP	10.69	-3.45	6.6E-03
CG9669	47.88	-3.46	8.0E-05
eIF3i	113.35	-3.46	1.5E-06
Sf3a1	7.56	-3.47	2.1E-04
baf	34.08	-3.47	2.2E-05
I(2)gl	35.81	-3.47	5.3E-07
Bap170	5.61	-3.48	8.7E-05
IleRS-m	1.77	-3.48	7.6E-03
vn	2.51	-3.48	9.2E-04
Eb1	48.39	-3.49	2.6E-07
aru	32.96	-3.49	3.0E-08
CG4281	7.45	-3.49	1.5E-05
Aprt	6.02	-3.49	4.6E-03
Iwa	96.37	-3.49	6.1E-08
grh	11.30	-3.49	1.4E-06
CG30069	87.87	-3.49	4.9E-04
Prp19	14.34	-3.49	1.1E-05
Membrin	8.33	-3.49	3.0E-03
CG15439	3.62	-3.50	3.9E-03
TfIIIFbeta	5.94	-3.50	4.2E-03
RpS8	609.00	-3.50	1.6E-03
Syb	51.57	-3.50	1.7E-05
CG30496	2.79	-3.50	6.2E-03
CG7200	4.78	-3.51	8.7E-04
CG1968	5.88	-3.51	9.7E-04

CG17202	19.72	-3.51	1.3E-04
fru	8.63	-3.51	1.1E-07
AnxB9	247.59	-3.51	4.5E-05
RpII18	23.68	-3.52	3.0E-04
PKD	16.76	-3.52	1.1E-07
CG6937	10.26	-3.52	1.2E-02
Ge-1	16.22	-3.52	1.4E-07
E2f2	4.11	-3.52	3.7E-03
Nop56	20.13	-3.53	8.4E-04
Vta1	22.61	-3.53	9.5E-06
CG33129	36.19	-3.54	5.8E-07
CG2016	28.64	-3.54	1.4E-04
CG3894	7.06	-3.54	3.6E-04
Ost48	63.00	-3.54	2.3E-08
eIF2Bepsilon	8.48	-3.55	1.7E-05
DCTN6-p27	18.31	-3.55	8.4E-04
CG13364	100.41	-3.55	9.0E-05
vnc	15.72	-3.55	1.5E-05
Cdc5	7.95	-3.55	3.0E-05
TfIIIEbeta	7.42	-3.55	2.7E-03
Mat1	5.12	-3.55	4.7E-03
Pol32	3.50	-3.56	5.0E-03
Nacalpa	292.76	-3.56	2.0E-06
CoRest	7.70	-3.56	8.1E-07
CG31495	2.14	-3.56	2.4E-02
MICU1	11.01	-3.56	6.5E-06
smt3	124.32	-3.57	9.0E-06
CG5510	20.29	-3.57	1.9E-06
CG1620	11.05	-3.57	4.1E-06
p47	24.82	-3.58	2.0E-06
CDK2AP1	6.85	-3.58	2.1E-04
TrpRS	9.92	-3.58	4.3E-05
pic	15.30	-3.58	3.3E-06
Tfb1	12.03	-3.59	1.9E-06
CG8152	2.63	-3.59	3.2E-02
CG7718	2.99	-3.59	1.6E-02
CG8860	98.25	-3.59	3.4E-05
CG11221	2.06	-3.59	1.8E-02
CG11882	4.38	-3.59	9.5E-03
Mtch	32.19	-3.59	1.9E-06
eRF3	32.43	-3.60	1.9E-08
CG3226	27.43	-3.60	3.9E-05
vers	2.76	-3.60	1.9E-02
CG9107	3.77	-3.60	6.9E-03
Arcp3A	16.89	-3.60	3.5E-06
wir	6.37	-3.60	2.0E-05
CG17059	28.84	-3.61	3.7E-04
CG8223	21.65	-3.61	1.8E-07
CG5168	34.61	-3.61	4.7E-07
pgant3	6.04	-3.61	6.7E-05
Rlb1	3.28	-3.61	9.8E-03
GCS1	5.99	-3.61	1.1E-05
nod	1.51	-3.61	2.6E-02
I(2)k09022	8.75	-3.61	1.3E-04
CG14414	4.66	-3.62	1.5E-02
tra2	5.70	-3.62	5.8E-04
CG13126	2.40	-3.62	1.3E-02
HP4	9.54	-3.62	3.4E-03
CG12880	3.90	-3.62	9.3E-03
LysRS	27.07	-3.62	6.4E-07
CG31457	3.16	-3.63	2.3E-02
Isn	9.03	-3.63	2.2E-03
CG12942	3.83	-3.64	4.3E-03
GstT1	26.52	-3.64	2.8E-05
CG8531	15.52	-3.64	1.9E-05
CG3773	5.11	-3.64	9.1E-03
Mtor	19.48	-3.64	3.4E-08
CG5590	37.12	-3.64	4.1E-07
Fnta	15.36	-3.64	1.7E-05
Pglym78	165.50	-3.65	6.9E-05
spd-2	2.74	-3.65	4.9E-04
CG1703	21.06	-3.65	1.1E-06
EMRE	26.87	-3.66	6.7E-06
Ufd1-like	16.76	-3.66	9.1E-05
GatB	2.11	-3.66	1.7E-02
CG4455	16.47	-3.66	4.6E-04
MED7	7.13	-3.67	3.5E-03
juh	7.65	-3.67	2.8E-06
CG4686	13.91	-3.67	1.1E-04
ergic53	73.26	-3.67	1.3E-08
CG5484	16.91	-3.67	5.6E-07
mol	12.22	-3.67	5.4E-05
CG13025	1.53	-3.68	6.4E-03
CG42336	16.86	-3.68	6.6E-06
Tgs1	2.06	-3.69	1.6E-02
CG14966	9.25	-3.69	5.9E-03
Gos28	11.45	-3.69	1.3E-03
ChLD3	1.44	-3.69	2.6E-02
EloB	31.28	-3.70	1.3E-04
CG17746	12.57	-3.70	2.5E-06
Pbgs	26.17	-3.70	1.4E-05
Rpt1	54.70	-3.70	2.3E-08
kin17	6.31	-3.70	9.9E-04
IntS9	3.63	-3.70	6.5E-03
AsnRS-m	2.51	-3.70	2.0E-02
RpL8	611.74	-3.70	4.0E-04
CG14220	4.79	-3.70	2.7E-03
dnk	6.99	-3.71	6.9E-04
CG8303	15.80	-3.71	5.4E-06
mRps14	6.82	-3.71	5.2E-03
Skp2	4.50	-3.71	2.2E-04
psidin	6.47	-3.71	3.6E-06
CG4210	8.02	-3.71	4.0E-03
bai	92.11	-3.72	1.2E-07
Nef-E	6.63	-3.72	3.8E-03
Myt1	3.38	-3.73	4.2E-03
CG12081	9.97	-3.73	2.5E-06
CG12279	14.47	-3.73	8.8E-04
CG42232	10.13	-3.73	5.6E-08
trol	229.76	-3.74	7.5E-04
CG34120	40.89	-3.74	1.3E-04

Hr78	2086	-3.74	5.6E-08
mRpS31	8.94	-3.74	5.9E-04
CypI	7.54	-3.74	8.0E-03
shtd	4.38	-3.75	2.3E-06
CG7889	4.83	-3.75	2.8E-03
CG31548	24.97	-3.75	1.5E-05
CG7656	12.76	-3.75	8.0E-07
Vha36-3	5.95	-3.76	2.1E-03
Rpl133	9.03	-3.76	9.4E-04
CG5961	2.58	-3.76	1.7E-02
Rpl22	383.97	-3.77	1.3E-05
Chi	10.63	-3.77	1.9E-05
slp1	1.98	-3.78	5.5E-03
mip130	8.88	-3.78	5.7E-06
CG5355	42.16	-3.78	6.4E-09
Thiolase	64.57	-3.78	3.1E-07
CG1622	4.98	-3.78	3.4E-04
Ir21a	2.31	-3.79	3.0E-03
CG10877	7.32	-3.79	1.3E-03
TppII	28.86	-3.79	5.2E-08
Lsm12	20.63	-3.79	4.8E-05
CG16892	5.28	-3.79	8.0E-04
GstS1	21.68	-3.79	1.0E-07
Bap111	11.88	-3.80	1.0E-04
Hexim	5.05	-3.80	2.8E-03
nero	10.35	-3.80	1.3E-04
CG12375	12.46	-3.80	1.3E-04
tsu	25.63	-3.80	2.2E-05
Smd2	30.81	-3.80	1.6E-06
eater	9.14	-3.80	8.0E-04
CG10217	37.09	-3.81	2.0E-07
mus308	1.75	-3.81	3.9E-04
CG5589	2.57	-3.81	8.5E-03
chinmo	12.97	-3.81	2.4E-07
CG14671	8.00	-3.81	4.5E-03
fzy	3.87	-3.81	3.7E-03
CG42675	8.35	-3.81	5.4E-06
grsm	32.44	-3.82	1.9E-09
CG12948	8.07	-3.82	1.8E-04
Dph5	11.92	-3.82	2.1E-04
CG2310	6.99	-3.82	7.0E-04
Rtml1	93.23	-3.82	2.1E-06
bowI	22.01	-3.83	3.0E-09
CG6607	8.53	-3.83	2.8E-04
Nrx-IV	29.08	-3.83	5.9E-09
RplP0	624.49	-3.83	1.8E-04
pza	18.04	-3.83	4.6E-08
OstDelta	67.32	-3.83	4.9E-09
Kank	44.44	-3.83	2.0E-07
CG5535	6.09	-3.83	1.4E-04
CG9521	9.70	-3.83	4.4E-03
Catsup	39.54	-3.84	2.8E-08
Cyp313b1	22.69	-3.84	7.6E-08
Ctf4	3.52	-3.84	1.4E-03
NT1	1.01	-3.84	2.8E-02
Nup50	13.24	-3.84	1.0E-06
CG17612	1.97	-3.85	1.8E-02
Cdk5	5.62	-3.85	4.8E-04
CG1236	15.64	-3.85	4.3E-06
Ufm1	28.34	-3.85	5.5E-05
Cenp-C	2.55	-3.86	1.3E-04
CG7872	11.64	-3.86	5.0E-06
nompC	0.50	-3.87	3.5E-02
Eaf6	3.93	-3.87	2.0E-02
Msp300	216.07	-3.87	4.4E-04
CG6142	5.18	-3.87	1.2E-04
A16	9.92	-3.87	1.3E-04
yem	4.14	-3.88	1.0E-05
U2af50	23.77	-3.88	7.6E-07
HIP-R	16.12	-3.88	2.4E-06
DCTN2-p50	41.69	-3.88	4.1E-07
chas	22.45	-3.88	1.2E-09
Sac1	23.94	-3.89	1.7E-07
CG8931	5.85	-3.89	1.3E-03
RpS2	583.32	-3.89	2.1E-04
mgl	79.48	-3.90	1.5E-04
CG1371	21.30	-3.90	6.5E-06
mTerf3	4.08	-3.90	1.6E-02
CG31549	11.60	-3.90	1.1E-04
CG10565	20.65	-3.90	7.6E-07
CG10555	6.19	-3.90	3.6E-06
shot	158.21	-3.90	3.4E-04
CG7504	1.63	-3.90	1.6E-03
CG30377	4.88	-3.91	1.0E-04
CG17904	11.14	-3.91	1.0E-04
esm	2.85	-3.91	1.5E-03
CG11777	6.50	-3.91	7.8E-03
Moe	113.80	-3.91	5.1E-06
ste14	6.96	-3.91	3.7E-03
CSN8	12.45	-3.91	2.2E-03
Arpc1	35.53	-3.91	5.7E-08
und	47.34	-3.92	1.3E-08
moi	2.18	-3.92	8.0E-03
CG45100	4.12	-3.93	2.2E-03
mEFTu1	27.82	-3.93	3.6E-08
CG14286	5.26	-3.93	1.4E-02
mhm	5.37	-3.93	5.2E-03
ValRS	18.72	-3.93	4.1E-07
CG9213	2.45	-3.93	4.1E-03
Nph	53.55	-3.93	1.2E-05
Cpsf73	6.17	-3.94	4.2E-04
glo	24.51	-3.94	3.5E-07
CG13175	1.54	-3.94	2.1E-02
See	4.84	-3.94	3.8E-03
bic	168.21	-3.94	5.8E-08
Rrp46	6.21	-3.94	6.3E-03
DNAPol-eta	1.48	-3.94	1.0E-02
pot	88.79	-3.94	3.3E-07
zF30C	12.18	-3.94	3.4E-06
lok	5.16	-3.94	7.3E-04
HnRNP-K	22.58	-3.94	7.3E-08

CG3542	5.96	-3.94	1.1E-05
Hrd3	16.42	-3.94	2.0E-08
CG10345	24.37	-3.94	1.3E-05
CG14636	5.01	-3.94	1.2E-02
ptc	11.54	-3.94	5.2E-06
CG9752	5.92	-3.95	1.2E-02
CG1943	55.82	-3.95	2.1E-08
Bap60	19.32	-3.96	9.8E-06
CG31100	8.14	-3.96	1.4E-05
CG3847	13.74	-3.96	1.9E-05
CG6094	5.24	-3.96	7.4E-03
mRNA-cap	11.37	-3.97	4.9E-06
Tasp1	2.95	-3.97	3.1E-03
CG42326	2.70	-3.97	1.8E-04
HisRS	15.20	-3.97	3.5E-07
Ibf2	6.54	-3.97	7.5E-03
Prosalpha5	55.72	-3.97	3.7E-06
CSN4	10.92	-3.97	2.5E-06
gtzf	13.51	-3.98	8.1E-09
BubR1	2.78	-3.98	1.9E-04
CG40006	23.44	-3.98	3.8E-08
Psn	20.72	-3.99	7.6E-07
Arl1	24.27	-3.99	7.4E-07
Dad1	53.26	-3.99	5.1E-07
Traf6	6.12	-4.00	7.5E-05
CG32152	0.96	-4.00	1.5E-02
deltaCOP	39.03	-4.00	8.3E-08
CG2614	4.69	-4.01	1.2E-04
CG1671	6.74	-4.01	6.6E-04
Gtp-bp	42.52	-4.01	3.0E-09
car	3.67	-4.02	7.0E-05
mab-21	10.09	-4.02	4.9E-05
CG1103	10.17	-4.03	5.3E-05
eEF1delta	94.28	-4.03	5.2E-07
Vps16B	3.10	-4.03	5.7E-03
Chd64	208.39	-4.03	3.9E-07
mus301	1.57	-4.04	2.7E-03
RnpS1	8.07	-4.04	1.5E-04
Phf5a	14.68	-4.04	4.9E-03
Art3	5.17	-4.04	2.6E-03
Dak1	37.48	-4.04	1.2E-07
Adk3	7.74	-4.05	1.4E-04
EndoG	4.24	-4.05	5.4E-03
Rpl4	620.89	-4.06	9.9E-04
lost	176.59	-4.06	5.4E-07
twf	10.39	-4.06	2.2E-04
Btk29A	13.16	-4.06	2.6E-10
Cbs	7.97	-4.06	6.6E-05
Hsp26	107.88	-4.06	2.8E-09
GstT4	47.25	-4.07	1.1E-06
BEAF-32	9.91	-4.07	5.2E-07
CG18048	2.10	-4.07	3.0E-02
CG11696	3.46	-4.07	3.8E-03
CG3939	12.83	-4.08	9.1E-05
CG11802	3.24	-4.08	5.2E-03
ArfGAP1	14.30	-4.08	5.6E-07
CG4332	8.98	-4.08	5.3E-07
Clp	4.29	-4.08	3.0E-03
Torsin	18.05	-4.08	1.7E-06
RplP1	1074.58	-4.09	4.5E-04
Pax	35.25	-4.09	1.2E-07
eIF2beta	74.99	-4.09	8.5E-09
M1BP	9.07	-4.10	1.7E-04
armi	4.67	-4.11	1.2E-04
su(Hw)	10.15	-4.11	4.4E-06
CG18641	3.70	-4.11	4.1E-03
La	28.22	-4.11	8.6E-07
CG7300	8.05	-4.12	6.9E-03
CG15211	7.43	-4.12	1.6E-03
tam	2.48	-4.12	6.4E-04
Mms19	8.60	-4.12	4.3E-07
Cdk4	5.86	-4.13	6.7E-05
pit	7.28	-4.13	1.2E-04
CG43345	1.45	-4.13	1.5E-02
RPA3	7.16	-4.13	4.7E-03
ND-B17	28.89	-4.13	1.2E-06
peng	12.48	-4.14	5.2E-06
CG34242	8.19	-4.14	2.8E-02
CG18081	32.11	-4.14	1.8E-06
EKBP59	39.57	-4.15	1.1E-07
CG31950	5.52	-4.15	1.4E-02
CG32022	4.54	-4.15	1.1E-02
Osbp	21.65	-4.15	8.7E-10
CG1662	6.55	-4.16	1.2E-04
mRpl134	13.08	-4.16	9.8E-03
Dle90F	48.46	-4.16	2.8E-07
His2Av	53.03	-4.16	7.1E-07
CG10126	44.09	-4.17	6.4E-06
CG12134	5.01	-4.17	1.6E-03
Mink	3.68	-4.17	5.4E-03
eIF3c	98.72	-4.17	4.9E-08
CG12056	8.34	-4.17	1.1E-03
CG31683	2.06	-4.18	3.0E-02
Snn43Aa	6.42	-4.18	3.4E-02
mu2	3.38	-4.18	9.1E-05
Dlip2	4.74	-4.18	9.2E-03
CG42382	2.78	-4.18	5.0E-02
Tg	13.31	-4.19	3.8E-06
CG18528	3.29	-4.19	4.8E-03
mus304	1.96	-4.19	3.8E-03
CG32856	6.91	-4.19	9.7E-03
NC2beta	5.88	-4.19	1.1E-02
eIF4H1	29.02	-4.19	2.4E-08
CG2617	2.42	-4.19	2.5E-02
FANCI	0.95	-4.20	9.4E-03
Xpac	2.62	-4.20	2.4E-02
GalNAc-T2	18.17	-4.21	1.4E-05
CG15365	4.22	-4.21	5.3E-05
fh	3.32	-4.21	2.1E-02
CG11752	29.11	-4.22	3.8E-04
neb	1.02	-4.22	1.4E-02

Cyp4p3	2.89	-4.22	1.5E-02
CG9578	6.81	-4.22	2.8E-03
bond	163.48	-4.23	1.6E-07
wash	4.14	-4.23	2.1E-03
Sgt1	20.57	-4.24	8.3E-07
thoc5	4.60	-4.24	7.5E-04
CG30291	16.13	-4.24	5.6E-08
CstF50	5.70	-4.24	1.4E-03
TORIP	16.77	-4.25	1.3E-07
Fpps	17.72	-4.26	3.0E-05
Inx3	71.85	-4.26	6.6E-10
Hmgcr	12.33	-4.26	6.1E-08
Su(fu)	12.09	-4.27	1.9E-07
dj-1beta	33.20	-4.27	3.5E-05
ko	19.90	-4.27	6.1E-10
Tango14	12.29	-4.27	2.1E-05
CG12259	4.98	-4.27	1.9E-03
Stt3A	24.70	-4.27	2.6E-07
CNMa	2.27	-4.27	2.4E-02
Snx3	27.49	-4.27	6.7E-10
Tudor-SN	72.45	-4.28	1.7E-08
CG10166	23.11	-4.28	2.6E-07
CG11257	2.20	-4.28	1.2E-02
CG44252	4.15	-4.28	1.4E-03
lha2	20.49	-4.28	3.7E-08
Sod3	43.22	-4.28	1.7E-09
CG1354	37.93	-4.29	1.2E-10
Arpc5	21.17	-4.29	5.7E-07
CG31999	17.97	-4.29	1.5E-08
Fuca	5.13	-4.30	1.1E-05
zormin	50.51	-4.30	1.6E-05
htl	24.41	-4.30	7.3E-09
CG30154	83.87	-4.30	3.8E-05
CG12237	14.63	-4.30	9.8E-08
dup	3.79	-4.30	4.2E-04
MED30	4.00	-4.30	8.3E-03
eIF3d1	77.28	-4.30	1.1E-08
grass	22.21	-4.30	1.8E-06
Tina-1	46.97	-4.31	1.3E-07
CG11858	17.88	-4.31	5.5E-04
CG4957	2.95	-4.31	3.7E-02
pasi1	15.89	-4.32	6.8E-05
cpa	34.21	-4.32	2.2E-07
hhl-1	4.40	-4.32	9.7E-05
Rpl35A	649.60	-4.33	6.4E-05
Spm77Ba	67.91	-4.33	3.8E-09
Nup43	6.30	-4.33	1.4E-03
CG2200	11.91	-4.33	3.3E-05
CG5886	5.36	-4.33	1.1E-04
RpS19a	401.53	-4.34	7.1E-05
CG12267	2.31	-4.35	1.1E-02
CG17806	1.96	-4.35	1.7E-02
ldbr	1.83	-4.35	1.9E-02
CG9312	16.34	-4.36	9.2E-04
CG31955	5.00	-4.36	4.9E-03
CG10602	36.71	-4.37	4.6E-10
PIG-P	5.55	-4.37	8.3E-03
Alr	4.25	-4.38	1.8E-03
CG10465	21.10	-4.39	2.3E-08
Rpn8	40.25	-4.39	6.9E-09
CG8399	68.70	-4.39	2.3E-10
CG5147	7.12	-4.39	1.3E-04
CG5721	19.68	-4.39	9.9E-07
Ndc80	1.47	-4.40	1.6E-02
Rfc38	5.81	-4.40	9.1E-04
IntS12	2.17	-4.40	3.3E-02
CG32407	18.67	-4.40	2.2E-07
CG14985	1.77	-4.40	2.4E-03
ebd2	2.09	-4.40	8.9E-03
Mco1	1.55	-4.40	4.2E-03
Swim	64.24	-4.41	1.7E-04
Nup160	4.90	-4.41	5.2E-06
nudC	12.10	-4.41	7.5E-07
CG30100	3.40	-4.41	3.4E-02
CG8066	36.86	-4.41	1.9E-05
Rpn12	43.38	-4.42	2.4E-06
mod	51.87	-4.42	1.8E-09
Tes	6.75	-4.42	1.3E-06
CG9531	2.82	-4.42	9.8E-03
Srp54k	39.17	-4.42	2.8E-09
Den1	9.70	-4.43	4.8E-05
Cyp12e1	10.32	-4.43	1.2E-05
CG7483	19.71	-4.43	8.1E-07
mof	4.09	-4.43	1.6E-05
Snx16	8.42	-4.44	2.8E-05
cana	8.77	-4.44	3.4E-08
asun	2.34	-4.44	1.9E-03
Sgf29	2.77	-4.45	1.6E-02
Ing3	2.84	-4.45	1.3E-03
Rpb11	12.59	-4.45	2.3E-03
CG3909	9.42	-4.45	1.6E-04
Rpl34b	243.07	-4.45	1.9E-05
CG5728	7.67	-4.46	2.7E-06
veli	10.66	-4.48	2.3E-05
Tsp74F	43.27	-4.48	3.5E-07
CG8635	22.50	-4.48	4.5E-08
Dronc	11.14	-4.49	4.5E-07
cl	80.62	-4.49	7.6E-08
CG14095	13.75	-4.49	4.7E-03
Ppa	15.71	-4.49	7.7E-08
CG4670	27.67	-4.50	8.6E-10
Gapdh2	689.46	-4.50	3.1E-05
mRpl10	7.30	-4.50	1.3E-03
Vha16-1	445.65	-4.50	2.3E-05
CG4282	2.76	-4.51	1.1E-03
CG10333	6.68	-4.51	1.6E-06
CCT7	51.74	-4.52	1.3E-07
timeout	3.04	-4.52	3.0E-05
CG7637	23.22	-4.52	1.9E-03
Nup58	3.62	-4.52	1.2E-03
CG7785	2.27	-4.53	8.7E-03

CG31249	5.62	-4.53	1.6E-03
CysRS	11.35	-4.53	1.7E-07
CG9302	17.49	-4.54	7.9E-06
DNA-ligI	3.05	-4.54	1.6E-03
CG1785	11.35	-4.54	1.7E-05
CG6227	5.04	-4.55	3.9E-06
Pgant35A	7.37	-4.55	1.1E-05
hlot	13.75	-4.55	7.1E-09
EndoGI	51.33	-4.56	2.7E-09
CG9581	4.98	-4.56	2.4E-04
LSm7	12.85	-4.57	8.6E-04
Ras85D	27.94	-4.57	6.3E-09
PSR	12.27	-4.57	1.6E-06
Mtc-c	97.24	-4.58	8.1E-11
Sry-delta	7.78	-4.58	1.7E-05
Non3	10.32	-4.59	5.7E-05
Ref1	36.92	-4.59	1.8E-09
CG12964	1.02	-4.59	1.2E-02
Aos1	19.58	-4.60	2.8E-07
Dpit47	8.50	-4.60	2.6E-05
CG7789	8.98	-4.60	1.0E-04
Hil	13.16	-4.61	2.8E-08
ppk13	5.49	-4.61	1.1E-03
crn	6.95	-4.61	7.3E-06
CG16935	17.40	-4.61	1.7E-07
CG9890	4.60	-4.61	1.1E-03
MESR6	5.63	-4.62	1.4E-04
grp	11.33	-4.63	9.5E-06
CG34112	2.71	-4.63	1.2E-02
yps	42.33	-4.63	3.0E-09
Smm	7.48	-4.63	8.6E-04
Rack1	526.71	-4.64	6.6E-06
CG43341	21.52	-4.64	1.2E-07
CG10646	3.95	-4.64	2.2E-03
CG9436	22.41	-4.64	5.1E-06
msd5	4.07	-4.65	1.3E-02
CG12171	22.16	-4.65	1.1E-06
CG15083	74.31	-4.65	1.9E-08
CG31213	4.65	-4.65	6.1E-07
CG9286	10.48	-4.66	2.0E-04
CG9853	8.91	-4.67	7.9E-06
GlyRS	24.63	-4.67	2.1E-08
Top3beta	8.70	-4.67	9.5E-08
CG9372	109.46	-4.68	3.9E-11
CG1142	9.14	-4.68	9.4E-04
CG3342	4.40	-4.68	1.2E-03
CG9839	2.86	-4.69	1.7E-03
ArgRS	18.18	-4.69	1.2E-07
Gdh	80.86	-4.69	3.6E-09
eIF2gamma	43.42	-4.69	6.8E-11
CG14543	8.35	-4.69	2.3E-03
CG10445	0.80	-4.69	2.7E-02
CG12320	2.07	-4.70	1.0E-02
Drice	16.45	-4.71	7.2E-08
akirin	29.87	-4.72	2.5E-09
Sans	1.48	-4.72	3.0E-02
CG14439	10.67	-4.72	2.5E-06
Strica	4.08	-4.73	3.2E-05
Pfdn2	36.13	-4.73	2.7E-07
Spec2	3.94	-4.73	5.6E-04
Rsf1	10.17	-4.73	4.7E-06
Vps2	21.07	-4.73	6.0E-09
CG8142	2.84	-4.73	1.3E-02
CG8630	161.28	-4.74	5.4E-08
CG33695	3.50	-4.74	1.2E-03
CG33506	7.08	-4.75	1.3E-03
CG7668	22.75	-4.75	1.5E-07
CG32365	2.81	-4.76	1.5E-03
Bub3	12.52	-4.76	4.1E-05
Tep3	63.57	-4.76	3.7E-09
Hakai	4.38	-4.76	8.8E-04
Art1	21.88	-4.77	1.4E-06
Zip71B	11.86	-4.78	2.3E-07
CG2816	49.47	-4.78	1.6E-06
BCAS2	7.61	-4.79	1.3E-03
CG3732	8.90	-4.80	1.7E-05
B-H2	1.20	-4.81	2.5E-02
CG8064	5.54	-4.81	2.1E-05
CycA	8.43	-4.82	3.6E-06
cmet	3.47	-4.82	1.9E-04
Tspo	148.55	-4.83	6.8E-10
I(2)35Bd	3.59	-4.83	3.5E-03
CG45078	9.75	-4.83	2.0E-04
CG11679	5.34	-4.84	7.3E-04
CG10584	4.59	-4.85	2.8E-03
rasp	7.22	-4.86	5.6E-05
Mcm5	5.66	-4.87	4.0E-05
CG6195	13.10	-4.87	1.9E-06
Cad96Cb	1.20	-4.87	1.2E-02
CG5787	10.47	-4.88	2.7E-08
Csat	10.20	-4.88	3.1E-06
CG15141	4.26	-4.88	6.7E-04
CG11069	14.20	-4.88	1.7E-07
loi	30.73	-4.89	3.5E-07
Sep2	27.15	-4.89	7.5E-09
TyrRS-m	3.71	-4.89	1.4E-03
CG6769	9.82	-4.90	2.1E-05
CaBP1	83.45	-4.90	4.2E-11
RpLP0-like	16.98	-4.90	1.9E-05
Nup205	7.93	-4.92	8.1E-09
CG2915	26.01	-4.92	6.8E-07
CCT6	65.37	-4.92	8.8E-11
IKKepsilon	5.62	-4.92	2.1E-03
SerRS	49.36	-4.92	1.1E-09
Rbf2	1.08	-4.93	2.5E-02
CG9967	3.65	-4.95	1.8E-03
hoip	32.01	-4.95	2.8E-06
CG5808	2.85	-4.96	2.2E-03
pelo	17.49	-4.96	1.4E-08
AIMP3	18.57	-4.96	1.1E-05
mTerF5	4.39	-4.97	3.3E-04

CG3817	5.77	-4.97	3.3E-03
Elp2	5.77	-4.97	3.0E-05
CG2453	4.36	-4.98	1.3E-03
mRpl36	7.32	-4.98	8.8E-03
Map205	61.35	-4.99	1.9E-09
CG17361	2.52	-4.99	4.8E-02
eIF2alpha	48.48	-5.00	3.4E-12
ThrRS	32.49	-5.00	1.9E-08
CG3009	15.48	-5.01	5.1E-07
l(2)37Cc	25.65	-5.01	2.7E-10
CG10576	85.75	-5.01	2.6E-10
CG8545	11.31	-5.01	2.7E-06
CG13751	44.74	-5.01	3.7E-06
CG10222	2.78	-5.02	8.1E-03
Pex19	15.22	-5.02	1.5E-07
ATPsvnF	166.57	-5.03	8.7E-05
Tsp26A	9.22	-5.03	1.1E-08
CG14230	5.09	-5.04	5.7E-05
CG32855	5.84	-5.04	9.2E-06
DNAPol-alpha60	2.52	-5.05	5.9E-03
rnh1	3.99	-5.05	4.5E-03
CG17544	13.12	-5.05	5.5E-07
Silp	5.89	-5.05	8.7E-04
Sec13	26.41	-5.07	9.1E-10
Tap42	7.76	-5.07	4.3E-05
Sbp2	9.19	-5.07	7.6E-05
beta' COP	40.59	-5.08	1.0E-11
eIF3a	71.50	-5.08	1.4E-10
CG8460	11.45	-5.08	7.5E-06
CG10424	15.23	-5.08	1.2E-06
Chrac-14	6.24	-5.08	8.1E-03
Sgf11	8.34	-5.08	9.1E-04
Rtc1	5.78	-5.09	1.1E-03
x16	13.04	-5.09	7.4E-07
CG43861	2.43	-5.09	1.3E-04
CG10348	2.40	-5.09	4.2E-03
CG12911	1.76	-5.10	2.8E-02
Calr	435.23	-5.10	1.7E-06
CHOP24	65.04	-5.11	6.8E-09
l(1)G0020	5.48	-5.11	4.0E-06
l(1)G0045	2.47	-5.12	1.0E-03
Rpb8	17.23	-5.12	5.0E-06
ncd	4.99	-5.12	8.1E-05
CG14544	2.13	-5.12	4.9E-02
CG8617	4.51	-5.12	8.6E-04
Myo61F	22.93	-5.13	2.8E-09
CG11961	6.93	-5.14	5.8E-09
CG8771	5.39	-5.15	3.1E-07
CG14618	3.74	-5.15	4.0E-03
CG33713	15.59	-5.15	1.5E-08
CG10286	10.38	-5.16	3.0E-07
mav	23.04	-5.16	1.3E-08
Apc2	4.08	-5.16	2.5E-06
CG11409	5.37	-5.17	1.3E-06
CG5104	20.27	-5.18	3.6E-06
Nedd8	29.67	-5.18	1.3E-06
MED17	5.15	-5.19	7.3E-05
Mettl3	3.09	-5.19	9.8E-04
ihog	9.44	-5.19	2.5E-07
ETHR	2.97	-5.19	5.5E-05
CG6610	9.06	-5.20	1.3E-03
Csl4	4.84	-5.21	3.8E-03
geminin	10.79	-5.22	1.1E-05
dmGlut	14.24	-5.22	8.9E-07
Rpl18	600.13	-5.22	5.8E-06
CG13157	1.22	-5.22	4.3E-02
Orc1	1.73	-5.23	2.0E-03
CG31121	18.94	-5.23	1.8E-10
Oseg4	1.12	-5.24	3.5E-03
CG43759	12.24	-5.24	2.8E-10
LamC	93.36	-5.24	8.4E-12
RplP2	979.37	-5.24	1.6E-06
DNAPol-alpha73	2.60	-5.25	1.0E-03
Sfxn2	12.68	-5.25	5.0E-09
Ntmt	7.01	-5.26	1.1E-04
alphaTub84D	30.41	-5.26	3.1E-10
Mps1	1.09	-5.27	3.9E-02
CG1840	3.25	-5.28	4.0E-02
Dro	3.10	-5.28	3.8E-02
CG11999	24.76	-5.28	7.0E-08
CHORD	10.56	-5.29	6.1E-06
CG16812	6.29	-5.29	5.1E-05
CycE	2.31	-5.30	1.5E-05
LanB1	31.14	-5.30	3.6E-13
PPP4R2r	12.72	-5.30	4.7E-08
Prp38	9.06	-5.31	1.5E-05
CG13003	20.77	-5.31	4.0E-12
Orc5	2.30	-5.31	5.9E-03
CG6543	100.42	-5.31	3.9E-11
scu	69.26	-5.32	1.4E-11
CG5412	6.86	-5.32	4.1E-04
yellow-b	30.74	-5.33	1.5E-06
Rlp67A	2.53	-5.34	5.0E-04
CG2321	2.40	-5.34	5.9E-04
CG7900	35.31	-5.34	7.3E-09
Non2	38.70	-5.35	6.5E-11
Rpl24	344.01	-5.35	4.4E-04
CG9147	6.30	-5.35	5.8E-05
CG11710	6.18	-5.35	9.6E-06
hbs	3.31	-5.36	8.7E-07
CNBP	108.54	-5.37	3.9E-11
borr	4.82	-5.37	1.1E-03
Smyd5	6.94	-5.37	6.4E-05
CG14805	9.66	-5.37	8.7E-07
CG42598	4.80	-5.38	2.9E-03
tex	5.16	-5.38	1.0E-03
e(y)1	5.61	-5.38	1.1E-03
CG2604	64.54	-5.38	9.1E-13
TBCD	9.94	-5.38	4.5E-08
CG12581	31.27	-5.39	9.0E-13
Nup37	4.47	-5.39	1.2E-03

CG9804	7.88	-5.39	3.9E-04
Hsc70-4	748.56	-5.39	9.8E-06
O-fut1	17.13	-5.40	1.9E-09
CG34215	74.25	-5.41	4.7E-05
Act5C	823.93	-5.41	4.9E-06
RpL6	676.47	-5.42	3.9E-06
Myo10A	19.88	-5.42	9.0E-13
SmydA-9	5.30	-5.43	9.9E-05
GC52beta	43.51	-5.43	3.2E-13
Cubn	6.68	-5.43	6.8E-04
CG31710	16.33	-5.44	6.9E-06
IRSp53	76.03	-5.44	2.8E-10
U4-U6-60K	6.28	-5.44	9.1E-06
Cdc42	42.29	-5.47	5.9E-12
l(1)1B1	5.49	-5.47	1.9E-07
Gapdh1	419.56	-5.48	1.1E-06
Gp210	12.27	-5.48	4.0E-10
Rrp4	7.83	-5.49	2.8E-04
CG8892	3.47	-5.50	2.6E-04
tsr	422.21	-5.51	1.0E-06
CG17337	59.52	-5.51	2.6E-11
Pex16	8.42	-5.52	2.3E-06
CG9590	12.82	-5.52	5.7E-09
Srp54	18.57	-5.53	9.7E-09
Argk	291.83	-5.53	1.1E-05
CG3709	2.40	-5.53	5.3E-03
Gem3	2.86	-5.54	6.6E-06
capt	43.71	-5.56	1.7E-13
Cpr65Au	26.73	-5.56	2.8E-03
gbb	34.28	-5.56	2.8E-10
CG3570	4.44	-5.56	1.5E-03
Ubc2	12.68	-5.57	1.7E-08
nop5	24.43	-5.57	8.6E-09
Not10	5.58	-5.57	4.1E-06
Vdup1	41.37	-5.57	9.2E-11
CG4390	37.07	-5.58	1.5E-09
Cap-D2	3.43	-5.59	1.1E-05
CG14174	2.30	-5.59	3.0E-02
Caf1-180	4.50	-5.61	6.0E-07
D1	40.62	-5.62	4.4E-10
CG4098	16.19	-5.63	6.7E-07
Rpl13	441.10	-5.64	1.5E-06
Sk2	12.09	-5.66	1.2E-08
CG8149	13.58	-5.66	3.7E-06
CG31633	2.87	-5.66	4.1E-03
dod	12.99	-5.67	1.6E-05
Rpl13A	680.65	-5.67	2.6E-06
thr	1.09	-5.67	1.4E-03
zip	78.22	-5.68	9.1E-09
CG8038	5.87	-5.68	1.3E-03
HDAC1	22.64	-5.70	4.6E-11
Naa15-16	16.39	-5.70	2.0E-11
Syx18	11.64	-5.71	1.6E-06
CG8306	74.57	-5.72	1.1E-12
CG14292	22.89	-5.72	4.0E-02
crok	18.58	-5.72	3.0E-08
e(y)2	11.63	-5.74	7.2E-04
lbf1	7.84	-5.76	3.7E-04
egg	6.19	-5.76	2.0E-08
grnd	15.27	-5.78	1.8E-09
AlaRS	39.26	-5.78	1.4E-13
PIG-X	2.14	-5.79	2.3E-02
CG3328	18.28	-5.79	2.1E-12
jafrac2	10.61	-5.79	2.9E-06
Ints14	3.96	-5.80	4.3E-04
CG6028	72.67	-5.80	6.5E-13
CG9705	45.78	-5.81	7.7E-14
CG10268	4.46	-5.82	1.3E-03
CG18004	6.86	-5.82	1.6E-04
Tango4	6.84	-5.83	8.1E-06
Spe105R	1.79	-5.83	2.2E-05
Ilk	21.94	-5.84	2.3E-11
flr	34.99	-5.84	1.7E-09
U2af38	8.79	-5.85	4.8E-06
CG7185	16.59	-5.86	2.9E-10
CG12702	1.23	-5.86	4.5E-03
CG30456	4.94	-5.87	1.3E-05
CG32409	11.86	-5.89	4.0E-06
SmydA-1	2.45	-5.89	7.3E-03
Pcd	89.71	-5.90	9.0E-07
TRAM	54.73	-5.91	1.3E-12
Cad88C	0.53	-5.94	8.3E-03
rt	3.20	-5.94	3.2E-05
CG31715	34.62	-5.96	1.3E-08
Nup93-1	11.41	-5.96	1.1E-08
CG7728	8.11	-5.96	1.3E-08
Caf1-55	22.48	-5.97	3.8E-08
br	14.19	-5.97	7.7E-11
CG14005	2.53	-5.99	7.0E-03
Spn42Dc	5.10	-6.00	2.2E-04
CG11444	34.90	-6.01	1.3E-10
CG42237	4.09	-6.02	5.2E-04
GXIVsPLA2	6.48	-6.04	2.0E-04
pre-mod(mdg4)-V	1.24	-6.04	1.0E-03
Nup54	4.31	-6.05	1.0E-04
RhoGAP54D	1.65	-6.06	7.6E-04
CG3760	46.39	-6.06	3.3E-12
CG14257	1.40	-6.06	9.1E-03
lwr	28.12	-6.07	1.4E-12
Eogt	14.89	-6.09	4.5E-09
Arp1	53.75	-6.09	5.2E-12
thoc6	3.40	-6.10	2.4E-05
Rpp30	4.02	-6.11	3.6E-03
Nopp140	16.40	-6.13	2.6E-10
CG12129	6.48	-6.13	1.5E-04
CG34382	1.64	-6.14	3.1E-03
CG33178	38.42	-6.14	1.2E-04
THADA	2.39	-6.15	2.8E-05
CG17109	7.39	-6.15	2.5E-03
NetA	2.91	-6.17	1.2E-04
dlp	25.10	-6.18	4.0E-13

Mcm6	8.13	-6.18	4.4E-07
Sf3a2	11.92	-6.20	2.0E-06
CG3793	5.77	-6.22	1.3E-05
eEF1beta	418.87	-6.22	7.3E-11
CG13377	70.99	-6.23	1.6E-13
Upf3	5.97	-6.23	1.4E-05
CG9135	15.03	-6.23	1.6E-09
CG40198	28.03	-6.24	8.6E-03
Rae1	9.36	-6.24	1.4E-05
Tgi	13.58	-6.24	8.8E-08
kst	92.94	-6.25	1.1E-07
in	4.19	-6.28	2.4E-06
Nup107	7.12	-6.29	1.2E-08
Hsp70Bb	99.68	-6.30	6.3E-12
Snr1	11.01	-6.30	9.5E-07
CG14434	4.28	-6.30	3.4E-04
CG17359	2.04	-6.31	1.7E-02
GstZ2	4.51	-6.31	1.8E-03
RtcB	10.61	-6.32	6.2E-08
mRpl12	16.31	-6.35	7.9E-07
CG5515	19.01	-6.35	9.7E-07
CG3165	5.63	-6.35	2.3E-04
eIF6	21.88	-6.36	5.1E-06
CG13601	8.53	-6.36	3.5E-05
CG15515	83.78	-6.37	1.3E-03
hng1	3.46	-6.38	4.5E-03
CG7860	7.57	-6.38	6.4E-04
RanGAP	10.17	-6.38	5.7E-09
Nox	2.12	-6.38	7.2E-05
epsilonCOP	27.95	-6.40	1.3E-09
cag	3.52	-6.40	1.5E-03
CG32857	5.48	-6.42	1.6E-03
cpb	30.39	-6.45	4.4E-11
CG32645	10.94	-6.47	2.5E-08
CG2157	46.68	-6.48	5.2E-10
Rrp42	4.82	-6.48	1.6E-03
CG16903	10.31	-6.51	2.0E-09
CG9577	15.19	-6.51	3.2E-07
sta	739.25	-6.52	1.5E-06
MED20	3.68	-6.52	4.3E-03
Flo1	32.63	-6.55	6.8E-12
Rfc3	3.37	-6.55	4.6E-03
ect	8.46	-6.56	3.6E-08
CCT4	56.40	-6.56	1.0E-14
CG17180	3.27	-6.56	4.2E-03
GlcAT1	7.42	-6.57	1.5E-06
CG8111	10.05	-6.57	3.9E-06
CG34232	24.43	-6.58	7.3E-08
GstO3	93.28	-6.59	1.3E-13
CG15529	5.64	-6.60	5.3E-04
CG14642	7.98	-6.60	1.3E-04
CG42498	5.94	-6.62	1.4E-03
CG17652	3.24	-6.63	3.9E-03
CG30467	3.83	-6.64	3.1E-04
CG17002	4.53	-6.65	2.4E-04
pont	15.62	-6.66	1.1E-09
CG31251	1.86	-6.66	4.9E-02
CycY	15.28	-6.67	2.5E-09
CG7702	2.45	-6.68	5.3E-04
Rhm13	5.12	-6.68	1.7E-04
rhi	3.19	-6.69	2.0E-03
salr	7.74	-6.69	5.8E-11
CG5554	46.79	-6.70	1.2E-13
yellow-h	9.35	-6.70	1.1E-05
mRpl4	9.72	-6.72	1.6E-05
CG32536	4.49	-6.73	3.6E-03
CG17027	14.33	-6.75	5.1E-07
CG4789	20.00	-6.76	1.3E-08
Cyp4e3	3.83	-6.76	5.5E-03
Faa	5.92	-6.76	1.3E-03
CG10175	0.50	-6.76	4.9E-02
CG14984	47.72	-6.76	6.2E-09
CG45071	5.79	-6.77	9.4E-06
rret	27.92	-6.78	6.8E-08
Cyp9c1	37.51	-6.79	8.3E-14
N	31.06	-6.79	3.5E-13
Sas-6	1.31	-6.79	4.4E-02
CG13096	13.14	-6.85	2.0E-09
ApepP	18.73	-6.85	7.7E-09
CG2812	3.85	-6.85	1.1E-03
CG30105	3.12	-6.85	4.3E-02
TAF1B	1.74	-6.87	5.2E-04
mmv	63.73	-6.87	3.7E-11
SLIRP1	15.60	-6.88	1.7E-10
stg	9.84	-6.88	3.7E-08
Map60	11.61	-6.89	3.5E-09
CG6310	26.23	-6.91	1.0E-07
CG8005	3.31	-6.91	3.4E-03
GstO1	4.31	-6.93	5.0E-03
CG14879	3.04	-6.94	5.3E-04
cher	147.89	-6.95	5.1E-08
CG9154	5.18	-6.96	3.1E-03
Ranbp9	12.42	-6.99	7.9E-10
mSSB	17.80	-6.99	1.5E-05
CG2852	311.54	-6.99	3.1E-11
Prm	68.04	-7.00	8.2E-11
Osi24	4.28	-7.01	5.5E-06
CG4199	54.30	-7.03	0.0E+00
Pu	38.64	-7.03	1.1E-11
bou	43.88	-7.04	3.1E-11
Hisl:CG33813	3.02	-7.05	1.1E-02
CG32803	9.31	-7.06	2.5E-04
Neurochondrin	14.59	-7.06	3.7E-08
vls	6.32	-7.07	1.1E-04
Lam	14.53	-7.08	1.2E-12
Zip89B	7.45	-7.08	6.7E-06
Hisl:CG31617	3.03	-7.10	9.7E-03
mEFTs	10.22	-7.11	5.2E-07
CG9338	76.30	-7.13	2.3E-13
Hs6st	32.78	-7.14	4.2E-15
Tm1	76.68	-7.15	4.6E-09

sqz	6.40	-7.15	3.1E-10
CG14830	51.69	-7.15	2.1E-15
Rrp1	7.46	-7.16	1.2E-08
cv	30.12	-7.17	1.1E-12
Lsp1beta	129.58	-7.19	2.7E-06
CG10467	38.52	-7.19	2.0E-06
CG15440	6.89	-7.20	7.2E-05
CG34437	5.30	-7.21	6.7E-03
sle	10.98	-7.21	9.3E-12
Ins2	73.11	-7.24	1.2E-13
CG32816	29.46	-7.24	4.2E-12
CG8180	36.62	-7.26	3.2E-13
CG1542	11.72	-7.28	3.8E-06
mago	20.37	-7.29	2.6E-09
DCTNS-p25	13.16	-7.30	1.1E-05
RpS10b	241.23	-7.32	5.9E-12
CG17211	0.65	-7.33	8.3E-03
beta-PheRS	14.27	-7.34	1.4E-11
CG14731	1.06	-7.34	3.3E-02
CG10053	2.23	-7.35	3.2E-02
Dhod	18.21	-7.36	7.2E-11
sit	5.56	-7.38	1.1E-03
holn1	5.43	-7.40	2.3E-04
mgr	30.97	-7.41	3.3E-10
CG32137	36.11	-7.42	0.0E+00
Top2	25.32	-7.43	0.0E+00
CG17350	7.06	-7.44	4.0E-04
Bap55	11.88	-7.46	1.2E-07
CG12910	1.25	-7.49	8.6E-03
CG30427	4.92	-7.49	8.8E-08
asr1	9.52	-7.51	1.3E-06
Arp10	12.91	-7.51	2.3E-10
CNT2	2.63	-7.52	6.2E-04
Tdc1	4.83	-7.52	2.7E-06
Ddx1	8.53	-7.52	5.9E-10
pgant2	15.56	-7.53	8.2E-11
CG6034	9.20	-7.53	1.6E-04
DENR	26.03	-7.55	6.0E-10
Ance	198.82	-7.58	8.3E-12
DNApol-epsilon255	2.76	-7.59	3.0E-08
Hsp70Ba	26.68	-7.61	5.3E-05
CG14304	6.01	-7.62	1.1E-05
U2A	6.68	-7.63	1.9E-04
wmd	17.07	-7.63	8.3E-11
iv	13.28	-7.64	1.6E-11
Dtg	10.11	-7.70	1.1E-08
ImpE3	5.30	-7.70	1.1E-03
ball	5.61	-7.72	1.8E-06
CG4374	3.90	-7.72	1.2E-09
ERp60	412.01	-7.73	3.1E-10
Mtr3	5.42	-7.73	2.0E-04
CCT2	61.60	-7.75	0.0E+00
CG5339	6.44	-7.76	9.9E-05
EndoU	22.01	-7.76	3.4E-11
mldr	1.61	-7.76	1.7E-03
mia	0.89	-7.81	2.6E-02
Cyp4d21	1.27	-7.82	2.7E-02
r	9.37	-7.83	1.9E-13
Mlp84B	65.97	-7.84	8.8E-11
CG8173	3.56	-7.85	6.2E-04
melt	12.21	-7.87	5.3E-14
CG10869	3.16	-7.89	2.3E-04
CG43333	0.54	-7.89	2.9E-02
CG7049	7.24	-7.90	9.4E-05
CG13926	7.96	-7.90	3.1E-04
Adgf-C	7.40	-7.92	6.1E-07
BBS4	1.53	-7.94	3.7E-02
Ctr1A	30.05	-7.96	5.3E-12
Rpb5	13.56	-7.97	4.5E-07
Rif1	4.27	-7.98	1.5E-09
Pp4-19C	12.67	-7.98	5.2E-11
CG1827	7.80	-7.98	6.5E-06
Blos4	2.24	-7.99	2.4E-02
CG12659	2.66	-8.01	2.5E-02
CG9692	2.55	-8.02	4.5E-03
CG31475	16.89	-8.03	1.6E-09
SP1173	87.89	-8.04	0.0E+00
Plap	15.36	-8.05	6.8E-11
DNApol-alpha180	4.54	-8.06	3.9E-10
Ponn	1.41	-8.06	8.2E-03
Knn2	4.08	-8.06	2.4E-02
CG5555	8.97	-8.07	9.8E-09
CG12075	21.72	-8.08	0.0E+00
O-fut2	5.08	-8.10	7.6E-05
sas	68.59	-8.10	5.0E-12
CG13994	11.27	-8.10	7.4E-05
Srp14	25.62	-8.10	5.7E-07
Prx6005	8.30	-8.11	8.6E-05
okr	1.66	-8.13	9.9E-04
CG6472	3.11	-8.14	3.0E-03
hgo	10.87	-8.17	5.0E-05
Rca1	3.10	-8.21	9.4E-04
vig2	73.46	-8.22	0.0E+00
CG34462	11.74	-8.23	2.3E-06
CG4914	6.85	-8.23	1.7E-05
CG15279	12.31	-8.23	6.8E-10
Zwilch	1.64	-8.28	4.5E-03
CG3770	12.14	-8.28	8.2E-08
caix	1378.25	-8.31	2.2E-09
Arpc4	39.31	-8.32	3.5E-12
CG10133	4.45	-8.33	8.9E-04
Nlp	80.62	-8.35	1.2E-14
SLIRP2	6.09	-8.36	2.1E-02
CG5181	6.02	-8.36	7.7E-05
CCT8	57.70	-8.36	0.0E+00
salt	3.00	-8.38	1.8E-02
I28up	19.62	-8.42	3.2E-10
udd	6.40	-8.43	3.6E-05
AIMP1	15.42	-8.43	3.8E-08
CCT5	75.73	-8.44	0.0E+00
CG17187	2.95	-8.44	3.4E-03

Cdc23	3.28	-8.45	7.9E-05
CG16798	3.92	-8.48	1.6E-05
CG31460	8.67	-8.50	2.6E-04
Tpi	202.26	-8.57	6.9E-13
mRpS24	8.39	-8.57	6.3E-04
CG15343	12.53	-8.60	9.3E-05
CG11123	5.25	-8.63	2.1E-06
CC11	60.68	-8.64	6.4E-13
mth	11.49	-8.65	2.4E-11
gammaTub23C	6.83	-8.66	1.4E-07
CG9125	5.76	-8.67	8.0E-05
GluRIID	3.58	-8.69	2.9E-05
Uch-L5	16.46	-8.70	1.2E-10
312	2.38	-8.70	3.1E-03
Axs	9.37	-8.71	8.3E-11
CG4096	15.44	-8.74	1.2E-12
Pvf2	3.67	-8.75	1.9E-04
slll	59.45	-8.75	0.0E+00
CG9812	233.37	-8.76	2.1E-15
Rrp40	4.99	-8.82	6.0E-04
mei-S332	1.54	-8.83	1.6E-02
CG5220	7.03	-8.84	9.4E-05
Pgam5	14.14	-8.87	5.4E-08
CG15545	2.11	-8.87	2.1E-02
grn	6.66	-8.88	9.7E-11
aurA	1.66	-8.88	1.6E-02
CG7182	10.64	-8.89	1.0E-10
Tsf3	26.37	-8.92	0.0E+00
CG7512	2.66	-8.92	3.8E-04
alphaTub84B	1206.79	-8.96	1.5E-09
RecQ4	2.10	-8.98	3.9E-06
Prp18	4.03	-8.98	3.7E-04
CG17919	88.46	-8.99	8.2E-13
Tsfl	1088.88	-8.99	4.8E-09
ems	3.22	-9.02	8.7E-05
PrBP	25.72	-9.02	2.9E-11
CG42747	1.88	-9.04	3.8E-04
Pbp49	6.87	-9.05	1.5E-06
CG31997	554.46	-9.06	3.8E-12
CG17600	11.23	-9.09	4.6E-11
CG13069	45.35	-9.09	1.0E-07
CG42394	55.13	-9.14	2.4E-11
CG11550	28.56	-9.14	5.1E-07
CG31313	407.24	-9.15	8.1E-08
CG5835	25.73	-9.18	9.7E-11
CG32075	3.47	-9.20	1.4E-04
Pxn	49.31	-9.20	2.8E-10
CG10585	8.87	-9.25	1.5E-08
betaTub56D	822.19	-9.25	6.2E-11
Rab23	6.00	-9.26	4.3E-07
Prat	5.14	-9.29	2.0E-06
CG42259	37.03	-9.29	2.7E-09
CG1890	42.44	-9.29	2.3E-12
E(spl)m3-HLH	7.39	-9.30	1.5E-05
spz6	1.69	-9.31	1.3E-02
Lrt	5.24	-9.32	1.8E-09
CG30196	8.30	-9.32	2.5E-03
Nnf1a	4.01	-9.32	1.3E-02
CG42255	4.29	-9.33	2.4E-04
CG5188	3.92	-9.37	2.1E-03
GstE13	19.82	-9.37	5.7E-10
CG11788	1.93	-9.39	1.2E-02
CG12909	5.40	-9.40	4.1E-04
CG33213	2.16	-9.41	1.3E-02
pio	105.24	-9.43	0.0E+00
Pen	14.61	-9.44	2.3E-11
CG8100	1.02	-9.47	1.2E-02
CG3788	1.57	-9.48	1.2E-02
CG32708	4.91	-9.50	2.1E-03
Oaz	2.94	-9.52	5.5E-07
icln	8.51	-9.53	1.0E-04
MCTS1	13.44	-9.54	1.2E-07
sad	3.57	-9.57	8.8E-03
AlkB	3.38	-9.57	1.8E-03
AAATL2	17.42	-9.62	3.3E-06
Hexo1	66.35	-9.65	0.0E+00
Cad96Ca	18.92	-9.66	1.2E-13
koko	3.03	-9.68	1.9E-03
CG5397	165.01	-9.70	1.0E-14
CG15879	4.12	-9.71	2.8E-04
CG8478	2.52	-9.72	3.5E-04
scra	6.50	-9.74	2.6E-09
CG5828	7.97	-9.74	8.4E-06
CG10098	17.88	-9.83	4.6E-12
Rlp3A	3.85	-9.84	2.6E-08
sti	4.07	-9.85	2.1E-10
CG14949	4.75	-9.85	5.0E-03
CG44245	74.08	-9.85	1.0E-13
nxf2	1.00	-9.86	1.0E-02
CG10889	2.01	-9.86	1.6E-03
slif	11.80	-9.91	1.1E-10
Cdk1	8.24	-9.91	6.5E-05
CG30438	8.73	-9.92	8.4E-07
MFS9	18.67	-9.97	1.5E-08
RnrS	20.82	-9.97	6.9E-12
CG15525	6.78	-10.04	1.5E-03
nst	28.31	-10.07	1.1E-13
lds	5.83	-10.08	1.1E-10
tum	5.64	-10.09	2.8E-07
Actn	56.98	-10.11	0.0E+00
alpha-PheRS	19.19	-10.13	3.0E-11
inv	1.56	-10.13	7.1E-05
CG12206	19.52	-10.17	1.4E-14
U3-55K	3.52	-10.17	2.9E-04
CG17190	100.64	-10.18	0.0E+00
Hsp70Bbb	13.90	-10.18	3.8E-08
Wnt6	8.30	-10.19	3.4E-09
CG12017	1.13	-10.29	8.9E-03
glu	4.74	-10.32	1.6E-10
CG1648	145.12	-10.34	0.0E+00
CG12164	1.92	-10.39	1.1E-02

nclb	15.21	-10.41	8.5E-10
CG3995	3.88	-10.44	1.3E-03
Tsp42Eo	3.54	-10.47	1.0E-02
CG4324	1.79	-10.48	8.2E-03
CG11836	2.28	-10.51	7.8E-03
FK506-bp1	45.15	-10.54	0.0E+00
mRpS25	12.00	-10.55	5.7E-05
Ran	90.27	-10.56	0.0E+00
CG1273	2.78	-10.63	5.0E-06
CG9572	37.29	-10.67	2.0E-08
DNApol-epsilon58	2.81	-10.70	1.0E-03
CalpC	13.41	-10.71	2.2E-11
Atu	9.29	-10.71	1.1E-11
CG2990	0.86	-10.76	6.9E-03
Spindly	1.87	-10.76	8.5E-04
dpv	98.96	-10.81	8.3E-11
polo	7.52	-10.84	2.3E-10
Cks30A	4.18	-10.85	9.3E-04
boi	2.22	-10.88	2.0E-06
CG2767	110.70	-10.90	0.0E+00
Hsp27	59.85	-10.91	0.0E+00
Set	27.74	-10.94	9.8E-12
esg	1.42	-10.95	6.0E-03
Sec61beta	91.36	-11.02	2.1E-15
CG13722	1.89	-11.04	1.0E-03
CG10570	42.78	-11.11	9.9E-10
CG17029	86.28	-11.14	0.0E+00
lft	36.94	-11.16	1.1E-13
CG1143	5.29	-11.21	2.9E-04
Tep4	54.88	-11.24	0.0E+00
spok	4.03	-11.25	2.9E-02
CG33671	20.61	-11.28	2.2E-12
Galphaf	1.86	-11.31	5.4E-03
CG4593	8.83	-11.33	3.7E-06
CG14291	28.35	-11.34	1.4E-14
CG15497	4.13	-11.35	5.6E-04
CG6294	3.72	-11.40	2.4E-07
CG13014	6.34	-11.44	7.5E-05
CG1299	153.80	-11.44	0.0E+00
snRNP-U1-C	14.80	-11.49	2.2E-06
Smf	18.05	-11.53	3.2E-05
dgt2	5.16	-11.54	5.3E-04
SAK	2.02	-11.55	1.1E-04
Cda5	17.28	-11.70	0.0E+00
CG18789	2.49	-11.74	3.9E-03
AnxB10	86.16	-11.76	0.0E+00
CG11835	6.36	-11.79	4.9E-08
CG2837	9.40	-11.83	3.8E-07
Dbp73D	3.16	-11.87	8.5E-05
CG42502	42.69	-11.94	4.1E-10
Hsp70Bc	12.53	-11.97	7.8E-08
CG10005	14.95	-12.01	2.5E-08
CG9596	3.77	-12.03	2.1E-05
CCT3	55.62	-12.08	0.0E+00
TwidT	2.22	-12.14	4.0E-03
CG46312	11.56	-12.26	2.3E-08
CG33082	1.57	-12.26	3.7E-03
CG14105	5.22	-12.29	1.0E-02
SP1029	68.05	-12.30	0.0E+00
CG34001	3.15	-12.37	4.7E-02
CG3594	6.38	-12.39	4.1E-04
WRNexo	3.66	-12.43	2.9E-04
Nle	6.97	-12.43	1.1E-06
mira	2.21	-12.47	5.6E-05
to	96.06	-12.54	7.5E-09
Rcc1	17.84	-12.57	1.4E-14
SeId	22.63	-12.58	1.4E-14
CG9194	1.26	-12.58	4.7E-03
CG15544	3.95	-12.59	1.7E-08
CG11164	2.50	-12.64	3.5E-03
wwpA	186.47	-12.68	0.0E+00
Cpr66D	5.25	-12.71	4.7E-04
Sptr	29.34	-12.71	1.1E-12
CG45064	5.61	-12.71	5.8E-09
Nsun5	6.28	-12.74	8.7E-06
scaf	78.02	-12.82	0.0E+00
CG1698	3.75	-12.83	1.2E-07
Hat1	8.06	-12.87	8.3E-08
snk	1.36	-12.89	4.4E-02
Ada1-1	3.48	-12.89	3.0E-03
CG13024	11.74	-12.90	1.1E-10
CG14259	24.24	-13.00	4.2E-08
CG14997	53.73	-13.14	0.0E+00
Spn42De	4.13	-13.16	4.1E-04
CG33502	3.74	-13.21	3.0E-03
Cpr67B	107.45	-13.21	3.4E-11
Cyp312a1	10.38	-13.33	3.7E-12
Obp56e	7.03	-13.35	6.4E-03
CG9265	19.90	-13.36	0.0E+00
tfc	11.81	-13.40	5.6E-08
Arl2	9.00	-13.40	2.1E-04
CG7946	9.61	-13.41	4.9E-10
CG8336	7.19	-13.44	2.0E-07
nle	46.22	-13.44	1.2E-13
CG16786	10.79	-13.57	3.2E-12
SMC2	3.77	-13.59	6.5E-08
Nup133	5.94	-13.61	3.0E-11
rept	11.28	-13.70	7.4E-11
CG9759	2.58	-13.71	2.8E-02
CG9427	46.21	-13.73	4.0E-14
[(2)03659	0.91	-13.75	2.4E-03
CG15554	2.61	-13.77	4.8E-02
[(2)09851	12.37	-13.88	2.9E-11
Cad99C	30.54	-13.95	0.0E+00
Mic2	683.16	-14.05	7.8E-11
dsx-c73A	0.61	-14.06	3.4E-02
Tsp42Ek	10.30	-14.17	5.6E-07
Fit2	5.24	-14.23	5.4E-08
CG45065	5.64	-14.25	4.6E-09
ez3	4.91	-14.26	7.0E-08
GstE11	22.04	-14.27	2.3E-11



CG34229	4.56	-14.31	3.2E-02
dpa	6.85	-14.40	3.6E-11
CG5645	3.89	-14.44	2.1E-06
CG10764	2.57	-14.45	3.2E-03
CG31473	2.23	-14.48	3.1E-02
CG14668	2.31	-14.49	3.2E-02
mRpl51	10.14	-14.49	1.5E-04
CG14223	0.63	-14.50	3.1E-02
abd-A	20.03	-14.53	0.0E+00
CG9815	7.40	-14.56	2.0E-06
CG6540	5.16	-14.57	1.3E-04
CG13551	124.25	-14.60	0.0E+00
Coop	10.14	-14.62	8.6E-09
pip	1.91	-14.64	1.6E-10
CG13742	0.86	-14.69	3.0E-02
GILT1	313.74	-14.81	0.0E+00
rtv	19.42	-14.82	4.1E-10
tx	8.11	-14.83	1.1E-09
unc-45	8.77	-14.91	4.7E-13
PCID2	5.17	-14.95	1.0E-04
HmgD	57.00	-15.00	0.0E+00
RanBP3	14.91	-15.01	6.5E-13
wus	3.14	-15.03	1.1E-04
E(spl)malph-BFM	3.35	-15.07	3.0E-02
pwn	12.26	-15.23	0.0E+00
CG30403	1.82	-15.24	2.8E-02
CG11699	29.46	-15.27	2.7E-12
Osi9	1.68	-15.28	2.8E-02
CG12301	3.58	-15.37	1.9E-05
CG1139	4.31	-15.42	1.7E-04
Mcm10	2.43	-15.47	1.3E-04
CG45076	23.11	-15.50	2.8E-14
Sld5	3.02	-15.51	2.6E-02
CG31321	35.65	-15.51	2.1E-15
CG42562	16.93	-15.56	2.0E-04
Pfdn1	30.54	-15.57	2.2E-09
asl	4.31	-15.62	7.0E-08
CG10359	20.69	-15.66	6.3E-14
Sodh-2	101.09	-15.70	0.0E+00
CG33672	12.83	-15.74	6.0E-13
CG2975	2.53	-15.86	1.2E-03
conv	17.67	-15.94	0.0E+00
CG33978	32.61	-16.20	0.0E+00
Hisl:CG33855	2.40	-16.52	2.2E-02
Hisl:CG33858	2.44	-16.56	2.2E-02
CG14445	5.63	-16.77	1.3E-04
CG10898	26.37	-16.81	0.0E+00
I(1)G0004	7.77	-16.86	4.5E-05
mth4	24.68	-16.95	0.0E+00
CG42561	9.07	-17.01	1.4E-03
spirit	9.23	-17.04	1.0E-06
CG30440	13.55	-17.07	2.1E-15
CG34056	38.44	-17.13	0.0E+00
CG30380	11.07	-17.14	7.0E-04
laccase2	57.86	-17.23	0.0E+00
CG8157	3.07	-17.25	2.4E-02
Hisl:CG33861	2.52	-17.27	2.0E-02
CG31176	21.13	-17.29	0.0E+00
CG9114	2.21	-17.36	6.5E-04
Psf1	3.75	-17.40	1.9E-02
lba5	24.97	-17.40	2.4E-14
CG5757	5.17	-17.42	7.0E-04
tant	3.09	-17.46	6.4E-04
I(2)35Cc	2.62	-17.82	1.7E-02
RIC4	9.29	-17.82	1.9E-06
CG10527	369.86	-17.85	0.0E+00
Nup75	7.52	-18.26	1.5E-08
wuho	7.37	-18.38	1.3E-06
Ser	9.57	-18.38	0.0E+00
CG17026	35.00	-18.60	1.1E-13
Pif1	2.13	-18.67	4.7E-04
CDC45L	4.96	-18.69	1.1E-06
PPO1	298.33	-18.69	1.0E-11
tw	15.47	-18.78	8.3E-15
up	255.00	-18.80	0.0E+00
Rpl12	5.33	-18.84	1.5E-02
wac	6.52	-18.84	4.1E-04
haf	21.95	-18.91	0.0E+00
CG18530	7.24	-18.92	5.7E-05
CG34446	16.16	-19.06	3.8E-04
nyo	0.76	-19.14	1.7E-02
Df31	177.66	-19.14	0.0E+00
Mcm7	7.87	-19.16	2.4E-09
uif	70.35	-19.20	0.0E+00
CG3119	6.67	-19.26	3.7E-04
CG5235	1.07	-19.27	1.4E-02
Gasp	190.82	-19.50	0.0E+00
ec	10.78	-19.52	0.0E+00
CG31559	1.51	-19.54	1.5E-02
CG5639	15.10	-19.65	0.0E+00
Cpr11B	11.15	-19.74	3.2E-04
CG8483	35.04	-19.74	0.0E+00
frac	5.41	-19.86	1.1E-10
CG14231	3.16	-20.01	3.2E-04
Mlp60A	60.33	-20.06	0.0E+00
CG34454	15.33	-20.08	1.1E-04
gen	1.32	-20.12	1.3E-02
CG17672	2.05	-20.13	1.4E-02
CAH1	1156.68	-20.22	1.0E-14
CG5731	6.84	-20.37	3.8E-07
Mic1	303.76	-20.38	0.0E+00
CG13679	6.21	-20.40	1.2E-02
CG5177	164.78	-20.54	0.0E+00
ea	39.45	-20.58	0.0E+00
RnrL	12.92	-20.61	7.1E-14
odd	1.33	-20.73	1.3E-02
qsm	64.17	-20.74	0.0E+00
CG4847	461.92	-20.77	8.3E-14
Ccp84Af	5.41	-20.89	1.2E-02
CG9737	1.92	-20.94	1.1E-02
CG13272	0.89	-21.07	1.6E-02

en	1.15	-21.22	1.2E-02
CG11852	279.27	-21.31	0.0E+00
Smb	20.16	-21.40	2.7E-08
Klp61F	4.98	-21.41	3.2E-09
PK1-R	2.54	-22.03	5.2E-04
CG13896	3.22	-22.14	8.8E-03
CG6414	1.64	-22.24	1.2E-02
CG40486	63.81	-22.41	0.0E+00
asp	2.61	-22.41	1.6E-08
mth3	80.73	-22.65	0.0E+00
CG15506	4.66	-22.66	2.7E-04
CG8492	16.05	-22.71	0.0E+00
CG31775	5.43	-22.72	1.0E-02
Gld	13.31	-22.76	1.7E-11
CG7778	30.94	-22.82	0.0E+00
Fib	18.24	-22.85	7.2E-11
CG17803	1.56	-23.07	7.8E-03
RhoGEF64C	16.51	-23.14	0.0E+00
CG17707	0.93	-23.29	8.4E-03
CG13038	6.91	-23.39	7.3E-03
Mcm3	6.23	-23.76	2.2E-08
Naa40	4.85	-23.98	6.9E-03
CG4702	7.24	-24.07	1.2E-05
Act87E	132.93	-24.14	0.0E+00
CG34445	47.22	-24.22	3.6E-12
CG9449	132.04	-24.30	0.0E+00
RhoGEF4	1.71	-24.42	7.0E-03
CG3746	10.61	-24.71	1.3E-04
Ts	8.21	-24.91	2.3E-06
CG8078	61.01	-24.92	0.0E+00
Dlsh	7.87	-24.95	2.3E-06
Tm2	191.19	-25.33	0.0E+00
RFase	14.06	-25.39	6.0E-08
CG16734	2.74	-25.60	6.0E-03
ds	9.39	-25.68	0.0E+00
CG10336	2.82	-25.91	5.7E-03
CG43134	115.77	-26.01	1.6E-11
CG42749	6.45	-26.28	1.2E-06
BCL7-like	7.05	-26.50	9.0E-07
CG16727	8.15	-26.59	1.8E-04
Fbp1	9.51	-26.62	1.9E-07
CG8501	18.52	-26.85	1.0E-07
CG1441	17.25	-26.86	1.9E-12
CG6739	18.90	-27.05	0.0E+00
He	11.66	-27.15	2.0E-04
qua	4.37	-27.22	1.4E-07
CG1632	11.66	-27.31	2.1E-15
thw	11.35	-27.39	3.2E-11
Incemp	5.70	-27.47	2.8E-08
CG5023	74.95	-27.56	0.0E+00
mth19	18.96	-27.58	0.0E+00
Spm88Ea	433.48	-27.78	0.0E+00
CG14968	9.57	-27.80	6.8E-07
CG8925	3.48	-28.16	6.4E-05
Hisp2B:CG33868	7.17	-28.19	4.3E-03
CG10663	15.72	-28.21	0.0E+00
CG8675	7.88	-28.52	5.9E-05
I(2)efl	80.02	-28.54	0.0E+00
sro	3.73	-28.91	4.5E-03
cutlet	2.66	-29.16	5.2E-05
Impl3	81.45	-29.56	0.0E+00
CG43386	7.80	-29.59	2.8E-07
PPO2	389.49	-29.74	3.0E-14
E(spl)mbeta-HLH	36.26	-29.78	3.4E-14
CG6296	2.07	-29.90	4.8E-03
CG12493	3.90	-30.17	3.8E-03
CG31337	5.38	-30.42	4.7E-03
Glat1	109.68	-30.49	0.0E+00
RPA2	9.48	-30.80	4.0E-05
CG33939	16.52	-30.95	4.5E-05
DI	54.78	-31.19	0.0E+00
CG15820	4.04	-31.35	4.0E-03
Fen1	3.44	-31.53	3.1E-03
CG1124	23.79	-31.71	6.6E-11
mei-38	2.75	-32.04	2.8E-03
Jheb3	122.73	-32.17	0.0E+00
CG13674	7.05	-32.35	2.8E-03
nesd	4.50	-32.40	2.8E-05
Fbp2	16.68	-32.49	3.6E-08
Mhc	504.57	-32.64	0.0E+00
feo	6.03	-32.74	3.5E-07
CG14353	3.37	-33.30	2.4E-03
CG44403	48.94	-33.34	0.0E+00
CG3038	10.76	-33.61	1.9E-09
Obp99b	82.83	-34.09	4.2E-15
CG3777	199.66	-34.18	0.0E+00
CG43131	10.98	-34.21	4.4E-03
CG17266	5.66	-34.34	2.2E-03
CG3502	11.99	-34.40	2.8E-11
CG17032	97.00	-34.44	0.0E+00
miple2	10.13	-34.47	1.8E-07
CG7365	10.52	-35.36	7.7E-08
sn	23.83	-35.56	0.0E+00
GluRIIC	1.77	-35.68	2.6E-03
CG14132	65.38	-35.75	0.0E+00
CG31028	20.82	-35.96	0.0E+00
CG12009	12.28	-36.45	4.3E-13
Cpr49Ac	2.73	-36.60	2.2E-03
Mp20	319.17	-36.95	0.0E+00
CG6300	11.06	-37.18	9.9E-05
PCNA	20.28	-37.23	4.7E-10
Scb	89.59	-37.63	0.0E+00
Hsp23	103.68	-38.63	0.0E+00
CG9747	12.31	-39.94	8.1E-12
Nha1	15.32	-40.28	1.2E-14
Cyp313a5	7.63	-40.41	3.8E-06
CG34140	3.54	-40.53	1.3E-03
Edg91	356.92	-41.33	0.0E+00
Cpr51A	176.81	-41.82	0.0E+00
Egfp2	10.18	-42.46	2.8E-06
ft	9.98	-43.15	0.0E+00

mtg	10.64	-43.42	9.3E-11
CG5863	8.66	-43.85	7.4E-06
yellow-e2	4.21	-44.00	1.2E-03
CG4115	226.49	-44.04	0.0E+00
wbl	15.08	-44.58	1.1E-08
cysu	28.49	-44.90	0.0E+00
St4	17.78	-45.78	4.2E-08
CG4576	20.05	-46.08	1.9E-12
knk	25.48	-46.55	0.0E+00
dUTPase	25.24	-46.75	3.4E-09
825-Oak	27.15	-47.44	2.3E-06
Phk-3	548.12	-47.93	0.0E+00
CAH2	90.63	-47.93	0.0E+00
fau	95.44	-47.98	0.0E+00
CG11382	7.91	-48.30	3.0E-05
CG8888	37.48	-48.56	0.0E+00
amd	6.10	-48.78	8.1E-06
yellow-c	42.16	-50.40	0.0E+00
Cht6	41.81	-50.72	0.0E+00
MFS3	43.83	-50.88	0.0E+00
CG13046	57.19	-51.27	4.2E-15
TpnC73F	175.76	-52.92	0.0E+00
Cpr97Eb	199.78	-53.05	0.0E+00
CG17104	14.88	-53.37	3.7E-12
CG8192	60.50	-53.40	0.0E+00
nav	5.11	-55.22	8.7E-07
CG14795	18.93	-57.84	6.2E-04
CG13640	68.65	-58.49	4.8E-12
l(2)k05911	68.72	-58.55	0.0E+00
sob	3.38	-58.75	3.9E-04
CG14564	10.21	-59.68	4.8E-04
Obp56d	954.07	-61.29	0.0E+00
CG2070	38.83	-62.39	0.0E+00
CG9993	5.11	-62.45	8.8E-04
CG7675	91.54	-62.91	0.0E+00
CG3292	6.22	-65.21	1.4E-03
d	4.80	-65.76	1.3E-10
Act57B	1351.88	-67.26	0.0E+00
PH4alphaMP	22.33	-68.98	1.9E-12
neo	3.50	-69.14	1.9E-04
Duox	17.39	-69.65	0.0E+00
Skeletor	46.11	-72.93	0.0E+00
CG10211	43.34	-73.59	0.0E+00
CG10205	36.49	-73.97	1.9E-10
CG9701	89.10	-76.53	0.0E+00
Cpr57A	115.33	-81.58	0.0E+00
mud	2.89	-86.58	1.6E-08
Ote	8.29	-86.90	6.1E-05
CG5391	17.39	-88.87	8.7E-05
CG8420	5.88	-89.73	5.5E-05
CG2121	39.00	-93.60	0.0E+00
CG32564	19.18	-93.64	7.3E-09
CG5928	11.71	-95.79	4.7E-05
alphaTub85E	18.48	-98.24	6.4E-08
CBP	44.91	-99.25	0.0E+00
CG14301	8.16	-100.84	5.7E-05
CG7402	51.57	-105.99	0.0E+00
Lsp1gamma	131.23	-108.40	0.0E+00
reb	44.92	-112.03	0.0E+00
Mcm2	5.86	-112.68	2.5E-05
exp	24.20	-114.70	0.0E+00
lj	9.70	-116.29	1.4E-09
Clect27	409.85	-117.91	0.0E+00
yellow-e	29.23	-119.87	3.1E-13
CG11029	30.06	-123.13	1.7E-13
CG42305	81.66	-130.00	2.1E-15
CG4000	205.52	-130.23	0.0E+00
Cad74A	17.11	-131.64	0.0E+00
ETH	132.49	-135.96	0.0E+00
Cpr49Ag	655.17	-136.57	0.0E+00
CG7896	28.57	-137.19	0.0E+00
CG11529	17.10	-138.07	1.0E-05
verm	398.62	-141.45	0.0E+00
fw	22.26	-141.69	0.0E+00
Cht7	92.91	-142.33	0.0E+00
Lsp1alpha	62.93	-144.03	0.0E+00
CG13067	4348.94	-145.76	0.0E+00
Cht2	43.62	-150.11	0.0E+00
Tmhs	13.76	-151.30	4.8E-06
CG10936	45.99	-152.80	0.0E+00
Fst	34.29	-155.45	1.5E-06
CG13047	73.39	-158.25	1.1E-10
CG13068	360.35	-159.78	0.0E+00
Cyp4c3	39.51	-166.00	6.1E-14
CG17325	83.17	-168.79	1.0E-14
serp	332.86	-174.89	0.0E+00
CG13676	93.64	-176.34	0.0E+00
CG8927	197.81	-178.95	0.0E+00
CG15414	20.06	-185.06	2.6E-06
AOX2	69.97	-196.73	0.0E+00
CG3588	109.95	-216.99	0.0E+00
kkv	77.71	-228.34	0.0E+00
CG17843	19.16	-230.20	6.8E-07
Cht10	334.09	-235.30	0.0E+00
Abd-B	8.94	-238.22	0.0E+00
SclA	36.70	-248.85	7.0E-07
hut	243.22	-249.56	0.0E+00
yellow-d2	87.15	-252.22	0.0E+00
CG8560	24.99	-259.74	3.9E-07
obst-A	130.32	-285.90	0.0E+00
Cpr78Ca	52.29	-306.79	3.0E-07
obst-B	120.04	-314.33	0.0E+00
obst-E	217.95	-314.96	0.0E+00
zyc	47.42	-318.61	0.0E+00
CG12607	48.25	-342.18	5.2E-07
spz5	26.39	-350.31	6.7E-08
l(3)mbn	67.85	-377.48	0.0E+00
CG13051	149.15	-383.10	3.9E-08
l(2)34Fc	688.67	-385.57	0.0E+00
CG42662	28.25	-515.36	8.3E-09
TwldX	58.73	-534.07	1.3E-08

Cpr78E	356.86	-548.98	0.0E+00
ckd	47.81	-554.71	5.9E-09
CG15353	43028.00	-555.46	0.0E+00
Cpr100A	189.54	-576.58	0.0E+00
CG42500	204.30	-588.27	9.2E-09
Cda4	96.96	-631.84	0.0E+00
CG17738	226.22	-639.26	7.7E-09
nw	96.59	-760.55	0.0E+00
Twldbeta	159.22	-767.57	9.3E-10
Peritrophin-A	177.93	-910.03	0.0E+00
Psd	53.08	-924.22	1.8E-10
CG13678	2719.70	-1054.82	0.0E+00
CG15597	279.70	-1266.26	3.4E-11
CG13705	273.41	-1477.33	0.0E+00
CG16884	1575.31	-1672.29	0.0E+00
Cpr49Ah	254.57	-1687.25	2.7E-12
CG15308	871.05	-1707.29	0.0E+00
Cpr65Av	405.39	-1719.09	3.4E-12
CG11350	179.74	-1773.54	4.6E-12
CG11370	6418.99	-1803.13	0.0E+00
Ccp84Ag	269.35	-1968.53	1.1E-12
frm	138.13	-2153.77	0.0E+00
CG7296	741.78	-2389.71	0.0E+00
CG1368	466.22	-2484.57	1.0E-12
Obp56a	828.37	-2994.47	8.6E-14
Nhp4	24541.49	-3073.59	0.0E+00
CG16885	2587.27	-3425.12	0.0E+00
Cpr92F	486.96	-5962.97	2.1E-15
CG32249	1955.92	-6192.42	0.0E+00
CG34227	1994.61	-6307.51	2.1E-15
Cpr62Bc	1685.85	-6397.84	0.0E+00
CG7214	1719.41	-11819.09	0.0E+00
Lcp3	9998.03	-16712.39	0.0E+00
Lcp1	2732.09	-19073.95	0.0E+00
Lcp65Ab1	21070.08	-2079919.47	3.8E-02
Lcp4	14677.83	-2770394.60	3.4E-02

## 6.7 GO terms for biological processes of airways from CS exposed 3<sup>rd</sup> instar larvae

Term	P-value	Fold enrichment
GO:0006749~glutathione metabolic process	2,6E-18	28,79
GO:0055114~oxidation-reduction process	3,0E-07	4,11
GO:0055085~transmembrane transport	6,0E-04	3,50
GO:0006979~response to oxidative stress	0,004	5,52
GO:0046425~regulation of JAK-STAT cascade	0,015	15,86
GO:0045454~cell redox homeostasis	0,023	6,51
GO:0046701~insecticide catabolic process	0,029	11,03
GO:0046427~positive regulation of JAK-STAT cascade	0,029	11,03
GO:0043697~cell dedifferentiation	0,035	56,39
GO:0046680~response to DDT	0,042	9,06
GO:0006820~anion transport	0,042	9,06
GO:0060729~intestinal epithelial structure maintenance	0,046	42,29

## 6.8 GO terms for biological processes of airways from 5 d CS exposed flies for upregulated DEGs

Term	P-value	Fold enrichment
GO:0007424~open tracheal system development	2,29E-13	3,56
GO:0007391~dorsal closure	3,35E-13	3,53
GO:0007476~imaginal disc-derived wing morphogenesis	1,59E-10	2,41
GO:0007298~border follicle cell migration	6,32E-09	2,71
GO:0008360~regulation of cell shape	2,76E-07	2,70
GO:0008340~determination of adult lifespan	5,71E-07	2,24
GO:0007426~tracheal outgrowth, open tracheal system	6,27E-07	4,97
GO:0007427~epithelial cell migration, open tracheal system	1,28E-06	4,17
GO:0030707~ovarian follicle cell development	1,82E-06	2,70
GO:0019991~septate junction assembly	3,27E-06	4,16
GO:0006909~phagocytosis	5,32E-06	1,99
GO:0030239~myofibril assembly	7,56E-06	5,91
GO:0045214~sarcomere organization	8,39E-06	4,14
GO:0007155~cell adhesion	9,35E-06	2,55
GO:0007507~heart development	1,07E-05	3,06
GO:0007498~mesoderm development	1,40E-05	2,91
GO:0033627~cell adhesion mediated by integrin	3,48E-05	4,65
GO:0016477~cell migration	3,90E-05	3,30
GO:0007411~axon guidance	7,46E-05	1,92
GO:0060857~establishment of glial blood-brain barrier	9,16E-05	4,67
GO:0006366~transcription from RNA polymerase II promoter	1,01E-04	2,65
GO:0035160~maintenance of epithelial integrity, open tracheal system	1,08E-04	5,91
GO:0007015~actin filament organization	1,09E-04	2,43
GO:0007419~ventral cord development	1,09E-04	2,43
GO:0001751~compound eye photoreceptor cell differentiation	1,24E-04	3,80
GO:0032509~endosome transport via multivesicular body sorting pathway	1,42E-04	4,99
GO:0045176~apical protein localization	1,42E-04	4,99
GO:0046331~lateral inhibition	1,57E-04	1,81
GO:0030431~sleep	1,69E-04	2,11
GO:0006955~immune response	2,01E-04	2,79
GO:0042060~wound healing	2,34E-04	2,66
GO:0035151~regulation of tube size, open tracheal system	2,36E-04	4,22
GO:0007435~salivary gland morphogenesis	2,54E-04	2,74
GO:0045186~zonula adherens assembly	2,84E-04	6,21
GO:0002009~morphogenesis of an epithelium	3,09E-04	3,75
GO:0034446~substrate adhesion-dependent cell spreading	3,11E-04	7,60
GO:0035001~dorsal trunk growth, open tracheal system	3,11E-04	7,60
GO:0035080~heat shock-mediated polytene chromosome puffing	3,11E-04	7,60
GO:0007494~midgut development	3,54E-04	3,43
GO:0007520~myoblast fusion	3,65E-04	2,89
GO:0007010~cytoskeleton organization	3,75E-04	3,20
GO:0006357~regulation of transcription from RNA polymerase II promoter	3,92E-04	1,85
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	4,50E-04	1,71
GO:0006749~glutathione metabolic process	4,67E-04	2,83
GO:0001736~establishment of planar polarity	4,85E-04	3,33
GO:0042127~regulation of cell proliferation	4,90E-04	2,96
GO:0006915~apoptotic process	4,98E-04	2,36
GO:0000902~cell morphogenesis	5,44E-04	2,68
GO:0008258~head involution	5,91E-04	2,77
GO:0035159~regulation of tube length, open tracheal system	6,18E-04	3,48
GO:0022416~chaeta development	6,53E-04	2,46
GO:0007399~nervous system development	6,62E-04	2,04
GO:0048190~wing disc dorsal/ventral pattern formation	7,43E-04	2,71
GO:0035330~regulation of hippo signaling	7,53E-04	6,65
GO:0001666~response to hypoxia	8,71E-04	3,13
GO:0030036~actin cytoskeleton organization	0,0010	2,76
GO:0006122~mitochondrial electron transport, ubiquinol to cytochrome c	0,0010	4,43
GO:0045087~innate immune response	0,0011	2,05
GO:0010906~regulation of glucose metabolic process	0,0012	1,75
GO:0050832~defense response to fungus	0,0013	2,70
GO:0007390~germ-band shortening	0,0013	3,80
GO:0007422~peripheral nervous system development	0,0021	2,11

GO:0007480~imaginal disc-derived leg morphogenesis	0,0022	2,36
GO:0001122~negative regulation of transcription from RNA polymerase II promoter	0,0022	1,79
GO:0043066~negative regulation of apoptotic process	0,0022	2,28
GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity	0,0023	3,94
GO:0007475~apposition of dorsal and ventral imaginal disc-derived wing surfaces	0,0026	2,96
GO:0007423~sensory organ development	0,0026	2,25
GO:0007398~ectoderm development	0,0026	3,47
GO:0007163~establishment or maintenance of cell polarity	0,0027	3,17
GO:0035206~regulation of hemocyte proliferation	0,0027	3,17
GO:0045167~asymmetric protein localization involved in cell fate determination	0,0027	4,43
GO:0006783~heme biosynthetic process	0,0027	4,43
GO:0061320~pericardial nephrocyte differentiation	0,0028	5,32
GO:0015031~protein transport	0,0029	2,11
GO:0008354~germ cell migration	0,0030	2,73
GO:0035099~hemocyte migration	0,0034	3,73
GO:0002181~cytoplasmic translation	0,0034	1,95
GO:0016318~ommatidial rotation	0,0035	3,06
GO:0048749~compound eye development	0,0037	1,82
GO:0008407~chaeta morphogenesis	0,0040	2,51
GO:0007425~epithelial cell fate determination, open tracheal system	0,0042	6,33
GO:0035011~melanotic encapsulation of foreign target	0,0045	2,96
GO:0008406~gonad development	0,0045	2,96
GO:0003007~heart morphogenesis	0,0046	4,84
GO:0002121~inter-male aggressive behavior	0,0050	2,25
GO:0007616~long-term memory	0,0056	2,09
GO:0008045~motor neuron axon guidance	0,0058	2,15
GO:0007409~axonogenesis	0,0059	2,22
GO:0007464~R3/R4 cell fate commitment	0,0060	3,88
GO:0007160~cell-matrix adhesion	0,0060	3,88
GO:0040008~regulation of growth	0,0062	3,07
GO:0008356~asymmetric cell division	0,0062	3,07
GO:0009620~response to fungus	0,0063	3,38
GO:0016203~muscle attachment	0,0064	2,64
GO:0007443~Malpighian tubule morphogenesis	0,0064	2,64
GO:0007525~somatic muscle development	0,0064	2,64
GO:0061327~anterior Malpighian tubule development	0,0072	4,43
GO:0007303~cytoplasmic transport, nurse cell to oocyte	0,0072	4,43
GO:0061343~cell adhesion involved in heart morphogenesis	0,0072	4,43
GO:0009408~response to heat	0,0077	2,09
GO:0010043~response to zinc ion	0,0077	5,54
GO:0007516~hemocyte development	0,0077	5,54
GO:0007173~epidermal growth factor receptor signaling pathway	0,0079	2,96
GO:0007254~JNK cascade	0,0079	2,96
GO:0007370~ventral furrow formation	0,0083	3,65
GO:0035147~branch fusion, open tracheal system	0,0084	3,22
GO:0035220~wing disc development	0,0084	1,91
GO:0030097~hemopoiesis	0,0109	3,08
GO:0045467~R7 cell development	0,0109	3,08
GO:0006952~defense response	0,0110	2,61
GO:0007166~cell surface receptor signaling pathway	0,0121	2,05
GO:0006986~response to unfolded protein	0,0127	4,93
GO:0043277~apoptotic cell clearance	0,0127	4,93
GO:0016332~establishment or maintenance of polarity of embryonic epithelium	0,0127	4,93
GO:0006099~tricarboxylic acid cycle	0,0136	2,38
GO:0045892~negative regulation of transcription, DNA-templated	0,0142	1,70
GO:0000381~regulation of alternative mRNA splicing, via spliceosome	0,0148	1,94
GO:0035019~somatic stem cell population maintenance	0,0150	3,27
GO:0035002~liquid clearance, open tracheal system	0,0151	3,80
GO:0042744~hydrogen peroxide catabolic process	0,0151	3,80
GO:0055114~oxidation-reduction process	0,0151	1,33
GO:0046843~dorsal appendage formation	0,0153	2,13
GO:0042067~establishment of ommatidial planar polarity	0,0154	2,66
GO:0007281~germ cell development	0,0161	2,32
GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	0,0179	1,81
GO:0045175~basal protein localization	0,0193	4,43
GO:0007229~integrin-mediated signaling pathway	0,0193	4,43
GO:0045571~negative regulation of imaginal disc growth	0,0193	4,43
GO:0042026~protein refolding	0,0193	4,43
GO:0046580~negative regulation of Ras protein signal transduction	0,0195	3,10
GO:0008105~asymmetric protein localization	0,0195	3,10
GO:0050830~defense response to Gram-positive bacterium	0,0202	2,06
GO:0035006~melanization defense response	0,0206	3,55
GO:0043065~positive regulation of apoptotic process	0,0217	2,73
GO:0030866~cortical actin cytoskeleton organization	0,0217	2,73
GO:0035096~larval midgut cell programmed cell death	0,0217	2,73
GO:0072499~photoreceptor cell axon guidance	0,0217	2,73
GO:0015992~proton transport	0,0217	2,73
GO:0034059~response to anoxia	0,0220	5,91
GO:0055065~metal ion homeostasis	0,0220	5,91
GO:0061088~regulation of sequestering of zinc ion	0,0220	5,91
GO:0030838~positive regulation of actin filament polymerization	0,0220	5,91
GO:0032869~cellular response to insulin stimulus	0,0220	5,91
GO:0042595~behavioral response to starvation	0,0220	5,91
GO:0035262~gonad morphogenesis	0,0220	5,91
GO:0046688~response to copper ion	0,0220	5,91
GO:0007043~cell-cell junction assembly	0,0220	5,91
GO:0055059~asymmetric neuroblast division	0,0226	2,49
GO:0048813~dendrite morphogenesis	0,0237	1,49
GO:0048542~lymph gland development	0,0247	2,96
GO:0035071~salivary gland cell autophagic cell death	0,0261	1,82
GO:0006096~glycolytic process	0,0266	2,63
GO:0019730~antimicrobial humoral response	0,0266	2,63
GO:0071456~cellular response to hypoxia	0,0266	2,63

GO:0007406~negative regulation of neuroblast proliferation	0,0266	2,63
GO:0006979~response to oxidative stress	0,0268	1,73
GO:0001738~morphogenesis of a polarized epithelium	0,0272	3,33
GO:0035172~hemocyte proliferation	0,0276	4,03
GO:0008299~isoprenoid biosynthetic process	0,0276	4,03
GO:0046621~negative regulation of organ growth	0,0276	4,03
GO:0046847~filopodium assembly	0,0276	4,03
GO:0006914~autophagy	0,0318	2,01
GO:0035212~cell competition in a multicellular organism	0,0351	3,13
GO:0035090~maintenance of apical/basal cell polarity	0,0352	8,87
GO:0042327~positive regulation of phosphorylation	0,0352	8,87
GO:0006613~cotranslational protein targeting to membrane	0,0352	8,87
GO:1902626~assembly of large subunit precursor of preribosome	0,0352	8,87
GO:0009786~regulation of asymmetric cell division	0,0352	8,87
GO:0040005~chitin-based cuticle attachment to epithelium	0,0352	8,87
GO:0007393~dorsal closure, leading edge cell fate determination	0,0352	8,87
GO:0030155~regulation of cell adhesion	0,0352	8,87
GO:0050766~positive regulation of phagocytosis	0,0352	8,87
GO:0071907~determination of digestive tract left/right asymmetry	0,0352	5,07
GO:0072593~reactive oxygen species metabolic process	0,0352	5,07
GO:0006098~pentose-phosphate shunt	0,0352	5,07
GO:0046662~regulation of oviposition	0,0352	5,07
GO:0032507~maintenance of protein location in cell	0,0352	5,07
GO:0006936~muscle contraction	0,0352	5,07
GO:0006351~transcription, DNA-templated	0,0357	1,30
GO:0008063~Toll signaling pathway	0,0374	2,28
GO:0016337~single organismal cell-cell adhesion	0,0379	2,70
GO:0046701~insecticide catabolic process	0,0379	2,70
GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	0,0383	2,45
GO:0031987~locomotion involved in locomotory behavior	0,0383	2,45
GO:0045893~positive regulation of transcription, DNA-templated	0,0435	1,56
GO:0035214~eye-antennal disc development	0,0442	2,96
GO:0046529~imaginal disc fusion, thorax closure	0,0442	2,96
GO:0008104~protein localization	0,0455	1,90
GO:0042594~response to starvation	0,0466	1,83
GO:0008285~negative regulation of cell proliferation	0,0471	2,06
GO:0007016~cytoskeletal anchoring at plasma membrane	0,0499	3,41
GO:0045196~establishment or maintenance of neuroblast polarity	0,0499	3,41
GO:0007436~larval salivary gland morphogenesis	0,0499	3,41
GO:0008585~female gonad development	0,0499	3,41
GO:0048082~regulation of adult chitin-containing cuticle pigmentation	0,0499	3,41
GO:0035152~regulation of tube architecture, open tracheal system	0,0499	3,41
GO:0007622~rhythmic behavior	0,0499	3,41

## 6.9 GO terms for biological processes of airways from 5 d CS exposed flies for downregulated DEGs

Term	P-value	Fold enrichment
GO:0007186~G-protein coupled receptor signaling pathway	1,20E-11	3,30
GO:0007605~sensory perception of sound	9,57E-08	3,96
GO:0055085~transmembrane transport	3,07E-07	2,10
GO:0007271~synaptic transmission, cholinergic	8,31E-07	7,68
GO:0003341~cilium movement	2,83E-06	5,53
GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	1,58E-05	4,76
GO:0007218~neuropeptide signaling pathway	2,21E-05	3,37
GO:0007528~neuromuscular junction development	7,66E-05	3,58
GO:0006812~cation transport	1,18E-04	3,95
GO:0007018~microtubule-based movement	2,55E-04	2,60
GO:0006813~potassium ion transport	2,99E-04	4,26
GO:0050808~synapse organization	3,36E-04	2,98
GO:0055114~oxidation-reduction process	4,58E-04	1,59
GO:0050965~detection of temperature stimulus involved in sensory perception of pain	0,001	3,25
GO:0070588~calcium ion transmembrane transport	0,002	5,04
GO:0019731~antibacterial humoral response	0,003	4,00
GO:0050830~defense response to Gram-positive bacterium	0,003	2,67
GO:0006811~ion transport	0,003	2,95
GO:0016079~synaptic vesicle exocytosis	0,003	3,84
GO:0007602~phototransduction	0,004	2,66
GO:1900074~negative regulation of neuromuscular synaptic transmission	0,005	6,40
GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	0,007	3,05
GO:0009755~hormone-mediated signaling pathway	0,008	5,76
GO:0045087~innate immune response	0,008	1,99
GO:0030431~sleep	0,009	1,89
GO:0008063~Toll signaling pathway	0,009	2,96
GO:0005975~carbohydrate metabolic process	0,009	1,96
GO:0017158~regulation of calcium ion-dependent exocytosis	0,011	7,68
GO:0010996~response to auditory stimulus	0,011	7,68
GO:0006959~humoral immune response	0,014	3,36
GO:0010579~positive regulation of adenylate cyclase activity involved in G-protein coupled receptor signaling pathway	0,017	6,58
GO:0007189~adenylate cyclase-activating G-protein coupled receptor signaling pathway	0,020	3,64
GO:0007269~neurotransmitter secretion	0,021	1,94
GO:0007601~visual perception	0,021	2,26
GO:0003333~amino acid transmembrane transport	0,021	2,79
GO:0006259~DNA metabolic process	0,021	11,51
GO:0007165~signal transduction	0,021	1,63
GO:0060271~cilium morphogenesis	0,023	2,53

GO:0006816~calcium ion transport	0,024	2,71
GO:0006730~one-carbon metabolic process	0,025	3,45
GO:0018298~protein-chromophore linkage	0,026	5,76
GO:0007210~serotonin receptor signaling pathway	0,026	5,76
GO:0048791~calcium ion-regulated exocytosis of neurotransmitter	0,026	5,76
GO:0035556~intracellular signal transduction	0,027	1,82
GO:0006508~proteolysis	0,033	1,31
GO:0050954~sensory perception of mechanical stimulus	0,040	8,64
GO:0046701~insecticide catabolic process	0,044	3,00
GO:0050975~sensory perception of touch	0,049	4,61
GO:0050774~negative regulation of dendrite morphogenesis	0,049	4,61

## 6.10 GO terms for biological processes of airways from 15 d CS exposed flies for upregulated DEGs

Term	P-value	Fold enrichment
GO:0009617~response to bacterium	1,03E-12	19,92
GO:0045087~innate immune response	1,81E-10	10,17
GO:0006749~glutathione metabolic process	7,66E-10	16,50
GO:0019731~antibacterial humoral response	1,96E-08	24,52
GO:0006952~defense response	3,77E-07	16,59
GO:0006959~humoral immune response	1,79E-05	17,62
GO:0050830~defense response to Gram-positive bacterium	1,29E-04	8,81
GO:0009408~response to heat	3,79E-04	7,26
GO:0034605~cellular response to heat	0,001	18,80
GO:0006979~response to oxidative stress	0,002	5,36
GO:0055114~oxidation-reduction process	0,002	2,57
GO:0007166~cell surface receptor signaling pathway	0,002	6,51
GO:0008063~Toll signaling pathway	0,013	8,06
GO:0042742~defense response to bacterium	0,015	5,26
GO:0030431~sleep	0,029	3,47
GO:0008340~determination of adult lifespan	0,033	2,90
GO:0006564~L-serine biosynthetic process	0,042	46,99
GO:0008344~adult locomotory behavior	0,048	4,86

## 6.11 GO terms for biological processes of airways from 15 d CS exposed flies for downregulated DEGs

Term	P-value	Fold enrichment
GO:0006030~chitin metabolic process	2,46E-05	11,78
GO:0002181~cytoplasmic translation	2,60E-05	11,66
GO:0045214~sarcomere organization	0,013	16,66

## 6.12 GO terms for biological processes of airways from old flies for upregulated DEGs

Term	P-value	Fold enrichment
GO:0050830~defense response to Gram-positive bacterium	6,5E-07	21,82
GO:0009617~response to bacterium	5,5E-06	22,77
GO:0019731~antibacterial humoral response	7,5E-06	37,94
GO:0045087~innate immune response	2,5E-05	11,75
GO:0006952~defense response	3,7E-05	25,67
GO:0050829~defense response to Gram-negative bacterium	3,5E-04	9,70
GO:0097017~renal protein absorption	0,011	174,54
GO:0055114~oxidation-reduction process	0,028	2,97
GO:0055065~metal ion homeostasis	0,033	58,18
GO:0097206~nephrocyte filtration	0,039	49,87
GO:0003012~muscle system process	0,039	49,87
GO:0019732~antifungal humoral response	0,044	43,63
GO:0010038~response to metal ion	0,044	43,63

## 6.13 GO terms for biological processes of airways from old flies for downregulated DEGs

Term	P-value	Fold enrichment
GO:0030497~fatty acid elongation	5,5E-10	40,39
GO:0042381~hemolymph coagulation	0,005	27,77
GO:0035336~long-chain fatty-acyl-CoA metabolic process	0,009	20,83
GO:0010025~wax biosynthetic process	0,009	20,83
GO:0006633~fatty acid biosynthetic process	0,011	18,51
GO:0007548~sex differentiation	0,015	15,87
GO:0008039~synaptic target recognition	0,035	10,10
GO:0007186~G-protein coupled receptor signaling pathway	0,039	3,88
GO:0007606~sensory perception of chemical stimulus	0,049	4,83

## 6.14 GO terms for biological processes of airways from CS recovered flies for upregulated DEGs

Term	P-value	Fold enrichment
GO:0002181~cytoplasmic translation	1,7E-23	5,34
GO:0007411~axon guidance	1,0E-10	2,82
GO:0007268~chemical synaptic transmission	5,4E-09	4,04
GO:0050808~synapse organization	1,1E-08	4,22
GO:0051124~synaptic growth at neuromuscular junction	1,3E-07	4,73
GO:0007616~long-term memory	1,7E-07	3,55
GO:0006120~mitochondrial electron transport, NADH to ubiquinone	2,5E-07	4,81
GO:0010906~regulation of glucose metabolic process	2,9E-07	2,45
GO:0006468~protein phosphorylation	8,3E-07	2,09
GO:0007271~synaptic transmission, cholinergic	1,1E-06	7,41
GO:0007528~neuromuscular junction development	4,7E-06	3,95
GO:0035556~intracellular signal transduction	7,2E-06	2,75
GO:0045475~locomotor rhythm	8,3E-06	3,30
GO:0006813~potassium ion transport	9,9E-06	4,94
GO:0008045~motor neuron axon guidance	1,3E-05	3,20
GO:0007269~neurotransmitter secretion	3,0E-05	2,75
GO:0006812~cation transport	3,1E-05	4,13
GO:0008582~regulation of synaptic growth at neuromuscular junction	7,7E-05	3,80
GO:0048477~oogenesis	9,3E-05	1,76
GO:0045433~male courtship behavior, veined wing generated song production	9,4E-05	4,83
GO:0050965~detection of temperature stimulus involved in sensory perception of pain	1,0E-04	3,71
GO:0008355~olfactory learning	1,5E-04	2,91
GO:0008306~associative learning	1,6E-04	5,93
GO:0007615~anesthesia-resistant memory	1,6E-04	7,08
GO:0007274~neuromuscular synaptic transmission	1,8E-04	2,86
GO:0007476~imaginal disc-derived wing morphogenesis	2,2E-04	1,90
GO:0070588~calcium ion transmembrane transport	2,6E-04	5,56
GO:0008088~axo-dendritic transport	2,6E-04	5,56
GO:0007210~serotonin receptor signaling pathway	2,6E-04	8,34
GO:0072499~photoreceptor cell axon guidance	2,8E-04	4,28
GO:0007613~memory	3,9E-04	4,12
GO:0007612~learning	4,0E-04	5,23
GO:0090328~regulation of olfactory learning	5,4E-04	7,41
GO:0007165~signal transduction	5,5E-04	1,96
GO:0007611~learning or memory	5,7E-04	3,14
GO:0048488~synaptic vesicle endocytosis	5,8E-04	3,60
GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	5,8E-04	3,60
GO:0086010~membrane depolarization during action potential	8,4E-04	9,27
GO:0048134~germ-line cyst formation	9,9E-04	6,67
GO:0016319~mushroom body development	0,001	2,38
GO:0000028~ribosomal small subunit assembly	0,001	4,45
GO:0055085~transmembrane transport	0,001	1,65
GO:0007614~short-term memory	0,001	3,85
GO:0007619~courtship behavior	0,001	3,85
GO:0016199~axon midline choice point recognition	0,001	3,85
GO:0042059~negative regulation of epidermal growth factor receptor signaling pathway	0,002	3,14
GO:0017148~negative regulation of translation	0,002	3,14
GO:0007416~synapse assembly	0,002	2,73
GO:0007314~oocyte anterior/posterior axis specification	0,003	3,57
GO:0010378~temperature compensation of the circadian clock	0,003	11,12
GO:0030431~sleep	0,003	2,00
GO:0008049~male courtship behavior	0,003	2,08
GO:0019233~sensory perception of pain	0,003	1,39
GO:0006357~regulation of transcription from RNA polymerase II promoter	0,003	1,80
GO:0007281~germ cell development	0,003	2,91
GO:0051260~protein homooligomerization	0,004	4,32
GO:0046716~muscle cell cellular homeostasis	0,004	3,34
GO:0045938~positive regulation of circadian sleep/wake cycle, sleep	0,004	5,13
GO:0070983~dendrite guidance	0,004	3,71
GO:0006836~neurotransmitter transport	0,004	3,71
GO:0016079~synaptic vesicle exocytosis	0,004	3,71
GO:0006351~transcription, DNA-templated	0,005	1,48
GO:0040040~thermosensory behavior	0,005	4,10

GO:2000331~regulation of terminal button organization	0,005	3,56
GO:0018105~peptidyl-serine phosphorylation	0,006	2,93
GO:0072347~response to anesthetic	0,006	6,18
GO:0048790~maintenance of presynaptic active zone structure	0,006	6,18
GO:0035075~response to ecdysone	0,006	4,76
GO:0019722~calcium-mediated signaling	0,006	4,76
GO:0040011~locomotion	0,006	3,13
GO:0007517~muscle organ development	0,007	2,14
GO:0008586~imaginal disc-derived wing vein morphogenesis	0,007	2,52
GO:0048813~dendrite morphogenesis	0,007	1,69
GO:0030707~ovarian follicle cell development	0,007	2,05
GO:0008039~synaptic target recognition	0,008	3,03
GO:0019730~antimicrobial humoral response	0,008	3,29
GO:0007406~negative regulation of neuroblast proliferation	0,008	3,29
GO:0007186~G-protein coupled receptor signaling pathway	0,009	1,79
GO:0007548~sex differentiation	0,009	3,71
GO:0042332~gravitaxis	0,009	3,71
GO:0006816~calcium ion transport	0,009	2,94
GO:0030154~cell differentiation	0,009	2,55
GO:0045893~positive regulation of transcription, DNA-templated	0,010	1,87
GO:0008345~larval locomotory behavior	0,010	3,18
GO:0007632~visual behavior	0,011	4,17
GO:0000381~regulation of alternative mRNA splicing, via spliceosome	0,012	2,13
GO:0042391~regulation of membrane potential	0,012	3,07
GO:0048675~axon extension	0,012	3,07
GO:0007294~germarium-derived oocyte fate determination	0,012	3,07
GO:0006811~ion transport	0,013	2,59
GO:0040034~regulation of development, heterochronic	0,013	5,05
GO:0045466~R7 cell differentiation	0,013	5,05
GO:0046959~habituation	0,013	5,05
GO:0045498~sex comb development	0,013	5,05
GO:0035073~pupariation	0,014	3,92
GO:0035011~melanotic encapsulation of foreign target	0,015	2,96
GO:0051298~centrosome duplication	0,016	1,85
GO:0045886~negative regulation of synaptic growth at neuromuscular junction	0,017	2,47
GO:0030727~germarium-derived female germ-line cyst formation	0,018	4,63
GO:0035332~positive regulation of hippo signaling	0,018	4,63
GO:0006936~muscle contraction	0,019	6,35
GO:0048789~cytoskeletal matrix organization at active zone	0,019	6,35
GO:0006898~receptor-mediated endocytosis	0,019	6,35
GO:0048172~regulation of short-term neuronal synaptic plasticity	0,019	6,35
GO:0048814~regulation of dendrite morphogenesis	0,023	3,51
GO:0007189~adenylate cyclase-activating G-protein coupled receptor signaling pathway	0,023	3,51
GO:0035023~regulation of Rho protein signal transduction	0,024	4,28
GO:0035094~response to nicotine	0,024	4,28
GO:0046928~regulation of neurotransmitter secretion	0,024	4,28
GO:0046777~protein autophosphorylation	0,025	2,99
GO:0016310~phosphorylation	0,025	2,99
GO:0048791~calcium ion-regulated exocytosis of neurotransmitter	0,029	5,56
GO:0008016~regulation of heart contraction	0,029	5,56
GO:0022416~chaeta development	0,029	2,05
GO:0048149~behavioral response to ethanol	0,029	2,15
GO:0090630~activation of GTPase activity	0,030	2,88
GO:0007417~central nervous system development	0,030	1,90
GO:0007432~salivary gland boundary specification	0,031	3,97
GO:0030833~regulation of actin filament polymerization	0,031	3,97
GO:0048489~synaptic vesicle transport	0,031	3,97
GO:0030322~stabilization of membrane potential	0,031	3,97
GO:0017085~response to insecticide	0,031	3,97
GO:0042052~rhabdomere development	0,034	2,54
GO:0008587~imaginal disc-derived wing margin morphogenesis	0,034	2,54
GO:0008285~negative regulation of cell proliferation	0,035	2,33
GO:0007422~peripheral nervous system development	0,036	1,85
GO:0007552~metamorphosis	0,038	2,47
GO:0010468~regulation of gene expression	0,039	1,96
GO:0016192~vesicle-mediated transport	0,040	1,67
GO:0006874~cellular calcium ion homeostasis	0,040	3,71
GO:0045732~positive regulation of protein catabolic process	0,040	3,71
GO:0007480~imaginal disc-derived leg morphogenesis	0,040	2,04
GO:0001963~synaptic transmission, dopaminergic	0,040	4,94
GO:0043044~ATP-dependent chromatin remodeling	0,040	4,94
GO:1900074~negative regulation of neuromuscular synaptic transmission	0,040	4,94
GO:0051259~protein oligomerization	0,040	4,94
GO:0090163~establishment of epithelial cell planar polarity	0,043	8,34
GO:0048013~ephrin receptor signaling pathway	0,043	8,34
GO:0034063~stress granule assembly	0,043	8,34
GO:0048499~synaptic vesicle membrane organization	0,043	8,34
GO:0048311~mitochondrion distribution	0,043	8,34
GO:0006914~autophagy	0,045	2,10
GO:0007474~imaginal disc-derived wing vein specification	0,045	2,10
GO:0007399~nervous system development	0,045	1,67
GO:0045887~positive regulation of synaptic growth at neuromuscular junction	0,048	2,59
GO:0050803~regulation of synapse structure or activity	0,049	3,47
GO:0016571~histone methylation	0,049	3,47
GO:0045467~R7 cell development	0,050	2,90



## 6.15 GO terms for biological processes of airways from CS recovered flies for downregulated DEGs

Term	P-value	Fold enrichment
GO:0009620~response to fungus	3,03E-07	6,59
GO:0015031~protein transport	1,07E-05	3,03
GO:0007391~dorsal closure	1,80E-05	2,69
GO:0007298~border follicle cell migration	4,70E-05	2,38
GO:0006952~defense response	8,58E-05	4,07
GO:0009617~response to bacterium	9,63E-05	3,51
GO:0000902~cell morphogenesis	1,17E-04	3,27
GO:0007155~cell adhesion	1,27E-04	2,58
GO:0009408~response to heat	1,74E-04	2,88
GO:0045087~innate immune response	1,91E-04	2,44
GO:0048102~autophagic cell death	1,98E-04	2,98
GO:0032509~endosome transport via multivesicular body sorting pathway	2,03E-04	5,77
GO:0006909~phagocytosis	2,37E-04	1,93
GO:0035220~wing disc development	4,54E-04	2,49
GO:0008360~regulation of cell shape	5,97E-04	2,31
GO:0016322~neuron remodeling	6,16E-04	3,12
GO:0006457~protein folding	8,67E-04	2,24
GO:0034605~cellular response to heat	0,001	5,38
GO:0033627~cell adhesion mediated by integrin	0,001	4,40
GO:0034976~response to endoplasmic reticulum stress	0,002	3,30
GO:0006897~endocytosis	0,002	2,56
GO:0035071~salivary gland cell autophagic cell death	0,003	2,37
GO:0019732~antifungal humoral response	0,003	7,21
GO:0007030~Golgi organization	0,004	2,25
GO:0060857~establishment of glial blood-brain barrier	0,004	4,25
GO:0030036~actin cytoskeleton organization	0,004	2,82
GO:0001736~establishment of planar polarity	0,005	3,25
GO:0040008~regulation of growth	0,005	3,55
GO:0016050~vesicle organization	0,006	9,23
GO:0006955~immune response	0,006	2,56
GO:0042048~olfactory behavior	0,006	2,42
GO:0007424~open tracheal system development	0,006	2,04
GO:0006310~DNA recombination	0,007	3,42
GO:0035151~regulation of tube size, open tracheal system	0,007	3,85
GO:0006357~regulation of transcription from RNA polymerase II promoter	0,007	1,73
GO:0006614~SRP-dependent cotranslational protein targeting to membrane	0,008	5,77
GO:0030589~pseudocleavage involved in syncytial blastoderm formation	0,008	5,77
GO:0000281~mitotic cytokinesis	0,009	2,31
GO:0008362~chitin-based embryonic cuticle biosynthetic process	0,009	3,67
GO:0005975~carbohydrate metabolic process	0,009	1,96
GO:0031987~locomotion involved in locomotory behavior	0,010	3,18
GO:0018344~protein geranylgeranylation	0,011	7,69
GO:0010389~regulation of G2/M transition of mitotic cell cycle	0,011	7,69
GO:0000301~retrograde transport, vesicle recycling within Golgi	0,011	7,69
GO:0051489~regulation of filopodium assembly	0,011	5,24
GO:0006487~protein N-linked glycosylation	0,012	4,07
GO:0007015~actin filament organization	0,013	2,06
GO:0042060~wound healing	0,013	2,31
GO:0061343~cell adhesion involved in heart morphogenesis	0,016	4,81
GO:0046529~imaginal disc fusion, thorax closure	0,016	3,85
GO:0035080~heat shock-mediated polytene chromosome puffing	0,017	6,59
GO:0035001~dorsal trunk growth, open tracheal system	0,017	6,59
GO:0030431~sleep	0,017	1,80
GO:0019991~septate junction assembly	0,018	2,88
GO:0010906~regulation of glucose metabolic process	0,018	1,63
GO:0006629~lipid metabolic process	0,019	2,02
GO:0006886~intracellular protein transport	0,020	1,85
GO:0035099~hemocyte migration	0,020	3,64
GO:0007498~mesoderm development	0,020	2,16
GO:0035167~larval lymph gland hemopoiesis	0,021	2,80
GO:0008340~determination of adult lifespan	0,021	1,63
GO:0007436~larval salivary gland morphogenesis	0,021	4,44
GO:0006613~cotranslational protein targeting to membrane	0,021	11,54
GO:0009589~detection of UV	0,021	11,54
GO:0033227~dsRNA transport	0,021	3,11
GO:0030866~cortical actin cytoskeleton organization	0,021	3,11
GO:0051726~regulation of cell cycle	0,022	1,92
GO:0032482~Rab protein signal transduction	0,024	2,71
GO:0007254~JNK cascade	0,025	2,99
GO:0010592~positive regulation of lamellipodium assembly	0,026	5,77
GO:0045752~positive regulation of Toll signaling pathway	0,026	5,77
GO:0030707~ovarian follicle cell development	0,026	1,88
GO:0006915~apoptotic process	0,027	2,00
GO:0008063~Toll signaling pathway	0,028	2,64
GO:0042052~rhabdomere development	0,028	2,64
GO:0008285~negative regulation of cell proliferation	0,029	2,41
GO:0009950~dorsal/ventral axis specification	0,030	2,88
GO:0035159~regulation of tube length, open tracheal system	0,030	2,88
GO:0055114~oxidation-reduction process	0,030	1,34
GO:0000422~mitophagy	0,030	3,30
GO:0007010~cytoskeleton organization	0,032	2,56
GO:0070374~positive regulation of ERK1 and ERK2 cascade	0,032	2,56
GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	0,035	2,79
GO:0006635~fatty acid beta-oxidation	0,035	2,79
GO:0016197~endosomal transport	0,035	2,79

GO:0007413~axonal fasciculation	0,035	3,85
GO:0046329~negative regulation of JNK cascade	0,037	3,15
GO:0034097~response to cytokine	0,040	8,65
GO:0006621~protein retention in ER lumen	0,040	8,65
GO:0035307~positive regulation of protein dephosphorylation	0,040	8,65
GO:0045887~positive regulation of synaptic growth at neuromuscular junction	0,041	2,69
GO:0035011~melanotic encapsulation of foreign target	0,041	2,69
GO:0010506~regulation of autophagy	0,042	2,43
GO:0046701~insecticide catabolic process	0,044	3,01
GO:0019731~antibacterial humoral response	0,044	3,01
GO:0007464~R3/R4 cell fate commitment	0,044	3,61
GO:0051491~positive regulation of filopodium assembly	0,044	3,61
GO:0007160~cell-matrix adhesion	0,044	3,61
GO:0007112~male meiosis cytokinesis	0,047	2,61
GO:0007494~midgut development	0,047	2,61
GO:0008354~germ cell migration	0,048	2,37
GO:0007229~integrin-mediated signaling pathway	0,049	4,62
GO:0071711~basement membrane organization	0,049	4,62
GO:0046856~phosphatidylinositol dephosphorylation	0,049	4,62
GO:0050830~defense response to Gram-positive bacterium	0,050	2,06

## 6.16 GO terms for biological processes of airways from the comparison of adult and larval airways

Term	P-value	Fold enrichment
GO:0007186~G-protein coupled receptor signaling pathway	2,0E-24	2,88
GO:0007218~neuropeptide signaling pathway	4,6E-20	3,75
GO:0050808~synapse organization	5,9E-15	3,34
GO:0007601~visual perception	4,9E-13	3,21
GO:0055085~transmembrane transport	1,9E-12	1,86
GO:0007268~chemical synaptic transmission	2,0E-11	2,87
GO:0007602~phototransduction	4,6E-11	3,09
GO:0007606~sensory perception of chemical stimulus	1,0E-08	2,31
GO:0007608~sensory perception of smell	2,1E-08	2,46
GO:0050965~detection of temperature stimulus involved in sensory perception of pain	2,9E-07	2,91
GO:0006813~potassium ion transport	4,3E-07	3,33
GO:0043052~thermotaxis	4,4E-07	3,94
GO:0035556~intracellular signal transduction	8,9E-07	2,06
GO:0045475~locomotor rhythm	1,1E-06	2,36
GO:0030431~sleep	1,3E-06	1,94
GO:0007271~synaptic transmission, cholinergic	1,9E-06	4,10
GO:0016059~deactivation of rhodopsin mediated signaling	1,9E-06	4,10
GO:0006508~proteolysis	2,8E-06	1,42
GO:0007623~circadian rhythm	5,7E-06	2,29
GO:0055114~oxidation-reduction process	8,4E-06	1,43
GO:0007619~courtship behavior	9,1E-06	3,09
GO:0007189~adenylate cyclase-activating G-protein coupled receptor signaling pathway	1,2E-05	3,48
GO:0016079~synaptic vesicle exocytosis	1,3E-05	3,15
GO:0008344~adult locomotory behavior	1,3E-05	2,28
GO:0009416~response to light stimulus	2,8E-05	3,31
GO:0009617~response to bacterium	5,0E-05	2,36
GO:0006811~ion transport	5,0E-05	2,42
GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	6,0E-05	2,77
GO:0006812~cation transport	7,2E-05	2,57
GO:0006836~neurotransmitter transport	7,7E-05	2,95
GO:0007603~phototransduction, visible light	1,2E-04	4,25
GO:0018298~protein-chromophore linkage	1,2E-04	4,73
GO:0007210~serotonin receptor signaling pathway	1,2E-04	4,73
GO:0007166~cell surface receptor signaling pathway	1,5E-04	2,04
GO:0050911~detection of chemical stimulus involved in sensory perception of smell	1,7E-04	1,97
GO:0046323~glucose import	1,8E-04	3,07
GO:0035428~hexose transmembrane transport	1,8E-04	3,07
GO:0006171~cAMP biosynthetic process	1,8E-04	3,47
GO:0019731~antibacterial humoral response	2,2E-04	2,88
GO:0007193~adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	2,6E-04	3,15
GO:0042391~regulation of membrane potential	2,7E-04	2,61
GO:0019933~cAMP-mediated signaling	3,3E-04	2,93
GO:0007605~sensory perception of sound	3,4E-04	2,01
GO:0003333~amino acid transmembrane transport	4,3E-04	2,44
GO:0043153~entrainment of circadian clock by photoperiod	4,5E-04	4,20
GO:1900074~negative regulation of neuromuscular synaptic transmission	4,5E-04	4,20
GO:0010579~positive regulation of adenylate cyclase activity involved in G-protein coupled receptor signaling pathway	5,1E-04	4,73
GO:0002121~inter-male aggressive behavior	5,1E-04	2,00
GO:0019722~calcium-mediated signaling	5,9E-04	3,38
GO:0006952~defense response	6,6E-04	2,36

GO:0045467~R7 cell development	1,0E-03	2,67
GO:0010906~regulation of glucose metabolic process	1,2E-03	1,50
GO:0008306~associative learning	1,2E-03	3,15
GO:0008039~synaptic target recognition	1,5E-03	2,29
GO:0016056~rhodopsin mediated signaling pathway	1,7E-03	4,14
GO:0048791~calcium ion-regulated exocytosis of neurotransmitter	1,7E-03	4,14
GO:0008049~male courtship behavior	1,8E-03	1,63
GO:0045938~positive regulation of circadian sleep/wake cycle, sleep	1,8E-03	3,27
GO:0035094~response to nicotine	1,8E-03	3,27
GO:0006182~cGMP biosynthetic process	1,8E-03	3,27
GO:0045087~innate immune response	2,0E-03	1,64
GO:0086010~membrane depolarization during action potential	2,1E-03	4,73
GO:0009813~flavonoid biosynthetic process	2,2E-03	2,22
GO:0052696~flavonoid glucuronidation	2,2E-03	2,22
GO:0070588~calcium ion transmembrane transport	2,2E-03	2,95
GO:0008345~larval locomotory behavior	2,4E-03	2,36
GO:0007615~anesthesia-resistant memory	2,8E-03	3,44
GO:0071482~cellular response to light stimulus	2,8E-03	3,44
GO:1900073~regulation of neuromuscular synaptic transmission	2,8E-03	3,44
GO:0007420~brain development	2,8E-03	2,11
GO:0006629~lipid metabolic process	2,9E-03	1,71
GO:0007528~neuromuscular junction development	3,1E-03	2,00
GO:0045187~regulation of circadian sleep/wake cycle, sleep	3,8E-03	2,78
GO:0042593~glucose homeostasis	4,1E-03	3,68
GO:0007416~synapse assembly	4,2E-03	1,87
GO:0048149~behavioral response to ethanol	4,7E-03	1,82
GO:0009190~cyclic nucleotide biosynthetic process	5,4E-03	3,15
GO:0009649~entrainment of circadian clock	5,4E-03	3,15
GO:0006959~humoral immune response	5,9E-03	2,36
GO:0048512~circadian behavior	6,0E-03	4,05
GO:0071329~cellular response to sucrose stimulus	6,0E-03	4,05
GO:0030728~ovulation	6,0E-03	4,05
GO:0005977~glycogen metabolic process	6,0E-03	4,05
GO:0048789~cytoskeletal matrix organization at active zone	6,0E-03	4,05
GO:0016057~regulation of membrane potential in photoreceptor cell	6,0E-03	4,05
GO:0007628~adult walking behavior	6,2E-03	2,63
GO:0006814~sodium ion transport	6,7E-03	1,81
GO:0007274~neuromuscular synaptic transmission	6,9E-03	1,72
GO:0007604~phototransduction, UV	8,3E-03	4,73
GO:0042749~regulation of circadian sleep/wake cycle	8,3E-03	4,73
GO:0046154~rhodopsin metabolic process	8,3E-03	4,73
GO:0007200~phospholipase C-activating G-protein coupled receptor signaling pathway	8,3E-03	4,73
GO:0050774~negative regulation of dendrite morphogenesis	8,5E-03	3,31
GO:0009755~hormone-mediated signaling pathway	8,5E-03	3,31
GO:0070050~neuron cellular homeostasis	8,5E-03	2,27
GO:0030497~fatty acid elongation	9,2E-03	2,36
GO:0008343~adult feeding behavior	9,6E-03	2,91
GO:0046928~regulation of neurotransmitter secretion	9,6E-03	2,91
GO:0019236~response to pheromone	9,9E-03	2,66
GO:0050804~modulation of synaptic transmission	1,0E-02	1,94
GO:0008152~metabolic process	1,1E-02	1,42
GO:0006821~chloride transport	1,4E-02	2,36
GO:0007269~neurotransmitter secretion	1,5E-02	1,54
GO:0007612~learning	1,5E-02	2,50
GO:0007465~R7 cell fate commitment	1,6E-02	2,70
GO:0071805~potassium ion transmembrane transport	1,6E-02	2,70
GO:0009744~response to sucrose	1,6E-02	2,70
GO:0032504~multicellular organism reproduction	1,8E-02	1,28
GO:0050830~defense response to Gram-positive bacterium	1,8E-02	1,69
GO:0007548~sex differentiation	2,0E-02	2,25
GO:0002028~regulation of sodium ion transport	2,1E-02	3,94
GO:0019432~triglyceride biosynthetic process	2,1E-02	3,94
GO:0035176~social behavior	2,1E-02	3,94
GO:0017158~regulation of calcium ion-dependent exocytosis	2,1E-02	3,94
GO:0009593~detection of chemical stimulus	2,3E-02	1,75
GO:0008355~olfactory learning	2,4E-02	1,60
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	2,4E-02	1,36
GO:0050908~detection of light stimulus involved in visual perception	2,5E-02	3,15
GO:0048047~mating behavior, sex discrimination	2,5E-02	3,15
GO:0007158~neuron cell-cell adhesion	2,5E-02	1,92
GO:0050907~detection of chemical stimulus involved in sensory perception	2,5E-02	2,76
GO:0042381~hemolymph coagulation	2,5E-02	2,76
GO:0007304~chorion-containing eggshell formation	2,6E-02	1,76
GO:0043171~peptide catabolic process	2,9E-02	1,96
GO:0051124~synaptic growth at neuromuscular junction	3,0E-02	1,77
GO:0007187~G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	3,2E-02	4,73
GO:0060086~circadian temperature homeostasis	3,2E-02	4,73
GO:0010841~positive regulation of circadian sleep/wake cycle, wakefulness	3,2E-02	4,73

GO:0007217~tachykinin receptor signaling pathway	3,2E-02	4,73
GO:0007411~axon guidance	3,2E-02	1,30
GO:0007362~terminal region determination	3,3E-02	2,00
GO:0060025~regulation of synaptic activity	3,5E-02	2,36
GO:0045433~male courtship behavior, veined wing generated song production	3,8E-02	2,06
GO:0007264~small GTPase mediated signal transduction	3,8E-02	1,53
GO:0035023~regulation of Rho protein signal transduction	3,9E-02	2,55
GO:0046835~carbohydrate phosphorylation	3,9E-02	2,55
GO:0050916~sensory perception of sweet taste	3,9E-02	2,55
GO:0007616~long-term memory	3,9E-02	1,51
GO:0006816~calcium ion transport	4,0E-02	1,81
GO:0006011~UDP-glucose metabolic process	4,1E-02	2,84
GO:0072375~medium-term memory	4,1E-02	2,84
GO:0048134~germ-line cyst formation	4,1E-02	2,84
GO:0019835~cytolysis	4,1E-02	2,84
GO:0050909~sensory perception of taste	4,4E-02	1,53
GO:0007611~learning or memory	4,7E-02	1,64
GO:0006906~vesicle fusion	5,0E-02	1,97

## 7 Curriculum Vitae

Name: Daniel Ruben Prange  
Date of birth: 14.12.1991  
Place of birth: Hamburg, Germany  
Nationality: German

### Education

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2016 – 2020 **PhD candidate** – Department of Molecular Physiology, Zoological Institute, Kiel University, Germany

Thesis:  
“A cigarette smoke induced *Drosophila* model identifies molecular mechanisms underlying COPD development”

2013 – 2016 **Master of Science, Biology** – Department of Molecular Physiology, Zoological Institute, Kiel University, Germany

Thesis:  
“Charakterisierung von Zielgenen und der Einfluss von Myokinen auf die Lebensspanne in einem *Drosophila melanogaster* COPD-Modell”

2010 – 2013 **Bachelor of Science, Biology** – University of Hamburg/PerkinElmer, Hamburg, Germany

Thesis:  
“Etablierung eines FRET-basierten Biosensors auf dem Operetta High Content Screening System“

2002 - 2010 **Abitur** – Emilie-Wüstenfeld Gymnasium, Hamburg, Germany

## 8 Publications

**Prange, R.**, Thiedmann, M., Bhandari, A., Mishra, N., Sinha, A., Häsler, R., Rosenstiel, P., Uliczka, K., Wagner, C., Yildirim, A. Ö., Fink, C. & Roeder, T. A *Drosophila* model of cigarette smoke induced COPD identifies Nrf2 signaling as an expedient target for intervention. *Aging (Albany, NY)*. **10**, 2122–2135 (2018).

Foitzik, A., **Prange, R.**, Boettcher, K., Schreiner, A. Opera Phenix High Content Screening System Technical Performance: Speed. PerkinElmer Technical Note (2016).

Mueller, HJ., **Prange, R.**, PCR-Polymerase Kettenreaktion. Springer Spektrum. 2016

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## 10 Declaration

Hereby I declare that I am the sole author of this dissertation titled “A cigarette smoke induced *Drosophila* model identifies molecular mechanisms underlying COPD development” and have not used sources other than those listed as references. This dissertation has not been submitted at any other institution in order to obtain an academic degree and was prepared according to the *Rules of Good Scientific Practice* of the German Research Foundation. Additionally, I confirm that I was not deprived an academic degree.

Hiermit erkläre ich, dass ich die vorliegende Dissertation mit dem Titel „A cigarette smoke induced *Drosophila* model identifies molecular mechanisms underlying COPD development“ selbstständig angefertigt habe und keine anderen als der von mir angegebenen Hilfsmittel verwendet habe. Diese Dissertation wurde an keiner anderen Institution zur Erlangung eines akademischen Grades eingereicht und wurde unter Berücksichtigung der *Regeln Guter Wissenschaftlicher Praxis* der Deutschen Forschungsgesellschaft angefertigt. Außerdem bestätige ich, dass mir kein akademischer Grad entzogen wurde.

Kiel, den

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Ruben Prange