

Supplementary Tables

Russell et al. *Wolbachia* endosymbionts manipulate GSC self-renewal and differentiation to enhance host fertility

source	type	target	citations
AGO1"	physical	bam	pubmed:33907499
AGO1"	physical	mei-P26	pubmed:22438571, pubmed:18528333, pubmed:29354790
bam"	physical	aub	pubmed:28441530
bgn"	physical	bam	pubmed:19556547, pubmed:25119050, pubmed:25412508, pubmed:19470484, pubmed:23526974, pubmed:20018853, pubmed:26291077, pubmed:28190776, pubmed:23122292
brat"	physical	bam	pubmed:33907499, pubmed:29354790
CG11700"	physical	bam	pubmed:28484036
CG6304"	physical	mei-P26	pubmed:22036573
CSN4"	physical	bam	pubmed:25119050
CycA"	physical	bam	pubmed:28484036
eIF4A"	physical	bam	pubmed:19556547
gw"	physical	mei-P26	pubmed:22438571
how"	physical	bam	pubmed:20362539
how"	physical	Sxl	pubmed:23788626
Mad"	physical	bam	pubmed:31097674
mei-P26"	physical	aub	pubmed:28441530
mei-P26"	physical	bam	pubmed:23122292
mei-P26"	physical	bam	pubmed:23526974, pubmed:29354790
mei-P26"	physical	bgn	pubmed:23122292
mei-P26"	physical	bgn	pubmed:23526974, pubmed:29354790
mei-P26"	physical	nos	pubmed:32654316, pubmed:23526974
mei-P26"	physical	nos	pubmed:22438571
mei-P26"	physical	orb	pubmed:22438571
mei-P26"	physical	pum	pubmed:24286029, pubmed:30590052
mei-P26"	physical	twin	pubmed:24286029

mir-137"	physical	mei-P26	pubmed:20400939
mir-7"	physical	bam	pubmed:19758565
mir-ban"	physical	mei-P26	pubmed:20400939
Myc"	physical	bam	pubmed:33907499
nos"	physical	bam	pubmed:32654316
nos"	physical	bam	pubmed:20018853
Not1"	physical	bam	pubmed:29255063
Not3"	physical	bam	pubmed:29255063
otu"	physical	bam	pubmed:28484036, pubmed:30879902
pum"	physical	bam	pubmed:20018853
Rbp9	physical	bam	pubmed:10082516
Rcd-1"	physical	bam	pubmed:29255063
Rga"	physical	bam	pubmed:29255063
Su(var)205"	physical	bam	pubmed:30867469
Sxl	physical	CG31908	pubmed:21663794
Sxl"	physical	aub	pubmed:28441530
Sxl"	physical	bam	pubmed:23526974
Sxl"	physical	bgcn	pubmed:23526974, pubmed:29354790
Sxl"	physical	brat	pubmed:29354790
Sxl"	physical	bru1	pubmed:17067567
Sxl"	physical	CG5050	pubmed:21663794
Sxl"	physical	ci	pubmed:14597576, pubmed:17284519
Sxl"	physical	cos	pubmed:14597576, pubmed:17284519
Sxl"	physical	eIF4E1	pubmed:21829374
Sxl"	physical	fl(2)d	pubmed:18245840
Sxl"	physical	fu	pubmed:14597576
Sxl"	physical	Gs2	pubmed:34029324
Sxl"	physical	hoe1	pubmed:21663794

Sxl"	physical	Hrb27C	pubmed:29635389
Sxl"	physical	loqs	pubmed:23788626
Sxl"	physical	Lrr47	pubmed:21663794
Sxl"	physical	me31B	pubmed:23788626
Sxl"	physical	mei-P26	pubmed:23526974, pubmed:29354790
Sxl"	physical	msl-2	pubmed:9144292, pubmed:29089381, pubmed:25209665, pubmed:30562515, pubmed:18203923, pubmed:21663794, pubmed:16452509, pubmed:29635389, pubmed:23788626, pubmed:14532129
Sxl"	physical	N	pubmed:17276344
Sxl"	physical	NetA	pubmed:30562515
Sxl"	physical	NHP2	pubmed:29845608
Sxl"	physical	nito	pubmed:26324914
Sxl"	physical	nos	pubmed:29845608, pubmed:22645327, pubmed:23526974, pubmed:32654316
Sxl"	physical	Pka-C3	pubmed:30562515
Sxl"	physical	Polr3E	pubmed:10521666
Sxl"	physical	pps	pubmed:20221253
Sxl"	physical	ptc	pubmed:17284519
Sxl"	physical	RpS14a	pubmed:21663794
Sxl"	physical	S-Lap3	pubmed:21663794
Sxl"	physical	sca	pubmed:30562515
Sxl"	physical	smo	pubmed:17284519
Sxl"	physical	snf	pubmed:19727396, pubmed:20221253
Sxl"	physical	snf	pubmed:19013444, pubmed:18245840, pubmed:20221253
Sxl"	physical	sog	pubmed:30562515
Sxl"	physical	ssx	pubmed:30590805
Sxl"	physical	Su(fu)	pubmed:14597576
Sxl"	physical	Sxl	pubmed:30562515, pubmed:28675155, pubmed:21829374, pubmed:27919081, pubmed:26324914, pubmed:20221253
Sxl"	physical	Sxl	pubmed:17284519

Sxl"	physical	tra	pubmed:20221253, pubmed:34029324, pubmed:25453831, pubmed:30562515
Sxl"	physical	tral	pubmed:23788626
Sxl"	physical	U2af50	pubmed:18245840
Sxl"	physical	Unr	pubmed:23788626, pubmed:16452509, pubmed:18203923
Sxl"	physical	Ythdc1	pubmed:28675155, pubmed:27919081
Sxl"	physical	Ythdf	pubmed:28675155
Traf6"	physical	bam	pubmed:30879902
tut	physical	mei-P26	pubmed:25412508
tut"	physical	bam	pubmed:28190776, pubmed:25412508
twin"	physical	bam	pubmed:29255063, pubmed:28190776, pubmed:26549449
U2A"	physical	mei-P26	pubmed:27035939
Ubi-p5E"	physical	bam	pubmed:28484036
Ubi-p63E"	physical	bam	pubmed:28484036
vas"	physical	mei-P26	pubmed:19952109
wuho"	physical	mei-P26	pubmed:31941704
wupA"	physical	Sxl	pubmed:34029324
bam	suppressible	mei-P26	pubmed:23122292
U2A	suppressible	mei-P26	pubmed:27035939
mei-P26	suppressible	eas	pubmed:15937125
mei-P26	suppressible	Dcr-1	pubmed:20400939
mei-P26	suppressible	twin	pubmed:24286029
mei-P26	suppressible	jus	pubmed:15937125
loqs	suppressible	mei-P26	pubmed:18528333
bam	enhanceable	mei-P26	pubmed:10924472
vas	enhanceable	mei-P26	pubmed:19952109

table S1. esyN references for *sxl* and *bam* interactions in Supplemental fig S1C and *mei-P26* interactions in Fig 9.

interaction	sex	reference
Bam is a translational repressor in female GSCs	females	Shen, R., Weng, C., Yu, J., and Xie, T. (2009). eIF4A controls germline stem cell self-renewal by directly inhibiting BAM function in the Drosophila ovary. <i>Proceedings of the National Academy of Sciences</i> 106, 11623–11628.
Bam and Bgcn bind the <i>nos</i> 3'-UTR and inhibit Nos translation in females	females	Li, Y., Minor, N.T., Park, J.K., McKearin, D.M., and Maines, J.Z. (2009). Bam and Bgcn antagonize Nanos-dependent germ-line stem cell maintenance. <i>Proceedings of the National Academy of Sciences</i> 106, 9304–9309.
Dpp GSC niche signalling silences <i>bam</i> transcription in females	females	Chen, D., and McKearin, D. (2003). Dpp Signaling Silences bam Transcription Directly to Establish Asymmetric Divisions of Germline Stem Cells. <i>Current Biology</i> 13, 1786–1791. 10.1016/j.cub.2003.09.033 .
BamF localizes to the fusome/spectrosome continuously and BamC localizes to the cytoplasm in CB-> 8-cell cysts	females	McKearin, D., and Ohlstein, B. (1995). A role for the Drosophila Bag-of-marbles protein in the differentiation of cystoblasts from germline stem cells. <i>Development</i> 121, 2937–2947.
Bam alters chromatin methylation to activate gene expression in the female germline	females	Mukai, M., Hira, S., Nakamura, K., Nakamura, S., Kimura, H., Sato, M., and Kobayashi, S. (2015). H3K36 Trimethylation-Mediated Epigenetic Regulation is Activated by Bam and Promotes Germ Cell Differentiation During Early Oogenesis in Drosophila. <i>Biology Open</i> 4, 119–124. 10.1242/bio.201410850 .
Bam binds Otu to deubiquitinate CycA during female TA mitoses	females	Ji, S., Li, C., Hu, L., Liu, K., Mei, J., Luo, Y., Tao, Y., Xia, Z., Sun, Q., and Chen, D. (2017). Bam-dependent deubiquitinase complex can disrupt germ-line stem cell maintenance by targeting cyclin A. <i>Proceedings of the National Academy of Sciences</i> 114, 6316–6321. 10.1073/pnas.1619188114 .
Bam interacts with Bgcn and the CCR4 deadenylase complex to repress GSC maintenance factors in the female germline	females	Sgromo, A., Raisch, T., Backhaus, C., Keskeny, C., Alva, V., Weichenrieder, O., and Izaurralde, E. (2018). Drosophila Bag-of-marbles directly interacts with the CAF40 subunit of the CCR4–NOT complex to elicit repression of mRNA targets. <i>RNA</i> 24, 381–395. 10.1261/rna.064584.117 .
In males, Tut binds the <i>mei-P26</i> 3'-UTR, which when bound to Bam and Bgcn represses Mei-P26 translation	males	Chen, D., Wu, C., Zhao, S., Geng, Q., Gao, Y., Li, X., Zhang, Y., and Wang, Z. (2014). Three RNA Binding Proteins Form a Complex to Promote Differentiation of Germline Stem Cell Lineage in Drosophila. <i>PLoS Genet</i> 10, e1004797. 10.1371/journal.pgen.1004797 .
Bam and Bgcn bind the <i>mei-P26</i> 3'-UTR and inhibit Mei-P26 translation in male spermatocytes	males	Insco, M.L., Bailey, A.S., Kim, J., Olivares, G.H., Wapinski, O.L., Tam, C.H., and Fuller, M.T. (2012). A Self-Limiting Switch Based on Translational Control Regulates the Transition from Proliferation to Differentiation in an Adult Stem Cell Lineage. <i>Cell Stem Cell</i> 11, 689–700. 10.1016/j.stem.2012.08.012 .
Bam is translationally regulated by miRNA binding to its 3'-UTR in the male germline	males	Eun, S.H., Stoiber, P.M., Wright, H.J., McMurdie, K.E., Choi, C.H., Gan, Q., Lim, C., and Chen, X. (2013). MicroRNAs downregulate Bag of marbles to ensure proper terminal differentiation in the Drosophila male germline. <i>Development</i> 140, 23–30. 10.1242/dev.086397 .
Bam is translationally regulated by miR-7 in the male germline	males	Pek, J.W., Lim, A.K., and Kai, T. (2009). Drosophila Maelstrom Ensures Proper Germline Stem Cell Lineage Differentiation by Repressing microRNA-7. <i>Developmental Cell</i> 17,

		417–424. 10.1016/j.devcel.2009.07.017.
Bam transcription is silenced by a histone linker protein	males	Carbonell, A., Pérez-Montero, S., Climent-Cantó, P., Reina, O., and Azorín, F. (2017). The Germline Linker Histone dBigH1 and the Translational Regulator Bam Form a Repressor Loop Essential for Male Germ Stem Cell Differentiation. <i>Cell Reports</i> 21, 3178–3189. 10.1016/j.celrep.2017.11.060.
mei-P26 genetically interacts with Bam as a dominant enhancer	females	Page, S.L., McKim, K.S., Deneen, B., Van Hook, T.L., and Hawley, R.S. (2000). Genetic Studies of <i>mei-P26</i> Reveal a Link Between the Processes That Control Germ Cell Proliferation in Both Sexes and Those That Control Meiotic Exchange in <i>Drosophila</i> . <i>Genetics</i> 155, 1757.
mei-P26 binds Ago1 through its NHL domain and inhibits miRNA production; loquacious knockdown suppresses mei-P26 knockdown phenotype	females	Neumüller, R.A., Betschinger, J., Fischer, A., Bushati, N., Poernbacher, I., Mechtler, K., Cohen, S.M., and Knoblich, J.A. (2008). Mei-P26 regulates microRNAs and cell growth in the <i>Drosophila</i> ovarian stem cell lineage. <i>Nature</i> 454, 241–245. 10.1038/nature07014.
Vas activates <i>mei-P26</i> translation by 3'-UTR binding and interaction with eIF5B	females	Liu, N., Han, H., and Lasko, P. (2009). Vasa promotes <i>Drosophila</i> germline stem cell differentiation by activating <i>mei-P26</i> translation by directly interacting with a (U)-rich motif in its 3' UTR. <i>Genes & Development</i> 23, 2742–2752. 10.1101/gad.1820709.
mei-P26 down-regulates eIF4E in GSCs	females	Song, Y., and Lu, B. (2011). Regulation of cell growth by Notch signaling and its differential requirement in normal vs. tumor-forming stem cells in <i>Drosophila</i> . <i>Genes Dev.</i> 25, 2644–2658. 10.1101/gad.171959.111.
mei-P26 inhibits Orb by Ago1-based miRNA-binding to the Orb 3'-UTR; mei-P26 also down-regulates Brat (and Bam because Brat-- pMad) expression in the GSC	females	Li, Y., Maines, J.Z., Tastan, O.Y., McKearin, D.M., and Buszczak, M. (2012). Mei-P26 regulates the maintenance of ovarian germline stem cells by promoting BMP signaling. <i>Development</i> 139, 1547–1556. 10.1242/dev.077412.
CCR4-NOT works with Nos and Pum to deadenylate mei-P26 in the GSC; CCR4 was present in the GSCs as well as in other cells in the germarium (Figure 1C) where it was mostly cytoplasmic and accumulated in discrete foci, as reported in other cell types in the ovary and embryo (Rouget et al., 2010; Temme et al., 2004; Zaessinger et al., 2006).	females	Joly, W., Chartier, A., Rojas-Rios, P., Busseau, I., and Simonelig, M. (2013). The CCR4 Deadenylase Acts with Nanos and Pumilio in the Fine-Tuning of Mei-P26 Expression to Promote Germline Stem Cell Self-Renewal. <i>Stem Cell Reports</i> 1, 411–424. 10.1016/j.stemcr.2013.09.007.
"Mei-P26 associates with Bam, Bgcn and Sxl and nanos mRNA during early cyst development, suggesting that this protein helps to repress the translation of nanos mRNA."	females	Li, Y., Zhang, Q., Carreira-Rosario, A., Maines, J.Z., McKearin, D.M., and Buszczak, M. (2013). Mei-P26 Cooperates with Bam, Bgcn and Sxl to Promote Early Germline Development in the <i>Drosophila</i> Ovary. <i>PLoS ONE</i> 8, e58301. 10.1371/journal.pone.0058301.
"Mei-P26 regulates PGC development"	females	Jankovics, F., Henn, L., Bujna, Á., Vilmos, P., Spirohn, K., Boutros, M., and Erdélyi, M. (2014). Functional Analysis of the <i>Drosophila</i> Embryonic Germ Cell Transcriptome by RNA Interference. <i>PLoS ONE</i> 9, e98579. 10.1371/journal.pone.0098579.
Mei-P26-Bgcn-Bam-Sxl-Brat-Ago1-miR980/miR-1 -- nos 3'-UTR	females	Malik, S., Jang, W., and Kim, C. (2017). Protein Interaction Mapping of Translational Regulators Affecting Expression of the Critical Stem Cell Factor Nos. <i>Development & Reproduction</i> 21, 449–456. 10.12717/DR.2017.21.4.449.

sisR-1, a stable intronic sequence RNA, negatively regulates mei-P26 in the GSC (through deadenylation)	females	Wong, J.T., Akhbar, F., Ng, A.Y.E., Tay, M.L.-I., Loi, G.J.E., and Pek, J.W. (2017). DIP1 modulates stem cell homeostasis in Drosophila through regulation of sisR-1. <i>Nat Commun</i> 8, 759. 10.1038/s41467-017-00684-4.
Wh regulates Mei-p26, and these proteins function together in multiple contexts to control GSC maintenance and differentiation	females	Rastegari, E., Kajal, K., Tan, B.-S., Huang, F., Chen, R.-H., Hsieh, T.-S., and Hsu, H.-J. (2020). WD40 protein Wuho controls germline homeostasis via TRIM-NHL tumor suppressor Mei-p26 in Drosophila. <i>Development</i> 147, dev182063. 10.1242/dev.182063.
Mei-P26 structure and RNA binding targets	females	Salerno-Kochan, A., Horn, A., Ghosh, P., Nithin, C., Kościelniak, A., Meindl, A., Strauss, D., Krutyhołowa, R., Rossbach, O., Bujnicki, J.M., et al. (2022). Molecular insights into RNA recognition and gene regulation by the TRIM-NHL protein Mei-P26. <i>Life Sci. Alliance</i> 5, e202201418. 10.26508/lsa.202201418.
Aub represses Mei-P26 translation through deadenylation	females	Rojas-Ríos, P., Chartier, A., Pierson, S., and Simonelig, M. (2017). Aubergine and pi RNA s promote germline stem cell self-renewal by repressing the proto-oncogene Cbl. <i>EMBO J</i> 36, 3194–3211. 10.15252/embj.201797259.
"mei-P26 mutant cystoblasts fail to downregulate dMyc protein, suggesting a role of Mei-P26 in dMyc repression during the stem cell-cystoblast transition"	females	Rhiner, C., Díaz, B., Portela, M., Poyatos, J.F., Fernández-Ruiz, I., López-Gay, J.M., Gerlitz, O., and Moreno, E. (2009). Persistent competition among stem cells and their daughters in the Drosophila ovary germline niche. <i>Development</i> 136, 995–1006. 10.1242/dev.033340.
Tut binds the long isoform of the mei-P26 3'-UTR; Bam binds Tut on its N-terminus and Bgcn on its C-Terminus to regulate Mei-P26	males	Chen, D., Wu, C., Zhao, S., Geng, Q., Gao, Y., Li, X., Zhang, Y., and Wang, Z. (2014). Three RNA Binding Proteins Form a Complex to Promote Differentiation of Germline Stem Cell Lineage in Drosophila. <i>PLoS Genet</i> 10, e1004797. 10.1371/journal.pgen.1004797.
Mei-P26 facilitates the accumulation of Bam, and then Bam with Bgcn represses the translation of mei-P26	males	Insko, M.L., Bailey, A.S., Kim, J., Olivares, G.H., Wapinski, O.L., Tam, C.H., and Fuller, M.T. (2012). A Self-Limiting Switch Based on Translational Control Regulates the Transition from Proliferation to Differentiation in an Adult Stem Cell Lineage. <i>Cell Stem Cell</i> 11, 689–700. 10.1016/j.stem.2012.08.012.
U2A is involved in mei-P26 splicing	males	Wu, H., Sun, L., Wen, Y., Liu, Y., Yu, J., Mao, F., Wang, Y., Tong, C., Guo, X., Hu, Z., et al. (2016). Major spliceosome defects cause male infertility and are associated with nonobstructive azoospermia in humans. <i>Proc Natl Acad Sci USA</i> 113, 4134–4139. 10.1073/pnas.1513682113.
Bruno binds to the sxl mRNA 3'-UTR to repress translation	females	Wang, Z., and Lin, H. (2007). Sex-lethal is a target of Bruno-mediated translational repression in promoting the differentiation of stem cell progeny during Drosophila oogenesis. <i>Developmental Biology</i> 302, 160–168. 10.1016/j.ydbio.2006.09.016.
Bam requires Sxl for differentiation	females	Chau, J., Kulnane, L.S., and Salz, H.K. (2009). Sex-lethal Facilitates the Transition From Germline Stem Cell to Committed Daughter Cell in the Drosophila Ovary. <i>Genetics</i> 182, 121–132. 10.1534/genetics.109.100693.

Sxl is required for cell autonomous PGC fate determination	females	Hashiyama, K., Hayashi, Y., and Kobayashi, S. (2011). <i>Drosophila</i> Sex lethal Gene Initiates Female Development in Germline Progenitors. <i>Science</i> 333, 885–888. 10.1126/science.1208146.
Sxl binds the nos 3'-UTR to down-regulate Nos translation	females	Chau, J., Kulnane, L.S., and Salz, H.K. (2012). Sex-lethal enables germline stem cell differentiation by down-regulating Nanos protein levels during <i>Drosophila</i> oogenesis. <i>Proceedings of the National Academy of Sciences</i> 109, 9465–9470. 10.1073/pnas.1120473109.
Sxl review	females	Moschall, R., Gaik, M., and Medenbach, J. (2017). Promiscuity in post-transcriptional control of gene expression: <i>Drosophila</i> sex-lethal and its regulatory partnerships. <i>FEBS Lett</i> 591, 1471–1488. 10.1002/1873-3468.12652.
Sxl binds to 3'-UTRs to control the length distribution of all transcripts	females	Sandler, J.E., Irizarry, J., Stepanik, V., Dunipace, L., Amrhein, H., and Stathopoulos, A. (2018). A Developmental Program Truncates Long Transcripts to Temporally Regulate Cell Signaling. <i>Developmental Cell</i> 47, 773-784.e6. 10.1016/j.devcel.2018.11.019.
SXL functions with SETDB1 in the assembly of H3K9me3 silencing islands in germ cells	females	Smolko, A.E., Shapiro-Kulnane, L., and Salz, H.K. (2018). The H3K9 methyltransferase SETDB1 maintains female identity in <i>Drosophila</i> germ cells. <i>Nat Commun</i> 9, 4155. 10.1038/s41467-018-06697-x.
Sxl transcription is repressed by histone lysine methyltransferase (HKMT) Eggless (Egg/dSETDB1), which catalyzes methylation of Histone H3 lysine 9 (H3K9)	females	Clough, E., Tedeschi, T., and Hazelrigg, T. (2014). Epigenetic regulation of oogenesis and germ stem cell maintenance by the <i>Drosophila</i> histone methyltransferase Eggless/dSetDB1. <i>Developmental Biology</i> 388, 181–191. 10.1016/j.ydbio.2014.01.014.
Sxl alters poly-A lengths in the female germline	females	Gawande, B., Robida, M.D., Rahn, A., and Singh, R. (2006). <i>Drosophila</i> Sex-lethal protein mediates polyadenylation switching in the female germline. <i>EMBO J</i> 25, 1263–1272. 10.1038/sj.emboj.7601022.
wMel TomO rescues Sxl function in GSC maintenance through derepression of Nos translation	females	Ote, M., Ueyama, M., and Yamamoto, D. (2016). Wolbachia protein TomO targets nanos mRNA and restores germ stem cells in <i>Drosophila</i> sex-lethal mutants. <i>Current Biology</i> 26, 2223–2232. 10.1016/j.cub.2016.06.054.
wPip's TomO sequence rescues Sxl in <i>D. melanogaster</i> via nos translational derepression	females	Ote, M., and Yamamoto, D. (2018). Enhancing Nanos expression via the bacterial TomO protein is a conserved strategy used by the symbiont Wolbachia to fuel germ stem cell maintenance in infected <i>Drosophila</i> females. <i>Archives of Insect Biochemistry and Physiology</i> , e21471. 10.1002/arch.21471.
"TomO associates with orb mRNA, inhibiting interaction with the translation repressor Cup, leading to the precocious translation of Orb"	females	Ote, M., and Yamamoto, D. (2018). The Wolbachia protein TomO interacts with a host RNA to induce polarization defects in <i>Drosophila</i> oocytes. <i>Archives of Insect Biochemistry and Physiology</i> 99, e21475. 10.1002/arch.21475.

table S2. Annotated references used to make fig S1A,B and the table in Fig. 9C.

table S3. Full fecundity dataset (n=3002). See "Table_S3_fecundity_assays - all_data.tsv" file.

category	group1	group2	n1	mean1	n2	mean2	differential offspring/day: mean1-mean2	proportion offspring/day: mean2/mean1	test	p-value
wild type (WT) fertility	WT_OreR_wMel	WT_OreR_uninf	115	25.72	164	24.75	0.96	0.96	Wilcoxon rank sum	8.09E-01
	WT_OreR_uninf	WT_F10_OreR_uninf	""	""	102	21.88	2.87	0.88	Wilcoxon rank sum	1.81E-01
	WT_OreR_wMel	WT_F10_OreR_uninf	""	""	""	""	3.84	0.85	Wilcoxon rank sum	1.23E-01
	nos:Gal4>RFP_wMel	nos:Gal4>RFP_uninf	23	23.03	21	31.58	-8.55	1.37	Wilcoxon rank sum	1.25E-01
	WT_OreR_wMel	nos:Gal4>RFP_wMel	""	""	""	""	-2.69	0.90	Wilcoxon rank sum	4.75E-01
	WT_OreR_uninf	nos:Gal4>RFP_uninf	""	""	""	""	6.83	1.28	Wilcoxon rank sum	1.05E-01
	CyO/nos:Gal4_wMel	CyO/nos:Gal4_uninf	83	40.26	55	27.09	13.18	0.67	Wilcoxon rank sum	2.20E-03
	Sb/nos:Gal4_wMel	Sb/nos:Gal4_uninf	43	34.39	26	31.93	2.46	0.93	Wilcoxon rank sum	7.41E-01
F mei-P26 knockdown	nos:Gal4>meiP26RNAi_F_wMel	nos:Gal4>meiP26RNAi_F_uninf	66	37.02	60	18.38	18.64	0.50	Wilcoxon rank sum	1.07E-04
	mei-P26[1]_F_wMel	mei-P26[1]_F_uninf	73	6.96	45	1.61	5.35	0.23	Wilcoxon rank sum	9.37E-05
	mei-P26[1/mfs1]_F_wMel	mei-P26[1/mfs1]_F_uninf	42	4.56	37	0.18	4.38	0.04	Fisher's exact test (with/without_offspring)	1.03E-05
	mei-P26[mfs1]_F_wMel	mei-P26[mfs1]_F_uninf	25	0.76	19	0.00	0.76	0.00	Fisher's exact test (with/without_offspring)	5.14E-06
WT vs F mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-11.30	1.44	Wilcoxon rank sum	1.15E-02
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	6.38	0.74	Wilcoxon rank sum	1.26E-02
	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	7.34	0.71	Wilcoxon rank sum	1.24E-02
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	12.26	1.50	Wilcoxon rank sum	5.78E-03
	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-13.98	1.61	Wilcoxon rank sum	3.49E-02
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	13.20	0.58	Wilcoxon rank sum	5.42E-03
	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	4.65	0.80	Wilcoxon rank sum	3.42E-01
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-5.44	1.17	Wilcoxon rank sum	7.18E-01
	WT_OreR_uninf	mei-P26[1]_F_wMel	""	""	""	""	-12.26	1.50	Wilcoxon rank sum	5.78E-03
	WT_OreR_wMel	mei-P26[1]_F_wMel	""	""	""	""	18.76	0.27	Wilcoxon rank sum	3.45E-12
	WT_OreR_uninf	mei-P26[1]_F_uninf	""	""	""	""	23.15	0.06	Wilcoxon rank sum	2.26E-14
	WT_OreR_wMel	mei-P26[1/mfs1]_F_wMel	""	""	""	""	21.15	0.18	Wilcoxon rank sum	5.01E-10
	WT_OreR_uninf	mei-P26[1/mfs1]_F_uninf	""	""	""	""	24.57	0.01	Wilcoxon rank sum	3.40E-04
WT_OreR_wMel	mei-P26[mfs1]_F_wMel	""	""	""	""	24.96	0.03	Wilcoxon rank sum	1.66E-09	

	WT_OreR_uninf	mei-P26[mfs1]_F_uninf	""	""	""	""	24.75	0.00	Fisher's exact test (with/without_offspring)	2.20E-16
M mei-P26 knockdown	nos:Gal4>meiP26RNAi_M_wMel	nos:Gal4>meiP26RNAi_M_uninf	35	36.11	35	32.45	3.67	0.90	Wilcoxon rank sum	4.41E-01
	mei-P26[1]_M_wMel	mei-P26[1]_M_uninf	32	43.38	21	32.49	10.89	0.75	Wilcoxon rank sum	1.58E-01
	mei-P26[mfs1]_M_wMel	mei-P26[mfs1]_M_uninf	21	24.84	24	0.40	24.45	0.02	Wilcoxon rank sum	2.85E-02
WT vs M mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_M_wMel	""	""	""	""	-10.40	1.40	Wilcoxon rank sum	3.72E-03
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_M_uninf	""	""	""	""	-7.69	1.31	Wilcoxon rank sum	6.54E-02
	WT_OreR_wMel	mei-P26[1]_M_wMel	""	""	""	""	-17.66	1.69	Wilcoxon rank sum	3.96E-04
	WT_OreR_uninf	mei-P26[1]_M_uninf	""	""	""	""	-7.74	1.31	Wilcoxon rank sum	6.60E-02
	WT_OreR_wMel	mei-P26[mfs1]_M_wMel	""	""	""	""	0.88	0.97	Wilcoxon rank sum	4.35E-01
	WT_OreR_uninf	mei-P26[mfs1]_M_uninf	""	""	""	""	24.36	0.02	Wilcoxon rank sum	4.28E-04
CI crosses	WT_OreR_Dmel_reciprocal-5d	WT_OreR_wMel	60	22.50	""	""	-3.21	1.14	Wilcoxon rank sum	2.74E-01
	WT_OreR_Dmel_reciprocal-5d	WT_OreR_uninf	""	""	""	""	-2.25	1.10	Wilcoxon rank sum	3.25E-01
	WT_OreR_Dmel_CI-0d	WT_OreR_Dmel_rescue-0d	70	16.11	69	22.08	-5.98	1.37	Wilcoxon rank sum	1.71E-02
	WT_OreR_Dmel_CI-0d	WT_OreR_Dmel_reciprocal-0d	""	""	14	29.69	-13.59	1.84	Wilcoxon rank sum	1.06E-02
	WT_OreR_Dmel_rescue-0d	WT_OreR_Dmel_reciprocal-0d	""	""	""	""	-7.61	1.34	Wilcoxon rank sum	1.71E-01
	WT_OreR_Dmel_CI-5d	WT_OreR_Dmel_rescue-5d	26	25.12	69	25.89	-0.77	1.03	Wilcoxon rank sum	9.27E-01
	WT_OreR_Dmel_CI-5d	WT_OreR_Dmel_reciprocal-5d	""	""	""	""	2.62	0.90	Wilcoxon rank sum	3.63E-01
	Dsimulans_CI-0d	Dsimulans_rescue-0d	31	2.24	33	23.88	-21.64	10.66	Wilcoxon rank sum	6.53E-07
Dsimulans_CI-5d	Dsimulans_rescue-5d	17	7.51	27	19.00	-11.49	2.53	Wilcoxon rank sum	5.00E-02	

table S4. Fecundity statistics: offspring produced per female per day in single female-by-single male crosses. Experimental genotypes, infection statuses, and sexes are listed. The mate for each cross was OreR, of the same infection status, and of the opposite sex as the experimental fly. Males were aged 3-6 days, except for the young male CI crosses, which were aged zero days (distinguished with “-0d” and “-5d” labels). P-values <0.01 are in light green and <0.05 are in dark green for clarity.

category	group1	group2	n1	mean1	n2	mean2	differential egg laid/day: mean1-mean2	proportion egg laid/day: mean2/mean1	test	p-value
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wild type (WT) fertility	WT_OreR_wMel	WT_OreR_uninf	115	27.49	164	27.69	-0.20	1.01	Wilcoxon rank sum	9.09E-01
	WT_OreR_uninf	WT_F10_OreR_uninf	""	""	102	25.62	2.07	0.93	Wilcoxon rank sum	4.78E-01
	WT_OreR_wMel	WT_F10_OreR_uninf	""	""	""	""	1.87	0.93	Wilcoxon rank sum	5.18E-01
	nos:Gal4>RFP_wMel	nos:Gal4>RFP_uninf	23	23.42	21	34.87	-11.46	1.49	Wilcoxon rank sum	7.22E-02
	WT_OreR_wMel	nos:Gal4>RFP_wMel	""	""	""	""	-4.08	0.85	Wilcoxon rank sum	3.15E-01
	WT_OreR_uninf	nos:Gal4>RFP_uninf	""	""	""	""	7.18	1.26	Wilcoxon rank sum	1.15E-01
	CyO/nos:Gal4_wMel	CyO/nos:Gal4_uninf	83	42.36	55	28.43	13.93	0.67	Wilcoxon rank sum	2.22E-03
	Sb/nos:Gal4_wMel	Sb/nos:Gal4_uninf	43	34.21	26	34.17	0.03	1.00	Wilcoxon rank sum	1.00E+00
F mei-P26 knockdown	nos:Gal4>meiP26RNAi_F_wMel	nos:Gal4>meiP26RNAi_F_uninf	66	45.89	60	28.89	17.01	0.63	Wilcoxon rank sum	1.17E-03
	mei-P26[1]_F_wMel	mei-P26[1]_F_uninf	73	16.09	45	6.09	10.00	0.38	Wilcoxon rank sum	2.82E-02
	mei-P26[1/mfs1]_F_wMel	mei-P26[1/mfs1]_F_uninf	42	8.40	37	0.18	8.22	0.02	Wilcoxon rank sum	4.71E-05
	mei-P26[mfs1]_F_wMel	mei-P26[mfs1]_F_uninf	25	2.52	19	0.00	2.52	0.00	Wilcoxon rank sum	3.04E-05
WT vs F mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-18.40	1.67	Wilcoxon rank sum	6.99E-05
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	-1.20	1.04	Wilcoxon rank sum	5.15E-01
	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	-1.40	1.05	Wilcoxon rank sum	5.29E-01
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	18.20	1.66	Wilcoxon rank sum	3.01E-05
	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-22.48	1.96	Wilcoxon rank sum	2.17E-03
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	5.99	0.83	Wilcoxon rank sum	1.68E-01
	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	-5.47	1.23	Wilcoxon rank sum	8.34E-01
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-11.02	1.32	Wilcoxon rank sum	1.76E-01
	WT_OreR_uninf	mei-P26[1]_F_wMel	""	""	""	""	-18.20	1.66	Wilcoxon rank sum	3.01E-05
	WT_OreR_wMel	mei-P26[1]_F_wMel	""	""	""	""	11.40	0.59	Wilcoxon rank sum	5.13E-06
	WT_OreR_uninf	mei-P26[1]_F_uninf	""	""	""	""	21.60	0.22	Wilcoxon rank sum	1.03E-11
	WT_OreR_wMel	mei-P26[1/mfs1]_F_wMel	""	""	""	""	19.09	0.31	Wilcoxon rank sum	2.67E-10
	WT_OreR_uninf	mei-P26[1/mfs1]_F_uninf	""	""	""	""	27.51	0.01	Wilcoxon rank sum	< 2.2e-16
	WT_OreR_wMel	mei-P26[mfs1]_F_wMel	""	""	""	""	24.97	0.09	Wilcoxon rank sum	1.12E-10
WT_OreR_uninf	mei-P26[mfs1]_F_uninf	""	""	""	""	27.69	0.00	Wilcoxon rank sum	6.31E-11	
M mei-P26 knockdown	nos:Gal4>meiP26RNAi_M_wMel	nos:Gal4>meiP26RNAi_M_uninf	38	34.84	41	36.30	-1.46	1.04	Wilcoxon rank sum	9.10E-01
	mei-P26[1]_M_wMel	mei-P26[1]_M_uninf	35	34.64	28	33.47	1.18	0.97	Wilcoxon rank sum	9.83E-01
	mei-P26[mfs1]_M_wMel	mei-P26[mfs1]_M_uninf	21	28.79	28	2.51	26.29	0.09	Wilcoxon rank sum	6.10E-06

WT vs M mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_M_wMel	""	""	""	""	-7.35	1.27	Wilcoxon rank sum	3.58E-02
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_M_uninf	""	""	""	""	-8.61	1.31	Wilcoxon rank sum	3.90E-02
	WT_OreR_wMel	mei-P26[1]_M_wMel	""	""	""	""	-7.15	1.26	Wilcoxon rank sum	2.32E-01
	WT_OreR_uninf	mei-P26[1]_M_uninf	""	""	""	""	-5.78	1.21	Wilcoxon rank sum	1.20E-01
	WT_OreR_wMel	mei-P26[mfs1]_M_wMel	""	""	""	""	-1.30	1.05	Wilcoxon rank sum	1.00E+00
	WT_OreR_uninf	mei-P26[mfs1]_M_uninf	""	""	""	""	25.18	0.09	Wilcoxon rank sum	8.59E-12

table S5. Fecundity statistics: eggs produced per female per day in single female-by-single male crosses. Experimental genotypes, infection statuses, and sexes are listed. The mate for each cross was OreR, of the same infection status, and of the opposite sex as the experimental fly. Males were aged 3-6 days, except for the young male CI crosses, which were aged zero days (distinguished with “-0d” and “-5d” labels). P-values <0.01 are in light green and <0.05 are in dark green for clarity.

category	group1(lay>=20)	group2(lay>=20)	n1	mean1	n2	mean2	differential hatch: mean1-mean2	proportion hatch/day: mean2/mean1	test	p-value
wild type (WT) fertility	WT_OreR_wMel	WT_OreR_uninf	76	88.40	104	83.18	5.22	0.94	Wilcoxon rank sum	3.46E-07
	WT_OreR_uninf	WT_F10_OreR_uninf	""	""	64	80.88	2.30	0.97	Wilcoxon rank sum	1.17E-01
	WT_OreR_wMel	WT_F10_OreR_uninf	""	""	""	""	7.51	0.92	Wilcoxon rank sum	8.98E-03
	nos:Gal4>RFP_wMel	nos:Gal4>RFP_uninf	12	88.49	16	90.50	-2.01	1.02	Wilcoxon rank sum	9.82E-01
	WT_OreR_wMel	nos:Gal4>RFP_wMel	""	""	""	""	0.09	1.00	Wilcoxon rank sum	7.15E-01
	WT_OreR_uninf	nos:Gal4>RFP_uninf	""	""	""	""	7.32	1.09	Wilcoxon rank sum	5.01E-03
	CyO/nos:Gal4_wMel	CyO/nos:Gal4_uninf	66	91.31	31	88.83	2.47	0.97	Wilcoxon rank sum	2.08E-03
	Sb/nos:Gal4_wMel	Sb/nos:Gal4_uninf	33	88.66	22	89.55	-0.89	1.01	Wilcoxon rank sum	8.37E-01
F mei-P26 knockdown	nos:Gal4>meiP26RNAi_F_wMel	nos:Gal4>meiP26RNAi_F_uninf	53	74.45	33	49.63	24.81	0.67	Wilcoxon rank sum	2.64E-08
	mei-P26[1]_F_wMel	mei-P26[1]_F_uninf	27(73)	24.91	5(45)	18.47	6.43	0.74	Fisher's exact test (with/without_hatch)	2.55E-03
	mei-P26[1/mfs1]_F_wMel	mei-P26[1/mfs1]_F_uninf	7(42)	27.74	5(35)	0.00	27.74	0.00	Wilcoxon rank sum (Fisher's exact test)	4.20E-03 (1.00E+00)
	mei-P26[mfs1]_F_wMel	mei-P26[mfs1]_F_uninf	5(25)	0.00	5(19)	0.00	0.00	0.00	NA - no females laid >=20 eggs/day	NA
WT vs F mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	13.95	0.84	Wilcoxon rank sum	9.11E-07
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	33.55	0.60	Wilcoxon rank sum	4.32E-15
	WT_OreR_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	38.76	0.56	Wilcoxon rank sum	3.57E-14
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	-8.73	0.90	Wilcoxon rank sum	1.38E-02

	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	14.04	0.84	Wilcoxon rank sum	1.42E-02
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	40.86	0.55	Wilcoxon rank sum	1.93E-08
	nos:Gal4>RFP_wMel	nos:Gal4>meiP26RNAi_F_uninf	""	""	""	""	38.85	0.56	Wilcoxon rank sum	8.26E-07
	nos:Gal4>RFP_uninf	nos:Gal4>meiP26RNAi_F_wMel	""	""	""	""	16.05	0.82	Wilcoxon rank sum	3.56E-03
	WT_OreR_uninf	mei-P26[1]_F_wMel	""	""	""	""	8.73	0.90	Wilcoxon rank sum	1.38E-02
	WT_OreR_wMel	mei-P26[1]_F_wMel	""	""	""	""	63.49	0.28	Wilcoxon rank sum	4.82E-13
	WT_OreR_uninf	mei-P26[1]_F_uninf	""	""	""	""	64.71	0.22	Wilcoxon rank sum	2.93E-04
	WT_OreR_wMel	mei-P26[1/mfs1]_F_wMel	""	""	""	""	60.66	0.31	Wilcoxon rank sum	5.32E-05
	WT_OreR_uninf	mei-P26[1/mfs1]_F_uninf	""	""	""	""	83.18	0.00	Wilcoxon rank sum	1.97E-04
	WT_OreR_wMel	mei-P26[mfs1]_F_wMel	""	""	""	""	88.40	0.00	Wilcoxon rank sum	2.41E-04
	WT_OreR_uninf	mei-P26[mfs1]_F_uninf	""	""	""	""	83.18	0.00	Wilcoxon rank sum	1.97E-04
M mei-P26 knockdown	nos:Gal4>meiP26RNAi_M_wMel	nos:Gal4>meiP26RNAi_M_uninf	28	90.58	26	72.61	17.97	0.80	Wilcoxon rank sum	3.42E-03
	mei-P26[1]_M_wMel	mei-P26[1]_M_uninf	21	94.86	16	90.64	4.22	0.96	Wilcoxon rank sum	1.03E-01
	mei-P26[mfs1]_M_wMel	mei-P26[mfs1]_M_uninf	15	71.00	2	0.00	71.00	0.00	Wilcoxon rank sum	1.07E-01
WT vs M mei-P26 knockdown	WT_OreR_wMel	nos:Gal4>meiP26RNAi_M_wMel	""	""	""	""	-2.18	1.02	Wilcoxon rank sum	1.65E-02
	WT_OreR_uninf	nos:Gal4>meiP26RNAi_M_uninf	""	""	""	""	10.57	0.87	Wilcoxon rank sum	9.00E-01
	WT_OreR_wMel	mei-P26[1]_M_wMel	""	""	""	""	-6.46	1.07	Wilcoxon rank sum	4.72E-04
	WT_OreR_uninf	mei-P26[1]_M_uninf	""	""	""	""	-7.46	1.09	Wilcoxon rank sum	5.00E-03
	WT_OreR_wMel	mei-P26[mfs1]_M_wMel	""	""	""	""	17.39	0.80	Wilcoxon rank sum	4.01E-01
	WT_OreR_uninf	mei-P26[mfs1]_M_uninf	""	""	""	""	83.18	0.00	Wilcoxon rank sum	1.73E-02
CI crosses	WT_OreR_Dmel_reciprocal-5d	WT_OreR_wMel	10	78.17	""	""	-10.22	1.13	Wilcoxon rank sum	0.612
	WT_OreR_Dmel_reciprocal-5d	WT_OreR_uninf	""	""	""	""	-5.01	1.06	Wilcoxon rank sum	9.91E-04
	WT_OreR_Dmel_CI-0d	WT_OreR_Dmel_rescue-0d	33	66.10	33	84.03	-17.93	1.27	Wilcoxon rank sum	4.63E-04
	WT_OreR_Dmel_CI-0d	WT_OreR_Dmel_reciprocal-0d	""	""	9	93.21	-27.11	1.41	Wilcoxon rank sum	4.56E-05
	WT_OreR_Dmel_rescue-0d	WT_OreR_Dmel_reciprocal-0d	""	""	""	""	-9.18	1.11	Wilcoxon rank sum	1.25E-01
	WT_OreR_Dmel_CI-5d	WT_OreR_Dmel_rescue-5d	20	89.22	45	88.66	0.56	0.99	Wilcoxon rank sum	9.15E-01
	WT_OreR_Dmel_CI-5d	WT_OreR_Dmel_reciprocal-5d	""	""	""	""	11.05	0.88	Wilcoxon rank sum	2.09E-01
	WT_OreR_Dmel_rescue-5d	WT_OreR_Dmel_reciprocal-5d	""	""	""	""	10.49	0.88	Wilcoxon rank sum	9.72E-02
	Dsimulans_CI-0d	Dsimulans_rescue-0d	24	6.07	28	68.43	-62.36	11.27	Wilcoxon rank sum	5.64E-08
Dsimulans_CI-5d	Dsimulans_rescue-5d	10	26.52	17	69.04	-42.51	2.60	Wilcoxon rank sum	3.63E-04	

table S6. Fecundity statistics: percentage of eggs that hatched from single female-by-single male crosses that laid ≥ 20 eggs. Experimental genotypes, infection statuses, and sexes are listed. The mate for each cross was OreR, of the same infection status, and of the opposite sex as the experimental fly. Males were aged 3-6 days, except for the young male CI crosses, which were aged zero days (distinguished with “-0d” and “-5d” labels). Sample counts (n1,n2) in parentheses are for Fisher Exact Tests (samples with hatched eggs vs no hatched eggs, opposed to % hatch for samples with 20 or more eggs laid). P-values <0.01 are in light green and <0.05 are in dark green for clarity.

group1	group2	test	egg lay (#/female/day) p-value	%egg hatch (>10 eggs laid) p-value	offspring (#/female/day) p-value
WT_OreR_wMel	WT_OreR_uninf	Kolmogorov-Smirnov	7.84E-02	7.06E-09	6.02E-02
meiP26RNAi_F_wMel	meiP26RNAi_F_uninf	Kolmogorov-Smirnov	5.92E-06	1.48E-11	3.87E-08
meiP261_F_wMel	meiP261_F_uninf	Kolmogorov-Smirnov	3.41E-02	6.36E-05	1.18E-04

table S7. Fecundity versus age statistics

category	group1	group2	n1	mean1	n2	mean2	test	p-value
wild type (WT)	WT_OreR_wMel-5d	WT_OreR_uninf-5d	8	2.313	13	1.923	Wilcoxon rank sum	1.81E-01
	WT_OreR_wMel-10d	WT_OreR_uninf-10d	15	1.600	15	1.867	Wilcoxon rank sum	3.47E-01
	WT_OreR_wMel-31d	WT_OreR_uninf-31d	14	1.321	15	1.533	Wilcoxon rank sum	7.64E-01
	WT_OreR_wMel-5d	WT_OreR_wMel-10d	""	""	""	""	Wilcoxon rank sum	1.93E-02
	WT_OreR_uninf-5d	WT_OreR_uninf-10d	""	""	""	""	Wilcoxon rank sum	8.24E-01
	WT_OreR_wMel-10d	WT_OreR_wMel-31d	""	""	""	""	Wilcoxon rank sum	0.2655
	WT_OreR_uninf-10d	WT_OreR_uninf-31d	""	""	""	""	Wilcoxon rank sum	0.249
F mei-P26 knockdown	meiP26RNAi_F_wMel-5d	meiP26RNAi_F_uninf-5d	31	2.048	23	1.848	Wilcoxon rank sum	6.68E-01
	meiP261_F_wMel-5d	meiP261_F_uninf-5d	42	1.024	73	0.575	Wilcoxon rank sum	2.88E-04
	meiP26RNAi_F_wMel-5d	meiP261_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	4.47E-08
	meiP26RNAi_F_wMel-5d	meiP261_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	4.04E-14
	meiP26RNAi_F_uninf-5d	meiP261_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	3.63E-08
	meiP26RNAi_F_uninf-5d	meiP261_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	3.15E-04
	meiP261_F_wMel-10d	meiP261_F_uninf-10d	14	1.464	16	0.938	Wilcoxon rank sum	1.48E-02
	meiP261_F_wMel-5d	meiP261_F_wMel-10d	""	""	""	""	Wilcoxon rank sum	1.32E-02
	meiP261_F_uninf-5d	meiP261_F_uninf-10d	""	""	""	""	Wilcoxon rank sum	1.37E-02
WT vs F mei-P26 knockdown	WT_OreR_wMel-5d	meiP26RNAi_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	1.94E-01
	WT_OreR_uninf-5d	meiP26RNAi_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	1.00E+00
	WT_OreR_uninf-5d	meiP26RNAi_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	6.12E-01
	WT_OreR_wMel-5d	meiP26RNAi_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	2.33E-01
	WT_OreR_uninf-5d	meiP261_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	3.18E-07
	WT_OreR_wMel-5d	meiP261_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	1.18E-04
	WT_OreR_wMel-5d	meiP261_F_uninf-5d	""	""	""	""	Wilcoxon rank sum	3.36E-06
	WT_OreR_uninf-5d	meiP261_F_wMel-5d	""	""	""	""	Wilcoxon rank sum	2.75E-04
	WT_OreR_wMel-10d	meiP261_F_wMel-10d	""	""	""	""	Wilcoxon rank sum	6.66E-01
	WT_OreR_wMel-10d	meiP261_F_uninf-10d	""	""	""	""	Wilcoxon rank sum	1.10E-02
	WT_OreR_uninf-10d	meiP261_F_wMel-10d	""	""	""	""	Wilcoxon rank sum	1.40E-01
WT_OreR_uninf-10d	meiP261_F_uninf-10d	""	""	""	""	Wilcoxon rank sum	1.24E-03	

table S8. Germline stem cell (GSC) counts per germarium.

category	group1	group2	n germaria	n GSCs	n pHH3+ GSCs	proportion GSCs mitotic	n germaria	n GSCs	n pHH3+ GSCs	proportion GSCs mitotic	test	p-value
wild type (WT)	WT_OreR_wMel	WT_OreR_uninf	81	179	10.000	0.056	68	143	9	0.063	Fisher's Exact Test	8.16E-01
mei-P26 knockdown	meiP261_F_wMel	meiP261_F_uninf	111	152	9.000	0.059	111	115	1	0.009	Fisher's Exact Test	4.69E-02
WT vs F mei-P26 knockdown	WT_OreR_uninf	meiP261_F_uninf	""	""		""	""	""		""	Fisher's Exact Test	4.62E-02
	WT_OreR_wMel	meiP261_F_wMel	""	""		""	""	""		""	Fisher's Exact Test	1.00E+00
	WT_OreR_wMel	meiP261_F_uninf	""	""		""	""	""		""	Fisher's Exact Test	5.51E-02
	WT_OreR_uninf	meiP261_F_wMel	""	""		""	""	""		""	Fisher's Exact Test	1.00E+00

table S9. Number of GSCs in mitosis (anti-pHH3-positive staining), per germarium.

category	group1	group2	n germaria	avg # mitotic cystocytes / germarium	n germaria	avg # mitotic cystocytes / germarium	test	p-value
wild type (WT)	WT_OreR_wMel	WT_OreR_uninf	81	1.079	68	1.957	Wilcoxon Rank Sum Test	3.01E-01
mei-P26 knockdown	meiP261_F_wMel	meiP261_F_uninf	111	2.545	111	1.817	Fisher's Exact Test	1.40E-01
WT vs F mei-P26 knockdown	WT_OreR_uninf	meiP261_F_uninf	""	""	""	""	Fisher's Exact Test	9.52E-01
	WT_OreR_wMel	meiP261_F_wMel	""	""	""	""	Fisher's Exact Test	1.34E-02
	WT_OreR_wMel	meiP261_F_uninf	""	""	""	""	Fisher's Exact Test	2.64E-01
	WT_OreR_uninf	meiP261_F_wMel	""	""	""	""	Fisher's Exact Test	2.26E-01

table S10. Number of cystocytes (CC) in mitosis (anti-pHH3-positive staining), per germarium.

category	group1	group2	n1	n2	test	region 1 - relative fluor mean1	region 1 - relative fluor mean2	differential region 1 - mean1-me an2	relative fluor region 1 p-value	region 2a - relative fluor mean1	region 2a - relative fluor mean2	differential region 2a - mean1-m ean2	relative fluor region 2a p-value	region 2b - relative fluor mean1	region 2b - relative fluor mean2	differential region 2b - mean1-m ean2	relative fluor region 2b p-value
wild type (WT)	WT_OreR _wMel-5d	WT_OreR _uninf-5d	26	40	Wilcoxon rank sum	0.644	0.639	0.005	5.02E-01	0.236	0.197	0.039	1.42E-02	0.172	0.155	0.02	2.64E-01
F mei-P26 knockdown	meiP261_ F_wMel-5 d	meiP261_ F_uninf-5 d	36	39	Wilcoxon rank sum	0.527	0.466	0.061	8.40E-03	0.222	0.236	0.014	1.77E-01	0.211	0.262	0.05	1.72E-02
WT vs F mei-P26 knockdown	WT_OreR _uninf-5d	meiP261_ F_uninf-5 d			Wilcoxon rank sum			0.173	5.67E-10			0.039	8.60E-04			0.11	2.30E-07
	WT_OreR _wMel-5d	meiP261_ F_wMel-5 d			Wilcoxon rank sum			0.117	2.87E-04			0.014	8.82E-01			0.04	2.21E-02
	WT_OreR _wMel-5d	meiP261_ F_uninf-5 d			Wilcoxon rank sum			0.178	9.90E-08			0.000	3.08E-01			0.09	5.33E-05
	WT_OreR _uninf-5d	meiP261_ F_wMel-5 d			Wilcoxon rank sum			0.112	3.78E-06			0.025	9.10E-02			0.06	1.16E-03

table S11. Sxl expression by germarium region, measured by fluorescence intensity.

category	group1	group2	n1	n2	test	GSC - relative fluor mean1	GSC - relative fluor mean2	differential GSC - mean1-mean2	relative fluor GSC p-value	CB - relative fluor mean1	CB - relative fluor mean2	differential CB - mean1-mean2	relative fluor CB p-value	region 2a - relative fluor mean1	region 2a - relative fluor mean2	differential region 2a - mean1-mean2	relative fluor region 2a p-value	region 2b - relative fluor mean1	region 2b - relative fluor mean2	differential region 2b - mean1-mean2	relative fluor region 2b p-value
wild type (WT)	WT_OreR_wMel-5d	WT_OreR_uninf-5d	33	29	Wilcoxon rank sum	0.102	0.089	0.012	1.72E-01	0.481	0.469	0.011	6.14E-01	0.174	0.195	0.021	1.72E-01	0.206	0.204	0.002	7.05E-01
F mei-P26 knockdown	meiP261_F_wMel-5d	meiP261_F_uninf-5d	34	39	Wilcoxon rank sum	0.056	0.069	0.012	4.25E-01	0.502	0.397	0.105	1.60E-02	0.179	0.220	0.041	6.21E-02	0.210	0.263	0.053	1.66E-01
WT vs F mei-P26 knockdown	WT_OreR_uninf-5d	meiP261_F_uninf-5d			Wilcoxon rank sum			0.021	1.42E-03			0.073	9.18E-02			0.025	1.74E-01			0.059	3.33E-02
	WT_OreR_wMel-5d	meiP261_F_wMel-5d			Wilcoxon rank sum			0.046	1.28E-06			0.021	4.58E-01			0.005	7.70E-01			0.004	6.14E-01
	WT_OreR_wMel-5d	meiP261_F_uninf-5d			Wilcoxon rank sum			0.033	4.32E-05			0.084	3.40E-02			0.046	1.99E-02			0.057	3.50E-02
	WT_OreR_uninf-5d	meiP261_F_wMel-5d			Wilcoxon rank sum			0.033	5.97E-05			0.033	3.27E-01			0.016	3.27E-01			0.006	5.15E-01

table S12. Bam expression by germarium region, measured by fluorescence intensity.

category	group1	group2	n1	n2	test	GSC - relative Bam/pMad fluor mean1	GSC - relative Bam/pMad fluor mean2	differential Bam/pMad GSC - mean1-mean2	relative Bam/pMad fluor GSC p-value	CB - relative Bam/pMad fluor mean1	CB - relative Bam/pMad fluor mean2	differential Bam/pMad CB - mean1-mean2	relative Bam/pMad fluor CB p-value
wild type (WT)	WT_OreR_wMel-5d	WT_OreR_uninf-5d	21	29	Wilcoxon rank sum	0.467	0.593	0.126	4.43E-02	1.841	1.767	0.074	5.11E-02
F mei-P26 knockdown	meiP261_F_wMel-5d	meiP261_F_uninf-5d	20	27	Wilcoxon rank sum	0.640	1.422	0.783	9.82E-03	2.814	2.142	0.673	1.43E-03
WT vs F mei-P26 knockdown	WT_OreR_uninf-5d	meiP261_F_uninf-5d			Wilcoxon rank sum			0.829	4.04E-04			0.374	2.82E-01
	WT_OreR_wMel-5d	meiP261_F_wMel-5d			Wilcoxon rank sum			0.173	9.08E-01			0.973	2.13E-02
	WT_OreR_wMel-5d	meiP261_F_uninf-5d			Wilcoxon rank sum			0.955	2.51E-04			0.300	3.86E-01
	WT_OreR_uninf-5d	meiP261_F_wMel-5d			Wilcoxon rank sum			0.047	8.57E-02			1.047	1.22E-06

table S13. Relative Bam vs pMad expression, measured by fluorescence, in GSCs.

category	group1	group2	n1	nurse cells in cyst			n2	nurse cells in cyst			test	p-value
				<15	15	>15		<15	15	>15		
wild type (WT)	WT_nos:Gal4_wMel	WT_nos:Gal4_uninf	215	0	212	3	216	0	216	0	Fisher's exact test	1.23E-01
F mei-P26 knockdown	meiP26RNAi_F_wMel	meiP26RNAi_F_uninf	86	10	62	14	190	16	107	67	Fisher's exact test	4.46E-03
	meiP261_F_wMel	meiP261_F_uninf	444	37	189	218	124	8	47	69	Fisher's exact test	4.44E-01
	meiP26RNAi_F_wMel	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	2.24E-08
	meiP26RNAi_F_wMel	meiP261_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	1.81E-08
	meiP26RNAi_F_uninf	meiP261_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	1.63E-03
	meiP26RNAi_F_uninf	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	3.87E-03
WT vs F mei-P26 knockdown	WT_nos:Gal4_wMel	meiP26RNAi_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	2.72E-12
	WT_nos:Gal4_uninf	meiP26RNAi_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
	WT_nos:Gal4_uninf	meiP26RNAi_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	5.94E-15
	WT_nos:Gal4_wMel	meiP26RNAi_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
	WT_nos:Gal4_uninf	meiP261_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
	WT_nos:Gal4_wMel	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
	WT_nos:Gal4_wMel	meiP261_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
WT_nos:Gal4_uninf	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16	
F mei-P26 OE	meiP26OE_F_wMel	meiP26OE_F_uninf	101	7	85	9	138	0	131	7	Fisher's exact test	1.63E-03
mei-P26 OE vs mei-P26 knockdown	meiP26OE_F_wMel	meiP26RNAi_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	1.36E-01
	meiP26OE_F_wMel	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	1.31E-15
	meiP26OE_F_wMel	meiP26RNAi_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	6.80E-07
	meiP26OE_F_wMel	meiP261_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	2.87E-14
	meiP26OE_F_uninf	meiP26RNAi_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	7.96E-07
	meiP26OE_F_uninf	meiP261_F_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	< 2.2e-16
	meiP26OE_F_uninf	meiP26RNAi_F_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	4.19E-16
WT vs F mei-P26 OE	meiP26OE_F_wMel	WT_nos:Gal4_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	1.23E-06
	meiP26OE_F_wMel	WT_nos:Gal4_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	4.73E-09
	meiP26OE_F_uninf	WT_nos:Gal4_wMel	***	***	***	***	***	***	***	***	Fisher's exact test	5.24E-02
	meiP26OE_F_uninf	WT_nos:Gal4_uninf	***	***	***	***	***	***	***	***	Fisher's exact test	1.24E-03

table S14. Tumorous germline cyst counts. Normal cysts contain 16 germline-derived cells, 15 nurse cells and one oocyte. Cysts containing greater or less than 15 nurse cells were scored as tumorous or abnormal, respectively.

category	group1	group2	n1	Y	M	N	n2	Y	M	N	test	p-value
wild type (WT)	WT_OreR_wMel-5d	WT_OreR_uninf-5d	53	50	2	1	64	58	6	0	Fisher's Exact Test	2.09E-01
F mei-P26 knockdown	meiP261_F_wMel-5d	meiP261_F_uninf-5d	66	40	15	11	63	16	4	43	Fisher's Exact Test	5.85E-09
WT vs F mei-P26 knockdown	WT_OreR_uninf-5d	meiP261_F_uninf-5d	""	""	""	""	""	""	""	""	Fisher's Exact Test	< 2.2e-16
	WT_OreR_wMel-5d	meiP261_F_wMel-5d	""	""	""	""	""	""	""	""	Fisher's Exact Test	5.61E-05
	WT_OreR_wMel-5d	meiP261_F_uninf-5d	""	""	""	""	""	""	""	""	Fisher's Exact Test	4.51E-16
	WT_OreR_uninf-5d	meiP261_F_wMel-5d	""	""	""	""	""	""	""	""	Fisher's Exact Test	2.97E-05

table S15. Counts of germline cysts exhibiting oocyte-specific Orb expression (Y), unclear staining (M), or no specific expression, indicating developmentally abnormal cysts lacking specified oocytes.

protocol	Sample ID	# Read pairs	Yield (Mbases)	Mean Quality Score	% Bases >= 30	Dmel mapped reads	Dmel %	Dmel coverage (calculated)	wMel mapped reads	wMel %	wMel coverage (calculated)
ribodepletion	mei-P261uninfected-1	16566114	4970	35.28	90.31	26794060	80.87%	21.73	142	0.00%	0.02
ribodepletion	mei-P261uninfected-2	24371726	7312	35.23	90.06	39374606	80.78%	31.93	1644	0.00%	0.22
ribodepletion	mei-P261uninfected-3	20726752	6218	35.2	89.96	31465602	75.91%	25.52	130	0.00%	0.02
ribodepletion	mei-P261uninfected-4	22725501	6818	34.99	89.1	33541934	73.80%	27.20	4742	0.01%	0.65
ribodepletion	mei-P261uninfected-5	25921666	7776	35.29	90.4	41658014	80.35%	33.79	92	0.00%	0.01
ribodepletion	mei-P261uninfected-6	21289976	6387	35.38	90.8	32541844	76.43%	26.39	48	0.00%	0.01
ribodepletion	mei-P261wMel-1	30205483	9061	32.9	80.16	36362650	60.19%	29.49	57237	0.09%	7.83
ribodepletion	mei-P261wMel-3	22849556	6855	35.36	90.65	35184986	76.99%	28.54	62646	0.14%	8.57
ribodepletion	mei-P261wMel-4	26232731	7870	35.37	90.71	42053352	80.15%	34.11	118236	0.23%	16.18
ribodepletion	mei-P261wMel-5	23786557	7136	35.41	90.93	39184612	82.37%	31.78	87424	0.18%	11.96
ribodepletion	mei-P261wMel-7	26403318	7921	35.34	90.59	41693804	78.96%	33.82	96438	0.18%	13.20
ribodepletion	mei-P261wMel-8	24804635	7441	35.33	90.55	39188718	78.99%	31.78	80004	0.16%	10.95
ribodepletion	OreRF10uninfected-4	21514878	6454	35.41	90.95	33544436	77.96%	27.21	1670	0.00%	0.23
ribodepletion	OreRF10uninfected-5	21887003	6566	35.4	90.9	33751420	77.10%	27.37	978	0.00%	0.13
ribodepletion	OreRF10uninfected-6	22033197	6610	35.13	89.72	32014844	72.65%	25.97	926	0.00%	0.13
ribodepletion	OreRuninfected-1	22902974	6871	35.42	91	38142430	83.27%	30.94	1000	0.00%	0.14
ribodepletion	OreRuninfected-2	19424258	5827	35.3	90.37	32687632	84.14%	26.51	556	0.00%	0.08
ribodepletion	OreRuninfected-3	25244059	7573	35.25	90.13	39497260	78.23%	32.03	576	0.00%	0.08
ribodepletion	OreRwMelDB-1	23669962	7101	35.36	90.66	40049364	84.60%	32.48	69074	0.15%	9.45
ribodepletion	OreRwMelDB-2	21342747	6403	35.28	90.3	31878812	74.68%	25.86	129552	0.30%	17.73
ribodepletion	OreRwMelDB-3	20997126	6299	35.33	90.52	32964512	78.50%	26.74	272124	0.65%	37.23
ribodepletion	OreRwMelDB-4	26137488	7841	35.31	90.46	44312894	84.77%	35.94	186630	0.36%	25.54
ribodepletion	OreRwMelDB-6	23976948	7193	35.38	90.75	38740764	80.79%	31.42	310028	0.65%	42.42
ribodepletion	OreRwMelDB-7	23816174	7145	35.37	90.75	37387940	78.49%	30.32	228366	0.48%	31.25
poly-A	nos-meiP26RNAi-wMel-1-resub	72190715	21657	35.97	93.99	137328600	95.12%	111.38	3948	0.00%	0.54
poly-A	nos-meiP26RNAi-wMel-2-resub	65207225	19562	35.96	93.99	123616024	94.79%	100.26	2204	0.00%	0.30

poly-A	nos-meip26RNAi-wMel-3	67418318	20225	35.87	93.54	126461294	93.79%	102.57	6748	0.01%	0.92
poly-A	nosGal4CyO-wMel-1	63388028	19016	35.92	93.81	120645078	95.16%	97.85	7462	0.01%	1.02
poly-A	nosGal4CyO-wMel-2	71148881	21345	35.81	93.18	133691906	93.95%	108.43	5078	0.00%	0.69
poly-A	nosGal4CyO-wMel-3-re sub	67506892	20252	35.96	93.95	128140108	94.91%	103.93	3636	0.00%	0.50

table S16. Transcriptomic dataset generated to test the impacts of mei-P26 knockdown and wMel infection. Data deposited under NCBI BioProjectnumber PRJNA992140.

gene_id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Dmel_CG32581	498.502	-7.545	0.348	-21.705	1.85E-104	1.97E-100
Dmel_CG12218	12376.792	5.652	0.285	19.841	1.31E-87	7.01E-84
Dmel_CG42565	636.741	-4.964	0.276	-17.965	3.68E-72	1.31E-68
Dmel_CR34601	1403.059	8.261	0.467	17.692	4.87E-70	1.30E-66
Dmel_CG32640	167.387	-7.771	0.501	-15.517	2.67E-54	5.72E-51
Dmel_CG7408	343.022	5.184	0.347	14.940	1.80E-50	3.21E-47
Dmel_CG15601	142.969	4.618	0.317	14.557	5.24E-48	8.01E-45
Dmel_CG33801	977.281	-4.316	0.304	-14.175	1.32E-45	1.76E-42
Dmel_CR45330	212.370	-3.991	0.289	-13.796	2.70E-43	3.21E-40
Dmel_CG11825	247.162	-3.656	0.277	-13.206	8.11E-40	8.67E-37
Dmel_CG33816	11696.267	-9.588	0.748	-12.825	1.18E-37	1.15E-34
Dmel_CG32975	49.803	4.811	0.385	12.492	8.24E-36	7.34E-33
Dmel_CG7052	166.253	-3.532	0.284	-12.447	1.45E-35	1.19E-32
Dmel_CG31997	498.060	-4.245	0.349	-12.147	5.97E-34	4.56E-31
Dmel_CG32474	120.332	-7.181	0.592	-12.135	6.88E-34	4.90E-31
Dmel_CR43257	129.071	-3.145	0.261	-12.032	2.40E-33	1.60E-30
Dmel_CG42584	108.987	4.408	0.374	11.777	5.12E-32	3.22E-29
Dmel_CG8357	611.808	-2.670	0.229	-11.662	2.00E-31	1.19E-28
Dmel_CG32475	179.753	-10.041	0.863	-11.639	2.62E-31	1.47E-28
Dmel_CG2947	1490.588	1.955	0.171	11.448	2.42E-30	1.29E-27
Dmel_CG4125	840.725	3.748	0.333	11.237	2.67E-29	1.36E-26
Dmel_CR45284	114.416	9.866	0.890	11.083	1.51E-28	7.36E-26
Dmel_CR46123	510.503	-3.518	0.323	-10.877	1.48E-27	6.87E-25
Dmel_CG31683	923.718	7.381	0.681	10.838	2.28E-27	1.02E-24
Dmel_CR45631	72.040	-5.945	0.554	-10.723	7.91E-27	3.38E-24
Dmel_CG32600	181.352	3.164	0.296	10.680	1.26E-26	5.17E-24
Dmel_CG10013	137.097	-3.508	0.335	-10.471	1.17E-25	4.65E-23
Dmel_CG14233	178.085	-2.132	0.206	-10.352	4.09E-25	1.56E-22

Dmel_CG6864	56.941	5.134	0.497	10.322	5.61E-25	2.07E-22
Dmel_CG18321	353.613	-2.824	0.274	-10.309	6.39E-25	2.28E-22
Dmel_CG17684	1222.833	2.837	0.277	10.237	1.36E-24	4.69E-22
Dmel_CG13941	124.885	-2.456	0.246	-10.003	1.47E-23	4.92E-21
Dmel_CG8376	116.256	-3.033	0.304	-9.985	1.77E-23	5.75E-21
Dmel_CR45567	40.179	8.757	0.888	9.863	6.00E-23	1.89E-20
Dmel_CG9453	343.636	-2.445	0.248	-9.859	6.28E-23	1.92E-20
Dmel_CG32647	110.757	-3.051	0.313	-9.739	2.05E-22	6.09E-20
Dmel_CG34380	118.947	4.239	0.436	9.712	2.69E-22	7.77E-20
Dmel_CG18188	45.646	-3.579	0.369	-9.703	2.93E-22	8.25E-20
Dmel_CG13138	209.177	4.323	0.449	9.625	6.27E-22	1.72E-19
Dmel_CG18853	75.915	-8.396	0.873	-9.621	6.49E-22	1.74E-19
Dmel_CG33852	7295.263	4.955	0.520	9.520	1.74E-21	4.53E-19
Dmel_CG1842	581.392	2.211	0.238	9.302	1.38E-20	3.51E-18
Dmel_CG42255	42.513	-3.971	0.428	-9.277	1.74E-20	4.24E-18
Dmel_CG42699	188.299	1.987	0.214	9.278	1.72E-20	4.24E-18
Dmel_CG6269	43.176	-3.049	0.330	-9.228	2.76E-20	6.56E-18
Dmel_CG13937	148.226	4.624	0.502	9.215	3.10E-20	7.21E-18
Dmel_CG12112	1047.365	-2.129	0.232	-9.196	3.72E-20	8.46E-18
Dmel_CG17470	57.133	4.145	0.461	8.986	2.57E-19	5.73E-17
Dmel_CG5559	36.773	5.491	0.616	8.919	4.69E-19	1.02E-16
Dmel_CG15312	1267.851	1.384	0.156	8.881	6.65E-19	1.42E-16
Dmel_CG31792	38.167	-4.478	0.506	-8.851	8.70E-19	1.82E-16
Dmel_CG9871	50.560	-6.238	0.716	-8.715	2.90E-18	5.97E-16
Dmel_CG4373	307.928	-4.950	0.573	-8.646	5.35E-18	1.08E-15
Dmel_CG3616	38.041	-3.219	0.374	-8.597	8.15E-18	1.61E-15
Dmel_CG12592	187.503	-3.278	0.382	-8.580	9.47E-18	1.84E-15
Dmel_CG12505	3126.415	-2.939	0.344	-8.542	1.32E-17	2.52E-15
Dmel_CG5744	82.115	-4.651	0.545	-8.534	1.42E-17	2.66E-15
Dmel_CG3578	148.306	-1.836	0.217	-8.471	2.43E-17	4.40E-15
Dmel_CG9170	356.887	-2.386	0.282	-8.472	2.41E-17	4.40E-15

Dmel_CG9168	50.760	3.256	0.386	8.433	3.38E-17	6.03E-15
Dmel_CR34602	25.163	8.166	0.970	8.417	3.85E-17	6.75E-15
Dmel_CG12414	1841.851	1.885	0.225	8.376	5.48E-17	9.46E-15
Dmel_CG32823	73.681	3.720	0.452	8.232	1.85E-16	3.13E-14
Dmel_CR46499	109.382	-2.030	0.248	-8.197	2.46E-16	4.11E-14
Dmel_CG31776	24.796	-8.050	0.984	-8.184	2.74E-16	4.51E-14
Dmel_CG12520	87.565	-2.304	0.285	-8.082	6.36E-16	1.03E-13
Dmel_CG14855	58.734	2.874	0.356	8.081	6.44E-16	1.03E-13
Dmel_CG13579	22.440	-8.336	1.034	-8.059	7.69E-16	1.21E-13
Dmel_CG12275	39.817	-5.503	0.693	-7.944	1.96E-15	3.03E-13
Dmel_CG8821	106.295	3.716	0.473	7.864	3.71E-15	5.67E-13
Dmel_CG16755	68.579	2.852	0.364	7.839	4.54E-15	6.85E-13
Dmel_CR44264	17.002	7.192	0.922	7.803	6.05E-15	8.99E-13
Dmel_CG2893	2410.997	1.218	0.156	7.793	6.53E-15	9.56E-13
Dmel_CG7002	154.856	-3.554	0.457	-7.781	7.19E-15	1.04E-12
Dmel_CG32789	795.569	-1.531	0.197	-7.778	7.35E-15	1.05E-12
Dmel_CG31617	8715.429	2.006	0.258	7.769	7.90E-15	1.10E-12
Dmel_CG33813	8715.429	2.006	0.258	7.769	7.90E-15	1.10E-12
Dmel_CG16957	23.805	5.408	0.697	7.759	8.59E-15	1.18E-12
Dmel_CG7900	157.605	3.411	0.441	7.744	9.66E-15	1.31E-12
Dmel_CG14444	6588.810	-0.958	0.124	-7.713	1.23E-14	1.64E-12
Dmel_CG6658	157.093	-3.339	0.433	-7.707	1.29E-14	1.70E-12
Dmel_CG33868	2586.412	-2.187	0.284	-7.690	1.47E-14	1.92E-12
Dmel_CG15706	424.122	1.599	0.209	7.659	1.88E-14	2.42E-12
Dmel_CR43960	157.786	-2.537	0.334	-7.598	3.00E-14	3.82E-12
Dmel_CR46481	1090.588	-1.945	0.257	-7.572	3.68E-14	4.63E-12
Dmel_CR45323	25.859	-6.703	0.889	-7.541	4.68E-14	5.81E-12
Dmel_CG12846	131.084	-2.264	0.302	-7.490	6.87E-14	8.44E-12
Dmel_CG6890	2345.639	1.977	0.264	7.476	7.65E-14	9.30E-12
Dmel_CG18405	1312.377	1.367	0.183	7.474	7.77E-14	9.33E-12
Dmel_CG1232	80.890	-3.916	0.524	-7.467	8.21E-14	9.76E-12

Dmel_CG31865	120.039	-2.432	0.327	-7.436	1.04E-13	1.22E-11
Dmel_CG32364	249.152	-2.558	0.344	-7.434	1.06E-13	1.23E-11
Dmel_CG11144	634.856	-1.765	0.239	-7.392	1.45E-13	1.67E-11
Dmel_CG1449	290.556	-2.023	0.275	-7.345	2.05E-13	2.33E-11
Dmel_CG7665	49.711	-2.544	0.352	-7.224	5.05E-13	5.68E-11
Dmel_CG6293	2110.091	2.582	0.358	7.217	5.33E-13	5.94E-11
Dmel_CG14204	32.050	2.302	0.321	7.173	7.33E-13	8.08E-11
Dmel_CG11354	35.882	-2.429	0.341	-7.125	1.04E-12	1.14E-10
Dmel_CG14253	132.269	2.126	0.299	7.123	1.06E-12	1.14E-10
Dmel_CG11099	22.666	-5.708	0.802	-7.116	1.11E-12	1.19E-10
Dmel_CG33837	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33840	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33843	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33846	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33849	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33864	2738.319	-2.233	0.314	-7.108	1.18E-12	1.19E-10
Dmel_CG33655	51.654	3.304	0.467	7.074	1.50E-12	1.50E-10
Dmel_CG32490	168.640	-2.039	0.288	-7.073	1.52E-12	1.51E-10
Dmel_CR45446	23.752	5.109	0.724	7.056	1.71E-12	1.68E-10
Dmel_CG4587	91.859	-2.577	0.366	-7.044	1.87E-12	1.82E-10
Dmel_CG8034	387.147	-1.379	0.196	-7.030	2.06E-12	1.99E-10
Dmel_CG9981	21.353	-6.048	0.861	-7.027	2.11E-12	2.02E-10
Dmel_CG14102	550.744	1.420	0.203	7.003	2.50E-12	2.37E-10
Dmel_CG6424	1178.291	-1.063	0.152	-6.977	3.01E-12	2.82E-10
Dmel_CG12548	110.057	2.956	0.424	6.971	3.14E-12	2.92E-10
Dmel_CG31279	99.274	-2.625	0.377	-6.961	3.39E-12	3.13E-10
Dmel_CG15632	24.357	-6.024	0.867	-6.950	3.65E-12	3.33E-10
Dmel_CG14808	573.015	-2.613	0.376	-6.941	3.89E-12	3.52E-10
Dmel_CG14518	13.705	6.644	0.962	6.905	5.02E-12	4.48E-10
Dmel_CR46350	65.211	2.397	0.347	6.905	5.00E-12	4.48E-10
Dmel_CR32881	15.023	6.709	0.976	6.877	6.13E-12	5.42E-10

Dmel_CG5106	180.963	-2.039	0.298	-6.852	7.29E-12	6.39E-10
Dmel_CG4573	407.261	0.986	0.144	6.838	8.02E-12	6.97E-10
Dmel_CG15673	374.682	2.079	0.305	6.808	9.91E-12	8.55E-10
Dmel_CG32261	8.393	6.641	0.976	6.801	1.04E-11	8.87E-10
Dmel_CG32540	27.797	-5.848	0.863	-6.776	1.23E-11	1.05E-09
Dmel_CG40470	117.571	2.521	0.374	6.743	1.55E-11	1.30E-09
Dmel_CG10654	255.238	-1.959	0.291	-6.723	1.78E-11	1.48E-09
Dmel_CG32319	43.380	2.630	0.396	6.640	3.15E-11	2.61E-09
Dmel_CG13876	343.928	-1.331	0.202	-6.595	4.25E-11	3.47E-09
Dmel_CG17142	69.912	-1.977	0.300	-6.595	4.25E-11	3.47E-09
Dmel_CR44603	26.607	-6.925	1.050	-6.592	4.33E-11	3.51E-09
Dmel_CG13848	572.438	-1.490	0.226	-6.590	4.40E-11	3.53E-09
Dmel_CG4116	39.770	2.830	0.430	6.578	4.75E-11	3.79E-09
Dmel_CG8321	886.301	-1.178	0.181	-6.515	7.27E-11	5.76E-09
Dmel_CG2397	133.002	-1.613	0.248	-6.499	8.08E-11	6.36E-09
Dmel_CR44441	70.571	2.873	0.444	6.472	9.70E-11	7.57E-09
Dmel_CG4666	110.138	-2.471	0.383	-6.451	1.11E-10	8.62E-09
Dmel_CG32944	92.791	-2.040	0.317	-6.441	1.19E-10	9.12E-09
Dmel_CR44649	14.040	5.807	0.902	6.440	1.19E-10	9.12E-09
Dmel_CG3592	24.833	3.723	0.579	6.435	1.24E-10	9.39E-09
Dmel_CG15267	102.975	2.512	0.391	6.432	1.26E-10	9.51E-09
Dmel_CG4181	124.651	-2.626	0.408	-6.430	1.28E-10	9.54E-09
Dmel_CG33861	849.240	-2.803	0.438	-6.394	1.61E-10	1.20E-08
Dmel_CG5130	868.620	-1.343	0.212	-6.343	2.26E-10	1.67E-08
Dmel_CG42343	28.745	-2.528	0.399	-6.331	2.43E-10	1.78E-08
Dmel_CG12405	52.075	-1.899	0.300	-6.320	2.62E-10	1.90E-08
Dmel_CR34573	15.764	5.560	0.880	6.317	2.66E-10	1.92E-08
Dmel_CG14162	1349.763	1.374	0.219	6.270	3.61E-10	2.58E-08
Dmel_CG4500	7.493	6.350	1.013	6.270	3.60E-10	2.58E-08
Dmel_CG32204	31.301	-2.860	0.456	-6.268	3.66E-10	2.59E-08
Dmel_CG11372	1894.097	1.758	0.281	6.264	3.75E-10	2.62E-08

Dmel_CG3134	31.621	-3.101	0.495	-6.265	3.73E-10	2.62E-08
Dmel_CG11160	16.059	-5.132	0.820	-6.261	3.82E-10	2.66E-08
Dmel_CG3653	339.374	2.166	0.346	6.258	3.89E-10	2.68E-08
Dmel_CG3832	660.172	1.414	0.226	6.254	4.00E-10	2.74E-08
Dmel_CR31853	15.583	-6.169	0.987	-6.248	4.17E-10	2.84E-08
Dmel_CG46315	1065.167	-0.931	0.149	-6.227	4.75E-10	3.22E-08
Dmel_CG10062	88.652	-2.498	0.402	-6.217	5.06E-10	3.41E-08
Dmel_CG45019	491.689	-1.639	0.264	-6.213	5.19E-10	3.47E-08
Dmel_CG18495	1721.586	-1.927	0.311	-6.193	5.92E-10	3.93E-08
Dmel_CG14416	20.114	3.533	0.571	6.187	6.12E-10	4.04E-08
Dmel_CG30401	80.682	-2.540	0.412	-6.167	6.96E-10	4.56E-08
Dmel_CR44285	16.737	-4.535	0.738	-6.149	7.81E-10	5.09E-08
Dmel_CR44842	51.141	2.339	0.381	6.139	8.31E-10	5.39E-08
Dmel_CG6644	396.732	-2.312	0.377	-6.137	8.42E-10	5.41E-08
Dmel_CR43957	57.161	-2.135	0.348	-6.136	8.44E-10	5.41E-08
Dmel_CG30026	144.278	2.596	0.423	6.135	8.50E-10	5.41E-08
Dmel_CG11263	812.988	1.589	0.260	6.120	9.33E-10	5.91E-08
Dmel_CG17959	18.151	3.189	0.522	6.114	9.69E-10	6.10E-08
Dmel_CG32191	18.062	3.536	0.579	6.104	1.03E-09	6.45E-08
Dmel_CG15695	15.117	-5.448	0.899	-6.058	1.38E-09	8.58E-08
Dmel_CG8964	30.624	-2.560	0.424	-6.041	1.53E-09	9.48E-08
Dmel_CR46147	58.757	-1.968	0.326	-6.035	1.59E-09	9.77E-08
Dmel_CG13426	9.974	6.113	1.016	6.018	1.77E-09	1.08E-07
Dmel_CG6352	20.044	-3.623	0.602	-6.017	1.78E-09	1.08E-07
Dmel_CG4486	56.498	2.700	0.449	6.015	1.80E-09	1.09E-07
Dmel_CG6829	1109.723	1.216	0.204	5.975	2.30E-09	1.38E-07
Dmel_CG18766	417.316	1.249	0.209	5.962	2.49E-09	1.49E-07
Dmel_CG9475	65.197	-1.919	0.322	-5.959	2.53E-09	1.51E-07
Dmel_CG4381	408.162	-1.619	0.273	-5.941	2.84E-09	1.68E-07
Dmel_CG7863	307.615	1.102	0.186	5.935	2.94E-09	1.73E-07
Dmel_CG13540	16.816	-4.164	0.703	-5.924	3.14E-09	1.84E-07

Dmel_CG11940	4570.884	1.039	0.176	5.892	3.81E-09	2.21E-07
Dmel_CG45781	99.356	2.496	0.424	5.880	4.10E-09	2.37E-07
Dmel_CG1544	56.811	3.186	0.543	5.869	4.38E-09	2.52E-07
Dmel_CR41257	19.191	3.731	0.637	5.859	4.67E-09	2.67E-07
Dmel_CG13375	172.764	-1.742	0.298	-5.852	4.85E-09	2.76E-07
Dmel_CG7084	38.686	-3.722	0.638	-5.838	5.29E-09	2.99E-07
Dmel_CG12370	119.708	-2.318	0.398	-5.825	5.71E-09	3.20E-07
Dmel_CR43635	28.969	-2.640	0.453	-5.826	5.68E-09	3.20E-07
Dmel_CG3036	780.679	-1.187	0.204	-5.821	5.86E-09	3.27E-07
Dmel_CG13617	40.995	2.463	0.425	5.801	6.60E-09	3.66E-07
Dmel_CG42639	16.055	-4.825	0.832	-5.796	6.77E-09	3.73E-07
Dmel_CR44648	7.481	5.743	0.999	5.747	9.08E-09	4.98E-07
Dmel_CG32187	11.172	6.232	1.085	5.745	9.19E-09	5.02E-07
Dmel_CG10650	150.114	-1.962	0.342	-5.741	9.43E-09	5.12E-07
Dmel_CG17836	1929.733	-1.570	0.274	-5.732	9.94E-09	5.37E-07
Dmel_CR43605	66.687	2.061	0.360	5.719	1.07E-08	5.75E-07
Dmel_CG3588	32.672	2.561	0.448	5.716	1.09E-08	5.83E-07
Dmel_CG7433	4321.842	-0.989	0.174	-5.689	1.27E-08	6.78E-07
Dmel_CG9701	11.604	-4.237	0.747	-5.676	1.38E-08	7.27E-07
Dmel_CR32886	5281.077	-1.355	0.239	-5.676	1.38E-08	7.27E-07
Dmel_CG44193	1265.153	-1.120	0.198	-5.661	1.50E-08	7.84E-07
Dmel_CG9411	11.974	-4.948	0.874	-5.661	1.50E-08	7.84E-07
Dmel_CG12986	9.202	-5.950	1.054	-5.645	1.66E-08	8.60E-07
Dmel_CG42566	568.495	-2.099	0.372	-5.643	1.67E-08	8.62E-07
Dmel_CG18789	575.054	-1.270	0.226	-5.613	1.99E-08	1.02E-06
Dmel_CR42861	395.796	-1.322	0.236	-5.607	2.06E-08	1.06E-06
Dmel_CG10246	507.936	-1.118	0.200	-5.587	2.31E-08	1.17E-06
Dmel_CG2381	70.702	2.064	0.369	5.587	2.31E-08	1.17E-06
Dmel_CG8165	279.924	0.802	0.144	5.583	2.37E-08	1.19E-06
Dmel_CG42694	322.776	1.171	0.210	5.571	2.53E-08	1.27E-06
Dmel_CR43836	1370.913	1.125	0.202	5.567	2.58E-08	1.29E-06

Dmel_CG11280	82.750	1.787	0.322	5.545	2.94E-08	1.46E-06
Dmel_CG30046	65.427	1.783	0.322	5.539	3.05E-08	1.51E-06
Dmel_CR34151	2597.926	1.281	0.232	5.528	3.24E-08	1.60E-06
Dmel_CR44105	111.289	1.812	0.328	5.522	3.35E-08	1.65E-06
Dmel_CG3926	50.891	-2.071	0.375	-5.518	3.43E-08	1.68E-06
Dmel_CG15422	16.358	-3.229	0.589	-5.478	4.30E-08	2.08E-06
Dmel_CG7970	1818.632	-0.761	0.139	-5.478	4.31E-08	2.08E-06
Dmel_CR45600	123.977	-1.441	0.264	-5.466	4.62E-08	2.22E-06
Dmel_CR42871	50.583	-2.562	0.471	-5.439	5.36E-08	2.57E-06
Dmel_CG10962	178.967	2.521	0.464	5.433	5.55E-08	2.65E-06
Dmel_CR44370	668.992	1.879	0.348	5.400	6.65E-08	3.16E-06
Dmel_CG14591	15.962	-3.474	0.643	-5.399	6.71E-08	3.17E-06
Dmel_CG45002	81.687	2.435	0.451	5.397	6.79E-08	3.20E-06
Dmel_CR43887	48.400	-2.054	0.381	-5.391	6.99E-08	3.28E-06
Dmel_CG8193	9.669	-5.178	0.963	-5.378	7.53E-08	3.52E-06
Dmel_CG10693	63.837	-2.304	0.429	-5.370	7.89E-08	3.67E-06
Dmel_CG17657	833.649	0.932	0.174	5.368	7.97E-08	3.69E-06
Dmel_CG9922	1514.484	-1.367	0.255	-5.357	8.45E-08	3.89E-06
Dmel_CG4998	35.482	-2.912	0.545	-5.344	9.07E-08	4.16E-06
Dmel_CG14615	327.742	1.131	0.212	5.326	1.00E-07	4.58E-06
Dmel_CG17669	10.096	-4.037	0.759	-5.317	1.06E-07	4.80E-06
Dmel_CG16779	55.503	-2.362	0.445	-5.311	1.09E-07	4.93E-06
Dmel_CG3548	367.754	1.676	0.319	5.258	1.46E-07	6.58E-06
Dmel_CG1629	52.870	-1.812	0.345	-5.255	1.48E-07	6.66E-06
Dmel_CG8666	1194.885	-1.041	0.198	-5.247	1.55E-07	6.94E-06
Dmel_CG13780	102.811	-3.674	0.701	-5.241	1.60E-07	7.11E-06
Dmel_CG30048	8.917	-5.534	1.060	-5.222	1.77E-07	7.84E-06
Dmel_CG45544	25.811	-2.041	0.391	-5.219	1.80E-07	7.97E-06
Dmel_CG10390	88.576	-1.834	0.352	-5.206	1.93E-07	8.49E-06
Dmel_CR43461	15.553	-2.544	0.489	-5.205	1.94E-07	8.51E-06
Dmel_CG12535	350.714	-1.351	0.260	-5.192	2.08E-07	9.08E-06

Dmel_CG14026	3581.522	0.517	0.100	5.176	2.26E-07	9.83E-06
Dmel_CR43334	902.502	1.433	0.278	5.161	2.46E-07	1.07E-05
Dmel_CG31956	7.679	-5.030	0.975	-5.159	2.48E-07	1.07E-05
Dmel_CG8256	121.600	-1.630	0.317	-5.150	2.61E-07	1.12E-05
Dmel_CG14424	11.673	4.159	0.809	5.138	2.77E-07	1.18E-05
Dmel_CR45714	39.803	2.530	0.492	5.138	2.78E-07	1.18E-05
Dmel_CG5927	130.550	3.518	0.685	5.134	2.83E-07	1.20E-05
Dmel_CG42711	9.934	-5.047	0.984	-5.130	2.90E-07	1.23E-05
Dmel_CG5022	23.972	2.232	0.436	5.117	3.10E-07	1.31E-05
Dmel_CG10559	18.084	-2.548	0.498	-5.112	3.18E-07	1.33E-05
Dmel_CG42362	214.695	-1.187	0.232	-5.107	3.28E-07	1.37E-05
Dmel_CG42363	214.695	-1.187	0.232	-5.107	3.28E-07	1.37E-05
Dmel_CG10245	245.057	-1.401	0.275	-5.096	3.47E-07	1.44E-05
Dmel_CG12582	1823.184	0.794	0.156	5.095	3.48E-07	1.44E-05
Dmel_CG3346	377.229	1.460	0.287	5.090	3.59E-07	1.48E-05
Dmel_CG34313	123.277	-1.216	0.239	-5.082	3.73E-07	1.53E-05
Dmel_CR46488	96.924	2.110	0.416	5.077	3.83E-07	1.56E-05
Dmel_CR43283	44.621	4.945	0.975	5.074	3.90E-07	1.58E-05
Dmel_CG15705	4.557	5.773	1.138	5.072	3.94E-07	1.60E-05
Dmel_CG43798	14.265	-2.669	0.527	-5.068	4.02E-07	1.62E-05
Dmel_CG1851	132.622	-1.408	0.278	-5.063	4.12E-07	1.66E-05
Dmel_CG34329	9.708	-5.152	1.018	-5.060	4.20E-07	1.68E-05
Dmel_CG11186	154.593	2.035	0.403	5.044	4.55E-07	1.82E-05
Dmel_CG1631	6.321	-5.205	1.033	-5.039	4.69E-07	1.86E-05
Dmel_CG2671	15581.812	1.147	0.228	5.039	4.67E-07	1.86E-05
Dmel_CG10247	12.494	-3.256	0.647	-5.034	4.81E-07	1.90E-05
Dmel_CG44102	63.130	2.047	0.407	5.024	5.07E-07	1.99E-05
Dmel_CG44328	42.014	-2.179	0.436	-4.999	5.75E-07	2.25E-05
Dmel_CG3546	24.816	1.961	0.392	4.996	5.84E-07	2.28E-05
Dmel_CG3767	118.430	-1.757	0.352	-4.996	5.86E-07	2.28E-05
Dmel_CG10391	295.990	1.311	0.263	4.985	6.19E-07	2.40E-05

Dmel_CG32595	13.102	-3.220	0.647	-4.979	6.38E-07	2.46E-05
Dmel_CG31174	20.644	-1.919	0.386	-4.970	6.71E-07	2.58E-05
Dmel_CG3598	12.213	4.080	0.823	4.958	7.10E-07	2.72E-05
Dmel_CR34621	154.656	1.896	0.383	4.956	7.19E-07	2.75E-05
Dmel_CG10160	13.374	-3.030	0.613	-4.944	7.64E-07	2.90E-05
Dmel_CG10287	102.780	-1.638	0.331	-4.945	7.62E-07	2.90E-05
Dmel_CG11450	84.360	1.490	0.302	4.942	7.75E-07	2.93E-05
Dmel_CG31901	28.374	-3.474	0.703	-4.939	7.84E-07	2.95E-05
Dmel_CG8051	10.915	-2.609	0.529	-4.930	8.24E-07	3.09E-05
Dmel_CG45058	655.515	1.169	0.237	4.929	8.27E-07	3.09E-05
Dmel_CG31693	14.293	-3.563	0.724	-4.921	8.63E-07	3.22E-05
Dmel_CG3022	27.256	-2.367	0.482	-4.916	8.85E-07	3.29E-05
Dmel_CG30383	49.644	-1.689	0.344	-4.913	8.98E-07	3.32E-05
Dmel_CG13916	111.331	2.194	0.447	4.905	9.33E-07	3.44E-05
Dmel_CG11205	397.986	-1.798	0.368	-4.892	1.00E-06	3.67E-05
Dmel_CG32814	302.950	-1.768	0.362	-4.887	1.02E-06	3.75E-05
Dmel_CG10695	3201.672	-1.191	0.244	-4.886	1.03E-06	3.76E-05
Dmel_CG12763	27.517	-6.787	1.391	-4.878	1.07E-06	3.89E-05
Dmel_CR46284	5.583	-5.554	1.139	-4.878	1.07E-06	3.89E-05
Dmel_CG14173	20.836	2.596	0.533	4.872	1.11E-06	3.99E-05
Dmel_CG15083	836.327	-1.186	0.244	-4.861	1.17E-06	4.21E-05
Dmel_CG6502	1593.297	0.700	0.144	4.856	1.20E-06	4.31E-05
Dmel_CG14502	161.282	1.211	0.250	4.843	1.28E-06	4.57E-05
Dmel_CG11125	345.793	1.079	0.224	4.819	1.44E-06	5.14E-05
Dmel_CG17523	9.395	-2.831	0.588	-4.816	1.46E-06	5.19E-05
Dmel_CG31718	13.955	-2.733	0.568	-4.815	1.47E-06	5.21E-05
Dmel_CG13401	706.768	0.814	0.169	4.813	1.49E-06	5.24E-05
Dmel_CG8942	20.884	-3.571	0.742	-4.813	1.49E-06	5.24E-05
Dmel_CG34002	25.029	-2.108	0.439	-4.807	1.53E-06	5.38E-05
Dmel_CG34251	4.631	-5.622	1.173	-4.793	1.64E-06	5.74E-05
Dmel_CG12473	121.417	1.006	0.210	4.788	1.69E-06	5.86E-05

Dmel_CG12500	121.417	1.006	0.210	4.788	1.69E-06	5.86E-05
Dmel_CG30101	46.664	2.599	0.543	4.783	1.73E-06	5.99E-05
Dmel_CG10794	23.361	-6.086	1.273	-4.782	1.74E-06	5.99E-05
Dmel_CG32845	27.360	-2.062	0.431	-4.780	1.75E-06	6.02E-05
Dmel_CG18095	35.302	4.346	0.910	4.775	1.80E-06	6.12E-05
Dmel_CG6798	39.400	2.450	0.513	4.774	1.80E-06	6.12E-05
Dmel_CG8561	48.662	-2.040	0.427	-4.774	1.80E-06	6.12E-05
Dmel_CR45215	6.526	3.592	0.752	4.774	1.80E-06	6.12E-05
Dmel_CG13091	80.925	2.136	0.447	4.773	1.81E-06	6.14E-05
Dmel_CG31619	134.708	-1.970	0.413	-4.773	1.82E-06	6.14E-05
Dmel_CG17604	2294.672	1.027	0.215	4.769	1.85E-06	6.23E-05
Dmel_CG10089	69.275	1.575	0.331	4.758	1.96E-06	6.56E-05
Dmel_CG12730	69.324	1.436	0.303	4.742	2.11E-06	7.06E-05
Dmel_CG17885	29.019	-1.638	0.346	-4.739	2.15E-06	7.15E-05
Dmel_CG1343	8.774	-4.947	1.046	-4.730	2.24E-06	7.42E-05
Dmel_CG14420	15.867	2.736	0.578	4.731	2.24E-06	7.42E-05
Dmel_CG14489	4874.516	0.630	0.134	4.717	2.39E-06	7.89E-05
Dmel_CG4476	2247.740	1.223	0.259	4.714	2.43E-06	7.98E-05
Dmel_CG5976	1222.502	-1.007	0.214	-4.712	2.46E-06	8.06E-05
Dmel_CR34645	9.943	4.238	0.900	4.708	2.51E-06	8.20E-05
Dmel_CG33531	10.591	3.263	0.696	4.688	2.76E-06	9.02E-05
Dmel_CG2505	44.932	3.869	0.826	4.683	2.83E-06	9.21E-05
Dmel_CG9921	462.165	-1.269	0.271	-4.676	2.92E-06	9.46E-05
Dmel_CG4780	256.282	-1.154	0.247	-4.675	2.94E-06	9.48E-05
Dmel_CG32485	670.585	0.877	0.188	4.674	2.96E-06	9.51E-05
Dmel_CG33494	73.278	-2.457	0.526	-4.674	2.96E-06	9.51E-05
Dmel_CG14584	13.563	-2.618	0.561	-4.667	3.06E-06	9.80E-05
Dmel_CR46075	89.606	1.330	0.286	4.660	3.17E-06	1.01E-04
Dmel_CG4563	4.531	-5.693	1.222	-4.658	3.19E-06	1.02E-04
Dmel_CG11700	93.380	-1.222	0.263	-4.655	3.24E-06	1.03E-04
Dmel_CR32773	602.990	1.163	0.251	4.639	3.50E-06	1.11E-04

Dmel_CG42338	533.899	-1.121	0.242	-4.637	3.53E-06	1.11E-04
Dmel_CG1483	10242.605	1.798	0.389	4.626	3.73E-06	1.17E-04
Dmel_CG43867	1609.935	1.111	0.241	4.615	3.93E-06	1.23E-04
Dmel_CR46231	7.957	-5.437	1.179	-4.613	3.97E-06	1.24E-04
Dmel_CG32459	8.115	-3.873	0.840	-4.610	4.02E-06	1.25E-04
Dmel_CG17610	1299.127	0.816	0.177	4.604	4.14E-06	1.29E-04
Dmel_CG10816	140.617	-3.652	0.794	-4.601	4.21E-06	1.30E-04
Dmel_CG1464	109.018	1.495	0.325	4.601	4.20E-06	1.30E-04
Dmel_CR44833	413.121	-0.980	0.213	-4.601	4.21E-06	1.30E-04
Dmel_CG1922	81.028	2.023	0.440	4.596	4.32E-06	1.33E-04
Dmel_CG14356	31.409	2.251	0.490	4.594	4.36E-06	1.33E-04
Dmel_CG6986	148.456	-1.258	0.274	-4.594	4.35E-06	1.33E-04
Dmel_CG13636	2287.981	3.194	0.696	4.587	4.50E-06	1.37E-04
Dmel_CG8279	98.613	1.543	0.336	4.587	4.49E-06	1.37E-04
Dmel_CR34558	120.892	1.745	0.381	4.575	4.77E-06	1.45E-04
Dmel_CG2657	34.331	-2.251	0.492	-4.573	4.81E-06	1.45E-04
Dmel_CG46313	39.798	4.693	1.027	4.568	4.93E-06	1.48E-04
Dmel_CG30382	3253.403	-1.858	0.408	-4.552	5.31E-06	1.59E-04
Dmel_CG14686	5.867	-5.206	1.144	-4.550	5.35E-06	1.60E-04
Dmel_CG18568	26.606	1.474	0.324	4.549	5.39E-06	1.61E-04
Dmel_CG8023	8.117	-4.055	0.891	-4.549	5.39E-06	1.61E-04
Dmel_CG15347	570.453	-1.578	0.348	-4.531	5.88E-06	1.75E-04
Dmel_CG14948	111.422	-1.570	0.347	-4.521	6.17E-06	1.83E-04
Dmel_CG8825	1165.276	-1.305	0.289	-4.511	6.45E-06	1.91E-04
Dmel_CG3397	15.052	-2.800	0.621	-4.507	6.58E-06	1.94E-04
Dmel_CG11094	251.870	-1.553	0.345	-4.502	6.73E-06	1.98E-04
Dmel_CG9169	13.677	2.700	0.600	4.502	6.74E-06	1.98E-04
Dmel_CG11390	112.637	-2.243	0.498	-4.500	6.78E-06	1.98E-04
Dmel_CG43326	10.654	-2.837	0.631	-4.497	6.89E-06	2.01E-04
Dmel_CG10151	33.822	-2.032	0.452	-4.492	7.05E-06	2.05E-04
Dmel_CG9093	881.441	-0.757	0.169	-4.491	7.07E-06	2.05E-04

Dmel_CG2297	30.219	-2.497	0.556	-4.487	7.24E-06	2.09E-04
Dmel_CG14931	1536.983	1.612	0.359	4.485	7.29E-06	2.10E-04
Dmel_CG2528	8.511	-4.082	0.910	-4.485	7.30E-06	2.10E-04
Dmel_CG1092	40.559	-2.093	0.467	-4.481	7.44E-06	2.13E-04
Dmel_CG14688	934.841	-0.685	0.153	-4.476	7.60E-06	2.17E-04
Dmel_CG15820	1082.505	0.912	0.204	4.477	7.59E-06	2.17E-04
Dmel_CG43088	13.320	-3.076	0.689	-4.464	8.04E-06	2.29E-04
Dmel_CG4950	13.824	-3.830	0.858	-4.461	8.16E-06	2.31E-04
Dmel_CG3323	48.498	1.884	0.423	4.457	8.31E-06	2.35E-04
Dmel_CG33481	45.632	-1.894	0.425	-4.455	8.39E-06	2.36E-04
Dmel_CG8145	489.756	-0.916	0.206	-4.455	8.39E-06	2.36E-04
Dmel_CR43264	294.406	-1.474	0.331	-4.453	8.45E-06	2.37E-04
Dmel_CG11052	8.299	4.274	0.962	4.442	8.91E-06	2.50E-04
Dmel_CG1960	4602.892	0.621	0.140	4.441	8.96E-06	2.50E-04
Dmel_CG7727	134.263	1.172	0.265	4.429	9.48E-06	2.64E-04
Dmel_CG32165	1153.177	-1.572	0.355	-4.427	9.54E-06	2.65E-04
Dmel_CG9742	1047.738	-1.639	0.371	-4.423	9.75E-06	2.70E-04
Dmel_CG43366	29.454	-2.231	0.505	-4.420	9.89E-06	2.73E-04
Dmel_CG12470	17.654	-2.391	0.542	-4.408	1.04E-05	2.87E-04
Dmel_CG6128	36.042	-2.440	0.554	-4.403	1.07E-05	2.94E-04
Dmel_CG6698	17.300	-3.573	0.812	-4.401	1.08E-05	2.96E-04
Dmel_CG1443	162.341	1.837	0.418	4.393	1.12E-05	3.05E-04
Dmel_CG41520	200.878	1.460	0.332	4.392	1.12E-05	3.07E-04
Dmel_CG18437	12.750	-2.891	0.660	-4.380	1.19E-05	3.24E-04
Dmel_CR34575	10.820	2.843	0.650	4.377	1.20E-05	3.27E-04
Dmel_CG7391	327.485	1.327	0.304	4.365	1.27E-05	3.44E-04
Dmel_CG5080	19.507	-2.449	0.562	-4.355	1.33E-05	3.60E-04
Dmel_CG14907	262.745	-1.083	0.249	-4.348	1.37E-05	3.70E-04
Dmel_CG10638	1166.946	-0.953	0.219	-4.343	1.40E-05	3.77E-04
Dmel_CG42829	4.622	-5.282	1.218	-4.337	1.45E-05	3.88E-04
Dmel_CG7918	20.384	2.296	0.530	4.334	1.46E-05	3.91E-04

Dmel_CR32914	35.179	-1.441	0.333	-4.331	1.49E-05	3.97E-04
Dmel_CG42368	30.697	1.790	0.414	4.319	1.57E-05	4.17E-04
Dmel_CG10936	307.998	1.283	0.297	4.313	1.61E-05	4.28E-04
Dmel_CG14423	8.974	3.751	0.872	4.299	1.71E-05	4.54E-04
Dmel_CR43989	55.193	-1.304	0.304	-4.297	1.73E-05	4.57E-04
Dmel_CR44183	4.078	4.873	1.134	4.296	1.74E-05	4.58E-04
Dmel_CG6044	14.793	2.702	0.630	4.289	1.79E-05	4.71E-04
Dmel_CG2812	61.353	-1.769	0.413	-4.287	1.81E-05	4.75E-04
Dmel_CG1506	66.867	-1.574	0.368	-4.273	1.93E-05	5.04E-04
Dmel_CG4620	4335.134	0.799	0.187	4.268	1.97E-05	5.14E-04
Dmel_CG7549	52.479	-1.357	0.318	-4.265	2.00E-05	5.20E-04
Dmel_CG31519	27.150	-2.340	0.550	-4.252	2.12E-05	5.50E-04
Dmel_CG42281	10048.584	0.592	0.139	4.251	2.13E-05	5.50E-04
Dmel_CR43302	6.039	3.219	0.758	4.248	2.16E-05	5.57E-04
Dmel_CG17077	839.671	0.783	0.186	4.204	2.63E-05	6.77E-04
Dmel_CG11961	335.734	-0.664	0.158	-4.201	2.66E-05	6.84E-04
Dmel_CG1969	470.276	-0.499	0.119	-4.186	2.83E-05	7.27E-04
Dmel_CG5399	18.394	-2.327	0.557	-4.180	2.92E-05	7.47E-04
Dmel_CG1873	30.188	-2.071	0.496	-4.176	2.97E-05	7.57E-04
Dmel_CG32017	173.619	1.439	0.345	4.174	3.00E-05	7.63E-04
Dmel_CG12749	4132.742	-0.630	0.151	-4.169	3.07E-05	7.79E-04
Dmel_CG7152	41.498	1.793	0.430	4.168	3.08E-05	7.80E-04
Dmel_CG31601	12.167	-3.060	0.735	-4.163	3.13E-05	7.92E-04
Dmel_CR18854	838.629	0.990	0.238	4.163	3.14E-05	7.92E-04
Dmel_CG9580	35.037	-1.839	0.442	-4.162	3.15E-05	7.93E-04
Dmel_CG31618	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG33814	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG33817	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG33820	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG33823	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG33826	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04

Dmel_CG33829	2229.642	-0.953	0.229	-4.154	3.26E-05	8.07E-04
Dmel_CG5792	3509.804	0.710	0.171	4.152	3.29E-05	8.12E-04
Dmel_CR45923	329.714	1.048	0.252	4.152	3.30E-05	8.12E-04
Dmel_CG11714	5.974	-3.867	0.934	-4.141	3.46E-05	8.50E-04
Dmel_CG8638	7.909	-2.815	0.680	-4.139	3.49E-05	8.56E-04
Dmel_CR43609	35.121	-2.292	0.554	-4.138	3.51E-05	8.58E-04
Dmel_CG10723	53.062	-1.426	0.345	-4.134	3.57E-05	8.69E-04
Dmel_CG5322	43.751	-2.396	0.580	-4.134	3.56E-05	8.69E-04
Dmel_CG9380	914.006	2.463	0.596	4.130	3.62E-05	8.80E-04
Dmel_CG34360	2556.488	0.835	0.202	4.129	3.64E-05	8.84E-04
Dmel_CR44366	13.310	-1.815	0.440	-4.122	3.76E-05	9.11E-04
Dmel_CG7395	11.002	2.961	0.719	4.120	3.79E-05	9.16E-04
Dmel_CR43898	11.698	2.122	0.515	4.116	3.85E-05	9.27E-04
Dmel_CG1004	121.543	1.633	0.397	4.112	3.93E-05	9.44E-04
Dmel_CG31288	22.525	-2.495	0.609	-4.095	4.21E-05	1.01E-03
Dmel_CG10877	88.197	-1.683	0.411	-4.093	4.26E-05	1.02E-03
Dmel_CR32896	10.122	-3.330	0.814	-4.093	4.26E-05	1.02E-03
Dmel_CG17681	14.570	-2.303	0.563	-4.090	4.31E-05	1.03E-03
Dmel_CG5338	70.237	-2.034	0.498	-4.086	4.39E-05	1.04E-03
Dmel_CG15143	100.498	1.533	0.375	4.083	4.44E-05	1.05E-03
Dmel_CG6067	10.429	-3.312	0.811	-4.084	4.43E-05	1.05E-03
Dmel_CG7882	16.945	-4.855	1.190	-4.080	4.51E-05	1.07E-03
Dmel_CG14640	9.690	-2.996	0.735	-4.075	4.60E-05	1.08E-03
Dmel_CG30170	20.719	-2.277	0.560	-4.065	4.80E-05	1.13E-03
Dmel_CG14606	111.001	4.228	1.042	4.059	4.92E-05	1.15E-03
Dmel_CG42486	7.794	-2.105	0.520	-4.053	5.06E-05	1.18E-03
Dmel_CR44914	34.591	2.238	0.552	4.051	5.09E-05	1.19E-03
Dmel_CG15599	55.457	-2.241	0.553	-4.050	5.13E-05	1.20E-03
Dmel_CG17572	7.733	2.997	0.743	4.032	5.52E-05	1.28E-03
Dmel_CG33779	7.876	2.716	0.674	4.032	5.54E-05	1.28E-03
Dmel_CG9907	59.516	-1.325	0.329	-4.031	5.56E-05	1.29E-03

Dmel_CG32313	7.303	3.037	0.754	4.029	5.60E-05	1.29E-03
Dmel_CG3008	1125.630	-0.785	0.195	-4.025	5.69E-05	1.31E-03
Dmel_CG32082	143.362	-1.201	0.299	-4.012	6.03E-05	1.38E-03
Dmel_CG32381	6.858	-3.414	0.851	-4.012	6.02E-05	1.38E-03
Dmel_CR45199	15.610	2.262	0.564	4.011	6.05E-05	1.38E-03
Dmel_CR45580	8.928	-1.996	0.499	-4.003	6.26E-05	1.43E-03
Dmel_CG3857	518.727	0.838	0.210	3.997	6.43E-05	1.47E-03
Dmel_CG15034	80.952	1.369	0.343	3.991	6.59E-05	1.50E-03
Dmel_CG1683	61.082	-1.424	0.357	-3.988	6.67E-05	1.51E-03
Dmel_CG15598	8.615	2.751	0.690	3.985	6.75E-05	1.53E-03
Dmel_CG43389	9.534	-2.635	0.664	-3.969	7.21E-05	1.63E-03
Dmel_CG7149	511.711	0.872	0.220	3.958	7.55E-05	1.70E-03
Dmel_CG7383	5.086	-4.596	1.162	-3.956	7.62E-05	1.72E-03
Dmel_CG12477	8.616	-4.050	1.027	-3.944	8.01E-05	1.80E-03
Dmel_CG6125	90.955	-1.593	0.404	-3.944	8.03E-05	1.80E-03
Dmel_CR45029	87.357	1.013	0.257	3.944	8.02E-05	1.80E-03
Dmel_CG32365	2522.157	0.876	0.222	3.939	8.17E-05	1.82E-03
Dmel_CG43395	5.634	-3.479	0.884	-3.937	8.24E-05	1.84E-03
Dmel_CG32793	17.470	2.676	0.680	3.933	8.38E-05	1.86E-03
Dmel_CG9738	2394.475	-0.619	0.157	-3.933	8.39E-05	1.86E-03
Dmel_CG17570	6.795	2.553	0.650	3.931	8.47E-05	1.87E-03
Dmel_CG31262	1828.361	0.790	0.201	3.930	8.49E-05	1.88E-03
Dmel_CG11155	1048.739	-1.266	0.323	-3.917	8.97E-05	1.98E-03
Dmel_CG34431	161.743	-1.020	0.261	-3.910	9.22E-05	2.03E-03
Dmel_CG34031	23.601	-2.008	0.514	-3.905	9.43E-05	2.07E-03
Dmel_CG9780	15.302	-2.148	0.550	-3.902	9.54E-05	2.09E-03
Dmel_CR46268	170.251	-1.026	0.263	-3.901	9.58E-05	2.10E-03
Dmel_CG14643	29.737	-2.214	0.568	-3.897	9.75E-05	2.13E-03
Dmel_CG7542	10.141	2.826	0.726	3.892	9.92E-05	2.16E-03
Dmel_CG42598	119.404	3.509	0.902	3.891	1.00E-04	2.17E-03
Dmel_CG14616	5403.289	0.544	0.140	3.890	1.00E-04	2.17E-03

Dmel_CG17907	42.096	-1.423	0.366	-3.887	1.01E-04	2.19E-03
Dmel_CG3448	358.908	-0.949	0.244	-3.888	1.01E-04	2.19E-03
Dmel_CG42335	49.366	4.755	1.224	3.884	1.03E-04	2.21E-03
Dmel_CG15150	6.838	-3.981	1.025	-3.884	1.03E-04	2.21E-03
Dmel_CR42254	371.532	0.984	0.254	3.881	1.04E-04	2.24E-03
Dmel_CG10091	216.140	-1.617	0.417	-3.876	1.06E-04	2.27E-03
Dmel_CG3796	20.569	-1.603	0.414	-3.873	1.08E-04	2.30E-03
Dmel_CR45334	5.283	-3.658	0.946	-3.869	1.09E-04	2.34E-03
Dmel_CR42910	65.924	1.696	0.439	3.866	1.11E-04	2.36E-03
Dmel_CG14639	7.664	-3.024	0.783	-3.863	1.12E-04	2.37E-03
Dmel_CR42743	4.749	-4.446	1.151	-3.863	1.12E-04	2.37E-03
Dmel_CR44348	10.906	2.269	0.588	3.862	1.13E-04	2.39E-03
Dmel_CG33658	6.283	4.239	1.100	3.855	1.16E-04	2.45E-03
Dmel_CG5392	15.491	-1.899	0.493	-3.850	1.18E-04	2.49E-03
Dmel_CR44953	22.110	-1.841	0.479	-3.845	1.21E-04	2.54E-03
Dmel_CG33111	598.892	0.612	0.159	3.841	1.23E-04	2.58E-03
Dmel_CG14933	32.287	-2.019	0.526	-3.839	1.24E-04	2.59E-03
Dmel_CG31801	8.478	-2.242	0.585	-3.833	1.27E-04	2.65E-03
Dmel_CR45124	51.575	1.671	0.436	3.832	1.27E-04	2.65E-03
Dmel_CG12910	6.836	3.245	0.847	3.832	1.27E-04	2.65E-03
Dmel_CG31015	538.599	1.076	0.281	3.831	1.28E-04	2.66E-03
Dmel_CG1743	114.738	-1.366	0.357	-3.827	1.29E-04	2.69E-03
Dmel_CG8003	1339.184	0.620	0.162	3.825	1.31E-04	2.71E-03
Dmel_CG6701	6459.136	0.625	0.163	3.823	1.32E-04	2.72E-03
Dmel_CG4608	113.986	-1.184	0.310	-3.821	1.33E-04	2.75E-03
Dmel_CG12410	544.961	0.593	0.155	3.817	1.35E-04	2.77E-03
Dmel_CG44835	2748.099	0.677	0.177	3.818	1.35E-04	2.77E-03
Dmel_CG6324	34.299	-1.676	0.439	-3.818	1.34E-04	2.77E-03
Dmel_CG9472	10.918	2.066	0.542	3.812	1.38E-04	2.82E-03
Dmel_CG13793	53.229	1.552	0.408	3.808	1.40E-04	2.86E-03
Dmel_CG14757	107.605	0.895	0.235	3.802	1.44E-04	2.93E-03

Dmel_CG18408	587.102	0.741	0.195	3.799	1.45E-04	2.94E-03
Dmel_CG34357	51.034	1.339	0.352	3.800	1.45E-04	2.94E-03
Dmel_CG5455	372.518	-1.046	0.275	-3.800	1.45E-04	2.94E-03
Dmel_CG11356	13.659	-2.148	0.566	-3.794	1.48E-04	2.99E-03
Dmel_CR45577	14.166	2.232	0.588	3.795	1.48E-04	2.99E-03
Dmel_CG5644	28.092	1.858	0.491	3.787	1.52E-04	3.08E-03
Dmel_CG42813	353.216	1.405	0.371	3.787	1.53E-04	3.08E-03
Dmel_CR44230	13.634	-2.024	0.535	-3.784	1.54E-04	3.10E-03
Dmel_CG16778	54.657	2.348	0.621	3.779	1.57E-04	3.15E-03
Dmel_CG8588	597.074	1.012	0.268	3.774	1.61E-04	3.22E-03
Dmel_CR43242	104.596	1.334	0.354	3.772	1.62E-04	3.23E-03
Dmel_CR34626	1126.535	1.548	0.411	3.768	1.64E-04	3.28E-03
Dmel_CG41434	7.270	-3.616	0.961	-3.762	1.68E-04	3.35E-03
Dmel_CG8274	6007.375	-0.557	0.148	-3.762	1.69E-04	3.35E-03
Dmel_CG3104	56.006	-1.293	0.344	-3.758	1.71E-04	3.40E-03
Dmel_CG14062	3.626	-4.929	1.313	-3.754	1.74E-04	3.44E-03
Dmel_CG42294	6.836	-3.208	0.855	-3.752	1.75E-04	3.47E-03
Dmel_CG13604	682.846	0.784	0.209	3.749	1.78E-04	3.50E-03
Dmel_CG13970	20.195	-2.312	0.617	-3.748	1.78E-04	3.51E-03
Dmel_CG11049	56.984	-1.611	0.430	-3.743	1.82E-04	3.57E-03
Dmel_CG1894	11.141	-2.082	0.557	-3.735	1.88E-04	3.68E-03
Dmel_CG10469	24.417	-1.430	0.383	-3.730	1.92E-04	3.76E-03
Dmel_CG4260	7777.907	0.530	0.142	3.727	1.93E-04	3.78E-03
Dmel_CG10868	20270.917	0.732	0.197	3.726	1.95E-04	3.80E-03
Dmel_CG9968	1175.027	-0.709	0.191	-3.710	2.07E-04	4.03E-03
Dmel_CG12800	317.337	-1.068	0.288	-3.705	2.11E-04	4.11E-03
Dmel_CG10776	280.046	0.841	0.228	3.687	2.26E-04	4.40E-03
Dmel_CG31477	8.939	-2.314	0.631	-3.669	2.43E-04	4.71E-03
Dmel_CG31721	43.300	-1.874	0.511	-3.669	2.43E-04	4.71E-03
Dmel_CG30000	890.667	-1.008	0.275	-3.665	2.48E-04	4.78E-03
Dmel_CG10440	6.298	2.592	0.708	3.662	2.50E-04	4.81E-03

Dmel_CG18522	301.389	-1.437	0.392	-3.662	2.50E-04	4.81E-03
Dmel_CG4209	16.847	-1.945	0.531	-3.661	2.51E-04	4.82E-03
Dmel_CG42316	192.031	-1.525	0.417	-3.658	2.54E-04	4.88E-03
Dmel_CG13772	15.539	-2.247	0.614	-3.657	2.55E-04	4.88E-03
Dmel_CG9339	7193.178	0.491	0.134	3.657	2.55E-04	4.88E-03
Dmel_CG12662	86.071	1.509	0.413	3.656	2.56E-04	4.89E-03
Dmel_CG3359	1017.402	-0.873	0.239	-3.654	2.58E-04	4.91E-03
Dmel_CG2679	77.051	0.973	0.266	3.654	2.59E-04	4.91E-03
Dmel_CG12190	1070.714	0.942	0.258	3.652	2.60E-04	4.92E-03
Dmel_CG15879	82.055	0.980	0.268	3.652	2.60E-04	4.92E-03
Dmel_CG17352	58.907	2.070	0.567	3.650	2.62E-04	4.96E-03
Dmel_CG9165	1988.485	-1.065	0.292	-3.647	2.65E-04	5.01E-03
Dmel_CR45510	7.744	-3.035	0.833	-3.645	2.67E-04	5.03E-03
Dmel_CG31436	22.798	-1.887	0.519	-3.639	2.74E-04	5.14E-03
Dmel_CG40305	50.491	1.110	0.305	3.639	2.74E-04	5.14E-03
Dmel_CG2641	219.749	-0.803	0.221	-3.637	2.76E-04	5.17E-03
Dmel_CG33474	26.760	-1.370	0.377	-3.634	2.79E-04	5.22E-03
Dmel_CG34120	382.219	-0.954	0.263	-3.631	2.82E-04	5.26E-03
Dmel_CG8606	869.507	0.588	0.162	3.624	2.90E-04	5.40E-03
Dmel_CG6232	43.952	-1.009	0.279	-3.622	2.92E-04	5.43E-03
Dmel_CG34411	5.697	-3.139	0.868	-3.617	2.98E-04	5.53E-03
Dmel_CG2985	15846.085	-1.395	0.386	-3.613	3.03E-04	5.60E-03
Dmel_CG33855	661.466	1.268	0.351	3.613	3.03E-04	5.60E-03
Dmel_CG33858	661.466	1.268	0.351	3.613	3.03E-04	5.60E-03
Dmel_CG18313	6.700	2.594	0.719	3.609	3.07E-04	5.67E-03
Dmel_CG34325	218.050	-1.043	0.289	-3.608	3.08E-04	5.67E-03
Dmel_CG43749	68.898	-1.747	0.484	-3.608	3.08E-04	5.67E-03
Dmel_CR45822	59.722	1.856	0.515	3.606	3.11E-04	5.71E-03
Dmel_CG31300	10.149	-2.756	0.765	-3.603	3.15E-04	5.77E-03
Dmel_CG15828	114.025	-2.543	0.706	-3.601	3.17E-04	5.79E-03
Dmel_CG7565	530.624	0.618	0.172	3.588	3.33E-04	6.08E-03

Dmel_CG13624	4837.368	0.626	0.175	3.587	3.35E-04	6.10E-03
Dmel_CR45472	12.276	2.189	0.611	3.584	3.38E-04	6.15E-03
Dmel_CG1532	1363.500	-0.736	0.205	-3.581	3.43E-04	6.22E-03
Dmel_CG1971	113.016	-0.924	0.258	-3.580	3.44E-04	6.23E-03
Dmel_CG31687	689.422	-0.814	0.228	-3.577	3.47E-04	6.28E-03
Dmel_CG7737	406.711	-0.897	0.251	-3.576	3.49E-04	6.31E-03
Dmel_CG3837	293.345	0.924	0.258	3.574	3.51E-04	6.34E-03
Dmel_CG13659	14.223	-1.963	0.550	-3.566	3.62E-04	6.52E-03
Dmel_CG8819	502.091	-0.591	0.166	-3.566	3.63E-04	6.52E-03
Dmel_CG12099	2772.921	-0.642	0.180	-3.563	3.67E-04	6.57E-03
Dmel_CG9068	9.058	3.563	1.000	3.563	3.67E-04	6.57E-03
Dmel_CG10481	27.823	-1.465	0.412	-3.559	3.72E-04	6.66E-03
Dmel_CG14307	1087.564	0.958	0.269	3.557	3.75E-04	6.70E-03
Dmel_CG31918	958.032	-0.742	0.209	-3.551	3.83E-04	6.83E-03
Dmel_CG32354	36.624	-1.592	0.448	-3.551	3.84E-04	6.83E-03
Dmel_CR46216	14.209	-2.633	0.741	-3.551	3.84E-04	6.83E-03
Dmel_CG14472	25993.883	0.315	0.089	3.549	3.87E-04	6.86E-03
Dmel_CG7466	1646.183	-0.502	0.142	-3.539	4.02E-04	7.10E-03
Dmel_CR43303	10.440	2.706	0.765	3.539	4.02E-04	7.10E-03
Dmel_CG18102	3933.133	0.395	0.112	3.538	4.03E-04	7.11E-03
Dmel_CG9652	17.219	1.772	0.501	3.537	4.05E-04	7.13E-03
Dmel_CG12066	170.368	-0.917	0.259	-3.535	4.07E-04	7.16E-03
Dmel_CG45057	104.242	-1.329	0.376	-3.532	4.12E-04	7.23E-03
Dmel_CG9925	8017.743	0.506	0.143	3.530	4.15E-04	7.28E-03
Dmel_CG2759	71.072	-1.197	0.339	-3.528	4.18E-04	7.33E-03
Dmel_CG3159	17.200	-1.981	0.562	-3.527	4.21E-04	7.35E-03
Dmel_CG40006	2376.258	0.767	0.217	3.526	4.21E-04	7.35E-03
Dmel_CG3329	5252.860	-0.707	0.201	-3.522	4.28E-04	7.45E-03
Dmel_CR45260	5.707	4.054	1.153	3.517	4.37E-04	7.60E-03
Dmel_CR44330	9.131	2.344	0.667	3.516	4.38E-04	7.60E-03
Dmel_CG15784	293.016	-1.201	0.342	-3.513	4.43E-04	7.67E-03

Dmel_CG9390	2169.006	-0.876	0.249	-3.513	4.43E-04	7.67E-03
Dmel_CG43921	462.043	0.947	0.270	3.511	4.47E-04	7.72E-03
Dmel_CG43052	15.089	1.909	0.544	3.508	4.52E-04	7.79E-03
Dmel_CG17292	1474.083	0.696	0.199	3.503	4.59E-04	7.91E-03
Dmel_CG13384	2664.424	0.482	0.138	3.500	4.65E-04	8.00E-03
Dmel_CG3565	6.277	-3.306	0.945	-3.499	4.67E-04	8.01E-03
Dmel_CG10833	21.891	-4.331	1.239	-3.496	4.72E-04	8.10E-03
Dmel_CG13539	9.683	2.242	0.642	3.495	4.74E-04	8.12E-03
Dmel_CG3879	12.492	-2.007	0.575	-3.491	4.81E-04	8.21E-03
Dmel_CG13140	9.747	-1.950	0.559	-3.485	4.93E-04	8.37E-03
Dmel_CG3209	1529.199	0.411	0.118	3.485	4.93E-04	8.37E-03
Dmel_CG4472	34.227	-1.331	0.382	-3.485	4.93E-04	8.37E-03
Dmel_CG7874	21.781	-4.907	1.408	-3.486	4.91E-04	8.37E-03
Dmel_CG34141	119.156	0.971	0.279	3.477	5.08E-04	8.60E-03
Dmel_CG31866	314.021	0.646	0.186	3.475	5.10E-04	8.63E-03
Dmel_CR44793	9.708	-2.928	0.843	-3.474	5.12E-04	8.65E-03
Dmel_CG7997	780.900	0.530	0.153	3.474	5.13E-04	8.65E-03
Dmel_CR34635	8.396	2.244	0.646	3.473	5.15E-04	8.67E-03
Dmel_CG16956	123.954	1.533	0.442	3.466	5.28E-04	8.87E-03
Dmel_CG3929	5193.590	-0.960	0.277	-3.463	5.35E-04	8.98E-03
Dmel_CG9901	6113.781	0.361	0.104	3.462	5.36E-04	8.98E-03
Dmel_CG6618	40.165	1.385	0.401	3.456	5.48E-04	9.17E-03
Dmel_CR43607	38.001	1.008	0.292	3.454	5.52E-04	9.22E-03
Dmel_CG17527	10.179	-2.272	0.658	-3.453	5.55E-04	9.27E-03
Dmel_CR44024	22.499	1.792	0.520	3.447	5.67E-04	9.45E-03
Dmel_CG3091	43.997	-1.541	0.447	-3.445	5.70E-04	9.49E-03
Dmel_CG7644	30.473	-1.781	0.517	-3.445	5.71E-04	9.49E-03
Dmel_CR45789	14.109	1.924	0.560	3.438	5.86E-04	9.72E-03
Dmel_CG30385	5.769	-2.845	0.829	-3.433	5.96E-04	9.84E-03
Dmel_CG4995	6.334	-2.402	0.700	-3.433	5.97E-04	9.84E-03
Dmel_CG6704	461.899	1.126	0.328	3.433	5.96E-04	9.84E-03

Dmel_CR43949	41.829	1.450	0.422	3.433	5.97E-04	9.84E-03
Dmel_CG10241	394.726	1.066	0.311	3.430	6.03E-04	9.87E-03
Dmel_CG10683	1174.214	0.730	0.213	3.431	6.02E-04	9.87E-03
Dmel_CG13516	62.853	-1.387	0.404	-3.430	6.03E-04	9.87E-03
Dmel_CG32350	8070.134	0.783	0.228	3.430	6.03E-04	9.87E-03
Dmel_CR32875	15.889	2.368	0.690	3.431	6.02E-04	9.87E-03
Dmel_CG10334	1524.281	0.510	0.149	3.430	6.04E-04	9.87E-03
Dmel_CG8595	16.500	1.613	0.471	3.428	6.08E-04	9.91E-03
Dmel_CG14898	511.421	0.874	0.255	3.425	6.15E-04	1.00E-02
Dmel_CG44246	646.353	0.760	0.222	3.423	6.20E-04	1.01E-02
Dmel_CG7224	1716.811	0.836	0.244	3.421	6.24E-04	1.01E-02
Dmel_CG15269	8.248	-3.161	0.924	-3.420	6.26E-04	1.01E-02
Dmel_CG40160	3039.300	0.735	0.215	3.418	6.31E-04	1.02E-02
Dmel_CR42452	1770.822	1.031	0.302	3.417	6.34E-04	1.02E-02
Dmel_CG9919	9.509	-2.393	0.701	-3.415	6.38E-04	1.03E-02
Dmel_CG16896	1701.150	0.433	0.127	3.412	6.46E-04	1.04E-02
Dmel_CG6604	39.186	1.492	0.437	3.412	6.46E-04	1.04E-02
Dmel_CG3314	19145.955	-1.176	0.345	-3.411	6.48E-04	1.04E-02
Dmel_CG14218	17.215	2.344	0.688	3.407	6.56E-04	1.05E-02
Dmel_CG13982	106.094	-1.105	0.324	-3.407	6.58E-04	1.05E-02
Dmel_CG10514	44.024	-3.242	0.952	-3.404	6.64E-04	1.06E-02
Dmel_CG4859	83.161	-1.139	0.335	-3.404	6.65E-04	1.06E-02
Dmel_CG18507	93.141	1.294	0.381	3.401	6.71E-04	1.07E-02
Dmel_CG8550	20.847	-2.053	0.604	-3.402	6.69E-04	1.07E-02
Dmel_CG9353	452.173	-1.013	0.298	-3.401	6.70E-04	1.07E-02
Dmel_CR43589	107.488	1.689	0.497	3.400	6.75E-04	1.07E-02
Dmel_CG14995	758.069	0.822	0.242	3.397	6.81E-04	1.08E-02
Dmel_CG42606	8.504	2.328	0.685	3.397	6.80E-04	1.08E-02
Dmel_CG11284	4635.783	0.581	0.171	3.390	7.00E-04	1.11E-02
Dmel_CG12342	308.203	1.065	0.314	3.389	7.01E-04	1.11E-02
Dmel_CG42365	650.988	-0.730	0.215	-3.387	7.05E-04	1.11E-02

Dmel_CG5096	38.054	-1.443	0.427	-3.382	7.18E-04	1.13E-02
Dmel_CG3984	9.224	3.722	1.101	3.382	7.20E-04	1.13E-02
Dmel_CR44756	369.555	0.923	0.273	3.378	7.30E-04	1.15E-02
Dmel_CG4700	8378.432	0.563	0.167	3.376	7.37E-04	1.15E-02
Dmel_CG9177	13081.628	0.723	0.214	3.375	7.38E-04	1.15E-02
Dmel_CG6718	2868.486	0.799	0.237	3.374	7.40E-04	1.16E-02
Dmel_CG46440	920.684	0.589	0.175	3.374	7.42E-04	1.16E-02
Dmel_CG18131	15.976	-1.772	0.525	-3.372	7.45E-04	1.16E-02
Dmel_CR44472	23.272	1.695	0.503	3.373	7.44E-04	1.16E-02
Dmel_CG8891	326.888	-1.078	0.320	-3.369	7.55E-04	1.17E-02
Dmel_CG43346	278.496	-1.055	0.313	-3.368	7.58E-04	1.17E-02
Dmel_CG14053	287.028	0.654	0.194	3.366	7.64E-04	1.18E-02
Dmel_CG4484	163.176	1.219	0.362	3.363	7.72E-04	1.19E-02
Dmel_CG7449	30.833	1.278	0.380	3.361	7.75E-04	1.20E-02
Dmel_CR45171	45.239	-1.316	0.392	-3.359	7.82E-04	1.20E-02
Dmel_CG31075	302.346	-1.178	0.351	-3.358	7.85E-04	1.21E-02
Dmel_CG31495	548.374	-0.665	0.198	-3.358	7.85E-04	1.21E-02
Dmel_CG2239	26.138	-1.554	0.463	-3.354	7.96E-04	1.22E-02
Dmel_CR34555	357.248	1.901	0.567	3.352	8.03E-04	1.23E-02
Dmel_CG30361	21.616	1.814	0.541	3.351	8.04E-04	1.23E-02
Dmel_CG5370	1911.098	-0.532	0.159	-3.349	8.11E-04	1.24E-02
Dmel_CG9331	286.658	-0.670	0.200	-3.347	8.17E-04	1.25E-02
Dmel_CG9173	16.362	1.790	0.535	3.346	8.19E-04	1.25E-02
Dmel_CG12789	42.944	-1.243	0.371	-3.345	8.22E-04	1.25E-02
Dmel_CG9586	483.605	-0.903	0.270	-3.344	8.25E-04	1.25E-02
Dmel_CR34531	17.468	-2.141	0.641	-3.343	8.30E-04	1.26E-02
Dmel_CG34235	13.980	1.569	0.470	3.341	8.34E-04	1.26E-02
Dmel_CG13855	5.891	-3.022	0.905	-3.339	8.41E-04	1.27E-02
Dmel_CG10315	393.534	-0.984	0.295	-3.333	8.58E-04	1.30E-02
Dmel_CG13833	4.924	-3.643	1.093	-3.332	8.61E-04	1.30E-02
Dmel_CG8389	831.413	0.536	0.161	3.331	8.64E-04	1.30E-02

Dmel_CR45121	50.125	1.516	0.455	3.331	8.64E-04	1.30E-02
Dmel_CG12344	38.021	-1.307	0.392	-3.330	8.69E-04	1.31E-02
Dmel_CG31666	208.145	-0.975	0.293	-3.327	8.76E-04	1.31E-02
Dmel_CG15362	501.697	-0.726	0.218	-3.327	8.79E-04	1.32E-02
Dmel_CG6282	29.876	-1.687	0.508	-3.322	8.93E-04	1.34E-02
Dmel_CG18155	80.770	1.100	0.331	3.321	8.97E-04	1.34E-02
Dmel_CG18550	29.990	-1.155	0.348	-3.321	8.97E-04	1.34E-02
Dmel_CG14644	19.112	-1.835	0.553	-3.319	9.03E-04	1.34E-02
Dmel_CG33978	236.502	-1.110	0.335	-3.316	9.12E-04	1.36E-02
Dmel_CG6953	7.399	-2.783	0.841	-3.308	9.38E-04	1.39E-02
Dmel_CG9155	396.786	-0.873	0.264	-3.308	9.39E-04	1.39E-02
Dmel_CR44841	147.190	2.036	0.616	3.304	9.53E-04	1.41E-02
Dmel_CR43278	17.357	1.816	0.550	3.303	9.56E-04	1.41E-02
Dmel_CG16727	9.877	-2.937	0.890	-3.302	9.59E-04	1.42E-02
Dmel_CG43772	8.841	2.289	0.694	3.299	9.70E-04	1.43E-02
Dmel_CG30058	14.018	1.569	0.476	3.295	9.85E-04	1.45E-02
Dmel_CG9503	341.519	-0.705	0.214	-3.294	9.86E-04	1.45E-02
Dmel_CG8453	48.480	-2.074	0.630	-3.292	9.95E-04	1.46E-02
Dmel_CG6202	3774.453	0.413	0.125	3.290	1.00E-03	1.47E-02
Dmel_CG9203	680.819	0.559	0.170	3.284	1.02E-03	1.50E-02
Dmel_CG10424	667.728	-0.482	0.147	-3.282	1.03E-03	1.51E-02
Dmel_CR34535	12.981	-2.039	0.621	-3.283	1.03E-03	1.51E-02
Dmel_CR45335	4.273	-3.693	1.126	-3.280	1.04E-03	1.51E-02
Dmel_CR46485	143.767	0.819	0.250	3.280	1.04E-03	1.51E-02
Dmel_CG5381	714.190	-0.894	0.273	-3.277	1.05E-03	1.53E-02
Dmel_CG42292	4.012	-3.931	1.201	-3.274	1.06E-03	1.54E-02
Dmel_CR45225	15.865	-1.435	0.438	-3.274	1.06E-03	1.54E-02
Dmel_CG11500	360.013	-0.970	0.297	-3.270	1.07E-03	1.55E-02
Dmel_CG32639	35.139	1.443	0.441	3.271	1.07E-03	1.55E-02
Dmel_CG30428	377.270	0.990	0.303	3.269	1.08E-03	1.56E-02
Dmel_CG5905	30.547	-1.520	0.465	-3.268	1.08E-03	1.57E-02

Dmel_CR34570	18.906	1.670	0.511	3.266	1.09E-03	1.57E-02
Dmel_CG12484	15.035	1.633	0.500	3.264	1.10E-03	1.58E-02
Dmel_CG9509	63.869	-1.305	0.400	-3.264	1.10E-03	1.58E-02
Dmel_CG12493	49.069	-1.106	0.339	-3.262	1.11E-03	1.59E-02
Dmel_CR46048	204.191	1.157	0.355	3.262	1.11E-03	1.59E-02
Dmel_CG12242	24.371	-1.881	0.577	-3.258	1.12E-03	1.61E-02
Dmel_CR33987	5.856	-3.176	0.976	-3.253	1.14E-03	1.63E-02
Dmel_CG11254	2543.570	0.494	0.152	3.253	1.14E-03	1.63E-02
Dmel_CR45052	9.726	1.810	0.557	3.252	1.15E-03	1.63E-02
Dmel_CG3180	5430.417	0.472	0.145	3.251	1.15E-03	1.64E-02
Dmel_CG13162	4958.261	0.650	0.200	3.248	1.16E-03	1.65E-02
Dmel_CG12355	88.195	1.418	0.438	3.239	1.20E-03	1.70E-02
Dmel_CG31661	694.811	1.283	0.396	3.239	1.20E-03	1.70E-02
Dmel_CG3533	709.897	0.595	0.184	3.240	1.20E-03	1.70E-02
Dmel_CG31760	6.061	-2.663	0.823	-3.235	1.22E-03	1.72E-02
Dmel_CG3526	23.555	1.393	0.431	3.234	1.22E-03	1.72E-02
Dmel_CG30345	500.338	-0.774	0.240	-3.227	1.25E-03	1.76E-02
Dmel_CG11937	394.841	1.254	0.389	3.226	1.26E-03	1.77E-02
Dmel_CG12692	6.274	-2.248	0.697	-3.226	1.26E-03	1.77E-02
Dmel_CG7938	124.712	-1.225	0.380	-3.225	1.26E-03	1.77E-02
Dmel_CG9281	6711.799	0.780	0.242	3.223	1.27E-03	1.78E-02
Dmel_CG14620	142.968	0.811	0.252	3.220	1.28E-03	1.79E-02
Dmel_CG43161	11.588	-1.841	0.572	-3.220	1.28E-03	1.79E-02
Dmel_CG12295	35.781	1.357	0.422	3.217	1.30E-03	1.81E-02
Dmel_CG32572	6.465	2.419	0.752	3.215	1.30E-03	1.82E-02
Dmel_CG3964	83.092	-1.019	0.317	-3.215	1.30E-03	1.82E-02
Dmel_CG8532	1616.996	-0.506	0.157	-3.216	1.30E-03	1.82E-02
Dmel_CG1618	539.997	0.960	0.299	3.214	1.31E-03	1.82E-02
Dmel_CG7672	11.702	1.904	0.593	3.211	1.32E-03	1.84E-02
Dmel_CG14419	12.691	1.942	0.605	3.209	1.33E-03	1.85E-02
Dmel_CG3239	15.410	-3.234	1.008	-3.208	1.34E-03	1.85E-02

Dmel_CG4821	225.884	-0.959	0.299	-3.206	1.35E-03	1.86E-02
Dmel_CG12194	17.091	-1.938	0.605	-3.204	1.36E-03	1.88E-02
Dmel_CG3252	14.207	-2.242	0.701	-3.199	1.38E-03	1.90E-02
Dmel_CG10207	23.822	-2.141	0.670	-3.197	1.39E-03	1.91E-02
Dmel_CG6449	103.030	-0.934	0.292	-3.197	1.39E-03	1.91E-02
Dmel_CG7221	353.424	0.505	0.158	3.192	1.41E-03	1.94E-02
Dmel_CR43866	19.789	1.269	0.397	3.192	1.41E-03	1.94E-02
Dmel_CR46451	4.256	-2.936	0.920	-3.192	1.42E-03	1.94E-02
Dmel_CG10630	13.277	-2.498	0.783	-3.191	1.42E-03	1.94E-02
Dmel_CG43968	34.300	-1.639	0.514	-3.190	1.42E-03	1.94E-02
Dmel_CG42326	4.987	-2.601	0.816	-3.189	1.43E-03	1.95E-02
Dmel_CG7083	1256.892	0.491	0.154	3.187	1.44E-03	1.96E-02
Dmel_CG11951	16.133	-1.770	0.556	-3.181	1.47E-03	2.00E-02
Dmel_CG33988	8.586	-1.871	0.588	-3.181	1.47E-03	2.00E-02
Dmel_CG42732	1224.002	0.612	0.193	3.180	1.47E-03	2.00E-02
Dmel_CG11255	998.369	-0.899	0.283	-3.179	1.48E-03	2.01E-02
Dmel_CG3918	1166.254	-0.917	0.289	-3.177	1.49E-03	2.02E-02
Dmel_CG10444	1982.603	-0.834	0.263	-3.176	1.49E-03	2.02E-02
Dmel_CG11387	867.178	0.889	0.280	3.172	1.51E-03	2.05E-02
Dmel_CG2857	23.133	-1.681	0.530	-3.172	1.51E-03	2.05E-02
Dmel_CG4496	194.538	0.797	0.252	3.166	1.55E-03	2.08E-02
Dmel_CG4715	932.204	1.110	0.351	3.165	1.55E-03	2.08E-02
Dmel_CG7054	954.374	0.660	0.209	3.165	1.55E-03	2.08E-02
Dmel_CR44987	153.397	0.870	0.275	3.166	1.55E-03	2.08E-02
Dmel_CG13871	15.439	2.691	0.851	3.163	1.56E-03	2.10E-02
Dmel_CG7497	146.135	-0.872	0.276	-3.162	1.57E-03	2.10E-02
Dmel_CG3176	41.451	-1.512	0.478	-3.161	1.57E-03	2.10E-02
Dmel_CR45471	11.922	1.836	0.581	3.161	1.57E-03	2.10E-02
Dmel_CG15102	2050.109	-0.525	0.166	-3.160	1.58E-03	2.11E-02
Dmel_CG44880	229.239	0.758	0.240	3.160	1.58E-03	2.11E-02
Dmel_CG30106	16.974	-2.048	0.649	-3.154	1.61E-03	2.14E-02

Dmel_CG5059	2186.489	0.800	0.254	3.152	1.62E-03	2.16E-02
Dmel_CG32373	792.364	1.121	0.356	3.148	1.65E-03	2.18E-02
Dmel_CR46029	29.522	-1.437	0.457	-3.148	1.64E-03	2.18E-02
Dmel_CG33181	2963.425	0.751	0.239	3.146	1.65E-03	2.19E-02
Dmel_CG5041	570.781	0.613	0.195	3.144	1.67E-03	2.20E-02
Dmel_CG11892	208.524	-2.690	0.856	-3.142	1.68E-03	2.22E-02
Dmel_CG8864	7.182	-3.023	0.962	-3.142	1.68E-03	2.22E-02
Dmel_CG5391	5.261	2.931	0.933	3.140	1.69E-03	2.23E-02
Dmel_CG33126	197.114	-1.147	0.366	-3.137	1.71E-03	2.24E-02
Dmel_CG9460	9.877	-1.909	0.608	-3.137	1.70E-03	2.24E-02
Dmel_CG33140	6.012	-2.506	0.800	-3.134	1.73E-03	2.27E-02
Dmel_CG5835	43.348	-0.978	0.312	-3.133	1.73E-03	2.27E-02
Dmel_CG3254	25.889	-1.471	0.470	-3.132	1.74E-03	2.28E-02
Dmel_CG34161	8.362	-2.108	0.674	-3.129	1.75E-03	2.29E-02
Dmel_CR34335	36494.636	-1.023	0.327	-3.127	1.76E-03	2.31E-02
Dmel_CG18870	2820.357	0.447	0.143	3.126	1.77E-03	2.32E-02
Dmel_CG10702	1150.706	0.814	0.261	3.124	1.78E-03	2.33E-02
Dmel_CG10734	120.828	0.968	0.310	3.121	1.80E-03	2.34E-02
Dmel_CG13784	2273.112	0.439	0.141	3.120	1.81E-03	2.35E-02
Dmel_CR32957	2001.447	0.688	0.221	3.120	1.81E-03	2.35E-02
Dmel_CG6503	26.425	-3.794	1.216	-3.119	1.81E-03	2.35E-02
Dmel_CG30334	16.024	1.724	0.553	3.119	1.82E-03	2.35E-02
Dmel_CG34331	7.516	-2.857	0.917	-3.114	1.85E-03	2.39E-02
Dmel_CG6584	2008.800	0.434	0.139	3.113	1.85E-03	2.40E-02
Dmel_CG4733	177.034	0.838	0.269	3.111	1.86E-03	2.41E-02
Dmel_CG9456	35.892	-1.475	0.475	-3.108	1.89E-03	2.43E-02
Dmel_CG9650	454.888	-0.791	0.255	-3.106	1.90E-03	2.45E-02
Dmel_CG15309	1390.190	0.451	0.145	3.105	1.90E-03	2.45E-02
Dmel_CR43962	8.553	-2.440	0.786	-3.103	1.92E-03	2.47E-02
Dmel_CG2060	1551.905	0.661	0.213	3.102	1.92E-03	2.47E-02
Dmel_CG41284	85.265	1.643	0.531	3.096	1.96E-03	2.51E-02

Dmel_CG8380	8.756	1.965	0.635	3.095	1.97E-03	2.52E-02
Dmel_CG31365	1258.248	0.778	0.251	3.094	1.98E-03	2.53E-02
Dmel_CG5612	169.169	-0.991	0.321	-3.091	2.00E-03	2.55E-02
Dmel_CG8083	13.191	-1.741	0.563	-3.091	2.00E-03	2.55E-02
Dmel_CG3705	1508.729	-0.635	0.205	-3.090	2.00E-03	2.55E-02
Dmel_CG13282	99.633	-1.054	0.341	-3.088	2.01E-03	2.56E-02
Dmel_CG16799	9.929	-2.275	0.737	-3.087	2.02E-03	2.57E-02
Dmel_CG12346	351.844	-0.783	0.254	-3.084	2.04E-03	2.59E-02
Dmel_CG10005	59.957	-1.055	0.342	-3.084	2.04E-03	2.59E-02
Dmel_CG12002	217.218	-1.329	0.432	-3.079	2.08E-03	2.63E-02
Dmel_CG12684	9.256	2.071	0.673	3.079	2.08E-03	2.63E-02
Dmel_CG17795	17.109	-1.962	0.638	-3.077	2.09E-03	2.64E-02
Dmel_CG17217	8.090	-2.152	0.700	-3.075	2.10E-03	2.65E-02
Dmel_CG6071	45.004	1.312	0.427	3.076	2.10E-03	2.65E-02
Dmel_CG18548	12.434	-1.665	0.542	-3.074	2.11E-03	2.66E-02
Dmel_CG7595	4521.269	0.400	0.130	3.072	2.13E-03	2.67E-02
Dmel_CG11634	4.279	-3.755	1.222	-3.071	2.13E-03	2.68E-02
Dmel_CG9207	300.491	-0.757	0.247	-3.069	2.15E-03	2.69E-02
Dmel_CR33686	13262.350	0.888	0.289	3.068	2.15E-03	2.70E-02
Dmel_CG17716	19.533	-1.772	0.578	-3.066	2.17E-03	2.71E-02
Dmel_CG40298	76.791	1.427	0.465	3.065	2.17E-03	2.72E-02
Dmel_CG17970	165.747	0.974	0.318	3.063	2.19E-03	2.74E-02
Dmel_CG7041	1004.052	0.604	0.197	3.063	2.19E-03	2.74E-02
Dmel_CG8339	1557.479	0.337	0.110	3.063	2.19E-03	2.74E-02
Dmel_CG32506	9.534	-1.944	0.635	-3.062	2.20E-03	2.74E-02
Dmel_CG9772	2989.847	0.486	0.159	3.060	2.21E-03	2.75E-02
Dmel_CG30047	10.082	-2.525	0.827	-3.055	2.25E-03	2.80E-02
Dmel_CG4257	9979.136	0.364	0.119	3.054	2.26E-03	2.80E-02
Dmel_CG5778	6.358	-1.972	0.646	-3.052	2.27E-03	2.81E-02
Dmel_CG6677	880.216	0.618	0.203	3.052	2.27E-03	2.81E-02
Dmel_CR45534	7.894	1.872	0.614	3.048	2.30E-03	2.85E-02

Dmel_CG1634	2307.073	-0.690	0.227	-3.047	2.31E-03	2.85E-02
Dmel_CG1806	80.643	0.842	0.276	3.046	2.32E-03	2.86E-02
Dmel_CG15576	10.175	-2.048	0.672	-3.045	2.32E-03	2.86E-02
Dmel_CG33093	9.378	2.029	0.667	3.041	2.36E-03	2.90E-02
Dmel_CG11899	1333.295	0.723	0.238	3.039	2.37E-03	2.92E-02
Dmel_CG34166	13.640	-3.258	1.073	-3.036	2.39E-03	2.94E-02
Dmel_CG6303	18054.014	0.312	0.103	3.035	2.40E-03	2.95E-02
Dmel_CG12120	10.092	-1.932	0.637	-3.034	2.41E-03	2.95E-02
Dmel_CG17524	127.121	-0.831	0.274	-3.033	2.42E-03	2.96E-02
Dmel_CG6575	11723.986	0.711	0.234	3.033	2.42E-03	2.96E-02
Dmel_CG3905	717.826	0.548	0.181	3.031	2.44E-03	2.98E-02
Dmel_CG9677	7820.096	0.424	0.140	3.030	2.45E-03	2.99E-02
Dmel_CG5904	373.382	0.587	0.194	3.028	2.46E-03	2.99E-02
Dmel_CG7913	6017.463	0.432	0.143	3.028	2.46E-03	2.99E-02
Dmel_CG3971	4591.617	0.532	0.176	3.027	2.47E-03	3.01E-02
Dmel_CG13315	109.740	-1.502	0.497	-3.026	2.48E-03	3.01E-02
Dmel_CR44115	21.000	-2.527	0.836	-3.023	2.50E-03	3.04E-02
Dmel_CG31673	855.982	-0.521	0.173	-3.022	2.51E-03	3.04E-02
Dmel_CR43018	20.119	-5.429	1.797	-3.022	2.51E-03	3.04E-02
Dmel_CG32656	29.905	-1.495	0.495	-3.021	2.52E-03	3.05E-02
Dmel_CG13663	409.022	-0.692	0.229	-3.019	2.53E-03	3.06E-02
Dmel_CG15040	6.619	-2.235	0.741	-3.018	2.54E-03	3.07E-02
Dmel_CG14275	101.798	0.985	0.326	3.017	2.55E-03	3.07E-02
Dmel_CR33674	23.624	1.375	0.456	3.016	2.56E-03	3.08E-02
Dmel_CG30195	12.984	-1.876	0.623	-3.014	2.58E-03	3.09E-02
Dmel_CG6511	1515.921	0.437	0.145	3.014	2.57E-03	3.09E-02
Dmel_CG8808	3822.949	0.618	0.205	3.012	2.59E-03	3.11E-02
Dmel_CG11064	2076.511	-1.666	0.554	-3.007	2.64E-03	3.16E-02
Dmel_CG6495	14.977	2.389	0.795	3.004	2.67E-03	3.19E-02
Dmel_CG33960	90.640	1.186	0.395	3.002	2.69E-03	3.21E-02
Dmel_CG42249	22.299	-1.121	0.374	-3.000	2.70E-03	3.22E-02

Dmel_CG9242	7363.625	0.548	0.183	3.000	2.70E-03	3.22E-02
Dmel_CG31898	1376.311	0.923	0.308	2.996	2.74E-03	3.26E-02
Dmel_CR42491	542.160	-0.920	0.307	-2.995	2.74E-03	3.26E-02
Dmel_CG2102	31.808	-1.577	0.527	-2.995	2.75E-03	3.26E-02
Dmel_CG31445	45.239	-1.471	0.491	-2.993	2.76E-03	3.27E-02
Dmel_CG43295	68.057	-0.972	0.325	-2.993	2.76E-03	3.27E-02
Dmel_CG5337	106.836	-0.633	0.212	-2.993	2.76E-03	3.27E-02
Dmel_CG10466	102.353	-1.024	0.342	-2.992	2.77E-03	3.28E-02
Dmel_CG11783	659.129	-0.599	0.200	-2.989	2.80E-03	3.30E-02
Dmel_CG3504	37.047	-1.060	0.355	-2.989	2.80E-03	3.30E-02
Dmel_CG4579	7553.916	0.337	0.113	2.989	2.80E-03	3.30E-02
Dmel_CG32146	3320.000	0.565	0.189	2.988	2.81E-03	3.31E-02
Dmel_CG6217	22.325	-1.437	0.481	-2.986	2.83E-03	3.32E-02
Dmel_CG12179	1309.413	0.444	0.149	2.983	2.85E-03	3.35E-02
Dmel_CG34323	38.530	-1.299	0.436	-2.982	2.86E-03	3.36E-02
Dmel_CG33926	47.226	-1.752	0.588	-2.981	2.87E-03	3.37E-02
Dmel_CG7447	113.824	1.091	0.366	2.979	2.89E-03	3.39E-02
Dmel_CR46083	34.947	1.067	0.360	2.967	3.01E-03	3.52E-02
Dmel_CG2706	50.078	-1.306	0.441	-2.966	3.02E-03	3.53E-02
Dmel_CG9098	194.284	0.586	0.198	2.963	3.05E-03	3.56E-02
Dmel_CG12708	73.374	1.280	0.432	2.961	3.07E-03	3.58E-02
Dmel_CG13827	209.725	0.751	0.254	2.958	3.09E-03	3.60E-02
Dmel_CG2736	76.651	-0.862	0.291	-2.959	3.09E-03	3.60E-02
Dmel_CR45179	43.006	1.321	0.447	2.958	3.10E-03	3.60E-02
Dmel_CG1950	10.505	-2.311	0.783	-2.950	3.18E-03	3.69E-02
Dmel_CG9611	723.808	0.458	0.155	2.949	3.19E-03	3.70E-02
Dmel_CR33753	103.198	1.049	0.356	2.947	3.21E-03	3.71E-02
Dmel_CG15848	101.067	1.135	0.386	2.944	3.24E-03	3.75E-02
Dmel_CG2194	15.037	-1.685	0.573	-2.939	3.29E-03	3.80E-02
Dmel_CR43493	219.103	0.871	0.296	2.940	3.28E-03	3.80E-02
Dmel_CG18372	32.607	-2.602	0.885	-2.938	3.30E-03	3.81E-02

Dmel_CG31764	398.620	-0.674	0.230	-2.938	3.31E-03	3.81E-02
Dmel_CG34392	202.441	1.223	0.417	2.935	3.34E-03	3.85E-02
Dmel_CG42600	8452.538	0.533	0.182	2.934	3.35E-03	3.85E-02
Dmel_CG42739	692.104	0.780	0.266	2.933	3.36E-03	3.86E-02
Dmel_CG46511	10.848	2.683	0.916	2.930	3.39E-03	3.89E-02
Dmel_CG8930	31.973	1.092	0.373	2.929	3.40E-03	3.90E-02
Dmel_CG11152	73.962	1.292	0.441	2.928	3.41E-03	3.91E-02
Dmel_CG14142	22.763	1.082	0.370	2.927	3.42E-03	3.91E-02
Dmel_CG10901	69851.455	0.493	0.169	2.927	3.43E-03	3.92E-02
Dmel_CG9610	35.323	-1.337	0.457	-2.926	3.43E-03	3.92E-02
Dmel_CG1112	34.251	-1.273	0.435	-2.924	3.45E-03	3.93E-02
Dmel_CG15035	33.968	1.521	0.520	2.925	3.45E-03	3.93E-02
Dmel_CG9414	984.747	-0.576	0.197	-2.924	3.45E-03	3.93E-02
Dmel_CG3757	66.606	-1.071	0.366	-2.924	3.46E-03	3.93E-02
Dmel_CG13309	45.049	-5.610	1.920	-2.922	3.47E-03	3.94E-02
Dmel_CG3694	9.047	2.078	0.711	2.922	3.48E-03	3.94E-02
Dmel_CG7660	20442.794	0.369	0.126	2.922	3.48E-03	3.94E-02
Dmel_CG42626	9.841	-1.383	0.474	-2.921	3.49E-03	3.95E-02
Dmel_CG43770	12411.707	0.490	0.168	2.921	3.49E-03	3.95E-02
Dmel_CG7910	43.394	1.649	0.565	2.919	3.51E-03	3.97E-02
Dmel_CG11852	53.225	-1.131	0.388	-2.918	3.52E-03	3.97E-02
Dmel_CG8014	7309.156	0.345	0.118	2.918	3.52E-03	3.97E-02
Dmel_CG8318	6370.629	0.435	0.149	2.915	3.55E-03	4.00E-02
Dmel_CG30339	24.402	-1.351	0.464	-2.912	3.59E-03	4.03E-02
Dmel_CG13113	571.943	1.134	0.390	2.912	3.59E-03	4.04E-02
Dmel_CG2849	5829.301	-0.601	0.207	-2.909	3.62E-03	4.06E-02
Dmel_CG40494	5617.941	0.382	0.131	2.909	3.62E-03	4.06E-02
Dmel_CG2699	9132.501	0.534	0.184	2.908	3.64E-03	4.07E-02
Dmel_CG43370	11.643	-1.723	0.593	-2.908	3.64E-03	4.07E-02
Dmel_CG42356	20.310	1.454	0.500	2.906	3.66E-03	4.09E-02
Dmel_CG3004	1347.285	0.378	0.130	2.904	3.69E-03	4.11E-02

Dmel_CG17294	289.599	-0.625	0.215	-2.903	3.69E-03	4.11E-02
Dmel_CG42357	20.533	1.583	0.545	2.903	3.69E-03	4.11E-02
Dmel_CG30156	45.744	0.920	0.317	2.900	3.74E-03	4.15E-02
Dmel_CR32900	11.168	1.445	0.498	2.900	3.73E-03	4.15E-02
Dmel_CG12605	8.184	-2.030	0.701	-2.894	3.80E-03	4.22E-02
Dmel_CG45088	63.539	1.460	0.505	2.893	3.81E-03	4.22E-02
Dmel_CG9256	405.857	-0.703	0.243	-2.893	3.81E-03	4.22E-02
Dmel_CR46094	67.098	0.875	0.302	2.894	3.81E-03	4.22E-02
Dmel_CR46090	25.206	0.995	0.344	2.893	3.82E-03	4.22E-02
Dmel_CG14341	124.607	-1.008	0.349	-2.892	3.83E-03	4.23E-02
Dmel_CG31038	332.270	0.559	0.193	2.892	3.83E-03	4.23E-02
Dmel_CG34433	25.355	1.353	0.468	2.892	3.83E-03	4.23E-02
Dmel_CG10777	10216.604	0.507	0.175	2.889	3.86E-03	4.25E-02
Dmel_CG13888	26.473	-0.993	0.344	-2.889	3.86E-03	4.25E-02
Dmel_CG4559	243.698	-0.610	0.211	-2.889	3.86E-03	4.25E-02
Dmel_CG3259	25.044	-1.221	0.423	-2.888	3.87E-03	4.25E-02
Dmel_CG15525	215.123	-0.719	0.249	-2.885	3.91E-03	4.29E-02
Dmel_CG32077	13.884	1.639	0.568	2.885	3.92E-03	4.29E-02
Dmel_CG17129	2764.223	0.763	0.264	2.884	3.93E-03	4.30E-02
Dmel_CG44195	214.639	0.979	0.339	2.884	3.93E-03	4.30E-02
Dmel_CG7607	91.260	0.863	0.299	2.883	3.93E-03	4.30E-02
Dmel_CG4170	1895.737	-0.667	0.231	-2.882	3.95E-03	4.30E-02
Dmel_CG8665	64.322	-0.946	0.328	-2.882	3.95E-03	4.30E-02
Dmel_CG17060	4727.730	0.355	0.123	2.880	3.97E-03	4.32E-02
Dmel_CG9492	5.030	-2.490	0.864	-2.880	3.97E-03	4.32E-02
Dmel_CG13317	26.761	1.699	0.590	2.879	3.99E-03	4.33E-02
Dmel_CG15739	27.147	-1.222	0.424	-2.879	3.99E-03	4.34E-02
Dmel_CG8651	11703.032	0.342	0.119	2.876	4.03E-03	4.38E-02
Dmel_CG6330	698.336	-0.683	0.238	-2.873	4.06E-03	4.40E-02
Dmel_CG6542	4210.347	0.424	0.148	2.872	4.08E-03	4.42E-02
Dmel_CG31743	245.562	0.807	0.281	2.871	4.09E-03	4.42E-02

Dmel_CG3424	18475.822	0.403	0.141	2.871	4.10E-03	4.42E-02
Dmel_CG17717	17.339	-1.491	0.520	-2.866	4.15E-03	4.48E-02
Dmel_CG44325	724.990	-0.660	0.230	-2.863	4.19E-03	4.52E-02
Dmel_CG7635	8.520	-2.027	0.708	-2.863	4.20E-03	4.52E-02
Dmel_CR45047	18.644	1.176	0.411	2.863	4.20E-03	4.52E-02
Dmel_CG11000	88.807	1.094	0.382	2.860	4.24E-03	4.56E-02
Dmel_CG10006	27.615	-1.283	0.449	-2.859	4.25E-03	4.56E-02
Dmel_CG1774	146.285	-0.977	0.342	-2.857	4.28E-03	4.58E-02
Dmel_CG31992	20913.729	0.405	0.142	2.856	4.29E-03	4.58E-02
Dmel_CG4180	1002.902	-0.407	0.143	-2.856	4.29E-03	4.58E-02
Dmel_CG7134	1948.993	0.544	0.190	2.857	4.28E-03	4.58E-02
Dmel_CG9682	8.008	-1.986	0.695	-2.855	4.30E-03	4.60E-02
Dmel_CG3544	5.634	-2.084	0.730	-2.854	4.31E-03	4.60E-02
Dmel_CG8827	140.828	-1.011	0.354	-2.854	4.31E-03	4.60E-02
Dmel_CG30343	277.129	-0.634	0.222	-2.853	4.34E-03	4.61E-02
Dmel_CG46520	3.070	-5.281	1.851	-2.853	4.34E-03	4.61E-02
Dmel_CG46522	3.070	-5.281	1.851	-2.853	4.34E-03	4.61E-02
Dmel_CG10146	15.302	-2.344	0.823	-2.849	4.39E-03	4.66E-02
Dmel_CG42854	30.574	-1.603	0.563	-2.849	4.39E-03	4.66E-02
Dmel_CG12423	221.162	-0.929	0.326	-2.845	4.44E-03	4.71E-02
Dmel_CG6490	2609.600	0.762	0.268	2.845	4.44E-03	4.71E-02
Dmel_CG8805	2531.220	0.438	0.154	2.844	4.45E-03	4.71E-02
Dmel_CG9372	9.420	-1.894	0.667	-2.840	4.52E-03	4.77E-02
Dmel_CR34607	29.650	1.410	0.497	2.838	4.53E-03	4.79E-02
Dmel_CG14193	12.461	-1.601	0.565	-2.837	4.56E-03	4.80E-02
Dmel_CG18473	60.517	1.180	0.416	2.836	4.56E-03	4.80E-02
Dmel_CG3039	3401.084	0.700	0.247	2.837	4.56E-03	4.80E-02
Dmel_CG1772	8275.607	0.661	0.233	2.833	4.61E-03	4.84E-02
Dmel_CG8205	2676.441	0.546	0.193	2.832	4.63E-03	4.86E-02
Dmel_CG6207	2745.065	0.598	0.212	2.825	4.72E-03	4.96E-02
Dmel_CG8316	213.397	-0.793	0.281	-2.825	4.73E-03	4.96E-02

Dmel_CG10479	75.907	1.041	0.369	2.821	4.79E-03	5.02E-02
Dmel_CR45758	6.430	2.623	0.930	2.820	4.81E-03	5.03E-02
Dmel_CG11128	2190.850	0.888	0.315	2.817	4.84E-03	5.06E-02
Dmel_CR46037	8285.229	-1.108	0.393	-2.817	4.84E-03	5.06E-02
Dmel_CG43079	631.857	-1.001	0.355	-2.816	4.86E-03	5.07E-02
Dmel_CG7460	93.172	1.036	0.368	2.814	4.89E-03	5.10E-02
Dmel_CG34220	261.387	1.093	0.388	2.813	4.91E-03	5.11E-02
Dmel_CG14695	5.018	-2.908	1.034	-2.812	4.93E-03	5.13E-02
Dmel_CG34455	1000.243	0.458	0.163	2.808	4.98E-03	5.18E-02
Dmel_CG15822	271.011	0.876	0.312	2.806	5.02E-03	5.21E-02
Dmel_CG14032	170.072	1.031	0.368	2.805	5.03E-03	5.21E-02
Dmel_CG2902	12.707	-1.599	0.570	-2.802	5.08E-03	5.26E-02
Dmel_CG3290	41.169	-5.759	2.055	-2.802	5.08E-03	5.26E-02
Dmel_CG10553	15.343	-2.517	0.898	-2.801	5.09E-03	5.26E-02
Dmel_CG7470	8.831	-2.032	0.725	-2.801	5.10E-03	5.27E-02
Dmel_CG32086	4.755	-2.790	0.998	-2.797	5.16E-03	5.33E-02
Dmel_CG7272	93.577	-0.653	0.234	-2.797	5.16E-03	5.33E-02
Dmel_CG3241	198.254	0.608	0.217	2.795	5.19E-03	5.35E-02
Dmel_CG11310	8.366	2.046	0.733	2.792	5.25E-03	5.40E-02
Dmel_CR45036	19.168	-1.346	0.483	-2.790	5.27E-03	5.42E-02
Dmel_CG4006	3810.911	0.486	0.174	2.789	5.29E-03	5.43E-02
Dmel_CG7363	14.727	-1.578	0.566	-2.789	5.29E-03	5.43E-02
Dmel_CG14064	16.145	1.903	0.683	2.788	5.31E-03	5.44E-02
Dmel_CG1307	973.268	-0.811	0.291	-2.787	5.32E-03	5.44E-02
Dmel_CG2767	1424.389	0.545	0.195	2.787	5.32E-03	5.44E-02

table S17. *D. melanogaster* genes Wald Test significant results for ~Genotype vs ~Genotype+Infection+Genotype*Infection

gene_id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Dmel_CG43079	631.857	-1.956	0.356	-5.494	3.92E-08	2.56E-04
Dmel_CG9871	50.560	-3.292	0.610	-5.399	6.69E-08	2.56E-04
Dmel_CG7002	154.856	-2.425	0.450	-5.387	7.17E-08	2.56E-04
Dmel_CG13772	15.539	-3.435	0.646	-5.318	1.05E-07	2.80E-04
Dmel_CG10593	2009.122	2.010	0.385	5.220	1.79E-07	3.83E-04
Dmel_CG15599	55.457	-2.867	0.557	-5.151	2.59E-07	4.61E-04
Dmel_CG6533	2736.531	4.123	0.808	5.101	3.38E-07	5.16E-04
Dmel_CG9073	36.796	-2.448	0.487	-5.031	4.89E-07	6.54E-04
Dmel_CG6524	6268.890	3.938	0.791	4.976	6.48E-07	7.54E-04
Dmel_CR46481	1090.588	-1.267	0.256	-4.947	7.54E-07	7.54E-04
Dmel_CG2187	500.405	1.275	0.258	4.937	7.95E-07	7.54E-04
Dmel_CG11941	16.019	-3.213	0.653	-4.924	8.46E-07	7.54E-04
Dmel_CG8663	114.131	-1.984	0.409	-4.856	1.19E-06	9.83E-04
Dmel_CG31973	444.390	-1.252	0.260	-4.814	1.48E-06	1.13E-03
Dmel_CG42711	9.934	-4.252	0.888	-4.790	1.66E-06	1.19E-03
Dmel_CG10287	102.780	-1.574	0.330	-4.776	1.79E-06	1.19E-03
Dmel_CR32368	12.082	-3.326	0.708	-4.699	2.61E-06	1.64E-03
Dmel_CG30046	65.427	1.508	0.322	4.685	2.80E-06	1.65E-03
Dmel_CG8942	20.884	-3.404	0.728	-4.676	2.93E-06	1.65E-03
Dmel_CG34323	38.530	-2.054	0.441	-4.661	3.14E-06	1.68E-03
Dmel_CG5644	28.092	2.236	0.486	4.598	4.26E-06	2.17E-03
Dmel_CG4373	307.928	-2.564	0.564	-4.547	5.44E-06	2.58E-03
Dmel_CG13084	2952.416	3.172	0.700	4.532	5.83E-06	2.58E-03
Dmel_CG4783	18.606	-2.194	0.484	-4.531	5.87E-06	2.58E-03
Dmel_CG3157	1113.612	0.878	0.194	4.524	6.08E-06	2.58E-03
Dmel_CG1091	2685.582	0.732	0.162	4.517	6.26E-06	2.58E-03
Dmel_CG6517	5048.988	3.842	0.857	4.483	7.35E-06	2.91E-03
Dmel_CG8388	689.979	0.544	0.121	4.474	7.66E-06	2.93E-03

Dmel_CG3635	29.922	-2.392	0.543	-4.406	1.05E-05	3.89E-03
Dmel_CG32640	167.387	-1.214	0.278	-4.373	1.22E-05	4.36E-03
Dmel_CG9663	323.692	1.203	0.276	4.355	1.33E-05	4.59E-03
Dmel_CR46350	65.211	-1.765	0.407	-4.332	1.48E-05	4.90E-03
Dmel_CG5937	33.106	-2.091	0.483	-4.327	1.51E-05	4.90E-03
Dmel_CG3625	103.288	-0.979	0.228	-4.284	1.84E-05	5.60E-03
Dmel_CG32082	143.362	-1.278	0.299	-4.279	1.87E-05	5.60E-03
Dmel_CG8805	2531.220	0.658	0.154	4.278	1.89E-05	5.60E-03
Dmel_CG6542	4210.347	0.628	0.148	4.254	2.10E-05	6.06E-03
Dmel_CG34325	218.050	-1.225	0.289	-4.241	2.23E-05	6.16E-03
Dmel_CG7050	174.496	-1.607	0.379	-4.239	2.25E-05	6.16E-03
Dmel_CG7676	35.784	-1.999	0.474	-4.219	2.45E-05	6.28E-03
Dmel_CG42854	30.574	-2.400	0.569	-4.218	2.47E-05	6.28E-03
Dmel_CG13000	15.067	-2.359	0.560	-4.214	2.51E-05	6.28E-03
Dmel_CG10726	2404.031	0.799	0.190	4.212	2.53E-05	6.28E-03
Dmel_CG6178	2685.460	0.496	0.119	4.180	2.91E-05	6.96E-03
Dmel_CG14193	12.461	-2.423	0.580	-4.179	2.93E-05	6.96E-03
Dmel_CG43749	68.898	-2.003	0.484	-4.138	3.50E-05	8.10E-03
Dmel_CG2191	17.249	-2.812	0.680	-4.134	3.56E-05	8.10E-03
Dmel_CG8262	752.433	1.089	0.265	4.107	4.00E-05	8.92E-03
Dmel_CG7178	1358.215	-1.725	0.421	-4.100	4.14E-05	9.03E-03
Dmel_CG3297	3125.993	0.709	0.173	4.092	4.27E-05	9.14E-03
Dmel_CG5252	4020.919	0.503	0.124	4.074	4.63E-05	9.53E-03
Dmel_CG14808	573.015	-1.527	0.375	-4.070	4.69E-05	9.53E-03
Dmel_CG6006	523.400	-1.228	0.302	-4.065	4.80E-05	9.53E-03
Dmel_CG7660	20442.794	0.514	0.126	4.065	4.81E-05	9.53E-03
Dmel_CG16995	24.742	-1.770	0.436	-4.056	5.00E-05	9.72E-03
Dmel_CG2275	1215.191	0.896	0.222	4.036	5.43E-05	1.04E-02
Dmel_CG18870	2820.357	0.576	0.143	4.030	5.57E-05	1.05E-02
Dmel_CG32944	92.791	-1.246	0.310	-4.016	5.91E-05	1.09E-02

Dmel_CG3879	12.492	-2.318	0.578	-4.008	6.12E-05	1.09E-02
Dmel_CG4476	2247.740	1.039	0.259	4.008	6.12E-05	1.09E-02
Dmel_CG12582	1823.184	0.624	0.156	4.005	6.20E-05	1.09E-02
Dmel_CG15814	1716.320	0.639	0.160	3.995	6.47E-05	1.11E-02
Dmel_CG15173	91.496	-1.131	0.284	-3.985	6.73E-05	1.11E-02
Dmel_CG9772	2989.847	0.632	0.159	3.980	6.90E-05	1.11E-02
Dmel_CG18547	97.360	-1.483	0.373	-3.980	6.90E-05	1.11E-02
Dmel_CG6698	17.300	-3.148	0.792	-3.976	7.00E-05	1.11E-02
Dmel_CG18619	37.742	-2.011	0.506	-3.974	7.06E-05	1.11E-02
Dmel_CG12002	217.218	-1.718	0.432	-3.974	7.08E-05	1.11E-02
Dmel_CG3631	610.954	0.637	0.161	3.967	7.29E-05	1.13E-02
Dmel_CG9650	454.888	-1.001	0.255	-3.933	8.40E-05	1.27E-02
Dmel_CG9411	11.974	-2.846	0.724	-3.932	8.44E-05	1.27E-02
Dmel_CG30101	46.664	2.134	0.544	3.923	8.75E-05	1.30E-02
Dmel_CG30489	122.263	-1.002	0.256	-3.916	8.99E-05	1.32E-02
Dmel_CG6477	1858.505	1.056	0.270	3.913	9.12E-05	1.32E-02
Dmel_CG6324	34.299	-1.701	0.436	-3.903	9.51E-05	1.36E-02
Dmel_CG31989	498.990	0.777	0.200	3.893	9.90E-05	1.39E-02
Dmel_CG17078	3064.101	0.927	0.239	3.885	1.02E-04	1.41E-02
Dmel_CG7084	38.686	-2.379	0.613	-3.884	1.03E-04	1.41E-02
Dmel_CG17927	1300.359	-1.575	0.406	-3.877	1.06E-04	1.43E-02
Dmel_CG18568	26.606	1.247	0.322	3.870	1.09E-04	1.44E-02
Dmel_CG14680	22.113	-1.898	0.491	-3.867	1.10E-04	1.44E-02
Dmel_CG8193	9.669	-2.935	0.759	-3.866	1.11E-04	1.44E-02
Dmel_CG10706	358.379	-1.147	0.298	-3.848	1.19E-04	1.54E-02
Dmel_CG42512	8.618	-2.278	0.593	-3.840	1.23E-04	1.57E-02
Dmel_CG43088	13.320	-2.541	0.663	-3.834	1.26E-04	1.57E-02
Dmel_CG8233	3636.327	0.540	0.141	3.834	1.26E-04	1.57E-02
Dmel_CG10638	1166.946	-0.838	0.219	-3.826	1.30E-04	1.60E-02
Dmel_CG17117	134.383	-1.721	0.451	-3.820	1.33E-04	1.62E-02
Dmel_CR45530	16.389	-1.740	0.456	-3.813	1.37E-04	1.65E-02

Dmel_CG13954	10.767	-1.844	0.484	-3.808	1.40E-04	1.66E-02
Dmel_CG16762	7.124	-3.388	0.893	-3.796	1.47E-04	1.71E-02
Dmel_CG14796	11568.819	1.541	0.406	3.795	1.48E-04	1.71E-02
Dmel_CG13928	13.709	-1.897	0.500	-3.793	1.49E-04	1.71E-02
Dmel_CG18522	301.389	-1.485	0.392	-3.787	1.52E-04	1.73E-02
Dmel_CG10521	195.366	-1.332	0.352	-3.784	1.54E-04	1.74E-02
Dmel_CG12283	681.554	-0.997	0.265	-3.759	1.70E-04	1.89E-02
Dmel_CG2893	2410.997	0.588	0.156	3.758	1.71E-04	1.89E-02
Dmel_CG6479	2633.182	0.946	0.252	3.749	1.78E-04	1.92E-02
Dmel_CR43461	15.553	-1.690	0.451	-3.748	1.78E-04	1.92E-02
Dmel_CG33472	105.352	-1.291	0.345	-3.745	1.80E-04	1.93E-02
Dmel_CG12449	143.489	-1.377	0.369	-3.730	1.91E-04	1.98E-02
Dmel_CG9338	181.285	-1.597	0.429	-3.727	1.94E-04	1.98E-02
Dmel_CG6958	2318.760	0.411	0.110	3.727	1.94E-04	1.98E-02
Dmel_CG10553	15.343	-3.397	0.912	-3.726	1.95E-04	1.98E-02
Dmel_CG4099	50.953	-1.505	0.404	-3.726	1.95E-04	1.98E-02
Dmel_CG3812	1006.282	0.566	0.152	3.724	1.96E-04	1.98E-02
Dmel_CG42486	7.794	-1.777	0.478	-3.716	2.02E-04	2.01E-02
Dmel_CG32642	1743.930	2.684	0.723	3.713	2.05E-04	2.01E-02
Dmel_CG42492	197.428	-1.605	0.432	-3.712	2.06E-04	2.01E-02
Dmel_CG15324	366.537	1.612	0.434	3.711	2.06E-04	2.01E-02
Dmel_CG9610	35.323	-1.695	0.458	-3.704	2.12E-04	2.03E-02
Dmel_CG10795	653.543	1.082	0.292	3.703	2.13E-04	2.03E-02
Dmel_CG5338	70.237	-1.831	0.495	-3.699	2.16E-04	2.04E-02
Dmel_CG14615	327.742	0.786	0.213	3.696	2.19E-04	2.04E-02
Dmel_CG6422	4864.193	0.631	0.171	3.692	2.22E-04	2.04E-02
Dmel_CG10550	16.054	-2.006	0.543	-3.692	2.23E-04	2.04E-02
Dmel_CG32364	249.152	-1.255	0.340	-3.690	2.24E-04	2.04E-02
Dmel_CG2857	23.133	-1.953	0.530	-3.688	2.26E-04	2.04E-02
Dmel_CG12375	831.121	0.541	0.147	3.684	2.29E-04	2.04E-02

Dmel_CG11125	345.793	0.825	0.224	3.683	2.30E-04	2.04E-02
Dmel_CG32577	132.606	-1.219	0.331	-3.683	2.30E-04	2.04E-02
Dmel_CR44472	23.272	1.829	0.497	3.679	2.34E-04	2.05E-02
Dmel_CR43144	234.567	-1.219	0.332	-3.674	2.39E-04	2.08E-02
Dmel_CG31901	28.374	-2.490	0.680	-3.664	2.49E-04	2.15E-02
Dmel_CG2246	2660.559	0.526	0.144	3.658	2.54E-04	2.15E-02
Dmel_CG41106	15.890	-1.904	0.521	-3.657	2.55E-04	2.15E-02
Dmel_CG9707	1943.581	0.589	0.161	3.649	2.63E-04	2.15E-02
Dmel_CG32019	11590.256	-1.412	0.387	-3.649	2.64E-04	2.15E-02
Dmel_CG7510	2088.312	0.558	0.153	3.648	2.64E-04	2.15E-02
Dmel_CG5041	570.781	0.710	0.195	3.648	2.64E-04	2.15E-02
Dmel_CG12423	221.162	-1.190	0.326	-3.647	2.65E-04	2.15E-02
Dmel_CG10336	664.150	0.885	0.243	3.646	2.66E-04	2.15E-02
Dmel_CG18039	57.006	-1.759	0.483	-3.644	2.69E-04	2.15E-02
Dmel_CG7564	14794.411	-1.158	0.318	-3.643	2.70E-04	2.15E-02
Dmel_CG42639	16.055	-2.624	0.721	-3.640	2.73E-04	2.16E-02
Dmel_CG15432	193.546	-1.233	0.339	-3.635	2.77E-04	2.18E-02
Dmel_CG45077	281.510	-1.509	0.416	-3.627	2.86E-04	2.23E-02
Dmel_CG13364	597.882	-1.546	0.427	-3.624	2.90E-04	2.23E-02
Dmel_CR34084	11.680	-2.032	0.561	-3.621	2.93E-04	2.23E-02
Dmel_CG46462	29.749	-1.810	0.500	-3.621	2.94E-04	2.23E-02
Dmel_CG10794	23.361	-4.266	1.179	-3.617	2.98E-04	2.23E-02
Dmel_CG33474	26.760	-1.326	0.367	-3.616	2.99E-04	2.23E-02
Dmel_CR45187	109.321	-1.218	0.337	-3.616	2.99E-04	2.23E-02
Dmel_CG32677	64.186	-1.706	0.472	-3.615	3.01E-04	2.23E-02
Dmel_CG15155	16.725	-1.854	0.513	-3.612	3.03E-04	2.24E-02
Dmel_CG31198	57.349	-5.117	1.419	-3.605	3.12E-04	2.29E-02
Dmel_CG13604	682.846	0.752	0.209	3.601	3.17E-04	2.29E-02
Dmel_CG31897	145.916	-0.865	0.241	-3.596	3.24E-04	2.29E-02

Dmel_CG32474	120.332	-1.621	0.451	-3.592	3.29E-04	2.29E-02
Dmel_CG4909	2833.384	0.845	0.235	3.590	3.30E-04	2.29E-02
Dmel_CG5596	653.286	-1.482	0.413	-3.590	3.30E-04	2.29E-02
Dmel_CG17716	19.533	-2.076	0.578	-3.590	3.31E-04	2.29E-02
Dmel_CG32017	173.619	-1.268	0.353	-3.589	3.32E-04	2.29E-02
Dmel_CG5867	86.914	-1.403	0.391	-3.588	3.33E-04	2.29E-02
Dmel_CG42309	229.779	-1.694	0.472	-3.587	3.35E-04	2.29E-02
Dmel_CG7128	682.992	1.249	0.348	3.586	3.35E-04	2.29E-02
Dmel_CG43758	309.775	-1.157	0.323	-3.586	3.36E-04	2.29E-02
Dmel_CG5445	1662.056	0.563	0.157	3.579	3.46E-04	2.33E-02
Dmel_CG3613	1120.960	0.860	0.240	3.577	3.47E-04	2.33E-02
Dmel_CG10364	1000.208	1.068	0.299	3.575	3.50E-04	2.33E-02
Dmel_CG1024	621.198	0.818	0.229	3.574	3.51E-04	2.33E-02
Dmel_CG8165	279.924	0.513	0.144	3.572	3.54E-04	2.34E-02
Dmel_CG8585	391.292	-1.143	0.320	-3.569	3.58E-04	2.35E-02
Dmel_CG3171	1422.762	0.794	0.223	3.561	3.69E-04	2.41E-02
Dmel_CG18536	49.200	-1.180	0.332	-3.556	3.77E-04	2.44E-02
Dmel_CG5038	341.144	0.614	0.173	3.554	3.80E-04	2.45E-02
Dmel_CG7083	1256.892	0.546	0.154	3.550	3.85E-04	2.46E-02
Dmel_CG34445	67.998	-1.639	0.462	-3.549	3.87E-04	2.46E-02
Dmel_CG9297	38.481	-1.620	0.458	-3.539	4.01E-04	2.54E-02
Dmel_CG15443	379.439	0.676	0.191	3.537	4.05E-04	2.55E-02
Dmel_CG1825	2353.709	1.329	0.376	3.532	4.13E-04	2.56E-02
Dmel_CG43664	825.006	0.783	0.222	3.531	4.14E-04	2.56E-02
Dmel_CR46482	19457.346	-1.042	0.295	-3.531	4.14E-04	2.56E-02
Dmel_CG13977	13.266	-2.838	0.804	-3.529	4.16E-04	2.56E-02
Dmel_CG4608	113.986	-1.087	0.308	-3.525	4.24E-04	2.59E-02
Dmel_CG30195	12.984	-2.196	0.623	-3.523	4.26E-04	2.59E-02
Dmel_CG14026	3581.522	0.351	0.100	3.521	4.30E-04	2.60E-02
Dmel_CG12106	309.494	0.865	0.246	3.515	4.40E-04	2.61E-02

Dmel_CG2184	1690.958	-1.347	0.383	-3.514	4.41E-04	2.61E-02
Dmel_CR33628	2075.290	-2.268	0.646	-3.512	4.45E-04	2.61E-02
Dmel_CR33921	2075.290	-2.268	0.646	-3.512	4.45E-04	2.61E-02
Dmel_CG7997	780.900	0.535	0.152	3.511	4.46E-04	2.61E-02
Dmel_CG1455	14.264	-1.917	0.546	-3.511	4.46E-04	2.61E-02
Dmel_CG9796	5516.729	0.623	0.178	3.503	4.60E-04	2.67E-02
Dmel_CG9057	16761.326	1.152	0.329	3.502	4.62E-04	2.67E-02
Dmel_CG15138	159.816	-1.071	0.306	-3.498	4.68E-04	2.68E-02
Dmel_CG18102	3933.133	0.390	0.112	3.498	4.69E-04	2.68E-02
Dmel_CG44007	82.476	-1.583	0.453	-3.494	4.76E-04	2.71E-02
Dmel_CG9423	10906.330	0.593	0.170	3.489	4.85E-04	2.73E-02
Dmel_CG14711	1052.838	0.629	0.180	3.488	4.86E-04	2.73E-02
Dmel_CG6957	112.117	-1.274	0.366	-3.485	4.92E-04	2.75E-02
Dmel_CG6202	3774.453	0.437	0.125	3.484	4.95E-04	2.75E-02
Dmel_CG12099	2772.921	0.627	0.180	3.483	4.96E-04	2.75E-02
Dmel_CG6927	4422.478	0.656	0.189	3.479	5.04E-04	2.76E-02
Dmel_CG1894	11.141	-1.881	0.541	-3.479	5.04E-04	2.76E-02
Dmel_CG5439	666.759	0.731	0.210	3.475	5.11E-04	2.78E-02
Dmel_CG3407	971.487	0.648	0.187	3.473	5.15E-04	2.78E-02
Dmel_CG12220	492.880	-1.064	0.306	-3.473	5.16E-04	2.78E-02
Dmel_CG4622	759.225	0.889	0.256	3.471	5.18E-04	2.78E-02
Dmel_CG6658	157.093	-1.473	0.425	-3.464	5.32E-04	2.85E-02
Dmel_CG18549	1584.276	0.459	0.133	3.462	5.35E-04	2.85E-02
Dmel_CG6930	714.992	-0.856	0.247	-3.459	5.41E-04	2.87E-02
Dmel_CG2072	1813.889	0.512	0.148	3.457	5.47E-04	2.87E-02
Dmel_CG8023	8.117	-2.756	0.798	-3.454	5.51E-04	2.87E-02
Dmel_CG3163	236.299	0.760	0.220	3.454	5.52E-04	2.87E-02
Dmel_CG12110	4136.182	0.530	0.154	3.451	5.58E-04	2.87E-02
Dmel_CG32641	631.055	-0.993	0.288	-3.450	5.60E-04	2.87E-02

Dmel_CG6357	882.290	-0.763	0.221	-3.450	5.60E-04	2.87E-02
Dmel_CG9155	396.786	-0.909	0.264	-3.450	5.61E-04	2.87E-02
Dmel_CG33344	7.747	-2.076	0.602	-3.449	5.63E-04	2.87E-02
Dmel_CG8316	213.397	-0.967	0.281	-3.447	5.67E-04	2.87E-02
Dmel_CG6665	468.601	0.565	0.164	3.444	5.74E-04	2.89E-02
Dmel_CG6040	548.589	-0.925	0.269	-3.441	5.81E-04	2.92E-02
Dmel_CG4274	2581.259	1.038	0.302	3.438	5.86E-04	2.93E-02
Dmel_CG7957	723.957	0.726	0.211	3.436	5.90E-04	2.93E-02
Dmel_CG4395	13.227	2.039	0.594	3.432	5.99E-04	2.93E-02
Dmel_CG13941	124.885	-0.800	0.233	-3.431	6.02E-04	2.93E-02
Dmel_CG6121	978.359	0.918	0.268	3.430	6.04E-04	2.93E-02
Dmel_CG4951	1445.689	0.530	0.155	3.428	6.09E-04	2.93E-02
Dmel_CG34200	556.763	-1.353	0.395	-3.426	6.12E-04	2.93E-02
Dmel_CR45132	40.764	-0.987	0.288	-3.426	6.14E-04	2.93E-02
Dmel_CG7289	1206.822	0.653	0.191	3.425	6.15E-04	2.93E-02
Dmel_CG7157	83.139	-1.164	0.340	-3.424	6.17E-04	2.93E-02
Dmel_CG11737	998.601	0.956	0.279	3.423	6.18E-04	2.93E-02
Dmel_CG6398	1931.984	0.944	0.276	3.423	6.18E-04	2.93E-02
Dmel_CG4686	727.346	0.684	0.200	3.423	6.19E-04	2.93E-02
Dmel_CG18642	441.573	0.918	0.268	3.421	6.25E-04	2.94E-02
Dmel_CG15201	9.880	-2.006	0.587	-3.420	6.27E-04	2.94E-02
Dmel_CG11210	1947.088	0.651	0.191	3.417	6.33E-04	2.94E-02
Dmel_CG1664	3508.885	0.707	0.207	3.417	6.34E-04	2.94E-02
Dmel_CG6962	1700.725	0.814	0.239	3.414	6.40E-04	2.94E-02
Dmel_CG10825	890.498	0.655	0.192	3.414	6.41E-04	2.94E-02
Dmel_CG13506	177.409	-1.083	0.317	-3.413	6.41E-04	2.94E-02
Dmel_CG34392	202.441	1.421	0.416	3.413	6.43E-04	2.94E-02
Dmel_CG4620	4335.134	0.639	0.187	3.411	6.47E-04	2.94E-02
Dmel_CG44325	724.990	-0.784	0.230	-3.405	6.62E-04	2.99E-02
Dmel_CG14946	22.832	-1.745	0.513	-3.403	6.66E-04	2.99E-02
Dmel_CG17084	133.181	-1.112	0.327	-3.403	6.66E-04	2.99E-02

Dmel_CG41265	266.240	-1.196	0.352	-3.398	6.78E-04	3.03E-02
Dmel_CG17149	1566.784	0.898	0.264	3.396	6.83E-04	3.04E-02
Dmel_CG7772	674.473	0.756	0.223	3.393	6.91E-04	3.04E-02
Dmel_CG4260	7777.907	0.482	0.142	3.393	6.91E-04	3.04E-02
Dmel_CG32115	14.590	-1.894	0.558	-3.393	6.91E-04	3.04E-02
Dmel_CR42451	792.575	-1.170	0.345	-3.391	6.96E-04	3.04E-02
Dmel_CG30170	20.719	-1.855	0.547	-3.391	6.96E-04	3.04E-02
Dmel_CG4262	252.039	-0.841	0.248	-3.387	7.07E-04	3.07E-02
Dmel_CG34133	4321.118	0.566	0.167	3.383	7.18E-04	3.11E-02
Dmel_CG12942	1863.699	0.587	0.174	3.381	7.23E-04	3.12E-02
Dmel_CG5725	1904.398	0.734	0.217	3.377	7.33E-04	3.14E-02
Dmel_CG1915	6242.146	-1.045	0.310	-3.376	7.34E-04	3.14E-02
Dmel_CG33147	9.630	-2.113	0.626	-3.374	7.40E-04	3.15E-02
Dmel_CG32506	9.534	-2.114	0.627	-3.372	7.46E-04	3.16E-02
Dmel_CG4267	559.666	0.880	0.261	3.371	7.48E-04	3.16E-02
Dmel_CG12391	1629.747	0.738	0.219	3.367	7.61E-04	3.20E-02
Dmel_CG10309	2135.421	1.285	0.382	3.366	7.62E-04	3.20E-02
Dmel_CG15848	101.067	-1.331	0.396	-3.364	7.68E-04	3.21E-02
Dmel_CG1911	1431.817	0.860	0.256	3.359	7.81E-04	3.25E-02
Dmel_CG8051	10.915	-1.571	0.468	-3.354	7.96E-04	3.30E-02
Dmel_CG33103	1003.050	-1.419	0.424	-3.351	8.04E-04	3.32E-02
Dmel_CG6207	2745.065	0.708	0.211	3.350	8.07E-04	3.32E-02
Dmel_CG32452	1457.804	0.813	0.243	3.349	8.12E-04	3.33E-02
Dmel_CG10240	935.082	0.709	0.212	3.347	8.18E-04	3.34E-02
Dmel_CR43626	142.895	-1.241	0.371	-3.346	8.20E-04	3.34E-02
Dmel_CG5222	595.645	0.896	0.268	3.344	8.27E-04	3.35E-02
Dmel_CG17462	1947.213	0.930	0.279	3.337	8.46E-04	3.39E-02
Dmel_CG2765	1659.825	0.624	0.187	3.337	8.48E-04	3.39E-02
Dmel_CG4029	5627.255	0.658	0.197	3.336	8.50E-04	3.39E-02
Dmel_CG12118	916.548	0.632	0.189	3.336	8.51E-04	3.39E-02
Dmel_CG4978	3421.524	0.862	0.259	3.334	8.55E-04	3.39E-02

Dmel_CG4821	225.884	-0.994	0.298	-3.332	8.62E-04	3.39E-02
Dmel_CG3041	913.876	0.915	0.275	3.332	8.63E-04	3.39E-02
Dmel_CG9712	1406.203	0.729	0.219	3.331	8.64E-04	3.39E-02
Dmel_CG11975	684.605	0.676	0.203	3.331	8.66E-04	3.39E-02
Dmel_CG44008	16.277	-1.804	0.542	-3.329	8.70E-04	3.40E-02
Dmel_CG6536	115.126	-1.090	0.328	-3.325	8.84E-04	3.43E-02
Dmel_CG11367	593.483	1.063	0.320	3.325	8.86E-04	3.43E-02
Dmel_CG17839	101.907	-1.084	0.326	-3.324	8.88E-04	3.43E-02
Dmel_CG8282	2013.871	0.529	0.159	3.322	8.94E-04	3.44E-02
Dmel_CG11804	8263.425	0.502	0.151	3.320	9.00E-04	3.44E-02
Dmel_CG8389	831.413	0.533	0.161	3.318	9.07E-04	3.44E-02
Dmel_CG9470	1461.555	-1.099	0.331	-3.317	9.09E-04	3.44E-02
Dmel_CG42253	66.402	-1.475	0.445	-3.316	9.14E-04	3.44E-02
Dmel_CG1674	540.658	-1.334	0.402	-3.316	9.14E-04	3.44E-02
Dmel_CG8411	7127.715	0.438	0.132	3.315	9.16E-04	3.44E-02
Dmel_CG5177	88.185	-1.824	0.550	-3.315	9.18E-04	3.44E-02
Dmel_CG34438	3017.459	0.722	0.218	3.311	9.29E-04	3.47E-02
Dmel_CG5602	1070.389	0.892	0.269	3.310	9.34E-04	3.48E-02
Dmel_CG5807	2244.113	0.476	0.144	3.308	9.39E-04	3.49E-02
Dmel_CG7107	460.078	-1.355	0.410	-3.303	9.56E-04	3.54E-02
Dmel_CG10895	11736.04 5	0.416	0.126	3.302	9.61E-04	3.54E-02
Dmel_CG7404	1099.831	0.354	0.107	3.299	9.69E-04	3.56E-02
Dmel_CG8994	15778.33 4	0.610	0.185	3.297	9.79E-04	3.58E-02
Dmel_CR43314	390.005	-1.144	0.347	-3.294	9.88E-04	3.61E-02
Dmel_CG10126	206.811	-1.209	0.367	-3.293	9.91E-04	3.61E-02
Dmel_CG34431	161.743	-0.853	0.259	-3.291	9.99E-04	3.62E-02
Dmel_CG9203	680.819	0.559	0.170	3.290	1.00E-03	3.62E-02
Dmel_CG9739	548.694	-1.009	0.307	-3.288	1.01E-03	3.63E-02
Dmel_CG31469	13.182	-1.602	0.487	-3.287	1.01E-03	3.63E-02

Dmel_CG9594	2785.003	0.659	0.201	3.285	1.02E-03	3.65E-02
Dmel_CG12004	4534.896	0.695	0.212	3.284	1.03E-03	3.65E-02
Dmel_CG9432	408.363	-1.247	0.380	-3.283	1.03E-03	3.65E-02
Dmel_CG4405	155.934	-1.333	0.406	-3.281	1.03E-03	3.66E-02
Dmel_CG13403	9.694	-2.267	0.691	-3.279	1.04E-03	3.68E-02
Dmel_CG4788	695.972	0.809	0.247	3.276	1.05E-03	3.70E-02
Dmel_CG42259	266.650	-1.368	0.418	-3.273	1.06E-03	3.72E-02
Dmel_CG1019	287.029	-0.997	0.305	-3.273	1.07E-03	3.72E-02
Dmel_CG4615	903.993	0.844	0.258	3.268	1.08E-03	3.78E-02
Dmel_CG3651	2573.552	0.462	0.141	3.266	1.09E-03	3.79E-02
Dmel_CG2990	1142.823	0.655	0.201	3.265	1.10E-03	3.79E-02
Dmel_CG5180	943.481	1.088	0.333	3.264	1.10E-03	3.79E-02
Dmel_CG8440	4400.552	0.398	0.122	3.263	1.10E-03	3.80E-02
Dmel_CR46254	14.144	-1.647	0.505	-3.261	1.11E-03	3.81E-02
Dmel_CG9123	285.710	0.970	0.298	3.259	1.12E-03	3.82E-02
Dmel_CG32758	1103.252	-0.563	0.173	-3.254	1.14E-03	3.88E-02
Dmel_CG30418	100.457	-1.346	0.414	-3.247	1.16E-03	3.94E-02
Dmel_CG31926	1397.870	2.466	0.759	3.247	1.17E-03	3.94E-02
Dmel_CG4139	67.549	-1.192	0.368	-3.243	1.18E-03	3.96E-02
Dmel_CG1109	2597.079	0.493	0.152	3.243	1.18E-03	3.96E-02
Dmel_CR45941	8.758	-2.186	0.674	-3.243	1.18E-03	3.96E-02
Dmel_CG11979	478.991	-1.044	0.322	-3.240	1.19E-03	3.96E-02
Dmel_CG33556	69.075	-1.477	0.456	-3.239	1.20E-03	3.96E-02
Dmel_CG8400	3643.172	0.672	0.207	3.239	1.20E-03	3.96E-02
Dmel_CG33720	267.591	-1.014	0.313	-3.237	1.21E-03	3.96E-02
Dmel_CG34250	185.219	-1.312	0.405	-3.237	1.21E-03	3.96E-02
Dmel_CG10387	2509.834	0.619	0.191	3.237	1.21E-03	3.96E-02
Dmel_CR44953	22.110	-1.516	0.468	-3.237	1.21E-03	3.96E-02
Dmel_CG6711	1884.750	0.427	0.132	3.236	1.21E-03	3.96E-02
Dmel_CG5938	1070.366	0.735	0.227	3.234	1.22E-03	3.98E-02
Dmel_CG12275	39.817	-1.912	0.592	-3.230	1.24E-03	4.03E-02

Dmel_CG16947	157.907	1.077	0.333	3.229	1.24E-03	4.03E-02
Dmel_CG17292	1474.083	0.641	0.199	3.224	1.26E-03	4.06E-02
Dmel_CG43273	105.193	-0.861	0.267	-3.224	1.27E-03	4.06E-02
Dmel_CG32096	237.586	-0.892	0.277	-3.223	1.27E-03	4.06E-02
Dmel_CG6329	64.231	-1.629	0.505	-3.223	1.27E-03	4.06E-02
Dmel_CG31753	71.034	-1.431	0.445	-3.216	1.30E-03	4.16E-02
Dmel_CG4433	1942.289	0.732	0.228	3.213	1.31E-03	4.18E-02
Dmel_CG42584	108.987	-1.531	0.477	-3.212	1.32E-03	4.18E-02
Dmel_CG4145	1028.805	-1.141	0.355	-3.212	1.32E-03	4.18E-02
Dmel_CG10063	16.237	-1.568	0.488	-3.209	1.33E-03	4.19E-02
Dmel_CG11098	1467.654	-0.416	0.130	-3.209	1.33E-03	4.19E-02
Dmel_CG32795	1510.068	0.441	0.137	3.208	1.34E-03	4.19E-02
Dmel_CG15435	899.900	0.762	0.238	3.207	1.34E-03	4.20E-02
Dmel_CG10570	76.217	-1.661	0.518	-3.203	1.36E-03	4.23E-02
Dmel_CG42502	76.217	-1.661	0.518	-3.203	1.36E-03	4.23E-02
Dmel_CR44042	410.787	-0.827	0.259	-3.196	1.40E-03	4.33E-02
Dmel_CG17360	1450.158	0.628	0.197	3.193	1.41E-03	4.36E-02
Dmel_CG3348	150.597	-1.169	0.366	-3.191	1.42E-03	4.36E-02
Dmel_CG11007	1087.406	0.493	0.154	3.190	1.42E-03	4.36E-02
Dmel_CG5905	30.547	-1.470	0.461	-3.190	1.43E-03	4.36E-02
Dmel_CG5181	242.756	1.037	0.325	3.189	1.43E-03	4.36E-02
Dmel_CG9046	18333.540	1.340	0.420	3.189	1.43E-03	4.36E-02
Dmel_CG9836	704.353	-0.686	0.215	-3.183	1.46E-03	4.42E-02
Dmel_CG12093	455.447	0.752	0.236	3.182	1.46E-03	4.42E-02
Dmel_CG2993	277.855	0.974	0.306	3.181	1.47E-03	4.42E-02
Dmel_CG10396	15.080	-1.532	0.482	-3.181	1.47E-03	4.42E-02
Dmel_CG9984	1897.020	0.676	0.213	3.180	1.47E-03	4.42E-02
Dmel_CG3403	2318.502	0.939	0.296	3.177	1.49E-03	4.45E-02
Dmel_CG31807	141.606	-0.932	0.293	-3.176	1.49E-03	4.45E-02
Dmel_CG46339	356.917	-0.968	0.305	-3.175	1.50E-03	4.45E-02

Dmel_CG7272	93.577	-0.737	0.232	-3.174	1.50E-03	4.45E-02
Dmel_CG5939	354.903	-1.070	0.337	-3.174	1.50E-03	4.45E-02
Dmel_CG10630	13.277	-2.459	0.775	-3.173	1.51E-03	4.45E-02
Dmel_CG11723	1410.373	0.585	0.184	3.172	1.51E-03	4.45E-02
Dmel_CR45897	10.683	-1.749	0.551	-3.171	1.52E-03	4.45E-02
Dmel_CG7930	574.112	-1.313	0.414	-3.171	1.52E-03	4.45E-02
Dmel_CG31365	1258.248	0.797	0.251	3.170	1.52E-03	4.45E-02
Dmel_CG13434	94.002	-0.939	0.297	-3.166	1.55E-03	4.50E-02
Dmel_CG42599	266.112	-1.010	0.319	-3.165	1.55E-03	4.50E-02
Dmel_CG7837	1051.188	0.740	0.234	3.164	1.56E-03	4.52E-02
Dmel_CG8811	8990.635	0.483	0.153	3.161	1.57E-03	4.53E-02
Dmel_CG3836	2301.302	0.722	0.228	3.161	1.57E-03	4.53E-02
Dmel_CG2330	77.759	-1.493	0.472	-3.160	1.58E-03	4.54E-02
Dmel_CG44246	646.353	0.700	0.222	3.158	1.59E-03	4.55E-02
Dmel_CG15721	6051.069	1.209	0.383	3.155	1.61E-03	4.59E-02
Dmel_CG18507	93.141	1.199	0.380	3.154	1.61E-03	4.59E-02
Dmel_CG32212	22.799	-1.623	0.515	-3.152	1.62E-03	4.60E-02
Dmel_CG32320	96.491	-1.370	0.435	-3.152	1.62E-03	4.60E-02
Dmel_CR44291	23.840	-1.339	0.425	-3.150	1.63E-03	4.62E-02
Dmel_CG8933	5203.559	0.513	0.163	3.145	1.66E-03	4.68E-02
Dmel_CG9379	238.648	-0.827	0.263	-3.145	1.66E-03	4.68E-02
Dmel_CG3065	790.124	1.218	0.387	3.144	1.67E-03	4.68E-02
Dmel_CG4214	1980.475	0.474	0.151	3.139	1.70E-03	4.75E-02
Dmel_CG8066	345.072	-0.741	0.236	-3.134	1.72E-03	4.81E-02
Dmel_CG1448	1370.609	-0.865	0.277	-3.128	1.76E-03	4.89E-02
Dmel_CG1745	4690.633	0.672	0.215	3.128	1.76E-03	4.89E-02
Dmel_CG7999	1414.777	0.475	0.152	3.126	1.77E-03	4.89E-02
Dmel_CG8114	6061.248	0.364	0.116	3.126	1.78E-03	4.89E-02
Dmel_CG12763	27.517	-3.900	1.248	-3.125	1.78E-03	4.89E-02
Dmel_CG5083	2062.330	0.757	0.242	3.123	1.79E-03	4.92E-02
Dmel_CG1487	3370.356	0.413	0.132	3.121	1.80E-03	4.93E-02

Dmel_CG5907	136.047	-1.175	0.377	-3.121	1.80E-03	4.93E-02
Dmel_CG14162	1349.763	0.684	0.219	3.120	1.81E-03	4.93E-02
Dmel_CG30118	7132.753	0.703	0.226	3.118	1.82E-03	4.96E-02
Dmel_CG9078	3970.323	0.435	0.140	3.115	1.84E-03	4.98E-02
Dmel_CG2249	2474.631	-0.901	0.289	-3.114	1.84E-03	4.98E-02
Dmel_CG9220	125.885	-0.824	0.265	-3.113	1.85E-03	4.98E-02
Dmel_CG8548	6621.909	0.439	0.141	3.113	1.85E-03	4.98E-02
Dmel_CG8338	594.660	-1.008	0.324	-3.112	1.86E-03	4.98E-02
Dmel_CG4407	1040.887	0.405	0.130	3.111	1.86E-03	4.98E-02
Dmel_CG3671	2152.230	0.679	0.218	3.111	1.86E-03	4.98E-02
Dmel_CR46037	8285.229	-1.223	0.393	-3.111	1.87E-03	4.98E-02
Dmel_CG9342	904.312	0.552	0.178	3.106	1.90E-03	5.03E-02
Dmel_CG33722	1440.994	0.563	0.181	3.106	1.90E-03	5.03E-02
Dmel_CG12242	24.371	-1.777	0.572	-3.105	1.90E-03	5.03E-02
Dmel_CG34333	20400.94 1	1.614	0.520	3.104	1.91E-03	5.04E-02
Dmel_CG15431	62.781	-0.872	0.281	-3.104	1.91E-03	5.04E-02
Dmel_CG32850	1595.721	-0.790	0.255	-3.100	1.93E-03	5.08E-02
Dmel_CG1311	1395.571	0.650	0.210	3.097	1.96E-03	5.13E-02
Dmel_CG12404	1283.354	0.419	0.136	3.095	1.97E-03	5.14E-02
Dmel_CR45146	7.571	-1.851	0.598	-3.094	1.98E-03	5.15E-02
Dmel_CG2934	5007.021	0.586	0.190	3.092	1.99E-03	5.17E-02
Dmel_CG14621	2331.371	0.753	0.244	3.087	2.02E-03	5.24E-02
Dmel_CG15094	334.092	0.800	0.259	3.084	2.04E-03	5.30E-02
Dmel_CG11263	812.988	-0.804	0.261	-3.078	2.09E-03	5.38E-02
Dmel_CG5848	5306.631	0.850	0.276	3.077	2.09E-03	5.38E-02
Dmel_CG3227	1353.712	1.111	0.361	3.077	2.09E-03	5.38E-02
Dmel_CG1569	2450.503	0.625	0.203	3.075	2.10E-03	5.39E-02
Dmel_CG3961	102.114	-0.958	0.312	-3.075	2.11E-03	5.39E-02
Dmel_CG7692	1472.997	0.524	0.170	3.074	2.11E-03	5.39E-02
Dmel_CG16840	80.024	-1.618	0.526	-3.073	2.12E-03	5.40E-02

Dmel_CG5857	1494.849	0.656	0.214	3.071	2.13E-03	5.42E-02
Dmel_CG34163	207.187	-1.039	0.338	-3.069	2.15E-03	5.44E-02

table S18. *D. melanogaster* genes Wald Test significant results for ~Infection vs ~Genotype+Infection+Genotype*Infection

gene_id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Dmel_CG32834	13.460	-21.521	2.735	-7.868	3.61E-15	3.64E-11
Dmel_CG2187	500.405	-2.857	0.369	-7.751	9.12E-15	4.59E-11
Dmel_CG3104	56.006	2.402	0.476	5.043	4.59E-07	1.54E-03
Dmel_CG10045	10067.445	-4.248	0.867	-4.901	9.52E-07	2.40E-03
Dmel_CG7404	1099.831	-0.694	0.152	-4.557	5.20E-06	1.05E-02
Dmel_CG5937	33.106	2.974	0.677	4.394	1.11E-05	1.86E-02
Dmel_CG9650	454.888	1.566	0.360	4.350	1.36E-05	1.96E-02
Dmel_CG8805	2531.220	-0.929	0.218	-4.270	1.95E-05	2.46E-02
Dmel_CG15599	55.457	3.314	0.789	4.200	2.67E-05	2.61E-02
Dmel_CG9155	396.786	1.554	0.373	4.164	3.12E-05	2.61E-02
Dmel_CG6178	2685.460	-0.699	0.168	-4.163	3.14E-05	2.61E-02
Dmel_CG17167	307.196	-1.705	0.411	-4.151	3.31E-05	2.61E-02
Dmel_CG13772	15.539	3.746	0.905	4.139	3.48E-05	2.61E-02
Dmel_CG8388	689.979	-0.713	0.173	-4.121	3.78E-05	2.61E-02
Dmel_CG3157	1113.612	-1.129	0.275	-4.114	3.89E-05	2.61E-02
Dmel_CG43079	631.857	2.061	0.503	4.096	4.21E-05	2.65E-02
Dmel_CG18870	2820.357	-0.823	0.202	-4.070	4.70E-05	2.78E-02
Dmel_CG18522	301.389	2.247	0.555	4.048	5.16E-05	2.89E-02
Dmel_CG12002	217.218	2.463	0.611	4.029	5.60E-05	2.93E-02
Dmel_CG31901	28.374	3.961	0.985	4.020	5.82E-05	2.93E-02
Dmel_CG10593	2009.122	-2.174	0.544	-3.993	6.52E-05	3.09E-02
Dmel_CG10573	175.250	1.302	0.327	3.985	6.75E-05	3.09E-02
Dmel_CR43461	15.553	2.695	0.680	3.965	7.34E-05	3.12E-02
Dmel_CG16762	7.124	4.634	1.172	3.955	7.66E-05	NA
Dmel_CG13871	15.439	-5.015	1.269	-3.952	7.75E-05	3.12E-02
Dmel_CG8663	114.131	2.257	0.573	3.941	8.11E-05	3.12E-02
Dmel_CG30046	65.427	-1.745	0.444	-3.929	8.54E-05	3.12E-02
Dmel_CR44115	21.000	4.551	1.163	3.913	9.12E-05	3.12E-02

Dmel_CG31973	444.390	1.434	0.367	3.906	9.40E-05	3.12E-02
Dmel_CG6542	4210.347	-0.815	0.209	-3.903	9.51E-05	3.12E-02
Dmel_CG5870	1313.514	1.321	0.339	3.894	9.84E-05	3.12E-02
Dmel_CG9610	35.323	2.525	0.648	3.893	9.90E-05	3.12E-02
Dmel_CG10726	2404.031	-1.042	0.268	-3.886	1.02E-04	3.12E-02
Dmel_CG15814	1716.320	-0.877	0.227	-3.871	1.09E-04	3.12E-02
Dmel_CG8256	121.600	1.720	0.445	3.865	1.11E-04	3.12E-02
Dmel_CG7660	20442.794	-0.690	0.179	-3.861	1.13E-04	3.12E-02
Dmel_CG9073	36.796	2.621	0.679	3.858	1.14E-04	3.12E-02
Dmel_CG32082	143.362	1.635	0.424	3.854	1.16E-04	3.12E-02
Dmel_CG9888	413.992	1.902	0.494	3.851	1.18E-04	3.12E-02
Dmel_CG9220	125.885	1.424	0.371	3.840	1.23E-04	3.18E-02
Dmel_CG9772	2989.847	-0.860	0.224	-3.833	1.27E-04	3.19E-02
Dmel_CG12283	681.554	1.430	0.375	3.819	1.34E-04	3.29E-02
Dmel_CG5252	4020.919	-0.666	0.175	-3.808	1.40E-04	3.37E-02
Dmel_CG12763	27.517	7.141	1.880	3.799	1.45E-04	3.41E-02
Dmel_CR44472	23.272	-2.646	0.702	-3.772	1.62E-04	3.69E-02
Dmel_CG43758	309.775	1.714	0.456	3.760	1.70E-04	3.69E-02
Dmel_CG2275	1215.191	-1.179	0.314	-3.754	1.74E-04	3.69E-02
Dmel_CG9559	4504.461	-1.078	0.287	-3.754	1.74E-04	3.69E-02
Dmel_CG1977	2140.679	1.065	0.284	3.752	1.76E-04	3.69E-02
Dmel_CG12375	831.121	-0.777	0.208	-3.739	1.85E-04	3.80E-02
Dmel_CG40813	5.158	8.173	2.197	3.720	1.99E-04	NA
Dmel_CG3812	1006.282	-0.794	0.215	-3.698	2.17E-04	4.33E-02
Dmel_CR46350	65.211	1.927	0.521	3.696	2.19E-04	4.33E-02
Dmel_CG3879	12.492	3.044	0.827	3.683	2.31E-04	4.43E-02
Dmel_CR45530	16.389	2.296	0.624	3.680	2.33E-04	4.43E-02
Dmel_CG12477	8.616	5.136	1.396	3.679	2.34E-04	NA
Dmel_CG17292	1474.083	-1.032	0.281	-3.674	2.39E-04	4.45E-02
Dmel_CG2807	1130.688	0.911	0.249	3.652	2.60E-04	4.76E-02
Dmel_CG9379	238.648	1.353	0.371	3.643	2.69E-04	4.79E-02

Dmel_CG17927	1300.359	2.092	0.574	3.641	2.71E-04	4.79E-02
Dmel_CG6006	523.400	1.551	0.427	3.636	2.77E-04	4.81E-02
Dmel_CG3407	971.487	-0.958	0.264	-3.625	2.89E-04	4.82E-02
Dmel_CG1462	323.655	1.723	0.476	3.621	2.94E-04	4.82E-02
Dmel_CG13000	15.067	2.743	0.759	3.615	3.00E-04	4.82E-02
Dmel_CG18375	181.968	1.050	0.291	3.614	3.01E-04	4.82E-02
Dmel_CG8262	752.433	-1.356	0.375	-3.614	3.02E-04	4.82E-02
Dmel_CG6227	371.074	1.175	0.326	3.604	3.13E-04	4.93E-02
Dmel_CG18549	1584.276	-0.675	0.188	-3.597	3.22E-04	4.93E-02
Dmel_CG5644	28.092	-2.406	0.670	-3.592	3.29E-04	4.93E-02
Dmel_CG34323	38.530	2.239	0.624	3.587	3.34E-04	4.93E-02
Dmel_CG17078	3064.101	-1.210	0.338	-3.584	3.39E-04	4.93E-02
Dmel_CR46481	1090.588	1.301	0.363	3.581	3.43E-04	4.93E-02
Dmel_CG3635	29.922	2.696	0.753	3.578	3.47E-04	4.93E-02
Dmel_CG9901	6113.781	-0.527	0.147	-3.577	3.47E-04	4.93E-02
Dmel_CG9707	1943.581	-0.814	0.228	-3.569	3.59E-04	5.02E-02
Dmel_CG3171	1422.762	-1.120	0.315	-3.552	3.82E-04	5.27E-02
Dmel_CG7002	154.856	2.295	0.648	3.539	4.02E-04	5.27E-02
Dmel_CG4620	4335.134	-0.936	0.265	-3.538	4.04E-04	5.27E-02
Dmel_CG6202	3774.453	-0.627	0.177	-3.537	4.04E-04	5.27E-02
Dmel_CG8411	7127.715	-0.661	0.187	-3.536	4.06E-04	5.27E-02
Dmel_CG11941	16.019	3.035	0.859	3.535	4.08E-04	5.27E-02
Dmel_CG12110	4136.182	-0.767	0.217	-3.531	4.14E-04	5.28E-02
Dmel_CG17839	101.907	1.620	0.459	3.526	4.22E-04	5.29E-02
Dmel_CG1024	621.198	-1.141	0.324	-3.521	4.30E-04	5.29E-02
Dmel_CG5445	1662.056	-0.783	0.223	-3.518	4.36E-04	5.29E-02
Dmel_CG16778	54.657	-3.076	0.875	-3.517	4.36E-04	5.29E-02
Dmel_CG5939	354.903	1.672	0.476	3.512	4.46E-04	5.34E-02

table S19. *D. melanogaster* genes with Wald Test significant results for ~Genotype*Infection vs ~Genotype+Infection+Genotype*Infection

gene_id	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
WD_RS03770	149.412	0.486	0.160	3.043	2.34E-03	7.92E-01
WD_RS05260	22.714	-1.127	0.380	-2.969	2.99E-03	7.92E-01
WD_RS06475	10.609	1.217	0.449	2.710	6.72E-03	7.92E-01
WD_RS05810	49.056	-0.535	0.199	-2.687	7.20E-03	7.92E-01
WD_RS04825	14.115	1.302	0.486	2.678	7.41E-03	7.92E-01
WD_RS04740	25.586	-1.220	0.461	-2.646	8.13E-03	7.92E-01
WD_RS04370	80.236	-0.387	0.148	-2.622	8.73E-03	7.92E-01
WD_RS01760	8.222	1.263	0.491	2.572	1.01E-02	7.92E-01
WD_RS01300	60.484	0.563	0.223	2.519	1.18E-02	7.92E-01
WD_RS05640	10.502	-1.425	0.567	-2.513	1.20E-02	7.92E-01
WD_RS02205	25.001	-1.221	0.496	-2.464	1.37E-02	8.26E-01
WD_RS01390	25.646	0.699	0.303	2.306	2.11E-02	9.96E-01
WD_RS03775	1404.573	0.354	0.161	2.207	2.73E-02	9.96E-01
WD_RS00480	8.281	1.001	0.454	2.204	2.76E-02	9.96E-01
WD_RS05480	70.888	-0.398	0.181	-2.203	2.76E-02	9.96E-01
WD_RS01110	12.261	-0.982	0.447	-2.198	2.80E-02	9.96E-01
WD_RS03920	32.007	-0.685	0.313	-2.190	2.85E-02	9.96E-01
WD_RS05665	11.884	0.905	0.422	2.145	3.19E-02	9.96E-01
WD_RS05520	17.489	0.821	0.388	2.118	3.42E-02	9.96E-01
WD_RS01790	16.771	-1.521	0.738	-2.062	3.92E-02	9.96E-01
WD_RS01335	36.739	-0.448	0.219	-2.050	4.03E-02	9.96E-01
WD_RS00655	32.020	-0.467	0.228	-2.046	4.07E-02	9.96E-01
WD_RS04175	9.229	0.982	0.483	2.034	4.20E-02	9.96E-01
WD_RS01525	14.722	0.836	0.417	2.002	4.52E-02	9.96E-01

WD_RS01990	15.357	0.803	0.405	1.985	4.72E-02	9.96E-01
WD_RS02935	45.227	0.477	0.240	1.985	4.72E-02	9.96E-01
WD_RS02225	22.418	0.650	0.333	1.949	5.13E-02	9.96E-01
WD_RS04020	7.360	0.942	0.485	1.940	5.23E-02	9.96E-01
WD_RS03070	8.315	1.286	0.665	1.934	5.32E-02	9.96E-01

table S20. wMel Wolbachia genes Wald Test significant results for ~Genotype vs ~1