

ABSTRACT

HUNTER, CHAD MICHAEL. Environmental and Genetic Determinants of Recombination Rate in *Drosophila melanogaster*. (Under the direction of Nadia D. Singh).

During meiosis, homologous chromosomes exchange genetic material through the process of recombination. Recombination helps ensure proper chromosome segregation. Recombination defects can have devastating consequences, including aneuploid gametes and cell mortality. Recombination is also a pivotal evolutionary force, creating new allelic combinations for selection to act upon. Interestingly, the frequency of recombination events and how those events are distributed genome-wide are highly variable. Here, I explore the environmental and genetic determinants of recombination rate variation in the model organism, *Drosophila melanogaster*.

In CHAPTER 2, I address how female and male genetic backgrounds individually and jointly affect crossover rates. I measured crossover rates of 10 inbred lines in a full diallel cross. The experimental design facilitates measuring the contributions of female and male genetic background, as well as female by male genetic background interaction effects on rates of crossing over in females. My results indicate that although female genetic background significantly affects crossover rates, male genetic background and the interaction of female and male genetic backgrounds have no significant effect. These findings thus suggest that male-mediated effects are unlikely to contribute greatly to natural variation in recombination rate in *Drosophila*.

In CHAPTER 3, I test the hypothesis that maternal age influences rates of crossing over in a genotypic-specific manner. After estimating rates of crossing over for individual *D. melanogaster* females from several strains as a function of maternal age, I find that both age and genetic background significantly contribute to variation in recombination frequency, as do genotype-age interactions. I further find differences in the effect of age on recombination in the two genomic regions surveyed. These results highlight the complexity of recombination rate variation and reveal a new role of genotype by environment interactions recombination rate variation.

In CHAPTER 4, I exploit natural variation in recombination rate among the sequenced lines of the *D. melanogaster* Genetic Reference Panel (DGRP) to map genetic variants affecting recombination rate. I measured rates of recombination in intervals on the X and 3R chromosomes for 205 DGRP lines. I found ~2-fold variation in recombination rates among

lines and that recombination rates are uncorrelated between the two chromosomal regions. I performed a genome-wide association study to identify genetic variants associated with natural variation in recombination rates. I selected twenty genes for functional variation and present strong evidence that four genes mediate natural variation in recombination rate. The results reveal the magnitude of population variation in recombination rate in *D. melanogaster* and identify new genetic factors modulating this variation.

In CHAPTER 5, I hypothesize that the connection between hybrid sterility and recombination illustrated with PRDM9 is not coincidental and that rather, hybrid sterility is a consequence of recombination defects. I asked whether genes involved in hybrid incompatibilities in *Drosophila* have yet unknown roles in meiotic recombination. My results suggest that two genes with clear functions in hybrid incompatibility, *JYalpha* and *Lhr*, mediate rates of recombination in *Drosophila*.

In CHAPTER 6, I utilize evolutionary rate covariation (ERC) to identify new genes mediating recombination rate variation. ERC is based on the idea that members of biological pathways are likely to experience similar evolutionary pressures, resulting in correlated rates of evolution. I analyzed ERC of 21 genes with known function in *Drosophila* meiotic recombination. My results confirm elevated ERC among meiotic recombination genes. I also identify thirteen candidate genes that have statistically significant ERC with at least eight meiotic recombination genes. Functional validation highlights two genes, *CG31898* and *CG2975*, that when disrupted significantly alter recombination rate in an interval on chromosome 3R. These results thus contribute two genetic factors involved in mediating recombination rate and demonstrate the potential of the ERC method.

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Environmental and Genetic Determinants of Recombination
Rate in *Drosophila melanogaster*

by
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DEDICATION

This dissertation is dedicated to my parents, Michael and Dori, and my fiancée, Kimberly, for always having faith in me. Without their continued support, you would not be reading this dissertation. I am forever grateful to them.

BIOGRAPHY

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CHAPTER 1. INTRODUCTION

For all organisms, the most basic biological goal is the production of offspring. For organisms that reproduce sexually, this requires the production and subsequent union of gametes. The process to create these gametes is known as meiosis. Meiosis is very similar to mitosis, as it generates new cells. However, after chromosomes are replicated, they undergo two cellular divisions, first separating homologous chromosomes, followed by separating sister chromatids. Meiosis is characterized by 4 stages (prophase, metaphase, anaphase and telophase), which repeat themselves during meiosis I and meiosis II. Briefly, during the precursor to meiosis (interphase), DNA is replicated (for a detailed review, see Bell and Dutta 2002). During prophase I, homologous chromosomes synapse and undergo homologous recombination. During metaphase I, chromosomes are aligned along the metaphase plate. During anaphase I, homologous chromosomes separate and during telophase I, the cleavage furrow forms and the cytoplasm is separated. This process is then repeated (minus recombination as present in prophase I) and 4 haploid cells are formed.

Meiotic recombination, one of the most intriguing and exciting biological processes, occurs during the lengthiest of the eight phases of meiosis, prophase I. In *Drosophila*, which is the subject of this thesis work, meiotic recombination occurs in females but not in males (Morgan 1912, 1914). Within females, recombination occurs within region 2a of the germarium (Mehrotra and McKim 2006), which is the most anterior portion of the ovariole. During recombination, homologous chromosomes first undergo synapsis with the formation of the synaptonemal complex (SC) which is made primarily of C(3)G (crossover suppressor on 3 of Gowen) (Page and Hawley 2001) and C(2)M (Manheim and McKim 2003). C(3)G is the transverse filament (Page and Hawley 2001) and C(2)M is the lateral element (Anderson et al. 2005), essentially forming a bridge between the homologous chromosomes. Following synapsis (**Figure 1.1A**), programmed DSBs are initiated by MEI-W68 (McKim and Hayashi-Hagihara 1998) (known as Spo11 in many other organisms) and MEI-P22 (Liu et al. 2002) (**Figure 1.1B**). Spo11 was originally discovered in yeast (Keeney et al. 1997). MEI-P22 mutants display the same phenotype as MEI-W68 mutants (Liu et al. 2002) which is surprising since most other organisms to date rely simply on Spo11 for the formation of DSBs. Additionally, before the recruitment of MEI-W68 and MEI-P22, Trade Embargo (Trem) is engaged in promoting locations for DSBs (Lake et al. 2011). A suite of proteins assist in repairing DSBs via the DSB repair model originally proposed by Szostak (1983).

Following the DSB, the ends are processed to produce 3' overhangs (Sun et al.

1991) (**Figure 1.1C**), this process is also known as resection. The next step is known as strand invasion (**Figure 1.1D**) in which one 3' end will invade the other strand (which does not contain a DSB). Proteins involved in this step and proceeding steps include OKRA, spindle-A (SPNA), spindle-B (SPNB), and spindle-C (SPNC) (Ghabrial et al. 1998; McCaffrey et al. 2006). This invasion creates what is known as displacement loop, or D-loop. DNA synthesis will occur following the template strand. Following this is second-end capture in which the other resected end anneals to the D-loop and synthesis begins for the upper portion of the D-loop. There are two possible fates for this structure. One pathway is through synthesis-dependent strand annealing pathway (**Figure 1.1G-H**). This involves disassociation (**Figure 1.1G**), followed by annealing which results in a non-crossover product (**Figure 1.1H**). The other pathway follows the typical DSB repair pathway. In **Figure 1.1E**, there is the formation of the double Holliday junction, named after Robin Holliday who originally proposed the structure (Holliday 1964). Following this structure formation is a process known as resolution in which the fate of the products will be decided (as either a noncrossover or crossover product). The fate of the products is decided by where the nicks in each strand are. The majority of nicks are aided by a RecQ DNA helicase (*BLM*) (Chu and Hickson 2009), which creates noncrossover products, with only a subset resulting in crossover products (shown in **Figure 1.1F**). There numerous proteins involved in the processing of a crossover product such as MEI-9 (Sekelsky et al. 1995), MUS312 (Yildiz et al. 2002), ERCC1 (Radford et al. 2005), and HDM (Joyce et al. 2009). Additionally, a recent study has shown that REC, MSH4 and MSH5 help block BLM in order to promote crossovers in *Drosophila* (Kohl et al. 2012).

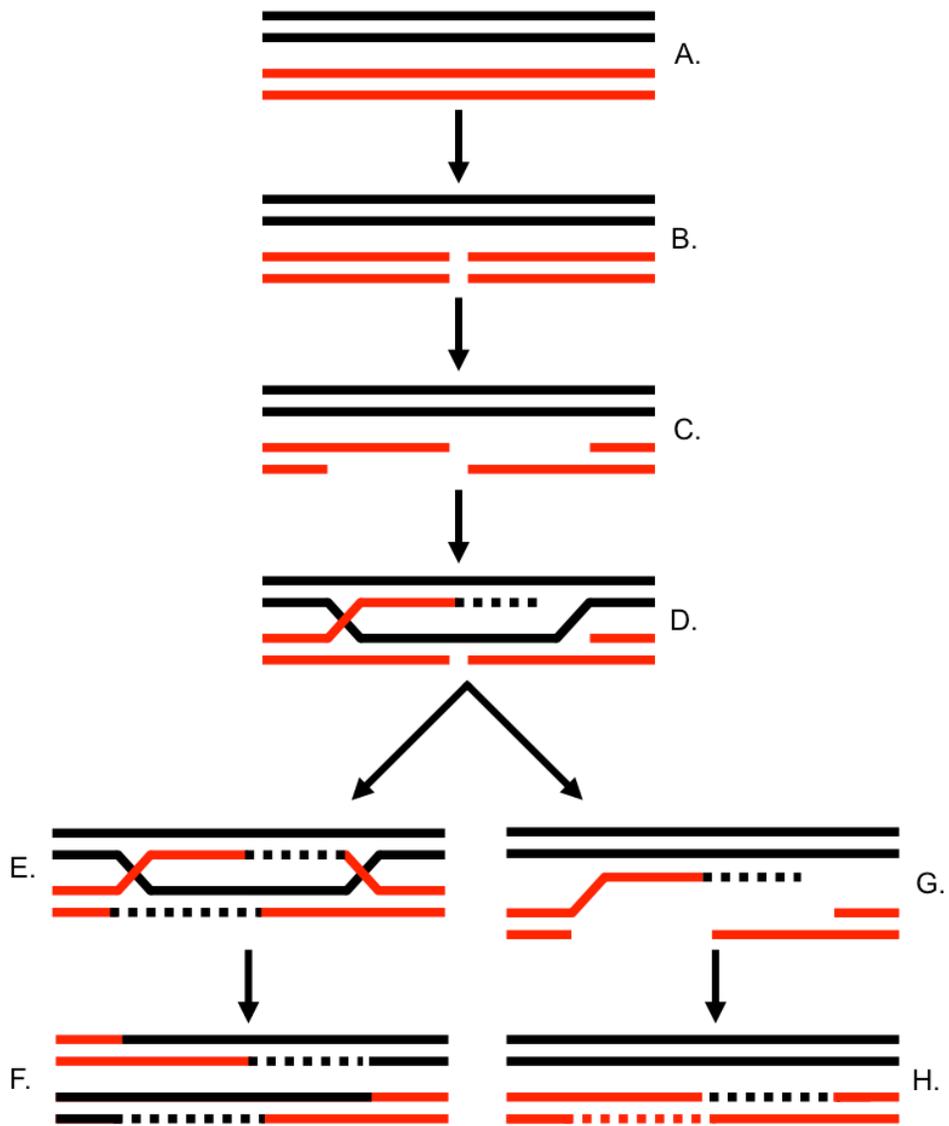


Figure 1.1 - Meiotic DSB repair pathway. Modeled after Andersen and Sekelsky (2010) and Bugreev et al. (2011). Originally proposed by Szostak (1983). The resulting products are either a (F) crossover or (H) noncrossover.

IMPORTANCE OF RECOMBINATION

Meiotic recombination is necessary for proper chromosome segregation in many organisms (Roeder 1997). Lack of recombination and aberrant placement of recombination events along the chromosome can generate aneuploid gametes; aneuploidy is the leading known cause of miscarriages and the principal genetic cause for developmental disability and delay in humans (Hassold and Hunt 2001). For example, reduced recombination has been repeatedly linked with human trisomies such as trisomy 15 (Robinson et al. 1998), 16 (Hassold et al. 1995), 18 (Bugge et al. 1998), 21 (Hassold and Sherman 2000) along with sex chromosome trisomies (Hassold et al. 1991; MacDonald et al. 1994).

In addition to its role in preserving genomic integrity between generations, recombination is a pivotal force in evolution, breaking down linkage disequilibrium. In this way, recombination can create new allelic combinations and may provide adaptive potential for populations (Rice 2002). Recombination also reduces Hill-Robertson interference between alleles thus increasing the efficacy of natural selection (Fisher 1930; Muller 1932; Hill and Robertson 1966). Consistent with the importance of recombination for genome evolution in particular, rates of recombination have been shown to correlate with a number of genomic traits such as the amount of DNA polymorphism (Aguadé et al. 1989a,b; Stephan and Langley 1989; Begun and Aquadro 1992), rates of protein evolution (Pál et al. 2001; Betancourt and Presgraves 2002), density of transposable elements (Bartolome et al. 2002; Rizzon et al. 2002; Petrov et al. 2011; Kofler et al. 2012), density of satellite DNA (Stephan 1986, 1987), and codon bias (Comeron et al. 1999; Marais and Piganeau 2002).

RECOMBINATION RATE VARIATION

Given the crucial role of recombination in meiosis and the devastating consequences of aberrant recombination, one might hypothesize that the process of recombination would be tightly regulated and finely-tuned so as to ensure proper chromosome segregation, yet both the rate and distribution of recombination are highly variable. Variation in recombination rate is present in almost all species studied to date such as yeast (Mancera et al. 2008; Tsai et al. 2010), worms (Barnes et al. 1995; Rockman and Kruglyak 2009), *Drosophila* (Brooks and Marks 1986; True et al. 1996; Stevison and Noor 2010; Comeron et al. 2012), honey bees (Ross et al. 2015), maize (Bauer et al. 2013), chickens (Rahn and Solari 1986), mice (Dumont et al. 2009), chimps (Ptak et al. 2004, 2005; Winckler et al. 2005) and humans (Kong et al. 2002; Crawford et al. 2004; Myers et al. 2005), to name a few. Variation is still present even on smaller scales such as within and between populations (Brooks and Marks

1986; Crawford et al. 2004; McVean et al. 2004; Fearnhead and Smith 2005; Graffelman et al. 2007; Dumont et al. 2009; Kong et al. 2010; Comeron et al. 2012) and among individuals (Brooks and Marks 1986; Yu et al. 1996; Coop et al. 2008; Dumont et al. 2009; Wang et al. 2012).

In many different organisms, there are differences in recombination rates between the sexes. According to Haldane-Huxley's rule (Haldane 1922; Huxley 1928), the heterogametic sex will typically have lower rates of recombination. We see a drastic example of this in *Drosophila melanogaster* and other Drosophilids with the males experiencing no recombination events (Morgan 1912, 1914). In numerous organisms, the heterogametic sex has lower rates of recombination such as in silk moths (Tanaka 1914), zebrafish (Singer et al. 2002), dogs (Neff et al. 1999), pigs (Marklund et al. 1996), mice (Dietrich et al. 1996), wallabies (Zenger et al. 2002) and humans (Dib et al. 1996). Yet there are also exceptions to this such as in sheep (Crawford et al. 1995) where the heterogametic sex has more crossovers, and also in chickens (Groenen et al. 2000) and pigeons (Pigozzi and Solari 1999) where there are no differences between sexes. It appears though that the majority of species have sex differences in recombination rates (for a more detailed list, see Lenormand and Dutheil 2005).

The distribution of recombination events within the genome also varies on both broad and fine scales (Lindsley et al. 1977; McVean et al. 2004; Cirulli et al. 2007; Paigen et al. 2008; Singh et al. 2009, 2013). This heterogeneity in rates of recombination across the genome can be seen in species such as in humans (Kong et al. 2002, 2010), mice (Nachman and Churchill 1996) and in *Drosophila* (Cirulli et al. 2007; Comeron et al. 2012). Typically, in regards to chromosome dynamics, there tend to be more crossover events in the middle of the chromosome, slight elevation near the telomeres in many species, and less crossover events near the centromere (Choo 1998). One hypothesis on why there are fewer crossovers near the centromere is because there is more heterochromatin in these regions as well as the fact that centromeres are needed for chromosome stability. In addition, in many species, there are areas of increased recombination known as "hotspots" (see Lichten and Goldman 1995 for review). Hotspots are local peaks of recombination exhibiting rates of recombination 10-1000 fold higher than adjacent regions. Some species are more extreme than others in their hotspot usage. In humans, roughly 80% of crossovers are believed to occur in these hotspots which only occupy 10-20% of the genome (Myers et al. 2005). A number of other organisms also exhibit these hotspots such as yeast (Gerton et al. 2000; Mancera et al. 2008), dogs (Axelsson et al. 2012), mice (Smagulova et al. 2011)

and chimps (Auton et al. 2012). In contrast, *Drosophila* do not have recombination hotspots though there is fine-scale heterogeneity of where crossovers occur (Cirulli et al. 2007; Singh et al. 2009, 2013; Comeron et al. 2012).

GENETIC FACTORS INFLUENCING RATES OF RECOMBINATION

Given the importance of recombination and the pervasive natural variation in recombination rate, it is perhaps unsurprising that the genetic basis of this variation has been an active area of research for the last decade. However, to date, only a small handful of genetic determinants have been identified that mediate the frequency of recombination. While CHAPTER 4 will go more in depth on what is known, there are a few key points that will be highlighted here. It is well-documented that recombination rate is a variable and heritable trait in *Drosophila*. For instance, classical genetic experiments indicate that the amount of crossing-over as well as the distribution of crossover events can vary among lines of *D. melanogaster* (Broadhead et al. 1977; Brooks and Marks 1986; Comeron et al. 2012; Hunter and Singh 2014), suggesting population-level variation in this trait. Additionally, there have been numerous artificial selection studies on rates of crossing over in *Drosophila* (Detlefsen and Roberts 1921; Parsons 1958; Acton 1961; Mukherjee 1961; Moyer 1964; Chinnici 1971a,b; Kidwell 1972a,b; Valentin 1973a,b; Charlesworth and Charlesworth 1985a,b; Charlesworth et al. 1985), many which have been successful in either increasing or decreasing rates of recombination in a given interval over many generations. Finally, changes in recombination rate have been shown to evolve as a correlated response to artificial selection on other characteristics, such as sternopleural bristle number (Rodell et al. 2004), DDT resistance (Flexon and Rodell 1982), geotaxis (Korol and Iliadit 1994), and resistance to temperature fluctuations (Zhuchenko et al. 1985), which is again consistent with segregating natural variation in recombination rate.

Chromosomal inversions are one of the most dramatic examples of a genetic element affecting recombination rate. Numerous studies in *Drosophila* (Sturtevant and Beadle 1936; Schultz and Redfield 1951; Novitski and Braver 1954; Stevison et al. 2011) have shown that inversions reduce recombination in the region of the inversion and increase recombination in other areas of the genome (also known as the interchromosomal effect; Schultz and Redfield 1951).

With respect to the genetic basis of the distribution of crossover events, the first known determinant of recombination distribution in metazoans was discovered recently (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010). This remarkable discovery

implicates PRDM9 in determining the locations of meiotic recombination hotspots in both humans and mice. Variation within PRDM9 also modulates hotspot activity in humans (Berg et al. 2010). PRDM9 is a histone methyltransferase that catalyzes histone H3 lysine 4 trimethylation (Baudat et al. 2013). This rapidly evolving protein (Oliver et al. 2009) was first associated with hybrid sterility in rodents (Mihola et al. 2009), and evidence continues to accumulate that it is a major component of recombination hotspot determination in mammalian systems (Berg et al. 2010, 2011; Kong et al. 2010; Hinch et al. 2011; Smagulova et al. 2011; Auton et al. 2012; Brick et al. 2012). Comparatively less is known in other systems such as *Drosophila*. Several studies have identified sequence motifs associated with recombination events (Cirulli et al. 2007; Kulathinal et al. 2008; Stevison and Noor 2010; Comeron et al. 2012; Heil and Noor 2012; Miller et al. 2012; Singh et al. 2013), but none have been functionally validated to date. *Drosophila* lacks PRDM9 (Oliver et al. 2009; Heil and Noor 2012), and perhaps relatedly, also lacks the highly punctate recombination landscape seen in mammals. Crossover distribution in *Drosophila* is far less heterogeneous (Comeron et al. 2012) and linkage disequilibrium decays over very small chromosomal spans (e.g. Mackay et al. 2012).

Recent work in mammals has also provided insight into the genetic architecture of global recombination rate. RNF212 has been repeatedly associated with natural variation in recombination rate in several systems including humans (Kong et al. 2008; Chowdhury et al. 2009), cattle (Sandor et al. 2012), and Soay sheep (Johnston et al. 2015). Consistent with a role of this protein in modulating recombination rate, mouse RNF212 is essential for meiotic recombination and has a key role in stabilizing meiosis-specific recombination factors (Reynolds et al. 2013). Moreover, in addition to its role with hotspot determination, PRDM9 has also been associated with heritable variation in recombination rate (Hinch et al. 2011; Capilla et al. 2014) in humans and mice. Other mediators of recombination rate include REC8 (Sandor et al. 2012), which is a cohesin that is required for proper chromosome segregation in many organisms (Bhatt et al. 1999; Parisi et al. 1999; Watanabe and Nurse 1999). In humans, inversion 17q21.31, a 900 kb inversion, is associated with increased recombination and fecundity in European females (Stefansson et al. 2005).

ENVIRONMENTAL FACTORS INFLUENCING RATES OF RECOMBINATION

Recombination rates are phenotypically plastic, meaning that rates of recombination can vary in response to environmental conditions even within a single genetic background. A common hypothesis is that environmental stress alters rates of recombination (Parsons

1988; Hoffmann and Parsons 1997; Hadany and Beker 2003), typically increasing recombination (Agrawal et al. 2005; Zhong and Priest 2011). Since the early days of *Drosophila* genetics, many different factors have been studied and continue to be studied (see CHAPTERS 2 & 3 for my addition to the current growing literature). For example, nutrition has been shown to alter rates of crossing over in both yeast (Abdullah and Borts 2001) and in *Drosophila* (Bergner 1928; Neel 1941). Other factors that have been examined that affect rates of crossing over include mating partner (Redfield 1966; Priest et al. 2007, 2008; Stevison 2012), maternal age (Bridges 1915, 1927; Plough 1917, 1921; Stern 1926; Neel 1941; Hayman and Parsons 1960; Redfield 1966; Brooks and Marks 1986; Tedman-Aucoin and Agrawal 2011), pathogen exposure (Singh et al. 2015), social stress (Belyaev and Borodin 1982), and temperature (Plough 1917, 1921; Stern 1926; Smith 1936; McNelly-Ingle et al. 1966; Rose and Baillie 1979; Ashburner et al. 2005; Lim et al. 2008).

DISSERTATION SUMMARY

The following dissertation will take you on a journey investigating both environmental and genetic determinants of recombination rate in *D. melanogaster*. CHAPTER 2 investigates the possibility that males can influence rates of crossing over in females that they are mated with, as proposed by Stevison (2012). The results were published in *Evolution* (Hunter and Singh 2014). CHAPTER 3 investigates how advancing maternal age affects rates of crossing over in *D. melanogaster* females, a topic that has been highly-studied and remains intensely-debated in *Drosophila* and in humans. The results are in revision at *G3: Genes | Genomes | Genetics*. CHAPTER 4 focuses on using the natural variation of the *Drosophila melanogaster* Genetic Reference Panel (Mackay et al. 2012) to complete a genome-wide association study of recombination rate variation and identifies new genetic factors possibly involved with meiotic recombination rate variation. The results are in review at *PLoS Genetics*. CHAPTER 5 investigates the hypothesis that genes involved in hybrid incompatibilities and hybrid sterility might have a dual role in modulating recombination rates. Finally, CHAPTER 6 investigates proteins that are evolving at similar rates to many known meiotic genes and if they also have a previously unidentified role in recombination. **Enjoy!**

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CHAPTER 2. DO MALES MATTER? TESTING THE EFFECTS OF MALE GENETIC BACKGROUND ON FEMALE MEIOTIC CROSSOVER RATES IN *DROSOPHILA MELANOGASTER*

Hunter, C. M., and N. D. Singh. 2014. Do males matter? Testing the effects of male genetic background on female meiotic crossover rates in *Drosophila melanogaster*. *Evolution* 68: 2718–2726.

The following paper was published in the journal, *Evolution*. The goal of the study was to address two outstanding questions related to male-mediated effects on female recombination rate. First, we were interested in investigating whether the effect of male genetic background is mediated in part by female genetic background. That is, are there female × male genetic background interaction effects on crossover rate? Second, we were interested in what the mechanism underlying the effect of male genetic background on female crossover rate was? Was it due to gametic selection or was it due to increased rates of crossing over?



DO MALES MATTER? TESTING THE EFFECTS OF MALE GENETIC BACKGROUND ON FEMALE MEIOTIC CROSSOVER RATES IN *DROSOPHILA MELANOGASTER*

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Meiotic recombination is a critical genetic process as well as a pivotal evolutionary force. Rates of crossing over are highly variable within and between species, due to both genetic and environmental factors. Early studies in *Drosophila* implicated female genetic background as a major determinant of crossover rate and recent work has highlighted male genetic background as a possible mediator as well. Our study employed classical genetics to address how female and male genetic backgrounds individually and jointly affect crossover rates. We measured rates of crossing over in a 33 cM region of the *Drosophila melanogaster* X chromosome using a two-step crossing scheme exploiting visible markers. In total, we measured crossover rates of 10 inbred lines in a full diallel cross. Our experimental design facilitates measuring the contributions of female genetic background, male genetic background, and female by male genetic background interaction effects on rates of crossing over in females. Our results indicate that although female genetic background significantly affects female meiotic crossover rates in *Drosophila*, male genetic background and the interaction of female and male genetic backgrounds have no significant effect. These findings thus suggest that male-mediated effects are unlikely to contribute greatly to variation in recombination rates in natural populations of *Drosophila*.

KEY WORDS: *Drosophila*, meiosis, recombination.

During meiosis, one of the most important cellular processes occurs when homologous chromosomes undergo meiotic recombination and exchange genetic material. Meiotic recombination begins with a programmed double-stranded break (DSB) in the DNA (Orr-Weaver et al. 1981; Szostak et al. 1983). These DSBs have two possible fates after processing via the DSB repair pathway, noncrossovers and crossovers. Crossovers not only aid in proper chromosome segregation but also help to maintain genome stability (Andersen and Sekelsky 2010).

Meiotic recombination is also a pivotal force in genome evolution. Recombination breaks down linkage disequilibrium and increases the efficacy of natural selection by reducing Hill–Robertson interference (Hill and Robertson 1966). Indeed, areas of the genome with higher rates of recombination also have a higher efficacy of natural selection (e.g., Berry et al. 1991;

Cameron et al. 1999; Haddrill et al. 2007). Additionally, rates of recombination have been shown to correlate with genomic features such as the amount of DNA polymorphism (Begun and Aquadro 1992), rates of protein evolution (Pál et al. 2001; Bétantcourt and Presgraves 2002), density of transposable elements (Rizzon et al. 2002), and codon bias (Cameron et al. 1999; Marais and Piganeau 2002), highlighting the biological significance of recombination rate for genome architecture and evolution.

Rates of meiotic recombination have been shown to be variable at all scales. Recombination rate varies among closely related species (True et al. 1996; Wall et al. 2003; Jensen-Seaman et al. 2004; Ptak et al. 2004, 2005; Winckler et al. 2005), among populations (Brooks and Marks 1986; Crawford et al. 2004; McVean et al. 2004; Fearnhead and Smith 2005; Graffelman et al. 2007; Dumont et al. 2009; Kong et al. 2010; Cameron et al. 2012),

among individuals (Brooks and Marks 1986; Yu et al. 1996; Coop et al. 2008; Dumont et al. 2009; Kong et al. 2010; Wang et al. 2012), and within the genome (Lindsley et al. 1977; McVean et al. 2004; Cirulli et al. 2007; Paigen et al. 2008; Singh et al. 2009, 2013).

In addition to being highly variable within and among species, recombination rates are also highly plastic. That is, recombination rate can vary in response to environmental conditions even within the context of a single genetic background. For instance, previous work indicates that stress alters recombination rate (Parsons 1988; Hadany and Beker 2003), typically increasing rates of recombination (Agrawal et al. 2005; Zhong and Priest 2011). Stressors that influence rates of crossing over include age (Stern 1926; Bridges 1927; Redfield 1966; Speed 1977; Kong et al. 2004; Tedman-Aucoin and Agrawal 2011; Vrooman et al. 2013), nutrition (Neel 1941; Abdullah and Borts 2001), pathogens (Lucht et al. 2002; Kovalchuk et al. 2003), and temperature (Plough 1917, 1921).

One stressor that most sexually reproducing organisms encounter is the act of mating. In *Drosophila*, mating has been shown to have detrimental effects on female fitness (Fowler and Partridge 1989) as well as to a lesser degree on male fitness (Markow et al. 1978; Dewsbury 1982). Previous work has suggested that mating stress, including the amount of mating and the age at which mating occurs, can significantly affect crossover rates in *Drosophila* (Redfield 1966; Priest et al. 2007, 2008). Moreover, a recent study indicated a significant effect of male genetic background on female crossover rate in *Drosophila melanogaster* (Stevison 2012). That is, genetically identical females produced different proportions of recombination progeny depending on the genetic background of the males to which they were mated. This could suggest that males are differentially stressful to females during mating and that one consequence of this variability is an effect of male genotype on female recombination rate.

The goal of our study was to address two outstanding questions related to male-mediated effects on female recombination rate. First, we were interested in investigating whether the effect of male genetic background is mediated in part by female genetic background. That is, are there female \times male genetic background interaction effects on crossover rate? Second, what is the mechanism underlying the effect of male genetic background on female crossover rate? Is this due to gametic selection or is it due to increased rates of crossing over?

To address these questions, we used a classical genetic approach. We measured crossover rate over a 33 cM region on the X chromosome by exploiting visible phenotypic markers in a two-step crossing scheme. Our study made use of 10 inbred strains from a North American population of flies. We used a full diallel cross, allowing us to investigate the effects of female genetic background, male genetic background, and female \times male ge-

netic background interaction effects. To distinguish between the two mechanistic hypotheses, we utilized the timing of oogenesis to separately analyze recombination events that occurred before and after the act of mating. Our results confirm a strong female genetic background effect as well as an effect of maternal age, as expected based on previous work (Plough 1917, 1921; Stern 1926; Bridges 1927; Redfield 1966; Brooks and Marks 1986; Tedman-Aucoin and Agrawal 2011). However, we see no evidence of an effect of male genetic background or a female \times male genetic background interaction effect. Our results thus suggest that male genetic background does not markedly contribute to variation in rates of crossing over in this population of *D. melanogaster*. We therefore suggest that male-mediated effects on female recombination rate in *Drosophila* are unlikely to be pervasive in natural populations.

Materials and Methods

STOCKS AND MARKERS

We randomly selected 10 lines from the *D. melanogaster* Genetic Reference Panel (DGRP) (Mackay et al. 2012). The 10 lines were RAL_21, RAL_26, RAL_38, RAL_40, RAL_45, RAL_57, RAL_59, RAL_73, RAL_75, and RAL_136. Three of lines (RAL_26, RAL_38, and RAL_136) contain autosomal inversions (Huang et al. 2014). The visible markers used in the study were *yellow* (*y*) and *vermillion* (*v*). These recessive markers are 33 cM apart on the X chromosome (Morgan and Bridges 1916). These markers were selected due to their apparent lack of viability defects (Morgan and Bridges 1916), ease of scoring and large genetic distance. Although *yellow* mutants show defects in male behavior and courtship (Barker 1962), such defects are unlikely to adversely affect our experiment because these males are not used in the experimental cross (see below). Rather, these males are simply used to generate females that are doubly heterozygous for visible markers such that recombination can be scored. The marker strain was constructed by using a $y^1 v^1$ mutant line (stock no. 1509 from the Bloomington *Drosophila* Stock Center) and introducing the doubly marked X chromosome into a Samarkand wild-type genetic background using balancers.

EXPERIMENTAL CROSSES

To score crossover frequency on the X chromosome, we used a two-step crossing scheme (Fig. 1). All crosses were performed at 25°C with a 12-h light–dark cycle on standard media using virgin females aged 12–24 h post eclosion. In the first cross, 20 virgin females from each of the 10 different DGRP lines were collected and then crossed to 20 *y v* males in 8 oz. bottles. $F_1 + + / y v$ virgin females were subsequently collected. Males and females were allowed to mate for 5 days, after which all adults were cleared from the bottles. In the second cross, 10 virgin F_1 females (12–24 h old) and 10 DGRP males (3–4 days old) were crossed in vials; this was

BRIEF COMMUNICATION

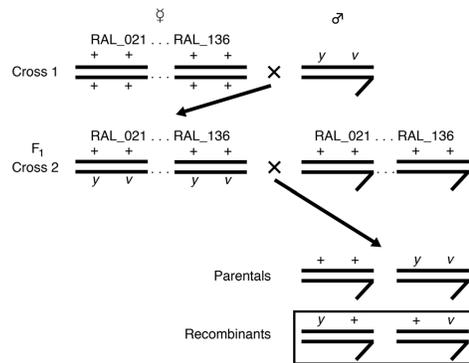


Figure 1. Two-step crossing scheme to score crossover rates. Only the X chromosome is shown for simplicity. Recombinant males are highlighted in the box outlined in black.

done for all 100 combinations of females and males (two vials per combination per block). After 6 h, males were removed from the vials. We chose a 6 h mating window because in our own experience, ~60–70% of single pair copulations for DGRP strains are successful over this time frame. Males were removed after this window to minimize the potential effects of multiple matings, as previous studies have suggested that increased mating increases crossover rates (Priest et al. 2007). Although *D. melanogaster* females display a lack of receptivity to remate soon after mating (Manning 1962, 1967; Bubis et al. 1998), remating within a 6-h window is not uncommon (e.g., Van Vianen and Bijlsma 1993; Drapeau et al. 2001). However, very young females (such as those used for the current experiment) show very low remating rates, on the order of 10% (Van Vianen and Bijlsma 1993). We are thus confident that remating is sufficiently rare in our experiment as to not compromise our ability to detect effects of various factors on crossover rate.

The experimental crosses were set up in two blocks, with two replicates per cross per block. The F₁ females were transferred to new vials every day for 10 days. After 15 days, the progeny were collected from each vial, frozen, and male progeny were scored for the recombinant phenotypes. Recombinant male progeny were identified as having only one visible marker (y + or + v). Previous work in our laboratory has demonstrated that freezing flies has no effect of the visible markers we are scoring. All of the raw data associated with this manuscript have been deposited into Dryad.

STATISTICS

All statistics were run using SAS version 9.3. To test for significant effects of crossover frequency, we used a mixed effects model

using random effects implemented in PROC MIXED in SAS software. The full model is as follows:

$$R_{ijklmn} = \mu + F_i + M_j + T_l + F_i \times M_j + F_i \times T_l + M_j \times T_l + F_i \times M_j \times T_l + B_k + V[F, M, B]_m + \varepsilon_n,$$

for $i = 1 \dots 10$; $j = 1 \dots 10$; $k = 1, 2$; $l = 1, 2$; $m = 1, 2$; $n = 1 \dots 800$

where R represents the crossover frequency, μ represents the mean of regression and ε represents the error. The model terms F and M stand for female and male genotype, respectively. T stands for time, either the first 5 days or the second 5 days. The timing of oogenesis allows us to separate crossover events that occurred before mating (the first 5 days) and crossover events that occurred after mating (the later 5 days) (McKim et al. 2002; Mehrotra and McKim 2006). F , M , and T are all fixed effects. Although modeling F and M as random effects could also be argued as appropriate, we note that modeling F and M as random effects does not change our results (data not shown). B is block and V is vial (replicate within block) and is nested within F , M , and B . Both B and V are random effects. There are also interaction effects between F , M , and T . We can estimate the proportion of phenotypic variation in recombination rate explained by each factor by taking the ratio of the sum of squares of a given factor to the total sum of squares. These proportions are converted to percentages and reported in Table 1.

Because inversions have an effect on recombination (Sturtevant and Beadle 1936; Schultz and Redfield 1951; Novitski and Braver 1954), we ran the model on two datasets: one with all lines included and one with only the seven inversion-free lines. Additionally, we utilized the SLICE function in SAS software to test for effects of each of these factors in the context of each time block, either the first 5 days or the second 5 days. The SLICE function allows for a test of simple effects; in this case, we are testing for an effect of M and F within each level of T (Winer 1971). We also repeated the analysis using our data coded as a binary response (whether an individual was recombinant or not) using a PROC GLIMMIX framework with the same parameters listed above, modeling after Stevison (2012).

Finally, to test for an effect of male genetic background on female fitness, we used a PROC MIXED framework described above. We use total number of progeny as a measure of female fitness. The full model is

$$P_{ijklmn} = \mu + F_i + M_j + F_i \times M_j + B_k + V[F, M, B]_m + \varepsilon_n,$$

for $i = 1 \dots 10$; $j = 1 \dots 10$; $k = 1, 2$; $m = 1, 2$; $n = 1 \dots 800$

where P represents the number of progeny, μ represents the mean of regression, and ε represents the error. The model terms F and M stand for female and male genotype, respectively. F and M are fixed effects. B is block and V is vial (replicate within block) and

Table 1. PROC MIXED fixed effects analysis.

Source	With inversions present				Without inversions present			
	df	F value	Pr > F	%	df	F value	Pr > F	%
<i>F</i>	9	9.62	<0.0001	16.23	6	6.73	<0.0001	16.03
<i>M</i>	9	0.72	0.69	-	6	1.08	0.39	-
<i>T</i>	1	46.94	<0.0001	3.06	1	20.81	<0.0001	3.08
<i>F</i> × <i>M</i>	81	0.68	0.96	-	36	0.71	0.86	-
<i>F</i> × <i>T</i>	9	1.40	0.19	-	6	1.12	0.35	-
<i>M</i> × <i>T</i>	9	0.46	0.90	-	6	0.20	0.98	-
<i>F</i> × <i>M</i> × <i>T</i>	81	0.87	0.78	-	36	0.74	0.86	-

% = percentage of variance explained by factor (reported only for significant factors); *F* = female genotype; *M* = male genotype; *T* = time (either the first 5 days or the second 5 days).

is nested within *F*, *M*, and *B*. Both *B* and *V* are random effects. There is also an interaction effect between *F* and *M*.

Results and Discussion

ROBUSTNESS OF CROSSOVER RATE ESTIMATION

In total, 152,547 progeny were collected from the experimental crosses, with 73,870 of those being males that were scored for recombination. Of these males, 12,356 were of the phenotype *y* + and 11,604 were of the phenotype *y* *v*. The average crossover frequency was 33 cM, which aligns perfectly with the expected genetic distance between these markers of 33 cM (Morgan and Bridges 1916). To test for deviations from expected ratios of phenotype classes, we performed *G*-tests for goodness of fit for all 100 combinations of female lines crossed to male lines for the following ratios: total males versus total females, total wild-type males versus total *y* *v* males and finally, total *y* + males versus total *y* *v* males. The null hypothesis for each comparison is a 1:1 ratio of phenotype classes. We used a Bonferroni correction with an initial $\alpha = 0.05$ to correct for multiple tests. For each of the 100 crosses, we summed progeny counts across the four replicates of that cross.

Comparing total females to total males, only six out of the 100 combinations show significant deviations from the expected 1:1 ratio ($P < 0.0004$, *G*-test). Interestingly, in all six cases, there were significantly more females than males. This is consistent with a very mild viability defect associated with the *y* *v* chromosome. Comparing wild-type males versus *y* *v* males, five out of the 100 combinations show a significant deviation from the expected 1:1 ratio ($P < 0.0001$, *G*-test). Again, all five of these lines show deviations in the same direction, with significantly more wild-type males than *y* *v* males. This is similarly consistent with a small viability defect associated with the doubly marked chromosome. Surprisingly, there was no overlap in the combination of lines from the two tests. Comparing the counts of *y* + males

versus *y* *v* males, none of the 100 crosses showed a significant difference between recombinant phenotypes ($P > 0.004$, all comparisons, *G*-test). Given the overall concordance of our results with null expectation, we believe that viability defects associated with the doubly marked chromosome are minute at best and as a consequence, we are confident that our approach to estimating crossover rate is robust.

FACTORS AFFECTING CROSSOVER RATE VARIATION

Overall, crossover frequency varies markedly among female genetic backgrounds (measured as an average across all 10 male genotypes for the entire 10-day collection period), ranging from 28.3 to 37.6 cM (Fig. 2A). The magnitude of variation in crossover frequency among lines (measured as the maximum observed crossover rate—minimum crossover rate) from the current study (9.26 cM) is comparable to the range in crossover frequency observed in this interval previously (8.8 cM; Brooks and Marks 1986; Fig. 2A). Measured in a slightly different way, our data show 1.33-fold variation in crossover rate among lines which is highly consistent with previous reports of 1.27-fold variation across strains in this same region (Brooks and Marks 1986).

To identify factors significantly contributing to crossover rate variation in this experiment, we used a mixed effects model. Our results indicate that female genetic background significantly affects crossover frequency ($P < 0.0001$), explaining 16.23% of the observed phenotypic variation in crossover rate (Table 1). This result is robust to the effect of inversions, as female genetic background remains a significant factor even if we restrict our analysis to the seven lines that are homozygous for a standard chromosome arrangement ($P < 0.0001$; Table 1). In addition, female genetic background contributes persistently to crossover rate variation, as this factor is clearly significant in both time points surveyed (Table 2). Our results are thus consistent with previous work highlighting a role of female genetic background in recombination rate variation (Brooks and Marks 1986; Cameron et al. 2012).

BRIEF COMMUNICATION

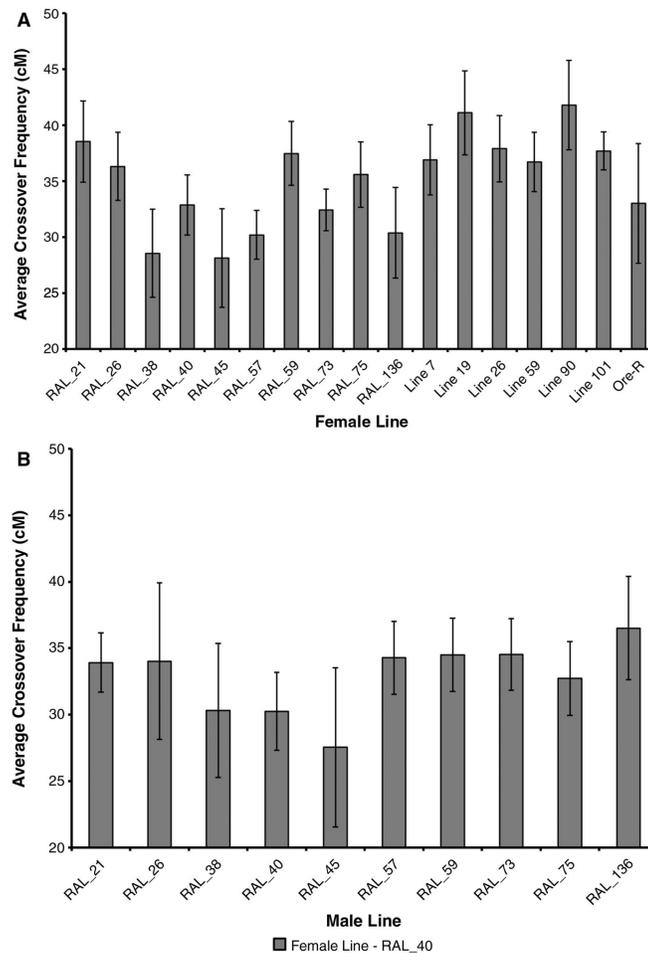


Figure 2. Crossover frequency over the entire 10-day period of (A) females averaged across male genetic backgrounds and (B) line RAL_40 females as a function of male genetic background. Error bars represent standard deviation. Note that in panel A, previous data are included for comparison (lines 7, 19, 26, 59, 90, 101, and Ore-R taken from Brooks and Marks 1986).

In contrast to previous results (Stevison 2012), we find no significant contribution of male genetic background to crossover rate variation ($P = 0.69$; Table 1). We also find no evidence in support of female \times male genetic background interaction effects on crossover rate ($P = 0.96$; Table 1). This is not due to confounding effects of inversions, as limiting the analysis to lines with standard arrangements produces similar results (Table 1). Indeed, very little variation in crossover frequency is observed for

a given female genetic background as a function of male genotype (e.g., Figs. 2B, S1–S9).

One formal possibility for this negative result is a lack of sexual conflict among the genotypes chosen for our study. Indeed, our study is motivated by the hypothesis that mating is stressful in *Drosophila* and that different males genotypes are differentially stressful to females. If the genotypes surveyed here do not vary in their consequences for female fitness, then perhaps a lack of

Table 2. PROC MIXED fixed effects analysis including time.

Source	Time	With inversions present			Without inversions present		
		df	<i>F</i> value	Pr > <i>F</i>	df	<i>F</i> value	Pr > <i>F</i>
<i>F</i>	Early	9	5.94	<0.0001	6	3.86	0.0013
<i>F</i>	Late	9	9.01	<0.0001	6	6.57	<0.0001
<i>M</i>	Early	9	0.83	0.59	6	1.03	0.41
<i>M</i>	Late	9	0.48	0.89	6	0.64	0.70
<i>F</i> × <i>M</i>	Early	99	1.07	0.32	48	1.01	0.46
<i>F</i> × <i>M</i>	Late	99	1.58	0.0017	48	1.57	0.021

F = female genotype; *M* = male genotype; *T* = time (either the first 5 days or the second 5 days).

male-mediated effects on recombination rate is unsurprising. To address this, we used a mixed effects model to test of the effect of male genetic background on female offspring production. This analysis reveals a strong effect of male genetic background on female offspring production ($P = 0.004$; Table S1), suggesting that the genotypes surveyed here do indeed play some role in mediating female fitness. It bears noting that this measure of fitness is somewhat crude, which may indicate that the effects of male genetic background on female reproductive fitness may be even more substantial than detected here. We further note that differential reproductive output as a function of male genetic background may result from differing numbers of eggs laid and/or other factors such as larval competition, as each vial in this assay contained 10 females.

Our finding of a lack of an effect of male genetic background on recombination rate in spite of a strong effect of male genetic background on offspring production prompted us to consider what size of an effect of male-mediated effects on female recombination rate we would be able to detect given our experimental design. Although the appropriateness of post hoc power analyses is quite uncertain (see Hoenig and Heisey 2001), we can conduct a rough calculation to provide qualitative insight into the quantitative scope of our result. The critical *F*-value for the effect of male genetic background is 1.96. Thus, the sum of squares for the male genetic background would need to be 2.7 times as large as was observed to achieve significance at an $\alpha = 0.05$. If the male genetic background effect was 2.7 times as large, it would explain only 3.3% of the variance in recombination rate observed in our experiment. This suggests male-mediated effects on female recombination explain at most 3.3% of the variance in female recombination rate, which is roughly 1/5 of the magnitude of the effect of female genetic background. This suggests strongly that male-mediated effects, if any, are minor in comparison to the effects of female genetic background.

However, depending on the mechanism underlying the previously observed male-mediated effects on female recombination rate (Stevison 2012), we might not expect to see an effect over the

entire 10-day collection period. Although the effects of gametic selection should be consistent across the experimental time frame, if the effect is due to increases in the number of crossover events, then the timing of the response should be notably different. During oogenesis, crossovers are initiated in region 2a of the gerarium (Mehrotra and McKim 2006). It takes roughly 4–5 days between when crossovers are initiated and when mature oocytes are laid by mated females. That is, crossovers are occurring well before a female has been mated (King et al. 1968; King 1970). Thus, it is possible that the effect of male genetic background does affect crossover rate, but that the effect would only be visible after 4–5 days.

To test this, we separated crossovers occurring before versus after mating by transferring females over the course of the experiment. We analyzed crossovers from the first 5 days (days 1–5) compared to the second 5 days (days 6–10); the first 5 days contained progeny that had crossovers initiated before a female was mated, whereas the second 5 days contained progeny that had crossovers initiated after mating and storage of sperm. Slicing (see Materials and Methods) the data into early (days 1–5) and late blocks (days 6–10) reveals no significant effects of paternal genotype (Table 2) in either block. Our results thus suggest that males play no detectable role in influencing crossover frequency in this population of *D. melanogaster*.

RECONCILING OUR RESULTS WITH PREVIOUS FINDINGS

Our results contrast significantly with previous work (Stevison 2012), which merits discussion. There are many factors that could serve to explain the differences between these studies. First, the strains used in the two studies are very different. The original study used flies collected in Zimbabwe, Africa whereas our study used flies from Raleigh, North Carolina (Mackay et al. 2012). If the effects of male genetic background on female crossover rates are population-specific, this could explain the differences in our results. This would also suggest that male-mediated effects are unlikely to dominate natural populations.

BRIEF COMMUNICATION

Another difference between the two studies is that crossover frequency was scored using molecular markers in the original study whereas our study used phenotypic markers. Phenotypic markers can have differences in viability whereas molecular markers are likely to be unbiased. Based on our *G*-test analyses presented above, we believe our results have not been adversely affected by viability defects associated with these mutations. However, it remains possible that the difference between the studies with respect to how crossovers were measured underlies the difference in outcomes.

Another important difference between the two studies is the environmental conditions under which the experiment was conducted. The temperature of the initial study was 21°C whereas our experiment was conducted at 25°C. Temperature, as mentioned before, will have an effect on crossover frequency (Plough 1917, 1921; Stern 1926). Notably, crossover frequency increases over 22°C (Ashburner 1989). One possibility is that crossover frequencies are near their extreme values at 25°C which reduces the capacity for phenotypic plasticity in crossover rate in response to male genetic background. Similarly, females in the initial experiment were held as virgins for 4 days in comparison to our females, which were held as virgin for 12–24 h. It is clear that maternal age affects crossover rate in *Drosophila* (Plough 1917, 1921; Bridges 1927; Neel 1941; Hayman and Parsons 1960; Redfield 1966; Priest et al. 2007; Tedman-Aucoin and Agrawal 2011), and it is possible that capacity for plasticity varies as a function of age as well. It is also possible that the duration of the aging window (4 days vs. 1 day) contributes to the difference between results observed in the current versus original study.

The final difference between the two studies that bears mentioning is the statistical framework in which the data were analyzed. Although the original study coded individuals as binary (recombinant vs. nonrecombinant), the current study estimated crossover frequency for a given replicate vial. To test whether this difference in analysis approach was sufficient to drive the difference in the results, we repeated our analysis using a statistical model similar to that employed previously. This analysis revealed no significant effect of paternal genotype on female crossover rate (Table S2). This result holds when we limit the analysis to inversion-free genotypes (Table S2) as well as when we control for the timing of crossover events during oogenesis (Table S2).

Thus, the precise reasons underlying the differences between our results and previous work remain unknown. However, we suggest that our results indicate that effects of male genotype on female genetic background are not pervasive in natural populations of *D. melanogaster*. Certainly in the case of this North American population, male genetic background appears to play no role in determining female crossover rates. In contrast, female genetic background contributes significantly to the variation in crossover rate observed in this experiment and is likely to

contribute markedly to natural variation in crossover rate in *D. melanogaster*.

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DATA ARCHIVING

The doi for our data is 10.5061/dryad.gk42k

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Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's website:

Table S1. PROC MIXED fixed effects analysis on fitness.

Table S2. PROC GLIMMIX fixed effects analysis.

Table S3. PROC GLIMMIX fixed effects analysis separated by time.

Figure S1. Crossover frequency of line RAL_21 females as a function of male genetic background.

Figure S2. Crossover frequency of line RAL_26 females as a function of male genetic background.

Figure S3. Crossover frequency of line RAL_38 females as a function of male genetic background.

Figure S4. Crossover frequency of line RAL_45 females as a function of male genetic background.

Figure S5. Crossover frequency of line RAL_57 females as a function of male genetic background.

Figure S6. Crossover frequency of line RAL_59 females as a function of male genetic background.

Figure S7. Crossover frequency of line RAL_73 females as a function of male genetic background.

Figure S8. Crossover frequency of line RAL_75 females as a function of male genetic background.

Figure S9. Crossover frequency of line RAL_136 females as a function of male genetic background.

SUPPORTING INFORMATION

Table 2.S1 - PROC MIXED fixed effects analysis on fitness.

	With Inversions Present		
Source	df	F Value	Pr > F
<i>F</i>	9	2.30	0.022
<i>M</i>	9	0.90	0.004
<i>F × M</i>	81	0.60	0.99

Key

F = female genotype; *M* = male genotype

Table 2.S2 - PROC GLIMMIX fixed effects analysis

Source	With Inversions Present			Without Inversions Present		
	df	F Value	Pr > F	df	F Value	Pr > F
<i>F</i>	9	7.80	<.0001	6	5.65	0.0002
<i>M</i>	9	0.90	0.53	6	1.04	0.41
<i>T</i>	1	47.61	<.0001	1	21.71	<.0001
<i>F × M</i>	81	0.60	0.99	36	0.57	0.96
<i>F × T</i>	9	0.98	0.45	6	1.21	0.30
<i>M × T</i>	9	0.39	0.94	6	0.48	0.82
<i>F × M × T</i>	81	1.08	0.29	36	1.08	0.36

KEY

F = female genotype; *M* = male genotype; *T* = time (either the first five days or the second five days)

Table 2.S3 - PROC GLIMMIX fixed effects analysis separated by time

		With Inversions Present			Without Inversions Present		
Source	Time	df	F Value	Pr > F	df	F Value	Pr > F
F	Early	9	5.79	<.0001	6	3.85	0.0008
F	Late	9	7.44	<.0001	6	5.62	<.0001
M	Early	9	0.89	0.56	6	1.32	0.25
M	Late	9	0.74	0.67	6	0.63	0.71
F × M	Early	99	1.08	0.29	48	1.02	0.43
F × M	Late	99	1.29	0.0029	48	1.24	0.13

KEY

F = female genotype; **M** = male genotype

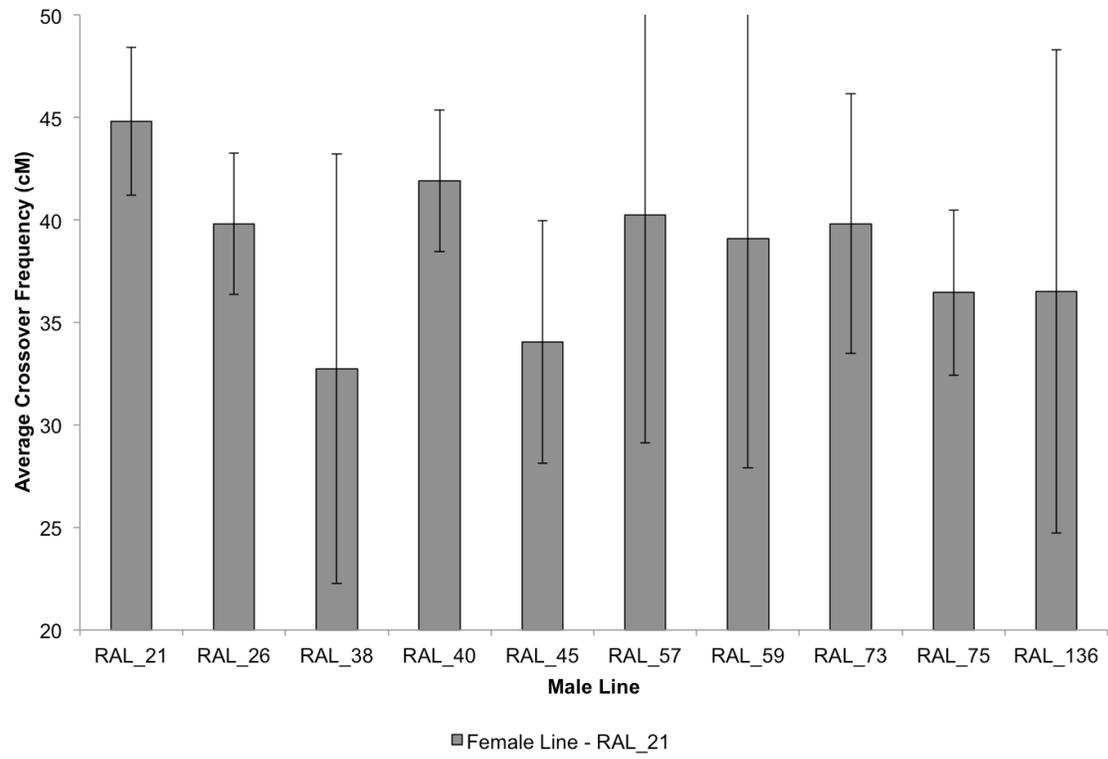


Figure 2.S1 - Crossover frequency of line RAL_21 females as a function of male genetic background. Error bars represent standard deviation across replicates.

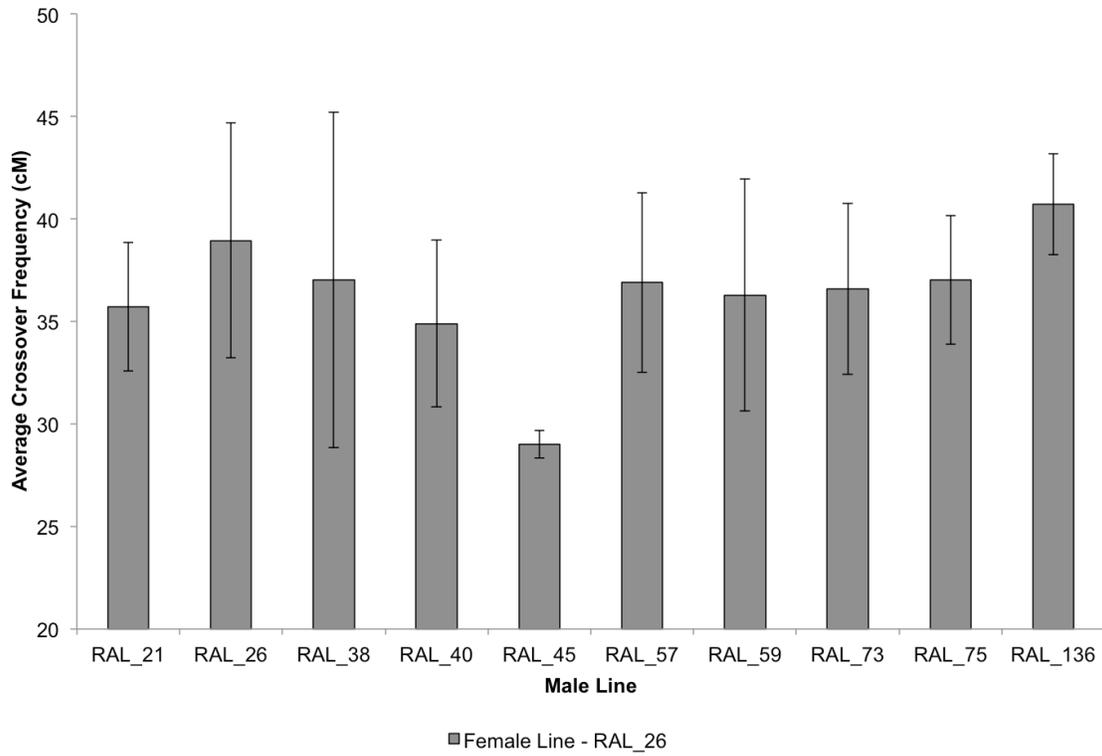


Figure 2.S2 - Crossover frequency of line RAL_26 females as a function of male genetic background. Error bars represent standard deviation across replicates.

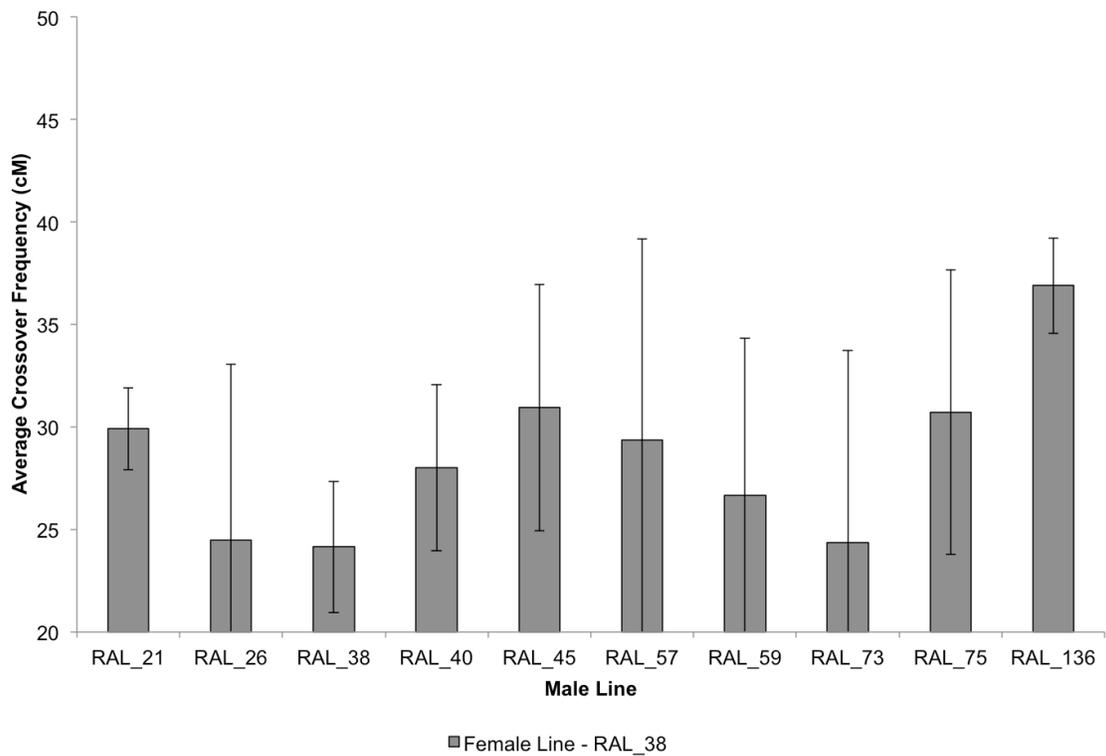


Figure 2.S3 - Crossover frequency of line RAL_38 females as a function of male genetic background. Error bars represent standard deviation across replicates.

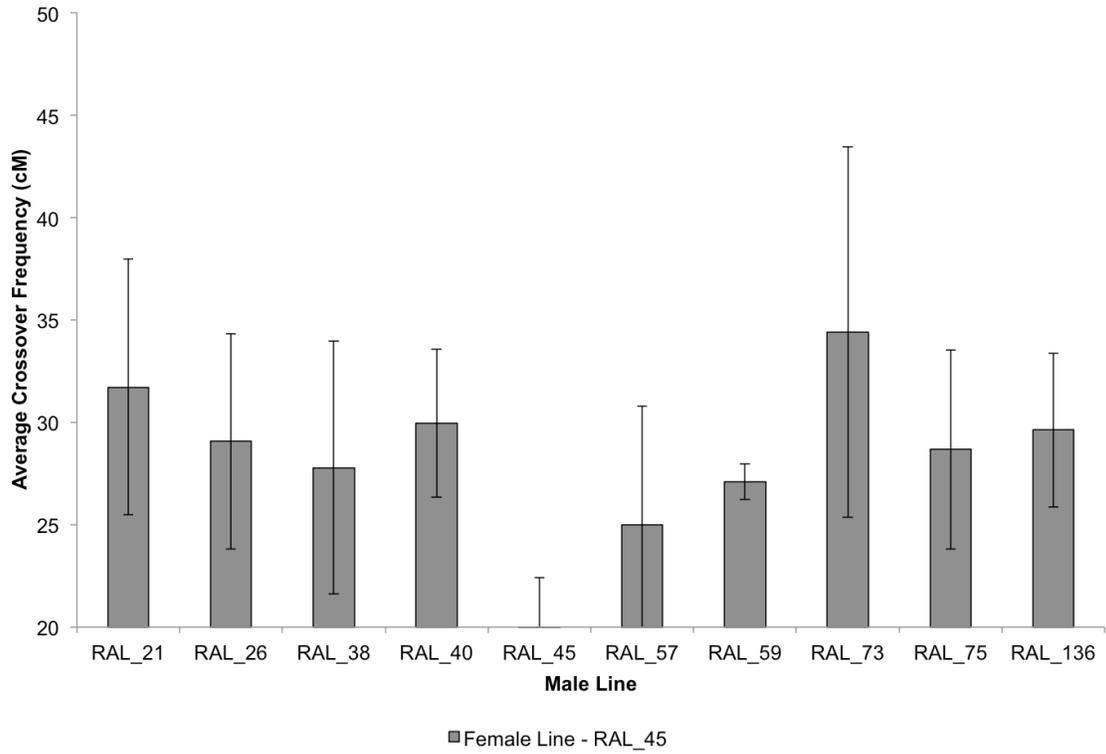


Figure 2.S4 - Crossover frequency of line RAL_45 females as a function of male genetic background. Error bars represent standard deviation across replicates.

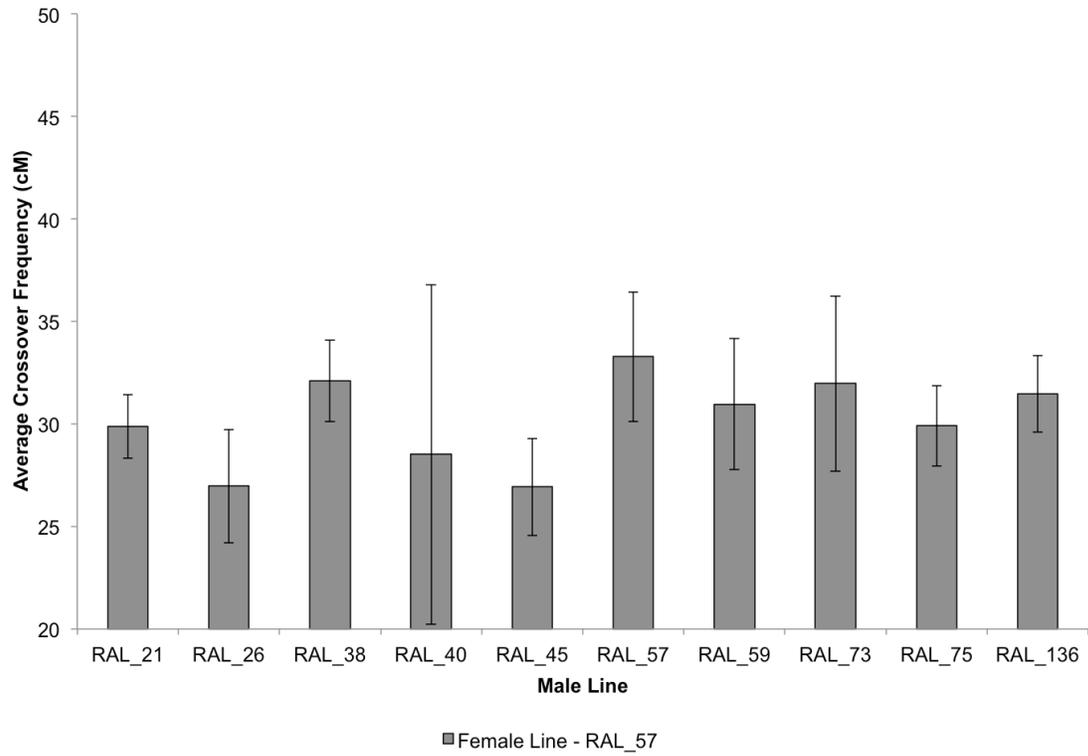


Figure 2.S5 - Crossover frequency of line RAL_57 females as a function of male genetic background. Error bars represent standard deviation across replicates.

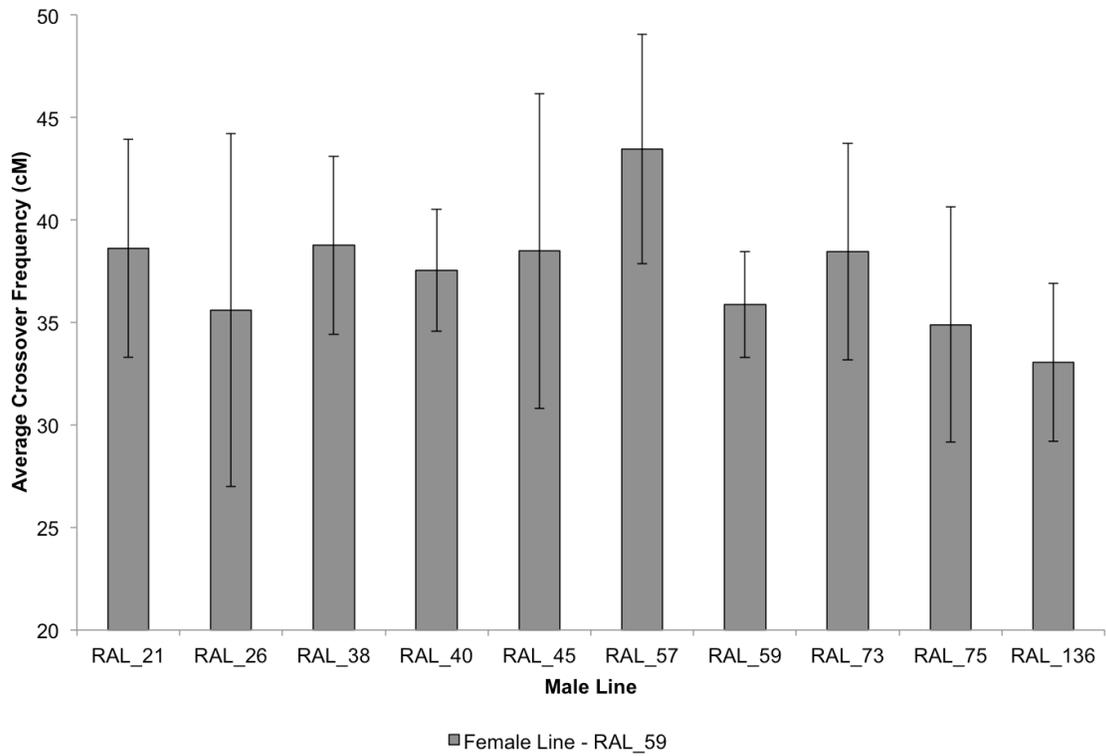


Figure 2.S6 - Crossover frequency of line RAL_59 females as a function of male genetic background. Error bars represent standard deviation across replicates.

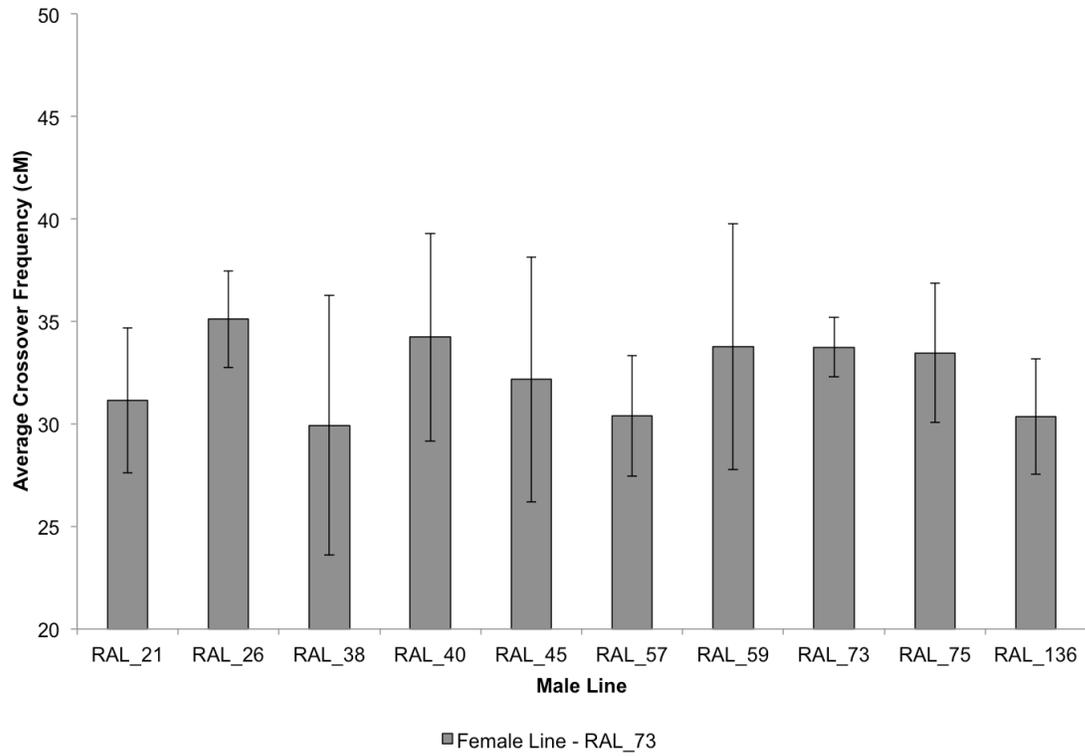


Figure 2.S7 - Crossover frequency of line RAL_73 females as a function of male genetic background. Error bars represent standard deviation across replicates.

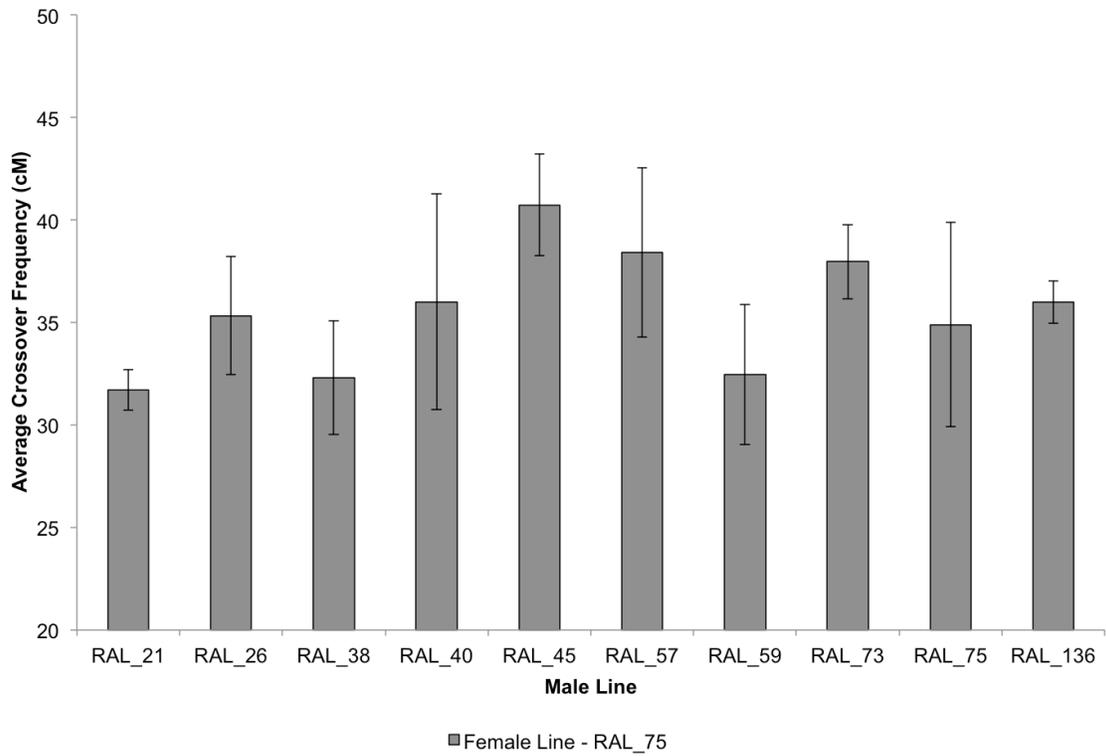


Figure 2.S8 - Crossover frequency of line RAL_75 females as a function of male genetic background. Error bars represent standard deviation across replicates.

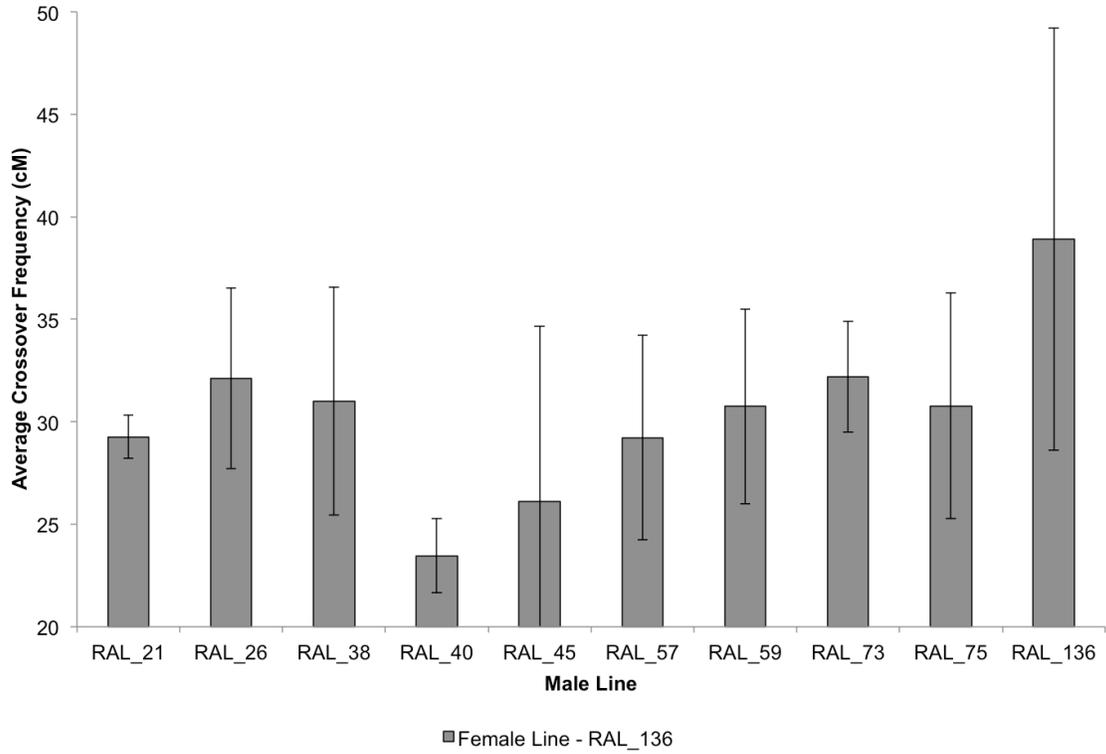


Figure 2.S9 - Crossover frequency of line RAL_136 females as a function of male genetic background. Error bars represent standard deviation across replicates.

CHAPTER 3. GENETIC BACKGROUND, MATERNAL AGE AND INTERACTION EFFECTS MEDIATE RATES OF CROSSING OVER IN *DROSOPHILA MELANOGASTER* FEMALES

AUTHORS

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ABSTRACT

Meiotic recombination is a genetic process that is indispensable for proper chromosome segregation in many organisms. Despite being fundamental for organismal fitness, rates of crossing over vary greatly at all levels of biological organization. Both genetic and environmental factors contribute to phenotypic variation in crossover frequency, as well as genotype-environment interactions. Here, we test that hypothesis maternal age influences rates of crossing over in a genotypic-specific manner. Using classical genetic techniques, we estimated rates of crossing over for individual *Drosophila melanogaster* females from several strains as a function of maternal age. We find that both age and genetic background significantly contribute to observed variation in recombination frequency, as do genotype-age interactions. We further find differences in the effect of age on recombination in the two genomic regions surveyed. Our results highlight the complexity of recombination rate variation and reveal a new role of genotype by environmental interactions in mediating recombination rate.

INTRODUCTION

Meiotic recombination is a critically important biological process, as chromosomal crossovers are required for proper chromosome segregation in many organisms (Roeder 1997). Defects in meiotic recombination can have detrimental consequences including increasing the probability of nondisjunction (Koehler et al. 1996; Hassold and Hunt 2001). The exchange of genetic material associated with crossing over can have important evolutionary consequences by combining or separating beneficial or deleterious alleles. Given the central importance of recombination for organismal fitness, one might hypothesize that this process would be highly regulated, with little to no variation present. However, a wealth of evidence in a variety of taxa points to the contrary. Variation in rates of recombination have been identified in yeast (Mancera et al. 2008), worms (Barnes et al. 1995; Rockman and Kruglyak 2009), fruit flies (Brooks and Marks 1986; Singh et al. 2009, 2013; Comeron et al. 2012), honey bees (Ross et al. 2015), maize (Bauer et al. 2013), chickens (Rahn and Solari 1986), mice (Dumont et al. 2009), chimps (Ptak et al. 2005; Winckler et al. 2005), and humans (Kong et al. 2002; Crawford et al. 2004; Myers et al. 2005), to name a few. This source of this variation is an intriguing evolutionary question, as both genetic factors such as PRDM9 (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010) and environmental variables such as nutrition (Neel 1941; Abdullah and Borts 2001) have been shown to greatly contribute to variation in rates of recombination.

It has long been known that recombination rates are plastic, meaning that a given genotype has the capability to exhibit different phenotypes in response to the environment. It has been noted that stress influences recombination rates, often increasing rates (Parsons 1988; Hadany and Beker 2003; Agrawal et al. 2005; Zhong and Priest 2011). Many studies have linked various types of stress to changes in recombination such as mating (Priest et al. 2007), nutrition (Neel 1941; Abdullah and Borts 2001), parasitism (Fischer and Schmid-Hempel 2005; Kerstes et al. 2012), social stress (Belyaev and Borodin 1982), and temperature (Plough 1917, 1921; Stern 1926; Smith 1936; Grushko et al. 1991).

For this study, we were interested in investigating how the stress of aging influenced rates of recombination in *D. melanogaster* females. Aging, “a steady progressive, irreversible decline in organismal performance” (Helfand and Rogina 2003), is a ubiquitous process with detrimental consequences, including an increase in genome instability (Vijg 2000). The accumulation of DNA damage associated with aging can lead to harmful mutations and ultimately to the occurrence of cancer (Hoeijmakers 2009). For most organisms, advancing age is accompanied by a decrease in overall fitness (Williams 1957;

Partridge and Barton 1993) and also a decrease in overall reproductive output (Stearns 1992).

Many studies have addressed the phenomenon of recombination rates changing with advancing maternal age in *Drosophila* (Bridges 1915, 1927, 1929; Plough 1917, 1921; Stern 1926; Bergner 1928; Neel 1941; Hayman and Parsons 1960; Redfield 1966; Lake and Cederberg 1984; Parsons 1988; Chadov et al. 2000; Priest et al. 2007; Tedman-Aucoin and Agrawal 2011; Stevison 2012; Manzano-Winkler et al. 2013; Hunter and Singh 2014) and in other species such as worms (Rose and Baillie 1979), tomatoes (Griffing and Langridge 1963), mice and hamsters (Henderson and Edwards 1968; Sugawara and Mikamo 1983) and humans (Kong et al. 2004; Coop et al. 2008; Hussin et al. 2011; Bleazard et al. 2013; Rowsey et al. 2014; Campbell et al. 2015). In spite of the depth of research on this topic, a clear picture of how maternal age affects rates of recombination has yet to emerge. In humans, for instance, while some studies show fewer crossovers over time (i.e. Kong et al. 2004; Hussin et al. 2011), others show more crossovers over time (i.e. Tanzi et al. 1992; Bleazard et al. 2013). The *Drosophila* literature shows similar discrepancies, with some studies showing clear increases in crossover frequency with increasing maternal age (i.e. Bridges, 1915; Stern, 1926; Bergner, 1928; Lake & Cederberg, 1984; Priest *et al.*, 2007; Hunter & Singh, 2014), others showing decreases (i.e. Bridges, 1915; Hayman & Parsons, 1960; Chadov *et al.*, 2000), some revealing non-linear effects (i.e. Plough, 1917, 1921; Bridges, 1927; Neel, 1941; Redfield, 1966; Tedman-Aucoin, 2008) and others yet finding no significant changes in recombination rates (i.e. Bridges, 1915; Plough, 1921; Stevison, 2012; Manzano-Winkler *et al.*, 2013).

It has proven difficult to compare these studies for a variety of reasons. First, many different strains have been employed in the above experiments, and it is not yet clear whether the effects of maternal age on recombination frequency are dependent on genetic background. Other factors such as repeated mating, which may affect rates of crossing over in *Drosophila* (Priest et al. 2007), have not been controlled for in all studies, further complicating the interpretation of previous data. Experimental design differs among studies as well, with some studies assaying recombination from single females while others assay recombination from a pool of females; this too may contribute to the observed differences in the effects of maternal age on recombination among studies. Finally, different regions of the genome have been surveyed, and it is possible that the affect of maternal age on recombination rate is not uniform across the genome.

The goal of this study is to test the hypothesis that the effects of maternal age on recombination rate are genotype and/or locus-specific. Demonstrating genotype-by-age interaction effects, or genomic heterogeneity in the magnitude/direction of age-associated changes in recombination rate is a critical first step in quantifying the extent of such effects and determining their genetic basis. To test for genotype-age interaction and locus-specific effects, we used multiple wild-type lines of *D. melanogaster* and measured recombination rates of individual females for a period of three weeks after a single mating event. This study estimated crossover rates in two different genomic locations. We find an increase of recombination rates with increasing maternal age on the X chromosome, though no significant age-dependency in recombination frequency on the 3R chromosome. This suggests that age-related changes in recombination rate are not constant genome-wide. In addition, our study confirms genotype-specific variation in recombination rate, and indicates that the effects of maternal age are indeed genotype-dependent. In moving forward, it will be important to control for genetic background effects when examining the effects of environmental factors on rates of crossing over. We demonstrate this in *Drosophila* and predict that genotype-environment interaction effects on crossover rates are likely to be pervasive in other species as well.

MATERIALS AND METHODS

Fly Lines

Five inbred wild-type strains of *Drosophila* were used in this study from the *Drosophila melanogaster* Genetic Reference Panel (DGRP) (Mackay et al. 2012; Huang et al. 2014). The five lines were RAL_21, RAL_59, RAL_73, RAL_75 and RAL_136. Four of the lines are free of chromosomal inversions and have the standard karyotype while one (RAL_136) is heterozygous for the Mourad inversion on 3L and heterozygous for the Kodani inversion on 3R (Huang et al. 2014). It should be noted that because of these inversions, RAL_136 was not used for estimating rates of recombination using markers on 3R. These lines were previously used in a study by the authors and were shown to be significantly variable for crossover rates (Hunter and Singh 2014).

To measure rates of recombination, we employed a classical genetic crossing scheme using homozygous, recessive visible markers. The markers used to measure recombination on the X chromosome were *yellow* (y^1) and *vermillion* (v^1) and are 33 cM apart (Morgan and Bridges 1916). The markers on the 3R chromosome were *ebony* (e^4) and *rough* (ro^1) and are 20.4 cM apart (Bridges and Morgan 1923). These markers were selected due to their genetic distance, ease of scoring and lack of viability defects.

Experimental Crosses

All crosses were executed at 25°C with a 12 hour light-dark cycle on standard cornmeal-molasses media. To score crossover frequency, we used a two-step crossing scheme (**Figure 3.1**). We conducted this experiment twice; once for the $y v$ marker pair and once for the $e ro$ marker pair. For the first cross, 20 virgin DGRP females were mated to 20 doubly-marked males for 5 days in 8 oz. bottles. (Doubly-marked males are denoted by $m^1 m^2$ for simplicity and refer to either $y v$ males or $e ro$ males.) After 5 days, parental flies were removed. Virgin F_1 females ($+ +/ m^1 m^2$) were collected within a two-hour period between 8AM and 10AM on the same day for all lines contemporaneously and held virgin for 24 hours in groups of 20. Twenty virgin females were mass-mated with twenty males in 8 oz. bottles for a period of 24 hours (for flies with the $y v$ markers) or for 48 hours (for flies with the $e ro$ markers). Males with $e ro$ markers seemed less enthusiastic to mating (a first trial of a 24 hour window produced very few gravid females), necessitating the longer mating window. Due to the apparent effect of repeated mating on rates of recombination (Priest et al. 2007), we limited females to mating attempts only in the short window of 24-48 hours. This short window allows for roughly one mating event since females become unresponsive

to remating for roughly one day after copulation (Manning 1962, 1967; Gromko et al. 1984). *Drosophila* females are able to store sperm for periods greater than two weeks (Kaufman and Demerec 1942; Lefevre and Jonsson 1962) so all progeny collected are a result of mating within that original 24-48 hour window. After mating, individual females were placed into vials and transferred every two days at the same time of day for 22 days. For *y v*, 150 replicate females were used for each line. For *e ro*, 175 replicate females were used for each line. The resulting progeny from each vial were scored for both sex and presence of morphological markers after the female had been removed from the vial. Recombinant progeny were identified by the presence of only one visible marker (recombinant genotypes are $m^1 + or + m^2$).

Statistics

All statistics were conducted using JMP®Pro v11.0.0 and/or R v3.2.0 unless otherwise noted. We used a repeated measures ANOVA (Winer 1971) on transformed data as a test for the effects of maternal age, genetic background, and the interaction between these factors. The full model is as follows:

$$R_{ij} = \mu + G_i + A_j + G_i \times A_j + \varepsilon_n,$$

for *y v*, $i = 1 \dots 5$; $j = 1 \dots 6$; and $n = 1 \dots 306$
and for *e ro*, $i = 1 \dots 2$; $j = 1 \dots 3$; and $n = 1 \dots 54$

where R represents crossover frequency, μ represents the mean of regression and ε represents the error. G represents female genetic background, modeled as a fixed effect and A represents maternal age, also modeled as a fixed effect, along with the interaction of the two. For the repeated measures ANOVA, we restricted our analysis to Days 1-12 for the interval on the X, as the number of females producing an appreciable number of progeny markedly decreased after day 12. For the same reason, we limited our analysis to Days 1-10 for the interval on 3R, as the number of females producing an appreciable number of progeny markedly decreased after day 10.

Additionally, we used a generalized linear model with a binomial distribution and logit link function to test for an effect of age, genetic background as well as the interaction of the two on recombination frequency. We treated each progeny as a realization of a binomial process (recombinant versus nonrecombinant) and summarized the data for a given vial by

the number of recombinants and the number of trials (total number of progeny per vial), The full model was as follows:

$$R_{ij} = \mu + G_i + A_j + G_i \times A_j + \varepsilon_n,$$

for y v: $i = 1 \dots 5, j = 10$, and $n = 1 \dots 2648$
and for e ro: $i = 1 \dots 4, j = 3$, and $n = 1 \dots 625$

where R represents crossover frequency, μ represents the mean of regression and ε represents the error. G represents female genetic background, modeled as a fixed effect and A represents maternal age, also modeled as a fixed effect, along with the interaction of the two.

RESULTS AND DISCUSSION

Robustness of Crossover Frequency Estimation

In total, we scored 105,378 progeny for both intervals combined (78,292 for the *y v* interval and 27,086 for the *e ro* interval). We performed G-tests for goodness of fit (Sokal and Rohlf 1994) on our combined data to validate that the correct proportions of females versus males, wild-type versus $m^1 m^2$, and $m^1 +$ versus $+ m^2$ were being recovered. It is expected that each member of these pair will be recovered in a 1:1 ratio due to Mendelian segregation. Comparing females versus males for the *y v* interval, only 1 out of 613 replicates showed a significant deviation from the 1:1 ratio (Bonferroni-corrected $P = 0.05$, G-test) while for the *e ro* interval, 0 out of 467 replicates showed a significant deviation from the 1:1 ratio (Bonferroni-corrected $P > 0.05$, all comparisons, G-test). Comparing wild-type versus $m^1 m^2$ (progeny with both markers), in the *y v* interval, 6 out of 613 replicates showed a significant deviation from the expected 1:1 ratio (Bonferroni-corrected $P < 0.05$, G-test) while for the *e ro* interval, none of the replicates showed a significant deviation from the 1:1 ratio (Bonferroni-corrected $P > 0.05$, all comparisons, G-test). Comparing the ratio of recombinant progeny ($m^1 +$ versus $+ m^2$), none of the replicates showed a significant deviation from the expected 1:1 ratio for the either the *y v* or *e ro* interval (Bonferroni-corrected $P > 0.05$, all comparisons, G-test). These results indicate that there is no viability defect associated with any of the mutations used in the current study and gives us confidence that our estimates of crossover are robust.

Interaction of Genetic Background and Maternal Age

The primary motivation for this study was to determine how crossover frequency varies in relation to genetic backgrounds, advancing maternal age and the interaction of the two. Although work has shown that meiotic nondisjunction increases with maternal age in *Drosophila* (using oocytes aged ~4 days; Jeffreys *et al.* 2003; Subramanian and Bickel 2008, 2009; Weng *et al.* 2014), the nature of the relationship between recombination rate and maternal age is less clear. As described before, increases, decreases, non-linear and no changes in rates of recombination with increasing maternal age have all been observed previously.

We analyzed recombination rates for individual females every two days for their lifetime. Analysis of the *y v* region data (up to day 12; see Materials and Methods) using a repeated measures ANOVA indicates that genetic background ($F_{4,302} = 12.56$; $P < 0.001$) and maternal age ($F_{1,1837} = 63.72$; $P < 0.001$) significantly contribute to recombination rate

observed in our study. Importantly, the interaction of genetic background and maternal age is also significant ($F_{4,1837} = 3.82$; $P = 0.004$; **Table 3.1**), indicating that the effects of maternal age on recombination rate are genotype-dependent. Analysis of the full data complement using a generalized linear model is consistent with these findings (**Table 3.2**), suggesting that our results are robust to sample size and method of statistical analysis. Additionally, removing RAL_136 which contains segregating inversions on arms 3L and 3R (see Materials and Methods) produces the same result (data not shown).

These data thus clearly indicate that the effects of age on recombination frequency are genotype-specific. While previous work showed that different strains of *D. melanogaster* containing different dominant deleterious mutations differed in the magnitude and extent of age-dependent changes in recombination (Tedman-Aucoin and Agrawal 2011), here we report that natural genetic variation can also drive changes in the effects of maternal age on recombination rate. Our data further indicate that rates of crossing over increase with maternal age within this genomic region (**Figure 3.2**), although these increases appear to not be strictly linear. The increase in recombination frequency with increasing maternal age is consistent with several previous studies in *Drosophila* (Bridges 1915; Stern 1926; Bergner 1928; Lake and Cederberg 1984; Priest et al. 2007; Hunter and Singh 2014) and other species (Kong et al. 2004; Coop et al. 2008).

Variation in recombination rates among individuals has been detailed in numerous different species such as in *Drosophila* (Brooks and Marks 1986), mice (Dumont et al. 2009), and humans (Yu et al. 1996; Coop et al. 2008; Wang et al. 2012). A significant effect of genetic background (Fig S1A-B) confirms previous work that has shown variation in recombination rates is associated with genetic background differences among DGRP lines (Comeron et al. 2012; Hunter and Singh 2014) as well as in *Drosophila* in general (Chinnici 1971a,b; Brooks and Marks 1986; Comeron et al. 2012).

It bears mentioning that our surveyed window does not fully capture the potential effects of age on recombination. Indeed, *Drosophila* can have lifespans of ~80 days and beyond (Grönke et al. 2010; Mockett et al. 2012; Ivanov et al. 2015). However, the average life span is ~45-60 days under optimal conditions (see Ivanov *et al.*, 2015) and usually less under normal conditions (Ashburner et al. 2005). Additionally, the act of mating can significantly reduce the average life span of a female as compared to her non-mated counterpart (Fowler and Partridge 1989). The average (unmated) lifespan for the five lines used in this study is ~56 days (Arya et al. 2010; Ivanov et al. 2015). Therefore, our measurements spanning 22 days encompass a large proportion of the adult lives of these

flies. While it is possible that were we able to survey recombination rates over a longer period of time we would see more dramatic effects of age on recombination, that we observe a significant effect of maternal age on recombination rates in the *y v* region indicates that the effects of age even within the first 22 days are biologically relevant.

Locus Effects

Previous research has indicated that rates of crossing vary along the genome, both on broad and fine scales (Lindsley et al. 1977; McVean et al. 2004; Cirulli et al. 2007; Paigen et al. 2008; Singh et al. 2009, 2013; Comeron et al. 2012). We hypothesized that changes in crossover frequency due to age might also be variable across the genome, and another goal of this work was to test the whether the effects of maternal age on recombination frequency are locus-dependent. By using markers on both the X and 3R chromosomes, we can compare the effect of maternal age and genetic background at two different genomic locations. For the recombination rate estimation on chromosome 3R, we limited our analysis to only the first 10 days, combining progeny from days 6 through 10. This maximized the useable data, as we recovered fewer progeny overall from this crossing scheme as compared with the crossing scheme used to survey recombination on the X chromosome. In addition, we did not include RAL_136 in this experiment due to the aforementioned segregating inversions.

A repeated measures ANOVA suggests that maternal age is a significant factor, but only marginally so ($P = 0.04$; **Table 3.1**). Using a generalized linear model (see Materials and Methods), we find that genetic background significantly contributes to the observed variation in recombination rate ($P = 0.05$) but neither maternal age ($P = 0.98$) nor the interaction term ($P = 0.65$) are significant. Given the sensitivity of these results to the method of analysis, it is difficult to interpret the results. However, it is worth noting that reducing the X chromosome dataset to the first 10 days only and combining days 6-10 confirms significant effects of genetic background ($P < 0.001$) and maternal age ($P < 0.001$) and the interaction of the two ($P = 0.002$) on recombination frequency in this X chromosome interval using a repeated measures ANOVA. This indicates that the lack of detectable effect of maternal age on crossover frequency on 3R is not due to the sampling structure of the experiment. That we detect no consistent effect of age or genetic background on recombination frequency in the third chromosome region surveyed is suggestive that crossover frequency at this locus is differentially sensitive to genetic and environmental variation.

Integrating our findings with previous work also points to genomic heterogeneity in the recombinational response to maternal age. Bridges (1915) found differences in the frequency of crossing over in two different broods from the same females for markers on the third chromosome (*pink* and *kidney*), while we observed no significant differences in crossover frequency associated with maternal age using our markers on the same chromosome. In addition, Bridges found no significant differences in crossover frequency in broods between markers on the X chromosome (*vermilion* and *fused*), while we observed a significant increase in crossover frequency between our X chromosome markers. Data in humans are similarly suggestive of chromosome-level variability in the effect of maternal age on crossover frequency (Hussin et al. 2011).

Conclusion

Our results indicate that crossover frequency is mediated by genetic background and maternal age. The novel contribution of our work is the finding of natural genetic variation for age-dependent changes in recombination rate in *Drosophila*. Future work will be aimed at quantifying the magnitude of genotype-age interaction effects in natural populations. Moreover, the DGRP provides an excellent community resource that can be used to uncover the genetic basis of these interaction effects, another area of future work. Our data are also suggestive of genomic variability in the effects of maternal age on recombination frequency, opening the possibility that environmental stressors may influence different parts of the genome in different ways. Future work will also be aimed testing for heterogeneity in the recombinational response to environmental stimuli at a genomic scale.

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TABLES

Table 3.1 - Repeated measures ANOVA effects.

X	Source	df	SS	MS	F Value	Prob>F
	Line	4	0.937	0.234	12.56	< 0.001
	Residuals	302	5.634	0.019		
	Maternal Age	4	0.855	0.855	63.72	< 0.001
	Line × Maternal Age	1	0.205	0.051	3.82	0.0043
	Residuals	1837	24.654	0.013		
3R	Source	df	SS	MS	F Value	Prob>F
	Line	2	0.00033	0.00017	0.017	0.98
	Residuals	14	0.14	0.0096		
	Maternal Age	2	0.057	0.029	3.72	0.036
	Line × Maternal Age	4	0.010	0.0025	0.33	0.86
	Residuals	30	0.23	0.0077		

Table 3.2 - GLM effects.

GLM				
X	Source	df	χ^2	Prob> χ^2
	Line	4	46.41	< 0.001
	Maternal Age	9	126.10	< 0.001
	Line × Maternal Age	36	48.80	0.075
3R	Source	df	χ^2	Prob> χ^2
	Line	3	7.84	0.0495
	Maternal Age	2	0.039	0.98
	Line × Maternal Age	6	4.22	0.65

FIGURES

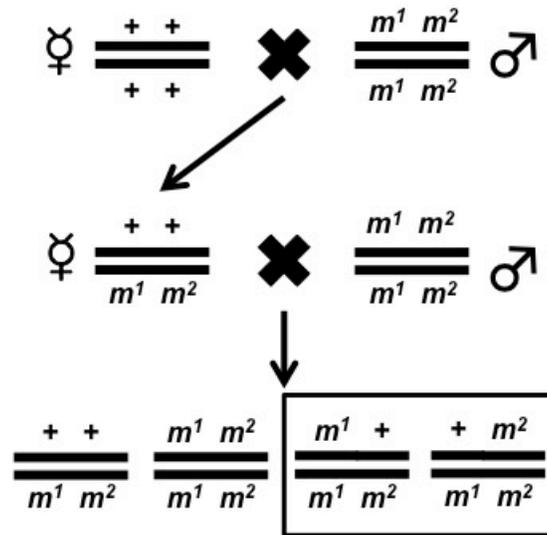


Figure 3.1 - Two-step crossing scheme used in order to generate crossover frequency. + + denotes wild-type genotype while $m^1 m^2$ denotes either marker combination *y v* or *e ro*. Recombinant progeny are denoted by having one visible marker (either $+ m^2$ or $m^1 +$) and are box outlined in black.

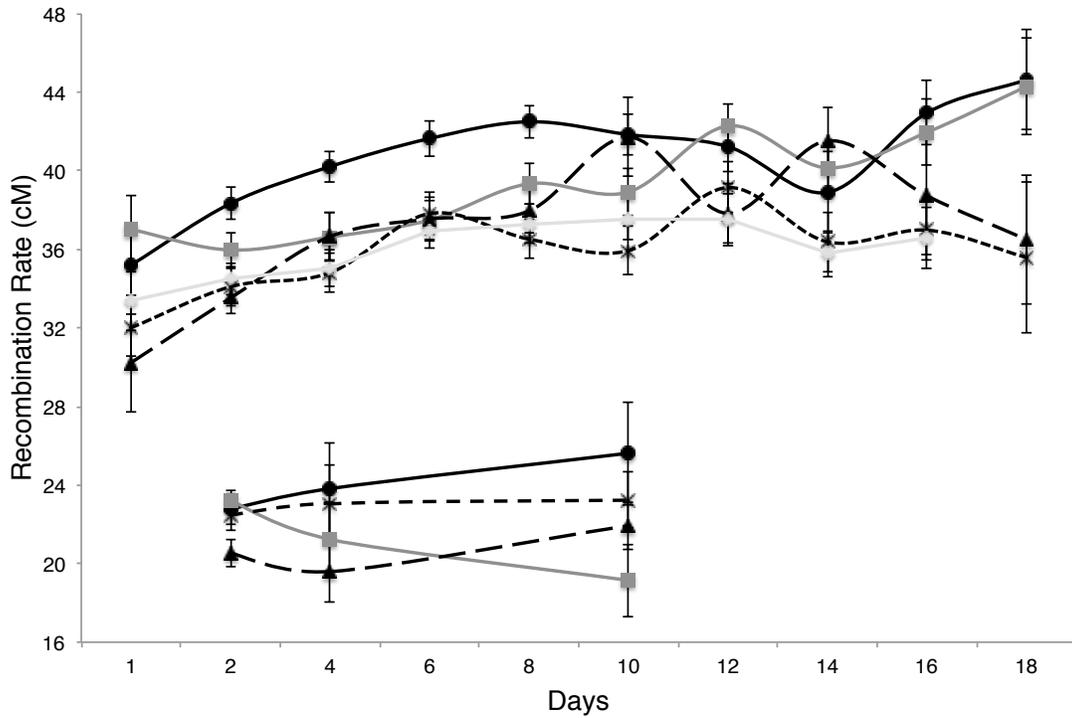


Figure 3.2 - Average crossover frequency separated by day. Data for RAL_21 (black line, ● data points), RAL_59 (dark grey line, ■ data points), RAL_73 (long-dashed black line, ▲ data points), RAL_75 (short-dashed black line, X data points) and RAL_136 (light grey line, ◆ data points) are shown. Error bars denote standard error.

CHAPTER 4. THE GENETIC ARCHITECTURE OF NATURAL VARIATION IN RECOMBINATION RATE IN
DROSOPHILA MELANOGASTER

AUTHORS

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ABSTRACT

Meiotic recombination ensures proper chromosome segregation in many sexually reproducing organisms. Despite this crucial function, rates of recombination are highly variable within and between taxa and the genetic basis of this variation remains poorly understood. Here, we exploit natural variation in the inbred, sequenced lines of the *D. melanogaster* Genetic Reference Panel (DGRP) to map genetic variants affecting recombination rate. We used a two-step crossing scheme and visible markers to measure rates of recombination in a 33 cM interval on the X chromosome and in a 20.4 cM interval on chromosome 3R for 205 DGRP lines. We find ~2-fold variation in recombination rates among lines. Interestingly, we further find that recombination rates are uncorrelated between the two chromosomal regions. We performed a genome-wide association study for genetic variants associated with recombination rates in the two intervals surveyed. We refined our list of candidate variants and genes associated with recombination rate variation and selected twenty genes for functional variation. We present strong evidence that four genes are likely to contribute to natural variation in recombination rate in *D. melanogaster* and lie outside of the canonical meiotic recombination pathway. Further, we find a weak effect of Wolbachia infection on recombination rate and we confirm the interchromosomal effect of polymorphic inversions in both regions. Our results highlight the magnitude of population variation in recombination rate present in *D. melanogaster* and implicate new genetic factors mediating natural variation in this quantitative trait.

INTRODUCTION

Meiotic recombination, the reciprocal exchange of genetic information between homologous chromosomes during meiosis, is necessary for proper chromosome segregation in many organisms (Roeder 1997). Lack of recombination and aberrant placement of recombination events along the chromosome can generate aneuploid gametes. Aneuploidy is the leading known cause of miscarriages and the principal genetic cause for developmental disability and delay in humans (Hassold and Hunt 2001). Given the crucial role of recombination in meiosis and the devastating consequences of aberrant recombination, one might hypothesize that the process of recombination would be tightly regulated so as to ensure proper chromosome segregation. In stark contrast to this expectation, recombination rates vary dramatically in almost all taxa studied to date. Recombination rate varies within and between species and populations in a huge diversity of species including humans, chimpanzees, flies, mice, worms, yeast, and many others (e.g. Brooks and Marks 1986; Rahn and Solari 1986; Barnes et al. 1995; True et al. 1996; Kong et al. 2002; Wall et al. 2003; Crawford et al. 2004; Ptak et al. 2004, 2005; Fearnhead and Smith 2005; Myers et al. 2005; Winckler et al. 2005; Wilfert et al. 2007; Mancera et al. 2008; Dumont et al. 2009; Rockman and Kruglyak 2009; Comeron et al. 2012; Bauer et al. 2013; Ross et al. 2015). Work in many species, particularly humans, mice, flies and yeast, also indicate that there is also considerable variation in how recombination events are distributed along the chromosome (Lindsley et al. 1977; Kong et al. 2002; Crawford et al. 2004; McVean et al. 2004; Myers et al. 2005; Cirulli et al. 2007; Mancera et al. 2008; Paigen et al. 2008; Singh et al. 2009, 2013; Comeron et al. 2012).

In addition to its role in preserving genomic integrity between generations, recombination is a pivotal force in evolution. Recombination can reduce interference between selected alleles and the genetic background in which they reside, thereby increasing the efficacy of natural selection (Fisher 1930; Muller 1932; Hill and Robertson 1966). Moreover, the exchange of genetic material between homologs creates new allelic combinations and thus provides the raw material for the process of evolution. Further highlighting its importance for evolution in general and genome evolution in particular, rates of recombination correlate with numerous genomic features such as the level of DNA polymorphism (Aguadé et al. 1989; Stephan and Langley 1989; Begun and Aquadro 1992), rates of protein evolution (Pál et al. 2001; Betancourt and Presgraves 2002), density of transposable elements (Bartolome et al. 2002; Rizzon et al. 2002; Petrov et al. 2011; Kofler

et al. 2012), density of satellite DNA (Stephan 1986, 1987), and codon bias (Comeron et al. 1999; Marais and Piganeau 2002).

Given the importance of recombination and the pervasive natural variation in recombination rate, it is perhaps unsurprising that the genetic basis of this variation has been an active area of research for the last decade. With respect to the genetic basis of the distribution of crossover events, the first known determinant of recombination distribution in metazoans was discovered recently (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010). This remarkable discovery implicates PRDM9 in determining the locations of meiotic recombination hotspots in both humans and mice. Sequence variation within *Prdm9* also modulates hotspot activity in humans (Berg et al. 2010). PRDM9 is a histone methyltransferase that catalyzes histone H3 lysine 4 trimethylation (Baudat et al. 2013). This rapidly evolving protein (Oliver et al. 2009) was first associated with hybrid sterility in rodents (Mihola et al. 2009), and evidence continues to accumulate that it is a major component of recombination hotspot determination in mammalian systems (Berg et al. 2010, 2011; Kong et al. 2010; Hinch et al. 2011; Smagulova et al. 2011; Auton et al. 2012; Brick et al. 2012).

Comparatively less is known in other systems such as *Drosophila*. Several studies have identified sequence motifs associated with recombination events (Cirulli et al. 2007; Kulathinal et al. 2008; Stevison and Noor 2010; Comeron et al. 2012; Heil and Noor 2012; Miller et al. 2012; Singh et al. 2013), but none have been functionally validated to date. *Drosophila* lacks PRDM9 (Oliver et al. 2009; Heil and Noor 2012), and perhaps relatedly, also lacks the highly punctate recombination landscape seen in mammals. While in humans up to 80% of recombination events fall in 10-20% of sequence (Myers et al. 2005), crossover distribution in *Drosophila* is far less heterogeneous (Comeron et al. 2012; Kaur and Rockman 2014).

Recent work in mammals has also provided insight into the genetic architecture of global recombination rate. RNF212 has been repeatedly associated with natural variation in recombination rate in several systems including humans (Kong et al. 2008; Chowdhury et al. 2009), cattle (Sandor et al. 2012), and Soay sheep (Johnston et al. 2015). Consistent with a role of this protein in modulating recombination rate, RNF212 is essential for meiotic recombination and has a key role in stabilizing meiosis-specific recombination factors in mice (Reynolds et al. 2013). PRDM9 has also been associated with heritable variation in recombination rate (Hinch et al. 2011; Capilla et al. 2014) in humans and mice. Other mediators of recombination rate include REC8 (Sandor et al. 2012), which is a cohesin that is required for proper chromosome segregation in many organisms (Bhatt et al. 1999; Parisi

et al. 1999; Watanabe and Nurse 1999). In humans, inversion 17q21.31, a 900 kb inversion, is associated with increased recombination and fecundity in European females (Stefansson et al. 2005).

The genetic architecture of recombination rate variation outside of mammals remains poorly understood, even in the model organism *Drosophila melanogaster*. However, it is well-documented that recombination rate is a variable and heritable trait in *Drosophila*. For instance, classical genetic experiments indicate that the amount of crossing-over as well as the distribution of crossover events can vary among lines of *D. melanogaster* (Broadhead et al. 1977; Brooks and Marks 1986; Comeron et al. 2012; Hunter and Singh 2014), suggesting population-level variation in this trait. Additionally, genetic control for crossover rate has been suggested by laboratory selection experiments in which recombination rate itself was successfully subject to artificial selection (Detlefsen and Roberts 1921; Parsons 1958; Mukherjee 1961; Moyer 1964, Chinnici 1971a,b, Kidwell 1972a,b, Valentin 1973a,c, Charlesworth and Charlesworth 1985a,b; Charlesworth et al. 1985). Finally, changes in recombination rate have been shown to evolve as a correlated response to artificial selection on other characteristics, such as sternopleural bristle number (Rodell et al. 2004), DDT resistance (Flexon and Rodell 1982), geotaxis (Korol and Iliadit 1994), and resistance to temperature fluctuations (Zhuchenko et al. 1985), which is again consistent with segregating natural variation in recombination rate. Additionally, the fact that modifiers of recombination rate are commonly linked to variants controlling completely unrelated traits suggests that the genetic regulation of recombination rate modifiers are pervasive in the genome and may have pleiotropic effects.

To gain the first insight into the genetic basis of population-level variation in recombination rate in *D. melanogaster*, we used an association mapping approach. We favored an unbiased approach in part because *D. melanogaster* lacks homologs of the three known determinants of recombination rate in mammals noted above: RNF212, REC8, and PRDM9. We measured recombination rates on both the 3R and X chromosomes in the 205 fully-sequenced inbred lines of the *Drosophila melanogaster* Genetic Reference Panel (DGRP) (Mackay et al. 2012; Huang et al. 2014) using a two-step crossing scheme. We find nearly 2-fold variation in recombination rate among lines. Unexpectedly, we find that recombination rates are uncorrelated between the X and 3rd chromosome. We leveraged this pervasive population-level variation in recombination rate for genome-wide association (GWA) mapping to identify variants associated with phenotypic variation in recombination rate on each chromosome. We selected the top 20 most promising candidate genes

associated with recombination rate and subjected these candidates to both gene-level and allele-level functional validation. Our functional assays implicate five highly promising candidates for novel mediators of recombination rate variation in *D. melanogaster*: *CG10864*, *CG33970*, *Eip75B*, *Iola*, and *Ptp61F*. Our results thus provide new insight into the scale and scope of population level variation in rates of recombination and more importantly implicate new determinants of natural variation in recombination rate in *Drosophila*.

RESULTS

Robustness of Data

To assay recombination rate variation in the DGRP, we used a classic two-step crossing scheme (**Figure 4.1**). We measured recombination rates in two different genomic intervals: a 20.4 cM interval between *ebony* (*e*) and *rough* (*ro*) on chromosome 3R and a 33 cM interval between *yellow* (*y*) and *vermillion* (*v*) on the X chromosome. In total, 506,045 progeny were scored for recombinant phenotypes (217,525 for the *e ro* interval and 288,520 for the *y v* interval). Each replicate (three per DGRP line per chromosome assay) contained an average of ~427 flies. We first verified that our data conformed to expectations given Mendelian inheritance. To do so, for each line we compared the number of wild-type progeny to the number of progeny possessing both markers (either *e ro* or *y v*), summing across all three replicates (**Table 4.S1**). We also compared the number of recombinant progeny possessing only one marker to the number of recombinant progeny containing only the other marker (either *e +* versus *+ ro* or *y +* versus *+ v*) (**Table 4.S1**). The null expectation is a 1:1 ratio for the aforementioned pairs of phenotype classes. We used a Bonferroni correction (Dunn 1959, 1961) with $\alpha = 0.05$ to correct for multiple tests. When comparing the ratios of the two non-recombinant haplotypes, we find 15 lines that deviate from the expected 1:1 wt: *e ro* ratio (Bonferroni-corrected $P < 0.03$, G-test) and 8 lines that deviate from the expected 1:1 wt: *y v* ratio (Bonferroni-corrected $P < 0.03$, G-test). In all but one case, the deviation is in the direction of a relative excess of wild type flies. Only one line deviated significantly in both intervals (DGRP_819), with more wild-type progeny in both intervals. When comparing the ratios of the two recombinant haplotypes, we find DGRP_31 deviates significantly from the expected 1:1 *e +/ + ro* ratio (Bonferroni-corrected $P < 0.0001$, G-test) and one line (DGRP_819) that deviates significantly from the expected 1:1 *y +/ + v* ratio (Bonferroni-corrected $P < 0.0001$ G-test).

Similarly, we tested for unity of sex ratio by comparing the numbers of female and male progeny. There are no deviations from the expected 1:1 male:female ratio in the 205 lines for the *e ro* region (Bonferroni-corrected $P > 0.10$, all comparisons, G-test). For the *y v* region only two lines significantly deviate from expectation (DGRP_41 AND DGRP_801) (Bonferroni-corrected $P < 0.0002$, G-test), both in the direction of a relative excess of females.

Together, these data indicate that our assays for measuring recombination rate faithfully conform to the expectation of Mendelian inheritance. Critically, the lack of systematic bias towards wild-type chromosomes indicates that there are no major viability

defects associated with any of these mutations alone or in the pairs in which they were used for the current experiment. This confirms previous descriptions of these mutants and their lack of viability defects (Morgan and Bridges 1916; Bridges and Morgan 1923).

Heritable Continuous Variation in Recombination Rate Among DGRP Lines

Following the crossing scheme detailed in the Materials and Methods and in **Figure 4.1**, we estimated crossover rate for each DGRP line in the *e ro* and the *y v* regions (**Figure 4.S1A-B Fig; Table 4.S2**). Analyzing only lines with a standard karyotype on all chromosomes ($n = 112$), the average crossover rate for *e ro* is 20.9 ± 0.2 cM (ranging from 14.2 cM to 26.12 cM) (**Figure 4.2A**). This agrees well with the published map distance of 20.4 cM (Bridges and Morgan 1923). Among these lines, we observe 1.84-fold variation in mean crossover rate. Analyzing only lines with a standard karyotype on all chromosomes, the average crossover rate for *y v* is 31.2 ± 0.3 cM (ranging from 23.6 cM to 39.30 cM) (**Figure 4.2B**), compared with the published map distance of 33 cM (Morgan and Bridges 1916). Similar to the magnitude of population-level variation in recombination rate on *3R*, here we observe 1.67-fold variation among these lines in mean crossover rate for the *y v* interval.

There is significant genetic variation for crossover rate among lines for both regions ($F_{e ro} = 1.34$, $P_{e ro} = 0.038$ and $F_{y v} = 3.00$, $P_{y v} < 0.0001$, ANOVA). Using only lines with a standard karyotype (112 lines), we estimated H^2 for *e ro* as 0.12 and for *y v* as 0.41 (**Table 4.S3**). Interestingly, there is no significant correlation between recombination rate in these two intervals (Spearman's $\rho = 0.09$, $P = 0.36$; **Figure 4.2C**). Consistent with this, a model fitting effects of line, genomic interval, and line-by-interval interaction effects reveals significant interaction effects ($P < 0.0001$, ANOVA), indicating that the magnitude of the difference in recombination frequency between the two loci surveyed varies significantly among lines. These analyses illustrate that recombination rate on chromosome *3R* and chromosome *X*, at least in the way they have been assayed here, are independent traits in this panel of flies.

Correlation with other Phenotypes

As a widely-used community resource, the DGRP offers a unique opportunity to examine the relationship between recombination rate and other phenotypes because a variety of phenotypes have been surveyed in this panel. We tested whether crossover rates in the *e ro* or *y v* region (of lines with standard karyotypes) were correlated with various traits

including aggression (Shorter et al. 2015), behavioral response to odorants (Swarup et al. 2013; Arya et al. 2015), chill coma recovery (Ayroles et al. 2009; Mackay et al. 2012), longevity (Ivanov et al. 2015), nutritional and immune indices (Unckless et al. 2015), oxidative stress (Weber et al. 2012), pigmentation (Dembeck et al. 2015), sleep phenotypes (Harbison et al. 2013), startle response (Ayroles et al. 2009; Mackay et al. 2012), and starvation (Mackay et al. 2012) stress (Ayroles et al. 2009; Mackay et al. 2012) (**Table 4.S4**). The majority of correlations were weak and not statistically significant. However, for the *e ro* region, crossover rates were significantly positively correlated with female response to citral (Spearman's $\rho = 0.20$, $P = 0.03$) and negatively correlated with female survival on paraquat-laced food (Spearman's $\rho = -0.25$, $P = 0.01$). For the *y v* region, crossover rates were negatively correlated with female and male response to ethyl butyrate (Spearman's $\rho = -0.21$, $P = 0.03$; Spearman's $\rho = -0.20$, $P = 0.04$) as well as female response to eugenol (Spearman's $\rho = -0.22$, $P = 0.02$). Also in the *y v* region, similar to the *e ro* region, crossover rates were positively correlated with female response to citral (Spearman's $\rho = 0.21$, $P = 0.03$), male response to citral (Spearman's $\rho = 0.28$, $P = 0.004$) and also to male response to hexanal (Spearman's $\rho = 0.20$, $P = 0.04$). We find no evidence of a relationship between recombination frequency and fitness (as measured as reproductive output in our recombination assay) in the *e ro* region (Spearman's $\rho = -0.10$, $P = 0.26$) but we do see a marginally significant negative correlation in the *y v* region (Spearman's $\rho = -0.19$, $P = 0.05$).

Interchromosomal Effect

Chromosomal inversions were first discovered in *D. melanogaster* (Sturtevant 1917). Recombination is suppressed within the inverted region, yet recombination elsewhere in the genome increases through what is known as the interchromosomal effect (Schultz and Redfield 1951; Lucchesi and Suzuki 1968). The interchromosomal effect has been repeatedly documented in *Drosophila* (Portin 1990; Joyce and McKim 2010; Stevison et al. 2011), and has also been observed in other species such as grasshopper (White and Morley 1955) and maize (Bellini and Bianchi 1963). A large number of the DGRP lines are either homozygous or polymorphic for a chromosomal inversion, as expected for natural North American populations of *Drosophila melanogaster* (Mettler et al. 1977). Within the DGRP, there are a total of sixteen different segregating inversions, all on the autosomes (Huang et al. 2014). Out of the 205 lines, 93 lines contain at least one inversion

To test for the interchromosomal effect, we separated lines with inversions from lines with standard karyotype and tested whether lines that possessed an inversion somewhere in

the genome had higher rates of recombination in our surveyed regions. Lines with inversions have significantly increased rates of recombination in the *y v* interval relative to lines with standard karyotypes (35.1 cM vs. 31.0 cM, $P < 0.0001$; t-test). This trend is echoed in the *e ro* region (20.9 cM vs. 20.7 cM) but the difference in recombination frequency between standard and inverted karyotypes is not statistically significant ($P = 0.66$, t-test). These data further illustrate the interchromosomal effect in *Drosophila*.

Effects of Wolbachia

In the DGRP, 108 lines are infected with *Wolbachia pipientis* (Huang et al. 2014). To test for an effect of *Wolbachia* infection on recombination frequency, we used a linear model (see MATERIALS AND METHODS) and fit effects of line and *Wolbachia* infection status for each interval surveyed. Analyzing only lines with standard karyotype, we find there is a significant effect of *Wolbachia* infection in the *y v* region ($P = 0.0003$, ANOVA), such that *Wolbachia*-infected lines had a higher crossover frequency (31.8 cM) than uninfected lines (30.0 cM). No effect of *Wolbachia* infection was found for the *e ro* region ($P = 0.35$, ANOVA).

Genome-wide Association Analyses

The continuous variation for recombination among lines described above suggests that the genetic architecture of this trait is likely complex and regulated by many independent genetic factors (**Figure 4.2A-B**). The observed variation in recombination rate in the DGRP motivates our association mapping approach to more finely define the genetic basis of this trait. To identify genetic variants contributing to variation in recombination rate variation, we performed genome wide association mapping on the mean crossover rates from the DGRP in the *e ro* and *y v* regions. We did the association mapping in three different ways for each interval because of the inversions segregating in the DGRP and the known effect of inversions on recombination frequency (see Lucchesi and Suzuki 1968 for review). None of these inversions are on the *X* chromosome. However, 49 lines contained at least one copy of the *C*, *K*, *Mo* or *P* inversion on chromosome arm *3R*; all four of these inversions span at least part of the *e ro* interval used to assay recombination rate (dos Santos et al. 2015). We thus completely exclude these lines when analyzing recombination rate data for the *3R* interval. The three datasets used for the *3R* analyses were: 1) lines with no inversion on *3R* ($n = 156$), 2) lines with neither *3R* inversions nor inversion polymorphisms elsewhere in the genome ($n = 130$), and 3) lines with the standard karyotype (lines lacking inversions; $n = 112$). The three datasets used for the *X* chromosome analyses were: 1) all lines ($n = 205$),

2) lines without inversion polymorphisms (n = 152) and 3) lines with a standard karyotype (n = 112).

The statistical model used to infer associations assesses and adjusts for significant associations of both *Wolbachia* status and inversions. For the *e ro* region, there is a significant association of the *NS* inversion (**Table 4.1**; $P = 0.003$, ANOVA) on crossover rate in the restricted data set that removes lines with inversions on *3R* and lines with inversion polymorphisms. For the *y v* region, *Wolbachia* infection is significantly associated with crossover rate in all three of our data sets (**Table 4.1**; $P < 0.01$, all cases, ANOVA). Additionally, inversions *t*, *NS*, *K*, and *Mo* are all significantly associated with crossover rate in the *y v* region (**Table 4.1**; $P < 0.05$, all cases, ANOVA). These data are summarized in **Table 4.1**.

The full results for all six GWA analyses are presented as supplementary tables (**Tables 4.S5-10**). To generate a list of candidate genes and alleles, we combined the results from the different GWAS for each chromosome interval, using a significance threshold of $P < 10^{-5}$. For a Venn diagram displaying overlap between the different data sets, see **Figure 4.S3**. We tested whether the distribution of these associated variants was significantly different from the null expectation of uniform distribution across chromosomes (as a function of the number of polymorphisms on each chromosome). Using lines with standard karyotypes, we find that the distribution of associated variants is significantly different from the distribution of variants in the genome for both intervals ($P < 0.02$, both comparisons, *G*-tests). It appears that in both intervals, there is an enrichment of associated variants on chromosome *2R* (*e ro*: 63 versus 33; *y v*: 29 versus 16; observed versus expected).

For the *e ro* region, the three GWAS yielded a combined total of 688 unique variants at a nominal significance threshold of $P < 10^{-5}$. Of these variants, 45 are deletions, 25 are insertions, 2 are multiple nucleotide polymorphisms (MNPs) and the remaining 616 are single nucleotide polymorphisms (SNPS). Of these variants, 132 are on chromosome *2L*, 126 are on chromosome *2R*, 98 are on chromosome *3L*, 263 are on chromosome *3R* and 69 are on chromosome *X*. For the 263 variants located on the *3R* chromosome, 79 were located within the *e ro* region. Analyzing the location of these variants in relation to gene regions, 174 variants were located in intergenic regions. The remaining variants were either a codon deletion (n=1), downstream modifiers (n=43), located within an exon (n=5), located within in an intron (n=327), non-synonymous coding (n=27), a gained start site (n=2), synonymous coding change (n=54), upstream (n=28), UTR 3' (n=15) or UTR 5' (n=12).

For the *y v* region, combining results from all three GWA analyses, we identified 160 unique variants at a nominal significance threshold of $P < 10^{-5}$. Of these variants, 9 are deletions, 3 are insertions, and the remaining 148 are SNPs. Of these variants, 45 are on chromosome *2L*, 41 are on chromosome *2R*, 31 are on chromosome *3L*, 17 are on chromosome *3R* and 26 are on chromosome *X*. For the 26 variants located on the *X* chromosome, 16 variants were located within the *y v* region. Analyzing the location of these variants in relation to gene regions, 38 variants were located in intergenic regions. The remaining variants were either downstream modifiers (n=8), located within in an intron (n=83), non-synonymous coding (n=5), synonymous coding change (n=12), upstream (n=12), UTR 3' (n=1) or UTR 5' (n=1). There were no variants that overlapped between the two regions, consistent with the lack of correlation between the two traits, although different variants in the same gene (see below) were found. Variants in 359 genes were implicated as potential candidates from the three *e ro* GWAS, and variants in 111 genes were associated with recombination rate variation in the *y v* GWAS. There is very little overlap between these gene lists; a total of fifteen genes showed overlapping (gene-level) associations between the *e ro* and *y v* GWAS (*bab1*, *bun*, *CG4440*, *CG5953*, *CG31817*, *CG32521*, *CR44199*, *dnr1*, *dpr6*, *Eip63E*, *Eip75B*, *Ptp61F*, *Sec16*, *Shroom*, and *SNF4Agamma*). Additionally, the effect sizes for these variants were moderate, averaging ~2.32 cM for both regions (**Figure 4.S2A-B**). **Figure 4.3A-B** displays the Manhattan plots and linkage disequilibrium plots for both regions for the lines with standard karyotypes while **Figures 4.S4-5** display the same information for the other data sets analyzed.

Candidate Genes

We sought to functionally validate a subset of the genes identified by our association mapping. We used several criteria to refine our list of candidate associations to a tractable set of 20 candidate genes. First, we restricted our focus to protein-coding genes harboring significantly associated genetic variants. We then integrated the *P*-value of the association, effect size, and the number of GWAS the gene was implicated in on either or both chromosomes to refine our list of putative candidates. We narrowed our list further by limiting ourselves to genes with documented expression in the ovaries (Chintapalli et al. 2007; Celniker et al. 2009; Adrian and Comeron 2013). Our final candidate gene list (**Table 4.2**) includes eleven genes from the *e ro* GWA, five genes from the *y v* GWA and four genes that were found in both. There was more than one significantly associated genetic variant in 8 of our 20 candidate genes (*CG1273*, *CG4440*, *CG7196*, *dpr6*, *Eip75B*, *jing*, *Ptp61F* and

Ubx) with *jing* and *Ptp61F* having the most significantly associated variants (17 and 13 respectively). The full list of variants within these genes and associated *P*-values are listed in **Table 4.S11** and the genotypes of each DGRP line at these variants are listed in **Table 4.S12**.

Functional Validation

If these identified candidate genes mediate recombination rate in some way, we expect that perturbing these genes will affect recombination rate. We used both mutant analysis and RNAi to either knock out or knock down expression of each of these genes, and compared recombination rate in the knock out/down lines to an appropriate genetic background control. We measured recombination rate in the *e ro* and *y v* intervals for available mutants and RNAi lines for all 20 candidate genes in the same way as described earlier. We used a combination of *P*-element insertions, chromosomal deletions, as well as any available RNAi lines. For the RNAi experiments, we used a *nanos GAL4* driver, which should target the effects of knockdown to oogenesis. For validation using the *e ro* markers, the only line tested that produced a significant difference from control line was a deletion line, *Df(3R)ED2* ($P = 0.004$, Dunnett's test) (**Figure 4.4A; Table 4.S14**); this line shows a significant increase in recombination frequency relative to the genetic background control. This deletion encompasses 71 full genes and part of 1 additional gene, including two of our candidate genes - *cdi* and *CG10864*. It should also be noted that this deletion is on chromosome *3R*, spanning the cytological region 91A5 to 91F1 (for reference *e* is at 93C7-93D1 and *ro* is at 97D4-97D5). Using the *y v* markers, seven genes tested show a significant deviation in recombination frequency relative to the appropriate control (**Figure 4.4B; Table 4.S15**). These included *alph*, *CG9650*, *CG33970*, *Eip75B*, *grp*, *lola*, and *Ptp61F* ($P < 0.05$, all comparisons, Dunnett's test). *Eip75B* and *CG9650* showed a decrease in recombination relative to the control while *alph*, *CG33970*, *Eip75B*, *lola*, and *Ptp61F* showed an increase in recombination relative to the control. Interestingly, one *P*-element insertion in *grp* showed a significant increase of recombination while a different *P*-element insertion in *grp* showed a significant decrease of recombination.

Expression Analysis

While the mutant/RNAi analysis provides insight as to whether the candidate genes function in some way to mediate recombination, we also wanted to test whether these candidate genes show significant differences at the allelic level. We hypothesized that the

effects of these genes on recombination rate were mediated by expression level differences and thus tested for differences in gene expression in ovaries between allelic variants of our 20 candidate genes. We measured gene expression as mRNA abundance using quantitative RT-PCR (qPCR). For each of our twenty candidate genes, we selected three DGRP lines containing the major allele and three lines containing the minor allele (**Table 4.S16**). For candidate genes that had that multiple significantly associated variants, all attempts were made to include lines in which all minor alleles were present. The genotypes of these lines at the gene surveyed can found in **Table 4.S17**. Once a line was selected to validate a candidate gene, it was not used to validate another candidate gene. RNA was extracted from dissected ovaries from virgin DGRP females. The qPCR data (normalized to *GAPDH*) reveal significant differential expression for 11 of our 20 candidate genes (**Figure 4.5; Table 4.S18**). DGRP lines with the major alleles of *CG4440*, *CG15365*, *CG33970*, and *Ptp61F* ($P < 0.003$, all comparisons, t-tests) display higher expression levels than lines with the minor alleles. Conversely, DGRP lines with the major alleles of *CG1273*, *CG10864*, *dpr6*, *Eip75B*, *lola*, *Oaz*, and *Ubx* ($P < 0.05$, all comparisons, t-tests) display lower expression levels than lines with the minor alleles. It should be noted for variants these eleven candidate genes, all minor alleles are associated with reduced rates of recombination. Comparisons of un-normalized data (with concern over unstable housekeeping gene expression - Guénin et al. 2009; Hruz et al. 2011) largely confirm these results (**Figure 4.S6; Table 4.S19**).

DISCUSSION

Population Level Variation in Recombination Rate

Here we report the largest population-level survey of recombination rate variation in *Drosophila* to date. We find significant genetic variation for recombination rate in this North American population of *D. melanogaster* for two independent genomic intervals. At the broadest scope, these data are consistent with previous work from other systems. Indeed, a wealth of data indicate that recombination rate varies between and within populations in species such as *Drosophila* (Brooks and Marks 1986; Comeron et al. 2012), mice (Dumont et al. 2009), and humans (McVean et al. 2004; Fearnhead and Smith 2005; Graffelman et al. 2007; Kong et al. 2010).

The magnitude of population-level variation in recombination rate exposed by our survey is comparable to what has been previously shown in *D. melanogaster*. For instance, we observe 1.67 fold-variation for the *y v* interval, and previous work in this region shows ~1.2-fold variation (Brooks and Marks 1986; Hunter and Singh 2014). Other genomic regions in *Drosophila* consistently show 1-2 fold variation in crossover frequency among strains (Brooks and Marks 1986). Although measured with a different approach, work from heterogeneous stock mice indicates crossover frequency varies ~2-fold in both males and females (Dumont et al. 2009). Work from cattle indicates average genome-wide recombination rate varies ~1.7 fold in males (Sandor et al. 2012), which aligns well with our survey. Similarly, humans show ~2-fold variation in crossover frequency in both males and females (Broman et al. 1998; Chowdhury et al. 2009).

It should be noted that the ~2 fold variation in recombination frequency that we report above is biased downward and is not truly reflective of segregating natural variation in recombination rate in *Drosophila*. When we include lines with inversions, which clearly segregate in natural populations, we see a much greater span in recombination rates in the DGRP: 5.2-fold for the *e ro* interval (excepting lines with an inversion on 3R) and 3.5-fold for the *y v* interval. This range of variation in recombination frequency is remarkable, nearly doubling previous estimates from *Drosophila*, mouse and humans.

Lack of Correlation Between Rates of Crossing Over on 3R and X

Our results indicate that recombination rate at the two intervals surveyed are uncorrelated in the DGRP. This independence does not appear to be universal, however. Previous work in humans showed a significant positive correlation of the number of maternal recombination events on individual chromosomes and the number of maternal

recombination events in the remaining genome complement for 20 out of 23 chromosomes, as well as a large significant correlation for the first eight chromosomes compared to chromosomes nine through twenty-two and the X chromosome (Kong et al. 2002). The difference between *Drosophila* and humans is interesting, and may point to different genetic architectures of this trait in these systems. Certainly, the molecular mechanics of meiotic recombination have diverged markedly between humans and *Drosophila* (e.g. Kohl et al. 2012) and the recombinational landscapes in humans and flies are qualitatively different as well.

Correlation with other Available DGRP Phenotypes

Although anecdotal evidence suggests a link between recombination rate and organismal fitness (Tucić et al. 1981; Kong et al. 2004), the adaptive significance of population-level variation in recombination rate remains unknown. We find no direct evidence of a relationship between recombination frequency and fitness in the *e ro* region but we do see a marginally significant negative correlation in the *y v* region. The direction of this correlation is opposite of what has been previously reported in humans (Kong et al. 2004) but similar to what has been reported in *Drosophila* (Tucić et al. 1981). It is unclear why humans and *Drosophila* differ in this way, and whether this is biologically relevant or an artifact of our experimental design. Indeed, our measurement of fitness is coarse and is likely a poor indicator of organismal fitness. Previously reported estimates of longevity in the DGRP, another aspect of organismal fitness, show no significant correlation with our estimates of recombination rate in either interval (**Table 4.S4**; Ivanov et al. 2015). Thus, any connection between recombination and fitness based on these data should be interpreted as tenuous at best.

However, if population-level variation in recombination rate has biological significance, one might expect that recombination rate would correlate with other organismal phenotypes. We mined published DGRP phenotype data to test this explicitly. While we saw correlations of crossover rate and behavioral responses to different naturally occurring odorants, the biological link between these remain unclear. The most intriguing significant correlation we uncovered is the correlation of rates of crossing over in the *e ro* region ($\rho = -0.25$, $P = 0.01$) to female survival time on paraquat-laced food. Paraquat can cause oxidative stress and single-base damage, often corrected through the base-excision repair pathway. Though paraquat exposure does not appear to plastically increase meiotic recombination (Langberg 2014), there is clearly a link between stress and recombination in

Drosophila and other systems (Stern 1926; Neel 1941; Belyaev and Borodin 1982; Parsons 1988; Abdullah and Borts 2001; Singh et al. 2015). This correlation between recombination and resistance to the toxic effects of oxidative stress specifically in females revealed here may be reflective of the general connection between stress and recombination. Interestingly, of seven candidate genes associated with oxidative stress susceptibility/resistance in the DGRP, two overlap with candidate genes selected for this study, *CG9650* and *Eip75B* (Weber et al. 2012). This overlap could suggest conserved players in the DNA damage repair pathway in both meiotically and mitotically dividing cells.

Heritability

Previous work has estimated heritability for recombination rate in many different species. While estimates of heritability are necessarily population-specific, mammalian estimates encompass a wide range, from as small as 0.14 (Fledel-Alon et al. 2009) and 0.30 (Coop et al. 2008) in humans to as large as 0.46 in mice (Dumont et al. 2009). In maize, heritability of recombination frequency is considerably higher (broad sense heritability 0.21-0.69; Hadad et al. 1996). Insects show a wide range as well, with estimates of narrow sense heritability of recombination rate ranging from 0.16 in *Tribolium* (Deweese 1975) to 0.27-0.49 in grasshoppers (Shaw 1972). Early estimates of narrow sense heritability of recombination frequency in *Drosophila* based on parent-offspring regression are comparable to ours (0.09-0.38; Valentin 1973b), and selection based approaches yield a narrow sense heritability of 0.12 (Kidwell 1972a). That estimates of heritability of recombination are low indicates that much of the observed variation in recombination frequency cannot be ascribed to genetic differences along lines. This is consistent with the remarkable phenotypic plasticity in recombination frequency in *Drosophila*, evidenced in response to temperature (Plough 1917, 1921; Stern 1926; Smith 1936; Grell and Chandley 1965; Grell 1966; Grushko et al. 1991; Jackson et al. 2015), maternal age (Bridges 1915, 1927, 1929; Plough 1917, 1921; Stern 1926; Bergner 1928; Neel 1941; Hayman and Parsons 1960; Redfield 1966; Lake and Cederberg 1984; Chadov et al. 2000; Priest et al. 2007; Tedman-Aucoin and Agrawal 2011; Hunter and Singh 2014), nutrition (Bergner 1928; Neel 1941), parasite pressure (Singh et al. 2015) and other environmental factors.

Effects of Wolbachia pipientis Infection

Wolbachia pipientis is a common endosymbiont that infects the reproductive tissues of many different arthropods (Werren 1997). Evidence points to the fact that over 40% of

arthropods are infected by *W. pipientis* (Jeyaprakash and Hoy 2000; Hilgenboecker et al. 2008; Zug and Hammerstein 2012). Roughly 29% of *Drosophila* stocks from Bloomington *Drosophila* Stock Center (Clark et al. 2005) are infected, along with 76% of the *Drosophila* Population Genomics Project (n = 116) (Richardson et al. 2012). In the DGRP, 108 of 205 (53%) lines are infected with *W. pipientis* (Huang et al. 2014). In *Drosophila*, there is clear infection in the ovaries (Dobson et al. 1999; Clark and Karr 2002) and infection has been shown to reduce egg production (Hoffmann et al. 1990).

Interestingly, we see a significant association with *Wolbachia* infection in crossover rates in the *y v* region yet not in the *e ro* region. This discrepancy between the two intervals surveyed is difficult to explain, and merits further investigation. More curious yet is the contrast with previous results. It has been shown that *Wolbachia* infection has no effect on rates of crossing over in the *w ct* region (18.5 cM) in the laboratory wild-type strain Canton S (Serga et al. 2010). The *w ct* region is actually within the *y v* region surveyed in this study, so the discrepancy between the two studies is puzzling. It may be that the effect of *Wolbachia* infection on recombination frequency is sufficiently minor that the previous study, using a single genetic background and smaller sample sizes than the present study, was underpowered to detect this small effect (an average increase of 1.8 cM associated with *Wolbachia* infection in our study). Our results, coupled with previous findings, suggest that *W. pipientis* might have differential effects on recombination frequencies in different parts of the genome. Testing explicitly for this heterogeneity will be a topic of future exploration. In the future, it will also be interesting to see if infecting DGRP lines with *Wolbachia* causes an increase of crossover rates and if curing DGRP lines via tetracycline yields a decrease in crossover rates.

Candidate Genes

The DGRP allows us to couple phenotypic variation with genetic variation such that the genetic basis of complex traits of interest can be dissected. One benefit of this association mapping approach is that it is unbiased, which means that new genes, outside of known pathways playing a role in the phenotype of interest, can be identified. For example, a recent study using the DGRP dissecting the genetic architecture of abdominal pigmentation yielded associations with several variants in the known pigmentation pathway but importantly, also functionally validated seventeen out of twenty-eight candidate genes that had not been previously associated with pigmentation (Dembeck et al. 2015). Because nothing was known regarding the genetic basis of population-level variation in recombination

rate in *Drosophila* and because *Drosophila* lacks homologs of all genes associated with recombination rate variation in other systems, we were eager to leverage this unbiased approach to gain novel insight into the genetic architecture of this fundamentally important trait.

Consistent with the power of GWAS to uncover novel genes associated with phenotypic variation, our top candidate genes involved with recombination rate variation contains genes outside of the meiotic recombination pathways, which have been characterized in exquisite detail (see McKim et al. 2002 for review). Among the top 20 candidates for functional validation, seven are computationally predicted genes which have no clearly defined biological function or human orthologs. Interestingly, four of our candidate genes have Cys₂His₂ zinc fingers (*CG9650*, *jing*, *lola*, and *Oaz*). This is particularly intriguing due to the link between the zinc-finger domain containing PRDM9 and hotspot determination, and it is tempting to speculate that these proteins bind to DNA and designate crossover sites in a way that is vaguely reminiscent of the role of PRDM9 in mammalian recombination (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010). Moreover, the *D. pseudoobscura* ortholog of *Oaz*, *GA14502*, was previously identified as a possible candidate gene involved in recombination as the frequency of its zinc finger binding motif was significantly negatively associated with recombination on a broad scale (Heil and Noor 2012). Consistent with a role for zinc-finger DNA binding in *Drosophila* recombination, Trem, which also contains zinc fingers, was recently shown to be necessary along with Mei-W68 and Mei-P22 for the formation of DSBs in *Drosophila* (Lake et al. 2011).

We chose two methods for validation. The first method involves is a gene-level approach and asks whether perturbation of candidate genes perturbs recombination frequencies. To complement this approach, we also compared expression levels of the different alleles in these candidate genes using qPCR. Significant differential expression of our candidate genes (separated based on major and minor alleles implicated in our GWA) could provide evidence for gene expression differences affecting rates of crossing over.

Overall, there were 5 genes (*bru-2*, *CG4440*, *jing*, *MESR3*, and *pk*) which showed no change in recombination frequency the *e ro* or *y v* region when perturbed and no difference in expression level between the major and minor allelic variants. However, lack of functional validation does not imply that a candidate gene has no role in modulating recombination rate in *Drosophila*. Indeed, validation of candidate genes is challenging. The effect sizes of the genetic variants are moderate at best (**Figure 4.S2A-B**), making detection of these changes quite difficult in the absence of very large sample sizes. Additionally recombination rate

variation is highly likely to be a polygenic trait (Chinnici 1971a,b), and our results confirm this. Further, it has been shown that in many quantitative traits within the DGRP, there is pervasive epistasis (Huang et al. 2012; Mackay 2013). Epistatic interactions may similarly contribute to recombination rate variation in *Drosophila*. Consistent with this is the observation that we see an increase in recombination rate relative to the appropriate background for one *P*-element insertion of *grp* and a decrease in recombination rate for another insertion line (though we note that this observation is also consistent with variation in allelic effects at a single locus if the two *P*-elements were inserted into different locations). Finally, the process of recombination is likely to be highly buffered, and one could hypothesize that there is redundancy in maintaining the approximate number of crossovers required. It is also possible that these statistical associations are false positives due to our lenient *P*-value.

However, integrating across both the gene- and allele-level functional analysis, we find five high quality candidate genes for further investigation. These genes show significant perturbations in recombination frequency relative to the appropriate genetic background control in addition to differential expression specifically in ovaries between allelic variants at this locus. These were *CG10864*, *CG33970*, *Eip75B*, *lola*, and *Ptp61F*. Two of these (*Eip75B* and *Ptp61F*) were identified in GWAS in both the *e ro* and *y v* region.

CG10864 is involved in potassium channel function (Döring et al. 2006). In humans, another protein involved in potassium channel function, *KCNQ1*, has been shown to somatically imprint regions of the genome with higher rates of recombination (Pàldi et al. 1995). While imprinting appears to be less common in *Drosophila* females (Coolon et al. 2012), it is unclear if *CG10864* is participating in a similar role as compared to *KCNQ1*.

CG33970 is predicted to be involved with ATP binding and transporter activity (dos Santos et al. 2015). A direct link between ATP binding and meiotic recombination has yet to be shown, but there have been some hints of connections in the literature. For example, mutations in the ATP-binding domain of *RecA* (Konola et al. 1994) in *Escherichia coli*, *DMC1* (Dresser et al. 1997), *Rad51* and *Rad55* in yeast (Shinohara et al. 1992; Johnson and Symington 1995) and *XRCC3* in humans (Rafii et al. 2003) cause defects in homologous recombination and meiosis. While speculative, this gives credence to the idea that the putative ATP-binding ability of *CG33970* may contribute to meiotic recombination. Further work is aimed at dissecting this link.

Eip75B (*Ecdysone-induced protein 75B*) is involved in mediating ecdysone signaling, a steroid hormone. Defective ecdysone signaling affects the early germarium, causing

defects with meiotic entry (Morris and Spradling 2012). Interestingly, ecdysone signaling is important for female fertility but not for male fertility (Garen et al. 1977; Bownes et al. 1983; Gaziova et al. 2004). *Drosophila* males do not undergo meiotic recombination (Morgan 1912, 1914). It remains to be seen whether the connection between recombination, fertility and ecdysone signaling is merely coincidence; however, the role of *Eip75B* in oogenesis makes it a particularly exciting candidate for further work.

lola, or *longitudinals lacking*, is BTB zinc finger containing transcription factor that is required for axon growth and guidance (Seeger et al. 1993; Giniger et al. 1994). As noted above, DNA binding ability along with zinc fingers is exciting as a possible link with recombination. The predicted human ortholog, *ZBTB46* or *BZEL*, was shown to repress a desumoylase (Shin et al. 2012). Sumoylation has been linked to DNA repair (Potts 2009) and therefore it is possible that *lola* is involved in early processes that could ultimately lead to crossover formation.

Ptp61F (*Protein tyrosine phosphatase 61F*) is a member of the protein tyrosine phosphatase family. *Ptp61F* is an induced antagonist of the JAK/STAT pathway (Baeg et al. 2005; Müller et al. 2005) and has been directly implicated in oogenesis (Ursuliak et al. 1997). In the female germline, expression of *Ptp61F* is targeted to the nucleus and cytoplasmic organelles (Fitzpatrick et al. 1995) and this gene is required for normal female fecundity (Buszard et al. 2013). Tentative links between *Ptp61F* and DNA damage can be made in mammals; *Ptp61F* is the *Drosophila* homolog of human *PTP1B* and knockout *PTP1B* mice show a higher sensitivity to irradiation and an upregulation of many genes in the DNA excision/repair pathway (Través et al. 2014). Homologous recombination, base excision repair, and nucleotide excision repair are the primary pathways by which DNA damage are repaired in *Drosophila*. While the role for *Ptp61F* in meiotic recombination is not obvious the clear function in oogenesis coupled with the tentative connection to DNA damage repair is promising.

Conclusion

In conclusion, we have quantified levels of recombination rate variation in a natural population of *D. melanogaster* and have shown that genetic background significantly drives phenotypic variation in this critically important phenotype. The magnitude of observed phenotypic variation in recombination rate is large, with almost 2-fold variation present in each genomic region analyzed. We demonstrate that inversions play a large role in mediating rates of recombination, indicative of the interchromosomal effect, and provide the

first evidence that *Wolbachia* infection can significantly increase rates of recombination. Through our GWA approach, we show that recombination rate is a highly polygenic trait, with many genetic factors of small effect associating with phenotypic variation. We show that a subset of our candidate genes (*CG10864*, *CG33970*, *Eip75B*, *lola*, and *Ptp61F*) play putative roles in modulating recombination rate variation in *Drosophila* through both gene-level and expression-level validation. Future work will be aimed at determining the role of these candidate genes in the molecular process of recombination.

MATERIALS AND METHODS

Fly Stocks

The *Drosophila* Genetic Reference Panel is a collection of 205 fully-sequenced inbred lines (Mackay et al. 2012; Huang et al. 2014). Mated, gravid *Drosophila melanogaster* females were originally collected in Raleigh, NC, USA in 2003. Their progeny underwent 20 generations of full-sibling matings and were then fully sequenced. A total of 4,853,802 single nucleotide polymorphisms (SNPs) and 1,296,080 non-SNP variants were identified among these lines (Huang et al. 2014). GWA studies can then be performed to identify genetic variants significantly associating with phenotypes of interest.

To assay recombination rate, we took advantage of visible, recessive markers in *D. melanogaster*. To measure recombination rates on the 3R chromosome, we used a strain marked with *ebony* (e^4) and *rough* (ro^1); these markers are 20.4 cM apart (Bridges and Morgan 1923). To measure recombination on the X chromosome, we used a strain marked with *yellow* (y^1) and *vermillion* (v^1); these markers are 33 cM apart (Morgan and Bridges 1916). These markers were chosen to examine due to the genetic distance between them, ease of scoring and also their apparent lack of viability defects (Morgan and Bridges 1916; Bridges and Morgan 1923). Each of the doubly marked chromosomes were substituted into a wild-type isogenic Samarkand genetic background, free of *P*-elements (Lyman et al. 1996), to allow for continuity between assays and to minimize marker genetic background effects.

Recombination Rate Assay

To assay recombination rate variation in the DGRP, we used a classic two-step crossing scheme (**Figure 4.1**). All crosses were executed at 25°C with a twelve:twelve hour light:dark cycle on standard media using virgin females aged roughly 24 hours. For each interval, all 205 lines were crossed simultaneously; this was repeated three times to yield three replicate estimates of recombination frequency per line per interval. For the first cross, ten virgin females from every DGRP line were crossed to ten doubly-marked males (either ero or yv) in eight ounce bottles. Males and females were allowed to mate for five days, after which all adults were cleared from the bottles. F_1 females resulting from this cross are doubly heterozygous; these females are the individuals in which recombination is occurring. To uncover these recombination events we backcross F_1 females to the doubly marked males. For this second cross, twenty heterozygous virgin females were collected and backcrossed to twenty doubly-marked males. Males and females were allowed to mate for

five days, after which all adults were cleared from the bottles. After eighteen days, BC₁ progeny were collected, frozen, and scored for sex and for visible phenotypes. Previous work in our lab has demonstrated that freezing flies has no effect on the visible markers we scored. Recombinant progeny were then identified as having only one visible marker ($m^1 +$ or $+ m^2$). For each replicate, recombination rates were estimated by taking the ratio of recombinant progeny to the total number of progeny. Double crossovers cannot be recovered with this assay, so our estimates of recombination frequency are likely to be biased downwards slightly. The estimated recombination for a given strain and interval was calculated as the average across the three replicates for use in the DGRP GWA pipeline.

Inversions

Freeze 2 of the DGRP contains 16 different segregating autosomal inversions verified by cytological methods (Huang et al. 2014). We therefore performed association mapping in three different ways for each interval. The *X* chromosome (in this population of flies) lacks inversions while 49 lines contained an inversion on chromosome arm *3R* which span at least part of the *e ro* interval used to assay recombination rate (dos Santos et al. 2015). We thus completely exclude these lines when analyzing recombination rate data for the *3R* interval. The three datasets used for the *3R* analyses were: 1) lines with no inversion on *3R* ($n = 156$), 2) lines with neither *3R* inversions nor inversion polymorphisms elsewhere in the genome ($n = 130$), and 3) lines with the standard karyotype ($n = 112$). The three datasets used for the *X* chromosome analyses were: 1) all lines ($n = 205$), 2) lines without inversion polymorphisms ($n = 152$) and 3) lines with a standard karyotype ($n = 112$).

Statistical and Quantitative Genetic Analyses

To estimate the broad-sense heritability (H^2) of recombination rate variation, we used an ANOVA framework. The ANOVA followed the form of $Y = \mu + L + \epsilon$, for each chromosome assayed where Y is recombination rate, μ is the overall mean, L is the random effect of line and ϵ is the residual. Additionally, we ran a similar ANOVA, adding the genomic region as a fixed factor, to test for a significant interaction. That ANOVA followed the form of $Y = \mu + L + R + L \times R + \epsilon$, with the terms remain the same and R is the genomic region assayed. To estimate H^2 , we followed the formula $H^2 = \sigma_L^2 / (\sigma_L^2 + \sigma_\epsilon^2)$ where σ_L^2 is the variance component among lines and σ_ϵ^2 is the residual variance or variance component attributed to error. The variance components were calculated using REML. All H^2 estimates were calculated using R Statistical Software, v3.2.1 and RStudio v0.99.467.

To test for a significant effect of Wolbachia infection, we used an ANOVA framework as well. That ANOVA followed the form of $Y = \mu + W + \epsilon$, for each chromosome assayed where Y is recombination rate (measured in cM), μ is the overall mean, W is fixed effect of Wolbachia infection status and ϵ is the residual, on all measurements (not average line means as used in the GWA described below).

Genome-wide Association

To identify genetic variants that are influencing differences in the mean crossover number in two different regions of the *Drosophila* genome, we performed a GWAS using the established web-based pipeline developed by the Mackay lab at NC State University, Raleigh, NC (<http://dgrp2.gnets.ncsu.edu/>) (Mackay et al. 2012; Huang et al. 2014). The first step in conducting the GWAS was to adjust line means for the effects of *Wolbachia pipientis* infection as well as the presence of inversions that are segregating in the DGRP. The adjusted line means are then used to fit a linear mixed model, $Y = \mathbf{X}b + \mathbf{Z}u + e$. Y is the adjusted phenotypic value, \mathbf{X} is the design matrix for the fixed SNP effect b , \mathbf{Z} is the incidence matrix for the random polygenic effect u and e is the residual. The vector of polygenic effects u has a covariance matrix in the form of $\mathbf{A}\sigma^2$, where σ^2 is the polygenic variance component and \mathbf{A} is the genomic relatedness. Additionally, Manhattan plots were constructed using the qqman package in R (Turner 2014).

Validation of Candidate Genes - Recombination Rate Assay

As described in the text, we selected 20 candidate genes to validate that contained at least one significantly associated genetic variant within them based on P -value of the SNP located within the gene, effect size of the SNP, and the number of GWAS the gene was implicated in and expression data. To validate these candidate genes, we took advantage of available P -element insertion lines and chromosomal deletions as well as RNAi lines (**Table 4.S13**). Lines containing a P -element insertion or chromosomal deletion (deleting the candidate gene) as well as appropriate controls (genetic background used to generate P -element insertion or chromosomal deletion) were used in the same crossing scheme (**Figure 4.1**) detailed above. For the first cross, ten virgin females from every line containing a P -element insertion or chromosomal deletion were crossed to ten doubly-marked males (either $e ro$ or $y v$) in eight oz. bottles. Males and females were allowed to mate for five days, after which all adults were cleared from the bottles. For the second cross, ten virgin heterozygous females were collected and backcrossed to ten doubly-marked

males in vials. Males and females were allowed to mate for five days, after which all adults were cleared from vials. BC₁ progeny were collected from each vial, frozen, and scored for sex and for visible phenotypes. For each *P*-element insertion or chromosomal deletion, there were 30 replicates. For each replicate, recombination rates were estimated by taking the ratio of recombinant progeny to the total number of progeny.

The RNAi lines followed a similar crossing scheme except for the males used in the F₀ cross. These males contained the doubly marked chromosome (*e ro*) along with *nanos-GAL4* driver (Rørth 1998; Van Doren et al. 1998). *nanos* is expressed throughout *Drosophila* oogenesis (Wang et al. 1994). All *P*-element insertions, chromosomal deletions or RNAi lines were compared to appropriate controls using Dunnett's Test (Dunnett 1955, 1964) using both the raw recombination proportions as well as arcsined transformed data. Statistics for validation were performed in JMP® Pro 11.2.0.

Validation of Candidate Genes - Expression Analysis

To test the hypothesis that gene expression differences between alleles are driving phenotypic variation, we analyzed mRNA abundance differences between the major and minor allele for each of our 20 candidate genes using quantitative RT-PCR (qPCR). For each candidate gene, three DGRP lines containing the major allele and three DGRP lines containing the minor allele were chosen (**Table 4.S16**). For the eight genes that had multiple significant genetic variants associated within the gene region, DGRP lines that contained the most major/minor alleles were selected (**Table 4.S17**). For each candidate gene, virgin females were collected from the six DGRP lines contemporaneously to minimize environmental variation. Females were aged three days in vials with roughly 0.5 mL of yeast paste. Ovaries were then dissected from anesthetized females in a solution of 1X PBS and stored in Life Technologies RNAlater® solution (Life Technologies). For each line, four replicates of ten pairs of ovaries were dissected. Total RNA was extracted from homogenized ovaries using Trizol® (Life Technologies) following manufacturer instructions. cDNA was generated using Bio-Rad iScript™ cDNA Synthesis and following manufacturer instructions. Primers for candidate genes were generated using FlyPrimerBank (Hu et al. 2013) (**Table 4.S20**). qPCR was run a BioRad CFX384 machine using Bio-Rad iQ™ SYBR® Green following manufacturer instructions. Four technical replicates for each sample were run on the same 384 plate, minimizing the contribution of between plate variation.

Samples were analyzed using *GAPDH* for normalization due to its relative consistent expression (Suzuki et al. 2000). For each candidate gene, there were six lines

analyzed, three that contained the major allele and three that contained the minor allele identified in our GWAS. For each line, we collected RNA in replicates of four. We ran each RNA sample (converted to cDNA) in replicates of four. Therefore, for each line, there are a total of 16 qPCR measurements for the candidate gene of interest and 16 qPCR measurements for the *GAPDH* control. Measurements from each DGRP line were normalized by dividing by the average Cq value of *GAPDH* for the corresponding DGRP line, modeled after common normalization procedures (Vandesompele et al. 2002). These 96 measurements (48 measurements for the major allele and 48 measurements for the minor allele) were then analyzed by comparing the means of the lines containing the major allele to the means of the lines containing the minor allele via a student's t-test using JMP Pro 11.2.0. In addition, the raw Cq values (before normalization) were also analyzed to ensure that differential *GAPDH* expression was not biasing results.

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TABLES

Table 4.1 - Analyses of variance of the effects of Wolbachia infection and inversions on recombination rate. .0.17

Region	Data Set	# of DGRP Lines	P values					
			Wolbachia Status	2L(t)	2R(NS)	3R(P)	3R(K)	3R(Mo)
<i>e ro</i>	All lines (with no 3R inversions)	156	0.17	0.12	0.59	-	-	-
<i>e ro</i>	No inversion polymorphisms (and no 3R inversions)	130	0.31	0.12	0.003	-	-	-
<i>e ro</i>	Only standard karyotypes	112	0.53	-	-	-	-	-
<i>y v</i>	All lines	205	0.01	< 0.0001	0.0006	0.1	0.002	0.001
<i>y v</i>	No inversion polymorphisms	152	0.006	< 0.0001	0.002	0.16	0.049	0.0004
<i>y v</i>	Only standard karyotypes	112	0.008	-	-	-	-	-

Table 4.2 - Summary of Candidate Genes identified during GWAS and selected for functional validation. Number of GWAS implicated in out of six total. FlyAtlas expression is listed as mRNA signal in ovaries as well as whole flies (i.e. ovary mRNA signal / whole fly mRNA signal). mRNA expression from Adrian and Comeron (2013) is listed as either expression in only 'early' meiosis (germaria to stage 3), 'late' meiosis (remaining ovarioles), 'both' phases, or significant differential expression ('DE') between the early and late.

Candidate Gene	GWAS	Number of GWAS	Lowest <i>P</i> -value	Largest Effect Size	modENCODE Expression	FlyAtlas Expression	Adrian & Comeron (2013)
<i>alph</i>	<i>y v</i>	1	2.29E-07	3.435	Very High	207 / 222	Both
<i>bru-2</i>	<i>e ro</i>	1	1.14E-05	1.565	-	2 / 9	Both
<i>cdi</i>	<i>e ro</i>	1	9.22E-06	1.634	Moderately High	6/60	Both
<i>CG1273</i>	<i>e ro</i>	1	3.47E-07	2.613	-	3 / 12	Both
<i>CG4440</i>	<i>e ro & y v</i>	6	1.10E-08	2.999	-	2 / 46	Early
<i>CG7196</i>	<i>e ro</i>	3	8.00E-07	3.029	-	2 / 80	Both
<i>CG9650</i>	<i>e ro</i>	1	5.54E-06	2.336	-	12 / 9	Both
<i>CG10864</i>	<i>e ro</i>	1	3.72E-06	2.394	-	5 / 6	Both
<i>CG15365</i>	<i>e ro</i>	1	3.55E-07	2.606	-	6 / 8	Both
<i>CG33970</i>	<i>y v</i>	1	5.66E-05	2.807	-	56 / 366	Both
<i>dpr6</i>	<i>e ro & y v</i>	4	9.37E-08	3.094	Moderate	20 / 13	Both
<i>Eip75B</i>	<i>e ro & y v</i>	2	5.98E-06	2.694	-	115 / 68	Both
<i>grp</i>	<i>e ro</i>	1	3.31E-06	-1.098	Very High	2137 / 1069	DE
<i>jing</i>	<i>e ro</i>	3	4.17E-08	2.786	Moderate	72 / 26	Both
<i>lola</i>	<i>e ro</i>	1	6.13E-08	2.755	Very High	112 / 95	DE
<i>MESR3</i>	<i>y v</i>	1	5.90E-06	2.281	Moderate	197 / 236	Both
<i>Oaz</i>	<i>y v</i>	1	8.84E-06	2.682	Moderate	1 / 1	Both
<i>pk</i>	<i>e ro</i>	1	7.20E-09	2.922	-	6 / 13	DE
<i>Ptp61F</i>	<i>e ro & y v</i>	3	3.36E-08	3.146	High	928 / 359	DE
<i>Ubx</i>	<i>y v</i>	1	4.82E-06	1.53	-	1 / 13	Both

FIGURES

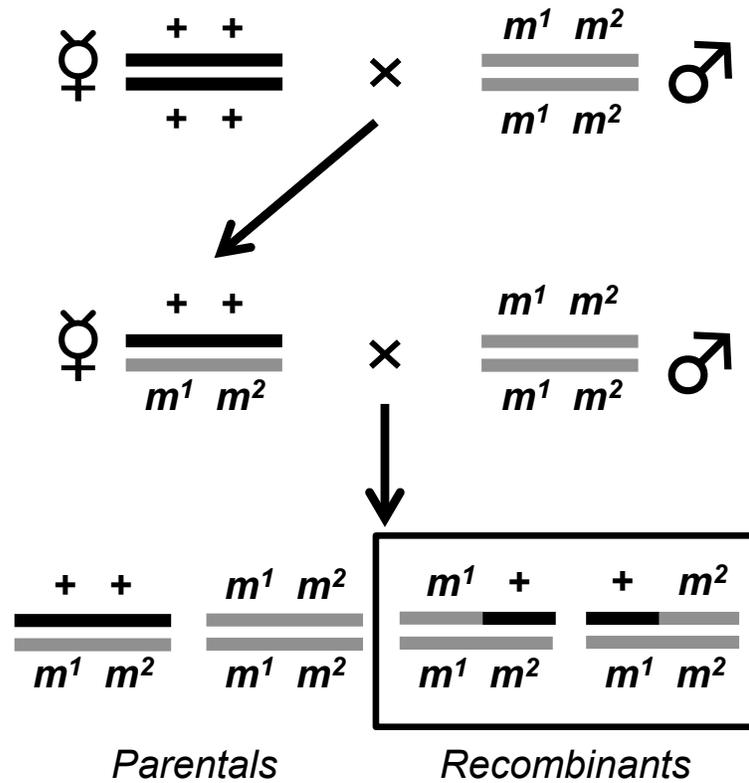
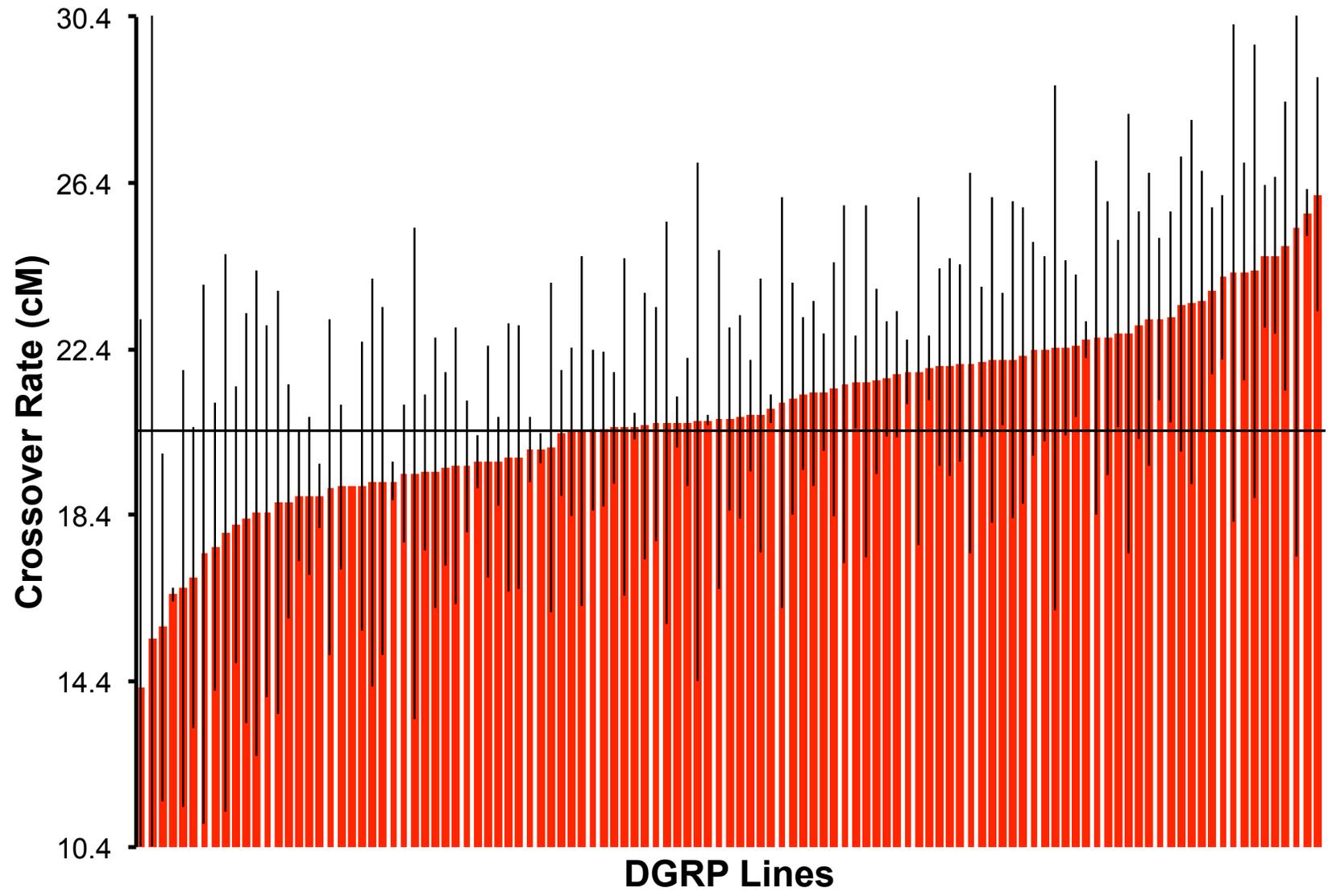


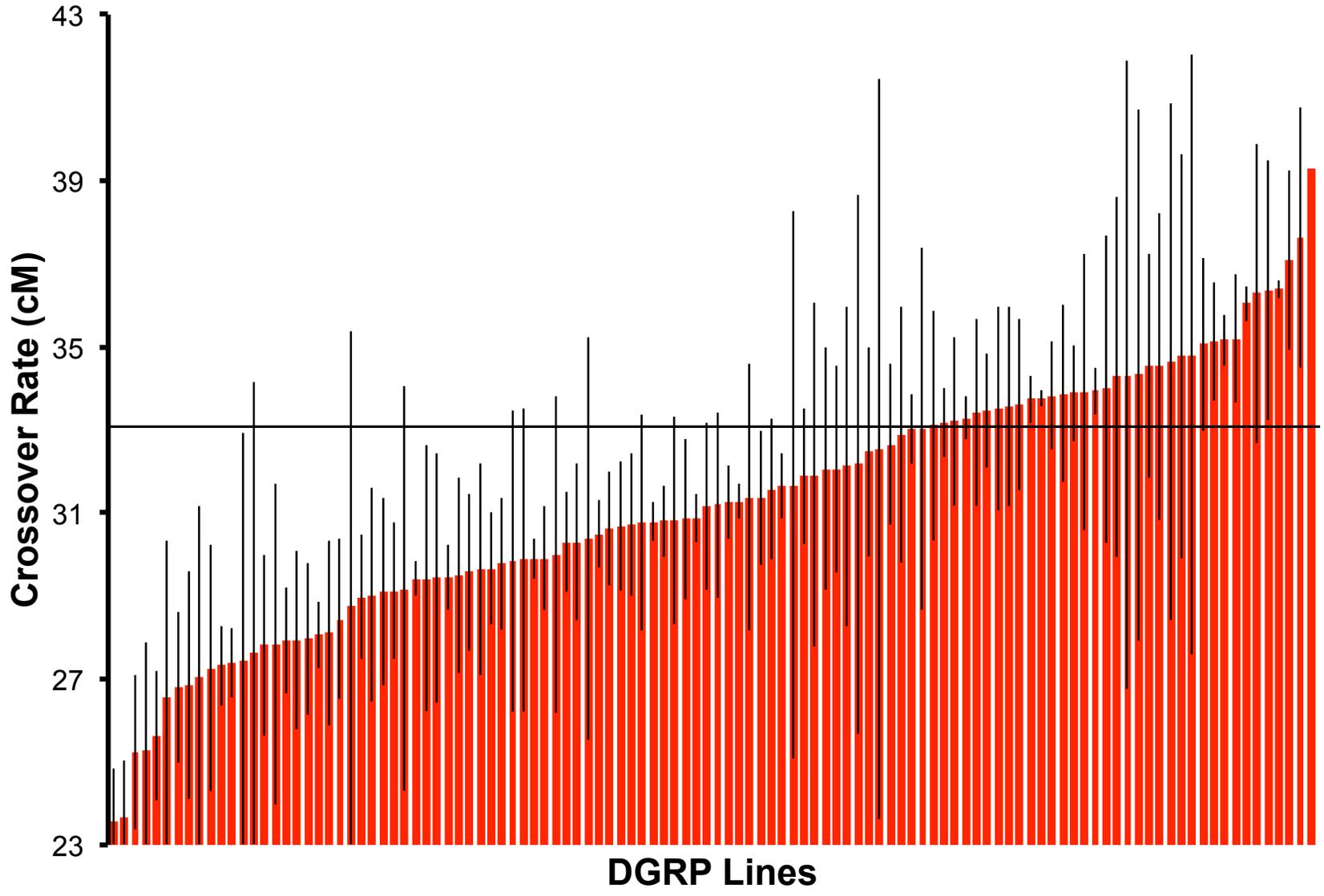
Figure 4.1 - Two-step crossing scheme to measure crossover frequency in the DGRP. ++ denotes wild-type and $m^1 m^2$ denotes either *e ro* on chromosome 3R or *y v* on the X chromosome. In addition, since males are heterogametic, only one copy of the *y* or *v* marker is needed to display a phenotype. Crossover frequency is calculated by taking the ratio of total recombinants (denoted by black box) to total number of progeny.

Figure 4.2 - Natural variation in recombination rate. Variation in crossover frequency in the DGRP (standard karyotypes only) in the (A) *e ro* region on chromosome 3R and (B) in the *y v* region on the X chromosome. The strains in each panel are ordered by recombination rate. Grey bars depict standard error. For reference, the reported map distance for the *e ro* region is 20.4 cM, while the reported map distance for the *y v* region is 33 cM, denoted by a horizontal line in both graphs. (C) Recombination rate on 3R as a function of recombination rate on the X chromosome (standard karyotypes only).

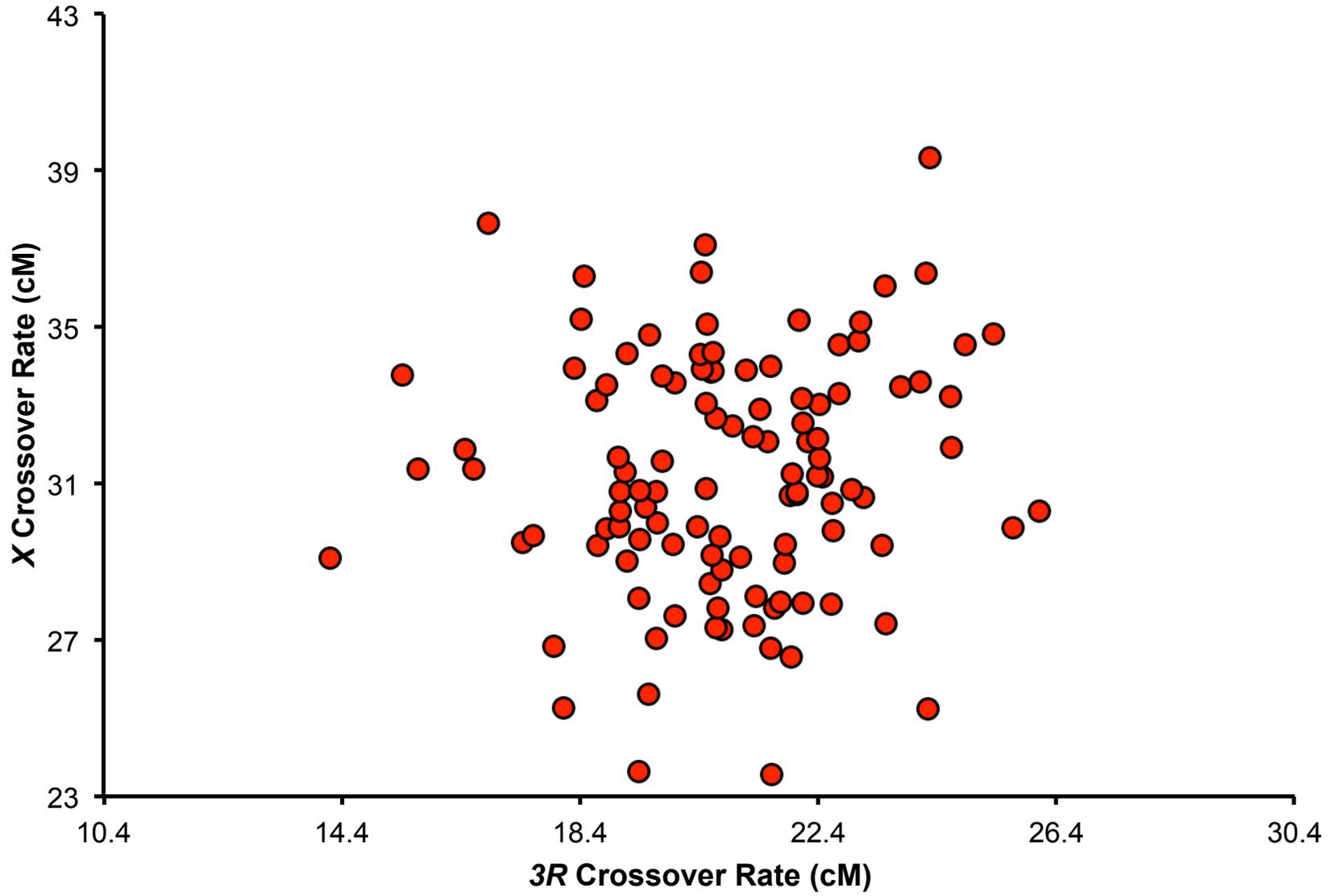
A



B



C



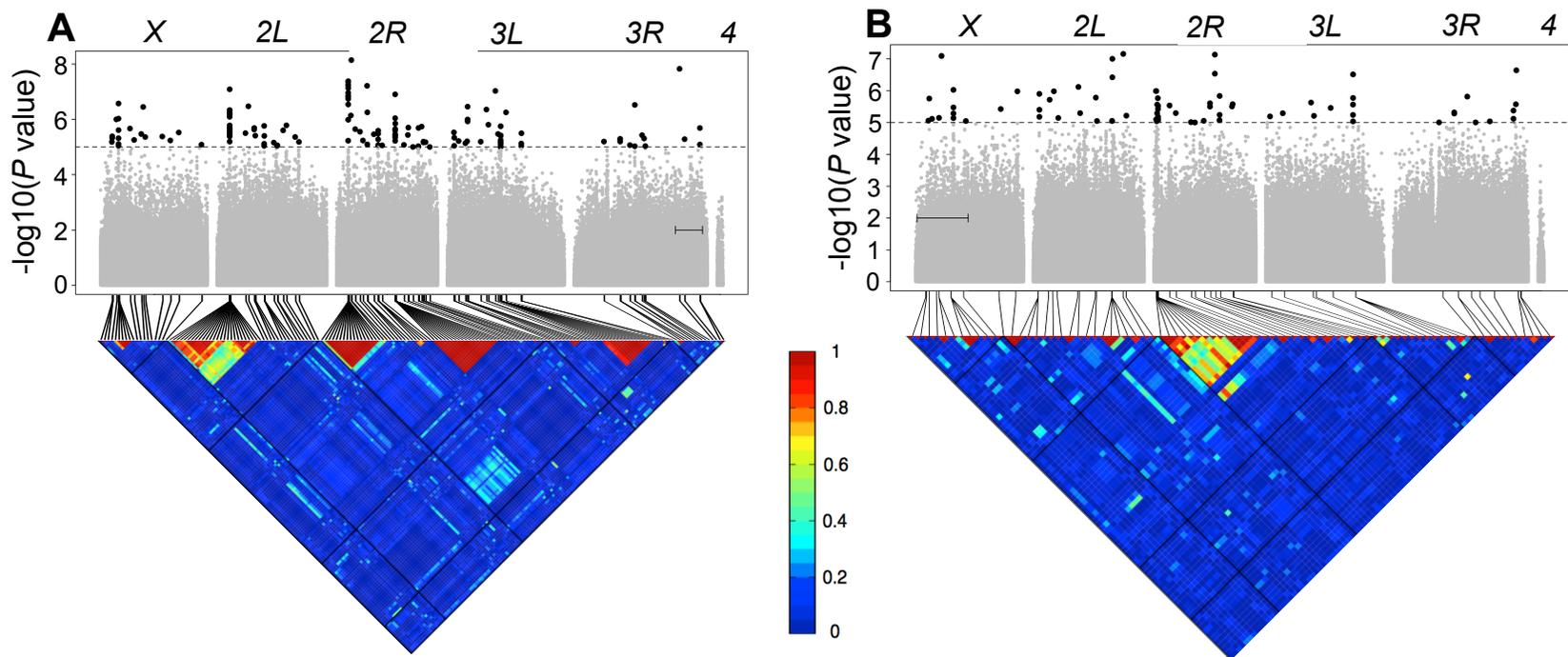
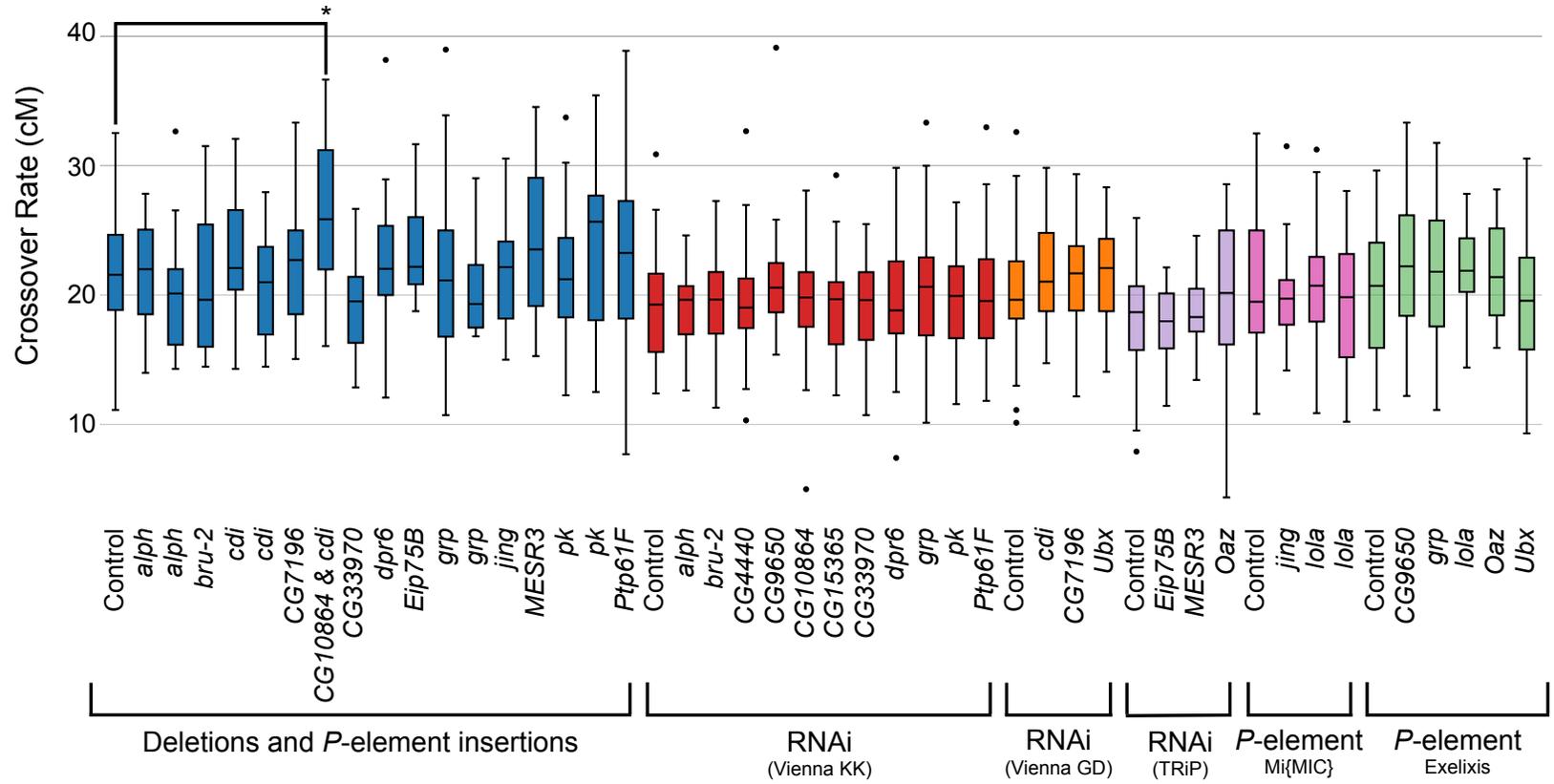


Figure 4.3 - Genome-wide association analyses. Manhattan plots and accompanying linkage disequilibrium heat maps are depicted for the (A) *e ro* region and (B) *y v* region for the standard karyotypes. A significance threshold of $P \leq 10^{-5}$ is denoted for Manhattan plots. Dots represent all tested genetic variants in the DGRP and dots above this threshold indicate significantly associating SNPs. Additionally, the surveyed region for each chromosome is bracketed. The triangular heat map displays the amount of linkage disequilibrium (LD, measured here as r^2) between variants. Each major chromosome is depicted. Red denotes complete LD and blue denotes absence of LD.

Figure 4.4 - Functional validation of candidate genes. Recombination rate of *P*-element insertions, chromosomal deletions and RNAi lines assayed in the (A) *e ro* region and (B) *y v* region. Darker grey boxes indicate control genetic background, followed by strains compared to that control genetic background. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. * indicates a $P < 0.05$, ** indicates $P < 0.01$ and *** indicates $P < 0.001$ (via Dunnett's test).

A



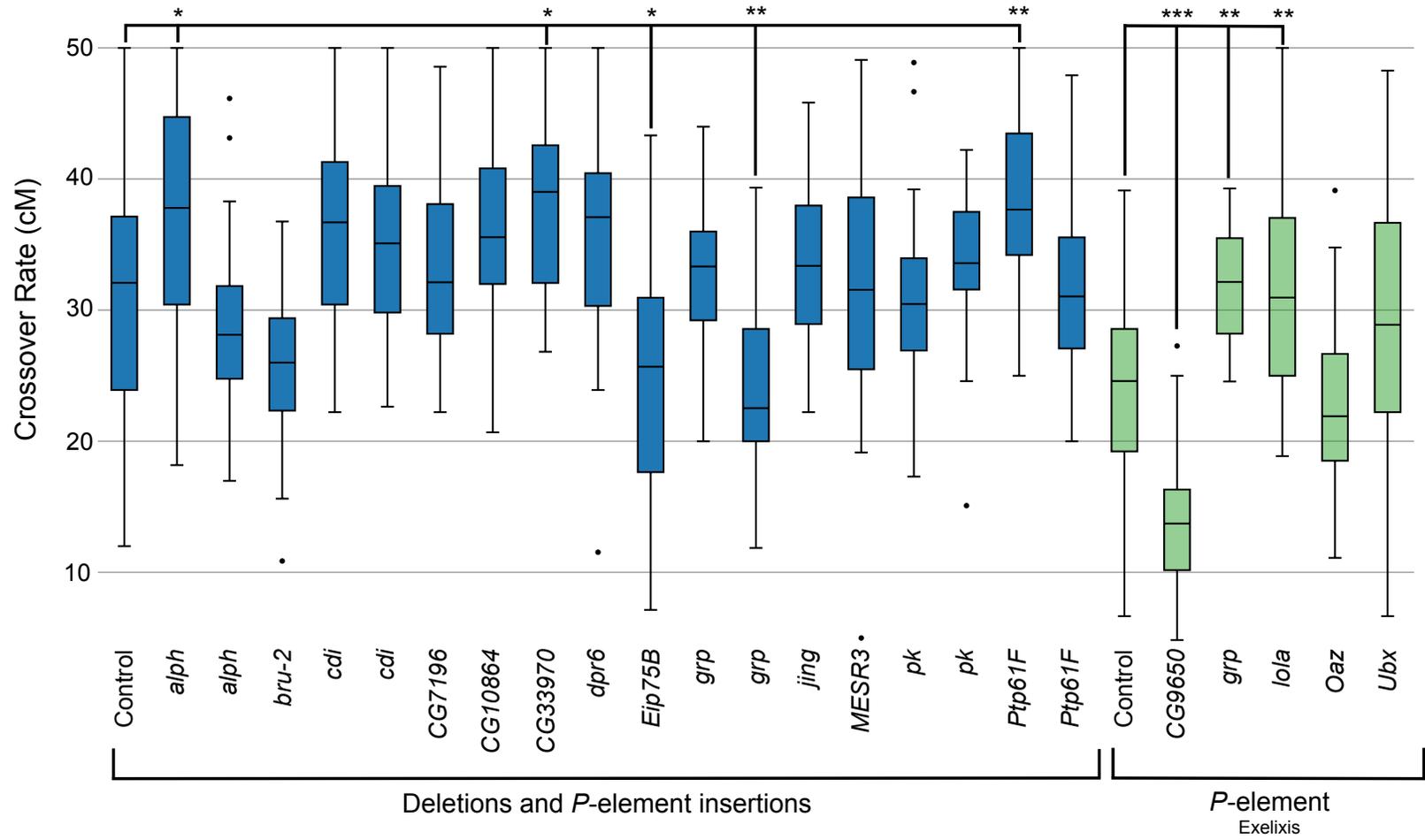
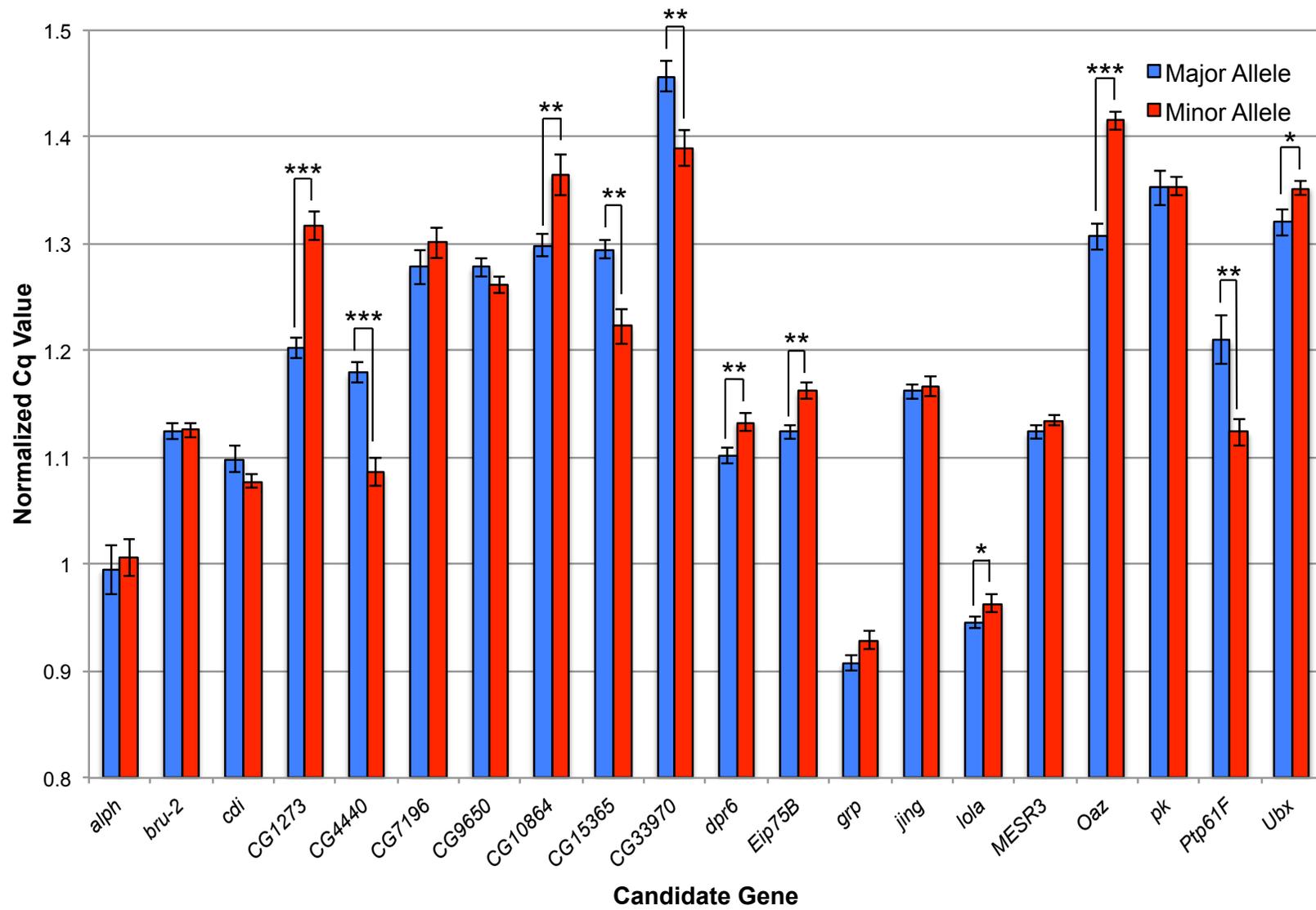
B

Figure 4.5 - Validation of expression difference in ovaries via qPCR. For each candidate gene, the normalized average expression of three lines with major allele (blue bars) and three lines with minor allele (red bars) are shown. Error bars denote standard error. * indicates a $P < 0.05$, ** indicates $P < 0.01$ and *** indicates $P < 0.001$ (via a student's t-test).



SUPPLEMENTAL TABLES

Table 4.S1 - Robustness of data. Raw counts, expected numbers and G-test *P*-values for number of males versus females, number of wild-type progeny versus doubly marked individuals ($m^1 m^2$), and number of recombinant progeny (either + m^2 or $m^1 +$).

DGRP Line	e ro. # of Males	e ro. # of Females	Expected	G-test <i>P</i> -value	e ro. # of ++	e ro. # of e ro	Expected	G-test <i>P</i> -value	e ro. # of + ro	e ro. # of e +	Expected	G-test <i>P</i> -value	yv # of Males	yv # of Females	Expected	G-test <i>P</i> -value	yv # of ++	yv # of y v	Expected	G-test <i>P</i> -value	yv # of + v	yv # of y +	Expected	G-test <i>P</i> -value
DGRP 21	723	786	754.5	0.25	592	549	570.5	0.37	176	192	184	0.56	666	603	634.5	0.21	425	383	404	0.30	229	232	230.5	0.92
DGRP 26	648	601	624.5	0.35	507	461	484	0.30	164	117	140.5	0.05	781	740	760.5	0.46	565	477	521	0.05	256	223	239.5	0.29
DGRP 28	381	333	357	0.20	330	384	357	0.15					593	666	629.5	0.15	376	384	380	0.84	264	235	249.5	0.36
DGRP 31	545	640	592.5	0.05	362	544	453	0.00	253	26	139.5	0.00	791	734	762.5	0.30	540	445	492.5	0.03	275	265	270	0.76
DGRP 32	424	400	412	0.55	414	369	391.5	0.26	13	28	20.5	0.09	739	720	729.5	0.73	484	438	461	0.28	280	257	268.5	0.48
DGRP 38	572	574	573	0.97	467	464	465.5	0.94	108	107	107.5	0.96	607	588	597.5	0.70	456	379	417.5	0.06	177	183	180	0.82
DGRP 40	766	786	776	0.72	682	594	638	0.08	137	139	138	0.93	708	661	684.5	0.37	521	420	470.5	0.02	220	208	214	0.68
DGRP 41	362	413	387.5	0.19	337	304	320.5	0.36	66	68	67	0.90	538	349	443.5	0.00	297	380	338.5	0.02	92	118	105	0.20
DGRP 42	266	263	264.5	0.93	219	209	214	0.73	52	49	50.5	0.83	519	518	518.5	0.98	382	335	358.5	0.21	176	144	160	0.21
DGRP 45	423	415	419	0.85	335	306	320.5	0.42	106	91	98.5	0.45	741	660	700.5	0.13	536	453	494.5	0.06	191	221	206	0.30
DGRP 48	518	503	510.5	0.74	435	390	412.5	0.27	94	102	98	0.69	597	541	569	0.24	370	317	343.5	0.15	227	224	225.5	0.92
DGRP 49	569	627	598	0.24	504	442	473	0.15	133	117	125	0.47	729	691	710	0.48	510	424	467	0.05	251	235	243	0.61
DGRP 57	417	430	423.5	0.75	371	302	336.5	0.06	98	76	87	0.24	647	530	588.5	0.02	400	429	414.5	0.48	147	201	174	0.04
DGRP 59	554	500	527	0.24	447	368	407.5	0.05	119	120	119.5	0.96	720	656	688	0.22	480	443	461.5	0.39	233	220	226.5	0.67
DGRP 69	201	217	209	0.58	161	149	155	0.63	50	58	54	0.59	694	631	662.5	0.22	483	404	443.5	0.06	233	205	219	0.34
DGRP 73	498	497	497.5	0.98	425	379	402	0.25	105	86	95.5	0.33	793	746	769.5	0.40	593	500	546.5	0.05	232	214	223	0.55
DGRP 75	537	549	543	0.80	497	358	427.5	0.00	122	109	115.5	0.55	552	559	555.5	0.88	458	298	378	0.00	178	177	177.5	0.97
DGRP 83	528	569	548.5	0.38	437	386	411.5	0.21	108	166	137	0.01	699	613	656	0.09	450	422	436	0.50	246	194	220	0.08
DGRP 85	582	584	583	0.97	455	444	449.5	0.80	116	151	133.5	0.13	762	774	768	0.83	535	466	500.5	0.12	269	266	267.5	0.93
DGRP 88	539	607	573	0.16	463	446	454.5	0.69	113	124	118.5	0.61	687	620	653.5	0.19	483	432	457.5	0.23	187	205	196	0.52
DGRP 91	456	471	463.5	0.73	403	338	370.5	0.09	71	115	93	0.02	753	666	709.5	0.10	517	479	498	0.39	197	226	211.5	0.32
DGRP 93	535	499	517	0.43	424	368	396	0.16	101	141	121	0.07	750	694	722	0.30	483	409	446	0.08	280	272	276	0.81
DGRP 100	622	567	594.5	0.26	683	506	594.5	0.00					855	804	829.5	0.38	580	499	539.5	0.08	308	272	290	0.29
DGRP 101	660	621	640.5	0.44	568	450	509	0.01	120	143	131.5	0.32	746	725	735.5	0.70	516	432	474	0.05	273	250	261.5	0.48
DGRP 105	536	528	532	0.86	565	470	517.5	0.04	25	4	14.5	0.00	824	635	729.5	0.00	527	396	461.5	0.00	279	257	268	0.50
DGRP 109	555	571	563	0.74	466	438	452	0.51	113	109	111	0.85	805	645	725	0.00	415	459	437	0.29	279	297	288	0.60
DGRP 129	421	444	432.5	0.58	346	316	331	0.41	91	112	101.5	0.30	478	462	470	0.71	324	321	322.5	0.93	146	149	147.5	0.90
DGRP 136	780	751	765.5	0.60	731	572	651.5	0.00	134	94	114	0.06	706	686	696	0.70	515	457	486	0.19	230	190	210	0.17
DGRP 138	416	403	409.5	0.75	426	358	392	0.09	21	14	17.5	0.40	832	768	800	0.26	599	486	542.5	0.02	277	238	257.5	0.22
DGRP 142	468	463	465.5	0.91	387	340	363.5	0.22	112	92	102	0.32	712	558	635	0.00	475	400	437.5	0.07	200	195	197.5	0.86
DGRP 149	656	647	651.5	0.86	527	482	504.5	0.32	166	128	147	0.12	615	625	620	0.84	447	404	425.5	0.30	216	173	194.5	0.12
DGRP 153	586	632	609	0.35	513	420	466.5	0.03	157	128	142.5	0.22	626	537	581.5	0.06	458	412	435	0.27	149	144	146.5	0.84
DGRP 158	560	574	567	0.77	459	451	455	0.85	111	113	112	0.92	633	630	631.5	0.95	479	446	462.5	0.44	198	140	169	0.03
DGRP 161	384	366	375	0.64	320	212	266	0.00	115	103	109	0.57	480	495	487.5	0.73	320	320	320	1.00	168	167	167.5	0.97
DGRP 176	584	605	594.5	0.67	491	472	481.5	0.67	114	112	113	0.93	871	738	804.5	0.02	594	525	559.5	0.14	258	232	245	0.41
DGRP 177	482	504	493	0.62	391	376	383.5	0.70	104	115	109.5	0.60	884	814	849	0.23	603	498	550.5	0.03	302	295	298.5	0.84
DGRP 181	720	677	698.5	0.42	610	496	553	0.02	133	158	145.5	0.30	466	533	499.5	0.13	358	302	330	0.12	188	151	169.5	0.15
DGRP 189																								
DGRP 195	524	525	524.5	0.98	469	343	406	0.00	111	126	118.5	0.49	782	739	760.5	0.44	613	484	548.5	0.01	214	210	212	0.89
DGRP 208	666	650	658	0.76	517	520	518.5	0.95	151	128	139.5	0.33	806	834	820	0.62	586	565	575.5	0.66	247	242	244.5	0.87
DGRP 217	398	415	406.5	0.67	316	319	317.5	0.93	86	92	89	0.75	687	635	661	0.31	487	430	458.5	0.18	208	197	202.5	0.70
DGRP 223	638	694	666	0.28	554	490	522	0.16	132	156	144	0.32	747	679	713	0.20	545	542	543.5	0.95	169	170	169.5	0.97
DGRP 227	519	520	519.5	0.98	429	412	420.5	0.68	111	87	99	0.23	803	739	771	0.25	569	505	537	0.17	238	230	234	0.79
DGRP 228	651	649	650	0.97	562	509	535.5	0.25	95	134	114.5	0.07	808	727	767.5	0.14	594	555	574.5	0.42	204	182	193	0.43
DGRP 229	743	746	744.5	0.96	652	549	600.5	0.04	149	139	144	0.68	816	743	779.5	0.19	581	581	581	1.00	211	186	198.5	0.37
DGRP 233	356	349	352.5	0.85	288	275	281.5	0.70	74	68	71	0.72	474	450	462	0.58	324	310	317	0.69	147	143	145	0.87
DGRP 235	358	401	379.5	0.27	304	296	300	0.82	76	83	79.5	0.69	743	761	752	0.74	530	485	507.5	0.32	255	234	244.5	0.50
DGRP 237	530	592	561	0.19	437	427	432	0.81	130	128	129	0.93	778	791	784.5	0.82	562	505	533.5	0.22	236	266	251	0.34
DGRP 239	538	514	526	0.60	633	369	501	0.00	36	14	25	0.02	513	453	483	0.17	334	311	322.5	0.52	160	161	160.5	0.97
DGRP 256	400	442	421	0.31	368	303	335.5	0.08	85	86	85.5	0.96												
DGRP 280	769	735	752	0.54	632	586	609	0.35	151	135	143	0.50	802	794	798	0.89	615	510	562.5	0.03	237	234	235.5	0.92
DGRP 287	315	317	316	0.96	284	224	254	0.06	58	66	62	0.61	586	602	594	0.74	402	392	397	0.80	191	203	197	0.67

Table 4.S1 Continued

DGRP Line	e ro: # of Males	e ro: # of Females	Expected	G-test P-value	e ro: # of ++	e ro: # of e ro	Expected	G-test P-value	e ro: # of + ro	e ro: # of e +	Expected	G-test P-value	y v: # of Males	y v: # of Females	Expected	G-test P-value	y v: # of ++	y v: # of y v	Expected	G-test P-value	y v: # of + v	y v: # of y +	Expected	G-test P-value
DGRP 301	315	324	319.5	0.80	256	244	250	0.70	67	72	69.5	0.76	585	558	571.5	0.57	422	368	395	0.17	184	169	176.5	0.57
DGRP 303	616	517	566.5	0.04	430	448	439	0.67	134	121	127.5	0.56	671	711	691	0.45	483	455	469	0.52	216	228	222	0.69
DGRP 304	432	422	427	0.81	342	337	339.5	0.89	94	81	87.5	0.49	760	672	716	0.10	481	473	477	0.85	252	226	239	0.40
DGRP 306	460	472	466	0.78	368	353	360.5	0.69	103	108	105.5	0.81	726	720	723	0.91	532	473	502.5	0.19	217	224	220.5	0.81
DGRP 307	623	588	605.5	0.48	533	467	500	0.14	100	111	105.5	0.59	748	746	747	0.97	531	437	484	0.03	253	273	263	0.54
DGRP 309	561	595	578	0.48	513	421	467	0.03	107	115	111	0.70	716	750	733	0.53	516	446	481	0.11	263	241	252	0.49
DGRP 310	655	644	649.5	0.83	520	497	508.5	0.61	142	140	141	0.93	592	523	557.5	0.14	394	352	373	0.28	179	190	184.5	0.69
DGRP 313	421	400	410.5	0.60	356	304	330	0.15	77	84	80.5	0.70	856	727	791.5	0.02	565	450	507.5	0.01	263	305	284	0.21
DGRP 315	333	336	334.5	0.93	292	230	261	0.05	71	76	73.5	0.77	757	739	748	0.74	566	465	515.5	0.03	247	218	232.5	0.34
DGRP 317	152	178	165	0.31	172	127	149.5	0.06	10	21	15.5	0.15	770	738	754	0.56	528	500	514	0.54	240	240	240	1.00
DGRP 318	680	693	686.5	0.80	579	528	553.5	0.28	139	127	133	0.60	788	744	766	0.43	517	487	502	0.50	286	242	264	0.18
DGRP 319	312	305	308.5	0.84	254	227	240.5	0.38	74	62	68	0.47	831	843	837	0.84	615	510	562.5	0.03	268	281	274.5	0.69
DGRP 320	377	386	381.5	0.82	306	279	292.5	0.43	117	61	89	0.00	589	640	614.5	0.30	395	392	393.5	0.94	217	225	221	0.79
DGRP 321	557	586	571.5	0.54	485	396	440.5	0.03	147	115	131	0.16	908	902	905	0.92	763	465	614	0.00	288	294	291	0.86
DGRP 324	535	578	556.5	0.36	619	450	534.5	0.00	18	26	22	0.39	944	948	946	0.95	754	664	709	0.09	249	225	237	0.44
DGRP 325	547	568	557.5	0.66	480	396	438	0.04	115	124	119.5	0.68	763	641	702	0.02	546	431	488.5	0.01	215	212	213.5	0.92
DGRP 332	363	348	355.5	0.69	288	275	281.5	0.70	59	89	74	0.08	650	541	595.5	0.03	405	383	394	0.58	209	194	201.5	0.60
DGRP 335	464	496	480	0.47	389	375	382	0.72	102	94	98	0.69	814	806	810	0.89	603	509	556	0.05	247	261	254	0.66
DGRP 336	608	545	576.5	0.19	523	369	446	0.00	143	118	130.5	0.27	701	575	638	0.01	422	389	405.5	0.41	254	211	232.5	0.16
DGRP 338	530	558	544	0.55	445	392	418.5	0.19	115	136	125.5	0.35	819	762	790.5	0.31	496	486	491	0.82	314	285	299.5	0.40
DGRP 340	562	542	552	0.67	472	406	439	0.11	115	111	113	0.85	814	636	725	0.00	497	478	487.5	0.67	264	211	237.5	0.08
DGRP 348	362	357	359.5	0.90	367	328	347.5	0.30	4	20	12	0.01	744	721	732.5	0.67	467	408	437.5	0.16	303	287	295	0.64
DGRP 350	447	462	454.5	0.72	439	448	443.5	0.83	9	13	11	0.54	884	777	830.5	0.06	525	449	487	0.08	342	345	343.5	0.94
DGRP 352	618	595	606.5	0.64	690	484	587	0.00	6	33	19.5	0.00	841	794	817.5	0.41	548	475	511.5	0.11	312	300	306	0.73
DGRP 354	387	430	408.5	0.29	354	309	331.5	0.22	73	81	77	0.65	775	765	770	0.86	578	501	539.5	0.10	250	211	230.5	0.20
DGRP 355	417	461	439	0.29	347	331	339	0.66	97	103	100	0.76	700	687	693.5	0.81	500	400	450	0.02	242	245	243.5	0.92
DGRP 356	313	294	303.5	0.59	242	214	228	0.35	76	75	75.5	0.95	740	674	707	0.21	473	488	480.5	0.73	221	232	226.5	0.71
DGRP 357	479	490	484.5	0.80	421	370	395.5	0.20	78	100	89	0.24	962	862	912	0.10	665	589	627	0.13	290	280	285	0.77
DGRP 358	398	419	408.5	0.60	444	347	395.5	0.01	11	15	13	0.58	748	703	725.5	0.40	442	380	411	0.13	342	287	314.5	0.12
DGRP 359	676	648	662	0.59	586	479	532.5	0.02	124	135	129.5	0.63	853	755	804	0.08	586	484	535	0.03	279	259	269	0.54
DGRP 360	542	511	526.5	0.50	422	413	417.5	0.83	109	109	109	1.00	721	671	696	0.34	483	446	464.5	0.39	244	219	231.5	0.41
DGRP 361	466	490	478	0.58	399	419	409	0.62	68	70	69	0.90	842	808	825	0.55	529	484	506.5	0.32	323	314	318.5	0.80
DGRP 362	525	582	553.5	0.23	455	403	429	0.21	130	119	124.5	0.62	765	653	709	0.04	498	446	472	0.23	235	239	237	0.90
DGRP 365	541	591	566	0.29	486	419	452.5	0.12	105	122	113.5	0.42	891	710	800.5	0.00	560	501	530.5	0.20	275	265	270	0.76
DGRP 367	342	367	354.5	0.51	291	259	275	0.33	72	87	79.5	0.40	726	658	692	0.20	489	463	476	0.55	234	198	216	0.22
DGRP 370	589	518	553.5	0.13	480	376	428	0.01	144	107	125.5	0.10	1009	957	983	0.41	738	624	681	0.03	297	307	302	0.77
DGRP 371	437	480	458.5	0.32	366	352	359	0.71	113	86	99.5	0.17	827	733	780	0.09	626	516	571	0.02	220	198	209	0.45
DGRP 373	389	416	402.5	0.50	372	306	339	0.07	57	70	63.5	0.41	846	664	755	0.00	555	462	508.5	0.04	255	238	246.5	0.59
DGRP 374	581	602	591.5	0.67	560	532	546	0.55	47	44	45.5	0.82	796	735	765.5	0.27	603	391	497	0.00	277	260	268.5	0.60
DGRP 375	574	543	558.5	0.51	491	400	445.5	0.03	107	119	113	0.57	513	436	474.5	0.08	341	297	319	0.22	155	156	155.5	0.97
DGRP 377	382	415	398.5	0.41	307	334	320.5	0.45	86	70	78	0.36	631	678	654.5	0.36	436	353	394.5	0.04	280	240	260	0.21
DGRP 379	445	453	449	0.85	452	279	365.5	0.00	85	82	83.5	0.87	751	598	674.5	0.00	505	480	492.5	0.57	198	166	182	0.24
DGRP 380	421	474	447.5	0.21	333	348	340.5	0.68	110	104	107	0.77	878	872	875	0.92	794	478	636	0.00	244	234	239	0.75
DGRP 381	691	625	658	0.20	548	446	497	0.02	174	148	161	0.31	552	404	478	0.00	292	308	300	0.64	179	177	178	0.94
DGRP 382	576	538	557	0.42	537	363	450	0.00	109	105	107	0.85	589	535	562	0.25	372	336	354	0.34	201	215	208	0.63
DGRP 383	555	566	560.5	0.82	420	424	422	0.92	148	129	138.5	0.42	885	836	860.5	0.40	549	506	527.5	0.35	363	303	333	0.10
DGRP 385	724	636	680	0.09	570	498	534	0.12	159	133	146	0.28	792	764	778	0.62	566	541	553.5	0.60	243	206	224.5	0.22
DGRP 386	540	527	533.5	0.78	484	370	427	0.01	98	115	106.5	0.41	859	864	861.5	0.93	689	550	619.5	0.01	230	254	242	0.44
DGRP 390	524	507	515.5	0.71	500	355	427.5	0.00	83	93	88	0.59	572	502	537	0.13	346	337	341.5	0.81	212	179	195.5	0.24
DGRP 391	579	646	612.5	0.18	554	421	487.5	0.00	125	125	125	1.00	676	611	643.5	0.20	461	376	418.5	0.04	242	208	225	0.26
DGRP 392	538	508	523	0.51	412	369	390.5	0.28	141	124	132.5	0.46	673	678	675.5	0.92	443	500	471.5	0.19	217	191	204	0.36

Table 4.S1 Continued

DGRP Line	e ro. # of Males	e ro. # of Females	Expected	G-test P-value	e ro. # of ++	e ro. # of e ro	Expected	G-test P-value	e ro. # of + ro	e ro. # of e +	Expected	G-test P-value	y v. # of Males	y v. # of Females	Expected	G-test P-value	y v. # of ++	y v. # of y v	Expected	G-test P-value	y v. # of + v	y v. # of y +	Expected	G-test P-value
DGRP 395	433	438	435.5	0.90	349	317	333	0.38	98	107	102.5	0.66	780	812	796	0.57	543	562	552.5	0.69	246	241	243.5	0.87
DGRP 397	761	626	693.5	0.01	608	526	567	0.08	120	133	126.5	0.56	797	779	788	0.75	528	530	529	0.97	282	236	259	0.15
DGRP 399	584	528	556	0.23	522	340	431	0.00	131	119	125	0.59	924	758	841	0.00	581	564	572.5	0.72	284	253	268.5	0.34
DGRP 405	578	558	568	0.67	511	384	447.5	0.00	123	118	120.5	0.82	924	801	862.5	0.04	651	502	576.5	0.00	304	268	286	0.29
DGRP 406	597	606	601.5	0.85	524	388	456	0.00	146	145	145.5	0.97	939	824	881.5	0.05	582	575	578.5	0.88	314	292	303	0.53
DGRP 409	543	554	548.5	0.81	581	516	548.5	0.17					777	773	775	0.94	511	479	495	0.47	272	288	280	0.63
DGRP 426	492	496	494	0.93	430	368	399	0.12	101	89	95	0.54	832	797	814.5	0.54	525	499	512	0.57	315	290	302.5	0.47
DGRP 427	518	544	531	0.57	425	402	413.5	0.57	130	105	117.5	0.25	699	630	664.5	0.18	490	469	479.5	0.63	196	174	185	0.42
DGRP 437	626	580	603	0.35	619	587	603	0.51					833	712	772.5	0.03	568	501	534.5	0.15	228	248	238	0.52
DGRP 439	668	632	650	0.48	577	472	524.5	0.02	153	98	125.5	0.01	818	779	798.5	0.49	588	468	528	0.01	276	265	270.5	0.74
DGRP 440	650	570	610	0.11	571	528	549.5	0.36	49	72	60.5	0.14	722	789	755.5	0.22	519	466	492.5	0.23	261	265	263	0.90
DGRP 441	609	627	618	0.72	540	454	497	0.05	116	126	121	0.65	695	574	634.5	0.02	501	348	424.5	0.00	218	202	210	0.58
DGRP 443	533	463	498	0.12	423	383	403	0.32	96	94	95	0.92	742	737	739.5	0.93	544	499	521.5	0.32	229	207	218	0.46
DGRP 461	462	437	449.5	0.56	385	322	353.5	0.09	75	117	96	0.03	565	476	520.5	0.05	366	331	348.5	0.35	167	177	172	0.70
DGRP 486	665	636	650.5	0.57	599	413	506	0.00	148	141	144.5	0.77	711	752	731.5	0.45	562	491	526.5	0.12	211	199	205	0.68
DGRP 491	649	702	675.5	0.31	587	511	549	0.10	117	136	126.5	0.40	587	530	558.5	0.23	428	365	396.5	0.11	180	144	162	0.16
DGRP 492	603	598	600.5	0.92	563	368	465.5	0.00	111	159	135	0.04	765	709	737	0.30	540	431	485.5	0.01	260	243	251.5	0.59
DGRP 502	335	356	345.5	0.57	258	285	271.5	0.41	59	89	74	0.08	633	630	631.5	0.95	489	475	482	0.75	147	152	149.5	0.84
DGRP 505	659	576	617.5	0.09	606	385	495.5	0.00	115	129	122	0.53	765	682	723.5	0.12	492	472	482	0.65	221	262	241.5	0.19
DGRP 508	594	591	592.5	0.95	525	403	464	0.00	121	136	128.5	0.51	855	792	823.5	0.27	613	557	585	0.25	230	247	238.5	0.58
DGRP 509	374	339	356.5	0.35	283	274	278.5	0.79	82	74	78	0.65	758	704	731	0.32	539	520	529.5	0.68	206	197	201.5	0.75
DGRP 513	439	490	464.5	0.24	382	322	352	0.11	105	120	112.5	0.48	405	413	409	0.84	271	265	268	0.85	168	114	141	0.02
DGRP 517	430	437	433.5	0.87	373	328	350.5	0.23	87	79	83	0.66	907	877	892	0.62	663	594	628.5	0.17	289	238	263.5	0.12
DGRP 528	570	532	551	0.42	444	412	428	0.44	108	138	123	0.18	790	755	772.5	0.53	519	510	514.5	0.84	268	248	258	0.53
DGRP 530	762	800	781	0.50	669	564	616.5	0.03	147	182	164.5	0.17	985	909	947	0.22	739	636	687.5	0.05	255	264	259.5	0.78
DGRP 531	574	450	512	0.01	461	314	387.5	0.00	115	134	124.5	0.39	946	861	903.5	0.16	631	565	598	0.18	322	289	305.5	0.34
DGRP 535	792	787	789.5	0.93	730	517	623.5	0.00	161	171	166	0.70	949	968	958.5	0.76	720	657	688.5	0.23	279	261	270	0.58
DGRP 551	673	696	684.5	0.66	646	488	567	0.00	123	112	117.5	0.61	848	852	850	0.95	630	475	552.5	0.00	301	294	297.5	0.84
DGRP 555	537	550	543.5	0.78	564	513	538.5	0.27	3	7	5	0.36	1016	970	993	0.47	636	603	619.5	0.51	380	367	373.5	0.74
DGRP 559	405	411	408	0.88	422	394	408	0.49					851	852	851.5	0.99	535	512	523.5	0.62	329	327	328	0.96
DGRP 563	322	331	326.5	0.80	305	216	260.5	0.01	73	59	66	0.39	506	517	511.5	0.81	336	359	347.5	0.54	170	158	164	0.64
DGRP 566	319	406	362.5	0.02	355	301	328	0.14	32	37	34.5	0.67	848	774	811	0.19	561	528	544.5	0.48	274	259	266.5	0.65
DGRP 584	369	432	400.5	0.12	315	316	315.5	0.98	86	84	85	0.91	720	671	695.5	0.35	484	419	451.5	0.13	254	234	244	0.52
DGRP 589	381	390	385.5	0.82	339	288	313.5	0.15	75	57	66	0.27	701	718	709.5	0.75	518	479	498.5	0.38	233	189	211	0.13
DGRP 595	471	492	481.5	0.63	351	375	363	0.53	137	100	118.5	0.09	466	440	453	0.54	322	292	307	0.39	171	121	146	0.04
DGRP 596	202	229	215.5	0.36	167	153	160	0.58	49	62	55.5	0.38	393	368	380.5	0.52	291	242	266.5	0.13	100	128	114	0.19
DGRP 627	598	646	622	0.34	527	430	478.5	0.03	140	147	143.5	0.77	790	803	796.5	0.82	516	507	511.5	0.84	293	277	285	0.64
DGRP 630	395	399	397	0.92	340	324	332	0.66	70	60	65	0.53	924	836	880	0.14	576	542	559	0.47	330	312	321	0.62
DGRP 634	450	415	432.5	0.40	405	401	403	0.92	17	42	29.5	0.02	670	619	644.5	0.32	487	363	425	0.00	233	206	219.5	0.36
DGRP 639	244	259	251.5	0.64	240	198	219	0.16	34	31	32.5	0.79	308	298	303	0.77	213	188	200.5	0.38	96	109	102.5	0.52
DGRP 642	445	442	443.5	0.94	364	328	346	0.33	90	105	97.5	0.45	691	666	678.5	0.63	453	393	423	0.14	261	250	255.5	0.73
DGRP 646	474	473	473.5	0.98	478	469	473.5	0.84					698	674	686	0.65	479	406	442.5	0.08	238	249	243.5	0.72
DGRP 703	404	397	400.5	0.86	362	278	320	0.02	80	81	80.5	0.96	881	771	826	0.06	632	568	600	0.19	216	236	226	0.51
DGRP 705	296	313	304.5	0.63	296	197	246.5	0.00	65	51	58	0.36	459	421	440	0.36	449	298	373.5	0.00	71	62	66.5	0.58
DGRP 707	329	402	365.5	0.06	382	341	361.5	0.28	2	6	4	0.30	442	434	438	0.85	302	273	287.5	0.39	163	138	150.5	0.31
DGRP 712	617	591	604	0.60	618	535	576.5	0.08	31	24	27.5	0.50	820	775	797.5	0.43	604	451	527.5	0.00	285	255	270	0.36
DGRP 714	392	427	409.5	0.39	428	391	409.5	0.36					563	512	537.5	0.27	343	323	333	0.58	218	191	204.5	0.34
DGRP 716	497	460	478.5	0.40	402	343	372.5	0.13	107	105	106	0.92	860	809	834.5	0.38	587	507	547	0.09	278	297	287.5	0.58
DGRP 721	487	488	487.5	0.98	422	349	385.5	0.06	112	92	102	0.32	805	782	793.5	0.68	504	493	498.5	0.81	277	313	295	0.29
DGRP 727	587	534	560.5	0.26	465	440	452.5	0.56	98	118	108	0.34	809	767	788	0.45	594	497	545.5	0.04	277	208	242.5	0.03
DGRP 730	422	421	421.5	0.98	399	276	337.5	0.00	78	90	84	0.51	815	725	770	0.10	493	487	490	0.89	275	285	280	0.77

Table 4.S1 Continued

DGRP Line	e ro. # of Males	e ro. # of Females	Expected	G-test P-value	e ro. # of ++	e ro. # of e ro	Expected	G-test P-value	e ro. # of + ro	e ro. # of e +	Expected	G-test P-value	y v. # of Males	y v. # of Females	Expected	G-test P-value	y v. # of ++	y v. # of y v	Expected	G-test P-value	y v. # of + v	y v. # of y +	Expected	G-test P-value
DGRP 732	532	519	525.5	0.78	504	394	449	0.01	83	70	76.5	0.46	751	773	762	0.69	515	495	505	0.66	262	252	257	0.76
DGRP 737	619	665	642	0.36	617	465	541	0.00	100	102	101	0.92	1011	872	941.5	0.02	678	616	647	0.22	313	276	294.5	0.28
DGRP 738	687	600	643.5	0.09	568	541	554.5	0.57	91	87	89	0.83	880	816	848	0.27	623	494	558.5	0.01	301	278	289.5	0.50
DGRP 748	449	405	427	0.29	368	312	340	0.13	79	95	87	0.39	864	810	837	0.35	563	488	525.5	0.10	321	302	311.5	0.59
DGRP 757	290	328	309	0.28	236	249	242.5	0.68	78	55	66.5	0.16	799	742	770.5	0.30	575	514	544.5	0.19	225	227	226	0.95
DGRP 761	322	306	314	0.65	252	247	249.5	0.87	57	72	64.5	0.35	622	561	591.5	0.21	426	393	409.5	0.41	186	178	182	0.77
DGRP 765	618	563	590.5	0.26	488	436	462	0.23	126	131	128.5	0.83	954	938	946	0.79	746	644	695	0.05	238	264	251	0.41
DGRP 774	577	560	568.5	0.72	488	422	455	0.12	118	109	113.5	0.67	810	728	769	0.14	586	527	556.5	0.21	217	208	212.5	0.76
DGRP 776	551	648	599.5	0.05	650	549	599.5	0.04					787	718	752.5	0.21	520	477	498.5	0.34	272	236	254	0.26
DGRP 783	466	508	487	0.34	395	373	384	0.57	115	91	103	0.24	843	779	811	0.26	626	545	585.5	0.09	255	196	225.5	0.05
DGRP 786	589	597	593	0.87	722	459	590.5	0.00					745	679	712	0.22	481	427	454	0.20	272	244	258	0.38
DGRP 787	495	429	462	0.12	397	329	363	0.07	88	110	99	0.27	568	575	571.5	0.88	431	326	378.5	0.01	194	192	193	0.94
DGRP 790	575	566	570.5	0.85	459	454	456.5	0.91	120	108	114	0.57	821	679	750	0.01	593	459	526	0.00	252	196	224	0.06
DGRP 796	619	657	638	0.45	520	448	484	0.10	163	145	154	0.47	573	512	542.5	0.19	350	373	361.5	0.55	169	193	181	0.37
DGRP 799	468	464	466	0.93	446	308	377	0.00	93	85	89	0.67	766	838	802	0.20	555	543	549	0.80	276	230	253	0.15
DGRP 801	405	377	391	0.48	328	283	305.5	0.20	72	99	85.5	0.14	671	462	566.5	0.00	386	389	387.5	0.94	158	200	179	0.12
DGRP 802	587	565	576	0.65	508	489	498.5	0.67	86	69	77.5	0.33	695	670	682.5	0.63	443	428	435.5	0.72	247	247	247	1.00
DGRP 804	695	722	708.5	0.61	598	535	566.5	0.19	158	126	142	0.18	909	953	931	0.47	697	583	640	0.02	283	299	291	0.64
DGRP 805	488	525	506.5	0.41	406	399	402.5	0.86	105	103	104	0.92	871	871	871	1.00	573	525	549	0.31	328	316	322	0.74
DGRP 808	477	436	456.5	0.34	432	329	380.5	0.01	81	71	76	0.57	725	683	704	0.43	547	451	499	0.03	227	183	205	0.12
DGRP 810	335	338	336.5	0.93	360	300	330	0.10	5	8	6.5	0.55	551	547	549	0.93	388	381	384.5	0.86	168	161	164.5	0.78
DGRP 812	362	387	374.5	0.52	294	245	269.5	0.14	100	110	105	0.63												
DGRP 818	514	487	500.5	0.55	390	391	390.5	0.98	123	97	110	0.21	798	720	759	0.16	493	519	506	0.56	258	248	253	0.75
DGRP 819	688	688	688	1.00	636	460	548	0.00	152	128	140	0.31	955	845	900	0.07	696	505	600.5	0.00	380	219	299.5	0.00
DGRP 820	561	558	559.5	0.95	601	513	557	0.06					810	682	746	0.02	522	453	487.5	0.12	261	256	258.5	0.88
DGRP 821	586	541	563.5	0.34	410	429	419.5	0.64	149	139	144	0.68	772	674	723	0.07	486	445	465.5	0.34	261	254	257.5	0.83
DGRP 822	424	434	429	0.81	408	309	358.5	0.01	72	69	70.5	0.86	791	767	779	0.67	519	544	531.5	0.59	275	220	247.5	0.08
DGRP 832	689	682	685.5	0.89	569	513	541	0.23	153	136	144.5	0.48	632	655	643.5	0.65	429	422	425.5	0.87	221	215	218	0.84
DGRP 837	668	656	662	0.82	521	530	525.5	0.84	149	124	136.5	0.28	823	825	824	0.97	605	541	573	0.18	267	235	251	0.31
DGRP 843	546	551	548.5	0.91	470	400	435	0.09	95	132	113.5	0.08	843	820	831.5	0.69	618	591	604.5	0.58	231	223	227	0.79
DGRP 849	566	597	581.5	0.52	443	450	446.5	0.87	119	151	135	0.17	575	623	599	0.33	490	361	425.5	0.00	189	158	173.5	0.24
DGRP 850	519	524	521.5	0.91	419	397	408	0.59	108	119	113.5	0.61	764	686	725	0.15	509	487	498	0.62	244	210	227	0.26
DGRP 852	695	706	700.5	0.84	575	520	547.5	0.24	138	168	153	0.22	503	456	479.5	0.28	313	290	301.5	0.51	165	191	178	0.33
DGRP 853	545	554	549.5	0.85	452	430	441	0.60	112	105	108.5	0.74	862	792	827	0.22	590	580	585	0.84	247	237	242	0.75
DGRP 855	553	588	570.5	0.46	583	508	545.5	0.11	25	25	25	1.00	626	604	615	0.66	457	353	405	0.01	202	218	210	0.58
DGRP 857	604	604	604	1.00	463	457	460	0.89	135	153	144	0.45	802	709	755.5	0.09	493	474	483.5	0.67	251	293	272	0.20
DGRP 859	673	703	688	0.57	593	470	531.5	0.01	172	141	156.5	0.21	847	742	794.5	0.06	562	503	532.5	0.20	245	279	262	0.29
DGRP 861	616	628	622	0.81	606	483	544.5	0.01	75	80	77.5	0.78	869	791	830	0.18	551	525	538	0.58	292	292	292	1.00
DGRP 879	413	529	471	0.01	376	352	364	0.53	89	125	107	0.08	817	854	835.5	0.52	615	540	577.5	0.12	250	266	258	0.62
DGRP 882	468	432	450	0.40	375	328	351.5	0.21	98	99	98.5	0.96	93	108	100.5	0.45	66	56	61	0.52	36	43	39.5	0.58
DGRP 884	692	683	687.5	0.86	686	541	613.5	0.00	77	71	74	0.73	866	821	843.5	0.44	626	557	591.5	0.16	262	242	252	0.53
DGRP 887	464	577	520.5	0.01	425	405	415	0.62	103	108	105.5	0.81	809	735	772	0.18	553	537	545	0.73	231	223	227	0.79
DGRP 890	452	486	469	0.43	393	352	372.5	0.29	98	95	96.5	0.88	785	735	760	0.36	561	524	542.5	0.43	236	199	217.5	0.21
DGRP 892	523	494	508.5	0.52	507	317	412	0.00	94	99	96.5	0.80	403	418	410.5	0.71	289	254	271.5	0.29	136	142	139	0.80
DGRP 894	598	546	572	0.28	496	420	458	0.08	124	104	114	0.35	185	166	175.5	0.47	109	119	114	0.64	56	67	61.5	0.48
DGRP 897	622	679	650.5	0.26	531	478	504.5	0.24	135	157	146	0.36	951	828	889.5	0.04	641	501	571	0.00	315	322	318.5	0.84
DGRP 900	548	569	558.5	0.66	486	418	452	0.11	113	100	106.5	0.53	758	706	732	0.34	549	502	525.5	0.31	232	181	206.5	0.08
DGRP 907	623	633	628	0.84	525	549	537	0.60	85	97	91	0.53	880	822	851	0.32	693	510	601.5	0.00	252	247	249.5	0.87
DGRP 908	606	614	610	0.87	625	591	608	0.49	1	3	2	0.46	850	836	843	0.81	584	487	535.5	0.04	302	313	307.5	0.75
DGRP 911	479	517	498	0.39	469	357	413	0.01	84	86	85	0.91	694	666	680	0.59	506	452	479	0.22	197	205	201	0.78
DGRP 913	558	599	578.5	0.39	614	415	514.5	0.00	68	60	64	0.62	835	828	831.5	0.90	615	492	553.5	0.01	269	287	278	0.59

Table 4.S2 - Recombination rate data for DGRP lines. Three replicates and average (in cM; used for GWA analysis) for both intervals (e ro and y v) are included along with inversion status and Wolbachia status of each line (Huang et al. 2014).

DGRP Line	e ro-1	e ro-2	e ro-3	e ro-Avg.	y v-1	y v-2	y v-3	y v-Avg.	In(2)Lt	In(2)RS	In(2)Y1	In(2)Y2	In(2)Y3	In(2)Y4	In(2)Y5	In(2)Y6	In(2)Y7	In(3)Lp	In(3)JM	In(3)Ly	In(3)RP	In(3)RK	In(3)Mo	In(3)IC	Infection Status
DGRP 21	0.188	0.307	0.232	24.227	0.331	0.394	0.366	36.366	ST	y															
DGRP 26	0.225	0.218	0.230	22.442	0.286	0.352	0.299	31.237	INV	ST	n														
DGRP 28		0.000	0.000	0.000	0.432	0.362	0.391	39.493	ST	INV	ST	n													
DGRP 31	0.344	0.117	0.303	25.441	0.356	0.393	0.314	35.465	ST	INV/ST	ST	ST	ST	INV/ST	ST	ST	n								
DGRP 32	0.089		0.033	6.115	0.314	0.406	0.397	37.239	INV	ST	INV	ST	n												
DGRP 38	0.199	0.144	0.219	18.740	0.276	0.348	0.287	30.350	ST	INV/ST	ST	ST	n												
DGRP 40	0.106	0.191	0.202	16.629	0.316	0.345	0.281	31.366	ST	y															
DGRP 41	0.136	0.255	0.191	19.407	0.227	0.246		23.650	ST	n															
DGRP 42			0.191	19.093	0.314	0.302		30.798	ST	n															
DGRP 45		0.210	0.260	23.484	0.291	0.292	0.299	29.419	ST	n															
DGRP 48		0.196	0.188	19.197		0.414	0.381	39.761	ST	INV/ST	ST	ST	y												
DGRP 49	0.190	0.199	0.225	20.462	0.301	0.360	0.357	33.906	ST	y															
DGRP 57	0.211		0.202	20.639	0.273	0.255	0.347	29.172	ST	n															
DGRP 59	0.203	0.224	0.245	22.430	0.335	0.320	0.335	33.008	ST	n															
DGRP 69		0.256	0.258	25.837	0.230	0.378	0.401	33.617	ST	INV	ST	INV/ST	ST	ST	ST	y									
DGRP 73		0.195	0.189	19.213	0.304	0.306	0.260	29.020	ST	y															
DGRP 75	0.233	0.196	0.211	21.325	0.362	0.357	0.247	32.190	ST	y															
DGRP 83	0.238	0.235	0.266	24.626	0.331	0.353	0.313	33.215	ST	n															
DGRP 85	0.214	0.242	0.224	22.666	0.336	0.370	0.333	34.620	INV/ST	ST	n														
DGRP 88	0.221	0.186	0.227	21.123	0.308	0.280	0.316	30.139	INV/ST	ST	n														
DGRP 91	0.185	0.203	0.204	19.707	0.256	0.316	0.327	29.985	ST	n															
DGRP 93	0.261	0.219	0.234	23.807	0.404	0.373	0.361	37.931	INV	ST	n														
DGRP 100	0.000	0.000	0.000	0.000	0.302	0.365	0.378	34.813	INV/ST	ST	INV	ST	ST	y											
DGRP 101	0.191	0.195	0.225	20.376	0.316	0.342	0.416	35.812	INV/ST	ST	n														
DGRP 105	0.102	0.000	0.000	3.392	0.325	0.402	0.359	36.166	ST	INV	ST	ST	n												
DGRP 109	0.115	0.203	0.245	18.767	0.388	0.404	0.400	39.713	INV/ST	ST	n														
DGRP 129	0.345	0.217	0.199	25.347	0.289	0.327	0.429	34.809	ST	n															
DGRP 136	0.207	0.126	0.136	15.615	0.301	0.300	0.305	30.190	ST	INV/ST	ST	ST	ST	INV/ST	ST	ST	n								
DGRP 138	0.136	0.000	0.005	4.705	0.282	0.351	0.335	32.275	ST	INV	ST	ST	ST	n											
DGRP 142	0.254	0.209	0.210	22.394	0.325	0.324	0.286	31.190	ST	y															
DGRP 149	0.195	0.247	0.217	21.970	0.303	0.321	0.314	31.244	ST	y															
DGRP 153	0.273	0.231	0.224	24.261	0.266	0.239		25.240	ST	y															
DGRP 158	0.190	0.199	0.202	19.690	0.239	0.317	0.255	27.035	ST	n															
DGRP 161		0.251	0.332	29.142		0.361	0.325	34.320	INV	ST	n														
DGRP 176	0.152	0.221	0.200	19.100	0.289	0.309	0.311	30.299	ST	y															
DGRP 177	0.206	0.241	0.215	22.084	0.358	0.346	0.351	35.162	ST	n															
DGRP 181	0.190	0.209	0.220	20.641		0.354	0.324	33.872	ST	INV	ST	ST	y												
DGRP 189									ST	n															
DGRP 195		0.230	0.223	22.637	0.276	0.293	0.269	27.923	ST	n															
DGRP 208	0.193	0.236	0.194	20.756	0.285	0.326	0.279	29.638	ST	n															
DGRP 217	0.228	0.218	0.212	21.950	0.291	0.307	0.322	30.690	ST	n															
DGRP 223	0.221	0.236	0.192	21.624	0.229	0.250	0.228	23.567	ST	y															
DGRP 227	0.181	0.207	0.178	18.859	0.279	0.340	0.276	29.833	ST	y															
DGRP 228	0.215	0.180	0.149	18.146	0.232	0.244	0.282	26.259	ST	n															
DGRP 229	0.230	0.164	0.193	19.570	0.249	0.246	0.274	26.621	ST	n															
DGRP 233		0.217	0.180	19.837		0.303	0.328	31.566	INV	ST	n														
DGRP 235		0.207	0.212	20.972	0.325	0.300	0.350	32.466	ST	n															
DGRP 237	0.256	0.246	0.197	23.288	0.313	0.353	0.295	32.025	INV/ST	INV/ST	ST	y													
DGRP 239	0.086	0.083	0.000	5.635	0.355	0.310	0.338	33.432	ST	n															
DGRP 256		0.218	0.190	20.400					ST	y															
DGRP 280	0.163	0.180	0.218	18.713	0.260	0.322	0.301	29.421	ST	y															
DGRP 287	0.175		0.202	18.660	0.350	0.349	0.307	33.508	ST	y															

Table 4.S2 Continued

DGRP Line	e ro -1	e ro -2	e ro -3	e ro -Avg.	y v -1	y v -2	y v -3	y v -Avg.	Int(L)I	Int(2R)WS	Int(2R)Y1	Int(2R)Y2	Int(2R)Y3	Int(2R)Y4	Int(2R)Y5	Int(2R)Y6	Int(2R)Y7	Int(3L)P	Int(3L)M	Int(3L)Y	Int(3R)P	Int(3R)K	Int(3R)Mo	Int(3R)C	Infection Status
DGRP 301		0.217	0.218	21.752	0.293	0.301	0.341	31.178	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 303	0.203	0.247	0.223	22.398	0.303	0.295	0.366	32.129	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n						
DGRP 304	0.183	0.204	0.232	20.632	0.296	0.337	0.360	33.104	ST	INV	ST	ST	ST	ST	ST	ST	ST	ST	y						
DGRP 306	0.273	0.190	0.216	22.656	0.309	0.310	0.296	30.479	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 307	0.252	0.154	0.148	18.441	0.335	0.366	0.354	35.188	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 309	0.059	0.257	0.207	17.447	0.345	0.383	0.301	34.318	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	n
DGRP 310	0.207	0.191	0.266	22.137	0.357	0.337	0.326	33.165	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 313	0.211	0.164	0.206	19.393	0.357	0.354	0.366	35.933	INV	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 315		0.237	0.213	22.487	0.293	0.309	0.333	31.153	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 317	0.077		0.130	10.310	0.346	0.282	0.327	31.844	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	y
DGRP 318	0.211	0.179	0.198	19.582	0.389	0.294	0.361	34.776	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 319	0.257		0.199	22.806	0.271	0.383	0.302	31.881	ST	ST	ST	ST	ST	ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 320	0.195	0.282	0.229	23.529		0.357	0.363	36.043	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 321	0.178	0.237	0.250	22.155	0.224	0.361	0.391	32.541	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 324	0.114	0.000	0.035	4.959	0.180	0.284	0.282	24.876	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	n
DGRP 325	0.225	0.212	0.211	21.613	0.266	0.318	0.337	30.691	ST	ST	ST	ST	ST	ST	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 332	0.280	0.229	0.174	22.765	0.323	0.325	0.388	34.532	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 335	0.174	0.186	0.232	19.744	0.296	0.328	0.309	31.081	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	y
DGRP 336	0.282	0.209	0.216	23.585	0.323	0.377	0.388	36.243	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y						
DGRP 338	0.211	0.218	0.263	23.087	0.389	0.381	0.368	37.971	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y						
DGRP 340	0.198	0.249	0.169	20.537	0.281	0.365	0.345	33.034	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 348	0.000	0.000	0.099	3.306	0.427	0.377	0.407	40.349	INV	ST	ST	ST	ST	ST	INV	ST	n								
DGRP 350	0.000	0.000	0.059	1.982	0.413	0.405	0.423	41.347	INV	ST	ST	ST	ST	ST	INV	ST	n								
DGRP 352	0.000	0.000	0.081	2.692	0.373	0.376	0.373	37.432	INV/ST	ST	ST	ST	ST	ST	INV	ST	y								
DGRP 354	0.192	0.170	0.210	19.077	0.286	0.299	0.311	29.891	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 355	0.246	0.209	0.238	23.128	0.345	0.342	0.367	35.120	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 356		0.233	0.260	24.654	0.273	0.352	0.352	31.908	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 357	0.230	0.166	0.188	19.426	0.305	0.335	0.285	30.814	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 358	0.000	0.000	0.068	2.263	0.413	0.433	0.453	43.312	INV	ST	ST	ST	ST	ST	INV	ST	n								
DGRP 359	0.190	0.181	0.214	19.530	0.361	0.319	0.333	33.773	INV	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 360	0.203	0.209	0.207	20.625	0.306	0.341	0.395	34.745	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 361	0.062	0.084	0.243	12.974	0.371	0.412	0.372	38.494	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	ST	ST	y
DGRP 362	0.179	0.207	0.262	21.614	0.315	0.321	0.383	33.983	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 365	0.166	0.199	0.230	19.805	0.342	0.331	0.339	33.739	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 367	0.193	0.235	0.234	22.055	0.313	0.331	0.279	30.759	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 370	0.261	0.222	0.213	23.175	0.291	0.318	0.310	30.626	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 371	0.247	0.203	0.209	21.967	0.222	0.282	0.292	29.566	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 373	0.261	0.087	0.138	16.190	0.353	0.349	0.281	32.771	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	ST	ST	n
DGRP 374	0.304	0.000	0.000	10.145	0.252	0.424	0.361	34.552	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	y
DGRP 375	0.144	0.209	0.219	19.061		0.363	0.270	31.673	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 377	0.000	0.272	0.278	18.313	0.377	0.400	0.419	39.861	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n						
DGRP 379	0.157	0.127	0.255	17.978	0.237	0.281	0.288	26.854	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 380		0.213	0.258	23.551	0.211	0.314	0.297	27.419	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 381	0.274	0.216	0.256	24.875	0.341	0.414		37.737	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 382	0.160	0.236	0.158	18.482	0.378	0.389	0.322	36.287	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 383	0.242	0.247	0.250	24.641	0.387	0.369	0.408	38.767	INV	ST	ST	ST	ST	ST	ST	ST	ST	y							
DGRP 385	0.170	0.230	0.224	20.800	0.258	0.243	0.363	28.780	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 386	0.156	0.192	0.222	19.002	0.279	0.296	0.267	28.028	INV	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 390	0.111	0.207	0.182	16.628		0.331	0.394	36.283	INV	ST	ST	ST	ST	ST	INV/ST	ST	n								
DGRP 391	0.229	0.219	0.169	20.547	0.361	0.327	0.365	35.060	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 392	0.289	0.261	0.233	26.117	0.282	0.318	0.309	30.301	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n

Table 4.S2 Continued

DGRP Line	e-ro-1	e-ro-2	e-ro-3	e-ro-Avg	Yv-1	Yv-2	Yv-3	Yv-Avg	Int2Lt	Int2RWS	Int2RY1	Int2RY2	Int2RY3	Int2RY4	Int2RY5	Int2RY6	Int2RY7	Int3LP	Int3LM	Int3LY	Int3RP	Int3RJK	Int3RMo	Int3RJC	Infection Status	
DGRP 395	0.168	0.253	0.241	22.062	0.316	0.287	0.318	30.715	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 397	0.199	0.148	0.204	18.364	0.334	0.314	0.343	33.038	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 399	0.167	0.232	0.248	21.562	0.295	0.314	0.352	32.054	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 405	0.194	0.204	0.230	20.959	0.315	0.334	0.347	33.177	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y								
DGRP 406	0.213	0.265	0.238	23.870	0.358	0.330	0.344	34.379	INV	ST	ST	ST	ST	ST	ST	ST	ST	n								
DGRP 409	0.000	0.000	0.000	0.000	0.345	0.342	0.395	36.078	ST	INV	ST	ST	ST	ST	ST	ST	ST	INV	y							
DGRP 426	0.247	0.161	0.188	19.867	0.405	0.317	0.392	37.131	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 427		0.210	0.233	22.151	0.300	0.257	0.262	27.946	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 437	0.000	0.000	0.000	0.000	0.302	0.296	0.330	30.931	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	n	
DGRP 439	0.262	0.184	0.173	20.617	0.346	0.324	0.343	33.827	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 440	0.062	0.108	0.115	9.480	0.350	0.358	0.330	34.609	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	y
DGRP 441	0.174	0.240	0.162	19.209	0.263	0.354	0.413	34.318	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 443	0.212	0.204	0.163	19.308	0.326	0.275	0.282	29.422	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n								
DGRP 461		0.236	0.193	21.442	0.351	0.307		32.884	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 486	0.201	0.223	0.230	21.784	0.282	0.296	0.260	27.959	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 491	0.222	0.178	0.186	19.517	0.324	0.249	0.339	30.383	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 492	0.154	0.277	0.207	21.277	0.368	0.366	0.286	34.002	INV/ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	n							
DGRP 502	0.198	0.250	0.189	21.224	0.227	0.258	0.226	23.708	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 505	0.206	0.158	0.236	20.012	0.325	0.319	0.363	33.562	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 508	0.226	0.211	0.218	21.839	0.306	0.288	0.276	28.968	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 509		0.227	0.207	21.683	0.270	0.303	0.261	27.816	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 513	0.279	0.211	0.257	24.884		0.364	0.326	34.526	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 517	0.193	0.176	0.214	19.421	0.283	0.317	0.287	29.572	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 528	0.167	0.234	0.257	21.921	0.344	0.323	0.337	33.479	INV/ST	INV/ST	ST	ST	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 530	0.196	0.222	0.206	20.795	0.269	0.304	0.245	27.259	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 531	0.219	0.255	0.250	24.126	0.317	0.358	0.333	33.588	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 535	0.229	0.201	0.211	21.366	0.255	0.294	0.294	28.114	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 551	0.188	0.194	0.150	17.730	0.332	0.362	0.346	35.336	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	y
DGRP 555	0.111	0.000	0.000	3.704	0.385	0.376	0.368	37.612	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 559	0.000	0.000	0.000	0.000	0.370	0.399	0.389	38.591	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	n
DGRP 563	0.238	0.182		21.028		0.280	0.358	31.915	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 566	0.137	0.091	0.072	9.985	0.307	0.347	0.332	32.858	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	INV/ST	n
DGRP 584	0.156	0.235	0.231	20.732	0.292	0.387	0.368	34.885	INV	ST	ST	ST	ST	ST	ST	ST	ST	ST	y							
DGRP 589	0.104	0.188	0.232	17.460	0.271	0.318	0.296	29.494	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 595	0.218	0.256	0.246	23.989	0.328	0.312		32.021	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y								
DGRP 596		0.261	0.253	25.679	0.297	0.336	0.263	29.867	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 627	0.213	0.234	0.239	22.887	0.380	0.391	0.303	35.812	INV	ST	ST	ST	ST	ST	ST	ST	ST	n								
DGRP 630	0.257		0.116	18.635	0.331	0.370	0.388	36.305	INV	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	n							
DGRP 634	0.098	0.043	0.093	7.801	0.336	0.356	0.331	34.136	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 639	0.305	0.000	0.158	15.441		0.339	0.336	33.749	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 642	0.189	0.221	0.243	21.780	0.366	0.374	0.391	37.721	ST	INV	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 646	0.000	0.000	0.000	0.000	0.339	0.338	0.382	35.290	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	y
DGRP 703	0.211	0.193	0.237	21.343	0.264	0.280	0.277	27.375	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n	
DGRP 705	0.183		0.194	18.864	0.191	0.060		12.535	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y	
DGRP 707	0.000	0.024	0.000	0.806	0.288	0.342	0.388	33.939	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	y
DGRP 712	0.000	0.000	0.115	3.843	0.353	0.283	0.375	33.696	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	y
DGRP 714		0.000	0.000	0.000	0.386	0.374		37.989	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV	ST	n
DGRP 716	0.134	0.242	0.243	20.649	0.276	0.349	0.404	34.326	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 721	0.188	0.224	0.214	20.875	0.366	0.406	0.346	37.279	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 727	0.226	0.194	0.171	19.697	0.309	0.312	0.303	30.780	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 730	0.224	0.204	0.185	20.452	0.361	0.364	0.366	36.388	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y

Table 4.S2 Continued

DGRP Line	e ro -1	e ro -2	e ro -3	e ro -Avg.	y v -1	y v -2	y v -3	y v -Avg.	In(2L)I	In(2R)IS	In(2R)Y1	In(2R)Y2	In(2R)Y3	In(2R)Y4	In(2R)Y5	In(2R)Y6	In(2R)Y7	In(3L)P	In(3L)M	In(3L)Y	In(3R)P	In(3R)K	In(3R)Mo	In(3R)C	Infection Status
DGRP 732	0.225	0.139	0.134	16.615	0.322	0.355	0.338	33.832	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 737	0.127	0.139	0.205	15.694	0.300	0.310	0.332	31.368	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 738	0.186	0.126	0.117	14.329	0.343	0.279	0.387	33.667	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 748	0.203		0.204	20.366	0.371	0.370	0.378	37.275	INV	ST	ST	ST	ST	ST	ST	ST	ST	y							
DGRP 757		0.248	0.189	21.856	0.304	0.261	0.318	29.431	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 761		0.203	0.208	20.542	0.304	0.307	0.315	30.873	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 765	0.203	0.224	0.221	21.612	0.247	0.282	0.274	26.794	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 774	0.204	0.197	0.199	20.006	0.244	0.351	0.234	27.627	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 776	0.000	0.000	0.000	0.000	0.312	0.364	0.329	33.517	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 783	0.189	0.232	0.201	20.728	0.245	0.269	0.321	27.828	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 786	0.000	0.000	0.014	0.462	0.366	0.347	0.374	36.230	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 787	0.180	0.232	0.224	21.204	0.351	0.338	0.328	33.888	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 790	0.221	0.193	0.198	20.382	0.296	0.304	0.296	29.888	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 796	0.215	0.254	0.245	23.796	0.344	0.325		33.450	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 799	0.228	0.202	0.164	19.789	0.315	0.333	0.299	31.560	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 801		0.180	0.269	22.428	0.322	0.311		31.638	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 802	0.186	0.123	0.124	14.444	0.341	0.375	0.362	35.938	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y							
DGRP 804	0.143	0.241	0.192	19.181	0.311	0.318	0.310	31.280	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 805		0.196	0.215	20.513	0.349	0.392	0.371	37.085	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 808	0.053	0.142	0.231	14.232	0.279	0.277	0.317	29.096	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 810	0.104	0.000	0.000	3.467	0.269	0.340	0.300	30.294	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 812		0.323	0.250	28.634					INV/ST	INV	ST	ST	ST	ST	ST	ST	ST	ST	n						
DGRP 818	0.247	0.233	0.203	22.761	0.328	0.339	0.331	33.282	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 819	0.130	0.229	0.202	18.703	0.352	0.300	0.342	33.100	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 820	0.000	0.011	0.000	0.370	0.308	0.395	0.339	34.744	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 821	0.215	0.319	0.210	24.802	0.329	0.343	0.387	35.299	ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	y						
DGRP 822	0.166		0.164	16.484	0.334	0.321	0.302	31.874	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 832	0.168	0.250	0.195	20.431	0.381	0.296	0.351	34.282	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 837	0.229	0.223	0.181	21.100	0.303	0.285	0.319	30.254	INV	ST	ST	ST	ST	ST	ST	ST	ST	y							
DGRP 843	0.208	0.205	0.207	20.692	0.263	0.281	0.276	27.317	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 849	0.226	0.237	0.230	23.085	0.323	0.302	0.261	29.531	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 850	0.252	0.233	0.183	22.243	0.326	0.342	0.293	32.058	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 852	0.245	0.241	0.171	21.884	0.385	0.357		37.121	ST	INV	ST	ST	ST	ST	ST	ST	ST	ST	y						
DGRP 853	0.268	0.181	0.184	21.104	0.309	0.288	0.277	29.121	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 855	0.000	0.007	0.124	4.370	0.357	0.323		33.997	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 857	0.248	0.224	0.246	23.948	0.376	0.336	0.365	35.896	ST	INV/ST	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 859	0.247	0.232	0.211	23.007	0.323	0.294	0.366	32.777	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 861	0.137	0.150	0.075	12.073	0.337	0.376	0.348	35.396	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 879	0.258	0.203	0.229	22.970	0.330	0.301	0.294	30.848	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 882	0.304	0.224	0.200	24.279	0.393			39.303	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 884	0.161	0.105	0.089	11.851	0.327	0.296	0.273	29.860	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	ST	y
DGRP 887	0.191	0.201	0.207	19.976	0.297	0.300	0.286	29.447	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 890	0.221	0.224	0.173	20.597	0.307	0.275	0.272	28.439	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 892	0.159	0.240	0.151	18.322		0.343	0.335	33.936	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 894		0.191	0.210	20.044		0.350		35.043	INV/ST	ST	ST	ST	ST	ST	ST	ST	ST	n							
DGRP 897	0.267	0.229	0.197	23.096	0.389	0.275	0.375	34.628	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 900	0.213	0.188	0.182	19.399	0.282	0.272	0.288	28.069	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 907	0.154	0.128	0.162	14.827	0.313	0.308	0.257	29.258	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	y
DGRP 908	0.000	0.007	0.000	0.218	0.375	0.346	0.367	36.247	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 911	0.204	0.137	0.188	17.640	0.281	0.302	0.307	29.658	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	n
DGRP 913	0.000	0.093	0.147	7.991	0.355	0.333	0.318	33.510	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	ST	INV/ST	ST	ST	INV/ST	ST	y

Table 4.S3 - Analyses of variance of recombination rate. Results are displayed for both the *e ro* and *y v* intervals (using only standard karyotypes). H^2 denotes broad sense heritability.

Region	Source	df	Type III SS	MS	F	P-value	σ^2	H^2
<i>e ro</i>	Line	110	0.211	0.00192	1.35	0.03497	1.95E-04	0.12
	Error	200	0.285	0.00143			1.41E-03	
<i>y v</i>	Line	109	0.330	0.00303	2.95	1.35E-11	0.0007168	0.41
	Error	204	0.209	0.00103			0.00105	

Table 4.S4 - Correlation with DGRP phenotypes. Spearman's rank correlation for crossover rates in the *e ro* and *y v* regions (using only standard karyotypes) compared to numerous DGRP published phenotypes. Sources of data are listed both within the main text as well as in the chart. Significant correlations are in bold.

Trait	<i>e ro</i> ρ	<i>e ro</i> P-value	<i>y v</i> ρ	<i>y v</i> P-value	Data Source
1-Hexanol_F	0.097	0.319	0.141	0.150	Arya et al. 2015
1-Hexanol_M	0.120	0.218	0.149	0.128	Arya et al. 2015
2-Heptanone_F	0.170	0.080	0.191	0.050	Arya et al. 2015
2_Heptanone_M	0.170	0.080	0.158	0.107	Arya et al. 2015
2-Phenyl_Ethyl_Alcohol_F	0.077	0.431	0.060	0.544	Arya et al. 2015
2-Phenyl_Ethyl_Alcohol_M	0.090	0.355	0.038	0.699	Arya et al. 2015
Acetophenone_F	0.084	0.387	0.151	0.123	Arya et al. 2015
Acetophenone_M	0.080	0.411	0.015	0.877	Arya et al. 2015
Aggression_M	0.097	0.310	0.080	0.404	Shorter et al. 2015
Benz_F	0.123	0.237	0.118	0.258	Swarup et al. 2013
Benz_M	0.121	0.241	0.033	0.754	Swarup et al. 2013
Benzaldehyde_F	0.057	0.560	0.058	0.555	Arya et al. 2015
Benzaldehyde_M	0.013	0.892	0.136	0.164	Arya et al. 2015
Chill_Coma_Recovery_F	0.025	0.806	-0.017	0.865	Ayroles et al. 2009; Mackay et al. 2012
Chill_Coma_Recovery_M	-0.015	0.879	0.012	0.903	Ayroles et al. 2009; Mackay et al. 2012
Citral_F	0.205	0.035	0.208	0.032	Arya et al. 2015
Citral_M	0.120	0.217	0.278	0.004	Arya et al. 2015
Day_Avg_Bout_Length_F	0.018	0.860	0.062	0.548	Harbison et al. 2013
Day_Avg_Bout_Length_M	-0.080	0.437	-0.106	0.307	Harbison et al. 2013
Day_Bout_Number_F	-0.140	0.171	0.093	0.368	Harbison et al. 2013
Day_Bout_Number_M	-0.079	0.442	0.009	0.931	Harbison et al. 2013
Day_Sleep_F	-0.126	0.218	0.060	0.560	Harbison et al. 2013
Day_Sleep_M	-0.059	0.566	0.110	0.288	Harbison et al. 2013
d-Carvone_F	0.149	0.125	-0.048	0.626	Arya et al. 2015
d-Carvone_M	0.116	0.236	0.020	0.836	Arya et al. 2015
Ethyl_Acetate_F	0.060	0.542	0.107	0.276	Arya et al. 2015
Ethyl_Acetate_M	0.112	0.253	0.046	0.639	Arya et al. 2015
Ethyl_Butyrate_F	0.063	0.519	-0.208	0.032	Arya et al. 2015
Ethyl_Butyrate_M	0.014	0.889	-0.204	0.036	Arya et al. 2015
Eugenol_F	-0.094	0.337	-0.222	0.022	Arya et al. 2015
Eugenol_M	-0.062	0.525	-0.036	0.712	Arya et al. 2015
Glucose_Low	-0.023	0.833	0.006	0.955	Unckless et al. 2015
Glucose_High	-0.087	0.433	0.082	0.463	Unckless et al. 2015
Glucose_Main	-0.077	0.478	0.090	0.408	Unckless et al. 2015
Glycogen_Low	-0.173	0.113	-0.087	0.432	Unckless et al. 2015
Glycogen_High	-0.125	0.258	0.187	0.090	Unckless et al. 2015
Glycogen_Main	-0.185	0.086	0.016	0.885	Unckless et al. 2015
Glycerol_Low	0.037	0.737	-0.203	0.064	Unckless et al. 2015
Glycerol_High	0.011	0.921	0.141	0.205	Unckless et al. 2015
Glycerol_Main	0.022	0.837	0.007	0.952	Unckless et al. 2015
Helional_F	-0.005	0.963	0.008	0.936	Arya et al. 2015
Helional_M	0.015	0.877	0.069	0.481	Arya et al. 2015

Table 4.S4 Continued

Trait	e r o p	e r o P-value	y v p	y v P-value	Data Source
Hexanal_F	0.061	0.531	0.162	0.098	Arya et al. 2015
Hexanal_M	0.101	0.300	0.198	0.042	Arya et al. 2015
I-Carvone_F	0.104	0.287	0.015	0.879	Arya et al. 2015
I-Carvone_M	0.125	0.198	0.055	0.578	Arya et al. 2015
Lifespan_Mean	-0.060	0.532	-0.019	0.842	Ivanov et al. 2015
Lifespan_Median	-0.126	0.233	0.045	0.673	Ivanov et al. 2015
Load_Low	-0.044	0.691	0.166	0.128	Unckless et al. 2015
Load_High	0.128	0.238	0.077	0.483	Unckless et al. 2015
Load_Main	0.054	0.623	0.120	0.271	Unckless et al. 2015
Mean_Weight_Low	-0.095	0.387	-0.028	0.801	Unckless et al. 2015
Mean_Weight_High	-0.166	0.132	0.124	0.265	Unckless et al. 2015
Mean_Weight_Main	-0.161	0.136	0.081	0.459	Unckless et al. 2015
Methyl_Salicylate_F	0.055	0.572	0.016	0.874	Arya et al. 2015
Methyl_Salicylate_M	0.143	0.143	-0.031	0.756	Arya et al. 2015
Neggeo_MSB_Sensitivity_F	0.085	0.387	-0.036	0.712	Weber et al. 2012
Neggeo_MSB_Sensitivity_M	0.018	0.855	-0.116	0.238	Weber et al. 2012
Night_Avg_Bout_Length_F	-0.017	0.867	-0.156	0.130	Harbison et al. 2013
Night_Avg_Bout_Length_M	-0.147	0.151	-0.118	0.251	Harbison et al. 2013
Night_Bout_Number_F	0.021	0.836	0.047	0.649	Harbison et al. 2013
Night_Bout_Number_M	0.107	0.298	0.149	0.146	Harbison et al. 2013
Night_Sleep_F	-0.064	0.532	-0.051	0.623	Harbison et al. 2013
Night_Sleep_M	-0.156	0.128	-0.006	0.955	Harbison et al. 2013
Protein_Low	0.104	0.344	-0.033	0.764	Unckless et al. 2015
Protein_High	0.058	0.598	-0.144	0.194	Unckless et al. 2015
Protein_Main	0.098	0.368	-0.066	0.544	Unckless et al. 2015
Startle_Response_F	-0.096	0.316	0.045	0.638	Ayroles et al. 2009; Mackay et al. 2012
Startle_Response_M	-0.113	0.237	0.062	0.517	Ayroles et al. 2009; Mackay et al. 2012
Startle_MSB_Sensitivity_F	0.073	0.457	0.071	0.471	Weber et al. 2012
Startle_MSB_Sensitivity_M	0.080	0.414	0.072	0.463	Weber et al. 2012
Starvation_Stress_F	-0.117	0.221	0.065	0.499	Ayroles et al. 2009; Mackay et al. 2012
Starvation_Stress_M	-0.087	0.366	-0.027	0.780	Ayroles et al. 2009; Mackay et al. 2012
Survival_MSB_F	-0.049	0.635	0.028	0.784	Weber et al. 2012
Survival_MSB_M	-0.039	0.702	0.124	0.228	Weber et al. 2012
Survival_Paraquat_F	-0.252	0.013	0.122	0.237	Weber et al. 2012
Survival_Paraquat_M	0.097	0.360	0.149	0.160	Weber et al. 2012
T5_Pigmentation	0.055	0.588	-0.105	0.300	Dembeck et al. 2015
T6_Pigmentation	0.030	0.770	-0.015	0.881	Dembeck et al. 2015
T6-T5_Pigmentation	0.023	0.822	0.029	0.779	Dembeck et al. 2015
Triglycerides_Low	-0.105	0.341	-0.179	0.104	Unckless et al. 2015
Triglycerides_High	-0.081	0.467	0.040	0.722	Unckless et al. 2015
Triglycerides_Main	-0.101	0.351	-0.055	0.616	Unckless et al. 2015
Walking_Activity_F	0.013	0.899	-0.042	0.685	Harbison et al. 2013
Walking_Activity_M	0.181	0.077	-0.075	0.471	Harbison et al. 2013

Table 4.S5 - Genome-wide association analyses for recombination rate. Results from GWA on *e ro* data set including all DGRP lines (except those containing an inversion on 3R).

D	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
2L 7766066 SNP	C	G	G	0.058	9	146	3.029	9.78E-10	FBgn0031944	CG7196	Downstream						
2L 2630304 SNP	C	T	T	0.105	16	137	2.116	4.91E-09									
2L 14502808 SNP	T	A	A	0.074	11	138	2.737	5.92E-09									
2R 16530532 SNP	A	C	C	0.060	9	141	2.899	9.54E-09	FBgn0061361	CG33786	Non_Synonymous_Coding	FBgn0061362	CG33785	UTR_3_Prime	FBgn0034535	CG11110	Downstream
2L 2630016 SNP	A	T	T	0.093	14	136	2.219	1.61E-08									
2L 2630015 SNP	T	A	A	0.093	14	137	2.216	1.68E-08									
2L 2630028 SNP	A	G	G	0.093	14	137	2.216	1.68E-08									
2L 2631679 SNP	T	C	C	0.080	12	138	2.522	1.76E-08									
2L 2630035 SNP	T	C	C	0.092	14	138	2.210	1.87E-08									
3R 11162200 SNP	G	A	A	0.058	9	147	2.652	2.68E-08	FBgn0038320	Sra-1	Synonymous_Coding						
2L 2630019 SNP	G	C	C	0.093	14	136	2.183	3.04E-08									
2L 9088828 SNP	T	C	C	0.061	9	138	2.627	4.01E-08	FBgn0032095	Toll-4	Synonymous_Coding						
3L 15591677 SNP	G	C	C	0.058	9	145	2.826	4.22E-08	FBgn0036518	RhoGAP71E	Intron						
3R 18726757 DEL	A	AA	AA	0.054	8	140	2.857	5.28E-08	FBgn0017590	klg	Intron						
3R 11711860 SNP	C	T	T	0.052	8	147	2.964	5.68E-08									
2R 9394974 SNP	T	C	C	0.053	8	143	2.924	5.71E-08	FBgn0033846	mip120	Intron	FBgn0024556	EFTuM	Upstream			
2R 9395041 SNP	A	T	T	0.053	8	143	2.924	5.71E-08	FBgn0033846	mip120	Intron	FBgn0024556	EFTuM	Upstream			
2R 9395335 SNP	C	T	T	0.054	8	141	2.924	5.78E-08	FBgn0024556	EFTuM	Synonymous_Coding	FBgn0033846	mip120	Intron			
2L 2631396 SNP	A	C	C	0.098	15	138	2.126	6.13E-08									
3R 20538756 SNP	A	C	C	0.052	8	146	2.276	7.10E-08	FBgn0039217	CG13627	UTR_5_Prime						
2L 16330317 SNP	T	A	A	0.067	10	140	2.580	7.99E-08	FBgn0040984	CG4440	UTR_3_Prime	FBgn0028899	CG31817	Downstream			
2L 2630587 SNP	A	G	G	0.092	14	138	2.125	8.03E-08									
2L 2631465 INS	GGTA	G	G	0.085	13	140	2.314	8.40E-08									
2L 2630393 SNP	G	T	T	0.091	14	140	2.129	8.47E-08									
3R 20537691 SNP	T	C	C	0.052	8	145	2.258	8.87E-08	FBgn0003429	slo	Downstream	FBgn0039217	CG13627	Upstream			
3R 20538757 SNP	A	C	C	0.052	8	147	2.257	9.25E-08	FBgn0039217	CG13627	UTR_5_Prime						
2L 2630918 SNP	G	A	A	0.060	9	140	2.737	9.31E-08									
2L 2629729 SNP	G	T	T	0.105	16	137	1.999	9.82E-08									
2L 2629944 SNP	T	C	C	0.105	16	137	1.999	9.82E-08									
2L 2629915 SNP	A	G	G	0.105	16	136	1.999	1.01E-07									
2L 2629929 SNP	C	T	T	0.093	14	137	2.113	1.04E-07									
2L 2628835 SNP	T	G	G	0.086	13	138	2.186	1.05E-07									
2L 2627934 SNP	C	A	A	0.099	15	137	2.028	1.34E-07									
3R 22077370 SNP	T	C	C	0.075	11	135	2.587	1.47E-07	FBgn0261708	CR42745	Exon						
2L 2631753 SNP	T	A	A	0.090	14	141	2.208	1.47E-07									
3R 11710508 INS	TGTT	T	T	0.059	8	128	2.881	1.50E-07									
3L 5796400 SNP	G	A	G	0.058	9	147	2.689	1.62E-07	FBgn0259167	CG42272	Non_Synonymous_Coding	FBgn0015806	S6k	Intron			
2R 7968428 SNP	G	C	C	0.074	11	138	2.293	1.87E-07	FBgn0033680	CG13186	Upstream						
2L 2628410 SNP	T	C	C	0.104	16	138	1.954	1.95E-07									
X 16373123 SNP	A	G	G	0.071	11	144	2.422	2.10E-07	FBgn0264255	para	Intron						
2R 7956889 SNP	T	C	C	0.093	14	136	2.029	2.11E-07	FBgn0033679	CG8888	Intron						
2L 10791112 INS	TTT	T	T	0.052	8	146	2.799	2.12E-07	FBgn0051869	CG31869	Intron	FBgn0051870	CG31870	Downstream			
2L 2628019 SNP	C	A	A	0.098	15	138	1.997	2.22E-07									
2L 2631459 DEL	C	CCCG	CCCG	0.072	11	141	2.427	2.26E-07									
3R 20527606 SNP	T	C	C	0.053	8	142	2.788	2.28E-07	FBgn0003429	slo	Intron						
2L 2628668 SNP	A	T	T	0.151	22	124	1.719	2.97E-07									
3R 11687896 SNP	T	G	G	0.052	8	147	2.909	3.08E-07	FBgn0051183	CG31183	Synonymous_Coding	FBgn0038377	CG9632	Downstream			
3R 11062857 SNP	A	C	C	0.058	9	147	2.473	3.21E-07	FBgn0045035	tefu	Non_Synonymous_Coding						
X 11925736 SNP	T	G	G	0.055	8	138	2.690	3.44E-07	FBgn0030367	Cyp311a1	Upstream	FBgn0030369	Cyp318a1	Upstream			
X 1882556 DEL	C	CTTCTGT	CTTCTGT	0.059	9	144	2.530	4.24E-07	FBgn0264562	Hr4	Intron						

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2
2L 7767080_SNP	A	G	G	0.078	12	142	2.217	4.24E-07	FBgn0031945	CG7191	Upstream			
3R 22348818_SNP	G	C	C	0.058	9	145	2.515	4.28E-07	FBgn0039431	CG6490	Intron			
2R 4951345_SNP	A	T	T	0.068	9	124	2.675	4.43E-07	FBgn0011746	ana	Intron			
3R 11688384_SNP	T	C	C	0.051	8	148	2.861	4.43E-07	FBgn0051183	CG31183	Non_Synonymous_Coding			
3L 4089328_SNP	A	C	C	0.086	12	128	2.236	4.57E-07	FBgn0035495	CG14989	Intron	FBgn0004516	Gad1	Upstream
3R 10834414_SNP	T	C	C	0.058	9	145	2.079	4.57E-07						
3R 11147348_SNP	C	G	G	0.071	11	144	1.929	4.68E-07	FBgn0026441	ear	Intron	FBgn0264832	CG44040	Downstream
2R 7960565_SNP	T	G	G	0.153	23	127	1.369	4.80E-07	FBgn0033679	CG8888	Intron			
2L 10057665_SNP	A	G	G	0.060	9	141	2.644	4.84E-07	FBgn0011823	Pen	UTR_5_Prime			
3L 9844532_SNP	T	A	A	0.059	9	144	2.672	4.98E-07	FBgn0004390	Gap1	Intron			
3L 1393055_SNP	A	G	G	0.058	9	147	2.646	5.84E-07	FBgn0003138	Ptp61F	Intron			
2L 13032232_SNP	A	C	C	0.060	9	140	2.618	6.45E-07	FBgn0262160	CG9932	Intron			
2R 9142403_SNP	T	C	C	0.053	8	143	2.674	6.51E-07	FBgn0265443	CR44343	Exon	FBgn0033819	CG4714	Upstream
X 11112246_SNP	A	G	G	0.052	8	147	2.667	6.80E-07						
2L 10170856_SNP	G	A	A	0.051	8	148	2.834	7.20E-07	FBgn0265002	CG44153	Intron			
X 17923037_SNP	C	G	G	0.052	8	146	2.807	7.43E-07	FBgn0003380	Sh	Intron	FBgn0030887	CG6867	Downstream
3R 20545307_SNP	A	T	T	0.052	8	147	2.173	7.54E-07	FBgn0004885	tok	Upstream	FBgn0039219	CG13630	Upstream
2R 7969265_SNP	T	C	C	0.072	11	141	2.158	7.71E-07	FBgn0033680	CG13186	UTR_3_Prime			
2L 2632099_SNP	A	G	G	0.122	18	129	1.868	7.90E-07						
2L 3612475_SNP	T	C	C	0.062	9	136	2.686	7.90E-07						
3R 26341342_SNP	T	A	A	0.072	11	141	2.512	8.19E-07	FBgn0039784	CG9698	Non_Synonymous_Coding			
3R 10771224_SNP	T	C	C	0.053	8	144	2.786	8.22E-07						
X 18036704_SNP	T	G	G	0.077	12	143	2.262	8.71E-07						
3R 10597721_SNP	C	T	T	0.060	9	142	2.495	8.87E-07	FBgn0263929	jvl	Intron			
2R 7970219_SNP	G	C	C	0.073	11	139	2.142	9.48E-07	FBgn0033680	CG13186	Downstream			
2L 10133276_DEL	T	TA	TA	0.067	10	139	2.418	9.93E-07	FBgn0265002	CG44153	Intron			
3R 21915444_SNP	A	T	T	0.052	8	147	2.886	1.04E-06	FBgn0039411	dys	Intron			
2L 2631452_SNP	T	C	C	0.084	13	141	2.154	1.09E-06						
2L 13032229_INS	GG	G	G	0.067	10	140	2.436	1.13E-06	FBgn0262160	CG9932	Intron			
2L 13032233_SNP	G	C	C	0.067	10	139	2.432	1.18E-06	FBgn0262160	CG9932	Intron			
2L 16519508_SNP	G	T	T	0.061	9	138	2.545	1.30E-06	FBgn0032587	CG5953	Intron			
2L 6804613_SNP	A	G	G	0.052	8	145	2.642	1.33E-06	FBgn0031861	CG17375	Downstream	FBgn0031860	CG11236	Downstream
2L 6102766_SNP	T	G	G	0.067	10	139	1.920	1.40E-06	FBgn0051641	stal	Intron			
3R 25322718_SNP	A	G	A	0.059	9	144	2.702	1.43E-06	FBgn0039667	CG2010	Intron			
2L 8096740_SNP	T	C	C	0.094	14	135	2.017	1.43E-06	FBgn0261822	Bsg	Intron			
3R 26341348_SNP	A	G	G	0.084	13	141	2.247	1.44E-06	FBgn0039784	CG9698	Synonymous_Coding			
3R 20539030_DEL	C	CAGCA	CAGCA	0.052	8	146	2.010	1.45E-06	FBgn0039217	CG13627	Intron			
2L 9687347_SNP	C	A	A	0.065	9	129	2.383	1.47E-06	FBgn0000273	Pka-C1	Intron			
X 16067327_SNP	A	C	A	0.071	11	143	2.295	1.48E-06						
X 16067311_SNP	G	T	G	0.071	11	145	2.292	1.48E-06						
3L 18254696_SNP	T	A	A	0.052	8	145	2.834	1.50E-06						
3R 8597698_INS	ACA	A	A	0.069	10	135	2.402	1.50E-06	FBgn0038084	beat-Vc	Intron			
2R 18195672_SNP	C	T	T	0.071	11	144	2.261	1.51E-06	FBgn0034718	wdp	Intron			
2L 10153087_SNP	A	G	G	0.052	8	147	2.657	1.55E-06	FBgn0265002	CG44153	Intron	FBgn0032187	CG4839	Synonymous_Coding
2L 7768177_SNP	G	T	T	0.057	8	133	2.581	1.57E-06	FBgn0031945	CG7191	Intron			
3R 23023994_SNP	C	T	T	0.059	9	144	2.623	1.59E-06						
X 16875596_SNP	C	A	A	0.061	9	138	2.550	1.64E-06	FBgn0030810	CG9059	Intron			
2R 7969137_SNP	T	C	C	0.080	12	138	1.979	1.79E-06	FBgn0033680	CG13186	Synonymous_Coding			
2L 9074788_SNP	A	T	T	0.053	8	142	2.618	1.81E-06						
2L 2630667_SNP	T	C	C	0.092	14	139	1.881	1.98E-06						

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
X_1951033_SNP	C	T	T	0.287	43	107	1.087	2.01E-06	FBgn0025625	<i>Sik2</i>	Non_Synonymous_Coding						
3R_19175421_SNP	A	G	G	0.077	12	143	2.325	2.07E-06	FBgn0264326	<i>DNApol-epsilon</i>	Synonymous_Coding						
X_1618822_SNP	A	G	G	0.073	11	140	2.194	2.08E-06									
2R_7921495_SNP	C	T	T	0.115	17	131	1.724	2.09E-06	FBgn0033677	<i>CG8321</i>	UTR_5_Prime	FBgn0260012	<i>pds5</i>	Downstream			
X_1876887_SNP	A	C	C	0.062	9	136	2.376	2.16E-06	FBgn0264562	<i>Hr4</i>	Intron						
2R_7956325_SNP	T	A	A	0.113	17	134	1.690	2.19E-06	FBgn0033679	<i>CG8888</i>	Intron						
3R_11802097_SNP	G	T	T	0.098	15	138	1.905	2.22E-06	FBgn0022787	<i>Hel89B</i>	Intron						
3L_1456902_SNP	T	C	C	0.053	8	144	2.574	2.25E-06	FBgn0003138	<i>Ptp61F</i>	Intron						
3R_20472162_SNP	T	G	G	0.052	8	147	2.581	2.26E-06	FBgn0039214	<i>CG5794</i>	Synonymous_Coding						
3R_10656276_SNP	G	A	A	0.072	11	141	2.158	2.35E-06	FBgn0264754	<i>btsz</i>	Intron						
2L_10060922_SNP	T	A	A	0.052	8	146	2.700	2.40E-06	FBgn0032178	<i>Spn31A</i>	UTR_5_Prime	FBgn0011823	<i>Pen</i>	Downstream			
2L_9096570_SNP	G	A	A	0.060	9	142	2.426	2.42E-06									
3L_14061273_SNP	C	T	T	0.051	8	148	2.634	2.47E-06	FBgn0052138	<i>CG32138</i>	Intron						
3L_8442127_SNP	T	C	C	0.052	8	146	2.680	2.50E-06	FBgn0035896	<i>CG6983</i>	Intron	FBgn0010825	<i>Gug</i>	Upstream			
2L_12473125_SNP	C	G	G	0.059	9	143	2.365	2.50E-06	FBgn0259176	<i>bun</i>	Intron						
2L_7719361_SNP	G	A	A	0.079	12	139	1.985	2.51E-06	FBgn0031935	<i>CG13793</i>	Synonymous_Coding	FBgn0031936	<i>CG13794</i>	Downstream			
X_8199556_SNP	G	A	A	0.052	8	147	2.602	2.52E-06	FBgn0015519	<i>nAcRalpha-7E</i>	Intron						
2R_8700325_SNP	C	T	T	0.112	17	135	1.777	2.52E-06									
3R_23142479_SNP	C	T	T	0.086	13	139	2.171	2.56E-06	FBgn0039510	<i>CG3339</i>	Intron						
2R_7970003_SNP	T	C	C	0.073	11	140	2.053	2.56E-06	FBgn0033680	<i>CG13186</i>	Downstream						
3L_9110092_SNP	A	C	C	0.058	9	147	2.562	2.65E-06	FBgn0011206	<i>bol</i>	Intron						
3R_19175539_SNP	C	T	T	0.091	14	140	2.139	2.70E-06	FBgn0264326	<i>DNApol-epsilon</i>	Synonymous_Coding						
2L_7765617_SNP	C	T	T	0.059	9	144	2.343	2.82E-06	FBgn0031944	<i>CG7196</i>	UTR_3_Prime						
2L_12113984_SNP	T	A	A	0.073	11	139	2.268	2.84E-06	FBgn0032414	<i>CG17211</i>	Upstream						
2L_17583652_SNP	G	C	C	0.059	9	143	2.442	2.91E-06									
3R_23505354_SNP	A	G	G	0.059	9	144	2.430	2.92E-06	FBgn0039538	<i>CG12883</i>	Synonymous_Coding	FBgn0039537	<i>CG5590</i>	Downstream	FBgn0003330	<i>Scp</i>	Downstream
2L_12817811_SNP	T	G	G	0.055	8	138	2.659	2.93E-06	FBgn0015399	<i>kek1</i>	UTR_3_Prime						
2R_9973083_SNP	T	C	C	0.382	55	89	-1.177	2.99E-06	FBgn0040752	<i>Prosap</i>	Intron						
2L_5493560_SNP	T	G	G	0.074	11	137	2.269	3.01E-06									
3L_15441280_SNP	G	C	C	0.059	9	144	2.415	3.03E-06									
2L_7767003_SNP	G	C	C	0.077	12	143	2.117	3.06E-06	FBgn0031945	<i>CG7191</i>	Upstream						
2L_2627548_SNP	T	A	A	0.068	10	138	2.098	3.11E-06									
3R_11722005_SNP	G	A	A	0.078	12	142	2.087	3.18E-06	FBgn0027657	<i>glob1</i>	Downstream						
2R_7969026_SNP	G	C	C	0.078	12	141	1.951	3.19E-06	FBgn0033680	<i>CG13186</i>	Synonymous_Coding						
2R_4868564_DEL	G	GTAGTACT	GTAGTACT	0.059	9	143	2.318	3.20E-06	FBgn0033359	<i>CG8213</i>	Intron						
2R_9142406_SNP	C	T	T	0.059	9	143	2.381	3.23E-06	FBgn0265443	<i>CR44343</i>	Exon	FBgn0033819	<i>CG4714</i>	Upstream			
3R_21590062_DEL	G	GCTGG	GCTGG	0.056	8	134	2.729	3.24E-06									
2R_7969666_SNP	T	G	G	0.081	12	136	1.921	3.25E-06	FBgn0033680	<i>CG13186</i>	Downstream						
3L_9843580_SNP	C	T	T	0.104	16	138	1.858	3.26E-06	FBgn0004390	<i>Gap1</i>	Intron						
3L_8744906_SNP	A	T	T	0.051	8	148	2.506	3.30E-06									
2L_16694744_SNP	A	T	T	0.280	40	103	-1.098	3.31E-06	FBgn0261278	<i>grp</i>	Intron						
X_9836934_SNP	T	A	A	0.051	8	148	2.657	3.32E-06									
X_9836936_SNP	A	G	G	0.051	8	148	2.657	3.32E-06									
X_9836977_SNP	C	A	A	0.051	8	148	2.657	3.32E-06									
3R_11698322_SNP	C	T	T	0.052	8	147	2.436	3.38E-06									
2L_13146425_SNP	A	T	T	0.069	9	121	2.388	3.40E-06	FBgn0265088	<i>CR44199</i>	Upstream						
2L_13745845_SNP	T	G	G	0.051	8	148	2.541	3.47E-06									
3R_11897570_SNP	G	A	A	0.059	9	143	1.895	3.53E-06	FBgn0026059	<i>Mhcl</i>	Intron						
2L_11333466_SNP	T	G	G	0.053	8	144	2.536	3.58E-06									
2R_7970010_SNP	T	C	C	0.080	12	138	1.939	3.63E-06	FBgn0033680	<i>CG13186</i>	Downstream						

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	Pvalue	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3	Flybase ID Gene 4	Gene Name 4	Site Class 4
3L 9285052 SNP	T	A	T	0.055	8	138	2.637	3.80E-06												
3R 21967979 SNP	T	A	A	0.052	8	147	2.678	3.80E-06												
2L 13785547 SNP	T	G	G	0.054	8	141	2.471	3.84E-06												
2R 7970197 MNP	GGG	ACC	ACC	0.079	12	139	1.934	3.91E-06	FBgn0033680	CG13186	Downstream									
2R 7970202 SNP	T	G	G	0.079	12	139	1.934	3.91E-06	FBgn0033680	CG13186	Downstream									
2R 7970204 DEL	G	GCAACAGAAAATT	GCAACAGAAAATT	0.079	12	139	1.934	3.91E-06	FBgn0033680	CG13186	Downstream									
2R 7970221 DEL	A	AC	AC	0.079	12	139	1.934	3.91E-06	FBgn0033680	CG13186	Downstream									
2R 7970232 DEL	G	GC	GC	0.079	12	139	1.934	3.91E-06	FBgn0033680	CG13186	Downstream									
X 19383384 SNP	G	A	A	0.090	14	142	1.822	3.94E-06	FBgn0020261	pcm	Synonymous_Coding									
3L 9843431 SNP	A	G	G	0.103	16	139	1.843	3.94E-06	FBgn004390	Gsp1	Intron									
3R 11721999 SNP	T	C	C	0.085	13	140	1.989	3.99E-06	FBgn0027657	glo1	Downstream									
2R 16529889 SNP	A	G	G	0.085	13	140	2.022	4.00E-06	FBgn0034535	CG11110	Synonymous_Coding	FBgn0061361	CG33786	Downstream	FBgn0061362	CG33785	Downstream	FBgn0034534	maf-S	Downstream
2R 7970220 SNP	G	C	C	0.080	12	138	1.933	4.00E-06	FBgn0033680	CG13186	Downstream									
3R 17704850 SNP	A	G	G	0.065	10	143	2.396	4.03E-06	FBgn0053092	P5CDh2	Synonymous_Coding	FBgn0083984	CG34148	Upstream						
2R 4950732 DEL	T	TT	TT	0.066	10	141	2.303	4.07E-06	FBgn0011746	ana	Intron									
2R 6536836 SNP	G	A	A	0.068	10	138	2.290	4.09E-06	FBgn0033541	CG12934	Synonymous_Coding	FBgn0033540	Elp2	Downstream						
3L 15440832 SNP	G	A	A	0.052	8	145	2.528	4.15E-06												
X 15659417 INS	GG	G	G	0.090	14	142	1.870	4.15E-06	FBgn0030687	CG17209	Intron									
X 15659431 INS	GAAACATGA	A	A	0.090	14	142	1.870	4.15E-06	FBgn0030687	CG17209	Intron									
X 16373000 SNP	T	C	C	0.084	13	142	1.898	4.20E-06	FBgn0264255	para	Intron									
2R 16531623 SNP	T	A	A	0.084	13	141	2.019	4.22E-06	FBgn0034537	DMAP1	UTR_5_Prime	FBgn0061361	CG33786	Upstream	FBgn0061362	CG33785	Upstream			
3R 11908663 SNP	A	C	C	0.052	8	145	1.876	4.24E-06	FBgn0026059	Mhcl	Intron									
X 18798247 DEL	T	TTTCGTTTT	TTTCGTTTT	0.052	8	147	2.541	4.38E-06	FBgn0030976	CG7378	Intron									
X 18798273 SNP	A	G	G	0.052	8	147	2.541	4.38E-06	FBgn0030976	CG7378	Intron									
3R 19414938 SNP	C	T	T	0.059	9	144	2.971	4.38E-06	FBgn0039091	CG10182	Non_Synonymous_Coding	FBgn0053337	CG33337	Downstream						
2L 1184262 SNP	C	T	T	0.079	12	139	2.036	4.43E-06	FBgn0031321	Tgt	Intron	FBgn0031320	CG5126	Upstream						
3R 10758623 SNP	A	G	G	0.052	8	146	2.521	4.45E-06												
2L 13032642 SNP	A	T	T	0.073	11	139	2.192	4.56E-06	FBgn0262160	CG9932	Intron									
3L 1456574 SNP	G	A	A	0.059	9	144	2.354	4.65E-06	FBgn0003138	Ptp61F	Intron									
3L 4441910 SNP	T	C	C	0.051	7	129	2.802	4.68E-06												
3R 26129471 SNP	T	A	A	0.084	12	131	1.662	4.83E-06	FBgn0101113	hdc	Intron									
2R 7959219 SNP	C	T	T	0.139	21	130	1.471	4.89E-06	FBgn0033679	CG8888	Intron									
3R 11686306 SNP	T	C	C	0.051	8	148	2.667	4.91E-06	FBgn0034883	spn-E	Synonymous_Coding									
3R 11920465 DEL	A	AGAGGCAA	AGAGGCAA	0.059	9	143	1.882	4.95E-06	FBgn0026059	Mhcl	Intron									
3L 9293237 INS	A	AA	A	0.054	8	140	2.602	4.95E-06												
3L 15499752 SNP	C	T	T	0.052	8	145	2.578	4.97E-06	FBgn0036502	CG7841	Intron									
3L 16908944 SNP	G	A	A	0.124	19	134	1.612	5.34E-06	FBgn0261565	Lmpt	Intron									
3R 11647604 SNP	T	C	C	0.058	9	146	2.346	5.37E-06	FBgn0029618	alpha-Man-IIIb	Synonymous_Coding									
2L 3386894 SNP	T	A	A	0.066	10	141	2.323	5.41E-06	FBgn0259449	Stp23F	Downstream									
3L 5354504 SNP	A	G	G	0.078	12	141	2.182	5.45E-06	FBgn0035600	CG4769	Intron									
3L 5354506 SNP	T	A	A	0.078	12	141	2.182	5.45E-06	FBgn0035600	CG4769	Intron									
X 18274161 SNP	G	A	A	0.052	8	146	2.292	5.53E-06	FBgn0030915	CG6179	Start_Gained	FBgn0004957	por	Upstream						
2L 14388712 SNP	C	A	A	0.072	11	142	2.117	5.56E-06												
X 16068818 SNP	T	A	T	0.078	12	141	2.118	5.68E-06												
2R 8949900 SNP	C	T	C	0.068	13	134	1.957	5.68E-06	FBgn0033791	Drl-2	Intron									
3L 5354438 SNP	A	C	C	0.073	11	140	2.281	5.77E-06	FBgn0035600	CG4769	Intron									
2L 2627549 SNP	T	C	C	0.075	11	136	1.974	5.91E-06												
3R 23226336 SNP	C	T	T	0.059	9	144	2.118	5.95E-06	FBgn0016061	side	Intron									
3L 18016881 SNP	G	A	A	0.053	8	143	2.562	5.98E-06	FBgn0000568	Elp75B	Intron									
2L 3798913 SNP	C	G	G	0.053	8	144	2.560	6.32E-06	FBgn0031571	CG3921	Synonymous_Coding									

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
3R 19425198_SNP	T	C	C	0.053	8	144	2.761	6.33E-06	FBgn0039093	CG10183	Upstream						
X 13282970_SNP	T	G	G	0.071	11	143	2.067	6.36E-06	FBgn0030481	CG1662	Downstream						
2L 10133218_SNP	G	A	A	0.071	11	143	2.175	6.68E-06	FBgn0265002	CG44153	Intron						
3R 20520926_SNP	T	C	C	0.058	9	146	1.892	6.70E-06	FBgn0003429	slo	Intron						
3R 11119592_SNP	G	A	G	0.071	11	144	1.729	6.86E-06	FBgn0003721	Tm1	Intron						
3R 17478255_SNP	A	G	G	0.055	8	138	2.447	7.11E-06	FBgn0011766	E2f	Intron						
2R 7970625_SNP	T	G	G	0.087	13	136	1.827	7.19E-06									
2L 18338977_SNP	C	G	G	0.052	8	145	2.668	7.22E-06	FBgn0000636	Fas3	Intron						
2R 17488762_SNP	T	G	G	0.056	8	136	2.427	7.25E-06									
3R 27069434_DEL	T	TCATCAGCATCAT	TCATCAGCATCAT	0.052	7	128	2.885	7.28E-06	FBgn0051005	gless	Intron						
3R 18366278_SNP	G	A	A	0.052	8	145	2.822	7.46E-06	FBgn0038983	CG5326	Upstream						
2R 7981259_INS	TT	T	T	0.290	40	98	1.177	7.48E-06	FBgn0086677	jeb	Intron						
3R 13913033_SNP	A	C	C	0.052	8	146	2.670	7.54E-06									
3L 14687810_SNP	A	C	C	0.065	10	143	2.302	7.55E-06	FBgn0259175	ome	Intron						
3R 13913027_SNP	A	G	G	0.052	8	147	2.668	7.59E-06									
3R 13913031_SNP	C	T	T	0.052	8	147	2.668	7.59E-06									
3R 23228359_SNP	A	G	G	0.060	9	140	2.104	7.74E-06	FBgn0016061	side	Intron						
X 21119512_SNP	T	A	A	0.065	10	145	2.402	8.08E-06	FBgn0052521	CG32521	Intron						
3L 16908877_SNP	T	C	C	0.118	18	134	1.618	8.21E-06	FBgn0261565	Lmpt	Intron						
2R 20106702_DEL	C	CC	CC	0.097	12	112	2.027	8.30E-06	FBgn0050419	CG30419	Intron						
2L 9258664_SNP	A	G	G	0.052	8	146	2.402	8.42E-06	FBgn0263984	CG43733	Intron	FBgn0028433	Ggamma30A	Intron			
2L 11950219_SNP	A	G	G	0.136	20	127	1.610	8.63E-06									
X 16066830_SNP	G	T	G	0.081	12	137	2.080	8.76E-06									
3L 10373349_SNP	T	C	T	0.136	21	133	1.573	8.94E-06									
3R 11076772_SNP	T	C	C	0.078	12	141	2.087	9.14E-06	FBgn0259823	CG42404	Intron						
X 12495370_SNP	T	C	C	0.090	14	141	1.912	9.16E-06	FBgn0052654	Sec16	Intron						
3R 10640029_SNP	T	C	C	0.078	12	141	2.080	9.16E-06	FBgn0264754	bisz	Intron						
2R 7951620_SNP	A	G	G	0.093	14	137	1.732	9.19E-06	FBgn0033679	CG8888	Downstream						
3R 20316507_SNP	A	G	G	0.065	10	145	2.355	9.24E-06	FBgn0000039	nAcRalpha-96A	Intron						
3R 22813583_SNP	T	C	C	0.054	8	141	2.475	9.28E-06	FBgn0051075	CG31075	Intron						
3R 10758617_SNP	G	C	C	0.053	8	144	2.458	9.29E-06									
3R 10597332_SNP	A	C	C	0.052	8	146	2.402	9.56E-06	FBgn0263929	jvl	Intron						
3R 21968056_SNP	G	C	C	0.058	9	146	2.422	9.62E-06									
3L 5354496_DEL	A	AT	AT	0.072	11	141	2.190	9.85E-06	FBgn0035600	CG4769	Intron						
3L 2388378_SNP	A	T	T	0.072	11	142	2.122	9.85E-06	FBgn0035338	CG13800	Intron	FBgn0261551	CG42669	Intron	FBgn0261858	CG42787	Upstream
2L 15840654_SNP	G	T	T	0.053	8	143	2.593	9.96E-06									
2L 7767035_SNP	T	C	C	0.083	13	143	1.939	1.00E-05	FBgn0031945	CG7191	Upstream						
3L 5354484_DEL	T	TTAAAAT	TTAAAAT	0.078	12	142	2.092	1.01E-05	FBgn0035600	CG4769	Intron						
2L 12102868_SNP	T	C	C	0.170	23	112	1.549	1.04E-05	FBgn0029137	Patsas	Non_Synonymous_Coding	FBgn0027081	Aats-thr	Upstream			
2R 13991527_SNP	T	C	C	0.053	8	144	2.382	1.08E-05	FBgn0034301	CG5756	Synonymous_Coding						
2L 9099191_SNP	G	T	T	0.059	9	144	2.254	1.09E-05									
3R 17478312_SNP	T	C	C	0.059	9	144	2.261	1.11E-05	FBgn0011766	E2f	Intron						
3L 1456971_SNP	A	T	T	0.058	9	146	2.266	1.12E-05	FBgn0003138	Ptp61F	Intron						
3L 1393071_SNP	A	G	G	0.071	11	143	2.151	1.15E-05	FBgn0003138	Ptp61F	Intron						
3R 24672203_SNP	A	G	G	0.052	8	145	2.598	1.17E-05	FBgn0264324	spg	Intron						
2R 10203282_DEL	A	AAC	AAC	0.058	9	147	2.269	1.18E-05	FBgn0085408	Shroom	Intron						
2R 19366641_SNP	C	G	G	0.073	11	140	2.137	1.19E-05	FBgn0264339	CG43795	Intron						
2R 18276634_SNP	A	C	C	0.079	12	140	2.061	1.20E-05	FBgn0034723	CG13506	Intron						
3R 18527884_SNP	A	G	G	0.077	12	143	2.176	1.21E-05	FBgn0039008	CG6972	UTR_5_Prime	FBgn0039007	Ccap	Upstream			
2L 4461905_SNP	T	C	C	0.051	8	148	2.529	1.21E-05	FBgn0031609	CG15443	Synonymous_Coding	FBgn0031608	CG15435	Downstream			

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2
3R 18581714 SNP	C	T	T	0.052	8	146	2.555	1.22E-05	FBgn0039025	<i>Usp12-46</i>	Intron	FBgn0039026	CG7029	Intron
X 16066810 SNP	A	T	A	0.072	11	142	2.112	1.23E-05						
3L 3590841 SNP	C	G	G	0.084	13	142	1.974	1.24E-05	FBgn0005640	<i>Eip63E</i>	Intron			
2L 21221587 SNP	A	C	C	0.054	8	140	2.482	1.24E-05	FBgn0026577	<i>CG8677</i>	Synonymous Coding			
3R 21535093 SNP	G	C	C	0.052	8	146	2.698	1.26E-05	FBgn0051092	<i>LpR2</i>	Intron			
3L 1456953 SNP	A	C	C	0.058	9	145	2.254	1.26E-05	FBgn0003138	<i>Ptp61F</i>	Intron			
3R 11047599 SNP	C	T	C	0.052	8	147	2.492	1.27E-05	FBgn0038304	<i>CG12241</i>	Synonymous Coding	FBgn0051155	<i>Rpb7</i>	Downstream
2L 16921930 SNP	T	A	A	0.054	8	141	2.431	1.27E-05						
3R 18288512 SNP	G	A	A	0.052	8	145	2.664	1.28E-05	FBgn0263351	<i>AP-50</i>	Intron	FBgn0028688	<i>Rpn7</i>	Upstream
3R 16736919 SNP	T	C	C	0.059	9	143	2.353	1.31E-05	FBgn0051191	<i>CG31191</i>	Utr_3 Prime	FBgn0264915	<i>CR44106</i>	Upstream
3R 15895429 SNP	A	G	G	0.086	13	138	2.036	1.31E-05						
3R 24026500 SNP	C	A	A	0.065	10	143	2.231	1.33E-05	FBgn0085383	<i>CG34354</i>	Intron			
3L 19933755 SNP	G	A	A	0.051	7	129	2.743	1.33E-05	FBgn0004852	<i>Ac76E</i>	Intron			
3R 26861298 SNP	A	T	A	0.060	9	141	2.306	1.34E-05	FBgn0053773	<i>CG33773</i>	Non Synonymous Coding			
2L 3386900 SNP	G	T	T	0.067	10	139	2.242	1.35E-05	FBgn0259949	<i>Sfp23F</i>	Downstream	FBgn0259950	CG42460	Downstream
2L 15538772 SNP	T	A	T	0.069	10	135	2.178	1.38E-05						
2L 7766818 SNP	T	A	A	0.099	15	136	1.849	1.42E-05	FBgn0031945	<i>CG7191</i>	Upstream			
3R 25812761 SNP	G	C	C	0.065	10	144	2.430	1.46E-05	FBgn0039728	<i>CG7896</i>	Non Synonymous Coding			
3R 23310671 SNP	A	T	T	0.065	10	145	2.372	1.49E-05						
3R 15895360 SNP	A	T	T	0.091	14	140	1.957	1.50E-05						
3R 23490177 SNP	G	A	A	0.058	9	145	2.358	1.50E-05	FBgn0039536	<i>CG18437</i>	Intron			
2R 1622838 SNP	A	C	C	0.054	8	139	2.429	1.51E-05						
X 16066844 SNP	G	A	G	0.075	11	135	2.098	1.53E-05						
3R 26750310 SNP	C	G	G	0.052	8	147	2.736	1.53E-05	FBgn0020912	<i>Ptx1</i>	Intron			
3R 26750338 SNP	T	A	A	0.052	8	147	2.736	1.53E-05	FBgn0020912	<i>Ptx1</i>	Intron			
3R 26750350 DEL	T	TA	TA	0.052	8	147	2.736	1.53E-05	FBgn0020912	<i>Ptx1</i>	Intron			
2L 8032747 SNP	G	A	A	0.058	9	146	2.242	1.54E-05	FBgn0044323	<i>Cka</i>	Intron	FBgn0031976	CG7367	Intron
2L 8032759 SNP	G	T	T	0.058	9	146	2.242	1.54E-05	FBgn0044323	<i>Cka</i>	Intron	FBgn0031976	CG7367	Intron
2L 7767021 INS	CCA	C	C	0.090	14	141	1.885	1.58E-05	FBgn0031945	<i>CG7191</i>	Upstream			
2L 7767024 DEL	T	TA	TA	0.090	14	141	1.885	1.58E-05	FBgn0031945	<i>CG7191</i>	Upstream			
2R 5106714 SNP	C	A	A	0.067	10	140	2.244	1.64E-05						
3R 25101028 SNP	A	G	G	0.052	8	146	2.480	1.66E-05						
X 18036389 SNP	A	G	G	0.052	8	146	2.368	1.67E-05						
3R 19917168 INS	TGCCAAA	T	T	0.072	11	141	2.251	1.68E-05	FBgn0053100	<i>4EHP</i>	Intron			
3R 25210392 SNP	T	A	A	0.052	8	146	2.591	1.68E-05	FBgn0004369	<i>Ptp99A</i>	Intron			
3R 19175562 SNP	C	T	T	0.097	15	140	1.932	1.69E-05	FBgn0264326	<i>DNApol-epsilon</i>	Synonymous Coding			
X 8549549 SNP	A	G	G	0.065	10	144	2.172	1.71E-05						
3R 19883791 DEL	ATC	A	ATC	0.053	8	143	2.504	1.72E-05	FBgn0040283	<i>SMC1</i>	Upstream	FBgn0001230	<i>Hsp68</i>	Upstream
3R 11552419 SNP	T	A	A	0.052	8	147	2.449	1.73E-05						
3R 3393781 SNP	T	G	G	0.077	12	144	2.090	1.78E-05						
3R 3393861 SNP	C	T	T	0.077	12	144	2.090	1.78E-05						
2R 2438252 INS	TCAT	T	T	0.055	8	138	2.367	1.80E-05	FBgn0086655	<i>jing</i>	Intron			
2L 12610157 SNP	A	G	G	0.059	9	144	2.284	1.82E-05	FBgn0085424	<i>nub</i>	Intron	FBgn0032439	<i>Ref2</i>	Downstream
X 6727249 SNP	T	A	T	0.166	25	126	1.453	1.84E-05	FBgn0263968	<i>nonC</i>	Intron	FBgn0029909	CG12796	Upstream
2R 18275974 SNP	A	T	T	0.059	9	144	2.297	1.84E-05	FBgn0034723	<i>CG13506</i>	Intron			
3R 23474742 DEL	C	AATA	AATA	0.052	8	146	2.487	1.85E-05	FBgn0051058	<i>CG31058</i>	Codon Deletion	FBgn0051057	<i>tau</i>	Intron
3R 24683972 SNP	T	G	G	0.079	12	140	2.009	1.87E-05	FBgn0265274	<i>Inx3</i>	Intron	FBgn0264324	<i>spg</i>	Intron
2L 12265179 SNP	A	C	C	0.066	10	142	2.286	1.88E-05	FBgn0000114	<i>aret</i>	Intron			
3R 21503055 SNP	T	G	G	0.052	8	147	2.546	1.89E-05	FBgn0039355	<i>CG4730</i>	Non Synonymous Coding	FBgn0039354	<i>Lgr3</i>	Downstream
3R 21503058 SNP	T	G	G	0.052	8	147	2.546	1.89E-05	FBgn0039355	<i>CG4730</i>	Non Synonymous Coding	FBgn0039354	<i>Lgr3</i>	Downstream

Table 4.S5 Continued

D	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
X 3333899	SNP	A	T	0.065	10	144	2.367	1.90E-05	FBgn0029657	CG12535	Intron						
X 17922048	SNP	T	A	0.059	9	144	2.333	1.97E-05	FBgn0003380	Sh	Intron	FBgn0030887	CG6867	Intron			
2L 9074827	SNP	A	G	0.053	8	143	2.350	2.05E-05									
3R 10586273	SNP	C	G	0.053	8	143	2.409	2.08E-05	FBgn0263929	ivl	Intron						
3R 20467872	SNP	T	A	0.052	8	146	2.378	2.10E-05	FBgn0039214	CG5794	Intron						
3R 13913000	SNP	T	G	0.052	8	146	2.626	2.11E-05									
3R 18876184	SNP	G	T	0.051	8	148	2.700	2.12E-05	FBgn0039044	p53	Intron						
2L 6552050	SNP	T	A	0.084	13	141	1.917	2.14E-05									
3R 19419676	SNP	G	C	0.058	9	145	2.484	2.14E-05	FBgn0039092	CG16723	Synonymous_Coding						
X 16030838	SNP	T	G	0.065	10	143	2.165	2.15E-05	FBgn0042650	disco-r	Intron						
3R 20468107	SNP	T	G	0.052	8	147	2.372	2.20E-05	FBgn0039214	CG5794	Intron						
3R 23736735	SNP	A	G	0.052	8	147	2.602	2.22E-05									
3L 5354499	SNP	C	T	0.072	11	141	2.127	2.22E-05	FBgn0035600	CG4769	Intron						
2L 1451509	SNP	T	C	0.053	8	143	2.468	2.28E-05									
3R 17321511	SNP	A	G	0.053	8	142	2.388	2.31E-05									
3R 11274414	SNP	A	G	0.071	11	145	2.222	2.32E-05	FBgn0038341	CG14869	Synonymous_Coding						
3R 12001472	SNP	T	A	0.052	8	146	2.415	2.37E-05	FBgn0038404	CG8925	Intron						
3R 19534459	SNP	T	A	0.071	10	130	2.371	2.39E-05	FBgn0051414	CG31414	Downstream						
2L 12262440	SNP	T	C	0.052	8	145	2.443	2.40E-05	FBgn0000114	aret	Intron						
3R 11078133	SNP	T	C	0.196	30	123	1.354	2.44E-05	FBgn0259823	CG42404	Synonymous_Coding						
3R 20482598	SNP	T	A	0.078	12	141	2.052	2.46E-05	FBgn0039215	CG6695	Non_Synonymous_Coding						
3R 19042575	SNP	G	C	0.053	8	144	2.613	2.48E-05	FBgn0262975	cnc	Intron						
3R 12001562	SNP	T	C	0.086	13	138	1.913	2.50E-05	FBgn0038404	CG8925	Intron						
3R 18272317	SNP	G	T	0.059	9	144	2.278	2.52E-05	FBgn0038968	CG12499	Upstream	FBgn0085317	CG34288	Downstream			
3R 23505823	DEL	A	ATAGAA	ATAGAA	0.067	10	139	2.224	2.57E-05	FBgn0039538	CG12883	UTR_3_Prime	FBgn0003330	See	Downstream		
3R 18726630	SNP	A	T	0.065	10	145	2.269	2.61E-05	FBgn0017590	klg	Intron						
X 17922690	SNP	T	A	0.065	10	145	2.191	2.66E-05	FBgn0003380	Sh	Intron	FBgn0030887	CG6867	Downstream			
X 18820629	SNP	T	C	0.072	11	142	2.029	2.66E-05									
X 6048541	SNP	T	C	0.058	9	146	2.361	2.68E-05	FBgn0264386	Ca-alpha1T	Intron						
3R 15852050	SNP	T	C	0.058	9	145	2.437	2.75E-05	FBgn0243511	psidin	UTR_3_Prime	FBgn0038765	CG4424	Downstream			
3R 20388331	SNP	G	A	0.113	17	134	1.724	2.88E-05	FBgn0039209	CG13624	Synonymous_Coding						
3L 9847103	SNP	A	G	0.092	14	138	1.860	2.94E-05	FBgn0004390	Gap1	Intron						
3R 17067496	INS	AAATTCCC	A	0.054	8	141	2.349	3.02E-05	FBgn0038873	CG5892	Upstream						
3R 11678198	SNP	A	G	0.051	8	148	2.387	3.10E-05	FBgn0265048	cv-d	Intron						
3R 18573126	SNP	C	T	0.059	9	143	2.500	3.10E-05	FBgn0039020	CG17141	Synonymous_Coding	FBgn0051139	CG31139	Downstream	FBgn0039019	HP1c	Downstream
3R 21923969	SNP	T	C	0.072	11	142	2.131	3.11E-05	FBgn0039411	dys	Upstream						
2L 13578133	DEL	G	GCAG	GCAG	0.073	11	139	2.115	3.23E-05	FBgn0259984	kuz	Intron					
X 3334548	SNP	G	A	0.052	8	146	2.250	3.27E-05	FBgn0029657	CG12535	Intron						
3L 20514590	SNP	T	C	0.059	9	144	2.264	3.28E-05	FBgn0037009	CG5104	Non_Synonymous_Coding	FBgn0037008	mTerf3	Upstream	FBgn0037010	CG4825	Downstream
3R 23287510	SNP	C	T	0.065	10	143	2.222	3.32E-05									
3R 11770432	SNP	A	G	0.072	11	142	2.087	3.38E-05	FBgn0013334	Sap47	Intron						
3R 18573137	SNP	A	G	0.053	8	144	2.612	3.51E-05	FBgn0039020	CG17141	Synonymous_Coding	FBgn0051139	CG31139	Downstream	FBgn0039019	HP1c	Downstream
3R 18573138	SNP	C	T	0.053	8	144	2.612	3.51E-05	FBgn0039020	CG17141	Synonymous_Coding	FBgn0051139	CG31139	Downstream	FBgn0039019	HP1c	Downstream
3R 26173969	SNP	G	A	0.052	8	147	2.477	3.52E-05	FBgn0010113	hdc	Intron						
2L 12266563	SNP	C	T	0.051	8	148	2.451	3.53E-05	FBgn0000114	aret	Intron						
2L 12266950	SNP	A	C	0.066	10	141	2.184	3.53E-05	FBgn0000114	aret	Intron						
3L 5354439	SNP	C	T	0.078	12	141	2.001	3.55E-05	FBgn0035600	CG4769	Intron						
3L 5354444	SNP	T	G	0.078	12	141	2.001	3.55E-05	FBgn0035600	CG4769	Intron						
3R 10759624	SNP	G	A	0.052	8	146	2.373	3.56E-05									
3R 10759634	SNP	A	C	0.052	8	146	2.373	3.56E-05									

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
3L_5354479_SNP	A	T	T	0.078	12	141	1.999	3.60E-05	FBgn0035600	CG4769	Intron						
3L_5354480_SNP	A	T	T	0.078	12	141	1.999	3.60E-05	FBgn0035600	CG4769	Intron						
3R_19917468_SNP	G	C	C	0.090	14	141	1.869	3.62E-05	FBgn0053100	4EHP	Intron						
3R_19417140_SNP	T	C	C	0.066	13	139	2.001	3.69E-05	FBgn0051163	SKIP	Intron						
3R_19414922_SNP	T	C	C	0.066	10	141	2.353	3.70E-05	FBgn0039091	CG10182	Synonymous_Coding	FBgn0053337	CG33337	Downstream			
3R_11076877_SNP	T	G	G	0.105	16	137	1.714	3.71E-05	FBgn0259823	CG42404	Intron						
3R_12410238_SNP	T	G	G	0.065	10	145	2.146	3.77E-05	FBgn0020907	Scp2	Upstream						
X_21119508_SNP	C	A	A	0.071	11	144	2.102	3.78E-05	FBgn0052521	CG32521	Intron						
3R_21971128_SNP	G	A	A	0.133	20	131	1.582	3.86E-05									
3L_5354472_SNP	A	T	T	0.078	12	142	1.991	3.88E-05	FBgn0035600	CG4769	Intron						
3R_17986421_DEL	C	GCGGG	GCGGG	0.099	15	136	1.861	3.90E-05	FBgn0051163	SKIP	Intron						
3R_24132048_SNP	C	T	C	0.085	13	140	2.027	4.01E-05									
3R_22857604_SNP	A	G	G	0.085	13	140	1.941	4.26E-05	FBgn0262473	Ti	Intron						
3R_21487418_SNP	A	T	T	0.073	11	140	2.147	4.39E-05	FBgn0261986	RASSF8	Upstream	FBgn0027508	tankyrase	Upstream			
3R_22348817_SNP	A	C	C	0.065	10	145	2.174	4.41E-05	FBgn0039431	CG6490	Intron						
3R_16924276_SNP	A	C	C	0.052	8	146	2.449	4.45E-05	FBgn0038854	CG7044	Synonymous_Coding	FBgn0038853	RhoGAP93B	Upstream			
3R_22707611_SNP	T	A	A	0.051	8	148	2.556	4.81E-05	FBgn0004359	T48	UTR_5_Prime	FBgn0003267	ro	Upstream			
3R_27123781_SNP	G	C	C	0.060	9	140	2.397	4.93E-05									
3R_19917361_SNP	G	A	A	0.097	15	139	1.804	4.99E-05	FBgn0053100	4EHP	Intron						
3R_23852854_DEL	C	CAATGCATTGAACA	CAATGCATTGAACA	0.052	8	147	2.585	5.10E-05	FBgn0085391	CG34362	Intron						
3R_24960120_SNP	A	C	C	0.058	9	145	2.377	5.18E-05	FBgn0028671	Vha100-1	Intron						
X_21120176_SNP	C	T	T	0.051	8	148	2.487	5.25E-05	FBgn0052521	CG32521	Intron	FBgn0031168	CG1722	Downstream			
3R_19883893_SNP	T	C	C	0.054	8	141	2.434	5.26E-05	FBgn0040283	SMC1	Upstream	FBgn0001230	Hsp68	Upstream			
2R_7444493_SNP	G	C	C	0.060	9	142	2.303	5.32E-05									
X_16036839_SNP	T	C	C	0.056	8	135	2.234	5.36E-05									
3R_27122262_SNP	G	C	C	0.058	9	146	2.365	5.43E-05									
3R_28972527_DEL	T	TACTCTATTCCGAAAAGTGCAGGCAT	TACTCTATTCCGAAAAGTGCAGGCAT	0.053	8	142	2.399	5.51E-05	FBgn0013973	Gycbeta100B	Intron						
3R_20776201_DEL	TT	T	TT	0.094	13	126	1.978	5.66E-05	FBgn0039255	CG13646	Downstream						
X_13159905_SNP	A	T	T	0.091	14	140	1.821	5.68E-05	FBgn0000346	camt	UTR_3_Prime	FBgn0041210	HDAC4	Downstream			
3R_20972622_SNP	G	C	C	0.072	11	142	2.175	5.71E-05									
3R_19917167_SNP	G	T	T	0.085	13	140	1.988	5.75E-05	FBgn0053100	4EHP	Intron						
3R_19409487_SNP	T	C	C	0.072	11	142	2.219	6.00E-05									
3R_25036969_SNP	G	A	A	0.124	19	134	1.863	6.24E-05									
3R_15895404_SNP	G	A	A	0.086	13	138	1.939	6.41E-05									
3R_21975013_SNP	T	C	C	0.051	8	148	2.383	6.49E-05									
3L_9846750_SNP	T	A	A	0.092	14	139	1.852	6.53E-05	FBgn0004390	Gap1	Intron						
2L_10550546_SNP	T	C	C	0.052	8	147	2.377	6.55E-05	FBgn0051721	Trim9	Intron						
3R_17986702_SNP	A	G	G	0.086	13	139	2.006	6.64E-05	FBgn0051163	SKIP	Intron						
3R_17986673_SNP	G	A	A	0.086	13	139	2.006	6.73E-05	FBgn0051163	SKIP	Intron						
3R_16020008_SNP	T	A	A	0.076	12	141	2.023	6.89E-05	FBgn0051163	SKIP	Intron						
2L_16304445_SNP	C	G	G	0.052	8	146	2.422	7.01E-05									
3R_26174080_SNP	T	A	A	0.052	8	147	2.408	7.05E-05	FBgn0010113	hdc	Intron						
3R_26691944_SNP	A	C	A	0.137	21	132	1.582	7.14E-05									
3R_26174077_SNP	C	T	T	0.052	8	146	2.406	7.40E-05	FBgn0010113	hdc	Intron						
3R_26341411_SNP	C	T	T	0.071	11	143	2.112	7.75E-05	FBgn0039784	CG9698	Synonymous_Coding						
3R_26341423_SNP	C	G	G	0.071	11	143	2.112	7.75E-05	FBgn0039784	CG9698	Non_Synonymous_Coding						
3R_15895827_SNP	C	G	G	0.058	9	145	2.310	8.17E-05									
2R_16532155_SNP	T	C	C	0.078	12	142	1.986	8.19E-05	FBgn0034537	DMAP1	Synonymous_Coding	FBgn0061361	CG33786	Upstream	FBgn0061362	CG33785	Upstream
3R_17146725_SNP	T	G	G	0.078	12	141	2.011	8.60E-05	FBgn0038881	CG16791	UTR_3_Prime						
3R_23852962_SNP	C	T	T	0.054	8	140	2.528	8.81E-05	FBgn0085391	CG34362	Intron						

Table 4.S5 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3	Flybase ID Gene 34	Gene Name 4	Site Class 4
3L 9591705_SNP	T	G	G	0.077	12	144	1.959	9.10E-05	FBgn0036014	CG3222	Upstream	FBgn0036013	CG14177	Downstream						
3R 26468719_SNP	G	A	A	0.052	8	145	2.526	9.17E-05	FBgn0051013	CG31013	Downstream									
3R 26468715_SNP	T	C	C	0.052	8	146	2.526	9.18E-05	FBgn0051013	CG31013	Downstream									
3R 27429311_SNP	C	A	A	0.052	8	145	2.467	9.25E-05	FBgn0039858	CycG	Intron									
3R 21492499_SNP	T	G	G	0.103	16	139	1.733	9.36E-05	FBgn0039354	Lg73	Intron									
ZL 12270571_SNP	G	A	A	0.053	8	144	2.431	9.36E-05	FBgn0000114	arot	Intron									
3R 1985728_SNP	C	T	T	0.112	17	135	1.706	9.43E-05	FBgn0085384	CG34355	Synonymous_Coding									
3R 20383055_DEL	G	GA	GA	0.058	9	145	2.288	9.45E-05	FBgn0004190	snRNA:U6.96A	Downstream	FBgn0039209	CG13624	Downstream	FBgn0004189	snRNA:U6.96A	Downstream	FBgn0039208	Esy2	Downstream
3R 25322453_SNP	T	C	C	0.065	10	143	2.198	9.67E-05	FBgn0039667	CG2010	Intron									

Table 4.S6 - Genome-wide association analyses for recombination rate. Results from GWA on *e ro* data set excluding DGRP lines with an inversion on 3R or any polymorphic inversions.

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
3R_22077370_SNP	T	C	C	0.066	8	114	3.369	3.72E-10	FBgn0261708	CR42745	Exon
3L_8201612_SNP	T	C	C	0.056	7	119	3.385	6.89E-10			
X_8549549_SNP	A	G	G	0.055	7	121	3.274	1.42E-09			
2L_2631679_SNP	T	C	C	0.088	11	114	2.739	2.06E-09			
2L_2630015_SNP	T	A	A	0.101	13	116	2.364	4.47E-09			
2L_2630016_SNP	A	T	T	0.101	13	116	2.364	4.47E-09			
2L_2630028_SNP	A	G	G	0.101	13	116	2.364	4.47E-09			
2L_2630035_SNP	T	C	C	0.101	13	116	2.364	4.47E-09			
2L_2630019_SNP	G	C	C	0.101	13	116	2.330	7.65E-09			
2L_2630918_SNP	G	A	A	0.064	8	117	3.062	8.22E-09			
3R_11711965_SNP	A	T	T	0.055	7	120	3.208	9.28E-09			
2L_7766066_SNP	C	G	G	0.069	9	121	2.858	9.81E-09	FBgn0031944	CG7196	Downstream
2L_16330317_SNP	T	A	A	0.062	8	121	2.999	1.10E-08	FBgn0040984	CG4440	UTR_3_Prime
2R_18451837_SNP	T	C	C	0.058	7	113	3.173	1.27E-08	FBgn0260866	<i>dnr1</i>	Non_Synonymous_Coding
2L_2631396_SNP	A	C	C	0.109	14	114	2.274	1.52E-08			
2L_2630587_SNP	A	G	G	0.101	13	116	2.280	1.78E-08			
2L_2631465_INS	GGTA	G	G	0.094	12	116	2.494	1.88E-08			
2L_2630393_SNP	G	T	T	0.101	13	116	2.287	1.94E-08			
2L_14502808_SNP	T	A	A	0.086	11	117	2.593	2.23E-08			
2L_2630304_SNP	C	T	T	0.123	16	114	2.026	2.44E-08			
2L_2629929_SNP	C	T	T	0.102	13	115	2.259	2.90E-08			
2L_2631753_SNP	T	A	A	0.100	13	117	2.371	3.35E-08			
3L_1456902_SNP	T	C	C	0.056	7	119	3.146	3.36E-08	FBgn0003138	<i>Ptp61F</i>	Intron
2L_2627934_SNP	C	A	A	0.110	14	113	2.172	3.45E-08			
3R_11811770_SNP	G	C	C	0.054	7	122	2.840	3.46E-08	FBgn0003507	<i>srp</i>	Upstream
2L_2629729_SNP	G	T	T	0.115	15	115	2.115	3.64E-08			
2L_2629915_SNP	A	G	G	0.115	15	115	2.115	3.64E-08			
2L_2629944_SNP	T	C	C	0.115	15	115	2.115	3.64E-08			
2L_2628410_SNP	T	C	C	0.115	15	115	2.099	4.36E-08			
2L_2628019_SNP	C	A	A	0.109	14	114	2.145	5.52E-08			
2L_2631459_DEL	C	CCCG	CCCG	0.079	10	117	2.650	5.64E-08			
3R_23142479_SNP	C	T	T	0.071	9	118	2.779	5.69E-08	FBgn0039510	CG3339	Intron
2L_7769581_SNP	G	C	C	0.054	7	123	3.121	5.94E-08	FBgn0031945	CG7191	Intron
2L_3612475_SNP	T	C	C	0.057	7	116	3.065	6.77E-08			
2L_2628668_SNP	A	T	T	0.163	21	108	1.821	8.67E-08			
3R_20541038_SNP	A	G	G	0.054	7	122	2.322	9.02E-08	FBgn0039217	CG13627	Synonymous_Coding
3R_20543333_SNP	A	C	C	0.054	7	122	2.317	1.06E-07	FBgn0039218	<i>Rpb10</i>	UTR_5_Prime
2L_9088828_SNP	T	C	C	0.071	9	118	2.444	1.10E-07	FBgn0032095	<i>Toll-4</i>	Synonymous_Coding
3R_11710508_INS	TGTT	T	T	0.052	6	109	3.258	1.20E-07			
2R_10706098_SNP	C	T	T	0.054	7	122	2.942	1.22E-07	FBgn0033969	CG10202	Synonymous_Coding
3L_1456574_SNP	G	A	A	0.063	8	119	2.829	1.28E-07	FBgn0003138	<i>Ptp61F</i>	Intron
2R_9395335_SNP	C	T	T	0.055	7	121	2.964	1.29E-07	FBgn0024556	<i>EFTuM</i>	Synonymous_Coding
2R_9394974_SNP	T	C	C	0.054	7	122	2.953	1.43E-07	FBgn0033846	<i>mip120</i>	Intron
2R_9395041_SNP	A	T	T	0.054	7	122	2.953	1.43E-07	FBgn0033846	<i>mip120</i>	Intron
2R_16530532_SNP	A	C	C	0.065	8	116	2.831	1.45E-07	FBgn0061361	CG33786	Non_Synonymous_Coding
3R_11711860_SNP	C	T	T	0.062	8	121	2.763	1.85E-07			
2R_6141292_SNP	A	T	T	0.054	7	122	3.046	2.04E-07	FBgn0033500	CG12913	Non_Synonymous_Coding
3R_11920465_DEL	A	AGAGG	AGAGG	0.056	7	119	2.239	2.39E-07	FBgn0026059	<i>Mhcl</i>	Intron
2L_9687347_SNP	C	A	A	0.056	7	117	2.807	2.98E-07	FBgn0000273	<i>Pka-C1</i>	Intron
2L_2631452_SNP	T	C	C	0.093	12	117	2.328	3.20E-07			

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
ZL_9074788_SNP	A	T	T	0.055	7	121	2.906	3.21E-07			
3R_23198956_SNP	A	C	C	0.055	7	121	2.239	3.53E-07	FBgn0260487	CG42534	Downstream
3R_20544983_SNP	G	T	T	0.076	10	119	2.060	3.68E-07	FBgn0039219	CG13630	Synonymous_Coding
3R_11687887_SNP	C	T	T	0.054	7	122	3.004	3.84E-07	FBgn0051183	CG31183	Synonymous_Coding
ZL_2632099_SNP	A	G	G	0.117	15	113	1.973	3.88E-07			
3L_1456971_SNP	A	T	T	0.062	8	121	2.728	3.89E-07	FBgn0003138	Ptp61F	Intron
3L_1456953_SNP	A	C	C	0.063	8	120	2.714	4.57E-07	FBgn0003138	Ptp61F	Intron
ZL_7767243_SNP	T	C	C	0.054	7	123	2.963	4.96E-07	FBgn0031945	CG7191	Upstream
X_3334702_SNP	G	C	C	0.058	7	114	2.876	5.23E-07	FBgn0029657	CG12535	Intron
3R_10834430_SNP	C	T	T	0.056	7	119	2.679	5.51E-07			
3L_1393055_SNP	A	G	G	0.062	8	122	2.734	5.60E-07	FBgn0003138	Ptp61F	Intron
3R_21967979_SNP	T	A	A	0.054	7	122	2.948	5.61E-07			
ZL_12817811_SNP	T	G	G	0.056	7	117	2.853	5.92E-07	FBgn0015399	kek1	UTR_3_Prime
ZL_2628835_SNP	T	G	G	0.102	13	115	2.073	6.21E-07			
ZR_8700325_SNP	C	T	T	0.109	14	114	1.986	6.33E-07			
X_17923037_SNP	C	G	G	0.055	7	121	2.925	6.54E-07	FBgn0003380	Sh	Intron
ZL_7760128_SNP	A	G	G	0.054	7	122	2.869	6.83E-07	FBgn0031944	CG7196	Intron
3R_22348818_SNP	G	C	C	0.063	8	120	2.524	6.99E-07	FBgn0039431	CG6490	Intron
X_16875596_SNP	C	A	A	0.057	7	116	2.892	7.63E-07	FBgn0030810	CG9059	Intron
ZR_7968428_SNP	G	C	C	0.087	11	115	2.155	7.72E-07	FBgn0033680	CG13186	Upstream
ZL_7763275_SNP	A	G	G	0.063	8	119	2.577	8.00E-07	FBgn0031944	CG7196	Intron
3R_11162200_SNP	G	A	A	0.062	8	122	2.509	8.13E-07	FBgn0038320	Sra-1	Synonymous_Coding
ZL_15840654_SNP	G	T	T	0.055	7	120	2.931	8.37E-07			
ZL_2630657_SNP	T	C	C	0.102	13	115	2.016	8.84E-07			
ZR_9143227_SNP	G	C	C	0.071	9	118	2.478	9.74E-07	FBgn0265443	CR44343	Upstream
3L_8912025_SNP	T	C	T	0.054	7	122	2.830	1.06E-06	FBgn0035936	Tsp66E	Intron
3R_20290651_SNP	A	C	C	0.103	13	113	2.099	1.13E-06			
3R_2841101_SNP	A	T	T	0.073	9	114	2.450	1.13E-06			
3L_1456916_SNP	A	C	C	0.069	9	121	2.474	1.14E-06	FBgn0003138	Ptp61F	Intron
3R_11687896_SNP	T	G	G	0.062	8	121	2.732	1.17E-06	FBgn0051183	CG31183	Synonymous_Coding
3L_1455925_SNP	T	G	G	0.085	11	116	2.136	1.16E-06	FBgn0003138	Ptp61F	Intron
3L_1455555_SNP	A	C	C	0.086	11	117	2.142	1.19E-06	FBgn0003138	Ptp61F	Intron
3R_10834367_SNP	A	G	G	0.056	7	116	2.694	1.27E-06			
3R_21827395_SNP	A	T	T	0.055	7	121	2.121	1.34E-06	FBgn0002735	E(spl)mgamma	Downstream
3R_24132048_SNP	C	T	C	0.079	10	117	2.575	1.35E-06			
3L_1074580_SNP	T	C	C	0.085	11	119	1.876	1.40E-06	FBgn0004870	bab1	Intron
3L_5796400_SNP	G	A	G	0.069	9	121	2.501	1.49E-06	FBgn0259167	CG42272	Non_Synonymous_Coding
3R_26341342_SNP	T	A	A	0.079	10	116	2.515	1.53E-06	FBgn0039784	CG9698	Non_Synonymous_Coding
ZL_2632236_SNP	G	A	A	0.194	25	104	1.429	1.53E-06			
X_3333899_SNP	A	T	T	0.062	8	121	2.428	1.58E-06	FBgn0029657	CG12535	Intron
ZL_10791112_INS	T	TTT	T	0.062	8	121	2.597	1.59E-06	FBgn0051869	CG31869	Intron
ZR_9355785_SNP	A	G	G	0.336	42	83	1.273	1.65E-06	FBgn0000119	arr	Intron
3R_11688384_SNP	T	C	C	0.062	8	122	2.675	1.67E-06	FBgn0051183	CG31183	Non_Synonymous_Coding
3L_19933755_SNP	G	A	A	0.053	6	108	2.994	1.71E-06	FBgn0004852	Ac76E	Intron
ZL_16550646_SNP	C	A	A	0.054	7	123	2.733	1.74E-06	FBgn0259735	CG42389	Intron
3R_17478255_SNP	A	G	G	0.057	7	116	2.613	1.76E-06	FBgn0011766	E2f	Intron
ZR_9142403_SNP	T	C	C	0.063	8	119	2.469	1.76E-06	FBgn0265443	CR44343	Exon
ZL_11953790_DEL	C	CTGATAAGTGGCTTTGATCTATCCCAC	CTGATAAGTGGCTTTGATCTATCCCAC	0.055	7	121	2.559	1.89E-06	FBgn0263019	CR43314	Exon
3R_20542837_SNP	A	G	G	0.054	7	122	2.069	1.96E-06	FBgn0039217	CG13627	Intron
3R_22151453_DEL	A	CCTTTTCAATCCCCGATGATTTTC	CCTTTTCAATCCCCGATGATTTTC	0.070	9	119	2.580	1.99E-06	FBgn0053970	CG33970	Intron

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
3R_20538756_SNP	A	C	C	0.055	7	121	2.083	2.00E-06	FBgn0039217	CG13627	UTR_5_Prime
3R_20520926_SNP	T	C	C	0.062	8	122	2.004	2.01E-06	FBgn0003429	slo	Intron
3R_22151484_DEL	T	TTTGCCACTT	TTTGCCACTT	0.071	9	118	2.563	2.02E-06	FBgn0053970	CG33970	Intron
3L_8442127_SNP	T	C	C	0.055	7	121	2.753	2.04E-06	FBgn0035896	CG6983	Intron
3R_23505354_SNP	A	G	G	0.055	7	120	2.668	2.04E-06	FBgn0039538	CG12883	Synonymous_Coding
3R_3393761_SNP	T	G	G	0.069	9	121	2.516	2.04E-06			
3R_3393861_SNP	C	T	T	0.069	9	121	2.516	2.04E-06			
3R_18726757_DEL	A	AA	AA	0.057	7	116	2.719	2.11E-06	FBgn0017590	klg	Intron
2L_10057665_SNP	A	G	G	0.072	9	116	2.469	2.23E-06	FBgn0011823	Pen	UTR_5_Prime
2R_10706468_SNP	G	A	A	0.078	10	118	2.269	2.29E-06	FBgn0033969	CG10202	Intron
X_13282970_SNP	T	G	G	0.078	10	118	2.191	2.32E-06	FBgn0030481	CG1662	Downstream
3R_21968056_SNP	G	C	C	0.082	8	121	2.628	2.36E-06			
3R_20776201_DEL	TT	T	TT	0.069	8	108	2.746	2.36E-06	FBgn0039255	CG13646	Downstream
3R_21590062_DEL	G	GCTGG	GCTGG	0.060	7	110	2.867	2.39E-06			
3L_1455295_SNP	G	A	A	0.093	12	117	1.993	2.42E-06	FBgn0003138	Ptp61F	Intron
3R_20383055_DEL	G	GA	GA	0.054	7	122	2.839	2.47E-06	FBgn0004190	snRNA:U6:96A	Downstream
X_16067327_SNP	A	C	A	0.078	10	119	2.279	2.49E-06			
3L_9844532_SNP	T	A	A	0.063	8	119	2.635	2.50E-06	FBgn0004390	Gap1	Intron
2R_13991527_SNP	T	C	C	0.054	7	122	2.637	2.57E-06	FBgn0034301	CG5756	Synonymous_Coding
3R_20537691_SNP	T	C	C	0.055	7	120	2.062	2.57E-06	FBgn0003429	slo	Downstream
2L_13032232_SNP	A	C	C	0.070	9	119	2.438	2.58E-06	FBgn0262160	CG9932	Intron
X_16067311_SNP	G	T	G	0.077	10	120	2.274	2.59E-06			
3R_20538757_SNP	A	C	C	0.054	7	122	2.060	2.65E-06	FBgn0039217	CG13627	UTR_5_Prime
2L_7760144_SNP	C	T	T	0.054	7	123	2.721	2.74E-06	FBgn0031944	CG7196	Intron
3R_23226336_SNP	C	T	T	0.063	8	119	2.198	2.82E-06	FBgn0016061	side	Intron
3R_10834414_SNP	T	C	C	0.070	9	119	1.924	2.87E-06			
X_16373123_SNP	A	G	G	0.070	9	120	2.436	2.93E-06	FBgn0264255	para	Intron
2L_10043927_INS	ATTCTACCA	A	A	0.050	6	114	2.934	2.93E-06			
3L_9110092_SNP	A	C	C	0.062	8	122	2.596	2.96E-06	FBgn0011206	bol	Intron
3R_11062857_SNP	A	C	C	0.062	8	122	2.374	3.08E-06	FBgn0045035	tefu	Non_Synonymous_Coding
2L_10170856_SNP	G	A	A	0.062	8	122	2.650	3.09E-06	FBgn0265002	CG44153	Intron
2R_20106702_DEL	C	CC	CC	0.103	11	96	2.226	3.12E-06	FBgn0050419	CG30419	Intron
3R_23023994_SNP	C	T	T	0.071	9	118	2.453	3.22E-06			
2R_7969265_SNP	T	C	C	0.085	11	118	2.014	3.23E-06	FBgn0033680	CG13186	UTR_3_Prime
3R_12052379_SNP	A	C	C	0.055	7	120	2.475	3.35E-06	FBgn0040071	tara	Intron
X_18036704_SNP	T	G	G	0.093	12	117	2.148	3.38E-06			
2R_7970219_SNP	G	C	C	0.086	11	117	2.007	3.55E-06	FBgn0033680	CG13186	Downstream
2R_4951345_SNP	A	T	T	0.071	8	104	2.607	3.59E-06	FBgn0011746	ana	Intron
3R_23226359_SNP	A	G	G	0.065	8	116	2.188	3.64E-06	FBgn0016061	side	Intron
3L_11506133_SNP	T	G	G	0.062	7	106	2.641	3.68E-06	FBgn0003373	Sgs3	Non_Synonymous_Coding
3R_25812761_SNP	GG	C	C	0.055	7	121	2.921	3.76E-06	FBgn0039728	CG7896	Non_Synonymous_Coding
2L_13032229_INS	GG	G	G	0.078	10	119	2.280	3.91E-06	FBgn0262160	CG9932	Intron
2L_13032233_SNP	G	C	C	0.078	10	119	2.280	3.91E-06	FBgn0262160	CG9932	Intron
3L_10748779_SNP	T	A	A	0.057	7	116	2.791	4.01E-06			
2L_6149005_SNP	T	G	G	0.054	7	123	2.690	4.15E-06			
2R_9106136_SNP	T	G	G	0.062	8	122	2.529	4.30E-06	FBgn0033809	CG4630	Intron
2R_7921495_SNP	C	T	T	0.136	17	108	1.654	4.35E-06	FBgn0033677	CG8321	UTR_5_Prime
2R_7956219_SNP	C	T	T	0.148	19	109	1.595	4.37E-06	FBgn0033679	CG8888	Intron
3R_10597721_SNP	C	T	T	0.063	8	118	2.400	4.41E-06	FBgn0263929	jvl	Intron
3R_19409487_SNP	T	C	C	0.055	7	121	2.928	4.50E-06			

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
3R_26341348_SNP	A	G	G	0.094	12	116	2.225	4.51E-06	FBgn0039784	CG9698	Synonymous_Coding
3R_16597923_SNP	A	G	G	0.102	13	115	2.164	4.56E-06	FBgn0046689	Tak1	Synonymous_Coding
3R_11802097_SNP	G	T	T	0.110	14	113	1.916	4.59E-06	FBgn0022787	Hel89B	Intron
2L_2085036_SNP	T	G	G	0.050	6	114	2.762	4.61E-06	FBgn0053516	dpr3	Intron
3R_16736919_SNP	T	C	C	0.063	8	118	2.461	4.65E-06	FBgn0051191	CG31191	UTR_3_Prime
3L_15441280_SNP	G	C	C	0.063	8	120	2.469	4.80E-06			
2L_7767080_SNP	A	G	G	0.094	12	116	2.091	4.82E-06	FBgn0031945	CG7191	Upstream
3R_25731500_SNP	A	T	T	0.086	11	117	2.258	4.96E-06	FBgn0039719	CG15515	Intron
3R_25731563_SNP	A	G	G	0.086	11	117	2.254	5.03E-06	FBgn0039719	CG15515	Intron
3R_5353631_INS	AA	A	A	0.075	9	111	2.263	5.05E-06	FBgn0000244	by	Downstream
2R_3896083_SNP	A	G	A	0.312	39	86	1.238	5.05E-06	FBgn0013308	Odc2	Synonymous_Coding
3R_22151481_SNP	C	T	T	0.078	10	118	2.354	5.07E-06	FBgn0053970	CG33970	Intron
3R_20482598_SNP	T	A	A	0.079	10	117	2.314	5.13E-06	FBgn0039215	CG6695	Non_Synonymous_Coding
2L_8096740_SNP	T	C	C	0.113	14	110	1.901	5.14E-06	FBgn0261822	Bsg	Intron
2L_10133276_DEL	T	TA	TA	0.079	10	116	2.252	5.27E-06	FBgn0265002	CG44153	Intron
3R_20545307_SNP	A	T	T	0.062	8	121	1.971	5.29E-06	FBgn0004885	tok	Upstream
3L_15440832_SNP	G	A	A	0.054	7	122	2.618	5.50E-06			
2R_7956889_SNP	T	C	C	0.109	14	114	1.780	5.58E-06	FBgn0033679	CG8888	Intron
3R_11559634_SNP	T	G	G	0.055	7	120	2.553	5.68E-06			
3R_17478312_SNP	T	C	C	0.063	8	119	2.348	5.72E-06	FBgn0011766	E2f	Intron
3R_25731525_SNP	C	G	G	0.086	11	117	2.248	5.74E-06	FBgn0039719	CG15515	Intron
X_1951033_SNP	C	T	T	0.286	36	90	1.139	5.80E-06	FBgn0025625	Sik2	Non_Synonymous_Coding
3R_19175421_SNP	A	G	G	0.093	12	117	2.198	6.00E-06	FBgn0264326	DNApol-epsilon	Synonymous_Coding
2R_7969137_SNP	T	C	C	0.094	12	115	1.858	6.16E-06	FBgn0033680	CG13186	Synonymous_Coding
3L_5796941_SNP	A	T	T	0.086	11	117	2.156	6.17E-06	FBgn0259167	CG42272	Intron
2L_6102766_SNP	T	G	G	0.078	10	118	1.760	6.18E-06	FBgn0051641	stai	Intron
2L_12292571_SNP	G	C	C	0.054	7	122	2.561	6.25E-06	FBgn0000114	aret	Intron
2L_10558851_SNP	A	G	G	0.063	8	118	2.298	6.32E-06	FBgn0051721	Trim9	Intron
X_17926074_DEL	T	TTTCATATACT	TTTCATATACT	0.063	8	119	2.519	6.61E-06	FBgn0003380	Sh	Intron
3R_20336079_SNP	A	T	T	0.054	7	123	2.803	6.69E-06	FBgn0004118	nAcRbeta-96A	Intron
2L_9074827_SNP	A	G	G	0.054	7	122	2.600	6.69E-06			
3R_10622238_SNP	T	A	A	0.063	8	120	2.471	6.72E-06	FBgn0038260	CG14855	UTR_5_Prime
3L_9843580_SNP	C	T	T	0.094	12	116	1.976	6.78E-06	FBgn0004390	Gap1	Intron
3R_13807546_SNP	C	A	A	0.055	7	121	2.450	6.81E-06	FBgn0263995	cpo	Intron
3L_17005116_SNP	A	G	G	0.054	7	122	2.631	6.99E-06	FBgn0036684	CG3764	Start_Gained
2L_16519508_SNP	G	T	T	0.072	9	116	2.371	7.08E-06	FBgn0032587	CG5953	Intron
X_8539183_SNP	T	C	C	0.052	6	109	2.959	7.11E-06	FBgn0004102	oc	Intron
2L_6804613_SNP	A	G	G	0.062	8	121	2.448	7.11E-06	FBgn0031861	CG17375	Downstream
3R_11722005_SNP	G	A	A	0.078	10	118	2.160	7.14E-06	FBgn0027657	glob1	Downstream
3R_19175539_SNP	C	T	T	0.109	14	114	2.037	7.16E-06	FBgn0264326	DNApol-epsilon	Synonymous_Coding
3R_23817615_SNP	T	A	A	0.059	7	111	2.514	7.32E-06			
3R_18457165_DEL	T	TGTTT	TGTTT	0.079	10	116	2.244	7.38E-06	FBgn0020278	loco	Intron
2L_10060922_SNP	T	A	A	0.062	8	121	2.503	7.55E-06	FBgn0032178	Spn31A	UTR_5_Prime
2L_1184262_SNP	C	T	T	0.085	11	119	2.025	7.58E-06	FBgn0031321	Tgt	Intron
3R_10612592_SNP	G	A	A	0.206	26	100	1.263	7.64E-06	FBgn0263929	jvl	Intron
3L_10373527_DEL	T	TT	TT	0.065	8	116	2.333	7.70E-06			
2L_10153087_SNP	A	G	G	0.062	8	122	2.448	7.74E-06	FBgn0265002	CG44153	Intron
2R_18936168_SNP	G	A	A	0.051	6	112	2.704	7.75E-06	FBgn0003900	twi	Downstream
3L_5990467_SNP	G	A	A	0.109	14	115	1.802	7.79E-06	FBgn0052406	CG32406	UTR_5_Prime
3R_26750342_SNP	A	T	T	0.055	7	121	2.835	7.93E-06	FBgn0020912	Ptx1	Intron

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
X_4645752_SNP	A	C	C	0.079	10	116	2.078	8.07E-06			
2L_7768177_SNP	G	T	T	0.068	8	110	2.392	8.10E-06	FBgn0031945	CG7191	Intron
X_12495370_SNP	T	C	C	0.093	12	117	2.057	8.17E-06	FBgn0052654	Sec16	Intron
3R_25085669_SNP	G	A	A	0.118	15	112	1.966	8.22E-06			
3L_9843431_SNP	A	G	G	0.093	12	117	1.959	8.23E-06	FBgn0004390	Gap1	Intron
2R_8761585_SNP	T	G	G	0.057	7	116	2.815	8.30E-06	FBgn0263446	CR43469	Exon
3R_11930686_SNP	G	A	A	0.056	7	118	2.329	8.42E-06	FBgn0010379	Akt1	Downstream
2R_9142406_SNP	C	T	T	0.070	9	120	2.195	8.46E-06	FBgn0265443	CR44343	Exon
2R_2440093_SNP	A	C	C	0.054	7	122	2.568	8.63E-06	FBgn0086655	jing	Intron
3R_20527606_SNP	T	C	C	0.056	7	118	2.648	8.69E-06	FBgn0003429	slo	Intron
3R_25322718_SNP	A	G	A	0.070	9	119	2.509	8.70E-06	FBgn0039667	CG2010	Intron
2R_2428894_SNP	T	G	G	0.055	7	121	2.564	8.84E-06	FBgn0086655	jing	Intron
3R_11698322_SNP	C	T	T	0.054	7	122	2.432	8.88E-06			
2R_8546690_SNP	G	C	C	0.054	7	123	2.614	9.05E-06	FBgn0033763	CG8646	Non_Synonymous_Coding
3R_11147034_SNP	A	T	T	0.062	8	121	2.469	9.18E-06	FBgn0026441	ear	Intron
2L_1451509_SNP	T	C	C	0.054	7	123	2.717	9.30E-06			
X_1950522_SNP	C	G	G	0.444	55	69	1.033	9.30E-06	FBgn0025625	Sik2	Non_Synonymous_Coding
3R_11930826_SNP	G	A	A	0.065	8	116	1.860	9.46E-06	FBgn0010379	Akt1	Downstream
3R_11721999_SNP	T	C	C	0.087	11	116	2.035	9.48E-06	FBgn0027657	glob1	Downstream
3R_17317394_SNP	A	G	G	0.054	7	122	2.585	9.54E-06			
2L_7742981_SNP	T	C	C	0.054	7	123	2.722	9.57E-06	FBgn0031940	CG7214	Downstream
2L_7743053_SNP	C	T	T	0.054	7	123	2.722	9.57E-06	FBgn0031940	CG7214	Downstream
3R_11688605_SNP	A	G	A	0.125	16	112	1.697	9.60E-06	FBgn0051183	CG31183	Intron
3R_11274414_SNP	A	G	A	0.077	10	120	2.344	9.62E-06	FBgn0038341	CG14869	Synonymous_Coding
2L_9096570_SNP	G	A	A	0.070	9	120	2.225	9.88E-06			
3R_18882288_SNP	A	G	G	0.054	7	123	2.804	1.04E-05	FBgn0039045	CG17119	Intron
3L_10266913_SNP	G	A	A	0.054	7	123	2.593	1.08E-05	FBgn0036080	Or67d	Synonymous_Coding
3L_11238459_SNP	T	G	G	0.062	8	121	2.622	1.08E-05			
X_8199556_SNP	G	A	A	0.062	8	121	2.398	1.11E-05	FBgn0015519	nAcRalpha-7E	Intron
2R_2428434_SNP	T	G	G	0.054	7	122	2.565	1.11E-05	FBgn0086655	jing	Intron
2R_2428451_SNP	T	G	G	0.054	7	122	2.565	1.11E-05	FBgn0086655	jing	Intron
3L_9285052_SNP	T	A	T	0.066	8	114	2.457	1.14E-05			
3R_20467878_SNP	A	T	T	0.055	7	121	2.535	1.15E-05	FBgn0039214	CG5794	Intron
3R_11663755_SNP	C	T	T	0.079	10	117	2.185	1.22E-05	FBgn0003483	spn-E	Intron
2R_2438252_INS	TCAT	T	T	0.066	8	113	2.395	1.25E-05	FBgn0086655	jing	Intron
3R_18876184_SNP	G	T	T	0.054	7	123	2.758	1.26E-05	FBgn0039044	p53	Intron
2R_8547582_SNP	A	G	G	0.085	11	119	2.044	1.29E-05	FBgn0261673	nemy	Utr_3_Prime
X_16066818_SNP	T	A	T	0.085	11	118	2.076	1.29E-05			
3R_9025512_SNP	T	A	A	0.055	7	121	2.628	1.34E-05			
3R_21535093_SNP	G	C	C	0.055	7	121	2.789	1.38E-05	FBgn0051092	LpR2	Intron
X_3334548_SNP	G	A	A	0.063	8	120	2.283	1.39E-05	FBgn0029657	CG12535	Intron
3L_9821508_SNP	A	G	G	0.070	9	120	2.255	1.39E-05	FBgn0264489	CG43897	Intron
3R_21971128_SNP	G	A	A	0.143	18	108	1.735	1.41E-05			
3R_24026500_SNP	C	A	A	0.063	8	119	2.389	1.41E-05	FBgn0085383	CG34354	Intron
2L_17583852_SNP	G	C	C	0.070	9	119	2.250	1.43E-05			
3L_1393071_SNP	A	G	G	0.078	10	119	2.175	1.53E-05	FBgn0003138	Ptp61F	Intron
3R_25856271_SNP	T	C	C	0.065	8	115	2.594	1.55E-05	FBgn0026597	Axn	Intron
3R_11047599_SNP	C	T	C	0.054	7	122	2.572	1.60E-05	FBgn0038304	CG12241	Synonymous_Coding
3R_10612837_SNP	A	C	C	0.063	8	118	2.357	1.60E-05	FBgn0263929	jvl	Intron
3L_3799081_SNP	A	G	G	0.109	14	114	1.869	1.65E-05	FBgn0052264	CG32264	Intron

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
3R_19414936_SNP	C	T	T	0.070	9	119	2.480	1.67E-05	FBgn0039091	CG10182	Non_Synonymous_Coding
3L_6577170_SNP	A	C	C	0.054	7	123	2.599	1.72E-05	FBgn0042185	CG18769	Intron
3R_26291690_SNP	A	C	C	0.063	8	120	2.556	1.73E-05	FBgn0039776	PH4alphaEFB	Upstream
X_6975869_SNP	G	A	G	0.056	6	102	2.609	1.74E-05	FBgn0264270	Sxl	Intron
3R_19425198_SNP	T	C	C	0.055	7	120	2.736	1.78E-05	FBgn0039093	CG10183	Upstream
2L_2628495_SNP	A	G	G	0.109	14	115	1.703	1.78E-05			
3R_18573137_SNP	A	G	G	0.056	7	119	2.769	1.78E-05	FBgn0039020	CG17141	Synonymous_Coding
3R_18573138_SNP	C	T	T	0.056	7	119	2.769	1.78E-05	FBgn0039020	CG17141	Synonymous_Coding
3R_26341411_SNP	C	T	T	0.070	9	119	2.441	1.81E-05	FBgn0039784	CG9698	Synonymous_Coding
3R_26341423_SNP	C	G	G	0.070	9	119	2.441	1.81E-05	FBgn0039784	CG9698	Non_Synonymous_Coding
3R_16018269_SNP	T	A	A	0.087	11	115	2.093	1.84E-05			
2L_21221587_SNP	A	C	C	0.056	7	118	2.532	1.86E-05	FBgn0026577	CG8677	Synonymous_Coding
3R_18573126_SNP	C	T	T	0.063	8	118	2.622	1.88E-05	FBgn0039020	CG17141	Synonymous_Coding
2L_13032642_SNP	A	T	T	0.085	11	118	2.049	1.91E-05	FBgn0262160	CG9932	Intron
3L_15499752_SNP	C	T	T	0.063	8	119	2.393	1.92E-05	FBgn0036502	CG7841	Intron
2L_15841761_SNP	T	A	A	0.085	11	118	2.086	1.97E-05			
3R_21975013_SNP	T	C	C	0.054	7	123	2.602	2.00E-05			
X_16068830_SNP	G	T	G	0.087	11	115	2.037	2.01E-05			
2R_6630668_SNP	A	C	C	0.054	7	123	2.547	2.04E-05	FBgn0053144	CG33144	Intron
3R_16288512_SNP	G	A	A	0.055	7	120	2.677	2.07E-05	FBgn0263351	AP-50	Intron
3R_17704850_SNP	A	G	G	0.079	10	117	2.241	2.13E-05	FBgn0053092	P5CDh2	Synonymous_Coding
3R_13985682_SNP	T	A	A	0.055	7	121	2.762	2.43E-05	FBgn0038568	CG14315	Downstream
3R_16280217_SNP	A	T	T	0.054	7	122	2.724	2.45E-05	FBgn0262869	mun	Intron
3L_5354438_SNP	A	C	C	0.072	9	116	2.356	2.46E-05	FBgn0035600	CG4769	Intron
3L_9293237_INS	A	AA	A	0.065	8	115	2.383	2.46E-05			
2L_5493560_SNP	T	G	G	0.088	11	114	2.102	2.56E-05			
3R_14308152_SNP	A	G	G	0.075	8	98	2.531	2.60E-05	FBgn0004652	fru	Intron
3R_18366278_SNP	G	A	A	0.063	8	119	2.616	2.60E-05	FBgn0038983	CG5326	Upstream
3L_5354504_SNP	A	G	G	0.079	10	117	2.225	2.65E-05	FBgn0035600	CG4769	Intron
3L_5354506_SNP	T	A	A	0.079	10	117	2.225	2.65E-05	FBgn0035600	CG4769	Intron
2L_12270571_SNP	G	A	A	0.056	7	119	2.657	2.65E-05	FBgn0000114	aret	Intron
3R_25083337_SNP	C	A	A	0.118	15	112	1.876	2.96E-05			
3R_14308136_SNP	G	T	T	0.083	9	100	2.366	2.98E-05	FBgn0004652	fru	Intron
3R_14308138_SNP	T	G	G	0.083	9	100	2.366	2.98E-05	FBgn0004652	fru	Intron
2L_7767003_SNP	G	C	C	0.093	12	117	1.992	3.00E-05	FBgn0031945	CG7191	Upstream
2L_18338977_SNP	C	G	G	0.062	8	122	2.451	3.10E-05	FBgn0000636	Fas3	Intron
3R_13913033_SNP	A	C	C	0.063	8	120	2.462	3.12E-05			
3R_25083340_DEL	T	GAGGGGCCAGCGATCAGATG	GAGGGGCCAGCGATCAGATG	0.129	16	108	1.832	3.12E-05			
3R_13913027_SNP	A	G	G	0.062	8	121	2.459	3.14E-05			
3R_13913031_SNP	C	T	T	0.062	8	121	2.459	3.14E-05			
3R_10640029_SNP	T	C	C	0.087	11	116	2.041	3.29E-05	FBgn0264754	btsz	Intron
3R_26691944_SNP	A	C	A	0.150	19	108	1.694	3.30E-05			
3R_18902906_SNP	T	A	A	0.050	6	113	2.854	3.55E-05	FBgn0039054	CG13830	Intron
3R_18527884_SNP	A	G	G	0.085	11	118	2.102	3.55E-05	FBgn0039008	CG6972	UTR_5_Prime
3R_27096203_INS	TTCA	T	T	0.054	7	122	2.609	3.58E-05			
3R_27096207_DEL	A	ATTT	ATTT	0.054	7	122	2.609	3.58E-05			
3R_23124758_SNP	C	G	G	0.054	7	122	2.696	3.60E-05	FBgn0039510	CG3339	Intron
3R_23078524_SNP	G	T	T	0.112	14	111	1.852	3.67E-05	FBgn0010441	pll	Synonymous_Coding
X_17928044_SNP	C	G	G	0.070	9	119	2.224	3.77E-05	FBgn0003380	Sh	Intron
3R_19917168_INS	TGCCAAA	T	T	0.087	11	115	2.115	3.92E-05	FBgn0053100	4EHP	Intron

Table 4.S6 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1
3R_27069434_DEL	T	TCATCAGCATCAT	TCATCAGCATCAT	0.061	7	107	2.662	3.94E-05	FBgn0051005	<i>gless</i>	Intron
3R_19175562_SNP	C	T	T	0.116	15	114	1.835	4.28E-05	FBgn0264326	<i>DNApol-epsilon</i>	Synonymous_Coding
3R_19408401_SNP	G	A	A	0.063	8	120	2.497	4.48E-05			
3R_23310671_SNP	A	T	T	0.070	9	120	2.337	4.65E-05			
3R_25210392_SNP	T	A	A	0.063	8	120	2.386	4.67E-05	FBgn0004369	<i>Ptp99A</i>	Intron
3R_27124443_SNP	G	A	A	0.054	7	122	2.628	4.72E-05			
3R_26750310_SNP	C	G	G	0.062	8	121	2.540	4.72E-05	FBgn0020912	<i>Ptx1</i>	Intron
3R_26750338_SNP	T	A	A	0.062	8	121	2.540	4.72E-05	FBgn0020912	<i>Ptx1</i>	Intron
3R_26750350_DEL	T	TA	TA	0.062	8	121	2.540	4.72E-05	FBgn0020912	<i>Ptx1</i>	Intron
3R_26339196_INS	CGATAGTTTGA	C	C	0.063	8	119	2.429	4.86E-05	FBgn0051524	<i>CG31524</i>	Intron
3R_26341622_SNP	A	G	G	0.062	8	121	2.437	5.12E-05	FBgn0039784	<i>CG9698</i>	Synonymous_Coding
3R_17478419_DEL	T	TAGTTGT	TAGTTGT	0.055	7	121	2.651	5.15E-05	FBgn0011766	<i>E2f</i>	Intron
3R_13659502_INS	GAAC	G	G	0.055	7	121	2.612	5.29E-05	FBgn0261649	<i>tinc</i>	Intron
X_21119803_SNP	A	T	T	0.054	7	123	2.644	5.31E-05	FBgn0052521	<i>CG32521</i>	Intron
3R_13659506_SNP	C	T	T	0.055	7	120	2.615	5.34E-05	FBgn0261649	<i>tinc</i>	Intron
3R_17477793_SNP	T	A	A	0.054	7	123	2.657	5.37E-05	FBgn0011766	<i>E2f</i>	Intron
3R_17478089_SNP	T	C	C	0.054	7	123	2.657	5.37E-05	FBgn0011766	<i>E2f</i>	Intron
3R_17478456_SNP	A	G	G	0.054	7	123	2.657	5.37E-05	FBgn0011766	<i>E2f</i>	Intron
3R_17478458_SNP	G	A	A	0.054	7	123	2.657	5.37E-05	FBgn0011766	<i>E2f</i>	Intron
3R_17478495_SNP	A	C	C	0.054	7	123	2.657	5.37E-05	FBgn0011766	<i>E2f</i>	Intron
3R_13659496_DEL	G	GGGGG	GGGGG	0.055	7	120	2.609	5.47E-05	FBgn0261649	<i>tinc</i>	Intron
3R_17566236_SNP	T	C	T	0.066	11	117	2.132	5.68E-05	FBgn0038897	<i>CG5849</i>	Non_Synonymous_Coding
3R_18001996_INS	TT	T	T	0.071	9	118	2.272	5.69E-05	FBgn0051163	<i>SKIP</i>	Intron
3R_13659504_SNP	C	T	T	0.055	7	121	2.604	5.89E-05	FBgn0261649	<i>tinc</i>	Intron
3R_13659525_SNP	G	C	C	0.055	7	120	2.600	5.93E-05	FBgn0261649	<i>tinc</i>	Intron
3R_18359008_SNP	G	A	A	0.070	9	119	2.270	6.33E-05	FBgn0038983	<i>CG5326</i>	Intron
3R_18417140_SNP	T	C	C	0.079	10	116	2.213	6.50E-05	FBgn0051158	<i>Efa6</i>	Intron
3R_16745968_SNP	C	G	G	0.071	9	117	2.331	6.51E-05	FBgn0038842	<i>CG5630</i>	Intron
3L_11352423_SNP	C	T	T	0.069	9	121	2.294	6.52E-05			
3R_16989964_SNP	T	C	C	0.063	8	118	2.404	6.71E-05	FBgn0264357	<i>SNF4Agamma</i>	Intron
3R_19705667_DEL	A	AGGTATATTAC	AGGTATATTAC	0.055	7	120	2.609	6.90E-05	FBgn0025574	<i>Pli</i>	Intron
3R_16745956_SNP	G	C	C	0.071	9	118	2.327	6.94E-05	FBgn0038842	<i>CG5630</i>	Intron
3R_23124267_SNP	G	A	A	0.054	7	122	2.626	7.20E-05	FBgn0039510	<i>CG3339</i>	Intron
3R_24637066_SNP	T	G	G	0.055	7	120	2.618	7.27E-05	FBgn0005642	<i>wdn</i>	Upstream
X_21119512_SNP	T	A	A	0.070	9	120	2.316	7.71E-05	FBgn0052521	<i>CG32521</i>	Intron
3R_16620589_SNP	C	G	G	0.071	9	117	2.242	8.71E-05	FBgn0038826	<i>Syp</i>	Intron
2R_3678764_SNP	G	T	T	0.055	7	120	2.490	8.78E-05	FBgn0033222	<i>CG12824</i>	Downstream
3R_24636358_SNP	A	G	G	0.054	7	122	2.605	9.04E-05	FBgn0005642	<i>wdn</i>	Synonymous_Coding
3R_15852050_SNP	T	C	C	0.070	9	120	2.257	9.17E-05	FBgn0243511	<i>psidin</i>	UTR_3_Prime
3R_17883673_SNP	C	T	T	0.055	7	120	2.552	9.17E-05	FBgn0264491	<i>how</i>	Intron
3R_19414922_SNP	T	C	C	0.079	10	116	2.177	9.86E-05	FBgn0039091	<i>CG10182</i>	Synonymous_Coding
3R_16745829_SNP	A	T	T	0.070	9	119	2.287	9.90E-05	FBgn0038842	<i>CG5630</i>	Intron

Table 4.S7 - Genome-wide association analyses for recombination rate. Results from GWA on *e ro* data set of DGRP lines only with standard karyotypes.

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2
2R_3083775_SNP	T	C	C	0.055	6	104	2.922	7.20E-09	FBgn0003090	<i>pk</i>	Intron			
3R_22077370_SNP	T	C	C	0.057	6	99	2.875	1.49E-08	FBgn0261708	<i>CR42745</i>	Intron			
2R_2440093_SNP	A	C	C	0.054	6	105	2.786	4.17E-08	FBgn0086655	<i>jing</i>	Intron			
2R_2428894_SNP	T	G	G	0.055	6	104	2.782	4.45E-08	FBgn0086655	<i>jing</i>	Intron			
2R_2428434_SNP	T	G	G	0.054	6	105	2.762	5.76E-08	FBgn0086655	<i>jing</i>	Intron			
2R_2428451_SNP	T	G	G	0.054	6	105	2.762	5.76E-08	FBgn0086655	<i>jing</i>	Intron			
2R_6379425_SNP	T	C	C	0.054	6	106	2.755	6.13E-08	FBgn0005630	<i>lola</i>				
2R_2446238_SNP	C	T	T	0.055	6	103	2.743	7.42E-08	FBgn0086655	<i>jing</i>	Intron			
2L_2631679_SNP	T	C	C	0.093	10	98	2.162	8.17E-08			Intron			
3L_10077092_SNP	A	G	G	0.063	7	104	2.524	9.37E-08	FBgn0040823	<i>dpr6</i>				
2R_2428634_SNP	A	T	T	0.069	7	94	2.530	1.10E-07	FBgn0086655	<i>jing</i>	Intron			
2R_12259374_SNP	C	T	T	0.073	8	101	2.357	1.25E-07			Intron			
2R_2438252_INS	TCAT	T	T	0.067	7	98	2.507	1.43E-07	FBgn0086655	<i>jing</i>	Intron			
2R_2428764_SNP	A	G	G	0.063	7	105	2.497	1.49E-07	FBgn0086655	<i>jing</i>	Intron			
2R_2428935_SNP	A	G	G	0.063	7	105	2.497	1.49E-07	FBgn0086655	<i>jing</i>	Intron			
2R_2429479_SNP	T	A	A	0.063	7	105	2.497	1.49E-07	FBgn0086655	<i>jing</i>	Intron			
2R_2440017_SNP	T	A	A	0.063	7	105	2.497	1.49E-07	FBgn0086655	<i>jing</i>	Intron			
2R_2438246_DEL	C	CTATG	CTATG	0.065	7	100	2.501	1.51E-07	FBgn0086655	<i>jing</i>	Utr_3_Prime			
2R_2436436_SNP	A	G	G	0.055	6	103	2.666	1.81E-07	FBgn0086655	<i>jing</i>	Intron			
X_3789383_DEL	G	GTCGG	GTCGG	0.064	7	103	2.447	2.67E-07	FBgn0260658	<i>CG42541</i>	Intron			
2R_2434296_SNP	A	C	C	0.074	7	88	2.456	2.89E-07	FBgn0086655	<i>jing</i>				
3R_12715089_SNP	A	C	C	0.082	9	101	2.180	3.00E-07	FBgn0264857	<i>iab-8</i>	Intron			
2L_6550827_SNP	C	A	A	0.054	6	105	2.613	3.36E-07			Synonymous_Coding			
3L_4268715_SNP	C	T	T	0.054	6	105	2.613	3.47E-07	FBgn0035522	<i>CG1273</i>				
X_8951785_SNP	T	C	C	0.055	6	104	2.606	3.55E-07	FBgn0030077	<i>CG15365</i>				
3L_8201612_SNP	T	C	C	0.056	6	102	2.589	4.41E-07						
2L_2630015_SNP	T	A	A	0.108	12	99	1.868	4.63E-07						
2L_2630016_SNP	A	T	T	0.108	12	99	1.868	4.63E-07						
2L_2630028_SNP	A	G	G	0.108	12	99	1.868	4.63E-07						
2L_2630035_SNP	T	C	C	0.108	12	99	1.868	4.63E-07						
2R_6435234_SNP	G	T	T	0.063	7	104	2.396	5.57E-07						
3L_12308349_SNP	T	G	T	0.063	7	104	2.392	5.58E-07						
2L_2631465_INS	GGTA	G	G	0.100	11	99	1.947	5.67E-07						
2L_2632238_SNP	G	A	A	0.106	12	99	1.869	6.18E-07						
2L_2631753_SNP	T	A	A	0.107	12	100	1.864	6.47E-07			Intron			
2L_2631396_SNP	A	C	C	0.118	13	97	1.791	6.90E-07						
2R_2983325_SNP	C	T	T	0.054	6	106	2.552	7.22E-07	FBgn0263934	<i>esn</i>				
2L_2630019_SNP	G	C	C	0.108	12	99	1.831	8.08E-07			UTR_3_Prime			
2R_12259403_SNP	G	A	A	0.075	8	99	2.217	9.03E-07			Intron			
X_3789312_SNP	T	C	C	0.064	7	103	2.346	9.37E-07	FBgn0260658	<i>CG42541</i>	Intron			
X_3334548_SNP	G	A	A	0.063	7	104	2.336	9.99E-07	FBgn0029657	<i>CG12535</i>	Intron			
3L_4268808_SNP	G	A	A	0.063	7	105	2.345	1.01E-06	FBgn0035522	<i>CG1273</i>	Intron			
3L_4268986_SNP	T	C	C	0.063	7	105	2.345	1.01E-06	FBgn0035522	<i>CG1273</i>	Intron			
2R_2433735_SNP	A	C	C	0.054	6	105	2.518	1.03E-06	FBgn0086655	<i>jing</i>	Intron			
2R_2438717_SNP	A	C	C	0.054	6	105	2.518	1.03E-06	FBgn0086655	<i>jing</i>	Intron			
3L_4268783_SNP	A	G	G	0.063	7	104	2.332	1.18E-06	FBgn0035522	<i>CG1273</i>	Synonymous_Coding			
2R_12286274_DEL	C	CC	CC	0.056	6	102	2.499	1.42E-06	FBgn0264273	<i>Sema-2b</i>				
3L_8615825_SNP	T	C	C	0.073	8	102	2.174	1.56E-06	FBgn0035916	<i>GAPsec</i>		FBgn0052351	<i>S-Lap2</i>	Downstream
2L_14502808_SNP	T	A	A	0.082	9	101	2.053	1.64E-06			Intron			
2L_2630918_SNP	G	A	A	0.065	7	101	2.306	1.65E-06			Intron			

Table 4.S7 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
2L 9845842 SNP	A	G	G	0.091	10	100	1.946	1.72E-06	FBgn0032151	nAcRalpha-30D	Intron						
3L 1118802 SNP	G	A	A	0.068	7	96	2.310	1.76E-06	FBgn0036144	GlcAT-P	Intron						
3L 11189542 SNP	C	A	A	0.063	7	104	2.299	1.78E-06	FBgn0036144	GlcAT-P	Intron						
2R 17793282 SNP	T	G	G	0.055	6	103	2.466	1.82E-06	FBgn0085397	Fili							
2R 15014954 SNP	T	A	A	0.148	16	92	1.593	1.98E-06	FBgn0034417	CG15117							
2L 2630393 SNP	G	T	T	0.108	12	99	1.773	1.98E-06									
2L 2629729 SNP	G	T	T	0.125	14	98	1.658	2.02E-06									
2L 2629915 SNP	A	G	G	0.125	14	98	1.658	2.02E-06									
2L 2629944 SNP	T	C	C	0.125	14	98	1.658	2.02E-06			Downstream						
2R 17141219 SNP	A	G	G	0.055	6	104	2.450	2.04E-06			Non_Synonymous_Coding						
2L 7768066 SNP	C	G	G	0.054	6	106	2.446	2.05E-06	FBgn0031944	CG7196	Synonymous_Coding						
3R 26341342 SNP	T	A	A	0.065	7	101	2.294	2.05E-06	FBgn0039784	CG9598							
X 6184573 SNP	T	C	T	0.128	14	97	1.673	2.14E-06	FBgn0028685	Rpl4		FBgn0029858	CG15896	Upstream	FBgn0029857	wuho	Downstream
2L 2630567 SNP	A	G	G	0.108	12	99	1.765	2.20E-06			Non_Synonymous_Coding						
2L 2629410 SNP	T	C	C	0.125	14	98	1.652	2.23E-06									
2R 3896298 SNP	A	T	A	0.072	8	103	2.139	2.25E-06	FBgn0013308	Odc2		FBgn0033250	CG14762	Downstream			
2R 12259348 DEL	C	CTACTTGA	CTACTTGA	0.082	9	101	2.030	2.25E-06									
2R 12259372 INS	AACTCT	A	A	0.082	9	101	2.030	2.25E-06			Synonymous_Coding						
2R 12259378 MNP	TACAA	ATGTT	ATGTT	0.082	9	101	2.030	2.25E-06			UTR_3_Prime						
2L 7756793 SNP	C	T	T	0.054	6	105	2.438	2.32E-06	FBgn0031943	CG14538	Intron	FBgn0031944	CG7196	Intron			
2L 2620646 INS	ACGAGGG	A	A	0.073	8	101	2.124	2.41E-06	FBgn0263322	CG43403	Non_Synonymous_Coding						
X 3792171 SNP	C	G	G	0.072	8	103	2.129	2.44E-06	FBgn0260658	CG42641							
2L 13816432 SNP	A	G	A	0.065	7	100	2.267	2.49E-06	FBgn0001965	Sos							
2R 12259376 SNP	C	A	A	0.083	9	100	2.022	2.54E-06									
2R 8698450 SNP	A	C	C	0.138	15	94	1.602	2.56E-06									
2L 2630304 SNP	C	T	T	0.134	15	97	1.587	2.60E-06			Intron						
2L 2629929 SNP	C	T	T	0.109	12	98	1.753	2.72E-06									
2R 4891539 SNP	C	G	G	0.107	11	92	1.835	2.79E-06	FBgn0265011	Np	Intron						
2L 2627934 SNP	C	A	A	0.119	13	96	1.691	2.81E-06			Intron						
3L 1400394 SNP	G	A	A	0.064	7	103	2.269	2.95E-06	FBgn0003138	Ptp61F		FBgn0052320	CG32320	Intron			
X 16402126 SNP	A	T	T	0.080	9	103	2.001	2.97E-06	FBgn0264255	para	Synonymous_Coding						
2L 2631459 DEL	C	CCCG	CCCG	0.083	9	100	2.007	3.07E-06			Intron						
2L 5936570 SNP	A	G	G	0.123	13	93	1.702	3.13E-06	FBgn0015381	dsf							
3L 15538418 SNP	T	A	A	0.055	6	104	2.415	3.17E-06	FBgn0004396	CrebA	Intron						
2R 8698641 SNP	G	C	C	0.144	16	95	1.543	3.28E-06									
3L 10642942 SNP	T	G	T	0.054	6	105	2.414	3.36E-06	FBgn0052066	CG32066	Intron						
X 8549549 SNP	A	G	G	0.055	6	104	2.395	3.36E-06			Intron						
2L 2628668 SNP	A	T	T	0.135	15	96	1.582	3.44E-06									
2R 7795952 SNP	G	A	A	0.054	6	106	2.402	3.44E-06	FBgn0033667	CG13183	Intron						
2R 12259412 SNP	T	C	C	0.093	10	98	1.934	3.48E-06									
2R 14913892 SNP	T	C	C	0.055	6	104	2.394	3.66E-06	FBgn0263116	5-HT1B							
2L 2628019 SNP	C	A	A	0.118	13	97	1.673	3.69E-06									
2R 12259391 SNP	A	T	T	0.092	10	99	1.899	3.69E-06									
2R 12259420 SNP	T	A	A	0.092	10	99	1.899	3.69E-06			Non_Synonymous_Coding						
2R 12259422 SNP	G	C	C	0.092	10	99	1.899	3.69E-06									
3R 14236729 SNP	C	A	A	0.055	6	103	2.394	3.72E-06	FBgn0038621	CG10864	Intron	FBgn0051122	CG31122	Intron			
2R 12259334 SNP	A	C	C	0.090	10	101	1.896	3.75E-06									
3L 11190112 SNP	T	G	G	0.063	7	104	2.232	3.78E-06	FBgn0036144	GlcAT-P							
2R 12259385 SNP	C	G	G	0.091	10	100	1.895	3.83E-06									
2R 12259393 INS	TTTTCC	A	A	0.091	10	100	1.895	3.83E-06									

Table 4.S7 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2
2R_12259398_SNP	A	T	T	0.091	10	100	1.895	3.83E-06			Intron			
2R_12259400_INS	GC	T	T	0.091	10	100	1.895	3.83E-06			Intron			
2R_12259415_SNP	T	A	A	0.091	10	100	1.895	3.83E-06			Intron			
2L_7997242_SNP	C	A	A	0.054	6	106	2.391	3.88E-06	FBgn0031970	CG7227	Intron			
3L_11188618_SNP	T	G	G	0.077	8	96	2.103	3.93E-06	FBgn0036144	GlcAT-P	Downstream			
2L_9877404_SNP	A	T	T	0.100	11	99	1.817	3.95E-06	FBgn0032151	nAcRalpha-30D				
X_2472342_SNP	C	A	A	0.135	15	96	1.577	4.08E-06	FBgn0040377	Vha36-3	Synonymous_Coding			
2L_2632099_SNP	A	G	G	0.118	13	97	1.674	4.12E-06						
X_12948230_SNP	T	G	G	0.063	7	104	2.220	4.16E-06	FBgn0030443	CG12715	Non_Synonymous_Coding	FBgn0261388	CG42629	Intron
2R_12259409_SNP	T	C	C	0.092	10	99	1.887	4.33E-06			Intron			
2L_16334771_SNP	G	A	G	0.072	8	103	2.077	4.34E-06	FBgn0028899	CG31817				
X_9375782_SNP	A	C	C	0.080	9	103	1.971	4.34E-06	FBgn0261260	mgl	Intron			
2R_12259414_SNP	G	A	A	0.093	10	98	1.884	4.51E-06			Downstream			
3L_1472460_SNP	A	G	G	0.055	6	104	2.374	4.60E-06	FBgn0003138	Ptp61F	Downstream	FBgn0052319	CG32319	Upstream
X_2471704_SNP	T	G	G	0.156	14	76	1.645	4.66E-06	FBgn0260753	Pdfr	Intron			
X_3788204_SNP	T	A	A	0.073	8	101	2.070	4.79E-06	FBgn0260658	CG42541				
3R_14654080_SNP	C	T	C	0.064	7	103	2.199	4.90E-06	FBgn0038653	CG18208	Intron			
3R_9651135_SNP	C	A	A	0.050	5	95	2.595	5.03E-06			Downstream			
3R_23142479_SNP	C	T	T	0.073	8	102	2.051	5.19E-06	FBgn0039510	CG3339				
2R_8695816_SNP	C	T	T	0.144	16	95	1.510	5.28E-06	FBgn0040755	CG17580	Intron			
3R_9651129_SNP	G	T	T	0.054	5	88	2.591	5.34E-06			Downstream			
X_7060779_SNP	T	G	G	0.058	6	97	2.336	5.54E-06	FBgn0029939	CG9650	Intron			
3L_11190959_SNP	G	A	A	0.075	8	99	2.067	5.65E-06	FBgn0036147	Plod	Intron	FBgn0036144	GlcAT-P	Upstream
X_14638074_SNP	G	A	A	0.083	9	100	1.909	5.78E-06	FBgn0015774	NetB	Intron			
2R_5511749_SNP	C	T	T	0.054	6	105	2.349	5.79E-06	FBgn0033438	Mmp2				
2R_2424152_SNP	C	T	T	0.054	6	106	2.353	5.89E-06	FBgn0086655	jing	Intron			
2R_12259423_SNP	T	C	C	0.100	11	99	1.783	5.97E-06			Downstream			
3L_2384202_SNP	T	G	G	0.083	9	100	1.926	6.06E-06	FBgn0035338	CG13800		FBgn0261551	CG42669	Intron
3L_4161537_SNP	A	T	T	0.059	6	95	2.350	6.20E-06	FBgn0011653	mas		FBgn0259986	nab	Upstream
3R_9651136_SNP	T	G	G	0.050	5	95	2.570	6.31E-06						
3R_6256029_SNP	G	T	T	0.054	6	105	2.346	6.33E-06			Downstream			
2L_2631452_SNP	T	C	C	0.099	11	100	1.779	6.35E-06			Intron			
2R_18174104_SNP	A	T	T	0.055	6	104	2.325	6.39E-06	FBgn0020307	dve	Intron			
3L_11187341_SNP	A	G	G	0.072	8	103	2.052	6.40E-06	FBgn0036144	GlcAT-P	Non_Synonymous_Coding			
3L_7010755_SNP	C	A	A	0.080	9	103	1.929	6.40E-06	FBgn0260680	mp	Intron			
2L_17133747_SNP	A	G	G	0.063	7	105	2.174	6.52E-06	FBgn0032627	beat-IIIa	Intron			
X_2391062_SNP	A	G	G	0.100	11	99	1.770	6.54E-06	FBgn0261451	trol	Synonymous_Coding			
2R_18600896_SNP	C	G	G	0.063	7	104	2.180	6.67E-06	FBgn0050268	CG30268	Downstream	FBgn0050275	CG30275	Downstream
3L_11196163_SNP	A	C	C	0.055	6	104	2.345	6.78E-06	FBgn0036147	Plod	Intron	FBgn0036146	CG14141	Downstream
2R_18174137_SNP	T	A	A	0.055	6	103	2.319	6.78E-06	FBgn0020307	dve	Upstream			
3L_11188458_SNP	C	T	T	0.071	8	104	2.047	6.88E-06	FBgn0036144	GlcAT-P	Upstream			
3L_11190895_SNP	T	A	A	0.071	8	104	2.047	6.88E-06	FBgn0036144	GlcAT-P	UTR_3_Prime	FBgn0036147	Plod	Downstream
3L_11190907_SNP	T	C	C	0.071	8	104	2.047	6.88E-06	FBgn0036144	GlcAT-P	Intron	FBgn0036147	Plod	Downstream
3L_11191270_SNP	A	T	T	0.071	8	104	2.047	6.88E-06	FBgn0036147	Plod	Intron	FBgn0036144	GlcAT-P	Upstream
2L_11866130_SNP	G	T	T	0.063	7	104	2.174	6.91E-06	FBgn0264815	Pde1c	Non_Synonymous_Coding			
3L_3800198_SNP	G	T	T	0.056	6	102	2.323	7.28E-06	FBgn0052264	CG32264	Intron			
3L_15494228_SNP	C	A	A	0.063	7	104	2.159	7.46E-06	FBgn0036501	CG7272	UTR_3_Prime	FBgn0036500	CG7275	Downstream
2L_9845069_SNP	A	G	G	0.055	6	103	2.314	7.63E-06	FBgn0032151	nAcRalpha-30D	Intron			
X_3789558_SNP	T	C	C	0.080	9	103	1.920	7.82E-06	FBgn0260658	CG42541				
3L_11190593_SNP	A	T	T	0.072	8	103	2.035	7.87E-06	FBgn0036144	GlcAT-P	Synonymous_Coding	FBgn0036147	Plod	Downstream

Table 4.S7 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3	Flybase ID Gene 4	Gene Name 4	Site Class 4
2R_6435436_SNP	T	C	C	0.054	6	105	2.315	8.05E-06			Upstream									
3R_26341348_SNP	A	G	G	0.082	9	101	1.933	8.07E-06	FBgn0039784	CG9698	Intron									
3L_11190896_SNP	A	T	T	0.072	8	103	2.032	8.15E-06	FBgn0036144	GlcAT-P		FBgn0036147	Piod	Downstream						
X_21150503_SNP	G	A	A	0.073	8	101	2.018	8.21E-06	FBgn0052521	CG32521	Synonymous_Coding									
2R_14092017_SNP	T	C	C	0.054	6	106	2.315	8.35E-06			Downstream									
3R_11687896_SNP	T	G	G	0.054	6	105	2.327	8.52E-06	FBgn0051183	CG31183	Intron	FBgn0038377	CG9632	Downstream						
2R_8696088_SNP	A	C	C	0.162	18	93	1.409	8.66E-06	FBgn0040755	CG17580	Intron									
2L_12611769_SNP	T	C	C	0.054	6	106	2.308	8.66E-06	FBgn0032439	Ref2	Downstream	FBgn0085424	nub	Intron						
2R_9538327_INS	TT	T	T	0.054	6	105	2.313	8.70E-06	FBgn0006333	fas	Intron									
X_3784535_SNP	A	T	T	0.083	7	105	2.140	8.97E-06	FBgn0029881	CG15239	Intron	FBgn0260658	CG42541	Downstream						
2L_9841599_SNP	T	G	G	0.067	7	98	2.150	8.96E-06	FBgn0032151	nAcRajpha-30D										
3L_1456802_SNP	T	C	C	0.055	6	103	2.308	9.01E-06	FBgn0003138	Ptp61F	Synonymous_Coding									
2L_12576177_SNP	T	C	C	0.054	6	106	2.305	9.02E-06			UTR_5_Prime									
3L_15497527_SNP	A	G	G	0.055	6	104	2.301	9.12E-06	FBgn0026738	CG7857	Intron	FBgn0036501	CG7272	Downstream	FBgn0036502	CG7841	Downstream			
3R_14913855_INS	GA	G	G	0.125	13	91	1.634	9.22E-06	FBgn0004876	cdi	Intron									
2R_17095944_SNP	G	C	C	0.064	7	103	2.149	9.29E-06	FBgn0265180	CG44245	Intron	FBgn0265191	Glycogenin	Intron						
3R_12710178_SNP	T	G	G	0.234	25	82	1.248	9.32E-06	FBgn0264857	ab-8	Intron									
2R_17098758_SNP	T	A	A	0.092	10	99	1.824	9.32E-06	FBgn0265180	CG44245	Intron	FBgn0265191	Glycogenin	Intron						
3L_11190111_SNP	T	G	G	0.063	7	104	2.145	9.84E-06	FBgn0036144	GlcAT-P	Intron									
3L_11190114_DEL	A	AG	AG	0.063	7	104	2.145	9.84E-06	FBgn0036144	GlcAT-P										
3L_11187357_SNP	G	C	C	0.080	9	103	1.908	9.85E-06	FBgn0036144	GlcAT-P	Non_Synonymous_Coding									
2R_15979607_SNP	T	C	C	0.081	9	102	1.904	9.89E-06			Intron									
2R_19488144_SNP	A	T	A	0.373	41	89	1.080	9.93E-06	FBgn0260761	CG42559	Intron	FBgn0067903	IM18	Downstream	FBgn0260455	CG10332	Downstream	FBgn0260762	CG42560	Upstream
2L_12359168_SNP	A	T	T	0.127	14	96	1.565	1.14E-05	FBgn0262475	bru-2	Intron									
3R_25965841_SNP	A	G	G	0.063	7	104	2.143	1.31E-05	FBgn0039747	AdoR	Intron									

Table 4.S8 - Genome-wide association analyses for recombination rate. Results from GWA on γ ν data set including all DGRP lines.

ρ	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
3L 16120637 SNP	G	C	C	0.149	29	186	1.658	3.89E-09									
3L 16978669 SNP	T	C	C	0.056	11	187	2.460	3.89E-07	FBgn0261547	<i>Exn</i>	Synonymous_Coding						
3L 16977837 SNP	G	A	A	0.056	11	186	2.465	4.53E-07	FBgn0261547	<i>Exn</i>	Intron						
2R 15938306 SNP	G	A	A	0.051	10	187	2.381	1.48E-06									
3R 15261408 SNP	A	T	T	0.055	10	172	2.495	2.00E-06	FBgn0051221	<i>CG31221</i>	Intron						
3R 15071916 SNP	A	T	T	0.242	44	138	1.200	2.57E-06	FBgn0038693	<i>unc79</i>	Upstream	FBgn0038694	<i>CG5217</i>	Downstream			
3R 15071915 SNP	T	C	C	0.245	45	139	1.178	2.96E-06	FBgn0038693	<i>unc79</i>	Upstream	FBgn0038694	<i>CG5217</i>	Downstream			
3L 13494037 SNP	G	A	A	0.061	12	186	2.019	3.41E-06	FBgn0036373	<i>CG10741</i>	Synonymous_Coding						
3L 19642073 SNP	G	C	C	0.070	13	174	-1.922	3.54E-06	FBgn0022774	<i>Oat</i>	Intron						
3L 7433675 SNP	C	G	G	0.106	21	178	1.810	3.78E-06	FBgn0259935	<i>CG42458</i>	Intron	FBgn0052382	<i>sphinx2</i>	Synonymous_Coding			
2L 13145874 SNP	T	C	C	0.420	76	105	-0.942	3.84E-06	FBgn0265088	<i>CR44199</i>	Upstream						
3L 1575811 SNP	A	C	C	0.085	17	184	1.608	4.08E-06	FBgn0035236	<i>CG12004</i>	Downstream	FBgn0035237	<i>CG13917</i>	Upstream			
3R 24845220 SNP	C	A	A	0.056	11	187	2.139	4.25E-06	FBgn0039620	<i>CG14443</i>	Intron						
3L 10065561 INS	AGCA	A	A	0.453	73	88	1.072	4.39E-06	FBgn0040823	<i>dpr6</i>	Downstream						
3L 16975214 SNP	G	A	A	0.050	10	190	2.317	4.72E-06	FBgn0261547	<i>Exn</i>	Synonymous_Coding						
X 12693381 SNP	A	T	A	0.175	35	165	-1.258	4.82E-06	FBgn0259171	<i>Pde9</i>	Intron						
2L 16532600 SNP	T	A	A	0.085	17	184	1.768	5.31E-06	FBgn0032587	<i>CG5953</i>	Intron						
2L 16532629 SNP	T	A	A	0.085	17	184	1.768	5.31E-06	FBgn0032587	<i>CG5953</i>	Intron						
3L 7501169 SNP	C	T	T	0.133	26	169	-1.413	5.40E-06									
X 10214530 SNP	A	G	G	0.055	11	189	2.116	5.50E-06	FBgn0259170	<i>alpha-Man-I</i>	Intron						
2L 16532387 SNP	A	C	C	0.089	13	175	2.071	6.41E-06	FBgn0032587	<i>CG5953</i>	Intron						
2L 1232314 SNP	A	G	G	0.059	11	177	2.363	6.63E-06									
3L 15938386 SNP	A	T	T	0.437	76	98	-1.073	7.18E-06	FBgn0000489	<i>Pka-C3</i>	Intron						
X 22115765 SNP	G	T	T	0.406	78	114	-1.022	7.20E-06									
2L 16391005 SNP	C	T	T	0.055	11	189	2.243	7.47E-06									
2R 18449694 SNP	T	G	G	0.135	26	167	1.380	7.64E-06	FBgn0034737	<i>CG11362</i>	Upstream	FBgn0003175	<i>px</i>	Upstream	FBgn0260866	<i>dnr1</i>	Downstream
2L 14438128 SNP	A	C	C	0.108	20	166	1.654	8.18E-06									
3R 11661615 SNP	C	T	T	0.106	20	169	1.691	8.20E-06	FBgn0017567	<i>ND23</i>	Downstream	FBgn0038389	<i>Arpc3A</i>	Downstream	FBgn0263525	<i>mir-4911</i>	Downstream
3L 1092924 SNP	T	C	C	0.064	13	189	2.079	8.52E-06	FBgn0004870	<i>bab1</i>	Intron						
2R 18449606 SNP	C	T	T	0.114	21	163	1.507	9.57E-06	FBgn0003175	<i>px</i>	Upstream	FBgn0034737	<i>CG11362</i>	Upstream			
2L 14509653 SNP	T	A	A	0.071	14	183	1.907	9.93E-06									
2R 10204647 SNP	A	G	G	0.061	12	186	2.191	1.22E-05	FBgn0085408	<i>Shroom</i>	Intron						
2L 20846741 SNP	T	G	G	0.124	23	162	1.655	1.23E-05	FBgn0051676	<i>CG31676</i>	Intron						
X 15026189 DEL	A	AAATTCT	AAATTCT	0.051	10	186	2.396	1.43E-05	FBgn0260006	<i>drd</i>	Intron						
2L 20568316 SNP	T	C	C	0.290	63	130	-1.116	1.57E-05									
2L 9357251 SNP	A	G	G	0.069	13	175	2.011	1.73E-05									
3R 18720166 SNP	C	G	G	0.152	30	167	1.409	1.85E-05									
2R 869699 SNP	A	G	G	0.141	27	164	1.500	3.10E-05	FBgn0040849	<i>Ir41a</i>	Intron						
2L 16330391 SNP	G	A	A	0.082	16	179	1.921	5.41E-05	FBgn0040984	<i>CG4440</i>	Non_Synonymous_Coding	FBgn0028899	<i>CG31817</i>	Downstream	FBgn0001995	<i>mRpL4</i>	Upstream
2L 16370516 SNP	C	G	G	0.195	37	153	1.306	6.51E-05									

Table 4.S9 - Genome-wide association analyses for recombination rate. Results from GWA on γ ν data set excluding DGRP lines with any polymorphic inversions.

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3	Flybase ID Gene 4	Gene Name 4	Site Class 4
3L 18120637 SNP	G	C	C	0.170	25	122	1.964	8.85E-10												
2R 11639518 SNP	A	C	C	0.107	16	133	2.092	2.69E-07	FBgn0050089	CG30089	Intron									
2L 9357251 SNP	A	G	G	0.063	9	134	2.777	4.57E-07												
X 22227370 SNP	T	G	G	0.095	14	134	2.225	5.71E-07	FBgn0000719	fog	Downstream									
X 5894773 SNP	T	C	C	0.053	8	142	2.873	8.78E-07	FBgn0027546	CG4766	UTR_5_Prime									
2R 4527850 SNP	T	G	G	0.090	13	132	2.219	1.27E-06												
2L 1232314 SNP	A	G	G	0.069	10	134	2.565	1.59E-06												
X 2676643 SNP	G	A	A	0.214	28	103	1.886	1.76E-06	FBgn0028369	kirre	Intron	FBgn0040384	CG32795	Downstream						
2L 16540093 SNP	T	G	G	0.101	15	134	1.960	1.90E-06												
2R 17323905 SNP	A	T	T	0.054	8	141	2.672	2.23E-06	FBgn0034622	CG15666	Synonymous_Coding									
2R 17681123 SNP	A	C	A	0.164	24	122	1.821	3.29E-06	FBgn0034659	CG4021	Intron									
3L 10022098 SNP	T	C	C	0.074	11	137	2.451	2.47E-06	FBgn0040823	dpn6	Intron									
X 22220180 SNP	A	T	T	0.060	9	140	2.604	2.64E-06												
3L 18135807 SNP	A	C	C	0.120	18	132	1.836	3.21E-06	FBgn0020300	pk	Intron									
2L 16532600 SNP	T	A	A	0.114	17	132	1.823	3.29E-06	FBgn0032587	CG5953	Intron									
2L 16532629 SNP	T	A	A	0.114	17	132	1.823	3.29E-06	FBgn0032587	CG5953	Intron									
2R 17232208 SNP	C	G	G	0.074	11	137	2.315	3.29E-06	FBgn0034622	CG15666	Intron									
2R 15936308 SNP	G	A	A	0.062	9	137	2.511	3.62E-06												
2L 16532387 SNP	A	C	C	0.092	13	128	2.093	3.67E-06	FBgn0032587	CG5953	Intron									
2L 1286196 SNP	G	C	C	0.061	9	138	2.528	4.03E-06	FBgn0041097	robo3	Synonymous_Coding									
3L 444413 SNP	T	A	A	0.074	11	136	2.328	4.04E-06	FBgn0001316	klar	Intron									
2L 16540148 SNP	G	A	A	0.096	14	132	1.969	4.11E-06												
3L 1433675 SNP	C	G	G	0.107	16	133	1.914	4.16E-06	FBgn0259935	CG42458	Intron	FBgn0052382	sphinx2	Synonymous_Coding						
2R 17376470 SNP	T	A	A	0.061	9	139	2.535	4.19E-06	FBgn0010470	Fkbp13	Intron									
2L 10472225 SNP	A	G	G	0.053	8	142	2.675	4.50E-06	FBgn0051719	RluA-1	Intron									
2L 18661173 SNP	G	A	A	0.239	33	105	1.499	4.68E-06	FBgn0003896	tup	Synonymous_Coding									
2L 16540258 SNP	G	T	T	0.129	19	126	1.749	5.00E-06												
2L 16391005 SNP	C	T	T	0.074	11	138	2.265	5.14E-06												
3L 5138344 SNP	T	G	G	0.054	8	139	2.575	5.37E-06	FBgn0035588	CG10671	Synonymous_Coding	FBgn0028962	Aats-ala-m	Upstream	FBgn0035587	CG4623	Downstream			
2R 4527815 SNP	C	T	T	0.081	12	136	2.257	5.48E-06												
2L 13142458 SNP	T	G	G	0.053	8	142	2.538	5.49E-06	FBgn0032472	CG9928	Downstream	FBgn0040972	CG16978	Downstream						
2L 18647760 SNP	C	G	G	0.083	12	133	2.281	5.90E-06	FBgn0032694	MESR3	Intron									
X 22227618 SNP	T	G	G	0.081	12	137	2.210	6.20E-06	FBgn0000719	fog	Downstream									
3L 1452328 SNP	G	T	T	0.103	15	130	2.015	6.74E-06	FBgn0003138	Ptp61F	Intron									
3L 17937317 SNP	A	T	T	0.463	63	73	1.251	6.79E-06	FBgn0262793	CG43174	Intron									
3L 13494037 SNP	G	A	A	0.054	8	139	2.409	6.97E-06	FBgn0036373	CG10741	Synonymous_Coding									
3R 10743458 SNP	T	G	G	0.054	8	140	2.538	8.16E-06	FBgn0038279	CG3837	Upstream									
2L 6712509 SNP	T	G	G	0.060	9	140	2.460	8.16E-06	FBgn0025595	GFRHR	Non_Synonymous_Coding									
2L 16330091 SNP	G	A	A	0.095	14	134	2.211	8.30E-06	FBgn0040984	CG4440	Non_Synonymous_Coding	FBgn0028899	CG31817	Downstream	FBgn0001995	mRpl4	Upstream			
2L 15831368 SNP	A	G	G	0.171	25	121	1.549	8.36E-06	FBgn0028518	CG18480	Synonymous_Coding									
2L 15831374 SNP	T	A	A	0.171	25	121	1.549	8.36E-06	FBgn0028518	CG18480	Synonymous_Coding									
3L 19280879 SNP	G	C	C	0.068	10	136	2.336	8.45E-06	FBgn0038857	CG9629	Synonymous_Coding	FBgn0036856	CG9666	Downstream	FBgn00259720	CG42374	Downstream			
2L 18914365 DEL	A	ACAAAAGTGCTTTAA	ACAAAAGTGCTTTAA	0.054	8	141	2.741	8.74E-06												
2L 18914393 DEL	T	TCTC	TCTC	0.054	8	141	2.741	8.74E-06												
2L 15907762 SNP	G	A	A	0.124	18	127	1.862	9.62E-06	FBgn0028645	beat-lb	Intron									
X 12494836 SNP	C	T	T	0.088	13	134	2.033	9.69E-06	FBgn0052654	Sec16	Intron									
X 16602847 SNP	A	G	G	0.094	14	135	1.803	9.72E-06	FBgn0030778	CG4678	Intron									
X 16602868 SNP	T	G	G	0.094	14	135	1.803	9.72E-06	FBgn0030778	CG4678	Intron									
2L 18914636 SNP	C	T	T	0.055	8	137	2.539	9.85E-06												
3L 16975214 SNP	G	A	A	0.054	8	141	2.607	1.05E-05	FBgn0261547	Exn	Synonymous_Coding									
X 1198690 SNP	A	G	G	0.088	13	135	2.132	1.09E-05	FBgn0025641	DAAM	Intron									
2R 5939839 INS	T	TAATGTTT	T	0.062	9	137	2.504	1.17E-05	FBgn0263280	sef	Upstream	FBgn0262169	magu	Upstream	FBgn0265343	CR44297	Downstream			
X 10315996 SNP	G	A	A	0.054	8	140	2.811	1.55E-05	FBgn0052683	CG32683	Intron									
3L 17950305 SNP	A	G	G	0.054	8	140	2.894	2.00E-05	FBgn0003568	Eip75B	Intron									
3R 17624832 DEL	G	GCAGAAAG	GCAGAAAG	0.061	9	139	2.452	3.70E-05	FBgn0013759	CASK	Intron	FBgn0263521	mir-4969	Upstream	FBgn0262331	mir-999	Upstream	FBgn0265344	CR44298	Downstream

Table 4.S10 - Genome-wide association analyses for recombination rate. Results from GWA on γ ν data set of DGRP lines only with standard karyotypes.

ρ	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2
2L 18647760 SNP	C	G	G	0.065	9	97	3.020	7.02E-08	FBgn0032694	MESR3	Intron			
2R 12634181 SNP	G	A	A	0.130	14	94	2.369	7.39E-08	FBgn0034151	CG15617	Upstream			
X 5399055 SNP	T	C	C	0.054	6	105	3.596	8.13E-08						
X 5399072 SNP	C	T	T	0.054	6	105	3.596	8.13E-08						
2L 16391005 SNP	C	T	T	0.073	8	102	3.095	9.99E-08						
3R 25440527 SNP	C	T	T	0.054	6	105	3.435	2.29E-07	FBgn0086361	alph	Intron			
2R 12634200 SNP	T	A	A	0.103	11	96	2.590	2.92E-07	FBgn0034151	CG15617	Upstream			
3L 18135786 DEL	T	TAAGAAATATATCTAT	TAAGAAATATATCTAT	0.129	12	81	2.504	3.09E-07	FBgn0020300	gk	Intron			
2L 16390942 SNP	G	T	T	0.063	7	104	3.189	3.79E-07						
2L 9357251 SNP	A	G	G	0.057	6	100	3.328	7.63E-07						
X 7870060 SNP	T	G	G	0.055	6	103	3.309	9.42E-07	FBgn0003447	sn	Intron			
2R 414917 SNP	G	A	A	0.065	7	101	2.899	1.03E-06						
2R 493011 SNP	C	G	G	0.065	7	101	2.899	1.03E-06	FBgn0280799	p120ctn	Intron			
2L 4275126 DEL	G	GTTTTCCCAACTACACGACTCGGTGTGCCCG	GTTTTCCCAACTACACGACTCGGTGTGCCCG	0.086	9	96	2.754	1.05E-06						
X 21125921 SNP	A	C	C	0.050	5	95	3.581	1.05E-06	FBgn0052521	CG32521	Intron			
2L 1268197 SNP	G	T	T	0.056	6	104	3.278	1.26E-06	FBgn0041097	robo3	Intron			
2R 13624433 SNP	C	G	C	0.102	11	97	2.377	1.46E-06	FBgn0034269	CG6406	Synonymous_Coding	FBgn0034270	CG6401	Downstream
3R 15261513 SNP	G	A	A	0.055	6	104	3.340	1.53E-06	FBgn0051221	CG31221	Intron			
2L 12965028 SNP	A	G	G	0.054	6	105	3.255	1.65E-06						
3L 18135807 SNP	A	C	C	0.108	12	99	2.353	1.69E-06	FBgn0020300	gk	Intron			
2R 803479 SNP	T	A	T	0.075	8	98	2.855	1.72E-06						
X 2884587 SNP	A	C	C	0.050	5	95	3.629	1.77E-06	FBgn0003285	rst	Intron	FBgn0028369	kirre	Intron
2L 3395090 SNP	C	T	T	0.055	6	103	3.215	1.93E-06						
3L 9418900 SNP	A	G	G	0.076	7	85	2.981	2.36E-06	FBgn0035989	CG3967	Intron			
2R 11618503 SNP	T	G	T	0.064	7	103	2.993	2.49E-06	FBgn0050089	CG30089	Intron			
2R 16325227 SNP	A	G	G	0.064	7	102	2.914	2.65E-06	FBgn0086604	CG12484	Intron			
3R 25337142 SNP	C	G	G	0.091	10	100	2.476	2.67E-06						
3L 18118614 DEL	A	AG	AG	0.137	14	88	2.171	2.73E-06						
2R 683700 SNP	G	C	C	0.056	6	102	3.179	2.73E-06						
2R 3237186 SNP	A	C	C	0.055	6	104	3.179	2.92E-06	FBgn0033159	Discam	Intron			
2R 865750 SNP	A	T	T	0.055	6	103	3.181	3.00E-06	FBgn0040849	Ir41a	Intron			
2R 18191946 SNP	A	G	G	0.138	15	94	2.074	3.13E-06	FBgn0034500	CG11200	Downstream			
2R 11621660 DEL	TCATGTT	T	TCATGTT	0.056	6	101	2.337	3.16E-06	FBgn0050089	CG30089	Intron			
X 7889864 SNP	G	A	A	0.063	7	104	2.895	3.36E-06	FBgn0003447	sn	Intron			
3L 13494037 SNP	G	A	A	0.065	7	101	2.720	3.48E-06	FBgn0036373	CG10741	Synonymous_Coding			
2R 844680 SNP	G	T	T	0.062	6	91	3.175	3.78E-06	FBgn0040849	Ir41a	Intron			
X 17678782 INS	AACCCCCCCCCCCC	A	A	0.051	5	93	3.423	3.78E-06						
2L 1267152 SNP	T	G	G	0.055	6	104	3.165	3.97E-06	FBgn0041097	robo3	Intron			
3R 24845220 SNP	C	A	A	0.064	7	103	2.673	4.22E-06	FBgn0039620	CG1443	Intron			
3R 12557674 SNP	A	C	C	0.308	32	72	1.530	4.82E-06	FBgn0003944	Ubx	Intron			
2R 4527850 SNP	T	G	G	0.065	7	100	2.894	5.05E-06						
2L 9712931 SNP	A	G	G	0.064	7	103	2.656	5.07E-06	FBgn0028704	Nckx30C	UTR_3_Prime			
3L 3561459 SNP	C	A	A	0.054	6	105	3.122	5.10E-06	FBgn0005640	Eip63E	Intron			
2R 870096 SNP	C	A	A	0.075	8	99	2.568	5.11E-06	FBgn0262970	CR43281	Intron			
X 7871098 SNP	A	G	G	0.055	6	103	3.102	5.20E-06	FBgn0003447	sn	Intron			
3R 12557680 SNP	G	A	A	0.314	33	72	1.530	5.21E-06	FBgn0003944	Ubx	Intron			
2R 13824780 SNP	T	G	G	0.126	14	97	1.890	5.74E-06	FBgn0034269	CG6406	Upstream	FBgn0034270	CG6401	Downstream
3L 18120637 SNP	G	C	C	0.167	18	90	1.724	5.78E-06						
2L 19290709 SNP	A	G	G	0.130	14	94	2.020	6.08E-06						
3L 10022196 SNP	G	T	T	0.055	6	103	3.094	6.17E-06	FBgn0040823	dpr6	Intron			

Table 4.S10 Continued

ID	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value	Flybase ID Gene 1	Gene Name 1	Site Class 1	Flybase ID Gene 2	Gene Name 2	Site Class 2	Flybase ID Gene 3	Gene Name 3	Site Class 3
3L 919772_DEL	G	GTG	GTG	0.327	33	68	1.465	6.43E-06	FBgn0264574	<i>Glut1</i>	Intron						
2L 1268225_SNP	G	A	A	0.063	7	104	2.879	6.62E-06	FBgn0041097	<i>robo3</i>	Intron						
2R 863958_SNP	A	C	C	0.064	7	102	2.874	6.68E-06	FBgn0040849	<i>Ir41a</i>	Intron						
X 4881162_SNP	A	C	C	0.057	6	100	2.946	7.13E-06									
2L 5187571_SNP	C	T	T	0.206	22	85	1.614	7.16E-06	FBgn0261836	<i>Msp-300</i>	Intron	FBgn0082990	<i>snoRNA:Psi283</i>	Upstream			
X 7870063_SNP	A	C	C	0.064	7	103	2.842	7.25E-06	FBgn0003447	<i>sn</i>	Intron						
3R 24845324_SNP	G	A	A	0.054	6	105	2.786	7.60E-06	FBgn0039620	<i>CG1443</i>	Intron						
X 3427639_SNP	T	A	T	0.194	21	87	1.678	7.65E-06	FBgn0052791	<i>CG32791</i>	Intron						
2R 863911_SNP	A	G	G	0.064	7	103	2.854	7.85E-06	FBgn0040849	<i>Ir41a</i>	Intron						
2R 864135_SNP	A	G	G	0.064	7	103	2.854	7.85E-06	FBgn0040849	<i>Ir41a</i>	Intron						
2R 470558_SNP	A	G	G	0.057	6	100	2.852	7.95E-06									
2R 864300_SNP	T	G	G	0.064	7	102	2.847	8.38E-06	FBgn0040849	<i>Ir41a</i>	Intron						
2R 13607386_SNP	C	T	T	0.055	6	104	3.054	8.48E-06	FBgn0028494	<i>CG6424</i>	Upstream						
X 2676643_SNP	G	A	A	0.229	22	74	1.767	8.72E-06	FBgn0028369	<i>kirre</i>	Intron	FBgn0040384	<i>CG32795</i>	Downstream			
2R 10335293_SNP	C	T	T	0.073	8	102	2.682	8.84E-06	FBgn0261613	<i>Oaz</i>	Intron						
2L 16330043_SNP	T	A	A	0.099	11	100	2.437	8.91E-06	FBgn0040984	<i>CG4440</i>	Intron	FBgn0028899	<i>CG31817</i>	Downstream	FBgn0001995	<i>mRpL4</i>	Upstream
2L 16330091_SNP	G	A	A	0.099	11	100	2.437	8.91E-06	FBgn0040984	<i>CG4440</i>	Non_Synonymous_Coding	FBgn0028899	<i>CG31817</i>	Downstream	FBgn0001995	<i>mRpL4</i>	Upstream
2L 16330185_SNP	T	G	G	0.099	11	100	2.437	8.91E-06	FBgn0040984	<i>CG4440</i>	Non_Synonymous_Coding	FBgn0028899	<i>CG31817</i>	Downstream			
X 10450665_SNP	A	T	T	0.081	9	102	2.404	8.96E-06	FBgn0085443	<i>spr1</i>	Intron						
2L 13207410_SNP	T	C	C	0.072	8	103	2.679	8.96E-06	FBgn0032482	<i>Pect</i>	Intron						
2R 566644_SNP	T	G	G	0.078	8	95	2.519	9.09E-06									
3R 19940569_SNP	T	G	G	0.056	6	102	2.992	9.19E-06	FBgn0039151	<i>CG13607</i>	Synonymous_Coding	FBgn0039152	<i>Rootletin</i>	Intron			
3L 18137546_SNP	T	C	C	0.308	33	74	1.493	9.20E-06	FBgn0020300	<i>gk</i>	Intron						
2R 7690985_SNP	G	A	A	0.055	6	104	2.867	9.73E-06	FBgn0033652	<i>ths</i>	Intron						
2R 7691008_SNP	T	C	C	0.055	6	104	2.867	9.73E-06	FBgn0033652	<i>ths</i>	Intron						
3R 9411977_SNP	C	T	T	0.306	33	75	1.499	9.91E-06									
3R 16988086_SNP	T	C	C	0.055	6	104	3.048	9.91E-06	FBgn0264357	<i>SNF4Agamma</i>	Intron						
2R 8500226_SNP	T	G	T	0.055	6	103	3.028	9.96E-06	FBgn0004435	<i>Galpha49B</i>	Upstream	FBgn0027356	<i>Amph</i>	Downstream			
3L 352461_SNP	T	G	G	0.064	7	103	2.849	1.01E-05	FBgn0261985	<i>Ptomeg</i>	Intron						
3L 342730_SNP	C	T	T	0.054	6	105	3.037	1.10E-05	FBgn0261985	<i>Ptomeg</i>	Intron	FBgn0035132	<i>mth10</i>	Intron	FBgn0023000	<i>mth</i>	Downstream
2L 12488902_SNP	G	T	T	0.054	6	105	3.026	1.25E-05	FBgn0259176	<i>bun</i>	Intron						
3L 357289_SNP	A	G	G	0.054	6	105	3.112	1.42E-05	FBgn0035134	<i>CG1231</i>	Non_Synonymous_Coding	FBgn0035136	<i>CG6905</i>	Downstream	FBgn0040291	<i>Roc1b</i>	Upstream
3L 5098012_SNP	C	G	G	0.128	13	89	2.156	1.43E-05	FBgn0054047	<i>CR34047</i>	Downstream						
2R 791438_SNP	G	A	A	0.055	6	104	3.078	1.60E-05	FBgn0264911	<i>CG44102</i>	Intron						
3R 17624832_DEL	G	GCAGAAAG	GCAGAAAG	0.082	9	101	2.520	1.71E-05	FBgn0013759	<i>CASK</i>	Intron	FBgn0263521	<i>mir-4969</i>	Upstream	FBgn0262331	<i>mir-999</i>	Upstream
2L 11046203_SNP	A	C	A	0.073	8	101	2.664	1.84E-05	FBgn0032330	<i>Samuel</i>	Intron						
2L 11045276_SNP	T	G	T	0.072	8	103	2.645	2.10E-05	FBgn0032330	<i>Samuel</i>	Intron						
2L 16331605_SNP	A	C	A	0.155	17	93	1.904	4.19E-05	FBgn0028899	<i>CG31817</i>	Non_Synonymous_Coding						

Table 4.S11 - Genetic variants from GWA. List of significantly associated genetic variants within candidate genes with corresponding *P*-value.

Candidate Gene	Region	Data Set	Variant	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value
<i>alph</i>	<i>y v</i>	Only ST	3R_25440527_SNP	C	T	T	0.054	6	105	3.435	2.29E-07
<i>bru-2</i>	<i>e ro</i>	Only ST	2L_12359168_SNP	A	T	T	0.127	14	96	1.565	1.14E-05
<i>cdi</i>	<i>e ro</i>	Only ST	3R_14913855_INS	GA	G	G	0.125	13	91	1.634	9.22E-06
<i>CG1273</i>	<i>e ro</i>	Only ST	3L_4268715_SNP	C	T	T	0.054	6	105	2.613	3.47E-07
<i>CG1273</i>	<i>e ro</i>	Only ST	3L_4268783_SNP	A	G	G	0.063	7	104	2.332	1.18E-06
<i>CG1273</i>	<i>e ro</i>	Only ST	3L_4268808_SNP	G	A	A	0.063	7	105	2.345	1.01E-06
<i>CG1273</i>	<i>e ro</i>	Only ST	3L_4268986_SNP	T	C	C	0.063	7	105	2.345	1.01E-06
<i>CG4440</i>	<i>y v</i>	Only ST	2L_16330043_SNP	T	A	A	0.099	11	100	2.437	8.91E-06
<i>CG4440</i>	<i>y v</i>	Only ST	2L_16330091_SNP	G	A	A	0.099	11	100	2.437	8.91E-06
<i>CG4440</i>	<i>y v</i>	No Poly	2L_16330091_SNP	G	A	A	0.095	14	134	2.211	8.30E-06
<i>CG4440</i>	<i>y v</i>	Full	2L_16330091_SNP	G	A	A	0.082	16	179	1.921	5.41E-05
<i>CG4440</i>	<i>y v</i>	Only ST	2L_16330185_SNP	T	G	G	0.099	11	100	2.437	8.91E-06
<i>CG4440</i>	<i>e ro</i>	No Poly	2L_16330317_SNP	T	A	A	0.062	8	121	2.999	1.10E-08
<i>CG4440</i>	<i>e ro</i>	Full	2L_16330317_SNP	T	A	A	0.067	10	140	2.580	7.99E-08
<i>CG7196</i>	<i>e ro</i>	No Poly	2L_7760128_SNP	A	G	G	0.054	7	122	2.869	6.83E-07
<i>CG7196</i>	<i>e ro</i>	No Poly	2L_7760144_SNP	C	T	T	0.054	7	123	2.721	2.74E-06
<i>CG7196</i>	<i>e ro</i>	No Poly	2L_7763275_SNP	A	G	G	0.063	8	119	2.577	8.00E-07
<i>CG7196</i>	<i>e ro</i>	Full	2L_7765617_SNP	C	T	T	0.059	9	144	2.343	2.82E-06
<i>CG7196</i>	<i>e ro</i>	Full	2L_7766066_SNP	C	G	G	0.058	9	146	3.029	9.78E-10
<i>CG7196</i>	<i>e ro</i>	No Poly	2L_7766066_SNP	C	G	G	0.069	9	121	2.858	9.81E-09
<i>CG7196</i>	<i>e ro</i>	Only ST	2L_7766066_SNP	C	G	G	0.054	6	106	2.446	2.05E-06
<i>CG9650</i>	<i>e ro</i>	Only ST	X_7060779_SNP	T	G	G	0.058	6	97	2.336	5.54E-06
<i>CG10864</i>	<i>e ro</i>	Only ST	3R_14236729_SNP	C	A	A	0.055	6	103	2.394	3.72E-06
<i>CG15365</i>	<i>e ro</i>	Only ST	X_8951785_SNP	T	C	C	0.055	6	104	2.606	3.55E-07
<i>CG33970</i>	<i>y v</i>	No Poly	3R_22168414_SNP	G	A	A	0.054	8	139	2.807	1.27E-04
<i>dpr6</i>	<i>y v</i>	No Poly	3L_10022098_SNP	T	C	C	0.074	11	137	2.451	2.47E-06
<i>dpr6</i>	<i>y v</i>	Only ST	3L_10022196_SNP	G	T	T	0.055	6	103	3.094	6.17E-06
<i>dpr6</i>	<i>y v</i>	Full	3L_10065561_INS	AGCA	A	A	0.453	73	88	1.072	4.39E-06
<i>dpr6</i>	<i>e ro</i>	Only ST	3L_10077092_SNP	A	G	G	0.063	7	104	2.524	9.37E-08
<i>Eip75B</i>	<i>y v</i>	No Poly	3L_17950305_SNP	A	G	G	0.054	8	140	2.694	2.00E-05
<i>Eip75B</i>	<i>e ro</i>	Full	3L_18016881_SNP	G	A	A	0.053	8	143	2.562	5.98E-06
<i>grp</i>	<i>e ro</i>	Full	2L_16694744_SNP	A	T	T	0.280	40	103	-1.098	3.31E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2424152_SNP	C	T	T	0.054	6	106	2.353	5.89E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428434_SNP	T	G	G	0.054	6	105	2.762	5.76E-08
<i>jing</i>	<i>e ro</i>	No Poly	2R_2428434_SNP	T	G	G	0.054	7	122	2.565	1.11E-05
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428451_SNP	T	G	G	0.054	6	105	2.762	5.76E-08
<i>jing</i>	<i>e ro</i>	No Poly	2R_2428451_SNP	T	G	G	0.054	7	122	2.565	1.11E-05
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428634_SNP	A	T	T	0.069	7	94	2.530	1.10E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428764_SNP	A	G	G	0.063	7	105	2.497	1.49E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428894_SNP	T	G	G	0.055	6	104	2.782	4.45E-08

Figure 4.S11 Continued

Candidate Gene	Region	Data Set	Variant	Minor Allele	Major Allele	Reference Allele	Minor Allele Frequency	Minor Allele Count	Major Allele Count	Effect	P-value
<i>jing</i>	<i>e ro</i>	No Poly	2R_2428894_SNP	T	G	G	0.055	7	121	2.564	8.84E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2428935_SNP	A	G	G	0.063	7	105	2.497	1.49E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2429479_SNP	T	A	A	0.063	7	105	2.497	1.49E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2433735_SNP	A	C	C	0.054	6	105	2.518	1.03E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2434296_SNP	A	C	C	0.074	7	88	2.456	2.89E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2436436_SNP	A	G	G	0.055	6	103	2.666	1.81E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2438246_DEL	C	CTATG	CTATG	0.065	7	100	2.501	1.51E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2438252_INS	TCAT	T	T	0.067	7	98	2.507	1.43E-07
<i>jing</i>	<i>e ro</i>	No Poly	2R_2438252_INS	TCAT	T	T	0.066	8	113	2.395	1.25E-05
<i>jing</i>	<i>e ro</i>	Full	2R_2438252_INS	TCAT	T	T	0.055	8	138	2.367	1.80E-05
<i>jing</i>	<i>e ro</i>	Only ST	2R_2438717_SNP	A	C	C	0.054	6	105	2.518	1.03E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2440017_SNP	T	A	A	0.063	7	105	2.497	1.49E-07
<i>jing</i>	<i>e ro</i>	Only ST	2R_2440093_SNP	A	C	C	0.054	6	105	2.786	4.17E-08
<i>jing</i>	<i>e ro</i>	No Poly	2R_2440093_SNP	A	C	C	0.054	7	122	2.568	8.63E-06
<i>jing</i>	<i>e ro</i>	Only ST	2R_2446238_SNP	C	T	T	0.055	6	103	2.743	7.42E-08
<i>jola</i>	<i>e ro</i>	Only ST	2R_6379425_SNP	T	C	C	0.054	6	106	2.755	6.13E-08
<i>MESR3</i>	<i>y v</i>	No Poly	2L_18647760_SNP	C	G	G	0.083	12	133	2.281	5.90E-06
<i>Oaz</i>	<i>y v</i>	Only ST	2R_10335293_SNP	C	T	T	0.073	8	102	2.682	8.84E-06
<i>pk</i>	<i>e ro</i>	Only ST	2R_3083775_SNP	T	C	C	0.055	6	104	2.922	7.20E-09
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1393055_SNP	A	G	G	0.062	8	122	2.734	5.60E-07
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1393055_SNP	A	G	G	0.058	9	147	2.646	5.84E-07
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1393071_SNP	A	G	G	0.078	10	119	2.175	1.53E-05
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1393071_SNP	A	G	G	0.071	11	143	2.151	1.15E-05
<i>Ptp61F</i>	<i>e ro</i>	Only ST	3L_1400394_SNP	G	A	A	0.064	7	103	2.269	2.95E-06
<i>Ptp61F</i>	<i>y v</i>	No Poly	3L_1452328_SNP	G	T	T	0.103	15	130	2.015	6.74E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1455295_SNP	G	A	A	0.093	12	117	1.993	2.42E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1455555_SNP	A	C	C	0.086	11	117	2.142	1.19E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1455925_SNP	T	G	G	0.085	11	118	2.138	1.18E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1456574_SNP	G	A	A	0.063	8	119	2.829	1.28E-07
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1456574_SNP	G	A	A	0.059	9	144	2.354	4.65E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1456902_SNP	T	C	C	0.056	7	119	3.146	3.36E-08
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1456902_SNP	T	C	C	0.053	8	144	2.574	2.25E-06
<i>Ptp61F</i>	<i>e ro</i>	Only ST	3L_1456902_SNP	T	C	C	0.055	6	103	2.308	9.01E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1456916_SNP	A	C	C	0.069	9	121	2.474	1.14E-06
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1456953_SNP	A	C	C	0.063	8	120	2.714	4.57E-07
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1456953_SNP	A	C	C	0.058	9	145	2.254	1.26E-05
<i>Ptp61F</i>	<i>e ro</i>	No Poly	3L_1456971_SNP	A	T	T	0.062	8	121	2.728	3.89E-07
<i>Ptp61F</i>	<i>e ro</i>	Full	3L_1456971_SNP	A	T	T	0.058	9	146	2.266	1.12E-05
<i>Ptp61F</i>	<i>e ro</i>	Only ST	3L_1472460_SNP	A	G	G	0.055	6	104	2.374	4.60E-06
<i>Ubx</i>	<i>y v</i>	Only ST	3R_12557674_SNP	A	C	C	0.308	32	72	1.530	4.82E-06
<i>Ubx</i>	<i>y v</i>	Only ST	3R_12557680_SNP	G	A	A	0.314	33	72	1.500	5.21E-06

Table 4.S12 - Genotypes of DGRP lines. Genotype of each DGRP line at each significantly associated genetic variant within candidate genes surveyed.

DGRP Line	chr3R:25440527_SNP	chr2L:12359168_SNP	chr3R:14913855_INS	chr3L:4268715_SNP	chr3L:4268783_SNP	chr3L:4268808_SNP	chr3L:4268986_SNP	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330043_SNP	chr2L:16330091_SNP	chr2L:16330185_SNP	chr2L:7760128_SNP	chr2L:7760144_SNP	chr2L:7763275_SNP	chr2L:7765617_SNP	chr2L:7766066_SNP	chrX:7060779_SNP	chr3R:14236729_SNP	chrX:8951785_SNP	chr3R:2216844_SNP	chr3L:10077092_SNP	chr3L:10022098_SNP	chr3L:10022196_SNP	chr3L:10065561_INS	chr3L:18016881_SNP	chr3L:17950305_SNP	chr2L:16684744_SNP	chr2R:2424152_SNP	chr2R:2428434_SNP	chr2R:2428457_SNP	
DGRP 21	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 26	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	G/G	A/A	C/C	A/A	C/C	T/T	G/G	A/A	A/A	C/C	A/A	G/G	T/T	G/G	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 28	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	A/A	C/C	A/A	C/C	T/T	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 31	T/T	T/T	J.	J.	J.	J.	J.	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 32	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 38	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 40	T/T	A/A	(G)A(G)A	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 41	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 42	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	C/C	J.	J.	
DGRP 45	T/T	T/T	(G)-(G)-	T/T	J.	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 48	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 49	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 57	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 59	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 69	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 73	T/T	A/A	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 75	T/T	J.	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 83	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 85	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	J.	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	J.	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G		
DGRP 88	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	J.	J.	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 91	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	C/C	G/G	A/A	C/C	T/T	J.	J.	G/G	T/T	T/T	G/G	G/G
DGRP 93	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 100	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	J.	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 101	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	J.	J.	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 105	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 109	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)-(A)-	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 129	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 136	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	J.	J.	J.	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	J.	J.
DGRP 138	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 142	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 149	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 153	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 158	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 161	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 176	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	C/C	T/T	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 177	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	J.	G/G	T/T	T/T	G/G	G/G	
DGRP 181	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 189	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 195	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 208	T/T	T/T	(G)A(G)A	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G		
DGRP 217	T/T	T/T	(G)A(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 223	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	G/G	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 227	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	C/C	G/G	G/G	
DGRP 228	T/T	T/T	(G)A(G)A	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 229	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	T/T	G/G	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 233	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 235	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 237	T/T	T/T	(G)-(G)-	T/T	G/G	J.	C/C	A/A	A/A	A/A	A/A	J.	J.	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 239	T/T	A/A	(G)A(G)A	C/C	A/A	G/G	T/T	T/T	T/T	A/A	A/A	A/A	G/G	A/A	C/C	A/A	C/C	C/C	T/T	C/C	T/T	A/A	A/A	C/C	T/T	J.	G/G	G/G	T/T	C/C	T/T	T/T	
DGRP 256	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 280	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G		
DGRP 287	T/T	T/T	(G)A(G)A	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	A/A	C/C	T/T	J.	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G

Table 4.S12 Continued

DGRP Line	chr3R:25440527_SNP	chr2L:12359168_SNP	chr3R:14913855_INS	chr3L:4268715_SNP	chr3L:4268783_SNP	chr3L:4268808_SNP	chr3L:4268986_SNP	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330043_SNP	chr2L:16330091_SNP	chr2L:16330185_SNP	chr2L:7760128_SNP	chr2L:7760144_SNP	chr2L:7763275_SNP	chr2L:7765617_SNP	chr2L:7766066_SNP	chrX:7060779_SNP	chr3R:14236729_SNP	chrX:8951785_SNP	chr3R:22168414_SNP	chr3L:10077092_SNP	chr3L:10022098_SNP	chr3L:10022196_SNP	chr3L:10065561_INS	chr3L:18016881_SNP	chr3L:17950305_SNP	chr2L:16694744_SNP	chr2R:2424152_SNP	chr2R:2428434_SNP	chr2R:2428451_SNP
DGRP 303	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	J.	J.	G/G	G/G
DGRP 304	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	G/G	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 306	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 307	T/T	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 309	T/T	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 310	T/T	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 313	T/T	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	C/C	T/T	T/T	G/G	
DGRP 315	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 317	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	J.	T/T	T/T	G/G	G/G	
DGRP 318	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 319	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	J.	J.	J.	
DGRP 320	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 321	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 324	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 325	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	J.	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	G/G	G/G	T/T	T/T	G/G	G/G		
DGRP 332	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	A/A	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 335	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 336	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	J.	J.	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 338	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	J.	G/G	T/T	J.	T/T	J.	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 340	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	J.	G/G	A/A	T/T	G/G	G/G	
DGRP 348	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 350	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	A/A	J.	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 352	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	C/C	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 354	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 355	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 356	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 357	T/T	A/A	(G)-(G)	J.	A/A	G/G	T/T	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 358	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 359	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 360	T/T	(G)-(G)	T/T	G/G	A/A	C/C	J.	J.	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 361	J.	J.	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	A/A	C/C	G/G	T/T	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	J.	G/G	T/T	T/T	G/G	G/G	
DGRP 362	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 365	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 367	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 370	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 371	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 373	T/T	(G)-(G)	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 374	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 375	T/T	A/A	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	T/T	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 377	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 379	C/C	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 380	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 381	T/T	J.	(G)A/(G)A	T/T	G/G	A/A	C/C	J.	J.	A/A	J.	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 382	T/T	(G)-(G)	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 383	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	G/G	G/G	T/T	T/T	G/G	G/G
DGRP 385	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	J.	A/A	G/G	C/C	T/T	(A)-(A)-	J.	G/G	T/T	T/T	G/G	G/G
DGRP 386	T/T	(G)-(G)	C/C	A/A	G/G	T/T	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 390	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	G/G	G/G	T/T	T/T	G/G	G/G	
DGRP 391	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 392	T/T	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	J.	T/T	T/T	G/G	G/G	

Table 4.S12 Continued

DGRP Line	chr3R:25440527_SNP	chr2L:12359168_SNP	chr3R:14913855_INS	chr3L:4268715_SNP	chr3L:4268783_SNP	chr3L:4268808_SNP	chr3L:4268986_SNP	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330043_SNP	chr2L:16330091_SNP	chr2L:16330185_SNP	chr2L:7760128_SNP	chr2L:7760144_SNP	chr2L:7763275_SNP	chr2L:7765617_SNP	chr2L:7766066_SNP	chrX:7060779_SNP	chr3R:14236729_SNP	chrX:8951785_SNP	chr3R:22168414_SNP	chr3L:10077092_SNP	chr3L:10022098_SNP	chr3L:10022196_SNP	chr3L:10065561_INS	chr3L:18016881_SNP	chr3L:17950305_SNP	chr2L:16694744_SNP	chr2R:2424152_SNP	chr2R:2428434_SNP	chr2R:2428451_SNP	
	alph	brv-2	cdi	CG1273	CG1273	CG1273	CG1273	CG4440	CG4440	CG4440	CG4440	CG4440	CG7196	CG7196	CG7196	CG7196	CG7196	CG9650	CG10864	CG15365	CG33970	dpr6	dpr6	dpr6	dpr6	Eip75B	Eip75B	grp	jing	jing	jing	
DGRP 397	T/T	J.	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	T/T	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 399	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 405	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 406	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 409	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 426	T/T	(G)-(G)	(G)-(G)	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	G/G	C/C	T/T	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 427	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	J.	G/G	T/T	G/G	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 437	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 439	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	C/C	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 440	T/T	(G)-(G)	(G)-(G)	C/C	A/A	G/G	T/T	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	J.	G/G	G/G
DGRP 441	T/T	(G)A/(G)A	(G)A/(G)A	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 443	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	J.	J.	A/A	J.	A/A	G/G	G/G	T/T	J.	T/T	G/G	A/A	C/C	G/G	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 461	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 486	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	G/G	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 491	T/T	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)GCA/(A)GCA	A/A	A/A	T/T	T/T	G/G	G/G	
DGRP 492	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	C/C	G/G	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 502	C/C	T/T	(G)-(G)	T/T	G/G	A/A	C/C	J.	J.	A/A	J.	A/A	G/G	J.	J.	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	J.	T/T	G/G	G/G
DGRP 505	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 508	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 509	T/T	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 513	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 517	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 528	T/T	J.	(G)-(G)	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 530	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 531	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	J.	C/C	G/G	T/T	G/G	J.	A/A	J.	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 535	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	A/A	A/A	T/T	G/G	G/G	
DGRP 551	T/T	J.	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 555	T/T	A/A	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 559	J.	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 563	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	J.	J.	J.	J.	G/G	J.	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 566	T/T	J.	J.	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 584	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	T/T	A/A	C/C	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 589	T/T	(G)A/(G)A	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	G/G	G/G	T/T	T/T	G/G	G/G
DGRP 595	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	J.	A/A	T/T	G/G	G/G
DGRP 596	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 627	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	A/A	T/T	J.	T/T	G/G	G/G	A/A	C/C	A/A	G/G	T/T	G/G	J.	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 630	T/T	J.	J.	T/T	G/G	A/A	C/C	J.	J.	A/A	G/G	G/G	J.	T/T	J.	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 634	J.	A/A	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 639	T/T	J.	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	C/C	C/C	T/T	A/A	C/C	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 642	T/T	(G)A/(G)A	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 646	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	J.	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 703	T/T	(G)A/(G)A	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	J.	T/T	G/G	G/G
DGRP 705	C/C	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	G/G	G/G	T/T	G/G	(A)GCA/(A)GCA	G/G	A/A	T/T	T/T	G/G	G/G
DGRP 707	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 712	T/T	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G
DGRP 714	T/T	(G)A/(G)A	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	J.	J.	J.	G/G	T/T	G/G	T/T	G/G	T/T	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	J.	T/T	G/G	G/G
DGRP 716	T/T	(G)-(G)	(G)-(G)	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 721	C/C	T/T	(G)-(G)	T/T	G/G	A/A	T/T	A/A	A/A	T/T	J.	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	J.	G/G	J.	G/G	G/G	T/T	T/T	G/G	G/G
DGRP 727	T/T	(G)-(G)	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	G/G	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	C/C	T/T	T/T
DGRP 730	T/T	A/A	(G)-(G)	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)	A/A	G/G	T/T	T/T	G/G	G/G

Table 4.S12 Continued

DGRP Line	chr3R:25440527_SNP	chr2L:12359168_SNP	chr3R:14913855_INS	chr3L:4268715_SNP	chr3L:4268783_SNP	chr3L:4268808_SNP	chr3L:4268986_SNP	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330043_SNP	chr2L:16330091_SNP	chr2L:16330185_SNP	chr2L:7760128_SNP	chr2L:7760144_SNP	chr2L:7763275_SNP	chr2L:7765617_SNP	chr2L:7766066_SNP	chrX:7060779_SNP	chr3R:14236729_SNP	chrX:8951785_SNP	chr3R:22168414_SNP	chr3L:10077092_SNP	chr3L:10022098_SNP	chr3L:10022196_SNP	chr3L:10065561_INS	chr3L:18016881_SNP	chr3L:17950305_SNP	chr2L:16684744_SNP	chr2R:2424152_SNP	chr2R:2428434_SNP	chr2R:2428451_SNP	
DGRP 737	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	A/A	C/C	G/G	T/T	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 738	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	J.	J.	A/A	A/A	G/G	G/G	T/T	G/G	T/T	C/C	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 748	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	A/A	C/C	G/G	T/T	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 757	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 761	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	C/C	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 765	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	C/C	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	J.	G/G	T/T	T/T	G/G	G/G	
DGRP 774	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	J.	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 776	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 783	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 786	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	T/T	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 787	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 790	T/T	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 796	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 799	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 801	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	J.	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 802	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 804	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	T/T	J.	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	J.	T/T	T/T	G/T	
DGRP 805	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 808	T/T	A/A	(G)-(G)-	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	T/T	C/C	T/T	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	T/T	T/T	
DGRP 810	T/T	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 812	T/T	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 818	T/T	A/A	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	J.	A/A	T/T	G/G	G/G	
DGRP 819	T/T	A/A	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	C/C	C/C	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 820	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	C/C	T/T	T/T	
DGRP 821	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 822	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	T/T	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	C/C	T/T	T/T	
DGRP 832	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	T/T	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 837	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 843	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 849	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	J.	T/T	G/G	G/G	A/A	C/C	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 850	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	G/G	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 852	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	G/G	A/A	T/T	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 853	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	J.	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	J.	T/T	G/G	G/G	
DGRP 855	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	T/T	A/A	A/A	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 857	T/T	A/A	(G)A/(G)A	C/C	A/A	G/G	T/T	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 859	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	J.	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 861	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	C/C	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 879	C/C	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	T/T	G/G	T/T	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 882	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 884	T/T	T/T	J.	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	A/A	C/C	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)GCA/(A)GCA	A/A	G/G	T/T	C/C	J.	T/T	
DGRP 887	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	C/C	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	J.	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 890	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	C/C	G/G	G/G	A/A	C/C	A/A	G/G	T/T	G/G	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 892	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	C/C	T/T	T/T	
DGRP 894	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	J.	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 897	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 900	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	T/T	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G
DGRP 907	T/T	T/T	(G)-(G)-	T/T	G/G	A/A	C/C	T/T	T/T	A/A	A/A	G/G	J.	J.	G/G	T/T	C/C	J.	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 908	T/T	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	A/A	T/T	G/G	G/G	
DGRP 911	T/T	T/T	(G)A/(G)A	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	A/A	T/T	G/G	J.	J.	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	
DGRP 913	T/T	J.	(G)-(G)-	T/T	G/G	A/A	C/C	A/A	A/A	A/A	A/A	G/G	G/G	T/T	G/G	T/T	G/G	G/G	A/A	C/C	A/A	G/G	C/C	T/T	(A)-(A)-	A/A	G/G	T/T	T/T	G/G	G/G	

Table 4.S13 - Genotypes of *P*-element insertions, chromosomal deletions and RNAi lines.
 Lines used for functional validation.

Candidate Gene	Genotype	Stock Center & Stock #
<i>alph</i>	<i>Df(3R)ED6316</i>	BDSC 8925
<i>alph</i>	<i>w¹¹¹⁸; PBac{w[+mC]=PB}alph[c04528]</i>	BDSC 11492
<i>alph</i>	<i>P{KK107730}VIE-260B</i>	VDRC 105483
<i>bru-2</i>	<i>w¹¹¹⁸; PBac{w[+mC]=WH}bru-2[f00171]</i>	BDSC 18300
<i>bru-2</i>	<i>P{KK108932}VIE-260B</i>	VDRC 109739
<i>cdi</i>	<i>w¹¹¹⁸; Df(3R)ED5911, P{w[+mW.Scer]FRT.hs3}=3'.RS5+3.3'}ED5911/TM6C, cu¹ Sb¹</i>	BDSC 8683
<i>cdi</i>	<i>w¹¹¹⁸; Mi{ET1}cdi[MB02390]</i>	BDSC 24441
<i>cdi</i>	<i>w¹¹¹⁸; P{GD8731}v43634</i>	VDRC 43634
<i>cdi, CG10864</i>	<i>Df(3R)ED2</i>	BDSC 6962
<i>CG4440</i>	<i>P{KK111759}VIE-260B</i>	VDRC 102475
<i>CG7196</i>	<i>Df(2L)ED508</i>	BDSC 8944
<i>CG7196</i>	<i>w¹¹¹⁸; P{GD12166}v22526</i>	VDRC 22526
<i>CG9650</i>	<i>PBac{RB}CG9650[e04580]</i>	Exelixis e04580
<i>CG9650</i>	<i>P{KK108364}VIE-260B</i>	VDRC 104402
<i>CG10864</i>	<i>P{KK104447}VIE-260B</i>	VDRC 107858
<i>CG15365</i>	<i>P{KK100288}VIE-260B</i>	VDRC 103369
<i>CG33970</i>	<i>P{KK109988}VIE-260B</i>	VDRC 101855
<i>CG33970</i>	<i>Df(3R)ED6232</i>	BDSC 8105
<i>dpr6</i>	<i>w¹¹¹⁸; Mi{ET1}dpr6[MB04096]</i>	BDSC 24673
<i>dpr6</i>	<i>P{KK112634}VIE-260B</i>	VDRC 103521
<i>Eip75B</i>	<i>Df(3L)ED4710</i>	BDSC 8100
<i>Eip75B</i>	<i>y¹ sc¹ v¹; P{y[+t7.7] v[+t1.8]=TRiP.GLC01418}attP2</i>	BDSC 43231
<i>grp</i>	<i>PBac{WH}grp[f03358]</i>	Exelixis f03358
<i>grp</i>	<i>w¹¹¹⁸; Mi{ET1}grp[MB08323]</i>	BDSC 26107
<i>grp</i>	<i>P{KK108548}VIE-260B</i>	VDRC 110076
<i>grp</i>	<i>Df(2L)ED1109</i>	BDSC 8945
<i>jing</i>	<i>Df(2R)ED1552</i>	BDSC 8044
<i>jing</i>	<i>y¹ w¹; Mi{y[+mDint2]=MIC}jing[Mi03555]/SM6a</i>	BDSC 36997
<i>lola</i>	<i>PBac{PB}lola[c01925]</i>	Exelixis c01925
<i>lola</i>	<i>y¹ w¹; Mi{y[+mDint2]=MIC}lola[Mi04800]</i>	BDSC 38056
<i>lola</i>	<i>y¹ w¹; Mi{y[+mDint2]=MIC}lola[Mi06282]/SM6a</i>	BDSC 40802
<i>MESR3</i>	<i>w¹¹¹⁸; Mi{ET1}MESR3[MB06218]</i>	BDSC 25484
<i>MESR3</i>	<i>y¹ v¹; P{y[+t7.7] v[+t1.8]=TRiP.GLC01393}attP2</i>	BDSC 50509
<i>Oaz</i>	<i>P{XP}Oaz[d09084]</i>	Exelixis d09084
<i>Oaz</i>	<i>y¹ sc¹ v¹; P{y[+t7.7] v[+t1.8]=TRiP.GLV21080}attP2</i>	BDSC 35715
<i>pk</i>	<i>w¹¹¹⁸; Mi{ET1}pk[MB11776] CG30384[MB11776]</i>	BDSC 29252
<i>pk</i>	<i>P{KK109294}VIE-260B</i>	VDRC 101480
<i>pk</i>	<i>Df(2R)ED1673</i>	BDSC 9062
<i>Ptp61F</i>	<i>Df(3L)ED207</i>	BDSC 8053
<i>Ptp61F</i>	<i>w¹¹¹⁸; Mi{ET1}Ptp61F[MB08823] CG32320[MB08823]</i>	BDSC 26133
<i>Ptp61F</i>	<i>P{KK101883}VIE-260B</i>	VDRC 108888
<i>Ubx</i>	<i>PBac{WH}Ubx[f07161]</i>	Exelixis f07161
<i>Ubx</i>	<i>w¹¹¹⁸; P{GD5049}v37825</i>	VDRC 37825
Control Line	<i>w¹¹¹⁸</i>	BDSC 5905
Control Line	<i>w¹¹¹⁸</i>	BDSC 6326
Control Line	<i>y¹ w¹¹¹⁸</i>	BDSC 6598
Control Line	<i>y¹ v¹; P{y[+t7.7]=CaryP}attP2</i>	BDSC 36303
Control Line	<i>w¹¹¹⁸ (For GD)</i>	VDRC 60000
Control Line	<i>y, w¹¹¹⁸; P{attP,y[+],w[3']} (For KK)</i>	VDRC 60100

Table 4.S14 - Functional validation results in the *e ro* interval. Raw counts and associated *P*-values from validation in the *e ro* interval.

Control w1118	alph 8925	alph 11492	bru-2 18300	cdi 8683	cdi 24441	CG7196 8944	CG10864 6962	CG33970 8105	dpr6 5905	Eip75B 8100	grp 8945	grp f03358	jing 8044	MESR3 25484	pk 9062	pk 29252	Ptp61F 8053	Control KK	alph 105483	bru-2 109739	CG4440 102475	CG9650 104402	CG10864 107858	
27.885	18.033	15.625	14.706	16.667	14.458	27.160	25.714	14.130	24.286	21.311	26.154	22.321	15.942	25.000	28.205	15.476	18.605	19.259	24.615	19.658	15.714	22.481	15.823	
23.729	25.806	15.789	16.505	20.253	15.854	20.455	22.535	15.909	21.978	31.667	21.053	17.526	20.238	32.468	23.529	25.843	17.969	21.176	19.277	22.330	21.277	21.168	21.368	
24.658	23.810	18.182	25.455	29.762	21.250	18.750	23.611	19.565	21.348	25.806	18.919	20.388	24.138	32.394	23.438	26.250	16.000	24.779	23.256	22.581	17.000	20.161	4.989	
20.000	22.727	15.584	19.753	23.656	22.105	20.968	21.277	19.512	22.500	20.833	33.898	26.316		21.875	12.245	18.056	23.596	22.330	20.690		10.309	21.008	16.912	
32.051	18.391	20.238	19.512	24.675	22.353	22.500	31.148	12.857	25.352	20.000	29.032	16.807	15.000	28.947	20.290	26.866	24.561	19.192	22.388	18.889	17.000	16.346	20.155	
11.111	17.284	22.000	18.333	27.059	14.474	18.421	31.481	25.000	38.182	18.750	16.418	19.101	21.053	30.769	21.333	28.395	16.667	21.212	19.811	15.873	19.048	17.778	19.863	
18.391	18.182	26.364	23.853	20.588	23.810	22.105	23.077	20.408	15.625	22.449	18.478	17.442	29.545	23.529	21.111	15.000	22.340	14.085	19.512	23.944	26.882	20.611	19.549	
25.758	13.978	21.622	15.517	27.586	27.586	27.059	36.364	19.802	23.077	26.923	14.493	19.512	22.727	17.544	33.735	27.692	18.182	15.238	14.400	16.842	18.605	24.779	14.815	
20.000	21.429	15.385	26.364	24.510	15.068	18.519	32.813	18.868	22.857	19.643	13.793	18.812	22.449	18.280	24.324	20.270	23.256	12.644	19.853	19.048	22.523	20.168	18.349	
28.723	21.296	16.162	26.718	25.581	18.644	23.077	31.373	23.958	16.438	30.137	12.346	17.073	30.556	27.907	28.000	18.987	31.818	20.870	13.462		24.096	23.894	21.951	
18.462	18.367	22.340	22.308	21.000	21.250	24.051	22.222	21.739	25.758	24.242	21.212	22.105	18.182	19.444	16.667	16.471	24.731	26.596	20.930	20.238	17.647	25.000	26.772	
21.348	26.437	18.478	23.853	21.250	15.278	15.789	29.851	19.192	24.490	26.582	23.188		22.951	29.412	28.205	25.532	8.696	18.750	20.270	21.818	22.917	18.667	12.644	
22.093	18.000	14.286	16.000	16.092	23.729	15.054	18.182	26.667	16.438	21.176	17.143	22.340	21.875	22.581	24.706	19.298	32.258	20.408	19.753	19.753	19.355	22.093	15.714	
18.841	25.243	25.333	14.953	19.318	23.750	18.095	33.333	14.943	26.027	21.429	30.380	23.529	24.176	20.548	19.780	35.443	27.273		24.615	11.290	32.673	17.391	18.548	
29.070	23.469	15.054	31.522	20.833	16.949	22.093	26.027	17.500	21.333	24.719	10.714	29.032	17.544	34.545	15.054	15.217	54.545		18.293	16.393	15.652	20.619	15.385	20.513
19.697	22.667	20.690	19.167	20.652	26.866	15.464	20.930		20.213	26.027	20.482	19.008		22.581	18.367	19.643	23.256	15.152	18.543	12.174	21.951	39.130	21.769	
21.538	27.835	22.881	14.458	16.484	22.581	25.275	16.049		26.250	19.444	21.429	17.273		16.418	20.000	21.053	25.000	14.286	12.621	19.643	17.442	25.833	19.118	
24.138	21.905	19.802	29.474	18.269	20.732	22.222			21.250	22.581	16.176			22.667	16.092	12.500	29.167	17.431	18.182	18.182	21.176	21.739	17.544	
32.530	27.083	16.495		21.008	27.957	31.507	27.692		28.947	21.667	25.000			27.273	19.767	27.451	38.889	15.094	18.421	21.429	26.966	19.298	26.724	
20.833		26.549		27.835	22.892	15.625	27.778		21.818	20.000	25.000			23.611	14.737	20.988	23.810	23.232	17.606	27.273	18.182	20.161	22.069	
18.919	22.000	17.708		22.936	19.444	22.917	26.087		22.078	30.769	23.529			27.869	19.417	18.033	21.429	15.714	19.835	19.626	18.919	18.750	28.082	
17.978	18.557	20.000		20.732	20.290	23.596	22.222		13.636	21.918	24.324			22.222	22.917	32.143	18.182	12.389	13.534	21.739	19.328	20.536	18.750	
12.360	25.243	15.385		28.571	15.909	25.000	36.667		12.069		20.000			15.556	14.754	28.947	20.000	18.605	15.385	24.615	17.647	18.421	17.829	
22.892	23.810	25.243		26.087	22.973	28.155	16.923		20.000					18.072	25.000	26.230	36.364	17.204	20.370	13.761	15.663	21.000	24.219	
17.647	23.596	17.391		14.286	25.974	24.752	25.862		15.517					31.034	16.495	15.625	7.692	30.882	18.354	18.868	19.000	20.202	22.314	
21.591	18.605	32.653		31.111	24.675	23.404	20.779		25.263					26.190	30.233	25.806	23.077	21.429	23.881	14.286	16.092	17.241	20.915	
27.500	20.370	21.359		25.926	20.000	24.510			25.373					15.278	24.176	26.866		25.000	20.652	17.188	19.048	16.667	20.325	
23.148	25.000	21.154		32.075	16.901	33.333			27.119					15.556	24.419	31.429		20.482	21.488	23.404	12.727	23.333	19.753	
22.105	26.786	20.755			18.841	28.829			17.241					29.508	22.340	31.646		25.000	14.634	21.127	19.811	22.523	20.000	
16.854	19.626	21.739			19.718	15.152			20.270						18.280	30.612		20.800	16.964	20.652	17.978	20.909	14.765	

Table 4.S14 Continued

CG15365	CG33970	dpr6	grp	pk	Ptp61F	Control	cdi	CG7196	Ubx	Control	Eip75B	MESR3	Oaz	Control	jing	lola	lola	Control	CG9650	grp	grp	lola	Oaz	Ubx	
103369	101855	103521	110076	101480	108888	GD	43634	22526	37825	36303	43231	50509	35715	6598	36977	38056	40802	6326	e04580	26107	26107	c01925	d09084	f07161	
19.231	17.757	20.968		21.649	21.053	21.429	21.260	21.229	14.063	18.543	13.953	18.286	28.571	20.213	31.507	24.242	24.096	27.551	19.101	26.437	18.841	21.008		23.585	
18.333	14.444	14.912	13.793	17.582	23.853	32.609	26.496	24.427	26.087	18.675	15.873	16.489	17.949	23.762	20.896	18.919	22.892	25.000	24.742	25.000	18.182	20.301	19.388	21.698	
14.894	25.490	17.073		16.667	13.846	11.111	20.000	21.951	22.148	17.241	18.590	16.471	25.714	21.818	16.832	24.590	23.171	16.667	25.676	20.879	20.238	14.394	25.301	22.936	
13.253	18.824	24.444	30.000	24.286	19.792	20.430	14.729	21.875	18.978	18.121	20.382	17.919	25.758	11.111	15.385	21.622	19.540	16.505	23.711	26.214	20.238	16.667	17.895	21.505	
15.116	17.500	21.111		15.625	16.239	16.279	21.311	19.380	20.438	18.889	15.172	21.186	20.732	21.359	21.429	19.355	19.355	19.753	12.195	23.171	29.8077	27.184	16.505	22.989	
20.000	20.482	18.333	23.457	21.739	23.256	18.947	29.839	25.203	20.270	18.543	20.765	13.433	19.540	17.094	25.490	14.493	21.795	12.222	30.380	25.000	23.8636	20.238	23.711	26.882	
29.268	19.388	22.472	20.635	25.301	19.298	19.277	21.053	16.667	24.540	15.476	16.959	20.455	14.706	17.500	14.167	21.667	20.270	22.989	22.667	21.918	31.7647	23.171	25.532	17.308	
16.667	19.318	16.883	33.333	16.456	25.000	20.213	18.045	22.156	23.232	14.943	16.667	16.568	17.910	27.027	20.000	21.154	20.482	22.330	29.167	29.268	22.0588	22.449	21.000	14.141	
16.190	10.714	24.444	17.000	18.182	21.239	24.242	20.667	27.632	18.750	21.970	14.371	22.297	14.634	10.811	15.000	20.513	28.049	24.051	18.310	23.611	16.8317	27.778	27.174	30.556	
21.649	21.818	18.812	18.000	25.806	23.457	19.048	18.367	27.206	22.881	20.192	20.769	16.384	23.457	31.034	19.388	10.938	17.978	29.630	16.162	16.901	27.6786	21.212	24.510	13.821	
21.739	17.949	15.574	21.296	22.222	28.571	29.213	19.205	12.162	28.333	19.108	19.091	15.663	25.676	17.241	24.096	19.444	15.190	11.111	33.333	26.761	25.2747	20.635	25.000	9.302	
18.667	19.828	24.490	16.092	12.389	21.053	22.353	22.222	21.359	24.786	21.875	22.137	18.354	26.829	22.449	20.879	31.250	10.390	26.596	28.866	22.619	21.6867	25.000	26.087	15.000	
19.355	12.857	29.839	16.842	23.404	18.750	12.987	25.828	21.678	20.567	21.481	13.855	17.647	16.364	18.072	20.732	22.951	21.818	14.815	25.714	19.718	17.284	15.957		20.253	
24.691	24.779	20.000	16.129	25.301	16.279	19.753	15.873	20.183	25.217	12.727	12.598	16.146	15.556	32.500	20.721	16.667	15.000	25.743	18.421	19.737	29.8701	18.085	22.667	14.286	
20.968	20.301	21.739	10.127	27.174	16.667	10.127	24.031	23.571	21.622	20.588	21.154	18.857	4.348	12.500	18.584	22.500	22.222	13.000	25.333	13.699	18	25.000	19.000	15.054	
20.000	23.810	12.500	17.822	20.408	17.143	15.217	18.543	25.466	20.492	18.713	19.266	17.178	28.571	26.866	15.909	29.508	15.000	20.588	21.429	23.611	25.3165	25.000	24.138	18.868	
23.158	22.302		15.217	19.588	25.843	22.917	18.750	15.033	18.261	20.168	17.763	23.669	20.000	27.397	19.444	18.519	19.672	13.978	14.035	22.034	15.6627	22.826	26.042	15.789	
20.238	16.216	19.540	19.737	20.408	13.415	22.222	23.448	29.348	24.370	20.952	18.919	20.359	20.513	27.586	23.077	25.373	19.643	26.667	27.536	18.310	27.381	24.390	16.216	21.429	
16.049	21.111	23.000	20.779	18.519	15.152	18.750	19.231	21.849	15.909	17.742	16.406	17.544	25.397	11.765	19.000	25.000	20.000	19.565	20.779	27.632	14.9425	23.301	15.909	18.421	
17.284	16.535	16.250	21.111	11.565	19.588	23.596	24.476	18.797	24.348	15.833	20.144	18.286	20.455	18.605	19.355	20.000	21.212	24.324	23.810	16.279	21.538	31.5217	22.609	16.832	23.077
20.202	20.000	26.718	15.464	17.610	32.979	24.000	27.007		22.535	15.116	17.647	21.472	25.000	15.625		18.056	24.359	15.909	30.986	17.188	24.1379	22.936	21.429	20.482	
21.000	18.644	7.407	24.419	15.652	18.391	19.000	18.699	18.803	24.460	9.524	12.987	17.213	16.176	18.750		11.111	19.298	21.978	15.625	27.419	18.2927	26.966	28.169	20.833	
13.115	16.312	19.091	26.263	21.970	18.182	19.512	21.019	17.037	16.000	21.600	18.182	21.893	17.333	16.364		19.697	14.286	13.793	25.287	30.159	12.0482	18.868	19.565	16.456	
18.947	21.600	25.424	21.951	18.421	11.818	17.476	18.182	21.250	23.077	7.895	20.863	17.544	24.138	17.172		21.739	12.727	18.987	20.000	27.778	16.6667	21.782	25.333	16.667	
23.077	15.748	18.421	19.780	20.270	19.512	18.182	24.806	27.160	22.727	25.962	17.391	19.209	20.313	25.000		23.188	23.810	24.359	28.889	24.719	13.2353	16.250	18.349	22.892	
15.385	20.879	16.923	17.172	14.583	14.286	22.609	27.941	16.364	17.931		11.429	20.492	15.385	21.212		17.949	10.204	18.519	22.222	16.901	13.2353	21.277	22.581	16.667	
12.245	13.934	18.699	21.622	19.588	19.565		20.619	19.444	22.034		19.689	18.310	18.750			15.663	16.216	12.048	18.750	24.286	18.3099	20.870	18.519	24.706	
20.000	23.423	18.812	28.846	22.680	18.072		25.828	23.256	22.973		18.797	20.382	15.625			20.930	11.111	20.833		17.857	11.1111	27.826	17.978	11.842	
25.676	21.769	18.391	23.232	16.522	20.370		19.108	22.308	15.957		16.923	24.581	15.385			10.870	25.352	21.978	20.000	26.531	16.9014	21.978	21.348	20.690	
20.833	22.603	18.321	21.429	21.019	22.772		25.581	18.548	17.273		20.130	21.512	23.077			16.364	26.316	23.611	12.500	18.033	12.1212	17.347	21.053	18.310	

Table 4.S15 - Functional validation results in the $y \nu$ interval. Raw counts and associated P -values from validation in the $y \nu$ interval.

Control w1118	alph 8925	alph 11492	bru-2 18300	cdi 8883	cdi 24441	CG7196 8944	CG10864 6962	CG33970 8105	dpr6 24673	Eip75B 8100	grp 8945	grp f03358	jing 8044	MESR3 25484	pk 9062	pk 29252	Ptp61F 8053	Ptp61F 26133	Control 6326	CG9650 e04580	grp 26107	lola c01925	Oaz d09084	Ubx f07161
32.673	29.187	21.176	25.806	32.184	24.000	23.958	30.864	30.687	32.110	23.404	25.000	19.130	24.528	25.000	24.348	28.896	25.000	27.869	15.385	15.584	23.770	20.536	22.917	25.806
28.767	38.842	26.287	13.976	17.391	32.895	27.473	35.385	32.556	13.208	27.083	30.000	14.876	32.767	24.324	20.755	27.174	29.670	21.905	16.800	13.333	26.203	20.370	15.464	11.538
18.072	17.391	15.789	33.673	29.630	32.500	25.490	28.571		36.364	27.711	26.429	10.000	20.755	28.250	23.333	29.213	26.087	28.000	10.526	11.268	28.000	18.627	12.500	23.810
19.565	26.667	21.739	26.087	33.784	27.381	27.027	20.253	34.177	16.949	19.118	31.333	18.478	29.508	34.906	29.213	25.000	40.580	24.675	12.500	15.278	22.222	21.818	20.000	18.182
25.373	28.571	25.263	14.407	23.438	28.696	38.961	31.429	30.769	25.000	33.333	29.412	19.167	31.707	18.182	28.829	26.852	34.848	20.430	17.241	15.476	19.685	28.182	19.672	18.421
18.824	10.526	26.471	20.833	25.893	25.000	25.926	32.468	26.667	25.373	22.222	23.333	27.885	29.268	20.930	33.684	26.415	38.028	25.714	24.390	13.115	21.538	31.148	16.667	26.316
27.358	24.000	25.806	14.019	32.222	22.881	27.907	17.742	36.047	26.000	21.053	28.226	14.815	31.481	23.596	31.731	31.731	33.333	23.478	21.875	16.667	25.688	23.438	19.540	20.968
20.732	35.294	20.430	18.421	30.435	28.868	27.848	21.053	23.077	23.077	28.971	23.276	24.138	25.000	25.714	30.928	30.088	38.554	27.273	15.217	11.881	25.439	27.193	17.045	15.094
27.586	28.281	28.190	19.658	29.348	28.302	26.923	32.911	38.842	33.621	26.923	24.771	27.160		28.070	29.545	27.941	31.429	30.303	23.077	14.063	32.710	15.126	12.903	21.591
26.829	45.763	22.222	23.762	38.235	22.581	22.973	27.397	24.390	31.313	22.093	25.000	22.826		25.843	23.684	26.000	29.545	17.213	17.391	10.390	27.857	28.814	16.456	22.857
32.941	38.095	19.753	20.792	30.556	32.000	21.053	24.731	28.431	26.882	22.034	25.000	16.364		5.970	16.071	25.714	28.000	22.340	10.753		25.373	27.119	30.189	33.333
24.324	25.581	17.647	11.364	23.881	30.556	23.881	21.250	38.272	17.978	23.256	24.590	16.379		23.140	21.905	32.099	22.680	21.839	23.881	20.313	25.862	22.222	20.290	30.357
22.826	15.625	11.765	16.216	34.884	31.707	29.032	29.268	37.500	25.000	24.324	29.851	14.894		24.000	25.000	23.913	32.955	25.439	19.753	10.714	25.424	15.625	16.667	17.241
13.924	31.250	31.250	23.423	37.255	22.222	20.968	26.667	48.077		26.154	29.348	25.000		18.667	24.272	11.785	25.000	21.649	17.143	10.909	27.865	23.256	12.000	18.750
35.616	39.024	28.389	19.540	25.000	33.000	22.034	27.273	29.487	20.732	24.324	26.889	18.367		23.529	37.776	24.856	29.545	23.077	23.810	11.111	22.951	38.583	12.281	22.368
22.059	33.333	11.429	18.462	29.333	34.000	28.768	35.088	25.714	30.769	5.714	28.766	24.299		25.243	25.000	26.667	30.189	19.841	16.071	20.339	23.967	14.953	23.729	28.750
17.045	34.615	23.529	22.314	40.000	20.238	30.667	43.137	45.455	20.000	11.290	23.000	21.000		30.172	32.110	30.263	31.395	25.000	10.769	6.522	15.385	20.000	16.071	15.116
25.000	22.642	29.762	15.385	25.000	23.438	27.397	32.051	43.750	25.510	12.048	25.556	14.815		20.732	27.586	23.423	34.177	23.364	17.910	17.647	24.800	19.565	23.750	26.966
27.869	30.952	28.169	16.667	25.758	30.952	21.538	29.730	40.278	27.027	14.865	21.505	19.608		28.440	27.679	19.048	32.967	18.681	23.729	13.333	25.185	22.059	17.647	25.882
26.667	34.146	23.171	20.619	25.581	27.143	22.826	25.301	33.333	27.273	10.638	23.333	11.667		33.000	26.923	27.206	34.694	23.711	13.725	14.583	23.485	23.457	18.557	31.034
23.529	18.438	21.505	24.752	31.707	28.571	28.866	20.000	38.372	25.862	13.333	30.769	14.851		20.462	33.333	22.472	26.667	23.596	22.474	15.929	24.000	23.810	18.519	20.690
27.869	25.000	20.408	17.308	20.588	33.333	24.444	24.444	25.283	32.636	10.906	26.667	16.484		15.842	40.217	30.088	31.183	29.703	15.000	6.537	32.468	28.431	29.412	15.873
22.727	45.833	#DIV/0!	23.750	25.806	32.308	24.359	31.081	31.579	19.643	6.897	32.727	30.097		20.690	29.126	37.500	30.328	25.352	15.584	23.622	22.414	15.909	12.500	
12.766	20.690	21.739		17.500	30.337	23.810	34.426	30.488	35.556	10.638	23.158	24.444		17.241		29.487	30.864	28.571	14.493	12.222	27.586	30.000	14.286	25.000
28.333	33.333	20.879		30.769	32.000	23.611	32.895	49.383	28.378	15.493	25.000	20.183		17.526		29.167	30.263	22.680	18.571	8.333	21.008	16.667	18.182	24.286
33.803	30.435	24.038		35.294	30.435	18.750	36.538	30.882	28.571	19.444	30.841	17.021		28.571		30.303	35.556	20.000	30.952	10.938	23.610	20.792	20.000	29.762
32.258	30.612	24.419		26.667	27.083	17.544	27.119	35.443	29.412	12.500	30.088			34.513		27.551	32.836	24.545	20.755	6.422	17.391	23.750	26.190	6.667
18.462	24.615	20.408		17.308	33.333	31.866	32.143	19.643	25.490	14.000	28.571			25.424		22.759	34.463	26.549	23.611	15.068	25.620	28.866	19.565	13.208
27.451	30.882	32.500		28.923	19.118	27.500	31.846	42.105	29.806	17.333	25.455			25.000		25.758	29.268	23.813	16.216	7.500		23.423	17.544	17.391
33.333	29.268	31.683		30.435	25.000	24.266	27.273	33.333	29.545	12.281	25.000			28.446		30.357	22.581	28.571	13.158	12.121	25.620	16.667	24.706	

Table 4.S16 - DGRP lines used for qPCR expression analysis. List of DGRP lines selected for each candidate gene for qPCR expression analysis.

Gene	Major Allele (#1)	Major Allele (#2)	Major Allele (#3)	Minor Allele (#1)	Minor Allele (#2)	Minor Allele (#3)
<i>alph</i>	DGRP_49	DGRP_310	DGRP_332	DGRP_379	DGRP_843	DGRP_879
<i>bru-2</i>	DGRP_59	DGRP_367	DGRP_761	DGRP_307	DGRP_491	DGRP_730
<i>cdi</i>	DGRP_757	DGRP_765	DGRP_774	DGRP_589	DGRP_703	DGRP_911
<i>CG1273</i>	DGRP_365	DGRP_370	DGRP_391	DGRP_287	DGRP_441	DGRP_716
<i>CG4440</i>	DGRP_315	DGRP_320	DGRP_321	DGRP_223	DGRP_530	DGRP_783
<i>CG7196</i>	DGRP_73	DGRP_75	DGRP_531	DGRP_57	DGRP_439	DGRP_737
<i>CG9650</i>	DGRP_356	DGRP_535	DGRP_787	DGRP_375	DGRP_395	DGRP_639
<i>CG10864</i>	DGRP_354	DGRP_355	DGRP_362	DGRP_91	DGRP_176	DGRP_505
<i>CG15365</i>	DGRP_392	DGRP_399	DGRP_596	DGRP_239	DGRP_804	DGRP_832
<i>CG33970</i>	DGRP_508	DGRP_513	DGRP_517	DGRP_304	DGRP_705	DGRP_850
<i>dpr6</i>	DGRP_21	DGRP_228	DGRP_235	DGRP_41	DGRP_229	DGRP_890
<i>Eip75B</i>	DGRP_83	DGRP_790	DGRP_796	DGRP_233	DGRP_386	DGRP_486
<i>grp</i>	DGRP_26	DGRP_101	DGRP_301	DGRP_161	DGRP_319	DGRP_406
<i>jing</i>	DGRP_158	DGRP_256	DGRP_900	DGRP_42	DGRP_227	DGRP_727
<i>lola</i>	DGRP_129	DGRP_142	DGRP_149	DGRP_40	DGRP_822	DGRP_892
<i>MESR3</i>	DGRP_45	DGRP_340	DGRP_371	DGRP_153	DGRP_208	DGRP_280
<i>Oaz</i>	DGRP_177	DGRP_181	DGRP_195	DGRP_306	DGRP_380	DGRP_801
<i>pk</i>	DGRP_217	DGRP_427	DGRP_887	DGRP_382	DGRP_808	DGRP_819
<i>Ptp61F</i>	DGRP_853	DGRP_859	DGRP_897	DGRP_357	DGRP_461	DGRP_799
<i>Ubx</i>	DGRP_805	DGRP_818	DGRP_882	DGRP_318	DGRP_385	DGRP_509

Table 4.S17 - Genotypes of DGRP lines used for qPCR. Genotype of DGRP lines selected for qPCR expression analysis at respective gene of choice.

	<i>alph</i>	chr3R:25440527_SNP				
Major Allele (#1)	DGRP_49	T/T				
Major Allele (#2)	DGRP_310	T/T				
Major Allele (#3)	DGRP_332	T/T				
Minor Allele (#1)	DGRP_379	C/C				
Minor Allele (#2)	DGRP_843	C/C				
Minor Allele (#3)	DGRP_879	C/C				
	<i>bru-2</i>	chr2L:12359168_SNP				
Major Allele (#1)	DGRP_59	T/T				
Major Allele (#2)	DGRP_367	T/T				
Major Allele (#3)	DGRP_761	T/T				
Minor Allele (#1)	DGRP_307	A/A				
Minor Allele (#2)	DGRP_491	A/A				
Minor Allele (#3)	DGRP_730	A/A				
	<i>cdi</i>	chr3R:14913855_INS				
Major Allele (#1)	DGRP_757	(G)-(G)-				
Major Allele (#2)	DGRP_765	(G)-(G)-				
Major Allele (#3)	DGRP_774	(G)-(G)-				
Minor Allele (#1)	DGRP_589	(G)A(G)A				
Minor Allele (#2)	DGRP_703	(G)A(G)A				
Minor Allele (#3)	DGRP_911	(G)A(G)A				
	CG1273	chr3L:4268808_SNP	chr3L:4268986_SNP			
Major Allele (#1)	DGRP_365	A/A	C/C			
Major Allele (#2)	DGRP_370	A/A	C/C			
Major Allele (#3)	DGRP_391	A/A	C/C			
Minor Allele (#1)	DGRP_287	G/G	T/T			
Minor Allele (#2)	DGRP_441	G/G	T/T			
Minor Allele (#3)	DGRP_716	G/G	T/T			
	CG4440	chr2L:16330317_SNP	chr2L:16330317_SNP	chr2L:16330043_SNP	chr2L:16330091_SNP	chr2L:16330185_SNP
Major Allele (#1)	DGRP_315	A/A	A/A	A/A	A/A	G/G
Major Allele (#2)	DGRP_320	A/A	A/A	A/A	A/A	G/G
Major Allele (#3)	DGRP_321	A/A	A/A	A/A	A/A	G/G
Minor Allele (#1)	DGRP_223	A/A	A/A	T/T	G/G	T/T
Minor Allele (#2)	DGRP_530	A/A	A/A	T/T	G/G	T/T
Minor Allele (#3)	DGRP_783	A/A	A/A	T/T	G/G	T/T
	CG7196	chr2L:7760128_SNP	chr2L:7760144_SNP	chr2L:7763275_SNP	chr2L:7765617_SNP	chr2L:7766066_SNP
Major Allele (#1)	DGRP_73	G/G	T/T	G/G	T/T	G/G
Major Allele (#2)	DGRP_75	G/G	T/T	G/G	T/T	G/G
Major Allele (#3)	DGRP_531	.	C/C	G/G	T/T	G/G
Minor Allele (#1)	DGRP_57	G/G	T/T	G/G	T/T	C/C
Minor Allele (#2)	DGRP_439	G/G	T/T	G/G	T/T	C/C
Minor Allele (#3)	DGRP_737	A/A	C/C	G/G	T/T	C/C
	CG9650	chrX:7060779_SNP				
Major Allele (#1)	DGRP_356	G/G				
Major Allele (#2)	DGRP_535	G/G				
Major Allele (#3)	DGRP_787	G/G				
Minor Allele (#1)	DGRP_375	T/T				
Minor Allele (#2)	DGRP_395	T/T				
Minor Allele (#3)	DGRP_639	T/T				
	CG10864	chr3R:14236729_SNP				
Major Allele (#1)	DGRP_354	A/A				
Major Allele (#2)	DGRP_355	A/A				
Major Allele (#3)	DGRP_362	A/A				
Minor Allele (#1)	DGRP_91	C/C				
Minor Allele (#2)	DGRP_176	C/C				
Minor Allele (#3)	DGRP_505	C/C				
	CG15365	chrX:8951785_SNP				
Major Allele (#1)	DGRP_392	C/C				
Major Allele (#2)	DGRP_399	C/C				
Major Allele (#3)	DGRP_596	C/C				
Minor Allele (#1)	DGRP_239	T/T				
Minor Allele (#2)	DGRP_804	T/T				
Minor Allele (#3)	DGRP_832	T/T				

Table 4.S17 Continued

	CG33970	chr3R:22168414_SNP								
Major Allele (#1)	DGRP_508	A/A								
Major Allele (#2)	DGRP_513	A/A								
Major Allele (#3)	DGRP_517	A/A								
Minor Allele (#1)	DGRP_304	G/G								
Minor Allele (#2)	DGRP_705	G/G								
Minor Allele (#3)	DGRP_890	G/G								
	dpr6	chr3L:10077092_SNP	chr3L:10022098_SNP	chr3L:10022196_SNP	chr3L:10065561_INS					
Major Allele (#1)	DGRP_21	G/G	C/C	T/T	(A)-(A)					
Major Allele (#2)	DGRP_228	G/G	C/C	T/T	J					
Major Allele (#3)	DGRP_235	G/G	C/C	T/T	(A)-(A)					
Minor Allele (#1)	DGRP_41	G/G	T/T	G/G	(A)GCA(A)GCA					
Minor Allele (#2)	DGRP_229	G/G	T/T	G/G	J					
Minor Allele (#3)	DGRP_890	G/G	T/T	G/G	(A)-(A)					
	Epf75B	chr3L:18016881_SNP	chr3L:17950305_SNP							
Major Allele (#1)	DGRP_83	A/A	G/G							
Major Allele (#2)	DGRP_790	A/A	G/G							
Major Allele (#3)	DGRP_796	A/A	G/G							
Minor Allele (#1)	DGRP_233	A/A	A/A							
Minor Allele (#2)	DGRP_388	A/A	A/A							
Minor Allele (#3)	DGRP_486	A/A	A/A							
	dpr	chr2L:16694744_SNP								
Major Allele (#1)	DGRP_26	T/T								
Major Allele (#2)	DGRP_101	T/T								
Major Allele (#3)	DGRP_301	T/T								
Minor Allele (#1)	DGRP_161	A/A								
Minor Allele (#2)	DGRP_319	A/A								
Minor Allele (#3)	DGRP_406	A/A								
	jing	chr2R:2424152_SNP	chr2R:2426434_SNP	chr2R:2428451_SNP	chr2R:2428634_SNP	chr2R:2428764_SNP	chr2R:2428894_SNP	chr2R:2428935_SNP	chr2R:2429479_SNP	chr2R:2433735_SNP
Major Allele (#1)	DGRP_158	T/T	G/G	G/G	T/T	G/G	G/G	G/G	A/A	C/C
Major Allele (#2)	DGRP_256	T/T	G/G	G/G	T/T	G/G	G/G	G/G	A/A	C/C
Major Allele (#3)	DGRP_900	T/T	G/G	G/G	T/T	G/G	G/G	G/G	A/A	C/C
Minor Allele (#1)	DGRP_42	C/C	J	J	A/A	A/A	T/T	A/A	T/T	A/A
Minor Allele (#2)	DGRP_227	C/C	G/G	G/G	T/T	G/G	G/G	G/G	A/A	C/C
Minor Allele (#3)	DGRP_727	C/C	T/T	T/T	A/A	A/A	J	A/A	T/T	A/A
	jing	chr2R:2434296_SNP	chr2R:2436436_SNP	chr2R:2438246_DEL	chr2R:2438252_INS	chr2R:2438717_SNP	chr2R:2440017_SNP	chr2R:2440093_SNP	chr2R:2446236_SNP	
Major Allele (#1)	DGRP_158	C/C	G/G	(C)TATG(C)TATG	(T)-(T)	C/C	A/A	C/C	T/T	
Major Allele (#2)	DGRP_256	C/C	G/G	J	J	C/C	A/A	C/C	T/T	
Major Allele (#3)	DGRP_900	C/C	G/G	(C)TATG(C)TATG	(T)-(T)	C/C	A/A	C/C	T/T	
Minor Allele (#1)	DGRP_42	A/A	A/A	(C)-(C)	(T)CAT(T)CAT	A/A	T/T	A/A	C/C	
Minor Allele (#2)	DGRP_227	C/C	G/G	(C)TATG(C)TATG	(T)-(T)	C/C	A/A	C/C	T/T	
Minor Allele (#3)	DGRP_727	A/A	A/A	(C)-(C)	(T)CAT(T)CAT	A/A	T/T	J	C/C	
	lola	chr2R:6379425_SNP								
Major Allele (#1)	DGRP_129	C/C								
Major Allele (#2)	DGRP_142	C/C								
Major Allele (#3)	DGRP_149	C/C								
Minor Allele (#1)	DGRP_40	T/T								
Minor Allele (#2)	DGRP_822	T/T								
Minor Allele (#3)	DGRP_892	T/T								
	MESR3	chr2L:18647760_SNP								
Major Allele (#1)	DGRP_45	G/G								
Major Allele (#2)	DGRP_340	G/G								
Major Allele (#3)	DGRP_371	G/G								
Minor Allele (#1)	DGRP_153	C/C								
Minor Allele (#2)	DGRP_208	C/C								
Minor Allele (#3)	DGRP_280	C/C								
	Oaz	chr2R:10335293_SNP								
Major Allele (#1)	DGRP_177	T/T								
Major Allele (#2)	DGRP_181	T/T								
Major Allele (#3)	DGRP_195	T/T								
Minor Allele (#1)	DGRP_306	C/C								
Minor Allele (#2)	DGRP_380	C/C								
Minor Allele (#3)	DGRP_801	C/C								

Table 4.S17 Continued

	pk	chr2R:3083775_SNP
Major Allele (#1)	DGRP_217	C/C
Major Allele (#2)	DGRP_427	C/C
Major Allele (#3)	DGRP_887	C/C
Minor Allele (#1)	DGRP_382	T/T
Minor Allele (#2)	DGRP_808	T/T
Minor Allele (#3)	DGRP_919	T/T

	Ptp61F	chr3L:1393055_SNP	chr3L:1393071_SNP	chr3L:1400394_SNP	chr3L:1455295_SNP	chr3L:1455555_SNP	chr3L:1455925_SNP	chr3L:1456574_SNP	chr3L:1456902_SNP	chr3L:1456916_SNP	chr3L:1456953_SNP	chr3L:1456971_SNP	chr3L:1472460_SNP	chr3L:1452328_SNP
Major Allele (#1)	DGRP_853	G/G	G/G	A/A	A/A	C/C	G/G	A/A	C/C	C/C	C/C	T/T	G/G	T/T
Major Allele (#2)	DGRP_859	G/G	G/G	A/A	A/A	C/C	G/G	A/A	C/C	C/C	C/C	T/T	G/G	T/T
Major Allele (#3)	DGRP_897	G/G	G/G	A/A	A/A	C/C	G/G	A/A	C/C	C/C	C/C	T/T	G/G	T/T
Minor Allele (#1)	DGRP_357	G/G	G/G	G/G	A/A	C/C	G/G	-	C/C	C/C	C/C	T/T	G/G	T/T
Minor Allele (#2)	DGRP_461	G/G	G/G	G/G	A/A	C/C	G/G	A/A	C/C	C/C	C/C	T/T	G/G	T/T
Minor Allele (#3)	DGRP_799	G/G	G/G	G/G	A/A	C/C	G/G	A/A	C/C	C/C	C/C	T/T	G/G	T/T

	Ubx	chr3R:12557674_SNP	chr3R:12557680_SNP
Major Allele (#1)	DGRP_805	C/C	A/A
Major Allele (#2)	DGRP_818	C/C	A/A
Major Allele (#3)	DGRP_882	C/C	A/A
Minor Allele (#1)	DGRP_318	A/A	G/G
Minor Allele (#2)	DGRP_385	A/A	G/G
Minor Allele (#3)	DGRP_509	A/A	G/G

Table 4.S18 - qPCR expression data. Cq values from qPCR expression analysis, normalized to GAPDH expression. Lines 1-3 for the major and minor allele correspond to lines in Table 4.S16.

	alph	bru-2	cdi	CG1273	CG4440	CG7196	CG9650	CG10864	CG15365	CG33970	dpr6	Eip75B	grp	jing	lola	MESR3	Oaz	pk	Ptp61F	Ubx
	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major
Line1_Replicate1_A	0.931	1.070	1.054	1.199	1.206	1.285	1.117	1.248	1.292	1.412	1.074	1.097	0.851	1.186	0.920	1.148	1.363	1.367	1.155	1.465
Line1_Replicate1_B	1.073	1.057	1.229	1.140	1.286	1.231	1.248	1.285	1.635	1.074	1.105	0.866	1.149	0.922	1.106	1.363	1.371	1.150	1.475	
Line1_Replicate1_C	0.914	1.084	1.594	1.275	1.163	1.320	1.274	1.254	1.300	1.463	1.086	1.096	0.850	1.169	0.916	1.124	1.381	1.376	1.201	1.516
Line1_Replicate1_D	0.920	1.078	1.174	1.196	1.212	1.449	1.198	1.249	1.317	1.077	1.077	1.101	0.823	1.174	0.936	1.118	1.396	1.397	1.137	1.518
Line1_Replicate2_A	1.167	1.046	1.094	1.244	1.159	1.264	1.239	1.282	1.203	1.407	1.339	1.080	0.925	1.112	0.926	1.174	1.275	1.195	1.375	1.300
Line1_Replicate2_B	0.939	1.047	1.111	1.266	1.106	1.289	1.295	1.292	1.239	1.448	1.062	1.110	0.908	1.081	0.942	1.152	1.227	1.194	1.302	1.282
Line1_Replicate2_C	0.918	1.098	1.124	1.273	1.111	1.282	1.345	1.281	1.257	1.408	1.079	1.098	0.913	1.089	0.977	1.159	1.240	1.177	1.391	1.313
Line1_Replicate2_D	0.919	1.080	1.115	1.237	1.184	1.505	1.286	1.307	1.281	1.462	1.052	1.118	0.825	1.109	0.940	1.164	1.233	1.188	1.351	1.317
Line1_Replicate3_A	0.984	1.071	1.042	1.301	1.346	1.189	1.199	1.333	1.325	1.076	1.111	0.985	1.111	0.900	1.113	1.133	1.133	1.133	1.553	1.250
Line1_Replicate3_B	0.910	1.086	1.034	1.287	1.359	1.182	1.302	1.246	1.340	1.348	1.048	1.139	0.908	1.141	0.878	1.127	1.145	1.384	1.519	1.273
Line1_Replicate3_C	0.921	1.075	1.127	1.285	1.319	1.186	1.314	1.224	1.370	1.323	1.078	1.121	0.891	1.149	0.877	1.104	1.147	1.368	1.576	1.261
Line1_Replicate3_D	1.320	1.071	1.064	1.288	1.352	1.529	1.256	1.226	1.368	1.383	1.058	1.114	0.893	1.136	0.899	1.111	1.163	1.373	1.469	1.287
Line1_Replicate4_A	0.907	1.067	1.097	1.128	1.157	1.203	1.312	1.329	1.472	1.048	1.095	0.977	1.156	0.981	1.135	1.254	1.228	1.101	1.160	
Line1_Replicate4_B	0.911	1.066	1.122	1.170	1.126	1.210	1.337	1.313	1.310	1.569	1.041	1.096	1.002	1.146	1.007	1.147	1.295	1.270	1.132	1.158
Line1_Replicate4_C	0.921	1.053	1.108	1.144	1.118	1.208	1.349	1.324	1.349	1.478	1.047	1.096	0.972	1.152	0.992	1.121	1.292	1.280	1.181	1.169
Line1_Replicate4_D	1.515	1.110	1.140	1.126	1.141	1.409	1.325	1.298	1.327	1.521	1.041	1.092	0.946	1.138	1.016	1.110	1.308	1.275	1.107	1.202
Line2_Replicate1_A	0.942	1.158	1.094	1.188	1.134	1.172	1.277	1.286	1.296	1.446	1.061	1.146	0.909	1.184	0.950	1.124	1.294	1.370	1.087	1.280
Line2_Replicate1_B	1.529	1.104	1.099	1.234	1.124	1.183	1.290	1.299	1.318	1.485	1.058	1.168	0.935	1.183	0.953	1.129	1.320	1.401	1.130	1.300
Line2_Replicate1_C	0.918	1.333	1.092	1.236	1.110	1.173	1.291	1.301	1.332	1.431	1.062	1.158	0.906	1.206	0.952	1.106	1.305	1.465	1.108	1.301
Line2_Replicate1_D	0.925	1.147	1.095	1.217	1.150	1.394	1.281	1.298	1.413	1.489	1.069	1.163	0.899	1.187	0.965	1.112	1.323	1.416	1.129	1.303
Line2_Replicate2_A	1.135	1.096	1.097	1.202	1.159	1.309	1.310	1.304	1.304	1.093	1.111	0.952	1.170	0.977	1.181	1.156	1.464	0.970	1.338	
Line2_Replicate2_B	0.927	1.121	1.118	1.114	1.224	1.173	1.322	1.303	1.321	1.105	1.109	1.003	1.194	0.978	1.192	1.219	1.471	1.024	1.337	
Line2_Replicate2_C	0.926	1.095	1.110	1.111	1.219	1.159	1.334	1.315	1.330	1.107	1.114	0.951	1.211	0.994	1.160	1.172	1.497	1.000	1.359	
Line2_Replicate2_D	0.949	1.109	1.108	1.106	1.241	1.416	1.331	1.300	1.370	1.101	1.120	0.934	1.174	0.988	1.143	1.230	1.498	1.035	1.366	
Line2_Replicate3_A	0.933	1.153	1.017	1.151	1.151	1.280	1.163	1.370	1.370	1.069	1.163	0.893	1.107	1.076	1.412	1.160	1.117	1.296		
Line2_Replicate3_B	1.063	1.138	1.034	1.183	1.171	1.104	1.318	1.121	1.200	1.397	1.127	1.092	0.932	1.188	0.929	1.126	1.423	1.203	1.135	1.351
Line2_Replicate3_C	1.055	1.148	1.026	1.180	1.170	1.150	1.298	1.350	1.209	1.353	1.123	1.075	0.875	1.230	0.940	1.052	1.401	1.269	1.056	1.334
Line2_Replicate3_D	1.071	1.138	1.031	1.150	1.150	1.509	1.306	1.340	1.252	1.423	1.133	1.083	0.871	1.129	0.951	1.060	1.461	1.176	1.189	1.323
Line2_Replicate4_A	1.163	1.120	1.134	1.158	1.200	1.362	1.353	1.209	1.712	1.153	1.206	0.878	1.136	0.882	1.059	1.270	1.226	1.114	1.286	
Line2_Replicate4_B	1.012	1.147	1.041	1.184	1.175	1.218	1.364	1.363	1.212	1.577	1.165	1.216	0.914	1.222	0.878	1.108	1.307	1.264	1.234	1.317
Line2_Replicate4_C	1.082	1.203	1.031	1.164	1.164	1.227	1.360	1.358	1.216	1.569	1.155	1.206	0.882	1.246	0.898	1.038	1.305	1.311	1.177	1.310
Line2_Replicate4_D	1.017	1.131	1.035	1.175	1.167	1.505	1.353	1.363	1.227	1.646	1.166	1.203	0.867	1.182	0.892	1.045	1.339	1.252	1.211	1.314
Line3_Replicate1_A	0.929	1.104	1.069	1.203	1.048	1.223	1.316	1.155	1.221	1.109	1.120	0.931	1.220	0.894	1.080	1.430	1.319	1.121	1.315	
Line3_Replicate1_B	0.913	1.131	1.275	1.161	1.089	1.232	1.247	1.161	1.253	1.093	1.110	0.970	1.270	0.905	1.074	1.426	1.350	1.168	1.401	
Line3_Replicate1_C	0.972	1.122	1.213	1.152	1.222	1.315	1.183	1.284	1.284	1.108	1.131	0.948	1.208	0.929	1.110	1.384	1.420	1.078	1.381	
Line3_Replicate1_D	0.980	1.167	1.091	1.204	1.201	1.231	1.319	1.177	1.254	1.098	1.121	0.965	1.258	0.934	1.113	1.419	1.405	1.102	1.416	
Line3_Replicate2_A	0.912	1.127	1.074	1.293	1.160	1.264	1.223	1.291	1.268	1.468	1.131	1.149	0.860	1.178	0.977	1.134	1.309	1.445	1.461	1.404
Line3_Replicate2_B	0.919	1.141	1.116	1.236	1.200	1.267	1.148	1.339	1.322	1.478	1.117	1.155	0.857	1.211	0.959	1.163	1.365	1.483	1.392	1.454
Line3_Replicate2_C	0.903	1.144	1.242	1.195	1.226	1.217	1.325	1.315	1.499	1.127	1.140	0.862	1.169	0.970	1.169	1.339	1.514	1.320	1.437	
Line3_Replicate2_D	0.921	1.178	1.097	1.265	1.253	1.275	1.212	1.342	1.332	1.550	1.126	1.151	0.863	1.204	0.995	1.169	1.385	1.601	1.336	1.465
Line3_Replicate3_A	0.916	1.141	1.068	1.294	1.165	1.422	1.198	1.313	1.232	1.355	1.145	1.177	0.841	1.121	0.981	1.055	1.349	1.434	1.411	1.230
Line3_Replicate3_B	1.145	1.074	1.237	1.203	1.443	1.133	1.326	1.375	1.406	1.147	1.184	0.846	1.154	0.996	1.128	1.372	1.434	1.383	1.311	
Line3_Replicate3_C	0.923	1.164	1.073	1.293	1.208	1.223	1.175	1.320	1.358	1.416	1.143	1.174	0.824	1.110	0.991	1.098	1.344	1.448	1.358	1.277
Line3_Replicate3_D	0.936	1.179	1.070	1.308	1.264	1.385	1.204	1.368	1.387	1.409	1.144	1.196	0.816	1.157	1.011	1.090	1.349	1.461	1.322	1.296
Line3_Replicate4_A	1.395	1.127	1.075	1.128	1.091	1.345	1.279	1.428	1.273	1.413	1.090	1.063	0.966	1.064	0.950	1.142	1.273	1.279	1.071	1.187
Line3_Replicate4_B	0.877	1.136	1.071	1.097	1.101	1.340	1.255	1.434	1.320	1.395	1.065	1.047	0.962	1.092	0.962	1.211	1.286	1.369	1.065	1.269
Line3_Replicate4_C	0.904	1.190	1.081	1.113	1.155	1.229	1.300	1.448	1.330	1.422	1.081	1.044	0.971	1.065	0.936	1.187	1.289	1.034	1.210	
Line3_Replicate4_D	0.934	1.194	1.093	1.113	1.208	1.349	1.287	1.445	1.364	1.444	1.103	1.059	0.969	1.095	0.976	1.193	1.257	1.357	1.059	1.270
Average	0.995	1.125	1.098	1.203	1.179	1.278	1.278	1.298	1.295	1.457	1.102	1.124	0.908	1.162	0.946	1.124	1.307	1.352	1.210	1.321
Standard Error	0.024	0.007	0.013	0.009	0.010	0.016	0.009	0.011	0.008	0.014	0.007	0.006	0.007	0.007	0.006	0.006	0.012	0.016	0.023	0.013
Count	44	48	46	47	47	48	47	47	48	39	47	48	48	48	47	48	48	48	48	48

Table 4.S18 Continued

	<i>alph</i>	<i>bru-2</i>	<i>cdi</i>	<i>CG1273</i>	<i>CG4440</i>	<i>CG7196</i>	<i>CG9650</i>	<i>CG10864</i>	<i>CG15365</i>	<i>CG33970</i>	<i>dpr6</i>	<i>Eip75B</i>	<i>grp</i>	<i>jing</i>	<i>lola</i>	<i>MESR3</i>	<i>Oaz</i>	<i>pk</i>	<i>Ptp61F</i>	<i>Ubx</i>
	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor
Line1_Replicate1_A	1.110	1.127	1.050	1.226	1.031	1.247	1.168	1.443	1.309	1.234	1.161	1.149	0.919	1.093	0.939	1.123	1.422	1.422	1.020	1.390
Line1_Replicate1_B	0.907	1.116	1.058	1.200	1.038	1.272	1.183	1.448	1.330	1.235	1.142	1.163	0.943	1.123	0.950	1.182	1.447	1.447	1.038	1.417
Line1_Replicate1_C	1.108	1.202	1.058	1.216	1.036	1.154	1.179	1.454	1.334	1.261	1.161	1.149	0.899	1.104	0.896	1.135	1.440	1.440	1.016	1.385
Line1_Replicate1_D	1.119	1.151	1.059	1.219	1.093	1.279	1.229	1.448	1.376	1.262	1.177	1.168	0.888	1.129	0.931	1.146	1.422	1.422	1.036	1.412
Line1_Replicate2_A	0.887	1.123	1.019	1.314	0.906	1.261	1.281	1.125	1.419	1.423	1.141	1.158	0.967	1.242	0.946	1.085	1.425	1.425	1.141	1.357
Line1_Replicate2_B	1.597	1.135	1.023	1.320	0.920	1.265	1.257	1.154	1.450	1.391	1.155	1.170	0.966	1.247	0.951	1.192	1.463	1.463	1.148	1.379
Line1_Replicate2_C	1.114	1.127	1.026	1.304	0.918	1.140	1.285	1.166	1.438	1.425	1.157	1.176	0.943	1.284	0.886	1.119	1.496	1.496	1.143	1.342
Line1_Replicate2_D	1.105	1.205	1.025	1.306	0.960	1.256	1.290	1.151	1.539	1.407	1.158	1.186	0.954	1.247	0.905	1.113	1.458	1.458	1.145	1.357
Line1_Replicate3_A	0.958	1.138	1.035	1.343	1.012	1.401	1.148	1.342	1.245	1.301	1.057	1.235	0.860	1.118	0.917	1.090	1.316	1.316	1.129	1.363
Line1_Replicate3_B	0.943	1.116	1.034	1.351	1.028	1.397	1.171	1.347	1.261	1.318	1.055	1.264	0.866	1.110	0.934	1.181	1.352	1.352	1.141	1.392
Line1_Replicate3_C	0.898	1.173	1.047	1.314	1.031	1.124	1.158	1.343	1.241	1.317	1.051	1.225	0.848	1.145	0.865	1.125	1.423	1.423	1.132	1.337
Line1_Replicate3_D	0.909	1.103	1.040	1.326	1.049	1.458	1.197	1.353	1.293	1.328	1.059	1.256	0.876	1.139	0.889	1.167	1.292	1.292	1.168	1.396
Line1_Replicate4_A	0.970	1.110	1.127	1.152	0.993	1.310	1.324	1.203	1.267	1.433	1.136	1.259	0.997	1.071	1.015	1.097	1.326	1.326	1.183	1.384
Line1_Replicate4_B	0.947	1.127	1.108	1.146	0.991	1.300	1.255	1.220	1.287	1.436	1.125	1.158	0.974	1.024	1.034	1.141	1.362	1.362	1.132	1.343
Line1_Replicate4_C	0.914	1.113	1.106	1.123	0.991	1.185	1.299	1.218	1.276	1.422	1.107	1.124	0.972	1.121	0.949	1.113	1.376	1.376	1.105	1.329
Line1_Replicate4_D	0.905	1.107	1.105	1.140	1.008	1.303	1.299	1.225	1.316	1.410	1.110	1.148	0.985	1.050	0.980	1.133	1.292	1.292	1.189	1.397
Line2_Replicate1_A	0.972	1.109	1.033	1.383	1.060	1.376	1.295	1.379	1.183	1.189	1.382	0.879	1.257	0.937	1.217	1.471	1.319	1.319	1.071	1.358
Line2_Replicate1_B	0.984	1.099	1.029	1.369	1.036	1.400	1.278	1.392	1.240	1.190	1.156	0.849	1.259	0.956	1.175	1.450	1.293	1.055	1.402	
Line2_Replicate1_C	0.946	1.109	1.043	1.303	1.035	1.338	1.392	1.202	1.180	1.159	0.833	1.293	0.957	1.181	1.446	1.278	1.014	1.365		
Line2_Replicate1_D	0.966	1.089	1.075	1.328	1.053	1.405	1.307	1.751	1.213	1.197	1.145	0.870	1.327	0.977	1.183	1.488	1.314	0.991	1.361	
Line2_Replicate2_A	0.973	1.094	1.122	1.392	1.157	1.410	1.261	1.331	1.033	1.424	1.208	1.132	1.044	1.153	1.008	1.166	1.313	1.358	1.097	1.390
Line2_Replicate2_B	0.962	1.094	1.129	1.335	1.163	1.462	1.269	1.344	1.092	1.643	1.212	1.131	1.005	1.146	1.022	1.107	1.390	1.398	1.070	1.384
Line2_Replicate2_C	0.949	1.082	1.126	1.287	1.126	1.418	1.298	1.331	1.057	1.550	1.201	1.126	0.973	1.176	0.988	1.089	1.346	1.386	1.075	1.375
Line2_Replicate2_D	0.979	1.084	1.165	1.299	1.146	1.440	1.342	1.647	1.038	1.528	1.215	1.131	1.420	1.168	1.021	1.122	1.368	1.374	1.101	1.370
Line2_Replicate3_A	1.103	1.117	1.047	1.318	1.123	1.187	1.216	1.211	1.108	1.479	1.206	1.136	0.933	1.121	0.997	1.133	1.426	1.331	1.103	1.305
Line2_Replicate3_B		1.133	1.041	1.304	1.140	1.257	1.261	1.241	1.121	1.749	1.213	1.136	0.918	1.121	1.026	1.112	1.486	1.318	1.316	1.340
Line2_Replicate3_C	0.994	1.089	1.045	1.254	1.149	1.228	1.270	1.230	1.108	1.519	1.224	1.119	0.894	1.155	1.019	1.103	1.479	1.328	1.384	1.321
Line2_Replicate3_D	0.988	1.090	1.048		1.097	1.179	1.301	1.270	1.121	1.484	1.203	1.143	0.912	1.179	1.026	1.114	1.494	1.359	1.080	1.311
Line2_Replicate4_A	0.961	1.129	1.101	1.414	1.056	1.217	1.254	1.391	1.063	1.421	1.074	1.119	0.879	1.111	1.002	1.159	1.416	1.277	1.056	1.316
Line2_Replicate4_B	0.984	1.238	1.093	1.390	1.025	1.263	1.301	1.403	1.045	1.433	1.057	1.137	0.837	1.116	1.027	1.155	1.443	1.319	1.044	1.392
Line2_Replicate4_C	0.992	1.176	1.089	1.351	1.023	1.239	1.277	1.387	1.051	1.421	1.057	1.122	0.817	1.127	1.001	1.128	1.406	1.292	1.025	1.353
Line2_Replicate4_D	0.984	1.111	1.108	1.369	1.021	1.185	1.347	1.452	1.045	1.509	1.080	1.126	0.858	1.138	1.031	1.157	1.467	1.357	1.052	1.333
Line3_Replicate1_A	1.388	1.024	1.339	1.223	1.343	1.241	1.445	1.225	1.313	1.090	1.205	1.012	1.148	0.991	1.151	1.351	1.237	1.136	1.290	
Line3_Replicate1_B	0.984	1.039	1.299	1.225	1.384	1.276	1.460	1.185	1.321	1.092	1.217	0.995	1.166	1.008	1.151	1.382	1.268	1.134	1.303	
Line3_Replicate1_C	0.969	1.024	1.274	1.205	1.301	1.260	1.442	1.213	1.312	1.087	1.205	0.955	1.164	0.989	1.138	1.338	1.248	1.112	1.293	
Line3_Replicate1_D	0.991	1.041	1.256	1.229	1.343	1.316	1.498	1.217	1.348	1.101	1.216	0.987	1.225	1.010	1.163	1.408	1.292	1.146	1.300	
Line3_Replicate2_A	1.040	1.112	1.433	1.100	1.274	1.280	1.498	1.193	1.280	1.080	1.157	0.934	1.141	0.838	1.150	1.461	1.294	1.043	1.258	
Line3_Replicate2_B	0.987	1.109	1.334	1.099	1.276	1.267	1.513	1.168	1.301	1.078	1.146	0.895	1.174	0.846	1.149	1.445	1.333	1.053	1.282	
Line3_Replicate2_C	0.973	1.108	1.361	1.079	1.279	1.288	1.491	1.174	1.274	1.082	1.155	0.882	1.138	0.840	1.136	1.414	1.304	1.033	1.256	
Line3_Replicate2_D	0.985	1.129	1.319	1.096	1.263	1.350	1.522	1.193	1.444	1.098	1.148	0.913	1.191	0.861	1.156	1.518	1.340	1.080	1.274	
Line3_Replicate3_A	0.929	1.109	1.345	1.172	1.192	1.252	1.312	1.270	1.361	1.091	1.136	0.983	1.208	0.988	1.081	1.525	1.365	1.243	1.354	
Line3_Replicate3_B	0.934	1.114	1.258	1.171	1.226	1.223	1.347	1.212	1.376	1.097	1.127	0.981	1.215	1.005	1.104	1.351	1.393	1.265	1.407	
Line3_Replicate3_C	1.026	1.106	1.319	1.157	1.215	1.264	1.312	1.204	1.349	1.095	1.133	0.974	1.195	0.988	1.092	1.356	1.392	1.219	1.371	
Line3_Replicate3_D	1.028	1.129	1.255	1.145	1.216	1.275	1.275	1.275	1.477	1.101	1.132	0.980	1.268	1.017	1.102	1.507	1.396	1.256	1.365	
Line3_Replicate4_A	0.949	1.105	1.508	1.235	1.451	1.250	1.375	1.245	1.278	1.125	1.109	0.919	1.174	0.964	1.114	1.457	1.370	1.179	1.348	
Line3_Replicate4_B	0.933	1.106	1.474	1.249	1.449	1.206	1.449	1.272	1.281	1.131	1.096	0.920	1.174	0.971	1.116	1.372	1.383	1.230	1.380	
Line3_Replicate4_C	1.040	1.105	1.533	1.212	1.454	1.229	1.386	1.257	1.266	1.268	1.094	0.937	1.162	0.959	1.111	1.398	1.339	1.196	1.328	
Line3_Replicate4_D	1.025	1.156	1.492	1.127	1.470	1.225	1.292	1.292	1.266	1.114	1.105	0.934	1.169	0.977	1.088	1.472	1.398	1.189	1.437	
Average	1.007	1.126	1.078	1.317	1.086	1.301	1.261	1.364	1.223	1.390	1.133	1.162	0.929	1.167	0.963	1.134	1.416	1.353	1.124	1.352
Standard Error	0.018	0.007	0.006	0.013	0.013	0.014	0.007	0.019	0.017	0.017	0.008	0.008	0.008	0.009	0.008	0.005	0.009	0.009	0.012	0.006
Count	47	32	48	47	48	47	48	45	48	43	48	48	48	48	48	48	48	48	47	48

	<i>alph</i>	<i>bru-2</i>	<i>cdi</i>	<i>CG1273</i>	<i>CG4440</i>	<i>CG7196</i>	<i>CG9650</i>	<i>CG10864</i>	<i>CG15365</i>	<i>CG33970</i>	<i>dpr6</i>	<i>Eip75B</i>	<i>grp</i>	<i>jing</i>	<i>lola</i>	<i>MESR3</i>	<i>Oaz</i>	<i>pk</i>	<i>Ptp61F</i>	<i>Ubx</i>
P-value	0.6947	0.9346	0.1469	<.0001	<.0001	0.2919	0.1376	0.004	0.0003	0.0032	0.0054	0.0002	0.0616	0.6837	0.0418	0.171	<.0001	0.9502	0.0013	0.028

Table 4.S19 - qPCR expression data before normalization. Cq values from qPCR expression analysis. Lines 1-3 for the major and minor allele correspond to lines in **Table 4.S16**.

	alph	bru-2	cdi	CG1273	CG4440	CG7196	CG9650	CG10864	CG15365	CG33970	dpr6	Eip75B	grp	jing	lola	MESR3	Oaz	pk	Ptp61F	Ubx
	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major	Major							
Line1_Replicate1_A	21.400	25.380	21.621	26.433	31.321	30.280	24.121	26.994	30.428	33.199	26.012	27.064	19.403	27.781	21.120	26.375	30.633	31.444	25.519	33.111
Line1_Replicate1_B		25.480	21.679	27.104	29.594	30.288	26.583	27.006	30.263	38.464	26.013	27.254	19.751	26.910	21.165	25.412	30.638	31.533	25.399	33.343
Line1_Replicate1_C	21.010	25.730	32.691	26.107	30.184	31.107	27.498	27.131	30.599	34.421	26.317	27.049	19.393	27.366	21.022	25.619	31.045	31.655	26.524	34.287
Line1_Replicate1_D	21.150	25.570	24.079	26.380	31.474	34.132	25.665	27.023	31.014				26.066							
Line1_Replicate2_A	26.830	24.630	22.445	27.442	30.055	29.776	26.751	27.739	28.310	33.101	32.439	26.646	21.100	26.049	21.272	26.958	28.648	27.479	30.377	29.375
Line1_Replicate2_B	21.600	24.850	22.784	27.913	28.716	30.367	27.958	27.957	29.159	34.063	25.722	27.380	20.706	25.319	21.640	26.473	27.568	27.458	28.756	28.983
Line1_Replicate2_C	21.110	26.050	23.067	26.064	28.848	30.201	29.039	27.716	29.596	33.125	26.130	27.093	20.829	25.512	21.061	26.613	27.863	27.072	30.730	29.678
Line1_Replicate2_D	21.130	25.630	22.863	27.280	30.214	35.469	27.771	26.278	30.163	34.383	25.482	27.583	18.807	25.983	21.591	26.737	27.709	27.316	29.847	29.764
Line1_Replicate3_A	22.830	25.410	21.368	26.680	34.950	28.003	25.952	25.945	31.374	31.165	26.114	27.425	22.460	27.495	20.670	25.568	25.461	30.611	34.306	28.258
Line1_Replicate3_B	20.820	25.780	21.219	28.366	35.292	27.845	28.113	26.964	31.547	31.696	25.388	28.105	20.697	26.716	20.164	25.883	25.728	31.817	33.562	28.773
Line1_Replicate3_C	21.170	25.520	23.112	28.336	34.251	27.933	26.376	26.493	32.259	31.118	26.128	27.684	20.321	26.906	20.142	25.360	25.780	31.467	34.821	28.504
Line1_Replicate3_D	30.350	25.410	21.825	28.401	35.095	36.014	27.110	26.519	32.213	32.526	25.641	27.500	20.356	26.611	20.653	25.510	26.136	31.567	32.460	29.075
Line1_Replicate4_A	20.860	25.320	22.501	24.878	30.033	28.347	28.321	28.561	31.296	34.617	25.394	27.014	22.270	27.065	22.533	26.061	28.176	28.233	24.318	26.223
Line1_Replicate4_B	20.940	25.290	23.011	25.802	29.224	28.515	28.875	28.407	30.852	36.894	25.211	27.046	22.853	26.827	23.129	26.338	29.106	29.196	25.016	26.180
Line1_Replicate4_C	21.190	24.980	22.728	25.220	29.021	28.461	29.119	28.655	31.754	34.755	25.354	27.033	22.156	26.987	22.777	25.754	29.046	29.434	26.092	26.427
Line1_Replicate4_D	34.830	26.340	23.384	24.799	29.618	33.202	28.607	28.088	31.233	35.769	25.230	26.949	21.574	26.644	23.338	25.505	29.394	29.327	24.458	27.157
Line2_Replicate1_A	21.480	26.270	23.388	25.225	26.647	27.825	29.076	27.866	30.301	31.519	24.973	26.679	19.577	25.203	21.088	25.533	26.943	29.172	23.100	29.079
Line2_Replicate1_B	34.860	25.060	23.494	26.201	26.412	28.065	29.381	28.155	30.821	32.372	24.903	27.183	19.908	25.175	21.154	25.656	27.499	29.823	24.004	29.532
Line2_Replicate1_C	20.940	30.260	23.339	26.234	26.064	27.830	29.400	28.202	31.148	31.197	25.007	26.966	19.278	25.664	21.131	25.131	27.183	31.192	23.537	29.544
Line2_Replicate1_D	21.100	26.020	23.400	25.834	27.023	33.094	29.155	28.130	33.039	32.463	25.160	27.063	19.133	25.259	21.426	25.261	27.563	30.137	23.984	29.595
Line2_Replicate2_A		25.760	23.431	23.285	28.229	27.504	29.801	28.383	30.478		25.727	25.860	20.273	24.910	21.673	26.829	24.067	31.167	20.616	30.396
Line2_Replicate2_B	21.130	25.450	23.906	23.642	28.757	27.828	30.092	28.240	30.893		26.014	25.815	21.346	25.411	21.702	27.089	25.387	31.323	21.761	30.363
Line2_Replicate2_C	21.110	24.850	23.726	23.585	27.507	30.380	28.489	31.102			26.059	25.924	20.240	25.783	22.067	26.352	24.409	31.862	21.240	30.856
Line2_Replicate2_D	21.640	25.170	23.678	23.478	29.150	33.599	30.302	28.180	32.025		25.927	26.082	19.879	24.998	21.920	25.975	25.613	31.892	21.992	31.032
Line2_Replicate3_A	21.280	26.160	21.744	27.249	27.309	29.153	28.857	27.198	29.865		26.202	25.140	18.997	23.565	20.777	24.446	29.413	24.892	23.746	29.444
Line2_Replicate3_B	24.230	25.820	22.099	25.115	27.518	26.197	30.014	24.285	28.052	30.463	26.543	25.422	19.833	25.279	20.622	25.594	29.629	25.602	24.117	30.680
Line2_Replicate3_C	24.060	26.060	21.936	25.047	27.480	27.298	29.544	29.254	28.273	29.507	26.429	25.026	18.619	26.187	20.857	23.910	29.185	27.012	22.449	30.290
Line2_Replicate3_D	24.410	25.820	22.033	24.399	27.021	35.819	29.737	29.047	29.270	31.018	26.670	25.220	18.529	24.037	21.094	24.088	30.433	25.045	25.262	30.039
Line2_Replicate4_A		26.390	23.941	24.072	27.196	28.479	31.019	29.318	28.278	37.334	27.153	28.081	18.696	24.179	19.579	24.054	26.458	26.099	23.665	29.199
Line2_Replicate4_B	23.070	26.020	22.244	25.125	27.602	26.895	31.054	29.539	28.345	34.394	27.436	28.297	19.445	26.004	19.489	25.171	27.222	26.911	26.216	29.912
Line2_Replicate4_C	24.680	27.290	22.029	24.704	27.339	29.119	30.961	29.427	28.421	34.202	27.197	28.075	18.763	26.531	19.919	23.577	27.178	27.903	25.006	29.764
Line2_Replicate4_D	23.200	25.670	22.118	24.933	27.410	35.708	30.812	29.544	28.685	35.896	27.448	28.006	18.457	25.150	19.922	23.753	27.690	26.649	25.736	29.837
Line3_Replicate1_A	20.330	25.310	22.136	26.371	25.533	28.434	29.174	23.427	27.050		25.815	25.860	21.776	27.619	20.222	24.179	32.318	29.298	24.324	29.202
Line3_Replicate1_B	19.970	25.930	26.412	27.387	26.536	28.659	27.652	23.556	27.751		25.447	25.649	22.689	28.754	20.488	24.045	32.232	29.986	25.346	31.112
Line3_Replicate1_C	21.260	25.730		26.605	28.060	26.405	29.159	23.989	28.005		25.774	26.137	22.185	27.354	21.029	24.852	31.281	31.532	23.381	30.675
Line3_Replicate1_D	21.440	26.750	22.589	28.391	29.275	26.816	29.238	23.869	27.795		25.542	25.910	22.578	28.490	21.129	24.929	32.066	31.197	23.899	31.449
Line3_Replicate2_A	19.950	25.830	22.251	30.513	28.252	29.399	27.116	26.192	28.104	34.460	26.313	26.547	20.119	26.682	22.118	25.389	29.574	32.096	31.699	31.183
Line3_Replicate2_B	20.110	26.160	23.118	29.196	29.250	29.457	25.442	27.159	29.301	34.697	26.001	26.678	20.054	27.427	21.710	26.040	30.840	32.942	30.194	32.301
Line3_Replicate2_C	19.760	26.220		29.298	29.116	28.503	26.987	26.877	29.140	35.180	26.228	26.338	20.160	26.471	21.951	26.174	30.261	33.618	28.628	31.926
Line3_Replicate2_D	20.160	27.020	22.711	29.846	30.536	29.636	26.870	27.215	29.516	36.368	26.202	26.591	20.182	27.257	22.513	26.173	31.302	35.552	28.975	32.535
Line3_Replicate3_A	20.030	26.160	22.116	30.536	28.390	33.071	26.547	26.641	27.289	31.801	26.655	27.205	19.668	25.382	22.191	23.610	30.478	31.837	30.606	27.312
Line3_Replicate3_B		26.250	22.245	29.190	29.311	33.542	25.120	26.893	30.458	33.004	26.683	27.366	19.787	26.146	22.535	25.248	31.006	31.846	29.998	29.124
Line3_Replicate3_C	20.200	26.690	22.222	30.500	29.432	28.441	26.047	26.766	30.083	33.231	26.606	27.117	19.273	25.128	22.413	24.592	30.385	32.164	29.460	28.367
Line3_Replicate3_D	20.470	27.040	22.169	30.853	30.795	32.200	26.699	27.745	30.730	33.067	26.616	27.672	19.092	26.191	22.885	24.408	30.493	32.453	26.675	28.781
Line3_Replicate4_A	30.520	25.830	22.256	26.613	26.590	31.266	28.343	28.975	28.200	33.166	25.364	24.551	22.599	24.099	21.489	25.559	28.769	28.411	23.235	26.364
Line3_Replicate4_B	19.180	26.050	22.174	25.880	26.825	31.155	27.821	29.063	29.244	32.729	24.794	24.201	22.498	24.732	21.762	27.113	29.074	30.409	23.103	28.195
Line3_Replicate4_C	19.780	27.280	22.382	26.262	28.131	28.582	28.813	29.368	29.464	33.374	25.168	24.117	22.722	24.121	21.179	26.571	29.135		22.432	26.884
Line3_Replicate4_D	20.440	27.380	22.629	26.249	29.439	31.376	28.523	29.305	30.226	33.888	25.660	24.479	22.668	24.801	22.087	26.704	28.410	30.131	22.982	28.199
Average	22.453	25.984	22.919	26.847	29.024	30.058	28.323	27.330	29.807	33.449	26.091	26.609	20.422	26.076	21.370	25.501	28.708	29.951	26.264	29.721
StdError	0.551	0.129	0.255	0.304	0.328	0.374	0.239	0.231	0.218	0.326	0.165	0.154	0.200	0.175	0.132	0.141	0.309	0.352	0.526	0.283
Count	44	48	46	47	48	48	48	48	48	39	48	48	48	48	48	48	48	48	47	48

Table 4.S19 Continued

	<i>alph</i>	<i>bru-2</i>	<i>cdi</i>	<i>CG1273</i>	<i>CG4440</i>	<i>CG7196</i>	<i>CG9650</i>	<i>CG10864</i>	<i>CG15365</i>	<i>CG33970</i>	<i>dpr6</i>	<i>Eip75B</i>	<i>grp</i>	<i>jing</i>	<i>lola</i>	<i>MESR3</i>	<i>Oaz</i>	<i>pk</i>	<i>Ptp61F</i>	<i>Ubx</i>	
	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	Minor	
Line1_Replicate1_A	20.080	26.270	22.239	28.796	28.109	30.048	26.342	30.248	29.574	26.976	26.707	26.884	20.657	24.798	21.145	25.317	30.464	27.823	23.638	29.806	
Line1_Replicate1_B	20.500	26.020	22.409	28.195	28.285	30.651	26.685	30.344	30.061	26.965	26.777	27.206	21.213	25.473	21.380	26.646	31.006	29.049	24.076	30.378	
Line1_Replicate1_C	25.040	28.020	22.415	28.561	28.243	27.806	26.599	30.466	30.151	27.559	26.707	26.887	20.220	25.038	20.167	25.581	30.841	28.242	23.566	29.694	
Line1_Replicate1_D	25.260	26.830	22.441	28.642	29.802	30.834	27.720	30.348	31.101	27.577	27.075	27.320	19.962	25.607	20.953	25.833	30.459	29.189	24.012	30.267	
Line1_Replicate2_A	20.050	26.170	21.588	30.861	24.684	30.400	28.880	23.567	32.057	31.114	26.254	27.083	21.751	26.168	21.302	24.471	30.525	28.666	26.456	29.079	
Line1_Replicate2_B	36.100	26.450	21.664	31.012	25.075	30.493	28.354	24.181	32.773	30.411	26.557	27.377	21.733	28.294	21.411	26.866	31.336	30.485	26.610	29.588	
Line1_Replicate2_C	25.180	26.260	21.727	30.624	25.033	27.472	28.973	24.431	32.491	31.152	26.605	27.511	21.201	29.121	19.939	25.222	32.051	30.050	26.502	28.761	
Line1_Replicate2_D	24.970	28.090	21.709	30.685	26.167	30.280	29.096	24.117	34.770	30.754	26.641	27.748	21.451	28.287	20.387	25.093	31.237	30.659	26.543	29.094	
Line1_Replicate3_A	21.660	26.520	21.924	31.555	27.586	33.769	25.889	28.133	28.124	28.435	24.314	28.896	19.338	25.349	20.648	24.570	28.195	29.287	26.183	29.224	
Line1_Replicate3_B	21.310	26.020	21.913	31.745	28.011	33.676	26.417	28.218	28.486	28.807	24.259	29.580	19.463	25.182	21.041	26.626	28.955	30.793	26.449	29.843	
Line1_Replicate3_C	20.290	27.340	22.177	30.866	28.112	27.089	28.122	28.153	28.052	28.765	24.174	28.650	19.064	25.965	19.470	25.361	30.478	29.412	26.233	28.661	
Line1_Replicate3_D	20.550	25.700	22.040	31.141	28.600	35.147	26.993	28.364	29.213	29.036	24.359	29.370	19.704	25.830	20.022	26.305	27.679	32.735	27.079	29.935	
Line1_Replicate4_A	21.920	25.860	23.869	27.062	27.069	31.574	29.859	25.212	28.623	31.320	26.118	29.462	22.424	24.295	22.857	24.731	28.404	30.315	27.422	29.678	
Line1_Replicate4_B	21.390	26.270	23.465	26.910	27.009	31.323	28.315	25.570	29.090	31.391	25.875	27.079	21.904	23.217	23.292	25.726	29.175	31.106	26.237	28.788	
Line1_Replicate4_C	20.650	25.930	23.429	26.389	27.008	28.549	29.294	25.524	28.832	31.078	25.469	26.305	21.859	25.422	21.357	25.090	29.484	30.013	26.628	28.488	
Line1_Replicate4_D	20.460	25.800	23.408	26.769	27.472	31.398	29.287	25.668	29.727	30.827	25.533	26.848	22.149	23.813	22.069	25.546	27.678	30.218	27.566	29.936	
Line2_Replicate1_A	20.820	25.670	21.387	30.248	30.307	31.540	29.962	29.832	28.626		27.122	32.633	19.280	27.758	20.261	26.402	31.683	30.443	23.685	29.634	
Line2_Replicate1_B	21.090	25.430	21.296	29.950	29.631	32.084	29.574	30.110	30.002		27.148	27.304	18.627	27.809	20.666	25.487	31.224	29.846	23.314	30.601	
Line2_Replicate1_C	20.280	25.670	21.585	28.511	29.955		30.969	30.116	29.074		26.924	27.383	18.269	28.556	20.695	25.611	31.133	29.500	22.407	29.805	
Line2_Replicate1_D	20.700	25.210	22.256	29.044	30.124	32.186	30.247	37.877	29.333		27.302	27.035	19.072	29.295	21.130	25.656	32.050	30.338	21.907	29.707	
Line2_Replicate2_A	20.860	25.320	23.233	30.444	33.083	32.318	29.179	28.802	25.001	31.216	27.559	26.737	22.894	25.462	21.784	25.306	28.287	31.351	24.261	30.348	
Line2_Replicate2_B	20.620	25.320	23.375	29.218	33.258	33.495	29.383	29.087	26.429	36.024	27.643	26.723	22.044	25.302	22.099	24.019	29.940	32.267	23.663	30.204	
Line2_Replicate2_C	20.330	25.040	23.302	28.147	32.205	32.499	30.040	28.805	25.567	33.977	27.394	26.602	21.326	25.965	21.364	23.633	28.994	31.994	23.772	30.020	
Line2_Replicate2_D	20.990	25.080	24.111	28.429	32.777	32.966	31.064	35.640	25.120	33.511	27.714	26.713	22.453	25.721	22.067	24.350	29.469	31.725	24.343	29.899	
Line2_Replicate3_A	23.630	25.860	21.667	28.831	32.121	27.192	28.151	26.198	26.812	32.437	27.527	26.831	20.453	24.749	21.545	24.576	30.720	30.738		28.479	
Line2_Replicate3_B		26.220	21.549	28.525	32.603	28.802	29.179	26.838	27.125	38.339	27.666	26.843	20.124	24.747	22.176	24.117	32.002	30.440	29.088	29.246	
Line2_Replicate3_C		21.310	25.200	21.632	27.435	32.644	28.139	29.397	26.607	26.804	33.301	27.925	26.438	19.608	25.505	22.039	23.934	31.860	30.667	30.585	28.832
Line2_Replicate3_D		21.170	25.230	21.688		31.362	27.016	30.113	27.478	27.115	32.527	27.452	27.003	19.969	26.033	22.189	24.159	32.175	31.378	23.880	28.616
Line2_Replicate4_A		20.600	26.140	22.764	30.946	30.205	27.893	29.021	30.095	25.709	31.165	24.506	26.437	19.261	24.540	21.669	25.143	30.493	29.487	23.347	28.724
Line2_Replicate4_B		21.080	26.640	22.632	30.421	29.315	28.940	30.111	30.346	25.284	31.413	24.123	26.848	18.349	24.652	22.203	25.048	31.074	30.449	23.075	30.377
Line2_Replicate4_C		21.250	27.220	22.534	29.555	29.246	28.381	29.551	30.000	25.431	31.156	24.116	26.491	17.911	24.894	21.652	24.465	30.287	29.830	22.664	29.532
Line2_Replicate4_D		21.080	25.720	22.934	29.945	29.191	27.164	31.180	31.419	25.272	33.095	24.652	26.588	18.806	25.132	22.293	25.092	31.594	31.324	23.252	29.103
Line3_Replicate1_A		30.170	25.600	20.752	28.846	29.793	29.880	27.853	30.138	27.916	30.907	24.952	28.839	21.866	25.607	22.849	26.122	28.375	27.057	24.539	29.120
Line3_Replicate1_B		21.390	26.620	21.057	27.991	29.857	30.802	26.631	30.453	27.007	31.089	24.993	29.123	21.495	26.019	23.229	26.119	29.033	27.738	24.491	29.396
Line3_Replicate1_C		21.050	25.420	20.744	27.450	29.357	28.961	28.290	30.071	27.644	30.881	24.894	28.835	20.639	25.975	22.797	25.829	28.107	27.304	24.022	29.166
Line3_Replicate1_D		21.530	25.440	21.102	27.062	29.940	29.877	29.540	31.245	27.737	31.723	25.206	29.105	21.332	27.323	23.291	26.384	29.592	28.261	24.741	29.331
Line3_Replicate2_A		22.610	26.110	22.530	30.865	26.791	28.345	28.737	31.246	27.189	30.119	24.737	27.675	20.180	25.442	19.306	26.090	30.704	28.303	22.520	28.397
Line3_Replicate2_B		21.440	26.860	22.474	28.745	26.786	28.402	28.435	31.548	26.619	30.619	24.675	27.418	19.334	26.196	19.500	26.061	30.360	29.161	22.740	28.931
Line3_Replicate2_C		21.140	25.240	22.454	29.315	26.296	28.468	28.921	31.093	26.759	29.978	24.766	27.623	19.055	25.376	19.365	25.778	29.717	28.527	22.313	28.332
Line3_Replicate2_D		21.410	24.780	22.884	28.418	26.699	28.095	30.300	31.746	27.177	33.977	25.144	27.477	19.730	26.565	19.845	26.228	31.898	29.305	23.321	28.742
Line3_Replicate3_A		20.190	26.640	22.466	28.979	28.562	26.525	28.108	27.366	28.949	32.513	24.988	27.233	21.253	26.949	22.782	24.537	32.042	29.853	26.836	30.547
Line3_Replicate3_B		20.300	26.280	22.577	27.097	28.526	27.275	27.461	28.086	27.608	32.384	25.108	26.975	21.193	27.102	23.170	25.056	28.387	30.469	27.311	31.748
Line3_Replicate3_C		22.290	24.920	22.411	28.418	28.186	27.041	28.364	27.365	27.439	31.762	25.070	27.119	21.055	26.662	22.784	24.774	28.499	30.452	26.334	30.927
Line3_Replicate3_D		22.350	25.250	22.867	27.041	27.890	27.053	28.629		29.043	34.769	25.209	27.081	21.181	28.274	23.444	24.999	31.671	30.522	27.135	30.796
Line3_Replicate4_A		20.620	26.290	22.366	32.496	30.100	32.287	28.056	28.688	28.372	30.072	25.748	26.540	19.866	26.183	22.220	25.287	30.607	29.959	25.455	30.425
Line3_Replicate4_B		20.280	26.250	22.408	31.758	30.425	32.243	27.070		28.965	30.159	25.885	26.224	19.893	26.187	22.384	25.312	28.628	30.250	26.569	31.147
Line3_Replicate4_C		22.600	25.230	22.366	33.024	29.542	32.344	27.587	28.897	28.635	29.800	29.041	26.164	20.244	25.916	22.101	25.203	29.371	29.283	25.827	29.959
Line3_Replicate4_D		22.270	25.570	23.426	32.139	27.465	32.703	27.493		29.445		25.516	26.441	20.190	26.082	22.513	24.685	30.933	30.583	25.680	32.427
Average		22.082	26.013	22.319	29.343	28.966	30.031	26.655	26.883	28.299	31.189	25.951	27.473	20.439	26.080	21.559	25.301	30.189	29.932	25.048	29.661
StdError		0.412	0.120	0.114	0.246	0.312	0.332	0.191	0.422	0.301	0.347	0.183	0.173	0.179	0.199	0.167	0.112	0.193	0.181	0.280	0.128
Count		47	48	48																	

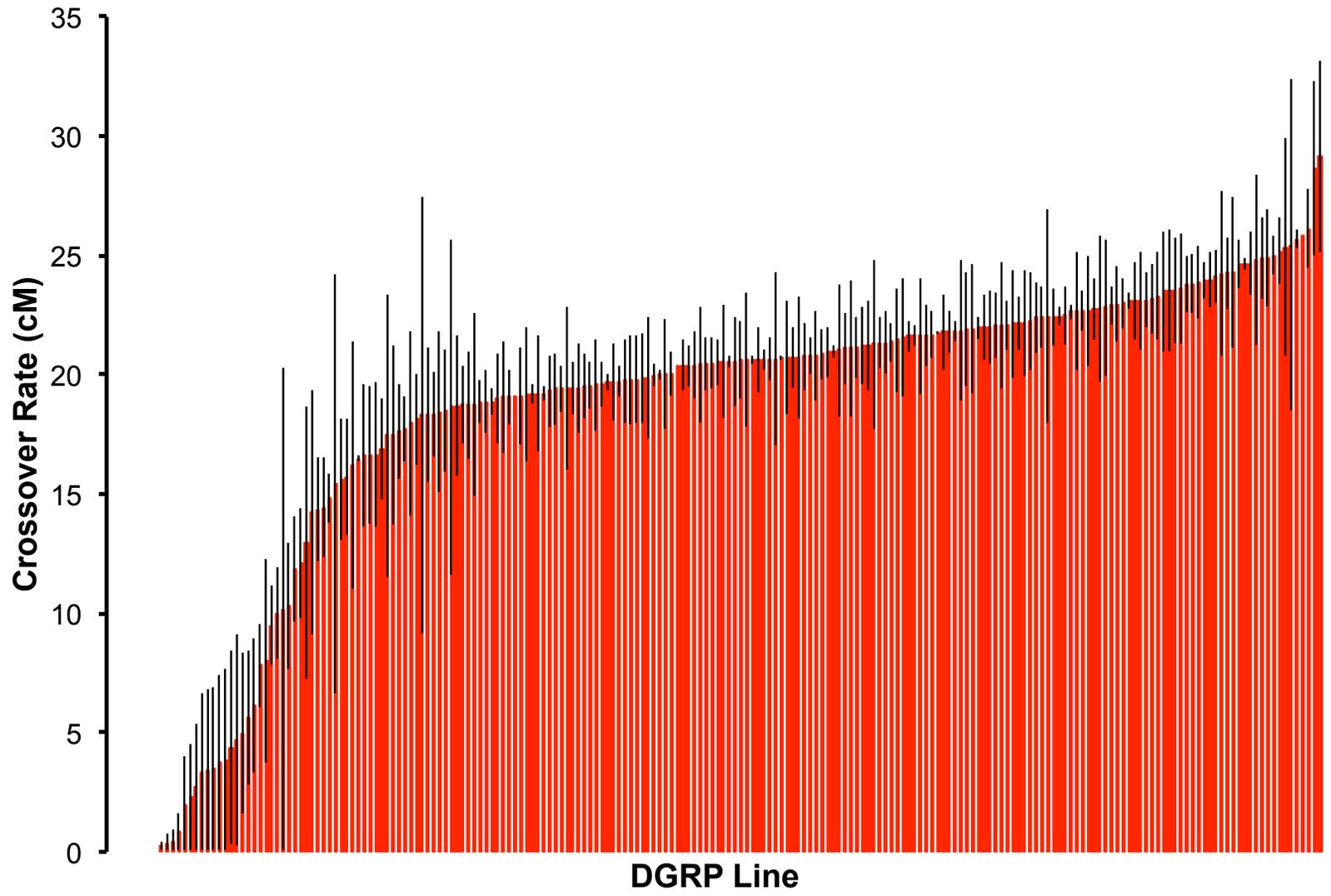
Table 4.S20 - Primers used for qPCR. Forward and reverse primers of candidate genes (and control) for qPCR expression analysis.

Candidate Gene and Direction	Sequence (5' to 3')
<i>alph</i> (Forward)	ATGGGCGGATTCCTGGATAAG
<i>alph</i> (Reverse)	GAGCGTAGTAGGCGTCCTC
<i>bru-2</i> (Forward)	CCCACCATTAATGCCGCAAC
<i>bru-2</i> (Reverse)	CCATCGACGGATTGGTACGT
<i>cdi</i> (Forward)	ATGAGCCTGAATCAGCACAGT
<i>cdi</i> (Reverse)	CGGCCAGATGAAAGGGGAG
<i>CG1273</i> (Forward)	TTACAACGGCTGCATTTATCGT
<i>CG1273</i> (Reverse)	CGGAAGGAACCCCTCAAAGC
<i>CG4440</i> (Forward)	AGTTCGGATTTCGGCGGATTT
<i>CG4440</i> (Reverse)	CCGCCAAAACCTTTCCTGCTG
<i>CG7196</i> (Forward)	ACTTGCGGTCACCACTCAAC
<i>CG7196</i> (Reverse)	CATCGTCCTCCATCGAAGGTT
<i>CG9650</i> (Forward)	GGAGGGCGTCAACCATCATC
<i>CG9650</i> (Reverse)	GCTGGGTTCTGTGTGGACTG
<i>CG10864</i> (Forward)	AGTCGCAAATAGCCGGAGTTG
<i>CG10864</i> (Reverse)	GACAGGCAGAACATTAGGGCA
<i>CG15365</i> (Forward)	CGGGAGTCACAGCAACTTG
<i>CG15365</i> (Reverse)	CTCAGCTCGAACATTTGTCGTAT
<i>CG33970</i> (Forward)	ATCTGCGTCAGCAGTATAATGC
<i>CG33970</i> (Reverse)	CGGCGTTTTCCCATGTTCT
<i>dpr6</i> (Forward)	CGGTCGGCTCGTACACCTA
<i>dpr6</i> (Reverse)	TCAGGCGAACGAAATAGCTGC
<i>Eip75B</i> (Forward)	CACCCAGGACGATAAGTTCAC
<i>Eip75B</i> (Reverse)	ACGAGTCAAACATGCAGATCAG
<i>GAPDH</i> (Forward)	CATTGTGGGCTCCGGCAA
<i>GAPDH</i> (Reverse)	CGCCCACGATTTTCGCTATG
<i>grp</i> (Forward)	TTCCTATGACCTGGTGGACTCG
<i>grp</i> (Reverse)	AGACTGCAGACGCTGCCTCTTA
<i>jing</i> (Forward)	ACTGGCTAGCAATGCACCAT
<i>jing</i> (Reverse)	TTCCACCATCGCAATGTCCA
<i>lola</i> (Forward)	GAATCGCTTCAGATCAAGGGC
<i>lola</i> (Reverse)	GTAGGCACCGCTCAGCTTA
<i>MESR3</i> (Forward)	AATCTATCGGACTACGAACGTGG
<i>MESR3</i> (Reverse)	CGCCGCTCACGAATATCTCT
<i>Oaz</i> (Forward)	GCGCTGAAAATAGCCAACAAG
<i>Oaz</i> (Reverse)	CCCCTCTCCTGTCAACTTATCA
<i>pk</i> (Forward)	CTTCTCGCAGATACCCGACG
<i>pk</i> (Reverse)	GGCGGAAGTTGATGGAGCAA
<i>Ptp61F</i> (Forward)	AGTCCAGAGCAGTTCTCATGC
<i>Ptp61F</i> (Reverse)	GTCGGCTCCCATCTCGTTG
<i>Ubx</i> (Forward)	ATGAACTCGTACTTTGAACAGGC
<i>Ubx</i> (Reverse)	CCAGCGAGAGAGGGAATCC

SUPPLEMENTAL FIGURES

Figure 4.S1 - Natural variation in recombination rate. Variation in crossover frequency in the DGRP (all lines) in the (A) *e ro* region on chromosome 3R and in the (B) *y v* region on the X chromosome. The lines for each panel are ordered by recombination rate. Error bars depict standard error. For reference, the reported map distance for the *e ro* region is 20.4 cM, while the reported map distance for the *y v* region is 33 cM, denoted by a horizontal line in both graphs.

A



B

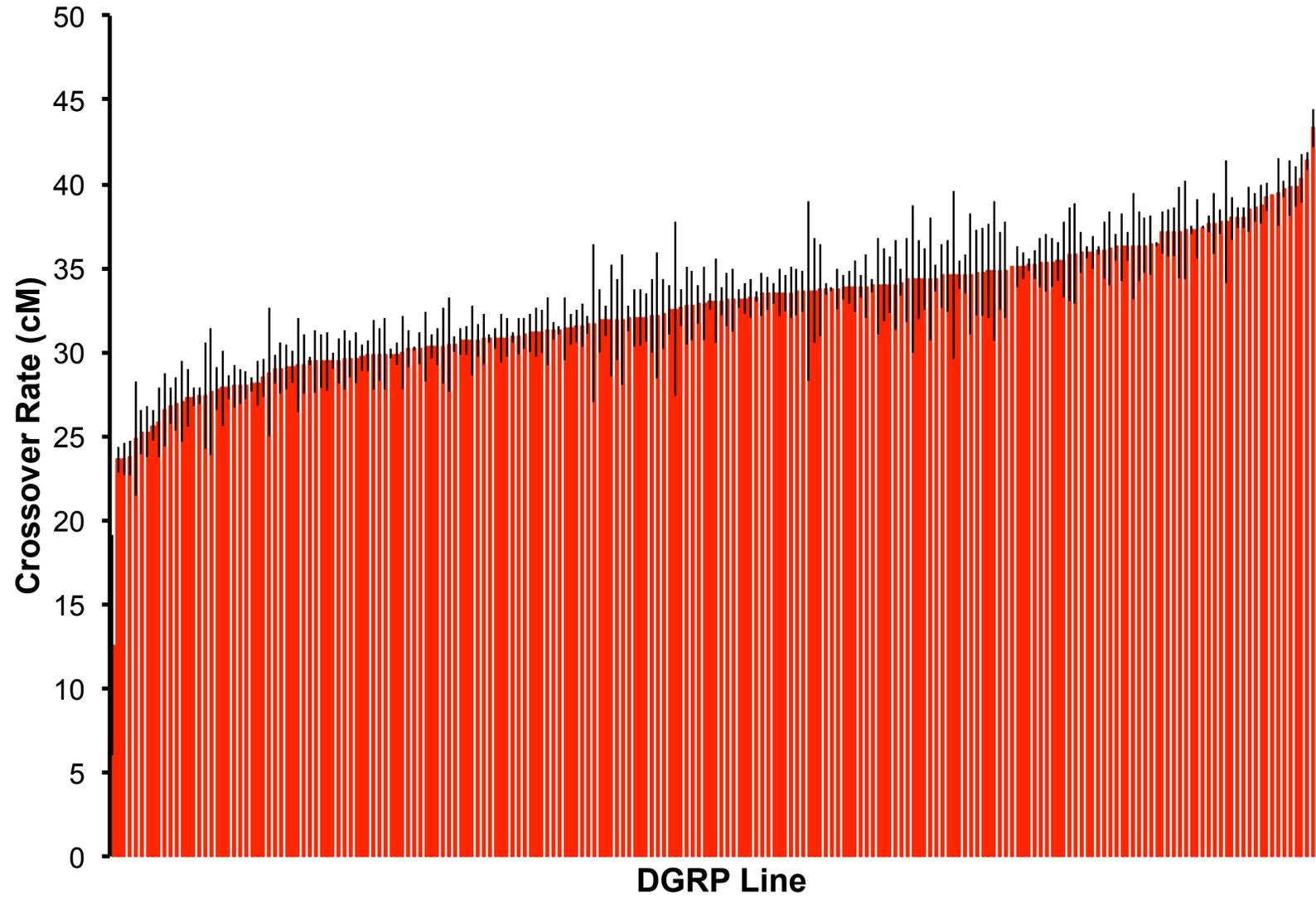
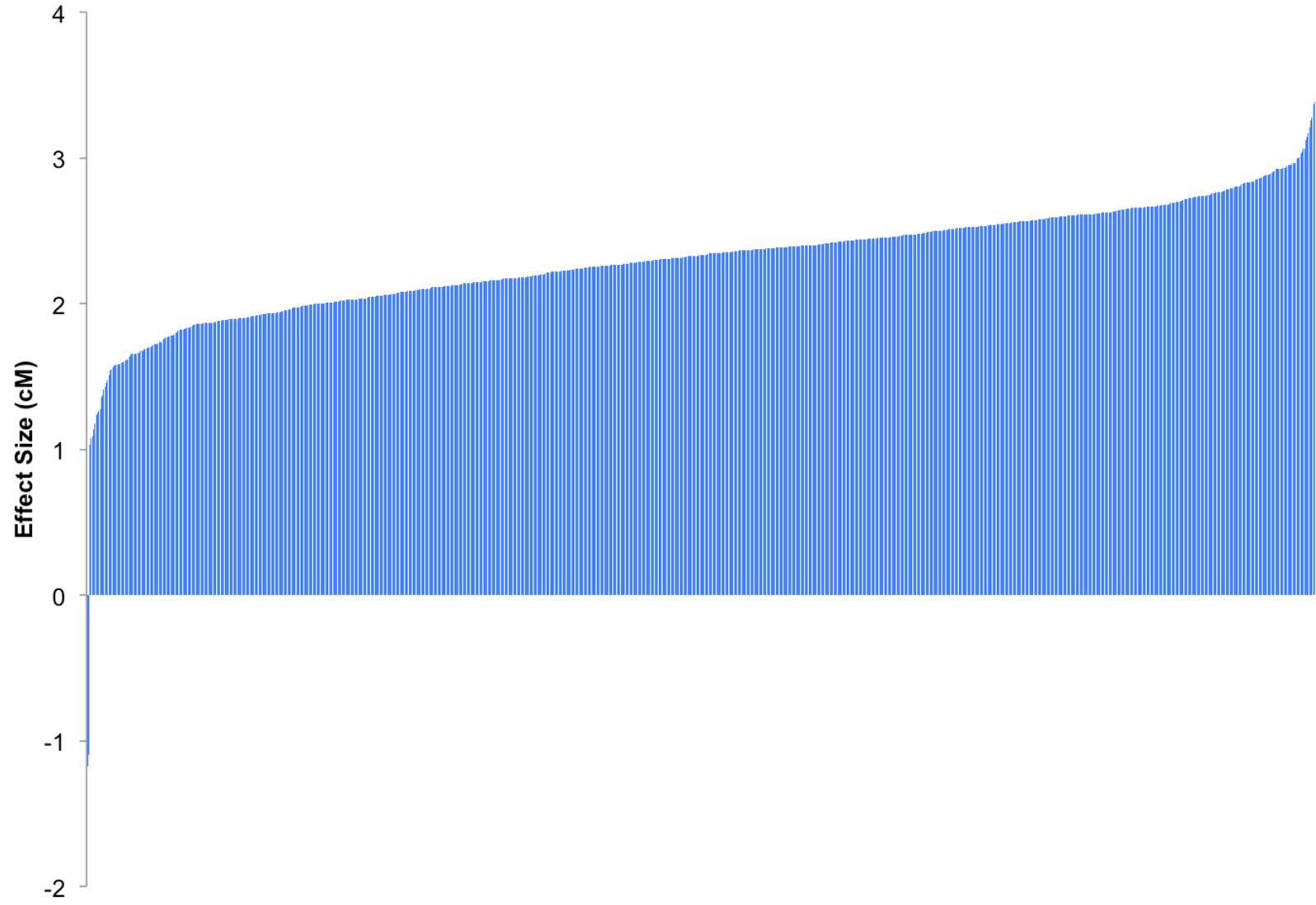
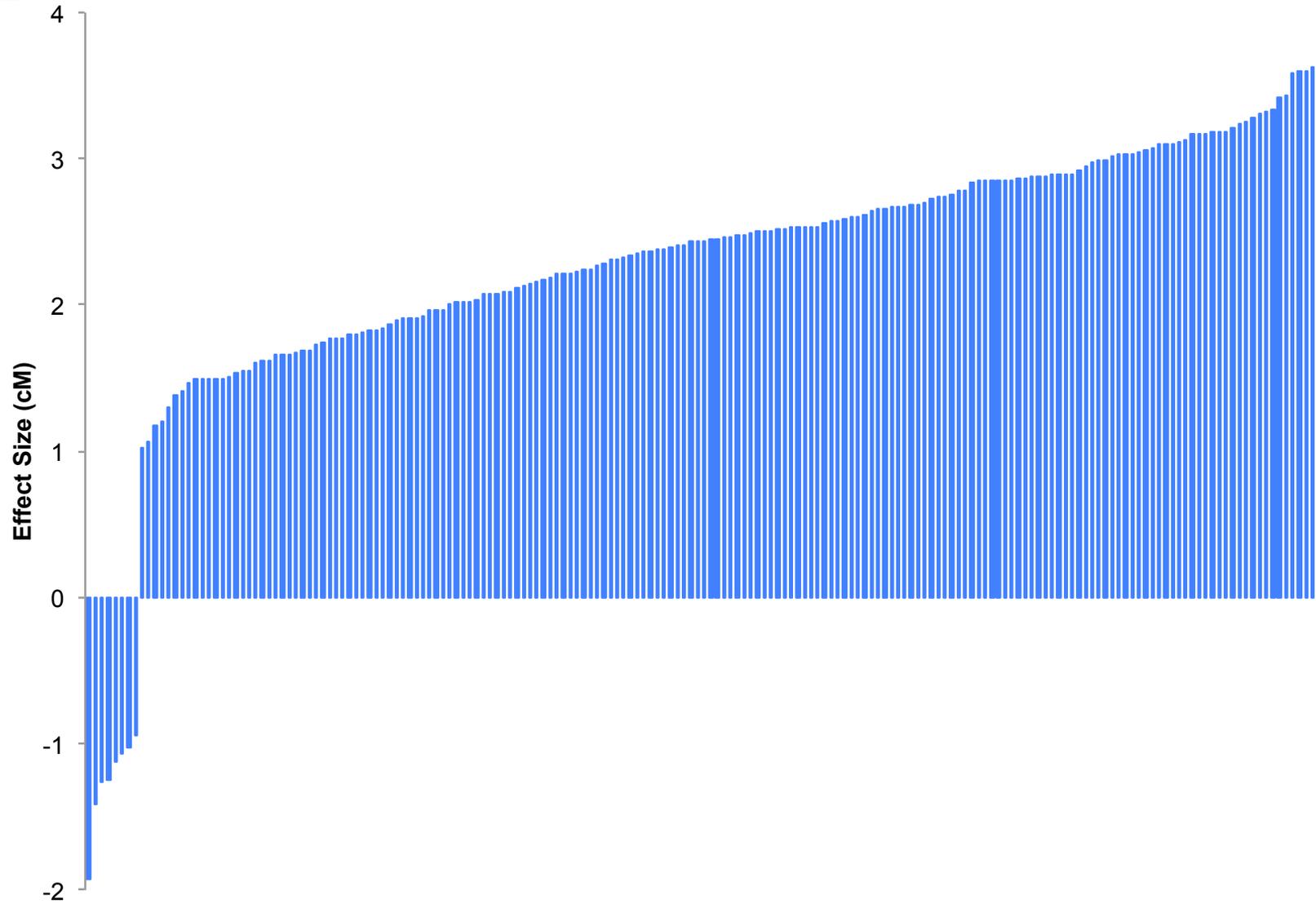


Figure 4.S2 - Distribution of effect sizes. Distribution of combined effect sizes for (A) *e ro* and (B) *y v* effect sizes from all GWA analyses.

A



B



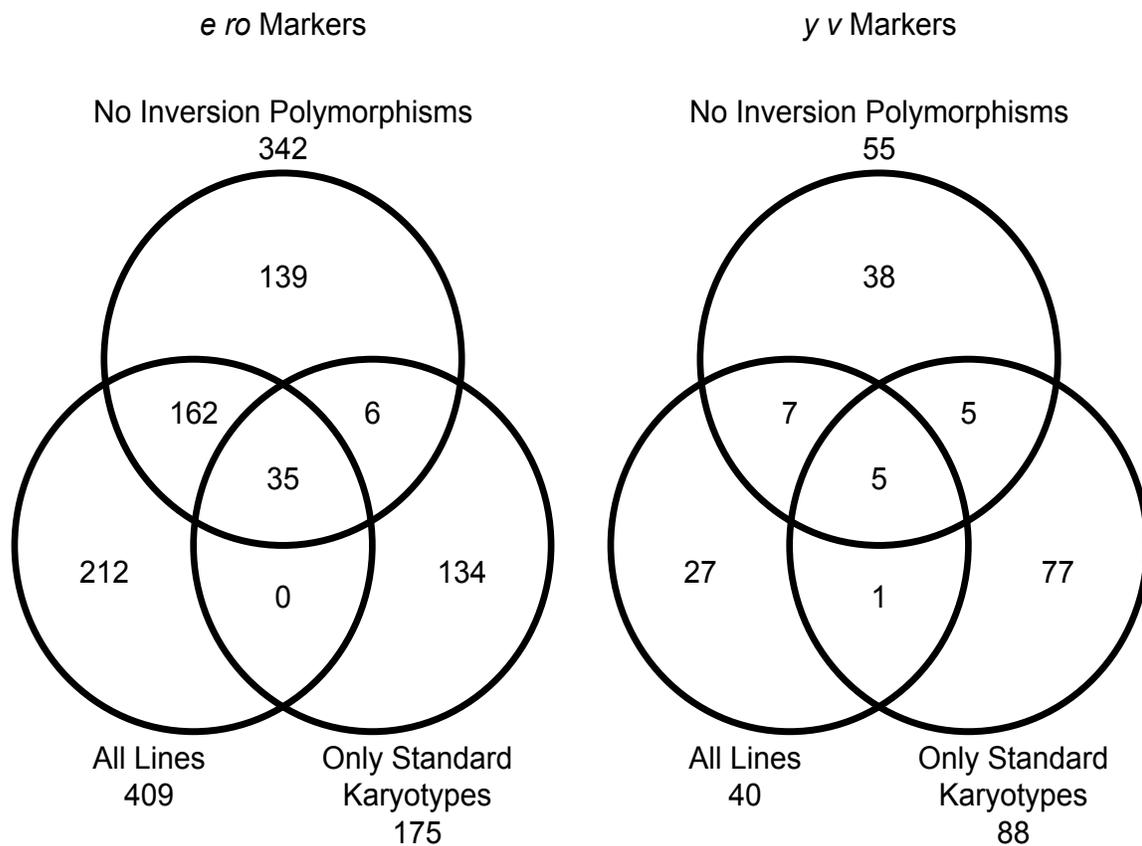


Figure 4.S3 - Venn diagram of SNPs uncovered from GWAS. Overlap of significantly associated genetic variants from the three different data sets for each chromosomal interval assayed.

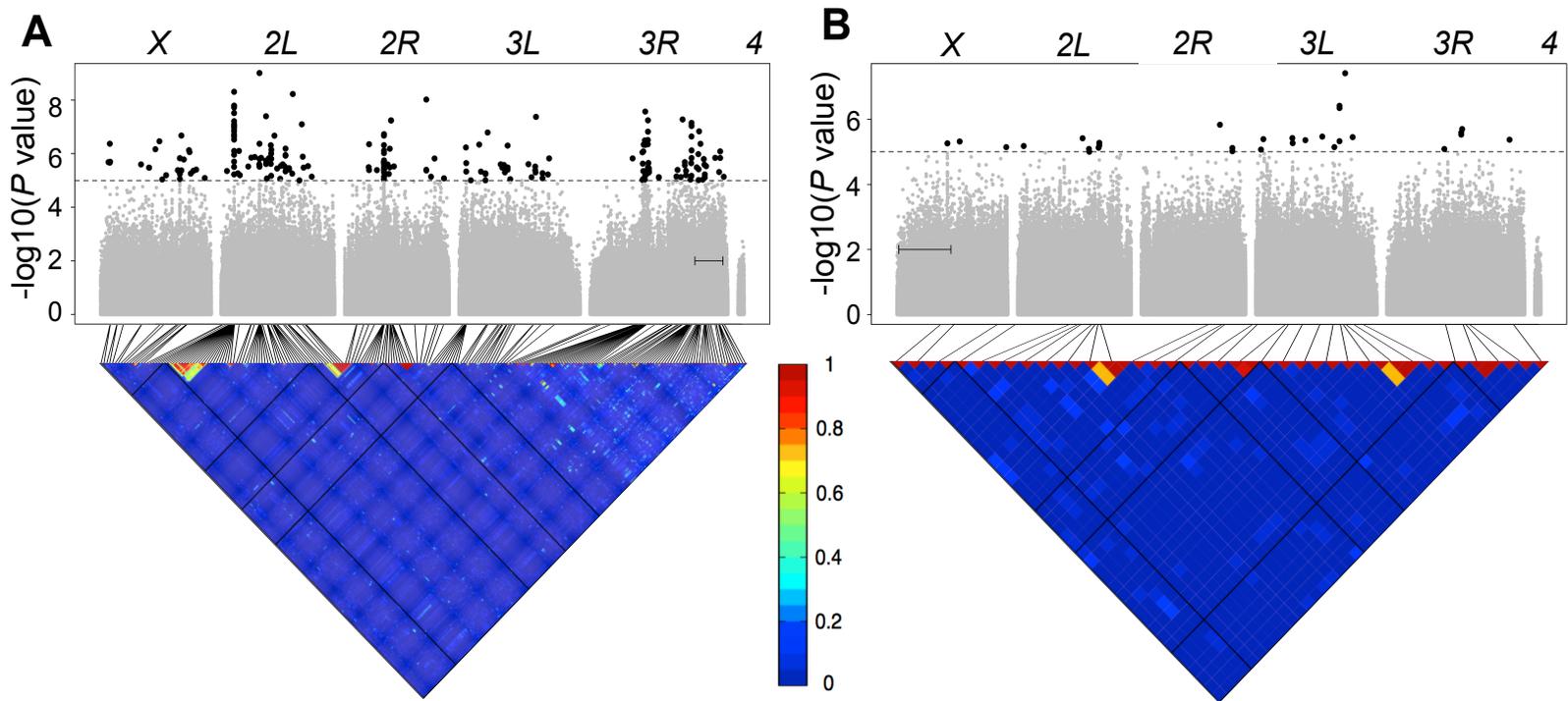


Figure 4.S4 - Genome-wide association analyses. Results are depicted for the (A) all lines in the *e ro* region (with no 3R inversions) and (B) all lines in the *y v* region. A significance threshold of $P \leq 10^{-5}$ is displayed. The triangular heat map displays the amount of linkage disequilibrium (LD or r^2) between variants. Each major chromosome is depicted. Brackets within Manhattan plot display chromosomal interval assayed. Red denotes complete LD and blue denotes absence of LD.

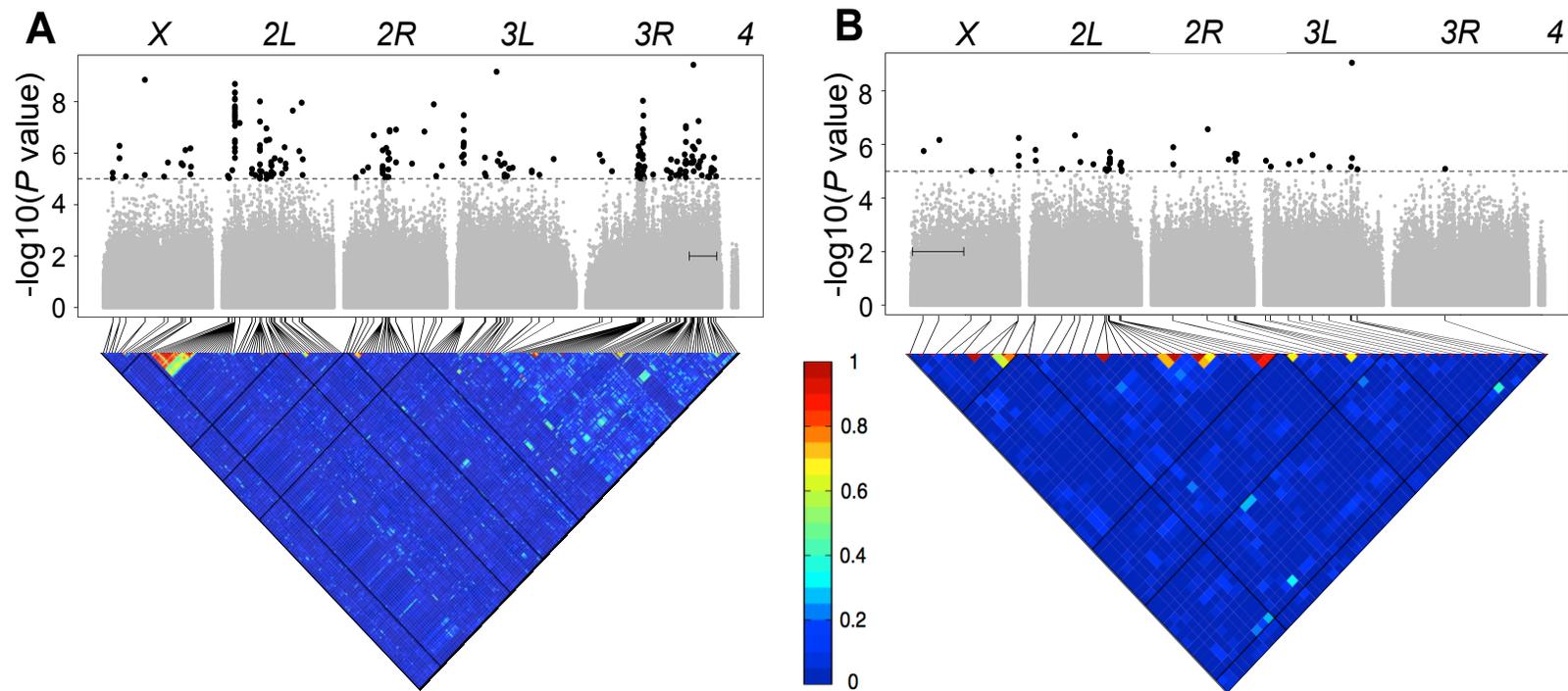


Figure 4.S5 - Genome-wide association analyses. Results are depicted for the (A) all lines in the *e ro* region (with no 3R inversions or polymorphic inversions) and (B) all lines in the *y v* region (with no polymorphic inversions). A significance threshold of $P \leq 10^{-5}$ is displayed. The triangular heat map displays the amount of linkage disequilibrium (LD or r^2) between variants. Each major chromosome is depicted. Brackets within Manhattan plot display chromosomal interval assayed. Red denotes complete LD and blue denotes absence of LD.

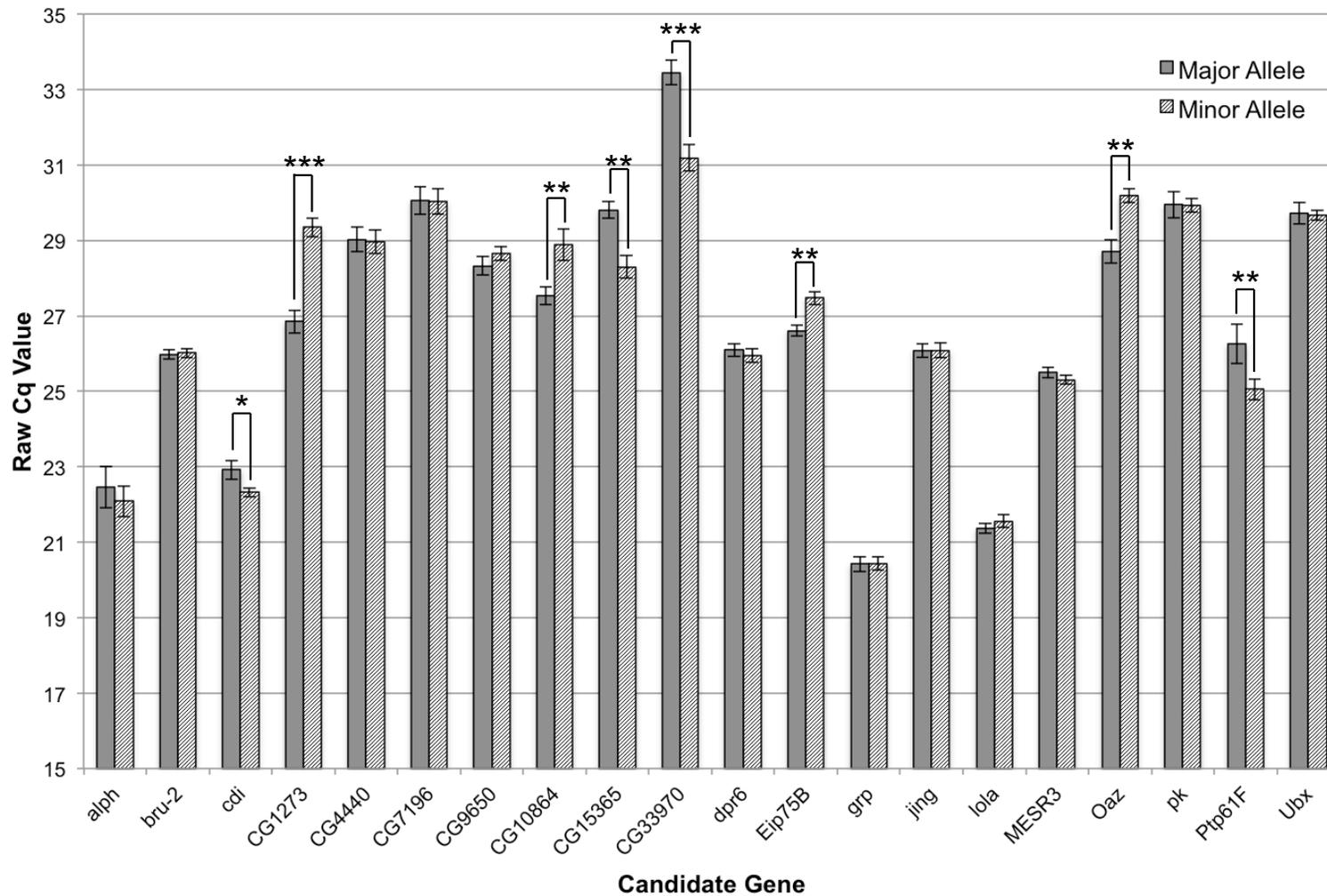


Figure 4.S6 - Validation of expression difference in ovaries via qPCR. For each candidate gene, the raw (before normalization) average expression of three lines with major allele (solid lines) and three lines with minor allele (shaded lines) are shown. Error bars denote standard error. * indicates a $P < 0.05$, ** indicates $P < 0.01$ and *** indicates $P < 0.001$.

CHAPTER 5. TWO HYBRID INCOMPATIBILITY GENES IMPLICATED IN MEDIATING RECOMBINATION RATE VARIATION IN *DROSOPHILA MELANOGASTER*

ABSTRACT

Within meiosis, homologous chromosomes exchange genetic material in a process known as meiotic recombination. This process helps ensure proper chromosome segregation. Defects in this process can lead to severe decreases in fitness, including aneuploid gametes and cell mortality. In addition, this process is also a pivotal evolutionary force, creating new allelic combinations for selection to act upon in future generations. Interestingly, the frequency of recombination as well as how recombination events are distributed across the genome are highly variable. Yet, the genetic factors underlying this variation remain poorly understood, especially in the model organism *Drosophila melanogaster*. Recently, PRDM9 was implicated in mediating both the distribution and location of recombination events in mammals. However, PRDM9 was first highlighted for its role in hybrid male sterility in mice. We hypothesized that this connection between hybrid sterility and recombination was not coincidental and that in fact, the hybrid sterility is a consequence of recombination defects. To test this hypothesis, we used *Drosophila* as a model system. Specifically, we asked whether genes involved in hybrid incompatibilities in *Drosophila* also have yet unknown roles in meiotic recombination. Our results suggest that two genes with clear functions in hybrid incompatibility, *JYalpha* and *Lhr*, mediate rates of recombination. Future work is aimed at exploring the molecular mechanisms of *JYalpha* and *Lhr* in meiotic recombination.

INTRODUCTION

Generating gametes is a necessity for organisms to produce offspring. Gametogenesis is accomplished by the cellular process of meiosis. During meiosis, DNA is replicated, and cells undergo two rounds of division. Before the first cellular division, homologous chromosomes are aligned along the metaphase plate and genetic material is exchanged. This exchange, also known as meiotic recombination, helps ensure proper chromosome segregation (Roeder 1997). Defects in this process can cause aneuploidy, the leading genetic cause of miscarriages in humans (Hassold and Hunt 2001). Despite being so essential, it is a highly variable process with rates varying between closely related species (True *et al.* 1996; Wall *et al.* 2003; Jensen-Seaman *et al.* 2004; Ptak *et al.* 2004, 2005; Winckler *et al.* 2005), between populations (Brooks and Marks 1986; McVean *et al.* 2004; Crawford *et al.* 2004; Fearnhead and Smith 2005; Graffelman *et al.* 2007; Dumont *et al.* 2009; Kong *et al.* 2010; Comeron *et al.* 2012), among individuals (Brooks and Marks 1986; Yu *et al.* 1996; Coop *et al.* 2008; Dumont *et al.* 2009; Wang *et al.* 2012), and even within the genome on both broad and fine scales (Lindsley *et al.* 1977; McVean *et al.* 2004; Cirulli *et al.* 2007; Paigen *et al.* 2008; Singh *et al.* 2009, 2013). Work has emphasized that both environmental and genetic factors contribute to recombination rate variation.

Recent work has highlighted PRDM9 as a key genetic factor in modulating recombination rate variation (e.g. Baudat *et al.* 2010; Myers *et al.* 2010; Parvanov *et al.* 2010; Berg *et al.* 2010, 2011; Kong *et al.* 2010; Fledel-Alon *et al.* 2011; Hinch *et al.* 2011). PRDM9 contains a KRAB domain, a PR/SET domain and multiple zinc fingers. PRDM9 was shown to bind a 13-base pair motif (Myers *et al.* 2005, 2008) that is enriched in mammalian recombination hotspots (Baudat *et al.* 2010; Myers *et al.* 2010; Parvanov *et al.* 2010). Further work demonstrated that allelic variation within the Cys₂His₂ zinc fingers of *Prdm9* is associated with the location and distribution of crossovers (Berg *et al.* 2010, 2011; Kong *et al.* 2010; Hinch *et al.* 2011). *Drosophila* does not possess a clear PRDM9 ortholog (Oliver *et al.* 2009; Heil and Noor 2012) and work has demonstrated that the zinc finger binding motifs of other proteins do not explain recombination rate variation within or between species of *Drosophila pseudoobscura* and *Drosophila miranda* (Heil and Noor 2012).

In addition to playing a role in hotspot usage, PRDM9 has also been linked with male sterility due to allelic incompatibilities in mice which cause defects in spermatogenesis (Forejt and Iványi 1974; Forejt 1996; Mihola *et al.* 2009). Because of this, PRDM9 has been commonly referred to as a hybrid incompatibility gene. In a popular model known as the Dobzhansky-Muller model of hybrid incompatibility (Dobzhansky 1937; Muller 1942), an

ancestral population is split into two and an allele (or alleles) diverge over time. If these populations are later reunited and try to mate with each other, divergent alleles are no longer compatible. Broadly speaking, hybrid incompatibility genes have detrimental effects on fitness in hybrids and often result in sterility or lethality (Maheshwari and Barbash 2011). In the case of PRDM9-associated sterility, the sterility phenotype is caused by failures in meiotic prophase, thus linking the hybrid dysfunction phenotype to the role of PRDM9 in recombination (which occurs during meiotic prophase). Due to PRDM9's dual role in meiotic recombination and hybrid sterility, we hypothesized that genes involved in hybrid incompatibilities more generally may have dual functions in meiotic recombination.

We tested this hypothesis using *Drosophila melanogaster* as a genetic model system. Many genes involved in hybrid incompatibility have been identified in *Drosophila melanogaster*. These include *JYalpha*, *Lhr*, *Hmr*, *Nup96*, *Nup160*, *Ods/OdsH*, and *Zhr*. A recent transposition of *JYalpha*, which is required for sperm motility, from the 3rd to 4th chromosome in *D. melanogaster* causes male sterility in *D. melanogaster*-*D. simulans* hybrids (Masly *et al.* 2006). *Lethal hybrid rescue* (*Lhr*), a loss-of-function mutation discovered from a natural population of *D. simulans*, rescues the lethality of the hybrid males from *D. melanogaster* females and *D. simulans* males (Watanabe 1979) while a loss-of-function mutation of *Hybrid male rescue* (*Hmr*) will allow for viable hybrid males from crosses between *D. melanogaster* females to *D. mauritiana*, *D. simulans*, and *D. sechellia* males (Barbash *et al.* 2000). Functional divergence of *Odysseus* (*Ods*) (known as *Ods-site homeobox* (*OdsH*) in *D. melanogaster*) causes hybrid male sterility between *D. simulans* and *D. mauritiana* (Perez *et al.* 1993; Perez and Wu 1995). *Nup96* and *Nup160* act in concert to cause hybrid incompatibility in *D. melanogaster*/*D. simulans* hybrids (Presgraves *et al.* 2003; Barbash 2007; Tang and Presgraves 2009; Sawamura *et al.* 2010). Finally, a variant of *Zygotic hybrid rescue* (*Zhr*) rescues the hybrid embryonic lethality in crosses between *D. simulans* females and *D. melanogaster* males (Sawamura *et al.* 1993).

To test our central hypothesis, we screened available mutants and RNAi lines of known hybrid incompatibility genes for changes in rates of crossing over using classical genetic techniques. Our results suggest that two genes, *JYalpha* and *Lhr*, have potential roles in determining rates of recombination. We hypothesize possible genetic roles of these proteins in recombination and discuss future experiments that could validate the connections between these genes and meiotic recombination.

MATERIAL AND METHODS

Fly Lines

We obtained available mutations, *P*-element insertions and UAS-RNAi lines for the following genes: *Hmr*, *JYalpha*, *Lhr*, *Nup96*, *Nup160*, *Ods/OdsH*, and *Zhr*. These lines tested in this study are listed in **Table 5.1**, separated by gene, and include genotype, source (with stock number if appropriate), genetic background control, and appropriate references. Construction of UAS-RNA lines from the Transgenic RNAi Project (TRiP) at Harvard Medical School and UAS-RNAo lines from the Vienna Drosophila Resource Center (VDRC) are detailed in Dietzl *et al.* 2007 and Ni *et al.* 2008.

Crossover Rate Assay in D. melanogaster and D. simulans

To assay crossover rates in *D. melanogaster* and *D. simulans*, we took advantage of classical genetic techniques and visible mutations. To measure recombination rates on the 3R chromosome in *D. melanogaster*, we used a fly strain marked with *ebony* (e^4) and *rough* (ro^1) (Bloomington Stock #496). These genes are roughly 20.4 cM apart (Bridges and Morgan 1923). The mutation in *ebony* causes dark pigmentation of the cuticle. The mutation in *rough* causes a reduction in the compound eye as well as rough texture on the eye. These markers were selected due to their genetic distance, lack of apparent viability defects and success in previous studies (Singh *et al.* 2015).

To measure recombination rates on the *D. melanogaster* X chromosome, we used a fly strain marker with *vermilion* (v^1) and *forked* (f^2) (Drosophila Species Stock Center #14021-0251.128). The mutation *vermilion* causes bright red compound eyes while the mutation in *forked* causes kinked thoracic bristles. These genes are roughly 26.65 cM apart (Barker and Moth 2001). These markers were selected due to their genetic distance and lack of apparent viability defects (Sturtevant 1929; Barker and Moth 2001).

To measure recombination rates on the *D. simulans* 3R chromosome, we used a fly strain marked with *scarlet* (st^1) and *ebony* (e^1) (Drosophila Species Stock Center #14021-0251.034). These genes are roughly 30.0 cM apart (Barker and Moth 2001). The mutation in *scarlet* causes a reduction in the compound eye as well as rough texture on the eye while the mutation in *ebony* causes dark pigmentation of the cuticle.

The crossover rate assay used a two-step crossing scheme (**Figure 5.1**). All crosses were executed at 25°C with a 12 hour: 12 hour light:dark cycle on standard media using virgin females aged roughly 24 hours. For the first cross, ten virgin females were crossed to ten doubly marked males in eight ounce bottles. Males and females were allowed to mate

for a total of five days, after which all adults were cleared from the bottles. For the second cross, virgin females were collected. These females are heterozygous for the visible markers and are the females in which crossing over is occurring and subsequently scored (via their progeny). Ten females were backcrossed to ten doubly marked males in 25 x 95 mm vials. There were 30 replicate backcrosses per line. Males and females were allowed to mate for five days, after which all adults were cleared from the vials. After eighteen days, BC₁ progeny were scored for both sex and presence/absence of visible markers. Recombinant progeny possessed only one morphological marker. The UAS-RNAi lines in *D. melanogaster* followed a similar crossing scheme except for the males used in this F₀ cross. These males contained the doubly marked chromosome along with *nanos*-GAL4 driver on the same chromosome arm (Van Doren *et al.* 1998; Rørth 1998). *nanos* is expressed throughout *Drosophila* oogenesis (Wang *et al.* 1994).

Nondisjunction Assay

To assay rates of nondisjunction in *D. melanogaster*, we used a multiply marked fly strain and a simple crossing scheme (**Figure 5.2**). The full genotype of this strain is *y cv v f / T(1:Y)B^S* (Kohl *et al.* 2012). All crosses were executed at 25°C with a 12 hour:12 hour light:dark cycle on standard media using virgin females aged roughly 24 hours. For the cross, ten virgin females from all lines were crossed to ten *y cv v f / T(1:Y)B^S* males in eight ounce bottles. We used five replicates per line. Males and females were allowed to mate for a total of five days, after which all adults were cleared from the bottles. All subsequent progeny were collected and scored for both sex and presence/absence of Bar eyes. Females displaying Bar eyes or males displaying wild-type eyes indicate a nondisjunction event. The total number of nondisjunction progeny observed was multiplied by two to account for triplo-X and nullo-X progeny, which are lethal (and thus not observable).

Statistics

To estimate the rate of crossing over for each vial, we took the ratio of recombinant progeny (flies possessing only one morphological marker) to the total number of progeny. These crossing over values were then arcsine transformed and compared to appropriate control via a student's t-test or Dunnett's test (Dunnett 1955, 1964) which controls for multiple testing. To calculate the rate of nondisjunction for each bottle, the total number of observed exceptional progeny was multiplied by two and then divided by the total number of progeny observed. These percentages were then arcsine transformed and compared to

appropriate controls using again a Dunnett's test. All statistics were performed using JMP® Pro 11.2.0.

RESULTS AND DISCUSSION

The genetic architecture of recombination rate variation remains poorly understood in the model organism *Drosophila melanogaster*. To identify new genes that may mediate recombination rate variation in this system, we used a candidate gene approach. Specifically, we focused on genes associated with hybrid incompatibility. This approach is motivated by previous work in mammals. Specifically, if PRMD9's role in determining hybrid sterility is a consequence of its role in designating crossover sites during gametogenesis, then perhaps other hybrid incompatibility genes could have similar roles in meiosis and meiotic recombination. Though *Drosophila* lacks an ortholog of PRDM9 (Oliver *et al.* 2009; Heil and Noor 2012), there have been numerous hybrid incompatibility genes identified in this system. Notable ones tested in this study include *Hmr* (Barbash *et al.* 2000, 2004; Barbash and Ashburner 2003; Barbash and Lorigan 2007), *JYalpha* (Masly *et al.* 2006), *Lhr* (Brideau *et al.* 2006; Prigent *et al.* 2009), *Nup96* (Presgraves *et al.* 2003; Presgraves and Stephan 2007; Presgraves 2007; Barbash 2007), *Nup160* (Tang and Presgraves 2009; Sawamura *et al.* 2010), *Ods/OdsH* (Ting *et al.* 1998; Bayes and Malik 2009), and *Zhr* (Sawamura and Yamamoto 1997; Ferree and Barbash 2009). We tested the hypothesis that disrupting hybrid incompatibility genes in *Drosophila* would also cause defects in rates of meiotic recombination. To assay recombination rates in *Drosophila*, we used a classic two-step crossing scheme (**Figure 5.1**) as detailed in the MATERIALS AND METHODS.

Five genes (*Hmr*, *Nup96*, *Nup160*, *Ods/OdsH*, and *Zhr*) showed no significant change in recombination rates as compared to genetic background control ($P > 0.08$, all comparisons, Dunnett's test; **Figure 5.3 & 5.4**) using various UAS-RNAi lines, *P*-elements, and loss-of-function alleles. However, two genes did display a significant change in recombination rate when perturbed as compared to appropriate genetic background control. These were *JYalpha* and *Lhr*.

JYalpha is a 4.1-kb gene located on the 4th chromosome in *D. melanogaster* that encodes a Na⁺/K⁺ ATPase. It is expressed in the testes (Chintapalli *et al.* 2007). Work has shown that this gene is located on the 3rd chromosome in *D. simulans* and this simple gene transposition causes hybrid incompatibility (Masly *et al.* 2006). *D. melanogaster* males homozygous for the *D. simulans* 4th chromosome produced immotile sperm and no progeny, while *D. melanogaster* males containing one copy of the *D. simulans* 4th chromosome and one copy of a *D. melanogaster* 4th chromosome displayed no reproductive defects and produced wild-type numbers of progeny. Mapping techniques isolated *JYalpha* as the culprit of these reproductive defects. Further work demonstrated that null mutants of *JYalpha* in

D. melanogaster produce sterile males (Masly *et al.* 2006). *JYalpha* is similar to the $\alpha 4$ isoform of Na^+/K^+ ATPases in mammals, also expressed in the testes (Woo *et al.* 1999). Like *JYalpha*, inhibition of this isoform causes fertility defects including problems with sperm motility (Woo *et al.* 2000), suggesting conserved function among taxa.

JYalpha mutants showed significant changes in recombination frequency in three instances (**Figure 5.5**). First, *4-sim/ey^D*, a line containing one copy of a *D. simulans* 4th chromosome (which lacks a functional copy of *JYalpha*) showed a significant increase in rates of recombination ($P = 0.04$, Dunnett's test) relative to a genetic background control. For clarification, our crossing scheme measures recombination in heterozygous females. Therefore *4-sim/ey^D* flies in our cross contain one copy of a *D. melanogaster* 4th chromosome and one copy of a *D. simulans* 4th chromosome. Second, a *P*-element insertion (KG09295) showed a significant decrease from control ($P = 0.03$, Dunnett's test) and finally, a precise *P*-element excision showed a significant increase from control ($P = 0.01$, Dunnett's test). *4-sim/ci^D* and the imprecise excision also showed an increase from control, although this increase was not statistically significant. The combination of these three results suggests that the loss of *JYalpha* can cause perturbations in recombination frequency that are dominant. Two UAS-RNAi lines for *JYalpha*, with knockdown expressed only in early meiotic prophase by use of GAL4-*nanos* (Wang *et al.* 1994; Van Doren *et al.* 1998; Rørth 1998), showed no significant change in recombination rates relative to the genetic background control ($P > 0.08$, both comparisons, Dunnett's test).

Expanding on these results, we also measured levels of nondisjunction using a simple crossing scheme (**Figure 5.2; see MATERIALS AND METHODS**). Abnormal rates of recombination have been associated with increased levels of nondisjunction (Koehler *et al.* 1996). For example, in humans, reduced recombination is present in many common trisomies (e.g. Hassold *et al.* 1995; Robinson *et al.* 1998; Hassold and Sherman 2000). The analyzed lines of *JYalpha* showed no elevated nondisjunction as compared to control ($P > 0.85$, all comparisons, **Table 5.2**), suggesting that the altered rates of recombination due to *JYalpha* are having no detectable effect on chromosome segregation.

JYalpha as a possible mediator of recombination in *Drosophila* is puzzling. First, evidence from mammals point to expression primarily located within the testes, with function directed at sperm motility. Analyzing *JYalpha* expression in *Drosophila* points to similar trends, with no detectable signal in the ovaries (Chintapalli *et al.* 2007; Adrian and Comeron 2013) or whole females (Celniker *et al.* 2009) as compared to readily-detectable levels in both testis and whole flies (combined sexes) (Chintapalli *et al.* 2007). It should be noted

here that *Drosophila* males do not undergo meiotic recombination (Morgan 1912, 1914) and male genotype has been shown not to significantly influence female rates of crossing over (Hunter and Singh 2014). How *JYalpha* can mediate rates of crossing over without being expressed in females is difficult to envision.

To explore possible mechanisms by which *JYalpha* mediates crossover frequency, we first tested for a possible role of allelic variation at *JYalpha* in mediating population-level variation in recombination rate by leveraging previous data. A prior experiment measured rates of recombination in the *Drosophila* Genetic Reference Panel (Mackay 2001; Huang *et al.* 2014) using the same experimental procedure in both the *e ro* interval as well as an additional interval on the X chromosome between *yellow* and *vermilion* (roughly ~33 cM apart) (Hunter *et al.*, In Preparation). Presumably because the 4th chromosome is largely heterochromatic and because it is difficult to sequence heterochromatin, the *JYalpha* region does not have a great deal of sequence coverage in the DGRP. Out of the 205 lines, 24 lines have genotypic data for this region; these data indicate that there are two polymorphic deletions at this locus. Among the 24 lines, 23 lines do not have either deletion and 1 line (RAL_307) has both. We used our recombination rate data (**Table 5.3**) to test for a significant difference between genotypes. Using an ANOVA framework, where genotype is the only fixed effect, we see no significant difference in the *e ro* region ($P = 0.57$) while we see a marginally significant effect in the *y v* region ($P = 0.064$). However, these results are underpowered with only one line having the minor allele. Future work will be aimed at genotyping this region in the DGRP to further strengthen this analysis to test if naturally occurring variants in *JYalpha* significantly contribute to population level variation in recombination rates.

A clear link between *JYalpha* and meiotic recombination does not emerge from these results. In order to further validate these results and potentially develop a mechanism for *JYalpha*'s role in modulating recombination rate, I plan additional experiments. First, I plan to analyze *JYalpha* expression in ovaries and whole females using quantitative RT-PCR with primers established in the FlyPrimerBank (Hu *et al.* 2013; **Table 5.4**). Meiotic recombination occurs only in the ovaries and *JYalpha* has only been detected in the testes of flies. Therefore, if expression of *JYalpha* is detected in the ovaries (even at a low level), this would indicate a secondary unexplored function of *JYalpha*. Second, I will analyze sensitivity to DNA damaging agents such as the oxidizing agent paraquat (methyl viologen dichloride). Meiotic recombination is initiated by programmed double-strand breaks and further resolved by DNA repair proteins. If *JYalpha* also has a unexplored role in DNA

damage repair, we would expect to see increased sensitivity of flies possessing only one functional copy of *JYalpha*. Finally, I will repeat the above experiments in hybrids using a cross between *D. simulans* females and *D. melanogaster* males (with and without the *JYalpha* P-element). Often, phenotypes from hybrid incompatibility genes are masked in non-hybrids. Perhaps, phenotypes from the above experiments will be exaggerated in hybrids, which would provide additional support for a role of *JYalpha* in recombination.

In addition to *JYalpha*, a UAS-RNAi knockdown of *Lhr* also showed a significant increase of recombination rate compared to genetic background control ($P = 0.003$, Dunnett's test; **Figure 3**). However, two other UAS-RNAi knockdowns of *Lhr* did not show any significant change in recombination rate ($P > 0.19$, both comparisons, Dunnett's test). Moreover, a previously established knockout of *Lhr* showed no significant perturbation in recombination frequency ($P = 0.99$, student's t-test). In addition, a known interactor with *Lhr*, *Hmr* (Brideau *et al.* 2006), did not show any significant change in recombination rate in four different UAS-RNAi lines ($P > 0.44$, all comparisons, Dunnett's test) or two deficiency lines ($P > 0.21$, both comparisons, Dunnett's test). Similar to *JYalpha*, these lines show no significant elevation in rates of nondisjunction as compared to control ($P > 0.92$, all comparisons; **Table 5.2**), suggesting that *Lhr* altering rates of recombination has no detectable effect on chromosome segregation.

Based on these results, we tested the hypothesis that *Lhr* might also affect rates of meiotic recombination in *D. simulans*. The first loss-of-function mutation of *Lhr* (*Lhr*¹) was discovered in a natural population of *D. simulans* (Watanabe 1979). We employed the same crossing scheme used in *D. melanogaster* (see **Figure 5.1**) with markers in *D. simulans*. Using *Lhr*¹, our results show a significant decrease in rates of crossing over in the *v f* interval ($P = 0.02$, Dunnett's test; **Figure 5.6**) but no significant difference in the *e st* interval ($P = 0.92$, Dunnett's test; **Figure 5.6**).

Both *Hmr* and *Lhr* are heterochromatin-associated proteins (Brideau *et al.* 2006; Greil *et al.* 2007) that interact in tandem with numerous centromeric proteins including HP1, Umbrea, and CENP-C (Thomae *et al.* 2013). While recombination is suppressed in the centromere (for review, see Choo 1998), it is clear that the centromere plays an integral role in the process of meiotic recombination. For example, CENP-C, a key centromeric protein, is a necessary component for the formation of the kinetochore which attaches homologous chromosomes in *Drosophila* (Przewloka *et al.* 2011). Defects in CENP-C disrupt synaptonemal complex formation and causes meiotic segregation problems (Unhavaithaya and Orr-Weaver 2013). In addition, mutations in HP1, another centromeric interactor with

Lhr and Hmr, has been shown to affect crossing over and nondisjunction in flies (Westphal and Reuter 2002). Centromeres represent just a fraction of heterochromatin within the genome. This tightly packed DNA elsewhere in the genome has been shown to be involved in meiotic chromosome pairing (Karpen *et al.* 1996; Dernburg *et al.* 1996; Yamagishi *et al.* 2008). In *Drosophila* Schneider cells, Hmr and Lhr depletion or overexpression causes defects in mitotic chromosome segregation. Another hybrid incompatibility gene mentioned above, *Zhr*, has been shown to be involved in mitotic defects (Ferree and Barbash 2009). Therefore, it seems possible that the role of Lhr might be similar to that of its centromeric interactors. That is, Lhr might have an unexplored role in kinetochore stability. It would not be surprising that defects with this process might cause changes in recombination rate. Future work is aimed at testing how depletion of both Lhr and Hmr affect recombination rates by testing dual knockdowns as it appears there might be a compensatory role of these interacting proteins (Brideau *et al.* 2006). In addition, analyzing *Lhr* in the background of a mutant with known kinetochore function such as *nod* (Theurkauf and Hawley 1992) might also help elucidate the role of *Lhr* in meiotic recombination if there are epistatic interactions.

Meiotic chromosome pairing is an essential component of determining species compatibility. For example, studies in *Drosophila* have highlighted that improper chromosome pairing can lead to species incompatibilities (Evgenev 1971; Madi-Ravazzi and Bicudo 1992; Madi-Ravazzi *et al.* 1997). It can be hypothesized that improper recombination can also lead to hybrid incompatibilities. The data presented here implicates both *JYalpha* and *Lhr*, both known hybrid incompatibility genes, in mediating rates of recombination. More work is needed to confirm these results, as our results were somewhat inconsistent internally. However our results are suggestive that identifying the genetic determinants of recombination rate variation might also provide insight into species divergence. Future work will be aimed at deciphering the molecular role of these two proteins in meiotic recombination as well as DNA damage repair.

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TABLES

Table 5.1 - List of *Drosophila* stocks used for crossover rate assay. Stocks are listed with genotype, stock center and ID # if applicable along with appropriate genetics background control. Genotypes of control backgrounds are also included for reference.

¹Stocks provided by D. A. Barbash; ²Stocks provided by J. P. Masly.

Gene	Genotype	Stock Center and ID #	Genetic Background Control & Reference (if applicable)
<i>Hmr</i>	$y^1 sc^* v^1; P\{y[+t7.7]v[+t1.8]=TRiP.GLV21024\}attP2$	Bloomington Stock #35659	Bloomington Stock #36303
	$w^{1118}; P\{GD9164\}v51849$	VDRRC Transformant ID #51849	VDRRC Transformant ID #60000
	$w^{1118}; P\{GD9164\}v51850$	VDRRC Transformant ID #51850	VDRRC Transformant ID #60000
	$P\{KK104035\}VIE-260B$	VDRRC transformant ID #101252	VDRRC Transformant ID #60100
	$Df(1)Hmr^-, y w v/ FM7I, Act-GFP$	N/A ¹	$y w v/ FM7I, Act-GFP$ (Barbash and Lorigan 2007)
	$P\{EPgy2\}Hmr^3$	N/A ¹	$y w$ F10 (Aruna <i>et al.</i> 2009; Satyaki <i>et al.</i> 2014).
	$mel-Hmr-HA$	N/A ¹	$y w$ F10; Hmr^3
	$sim-Hmr-HA$	N/A ¹	$y w$ F10; Hmr^3
<i>Jyalpha</i>	$y^1; P\{y[+mDint2] w[BR.E.BR]=SUPor-P\}JYalpha[KG09295]$	Bloomington Stock #16983	Bloomington Stock #169
	$w^{1118}; 4-sim/ci^D$	N/A ²	w^{1118} (Masly <i>et al.</i> 2006)
	$w^{1118}; 4-sim/ey^D$	N/A ²	w^{1118} (Masly <i>et al.</i> 2006)
	imprecise <i>P</i> -element excision ($20a/ey^D$)	N/A ²	w^{1118} (Masly <i>et al.</i> 2006)
	precise <i>P</i> -element excision ($12a/12a$)	N/A ²	w^{1118} (Masly <i>et al.</i> 2006)
	$w^{1118}; P\{GD1823\}v3976$	VDRRC Transformant ID #3976	VDRRC Transformant ID #60000
	$P\{KK111805\}VIE-260B$	VDRRC Transformant ID #106410	VDRRC Transformant ID #601000
<i>Lhr</i>	$y^1 sc^* v^1; P\{TRiP.GLC01649\}attP2$	Bloomington Stock #50531	Bloomington Stock #36303
	$w^{1118}; P\{GD9581\}v25340$	VDRRC Transformant ID #25340	VDRRC Transformant ID #60000
	$P\{KK106339\}VIE-260B$	VDRRC Transformant ID #100529	VDRRC Transformant ID #60100
	Lhr^{KO}	N/A ¹	$y w$ (Satyaki <i>et al.</i> 2014)
	$Lhr^1 (D. simulans)$	N/A ¹	$w^{501} (D. simulans)$ (Brideau <i>et al.</i> 2006; Satyaki <i>et al.</i> 2014)

Table 5.1 Continued

Gene	Genotype	Stock Center and ID #	Genetic Background Control & Reference (if applicable)
<i>Nup96</i>	$y^1 w^+$; $P\{w[+mC]=EP\}Nup98-96[G2120]/TM3, Sb^1 Ser^1$	Bloomington Stock #28433	Bloomington Stock #6598
<i>Nup160</i>	$w^{1118}; P\{w[+mC]=EP\}Nup160[EP372]/CyO$	Bloomington Stock #17278	Bloomington Stock #5905/#6326
<i>OdsH</i>	$PBac\{y[+mDint2] w[+mC]=OdsH-GFP.FPTB\}VK00033$	Bloomington Stock #42282	Bloomington Stock #5905/#6326
<i>Zhr</i>	Zhr^1	Bloomington Stock #25140	Bloomington Stock #5

	Genotype	Stock Center and ID
Control	$y^1 v^1; P\{CaryP\}attP2$	Bloomington Stock #36303
Control	isogenic host strain, w^{1118}	VDRC Transformant ID #60000
Control	host line $y, w^{1118}; P\{attP, y^+, w^3\}$	VDRC Transformant ID #60100
Control	y^1	Bloomington Stock #169
Control	w^{1118} stock which was originally $w^{1118}; ; ci^D/ey^D$	Bloomington Stock #464
Control	$y^1 w^{1118}$	Bloomington Stock #6598
Control	w^{1118}	Bloomington Stock #5905
Control	w^{1118}	Bloomington Stock #6326
Control	OreR	Bloomington Stock #5

Table 5.2 - Nondisjunction Counts for *JYalpha* and *Lhr*. Total number of flies and exceptional progeny are summed from five separate replicates. Exceptional progeny indicate a fly that has experienced a nondisjunction event.

<i>JYalpha</i>	Total # of Flies	Exceptional Progeny
Control for KG09295	2724	5
$y^1; P\{y[+mDint2] w[BR.E.BR]=SUPor-P\}JYalpha[KG09295]$	2166	1
Control for 4-sim, imprecise and precise <i>P</i> -element	1839	2
$w^{1118};;4-sim/ci^D$	1738	0
$w^{1118};;4-sim/ey^D$	1886	2
imprecise <i>P</i> -element excision ($20a/ey^D$)	1722	0
precise <i>P</i> -element excision ($12a/12a$)	1479	0
Control for GD	2045	0
$w^{1118}; P\{GD1823\}v3976$	2261	5
Control for KK	2100	9
$P\{KK111805\}VIE-260B$	2815	1

<i>Lhr</i>	Total # of Flies	Exceptional Progeny
<i>TRiP Control</i>	1449	1
$y^1sc^*v^1;P\{TRiP.GLC01649\}attP2$	2745	2
GD Control for GD	2045	0
$w^{1118}; P\{GD9581\}v25340$	2271	2
KK Control for KK	2100	9
$P\{KK106339\}VIE-260B$	2520	2
Lhr^{KO} Control	2049	22
Lhr^{KO}	1426	5

Table 5.3 - *JYalpha* genotype and crossover rate data from the DGRP.

DGRP Line	chr4:2538-2542 Genotype	chr4:2538-2542 Genotype	e ro - 1	e ro - 2	e ro - 3	e ro - Avg.	y v - 1	y v - 2	y v - 3	y v - Avg.
DGRP_32	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	8.94		3.29	6.12	31.44	40.62	39.66	37.24
DGRP_57	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	21.08		20.19	20.64	27.30	25.53	34.69	29.17
DGRP_75	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	23.26	19.61	21.11	21.33	36.16	35.69	24.68	32.18
DGRP_109	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	11.50	20.25	24.55	18.77	38.75	40.39	40.00	39.71
DGRP_142	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	25.36	20.87	20.95	22.39	32.55	32.42	28.60	31.19
DGRP_229	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	23.04	16.39	19.28	19.57	24.87	24.59	27.40	25.62
DGRP_307	(C)-/(C)-	(C)-/(C)-	25.17	15.38	14.77	18.44	33.55	36.60	35.42	35.19
DGRP_315	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC		23.71	21.26	22.49	29.26	30.94	33.26	31.15
DGRP_324	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	11.40	0.00	3.47	4.96	18.03	28.39	28.21	24.88
DGRP_354	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	19.20	17.02	21.01	19.08	28.64	29.90	31.14	29.89
DGRP_355	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	24.63	20.91	23.84	23.13	34.46	34.16	36.74	35.12
DGRP_371	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	24.69	20.32	20.89	21.97	22.25	28.21	29.24	26.57
DGRP_380	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC		21.33	25.77	23.55	21.13	31.38	29.74	27.42
DGRP_437	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	0.00	0.00	0.00	0.00	30.20	29.55	33.04	30.93
DGRP_596	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC		26.07	25.29	25.68	29.71	33.60	26.29	29.87
DGRP_634	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	9.76	4.32	9.33	7.80	33.64	35.64	33.12	34.14
DGRP_727	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	22.64	19.39	17.06	19.70	30.92	31.17	30.26	30.78
DGRP_774	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	20.41	19.74	19.87	20.01	24.40	35.11	23.37	27.63
DGRP_808	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	5.34	14.23	23.13	14.23	27.91	27.66	31.71	29.10
DGRP_843	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	20.81	20.53	20.73	20.69	26.25	28.13	27.57	27.32
DGRP_849	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	22.58	23.67	23.01	23.09	32.29	30.19	26.11	29.53
DGRP_853	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	26.80	18.09	18.41	21.10	30.91	28.80	27.66	29.12
DGRP_887	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	19.13	20.14	20.66	19.98	29.72	30.04	28.57	29.45
DGRP_900	(C)TCCGC/(C)TCCGC	(C)TCCGC/(C)TCCGC	21.29	18.75	18.16	19.40	28.21	27.20	28.80	28.07

Table 5.4 - *JYalpha* primer pairs for use with future qRT-PCR expression analysis.

Primer Pair	Direction	Sequence	Tm	PCR Product Length
PD40549	Forward	GGCAGAACATGGATTCCCCC	60.75°C	234 bp
	Reverse	TTGCCCATACCTTGTTGCAA	58.29°C	
PD40550	Forward	GGCAGAACATGGATTCCCCC	60.75°C	235 bp
	Reverse	ATTGCCCATACCTTGTTGCA	58.06°C	
PD40551	Forward	GGCAGAACATGGATTCCCCC	60.75°C	150 bp
	Reverse	AAAAACCCGGTGCCTGCT	60.12°C	

FIGURES

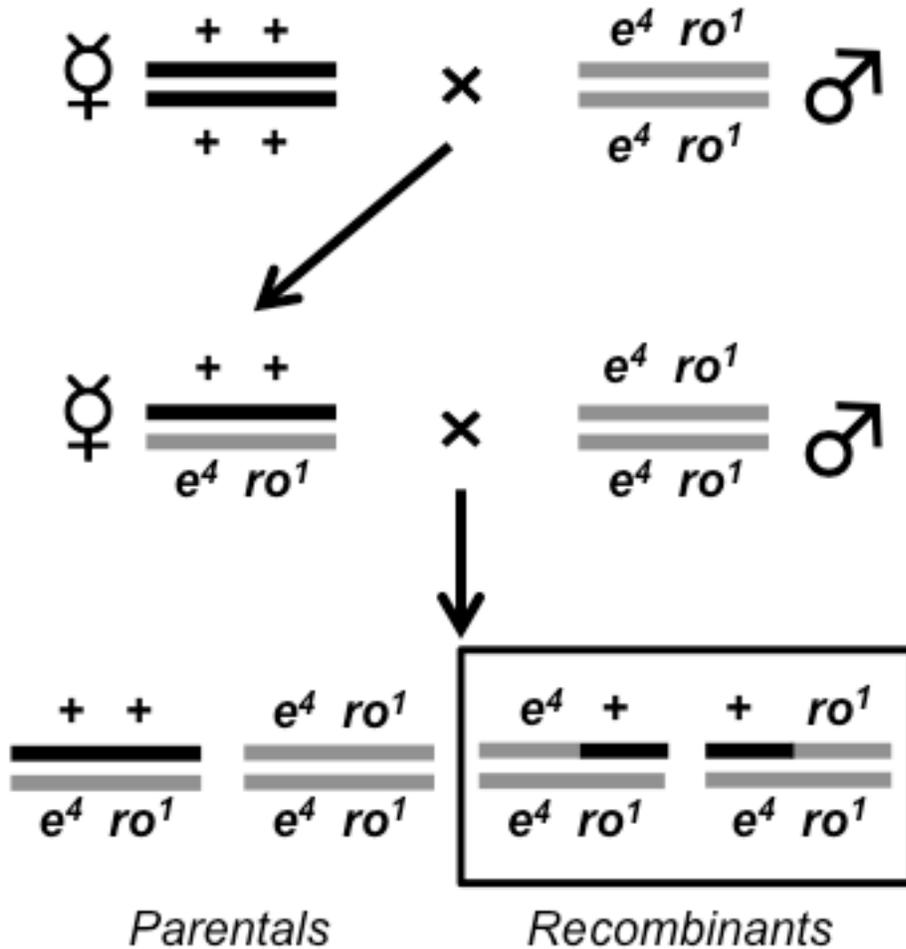


Figure 5.1 - Two step crossing scheme to measure crossover frequency in candidate genes. ++ denotes wild-type and e⁴ ro¹ denotes the doubly marked chromosome on 3R. Stocks used in this cross include the genetic background control as well as P-element insertion or RNAi stocks. Crossover frequency is calculated by taking the ratio of total recombinants (denoted by black box) to total number of progeny. Crosses with *D. simulans* follow the same scheme with the marked chromosome being either st¹ e¹ or v¹ f².

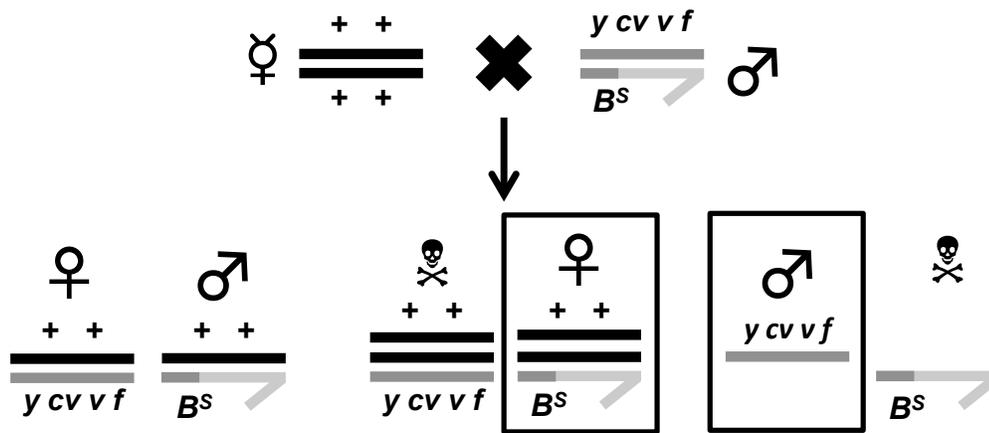


Figure 5.2 - Crossing scheme to measure nondisjunction in *D. melanogaster*. ++ denotes wild-type. A skull and crossbones indicates a lethal genotype that is unrecoverable. Black boxes indicate progeny that have experienced a nondisjunction event. Aneuploid progeny can be identified as such by the sex along with presence or absence of the *Bar* (B^S) eye phenotype.

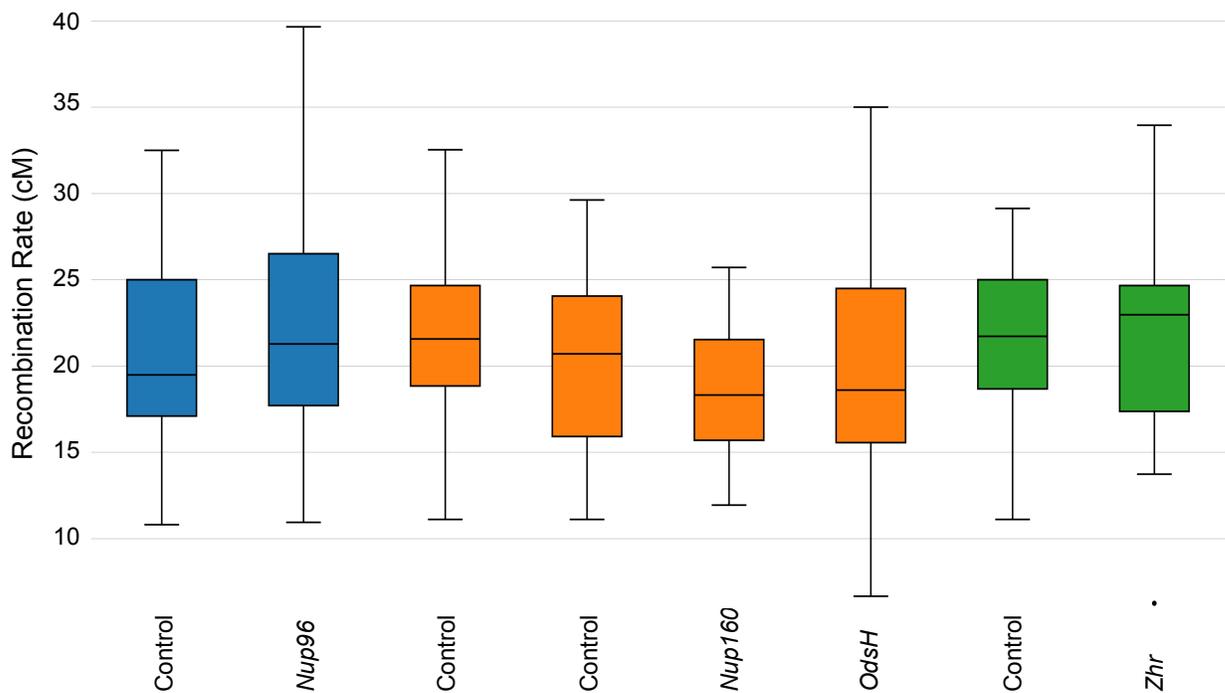


Figure 5.3 - Recombination rate of *Nup96*, *Nup160*, *OdsH*, and *Zhr* in the *e ro* region. Control genetic background and strains compared to that background are denoted by similar colors. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. No experimental lines tested are significant (via Dunnett's test)

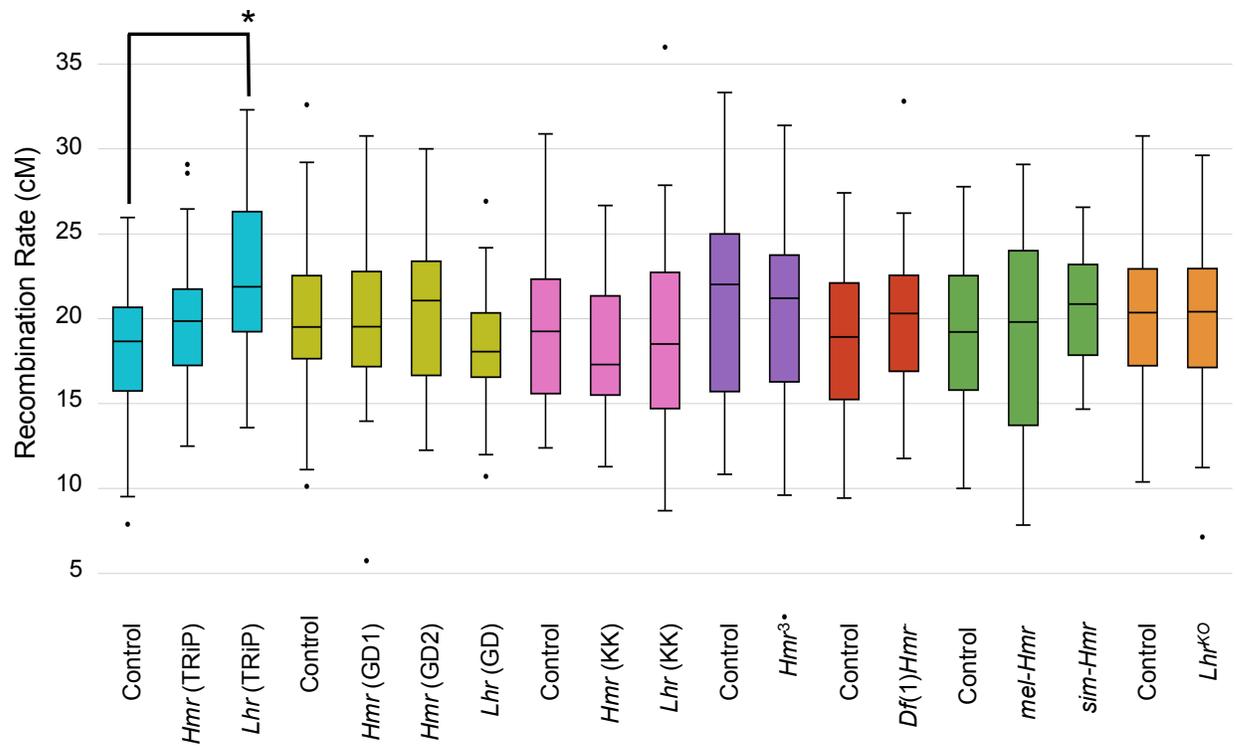


Figure 5.4 - Recombination rate of *P*-element insertions and UAS-RNAi lines of *Lhr* and *Hmr* in the *e ro* region. Control genetic background and strains compared to that background are denoted by similar colors. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. * indicates a $P < 0.05$ (via Dunnett's test).

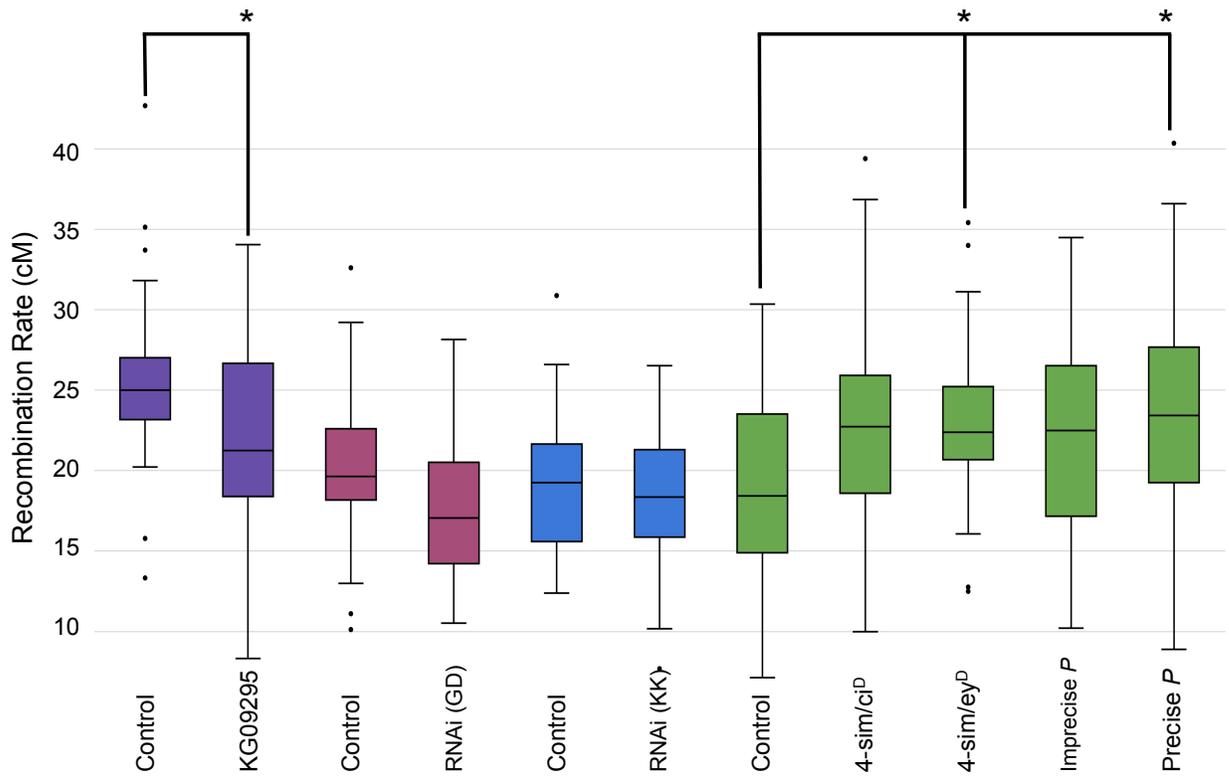


Figure 5.5 - Recombination rate of *P*-element insertions, UAS-RNAi, and chromosomal replacement lines of *JYalpha* in the *e ro* region. Control genetic background and strains compared to that background are denoted by similar colors. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. * indicates a $P < 0.05$ (via Dunnett's test).

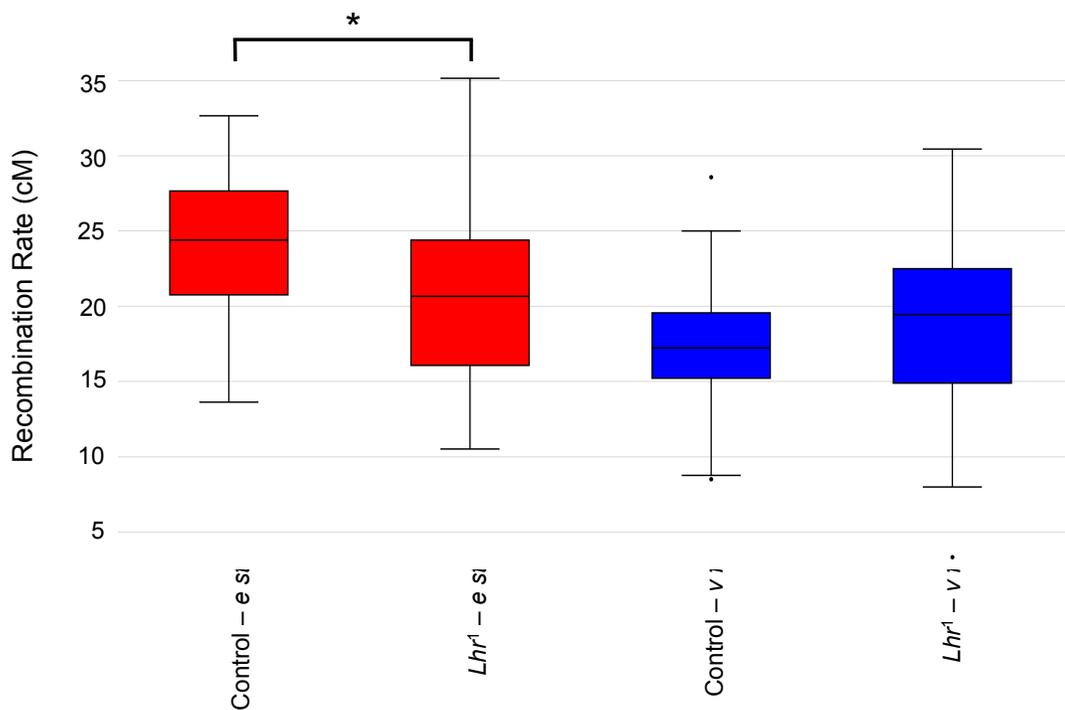


Figure 5.6 - Recombination rate of *Lhr*¹ in the *e st* and *v f* region in *D. simulans*. The two different intervals are separated by color. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. * indicates a $P < 0.05$ (via Dunnett's test).

CHAPTER 6. EVOLUTIONARY RATE COVARIATION UNCOVERS NEW GENETIC FACTORS INVOLVED IN MODULATING RECOMBINATION RATE VARIATION

ABSTRACT

Meiotic recombination is an essential biological process. Not only does it ensure proper chromosome segregation, it is also a pivotal evolutionary force that creates new allelic combinations upon which natural selection can act. Interestingly, rates of recombination are highly variable, due to both environmental and genetic factors. In order to identify genetic factors playing a role in mediating this variation, we utilized a method entitled evolutionary rate covariation (ERC). The method exploits the fact that members of biological pathways are likely to experience similar evolutionary pressures, which could result in correlated changes in rates of coding sequence evolution. ERC identifies genes that experience similar rates of evolution by analyzing phylogenetic trends; genes with highly correlated rates of evolution may be functionally connected in gene networks or biological networks. Here, we attempt to identify genes that modulate rates of recombination by analyzing evolutionary rate covariation of 21 genes with known function in *Drosophila* meiotic recombination. Our results confirm elevated ERC among meiotic recombination genes within *Drosophila*. We also identify thirteen candidate genes that have statistically significant ERC with at least eight meiotic recombination genes. A majority of these candidate genes have no known function though two have been previously implicated in mitotic chromosome segregation. Functional validation highlights two genes, *CG31898* and *CG2975*, that when disrupted significantly alter rates of recombination rate in an interval on chromosome 3R. Our results thus contribute two genetic factors involved in possibly mediating recombination rate in *Drosophila*. Our findings also demonstrate the potential of the ERC method in predicting new members of existing biological pathways.

INTRODUCTION

During meiosis, homologous chromosomes exchange genetic material in a process known as meiotic recombination. This process is essential for proper chromosome segregation and cell viability (Roeder 1997; Hassold and Hunt 2001). For example, abnormal recombination is a hallmark of many human trisomies (Hassold et al. 1991, 1995; MacDonald et al. 1994; Bugge et al. 1998; Robinson et al. 1998; Hassold and Sherman 2000). Despite this intrinsic importance, rates of recombination are highly variable. Variation in recombination rate is present in almost all species studied to date such as yeast (Mancera et al. 2008; Tsai et al. 2010), worms (Barnes et al. 1995; Rockman and Kruglyak 2009), *Drosophila* (Brooks and Marks 1986; True et al. 1996; Stevison and Noor 2010; Comeron et al. 2012), honey bees (Ross et al. 2015), maize (Bauer et al. 2013), chickens (Rahn and Solari 1986), mice (Dumont et al. 2009), chimps (Ptak et al. 2004, 2005; Winckler et al. 2005) and humans (Kong et al. 2002; Crawford et al. 2004; Myers et al. 2005), to name a few.

This variation arises from both environmental and genetic factors. To date, very few genetic factors influencing recombination rate variation have been identified. The most promising discovery so far has been the link of PRDM9 to determination of meiotic recombination hotspot locations (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010) as well as crossover number (Hinch et al. 2011; Capilla et al. 2014) in mammals. Other genetic factors identified as mediators of crossover number include RNF212 (Kong et al. 2008; Chowdhury et al. 2009; Sandor et al. 2012; Johnston et al. 2015) and REC8 (Sandor et al. 2012). Strikingly, these genetic factors are all absent in *Drosophila* and despite being an active area of research, the genetic factors mediating recombination rate variation in *Drosophila* still remain poorly understood.

In order to identify genetic factors involved in this process, we utilized a technique entitled evolutionary rate covariation (ERC). This technique examines tractable phylogenetic signatures of co-variation of proteins (Clark et al. 2012). This method analyzes amino acid divergence in species trees and identifies proteins that have more correlated rates of evolution than expected. This method was inspired by lines of evidence indicating that proteins that physically interact tend to experience similar evolutionary pressures and thus display correlated sequence changes (Pazos et al. 1997; Pazos and Valencia 2001; Hakes et al. 2007; Clark et al. 2009; Clark and Aquadro 2010).

Previous work has spotlighted the success of this method. For example, in yeast, ERC is elevated for genes that have similar biological functions (Clark et al. 2012). Further,

an analysis in yeast and mammals demonstrated significantly strong ERC for genes involved in meiotic crossing over pathways (Clark et al. 2013). Finally, a recent study used ERC to successfully identify new members of protein networks required for *Drosophila* female post-mating responses (Findlay et al. 2014). Based on this evidence, ERC is a powerful tool to identify new players in existing networks and prioritize them for functional testing.

We hypothesized that genes involved in recombination rate variation would display elevated ERC with known meiotic recombination genes. We first demonstrated that meiotic recombination genes displayed elevated ERC values, as would be predicted under the assumption that genes in a shared pathway show correlated rates of evolution because of shared evolutionary pressures. In addition, our results point to thirteen candidate genes that show significant, high correlations in evolutionary rate with eight or more of 21 known meiotic recombination genes. We show that disruptions in two of these candidate genes, *CG31898* and *CG2975*, cause significantly altered rates of recombination as compared to genetic controls. Our results thus reveal two possible new genetic factors involved in mediating recombination rate in *Drosophila* as well as demonstrate the strength of the ERC method in identifying and prioritizing candidate genes for validation.

MATERIAL AND METHODS

ERC Analysis

We made a list of 41 meiotic genes gathered from previous collections (Mehrotra et al. 2008; Anderson et al. 2009; Lake et al. 2011). We refined this list to a total of 21 genes for use in downstream ERC analyses (**Table 6.1**). These 21 genes, in addition to being involved in meiotic recombination, all show either a defect in double-strand break (DSB) repair or crossing over in a null mutant background (see Mehrotra et al. 2008 and references therein).

The ERC method (Clark and Aquadro 2010) analyzes orthologous genes across a phylogeny and calculates amino acid divergence of each gene on each branch in the species tree, utilizing PAML (Yang 2007). In our case, method leverages sequence and alignment data generated as part of the Drosophila 12 Genomes project (Drosophila 12 Genomes Consortium 2007). Protein alignments are only used if there is available data from a minimum of five species. Following this, branch lengths are transformed into a relative rate of evolution compared to the genome-wide average tree. Due to differences in number of species used to create the ERC, these values undergo what is known as a projection operation (Sato et al. 2005), which allows for direct comparisons between ERCs calculated from different sets of Drosophila species. These ERC values are then also assigned a *P*-value based on the genome-wide distribution of ERC values for the particular set of Drosophila species used in the calculation.

All ERC analyses were performed using the ERC webserver (available at http://csb.pitt.edu/erc_analysis/). First, we aimed to test the hypothesis that our compiled list of meiotic genes displayed higher ERC within this group than expected by chance. To do this, we used the *Group Analysis* option. This analyzes the ERC values within a queried list of genes and returns the ERC value between all gene pairs as well as accompanying *P*-values based 100,000 permutations (**Figure 6.2; Table 6.S1**). The *P*-values describe the significance of the difference in ERC values of the focal set relative to the background distribution of ERC values for that collection of species.

After confirming elevated ERC values among meiotic recombination genes, we analyzed each meiotic gene separately to identify potential novel genes that share similar evolutionary pressures because of shared function. This analysis, implemented using the *Top Genes* option, reports the ERC values between a queried gene and all possible genes in the genome (~11,100). For each of the 21 meiotic genes, we restricted our analysis to

genes with a $P \leq 0.10$. These lists are included as **Supplemental Tables 6.2-22**. Finally, genes that were found in greater than six *Top Genes* analyses were used for further analyses (**Table 6.S23**).

Interpretation of Gene Lists

In order to analyze our generated gene list (**Table 6.S23**) for possible trends, we used a pre-established pipeline, BioProfiling.de (available at <http://www.bioprofiling.de/>). This pipeline takes queried gene lists and analyzes them for similar gene function, interactions, pathway involvements and known previous functions (Antonov 2011). The server uses the novel profiling of complex functionality (Antonov et al. 2008), which can analyze functions based on ‘and’, ‘or’ and ‘not’ statements. (For example, *DNA binding capability* ‘and’ *expression in the ovary*.) The server gathers data from the Gene Ontology database (Ashburner et al. 2000; The Gene Ontology Consortium 2015) as well as the InterPro database (Jones et al. 2014; Mitchell et al. 2015). Statistics for these enriched categories are computed using a modified χ^2 test along with a Monte-Carlo simulation approach to adjust for multiple testing (Antonov and Mewes 2006).

Fly Stocks

To assay crossover rates, we took advantage of classical genetic techniques and visible mutations. To measure recombination rates on the 3R chromosome, we used a fly strain marked with *ebony* (e^4) and *rough* (ro^1) (Bloomington Stock #496). These genes are roughly 20.4 cM apart (Bridges and Morgan 1923). These markers were selected due to their genetic distance, lack of apparent viability defects and as well as success in previous studies (Singh et al. 2015). To functionally validate possible candidate genes, we obtained multiple *P*-element insertion and UAS-RNAi lines from the Bloomington Drosophila Stock Center, Vienna Drosophila Resource Center (Dietzl et al. 2007) and Exelixis Collection at Harvard Medical School (Parks et al. 2004; Thibault et al. 2004) for use in our crossover rate assay described below. These stocks are listed in **Table 6.S24**.

Crossover Rate Assay

To assay crossover rates in the *e ro* region on the third chromosome, we used a two-step crossing scheme (**Figure 6.1**). All crosses were executed at 25°C with a 12 hour: 12 hour light:dark cycle on standard media using virgin females aged roughly 24 hours. For the first cross, ten virgin females were crossed to ten *e ro* males in eight ounce bottles. Males

and females were allowed to mate for a total of five days, after which all adults were cleared from the bottles. For the second cross, once again virgin females were collected. These females are doubly heterozygous for the visible markers and are the females in which crossing over is occurring and subsequently scored via their progeny. Ten females were backcrossed to ten males in 25 x 95 mm vials. There were thirty replicates per line. Males and females were once again allowed to mate for five days, after which all adults were cleared from the vials. After eighteen days, BC₁ progeny were collected and scored for both sex and presence/absence of visible markers. The UAS-RNAi lines followed a similar crossing scheme except for the males used in this F₀ cross. These males instead contained both the doubly marked chromosome (*e ro*) along with *nanos*-GAL4 driver on the same chromosome arm (Rørth 1998; Van Doren et al. 1998). *nanos* is expressed throughout *Drosophila* oogenesis (Wang et al. 1994). Recombinant progeny possessed only one morphological marker (either *ebony* or *rough*). The ratio of recombinant progeny to total number progeny for each line was compared to the same ratio from the appropriate genetic background control using a Dunnett's test (Dunnett 1955, 1964) which controls for multiple tests. All statistics were performed using JMP®Pro 11.2.0.

RESULTS AND DISCUSSION

Why rates of recombination are highly variable remains an intriguing biological question. A large amount of research has been aimed at understanding the genetic architecture of natural variation in this trait. It is clear from a wealth of literature that genetics plays a large role in determining recombination rate variation in both *Drosophila* (Broadhead et al. 1977; Brooks and Marks 1986; Cirulli et al. 2007; Comeron et al. 2012; Hunter and Singh 2014) and other species (e.g. Jensen-Seaman et al. 2004; Dumont et al. 2009; Kong et al. 2010). Despite this, only a handful of genetic factors have been identified that mediate recombination rate variation. These genes include PRDM9 (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010), RNF212 (Kong et al. 2008; Chowdhury et al. 2009; Sandor et al. 2012; Johnston et al. 2015) and REC8 (Sandor et al. 2012). *Drosophila* lacks orthologs of all these genes, and moreover, the genetic architecture of recombination in *Drosophila* remains almost completely unknown. We sought to address this critical knowledge gap by identifying genes exhibiting high ERC values with other known meiotic recombination genes under the assumption that the correlated rates of evolution were driven by shared function in meiotic recombination.

Constructing an accurate list of previously identified genes that are involved in meiotic recombination *Drosophila* was of utmost importance. This list (summarized in **Table 6.1**) was compiled using various reviews and primary literature (Mehrotra et al. 2008; Anderson et al. 2009; Lake et al. 2011) and includes genes in the major steps of the crossover pathway. The genes used for analysis include the two members of the synaptonemal complex: *c(2)M* (Manheim and McKim 2003) and *c(3)G* (Page and Hawley 2001) and the three known genes involved in double-strand break (DSB) formation: *mei-W68* (McKim and Hayashi-Hagihara 1998), *mei-P22* (Liu et al. 2002), and *trem* (Lake et al. 2011). It also includes genes involved in meiotic DSB repair: *mre11* (Ciapponi et al. 2004), *mus301* (McCaffrey et al. 2006), *okr* (Ghabrial et al. 1998), *rad50* (Ciapponi et al. 2004), *spn-A* (Staeva-Vieira et al. 2003), *spn-B* (Ghabrial et al. 1998), and *spn-D* (Abdu et al. 2003). *pds5*, involved in DSB repair, is also involved in sister chromatid cohesion (Dorsett et al. 2005; Barbosa et al. 2007) along with *ord* (Bickel et al. 1996). Other categories include exchange class genes: *Ercc1* (Radford et al. 2005), *mei-9* (Sekelsky et al. 1995), and *mus312* (Yildiz et al. 2002); and also precondition genes: *Mcm5* (Lake et al. 2007), *mei-218* (McKim et al. 1996), and *rec* (Blanton et al. 2005). Finally, *mei-41* was included, which is involved in checkpoint response (Hari et al. 1995). It should be noted again that in a null mutant background, all of these genes show either a defect in DSB repair or crossing over.

For this ERC approach to be successful, it is imperative that our list of meiotic recombination genes exhibits high ERC values between pairs of genes within this annotated group. To test this, we analyzed the strength of ERC among only these 21 genes. As mentioned in the introduction, the ERC can be interpreted as a measure of shared evolutionary pressure. Therefore, one would hypothesize that we should observe elevated ERC values among these genes due to their shared involvement in the meiotic recombination pathway as compared to genomic background. The data provided in **Table 6.S1** are the estimates of ERC in all pairwise combinations of these 21 genes. **Figure 6.2** displays a heat map of these values. ERC values range from 1 to -1 with 1 being a perfect positive correlation and -1 being a perfect negative correlation. The largest positive ERC value (0.77) was between *mei-41* and *mus301*. This large ERC value is validated with physical interaction of these proteins (Ghabrial and Schüpbach 1999; Masrouha et al. 2003). The largest negative ERC value (-0.91) was between *mei-P22* and *ord*. *mei-P22* is needed for induction of double-strand breaks (Liu et al. 2002) while *ord* is essential for sister chromatid cohesion (Bickel et al. 1996). The mean value of all ERC values between pairs of proteins ($n = 400$) was 0.15. This value is much larger than the *Drosophila* proteome-wide mean (0.0019) from ~11,100 genes (Findlay et al. 2014). The large average value of ERC, coupled with previous success of this method in *Drosophila* and other organisms (Clark et al. 2012, 2013; Findlay et al. 2014) gave us confidence with this approach for identifying candidate genes modulation recombination rate variation.

Our hypothesis was that proteins that demonstrated elevated ERC values with a large proportion of our list of meiotic recombination proteins would also have unexplored roles in meiotic recombination. We individually ran our 21 meiotic recombination genes (for simplicity, we also refer to these as the “bait” genes) through the *Top Genes* option in the ERC webserver. This tool computes the ERC values between every annotated gene and the “bait” gene and returns an ERC value along with a *P*-value of that correlation based on the distribution of ERC values for that species comparison. From each “bait”, we compiled a list of genes that have a higher ERC than genomic background with a $P \leq 0.10$ (for simplicity, we also refer to these as “correlated” genes). A lenient *P*-value ≤ 0.10 was chosen to allow for a greater chance of identifying proteins that do indeed interact or operate in the same network. (For example, when looking at the two components of the synaptonemal complex, *c(3)G* has an ERC value of 0.53 with *c(2)M* yet has a *P*-value of 0.08.) “Bait” genes along with their “correlated” genes are included as supplemental tables (**Supplemental Tables 6.2-6.22**). The *Top Genes* analyses generated a list on average of 1,113 “correlated” genes

per “bait” gene with a P -value ≤ 0.10 . These lists were then collated and analyzed for reoccurring “correlated” genes across our analyses with “bait” genes.

Our combined gene lists consisted of 23,370 genes. Within this list were 150 “correlated” genes that were present in at least six of the *Top Genes* lists from our 21 “bait” analyses (**Table 6.S23**). Four of our “baits” are included in this list of 150 “correlated” genes. These were *spn-B*, *mei-41*, *mus301*, and *trem* and were excluded from future analysis due to their preexisting known roles in meiotic recombination.

The 146 genes were analyzed to see whether they shared any similar functions or pathways using the BioProfiling.de pipeline (Antonov 2011). We observe significant enrichment for distinct categories. These include *nucleic acid binding* ($P = 0.01$, Gene Ontology database), *zinc ion binding* ($P = 0.03$), *nucleus* ($P = 0.04$), and *zinc finger, AD-type* ($P = 0.01$). These results are summarized in **Table 6.S25**. *Nucleic acid binding* is an interesting gene ontology category because PRDM9, which localizes to recombination hotspots, has been shown to bind to DNA in the center of hotspots (Grey et al. 2011). In addition, MUS312, which is involved in Holliday junction resolution, also has DNA binding domains in *Drosophila* (Andersen et al. 2009). Finally, the *zinc finger* category is intriguing because of the role of PRDM9, a zinc finger containing protein, in determining meiotic recombination hotspots (Baudat et al. 2010; Myers et al. 2010; Parvanov et al. 2010) and crossover number (Hinch et al. 2011; Capilla et al. 2014) in mammals. In further support of a role of zinc fingers for mediating recombination, Trade Embargo, a *Drosophila* zinc finger containing protein, works in tandem with Mei-W68 and Mei-P22 to form DSBs (Lake et al. 2011).

We narrowed our list to “correlated” genes that were present in either eight or nine of our “bait” lists for a manageable amount for functional validation. No “correlated” genes were present in ten or more “bait” lists. These “correlated” genes are summarized in **Table 6.2** and emerge as the most promising candidates for functional validation. Three of these showed significantly elevated ERC with nine “baits” (*CG10560*, *CG31898*, and *Nnf1a*) and the other ten showed significantly elevated ERC with eight “baits” (*CG10274*, *CG11778*, *CG18806*, *CG2975*, *CG34012*, *CG7069*, *CG7597*, *dm*, *ft*, and *Kmn1*). A majority of our candidate genes are CGs or computationally predicted genes with no known function.

If these genes function in some way to mediate recombination rate, then we expect that disrupting these genes will perturb recombination. To functionally test this, we used available P -element insertions and UAS-RNAi lines and measured rates of recombination in these strains in the *e ro* interval on chromosome 3R. Two of 13 candidate genes produce a

significant change in recombination rate relative to the appropriate genetic background control: *CG31898* ($P < 0.035$, Dunnett's test) and *CG2975* ($P < 0.009$, Dunnett's test) (**Figure 6.3; Table 6.S24**). These results thus link both *CG31898* and *CG2975* with meiotic recombination. Unfortunately, not much is known about either of these genes. *CG31898*, located on chromosome 2L, encodes a protein of 334 amino acids. Based on expression data from FlyAtlas, there is ~3.4X more expression of *CG31898* in the ovaries compared to whole fly expression (Chintapalli et al. 2007). The second significant gene, *CG2975*, is also on chromosome 2L and encodes a protein of 386 amino acids. It shows minimal expression in the ovaries (Chintapalli et al. 2007; Adrian and Comeron 2013), but clear expression in ovarian nurse cells (Lin et al. 2008). Future work is aimed at further characterizing these two genes for their role in meiosis such as analyzing protein interactions between other meiotic proteins as well as expression profiles.

Our candidate gene list also contained four genes that have previously described functions: *dm*, *Nnf1a*, *Kmn1*, and *ft*. It is important to note what is already known about these genes and their possible relationship to meiosis and meiotic recombination. Even though perturbing these genes did not significantly affect recombination in the *ebony rough* region as detected through our assay, this does not preclude a role of these genes in modulating recombination rate elsewhere in the genome or under different conditions. *Dm*, or *Myc*, has been heavily studied due to its role as an oncogene in humans (see Meyer and Penn 2008 for review). In *Drosophila*, *dm/Myc* can have detrimental effects on fitness including delayed development, female sterility and even larval fatality (Johnston et al. 1999; Pierce et al. 2004, 2008). *Myc*, along with other proto-oncogenes, is expressed before entry into meiotic prophase in mice spermatogenesis (Wolfes et al. 1989). Overexpression induces apoptosis in prophase and causes sterility in male rats (Kodaira et al. 1996). Work has shown that both somatic and meiotic DSBs tend to occur near the *Myc* gene region in mice (Ng et al. 2009), suggesting that *Myc* might have a role in regulating double-strand break (DSB) placements.

Not much is known about *Nnf1a* in *Drosophila*. The yeast ortholog, *NNF1*, is required for proper spindle orientation and nucleolar and nuclear envelope structure (Shan et al. 1997) and is a member of the Mis12 complex (Santaguida and Musacchio 2009). Work has also proposed that *NNF1* is essential for mitotic chromosome segregation in yeast (Euskirchen 2002). In *Drosophila*, it was shown that *Nnf1a* interacts with Centromeric protein C which is essential for the formation of the kinetochore during mitosis (Przewloka et al. 2011). *Kmn1*, or *kinetochore Mis12-Ndc80 network component 1*, (also known as *Nsl1*) is

also involved in kinetochore formation. Interestingly, *Kmn1* directly interacts with *Nnf1a* (Santaguida and Musacchio 2009) as members of the Mis12 complex. In *Drosophila*, null mutants of *Kmn1* have been linked with mitotic chromosome segregation defects (Venkei et al. 2011). It is unclear whether *Nnf1a* and *Kmn1* have dual roles in meiosis kinetochore formation but this is an interesting hypothesis to test. Finally, a mutation in *ft*, or *fat*, causes a short and fat abdomen phenotype (Lindsley and Zimm 1992). A member of the Hippo pathway, *ft* controls growth, polarity, and patterning (Bosch et al. 2014). The role of *ft* in meiosis or meiotic recombination remains unclear as work has shown that induction of a mutant clone of *ft* in *Drosophila* ovaries causes no observable phenotypes (Sun et al. 2008). Separate of its function, *ft* has been shown to interact with *dm/Myc* (Ziosi et al. 2010), highlighting once again the strength of using ERC to identify possible protein interactions.

In conclusion, our results thus expose two genes, *CG31898* and *CG2975*, that have possible previously unreported roles in meiotic recombination. Future work will be aimed at functionally dissecting these two genes and identifying possible interactions with known meiotic recombination genes. In addition, while two other candidate genes, *Nnf1a* and *Kmn1*, failed to validate in our assay, they both have roles in mitotic chromosome segregation. Given the functional and evolutionary similarity of meiosis and mitosis, these genes may also have roles in meiotic chromosome segregation. This will be another future avenue of exploration. Our results demonstrate the promise and potential power of using correlated rates of evolution to identify novel genes in well-established gene networks and pathways.

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TABLES

Table 6.1 - List of *Drosophila* genes involved in meiotic recombination along with major contribution. See main texts for citations.

	Gene Name	Pathway Involvement
1.	<i>c(2)M</i>	Synaptonemal Complex
2.	<i>c(3)G</i>	Synaptonemal Complex
3.	<i>Ercc1</i>	Exchange Class
4.	<i>Mcm5</i>	Precondition
5.	<i>mei-9</i>	Exchange Class
6.	<i>mei-41</i>	Checkpoint Response
7.	<i>mei-218</i>	Precondition
8.	<i>mei-P22</i>	DSB Formation
9.	<i>mei-W68</i>	DSB Formation
10.	<i>mre11</i>	DSB Repair
11.	<i>mus301</i>	DSB Repair
12.	<i>mus312</i>	Exchange Class
13.	<i>okr</i>	DSB Repair
14.	<i>ord</i>	Sister Chromatid Cohesion
15.	<i>pds5</i>	Sister Chromatid Cohesion, DSB Repair
16.	<i>rad50</i>	DSB Repair
17.	<i>rec</i>	Precondition
18.	<i>spn-A</i>	DSB Repair
19.	<i>spn-B</i>	DSB Repair
20.	<i>spn-D</i>	DSB Repair
21.	<i>trem</i>	DSB Formation

Table 6.2 - List of candidate genes used for functional validation. Also included is what *Top Genes* analysis each candidate gene was present in along with the sum of counts for each of meiotic recombination gene class.

Gene Name	c(2)M - SC	c(3)G - SC	mei-P22 - DSB Formation	mei-W68 - DSB Formation	lrem - DSB Formation	ord - Sister Chromatid Cohesion	pds5 - Sister Chromatid Cohesion	mre11 - DSB Repair	mus301 - DSB Repair	okr - DSB Repair	rad50 - DSB Repair	spn-A - DSB Repair	spn-B - DSB Repair	spn-D - DSB Repair	Mcm5 - Precondition	mei-218 - Precondition	rec - Precondition	mei-41 - Checkpoint Response	Efcc1 - Exchange Class	mus312 - Exchange Class	mei-9 - Exchange Class	Total SC (Max = 2)	Total DSB Formation (Max = 2)	Total Sister Chromatid Cohesion (Max = 2)	Total DSB Repair (Max = 8)	Total Precondition (Max = 3)	Total Checkpoint Response (Max = 3)	Total Exchange Class (Max = 3)	Overall Total (Max = 21)
CG10560	X		X		X		X		X			X	X			X	X					1	1	1	4	1	1	0	9
CG31898			X					X	X		X	X	X			X	X		X			0	1	0	5	1	1	1	9
Nnf1a	X			X	X		X		X			X					X	X		X		1	1	1	3	0	1	2	9
CG10274			X	X		X	X					X				X	X					0	2	1	4	1	1	0	8
CG11778	X			X			X		X	X		X					X	X				1	1	0	4	0	1	1	8
CG18806	X			X					X	X		X					X	X		X		1	1	0	3	0	1	2	8
CG2975	X		X	X			X				X		X	X				X				1	2	0	4	0	1	0	8
CG34012		X		X	X		X	X							X	X		X		X		1	1	1	2	1	1	1	8
CG7069	X		X	X	X		X					X					X		X		X	1	2	1	2	0	0	2	8
CG7597			X	X	X	X	X	X			X	X					X				X	0	2	1	5	0	1	0	8
dm	X		X	X	X		X	X	X									X				1	2	1	3	0	0	1	8
ft			X	X			X	X	X			X				X	X					0	2	0	4	1	1	0	8
Kmn1	X		X	X	X		X		X			X					X					1	2	1	3	0	1	0	8

FIGURES

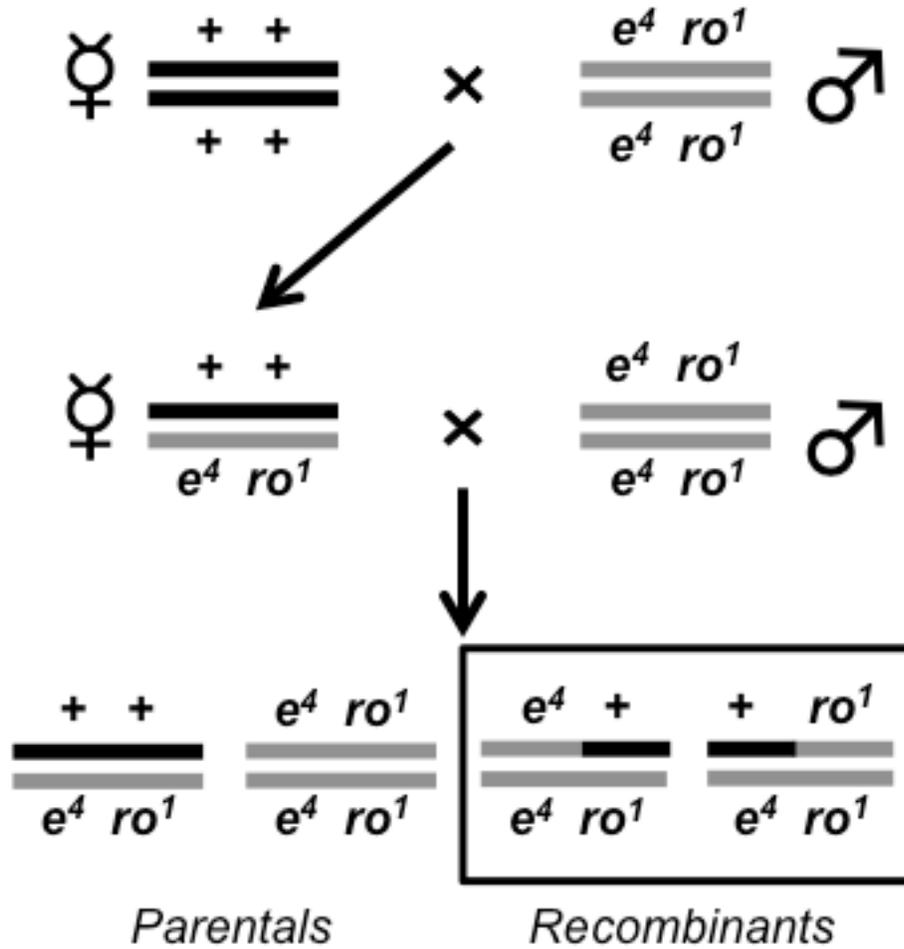


Figure 6.1 - Two step crossing scheme to measure crossover frequency. ++ denotes wild-type and $e^4 ro^1$ denotes the doubly marked chromosome on 3R. For UAS-RNAi lines, males in the first cross also carried a *nanos*-GAL4 driver on the same chromosome as the visible markers. Crossover frequency is calculated by taking the ratio of total recombinants (denoted by black box) to the total number of progeny.

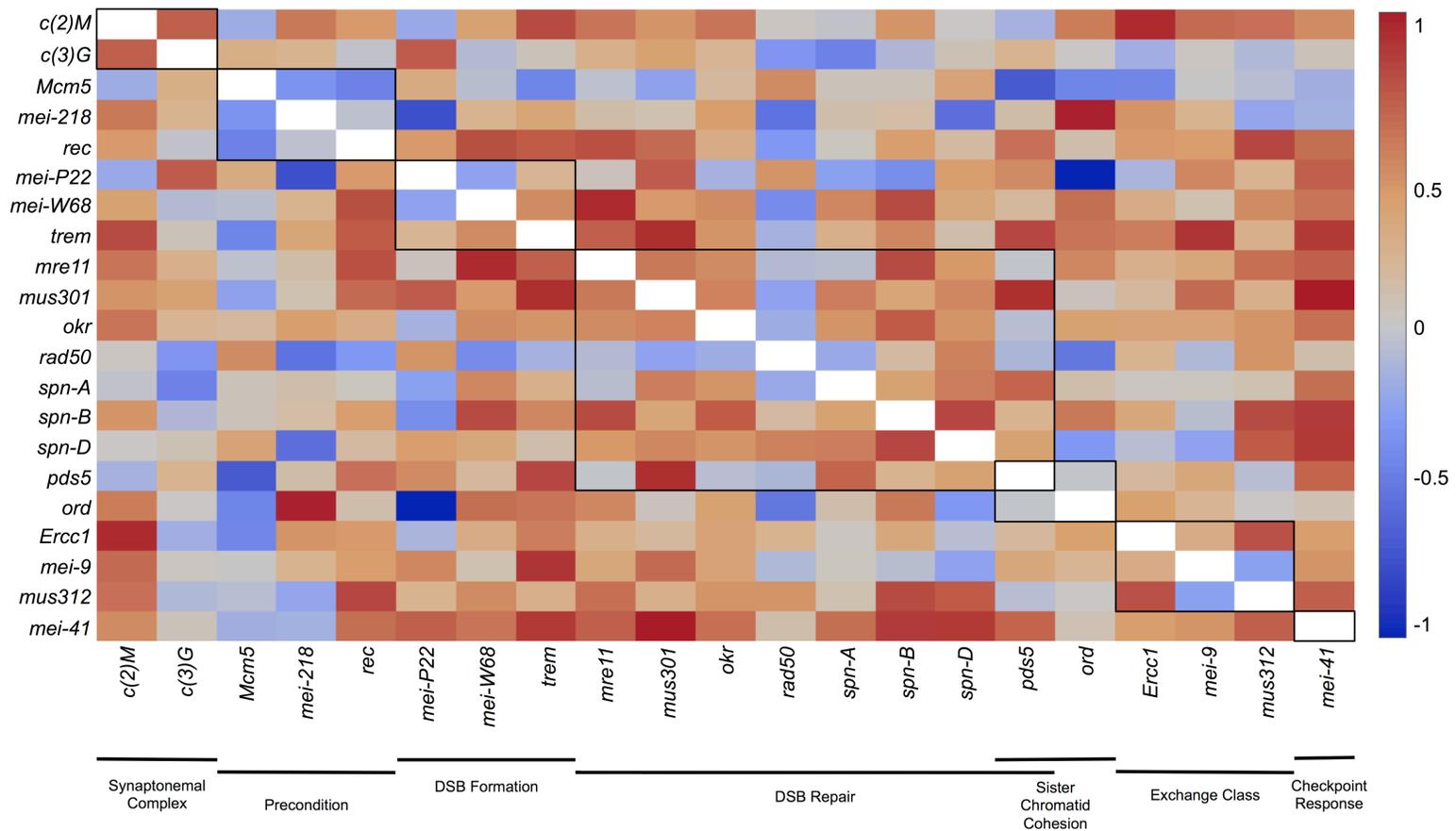


Figure 6.2 - Heat map of ERC values from meiotic recombination genes. See **Table 6.2-3** for ERC values and associated *P*-values. Dark red indicates larger positive ERC values while dark blue indicates larger negative ERC values (values range from -1 to 1). Genes are organized according to involvement in meiotic recombination.

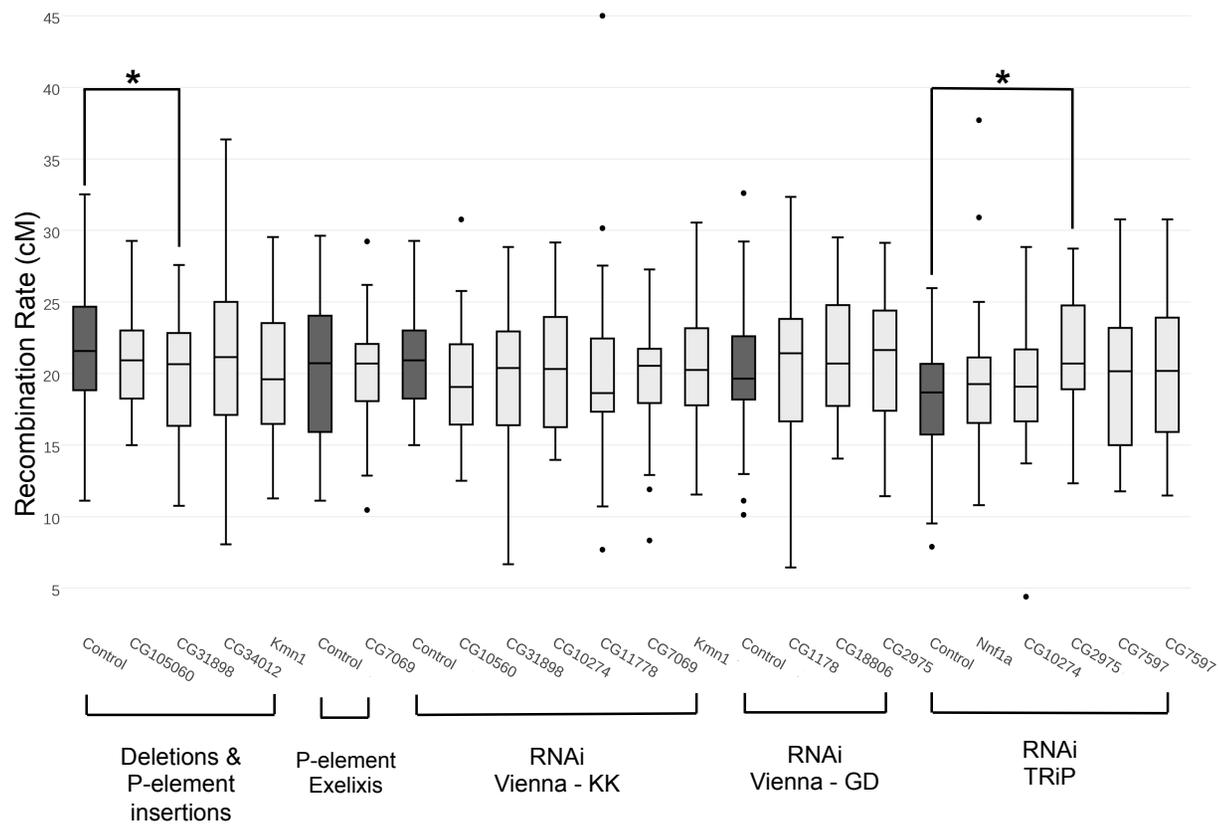


Figure 6.3 - Functional validation of candidate genes. Recombination rates of *P*-element insertions and RNAi lines assayed in the *e ro* region. Darker grey boxes indicate control genetic background, followed by mutant/knockdown strains in that genetic background. Boxplots show first to third quartiles with whiskers extending to the smallest and largest nonoutliers. * indicates a $P < 0.05$ (via Dunnett's test).

SUPPLEMENTAL TABLES

Table 6.S1 - ERC values with associated *P*-values of meiotic recombination genes. Bold ERC values indicate a *P*-value ≤ 0.10.

Genes are organized in the same pattern as displayed in Figure 6.2.

	<i>c(3)G</i>	<i>c(2)M</i>	<i>Ercc1</i>	<i>rad50</i>	<i>Mcm5</i>	<i>mei-218</i>	<i>ord</i>	<i>mei-W68</i>	<i>mre11</i>	<i>rec</i>	<i>mus312</i>	<i>spn-B</i>	<i>okr</i>	<i>spn-A</i>	<i>spn-D</i>	<i>mei-41</i>	<i>mus301</i>	<i>pds5</i>	<i>trem</i>	<i>mei-9</i>	<i>mei-P22</i>
<i>c(3)G</i>	N/A	0.53	-0.22	-0.35	0.16	0.12	-0.06	-0.14	0.15	-0.10	-0.16	-0.17	0.11	-0.46	-0.01	-0.02	0.25	0.12	-0.02	-0.05	0.53
<i>c(2)M</i>	0.53	N/A	0.73	-0.05	-0.23	0.41	0.41	0.24	0.45	0.29	0.45	0.31	0.44	-0.10	-0.06	0.34	0.32	-0.20	0.60	0.48	-0.25
<i>Ercc1</i>	-0.22	0.73	N/A	0.11	-0.43	0.32	0.26	0.17	0.15	0.28	0.57	0.21	0.23	-0.05	-0.13	0.28	0.07	0.06	0.40	0.17	-0.18
<i>rad50</i>	-0.35	-0.05	0.11	N/A	0.34	-0.53	-0.52	-0.41	-0.14	-0.34	0.30	0.06	-0.23	-0.25	0.38	0.02	-0.29	-0.17	-0.20	-0.16	0.32
<i>Mcm5</i>	0.16	-0.23	-0.43	0.34	N/A	-0.36	-0.44	-0.12	-0.10	-0.46	-0.14	-0.03	0.06	-0.03	0.24	-0.21	-0.28	-0.66	-0.45	-0.07	0.18
<i>mei-218</i>	0.12	0.41	0.32	-0.53	-0.36	N/A	0.75	0.12	0.03	-0.11	-0.26	0.04	0.27	0.03	-0.55	-0.21	0.00	0.04	0.22	0.11	-0.71
<i>ord</i>	-0.06	0.41	0.26	-0.52	-0.44	0.75	N/A	0.47	0.36	0.02	-0.06	0.43	0.26	0.03	-0.33	0.00	-0.03	-0.09	0.45	0.11	-0.91
<i>mei-W68</i>	-0.14	0.24	0.17	-0.41	-0.12	0.12	0.47	N/A	0.72	0.59	0.34	0.60	0.34	0.37	0.21	0.45	0.29	0.07	0.34	0.00	-0.29
<i>mre11</i>	0.15	0.45	0.15	-0.14	-0.10	0.03	0.36	0.72	N/A	0.58	0.46	0.61	0.35	-0.12	0.29	0.53	0.42	-0.09	0.53	0.20	-0.03
<i>rec</i>	-0.10	0.29	0.28	-0.34	-0.46	-0.11	0.02	0.59	0.58	N/A	0.61	0.26	0.17	-0.03	0.06	0.47	0.48	0.45	0.54	0.27	0.29
<i>mus312</i>	-0.16	0.45	0.57	0.30	-0.14	-0.26	-0.06	0.34	0.46	0.61	N/A	0.60	0.31	0.00	0.54	0.52	0.14	-0.13	0.13	-0.30	0.12
<i>spn-B</i>	-0.17	0.31	0.21	0.06	-0.03	0.04	0.43	0.60	0.61	0.26	0.60	N/A	0.54	0.54	0.62	0.66	0.22	0.11	0.37	-0.12	-0.40
<i>okr</i>	0.11	0.44	0.23	-0.23	0.06	0.27	0.26	0.34	0.35	0.17	0.31	0.54	N/A	0.31	0.31	0.46	0.37	-0.12	0.31	0.23	-0.20
<i>spn-A</i>	-0.46	-0.10	-0.05	-0.25	-0.03	0.03	0.03	0.37	-0.12	-0.03	0.00	0.25	0.31	N/A	0.41	0.46	0.41	0.50	0.14	-0.04	-0.30
<i>spn-D</i>	-0.01	-0.06	-0.13	0.38	0.24	-0.55	-0.33	0.21	0.29	0.06	0.54	0.62	0.31	0.41	N/A	0.67	0.37	0.24	0.03	-0.29	0.28
<i>mei-41</i>	-0.02	0.34	0.28	0.02	-0.21	-0.21	0.00	0.45	0.53	0.47	0.52	0.66	0.46	0.46	0.67	N/A	0.77	0.49	0.67	0.30	0.53
<i>mus301</i>	0.25	0.32	0.07	-0.29	-0.28	0.00	-0.03	0.29	0.42	0.48	0.14	0.22	0.37	0.41	0.37	0.77	N/A	0.71	0.71	0.48	0.53
<i>pds5</i>	0.12	-0.20	0.06	-0.17	-0.66	0.04	-0.09	0.07	-0.09	0.45	-0.13	0.11	-0.12	0.50	0.24	0.49	0.71	N/A	0.62	0.21	0.34
<i>trem</i>	-0.02	0.60	0.40	-0.20	-0.45	0.22	0.45	0.34	0.53	0.54	0.13	0.37	0.31	0.14	0.03	0.67	0.71	0.62	N/A	0.69	0.10
<i>mei-9</i>	-0.05	0.48	0.17	-0.16	-0.07	0.11	0.11	0.00	0.20	0.27	-0.30	-0.12	0.23	-0.04	-0.29	0.30	0.48	0.21	0.69	N/A	0.37
<i>mei-P22</i>	0.53	-0.25	-0.18	0.32	0.18	-0.71	-0.91	-0.29	-0.03	0.29	0.12	-0.40	-0.20	-0.30	0.28	0.53	0.53	0.34	0.10	0.37	N/A

ND indicates that no value exists in the dataset between those two genes.

Mean ERC-value: 0.15
 Median ERC value: 0.17
 Probability of observed mean by chance: 0.006
 100,000 permutations

Table 6.S1 Continued

	<i>c(3)G</i>	<i>c(2)M</i>	<i>Erccl</i>	<i>rad50</i>	<i>Mcm5</i>	<i>mei-218</i>	<i>ord</i>	<i>mei-W68</i>	<i>mre11</i>	<i>rec</i>	<i>mus312</i>	<i>spn-B</i>	<i>okr</i>	<i>spn-A</i>	<i>spn-D</i>	<i>mei-41</i>	<i>mus301</i>	<i>pds5</i>	<i>trem</i>	<i>mei-9</i>	<i>mei-P22</i>
<i>c(3)G</i>	N/A	0.07	0.74	0.85	0.32	0.36	0.58	0.67	0.33	0.61	0.68	0.70	0.37	0.92	0.53	0.53	0.24	0.36	0.53	0.57	0.06
<i>c(2)M</i>	0.08	N/A	0.02	0.55	0.75	0.14	0.14	0.27	0.12	0.23	0.12	0.22	0.13	0.61	0.57	0.19	0.21	0.72	0.05	0.10	0.76
<i>Erccl</i>	0.77	0.01	N/A	0.37	0.92	0.18	0.23	0.31	0.33	0.20	0.04	0.27	0.25	0.58	0.67	0.21	0.43	0.43	0.12	0.31	0.72
<i>rad50</i>	0.84	0.54	0.37	N/A	0.17	0.94	0.94	0.88	0.65	0.82	0.20	0.43	0.74	0.75	0.15	0.47	0.79	0.68	0.70	0.67	0.19
<i>Mcm5</i>	0.32	0.73	0.89	0.15	N/A	0.84	0.90	0.62	0.60	0.91	0.64	0.52	0.42	0.52	0.24	0.71	0.78	0.99	0.90	0.57	0.30
<i>mei-218</i>	0.35	0.13	0.19	0.95	0.85	N/A	0.01	0.35	0.42	0.63	0.76	0.41	0.23	0.43	0.95	0.72	0.45	0.42	0.26	0.35	1.00
<i>ord</i>	0.57	0.15	0.26	0.92	0.88	0.02	N/A	0.12	0.19	0.47	0.58	0.14	0.27	0.46	0.81	0.52	0.55	0.60	0.13	0.39	1.00
<i>mei-W68</i>	0.67	0.28	0.34	0.89	0.64	0.40	0.11	N/A	0.01	0.05	0.19	0.05	0.19	0.17	0.31	0.12	0.24	0.44	0.19	0.51	0.81
<i>mre11</i>	0.35	0.12	0.35	0.67	0.63	0.47	0.18	0.02	N/A	0.06	0.11	0.05	0.18	0.65	0.23	0.08	0.14	0.61	0.08	0.30	0.55
<i>rec</i>	0.61	0.25	0.25	0.82	0.90	0.62	0.47	0.07	0.07	N/A	0.06	0.27	0.34	0.55	0.43	0.13	0.13	0.14	0.09	0.27	0.25
<i>mus312</i>	0.68	0.13	0.06	0.24	0.66	0.77	0.60	0.21	0.13	0.05	N/A	0.05	0.24	0.52	0.08	0.09	0.39	0.66	0.39	0.79	0.41
<i>spn-B</i>	0.70	0.19	0.28	0.42	0.55	0.44	0.12	0.04	0.04	0.23	0.04	N/A	0.06	0.24	0.03	0.02	0.27	0.37	0.16	0.65	0.90
<i>okr</i>	0.36	0.05	0.21	0.82	0.42	0.18	0.18	0.11	0.10	0.28	0.13	0.02	N/A	0.14	0.14	0.04	0.09	0.69	0.14	0.21	0.79
<i>spn-A</i>	0.93	0.63	0.57	0.79	0.54	0.45	0.45	0.12	0.65	0.55	0.48	0.21	0.17	N/A	0.10	0.07	0.10	0.06	0.31	0.55	0.82
<i>spn-D</i>	0.52	0.58	0.65	0.14	0.25	0.95	0.83	0.28	0.21	0.43	0.05	0.03	0.19	0.12	N/A	0.02	0.15	0.25	0.46	0.80	0.22
<i>mei-41</i>	0.53	0.19	0.23	0.48	0.73	0.73	0.51	0.11	0.07	0.10	0.08	0.03	0.11	0.10	0.02	N/A	0.01	0.09	0.02	0.22	0.07
<i>mus301</i>	0.25	0.20	0.43	0.79	0.78	0.49	0.53	0.22	0.13	0.09	0.36	0.28	0.16	0.14	0.16	0.01	N/A	0.01	0.01	0.09	0.07
<i>pds5</i>	0.39	0.70	0.44	0.67	0.97	0.46	0.59	0.44	0.60	0.13	0.64	0.39	0.63	0.10	0.28	0.11	0.02	N/A	0.05	0.31	0.21
<i>trem</i>	0.53	0.04	0.14	0.71	0.91	0.28	0.11	0.18	0.07	0.06	0.37	0.16	0.21	0.36	0.47	0.02	0.02	0.03	N/A	0.02	0.40
<i>mei-9</i>	0.60	0.04	0.28	0.72	0.63	0.35	0.36	0.49	0.25	0.18	0.84	0.68	0.22	0.58	0.84	0.15	0.04	0.24	0.00	N/A	0.10
<i>mei-P22</i>	0.08	0.74	0.68	0.22	0.34	0.98	1.00	0.78	0.55	0.24	0.40	0.85	0.70	0.78	0.25	0.09	0.08	0.21	0.41	0.18	N/A

Mean p-value: 0.38

Median p-value: 0.32

_____ Z-test of observed p-values _____

mean 0.38 expected 0.5 difference -0.12

exp std error of mean 0.02 z_score -6.04

lower probability of the normal distribution = 0.00e+000

Table 6.S2 - Top Genes ERC values for *c(2)M* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Rad51D</i>	0.956	0.0001
<i>CG31682</i>	0.952	0.0002
<i>Or65a</i>	0.945	0.0003
<i>Ir56a</i>	0.925	0.0004
<i>CG8319</i>	0.919	0.0005
<i>CG12307</i>	0.916	0.0005
<i>CG14450</i>	0.914	0.0006
<i>vlc</i>	0.913	0.0007
<i>CG11778</i>	0.909	0.0008
<i>Sep5</i>	0.905	0.0009
<i>CG12126</i>	0.899	0.001
<i>CG32573</i>	0.898	0.0011
<i>Stim</i>	0.898	0.0011
<i>CG5265</i>	0.894	0.0013
<i>Anxb11</i>	0.888	0.0014
<i>CG5565</i>	0.887	0.0014
<i>CG14408</i>	0.884	0.0015
<i>Spn42Db</i>	0.882	0.0016
<i>CG8974</i>	0.881	0.0017
<i>CG2975</i>	0.878	0.0018
<i>CG7849</i>	0.874	0.0019
<i>Spargel</i>	0.869	0.002
<i>CG10424</i>	0.866	0.0021
<i>beat-la</i>	0.864	0.0022
<i>CG33172</i>	0.864	0.0022
<i>Pp2B-14D</i>	0.863	0.0023
<i>CG11163</i>	0.859	0.0024
<i>Hsp60</i>	0.857	0.0025
<i>RhoGAP18E</i>	0.857	0.0025
<i>pie</i>	0.854	0.0027
<i>CG18418</i>	0.853	0.0028
<i>Sptr</i>	0.852	0.0029
<i>Eaf</i>	0.851	0.003
<i>CG10166</i>	0.845	0.0031
<i>CG14834</i>	0.845	0.0031
<i>CG8245</i>	0.845	0.0031
<i>CG9879</i>	0.845	0.0031
<i>glec</i>	0.842	0.0034
<i>CG1138</i>	0.84	0.0035
<i>CG3812</i>	0.837	0.0036
<i>CG2091</i>	0.831	0.0037
<i>CG3592</i>	0.83	0.0038
<i>zpg</i>	0.83	0.0038
<i>CG1492</i>	0.829	0.004
<i>Ir54c</i>	0.826	0.0041
<i>CG32350</i>	0.825	0.0041
<i>CG32088</i>	0.824	0.0042
<i>Fbw5</i>	0.82	0.0043
<i>Jon74E</i>	0.819	0.0044
<i>CG18806</i>	0.818	0.0045
<i>CG34140</i>	0.818	0.0045
<i>CG11570</i>	0.815	0.0047
<i>mod</i>	0.815	0.0047
<i>CG7069</i>	0.814	0.0049
<i>CG9804</i>	0.814	0.0049
<i>llp5</i>	0.814	0.0049

Gene Name	ERC Value	P-value
<i>Kaz1-ORFB</i>	0.814	0.0049
<i>CG9044</i>	0.813	0.0052
<i>CG6523</i>	0.812	0.0053
<i>Spc105R</i>	0.812	0.0053
<i>CG11470</i>	0.81	0.0055
<i>Ckl1beta</i>	0.809	0.0056
<i>CG31815</i>	0.808	0.0057
<i>CG40191</i>	0.808	0.0057
<i>ald</i>	0.807	0.0059
<i>CG15116</i>	0.807	0.0059
<i>CG15404</i>	0.807	0.0059
<i>CG3281</i>	0.807	0.0059
<i>CG10481</i>	0.805	0.0062
<i>CG17162</i>	0.805	0.0062
<i>CG7408</i>	0.805	0.0062
<i>CG31755</i>	0.802	0.0065
<i>Doa</i>	0.802	0.0065
<i>CG2201</i>	0.801	0.0067
<i>CG30441</i>	0.8	0.0068
<i>Yet1</i>	0.799	0.0068
<i>CG14470</i>	0.796	0.0069
<i>CG31380</i>	0.795	0.007
<i>CG11555</i>	0.794	0.0071
<i>CG13741</i>	0.794	0.0071
<i>CG11227</i>	0.793	0.0073
<i>CG14717</i>	0.793	0.0073
<i>ppk7</i>	0.792	0.0075
<i>CG2453</i>	0.79	0.0076
<i>CG2316</i>	0.788	0.0077
<i>mGluRA</i>	0.788	0.0077
<i>CG9947</i>	0.787	0.0078
<i>Spf45</i>	0.787	0.0078
<i>spz</i>	0.787	0.0078
<i>CG10560</i>	0.786	0.0081
<i>CG5955</i>	0.784	0.0082
<i>CG7845</i>	0.783	0.0083
<i>CG42827</i>	0.782	0.0084
<i>CG4480</i>	0.781	0.0085
<i>CG5532</i>	0.78	0.0086
<i>CG15124</i>	0.779	0.0086
<i>dbp</i>	0.779	0.0086
<i>dm</i>	0.779	0.0086
<i>CG4045</i>	0.778	0.0089
<i>l(2)09851</i>	0.776	0.009
<i>SPoCk</i>	0.776	0.009
<i>CG10713</i>	0.775	0.0092
<i>CG12012</i>	0.775	0.0092
<i>CG14302</i>	0.775	0.0092
<i>CG3107</i>	0.774	0.0095
<i>CG16743</i>	0.773	0.0095
<i>CG17528</i>	0.773	0.0095
<i>CG7587</i>	0.773	0.0095
<i>CG8939</i>	0.772	0.0098
<i>CG11668</i>	0.771	0.0099
<i>CG31643</i>	0.771	0.0099
<i>CG33641</i>	0.771	0.0099

Gene Name	ERC Value	P-value
<i>gp210</i>	0.77	0.0102
<i>CG13837</i>	0.768	0.0103
<i>CG32832</i>	0.768	0.0103
<i>CG7837</i>	0.768	0.0103
<i>CG13876</i>	0.767	0.0105
<i>CG8931</i>	0.767	0.0105
<i>CG1513</i>	0.766	0.0107
<i>CG14590</i>	0.765	0.0108
<i>l(2)NC136</i>	0.763	0.0109
<i>beta3GalTII</i>	0.761	0.011
<i>CG18234</i>	0.759	0.0111
<i>CG3808</i>	0.758	0.0112
<i>Prosalpha6T</i>	0.758	0.0112
<i>CG17562</i>	0.757	0.0114
<i>CG31760</i>	0.755	0.0114
<i>Rod2</i>	0.755	0.0114
<i>Cyp28a5</i>	0.754	0.0116
<i>l(2)01289</i>	0.754	0.0116
<i>CG3305</i>	0.753	0.0118
<i>Su(var)2-HP</i>	0.753	0.0118
<i>CG4815</i>	0.752	0.012
<i>CG8677</i>	0.752	0.012
<i>CG11109</i>	0.751	0.0122
<i>CG31698</i>	0.751	0.0122
<i>B-H1</i>	0.749	0.0123
<i>Or98b</i>	0.749	0.0123
<i>Chc</i>	0.748	0.0125
<i>mRpl3</i>	0.748	0.0125
<i>CG17190</i>	0.747	0.0127
<i>kek5</i>	0.747	0.0127
<i>cin</i>	0.746	0.0129
<i>Rhp</i>	0.746	0.0129
<i>Cyp28d1</i>	0.745	0.0131
<i>Ddr</i>	0.745	0.0131
<i>CG1890</i>	0.744	0.0132
<i>Sdc</i>	0.744	0.0132
<i>CG1344</i>	0.743	0.0134
<i>KH1</i>	0.742	0.0135
<i>Acp53C14c</i>	0.741	0.0136
<i>calypso</i>	0.741	0.0136
<i>ed</i>	0.741	0.0136
<i>It</i>	0.741	0.0136
<i>CG32732</i>	0.74	0.014
<i>CG40006</i>	0.74	0.014
<i>Ser8</i>	0.74	0.014
<i>CG3226</i>	0.739	0.0142
<i>scf</i>	0.739	0.0142
<i>CG9471</i>	0.738	0.0144
<i>CG8671</i>	0.737	0.0145
<i>CG9253</i>	0.737	0.0145
<i>Vm32E</i>	0.737	0.0145
<i>Zyx102EF</i>	0.736	0.0148
<i>CG30466</i>	0.735	0.0149
<i>CG32551</i>	0.735	0.0149
<i>CG6216</i>	0.735	0.0149
<i>Gr89a</i>	0.735	0.0149

Gene Name	ERC Value	P-value
<i>Mt2</i>	0.735	0.0149
<i>Ir40a</i>	0.734	0.0153
<i>SmD2</i>	0.734	0.0153
<i>CG14693</i>	0.733	0.0155
<i>CG31752</i>	0.733	0.0155
<i>mei-S332</i>	0.733	0.0155
<i>Prosbeta7</i>	0.732	0.0158
<i>CG10830</i>	0.731	0.0159
<i>CG17707</i>	0.731	0.0159
<i>Sbp2</i>	0.731	0.0159
<i>CG17691</i>	0.73	0.0161
<i>CG31676</i>	0.73	0.0161
<i>Elp2</i>	0.73	0.0161
<i>CG17186</i>	0.729	0.0164
<i>CG9592</i>	0.728	0.0165
<i>tectonic</i>	0.728	0.0165
<i>CG11912</i>	0.727	0.0167
<i>CG14882</i>	0.727	0.0167
<i>l(2)k14505</i>	0.727	0.0167
<i>Ercct1</i>	0.726	0.0169
<i>H2.0</i>	0.726	0.0169
<i>Nnfta</i>	0.726	0.0169
<i>CG11279</i>	0.725	0.0172
<i>mRps30</i>	0.725	0.0172
<i>CG12121</i>	0.724	0.0174
<i>CG32006</i>	0.722	0.0175
<i>Kmn1</i>	0.722	0.0175
<i>CG15028</i>	0.721	0.0177
<i>CG3191</i>	0.721	0.0177
<i>Gint3</i>	0.721	0.0177
<i>nimC1</i>	0.72	0.0179
<i>timeout</i>	0.72	0.0179
<i>beat-1c</i>	0.719	0.0181
<i>CG5194</i>	0.719	0.0181
<i>CG12288</i>	0.718	0.0183
<i>CG15482</i>	0.718	0.0183
<i>CG15914</i>	0.718	0.0183
<i>CG6204</i>	0.718	0.0183
<i>FLASH</i>	0.718	0.0183
<i>CG9523</i>	0.717	0.0187
<i>CG9886</i>	0.717	0.0187
<i>nAcRbeta-2</i>	0.717	0.0187
<i>Traf6</i>	0.717	0.0187
<i>CG11665</i>	0.716	0.0191
<i>oc</i>	0.716	0.0191
<i>CG11141</i>	0.715	0.0193
<i>CG12182</i>	0.715	0.0193
<i>llp1</i>	0.714	0.0195
<i>CG6838</i>	0.713	0.0195
<i>mus308</i>	0.713	0.0195
<i>Hr39</i>	0.712	0.0197
<i>Bj1</i>	0.711	0.0198
<i>cenB1A</i>	0.71	0.0199
<i>CG30008</i>	0.709	0.02
<i>CG32686</i>	0.709	0.02
<i>CG33919</i>	0.708	0.0202

Gene Name	ERC Value	P-value
<i>CG30440</i>	0.706	0.0203
<i>CG7328</i>	0.706	0.0203
<i>mRpl19</i>	0.706	0.0203
<i>cmel</i>	0.705	0.0205
<i>CG5871</i>	0.704	0.0206
<i>CG17270</i>	0.703	0.0207
<i>CG10581</i>	0.702	0.0208
<i>d4</i>	0.702	0.0208
<i>Eps-15</i>	0.702	0.0208
<i>Est-Q</i>	0.702	0.0208
<i>Rrp42</i>	0.702	0.0208
<i>CG32281</i>	0.701	0.0213
<i>CG32409</i>	0.701	0.0213
<i>CG42487</i>	0.701	0.0213
<i>CG9691</i>	0.701	0.0213
<i>cta</i>	0.701	0.0213
<i>adat</i>	0.7	0.0217
<i>CG12990</i>	0.7	0.0217
<i>CG31195</i>	0.7	0.0217
<i>GstD8</i>	0.7	0.0217
<i>Rheb</i>	0.7	0.0217
<i>CG10324</i>	0.699	0.0222
<i>CG10924</i>	0.699	0.0222
<i>pkc</i>	0.699	0.0222
<i>CG10417</i>	0.698	0.0224
<i>CG4424</i>	0.698	0.0224
<i>Nca</i>	0.698	0.0224
<i>sra</i>	0.698	0.0224
<i>CG12206</i>	0.697	0.0228
<i>CG7603</i>	0.697	0.0228
<i>CG9109</i>	0.697	0.0228
<i>rg</i>	0.696	0.0231
<i>Fs</i>	0.695	0.0232
<i>Btd</i>	0.694	0.0232
<i>CG14618</i>	0.694	0.0232
<i>CG15890</i>	0.694	0.0232
<i>CG18764</i>	0.694	0.0232
<i>Dg</i>	0.694	0.0232
<i>psd</i>	0.694	0.0232
<i>fs(1)N</i>	0.693	0.0238
<i>Ak6</i>	0.692	0.0239
<i>CG11784</i>	0.692	0.0239
<i>CG17283</i>	0.692	0.0239
<i>CG17917</i>	0.691	0.0241
<i>CG31600</i>	0.691	0.0241
<i>CG7488</i>	0.691	0.0241
<i>nimB3</i>	0.69	0.0244
<i>Nhe3</i>	0.689	0.0245
<i>CG1234</i>	0.688	0.0246
<i>CG13955</i>	0.688	0.0246
<i>CG11882</i>	0.687	0.0248
<i>CG8180</i>	0.686	0.0249
<i>CG10265</i>	0.685	0.025
<i>CG11870</i>	0.685	0.025
<i>CG31482</i>	0.684	0.0251
<i>CG7071</i>	0.684	0.0251

Table 6.S2 Continued

Gene Name	ERC Value	P-value
<i>tw</i>	0.684	0.0251
<i>cav</i>	0.683	0.0254
<i>CG11133</i>	0.683	0.0254
<i>CG9247</i>	0.683	0.0254
<i>G9a</i>	0.683	0.0254
<i>CG13377</i>	0.682	0.0258
<i>CG33263</i>	0.682	0.0258
<i>CG13748</i>	0.681	0.0259
<i>CG3534</i>	0.681	0.0259
<i>yl</i>	0.68	0.0261
<i>CG13001</i>	0.679	0.0262
<i>CG14301</i>	0.679	0.0262
<i>CG42402</i>	0.679	0.0262
<i>DhpD</i>	0.679	0.0262
<i>l(2)37Ce</i>	0.679	0.0262
<i>NfR</i>	0.679	0.0262
<i>CG17575</i>	0.678	0.0268
<i>CG18258</i>	0.678	0.0268
<i>CG17683</i>	0.677	0.0269
<i>CG3165</i>	0.677	0.0269
<i>CG6914</i>	0.677	0.0269
<i>CG7551</i>	0.677	0.0269
<i>CG9519</i>	0.677	0.0269
<i>CG14407</i>	0.676	0.0274
<i>CG18347</i>	0.676	0.0274
<i>GluRIIB</i>	0.676	0.0274
<i>CG12818</i>	0.675	0.0277
<i>CG14322</i>	0.675	0.0277
<i>CG7956</i>	0.675	0.0277
<i>RpL35A</i>	0.675	0.0277
<i>DIP1</i>	0.674	0.028
<i>Nipsnap</i>	0.674	0.028
<i>CG14931</i>	0.672	0.0282
<i>CG1732</i>	0.672	0.0282
<i>CG34045</i>	0.672	0.0282
<i>hkb</i>	0.672	0.0282
<i>CG11155</i>	0.671	0.0286
<i>Elo68beta</i>	0.671	0.0286
<i>Lis-1</i>	0.671	0.0286
<i>Muc55B</i>	0.671	0.0286
<i>CG30152</i>	0.67	0.0289
<i>CG12539</i>	0.669	0.029
<i>CG3262</i>	0.669	0.029
<i>CG8833</i>	0.669	0.029
<i>CG13557</i>	0.668	0.0293
<i>na</i>	0.668	0.0293
<i>p53</i>	0.668	0.0293
<i>CG15025</i>	0.667	0.0295
<i>CG4565</i>	0.667	0.0295
<i>CG5909</i>	0.667	0.0295
<i>CG8501</i>	0.667	0.0295
<i>CG12272</i>	0.666	0.0299
<i>CG6745</i>	0.666	0.0299
<i>Myb</i>	0.666	0.0299
<i>CG13423</i>	0.665	0.0302
<i>CG14316</i>	0.665	0.0302

Gene Name	ERC Value	P-value
<i>CG40198</i>	0.665	0.0302
<i>CG9960</i>	0.665	0.0302
<i>GluRIIA</i>	0.665	0.0302
<i>CG13500</i>	0.664	0.0306
<i>CG15865</i>	0.664	0.0306
<i>CG5921</i>	0.664	0.0306
<i>CG18011</i>	0.663	0.0309
<i>CG9509</i>	0.663	0.0309
<i>ct</i>	0.663	0.0309
<i>lrr1a</i>	0.663	0.0309
<i>Prosbeta1</i>	0.663	0.0309
<i>sqv</i>	0.663	0.0309
<i>CG11638</i>	0.662	0.0314
<i>CG15130</i>	0.662	0.0314
<i>Hen1</i>	0.661	0.0316
<i>CG31784</i>	0.66	0.0317
<i>Cpr47Ed</i>	0.66	0.0317
<i>fs(1)Yb</i>	0.66	0.0317
<i>CG42329</i>	0.659	0.032
<i>Proc-R</i>	0.659	0.032
<i>VhaM9.7-d</i>	0.659	0.032
<i>CG2641</i>	0.658	0.0323
<i>Hmr</i>	0.658	0.0323
<i>aux</i>	0.657	0.0324
<i>Pph13</i>	0.657	0.0324
<i>CG32529</i>	0.656	0.0326
<i>CG6712</i>	0.656	0.0326
<i>CG10486</i>	0.655	0.0328
<i>CG17633</i>	0.655	0.0328
<i>CG9203</i>	0.655	0.0328
<i>CG7224</i>	0.654	0.0331
<i>eco</i>	0.654	0.0331
<i>RpL34a</i>	0.654	0.0331
<i>CG10362</i>	0.653	0.0333
<i>Roc2</i>	0.653	0.0333
<i>Ugt36Ba</i>	0.653	0.0333
<i>CG42369</i>	0.652	0.0336
<i>Ndc80</i>	0.652	0.0336
<i>salt</i>	0.651	0.0338
<i>Ets21C</i>	0.65	0.0339
<i>Rfabg</i>	0.65	0.0339
<i>CG10075</i>	0.649	0.0341
<i>CG13169</i>	0.649	0.0341
<i>CG31053</i>	0.649	0.0341
<i>CG7949</i>	0.649	0.0341
<i>gd</i>	0.649	0.0341
<i>LRP1</i>	0.649	0.0341
<i>Pbprp2</i>	0.649	0.0341
<i>CG11210</i>	0.648	0.0347
<i>CG8001</i>	0.648	0.0347
<i>Rrp46</i>	0.648	0.0347
<i>CG13897</i>	0.647	0.035
<i>CG6933</i>	0.647	0.035
<i>CG8777</i>	0.647	0.035
<i>dlimm</i>	0.647	0.035
<i>CG31269</i>	0.646	0.0353

Gene Name	ERC Value	P-value
<i>lrr94f</i>	0.646	0.0353
<i>Syt112</i>	0.646	0.0353
<i>kat80</i>	0.645	0.0356
<i>Pros35</i>	0.645	0.0356
<i>CG3014</i>	0.644	0.0358
<i>CG42255</i>	0.644	0.0358
<i>Gr43b</i>	0.644	0.0358
<i>Rpb4</i>	0.644	0.0358
<i>shl</i>	0.644	0.0358
<i>CG14906</i>	0.643	0.0362
<i>CG31224</i>	0.643	0.0362
<i>CG34136</i>	0.643	0.0362
<i>CG4956</i>	0.643	0.0362
<i>CG6380</i>	0.643	0.0362
<i>CG8116</i>	0.643	0.0362
<i>shu</i>	0.643	0.0362
<i>CG11345</i>	0.642	0.0368
<i>CG13343</i>	0.642	0.0368
<i>CycD</i>	0.642	0.0368
<i>CG11762</i>	0.641	0.0371
<i>Or23a</i>	0.641	0.0371
<i>RhoGAP5A</i>	0.641	0.0371
<i>CG11425</i>	0.639	0.0374
<i>CG12204</i>	0.639	0.0374
<i>CG14930</i>	0.639	0.0374
<i>CG15418</i>	0.639	0.0374
<i>CG6106</i>	0.639	0.0374
<i>CG42748</i>	0.638	0.0378
<i>CG6757</i>	0.638	0.0378
<i>Ku80</i>	0.638	0.0378
<i>Scfp</i>	0.638	0.0378
<i>BubR1</i>	0.637	0.0382
<i>CG31777</i>	0.637	0.0382
<i>CG8928</i>	0.637	0.0382
<i>Uchr</i>	0.637	0.0382
<i>aust</i>	0.636	0.0386
<i>CG12983</i>	0.636	0.0386
<i>CG3921</i>	0.636	0.0386
<i>DAAM</i>	0.636	0.0386
<i>Dcp2</i>	0.636	0.0386
<i>lr</i>	0.636	0.0386
<i>Sas</i>	0.636	0.0386
<i>CG34298</i>	0.635	0.0392
<i>CG4019</i>	0.635	0.0392
<i>CG6325</i>	0.635	0.0392
<i>CG11367</i>	0.634	0.0395
<i>CG30157</i>	0.634	0.0395
<i>CG6144</i>	0.634	0.0395
<i>CG8316</i>	0.634	0.0395
<i>sun</i>	0.634	0.0395
<i>CG12042</i>	0.633	0.0399
<i>CG14561</i>	0.633	0.0399
<i>CG7265</i>	0.633	0.0399
<i>CG1806</i>	0.632	0.0402
<i>GluRIIE</i>	0.632	0.0402
<i>Jhedup</i>	0.632	0.0402

Gene Name	ERC Value	P-value
<i>Pgk</i>	0.632	0.0402
<i>CG16970</i>	0.631	0.0405
<i>Grd</i>	0.631	0.0405
<i>Mst89B</i>	0.631	0.0405
<i>Obp99c</i>	0.631	0.0405
<i>CG10465</i>	0.63	0.0409
<i>CG32195</i>	0.63	0.0409
<i>CG4666</i>	0.63	0.0409
<i>dUTPase</i>	0.63	0.0409
<i>l(1)G0289</i>	0.63	0.0409
<i>CG12788</i>	0.629	0.0414
<i>CG4942</i>	0.629	0.0414
<i>CG33775</i>	0.628	0.0415
<i>CG8678</i>	0.628	0.0415
<i>Nfl</i>	0.628	0.0415
<i>CG10752</i>	0.627	0.0418
<i>scpr-C</i>	0.627	0.0418
<i>Mis12</i>	0.626	0.042
<i>Pngl</i>	0.626	0.042
<i>CG10395</i>	0.625	0.0422
<i>CG2712</i>	0.625	0.0422
<i>CG4877</i>	0.625	0.0422
<i>l(1)G0045</i>	0.625	0.0422
<i>Map205</i>	0.625	0.0422
<i>CG31551</i>	0.624	0.0426
<i>CG5122</i>	0.624	0.0426
<i>Cyp4ae1</i>	0.624	0.0426
<i>gm</i>	0.624	0.0426
<i>CG33266</i>	0.623	0.043
<i>Dcr-1</i>	0.623	0.043
<i>plu</i>	0.623	0.043
<i>CG12866</i>	0.622	0.0432
<i>CG1315</i>	0.622	0.0432
<i>CG14482</i>	0.622	0.0432
<i>CG2974</i>	0.622	0.0432
<i>CG10462</i>	0.621	0.0436
<i>CG11188</i>	0.621	0.0436
<i>CG32712</i>	0.621	0.0436
<i>CG7882</i>	0.621	0.0436
<i>atms</i>	0.62	0.044
<i>CG10000</i>	0.62	0.044
<i>CG3194</i>	0.62	0.044
<i>CG8100</i>	0.62	0.044
<i>CG9795</i>	0.619	0.0443
<i>DNApol-garr</i>	0.619	0.0443
<i>Jhf-21</i>	0.619	0.0443
<i>CG31457</i>	0.618	0.0446
<i>CG11327</i>	0.617	0.0447
<i>CG32809</i>	0.617	0.0447
<i>CG7248</i>	0.617	0.0447
<i>CG8602</i>	0.617	0.0447
<i>ilp2</i>	0.617	0.0447
<i>Ym26Ab</i>	0.617	0.0447
<i>CG13982</i>	0.616	0.0452
<i>CG8498</i>	0.616	0.0452
<i>CCKLR-17D</i>	0.615	0.0454

Gene Name	ERC Value	P-value
<i>CG12609</i>	0.615	0.0454
<i>CG3635</i>	0.615	0.0454
<i>CG9117</i>	0.615	0.0454
<i>CG1103</i>	0.614	0.0458
<i>CG14306</i>	0.614	0.0458
<i>CG14767</i>	0.614	0.0458
<i>CG15876</i>	0.614	0.0458
<i>CG8539</i>	0.614	0.0458
<i>Crk</i>	0.614	0.0458
<i>l(1)sc</i>	0.614	0.0458
<i>mamo</i>	0.614	0.0458
<i>CG10911</i>	0.613	0.0465
<i>CG32016</i>	0.613	0.0465
<i>Saf-B</i>	0.613	0.0465
<i>CG14591</i>	0.612	0.0468
<i>CG34316</i>	0.612	0.0468
<i>HLHm3</i>	0.612	0.0468
<i>l(2)05714</i>	0.612	0.0468
<i>Asph</i>	0.611	0.0471
<i>CG17669</i>	0.611	0.0471
<i>CG9766</i>	0.611	0.0471
<i>Rbcn-3A</i>	0.611	0.0471
<i>tinc</i>	0.611	0.0471
<i>CG10459</i>	0.61	0.0476
<i>CG9919</i>	0.61	0.0476
<i>coil</i>	0.61	0.0476
<i>calc</i>	0.609	0.0478
<i>CG5010</i>	0.609	0.0478
<i>CG15725</i>	0.608	0.048
<i>CG5791</i>	0.608	0.048
<i>CG8412</i>	0.608	0.048
<i>CG9917</i>	0.608	0.048
<i>mRpL34</i>	0.608	0.048
<i>ppk11</i>	0.608	0.048
<i>CG33969</i>	0.607	0.0486
<i>CG3603</i>	0.607	0.0486
<i>CG7634</i>	0.607	0.0486
<i>Spe25</i>	0.607	0.0486
<i>beta4GalT7</i>	0.606	0.0489
<i>CG1909</i>	0.606	0.0489
<i>CG33234</i>	0.606	0.0489
<i>Prosbeta3</i>	0.606	0.0489
<i>Gem3</i>	0.605	0.0493
<i>Hrd3</i>	0.605	0.0493
<i>sty</i>	0.605	0.0493
<i>CG5883</i>	0.604	0.0495
<i>Hcf</i>	0.604	0.0495
<i>CG12179</i>	0.603	0.0497
<i>CG12783</i>	0.603	0.0497
<i>CG14695</i>	0.603	0.0497
<i>CG16863</i>	0.602	0.05
<i>CG32117</i>	0.602	0.05
<i>CG7881</i>	0.602	0.05
<i>RanBPM</i>	0.602	0.05
<i>Scr</i>	0.602	0.05
<i>Ars2</i>	0.601	0.0505

Table 6.S2 Continued

Gene Name	ERC Value	P-value
CG13725	0.601	0.0505
CG15643	0.601	0.0505
CG3198	0.601	0.0505
CG6980	0.601	0.0505
CG8141	0.601	0.0505
CG15169	0.6	0.051
CG7330	0.6	0.051
Ssl1	0.6	0.051
vap	0.6	0.051
CG13334	0.599	0.0514
CG2789	0.599	0.0514
CG31922	0.599	0.0514
CG14440	0.598	0.0516
CG16700	0.598	0.0516
Uba2	0.598	0.0516
xmas-2	0.598	0.0516
ATPsyn-garr	0.597	0.052
CG3940	0.597	0.052
trem	0.597	0.052
CG2813	0.596	0.0523
ird5	0.596	0.0523
Kdm4B	0.596	0.0523
rab3-GEF	0.596	0.0523
Acp65Aa	0.595	0.0526
CG32850	0.595	0.0526
CG42245	0.595	0.0526
rhea	0.595	0.0526
Suz12	0.595	0.0526
tbce	0.595	0.0526
Cas	0.594	0.0532
CG31267	0.594	0.0532
CG5087	0.594	0.0532
CG5746	0.594	0.0532
CG9346	0.594	0.0532
Tbp	0.594	0.0532
Tsp68C	0.594	0.0532
CG5399	0.593	0.0538
boca	0.592	0.0539
pain	0.592	0.0539
Surf1	0.592	0.0539
Tsp97E	0.592	0.0539
wgn	0.592	0.0539
CG4198	0.591	0.0543
corv	0.591	0.0543
Vps36	0.591	0.0543
Alh	0.59	0.0546
CG13965	0.59	0.0546
CG17272	0.59	0.0546
CG30373	0.59	0.0546
CS-2	0.59	0.0546
DNApol- α ph	0.59	0.0546
Treh	0.59	0.0546
Adk3	0.589	0.0552
CG4611	0.589	0.0552
CG7255	0.589	0.0552
toy	0.589	0.0552

Gene Name	ERC Value	P-value
CG17841	0.588	0.0556
CG6927	0.588	0.0556
CG9682	0.588	0.0556
Dis3	0.588	0.0556
spag4	0.588	0.0556
ATPsyn-Cf6	0.587	0.056
CG11247	0.587	0.056
CG31926	0.587	0.056
Cyp313b1	0.587	0.056
CG12582	0.586	0.0564
CG32487	0.586	0.0564
desat2	0.586	0.0564
Octbeta2R	0.586	0.0564
CG12129	0.585	0.0568
cuff	0.585	0.0568
CG15863	0.584	0.0569
CG7024	0.584	0.0569
gfp	0.584	0.0569
Orc4	0.584	0.0569
wdb	0.584	0.0569
bam	0.583	0.0574
betaggt-ll	0.583	0.0574
CG12105	0.583	0.0574
CG33509	0.583	0.0574
CG8289	0.583	0.0574
galectin	0.583	0.0574
Arp87C	0.582	0.0579
Cda4	0.582	0.0579
CG5877	0.582	0.0579
Os-E	0.582	0.0579
CG31324	0.581	0.0583
CG9135	0.581	0.0583
Nap1	0.581	0.0583
Nmd3	0.581	0.0583
Or13a	0.581	0.0583
Ric	0.581	0.0583
CG4434	0.58	0.0588
CG5924	0.58	0.0588
Elp3	0.58	0.0588
Or43b	0.58	0.0588
retm	0.58	0.0588
sle	0.58	0.0588
vps24	0.58	0.0588
Andorra	0.579	0.0595
CG15236	0.579	0.0595
Aly	0.578	0.0596
CG12507	0.578	0.0596
ns3	0.578	0.0596
piwi	0.578	0.0596
asl	0.577	0.06
nec	0.577	0.06
CG1358	0.576	0.0602
Dhcb4C	0.576	0.0602
Rbp2	0.576	0.0602
CG31959	0.575	0.0605
Eno	0.575	0.0605

Gene Name	ERC Value	P-value
Nrx-IV	0.575	0.0605
Orc7a	0.575	0.0605
CG14187	0.574	0.0608
CG5255	0.574	0.0608
lbi	0.574	0.0608
Tif-IA	0.574	0.0608
CG11577	0.573	0.0612
CG9926	0.573	0.0612
RpLP2	0.573	0.0612
kune	0.572	0.0614
tlilB	0.572	0.0614
CG4733	0.571	0.0616
EloA	0.571	0.0616
CG10418	0.57	0.0618
CG11158	0.57	0.0618
CG8485	0.57	0.0618
ll(1)G0230	0.57	0.0618
Tsf1	0.57	0.0618
CG10092	0.569	0.0623
Hand	0.569	0.0623
Map60	0.569	0.0623
Rb97D	0.569	0.0623
CG12432	0.568	0.0626
CG12716	0.568	0.0626
CG34008	0.568	0.0626
CG34448	0.568	0.0626
CG7791	0.568	0.0626
Ciao1	0.568	0.0626
Orc2	0.568	0.0626
CG11902	0.567	0.0632
CG1421	0.567	0.0632
CG4468	0.567	0.0632
dor	0.567	0.0632
Snp	0.567	0.0632
beat-VI	0.566	0.0637
c12.1	0.566	0.0637
CG11634	0.566	0.0637
CG1231	0.566	0.0637
Mapmodulin	0.566	0.0637
Pez	0.566	0.0637
Rpl1140	0.565	0.0642
CG12721	0.564	0.0643
CG13002	0.564	0.0643
CG13427	0.564	0.0643
pgant4	0.564	0.0643
Ppt2	0.564	0.0643
sna	0.564	0.0643
Tob	0.564	0.0643
CG13031	0.563	0.065
CG2694	0.563	0.065
CG32548	0.563	0.065
CG6463	0.563	0.065
Manf	0.563	0.065
mav	0.563	0.065
Ser	0.563	0.065
Sps2	0.563	0.065

Gene Name	ERC Value	P-value
betalnt-nu	0.562	0.0657
CG14476	0.562	0.0657
CG32702	0.562	0.0657
CG5626	0.562	0.0657
CG11703	0.561	0.066
CG4374	0.561	0.066
CG8097	0.561	0.066
Rad17	0.561	0.066
CG30376	0.559	0.0664
CG31704	0.559	0.0664
CG4789	0.559	0.0664
elF-3p66	0.559	0.0664
CG13773	0.558	0.0668
CG42358	0.558	0.0668
CG5073	0.558	0.0668
Grip75	0.558	0.0668
tej	0.558	0.0668
CG11403	0.557	0.0672
CG14929	0.557	0.0672
CG31739	0.557	0.0672
CG3556	0.557	0.0672
CG9876	0.557	0.0672
fog	0.557	0.0672
nut	0.557	0.0672
Tim17b1	0.557	0.0672
ZC3H3	0.557	0.0672
CG17658	0.556	0.068
dre4	0.556	0.068
Shroom	0.556	0.068
Slip1	0.556	0.068
XNP	0.556	0.068
CG11674	0.555	0.0685
CG33262	0.555	0.0685
CG8323	0.555	0.0685
Psc	0.555	0.0685
Ucp4A	0.555	0.0685
CG3511	0.554	0.0689
CG32277	0.553	0.069
CG10053	0.552	0.0691
CG10916	0.552	0.0691
CG14212	0.552	0.0691
CG18128	0.552	0.0691
CG10576	0.551	0.0695
CG17508	0.551	0.0695
CG18262	0.551	0.0695
CG5860	0.551	0.0695
Dp	0.551	0.0695
Gtp-bp	0.551	0.0695
ver	0.551	0.0695
CG14715	0.55	0.0701
CG3021	0.55	0.0701
Drep-4	0.55	0.0701
be	0.549	0.0704
CG17636	0.549	0.0704
CG31805	0.549	0.0704
CG5690	0.549	0.0704

Gene Name	ERC Value	P-value
CG7135	0.549	0.0704
hang	0.549	0.0704
Naam	0.549	0.0704
nahoda	0.549	0.0704
RhoGAP100	0.549	0.0704
CG14314	0.548	0.0712
CG33090	0.548	0.0712
Hsp67Ba	0.548	0.0712
nAcRalpha-7	0.548	0.0712
Cdc6	0.547	0.0715
CG10177	0.547	0.0715
CG42232	0.547	0.0715
CG8273	0.547	0.0715
Pglym87	0.547	0.0715
CG15517	0.546	0.072
CG1647	0.546	0.072
CG3650	0.546	0.072
CG5543	0.546	0.072
CG9542	0.546	0.072
Atac1	0.545	0.0724
CG11699	0.545	0.0724
CG14245	0.545	0.0724
CG16742	0.545	0.0724
CG1824	0.545	0.0724
CG32055	0.545	0.0724
Neos	0.545	0.0724
CG5968	0.544	0.0731
CG12744	0.543	0.0732
CG13283	0.543	0.0732
CG31974	0.543	0.0732
CG6409	0.543	0.0732
CG7376	0.543	0.0732
CG9649	0.543	0.0732
bchs	0.542	0.0737
CG11835	0.542	0.0737
CG14823	0.542	0.0737
CG17278	0.542	0.0737
CG3246	0.542	0.0737
CG32772	0.542	0.0737
CG7945	0.542	0.0737
CG9172	0.542	0.0737
CG1902	0.541	0.0744
CG31365	0.541	0.0744
Klp31E	0.541	0.0744
CG16825	0.54	0.0747
CG40160	0.54	0.0747
Ckl1alpha-1	0.54	0.0747
CG32196	0.539	0.075
CG4038	0.539	0.075
CG6055	0.539	0.075
CG7065	0.539	0.075
Menl-2	0.539	0.075
CG13144	0.538	0.0754
CG1427	0.538	0.0754
CG34130	0.538	0.0754
CG5613	0.538	0.0754

Table 6.S2 Continued

Gene Name	ERC Value	P-value
CG6048	0.538	0.0754
CG9125	0.538	0.0754
Kr-h1	0.538	0.0754
m2	0.538	0.0754
Roc1b	0.538	0.0754
CG11263	0.537	0.0762
CG11906	0.537	0.0762
CG31278	0.537	0.0762
CG31530	0.537	0.0762
CG32164	0.537	0.0762
CG32533	0.537	0.0762
CG4872	0.537	0.0762
CG6766	0.537	0.0762
CG16790	0.536	0.0769
CG9521	0.536	0.0769
CG9988	0.536	0.0769
betaTub97E	0.535	0.0772
CG14797	0.535	0.0772
CG4995	0.535	0.0772
CG8661	0.535	0.0772
hdm	0.535	0.0772
Or45a	0.535	0.0772
Akt1	0.534	0.0777
C901	0.534	0.0777
CG16369	0.534	0.0777
CG32343	0.534	0.0777
CG8578	0.534	0.0777
RpL39	0.534	0.0777
shep	0.534	0.0777
Ast-C	0.533	0.0784
CG34104	0.533	0.0784
CG4771	0.533	0.0784
CG9246	0.533	0.0784
CG9377	0.533	0.0784
CaMKI	0.532	0.0788
CG14933	0.532	0.0788
CG8952	0.532	0.0788
CG9098	0.532	0.0788
CG17068	0.531	0.0792
CG30196	0.531	0.0792
CG6808	0.531	0.0792
CG7716	0.531	0.0792
CG9791	0.531	0.0792
Lsm11	0.531	0.0792
Lsm7	0.531	0.0792
CG10702	0.53	0.0798
CG10749	0.53	0.0798
CG13148	0.53	0.0798
CG16896	0.53	0.0798
CG3223	0.53	0.0798
CG5808	0.53	0.0798
CG7211	0.53	0.0798
CG8690	0.53	0.0798
hay	0.53	0.0798
CG11722	0.529	0.0806
CG13253	0.529	0.0806

Gene Name	ERC Value	P-value
CG14205	0.529	0.0806
elF2B-alpha	0.529	0.0806
l(2)01810	0.529	0.0806
cc(3)G	0.528	0.0811
CG15649	0.528	0.0811
CG2862	0.528	0.0811
CG31010	0.528	0.0811
CG5327	0.528	0.0811
scb	0.528	0.0811
CG3823	0.527	0.0816
CG5118	0.527	0.0816
CG5611	0.527	0.0816
CG5961	0.527	0.0816
ChT11	0.527	0.0816
Gr39b	0.527	0.0816
nimb4	0.527	0.0816
Pros26	0.527	0.0816
Asx	0.526	0.0823
CG31910	0.526	0.0823
CG34305	0.526	0.0823
Cyp6a21	0.526	0.0823
wde	0.526	0.0823
X11Lbeta	0.526	0.0823
boly	0.525	0.0829
CG1316	0.525	0.0829
CG14966	0.525	0.0829
CG8006	0.525	0.0829
CG10512	0.524	0.0832
CG14174	0.524	0.0832
CG14317	0.524	0.0832
CG30456	0.524	0.0832
CG32262	0.524	0.0832
HipHop	0.524	0.0832
Tsp42Ea	0.524	0.0832
CG11241	0.523	0.0839
CG13040	0.523	0.0839
CG14764	0.523	0.0839
CG17493	0.523	0.0839
Lip2	0.523	0.0839
Snm1	0.523	0.0839
Ac3	0.522	0.0844
CG14457	0.522	0.0844
CG32758	0.522	0.0844
CG4891	0.522	0.0844
CG14130	0.521	0.0848
CG14262	0.521	0.0848
CG31464	0.521	0.0848
CG3408	0.521	0.0848
CG6511	0.521	0.0848
Su(var)2-10	0.521	0.0848
CG14074	0.519	0.0853
CG15522	0.519	0.0853
CG42374	0.519	0.0853
CG15311	0.518	0.0856
CG18065	0.518	0.0856
CG4603	0.518	0.0856

Gene Name	ERC Value	P-value
CG5946	0.518	0.0856
CG9399	0.518	0.0856
Atox1	0.517	0.086
gatA	0.517	0.086
Pros25	0.517	0.086
tsl	0.517	0.086
CG1970	0.516	0.0864
CG34115	0.516	0.0864
CtBP	0.516	0.0864
Liev1A	0.516	0.0864
CG12768	0.515	0.0868
CG14562	0.515	0.0868
CG2807	0.515	0.0868
CG9053	0.515	0.0868
CG9740	0.515	0.0868
eater	0.515	0.0868
fs(1)K10	0.515	0.0868
ste24b	0.515	0.0868
CG1545	0.514	0.0875
CG1628	0.514	0.0875
CG18268	0.514	0.0875
CG2162	0.514	0.0875
CG31646	0.514	0.0875
CG34148	0.514	0.0875
Dlcr90F	0.514	0.0875
Hem	0.514	0.0875
Pka-C1	0.514	0.0875
se	0.514	0.0875
CG12078	0.513	0.0884
CG33306	0.513	0.0884
CG4078	0.513	0.0884
CG6345	0.513	0.0884
CG7049	0.513	0.0884
Rp11	0.513	0.0884
btd	0.512	0.0889
CG11076	0.512	0.0889
CG1271	0.512	0.0889
CG15172	0.512	0.0889
CG30356	0.512	0.0889
Muc18B	0.512	0.0889
PpY-55A	0.512	0.0889
stnB	0.512	0.0889
car	0.511	0.0896
CG1537	0.511	0.0896
CG15376	0.511	0.0896
CG15661	0.511	0.0896
CG6418	0.511	0.0896
lr67c	0.511	0.0896
kcc	0.511	0.0896
Lhr	0.511	0.0896
Pbprp5	0.511	0.0896
RSg7	0.511	0.0896
sba	0.511	0.0896
ASPP	0.51	0.0906
CG31550	0.51	0.0906
CG5431	0.51	0.0906

Gene Name	ERC Value	P-value
CG7298	0.51	0.0906
Hsp60D	0.51	0.0906
sbr	0.51	0.0906
wds	0.51	0.0906
CG14722	0.509	0.0913
CG15251	0.509	0.0913
CG30192	0.509	0.0913
CG31928	0.509	0.0913
Hpr1	0.509	0.0913
icln	0.509	0.0913
CG13902	0.508	0.0918
CG4676	0.508	0.0918
CG7519	0.508	0.0918
lr60e	0.508	0.0918
Skeletor	0.508	0.0918
BRWD3	0.507	0.0923
CG12278	0.507	0.0923
CG13310	0.507	0.0923
ldgf5	0.507	0.0923
lat	0.507	0.0923
Ance-3	0.506	0.0927
cact	0.506	0.0927
CG10414	0.506	0.0927
CG13116	0.506	0.0927
CG14103	0.506	0.0927
CG17816	0.506	0.0927
CG33771	0.506	0.0927
CG9170	0.506	0.0927
sad	0.506	0.0927
CG10631	0.505	0.0935
CG10992	0.505	0.0935
CG7458	0.505	0.0935
Dip3	0.505	0.0935
CG10444	0.504	0.0939
CG32750	0.504	0.0939
GstD10	0.504	0.0939
TllEalpha	0.504	0.0939
CG2258	0.503	0.0942
CG32418	0.503	0.0942
chb	0.503	0.0942
DppIII	0.503	0.0942
CG12299	0.502	0.0946
CG6255	0.502	0.0946
CG11977	0.501	0.0948
CG17724	0.501	0.0948
CG31089	0.501	0.0948
CG6136	0.501	0.0948
CG8366	0.501	0.0948
Cafl-105	0.5	0.0952
Cbp53E	0.5	0.0952
CG11251	0.5	0.0952
CG12680	0.5	0.0952
CG5910	0.5	0.0952
CG4726	0.499	0.0957
CG5527	0.499	0.0957
CG7707	0.499	0.0957

Gene Name	ERC Value	P-value
CG9021	0.499	0.0957
Gem2	0.499	0.0957
CG15471	0.498	0.0961
CG34116	0.498	0.0961
CG5515	0.498	0.0961
CG6568	0.498	0.0961
CG8320	0.498	0.0961
elF-Zalpha	0.498	0.0961
Sgt11	0.498	0.0961
unc-119	0.498	0.0961
a6	0.497	0.0968
CG1218	0.497	0.0968
CG16704	0.497	0.0968
CG2943	0.497	0.0968
CG32191	0.497	0.0968
CG5398	0.497	0.0968
CG8080	0.497	0.0968
scafb	0.497	0.0968
ap	0.496	0.0976
CG11807	0.496	0.0976
CG15209	0.496	0.0976
cnlg	0.496	0.0976
NetA	0.496	0.0976
CG10073	0.495	0.098
CG34236	0.495	0.098
CG7372	0.495	0.098
CG9672	0.495	0.098
Hsc70-1	0.495	0.098
CG12657	0.494	0.0985
CG42258	0.494	0.0985
CG6621	0.494	0.0985
CG9723	0.494	0.0985
La	0.494	0.0985
Wnt6	0.494	0.0985
CG31690	0.493	0.099
CG32176	0.493	0.099
CG33672	0.493	0.099
CG9027	0.492	0.0993
Moca-cyp	0.492	0.0993
mRpl22	0.492	0.0993
Ranbp16	0.492	0.0993
CG15533	0.491	0.0996
CG18809	0.491	0.0996
CG2790	0.491	0.0996
CG34012	0.491	0.0996
spn-E	0.491	0.0996
Ssadh	0.491	0.0996
tap	0.491	0.0996

Table 6.S3 - Top Genes ERC values for c(3)G arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value
CG4820	0.969	0.0001	endoB	0.819	0.005	CG15594	0.762	0.0102	CG6236	0.723	0.015	SMSr	0.694	0.0202
wac	0.926	0.0002	CG11298	0.819	0.005	tacc	0.762	0.0102	TTLL3A	0.722	0.0153	CG9866	0.694	0.0202
CG13727	0.923	0.0003	CG4666	0.818	0.0053	CG34229	0.76	0.0104	CG14352	0.722	0.0153	CG30270	0.692	0.0205
CG13097	0.92	0.0004	CG10513	0.815	0.0054	Acon	0.759	0.0105	CG10164	0.721	0.0155	CG11784	0.692	0.0205
CG10680	0.912	0.0005	CG10383	0.814	0.0055	CG4926	0.759	0.0105	CG9486	0.721	0.0155	lr75d	0.692	0.0205
CG33703	0.91	0.0005	MtnB	0.814	0.0055	Ero1L	0.758	0.0106	CG4325	0.721	0.0155	CG13042	0.692	0.0205
CG6914	0.898	0.0006	Cpr30F	0.813	0.0057	CG12608	0.758	0.0106	CG42669	0.72	0.0158	CG17272	0.692	0.0205
CG15025	0.892	0.0007	CG4842	0.812	0.0058	CG7115	0.758	0.0106	RASSF8	0.719	0.0159	CG15731	0.691	0.0209
PI3K59F	0.889	0.0008	CG4038	0.812	0.0058	CG12126	0.758	0.0106	CG3288	0.719	0.0159	CG6752	0.689	0.021
CG8258	0.886	0.0009	l(3)mbr	0.808	0.0059	numb	0.758	0.0106	ninaA	0.719	0.0159	CG9192	0.689	0.021
CG6000	0.885	0.001	CG15337	0.807	0.006	CG2064	0.757	0.0111	CG12278	0.717	0.0161	alpha-Man-II	0.689	0.021
CG32544	0.885	0.001	CG3817	0.803	0.0061	CG4019	0.757	0.0111	CG13121	0.717	0.0161	CG12111	0.688	0.0213
Cpr72Ea	0.884	0.0012	CG18815	0.801	0.0062	cdi	0.756	0.0113	CG17618	0.717	0.0161	CG7834	0.688	0.0213
sec24	0.883	0.0013	CG34204	0.8	0.0063	PGRP-SB2	0.755	0.0114	Dhc93AB	0.715	0.0164	her	0.688	0.0213
CG34223	0.879	0.0014	CG15168	0.8	0.0063	vps2	0.753	0.0114	CG9286	0.715	0.0164	pelo	0.687	0.0215
CG17121	0.877	0.0014	CG4813	0.798	0.0065	Adk2	0.753	0.0114	CG14077	0.715	0.0164	lr	0.687	0.0215
Scgbeta	0.873	0.0015	CG9825	0.798	0.0065	ATPsyn-gam	0.751	0.0116	CG8611	0.715	0.0164	Tango3	0.687	0.0215
CG9143	0.87	0.0016	CG31665	0.797	0.0067	CG13438	0.748	0.0117	Zip3	0.714	0.0168	su(s)	0.687	0.0215
Rbcn-3A	0.87	0.0016	CG13075	0.796	0.0068	TpnC4	0.747	0.0118	CG3609	0.714	0.0168	CG12307	0.687	0.0215
CG9297	0.869	0.0018	wek	0.795	0.0068	mars	0.746	0.0119	CG6045	0.713	0.0169	CG13078	0.686	0.022
CG8545	0.867	0.0019	CG14659	0.795	0.0068	Srp14	0.746	0.0119	CG15485	0.712	0.017	CG2014	0.686	0.022
CG9589	0.863	0.002	Rpl3R	0.794	0.007	Ttb5	0.744	0.0121	CG17221	0.71	0.0171	mirr	0.685	0.0222
CG1458	0.859	0.0021	CG42505	0.793	0.0071	fill	0.742	0.0122	CG10444	0.71	0.0171	CG14974	0.684	0.0223
CG13566	0.858	0.0022	Hydr1	0.792	0.0072	Art2	0.742	0.0122	CG5964	0.71	0.0171	Osi4	0.684	0.0223
CG31126	0.857	0.0023	CG33278	0.79	0.0073	CG11210	0.742	0.0122	CG14292	0.71	0.0171	Tsp33B	0.684	0.0223
CG10466	0.856	0.0023	CG7031	0.787	0.0074	CG16719	0.742	0.0122	pr	0.709	0.0175	lde	0.684	0.0223
CG3077	0.85	0.0024	vri	0.787	0.0074	CG14934	0.742	0.0122	nAcRalpha-6	0.709	0.0175	CG17652	0.684	0.0223
Cpr64Ac	0.849	0.0025	isopeptidase	0.786	0.0076	CG2543	0.741	0.0126	CG2256	0.708	0.0177	Scsalpha	0.684	0.0223
FucTD	0.847	0.0026	CG33770	0.786	0.0076	CG30015	0.741	0.0126	elyj3	0.707	0.0177	CG5339	0.683	0.0228
CG16711	0.847	0.0026	CG11858	0.785	0.0077	Mic2	0.74	0.0128	CG12402	0.707	0.0177	Mocs2	0.683	0.0228
CG31816	0.844	0.0028	f-cup	0.785	0.0077	CG15014	0.74	0.0128	Neb-cGP	0.707	0.0177	CG31226	0.682	0.023
CG42574	0.844	0.0028	CG15353	0.785	0.0077	Meics	0.74	0.0128	CG3735	0.706	0.018	CG31099	0.682	0.023
CG10969	0.843	0.003	CG17127	0.785	0.0077	Cpr35B	0.739	0.0131	CG15922	0.706	0.018	CG5792	0.682	0.023
CG18130	0.841	0.0031	Nca	0.785	0.0077	Esyt2	0.739	0.0131	CG5521	0.705	0.0182	h	0.68	0.0232
chb	0.84	0.0032	CG9570	0.782	0.0082	Bace	0.738	0.0132	Arp66B	0.704	0.0183	Obp50b	0.68	0.0232
CG6388	0.839	0.0032	Cpr65Av	0.782	0.0082	CG33964	0.738	0.0132	CG14861	0.704	0.0183	CG5756	0.68	0.0232
CG5388	0.839	0.0032	CG30471	0.781	0.0084	CG9119	0.735	0.0134	Nmda1	0.703	0.0185	DptB	0.68	0.0232
CG6905	0.838	0.0034	CG1889	0.781	0.0084	CG5111	0.735	0.0134	CG8701	0.703	0.0185	Apc	0.679	0.0236
Bub1	0.838	0.0034	CG31551	0.781	0.0084	CG15461	0.735	0.0134	Lsd-2	0.703	0.0185	CG3773	0.678	0.0237
CG13663	0.838	0.0034	CG32150	0.78	0.0086	CG1340	0.733	0.0137	l(1)G0045	0.702	0.0187	CG5323	0.678	0.0237
CG7110	0.838	0.0034	CG1109	0.779	0.0087	CG5969	0.731	0.0138	CG9759	0.701	0.0188	Cyp12a1	0.678	0.0237
CG3819	0.836	0.0038	CG17601	0.778	0.0088	CG32643	0.731	0.0138	CG16820	0.701	0.0188	CG12155	0.678	0.0237
CG14752	0.835	0.0039	FK506-bp1	0.777	0.0089	l(2)34Fd	0.731	0.0138	cdm	0.701	0.0188	CG5543	0.678	0.0237
CG12164	0.833	0.004	CG14151	0.775	0.009	CG12428	0.729	0.0141	CG3338	0.7	0.0191	CG34172	0.678	0.0237
CG3624	0.832	0.0041	Tbp	0.775	0.009	Bsg25D	0.728	0.0141	CG9941	0.698	0.0192	Pp2A-29B	0.677	0.0242
CG14635	0.831	0.0041	awd	0.774	0.0092	CG31675	0.727	0.0142	Tal	0.698	0.0192	CG34022	0.677	0.0242
CG31106	0.829	0.0042	ben	0.772	0.0093	CG7813	0.727	0.0142	CG5482	0.698	0.0192	Prosbeta1	0.677	0.0242
CG31098	0.829	0.0042	CG8323	0.772	0.0093	CG15255	0.727	0.0142	CG4363	0.698	0.0192	skd	0.674	0.0245
CG12902	0.828	0.0044	elif2B-beta	0.769	0.0095	CG2120	0.727	0.0142	Mys45A	0.698	0.0192	Vps4	0.674	0.0245
CG11227	0.827	0.0045	mip-120	0.768	0.0095	CycD	0.727	0.0142	CG17806	0.698	0.0192	crm	0.674	0.0245
CG16787	0.823	0.0046	Rab30	0.767	0.0096	ade2	0.727	0.0142	CG12011	0.697	0.0197	CG10898	0.673	0.0248
CG32591	0.822	0.0047	pug	0.766	0.0097	pull	0.726	0.0148	CG3214	0.697	0.0197	CG2767	0.673	0.0248
CG34007	0.822	0.0047	CG1983	0.766	0.0097	CG14354	0.724	0.0149	CG5961	0.696	0.0199	CG6843	0.673	0.0248
CG6041	0.821	0.0049	CG9392	0.763	0.0099	CG15247	0.724	0.0149	CG7829	0.696	0.0199	CG16974	0.673	0.0248
CG5446	0.82	0.005	sut1	0.763	0.0099	CG8552	0.723	0.015	CG12643	0.696	0.0199	yu	0.671	0.0251
CG6830	0.819	0.005	cbx	0.763	0.0099	Cpr78Ca	0.723	0.015	CG6290	0.694	0.0202	CG1667	0.671	0.0251

Table 6.S3 Continued

Gene Name	ERC Value	P-value
CG32248	0.671	0.0251
Gprk2	0.67	0.0254
Roc2	0.67	0.0254
CG14509	0.667	0.0256
CG13712	0.667	0.0256
primo-2	0.667	0.0256
CG31224	0.667	0.0256
CG3061	0.666	0.0259
CG17075	0.666	0.0259
CG32556	0.665	0.0261
Sug	0.665	0.0261
glob1	0.665	0.0261
Aats-cys	0.665	0.0261
CG10909	0.664	0.0265
CG12344	0.664	0.0265
CG13708	0.664	0.0265
CG8314	0.664	0.0265
CG14686	0.664	0.0265
Ir1d	0.663	0.0269
ac	0.663	0.0269
bw	0.662	0.0271
alpha-Est3	0.662	0.0271
CG34242	0.662	0.0271
CG2816	0.662	0.0271
CG34228	0.662	0.0271
CG12795	0.662	0.0271
CG8498	0.661	0.0277
CG7188	0.66	0.0277
wah	0.659	0.0278
a	0.659	0.0278
CG31459	0.658	0.028
CG7029	0.658	0.028
Ack	0.657	0.0282
Crc	0.657	0.0282
Z600	0.657	0.0282
plm	0.656	0.0285
CG14153	0.656	0.0285
CG4872	0.656	0.0285
CG3192	0.656	0.0285
Cyp6a8	0.655	0.0288
CG4041	0.655	0.0288
CaBP1	0.655	0.0288
CG10089	0.655	0.0288
tipE	0.655	0.0288
Sans	0.653	0.0293
Nak	0.653	0.0293
CG17646	0.652	0.0295
CG5800	0.651	0.0295
CG6066	0.651	0.0295
CG31029	0.651	0.0295
SpdS	0.65	0.0298
MED1	0.649	0.0299
HERC2	0.648	0.03
CG17639	0.648	0.03
CG14823	0.648	0.03
RpLP0	0.648	0.03

Gene Name	ERC Value	P-value
Nup62	0.647	0.0304
Aats-val	0.647	0.0304
ine	0.647	0.0304
Oscp	0.647	0.0304
CG31802	0.646	0.0307
CG32668	0.646	0.0307
CG6115	0.646	0.0307
Or42b	0.646	0.0307
CG12027	0.646	0.0307
CG18628	0.645	0.0312
CG7179	0.644	0.0313
CG15564	0.643	0.0314
CG14325	0.643	0.0314
CG14024	0.643	0.0314
CAP	0.643	0.0314
CG7173	0.642	0.0317
nos	0.642	0.0317
unc79	0.642	0.0317
CG14010	0.642	0.0317
CG7006	0.641	0.0321
CG6852	0.641	0.0321
GstD8	0.641	0.0321
CG32119	0.64	0.0323
CG34012	0.64	0.0323
Ir67c	0.64	0.0323
vanin-like	0.64	0.0323
CG4962	0.639	0.0327
CG1523	0.639	0.0327
Mlp84B	0.638	0.0329
CG6712	0.638	0.0329
Prp19	0.638	0.0329
CG34291	0.637	0.0332
CG13671	0.636	0.0332
CG4681	0.636	0.0332
mi	0.635	0.0334
CG7484	0.635	0.0334
Incenp	0.634	0.0336
Pglym87	0.634	0.0336
Rpn2	0.633	0.0338
MESR4	0.633	0.0338
Snx6	0.633	0.0338
caz	0.633	0.0338
ens	0.632	0.0341
mRpL55	0.632	0.0341
CG13907	0.632	0.0341
Lsm10	0.631	0.0344
CG1675	0.63	0.0345
CG13617	0.629	0.0346
CG10730	0.629	0.0346
CG10154	0.629	0.0346
CG7968	0.629	0.0346
phf	0.628	0.035
CG5199	0.628	0.035
PpD5	0.627	0.0351
CG30099	0.627	0.0351
CG31659	0.627	0.0351

Gene Name	ERC Value	P-value
mei-38	0.626	0.0354
CG18432	0.626	0.0354
CG2186	0.626	0.0354
CG10949	0.626	0.0354
CG7420	0.625	0.0358
CG5039	0.625	0.0358
CG30421	0.625	0.0358
MAN1	0.624	0.036
CG9988	0.623	0.0361
CG5327	0.622	0.0362
CG3592	0.622	0.0362
Lcp1	0.622	0.0362
CG32987	0.622	0.0362
nrv1	0.621	0.0366
CG5794	0.621	0.0366
Trax	0.62	0.0368
CG7251	0.62	0.0368
CG31345	0.62	0.0368
CG30463	0.619	0.037
chp	0.619	0.037
RpL22	0.618	0.0372
vir-1	0.618	0.0372
Src64B	0.618	0.0372
CG14419	0.618	0.0372
Cyp12d1-p	0.617	0.0376
CG9121	0.614	0.0377
CG8135	0.614	0.0377
CG13779	0.614	0.0377
Adgf-E	0.613	0.0379
Ag5r	0.613	0.0379
CG2789	0.612	0.0381
CG7582	0.612	0.0381
CG5968	0.611	0.0383
CG15096	0.611	0.0383
Tim13	0.61	0.0385
Vha68-2	0.609	0.0386
CG7414	0.609	0.0386
CG31496	0.609	0.0386
CG1902	0.608	0.0388
Fbp1	0.608	0.0388
Cap-D3	0.608	0.0388
CG16739	0.608	0.0388
alpha-Est7	0.607	0.0392
CG10253	0.607	0.0392
SdhB	0.607	0.0392
Ost48	0.606	0.0395
king-tubby	0.606	0.0395
Marcal1	0.606	0.0395
CG3173	0.606	0.0395
CG5728	0.606	0.0395
CG8034	0.606	0.0395
cpb	0.605	0.04
Thiolase	0.605	0.04
CG11815	0.605	0.04
CG5892	0.605	0.04
CG11286	0.605	0.04

Gene Name	ERC Value	P-value
CG6455	0.605	0.04
CG3323	0.604	0.0405
oc	0.604	0.0405
Scamp	0.604	0.0405
CG9007	0.603	0.0408
CG17838	0.603	0.0408
CG4386	0.603	0.0408
CG10470	0.602	0.0411
CG10341	0.602	0.0411
CG8861	0.602	0.0411
Es2	0.601	0.0414
CG12972	0.601	0.0414
kcc	0.6	0.0415
cp309	0.6	0.0415
CG3736	0.6	0.0415
CG14962	0.599	0.0418
CG6497	0.599	0.0418
CG1236	0.599	0.0418
CG5767	0.599	0.0418
CG12991	0.599	0.0418
ird5	0.599	0.0418
mol	0.599	0.0418
CG1146	0.598	0.0424
CG11750	0.598	0.0424
CG4570	0.598	0.0424
Nmd3	0.597	0.0427
CG1824	0.597	0.0427
CG14870	0.595	0.0429
Hydr2	0.594	0.043
Vm26Ab	0.593	0.0431
CG13334	0.593	0.0431
CG9935	0.593	0.0431
Cpr64Aa	0.593	0.0431
CG31161	0.593	0.0431
Smg5	0.593	0.0431
Vha68-1	0.592	0.0436
bsk	0.592	0.0436
Cpr65Az	0.591	0.0438
CG9836	0.591	0.0438
Prosbeta7	0.591	0.0438
CG31957	0.59	0.0441
CG7191	0.59	0.0441
CG16799	0.59	0.0441
CG4377	0.589	0.0443
CG34144	0.589	0.0443
CG4282	0.589	0.0443
CG31715	0.589	0.0443
CG14118	0.589	0.0443
CG14340	0.589	0.0443
CG1662	0.588	0.0449
CG5880	0.588	0.0449
CG15249	0.588	0.0449
CG3353	0.588	0.0449
CG12723	0.588	0.0449
CG6051	0.587	0.0453
Syx17	0.587	0.0453

Gene Name	ERC Value	P-value
CG4741	0.587	0.0453
Twid1N	0.586	0.0456
CG8042	0.586	0.0456
r-cup	0.586	0.0456
CG2187	0.586	0.0456
lqf	0.586	0.0456
Sas-4	0.585	0.046
CG10470	0.602	0.0411
jar	0.585	0.046
SP1029	0.585	0.046
Nup358	0.585	0.046
CG11529	0.584	0.0464
CG13364	0.584	0.0464
CG3124	0.584	0.0464
Pcd	0.583	0.0467
CG12985	0.583	0.0467
ninaC	0.582	0.0468
Ir100a	0.582	0.0468
tkk	0.581	0.047
CG14230	0.581	0.047
CG16126	0.581	0.047
mRpS26	0.581	0.047
CG10804	0.581	0.047
phi	0.581	0.047
Nsf2	0.581	0.047
eIF2B-gamma	0.581	0.047
CG34293	0.58	0.0477
Pde11	0.58	0.0477
CG13035	0.58	0.0477
Cpr64Ad	0.579	0.048
CG13436	0.579	0.048
CG14500	0.579	0.048
CG40127	0.579	0.048
CG33691	0.578	0.0484
Trh	0.578	0.0484
RpL24-like	0.578	0.0484
CG32679	0.578	0.0484
mas	0.578	0.0484
mask	0.577	0.0488
CG5150	0.577	0.0488
CG14537	0.577	0.0488
HP1b	0.577	0.0488
CG31086	0.577	0.0488
dia	0.576	0.0493
CG12950	0.576	0.0493
Cyp4d2	0.575	0.0495
alpha-Man-II	0.575	0.0495
Dmn	0.575	0.0495
CG9870	0.575	0.0495
bigmax	0.575	0.0495
CG17919	0.574	0.0499
CG12818	0.574	0.0499
CG5933	0.573	0.0501
CG9135	0.573	0.0501
shot	0.572	0.0503
CG15382	0.572	0.0503
CG5742	0.571	0.0505

Table 6.S3 Continued

Gene Name	ERC Value	P-value
CG8343	0.571	0.0505
CG42449	0.57	0.0506
Lcp65Ac	0.57	0.0506
CG2772	0.569	0.0508
CG15024	0.568	0.0509
Arr1	0.568	0.0509
CG8607	0.567	0.0511
t-cup	0.567	0.0511
CG3822	0.567	0.0511
CG42360	0.566	0.0514
CG9253	0.565	0.0514
CG8600	0.564	0.0515
CG8257	0.564	0.0515
Vha55	0.564	0.0515
CG17385	0.564	0.0515
CG9500	0.563	0.0519
CG5618	0.563	0.0519
CG4585	0.563	0.0519
Best2	0.562	0.0522
CG8997	0.562	0.0522
CG15615	0.562	0.0522
CG11456	0.562	0.0522
CG1781	0.561	0.0525
Zw	0.561	0.0525
CG42251	0.561	0.0525
CG1090	0.56	0.0528
CG1572	0.56	0.0528
Pxt	0.56	0.0528
CG12016	0.56	0.0528
CG15706	0.559	0.0532
Nopp140	0.559	0.0532
CG9238	0.559	0.0532
CG8878	0.559	0.0532
nwk	0.559	0.0532
CG11967	0.559	0.0532
TM9SF4	0.559	0.0532
CG5863	0.559	0.0532
CSN1b	0.558	0.0539
gcm	0.558	0.0539
CG1742	0.558	0.0539
CG7497	0.558	0.0539
CG5556	0.558	0.0539
CG34179	0.558	0.0539
Adgf-A	0.557	0.0544
fl(2)d	0.557	0.0544
CG11414	0.557	0.0544
CG42322	0.557	0.0544
mj	0.557	0.0544
CG42784	0.557	0.0544
CG7956	0.556	0.055
Fsh	0.556	0.055
CG2107	0.556	0.055
Baldspot	0.556	0.055
Arc-p34	0.555	0.0553
CG33156	0.555	0.0553
Der-1	0.554	0.0555

Gene Name	ERC Value	P-value
ssp5	0.554	0.0555
calypso	0.554	0.0555
CG3907	0.554	0.0555
CG10166	0.553	0.0559
Jafrac1	0.553	0.0559
CG13748	0.553	0.0559
gammaSnap	0.552	0.0561
CG4972	0.552	0.0561
fd96Cb	0.551	0.0563
CG15440	0.551	0.0563
inaC	0.551	0.0563
CG7509	0.551	0.0563
l(1)G0020	0.551	0.0563
mnd	0.55	0.0568
Eaat2	0.55	0.0568
CG13949	0.55	0.0568
CG5514	0.55	0.0568
CG33288	0.55	0.0568
CG42770	0.549	0.0572
qkr58E-2	0.549	0.0572
CG11068	0.549	0.0572
bc10	0.549	0.0572
l(3)J2D3	0.549	0.0572
CG18437	0.549	0.0572
bwa	0.549	0.0572
CG6812	0.548	0.0578
CG18004	0.548	0.0578
Cyp313a4	0.547	0.058
Gtp-bp	0.547	0.058
CG11200	0.547	0.058
CG12130	0.547	0.058
CG8918	0.547	0.058
Prp18	0.546	0.0585
Prosbeta4R2	0.546	0.0585
CG8026	0.546	0.0585
dnk	0.545	0.0587
dtr	0.545	0.0587
Atf-2	0.545	0.0587
CG1371	0.545	0.0587
CG15173	0.544	0.0591
Kip98A	0.543	0.0592
Cpr49Ab	0.543	0.0592
sad	0.542	0.0594
CG7993	0.542	0.0594
CG14199	0.542	0.0594
kdn	0.542	0.0594
CG5506	0.541	0.0597
CG18269	0.541	0.0597
CG13836	0.54	0.0599
Unc-89	0.54	0.0599
Ugt	0.539	0.0601
CG1137	0.539	0.0601
CG13318	0.539	0.0601
CG10581	0.539	0.0601
l(3)87Df	0.538	0.0605
Crtp	0.538	0.0605

Gene Name	ERC Value	P-value
kek6	0.538	0.0605
tsh	0.538	0.0605
CG3590	0.538	0.0605
CG12341	0.538	0.0605
CG33169	0.538	0.0605
CG12370	0.537	0.0611
CG13025	0.537	0.0611
CG32801	0.537	0.0611
CG13856	0.536	0.0614
CG8006	0.536	0.0614
CG2371	0.536	0.0614
CG31248	0.536	0.0614
CG16857	0.536	0.0614
CG13442	0.535	0.0618
TyrRll	0.535	0.0618
CG42823	0.535	0.0618
nes	0.534	0.0621
Scgalpha	0.534	0.0621
CG13319	0.534	0.0621
CG1750	0.534	0.0621
CG17580	0.534	0.0621
p115	0.534	0.0621
PpY-55A	0.534	0.0621
lack	0.533	0.0627
CG16886	0.533	0.0627
Sec22	0.533	0.0627
Tsp2A	0.533	0.0627
CG31635	0.532	0.0631
mel-P22	0.532	0.0631
CG12703	0.532	0.0631
Ugt86Dd	0.531	0.0633
Cpr92A	0.531	0.0633
car	0.531	0.0633
CG17048	0.531	0.0633
CheA75a	0.531	0.0633
pcx	0.531	0.0633
CG13875	0.53	0.0639
CG3790	0.53	0.0639
Dh31-R1	0.53	0.0639
GRHRll	0.53	0.0639
Prx5	0.53	0.0639
CG18769	0.529	0.0643
CG1677	0.529	0.0643
ligatin	0.529	0.0643
CG6227	0.529	0.0643
Rho1	0.529	0.0643
CG11267	0.529	0.0643
CG9669	0.528	0.0649
c(2)M	0.528	0.0649
CG12858	0.528	0.0649
GstD9	0.528	0.0649
CG8965	0.527	0.0652
CG32459	0.527	0.0652
ago	0.527	0.0652
Gr21a	0.526	0.0655
Atg6	0.526	0.0655

Gene Name	ERC Value	P-value
Sop2	0.526	0.0655
alpha-catenin	0.525	0.0658
CG7611	0.525	0.0658
CG17734	0.525	0.0658
CG15863	0.524	0.066
CG13607	0.524	0.066
CG7203	0.524	0.066
CG17664	0.524	0.066
Hel89B	0.524	0.066
CG14013	0.524	0.066
lox	0.523	0.0666
CG33177	0.523	0.0666
Tsf3	0.523	0.0666
CG10543	0.523	0.0666
CG10280	0.522	0.0669
Spn	0.522	0.0669
Cpr30B	0.522	0.0669
CG6330	0.522	0.0669
CG6116	0.521	0.0673
or	0.521	0.0673
CG13994	0.521	0.0673
CG10073	0.52	0.0676
CG32232	0.52	0.0676
CG13646	0.52	0.0676
Rpn7	0.52	0.0676
CG13700	0.52	0.0676
CG32038	0.52	0.0676
CG10732	0.52	0.0676
Gmap	0.52	0.0676
Prosalpha5	0.519	0.0683
CG10151	0.519	0.0683
kermit	0.519	0.0683
ave	0.518	0.0686
CG12744	0.518	0.0686
fh	0.518	0.0686
CG15432	0.518	0.0686
Fkbp13	0.518	0.0686
RacGAP84C	0.518	0.0686
CG3630	0.518	0.0686
CG12948	0.518	0.0686
Scgdelta	0.517	0.0693
CG15141	0.517	0.0693
CG34202	0.517	0.0693
CG10866	0.517	0.0693
CG11381	0.517	0.0693
ca	0.516	0.0697
CG6454	0.516	0.0697
CG5131	0.516	0.0697
CG10953	0.516	0.0697
CG9548	0.515	0.0701
CG11836	0.515	0.0701
bap	0.515	0.0701
CG3036	0.515	0.0701
CG5903	0.515	0.0701
CG4502	0.514	0.0705
CG6800	0.514	0.0705

Gene Name	ERC Value	P-value
Sox14	0.513	0.0707
CG17237	0.513	0.0707
CG9010	0.513	0.0707
Rab1	0.512	0.071
Mtk	0.512	0.071
Ede3	0.512	0.071
Trf4-1	0.512	0.071
Prosbeta2	0.512	0.071
Acox57D-p	0.512	0.071
CG14071	0.511	0.0715
CG8248	0.511	0.0715
CG17150	0.511	0.0715
CG34282	0.511	0.0715
CG4613	0.51	0.0719
lima	0.51	0.0719
CG4230	0.51	0.0719
elm	0.51	0.0719
CG5091	0.509	0.0723
Or35a	0.509	0.0723
CG3045	0.509	0.0723
CG4151	0.509	0.0723
CG9642	0.509	0.0723
pdfr	0.509	0.0723
CalpA	0.508	0.0728
CG32154	0.508	0.0728
Tcp1	0.508	0.0728
CG31087	0.508	0.0728
Past1	0.508	0.0728
CG42820	0.508	0.0728
beat-lla	0.508	0.0728
CG12680	0.508	0.0728
CG12558	0.507	0.0735
ave	0.507	0.0735
garz	0.507	0.0735
CG8407	0.507	0.0735
CG16782	0.506	0.0739
Pgan135A	0.506	0.0739
Hsp67Bc	0.506	0.0739
CG8031	0.505	0.0741
Zmit	0.504	0.0742
CG32564	0.504	0.0742
VGAT	0.503	0.0744
asun	0.503	0.0744
CG7839	0.502	0.0746
akirin	0.502	0.0746
snRNP-U1-C	0.502	0.0746
CG3690	0.502	0.0746
CG6785	0.502	0.0746
ninaB	0.502	0.0746
Cnx99A	0.502	0.0746
CG10075	0.502	0.0746
CG11694	0.501	0.0753
lpp	0.501	0.0753
rdgB	0.501	0.0753
CG9801	0.501	0.0753
Nha1	0.501	0.0753

Table 6.S3 Continued

Gene Name	ERC Value	P-value
Rpn6	0.5	0.0758
CG10361	0.5	0.0758
Tg	0.5	0.0758
rho	0.499	0.076
CG10362	0.499	0.076
Gclc	0.499	0.076
CG13455	0.499	0.076
CG5554	0.499	0.076
Lim3	0.499	0.076
CG5731	0.499	0.076
CG5149	0.499	0.076
CG6026	0.498	0.0768
Chi	0.498	0.0768
CG5539	0.498	0.0768
CdGAPr	0.498	0.0768
CG5204	0.498	0.0768
CG30195	0.497	0.0772
CG3244	0.497	0.0772
Kdm4A	0.496	0.0774
CG7747	0.496	0.0774
CG14353	0.496	0.0774
CG14200	0.496	0.0774
CG34127	0.496	0.0774
CG18539	0.496	0.0774
CG1552	0.495	0.0779
CG10657	0.495	0.0779
CG17896	0.494	0.0781
Gbeta5	0.494	0.0781
CG2812	0.494	0.0781
CG42404	0.494	0.0781
CG16903	0.494	0.0781
CG11811	0.494	0.0781
CG7518	0.493	0.0786
Set2	0.493	0.0786
Gal	0.492	0.0788
Prosalpha7	0.492	0.0788
CG8436	0.492	0.0788
Pdp	0.491	0.0791
CG8419	0.491	0.0791
CG1575	0.491	0.0791
Gr64b	0.491	0.0791
ncm	0.491	0.0791
CG13599	0.49	0.0795
ssp3	0.49	0.0795
elF3-S8	0.49	0.0795
fu2	0.489	0.0798
CG7311	0.489	0.0798
CG15649	0.489	0.0798
RpS17	0.489	0.0798
Pp1-Y2	0.489	0.0798
nAcRbeta-9d	0.489	0.0798
CG10337	0.488	0.0804
AICR2	0.488	0.0804
fdl	0.488	0.0804
alien	0.488	0.0804
CG17002	0.488	0.0804

Gene Name	ERC Value	P-value
CG11474	0.488	0.0804
asrij	0.487	0.0809
CG12885	0.486	0.081
TpnC73F	0.486	0.081
CG6523	0.486	0.081
CG31516	0.486	0.081
CG16716	0.486	0.081
CG14905	0.486	0.081
Trf	0.486	0.081
CG3491	0.486	0.081
CG31661	0.485	0.0817
CG11048	0.485	0.0817
CG13250	0.485	0.0817
CG10283	0.485	0.0817
CG15438	0.485	0.0817
CG8297	0.484	0.0822
Or59b	0.484	0.0822
CG42375	0.484	0.0822
Hip14	0.484	0.0822
CG15571	0.484	0.0822
CG7616	0.483	0.0826
Cyp9h1	0.483	0.0826
Tango14	0.483	0.0826
CG4860	0.483	0.0826
NC2beta	0.483	0.0826
cer	0.483	0.0826
CG7739	0.482	0.0832
CG13409	0.482	0.0832
Pino	0.482	0.0832
CG11345	0.482	0.0832
CanA-14F	0.481	0.0835
CG10469	0.481	0.0835
CG13049	0.481	0.0835
Arma	0.48	0.0838
CG32647	0.48	0.0838
Fst	0.48	0.0838
CG11985	0.48	0.0838
sesB	0.479	0.0841
CG9646	0.479	0.0841
CG31195	0.478	0.0843
Bet3	0.478	0.0843
CG15408	0.478	0.0843
CG7686	0.478	0.0843
Pf1B	0.478	0.0843
Liprin-alpha	0.476	0.0848
CG13168	0.476	0.0848
CG17477	0.476	0.0848
enok	0.476	0.0848
sle	0.476	0.0848
CG14949	0.476	0.0848
dalao	0.476	0.0848
KrT95D	0.476	0.0848
Dic90F	0.475	0.0855
CG11122	0.475	0.0855
CG14687	0.474	0.0857
CG3669	0.474	0.0857

Gene Name	ERC Value	P-value
bcr92	0.474	0.0857
sip3	0.474	0.0857
Apf	0.474	0.0857
CG6767	0.474	0.0857
dream	0.473	0.0862
GlyP	0.473	0.0862
CG32053	0.473	0.0862
Pros26.4	0.473	0.0862
Sras	0.473	0.0862
CG3740	0.472	0.0867
CG5873	0.472	0.0867
CG42296	0.472	0.0867
Nf-YB	0.472	0.0867
CG7488	0.471	0.087
CG3588	0.471	0.087
CG17186	0.471	0.087
CG15279	0.471	0.087
CG6656	0.471	0.087
CG3011	0.471	0.087
CG3448	0.471	0.087
CG3125	0.47	0.0877
CG13036	0.47	0.0877
CG14521	0.469	0.0878
st	0.469	0.0878
CG15094	0.469	0.0878
Dh31	0.469	0.0878
RplI215	0.469	0.0878
CG4911	0.468	0.0883
CG17816	0.468	0.0883
CG5002	0.468	0.0883
CG11927	0.468	0.0883
Or63a	0.468	0.0883
tamo	0.468	0.0883
CG8837	0.467	0.0888
CG4511	0.467	0.0888
CG6441	0.467	0.0888
CG15543	0.467	0.0888
FucT6	0.467	0.0888
CG13972	0.466	0.0893
CG11505	0.466	0.0893
CG7441	0.466	0.0893
CG10830	0.465	0.0895
ns1	0.465	0.0895
SP555	0.465	0.0895
cni	0.465	0.0895
CG34247	0.465	0.0895
ST6Gal	0.464	0.09
CG10083	0.464	0.09
CG7546	0.464	0.09
Cad86C	0.464	0.09
CG15036	0.464	0.09
Su(var)3-3	0.463	0.0905
CG8851	0.463	0.0905
CG10131	0.463	0.0905
CG8136	0.463	0.0905
Gp93	0.463	0.0905

Gene Name	ERC Value	P-value
Nop56	0.463	0.0905
CG4050	0.463	0.0905
CG32755	0.462	0.0911
ras	0.462	0.0911
sty	0.462	0.0911
Fer1	0.462	0.0911
Mpk2	0.461	0.0914
RecQ5	0.461	0.0914
CG6662	0.461	0.0914
CG8218	0.461	0.0914
hoe2	0.461	0.0914
CG8525	0.461	0.0914
CG33639	0.46	0.092
CG6118	0.46	0.092
CG8785	0.46	0.092
CG1815	0.46	0.092
Klp54D	0.46	0.092
Rpn5	0.46	0.092
e(3)G	0.46	0.092
CG32270	0.46	0.092
CG32202	0.459	0.0927
Tsp42Ei	0.459	0.0927
CG12321	0.459	0.0927
Esp	0.459	0.0927
ade3	0.458	0.0931
CG30120	0.458	0.0931
Pxd	0.458	0.0931
mnb	0.458	0.0931
Mppc	0.458	0.0931
Wnt10	0.457	0.0935
CG32972	0.457	0.0935
CG13653	0.457	0.0935
vis	0.457	0.0935
tim	0.457	0.0935
sno	0.456	0.094
CG3371	0.456	0.094
CG3016	0.456	0.094
CG14397	0.456	0.094
CG15563	0.456	0.094
CG7630	0.456	0.094
CG4908	0.455	0.0945
CG10778	0.455	0.0945
CG32260	0.455	0.0945
gammaCop	0.455	0.0945
SIFR	0.454	0.0949
CG15666	0.454	0.0949
CG31091	0.454	0.0949
Klp59D	0.454	0.0949
CG9576	0.454	0.0949
CG4562	0.454	0.0949
TwdIV	0.453	0.0954
CG8021	0.453	0.0954
CG34355	0.453	0.0954
Cap-H2	0.453	0.0954
mib2	0.453	0.0954
CG12507	0.453	0.0954

Gene Name	ERC Value	P-value
CG4572	0.453	0.0954
CG10459	0.452	0.096
mr	0.452	0.096
debcI	0.452	0.096
CG8866	0.452	0.096
CG14864	0.452	0.096
CG3198	0.452	0.096
dpr15	0.452	0.096
sns	0.452	0.096
CG3040	0.451	0.0968
Eiqt71Ef	0.451	0.0968
Eip1	0.451	0.0968
Ppcs	0.451	0.0968
CG14540	0.451	0.0968
CG31207	0.451	0.0968
Df31	0.451	0.0968
dit	0.451	0.0968
glo	0.451	0.0968
CG8184	0.45	0.0976
SmD2	0.45	0.0976
thoc5	0.45	0.0976
CG10979	0.45	0.0976
Gr63a	0.45	0.0976
cyc	0.45	0.0976
Uch	0.45	0.0976
Oatp33Eb	0.45	0.0976
CG17781	0.45	0.0976
yellow-c	0.45	0.0976
CG3104	0.449	0.0985
beat-IV	0.449	0.0985
mRpS21	0.449	0.0985
Uch-L3	0.449	0.0985
dgo	0.449	0.0985
CG6379	0.449	0.0985
CG5973	0.449	0.0985
Gyc88E	0.448	0.0991
Xpd	0.448	0.0991
Pdf	0.448	0.0991
CG18404	0.448	0.0991
CG5762	0.448	0.0991
Clk	0.448	0.0991
CG30497	0.448	0.0991
Catsup	0.447	0.0997
CG31682	0.447	0.0997
CG33322	0.447	0.0997
CG30383	0.446	0.1
gogo	0.446	0.1
SK	0.446	0.1
CG9664	0.446	0.1
CG18631	0.446	0.1
CG8372	0.446	0.1
CG14476	0.446	0.1
CG34313	0.446	0.1

Table 6.S4 - Top Genes ERC values for *Ercc1* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG12126	0.901	0.0001
CG10366	0.892	0.0002
CG7587	0.887	0.0003
CG12204	0.885	0.0004
gp210	0.87	0.0005
CG13742	0.868	0.0005
CG31815	0.865	0.0006
fs(1)Yb	0.865	0.0006
CG14717	0.862	0.0008
CG18418	0.861	0.0009
CG12182	0.856	0.001
CG14834	0.849	0.0011
CG31755	0.845	0.0012
Nap1	0.845	0.0012
CG9592	0.843	0.0014
glic	0.843	0.0014
CG7849	0.841	0.0015
Cyp28d1	0.841	0.0015
CG31760	0.839	0.0017
pain	0.839	0.0017
CG31643	0.836	0.0019
CG31600	0.835	0.002
llp5	0.833	0.0021
CG18806	0.831	0.0022
nimB3	0.831	0.0022
CG7845	0.827	0.0023
Mapmodulin	0.825	0.0024
CG33172	0.824	0.0025
CG4434	0.823	0.0026
CG14316	0.822	0.0027
CG5265	0.821	0.0028
CG13427	0.819	0.0029
CG16896	0.819	0.0029
beat-la	0.818	0.0031
hppy	0.816	0.0032
mm	0.815	0.0032
Su(var)2-HP	0.815	0.0032
CG14662	0.811	0.0034
HLHm3	0.811	0.0034
lr56a	0.811	0.0034
CG32088	0.809	0.0037
scf	0.809	0.0037
CG1513	0.808	0.0039
Lis-1	0.808	0.0039
CG12307	0.807	0.0041
kek5	0.805	0.0041
CG31926	0.804	0.0042
CG17186	0.796	0.0043
Kaz1-ORFB	0.788	0.0044
tectonic	0.788	0.0044
CG5877	0.787	0.0046
Mst89B	0.787	0.0046
cav	0.786	0.0048
CG13557	0.786	0.0048
CG30157	0.784	0.005
Spn42Db	0.779	0.005

Gene Name	ERC Value	P-value
CG18234	0.778	0.0051
CG7488	0.778	0.0051
Cpr47Ed	0.774	0.0053
pie	0.774	0.0053
vic	0.773	0.0055
CG42566	0.772	0.0056
cenB1A	0.771	0.0057
Lhr	0.77	0.0058
CG34140	0.768	0.0059
nimC1	0.768	0.0059
CG10459	0.766	0.006
CG5565	0.766	0.006
CG34148	0.765	0.0062
Hem	0.765	0.0062
CG4884	0.763	0.0064
CG4942	0.762	0.0065
CG11085	0.76	0.0066
FLASH	0.758	0.0067
CG33234	0.757	0.0068
Octbeta2R	0.755	0.0068
spag4	0.755	0.0068
CG9879	0.754	0.007
Su(z)12	0.754	0.007
CG1537	0.749	0.0072
CG3592	0.747	0.0073
Poc1	0.747	0.0073
CG16713	0.744	0.0075
CG3823	0.743	0.0076
CG3123	0.742	0.0077
CG7248	0.74	0.0077
Arpc3A	0.738	0.0078
CG9399	0.738	0.0078
lr94c	0.738	0.0078
CG34305	0.736	0.0081
Vps135	0.735	0.0082
timeout	0.735	0.0082
CG13862	0.734	0.0084
adat	0.731	0.0085
CG11470	0.731	0.0085
CG15116	0.731	0.0085
CG42255	0.731	0.0085
CaMKI	0.729	0.0088
CG5079	0.728	0.0089
e(2)M	0.726	0.009
CG34033	0.725	0.0091
boly	0.723	0.0092
CG6044	0.723	0.0092
CG6523	0.722	0.0094
CG14470	0.721	0.0095
CG6845	0.721	0.0095
l(1)sc	0.721	0.0095
Vsx2	0.72	0.0097
CG17658	0.719	0.0098
CG7882	0.719	0.0098
Ckl1beta	0.719	0.0098
CG3808	0.718	0.0101

Gene Name	ERC Value	P-value
CG8316	0.718	0.0101
CG11163	0.717	0.0103
CG14322	0.717	0.0103
CG9117	0.717	0.0103
CG11882	0.716	0.0105
CG12617	0.716	0.0105
CG13876	0.715	0.0107
CG14693	0.715	0.0107
Stim	0.715	0.0107
CG2941	0.714	0.011
CG5690	0.714	0.011
CG1138	0.713	0.0112
Rcd2	0.713	0.0112
lr40a	0.712	0.0114
CG12272	0.711	0.0114
CG42729	0.71	0.0115
CG9523	0.71	0.0115
Npc2g	0.709	0.0117
Btd	0.707	0.0118
CG11158	0.707	0.0118
CG34296	0.707	0.0118
CG1890	0.706	0.0121
l(2)01810	0.706	0.0121
CG7837	0.705	0.0123
abr	0.705	0.0123
CG10338	0.704	0.0124
CG14220	0.704	0.0124
CG14377	0.704	0.0124
CG31288	0.704	0.0124
Rop	0.704	0.0124
sty	0.704	0.0124
CG11570	0.703	0.013
CG33263	0.703	0.013
CG8774	0.702	0.0132
Vps36	0.702	0.0132
CG42564	0.7	0.0133
CG7211	0.7	0.0133
CG17575	0.698	0.0135
CG8539	0.697	0.0136
su(Hw)	0.696	0.0137
CG40191	0.695	0.0138
CG32732	0.694	0.0139
be	0.693	0.014
CG3165	0.693	0.014
Ranbp16	0.693	0.014
Ucp4B	0.693	0.014
Sec61beta	0.692	0.0143
CG31482	0.691	0.0144
CG7408	0.691	0.0144
Psa	0.69	0.0146
beta3GalTII	0.689	0.0147
CG10924	0.688	0.0148
CG13970	0.688	0.0148
CG14797	0.688	0.0148
CG31269	0.688	0.0148
CG14882	0.686	0.0151

Gene Name	ERC Value	P-value
CG4269	0.686	0.0151
msv	0.686	0.0151
CG14408	0.685	0.0154
CG18171	0.684	0.0155
Pp2B-14D	0.684	0.0155
CG13741	0.682	0.0157
CG15471	0.682	0.0157
CG11778	0.681	0.0159
CG9947	0.68	0.0159
toy	0.68	0.0159
CG30441	0.678	0.0161
CG14590	0.676	0.0162
CG12783	0.675	0.0163
CG30275	0.675	0.0163
lr94f	0.673	0.0165
CG13748	0.672	0.0166
Or23a	0.672	0.0166
CG30440	0.671	0.0168
Ser8	0.671	0.0168
lr67c	0.67	0.0169
GluRIIB	0.669	0.017
Pat-AHalp	0.669	0.017
psd	0.669	0.017
CG13500	0.668	0.0173
CG15048	0.666	0.0174
ct	0.666	0.0174
Cyp4ae1	0.666	0.0174
CG6012	0.665	0.0177
CG8974	0.665	0.0177
cta	0.665	0.0177
KH1	0.665	0.0177
Pms2	0.665	0.0177
CG7224	0.664	0.0181
CG8777	0.664	0.0181
se	0.664	0.0181
CG10417	0.663	0.0184
CG14212	0.663	0.0184
Rfabg	0.663	0.0184
Cda4	0.662	0.0186
Sbp2	0.661	0.0187
lr47a	0.66	0.0188
Spc25	0.66	0.0188
tw	0.66	0.0188
CG33489	0.659	0.0191
CG1421	0.658	0.0192
CG17816	0.658	0.0192
CG6149	0.658	0.0192
Spl45	0.658	0.0192
CG9804	0.657	0.0195
Clic	0.657	0.0195
NHR	0.657	0.0195
Psc	0.657	0.0195
CG30033	0.656	0.0199
mod	0.656	0.0199
Rb97D	0.656	0.0199
CG13377	0.655	0.0202

Gene Name	ERC Value	P-value
Shroom	0.655	0.0202
CG14306	0.654	0.0204
CG34116	0.654	0.0204
CG11333	0.653	0.0205
Or65a	0.653	0.0205
pex2	0.653	0.0205
Ser	0.653	0.0205
svr	0.653	0.0205
CG15124	0.652	0.021
CG7458	0.652	0.021
Elp3	0.652	0.021
CG14945	0.65	0.0213
CG32487	0.65	0.0213
CG3281	0.65	0.0213
CG31682	0.649	0.0215
CG33919	0.648	0.0216
CG9377	0.648	0.0216
CG12301	0.646	0.0218
CG13476	0.646	0.0218
Tre1	0.646	0.0218
lr41a	0.645	0.0221
Sdhc	0.645	0.0221
CG31974	0.644	0.0223
Gr89a	0.644	0.0223
DNApol- <i>alph</i>	0.643	0.0224
FucTD	0.643	0.0224
mRpL19	0.643	0.0224
sra	0.643	0.0224
CG10424	0.642	0.0228
unc-119	0.642	0.0228
CG32379	0.641	0.023
CG33642	0.641	0.023
CG9308	0.641	0.023
upd3	0.641	0.023
CG7881	0.64	0.0233
nopo	0.64	0.0233
Spc105R	0.64	0.0233
X11Lbeta	0.64	0.0233
CG14229	0.638	0.0237
CG17982	0.638	0.0237
CG6985	0.638	0.0237
CG14450	0.637	0.024
CG7049	0.637	0.024
Apc7	0.636	0.0241
CG5626	0.636	0.0241
Hmr	0.636	0.0241
Skeletor	0.636	0.0241
CG30203	0.635	0.0245
CG2453	0.634	0.0246
CG34045	0.633	0.0247
CG9109	0.633	0.0247
dhd	0.633	0.0247
Eps-15	0.633	0.0247
CG10825	0.632	0.025
CG34130	0.632	0.025
CG5910	0.632	0.025

Table 6.S4 Continued

Gene Name	ERC Value	P-value
<i>mRpl20</i>	0.632	0.025
<i>CG4480</i>	0.631	0.0254
<i>cmet</i>	0.631	0.0254
<i>CG13902</i>	0.629	0.0256
<i>CG17806</i>	0.629	0.0256
<i>CG18088</i>	0.629	0.0256
<i>mRpl41</i>	0.629	0.0256
<i>CG5871</i>	0.628	0.0259
<i>CG1545</i>	0.627	0.026
<i>CG17528</i>	0.627	0.026
<i>CG11227</i>	0.626	0.0262
<i>CG3358</i>	0.626	0.0262
<i>sle</i>	0.626	0.0262
<i>Hsp60</i>	0.625	0.0265
<i>CG11977</i>	0.624	0.0266
<i>CG13713</i>	0.624	0.0266
<i>desat2</i>	0.624	0.0266
<i>CG14354</i>	0.623	0.0266
<i>CG5122</i>	0.623	0.0268
<i>l(2)k14505</i>	0.623	0.0268
<i>CG7791</i>	0.622	0.0271
<i>CG12866</i>	0.621	0.0272
<i>CG18268</i>	0.621	0.0272
<i>CG11123</i>	0.62	0.0274
<i>Mio</i>	0.62	0.0274
<i>Ugt86Dj</i>	0.62	0.0274
<i>btd</i>	0.619	0.0277
<i>CG7634</i>	0.619	0.0277
<i>CG9044</i>	0.619	0.0277
<i>GGBP2</i>	0.619	0.0277
<i>Irc</i>	0.619	0.0277
<i>CG30192</i>	0.618	0.0281
<i>CG31010</i>	0.618	0.0281
<i>dm</i>	0.617	0.0283
<i>mth1</i>	0.617	0.0283
<i>CG10911</i>	0.616	0.0285
<i>llp1</i>	0.616	0.0285
<i>Cdk8</i>	0.615	0.0286
<i>CG12788</i>	0.615	0.0286
<i>CG12990</i>	0.615	0.0286
<i>CG14407</i>	0.615	0.0286
<i>Sas</i>	0.615	0.0286
<i>CG16825</i>	0.614	0.0291
<i>CG6980</i>	0.614	0.0291
<i>sPLA2</i>	0.614	0.0291
<i>CG17324</i>	0.613	0.0294
<i>CG9471</i>	0.613	0.0294
<i>CG11327</i>	0.612	0.0295
<i>CG7551</i>	0.612	0.0295
<i>CG6353</i>	0.611	0.0297
<i>CG6947</i>	0.611	0.0297
<i>CG7357</i>	0.611	0.0297
<i>Asator</i>	0.61	0.03
<i>CG5048</i>	0.61	0.03
<i>dmt</i>	0.61	0.03
<i>gd</i>	0.61	0.03

Gene Name	ERC Value	P-value
<i>CG11035</i>	0.609	0.0304
<i>CG12042</i>	0.609	0.0304
<i>CG32016</i>	0.609	0.0304
<i>Cas</i>	0.608	0.0306
<i>CG31612</i>	0.608	0.0306
<i>CG10830</i>	0.607	0.0308
<i>Ddr</i>	0.607	0.0308
<i>Tob</i>	0.607	0.0308
<i>CG3701</i>	0.606	0.0311
<i>CG5087</i>	0.606	0.0311
<i>CG8771</i>	0.606	0.0311
<i>GaiNAc-T2</i>	0.606	0.0311
<i>RplP2</i>	0.606	0.0311
<i>Spargel</i>	0.606	0.0311
<i>CG18635</i>	0.605	0.0316
<i>CG1344</i>	0.604	0.0317
<i>CG15386</i>	0.604	0.0317
<i>Rbp2</i>	0.604	0.0317
<i>CG8602</i>	0.603	0.032
<i>mbm</i>	0.603	0.032
<i>Acp1</i>	0.602	0.0322
<i>CG11912</i>	0.602	0.0322
<i>CG17150</i>	0.602	0.0322
<i>CG4714</i>	0.602	0.0322
<i>nAcRbeta-2</i>	0.602	0.0322
<i>CG11249</i>	0.601	0.0326
<i>CG15201</i>	0.601	0.0326
<i>CG4407</i>	0.601	0.0326
<i>CG1783</i>	0.601	0.0326
<i>mRplS30</i>	0.601	0.0326
<i>Pez</i>	0.601	0.0326
<i>scaf</i>	0.601	0.0326
<i>CG12818</i>	0.6	0.0332
<i>RhoGAP1A</i>	0.6	0.0332
<i>CG5527</i>	0.599	0.0334
<i>CG9766</i>	0.599	0.0334
<i>tef</i>	0.599	0.0334
<i>CG17493</i>	0.598	0.0337
<i>Hrd3</i>	0.598	0.0337
<i>mGluRA</i>	0.598	0.0337
<i>Neos</i>	0.598	0.0337
<i>galectin</i>	0.597	0.0341
<i>Yell</i>	0.597	0.0341
<i>CG12121</i>	0.596	0.0342
<i>CG15890</i>	0.596	0.0342
<i>CG1732</i>	0.596	0.0342
<i>CG3107</i>	0.596	0.0342
<i>CG12206</i>	0.594	0.0346
<i>CG32533</i>	0.594	0.0346
<i>CG33155</i>	0.594	0.0346
<i>CG6947</i>	0.594	0.0346
<i>CG4424</i>	0.594	0.0346
<i>Ucp4A</i>	0.594	0.0346
<i>CG11180</i>	0.593	0.0351
<i>CG15914</i>	0.593	0.0351
<i>CG31784</i>	0.593	0.0351

Gene Name	ERC Value	P-value
<i>CG6153</i>	0.593	0.0351
<i>Pngl</i>	0.593	0.0351
<i>Rrp46</i>	0.593	0.0351
<i>ACXE</i>	0.592	0.0357
<i>CG18809</i>	0.592	0.0357
<i>CG32006</i>	0.592	0.0357
<i>CG42487</i>	0.591	0.0359
<i>CG3650</i>	0.59	0.036
<i>l(3)neo43</i>	0.59	0.036
<i>Anxb11</i>	0.589	0.0362
<i>CG10311</i>	0.589	0.0362
<i>Eaf</i>	0.589	0.0362
<i>mRpl34</i>	0.587	0.0365
<i>tap</i>	0.587	0.0365
<i>CG15087</i>	0.586	0.0367
<i>CG31278</i>	0.586	0.0367
CG7069	0.586	0.0367
<i>Rhp</i>	0.586	0.0367
<i>sqv</i>	0.586	0.0367
<i>tbce</i>	0.586	0.0367
<i>CG10265</i>	0.585	0.0372
<i>CG10631</i>	0.585	0.0372
<i>CG3305</i>	0.585	0.0372
<i>CG9791</i>	0.584	0.0375
<i>CG13040</i>	0.583	0.0376
<i>CG6432</i>	0.583	0.0376
<i>CG9926</i>	0.583	0.0376
<i>VhaM9-7-d</i>	0.583	0.0376
<i>CG17135</i>	0.582	0.0379
<i>Gem3</i>	0.582	0.0379
<i>p53</i>	0.582	0.0379
<i>CG14913</i>	0.581	0.0382
<i>Cha</i>	0.581	0.0382
<i>CG11703</i>	0.58	0.0384
<i>CG32548</i>	0.58	0.0384
<i>C901</i>	0.579	0.0386
<i>CG8079</i>	0.578	0.0386
<i>CG17636</i>	0.577	0.0387
<i>CG32712</i>	0.577	0.0387
<i>CG40485</i>	0.577	0.0387
<i>l(2)37Ce</i>	0.577	0.0387
<i>ttm50</i>	0.577	0.0387
<i>Actbeta</i>	0.576	0.0392
<i>CG32281</i>	0.576	0.0392
<i>CG13028</i>	0.575	0.0394
<i>CG17283</i>	0.575	0.0394
<i>CG3191</i>	0.575	0.0394
<i>CG5612</i>	0.575	0.0394
<i>Nfi</i>	0.575	0.0394
<i>CG14721</i>	0.574	0.0398
<i>CG9247</i>	0.573	0.0399
<i>sun</i>	0.573	0.0399
<i>CG3502</i>	0.572	0.0401
mus312	0.572	0.0401
<i>CG33969</i>	0.571	0.0403
<i>dgt6</i>	0.571	0.0403

Gene Name	ERC Value	P-value
<i>l(2)JNC136</i>	0.571	0.0403
<i>Tango11</i>	0.571	0.0403
<i>Tsp97E</i>	0.571	0.0403
<i>Ance</i>	0.57	0.0407
<i>CG17278</i>	0.57	0.0407
<i>CG31457</i>	0.57	0.0407
<i>Rpp30</i>	0.57	0.0407
<i>CG33340</i>	0.569	0.0411
<i>dimm</i>	0.569	0.0411
<i>plu</i>	0.569	0.0411
<i>CG2444</i>	0.568	0.0414
<i>CG32277</i>	0.568	0.0414
<i>CG7506</i>	0.568	0.0414
<i>CG9588</i>	0.568	0.0414
<i>Nnfta</i>	0.568	0.0414
<i>l(2)35Di</i>	0.567	0.0418
<i>140up</i>	0.566	0.0419
<i>CG14906</i>	0.566	0.0419
<i>CG6672</i>	0.566	0.0419
<i>Elp2</i>	0.566	0.0419
<i>YL-1</i>	0.566	0.0419
<i>CG17683</i>	0.565	0.0423
<i>CG7071</i>	0.565	0.0423
<i>dpr6</i>	0.565	0.0423
<i>lbi</i>	0.565	0.0423
<i>CG11762</i>	0.564	0.0427
<i>CG9925</i>	0.564	0.0427
<i>corrv</i>	0.564	0.0427
<i>l(2)gd1</i>	0.564	0.0427
<i>scpr-C</i>	0.564	0.0427
<i>CG31704</i>	0.563	0.0432
<i>CG8097</i>	0.563	0.0432
<i>l(2)09851</i>	0.563	0.0432
<i>Pbprp2</i>	0.563	0.0432
<i>Pglym87</i>	0.563	0.0432
<i>CG4406</i>	0.562	0.0436
<i>CG8080</i>	0.562	0.0436
<i>CG10347</i>	0.561	0.0438
<i>CG1791</i>	0.561	0.0438
<i>CG18128</i>	0.561	0.0438
<i>Orc4</i>	0.561	0.0438
<i>Tsp3A</i>	0.561	0.0438
<i>CG8833</i>	0.56	0.0442
<i>Nfi</i>	0.56	0.0442
<i>CG8507</i>	0.559	0.0444
<i>Taf7</i>	0.559	0.0444
<i>CG12288</i>	0.558	0.0446
<i>CG33977</i>	0.558	0.0446
<i>CG11279</i>	0.557	0.0448
<i>CG5285</i>	0.557	0.0448
<i>CG9175</i>	0.557	0.0448
<i>CG9507</i>	0.557	0.0448
<i>CG9799</i>	0.557	0.0448
<i>CG13376</i>	0.556	0.0452
<i>CG31808</i>	0.556	0.0452
<i>CG3226</i>	0.556	0.0452

Gene Name	ERC Value	P-value
<i>CG5746</i>	0.556	0.0452
<i>CG17162</i>	0.555	0.0456
<i>H2.0</i>	0.555	0.0456
<i>CG15634</i>	0.554	0.0458
<i>CG31676</i>	0.554	0.0458
<i>CG7544</i>	0.554	0.0458
<i>CG6255</i>	0.553	0.046
<i>CG9609</i>	0.553	0.046
<i>spag</i>	0.552	0.0462
<i>CG13405</i>	0.551	0.0463
<i>PPP4R2r</i>	0.551	0.0463
<i>CG32350</i>	0.55	0.0465
<i>CG3709</i>	0.55	0.0465
<i>CG9235</i>	0.55	0.0465
<i>Dip3</i>	0.55	0.0465
<i>CG10702</i>	0.549	0.0468
<i>CG11109</i>	0.548	0.0469
<i>CG12024</i>	0.548	0.0469
<i>CG15482</i>	0.548	0.0469
<i>Taf2</i>	0.548	0.0469
<i>CG18879</i>	0.547	0.0473
<i>CG5946</i>	0.547	0.0473
<i>d4</i>	0.547	0.0473
<i>Hr39</i>	0.547	0.0473
<i>mus308</i>	0.547	0.0473
<i>l(1)G0007</i>	0.546	0.0477
<i>wdb</i>	0.546	0.0477
<i>CG17633</i>	0.545	0.0479
<i>CG5431</i>	0.545	0.0479
<i>CG8245</i>	0.545	0.0479
<i>ed</i>	0.545	0.0479
<i>CG15881</i>	0.544	0.0483
<i>CG32164</i>	0.544	0.0483
<i>CG32832</i>	0.544	0.0483
<i>CG4789</i>	0.544	0.0483
<i>Fs</i>	0.544	0.0483
<i>CG12721</i>	0.542	0.0487
<i>CG31959</i>	0.542	0.0487
<i>CG34316</i>	0.542	0.0487
<i>CG9509</i>	0.542	0.0487
<i>Rrp40</i>	0.542	0.0487
<i>sowah</i>	0.542	0.0487
<i>CG11594</i>	0.541	0.0493
<i>Kap-alpha1</i>	0.541	0.0493
<i>Ndc80</i>	0.541	0.0493
<i>ast</i>	0.54	0.0495
<i>CG10581</i>	0.54	0.0495
<i>CG11077</i>	0.54	0.0495
<i>CG11590</i>	0.54	0.0495
<i>CG30007</i>	0.54	0.0495
<i>CG5537</i>	0.54	0.0495
<i>CG8116</i>	0.54	0.0495
<i>CG32195</i>	0.539	0.0502
<i>CG32263</i>	0.539	0.0502
<i>CG3528</i>	0.539	0.0502
<i>CG7692</i>	0.539	0.0502

Table 6.S4 Continued

Gene Name	ERC Value	P-value
<i>Elo88beta</i>	0.539	0.0502
<i>ERR</i>	0.539	0.0502
<i>Rme-8</i>	0.539	0.0502
<i>Traf6</i>	0.539	0.0502
<i>CCKLR-17D</i>	0.538	0.0509
<i>CG13392</i>	0.538	0.0509
<i>CG32079</i>	0.538	0.0509
<i>ck</i>	0.538	0.0509
<i>tsl</i>	0.538	0.0509
<i>Atox1</i>	0.537	0.0514
<i>Mfap1</i>	0.537	0.0514
<i>ver</i>	0.537	0.0514
<i>CG10189</i>	0.536	0.0516
<i>CG18233</i>	0.536	0.0516
<i>Kmn1</i>	0.536	0.0516
<i>Tsp66A</i>	0.536	0.0516
<i>CG16863</i>	0.535	0.052
<i>CG18675</i>	0.535	0.052
<i>CG32412</i>	0.535	0.052
<i>Pros26</i>	0.535	0.052
<i>vib</i>	0.535	0.052
<i>CG13226</i>	0.534	0.0524
<i>CG2091</i>	0.534	0.0524
<i>Hsp23</i>	0.534	0.0524
<i>CG13982</i>	0.533	0.0527
<i>CG2316</i>	0.533	0.0527
<i>CG6511</i>	0.533	0.0527
<i>CG6659</i>	0.533	0.0527
<i>CG13252</i>	0.532	0.0531
<i>CG8435</i>	0.532	0.0531
<i>Myb</i>	0.532	0.0531
<i>CG31287</i>	0.531	0.0533
<i>rg</i>	0.531	0.0533
<i>tos</i>	0.531	0.0533
<i>CG10343</i>	0.53	0.0536
<i>CG11133</i>	0.53	0.0536
<i>CG15865</i>	0.53	0.0536
<i>CG17669</i>	0.53	0.0536
<i>CG32251</i>	0.53	0.0536
<i>Ast-CC</i>	0.529	0.0541
<i>CG10688</i>	0.529	0.0541
<i>CG14695</i>	0.529	0.0541
<i>CG5322</i>	0.529	0.0541
<i>CG6745</i>	0.529	0.0541
<i>E(spl)</i>	0.529	0.0541
<i>CG2975</i>	0.528	0.0546
<i>CG6762</i>	0.528	0.0546
<i>hkb</i>	0.528	0.0546
<i>CG11155</i>	0.527	0.0549
<i>hang</i>	0.527	0.0549
<i>CG15025</i>	0.526	0.055
<i>CG42827</i>	0.526	0.055
<i>Cp15</i>	0.526	0.055
<i>Cyp4aa1</i>	0.526	0.055
<i>llp2</i>	0.526	0.055
<i>Myo31DF</i>	0.526	0.055

Gene Name	ERC Value	P-value
<i>p-cup</i>	0.526	0.055
<i>Tango2</i>	0.526	0.055
<i>CG12923</i>	0.525	0.0558
<i>dre4</i>	0.525	0.0558
<i>Or10a</i>	0.525	0.0558
<i>Bj1</i>	0.524	0.056
<i>Caff1-105</i>	0.524	0.056
<i>CG1239</i>	0.524	0.056
<i>CG14931</i>	0.524	0.056
<i>CG4565</i>	0.524	0.056
<i>CG5724</i>	0.524	0.056
<i>CG9150</i>	0.524	0.056
<i>Est-Q</i>	0.524	0.056
<i>retm</i>	0.524	0.056
<i>CG5532</i>	0.523	0.0568
<i>CG6024</i>	0.523	0.0568
<i>CG9917</i>	0.523	0.0568
<i>gm</i>	0.523	0.0568
<i>ana1</i>	0.522	0.0572
<i>CG11247</i>	0.521	0.0573
<i>CG31910</i>	0.521	0.0573
<i>CG33493</i>	0.521	0.0573
<i>Rab7</i>	0.521	0.0573
<i>CG13841</i>	0.52	0.0577
<i>CG3557</i>	0.52	0.0577
<i>Listencin</i>	0.52	0.0577
<i>Mis12</i>	0.52	0.0577
<i>alphaTry</i>	0.519	0.058
<i>CG11665</i>	0.519	0.058
<i>CG32700</i>	0.519	0.058
<i>inaF-A</i>	0.519	0.058
<i>Spn47C</i>	0.519	0.058
<i>ll(1)G0230</i>	0.518	0.0585
<i>CG13101</i>	0.517	0.0586
<i>CG32147</i>	0.517	0.0586
<i>CG33509</i>	0.517	0.0586
<i>CG3356</i>	0.517	0.0586
<i>CG42308</i>	0.517	0.0586
<i>CG4877</i>	0.517	0.0586
<i>GluRIIE</i>	0.517	0.0586
<i>CG12773</i>	0.516	0.0592
<i>CG6204</i>	0.516	0.0592
<i>Dis3</i>	0.516	0.0592
<i>CG32986</i>	0.515	0.0595
<i>Fs(2)Ket</i>	0.515	0.0595
<i>mRpl3</i>	0.515	0.0595
<i>CG14933</i>	0.514	0.0597
<i>CG18764</i>	0.514	0.0597
<i>Cyp28a5</i>	0.514	0.0597
<i>homer</i>	0.514	0.0597
<i>CG11555</i>	0.513	0.0601
<i>CG11629</i>	0.513	0.0601
<i>CG13850</i>	0.513	0.0601
<i>CG31917</i>	0.513	0.0601
<i>CG4956</i>	0.513	0.0601
<i>CG5421</i>	0.513	0.0601

Gene Name	ERC Value	P-value
<i>c12.1</i>	0.512	0.0606
<i>CG10395</i>	0.512	0.0606
<i>CG16742</i>	0.512	0.0606
<i>CG3337</i>	0.512	0.0606
<i>CG3635</i>	0.512	0.0606
<i>CG5642</i>	0.512	0.0606
<i>CG6216</i>	0.512	0.0606
<i>shl</i>	0.512	0.0606
<i>CG9619</i>	0.511	0.0614
<i>mRpl35</i>	0.511	0.0614
<i>Rrp42</i>	0.511	0.0614
<i>CG14314</i>	0.51	0.0616
<i>CG14457</i>	0.51	0.0616
<i>Doa</i>	0.51	0.0616
<i>piwi</i>	0.51	0.0616
<i>CG5860</i>	0.509	0.062
<i>CG8578</i>	0.509	0.062
<i>Kai1RIA</i>	0.509	0.062
<i>CG14618</i>	0.508	0.0623
<i>Uchr</i>	0.508	0.0623
<i>CG10512</i>	0.507	0.0624
<i>Crk</i>	0.507	0.0624
<i>G9a</i>	0.507	0.0624
<i>ll(2)37Cd</i>	0.507	0.0624
<i>NetA</i>	0.507	0.0624
<i>Not1</i>	0.507	0.0624
<i>CG10486</i>	0.506	0.063
<i>CG14177</i>	0.506	0.063
<i>CG17159</i>	0.506	0.063
<i>RhoGAP18E</i>	0.506	0.063
<i>Tsp42Ea</i>	0.506	0.063
<i>CG13725</i>	0.505	0.0634
<i>eco</i>	0.505	0.0634
<i>GstD8</i>	0.505	0.0634
<i>RhoGAP5A</i>	0.505	0.0634
<i>CG13717</i>	0.504	0.0638
<i>CG2260</i>	0.504	0.0638
<i>CtBP</i>	0.504	0.0638
<i>Mit2</i>	0.504	0.0638
<i>Scip</i>	0.504	0.0638
<i>CG11668</i>	0.503	0.0642
<i>CG8417</i>	0.503	0.0642
<i>Or98b</i>	0.503	0.0642
<i>tsq</i>	0.503	0.0642
<i>CG10752</i>	0.502	0.0646
<i>CG18065</i>	0.502	0.0646
<i>CG34447</i>	0.502	0.0646
<i>CG7829</i>	0.502	0.0646
<i>it</i>	0.502	0.0646
<i>Vha16-3</i>	0.502	0.0646
<i>Xpac</i>	0.502	0.0646
<i>CG11674</i>	0.501	0.0652
<i>CG14561</i>	0.501	0.0652
<i>CG30466</i>	0.501	0.0652
<i>ATPsyn-Cf6</i>	0.5	0.0655
<i>CG9682</i>	0.5	0.0655

Gene Name	ERC Value	P-value
<i>pAbp</i>	0.5	0.0655
<i>Snm1</i>	0.5	0.0655
<i>lko</i>	0.5	0.0655
<i>CG11029</i>	0.499	0.0659
<i>CG15747</i>	0.499	0.0659
<i>CG6180</i>	0.499	0.0659
<i>CG8931</i>	0.499	0.0659
<i>Lam</i>	0.499	0.0659
<i>Rcp</i>	0.499	0.0659
<i>Vmi</i>	0.499	0.0659
<i>CG10195</i>	0.498	0.0666
<i>CG11638</i>	0.498	0.0666
<i>CG31530</i>	0.498	0.0666
<i>CG31920</i>	0.498	0.0666
<i>CG9451</i>	0.498	0.0666
<i>edl</i>	0.498	0.0666
<i>m1TF</i>	0.498	0.0666
<i>pallidin</i>	0.498	0.0666
<i>ste14</i>	0.498	0.0666
<i>bs</i>	0.497	0.0674
<i>CG12934</i>	0.497	0.0674
<i>Phax</i>	0.497	0.0674
<i>Cdep</i>	0.496	0.0677
<i>CG11196</i>	0.496	0.0677
<i>CG13901</i>	0.496	0.0677
<i>CG14712</i>	0.496	0.0677
<i>mus210</i>	0.496	0.0677
<i>CG11634</i>	0.495	0.0681
<i>CG2974</i>	0.495	0.0681
<i>CG3262</i>	0.495	0.0681
<i>how</i>	0.495	0.0681
<i>sbr</i>	0.495	0.0681
<i>Trxr-2</i>	0.495	0.0681
<i>BubR1</i>	0.494	0.0686
<i>CG10375</i>	0.494	0.0686
<i>CG2144</i>	0.494	0.0686
<i>CG32772</i>	0.494	0.0686
<i>CG3748</i>	0.494	0.0686
<i>Hsc70-2</i>	0.494	0.0686
<i>CG15876</i>	0.493	0.0692
<i>CG17691</i>	0.493	0.0692
<i>CG7265</i>	0.493	0.0692
<i>CG7914</i>	0.493	0.0692
<i>Ptp52F</i>	0.493	0.0692
<i>tlilB</i>	0.493	0.0692
<i>CG8197</i>	0.492	0.0697
<i>Rheb</i>	0.492	0.0697
<i>CG10166</i>	0.491	0.0699
<i>CG11107</i>	0.491	0.0699
<i>CG17917</i>	0.491	0.0699
<i>CG3921</i>	0.491	0.0699
<i>Hen1</i>	0.491	0.0699
<i>Rga</i>	0.491	0.0699
<i>CG13110</i>	0.49	0.0705
<i>Pros28.1</i>	0.49	0.0705
<i>Andorra</i>	0.489	0.0706

Gene Name	ERC Value	P-value
<i>CG3520</i>	0.489	0.0706
<i>CG8677</i>	0.489	0.0706
<i>ns3</i>	0.489	0.0706
<i>ppk13</i>	0.489	0.0706
<i>Rpb4</i>	0.489	0.0706
<i>shu</i>	0.489	0.0706
<i>CG8289</i>	0.488	0.0713
<i>Or62a</i>	0.488	0.0713
<i>CG11403</i>	0.487	0.0714
<i>DIP1</i>	0.487	0.0714
<i>CG15369</i>	0.486	0.0716
<i>CG6136</i>	0.486	0.0716
<i>mRPL52</i>	0.486	0.0716
<i>CG11437</i>	0.485	0.0719
<i>CG12179</i>	0.485	0.0719
<i>CG12983</i>	0.485	0.0719
<i>CG18302</i>	0.485	0.0719
<i>CG34203</i>	0.485	0.0719
<i>CG42811</i>	0.485	0.0719
<i>CG4619</i>	0.485	0.0719
<i>CG7341</i>	0.485	0.0719
<i>DhpD</i>	0.485	0.0719
<i>knk</i>	0.485	0.0719
<i>CG10324</i>	0.484	0.0728
<i>CG2862</i>	0.484	0.0728
<i>CG5255</i>	0.484	0.0728
<i>CG6380</i>	0.484	0.0728
<i>CG7707</i>	0.484	0.0728
<i>Phk-3</i>	0.484	0.0728
<i>CalpC</i>	0.483	0.0733
<i>CG10463</i>	0.483	0.0733
<i>CG13365</i>	0.483	0.0733
<i>CG2901</i>	0.483	0.0733
<i>Hand</i>	0.483	0.0733
<i>mRpS25</i>	0.483	0.0733
<i>CG30380</i>	0.482	0.0739
<i>CG4984</i>	0.482	0.0739
<i>ste24b</i>	0.482	0.0739
<i>CG10749</i>	0.481	0.0741
<i>CG12263</i>	0.481	0.0741
<i>CG13423</i>	0.481	0.0741
<i>CG3795</i>	0.481	0.0741
<i>CG14829</i>	0.48	0.0745
<i>Ppm1</i>	0.48	0.0745
<i>Ssb-c31a</i>	0.48	0.0745
<i>CG14635</i>	0.479	0.0748
<i>Dbp45A</i>	0.479	0.0748
<i>Grip75</i>	0.479	0.0748
<i>Vha100-3</i>	0.479	0.0748
<i>CG32809</i>	0.478	0.0751
<i>CG8928</i>	0.478	0.0751
<i>Vago</i>	0.478	0.0751
<i>vap</i>	0.478	0.0751
<i>CG11425</i>	0.477	0.0755
<i>CG13999</i>	0.477	0.0755
<i>CG15896</i>	0.477	0.0755

Table 6.S4 Continued

Gene Name	ERC Value	P-value
CG17168	0.477	0.0755
CG31198	0.477	0.0755
CG33775	0.477	0.0755
Fer3HCH	0.477	0.0755
mRpL10	0.477	0.0755
spt4	0.477	0.0755
CG10075	0.476	0.0763
EloA	0.476	0.0763
Prosbeta1	0.476	0.0763
CG11722	0.475	0.0766
CG13310	0.475	0.0766
CG14187	0.475	0.0766
CG5630	0.475	0.0766
CG16890	0.474	0.0769
CG4836	0.474	0.0769
fs(1)K10	0.474	0.0769
l(2)35Df	0.474	0.0769
PGRP-LE	0.474	0.0769
Ast-C	0.473	0.0774
CG10801	0.473	0.0774
CG12134	0.473	0.0774
CG16957	0.473	0.0774
CG32488	0.473	0.0774
CG4612	0.473	0.0774
CG8654	0.473	0.0774
Bruce	0.472	0.078
calypso	0.472	0.078
CG32103	0.472	0.078
CG34253	0.472	0.078
CG42259	0.472	0.078
CG8678	0.472	0.078
DAAM	0.472	0.078
Nipsnap	0.472	0.078
bam	0.471	0.0787
betalnt-nu	0.471	0.0787
CG1218	0.471	0.0787
CG1315	0.471	0.0787
CG1358	0.471	0.0787
rhea	0.471	0.0787
CG16941	0.47	0.0793
CG7427	0.47	0.0793
CG7971	0.47	0.0793
RhoGAP100	0.47	0.0793
CG14764	0.469	0.0796
geminin	0.469	0.0796
mei-S332	0.469	0.0796
primo-2	0.469	0.0796
CG31195	0.468	0.08
Nrx-IV	0.468	0.08
CG34231	0.467	0.0802
CG5116	0.467	0.0802
CG8412	0.467	0.0802
nerfin-2	0.467	0.0802
yl	0.467	0.0802
CG11345	0.466	0.0806
CG1271	0.466	0.0806

Gene Name	ERC Value	P-value
CG33286	0.466	0.0806
CG6048	0.466	0.0806
Chc	0.466	0.0806
CG10465	0.465	0.0811
CG10481	0.465	0.0811
CG11902	0.465	0.0811
CG42358	0.464	0.0814
CG9886	0.464	0.0814
eIF5	0.464	0.0814
Glut3	0.464	0.0814
icln	0.464	0.0814
MED17	0.464	0.0814
nAcRalpha-7	0.464	0.0814
CG10713	0.463	0.082
CG11263	0.463	0.082
CG11739	0.463	0.082
CG13086	0.463	0.082
CG13144	0.463	0.082
CG16704	0.463	0.082
CG42376	0.463	0.082
CG5550	0.463	0.082
CG33228	0.462	0.0827
CG40451	0.462	0.0827
mRpL48	0.462	0.0827
pgant3	0.462	0.0827
5-HT1A	0.461	0.0831
CG11870	0.461	0.0831
CG30385	0.461	0.0831
CG3306	0.461	0.0831
CG6927	0.461	0.0831
CG7573	0.461	0.0831
fs(1)N	0.461	0.0831
CG11141	0.46	0.0837
CG14815	0.46	0.0837
CG31089	0.46	0.0837
CG9542	0.46	0.0837
Ets21C	0.46	0.0837
hpo	0.46	0.0837
l(1)G0289	0.46	0.0837
Nca	0.46	0.0837
CG16854	0.459	0.0844
CG31862	0.459	0.0844
CG5895	0.459	0.0844
Gr39b	0.459	0.0844
L	0.459	0.0844
CG34012	0.458	0.0849
CG6463	0.458	0.0849
Gem2	0.458	0.0849
Sep5	0.457	0.0851
CG11872	0.457	0.0851
CG33213	0.457	0.0851
CG42329	0.457	0.0851
CG5844	0.457	0.0851
CG7755	0.457	0.0851
CG7787	0.457	0.0851
Cyp6a8	0.457	0.0851

Gene Name	ERC Value	P-value
D1	0.457	0.0851
Lip2	0.457	0.0851
shcp	0.457	0.0851
beat-1c	0.456	0.0861
CG42540	0.456	0.0861
nxf2	0.456	0.0861
Skil6	0.456	0.0861
Eno	0.455	0.0865
Hf	0.455	0.0865
polybromo	0.455	0.0865
Rev1	0.455	0.0865
CG10000	0.454	0.0868
CG30196	0.454	0.0868
CG33060	0.454	0.0868
CG6613	0.454	0.0868
CG8414	0.454	0.0868
CG9410	0.454	0.0868
Gprk1	0.454	0.0868
xmas-2	0.454	0.0868
CG2794	0.453	0.0876
CG3515	0.453	0.0876
CG8501	0.453	0.0876
CTCF	0.453	0.0876
DppIII	0.453	0.0876
pgant4	0.453	0.0876
Pi3K92E	0.453	0.0876
Surf1	0.453	0.0876
CG9395	0.452	0.0883
CG9521	0.452	0.0883
Mcm7	0.452	0.0883
Syt12	0.452	0.0883
ATPsyn-beta	0.451	0.0886
CG32702	0.451	0.0886
CG7024	0.451	0.0886
ald	0.45	0.0889
CG13127	0.45	0.0889
CG14744	0.45	0.0889
CG31025	0.45	0.0889
CG7330	0.45	0.0889
CG8671	0.45	0.0889
CG9021	0.45	0.0889
RpL37a	0.45	0.0889
vn	0.45	0.0889
Best4	0.449	0.0897
CG1394	0.449	0.0897
CG15252	0.449	0.0897
CG42374	0.449	0.0897
CG4743	0.449	0.0897
CG6933	0.449	0.0897
gl	0.449	0.0897
mbt	0.449	0.0897
Menl-1	0.449	0.0897
obst-H	0.449	0.0897
Ca-alpha1D	0.448	0.0906
CG31627	0.448	0.0906
CG32191	0.448	0.0906

Gene Name	ERC Value	P-value
CG34117	0.448	0.0906
CG8292	0.448	0.0906
GluRIIC	0.448	0.0906
mRpS10	0.448	0.0906
slam	0.448	0.0906
Arp11	0.447	0.0914
CG1492	0.447	0.0914
CG1635	0.447	0.0914
CG31469	0.447	0.0914
CG8026	0.447	0.0914
drk	0.447	0.0914
Jhl-21	0.447	0.0914
LRP1	0.447	0.0914
B-H1	0.446	0.0921
CG14130	0.446	0.0921
CG33307	0.446	0.0921
CG42335	0.446	0.0921
Sac1	0.446	0.0921
CG10092	0.445	0.0925
CG10217	0.445	0.0925
CG42272	0.445	0.0925
CG5909	0.444	0.0928
CG6144	0.444	0.0928
CycG	0.444	0.0928
hbn	0.444	0.0928
RpL34a	0.444	0.0928
Sulf1	0.444	0.0928
CG14881	0.443	0.0933
CG2790	0.443	0.0933
CG32409	0.443	0.0933
CG42382	0.443	0.0933
CG40006	0.442	0.0937
CG7603	0.442	0.0937
dbe	0.442	0.0937
Prosbeta3	0.442	0.0937
Tsp29Fb	0.442	0.0937
Adk3	0.441	0.0941
CG12391	0.441	0.0941
CG31053	0.441	0.0941
CG5883	0.441	0.0941
CG9302	0.441	0.0941
Men	0.441	0.0941
net	0.441	0.0941
Proc-R	0.441	0.0941
pst	0.441	0.0941
Rpp20	0.441	0.0941
CG10495	0.44	0.095
CG13322	0.44	0.095
CG31368	0.44	0.095
CG32758	0.44	0.095
CG9086	0.44	0.095
mod(r)	0.44	0.095
RpL35A	0.44	0.095
CG14103	0.439	0.0957
CG14414	0.439	0.0957
CG32298	0.439	0.0957

Gene Name	ERC Value	P-value
escl	0.439	0.0957
kat80	0.439	0.0957
pn	0.439	0.0957
Tango5	0.439	0.0957
CG11052	0.438	0.0963
CG11475	0.438	0.0963
CG17270	0.438	0.0963
CG42369	0.438	0.0963
CG42402	0.438	0.0963
CG6043	0.438	0.0963
lat	0.438	0.0963
m2	0.438	0.0963
mtSSB	0.438	0.0963
Ogg1	0.438	0.0963
betaggt-II	0.437	0.0972
cdc2c	0.437	0.0972
CG10462	0.437	0.0972
CG3198	0.437	0.0972
CG33090	0.437	0.0972
CG3612	0.437	0.0972
Muc55B	0.437	0.0972
nahoda	0.437	0.0972
CG10731	0.436	0.0979
CG11699	0.436	0.0979
CG12736	0.436	0.0979
CG1291	0.436	0.0979
CG4678	0.436	0.0979
CG8455	0.436	0.0979
CG10418	0.435	0.0985
CG14543	0.435	0.0985
CG30101	0.435	0.0985
CG32343	0.435	0.0985
CG3887	0.435	0.0985
Vps13	0.435	0.0985
yip3	0.435	0.0985
CG1909	0.434	0.0991
CG6409	0.434	0.0991
Hsp60D	0.434	0.0991
Sgt1	0.434	0.0991
Taff1	0.434	0.0991
Tfb4	0.434	0.0991
WRNexo	0.434	0.0991
aux	0.433	0.0997
CG17841	0.433	0.0997
CG31525	0.433	0.0997
CG6218	0.433	0.0997
CG6325	0.433	0.0997
CG9997	0.433	0.0997
Sdc	0.433	0.0997

Table 6.S5 - Top Genes ERC values for *Mcm5* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Obp50c</i>	0.902	0.0001
<i>dpr3</i>	0.842	0.0002
<i>Or49b</i>	0.833	0.0003
<i>dpp</i>	0.824	0.0004
<i>Scamp</i>	0.812	0.0005
<i>Flo-2</i>	0.811	0.0005
<i>CG13893</i>	0.808	0.0006
<i>Twd1X</i>	0.805	0.0007
<i>CG13606</i>	0.804	0.0008
<i>CG13857</i>	0.803	0.0009
<i>CG33766</i>	0.79	0.001
<i>CG31659</i>	0.787	0.0011
<i>rumi</i>	0.784	0.0012
<i>CG14491</i>	0.774	0.0013
<i>CG15887</i>	0.77	0.0014
<i>Pk17E</i>	0.765	0.0014
<i>CheB42c</i>	0.764	0.0015
<i>CG17664</i>	0.758	0.0016
<i>inaF-C</i>	0.758	0.0016
<i>st</i>	0.758	0.0016
<i>CG1124</i>	0.757	0.0019
<i>Ubc-E2H</i>	0.756	0.002
<i>CG17323</i>	0.755	0.0021
<i>ldgf3</i>	0.755	0.0021
<i>mRpL32</i>	0.755	0.0021
<i>fu12</i>	0.753	0.0023
<i>Twd1F</i>	0.751	0.0024
<i>Gr21a</i>	0.75	0.0025
<i>CG15545</i>	0.749	0.0026
<i>Cyp9f2</i>	0.745	0.0027
<i>CG16800</i>	0.744	0.0028
<i>CG14546</i>	0.743	0.0029
<i>NT1</i>	0.742	0.003
<i>sns</i>	0.737	0.0031
<i>CG17322</i>	0.735	0.0032
<i>Rh4</i>	0.731	0.0032
<i>RhoGAP102</i>	0.731	0.0032
<i>Cpr64Ac</i>	0.73	0.0034
<i>Hsp22</i>	0.73	0.0034
<i>Osi20</i>	0.73	0.0034
<i>CG13792</i>	0.726	0.0037
<i>CG7924</i>	0.724	0.0038
<i>CG17036</i>	0.723	0.0039
<i>CG15408</i>	0.722	0.004
<i>CG12398</i>	0.721	0.0041
<i>LvpD</i>	0.72	0.0041
<i>epsilonTry</i>	0.718	0.0042
<i>CG17780</i>	0.717	0.0043
<i>Gr63a</i>	0.717	0.0043
<i>C3G</i>	0.713	0.0045
<i>fin</i>	0.712	0.0046
<i>CG14949</i>	0.708	0.0047
<i>CG13994</i>	0.706	0.0048
<i>Atg2</i>	0.705	0.0049
<i>CG10591</i>	0.705	0.0049
<i>HLHm5</i>	0.705	0.0049

Gene Name	ERC Value	P-value
<i>CG13827</i>	0.703	0.0051
<i>CG13875</i>	0.703	0.0051
<i>CG11811</i>	0.702	0.0053
<i>Rab35</i>	0.702	0.0053
<i>uzip</i>	0.702	0.0053
<i>CG7029</i>	0.701	0.0056
<i>ben</i>	0.699	0.0057
<i>CG9813</i>	0.699	0.0057
<i>CtrlC</i>	0.698	0.0059
<i>Gr64b</i>	0.698	0.0059
<i>AnnX</i>	0.697	0.006
<i>CG8891</i>	0.697	0.006
<i>CG9400</i>	0.697	0.006
<i>CG9717</i>	0.697	0.006
<i>CG18005</i>	0.695	0.0064
<i>CG1140</i>	0.693	0.0065
<i>CG1607</i>	0.693	0.0065
<i>OstSht3</i>	0.693	0.0065
<i>rols</i>	0.693	0.0065
<i>drono</i>	0.692	0.0068
<i>scramb2</i>	0.688	0.0069
<i>CG17549</i>	0.687	0.007
<i>Mdr65</i>	0.686	0.0071
<i>CG5687</i>	0.685	0.0072
<i>trp</i>	0.685	0.0072
<i>CG33514</i>	0.684	0.0074
<i>CG7420</i>	0.684	0.0074
<i>CG11286</i>	0.683	0.0076
<i>CG12170</i>	0.681	0.0077
<i>CG30148</i>	0.681	0.0077
<i>CG34172</i>	0.681	0.0077
<i>Rh2</i>	0.679	0.0079
<i>CG12370</i>	0.678	0.008
<i>CG5973</i>	0.678	0.008
<i>gammaSnap</i>	0.677	0.0082
<i>Gyc-89Da</i>	0.677	0.0082
<i>Rh6</i>	0.677	0.0082
<i>yellow-c</i>	0.677	0.0082
<i>CG32374</i>	0.676	0.0086
<i>bnb</i>	0.675	0.0086
<i>CG7896</i>	0.675	0.0086
<i>S2P</i>	0.675	0.0086
<i>sni</i>	0.675	0.0086
<i>CG15249</i>	0.674	0.009
<i>CG12520</i>	0.673	0.0091
<i>Ost48</i>	0.672	0.0092
<i>CG15822</i>	0.671	0.0093
<i>Or42b</i>	0.671	0.0093
<i>CG3016</i>	0.67	0.0095
<i>m1</i>	0.669	0.0095
<i>CG32052</i>	0.667	0.0096
<i>CG13193</i>	0.666	0.0097
<i>CG8909</i>	0.664	0.0098
<i>Ser7</i>	0.664	0.0098
<i>CG31441</i>	0.663	0.01
<i>CG5404</i>	0.66	0.0101

Gene Name	ERC Value	P-value
<i>v(2)k05816</i>	0.66	0.0101
<i>Hey</i>	0.659	0.0103
<i>ade5</i>	0.658	0.0104
<i>CG13912</i>	0.658	0.0104
<i>CG32305</i>	0.658	0.0104
<i>CG33232</i>	0.658	0.0104
<i>[(1)G0196</i>	0.658	0.0104
<i>simA</i>	0.658	0.0104
<i>Cpr64Aa</i>	0.657	0.0109
<i>Twd1R</i>	0.657	0.0109
<i>CG12950</i>	0.655	0.0111
<i>CG3835</i>	0.655	0.0111
<i>CG4467</i>	0.655	0.0111
<i>CG14971</i>	0.652	0.0114
<i>CG8560</i>	0.651	0.0114
<i>nnr1</i>	0.651	0.0114
<i>inx7</i>	0.65	0.0116
<i>CG15414</i>	0.649	0.0117
<i>CG3215</i>	0.649	0.0117
<i>gce</i>	0.649	0.0117
<i>CG8965</i>	0.647	0.012
<i>CG32679</i>	0.646	0.0121
<i>Obp19c</i>	0.646	0.0121
<i>Wnt10</i>	0.646	0.0121
<i>Gr66a</i>	0.645	0.0123
<i>CG5902</i>	0.644	0.0124
<i>CG17565</i>	0.643	0.0125
<i>y</i>	0.643	0.0125
<i>CG5521</i>	0.641	0.0127
<i>Cralbp</i>	0.641	0.0127
<i>GV1</i>	0.641	0.0127
<i>CG31473</i>	0.638	0.013
<i>CG6084</i>	0.638	0.013
<i>ssp5</i>	0.638	0.013
<i>CG34291</i>	0.636	0.0132
<i>CG6231</i>	0.636	0.0132
<i>Gr39a</i>	0.636	0.0132
<i>CG8249</i>	0.635	0.0135
<i>CG3961</i>	0.634	0.0136
<i>Ir68b</i>	0.634	0.0136
<i>CG13023</i>	0.633	0.0138
<i>CG13278</i>	0.633	0.0138
<i>CG14168</i>	0.633	0.0138
<i>GlcAT-I</i>	0.632	0.0141
<i>Ir56d</i>	0.632	0.0141
<i>CG34256</i>	0.631	0.0142
<i>botv</i>	0.63	0.0143
<i>Ir75c</i>	0.63	0.0143
<i>Impl3</i>	0.629	0.0145
<i>CG15706</i>	0.628	0.0146
<i>Cyp310a1</i>	0.628	0.0146
<i>Rab39</i>	0.628	0.0146
<i>Vps16A</i>	0.627	0.0149
<i>CG11505</i>	0.624	0.015
<i>Cpr65Ea</i>	0.624	0.015
<i>lush</i>	0.624	0.015

Gene Name	ERC Value	P-value
<i>CheA75a</i>	0.623	0.0152
<i>CG15431</i>	0.622	0.0153
<i>CG4734</i>	0.622	0.0153
<i>CG71781</i>	0.622	0.0153
<i>CG13704</i>	0.621	0.0156
<i>MED9</i>	0.621	0.0156
<i>CG16820</i>	0.62	0.0158
<i>CG33630</i>	0.62	0.0158
<i>Obp47a</i>	0.62	0.0158
<i>Obp56h</i>	0.62	0.0158
<i>Pdi</i>	0.62	0.0158
<i>CG11360</i>	0.619	0.0162
<i>CG7953</i>	0.619	0.0162
<i>CG10657</i>	0.618	0.0164
<i>CG6567</i>	0.618	0.0164
<i>Cyp4d2</i>	0.618	0.0164
<i>CG32459</i>	0.616	0.0167
<i>Sps2</i>	0.615	0.0168
<i>Cyp4g1</i>	0.614	0.0168
<i>mtm</i>	0.614	0.0168
<i>Atas-cys</i>	0.613	0.017
<i>CG6359</i>	0.613	0.017
<i>CG4461</i>	0.612	0.0172
<i>CG2493</i>	0.611	0.0173
<i>Cpr11A</i>	0.611	0.0173
<i>Dhc62B</i>	0.611	0.0173
<i>DNaseII</i>	0.611	0.0173
<i>Slob</i>	0.611	0.0173
<i>CG17264</i>	0.609	0.0177
<i>CG31106</i>	0.609	0.0177
<i>CG13334</i>	0.608	0.0179
<i>CG15082</i>	0.608	0.0179
<i>akirin</i>	0.607	0.0181
<i>CG13333</i>	0.607	0.0181
<i>CG14330</i>	0.606	0.0183
<i>CG31005</i>	0.606	0.0183
<i>CG3238</i>	0.606	0.0183
<i>CG42770</i>	0.606	0.0183
<i>per</i>	0.606	0.0183
<i>CG11655</i>	0.605	0.0187
<i>CG12069</i>	0.605	0.0187
<i>MAN1</i>	0.605	0.0187
<i>Rph</i>	0.605	0.0187
<i>cp309</i>	0.604	0.0191
<i>CG6045</i>	0.603	0.0192
<i>CG9911</i>	0.603	0.0192
<i>Spred</i>	0.603	0.0192
<i>alpha-catenin</i>	0.602	0.0195
<i>Adh</i>	0.601	0.0195
<i>CG13814</i>	0.601	0.0195
<i>lox</i>	0.601	0.0195
<i>wntD</i>	0.601	0.0195
<i>CG15170</i>	0.6	0.0199
<i>Mkk4</i>	0.6	0.0199
<i>CG7582</i>	0.599	0.0201
<i>Gr59d</i>	0.599	0.0201

Gene Name	ERC Value	P-value
<i>CG6503</i>	0.598	0.0203
<i>CG14741</i>	0.597	0.0204
<i>CG5916</i>	0.597	0.0204
<i>CG8299</i>	0.596	0.0205
<i>CG12826</i>	0.595	0.0206
<i>CG3650</i>	0.594	0.0207
<i>CG11357</i>	0.593	0.0208
<i>mRpS18C</i>	0.593	0.0208
<i>Or59b</i>	0.593	0.0208
<i>CG11550</i>	0.592	0.0211
<i>CG3669</i>	0.592	0.0211
<i>CG8460</i>	0.592	0.0211
<i>CG8945</i>	0.592	0.0211
<i>Rab26</i>	0.592	0.0211
<i>CG13082</i>	0.591	0.0215
<i>CG13018</i>	0.59	0.0216
<i>RhoGAPp19</i>	0.59	0.0216
<i>Tlls</i>	0.59	0.0216
<i>Twd1C</i>	0.59	0.0216
<i>vfl</i>	0.59	0.0216
<i>CG34266</i>	0.589	0.0221
<i>Vha100-1</i>	0.589	0.0221
<i>CG12325</i>	0.588	0.0223
<i>Eip93F</i>	0.588	0.0223
<i>gol</i>	0.587	0.0224
<i>Or94b</i>	0.587	0.0224
<i>wun</i>	0.587	0.0224
<i>CG3942</i>	0.585	0.0227
<i>CG12018</i>	0.584	0.0228
<i>CG14516</i>	0.584	0.0228
<i>CG15803</i>	0.584	0.0228
<i>CG5968</i>	0.584	0.0228
<i>CG8481</i>	0.584	0.0228
<i>CG9430</i>	0.584	0.0228
<i>CG4681</i>	0.583	0.0233
<i>Ahcy89E</i>	0.582	0.0234
<i>CG31148</i>	0.582	0.0234
<i>CG5357</i>	0.582	0.0234
<i>CG10863</i>	0.581	0.0237
<i>CG7023</i>	0.581	0.0237
<i>CG34120</i>	0.58	0.0239
<i>CG4500</i>	0.58	0.0239
<i>mnb</i>	0.58	0.0239
<i>bw</i>	0.579	0.0241
<i>CG34355</i>	0.579	0.0241
<i>Cpr49Ab</i>	0.579	0.0241
<i>CG33703</i>	0.578	0.0244
<i>cpb</i>	0.578	0.0244
<i>VGAT</i>	0.578	0.0244
<i>ABC7</i>	0.577	0.0247
<i>CG3907</i>	0.577	0.0247
<i>CG7735</i>	0.577	0.0247
<i>ema</i>	0.577	0.0247
<i>CG1969</i>	0.575	0.025
<i>CG5937</i>	0.575	0.025
<i>CG9631</i>	0.575	0.025

Table 6.S5 Continued

Gene Name	ERC Value	P-value
CG31630	0.574	0.0253
CG11563	0.573	0.0254
CG33156	0.573	0.0254
CG3860	0.573	0.0254
CG7509	0.573	0.0254
Pgd	0.573	0.0254
Ir56c	0.572	0.0259
smi35A	0.572	0.0259
VhaM9.7-a	0.571	0.026
CG2656	0.57	0.0261
Ckl1alpha	0.57	0.0261
CG6888	0.569	0.0263
CheA7a	0.569	0.0263
Adhr	0.568	0.0265
Osi16	0.568	0.0265
SelG	0.568	0.0265
CG10339	0.567	0.0268
CG10444	0.567	0.0268
CG1139	0.567	0.0268
CG17855	0.567	0.0268
CG2774	0.567	0.0268
Or30a	0.567	0.0268
Spn77Ba	0.567	0.0268
Ccn	0.566	0.0274
CG33061	0.566	0.0274
CG42375	0.566	0.0274
Nmdmc	0.566	0.0274
CG10483	0.565	0.0277
nab	0.565	0.0277
Oseg4	0.565	0.0277
CG18598	0.564	0.028
CG3121	0.564	0.028
CG34394	0.563	0.0282
lM4	0.563	0.0282
obst-J	0.563	0.0282
CG12054	0.562	0.0285
CG13604	0.562	0.0285
CG31030	0.562	0.0285
CG13344	0.561	0.0287
Or42a	0.561	0.0287
Updo	0.561	0.0287
CG3916	0.56	0.029
deltaCOP	0.56	0.029
Fmo-1	0.56	0.029
Gapdh2	0.56	0.029
CG1143	0.559	0.0294
CG31004	0.559	0.0294
CG5554	0.559	0.0294
Cpr49Ah	0.559	0.0294
Edg78E	0.559	0.0294
Mvl	0.559	0.0294
pburs	0.559	0.0294
ppk10	0.559	0.0294
Aats-val	0.558	0.0301
HP1b	0.558	0.0301
shot	0.558	0.0301

Gene Name	ERC Value	P-value
CG1572	0.557	0.0304
CG5614	0.557	0.0304
CG10286	0.555	0.0305
CG12428	0.555	0.0305
CG42331	0.555	0.0305
Or74a	0.555	0.0305
Osi1	0.555	0.0305
CG5873	0.554	0.031
CG6041	0.554	0.031
CG11836	0.553	0.0312
CG3209	0.553	0.0312
CG5321	0.553	0.0312
CG5435	0.553	0.0312
CG5602	0.553	0.0312
CG12436	0.552	0.0316
CG15353	0.552	0.0316
CG30274	0.552	0.0316
CG3376	0.552	0.0316
lack	0.552	0.0316
Sk1	0.552	0.0316
CG14636	0.551	0.0322
CG2736	0.551	0.0322
Dap160	0.551	0.0322
rost	0.551	0.0322
CG12964	0.55	0.0325
Mekk1	0.55	0.0325
bsf	0.549	0.0327
CG31105	0.549	0.0327
CG8586	0.549	0.0327
Mgat2	0.549	0.0327
Sp212	0.549	0.0327
Sodh-2	0.548	0.0332
CG15440	0.547	0.0332
CG31559	0.547	0.0332
CG4038	0.547	0.0332
krz	0.547	0.0332
Arc-p34	0.546	0.0336
CG13443	0.546	0.0336
CG14507	0.546	0.0336
CG17127	0.546	0.0336
CG31644	0.546	0.0336
CG5039	0.546	0.0336
PH4alphaNE	0.546	0.0336
Rab1	0.546	0.0336
alpha-Est3	0.545	0.0343
CG11926	0.545	0.0343
CG14062	0.545	0.0343
CG9314	0.545	0.0343
CG14221	0.544	0.0347
CG32972	0.544	0.0347
CG7236	0.544	0.0347
Edem2	0.544	0.0347
egr	0.544	0.0347
CG14500	0.543	0.0351
CG1889	0.543	0.0351
CG3546	0.543	0.0351

Gene Name	ERC Value	P-value
crq	0.543	0.0351
Unc-89	0.543	0.0351
CG6272	0.542	0.0356
CG7653	0.542	0.0356
CG8083	0.542	0.0356
CG9444	0.542	0.0356
RpS3	0.542	0.0356
CG14962	0.541	0.036
CG15536	0.541	0.036
CG17776	0.541	0.036
scaf6	0.541	0.036
CG17292	0.54	0.0364
CG42534	0.54	0.0364
CG7713	0.54	0.0364
CG9864	0.54	0.0364
Glycogenin	0.54	0.0364
Vha55	0.54	0.0364
CG14397	0.539	0.0369
CG5945	0.539	0.0369
Il(1)G0193	0.539	0.0369
Myo28B1	0.539	0.0369
Ork1	0.539	0.0369
pum	0.539	0.0369
sec63	0.539	0.0369
CG14352	0.538	0.0376
CG31665	0.538	0.0376
CG7906	0.538	0.0376
CG1126	0.537	0.0378
ens	0.537	0.0378
CG15740	0.536	0.038
CG1850	0.536	0.038
CG6709	0.536	0.038
Hdc	0.536	0.038
NitFhit	0.536	0.038
CG15422	0.535	0.0385
CG8888	0.535	0.0385
Spn6	0.535	0.0385
CG10910	0.534	0.0387
Cpr78Ca	0.534	0.0387
sdk	0.534	0.0387
CG10186	0.533	0.039
CG7497	0.533	0.039
danr	0.533	0.039
Dph5	0.533	0.039
Ela	0.533	0.039
CG32699	0.532	0.0395
Obp19a	0.532	0.0395
tgy	0.532	0.0395
mwh	0.531	0.0397
Oatp33Eb	0.531	0.0397
Osi19	0.531	0.0397
ppk6	0.531	0.0397
RpL21	0.531	0.0397
trc	0.531	0.0397
CG13603	0.53	0.0403
CG32230	0.53	0.0403

Gene Name	ERC Value	P-value
CG34194	0.53	0.0403
CG5045	0.53	0.0403
CG5969	0.53	0.0403
CG6279	0.53	0.0403
LvpH	0.53	0.0403
Poxm	0.53	0.0403
sals	0.53	0.0403
bnf	0.529	0.0411
CG10089	0.529	0.0411
CG13607	0.529	0.0411
CG15579	0.529	0.0411
CG13921	0.528	0.0414
CG6361	0.528	0.0414
CG7772	0.528	0.0414
neo	0.528	0.0414
pigs	0.528	0.0414
CG32299	0.527	0.0419
CG5002	0.527	0.0419
CG6403	0.527	0.0419
CG6938	0.527	0.0419
mlt	0.527	0.0419
CG34229	0.526	0.0423
CG6123	0.526	0.0423
Osi7	0.526	0.0423
CG9780	0.526	0.0423
Spn43Aa	0.526	0.0423
beat-Va	0.525	0.0428
CG10208	0.525	0.0428
CG1399	0.525	0.0428
CG2680	0.525	0.0428
CG4053	0.525	0.0428
CG6749	0.525	0.0428
yellow-d2	0.525	0.0428
CG31549	0.524	0.0434
CG7580	0.524	0.0434
Syx17	0.524	0.0434
CG11267	0.523	0.0437
CG14598	0.523	0.0437
CG6321	0.523	0.0437
Cyp6d5	0.523	0.0437
Gyc88E	0.523	0.0437
lrr7d	0.523	0.0437
CG17140	0.522	0.0442
CG42671	0.522	0.0442
CG5028	0.522	0.0442
CG5455	0.522	0.0442
CG6865	0.522	0.0442
CG8407	0.522	0.0442
And	0.521	0.0448
Catsup	0.521	0.0448
Gap69C	0.521	0.0448
sar1	0.521	0.0448
CG10132	0.52	0.0451
CG4484	0.52	0.0451
CG8550	0.52	0.0451
inaD	0.52	0.0451

Gene Name	ERC Value	P-value
Mpk2	0.52	0.0451
CG32068	0.519	0.0456
CG34462	0.519	0.0456
chp	0.519	0.0456
Obp44a	0.519	0.0456
Uro	0.519	0.0456
CG10804	0.518	0.046
CG17784	0.518	0.046
CG32119	0.518	0.046
CG9740	0.518	0.046
Vha68-2	0.518	0.046
CG6769	0.517	0.0465
Fbp2	0.517	0.0465
Ho	0.517	0.0465
lrr84a	0.517	0.0465
CG13064	0.516	0.0468
CG42322	0.516	0.0468
Or35a	0.516	0.0468
CG11370	0.515	0.0471
CG4586	0.515	0.0471
Zip3	0.515	0.0471
CG13836	0.513	0.0474
CG17119	0.513	0.0474
CG8008	0.513	0.0474
CG9780	0.513	0.0474
Or9a	0.513	0.0474
yrt	0.513	0.0474
CG14044	0.512	0.0479
CG14565	0.512	0.0479
CG6420	0.512	0.0479
CG6785	0.512	0.0479
Gr64a	0.512	0.0479
lrr75d	0.512	0.0479
CG10116	0.511	0.0485
CG17840	0.511	0.0485
CG3008	0.511	0.0485
CG3216	0.511	0.0485
CG33725	0.511	0.0485
CG33772	0.511	0.0485
CG4151	0.511	0.0485
CG6283	0.511	0.0485
TTL3A	0.511	0.0485
CG13693	0.51	0.0493
CG6425	0.51	0.0493
CG30280	0.509	0.0495
CG34144	0.509	0.0495
CG8866	0.509	0.0495
LanB1	0.509	0.0495
lyn	0.509	0.0495
CG3523	0.508	0.0499
Klp98A	0.508	0.0499
mRpl17	0.508	0.0499
Pfrx	0.508	0.0499
CG11342	0.507	0.0503
CG30122	0.507	0.0503
CG4866	0.507	0.0503

Table 6.S5 Continued

Gene Name	ERC Value	P-value
CREG	0.507	0.0503
Cyp311a1	0.507	0.0503
Obp56d	0.507	0.0503
CG14455	0.506	0.0508
CG14606	0.506	0.0508
CG3703	0.506	0.0508
ppk21	0.506	0.0508
CG10353	0.505	0.0512
CG15537	0.505	0.0512
CG33639	0.505	0.0512
CG9287	0.505	0.0512
Con	0.505	0.0512
Ir21a	0.505	0.0512
VhaPPA1-2	0.505	0.0512
CG14642	0.504	0.0518
Atx2	0.503	0.0519
CG17662	0.503	0.0519
CG3505	0.503	0.0519
CG4729	0.503	0.0519
CG7201	0.503	0.0519
Cpr67Fb	0.503	0.0519
dnt	0.503	0.0519
Esyt2	0.503	0.0519
mRpL45	0.503	0.0519
aph-1	0.502	0.0527
CalpB	0.502	0.0527
CG34376	0.502	0.0527
Chit	0.502	0.0527
jagn	0.502	0.0527
RpS5a	0.502	0.0527
CG13887	0.501	0.0532
CG16716	0.501	0.0532
CG7079	0.501	0.0532
Cpr65Eb	0.501	0.0532
MtnB	0.501	0.0532
CG10869	0.5	0.0537
CG17124	0.5	0.0537
CG5646	0.5	0.0537
gb	0.5	0.0537
nrn3	0.5	0.0537
CG11353	0.499	0.0541
CG5144	0.499	0.0541
CG6793	0.499	0.0541
ea	0.499	0.0541
Ir8a	0.499	0.0541
Akap200	0.498	0.0546
CG13872	0.498	0.0546
CG4229	0.498	0.0546
PKD	0.498	0.0546
ref(2)P	0.498	0.0546
alpha-Cat	0.497	0.055
CG15615	0.497	0.055
CG18539	0.497	0.055
CG33627	0.497	0.055
CG4465	0.497	0.055
Fen1	0.497	0.055

Gene Name	ERC Value	P-value
Nha1	0.497	0.055
Spn	0.497	0.055
CG8800	0.496	0.0558
Dcp1	0.496	0.0558
Hsp26	0.496	0.0558
CG1275	0.495	0.056
Obp99b	0.495	0.056
Past1	0.495	0.056
Srp14	0.495	0.056
Vha100-4	0.495	0.056
CG13309	0.494	0.0565
CG14199	0.494	0.0565
CG15362	0.494	0.0565
Chi	0.494	0.0565
Npc2b	0.494	0.0565
PGRP-LF	0.494	0.0565
Smg5	0.494	0.0565
alpha-Estf6	0.493	0.0571
CG13575	0.493	0.0571
CG15525	0.493	0.0571
CG17121	0.493	0.0571
CG9812	0.493	0.0571
CG9981	0.493	0.0571
Set	0.493	0.0571
Src64B	0.493	0.0571
CG7203	0.492	0.0578
DF31	0.492	0.0578
Arr2	0.491	0.058
Atg8b	0.491	0.058
CG11652	0.491	0.058
CG12861	0.491	0.058
CG3077	0.491	0.058
CG33774	0.491	0.058
Obp56c	0.491	0.058
ppk14	0.491	0.058
Spn100A	0.491	0.058
CG3476	0.49	0.0588
Tina-1	0.49	0.0588
ACXC	0.489	0.059
CG18641	0.489	0.059
CG31019	0.489	0.059
CG6543	0.489	0.059
CG8596	0.489	0.059
CG9139	0.489	0.059
cola	0.489	0.059
dan	0.489	0.059
Dnz1	0.489	0.059
en	0.489	0.059
Fer2	0.489	0.059
Ncc69	0.489	0.059
Osi3	0.489	0.059
Ugt36Ba	0.489	0.059
CG13133	0.488	0.0603
CG15068	0.488	0.0603
CG2938	0.488	0.0603
CG3590	0.488	0.0603

Gene Name	ERC Value	P-value
CG7900	0.488	0.0603
CG15922	0.487	0.0607
CG30010	0.487	0.0607
CG30339	0.487	0.0607
CG31294	0.487	0.0607
CG9339	0.487	0.0607
Lsp1gamma	0.487	0.0607
Whamy	0.487	0.0607
CG14239	0.486	0.0614
CG1827	0.486	0.0614
CG31111	0.486	0.0614
CG3501	0.486	0.0614
coif	0.486	0.0614
Ady43A	0.485	0.0618
CG11899	0.485	0.0618
CG14446	0.485	0.0618
CG18519	0.485	0.0618
CG9416	0.485	0.0618
Glut3	0.485	0.0618
lgs	0.485	0.0618
Tal	0.485	0.0618
CG12811	0.484	0.0625
CG17544	0.484	0.0625
CG31937	0.484	0.0625
CG7084	0.484	0.0625
comm3	0.484	0.0625
LanA	0.484	0.0625
woc	0.484	0.0625
CG14872	0.483	0.0632
CG15589	0.483	0.0632
CG18507	0.483	0.0632
CG2964	0.483	0.0632
CG32668	0.483	0.0632
CG32686	0.483	0.0632
CG34179	0.483	0.0632
CG11843	0.482	0.0638
CG14259	0.482	0.0638
CG3769	0.482	0.0638
Meics	0.482	0.0638
Oscillin	0.482	0.0638
ran	0.482	0.0638
sesB	0.482	0.0638
zormin	0.482	0.0638
Abd-B	0.481	0.0645
CG11148	0.481	0.0645
CG11200	0.481	0.0645
CG18367	0.481	0.0645
CG11349	0.48	0.0649
CG15270	0.48	0.0649
CG32238	0.48	0.0649
Osi15	0.48	0.0649
Pcp	0.48	0.0649
ATPsyn-b	0.479	0.0653
CG11444	0.479	0.0653
CG17075	0.479	0.0653
CG4962	0.479	0.0653

Gene Name	ERC Value	P-value
Lcp65Ac	0.479	0.0653
Mov34	0.479	0.0653
MtnC	0.479	0.0653
CG14369	0.478	0.0659
CG15695	0.478	0.0659
CG34159	0.478	0.0659
Pur-alpha	0.478	0.0659
TwdIV	0.478	0.0659
CG14609	0.477	0.0664
CG14905	0.477	0.0664
CG30324	0.477	0.0664
CG5023	0.477	0.0664
ECSIT	0.477	0.0664
RpS11	0.477	0.0664
CG18745	0.476	0.0669
CG4267	0.476	0.0669
CG6125	0.476	0.0669
GalNac-T1	0.476	0.0669
Ac76E	0.475	0.0673
CG11760	0.475	0.0673
CG12795	0.475	0.0673
lpk1	0.475	0.0673
shark	0.475	0.0673
CG11162	0.474	0.0677
CG16718	0.474	0.0677
CG34133	0.474	0.0677
LanA	0.474	0.0677
Tsp42Eq	0.474	0.0677
CG1636	0.473	0.0682
CG31125	0.473	0.0682
CG4213	0.473	0.0682
CG8032	0.473	0.0682
fd64A	0.473	0.0682
MED6	0.473	0.0682
mRpL2	0.473	0.0682
RpL3	0.473	0.0682
SPE	0.473	0.0682
CG13312	0.472	0.0689
CG15773	0.472	0.0689
CG33301	0.472	0.0689
CG7442	0.472	0.0689
mRpS17	0.472	0.0689
CG3163	0.471	0.0695
Nhe2	0.471	0.0695
CG11898	0.47	0.0696
CG4186	0.47	0.0696
CG42449	0.47	0.0696
CG4623	0.47	0.0696
mol	0.47	0.0696
sas	0.47	0.0696
CG13795	0.469	0.0702
endoB	0.469	0.0702
GstE9	0.469	0.0702
CG1077	0.468	0.0705
CG13544	0.468	0.0705
CG17639	0.468	0.0705

Gene Name	ERC Value	P-value
CG30463	0.468	0.0705
CG42489	0.468	0.0705
CG9486	0.468	0.0705
Cp18	0.468	0.0705
DNApol-delta	0.468	0.0705
Drip	0.468	0.0705
Gp93	0.468	0.0705
CG16886	0.467	0.0714
CG5780	0.467	0.0714
CG7145	0.467	0.0714
Cpr47Ec	0.467	0.0714
Pdp1	0.467	0.0714
W	0.467	0.0714
CG4598	0.466	0.0719
CG7920	0.466	0.0719
Cpr30F	0.466	0.0719
iPLA2-VIA	0.466	0.0719
mdy	0.466	0.0719
Tsc1	0.466	0.0719
yellow-e	0.466	0.0719
CG30502	0.465	0.0725
CG8675	0.465	0.0725
oc	0.465	0.0725
scrt	0.465	0.0725
XRCC1	0.465	0.0725
Arr1	0.464	0.073
Best1	0.464	0.073
Bka	0.464	0.073
CG17646	0.464	0.073
CG9192	0.464	0.073
nimC4	0.464	0.073
CG3004	0.463	0.0735
CG5130	0.463	0.0735
CG7708	0.463	0.0735
hoe2	0.463	0.0735
Rappap1	0.463	0.0735
ScpX	0.463	0.0735
CG13442	0.462	0.0741
CG7603	0.462	0.0741
Fas2	0.462	0.0741
p38b	0.462	0.0741
CG10237	0.461	0.0744
CG1319	0.461	0.0744
CG13822	0.461	0.0744
CG17271	0.461	0.0744
CG31233	0.461	0.0744
CG32572	0.461	0.0744
CG42505	0.461	0.0744
CG6974	0.461	0.0744
CG7191	0.461	0.0744
Ero1L	0.461	0.0744
PHDP	0.461	0.0744
stai	0.461	0.0744
CG9993	0.46	0.0755
Nep5	0.46	0.0755
Sam-S	0.46	0.0755

Table 6.S5 Continued

Gene Name	ERC Value	P-value
<i>su(s)</i>	0.46	0.0755
<i>Vhl</i>	0.46	0.0755
<i>CG15614</i>	0.459	0.0759
<i>CG34349</i>	0.459	0.0759
<i>CG5938</i>	0.459	0.0759
<i>CG7337</i>	0.459	0.0759
<i>CG9184</i>	0.459	0.0759
<i>mbf1</i>	0.459	0.0759
<i>CG4301</i>	0.458	0.0765
<i>CG4955</i>	0.458	0.0765
<i>CG8607</i>	0.458	0.0765
<i>lolal</i>	0.458	0.0765
<i>primo-1</i>	0.458	0.0765
<i>puc</i>	0.458	0.0765
<i>CG17349</i>	0.457	0.077
<i>dnk</i>	0.457	0.077
<i>fusl</i>	0.457	0.077
<i>GstD9</i>	0.457	0.077
<i>pr</i>	0.457	0.077
<i>Bk29A</i>	0.456	0.0775
<i>CG2543</i>	0.456	0.0775
<i>CG32556</i>	0.456	0.0775
<i>CG8353</i>	0.456	0.0775
<i>ppk23</i>	0.456	0.0775
<i>sno</i>	0.456	0.0775
<i>CG13077</i>	0.455	0.078
<i>CG13578</i>	0.455	0.078
<i>CG6767</i>	0.455	0.078
<i>Ets65A</i>	0.455	0.078
<i>plinta</i>	0.455	0.078
<i>wus</i>	0.455	0.078
<i>CG8303</i>	0.454	0.0786
<i>ldgf4</i>	0.454	0.0786
<i>pyd</i>	0.454	0.0786
<i>PyK</i>	0.454	0.0786
<i>rho-4</i>	0.454	0.0786
<i>ric8a</i>	0.454	0.0786
<i>CG42390</i>	0.453	0.0791
<i>Cpr49Ad</i>	0.453	0.0791
<i>pex13</i>	0.453	0.0791
<i>CG14200</i>	0.452	0.0794
<i>ey</i>	0.452	0.0794
<i>moody</i>	0.452	0.0794
<i>CG12011</i>	0.451	0.0796
<i>CG34284</i>	0.451	0.0796
<i>dia</i>	0.451	0.0796
<i>CG16836</i>	0.45	0.0799
<i>CG5458</i>	0.45	0.0799
<i>CG5597</i>	0.45	0.0799
<i>CG8214</i>	0.45	0.0799
<i>CG14795</i>	0.449	0.0803
<i>eag</i>	0.449	0.0803
<i>ns4</i>	0.449	0.0803
<i>Or67d</i>	0.449	0.0803
<i>CG13510</i>	0.448	0.0806
<i>CG5958</i>	0.448	0.0806

Gene Name	ERC Value	P-value
<i>CG8661</i>	0.448	0.0806
<i>mars</i>	0.448	0.0806
<i>Nc</i>	0.448	0.0806
<i>Pglym78</i>	0.448	0.0806
<i>CG5386</i>	0.447	0.0812
<i>Cht5</i>	0.447	0.0812
<i>CG1246</i>	0.446	0.0814
<i>CG31347</i>	0.446	0.0814
<i>CheA87a</i>	0.446	0.0814
<i>ci</i>	0.446	0.0814
<i>CG11820</i>	0.445	0.0817
<i>CG13075</i>	0.445	0.0817
<i>CG14518</i>	0.445	0.0817
<i>CG7997</i>	0.445	0.0817
<i>l(1)G0136</i>	0.445	0.0817
<i>Or85f</i>	0.445	0.0817
<i>CG32631</i>	0.444	0.0823
<i>CG5500</i>	0.444	0.0823
<i>CG9222</i>	0.444	0.0823
<i>Bk2</i>	0.444	0.0823
<i>ninaD</i>	0.444	0.0823
<i>Pbgs</i>	0.444	0.0823
<i>sut1</i>	0.444	0.0823
<i>CG10660</i>	0.443	0.0829
<i>CG14298</i>	0.443	0.0829
<i>CG14767</i>	0.443	0.0829
<i>CG14961</i>	0.443	0.0829
<i>CG1698</i>	0.443	0.0829
<i>CG17082</i>	0.443	0.0829
<i>CG32150</i>	0.443	0.0829
<i>CG32407</i>	0.443	0.0829
<i>Cpr51A</i>	0.443	0.0829
<i>Mdr50</i>	0.443	0.0829
<i>CG11120</i>	0.442	0.0838
<i>CG31199</i>	0.442	0.0838
<i>CG4302</i>	0.442	0.0838
<i>dsd</i>	0.442	0.0838
<i>CG13631</i>	0.441	0.0841
<i>CG13856</i>	0.441	0.0841
<i>CG16779</i>	0.441	0.0841
<i>CG32263</i>	0.441	0.0841
<i>hipk</i>	0.441	0.0841
<i>CG13318</i>	0.44	0.0846
<i>CG30427</i>	0.44	0.0846
<i>CG31091</i>	0.44	0.0846
<i>CG42269</i>	0.44	0.0846
<i>Cyp312a1</i>	0.44	0.0846
<i>E23</i>	0.44	0.0846
<i>Or47b</i>	0.44	0.0846
<i>Pif1B</i>	0.44	0.0846
<i>ppk19</i>	0.44	0.0846
<i>sing</i>	0.44	0.0846
<i>swa</i>	0.44	0.0846
<i>Vha68-1</i>	0.44	0.0846
<i>CG14070</i>	0.439	0.0857
<i>CG16985</i>	0.439	0.0857

Gene Name	ERC Value	P-value
<i>CG17404</i>	0.439	0.0857
<i>CG18404</i>	0.439	0.0857
<i>CG31548</i>	0.439	0.0857
<i>CG8910</i>	0.439	0.0857
<i>miple2</i>	0.439	0.0857
<i>cag</i>	0.438	0.0863
<i>CAH2</i>	0.438	0.0863
<i>CG11221</i>	0.438	0.0863
<i>CG13712</i>	0.438	0.0863
<i>CG18609</i>	0.438	0.0863
<i>CG14127</i>	0.437	0.0868
<i>CG14740</i>	0.437	0.0868
<i>CG30172</i>	0.437	0.0868
<i>CG31248</i>	0.437	0.0868
<i>CG8272</i>	0.437	0.0868
<i>mRpS26</i>	0.437	0.0868
<i>Rab10</i>	0.437	0.0868
<i>Tsp5D</i>	0.437	0.0868
<i>CG13437</i>	0.436	0.0875
<i>CG3156</i>	0.436	0.0875
<i>CG31675</i>	0.436	0.0875
<i>CG33558</i>	0.436	0.0875
<i>CG6966</i>	0.436	0.0875
<i>Cyp4s3</i>	0.436	0.0875
<i>Hexo2</i>	0.436	0.0875
<i>RpS18</i>	0.436	0.0875
<i>CG5010</i>	0.435	0.0882
<i>Cyp4d14</i>	0.435	0.0882
<i>Eip63F-1</i>	0.435	0.0882
<i>Ca-beta</i>	0.434	0.0885
<i>CG11210</i>	0.434	0.0885
<i>CG1648</i>	0.434	0.0885
<i>CG30431</i>	0.434	0.0885
<i>comt</i>	0.434	0.0885
<i>Cpr78Cb</i>	0.434	0.0885
<i>lpp</i>	0.434	0.0885
<i>Mlc2</i>	0.434	0.0885
<i>yin</i>	0.434	0.0885
<i>CG10738</i>	0.433	0.0893
<i>CG18659</i>	0.433	0.0893
<i>CG32483</i>	0.433	0.0893
<i>l(1)G0156</i>	0.433	0.0893
<i>star1</i>	0.433	0.0893
<i>Caix</i>	0.432	0.0897
<i>CG10973</i>	0.432	0.0897
<i>CG15111</i>	0.432	0.0897
<i>CG31075</i>	0.432	0.0897
<i>CG9921</i>	0.432	0.0897
<i>fd19B</i>	0.432	0.0897
<i>inv</i>	0.432	0.0897
<i>RpL10Ab</i>	0.432	0.0897
<i>sing</i>	0.432	0.0897
<i>Tao-1</i>	0.432	0.0897
<i>Cad99C</i>	0.431	0.0906
<i>CG10470</i>	0.431	0.0906
<i>CG13506</i>	0.431	0.0906

Gene Name	ERC Value	P-value
<i>CG14315</i>	0.431	0.0906
<i>CG32544</i>	0.431	0.0906
<i>CG34391</i>	0.431	0.0906
<i>CG6675</i>	0.431	0.0906
<i>CG8791</i>	0.431	0.0906
<i>CG8834</i>	0.431	0.0906
<i>Sox102F</i>	0.431	0.0906
<i>Top2</i>	0.431	0.0906
<i>tm</i>	0.431	0.0906
<i>CG14042</i>	0.43	0.0917
<i>CG1441</i>	0.43	0.0917
<i>onecut</i>	0.43	0.0917
<i>CG13796</i>	0.429	0.092
<i>CG4313</i>	0.429	0.092
<i>CG7794</i>	0.429	0.092
<i>Cp15</i>	0.429	0.092
<i>Cyp317a1</i>	0.429	0.092
<i>E(bx)</i>	0.429	0.092
<i>plx</i>	0.429	0.092
<i>Pxd</i>	0.429	0.092
<i>Toll-9</i>	0.429	0.092
<i>CG12910</i>	0.428	0.0928
<i>CG31998</i>	0.428	0.0928
<i>Gr97a</i>	0.428	0.0928
<i>Snx6</i>	0.428	0.0928
<i>CG10035</i>	0.427	0.0932
<i>CG14375</i>	0.427	0.0932
<i>CG33993</i>	0.427	0.0932
<i>CG6287</i>	0.427	0.0932
<i>h</i>	0.427	0.0932
<i>CG10748</i>	0.426	0.0936
<i>CG12400</i>	0.426	0.0936
<i>CG5323</i>	0.426	0.0936
<i>CG5591</i>	0.426	0.0936
<i>debel</i>	0.426	0.0936
<i>Cctgamma3</i>	0.425	0.0941
<i>CG13473</i>	0.425	0.0941
<i>lrl00a</i>	0.425	0.0941
<i>Lsp2</i>	0.425	0.0941
<i>Nmda1</i>	0.425	0.0941
<i>skd</i>	0.425	0.0941
<i>slow</i>	0.425	0.0941
<i>spz5</i>	0.425	0.0941
<i>Thiolase</i>	0.425	0.0941
<i>Aats-ser</i>	0.424	0.0949
<i>arg</i>	0.424	0.0949
<i>CG15564</i>	0.424	0.0949
<i>CG18631</i>	0.424	0.0949
<i>CG9509</i>	0.424	0.0949
<i>Keap1</i>	0.424	0.0949
<i>m</i>	0.424	0.0949
<i>me31B</i>	0.424	0.0949
<i>tefu</i>	0.424	0.0949
<i>CG13054</i>	0.423	0.0957
<i>CG13627</i>	0.423	0.0957
<i>CG13640</i>	0.423	0.0957

Gene Name	ERC Value	P-value
<i>CG8907</i>	0.423	0.0957
<i>Ckialpha</i>	0.423	0.0957
<i>EifSec</i>	0.423	0.0957
<i>CG2962</i>	0.422	0.0962
<i>CG34210</i>	0.422	0.0962
<i>CG5246</i>	0.422	0.0962
<i>CG8861</i>	0.422	0.0962
<i>Gpo-1</i>	0.422	0.0962
<i>CG11320</i>	0.421	0.0967
<i>CG13120</i>	0.421	0.0967
<i>CG31800</i>	0.421	0.0967
<i>CG6765</i>	0.421	0.0967
<i>fray</i>	0.421	0.0967
<i>app</i>	0.42	0.0971
<i>CG14043</i>	0.42	0.0971
<i>CG3817</i>	0.42	0.0971
<i>CG9940</i>	0.42	0.0971
<i>eEF1delta</i>	0.42	0.0971
<i>Pdf</i>	0.42	0.0971
<i>CG14380</i>	0.419	0.0977
<i>CG31226</i>	0.419	0.0977
<i>CG5932</i>	0.419	0.0977
<i>CG6904</i>	0.419	0.0977
<i>Oatp26F</i>	0.419	0.0977
<i>Rab27</i>	0.419	0.0977
<i>Trh</i>	0.419	0.0977
<i>Adgf-E</i>	0.418	0.0983
<i>CAP</i>	0.418	0.0983
<i>CG14687</i>	0.418	0.0983
<i>CG15199</i>	0.418	0.0983
<i>CG15824</i>	0.418	0.0983
<i>CG30120</i>	0.418	0.0983
<i>CG4049</i>	0.418	0.0983
<i>CG6435</i>	0.418	0.0983
<i>CG6915</i>	0.418	0.0983
<i>l(3)mbn</i>	0.418	0.0983
<i>Nf1</i>	0.418	0.0983
<i>CG32564</i>	0.417	0.0993
<i>CG7970</i>	0.417	0.0993
<i>cyc</i>	0.417	0.0993
<i>Fmf</i>	0.417	0.0993
<i>lce</i>	0.417	0.0993
<i>lds</i>	0.417	0.0993
<i>Npc2c</i>	0.417	0.0993
<i>pasha</i>	0.417	0.0993
<i>CG10795</i>	0.416	0.1
<i>CG11426</i>	0.416	0.1
<i>CG5038</i>	0.416	0.1
<i>CG8343</i>	0.416	0.1
<i>Prestin</i>	0.416	0.1

Table 6.S6 - Top Genes ERC values for *mei-9* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG15172	0.84	0.0001
CG4587	0.83	0.0002
CG2931	0.826	0.0003
CG31815	0.823	0.0004
CG3301	0.805	0.0005
Ac3	0.803	0.0005
CG15035	0.798	0.0006
CG3645	0.793	0.0007
mRpl21	0.791	0.0008
CG12609	0.78	0.0009
Cp15	0.78	0.0009
CG3305	0.77	0.0011
hkb	0.77	0.0011
Syt4	0.768	0.0013
CG14451	0.764	0.0014
CG31682	0.762	0.0014
CG31926	0.738	0.0015
CG9879	0.735	0.0016
CG7650	0.726	0.0017
CG1792	0.724	0.0018
spen	0.723	0.0019
CG31482	0.719	0.002
stnB	0.717	0.0021
Prosbeta3	0.711	0.0022
Klf3C	0.707	0.0023
Tango7	0.706	0.0023
Cap	0.705	0.0024
CG15130	0.702	0.0025
CG17490	0.702	0.0025
CG1074	0.701	0.0027
Sox100B	0.701	0.0027
CG33178	0.7	0.0029
disco-r	0.698	0.003
CG13862	0.695	0.0031
CG12994	0.694	0.0032
ms(3)K81	0.687	0.0032
trm	0.685	0.0033
CG8677	0.681	0.0034
CG30008	0.679	0.0035
SMC1	0.679	0.0035
CG5003	0.677	0.0037
CG5431	0.676	0.0038
CG6972	0.674	0.0039
CG7824	0.674	0.0039
CG2807	0.672	0.0041
CG8187	0.672	0.0041
Drep-4	0.672	0.0041
CG4896	0.671	0.0043
Obp8a	0.671	0.0043
sax	0.67	0.0045
CG11906	0.667	0.0046
CG4115	0.667	0.0046
dsf	0.666	0.0048
FLASH	0.664	0.0049
TllfBpeta	0.662	0.005
CG14739	0.661	0.005

Gene Name	ERC Value	P-value
<i>llp1</i>	0.661	0.005
<i>LSm7</i>	0.66	0.0052
<i>tef</i>	0.66	0.0052
<i>nompB</i>	0.659	0.0054
<i>Tbp-1</i>	0.659	0.0054
<i>RpL30</i>	0.658	0.0056
<i>Acyp</i>	0.657	0.0057
<i>CG18234</i>	0.657	0.0057
<i>CG31777</i>	0.657	0.0057
<i>CG32354</i>	0.657	0.0057
<i>pcs</i>	0.657	0.0057
<i>CG32344</i>	0.656	0.0061
<i>betaTub60D</i>	0.655	0.0062
<i>RhoL</i>	0.655	0.0062
<i>FK506-bp1</i>	0.653	0.0064
<i>[[2]05714</i>	0.653	0.0064
<i>CG13362</i>	0.652	0.0066
<i>CG9795</i>	0.652	0.0066
<i>CG2790</i>	0.651	0.0068
<i>Su[var]2-10</i>	0.651	0.0068
<i>CG5214</i>	0.65	0.0069
<i>CG9346</i>	0.65	0.0069
<i>CG8960</i>	0.647	0.0071
<i>CG9776</i>	0.647	0.0071
<i>CG42358</i>	0.646	0.0073
<i>vir-1</i>	0.646	0.0073
<i>CG7829</i>	0.644	0.0075
<i>growl</i>	0.644	0.0075
<i>aux</i>	0.643	0.0077
<i>CG10694</i>	0.643	0.0077
<i>CG11837</i>	0.643	0.0077
<i>CG17883</i>	0.643	0.0077
<i>Ric</i>	0.643	0.0077
<i>CG15571</i>	0.642	0.0081
<i>CG13376</i>	0.64	0.0082
<i>CG17802</i>	0.64	0.0082
<i>Ccap</i>	0.639	0.0084
<i>Orc1</i>	0.639	0.0084
<i>Rrp42</i>	0.639	0.0084
<i>Trxr-2</i>	0.638	0.0086
<i>CG4164</i>	0.637	0.0087
<i>Cpr76Ba</i>	0.637	0.0087
<i>CG7530</i>	0.632	0.0089
<i>Spf45</i>	0.632	0.0089
<i>CG32712</i>	0.631	0.0091
<i>CG7707</i>	0.631	0.0091
<i>fog</i>	0.631	0.0091
<i>Pp2B-14D</i>	0.631	0.0091
<i>CG9723</i>	0.63	0.0095
<i>CG10459</i>	0.629	0.0095
<i>Pvf2</i>	0.629	0.0095
<i>CG1394</i>	0.627	0.0097
<i>CCKLR-17D</i>	0.626	0.0098
<i>CG8501</i>	0.626	0.0098
<i>dUTPase</i>	0.626	0.0098
<i>CG33288</i>	0.625	0.0101

Gene Name	ERC Value	P-value
<i>CG7694</i>	0.624	0.0102
<i>CG8141</i>	0.624	0.0102
<i>HLHmdelta</i>	0.624	0.0102
<i>cid</i>	0.623	0.0105
<i>Spn43Ad</i>	0.622	0.0105
<i>CG14482</i>	0.621	0.0106
<i>CG3191</i>	0.621	0.0106
<i>Tim17b1</i>	0.621	0.0106
<i>Rsf1</i>	0.62	0.0109
<i>CG14570</i>	0.619	0.011
<i>CG17168</i>	0.619	0.011
<i>CG42346</i>	0.619	0.011
<i>Cyp305a1</i>	0.619	0.011
<i>CG14341</i>	0.617	0.0114
<i>Dp1</i>	0.617	0.0114
<i>CG40351</i>	0.616	0.0115
<i>CG9953</i>	0.615	0.0116
<i>mRpl34</i>	0.613	0.0117
<i>nuf</i>	0.612	0.0118
<i>Tom34</i>	0.612	0.0118
<i>CG11577</i>	0.61	0.012
<i>CG1427</i>	0.61	0.012
<i>CG5515</i>	0.609	0.0122
<i>CG17494</i>	0.607	0.0123
<i>CG6418</i>	0.607	0.0123
<i>CG8641</i>	0.607	0.0123
<i>CG15863</i>	0.606	0.0125
<i>CG3651</i>	0.606	0.0125
<i>CG6739</i>	0.606	0.0125
<i>CG13026</i>	0.605	0.0128
<i>CG30007</i>	0.605	0.0128
<i>PpD3</i>	0.605	0.0128
<i>CG12126</i>	0.604	0.0131
<i>CG9636</i>	0.604	0.0131
<i>beat-lb</i>	0.603	0.0132
<i>CG14316</i>	0.603	0.0132
<i>CG16970</i>	0.603	0.0132
<i>CG5199</i>	0.603	0.0132
<i>CG16957</i>	0.602	0.0136
<i>CG9804</i>	0.602	0.0136
<i>fax</i>	0.602	0.0136
<i>GlcAT-I</i>	0.602	0.0136
<i>Drep-3</i>	0.601	0.014
<i>CG15028</i>	0.6	0.0141
<i>Sec61gamm</i>	0.6	0.0141
<i>ttm3</i>	0.6	0.0141
<i>RhoGAP71E</i>	0.599	0.0143
<i>Tsp39D</i>	0.598	0.0144
<i>CG15124</i>	0.597	0.0145
<i>CG17154</i>	0.597	0.0145
<i>CG8289</i>	0.597	0.0145
<i>CG8726</i>	0.597	0.0145
<i>tio</i>	0.597	0.0145
<i>CG9640</i>	0.595	0.015
<i>Flo</i>	0.595	0.015
<i>CG13876</i>	0.594	0.0151

Gene Name	ERC Value	P-value
<i>CG15443</i>	0.594	0.0151
<i>Nnp-1</i>	0.594	0.0151
<i>Vm26Ab</i>	0.593	0.0154
<i>CG18011</i>	0.592	0.0155
<i>CG30280</i>	0.592	0.0155
<i>CG4666</i>	0.592	0.0155
<i>ninaE</i>	0.592	0.0155
<i>Dref</i>	0.591	0.0159
<i>Atf6</i>	0.59	0.0159
<i>koi</i>	0.59	0.0159
<i>LSm1</i>	0.59	0.0159
<i>ato</i>	0.589	0.0162
<i>CG3626</i>	0.589	0.0162
<i>Spargel</i>	0.589	0.0162
<i>Nuf2</i>	0.588	0.0165
<i>CG32945</i>	0.587	0.0166
<i>Rpn9</i>	0.587	0.0166
<i>Cks85A</i>	0.586	0.0168
<i>Pink1</i>	0.586	0.0168
<i>CG1208</i>	0.585	0.0169
<i>CG13692</i>	0.585	0.0169
<i>CG14331</i>	0.585	0.0169
<i>CG9691</i>	0.585	0.0169
<i>Or59c</i>	0.585	0.0169
<i>CG11555</i>	0.584	0.0174
<i>CG31301</i>	0.584	0.0174
<i>elfF4E-7</i>	0.584	0.0174
<i>CG14230</i>	0.582	0.0177
<i>CG8550</i>	0.582	0.0177
<i>CG11412</i>	0.581	0.0178
<i>CG9125</i>	0.58	0.0179
<i>mtacp1</i>	0.579	0.018
<i>Neurochond</i>	0.579	0.018
<i>Ranbp9</i>	0.579	0.018
<i>ac</i>	0.578	0.0183
<i>CG10399</i>	0.578	0.0183
<i>Dent1</i>	0.578	0.0183
<i>BEAF-32</i>	0.577	0.0186
<i>CG31959</i>	0.577	0.0186
<i>CG14085</i>	0.576	0.0187
<i>Roc1b</i>	0.576	0.0187
<i>DNApol-alpha</i>	0.575	0.0189
<i>EFSc</i>	0.575	0.0189
<i>alpha4GT1</i>	0.574	0.0191
<i>CG11327</i>	0.574	0.0191
<i>CG13343</i>	0.574	0.0191
<i>CG5955</i>	0.574	0.0191
<i>CycK</i>	0.574	0.0191
<i>CG7265</i>	0.572	0.0195
<i>Dpy-30L1</i>	0.572	0.0195
<i>CG3605</i>	0.571	0.0197
<i>CG11617</i>	0.569	0.0198
<i>CcapR</i>	0.568	0.0199
<i>CG51509</i>	0.568	0.0199
<i>CG34116</i>	0.568	0.0199
<i>swa</i>	0.568	0.0199

Gene Name	ERC Value	P-value
<i>CG40042</i>	0.567	0.0203
<i>CG9426</i>	0.567	0.0203
<i>irc</i>	0.566	0.0205
<i>CG1090</i>	0.565	0.0205
<i>CG10283</i>	0.564	0.0206
<i>CG12206</i>	0.564	0.0206
<i>CG6766</i>	0.564	0.0206
<i>dre4</i>	0.564	0.0206
<i>Gmd</i>	0.564	0.0206
<i>CG10414</i>	0.563	0.0211
<i>for</i>	0.563	0.0211
<i>CG14050</i>	0.562	0.0213
<i>CG8408</i>	0.562	0.0213
<i>piwi</i>	0.562	0.0213
<i>14-3-3[m]</i>	0.561	0.0215
<i>CG12942</i>	0.56	0.0216
<i>CG6540</i>	0.56	0.0216
<i>kune</i>	0.559	0.0218
Nnfta	0.558	0.0219
<i>CG11227</i>	0.557	0.022
<i>CG34305</i>	0.557	0.022
<i>CG5805</i>	0.557	0.022
<i>CG8078</i>	0.557	0.022
<i>CG33489</i>	0.556	0.0223
<i>CG3631</i>	0.556	0.0223
<i>CG6808</i>	0.556	0.0223
<i>CG15445</i>	0.555	0.0226
<i>CG34331</i>	0.554	0.0227
<i>CG5204</i>	0.554	0.0227
<i>Mcm10</i>	0.554	0.0227
<i>Pros26</i>	0.554	0.0227
<i>Tm2</i>	0.554	0.0227
<i>Dhc64C</i>	0.553	0.0232
<i>Npjp1</i>	0.553	0.0232
<i>CG15881</i>	0.552	0.0233
<i>CG14650</i>	0.551	0.0234
<i>CG12945</i>	0.55	0.0235
<i>CG15262</i>	0.55	0.0235
<i>CG17841</i>	0.549	0.0237
<i>CG2051</i>	0.548	0.0238
<i>CG42258</i>	0.548	0.0238
<i>Rheb</i>	0.548	0.0238
<i>CG10075</i>	0.547	0.0241
<i>CG6136</i>	0.547	0.0241
<i>CG6142</i>	0.547	0.0241
<i>DNApol-alpha</i>	0.547	0.0241
<i>CdsA</i>	0.546	0.0244
<i>CG6470</i>	0.546	0.0244
<i>CG13375</i>	0.545	0.0246
<i>CG2694</i>	0.545	0.0246
<i>CG42748</i>	0.545	0.0246
<i>CG5322</i>	0.545	0.0246
<i>CG9109</i>	0.545	0.0246
<i>CG9510</i>	0.545	0.0246
<i>Gprk2</i>	0.545	0.0246
<i>CG14106</i>	0.544	0.0252

Table 6.S6 Continued

Gene Name	ERC Value	P-value
CG15116	0.544	0.0252
CG18806	0.544	0.0252
<i>lds</i>	0.544	0.0252
CG14718	0.543	0.0256
CG8089	0.543	0.0256
U2A	0.543	0.0256
VGlut	0.543	0.0256
CG13897	0.542	0.0259
CG7427	0.542	0.0259
PGRP-LE	0.542	0.0259
CG13287	0.541	0.0262
CG2247	0.541	0.0262
<i>Chrac-14</i>	0.541	0.0262
CG15219	0.54	0.0265
CG7837	0.539	0.0266
CG8565	0.539	0.0266
CG12007	0.538	0.0268
CG12395	0.537	0.0268
CG18858	0.537	0.0268
CG42377	0.536	0.027
CG8366	0.536	0.027
CG13476	0.535	0.0272
CG2091	0.535	0.0272
Saf-B	0.535	0.0272
Su(z)12	0.535	0.0272
CG15153	0.533	0.0276
HipHop	0.533	0.0276
RnpS1	0.533	0.0276
CG14346	0.532	0.0278
CG12299	0.531	0.0279
CG14693	0.531	0.0279
CG32069	0.531	0.0279
Prosbeta1	0.531	0.0279
CG10576	0.53	0.0283
CG18065	0.53	0.0283
<i>xmas-2</i>	0.53	0.0283
RpL34a	0.529	0.0286
CG10177	0.528	0.0286
CG16885	0.528	0.0286
CG17508	0.528	0.0286
CG8326	0.528	0.0286
CG12320	0.527	0.029
CG12362	0.527	0.029
CG2974	0.527	0.029
CG9634	0.527	0.029
CG8952	0.526	0.0294
<i>l(1)dd4</i>	0.526	0.0294
<i>rgr</i>	0.525	0.0295
CG4892	0.524	0.0296
CG8552	0.524	0.0296
CG14984	0.523	0.0298
CG3669	0.523	0.0298
Cpsf73	0.523	0.0298
CG10053	0.521	0.0301
CG34302	0.521	0.0301
CG5899	0.521	0.0301

Gene Name	ERC Value	P-value
<i>Psi</i>	0.521	0.0301
CG31221	0.52	0.0305
CG30020	0.519	0.0305
CG9027	0.519	0.0305
CG4820	0.518	0.0307
DNApol-eta	0.518	0.0307
<i>m4</i>	0.518	0.0307
<i>Tif-1A</i>	0.518	0.0307
CG14130	0.517	0.0311
CG14931	0.517	0.0311
CG33752	0.517	0.0311
CG7338	0.517	0.0311
<i>Nmdar2</i>	0.517	0.0311
<i>Coq2</i>	0.516	0.0315
<i>Tsp42Ea</i>	0.516	0.0315
CG10324	0.515	0.0317
CG42399	0.514	0.0318
RpL13	0.514	0.0318
CG42749	0.513	0.032
CG7849	0.513	0.032
CG8209	0.513	0.032
<i>dod</i>	0.513	0.032
<i>pyr</i>	0.513	0.032
<i>sowah</i>	0.512	0.0324
<i>Spn42Db</i>	0.512	0.0324
CG6523	0.511	0.0326
CG34441	0.51	0.0327
<i>Caf1-105</i>	0.509	0.0328
<i>ppk10</i>	0.509	0.0328
CG10465	0.508	0.033
CG1315	0.508	0.033
CG3223	0.508	0.033
<i>Tis11</i>	0.508	0.033
<i>Ca-alpha1T</i>	0.507	0.0333
CG12703	0.507	0.0333
CG13315	0.507	0.0333
CG7149	0.507	0.0333
CG12923	0.506	0.0337
CG18764	0.506	0.0337
CG34140	0.506	0.0337
<i>hppy</i>	0.506	0.0337
<i>Syt12</i>	0.506	0.0337
<i>Aats-arg</i>	0.505	0.0341
CG14898	0.505	0.0341
CG15236	0.505	0.0341
CG4462	0.505	0.0341
CG4607	0.505	0.0341
<i>ret</i>	0.505	0.0341
<i>Uev1A</i>	0.505	0.0341
<i>cal1</i>	0.504	0.0348
CG12581	0.504	0.0348
RpL1128	0.504	0.0348
<i>Cdk7</i>	0.503	0.035
CG17633	0.503	0.035
CG6325	0.503	0.035
<i>bsh</i>	0.501	0.0353

Gene Name	ERC Value	P-value
CG14626	0.501	0.0353
CG3021	0.501	0.0353
CG5180	0.501	0.0353
CG8368	0.501	0.0353
<i>ftp</i>	0.501	0.0353
<i>icln</i>	0.501	0.0353
<i>nimB4</i>	0.501	0.0353
<i>wal</i>	0.501	0.0353
CG3812	0.5	0.0361
CG4785	0.5	0.0361
CG6996	0.5	0.0361
CG8180	0.5	0.0361
<i>Cyp28a5</i>	0.5	0.0361
HLHm5	0.5	0.0361
<i>pie</i>	0.5	0.0361
CG4880	0.499	0.0368
<i>Crag</i>	0.499	0.0368
<i>dbr</i>	0.499	0.0368
<i>yellow-h</i>	0.499	0.0368
CG15269	0.498	0.0371
CG40191	0.498	0.0371
CG8335	0.498	0.0371
<i>tna</i>	0.498	0.0371
<i>Cdc6</i>	0.497	0.0375
CG3925	0.496	0.0376
<i>Pros54</i>	0.496	0.0376
<i>blos3</i>	0.495	0.0377
<i>cav</i>	0.495	0.0377
CG12078	0.495	0.0377
<i>mRpL14</i>	0.495	0.0377
<i>Tsp42E1</i>	0.495	0.0377
<i>TwdlH</i>	0.495	0.0377
BRWD3	0.494	0.0383
CG14274	0.494	0.0383
CG16743	0.494	0.0383
CG30046	0.494	0.0383
<i>hoip</i>	0.494	0.0383
<i>mRpL13</i>	0.494	0.0383
<i>ttm2</i>	0.494	0.0383
<i>beat-la</i>	0.493	0.0389
CG30466	0.493	0.0389
<i>eIF-3p40</i>	0.493	0.0389
CG17343	0.492	0.0392
CG30291	0.492	0.0392
CG31928	0.492	0.0392
CG7786	0.492	0.0392
CG7928	0.492	0.0392
<i>Mat1</i>	0.492	0.0392
<i>Rassf</i>	0.492	0.0392
<i>Bet5</i>	0.491	0.0398
CG30438	0.491	0.0398
CG32536	0.491	0.0398
<i>Spz25</i>	0.491	0.0398
CG10721	0.49	0.0402
CG30440	0.49	0.0402
CG33680	0.49	0.0402

Gene Name	ERC Value	P-value
<i>Df31</i>	0.49	0.0402
<i>l(2)gl</i>	0.49	0.0402
CG14711	0.489	0.0406
CG6833	0.489	0.0406
<i>Mtr3</i>	0.489	0.0406
CG11919	0.488	0.0409
CG17181	0.488	0.0409
<i>norpA</i>	0.488	0.0409
CG3635	0.487	0.0412
<i>chinmo</i>	0.487	0.0412
<i>desat2</i>	0.487	0.0412
<i>sina</i>	0.487	0.0412
<i>srp</i>	0.487	0.0412
<i>Su(H)</i>	0.487	0.0412
CG10373	0.486	0.0417
CG14715	0.486	0.0417
CG6083	0.486	0.0417
CG14636	0.485	0.042
CG32772	0.485	0.042
CG33110	0.485	0.042
<i>clb</i>	0.485	0.042
<i>exu</i>	0.485	0.042
<i>Nup44A</i>	0.485	0.042
<i>bcr92</i>	0.484	0.0425
CG1344	0.484	0.0425
CG1421	0.484	0.0425
CG17707	0.484	0.0425
<i>RpL18A</i>	0.484	0.0425
mus301	0.484	0.0425
<i>RhoGAP100</i>	0.484	0.0425
SF2	0.484	0.0425
<i>Unr</i>	0.484	0.0425
g(2)M	0.483	0.0433
CD98hc	0.483	0.0433
CG11377	0.483	0.0433
CG13585	0.483	0.0433
CG1832	0.483	0.0433
CG2857	0.483	0.0433
CG31530	0.483	0.0433
CG6024	0.483	0.0433
<i>Arf102F</i>	0.482	0.0441
CG5790	0.482	0.0441
CG11334	0.481	0.0442
CG14720	0.481	0.0442
<i>ppk7</i>	0.481	0.0442
<i>alpha-Man-I</i>	0.48	0.0445
CG17190	0.48	0.0445
CG7083	0.48	0.0445
<i>comm2</i>	0.48	0.0445
<i>pgant4</i>	0.48	0.0445
<i>B-H2</i>	0.479	0.045
CG4415	0.479	0.045
CG6255	0.479	0.045
CG8273	0.479	0.045
<i>Karybeta3</i>	0.479	0.045
<i>mus81</i>	0.479	0.045

Gene Name	ERC Value	P-value
<i>rump</i>	0.479	0.045
<i>Asx</i>	0.478	0.0456
Hsp60C	0.478	0.0456
Bap60	0.477	0.0458
<i>cer</i>	0.477	0.0458
CG12831	0.477	0.0458
CG14107	0.477	0.0458
<i>Tim17a1</i>	0.477	0.0458
TM4SF	0.477	0.0458
CG15817	0.476	0.0463
CG31778	0.476	0.0463
CG5428	0.476	0.0463
<i>krz</i>	0.476	0.0463
<i>l(2)37Cb</i>	0.476	0.0463
<i>tud</i>	0.476	0.0463
CG12788	0.475	0.0468
<i>nct</i>	0.475	0.0468
<i>Obp59a</i>	0.475	0.0468
CG15418	0.474	0.0471
CG32440	0.474	0.0471
CG9053	0.474	0.0471
CG1236	0.473	0.0474
CG15649	0.473	0.0474
CG2046	0.473	0.0474
CG3530	0.473	0.0474
Hsc70-1	0.473	0.0474
Nf-YB	0.473	0.0474
RpL18A	0.473	0.0474
CG15535	0.471	0.048
CG18363	0.471	0.048
CG43066	0.471	0.048
CG7069	0.471	0.048
DLP	0.471	0.048
<i>Or92a</i>	0.471	0.048
<i>Aly</i>	0.47	0.0486
CG3744	0.47	0.0486
CG8027	0.47	0.0486
Dip-C	0.47	0.0486
pHCl	0.47	0.0486
CanA1	0.469	0.049
CG11882	0.469	0.049
CG14630	0.469	0.049
<i>pkf</i>	0.469	0.049
Sps2	0.469	0.049
<i>Su(Tp1)</i>	0.469	0.049
Sym	0.469	0.049
CG34381	0.468	0.0496
<i>Jon44E</i>	0.468	0.0496
<i>lbe</i>	0.468	0.0496
<i>wbl</i>	0.468	0.0496
<i>Awh</i>	0.467	0.05
CG12885	0.467	0.05
CG4424	0.467	0.05
<i>amx</i>	0.466	0.0503
<i>beat-VI</i>	0.466	0.0503
CG12384	0.466	0.0503

Table 6.S6 Continued

Gene Name	ERC Value	P-value
CG31619	0.466	0.0503
CG32687	0.466	0.0503
CG3501	0.466	0.0503
CG5361	0.466	0.0503
Cpr49Ac	0.466	0.0503
fd19B	0.466	0.0503
Glu-Rl	0.466	0.0503
ImpE3	0.466	0.0503
kraken	0.466	0.0503
Mur29B	0.466	0.0503
pch2	0.466	0.0503
SA-2	0.466	0.0503
CG11723	0.465	0.0516
CG12012	0.465	0.0516
CG34360	0.465	0.0516
l(1)G0289	0.465	0.0516
mn	0.465	0.0516
Pvf1	0.465	0.0516
Cat	0.464	0.0522
CG10839	0.464	0.0522
CG6621	0.464	0.0522
ine	0.464	0.0522
CG12119	0.463	0.0525
CG40198	0.463	0.0525
pico	0.463	0.0525
CG12278	0.462	0.0528
CG7251	0.462	0.0528
Yippee	0.462	0.0528
CG42507	0.461	0.0531
CG6006	0.461	0.0531
CG6254	0.461	0.0531
CG8193	0.461	0.0531
iPLA2-VIA	0.461	0.0531
shu	0.461	0.0531
smt3	0.461	0.0531
CG11841	0.46	0.0537
CG31365	0.46	0.0537
SdhB	0.46	0.0537
CG10254	0.459	0.054
CG10858	0.459	0.054
CG15322	0.459	0.054
CG30401	0.459	0.054
CG4747	0.458	0.0543
CG5924	0.458	0.0543
CG7946	0.458	0.0543
CG8503	0.458	0.0543
egg	0.458	0.0543
llp5	0.458	0.0543
CG10741	0.457	0.0549
CG13350	0.457	0.0549
CG17018	0.457	0.0549
CG5626	0.457	0.0549
CG9602	0.457	0.0549
Acf1	0.456	0.0553
CG4936	0.456	0.0553
exba	0.456	0.0553

Gene Name	ERC Value	P-value
gammaTub3	0.456	0.0553
RhoGAP102	0.456	0.0553
Yeti	0.456	0.0553
CG17078	0.455	0.0559
CG30460	0.455	0.0559
CG3224	0.455	0.0559
CG9760	0.455	0.0559
Kaz1-ORFB	0.455	0.0559
CG34045	0.454	0.0563
Ork1	0.454	0.0563
l(1)G0222	0.453	0.0565
CG17691	0.452	0.0566
CG9249	0.452	0.0566
Ets96B	0.452	0.0566
Tom40	0.452	0.0566
CG14834	0.451	0.0569
CG31600	0.451	0.0569
CG7510	0.451	0.0569
Or2a	0.451	0.0569
twe	0.451	0.0569
Adam	0.45	0.0574
CG32732	0.45	0.0574
Galpha73B	0.45	0.0574
La	0.45	0.0574
TfllEbata	0.45	0.0574
CG1092	0.449	0.0578
CG12432	0.449	0.0578
CG13454	0.449	0.0578
CG9839	0.449	0.0578
lz	0.449	0.0578
ATPsyn-Cf6	0.448	0.0583
CG11784	0.448	0.0583
CG15890	0.448	0.0583
llp2	0.448	0.0583
CG10830	0.447	0.0586
CG6662	0.447	0.0586
ds	0.447	0.0586
Rab27	0.447	0.0586
CG4338	0.446	0.059
Kul	0.446	0.059
Pof	0.446	0.059
wde	0.446	0.059
BCL7-like	0.445	0.0594
CG31870	0.445	0.0594
Grip75	0.445	0.0594
Map60	0.445	0.0594
CG11570	0.444	0.0597
CG14540	0.444	0.0597
CG15482	0.444	0.0597
CG17493	0.444	0.0597
CG32087	0.444	0.0597
CG33260	0.444	0.0597
CG4968	0.444	0.0597
CG8613	0.444	0.0597
Ptp52F	0.444	0.0597
CG14866	0.443	0.0605

Gene Name	ERC Value	P-value
CG14906	0.443	0.0605
CG33695	0.443	0.0605
Gem3	0.443	0.0605
CG12481	0.442	0.0609
Eaf	0.442	0.0609
elf3-S8	0.442	0.0609
CG3777	0.441	0.0612
tsh	0.441	0.0612
CG14684	0.44	0.0614
CG30152	0.44	0.0614
CG6847	0.44	0.0614
CG8924	0.44	0.0614
Elo68beta	0.44	0.0614
nompA	0.44	0.0614
Prosbeta7	0.44	0.0614
qkr58E-2	0.44	0.0614
CG10664	0.439	0.0621
CG17751	0.439	0.0621
CG31869	0.439	0.0621
CG32626	0.439	0.0621
CG3880	0.439	0.0621
CG5045	0.439	0.0621
Eip78C	0.439	0.0621
pita	0.439	0.0621
CG11778	0.438	0.0628
CG15699	0.438	0.0628
CG17928	0.438	0.0628
CG6769	0.438	0.0628
Hrb98DE	0.438	0.0628
pix	0.438	0.0628
skpB	0.438	0.0628
CG7429	0.437	0.0634
gp210	0.437	0.0634
zwilch	0.437	0.0634
CG10098	0.436	0.0637
CG15725	0.436	0.0637
CG8916	0.436	0.0637
CheA7a	0.436	0.0637
H2.0	0.436	0.0637
Nhe3	0.436	0.0637
Aats-thr	0.435	0.0642
CG9316	0.435	0.0642
DAAM	0.435	0.0642
ZC3H3	0.435	0.0642
Cad87A	0.434	0.0646
CG18258	0.434	0.0646
Fbw5	0.434	0.0646
Shaw	0.434	0.0646
Bruce	0.433	0.065
bs	0.433	0.065
CG10321	0.433	0.065
CG14573	0.433	0.065
Stat92E	0.433	0.065
CG11453	0.432	0.0654
CG13717	0.432	0.0654
CG31142	0.432	0.0654

Gene Name	ERC Value	P-value
CG6610	0.432	0.0654
CG7963	0.432	0.0654
opa1-like	0.432	0.0654
ara	0.431	0.0659
CG13745	0.431	0.0659
CG17724	0.431	0.0659
CG18131	0.431	0.0659
CG32164	0.431	0.0659
dpr2	0.431	0.0659
fs(1)N	0.431	0.0659
spz6	0.431	0.0659
CG42807	0.43	0.0667
CG8359	0.43	0.0667
CG15914	0.429	0.0668
CG2685	0.429	0.0668
CG30441	0.429	0.0668
Cont	0.429	0.0668
Hpr1	0.429	0.0668
Spc105R	0.429	0.0668
wac	0.429	0.0668
CG15014	0.428	0.0675
CG3306	0.428	0.0675
CG42817	0.428	0.0675
Fs	0.428	0.0675
l(3)psg7	0.428	0.0675
Sdc	0.428	0.0675
tomb	0.428	0.0675
CG14239	0.427	0.0681
CG2258	0.427	0.0681
CG6859	0.427	0.0681
CG9855	0.427	0.0681
HP1c	0.427	0.0681
sds22	0.427	0.0681
CG10424	0.426	0.0686
lrs4a	0.426	0.0686
Teh3	0.426	0.0686
Bj1	0.425	0.0689
CG14109	0.425	0.0689
CG15876	0.425	0.0689
CG6568	0.425	0.0689
CG10463	0.424	0.0693
CG12866	0.424	0.0693
CG5292	0.424	0.0693
CG6388	0.424	0.0693
CG8116	0.424	0.0693
elf-2alpha	0.424	0.0693
CG10107	0.423	0.0698
CG13339	0.423	0.0698
CG9135	0.423	0.0698
CG9586	0.423	0.0698
mRpl.52	0.423	0.0698
Uba2	0.423	0.0698
CG10035	0.422	0.0704
CG1896	0.422	0.0704
RpA-70	0.422	0.0704
CG13148	0.421	0.0706

Gene Name	ERC Value	P-value
CG2924	0.421	0.0706
CG8915	0.421	0.0706
Egfr	0.421	0.0706
Mrtf	0.421	0.0706
Spase25	0.421	0.0706
CG17162	0.42	0.0712
CG5326	0.42	0.0712
CG6700	0.42	0.0712
Chd1	0.42	0.0712
Rbp4	0.42	0.0712
CG14006	0.419	0.0716
CG5931	0.419	0.0716
CG8405	0.419	0.0716
dao	0.419	0.0716
TfllEalpha	0.419	0.0716
Tsp42Ef	0.419	0.0716
Vsx2	0.419	0.0716
Adar	0.418	0.0723
CG11490	0.418	0.0723
CG15754	0.418	0.0723
CG3308	0.418	0.0723
CG8379	0.418	0.0723
CREG	0.418	0.0723
Gel	0.418	0.0723
lrf7c	0.418	0.0723
Rae1	0.418	0.0723
CG34005	0.417	0.0731
Dg	0.417	0.0731
Lcch3	0.417	0.0731
pck	0.417	0.0731
Pros28.1B	0.417	0.0731
SeIR	0.417	0.0731
slp1	0.417	0.0731
WRNexo	0.417	0.0731
bun	0.416	0.0738
CG10641	0.416	0.0738
CG33692	0.416	0.0738
conv	0.416	0.0738
Oatp58Da	0.416	0.0738
oho23B	0.416	0.0738
Uchr	0.416	0.0738
CG11967	0.415	0.0744
CG13970	0.415	0.0744
CG14036	0.415	0.0744
CG1746	0.415	0.0744
RIC-3	0.415	0.0744
run	0.415	0.0744
CG13982	0.414	0.075
CG17187	0.414	0.075
sd	0.414	0.075
CG12582	0.413	0.0752
Cht3	0.413	0.0752
DnaJ-1	0.413	0.0752
h-cup	0.413	0.0752
Sug	0.413	0.0752
CG10267	0.412	0.0757

Table 6.S6 Continued

Gene Name	ERC Value	P-value
CG2972	0.412	0.0757
CG33977	0.412	0.0757
CG7453	0.412	0.0757
CG8611	0.412	0.0757
ecd	0.412	0.0757
Herp	0.412	0.0757
msl-3	0.412	0.0757
CG13743	0.411	0.0764
CG6724	0.411	0.0764
ix	0.411	0.0764
LpR1	0.411	0.0764
Mcm6	0.411	0.0764
Scp2	0.411	0.0764
yl	0.411	0.0764
CG11318	0.41	0.077
CG11321	0.41	0.077
CG12558	0.41	0.077
CG15169	0.41	0.077
pex12	0.41	0.077
Vps33B	0.41	0.077
Cg25C	0.409	0.0776
CG5500	0.409	0.0776
CG9287	0.409	0.0776
eIF-3p66	0.409	0.0776
Fancd2	0.409	0.0776
kay	0.409	0.0776
Kr	0.409	0.0776
CG11912	0.408	0.0782
CG13599	0.408	0.0782
CG14749	0.408	0.0782
CG17683	0.408	0.0782
CG7914	0.408	0.0782
rg	0.408	0.0782
Treh	0.408	0.0782
CG11590	0.407	0.0788
CG12106	0.407	0.0788
CG14647	0.407	0.0788
CG33635	0.407	0.0788
CG6443	0.407	0.0788
CG7685	0.407	0.0788
l(2)09851	0.407	0.0788
unc-4	0.407	0.0788
CG10722	0.406	0.0795
CG10936	0.406	0.0795
CG14238	0.406	0.0795
CG6230	0.406	0.0795
met1	0.406	0.0795
prp	0.406	0.0795
CG18472	0.405	0.0801
CG5921	0.405	0.0801
NeptYr	0.405	0.0801
CG4452	0.404	0.0804
CG5122	0.404	0.0804
CG5235	0.404	0.0804
CG6762	0.404	0.0804
Jupiter	0.404	0.0804

Gene Name	ERC Value	P-value
beat-1c	0.403	0.0808
cdc23	0.403	0.0808
CG3294	0.403	0.0808
CG9577	0.403	0.0808
Snr1	0.403	0.0808
SPoCk	0.403	0.0808
blos1	0.402	0.0814
CG8237	0.402	0.0814
CG8778	0.402	0.0814
CG9090	0.402	0.0814
E(bx)	0.402	0.0814
CG1271	0.401	0.0818
CG14608	0.401	0.0818
CG6915	0.401	0.0818
E(spl)	0.401	0.0818
Nrx-IV	0.401	0.0818
pnr	0.401	0.0818
poe	0.401	0.0818
CG10184	0.4	0.0824
CG17665	0.4	0.0824
CG5863	0.4	0.0824
CG7213	0.4	0.0824
CG9004	0.4	0.0824
mRpS18B	0.4	0.0824
AR-2	0.399	0.083
CG12439	0.399	0.083
CG12910	0.399	0.083
CG13377	0.399	0.083
CG2121	0.399	0.083
CG31787	0.399	0.083
CG42268	0.399	0.083
Dpy-30L2	0.399	0.083
nimC1	0.399	0.083
a6	0.398	0.0838
CG12590	0.398	0.0838
CG1571	0.398	0.0838
CG3162	0.398	0.0838
CG3430	0.398	0.0838
CG6959	0.398	0.0838
Andorra	0.397	0.0843
CG10516	0.397	0.0843
CG12540	0.397	0.0843
CG3680	0.397	0.0843
CG5895	0.397	0.0843
Lsp1beta	0.397	0.0843
rev7	0.397	0.0843
ssp3	0.397	0.0843
CG10326	0.396	0.085
CG5104	0.396	0.085
CG9519	0.396	0.085
ImpL2	0.396	0.085
lr60a	0.396	0.085
CG10915	0.395	0.0855
CG11762	0.395	0.0855
CG12773	0.395	0.0855
CG14770	0.395	0.0855

Gene Name	ERC Value	P-value
CG18171	0.395	0.0855
CG3919	0.395	0.0855
CG5181	0.395	0.0855
heix	0.395	0.0855
Ndc80	0.395	0.0855
stau	0.395	0.0855
yps	0.395	0.0855
CG34380	0.394	0.0865
cora	0.394	0.0865
Hsp67Ba	0.394	0.0865
lr56a	0.394	0.0865
Octbeta2R	0.394	0.0865
sced	0.394	0.0865
Syt14	0.394	0.0865
CG30428	0.393	0.0871
CG42235	0.393	0.0871
Dbp73D	0.393	0.0871
E(var)3-9	0.393	0.0871
Int6	0.393	0.0871
CG13901	0.392	0.0876
CG14710	0.392	0.0876
CG5514	0.392	0.0876
CG8490	0.392	0.0876
jing	0.392	0.0876
tho2	0.392	0.0876
ana3	0.391	0.0881
CG11163	0.391	0.0881
CG15630	0.391	0.0881
CG31919	0.391	0.0881
CG4577	0.391	0.0881
CG5669	0.391	0.0881
cta	0.391	0.0881
Hsp60	0.391	0.0881
Syn2	0.391	0.0881
CG13042	0.39	0.0889
CG33052	0.39	0.0889
CG8468	0.39	0.0889
CG1492	0.389	0.0892
CG2183	0.389	0.0892
CG8443	0.389	0.0892
CG9692	0.389	0.0892
Gfat2	0.389	0.0892
l(2)35Bg	0.389	0.0892
sinah	0.389	0.0892
bel	0.388	0.0898
bip1	0.388	0.0898
CG10581	0.388	0.0898
CG12879	0.388	0.0898
CG13386	0.388	0.0898
CG7627	0.388	0.0898
Pka-C1	0.388	0.0898
Vha14-1	0.388	0.0898
armi	0.387	0.0905
CG3292	0.387	0.0905
CG6712	0.387	0.0905
CG10877	0.386	0.0908

Gene Name	ERC Value	P-value
CG3184	0.386	0.0908
CG32343	0.386	0.0908
Git	0.386	0.0908
Mad1	0.386	0.0908
Rev1	0.386	0.0908
ald	0.385	0.0914
CG10924	0.385	0.0914
CG11247	0.385	0.0914
CG18005	0.385	0.0914
CG4645	0.385	0.0914
CG9170	0.385	0.0914
CG9821	0.385	0.0914
fs(1)Ya	0.385	0.0914
Mtor	0.385	0.0914
Rpn6	0.385	0.0914
RYBP	0.385	0.0914
Top2	0.385	0.0914
gcm	0.384	0.0924
glob3	0.384	0.0924
Nup358	0.384	0.0924
CG14229	0.383	0.0927
CG32816	0.383	0.0927
CG7332	0.383	0.0927
eIF-4E	0.383	0.0927
mRpS28	0.383	0.0927
CG1750	0.382	0.0932
CG5027	0.382	0.0932
tbl6	0.382	0.0932
ft	0.382	0.0932
sas	0.382	0.0932
Shal	0.382	0.0932
CG14803	0.381	0.0937
CG14882	0.381	0.0937
CG32266	0.381	0.0937
CG5399	0.381	0.0937
Anxb11	0.38	0.0941
Baldspot	0.38	0.0941
CG12681	0.38	0.0941
CG7692	0.38	0.0941
Gr89a	0.38	0.0941
CG4004	0.379	0.0945
CG9875	0.379	0.0945
CSN3	0.379	0.0945
achi	0.378	0.0948
Dip2	0.378	0.0948
elav	0.378	0.0948
Faf	0.378	0.0948
Rab7	0.378	0.0948
Tango2	0.378	0.0948
blos4	0.377	0.0953
Cda5	0.377	0.0953
CG11044	0.377	0.0953
CG13296	0.377	0.0953
CG14561	0.377	0.0953
CG9975	0.377	0.0953
D19A	0.377	0.0953

Gene Name	ERC Value	P-value
ems	0.377	0.0953
mRpL4	0.377	0.0953
ran	0.377	0.0953
CG14508	0.376	0.0962
CG16965	0.376	0.0962
CG4810	0.376	0.0962
CG9014	0.376	0.0962
d4	0.376	0.0962
Oatp33Eb	0.376	0.0962
Ppt2	0.376	0.0962
CG11875	0.375	0.0968
CG13288	0.375	0.0968
CG17270	0.375	0.0968
CG3534	0.375	0.0968
CG9451	0.375	0.0968
mi	0.375	0.0968
mys	0.375	0.0968
Pcl	0.375	0.0968
Sgt1	0.375	0.0968
CG14223	0.374	0.0977
CG14442	0.374	0.0977
dx	0.374	0.0977
eIF5B	0.374	0.0977
pirk	0.374	0.0977
Usp7	0.374	0.0977
CG1737	0.373	0.0982
CG31646	0.373	0.0982
CG8100	0.373	0.0982
mRpS24	0.373	0.0982
Ski6	0.373	0.0982
Vha13	0.373	0.0982
aub	0.372	0.0987
CG17209	0.372	0.0987
CG1888	0.372	0.0987
CG7120	0.372	0.0987
CG7320	0.372	0.0987
GX1VspLA2	0.372	0.0987
wdp	0.372	0.0987
CG5674	0.371	0.0994
CG8892	0.371	0.0994
met-P22	0.371	0.0994
UbcD4	0.371	0.0994
CG17370	0.37	0.0997
CG31223	0.37	0.0997
CG13126	0.37	0.0997
eIF-4a	0.37	0.0997
Lrt	0.37	0.0997
slim	0.37	0.0997

Table 6.S7 - Top Genes ERC values for *mei-41* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>zpg</i>	0.942	0.0001
<i>Rad51D</i>	0.921	0.0002
<i>CG12420</i>	0.881	0.0003
CG31898	0.879	0.0004
<i>dos</i>	0.874	0.0005
<i>Sulf1</i>	0.872	0.0005
<i>CG31793</i>	0.87	0.0006
<i>CG31812</i>	0.868	0.0007
<i>pll</i>	0.864	0.0008
<i>Ptth</i>	0.855	0.0009
<i>Sym</i>	0.854	0.001
<i>CG31365</i>	0.851	0.0011
<i>HLH106</i>	0.85	0.0012
CG2975	0.848	0.0013
<i>CG10824</i>	0.845	0.0014
<i>Rad51C</i>	0.841	0.0014
<i>ome</i>	0.838	0.0015
<i>Gr9a</i>	0.834	0.0016
<i>CG1602</i>	0.833	0.0017
<i>CG1311</i>	0.832	0.0018
<i>CG32579</i>	0.832	0.0018
<i>CG32437</i>	0.829	0.002
<i>CG8642</i>	0.829	0.002
<i>lHog</i>	0.829	0.002
<i>CG13745</i>	0.827	0.0023
<i>gsb-n</i>	0.827	0.0023
<i>Tim17b1</i>	0.825	0.0024
<i>CG12104</i>	0.822	0.0025
<i>CG13884</i>	0.821	0.0026
<i>CG11377</i>	0.819	0.0027
<i>CG14650</i>	0.818	0.0028
<i>ix</i>	0.816	0.0029
<i>CG14109</i>	0.814	0.003
<i>CG32791</i>	0.813	0.0031
<i>CG42351</i>	0.811	0.0032
<i>ETH</i>	0.811	0.0032
<i>ft</i>	0.811	0.0032
<i>lrk</i>	0.811	0.0032
<i>CG4751</i>	0.809	0.0035
<i>beat-lla</i>	0.807	0.0036
<i>Ptp52F</i>	0.806	0.0037
<i>CG11211</i>	0.804	0.0038
<i>CG32573</i>	0.804	0.0038
<i>CG6745</i>	0.804	0.0038
<i>CG8191</i>	0.804	0.0038
<i>Taspase1</i>	0.802	0.0041
<i>CG13837</i>	0.8	0.0042
<i>CG33784</i>	0.796	0.0043
<i>CG7510</i>	0.791	0.0044
<i>CG14401</i>	0.788	0.0045
<i>rump</i>	0.788	0.0045
<i>CG14321</i>	0.787	0.0047
<i>GNBP1</i>	0.787	0.0047
<i>CG14302</i>	0.785	0.0049
<i>CG15116</i>	0.785	0.0049
<i>llil</i>	0.785	0.0049

Gene Name	ERC Value	P-value
<i>Rga</i>	0.785	0.0049
<i>CG9839</i>	0.784	0.0052
<i>a6</i>	0.782	0.0053
CG11778	0.781	0.0054
<i>GstD9</i>	0.78	0.0055
<i>Rab7</i>	0.78	0.0055
<i>Pbp45</i>	0.779	0.0057
<i>CG12316</i>	0.778	0.0058
<i>CHKov2</i>	0.776	0.0059
<i>CG9776</i>	0.773	0.0059
<i>CG30001</i>	0.772	0.006
<i>eyg</i>	0.772	0.006
<i>Nlp</i>	0.772	0.006
<i>CG10741</i>	0.77	0.0063
<i>CG31224</i>	0.769	0.0064
<i>CG42678</i>	0.768	0.0065
<i>CG7787</i>	0.768	0.0065
<i>CG16743</i>	0.767	0.0067
<i>CG16868</i>	0.767	0.0067
<i>CG8159</i>	0.765	0.0068
mus301	0.765	0.0068
<i>CG2162</i>	0.764	0.007
<i>glob3</i>	0.764	0.007
<i>hk</i>	0.764	0.007
<i>CG18265</i>	0.759	0.0073
<i>CG31102</i>	0.759	0.0073
<i>CG3168</i>	0.759	0.0073
<i>Gyk</i>	0.759	0.0073
<i>CG8199</i>	0.758	0.0077
CG18806	0.757	0.0077
<i>blue</i>	0.753	0.0078
<i>CG34401</i>	0.753	0.0078
<i>phol</i>	0.753	0.0078
<i>Vdup1</i>	0.753	0.0078
<i>CG6325</i>	0.752	0.0082
<i>CG8539</i>	0.752	0.0082
<i>CG7372</i>	0.749	0.0084
<i>CG8960</i>	0.748	0.0085
<i>net</i>	0.748	0.0085
<i>Phipp</i>	0.748	0.0085
<i>Taff1</i>	0.748	0.0085
<i>CG10916</i>	0.747	0.0088
<i>ear</i>	0.746	0.0089
<i>Gr85a</i>	0.746	0.0089
<i>tutl</i>	0.746	0.0089
<i>CG2321</i>	0.745	0.0092
<i>CG8202</i>	0.744	0.0093
<i>CG13802</i>	0.743	0.0094
<i>MED31</i>	0.743	0.0094
<i>icln</i>	0.742	0.0095
<i>zwilch</i>	0.741	0.0096
<i>CG3651</i>	0.739	0.0097
<i>Sox15</i>	0.738	0.0098
<i>CG17562</i>	0.737	0.0099
<i>CG32121</i>	0.735	0.01
<i>CG33229</i>	0.735	0.01

Gene Name	ERC Value	P-value
<i>G59b</i>	0.735	0.01
<i>CG12995</i>	0.734	0.0103
<i>Jon74E</i>	0.733	0.0104
<i>PTP-ER</i>	0.733	0.0104
<i>CG32803</i>	0.732	0.0105
<i>InR</i>	0.732	0.0105
<i>PGRP-LD</i>	0.732	0.0105
<i>CG4074</i>	0.731	0.0108
<i>CG6024</i>	0.731	0.0108
<i>GstE6</i>	0.731	0.0108
<i>CG9673</i>	0.73	0.0111
<i>Map205</i>	0.73	0.0111
<i>cg</i>	0.728	0.0113
<i>CG6254</i>	0.728	0.0113
<i>Ets96B</i>	0.727	0.0114
<i>sced</i>	0.726	0.0115
<i>MSBP</i>	0.724	0.0116
<i>CG10399</i>	0.723	0.0117
<i>CG18558</i>	0.723	0.0117
<i>alpha4GT1</i>	0.722	0.0119
<i>CG31689</i>	0.722	0.0119
CG7597	0.721	0.0121
<i>CG34315</i>	0.72	0.0122
<i>CG5895</i>	0.72	0.0122
<i>CG7739</i>	0.72	0.0122
<i>Spt20</i>	0.72	0.0122
<i>Abi</i>	0.717	0.0125
<i>CG15167</i>	0.717	0.0125
<i>CG34007</i>	0.717	0.0125
<i>CG8370</i>	0.717	0.0125
<i>rev7</i>	0.717	0.0125
<i>RpA-70</i>	0.717	0.0125
<i>CG30403</i>	0.715	0.0131
<i>kto</i>	0.715	0.0131
<i>CG11851</i>	0.714	0.0132
<i>CG5872</i>	0.714	0.0132
<i>fy</i>	0.713	0.0134
<i>NK7.1</i>	0.713	0.0134
<i>CG8959</i>	0.711	0.0136
<i>CG10077</i>	0.71	0.0137
<i>CG32790</i>	0.71	0.0137
<i>CG5550</i>	0.71	0.0137
<i>CG15861</i>	0.709	0.014
<i>CG17184</i>	0.709	0.014
<i>CG32221</i>	0.708	0.0141
<i>CG15376</i>	0.707	0.0142
<i>CG8490</i>	0.707	0.0142
<i>pgant6</i>	0.707	0.0142
<i>CG6985</i>	0.706	0.0145
<i>Hk</i>	0.703	0.0146
<i>lkb1</i>	0.703	0.0146
<i>CG13488</i>	0.702	0.0148
<i>CG14562</i>	0.702	0.0148
<i>CG42399</i>	0.702	0.0148
<i>CG3542</i>	0.701	0.015
<i>Su(H)</i>	0.701	0.015

Gene Name	ERC Value	P-value
<i>cag</i>	0.699	0.0152
<i>CG10249</i>	0.699	0.0152
<i>CG10051</i>	0.698	0.0154
<i>CG12986</i>	0.698	0.0154
<i>CG16826</i>	0.698	0.0154
<i>CG7265</i>	0.697	0.0157
<i>CG8319</i>	0.696	0.0158
<i>CG9879</i>	0.696	0.0158
<i>pnr</i>	0.696	0.0158
<i>mus309</i>	0.695	0.016
<i>Cpr72Ea</i>	0.694	0.0161
<i>H</i>	0.694	0.0161
<i>KailRIA</i>	0.694	0.0161
<i>CG13377</i>	0.693	0.0164
<i>CG13766</i>	0.693	0.0164
<i>CG15435</i>	0.693	0.0164
<i>omd</i>	0.693	0.0164
<i>Pc</i>	0.693	0.0164
<i>wit</i>	0.693	0.0164
<i>CG14956</i>	0.692	0.0169
<i>Grip734</i>	0.692	0.0169
<i>thr</i>	0.692	0.0169
CG10274	0.691	0.0172
<i>CG31380</i>	0.691	0.0172
<i>sba</i>	0.691	0.0172
<i>m4</i>	0.69	0.0175
<i>RhoL</i>	0.69	0.0175
<i>CG12050</i>	0.689	0.0177
<i>CG13408</i>	0.689	0.0177
<i>esn</i>	0.689	0.0177
<i>mthl14</i>	0.689	0.0177
<i>CG8301</i>	0.688	0.018
<i>sad</i>	0.688	0.018
<i>CG5255</i>	0.687	0.0182
<i>Oatp58Da</i>	0.687	0.0182
<i>Tbp-1</i>	0.687	0.0182
<i>Vm32E</i>	0.687	0.0182
<i>beta4GalNA</i>	0.686	0.0186
<i>CG34404</i>	0.686	0.0186
<i>CG9801</i>	0.686	0.0186
<i>d</i>	0.686	0.0186
<i>CG11248</i>	0.685	0.0189
<i>DNApol-eta</i>	0.685	0.0189
<i>Arp5</i>	0.683	0.0191
<i>BubR1</i>	0.682	0.0192
<i>Psi</i>	0.682	0.0192
<i>Sec61beta</i>	0.682	0.0192
<i>ash1</i>	0.681	0.0195
<i>CG11367</i>	0.681	0.0195
<i>CG12206</i>	0.681	0.0195
<i>CG9386</i>	0.681	0.0195
<i>llp2</i>	0.681	0.0195
<i>vig</i>	0.681	0.0195
<i>wb</i>	0.681	0.0195
<i>CG12693</i>	0.68	0.0201
<i>Tl</i>	0.68	0.0201

Gene Name	ERC Value	P-value
<i>yki</i>	0.68	0.0201
<i>CG31431</i>	0.679	0.0204
<i>ham</i>	0.679	0.0204
<i>Start1</i>	0.679	0.0204
<i>CG32962</i>	0.678	0.0206
<i>CG3532</i>	0.678	0.0206
<i>CG5849</i>	0.678	0.0206
<i>Dref</i>	0.678	0.0206
<i>lbr</i>	0.678	0.0206
<i>BtbVII</i>	0.677	0.0211
<i>CG14435</i>	0.677	0.0211
<i>CG7222</i>	0.677	0.0211
<i>Cks85A</i>	0.677	0.0211
<i>X11L</i>	0.677	0.0211
<i>CG30115</i>	0.676	0.0215
<i>MBD-like</i>	0.676	0.0215
<i>CG32442</i>	0.675	0.0217
<i>GluRIIE</i>	0.675	0.0217
<i>pcs</i>	0.674	0.0219
<i>Prosbeta7</i>	0.674	0.0219
<i>CG6734</i>	0.673	0.0221
<i>Gr93a</i>	0.673	0.0221
<i>CG31607</i>	0.672	0.0223
<i>DAT</i>	0.672	0.0223
<i>dome</i>	0.672	0.0223
<i>Or65a</i>	0.672	0.0223
<i>Rab40</i>	0.672	0.0223
<i>trem</i>	0.672	0.0223
spn-D	0.671	0.0228
<i>Spn43Ad</i>	0.67	0.0229
<i>blos3</i>	0.669	0.023
<i>Cas</i>	0.669	0.023
<i>CG10435</i>	0.669	0.023
<i>CG13877</i>	0.669	0.023
<i>CG5830</i>	0.669	0.023
<i>CG2046</i>	0.668	0.0234
CG34012	0.668	0.0234
<i>CG41434</i>	0.668	0.0234
<i>CG7102</i>	0.668	0.0234
<i>CG12851</i>	0.667	0.0238
<i>CG5746</i>	0.667	0.0238
<i>ss</i>	0.667	0.0238
<i>CG10732</i>	0.666	0.0241
<i>slam</i>	0.666	0.0241
<i>CG5924</i>	0.665	0.0242
<i>Spc105R</i>	0.665	0.0242
<i>Aef1</i>	0.664	0.0244
<i>CG14550</i>	0.664	0.0244
<i>mRpl14</i>	0.664	0.0244
<i>CG15571</i>	0.663	0.0247
<i>CG6276</i>	0.662	0.0248
<i>Rpl115</i>	0.662	0.0248
<i>TyrR</i>	0.662	0.0248
<i>ZC3H3</i>	0.662	0.0248
<i>CG8677</i>	0.661	0.0251
<i>Klc</i>	0.66	0.0252

Table 6.S7 Continued

Gene Name	ERC Value	P-value
CG2126	0.659	0.0253
CG31371	0.659	0.0253
Gpi1	0.659	0.0253
ORMDL	0.659	0.0253
Brf	0.658	0.0257
CG13539	0.658	0.0257
CG13640	0.658	0.0257
CG16957	0.658	0.0257
CG3292	0.658	0.0257
MED18	0.658	0.0257
Bin1	0.657	0.0262
CG13362	0.657	0.0262
CG32563	0.657	0.0262
CG3558	0.657	0.0262
CG9147	0.657	0.0262
fax	0.657	0.0262
CG2694	0.656	0.0268
spn-B	0.655	0.0268
Dot	0.654	0.0269
Kmn1	0.654	0.0269
mahj	0.654	0.0269
Map60	0.654	0.0269
bnk	0.653	0.0273
CG7197	0.653	0.0273
ds	0.653	0.0273
CG12299	0.652	0.0276
CG2182	0.652	0.0276
pzg	0.652	0.0276
CG11454	0.651	0.0278
Hus1-like	0.651	0.0278
repo	0.651	0.0278
CG6520	0.65	0.0281
S1P	0.65	0.0281
Trs23	0.65	0.0281
CG10543	0.649	0.0284
14-3-3j	0.647	0.0285
CG9004	0.647	0.0285
CG9384	0.647	0.0285
Dsk	0.647	0.0285
Reck	0.647	0.0285
Sep5	0.646	0.0289
CG5773	0.646	0.0289
CG42676	0.645	0.0291
CG3808	0.644	0.0292
CG5098	0.644	0.0292
CG8501	0.644	0.0292
CG14132	0.643	0.0295
CG15443	0.643	0.0295
dao	0.643	0.0295
DNApol-gam	0.643	0.0295
Tak1	0.643	0.0295
bsh	0.642	0.0299
Or45a	0.642	0.0299
CG17660	0.64	0.0301
nimA	0.64	0.0301
CG4820	0.639	0.0303

Gene Name	ERC Value	P-value
pex1	0.639	0.0303
CG17724	0.638	0.0305
CG6923	0.638	0.0305
Rtc1	0.638	0.0305
CG16799	0.637	0.0307
CG3502	0.637	0.0307
CG7158	0.637	0.0307
Gr89a	0.637	0.0307
CG17807	0.636	0.0311
Elo68beta	0.636	0.0311
CG33641	0.634	0.0313
CG5867	0.634	0.0313
tj	0.634	0.0313
CG1738	0.633	0.0315
CG34313	0.633	0.0315
trr	0.633	0.0315
CG13169	0.632	0.0318
mus101	0.632	0.0318
Ssl1	0.632	0.0318
CG14647	0.631	0.0321
CG15738	0.631	0.0321
CG3570	0.63	0.0323
CG4424	0.63	0.0323
sax	0.63	0.0323
slbo	0.63	0.0323
CG13694	0.629	0.0326
CG8232	0.629	0.0326
Tsp	0.629	0.0326
bs	0.628	0.0329
CG14607	0.628	0.0329
Tsp42E1	0.628	0.0329
CG14715	0.627	0.0332
CG17782	0.627	0.0332
Fer1HCH	0.627	0.0332
Taf13	0.627	0.0332
CG10561	0.626	0.0335
CG3880	0.626	0.0335
CG7453	0.626	0.0335
l(2)05510	0.626	0.0335
CG13125	0.625	0.0339
e(y)3	0.625	0.0339
fdlipdiline	0.625	0.0339
Gr61a	0.625	0.0339
brk	0.624	0.0342
CG33703	0.624	0.0342
CG6465	0.624	0.0342
Dpy-30L1	0.624	0.0342
srw	0.624	0.0342
Apc2	0.623	0.0347
clt	0.622	0.0348
DIP2	0.622	0.0348
glo	0.622	0.0348
CG13561	0.621	0.035
CG14618	0.621	0.035
CG1832	0.621	0.035
CG18812	0.621	0.035

Gene Name	ERC Value	P-value
CG31053	0.621	0.035
CG5073	0.621	0.035
CG9892	0.621	0.035
CG11983	0.62	0.0357
CG1792	0.62	0.0357
Nuf2	0.62	0.0357
POSH	0.62	0.0357
RPA2	0.62	0.0357
CG1315	0.619	0.0361
Galpha73B	0.619	0.0361
Klp67A	0.619	0.0361
Rassf	0.619	0.0361
CG12075	0.618	0.0365
CG14882	0.618	0.0365
CG9804	0.618	0.0365
jim	0.618	0.0365
phm	0.618	0.0365
CG10920	0.617	0.0369
CG32043	0.617	0.0369
CG4753	0.617	0.0369
Med	0.617	0.0369
D12	0.616	0.0373
mus205	0.616	0.0373
Fancd2	0.615	0.0375
CG15093	0.614	0.0376
CG6908	0.614	0.0376
CG7407	0.613	0.0377
dmrt11E	0.613	0.0377
jub	0.613	0.0377
CG17490	0.612	0.038
Nnf1a	0.612	0.038
CG15514	0.611	0.0382
CG11970	0.61	0.0383
CG13339	0.61	0.0383
CG17691	0.61	0.0383
CG31849	0.61	0.0383
CG32635	0.61	0.0383
mts	0.61	0.0383
Cortactin	0.609	0.0388
H2.0	0.609	0.0388
CG10560	0.608	0.039
CG10659	0.608	0.039
CG13545	0.608	0.039
CG9634	0.608	0.039
Mat89Ba	0.608	0.039
slpr	0.608	0.039
Tsp39D	0.608	0.039
CG18599	0.607	0.0396
CG31191	0.607	0.0396
CG32343	0.607	0.0396
CG3838	0.607	0.0396
CG10669	0.606	0.04
CG11109	0.606	0.04
CG11317	0.606	0.04
CG4374	0.606	0.04
CG9427	0.606	0.04

Gene Name	ERC Value	P-value
in	0.606	0.04
Prosalpha67	0.606	0.04
Psfl	0.606	0.04
Sema-1b	0.606	0.04
CG3223	0.605	0.0408
CG14113	0.604	0.0409
CG10646	0.603	0.041
CG14749	0.603	0.041
CG8646	0.603	0.041
rod	0.603	0.041
CG13295	0.602	0.0414
CG14883	0.602	0.0414
CG42863	0.602	0.0414
CG9418	0.602	0.0414
Best3	0.601	0.0417
Magi	0.601	0.0417
mth5	0.601	0.0417
stf	0.601	0.0417
CG14177	0.6	0.0421
CG18476	0.6	0.0421
CG5585	0.6	0.0421
CG9300	0.6	0.0421
dbf	0.6	0.0421
pck	0.6	0.0421
smt3	0.6	0.0421
CG31698	0.599	0.0427
Cpr47E	0.599	0.0427
CG14661	0.598	0.0429
CG15888	0.598	0.0429
E5	0.598	0.0429
CG31855	0.597	0.0432
CG33096	0.597	0.0432
CG8247	0.597	0.0432
Rad9	0.597	0.0432
Art4	0.596	0.0435
CG1299	0.596	0.0435
CG34284	0.596	0.0435
CG3939	0.596	0.0435
bip1	0.595	0.0439
CG13086	0.595	0.0439
CG14023	0.595	0.0439
cn	0.595	0.0439
DNApol-alpha	0.595	0.0439
dx	0.595	0.0439
Or23a	0.595	0.0439
wgn	0.595	0.0439
CG18095	0.594	0.0446
CG6751	0.594	0.0446
CG9592	0.594	0.0446
Gr59e	0.594	0.0446
mri	0.594	0.0446
CG10495	0.593	0.045
CG14330	0.593	0.045
CG9063	0.593	0.045
coro	0.593	0.045
l(2)k05819	0.593	0.045

Gene Name	ERC Value	P-value
Ndc80	0.593	0.045
Uchr	0.593	0.045
CalpC	0.592	0.0457
CG4705	0.592	0.0457
CG7246	0.592	0.0457
GluRIIA	0.592	0.0457
CG11381	0.591	0.046
CG14803	0.591	0.046
CG31076	0.591	0.046
Cypl	0.591	0.046
HipHop	0.591	0.046
CG14341	0.59	0.0465
CG7227	0.59	0.0465
CG13594	0.589	0.0467
CG15630	0.589	0.0467
dpr16	0.589	0.0467
DNApol-alpha	0.588	0.0469
trbd	0.588	0.0469
l(2)k09022	0.587	0.0471
NKAIN	0.587	0.0471
Sse	0.587	0.0471
zen	0.587	0.0471
CG8378	0.586	0.0475
scro	0.586	0.0475
CG13624	0.585	0.0477
CG14676	0.585	0.0477
CG17181	0.585	0.0477
CG6225	0.585	0.0477
CG14314	0.584	0.048
CG17912	0.584	0.048
CG4393	0.584	0.048
CG6576	0.584	0.048
Tehao	0.584	0.048
CG15522	0.583	0.0485
magu	0.583	0.0485
vtb	0.583	0.0485
CG13931	0.582	0.0487
CG3036	0.582	0.0487
CG3216	0.582	0.0487
Glu-RI	0.582	0.0487
Andorra	0.581	0.0491
CG4996	0.581	0.0491
Gen	0.581	0.0491
Su(Tpl)	0.581	0.0491
Cpr49Aa	0.58	0.0495
La	0.58	0.0495
Ssb-c31a	0.58	0.0495
CG1888	0.579	0.0497
CG6867	0.579	0.0497
CG9248	0.579	0.0497
Drep-2	0.579	0.0497
l(2)35Bc	0.579	0.0497
nimB5	0.579	0.0497
Ast-CC	0.578	0.0503
CG12207	0.578	0.0503
CG14570	0.578	0.0503

Table 6.S7 Continued

Gene Name	ERC Value	P-value
CG33120	0.577	0.0505
comm	0.577	0.0505
CG18110	0.576	0.0507
CG34282	0.576	0.0507
CG42404	0.576	0.0507
Glt	0.576	0.0507
CG9609	0.575	0.0511
Cpr60D	0.575	0.0511
dbo	0.575	0.0511
Dg	0.575	0.0511
fend	0.575	0.0511
pex10	0.575	0.0511
Tom	0.575	0.0511
CG12213	0.574	0.0517
CG4615	0.574	0.0517
CG9747	0.573	0.0519
dm	0.573	0.0519
lace	0.573	0.0519
Orc2	0.573	0.0519
CG13005	0.572	0.0523
CG30020	0.572	0.0523
CG3631	0.572	0.0523
put	0.572	0.0523
RhoGAP100	0.572	0.0523
CG13424	0.571	0.0527
CG2993	0.571	0.0527
Oatp74D	0.571	0.0527
robo	0.571	0.0527
CG14963	0.57	0.0531
CG9894	0.57	0.0531
Drep-3	0.57	0.0531
Nup214	0.57	0.0531
sv	0.57	0.0531
CG4892	0.569	0.0535
cid	0.569	0.0535
Pi3K92E	0.569	0.0535
CG3655	0.568	0.0538
CG6758	0.568	0.0538
CG10140	0.567	0.054
CG4289	0.567	0.054
CG6927	0.567	0.054
CG9452	0.567	0.054
Lrrk	0.567	0.054
sec15	0.567	0.054
CG10326	0.566	0.0545
hkb	0.566	0.0545
CG10035	0.565	0.0547
CG8550	0.565	0.0547
Dip2	0.565	0.0547
EloA	0.565	0.0547
Hr7B	0.565	0.0547
SoxN	0.565	0.0547
CG12929	0.564	0.0552
D	0.563	0.0553
Dip3	0.563	0.0553
Hr96	0.563	0.0553

Gene Name	ERC Value	P-value
Nhe1	0.563	0.0553
Tsp97E	0.563	0.0553
CG11877	0.562	0.0558
CG12241	0.562	0.0558
CG13957	0.562	0.0558
CG15083	0.562	0.0558
CG18746	0.562	0.0558
CG10743	0.561	0.0562
CG31326	0.561	0.0562
CG32016	0.561	0.0562
CG4683	0.561	0.0562
CG5791	0.561	0.0562
CG7328	0.561	0.0562
Mad	0.561	0.0562
Saf-B	0.561	0.0562
SIDL	0.561	0.0562
CG14115	0.56	0.057
CG3744	0.56	0.057
CG4612	0.56	0.057
CG6144	0.56	0.057
Hsp67Ba	0.56	0.057
sec31	0.56	0.057
CG11919	0.559	0.0576
CG12003	0.559	0.0576
CG2003	0.559	0.0576
CG6792	0.559	0.0576
cact	0.558	0.0579
CG9760	0.558	0.0579
Gef26	0.558	0.0579
Hcs	0.558	0.0579
l(2)05714	0.558	0.0579
Tsp47F	0.558	0.0579
CG14627	0.557	0.0585
GlcAT-P	0.557	0.0585
MED10	0.557	0.0585
RnpS1	0.557	0.0585
Taf4	0.557	0.0585
CG13920	0.556	0.0589
CG9053	0.556	0.0589
cort	0.556	0.0589
dpr2	0.556	0.0589
Edg84A	0.556	0.0589
sunz	0.556	0.0589
CG10830	0.555	0.0595
CG3493	0.555	0.0595
lab	0.555	0.0595
sens-2	0.555	0.0595
CG17328	0.554	0.0598
CG5726	0.554	0.0598
gbb	0.554	0.0598
CG15322	0.553	0.0601
CG2811	0.553	0.0601
UbcD2	0.553	0.0601
brat	0.552	0.0604
CG34447	0.552	0.0604
CG7789	0.552	0.0604

Gene Name	ERC Value	P-value
CG8818	0.552	0.0604
CTCF	0.552	0.0604
Cyp4ae1	0.552	0.0604
Tusp	0.552	0.0604
ara	0.551	0.061
BBS1	0.551	0.061
CG14856	0.551	0.061
Rpn7	0.551	0.061
Syx13	0.551	0.061
CG11155	0.55	0.0614
CG16941	0.55	0.0614
CG33281	0.55	0.0614
Corp	0.55	0.0614
N	0.55	0.0614
aru	0.548	0.0619
CG8814	0.548	0.0619
Liprin-alpha	0.548	0.0619
CG12253	0.547	0.0622
CG7079	0.547	0.0622
SuUR	0.547	0.0622
swm	0.547	0.0622
CG31975	0.546	0.0625
CG3679	0.546	0.0625
CG8100	0.546	0.0625
if	0.546	0.0625
mRipS10	0.546	0.0625
ver	0.546	0.0625
CG14823	0.545	0.0631
CG3356	0.545	0.0631
Ge-1	0.545	0.0631
LpR1	0.545	0.0631
Nf-YC	0.545	0.0631
sina	0.545	0.0631
ato	0.544	0.0636
CG10681	0.544	0.0636
CG12038	0.544	0.0636
CG12012	0.543	0.0639
CG31226	0.543	0.0639
CG31706	0.543	0.0639
CG4452	0.543	0.0639
Cpr66Cb	0.543	0.0639
xmas-2	0.543	0.0639
CG6201	0.542	0.0644
CG7526	0.542	0.0644
Cyp49a1	0.542	0.0644
hb	0.542	0.0644
CG12507	0.541	0.0648
CG14072	0.541	0.0648
CG4328	0.541	0.0648
cv	0.541	0.0648
ksr	0.541	0.0648
Anxb11	0.54	0.0652
CG32541	0.54	0.0652
CG34331	0.54	0.0652
CG4398	0.54	0.0652
CG4496	0.54	0.0652

Gene Name	ERC Value	P-value
Fak56D	0.54	0.0652
Rb97D	0.54	0.0652
Vps45	0.54	0.0652
Cad96Cb	0.539	0.0659
CG14529	0.539	0.0659
CG15478	0.539	0.0659
FBX011	0.539	0.0659
l(2)INC136	0.539	0.0659
Rfx	0.539	0.0659
CG11131	0.538	0.0665
CG32832	0.538	0.0665
comm3	0.538	0.0665
mGluRA	0.538	0.0665
TwdlW	0.538	0.0665
Act88F	0.537	0.0669
CG2083	0.537	0.0669
CG4459	0.537	0.0669
Cpr65Ec	0.537	0.0669
Or88a	0.537	0.0669
CG10462	0.536	0.0674
CG9172	0.536	0.0674
cnk	0.536	0.0674
Cpr64Ad	0.536	0.0674
CG31688	0.535	0.0677
CG8397	0.535	0.0677
stj	0.535	0.0677
CG30273	0.534	0.068
CG32459	0.534	0.068
CG6136	0.534	0.068
lr94c	0.534	0.068
Bap170	0.533	0.0684
CG13350	0.533	0.0684
CG1529	0.533	0.0684
CG18031	0.533	0.0684
CG33510	0.533	0.0684
CG8683	0.533	0.0684
Spt3	0.533	0.0684
CG14442	0.532	0.069
CG2519	0.532	0.069
fz4	0.532	0.069
CG34293	0.531	0.0693
CG4619	0.531	0.0693
llp1	0.531	0.0693
Tsp42Eg	0.531	0.0693
CG30008	0.53	0.0696
CG34289	0.53	0.0696
CG7692	0.53	0.0696
CG9649	0.53	0.0696
DNApol-alpha	0.53	0.0696
NPFR1	0.53	0.0696
Rad1	0.53	0.0696
Spase18-21	0.53	0.0696
fs(1)N	0.529	0.0704
Gr77a	0.529	0.0704
sname	0.529	0.0704
BEAF-32	0.528	0.0706

Gene Name	ERC Value	P-value
CG11417	0.528	0.0706
CG31275	0.528	0.0706
CG4829	0.528	0.0706
CG5466	0.528	0.0706
Csk	0.528	0.0706
CG15744	0.527	0.0712
CG3386	0.527	0.0712
CG3611	0.527	0.0712
CG7781	0.527	0.0712
corn	0.527	0.0712
Orc5	0.527	0.0712
CG6689	0.526	0.0717
ect	0.526	0.0717
mre11	0.526	0.0717
capu	0.525	0.072
CG17026	0.525	0.072
CG31065	0.525	0.072
CG31211	0.525	0.072
CG3632	0.525	0.072
ct	0.525	0.072
Hsp67Bb	0.525	0.072
lic	0.525	0.072
mei-P22	0.525	0.072
Nhe3	0.525	0.072
Oatp26F	0.525	0.072
CG10713	0.524	0.073
CG6142	0.524	0.073
Lip1	0.524	0.073
CG10188	0.523	0.0732
CG14906	0.523	0.0732
CG33635	0.523	0.0732
Cpr72Eb	0.523	0.0732
Dip-B	0.523	0.0732
klg	0.523	0.0732
Mih1	0.523	0.0732
Ripalpha	0.523	0.0732
CG10251	0.522	0.074
CG14442	0.522	0.074
CG15212	0.522	0.074
CG32305	0.522	0.074
Gr58c	0.522	0.074
HLH54F	0.522	0.074
san	0.522	0.074
snRNP-U1-C	0.522	0.074
Tango9	0.522	0.074
CG3353	0.521	0.0748
CG8116	0.521	0.0748
CG8389	0.521	0.0748
CG9175	0.521	0.0748
CG10962	0.52	0.0751
CG12680	0.52	0.0751
Eap	0.52	0.0751
Lgr3	0.52	0.0751
Mst85C	0.52	0.0751
tsh	0.52	0.0751
Atg4	0.519	0.0757

Table 6.S7 Continued

Gene Name	ERC Value	P-value
CG10947	0.519	0.0757
CG17019	0.519	0.0757
CHLD3	0.519	0.0757
Sap130	0.519	0.0757
CG42748	0.518	0.0761
exo70	0.518	0.0761
Hmt-1	0.518	0.0761
Plip	0.518	0.0761
CG1647	0.517	0.0765
CG31798	0.517	0.0765
CG4022	0.517	0.0765
CG10588	0.516	0.0768
CG1104	0.516	0.0768
CG11889	0.516	0.0768
CG32379	0.516	0.0768
CG34174	0.516	0.0768
CG7251	0.516	0.0768
CG8141	0.516	0.0768
CG8552	0.516	0.0768
Cyp611	0.516	0.0768
m2	0.516	0.0768
Pp2B-14D	0.516	0.0768
CG1120	0.515	0.0777
CG16970	0.515	0.0777
CG5439	0.515	0.0777
d4	0.515	0.0777
mus312	0.515	0.0777
CG12831	0.514	0.0782
CG16926	0.514	0.0782
CG33704	0.514	0.0782
CG9068	0.514	0.0782
mRpS31	0.514	0.0782
CG10362	0.513	0.0786
CG2712	0.513	0.0786
CG33786	0.513	0.0786
Ir54a	0.513	0.0786
SeiR	0.513	0.0786
dimm	0.512	0.0791
HLHdelta	0.512	0.0791
amx	0.511	0.0793
CG13298	0.511	0.0793
CG9215	0.511	0.0793
crb	0.511	0.0793
slim	0.511	0.0793
sawah	0.511	0.0793
trus	0.511	0.0793
dpr20	0.51	0.0799
Os-E	0.51	0.0799
sens	0.51	0.0799
wek	0.51	0.0799
CG11164	0.509	0.0803
CG32846	0.509	0.0803
CG8317	0.509	0.0803
gek	0.509	0.0803
Lap1	0.509	0.0803
CG18480	0.508	0.0807

Gene Name	ERC Value	P-value
CG7384	0.508	0.0807
CG9044	0.508	0.0807
CG9426	0.507	0.081
Fsh	0.507	0.081
phi	0.507	0.081
Ptp69D	0.507	0.081
ca	0.506	0.0814
CG15035	0.506	0.0814
CG5056	0.506	0.0814
CG5322	0.506	0.0814
PR2	0.506	0.0814
bl	0.505	0.0818
CG30499	0.505	0.0818
Gdh	0.505	0.0818
Myd88	0.505	0.0818
CG10428	0.504	0.0822
CG10710	0.504	0.0822
CG11070	0.504	0.0822
CG12307	0.503	0.0824
CG18577	0.503	0.0824
CG3448	0.503	0.0824
CG4462	0.503	0.0824
D19A	0.503	0.0824
fus	0.503	0.0824
Hpr1	0.503	0.0824
[(1)G0289	0.503	0.0824
sda	0.503	0.0824
Trm-SR	0.503	0.0824
ana	0.502	0.0833
CG7860	0.502	0.0833
mp	0.502	0.0833
RagC	0.502	0.0833
CG13692	0.501	0.0837
CG15740	0.501	0.0837
CG18585	0.501	0.0837
CG5871	0.501	0.0837
CG6523	0.501	0.0837
grk	0.501	0.0837
jumu	0.501	0.0837
CG13185	0.5	0.0843
Mif	0.5	0.0843
CG14815	0.499	0.0845
CG6418	0.499	0.0845
E(spl)	0.499	0.0845
Bzd	0.498	0.0848
CG17190	0.498	0.0848
CG4592	0.498	0.0848
CG7146	0.498	0.0848
CG9752	0.498	0.0848
fog	0.498	0.0848
miple2	0.498	0.0848
phf1	0.498	0.0848
Syx4	0.498	0.0848
Act42A	0.497	0.0856
CG42554	0.497	0.0856
Tektin-A	0.497	0.0856

Gene Name	ERC Value	P-value
CG14086	0.496	0.0859
CG14459	0.496	0.0859
CG2789	0.496	0.0859
Lrt	0.496	0.0859
beat-1a	0.495	0.0862
CG10158	0.495	0.0862
CG12269	0.495	0.0862
CG3305	0.495	0.0862
CG4537	0.495	0.0862
Madm	0.495	0.0862
itk	0.495	0.0862
CG11395	0.494	0.0868
CG11448	0.494	0.0868
CG6480	0.494	0.0868
Dip-C	0.494	0.0868
mRpl1	0.494	0.0868
pds5	0.494	0.0868
CG10809	0.493	0.0874
CG13567	0.493	0.0874
CG32732	0.493	0.0874
CG3326	0.493	0.0874
CG6472	0.493	0.0874
Oaz	0.493	0.0874
Ret	0.493	0.0874
CG11668	0.492	0.088
CG12084	0.492	0.088
CG14195	0.492	0.088
CG15020	0.492	0.088
kar	0.492	0.088
malpha	0.492	0.088
nmd	0.492	0.088
Pink1	0.492	0.088
CG10555	0.491	0.0887
CG1671	0.491	0.0887
CG33155	0.491	0.0887
CG4553	0.491	0.0887
disco	0.491	0.0887
mbt	0.491	0.0887
wg	0.491	0.0887
CG13287	0.49	0.0894
CG6282	0.49	0.0894
Ent2	0.49	0.0894
gcm	0.49	0.0894
sec6	0.49	0.0894
CG31803	0.489	0.0898
CG4101	0.489	0.0898
CG13751	0.488	0.09
CG40198	0.488	0.09
Lig4	0.488	0.09
Su(z)12	0.488	0.09
AP-1sigma	0.487	0.0904
CG13375	0.487	0.0904
CG13875	0.487	0.0904
CG15099	0.487	0.0904
CG6511	0.487	0.0904
CG9344	0.487	0.0904

Gene Name	ERC Value	P-value
dpr11	0.487	0.0904
mus304	0.487	0.0904
Stam	0.487	0.0904
CG12379	0.486	0.0912
CG14989	0.486	0.0912
CG18234	0.486	0.0912
pkf	0.486	0.0912
Adgf-D	0.485	0.0915
beta3GalTII	0.485	0.0915
CDase	0.485	0.0915
CG18863	0.485	0.0915
CG2943	0.485	0.0915
CG8089	0.485	0.0915
CG9797	0.485	0.0915
Eig71Ef	0.485	0.0915
Spn27A	0.485	0.0915
Syt12	0.485	0.0915
Rpil140	0.484	0.0924
CG30421	0.484	0.0924
Pal	0.484	0.0924
Rrf1	0.484	0.0924
CG1316	0.483	0.0928
CG13454	0.483	0.0928
CG17083	0.483	0.0928
m6	0.483	0.0928
RpS16	0.483	0.0928
CG7028	0.482	0.0932
DNApol- α	0.482	0.0932
ppk7	0.482	0.0932
Rab-RP3	0.482	0.0932
Cdk9	0.481	0.0936
CG14894	0.481	0.0936
CG32040	0.481	0.0936
CG42251	0.481	0.0936
CG4607	0.481	0.0936
CG5116	0.481	0.0936
CG8366	0.481	0.0936
Cpsf73	0.481	0.0936
Pez	0.481	0.0936
Cad74A	0.48	0.0944
CG11534	0.48	0.0944
CG12219	0.48	0.0944
CG14834	0.48	0.0944
CG6461	0.48	0.0944
CG7120	0.48	0.0944
CG9410	0.48	0.0944
Prosbeta3	0.48	0.0944
pwn	0.48	0.0944
RhoGAP19C	0.48	0.0944
Sbf	0.48	0.0944
Stim	0.48	0.0944
CG15609	0.479	0.0955
CG6700	0.479	0.0955
dalao	0.479	0.0955
MED17	0.479	0.0955
Spt5	0.479	0.0955

Gene Name	ERC Value	P-value
CG13919	0.478	0.0959
CG33172	0.478	0.0959
CG4660	0.478	0.0959
CG6230	0.478	0.0959
CG7627	0.478	0.0959
Chd1	0.478	0.0959
eg	0.478	0.0959
Pask	0.478	0.0959
aref	0.477	0.0967
CG13044	0.477	0.0967
CG16789	0.477	0.0967
CG32354	0.477	0.0967
CG4554	0.477	0.0967
Cpr65Ay	0.477	0.0967
CstF-64	0.477	0.0967
Cyp28a5	0.477	0.0967
Or47a	0.477	0.0967
beat-lib	0.476	0.0975
CG13116	0.476	0.0975
CG13192	0.476	0.0975
CG6188	0.476	0.0975
CG8963	0.476	0.0975
mys	0.476	0.0975
Atg13	0.475	0.098
CG6796	0.475	0.098
p53	0.475	0.098
Pros25	0.475	0.098
CG10814	0.474	0.0984
CG1951	0.474	0.0984
CG34005	0.474	0.0984
CG9437	0.474	0.0984
grass	0.474	0.0984
Tsp42EK	0.474	0.0984
CG15570	0.473	0.0989
CG31373	0.473	0.0989
CG7695	0.473	0.0989
AlkB	0.472	0.0992
boss	0.472	0.0992
CG13239	0.472	0.0992
CG17304	0.472	0.0992
CG31221	0.472	0.0992
NTPase	0.472	0.0992
Or43b	0.472	0.0992
SPoCk	0.472	0.0992
CG11055	0.471	0.0999
CG13616	0.471	0.0999
CG1575	0.471	0.0999
CG18870	0.471	0.0999
CG9917	0.471	0.0999
enok	0.471	0.0999
fvd	0.471	0.0999
Myb	0.471	0.0999

Table 6.S8 - Top Genes ERC values for *mei-218* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Nup160</i>	0.924	0.0001
<i>spn-E</i>	0.916	0.0002
<i>CG8173</i>	0.915	0.0003
<i>CG10013</i>	0.913	0.0004
<i>CG4771</i>	0.912	0.0005
<i>CG31525</i>	0.91	0.0005
<i>CG18731</i>	0.907	0.0006
<i>CG12078</i>	0.901	0.0007
<i>CG4877</i>	0.898	0.0008
<i>CG10752</i>	0.894	0.0009
<i>CG13984</i>	0.889	0.001
<i>CG5762</i>	0.889	0.001
<i>fs(1)K10</i>	0.886	0.0012
<i>Dcr-2</i>	0.878	0.0013
<i>CG2147</i>	0.877	0.0014
<i>CG3056</i>	0.875	0.0014
<i>CG7332</i>	0.874	0.0015
<i>CG12857</i>	0.872	0.0016
<i>CG8097</i>	0.87	0.0017
<i>CG14303</i>	0.869	0.0018
<i>mus308</i>	0.869	0.0018
<i>Pros35</i>	0.863	0.002
<i>tej</i>	0.86	0.0021
<i>Ppm1</i>	0.856	0.0022
<i>coil</i>	0.85	0.0023
<i>Rpl133</i>	0.85	0.0023
<i>CG31320</i>	0.847	0.0024
<i>CG4449</i>	0.847	0.0024
<i>NetB</i>	0.846	0.0026
<i>CG2990</i>	0.844	0.0027
<i>CG32812</i>	0.844	0.0027
<i>bam</i>	0.843	0.0029
<i>CG13131</i>	0.842	0.003
<i>CG9650</i>	0.841	0.0031
<i>CG5642</i>	0.84	0.0032
<i>CG18065</i>	0.839	0.0032
<i>CG4593</i>	0.839	0.0032
<i>CG8090</i>	0.839	0.0032
<i>CG17826</i>	0.838	0.0035
<i>CG18605</i>	0.835	0.0036
<i>CG8105</i>	0.834	0.0037
<i>Spec2</i>	0.833	0.0038
<i>CG15311</i>	0.831	0.0039
<i>Tom70</i>	0.831	0.0039
<i>acj6</i>	0.83	0.0041
<i>CG3940</i>	0.83	0.0041
<i>CG13741</i>	0.829	0.0042
<i>CG4362</i>	0.826	0.0043
<i>sbr</i>	0.825	0.0044
<i>CG4294</i>	0.824	0.0045
<i>Scp</i>	0.824	0.0045
<i>CG2533</i>	0.823	0.0047
<i>Fs(2)Ket</i>	0.823	0.0047
<i>CG7691</i>	0.822	0.0049
<i>Hrd3</i>	0.822	0.0049
<i>shu</i>	0.821	0.005

Gene Name	ERC Value	P-value
<i>CG12179</i>	0.82	0.0051
<i>ttm50</i>	0.82	0.0051
<i>CG11133</i>	0.814	0.0053
<i>CG15601</i>	0.814	0.0053
<i>CG2972</i>	0.814	0.0053
<i>CG13197</i>	0.813	0.0056
<i>CG3847</i>	0.813	0.0056
<i>CG9926</i>	0.813	0.0056
<i>CG7366</i>	0.808	0.0059
<i>cuff</i>	0.806	0.0059
<i>Ars2</i>	0.805	0.006
<i>Sh</i>	0.804	0.0061
<i>Moca-cyp</i>	0.802	0.0062
<i>CG15368</i>	0.799	0.0063
<i>Hand</i>	0.799	0.0063
<i>Pbprp2</i>	0.798	0.0065
<i>CG15876</i>	0.797	0.0066
<i>CG17928</i>	0.797	0.0066
<i>CG31752</i>	0.795	0.0068
<i>luna</i>	0.795	0.0068
<i>CG12590</i>	0.792	0.0069
<i>Pros28.1</i>	0.792	0.0069
<i>CG13865</i>	0.789	0.0071
<i>CG32712</i>	0.788	0.0072
<i>CG2129</i>	0.786	0.0073
<i>Art9</i>	0.785	0.0074
<i>CG8683</i>	0.785	0.0074
<i>Gem3</i>	0.784	0.0076
<i>Aos1</i>	0.78	0.0077
<i>CG32075</i>	0.78	0.0077
<i>CG16753</i>	0.778	0.0078
<i>CG30376</i>	0.778	0.0078
<i>CG6967</i>	0.777	0.008
<i>RhoGAP18E</i>	0.776	0.0081
<i>Taf12L</i>	0.776	0.0081
<i>MBD-R2</i>	0.773	0.0083
<i>CG1646</i>	0.772	0.0084
<i>ef(y)1</i>	0.772	0.0084
<i>E(var)3-9</i>	0.771	0.0086
<i>CG42707</i>	0.77	0.0086
<i>CG5398</i>	0.77	0.0086
<i>CG6304</i>	0.77	0.0086
<i>CG7101</i>	0.77	0.0086
<i>CSN1a</i>	0.767	0.009
<i>ttm2</i>	0.767	0.009
<i>CG12029</i>	0.766	0.0092
<i>CG13380</i>	0.765	0.0093
<i>CG9581</i>	0.765	0.0093
<i>Dlic</i>	0.765	0.0093
<i>CG13733</i>	0.764	0.0095
<i>CG10317</i>	0.763	0.0096
<i>CG31950</i>	0.763	0.0096
<i>CG6962</i>	0.763	0.0096
<i>CG5660</i>	0.762	0.0099
<i>CG9203</i>	0.762	0.0099
<i>dgt1</i>	0.762	0.0099

Gene Name	ERC Value	P-value
<i>HmgZ</i>	0.761	0.0102
<i>XNP</i>	0.761	0.0102
<i>CG14931</i>	0.76	0.0104
<i>c12.1</i>	0.759	0.0105
<i>CG1231</i>	0.759	0.0105
<i>CG11912</i>	0.758	0.0106
<i>CG30417</i>	0.758	0.0106
<i>THIA-L</i>	0.758	0.0106
<i>CG7504</i>	0.756	0.0109
<i>CG8038</i>	0.756	0.0109
<i>CG1421</i>	0.755	0.0111
<i>CG15124</i>	0.755	0.0111
<i>CG9925</i>	0.754	0.0113
<i>dy</i>	0.754	0.0113
<i>Hsc70-4</i>	0.754	0.0113
<i>DAAM</i>	0.753	0.0115
<i>can</i>	0.752	0.0116
<i>CG1764</i>	0.752	0.0116
<i>vis</i>	0.752	0.0116
<i>CG12442</i>	0.751	0.0119
<i>knimp</i>	0.751	0.0119
<i>SMC2</i>	0.751	0.0119
<i>CG14438</i>	0.75	0.0122
<i>CG30154</i>	0.75	0.0122
<i>Neos</i>	0.75	0.0122
<i>ord</i>	0.749	0.0124
<i>APP-BP1</i>	0.748	0.0125
<i>Dcp2</i>	0.748	0.0125
<i>PCID2</i>	0.748	0.0125
<i>Upf2</i>	0.748	0.0125
<i>CG8974</i>	0.745	0.0129
<i>Tango2</i>	0.745	0.0129
<i>CG12010</i>	0.744	0.0131
<i>PK34A</i>	0.744	0.0131
<i>CG10265</i>	0.743	0.0132
<i>Fs</i>	0.743	0.0132
<i>Hen1</i>	0.743	0.0132
<i>CG31805</i>	0.742	0.0135
<i>Rrp45</i>	0.741	0.0136
<i>t-cup</i>	0.741	0.0136
<i>CG33286</i>	0.74	0.0138
<i>CG11092</i>	0.739	0.0139
<i>CG4854</i>	0.739	0.0139
<i>Bruce</i>	0.738	0.0141
<i>CG4788</i>	0.738	0.0141
<i>CG7213</i>	0.738	0.0141
<i>aly</i>	0.737	0.0143
<i>CG3394</i>	0.737	0.0143
<i>SrnB</i>	0.737	0.0143
<i>CG15399</i>	0.736	0.0146
<i>CG10414</i>	0.735	0.0147
<i>CG1134</i>	0.735	0.0147
<i>CG6808</i>	0.734	0.0149
<i>DLP</i>	0.734	0.0149
<i>l(2)35Cc</i>	0.733	0.015
<i>CG2258</i>	0.732	0.0151

Gene Name	ERC Value	P-value
<i>CG3726</i>	0.732	0.0151
<i>CG2750</i>	0.731	0.0153
<i>CG34115</i>	0.731	0.0153
<i>CG13725</i>	0.73	0.0155
<i>CG3071</i>	0.73	0.0155
<i>CG5862</i>	0.73	0.0155
<i>CG8298</i>	0.73	0.0155
<i>CG9692</i>	0.73	0.0155
<i>JIL-1</i>	0.73	0.0155
<i>CG13894</i>	0.729	0.016
<i>mRNA-capp</i>	0.728	0.0161
<i>rut</i>	0.728	0.0161
<i>Got2</i>	0.727	0.0163
<i>Gtp-bp</i>	0.727	0.0163
<i>Adff</i>	0.725	0.0165
<i>CG16815</i>	0.725	0.0165
<i>CG1690</i>	0.725	0.0165
<i>CG6893</i>	0.725	0.0165
<i>Snm1</i>	0.725	0.0165
<i>Opbp</i>	0.724	0.0169
<i>CG8798</i>	0.723	0.017
<i>CG14930</i>	0.722	0.0171
<i>Mis12</i>	0.722	0.0171
<i>CG32095</i>	0.721	0.0173
<i>Nop60B</i>	0.721	0.0173
<i>Use1</i>	0.721	0.0173
<i>blp</i>	0.72	0.0176
<i>CG15549</i>	0.72	0.0176
<i>CG33262</i>	0.72	0.0176
<i>CG34205</i>	0.72	0.0176
<i>CG32319</i>	0.719	0.0179
<i>CG6579</i>	0.719	0.0179
<i>CG2199</i>	0.718	0.0181
<i>CG31820</i>	0.718	0.0181
<i>CG11560</i>	0.717	0.0183
<i>poe</i>	0.717	0.0183
<i>rdgA</i>	0.716	0.0185
<i>CG15369</i>	0.715	0.0186
<i>Syx18</i>	0.715	0.0186
<i>CG14383</i>	0.713	0.0187
<i>Hmr</i>	0.713	0.0187
<i>Irk2</i>	0.713	0.0187
<i>CG10254</i>	0.712	0.019
<i>CG13220</i>	0.712	0.019
<i>Prosbeta2R</i>	0.712	0.019
<i>blw</i>	0.711	0.0193
<i>CG15711</i>	0.709	0.0194
<i>CG9133</i>	0.709	0.0194
<i>lin-52</i>	0.709	0.0194
<i>sws</i>	0.709	0.0194
<i>CG2617</i>	0.708	0.0197
<i>csul</i>	0.708	0.0197
<i>CG10931</i>	0.706	0.0199
<i>CG12118</i>	0.706	0.0199
<i>CG34104</i>	0.706	0.0199
<i>nht</i>	0.706	0.0199

Gene Name	ERC Value	P-value
<i>bol</i>	0.705	0.0203
<i>CG32533</i>	0.705	0.0203
<i>RpS25</i>	0.705	0.0203
<i>CG31862</i>	0.704	0.0205
<i>Cpr47Ef</i>	0.704	0.0205
<i>Fsn</i>	0.704	0.0205
<i>Tango4</i>	0.703	0.0208
<i>Trf4-2</i>	0.703	0.0208
<i>Jupiter</i>	0.7	0.021
<i>Aly</i>	0.699	0.0211
<i>IP3K2</i>	0.699	0.0211
<i>CG13148</i>	0.698	0.0213
<i>nmo</i>	0.698	0.0213
<i>Ckl1alpha-1</i>	0.697	0.0214
<i>CG32810</i>	0.696	0.0215
<i>CG9863</i>	0.696	0.0215
<i>shep</i>	0.696	0.0215
<i>CG14006</i>	0.695	0.0218
<i>CG7387</i>	0.695	0.0218
<i>tomb</i>	0.695	0.0218
<i>Vsx2</i>	0.695	0.0218
<i>AIF</i>	0.694	0.0222
<i>Marf</i>	0.694	0.0222
<i>CG5355</i>	0.693	0.0223
<i>CG9153</i>	0.693	0.0223
<i>ees</i>	0.693	0.0223
<i>inx6</i>	0.693	0.0223
<i>Synd</i>	0.693	0.0223
<i>Bj1</i>	0.692	0.0228
<i>DmsR-2</i>	0.691	0.0229
<i>armi</i>	0.69	0.023
<i>ab</i>	0.689	0.0231
<i>CG13253</i>	0.689	0.0231
<i>CG32006</i>	0.689	0.0231
<i>CG4617</i>	0.689	0.0231
<i>l(3)psg2</i>	0.689	0.0231
<i>CG18266</i>	0.688	0.0235
<i>CG5265</i>	0.687	0.0236
<i>CG10063</i>	0.686	0.0237
<i>CG17261</i>	0.686	0.0237
<i>CG9934</i>	0.686	0.0237
<i>CG9973</i>	0.686	0.0237
<i>Dis3</i>	0.686	0.0237
<i>CG5194</i>	0.683	0.0241
<i>comr</i>	0.682	0.0242
<i>HP54</i>	0.682	0.0242
<i>CG15649</i>	0.681	0.0244
<i>Oamb</i>	0.681	0.0244
<i>CG6308</i>	0.68	0.0246
<i>CG8931</i>	0.68	0.0246
<i>CG3698</i>	0.679	0.0248
<i>Roc2</i>	0.679	0.0248
<i>CG14589</i>	0.678	0.025
<i>CG1317</i>	0.677	0.025
<i>for</i>	0.677	0.025
<i>CG16712</i>	0.676	0.0252

Table 6.S8 Continued

Gene Name	ERC Value	P-value
CG5161	0.676	0.0252
CG8915	0.676	0.0252
Ptpa	0.676	0.0252
mRpl3	0.675	0.0256
CG12438	0.674	0.0257
elF4E-5	0.674	0.0257
mud	0.674	0.0257
vig2	0.674	0.0257
CG14103	0.673	0.026
CG9125	0.673	0.026
unc	0.673	0.026
yuri	0.673	0.026
asl	0.672	0.0264
Klp59C	0.672	0.0264
O-fut2	0.672	0.0264
Rev1	0.672	0.0264
CG13108	0.671	0.0268
CG4789	0.671	0.0268
Nca	0.671	0.0268
Doa	0.67	0.027
CG4836	0.668	0.0271
CG7071	0.668	0.0271
Scgalpha	0.668	0.0271
sra	0.668	0.0271
Tim9a	0.668	0.0271
CG6628	0.667	0.0276
Mad1	0.667	0.0276
Nup358	0.667	0.0276
CG32246	0.666	0.0278
exd	0.666	0.0278
Nup107	0.666	0.0278
CG2247	0.665	0.0281
CG6179	0.665	0.0281
CG9346	0.665	0.0281
mge	0.665	0.0281
CG14407	0.664	0.0285
CG32576	0.664	0.0285
mmps	0.664	0.0285
Prp8	0.664	0.0285
CG31922	0.663	0.0288
CG34029	0.663	0.0288
CG6299	0.663	0.0288
CG3408	0.662	0.0291
CG5703	0.662	0.0291
CG7017	0.662	0.0291
Kdm4B	0.661	0.0294
Taf10b	0.661	0.0294
CG12236	0.66	0.0295
CG7065	0.66	0.0295
CG8771	0.66	0.0295
Hyd2	0.66	0.0295
CG12721	0.659	0.0299
CG13284	0.659	0.0299
CG31550	0.659	0.0299
CG7675	0.659	0.0299
CG9240	0.659	0.0299

Gene Name	ERC Value	P-value
vial	0.658	0.0304
CG11570	0.657	0.0305
CG9514	0.657	0.0305
CG12860	0.656	0.0306
CG1815	0.656	0.0306
CG30356	0.656	0.0306
CG1463	0.655	0.0309
CG17293	0.655	0.0309
CG10638	0.654	0.0311
CG12096	0.654	0.0311
CG32703	0.654	0.0311
Mtor	0.654	0.0311
CG17732	0.653	0.0314
CG34181	0.653	0.0314
CG4198	0.653	0.0314
Nup153	0.653	0.0314
scrib	0.653	0.0314
CG13474	0.652	0.0319
Marcal1	0.652	0.0319
CG10673	0.651	0.0321
CG12035	0.651	0.0321
Ets97D	0.651	0.0321
mu2	0.651	0.0321
CG33213	0.65	0.0324
CG5859	0.65	0.0324
CG8728	0.65	0.0324
CG9247	0.65	0.0324
CG34302	0.649	0.0328
CG7766	0.649	0.0328
CG8273	0.649	0.0328
casp	0.648	0.0331
CG13744	0.648	0.0331
CG30156	0.648	0.0331
CG8629	0.648	0.0331
CG9235	0.648	0.0331
CG3517	0.647	0.0335
CG3680	0.647	0.0335
l(1)dd4	0.647	0.0335
CG11263	0.646	0.0338
CG1234	0.646	0.0338
CG15874	0.646	0.0338
CG31848	0.646	0.0338
CG12672	0.645	0.0341
CG33051	0.645	0.0341
maf-S	0.644	0.0343
yellow-g2	0.644	0.0343
CG12535	0.643	0.0345
CG7884	0.643	0.0345
CG4956	0.642	0.0347
CG9003	0.642	0.0347
4EHP	0.641	0.0349
CG11110	0.641	0.0349
CG17048	0.641	0.0349
CG10267	0.64	0.0351
CG7945	0.64	0.0351
l(3)mbt	0.64	0.0351

Gene Name	ERC Value	P-value
RanBPM	0.64	0.0351
CG3893	0.639	0.0355
CG7886	0.639	0.0355
prtp	0.639	0.0355
CG16940	0.637	0.0358
CG31010	0.637	0.0358
CG1055	0.637	0.0358
CG7376	0.637	0.0358
l(2)03709	0.637	0.0358
CG11638	0.636	0.0362
cyp33	0.636	0.0362
Oscp	0.636	0.0362
CG13558	0.635	0.0365
CG32685	0.635	0.0365
CG6540	0.635	0.0365
Hrs	0.635	0.0365
mRps30	0.635	0.0365
CG15814	0.634	0.0369
CG5050	0.634	0.0369
CG32803	0.633	0.0371
CG3436	0.633	0.0371
CG4806	0.633	0.0371
CG5071	0.633	0.0371
CG5196	0.633	0.0371
CG6621	0.633	0.0371
CG11279	0.632	0.0377
CG13026	0.632	0.0377
CG42516	0.632	0.0377
RhoGAP15E	0.632	0.0377
CG11526	0.631	0.038
CG1732	0.631	0.038
CG10979	0.63	0.0382
CG1468	0.63	0.0382
CG2974	0.63	0.0382
CG4400	0.63	0.0382
CG7429	0.63	0.0382
CG7518	0.63	0.0382
CG9548	0.63	0.0382
r2d2	0.63	0.0382
ana3	0.629	0.0389
CG12129	0.629	0.0389
Rrp42	0.629	0.0389
Bx42	0.628	0.0392
CG11018	0.628	0.0392
Rnp4F	0.628	0.0392
tex	0.628	0.0392
CG8414	0.627	0.0395
CG42327	0.626	0.0396
CG4676	0.626	0.0396
CG5543	0.626	0.0396
clin	0.626	0.0396
MED4	0.626	0.0396
vir	0.626	0.0396
CG14087	0.625	0.0402
CG3919	0.625	0.0402
row	0.625	0.0402

Gene Name	ERC Value	P-value
CG16825	0.624	0.0405
CG9682	0.624	0.0405
CG14646	0.623	0.0406
CG17272	0.623	0.0406
CG31739	0.623	0.0406
CG6197	0.623	0.0406
Sfp53D	0.623	0.0406
Akt1	0.621	0.0411
CG10616	0.621	0.0411
CG10880	0.621	0.0411
fry	0.621	0.0411
CG18869	0.62	0.0414
CG4933	0.62	0.0414
CG7557	0.62	0.0414
Bet5	0.619	0.0417
CAH1	0.619	0.0417
CG14839	0.619	0.0417
se	0.619	0.0417
CG8320	0.618	0.0421
ecd	0.618	0.0421
Sirt2	0.618	0.0421
CG10803	0.617	0.0423
CG18155	0.617	0.0423
CG1902	0.617	0.0423
park	0.617	0.0423
Taf1	0.617	0.0423
CG14812	0.616	0.0428
CG8066	0.616	0.0428
tst	0.616	0.0428
tsu	0.616	0.0428
CG15917	0.615	0.0432
CG42455	0.615	0.0432
CG12081	0.614	0.0433
CG15863	0.614	0.0433
wfs1	0.614	0.0433
LRP1	0.613	0.0436
Taf6	0.613	0.0436
Ube3a	0.613	0.0436
CG11658	0.612	0.0439
CG15482	0.612	0.0439
CG15657	0.612	0.0439
CG15705	0.612	0.0439
CG34040	0.612	0.0439
CG42675	0.612	0.0439
Atg8a	0.611	0.0444
CG17658	0.611	0.0444
Ccp84Ag	0.61	0.0446
CG7077	0.61	0.0446
Taf2	0.61	0.0446
CG11807	0.609	0.0449
CG31551	0.609	0.0449
CG8184	0.609	0.0449
ely2	0.609	0.0449
CycJ	0.608	0.0452
Elip78C	0.608	0.0452
CG14269	0.607	0.0454

Gene Name	ERC Value	P-value
CG8712	0.607	0.0454
ort	0.607	0.0454
pita	0.607	0.0454
Tob	0.606	0.0458
Ubc84D	0.606	0.0458
Ufd1-like	0.606	0.0458
CG1707	0.605	0.046
CG40045	0.605	0.046
ns3	0.605	0.046
sfl	0.605	0.046
elF-2alpha	0.604	0.0464
lrtp	0.604	0.0464
RASSF8	0.604	0.0464
Art51F	0.603	0.0467
CG17098	0.603	0.0467
CG3815	0.603	0.0467
Mes-4	0.603	0.0467
Rhp	0.603	0.0467
CG10694	0.602	0.0471
CG7094	0.602	0.0471
CG4995	0.601	0.0473
CHES-1-like	0.601	0.0473
CG10496	0.6	0.0475
CG3014	0.6	0.0475
CG34130	0.6	0.0475
Jheh1	0.6	0.0475
CG6175	0.599	0.0478
CG7295	0.599	0.0478
Aih	0.598	0.048
ATPsyn-garr	0.598	0.048
CG14322	0.598	0.048
CG4520	0.598	0.048
CG6568	0.598	0.048
Taz	0.598	0.048
CG14937	0.597	0.0486
Hs6st	0.597	0.0486
CG15458	0.596	0.0487
Cyp313b1	0.596	0.0487
CG16721	0.595	0.0489
CG5292	0.595	0.0489
Spargel	0.595	0.0489
CG10263	0.594	0.0492
CG9014	0.594	0.0492
Muc18B	0.594	0.0492
squ	0.594	0.0492
Uba2	0.594	0.0492
CG14624	0.593	0.0496
CG15278	0.593	0.0496
CG1677	0.593	0.0496
CG5118	0.593	0.0496
CG15172	0.592	0.05
CSN3	0.592	0.05
inx5	0.592	0.05
Sema-1a	0.592	0.0504
CG2901	0.591	0.0504
Kdm4A	0.591	0.0504

Table 6.S8 Continued

Gene Name	ERC Value	P-value
<i>Su(var)3-3</i>	0.591	0.0504
<i>CG15034</i>	0.59	0.0506
<i>CG9413</i>	0.59	0.0506
<i>rab3-GEF</i>	0.589	0.0508
<i>Smg1</i>	0.589	0.0508
<i>tat1</i>	0.589	0.0508
<i>CG12384</i>	0.587	0.0511
<i>CG13393</i>	0.587	0.0511
<i>CG15605</i>	0.587	0.0511
<i>CG1824</i>	0.587	0.0511
<i>CG2292</i>	0.587	0.0511
<i>CG31679</i>	0.587	0.0511
<i>CG33960</i>	0.587	0.0511
<i>CG3491</i>	0.587	0.0511
<i>CG7202</i>	0.587	0.0511
<i>CG7990</i>	0.587	0.0511
<i>lswi</i>	0.587	0.0511
<i>Pbp49</i>	0.586	0.0521
<i>CG33199</i>	0.585	0.0522
<i>heph</i>	0.584	0.0523
<i>CG5539</i>	0.583	0.0523
<i>CG7262</i>	0.583	0.0523
<i>CG12279</i>	0.582	0.0525
<i>CG12413</i>	0.582	0.0525
<i>CG14300</i>	0.582	0.0525
<i>CG5482</i>	0.582	0.0525
<i>CG6230</i>	0.582	0.0525
<i>CG7139</i>	0.582	0.0525
<i>CG8316</i>	0.582	0.0525
<i>ena</i>	0.582	0.0525
<i>RpL32</i>	0.582	0.0525
<i>CG11379</i>	0.581	0.0533
<i>CG14739</i>	0.581	0.0533
<i>CG14151</i>	0.58	0.0535
<i>CG3887</i>	0.58	0.0535
<i>inaC</i>	0.58	0.0535
<i>l(1)10Bb</i>	0.58	0.0535
<i>CG5532</i>	0.579	0.0539
<i>CG8100</i>	0.579	0.0539
<i>Ddr</i>	0.579	0.0539
<i>Naam</i>	0.579	0.0539
<i>caz</i>	0.578	0.0542
<i>CG32240</i>	0.578	0.0542
<i>CG5928</i>	0.578	0.0542
<i>mod</i>	0.578	0.0542
<i>A16</i>	0.577	0.0546
<i>CG11345</i>	0.577	0.0546
<i>dwg</i>	0.577	0.0546
<i>PpN58A</i>	0.577	0.0546
<i>ATPsyn-Cf6</i>	0.576	0.055
<i>cal1</i>	0.576	0.055
<i>CG3106</i>	0.576	0.055
<i>CG4165</i>	0.576	0.055
<i>Stmbt</i>	0.576	0.055
<i>Att3</i>	0.575	0.0554
<i>CG1523</i>	0.575	0.0554

Gene Name	ERC Value	P-value
<i>CG3162</i>	0.575	0.0554
<i>CG1908</i>	0.574	0.0557
<i>CG2641</i>	0.574	0.0557
<i>yellow-g</i>	0.574	0.0557
<i>CG11943</i>	0.573	0.0559
<i>CG2662</i>	0.573	0.0559
<i>CG6766</i>	0.573	0.0559
<i>Or66a</i>	0.573	0.0559
<i>raw</i>	0.573	0.0559
<i>Ubqn</i>	0.573	0.0559
<i>z</i>	0.573	0.0559
<i>CG3894</i>	0.572	0.0566
<i>CG4364</i>	0.572	0.0566
<i>gp210</i>	0.572	0.0566
<i>Snap</i>	0.572	0.0566
<i>CG12362</i>	0.571	0.0569
<i>CG12395</i>	0.571	0.0569
<i>CG1503</i>	0.571	0.0569
<i>CG6597</i>	0.571	0.0569
<i>Rae1</i>	0.571	0.0569
<i>Rel</i>	0.571	0.0569
<i>CG12985</i>	0.57	0.0575
<i>CG17068</i>	0.57	0.0575
<i>CG18643</i>	0.57	0.0575
<i>Klp10A</i>	0.57	0.0575
<i>Rcd1</i>	0.57	0.0575
<i>Smg6</i>	0.57	0.0575
<i>Srp19</i>	0.57	0.0575
<i>Cad87A</i>	0.569	0.0581
<i>ena</i>	0.569	0.0581
<i>CG14005</i>	0.569	0.0581
<i>CG9875</i>	0.569	0.0581
<i>fl(2)d</i>	0.569	0.0581
<i>mael</i>	0.569	0.0581
<i>CG10459</i>	0.568	0.0586
<i>kni</i>	0.568	0.0586
<i>ncm</i>	0.568	0.0586
<i>stwl</i>	0.568	0.0586
<i>CG10631</i>	0.567	0.059
<i>CG14130</i>	0.567	0.059
<i>CG15357</i>	0.567	0.059
<i>tud</i>	0.567	0.059
<i>Arp87C</i>	0.566	0.0594
<i>CG12446</i>	0.566	0.0594
<i>CG18258</i>	0.566	0.0594
<i>CG31682</i>	0.566	0.0594
<i>CG13003</i>	0.565	0.0597
<i>CG13123</i>	0.565	0.0597
<i>CG14797</i>	0.565	0.0597
<i>RluA-2</i>	0.565	0.0597
<i>CG15725</i>	0.564	0.0601
<i>CG34296</i>	0.564	0.0601
<i>Dh</i>	0.564	0.0601
<i>CG11251</i>	0.563	0.0604
<i>CG15262</i>	0.563	0.0604
<i>Sec22</i>	0.563	0.0604

Gene Name	ERC Value	P-value
<i>CG9970</i>	0.562	0.0606
<i>Rgk1</i>	0.561	0.0607
<i>SmG</i>	0.561	0.0607
<i>CG4810</i>	0.56	0.0609
<i>CG6380</i>	0.56	0.0609
<i>CG8010</i>	0.56	0.0609
<i>Trax</i>	0.56	0.0609
<i>CG33282</i>	0.559	0.0613
<i>CG33172</i>	0.558	0.0614
<i>otu</i>	0.558	0.0614
<i>Set2</i>	0.558	0.0614
<i>snf</i>	0.558	0.0614
<i>mito</i>	0.556	0.0617
<i>Rrp46</i>	0.556	0.0617
<i>CG15643</i>	0.555	0.0619
<i>CG32649</i>	0.555	0.0619
<i>mle</i>	0.555	0.0619
<i>CG1120</i>	0.554	0.0622
<i>CG15771</i>	0.554	0.0622
<i>Dhc64C</i>	0.554	0.0622
<i>tral</i>	0.554	0.0622
<i>CG11927</i>	0.553	0.0625
<i>CG11985</i>	0.553	0.0625
<i>CG18269</i>	0.553	0.0625
<i>soti</i>	0.553	0.0625
<i>CG11964</i>	0.552	0.0629
<i>Art3</i>	0.551	0.063
<i>CG1695</i>	0.551	0.063
<i>CG14913</i>	0.55	0.0632
<i>CG15317</i>	0.55	0.0632
<i>Ucp4A</i>	0.55	0.0632
<i>CG17378</i>	0.549	0.0634
<i>CG6412</i>	0.549	0.0634
<i>mago</i>	0.549	0.0634
<i>CG31528</i>	0.548	0.0637
<i>Tim10</i>	0.548	0.0637
<i>CG2051</i>	0.547	0.0639
<i>CG30383</i>	0.547	0.0639
<i>dre4</i>	0.547	0.0639
<i>Rdl</i>	0.547	0.0639
<i>Ten-m</i>	0.547	0.0639
<i>dgt2</i>	0.546	0.0643
<i>ps</i>	0.546	0.0643
<i>CAP-D2</i>	0.545	0.0645
<i>CG11779</i>	0.545	0.0645
<i>slo</i>	0.545	0.0645
<i>Caf1-180</i>	0.544	0.0648
<i>CG43078</i>	0.544	0.0648
<i>CG5514</i>	0.544	0.0648
<i>Klp31E</i>	0.544	0.0648
<i>pch2</i>	0.544	0.0648
<i>Smc5</i>	0.544	0.0648
<i>CG32302</i>	0.543	0.0653
<i>CG34360</i>	0.543	0.0653
<i>CG4951</i>	0.543	0.0653
<i>CG7556</i>	0.543	0.0653

Gene Name	ERC Value	P-value
<i>TFAM</i>	0.543	0.0653
<i>CG32055</i>	0.542	0.0658
<i>CG8141</i>	0.542	0.0658
<i>cry</i>	0.542	0.0658
<i>CG2061</i>	0.541	0.066
<i>CG6650</i>	0.541	0.066
<i>Ptp98A</i>	0.541	0.066
<i>Rrp40</i>	0.541	0.066
<i>seq</i>	0.541	0.066
<i>CG15909</i>	0.54	0.0665
<i>CG3511</i>	0.54	0.0665
<i>CG8079</i>	0.54	0.0665
<i>Mob4</i>	0.54	0.0665
<i>msk</i>	0.54	0.0665
<i>CG10365</i>	0.539	0.0669
<i>CG31646</i>	0.539	0.0669
<i>CG4936</i>	0.539	0.0669
<i>CG7707</i>	0.539	0.0669
<i>c-cup</i>	0.538	0.0673
<i>CG14684</i>	0.538	0.0673
<i>CG30466</i>	0.538	0.0673
<i>CG5798</i>	0.538	0.0673
<i>CG6459</i>	0.538	0.0673
<i>Chc</i>	0.538	0.0673
<i>Kr-h2</i>	0.538	0.0673
<i>CG14358</i>	0.537	0.0679
<i>CG3306</i>	0.537	0.0679
<i>Pcl</i>	0.537	0.0679
<i>Scgdelta</i>	0.537	0.0679
<i>vap</i>	0.537	0.0679
<i>CG33308</i>	0.536	0.0684
<i>CG6204</i>	0.536	0.0684
<i>CG8830</i>	0.536	0.0684
<i>CG10163</i>	0.535	0.0686
<i>CG31251</i>	0.535	0.0686
<i>CG31910</i>	0.535	0.0686
<i>Est-Q</i>	0.535	0.0686
<i>Arp8</i>	0.534	0.069
<i>CG17230</i>	0.534	0.069
<i>CG18131</i>	0.534	0.069
<i>CG2116</i>	0.534	0.069
<i>CG31627</i>	0.534	0.069
<i>CG31851</i>	0.534	0.069
<i>CG7837</i>	0.534	0.069
<i>tomosyn</i>	0.534	0.069
<i>vav</i>	0.534	0.069
<i>CG13889</i>	0.533	0.0698
<i>CG14805</i>	0.533	0.0698
<i>CG5217</i>	0.533	0.0698
<i>Jon65Aiii</i>	0.533	0.0698
<i>Pp2C1</i>	0.533	0.0698
<i>CG6171</i>	0.532	0.0703
<i>CG9323</i>	0.532	0.0703
<i>D1</i>	0.532	0.0703
<i>dym-p25</i>	0.532	0.0703
<i>retm</i>	0.532	0.0703

Gene Name	ERC Value	P-value
<i>CG11768</i>	0.531	0.0707
<i>CG14317</i>	0.531	0.0707
<i>CG15708</i>	0.531	0.0707
<i>CG2698</i>	0.531	0.0707
<i>CG3342</i>	0.531	0.0707
<i>CG6729</i>	0.531	0.0707
<i>Dsp1</i>	0.531	0.0707
<i>Roc1b</i>	0.531	0.0707
<i>CG10654</i>	0.53	0.0714
<i>CG3092</i>	0.53	0.0714
<i>CG33080</i>	0.53	0.0714
<i>CG6569</i>	0.53	0.0714
<i>Ino80</i>	0.53	0.0714
<i>Sbp2</i>	0.53	0.0714
<i>SPoCk</i>	0.53	0.0714
<i>CG10306</i>	0.529	0.0721
<i>CG17209</i>	0.529	0.0721
<i>CG2183</i>	0.529	0.0721
<i>CG7326</i>	0.529	0.0721
<i>CG8334</i>	0.529	0.0721
<i>Rbp9</i>	0.529	0.0721
<i>CG4230</i>	0.528	0.0726
<i>CG9518</i>	0.528	0.0726
<i>Eaf</i>	0.528	0.0726
<i>Ace</i>	0.527	0.0729
<i>CG14593</i>	0.527	0.0729
<i>CG1826</i>	0.527	0.0729
<i>CG2941</i>	0.527	0.0729
<i>Cep97</i>	0.526	0.0732
<i>CG9308</i>	0.526	0.0732
<i>Jhl-21</i>	0.526	0.0732
<i>KP78a</i>	0.526	0.0732
<i>para</i>	0.526	0.0732
<i>Bx</i>	0.524	0.0737
<i>CG1812</i>	0.524	0.0737
<i>CG5139</i>	0.524	0.0737
<i>lqf</i>	0.524	0.0737
<i>CG10959</i>	0.523	0.0741
<i>CG13300</i>	0.523	0.0741
<i>CG18418</i>	0.523	0.0741
<i>CG3330</i>	0.523	0.0741
<i>CG5204</i>	0.523	0.0741
<i>CG5790</i>	0.523	0.0741
<i>Dp</i>	0.523	0.0741
<i>Miro</i>	0.523	0.0741
<i>Pros28.1B</i>	0.523	0.0741
<i>Usp7</i>	0.523	0.0741
<i>CG31068</i>	0.522	0.075
<i>CG32945</i>	0.522	0.075
<i>CG42232</i>	0.522	0.075
<i>CG42540</i>	0.522	0.075
<i>Nos</i>	0.522	0.075
<i>Pino</i>	0.522	0.075
<i>Su(var)205</i>	0.522	0.075
<i>U4-U6-60K</i>	0.522	0.075
<i>uri</i>	0.522	0.075

Table 6.S8 Continued

Gene Name	ERC Value	P-value
CG10298	0.521	0.0758
CG12909	0.521	0.0758
CG18273	0.521	0.0758
CG2875	0.521	0.0758
Rcd5	0.521	0.0758
sty	0.521	0.0758
CG42258	0.52	0.0763
CG4957	0.52	0.0763
Myb	0.52	0.0763
CG13597	0.519	0.0766
nAcRalpha-7	0.519	0.0766
CG43073	0.518	0.0768
mRpL22	0.518	0.0768
CG15117	0.517	0.0769
CG1737	0.517	0.0769
hiw	0.517	0.0769
qkr54B	0.517	0.0769
Tsf1	0.517	0.0769
unc-13-4A	0.517	0.0769
Upf1	0.517	0.0769
CG15642	0.516	0.0776
Mcm7	0.516	0.0776
pex16	0.516	0.0776
Ssl	0.516	0.0776
CG17829	0.515	0.0779
l(2)37Ce	0.515	0.0779
Mst89B	0.515	0.0779
Rab21	0.515	0.0779
slmo	0.515	0.0779
CG34325	0.514	0.0784
CG34459	0.514	0.0784
CG42256	0.514	0.0784
CG7519	0.514	0.0784
CG14718	0.513	0.0787
CG4065	0.513	0.0787
CG9754	0.513	0.0787
ChT11	0.513	0.0787
Nc73EF	0.513	0.0787
Sec16	0.513	0.0787
CG15497	0.512	0.0793
CG32277	0.512	0.0793
mRpL41	0.512	0.0793
beat-lb	0.511	0.0795
CG1271	0.511	0.0795
CG14561	0.511	0.0795
CG17154	0.511	0.0795
CG31755	0.511	0.0795
scf	0.511	0.0795
bin	0.51	0.0801
CG17922	0.51	0.0801
CG4701	0.51	0.0801
Ucp4C	0.51	0.0801
ZC3H3	0.51	0.0801
CG15236	0.509	0.0805
CG33159	0.509	0.0805
CG11504	0.508	0.0807

Gene Name	ERC Value	P-value
CG11885	0.508	0.0807
CG31773	0.508	0.0807
CG4293	0.508	0.0807
Kap-alpha1	0.508	0.0807
sgl	0.508	0.0807
Smn	0.508	0.0807
CG14262	0.507	0.0814
dpr4	0.507	0.0814
CG14695	0.506	0.0815
CG5379	0.506	0.0815
Prosbeta1	0.506	0.0815
Tim17b1	0.506	0.0815
CBP	0.505	0.0819
CG12288	0.505	0.0819
CG14762	0.505	0.0819
Eaat1	0.505	0.0819
pad	0.505	0.0819
agt	0.504	0.0823
CG14074	0.504	0.0823
CG3313	0.504	0.0823
CG34334	0.504	0.0823
CG5807	0.504	0.0823
Gbeta76C	0.504	0.0823
Prosbeta2	0.504	0.0823
CG12229	0.503	0.083
CG16704	0.503	0.083
CG17777	0.503	0.083
Hsp83	0.503	0.083
kuk	0.503	0.083
CG13993	0.502	0.0834
CG2982	0.502	0.0834
CG7024	0.502	0.0834
CHIP	0.502	0.0834
HLHm7	0.502	0.0834
RSG7	0.502	0.0834
yemalpha	0.502	0.0834
CG33775	0.501	0.0841
CG34127	0.501	0.0841
CG5180	0.501	0.0841
LIMK1	0.501	0.0841
Tsp33B	0.501	0.0841
CG10462	0.5	0.0845
CG13373	0.5	0.0845
Shal	0.5	0.0845
CG10802	0.499	0.0848
CG10948	0.499	0.0848
CG11149	0.499	0.0848
CG12848	0.499	0.0848
CG15890	0.499	0.0848
CG42339	0.499	0.0848
CG9769	0.499	0.0848
CG13040	0.498	0.0854
CG4678	0.498	0.0854
CG14840	0.497	0.0856
CG16957	0.497	0.0856
CG3198	0.497	0.0856

Gene Name	ERC Value	P-value
CG32676	0.497	0.0856
CG8366	0.497	0.0856
CG9027	0.497	0.0856
jet	0.497	0.0856
Arp53D	0.496	0.0862
CG10761	0.496	0.0862
CG11737	0.496	0.0862
CG12680	0.496	0.0862
CG17324	0.496	0.0862
CG3437	0.496	0.0862
Dscam	0.496	0.0862
TpnC41C	0.496	0.0862
Andorra	0.495	0.0869
CG32551	0.495	0.0869
CG7231	0.495	0.0869
CG8878	0.495	0.0869
dm	0.495	0.0869
larp	0.495	0.0869
SmD3	0.495	0.0869
CG11099	0.494	0.0876
CG13047	0.494	0.0876
CG5815	0.494	0.0876
CG8833	0.494	0.0876
CG9376	0.494	0.0876
elf-3p66	0.494	0.0876
ox	0.494	0.0876
Saf-B	0.494	0.0876
betaTub97E	0.493	0.0883
CG12121	0.493	0.0883
CG15109	0.493	0.0883
stau	0.493	0.0883
xmas-2	0.493	0.0883
Art8	0.492	0.0887
CG17147	0.492	0.0887
fs(1)Yb	0.492	0.0887
CG33263	0.491	0.089
CG6345	0.491	0.089
fig	0.491	0.089
Nf-YB	0.491	0.089
Pdp	0.491	0.089
betaTub60D	0.49	0.0895
CG15125	0.49	0.0895
CG17005	0.49	0.0895
CG6048	0.49	0.0895
HDAC6	0.49	0.0895
pcm	0.49	0.0895
Ser8	0.49	0.0895
wds	0.49	0.0895
beat-llb	0.489	0.0902
CG13966	0.489	0.0902
CG3635	0.489	0.0902
elf4AIII	0.489	0.0902
mRpL23	0.489	0.0902
RpL19	0.489	0.0902
Vps4	0.489	0.0902
CG13423	0.488	0.0908

Gene Name	ERC Value	P-value
CG15925	0.488	0.0908
CG3492	0.488	0.0908
chb	0.488	0.0908
l(3)73Ah	0.488	0.0908
Surf1	0.488	0.0908
CG14125	0.487	0.0914
CG15471	0.487	0.0914
CG7339	0.487	0.0914
RnrS	0.487	0.0914
CG32432	0.486	0.0917
cype	0.486	0.0917
ste24c	0.486	0.0917
CG32364	0.485	0.092
CG4627	0.485	0.092
CG4872	0.485	0.092
elf4E-4	0.485	0.092
rg	0.485	0.092
CG11727	0.484	0.0924
CG4300	0.484	0.0924
CG8001	0.484	0.0924
CG8281	0.484	0.0924
cmet	0.484	0.0924
kdn	0.484	0.0924
CG31287	0.483	0.093
CG4415	0.483	0.093
CG7963	0.483	0.093
Msi	0.483	0.093
CG11137	0.482	0.0933
CG34012	0.482	0.0933
CG3603	0.482	0.0933
elav	0.482	0.0933
Rlip	0.482	0.0933
RpL35A	0.482	0.0933
CG32772	0.481	0.0939
CG8557	0.481	0.0939
eco	0.481	0.0939
eRF1	0.481	0.0939
klar	0.481	0.0939
pgant6	0.481	0.0939
Zyx102EF	0.481	0.0939
CG10750	0.48	0.0945
CG1545	0.48	0.0945
CG42732	0.48	0.0945
hts	0.48	0.0945
CG8086	0.479	0.0949
MSBP	0.478	0.095
thoc6	0.478	0.095
CG11333	0.477	0.0951
CG12484	0.477	0.0951
CG14215	0.477	0.0951
CG14297	0.477	0.0951
CG31360	0.477	0.0951
Cyp12e1	0.477	0.0951
Ard1	0.476	0.0957
Cdc6	0.476	0.0957
CG18596	0.476	0.0957

Gene Name	ERC Value	P-value
CG7054	0.476	0.0957
CG9672	0.476	0.0957
wor	0.476	0.0957
CG2889	0.475	0.0962
Or98a	0.475	0.0962
CG14476	0.474	0.0964
CG17665	0.474	0.0964
CG31195	0.474	0.0964
CG31921	0.474	0.0964
CG5043	0.474	0.0964
RpL34a	0.474	0.0964
Skil6	0.474	0.0964
TpnC73F	0.474	0.0964
CG14929	0.473	0.0971
CG5073	0.473	0.0971
dom	0.473	0.0971
CG14511	0.472	0.0974
CG33713	0.472	0.0974
CG9101	0.472	0.0974
CG13142	0.471	0.0977
CG16890	0.471	0.0977
CG4629	0.471	0.0977
CG9336	0.471	0.0977
Rpn11	0.471	0.0977
CG13392	0.471	0.0981
CG14301	0.47	0.0981
DMAP1	0.47	0.0981
dod	0.47	0.0981
HtrA2	0.47	0.0981
CG8757	0.469	0.0986
CG10333	0.468	0.0986
CG17199	0.468	0.0986
CG33191	0.468	0.0986
Mef2	0.468	0.0986
tmod	0.468	0.0986
vg	0.468	0.0986
CG13376	0.467	0.0992
p53	0.467	0.0992
REG	0.467	0.0992
beat-VII	0.466	0.0995
CG2256	0.466	0.0995
CG6506	0.466	0.0995
exu	0.466	0.0995
CG6241	0.465	0.0998
CG8408	0.465	0.0998
Hsp60	0.465	0.0998

Table 6.S9 - Top Genes ERC values for *mei-P22* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>ac</i>	0.976	0.0001
<i>CG13692</i>	0.959	0.0002
<i>Kul</i>	0.951	0.0003
<i>Psn</i>	0.948	0.0004
<i>dao</i>	0.947	0.0005
<i>CG3669</i>	0.934	0.0005
<i>ST6Gal</i>	0.927	0.0006
<i>TwidJ</i>	0.927	0.0006
<i>phl</i>	0.919	0.0008
<i>MED10</i>	0.91	0.0009
<i>CG11919</i>	0.909	0.001
<i>bun</i>	0.906	0.0011
<i>CG32241</i>	0.906	0.0011
<i>Sox100B</i>	0.905	0.0013
<i>CG11317</i>	0.904	0.0014
<i>CG3301</i>	0.903	0.0014
<i>CG12643</i>	0.896	0.0015
<i>CG34348</i>	0.896	0.0015
<i>CG11248</i>	0.89	0.0017
<i>CG3825</i>	0.888	0.0018
<i>CG10508</i>	0.885	0.0019
<i>FLASH</i>	0.88	0.002
<i>CypI</i>	0.879	0.0021
<i>CG8326</i>	0.876	0.0022
<i>Cpr92A</i>	0.875	0.0023
<i>Thor</i>	0.875	0.0023
<i>CG34441</i>	0.871	0.0024
<i>CG9760</i>	0.87	0.0025
<i>nan</i>	0.866	0.0026
<i>phol</i>	0.856	0.0027
<i>CG15220</i>	0.852	0.0028
<i>CG6410</i>	0.852	0.0028
<i>CG3156</i>	0.851	0.003
<i>ato</i>	0.85	0.0031
<i>Efr</i>	0.848	0.0032
<i>PHDP</i>	0.848	0.0032
<i>CG1090</i>	0.846	0.0033
<i>CG6734</i>	0.845	0.0034
<i>Glu-RI</i>	0.844	0.0035
<i>kis</i>	0.844	0.0035
<i>paII</i>	0.843	0.0037
<i>Fer1</i>	0.842	0.0038
<i>CG13077</i>	0.84	0.0039
<i>Rpn2</i>	0.839	0.004
<i>dx</i>	0.837	0.0041
<i>vig</i>	0.837	0.0041
<i>CG14330</i>	0.836	0.0042
<i>CG6454</i>	0.836	0.0042
<i>bsk</i>	0.835	0.0044
<i>CG9067</i>	0.835	0.0044
<i>Cpr64Ab</i>	0.835	0.0044
<i>Gycbeta100</i>	0.835	0.0044
<i>CG12831</i>	0.834	0.0048
<i>CG9317</i>	0.834	0.0048
<i>CG10158</i>	0.833	0.005
<i>cue</i>	0.833	0.005

Gene Name	ERC Value	P-value
<i>CG8839</i>	0.831	0.0051
<i>CG9752</i>	0.831	0.0051
<i>CG7371</i>	0.829	0.0053
<i>CG14107</i>	0.826	0.0054
<i>CG14806</i>	0.826	0.0054
<i>CG11211</i>	0.825	0.0056
<i>CG31199</i>	0.824	0.0057
<i>CG5160</i>	0.824	0.0057
<i>Pros45</i>	0.823	0.0059
<i>CG2126</i>	0.82	0.0059
<i>Cp36</i>	0.82	0.0059
<i>PEK</i>	0.82	0.0059
<i>Ero1L</i>	0.818	0.0062
<i>CG13868</i>	0.817	0.0063
<i>CG34195</i>	0.815	0.0064
<i>bap</i>	0.814	0.0065
<i>Cyp301a1</i>	0.814	0.0065
<i>tsh</i>	0.814	0.0065
<i>CG6792</i>	0.813	0.0068
<i>Cks85A</i>	0.813	0.0068
<i>CG2818</i>	0.81	0.0069
<i>CG4585</i>	0.809	0.007
<i>CG4587</i>	0.809	0.007
<i>CG15480</i>	0.805	0.0072
<i>CG9300</i>	0.805	0.0072
<i>CG14550</i>	0.802	0.0074
<i>CG12237</i>	0.801	0.0075
<i>CG32150</i>	0.801	0.0075
<i>CG4476</i>	0.801	0.0075
<i>CG9596</i>	0.801	0.0075
<i>zen</i>	0.801	0.0075
<i>CG6115</i>	0.8	0.0079
<i>CanA1</i>	0.799	0.008
<i>CG13920</i>	0.799	0.008
<i>elF2B-beta</i>	0.798	0.0082
<i>Brd8</i>	0.797	0.0083
<i>pHCl</i>	0.796	0.0084
<i>primo-2</i>	0.796	0.0084
<i>Tom</i>	0.795	0.0086
<i>AttC</i>	0.792	0.0086
<i>CG12998</i>	0.792	0.0086
<i>CG34214</i>	0.79	0.0088
<i>CG12213</i>	0.789	0.0089
<i>Obp58c</i>	0.789	0.0089
<i>CG6664</i>	0.788	0.0091
<i>CG10361</i>	0.787	0.0092
<i>CG34261</i>	0.787	0.0092
<i>Ocho</i>	0.784	0.0094
<i>spz6</i>	0.784	0.0094
<i>Arp5</i>	0.783	0.0095
<i>CG9953</i>	0.78	0.0096
<i>dlt</i>	0.78	0.0096
<i>cup</i>	0.779	0.0098
<i>Dfd</i>	0.779	0.0098
<i>CG1575</i>	0.778	0.01
<i>Txl</i>	0.777	0.0101

Gene Name	ERC Value	P-value
<i>CG7686</i>	0.776	0.0102
<i>efly3</i>	0.775	0.0103
<i>CG9640</i>	0.773	0.0104
<i>CG11874</i>	0.771	0.0105
<i>Menf-1</i>	0.771	0.0105
<i>CG31870</i>	0.77	0.0106
<i>CG11897</i>	0.769	0.0107
<i>qkr58E-2</i>	0.769	0.0107
<i>RhoGEF3</i>	0.769	0.0107
<i>Sym</i>	0.769	0.0107
<i>CG31460</i>	0.768	0.0111
<i>rump</i>	0.766	0.0112
<i>Ag5r</i>	0.763	0.0113
<i>m4</i>	0.763	0.0113
<i>CG12038</i>	0.762	0.0114
<i>CG12093</i>	0.759	0.0115
<i>CG9850</i>	0.759	0.0115
<i>noa5</i>	0.758	0.0117
<i>piwi</i>	0.758	0.0117
<i>NPFR1</i>	0.757	0.0119
<i>Su(H)</i>	0.757	0.0119
<i>CG3542</i>	0.756	0.0121
<i>CG34282</i>	0.755	0.0122
<i>CG14340</i>	0.754	0.0123
<i>CG5861</i>	0.754	0.0123
<i>mRpl21</i>	0.754	0.0123
<i>CG12241</i>	0.752	0.0125
<i>CG14608</i>	0.749	0.0126
<i>l(1)G0320</i>	0.749	0.0126
<i>mts</i>	0.749	0.0126
<i>Rpl37A</i>	0.749	0.0126
<i>CG13624</i>	0.748	0.013
<i>Discam3</i>	0.748	0.013
<i>Jafract1</i>	0.747	0.0132
<i>CG12269</i>	0.746	0.0132
<i>CG30429</i>	0.746	0.0132
<i>CG30273</i>	0.745	0.0134
<i>CG42505</i>	0.745	0.0134
<i>CG9839</i>	0.745	0.0134
<i>CG10326</i>	0.744	0.0137
<i>CG33704</i>	0.743	0.0138
<i>dpn</i>	0.743	0.0138
<i>Tsp47F</i>	0.743	0.0138
<i>CG13594</i>	0.742	0.0141
<i>CG5466</i>	0.742	0.0141
<i>CG6026</i>	0.742	0.0141
<i>Cpr65Ec</i>	0.742	0.0141
<i>CG1951</i>	0.741	0.0144
<i>CG32155</i>	0.741	0.0144
<i>CG42246</i>	0.741	0.0144
<i>CG13877</i>	0.74	0.0147
<i>CG42351</i>	0.74	0.0147
<i>CG4452</i>	0.74	0.0147
<i>CG13296</i>	0.739	0.015
<i>CG33786</i>	0.738	0.015
<i>CG33964</i>	0.738	0.015

Gene Name	ERC Value	P-value
<i>phyl</i>	0.738	0.015
<i>CG18271</i>	0.736	0.0153
<i>CG8841</i>	0.735	0.0154
<i>Nup62</i>	0.734	0.0155
<i>CG1113</i>	0.733	0.0156
<i>Dmn</i>	0.733	0.0156
<i>CG13708</i>	0.732	0.0158
<i>CG3168</i>	0.732	0.0158
<i>CG6726</i>	0.732	0.0158
<i>CG3784</i>	0.732	0.0158
<i>MKP-4</i>	0.732	0.0158
<i>Rab23</i>	0.732	0.0158
<i>robo3</i>	0.732	0.0158
<i>CG32069</i>	0.731	0.0164
<i>CG11693</i>	0.73	0.0165
<i>CG9941</i>	0.729	0.0166
<i>lpl1</i>	0.729	0.0166
<i>dpa</i>	0.728	0.0168
<i>l(2)35Bg</i>	0.728	0.0168
<i>CG32037</i>	0.727	0.0169
<i>CG6116</i>	0.727	0.0169
<i>Tsf3</i>	0.727	0.0169
<i>CG10280</i>	0.726	0.0172
<i>CG42371</i>	0.726	0.0172
<i>CG9339</i>	0.726	0.0172
<i>CG9894</i>	0.726	0.0172
<i>Fatp</i>	0.726	0.0172
<i>CG34159</i>	0.725	0.0177
<i>cbs</i>	0.724	0.0177
<i>CG11369</i>	0.724	0.0177
<i>CG9822</i>	0.724	0.0177
<i>Corp</i>	0.724	0.0177
<i>Klp68D</i>	0.724	0.0177
<i>SP555</i>	0.724	0.0177
<i>CG31812</i>	0.723	0.0183
<i>CG7158</i>	0.723	0.0183
<i>msl-3</i>	0.723	0.0183
<i>Rat1</i>	0.723	0.0183
<i>Takr99D</i>	0.723	0.0183
<i>CG9547</i>	0.722	0.0187
<i>t</i>	0.722	0.0187
<i>CG8837</i>	0.721	0.0189
<i>CG11034</i>	0.72	0.019
<i>hwd</i>	0.72	0.019
<i>RagA</i>	0.72	0.019
<i>msd1</i>	0.719	0.0193
<i>Nacalpa</i>	0.719	0.0193
<i>Prx5</i>	0.719	0.0193
<i>ncup</i>	0.719	0.0193
<i>CG31800</i>	0.717	0.0196
<i>dgo</i>	0.717	0.0196
<i>vri</i>	0.717	0.0196
<i>CG11883</i>	0.716	0.0199
<i>CG6362</i>	0.716	0.0199
<i>Cpr65Ay</i>	0.716	0.0199
<i>ird1</i>	0.716	0.0199

Gene Name	ERC Value	P-value
<i>CG13046</i>	0.715	0.0203
<i>CG32695</i>	0.715	0.0203
<i>mo</i>	0.715	0.0203
<i>smt3</i>	0.715	0.0203
<i>l(3)2D3</i>	0.714	0.0206
<i>cer</i>	0.713	0.0207
<i>CG4820</i>	0.713	0.0207
<i>CG8388</i>	0.713	0.0207
<i>boss</i>	0.712	0.021
<i>CG13737</i>	0.712	0.021
<i>CG14856</i>	0.712	0.021
<i>Phlpp</i>	0.712	0.021
<i>tj</i>	0.712	0.021
<i>Cpr65Ea</i>	0.711	0.0214
<i>Pole2</i>	0.71	0.0215
<i>CG5569</i>	0.709	0.0216
<i>CG7453</i>	0.709	0.0216
<i>ETH</i>	0.709	0.0216
<i>Patsas</i>	0.709	0.0216
<i>Sema-1b</i>	0.709	0.0216
<i>Aats-gln</i>	0.708	0.0221
<i>CG18599</i>	0.708	0.0221
<i>dpr3</i>	0.708	0.0221
<i>ple</i>	0.708	0.0221
<i>SRm160</i>	0.708	0.0221
<i>Fit1</i>	0.707	0.0225
<i>comm3</i>	0.706	0.0226
<i>CG13712</i>	0.705	0.0227
<i>CG34309</i>	0.704	0.0228
<i>Syx8</i>	0.704	0.0228
<i>CG31029</i>	0.703	0.023
<i>CG12879</i>	0.702	0.0231
<i>CG13700</i>	0.702	0.0231
<i>CG14010</i>	0.702	0.0231
<i>CG33257</i>	0.702	0.0231
<i>CG4998</i>	0.702	0.0231
<i>CG5639</i>	0.702	0.0231
<i>CG7484</i>	0.702	0.0231
<i>CG7759</i>	0.701	0.0237
<i>elF5B</i>	0.701	0.0237
<i>mRpl55</i>	0.701	0.0237
<i>CG1738</i>	0.7	0.024
<i>CG34015</i>	0.7	0.024
<i>DNApol-eta</i>	0.7	0.024
<i>Tango6</i>	0.7	0.024
<i>CG16799</i>	0.699	0.0243
<i>CG32344</i>	0.699	0.0243
<i>CG32638</i>	0.699	0.0243
<i>CG34404</i>	0.699	0.0243
<i>Cps73</i>	0.699	0.0243
<i>l(1)G0045</i>	0.699	0.0243
<i>mRplS24</i>	0.699	0.0243
<i>Arp66B</i>	0.697	0.025
<i>CG13398</i>	0.697	0.025
<i>CG17646</i>	0.696	0.0251
<i>CG31793</i>	0.696	0.0251

Table 6.S9 Continued

Gene Name	ERC Value	P-value
CG4367	0.696	0.0251
CG42673	0.695	0.0254
Cdc37	0.694	0.0255
CG12290	0.694	0.0255
CG13298	0.694	0.0255
lin	0.694	0.0255
lkb1	0.694	0.0255
CG14111	0.693	0.0259
CG17807	0.693	0.0259
CG18004	0.693	0.0259
CG13071	0.692	0.0262
CG14292	0.692	0.0262
CG1702	0.692	0.0262
fritz	0.692	0.0262
thr	0.692	0.0262
CG9634	0.691	0.0267
CG9642	0.691	0.0267
CG5458	0.69	0.0268
CG6196	0.69	0.0268
CG6406	0.689	0.027
beta4GalNA	0.688	0.0271
CG32264	0.688	0.0271
Mms19	0.688	0.0271
CG15094	0.686	0.0274
Atg13	0.685	0.0275
CG6619	0.685	0.0275
Ent1	0.685	0.0275
CG31183	0.684	0.0277
CG4973	0.684	0.0277
Osi9	0.684	0.0277
CG12540	0.683	0.028
Lap1	0.683	0.028
Nrt	0.683	0.028
Oatp58Dc	0.683	0.028
phr6-4	0.683	0.028
scat	0.683	0.028
bru	0.682	0.0286
CG17075	0.682	0.0286
CG6000	0.682	0.0286
lr93a	0.682	0.0286
CG32221	0.681	0.0289
pix	0.681	0.0289
CG13086	0.679	0.0291
CG17660	0.679	0.0291
Dpy-30L2	0.679	0.0291
Drep-3	0.679	0.0291
pcx	0.679	0.0291
Apc	0.677	0.0295
ave	0.677	0.0295
CG14023	0.676	0.0297
CG9427	0.676	0.0297
CG9467	0.676	0.0297
CG12194	0.675	0.03
CG14546	0.675	0.03
CG5199	0.675	0.03
kar	0.675	0.03

Gene Name	ERC Value	P-value
CG17839	0.674	0.0304
CG4753	0.674	0.0304
CG5849	0.674	0.0304
Ckl1alpha	0.674	0.0304
mri	0.674	0.0304
CG15564	0.673	0.0308
CG17746	0.673	0.0308
pinta	0.673	0.0308
CG13875	0.672	0.0311
CG31954	0.672	0.0311
CG42678	0.672	0.0311
CG5013	0.672	0.0311
Neif-A	0.672	0.0311
CG4393	0.671	0.0315
sec15	0.671	0.0315
CG13035	0.67	0.0317
cnk	0.67	0.0317
VhaAC45	0.67	0.0317
CG10277	0.669	0.032
CG1434	0.669	0.032
CG1571	0.669	0.032
CG7839	0.669	0.032
Rsf1	0.668	0.0323
TwdlN	0.668	0.0323
CG10602	0.667	0.0325
CG11388	0.667	0.0325
CG4563	0.667	0.0325
CG9164	0.666	0.0328
Osi6	0.666	0.0328
Syx13	0.666	0.0328
Fps85D	0.665	0.0331
Gr85a	0.665	0.0331
Ef1gamma	0.664	0.0332
Nf1	0.664	0.0332
Orc6	0.664	0.0332
RpS5b	0.664	0.0332
CG11679	0.663	0.0336
Fak56D	0.663	0.0336
CG15731	0.662	0.0338
CG32260	0.662	0.0338
CG3353	0.662	0.0338
CG3493	0.662	0.0338
fab1	0.662	0.0338
Hsp22	0.662	0.0338
sec23	0.662	0.0338
CG12895	0.661	0.0344
CG5924	0.661	0.0344
CG6503	0.661	0.0344
deltaCOP	0.661	0.0344
Kip98A	0.661	0.0344
mms101	0.661	0.0344
Nnp-1	0.661	0.0344
CG14964	0.66	0.035
CG6425	0.659	0.0351
ImpL2	0.659	0.0351
CG3356	0.658	0.0353

Gene Name	ERC Value	P-value
ndl	0.658	0.0353
CG5885	0.657	0.0355
DNApol-alpha	0.657	0.0355
unc79	0.657	0.0355
CG13216	0.656	0.0358
CG33120	0.656	0.0358
CG34022	0.656	0.0358
Oscillin	0.656	0.0358
sut2	0.656	0.0358
Teh4	0.656	0.0358
bic	0.655	0.0363
CG4282	0.655	0.0363
SoxN	0.655	0.0363
a	0.653	0.0366
CG10006	0.653	0.0366
CG4842	0.653	0.0366
CG5872	0.653	0.0366
CG14570	0.652	0.0369
CG5500	0.652	0.0369
Cpr49Af	0.652	0.0369
Nlp	0.651	0.0372
CG13443	0.65	0.0373
CG31344	0.65	0.0373
CG9780	0.65	0.0373
CG10359	0.649	0.0376
CG33288	0.649	0.0376
CG5608	0.649	0.0376
Or92a	0.649	0.0376
RpL35	0.649	0.0376
CG30471	0.647	0.038
pyd3	0.647	0.038
rab3-GAP	0.647	0.038
alc	0.646	0.0383
CG16886	0.646	0.0383
CG3192	0.646	0.0383
miple2	0.646	0.0383
Sos	0.646	0.0383
CG18558	0.645	0.0387
CG9328	0.645	0.0387
CG3645	0.644	0.0389
CG9536	0.644	0.0389
Hmt-1	0.644	0.0389
CG14036	0.643	0.0392
Su(z)2	0.643	0.0392
CG34293	0.642	0.0394
CG6236	0.642	0.0394
Taf13	0.642	0.0394
CG11997	0.641	0.0396
CG17328	0.641	0.0396
CG4324	0.641	0.0396
CG9018	0.641	0.0396
CG9297	0.641	0.0396
Ranbp11	0.641	0.0396
CG13950	0.64	0.0402
CG18304	0.64	0.0402
drpr	0.64	0.0402

Gene Name	ERC Value	P-value
TwdlR	0.64	0.0402
yellow-d	0.64	0.0402
CG7457	0.639	0.0406
Hexo1	0.639	0.0406
CG34247	0.638	0.0408
CG5964	0.638	0.0408
Osi10	0.638	0.0408
Syx17	0.638	0.0408
CG32792	0.637	0.0412
CG7196	0.637	0.0412
CG13430	0.636	0.0414
Cpr23B	0.636	0.0414
CG18136	0.635	0.0415
CG5126	0.634	0.0416
dome	0.634	0.0416
Pdk	0.634	0.0416
ppk6	0.634	0.0416
CG7102	0.633	0.042
dap	0.633	0.042
Gr58c	0.633	0.042
HLHmdelta	0.633	0.042
CG33998	0.632	0.0423
CG8818	0.632	0.0423
CG6870	0.631	0.0425
MED31	0.631	0.0425
CG10920	0.63	0.0427
CG15210	0.63	0.0427
CG16926	0.63	0.0427
CG32100	0.63	0.0427
CG4497	0.63	0.0427
torp4a	0.63	0.0427
CG16718	0.629	0.0432
CG6724	0.629	0.0432
CG7251	0.628	0.0434
CG9920	0.628	0.0434
CG9010	0.627	0.0436
CG7342	0.626	0.0437
Cyp4d2	0.626	0.0437
RpA-70	0.626	0.0437
Bsg25D	0.625	0.044
CG13157	0.625	0.044
CG3119	0.625	0.044
Cpr67Fb	0.625	0.044
Rab-RP4	0.625	0.044
remA	0.625	0.044
BicC	0.624	0.0445
CG16868	0.624	0.0445
rho-6	0.624	0.0445
CG16743	0.623	0.0448
CG33722	0.623	0.0448
CG3409	0.623	0.0448
CG4377	0.623	0.0448
dream	0.623	0.0448
E(Pc)	0.623	0.0448
Ets96B	0.623	0.0448
ts(1)Ya	0.622	0.0454

Gene Name	ERC Value	P-value
lectin-46Ca	0.622	0.0454
slpr	0.622	0.0454
Apc2	0.621	0.0457
CG42319	0.621	0.0457
CG9883	0.621	0.0457
tacc	0.621	0.0457
CG6388	0.62	0.046
CG6428	0.62	0.046
Phm	0.62	0.046
Thiolase	0.62	0.046
CG13458	0.619	0.0464
CG9775	0.619	0.0464
gsb-n	0.619	0.0464
mus304	0.619	0.0464
Rab3	0.619	0.0464
RhoGAP92E	0.619	0.0464
CG10096	0.618	0.0469
CG1236	0.618	0.0469
CG13409	0.618	0.0469
CG33291	0.618	0.0469
Tsp42Ei	0.618	0.0469
CG13472	0.617	0.0474
Cpr60D	0.617	0.0474
CG5805	0.616	0.0476
Hsp27	0.616	0.0476
pgc	0.616	0.0476
bwa	0.615	0.0478
CG33770	0.615	0.0478
CG8481	0.615	0.0478
Spt3	0.615	0.0478
CG33696	0.614	0.0482
tio	0.614	0.0482
by	0.613	0.0484
CG12911	0.613	0.0484
CG3822	0.613	0.0484
santa-maria	0.613	0.0484
CG11162	0.612	0.0487
CG11858	0.612	0.0487
CG17712	0.612	0.0487
CG34456	0.612	0.0487
CG4610	0.612	0.0487
NC2beta	0.612	0.0487
npf	0.612	0.0487
sec31	0.612	0.0487
CG9935	0.611	0.0495
Lrk	0.611	0.0495
mirr	0.611	0.0495
SP1173	0.611	0.0495
Fer2LCH	0.61	0.0498
CG12679	0.609	0.0499
CG4882	0.609	0.0499
qua	0.609	0.0499
Arr1	0.608	0.0502
HipHop	0.608	0.0502
Klp54D	0.608	0.0502
nct	0.608	0.0502

Table 6.S9 Continued

Gene Name	ERC Value	P-value
<i>Pcf11</i>	0.608	0.0502
<i>cad</i>	0.607	0.0506
<i>CG10903</i>	0.607	0.0506
<i>CG13751</i>	0.607	0.0506
<i>CG17181</i>	0.607	0.0506
<i>CG18539</i>	0.607	0.0506
<i>CG33330</i>	0.607	0.0506
<i>Lsd-2</i>	0.607	0.0506
<i>RPA2</i>	0.607	0.0506
<i>CG13350</i>	0.606	0.0514
<i>CG8795</i>	0.606	0.0514
<i>mas</i>	0.606	0.0514
<i>CG3065</i>	0.605	0.0516
<i>nes</i>	0.605	0.0516
<i>Pnn</i>	0.605	0.0516
<i>CG16947</i>	0.604	0.0519
<i>CG33169</i>	0.604	0.0519
<i>CG6688</i>	0.604	0.0519
<i>CG31531</i>	0.603	0.0522
<i>CG6129</i>	0.603	0.0522
<i>HGTX</i>	0.603	0.0522
<i>nwk</i>	0.603	0.0522
<i>alpha4GT1</i>	0.602	0.0525
<i>Oatp26F</i>	0.602	0.0525
<i>simj</i>	0.602	0.0525
<i>CG11349</i>	0.601	0.0528
<i>CG4613</i>	0.601	0.0528
<i>hale</i>	0.601	0.0528
<i>Jhl-1</i>	0.601	0.0528
<i>hd</i>	0.6	0.0532
<i>CG11913</i>	0.599	0.0532
<i>CG4288</i>	0.599	0.0532
<i>Npc2b</i>	0.599	0.0532
<i>CG13565</i>	0.598	0.0535
<i>CG13727</i>	0.598	0.0535
<i>CG14200</i>	0.598	0.0535
<i>CG17026</i>	0.598	0.0535
<i>GATAd</i>	0.598	0.0535
<i>scw</i>	0.598	0.0535
<i>CG5018</i>	0.597	0.0541
<i>CG8550</i>	0.597	0.0541
<i>CG9531</i>	0.597	0.0541
<i>CG11900</i>	0.596	0.0543
<i>CG12321</i>	0.596	0.0543
<i>CG14564</i>	0.596	0.0543
<i>CG33229</i>	0.596	0.0543
<i>CG6945</i>	0.596	0.0543
<i>Jarid2</i>	0.596	0.0543
<i>mi</i>	0.596	0.0543
<i>CG15674</i>	0.595	0.055
<i>CG8195</i>	0.595	0.055
<i>mars</i>	0.595	0.055
<i>san</i>	0.595	0.055
<i>Spn77Ba</i>	0.595	0.055
<i>Ast</i>	0.594	0.0554
<i>CG12171</i>	0.594	0.0554

Gene Name	ERC Value	P-value
<i>CG14500</i>	0.594	0.0554
<i>CG15653</i>	0.594	0.0554
<i>CG5255</i>	0.594	0.0554
<i>CG7110</i>	0.594	0.0554
<i>CG7381</i>	0.594	0.0554
<i>mf6</i>	0.594	0.0554
<i>CG16838</i>	0.593	0.0561
<i>CrebA</i>	0.593	0.0561
<i>CG10399</i>	0.592	0.0563
<i>CG30271</i>	0.592	0.0563
<i>CG7631</i>	0.592	0.0563
<i>tum</i>	0.592	0.0563
<i>CD98hc</i>	0.591	0.0567
<i>CG31357</i>	0.591	0.0567
<i>CG8248</i>	0.591	0.0567
<i>mRpS25</i>	0.591	0.0567
<i>Yippee</i>	0.591	0.0567
<i>CG10814</i>	0.59	0.0571
<i>CG31207</i>	0.59	0.0571
<i>CG34376</i>	0.59	0.0571
<i>CG8907</i>	0.59	0.0571
<i>lr85a</i>	0.59	0.0571
<i>r-I</i>	0.59	0.0571
<i>CG2765</i>	0.589	0.0577
<i>CG33298</i>	0.589	0.0577
<i>CG5361</i>	0.589	0.0577
<i>CG5715</i>	0.589	0.0577
<i>eg</i>	0.589	0.0577
<i>mask</i>	0.589	0.0577
<i>AcpH-1</i>	0.588	0.0582
<i>ash1</i>	0.588	0.0582
<i>beat-1b</i>	0.588	0.0582
<i>CG17782</i>	0.588	0.0582
<i>CG1868</i>	0.588	0.0582
<i>CG33054</i>	0.588	0.0582
<i>fy</i>	0.588	0.0582
<i>CG14015</i>	0.587	0.0588
<i>CG34144</i>	0.587	0.0588
<i>CG7120</i>	0.587	0.0588
<i>Or47a</i>	0.587	0.0588
<i>CG10927</i>	0.586	0.0592
<i>CG11381</i>	0.586	0.0592
<i>CG7630</i>	0.586	0.0592
<i>CG7968</i>	0.586	0.0592
<i>ltk</i>	0.586	0.0592
<i>CG11474</i>	0.585	0.0596
<i>CG13617</i>	0.585	0.0596
<i>CG15269</i>	0.585	0.0596
<i>CG17930</i>	0.585	0.0596
<i>CG32333</i>	0.585	0.0596
<i>CG5273</i>	0.585	0.0596
<i>CG5599</i>	0.585	0.0596
<i>mRpL45</i>	0.585	0.0596
<i>obst-H</i>	0.585	0.0596
<i>Top2</i>	0.585	0.0596
<i>CG5873</i>	0.584	0.0605

Gene Name	ERC Value	P-value
<i>Cpr47Ee</i>	0.584	0.0605
<i>amx</i>	0.583	0.0607
<i>CG13349</i>	0.583	0.0607
<i>CG3773</i>	0.583	0.0607
<i>CG7888</i>	0.583	0.0607
<i>CG8738</i>	0.583	0.0607
<i>l(3)Ineo43</i>	0.583	0.0607
<i>mRpL1</i>	0.583	0.0607
<i>Nep2</i>	0.583	0.0607
<i>CG13090</i>	0.582	0.0614
<i>CG3121</i>	0.582	0.0614
<i>CG5377</i>	0.582	0.0614
<i>CG8455</i>	0.581	0.0617
<i>chico</i>	0.581	0.0617
<i>pcs</i>	0.581	0.0617
<i>CG33111</i>	0.58	0.062
<i>CG8319</i>	0.58	0.062
<i>CG8545</i>	0.58	0.062
<i>Cyp1</i>	0.58	0.062
<i>Hcs</i>	0.58	0.062
<i>Phax</i>	0.58	0.062
<i>CG10321</i>	0.579	0.0625
<i>CG13562</i>	0.579	0.0625
<i>CG17282</i>	0.579	0.0625
<i>CG30000</i>	0.579	0.0625
<i>Cry</i>	0.579	0.0625
<i>sec5</i>	0.579	0.0625
<i>ca</i>	0.578	0.0631
<i>CG13694</i>	0.578	0.0631
<i>CG6697</i>	0.578	0.0631
<i>CG9517</i>	0.578	0.0631
<i>Edg84A</i>	0.578	0.0631
<i>sim</i>	0.578	0.0631
<i>swm</i>	0.578	0.0631
<i>CG11414</i>	0.577	0.0637
<i>CG13561</i>	0.577	0.0637
<i>grau</i>	0.577	0.0637
<i>lr21a</i>	0.577	0.0637
<i>l(1)G0269</i>	0.577	0.0637
<i>Sc2</i>	0.577	0.0637
<i>CG14647</i>	0.576	0.0642
<i>CG3819</i>	0.576	0.0642
<i>Klc</i>	0.576	0.0642
<i>Lcp1</i>	0.576	0.0642
<i>SmD1</i>	0.576	0.0642
<i>sut1</i>	0.576	0.0642
<i>BBS8</i>	0.575	0.0648
<i>CG1399</i>	0.575	0.0648
<i>CG8087</i>	0.575	0.0648
<i>CG18769</i>	0.574	0.065
<i>CG5787</i>	0.574	0.065
<i>CG7079</i>	0.574	0.065
<i>CG7787</i>	0.574	0.065
<i>Rib1</i>	0.574	0.065
<i>asp</i>	0.573	0.0655
<i>CG2046</i>	0.573	0.0655

Gene Name	ERC Value	P-value
<i>CG13627</i>	0.572	0.0657
<i>CG1910</i>	0.572	0.0657
<i>tgo</i>	0.572	0.0657
<i>CG13042</i>	0.571	0.0659
<i>CG1443</i>	0.571	0.0659
<i>CG14815</i>	0.571	0.0659
<i>Klp67A</i>	0.571	0.0659
<i>CG13097</i>	0.57	0.0663
<i>CG42404</i>	0.57	0.0663
<i>chif</i>	0.57	0.0663
<i>fh</i>	0.57	0.0663
<i>Cdk5</i>	0.569	0.0667
<i>CG12004</i>	0.569	0.0667
<i>CG12128</i>	0.569	0.0667
<i>CG16711</i>	0.569	0.0667
<i>CG6282</i>	0.568	0.067
<i>coro</i>	0.568	0.067
<i>FK506-bp1</i>	0.568	0.067
<i>Myo28B1</i>	0.568	0.067
<i>omd</i>	0.568	0.067
<i>vir-1</i>	0.568	0.067
<i>Adgf-A</i>	0.567	0.0676
<i>CG10505</i>	0.567	0.0676
<i>CG11490</i>	0.567	0.0676
<i>CG11652</i>	0.567	0.0676
<i>CG12974</i>	0.567	0.0676
<i>CG31976</i>	0.567	0.0676
<i>v(2)k05816</i>	0.567	0.0676
<i>Vha100-2</i>	0.567	0.0676
<i>CG32278</i>	0.566	0.0683
<i>CG17179</i>	0.566	0.0683
<i>CG7582</i>	0.566	0.0683
<i>Pcp</i>	0.566	0.0683
<i>CG13510</i>	0.565	0.0686
<i>CG18265</i>	0.565	0.0686
<i>CG31815</i>	0.565	0.0686
<i>CG33691</i>	0.565	0.0686
<i>CG3735</i>	0.565	0.0686
<i>CG6432</i>	0.565	0.0686
<i>CG12703</i>	0.564	0.0692
<i>Ror</i>	0.564	0.0692
<i>cathD</i>	0.563	0.0694
<i>CG18003</i>	0.563	0.0694
<i>CG32762</i>	0.563	0.0694
<i>TwdlC</i>	0.563	0.0694
<i>bnb</i>	0.562	0.0697
<i>Bzd</i>	0.562	0.0697
<i>CG14110</i>	0.562	0.0697
<i>CG15754</i>	0.562	0.0697
<i>CG42574</i>	0.562	0.0697
<i>Csk</i>	0.562	0.0697
<i>DR31</i>	0.562	0.0697
<i>l(1)G0334</i>	0.562	0.0697
<i>lva</i>	0.562	0.0697
<i>CG12730</i>	0.561	0.0705
<i>CstF-64</i>	0.561	0.0705

Gene Name	ERC Value	P-value
<i>Teh3</i>	0.561	0.0705
<i>CG9068</i>	0.56	0.0708
<i>hug</i>	0.559	0.0709
<i>pxb</i>	0.559	0.0709
<i>CG10184</i>	0.558	0.0711
<i>CG3570</i>	0.558	0.0711
<i>ari-2</i>	0.557	0.0713
<i>Cpr30F</i>	0.557	0.0713
<i>CG7172</i>	0.556	0.0714
<i>malpha</i>	0.556	0.0714
<i>MtnB</i>	0.556	0.0714
<i>pic</i>	0.556	0.0714
<i>CG9865</i>	0.555	0.0718
<i>RN-tre</i>	0.555	0.0718
<i>CG10495</i>	0.554	0.072
<i>CG4433</i>	0.554	0.072
<i>CG5984</i>	0.554	0.072
<i>srw</i>	0.554	0.072
<i>enok</i>	0.553	0.0723
<i>jhamt</i>	0.553	0.0723
<i>RNaseX25</i>	0.553	0.0723
<i>tow</i>	0.553	0.0723
<i>CG11889</i>	0.552	0.0727
<i>CG12835</i>	0.552	0.0727
<i>CG14892</i>	0.552	0.0727
<i>CG4291</i>	0.552	0.0727
<i>CG8235</i>	0.552	0.0727
<i>Hs2st</i>	0.552	0.0727
<i>TwdlD</i>	0.552	0.0727
<i>glo</i>	0.551	0.0733
<i>ImpL3</i>	0.551	0.0733
<i>CG6013</i>	0.55	0.0735
<i>TwdlY</i>	0.55	0.0735
<i>CG10467</i>	0.549	0.0737
<i>CG17184</i>	0.549	0.0737
<i>CG32043</i>	0.549	0.0737
<i>CG8419</i>	0.549	0.0737
<i>Cpr97Ea</i>	0.549	0.0737
<i>Psi</i>	0.549	0.0737
<i>Vha14-1</i>	0.549	0.0737
<i>zpg</i>	0.549	0.0737
<i>CG4537</i>	0.548	0.0744
<i>CG8317</i>	0.548	0.0744
<i>CG10981</i>	0.547	0.0746
<i>CG14671</i>	0.547	0.0746
<i>CG32248</i>	0.547	0.0746
<i>mp</i>	0.547	0.0746
<i>WASp</i>	0.547	0.0746
<i>CG42784</i>	0.546	0.075
<i>CG6660</i>	0.546	0.075
<i>numb</i>	0.546	0.075
<i>sced</i>	0.546	0.075
<i>CG11475</i>	0.545	0.0754
<i>CG12007</i>	0.545	0.0754
<i>CG13949</i>	0.545	0.0754
<i>CG14298</i>	0.545	0.0754

Table 6.S9 Continued

Gene Name	ERC Value	P-value
CG5682	0.545	0.0754
CG7747	0.545	0.0754
CG8486	0.545	0.0754
d	0.545	0.0754
Or35a	0.545	0.0754
CG17834	0.544	0.0762
CG3004	0.544	0.0762
Gefb4C	0.544	0.0762
CG10657	0.543	0.0765
CG11242	0.543	0.0765
GRHRll	0.543	0.0765
Jheh3	0.543	0.0765
LpR1	0.543	0.0765
Papst2	0.543	0.0765
alpha-Est7	0.542	0.077
CG15237	0.542	0.077
CG8094	0.542	0.077
CG9192	0.542	0.077
CG6414	0.54	0.0774
smg	0.54	0.0774
Atf-2	0.539	0.0776
bsh	0.539	0.0776
CG12056	0.539	0.0776
CG18568	0.539	0.0776
CG31321	0.539	0.0776
CG8353	0.539	0.0776
Tg	0.539	0.0776
TwdlV	0.539	0.0776
CG4119	0.538	0.0783
CG5591	0.538	0.0783
CG8138	0.538	0.0783
CG9510	0.538	0.0783
tau	0.538	0.0783
unpg	0.538	0.0783
cbx	0.537	0.0788
CG3862	0.537	0.0788
CG3939	0.537	0.0788
CG4829	0.537	0.0788
CG6404	0.537	0.0788
CG9643	0.537	0.0788
PHGPx	0.537	0.0788
CG14132	0.536	0.0795
CG5773	0.536	0.0795
CG8237	0.536	0.0795
Sip1	0.536	0.0795
stg	0.536	0.0795
CG16884	0.535	0.0799
Atg4	0.534	0.08
CG15809	0.534	0.08
CG16836	0.534	0.08
CG3244	0.534	0.08
CG8236	0.534	0.08
CG9384	0.534	0.08
D12	0.534	0.08
SP1029	0.534	0.08
VhaM9.7-b	0.534	0.08

Gene Name	ERC Value	P-value
CG13837	0.533	0.0808
Tie	0.533	0.0808
c(3)G	0.532	0.081
CG15753	0.532	0.081
CG17477	0.532	0.081
CG31957	0.532	0.081
CG42508	0.532	0.081
RpLP0	0.532	0.081
Smox	0.532	0.081
Cat	0.531	0.0816
CG1161	0.531	0.0816
CG14642	0.531	0.0816
CG1943	0.531	0.0816
CG32112	0.531	0.0816
CG34194	0.531	0.0816
CG3699	0.531	0.0816
CG8960	0.531	0.0816
Pask	0.531	0.0816
sina	0.531	0.0816
TllfBeta	0.531	0.0816
CG14086	0.53	0.0826
CG7564	0.53	0.0826
hk	0.53	0.0826
mus301	0.53	0.0826
CG14946	0.529	0.083
CG5112	0.529	0.083
Ch8	0.529	0.083
Geklll	0.529	0.083
Odc1	0.529	0.083
Spp	0.529	0.083
CG13640	0.528	0.0835
CG15147	0.528	0.0835
CG15888	0.528	0.0835
CG5150	0.528	0.0835
nbs	0.528	0.0835
Nha1	0.528	0.0835
Utx	0.528	0.0835
CG13282	0.527	0.0841
CG31728	0.527	0.0841
CG4238	0.527	0.0841
ird5	0.527	0.0841
MED8	0.527	0.0841
nub	0.527	0.0841
ome	0.527	0.0841
CG1308	0.526	0.0848
CG42336	0.526	0.0848
CG14375	0.525	0.085
CG30413	0.525	0.085
CG6843	0.525	0.085
CG7611	0.525	0.085
CG9849	0.525	0.085
dalac	0.525	0.085
mei-41	0.525	0.085
Mvl	0.525	0.085
CG8642	0.524	0.0857
cib	0.524	0.0857

Gene Name	ERC Value	P-value
HSPC300	0.524	0.0857
tin	0.524	0.0857
CG11656	0.523	0.086
CG5261	0.523	0.086
CG8726	0.523	0.086
CG9238	0.523	0.086
Est-6	0.523	0.086
pallidin	0.523	0.086
Pxx5037	0.523	0.086
Sp7	0.523	0.086
Aats-gly	0.522	0.0868
CG33303	0.522	0.0868
CG6470	0.522	0.0868
CG8021	0.522	0.0868
Drip	0.522	0.0868
Sas-4	0.522	0.0868
CG2812	0.521	0.0873
oho23B	0.521	0.0873
RpS29	0.521	0.0873
Tbp-1	0.521	0.0873
Cerk	0.52	0.0877
CG1104	0.52	0.0877
CG1461	0.52	0.0877
CG3036	0.52	0.0877
CG5493	0.52	0.0877
mus201	0.52	0.0877
Rab4	0.52	0.0877
Tace	0.52	0.0877
CG11164	0.519	0.0884
CG31248	0.519	0.0884
CG4101	0.519	0.0884
CG4752	0.519	0.0884
ear	0.519	0.0884
Nek2	0.519	0.0884
PGRP-LE	0.519	0.0884
Syb	0.519	0.0884
BBS4	0.518	0.0891
CG12370	0.518	0.0891
Bub3	0.517	0.0893
cdl	0.517	0.0893
CG15861	0.517	0.0893
CG3880	0.517	0.0893
CG6495	0.517	0.0893
Kr	0.517	0.0893
rb	0.517	0.0893
CG10804	0.516	0.0899
CG13917	0.516	0.0899
CycD	0.516	0.0899
dj-1beta	0.516	0.0899
HLH54F	0.516	0.0899
CG11854	0.515	0.0904
CG31729	0.515	0.0904
CG4116	0.515	0.0904
CG4972	0.515	0.0904
CG5706	0.515	0.0904
amon	0.514	0.0908

Gene Name	ERC Value	P-value
CG13250	0.514	0.0908
CG5262	0.514	0.0908
Dhc93AB	0.514	0.0908
Eff1beta	0.514	0.0908
pzg	0.514	0.0908
Surf4	0.514	0.0908
7B2	0.513	0.0914
bbg	0.513	0.0914
CG10178	0.513	0.0914
CG14607	0.513	0.0914
MED28	0.513	0.0914
Mgat2	0.513	0.0914
CG14516	0.512	0.092
CG34447	0.512	0.092
l(2)gl	0.512	0.092
Mpk2	0.512	0.092
Or88a	0.512	0.092
Rh2	0.512	0.092
Tsp74F	0.512	0.092
CG3560	0.511	0.0926
CG4757	0.511	0.0926
CG8031	0.511	0.0926
Moe	0.511	0.0926
bmm	0.51	0.093
CG17385	0.51	0.093
Act88F	0.509	0.0932
CG13581	0.509	0.0932
CG3532	0.509	0.0932
CG8509	0.509	0.0932
E2f2	0.509	0.0932
Pros54	0.509	0.0932
B-H2	0.508	0.0937
Ccap	0.508	0.0937
CG11781	0.508	0.0937
gek	0.508	0.0937
Gr22e	0.508	0.0937
TllIS	0.508	0.0937
CG5254	0.507	0.0942
CG6330	0.507	0.0942
cag	0.506	0.0944
CG3651	0.506	0.0944
CG31076	0.505	0.0946
dpr19	0.505	0.0946
Psf1	0.505	0.0946
Sep2	0.504	0.0949
CG13745	0.504	0.0949
CG18598	0.504	0.0949
CG1986	0.504	0.0949
CG33784	0.504	0.0949
CG3907	0.504	0.0949
CG14803	0.503	0.0954
CG1622	0.503	0.0954
CG31516	0.503	0.0954
CG9222	0.503	0.0954
CycB	0.503	0.0954
kuz	0.503	0.0954

Gene Name	ERC Value	P-value
CG12849	0.502	0.0959
CG13287	0.502	0.0959
CG15201	0.502	0.0959
CG33988	0.502	0.0959
CG7142	0.502	0.0959
dpr9	0.502	0.0959
CG11376	0.501	0.0965
CG11449	0.501	0.0965
CG14259	0.501	0.0965
CG2837	0.501	0.0965
CG33511	0.501	0.0965
CG5614	0.501	0.0965
Crtp	0.501	0.0965
GM130	0.501	0.0965
l(2)gl	0.501	0.0965
PSR	0.501	0.0965
brat	0.5	0.0974
CG12869	0.5	0.0974
CG14720	0.5	0.0974
CG30291	0.5	0.0974
CG6337	0.5	0.0974
CG8861	0.5	0.0974
Lerp	0.5	0.0974
CG13036	0.499	0.098
CG17343	0.499	0.098
CG9143	0.499	0.098
CG42741	0.498	0.0983
CG5521	0.498	0.0983
CG6800	0.498	0.0983
geminin	0.498	0.0983
Hsp67Bc	0.498	0.0983
l(2)35Bc	0.498	0.0983
ea	0.497	0.0988
l(2)dfl	0.497	0.0988
Obp47b	0.497	0.0988
alpha-Est10	0.496	0.0991
CG30016	0.496	0.0991
CG6928	0.496	0.0991
snRNP-U1-C	0.496	0.0991
Tim9b	0.496	0.0991
Arc-p34	0.495	0.0995
CG13605	0.495	0.0995
CG14866	0.495	0.0995
CG31706	0.495	0.0995
CG37378	0.495	0.0995
PTP-ER	0.495	0.0995

Table 6.S10 - Top Genes ERC values for *mei-W68* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Ir7g</i>	0.955	0.0001
<i>CG13955</i>	0.896	0.0002
<i>sunz</i>	0.884	0.0003
<i>btd</i>	0.873	0.0004
<i>ru</i>	0.873	0.0004
<i>CG15639</i>	0.872	0.0005
<i>CG32750</i>	0.872	0.0005
<i>wg</i>	0.865	0.0007
<i>CG10249</i>	0.856	0.0008
<i>unc-4</i>	0.852	0.0009
<i>mRp56</i>	0.851	0.001
<i>Lig4</i>	0.849	0.0011
<i>CG11262</i>	0.848	0.0012
<i>CG15717</i>	0.845	0.0013
<i>CG42374</i>	0.845	0.0013
<i>Vps28</i>	0.836	0.0014
<i>CG14442</i>	0.835	0.0015
<i>os</i>	0.835	0.0015
<i>trk</i>	0.833	0.0017
<i>MagI</i>	0.832	0.0018
<i>CG8401</i>	0.831	0.0019
<i>CG14695</i>	0.827	0.002
<i>CG12594</i>	0.825	0.0021
<i>CG9649</i>	0.825	0.0021
<i>CG13121</i>	0.822	0.0023
<i>CG34331</i>	0.82	0.0023
<i>CG5909</i>	0.819	0.0024
<i>CG8617</i>	0.819	0.0024
<i>trus</i>	0.819	0.0024
<i>CG13272</i>	0.816	0.0027
<i>mos</i>	0.814	0.0028
<i>CG34284</i>	0.813	0.0029
<i>CG6607</i>	0.813	0.0029
<i>CG2321</i>	0.812	0.0031
<i>CG10669</i>	0.804	0.0032
<i>CG42366</i>	0.793	0.0032
<i>boly</i>	0.792	0.0033
<i>Hr39</i>	0.791	0.0034
<i>Tsp42Ek</i>	0.791	0.0034
<i>ana</i>	0.79	0.0036
<i>CG15404</i>	0.79	0.0036
<i>Vm32E</i>	0.79	0.0036
<i>CG5734</i>	0.789	0.0039
<i>Ret</i>	0.788	0.004
<i>CG1885</i>	0.785	0.0041
<i>CG3239</i>	0.785	0.0041
<i>CG6234</i>	0.785	0.0041
<i>fs(1)M3</i>	0.782	0.0043
<i>Hsp57Bb</i>	0.782	0.0043
<i>TyrR</i>	0.782	0.0043
<i>CG10479</i>	0.779	0.0046
<i>CG11802</i>	0.779	0.0046
<i>CG34195</i>	0.779	0.0046
<i>cos</i>	0.779	0.0046
<i>Cpr62Ba</i>	0.778	0.005
<i>Dok</i>	0.778	0.005

Gene Name	ERC Value	P-value
<i>CG2124</i>	0.777	0.0051
<i>CG2794</i>	0.775	0.0052
<i>Gpi1</i>	0.775	0.0052
<i>Pask</i>	0.775	0.0052
<i>La</i>	0.773	0.0055
<i>CG31922</i>	0.766	0.0056
<i>Jon44E</i>	0.766	0.0056
CG31898	0.764	0.0058
<i>CG11418</i>	0.763	0.0059
<i>CG12042</i>	0.762	0.0059
<i>CG15522</i>	0.762	0.0059
<i>CG7550</i>	0.762	0.0059
<i>CG15118</i>	0.76	0.0062
<i>CG4496</i>	0.76	0.0062
<i>melt</i>	0.758	0.0064
<i>CG31475</i>	0.757	0.0065
<i>CG7884</i>	0.757	0.0065
<i>CG13502</i>	0.756	0.0067
<i>CG15912</i>	0.755	0.0068
<i>CG5541</i>	0.755	0.0068
<i>CG9335</i>	0.755	0.0068
<i>CG15376</i>	0.753	0.007
<i>CG6927</i>	0.752	0.0071
<i>CG7320</i>	0.752	0.0071
<i>CG4017</i>	0.751	0.0073
<i>fu</i>	0.751	0.0073
<i>Rpb8</i>	0.751	0.0073
<i>tap</i>	0.751	0.0073
<i>CG10713</i>	0.749	0.0077
<i>CG18316</i>	0.749	0.0077
<i>CG12851</i>	0.748	0.0078
<i>SP2363</i>	0.748	0.0078
<i>CG11593</i>	0.747	0.008
<i>CG14997</i>	0.747	0.008
<i>bow1</i>	0.746	0.0082
<i>CG31150</i>	0.746	0.0082
<i>CG34314</i>	0.745	0.0084
CG7069	0.745	0.0084
<i>Tsp</i>	0.745	0.0084
<i>CG13126</i>	0.744	0.0086
<i>thetaTry</i>	0.743	0.0087
<i>nerfin-2</i>	0.742	0.0088
<i>ths</i>	0.742	0.0088
<i>Cyp28c1</i>	0.74	0.009
<i>lr54a</i>	0.739	0.0091
<i>salm</i>	0.739	0.0091
<i>Sirt6</i>	0.739	0.0091
<i>CG13813</i>	0.738	0.0094
<i>CG14722</i>	0.738	0.0094
<i>CG15479</i>	0.738	0.0094
<i>sl</i>	0.738	0.0094
<i>GstD10</i>	0.737	0.0097
<i>CG8668</i>	0.736	0.0098
<i>CG5919</i>	0.735	0.0099
<i>Ptp61F</i>	0.735	0.0099
<i>CG30217</i>	0.734	0.0101

Gene Name	ERC Value	P-value
<i>CG33057</i>	0.734	0.0101
<i>MeF2</i>	0.734	0.0101
<i>sca</i>	0.734	0.0101
<i>GlcAT-P</i>	0.733	0.0105
<i>CG2083</i>	0.732	0.0105
<i>CG4398</i>	0.732	0.0105
<i>mRpL36</i>	0.731	0.0107
<i>Oatp74D</i>	0.731	0.0107
<i>stI</i>	0.731	0.0107
<i>bdg</i>	0.73	0.011
<i>CG12516</i>	0.73	0.011
<i>CG15120</i>	0.729	0.0112
<i>CG30423</i>	0.729	0.0112
<i>CG9114</i>	0.729	0.0112
<i>CG11576</i>	0.728	0.0114
<i>CG14562</i>	0.728	0.0114
<i>CG15020</i>	0.726	0.0116
<i>CG5746</i>	0.725	0.0117
<i>CG9215</i>	0.725	0.0117
<i>Ir2a</i>	0.725	0.0117
<i>Os-E</i>	0.725	0.0117
CG10560	0.724	0.0121
<i> fend</i>	0.724	0.0121
<i>Jhe</i>	0.724	0.0121
<i>magu</i>	0.724	0.0121
<i>CG1403</i>	0.723	0.0124
<i>CG8134</i>	0.723	0.0124
<i>CG9542</i>	0.723	0.0124
<i>Mif</i>	0.722	0.0127
<i>ms(3)K81</i>	0.722	0.0127
<i>vg</i>	0.722	0.0127
<i>yki</i>	0.722	0.0127
<i>CG10209</i>	0.721	0.0131
<i>Prx5037</i>	0.721	0.0131
<i>CG11454</i>	0.72	0.0132
<i>CG7781</i>	0.72	0.0132
<i>dsh</i>	0.72	0.0132
<i>CG5550</i>	0.719	0.0135
<i>CG7860</i>	0.719	0.0135
<i>dbo</i>	0.719	0.0135
<i>hfw</i>	0.719	0.0135
<i>dpr20</i>	0.718	0.0139
<i>Klp31E</i>	0.718	0.0139
<i>NetA</i>	0.718	0.0139
<i>Sox21b</i>	0.718	0.0139
CG7597	0.717	0.0142
<i>EndoG1</i>	0.717	0.0142
<i>tz4</i>	0.717	0.0142
<i>tsg</i>	0.717	0.0142
<i>pdm3</i>	0.716	0.0146
<i>CG16771</i>	0.715	0.0147
<i>mre11</i>	0.715	0.0147
<i>CG15643</i>	0.714	0.0149
<i>CG30183</i>	0.713	0.015
<i>CG31886</i>	0.713	0.015
<i>TpnC41C</i>	0.712	0.0151

Gene Name	ERC Value	P-value
<i>CG3837</i>	0.71	0.0152
<i>CG7091</i>	0.71	0.0152
<i>CG8209</i>	0.71	0.0152
<i>CG17047</i>	0.709	0.0155
<i>CG6254</i>	0.709	0.0155
<i>CG8397</i>	0.709	0.0155
<i>PICK1</i>	0.708	0.0158
<i>qkr54B</i>	0.708	0.0158
<i>Ir11a</i>	0.707	0.0159
<i>Arp11</i>	0.706	0.016
<i>CG31371</i>	0.706	0.016
<i>Abi</i>	0.705	0.0162
<i>CG11975</i>	0.704	0.0163
<i>CG10702</i>	0.703	0.0164
<i>CG33985</i>	0.703	0.0164
<i>CG8389</i>	0.703	0.0164
<i>Vps33B</i>	0.703	0.0164
<i>CG11294</i>	0.702	0.0168
<i>MED30</i>	0.702	0.0168
<i>B-H1</i>	0.701	0.0169
<i>caasp</i>	0.701	0.0169
<i>caup</i>	0.701	0.0169
<i>CG12253</i>	0.701	0.0169
<i>CG12263</i>	0.701	0.0169
<i>CG14069</i>	0.701	0.0169
<i>DNApol-αph</i>	0.701	0.0169
<i>gbb</i>	0.7	0.0176
<i>Osi12</i>	0.7	0.0176
<i>CG12943</i>	0.699	0.0177
<i>CTCF</i>	0.699	0.0177
<i>CG10741</i>	0.698	0.0179
<i>CG1359</i>	0.698	0.0179
<i>CG32846</i>	0.698	0.0179
<i>Traf6</i>	0.697	0.0182
<i>N</i>	0.696	0.0183
<i>Sir2</i>	0.696	0.0183
<i>CG14177</i>	0.694	0.0185
CG10274	0.693	0.0186
<i>CG15534</i>	0.692	0.0186
<i>fs(1)N</i>	0.692	0.0186
<i>ftz</i>	0.692	0.0186
<i>CG4334</i>	0.691	0.0189
<i>CG8370</i>	0.691	0.0189
<i>CG14314</i>	0.69	0.0191
<i>CG7200</i>	0.69	0.0191
<i>comm</i>	0.69	0.0191
<i>CG16863</i>	0.689	0.0194
<i>CG6923</i>	0.689	0.0194
<i>ilc</i>	0.689	0.0194
<i>CG9072</i>	0.688	0.0196
<i>Stp84E</i>	0.688	0.0196
<i>CG4542</i>	0.687	0.0198
<i>Cpr47Ed</i>	0.687	0.0198
<i>Mes4</i>	0.687	0.0198
<i>CG14238</i>	0.686	0.0201
<i>KH1</i>	0.686	0.0201

Gene Name	ERC Value	P-value
<i>CG14826</i>	0.685	0.0203
<i>osk</i>	0.684	0.0204
<i>CG7255</i>	0.683	0.0205
<i>tfh</i>	0.683	0.0205
<i>crb</i>	0.681	0.0206
<i>Ptp4E</i>	0.681	0.0206
<i>sda</i>	0.681	0.0206
<i>CG13059</i>	0.68	0.0209
<i>CG9861</i>	0.68	0.0209
<i>hdm</i>	0.68	0.0209
<i>kon</i>	0.68	0.0209
<i>AQP</i>	0.678	0.0213
<i>CG11762</i>	0.678	0.0213
<i>CG4751</i>	0.678	0.0213
<i>Mer</i>	0.678	0.0213
<i>Obp99b</i>	0.678	0.0213
<i>sna</i>	0.678	0.0213
<i>CG8963</i>	0.677	0.0218
<i>Git</i>	0.677	0.0218
<i>CG13958</i>	0.676	0.022
<i>Galpha73B</i>	0.676	0.022
<i>CG12104</i>	0.675	0.0222
<i>CG30268</i>	0.675	0.0222
<i>CG3308</i>	0.674	0.0223
<i>CG9951</i>	0.674	0.0223
<i>Hpr1</i>	0.674	0.0223
<i>Or46a</i>	0.674	0.0223
<i>Skeletor</i>	0.674	0.0223
<i>Ssadh</i>	0.674	0.0223
<i>CG32104</i>	0.673	0.0229
<i>Saf6</i>	0.673	0.0229
<i>bib</i>	0.672	0.0231
<i>CG13339</i>	0.672	0.0231
<i>CG32343</i>	0.672	0.0231
<i>CG6520</i>	0.672	0.0231
<i>Gr9a</i>	0.672	0.0231
<i>CG15478</i>	0.671	0.0235
<i>Oseg5</i>	0.671	0.0235
<i>Pros25</i>	0.671	0.0235
<i>CG7526</i>	0.67	0.0238
<i>CG7985</i>	0.67	0.0238
<i>Gr39b</i>	0.67	0.0238
<i>CG1311</i>	0.669	0.0241
<i>CG3386</i>	0.669	0.0241
<i>HisCl1</i>	0.669	0.0241
<i>Obp8a</i>	0.669	0.0241
<i>CG10809</i>	0.668	0.0244
<i>CG9330</i>	0.668	0.0244
<i>CS-2</i>	0.668	0.0244
<i>CG10000</i>	0.667	0.0247
<i>CG13908</i>	0.667	0.0247
<i>CG15865</i>	0.667	0.0247
<i>O-fut1</i>	0.667	0.0247
<i>heix</i>	0.666	0.025
<i>CG11155</i>	0.665	0.0251
<i>CG14174</i>	0.665	0.0251

Table 6.S10 Continued

Gene Name	ERC Value	P-value
<i>Nrg</i>	0.665	0.0251
<i>B-H2</i>	0.664	0.0254
<i>bal</i>	0.664	0.0254
<i>CG5895</i>	0.664	0.0254
<i>CG13229</i>	0.663	0.0257
<i>CG32040</i>	0.663	0.0257
<i>CG9932</i>	0.663	0.0257
<i>kek3</i>	0.663	0.0257
<i>Rh7</i>	0.663	0.0257
<i>CG14423</i>	0.662	0.0261
<i>CG30196</i>	0.662	0.0261
<i>htl</i>	0.662	0.0261
<i>Pngl</i>	0.662	0.0261
<i>CG10264</i>	0.661	0.0265
<i>CG14969</i>	0.661	0.0265
<i>CG6654</i>	0.661	0.0265
<i>CG32649</i>	0.66	0.0268
<i>CG9376</i>	0.66	0.0268
<i>HLHmbeta</i>	0.66	0.0268
<i>salt</i>	0.66	0.0268
<i>CalpC</i>	0.659	0.0271
<i>CG14906</i>	0.659	0.0271
<i>CG2182</i>	0.659	0.0271
<i>Ssl1</i>	0.659	0.0271
<i>Ucp4C</i>	0.659	0.0271
<i>CG31646</i>	0.658	0.0276
<i>su(wfaj)</i>	0.658	0.0276
<i>beat-11b</i>	0.657	0.0277
<i>sut4</i>	0.657	0.0277
<i>Djp3</i>	0.656	0.0279
<i>SC35</i>	0.656	0.0279
<i>Syx4</i>	0.656	0.0279
<i>yellow-k</i>	0.656	0.0279
<i>CG7785</i>	0.655	0.0283
<i>scro</i>	0.655	0.0283
<i>wgn</i>	0.655	0.0283
<i>ase</i>	0.654	0.0286
<i>CG12913</i>	0.653	0.0286
<i>Lk6</i>	0.653	0.0286
<i>Cpr72Eb</i>	0.652	0.0288
<i>sob</i>	0.652	0.0288
<i>CG12050</i>	0.651	0.029
<i>CG5835</i>	0.651	0.029
<i>CG6040</i>	0.651	0.029
<i>fd59A</i>	0.65	0.0293
<i>Scm</i>	0.65	0.0293
<i>Aldh</i>	0.649	0.0295
<i>CG15745</i>	0.649	0.0295
<i>CG32573</i>	0.649	0.0295
<i>CG9992</i>	0.649	0.0295
<i>CG32579</i>	0.648	0.0298
<i>da</i>	0.648	0.0298
<i>slp2</i>	0.648	0.0298
<i>CG10428</i>	0.647	0.0301
<i>CG8159</i>	0.646	0.0302
<i>hop</i>	0.646	0.0302

Gene Name	ERC Value	P-value
<i>dah</i>	0.645	0.0304
<i>usnp</i>	0.644	0.0305
<i>ORMDL</i>	0.643	0.0305
<i>RunxB</i>	0.643	0.0305
<i>CG4753</i>	0.642	0.0307
<i>D12</i>	0.642	0.0307
<i>CG31464</i>	0.641	0.0309
<i>CG32206</i>	0.641	0.0309
<i>CG8950</i>	0.641	0.0309
<i>CG9304</i>	0.641	0.0309
<i>Drak</i>	0.641	0.0309
<i>Kmn1</i>	0.641	0.0309
<i>slv</i>	0.641	0.0309
<i>CG11660</i>	0.64	0.0315
<i>CG14408</i>	0.64	0.0315
<i>CG14435</i>	0.64	0.0315
<i>CG17751</i>	0.64	0.0315
<i>CG3995</i>	0.64	0.0315
<i>Dg</i>	0.64	0.0315
<i>CG10348</i>	0.639	0.0321
<i>CG6847</i>	0.639	0.0321
<i>disp</i>	0.639	0.0321
<i>Ent2</i>	0.639	0.0321
<i>CG9727</i>	0.638	0.0324
<i>Inrx-IV</i>	0.638	0.0324
<i>NKAIN</i>	0.637	0.0326
<i>png</i>	0.637	0.0326
<i>ds</i>	0.636	0.0328
<i>ft</i>	0.636	0.0328
<i>CG9505</i>	0.635	0.033
<i>RpL34a</i>	0.635	0.033
<i>CG12773</i>	0.634	0.0332
<i>CG12986</i>	0.634	0.0332
<i>CG13305</i>	0.634	0.0332
<i>Pros35</i>	0.634	0.0332
<i>sens</i>	0.634	0.0332
<i>ZC3H3</i>	0.634	0.0332
<i>CG30007</i>	0.632	0.0337
<i>CG30403</i>	0.632	0.0337
<i>Brl40</i>	0.631	0.0339
<i>CG14417</i>	0.631	0.0339
<i>CG15877</i>	0.631	0.0339
<i>CG17048</i>	0.631	0.0339
<i>CG31698</i>	0.631	0.0339
<i>CG6329</i>	0.631	0.0339
<i>CG10725</i>	0.63	0.0344
<i>CG18012</i>	0.63	0.0344
<i>CG5597</i>	0.63	0.0344
<i>CG6276</i>	0.63	0.0344
<i>Src42A</i>	0.63	0.0344
<i>CG3838</i>	0.629	0.0349
<i>GLaz</i>	0.629	0.0349
<i>PGRP-SD</i>	0.629	0.0349
<i>Scr</i>	0.629	0.0349
<i>CG13074</i>	0.628	0.0352
<i>InR</i>	0.628	0.0352

Gene Name	ERC Value	P-value
<i>Ir48b</i>	0.628	0.0352
<i>lrx</i>	0.628	0.0352
<i>Asph</i>	0.627	0.0356
<i>CG14463</i>	0.627	0.0356
<i>CG2852</i>	0.627	0.0356
<i>CG32541</i>	0.627	0.0356
<i>CG31431</i>	0.626	0.0359
<i>CG8180</i>	0.626	0.0359
<i>CG9147</i>	0.626	0.0359
<i>Cyp49a1</i>	0.626	0.0359
<i>CG1809</i>	0.625	0.0363
<i>CG32459</i>	0.625	0.0363
<i>CG3368</i>	0.625	0.0363
<i>CG6733</i>	0.625	0.0363
<i>CG14658</i>	0.624	0.0367
<i>CG6201</i>	0.624	0.0367
<i>Obp50a</i>	0.624	0.0367
<i>CG11835</i>	0.623	0.0369
<i>CG15443</i>	0.623	0.0369
<i>ct</i>	0.623	0.0369
<i>dm</i>	0.623	0.0369
<i>sli</i>	0.623	0.0369
<i>snk</i>	0.623	0.0369
<i>snz</i>	0.623	0.0369
<i>CG2975</i>	0.622	0.0376
<i>CG8116</i>	0.622	0.0376
<i>Di</i>	0.622	0.0376
<i>ferrochelatas</i>	0.622	0.0376
<i>scyl1</i>	0.622	0.0376
<i>wb</i>	0.622	0.0376
<i>AlkB</i>	0.621	0.0381
<i>CG11178</i>	0.621	0.0381
<i>CG11448</i>	0.621	0.0381
<i>CG13016</i>	0.62	0.0384
<i>CG15744</i>	0.62	0.0384
<i>CG33307</i>	0.62	0.0384
<i>Plip</i>	0.62	0.0384
<i>CG10424</i>	0.619	0.0387
<i>CG11211</i>	0.619	0.0387
<i>CG11417</i>	0.619	0.0387
<i>CG4374</i>	0.619	0.0387
<i>CG7265</i>	0.619	0.0387
<i>Pka-C1</i>	0.619	0.0387
<i>CG6409</i>	0.618	0.0393
<i>CG9922</i>	0.618	0.0393
<i>l(2)k16918</i>	0.618	0.0393
<i>aff</i>	0.617	0.0395
<i>CG15317</i>	0.617	0.0395
<i>CG6106</i>	0.617	0.0395
<i>CG5414</i>	0.616	0.0398
<i>CG8100</i>	0.616	0.0398
<i>sisA</i>	0.616	0.0398
<i>az2</i>	0.615	0.0401
<i>capa</i>	0.615	0.0401
<i>CG14057</i>	0.615	0.0401
<i>disco-r</i>	0.615	0.0401

Gene Name	ERC Value	P-value
<i>Fem-1</i>	0.615	0.0401
<i>CG10654</i>	0.614	0.0405
<i>CG17118</i>	0.614	0.0405
<i>CG31221</i>	0.614	0.0405
<i>CG11870</i>	0.613	0.0408
<i>CG17562</i>	0.612	0.0409
<i>CG31296</i>	0.612	0.0409
<i>CG4078</i>	0.612	0.0409
<i>CG5026</i>	0.612	0.0409
<i>Menl-1</i>	0.612	0.0409
<i>CG10465</i>	0.611	0.0414
<i>CG11071</i>	0.611	0.0414
<i>Ir40a</i>	0.611	0.0414
<i>CG10496</i>	0.61	0.0416
<i>CG14644</i>	0.61	0.0416
<i>CG14856</i>	0.61	0.0416
<i>CG14966</i>	0.61	0.0416
<i>CG3021</i>	0.61	0.0416
<i>CG12432</i>	0.609	0.0421
<i>CG6488</i>	0.609	0.0421
<i>Spz2</i>	0.609	0.0421
<i>Poxn</i>	0.608	0.0423
<i>beat-111b</i>	0.607	0.0424
<i>exba</i>	0.607	0.0424
<i>CG31025</i>	0.606	0.0426
<i>CG31036</i>	0.606	0.0426
<i>CG14451</i>	0.605	0.0428
<i>CG4617</i>	0.605	0.0428
<i>mGluRA</i>	0.605	0.0428
<i>mthl5</i>	0.605	0.0428
<i>RpLP1</i>	0.605	0.0428
<i>CG31690</i>	0.604	0.0432
<i>CG32442</i>	0.604	0.0432
<i>Gr98a</i>	0.604	0.0432
<i>CG14186</i>	0.603	0.0435
<i>CG15896</i>	0.603	0.0435
<i>CG31326</i>	0.603	0.0435
<i>Cp7Fc</i>	0.603	0.0435
<i>tw</i>	0.603	0.0435
<i>ventrally-exp</i>	0.603	0.0435
<i>Aeft1</i>	0.602	0.0441
<i>CG11877</i>	0.602	0.0441
<i>CG14956</i>	0.602	0.0441
<i>CG15322</i>	0.602	0.0441
<i>CG31381</i>	0.602	0.0441
<i>CG4582</i>	0.602	0.0441
<i>CG14853</i>	0.601	0.0446
<i>CG34186</i>	0.601	0.0446
<i>H2.0</i>	0.601	0.0446
<i>homer</i>	0.601	0.0446
<i>hpo</i>	0.601	0.0446
<i>Sytl</i>	0.601	0.0446
<i>trbd</i>	0.601	0.0446
<i>CG17922</i>	0.6	0.0452
<i>CG32121</i>	0.6	0.0452
<i>Ser</i>	0.6	0.0452

Gene Name	ERC Value	P-value
<i>spn-B</i>	0.6	0.0452
<i>CG17490</i>	0.599	0.0456
<i>CG17724</i>	0.599	0.0456
<i>CG5613</i>	0.599	0.0456
<i>l(2)37Cd</i>	0.599	0.0456
<i>CG11970</i>	0.598	0.0459
<i>CG12123</i>	0.598	0.0459
<i>CG14126</i>	0.598	0.0459
<i>CG14450</i>	0.598	0.0459
<i>CG14696</i>	0.598	0.0459
<i>CG2162</i>	0.598	0.0459
<i>Rab9</i>	0.598	0.0459
<i>repo</i>	0.598	0.0459
<i>Rpb4</i>	0.598	0.0459
<i>Bx</i>	0.597	0.0468
<i>CG12272</i>	0.597	0.0468
<i>CG9384</i>	0.597	0.0468
<i>CG9449</i>	0.597	0.0468
<i>CG10019</i>	0.596	0.0471
<i>CG11560</i>	0.596	0.0471
<i>CG3194</i>	0.596	0.0471
<i>CG32195</i>	0.595	0.0474
<i>CG40351</i>	0.595	0.0474
<i>CG9247</i>	0.595	0.0474
<i>RIC-3</i>	0.595	0.0474
<i>Sap47</i>	0.595	0.0474
<i>stnA</i>	0.595	0.0474
<i>Taspase1</i>	0.595	0.0474
<i>CG1529</i>	0.594	0.048
<i>CG17270</i>	0.594	0.048
<i>CG3556</i>	0.594	0.048
<i>Cpr49Aa</i>	0.594	0.048
<i>CG3292</i>	0.593	0.0484
<i>CG7369</i>	0.593	0.0484
<i>CG6465</i>	0.593	0.0484
<i>jet</i>	0.593	0.0484
<i>por</i>	0.593	0.0484
<i>CG11251</i>	0.592	0.0488
<i>CG31102</i>	0.592	0.0488
<i>CG8538</i>	0.592	0.0488
<i>CG13245</i>	0.591	0.0491
<i>CG3558</i>	0.591	0.0491
<i>Ppt1</i>	0.591	0.0491
<i>rec</i>	0.591	0.0491
<i>Tsp42Eg</i>	0.591	0.0491
<i>grp</i>	0.59	0.0495
<i>CG13116</i>	0.589	0.0496
<i>CG5270</i>	0.589	0.0496
<i>CG5791</i>	0.589	0.0496
<i>CYLD</i>	0.589	0.0496
<i>LIMK1</i>	0.589	0.0496
<i>CG11562</i>	0.588	0.0501
<i>CG12299</i>	0.588	0.0501
<i>CG14544</i>	0.588	0.0501
<i>CG15093</i>	0.588	0.0501
<i>sax</i>	0.588	0.0501

Table 6.S10 Continued

Gene Name	ERC Value	P-value
Xbp1	0.588	0.0501
CG11534	0.587	0.0506
CG1688	0.587	0.0506
CG3775	0.587	0.0506
CG18476	0.586	0.0509
CG7879	0.586	0.0509
lama	0.586	0.0509
CG1942	0.585	0.0512
CG2003	0.585	0.0512
CG3652	0.585	0.0512
Pph13	0.585	0.0512
CG10864	0.584	0.0515
CG13667	0.584	0.0515
CG15365	0.584	0.0515
CG42487	0.584	0.0515
CG6796	0.584	0.0515
Cyp6v1	0.584	0.0515
Btbv11	0.583	0.0521
CG14300	0.583	0.0521
CG14787	0.583	0.0521
CG31360	0.583	0.0521
CG3191	0.583	0.0521
Gp150	0.583	0.0521
PGRP-LD	0.583	0.0521
Sry-alpha	0.583	0.0521
ssh	0.583	0.0521
bou	0.582	0.0529
CG12134	0.582	0.0529
CG30499	0.582	0.0529
CycG	0.582	0.0529
polo	0.582	0.0529
Usf	0.582	0.0529
aust	0.581	0.0534
CG5726	0.581	0.0534
cwo	0.581	0.0534
f	0.581	0.0534
jim	0.581	0.0534
Jra	0.581	0.0534
mth110	0.581	0.0534
CG13003	0.58	0.0541
CG14512	0.58	0.0541
CG10916	0.579	0.0542
CG5439	0.579	0.0542
na	0.579	0.0542
CG11279	0.578	0.0545
CG32176	0.578	0.0545
CG32792	0.578	0.0545
CG7692	0.578	0.0545
CG8319	0.578	0.0545
Dpy-30L1	0.578	0.0545
org-1	0.578	0.0545
Spn43Ad	0.578	0.0545
CG10646	0.577	0.0552
CG14352	0.577	0.0552
CG15012	0.577	0.0552
CG4678	0.577	0.0552

Gene Name	ERC Value	P-value
Cyp9b2	0.577	0.0552
MTF-1	0.577	0.0552
CG11137	0.576	0.0558
CG13362	0.576	0.0558
CG13685	0.576	0.0558
CG14280	0.576	0.0558
CG3149	0.576	0.0558
CG33695	0.576	0.0558
CG6362	0.575	0.0563
CG9220	0.575	0.0563
lr94h	0.575	0.0563
Msi	0.575	0.0563
lko	0.575	0.0563
CG14223	0.574	0.0568
CG17360	0.574	0.0568
CG2269	0.574	0.0568
CG9437	0.574	0.0568
CG9577	0.574	0.0568
CG7382	0.573	0.0572
CG9986	0.573	0.0572
srp	0.573	0.0572
Syt12	0.573	0.0572
Syt14	0.573	0.0572
CG31109	0.572	0.0577
cyr	0.572	0.0577
llp6	0.572	0.0577
mahj	0.572	0.0577
CG12177	0.571	0.058
Map60	0.571	0.058
zpg	0.571	0.058
Aats-ala-m	0.57	0.0583
Ance-3	0.57	0.0583
blot	0.57	0.0583
CG3457	0.57	0.0583
H	0.57	0.0583
Ku80	0.57	0.0583
plexA	0.57	0.0583
RhoGAP19D	0.57	0.0583
beat-11la	0.569	0.059
CG42795	0.569	0.059
CG5589	0.569	0.059
CG8408	0.569	0.059
kek1	0.569	0.059
kek5	0.569	0.059
NK7.1	0.569	0.059
rod	0.569	0.059
CG11356	0.568	0.0597
CG1315	0.568	0.0597
CG30456	0.568	0.0597
CG4022	0.568	0.0597
nec	0.568	0.0597
net	0.568	0.0597
Snp	0.568	0.0597
stan	0.568	0.0597
Stat92E	0.568	0.0597
Sulf1	0.568	0.0597

Gene Name	ERC Value	P-value
CG4984	0.567	0.0606
CG6415	0.567	0.0606
CG6860	0.567	0.0606
Ravus	0.567	0.0606
CG13532	0.566	0.061
CG14105	0.566	0.061
CG8079	0.566	0.061
Lip1	0.566	0.061
wdp	0.566	0.061
CG10914	0.564	0.0614
CG15701	0.564	0.0614
CG7598	0.564	0.0614
pnr	0.564	0.0614
ppk11	0.564	0.0614
Rtf1	0.564	0.0614
CG18431	0.563	0.062
CG31798	0.563	0.062
CG7453	0.563	0.062
CG9243	0.563	0.062
fidipidine	0.563	0.062
nAcRbeta-2	0.563	0.062
Syt10A31	0.562	0.0625
CG14629	0.562	0.0625
CG17059	0.562	0.0625
CG18262	0.562	0.0625
CG3744	0.562	0.0625
CG5510	0.562	0.0625
CG7222	0.562	0.0625
Nfl	0.562	0.0625
bin3	0.561	0.0632
CG11286	0.561	0.0632
CG13361	0.561	0.0632
CG13837	0.561	0.0632
Notum	0.561	0.0632
PsGEF	0.561	0.0632
RhoGAP5A	0.561	0.0632
CG10171	0.56	0.0639
CG15528	0.56	0.0639
CG9967	0.56	0.0639
ldgf5	0.56	0.0639
mus81	0.56	0.0639
CG14070	0.559	0.0643
CG1561	0.559	0.0643
Bteb2	0.558	0.0645
CG13640	0.558	0.0645
CG14321	0.558	0.0645
Def	0.558	0.0645
CG11637	0.557	0.0649
CG14736	0.557	0.0649
CG31053	0.557	0.0649
HP1c	0.557	0.0649
kat80	0.557	0.0649
sad	0.557	0.0649
CG14323	0.556	0.0654
CG5068	0.556	0.0654
how	0.556	0.0654

Gene Name	ERC Value	P-value
Or43b	0.556	0.0654
pgant8	0.556	0.0654
Sara	0.556	0.0654
Csas	0.555	0.0659
CG14625	0.554	0.066
CG4553	0.554	0.066
CG6980	0.554	0.066
CG8312	0.554	0.066
Germ2	0.554	0.066
SPoCk	0.554	0.066
ACXE	0.553	0.0666
CG13244	0.553	0.0666
CG18178	0.553	0.0666
CG31414	0.553	0.0666
RpS29	0.553	0.0666
CG10623	0.552	0.067
CG18528	0.552	0.067
CG33958	0.552	0.067
mRpS30	0.552	0.067
plc	0.552	0.067
dup	0.551	0.0675
thr	0.551	0.0675
CG10824	0.55	0.0677
CG1136	0.55	0.0677
CG9541	0.55	0.0677
ERR	0.55	0.0677
Gr93c	0.55	0.0677
CG10680	0.549	0.0681
CG30127	0.549	0.0681
ia2	0.549	0.0681
nxf2	0.549	0.0681
retm	0.549	0.0681
trr	0.549	0.0681
a6	0.548	0.0686
btlv	0.548	0.0686
CG4914	0.548	0.0686
CG7277	0.548	0.0686
Gyk	0.548	0.0686
Mlh1	0.548	0.0686
Rpp20	0.548	0.0686
CG5897	0.547	0.0693
CG9053	0.547	0.0693
Hsp67Ba	0.547	0.0693
Sbf	0.547	0.0693
CCKLR-17D	0.546	0.0696
CG15336	0.546	0.0696
CG1602	0.546	0.0696
CG30440	0.546	0.0696
CG42557	0.546	0.0696
CG8944	0.546	0.0696
Eps-15	0.546	0.0696
lute	0.546	0.0696
Proc-R	0.546	0.0696
CG10376	0.545	0.0705
CG12420	0.545	0.0705
CG1344	0.545	0.0705

Gene Name	ERC Value	P-value
CG14989	0.545	0.0705
CG3483	0.545	0.0705
Sdc	0.545	0.0705
Sp7	0.545	0.0705
Bap170	0.544	0.0711
CG1888	0.544	0.0711
CG34196	0.544	0.0711
CG9817	0.544	0.0711
Ndc80	0.544	0.0711
tan	0.544	0.0711
CG13084	0.543	0.0716
CG1647	0.543	0.0716
CG7017	0.543	0.0716
CG8300	0.543	0.0716
CG9740	0.543	0.0716
ix	0.543	0.0716
Ptp69D	0.543	0.0716
CG12680	0.542	0.0723
CG15130	0.542	0.0723
CG15756	0.542	0.0723
Dip-C	0.542	0.0723
l(2)37Ce	0.542	0.0723
tera	0.542	0.0723
CG10435	0.54	0.0728
CG10889	0.54	0.0728
CG11095	0.54	0.0728
CG16986	0.54	0.0728
cact	0.539	0.0732
CG9386	0.539	0.0732
CG9733	0.539	0.0732
Pbp45	0.539	0.0732
yl	0.539	0.0732
CG11668	0.538	0.0736
CG15199	0.538	0.0736
CG3732	0.538	0.0736
CG3841	0.538	0.0736
Nfn1a	0.538	0.0736
RpS5a	0.538	0.0736
CG1578	0.537	0.0741
CG3281	0.537	0.0741
CG33286	0.537	0.0741
CG4907	0.537	0.0741
CG4950	0.537	0.0741
CG7979	0.537	0.0741
Hr83	0.537	0.0741
mRpL54	0.537	0.0741
CG12207	0.536	0.0749
CG13322	0.536	0.0749
CG32281	0.536	0.0749
Chf11	0.536	0.0749
E5	0.536	0.0749
MED15	0.536	0.0749
Psf2	0.536	0.0749
CG14967	0.535	0.0755
CG33672	0.535	0.0755
CG42382	0.535	0.0755

Table 6.S10 Continued

Gene Name	ERC Value	P-value
<i>grk</i>	0.535	0.0755
<i>Orc4</i>	0.535	0.0755
<i>Pc</i>	0.535	0.0755
<i>CG32685</i>	0.533	0.076
<i>CG4424</i>	0.533	0.076
<i>CG4679</i>	0.533	0.076
<i>Nuf2</i>	0.533	0.076
<i>sha</i>	0.533	0.076
<i>CG11299</i>	0.532	0.0765
<i>CG17883</i>	0.532	0.0765
<i>CG33096</i>	0.532	0.0765
<i>esn</i>	0.532	0.0765
<i>Abl</i>	0.531	0.0768
<i>CG11872</i>	0.531	0.0768
<i>CG13843</i>	0.531	0.0768
<i>CG6136</i>	0.531	0.0768
<i>CG7280</i>	0.531	0.0768
<i>EF2b</i>	0.531	0.0768
<i>PR2</i>	0.531	0.0768
<i>blue</i>	0.53	0.0775
<i>CG5235</i>	0.53	0.0775
<i>CG5773</i>	0.53	0.0775
<i>lambdaTry</i>	0.53	0.0775
<i>Pi3K21B</i>	0.53	0.0775
<i>Rac1</i>	0.53	0.0775
<i>robo</i>	0.53	0.0775
<i>CG13877</i>	0.529	0.0781
<i>CG14543</i>	0.529	0.0781
<i>CG7927</i>	0.529	0.0781
<i>jub</i>	0.529	0.0781
<i>bru-2</i>	0.528	0.0785
<i>CG11109</i>	0.528	0.0785
<i>CG33340</i>	0.528	0.0785
<i>Obp83cd</i>	0.528	0.0785
<i>obst-F</i>	0.528	0.0785
<i>rictor</i>	0.528	0.0785
<i>sub</i>	0.528	0.0785
<i>CG9422</i>	0.527	0.0791
<i>l(1)sc</i>	0.527	0.0791
<i>CG10600</i>	0.526	0.0793
<i>CG12768</i>	0.526	0.0793
<i>CG13321</i>	0.526	0.0793
<i>CG13565</i>	0.526	0.0793
<i>CG6325</i>	0.526	0.0793
<i>DAT</i>	0.526	0.0793
<i>Ets21C</i>	0.526	0.0793
<i>lr67b</i>	0.526	0.0793
<i>pigeon</i>	0.526	0.0793
<i>CG32105</i>	0.525	0.0801
<i>CG4749</i>	0.525	0.0801
<i>CG8964</i>	0.525	0.0801
<i>lr56a</i>	0.525	0.0801
<i>CG10077</i>	0.524	0.0805
<i>CG42245</i>	0.524	0.0805
<i>Orc5</i>	0.524	0.0805
<i>CG10144</i>	0.523	0.0807

Gene Name	ERC Value	P-value
<i>CG13114</i>	0.523	0.0807
<i>CG13500</i>	0.523	0.0807
<i>CG2016</i>	0.523	0.0807
<i>CG31380</i>	0.523	0.0807
<i>CG7227</i>	0.523	0.0807
<i>CG13384</i>	0.522	0.0813
<i>CG3407</i>	0.522	0.0813
<i>CG9876</i>	0.522	0.0813
<i>ect</i>	0.522	0.0813
<i>llp2</i>	0.522	0.0813
<i>scb</i>	0.522	0.0813
<i>Tollo</i>	0.522	0.0813
<i>bip1</i>	0.521	0.0819
<i>CG13169</i>	0.521	0.0819
<i>CG17691</i>	0.521	0.0819
<i>CG34039</i>	0.521	0.0819
<i>lat</i>	0.521	0.0819
<i>beat-VI</i>	0.52	0.0823
<i>CG11396</i>	0.52	0.0823
<i>CG5978</i>	0.52	0.0823
<i>CG6550</i>	0.52	0.0823
<i>brk</i>	0.519	0.0827
<i>CG3223</i>	0.519	0.0827
<i>CG6739</i>	0.519	0.0827
<i>ImpL2</i>	0.519	0.0827
<i>Ptx1</i>	0.519	0.0827
<i>beat-1c</i>	0.518	0.0832
<i>CG10710</i>	0.518	0.0832
<i>Cic</i>	0.518	0.0832
<i>Mnt</i>	0.518	0.0832
<i>Att3</i>	0.517	0.0835
<i>CG42353</i>	0.517	0.0835
<i>CG7593</i>	0.517	0.0835
<i>Gs1f</i>	0.517	0.0835
<i>CG10222</i>	0.516	0.0839
<i>CG12582</i>	0.516	0.0839
<i>CG15269</i>	0.516	0.0839
<i>CG7156</i>	0.516	0.0839
<i>mod</i>	0.516	0.0839
<i>BubR1</i>	0.515	0.0843
<i>corn</i>	0.515	0.0843
<i>CG10936</i>	0.514	0.0845
<i>CG32635</i>	0.514	0.0845
<i>CG3679</i>	0.514	0.0845
<i>sens-2</i>	0.514	0.0845
<i>CG14100</i>	0.513	0.0849
<i>CG6503</i>	0.513	0.0849
<i>CG9175</i>	0.513	0.0849
<i>lr7a</i>	0.513	0.0849
<i>mrRpS29</i>	0.513	0.0849
<i>pot</i>	0.513	0.0849
<i>CG17111</i>	0.512	0.0854
<i>CG2813</i>	0.512	0.0854
<i>CG34315</i>	0.512	0.0854
<i>CG4896</i>	0.512	0.0854
<i>Orc2</i>	0.512	0.0854

Gene Name	ERC Value	P-value
<i>Rad1</i>	0.512	0.0854
<i>Takr99D</i>	0.512	0.0854
<i>CG4660</i>	0.511	0.086
<i>CG5367</i>	0.511	0.086
<i>CG7099</i>	0.511	0.086
<i>GlcT-1</i>	0.511	0.086
<i>grim</i>	0.511	0.086
<i>CG8097</i>	0.51	0.0865
<i>Drep-2</i>	0.51	0.0865
<i>Bet1</i>	0.509	0.0867
<i>CG3808</i>	0.509	0.0867
<i>CG42404</i>	0.509	0.0867
<i>Lrt</i>	0.509	0.0867
<i>NaCP60E</i>	0.509	0.0867
<i>sec8</i>	0.509	0.0867
<i>CG11902</i>	0.508	0.0872
<i>CG17265</i>	0.508	0.0872
<i>CG5445</i>	0.508	0.0872
<i>wda</i>	0.508	0.0872
<i>CG11966</i>	0.507	0.0876
<i>CG13366</i>	0.507	0.0876
<i>CG14882</i>	0.507	0.0876
<i>CG9886</i>	0.507	0.0876
<i>Rga</i>	0.507	0.0876
<i>Spn27A</i>	0.507	0.0876
<i>Sse</i>	0.507	0.0876
<i>CG13005</i>	0.506	0.0882
<i>CG13239</i>	0.506	0.0882
<i>CG16970</i>	0.506	0.0882
<i>CG34244</i>	0.506	0.0882
<i>Bro</i>	0.505	0.0886
<i>CG12998</i>	0.505	0.0886
<i>CG14195</i>	0.505	0.0886
<i>CG14607</i>	0.505	0.0886
<i>CG2862</i>	0.505	0.0886
<i>CG3823</i>	0.505	0.0886
<i>CG6197</i>	0.505	0.0886
<i>cv-2</i>	0.505	0.0886
<i>Nrk</i>	0.505	0.0886
<i>vtd</i>	0.505	0.0886
<i>CG13999</i>	0.504	0.0895
<i>idbr</i>	0.504	0.0895
<i>caps</i>	0.503	0.0896
<i>CG13283</i>	0.503	0.0896
<i>CG32803</i>	0.503	0.0896
<i>CG9747</i>	0.503	0.0896
<i>CG11289</i>	0.502	0.09
<i>CG11851</i>	0.502	0.09
<i>CG13728</i>	0.502	0.09
<i>CG15738</i>	0.502	0.09
<i>CG33155</i>	0.502	0.09
<i>CG3511</i>	0.502	0.09
<i>pil</i>	0.502	0.09
<i>Ptp52F</i>	0.502	0.09
<i>CG10912</i>	0.501	0.0907
<i>CG11060</i>	0.501	0.0907

Gene Name	ERC Value	P-value
<i>CG13970</i>	0.501	0.0907
<i>CG30047</i>	0.501	0.0907
<i>CG31823</i>	0.501	0.0907
<i>Ppt2</i>	0.501	0.0907
<i>CG11263</i>	0.5	0.0913
<i>CG14879</i>	0.5	0.0913
<i>CG31342</i>	0.5	0.0913
<i>CG4611</i>	0.5	0.0913
<i>CG4949</i>	0.5	0.0913
<i>cn</i>	0.5	0.0913
<i>Hex-t2</i>	0.5	0.0913
<i>Mt2</i>	0.5	0.0913
<i>Ogg1</i>	0.5	0.0913
<i>Tsp42Ec</i>	0.5	0.0913
<i>CG11843</i>	0.499	0.0922
<i>CG12333</i>	0.499	0.0922
<i>CG14103</i>	0.499	0.0922
<i>CG14115</i>	0.499	0.0922
<i>CG33172</i>	0.498	0.0925
<i>DNApol-ι</i>	0.498	0.0925
<i>Or23a</i>	0.498	0.0925
<i>CG13185</i>	0.497	0.0928
<i>CG31688</i>	0.497	0.0928
<i>CG34045</i>	0.497	0.0928
<i>Rfx</i>	0.497	0.0928
<i>Wnt4</i>	0.497	0.0928
<i>CG10845</i>	0.496	0.0932
<i>CG11165</i>	0.496	0.0932
<i>CG7519</i>	0.496	0.0932
<i>Cpr65Eb</i>	0.496	0.0932
<i>kay</i>	0.496	0.0932
<i>RluA-2</i>	0.496	0.0932
<i>CG5195</i>	0.495	0.0938
<i>pkf</i>	0.495	0.0938
<i>CG42726</i>	0.494	0.094
<i>LpR1</i>	0.494	0.094
<i>Mst85C</i>	0.494	0.094
<i>CG12316</i>	0.493	0.0942
<i>CG14050</i>	0.493	0.0942
<i>CG7786</i>	0.493	0.0942
<i>Lsm11</i>	0.493	0.0942
<i>wit</i>	0.493	0.0942
<i>CG13616</i>	0.492	0.0947
<i>CG18048</i>	0.492	0.0947
<i>CG32354</i>	0.492	0.0947
<i>CG32832</i>	0.492	0.0947
<i>CG6370</i>	0.492	0.0947
<i>CG6576</i>	0.492	0.0947
<i>CG8329</i>	0.492	0.0947
<i>CycK</i>	0.492	0.0947
<i>eco</i>	0.492	0.0947
<i>Osi23</i>	0.492	0.0947
<i>CG3894</i>	0.491	0.0956
<i>CG4297</i>	0.491	0.0956
<i>CG4360</i>	0.491	0.0956
<i>CG7322</i>	0.491	0.0956

Gene Name	ERC Value	P-value
<i>CG8089</i>	0.491	0.0956
<i>Tsp97E</i>	0.491	0.0956
<i>ara</i>	0.49	0.0961
<i>CG4629</i>	0.49	0.0961
<i>CG4844</i>	0.49	0.0961
<i>CG5073</i>	0.49	0.0961
<i>Cct1</i>	0.489	0.0965
<i>CG5399</i>	0.489	0.0965
<i>Lip2</i>	0.489	0.0965
<i>mus309</i>	0.489	0.0965
<i>Ssdp</i>	0.489	0.0965
<i>CG14903</i>	0.488	0.0969
<i>GluRIIC</i>	0.488	0.0969
<i>hh</i>	0.488	0.0969
<i>CG12391</i>	0.487	0.0972
<i>Dcr-1</i>	0.487	0.0972
<i>Rpn5</i>	0.487	0.0972
<i>Andorra</i>	0.486	0.0975
<i>CG12012</i>	0.486	0.0975
<i>mus309</i>	0.486	0.0975
<i>CG15395</i>	0.486	0.0975
<i>CG17278</i>	0.486	0.0975
<i>CG5612</i>	0.486	0.0975
<i>Spn5</i>	0.486	0.0975
<i>CG17083</i>	0.485	0.0981
<i>yps</i>	0.485	0.0981
<i>CG10140</i>	0.484	0.0983
<i>CG13690</i>	0.484	0.0983
<i>CG13962</i>	0.484	0.0983
<i>CG14302</i>	0.484	0.0983
<i>CG14441</i>	0.484	0.0983
<i>CG1542</i>	0.484	0.0983
<i>CG9689</i>	0.484	0.0983
<i>CG13258</i>	0.483	0.0989
<i>CG2909</i>	0.483	0.0989
<i>CHKov2</i>	0.483	0.0989
<i>Kif3C</i>	0.483	0.0989
<i>blos3</i>	0.482	0.0993
<i>CG13516</i>	0.482	0.0993
<i>CG15083</i>	0.482	0.0993
<i>CG31637</i>	0.482	0.0993
<i>CG6005</i>	0.482	0.0993
<i>CG7789</i>	0.482	0.0993
<i>CG9109</i>	0.482	0.0993
<i>CG34266</i>	0.48	0.0999
<i>CG4025</i>	0.48	0.0999
<i>Det</i>	0.48	0.0999
<i>Muc91C</i>	0.48	0.0999

Table 6.S11 - Top Genes ERC values for *mre11* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG7369	0.936	0.0001
CG10560	0.916	0.0002
CG11835	0.91	0.0003
CG15376	0.909	0.0004
CG6409	0.907	0.0005
CG32573	0.906	0.0005
CG13074	0.897	0.0006
Magi	0.89	0.0007
os	0.884	0.0008
CG3386	0.882	0.0009
Rh7	0.882	0.0009
CG5414	0.881	0.0011
rod	0.881	0.0011
CG7069	0.879	0.0013
CG17562	0.874	0.0014
Cpr62Ba	0.871	0.0014
CG9649	0.864	0.0015
RhoGAP18E	0.863	0.0016
CG31698	0.857	0.0017
CS-2	0.856	0.0018
CG12851	0.855	0.0019
CG11289	0.852	0.002
CG34284	0.848	0.0021
Aldh	0.847	0.0022
Rad51D	0.846	0.0023
CG11095	0.845	0.0023
CG15478	0.844	0.0024
Rp55a	0.841	0.0025
salr	0.841	0.0025
CG5399	0.84	0.0027
CG2813	0.836	0.0028
CG3368	0.832	0.0029
CG10713	0.831	0.003
TfllEalpha	0.83	0.0031
Vm32E	0.83	0.0031
CG10947	0.829	0.0032
CG42487	0.829	0.0032
CG10479	0.828	0.0034
CG3223	0.826	0.0035
CG13384	0.825	0.0036
CG33641	0.825	0.0036
Rab9	0.824	0.0038
CG3556	0.821	0.0039
CG14100	0.818	0.004
CG32803	0.817	0.0041
nerfin-2	0.817	0.0041
CG4334	0.814	0.0042
CG32750	0.812	0.0043
CG2794	0.811	0.0044
CG8370	0.811	0.0044
Pep	0.811	0.0044
dikar	0.81	0.0047
Gr9a	0.81	0.0047
Pros35	0.81	0.0047
CG31053	0.809	0.005
CG9733	0.807	0.005

Gene Name	ERC Value	P-value
wgn	0.805	0.0051
CG11975	0.803	0.0052
CG9114	0.801	0.0053
l(3)04053	0.801	0.0053
CG14302	0.799	0.0055
CG10376	0.798	0.0056
CG15912	0.798	0.0056
CG2162	0.798	0.0056
CG9886	0.798	0.0056
CG11109	0.797	0.0059
CG6927	0.797	0.0059
melt	0.796	0.0061
BubR1	0.792	0.0062
lrb0e	0.792	0.0062
CG15404	0.791	0.0064
CG31150	0.789	0.0065
Jon74E	0.788	0.0066
Pph13	0.788	0.0066
Scr	0.787	0.0068
CG7598	0.786	0.0068
Rpb8	0.786	0.0068
CG11668	0.783	0.007
Ent2	0.783	0.007
Or46a	0.783	0.007
Os-E	0.781	0.0073
CG13169	0.78	0.0074
Det	0.78	0.0074
Dyrk3	0.78	0.0074
CG32541	0.778	0.0077
CG6838	0.777	0.0077
f	0.775	0.0078
CG10264	0.773	0.0079
CG14562	0.772	0.008
Hsp67Ba	0.77	0.0081
Vps33B	0.77	0.0081
CG11155	0.769	0.0083
jim	0.769	0.0083
CG34391	0.768	0.0085
CG9335	0.768	0.0085
CG32006	0.767	0.0086
CG34199	0.767	0.0086
CG10249	0.766	0.0088
CG11870	0.766	0.0088
CG7985	0.766	0.0088
Ance-3	0.765	0.0091
Pros25	0.765	0.0091
Vps28	0.765	0.0091
CG7880	0.764	0.0094
CG8389	0.762	0.0095
CG12316	0.761	0.0095
CG15118	0.761	0.0095
ldbr	0.759	0.0097
CG6796	0.758	0.0098
CG13111	0.757	0.0099
CG31380	0.756	0.01
Sdc	0.756	0.01

Gene Name	ERC Value	P-value
CG2022	0.754	0.0102
CG7320	0.754	0.0102
a6	0.753	0.0104
CG14826	0.753	0.0104
CG1599	0.753	0.0104
CG6607	0.753	0.0104
mei-S332	0.753	0.0104
CG10710	0.751	0.0108
CG13424	0.75	0.0109
CG13616	0.749	0.011
CG4554	0.748	0.0111
CG8180	0.747	0.0112
l(2)k10201	0.747	0.0112
CG12012	0.745	0.0114
gatA	0.745	0.0114
Satf	0.745	0.0114
CG31690	0.744	0.0116
CG14618	0.743	0.0117
scod	0.743	0.0117
CG6733	0.742	0.0119
Ykt6	0.742	0.0119
CG14253	0.741	0.0121
katanin-60	0.741	0.0121
mos	0.74	0.0123
CG15353	0.739	0.0123
CG2709	0.738	0.0124
Dcr-1	0.738	0.0124
CG12104	0.737	0.0126
CG11902	0.736	0.0127
CG3407	0.736	0.0127
CG15020	0.735	0.0129
CG3194	0.735	0.0129
CG12432	0.733	0.0131
CG32459	0.731	0.0132
Fbw5	0.731	0.0132
gd	0.731	0.0132
CG5909	0.729	0.0134
CG10424	0.728	0.0135
CG1358	0.728	0.0135
CG8538	0.728	0.0135
CG30046	0.727	0.0138
CG3652	0.726	0.0139
CG4611	0.726	0.0139
Ppt2	0.726	0.0139
CG15093	0.725	0.0141
CG10344	0.724	0.0142
CG14417	0.724	0.0142
CG17026	0.724	0.0142
CG31371	0.724	0.0142
CG7222	0.724	0.0142
pod1	0.724	0.0142
CG15928	0.723	0.0148
CG17118	0.723	0.0148
Or43b	0.723	0.0148
DNApol-gam	0.722	0.015
mth19	0.722	0.015

Gene Name	ERC Value	P-value
CG9747	0.721	0.0152
Asph	0.72	0.0153
Pbp45	0.72	0.0153
hop	0.719	0.0155
CG11403	0.718	0.0156
CG14879	0.716	0.0157
CG31682	0.716	0.0157
CG7884	0.716	0.0157
Fem-1	0.716	0.0157
kon	0.716	0.0157
Sox15	0.716	0.0157
mei-W68	0.715	0.0162
aft	0.714	0.0163
CG11345	0.714	0.0163
CG8159	0.714	0.0163
Jon44E	0.714	0.0163
Dredd	0.713	0.0167
CG32281	0.711	0.0168
zpg	0.711	0.0168
CG14930	0.71	0.0169
CG31922	0.71	0.0169
CG6520	0.71	0.0169
GlurIIIC	0.71	0.0169
mth5	0.71	0.0169
CG10418	0.709	0.0174
CG13741	0.709	0.0174
mRpl38	0.709	0.0174
Prosalpha6T	0.709	0.0174
CG14722	0.708	0.0177
CG3837	0.708	0.0177
CG6234	0.708	0.0177
SatD10	0.708	0.0177
CG10669	0.707	0.0181
CG15865	0.707	0.0181
CG32537	0.707	0.0181
CG5439	0.707	0.0181
PGRP-SD	0.706	0.0185
Spn27A	0.706	0.0185
nAcRbeta-2	0.705	0.0186
lr56a	0.704	0.0187
Suff	0.704	0.0187
B-H1	0.703	0.0189
CG10469	0.703	0.0189
CG11454	0.703	0.0189
Tollo	0.703	0.0189
CG14408	0.702	0.0193
RhoGAP5A	0.702	0.0193
CG15661	0.701	0.0195
Orb5a	0.701	0.0195
CG13837	0.7	0.0196
CG15643	0.7	0.0196
Csl4	0.7	0.0196
Mif	0.7	0.0196
Pdp	0.7	0.0196
qkr54B	0.7	0.0196
Traf6	0.7	0.0196

Gene Name	ERC Value	P-value
CG4573	0.699	0.0203
mGluRA	0.699	0.0203
Abi	0.698	0.0205
CG8093	0.698	0.0205
Drak	0.698	0.0205
SC35	0.698	0.0205
CG30403	0.697	0.0208
ds	0.696	0.0209
CG32832	0.695	0.021
CG6503	0.695	0.021
Dg	0.695	0.021
Kmn1	0.695	0.021
Sep5	0.694	0.0214
ia2	0.694	0.0214
lr7g	0.694	0.0214
Snp	0.694	0.0214
beat-IIIb	0.693	0.0217
CycT	0.693	0.0217
dUTPase	0.693	0.0217
ss	0.693	0.0217
CG42399	0.692	0.0221
fs(1)N	0.692	0.0221
CG31849	0.691	0.0223
dor	0.691	0.0223
sna	0.691	0.0223
CG13272	0.69	0.0225
CG9542	0.69	0.0225
ft	0.69	0.0225
GlurIIIA	0.69	0.0225
hh	0.69	0.0225
nimB5	0.69	0.0225
Orc2	0.69	0.0225
eco	0.689	0.0232
CG6254	0.688	0.0232
CG17691	0.687	0.0233
CG32635	0.687	0.0233
CG5746	0.687	0.0233
Ssl1	0.687	0.0233
CG6847	0.686	0.0237
net	0.686	0.0237
sda	0.686	0.0237
snopin	0.686	0.0237
CG15322	0.685	0.0241
CG2765	0.684	0.0241
CG31251	0.684	0.0241
Ptp52F	0.684	0.0241
Tjrr	0.684	0.0241
D12	0.681	0.0245
RhoGEF3	0.681	0.0245
yki	0.681	0.0245
aid	0.68	0.0248
CG14450	0.68	0.0248
CG9384	0.68	0.0248
CG7146	0.679	0.025
CG10680	0.678	0.0251
CG7156	0.678	0.0251

Table 6.S11 Continued

Gene Name	ERC Value	P-value
Pip61F	0.678	0.0251
CG33784	0.677	0.0254
CG9386	0.677	0.0254
CG42726	0.676	0.0256
CG15124	0.675	0.0257
CG15395	0.675	0.0257
fz4	0.675	0.0257
Mt2	0.675	0.0257
CG3841	0.674	0.026
CG42374	0.674	0.026
CG8617	0.674	0.026
CG11778	0.673	0.0263
CG12163	0.673	0.0263
Ptth	0.673	0.0263
CG3838	0.671	0.0266
Map60	0.671	0.0266
CG12355	0.67	0.0268
CG14314	0.67	0.0268
CG16863	0.67	0.0268
CG2975	0.67	0.0268
CG31344	0.67	0.0268
Sp7	0.67	0.0268
CG14435	0.669	0.0273
CG4017	0.669	0.0273
Cpr72Eb	0.669	0.0273
dmt193B	0.669	0.0273
Fist	0.669	0.0273
Spn43Ad	0.669	0.0273
Sap47	0.668	0.0278
thoc7	0.668	0.0278
Def	0.667	0.028
Dip-C	0.667	0.028
vsg	0.667	0.028
borr	0.666	0.0283
CG18178	0.666	0.0283
CG3292	0.666	0.0283
Irp-1B	0.666	0.0283
CG15533	0.665	0.0286
CG33919	0.665	0.0286
dbo	0.665	0.0286
EioA	0.665	0.0286
H2.0	0.665	0.0286
Hpr1	0.665	0.0286
CG33695	0.664	0.0292
CG7550	0.664	0.0292
CG8087	0.664	0.0292
CG14882	0.663	0.0295
CG9147	0.663	0.0295
G-alpha47A	0.663	0.0295
CG10581	0.662	0.0297
CG16790	0.662	0.0297
Jhl-26	0.662	0.0297
trbd	0.662	0.0297
ventrally-exp	0.662	0.0297
CG15756	0.661	0.0302
CG30456	0.661	0.0302

Gene Name	ERC Value	P-value
CG6074	0.661	0.0302
CG3308	0.66	0.0305
CG3434	0.66	0.0305
CG8312	0.66	0.0305
Rpb4	0.66	0.0305
CG30196	0.659	0.0308
hep	0.659	0.0308
MED15	0.659	0.0308
tap	0.659	0.0308
CG10725	0.658	0.0312
Dip3	0.658	0.0312
EndoG1	0.658	0.0312
Proc-R	0.658	0.0312
CG4725	0.657	0.0315
Git	0.657	0.0315
bdg	0.656	0.0317
CG30197	0.656	0.0317
CG7927	0.656	0.0317
KH1	0.656	0.0317
Pvf1	0.656	0.0317
Syt12	0.656	0.0317
Ir92a	0.655	0.0323
thetaTry	0.655	0.0323
CG14273	0.654	0.0324
CG2321	0.653	0.0325
CG7922	0.653	0.0325
CG8690	0.653	0.0325
RpS30	0.653	0.0325
snk	0.653	0.0325
DJ	0.652	0.033
Fsh	0.652	0.033
CG14906	0.651	0.0332
CG15896	0.651	0.0332
CG42817	0.651	0.0332
put	0.651	0.0332
CG1647	0.65	0.0335
ru	0.65	0.0335
CG2789	0.649	0.0337
CG31646	0.649	0.0337
CG14627	0.648	0.0339
La	0.648	0.0339
CG14650	0.647	0.0341
CG15639	0.647	0.0341
CG32563	0.647	0.0341
CG8202	0.647	0.0341
Aats-pro	0.646	0.0344
CG12943	0.646	0.0344
CG3281	0.646	0.0344
tw	0.646	0.0344
bip1	0.645	0.0348
CG14695	0.645	0.0348
CG14853	0.645	0.0348
Cyp28c1	0.645	0.0348
Jra	0.645	0.0348
Syt7	0.645	0.0348
unc-4	0.645	0.0348

Gene Name	ERC Value	P-value
dpr17	0.643	0.0354
tutl	0.641	0.0355
CG14105	0.64	0.0356
CG9279	0.64	0.0356
CG42353	0.639	0.0358
CG5921	0.639	0.0358
CG7028	0.639	0.0358
CG9418	0.639	0.0358
Cpr65Eb	0.639	0.0358
NKAIN	0.639	0.0358
CG8319	0.638	0.0363
Cyp28a5	0.638	0.0363
Psf2	0.638	0.0363
Ret	0.638	0.0363
CG33057	0.637	0.0367
CG13239	0.636	0.0368
CG34186	0.636	0.0368
CG9243	0.636	0.0368
ldgf5	0.636	0.0368
CG12420	0.635	0.0371
CG31133	0.635	0.0371
Cyp49a1	0.635	0.0371
SIDL	0.635	0.0371
CG12042	0.634	0.0375
fs(1)M3	0.634	0.0375
Hsp67Bb	0.634	0.0375
CG17724	0.633	0.0377
CG9691	0.633	0.0377
Gpi1	0.633	0.0377
CG30122	0.632	0.038
Cyp6v1	0.632	0.038
CdsA	0.631	0.0382
CG10000	0.631	0.0382
Kaz1-ORFB	0.63	0.0384
CG11851	0.629	0.0385
CG5265	0.629	0.0385
CG5978	0.629	0.0385
CG9044	0.629	0.0385
lr	0.629	0.0385
Rpn7	0.629	0.0385
CG10077	0.628	0.039
CG10098	0.628	0.039
CG11637	0.628	0.039
CG11762	0.628	0.039
CG11841	0.628	0.039
CG12582	0.628	0.039
CG15172	0.628	0.039
CG4860	0.628	0.039
CG10809	0.627	0.0397
CG32195	0.627	0.0397
Ppm1	0.627	0.0397
CG14572	0.626	0.04
CG34012	0.626	0.04
dm	0.625	0.0402
obst-J	0.625	0.0402
Ssadh	0.625	0.0402

Gene Name	ERC Value	P-value
CG13500	0.624	0.0405
CG7526	0.624	0.0405
GluRIIE	0.624	0.0405
X11L	0.624	0.0405
MrgBP	0.623	0.0408
CG12288	0.622	0.0409
CG13454	0.622	0.0409
CG13643	0.622	0.0409
CG14442	0.622	0.0409
CG14658	0.622	0.0409
CG9497	0.622	0.0409
CG13361	0.621	0.0414
CG14667	0.621	0.0414
CG9021	0.621	0.0414
CG5776	0.62	0.0417
CG7785	0.62	0.0417
DAT	0.62	0.0417
I(2)37Bb	0.62	0.0417
Tsp	0.62	0.0417
ZC3H3	0.62	0.0417
CG11872	0.619	0.0423
CG12159	0.619	0.0423
CG12986	0.619	0.0423
CG4553	0.619	0.0423
CG6300	0.619	0.0423
galectin	0.619	0.0423
CG12716	0.618	0.0428
icln	0.618	0.0428
Olii	0.618	0.0428
CG42366	0.617	0.0431
arg-1	0.617	0.0431
ths	0.617	0.0431
CG11241	0.616	0.0433
CG12990	0.616	0.0433
CG14238	0.616	0.0433
fil	0.616	0.0433
wit	0.616	0.0433
CG13121	0.615	0.0438
CG31360	0.615	0.0438
CG33985	0.615	0.0438
PGRP-LD	0.615	0.0438
CG11593	0.614	0.0441
RpL15	0.614	0.0441
Spc105R	0.614	0.0441
CG3409	0.613	0.0444
CG8243	0.613	0.0444
scriy	0.612	0.0446
CG11070	0.611	0.0447
CG15130	0.611	0.0447
CG5390	0.611	0.0447
CG6613	0.611	0.0447
CG7255	0.611	0.0447
Fit2	0.611	0.0447
CG14102	0.61	0.0452
CG17270	0.61	0.0452
CG34195	0.61	0.0452

Gene Name	ERC Value	P-value
CycK	0.61	0.0452
Grx-1	0.61	0.0452
mRpS10	0.61	0.0452
spn-B	0.61	0.0452
CG2862	0.609	0.0459
comm	0.609	0.0459
CG10274	0.608	0.046
CG14177	0.608	0.046
CG15534	0.608	0.046
coot	0.608	0.046
Hr39	0.608	0.046
m2	0.608	0.046
Aef1	0.607	0.0466
CDase	0.607	0.0466
CG14280	0.607	0.0466
CG4835	0.607	0.0466
CG5522	0.607	0.0466
aust	0.606	0.047
CG17669	0.606	0.047
Ets21C	0.606	0.047
kat80	0.606	0.047
CG4050	0.605	0.0474
Jhe	0.605	0.0474
CG4751	0.604	0.0476
eyg	0.604	0.0476
CG12995	0.603	0.0477
CG15522	0.603	0.0477
Gef64C	0.603	0.0477
Ca-alpha1D	0.602	0.048
CG12507	0.601	0.0481
CG13667	0.601	0.0481
CG13875	0.601	0.0481
CG14300	0.601	0.0481
CG8230	0.601	0.0481
CG8974	0.601	0.0481
Tfb5	0.601	0.0481
CG12278	0.6	0.0487
CG1344	0.6	0.0487
CG12272	0.599	0.0489
CG30338	0.599	0.0489
CG4679	0.599	0.0489
Rad51C	0.599	0.0489
sunz	0.599	0.0489
CG14195	0.598	0.0494
CG14749	0.598	0.0494
CG3239	0.598	0.0494
Nnfta	0.598	0.0494
CG14423	0.597	0.0497
CG15251	0.597	0.0497
CG31381	0.597	0.0497
CG32343	0.597	0.0497
CG32529	0.597	0.0497
CG7781	0.597	0.0497
Mer	0.597	0.0497
Rab40	0.597	0.0497
RpL9	0.597	0.0497

Table 6.S11 Continued

Gene Name	ERC Value	P-value
<i>Cpr6Cb</i>	0.596	0.0505
<i>l(2)k16918</i>	0.596	0.0505
<i>Rpn11</i>	0.596	0.0505
<i>B-H2</i>	0.595	0.0508
<i>CG14903</i>	0.595	0.0508
<i>CG5734</i>	0.595	0.0508
<i>CTCF</i>	0.595	0.0508
<i>Or98b</i>	0.595	0.0508
<i>ptc</i>	0.595	0.0508
<i>SPoCk</i>	0.595	0.0508
<i>CG8116</i>	0.594	0.0514
<i>lrl1a</i>	0.594	0.0514
<i>mus205</i>	0.594	0.0514
<i>CG4042</i>	0.593	0.0517
<i>ihog</i>	0.593	0.0517
<i>mo</i>	0.593	0.0517
<i>salt</i>	0.592	0.052
<i>CG42361</i>	0.591	0.0521
<i>CG9269</i>	0.591	0.0521
<i>Lrt</i>	0.591	0.0521
<i>Prx5037</i>	0.591	0.0521
<i>CG10992</i>	0.59	0.0524
<i>hd</i>	0.59	0.0524
<i>lrf4a</i>	0.59	0.0524
<i>mus81</i>	0.59	0.0524
<i>CG11294</i>	0.589	0.0528
<i>CG14566</i>	0.589	0.0528
<i>CG14877</i>	0.589	0.0528
<i>CG3808</i>	0.589	0.0528
<i>fend</i>	0.589	0.0528
<i>trus</i>	0.589	0.0528
<i>CG11262</i>	0.588	0.0533
<i>CG9422</i>	0.588	0.0533
<i>Ch2</i>	0.588	0.0533
<i>Cog3</i>	0.588	0.0533
<i>Nca</i>	0.588	0.0533
<i>zwlch</i>	0.588	0.0533
<i>CG3683</i>	0.587	0.0539
<i>VhaM9.7-d</i>	0.587	0.0539
<i>CG10140</i>	0.586	0.0541
<i>salm</i>	0.585	0.0541
<i>Atg7</i>	0.584	0.0542
<i>beat-lb</i>	0.584	0.0542
<i>Bln1</i>	0.584	0.0542
<i>CG3021</i>	0.584	0.0542
<i>CG33511</i>	0.584	0.0542
<i>CG6429</i>	0.584	0.0542
<i>elF3-58</i>	0.584	0.0542
<i>l(2)05714</i>	0.584	0.0542
<i>levy</i>	0.584	0.0542
<i>CG1732</i>	0.583	0.055
<i>CG4374</i>	0.583	0.055
<i>Pink1</i>	0.583	0.055
<i>Ucp4C</i>	0.583	0.055
<i>CG14397</i>	0.582	0.0554
<i>CG1492</i>	0.582	0.0554

Gene Name	ERC Value	P-value
<i>RpL34a</i>	0.582	0.0554
<i>Antp</i>	0.581	0.0557
<i>CG11367</i>	0.581	0.0557
<i>CG14569</i>	0.581	0.0557
<i>CG1806</i>	0.581	0.0557
<i>GloAT-P</i>	0.581	0.0557
<i>kek3</i>	0.581	0.0557
<i>lama</i>	0.581	0.0557
<i>tsg</i>	0.581	0.0557
<i>wg</i>	0.581	0.0557
<i>CG18811</i>	0.58	0.0565
<i>Gem2</i>	0.58	0.0565
<i>RhoGAP16F</i>	0.58	0.0565
<i>CG17352</i>	0.579	0.0568
<i>CG18234</i>	0.579	0.0568
<i>CG14301</i>	0.578	0.0569
<i>CG34208</i>	0.578	0.0569
<i>CG4542</i>	0.578	0.0569
<i>Dpy-30L1</i>	0.578	0.0569
<i>Tsp42Ek</i>	0.578	0.0569
<i>CG11418</i>	0.577	0.0574
<i>CG16970</i>	0.577	0.0574
<i>CG18476</i>	0.577	0.0574
<i>fs(1)Ya</i>	0.577	0.0574
<i>CG15861</i>	0.576	0.0577
<i>CG42404</i>	0.576	0.0577
<i>mRpl.1</i>	0.576	0.0577
<i>CG5726</i>	0.575	0.058
<i>CG5924</i>	0.575	0.058
<i>clt</i>	0.575	0.058
<i>muskelin</i>	0.575	0.058
<i>rec</i>	0.575	0.058
<i>CG13154</i>	0.574	0.0585
<i>CG18262</i>	0.574	0.0585
<i>CG6723</i>	0.574	0.0585
<i>lilli</i>	0.574	0.0585
<i>Plip</i>	0.574	0.0585
<i>CG10165</i>	0.573	0.0589
<i>CG4025</i>	0.573	0.0589
<i>Doa</i>	0.573	0.0589
<i>hdm</i>	0.573	0.0589
<i>xmas-2</i>	0.573	0.0589
<i>CG10924</i>	0.572	0.0594
<i>CG11279</i>	0.572	0.0594
<i>CG15634</i>	0.571	0.0595
<i>CG30047</i>	0.571	0.0595
<i>homer</i>	0.571	0.0595
<i>CG15443</i>	0.57	0.0598
<i>CG34316</i>	0.57	0.0598
<i>CG8485</i>	0.57	0.0598
<i>mRps30</i>	0.57	0.0598
<i>pex16</i>	0.57	0.0598
<i>CG32554</i>	0.569	0.0603
<i>CG8209</i>	0.569	0.0603
<i>CG13707</i>	0.568	0.0605
<i>CG13877</i>	0.568	0.0605

Gene Name	ERC Value	P-value
<i>NC2beta</i>	0.568	0.0605
<i>usnp</i>	0.568	0.0605
<i>btd</i>	0.567	0.0608
<i>CG9215</i>	0.567	0.0608
<i>Cpr65Au</i>	0.567	0.0608
<i>lambdaTry</i>	0.567	0.0608
<i>Nlp</i>	0.567	0.0608
<i>pico</i>	0.567	0.0608
<i>CG4996</i>	0.566	0.0614
<i>CG8134</i>	0.566	0.0614
<i>fog</i>	0.566	0.0614
<i>Osi12</i>	0.566	0.0614
<i>tectonic</i>	0.566	0.0614
<i>CG11137</i>	0.564	0.0618
<i>CG14070</i>	0.564	0.0618
<i>CG3679</i>	0.564	0.0618
<i>jub</i>	0.564	0.0618
<i>CG14573</i>	0.563	0.0622
<i>CG14966</i>	0.563	0.0622
<i>CG15738</i>	0.563	0.0622
<i>CG9673</i>	0.563	0.0622
<i>Muc91C</i>	0.563	0.0622
<i>toe</i>	0.563	0.0622
<i>CG1265</i>	0.562	0.0627
<i>CG14057</i>	0.562	0.0627
<i>CG31365</i>	0.562	0.0627
<i>jet</i>	0.562	0.0627
<i>CG4424</i>	0.561	0.0631
<i>lic</i>	0.561	0.0631
<i>Saf-B</i>	0.561	0.0631
<i>CG6550</i>	0.56	0.0633
<i>Tsp42Eg</i>	0.56	0.0633
<i>CG10035</i>	0.559	0.0635
<i>CG1674</i>	0.559	0.0635
<i>CG30008</i>	0.559	0.0635
<i>Lig4</i>	0.559	0.0635
<i>vps24</i>	0.559	0.0635
<i>grass</i>	0.558	0.064
<i>CG31326</i>	0.557	0.0641
<i>CG9249</i>	0.557	0.0641
<i>Aats-trp</i>	0.556	0.0642
<i>CG10222</i>	0.556	0.0642
<i>CG12299</i>	0.556	0.0642
<i>CG17068</i>	0.556	0.0642
<i>CG42863</i>	0.556	0.0642
<i>CG5919</i>	0.556	0.0642
<i>CG9247</i>	0.556	0.0642
<i>H</i>	0.556	0.0642
<i>hay</i>	0.556	0.0642
<i>htt</i>	0.556	0.0642
<i>l(3)05822</i>	0.556	0.0642
<i>su(w[a])</i>	0.556	0.0642
<i>Aats-ala-m</i>	0.555	0.0653
<i>CG16838</i>	0.555	0.0653
<i>CG4848</i>	0.555	0.0653
<i>l(2)k09022</i>	0.555	0.0653

Gene Name	ERC Value	P-value
<i>CG10324</i>	0.554	0.0657
<i>CG13283</i>	0.554	0.0657
<i>CG13802</i>	0.554	0.0657
<i>CG14786</i>	0.554	0.0657
<i>CG42345</i>	0.554	0.0657
<i>CG9246</i>	0.554	0.0657
<i>Kr-h1</i>	0.554	0.0657
<i>CG14023</i>	0.553	0.0663
<i>CG32846</i>	0.553	0.0663
<i>l(2)05510</i>	0.553	0.0663
<i>polo</i>	0.553	0.0663
<i>CG11178</i>	0.552	0.0667
<i>CG42360</i>	0.552	0.0667
<i>CG4468</i>	0.552	0.0667
<i>CG6950</i>	0.552	0.0667
<i>Obp8a</i>	0.552	0.0667
<i>CG12680</i>	0.551	0.0671
<i>CG33557</i>	0.551	0.0671
<i>CG5791</i>	0.551	0.0671
<i>Gs1</i>	0.551	0.0671
<i>mspo</i>	0.551	0.0671
<i>Osi21</i>	0.551	0.0671
<i>CG33229</i>	0.55	0.0677
<i>CG42827</i>	0.55	0.0677
<i>Taspase1</i>	0.55	0.0677
<i>TwdlW</i>	0.55	0.0677
<i>CG31688</i>	0.549	0.068
<i>CG7461</i>	0.549	0.068
<i>ix</i>	0.549	0.068
<i>lat</i>	0.549	0.068
<i>mRps6</i>	0.549	0.068
<i>sad</i>	0.549	0.068
<i>Scm</i>	0.549	0.068
<i>CG4221</i>	0.548	0.0686
<i>CG8785</i>	0.548	0.0686
<i>ct</i>	0.548	0.0686
<i>Sptr</i>	0.548	0.0686
<i>CCKLR-17D</i>	0.547	0.069
<i>CG10348</i>	0.547	0.069
<i>CG1332</i>	0.547	0.069
<i>CG4480</i>	0.547	0.069
<i>Or45a</i>	0.547	0.069
<i>CG14333</i>	0.546	0.0695
<i>CG31373</i>	0.546	0.0695
<i>Chf11</i>	0.546	0.0695
<i>sax</i>	0.546	0.0695
<i>HLHmbeta</i>	0.545	0.0698
<i>NetA</i>	0.545	0.0698
<i>Stat92E</i>	0.545	0.0698
<i>Ak6</i>	0.544	0.0701
<i>Bro</i>	0.544	0.0701
<i>CG13908</i>	0.544	0.0701
<i>CG14050</i>	0.544	0.0701
<i>CG1832</i>	0.544	0.0701
<i>CG32204</i>	0.544	0.0701
<i>CG7597</i>	0.544	0.0701

Gene Name	ERC Value	P-value
<i>CG9992</i>	0.544	0.0701
<i>Lip1</i>	0.544	0.0701
<i>nahoda</i>	0.544	0.0701
<i>atms</i>	0.543	0.071
<i>CG10646</i>	0.543	0.071
<i>CG31414</i>	0.543	0.071
<i>CG33260</i>	0.543	0.071
<i>corn</i>	0.543	0.071
<i>Obp99d</i>	0.543	0.071
<i>CG13813</i>	0.542	0.0715
<i>CG15317</i>	0.542	0.0715
<i>Lsm11</i>	0.542	0.0715
<i>SPE</i>	0.542	0.0715
<i>CG12516</i>	0.541	0.0719
<i>CG32409</i>	0.541	0.0719
<i>CG4678</i>	0.541	0.0719
<i>ssh</i>	0.541	0.0719
<i>blue</i>	0.54	0.0723
<i>CG4462</i>	0.54	0.0723
<i>CG8191</i>	0.541	0.0723
<i>CG8401</i>	0.54	0.0723
<i>CG9657</i>	0.54	0.0723
<i>obst-F</i>	0.54	0.0723
<i>Sy11</i>	0.54	0.0723
<i>CG11396</i>	0.539	0.0729
<i>CG14803</i>	0.539	0.0729
<i>CG6463</i>	0.539	0.0729
<i>hllB</i>	0.539	0.0729
<i>Cdc6</i>	0.538	0.0732
<i>CG34126</i>	0.538	0.0732
<i>mav</i>	0.538	0.0732
<i>Ndc80</i>	0.538	0.0732
<i>Rpp20</i>	0.538	0.0732
<i>yellow-e3</i>	0.538	0.0732
<i>CG13287</i>	0.537	0.0738
<i>CG7246</i>	0.537	0.0738
<i>CG30183</i>	0.536	0.074
<i>CG7519</i>	0.536	0.074
<i>CG7879</i>	0.536	0.074
<i>KLHL18</i>	0.536	0.074
<i>l(2)01289</i>	0.536	0.074
<i>mms4</i>	0.536	0.074
<i>Spt20</i>	0.536	0.074
<i>CG14608</i>	0.535	0.0746
<i>CG34040</i>	0.535	0.0746
<i>Gr36d</i>	0.535	0.0746
<i>Klp31E</i>	0.535	0.0746
<i>Rhf1</i>	0.535	0.0746
<i>CG32232</i>	0.534	0.075
<i>Thlfbeta</i>	0.534	0.075
<i>CG12206</i>	0.533	0.0752
<i>CG18581</i>	0.533	0.0752
<i>CG4995</i>	0.533	0.0752
<i>Ku80</i>	0.533	0.0752
<i>slp2</i>	0.533	0.0752
<i>Tim17b1</i>	0.533	0.0752

Table 6.S11 Continued

Gene Name	ERC Value	P-value
<i>MTF-1</i>	0.532	0.0758
<i>PGRP-LA</i>	0.532	0.0758
<i>plexA</i>	0.532	0.0758
<i>spz6</i>	0.532	0.0758
<i>7B2</i>	0.531	0.0761
<i>CG11127</i>	0.531	0.0761
<i>CG17190</i>	0.531	0.0761
<i>CG7407</i>	0.531	0.0761
<i>MSBP</i>	0.531	0.0761
<i>CG11275</i>	0.53	0.0766
<i>CG12020</i>	0.53	0.0766
<i>CG2604</i>	0.53	0.0766
<i>CG32643</i>	0.53	0.0766
<i>CG34350</i>	0.53	0.0766
<i>l(2)37Ce</i>	0.53	0.0766
<i>Tango9</i>	0.53	0.0766
<i>CG1750</i>	0.529	0.0772
<i>CG13003</i>	0.528	0.0773
<i>CG15005</i>	0.528	0.0773
<i>CG15365</i>	0.528	0.0773
<i>CG32850</i>	0.528	0.0773
<i>CG5466</i>	0.528	0.0773
<i>CG7971</i>	0.528	0.0773
<i>PH4alphaPv</i>	0.528	0.0773
<i>trom</i>	0.528	0.0773
<i>CG14712</i>	0.527	0.078
<i>CG31195</i>	0.527	0.078
<i>CG34424</i>	0.527	0.078
<i>CG42796</i>	0.527	0.078
<i>CG4565</i>	0.527	0.078
<i>CG10435</i>	0.526	0.0785
<i>CG14275</i>	0.526	0.0785
<i>CG15236</i>	0.526	0.0785
<i>CG15269</i>	0.526	0.0785
<i>CG6739</i>	0.526	0.0785
<i>mei-41</i>	0.526	0.0785
<i>repo</i>	0.526	0.0785
<i>Rpb10</i>	0.526	0.0785
<i>rtet</i>	0.526	0.0785
<i>casp</i>	0.525	0.0793
<i>CG13897</i>	0.525	0.0793
<i>Gr93c</i>	0.525	0.0793
<i>beat-11b</i>	0.524	0.0795
<i>CG16904</i>	0.524	0.0795
<i>CG4914</i>	0.524	0.0795
<i>CG6933</i>	0.524	0.0795
<i>Nek2</i>	0.524	0.0795
<i>RpL39</i>	0.524	0.0795
<i>tan</i>	0.524	0.0795
<i>Ugt86Dc</i>	0.524	0.0795
<i>CG17111</i>	0.523	0.0803
<i>CG18522</i>	0.523	0.0803
<i>Sse</i>	0.523	0.0803
<i>Tor</i>	0.523	0.0803
<i>CG11356</i>	0.522	0.0806
<i>CG15745</i>	0.522	0.0806

Gene Name	ERC Value	P-value
<i>CG8683</i>	0.522	0.0806
<i>NurF2</i>	0.522	0.0806
<i>Reg-2</i>	0.522	0.0806
<i>CG31935</i>	0.521	0.0811
<i>CG5800</i>	0.52	0.0812
<i>CG9853</i>	0.52	0.0812
<i>E5</i>	0.52	0.0812
<i>fzy</i>	0.52	0.0812
<i>Oatp74D</i>	0.52	0.0812
<i>p24-1</i>	0.52	0.0812
<i>Tsp42E1</i>	0.52	0.0812
<i>awd</i>	0.519	0.0818
<i>CG10131</i>	0.519	0.0818
<i>CG13306</i>	0.519	0.0818
<i>CG14544</i>	0.519	0.0818
<i>CG6325</i>	0.519	0.0818
<i>GABA-B-R3</i>	0.519	0.0818
<i>hkl</i>	0.519	0.0818
<i>Toll-6</i>	0.519	0.0818
<i>CG10431</i>	0.518	0.0825
<i>CG2811</i>	0.518	0.0825
<i>CG32702</i>	0.518	0.0825
<i>CG8170</i>	0.518	0.0825
<i>ect</i>	0.518	0.0825
<i>mab-21</i>	0.518	0.0825
<i>Obp83cd</i>	0.518	0.0825
<i>CG10703</i>	0.517	0.0832
<i>CG10824</i>	0.517	0.0832
<i>CG13305</i>	0.517	0.0832
<i>CG1809</i>	0.517	0.0832
<i>CG30503</i>	0.517	0.0832
<i>Sap130</i>	0.517	0.0832
<i>CG10732</i>	0.516	0.0837
<i>CG12481</i>	0.516	0.0837
<i>CG13955</i>	0.516	0.0837
<i>CG7227</i>	0.516	0.0837
<i>CG9175</i>	0.516	0.0837
<i>fu</i>	0.516	0.0837
<i>l(1)G0045</i>	0.516	0.0837
<i>CG18316</i>	0.515	0.0843
<i>CG32206</i>	0.515	0.0843
<i>mRpS29</i>	0.515	0.0843
<i>Sara</i>	0.515	0.0843
<i>trk</i>	0.515	0.0843
<i>wdp</i>	0.515	0.0843
<i>CG12134</i>	0.514	0.0849
<i>CG14459</i>	0.514	0.0849
<i>CG4239</i>	0.514	0.0849
<i>gdl</i>	0.514	0.0849
<i>gem</i>	0.514	0.0849
<i>oc</i>	0.514	0.0849
<i>thoc6</i>	0.514	0.0849
<i>CG15877</i>	0.513	0.0855
<i>CG1602</i>	0.513	0.0855
<i>CG34448</i>	0.513	0.0855
<i>Dok</i>	0.513	0.0855

Gene Name	ERC Value	P-value
<i>key</i>	0.513	0.0855
<i>RpS29</i>	0.513	0.0855
<i>Stim</i>	0.513	0.0855
<i>Zmit</i>	0.512	0.0861
<i>CG13775</i>	0.512	0.0861
<i>Grip75</i>	0.512	0.0861
<i>Sp212</i>	0.512	0.0861
<i>RpII140</i>	0.511	0.0865
<i>CG12920</i>	0.511	0.0865
<i>CG6048</i>	0.511	0.0865
<i>Eps-15</i>	0.511	0.0865
<i>cdc23</i>	0.51	0.0868
<i>CG10428</i>	0.51	0.0868
<i>CG12105</i>	0.51	0.0868
<i>CG9634</i>	0.51	0.0868
<i>Pngl</i>	0.51	0.0868
<i>CG7265</i>	0.509	0.0873
<i>CG9801</i>	0.509	0.0873
<i>Gr94a</i>	0.509	0.0873
<i>RunxB</i>	0.509	0.0873
<i>sowah</i>	0.509	0.0873
<i>Spase18-21</i>	0.509	0.0873
<i>Anxb11</i>	0.508	0.0878
<i>CG12818</i>	0.508	0.0878
<i>CG5068</i>	0.508	0.0878
<i>CG12130</i>	0.507	0.0881
<i>CG17739</i>	0.507	0.0881
CG18806	0.507	0.0881
<i>CG31267</i>	0.507	0.0881
<i>CG9523</i>	0.507	0.0881
<i>CG34230</i>	0.506	0.0886
<i>CG4658</i>	0.506	0.0886
<i>Rib1</i>	0.506	0.0886
<i>alpha-Est10</i>	0.505	0.0888
<i>CG10352</i>	0.505	0.0888
<i>CG10743</i>	0.505	0.0888
<i>CG31607</i>	0.505	0.0888
<i>CG8738</i>	0.505	0.0888
<i>lr7a</i>	0.505	0.0888
<i>Pv2</i>	0.505	0.0888
<i>blot</i>	0.504	0.0895
<i>CG11658</i>	0.504	0.0895
<i>CG11699</i>	0.504	0.0895
<i>CG5819</i>	0.504	0.0895
<i>CG6867</i>	0.504	0.0895
<i>Cp1</i>	0.504	0.0895
<i>lr94h</i>	0.504	0.0895
<i>pHCl</i>	0.504	0.0895
<i>run</i>	0.504	0.0895
<i>CG14607</i>	0.502	0.0903
<i>CG31342</i>	0.502	0.0903
<i>CG7382</i>	0.502	0.0903
<i>CG8051</i>	0.502	0.0903
<i>pea</i>	0.502	0.0903
<i>pil</i>	0.502	0.0903
<i>AlkB</i>	0.501	0.0908

Gene Name	ERC Value	P-value
<i>CG11188</i>	0.501	0.0908
<i>CG1273</i>	0.501	0.0908
<i>CG13982</i>	0.501	0.0908
<i>CG1847</i>	0.501	0.0908
<i>CG6860</i>	0.501	0.0908
<i>cngl</i>	0.501	0.0908
<i>hfw</i>	0.501	0.0908
<i>Ravus</i>	0.501	0.0908
<i>CG10465</i>	0.5	0.0916
<i>CG34246</i>	0.5	0.0916
<i>CG4949</i>	0.5	0.0916
<i>ImpL2</i>	0.5	0.0916
<i>nbs</i>	0.5	0.0916
<i>Buffy</i>	0.499	0.0921
<i>CG17266</i>	0.499	0.0921
<i>CG30359</i>	0.499	0.0921
<i>CG33108</i>	0.499	0.0921
<i>CG6106</i>	0.499	0.0921
<i>CG8408</i>	0.499	0.0921
<i>cyr</i>	0.499	0.0921
<i>CG11236</i>	0.498	0.0927
<i>CG14869</i>	0.498	0.0927
<i>CG4496</i>	0.498	0.0927
<i>CG5270</i>	0.498	0.0927
<i>CG5541</i>	0.498	0.0927
<i>PICK1</i>	0.498	0.0927
<i>CG1513</i>	0.497	0.0932
<i>CG2453</i>	0.497	0.0932
<i>CG31689</i>	0.497	0.0932
<i>CG3323</i>	0.497	0.0932
<i>CG5674</i>	0.497	0.0932
<i>Arp11</i>	0.496	0.0937
<i>CG14341</i>	0.496	0.0937
<i>CG14515</i>	0.496	0.0937
<i>CG2091</i>	0.496	0.0937
<i>CG7956</i>	0.496	0.0937
<i>DIP1</i>	0.496	0.0937
<i>DNApol-iota</i>	0.496	0.0937
<i>lr40a</i>	0.496	0.0937
<i>Mef2</i>	0.496	0.0937
<i>Os-C</i>	0.496	0.0937
<i>sina</i>	0.496	0.0937
<i>Sul(H)</i>	0.496	0.0937
<i>CG11417</i>	0.495	0.0948
<i>Efr</i>	0.495	0.0948
<i>RpL11</i>	0.495	0.0948
<i>CG4660</i>	0.494	0.095
<i>Der-2</i>	0.494	0.095
<i>Orc5</i>	0.494	0.095
<i>Spt6</i>	0.494	0.095
<i>CG14327</i>	0.493	0.0954
<i>CG8359</i>	0.493	0.0954
<i>CG10962</i>	0.492	0.0956
<i>CG33155</i>	0.492	0.0956
<i>CG42456</i>	0.492	0.0956
<i>CG8097</i>	0.492	0.0956

Gene Name	ERC Value	P-value
<i>beat-11a</i>	0.491	0.0959
<i>CG30217</i>	0.491	0.0959
<i>CG7564</i>	0.491	0.0959
<i>Gr98a</i>	0.491	0.0959
<i>Gycbeta100</i>	0.491	0.0959
<i>mlo</i>	0.491	0.0959
<i>Bet1</i>	0.49	0.0965
<i>CG13422</i>	0.49	0.0965
<i>CG17059</i>	0.49	0.0965
<i>CG33172</i>	0.49	0.0965
<i>CG4670</i>	0.49	0.0965
<i>RhoGAP19C</i>	0.49	0.0965
<i>Ttb1</i>	0.49	0.0965
<i>CG15701</i>	0.489	0.0971
<i>CG32623</i>	0.489	0.0971
<i>cwo</i>	0.489	0.0971
<i>disp</i>	0.489	0.0971
<i>mRpL54</i>	0.489	0.0971
<i>sca</i>	0.489	0.0971
<i>thr</i>	0.489	0.0971
<i>CG12307</i>	0.488	0.0977
<i>CG13031</i>	0.488	0.0977
<i>CG13114</i>	0.488	0.0977
<i>CG32809</i>	0.488	0.0977
<i>Sp2</i>	0.488	0.0977
<i>CG15024</i>	0.487	0.0982
<i>CG17528</i>	0.487	0.0982
<i>CG33543</i>	0.487	0.0982
<i>CG8740</i>	0.487	0.0982
<i>mRpS31</i>	0.487	0.0982
<i>Oatp58Da</i>	0.487	0.0982
<i>vg</i>	0.487	0.0982
<i>mahj</i>	0.486	0.0988
<i>Sas</i>	0.486	0.0988
<i>Ssdp</i>	0.486	0.0988
<i>CG32246</i>	0.485	0.0991
<i>CG7988</i>	0.485	0.0991
<i>O-fut1</i>	0.485	0.0991
<i>CG7280</i>	0.484	0.0994
<i>mRpL48</i>	0.484	0.0994
<i>CG11030</i>	0.483	0.0995
<i>CG4753</i>	0.483	0.0995
<i>CG11122</i>	0.482	0.0997
<i>CG1688</i>	0.482	0.0997
<i>CG30440</i>	0.482	0.0997
<i>CG32685</i>	0.482	0.0997
<i>CG5895</i>	0.482	0.0997
<i>CG8193</i>	0.482	0.0997
<i>ebi</i>	0.482	0.0997
<i>esn</i>	0.482	0.0997
<i>Rip11</i>	0.482	0.0997
<i>Sr-CJ</i>	0.482	0.0997
<i>stumps</i>	0.482	0.0997

Table 6.S12 - Top Genes ERC values for *mus301* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Oatp58Da</i>	0.924	0.0001
<i>CG32790</i>	0.904	0.0002
<i>pzg</i>	0.903	0.0003
<i>CG12693</i>	0.884	0.0004
<i>CG18812</i>	0.877	0.0005
<i>CG1602</i>	0.866	0.0005
<i>ash1</i>	0.855	0.0006
<i>CG13802</i>	0.851	0.0007
<i>gcm</i>	0.85	0.0008
<i>CG4892</i>	0.849	0.0009
<i>CG16868</i>	0.848	0.001
<i>CG18265</i>	0.848	0.001
<i>CG3542</i>	0.847	0.0012
<i>phol</i>	0.832	0.0013
<i>CG11889</i>	0.829	0.0014
<i>lrv</i>	0.823	0.0014
<i>san</i>	0.823	0.0014
<i>pnr</i>	0.817	0.0016
<i>swm</i>	0.817	0.0016
<i>Tim17b1</i>	0.815	0.0018
<i>beta4GalNA</i>	0.814	0.0019
<i>Sym</i>	0.812	0.002
<i>Psi</i>	0.81	0.0021
<i>CG6695</i>	0.809	0.0022
<i>CG32982</i>	0.806	0.0023
<i>CG4452</i>	0.804	0.0023
<i>CG8159</i>	0.804	0.0023
<i>CG5872</i>	0.803	0.0025
<i>CG6700</i>	0.799	0.0026
<i>sba</i>	0.799	0.0026
<i>CG10077</i>	0.798	0.0028
<i>CG31211</i>	0.788	0.0029
<i>CG3532</i>	0.788	0.0029
<i>CG8319</i>	0.787	0.0031
<i>omd</i>	0.787	0.0031
<i>gammaTub2</i>	0.785	0.0032
<i>CG13350</i>	0.784	0.0033
<i>eyj3</i>	0.784	0.0033
<i>CG34214</i>	0.783	0.0035
<i>CG17181</i>	0.782	0.0036
<i>CG14650</i>	0.78	0.0037
<i>CG14956</i>	0.778	0.0038
<i>dos</i>	0.778	0.0038
<i>Klp67A</i>	0.778	0.0038
<i>CG9839</i>	0.777	0.0041
<i>zwilch</i>	0.773	0.0041
<i>bsh</i>	0.772	0.0042
<i>Rad51D</i>	0.772	0.0042
<i>Bap170</i>	0.771	0.0044
<i>CG15514</i>	0.77	0.0045
<i>pgant8</i>	0.77	0.0045
<i>CG15167</i>	0.769	0.0047
<i>CG10543</i>	0.768	0.0048
<i>CG12420</i>	0.768	0.0048
<i>CG17328</i>	0.768	0.0048
<i>CG30020</i>	0.768	0.0048

Gene Name	ERC Value	P-value
<i>RpA-70</i>	0.768	0.0048
<i>CG6254</i>	0.766	0.0052
<i>dpr2</i>	0.766	0.0052
<i>PR2</i>	0.766	0.0052
<i>HLH106</i>	0.765	0.0055
<i>mel-41</i>	0.765	0.0055
<i>zen</i>	0.765	0.0055
<i>CG5098</i>	0.764	0.0058
<i>DNApol-alpha</i>	0.763	0.0059
<i>CG12316</i>	0.762	0.0059
<i>CG14540</i>	0.761	0.006
<i>CG8087</i>	0.761	0.006
<i>Chrac-14</i>	0.76	0.0062
<i>CG34313</i>	0.759	0.0063
<i>Su(H)</i>	0.759	0.0063
<i>Su(Tp)</i>	0.759	0.0063
<i>CG14749</i>	0.758	0.0066
<i>Stam</i>	0.758	0.0066
<i>CG6576</i>	0.757	0.0068
<i>CG9418</i>	0.757	0.0068
<i>CG13169</i>	0.754	0.0069
<i>CG1832</i>	0.753	0.007
<i>CG11248</i>	0.751	0.0071
<i>CG7597</i>	0.751	0.0071
<i>Aef1</i>	0.75	0.0073
<i>CG31380</i>	0.75	0.0073
<i>CG31191</i>	0.749	0.0075
<i>corn</i>	0.749	0.0075
<i>Rassf</i>	0.748	0.0077
<i>CG13226</i>	0.747	0.0077
<i>mts</i>	0.747	0.0077
<i>sd</i>	0.747	0.0077
<i>Arp5</i>	0.745	0.008
<i>CG1311</i>	0.745	0.008
<i>Ge-1</i>	0.745	0.008
<i>CG32791</i>	0.743	0.0083
<i>Rab40</i>	0.743	0.0083
<i>hkl</i>	0.741	0.0085
<i>CG5056</i>	0.74	0.0086
<i>rump</i>	0.739	0.0086
<i>Pbp45</i>	0.738	0.0087
<i>ZC3H3</i>	0.737	0.0088
<i>CG12680</i>	0.735	0.0089
<i>CG6418</i>	0.735	0.0089
<i>tsh</i>	0.735	0.0089
<i>ksr</i>	0.734	0.0092
<i>CG1575</i>	0.733	0.0093
<i>CG18476</i>	0.733	0.0093
<i>CG3605</i>	0.733	0.0093
<i>CG9894</i>	0.733	0.0093
<i>Ric1</i>	0.733	0.0093
<i>SelR</i>	0.732	0.0097
<i>CG13287</i>	0.731	0.0098
<i>CG3611</i>	0.731	0.0098
<i>eyg</i>	0.731	0.0098
<i>Klp61F</i>	0.73	0.0101

Gene Name	ERC Value	P-value
<i>CG15435</i>	0.729	0.0102
<i>CG16812</i>	0.729	0.0102
<i>ome</i>	0.729	0.0102
<i>Pink1</i>	0.729	0.0102
<i>CG11211</i>	0.728	0.0105
<i>dx</i>	0.728	0.0105
<i>E5</i>	0.727	0.0107
<i>SelD</i>	0.727	0.0107
<i>CG14321</i>	0.726	0.0109
<i>Dot</i>	0.726	0.0109
<i>Map60</i>	0.725	0.0111
<i>Or45a</i>	0.725	0.0111
<i>PGRP-LD</i>	0.724	0.0113
<i>CG10326</i>	0.723	0.0114
<i>CG6230</i>	0.723	0.0114
<i>CG3223</i>	0.721	0.0115
<i>CG8155</i>	0.721	0.0115
<i>CG8202</i>	0.721	0.0115
<i>m6</i>	0.721	0.0115
<i>CG9300</i>	0.72	0.0119
<i>dom</i>	0.72	0.0119
<i>CG14570</i>	0.719	0.0121
<i>CG31688</i>	0.719	0.0121
<i>CG12439</i>	0.718	0.0123
<i>CG13745</i>	0.718	0.0123
<i>D12</i>	0.718	0.0123
<i>Glu-R1</i>	0.718	0.0123
<i>mus101</i>	0.718	0.0123
<i>sina</i>	0.718	0.0123
<i>CG14803</i>	0.717	0.0128
<i>CG7407</i>	0.717	0.0128
<i>CG7627</i>	0.717	0.0128
<i>mRpl14</i>	0.717	0.0128
<i>argos</i>	0.716	0.0132
<i>CG32573</i>	0.715	0.0132
<i>CG4377</i>	0.715	0.0132
<i>dao</i>	0.715	0.0132
<i>Taspase1</i>	0.715	0.0132
<i>CG34007</i>	0.714	0.0136
<i>CG34404</i>	0.714	0.0136
<i>Nhe3</i>	0.714	0.0136
<i>pds5</i>	0.713	0.0139
<i>a6</i>	0.712	0.014
<i>Atg4</i>	0.712	0.014
<i>CG12038</i>	0.711	0.0141
<i>Gen</i>	0.711	0.0141
<i>CG12050</i>	0.71	0.0143
<i>CG17782</i>	0.71	0.0143
<i>CG42678</i>	0.71	0.0143
<i>CG9004</i>	0.71	0.0143
<i>PTP-ER</i>	0.709	0.0147
<i>rogdi</i>	0.708	0.0148
<i>Aac11</i>	0.707	0.0149
<i>CG4587</i>	0.707	0.0149
<i>thr</i>	0.707	0.0149
<i>trom</i>	0.707	0.0149

Gene Name	ERC Value	P-value
<i>CG3744</i>	0.706	0.0152
<i>CG42676</i>	0.705	0.0153
<i>CG8501</i>	0.705	0.0153
<i>l(2)05510</i>	0.705	0.0153
<i>pcs</i>	0.705	0.0153
<i>CG13454</i>	0.704	0.0157
<i>lrv</i>	0.704	0.0157
<i>CG2694</i>	0.702	0.0159
<i>lrv</i>	0.702	0.0159
<i>sad</i>	0.702	0.0159
<i>CG9269</i>	0.701	0.0161
<i>CG12241</i>	0.7	0.0162
<i>CG30403</i>	0.699	0.0163
<i>CG9609</i>	0.699	0.0163
<i>Sema-1b</i>	0.699	0.0163
<i>CG4074</i>	0.698	0.0166
<i>Ets96B</i>	0.698	0.0166
<i>mth15</i>	0.697	0.0168
<i>Sin3A</i>	0.697	0.0168
<i>CG10824</i>	0.696	0.0169
<i>chm</i>	0.695	0.017
<i>CG10435</i>	0.694	0.0171
<i>CG7372</i>	0.694	0.0171
<i>Lap1</i>	0.694	0.0171
<i>MAGE</i>	0.693	0.0174
<i>CG9427</i>	0.692	0.0175
<i>CG8366</i>	0.691	0.0176
<i>CG11970</i>	0.69	0.0177
<i>CG34012</i>	0.689	0.0177
<i>psq</i>	0.688	0.0178
<i>CG14109</i>	0.688	0.0179
<i>Bsg25A</i>	0.685	0.018
<i>CG18031</i>	0.685	0.018
<i>Cpsf100</i>	0.685	0.018
<i>enok</i>	0.685	0.018
<i>MED31</i>	0.684	0.0184
<i>Cas</i>	0.683	0.0185
<i>CG4820</i>	0.683	0.0185
<i>CG10251</i>	0.682	0.0186
<i>pav</i>	0.682	0.0186
<i>RhoGAP19C</i>	0.682	0.0186
<i>CG14647</i>	0.681	0.0189
<i>CG5180</i>	0.681	0.0189
<i>CG14036</i>	0.68	0.0191
<i>CG34319</i>	0.68	0.0191
<i>Nlp</i>	0.68	0.0191
<i>Sse</i>	0.68	0.0191
<i>CG14341</i>	0.679	0.0195
<i>tud</i>	0.679	0.0195
<i>Prosalpha6T</i>	0.678	0.0196
<i>CG10588</i>	0.677	0.0197
<i>ds</i>	0.677	0.0197
<i>phl</i>	0.677	0.0197
<i>Rpn6</i>	0.677	0.0197
<i>Tusp</i>	0.677	0.0197
<i>CG11164</i>	0.676	0.0202

Gene Name	ERC Value	P-value
<i>CG5885</i>	0.676	0.0202
<i>CG6024</i>	0.676	0.0202
<i>iHog</i>	0.676	0.0202
<i>pps</i>	0.676	0.0202
<i>Rad51C</i>	0.676	0.0202
<i>CG33703</i>	0.675	0.0207
<i>CG13667</i>	0.674	0.0208
<i>CG15024</i>	0.674	0.0208
<i>CG33784</i>	0.674	0.0208
<i>CG8301</i>	0.674	0.0208
<i>robo</i>	0.674	0.0208
<i>CG11983</i>	0.673	0.0213
<i>CG17807</i>	0.673	0.0213
<i>CG91724</i>	0.672	0.0214
<i>CG31812</i>	0.672	0.0214
<i>CG6745</i>	0.672	0.0214
<i>Pros54</i>	0.671	0.0217
<i>Ss1</i>	0.671	0.0217
<i>CG6792</i>	0.67	0.0219
<i>ird5</i>	0.67	0.0219
<i>BEAF-32</i>	0.669	0.0221
<i>Cpr64Ad</i>	0.669	0.0221
<i>Dref</i>	0.669	0.0221
<i>seq</i>	0.669	0.0221
<i>CG15553</i>	0.668	0.0224
<i>CG18599</i>	0.668	0.0224
<i>CG31365</i>	0.668	0.0224
<i>CG3493</i>	0.668	0.0224
<i>CG4751</i>	0.668	0.0224
<i>ix</i>	0.668	0.0224
<i>nocte</i>	0.668	0.0224
<i>CG11070</i>	0.667	0.0231
<i>CG1434</i>	0.667	0.0231
<i>CG15528</i>	0.667	0.0231
<i>CG13239</i>	0.666	0.0233
<i>CG15237</i>	0.666	0.0233
<i>mel-P26</i>	0.666	0.0233
<i>CG16979</i>	0.664	0.0236
<i>CG6621</i>	0.664	0.0236
<i>qua</i>	0.663	0.0238
<i>CG15093</i>	0.662	0.0239
<i>CG4476</i>	0.662	0.0239
<i>Tango9</i>	0.662	0.0239
<i>CG1227</i>	0.661	0.0241
<i>CG13837</i>	0.661	0.0241
<i>CG14720</i>	0.661	0.0241
<i>CG4988</i>	0.661	0.0241
<i>trbd</i>	0.661	0.0241
<i>bip1</i>	0.66	0.0246
<i>toe</i>	0.66	0.0246
<i>CG10399</i>	0.659	0.0248
<i>CG30291</i>	0.659	0.0248
<i>l(2)k09022</i>	0.659	0.0248
<i>Sap130</i>	0.659	0.0248
<i>CG14085</i>	0.658	0.0251
<i>CG31793</i>	0.658	0.0251

Table 6.S12 Continued

Gene Name	ERC Value	P-value
<i>glob3</i>	0.658	0.0251
<i>mahj</i>	0.658	0.0251
<i>Acp53C14c</i>	0.657	0.0255
<i>CG13185</i>	0.657	0.0255
<i>CG18577</i>	0.657	0.0255
<i>CG11396</i>	0.656	0.0258
<i>sced</i>	0.656	0.0258
<i>icl1n</i>	0.655	0.0259
<i>MSBP</i>	0.655	0.0259
<i>Taf10</i>	0.655	0.0259
<i>CG13424</i>	0.654	0.0262
<i>CG6480</i>	0.654	0.0262
<i>SC35</i>	0.654	0.0262
<i>vig</i>	0.654	0.0262
<i>alpha4GT1</i>	0.653	0.0266
<i>CG3558</i>	0.653	0.0266
<i>DNApol-eta</i>	0.653	0.0266
<i>CG42399</i>	0.651	0.0268
<i>CG9992</i>	0.651	0.0268
<i>[(2)05714</i>	0.651	0.0268
<i>Mrf1</i>	0.651	0.0268
<i>CG16957</i>	0.65	0.0272
<i>CG34441</i>	0.65	0.0272
<i>CG42351</i>	0.65	0.0272
<i>CG4936</i>	0.65	0.0272
<i>cup</i>	0.65	0.0272
<i>MED15</i>	0.65	0.0272
<i>CG5924</i>	0.649	0.0277
<i>Cpr72Ea</i>	0.649	0.0277
<i>CG17660</i>	0.648	0.0279
<i>CG9754</i>	0.648	0.0279
<i>Mih1</i>	0.648	0.0279
<i>CG9586</i>	0.647	0.0282
<i>CG9818</i>	0.645	0.0283
<i>Chd1</i>	0.645	0.0283
<i>Apc2</i>	0.644	0.0285
<i>CG18558</i>	0.644	0.0285
<i>CG31607</i>	0.644	0.0285
CG31898	0.644	0.0285
<i>CG42569</i>	0.644	0.0285
<i>CG7789</i>	0.644	0.0285
<i>CG6325</i>	0.643	0.029
<i>Cortactin</i>	0.643	0.029
<i>CG12299</i>	0.642	0.0292
<i>CG13409</i>	0.642	0.0292
<i>CG14352</i>	0.642	0.0292
<i>CG5181</i>	0.642	0.0292
<i>CG10646</i>	0.64	0.0295
<i>CG11874</i>	0.64	0.0295
<i>CG14435</i>	0.64	0.0295
<i>CG41434</i>	0.64	0.0295
<i>CG8765</i>	0.64	0.0295
<i>DAT</i>	0.64	0.0295
<i>CG10321</i>	0.639	0.0301
<i>CG4753</i>	0.639	0.0301
<i>CG7457</i>	0.638	0.0303

Gene Name	ERC Value	P-value
<i>cnk</i>	0.638	0.0303
<i>[(3)2D3</i>	0.638	0.0303
<i>Saf-B</i>	0.638	0.0303
<i>CG13044</i>	0.637	0.0306
<i>CG2162</i>	0.637	0.0306
<i>Chro</i>	0.637	0.0306
<i>fy</i>	0.636	0.0309
<i>Hk</i>	0.636	0.0309
<i>pll</i>	0.636	0.0309
<i>CG14023</i>	0.635	0.0312
<i>E(Pc)</i>	0.634	0.0313
<i>CG5808</i>	0.633	0.0314
<i>GstE6</i>	0.633	0.0314
<i>CG31224</i>	0.632	0.0315
<i>CG33169</i>	0.632	0.0315
<i>Drep-3</i>	0.632	0.0315
<i>CG4462</i>	0.631	0.0318
<i>Cks85A</i>	0.631	0.0318
<i>tum</i>	0.631	0.0318
<i>CG14550</i>	0.63	0.0321
<i>CG7120</i>	0.63	0.0321
<i>CG7222</i>	0.63	0.0321
<i>Ptp52F</i>	0.63	0.0321
<i>slim</i>	0.63	0.0321
<i>thoc5</i>	0.63	0.0321
<i>Dip-B</i>	0.628	0.0326
<i>CG9452</i>	0.627	0.0327
<i>CG13624</i>	0.626	0.0328
<i>CG3939</i>	0.626	0.0328
<i>Trs23</i>	0.626	0.0328
<i>wit</i>	0.626	0.0328
<i>CG13920</i>	0.625	0.0332
<i>CG32803</i>	0.625	0.0332
<i>CG7102</i>	0.625	0.0332
<i>CG7739</i>	0.625	0.0332
<i>Smg6</i>	0.625	0.0332
<i>Spt5</i>	0.625	0.0332
<i>CG30046</i>	0.624	0.0337
<i>Ranbp9</i>	0.624	0.0337
<i>BtbVII</i>	0.623	0.0339
<i>CG9279</i>	0.623	0.0339
<i>opa1-like</i>	0.623	0.0339
<i>CG9147</i>	0.622	0.0341
<i>CstF-50</i>	0.622	0.0341
<i>malpha</i>	0.621	0.0343
<i>mri</i>	0.621	0.0343
<i>CG13640</i>	0.62	0.0345
<i>CG14401</i>	0.62	0.0345
<i>CG1792</i>	0.62	0.0345
<i>CG5322</i>	0.62	0.0345
<i>CG9727</i>	0.62	0.0345
<i>Ndc80</i>	0.62	0.0345
<i>CD98hc</i>	0.619	0.035
<i>CG32061</i>	0.619	0.035
<i>Sox15</i>	0.619	0.035
<i>Spc105R</i>	0.619	0.035

Gene Name	ERC Value	P-value
<i>CG16826</i>	0.618	0.0354
<i>CG32221</i>	0.618	0.0354
<i>CG3457</i>	0.618	0.0354
<i>ear</i>	0.618	0.0354
<i>sax</i>	0.617	0.0358
<i>SIDL</i>	0.617	0.0358
<i>sname</i>	0.617	0.0358
<i>CG31635</i>	0.616	0.036
<i>CG6734</i>	0.616	0.036
<i>CG8100</i>	0.616	0.036
<i>slv</i>	0.616	0.036
<i>CG13594</i>	0.615	0.0364
<i>Karybeta3</i>	0.615	0.0364
<i>CG15236</i>	0.614	0.0366
<i>CG4615</i>	0.614	0.0366
<i>Dg</i>	0.614	0.0366
<i>Sox100B</i>	0.614	0.0366
<i>X11L</i>	0.614	0.0366
<i>CG16926</i>	0.613	0.037
<i>Cp190</i>	0.613	0.037
<i>Hpr1</i>	0.613	0.037
<i>MED10</i>	0.613	0.037
<i>Nup44A</i>	0.613	0.037
<i>Phlpp</i>	0.613	0.037
<i>tkk</i>	0.613	0.037
<i>CG8329</i>	0.612	0.0377
<i>Spn43Ad</i>	0.612	0.0377
<i>Vdup1</i>	0.612	0.0377
<i>aret</i>	0.611	0.0379
<i>CG10681</i>	0.611	0.0379
<i>CG12851</i>	0.611	0.0379
<i>CG8677</i>	0.611	0.0379
<i>az2</i>	0.61	0.0383
<i>CG10140</i>	0.61	0.0383
<i>CG42246</i>	0.61	0.0383
<i>CG8027</i>	0.61	0.0383
<i>lab</i>	0.61	0.0383
<i>CG32459</i>	0.609	0.0387
<i>CG6758</i>	0.609	0.0387
<i>ETH</i>	0.609	0.0387
<i>beat-1la</i>	0.608	0.039
<i>CG7251</i>	0.608	0.039
<i>Sulf1</i>	0.608	0.039
<i>CG13386</i>	0.607	0.0393
<i>CG14711</i>	0.607	0.0393
<i>CG15322</i>	0.607	0.0393
<i>CG4289</i>	0.607	0.0393
<i>CG5466</i>	0.607	0.0393
<i>CG7172</i>	0.607	0.0393
<i>jub</i>	0.607	0.0393
<i>CG11122</i>	0.606	0.0399
<i>CG13747</i>	0.606	0.0399
<i>m4</i>	0.606	0.0399
<i>CG13692</i>	0.605	0.0402
<i>CG30001</i>	0.605	0.0402
<i>Tbp-1</i>	0.605	0.0402

Gene Name	ERC Value	P-value
<i>Br140</i>	0.604	0.0405
<i>CG10107</i>	0.604	0.0405
<i>CG1368</i>	0.604	0.0405
<i>CG17026</i>	0.604	0.0405
<i>CG6276</i>	0.604	0.0405
<i>Galpha73B</i>	0.604	0.0405
<i>RhoL</i>	0.604	0.0405
<i>trr</i>	0.604	0.0405
<i>CG4497</i>	0.603	0.0412
<i>lim</i>	0.603	0.0412
<i>Stmbt</i>	0.602	0.0414
<i>TyrR</i>	0.602	0.0414
<i>CG8191</i>	0.601	0.0415
<i>labr</i>	0.601	0.0415
<i>mus205</i>	0.601	0.0415
<i>CG10730</i>	0.6	0.0418
<i>CG13398</i>	0.6	0.0418
<i>Pcl</i>	0.6	0.0418
<i>CG12269</i>	0.599	0.0421
<i>CG15172</i>	0.599	0.0421
<i>CG2712</i>	0.599	0.0421
<i>CG31870</i>	0.599	0.0421
<i>CG34005</i>	0.599	0.0421
<i>CG5669</i>	0.599	0.0421
<i>CG15160</i>	0.598	0.0426
<i>gdl</i>	0.598	0.0426
<i>Sytl</i>	0.598	0.0426
<i>CG5199</i>	0.597	0.0429
<i>CG9007</i>	0.597	0.0429
<i>ato</i>	0.596	0.0431
<i>CG32635</i>	0.596	0.0431
<i>CG1622</i>	0.595	0.0432
<i>mRpL21</i>	0.595	0.0432
<i>Pof</i>	0.595	0.0432
<i>ac</i>	0.594	0.0435
<i>cg</i>	0.594	0.0435
<i>CG32846</i>	0.594	0.0435
<i>CG34401</i>	0.594	0.0435
<i>CG9776</i>	0.594	0.0435
<i>fai</i>	0.594	0.0435
<i>pkf</i>	0.594	0.0435
<i>ald</i>	0.593	0.0441
<i>CG14302</i>	0.593	0.0441
<i>CG5726</i>	0.593	0.0441
<i>CG7510</i>	0.593	0.0441
<i>Prosalpha7</i>	0.593	0.0441
<i>sec15</i>	0.593	0.0441
<i>adp</i>	0.592	0.0447
<i>CG13565</i>	0.592	0.0447
<i>CG13751</i>	0.592	0.0447
<i>Nf-YC</i>	0.592	0.0447
<i>CG15099</i>	0.591	0.045
<i>CG31803</i>	0.591	0.045
<i>CG4393</i>	0.591	0.045
<i>DNApol-lota</i>	0.591	0.045
<i>exo70</i>	0.591	0.045

Gene Name	ERC Value	P-value
CG10274	0.59	0.0455
<i>CG10732</i>	0.59	0.0455
<i>CG12320</i>	0.59	0.0455
<i>CG5787</i>	0.59	0.0455
<i>clt</i>	0.59	0.0455
<i>CG11377</i>	0.589	0.0459
<i>CG11919</i>	0.589	0.0459
<i>CG4554</i>	0.589	0.0459
<i>CG9801</i>	0.589	0.0459
<i>bwa</i>	0.588	0.0463
<i>CG14564</i>	0.588	0.0463
<i>CG42404</i>	0.588	0.0463
<i>CG5018</i>	0.588	0.0463
<i>CG6689</i>	0.588	0.0463
<i>CG30015</i>	0.587	0.0468
<i>CG5830</i>	0.587	0.0468
<i>CycA</i>	0.587	0.0468
<i>fdlipidine</i>	0.587	0.0468
<i>Git</i>	0.587	0.0468
<i>cact</i>	0.586	0.0472
<i>CG11637</i>	0.586	0.0472
<i>CG12104</i>	0.586	0.0472
<i>CG14607</i>	0.586	0.0472
<i>CG15571</i>	0.586	0.0472
<i>CG3570</i>	0.586	0.0472
dm	0.586	0.0472
<i>brat</i>	0.585	0.0478
<i>CG12214</i>	0.585	0.0478
<i>CG15919</i>	0.585	0.0478
<i>CG18811</i>	0.585	0.0478
<i>CG5728</i>	0.585	0.0478
ft	0.585	0.0478
<i>gfzf</i>	0.584	0.0484
<i>in</i>	0.584	0.0484
<i>mask</i>	0.584	0.0484
<i>Sep2</i>	0.583	0.0486
<i>glo</i>	0.583	0.0486
<i>lilji</i>	0.583	0.0486
<i>Ror</i>	0.583	0.0486
<i>repo</i>	0.582	0.049
<i>SmD1</i>	0.582	0.049
<i>CG14667</i>	0.581	0.0492
<i>CG5720</i>	0.581	0.0492
<i>CG9804</i>	0.581	0.0492
<i>Gr85a</i>	0.581	0.0492
<i>N</i>	0.581	0.0492
<i>CG13931</i>	0.58	0.0496
<i>CG16799</i>	0.58	0.0496
<i>Pros25</i>	0.58	0.0496
<i>CG9760</i>	0.579	0.0499
<i>NPFR1</i>	0.579	0.0499
<i>Nup214</i>	0.579	0.0499
<i>Oppp</i>	0.579	0.0499
<i>CG8550</i>	0.578	0.0503
<i>CG9053</i>	0.578	0.0503
<i>Gr9a</i>	0.578	0.0503

Table 6.S12 Continued

Gene Name	ERC Value	P-value
<i>MED16</i>	0.578	0.0503
<i>beat-11b</i>	0.577	0.0506
<i>CG11985</i>	0.577	0.0506
<i>CG13622</i>	0.577	0.0506
<i>CG2685</i>	0.577	0.0506
<i>Edg84A</i>	0.577	0.0506
<i>Rpb5</i>	0.577	0.0506
<i>Cyp4c3</i>	0.576	0.0512
<i>La</i>	0.576	0.0512
<i>Tsp42Ef</i>	0.576	0.0512
<i>cbs</i>	0.575	0.0514
<i>CG7911</i>	0.575	0.0514
<i>CG8187</i>	0.575	0.0514
<i>mspo</i>	0.575	0.0514
<i>Abi</i>	0.574	0.0518
<i>CG30460</i>	0.574	0.0518
<i>CG4810</i>	0.574	0.0518
<i>CG9875</i>	0.574	0.0518
<i>CG15861</i>	0.573	0.0522
<i>CG32442</i>	0.573	0.0522
<i>CG3651</i>	0.573	0.0522
<i>CG8193</i>	0.573	0.0522
<i>CG9673</i>	0.573	0.0522
<i>dgo</i>	0.573	0.0522
<i>sub</i>	0.573	0.0522
<i>trx</i>	0.573	0.0522
<i>CG32479</i>	0.572	0.0529
<i>Cdk7</i>	0.571	0.053
<i>CG4557</i>	0.571	0.053
<i>Taf13</i>	0.571	0.053
<i>CG10669</i>	0.57	0.0532
<i>CG11593</i>	0.57	0.0532
<i>CG42506</i>	0.57	0.0532
<i>CG5746</i>	0.57	0.0532
<i>qkr58E-2</i>	0.57	0.0532
<i>zpg</i>	0.57	0.0532
<i>CG12253</i>	0.568	0.0538
<i>CG12355</i>	0.568	0.0538
<i>CG14718</i>	0.568	0.0538
<i>melt</i>	0.568	0.0538
<i>nkd</i>	0.568	0.0538
<i>pad</i>	0.568	0.0538
<i>capu</i>	0.567	0.0543
<i>CG3292</i>	0.567	0.0543
<i>CG8509</i>	0.567	0.0543
<i>D19A</i>	0.567	0.0543
<i>HLHdelta</i>	0.567	0.0543
<i>MED23</i>	0.567	0.0543
<i>Rpil33</i>	0.567	0.0543
<i>twi</i>	0.567	0.0543
<i>CG2046</i>	0.566	0.055
<i>LSm7</i>	0.566	0.055
<i>ns3</i>	0.566	0.055
<i>mo</i>	0.566	0.055
<i>Brf</i>	0.565	0.0554
<i>CG10277</i>	0.565	0.0554

Gene Name	ERC Value	P-value
<i>CG18011</i>	0.565	0.0554
<i>GluRIIA</i>	0.565	0.0554
<i>Axn</i>	0.564	0.0558
<i>CG18004</i>	0.564	0.0558
<i>CG9386</i>	0.564	0.0558
<i>Cp7Fc</i>	0.564	0.0558
<i>Prosbeta3</i>	0.564	0.0558
<i>asun</i>	0.563	0.0562
<i>CG10011</i>	0.563	0.0562
<i>CG10055</i>	0.563	0.0562
<i>CG32792</i>	0.563	0.0562
<i>HLHmbeta</i>	0.563	0.0562
<i>Rpn7</i>	0.563	0.0562
<i>stii</i>	0.563	0.0562
<i>CG13727</i>	0.562	0.0568
<i>CG15376</i>	0.562	0.0568
<i>CG32563</i>	0.562	0.0568
<i>Hsf</i>	0.561	0.0571
<i>Lrrk</i>	0.561	0.0571
<i>srw</i>	0.561	0.0571
<i>Su(var)2-10</i>	0.561	0.0571
<i>RPA2</i>	0.56	0.0575
<i>CG1120</i>	0.559	0.0576
<i>CG31802</i>	0.559	0.0576
<i>Dcr-1</i>	0.559	0.0576
<i>exex</i>	0.559	0.0576
<i>CG12734</i>	0.558	0.0579
<i>CG42336</i>	0.558	0.0579
<i>CG6568</i>	0.558	0.0579
<i>CG6923</i>	0.558	0.0579
<i>crp</i>	0.558	0.0579
<i>pck</i>	0.558	0.0579
<i>CG12929</i>	0.557	0.0585
<i>CG8067</i>	0.557	0.0585
<i>d</i>	0.557	0.0585
<i>GlcAT-P</i>	0.557	0.0585
<i>llp1</i>	0.557	0.0585
<i>wge</i>	0.557	0.0585
<i>Yippee</i>	0.557	0.0585
<i>CG4607</i>	0.556	0.0591
<i>CG5535</i>	0.556	0.0591
<i>sti</i>	0.556	0.0591
<i>CG1104</i>	0.555	0.0594
<i>CG6520</i>	0.555	0.0594
<i>Cpsf73</i>	0.555	0.0594
<i>D</i>	0.555	0.0594
<i>RhoGAP68F</i>	0.555	0.0594
<i>Rtf1</i>	0.555	0.0594
<i>Uch-L3</i>	0.555	0.0594
<i>CG17490</i>	0.554	0.06
<i>CG13539</i>	0.553	0.0601
<i>Prp18</i>	0.553	0.0601
<i>CG7879</i>	0.552	0.0603
<i>Hr78</i>	0.552	0.0603
<i>Spt20</i>	0.552	0.0603
<i>CG1758</i>	0.551	0.0605

Gene Name	ERC Value	P-value
<i>CG7593</i>	0.551	0.0605
<i>CG8312</i>	0.551	0.0605
<i>Fer1</i>	0.551	0.0605
<i>GluRIIE</i>	0.551	0.0605
<i>HGTX</i>	0.551	0.0605
<i>rod</i>	0.551	0.0605
<i>Cdc27</i>	0.55	0.0612
<i>CG12986</i>	0.55	0.0612
<i>CG3104</i>	0.55	0.0612
<i>sds22</i>	0.55	0.0612
<i>CG1271</i>	0.549	0.0615
<i>CG31029</i>	0.549	0.0615
<i>Hcs</i>	0.549	0.0615
<i>CG10933</i>	0.548	0.0618
<i>CG13616</i>	0.548	0.0618
<i>CG5604</i>	0.548	0.0618
<i>snRNP-U1-7</i>	0.548	0.0618
<i>tj</i>	0.548	0.0618
<i>CG10075</i>	0.547	0.0623
<i>CG1553</i>	0.547	0.0623
<i>CG2269</i>	0.547	0.0623
<i>CG5773</i>	0.547	0.0623
<i>CG8199</i>	0.547	0.0623
<i>ventrally-exp</i>	0.547	0.0623
<i>CG14618</i>	0.546	0.0628
<i>CG17233</i>	0.546	0.0628
<i>ChLD3</i>	0.546	0.0628
<i>dpr20</i>	0.546	0.0628
<i>hk</i>	0.546	0.0628
<i>CG8690</i>	0.545	0.0632
<i>C5N1b</i>	0.545	0.0632
<i>thoc7</i>	0.545	0.0632
<i>CG1172</i>	0.544	0.0635
<i>CG13114</i>	0.544	0.0635
<i>CG13123</i>	0.544	0.0635
<i>CG14823</i>	0.544	0.0635
<i>CG15035</i>	0.544	0.0635
<i>CG2091</i>	0.544	0.0635
<i>CG32343</i>	0.544	0.0635
<i>CG8642</i>	0.544	0.0635
<i>CG4004</i>	0.543	0.0642
<i>CG7461</i>	0.543	0.0642
<i>CG9132</i>	0.543	0.0642
<i>Nrk</i>	0.543	0.0642
<i>vsg</i>	0.543	0.0642
<i>CG8165</i>	0.542	0.0647
<i>CG10144</i>	0.541	0.0648
<i>CG14314</i>	0.541	0.0648
<i>CG7860</i>	0.541	0.0648
<i>Cpr47Ea</i>	0.541	0.0648
<i>CG12672</i>	0.54	0.0651
<i>CG31682</i>	0.54	0.0651
<i>CHES-1-like</i>	0.54	0.0651
<i>mRpl1</i>	0.54	0.0651
<i>Pnn</i>	0.54	0.0651
<i>CG12995</i>	0.539	0.0656

Gene Name	ERC Value	P-value
<i>CG15212</i>	0.539	0.0656
<i>CG34282</i>	0.539	0.0656
<i>CG9248</i>	0.539	0.0656
<i>Crag</i>	0.539	0.0656
<i>CG32685</i>	0.538	0.066
<i>CG3338</i>	0.538	0.066
<i>kermit</i>	0.538	0.066
<i>Pthh</i>	0.538	0.066
<i>Tsp42E1</i>	0.538	0.066
<i>Ubp64E</i>	0.538	0.066
<i>CG14573</i>	0.537	0.0666
<i>CG5013</i>	0.537	0.0666
<i>CG8920</i>	0.537	0.0666
<i>rab3-GAP</i>	0.537	0.0666
<i>CG10249</i>	0.536	0.0669
<i>CG13375</i>	0.536	0.0669
<i>CG15083</i>	0.536	0.0669
<i>CG8468</i>	0.536	0.0669
<i>CG9797</i>	0.536	0.0669
<i>dod</i>	0.536	0.0669
<i>muskelin</i>	0.536	0.0669
<i>NK7.1</i>	0.536	0.0669
<i>CG18190</i>	0.535	0.0677
<i>CG2107</i>	0.535	0.0677
<i>CG3168</i>	0.535	0.0677
<i>Dgp-1</i>	0.535	0.0677
<i>Or47a</i>	0.535	0.0677
<i>CG2811</i>	0.534	0.0681
<i>CG42258</i>	0.534	0.0681
<i>CG7927</i>	0.534	0.0681
<i>CG8892</i>	0.534	0.0681
<i>CTCF</i>	0.534	0.0681
<i>HLH54F</i>	0.534	0.0681
<i>CG11448</i>	0.533	0.0686
<i>CG13154</i>	0.533	0.0686
<i>CG5510</i>	0.533	0.0686
<i>dwg</i>	0.532	0.0689
<i>pigeon</i>	0.532	0.0689
<i>CG17912</i>	0.531	0.0691
<i>sut2</i>	0.531	0.0691
<i>cag</i>	0.53	0.0693
<i>CG15168</i>	0.53	0.0693
<i>CG2321</i>	0.53	0.0693
<i>CG2807</i>	0.53	0.0693
<i>mel-P22</i>	0.53	0.0693
<i>silbo</i>	0.53	0.0693
<i>vimar</i>	0.53	0.0693
<i>CG10561</i>	0.529	0.0699
<i>CG15478</i>	0.529	0.0699
<i>CG31102</i>	0.529	0.0699
<i>CG8959</i>	0.529	0.0699
<i>Cpr72Eb</i>	0.529	0.0699
<i>CG5978</i>	0.528	0.0704
<i>CG9879</i>	0.528	0.0704
<i>Cpr49Aa</i>	0.528	0.0704
<i>Fancd2</i>	0.528	0.0704

Gene Name	ERC Value	P-value
<i>KalRIIA</i>	0.528	0.0704
<i>mp</i>	0.528	0.0704
<i>CG11317</i>	0.527	0.0709
<i>CG13599</i>	0.527	0.0709
<i>CG15220</i>	0.527	0.0709
<i>CG4570</i>	0.527	0.0709
<i>CG7028</i>	0.527	0.0709
<i>Reck</i>	0.527	0.0709
<i>CG3925</i>	0.526	0.0714
<i>CG9437</i>	0.526	0.0714
<i>HdacX</i>	0.526	0.0714
<i>sec8</i>	0.526	0.0714
<i>CG4577</i>	0.525	0.0718
<i>Cyp49a1</i>	0.525	0.0718
<i>PNUTS</i>	0.525	0.0718
<i>Psf1</i>	0.525	0.0718
<i>CG12825</i>	0.524	0.0722
<i>CG9883</i>	0.524	0.0722
<i>gsb-n</i>	0.524	0.0722
<i>mus309</i>	0.524	0.0722
<i>tadr</i>	0.524	0.0722
<i>CG33770</i>	0.523	0.0726
<i>poe</i>	0.523	0.0726
<i>Prosbeta7</i>	0.523	0.0726
<i>CG10962</i>	0.522	0.0729
<i>CG12016</i>	0.522	0.0729
<i>CG4119</i>	0.522	0.0729
<i>CG4218</i>	0.522	0.0729
<i>CG5361</i>	0.522	0.0729
<i>CG6800</i>	0.522	0.0729
<i>CG8378</i>	0.522	0.0729
<i>CG8852</i>	0.522	0.0729
<i>CG8960</i>	0.522	0.0729
<i>gpp</i>	0.522	0.0729
<i>lkb1</i>	0.522	0.0729
<i>tob1</i>	0.522	0.0729
<i>CG15666</i>	0.521	0.074
<i>CG7747</i>	0.521	0.074
<i>CG1315</i>	0.52	0.0741
<i>l(3)78Bdm</i>	0.52	0.0741
<i>ro</i>	0.52	0.0741
<i>Vha14-1</i>	0.52	0.0741
<i>CG7384</i>	0.519	0.0745
<i>DNApol-gam</i>	0.519	0.0745
<i>ss</i>	0.519	0.0745
<i>CG32155</i>	0.518	0.0748
<i>CG33178</i>	0.518	0.0748
<i>CG8552</i>	0.518	0.0748
<i>fend</i>	0.518	0.0748
<i>RnpS1</i>	0.518	0.0748
<i>Tak1</i>	0.518	0.0748
<i>CG4230</i>	0.517	0.0753
<i>CG4612</i>	0.517	0.0753
<i>Hmt-1</i>	0.517	0.0753
<i>Klc</i>	0.517	0.0753
<i>CG14340</i>	0.516	0.0757

Table 6.S12 Continued

Gene Name	ERC Value	P-value
CG9676	0.516	0.0757
mus304	0.515	0.0759
tuff	0.515	0.0759
CG17184	0.514	0.076
cid	0.514	0.076
beat-lb	0.513	0.0762
CG10947	0.513	0.0762
CG12213	0.513	0.0762
CG13950	0.513	0.0762
CG15888	0.513	0.0762
CG5849	0.513	0.0762
pim	0.513	0.0762
CG1090	0.512	0.0768
CG16790	0.512	0.0768
CG17343	0.512	0.0768
CG7065	0.512	0.0768
EloA	0.512	0.0768
Apc10	0.511	0.0773
CG31646	0.511	0.0773
CG32100	0.511	0.0773
CG7985	0.511	0.0773
CG8370	0.511	0.0773
DNApol-alpha	0.511	0.0773
CG42377	0.51	0.0778
RIC-3	0.51	0.0778
smt3	0.51	0.0778
CG34039	0.509	0.0781
SAK	0.509	0.0781
fs(1)N	0.508	0.0783
gek	0.508	0.0783
ine	0.508	0.0783
CG33696	0.507	0.0786
mRpS31	0.507	0.0786
Sc2	0.507	0.0786
Tfllfbeta	0.507	0.0786
CG14715	0.506	0.0789
CG14856	0.506	0.0789
spen	0.506	0.0789
Anxb11	0.505	0.0792
CG13036	0.505	0.0792
RpIII128	0.505	0.0792
sens-2	0.505	0.0792
sob	0.505	0.0792
Tsp	0.505	0.0792
Tsp42Ek	0.505	0.0792
xmas-2	0.505	0.0792
CG6985	0.504	0.0799
CG8141	0.504	0.0799
CG14132	0.503	0.0801
CG33985	0.503	0.0801
Gr59b	0.503	0.0801
Plip	0.503	0.0801
CG10809	0.502	0.0805
CG15418	0.502	0.0805
CG32333	0.502	0.0805
CG32801	0.502	0.0805

Gene Name	ERC Value	P-value
chico	0.502	0.0805
hkb	0.502	0.0805
CG32437	0.501	0.081
Cpr47Ed	0.501	0.081
croI	0.501	0.081
Ddx1	0.501	0.081
Drep-2	0.501	0.081
Syx7	0.501	0.081
mus301	0.5	0.0815
CG11873	0.5	0.0815
CG14608	0.5	0.0815
CG31296	0.5	0.0815
CG9246	0.5	0.0815
HP4	0.5	0.0815
MTA1-like	0.5	0.0815
Adar	0.499	0.0822
CG32832	0.499	0.0822
Exn	0.499	0.0822
bs	0.498	0.0824
CG10979	0.498	0.0824
CG31360	0.498	0.0824
CG31675	0.498	0.0824
Or43b	0.498	0.0824
srp	0.498	0.0824
Cap-G	0.497	0.083
CG12831	0.497	0.083
CG33692	0.497	0.083
CG8388	0.497	0.083
coot	0.497	0.083
CG13283	0.496	0.0834
CG31630	0.496	0.0834
CG32121	0.496	0.0834
CG9634	0.496	0.0834
Tango6	0.496	0.0834
CG13617	0.495	0.0839
CG18269	0.495	0.0839
CG42820	0.495	0.0839
Den1	0.495	0.0839
Snp	0.495	0.0839
yemalphi	0.495	0.0839
CG13545	0.494	0.0844
CG14515	0.494	0.0844
CG32087	0.494	0.0844
CG34116	0.494	0.0844
CG6550	0.494	0.0844
Grip75	0.494	0.0844
POSH	0.494	0.0844
CG10226	0.493	0.085
CG15387	0.493	0.085
CG4658	0.493	0.085
CG6388	0.493	0.085
CG8503	0.493	0.085
Dip1	0.493	0.085
Hsp67Ba	0.493	0.085
ana2	0.492	0.0857
CG14657	0.492	0.0857

Gene Name	ERC Value	P-value
CG17068	0.492	0.0857
CG5412	0.492	0.0857
scny	0.492	0.0857
Sep1	0.491	0.0861
CG17672	0.491	0.0861
CG5823	0.491	0.0861
Hek2	0.491	0.0861
Spase18-21	0.491	0.0861
Bin1	0.49	0.0866
CG1394	0.49	0.0866
CG32113	0.49	0.0866
CG3610	0.49	0.0866
CG8064	0.49	0.0866
hbs	0.49	0.0866
CG12171	0.489	0.0871
CG13949	0.489	0.0871
CG17691	0.489	0.0871
chn	0.489	0.0871
tan	0.489	0.0871
imd	0.488	0.0876
7B2	0.487	0.0877
CG4666	0.487	0.0877
CG7928	0.487	0.0877
Spt3	0.487	0.0877
Taf11	0.487	0.0877
CG11851	0.486	0.0881
Mob4	0.486	0.0881
CG12012	0.485	0.0883
CG31053	0.485	0.0883
CG42707	0.485	0.0883
ewg	0.485	0.0883
Hexo1	0.485	0.0883
CG15443	0.484	0.0887
CG5888	0.484	0.0887
CG9384	0.484	0.0887
Dpy-30L1	0.484	0.0887
foi	0.484	0.0887
Kul	0.484	0.0887
mel-9	0.484	0.0887
CG10158	0.483	0.0894
CG8230	0.483	0.0894
CG9747	0.483	0.0894
Kap-alpha3	0.483	0.0894
mRpl55	0.483	0.0894
mRplS10	0.483	0.0894
Rcd5	0.483	0.0894
tey	0.483	0.0894
CG15480	0.482	0.0901
CG33158	0.482	0.0901
CG8031	0.482	0.0901
Gpi1	0.482	0.0901
mi	0.482	0.0901
Dip1	0.482	0.0901
Su(z)12	0.482	0.0901
ana2	0.481	0.0907
CG10467	0.481	0.0907

Gene Name	ERC Value	P-value
CG10889	0.481	0.0907
CG17352	0.481	0.0907
CG42449	0.481	0.0907
CG6796	0.481	0.0907
CG7759	0.481	0.0907
Fbw5	0.481	0.0907
Jon74E	0.481	0.0907
CG14937	0.48	0.0915
CG3409	0.48	0.0915
CG7246	0.48	0.0915
CG7453	0.48	0.0915
Cyp301a1	0.48	0.0915
skpB	0.48	0.0915
cdm	0.479	0.0921
CG13035	0.479	0.0921
CG2083	0.479	0.0921
CG6950	0.479	0.0921
Gas41	0.479	0.0921
Rpn11	0.479	0.0921
CG13875	0.478	0.0926
CG17562	0.478	0.0926
Myt1	0.478	0.0926
cbx	0.477	0.0929
CG32053	0.477	0.0929
comm	0.477	0.0929
Myd88	0.477	0.0929
Oatp74D	0.477	0.0929
Orc2	0.477	0.0929
Pc	0.477	0.0929
RanBP3	0.477	0.0929
RpS28-like	0.477	0.0929
CG10898	0.476	0.0937
CG11870	0.476	0.0937
CG18619	0.476	0.0937
GstD10	0.476	0.0937
mrt	0.476	0.0937
Muc91C	0.476	0.0937
CG12107	0.475	0.0942
CG2931	0.475	0.0942
CG32579	0.475	0.0942
CG33281	0.475	0.0942
CG8170	0.475	0.0942
CstF-64	0.475	0.0942
gbb	0.475	0.0942
rec	0.475	0.0942
RpS29	0.475	0.0942
TllEalpha	0.475	0.0942
CG13725	0.474	0.0951
CG33786	0.474	0.0951
CG4210	0.474	0.0951
borr	0.473	0.0954
CG12219	0.473	0.0954
CG30372	0.473	0.0954
CG3353	0.473	0.0954
CG7839	0.473	0.0954
CG8683	0.473	0.0954

Gene Name	ERC Value	P-value
CG13775	0.472	0.0959
CG17839	0.472	0.0959
CG32541	0.471	0.0961
CG3631	0.471	0.0961
CG6724	0.471	0.0961
Liprin-alpha	0.471	0.0961
mtacp1	0.471	0.0961
Or46a	0.471	0.0961
Sid5	0.471	0.0961
Tsp97E	0.471	0.0961
CG1962	0.47	0.0968
CG6733	0.47	0.0968
CG7139	0.47	0.0968
da	0.47	0.0968
Pal	0.47	0.0968
Rpn9	0.47	0.0968
CG30008	0.469	0.0974
CG31221	0.469	0.0974
CG4069	0.469	0.0974
CG4525	0.469	0.0974
CG6927	0.469	0.0974
CG8490	0.469	0.0974
Dip-C	0.469	0.0974
nmd	0.469	0.0974
Su(var)3-3	0.469	0.0974
CG14562	0.468	0.0982
CG18870	0.468	0.0982
CG3437	0.468	0.0982
CG4374	0.468	0.0982
CG7265	0.468	0.0982
CG8979	0.468	0.0982
Cpr47Ee	0.468	0.0982
cuff	0.468	0.0982
wgn	0.468	0.0982
CG18682	0.467	0.099
Gr98a	0.467	0.099
net	0.467	0.099
RhoGAP54D	0.467	0.099
CG33120	0.466	0.0994
CG7786	0.466	0.0994
CG8180	0.466	0.0994
dalaio	0.466	0.0994
Os-E	0.466	0.0994
pb	0.466	0.0994
CG15278	0.465	0.0999
CG15482	0.465	0.0999
CG18262	0.465	0.0999
CG7889	0.465	0.0999
growl	0.465	0.0999
hb	0.465	0.0999
Prx5	0.465	0.0999

Table 6.S13 - Top Genes ERC values for *mus312* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG30381	0.94	0.0001
CG32305	0.935	0.0002
mRps10	0.922	0.0003
Actbeta	0.896	0.0004
lgy	0.896	0.0004
CG17150	0.89	0.0005
CG31226	0.888	0.0006
CG3502	0.887	0.0007
CG9175	0.883	0.0008
MED17	0.882	0.0009
m2	0.88	0.001
CG9837	0.879	0.0011
CG32016	0.878	0.0012
l(2)35Df	0.878	0.0012
Men1-2	0.865	0.0014
CG10495	0.864	0.0014
net	0.862	0.0015
CG16854	0.861	0.0016
l(2)37Bb	0.86	0.0017
Adgf-E	0.859	0.0018
nerfin-2	0.858	0.0019
obst-H	0.858	0.0019
TwlJ	0.858	0.0019
CG1239	0.852	0.0022
CG11674	0.851	0.0023
sv	0.85	0.0023
CG3091	0.849	0.0024
CG4365	0.849	0.0024
CG5537	0.848	0.0026
CG5116	0.847	0.0027
nimC2	0.842	0.0028
mav	0.834	0.0029
slam	0.833	0.003
CG10710	0.831	0.0031
CG17636	0.831	0.0031
GNBP2	0.83	0.0032
CG13334	0.829	0.0033
Ephrin	0.829	0.0033
l(3)76BDr	0.825	0.0035
Tango11	0.824	0.0036
CG4619	0.823	0.0037
CSN5	0.818	0.0038
CG11035	0.817	0.0039
CG3701	0.817	0.0039
CG4407	0.817	0.0039
tos	0.816	0.0041
CG42729	0.815	0.0042
CG7785	0.815	0.0042
CG15896	0.814	0.0044
CG7458	0.814	0.0044
CG32809	0.813	0.0046
CG6277	0.813	0.0046
CG18268	0.812	0.0048
CG8539	0.811	0.0049
CG31808	0.81	0.005
Shroom	0.81	0.005

Gene Name	ERC Value	P-value
aft	0.809	0.0051
CG33642	0.807	0.0052
CG5255	0.807	0.0052
CG14661	0.806	0.0054
CG33155	0.806	0.0054
CG9021	0.806	0.0054
CG10073	0.805	0.0057
CG15523	0.805	0.0057
CG5910	0.805	0.0057
CG31921	0.804	0.0059
CG9917	0.803	0.006
Elp3	0.802	0.0061
GluRIIE	0.802	0.0061
MED18	0.802	0.0061
Syx13	0.801	0.0064
CG16941	0.799	0.0065
CG31550	0.799	0.0065
gd	0.799	0.0065
CG9782	0.798	0.0068
CG32412	0.797	0.0068
CG9961	0.797	0.0068
CG2794	0.796	0.007
CG10481	0.795	0.0071
tam	0.792	0.0072
toy	0.792	0.0072
CG6409	0.791	0.0074
Hf	0.791	0.0074
CG13850	0.79	0.0076
Dms	0.787	0.0077
Pl3K92E	0.787	0.0077
sPLA2	0.785	0.0078
tectonic	0.785	0.0078
CG7011	0.784	0.008
Gprk1	0.784	0.008
CG11029	0.782	0.0082
CG14894	0.782	0.0082
os	0.782	0.0082
Cpr47Ed	0.781	0.0085
Acp1	0.779	0.0086
CG32241	0.779	0.0086
Traf-like	0.778	0.0087
CG17294	0.777	0.0088
CG31974	0.777	0.0088
gw	0.777	0.0088
CG4592	0.775	0.0091
CG5819	0.775	0.0091
esn	0.775	0.0091
lr56a	0.775	0.0091
Or33c	0.774	0.0095
BBS1	0.773	0.0095
CG11872	0.773	0.0095
CG5724	0.773	0.0095
CG8128	0.773	0.0095
CG10092	0.772	0.0099
CG17816	0.772	0.0099
CG31259	0.772	0.0099

Gene Name	ERC Value	P-value
CG6927	0.772	0.0099
CG9747	0.772	0.0099
CG11395	0.77	0.0104
CG3165	0.769	0.0105
Rfabg	0.769	0.0105
CG7881	0.768	0.0106
Cpr	0.768	0.0106
l(2)k10201	0.768	0.0106
AiKb	0.767	0.0109
CG14627	0.766	0.011
CG31065	0.766	0.011
CG6074	0.766	0.011
fs(1)Yb	0.766	0.011
Aats-ile	0.764	0.0114
Cdk8	0.764	0.0114
CG13422	0.763	0.0115
CG32379	0.763	0.0115
ftz-f1	0.763	0.0115
CG11127	0.761	0.0118
POSH	0.761	0.0118
CG42811	0.76	0.012
CG6225	0.76	0.012
CG16879	0.758	0.0122
GstD9	0.756	0.0123
CG10585	0.755	0.0123
CG8526	0.755	0.0123
CG15211	0.753	0.0125
CG31053	0.752	0.0126
CG14882	0.751	0.0127
CG18480	0.751	0.0127
Reps	0.751	0.0127
cnir	0.749	0.013
tw	0.749	0.013
CG14881	0.747	0.0132
Taff1	0.747	0.0132
CG12272	0.746	0.0133
CG2177	0.746	0.0133
Osi13	0.746	0.0133
CG4835	0.745	0.0136
ppk13	0.745	0.0136
SIDL	0.745	0.0136
CG1347	0.744	0.0139
CG30275	0.744	0.0139
modSP	0.744	0.0139
rol122E	0.743	0.0141
Ast-CC	0.742	0.0142
CG3841	0.742	0.0142
CG14062	0.741	0.0144
CG7616	0.741	0.0144
mm	0.741	0.0144
CG4705	0.739	0.0147
Megaln	0.737	0.0148
CG6912	0.736	0.0149
Gr85a	0.735	0.015
GalNAc-T2	0.734	0.015
dpr9	0.733	0.0151

Gene Name	ERC Value	P-value
CG42255	0.731	0.0152
CG4611	0.731	0.0152
HmgD	0.731	0.0152
CG11141	0.73	0.0155
CG14100	0.73	0.0155
CG14418	0.73	0.0155
CG7091	0.73	0.0155
Bet3	0.729	0.0159
CG11835	0.729	0.0159
CG13614	0.729	0.0159
CG15928	0.729	0.0159
CG8774	0.729	0.0159
Jhedup	0.729	0.0159
Nfl	0.729	0.0159
CG32032	0.728	0.0165
lr87a	0.728	0.0165
Poc1	0.728	0.0165
CG13028	0.727	0.0168
Ugt86Dj	0.727	0.0168
CG31855	0.726	0.0169
CG6672	0.726	0.0169
CG30203	0.724	0.0171
pst	0.724	0.0171
salt	0.724	0.0171
CG14662	0.723	0.0174
CG31288	0.723	0.0174
CG10486	0.722	0.0176
CG6613	0.722	0.0176
See	0.72	0.0177
CG14314	0.719	0.0178
mRps31	0.719	0.0178
pb	0.719	0.0178
CG30184	0.718	0.0181
CG33771	0.718	0.0181
rictor	0.718	0.0181
CG10189	0.717	0.0184
CG4098	0.717	0.0184
CG9410	0.717	0.0184
Jheh2	0.717	0.0184
CG7222	0.716	0.0187
Ama	0.714	0.0188
CG14235	0.714	0.0188
CG7211	0.714	0.0188
mGluRA	0.714	0.0188
CG34203	0.713	0.0192
nahoda	0.713	0.0192
CG32832	0.712	0.0194
CG3808	0.712	0.0194
CG14815	0.711	0.0195
CG6154	0.711	0.0195
CG7009	0.711	0.0195
DhpD	0.711	0.0195
Rpl1140	0.71	0.0199
CG32350	0.71	0.0199
Pms2	0.71	0.0199
cif	0.709	0.0202

Gene Name	ERC Value	P-value
CG7330	0.708	0.0203
Nha2	0.708	0.0203
CG15067	0.707	0.0205
CG10219	0.706	0.0205
Or85c	0.706	0.0205
Phax	0.706	0.0205
tutl	0.706	0.0205
CG32277	0.705	0.0209
CG5386	0.705	0.0209
CG9386	0.705	0.0209
CG10650	0.704	0.0212
nimB3	0.704	0.0212
Patsas	0.704	0.0212
Os-C	0.703	0.0214
wdn	0.703	0.0214
CG13127	0.702	0.0216
CG14618	0.702	0.0216
Cpr66Cb	0.702	0.0216
Rbf	0.701	0.0219
Gr9a	0.699	0.022
Atg7	0.698	0.0221
betalnt-nu	0.698	0.0221
CG13144	0.698	0.0221
CG5844	0.698	0.0221
CG7059	0.698	0.0221
CG11437	0.697	0.0225
CG1635	0.697	0.0225
proPO-A1	0.697	0.0225
CG9592	0.696	0.0228
NP15.6	0.695	0.0229
CG31021	0.694	0.023
CG9269	0.694	0.023
CG13160	0.693	0.0232
CG13322	0.693	0.0232
CG14177	0.692	0.0233
CG18095	0.692	0.0233
CG4573	0.692	0.0233
CG5909	0.692	0.0233
galectin	0.692	0.0233
SerT	0.692	0.0233
CG14826	0.691	0.0239
fh	0.691	0.0239
CG2034	0.69	0.0241
CG2144	0.69	0.0241
CG33172	0.69	0.0241
CG1233	0.689	0.0243
CG13705	0.689	0.0243
CG4553	0.689	0.0243
Or48a	0.689	0.0243
Tre	0.689	0.0243
Vps13	0.689	0.0243
put	0.688	0.0249
Rpl1140	0.687	0.025
CG31048	0.687	0.025
Nap1	0.687	0.025
Pl4K1alpha	0.687	0.025

Table 6.S13 Continued

Gene Name	ERC Value	P-value
CG10725	0.686	0.0253
CG8498	0.686	0.0253
CG7587	0.685	0.0255
shl	0.685	0.0255
CG16789	0.684	0.0257
CG6656	0.684	0.0257
Spn42Dc	0.684	0.0257
dimm	0.683	0.0259
CG18744	0.682	0.026
ABCB7	0.681	0.0261
CG14070	0.681	0.0261
CG16952	0.681	0.0261
CG5270	0.681	0.0261
CG31373	0.68	0.0265
CG3434	0.68	0.0265
stv	0.68	0.0265
arr	0.679	0.0268
Cwc25	0.679	0.0268
CG32635	0.678	0.0269
CG5846	0.678	0.0269
spin	0.678	0.0269
CG13500	0.676	0.0272
CG4398	0.676	0.0272
nimB2	0.676	0.0272
S	0.676	0.0272
skpA	0.675	0.0276
CG12883	0.674	0.0277
CG14205	0.674	0.0277
Gr98b	0.674	0.0277
CG34447	0.673	0.0279
Gr47b	0.672	0.028
Sulf1	0.672	0.028
Tsp29Fb	0.672	0.028
CG11077	0.671	0.0283
Atox1	0.67	0.0284
CG30196	0.67	0.0284
CG31731	0.67	0.0284
L	0.67	0.0284
Sec61beta	0.67	0.0284
CG1358	0.669	0.0288
Obp99a	0.669	0.0288
Best3	0.668	0.029
CG13002	0.668	0.029
CG6484	0.668	0.029
CG16857	0.667	0.0293
CG34012	0.667	0.0293
CG12990	0.666	0.0295
pain	0.666	0.0295
shf	0.666	0.0295
CG14777	0.665	0.0297
CG2789	0.665	0.0297
CG42330	0.665	0.0297
CG12177	0.664	0.03
CG13711	0.664	0.03
CG1640	0.664	0.03
CG3589	0.664	0.03

Gene Name	ERC Value	P-value
Hely	0.664	0.03
CG13086	0.663	0.0305
CG15534	0.663	0.0305
CG15674	0.663	0.0305
CG15828	0.663	0.0305
cv	0.663	0.0305
CG12970	0.662	0.0309
PGRP-SD	0.662	0.0309
CG34266	0.661	0.0311
CG15478	0.66	0.0312
CG42724	0.66	0.0312
CG9107	0.66	0.0312
lil	0.66	0.0312
FancI	0.659	0.0315
spag4	0.659	0.0315
CG15701	0.658	0.0317
CG18585	0.658	0.0317
CG2943	0.658	0.0317
CG33506	0.658	0.0317
Or83c	0.657	0.0321
CG8562	0.656	0.0322
Lerp	0.656	0.0322
BubR1	0.655	0.0323
CG13965	0.655	0.0323
CG2224	0.655	0.0323
Cpr60D	0.654	0.0326
Crz	0.654	0.0326
CG6421	0.653	0.0328
CG6796	0.653	0.0328
Hr39	0.653	0.0328
p-cup	0.653	0.0328
CG15432	0.652	0.0332
CG32686	0.652	0.0332
CG5565	0.652	0.0332
CG6980	0.651	0.0334
CG12567	0.65	0.0335
CG30016	0.65	0.0335
Oaz	0.65	0.0335
CG10362	0.649	0.0338
CG11109	0.649	0.0338
CG13295	0.649	0.0338
CG15283	0.649	0.0338
CG11123	0.648	0.0341
CG1299	0.648	0.0341
Gr22e	0.648	0.0341
su(Hw)	0.648	0.0341
upd3	0.648	0.0341
CG2993	0.647	0.0346
CG5924	0.647	0.0346
plo	0.647	0.0346
Ptp52F	0.646	0.0349
Smt	0.646	0.0349
CG8889	0.645	0.035
Rpl37a	0.645	0.035
CG13252	0.644	0.0352
CG31414	0.644	0.0352

Gene Name	ERC Value	P-value
CG31898	0.644	0.0352
CG8245	0.643	0.0355
CG13742	0.642	0.0356
CG32017	0.642	0.0356
Ugt35a	0.642	0.0356
CG11637	0.641	0.0359
CG15198	0.641	0.0359
CG3326	0.641	0.0359
CG6462	0.641	0.0359
Corp	0.641	0.0359
CG7695	0.64	0.0363
Hem	0.64	0.0363
l77g	0.64	0.0363
IdlCp	0.64	0.0363
CG2862	0.639	0.0367
CG32537	0.639	0.0367
CG1970	0.636	0.0368
svr	0.636	0.0368
CG12325	0.635	0.037
CG30340	0.635	0.037
GluRIIC	0.635	0.037
CG16713	0.634	0.0373
Pgym87	0.634	0.0373
Rcp	0.634	0.0373
zfh2	0.634	0.0373
CG1246	0.633	0.0377
CG3655	0.633	0.0377
CG7255	0.633	0.0377
Gr36d	0.633	0.0377
Rab7	0.633	0.0377
CG42726	0.632	0.0381
CG8642	0.632	0.0381
Fk61C	0.632	0.0381
Ptpmeg	0.632	0.0381
CG10195	0.631	0.0385
CG1104	0.631	0.0385
CG9377	0.631	0.0385
CG33307	0.63	0.0387
cyr	0.63	0.0387
CG33145	0.629	0.0389
Ntl	0.629	0.0389
ptc	0.629	0.0389
T48	0.629	0.0389
CG10731	0.628	0.0393
CG12818	0.628	0.0393
CG17669	0.628	0.0393
CG1791	0.628	0.0393
CG8852	0.628	0.0393
CG8945	0.628	0.0393
CG16896	0.627	0.0398
CG18417	0.627	0.0398
CG7781	0.627	0.0398
Jhl-26	0.627	0.0398
CG31689	0.626	0.0402
CG33340	0.626	0.0402
CG10116	0.625	0.0404

Gene Name	ERC Value	P-value
CG4325	0.625	0.0404
hk	0.625	0.0404
Adgf-B	0.624	0.0406
Dsk	0.624	0.0406
CG14963	0.623	0.0408
CG7197	0.623	0.0408
CG9044	0.623	0.0408
ced-6	0.622	0.0411
CG33289	0.622	0.0411
Kap3	0.622	0.0411
magu	0.622	0.0411
CG10680	0.621	0.0414
Fmrf	0.621	0.0414
Cdc42	0.62	0.0416
CG6234	0.62	0.0416
Twid2	0.62	0.0416
CG1909	0.619	0.0419
CG33090	0.619	0.0419
scaf	0.619	0.0419
CG13869	0.618	0.0422
CG31089	0.618	0.0422
CG31760	0.618	0.0422
dpr18	0.618	0.0422
mRpS25	0.618	0.0422
ste14	0.618	0.0422
CG5026	0.617	0.0427
CG5265	0.617	0.0427
CG7882	0.617	0.0427
CG8321	0.617	0.0427
CG3700	0.616	0.0431
Myo10A	0.616	0.0431
cal5	0.615	0.0432
CG14079	0.615	0.0432
CG32195	0.615	0.0432
CG5705	0.615	0.0432
Obp99d	0.615	0.0432
CG13427	0.614	0.0437
GABPI	0.614	0.0437
mRpS33	0.614	0.0437
CG12995	0.613	0.044
CG32778	0.613	0.044
CG6511	0.613	0.044
CG8102	0.613	0.044
Or23a	0.613	0.044
rec	0.613	0.044
sens	0.613	0.044
CG9302	0.612	0.0446
Obp50d	0.612	0.0446
rod	0.612	0.0446
TORC	0.612	0.0446
CG11262	0.611	0.045
CG14277	0.611	0.045
CG7526	0.611	0.045
CG8247	0.611	0.045
Lin29	0.611	0.045
CG9673	0.61	0.0454

Gene Name	ERC Value	P-value
KH1	0.61	0.0454
pex1	0.61	0.0454
ppk19	0.61	0.0454
Stim	0.61	0.0454
tap	0.61	0.0454
CG17564	0.609	0.0459
ETH	0.609	0.0459
GNBP1	0.609	0.0459
RagC	0.609	0.0459
CG31189	0.608	0.0463
CG8060	0.608	0.0463
ImpL1	0.607	0.0465
MED27	0.607	0.0465
ND42	0.607	0.0465
CG14411	0.606	0.0468
CG7145	0.606	0.0468
CG8777	0.606	0.0468
Gr59b	0.606	0.0468
Nup214	0.606	0.0468
RhoGAP18E	0.606	0.0468
312	0.605	0.0473
Aats-phe	0.605	0.0473
CG10469	0.605	0.0473
CG7277	0.605	0.0473
CG7509	0.605	0.0473
CG9400	0.605	0.0473
CG11367	0.604	0.0478
CG3119	0.604	0.0478
CG11131	0.603	0.048
CG11155	0.603	0.048
CG6830	0.603	0.048
Tsp42Eg	0.603	0.048
CG4020	0.602	0.0484
CG7488	0.602	0.0484
Cyp6a13	0.602	0.0484
lmd	0.602	0.0484
RhoGAPp19	0.602	0.0484
CG11665	0.601	0.0488
GABPI	0.601	0.0488
CG6012	0.601	0.0488
CG9248	0.601	0.0488
Rad51C	0.601	0.0488
spn-B	0.601	0.0488
CG14273	0.6	0.0493
CG14408	0.6	0.0493
CG15861	0.6	0.0493
psd	0.6	0.0493
Rab10	0.6	0.0493
Rop	0.6	0.0493
Adgf-C	0.599	0.0498
CG10352	0.599	0.0498
CG13488	0.599	0.0498
CG3358	0.599	0.0498
CG6586	0.599	0.0498
CG8785	0.599	0.0498
lrs4c	0.599	0.0498
CG33229	0.598	0.0505

Table 6.S13 Continued

Gene Name	ERC Value	P-value
CG8407	0.598	0.0505
CG14562	0.597	0.0506
CG1806	0.597	0.0506
CG3246	0.597	0.0506
Mlo	0.597	0.0506
att-ORFA	0.596	0.051
CG12204	0.596	0.051
CG5613	0.596	0.051
Ckllbeta	0.596	0.051
CG13192	0.595	0.0514
CG31706	0.595	0.0514
CG4660	0.595	0.0514
CG7224	0.595	0.0514
CG7309	0.595	0.0514
CG13531	0.594	0.0518
CG6836	0.594	0.0518
TwdIG	0.594	0.0518
wdb	0.594	0.0518
CG18233	0.593	0.0522
CG34217	0.593	0.0522
Cys	0.593	0.0522
ppk14	0.593	0.0522
timeout	0.593	0.0522
TMS1	0.593	0.0522
be	0.592	0.0527
CG12917	0.592	0.0527
CG13463	0.592	0.0527
CG34231	0.592	0.0527
CG5522	0.592	0.0527
CG10527	0.591	0.0532
CG14526	0.591	0.0532
CG8958	0.591	0.0532
CG9010	0.591	0.0532
ft	0.591	0.0532
Gr59a	0.591	0.0532
serp	0.591	0.0532
adat	0.59	0.0538
CG10252	0.59	0.0538
CG31975	0.59	0.0538
CG32043	0.59	0.0538
CG9335	0.59	0.0538
Dhod	0.59	0.0538
Ir11a	0.59	0.0538
VhaM9.7-d	0.59	0.0538
CG11750	0.589	0.0545
CG13310	0.589	0.0545
bgm	0.588	0.0547
CG15252	0.588	0.0547
CG4683	0.588	0.0547
Ir41a	0.588	0.0547
mbm	0.588	0.0547
CG33509	0.587	0.0551
PKD	0.587	0.0551
CG11739	0.586	0.0553
CG11870	0.586	0.0553
CG13085	0.586	0.0553

Gene Name	ERC Value	P-value
CG15766	0.586	0.0553
CG15922	0.586	0.0553
CG2278	0.586	0.0553
dlp	0.586	0.0553
Gint3	0.586	0.0553
Gyc32E	0.586	0.0553
Ogg1	0.586	0.0553
bdg	0.585	0.0562
CG13795	0.585	0.0562
CG14414	0.585	0.0562
CG15563	0.585	0.0562
Vm34Ca	0.585	0.0562
CG18234	0.584	0.0567
CG18519	0.584	0.0567
CG30192	0.584	0.0567
CG31087	0.584	0.0567
CG3683	0.584	0.0567
Fen1	0.584	0.0567
Taf4	0.584	0.0567
CG17184	0.583	0.0573
CG3123	0.583	0.0573
CG34227	0.583	0.0573
hale	0.583	0.0573
NKAIN	0.583	0.0573
rhea	0.583	0.0573
CDase	0.582	0.0578
CG12042	0.582	0.0578
CG12130	0.582	0.0578
CG32196	0.582	0.0578
DNApol-gam	0.582	0.0578
Atx2	0.581	0.0583
beta3GalTII	0.581	0.0583
CG3214	0.581	0.0583
CG6947	0.581	0.0583
CG8401	0.581	0.0583
csw	0.581	0.0583
CG10962	0.58	0.0588
CG32079	0.58	0.0588
CG34195	0.579	0.059
Hex-t2	0.579	0.059
Gs2	0.578	0.0592
c12.2	0.577	0.0593
CG10702	0.577	0.0593
CG8257	0.577	0.0593
Crk	0.577	0.0593
KairRIA	0.577	0.0593
CG13125	0.576	0.0597
CG7058	0.576	0.0597
CG7431	0.576	0.0597
CG8248	0.576	0.0597
frtz	0.576	0.0597
icln	0.576	0.0597
RhoGAP93E	0.576	0.0597
Top3alpha	0.576	0.0597
Ald	0.575	0.0605
CG10841	0.575	0.0605

Gene Name	ERC Value	P-value
CG14834	0.575	0.0605
CG8176	0.575	0.0605
RpL13A	0.575	0.0605
CG4374	0.574	0.0609
CG7146	0.574	0.0609
CG10738	0.573	0.0611
CG14196	0.573	0.0611
CG30380	0.573	0.0611
CG7777	0.573	0.0611
mRpL54	0.573	0.0611
CG31659	0.572	0.0615
CG7227	0.572	0.0615
CG8417	0.572	0.0615
Eccc1	0.572	0.0615
CG15201	0.571	0.0619
homer	0.571	0.0619
CG5871	0.57	0.0621
CG6985	0.57	0.0621
Dip3	0.57	0.0621
Listericiin	0.57	0.0621
mRpL39	0.57	0.0621
pgant3	0.57	0.0621
CG17726	0.569	0.0626
CG5357	0.569	0.0626
CG6761	0.569	0.0626
CG6812	0.569	0.0626
CG9799	0.569	0.0626
Elo6beta	0.569	0.0626
CG15739	0.568	0.0632
CG4424	0.568	0.0632
Got1	0.568	0.0632
Gr8a	0.568	0.0632
CG33056	0.567	0.0635
CG33919	0.567	0.0635
RhoGEF2	0.567	0.0635
Vang	0.567	0.0635
CG18418	0.566	0.0639
CG9981	0.566	0.0639
CG10512	0.565	0.0641
CG16742	0.565	0.0641
CG5048	0.565	0.0641
hug	0.565	0.0641
Il1isc	0.565	0.0641
Il2j01289	0.565	0.0641
Best4	0.564	0.0646
CG15570	0.564	0.0646
CG2126	0.564	0.0646
CG4393	0.564	0.0646
Prosalpha5	0.564	0.0646
RpL7-like	0.564	0.0646
CG3837	0.563	0.0651
CG8520	0.563	0.0651
Eap	0.563	0.0651
RhoGAP5A	0.563	0.0651
Trm-SR	0.563	0.0651
CG12659	0.562	0.0656

Gene Name	ERC Value	P-value
CG33672	0.562	0.0656
CG5757	0.562	0.0656
mus205	0.562	0.0656
Pngl	0.562	0.0656
tor	0.562	0.0656
BBS8	0.561	0.0661
CG34348	0.561	0.0661
CG9555	0.561	0.0661
Gr57a	0.561	0.0661
Il2j35Bc	0.561	0.0661
Or88a	0.561	0.0661
CG11060	0.56	0.0667
CG14655	0.56	0.0667
CG17322	0.56	0.0667
poly	0.56	0.0667
vap	0.56	0.0667
GlurIIIA	0.559	0.0671
sea	0.559	0.0671
CG14427	0.558	0.0673
CG6619	0.558	0.0673
CG17217	0.557	0.0675
CG31704	0.557	0.0675
CG5877	0.557	0.0675
CG6153	0.557	0.0675
CG7551	0.557	0.0675
CG8097	0.557	0.0675
CG8974	0.557	0.0675
CG9702	0.557	0.0675
mus201	0.557	0.0675
beat-lla	0.556	0.0683
Cht8	0.556	0.0683
Bteb2	0.555	0.0685
CG18788	0.555	0.0685
CG31437	0.555	0.0685
CG34448	0.555	0.0685
CG42240	0.555	0.0685
CG4942	0.555	0.0685
CG5746	0.555	0.0685
E2f	0.555	0.0685
CG11236	0.554	0.0692
CG31534	0.554	0.0692
Fuc7D	0.554	0.0692
Ir52a	0.554	0.0692
shg	0.554	0.0692
cbc	0.553	0.0696
CG42335	0.553	0.0696
knk	0.553	0.0696
gb	0.553	0.0696
Glycogenin	0.553	0.0696
levy	0.553	0.0696
Oseg5	0.553	0.0696
SKIP	0.553	0.0696
CG11249	0.552	0.0703
CG14380	0.552	0.0703
CG3239	0.552	0.0703
CG7328	0.552	0.0703
CG8197	0.552	0.0703

Gene Name	ERC Value	P-value
CG9649	0.552	0.0703
mRpS6	0.552	0.0703
Nca	0.552	0.0703
p53	0.552	0.0703
Ssb-c31a	0.552	0.0703
Uchr	0.552	0.0703
CG13436	0.551	0.0713
CG4323	0.551	0.0713
Reck	0.551	0.0713
Sox15	0.551	0.0713
ver	0.551	0.0713
CG14869	0.55	0.0717
CG2219	0.55	0.0717
CG31102	0.55	0.0717
CG3568	0.55	0.0717
CG42513	0.55	0.0717
dysb	0.55	0.0717
mTTF	0.55	0.0717
CG7349	0.549	0.0723
CG9596	0.549	0.0723
ldbr	0.549	0.0723
Mt2	0.549	0.0723
sawah	0.549	0.0723
CG10083	0.548	0.0728
CG13724	0.548	0.0728
CG7956	0.548	0.0728
CG9935	0.548	0.0728
Doa	0.548	0.0728
Obp57c	0.548	0.0728
CG13005	0.547	0.0733
CG30217	0.547	0.0733
CG30359	0.547	0.0733
CG6353	0.547	0.0733
ct	0.547	0.0733
Gr2a	0.547	0.0733
Mitf	0.547	0.0733
Tsp66A	0.547	0.0733
CG12918	0.546	0.0741
CG14528	0.546	0.0741
CG1983	0.546	0.0741
Gr89a	0.546	0.0741
Hsp67Bc	0.546	0.0741
Nipsnap	0.546	0.0741
CG1868	0.545	0.0746
CG4045	0.545	0.0746
knk	0.545	0.0746
out	0.545	0.0746
CG17333	0.544	0.075
CG2135	0.544	0.075
CG32425	0.544	0.075
wb	0.544	0.075
Asator	0.543	0.0753
CG12730	0.543	0.0753
CG14290	0.543	0.0753
CG33510	0.543	0.0753
CG9886	0.543	0.0753

Table 6.S13 Continued

Gene Name	ERC Value	P-value
<i>grp</i>	0.543	0.0753
<i>PH4alphaS</i>	0.543	0.0753
<i>sun</i>	0.543	0.0753
<i>CG10713</i>	0.542	0.076
<i>CG12716</i>	0.542	0.076
<i>CG2811</i>	0.542	0.076
<i>CG31954</i>	0.542	0.076
<i>CG4839</i>	0.542	0.076
<i>CG9507</i>	0.542	0.076
<i>Or67b</i>	0.542	0.076
<i>Ret</i>	0.542	0.076
<i>spn-D</i>	0.542	0.076
<i>Tusp</i>	0.542	0.076
<i>CG14933</i>	0.541	0.0769
<i>CG4169</i>	0.541	0.0769
<i>CG8080</i>	0.541	0.0769
<i>SdhC</i>	0.541	0.0769
<i>CG2813</i>	0.54	0.0773
<i>CG3009</i>	0.54	0.0773
<i>CG32000</i>	0.54	0.0773
<i>CG32281</i>	0.54	0.0773
<i>CG33060</i>	0.54	0.0773
<i>CG3520</i>	0.54	0.0773
<i>cl</i>	0.54	0.0773
<i>flr</i>	0.54	0.0773
<i>Rab5</i>	0.54	0.0773
<i>spt4</i>	0.54	0.0773
<i>CG2701</i>	0.539	0.0782
<i>CG30385</i>	0.539	0.0782
<i>CG7135</i>	0.539	0.0782
<i>CG7568</i>	0.539	0.0782
<i>ERR</i>	0.539	0.0782
<i>CG15412</i>	0.538	0.0786
<i>CG16739</i>	0.538	0.0786
<i>CG30272</i>	0.538	0.0786
<i>CG32702</i>	0.538	0.0786
<i>Spc105R</i>	0.538	0.0786
<i>CG11475</i>	0.537	0.0791
<i>CG32850</i>	0.537	0.0791
<i>CG5961</i>	0.537	0.0791
<i>CG8331</i>	0.537	0.0791
<i>fd102C</i>	0.537	0.0791
<i>Or94a</i>	0.537	0.0791
<i>spi</i>	0.537	0.0791
<i>vn</i>	0.537	0.0791
<i>CG15634</i>	0.536	0.0798
<i>CG1774</i>	0.536	0.0798
<i>CG31469</i>	0.536	0.0798
<i>CG31920</i>	0.536	0.0798
<i>CG3652</i>	0.536	0.0798
<i>CG7580</i>	0.536	0.0798
<i>ETHR</i>	0.536	0.0798
<i>smi35A</i>	0.536	0.0798
<i>Syt12</i>	0.536	0.0798
<i>Ugt58Fa</i>	0.536	0.0798
<i>CG13089</i>	0.535	0.0807

Gene Name	ERC Value	P-value
<i>CG13766</i>	0.535	0.0807
<i>CG31728</i>	0.535	0.0807
<i>CG3823</i>	0.535	0.0807
<i>gkt</i>	0.535	0.0807
<i>Nurf-38</i>	0.535	0.0807
<i>tin</i>	0.535	0.0807
<i>CG16865</i>	0.534	0.0814
<i>CG3448</i>	0.534	0.0814
<i>CG4078</i>	0.534	0.0814
<i>CG5630</i>	0.534	0.0814
<i>Spn43Ab</i>	0.534	0.0814
<i>14-3-3<i>l</i>_u</i>	0.533	0.0818
<i>CG13377</i>	0.533	0.0818
<i>CG16826</i>	0.533	0.0818
<i>CG31267</i>	0.533	0.0818
<i>wgn</i>	0.533	0.0818
<i>Tfb5</i>	0.532	0.0823
<i>CG11009</i>	0.531	0.0823
<i>CG30488</i>	0.531	0.0823
<i>CG32627</i>	0.531	0.0823
<i>CG6180</i>	0.531	0.0823
<i>CG9356</i>	0.531	0.0823
<i>mbt</i>	0.531	0.0823
<i>Moe</i>	0.531	0.0823
<i>stl</i>	0.531	0.0823
<i>Try29F</i>	0.531	0.0823
<i>CG15661</i>	0.53	0.0832
<i>CG31784</i>	0.53	0.0832
<i>dock</i>	0.53	0.0832
<i>Gr61a</i>	0.53	0.0832
<i>alpha-Est1</i>	0.529	0.0835
<i>CG4836</i>	0.529	0.0835
<i>l(1)G0230</i>	0.529	0.0835
<i>CG14712</i>	0.528	0.0838
<i>CG15525</i>	0.528	0.0838
<i>CG17807</i>	0.528	0.0838
<i>CG6018</i>	0.528	0.0838
<i>meso18E</i>	0.528	0.0838
<i>CG15429</i>	0.527	0.0842
<i>Lcp1</i>	0.527	0.0842
<i>PICK1</i>	0.527	0.0842
<i>CG13936</i>	0.526	0.0845
<i>CG14969</i>	0.526	0.0845
<i>CG15020</i>	0.526	0.0845
<i>CG17266</i>	0.526	0.0845
<i>CG31371</i>	0.526	0.0845
<i>CG4658</i>	0.526	0.0845
<i>GluRIIB</i>	0.526	0.0845
<i>CG14450</i>	0.525	0.0851
<i>CG2162</i>	0.525	0.0851
<i>CG6028</i>	0.525	0.0851
<i>CG6347</i>	0.525	0.0851
<i>DIP1</i>	0.525	0.0851
<i>Lip4</i>	0.525	0.0851
<i>miple2</i>	0.525	0.0851
<i>Zw</i>	0.525	0.0851

Gene Name	ERC Value	P-value
<i>CG5690</i>	0.524	0.0859
<i>CG5867</i>	0.524	0.0859
<i>S6kl</i>	0.524	0.0859
<i>CG4269</i>	0.523	0.0861
<i>Tak1</i>	0.523	0.0861
<i>ast</i>	0.522	0.0863
<i>CG13397</i>	0.522	0.0863
<i>dj-1beta</i>	0.522	0.0863
<i>hbn</i>	0.522	0.0863
<i>Aats-met</i>	0.521	0.0867
<i>CG11255</i>	0.521	0.0867
<i>CG3356</i>	0.521	0.0867
<i>escl</i>	0.521	0.0867
<i>Spn27A</i>	0.521	0.0867
<i>CG10628</i>	0.52	0.0871
<i>CG14565</i>	0.52	0.0871
<i>CG3262</i>	0.52	0.0871
<i>CG9150</i>	0.52	0.0871
<i>niki</i>	0.52	0.0871
<i>CG11286</i>	0.519	0.0876
<i>CG13760</i>	0.519	0.0876
<i>CG16904</i>	0.519	0.0876
<i>CG31793</i>	0.519	0.0876
<i>CG32599</i>	0.519	0.0876
<i>CG34001</i>	0.519	0.0876
<i>CG4565</i>	0.519	0.0876
<i>Hml</i>	0.519	0.0876
<i>l(1)G0289</i>	0.519	0.0876
<i>burs</i>	0.518	0.0884
<i>mtRNApol</i>	0.518	0.0884
<i>CG17036</i>	0.517	0.0886
<i>sut4</i>	0.517	0.0886
<i>tkv</i>	0.517	0.0886
<i>Ast</i>	0.516	0.0888
<i>CG3515</i>	0.516	0.0888
<i>CG5421</i>	0.516	0.0888
<i>CycY</i>	0.516	0.0888
<i>bnk</i>	0.515	0.0892
<i>CG10916</i>	0.515	0.0892
<i>CG11436</i>	0.515	0.0892
<i>CG15093</i>	0.515	0.0892
<i>CG3987</i>	0.515	0.0892
<i>CG4367</i>	0.515	0.0892
<i>CG4434</i>	0.515	0.0892
<i>lr40a</i>	0.515	0.0892
<i>mei-41</i>	0.515	0.0892
<i>mRpl16</i>	0.515	0.0892
<i>CG10825</i>	0.514	0.0901
<i>CG14212</i>	0.514	0.0901
<i>CG2162</i>	0.514	0.0901
<i>ss</i>	0.514	0.0901
<i>CG14194</i>	0.513	0.0905
<i>CG15161</i>	0.513	0.0905
<i>CG30115</i>	0.513	0.0905
<i>CG5830</i>	0.513	0.0905
<i>Cyp4ad1</i>	0.513	0.0905

Gene Name	ERC Value	P-value
<i>l(1)G0269</i>	0.513	0.0905
<i>Rab6</i>	0.513	0.0905
<i>wcd</i>	0.513	0.0905
<i>Ast-C</i>	0.512	0.0912
<i>CG12539</i>	0.512	0.0912
<i>Psc</i>	0.512	0.0912
<i>m</i>	0.512	0.0912
<i>CG12024</i>	0.511	0.0915
<i>CG14195</i>	0.511	0.0915
<i>CG14695</i>	0.511	0.0915
<i>CG1561</i>	0.511	0.0915
<i>CG3033</i>	0.511	0.0915
<i>CG42686</i>	0.511	0.0915
<i>CSN6</i>	0.511	0.0915
<i>ninaA</i>	0.511	0.0915
<i>CG16790</i>	0.51	0.0923
<i>CG30104</i>	0.51	0.0923
<i>CG4586</i>	0.51	0.0923
<i>dmrt11E</i>	0.51	0.0923
<i>ttk</i>	0.51	0.0923
<i>Yps45</i>	0.51	0.0923
<i>aur</i>	0.509	0.0928
<i>CG3719</i>	0.509	0.0928
<i>CG4612</i>	0.509	0.0928
<i>CG8147</i>	0.509	0.0928
<i>dor</i>	0.509	0.0928
<i>CG13562</i>	0.508	0.0932
<i>CG17337</i>	0.508	0.0932
<i>CG34251</i>	0.508	0.0932
<i>CG3508</i>	0.508	0.0932
<i>CG8678</i>	0.508	0.0932
<i>iHog</i>	0.508	0.0932
<i>Psa</i>	0.508	0.0932
<i>CG11048</i>	0.507	0.0939
<i>CG1115</i>	0.507	0.0939
<i>CG31291</i>	0.507	0.0939
<i>CG5451</i>	0.507	0.0939
<i>CG7156</i>	0.507	0.0939
<i>disp</i>	0.507	0.0939
<i>polo</i>	0.507	0.0939
<i>Tom</i>	0.507	0.0939
<i>VhaM9.7-a</i>	0.507	0.0939
<i>CG10479</i>	0.506	0.0947
<i>CG14543</i>	0.506	0.0947
<i>Cyp28a5</i>	0.506	0.0947
<i>Taf7</i>	0.506	0.0947
<i>CG14321</i>	0.505	0.095
<i>CG2249</i>	0.505	0.095
<i>Kmn1</i>	0.505	0.095
<i>pen</i>	0.505	0.095
<i>PH4alphaMf</i>	0.505	0.095
<i>B4</i>	0.504	0.0955
<i>CG10581</i>	0.504	0.0955
<i>CG16734</i>	0.504	0.0955
<i>CG17781</i>	0.504	0.0955
<i>Jafra2</i>	0.504	0.0955

Gene Name	ERC Value	P-value
<i>Rab3</i>	0.504	0.0955
<i>CG9523</i>	0.503	0.096
<i>Duox</i>	0.503	0.096
<i>KCNQ</i>	0.503	0.096
<i>Anxb11</i>	0.502	0.0963
<i>CG12617</i>	0.502	0.0963
<i>CG13902</i>	0.502	0.0963
<i>CG7025</i>	0.502	0.0963
<i>CG7845</i>	0.502	0.0963
<i>Cyp6d5</i>	0.502	0.0963
<i>nopo</i>	0.502	0.0963
<i>Nufip</i>	0.502	0.0963
<i>Oli</i>	0.502	0.0963
<i>pallidin</i>	0.502	0.0963
<i>CG11902</i>	0.501	0.0972
<i>CG2604</i>	0.501	0.0972
<i>CG3332</i>	0.501	0.0972
<i>CG8455</i>	0.501	0.0972
<i>CG9253</i>	0.501	0.0972
<i>ome</i>	0.501	0.0972
<i>Sur-8</i>	0.501	0.0972
<i>CG33301</i>	0.5	0.0978
<i>Cyp4d8</i>	0.5	0.0978
<i>CG12851</i>	0.499	0.098
<i>CG32631</i>	0.499	0.098
<i>CG5612</i>	0.499	0.098
<i>CG5793</i>	0.499	0.098
<i>CG8232</i>	0.499	0.098
<i>Dic90F</i>	0.499	0.098
<i>ldgf5</i>	0.499	0.098
<i>mRpl48</i>	0.499	0.098
<i>CG8671</i>	0.498	0.0987
<i>Mes2</i>	0.498	0.0987
<i>plexA</i>	0.498	0.0987
<i>CG1537</i>	0.497	0.099
<i>CG15609</i>	0.497	0.099
<i>CG18769</i>	0.497	0.099
<i>CG30085</i>	0.497	0.099
<i>CG32579</i>	0.497	0.099
<i>CG42487</i>	0.497	0.099
<i>CG9067</i>	0.497	0.099
<i>Timp</i>	0.497	0.099
<i>CG13855</i>	0.496	0.0997
<i>CG34193</i>	0.496	0.0997
<i>CG9215</i>	0.496	0.0997
<i>Esp</i>	0.496	0.0997
<i>if</i>	0.496	0.0997

Table 6.S14 - Top Genes ERC values for *okr* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>sw</i>	0.882	0.0001
<i>nAcRalpha-1</i>	0.754	0.0002
<i>CG11367</i>	0.753	0.0003
<i>scro</i>	0.751	0.0004
<i>CG3632</i>	0.739	0.0005
<i>pot</i>	0.733	0.0005
<i>oc</i>	0.731	0.0006
<i>sl</i>	0.729	0.0007
<i>CG12773</i>	0.722	0.0008
<i>CG11417</i>	0.716	0.0009
<i>CG1315</i>	0.709	0.001
<i>hfw</i>	0.699	0.0011
<i>pck</i>	0.698	0.0012
<i>CG2201</i>	0.696	0.0013
<i>Eph</i>	0.69	0.0014
<i>CG42827</i>	0.679	0.0014
<i>CG9947</i>	0.676	0.0015
<i>CG5073</i>	0.675	0.0016
<i>CG7739</i>	0.675	0.0016
<i>CG42402</i>	0.674	0.0018
<i>MBD-like</i>	0.674	0.0018
<i>CG1492</i>	0.673	0.002
<i>vtD</i>	0.673	0.002
<i>CG32409</i>	0.671	0.0022
<i>CG42795</i>	0.669	0.0023
<i>CG14401</i>	0.667	0.0023
<i>CG14352</i>	0.666	0.0024
<i>CG6201</i>	0.666	0.0024
<i>CG15251</i>	0.664	0.0026
<i>Cyp313b1</i>	0.662	0.0027
<i>dmrt11E</i>	0.662	0.0027
<i>CG31109</i>	0.66	0.0029
<i>d4</i>	0.66	0.0029
<i>Ku80</i>	0.655	0.0031
<i>NK7.1</i>	0.654	0.0032
<i>Nca</i>	0.653	0.0032
<i>Proc-R</i>	0.652	0.0033
<i>mGluRA</i>	0.65	0.0034
<i>CG3198</i>	0.644	0.0035
<i>CG33672</i>	0.643	0.0036
<i>CG14321</i>	0.64	0.0037
<i>plexA</i>	0.64	0.0037
<i>CG11665</i>	0.639	0.0039
<i>rg</i>	0.637	0.004
<i>CG33958</i>	0.636	0.0041
<i>SCAP</i>	0.632	0.0041
<i>Zyx102EF</i>	0.632	0.0041
<i>CG14883</i>	0.631	0.0043
<i>CG14966</i>	0.631	0.0043
<i>CG15376</i>	0.631	0.0043
<i>Dlic</i>	0.625	0.0046
<i>Gr39b</i>	0.623	0.0047
<i>UbcD2</i>	0.623	0.0047
<i>GstE6</i>	0.622	0.0049
<i>CG14854</i>	0.621	0.005
<i>CG11131</i>	0.62	0.005

Gene Name	ERC Value	P-value
<i>CG9098</i>	0.62	0.005
<i>CG12680</i>	0.619	0.0052
<i>CG14709</i>	0.619	0.0052
<i>CG5142</i>	0.619	0.0052
<i>14-3-3μ</i>	0.618	0.0055
<i>CG17019</i>	0.618	0.0055
<i>l(2)NC136</i>	0.618	0.0055
<i>Nipsnap</i>	0.615	0.0058
<i>Cbl</i>	0.614	0.0059
<i>Ubx</i>	0.614	0.0059
<i>Kdm4B</i>	0.613	0.006
<i>Rad51C</i>	0.613	0.006
<i>CG33172</i>	0.612	0.0062
<i>Doa</i>	0.612	0.0062
<i>RpL35A</i>	0.61	0.0064
<i>CG31739</i>	0.608	0.0065
<i>na</i>	0.608	0.0065
<i>Tsp5D</i>	0.608	0.0065
<i>CG5611</i>	0.607	0.0068
<i>SPoCk</i>	0.606	0.0068
<i>CG10035</i>	0.603	0.0069
<i>CG32529</i>	0.603	0.0069
<i>DIP1</i>	0.603	0.0069
<i>CG9172</i>	0.602	0.0072
<i>CG12084</i>	0.601	0.0073
<i>CG32305</i>	0.601	0.0073
<i>p53</i>	0.601	0.0073
<i>Rpl115</i>	0.601	0.0073
<i>CG41434</i>	0.6	0.0077
<i>CG11155</i>	0.599	0.0077
<i>Tsp39D</i>	0.599	0.0077
<i>Gp1</i>	0.598	0.0079
<i>vg</i>	0.598	0.0079
<i>CG10916</i>	0.597	0.0081
<i>CG30421</i>	0.597	0.0081
<i>RanGap</i>	0.596	0.0083
<i>CG9817</i>	0.594	0.0084
<i>beat-lc</i>	0.593	0.0085
<i>CG1909</i>	0.593	0.0085
<i>hdm</i>	0.593	0.0085
<i>Kmn1</i>	0.593	0.0085
<i>Tsp68C</i>	0.593	0.0085
<i>CG11306</i>	0.592	0.0089
<i>CG14431</i>	0.592	0.0089
<i>CG8245</i>	0.592	0.0089
<i>Ch12</i>	0.59	0.0092
<i>Klp31E</i>	0.589	0.0093
<i>shi</i>	0.589	0.0093
<i>CG8100</i>	0.587	0.0095
<i>Grd</i>	0.585	0.0095
<i>Adgf-E</i>	0.583	0.0096
<i>CG12413</i>	0.583	0.0096
<i>CG30001</i>	0.582	0.0098
<i>CG3262</i>	0.582	0.0098
<i>CG4680</i>	0.582	0.0098
<i>Gef26</i>	0.582	0.0098

Gene Name	ERC Value	P-value
<i>CG6345</i>	0.58	0.0102
<i>CG8116</i>	0.58	0.0102
<i>CG1888</i>	0.579	0.0104
<i>CG4019</i>	0.578	0.0105
<i>Trl</i>	0.576	0.0105
<i>dec-1</i>	0.575	0.0106
<i>beat-lla</i>	0.573	0.0107
<i>bt</i>	0.572	0.0108
<i>CG31676</i>	0.572	0.0108
<i>CG31898</i>	0.572	0.0108
<i>CG17333</i>	0.571	0.0111
<i>PpV</i>	0.571	0.0111
<i>lic</i>	0.57	0.0113
<i>CG15353</i>	0.569	0.0114
<i>CG6325</i>	0.569	0.0114
<i>trk</i>	0.569	0.0114
<i>CG13343</i>	0.566	0.0118
<i>CG18619</i>	0.566	0.0118
<i>Ddr</i>	0.566	0.0118
<i>CG6465</i>	0.564	0.0119
<i>CG5895</i>	0.563	0.012
<i>lr56a</i>	0.563	0.012
<i>CG11778</i>	0.562	0.0122
<i>CG30428</i>	0.562	0.0122
<i>CG8944</i>	0.562	0.0122
<i>Cul-5</i>	0.562	0.0122
<i>CG12307</i>	0.561	0.0125
<i>CG17190</i>	0.561	0.0125
<i>CG1970</i>	0.561	0.0125
<i>CG40006</i>	0.561	0.0125
<i>Hk</i>	0.56	0.0129
<i>lr</i>	0.56	0.0129
<i>mus309</i>	0.56	0.0129
<i>CG32016</i>	0.559	0.0132
<i>CG9992</i>	0.559	0.0132
<i>Chc</i>	0.559	0.0132
<i>Arp87C</i>	0.558	0.0134
<i>CG14805</i>	0.558	0.0134
<i>CG3448</i>	0.558	0.0134
<i>DAT</i>	0.558	0.0134
<i>CG14442</i>	0.557	0.0138
<i>ed</i>	0.557	0.0138
<i>NKAIN</i>	0.557	0.0138
<i>CG8974</i>	0.556	0.0141
<i>CG9801</i>	0.556	0.0141
<i>Eaf</i>	0.556	0.0141
<i>hyd</i>	0.556	0.0141
<i>CG17211</i>	0.555	0.0144
<i>CG4078</i>	0.555	0.0144
<i>CG9215</i>	0.555	0.0144
<i>Appl</i>	0.554	0.0147
<i>dpr14</i>	0.553	0.0148
<i>png</i>	0.553	0.0148
<i>Andorra</i>	0.552	0.015
<i>Trus</i>	0.552	0.015
<i>Tsf1</i>	0.552	0.015

Gene Name	ERC Value	P-value
<i>CG2321</i>	0.551	0.0152
<i>Ets21C</i>	0.551	0.0152
<i>lrtp</i>	0.55	0.0154
<i>Orc5</i>	0.55	0.0154
<i>CG12288</i>	0.549	0.0156
<i>CG5327</i>	0.549	0.0156
<i>CG7956</i>	0.548	0.0158
<i>CG14047</i>	0.547	0.0159
<i>CG32459</i>	0.547	0.0159
<i>CG9293</i>	0.547	0.0159
<i>Rbcn-3A</i>	0.547	0.0159
<i>CG11251</i>	0.546	0.0162
<i>Mtl</i>	0.546	0.0162
<i>stai</i>	0.546	0.0162
<i>CG14075</i>	0.545	0.0165
<i>TMS1</i>	0.545	0.0165
<i>CG13121</i>	0.544	0.0167
<i>CG16989</i>	0.544	0.0167
<i>CG34104</i>	0.544	0.0167
<i>CG3984</i>	0.544	0.0167
<i>Moca-cyp</i>	0.544	0.0167
<i>ver</i>	0.543	0.0171
<i>CG11071</i>	0.542	0.0172
<i>CG32442</i>	0.542	0.0172
<i>CG5439</i>	0.542	0.0172
<i>CG17528</i>	0.541	0.0175
<i>CG14839</i>	0.54	0.0176
<i>CG1806</i>	0.54	0.0176
<i>glsh</i>	0.54	0.0176
<i>gol</i>	0.54	0.0176
<i>Gr59b</i>	0.54	0.0176
<i>CG34284</i>	0.539	0.018
<i>Or65a</i>	0.538	0.0181
<i>CG10481</i>	0.537	0.0182
<i>CG9109</i>	0.537	0.0182
<i>l(2)01289</i>	0.537	0.0182
<i>Sp1</i>	0.537	0.0182
<i>a6</i>	0.536	0.0186
<i>CG10948</i>	0.536	0.0186
<i>CG34401</i>	0.536	0.0186
<i>CG8323</i>	0.536	0.0186
<i>spn-B</i>	0.536	0.0186
<i>CG8552</i>	0.535	0.019
<i>CG8909</i>	0.535	0.019
<i>llp2</i>	0.535	0.019
<i>Prosalpha5</i>	0.535	0.019
<i>Sptr</i>	0.534	0.0194
<i>CG8538</i>	0.533	0.0195
<i>Cpr72Ea</i>	0.533	0.0195
<i>Nfl</i>	0.533	0.0195
<i>CG10681</i>	0.532	0.0197
<i>CG13334</i>	0.532	0.0197
<i>CG31226</i>	0.531	0.0199
<i>CG3894</i>	0.531	0.0199
<i>CG7536</i>	0.531	0.0199
<i>CG11668</i>	0.53	0.0202

Gene Name	ERC Value	P-value
<i>CG2059</i>	0.529	0.0203
<i>Samuel</i>	0.529	0.0203
<i>CG32121</i>	0.528	0.0205
<i>lpk2</i>	0.528	0.0205
<i>It</i>	0.528	0.0205
<i>rut</i>	0.528	0.0205
<i>Atx2</i>	0.527	0.0208
<i>CG32732</i>	0.527	0.0208
<i>CG3568</i>	0.527	0.0208
<i>CG4045</i>	0.527	0.0208
<i>CG4565</i>	0.527	0.0208
<i>CG8678</i>	0.527	0.0208
<i>mthl14</i>	0.527	0.0208
<i>Alk</i>	0.526	0.0214
<i>CG9505</i>	0.526	0.0214
<i>Sox21a</i>	0.526	0.0214
<i>AP-1gamma</i>	0.525	0.0217
<i>CG11750</i>	0.525	0.0217
<i>ft</i>	0.525	0.0217
<i>sca6</i>	0.525	0.0217
<i>CG33096</i>	0.523	0.0221
<i>vap</i>	0.523	0.0221
<i>CG10424</i>	0.522	0.0223
<i>CG15643</i>	0.521	0.0223
<i>CG9053</i>	0.521	0.0223
<i>dbr</i>	0.521	0.0223
<i>alpha-Cat</i>	0.52	0.0226
<i>CG2617</i>	0.52	0.0226
<i>CG7509</i>	0.52	0.0226
<i>Prosbeta7</i>	0.52	0.0226
<i>CG11454</i>	0.519	0.023
<i>CG17048</i>	0.519	0.023
<i>CG5791</i>	0.519	0.023
<i>Cpr49Aa</i>	0.519	0.023
<i>D2R</i>	0.519	0.023
<i>CG1233</i>	0.518	0.0234
<i>Sp1</i>	0.518	0.0234
<i>InR</i>	0.518	0.0234
<i>Vha36-1</i>	0.518	0.0234
<i>CG15020</i>	0.517	0.0238
<i>CG42251</i>	0.517	0.0238
<i>CG9917</i>	0.517	0.0238
<i>Cyp9b2</i>	0.517	0.0238
<i>ldbr</i>	0.517	0.0238
<i>CG6204</i>	0.516	0.0242
<i>mRps30</i>	0.516	0.0242
<i>CG1120</i>	0.515	0.0244
<i>CG1240</i>	0.515	0.0244
<i>CG1316</i>	0.515	0.0244
<i>CG15117</i>	0.515	0.0244
<i>Muc91C</i>	0.515	0.0244
<i>r</i>	0.515	0.0244
<i>Bin1</i>	0.514	0.025
<i>CG10561</i>	0.514	0.025
<i>CG2943</i>	0.514	0.025
<i>CG32350</i>	0.514	0.025

Table 6.S14 Continued

Gene Name	ERC Value	P-value
<i>Hex-A</i>	0.512	0.0253
<i>Obp44a</i>	0.512	0.0253
<i>trio</i>	0.512	0.0253
<i>Wnt6</i>	0.512	0.0253
<i>Ama</i>	0.511	0.0257
<i>CG7227</i>	0.511	0.0257
<i>Dip2</i>	0.511	0.0257
<i>Ucrh</i>	0.511	0.0257
<i>CG1109</i>	0.51	0.026
<i>CG17669</i>	0.51	0.026
<i>dor</i>	0.51	0.026
<i>Pfxf</i>	0.51	0.026
<i>CG2694</i>	0.509	0.0264
<i>ZC3H3</i>	0.509	0.0264
<i>CG17270</i>	0.508	0.0266
<i>CG31675</i>	0.508	0.0266
<i>CG33281</i>	0.508	0.0266
<i>CG7146</i>	0.508	0.0266
<i>CG2865</i>	0.507	0.0269
<i>CG13116</i>	0.506	0.027
<i>CG2712</i>	0.506	0.027
<i>CG6933</i>	0.506	0.027
<i>Spf45</i>	0.506	0.027
<i>awd</i>	0.505	0.0274
<i>bigmax</i>	0.505	0.0274
<i>CG13377</i>	0.505	0.0274
<i>CG16700</i>	0.505	0.0274
<i>mRplL3</i>	0.505	0.0274
<i>Ptp4E</i>	0.505	0.0274
<i>SmD3</i>	0.505	0.0274
<i>CG12012</i>	0.504	0.028
<i>CG32982</i>	0.504	0.028
<i>CG42360</i>	0.504	0.028
<i>CG31004</i>	0.503	0.0283
<i>CG10133</i>	0.502	0.0284
<i>grk</i>	0.502	0.0284
<i>Muc55B</i>	0.502	0.0284
<i>CG15738</i>	0.5	0.0286
<i>CG7772</i>	0.5	0.0286
<i>CG34230</i>	0.499	0.0288
<i>CG4872</i>	0.499	0.0288
<i>pll</i>	0.499	0.0288
<i>Tl</i>	0.499	0.0288
<i>wuho</i>	0.499	0.0288
<i>CG10362</i>	0.498	0.0293
<i>CG10486</i>	0.498	0.0293
<i>fidipidine</i>	0.498	0.0293
<i>wupA</i>	0.498	0.0293
<i>CG14115</i>	0.497	0.0296
<i>CG31224</i>	0.497	0.0296
<i>CG5543</i>	0.497	0.0296
<i>CG7265</i>	0.497	0.0296
<i>Lsm11</i>	0.497	0.0296
<i>Rad17</i>	0.497	0.0296
<i>spz</i>	0.497	0.0296
<i>sv</i>	0.497	0.0296

Gene Name	ERC Value	P-value
<i>BM-40-SPA</i>	0.496	0.0304
<i>f</i>	0.496	0.0304
<i>Lasp</i>	0.496	0.0304
<i>Rhp</i>	0.496	0.0304
<i>CG7126</i>	0.495	0.0307
<i>CG7510</i>	0.495	0.0307
<i>Src42A</i>	0.495	0.0307
<i>CG10654</i>	0.493	0.031
<i>CG17278</i>	0.493	0.031
<i>CG31431</i>	0.493	0.031
<i>Dp</i>	0.493	0.031
<i>Gr43b</i>	0.493	0.031
<i>CG12655</i>	0.492	0.0314
<i>CG13001</i>	0.492	0.0314
<i>CG8677</i>	0.492	0.0314
<i>CG31326</i>	0.491	0.0317
<i>CG34266</i>	0.491	0.0317
<i>CG5482</i>	0.491	0.0317
<i>pie</i>	0.491	0.0317
<i>Cad74A</i>	0.49	0.0321
<i>CG10659</i>	0.49	0.0321
<i>CG11211</i>	0.49	0.0321
<i>CG13192</i>	0.49	0.0321
<i>CG13972</i>	0.489	0.0324
<i>CG7755</i>	0.489	0.0324
<i>Nnf1a</i>	0.489	0.0324
<i>CG13500</i>	0.488	0.0327
<i>PpY-55A</i>	0.488	0.0327
<i>Sxl</i>	0.488	0.0327
<i>CG11755</i>	0.487	0.033
<i>CG15661</i>	0.487	0.033
<i>CG3592</i>	0.487	0.033
<i>CG4749</i>	0.487	0.033
<i>Scgdelta</i>	0.487	0.033
<i>CG12121</i>	0.485	0.0334
<i>CG6230</i>	0.485	0.0334
<i>Eps-15</i>	0.485	0.0334
<i>Cortactin</i>	0.484	0.0337
<i>dpr11</i>	0.484	0.0337
<i>shg</i>	0.484	0.0337
<i>xmas-2</i>	0.484	0.0337
<i>blue</i>	0.483	0.0341
<i>CG14695</i>	0.483	0.0341
<i>CG30441</i>	0.483	0.0341
<i>CG6216</i>	0.483	0.0341
<i>CG40191</i>	0.482	0.0344
<i>glec</i>	0.482	0.0344
<i>Tsp96F</i>	0.482	0.0344
<i>CG12379</i>	0.481	0.0347
<i>CG30497</i>	0.481	0.0347
<i>CG3338</i>	0.481	0.0347
<i>CG9672</i>	0.481	0.0347
<i>arm</i>	0.48	0.035
<i>CG11141</i>	0.48	0.035
<i>CG15464</i>	0.48	0.035
<i>Drak</i>	0.48	0.035

Gene Name	ERC Value	P-value
<i>Hr39</i>	0.48	0.035
<i>ome</i>	0.48	0.035
<i>Pino</i>	0.48	0.035
<i>beta3GalTII</i>	0.479	0.0357
<i>CG10073</i>	0.479	0.0357
<i>CG1647</i>	0.479	0.0357
<i>H2.0</i>	0.479	0.0357
<i>Nmdar2</i>	0.479	0.0357
<i>sda</i>	0.479	0.0357
<i>CG30281</i>	0.478	0.0362
<i>CG4726</i>	0.478	0.0362
<i>CG8498</i>	0.478	0.0362
<i>CG14722</i>	0.477	0.0365
<i>fit</i>	0.477	0.0365
<i>RpS26</i>	0.477	0.0365
<i>koko</i>	0.476	0.0368
<i>RFC38</i>	0.476	0.0368
<i>CG13339</i>	0.475	0.0369
<i>Eio68beta</i>	0.475	0.0369
<i>kkv</i>	0.475	0.0369
<i>ap</i>	0.474	0.0372
<i>CG4390</i>	0.474	0.0372
<i>Synd</i>	0.474	0.0372
<i>TBPH</i>	0.474	0.0372
<i>CG2124</i>	0.473	0.0376
<i>CG40198</i>	0.473	0.0376
<i>elF2B-alpha</i>	0.473	0.0376
<i>RhoL</i>	0.473	0.0376
<i>Roc2</i>	0.473	0.0376
<i>CG13532</i>	0.472	0.038
<i>CG17490</i>	0.472	0.038
<i>CG3592</i>	0.472	0.038
<i>CG3566</i>	0.472	0.038
<i>CG3812</i>	0.472	0.038
<i>CG7903</i>	0.472	0.038
<i>Gr77a</i>	0.472	0.038
<i>CG17683</i>	0.471	0.0386
<i>LRP1</i>	0.471	0.0386
<i>Mef2</i>	0.471	0.0386
<i>CG10165</i>	0.47	0.0389
<i>CG12502</i>	0.47	0.0389
<i>CG2852</i>	0.47	0.0389
<i>CG33703</i>	0.47	0.0389
<i>klar</i>	0.47	0.0389
<i>CG5550</i>	0.469	0.0394
<i>N</i>	0.469	0.0394
<i>Pez</i>	0.469	0.0394
<i>CG8191</i>	0.468	0.0396
<i>l(2)k14505</i>	0.468	0.0396
<i>CG10830</i>	0.466	0.0398
<i>CG5961</i>	0.466	0.0398
<i>beat-VI</i>	0.465	0.04
<i>arm</i>	0.465	0.04
<i>CG9413</i>	0.465	0.04
<i>stj</i>	0.465	0.04
<i>CG3776</i>	0.464	0.0404

Gene Name	ERC Value	P-value
<i>kat80</i>	0.464	0.0404
<i>mRpl19</i>	0.464	0.0404
<i>CG33057</i>	0.463	0.0406
<i>CG3376</i>	0.463	0.0406
<i>CG8370</i>	0.463	0.0406
<i>Rad1</i>	0.463	0.0406
<i>CG31712</i>	0.462	0.041
<i>CG6084</i>	0.462	0.041
<i>CG8159</i>	0.462	0.041
<i>DhpD</i>	0.462	0.041
<i>Rb97D</i>	0.462	0.041
<i>Traf-like</i>	0.462	0.041
<i>CG11377</i>	0.461	0.0415
<i>CG15571</i>	0.461	0.0415
<i>CG7328</i>	0.461	0.0415
<i>Sh</i>	0.461	0.0415
<i>CG32040</i>	0.46	0.0419
<i>exd</i>	0.46	0.0419
<i>Vps45</i>	0.46	0.0419
<i>CG31036</i>	0.459	0.0422
<i>CG31787</i>	0.459	0.0422
<i>CG33969</i>	0.459	0.0422
<i>CG5585</i>	0.459	0.0422
<i>Ripalpha</i>	0.459	0.0422
<i>CG15865</i>	0.458	0.0426
<i>CG4022</i>	0.458	0.0426
<i>S6kII</i>	0.458	0.0426
<i>shu</i>	0.458	0.0426
<i>CG14629</i>	0.457	0.043
<i>CG8539</i>	0.457	0.043
<i>hkl</i>	0.457	0.043
<i>l(2)37Ce</i>	0.457	0.043
<i>TwdIG</i>	0.457	0.043
<i>CG10417</i>	0.456	0.0434
<i>CG10462</i>	0.456	0.0434
<i>CG12848</i>	0.456	0.0434
<i>CG12851</i>	0.456	0.0434
<i>CG16704</i>	0.456	0.0434
<i>CG7597</i>	0.456	0.0434
<i>Cyp611</i>	0.456	0.0434
<i>mei-41</i>	0.456	0.0434
<i>Rpl1140</i>	0.455	0.0441
CG10560	0.455	0.0441
<i>CG13745</i>	0.455	0.0441
<i>CG14780</i>	0.455	0.0441
<i>CG3014</i>	0.455	0.0441
<i>CG31065</i>	0.454	0.0446
<i>KH1</i>	0.454	0.0446
<i>Brf</i>	0.452	0.0448
<i>CG16985</i>	0.452	0.0448
<i>CG1907</i>	0.452	0.0448
<i>CG42748</i>	0.452	0.0448
<i>Ugt36Ba</i>	0.452	0.0448
<i>CG11870</i>	0.451	0.0452
<i>CG6656</i>	0.451	0.0452
<i>CG8814</i>	0.451	0.0452

Gene Name	ERC Value	P-value
<i>dm</i>	0.451	0.0452
<i>CG31689</i>	0.45	0.0456
<i>MSBP</i>	0.45	0.0456
<i>prc</i>	0.45	0.0456
<i>Spn43Ad</i>	0.45	0.0456
<i>AlkB</i>	0.449	0.0459
<i>CG13253</i>	0.449	0.0459
<i>CG15028</i>	0.449	0.0459
<i>CG18480</i>	0.449	0.0459
<i>eIF5</i>	0.449	0.0459
<i>Gr89a</i>	0.449	0.0459
<i>CG15523</i>	0.448	0.0465
<i>CG3091</i>	0.448	0.0465
<i>CG3534</i>	0.448	0.0465
<i>CG5780</i>	0.448	0.0465
<i>CrebB-17A</i>	0.448	0.0465
<i>dimm</i>	0.448	0.0465
<i>disp</i>	0.448	0.0465
<i>lilli</i>	0.448	0.0465
<i>Ptth</i>	0.448	0.0465
<i>Arp11</i>	0.447	0.0473
<i>CG30466</i>	0.447	0.0473
<i>CG31659</i>	0.447	0.0473
<i>CG5734</i>	0.447	0.0473
<i>Kif3C</i>	0.447	0.0473
<i>PsGEF</i>	0.447	0.0473
<i>CG13707</i>	0.446	0.0478
CG18806	0.446	0.0478
<i>cmet</i>	0.446	0.0478
<i>CS-2</i>	0.445	0.0481
<i>Lrt</i>	0.445	0.0481
<i>Map205</i>	0.445	0.0481
<i>Sbf</i>	0.445	0.0481
<i>yl</i>	0.445	0.0481
<i>Atf3</i>	0.444	0.0486
<i>CG13444</i>	0.444	0.0486
<i>CG2641</i>	0.444	0.0486
<i>CG31098</i>	0.444	0.0486
<i>CG5955</i>	0.444	0.0486
<i>CG9203</i>	0.444	0.0486
<i>Gap1</i>	0.444	0.0486
<i>CG31917</i>	0.443	0.0492
<i>CG9044</i>	0.443	0.0492
<i>tna</i>	0.443	0.0492
<i>CG3808</i>	0.442	0.0495
<i>drl</i>	0.442	0.0495
<i>Dsk</i>	0.442	0.0495
<i>GABA-B-R2</i>	0.442	0.0495
<i>Rac1</i>	0.442	0.0495
<i>Ac3</i>	0.441	0.0499
<i>cals</i>	0.441	0.0499
<i>CG4683</i>	0.441	0.0499
<i>net</i>	0.441	0.0499
<i>osm-1</i>	0.441	0.0499
<i>Ant2</i>	0.44	0.0504
c(2)M	0.44	0.0504

Table 6.S14 Continued

Gene Name	ERC Value	P-value
CG12484	0.44	0.0504
CG5933	0.44	0.0504
CG6689	0.44	0.0504
Eaat1	0.44	0.0504
granny-smith	0.44	0.0504
Inos	0.44	0.0504
phf	0.44	0.0504
VhaM9.7-d	0.44	0.0504
CG42826	0.439	0.0513
CG5398	0.439	0.0513
RhoGAPp19	0.439	0.0513
tsl	0.439	0.0513
CG11638	0.438	0.0516
CG15914	0.438	0.0516
CG16865	0.438	0.0516
CG5746	0.438	0.0516
CG5909	0.438	0.0516
CG7945	0.438	0.0516
CG8006	0.438	0.0516
E(bx)	0.438	0.0516
CG16941	0.437	0.0523
mel-S332	0.437	0.0523
CG11851	0.436	0.0525
CG17283	0.436	0.0525
CG5379	0.436	0.0525
CG8931	0.436	0.0525
Fs	0.436	0.0525
Ttb5	0.436	0.0525
Vdup1	0.436	0.0525
CG10512	0.435	0.0532
CG13272	0.435	0.0532
CG15404	0.435	0.0532
CG30046	0.435	0.0532
SP2353	0.435	0.0532
Taf4	0.435	0.0532
CG2774	0.434	0.0537
CG5217	0.434	0.0537
lr94c	0.434	0.0537
Liprin-alpha	0.434	0.0537
ppk7	0.434	0.0537
CG13126	0.433	0.0541
CG14764	0.433	0.0541
CG8202	0.433	0.0541
CG9592	0.433	0.0541
Atac1	0.432	0.0545
CG5793	0.432	0.0545
CG6023	0.432	0.0545
Or98b	0.432	0.0545
Pi3K21B	0.432	0.0545
bib	0.431	0.055
CG14676	0.431	0.055
CG16775	0.431	0.055
CG34007	0.431	0.055
cin	0.431	0.055
eve	0.431	0.055
mth	0.431	0.055

Gene Name	ERC Value	P-value
Rab-RP3	0.431	0.055
Tif-1A	0.431	0.055
timeout	0.431	0.055
vps2	0.431	0.055
Yeti	0.431	0.055
CG11210	0.43	0.056
CG17162	0.43	0.056
CSN4	0.43	0.056
HLH106	0.43	0.056
CG10713	0.429	0.0564
CG11069	0.429	0.0564
CG1832	0.429	0.0564
CG3838	0.429	0.0564
CG6340	0.429	0.0564
CG6745	0.429	0.0564
Gr2a	0.429	0.0564
Pk61C	0.429	0.0564
CG10732	0.428	0.0571
CG11356	0.428	0.0571
CG12637	0.428	0.0571
CG32437	0.428	0.0571
Crk	0.428	0.0571
CG12050	0.427	0.0576
CG15740	0.427	0.0576
CG1637	0.427	0.0576
Hex-12	0.427	0.0576
Mat89Ba	0.427	0.0576
RhoGAP15E	0.427	0.0576
a10	0.426	0.0581
CG14195	0.426	0.0581
CG32750	0.426	0.0581
CG3769	0.426	0.0581
CG7992	0.426	0.0581
CG8079	0.426	0.0581
Fur2	0.426	0.0581
kek1	0.426	0.0581
Patj	0.426	0.0581
CG2993	0.425	0.0589
mus308	0.425	0.0589
CG30291	0.424	0.0591
CG9007	0.424	0.0591
ppk11	0.424	0.0591
CG12179	0.423	0.0594
CG13640	0.423	0.0594
CG14565	0.423	0.0594
CG33289	0.423	0.0594
CG5808	0.423	0.0594
CG8671	0.423	0.0594
grass	0.423	0.0594
RhoGAP100	0.423	0.0594
Smb	0.423	0.0594
Ca-alpha1T	0.422	0.0602
CG11674	0.422	0.0602
CG31145	0.422	0.0602
CG8959	0.422	0.0602
CG9919	0.422	0.0602

Gene Name	ERC Value	P-value
Glycogenin	0.422	0.0602
Grip75	0.422	0.0602
Nup154	0.422	0.0602
Or23a	0.422	0.0602
Sps2	0.422	0.0602
Stim	0.422	0.0602
CG14174	0.421	0.0612
CG32850	0.421	0.0612
Hr4	0.421	0.0612
ll2j09851	0.421	0.0612
Asph	0.42	0.0615
CG13284	0.42	0.0615
CG14767	0.42	0.0615
CG2862	0.42	0.0615
CG4678	0.42	0.0615
CG5235	0.42	0.0615
Ssb-c31a	0.42	0.0615
CG1983	0.419	0.0622
CG42330	0.419	0.0622
CG4404	0.419	0.0622
DNApol-gam	0.419	0.0622
sens	0.419	0.0622
Sra-1	0.419	0.0622
beat-1a	0.418	0.0627
CG12187	0.418	0.0627
CG30008	0.418	0.0627
CG5287	0.418	0.0627
Cyp28a5	0.418	0.0627
Mp20	0.418	0.0627
Syt7	0.418	0.0627
CG11267	0.417	0.0633
CG2162	0.417	0.0633
CG3502	0.417	0.0633
CG4789	0.417	0.0633
g	0.417	0.0633
CG11133	0.416	0.0638
CG15570	0.416	0.0638
CG34045	0.416	0.0638
CG34127	0.416	0.0638
CG4198	0.416	0.0638
CG7009	0.416	0.0638
Ssl1	0.416	0.0638
vsg	0.416	0.0638
wmd	0.416	0.0638
Act42A	0.415	0.0646
CG7330	0.415	0.0646
Ciao1	0.415	0.0646
magu	0.415	0.0646
Sbp2	0.415	0.0646
Ten-m	0.415	0.0646
CG16970	0.414	0.0651
CG8378	0.414	0.0651
NP15.6	0.414	0.0651
Nsf2	0.414	0.0651
Aats-met	0.413	0.0655
bl	0.413	0.0655

Gene Name	ERC Value	P-value
blot	0.413	0.0655
CG10092	0.413	0.0655
CG13725	0.413	0.0655
CG14624	0.413	0.0655
CG15922	0.413	0.0655
CG3107	0.413	0.0655
CG34297	0.413	0.0655
grp	0.413	0.0655
Sep5	0.412	0.0664
CG14314	0.412	0.0664
CG4666	0.412	0.0664
CHKov2	0.412	0.0664
Dcr-1	0.412	0.0664
Ets96B	0.412	0.0664
gp210	0.412	0.0664
CG12539	0.411	0.067
CG14441	0.411	0.067
CG18659	0.411	0.067
Su(fu)	0.411	0.067
tud	0.411	0.067
asun	0.41	0.0675
CG12140	0.41	0.0675
CG14894	0.41	0.0675
CG31266	0.41	0.0675
CG4877	0.41	0.0675
CG13031	0.409	0.0679
CG31890	0.409	0.0679
Cpr65Eb	0.409	0.0679
Rfx	0.409	0.0679
CG31551	0.408	0.0683
CG9253	0.408	0.0683
Pp1-87B	0.408	0.0683
wgn	0.408	0.0683
CG10680	0.407	0.0686
CG12926	0.407	0.0686
CG14515	0.407	0.0686
sli	0.407	0.0686
CalpC	0.406	0.069
CG32758	0.406	0.069
Atox1	0.405	0.0692
CG10188	0.405	0.0692
CG42313	0.405	0.0692
CG9171	0.405	0.0692
sad	0.405	0.0692
Mad	0.404	0.0696
CG12594	0.403	0.0697
CG1552	0.403	0.0697
CG2316	0.403	0.0697
Cp38	0.403	0.0697
lz	0.403	0.0697
toy	0.403	0.0697
Cdk4	0.402	0.0703
CG10166	0.402	0.0703
CG11163	0.402	0.0703
CG13884	0.402	0.0703
gwg	0.402	0.0703

Gene Name	ERC Value	P-value
Ppf1	0.402	0.0703
RpL29	0.402	0.0703
Taz	0.402	0.0703
tsu	0.402	0.0703
CG1275	0.401	0.0711
CG17083	0.401	0.0711
CG33286	0.401	0.0711
CG34317	0.401	0.0711
CG9449	0.401	0.0711
CG9904	0.401	0.0711
lab	0.401	0.0711
CG10669	0.4	0.0717
CG13319	0.4	0.0717
CG32832	0.4	0.0717
CG3760	0.4	0.0717
Femcoat	0.4	0.0717
Fer1HCH	0.4	0.0717
Orc4	0.4	0.0717
repo	0.4	0.0717
Bteb2	0.399	0.0724
CG10395	0.399	0.0724
CG13407	0.399	0.0724
CG32017	0.399	0.0724
CG4741	0.399	0.0724
CG6927	0.399	0.0724
pes	0.399	0.0724
CG12126	0.398	0.0731
CG9147	0.398	0.0731
gbb	0.398	0.0731
Gr93a	0.398	0.0731
Mo25	0.398	0.0731
CcapR	0.397	0.0735
CG12507	0.397	0.0735
CG15432	0.397	0.0735
CG31698	0.397	0.0735
CG6005	0.397	0.0735
pnr	0.397	0.0735
CG14655	0.396	0.0741
CG32712	0.396	0.0741
CG33641	0.396	0.0741
CG42554	0.396	0.0741
CG7593	0.396	0.0741
GABPI	0.396	0.0741
CG10496	0.395	0.0746
CG11927	0.395	0.0746
CG13376	0.395	0.0746
CG30440	0.395	0.0746
CG3226	0.395	0.0746
CG34008	0.395	0.0746
obst-G	0.395	0.0746
RpII18	0.395	0.0746
betaInt-nu	0.394	0.0753
CG14239	0.394	0.0753
CG5705	0.394	0.0753
CG8239	0.394	0.0753
MED21	0.394	0.0753

Table 6.S14 Continued

Gene Name	ERC Value	P-value
<i>Or83b</i>	0.394	0.0753
<i>Pdp</i>	0.394	0.0753
<i>RASSF8</i>	0.394	0.0753
<i>CG11985</i>	0.393	0.076
<i>CG13074</i>	0.393	0.076
<i>CG9004</i>	0.393	0.076
<i>ds</i>	0.393	0.076
<i>wdb</i>	0.393	0.076
<i>ara</i>	0.392	0.0765
<i>CG31752</i>	0.392	0.0765
<i>CG3223</i>	0.392	0.0765
<i>CG6055</i>	0.392	0.0765
<i>CG9825</i>	0.392	0.0765
<i>cuff</i>	0.392	0.0765
<i>gb</i>	0.392	0.0765
<i>l(1)G0289</i>	0.392	0.0765
<i>Reps</i>	0.392	0.0765
<i>CG3790</i>	0.391	0.0773
<i>CG6254</i>	0.391	0.0773
<i>CG9135</i>	0.391	0.0773
<i>CtBP</i>	0.391	0.0773
<i>Map60</i>	0.391	0.0773
<i>Rrp42</i>	0.391	0.0773
<i>CG10702</i>	0.39	0.0778
<i>CG17707</i>	0.39	0.0778
<i>CG31646</i>	0.39	0.0778
<i>CG4705</i>	0.39	0.0778
<i>CG6144</i>	0.39	0.0778
<i>Got2</i>	0.39	0.0778
<i>Tps1</i>	0.39	0.0778
<i>capaR</i>	0.389	0.0785
<i>CG1077</i>	0.389	0.0785
<i>CG12499</i>	0.389	0.0785
<i>CG14182</i>	0.389	0.0785
<i>CG31777</i>	0.389	0.0785
<i>CG5339</i>	0.389	0.0785
<i>CG9631</i>	0.389	0.0785
<i>La</i>	0.389	0.0785
<i>lace</i>	0.389	0.0785
<i>CG32343</i>	0.388	0.0793
<i>CG9247</i>	0.388	0.0793
<i>CG14635</i>	0.387	0.0795
<i>CG4751</i>	0.387	0.0795
<i>Gr36d</i>	0.387	0.0795
<i>proPO-A1</i>	0.387	0.0795
<i>beat-IIIb</i>	0.386	0.0798
<i>CG14882</i>	0.386	0.0798
<i>CG14997</i>	0.386	0.0798
<i>CG3517</i>	0.386	0.0798
<i>CG40351</i>	0.386	0.0798
<i>CG9008</i>	0.386	0.0798
<i>Lcch3</i>	0.386	0.0798
<i>Pomp</i>	0.386	0.0798
<i>rab3-GEF</i>	0.386	0.0798
<i>Ric</i>	0.386	0.0798
<i>RpL4</i>	0.386	0.0798

Gene Name	ERC Value	P-value
<i>Spc105R</i>	0.386	0.0798
<i>tutl</i>	0.386	0.0798
<i>beta-Spec</i>	0.385	0.081
<i>CG33985</i>	0.385	0.081
<i>CG42256</i>	0.385	0.081
<i>cos</i>	0.385	0.081
<i>Dic90F</i>	0.385	0.081
<i>squ</i>	0.385	0.081
<i>CG1138</i>	0.384	0.0815
<i>CG3259</i>	0.384	0.0815
<i>Ggamma1</i>	0.384	0.0815
<i>CG12182</i>	0.383	0.0818
<i>CG14082</i>	0.383	0.0818
<i>CG14435</i>	0.383	0.0818
<i>CG17751</i>	0.383	0.0818
<i>CG9797</i>	0.383	0.0818
<i>Spt20</i>	0.383	0.0818
<i>Ance-3</i>	0.382	0.0823
<i>CaMKI</i>	0.382	0.0823
<i>CKLR-17D</i>	0.382	0.0823
<i>CG13931</i>	0.382	0.0823
<i>CG42374</i>	0.382	0.0823
<i>CG7211</i>	0.382	0.0823
<i>CG7694</i>	0.382	0.0823
<i>eater</i>	0.382	0.0823
<i>glob.3</i>	0.382	0.0823
<i>lrd0a</i>	0.382	0.0823
<i>Wnt5</i>	0.382	0.0823
<i>CG10384</i>	0.381	0.0833
<i>CG10824</i>	0.381	0.0833
<i>CG11403</i>	0.381	0.0833
<i>CG11872</i>	0.381	0.0833
<i>CG3408</i>	0.381	0.0833
<i>CG9542</i>	0.381	0.0833
<i>CG9747</i>	0.381	0.0833
<i>dsd</i>	0.381	0.0833
<i>Pros29</i>	0.381	0.0833
<i>snv</i>	0.381	0.0833
<i>CG13295</i>	0.38	0.0842
<i>disco</i>	0.38	0.0842
<i>Ranbp16</i>	0.38	0.0842
<i>sun</i>	0.38	0.0842
<i>Syn2</i>	0.38	0.0842
<i>Treh</i>	0.38	0.0842
<i>Cda4</i>	0.379	0.0848
<i>CG12986</i>	0.379	0.0848
<i>CG17549</i>	0.379	0.0848
<i>CG17922</i>	0.379	0.0848
<i>CG5664</i>	0.379	0.0848
<i>Nmd3</i>	0.379	0.0848
<i>Pngl</i>	0.379	0.0848
<i>CG10222</i>	0.378	0.0854
<i>CG10650</i>	0.378	0.0854
<i>CG14072</i>	0.378	0.0854
<i>CG30203</i>	0.378	0.0854
<i>CG3106</i>	0.378	0.0854

Gene Name	ERC Value	P-value
<i>CG4844</i>	0.378	0.0854
<i>erm</i>	0.378	0.0854
<i>Rad51D</i>	0.378	0.0854
<i>CG10465</i>	0.377	0.0861
<i>CG14967</i>	0.377	0.0861
<i>CG34140</i>	0.377	0.0861
<i>CG6985</i>	0.377	0.0861
<i>lrf51b</i>	0.377	0.0861
<i>qkr58E-1</i>	0.377	0.0861
<i>Rp11</i>	0.377	0.0861
<i>CG31159</i>	0.376	0.0868
<i>CG42676</i>	0.376	0.0868
<i>CG9095</i>	0.376	0.0868
<i>CycD</i>	0.376	0.0868
<i>ras</i>	0.376	0.0868
<i>CG14302</i>	0.375	0.0872
<i>CG5860</i>	0.375	0.0872
<i>CG6296</i>	0.375	0.0872
<i>betaTub97E</i>	0.374	0.0875
<i>CG10265</i>	0.374	0.0875
<i>CG32463</i>	0.374	0.0875
<i>CG7120</i>	0.374	0.0875
<i>CG9541</i>	0.374	0.0875
<i>Gr9a</i>	0.374	0.0875
<i>mus301</i>	0.374	0.0875
<i>Scfp</i>	0.374	0.0875
<i>lchs</i>	0.373	0.0882
<i>CG14937</i>	0.373	0.0882
<i>CG5978</i>	0.373	0.0882
<i>CG9986</i>	0.373	0.0882
<i>Gr61a</i>	0.373	0.0882
<i>Kaz1-ORFB</i>	0.373	0.0882
<i>kto</i>	0.373	0.0882
<i>melt</i>	0.373	0.0882
<i>S1P</i>	0.373	0.0882
<i>Atg4</i>	0.372	0.089
<i>casp</i>	0.372	0.089
<i>CG14969</i>	0.372	0.089
<i>CG15438</i>	0.372	0.089
<i>CG7222</i>	0.372	0.089
<i>CG9649</i>	0.372	0.089
<i>krz</i>	0.372	0.089
<i>Art4</i>	0.371	0.0896
<i>CG11357</i>	0.371	0.0896
<i>CG11835</i>	0.371	0.0896
<i>CG12374</i>	0.371	0.0896
<i>CG12943</i>	0.371	0.0896
<i>CG14007</i>	0.371	0.0896
<i>CG14929</i>	0.371	0.0896
<i>CG2990</i>	0.371	0.0896
<i>CG33771</i>	0.371	0.0896
<i>Edem2</i>	0.371	0.0896
<i>Hsp60D</i>	0.371	0.0896
<i>Rpb4</i>	0.371	0.0896
<i>scb</i>	0.371	0.0896
<i>slam</i>	0.371	0.0896

Gene Name	ERC Value	P-value
<i>calyso</i>	0.37	0.0909
<i>CG10249</i>	0.37	0.0909
<i>CG13049</i>	0.37	0.0909
<i>CG13982</i>	0.37	0.0909
<i>CG14526</i>	0.37	0.0909
<i>CG15522</i>	0.37	0.0909
<i>CG15649</i>	0.37	0.0909
<i>CG1902</i>	0.37	0.0909
<i>CG8097</i>	0.37	0.0909
<i>Lgr3</i>	0.37	0.0909
<i>Lig4</i>	0.37	0.0909
<i>pgant3</i>	0.37	0.0909
<i>SMC2</i>	0.37	0.0909
<i>Ugt35a</i>	0.37	0.0909
<i>CG16854</i>	0.369	0.0922
<i>CG1962</i>	0.369	0.0922
<i>CG8408</i>	0.369	0.0922
<i>Eno</i>	0.369	0.0922
<i>GstD9</i>	0.369	0.0922
<i>prominin-like</i>	0.369	0.0922
<i>Prosalpha6T</i>	0.369	0.0922
<i>shcp</i>	0.369	0.0922
<i>CG11149</i>	0.368	0.0929
<i>CG14826</i>	0.368	0.0929
<i>CG1561</i>	0.368	0.0929
<i>CG15753</i>	0.368	0.0929
<i>CG33253</i>	0.368	0.0929
<i>Fs(2)Ket</i>	0.368	0.0929
<i>jim</i>	0.368	0.0929
<i>por</i>	0.368	0.0929
<i>Vsx1</i>	0.368	0.0929
<i>CG12420</i>	0.367	0.0937
<i>CG31360</i>	0.367	0.0937
<i>CG6523</i>	0.367	0.0937
<i>CG7069</i>	0.367	0.0937
<i>CG8928</i>	0.367	0.0937
<i>coil</i>	0.367	0.0937
<i>D12</i>	0.367	0.0937
<i>Myb</i>	0.367	0.0937
<i>Patr-1</i>	0.367	0.0937
<i>silbo</i>	0.367	0.0937
<i>BicD</i>	0.366	0.0946
<i>l(1)G0007</i>	0.366	0.0946
<i>wg</i>	0.366	0.0946
<i>Art8</i>	0.365	0.0949
<i>CG14450</i>	0.365	0.0949
<i>CG14618</i>	0.365	0.0949
<i>CG30419</i>	0.365	0.0949
<i>CG8916</i>	0.365	0.0949
<i> fend</i>	0.365	0.0949
<i>l(2)k09022</i>	0.365	0.0949
<i>Mis12</i>	0.365	0.0949
<i>myoglianin</i>	0.365	0.0949
<i>CG11560</i>	0.364	0.0957
<i>CG13895</i>	0.364	0.0957
<i>CG6607</i>	0.364	0.0957

Gene Name	ERC Value	P-value
<i>CG7488</i>	0.364	0.0957
<i>Cyp49a1</i>	0.364	0.0957
<i>fw</i>	0.364	0.0957
<i>H</i>	0.363	0.0962
<i>l(2)k05819</i>	0.363	0.0962
<i>nimA</i>	0.363	0.0962
<i>CG12042</i>	0.362	0.0965
<i>Fanc1</i>	0.362	0.0965
<i>ix</i>	0.362	0.0965
<i>kek5</i>	0.362	0.0965
<i>CG15696</i>	0.361	0.0968
<i>Dip-B</i>	0.361	0.0968
<i>Hcf</i>	0.361	0.0968
<i>kcc</i>	0.361	0.0968
<i>levy</i>	0.361	0.0968
<i>Obp99c</i>	0.361	0.0968
<i>CG11137</i>	0.36	0.0974
<i>CG33635</i>	0.36	0.0974
<i>CG6503</i>	0.36	0.0974
<i>CG8031</i>	0.36	0.0974
<i>sinu</i>	0.36	0.0974
<i>CG12439</i>	0.359	0.0978
<i>CG14301</i>	0.359	0.0978
<i>CG31812</i>	0.359	0.0978
<i>CG4038</i>	0.359	0.0978
<i>CG42449</i>	0.359	0.0978
<i>CG6276</i>	0.359	0.0978
<i>mip120</i>	0.359	0.0978
<i>Pp2B-14D</i>	0.359	0.0978
<i>VhaM9.7-a</i>	0.359	0.0978
<i>CG32563</i>	0.358	0.0986
<i>Mih1</i>	0.358	0.0986
<i>CG13876</i>	0.357	0.0988
<i>CG14103</i>	0.357	0.0988
<i>CG14657</i>	0.357	0.0988
<i>CG17304</i>	0.357	0.0988
<i>CG34355</i>	0.357	0.0988
<i>CG4480</i>	0.357	0.0988
<i>CG6908</i>	0.357	0.0988
<i>CTCF</i>	0.357	0.0988
<i>Syt14</i>	0.357	0.0988
<i>CG16771</i>	0.356	0.0996
<i>CG4293</i>	0.356	0.0996
<i>CG5669</i>	0.356	0.0996
<i>CG6136</i>	0.356	0.0996
<i>DAAM</i>	0.356	0.0996
<i>Gr93c</i>	0.356	0.0996
<i>iotaTry</i>	0.356	0.0996
<i>rhea</i>	0.356	0.0996

Table 6.S15 - Top Genes ERC values for *ord* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Hsp60D</i>	0.969	0.0001
<i>Cpr62Ba</i>	0.95	0.0002
<i>CG12721</i>	0.944	0.0003
<i>Snp</i>	0.941	0.0004
<i>rms(2)35C1</i>	0.937	0.0005
<i>CG13884</i>	0.93	0.0005
<i>CG14695</i>	0.93	0.0005
<i>CG11251</i>	0.923	0.0007
<i>CG11560</i>	0.91	0.0008
<i>CG12027</i>	0.901	0.0009
<i>CG13894</i>	0.901	0.0009
<i>CG32591</i>	0.897	0.0011
<i>CG30356</i>	0.889	0.0012
<i>MED4</i>	0.888	0.0013
<i>CG6733</i>	0.887	0.0014
<i>exd</i>	0.887	0.0014
<i>CG5122</i>	0.884	0.0015
<i>glic</i>	0.881	0.0016
<i>fs(1)M3</i>	0.88	0.0017
<i>hhl</i>	0.88	0.0017
<i>Tsf1</i>	0.878	0.0019
<i>CG9468</i>	0.877	0.002
<i>CG17802</i>	0.873	0.0021
<i>Ckl1alpha-f1</i>	0.871	0.0022
<i>CG4198</i>	0.869	0.0023
<i>CG6568</i>	0.863	0.0023
<i>CG8105</i>	0.863	0.0023
<i>CG15643</i>	0.853	0.0025
<i>wor</i>	0.85	0.0026
<i>l(3)psg2</i>	0.849	0.0027
<i>Arf51F</i>	0.848	0.0028
<i>vir</i>	0.848	0.0028
<i>CG12147</i>	0.844	0.003
<i>CG6791</i>	0.844	0.003
<i>CG14926</i>	0.841	0.0032
<i>CG9247</i>	0.84	0.0032
<i>hop</i>	0.833	0.0033
<i>CG14913</i>	0.832	0.0034
<i>CG34296</i>	0.829	0.0035
<i>LIMK1</i>	0.829	0.0035
<i>CG10013</i>	0.828	0.0037
<i>CG8629</i>	0.826	0.0038
<i>Doa</i>	0.826	0.0038
<i>CG13253</i>	0.824	0.004
<i>CG14635</i>	0.823	0.0041
<i>CG13131</i>	0.822	0.0041
<i>CG14929</i>	0.821	0.0042
<i>CG4565</i>	0.821	0.0042
<i>CG31418</i>	0.82	0.0044
<i>Hand</i>	0.82	0.0044
<i>Klp31E</i>	0.82	0.0044
<i>Ssadh</i>	0.82	0.0044
<i>Aos1</i>	0.819	0.0048
<i>CG13741</i>	0.819	0.0048
<i>CG8924</i>	0.818	0.005
<i>XNP</i>	0.817	0.005

Gene Name	ERC Value	P-value
<i>CG13895</i>	0.814	0.0051
<i>bfp</i>	0.812	0.0052
<i>RplL39</i>	0.812	0.0052
<i>CG18731</i>	0.811	0.0054
<i>CG15317</i>	0.81	0.0055
<i>CG32649</i>	0.81	0.0055
<i>CG8316</i>	0.81	0.0055
<i>CG13003</i>	0.809	0.0058
<i>CG10263</i>	0.808	0.0059
<i>CG10752</i>	0.808	0.0059
<i>row</i>	0.808	0.0059
<i>vap</i>	0.806	0.0061
<i>CG13040</i>	0.804	0.0062
<i>CG15311</i>	0.804	0.0062
<i>CG31752</i>	0.804	0.0062
<i>Mis12</i>	0.804	0.0062
<i>RSG7</i>	0.804	0.0062
<i>CG8173</i>	0.803	0.0067
<i>CG1234</i>	0.801	0.0068
<i>fs(1)K10</i>	0.801	0.0068
<i>Synd</i>	0.801	0.0068
<i>CG33286</i>	0.8	0.007
<i>boly</i>	0.798	0.0071
<i>CG3394</i>	0.798	0.0071
<i>mRpS30</i>	0.798	0.0071
<i>CG10600</i>	0.797	0.0074
<i>CG13865</i>	0.797	0.0074
<i>slmo</i>	0.797	0.0074
<i>CG2258</i>	0.796	0.0077
<i>CG4617</i>	0.796	0.0077
<i>CG11668</i>	0.795	0.0078
<i>CG12442</i>	0.795	0.0078
<i>CG13966</i>	0.795	0.0078
<i>CG14451</i>	0.795	0.0078
CG7069	0.794	0.0082
<i>CG15395</i>	0.793	0.0083
<i>CG6345</i>	0.793	0.0083
<i>RanBPM</i>	0.793	0.0083
<i>CG15404</i>	0.792	0.0086
<i>CG4017</i>	0.792	0.0086
<i>CG6048</i>	0.792	0.0086
<i>CG17928</i>	0.791	0.0088
<i>CG42827</i>	0.79	0.0089
<i>vig2</i>	0.79	0.0089
<i>CG6893</i>	0.789	0.0091
<i>CG13558</i>	0.788	0.0092
<i>CG2990</i>	0.788	0.0092
<i>CG11638</i>	0.787	0.0094
<i>CG1688</i>	0.787	0.0094
<i>bam</i>	0.785	0.0095
<i>Cdc6</i>	0.785	0.0095
<i>Cyp6a8</i>	0.785	0.0095
<i>CG15917</i>	0.784	0.0098
<i>CG32095</i>	0.782	0.0099
<i>ms(3)K81</i>	0.782	0.0099
<i>Nop60B</i>	0.782	0.0099

Gene Name	ERC Value	P-value
<i>CG30466</i>	0.781	0.0102
<i>CG12783</i>	0.779	0.0103
<i>CG3014</i>	0.777	0.0104
<i>CAP-D2</i>	0.776	0.0105
<i>CG1523</i>	0.776	0.0105
<i>casp</i>	0.775	0.0106
<i>SmB</i>	0.775	0.0106
<i>CG3940</i>	0.774	0.0108
<i>CG4854</i>	0.774	0.0108
<i>Scp</i>	0.774	0.0108
<i>CG42487</i>	0.773	0.0111
<i>Klp59C</i>	0.773	0.0111
<i>CG1722</i>	0.772	0.0113
<i>CG9422</i>	0.771	0.0114
<i>CG13897</i>	0.77	0.0114
<i>CG18278</i>	0.769	0.0115
<i>CG12179</i>	0.767	0.0116
<i>CG30389</i>	0.766	0.0117
<i>CG32685</i>	0.766	0.0117
<i>Kaz1-ORFB</i>	0.766	0.0117
<i>scpr-C</i>	0.766	0.0117
<i>ACXE</i>	0.765	0.0121
<i>CG1646</i>	0.765	0.0121
<i>CG17048</i>	0.765	0.0121
<i>CG31251</i>	0.765	0.0121
<i>CG5642</i>	0.765	0.0121
<i>mRpL3</i>	0.765	0.0121
<i>CG14317</i>	0.764	0.0126
<i>CG18316</i>	0.764	0.0126
<i>CG2147</i>	0.764	0.0126
<i>CG4877</i>	0.764	0.0126
<i>CG11658</i>	0.763	0.013
<i>CG12121</i>	0.763	0.013
<i>CG17665</i>	0.763	0.013
<i>CG7077</i>	0.763	0.013
<i>IP3K2</i>	0.763	0.013
<i>O-fut2</i>	0.763	0.013
<i>Os-E</i>	0.762	0.0135
<i>Pbp95</i>	0.762	0.0135
<i>CG16700</i>	0.761	0.0137
<i>Ets21C</i>	0.761	0.0137
<i>Itm50</i>	0.761	0.0137
<i>yl</i>	0.761	0.0137
<i>CG11052</i>	0.76	0.0141
<i>CG12691</i>	0.76	0.0141
<i>CG4004</i>	0.76	0.0141
<i>Pgan135A</i>	0.76	0.0141
<i>ppa</i>	0.76	0.0141
<i>Pk34A</i>	0.759	0.0145
<i>CG32246</i>	0.758	0.0146
<i>pex16</i>	0.757	0.0147
<i>CG17068</i>	0.756	0.0148
<i>CG3436</i>	0.756	0.0148
<i>CG8757</i>	0.756	0.0148
<i>qkr54B</i>	0.756	0.0148
<i>Saf6</i>	0.755	0.0151

Gene Name	ERC Value	P-value
<i>CG3056</i>	0.754	0.0152
<i>CG9203</i>	0.754	0.0152
<i>klar</i>	0.754	0.0152
<i>Nup107</i>	0.754	0.0152
<i>CG7101</i>	0.752	0.0156
<i>CG34360</i>	0.751	0.0157
<i>CG3526</i>	0.751	0.0157
<i>hdm</i>	0.751	0.0157
<i>CG10496</i>	0.75	0.0159
<i>CG1142</i>	0.75	0.0159
<i>CG12229</i>	0.75	0.0159
<i>Rhp</i>	0.75	0.0159
<i>CG14797</i>	0.749	0.0163
mei-218	0.749	0.0163
<i>SMC2</i>	0.749	0.0163
<i>CG10298</i>	0.747	0.0166
<i>CG13169</i>	0.747	0.0166
<i>CG31320</i>	0.747	0.0166
<i>CG18011</i>	0.746	0.0168
<i>Cyp313b1</i>	0.746	0.0168
<i>CG31525</i>	0.745	0.017
<i>MTF-1</i>	0.745	0.017
<i>CG4836</i>	0.744	0.0172
<i>CSN1a</i>	0.744	0.0172
<i>CG8974</i>	0.743	0.0174
<i>CG6838</i>	0.742	0.0175
<i>Ect3</i>	0.742	0.0175
<i>A16</i>	0.741	0.0177
<i>bid</i>	0.741	0.0177
<i>CG34130</i>	0.741	0.0177
<i>CG8334</i>	0.741	0.0177
<i>l(3)L1231</i>	0.741	0.0177
<i>Zyx102EF</i>	0.741	0.0177
<i>CG1134</i>	0.74	0.0182
<i>CG7376</i>	0.74	0.0182
<i>east</i>	0.74	0.0182
<i>luna</i>	0.74	0.0182
<i>CG31820</i>	0.739	0.0186
<i>cuff</i>	0.739	0.0186
<i>CG8239</i>	0.738	0.0187
<i>mus308</i>	0.737	0.0188
<i>aly</i>	0.736	0.0189
<i>CG11660</i>	0.736	0.0189
<i>CG13802</i>	0.736	0.0189
<i>CG4390</i>	0.736	0.0189
<i>kni</i>	0.736	0.0189
<i>RplL34a</i>	0.736	0.0189
CG10560	0.735	0.0195
<i>CG2129</i>	0.735	0.0195
<i>CG4676</i>	0.735	0.0195
<i>CG9542</i>	0.735	0.0195
<i>Act42A</i>	0.734	0.0198
<i>CG11263</i>	0.734	0.0198
<i>CG14297</i>	0.733	0.02
<i>Roc2</i>	0.733	0.02
<i>CG34104</i>	0.732	0.0202

Gene Name	ERC Value	P-value
<i>Ddr</i>	0.731	0.0203
<i>CG31551</i>	0.73	0.0204
<i>CG8808</i>	0.73	0.0204
<i>mei-S332</i>	0.73	0.0204
<i>CG18262</i>	0.729	0.0206
<i>CG32088</i>	0.729	0.0206
<i>GstD8</i>	0.729	0.0206
<i>jet</i>	0.729	0.0206
<i>tst</i>	0.729	0.0206
<i>CG14174</i>	0.728	0.0211
<i>wds</i>	0.728	0.0211
<i>CG14303</i>	0.727	0.0213
<i>CG15865</i>	0.725	0.0214
<i>CG8931</i>	0.725	0.0214
<i>CG11403</i>	0.724	0.0215
<i>scyl</i>	0.724	0.0215
<i>CG4294</i>	0.722	0.0217
<i>Fem-1</i>	0.722	0.0217
<i>MED30</i>	0.722	0.0217
<i>Or98b</i>	0.722	0.0217
<i>Ppm1</i>	0.722	0.0217
<i>CG14930</i>	0.721	0.0222
<i>CG16863</i>	0.721	0.0222
<i>CG1764</i>	0.721	0.0222
<i>CG34115</i>	0.721	0.0222
<i>Moca-cyp</i>	0.721	0.0222
<i>CG5514</i>	0.72	0.0226
<i>CG7518</i>	0.719	0.0227
<i>CG7884</i>	0.719	0.0227
<i>CG9861</i>	0.719	0.0227
<i>Prosalpha6T</i>	0.719	0.0227
<i>Rbcn-3A</i>	0.719	0.0227
<i>Art8</i>	0.718	0.0232
<i>CG15639</i>	0.718	0.0232
<i>CG2199</i>	0.718	0.0232
<i>CG7945</i>	0.718	0.0232
<i>lat</i>	0.718	0.0232
<i>nht</i>	0.718	0.0232
<i>por</i>	0.718	0.0232
<i>RhoGAP18B</i>	0.718	0.0232
<i>CG9934</i>	0.717	0.0239
<i>cal5</i>	0.715	0.024
<i>CG42707</i>	0.715	0.024
<i>CG8298</i>	0.715	0.024
<i>CG4449</i>	0.714	0.0242
<i>CG5823</i>	0.714	0.0242
<i>ein</i>	0.714	0.0242
<i>CG12535</i>	0.713	0.0245
<i>CycG</i>	0.712	0.0246
<i>Proc-R</i>	0.712	0.0246
<i>CG10654</i>	0.711	0.0248
<i>CG6197</i>	0.711	0.0248
<i>CG9581</i>	0.711	0.0248
<i>CG33262</i>	0.71	0.025
<i>CG3397</i>	0.71	0.025
<i>CG9485</i>	0.71	0.025

Table 6.S15 Continued

Gene Name	ERC Value	P-value
Dh	0.71	0.025
Arg87C	0.708	0.0254
CG1695	0.708	0.0254
CG31921	0.708	0.0254
CG6241	0.708	0.0254
CG17658	0.707	0.0258
CG9593	0.707	0.0258
Pep	0.707	0.0258
CG13001	0.706	0.026
CG8408	0.706	0.026
eas	0.706	0.026
acj6	0.705	0.0263
CG18065	0.705	0.0263
CG32409	0.705	0.0263
CG42327	0.705	0.0263
Su(var)2-HP	0.705	0.0263
THIA-L	0.705	0.0263
tomb	0.705	0.0263
Pbprp2	0.704	0.0269
shu	0.704	0.0269
Hrs	0.702	0.0271
LRP1	0.702	0.0271
CG8915	0.701	0.0273
DmsR-2	0.701	0.0273
Pbp49	0.7	0.0275
Sfp53D	0.7	0.0275
su(wa)	0.7	0.0275
CG33641	0.699	0.0277
Dic90F	0.699	0.0277
Klp59D	0.699	0.0277
CHES-1-like	0.698	0.028
Drak	0.698	0.028
sbr	0.698	0.028
CG12096	0.697	0.0283
CG4678	0.697	0.0283
CG31922	0.696	0.0285
CG32643	0.696	0.0285
CG42374	0.696	0.0285
Bj1	0.695	0.0287
Scr	0.695	0.0287
tsg	0.695	0.0287
Tsp42Er	0.695	0.0287
CG34012	0.694	0.0291
coil	0.694	0.0291
CG12288	0.693	0.0293
Eps-15	0.693	0.0293
Nca	0.693	0.0293
RpL35A	0.693	0.0293
CG17283	0.692	0.0296
CG17568	0.692	0.0296
PhKgamma	0.692	0.0296
CG14966	0.691	0.0299
CG7200	0.691	0.0299
Rad17	0.69	0.0301
CG8097	0.689	0.0302
fl(2)d	0.689	0.0302

Gene Name	ERC Value	P-value
CG13984	0.688	0.0304
Saf-B	0.688	0.0304
asl	0.687	0.0305
CG9514	0.687	0.0305
CTCF	0.687	0.0305
sna	0.687	0.0305
sws	0.687	0.0305
CG11768	0.686	0.031
CG14050	0.686	0.031
CG30376	0.686	0.031
gp210	0.686	0.031
Mlf	0.686	0.031
Aly	0.685	0.0314
CG11133	0.685	0.0314
CG15602	0.685	0.0314
CG31550	0.685	0.0314
Map205	0.685	0.0314
Bx	0.684	0.0319
CG15916	0.684	0.0319
mRpL22	0.684	0.0319
tlilB	0.684	0.0319
CG31805	0.683	0.0323
CG33282	0.683	0.0323
Taz	0.683	0.0323
Isl	0.682	0.0325
CG10845	0.681	0.0326
CG2641	0.681	0.0326
Tsp68C	0.68	0.0328
CG10177	0.679	0.0329
CG10588	0.679	0.0329
CG7927	0.679	0.0329
Vsx2	0.679	0.0329
CG9170	0.678	0.0332
D1	0.678	0.0332
CG15236	0.677	0.0334
CG31542	0.677	0.0334
E(var)3-9	0.677	0.0334
CG6628	0.675	0.0337
Gem3	0.675	0.0337
Km	0.674	0.0339
CG8944	0.673	0.034
CG16853	0.672	0.0341
CG31646	0.672	0.0341
CG5762	0.672	0.0341
Mer	0.672	0.0341
nimB5	0.672	0.0341
CG10462	0.671	0.0345
CG14722	0.671	0.0345
CG14997	0.671	0.0345
CG31109	0.671	0.0345
CG3262	0.671	0.0345
CG7557	0.671	0.0345
CG7607	0.671	0.0345
CG13306	0.67	0.0351
CG7429	0.67	0.0351
DIP1	0.67	0.0351

Gene Name	ERC Value	P-value
nAcRalpha-9	0.67	0.0351
retm	0.67	0.0351
CG30423	0.669	0.0356
CG4045	0.669	0.0356
CG7332	0.669	0.0356
CG8100	0.669	0.0356
CG32055	0.668	0.0359
CG8134	0.668	0.0359
tral	0.668	0.0359
eco	0.667	0.0362
plu	0.667	0.0362
Syx18	0.666	0.0364
CG13031	0.665	0.0365
CG9376	0.665	0.0365
CG15745	0.663	0.0367
CG34448	0.662	0.0368
Cpr97Eb	0.662	0.0368
kek3	0.662	0.0368
Uba2	0.662	0.0368
CG14407	0.661	0.0371
CG4771	0.661	0.0371
CG8929	0.661	0.0371
laf	0.661	0.0371
CG31698	0.66	0.0375
Gr43b	0.66	0.0375
CG10948	0.659	0.0377
CG18600	0.659	0.0377
CG8116	0.659	0.0377
ct	0.659	0.0377
Got2	0.659	0.0377
CG11418	0.658	0.0381
CG2901	0.658	0.0381
CG2972	0.658	0.0381
Fs	0.657	0.0384
CG1231	0.656	0.0385
CG12516	0.656	0.0385
boca	0.655	0.0386
CG3775	0.655	0.0386
Ucp4C	0.655	0.0386
CG10139	0.654	0.0389
CG7691	0.654	0.0389
MSBP	0.653	0.0391
Rrp6	0.653	0.0391
APP-BP1	0.652	0.0393
Bem46	0.652	0.0393
CG11762	0.652	0.0393
CG18128	0.652	0.0393
CG31142	0.652	0.0393
CG4788	0.652	0.0393
CG4936	0.652	0.0393
Stim	0.652	0.0393
CG34181	0.651	0.04
CG8916	0.651	0.04
Nup358	0.651	0.04
CG12236	0.65	0.0403
CG14300	0.65	0.0403

Gene Name	ERC Value	P-value
CG15036	0.65	0.0403
CG31705	0.65	0.0403
CG31862	0.65	0.0403
Yps28	0.649	0.0407
CG10317	0.648	0.0408
CG10333	0.648	0.0408
CG11071	0.648	0.0408
CG14812	0.648	0.0408
CG32302	0.648	0.0408
CG7789	0.648	0.0408
Rh7	0.648	0.0408
CG14105	0.647	0.0414
Hsc70-4	0.647	0.0414
RunxB	0.647	0.0414
CG31802	0.646	0.0417
CG32541	0.646	0.0417
CG34008	0.646	0.0417
CG33695	0.645	0.042
CG3726	0.645	0.042
Marf	0.645	0.042
S6kill	0.645	0.042
Surf1	0.645	0.042
Tob	0.645	0.042
CG14103	0.644	0.0425
CG18258	0.643	0.0426
CG5928	0.643	0.0426
Nipsnap	0.643	0.0426
CG8636	0.642	0.0429
CG10431	0.641	0.043
CG13197	0.641	0.043
CG2533	0.641	0.043
SPoCk	0.641	0.043
CG16825	0.64	0.0433
Skeletor	0.64	0.0433
Aldh	0.639	0.0435
CG1677	0.639	0.0435
wde	0.639	0.0435
Ars2	0.638	0.0438
CG15124	0.638	0.0438
AP-1gamma	0.637	0.044
CG11912	0.637	0.044
CG3281	0.637	0.044
CG7017	0.637	0.044
CG14125	0.636	0.0443
RpL37a	0.636	0.0443
Est-Q	0.635	0.0445
CG1737	0.634	0.0446
CG5194	0.634	0.0446
Def	0.634	0.0446
Elf	0.634	0.0446
Hpr1	0.634	0.0446
xmas-2	0.634	0.0446
CG13532	0.633	0.0451
CG3342	0.633	0.0451
dm	0.633	0.0451
fl(2)37Cd	0.633	0.0451

Gene Name	ERC Value	P-value
Bet5	0.632	0.0455
CG15365	0.632	0.0455
CG9027	0.632	0.0455
Sara	0.632	0.0455
Atf3	0.631	0.0459
CG13305	0.63	0.0459
CG2104	0.63	0.0459
Kmn1	0.63	0.0459
RASSF8	0.63	0.0459
soti	0.63	0.0459
Art9	0.629	0.0464
NnfxA	0.629	0.0464
CG5718	0.628	0.0466
CG8273	0.628	0.0466
Eno	0.628	0.0466
ftz	0.628	0.0466
SMD3	0.628	0.0466
ssh	0.628	0.0466
CG2813	0.627	0.0471
CG4362	0.627	0.0471
fit	0.627	0.0471
Traf6	0.627	0.0471
CG12857	0.625	0.0475
CG1824	0.625	0.0475
CG1902	0.625	0.0475
CG33919	0.625	0.0475
CG3603	0.625	0.0475
CG7519	0.625	0.0475
l(1)G0148	0.625	0.0475
NetB	0.625	0.0475
CG11137	0.624	0.0482
CG17047	0.624	0.0482
Dlhc	0.624	0.0482
fog	0.624	0.0482
CG5398	0.623	0.0486
cmet	0.623	0.0486
pad	0.623	0.0486
Stat92E	0.623	0.0486
CG11149	0.622	0.0489
CG34317	0.622	0.0489
CG42458	0.622	0.0489
Ndc80	0.622	0.0489
Tsp33B	0.622	0.0489
CG12012	0.621	0.0494
CG32750	0.621	0.0494
CG9003	0.621	0.0494
CG9125	0.621	0.0494
Pcl	0.621	0.0494
Sfmbt	0.621	0.0494
Elf	0.62	0.0499
CG3680	0.62	0.0499
CG5859	0.62	0.0499
mod	0.62	0.0499
Alf	0.619	0.0503
CG11985	0.619	0.0503
CG32573	0.619	0.0503

Table 6.S15 Continued

Gene Name	ERC Value	P-value
CG42516	0.619	0.0503
CG8928	0.619	0.0503
CG6506	0.618	0.0507
Nup160	0.618	0.0507
RluA-2	0.618	0.0507
trus	0.618	0.0507
Atox1	0.617	0.0511
CG4603	0.617	0.0511
Sir2	0.617	0.0511
CG14512	0.616	0.0514
CG31787	0.616	0.0514
Pino	0.616	0.0514
RhoGAP19C	0.616	0.0514
thoc6	0.616	0.0514
cal1	0.615	0.0518
CG10979	0.615	0.0518
CG6280	0.615	0.0518
Obp99c	0.615	0.0518
CG10264	0.614	0.0522
CG13773	0.614	0.0522
CG14306	0.614	0.0522
Map60	0.614	0.0522
Axs	0.613	0.0525
CG10265	0.613	0.0525
CG13148	0.613	0.0525
CG17917	0.613	0.0525
shcp	0.613	0.0525
Atg18	0.612	0.053
bchs	0.612	0.053
CG10414	0.612	0.053
CG14646	0.612	0.053
CG17734	0.612	0.053
tex	0.612	0.053
CG10481	0.611	0.0535
CG15876	0.611	0.0535
CG18048	0.611	0.0535
CG32117	0.611	0.0535
lr56a	0.611	0.0535
CG13284	0.61	0.054
CG5217	0.61	0.054
CG8538	0.61	0.054
Dip-C	0.61	0.054
mms4	0.61	0.054
stnA	0.61	0.054
CG12991	0.609	0.0545
CG15914	0.609	0.0545
Hsp67Ba	0.609	0.0545
ns3	0.609	0.0545
CG11279	0.608	0.0549
CG42324	0.608	0.0549
CG7082	0.608	0.0549
CG7335	0.608	0.0549
Gem2	0.608	0.0549
Jheh1	0.608	0.0549
Spn42Db	0.608	0.0549
Su(var)205	0.608	0.0549

Gene Name	ERC Value	P-value
CG12360	0.607	0.0556
Chc	0.607	0.0556
fd68A	0.607	0.0556
Kdm4B	0.607	0.0556
sra	0.607	0.0556
Tom40	0.607	0.0556
c12.1	0.606	0.0561
can	0.606	0.0561
kat80	0.606	0.0561
ppk11	0.606	0.0561
spn-E	0.606	0.0561
Ance-3	0.605	0.0566
EndoG1	0.605	0.0566
rab3-GEF	0.605	0.0566
Sbp2	0.605	0.0566
Efz2b	0.604	0.0569
Ppt1	0.604	0.0569
Tango2	0.604	0.0569
CG13725	0.603	0.0572
CG12590	0.602	0.0573
CG13116	0.602	0.0573
CG3887	0.602	0.0573
CG7702	0.602	0.0573
CG3984	0.601	0.0577
Gr68a	0.601	0.0577
CG10669	0.6	0.0578
CG7911	0.6	0.0578
Fs(2)Ket	0.6	0.0578
mth19	0.6	0.0578
yip3	0.6	0.0578
bai	0.599	0.0583
CG10417	0.599	0.0583
CG14238	0.599	0.0583
CG5790	0.599	0.0583
MeF2	0.599	0.0583
CG10000	0.598	0.0587
CG14383	0.598	0.0587
CG2889	0.598	0.0587
CG3592	0.598	0.0587
CG5550	0.598	0.0587
CG6106	0.598	0.0587
Crk	0.598	0.0587
Dcr-2	0.598	0.0587
prtp	0.598	0.0587
Spec2	0.598	0.0587
CG10680	0.597	0.0596
CG12263	0.597	0.0596
CG30440	0.597	0.0596
Obp50b	0.597	0.0596
Aats-ala-m	0.596	0.06
CG14693	0.596	0.06
CG3847	0.596	0.06
Tif-1A	0.596	0.06
CG12975	0.595	0.0604
CG32812	0.595	0.0604
CG7071	0.595	0.0604

Gene Name	ERC Value	P-value
CG9099	0.595	0.0604
dwg	0.595	0.0604
ths	0.595	0.0604
beat-11b	0.594	0.0609
CG10424	0.594	0.0609
CG13717	0.593	0.0611
CG17528	0.593	0.0611
CG32856	0.593	0.0611
CG13733	0.592	0.0614
l(2)37Ce	0.592	0.0614
CG4480	0.591	0.0615
CG9147	0.591	0.0615
CG9692	0.591	0.0615
Osi21	0.591	0.0615
CG10413	0.59	0.0619
CG10486	0.59	0.0619
CG1513	0.59	0.0619
Pkg21D	0.59	0.0619
ATPsyn-gam	0.589	0.0623
CAH1	0.589	0.0623
CG10418	0.589	0.0623
Cyp316a1	0.589	0.0623
Cyp6v1	0.589	0.0623
Pdp	0.589	0.0623
CG5265	0.588	0.0628
CG9682	0.588	0.0628
CG12307	0.587	0.063
CG9098	0.587	0.063
myoglianin	0.587	0.063
CG18581	0.586	0.0632
CG6163	0.586	0.0632
Cul-5	0.586	0.0632
GlcT-1	0.586	0.0632
l(2)09851	0.586	0.0632
mRpl23	0.586	0.0632
Pros35	0.586	0.0632
CG11247	0.585	0.0639
CG2862	0.585	0.0639
CG6744	0.585	0.0639
CG7366	0.585	0.0639
dgt2	0.585	0.0639
eIF5	0.585	0.0639
CG2807	0.584	0.0644
CG7991	0.584	0.0644
Eaf	0.584	0.0644
GstD10	0.584	0.0644
CG18269	0.583	0.0648
CG4907	0.583	0.0648
Grip163	0.583	0.0648
CG2091	0.582	0.065
CG4078	0.582	0.065
Spargel	0.582	0.065
Andorra	0.581	0.0653
CG15376	0.581	0.0653
CG6933	0.581	0.0653
CG8320	0.581	0.0653

Gene Name	ERC Value	P-value
Gtp-bp	0.581	0.0653
Hen1	0.581	0.0653
Toll-7	0.581	0.0653
yellow-g	0.581	0.0653
CG13323	0.58	0.066
CG7956	0.58	0.066
Or65a	0.58	0.066
CG11158	0.579	0.0663
CG15725	0.579	0.0663
CG5089	0.579	0.0663
Dcp2	0.579	0.0663
fon	0.579	0.0663
Pvr	0.579	0.0663
nut	0.579	0.0663
CG13500	0.578	0.0669
CG15399	0.578	0.0669
CG43078	0.578	0.0669
CG7099	0.578	0.0669
sisA	0.578	0.0669
stwl	0.578	0.0669
alpha-Est2	0.577	0.0675
CG12866	0.577	0.0675
CG30373	0.577	0.0675
CG9926	0.577	0.0675
fund	0.577	0.0675
CG5862	0.576	0.0679
cos	0.576	0.0679
JIL-1	0.576	0.0679
CG15549	0.575	0.0682
eIF-3p66	0.575	0.0682
CG12042	0.574	0.0684
CG13970	0.574	0.0684
CG17272	0.574	0.0684
CG31055	0.574	0.0684
CG12029	0.573	0.0687
CG17494	0.573	0.0687
CG9323	0.573	0.0687
Rpn11	0.573	0.0687
Sec16	0.573	0.0687
Tango4	0.573	0.0687
CG1077	0.572	0.0693
CG42258	0.572	0.0693
CG42557	0.572	0.0693
CG4880	0.572	0.0693
ChT11	0.572	0.0693
Jhe	0.572	0.0693
l(1)G0230	0.572	0.0693
Ppt2	0.572	0.0693
ZC3H3	0.572	0.0693
CG4660	0.571	0.0701
CG9919	0.571	0.0701
CG14931	0.57	0.0703
CG4360	0.57	0.0703
CS-2	0.57	0.0703
CG5711	0.569	0.0705
CG3511	0.569	0.0705

Gene Name	ERC Value	P-value
poe	0.569	0.0705
CG13982	0.568	0.0708
CG17221	0.568	0.0708
CG7757	0.568	0.0708
how	0.568	0.0708
btz	0.567	0.0712
CG5196	0.567	0.0712
CG6361	0.567	0.0712
CG9426	0.567	0.0712
ferrochelatase	0.567	0.0712
RhoGAP15E	0.567	0.0712
fon	0.566	0.0717
CG2061	0.566	0.0717
CG9119	0.566	0.0717
Rad23	0.566	0.0717
CG32437	0.565	0.0721
Rpl32	0.565	0.0721
CG13999	0.564	0.0723
CG14839	0.564	0.0723
Atac1	0.563	0.0724
crm	0.563	0.0724
Nsf2	0.562	0.0726
CG9932	0.561	0.0727
EloA	0.561	0.0727
RplP1	0.561	0.0727
Acp65Aa	0.56	0.073
Adk3	0.56	0.073
CG31380	0.56	0.073
CG32281	0.56	0.073
CG5379	0.56	0.073
Hrd3	0.56	0.073
CG10802	0.559	0.0735
CG15213	0.559	0.0735
CG30495	0.559	0.0735
CG4872	0.559	0.0735
CG8771	0.559	0.0735
Sox14	0.559	0.0735
tth	0.559	0.0735
CG13384	0.558	0.0741
CG17691	0.558	0.0741
CG2926	0.558	0.0741
CG3568	0.558	0.0741
CG8939	0.558	0.0741
Pros25	0.558	0.0741
RhoGAP5A	0.558	0.0741
CG4956	0.557	0.0748
CG1764	0.557	0.0748
CycT	0.557	0.0748
pita	0.557	0.0748
nu	0.557	0.0748
tsu	0.557	0.0748
aust	0.556	0.0753
CG10254	0.556	0.0753
CG12134	0.556	0.0753
CG15912	0.556	0.0753
CG31676	0.556	0.0753

Table 6.S15 Continued

Gene Name	ERC Value	P-value
CG34040	0.556	0.0753
CG10947	0.555	0.0759
CG14431	0.555	0.0759
CG15708	0.555	0.0759
CG17230	0.555	0.0759
CG5161	0.555	0.0759
comr	0.555	0.0759
Gbeta5	0.555	0.0759
Obp58b	0.555	0.0759
Trf4-2	0.555	0.0759
CG34033	0.554	0.0767
Jon25Bii	0.554	0.0767
B-H1	0.553	0.0768
CG14274	0.553	0.0768
CG14591	0.553	0.0768
CG15130	0.553	0.0768
Grd	0.553	0.0768
lambdaTry	0.553	0.0768
mu2	0.553	0.0768
Oscp	0.553	0.0768
CG10166	0.552	0.0776
CG14767	0.552	0.0776
CG5071	0.552	0.0776
CG12078	0.551	0.0778
CG14937	0.551	0.0778
CG15863	0.551	0.0778
CG32225	0.551	0.0778
CG8141	0.551	0.0778
CG18624	0.55	0.0783
CG31755	0.55	0.0783
mamo	0.55	0.0783
CG18869	0.549	0.0786
CG6066	0.549	0.0786
Opbp	0.549	0.0786
CG11092	0.548	0.0788
CG1120	0.548	0.0788
CG31279	0.548	0.0788
CG32712	0.548	0.0788
CG4896	0.548	0.0788
CG17922	0.547	0.0793
CG7461	0.547	0.0793
CG9548	0.547	0.0793
KH1	0.547	0.0793
CG32104	0.546	0.0796
CG42402	0.546	0.0796
CG7786	0.546	0.0796
CG9346	0.546	0.0796
Hsp60	0.546	0.0796
Ino80	0.546	0.0796
Ca-alpha1D	0.545	0.0802
CG12413	0.545	0.0802
CG33052	0.545	0.0802
CG4806	0.545	0.0802
CG5033	0.545	0.0802
CG9172	0.545	0.0802
It	0.545	0.0802

Gene Name	ERC Value	P-value
mfm	0.545	0.0802
SH3PX1	0.545	0.0802
CG32298	0.544	0.081
DAAM	0.544	0.081
CG6308	0.543	0.0812
kel	0.543	0.0812
CG14423	0.542	0.0814
CG33791	0.542	0.0814
CG3812	0.542	0.0814
CG9392	0.542	0.0814
plexA	0.542	0.0814
usnp	0.542	0.0814
CG5835	0.541	0.0819
elf3-S8	0.541	0.0819
Scgalpha	0.541	0.0819
Src42A	0.541	0.0819
CG10171	0.54	0.0823
CG3517	0.54	0.0823
nAcRbeta-2	0.54	0.0823
CG33057	0.539	0.0825
CG42361	0.539	0.0825
CG5798	0.539	0.0825
Hrb98DE	0.539	0.0825
kek5	0.539	0.0825
l(3)mbt	0.538	0.083
CG13123	0.537	0.0831
CG9406	0.537	0.0831
La	0.537	0.0831
Itm3	0.537	0.0831
CG17669	0.536	0.0834
CG34148	0.536	0.0834
DLP	0.536	0.0834
CG31381	0.535	0.0837
ecd	0.535	0.0837
CG14826	0.534	0.0839
CG4725	0.534	0.0839
CG7295	0.534	0.0839
Gef26	0.534	0.0839
inaC	0.534	0.0839
CG15117	0.533	0.0843
CG17724	0.533	0.0843
CG31690	0.533	0.0843
CG7408	0.533	0.0843
CG8001	0.533	0.0843
Cnx99A	0.533	0.0843
hay	0.533	0.0843
CG12432	0.532	0.085
CG15705	0.532	0.085
CG31739	0.532	0.085
CG7407	0.532	0.085
mRpl19	0.532	0.085
mssp	0.532	0.085
CG10465	0.531	0.0855
CG13407	0.531	0.0855
CG15369	0.531	0.0855
CG33263	0.531	0.0855

Gene Name	ERC Value	P-value
CG42675	0.531	0.0855
l(2)INC136	0.531	0.0855
nAcRalpha-1	0.531	0.0855
osk	0.531	0.0855
tap	0.531	0.0855
CG10912	0.53	0.0863
CG31176	0.53	0.0863
CG3124	0.53	0.0863
CG8300	0.53	0.0863
Dip3	0.53	0.0863
dy	0.53	0.0863
HtrA2	0.53	0.0863
Ada	0.529	0.0869
blw	0.529	0.0869
CG15877	0.529	0.0869
Dip1	0.528	0.0872
CG11345	0.527	0.0873
CG4629	0.527	0.0873
na	0.527	0.0873
Slip1	0.527	0.0873
CG14736	0.526	0.0877
CG31712	0.526	0.0877
CG32075	0.526	0.0877
CG3838	0.526	0.0877
CG7094	0.526	0.0877
Grip75	0.526	0.0877
Hydr2	0.526	0.0877
Upf2	0.526	0.0877
CG13476	0.525	0.0884
CG9523	0.525	0.0884
dsh	0.525	0.0884
RpL24	0.525	0.0884
Tbp	0.525	0.0884
beat-1c	0.524	0.0888
CG12299	0.524	0.0888
CG13928	0.524	0.0888
CG14322	0.524	0.0888
CG6216	0.524	0.0888
Jupiter	0.524	0.0888
l(2)05714	0.524	0.0888
salr	0.524	0.0888
calypso	0.523	0.0895
CG11155	0.523	0.0895
CG11526	0.523	0.0895
Cp16	0.523	0.0895
Ten-m	0.523	0.0895
wmd	0.523	0.0895
CG11927	0.522	0.0901
CG12914	0.522	0.0901
CG3534	0.522	0.0901
Ets97D	0.522	0.0901
mssp	0.522	0.0901
vps2	0.522	0.0901
CG14020	0.521	0.0906
Lip2	0.521	0.0906
srp	0.521	0.0906

Gene Name	ERC Value	P-value
vis	0.521	0.0906
CG11262	0.52	0.091
CG14450	0.52	0.091
CG1815	0.52	0.091
CG5921	0.52	0.091
Neos	0.52	0.091
wdp	0.52	0.091
CG32576	0.519	0.0915
CG15909	0.518	0.0916
CG4802	0.518	0.0916
igl	0.518	0.0916
CG17508	0.517	0.0919
CG31195	0.517	0.0919
CG3194	0.517	0.0919
CG5482	0.517	0.0919
exba	0.517	0.0919
PNUTS	0.517	0.0919
RhoGEF4	0.517	0.0919
betaTub97E	0.516	0.0925
CG12010	0.516	0.0925
CG3556	0.516	0.0925
CG7054	0.516	0.0925
CG15251	0.515	0.0929
CG1628	0.515	0.0929
CG34205	0.515	0.0929
HP1c	0.515	0.0929
hts	0.515	0.0929
pck	0.515	0.0929
point	0.515	0.0929
Bteb2	0.514	0.0935
CG18431	0.514	0.0935
Snm1	0.514	0.0935
CG3698	0.513	0.0938
CG10469	0.512	0.0939
CG33672	0.512	0.0939
CG34302	0.512	0.0939
CG3995	0.512	0.0939
CG42232	0.512	0.0939
CG6136	0.512	0.0939
cdc2c	0.511	0.0944
CG16903	0.511	0.0944
CG40045	0.511	0.0944
CG6607	0.511	0.0944
CG7536	0.511	0.0944
CG8090	0.511	0.0944
larp	0.511	0.0944
Ulp1	0.511	0.0944
CG13386	0.51	0.0951
CG5919	0.51	0.0951
CG6429	0.51	0.0951
CG8292	0.51	0.0951
Fsn	0.51	0.0951
Rrp42	0.51	0.0951
CG10732	0.509	0.0957
CG15464	0.509	0.0957
nerfin-1	0.509	0.0957

Gene Name	ERC Value	P-value
CG10822	0.508	0.0959
CG14301	0.508	0.0959
CG7139	0.508	0.0959
l(2)k09022	0.508	0.0959
CG15432	0.507	0.0963
CG30383	0.507	0.0963
CG33340	0.507	0.0963
CG8369	0.507	0.0963
Rtf1	0.507	0.0963
CG4802	0.507	0.0963
Tollo	0.507	0.0963
CG11334	0.506	0.0969
CG12672	0.506	0.0969
CG15167	0.506	0.0969
CG17806	0.506	0.0969
CG30417	0.506	0.0969
gukh	0.506	0.0969
Msi	0.506	0.0969
Or43b	0.506	0.0969
rg	0.506	0.0969
CG11865	0.505	0.0977
CG14333	0.505	0.0977
CG18605	0.505	0.0977
CG30154	0.505	0.0977
CG4042	0.505	0.0977
CG42353	0.505	0.0977
CG5278	0.505	0.0977
CG7239	0.505	0.0977
Hmr	0.505	0.0977
Mes4	0.505	0.0977
Tom70	0.505	0.0977
CG13958	0.504	0.0987
CG42455	0.504	0.0987
CG4612	0.504	0.0987
CG5807	0.504	0.0987
CG6579	0.504	0.0987
CG6967	0.504	0.0987
Cyp318a1	0.504	0.0987
PpN58A	0.504	0.0987
rdgA	0.504	0.0987
CG1358	0.503	0.0995
CG4789	0.503	0.0995
beat-IIIb	0.502	0.0997
CG1233	0.502	0.0997
CG32986	0.502	0.0997
CG34112	0.502	0.0997
CG7255	0.502	0.0997
CG9101	0.502	0.0997
Ort3a	0.502	0.0997
ppk7	0.502	0.0997

Table 6.S16 - Top Genes ERC values for *pds5* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>itm3</i>	0.955	0.0001
<i>Ge-1</i>	0.941	0.0002
<i>CG15167</i>	0.937	0.0003
<i>CG3610</i>	0.928	0.0004
<i>CG18190</i>	0.916	0.0005
<i>Tango3</i>	0.916	0.0005
<i>CG8455</i>	0.91	0.0006
<i>CG3611</i>	0.903	0.0007
<i>CG14613</i>	0.9	0.0008
<i>CG11164</i>	0.895	0.0009
<i>CstF-50</i>	0.895	0.0009
<i>CG6576</i>	0.893	0.0011
<i>mei-P26</i>	0.891	0.0012
<i>robo</i>	0.88	0.0013
<i>CG2202</i>	0.878	0.0014
<i>CG5098</i>	0.874	0.0014
<i>CG10055</i>	0.872	0.0015
<i>Golgin84</i>	0.871	0.0016
<i>CG12038</i>	0.869	0.0017
<i>nkd</i>	0.869	0.0017
<i>RanBP3</i>	0.866	0.0019
<i>rob62A</i>	0.866	0.0019
<i>CG18265</i>	0.863	0.0021
<i>CG15514</i>	0.862	0.0022
<i>Klp67A</i>	0.862	0.0022
<i>still</i>	0.861	0.0023
<i>CG4497</i>	0.859	0.0024
<i>CG30278</i>	0.856	0.0025
<i>CG13870</i>	0.854	0.0026
<i>CG31211</i>	0.849	0.0027
<i>CG12214</i>	0.847	0.0028
<i>CG30020</i>	0.846	0.0029
<i>CG4557</i>	0.844	0.003
<i>NPFR1</i>	0.844	0.003
<i>kto</i>	0.843	0.0032
<i>SmD1</i>	0.843	0.0032
<i>rogdi</i>	0.842	0.0033
<i>MED23</i>	0.841	0.0034
<i>DNApol-αph</i>	0.837	0.0035
<i>CG7172</i>	0.836	0.0036
<i>CG13802</i>	0.835	0.0037
<i>CG15653</i>	0.835	0.0037
<i>CG15387</i>	0.834	0.0039
<i>CG5897</i>	0.834	0.0039
<i>pzg</i>	0.833	0.0041
<i>lumu</i>	0.832	0.0041
<i>CG18870</i>	0.831	0.0042
<i>in</i>	0.83	0.0043
<i>pim</i>	0.83	0.0043
<i>CG10321</i>	0.828	0.0045
<i>CG5290</i>	0.827	0.0046
<i>chm</i>	0.827	0.0046
<i>cnk</i>	0.827	0.0046
<i>kermit</i>	0.826	0.0049
<i>san</i>	0.825	0.005
<i>Axn</i>	0.824	0.005

Gene Name	ERC Value	P-value
<i>CG7789</i>	0.824	0.005
<i>SellR</i>	0.824	0.005
<i>CG11970</i>	0.823	0.0053
<i>CG31029</i>	0.823	0.0053
<i>E(Pc)</i>	0.823	0.0053
<i>CG3542</i>	0.822	0.0056
<i>ksr</i>	0.822	0.0056
<i>CG17328</i>	0.821	0.0058
<i>CG13747</i>	0.82	0.0059
<i>CG17233</i>	0.82	0.0059
<i>CG4282</i>	0.82	0.0059
<i>PTP-ER</i>	0.818	0.0061
<i>pgant8</i>	0.817	0.0062
<i>PpD5</i>	0.817	0.0062
<i>PR2</i>	0.817	0.0062
<i>CG10778</i>	0.816	0.0065
<i>CG10907</i>	0.816	0.0065
<i>CdGAPr</i>	0.813	0.0067
<i>CG15435</i>	0.813	0.0067
<i>pps</i>	0.81	0.0068
<i>CG12929</i>	0.808	0.0069
<i>CG33169</i>	0.808	0.0069
<i>CG6480</i>	0.808	0.0069
<i>CG12439</i>	0.807	0.0072
<i>Taf10</i>	0.806	0.0073
<i>CG11298</i>	0.805	0.0074
<i>CG9300</i>	0.805	0.0074
<i>trx</i>	0.803	0.0076
<i>mrt</i>	0.799	0.0077
<i>swm</i>	0.798	0.0077
<i>CG4892</i>	0.797	0.0078
<i>Pof</i>	0.796	0.0079
<i>CG11329</i>	0.794	0.008
<i>CG11874</i>	0.792	0.0081
<i>wge</i>	0.792	0.0081
<i>CG17802</i>	0.79	0.0083
<i>CG4936</i>	0.789	0.0084
<i>Bzd</i>	0.788	0.0085
<i>CG6945</i>	0.788	0.0085
<i>CG15160</i>	0.787	0.0086
<i>CG7102</i>	0.787	0.0086
<i>CG32479</i>	0.785	0.0088
<i>Ptp69D</i>	0.785	0.0088
<i>CG5787</i>	0.784	0.009
<i>Mrtf</i>	0.784	0.009
<i>CG8436</i>	0.782	0.0092
<i>m6</i>	0.782	0.0092
<i>Pal</i>	0.782	0.0092
<i>tj</i>	0.782	0.0092
<i>CG3558</i>	0.781	0.0095
<i>CG14540</i>	0.78	0.0096
<i>CG14647</i>	0.78	0.0096
<i>CG15337</i>	0.78	0.0096
<i>CG17930</i>	0.779	0.0099
<i>CG30391</i>	0.779	0.0099
<i>MEP-1</i>	0.779	0.0099

Gene Name	ERC Value	P-value
<i>Sep2</i>	0.778	0.0102
<i>CG9437</i>	0.777	0.0103
<i>sba</i>	0.777	0.0103
<i>dpr2</i>	0.776	0.0105
<i>jub</i>	0.776	0.0105
<i>MED10</i>	0.776	0.0105
<i>CG10277</i>	0.775	0.0107
<i>CG15528</i>	0.775	0.0107
<i>CG6852</i>	0.775	0.0107
<i>CG8979</i>	0.775	0.0107
<i>HGTX</i>	0.774	0.0111
<i>CG34386</i>	0.773	0.0112
<i>zen</i>	0.773	0.0112
<i>mts</i>	0.772	0.0114
<i>Psi</i>	0.772	0.0114
<i>Ada1-2</i>	0.771	0.0115
<i>par-6</i>	0.771	0.0115
<i>CG31920</i>	0.77	0.0117
<i>CIC-a</i>	0.769	0.0118
<i>t</i>	0.768	0.0119
<i>CG18616</i>	0.766	0.012
<i>phol</i>	0.766	0.012
<i>Aac11</i>	0.765	0.0122
<i>CG42788</i>	0.765	0.0122
<i>Chro</i>	0.763	0.0123
<i>slim</i>	0.763	0.0123
<i>CG32790</i>	0.762	0.0125
<i>Mh1</i>	0.761	0.0126
<i>MED28</i>	0.76	0.0127
<i>Taspase1</i>	0.76	0.0127
<i>CG16979</i>	0.759	0.0129
<i>CG32441</i>	0.759	0.0129
<i>malpha</i>	0.759	0.0129
<i>CG4607</i>	0.758	0.0132
<i>CG7911</i>	0.758	0.0132
<i>CG10069</i>	0.755	0.0133
<i>CG32536</i>	0.755	0.0133
<i>CG8155</i>	0.755	0.0133
<i>Notf</i>	0.755	0.0133
<i>CG10251</i>	0.754	0.0137
<i>CG17131</i>	0.754	0.0137
<i>RpS28-like</i>	0.754	0.0137
<i>CG6470</i>	0.753	0.014
<i>CG9839</i>	0.753	0.014
<i>Nrk</i>	0.753	0.014
<i>bwa</i>	0.752	0.0142
<i>CG6654</i>	0.752	0.0142
<i>Dro</i>	0.752	0.0142
<i>MAGE</i>	0.751	0.0145
<i>CG5056</i>	0.749	0.0146
<i>CG5720</i>	0.749	0.0146
<i>DNApol-Iota</i>	0.749	0.0146
<i>CG9589</i>	0.748	0.0149
<i>tabi</i>	0.746	0.015
<i>Bsg25A</i>	0.745	0.015
<i>CG11211</i>	0.745	0.015

Gene Name	ERC Value	P-value
<i>CG30457</i>	0.745	0.015
<i>CG8301</i>	0.745	0.015
<i>CG9004</i>	0.745	0.015
<i>CG12003</i>	0.744	0.0155
<i>CG5861</i>	0.744	0.0155
<i>CG13920</i>	0.743	0.0157
<i>CG32022</i>	0.743	0.0157
<i>mahj</i>	0.742	0.0159
<i>Stam</i>	0.742	0.0159
<i>Br140</i>	0.741	0.016
<i>CG12219</i>	0.741	0.016
<i>Chd1</i>	0.741	0.016
<i>Cpsf100</i>	0.741	0.016
<i>sqz</i>	0.741	0.016
<i>CG3124</i>	0.74	0.0165
<i>lft</i>	0.74	0.0165
<i>CG10051</i>	0.739	0.0167
<i>CG30089</i>	0.739	0.0167
<i>chico</i>	0.739	0.0167
<i>sd</i>	0.739	0.0167
<i>CG1603</i>	0.738	0.017
<i>ES</i>	0.738	0.017
<i>epsilonCOP</i>	0.738	0.017
<i>Eap</i>	0.737	0.0173
<i>glob3</i>	0.737	0.0173
<i>str</i>	0.737	0.0173
<i>CG5888</i>	0.736	0.0176
<i>Gen</i>	0.736	0.0176
<i>CG3939</i>	0.735	0.0177
<i>CG10920</i>	0.733	0.0178
<i>nocte</i>	0.733	0.0178
<i>CG14488</i>	0.732	0.018
<i>CG14956</i>	0.732	0.018
<i>ash1</i>	0.731	0.0182
<i>CG15580</i>	0.731	0.0182
<i>CG4447</i>	0.731	0.0182
<i>CG3123</i>	0.73	0.0185
<i>CG13405</i>	0.729	0.0186
<i>CG14036</i>	0.729	0.0186
<i>Sym</i>	0.729	0.0186
<i>pen</i>	0.728	0.0188
<i>SamDC</i>	0.728	0.0188
<i>ear</i>	0.727	0.019
<i>spd-2</i>	0.727	0.019
<i>Rpn6</i>	0.725	0.0192
<i>CG2269</i>	0.724	0.0193
<i>CG42569</i>	0.723	0.0194
<i>CG6347</i>	0.722	0.0195
<i>CG9609</i>	0.721	0.0195
<i>Corp</i>	0.721	0.0195
<i>pr-set7</i>	0.721	0.0195
<i>gtzf</i>	0.72	0.0198
<i>kappaB-Ras</i>	0.72	0.0198
<i>MED31</i>	0.72	0.0198
<i>CG10494</i>	0.719	0.0201
<i>CG9894</i>	0.719	0.0201

Gene Name	ERC Value	P-value
<i>D19A</i>	0.719	0.0201
<i>CG5022</i>	0.718	0.0204
<i>Galpha73B</i>	0.718	0.0204
<i>Rcd5</i>	0.717	0.0205
<i>CG13298</i>	0.716	0.0206
<i>CG3213</i>	0.716	0.0206
<i>sob</i>	0.716	0.0206
<i>torp4a</i>	0.716	0.0206
<i>CG14718</i>	0.715	0.021
<i>CG31708</i>	0.715	0.021
<i>Yippee</i>	0.715	0.021
<i>CG4363</i>	0.714	0.0213
<i>CG7461</i>	0.714	0.0213
<i>CG13044</i>	0.713	0.0214
<i>CG14711</i>	0.713	0.0214
<i>CG8920</i>	0.713	0.0214
<i>mus301</i>	0.713	0.0214
<i>argos</i>	0.712	0.0218
<i>BHD</i>	0.712	0.0218
<i>BtbVII</i>	0.712	0.0218
<i>CG12241</i>	0.712	0.0218
<i>CG31710</i>	0.712	0.0218
<i>CG30273</i>	0.711	0.0223
<i>CG3605</i>	0.711	0.0223
<i>Oatp58Dc</i>	0.711	0.0223
<i>RpS24</i>	0.711	0.0223
<i>sec15</i>	0.711	0.0223
<i>CG11983</i>	0.71	0.0227
<i>CG6770</i>	0.709	0.0228
<i>eyg</i>	0.709	0.0228
<i>bip1</i>	0.708	0.023
<i>CG15766</i>	0.708	0.023
<i>CG4289</i>	0.708	0.023
<i>Cp190</i>	0.708	0.023
<i>CG2182</i>	0.707	0.0233
<i>CG7120</i>	0.706	0.0234
<i>CG7492</i>	0.706	0.0234
<i>hk</i>	0.706	0.0234
<i>vlg</i>	0.706	0.0234
<i>cbs</i>	0.705	0.0238
<i>CG11369</i>	0.705	0.0238
<i>Sam984</i>	0.705	0.0238
<i>CG2277</i>	0.705	0.0238
<i>CG33178</i>	0.705	0.0238
<i>CG42542</i>	0.705	0.0238
<i>CG2700</i>	0.705	0.0238
<i>CG7082</i>	0.705	0.0238
<i>gcm</i>	0.705	0.0238
<i>mus101</i>	0.705	0.0238
<i>RhoGAP19C</i>	0.705	0.0238
<i>Aef1</i>	0.704	0.0248
<i>Cda9</i>	0.704	0.0248
<i>CG12320</i>	0.703	0.025
<i>CG3860</i>	0.703	0.025
<i>CG10077</i>	0.701	0.0251
<i>CG42506</i>	0.701	0.0251

Table 6.S16 Continued

Gene Name	ERC Value	P-value
Drep-3	0.701	0.0251
PNUTS	0.701	0.0251
CG30460	0.7	0.0255
CG7718	0.7	0.0255
CG13786	0.699	0.0257
CG34425	0.699	0.0257
Klp61F	0.699	0.0257
CG10326	0.698	0.0259
CG14282	0.698	0.0259
CG8027	0.698	0.0259
CG9727	0.698	0.0259
gpp	0.698	0.0259
CG4810	0.697	0.0264
pav	0.697	0.0264
CG11248	0.696	0.0266
CG16813	0.696	0.0266
CG4073	0.696	0.0266
CG5728	0.696	0.0266
CG6385	0.696	0.0266
fg96Cb	0.696	0.0266
RhoGAP68F	0.696	0.0266
CG11889	0.695	0.0272
CG1553	0.695	0.0272
tsh	0.694	0.0274
CG15073	0.692	0.0275
CG32792	0.692	0.0275
l(2)k09022	0.692	0.0275
MEQ16	0.692	0.0275
Pros54	0.692	0.0275
Apc10	0.691	0.0279
CG12099	0.691	0.0279
CG17180	0.691	0.0279
CG18682	0.691	0.0279
CG7597	0.691	0.0279
CG7759	0.691	0.0279
Cyp12d1-p	0.691	0.0279
dpr16	0.691	0.0279
MTA1-like	0.691	0.0279
CG7627	0.69	0.0287
brk	0.689	0.0288
CG13375	0.689	0.0288
CG17181	0.689	0.0288
CG4612	0.689	0.0288
CG10274	0.688	0.0292
CG6509	0.688	0.0292
CG8918	0.688	0.0292
CG9395	0.688	0.0292
tey	0.688	0.0292
Tsp26A	0.688	0.0292
CG10588	0.687	0.0297
CG13408	0.687	0.0297
CG18599	0.687	0.0297
CycA	0.687	0.0297
Herp	0.687	0.0297
Sln	0.687	0.0297
CG5830	0.686	0.0303

Gene Name	ERC Value	P-value
E2f	0.686	0.0303
CG42666	0.685	0.0305
CG4230	0.684	0.0305
CG4538	0.684	0.0305
pcs	0.684	0.0305
Ranbp9	0.684	0.0305
tamo	0.684	0.0305
CG13745	0.683	0.031
CG5524	0.683	0.031
CG10555	0.682	0.0312
CG6792	0.682	0.0312
CG10435	0.681	0.0314
CG14085	0.681	0.0314
mRpl14	0.681	0.0314
CG31803	0.68	0.0316
srw	0.68	0.0316
CG12026	0.678	0.0318
CG13594	0.678	0.0318
CG2083	0.678	0.0318
CG6568	0.678	0.0318
CG9248	0.678	0.0318
llp4	0.677	0.0323
eEF1delta	0.676	0.0323
Sin3A	0.676	0.0323
aay	0.675	0.0325
tadr	0.675	0.0325
CG13287	0.674	0.0327
CG3493	0.674	0.0327
CG2126	0.673	0.0329
Fancd2	0.673	0.0329
beta4GalNA	0.672	0.0331
CG12253	0.671	0.0332
polybromo	0.671	0.0332
Arp5	0.67	0.0333
CG14439	0.67	0.0333
Ets96B	0.67	0.0333
Patsas	0.67	0.0333
Pcl	0.67	0.0333
seq	0.67	0.0333
CG14511	0.669	0.0339
CG3457	0.669	0.0339
dpr	0.669	0.0339
RluA-2	0.669	0.0339
Spp	0.669	0.0339
U2af50	0.669	0.0339
unpg	0.669	0.0339
Wnk	0.669	0.0339
CG10516	0.668	0.0346
Sirt7	0.668	0.0346
CG10927	0.667	0.0348
CG11964	0.667	0.0348
CG4041	0.667	0.0348
CG9427	0.667	0.0348
Hira	0.667	0.0348
CG17343	0.666	0.0352
CG31798	0.666	0.0352

Gene Name	ERC Value	P-value
CG7372	0.666	0.0352
DnaJ-60	0.666	0.0352
HLH54F	0.666	0.0352
ppk	0.666	0.0352
Tak1	0.666	0.0352
tomb	0.666	0.0352
CG9005	0.665	0.0359
Den1	0.665	0.0359
CG11977	0.664	0.0361
CG17672	0.664	0.0361
CG33696	0.664	0.0361
CG6067	0.664	0.0361
Chrac-14	0.664	0.0361
CG12207	0.663	0.0366
CG17387	0.663	0.0366
CG18558	0.663	0.0366
corn	0.663	0.0366
CG12576	0.662	0.0369
CG30015	0.662	0.0369
Oatp58Da	0.662	0.0369
CG1529	0.661	0.0372
CG6441	0.661	0.0372
CG10566	0.66	0.0374
CG12869	0.66	0.0374
CG3104	0.66	0.0374
CG34176	0.66	0.0374
wit	0.66	0.0374
CG9676	0.659	0.0378
twi	0.659	0.0378
CG11317	0.658	0.038
CG31183	0.658	0.038
CG4218	0.658	0.038
her	0.658	0.038
CG5823	0.657	0.0384
CG6673	0.657	0.0384
CG7140	0.657	0.0384
comr	0.657	0.0384
dx	0.657	0.0384
Hmt-1	0.657	0.0384
mRps14	0.657	0.0384
CG1951	0.656	0.039
CG34388	0.656	0.039
CG12420	0.655	0.0392
CG6734	0.655	0.0392
pad	0.655	0.0392
Prp18	0.655	0.0392
Riff1	0.655	0.0392
CG11060	0.654	0.0396
CG13917	0.654	0.0396
CG3092	0.654	0.0396
CG3532	0.654	0.0396
KalIRIA	0.654	0.0396
mxc	0.654	0.0396
sub	0.654	0.0396
Ubp64E	0.654	0.0396
CG31730	0.653	0.0404

Gene Name	ERC Value	P-value
CG42820	0.653	0.0404
CG4324	0.653	0.0404
CG34319	0.652	0.0406
Nhe3	0.652	0.0406
CG13539	0.651	0.0408
CG31531	0.651	0.0408
CG42533	0.651	0.0408
wda	0.651	0.0408
Aats-gly	0.65	0.0412
Crz	0.65	0.0412
Glu-RI	0.65	0.0412
noc	0.65	0.0412
odd	0.65	0.0412
sds22	0.65	0.0412
Spt5	0.65	0.0412
beat-11b	0.649	0.0418
CG11534	0.649	0.0418
CG12304	0.649	0.0418
CG13183	0.649	0.0418
CG3548	0.649	0.0418
CG8818	0.649	0.0418
CG9883	0.649	0.0418
Su(Tpl)	0.649	0.0418
fy	0.648	0.0425
Gdh	0.648	0.0425
imd	0.648	0.0425
lok	0.648	0.0425
sage	0.648	0.0425
CG4476	0.647	0.043
Tim17b1	0.646	0.0431
bs	0.645	0.0432
CG12360	0.645	0.0432
CG14803	0.645	0.0432
CG14817	0.645	0.0432
CG15099	0.645	0.0432
CG9368	0.645	0.0432
CG13055	0.644	0.0437
CG34039	0.644	0.0437
RPA2	0.644	0.0437
CG13250	0.643	0.044
CG7194	0.643	0.044
HP4	0.643	0.044
pnr	0.643	0.044
CG15278	0.642	0.0443
Obp59a	0.642	0.0443
CG11985	0.641	0.0445
CG8765	0.641	0.0445
omd	0.641	0.0445
CG42676	0.64	0.0448
CG7747	0.64	0.0448
KCNQ	0.64	0.0448
bond	0.639	0.045
CG10107	0.639	0.045
CG31870	0.638	0.0452
CG33322	0.638	0.0452
CG7148	0.638	0.0452

Gene Name	ERC Value	P-value
CG9393	0.638	0.0452
Hel25E	0.638	0.0452
Sec16	0.638	0.0452
Suv4-20	0.638	0.0452
LBR	0.637	0.0459
mRps24	0.637	0.0459
ORMDL	0.637	0.0459
RhoGAP54C	0.637	0.0459
CG8087	0.636	0.0462
Max	0.636	0.0462
sina	0.636	0.0462
CG17184	0.635	0.0465
CG34015	0.635	0.0465
CG17648	0.634	0.0467
CG31851	0.634	0.0467
CG4676	0.634	0.0467
CG5726	0.634	0.0467
CG9305	0.634	0.0467
Rrp4	0.634	0.0467
alpha4GT1	0.633	0.0472
CG12540	0.633	0.0472
CG18476	0.633	0.0472
CG31191	0.633	0.0472
CG5850	0.633	0.0472
SeiD	0.633	0.0472
wek	0.633	0.0472
aru	0.632	0.0478
CaipA	0.632	0.0478
CG17290	0.63	0.048
CG4074	0.63	0.048
CG4820	0.63	0.048
Lrk	0.63	0.048
CG5018	0.629	0.0484
ix	0.629	0.0484
Sox100B	0.629	0.0484
biv	0.628	0.0486
CG11015	0.628	0.0486
CG12464	0.628	0.0486
CG5116	0.627	0.0489
ETHR	0.627	0.0489
Ptp45	0.627	0.0489
CG13185	0.626	0.0492
CG3508	0.626	0.0492
Std5	0.626	0.0492
CG15577	0.625	0.0495
CG42336	0.625	0.0495
CG4452	0.625	0.0495
Cpr64Ad	0.625	0.0495
Art6	0.624	0.0498
CG12744	0.624	0.0498
Csk	0.624	0.0498
CstF-64	0.624	0.0498
CG17490	0.623	0.0502
CG30403	0.623	0.0502
CG9951	0.623	0.0502
neuroligin	0.623	0.0502

Table 6.S16 Continued

Gene Name	ERC Value	P-value
CG14607	0.622	0.0505
CG3509	0.622	0.0505
CG4406	0.622	0.0505
mtacp1	0.622	0.0505
CG12299	0.621	0.0509
CG17199	0.621	0.0509
CG31688	0.621	0.0509
CG33120	0.621	0.0509
CG4360	0.621	0.0509
CG9586	0.621	0.0509
Dref	0.621	0.0509
Sgfl1	0.621	0.0509
CG11808	0.62	0.0516
CG18269	0.62	0.0516
CG4953	0.62	0.0516
CG9418	0.62	0.0516
Opbp	0.62	0.0516
X11L	0.62	0.0516
aret	0.619	0.0522
beta4GalNA	0.619	0.0522
CG10428	0.619	0.0522
CG10984	0.619	0.0522
CG18011	0.619	0.0522
Rab21	0.619	0.0522
trem	0.619	0.0522
CG14132	0.618	0.0528
Phlpp	0.618	0.0528
qua	0.618	0.0528
Sap130	0.618	0.0528
CG3570	0.617	0.0532
CG8187	0.617	0.0532
sec23	0.617	0.0532
sev	0.617	0.0532
Shawn	0.617	0.0532
Sos	0.617	0.0532
CG12643	0.616	0.0537
CG32793	0.616	0.0537
HLLHmdelta	0.616	0.0537
Sry-delta	0.616	0.0537
CG10889	0.615	0.0541
CG4570	0.615	0.0541
CG8298	0.615	0.0541
dwg	0.615	0.0541
trr	0.615	0.0541
CG10064	0.614	0.0545
CG12693	0.614	0.0545
CG4925	0.614	0.0545
Sfmbt	0.614	0.0545
CG13366	0.613	0.0549
CG2889	0.613	0.0549
CG3437	0.613	0.0549
fend	0.613	0.0549
Hr78	0.613	0.0549
CG12825	0.612	0.0553
CG4393	0.612	0.0553
CG13617	0.611	0.0555

Gene Name	ERC Value	P-value
CG5214	0.611	0.0555
RFC3	0.611	0.0555
CG10543	0.61	0.0558
CG4238	0.61	0.0558
CG4768	0.61	0.0558
Cpr72Ea	0.61	0.0558
Sc2	0.61	0.0558
Obp47a	0.609	0.0562
CG13717	0.608	0.0563
CG5385	0.608	0.0563
POSH	0.608	0.0563
Bap170	0.607	0.0566
CG12171	0.607	0.0566
CG16868	0.607	0.0566
CG17777	0.607	0.0566
poe	0.607	0.0566
CG12316	0.606	0.057
CG1962	0.606	0.057
CG6418	0.606	0.057
CSN8	0.606	0.057
Ccp84Ac	0.605	0.0574
CG17807	0.605	0.0574
Dscam3	0.605	0.0574
stf	0.605	0.0574
CG1602	0.604	0.0577
CG33339	0.604	0.0577
CG6689	0.604	0.0577
Cul-2	0.604	0.0577
Cyp4c3	0.604	0.0577
iHog	0.604	0.0577
Sans	0.604	0.0577
CG31793	0.603	0.0584
CG9752	0.603	0.0584
Sin1	0.603	0.0584
ssp4	0.603	0.0584
CG7196	0.602	0.0587
Ndc80	0.602	0.0587
CG34007	0.601	0.0589
Egfr	0.601	0.0589
CG1675	0.6	0.0591
CG34214	0.6	0.0591
CG4119	0.6	0.0591
ind	0.6	0.0591
CG31898	0.599	0.0595
CG33341	0.599	0.0595
CG9673	0.599	0.0595
ftz	0.599	0.0595
Lap1	0.599	0.0595
robl22E	0.599	0.0595
Acp32CD	0.598	0.06
CG1657	0.598	0.06
CG3955	0.598	0.06
Git	0.598	0.06
PHGPx	0.598	0.06
CG6379	0.597	0.0605
CG8004	0.597	0.0605

Gene Name	ERC Value	P-value
da	0.597	0.0605
Su(H)	0.597	0.0605
CG32082	0.596	0.0608
CG33051	0.596	0.0608
Pros28.1B	0.596	0.0608
Apc2	0.595	0.0611
CG14760	0.595	0.0611
tor	0.595	0.0611
bsh	0.594	0.0614
Cas	0.594	0.0614
CG3831	0.594	0.0614
CG9629	0.594	0.0614
r-cup	0.594	0.0614
S	0.594	0.0614
CG33111	0.593	0.0619
CG4662	0.593	0.0619
cid	0.593	0.0619
Pdk	0.593	0.0619
Vps16B	0.593	0.0619
CG7197	0.592	0.0623
CG8159	0.592	0.0623
CHES-1-like	0.592	0.0623
pk	0.592	0.0623
CG10623	0.591	0.0627
CG14005	0.591	0.0627
CG15256	0.591	0.0627
CG42514	0.591	0.0627
fu2	0.591	0.0627
nes	0.591	0.0627
CG13297	0.589	0.0632
CG17032	0.589	0.0632
CG2014	0.589	0.0632
CG6908	0.589	0.0632
Dot	0.589	0.0636
Fjp1	0.589	0.0636
cg	0.588	0.0638
CG15087	0.588	0.0638
CG3797	0.588	0.0638
dve	0.588	0.0638
D	0.587	0.0641
Poxn	0.587	0.0641
Sema-1b	0.587	0.0641
Task7	0.587	0.0641
Cep97	0.586	0.0645
CG17782	0.586	0.0645
RhoGAP15E	0.586	0.0645
CG13843	0.585	0.0648
zf30C	0.585	0.0648
BBS4	0.584	0.065
CG12995	0.584	0.065
CG32437	0.584	0.065
CG42508	0.584	0.065
CG4377	0.584	0.065
Drep-2	0.584	0.065
lMdr49	0.584	0.065
MED24	0.584	0.065

Gene Name	ERC Value	P-value
CG34367	0.583	0.0657
CG5556	0.582	0.0658
Sb	0.582	0.0658
CG12321	0.581	0.0659
CG31635	0.581	0.0659
CG42769	0.581	0.0659
CG7609	0.581	0.0659
CG8388	0.581	0.0659
croI	0.581	0.0659
fok	0.581	0.0659
pros	0.581	0.0659
Rpb5	0.581	0.0659
Tusp	0.581	0.0659
CG13531	0.58	0.0668
CG16926	0.58	0.0668
CG13350	0.579	0.067
CG6695	0.579	0.067
ds	0.579	0.067
PSR	0.579	0.067
Spindly	0.579	0.067
CG5180	0.578	0.0675
CG5346	0.578	0.0675
CG6310	0.578	0.0675
CG9053	0.578	0.0675
CG9797	0.578	0.0675
kat-60L1	0.578	0.0675
capu	0.577	0.068
CG12395	0.577	0.068
CG1575	0.577	0.068
CG3491	0.577	0.068
TwilZ	0.577	0.068
CG13474	0.576	0.0685
CG3925	0.576	0.0685
CG4300	0.576	0.0685
CG8329	0.576	0.0685
l(3)psg2	0.576	0.0685
opa1-like	0.576	0.0685
Tbp-1	0.576	0.0685
CG8509	0.575	0.0691
pkaap	0.575	0.0691
Sse	0.575	0.0691
CG11377	0.574	0.0694
CG12438	0.574	0.0694
CG13038	0.574	0.0694
CG3492	0.574	0.0694
CG42678	0.574	0.0694
CG8281	0.574	0.0694
Jafrac1	0.574	0.0694
CG31296	0.573	0.07
CG6142	0.573	0.07
CG6984	0.573	0.07
Coq2	0.573	0.07
dom	0.573	0.07
Nf-YC	0.573	0.07
Taf11	0.573	0.07
Vsx2	0.573	0.07

Gene Name	ERC Value	P-value
CG10399	0.572	0.0707
CG13306	0.572	0.0707
CG34401	0.572	0.0707
CG4004	0.572	0.0707
CG9452	0.572	0.0707
Cyp9c1	0.572	0.0707
Nacalpa	0.572	0.0707
Abi	0.571	0.0714
CG17593	0.571	0.0714
CG3975	0.571	0.0714
exo70	0.571	0.0714
FucTA	0.571	0.0714
kel	0.571	0.0714
Parg	0.571	0.0714
CG31607	0.57	0.072
CG32113	0.57	0.072
Aps	0.569	0.0722
CG11448	0.569	0.0722
Myt1	0.569	0.0722
Or45b	0.569	0.0722
sad	0.569	0.0722
CG10979	0.568	0.0726
CG13409	0.568	0.0726
Nlp	0.568	0.0726
CG4286	0.567	0.0729
sec6	0.567	0.0729
wls	0.567	0.0729
CG7872	0.566	0.0732
CG8735	0.566	0.0732
CG8959	0.566	0.0732
Tektin-A	0.566	0.0732
wfs1	0.566	0.0732
CG34404	0.565	0.0736
CG34457	0.565	0.0736
Edg84A	0.565	0.0736
LSm7	0.565	0.0736
Moe	0.565	0.0736
MRG15	0.565	0.0736
RagC	0.565	0.0736
RpL34b	0.565	0.0736
CG34116	0.564	0.0743
CG3698	0.564	0.0743
lab	0.564	0.0743
orb	0.564	0.0743
phyl	0.564	0.0743
skf	0.564	0.0743
smt3	0.564	0.0743
CG13111	0.563	0.075
CG13151	0.563	0.075
CG5623	0.563	0.075
CG6841	0.563	0.075
CG7139	0.563	0.075
CG9130	0.563	0.075
Nup214	0.563	0.075
CG13123	0.562	0.0756
CG7080	0.562	0.0756

Table 6.S16 Continued

Gene Name	ERC Value	P-value
CG11165	0.561	0.0758
CG1271	0.561	0.0758
CG14529	0.561	0.0758
CG14721	0.561	0.0758
CG7251	0.561	0.0758
pfk	0.561	0.0758
CG14659	0.56	0.0763
CG14892	0.56	0.0763
ems	0.56	0.0763
foi	0.56	0.0763
Acp53C14c	0.559	0.0767
Ance-2	0.558	0.0768
caup	0.558	0.0768
CG6745	0.558	0.0768
CG7692	0.558	0.0768
CG7879	0.558	0.0768
hig	0.558	0.0768
Rlc1	0.558	0.0768
Su(var)3-3	0.558	0.0768
CG10104	0.557	0.0775
CG3292	0.557	0.0775
CG42288	0.557	0.0775
CG5110	0.557	0.0775
CG7841	0.557	0.0775
frtz	0.557	0.0775
Hip1	0.557	0.0775
NlPp1	0.557	0.0775
CG7154	0.556	0.0782
ncm	0.556	0.0782
Sir2	0.556	0.0782
skl	0.556	0.0782
CG32280	0.555	0.0786
Syx5	0.555	0.0786
CG12379	0.554	0.0787
CG13204	0.554	0.0787
CG15651	0.554	0.0787
CG18004	0.554	0.0787
CG10914	0.553	0.0791
CG13322	0.553	0.0791
CG30104	0.553	0.0791
CG7173	0.553	0.0791
CG8165	0.553	0.0791
CG11125	0.552	0.0795
CG4338	0.552	0.0795
pwn	0.552	0.0795
sut2	0.552	0.0795
CG10164	0.551	0.0799
CG17266	0.551	0.0799
CG4615	0.551	0.0799
CG5089	0.551	0.0799
CG6024	0.551	0.0799
bcd	0.55	0.0804
CG6971	0.55	0.0804
CG9541	0.55	0.0804
CTCF	0.55	0.0804
CG4069	0.549	0.0807

Gene Name	ERC Value	P-value
Nup107	0.549	0.0807
tum	0.549	0.0807
CG12734	0.548	0.081
CG13436	0.548	0.081
CG14921	0.548	0.081
HLH106	0.548	0.081
mri	0.548	0.081
CG11596	0.547	0.0814
CG12075	0.547	0.0814
CG18812	0.547	0.0814
CG3880	0.547	0.0814
CG9855	0.547	0.0814
zwlch	0.547	0.0814
CG5024	0.546	0.082
CG32221	0.545	0.0821
CG34204	0.545	0.0821
CG5198	0.545	0.0821
Myd88	0.545	0.0821
Trn-SR	0.545	0.0821
CG17098	0.544	0.0825
CG1792	0.544	0.0825
CG4996	0.544	0.0825
pgant3	0.544	0.0825
Ranbp11	0.544	0.0825
CG7787	0.543	0.083
gogo	0.543	0.083
l(3)2D3	0.543	0.083
psq	0.543	0.083
spen	0.543	0.083
CG17768	0.542	0.0834
CG31869	0.542	0.0834
CG8230	0.542	0.0834
CG9934	0.542	0.0834
Lam	0.542	0.0834
Mob4	0.542	0.0834
CG14626	0.541	0.084
CG15888	0.541	0.084
CG7264	0.541	0.084
fus	0.541	0.084
ninaE	0.541	0.084
CG3309	0.54	0.0844
CG6006	0.54	0.0844
CG6592	0.54	0.0844
CG8852	0.54	0.0844
Exn	0.54	0.0844
Pp2C1	0.54	0.0844
thr	0.54	0.0844
asun	0.539	0.085
CG12091	0.539	0.085
CG13398	0.539	0.085
CG3168	0.539	0.085
CG8564	0.539	0.085
SC35	0.539	0.085
CG11447	0.538	0.0856
CG12107	0.538	0.0856
CG12134	0.538	0.0856

Gene Name	ERC Value	P-value
CG13086	0.538	0.0856
CG14752	0.538	0.0856
CG15744	0.538	0.0856
CG15817	0.538	0.0856
CG30115	0.538	0.0856
CG32579	0.538	0.0856
phm	0.538	0.0856
pigeon	0.538	0.0856
SAK	0.538	0.0856
blos2	0.537	0.0867
c11.1	0.537	0.0867
CG15142	0.537	0.0867
CG32685	0.537	0.0867
CG5863	0.537	0.0867
Sg729	0.537	0.0867
CG34301	0.536	0.0872
dgo	0.536	0.0872
l(3)76BDM	0.536	0.0872
Rga	0.536	0.0872
CG13186	0.535	0.0876
CG18811	0.535	0.0876
Cpr47Eb	0.535	0.0876
Atg12	0.534	0.0878
CG10163	0.534	0.0878
CG10741	0.534	0.0878
CG5859	0.534	0.0878
CG6293	0.534	0.0878
CG6332	0.534	0.0878
Adgf-D	0.533	0.0884
CG14710	0.533	0.0884
CG5931	0.533	0.0884
CG7246	0.533	0.0884
CG14126	0.532	0.0887
Cpr78Cc	0.532	0.0887
RpL35	0.532	0.0887
CG17764	0.531	0.089
CG3651	0.531	0.089
RIC-3	0.531	0.089
Aats-thr	0.53	0.0893
Act88F	0.53	0.0893
CG1227	0.53	0.0893
CG31913	0.53	0.0893
CG7394	0.53	0.0893
Nup98	0.53	0.0893
Ugt	0.53	0.0893
CG10646	0.529	0.0899
CG14823	0.529	0.0899
CG15258	0.529	0.0899
CG3589	0.529	0.0899
Map60	0.529	0.0899
mew	0.529	0.0899
mthl5	0.529	0.0899
E2f2	0.528	0.0905
glo	0.528	0.0905
MSBP	0.528	0.0905
CG3687	0.527	0.0908

Gene Name	ERC Value	P-value
CG4802	0.527	0.0908
CG4829	0.527	0.0908
fff	0.527	0.0908
Nup44A	0.527	0.0908
skpB	0.527	0.0908
BBS1	0.526	0.0914
CG14377	0.526	0.0914
CG32846	0.526	0.0914
CG42284	0.526	0.0914
CG9063	0.526	0.0914
Rho1	0.526	0.0914
ana2	0.525	0.0919
CG3499	0.525	0.0919
CG5013	0.525	0.0919
CG8366	0.525	0.0919
l(2)05714	0.525	0.0919
CG9257	0.524	0.0923
enok	0.524	0.0923
fdlipidine	0.524	0.0923
CG13362	0.523	0.0926
CG4901	0.523	0.0926
CG7358	0.523	0.0926
CG7530	0.523	0.0926
Dgp-1	0.523	0.0926
dos	0.523	0.0926
l(2)05510	0.523	0.0926
Brf	0.522	0.0932
CG12680	0.522	0.0932
CG18327	0.522	0.0932
CG4203	0.522	0.0932
CG4374	0.522	0.0932
CG4757	0.522	0.0932
dpr20	0.522	0.0932
h-cup	0.522	0.0932
porln	0.522	0.0932
wee	0.522	0.0932
CG13386	0.521	0.0941
CG15093	0.521	0.0941
CG4751	0.521	0.0941
gro	0.521	0.0941
Tsp42Eh	0.521	0.0941
CG1120	0.52	0.0946
CG13198	0.52	0.0946
CG13743	0.52	0.0946
CG31871	0.52	0.0946
ETH	0.52	0.0946
MCPH1	0.52	0.0946
Acyp	0.519	0.0951
CG42258	0.519	0.0951
CG42455	0.519	0.0951
TI	0.519	0.0951
CG10144	0.518	0.0955
CG14915	0.518	0.0955
CG9666	0.518	0.0955
Deaf1	0.518	0.0955
hb	0.518	0.0955

Gene Name	ERC Value	P-value
ome	0.518	0.0955
tlk	0.518	0.0955
CG15571	0.517	0.0961
CG17922	0.517	0.0961
CG4080	0.517	0.0961
CG5872	0.517	0.0961
CG6664	0.517	0.0961
CG9147	0.517	0.0961
Prp31	0.517	0.0961
Snm1	0.517	0.0961
yemalpha	0.517	0.0961
CG10732	0.516	0.0969
CG34313	0.516	0.0969
Roc1b	0.516	0.0969
trk	0.516	0.0969
Ugt58Fa	0.516	0.0969
Utx	0.516	0.0969
CG10068	0.515	0.0975
CG12479	0.515	0.0975
CG3419	0.515	0.0975
CG9801	0.515	0.0975
pdm3	0.515	0.0975
phf1	0.515	0.0975
CG34282	0.514	0.098
CG3868	0.514	0.098
CG8963	0.514	0.098
Hrb87F	0.514	0.098
CG11380	0.513	0.0984
CG13565	0.513	0.0984
CG13624	0.513	0.0984
CG13700	0.513	0.0984
CG14720	0.513	0.0984
CG5498	0.513	0.0984
l(1)G0144	0.513	0.0984
MED8	0.513	0.0984
nmdyn-D7	0.513	0.0984
CG30161	0.512	0.0992
HPS1	0.512	0.0992
hyx	0.512	0.0992
Mst98Ca	0.512	0.0992
tau	0.512	0.0992
Mtor	0.511	0.0996
Rab40	0.511	0.0996
CG12173	0.51	0.0998
ns3	0.51	0.0998
tud	0.51	0.0998

Table 6.S17 - Top Genes ERC values for *rad50* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG6279	0.931	0.0001
CG2975	0.913	0.0002
<i>swif</i>	0.902	0.0003
CG8791	0.898	0.0004
<i>Eft1alpha100</i>	0.873	0.0005
CG16743	0.871	0.0005
CG14330	0.862	0.0006
<i>zpg</i>	0.862	0.0006
CG18806	0.861	0.0008
<i>ppk25</i>	0.86	0.0009
<i>CG15116</i>	0.845	0.001
CG33145	0.842	0.0011
CG3156	0.84	0.0012
<i>LanB2</i>	0.838	0.0013
<i>CiC-b</i>	0.836	0.0014
CG17765	0.834	0.0014
<i>cas</i>	0.833	0.0015
CG12674	0.828	0.0016
<i>Mes2</i>	0.828	0.0016
CG17124	0.826	0.0018
CG33689	0.826	0.0018
<i>tefu</i>	0.825	0.002
<i>sog</i>	0.824	0.0021
CG14662	0.823	0.0022
<i>bnb</i>	0.821	0.0023
<i>B4</i>	0.817	0.0023
CG33003	0.816	0.0024
CG11778	0.812	0.0025
<i>Pk17E</i>	0.809	0.0026
CG13333	0.806	0.0027
CG6277	0.806	0.0027
<i>Spn77Ba</i>	0.802	0.0029
CG4335	0.801	0.003
CG5976	0.79	0.0031
CG15674	0.787	0.0032
CG11360	0.785	0.0032
CG6044	0.785	0.0032
<i>pex1</i>	0.785	0.0032
<i>HipHop</i>	0.781	0.0035
<i>Hs2st</i>	0.78	0.0036
CG12883	0.778	0.0037
CG9899	0.778	0.0037
<i>LvpL</i>	0.777	0.0039
CG13312	0.775	0.004
CG31021	0.775	0.004
<i>Pgd</i>	0.774	0.0041
<i>Cdk8</i>	0.771	0.0042
CG10353	0.771	0.0042
CG15754	0.77	0.0044
<i>W</i>	0.77	0.0044
CG18234	0.767	0.0046
<i>plx</i>	0.766	0.0047
CG5958	0.759	0.0048
CG31636	0.758	0.0049
<i>Vm26Aa</i>	0.758	0.0049
<i>yrt</i>	0.758	0.0049

Gene Name	ERC Value	P-value
CG9993	0.757	0.0051
<i>cola</i>	0.757	0.0051
<i>scramb2</i>	0.757	0.0051
CG12898	0.756	0.0054
CG5602	0.756	0.0054
<i>puc</i>	0.755	0.0056
CG14380	0.754	0.0057
<i>sowah</i>	0.754	0.0057
CG13278	0.753	0.0059
<i>RpS18</i>	0.753	0.0059
CG30339	0.751	0.006
CG30381	0.751	0.006
CG7882	0.75	0.0062
CG18446	0.749	0.0063
CG3476	0.749	0.0063
<i>RpL31</i>	0.748	0.0065
CG4323	0.747	0.0066
<i>ppk12</i>	0.744	0.0067
<i>Kua</i>	0.743	0.0068
<i>CheB42c</i>	0.742	0.0068
CG8080	0.736	0.0069
<i>Fen1</i>	0.735	0.007
CG31199	0.734	0.0071
CG17140	0.733	0.0072
<i>Aats-ser</i>	0.732	0.0073
<i>Obp46a</i>	0.731	0.0074
CG13578	0.729	0.0075
<i>Ir68b</i>	0.729	0.0075
<i>wus</i>	0.728	0.0077
<i>ldh</i>	0.727	0.0077
CG12325	0.725	0.0078
CG30458	0.725	0.0078
CG31105	0.725	0.0078
CG15203	0.724	0.0081
CG11897	0.723	0.0082
CG15579	0.723	0.0082
CG17544	0.723	0.0082
CG31547	0.723	0.0082
CG7778	0.723	0.0082
<i>mRplL33</i>	0.723	0.0082
CG13919	0.72	0.0087
CG6356	0.72	0.0087
<i>Cp19</i>	0.72	0.0087
<i>Yp3</i>	0.72	0.0087
<i>GstD9</i>	0.718	0.0091
CG11327	0.716	0.0092
CG31731	0.715	0.0093
<i>Sox102F</i>	0.715	0.0093
CG6660	0.714	0.0095
CG8481	0.714	0.0095
CG32269	0.713	0.0096
CG5853	0.713	0.0096
CG42811	0.712	0.0098
<i>Or85d</i>	0.71	0.0099
CG2177	0.708	0.01
<i>Eig71Ef</i>	0.708	0.01

Gene Name	ERC Value	P-value
<i>NitFhit</i>	0.708	0.01
<i>Or83c</i>	0.708	0.01
CG13983	0.707	0.0104
CG30181	0.707	0.0104
CG8460	0.707	0.0104
CG9780	0.707	0.0104
CG16826	0.706	0.0107
CG8353	0.705	0.0108
CG9626	0.705	0.0108
<i>Or67b</i>	0.704	0.011
<i>Cyp4g1</i>	0.703	0.0111
CG5916	0.701	0.0112
CG13636	0.7	0.0113
CG6272	0.7	0.0113
<i>Nf1</i>	0.7	0.0113
CG30488	0.698	0.0115
CG4991	0.698	0.0115
CG8632	0.698	0.0115
<i>Gr64b</i>	0.698	0.0115
<i>Obp50d</i>	0.698	0.0115
<i>Or59a</i>	0.698	0.0115
<i>r-cup</i>	0.697	0.0121
<i>Thd1</i>	0.697	0.0121
<i>yellow-e</i>	0.697	0.0121
CG8490	0.696	0.0123
<i>Oatp33Ea</i>	0.696	0.0123
<i>p-cup</i>	0.696	0.0123
CG11505	0.695	0.0126
<i>Gs1</i>	0.695	0.0126
CG10096	0.693	0.0128
<i>ial</i>	0.693	0.0128
CG18609	0.692	0.013
<i>Cyp12b2</i>	0.692	0.013
CG14701	0.691	0.0132
CG5941	0.691	0.0132
<i>Osi1</i>	0.691	0.0132
<i>wntD</i>	0.691	0.0132
CG30010	0.69	0.0135
CG30371	0.689	0.0136
CG14691	0.688	0.0137
CG11320	0.686	0.0138
CG9740	0.684	0.0139
<i>loj</i>	0.684	0.0139
<i>Orc6</i>	0.684	0.0139
CG5254	0.683	0.0141
<i>Gr97a</i>	0.683	0.0141
<i>Cad89D</i>	0.681	0.0143
<i>Gr66a</i>	0.681	0.0143
<i>Ir56d</i>	0.681	0.0143
<i>Ir94f</i>	0.681	0.0143
<i>Arc42</i>	0.68	0.0147
CG13506	0.679	0.0148
<i>E2f2</i>	0.679	0.0148
CG16996	0.678	0.015
CG32103	0.677	0.015
CG12811	0.676	0.0151

Gene Name	ERC Value	P-value
CG16908	0.676	0.0151
CG31357	0.676	0.0151
CG33558	0.676	0.0151
<i>dsx</i>	0.675	0.0155
<i>Prestin</i>	0.675	0.0155
<i>Adgf-B</i>	0.674	0.0157
CG1213	0.674	0.0157
CG14286	0.674	0.0157
<i>yin</i>	0.674	0.0157
CG15625	0.673	0.016
CG13544	0.672	0.0161
CG5569	0.672	0.0161
<i>aph-1</i>	0.671	0.0163
<i>beat-Vc</i>	0.671	0.0163
CG14040	0.671	0.0163
CG14277	0.671	0.0163
<i>Vha100-2</i>	0.671	0.0163
CG13344	0.67	0.0168
CG9569	0.67	0.0168
CG9981	0.67	0.0168
<i>upd2</i>	0.67	0.0168
CG14234	0.669	0.0171
<i>kappaTry</i>	0.669	0.0171
<i>Aats-gln</i>	0.667	0.0173
CG3825	0.667	0.0173
CG9990	0.667	0.0173
CG14200	0.666	0.0176
CG42269	0.666	0.0176
<i>Tb</i>	0.666	0.0176
CG13887	0.665	0.0178
CG1394	0.665	0.0178
CG17264	0.665	0.0178
CG17597	0.665	0.0178
CG17565	0.664	0.0182
CG13795	0.663	0.0183
<i>Cyp6i3</i>	0.663	0.0183
CG6196	0.662	0.0185
CG8837	0.662	0.0185
<i>Twid1D</i>	0.662	0.0185
CG6865	0.661	0.0187
CG14483	0.66	0.0188
CG13893	0.66	0.0188
<i>NAAT1</i>	0.659	0.019
CG18271	0.658	0.0191
CG31200	0.658	0.0191
CG5261	0.658	0.0191
CG12426	0.656	0.0194
CG14609	0.656	0.0194
CG6178	0.656	0.0194
<i>Rad51D</i>	0.656	0.0194
<i>WASp</i>	0.656	0.0194
<i>Impl3</i>	0.655	0.0198
<i>Pak3</i>	0.655	0.0198
CG7329	0.654	0.02
CG14302	0.653	0.0201
CG5630	0.653	0.0201

Gene Name	ERC Value	P-value
<i>Flo-2</i>	0.653	0.0201
<i>Hml</i>	0.653	0.0201
<i>Gr22e</i>	0.652	0.0205
<i>moody</i>	0.652	0.0205
<i>Myb</i>	0.652	0.0205
<i>RtnI1</i>	0.652	0.0205
CG31233	0.651	0.0208
<i>ppk19</i>	0.651	0.0208
<i>CalpB</i>	0.65	0.021
CG5246	0.65	0.021
<i>scr1</i>	0.65	0.021
CG3119	0.649	0.0213
<i>Vha16-1</i>	0.649	0.0213
CG7058	0.648	0.0214
<i>Ephrin</i>	0.648	0.0214
<i>Nnp-1</i>	0.648	0.0214
CG9086	0.647	0.0217
<i>LanB1</i>	0.647	0.0217
CG8563	0.646	0.0219
<i>brn</i>	0.645	0.022
CG7580	0.645	0.022
CG13581	0.644	0.0222
CG1850	0.644	0.0222
CG31976	0.644	0.0222
<i>epsilonTry</i>	0.644	0.0222
CG15739	0.643	0.0225
<i>mbc</i>	0.642	0.0226
CG12679	0.64	0.0227
<i>Spn42Dc</i>	0.64	0.0227
CG6283	0.639	0.0229
<i>glg</i>	0.639	0.0229
<i>r1</i>	0.638	0.0231
<i>zfh2</i>	0.638	0.0231
CG3513	0.637	0.0232
<i>Fit1</i>	0.637	0.0232
<i>mia</i>	0.637	0.0232
<i>Best1</i>	0.636	0.0235
<i>Bgb</i>	0.636	0.0235
CG10584	0.636	0.0235
CG11284	0.635	0.0238
CG11563	0.635	0.0238
CG13893	0.635	0.0238
CG2680	0.635	0.0238
<i>Men1-2</i>	0.635	0.0238
CG14111	0.634	0.0242
CG14641	0.634	0.0242
CG31694	0.634	0.0242
<i>dj-1beta</i>	0.634	0.0242
CG10289	0.633	0.0246
CG11601	0.633	0.0246
CG7371	0.633	0.0246
CG13501	0.632	0.0249
CG13936	0.632	0.0249
CG3544	0.632	0.0249
<i>wa-cup</i>	0.632	0.0249
CG10116	0.631	0.0252

Table 6.S17 Continued

Gene Name	ERC Value	P-value
CG10591	0.631	0.0252
CG13463	0.631	0.0252
ms(2)34Fe	0.631	0.0252
CG34202	0.63	0.0256
CG8665	0.63	0.0256
Ppdc	0.63	0.0256
ABCB7	0.629	0.0259
CG3085	0.629	0.0259
LamC	0.629	0.0259
CG14194	0.628	0.0261
CG7830	0.628	0.0261
Chit	0.628	0.0261
alpha-Est8	0.627	0.0264
CG11221	0.627	0.0264
CG42558	0.627	0.0264
Cyp9f2	0.627	0.0264
Nurf-38	0.627	0.0264
CG14606	0.625	0.0268
CG15173	0.625	0.0268
mtg	0.625	0.0268
Ppn	0.625	0.0268
CG17337	0.624	0.0272
CG34201	0.624	0.0272
Or85f	0.624	0.0272
Pdi	0.624	0.0272
Rh4	0.624	0.0272
CG9643	0.623	0.0277
CG1698	0.622	0.0277
CG30384	0.622	0.0277
Or94a	0.622	0.0277
Ac78E	0.621	0.028
CG10311	0.621	0.028
CG6617	0.621	0.028
CG8774	0.621	0.028
CG30502	0.62	0.0284
CG13065	0.619	0.0285
CG16762	0.619	0.0285
CG9536	0.619	0.0285
Fbp2	0.619	0.0285
att-ORFA	0.618	0.0288
CG13088	0.618	0.0288
CG31814	0.618	0.0288
onecut	0.618	0.0288
aop	0.617	0.0292
Or9a	0.617	0.0292
CG5376	0.616	0.0294
CG8596	0.616	0.0294
lrf0a	0.616	0.0294
Npc1b	0.616	0.0294
Or22c	0.616	0.0294
CG11655	0.615	0.0298
CG5783	0.615	0.0298
elF4G	0.615	0.0298
lgs	0.615	0.0298
lox	0.615	0.0298
Or67d	0.615	0.0298

Gene Name	ERC Value	P-value
CG13847	0.614	0.0304
CG33061	0.614	0.0304
lpp	0.614	0.0304
scaf	0.614	0.0304
CG1124	0.613	0.0307
CG31189	0.613	0.0307
CG32112	0.613	0.0307
CG11349	0.612	0.031
CG13250	0.612	0.031
CG6114	0.612	0.031
CG8177	0.612	0.031
Fps85D	0.612	0.031
Hn	0.612	0.031
Obp58c	0.612	0.031
RpL21	0.612	0.031
Cdk5	0.611	0.0317
CG30344	0.611	0.0317
CG4409	0.611	0.0317
COQ7	0.611	0.0317
Mekk1	0.611	0.0317
AnnX	0.61	0.0322
CG8525	0.61	0.0322
CG9222	0.61	0.0322
Or35a	0.609	0.0324
Or85c	0.609	0.0324
bgm	0.608	0.0326
CG13102	0.608	0.0326
MP1	0.608	0.0326
Rh6	0.608	0.0326
CG17746	0.607	0.033
CG2187	0.607	0.033
CG31441	0.607	0.033
CG9865	0.607	0.033
Orct	0.607	0.033
CG15555	0.606	0.0334
CG3032	0.606	0.0334
CG33722	0.606	0.0334
CG7816	0.606	0.0334
CG8839	0.606	0.0334
LanA	0.606	0.0334
CG13833	0.605	0.034
CG15554	0.605	0.034
CG8303	0.605	0.034
Mpp6	0.605	0.034
CG10970	0.604	0.0343
CG17267	0.604	0.0343
Hsp26	0.604	0.0343
ppk6	0.604	0.0343
rk	0.604	0.0343
RpL36	0.604	0.0343
CG14815	0.603	0.0349
gwl	0.603	0.0349
Hf	0.603	0.0349
CG12971	0.602	0.0351
CG1319	0.602	0.0351
CG17999	0.602	0.0351

Gene Name	ERC Value	P-value
CG2082	0.602	0.0351
Obp56a	0.602	0.0351
CG13120	0.601	0.0356
CG15406	0.601	0.0356
CG15824	0.601	0.0356
CG18675	0.601	0.0356
CG4586	0.601	0.0356
CG8693	0.601	0.0356
ema	0.601	0.0356
Mkrr1	0.601	0.0356
pst	0.601	0.0356
stck	0.601	0.0356
whd	0.601	0.0356
CG11353	0.6	0.0366
CG33704	0.6	0.0366
CG5932	0.6	0.0366
Neif-A	0.6	0.0366
Vang	0.6	0.0366
upd3	0.599	0.037
CG13458	0.598	0.0371
CG14420	0.598	0.0371
CG32528	0.598	0.0371
CG6961	0.598	0.0371
Obp56d	0.598	0.0371
CG10202	0.597	0.0376
CG13071	0.597	0.0376
jagn	0.597	0.0376
Accox57D-d	0.596	0.0378
Mcm2	0.596	0.0378
Mec2	0.596	0.0378
Mur89F	0.596	0.0378
Papst2	0.596	0.0378
Tsc1	0.596	0.0378
CG34124	0.595	0.0384
C15	0.594	0.0385
dpr3	0.594	0.0385
MESR6	0.594	0.0385
Tsp29Fa	0.594	0.0385
CG11876	0.593	0.0388
CG32251	0.593	0.0388
CG3916	0.593	0.0388
GNBP2	0.593	0.0388
CG32000	0.592	0.0392
CG34376	0.592	0.0392
CG4091	0.592	0.0392
CG10176	0.591	0.0395
CG17168	0.591	0.0395
CG4116	0.591	0.0395
CG6912	0.591	0.0395
etaTry	0.591	0.0395
fd102C	0.591	0.0395
Fmrf	0.591	0.0395
CG15545	0.59	0.0401
CG33228	0.59	0.0401
CG34261	0.59	0.0401
CG5130	0.59	0.0401

Gene Name	ERC Value	P-value
CG6428	0.59	0.0401
Ch15	0.59	0.0401
Obp56h	0.59	0.0401
CG13313	0.589	0.0407
CG5966	0.589	0.0407
CG7587	0.589	0.0407
Tig	0.589	0.0407
CG11693	0.588	0.0411
CG6149	0.588	0.0411
CG6231	0.588	0.0411
CG7900	0.588	0.0411
dmt	0.588	0.0411
FancI	0.588	0.0411
CG18493	0.587	0.0416
salt	0.587	0.0416
CG13117	0.586	0.0418
CG5205	0.585	0.0419
Chd64	0.585	0.0419
Tina-1	0.585	0.0419
Ance-5	0.584	0.0422
CG17470	0.584	0.0422
CG5262	0.584	0.0422
CG8891	0.584	0.0422
Ets65A	0.584	0.0422
NUCB1	0.584	0.0422
CG11703	0.583	0.0427
Glut3	0.583	0.0427
Spase22-23	0.583	0.0427
CG6059	0.582	0.043
spirit	0.582	0.043
Tab2	0.582	0.043
CG33160	0.581	0.0432
CG34185	0.581	0.0432
CG7430	0.581	0.0432
CG13615	0.58	0.0435
CG8800	0.58	0.0435
PGRP-SC2	0.58	0.0435
CG10083	0.579	0.0438
CG1246	0.579	0.0438
CG17985	0.579	0.0438
Gyc88E	0.579	0.0438
ns4	0.579	0.0438
Smtv	0.579	0.0438
Whamy	0.579	0.0438
CG12746	0.578	0.0444
CG30094	0.578	0.0444
CG32017	0.578	0.0444
CG42561	0.578	0.0444
Cpr47Eg	0.577	0.0448
GV1	0.577	0.0448
Mio	0.577	0.0448
CG14110	0.576	0.045
CG42686	0.576	0.045
CG4389	0.576	0.045
Ucp4B	0.576	0.045
Npc2c	0.575	0.0454

Gene Name	ERC Value	P-value
CG14818	0.574	0.0455
CG7272	0.574	0.0455
CG8237	0.574	0.0455
CG8783	0.574	0.0455
Mur18B	0.574	0.0455
SP555	0.574	0.0455
CheA87a	0.573	0.046
CG11693	0.588	0.0411
CtrlB	0.572	0.0461
B-H2	0.571	0.0462
CG30184	0.571	0.0462
CG33767	0.571	0.0462
Cyp28d1	0.571	0.0462
CG14693	0.57	0.0466
CG6719	0.57	0.0466
Esp	0.57	0.0466
TfIIIS	0.57	0.0466
th	0.57	0.0466
Uro	0.57	0.0466
CG15517	0.569	0.0471
CG1774	0.569	0.0471
Osbp	0.569	0.0471
vkg	0.569	0.0471
CG14205	0.568	0.0475
mRps535	0.568	0.0475
Pcp	0.568	0.0475
CG15629	0.567	0.0477
CG2837	0.567	0.0477
CG8486	0.567	0.0477
ci	0.567	0.0477
CG9572	0.566	0.0481
Cp18	0.566	0.0481
CG3660	0.565	0.0483
lrl10a	0.565	0.0483
Lerp	0.565	0.0483
Npc2f	0.565	0.0483
Or24a	0.565	0.0483
CG13604	0.564	0.0487
Hexo2	0.564	0.0487
CG11242	0.563	0.0489
CG1347	0.563	0.0489
CG6763	0.563	0.0489
CG16718	0.562	0.0492
CG8586	0.562	0.0492
CG2249	0.561	0.0494
CG33766	0.561	0.0494
Gr64f	0.561	0.0494
bgcn	0.56	0.0496
CG1140	0.56	0.0496
CG17082	0.56	0.0496
CG31530	0.56	0.0496
CG7953	0.56	0.0496
Cpr23B	0.56	0.0496
Osi22	0.56	0.0496
Sep5	0.559	0.0503
CG13023	0.559	0.0503
pgant2	0.559	0.0503

Table 6.S17 Continued

Gene Name	ERC Value	P-value
CG4623	0.558	0.0505
Edg78E	0.558	0.0505
CG11077	0.557	0.0507
CG16713	0.557	0.0507
Gr98b	0.557	0.0507
mav	0.557	0.0507
CG17323	0.556	0.0511
CG32631	0.556	0.0511
CG6878	0.556	0.0511
Ote	0.556	0.0511
pinta	0.556	0.0511
Tsp42Ed	0.556	0.0511
CG9515	0.555	0.0516
Duox	0.555	0.0516
Pde6	0.555	0.0516
CG13430	0.554	0.0519
CG15362	0.554	0.0519
CG31343	0.554	0.0519
CG34001	0.554	0.0519
CG4576	0.554	0.0519
NAT1	0.554	0.0519
swi2	0.554	0.0519
CG11796	0.553	0.0525
CG12470	0.553	0.0525
CG5665	0.553	0.0525
Klp98A	0.553	0.0525
CG3097	0.552	0.0529
CG13330	0.551	0.053
CG13837	0.551	0.053
CG17258	0.551	0.053
CG1943	0.551	0.053
CG34426	0.551	0.053
Scs	0.551	0.053
Tsp42En	0.551	0.053
usp	0.551	0.053
CG10005	0.55	0.0537
CG13081	0.55	0.0537
CG13170	0.55	0.0537
Gr59a	0.55	0.0537
Or42a	0.55	0.0537
rumi	0.55	0.0537
CG14881	0.549	0.0542
CG17739	0.549	0.0542
CG17834	0.549	0.0542
CG7381	0.549	0.0542
obst-J	0.549	0.0542
Ugt36Bc	0.549	0.0542
CG12964	0.548	0.0548
CG17571	0.548	0.0548
CG8249	0.548	0.0548
hebe	0.548	0.0548
CG3065	0.547	0.0551
CG5323	0.547	0.0551
Cht6	0.547	0.0551
spict	0.547	0.0551
Ahcy13	0.546	0.0555

Gene Name	ERC Value	P-value
Atg2	0.546	0.0555
atl	0.546	0.0555
ball	0.546	0.0555
CG12194	0.546	0.0555
CG14777	0.546	0.0555
CG30431	0.546	0.0555
CG3362	0.546	0.0555
CG6337	0.546	0.0555
pgc	0.546	0.0555
Spn100A	0.546	0.0555
CG14062	0.545	0.0565
CG5084	0.545	0.0565
CG7730	0.545	0.0565
CG16779	0.544	0.0568
CG17639	0.544	0.0568
Rab35	0.544	0.0568
CG13713	0.543	0.057
CG3209	0.543	0.057
CG9400	0.543	0.057
CG9498	0.543	0.057
CG9550	0.543	0.057
CG9987	0.543	0.057
fusi	0.543	0.057
CG31148	0.542	0.0577
Pros45	0.542	0.0577
C1GalTA	0.541	0.0578
CG15100	0.541	0.0578
CG4278	0.541	0.0578
CG8736	0.541	0.0578
CG12393	0.54	0.0582
CG17290	0.54	0.0582
CG32119	0.54	0.0582
CG34265	0.54	0.0582
CG4199	0.54	0.0582
CG7175	0.54	0.0582
CG8036	0.54	0.0582
CG8526	0.54	0.0582
CG9684	0.54	0.0582
gnu	0.54	0.0582
l(1)G0320	0.54	0.0582
Obp58d	0.54	0.0582
PebIII	0.54	0.0582
Rh2	0.54	0.0582
Aats-asn	0.539	0.0595
Acph-1	0.539	0.0595
CG12617	0.539	0.0595
mdy	0.539	0.0595
Or74a	0.539	0.0595
CG33509	0.538	0.0599
Or65a	0.538	0.0599
CG14044	0.537	0.0601
CG32079	0.537	0.0601
Gs2	0.537	0.0601
Pur-alpha	0.537	0.0601
CG10910	0.536	0.0605
CG17784	0.536	0.0605

Gene Name	ERC Value	P-value
CG7051	0.536	0.0605
CG9796	0.536	0.0605
dpp	0.536	0.0605
CG13700	0.534	0.0609
CG7912	0.534	0.0609
Fhos	0.534	0.0609
m1	0.534	0.0609
MED26	0.534	0.0609
shf	0.534	0.0609
CG10585	0.533	0.0614
CG1126	0.533	0.0614
CG11679	0.533	0.0614
CG11926	0.533	0.0614
CG9826	0.533	0.0614
CG9920	0.533	0.0614
MED6	0.533	0.0614
sNPF	0.533	0.0614
Srp54k	0.533	0.0614
CG2701	0.532	0.0623
CG2781	0.532	0.0623
CG7349	0.532	0.0623
CG8834	0.532	0.0623
CG9849	0.532	0.0623
dao	0.532	0.0623
m	0.532	0.0623
SuUR	0.532	0.0623
CG11686	0.531	0.063
Cyp6a23	0.531	0.063
CG11669	0.53	0.0632
CG13869	0.53	0.0632
CG14546	0.53	0.0632
Cdc37	0.529	0.0634
CG10041	0.529	0.0634
CG2336	0.529	0.0634
CG32573	0.529	0.0634
CG40485	0.529	0.0634
CG5404	0.529	0.0634
CG9259	0.529	0.0634
dap	0.529	0.0634
Mitf	0.529	0.0634
pic	0.529	0.0634
Arr1	0.528	0.0643
bur	0.528	0.0643
CG14258	0.528	0.0643
CG14857	0.528	0.0643
CG15084	0.528	0.0643
CG18371	0.528	0.0643
CG9314	0.528	0.0643
Nhe1	0.528	0.0643
npf	0.528	0.0643
CG6675	0.527	0.0651
CG7968	0.527	0.0651
CG9940	0.527	0.0651
geminin	0.527	0.0651
CG3264	0.525	0.0655
CG34455	0.525	0.0655

Gene Name	ERC Value	P-value
CG7777	0.525	0.0655
CG7920	0.525	0.0655
CG8866	0.525	0.0655
meso18E	0.525	0.0655
Caps	0.524	0.066
CG10089	0.524	0.066
CG13085	0.524	0.066
CG31272	0.524	0.066
CklIbeta	0.524	0.066
csw	0.524	0.066
Cyp4d20	0.524	0.066
Uch	0.524	0.066
CG11148	0.523	0.0668
CG3238	0.523	0.0668
CG6023	0.523	0.0668
Dcp-1	0.523	0.0668
Plf	0.523	0.0668
RhoGAP92E	0.523	0.0668
CG2893	0.522	0.0673
CG8089	0.522	0.0673
CG9547	0.522	0.0673
Cyp6a22	0.522	0.0673
nrv3	0.522	0.0673
CG15198	0.521	0.0677
CG2616	0.521	0.0677
CG4770	0.521	0.0677
CG7442	0.521	0.0677
dpr18	0.521	0.0677
Vm32E	0.521	0.0677
CG1291	0.52	0.0683
CG13705	0.52	0.0683
CG14958	0.52	0.0683
CG2219	0.52	0.0683
CG33331	0.52	0.0683
CG9791	0.52	0.0683
Gdi	0.52	0.0683
Glat1	0.52	0.0683
ssp2	0.52	0.0683
CG11269	0.519	0.0691
CG15082	0.519	0.0691
CG31784	0.519	0.0691
CG9010	0.519	0.0691
gce	0.519	0.0691
Hnf4	0.519	0.0691
Or30a	0.519	0.0691
CG13133	0.518	0.0697
CG14717	0.518	0.0697
CG7337	0.518	0.0697
CG8814	0.518	0.0697
TfIIA-S	0.518	0.0697
CG31265	0.517	0.0702
Dhc62B	0.517	0.0702
mRps17	0.517	0.0702
ppk13	0.517	0.0702
CG11160	0.516	0.0705
CG11788	0.516	0.0705

Gene Name	ERC Value	P-value
CG12126	0.516	0.0705
CG15254	0.516	0.0705
Cg25C	0.516	0.0705
CG6015	0.516	0.0705
CG8889	0.516	0.0705
inx2	0.516	0.0705
CG17189	0.515	0.0713
CG18539	0.515	0.0713
CG4646	0.515	0.0713
CG9377	0.515	0.0713
CG9416	0.515	0.0713
Cyp6d5	0.515	0.0713
Ndg	0.515	0.0713
CG10863	0.514	0.0719
CG11438	0.514	0.0719
CG17574	0.514	0.0719
Cpr47Ec	0.514	0.0719
Cry	0.514	0.0719
Cyp1	0.514	0.0719
modSP	0.514	0.0719
CG42331	0.513	0.0725
Cpr67Fb	0.513	0.0725
ey	0.513	0.0725
gsb	0.513	0.0725
Tudor-SN	0.513	0.0725
CG8417	0.512	0.073
CG9104	0.512	0.073
SoxN	0.512	0.073
CG16953	0.511	0.0732
CG31698	0.511	0.0732
CG8297	0.511	0.0732
Gprk1	0.511	0.0732
arg	0.51	0.0736
CG10674	0.51	0.0736
CG30272	0.51	0.0736
CG7191	0.51	0.0736
Cpr11B	0.51	0.0736
CrebA	0.51	0.0736
Nrt	0.51	0.0736
CG1416	0.509	0.0742
CG14569	0.509	0.0742
CG31630	0.509	0.0742
CG9911	0.509	0.0742
swa	0.509	0.0742
yellow-b	0.509	0.0742
CG10178	0.508	0.0748
CG11406	0.508	0.0748
CG8671	0.508	0.0748
CG7966	0.508	0.0748
sav	0.508	0.0748
CG5455	0.507	0.0752
CG8671	0.507	0.0752
Jon74E	0.507	0.0752
mRps18A	0.507	0.0752
RpS27A	0.507	0.0752
CG13872	0.506	0.0757

Table 6.S17 Continued

Gene Name	ERC Value	P-value
CG17664	0.506	0.0757
CG34179	0.506	0.0757
CG42724	0.506	0.0757
CG7025	0.506	0.0757
Nc	0.506	0.0757
Or88a	0.506	0.0757
stops	0.506	0.0757
CG15414	0.505	0.0764
clin3	0.505	0.0764
lolal	0.505	0.0764
mbf1	0.505	0.0764
nimC1	0.505	0.0764
Obp49e	0.505	0.0764
CG3309	0.504	0.0769
CG3332	0.504	0.0769
CG9527	0.504	0.0769
skpA	0.504	0.0769
CG15525	0.503	0.0773
CG15828	0.503	0.0773
CG34309	0.503	0.0773
CG8517	0.503	0.0773
crc	0.503	0.0773
frtz	0.503	0.0773
lr8a	0.503	0.0773
SdhA	0.503	0.0773
CG11168	0.502	0.078
CG11309	0.502	0.078
CG17224	0.502	0.078
Gr85a	0.502	0.078
inaF-D	0.502	0.078
CG15270	0.501	0.0785
CG18788	0.501	0.0785
CG32305	0.501	0.0785
Nmdmc	0.501	0.0785
SerT	0.501	0.0785
yellow-d	0.501	0.0785
CG11470	0.5	0.079
CG4500	0.5	0.079
CG5608	0.5	0.079
CG3719	0.499	0.0793
TwidF	0.499	0.0793
CG9149	0.498	0.0795
TepII	0.498	0.0795
CG12835	0.497	0.0796
CG2493	0.497	0.0796
mtl18	0.497	0.0796
Rab-RP4	0.497	0.0796
Sur-8	0.497	0.0796
Try29F	0.497	0.0796
alc	0.496	0.0802
CG14315	0.496	0.0802
CG17562	0.496	0.0802
CG32448	0.496	0.0802
CG34375	0.496	0.0802
CG9360	0.496	0.0802
Cpr49Af	0.496	0.0802

Gene Name	ERC Value	P-value
nab	0.496	0.0802
U3-55K	0.496	0.0802
CG16758	0.495	0.081
CG3326	0.495	0.081
mtm	0.495	0.081
Nha2	0.495	0.081
CG18304	0.494	0.0814
CG3303	0.494	0.0814
CG34217	0.494	0.0814
CG4213	0.494	0.0814
CG5160	0.494	0.0814
lig	0.494	0.0814
Or33c	0.494	0.0814
sro	0.494	0.0814
CG12204	0.493	0.0821
CG30192	0.493	0.0821
CG32488	0.493	0.0821
CG3588	0.493	0.0821
Cyp6g1	0.493	0.0821
Gr32a	0.493	0.0821
Moe	0.493	0.0821
Obp83cd	0.493	0.0821
CG11340	0.492	0.0828
CG12970	0.492	0.0828
CG14946	0.492	0.0828
CG30148	0.492	0.0828
Cyp310a1	0.492	0.0828
lr76a	0.492	0.0828
lr94e	0.492	0.0828
nimB1	0.492	0.0828
Obp93a	0.492	0.0828
primo-1	0.492	0.0828
robo3	0.492	0.0828
CG15408	0.491	0.0838
CG5910	0.491	0.0838
CG9961	0.491	0.0838
ChT3	0.491	0.0838
colt	0.491	0.0838
Eip71CD	0.491	0.0838
inct	0.491	0.0838
Spn	0.491	0.0838
RpL8	0.49	0.0845
CG3618	0.489	0.0846
CG4301	0.489	0.0846
CG5458	0.489	0.0846
fu12	0.489	0.0846
Osi6	0.489	0.0846
CG13868	0.488	0.085
CG14377	0.488	0.085
CG5397	0.488	0.085
Cyp6a13	0.488	0.085
RpL3	0.488	0.085
bni	0.487	0.0855
CG14856	0.487	0.0855
CG3277	0.487	0.0855
Cyp311a1	0.487	0.0855

Gene Name	ERC Value	P-value
ogre	0.487	0.0855
uzip	0.487	0.0855
CG13002	0.486	0.086
CG15650	0.486	0.086
CG32260	0.486	0.086
CG7261	0.486	0.086
kraken	0.486	0.086
Myo28B1	0.486	0.086
CG14259	0.485	0.0866
CG7881	0.485	0.0866
Snmp	0.485	0.0866
CG13603	0.484	0.0868
CG18745	0.484	0.0868
CG31005	0.484	0.0868
CG31549	0.484	0.0868
CG33784	0.484	0.0868
CG33934	0.484	0.0868
CG7914	0.484	0.0868
CG8407	0.484	0.0868
Gr32a	0.483	0.0876
CG10747	0.483	0.0876
CG14971	0.483	0.0876
CG31259	0.483	0.0876
CG33970	0.483	0.0876
CG7735	0.483	0.0876
CG9318	0.483	0.0876
gb	0.483	0.0876
Rab23	0.483	0.0876
Spn47C	0.483	0.0876
CG16734	0.482	0.0885
CG33054	0.482	0.0885
CG4404	0.482	0.0885
CG5757	0.482	0.0885
Lin29	0.482	0.0885
CG3165	0.481	0.0889
CG42512	0.481	0.0889
CG9917	0.481	0.0889
CREG	0.481	0.0889
CG31106	0.48	0.0893
Fibp	0.48	0.0893
ppk14	0.48	0.0893
Rph	0.48	0.0893
TwidIN	0.48	0.0893
wash	0.48	0.0893
CG2076	0.479	0.0898
CG4743	0.479	0.0898
KCNQ	0.479	0.0898
Ark	0.478	0.0901
CG13737	0.478	0.0901
CG5397	0.478	0.0901
DppIII	0.478	0.0901
irc	0.478	0.0901
Ance	0.477	0.0905
CG3348	0.477	0.0905
CG4098	0.477	0.0905
Lsp1beta	0.477	0.0905

Gene Name	ERC Value	P-value
WRNexo	0.477	0.0905
CG14107	0.476	0.091
CG14949	0.476	0.091
CG7431	0.476	0.091
Sibp	0.476	0.091
CG30413	0.475	0.0914
CG34396	0.475	0.0914
CG3527	0.475	0.0914
CG7943	0.475	0.0914
Cpr49Ah	0.475	0.0914
hoe2	0.475	0.0914
Oscillin	0.475	0.0914
CG12659	0.474	0.092
CG14528	0.474	0.092
CG18622	0.474	0.092
CG3074	0.474	0.092
CG42351	0.474	0.092
Esyt2	0.474	0.092
Or59b	0.474	0.092
Tap42	0.474	0.092
Bicc	0.473	0.0927
CG10513	0.473	0.0927
CG10562	0.473	0.0927
CG14516	0.473	0.0927
p130CAS	0.473	0.0927
CG10359	0.472	0.0932
CG13426	0.472	0.0932
Kklalpha	0.472	0.0932
Spat	0.472	0.0932
TwidIO	0.472	0.0932
CaBP1	0.471	0.0936
cag	0.471	0.0936
CG33692	0.471	0.0936
CG33769	0.471	0.0936
Fcp3C	0.471	0.0936
ZIP1	0.471	0.0936
CG15210	0.47	0.0941
CG42319	0.47	0.0941
CG4325	0.47	0.0941
hale	0.47	0.0941
Lsp1gamma	0.47	0.0941
ppl	0.47	0.0941
cbc	0.469	0.0947
CG18418	0.469	0.0947
CG2316	0.469	0.0947
CG2519	0.469	0.0947
CG31275	0.469	0.0947
Tim17a1	0.469	0.0947
tkv	0.469	0.0947
Ady43A	0.468	0.0953
CG11753	0.468	0.0953
CG31169	0.468	0.0953
CG5623	0.468	0.0953
CG6602	0.468	0.0953
Cpr30B	0.468	0.0953
Start1	0.468	0.0953

Gene Name	ERC Value	P-value
CG31855	0.467	0.0959
CG4302	0.467	0.0959
Topors	0.467	0.0959
by	0.466	0.0962
CG11437	0.466	0.0962
CG32372	0.466	0.0962
Cyp317a1	0.466	0.0962
EndoG	0.466	0.0962
lr21a	0.466	0.0962
And	0.466	0.0968
CG10186	0.465	0.0968
CG12917	0.465	0.0968
CG13069	0.465	0.0968
CG13724	0.465	0.0968
CG17821	0.465	0.0968
CG18668	0.465	0.0968
Cyp3514	0.465	0.0968
CG4882	0.465	0.0968
CG5844	0.465	0.0968
Dsor1	0.465	0.0968
Gr8a	0.465	0.0968
nmy	0.465	0.0968
Catsup	0.464	0.0979
CG42308	0.464	0.0979
CG7029	0.464	0.0979
Gr39a	0.464	0.0979
Odc1	0.464	0.0979
pasha	0.464	0.0979
prd	0.464	0.0979
Thiolase	0.464	0.0979
CG12736	0.463	0.0986
CG1927	0.463	0.0986
CG3008	0.463	0.0986
CG5190	0.463	0.0986
CG6359	0.463	0.0986
CG9287	0.463	0.0986
ChT9	0.463	0.0986
pyd	0.463	0.0986
CG14292	0.462	0.0994
Mur29B	0.462	0.0994
CG10208	0.461	0.0995
CG10657	0.461	0.0995
CG15170	0.461	0.0995
CG8299	0.461	0.0995
CG9213	0.461	0.0995
nrv2	0.461	0.0995

Table 6.S18 - Top Genes ERC values for *rec* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value	Gene Name	ERC Value	P-value
<i>Lip1</i>	0.915	0.0001	<i>CG7889</i>	0.813	0.005	<i>pk</i>	0.772	0.01	<i>GstD10</i>	0.74	0.0152	<i>CG6418</i>	0.717	0.0202
<i>CG13565</i>	0.908	0.0002	<i>RunxB</i>	0.813	0.005	<i>ds</i>	0.771	0.0103	<i>CG10814</i>	0.739	0.0153	<i>Ret</i>	0.717	0.0202
<i>CG8319</i>	0.906	0.0003	<i>l(3)76BDM</i>	0.811	0.0053	<i>Aats-ala-m</i>	0.77	0.0104	<i>CG15919</i>	0.739	0.0153	<i>CG42404</i>	0.716	0.0205
<i>CG4753</i>	0.901	0.0004	<i>mRpL44</i>	0.811	0.0053	<i>CG12299</i>	0.77	0.0104	<i>CG32816</i>	0.738	0.0155	<i>muskelin</i>	0.716	0.0205
<i>B-H2</i>	0.892	0.0005	<i>CG13908</i>	0.809	0.0055	<i>CG13643</i>	0.769	0.0105	<i>CG2811</i>	0.737	0.0156	<i>Nox</i>	0.716	0.0205
<i>CG10889</i>	0.891	0.0005	<i>BBS8</i>	0.805	0.0056	<i>Sfp84E</i>	0.769	0.0105	<i>CG4619</i>	0.737	0.0156	<i>CG16863</i>	0.715	0.0207
<i>Pask</i>	0.889	0.0006	<i>CG5322</i>	0.805	0.0056	<i>Pros25</i>	0.767	0.0107	<i>dpr17</i>	0.736	0.0158	<i>CG17181</i>	0.714	0.0208
<i>btv</i>	0.888	0.0007	<i>PGRP-LA</i>	0.805	0.0056	<i>mlo</i>	0.764	0.0108	<i>dpr9</i>	0.734	0.0159	<i>CG8641</i>	0.714	0.0208
<i>pb</i>	0.886	0.0008	<i>CG9175</i>	0.804	0.0059	<i>CG11448</i>	0.763	0.0109	<i>CG2017</i>	0.733	0.0159	<i>CG15322</i>	0.713	0.021
<i>CG18262</i>	0.879	0.0009	<i>boly</i>	0.803	0.0059	<i>CG13837</i>	0.763	0.0109	<i>CG4835</i>	0.733	0.0159	<i>CG15522</i>	0.713	0.021
<i>CG32846</i>	0.874	0.001	<i>CG14177</i>	0.802	0.006	<i>CG34039</i>	0.762	0.0111	<i>lbk</i>	0.733	0.0159	<i>CG33155</i>	0.713	0.021
<i>CG6234</i>	0.874	0.001	<i>CG42337</i>	0.802	0.006	<i>CstF-64</i>	0.762	0.0111	<i>CG14100</i>	0.732	0.0162	<i>corn</i>	0.713	0.021
<i>CG5270</i>	0.873	0.0012	<i>lrfg</i>	0.802	0.006	<i>Sse</i>	0.762	0.0111	<i>llp1</i>	0.732	0.0162	<i>mRpS10</i>	0.713	0.021
<i>CG14856</i>	0.867	0.0013	<i>Snp</i>	0.802	0.006	<i>vps24</i>	0.762	0.0111	<i>sut4</i>	0.732	0.0162	<i>alpha4GT1</i>	0.712	0.0214
<i>CG8852</i>	0.863	0.0014	<i>Obp8a</i>	0.801	0.0064	<i>CG8312</i>	0.761	0.0114	<i>CG34331</i>	0.731	0.0165	<i>CG8027</i>	0.712	0.0214
<i>CG12432</i>	0.855	0.0014	<i>dah</i>	0.8	0.0065	<i>rod</i>	0.761	0.0114	<i>CG6550</i>	0.73	0.0166	<i>adp</i>	0.711	0.0216
<i>CG15701</i>	0.855	0.0014	<i>Cdep</i>	0.798	0.0066	<i>Rpb10</i>	0.76	0.0116	<i>CG9384</i>	0.73	0.0166	<i>CG4853</i>	0.711	0.0216
<i>CG11637</i>	0.854	0.0016	<i>CG10864</i>	0.797	0.0067	CG10274	0.757	0.0117	<i>Rpl39</i>	0.73	0.0166	<i>CG9452</i>	0.711	0.0216
<i>CG13955</i>	0.854	0.0016	<i>CG12355</i>	0.797	0.0067	<i>CG14562</i>	0.757	0.0117	<i>CG14274</i>	0.728	0.0168	<i>CG6734</i>	0.71	0.0219
<i>CG15717</i>	0.852	0.0018	<i>CG15093</i>	0.796	0.0068	<i>Pph13</i>	0.757	0.0117	<i>CG7130</i>	0.728	0.0168	<i>Drep-2</i>	0.71	0.0219
<i>CG34186</i>	0.846	0.0019	<i>mos</i>	0.795	0.0069	<i>CG10646</i>	0.756	0.012	<i>CG10098</i>	0.727	0.017	<i>CG18012</i>	0.709	0.0221
<i>CG4658</i>	0.846	0.0019	<i>Oatp74D</i>	0.795	0.0069	<i>ru</i>	0.756	0.012	<i>CG32635</i>	0.727	0.017	<i>CG3655</i>	0.709	0.0221
<i>CG11127</i>	0.843	0.0021	<i>CG42374</i>	0.793	0.0071	<i>CG4476</i>	0.755	0.0122	<i>ldgf5</i>	0.726	0.0172	<i>kel</i>	0.709	0.0221
<i>CG10428</i>	0.842	0.0022	<i>mab-21</i>	0.793	0.0071	<i>dsh</i>	0.755	0.0122	<i>CG13422</i>	0.725	0.0173	<i>Takr99D</i>	0.709	0.0221
<i>CG30183</i>	0.836	0.0023	<i>Vps33B</i>	0.793	0.0071	<i>pHCl</i>	0.755	0.0122	<i>CG4297</i>	0.725	0.0173	<i>aru</i>	0.708	0.0224
<i>CG9335</i>	0.836	0.0023	<i>CG14807</i>	0.792	0.0074	<i>CG18599</i>	0.754	0.0124	<i>CG9269</i>	0.725	0.0173	<i>CG15443</i>	0.708	0.0224
<i>E5</i>	0.833	0.0024	<i>CG17807</i>	0.792	0.0074	<i>BtvV11</i>	0.752	0.0125	<i>CG13185</i>	0.724	0.0176	<i>CG9422</i>	0.708	0.0224
<i>salM</i>	0.832	0.0025	<i>Ca-alpha1D</i>	0.79	0.0076	<i>CG9951</i>	0.752	0.0125	<i>spl</i>	0.724	0.0176	<i>CG9629</i>	0.708	0.0224
<i>CG4324</i>	0.831	0.0026	<i>CG4554</i>	0.789	0.0077	<i>CG14085</i>	0.751	0.0127	<i>Dip3</i>	0.723	0.0177	<i>GlurRIIE</i>	0.708	0.0224
<i>CG2144</i>	0.83	0.0027	<i>kon</i>	0.789	0.0077	<i>CG8060</i>	0.751	0.0127	<i>E(spl)</i>	0.723	0.0177	<i>bonsai</i>	0.707	0.0229
<i>CG4553</i>	0.829	0.0028	<i>l(2)37Bb</i>	0.787	0.0078	<i>Gst1</i>	0.751	0.0127	<i>ft4</i>	0.723	0.0177	<i>CG10927</i>	0.707	0.0229
<i>CG8170</i>	0.829	0.0028	<i>waw</i>	0.787	0.0078	<i>Magi</i>	0.751	0.0127	<i>Gen</i>	0.723	0.0177	<i>CG15766</i>	0.707	0.0229
<i>cyr</i>	0.829	0.0028	<i>CG12516</i>	0.785	0.008	<i>CG9676</i>	0.75	0.0131	<i>stf</i>	0.723	0.0177	<i>CG3651</i>	0.707	0.0229
<i>CG11262</i>	0.827	0.0031	<i>CG13711</i>	0.784	0.0081	<i>CG31053</i>	0.749	0.0132	<i>CG12134</i>	0.722	0.0182	<i>Cpr65Au</i>	0.707	0.0229
<i>Git</i>	0.827	0.0031	<i>CG17672</i>	0.784	0.0081	<i>CG4679</i>	0.749	0.0132	<i>CG9427</i>	0.722	0.0182	<i>icln</i>	0.707	0.0229
<i>CG15429</i>	0.826	0.0032	<i>CG2269</i>	0.783	0.0083	<i>CG6462</i>	0.749	0.0132	<i>CG1104</i>	0.721	0.0184	<i>CG13690</i>	0.706	0.0234
<i>CG1358</i>	0.825	0.0033	<i>Os-E</i>	0.783	0.0083	<i>CG7567</i>	0.749	0.0132	<i>CG32281</i>	0.721	0.0184	<i>CG9243</i>	0.706	0.0234
<i>CG3194</i>	0.825	0.0033	<i>CG5535</i>	0.781	0.0085	<i>djp</i>	0.749	0.0132	<i>CG6129</i>	0.721	0.0184	<i>PR2</i>	0.706	0.0234
<i>m2</i>	0.825	0.0033	<i>Vps16B</i>	0.781	0.0085	<i>CG11418</i>	0.748	0.0136	<i>CG7154</i>	0.721	0.0184	<i>CG13759</i>	0.704	0.0237
<i>SC35</i>	0.825	0.0033	<i>Aeff1</i>	0.78	0.0086	<i>CG2794</i>	0.748	0.0136	<i>CG7927</i>	0.721	0.0184	<i>CG2260</i>	0.704	0.0237
<i>CG17352</i>	0.823	0.0037	<i>CG1172</i>	0.78	0.0086	<i>CG6511</i>	0.748	0.0136	<i>CG1273</i>	0.72	0.0188	<i>CG2813</i>	0.704	0.0237
<i>CG34447</i>	0.823	0.0037	<i>CG7156</i>	0.78	0.0086	<i>l(2)k16918</i>	0.748	0.0136	<i>CG32832</i>	0.72	0.0188	<i>ftz</i>	0.704	0.0237
<i>CG13531</i>	0.821	0.0039	<i>CG10703</i>	0.779	0.0089	<i>Syr12</i>	0.748	0.0136	<i>CG5645</i>	0.72	0.0188	<i>Toll-6</i>	0.704	0.0237
<i>CG3652</i>	0.821	0.0039	<i>CG15478</i>	0.779	0.0089	<i>beat-lb</i>	0.747	0.0141	<i>mus101</i>	0.72	0.0188	<i>CG7598</i>	0.703	0.0241
<i>SIDL</i>	0.821	0.0039	<i>CG13306</i>	0.778	0.0091	<i>CG13813</i>	0.747	0.0141	<i>Spt6</i>	0.72	0.0188	<i>Jon44E</i>	0.703	0.0241
<i>fs(1)N</i>	0.819	0.0041	<i>CG14882</i>	0.778	0.0091	<i>CG30053</i>	0.747	0.0141	<i>CG4221</i>	0.719	0.0193	<i>CG15861</i>	0.702	0.0243
<i>CG12582</i>	0.817	0.0042	<i>Su(H)</i>	0.778	0.0091	<i>CG14036</i>	0.746	0.0143	<i>CG5984</i>	0.719	0.0193	<i>CG5195</i>	0.702	0.0243
<i>Cyp28c1</i>	0.816	0.0043	<i>CG15896</i>	0.777	0.0094	<i>Fit2</i>	0.746	0.0143	<i>CG10435</i>	0.718	0.0195	<i>CG5919</i>	0.702	0.0243
<i>CG11447</i>	0.815	0.0044	<i>CG9248</i>	0.777	0.0094	<i>CG13366</i>	0.745	0.0145	<i>CG14749</i>	0.718	0.0195	<i>CG7222</i>	0.702	0.0243
<i>CG17266</i>	0.814	0.0045	<i>mthi5</i>	0.777	0.0094	<i>CG2906</i>	0.745	0.0145	<i>CG14906</i>	0.718	0.0195	<i>CG7879</i>	0.702	0.0243
<i>CG2083</i>	0.814	0.0045	<i>MED15</i>	0.776	0.0096	<i>CG31380</i>	0.745	0.0145	<i>CG6592</i>	0.718	0.0195	<i>lrf1a</i>	0.702	0.0243
<i>CG7692</i>	0.814	0.0045	<i>CG11534</i>	0.775	0.0097	<i>CG7320</i>	0.745	0.0145	<i>CG8230</i>	0.718	0.0195	<i>sax</i>	0.702	0.0243
<i>sob</i>	0.814	0.0045	<i>CG42353</i>	0.775	0.0097	<i>CG13594</i>	0.744	0.0149	<i>CG8765</i>	0.718	0.0195	<i>thr</i>	0.702	0.0243
<i>unc-4</i>	0.814	0.0045	<i>Cpr72Eb</i>	0.773	0.0099	<i>CG16813</i>	0.744	0.0149	<i>Hcs</i>	0.718	0.0195	<i>CG10623</i>	0.7	0.025
<i>wcd</i>	0.814	0.0045	<i>aft</i>	0.772	0.01	<i>MTA1-like</i>	0.743	0.015	<i>Mgstf</i>	0.718	0.0195	<i>CG10914</i>	0.7	0.025
<i>CG13283</i>	0.813	0.005	<i>mRpS31</i>	0.772	0.01	<i>CG11873</i>	0.742	0.0151	<i>CG5367</i>	0.717	0.0202	<i>ex</i>	0.7	0.025

Table 6.S18 Continued

Gene Name	ERC Value	P-value
<i>RunxA</i>	0.7	0.025
<i>CG10588</i>	0.699	0.0254
<i>CG15745</i>	0.699	0.0254
<i>CG17691</i>	0.699	0.0254
<i>Iva</i>	0.699	0.0254
<i>CG11593</i>	0.698	0.0258
<i>mus81</i>	0.698	0.0258
<i>osk</i>	0.698	0.0258
<i>sha</i>	0.698	0.0258
<i>CG12290</i>	0.697	0.0261
<i>GABA-B-R3</i>	0.697	0.0261
<i>sad</i>	0.697	0.0261
<i>tap</i>	0.697	0.0261
<i>caup</i>	0.696	0.0265
<i>CG17047</i>	0.696	0.0265
<i>CG31414</i>	0.696	0.0265
<i>CG32573</i>	0.696	0.0265
<i>Ptp61F</i>	0.696	0.0265
<i>CG10669</i>	0.695	0.0269
<i>CG5431</i>	0.695	0.0269
<i>CG10725</i>	0.694	0.0271
<i>comm</i>	0.693	0.0272
<i>DNApol-alpha</i>	0.693	0.0272
<i>CG4374</i>	0.692	0.0274
<i>CG5013</i>	0.692	0.0274
<i>CG33108</i>	0.691	0.0276
<i>CG3520</i>	0.691	0.0276
<i>D12</i>	0.691	0.0276
<i>melt</i>	0.691	0.0276
<i>dx</i>	0.69	0.0279
<i>HLHmbeta</i>	0.69	0.0279
<i>Or43b</i>	0.69	0.0279
<i>RhoGAP5A</i>	0.69	0.0279
<i>CG12772</i>	0.689	0.0283
<i>CG2091</i>	0.689	0.0283
<i>CG15480</i>	0.688	0.0285
<i>CG4611</i>	0.688	0.0285
<i>CG7550</i>	0.688	0.0285
<i>mus205</i>	0.688	0.0285
<i>CG14463</i>	0.687	0.0288
<i>CG9861</i>	0.687	0.0288
<i>bdg</i>	0.686	0.029
<i>CG10249</i>	0.686	0.029
<i>CG30047</i>	0.686	0.029
<i>CG3841</i>	0.686	0.029
<i>CG6613</i>	0.686	0.029
<i>SelR</i>	0.686	0.029
<i>CG5924</i>	0.685	0.0295
<i>Nlp</i>	0.685	0.0295
<i>remA</i>	0.685	0.0295
<i>CG10741</i>	0.684	0.0298
<i>CG10144</i>	0.683	0.0299
<i>CG13111</i>	0.683	0.0299
<i>CG13169</i>	0.683	0.0299
<i>CG14223</i>	0.683	0.0299
<i>CG32541</i>	0.683	0.0299

Gene Name	ERC Value	P-value
<i>CG3409</i>	0.683	0.0299
<i>Aats-leu</i>	0.682	0.0305
<i>TwidZ</i>	0.682	0.0305
<i>bcd</i>	0.681	0.0306
<i>CG11870</i>	0.681	0.0306
<i>CG17184</i>	0.681	0.0306
<i>I-2</i>	0.681	0.0306
<i>CG11802</i>	0.68	0.031
<i>CG4286</i>	0.68	0.031
<i>CG6733</i>	0.68	0.031
<i>CG8089</i>	0.68	0.031
<i>CG3292</i>	0.679	0.0314
<i>CG9386</i>	0.679	0.0314
<i>CG10019</i>	0.678	0.0315
<i>CG8301</i>	0.678	0.0315
<i>CG8617</i>	0.678	0.0315
<i>CG9666</i>	0.678	0.0315
<i>Dot</i>	0.676	0.0319
CG31898	0.675	0.032
<i>CG6847</i>	0.675	0.032
<i>Lrr47</i>	0.675	0.032
<i>pgant8</i>	0.675	0.032
CG10560	0.674	0.0323
<i>CG13074</i>	0.674	0.0323
<i>CG15387</i>	0.674	0.0323
<i>CG15528</i>	0.674	0.0323
<i>CG7526</i>	0.674	0.0323
<i>mats</i>	0.674	0.0323
<i>ald</i>	0.673	0.0329
<i>CG5597</i>	0.673	0.0329
<i>CG7985</i>	0.672	0.0331
<i>CG8963</i>	0.672	0.0331
<i>Fem-1</i>	0.672	0.0331
<i>ft</i>	0.672	0.0331
<i>ia2</i>	0.672	0.0331
<i>Aats-gly</i>	0.671	0.0335
<i>Atg9</i>	0.671	0.0335
<i>CG11236</i>	0.671	0.0335
<i>CG2182</i>	0.671	0.0335
<i>CG30273</i>	0.67	0.0339
<i>CG15153</i>	0.669	0.034
<i>CG15514</i>	0.669	0.034
<i>DNApol-alpha</i>	0.669	0.034
<i>Gef64C</i>	0.669	0.034
<i>RhoGAP18E</i>	0.669	0.034
<i>salr</i>	0.669	0.034
<i>TyrR</i>	0.669	0.034
<i>CG13287</i>	0.668	0.0346
<i>CG3309</i>	0.668	0.0346
<i>CG14879</i>	0.667	0.0348
<i>jub</i>	0.667	0.0348
<i>pirk</i>	0.667	0.0348
<i>Tango9</i>	0.667	0.0348
<i>blos1</i>	0.666	0.0351
<i>CG9246</i>	0.666	0.0351
<i>fra</i>	0.666	0.0351

Gene Name	ERC Value	P-value
<i>KLHL18</i>	0.666	0.0351
<i>stnA</i>	0.666	0.0351
<i>Obp59a</i>	0.665	0.0356
<i>zwilch</i>	0.665	0.0356
<i>CG12825</i>	0.664	0.0358
<i>CG14238</i>	0.664	0.0358
<i>CG9377</i>	0.664	0.0358
<i>CG9673</i>	0.664	0.0358
<i>nerfin-2</i>	0.664	0.0358
<i>PGRP-SD</i>	0.664	0.0358
<i>Shawn</i>	0.664	0.0358
<i>CG6607</i>	0.663	0.0364
<i>fy</i>	0.663	0.0364
<i>heix</i>	0.663	0.0364
<i>Ptp52F</i>	0.663	0.0364
<i>CG11889</i>	0.662	0.0368
<i>CG4300</i>	0.662	0.0368
<i>CG11562</i>	0.661	0.0369
<i>CG12986</i>	0.661	0.0369
<i>CG3862</i>	0.661	0.0369
<i>CG34214</i>	0.66	0.0372
<i>Men1-1</i>	0.66	0.0372
<i>run</i>	0.66	0.0372
<i>CG10479</i>	0.659	0.0375
<i>Gr9a</i>	0.659	0.0375
<i>imd</i>	0.659	0.0375
<i>phr</i>	0.659	0.0375
<i>blow</i>	0.658	0.0378
<i>bowl</i>	0.658	0.0378
<i>CG31871</i>	0.657	0.038
<i>CG42336</i>	0.657	0.038
<i>CG7028</i>	0.657	0.038
<i>MED30</i>	0.657	0.038
<i>Tor</i>	0.657	0.038
<i>CG10000</i>	0.656	0.0385
<i>CG15479</i>	0.656	0.0385
<i>CG2162</i>	0.656	0.0385
<i>CG34246</i>	0.656	0.0385
<i>CG5830</i>	0.656	0.0385
<i>FLASH</i>	0.656	0.0385
<i>toe</i>	0.655	0.039
<i>CG12207</i>	0.654	0.0391
<i>CG31688</i>	0.654	0.0391
<i>CG32397</i>	0.654	0.0391
<i>CG42817</i>	0.654	0.0391
<i>Vm32E</i>	0.654	0.0391
<i>CG32069</i>	0.653	0.0395
<i>CG6443</i>	0.653	0.0395
<i>CG7884</i>	0.653	0.0395
<i>da</i>	0.653	0.0395
<i>Dg</i>	0.653	0.0395
<i>RhoGEF3</i>	0.653	0.0395
<i>THIFbeta</i>	0.653	0.0395
<i>CG42726</i>	0.652	0.0402
<i>CG12272</i>	0.651	0.0403
<i>CG14314</i>	0.651	0.0403

Gene Name	ERC Value	P-value
<i>KH1</i>	0.651	0.0403
<i>Aats-pro</i>	0.65	0.0405
<i>CG10251</i>	0.65	0.0405
<i>CG11975</i>	0.65	0.0405
<i>CG32204</i>	0.65	0.0405
<i>CG33057</i>	0.65	0.0405
<i>CG9300</i>	0.65	0.0405
<i>in</i>	0.65	0.0405
<i>wor</i>	0.65	0.0405
<i>CG10710</i>	0.649	0.0413
<i>CG30403</i>	0.649	0.0413
<i>CG12105</i>	0.648	0.0414
<i>CG33158</i>	0.648	0.0414
<i>CG6409</i>	0.648	0.0414
<i>CG7564</i>	0.648	0.0414
<i>CG7781</i>	0.648	0.0414
<i>CG9410</i>	0.648	0.0414
<i>Lrrk</i>	0.648	0.0414
<i>Pal</i>	0.648	0.0414
<i>RhoGAP54C</i>	0.648	0.0414
<i>sunz</i>	0.648	0.0414
<i>CG13667</i>	0.647	0.0423
<i>CG17026</i>	0.647	0.0423
<i>CG42246</i>	0.647	0.0423
<i>CG4360</i>	0.647	0.0423
<i>CG6136</i>	0.647	0.0423
<i>elf2B-delta</i>	0.647	0.0423
<i>CG17026</i>	0.647	0.0423
<i>CG42246</i>	0.647	0.0423
<i>CG4360</i>	0.647	0.0423
<i>CG6136</i>	0.647	0.0423
<i>elf2B-delta</i>	0.647	0.0423
<i>CG17026</i>	0.647	0.0423
<i>ash1</i>	0.646	0.043
<i>CG31326</i>	0.646	0.043
<i>CG4709</i>	0.646	0.043
<i>CG7737</i>	0.646	0.043
<i>HisCl1</i>	0.646	0.043
<i>ret</i>	0.646	0.043
<i>CG11109</i>	0.645	0.0435
<i>CG15130</i>	0.645	0.0435
<i>CG32206</i>	0.645	0.0435
<i>CG33543</i>	0.645	0.0435
<i>CG7453</i>	0.645	0.0435
<i>LpR1</i>	0.645	0.0435
<i>CG18811</i>	0.644	0.0441
<i>CG4984</i>	0.643	0.0441
<i>CG32750</i>	0.642	0.0442
<i>Dpy-30L1</i>	0.642	0.0442
<i>sec15</i>	0.642	0.0442
<i>CG7544</i>	0.641	0.0445
<i>EndoGl</i>	0.641	0.0445
<i>Fbw5</i>	0.641	0.0445
<i>kek3</i>	0.641	0.0445
<i>Sulf1</i>	0.641	0.0445
<i>CG18616</i>	0.64	0.045
<i>emc</i>	0.64	0.045
<i>Hsp67Ba</i>	0.64	0.045
<i>Syx13</i>	0.64	0.045
<i>CG6796</i>	0.639	0.0453
<i>key</i>	0.639	0.0453

Gene Name	ERC Value	P-value
<i>mahj</i>	0.639	0.0453
<i>POSH</i>	0.639	0.0453
<i>X11L</i>	0.639	0.0453
<i>CG14945</i>	0.638	0.0458
<i>CG6040</i>	0.638	0.0458
<i>CG8401</i>	0.638	0.0458
<i>cit</i>	0.638	0.0458
<i>Abi</i>	0.637	0.0461
<i>CG5463</i>	0.637	0.0461
<i>CG9747</i>	0.637	0.0461
<i>CG6415</i>	0.636	0.0464
<i>Mih1</i>	0.636	0.0464
<i>CG3837</i>	0.635	0.0466
<i>CG4424</i>	0.635	0.0466
<i>os</i>	0.635	0.0466
<i>Rpb4</i>	0.635	0.0466
<i>Sema-1b</i>	0.635	0.0466
<i>CG10581</i>	0.634	0.047
<i>esg</i>	0.634	0.047
<i>CG12734</i>	0.633	0.0472
CG34012	0.633	0.0472
<i>mit(1)15</i>	0.633	0.0472
<i>pigeon</i>	0.632	0.0475
<i>Taspase1</i>	0.632	0.0475
<i>wgn</i>	0.632	0.0475
<i>CG13322</i>	0.631	0.0477
<i>gloB3</i>	0.631	0.0477
<i>Pink1</i>	0.631	0.0477
<i>RhoGAP19C</i>	0.631	0.0477
<i>CG13012</i>	0.63	0.0481
<i>CG34284</i>	0.63	0.0481
<i>CG6695</i>	0.63	0.0481
<i>Art7</i>	0.629	0.0484
<i>CG1265</i>	0.629	0.0484
<i>CG1885</i>	0.629	0.0484
<i>RpS15</i>	0.629	0.0484
<i>Sir2</i>	0.629	0.0484
<i>CG16956</i>	0.628	0.0488
<i>CG8321</i>	0.628	0.0488
<i>par-6</i>	0.628	0.0488
<i>PGRP-SB1</i>	0.628	0.0488
<i>CG11835</i>	0.627	0.0492
<i>CG3223</i>	0.627	0.0492
<i>CG3239</i>	0.627	0.0492
<i>CG3709</i>	0.627	0.0492
<i>CG5116</i>	0.627	0.0492
<i>Hr83</i>	0.627	0.0492
<i>SPR</i>	0.627	0.0492
<i>trk</i>	0.627	0.0492
<i>CG14132</i>	0.626	0.0499
<i>ct</i>	0.626	0.0499
<i>Pros35</i>	0.626	0.0499
<i>CG8785</i>	0.625	0.0502
<i>CG9279</i>	0.625	0.0502
<i>Hmt-1</i>	0.625	0.0502
<i>Lig4</i>	0.625	0.0502

Table 6.S18 Continued

Gene Name	ERC Value	P-value
<i>tan</i>	0.625	0.0502
<i>Tapdelta</i>	0.625	0.0502
<i>caps</i>	0.624	0.0507
<i>CG14395</i>	0.624	0.0507
<i>dbo</i>	0.624	0.0507
<i>Fip1</i>	0.624	0.0507
<i>CG16790</i>	0.623	0.0511
<i>dare</i>	0.623	0.0511
<i>m4</i>	0.623	0.0511
<i>mts</i>	0.623	0.0511
<i>Aplp1</i>	0.622	0.0514
<i>CG10373</i>	0.622	0.0514
<i>CG11617</i>	0.622	0.0514
<i>CG12123</i>	0.622	0.0514
<i>CG6385</i>	0.622	0.0514
<i>CG14618</i>	0.621	0.0519
<i>Corp</i>	0.621	0.0519
<i>ear</i>	0.621	0.0519
<i>ewg</i>	0.621	0.0519
<i>ndl</i>	0.621	0.0519
<i>Ocho</i>	0.621	0.0519
<i>sens-2</i>	0.621	0.0519
<i>CG12263</i>	0.62	0.0525
<i>CG17244</i>	0.62	0.0525
<i>CG6254</i>	0.62	0.0525
<i>DNApol-gam</i>	0.62	0.0525
<i>CG8102</i>	0.619	0.0529
<i>CG11762</i>	0.618	0.053
<i>CG14710</i>	0.618	0.053
<i>mRpL50</i>	0.618	0.053
<i>CG10376</i>	0.617	0.0532
<i>CG11872</i>	0.617	0.0532
<i>CG17883</i>	0.617	0.0532
<i>CG18178</i>	0.617	0.0532
<i>CG6406</i>	0.617	0.0532
<i>CG9249</i>	0.617	0.0532
<i>jim</i>	0.617	0.0532
<i>TwdlJ</i>	0.617	0.0532
<i>CG33704</i>	0.616	0.054
<i>CG4004</i>	0.616	0.054
<i>CG42807</i>	0.616	0.054
<i>CG4338</i>	0.616	0.054
<i>CG8485</i>	0.616	0.054
<i>DNApol-eta</i>	0.616	0.054
<i>ths</i>	0.616	0.054
<i>CG11241</i>	0.615	0.0546
<i>CG3921</i>	0.615	0.0546
<i>Det</i>	0.615	0.0546
<i>Shroom</i>	0.615	0.0546
<i>TORC</i>	0.615	0.0546
<i>CG18094</i>	0.614	0.055
<i>CG4334</i>	0.614	0.055
<i>phol</i>	0.614	0.055
<i>rob/22E</i>	0.614	0.055
<i>CG11070</i>	0.613	0.0554
<i>CG18581</i>	0.613	0.0554

Gene Name	ERC Value	P-value
<i>CG33060</i>	0.613	0.0554
<i>CG33303</i>	0.613	0.0554
<i>CG42729</i>	0.613	0.0554
<i>CG4497</i>	0.613	0.0554
<i>CG5022</i>	0.613	0.0554
<i>mus312</i>	0.613	0.0554
<i>Or45a</i>	0.613	0.0554
<i>Osi9</i>	0.613	0.0554
<i>CG12104</i>	0.612	0.0563
<i>CG13239</i>	0.612	0.0563
<i>CG1529</i>	0.612	0.0563
<i>CG8004</i>	0.612	0.0563
<i>GluRIIA</i>	0.612	0.0563
<i>O-fut1</i>	0.612	0.0563
<i>blos4</i>	0.611	0.0568
<i>CG4573</i>	0.611	0.0568
<i>dpr20</i>	0.611	0.0568
<i>Elp2</i>	0.61	0.0571
<i>La</i>	0.61	0.0571
<i>polo</i>	0.61	0.0571
<i>Sym</i>	0.61	0.0571
<i>beat-11b</i>	0.609	0.0575
<i>CG10431</i>	0.609	0.0575
<i>CG10467</i>	0.609	0.0575
<i>CG14512</i>	0.609	0.0575
<i>CG33511</i>	0.609	0.0575
<i>CG9782</i>	0.609	0.0575
<i>Fbp45</i>	0.609	0.0575
<i>Sox15</i>	0.609	0.0575
<i>Cpr76Bb</i>	0.608	0.0582
<i>homer</i>	0.608	0.0582
<i>hop</i>	0.608	0.0582
<i>hug</i>	0.608	0.0582
<i>CG14608</i>	0.607	0.0586
<i>CG8818</i>	0.607	0.0586
<i>Prosalpha7</i>	0.607	0.0586
<i>Tsp26A</i>	0.607	0.0586
<i>TllIEalpha</i>	0.606	0.0589
<i>tth</i>	0.606	0.0589
<i>CG13154</i>	0.605	0.0591
<i>CG7427</i>	0.605	0.0591
<i>lrb8a</i>	0.605	0.0591
<i>Klp61F</i>	0.605	0.0591
<i>Rab9</i>	0.605	0.0591
<i>Atg13</i>	0.604	0.0595
<i>CG11165</i>	0.604	0.0595
<i>CG13125</i>	0.604	0.0595
<i>CG13802</i>	0.604	0.0595
<i>CG1792</i>	0.604	0.0595
<i>CG6074</i>	0.604	0.0595
<i>CG7056</i>	0.604	0.0595
<i>CG8397</i>	0.604	0.0595
<i>wit</i>	0.604	0.0595
<i>CG33260</i>	0.603	0.0604
<i>CG5361</i>	0.603	0.0604
<i>lrb6a</i>	0.603	0.0604

Gene Name	ERC Value	P-value
<i>lrg4h</i>	0.603	0.0604
<i>msn</i>	0.603	0.0604
<i>Scr</i>	0.603	0.0604
<i>CD98hc</i>	0.602	0.0609
<i>CG13587</i>	0.602	0.0609
<i>CG32176</i>	0.602	0.0609
<i>CG5428</i>	0.602	0.0609
<i>CG6619</i>	0.602	0.0609
<i>CG12241</i>	0.601	0.0614
<i>CG7695</i>	0.601	0.0614
<i>MKP-4</i>	0.601	0.0614
<i>tin</i>	0.601	0.0614
<i>CG13204</i>	0.6	0.0617
<i>CG13841</i>	0.6	0.0617
<i>CG5676</i>	0.6	0.0617
<i>GlcAT-P</i>	0.6	0.0617
<i>Sc2</i>	0.6	0.0617
<i>Wnt4</i>	0.6	0.0617
<i>CG14720</i>	0.599	0.0623
<i>CG5808</i>	0.599	0.0623
<i>Klp68D</i>	0.599	0.0623
<i>CG18476</i>	0.598	0.0625
<i>CG5746</i>	0.598	0.0625
<i>CG6579</i>	0.598	0.0625
<i>CG7049</i>	0.598	0.0625
<i>dao</i>	0.598	0.0625
<i>PGRP-LD</i>	0.598	0.0625
<i>tw</i>	0.598	0.0625
<i>CG5612</i>	0.597	0.0632
<i>CG8155</i>	0.597	0.0632
<i>ImpL1</i>	0.597	0.0632
<i>Nek2</i>	0.597	0.0632
<i>sa</i>	0.596	0.0635
<i>sna</i>	0.596	0.0635
<i>CG10006</i>	0.595	0.0637
<i>CG12818</i>	0.595	0.0637
<i>CG3732</i>	0.595	0.0637
<i>CG5018</i>	0.595	0.0637
<i>CG5522</i>	0.595	0.0637
<i>CG9727</i>	0.595	0.0637
<i>CTCF</i>	0.595	0.0637
<i>Ent2</i>	0.595	0.0637
<i>Gas41</i>	0.595	0.0637
<i>lmd</i>	0.595	0.0637
<i>Syt1</i>	0.595	0.0637
<i>Taf13</i>	0.595	0.0637
<i>CG8519</i>	0.594	0.0648
<i>Hpr1</i>	0.594	0.0648
<i>Oatp58Da</i>	0.594	0.0648
<i>aust</i>	0.593	0.065
<i>CG14070</i>	0.593	0.065
<i>CG3386</i>	0.593	0.065
<i>Cpr62Ba</i>	0.593	0.065
<i>EcR</i>	0.593	0.065
<i>mo</i>	0.593	0.065
<i>spd-2</i>	0.593	0.065

Gene Name	ERC Value	P-value
<i>isg</i>	0.593	0.065
<i>CG12042</i>	0.592	0.0658
<i>CG18812</i>	0.592	0.0658
<i>epsilonCOP</i>	0.592	0.0658
<i>lrb54a</i>	0.592	0.0658
<i>wg</i>	0.592	0.0658
<i>zen</i>	0.592	0.0658
<i>CG6024</i>	0.591	0.0663
<i>l(3)76BDr</i>	0.591	0.0663
<i>mei-W68</i>	0.591	0.0663
<i>CG7785</i>	0.59	0.0666
<i>dgo</i>	0.59	0.0666
<i>gdl</i>	0.59	0.0666
<i>mRpL36</i>	0.59	0.0666
<i>Probeta3</i>	0.59	0.0666
<i>CG13640</i>	0.589	0.067
<i>CG5110</i>	0.589	0.067
<i>Poxn</i>	0.589	0.067
<i>Rtf1</i>	0.589	0.067
<i>Tsp</i>	0.589	0.067
<i>babo</i>	0.588	0.0675
<i>MED17</i>	0.588	0.0675
<i>odd</i>	0.588	0.0675
<i>cav</i>	0.587	0.0677
<i>CG13310</i>	0.587	0.0677
<i>CG13829</i>	0.587	0.0677
<i>CG14572</i>	0.587	0.0677
<i>CG15083</i>	0.587	0.0677
<i>CG16798</i>	0.587	0.0677
<i>CG17328</i>	0.587	0.0677
<i>CG3532</i>	0.587	0.0677
<i>CG7255</i>	0.587	0.0677
<i>dpr2</i>	0.587	0.0677
<i>mRpL54</i>	0.587	0.0677
<i>CG12316</i>	0.586	0.0687
<i>cnk</i>	0.586	0.0687
<i>Golgin84</i>	0.586	0.0687
<i>CG10713</i>	0.585	0.069
<i>CG1809</i>	0.585	0.069
<i>CG3281</i>	0.585	0.069
<i>CG5541</i>	0.585	0.069
<i>CG6067</i>	0.585	0.069
<i>CG6792</i>	0.585	0.069
<i>CG14222</i>	0.584	0.0695
<i>CG6927</i>	0.584	0.0695
<i>Sps2</i>	0.584	0.0695
<i>Tak1</i>	0.584	0.0695
<i>CG13005</i>	0.583	0.0699
<i>CG13766</i>	0.583	0.0699
<i>CG14069</i>	0.583	0.0699
<i>CG3356</i>	0.583	0.0699
<i>CG9542</i>	0.583	0.0699
<i>CG12929</i>	0.582	0.0704
<i>CG13038</i>	0.582	0.0704
<i>CG13843</i>	0.582	0.0704
<i>CG4822</i>	0.582	0.0704

Gene Name	ERC Value	P-value
<i>CG7082</i>	0.582	0.0704
<i>CycK</i>	0.582	0.0704
<i>ksr</i>	0.582	0.0704
<i>l(2)05714</i>	0.582	0.0704
<i>mthl1</i>	0.582	0.0704
<i>Phax</i>	0.582	0.0704
<i>Pngl</i>	0.582	0.0704
<i>CG3764</i>	0.581	0.0714
<i>CG10348</i>	0.58	0.0714
<i>CG10602</i>	0.58	0.0714
<i>CG13424</i>	0.58	0.0714
<i>CG15172</i>	0.58	0.0714
<i>CG3191</i>	0.58	0.0714
<i>CG7789</i>	0.58	0.0714
<i>CG8149</i>	0.58	0.0714
<i>pdm3</i>	0.58	0.0714
<i>pnt</i>	0.58	0.0714
<i>pon</i>	0.58	0.0714
<i>Rad51D</i>	0.58	0.0714
<i>thoc7</i>	0.58	0.0714
<i>CG7911</i>	0.579	0.0725
<i>CG8193</i>	0.579	0.0725
<i>CG9577</i>	0.579	0.0725
<i>CG18171</i>	0.578	0.0728
<i>CG32195</i>	0.578	0.0728
<i>CG9691</i>	0.578	0.0728
<i>Epac</i>	0.578	0.0728
<i>hyx</i>	0.578	0.0728
<i>Snr1</i>	0.578	0.0728
<i>stan</i>	0.578	0.0728
<i>CG15011</i>	0.577	0.0734
<i>CG1674</i>	0.577	0.0734
<i>CG3301</i>	0.577	0.0734
<i>Nrk</i>	0.577	0.0734
<i>pkaap</i>	0.577	0.0734
<i>CG12713</i>	0.576	0.0739
<i>bs</i>	0.575	0.074
<i>CG13454</i>	0.575	0.074
<i>CG14711</i>	0.575	0.074
<i>ETH</i>	0.575	0.074
<i>Gcn2</i>	0.575	0.074
<i>HDAC4</i>	0.575	0.074
<i>mre11</i>	0.575	0.074
<i>mRpL14</i>	0.575	0.074
<i>nes</i>	0.575	0.074
<i>ana</i>	0.574	0.0748
<i>Bsg25D</i>	0.574	0.0748
<i>CG31935</i>	0.574	0.0748
<i>Hsp67Bb</i>	0.574	0.0748
<i>Arp5</i>	0.573	0.0751
<i>CG15435</i>	0.573	0.0751
<i>CG3021</i>	0.573	0.0751
<i>CG3308</i>	0.573	0.0751
<i>CG5466</i>	0.573	0.0751
<i>Galpha73B</i>	0.573	0.0751
<i>Prx5037</i>	0.573	0.0751

Table 6.S18 Continued

Gene Name	ERC Value	P-value
<i>tor</i>	0.573	0.0751
<i>dm</i>	0.572	0.0759
<i>CG12420</i>	0.571	0.0759
<i>Ssadh</i>	0.571	0.0759
<i>Bet1</i>	0.57	0.0761
<i>CG10933</i>	0.57	0.0761
<i>CG14696</i>	0.57	0.0761
<i>CG15553</i>	0.57	0.0761
<i>CG15634</i>	0.57	0.0761
<i>mRpS6</i>	0.57	0.0761
<i>Plip</i>	0.57	0.0761
<i>PSR</i>	0.57	0.0761
<i>CG14803</i>	0.569	0.0768
<i>dock</i>	0.569	0.0768
<i>Spc105R</i>	0.569	0.0768
<i>nAcRbeta-2</i>	0.568	0.0771
<i>snz</i>	0.568	0.0771
<i>Stam</i>	0.568	0.0771
<i>CG5909</i>	0.567	0.0774
<i>CG8538</i>	0.567	0.0774
<i>Csk</i>	0.567	0.0774
<i>Atg7</i>	0.566	0.0777
<i>bin3</i>	0.566	0.0777
<i>CG10352</i>	0.566	0.0777
<i>CG11178</i>	0.566	0.0777
<i>CG30085</i>	0.566	0.0777
<i>CG9336</i>	0.566	0.0777
<i>crb</i>	0.566	0.0777
<i>GlcT-1</i>	0.566	0.0777
<i>hh</i>	0.566	0.0777
<i>Mnn1</i>	0.566	0.0777
<i>mRpL48</i>	0.566	0.0777
<i>Or46a</i>	0.566	0.0777
<i>pbl</i>	0.566	0.0777
<i>RagC</i>	0.566	0.0777
<i>CG11159</i>	0.565	0.0789
<i>CG12990</i>	0.565	0.0789
<i>Ppm1</i>	0.565	0.0789
<i>SdhC</i>	0.565	0.0789
<i>srp</i>	0.565	0.0789
<i>CG3548</i>	0.564	0.0794
<i>CG4892</i>	0.564	0.0794
<i>CG9649</i>	0.564	0.0794
<i>lab</i>	0.564	0.0794
<i>mRpL30</i>	0.564	0.0794
<i>CG17078</i>	0.563	0.0798
<i>CG18265</i>	0.563	0.0798
<i>CG4587</i>	0.563	0.0798
<i>fas</i>	0.563	0.0798
<i>rho-6</i>	0.563	0.0798
<i>BubR1</i>	0.562	0.0803
<i>CG1575</i>	0.562	0.0803
<i>Cp7Fb</i>	0.562	0.0803
<i>HLH54F</i>	0.562	0.0803
<i>Rrp46</i>	0.562	0.0803
<i>CG34005</i>	0.561	0.0807

Gene Name	ERC Value	P-value
<i>CG7069</i>	0.561	0.0807
<i>Cks85A</i>	0.561	0.0807
<i>malpha</i>	0.561	0.0807
<i>Ssl1</i>	0.561	0.0807
<i>Usf</i>	0.561	0.0807
<i>CG11248</i>	0.56	0.0813
<i>CG33695</i>	0.56	0.0813
<i>lr7a</i>	0.56	0.0813
<i>Ucp4C</i>	0.56	0.0813
<i>CG30157</i>	0.559	0.0816
<i>l(2)05510</i>	0.559	0.0816
<i>mex1</i>	0.559	0.0816
<i>Reck</i>	0.559	0.0816
<i>Tsp42Ek</i>	0.559	0.0816
<i>CG32685</i>	0.558	0.0821
<i>CG4041</i>	0.558	0.0821
<i>CG2915</i>	0.557	0.0823
<i>CG30101</i>	0.557	0.0823
<i>CG31089</i>	0.557	0.0823
<i>CG6153</i>	0.557	0.0823
<i>CG6724</i>	0.557	0.0823
<i>CG9288</i>	0.557	0.0823
<i>ptc</i>	0.557	0.0823
<i>sd</i>	0.557	0.0823
<i>CG4377</i>	0.556	0.083
<i>CG7382</i>	0.556	0.083
<i>CG14050</i>	0.555	0.0832
<i>rgr</i>	0.555	0.0832
<i>Syt14</i>	0.555	0.0832
<i>zpg</i>	0.555	0.0832
<i>Aldh</i>	0.554	0.0835
<i>CG33229</i>	0.554	0.0835
<i>CG8159</i>	0.554	0.0835
<i>hoip</i>	0.554	0.0835
<i>Klp67A</i>	0.554	0.0835
<i>Pc</i>	0.554	0.0835
<i>Syx4</i>	0.554	0.0835
<i>CG31922</i>	0.553	0.0841
<i>CG5255</i>	0.553	0.0841
<i>CG5325</i>	0.553	0.0841
<i>mrt</i>	0.553	0.0841
<i>net</i>	0.553	0.0841
<i>CG11155</i>	0.552	0.0846
<i>CG12075</i>	0.552	0.0846
<i>CG4025</i>	0.552	0.0846
<i>eyg</i>	0.552	0.0846
<i>PGRP-LE</i>	0.552	0.0846
<i>BBS4</i>	0.551	0.085
<i>CG34195</i>	0.551	0.085
<i>CG40228</i>	0.551	0.085
<i>CG5414</i>	0.551	0.085
<i>exex</i>	0.551	0.085
<i>CG12237</i>	0.55	0.0855
<i>CG15365</i>	0.55	0.0855
<i>CG31344</i>	0.55	0.0855
<i>CG31371</i>	0.55	0.0855

Gene Name	ERC Value	P-value
<i>CG3744</i>	0.55	0.0855
<i>CG5897</i>	0.55	0.0855
<i>CG6488</i>	0.55	0.0855
<i>CG8209</i>	0.55	0.0855
<i>CG4996</i>	0.549	0.0862
<i>CG8892</i>	0.549	0.0862
<i>fz3</i>	0.549	0.0862
<i>KailRIA</i>	0.549	0.0862
<i>nimB5</i>	0.549	0.0862
<i>bip1</i>	0.548	0.0867
<i>CG31957</i>	0.548	0.0867
<i>CG3626</i>	0.548	0.0867
<i>CG5026</i>	0.548	0.0867
<i>Sin3A</i>	0.548	0.0867
<i>sina</i>	0.548	0.0867
<i>yellow-e2</i>	0.548	0.0867
<i>ase</i>	0.547	0.0873
<i>CG12913</i>	0.547	0.0873
<i>CG4080</i>	0.547	0.0873
<i>NKAIN</i>	0.547	0.0873
<i>spz6</i>	0.547	0.0873
<i>wdp</i>	0.547	0.0873
<i>Ykt6</i>	0.547	0.0873
<i>CG11583</i>	0.546	0.0879
<i>CG12171</i>	0.546	0.0879
<i>CG13296</i>	0.546	0.0879
<i>CG8745</i>	0.546	0.0879
<i>CG9922</i>	0.546	0.0879
<i>CG2950</i>	0.545	0.0884
<i>CG32590</i>	0.545	0.0884
<i>Cp190</i>	0.545	0.0884
<i>Prp38</i>	0.545	0.0884
<i>Acp32CD</i>	0.544	0.0887
<i>CG13229</i>	0.544	0.0887
<i>CG14408</i>	0.544	0.0887
<i>Hph</i>	0.544	0.0887
<i>CG10107</i>	0.543	0.0891
<i>CG10158</i>	0.543	0.0891
<i>CG10822</i>	0.543	0.0891
<i>CG11699</i>	0.543	0.0891
<i>CG13950</i>	0.543	0.0891
<i>CG13970</i>	0.543	0.0891
<i>CG14023</i>	0.543	0.0891
<i>CG33012</i>	0.543	0.0891
<i>eco</i>	0.543	0.0891
<i>RpS29</i>	0.543	0.0891
<i>trem</i>	0.543	0.0891
<i>Tsp66A</i>	0.543	0.0891
<i>CG31550</i>	0.542	0.0902
<i>CG32803</i>	0.542	0.0902
<i>CG4393</i>	0.542	0.0902
<i>ird5</i>	0.542	0.0902
<i>CG2016</i>	0.541	0.0905
<i>CG5390</i>	0.541	0.0905
<i>Taf10</i>	0.541	0.0905
<i>CG11475</i>	0.54	0.0908

Gene Name	ERC Value	P-value
<i>CG16926</i>	0.54	0.0908
<i>CG2233</i>	0.54	0.0908
<i>CG34350</i>	0.54	0.0908
<i>CG8562</i>	0.54	0.0908
<i>CG8858</i>	0.54	0.0908
<i>vig</i>	0.54	0.0908
<i>CG1074</i>	0.539	0.0914
<i>CG11034</i>	0.539	0.0914
<i>CG11095</i>	0.539	0.0914
<i>CG31102</i>	0.539	0.0914
<i>CG6197</i>	0.539	0.0914
<i>CG7705</i>	0.539	0.0914
<i>CG9063</i>	0.539	0.0914
<i>Gr98a</i>	0.539	0.0914
<i>mus304</i>	0.539	0.0914
<i>Sas-4</i>	0.539	0.0914
<i>CG10825</i>	0.538	0.0923
<i>CG16743</i>	0.538	0.0923
<i>CG42487</i>	0.538	0.0923
<i>CG4287</i>	0.538	0.0923
<i>Cpr49Aq</i>	0.538	0.0923
<i>mms4</i>	0.538	0.0923
<i>mtTFB1</i>	0.538	0.0923
<i>tey</i>	0.538	0.0923
<i>Dgp-1</i>	0.537	0.0931
<i>Fks-C1</i>	0.537	0.0931
<i>Vti1</i>	0.537	0.0931
<i>CG13036</i>	0.536	0.0933
<i>CG3542</i>	0.536	0.0933
<i>CG5726</i>	0.536	0.0933
<i>CG7277</i>	0.536	0.0933
<i>CG9667</i>	0.536	0.0933
<i>mav</i>	0.536	0.0933
<i>CG7860</i>	0.535	0.0939
<i>CG8116</i>	0.535	0.0939
<i>Cp36</i>	0.535	0.0939
<i>dve</i>	0.535	0.0939
<i>Mcr</i>	0.535	0.0939
<i>nudE</i>	0.535	0.0939
<i>Ptx1</i>	0.535	0.0939
<i>Rtc1</i>	0.535	0.0939
<i>Tdc2</i>	0.535	0.0939
<i>CG3939</i>	0.534	0.0947
<i>CG8476</i>	0.534	0.0947
<i>Cyp301a1</i>	0.534	0.0947
<i>Ets96B</i>	0.534	0.0947
<i>mRpL35</i>	0.534	0.0947
<i>rogdi</i>	0.534	0.0947
<i>Br140</i>	0.533	0.0952
<i>CG14340</i>	0.533	0.0952
<i>CG17562</i>	0.533	0.0952
<i>CG8389</i>	0.533	0.0952
<i>Ndc80</i>	0.533	0.0952
<i>rab3-GAP</i>	0.533	0.0952
<i>AttD</i>	0.532	0.0958
<i>CG13305</i>	0.532	0.0958

Gene Name	ERC Value	P-value
<i>CG30380</i>	0.532	0.0958
<i>CG31365</i>	0.532	0.0958
<i>CG34404</i>	0.532	0.0958
<i>Dscam3</i>	0.532	0.0958
<i>Vps28</i>	0.532	0.0958
<i>CG12424</i>	0.531	0.0964
<i>CG15005</i>	0.531	0.0964
<i>CG15118</i>	0.531	0.0964
<i>Rpn9</i>	0.531	0.0964
<i>CG14647</i>	0.53	0.0968
<i>CG4447</i>	0.53	0.0968
<i>nerfin-1</i>	0.53	0.0968
<i>CG10418</i>	0.529	0.097
<i>CG11874</i>	0.529	0.097
<i>CG13850</i>	0.529	0.097
<i>CG31025</i>	0.529	0.097
<i>CG3168</i>	0.529	0.097
<i>CG32537</i>	0.529	0.097
<i>CG33234</i>	0.529	0.097
<i>CG5589</i>	0.529	0.097
<i>GM130</i>	0.529	0.097
<i>CG13897</i>	0.528	0.0978
<i>CG15534</i>	0.528	0.0978
<i>CG17724</i>	0.528	0.0978
<i>ec</i>	0.528	0.0978
<i>lap2</i>	0.528	0.0978
<i>Sp7</i>	0.528	0.0978
<i>Cpr65Ec</i>	0.527	0.0984
<i>HLHm3</i>	0.527	0.0984
<i>Nhe3</i>	0.527	0.0984
<i>ome</i>	0.527	0.0984
<i>RpLP1</i>	0.527	0.0984
<i>sr</i>	0.527	0.0984
<i>CG13405</i>	0.526	0.0989
<i>CG32354</i>	0.526	0.0989
<i>CG42346</i>	0.526	0.0989
<i>CG42358</i>	0.526	0.0989
<i>CG4612</i>	0.526	0.0989
<i>CG6388</i>	0.526	0.0989
<i>GluRIIC</i>	0.526	0.0989
<i>obst-F</i>	0.526	0.0989
<i>CG11164</i>	0.525	0.0996
<i>CG17782</i>	0.525	0.0996
<i>CG5048</i>	0.525	0.0996
<i>CG8087</i>	0.525	0.0996
<i>gry</i>	0.525	0.0996

Table 6.S19 - Top Genes ERC values for *spn-A* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG4691	0.902	0.0001
CG3610	0.897	0.0002
CG6689	0.884	0.0003
CG13957	0.882	0.0004
CG7126	0.877	0.0005
CG11211	0.857	0.0005
CG8564	0.855	0.0006
SAK	0.85	0.0007
Sbf	0.85	0.0007
CG31870	0.841	0.0009
CG17387	0.837	0.001
MED20	0.835	0.0011
Or13a	0.835	0.0011
CG5549	0.833	0.0013
CG4476	0.826	0.0014
mus309	0.826	0.0014
CG34214	0.821	0.0015
CG8349	0.81	0.0016
Vha14-1	0.809	0.0017
CG6654	0.808	0.0018
CG3621	0.806	0.0019
CG31036	0.805	0.002
CG4844	0.805	0.002
CG12439	0.804	0.0022
CG17751	0.804	0.0022
CG9541	0.804	0.0022
grh	0.804	0.0022
msl(2)35Ci	0.804	0.0022
dpr5	0.798	0.0026
CG14956	0.796	0.0027
CG5934	0.794	0.0028
CG3760	0.791	0.0029
RluA-1	0.786	0.003
CG4324	0.785	0.0031
CG15653	0.784	0.0032
CG9797	0.784	0.0032
CG2652	0.783	0.0033
CG32442	0.783	0.0033
CG5198	0.781	0.0035
CG31296	0.775	0.0036
CG8646	0.772	0.0037
CG31803	0.771	0.0038
MED10	0.771	0.0038
CG2003	0.77	0.004
CG13565	0.768	0.0041
CG12998	0.764	0.0041
Rad1	0.763	0.0042
CG14182	0.762	0.0043
CG13931	0.761	0.0044
RFC4	0.76	0.0045
CG14401	0.755	0.0046
rob162A	0.755	0.0046
dao	0.75	0.0048
MYPT-75D	0.75	0.0048
CG3570	0.749	0.005
DNApol- α ph	0.749	0.005

Gene Name	ERC Value	P-value
laf	0.747	0.0051
CG5366	0.745	0.0052
klu	0.745	0.0052
CG5337	0.744	0.0054
al	0.743	0.0055
Ripalpha	0.743	0.0055
CG6201	0.741	0.0057
CG8909	0.741	0.0057
SBf	0.74	0.0059
Wnt5	0.739	0.0059
Lcch3	0.738	0.006
N	0.737	0.0061
CG31235	0.736	0.0062
CG42288	0.734	0.0063
CG10440	0.733	0.0064
CG13248	0.732	0.0065
Obp50e	0.732	0.0065
pim	0.73	0.0067
CG8329	0.729	0.0068
CG14989	0.728	0.0068
Pask	0.728	0.0068
CG31898	0.727	0.007
exo70	0.724	0.0071
CG7627	0.723	0.0072
CG13958	0.722	0.0073
CG5773	0.719	0.0074
CG6182	0.718	0.0075
bond	0.717	0.0076
CG7841	0.716	0.0077
eEF1delta	0.716	0.0077
CG1888	0.714	0.0078
CG12050	0.713	0.0079
CG4065	0.712	0.008
Sirt6	0.711	0.0081
CG17593	0.71	0.0082
srw	0.71	0.0082
CG32187	0.708	0.0084
CG16771	0.706	0.0085
RpA-70	0.706	0.0085
CG10984	0.705	0.0086
CG14856	0.705	0.0086
CG32121	0.705	0.0086
CG7456	0.705	0.0086
CG4753	0.704	0.009
Obp47a	0.704	0.009
CG32113	0.703	0.0092
robo	0.703	0.0092
CG14644	0.702	0.0094
NlPp1	0.702	0.0094
a10	0.701	0.0095
CG6923	0.701	0.0095
Src42A	0.701	0.0095
CG7609	0.7	0.0098
dsd	0.7	0.0098
CG33253	0.699	0.01
GstE6	0.699	0.01

Gene Name	ERC Value	P-value
CG6576	0.697	0.0102
Cpr49Aa	0.696	0.0103
daw	0.696	0.0103
CG15128	0.695	0.0105
Dref	0.695	0.0105
Uzaf50	0.695	0.0105
CG32428	0.694	0.0107
Patr-1	0.694	0.0107
trr	0.694	0.0107
CG10516	0.692	0.011
Las	0.691	0.0111
Rab8	0.689	0.0112
CG17180	0.687	0.0113
AlstR	0.686	0.0114
CG1962	0.684	0.0114
CG4328	0.681	0.0115
MtnC	0.681	0.0115
synaptogyrin	0.681	0.0115
CG17572	0.68	0.0118
CG6422	0.68	0.0118
CG7044	0.678	0.012
CG13567	0.677	0.0121
CG14075	0.677	0.0121
veil	0.677	0.0121
CG12502	0.676	0.0123
CG15577	0.675	0.0124
CG12253	0.674	0.0125
CG42506	0.674	0.0125
CG11298	0.673	0.0127
CG31075	0.673	0.0127
Tom20	0.673	0.0127
CG14676	0.672	0.013
CG15580	0.672	0.013
CHKov2	0.671	0.0132
Ubp64E	0.671	0.0132
CG32040	0.67	0.0133
nmd	0.67	0.0133
Parg	0.67	0.0133
CG10973	0.669	0.0136
CG13284	0.669	0.0136
Ogg1	0.668	0.0138
Sox21b	0.668	0.0138
CG31145	0.666	0.014
CG34007	0.665	0.0141
snama	0.665	0.0141
CG10996	0.664	0.0142
CG17570	0.664	0.0142
CG3776	0.664	0.0142
CG10133	0.663	0.0145
brk	0.662	0.0146
amos	0.66	0.0147
CG7928	0.66	0.0147
trk	0.66	0.0147
CG8993	0.658	0.015
chm	0.658	0.015
SCAR	0.658	0.015

Gene Name	ERC Value	P-value
CG17922	0.657	0.0152
CG12099	0.656	0.0153
CG5056	0.656	0.0153
Chd1	0.656	0.0153
pwn	0.656	0.0153
CG12014	0.655	0.0157
CG15546	0.655	0.0157
CG33704	0.655	0.0157
CG8916	0.655	0.0157
Gl	0.655	0.0157
CG12171	0.654	0.0161
CG14839	0.653	0.0162
AQP	0.652	0.0163
Cad74A	0.652	0.0163
CG14007	0.652	0.0163
CG34314	0.651	0.0166
CG3611	0.651	0.0166
CG9505	0.651	0.0166
null0	0.65	0.0168
gro	0.649	0.0169
CG13375	0.648	0.017
CG13727	0.648	0.017
Dro	0.648	0.017
Tsp97E	0.648	0.017
CG13545	0.646	0.0174
CG14321	0.646	0.0174
Hlp1	0.646	0.0174
CYLD	0.645	0.0177
CG1387	0.644	0.0177
CG5727	0.644	0.0177
Dab	0.644	0.0177
CG6908	0.643	0.018
ana	0.642	0.0181
CG5550	0.642	0.0181
CG1275	0.64	0.0183
S1P	0.64	0.0183
chs	0.639	0.0185
CG16989	0.639	0.0185
CG30391	0.639	0.0185
PTP-ER	0.639	0.0185
CG13339	0.638	0.0188
Tango3	0.638	0.0188
CG18558	0.635	0.019
CG5720	0.634	0.0191
drl	0.634	0.0191
CG12084	0.633	0.0193
CG12219	0.633	0.0193
CG6959	0.633	0.0193
RhoGAP15E	0.633	0.0193
Utx	0.633	0.0193
CG4582	0.632	0.0197
escl	0.631	0.0198
CG5669	0.63	0.0199
Dip-B	0.63	0.0199
Fas2	0.63	0.0199
PH4alphaNE	0.63	0.0199

Gene Name	ERC Value	P-value
CG4901	0.629	0.0203
Lasp	0.629	0.0203
CG17780	0.628	0.0205
CG34317	0.628	0.0205
CG5897	0.628	0.0205
Nep4	0.628	0.0205
CG13747	0.627	0.0208
CG34176	0.627	0.0208
CG11398	0.626	0.021
CG3894	0.626	0.021
CG1227	0.625	0.0212
CG15537	0.625	0.0212
CG9240	0.624	0.0214
CG6971	0.623	0.0214
CG12479	0.622	0.0215
Der-1	0.621	0.0216
MED23	0.621	0.0216
Msl	0.621	0.0216
CG6276	0.62	0.0219
CG42553	0.619	0.022
CG7597	0.619	0.022
CG12374	0.618	0.0222
CG3104	0.618	0.0222
CG33770	0.618	0.0222
Dfd	0.618	0.0222
kto	0.618	0.0222
Met	0.618	0.0222
CG13561	0.617	0.0227
CG13992	0.616	0.0228
CG11299	0.615	0.0229
CG3257	0.615	0.0229
Npc2a	0.615	0.0229
CG13408	0.614	0.0232
CG9727	0.614	0.0232
chrh	0.614	0.0232
Cic-a	0.614	0.0232
CG4615	0.613	0.0235
CG10824	0.612	0.0236
CG10948	0.612	0.0236
egl	0.612	0.0236
sds22	0.612	0.0236
silbo	0.612	0.0236
ssp4	0.612	0.0236
Sur	0.612	0.0236
lr67b	0.611	0.0242
Br140	0.61	0.0243
CG10069	0.61	0.0243
CG10881	0.61	0.0243
CG40351	0.61	0.0243
Ent3	0.61	0.0243
wrapper	0.61	0.0243
CG31109	0.609	0.0249
brat	0.608	0.025
CG15373	0.608	0.025
CG18594	0.608	0.025
CG7872	0.608	0.025

Table 6.S19 Continued

Gene Name	ERC Value	P-value
<i>atp</i>	0.608	0.025
<i>ver</i>	0.608	0.025
<i>CG1971</i>	0.607	0.0255
<i>CG42676</i>	0.607	0.0255
<i>CG5235</i>	0.607	0.0255
<i>trx</i>	0.607	0.0255
<i>CG12637</i>	0.606	0.0259
<i>Hira</i>	0.606	0.0259
<i>CG32792</i>	0.604	0.026
<i>oaf</i>	0.604	0.026
<i>CG14126</i>	0.603	0.0262
<i>CG17931</i>	0.603	0.0262
<i>CG42554</i>	0.602	0.0264
<i>CG1136</i>	0.601	0.0265
<i>CG15891</i>	0.601	0.0265
<i>CG8436</i>	0.601	0.0265
<i>Ras85D</i>	0.601	0.0265
<i>Trxr-1</i>	0.601	0.0265
<i>beta4GalNA</i>	0.6	0.0269
<i>CG14424</i>	0.6	0.0269
<i>CG1494</i>	0.599	0.0271
<i>CG16826</i>	0.599	0.0271
<i>CG17233</i>	0.599	0.0271
<i>CG8072</i>	0.598	0.0274
<i>CG5535</i>	0.597	0.0275
<i>Tehao</i>	0.597	0.0275
<i>CG1603</i>	0.596	0.0277
<i>Fancd2</i>	0.595	0.0277
<i>stj</i>	0.594	0.0278
<i>Ten-m</i>	0.594	0.0278
<i>BRWD3</i>	0.593	0.028
<i>CG8319</i>	0.593	0.028
<i>vih</i>	0.593	0.028
<i>Cf2</i>	0.592	0.0283
<i>CG11504</i>	0.592	0.0283
<i>GNBP1</i>	0.592	0.0283
<i>hfw</i>	0.592	0.0283
<i>CG11790</i>	0.591	0.0286
<i>CG9272</i>	0.591	0.0286
<i>Madm</i>	0.591	0.0286
<i>UbcD10</i>	0.591	0.0286
<i>AdoR</i>	0.59	0.029
<i>Cyp9b2</i>	0.59	0.029
<i>ko</i>	0.59	0.029
<i>pex10</i>	0.59	0.029
<i>pros</i>	0.59	0.029
<i>qkr58E-1</i>	0.59	0.029
<i>Spn31A</i>	0.59	0.029
<i>cact</i>	0.589	0.0296
<i>CG7492</i>	0.589	0.0296
<i>CG9945</i>	0.589	0.0296
<i>Cpr72Ea</i>	0.589	0.0296
<i>Mst85C</i>	0.589	0.0296
<i>Rab-RP3</i>	0.589	0.0296
<i>wge</i>	0.588	0.0302
<i>RplL34b</i>	0.587	0.0303

Gene Name	ERC Value	P-value
<i>Tektin-A</i>	0.587	0.0303
<i>CG14626</i>	0.586	0.0305
<i>CG31038</i>	0.585	0.0305
<i>Cyp6t1</i>	0.585	0.0305
<i>D2R</i>	0.585	0.0305
<i>MBD-like</i>	0.585	0.0305
<i>RpII128</i>	0.585	0.0305
<i>star1</i>	0.585	0.0305
<i>vig</i>	0.585	0.0305
<i>llp4</i>	0.584	0.0312
<i>Ptp69D</i>	0.584	0.0312
<i>sas</i>	0.584	0.0312
<i>CG11369</i>	0.583	0.0314
<i>CG31886</i>	0.583	0.0314
<i>dpr4</i>	0.583	0.0314
<i>CG3680</i>	0.582	0.0317
<i>asun</i>	0.581	0.0318
<i>CG14921</i>	0.581	0.0318
<i>CG17490</i>	0.581	0.0318
<i>CG31191</i>	0.581	0.0318
<i>CG32104</i>	0.581	0.0318
<i>LSm-4</i>	0.581	0.0318
<i>CG1602</i>	0.58	0.0323
<i>CG18746</i>	0.58	0.0323
<i>CG6412</i>	0.58	0.0323
<i>Gpi1</i>	0.58	0.0323
<i>sub</i>	0.58	0.0323
<i>Ggamma1</i>	0.579	0.0328
<i>RFC3</i>	0.579	0.0328
<i>Cad99C</i>	0.577	0.033
<i>CG30268</i>	0.577	0.033
<i>CG8550</i>	0.577	0.033
<i>nej</i>	0.577	0.033
<i>Rassf</i>	0.577	0.033
<i>CG16852</i>	0.576	0.0334
<i>CG34319</i>	0.576	0.0334
<i>dpr</i>	0.576	0.0334
<i>Gr59f</i>	0.576	0.0334
<i>pita</i>	0.576	0.0334
<i>CG10659</i>	0.575	0.0339
<i>CG31431</i>	0.575	0.0339
<i>Cp110</i>	0.575	0.0339
<i>Mgat1</i>	0.575	0.0339
<i>CG13247</i>	0.574	0.0342
<i>CG32982</i>	0.574	0.0342
<i>pUf68</i>	0.574	0.0342
<i>CG14561</i>	0.573	0.0345
<i>CG4069</i>	0.573	0.0345
<i>CG4751</i>	0.573	0.0345
<i>CG9003</i>	0.573	0.0345
<i>dod</i>	0.573	0.0345
<i>CG3213</i>	0.572	0.035
<i>Obp83ef</i>	0.572	0.035
<i>Cyp309a1</i>	0.571	0.0351
<i>orb</i>	0.571	0.0351
<i>CG6362</i>	0.57	0.0353

Gene Name	ERC Value	P-value
<i>CG8925</i>	0.57	0.0353
<i>ergic53</i>	0.57	0.0353
<i>CG31751</i>	0.568	0.0356
<i>CG9586</i>	0.568	0.0356
<i>lr48b</i>	0.568	0.0356
<i>phm</i>	0.566	0.0359
<i>CG5385</i>	0.565	0.0359
<i>CG9992</i>	0.565	0.0359
<i>CG5098</i>	0.564	0.0361
<i>mys</i>	0.564	0.0361
<i>rln</i>	0.564	0.0361
<i>CG14180</i>	0.563	0.0364
<i>Mfap1</i>	0.563	0.0364
<i>prominin-like</i>	0.562	0.0366
<i>dpr4</i>	0.561	0.0367
<i>CG6472</i>	0.561	0.0367
<i>CG8661</i>	0.561	0.0367
<i>glo</i>	0.561	0.0367
<i>sec6</i>	0.56	0.037
<i>wb</i>	0.56	0.037
<i>gsb-n</i>	0.559	0.0372
<i>Hsf</i>	0.559	0.0372
<i>CG17974</i>	0.558	0.0374
<i>CG30001</i>	0.558	0.0374
<i>CG8142</i>	0.558	0.0374
<i>Tom40</i>	0.558	0.0374
<i>Atac1</i>	0.557	0.0377
<i>CG4972</i>	0.557	0.0377
<i>Exn</i>	0.557	0.0377
<i>RpL36A</i>	0.556	0.038
<i>CG1942</i>	0.555	0.0381
<i>CG5027</i>	0.555	0.0381
<i>CG13116</i>	0.554	0.0383
<i>CG34367</i>	0.554	0.0383
<i>fidipidine</i>	0.554	0.0383
<i>beat-Va</i>	0.553	0.0386
<i>CG10555</i>	0.553	0.0386
<i>CG34371</i>	0.553	0.0386
<i>Dek</i>	0.553	0.0386
<i>Spn5</i>	0.553	0.0386
<i>CG7755</i>	0.552	0.039
<i>ms(3)K81</i>	0.552	0.039
<i>Rpn12R</i>	0.552	0.039
<i>cg</i>	0.551	0.0393
<i>CG5888</i>	0.551	0.0393
<i>wmd</i>	0.551	0.0393
<i>CG3330</i>	0.55	0.0395
<i>eve</i>	0.55	0.0395
<i>alpha-Man-II</i>	0.549	0.0397
<i>CG13126</i>	0.548	0.0398
<i>CG5849</i>	0.548	0.0398
<i>CG6512</i>	0.548	0.0398
<i>Mkp3</i>	0.547	0.0401
<i>Orb7c</i>	0.547	0.0401
<i>pgant8</i>	0.547	0.0401
<i>CG15147</i>	0.546	0.0404

Gene Name	ERC Value	P-value
<i>CG6398</i>	0.546	0.0404
<i>crp</i>	0.546	0.0404
<i>rdgC</i>	0.546	0.0404
<i>CG3062</i>	0.545	0.0407
<i>CG10384</i>	0.544	0.0408
<i>CG10916</i>	0.544	0.0408
<i>CG12484</i>	0.544	0.0408
<i>CG13532</i>	0.544	0.0408
<i>CG16986</i>	0.544	0.0408
<i>CG31798</i>	0.544	0.0408
<i>CG34425</i>	0.544	0.0408
<i>CG3975</i>	0.544	0.0408
<i>CG4218</i>	0.544	0.0408
<i>en</i>	0.544	0.0408
<i>dpr14</i>	0.543	0.0417
<i>lox2</i>	0.543	0.0417
<i>MED21</i>	0.543	0.0417
<i>pnr</i>	0.543	0.0417
<i>Task7</i>	0.543	0.0417
<i>CG13285</i>	0.542	0.0422
<i>CG2694</i>	0.542	0.0422
<i>CG34404</i>	0.542	0.0422
<i>CG15925</i>	0.541	0.0424
<i>CG18249</i>	0.541	0.0424
<i>CG9706</i>	0.541	0.0424
<i>CkIIalpha-1</i>	0.541	0.0424
<i>CG31712</i>	0.54	0.0428
<i>CG32572</i>	0.54	0.0428
<i>Pp1-87B</i>	0.54	0.0428
<i>Sox21a</i>	0.539	0.0431
<i>Nrk</i>	0.538	0.0432
<i>Art4</i>	0.537	0.0432
<i>CG15160</i>	0.537	0.0432
<i>CG6020</i>	0.537	0.0432
<i>Hel69B</i>	0.537	0.0432
<i>pkf</i>	0.537	0.0432
<i>Rfx</i>	0.537	0.0432
<i>vtd</i>	0.537	0.0432
<i>D19A</i>	0.536	0.0439
<i>Fas1</i>	0.536	0.0439
<i>CG14806</i>	0.535	0.0441
<i>CG1958</i>	0.535	0.0441
<i>CG32801</i>	0.535	0.0441
<i>hb</i>	0.535	0.0441
<i>Adgf-D</i>	0.534	0.0444
<i>CG15366</i>	0.534	0.0444
<i>CG6852</i>	0.534	0.0444
<i>mew</i>	0.534	0.0444
<i>CG1271</i>	0.533	0.0448
<i>CG16853</i>	0.533	0.0448
<i>CG2321</i>	0.533	0.0448
<i>Egfr</i>	0.533	0.0448
<i>Tsp68C</i>	0.533	0.0448
<i>CG11125</i>	0.532	0.0452
<i>CG13745</i>	0.532	0.0452
<i>CG14709</i>	0.532	0.0452

Gene Name	ERC Value	P-value
<i>CG34315</i>	0.532	0.0452
<i>Lip4</i>	0.532	0.0452
<i>Ptp4E</i>	0.532	0.0452
<i>SmB</i>	0.532	0.0452
<i>CG1120</i>	0.53	0.0459
<i>CG5885</i>	0.53	0.0459
<i>gus</i>	0.53	0.0459
<i>IP3K1</i>	0.53	0.0459
<i>CG11055</i>	0.529	0.0462
<i>CG9449</i>	0.529	0.0462
<i>abd-A</i>	0.528	0.0464
<i>CG12106</i>	0.528	0.0464
<i>CG13579</i>	0.528	0.0464
<i>CG13877</i>	0.528	0.0464
<i>CG14086</i>	0.528	0.0464
<i>CG42674</i>	0.528	0.0464
<i>CG5217</i>	0.528	0.0464
<i>CG6765</i>	0.528	0.0464
<i>CG6984</i>	0.528	0.0464
<i>Fur2</i>	0.528	0.0464
<i>HPS1</i>	0.528	0.0464
<i>Nrg</i>	0.528	0.0464
<i>sens</i>	0.528	0.0464
<i>yemalpha</i>	0.528	0.0464
<i>CG11970</i>	0.527	0.0477
<i>CG30281</i>	0.527	0.0477
<i>CG3605</i>	0.527	0.0477
<i>CG5860</i>	0.527	0.0477
<i>iz</i>	0.527	0.0477
<i>CG18265</i>	0.526	0.0481
<i>LRP1</i>	0.526	0.0481
<i>RluA-2</i>	0.525	0.0483
<i>beat-lc</i>	0.524	0.0484
<i>CG5142</i>	0.524	0.0484
<i>CSN4</i>	0.524	0.0484
<i>ApepP</i>	0.523	0.0486
<i>Atg4</i>	0.523	0.0486
<i>CG9215</i>	0.523	0.0486
<i>Gap1</i>	0.522	0.0489
<i>NK7.1</i>	0.522	0.0489
<i>sunz</i>	0.522	0.0489
<i>Taz</i>	0.522	0.0489
<i>CG10051</i>	0.521	0.0493
<i>CG8397</i>	0.521	0.0493
<i>CG9008</i>	0.521	0.0493
<i>Osepg6</i>	0.521	0.0493
<i>CG3295</i>	0.52	0.0496
<i>CG6985</i>	0.52	0.0496
<i>CG7510</i>	0.52	0.0496
<i>CG15120</i>	0.519	0.0499
<i>Cyp4c3</i>	0.519	0.0499
<i>magu</i>	0.519	0.0499
<i>slim</i>	0.519	0.0499
<i>CG17321</i>	0.518	0.0503
<i>Moca-cyp</i>	0.518	0.0503
<i>argos</i>	0.517	0.0505

Table 6.S19 Continued

Gene Name	ERC Value	P-value
<i>Cic</i>	0.517	0.0505
<i>M6</i>	0.517	0.0505
<i>sinah</i>	0.517	0.0505
<i>CG12825</i>	0.516	0.0508
<i>CG34301</i>	0.516	0.0508
<i>CG8239</i>	0.516	0.0508
<i>h-cup</i>	0.516	0.0508
<i>RabX4</i>	0.516	0.0508
<i>slv</i>	0.516	0.0508
<i>Galpha73B</i>	0.515	0.0514
<i>CG34457</i>	0.514	0.0514
<i>CG5062</i>	0.514	0.0514
<i>ems</i>	0.514	0.0514
<i>CG6490</i>	0.513	0.0517
<i>nkd</i>	0.513	0.0517
<i>asf1</i>	0.512	0.0519
<i>CG4674</i>	0.512	0.0519
<i>CG5510</i>	0.512	0.0519
<i>Cortactin</i>	0.512	0.0519
<i>deff</i>	0.512	0.0519
<i>fd96Ca</i>	0.512	0.0519
<i>tara</i>	0.512	0.0519
<i>CG32772</i>	0.511	0.0525
<i>dos</i>	0.511	0.0525
<i>CG1240</i>	0.51	0.0527
<i>CG17019</i>	0.51	0.0527
<i>CG32036</i>	0.51	0.0527
<i>CG42788</i>	0.51	0.0527
<i>CG8199</i>	0.51	0.0527
<i>cooro</i>	0.51	0.0527
<i>Dnz1</i>	0.51	0.0527
<i>hpo</i>	0.51	0.0527
<i>RIC-3</i>	0.51	0.0527
<i>CG11779</i>	0.509	0.0535
<i>CG14657</i>	0.509	0.0535
<i>CG6746</i>	0.509	0.0535
<i>Mrf</i>	0.509	0.0535
<i>nmdyn-D7</i>	0.509	0.0535
<i>CG13014</i>	0.508	0.054
<i>CG14529</i>	0.508	0.054
<i>CG3457</i>	0.508	0.054
<i>CG42533</i>	0.508	0.054
<i>CG4630</i>	0.508	0.054
<i>Cyp317a1</i>	0.508	0.054
<i>lin19</i>	0.508	0.054
<i>Atf3</i>	0.507	0.0546
<i>CG13539</i>	0.507	0.0546
<i>CG13751</i>	0.507	0.0546
<i>CG33958</i>	0.507	0.0546
<i>CG5282</i>	0.507	0.0546
<i>mtacp1</i>	0.507	0.0546
<i>Psi</i>	0.507	0.0546
<i>CG10494</i>	0.506	0.0552
<i>CG5024</i>	0.506	0.0552
<i>CG32109</i>	0.505	0.0554
<i>CG32221</i>	0.505	0.0554

Gene Name	ERC Value	P-value
<i>CG34161</i>	0.505	0.0554
<i>SuUR</i>	0.505	0.0554
<i>CG13024</i>	0.504	0.0558
<i>CG6750</i>	0.504	0.0558
<i>CG8100</i>	0.504	0.0558
<i>RpL17</i>	0.504	0.0558
<i>CG13064</i>	0.503	0.0562
<i>CG14147</i>	0.503	0.0562
<i>CG32161</i>	0.503	0.0562
<i>CG5073</i>	0.503	0.0562
<i>DnaJ-60</i>	0.503	0.0562
<i>pgant3</i>	0.503	0.0562
<i>CG5694</i>	0.502	0.0568
<i>Or45b</i>	0.502	0.0568
<i>CG5804</i>	0.501	0.0569
<i>CG14317</i>	0.5	0.057
<i>CG14451</i>	0.5	0.057
<i>CG4729</i>	0.5	0.057
<i>CG9293</i>	0.5	0.057
<i>cv</i>	0.5	0.057
<i>Wnk</i>	0.5	0.057
<i>CG3708</i>	0.499	0.0576
<i>CG8959</i>	0.499	0.0576
<i>CG9305</i>	0.499	0.0576
<i>InR</i>	0.499	0.0576
<i>pds5</i>	0.499	0.0576
<i>SIP2</i>	0.499	0.0576
<i>Andorra</i>	0.498	0.0581
<i>CG31111</i>	0.498	0.0581
<i>Xbp1</i>	0.498	0.0581
<i>CG11377</i>	0.497	0.0584
<i>CG14929</i>	0.497	0.0584
<i>pll</i>	0.497	0.0584
<i>btd</i>	0.496	0.0586
<i>CG15117</i>	0.496	0.0586
<i>CG3328</i>	0.496	0.0586
<i>ham</i>	0.495	0.0589
<i>Osi3</i>	0.495	0.0589
<i>Billi</i>	0.494	0.0591
<i>CG31158</i>	0.494	0.0591
<i>CG4953</i>	0.494	0.0591
<i>Flo</i>	0.494	0.0591
<i>llp2</i>	0.494	0.0591
<i>CG10104</i>	0.493	0.0595
<i>CG12187</i>	0.493	0.0595
<i>CG13049</i>	0.493	0.0595
<i>CG6461</i>	0.493	0.0595
<i>DIP2</i>	0.493	0.0595
<i>Dpck</i>	0.493	0.0595
<i>Hr4</i>	0.493	0.0595
<i>mtb</i>	0.493	0.0595
<i>spict</i>	0.493	0.0595
<i>CG12391</i>	0.492	0.0604
<i>CG17304</i>	0.492	0.0604
<i>CG3092</i>	0.492	0.0604
<i>da</i>	0.492	0.0604

Gene Name	ERC Value	P-value
<i>didum</i>	0.492	0.0604
<i>eg</i>	0.492	0.0604
<i>vg</i>	0.492	0.0604
<i>CG14427</i>	0.491	0.061
<i>CG4398</i>	0.491	0.061
<i>gpp</i>	0.491	0.061
<i>Tis11</i>	0.491	0.061
<i>CG14352</i>	0.49	0.0614
<i>ltbp</i>	0.49	0.0614
<i>mRipS21</i>	0.49	0.0614
<i>RhoPPA100</i>	0.49	0.0614
<i>Tl</i>	0.49	0.0614
<i>CG13016</i>	0.489	0.0618
<i>CG14435</i>	0.489	0.0618
<i>CG17331</i>	0.489	0.0618
<i>CG3294</i>	0.489	0.0618
<i>Lkr</i>	0.489	0.0618
<i>osp</i>	0.489	0.0618
<i>CG13829</i>	0.488	0.0623
<i>cv</i>	0.488	0.0623
<i>VhaPPA1-2</i>	0.488	0.0623
<i>alpha-Cat</i>	0.487	0.0626
<i>CG14593</i>	0.487	0.0626
<i>CG15651</i>	0.487	0.0626
<i>CG3964</i>	0.487	0.0626
<i>CG42458</i>	0.487	0.0626
<i>CG13192</i>	0.486	0.0631
<i>CG1968</i>	0.486	0.0631
<i>CG4896</i>	0.486	0.0631
<i>Xbp1</i>	0.486	0.0631
<i>Gyk</i>	0.486	0.0631
<i>Mipp1</i>	0.486	0.0631
<i>Pnn</i>	0.486	0.0631
<i>Synd</i>	0.486	0.0631
<i>CG13991</i>	0.485	0.0638
<i>CG30419</i>	0.485	0.0638
<i>inv</i>	0.485	0.0638
<i>Lig4</i>	0.485	0.0638
<i>Reg-5</i>	0.485	0.0638
<i>Cdk9</i>	0.484	0.0642
<i>cos</i>	0.484	0.0642
<i>Opbp</i>	0.484	0.0642
<i>Bap170</i>	0.483	0.0645
<i>CG12214</i>	0.483	0.0645
<i>CG13728</i>	0.483	0.0645
<i>CG14760</i>	0.483	0.0645
<i>Djp2</i>	0.483	0.0645
<i>pck</i>	0.483	0.0645
<i>azz</i>	0.482	0.065
<i>CG13843</i>	0.482	0.065
<i>CG15744</i>	0.482	0.065
<i>CG32043</i>	0.482	0.065
<i>CG34196</i>	0.482	0.065
<i>CG7593</i>	0.482	0.065
<i>CG9004</i>	0.482	0.065
<i>Taf4</i>	0.482	0.065

Gene Name	ERC Value	P-value
<i>CG11357</i>	0.481	0.0658
<i>CG31275</i>	0.481	0.0658
<i>dpr20</i>	0.481	0.0658
<i>Rpn1</i>	0.481	0.0658
<i>Tsp42Ek</i>	0.481	0.0658
<i>CG12038</i>	0.48	0.0662
<i>CG16984</i>	0.48	0.0662
<i>CG32302</i>	0.48	0.0662
<i>MED19</i>	0.48	0.0662
<i>obst-G</i>	0.48	0.0662
<i>stl</i>	0.48	0.0662
<i>Atf6</i>	0.479	0.0668
<i>blos2</i>	0.479	0.0668
<i>CG11839</i>	0.479	0.0668
<i>CG12379</i>	0.479	0.0668
<i>CG13791</i>	0.479	0.0668
<i>CG14290</i>	0.479	0.0668
<i>CG14439</i>	0.479	0.0668
<i>CG33635</i>	0.479	0.0668
<i>CG5181</i>	0.479	0.0668
<i>SamDC</i>	0.479	0.0668
<i>Sym</i>	0.479	0.0668
<i>CG10561</i>	0.478	0.0677
<i>CG15708</i>	0.478	0.0677
<i>CG2046</i>	0.478	0.0677
<i>CG5742</i>	0.478	0.0677
<i>CG9948</i>	0.478	0.0677
<i>Gef26</i>	0.478	0.0677
<i>polybramo</i>	0.478	0.0677
<i>disco-r</i>	0.477	0.0684
<i>DNApol-alpha</i>	0.477	0.0684
<i>CG2113</i>	0.476	0.0686
<i>CG7607</i>	0.476	0.0686
<i>chn</i>	0.476	0.0686
<i>wda</i>	0.475	0.0688
<i>CG4950</i>	0.474	0.0689
<i>gol</i>	0.474	0.0689
<i>VhaPPA1-1</i>	0.474	0.0689
<i>Cep97</i>	0.473	0.0692
<i>Axn</i>	0.472	0.0693
<i>CG16985</i>	0.472	0.0693
<i>CG42508</i>	0.472	0.0693
<i>crb</i>	0.472	0.0693
<i>CG42557</i>	0.471	0.0696
<i>CG6751</i>	0.471	0.0696
<i>CG7102</i>	0.471	0.0696
<i>CG8501</i>	0.471	0.0696
<i>GLaz</i>	0.471	0.0696
<i>lok</i>	0.471	0.0696
<i>Bruce</i>	0.47	0.0702
<i>CG2852</i>	0.47	0.0702
<i>CG31102</i>	0.47	0.0702
<i>CG33692</i>	0.47	0.0702
<i>CG6006</i>	0.47	0.0702
<i>Deaf1</i>	0.47	0.0702
<i>erm</i>	0.47	0.0702

Gene Name	ERC Value	P-value
<i>Sid5</i>	0.47	0.0702
<i>CG14550</i>	0.469	0.0709
<i>CG5938</i>	0.469	0.0709
<i>Smg6</i>	0.469	0.0709
<i>Syx4</i>	0.469	0.0709
<i>CG13244</i>	0.468	0.0713
<i>Pi3K21B</i>	0.468	0.0713
<i>bsh</i>	0.467	0.0714
<i>CG31910</i>	0.467	0.0714
<i>CG8368</i>	0.467	0.0714
<i>pzg</i>	0.467	0.0714
<i>Cas</i>	0.466	0.0718
<i>CG14186</i>	0.466	0.0718
<i>CG3376</i>	0.466	0.0718
<i>CG8788</i>	0.466	0.0718
<i>Dh</i>	0.466	0.0718
<i>mRpS24</i>	0.466	0.0718
<i>Rad51C</i>	0.466	0.0718
<i>rho-7</i>	0.466	0.0718
<i>CG14103</i>	0.465	0.0725
<i>CG15673</i>	0.465	0.0725
<i>CG3558</i>	0.465	0.0725
<i>CG7120</i>	0.465	0.0725
<i>ed</i>	0.465	0.0725
<i>hk</i>	0.465	0.0725
<i>Srp68</i>	0.465	0.0725
<i>sti</i>	0.465	0.0725
<i>CG13837</i>	0.464	0.0732
<i>fal</i>	0.464	0.0732
<i>RhoBTB</i>	0.464	0.0732
<i>CG3731</i>	0.463	0.0735
<i>mei-41</i>	0.463	0.0735
<i>so</i>	0.463	0.0735
<i>thoc5</i>	0.463	0.0735
<i>CG10730</i>	0.462	0.0739
<i>CG13295</i>	0.462	0.0739
<i>CG7745</i>	0.462	0.0739
<i>CG7786</i>	0.462	0.0739
<i>CG9813</i>	0.462	0.0739
<i>GlcAT-P</i>	0.462	0.0739
<i>Smc5</i>	0.462	0.0739
<i>wfs1</i>	0.462	0.0739
<i>CG11329</i>	0.461	0.0746
<i>CG32299</i>	0.461	0.0746
<i>CG4570</i>	0.461	0.0746
<i>CG5589</i>	0.461	0.0746
<i>CG7148</i>	0.461	0.0746
<i>CG8336</i>	0.461	0.0746
<i>CG9570</i>	0.461	0.0746
<i>epsilonCOP</i>	0.461	0.0746
<i>GIIIspIa2</i>	0.461	0.0746
<i>Sb</i>	0.461	0.0746
<i>Aats-thr</i>	0.46	0.0755
<i>Arp87C</i>	0.46	0.0755
<i>CG11191</i>	0.46	0.0755
<i>CG16979</i>	0.46	0.0755

Table 6.S19 Continued

Gene Name	ERC Value	P-value
CG9007	0.46	0.0755
CG9904	0.46	0.0755
DNApol-eps1	0.46	0.0755
Hus1-like	0.46	0.0755
tud	0.46	0.0755
aay	0.459	0.0763
CG33960	0.459	0.0763
CG34116	0.459	0.0763
Drep-3	0.459	0.0763
gskt	0.459	0.0763
RnpS1	0.459	0.0763
cdm	0.458	0.0768
CG11192	0.458	0.0768
CG14011	0.458	0.0768
CG15822	0.458	0.0768
CG17768	0.458	0.0768
CG4945	0.458	0.0768
Lgr3	0.458	0.0768
Lin29	0.458	0.0768
TBPH	0.458	0.0768
CG11379	0.457	0.0777
CG12229	0.457	0.0777
CG13905	0.457	0.0777
CG15400	0.457	0.0777
CG32226	0.457	0.0777
CG6230	0.457	0.0777
CG13694	0.456	0.0782
CG14115	0.456	0.0782
CG1561	0.456	0.0782
CG17278	0.456	0.0782
CG33985	0.456	0.0782
twi	0.456	0.0782
CG15630	0.455	0.0787
CG33281	0.455	0.0787
CG34200	0.455	0.0787
dpr19	0.455	0.0787
beat-Vb	0.454	0.0791
[[2]]NC136	0.454	0.0791
Pof	0.454	0.0791
CG14883	0.453	0.0794
CG9689	0.453	0.0794
CG4709	0.452	0.0795
CG5644	0.452	0.0795
PGRP-LB	0.452	0.0795
CG13488	0.451	0.0798
CG13581	0.451	0.0798
CG6055	0.451	0.0798
Pp2C1	0.451	0.0798
Rad17	0.451	0.0798
CG1142	0.45	0.0803
CG14160	0.45	0.0803
CG5895	0.45	0.0803
CG10741	0.449	0.0805
CG14431	0.449	0.0805
CG30159	0.449	0.0805
CG31465	0.449	0.0805

Gene Name	ERC Value	P-value
CG6073	0.449	0.0805
Cul-3	0.448	0.081
Alk	0.447	0.0811
CcapR	0.447	0.0811
CG10267	0.447	0.0811
CG14540	0.447	0.0811
CG15609	0.447	0.0811
CG18031	0.447	0.0811
CG3744	0.447	0.0811
CG42797	0.447	0.0811
opa1-like	0.447	0.0811
Pten	0.447	0.0811
rev7	0.447	0.0811
CG11453	0.446	0.0821
ppk11	0.446	0.0821
repo	0.446	0.0821
RhoGEF2	0.446	0.0821
Rlc1	0.446	0.0821
CG10405	0.445	0.0825
CG6254	0.445	0.0825
Gr93a	0.445	0.0825
Paip2	0.445	0.0825
Poxn	0.445	0.0825
tj	0.445	0.0825
Akt1	0.444	0.0831
CG10920	0.444	0.0831
CG15544	0.444	0.0831
CG10326	0.443	0.0833
CG13473	0.443	0.0833
CG15073	0.443	0.0833
CG4161	0.443	0.0833
CG5872	0.443	0.0833
kat-60L1	0.443	0.0833
pps	0.443	0.0833
rpr	0.443	0.0833
wds	0.443	0.0833
Bx	0.442	0.0841
CG6859	0.442	0.0841
pr-set7	0.442	0.0841
CG13398	0.441	0.0844
CG5728	0.441	0.0844
D	0.441	0.0844
Gr58c	0.441	0.0844
Gr59e	0.441	0.0844
hyd	0.441	0.0844
Rho1	0.441	0.0844
vav	0.441	0.0844
CG4496	0.44	0.0851
Grd	0.44	0.0851
Pkc53E	0.44	0.0851
Rgk1	0.44	0.0851
pdm3	0.439	0.0855
seq	0.439	0.0855
CG10979	0.438	0.0857
CG14442	0.438	0.0857
CG14837	0.438	0.0857

Gene Name	ERC Value	P-value
CG17098	0.438	0.0857
GABA-B-R1	0.438	0.0857
rump	0.438	0.0857
Sema-2a	0.438	0.0857
Spase18-21	0.438	0.0857
sv	0.438	0.0857
CG13999	0.437	0.0865
CG6441	0.437	0.0865
CG7739	0.437	0.0865
CG8366	0.437	0.0865
CG9132	0.437	0.0865
Got2	0.437	0.0865
Appl	0.436	0.087
CG15278	0.436	0.087
CG7903	0.436	0.087
desat1	0.436	0.087
Srp19	0.436	0.087
Tango5	0.436	0.087
CG11068	0.435	0.0876
CG14052	0.435	0.0876
CG4686	0.435	0.0876
CG9483	0.435	0.0876
wls	0.435	0.0876
CG10660	0.434	0.088
CG1295	0.434	0.088
CG30259	0.434	0.088
CG5867	0.434	0.088
Osi13	0.434	0.088
tamo	0.434	0.088
CG11071	0.433	0.0886
CG4074	0.433	0.0886
CG5604	0.433	0.0886
Obp56c	0.433	0.0886
Wscck	0.433	0.0886
CG1675	0.432	0.089
CG33205	0.432	0.089
La	0.432	0.089
CG12003	0.431	0.0893
CG1340	0.431	0.0893
CG31679	0.431	0.0893
CG34420	0.431	0.0893
CG33275	0.43	0.0896
Gr59b	0.43	0.0896
spas	0.43	0.0896
Uev1A	0.43	0.0896
CG10226	0.429	0.09
CG13640	0.429	0.09
CG13671	0.429	0.09
CG9053	0.429	0.09
HP1c	0.429	0.09
CG16833	0.428	0.0905
CG16837	0.428	0.0905
CG30105	0.428	0.0905
CG5577	0.428	0.0905
CG7906	0.428	0.0905
fend	0.428	0.0905

Gene Name	ERC Value	P-value
pyx	0.428	0.0905
ACXD	0.427	0.0911
CG34331	0.427	0.0911
CG4627	0.427	0.0911
CG4683	0.427	0.0911
gek	0.427	0.0911
PR2	0.427	0.0911
Su(z)12	0.427	0.0911
Taspase1	0.427	0.0911
Trn-SR	0.427	0.0911
CG7215	0.426	0.0919
Sbp2	0.426	0.0919
zormin	0.426	0.0919
CG11190	0.425	0.0922
CG15658	0.425	0.0922
CG1812	0.425	0.0922
CG3919	0.425	0.0922
CG8490	0.425	0.0922
neuroigin	0.425	0.0922
CG13362	0.424	0.0927
Tsp	0.424	0.0927
CG11454	0.423	0.0929
ix	0.423	0.0929
Su(fu)	0.423	0.0929
CG12955	0.422	0.0932
CG14072	0.422	0.0932
Fak56D	0.422	0.0932
Or82a	0.422	0.0932
PrBP	0.422	0.0932
bnk	0.421	0.0936
CG10188	0.421	0.0936
CG34001	0.421	0.0936
CG9072	0.421	0.0936
fd59A	0.421	0.0936
Gr98a	0.421	0.0936
llic	0.421	0.0936
Snm1	0.421	0.0936
CG33299	0.42	0.0943
CG5791	0.42	0.0943
CG9589	0.42	0.0943
enc	0.42	0.0943
Mtor	0.42	0.0943
Secm	0.42	0.0943
scs8	0.42	0.0943
CG2124	0.419	0.095
CG31716	0.419	0.095
CG34401	0.419	0.095
Dbp73D	0.419	0.095
CG31787	0.418	0.0953
CG3492	0.418	0.0953
CG3995	0.418	0.0953
CG7099	0.418	0.0953
FBX011	0.418	0.0953
jeb	0.418	0.0953
CG5412	0.417	0.0959
CG5854	0.417	0.0959

Gene Name	ERC Value	P-value
CG9130	0.417	0.0959
Cyp4aa1	0.417	0.0959
lea	0.417	0.0959
Phm	0.417	0.0959
Rpl115	0.417	0.0959
yellow-e2	0.417	0.0959
CG31326	0.416	0.0966
CG9154	0.416	0.0966
nimb4	0.416	0.0966
CG13331	0.415	0.0968
CG3173	0.415	0.0968
CG5157	0.415	0.0968
CG6878	0.415	0.0968
CG7589	0.415	0.0968
CG8944	0.415	0.0968
CG9839	0.415	0.0968
Cp7Fc	0.415	0.0968
Phlpp	0.415	0.0968
AP-2	0.414	0.0977
Apc2	0.414	0.0977
CG13725	0.414	0.0977
CG4701	0.414	0.0977
CG9754	0.414	0.0977
Lnk	0.414	0.0977
Pk92B	0.414	0.0977
bru-2	0.413	0.0983
CG13786	0.413	0.0983
CG31065	0.413	0.0983
CG42516	0.413	0.0983
CG6024	0.413	0.0983
ecd	0.413	0.0983
pgant5	0.413	0.0983
CalpC	0.412	0.0989
CG10809	0.412	0.0989
CG12091	0.412	0.0989
CG17349	0.412	0.0989
CG18870	0.412	0.0989
CG2371	0.412	0.0989
CG3925	0.412	0.0989
CG5382	0.412	0.0989
mbt	0.412	0.0989
SP2637	0.412	0.0989
trus	0.412	0.0989
CG1287	0.411	0.0999
CG15450	0.411	0.0999
CG16868	0.411	0.0999
CG1907	0.411	0.0999
CG9098	0.411	0.0999
Pif1A	0.411	0.0999

Table 6.S20 - Top Genes ERC values for *spn-B* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG11668	0.911	0.0001
CG3838	0.911	0.0001
14-3-3 <i>β</i>	0.895	0.0003
CG15404	0.893	0.0004
CG11251	0.886	0.0005
CG5439	0.865	0.0005
blue	0.861	0.0006
Doa	0.851	0.0007
CG13884	0.85	0.0008
CG14883	0.846	0.0009
Nca	0.841	0.001
CG4565	0.839	0.0011
CG17568	0.837	0.0012
CG4660	0.832	0.0013
CG32579	0.827	0.0014
CG8370	0.826	0.0014
CHKov2	0.826	0.0014
proPO-A1	0.819	0.0016
CG33672	0.818	0.0017
CG13001	0.817	0.0018
CG17083	0.816	0.0019
CG15376	0.811	0.002
Drak	0.81	0.0021
CG11367	0.809	0.0022
CG5073	0.809	0.0022
CG2321	0.807	0.0023
CG31698	0.805	0.0024
Bin1	0.799	0.0025
CG1909	0.798	0.0026
magu	0.798	0.0026
CG30115	0.797	0.0028
CG14115	0.796	0.0029
Gef26	0.795	0.003
disp	0.794	0.0031
CG32409	0.789	0.0032
if	0.788	0.0032
CG14072	0.787	0.0033
CG31898	0.787	0.0033
RpS26	0.787	0.0033
CG5734	0.786	0.0036
CG5846	0.786	0.0036
CG31065	0.785	0.0038
CG11155	0.784	0.0039
CG8191	0.784	0.0039
lr7g	0.784	0.0039
NK7.1	0.783	0.0041
CG6005	0.781	0.0042
CG1233	0.78	0.0043
CG31849	0.78	0.0043
CG42827	0.78	0.0043
plexA	0.779	0.0046
InR	0.777	0.0047
CG11877	0.774	0.0048
CG7146	0.774	0.0048
MED18	0.773	0.005
beat-IIIb	0.769	0.005

Gene Name	ERC Value	P-value
CG13500	0.768	0.0051
Cpr72Ea	0.768	0.0051
Kmnl	0.768	0.0051
CG10741	0.767	0.0054
tull	0.767	0.0054
CG10103	0.766	0.0056
lic	0.766	0.0056
Proc-R	0.766	0.0056
Rad51C	0.765	0.0059
Skill	0.765	0.0059
beat-IIIa	0.764	0.006
CG11071	0.763	0.0061
lpk2	0.763	0.0061
Ets21C	0.759	0.0063
CG15464	0.757	0.0064
CG1806	0.757	0.0064
CG11262	0.756	0.0066
CG9098	0.755	0.0067
CG12507	0.754	0.0068
CG2862	0.754	0.0068
CG11851	0.753	0.0069
CG14655	0.752	0.007
dmrt11E	0.752	0.007
CG32121	0.751	0.0072
lr87a	0.751	0.0072
CG13295	0.75	0.0074
Nipsnap	0.75	0.0074
Ama	0.749	0.0076
CG13877	0.747	0.0077
CG17669	0.747	0.0077
CG9801	0.746	0.0078
CG8401	0.745	0.0079
DIP1	0.745	0.0079
mthl14	0.743	0.0081
CG11417	0.741	0.0082
lilli	0.741	0.0082
CG11141	0.74	0.0084
Twd1G	0.74	0.0084
Nfi	0.739	0.0086
Spt20	0.737	0.0086
CG33096	0.736	0.0087
Fancl	0.735	0.0088
gw	0.735	0.0088
Ptth	0.735	0.0088
CG3632	0.734	0.0091
Snoo	0.734	0.0091
Traf-like	0.732	0.0093
CG13431	0.731	0.0094
CG7009	0.731	0.0094
wg	0.731	0.0094
CG30421	0.73	0.0096
CG4705	0.73	0.0096
CG5550	0.73	0.0096
hdm	0.729	0.0099
CG10560	0.728	0.01
sda	0.727	0.0101

Gene Name	ERC Value	P-value
CG11306	0.726	0.0102
CG31150	0.726	0.0102
Rpl35A	0.726	0.0102
H	0.725	0.0105
CG32803	0.723	0.0105
Gr77a	0.723	0.0105
CG1316	0.721	0.0107
CG13488	0.721	0.0107
CG14411	0.721	0.0107
CG1647	0.721	0.0107
CG12075	0.72	0.0111
CG12995	0.72	0.0111
hfw	0.72	0.0111
CG10916	0.719	0.0114
Med	0.718	0.0114
DAT	0.716	0.0115
Gr59b	0.715	0.0116
os	0.715	0.0116
CG7956	0.714	0.0118
pll	0.714	0.0118
CG13995	0.713	0.012
CG7739	0.713	0.012
comm3	0.713	0.012
Cpr62Ba	0.713	0.012
CG14661	0.712	0.0123
nfm	0.712	0.0123
CG10680	0.711	0.0125
Gpi1	0.711	0.0125
CG3880	0.708	0.0127
Atox1	0.706	0.0128
CG2993	0.706	0.0128
sv	0.706	0.0128
trus	0.706	0.0128
CG17636	0.704	0.0132
Hsp90D	0.704	0.0132
Sulf1	0.704	0.0132
l(2)k05819	0.703	0.0134
Pi3K21B	0.703	0.0134
Cyp318a1	0.702	0.0136
MBD-like	0.702	0.0136
Orc5	0.701	0.0138
yki	0.701	0.0138
CG6201	0.7	0.014
CG42330	0.699	0.0141
cv	0.699	0.0141
CG14933	0.698	0.0142
CG17662	0.698	0.0142
CG34284	0.698	0.0142
CG4751	0.698	0.0142
Mif	0.698	0.0142
CG11778	0.697	0.0147
CG11131	0.696	0.0148
CG32437	0.696	0.0148
CG7536	0.696	0.0148
CG11403	0.695	0.015
CG14963	0.695	0.015

Gene Name	ERC Value	P-value
CG5895	0.694	0.0152
fend	0.693	0.0153
slam	0.693	0.0153
UbcD2	0.693	0.0153
CG10249	0.692	0.0156
CG16700	0.691	0.0157
Tsfl	0.691	0.0157
CG18278	0.69	0.0159
CG31371	0.69	0.0159
Crk	0.69	0.0159
Ugt35a	0.69	0.0159
CG14195	0.689	0.0162
CG2003	0.689	0.0162
CG32006	0.689	0.0162
CG3502	0.689	0.0162
CG3679	0.687	0.0166
CG8959	0.687	0.0166
Magi	0.687	0.0166
CG12288	0.686	0.0168
lute	0.686	0.0168
CG12420	0.685	0.017
CG5585	0.684	0.0171
CG9215	0.684	0.0171
CG12986	0.683	0.0173
disco	0.682	0.0174
Src42A	0.682	0.0174
wgn	0.682	0.0174
CG14069	0.681	0.0177
CG31102	0.681	0.0177
CG40117	0.681	0.0177
cn	0.681	0.0177
Su(fu)	0.681	0.0177
Uchr	0.681	0.0177
Act42A	0.68	0.0182
Gr9a	0.68	0.0182
CG12084	0.678	0.0184
CG13083	0.678	0.0184
CG31226	0.678	0.0184
Tl	0.678	0.0184
Gr43b	0.677	0.0187
lr56a	0.677	0.0187
l(2)k10201	0.675	0.0189
nimA	0.675	0.0189
CG30001	0.674	0.0191
CG42678	0.674	0.0191
CG8974	0.674	0.0191
Gr2a	0.674	0.0191
Abi	0.673	0.0195
Rfx	0.673	0.0195
CG14562	0.672	0.0196
CG32305	0.672	0.0196
Mat89Ba	0.672	0.0196
CalpC	0.671	0.0199
CG33057	0.67	0.02
CG4496	0.67	0.02
Trn-SR	0.67	0.02

Gene Name	ERC Value	P-value
CG33771	0.669	0.0203
Kip31E	0.669	0.0203
CG14903	0.668	0.0205
CG7227	0.668	0.0205
Gyc32E	0.668	0.0205
Ret	0.668	0.0205
sens	0.668	0.0205
CDase	0.667	0.0209
CG8944	0.667	0.0209
ft	0.667	0.0209
net	0.667	0.0209
Ptp4E	0.667	0.0209
tz4	0.666	0.0214
ldbr	0.666	0.0214
CG32850	0.665	0.0215
CG5791	0.665	0.0215
CG8134	0.665	0.0215
Gr61a	0.665	0.0215
Oseg5	0.665	0.0215
CG10222	0.664	0.022
CG10486	0.664	0.022
CG2059	0.664	0.022
CG42686	0.664	0.022
CG14736	0.663	0.0223
CG17333	0.663	0.0223
CG8023	0.663	0.0223
CG6361	0.663	0.0223
trk	0.662	0.0227
CG13362	0.661	0.0228
CG15865	0.66	0.0229
nimB5	0.659	0.023
Fbp45	0.658	0.0231
CG14894	0.657	0.0232
eyg	0.657	0.0232
ix	0.657	0.0232
beta3GalTII	0.656	0.0234
CG8247	0.656	0.0234
mel-41	0.655	0.0236
Vm32E	0.655	0.0236
CG6484	0.654	0.0238
blos3	0.653	0.0239
fidipidine	0.653	0.0239
shg	0.653	0.0239
CG15570	0.652	0.0241
CG42863	0.652	0.0241
Jhl-26	0.652	0.0241
Andorra	0.651	0.0244
CG10732	0.65	0.0245
CG6465	0.65	0.0245
CG9917	0.65	0.0245
Dsk	0.65	0.0245
RhoGAP93E	0.65	0.0245
yl	0.649	0.025
CG17019	0.648	0.025
Elo88beta	0.648	0.025
f	0.648	0.025

Table 6.S20 Continued

Gene Name	ERC Value	P-value
<i>TMS1</i>	0.648	0.025
<i>vtd</i>	0.647	0.0254
<i>Hk</i>	0.646	0.0255
<i>CG11436</i>	0.645	0.0256
<i>Pros29</i>	0.645	0.0256
<i>ver</i>	0.645	0.0256
<i>CG9992</i>	0.644	0.0259
<i>lat</i>	0.644	0.0259
<i>Pt3K92E</i>	0.644	0.0259
<i>CG18095</i>	0.643	0.0261
<i>CG3262</i>	0.643	0.0261
<i>CG42402</i>	0.643	0.0261
<i>Ptpmeg</i>	0.643	0.0261
<i>Spn27A</i>	0.643	0.0261
<i>CG11750</i>	0.642	0.0266
<i>CG34266</i>	0.642	0.0266
<i>Ent2</i>	0.642	0.0266
<i>bdg</i>	0.641	0.0268
<i>CG1529</i>	0.641	0.0268
<i>S1P</i>	0.64	0.027
<i>CG10561</i>	0.639	0.0271
<i>CG13125</i>	0.639	0.0271
<i>CG9172</i>	0.639	0.0271
<i>Dic90F</i>	0.639	0.0271
<i>Rac1</i>	0.639	0.0271
<i>Rpl115</i>	0.639	0.0271
<i>shi</i>	0.639	0.0271
<i>CG11665</i>	0.638	0.0277
<i>CG32541</i>	0.638	0.0277
<i>snk</i>	0.638	0.0277
<i>Adgf-E</i>	0.637	0.028
<i>beat-VI</i>	0.637	0.028
<i>CG13766</i>	0.637	0.028
<i>CG15928</i>	0.637	0.028
<i>CG31109</i>	0.637	0.028
<i>CG3386</i>	0.637	0.028
<i>CG5902</i>	0.637	0.028
<i>CG6461</i>	0.637	0.028
<i>Grip75</i>	0.637	0.028
<i>CG18480</i>	0.636	0.0288
<i>Rga</i>	0.636	0.0288
<i>CG15251</i>	0.635	0.029
<i>CG6225</i>	0.635	0.029
<i>cos</i>	0.635	0.029
<i>Obp44a</i>	0.635	0.029
<i>Mad</i>	0.634	0.0294
<i>tsl</i>	0.634	0.0294
<i>CG13982</i>	0.633	0.0295
<i>Eps-15</i>	0.633	0.0295
<i>grk</i>	0.633	0.0295
<i>klar</i>	0.633	0.0295
<i>CG7526</i>	0.632	0.0299
<i>Slip1</i>	0.632	0.0299
<i>Ance-3</i>	0.631	0.0301
<i>CG6345</i>	0.631	0.0301
<i>ct</i>	0.631	0.0301

Gene Name	ERC Value	P-value
<i>d4</i>	0.631	0.0301
<i>Lgr3</i>	0.631	0.0301
<i>Mer</i>	0.631	0.0301
<i>CG11872</i>	0.63	0.0306
<i>CG30403</i>	0.63	0.0306
<i>CG32017</i>	0.63	0.0306
<i>CG8814</i>	0.63	0.0306
<i>Taf4</i>	0.63	0.0306
<i>CG14102</i>	0.629	0.0311
<i>CG31798</i>	0.629	0.0311
<i>CG7992</i>	0.629	0.0311
<i>Cpr65Eb</i>	0.629	0.0311
<i>mRpS6</i>	0.629	0.0311
<i>Nnfla</i>	0.629	0.0311
<i>Sox15</i>	0.628	0.0316
<i>Rben-3A</i>	0.627	0.0317
<i>Vdup1</i>	0.627	0.0317
<i>CG30467</i>	0.626	0.0319
<i>Ir84a</i>	0.626	0.0319
<i>Obp99a</i>	0.626	0.0319
<i>CG10469</i>	0.625	0.0322
<i>scro</i>	0.625	0.0322
<i>ssh</i>	0.625	0.0322
<i>klg</i>	0.624	0.0324
<i>Myb</i>	0.624	0.0324
<i>Or98b</i>	0.624	0.0324
<i>Taff1</i>	0.624	0.0324
<i>Grd</i>	0.623	0.0328
<i>Or88a</i>	0.623	0.0328
<i>Pkg21D</i>	0.623	0.0328
<i>CG17528</i>	0.622	0.0331
<i>Fmrf</i>	0.622	0.0331
<i>It</i>	0.622	0.0331
<i>CG14062</i>	0.621	0.0333
<i>CG18585</i>	0.621	0.0333
<i>CG3397</i>	0.621	0.0333
<i>spn-D</i>	0.621	0.0333
<i>mus309</i>	0.62	0.0337
<i>CG3568</i>	0.619	0.0338
<i>CG8539</i>	0.619	0.0338
<i>CG17283</i>	0.618	0.034
<i>CS-2</i>	0.618	0.034
<i>fit</i>	0.617	0.0341
<i>Tsp96F</i>	0.617	0.0341
<i>CG14722</i>	0.616	0.0343
<i>CG1907</i>	0.616	0.0343
<i>CG31025</i>	0.616	0.0343
<i>CG10274</i>	0.615	0.0346
<i>CG14301</i>	0.615	0.0346
<i>CG16985</i>	0.615	0.0346
<i>CG17304</i>	0.615	0.0346
<i>CG31689</i>	0.615	0.0346
<i>Hr96</i>	0.615	0.0346
<i>Dip2</i>	0.614	0.0351
<i>pygo</i>	0.614	0.0351
<i>RpS16</i>	0.614	0.0351

Gene Name	ERC Value	P-value
<i>CG2278</i>	0.613	0.0354
<i>drl</i>	0.613	0.0354
<i>MSBP</i>	0.613	0.0354
<i>sil</i>	0.613	0.0354
<i>CG34391</i>	0.612	0.0358
<i>CG8116</i>	0.612	0.0358
<i>CG9095</i>	0.612	0.0358
<i>mGluRA</i>	0.612	0.0358
<i>oa2</i>	0.612	0.0358
<i>CG10669</i>	0.611	0.0362
<i>CG9542</i>	0.611	0.0362
<i>Gr36d</i>	0.611	0.0362
<i>myoglianin</i>	0.611	0.0362
<i>CG8507</i>	0.61	0.0366
<i>l(2)NC136</i>	0.61	0.0366
<i>mre11</i>	0.61	0.0366
<i>CG14401</i>	0.609	0.0368
<i>CG2789</i>	0.609	0.0368
<i>CG12012</i>	0.608	0.037
<i>CG2162</i>	0.608	0.037
<i>CG2604</i>	0.608	0.037
<i>CG9468</i>	0.608	0.037
<i>CG12851</i>	0.607	0.0374
<i>lid</i>	0.607	0.0374
<i>CG12104</i>	0.606	0.0376
<i>CG14526</i>	0.606	0.0376
<i>nav</i>	0.606	0.0376
<i>mnd</i>	0.606	0.0376
<i>repo</i>	0.606	0.0376
<i>CG1311</i>	0.605	0.038
<i>CG6409</i>	0.605	0.038
<i>CG14235</i>	0.604	0.0382
<i>CG6325</i>	0.604	0.0382
<i>CG7884</i>	0.604	0.0382
<i>l(2)01289</i>	0.604	0.0382
<i>CG2943</i>	0.603	0.0386
<i>CG4847</i>	0.603	0.0386
<i>CG9008</i>	0.603	0.0386
<i>CG9400</i>	0.603	0.0386
<i>NKAIN</i>	0.603	0.0386
<i>oc</i>	0.603	0.0386
<i>CG13377</i>	0.602	0.0391
<i>CG15744</i>	0.602	0.0391
<i>CG9114</i>	0.602	0.0391
<i>Edem2</i>	0.602	0.0391
<i>AP-1gamma</i>	0.601	0.0395
<i>CG10140</i>	0.601	0.0395
<i>mus312</i>	0.601	0.0395
<i>Stim</i>	0.601	0.0395
<i>Ant2</i>	0.6	0.0398
<i>comm</i>	0.6	0.0398
<i>mel-W68</i>	0.6	0.0398
<i>CG10702</i>	0.599	0.0401
<i>CG2104</i>	0.599	0.0401
<i>CG32563</i>	0.599	0.0401
<i>CG3984</i>	0.599	0.0401

Gene Name	ERC Value	P-value
<i>CG7099</i>	0.599	0.0401
<i>mel-S332</i>	0.599	0.0401
<i>Skeletor</i>	0.598	0.0406
<i>CG10035</i>	0.597	0.0407
<i>CG2975</i>	0.597	0.0407
<i>CG10300</i>	0.596	0.0409
<i>CG12316</i>	0.596	0.0409
<i>CG32485</i>	0.596	0.0409
<i>CG7197</i>	0.596	0.0409
<i>dor</i>	0.596	0.0409
<i>Ir60e</i>	0.596	0.0409
<i>Jra</i>	0.596	0.0409
<i>TwdlW</i>	0.596	0.0409
<i>CG15522</i>	0.595	0.0416
<i>CG8245</i>	0.595	0.0416
<i>Gr93a</i>	0.595	0.0416
<i>how</i>	0.595	0.0416
<i>stj</i>	0.595	0.0416
<i>AlkB</i>	0.594	0.0421
<i>CG1053</i>	0.594	0.0421
<i>CG31676</i>	0.594	0.0421
<i>CG42251</i>	0.594	0.0421
<i>GstE6</i>	0.594	0.0421
<i>lgs</i>	0.594	0.0421
<i>NF-YC</i>	0.594	0.0421
<i>Art4</i>	0.593	0.0427
<i>CG17562</i>	0.593	0.0427
<i>CG33641</i>	0.593	0.0427
<i>CG5726</i>	0.593	0.0427
<i>CG10344</i>	0.592	0.0431
<i>CG13005</i>	0.592	0.0431
<i>CG7277</i>	0.591	0.0432
<i>Or65a</i>	0.591	0.0432
<i>SP2353</i>	0.591	0.0432
<i>CG1732</i>	0.59	0.0435
<i>CG34174</i>	0.59	0.0435
<i>CG7265</i>	0.59	0.0435
<i>CG34331</i>	0.589	0.0438
<i>rimC4</i>	0.589	0.0438
<i>phf</i>	0.589	0.0438
<i>Vang</i>	0.589	0.0438
<i>CG14969</i>	0.588	0.0441
<i>Abx2</i>	0.587	0.0442
<i>esn</i>	0.587	0.0442
<i>CG6607</i>	0.586	0.0444
<i>Gr33a</i>	0.586	0.0444
<i>PGRP-SD</i>	0.586	0.0444
<i>Taspase1</i>	0.586	0.0444
<i>Bteb2</i>	0.585	0.0448
<i>CG12539</i>	0.585	0.0448
<i>CG14695</i>	0.585	0.0448
<i>CG5038</i>	0.585	0.0448
<i>CG7597</i>	0.584	0.0451
<i>png</i>	0.584	0.0451
<i>CG2182</i>	0.583	0.0453
<i>Prosbeta7</i>	0.583	0.0453

Gene Name	ERC Value	P-value
<i>CG14047</i>	0.582	0.0455
<i>CG8159</i>	0.582	0.0455
<i>Gdh</i>	0.581	0.0457
<i>l(2)k09022</i>	0.581	0.0457
<i>l(3)87Df</i>	0.581	0.0457
<i>stumps</i>	0.581	0.0457
<i>CG12341</i>	0.58	0.046
<i>CG30281</i>	0.58	0.046
<i>CG9063</i>	0.58	0.046
<i>CG9904</i>	0.58	0.046
<i>wb</i>	0.58	0.046
<i>bl</i>	0.579	0.0465
<i>CG15661</i>	0.579	0.0465
<i>CG33784</i>	0.579	0.0465
<i>Spase18-21</i>	0.579	0.0465
<i>CG32732</i>	0.578	0.0468
<i>CG4683</i>	0.578	0.0468
<i>dbo</i>	0.578	0.0468
<i>CG13745</i>	0.577	0.0471
<i>CG18806</i>	0.577	0.0471
<i>CG7069</i>	0.577	0.0471
<i>CG7755</i>	0.577	0.0471
<i>CG9386</i>	0.577	0.0471
<i>Fur2</i>	0.577	0.0471
<i>Hsp67Ba</i>	0.577	0.0471
<i>Hsp67Bb</i>	0.577	0.0471
<i>put</i>	0.577	0.0471
<i>BubR1</i>	0.576	0.0479
<i>Cad96Cb</i>	0.576	0.0479
<i>CG10743</i>	0.576	0.0479
<i>CG6745</i>	0.576	0.0479
<i>CG7922</i>	0.576	0.0479
<i>CG9147</i>	0.576	0.0479
<i>fu</i>	0.576	0.0479
<i>CG10051</i>	0.575	0.0486
<i>CG11581</i>	0.575	0.0486
<i>CG31265</i>	0.575	0.0486
<i>CG33172</i>	0.575	0.0486
<i>CG6980</i>	0.574	0.0489
<i>Gr68a</i>	0.574	0.0489
<i>RpL7-like</i>	0.574	0.0489
<i>CG34230</i>	0.573	0.0492
<i>DNApol-alpha</i>	0.573	0.0492
<i>l(2)09851</i>	0.573	0.0492
<i>caIs</i>	0.572	0.0495
<i>CG18128</i>	0.572	0.0495
<i>CG31158</i>	0.572	0.0495
<i>Gap1</i>	0.572	0.0495
<i>tam</i>	0.572	0.0495
<i>CG12134</i>	0.571	0.0499
<i>CG34199</i>	0.571	0.0499
<i>fd102C</i>	0.571	0.0499
<i>nerfin-2</i>	0.571	0.0499
<i>ppk7</i>	0.571	0.0499
<i>CG10092</i>	0.57	0.0504
<i>CG5287</i>	0.57	0.0504

Table 6.S20 Continued

Gene Name	ERC Value	P-value
CG8389	0.57	0.0504
<i>Ice</i>	0.57	0.0504
<i>a6</i>	0.569	0.0507
CG10362	0.569	0.0507
CG31048	0.569	0.0507
CG7091	0.569	0.0507
<i>RpS5a</i>	0.569	0.0507
<i>Syt7</i>	0.569	0.0507
CG13086	0.568	0.0513
CG8617	0.568	0.0513
CG9426	0.568	0.0513
<i>iHog</i>	0.568	0.0513
<i>KH1</i>	0.568	0.0513
CG11377	0.567	0.0517
CG12914	0.567	0.0517
CG18234	0.567	0.0517
CG2736	0.567	0.0517
CG3292	0.567	0.0517
CG4022	0.567	0.0517
<i>Hust1-like</i>	0.567	0.0517
<i>sced</i>	0.567	0.0517
CG13074	0.566	0.0524
CG13272	0.566	0.0524
CG2794	0.566	0.0524
CG30288	0.566	0.0524
CG32016	0.566	0.0524
CG32350	0.566	0.0524
CG34448	0.566	0.0524
CG7246	0.566	0.0524
CG15896	0.565	0.0532
CG16941	0.565	0.0532
CG5357	0.565	0.0532
CG8202	0.565	0.0532
CSN6	0.563	0.0535
CG10738	0.562	0.0536
CG14997	0.562	0.0536
CG4630	0.562	0.0536
CG11109	0.56	0.0539
<i>Tsp68C</i>	0.56	0.0539
CG18110	0.559	0.0541
CG32463	0.559	0.0541
<i>kek1</i>	0.559	0.0541
CG17564	0.558	0.0543
<i>glob3</i>	0.558	0.0543
CG13999	0.557	0.0545
CG15643	0.557	0.0545
CG40006	0.557	0.0545
<i>Chf12</i>	0.557	0.0545
CG10912	0.556	0.0549
CG1344	0.556	0.0549
CG14442	0.556	0.0549
CG18048	0.556	0.0549
<i>cav</i>	0.555	0.0552
CG12307	0.555	0.0552
CG8128	0.555	0.0552
<i>Dip3</i>	0.555	0.0552

Gene Name	ERC Value	P-value
CG34008	0.554	0.0556
CG10481	0.553	0.0557
CG13532	0.553	0.0557
CG1516	0.553	0.0557
CG31855	0.553	0.0557
CG33514	0.553	0.0557
CG4553	0.553	0.0557
<i>Fsh</i>	0.553	0.0557
<i>l(1)G0289</i>	0.553	0.0557
<i>X11L</i>	0.553	0.0557
CG4398	0.552	0.0565
<i>rasp</i>	0.552	0.0565
<i>Tsp29Fb</i>	0.552	0.0565
CG12177	0.551	0.0568
CG14431	0.551	0.0568
CG7222	0.551	0.0568
<i>Pp1-87B</i>	0.551	0.0568
<i>capa</i>	0.55	0.0571
CG10165	0.55	0.0571
CG10725	0.55	0.0571
CG15738	0.55	0.0571
CG3683	0.55	0.0571
CG6216	0.55	0.0571
CG7906	0.55	0.0571
CG8516	0.55	0.0571
CG8642	0.55	0.0571
<i>ERR</i>	0.55	0.0571
<i>mRpS30</i>	0.55	0.0571
CG32105	0.549	0.0581
CG3376	0.549	0.0581
CG4459	0.549	0.0581
CG5835	0.549	0.0581
CG6933	0.549	0.0581
CG7785	0.549	0.0581
CG9505	0.549	0.0581
<i>osp</i>	0.549	0.0581
<i>Rab9</i>	0.549	0.0581
CG10417	0.548	0.0589
CG14459	0.548	0.0589
CG15438	0.548	0.0589
CG4725	0.548	0.0589
CG6927	0.548	0.0589
CG9119	0.548	0.0589
CG10947	0.547	0.0595
CG30217	0.547	0.0595
CG4078	0.547	0.0595
CG6656	0.547	0.0595
<i>nimB2</i>	0.547	0.0595
<i>pck</i>	0.547	0.0595
<i>xmas-2</i>	0.547	0.0595
CG4612	0.546	0.0601
CG5265	0.546	0.0601
<i>levy</i>	0.546	0.0601
CG3808	0.545	0.0604
CG8498	0.545	0.0604
<i>CF2</i>	0.544	0.0605

Gene Name	ERC Value	P-value
CG31224	0.544	0.0605
<i>DNApol-gam</i>	0.544	0.0605
<i>gish</i>	0.543	0.0608
<i>Rb97D</i>	0.543	0.0608
CG11672	0.542	0.061
CG30440	0.542	0.061
CG33155	0.542	0.061
CG33340	0.542	0.061
CG42361	0.542	0.061
<i>glec</i>	0.542	0.061
<i>GNBP1</i>	0.542	0.061
<i>llp2</i>	0.542	0.061
CG31365	0.541	0.0617
CG32442	0.541	0.0617
<i>Eap</i>	0.541	0.0617
<i>GluRIIB</i>	0.541	0.0617
CG10133	0.54	0.0621
CG10710	0.54	0.0621
CG15432	0.54	0.0621
CG33229	0.54	0.0621
CG5142	0.54	0.0621
<i>LpR2</i>	0.54	0.0621
<i>Obp83cd</i>	0.54	0.0621
CG31464	0.539	0.0627
CG34401	0.539	0.0627
CG42554	0.539	0.0627
<i>ERR</i>	0.53895	0.063
CG14205	0.538	0.063
CG5819	0.538	0.063
CG6144	0.538	0.063
<i>RhoB7B</i>	0.538	0.063
CG14321	0.537	0.0634
CG33289	0.537	0.0634
CG5611	0.537	0.0634
CG1315	0.536	0.0637
CG33958	0.536	0.0637
CG7059	0.536	0.0637
CG7772	0.536	0.0637
<i>okr</i>	0.536	0.0637
<i>ss</i>	0.536	0.0637
<i>Ykt6</i>	0.536	0.0637
CG10077	0.535	0.0643
CG32573	0.535	0.0643
CG3775	0.535	0.0643
CG3091	0.534	0.0646
<i>mahj</i>	0.534	0.0646
CG11576	0.533	0.0648
CG14627	0.533	0.0648
CG34007	0.533	0.0648
CG6836	0.533	0.0648
CG9649	0.533	0.0648
<i>COQ7</i>	0.533	0.0648
<i>Ephrin</i>	0.533	0.0648
<i>Vps28</i>	0.533	0.0648
<i>boly</i>	0.532	0.0655
CG12680	0.532	0.0655

Gene Name	ERC Value	P-value
CG1561	0.532	0.0655
CG4328	0.532	0.0655
<i>clt</i>	0.532	0.0655
CG17190	0.531	0.0659
CG32702	0.531	0.0659
CG7369	0.531	0.0659
CG7903	0.531	0.0659
CG10654	0.53	0.0663
CG5026	0.53	0.0663
<i>ara</i>	0.529	0.0665
<i>ash2</i>	0.529	0.0665
CG9673	0.529	0.0665
<i>Hml</i>	0.529	0.0665
<i>Nup154</i>	0.529	0.0665
<i>Sep5</i>	0.528	0.0669
CG30385	0.528	0.0669
CG31030	0.528	0.0669
CG9986	0.528	0.0669
<i>fog</i>	0.528	0.0669
<i>Gyk</i>	0.528	0.0669
<i>Prosalpha5</i>	0.528	0.0669
<i>Tig</i>	0.528	0.0669
CG10462	0.527	0.0677
CG14423	0.527	0.0677
CG3790	0.527	0.0677
<i>Cortactin</i>	0.527	0.0677
<i>Cpr49Ae</i>	0.527	0.0677
<i>Map205</i>	0.527	0.0677
CG14070	0.526	0.0682
CG16863	0.526	0.0682
<i>Git</i>	0.526	0.0682
<i>tectonic</i>	0.526	0.0682
<i>wek</i>	0.526	0.0682
CG13407	0.525	0.0686
CG14528	0.525	0.0686
CG2016	0.525	0.0686
CG30050	0.525	0.0686
CG31808	0.525	0.0686
CG3434	0.525	0.0686
CG42382	0.525	0.0686
CG4374	0.525	0.0686
CG4802	0.525	0.0686
<i>Def</i>	0.525	0.0686
<i>smo</i>	0.525	0.0686
CG40198	0.524	0.0696
<i>AlstR</i>	0.523	0.0697
<i>sowah</i>	0.523	0.0697
CG7328	0.522	0.0699
<i>Kaz1-ORFB</i>	0.522	0.0699
<i>Pez</i>	0.522	0.0699
<i>sunz</i>	0.522	0.0699
CG11835	0.521	0.0703
CG12206	0.521	0.0703
CG18744	0.52	0.0705
CG31125	0.52	0.0705
CG42724	0.519	0.0706

Gene Name	ERC Value	P-value
CG8646	0.519	0.0706
<i>omet</i>	0.519	0.0706
<i>Dok</i>	0.519	0.0706
<i>rt</i>	0.519	0.0706
CG13323	0.518	0.0711
CG34317	0.518	0.0711
CG5382	0.518	0.0711
CG6908	0.518	0.0711
<i>Nurf-38</i>	0.518	0.0711
<i>wit</i>	0.518	0.0711
CG5793	0.517	0.0716
<i>Rpn7</i>	0.517	0.0716
CG17974	0.516	0.0718
<i>eca</i>	0.516	0.0718
<i>AdoR</i>	0.515	0.072
<i>Cyp9h1</i>	0.515	0.072
<i>Tehao</i>	0.515	0.072
CG11454	0.514	0.0723
CG13116	0.514	0.0723
CG13121	0.514	0.0723
<i>Jon25Bii</i>	0.514	0.0723
<i>Tig</i>	0.514	0.0723
<i>Orc4</i>	0.514	0.0723
CG14989	0.513	0.0728
<i>jub</i>	0.513	0.0728
CG12003	0.512	0.073
CG9747	0.512	0.073
<i>btd</i>	0.511	0.0732
CG3062	0.511	0.0732
CG32196	0.511	0.0732
CG5746	0.511	0.0732
CG8301	0.511	0.0732
CG8790	0.511	0.0732
CG9437	0.511	0.0732
<i>Cyp28d1</i>	0.511	0.0732
<i>Dlp-C</i>	0.511	0.0732
<i>FBX011</i>	0.511	0.0732
<i>GluRIIA</i>	0.511	0.0732
<i>grp</i>	0.511	0.0732
<i>Ppt1</i>	0.511	0.0732
<i>usnp</i>	0.511	0.0732
<i>Arp87C</i>	0.51	0.0744
CG15343	0.51	0.0744
CG3558	0.51	0.0744
<i>Tif-IA</i>	0.51	0.0744
<i>Tsp42Eg</i>	0.51	0.0744
CG10479	0.509	0.0749
CG14435	0.509	0.0749
CG30196	0.509	0.0749
CG34315	0.509	0.0749
CG4325	0.509	0.0749
CG5451	0.509	0.0749
CG7509	0.509	0.0749
<i>hk</i>	0.509	0.0749
<i>pot</i>	0.509	0.0749
<i>RhoGAPp19</i>	0.509	0.0749

Table 6.S20 Continued

Gene Name	ERC Value	P-value
Rpb4	0.509	0.0749
CG1120	0.508	0.0759
CG12783	0.508	0.0759
CG17278	0.508	0.0759
CG32790	0.508	0.0759
CG7918	0.508	0.0759
dos	0.508	0.0759
CG14650	0.507	0.0764
CG33307	0.507	0.0764
erm	0.507	0.0764
CG14906	0.506	0.0767
CG8538	0.506	0.0767
H2.0	0.506	0.0767
amd	0.505	0.0769
casp	0.505	0.0769
CG14926	0.505	0.0769
CG18659	0.505	0.0769
lr	0.505	0.0769
Jon74E	0.505	0.0769
Start1	0.505	0.0769
CG11880	0.504	0.0776
CG4098	0.504	0.0776
dimm	0.504	0.0776
GNBP2	0.504	0.0776
Gr89a	0.504	0.0776
trpm	0.504	0.0776
CG32225	0.503	0.0781
Lig4	0.503	0.0781
Reps	0.503	0.0781
Arp11	0.502	0.0784
CG31998	0.502	0.0784
CG4301	0.502	0.0784
EloA	0.502	0.0784
Fer1HCH	0.502	0.0784
shf	0.502	0.0784
T48	0.502	0.0784
tap	0.502	0.0784
Adh	0.501	0.0791
bib	0.501	0.0791
CG10073	0.501	0.0791
CG10424	0.501	0.0791
CG13502	0.501	0.0791
CG4996	0.501	0.0791
CG9593	0.501	0.0791
CTCF	0.501	0.0791
CG33969	0.5	0.0798
CG4949	0.5	0.0798
CG8100	0.5	0.0798
ru	0.5	0.0798
CG12207	0.499	0.0802
CG13890	0.499	0.0802
CG31269	0.499	0.0802
CG40191	0.499	0.0802
escl	0.499	0.0802
CG14174	0.498	0.0806
CG16854	0.498	0.0806

Gene Name	ERC Value	P-value
CG7408	0.498	0.0806
CG15118	0.497	0.0809
CG42360	0.497	0.0809
CG5909	0.497	0.0809
CG11060	0.496	0.0812
CG14618	0.496	0.0812
CG32459	0.496	0.0812
CG6838	0.496	0.0812
Fer2	0.496	0.0812
Bem46	0.495	0.0816
CG14693	0.495	0.0816
CG14882	0.495	0.0816
CG30466	0.495	0.0816
CG6276	0.495	0.0816
Cyp28c1	0.495	0.0816
org-1	0.495	0.0816
toy	0.495	0.0816
vg	0.495	0.0816
CG10824	0.494	0.0824
CG3368	0.494	0.0824
Chc	0.494	0.0824
Cul-5	0.494	0.0824
Ssb-c31a	0.494	0.0824
BBS1	0.493	0.0829
CG14956	0.493	0.0829
CG15861	0.493	0.0829
CG7787	0.493	0.0829
CG8783	0.493	0.0829
PICK1	0.493	0.0829
rab3-GEF	0.493	0.0829
ACXE	0.492	0.0835
Antp	0.492	0.0835
CG34112	0.492	0.0835
CG5644	0.492	0.0835
CG5830	0.492	0.0835
Pgani35A	0.492	0.0835
Ugt86Dj	0.492	0.0835
CG13957	0.491	0.0841
CG2519	0.491	0.0841
lir40a	0.491	0.0841
CG31793	0.49	0.0844
CG7431	0.49	0.0844
Ptp61F	0.49	0.0844
SPoCk	0.49	0.0844
Treh	0.49	0.0844
CG10345	0.489	0.0849
CG2316	0.489	0.0849
Ptp52F	0.489	0.0849
Zyx102EF	0.489	0.0849
Acsl	0.488	0.0852
CG12943	0.488	0.0852
CG6499	0.488	0.0852
CG9109	0.488	0.0852
Bet1	0.487	0.0856
CG42313	0.487	0.0856
cl	0.487	0.0856

Gene Name	ERC Value	P-value
MED1	0.487	0.0856
Itf5	0.487	0.0856
CG10845	0.486	0.086
CG5945	0.486	0.086
Femcoat	0.486	0.086
G-salpa60A	0.486	0.086
Galpa73B	0.486	0.086
ZC3H3	0.486	0.086
CG11255	0.485	0.0866
CG14937	0.485	0.0866
CG33281	0.485	0.0866
CG3841	0.485	0.0866
CG42345	0.485	0.0866
fax	0.485	0.0866
Ddr	0.484	0.0871
Ku80	0.484	0.0871
ictor	0.484	0.0871
sNPF	0.484	0.0871
CCKLR-17D	0.483	0.0875
CG13408	0.483	0.0875
CG17931	0.483	0.0875
CG1970	0.483	0.0875
cv-2	0.483	0.0875
gd	0.483	0.0875
Rab7	0.483	0.0875
CG4198	0.482	0.0881
scaf6	0.482	0.0881
CG4045	0.481	0.0883
CG12042	0.48	0.0884
CG13334	0.48	0.0884
CG15822	0.48	0.0884
CG33791	0.48	0.0884
Map60	0.48	0.0884
CG11211	0.479	0.0888
CG11970	0.479	0.0888
CG13707	0.479	0.0888
CG17184	0.479	0.0888
CG9416	0.479	0.0888
Nuf2	0.479	0.0888
Tyrr	0.479	0.0888
CG10188	0.478	0.0895
CG10713	0.478	0.0895
CG3701	0.478	0.0895
CG42374	0.478	0.0895
CG8671	0.478	0.0895
CG9384	0.478	0.0895
Nlp	0.478	0.0895
Pep	0.478	0.0895
CG14715	0.477	0.0902
CG17490	0.477	0.0902
CG2813	0.477	0.0902
CG6499	0.477	0.0902
VhaM9-T-d	0.477	0.0902
Vps45	0.477	0.0902
CG3884	0.476	0.0906
CG7702	0.476	0.0906
CG9592	0.476	0.0906

Gene Name	ERC Value	P-value
Proct	0.476	0.0906
bgm	0.475	0.091
CG34293	0.475	0.091
Lip2	0.475	0.091
Rad17	0.475	0.091
rod	0.475	0.091
CG12991	0.474	0.0914
CG13802	0.474	0.0914
CG4726	0.474	0.0914
CG8232	0.474	0.0914
CG8490	0.474	0.0914
Kif3C	0.474	0.0914
Orct2	0.474	0.0914
Scs	0.474	0.0914
CG13972	0.473	0.0922
CG5414	0.473	0.0922
CG6136	0.473	0.0922
hb	0.473	0.0922
hh	0.473	0.0922
Wscck	0.473	0.0922
PTP-ER	0.472	0.0927
ths	0.472	0.0927
CG14529	0.471	0.0929
CG17843	0.471	0.0929
Glycogenin	0.471	0.0929
hpo	0.471	0.0929
ome	0.471	0.0929
CG2652	0.47	0.0933
KalRIA	0.47	0.0933
CG1239	0.469	0.0935
CG15443	0.469	0.0935
CG33557	0.469	0.0935
Cyp316a1	0.469	0.0935
tsg	0.469	0.0935
CG14177	0.468	0.094
CG8142	0.468	0.094
granny-smith	0.468	0.094
Ho	0.468	0.094
Hrb98DE	0.468	0.094
mthl9	0.468	0.094
Roc2	0.468	0.094
Spn43Ad	0.468	0.094
Tsp42Ep	0.468	0.094
CG3592	0.467	0.0948
CG5280	0.467	0.0948
CG6503	0.467	0.0948
GalINAc-T2	0.467	0.0948
osm-1	0.467	0.0948
Tango11	0.467	0.0948
CG10209	0.466	0.0953
CG10352	0.466	0.0953
CG14314	0.466	0.0953
CG8678	0.466	0.0953
Cyp28a5	0.466	0.0953
jim	0.466	0.0953
pex1	0.466	0.0953

Gene Name	ERC Value	P-value
RpS3A	0.466	0.0953
CG1358	0.465	0.096
CG31712	0.465	0.096
CG4390	0.465	0.096
CG9099	0.465	0.096
ear	0.465	0.096
Mst85C	0.465	0.096
CG11902	0.464	0.0966
CG16739	0.464	0.0966
CG16865	0.464	0.0966
CG32591	0.464	0.0966
Hcf	0.464	0.0966
kto	0.464	0.0966
lama	0.464	0.0966
Reck	0.464	0.0966
CG13741	0.463	0.0973
dyl	0.463	0.0973
fy	0.463	0.0973
kek5	0.463	0.0973
Mp20	0.463	0.0973
Cdk4	0.462	0.0977
CG3448	0.462	0.0977
CG8562	0.462	0.0977
Def	0.462	0.0977
dm	0.462	0.0977
CG3652	0.461	0.0982
CG8963	0.461	0.0982
SH3PX1	0.461	0.0982
stf	0.461	0.0982
CG10465	0.46	0.0986
CG17691	0.46	0.0986
CG5276	0.46	0.0986
CG5386	0.46	0.0986
CG7607	0.46	0.0986
CG7777	0.46	0.0986
CG9951	0.46	0.0986
Os-E	0.46	0.0986
Pdp	0.46	0.0986
sPLA2	0.46	0.0986
yps	0.46	0.0986
Aats-met	0.459	0.0995
CG10428	0.459	0.0995
CG11406	0.459	0.0995
CG11983	0.459	0.0995
CG14826	0.459	0.0995
CG31036	0.459	0.0995
CG32750	0.459	0.0995
CG4407	0.459	0.0995
IP3K1	0.459	0.0995
Ppn	0.459	0.0995
Rpb8	0.459	0.0995

Table 6.S21 - Top Genes ERC values for *spn-D* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
<i>Gr61a</i>	0.935	0.0001
<i>Rad51D</i>	0.92	0.0002
<i>Or88a</i>	0.913	0.0003
<i>Start1</i>	0.908	0.0004
<i>CG32573</i>	0.904	0.0005
<i>CG13295</i>	0.901	0.0005
<i>CG34007</i>	0.894	0.0006
<i>Hr96</i>	0.878	0.0007
<i>CG8247</i>	0.877	0.0008
<i>Hus1-like</i>	0.866	0.0009
<i>CG32043</i>	0.862	0.001
<i>CG13085</i>	0.859	0.0011
<i>CG6188</i>	0.85	0.0012
<i>CG42554</i>	0.84	0.0013
<i>cag</i>	0.839	0.0014
<i>CG8319</i>	0.839	0.0014
<i>Gr59b</i>	0.835	0.0015
<i>Art4</i>	0.834	0.0016
<i>Tehao</i>	0.829	0.0017
<i>CG7431</i>	0.827	0.0018
<i>CG33703</i>	0.825	0.0019
<i>nima</i>	0.821	0.002
<i>CG42678</i>	0.819	0.0021
<i>smo</i>	0.818	0.0022
<i>CG11191</i>	0.814	0.0023
<i>CG15082</i>	0.813	0.0023
<i>CG13837</i>	0.812	0.0024
<i>CG16826</i>	0.811	0.0025
<i>Rad51C</i>	0.811	0.0025
<i>CG31630</i>	0.81	0.0027
<i>GNBP1</i>	0.81	0.0027
CG10560	0.809	0.0029
<i>CG33784</i>	0.807	0.003
<i>zpg</i>	0.807	0.003
<i>Gr77a</i>	0.805	0.0032
<i>Vdup1</i>	0.805	0.0032
<i>CG32563</i>	0.801	0.0033
<i>CG13545</i>	0.799	0.0034
<i>CG31380</i>	0.799	0.0034
<i>CG42863</i>	0.798	0.0036
<i>CG14330</i>	0.795	0.0037
<i>Gr93a</i>	0.794	0.0038
CG31898	0.793	0.0039
<i>CG18110</i>	0.791	0.004
<i>MRP</i>	0.79	0.0041
<i>snw</i>	0.789	0.0041
<i>CG10300</i>	0.788	0.0042
<i>CG31793</i>	0.787	0.0043
<i>CG10339</i>	0.783	0.0044
<i>dos</i>	0.783	0.0044
<i>CG13169</i>	0.782	0.0046
<i>CG13488</i>	0.782	0.0046
<i>CG17931</i>	0.782	0.0046
<i>CG32631</i>	0.779	0.0049
<i>CG13912</i>	0.778	0.005
<i>CG2278</i>	0.775	0.005

Gene Name	ERC Value	P-value
<i>CG5867</i>	0.774	0.0051
<i>dome</i>	0.774	0.0051
<i>dpr3</i>	0.771	0.0053
<i>Gr65a</i>	0.771	0.0053
<i>Os-E</i>	0.771	0.0053
<i>CG11286</i>	0.77	0.0056
<i>CG18585</i>	0.77	0.0056
<i>Gr59e</i>	0.77	0.0056
<i>CG33289</i>	0.767	0.0059
<i>CG8199</i>	0.766	0.0059
<i>CG9416</i>	0.766	0.0059
<i>CG6733</i>	0.764	0.0061
<i>TwdlX</i>	0.764	0.0061
<i>CG31102</i>	0.763	0.0063
<i>CG13033</i>	0.762	0.0064
<i>CG14302</i>	0.762	0.0064
<i>Cdk9</i>	0.761	0.0066
<i>Cpr60D</i>	0.76	0.0067
<i>CG17562</i>	0.759	0.0068
<i>CG14401</i>	0.757	0.0068
<i>Obp19a</i>	0.757	0.0068
<i>cv</i>	0.756	0.007
<i>CG10591</i>	0.753	0.0071
<i>CG7906</i>	0.753	0.0071
<i>Cyp309a1</i>	0.753	0.0071
<i>Rpl31</i>	0.752	0.0074
<i>Vm32E</i>	0.751	0.0075
<i>CG14115</i>	0.75	0.0076
<i>Cpr62Ba</i>	0.749	0.0077
<i>CG14290</i>	0.748	0.0077
<i>CG32121</i>	0.747	0.0078
<i>CG8642</i>	0.747	0.0078
<i>SoxN</i>	0.747	0.0078
<i>CG3860</i>	0.746	0.0081
<i>CG5846</i>	0.745	0.0082
<i>ppk19</i>	0.745	0.0082
<i>Proct</i>	0.745	0.0082
<i>CG15609</i>	0.74	0.0085
<i>CG4753</i>	0.739	0.0086
<i>CG13408</i>	0.738	0.0086
<i>Gr22e</i>	0.737	0.0087
<i>Dsk</i>	0.736	0.0088
<i>CG3285</i>	0.734	0.0089
<i>Fen1</i>	0.734	0.0089
<i>CG14427</i>	0.733	0.0091
<i>CG31091</i>	0.733	0.0091
<i>CG9400</i>	0.733	0.0091
<i>CG4592</i>	0.73	0.0094
<i>Jon74E</i>	0.73	0.0094
<i>CG11388</i>	0.729	0.0095
<i>CG5386</i>	0.729	0.0095
<i>Reck</i>	0.729	0.0095
<i>synaptogyrin</i>	0.729	0.0095
<i>repo</i>	0.728	0.0099
<i>CG1998</i>	0.727	0.01
<i>CG12995</i>	0.726	0.0101

Gene Name	ERC Value	P-value
<i>CG15888</i>	0.726	0.0101
<i>CG8516</i>	0.726	0.0101
<i>sec31</i>	0.725	0.0104
<i>Rpl115</i>	0.723	0.0105
<i>CG14963</i>	0.722	0.0105
<i>CG33514</i>	0.722	0.0105
<i>CG4729</i>	0.722	0.0105
<i>esn</i>	0.722	0.0105
<i>CG31431</i>	0.721	0.0109
<i>Spt20</i>	0.721	0.0109
<i>Hk</i>	0.72	0.0111
<i>CG31272</i>	0.717	0.0112
<i>Gr64f</i>	0.717	0.0112
<i>CG30115</i>	0.716	0.0114
<i>CG3376</i>	0.716	0.0114
<i>CG34266</i>	0.716	0.0114
<i>DIP2</i>	0.716	0.0114
<i>CG13814</i>	0.715	0.0117
<i>COQ7</i>	0.715	0.0117
<i>Atx2</i>	0.714	0.0119
<i>Cdk5</i>	0.714	0.0119
<i>CG15740</i>	0.714	0.0119
<i>CHKov2</i>	0.713	0.0122
<i>SP2</i>	0.709	0.0123
<i>CG6225</i>	0.708	0.0123
<i>CG31065</i>	0.707	0.0124
<i>CG18095</i>	0.705	0.0125
<i>Gr58c</i>	0.705	0.0125
<i>CG11395</i>	0.704	0.0127
<i>CG14321</i>	0.704	0.0127
<i>CG31607</i>	0.704	0.0127
<i>Spase18-21</i>	0.704	0.0127
<i>Vha100-4</i>	0.703	0.0131
<i>Cdc42</i>	0.702	0.0132
<i>nimB2</i>	0.702	0.0132
<i>Cad89D</i>	0.701	0.0133
<i>CG6751</i>	0.701	0.0133
<i>GstD10</i>	0.701	0.0133
<i>Orct2</i>	0.701	0.0133
<i>Dnz1</i>	0.7	0.0137
<i>Osi3</i>	0.7	0.0137
<i>hk</i>	0.699	0.0139
<i>gek</i>	0.698	0.014
<i>CG2519</i>	0.697	0.0141
<i>ome</i>	0.697	0.0141
<i>Or47a</i>	0.697	0.0141
<i>Or43b</i>	0.696	0.0143
<i>CG7158</i>	0.695	0.0144
<i>wrapper</i>	0.695	0.0144
<i>CG42371</i>	0.694	0.0146
<i>obst-J</i>	0.694	0.0146
<i>CG34196</i>	0.693	0.0148
<i>slbo</i>	0.693	0.0148
<i>dmt11E</i>	0.692	0.015
<i>boss</i>	0.691	0.015
<i>CG11851</i>	0.691	0.015

Gene Name	ERC Value	P-value
<i>CG33510</i>	0.691	0.015
<i>CG3679</i>	0.691	0.015
<i>disp</i>	0.691	0.015
<i>CG7197</i>	0.69	0.0155
<i>Nhe1</i>	0.69	0.0155
<i>Oaz</i>	0.69	0.0155
<i>RpS26</i>	0.689	0.0158
<i>CG14915</i>	0.688	0.0159
<i>Fas2</i>	0.688	0.0159
<i>gsb-n</i>	0.688	0.0159
<i>ACXD</i>	0.687	0.0161
<i>CG18746</i>	0.687	0.0161
<i>Lerp</i>	0.687	0.0161
<i>nab</i>	0.687	0.0161
<i>Cpr72Ea</i>	0.686	0.0165
<i>sv</i>	0.686	0.0165
<i>CG17660</i>	0.685	0.0167
<i>CG1246</i>	0.684	0.0168
<i>CG34001</i>	0.684	0.0168
<i>Gr59f</i>	0.684	0.0168
<i>CG1671</i>	0.683	0.017
<i>Obp50d</i>	0.683	0.017
<i>ppk16</i>	0.683	0.017
<i>CG14424</i>	0.682	0.0173
<i>CG9663</i>	0.681	0.0174
<i>Tektm-A</i>	0.679	0.0175
<i>MED19</i>	0.678	0.0176
<i>Cpr78E</i>	0.677	0.0177
<i>ema</i>	0.677	0.0177
<i>B4</i>	0.675	0.0178
<i>CG8646</i>	0.675	0.0178
<i>Pask</i>	0.675	0.0178
<i>Pbprp3</i>	0.675	0.0178
<i>Adgf-B</i>	0.674	0.0182
<i>SuUR</i>	0.674	0.0182
<i>CG16786</i>	0.673	0.0184
<i>lHog</i>	0.672	0.0185
<i>brat</i>	0.671	0.0186
<i>CG8067</i>	0.671	0.0186
<i>dsd</i>	0.671	0.0186
mel-41	0.671	0.0186
<i>Mpk2</i>	0.671	0.0186
<i>pll</i>	0.671	0.0186
<i>CG11055</i>	0.669	0.0191
<i>CG30411</i>	0.669	0.0191
<i>Osi13</i>	0.669	0.0191
<i>T48</i>	0.669	0.0191
<i>CG31373</i>	0.667	0.0195
<i>CG14313</i>	0.666	0.0195
<i>CG4586</i>	0.666	0.0195
<i>pep1</i>	0.666	0.0195
<i>npf</i>	0.665	0.0198
<i>Rab3</i>	0.665	0.0198
<i>bnb</i>	0.664	0.02
<i>CG1443</i>	0.664	0.02
<i>CG33641</i>	0.664	0.02

Gene Name	ERC Value	P-value
<i>CG34420</i>	0.663	0.0203
<i>CG5287</i>	0.663	0.0203
<i>CG4074</i>	0.662	0.0205
<i>cort</i>	0.662	0.0205
<i>CG42319</i>	0.661	0.0206
<i>lkb1</i>	0.661	0.0206
<i>spict</i>	0.661	0.0206
<i>lox2</i>	0.66	0.0209
<i>Cpr49Aa</i>	0.659	0.021
<i>CG15099</i>	0.658	0.0211
<i>CG5902</i>	0.655	0.0212
<i>CG6688</i>	0.655	0.0212
<i>CG31689</i>	0.654	0.0214
<i>Gas8</i>	0.654	0.0214
<i>Apc2</i>	0.653	0.0215
<i>CG17974</i>	0.653	0.0215
<i>CG7777</i>	0.653	0.0215
<i>CG7787</i>	0.652	0.0218
<i>CG9088</i>	0.652	0.0218
<i>Or45b</i>	0.652	0.0218
<i>CG17782</i>	0.651	0.0221
<i>CG42508</i>	0.651	0.0221
<i>tufl</i>	0.65	0.0223
<i>TwdlF</i>	0.65	0.0223
<i>CG1299</i>	0.649	0.0224
<i>ss</i>	0.649	0.0224
<i>frr</i>	0.649	0.0224
<i>CG10910</i>	0.648	0.0227
<i>DAT</i>	0.646	0.0228
<i>frtz</i>	0.646	0.0228
<i>CG10505</i>	0.645	0.023
<i>CG15626</i>	0.645	0.023
<i>CG31275</i>	0.645	0.023
<i>FancI</i>	0.645	0.023
<i>CG5938</i>	0.644	0.0233
<i>CG5872</i>	0.643	0.0234
<i>GaiNac-T1</i>	0.643	0.0234
<i>pgc</i>	0.643	0.0234
<i>CG7079</i>	0.642	0.0237
<i>rost</i>	0.642	0.0237
<i>lr84a</i>	0.641	0.0239
<i>CG30050</i>	0.64	0.024
<i>CG3303</i>	0.64	0.024
<i>CG8490</i>	0.64	0.024
<i>CDase</i>	0.639	0.0242
<i>CG13022</i>	0.639	0.0242
<i>CG2680</i>	0.639	0.0242
CG2975	0.639	0.0242
<i>Gr2a</i>	0.639	0.0242
<i>Gr33a</i>	0.639	0.0242
<i>mus309</i>	0.639	0.0242
<i>Ripalpha</i>	0.639	0.0242
<i>Cpr64Ad</i>	0.638	0.025
<i>put</i>	0.638	0.025
<i>net</i>	0.637	0.0251
<i>CG14459</i>	0.636	0.0252

Table 6.S21 Continued

Gene Name	ERC Value	P-value
kar	0.636	0.0252
CG1387	0.634	0.0254
CG14277	0.634	0.0254
FBX011	0.634	0.0254
THIA-S	0.634	0.0254
capa	0.633	0.0258
CG17784	0.633	0.0258
CG8353	0.633	0.0258
CG7044	0.632	0.026
Eig71Ef	0.632	0.026
Gyc32E	0.632	0.026
CG12971	0.631	0.0263
CG14857	0.631	0.0263
comm3	0.631	0.0263
neo	0.631	0.0263
CG4267	0.63	0.0267
CG8546	0.63	0.0267
HSPC300	0.63	0.0267
slam	0.63	0.0267
sname	0.629	0.027
Cyp6d5	0.628	0.0271
For2	0.628	0.0271
CG2126	0.627	0.0273
CG30431	0.627	0.0273
ETH	0.627	0.0273
Or49a	0.627	0.0273
14-3-3μ	0.626	0.0277
Sep5	0.626	0.0277
CG31076	0.626	0.0277
CG3216	0.626	0.0277
CG34396	0.626	0.0277
Ir56d	0.626	0.0277
CG4829	0.625	0.0282
Klc	0.625	0.0282
amon	0.624	0.0284
CG18745	0.624	0.0284
CG31048	0.624	0.0284
CG6867	0.624	0.0284
CG8202	0.624	0.0284
Gr57a	0.624	0.0284
Irt0a	0.624	0.0284
CG10743	0.623	0.029
CG17780	0.623	0.029
CG30372	0.623	0.029
CG31191	0.623	0.029
CG4734	0.623	0.029
CG18766	0.622	0.0295
Tab2	0.622	0.0295
Adgf-D	0.621	0.0296
spn-B	0.621	0.0296
CG13250	0.62	0.0298
CG33257	0.62	0.0298
CG5773	0.62	0.0298
Prosalpha6T	0.62	0.0298
CG9865	0.619	0.0302
RpL17	0.619	0.0302

Gene Name	ERC Value	P-value
CG10086	0.618	0.0304
CG14234	0.618	0.0304
Nedd4	0.618	0.0304
CG1143	0.617	0.0306
CG14257	0.617	0.0306
CG15537	0.617	0.0306
CG34193	0.617	0.0306
CG42676	0.617	0.0306
CG4751	0.617	0.0306
CG7272	0.616	0.0312
exo84	0.616	0.0312
CG14880	0.615	0.0314
Try29F	0.615	0.0314
CG9267	0.614	0.0315
RhoGEF2	0.614	0.0315
RpL21	0.614	0.0315
CG30381	0.613	0.0318
CG33253	0.613	0.0318
CG3448	0.613	0.0318
Madm	0.613	0.0318
CG32437	0.612	0.0322
CG9752	0.612	0.0322
PH4alphaMF	0.612	0.0322
Rab40	0.612	0.0322
CG10841	0.611	0.0325
CG31698	0.611	0.0325
Cyp4d2	0.611	0.0325
LvpD	0.611	0.0325
l(2)35Bc	0.61	0.0329
Illil	0.61	0.0329
CG14113	0.609	0.0331
Slide	0.609	0.0331
CG13931	0.608	0.0332
CG30016	0.608	0.0332
Npc2a	0.608	0.0332
CG13636	0.607	0.0335
CG6484	0.607	0.0335
Or83c	0.607	0.0335
TMS1	0.607	0.0335
CG2774	0.606	0.0339
CG34401	0.606	0.0339
CG42456	0.606	0.0339
CG13640	0.605	0.0341
CG6282	0.605	0.0341
CG13157	0.604	0.0343
CG31659	0.603	0.0344
GstE6	0.603	0.0344
Reps	0.603	0.0344
CG31226	0.602	0.0347
pwn	0.602	0.0347
CG2993	0.601	0.0349
CG7896	0.601	0.0349
Lgr3	0.601	0.0349
Tsc1	0.601	0.0349
ham	0.6	0.0352
Adhr	0.599	0.0353

Gene Name	ERC Value	P-value
Atg6	0.599	0.0353
CG13875	0.599	0.0353
rk	0.599	0.0353
CG3168	0.598	0.0357
drpr	0.598	0.0357
CG42351	0.597	0.0359
Ext2	0.597	0.0359
IP3K1	0.597	0.0359
Mst85C	0.597	0.0359
Rad1	0.597	0.0359
RhoBTB	0.597	0.0359
Act88F	0.596	0.0364
blue	0.596	0.0364
Myd88	0.596	0.0364
CG33281	0.595	0.0367
wdn	0.595	0.0367
CG10495	0.594	0.0368
CG14883	0.594	0.0368
coro	0.594	0.0368
sro	0.594	0.0368
CG4496	0.593	0.0372
Cpr66Cb	0.593	0.0372
Gr94a	0.593	0.0372
smg	0.593	0.0372
Adh	0.592	0.0376
CG15404	0.592	0.0376
CG30394	0.592	0.0376
CG33096	0.592	0.0376
CG10730	0.591	0.0379
CG10824	0.591	0.0379
CG13575	0.591	0.0379
CG16743	0.591	0.0379
CG30001	0.591	0.0379
CG3884	0.591	0.0379
CG4770	0.591	0.0379
neur	0.591	0.0379
Rab5	0.591	0.0379
CG15738	0.59	0.0387
CG5665	0.59	0.0387
CG2774	0.59	0.0387
Nf1	0.589	0.039
CG32791	0.588	0.0391
dpr16	0.588	0.0391
Esp	0.588	0.0391
TwdlR	0.588	0.0391
CG10188	0.587	0.0395
l(2)k05819	0.587	0.0395
CG12325	0.586	0.0396
CG13331	0.586	0.0396
CG34174	0.586	0.0396
CG6182	0.586	0.0396
Or45a	0.586	0.0396
CG13955	0.585	0.0401
CG30094	0.585	0.0401
CG32305	0.585	0.0401
Sin1	0.585	0.0401

Gene Name	ERC Value	P-value
Ccn	0.584	0.0405
CG14676	0.584	0.0405
CG31812	0.584	0.0405
CG8191	0.584	0.0405
Nha1	0.584	0.0405
niki	0.584	0.0405
Taf4	0.584	0.0405
CG13298	0.583	0.0411
CG6196	0.583	0.0411
Cyp9h1	0.583	0.0411
Rab-RP3	0.583	0.0411
Whamy	0.583	0.0411
mtth14	0.582	0.0415
S1P	0.582	0.0415
shark	0.582	0.0415
alpha-Est8	0.581	0.0418
CG3502	0.581	0.0418
Oseg1	0.581	0.0418
Tak1	0.581	0.0418
Ark	0.58	0.0422
CG14109	0.58	0.0422
CG6984	0.58	0.0422
CG8959	0.58	0.0422
CG15212	0.579	0.0425
CG17912	0.579	0.0425
PGRP-LD	0.579	0.0425
CG7992	0.578	0.0428
CG11131	0.577	0.0429
Cfz	0.577	0.0429
CG13344	0.577	0.0429
CG5435	0.577	0.0429
Cpr49Ae	0.577	0.0429
CG30259	0.576	0.0432
Psf2	0.576	0.0432
RpL13A	0.576	0.0432
Sb	0.576	0.0432
bgm	0.575	0.0436
CG13183	0.575	0.0436
CG15506	0.575	0.0436
CG15743	0.575	0.0436
CG15822	0.575	0.0436
CG8783	0.575	0.0436
cn	0.575	0.0436
fd96Ca	0.575	0.0436
AistR	0.574	0.0443
CG11750	0.574	0.0443
CG13278	0.574	0.0443
Jarid2	0.574	0.0443
CG14062	0.573	0.0447
CG3091	0.573	0.0447
GstD9	0.573	0.0447
Obp47a	0.573	0.0447
Idbr	0.572	0.045
Tyrril	0.572	0.045
CG12420	0.571	0.0452
CG2336	0.571	0.0452
Gyk	0.571	0.0452

Gene Name	ERC Value	P-value
Oatp26F	0.571	0.0452
CG12003	0.57	0.0456
ChLD3	0.57	0.0456
MED10	0.57	0.0456
mus304	0.57	0.0456
CG15044	0.569	0.0459
CG7146	0.569	0.0459
Ho	0.569	0.0459
Ir87a	0.569	0.0459
CG10920	0.568	0.0463
grau	0.568	0.0463
CG32052	0.567	0.0465
bnk	0.566	0.0466
CG14627	0.566	0.0466
CG2135	0.566	0.0466
CG3326	0.566	0.0466
CG5073	0.566	0.0466
CG5535	0.566	0.0466
CG5948	0.566	0.0466
CG6974	0.566	0.0466
CG14565	0.565	0.0473
scramb2	0.565	0.0473
CG4844	0.564	0.0475
Est65A	0.564	0.0475
CG13937	0.563	0.0477
CG14102	0.563	0.0477
CG7992	0.563	0.0477
Npc2f	0.563	0.0477
CG14856	0.562	0.048
CG7222	0.562	0.048
Cpr23B	0.561	0.0482
NiPp1	0.561	0.0482
CG31075	0.56	0.0484
Ephrin	0.56	0.0484
Fer1HCH	0.56	0.0484
magu	0.56	0.0484
MED18	0.56	0.0484
CG4210	0.559	0.0488
CG8539	0.559	0.0488
grk	0.559	0.0488
CG13884	0.558	0.0491
CG14491	0.558	0.0491
Dgkepsilon	0.558	0.0491
Gal	0.558	0.0491
SCAP	0.558	0.0491
CG11060	0.557	0.0495
CG31266	0.557	0.0495
eyg	0.557	0.0495
CG12516	0.556	0.0498
CG13565	0.556	0.0498
CG2652	0.556	0.0498
CG5903	0.556	0.0498
CG8814	0.556	0.0498
NAT1	0.556	0.0498
slpr	0.556	0.0498
lin	0.555	0.0505

Table 6.S21 Continued

Gene Name	ERC Value	P-value
<i>miple2</i>	0.555	0.0505
<i>CG5157</i>	0.554	0.0506
<i>Csk</i>	0.554	0.0506
<i>POSH</i>	0.554	0.0506
<i>Taf11</i>	0.554	0.0506
<i>CG1738</i>	0.553	0.051
<i>CG9904</i>	0.553	0.051
<i>lace</i>	0.553	0.051
<i>llc</i>	0.553	0.051
<i>CG13847</i>	0.552	0.0514
<i>CG14989</i>	0.552	0.0514
<i>CG16868</i>	0.552	0.0514
<i>CG3062</i>	0.552	0.0514
<i>CG32627</i>	0.552	0.0514
<i>HLH54F</i>	0.552	0.0514
<i>lpk1</i>	0.552	0.0514
<i>yki</i>	0.552	0.0514
<i>CG12835</i>	0.551	0.0521
<i>CG18609</i>	0.551	0.0521
<i>CG32459</i>	0.551	0.0521
<i>CG33772</i>	0.551	0.0521
<i>lox</i>	0.551	0.0521
<i>CG14070</i>	0.55	0.0525
<i>CG33988</i>	0.55	0.0525
<i>Sry-alpha</i>	0.55	0.0525
<i>AP-1sigma</i>	0.549	0.0528
<i>Atg2</i>	0.549	0.0528
<i>CG1275</i>	0.549	0.0528
<i>CG32351</i>	0.549	0.0528
<i>CG9344</i>	0.549	0.0528
<i>trbd</i>	0.549	0.0528
<i>CG4393</i>	0.548	0.0533
<i>CG5002</i>	0.548	0.0533
<i>CG6617</i>	0.548	0.0533
<i>CG7009</i>	0.547	0.0536
<i>Edg84A</i>	0.547	0.0536
<i>CG11679</i>	0.546	0.0538
<i>Cyp49a1</i>	0.546	0.0538
<i>Rlc1</i>	0.546	0.0538
<i>CG8861</i>	0.545	0.0541
<i>CG9801</i>	0.545	0.0541
<i>Cys</i>	0.545	0.0541
<i>p38b</i>	0.544	0.0543
<i>CG17999</i>	0.543	0.0544
<i>CG5734</i>	0.543	0.0544
<i>CG8370</i>	0.543	0.0544
<i>Dhod</i>	0.543	0.0544
<i>CG13627</i>	0.542	0.0548
<i>CG31855</i>	0.542	0.0548
<i>CG8596</i>	0.542	0.0548
<i>lute</i>	0.542	0.0548
<i>mus312</i>	0.542	0.0548
<i>CG12986</i>	0.541	0.0552
<i>CG30497</i>	0.541	0.0552
<i>CG32068</i>	0.541	0.0552
<i>CG7912</i>	0.541	0.0552

Gene Name	ERC Value	P-value
<i>Tsp42Eg</i>	0.541	0.0552
<i>CG13193</i>	0.54	0.0557
<i>CG1347</i>	0.54	0.0557
<i>Slid5</i>	0.54	0.0557
<i>Ssb-c31a</i>	0.54	0.0557
<i>CG14195</i>	0.539	0.056
<i>CG4705</i>	0.539	0.056
<i>CG9444</i>	0.539	0.056
<i>Chi</i>	0.539	0.056
<i>Moe</i>	0.539	0.056
<i>PHDP</i>	0.539	0.056
<i>CG10973</i>	0.538	0.0566
<i>CG11406</i>	0.538	0.0566
<i>CG17265</i>	0.538	0.0566
<i>CG17267</i>	0.538	0.0566
<i>mew</i>	0.538	0.0566
<i>Tsp42En</i>	0.538	0.0566
<i>CG12911</i>	0.537	0.0571
<i>CG14956</i>	0.537	0.0571
<i>CG5024</i>	0.537	0.0571
<i>CG5945</i>	0.537	0.0571
<i>lox</i>	0.537	0.0571
<i>Lip4</i>	0.537	0.0571
<i>nmd</i>	0.537	0.0571
<i>Or65a</i>	0.537	0.0571
<i>Sox15</i>	0.537	0.0571
<i>sut2</i>	0.537	0.0571
<i>CG13634</i>	0.536	0.058
<i>CG13766</i>	0.536	0.058
<i>CG18135</i>	0.536	0.058
<i>CG30105</i>	0.536	0.058
<i>CG31849</i>	0.536	0.058
<i>CG32790</i>	0.536	0.058
<i>CG5618</i>	0.536	0.058
<i>CG7918</i>	0.536	0.058
<i>CG14551</i>	0.535	0.0587
<i>CG14661</i>	0.535	0.0587
<i>CG5569</i>	0.535	0.0587
<i>Hr78</i>	0.535	0.0587
<i>CG5276</i>	0.534	0.0591
<i>CG8800</i>	0.534	0.0591
<i>CG13430</i>	0.533	0.0593
<i>CG9797</i>	0.533	0.0593
<i>CG10226</i>	0.532	0.0595
<i>CG12057</i>	0.532	0.0595
<i>CG2321</i>	0.532	0.0595
<i>CG4576</i>	0.532	0.0595
<i>CG5591</i>	0.532	0.0595
<i>Cyp4e2</i>	0.532	0.0595
<i>Hex-12</i>	0.532	0.0595
<i>bl</i>	0.531	0.0601
<i>CG30120</i>	0.531	0.0601
<i>InR</i>	0.531	0.0601
<i>Mdr50</i>	0.531	0.0601
<i>MED31</i>	0.531	0.0601
<i>sNPF</i>	0.531	0.0601

Gene Name	ERC Value	P-value
<i>Tom</i>	0.531	0.0601
<i>CG14550</i>	0.53	0.0607
<i>lr56c</i>	0.53	0.0607
<i>alpha-catenin</i>	0.529	0.0609
<i>CG13813</i>	0.529	0.0609
<i>CG14894</i>	0.529	0.0609
<i>clt</i>	0.529	0.0609
<i>en</i>	0.529	0.0609
<i>PTP-ER</i>	0.529	0.0609
<i>BBS1</i>	0.528	0.0614
<i>CG15928</i>	0.528	0.0614
<i>CG7739</i>	0.528	0.0614
<i>Csl4</i>	0.528	0.0614
<i>Obp50e</i>	0.528	0.0614
<i>CG13613</i>	0.527	0.0619
<i>CG14047</i>	0.527	0.0619
<i>CG15221</i>	0.527	0.0619
<i>CG4459</i>	0.527	0.0619
<i>CG8419</i>	0.527	0.0619
<i>CG9911</i>	0.527	0.0619
<i>Ptth</i>	0.527	0.0619
<i>CG8128</i>	0.526	0.0625
<i>CG5621</i>	0.526	0.0625
<i>CG9430</i>	0.526	0.0625
<i>rasp</i>	0.526	0.0625
<i>a6</i>	0.525	0.0629
<i>CG17549</i>	0.525	0.0629
<i>CG34349</i>	0.525	0.0629
<i>CG6746</i>	0.525	0.0629
<i>Gr32a</i>	0.525	0.0629
<i>Rbf</i>	0.525	0.0629
<i>TwidC</i>	0.525	0.0629
<i>CG14213</i>	0.524	0.0635
<i>CG17739</i>	0.524	0.0635
<i>lj</i>	0.524	0.0635
<i>CG11454</i>	0.523	0.0638
<i>CG11778</i>	0.523	0.0638
<i>CG7246</i>	0.523	0.0638
<i>CG7759</i>	0.523	0.0638
<i>l 2 05510</i>	0.523	0.0638
<i>Brf</i>	0.522	0.0642
<i>CG13745</i>	0.522	0.0642
<i>CG7227</i>	0.522	0.0642
<i>Tsp42Eg</i>	0.522	0.0642
<i>CG13160</i>	0.521	0.0646
<i>CG3476</i>	0.521	0.0646
<i>CG5357</i>	0.521	0.0646
<i>ear</i>	0.521	0.0646
<i>Gr66a</i>	0.521	0.0646
<i>Osi17</i>	0.521	0.0646
<i>CG10738</i>	0.52	0.0651
<i>CG11619</i>	0.52	0.0651
<i>CG15438</i>	0.52	0.0651
<i>CG17839</i>	0.52	0.0651
<i>CG32016</i>	0.52	0.0651
<i>CG34217</i>	0.52	0.0651

Gene Name	ERC Value	P-value
<i>CG34456</i>	0.52	0.0651
<i>CG7084</i>	0.52	0.0651
<i>sced</i>	0.52	0.0651
<i>skpA</i>	0.52	0.0651
<i>TwidY</i>	0.52	0.0651
<i>ABCB7</i>	0.519	0.0661
<i>beat-lla</i>	0.519	0.0661
<i>CG30263</i>	0.519	0.0661
<i>CG6425</i>	0.519	0.0661
<i>obst-F</i>	0.519	0.0661
<i>proPO-A1</i>	0.519	0.0661
<i>Akap200</i>	0.518	0.0667
<i>CG15717</i>	0.518	0.0667
<i>CG5554</i>	0.518	0.0667
<i>CG9917</i>	0.518	0.0667
<i>Act42A</i>	0.517	0.067
<i>CG11306</i>	0.517	0.067
<i>CG11668</i>	0.517	0.067
<i>CG18549</i>	0.517	0.067
<i>CG6520</i>	0.517	0.067
<i>dri</i>	0.517	0.067
<i>Fsh</i>	0.517	0.067
<i>Patj</i>	0.517	0.067
<i>CG13616</i>	0.516	0.0677
<i>CG17290</i>	0.516	0.0677
<i>CG32579</i>	0.516	0.0677
<i>CG4741</i>	0.516	0.0677
<i>Ckllalpha</i>	0.516	0.0677
<i>osp</i>	0.516	0.0677
<i>Pk17E</i>	0.516	0.0677
<i>Sema-1b</i>	0.516	0.0677
<i>CG9008</i>	0.513	0.0685
<i>Npc2e</i>	0.513	0.0685
<i>CG11211</i>	0.512	0.0686
<i>CG11436</i>	0.512	0.0686
<i>kek1</i>	0.512	0.0686
<i>lgs</i>	0.512	0.0686
<i>CG10103</i>	0.511	0.069
<i>CG11068</i>	0.511	0.069
<i>CG14606</i>	0.511	0.069
<i>CG42826</i>	0.511	0.069
<i>Gr9a</i>	0.511	0.069
<i>tefu</i>	0.511	0.069
<i>UbcD2</i>	0.511	0.069
<i>beta4GalNA</i>	0.51	0.0696
<i>NTPase</i>	0.51	0.0696
<i>CG5280</i>	0.509	0.0698
<i>Traf-like</i>	0.509	0.0698
<i>CG8008</i>	0.508	0.07
<i>dpr19</i>	0.508	0.07
<i>Fmrf</i>	0.508	0.07
<i>ImpE1</i>	0.508	0.07
<i>lld</i>	0.508	0.07
<i>CG13215</i>	0.507	0.0705
<i>CG13924</i>	0.507	0.0705
<i>CG16926</i>	0.507	0.0705

Gene Name	ERC Value	P-value
<i>foi</i>	0.507	0.0705
<i>halo</i>	0.507	0.0705
<i>Phlpp</i>	0.507	0.0705
<i>Sos</i>	0.507	0.0705
<i>Sulf1</i>	0.507	0.0705
<i>CG3339</i>	0.506	0.0712
<i>CG7966</i>	0.506	0.0712
<i>dao</i>	0.506	0.0712
<i>CG33061</i>	0.505	0.0714
<i>CG42330</i>	0.505	0.0714
<i>dpr11</i>	0.505	0.0714
<i>omd</i>	0.505	0.0714
<i>Or35a</i>	0.505	0.0714
<i>Pk61C</i>	0.505	0.0714
<i>SP1173</i>	0.505	0.0714
<i>bic</i>	0.504	0.0721
<i>CG10510</i>	0.504	0.0721
<i>CG18558</i>	0.504	0.0721
<i>CG31814</i>	0.504	0.0721
<i>gw</i>	0.504	0.0721
<i>pigs</i>	0.504	0.0721
<i>Snoo</i>	0.504	0.0721
<i>ATP7</i>	0.503	0.0727
<i>CG11752</i>	0.503	0.0727
<i>CG12213</i>	0.503	0.0727
<i>CG1907</i>	0.503	0.0727
<i>CG5882</i>	0.503	0.0727
<i>CG13877</i>	0.502	0.0732
<i>CG30268</i>	0.502	0.0732
<i>CG3253</i>	0.502	0.0732
<i>Or9a</i>	0.502	0.0732
<i>wek</i>	0.502	0.0732
<i>Adgf-E</i>	0.501	0.0736
<i>CG17364</i>	0.501	0.0736
<i>CG7102</i>	0.501	0.0736
<i>CG9883</i>	0.501	0.0736
<i>Ada1-2</i>	0.5	0.074
<i>CG12050</i>	0.5	0.074
<i>CG16941</i>	0.5	0.074
<i>CG3907</i>	0.5	0.074
<i>CG4562</i>	0.5	0.074
<i>CG5455</i>	0.5	0.074
<i>CG8683</i>	0.5	0.074
<i>Cyp4g1</i>	0.5	0.074
<i>Pp1-87B</i>	0.5	0.074
<i>CG10133</i>	0.499	0.0748
<i>CG14526</i>	0.499	0.0748
<i>CG17570</i>	0.499	0.0748
<i>Cyp1</i>	0.499	0.0748
<i>Cerk</i>	0.498	0.0751
<i>CG13049</i>	0.498	0.0751
<i>CG15161</i>	0.498	0.0751
<i>CG32564</i>	0.498	0.0751
<i>Sp3</i>	0.498	0.0751
<i>sug</i>	0.498	0.0751
<i>CG10543</i>	0.497	0.0757

Table 6.S21 Continued

Gene Name	ERC Value	P-value
CG10659	0.497	0.0757
CG1602	0.497	0.0757
CG6908	0.497	0.0757
Crz	0.497	0.0757
Nup154	0.497	0.0757
ppk12	0.497	0.0757
Rad9	0.497	0.0757
Tace	0.497	0.0757
TopIII	0.497	0.0757
wb	0.497	0.0757
CG13983	0.496	0.0767
CG34291	0.496	0.0767
ix	0.496	0.0767
sens	0.496	0.0767
Ac76E	0.495	0.077
CG6800	0.495	0.077
fidipidine	0.495	0.077
Patsas	0.495	0.077
alphaTub67C	0.494	0.0774
CG17029	0.494	0.0774
CG3119	0.494	0.0774
GABA-B-R1	0.494	0.0774
NK7.1	0.494	0.0774
oa2	0.494	0.0774
CG17930	0.493	0.0779
dream	0.493	0.0779
Rab35	0.493	0.0779
RPA2	0.493	0.0779
CG10062	0.492	0.0783
CG1124	0.492	0.0783
CG14709	0.491	0.0785
CG3434	0.491	0.0785
CG6201	0.491	0.0785
CG6923	0.491	0.0785
erm	0.491	0.0785
Fak56D	0.491	0.0785
GABPI	0.491	0.0785
MBD-like	0.491	0.0785
nimC4	0.491	0.0785
Oatp58Dc	0.491	0.0785
Ror	0.491	0.0785
Bin1	0.49	0.0795
CG17032	0.49	0.0795
CG4630	0.49	0.0795
CG6576	0.49	0.0795
Cpr	0.49	0.0795
GlcAT-P	0.49	0.0795
CG10301	0.489	0.08
CG13120	0.489	0.08
CG6985	0.489	0.08
CG7059	0.489	0.08
NPFR1	0.489	0.08
Atg4	0.487	0.0805
CG13390	0.487	0.0805
CG13581	0.487	0.0805
CG18744	0.487	0.0805

Gene Name	ERC Value	P-value
CG32442	0.487	0.0805
CG3690	0.487	0.0805
CG6656	0.487	0.0805
CG7735	0.487	0.0805
CG8600	0.487	0.0805
Trs23	0.487	0.0805
CG10681	0.486	0.0814
CG42686	0.486	0.0814
Ac78C	0.485	0.0815
CG12084	0.485	0.0815
CG13125	0.485	0.0815
CG42489	0.485	0.0815
CG5687	0.485	0.0815
ckd	0.485	0.0815
Tsp42Ep	0.485	0.0815
Tusp	0.485	0.0815
Atg13	0.484	0.0823
CG11796	0.484	0.0823
CG12316	0.484	0.0823
CG14015	0.484	0.0823
dyl	0.484	0.0823
Scs	0.484	0.0823
CG11349	0.483	0.0828
CG3548	0.483	0.0828
CG8248	0.483	0.0828
Cyp317a1	0.483	0.0828
Cad99C	0.482	0.0832
CG32226	0.482	0.0832
htt	0.482	0.0832
CG11168	0.481	0.0834
CG17184	0.481	0.0834
CG3790	0.481	0.0834
CG5849	0.481	0.0834
if	0.481	0.0834
wit	0.481	0.0834
Dgp-1	0.48	0.084
dpr20	0.48	0.084
CG30172	0.479	0.0841
CG3735	0.479	0.0841
CG6026	0.479	0.0841
serp	0.479	0.0841
SerT	0.479	0.0841
beat-Va	0.478	0.0846
CG10073	0.478	0.0846
CG10962	0.478	0.0846
CG11672	0.478	0.0846
CG31675	0.478	0.0846
CG41434	0.478	0.0846
CG7922	0.478	0.0846
Hsp67Bb	0.478	0.0846
ns4	0.478	0.0846
shf	0.478	0.0846
CG15147	0.477	0.0855
CG4537	0.477	0.0855
PH4alphaNE	0.477	0.0855
CG12341	0.476	0.0858

Gene Name	ERC Value	P-value
CG4653	0.476	0.0858
CG9215	0.476	0.0858
ldgf3	0.475	0.086
Mat89Ba	0.475	0.086
Rh6	0.475	0.086
CG14760	0.474	0.0863
CG16953	0.474	0.0863
CG5623	0.474	0.0863
CG6414	0.474	0.0863
CG6843	0.474	0.0863
Djp-B	0.474	0.0863
RpA-70	0.474	0.0863
CG32803	0.473	0.0869
CG4398	0.473	0.0869
CG9864	0.473	0.0869
al	0.472	0.0872
CG17019	0.472	0.0872
CG31321	0.472	0.0872
CG3621	0.472	0.0872
CG3759	0.472	0.0872
CG8813	0.472	0.0872
CG13285	0.471	0.0877
CG15254	0.471	0.0877
CG4325	0.471	0.0877
CG6761	0.471	0.0877
Sc2	0.471	0.0877
CG10035	0.47	0.0882
CG33786	0.47	0.0882
CG4996	0.47	0.0882
lr7c	0.47	0.0882
jhamt	0.47	0.0882
tok	0.47	0.0882
CG10051	0.469	0.0887
CG18581	0.469	0.0887
CG30502	0.469	0.0887
CG7328	0.469	0.0887
fy	0.469	0.0887
Gr10a	0.469	0.0887
Mad	0.469	0.0887
Ast	0.468	0.0894
Gdh	0.468	0.0894
Rab7	0.468	0.0894
RpS5a	0.468	0.0894
CG13192	0.467	0.0897
CG8891	0.467	0.0897
DNApol-delta	0.467	0.0897
Gr58b	0.467	0.0897
ifc	0.467	0.0897
iotaTry	0.467	0.0897
nord	0.467	0.0897
Pbp45	0.467	0.0897
scro	0.467	0.0897
CG13473	0.466	0.0905
CG31005	0.466	0.0905
CG34408	0.466	0.0905
CG5705	0.466	0.0905

Gene Name	ERC Value	P-value
CG5830	0.466	0.0905
Lcp65Ac	0.466	0.0905
nimC2	0.466	0.0905
Oat	0.466	0.0905
CG4991	0.465	0.0913
Gr97a	0.465	0.0913
Med	0.465	0.0913
CG31224	0.464	0.0915
CG32668	0.464	0.0915
CG8784	0.464	0.0915
Him	0.464	0.0915
Npc2c	0.464	0.0915
CG11367	0.463	0.092
CG18249	0.463	0.092
Pc	0.463	0.092
s-cup	0.463	0.092
Sply	0.463	0.092
TyrR	0.463	0.092
CG10137	0.462	0.0925
CG15754	0.462	0.0925
CG18031	0.462	0.0925
Hml	0.462	0.0925
lack	0.462	0.0925
CG12177	0.461	0.093
CG13957	0.461	0.093
CG14650	0.461	0.093
CG14815	0.461	0.093
CG15922	0.461	0.093
H	0.461	0.093
CG15412	0.46	0.0935
CG17337	0.46	0.0935
CG18659	0.46	0.0935
CG4615	0.46	0.0935
CG5783	0.46	0.0935
CG7597	0.46	0.0935
Cyp6d2	0.46	0.0935
AlkB	0.459	0.0941
CG12512	0.459	0.0941
CG16734	0.459	0.0941
CG3769	0.459	0.0941
Tm-SR	0.459	0.0941
CG7839	0.458	0.0946
CG9914	0.458	0.0946
gho	0.458	0.0946
mRps33	0.458	0.0946
ca	0.457	0.095
CG12011	0.457	0.095
CG14072	0.457	0.095
CG17083	0.457	0.095
ssp2	0.457	0.095
CG13282	0.456	0.0954
CG13539	0.456	0.0954
Gip	0.456	0.0954
CG34247	0.455	0.0957
CG4301	0.455	0.0957
CG4329	0.455	0.0957

Gene Name	ERC Value	P-value
CG5611	0.455	0.0957
CG9452	0.455	0.0957
CG14598	0.454	0.0961
CG31021	0.454	0.0961
CG42509	0.454	0.0961
CG8072	0.454	0.0961
GABA-B-R2	0.454	0.0961
mask	0.454	0.0961
oys	0.454	0.0961
CG13463	0.453	0.0968
CG13705	0.453	0.0968
CG16789	0.453	0.0968
CtrlB	0.453	0.0968
dpp	0.453	0.0968
stj	0.453	0.0968
bay	0.452	0.0973
CG16884	0.452	0.0973
CG17664	0.452	0.0973
CG34199	0.452	0.0973
CG42511	0.452	0.0973
MED25	0.452	0.0973
Su(z)2	0.452	0.0973
zetaTry	0.452	0.0973
CG2177	0.451	0.098
CG2604	0.451	0.098
CG9961	0.451	0.098
Bap170	0.45	0.0983
CG13857	0.45	0.0983
CG15019	0.45	0.0983
CG15202	0.45	0.0983
Lig4	0.45	0.0983
CG7510	0.449	0.0987
E23	0.449	0.0987
fab1	0.449	0.0987
Pi3K21B	0.449	0.0987
sec15	0.449	0.0987
CG13795	0.448	0.0992
CG15553	0.448	0.0992
CheB42c	0.448	0.0992
Hr38	0.448	0.0992
Or46a	0.448	0.0992
Oseg4	0.448	0.0992
Bub3	0.447	0.0997
CG2059	0.447	0.0997
CG31105	0.447	0.0997
CG31125	0.447	0.0997
CG31731	0.447	0.0997
CG4945	0.447	0.0997
CG6564	0.447	0.0997
tam	0.447	0.0997

Table 6.S22 - Top Genes ERC values for *trem* arranged by largest ERC value. “Bait” genes and candidate genes are shaded in grey as well as bolded.

Gene Name	ERC Value	P-value
CG31815	0.908	0.0001
<i>l(2)05714</i>	0.894	0.0002
Nnfta	0.893	0.0003
CG18806	0.883	0.0004
CG7372	0.878	0.0005
CG31365	0.875	0.0005
<i>Tim17b1</i>	0.873	0.0006
<i>Map60</i>	0.864	0.0007
CG30020	0.862	0.0008
CG6745	0.86	0.0009
CG1792	0.859	0.001
CG12299	0.855	0.0011
CG30008	0.855	0.0011
CG15116	0.853	0.0013
CG31682	0.853	0.0013
<i>fog</i>	0.853	0.0013
CG18011	0.844	0.0015
CG10588	0.843	0.0016
<i>hkb</i>	0.842	0.0017
<i>Saf-B</i>	0.839	0.0018
CG18234	0.836	0.0019
<i>pcs</i>	0.836	0.0019
<i>Ndc80</i>	0.834	0.0021
CG11778	0.829	0.0022
<i>xmas-2</i>	0.825	0.0023
CG2712	0.824	0.0023
CG8677	0.824	0.0023
<i>Dpy-30L1</i>	0.822	0.0025
CG15172	0.821	0.0026
<i>Hsp67Ba</i>	0.821	0.0026
<i>mRpl14</i>	0.821	0.0026
<i>Dip-C</i>	0.819	0.0029
<i>lfp1</i>	0.819	0.0029
<i>lr56a</i>	0.818	0.0031
<i>icln</i>	0.812	0.0032
CG6325	0.808	0.0032
CG13802	0.806	0.0033
<i>Su(z)12</i>	0.806	0.0033
CG15130	0.804	0.0035
<i>Grip75</i>	0.8	0.0036
CG30466	0.799	0.0037
CG4587	0.799	0.0037
CG7069	0.799	0.0037
CG9879	0.797	0.004
<i>Kaz1-ORFB</i>	0.797	0.004
<i>Ser8</i>	0.797	0.004
CG5180	0.796	0.0042
CG7789	0.795	0.0043
CG17802	0.794	0.0044
CG8501	0.793	0.0045
<i>ds</i>	0.791	0.0046
<i>Su(var)2-HP</i>	0.791	0.0046
CG10399	0.789	0.0048
CG17691	0.789	0.0048
<i>Cpr47Ed</i>	0.788	0.005
CG15035	0.783	0.005

Gene Name	ERC Value	P-value
CG2694	0.783	0.005
<i>Taspase1</i>	0.783	0.005
<i>zpg</i>	0.783	0.005
<i>Prosbeta3</i>	0.781	0.0054
dm	0.78	0.0055
CG14715	0.779	0.0056
CG3223	0.779	0.0056
CG42399	0.779	0.0056
CG32803	0.778	0.0059
CG9804	0.778	0.0059
FLASH	0.778	0.0059
ZC3H3	0.778	0.0059
<i>cav</i>	0.777	0.0062
CG12206	0.775	0.0063
CG6418	0.775	0.0063
CG2162	0.774	0.0065
<i>glob3</i>	0.772	0.0066
<i>alpha4GT1</i>	0.771	0.0067
<i>Aeff1</i>	0.77	0.0068
CG15571	0.769	0.0068
CG9839	0.769	0.0068
<i>Sym</i>	0.769	0.0068
CG14906	0.768	0.0071
<i>KalRIA</i>	0.767	0.0072
CG15435	0.765	0.0073
CG17490	0.765	0.0073
<i>Galpha73B</i>	0.765	0.0073
CG2975	0.763	0.0076
<i>Sulf1</i>	0.76	0.0077
CG12104	0.758	0.0077
CG2807	0.758	0.0077
CG9004	0.758	0.0077
<i>beat-lb</i>	0.756	0.008
CG15443	0.754	0.0081
CG6136	0.754	0.0081
CG6254	0.754	0.0081
<i>EloA</i>	0.754	0.0081
<i>Spargel</i>	0.754	0.0081
CG6568	0.753	0.0086
CG9426	0.752	0.0086
<i>Dg</i>	0.752	0.0086
<i>sba</i>	0.752	0.0086
CG7265	0.751	0.0089
<i>zwilch</i>	0.75	0.009
CG6838	0.748	0.0091
CG1311	0.747	0.0092
CG34045	0.747	0.0092
<i>Arp5</i>	0.746	0.0094
CG3651	0.746	0.0094
CG4892	0.746	0.0094
CG32343	0.745	0.0096
CG14341	0.744	0.0097
<i>LSm7</i>	0.744	0.0097
CG8116	0.743	0.0099
CG12316	0.742	0.01
CG2091	0.742	0.01

Gene Name	ERC Value	P-value
CG8100	0.741	0.0102
<i>Ptp52F</i>	0.741	0.0102
CG6024	0.739	0.0104
<i>BtbVII</i>	0.738	0.0105
CG4936	0.738	0.0105
CG30440	0.736	0.0106
<i>Pink1</i>	0.736	0.0106
CG15482	0.735	0.0108
<i>Psi</i>	0.735	0.0108
<i>HLHmdelta</i>	0.732	0.011
CG14882	0.731	0.0111
CG33695	0.731	0.0111
<i>Pp2B-14D</i>	0.731	0.0111
<i>Snp</i>	0.731	0.0111
<i>bs</i>	0.73	0.0114
CG7692	0.73	0.0114
CG1983	0.729	0.0116
CG14650	0.729	0.0116
<i>SeifR</i>	0.728	0.0118
CG3281	0.727	0.0119
CG12134	0.726	0.012
<i>RhoGAP18E</i>	0.724	0.0121
CG14711	0.722	0.0122
CG8408	0.722	0.0122
<i>Ge-1</i>	0.722	0.0122
<i>glic</i>	0.721	0.0124
<i>Spn42Db</i>	0.721	0.0124
<i>Ptp45</i>	0.72	0.0126
<i>CCKLR-17D</i>	0.719	0.0127
<i>La</i>	0.719	0.0127
<i>ns3</i>	0.719	0.0127
CG11109	0.718	0.013
CG13375	0.718	0.013
<i>ix</i>	0.718	0.013
CG42258	0.717	0.0132
CG9053	0.717	0.0132
CG13454	0.716	0.0134
<i>DNApol-gam</i>	0.716	0.0134
<i>Or65a</i>	0.716	0.0134
<i>sad</i>	0.716	0.0134
CG12126	0.715	0.0138
CG17724	0.715	0.0138
<i>sina</i>	0.715	0.0138
CG3292	0.714	0.0141
CG8366	0.714	0.0141
<i>fs(1)N</i>	0.713	0.0142
Kmnl1	0.713	0.0142
<i>sax</i>	0.713	0.0142
<i>Spc105R</i>	0.713	0.0142
<i>dUTPase</i>	0.712	0.0146
<i>nimB5</i>	0.711	0.0147
CG12432	0.71	0.0148
CG8960	0.71	0.0148
CG9776	0.708	0.015
CG9673	0.707	0.015
mus301	0.707	0.015

Gene Name	ERC Value	P-value
CG32541	0.706	0.0152
<i>MSBP</i>	0.706	0.0152
<i>sd</i>	0.706	0.0152
<i>bip1</i>	0.705	0.0155
CG10947	0.705	0.0155
CG4462	0.705	0.0155
<i>CTCF</i>	0.705	0.0155
<i>Cdc6</i>	0.704	0.0159
CG4374	0.704	0.0159
<i>Nhe3</i>	0.704	0.0159
<i>RhoGAP19C</i>	0.704	0.0159
CG7082	0.703	0.0162
CG11882	0.702	0.0163
<i>dpr2</i>	0.701	0.0164
<i>Abi</i>	0.7	0.0165
CG3301	0.7	0.0165
CG4612	0.7	0.0165
<i>HLH106</i>	0.7	0.0165
<i>Cas</i>	0.699	0.0168
ft	0.699	0.0168
<i>Spn43Ad</i>	0.699	0.0168
CG11377	0.697	0.0171
CG12420	0.697	0.0171
CG16957	0.697	0.0171
CG3305	0.697	0.0171
<i>fax</i>	0.697	0.0171
<i>CycA</i>	0.696	0.0176
<i>Tsp42E1</i>	0.696	0.0176
CG16863	0.695	0.0177
CG5924	0.695	0.0177
CG14618	0.694	0.0179
CG30403	0.694	0.0179
<i>Su(Tp1)</i>	0.694	0.0179
CG15236	0.692	0.0182
<i>Tbp-1</i>	0.692	0.0182
CG11762	0.691	0.0184
<i>Prosbeta7</i>	0.691	0.0184
CG34116	0.69	0.0186
<i>pnr</i>	0.69	0.0186
CG10077	0.689	0.0187
CG10274	0.689	0.0187
<i>l(2)k09022</i>	0.689	0.0187
CG15376	0.687	0.019
<i>Drop-3</i>	0.686	0.0191
CG2931	0.685	0.0192
<i>E(spl)</i>	0.685	0.0192
mei-9	0.685	0.0192
CG33178	0.684	0.0195
<i>Oatp58Da</i>	0.684	0.0195
CG1315	0.682	0.0196
<i>sob</i>	0.682	0.0196
CG30046	0.681	0.0198
<i>BubR1</i>	0.68	0.0199
<i>Ca-alpha1D</i>	0.68	0.0199
CG34012	0.68	0.0199
<i>Rad51D</i>	0.68	0.0199

Gene Name	ERC Value	P-value
<i>ald</i>	0.679	0.0203
<i>beat-11b</i>	0.679	0.0203
<i>CdsA</i>	0.679	0.0203
CG10669	0.679	0.0203
<i>CycK</i>	0.679	0.0203
<i>Sdc</i>	0.679	0.0203
<i>TllEalpha</i>	0.678	0.0208
CG10075	0.677	0.0209
CG34148	0.677	0.0209
CG5746	0.677	0.0209
<i>jub</i>	0.677	0.0209
<i>mei-P26</i>	0.677	0.0209
<i>wgn</i>	0.677	0.0209
CG4004	0.676	0.0214
CG8159	0.676	0.0214
CG9147	0.676	0.0214
CG9592	0.674	0.0217
<i>Hpr1</i>	0.673	0.0218
CG13897	0.672	0.0219
<i>dbo</i>	0.672	0.0219
<i>Git</i>	0.672	0.0219
mei-41	0.672	0.0219
<i>Anxb11</i>	0.671	0.0223
CG42374	0.67	0.0223
CG8191	0.67	0.0223
CG10424	0.669	0.0225
<i>ct</i>	0.668	0.0226
<i>beat-1a</i>	0.667	0.0227
<i>B-H2</i>	0.666	0.0228
CG13287	0.666	0.0228
CG14085	0.666	0.0228
CG16743	0.666	0.0228
CG10462	0.665	0.0232
<i>cmet</i>	0.664	0.0232
<i>Gr9a</i>	0.664	0.0232
<i>kto</i>	0.664	0.0232
CG12680	0.663	0.0235
CG17068	0.663	0.0235
CG8641	0.663	0.0235
CG12693	0.662	0.0238
CG31211	0.662	0.0238
CG14647	0.661	0.024
CG18262	0.661	0.024
CG8027	0.661	0.024
<i>mRpl34</i>	0.661	0.024
<i>Nlp</i>	0.661	0.024
<i>Nplp1</i>	0.661	0.024
<i>Su(var)2-10</i>	0.661	0.024
CG31600	0.66	0.0246
CG12012	0.657	0.0247
CG14274	0.657	0.0247
CG3191	0.657	0.0247
<i>MED4</i>	0.657	0.0247
CG14749	0.656	0.025
CG15322	0.656	0.025
CG7837	0.656	0.025

Table 6.S22 Continued

Gene Name	ERC Value	P-value
<i>Dref</i>	0.656	0.025
<i>H2.0</i>	0.656	0.025
<i>CG14562</i>	0.655	0.0255
<i>CG32685</i>	0.655	0.0255
<i>CG14718</i>	0.654	0.0257
<i>CG14803</i>	0.654	0.0257
<i>E5</i>	0.654	0.0257
<i>Dip3</i>	0.653	0.0259
<i>spen</i>	0.653	0.0259
<i>Pros25</i>	0.652	0.0261
<i>Ssl1</i>	0.652	0.0261
<i>corn</i>	0.651	0.0263
<i>CG12307</i>	0.65	0.0264
<i>CG2182</i>	0.65	0.0264
<i>CG6808</i>	0.65	0.0264
<i>Pros26</i>	0.65	0.0264
<i>CG13745</i>	0.649	0.0268
<i>CG16970</i>	0.649	0.0268
<i>CG18265</i>	0.649	0.0268
<i>CG34033</i>	0.649	0.0268
<i>CG31053</i>	0.648	0.0271
<i>CG9542</i>	0.648	0.0271
<i>Mif</i>	0.648	0.0271
<i>RplL34a</i>	0.648	0.0271
<i>CG2813</i>	0.647	0.0275
<i>CG5399</i>	0.647	0.0275
<i>CG6230</i>	0.647	0.0275
<i>DNApol-αph</i>	0.647	0.0275
<i>pad</i>	0.646	0.0278
<i>CG10732</i>	0.645	0.0279
<i>CG15418</i>	0.645	0.0279
<i>CG7849</i>	0.645	0.0279
<i>Ric</i>	0.645	0.0279
<i>Rrp46</i>	0.645	0.0279
<i>CG14302</i>	0.643	0.0284
<i>CG1513</i>	0.643	0.0284
<i>CG7065</i>	0.643	0.0284
<i>iHog</i>	0.643	0.0284
<i>Spf45</i>	0.642	0.0287
<i>CG11070</i>	0.641	0.0288
<i>CG7407</i>	0.641	0.0288
<i>Ranbp9</i>	0.641	0.0288
<i>a6</i>	0.64	0.0291
<i>CG14937</i>	0.64	0.0291
<i>CG9691</i>	0.64	0.0291
<i>rod</i>	0.64	0.0291
<i>CG13982</i>	0.639	0.0295
<i>pkf</i>	0.638	0.0295
<i>X11L</i>	0.638	0.0295
<i>CG7911</i>	0.637	0.0297
<i>SC35</i>	0.636	0.0298
<i>sna</i>	0.636	0.0298
<i>CG33229</i>	0.635	0.03
<i>mth5</i>	0.635	0.03
<i>sp</i>	0.635	0.03
<i>CG4607</i>	0.634	0.0303

Gene Name	ERC Value	P-value
<i>phol</i>	0.634	0.0303
<i>CG1832</i>	0.633	0.0305
<i>CG9247</i>	0.633	0.0305
<i>slim</i>	0.633	0.0305
<i>CG1344</i>	0.632	0.0307
<i>CG11263</i>	0.631	0.0308
<i>CHES-1-like</i>	0.631	0.0308
<i>Cks85A</i>	0.631	0.0308
<i>pie</i>	0.631	0.0308
<i>CG13405</i>	0.63	0.0312
<i>GluRIIA</i>	0.63	0.0312
<i>CG13386</i>	0.628	0.0314
<i>CG3631</i>	0.628	0.0314
<i>CstF-50</i>	0.628	0.0314
<i>GluRIIE</i>	0.628	0.0314
<i>tud</i>	0.628	0.0314
<i>CG1074</i>	0.627	0.0318
<i>CG14667</i>	0.627	0.0318
<i>CG4785</i>	0.627	0.0318
<i>Ccap</i>	0.625	0.0321
<i>CG12439</i>	0.625	0.0321
<i>CG13539</i>	0.625	0.0321
<i>CG32635</i>	0.625	0.0321
<i>CG3386</i>	0.625	0.0321
<i>fil</i>	0.625	0.0321
<i>pck</i>	0.625	0.0321
<i>CG6523</i>	0.624	0.0327
<i>CG11906</i>	0.623	0.0328
<i>CG13377</i>	0.623	0.0328
<i>CG32006</i>	0.622	0.033
<i>Rpn11</i>	0.622	0.033
<i>stil</i>	0.622	0.033
<i>BEAF-32</i>	0.621	0.0332
<i>CG10249</i>	0.621	0.0332
<i>Pep</i>	0.621	0.0332
<i>CG31224</i>	0.62	0.0335
<i>CG6480</i>	0.62	0.0335
<i>mitf(1)15</i>	0.62	0.0335
<i>CG14050</i>	0.619	0.0338
<i>Jon44E</i>	0.619	0.0338
<i>pds5</i>	0.619	0.0338
<i>Tob</i>	0.619	0.0338
<i>CG10324</i>	0.618	0.0341
<i>CG13148</i>	0.618	0.0341
<i>CG14823</i>	0.618	0.0341
<i>CG15643</i>	0.618	0.0341
<i>CG6739</i>	0.618	0.0341
<i>D19A</i>	0.618	0.0341
<i>l(2)37Ce</i>	0.618	0.0341
<i>Not1</i>	0.618	0.0341
<i>Nuf2</i>	0.618	0.0341
<i>RhoL</i>	0.618	0.0341
<i>unc-4</i>	0.618	0.0341
<i>beat-lla</i>	0.617	0.0351
<i>CG6230</i>	0.617	0.0351
<i>CG9609</i>	0.617	0.0351

Gene Name	ERC Value	P-value
<i>Det</i>	0.617	0.0351
<i>lppy</i>	0.617	0.0351
<i>m4</i>	0.617	0.0351
<i>CG3542</i>	0.616	0.0357
<i>Cp190</i>	0.616	0.0357
<i>sowah</i>	0.616	0.0357
<i>CG13717</i>	0.615	0.0359
<i>CG32536</i>	0.615	0.0359
<i>CG8485</i>	0.614	0.0361
<i>CG34360</i>	0.613	0.0362
<i>ato</i>	0.612	0.0363
<i>CG33489</i>	0.612	0.0363
<i>Sfmbt</i>	0.612	0.0363
<i>CG11418</i>	0.611	0.0366
<i>CG12278</i>	0.611	0.0366
<i>CG31646</i>	0.611	0.0366
<i>CG9418</i>	0.611	0.0366
<i>Asx</i>	0.61	0.0369
<i>CG6700</i>	0.61	0.0369
<i>HLHm3</i>	0.61	0.0369
<i>Rpn7</i>	0.61	0.0369
<i>Aly</i>	0.609	0.0373
<i>CG12507</i>	0.609	0.0373
<i>CG9894</i>	0.609	0.0373
<i>cnk</i>	0.609	0.0373
<i>ara</i>	0.608	0.0377
<i>CG1602</i>	0.608	0.0377
<i>CG18811</i>	0.608	0.0377
<i>CG32791</i>	0.608	0.0377
<i>wde</i>	0.608	0.0377
<i>CG2083</i>	0.607	0.0381
<i>CG10107</i>	0.606	0.0382
<i>CG5895</i>	0.606	0.0382
<i>elF3-S8</i>	0.606	0.0382
<i>Fbw5</i>	0.606	0.0382
<i>run</i>	0.606	0.0382
<i>sced</i>	0.606	0.0382
<i>hop</i>	0.604	0.0387
<i>Mtr3</i>	0.604	0.0387
<i>rump</i>	0.604	0.0387
<i>CG18812</i>	0.603	0.039
<i>CG34186</i>	0.602	0.0391
<i>CG4338</i>	0.602	0.0391
<i>CG4557</i>	0.602	0.0391
<i>Sap130</i>	0.602	0.0391
<i>CG8141</i>	0.601	0.0395
<i>san</i>	0.601	0.0395
<i>Su(H)</i>	0.601	0.0395
<i>CG9386</i>	0.6	0.0397
<i>ths</i>	0.6	0.0397
<i>Tango7</i>	0.599	0.0399
<i>CG13725</i>	0.598	0.04
<i>CG15514</i>	0.598	0.04
<i>CG15817</i>	0.598	0.04
<i>CG4452</i>	0.598	0.04
<i>CG5214</i>	0.598	0.04

Gene Name	ERC Value	P-value
<i>Magi</i>	0.598	0.04
<i>Sox100B</i>	0.598	0.04
<i>c(2)M</i>	0.597	0.0406
<i>CG6621</i>	0.597	0.0406
<i>eyg</i>	0.597	0.0406
<i>ash1</i>	0.596	0.0409
<i>CG3611</i>	0.596	0.0409
<i>RhoGAP100</i>	0.596	0.0409
<i>Syt12</i>	0.596	0.0409
<i>Vsx2</i>	0.596	0.0409
<i>CG1358</i>	0.595	0.0414
<i> fend</i>	0.595	0.0414
<i>mRpL21</i>	0.595	0.0414
<i>CG15634</i>	0.594	0.0416
<i>CG4424</i>	0.594	0.0416
<i>CG4820</i>	0.594	0.0416
<i>CG9125</i>	0.594	0.0416
<i> dbr</i>	0.594	0.0416
<i>fz4</i>	0.594	0.0416
<i>shu</i>	0.594	0.0416
<i>CG14109</i>	0.593	0.0423
<i>CG14710</i>	0.593	0.0423
<i>CG15522</i>	0.593	0.0423
<i>CG7914</i>	0.592	0.0425
<i>nAcRbeta-2</i>	0.592	0.0425
<i>CG11889</i>	0.591	0.0427
<i>CG5515</i>	0.591	0.0427
<i>Pci</i>	0.591	0.0427
<i>tomb</i>	0.591	0.0427
<i>Ets96B</i>	0.59	0.0431
<i>Jumu</i>	0.59	0.0431
<i>RanBP3</i>	0.59	0.0431
<i>Roc1b</i>	0.59	0.0431
<i>CG1394</i>	0.589	0.0434
<i>pzg</i>	0.589	0.0434
<i>Rpb4</i>	0.589	0.0434
<i>skpB</i>	0.589	0.0434
<i>SFPoCk</i>	0.589	0.0434
<i>CG34140</i>	0.588	0.0439
<i>dwg</i>	0.588	0.0439
<i>Klp31E</i>	0.588	0.0439
<i>Lip1</i>	0.588	0.0439
<i>pico</i>	0.588	0.0439
<i>ppk7</i>	0.588	0.0439
<i>Rpn9</i>	0.588	0.0439
<i>CG32281</i>	0.587	0.0445
<i>CG7786</i>	0.587	0.0445
<i>Jon74E</i>	0.586	0.0447
<i>CG42404</i>	0.585	0.0448
<i>CG5726</i>	0.585	0.0448
<i>CG8089</i>	0.585	0.0448
<i>CG8920</i>	0.585	0.0448
<i>Coq2</i>	0.585	0.0448
<i>dre4</i>	0.585	0.0448
<i>CG14442</i>	0.584	0.0453
<i>CG3558</i>	0.584	0.0453

Gene Name	ERC Value	P-value
<i>CG5823</i>	0.584	0.0453
<i>CG6847</i>	0.584	0.0453
<i>zen</i>	0.584	0.0453
<i>CG14036</i>	0.583	0.0458
<i>CG14057</i>	0.583	0.0458
<i>CG14570</i>	0.583	0.0458
<i>CG18065</i>	0.583	0.0458
<i>MTA1-like</i>	0.583	0.0458
<i>Rb97D</i>	0.583	0.0458
<i>bsh</i>	0.582	0.0463
<i>CG10713</i>	0.582	0.0463
<i>CG13476</i>	0.582	0.0463
<i>CG17181</i>	0.581	0.0466
<i>CG9279</i>	0.581	0.0466
<i>Mih1</i>	0.581	0.0466
<i>CG13362</i>	0.58	0.0468
<i>CG8001</i>	0.58	0.0468
<i>cuff</i>	0.58	0.0468
<i>lr54a</i>	0.58	0.0468
<i>l(3)psg2</i>	0.58	0.0468
<i>mRpS30</i>	0.58	0.0468
<i>Ac3</i>	0.579	0.0474
<i>CG10265</i>	0.579	0.0474
<i>CG11985</i>	0.579	0.0474
<i>CG42353</i>	0.579	0.0474
<i>HP1c</i>	0.579	0.0474
<i>CG10741</i>	0.578	0.0478
<i>CG32732</i>	0.578	0.0478
<i>CG7427</i>	0.578	0.0478
<i>Dcr-1</i>	0.578	0.0478
<i>lr67c</i>	0.578	0.0478
<i>lat</i>	0.578	0.0478
<i>Obp59a</i>	0.578	0.0478
<i>Obp8a</i>	0.578	0.0478
<i>Tsp</i>	0.578	0.0478
<i>CG10418</i>	0.577	0.0486
<i>CG32712</i>	0.577	0.0486
<i>CG34284</i>	0.577	0.0486
<i>CG6511</i>	0.577	0.0486
<i>RIC-3</i>	0.577	0.0486
<i>CG11155</i>	0.576	0.0491
<i>CG34039</i>	0.576	0.0491
<i>CG42817</i>	0.576	0.0491
<i>Cyp28a5</i>	0.576	0.0491
<i>cenB1A</i>	0.575	0.0495
<i>CG14834</i>	0.575	0.0495
<i>CG31326</i>	0.575	0.0495
<i>CG32846</i>	0.575	0.0495
<i>CG3808</i>	0.575	0.0495
<i>CG4996</i>	0.575	0.0495
<i>CG32246</i>	0.574	0.05
CG7597	0.574	0.05
<i>CG6301</i>	0.574	0.05
<i>Jhl-21</i>	0.574	0.05
<i>Traf6</i>	0.574	0.05
<i>blue</i>	0.573	0.0505

Table 6.S22 Continued

Gene Name	ERC Value	P-value
CG4676	0.573	0.0505
Cyp305a1	0.573	0.0505
mus205	0.573	0.0505
Cdk7	0.572	0.0508
CG10561	0.572	0.0508
CG42358	0.572	0.0508
ear	0.572	0.0508
PNUTS	0.572	0.0508
SIDL	0.572	0.0508
beta4GalNA4	0.571	0.0514
CG13424	0.571	0.0514
CG3744	0.571	0.0514
Pthh	0.571	0.0514
CG14607	0.57	0.0517
kek5	0.57	0.0517
CG10055	0.569	0.0519
CG7461	0.569	0.0519
Fs	0.569	0.0519
CG32354	0.568	0.0522
CG8273	0.568	0.0522
CG8915	0.568	0.0522
Illl	0.568	0.0522
CG5265	0.567	0.0525
CG7889	0.567	0.0525
Cpr76Ba	0.567	0.0525
DNApol-alpha	0.567	0.0525
CG14450	0.566	0.0529
CG6470	0.566	0.0529
cid	0.566	0.0529
Klp67A	0.566	0.0529
Uba2	0.566	0.0529
blos3	0.565	0.0533
CG12007	0.565	0.0533
CG4658	0.565	0.0533
Ppt2	0.565	0.0533
PR2	0.565	0.0533
CG8690	0.564	0.0538
Cyp4ae1	0.564	0.0538
Gpi1	0.564	0.0538
hkl	0.564	0.0538
Sirt7	0.564	0.0538
Vps33B	0.564	0.0538
CG31371	0.563	0.0543
CG3838	0.563	0.0543
CG3939	0.563	0.0543
CG5098	0.563	0.0543
CG7510	0.563	0.0543
CG14238	0.562	0.0548
CG34296	0.562	0.0548
CG5585	0.562	0.0548
CG30157	0.561	0.055
CG33641	0.561	0.055
CG8209	0.561	0.055
RhoGAP5A	0.561	0.055
yl	0.561	0.055
CG10177	0.56	0.0555

Gene Name	ERC Value	P-value
CG9437	0.56	0.0555
Mrtf	0.56	0.0555
Rrp4	0.56	0.0555
Best3	0.559	0.0559
CG17658	0.559	0.0559
Drep-2	0.559	0.0559
l(3)j2D3	0.559	0.0559
Rpb5	0.559	0.0559
Stam	0.559	0.0559
toe	0.559	0.0559
CG10098	0.558	0.0565
CG11248	0.558	0.0565
CG32088	0.558	0.0565
CG4707	0.558	0.0565
CG8959	0.558	0.0565
Elo68beta	0.558	0.0565
Rga	0.557	0.057
AP-1gamma	0.556	0.0571
CG14177	0.556	0.0571
CG18599	0.556	0.0571
CG5255	0.556	0.0571
CG7879	0.556	0.0571
Dot	0.556	0.0571
CG1271	0.555	0.0577
CG7650	0.555	0.0577
CG8298	0.555	0.0577
CG11660	0.554	0.0579
CG15093	0.554	0.0579
CG16790	0.554	0.0579
CG8370	0.554	0.0579
opa1-like	0.554	0.0579
Rrp42	0.554	0.0579
TllIFbeta	0.554	0.0579
CG12075	0.553	0.0586
CG8316	0.553	0.0586
Rab7	0.553	0.0586
CG14511	0.552	0.0588
CG9992	0.552	0.0588
Fancd2	0.552	0.0588
Mat1	0.552	0.0588
Pph13	0.552	0.0588
seq	0.552	0.0588
CG10428	0.551	0.0594
CG10465	0.551	0.0594
CG4198	0.551	0.0594
gp210	0.551	0.0594
CG13999	0.55	0.0597
CG14717	0.55	0.0597
CG4810	0.55	0.0597
CG7685	0.55	0.0597
l(3)04053	0.55	0.0597
scpr-C	0.55	0.0597
Tsp42Ea	0.55	0.0597
CG5955	0.549	0.0604
CG7526	0.549	0.0604
Cpr72Ea	0.549	0.0604

Gene Name	ERC Value	P-value
mus81	0.549	0.0604
Tsp97E	0.549	0.0604
CG10459	0.548	0.0608
CG10830	0.548	0.0608
CG12182	0.548	0.0608
CG31688	0.548	0.0608
CG31935	0.548	0.0608
CG32479	0.548	0.0608
CG34313	0.548	0.0608
phf	0.548	0.0608
heix	0.547	0.0615
mei-S332	0.547	0.0615
CG10581	0.546	0.0617
CG3626	0.546	0.0617
pll	0.546	0.0617
RrpS1	0.546	0.0617
CG15317	0.545	0.0621
CG3532	0.545	0.0621
CG6950	0.545	0.0621
Drep-4	0.545	0.0621
CG10877	0.544	0.0624
Rassf	0.544	0.0624
CG14930	0.543	0.0626
CG17807	0.543	0.0626
CG32772	0.543	0.0626
CG42569	0.543	0.0626
CG8180	0.543	0.0626
rec	0.543	0.0626
cg	0.542	0.0632
CG11378	0.542	0.0632
CG14540	0.542	0.0632
CG1737	0.542	0.0632
ksr	0.542	0.0632
Taf11	0.542	0.0632
CG13306	0.541	0.0637
CG17928	0.541	0.0637
CG9801	0.541	0.0637
Pros35	0.541	0.0637
CG10131	0.54	0.0641
CG5860	0.54	0.0641
cro1	0.54	0.0641
gfzf	0.54	0.0641
Pros54	0.54	0.0641
beat-VI	0.539	0.0645
CG12929	0.539	0.0645
CG40191	0.539	0.0645
Chrac-14	0.539	0.0645
DNApol-eta	0.539	0.0645
osk	0.539	0.0645
Proc-R	0.539	0.0645
CG7139	0.538	0.0651
Klp61F	0.538	0.0651
l(2)09851	0.538	0.0651
Sox15	0.538	0.0651
Tsp42Ef	0.538	0.0651
cact	0.537	0.0656

Gene Name	ERC Value	P-value
CG1234	0.537	0.0656
CG4678	0.537	0.0656
CG6540	0.537	0.0656
pps	0.537	0.0656
stnB	0.537	0.0656
CG12105	0.536	0.0661
CG12582	0.536	0.0661
CG17562	0.536	0.0661
CG31221	0.536	0.0661
CG3194	0.536	0.0661
CG3812	0.536	0.0661
CG6972	0.536	0.0661
mus101	0.536	0.0661
CG12990	0.535	0.0668
CG30001	0.535	0.0668
CG10321	0.534	0.067
CG10924	0.534	0.067
CG11560	0.534	0.067
CG31698	0.534	0.067
CG31787	0.534	0.067
CG7028	0.534	0.067
Chro	0.534	0.067
NK7.1	0.534	0.067
CG7049	0.533	0.0677
CG8490	0.533	0.0677
Cyp28d1	0.533	0.0677
CG14132	0.532	0.068
CG6142	0.532	0.068
CG7627	0.532	0.068
mtacp1	0.532	0.068
CG11723	0.531	0.0684
CG14722	0.531	0.0684
CG9300	0.531	0.0684
polybromo	0.531	0.0684
Scr	0.531	0.0684
CG17266	0.53	0.0688
CG31777	0.53	0.0688
CG32982	0.53	0.0688
CG5510	0.53	0.0688
CG6409	0.53	0.0688
CG7739	0.53	0.0688
CG11970	0.529	0.0694
CG13500	0.529	0.0694
CG6734	0.529	0.0694
llp5	0.529	0.0694
Nup107	0.529	0.0694
wit	0.529	0.0694
Bin1	0.528	0.0699
CG11412	0.528	0.0699
CG13376	0.528	0.0699
CG8312	0.528	0.0699
CG8550	0.528	0.0699
dx	0.528	0.0699
mnf1	0.528	0.0699
qkr58E-2	0.528	0.0699
adat	0.527	0.0706

Gene Name	ERC Value	P-value
CG15865	0.527	0.0706
CG7530	0.527	0.0706
CG9109	0.527	0.0706
CG14407	0.526	0.071
CG16868	0.526	0.071
CG9243	0.526	0.071
Fem-1	0.526	0.071
NF-YC	0.526	0.071
hllB	0.526	0.071
Ish	0.526	0.071
CG12395	0.525	0.0716
CG5431	0.525	0.0716
CG9634	0.525	0.0716
Pof	0.525	0.0716
Prosalpha6T	0.525	0.0716
rtet	0.524	0.0721
lhoc7	0.524	0.0721
CG10264	0.523	0.0723
llp2	0.523	0.0723
psq	0.523	0.0723
Ucrh	0.523	0.0723
CG17190	0.522	0.0726
CG2453	0.522	0.0726
CG32832	0.522	0.0726
CG8765	0.522	0.0726
mmd	0.522	0.0726
CG17883	0.521	0.0731
dsf	0.521	0.0731
Hsc70-2	0.521	0.0731
mts	0.521	0.0731
rgr	0.521	0.0731
Tango2	0.521	0.0731
CG10326	0.52	0.0736
CG5514	0.52	0.0736
e(r)	0.52	0.0736
ORMDL	0.52	0.0736
CG11658	0.519	0.074
CG13110	0.519	0.074
CG9427	0.519	0.074
Dip2	0.519	0.074
Acp53C14c	0.518	0.0743
CG10824	0.518	0.0743
CG14720	0.518	0.0743
CG15863	0.518	0.0743
jim	0.518	0.0743
CG10694	0.517	0.0748
CG17078	0.517	0.0748
KH1	0.517	0.0748
B-H1	0.516	0.075
CG11334	0.516	0.075
CG3124	0.516	0.075
ladr	0.516	0.075
MED31	0.516	0.075
CG3308	0.515	0.0755
CG6144	0.515	0.0755
poe	0.515	0.0755

Table 6.S22 Continued

Gene Name	ERC Value	P-value
<i>Ppm1</i>	0.515	0.0755
<i>Rtf1</i>	0.515	0.0755
<i>CG11870</i>	0.514	0.0759
<i>CG8320</i>	0.514	0.0759
<i>Aac11</i>	0.513	0.0761
<i>CG15083</i>	0.513	0.0761
<i>CG31251</i>	0.513	0.0761
<i>CG3880</i>	0.513	0.0761
<i>growl</i>	0.513	0.0761
<i>pk</i>	0.513	0.0761
<i>CG11247</i>	0.512	0.0767
<i>CG12734</i>	0.512	0.0767
<i>CG3652</i>	0.512	0.0767
<i>CG9044</i>	0.512	0.0767
<i>CG9861</i>	0.512	0.0767
<i>Pc</i>	0.512	0.0767
<i>sunz</i>	0.512	0.0767
<i>CG11902</i>	0.511	0.0773
<i>CG14435</i>	0.511	0.0773
<i>CG5978</i>	0.511	0.0773
<i>Den1</i>	0.511	0.0773
<i>smt3</i>	0.511	0.0773
<i>CG15478</i>	0.51	0.0777
<i>CG32573</i>	0.51	0.0777
<i>Cyp28c1</i>	0.51	0.0777
<i>RanBPM</i>	0.51	0.0777
<i>Rrp6</i>	0.51	0.0777
<i>CG10752</i>	0.509	0.0782
<i>CG17059</i>	0.509	0.0782
<i>CG4751</i>	0.509	0.0782
<i>Sec16</i>	0.509	0.0782
<i>Tl</i>	0.509	0.0782
<i>CG13837</i>	0.508	0.0786
<i>CG15153</i>	0.508	0.0786
<i>CG15861</i>	0.508	0.0786
<i>CG34404</i>	0.508	0.0786
<i>CG4553</i>	0.508	0.0786
<i>Ssadh</i>	0.508	0.0786
<i>CG10435</i>	0.507	0.0792
<i>CG10688</i>	0.507	0.0792
<i>CG17633</i>	0.507	0.0792
<i>CG3409</i>	0.507	0.0792
<i>CG34331</i>	0.507	0.0792
<i>CG4854</i>	0.507	0.0792
<i>melt</i>	0.507	0.0792
<i>CG12609</i>	0.506	0.0798
<i>CG13599</i>	0.506	0.0798
<i>CG18316</i>	0.506	0.0798
<i>CG31869</i>	0.506	0.0798
<i>CG5439</i>	0.506	0.0798
<i>CG9649</i>	0.506	0.0798
<i>kai</i>	0.506	0.0798
<i>Mer</i>	0.506	0.0798
<i>CG11851</i>	0.505	0.0805
<i>CG15024</i>	0.505	0.0805
<i>CG31025</i>	0.505	0.0805

Gene Name	ERC Value	P-value
<i>CG32750</i>	0.505	0.0805
<i>CG8165</i>	0.505	0.0805
<i>CG8202</i>	0.505	0.0805
<i>CG9384</i>	0.505	0.0805
<i>DNApol-iota</i>	0.505	0.0805
<i>mri</i>	0.505	0.0805
<i>SelD</i>	0.505	0.0805
<i>trk</i>	0.505	0.0805
<i>amx</i>	0.504	0.0815
<i>CG15528</i>	0.504	0.0815
<i>CG7884</i>	0.504	0.0815
<i>l(1)G0289</i>	0.504	0.0815
<i>mRpL44</i>	0.504	0.0815
<i>CG13350</i>	0.503	0.082
<i>CG32437</i>	0.503	0.082
<i>CG4666</i>	0.503	0.082
<i>CG9855</i>	0.503	0.082
<i>rut</i>	0.503	0.082
<i>wdp</i>	0.503	0.082
<i>Sep5</i>	0.502	0.0825
<i>CG13876</i>	0.502	0.0825
<i>CG9249</i>	0.502	0.0825
<i>mspo</i>	0.502	0.0825
<i>Stat92E</i>	0.502	0.0825
<i>Chd1</i>	0.501	0.083
<i>ome</i>	0.501	0.083
<i>brk</i>	0.5	0.0832
<i>CG18605</i>	0.5	0.0832
<i>CG1951</i>	0.5	0.0832
<i>CG7927</i>	0.5	0.0832
<i>CycT</i>	0.5	0.0832
<i>Gs1l</i>	0.5	0.0832
<i>hh</i>	0.5	0.0832
<i>CG32816</i>	0.499	0.0838
<i>CG3645</i>	0.499	0.0838
<i>ACXE</i>	0.498	0.084
<i>CG8097</i>	0.498	0.084
<i>Gem3</i>	0.498	0.084
<i>Men1-1</i>	0.498	0.084
<i>wor</i>	0.498	0.084
<i>CG10916</i>	0.497	0.0844
<i>CG14573</i>	0.497	0.0844
<i>CG7457</i>	0.497	0.0844
<i>cal1</i>	0.496	0.0847
<i>capu</i>	0.496	0.0847
<i>CG13003</i>	0.496	0.0847
<i>CG13692</i>	0.496	0.0847
<i>CG14314</i>	0.496	0.0847
<i>CG3605</i>	0.496	0.0847
<i>CG8389</i>	0.496	0.0847
<i>CG13970</i>	0.495	0.0853
<i>Hmt-1</i>	0.495	0.0853
<i>Bruce</i>	0.494	0.0855
<i>CG13339</i>	0.494	0.0855
<i>CG7376</i>	0.494	0.0855
<i>eco</i>	0.494	0.0855

Gene Name	ERC Value	P-value
<i>fy</i>	0.494	0.0855
<i>Glu-Rl</i>	0.494	0.0855
<i>Pvfl</i>	0.494	0.0855
<i>CG31010</i>	0.493	0.0861
<i>CG32790</i>	0.493	0.0861
<i>CG8187</i>	0.493	0.0861
<i>CG13123</i>	0.492	0.0864
<i>Gr89a</i>	0.492	0.0864
<i>nkd</i>	0.492	0.0864
<i>Stim</i>	0.492	0.0864
<i>calypso</i>	0.491	0.0868
<i>CG10889</i>	0.491	0.0868
<i>CG15896</i>	0.491	0.0868
<i>CG34447</i>	0.491	0.0868
<i>CG42251</i>	0.491	0.0868
<i>Gyk</i>	0.491	0.0868
<i>l(2)NC136</i>	0.491	0.0868
<i>CG10051</i>	0.49	0.0874
<i>CG14967</i>	0.49	0.0874
<i>CG1622</i>	0.49	0.0874
<i>CG34115</i>	0.49	0.0874
<i>CG4725</i>	0.49	0.0874
<i>CG8552</i>	0.49	0.0874
<i>rev7</i>	0.49	0.0874
<i>Bt140</i>	0.489	0.088
<i>CG42507</i>	0.489	0.088
<i>D12</i>	0.489	0.088
<i>Sec61beta</i>	0.489	0.088
<i>boly</i>	0.488	0.0884
<i>BRWD3</i>	0.488	0.0884
<i>CG13594</i>	0.488	0.0884
<i>CG14739</i>	0.488	0.0884
<i>CG15387</i>	0.488	0.0884
<i>CG6927</i>	0.488	0.0884
<i>Taf10</i>	0.488	0.0884
<i>CG11211</i>	0.487	0.089
<i>CG11590</i>	0.487	0.089
<i>CG12207</i>	0.487	0.089
<i>CalpC</i>	0.486	0.0893
<i>CG12320</i>	0.486	0.0893
<i>CG30460</i>	0.486	0.0893
<i>CG42666</i>	0.486	0.0893
<i>CG9335</i>	0.486	0.0893
<i>CG9876</i>	0.486	0.0893
<i>gcm</i>	0.486	0.0893
<i>Opbp</i>	0.486	0.0893
<i>CG1427</i>	0.485	0.09
<i>CG5626</i>	0.485	0.09
<i>CG9114</i>	0.485	0.09
<i>ine</i>	0.485	0.09
<i>Karybeta3</i>	0.485	0.09
<i>mRpL22</i>	0.485	0.09
<i>Pez</i>	0.485	0.09
<i>trus</i>	0.485	0.09
<i>CG12994</i>	0.484	0.0907
<i>CG13283</i>	0.484	0.0907

Gene Name	ERC Value	P-value
<i>CG42346</i>	0.484	0.0907
<i>malpha</i>	0.484	0.0907
<i>CG7985</i>	0.483	0.0911
<i>lrl1a</i>	0.483	0.0911
<i>Taf13</i>	0.483	0.0911
<i>TllEbata</i>	0.483	0.0911
<i>Art3</i>	0.482	0.0914
<i>casp</i>	0.482	0.0914
<i>CG6083</i>	0.482	0.0914
<i>CG8963</i>	0.482	0.0914
<i>pita</i>	0.482	0.0914
<i>CG11637</i>	0.481	0.0919
<i>CG14229</i>	0.481	0.0919
<i>CG18643</i>	0.481	0.0919
<i>Contactin</i>	0.481	0.0919
<i>kon</i>	0.481	0.0919
<i>Psf1</i>	0.481	0.0919
<i>Rae1</i>	0.481	0.0919
<i>Rbp1-like</i>	0.481	0.0919
<i>wge</i>	0.481	0.0919
<i>CG6712</i>	0.48	0.0927
<i>CG7320</i>	0.48	0.0927
<i>CG7332</i>	0.48	0.0927
<i>Trs23</i>	0.48	0.0927
<i>yemalpha</i>	0.48	0.0927
<i>CG42455</i>	0.479	0.0932
<i>CG5466</i>	0.479	0.0932
<i>m2</i>	0.479	0.0932
<i>Mis12</i>	0.479	0.0932
<i>Nek2</i>	0.479	0.0932
<i>RluA-2</i>	0.479	0.0932
<i>CG1120</i>	0.478	0.0937
<i>CG12851</i>	0.478	0.0937
<i>CG32643</i>	0.478	0.0937
<i>CG4554</i>	0.478	0.0937
<i>CG9760</i>	0.478	0.0937
<i>E(Pc)</i>	0.478	0.0937
<i>vps24</i>	0.478	0.0937
<i>CG11570</i>	0.477	0.0943
<i>CG12078</i>	0.477	0.0943
<i>CG32232</i>	0.477	0.0943
<i>CG33155</i>	0.477	0.0943
<i>GstD8</i>	0.477	0.0943
<i>Hsp23</i>	0.477	0.0943
<i>Or98b</i>	0.477	0.0943
<i>CG10543</i>	0.476	0.095
<i>CG15398</i>	0.476	0.095
<i>Snr1</i>	0.476	0.095
<i>adp</i>	0.475	0.0952
<i>CG10263</i>	0.475	0.0952
<i>CG12263</i>	0.475	0.0952
<i>CG13074</i>	0.475	0.0952
<i>CG14408</i>	0.475	0.0952
<i>CG31812</i>	0.475	0.0952
<i>CG32087</i>	0.475	0.0952
<i>CG7246</i>	0.475	0.0952

Gene Name	ERC Value	P-value
<i>CG7550</i>	0.475	0.0952
<i>CG8944</i>	0.475	0.0952
<i>Fit2</i>	0.475	0.0952
<i>in</i>	0.475	0.0952
<i>mahj</i>	0.475	0.0952
<i>MED15</i>	0.475	0.0952
<i>Sin3A</i>	0.475	0.0952
<i>CG18190</i>	0.474	0.0966
<i>CG31301</i>	0.474	0.0966
<i>ttn2</i>	0.474	0.0966
<i>CG2685</i>	0.473	0.0968
<i>CG5669</i>	0.473	0.0968
<i>dom</i>	0.473	0.0968
<i>InR</i>	0.473	0.0968
<i>Tif-1A</i>	0.473	0.0968
<i>Aats-gly</i>	0.472	0.0973
<i>bin3</i>	0.472	0.0973
<i>CG10933</i>	0.472	0.0973
<i>CG13366</i>	0.472	0.0973
<i>Hrb87F</i>	0.472	0.0973
<i>az2</i>	0.471	0.0977
<i>CG15124</i>	0.471	0.0977
<i>CG1896</i>	0.471	0.0977
<i>CG9676</i>	0.471	0.0977
<i>CG13046</i>	0.47	0.0981
<i>Gen</i>	0.47	0.0981
<i>Hrs</i>	0.47	0.0981
<i>lab</i>	0.47	0.0981
<i>CG1172</i>	0.469	0.0985
<i>CG12818</i>	0.469	0.0985
<i>CG13862</i>	0.469	0.0985
<i>CG15262</i>	0.469	0.0985
<i>CG17233</i>	0.469	0.0985
<i>CG9723</i>	0.469	0.0985
<i>disco-r</i>	0.469	0.0985
<i>CG34040</i>	0.468	0.0991
<i>CG6985</i>	0.468	0.0991
<i>Eps-15</i>	0.467	0.0993
<i>Ykt6</i>	0.467	0.0993
<i>CG11835</i>	0.466	0.0995
<i>CG18171</i>	0.466	0.0995
<i>CG42337</i>	0.466	0.0995
<i>CG9007</i>	0.466	0.0995
<i>Myb</i>	0.466	0.0995
<i>Prp18</i>	0.466	0.0995
<i>CG10414</i>	0.465	0.1
<i>Med</i>	0.465	0.1
<i>Pvr2</i>	0.465	0.1

Table 6.S23 - Genes with ≥ 6 significant ERC values with *Drosophila* meiotic recombination gene set.

Gene Name	Number	Gene Name	Number	Gene Name	Number
CG10560	9	Rad51D	7	CG33641	6
CG31898	9	RhoGAP18B	7	CG33703	6
Nnf1a	9	Sulf1	7	CG3808	6
CG10274	8	Taspase1	7	CG4424	6
CG11778	8	trk	7	CG5924	6
CG18806	8	Vm32E	7	CG7222	6
CG2975	8	Abi	6	CG7884	6
CG34012	8	alpha4GT1	6	CG8100	6
CG7069	8	BubR1	6	CG8191	6
CG7597	8	CG10249	6	CG8501	6
dm	8	CG10424	6	CG8677	6
ft	8	CG10669	6	CG9147	6
Kmn1	8	CG11762	6	CG9247	6
Aef1	7	CG12012	6	CG9386	6
CG11109	7	CG12104	6	CG9804	6
CG11155	7	CG12272	6	CG9992	6
CG11211	7	CG12288	6	cmet	6
CG12420	7	CG12851	6	Cpr47Ed	6
CG1311	7	CG13377	6	DAT	6
CG13169	7	CG1344	6	dbr	6
CG13745	7	CG13500	6	Dg	6
CG14302	7	CG13837	6	ds	6
CG14882	7	CG14401	6	FLASH	6
CG16743	7	CG14562	6	GluRIIE	6
CG2162	7	CG14695	6	Gpi1	6
CG30403	7	CG14906	6	GstE6	6
CG31053	7	CG14956	6	Hr39	6
CG31698	7	CG15116	6	icl1	6
CG32573	7	CG15124	6	llp1	6
CG34284	7	CG15376	6	ldbr	6
CG4751	7	CG15404	6	Magi	6
CG4753	7	CG15522	6	magu	6
CG4820	7	CG15865	6	mRpS30	6
CG6325	7	CG16863	6	MSBP	6
CG7265	7	CG17181	6	mthl5	6
CG8116	7	CG17490	6	Nca	6
CG8159	7	CG17562	6	Ndc80	6
CG8319	7	CG2182	6	net	6
CG8539	7	CG2321	6	Pbp45	6
CG8974	7	CG2694	6	Prosalph6T	6
Cpr72Ea	7	CG30001	6	Prosbeta7	6
ct	7	CG31224	6	Ptp52F	6
eyg	7	CG31380	6	Spc105R	6
Gr9a	7	CG31431	6	spn-B	6
H2.0	7	CG32006	6	Spn43Ad	6
lr56a	7	CG32121	6	Su(H)	6
KH1	7	CG3223	6	Sym	6
mGluRA	7	CG32541	6	wgn	6
Or65a	7	CG32635	6	ZC3H3	6
Rad51C	7	CG32803	6	zpg	6

Table 6.S24 - List of Drosophila stocks used for functional validation.

Gene Name	Stock Center and Number	Genotype
<i>CG10560</i>	BDSC #18339	w[1118]; PBac{w[+mC]=WH}CG10560[f00512]
<i>CG10560</i>	VDRC #104272	P{KK106578}VIE-260B
<i>CG31898</i>	BDSC #18211	w[1118]; PBac{w[+mC]=RB}CG31898[e03937]
<i>CG31898</i>	VDRC #108688	P{KK104442}VIE-260B
<i>Nnf1a</i>	BDSC #52973	y[1] v[1]; P{y[+t7.7] v[+t1.8]=TRiP.HMJ21658}attP40
<i>CG10274</i>	BDSC #26239	y[1] v[1]; P{y[+t7.7] v[+t1.8]=TRiP.JF02137}attP2/TM3, Sb[1]
<i>CG10274</i>	VDRC #110232	P{KK112732}VIE-260B
<i>CG11778</i>	VDRC #106218	P{KK105246}VIE-260B
<i>CG11778</i>	VDRC #7374	w[1118]; P{GD1888}v7374/TM3
<i>CG18806</i>	VDRC #19197	w[1118]; P{GD8823}v19197
<i>CG2975</i>	BDSC #43290	y[1] sc[*] v[1]; P{y[+t7.7] v[+t1.8]=TRiP.HMS02662}attP40
<i>CG2975</i>	VDRC #2601	w[1118]; P{GD847}v2601
<i>CG34012</i>	Harvard Exelixis c02254	PBac{PB}CG34012c02254
<i>CG7069</i>	BDSC #17266	w[1118]; P{w[+mC]=EP}CG7069[EP3224]/TM3, Sb[1] Ser[1]
<i>CG7069</i>	VDRC #101116	P{KK106952}VIE-260B
<i>CG7597</i>	BDSC #35163	y[1] sc[*] v[1]; P{y[+t7.7] v[+t1.8]=TRiP.GL00031}attP2
<i>CG7597</i>	BDSC #42775	y[1] sc[*] v[1]; P{y[+t7.7] v[+t1.8]=TRiP.GL01137}attP2
<i>dm</i>	BDSC #11298	P{P-Sal}dmP0/C(1)DX, y1 f1; bw1; st1
<i>ft</i>	BDSC #304	ft[1]
<i>ft</i>	VDRC #108863	P{KK101190}VIE-260B
<i>Kmn1</i>	BDSC #18932	w1118 PBac{WH}Kmn1f06049
<i>Kmn1</i>	VDRC #106889	P{KK111826}VIE-260B

Table 6.S25 - Gene ontology analysis of genes with ≥ 6 significant ERC values from *Drosophila* meiotic recombination genes

Gene Ontology Category	I^A	I^B	Odds Ratio	P-value
Nucleic Acid Binding	14 (148)	389 (11478)	2.79	0.01
Zinc Ion Binding	19 (148)	880 (11478)	1.67	0.03
Nucleus	22 (148)	1171 (11478)	1.46	0.04

Gene Ontology Category	I^A	I^B	Odds Ratio	P-value
Nucleus and Zinc Ion Binding	12 (148)	309 (11478)	3.01	0.01
Nucleic Acid Binding and Nucleus	8 (148)	127 (11478)	4.89	0.01
Nucleic Acid Binding and Zinc Ion Binding	10 (148)	182 (11478)	4.26	0.01

Gene Ontology Category	I^A	I^B	Odds Ratio	P-value
((Nucleus and Zinc Ion Binding) and Nucleic Acid Binding)	8 (148)	93 (11478)	6.67	0.01
((Nucleic Acid Binding and Nucleus) and Zinc Ion Binding)	8 (148)	93 (11478)	6.67	0.01
((Nucleic Acid Binding and Zinc Ion Binding) and Nucleus)	8 (148)	93 (11478)	6.67	0.01

Gene Ontology Category	I^A	I^B	Odds Ratio	P-value
(((Nucleic Acid Binding and Zinc Ion Binding) and Nucleus) not RNA Polymerase II Transcription Factor Activity)	8 (148)	82 (11478)	7.57	0.01
(((Nucleic Acid Binding and Nucleus) and Zinc Ion Binding) not RNA Polymerase II Transcription Factor Activity)	8 (148)	82 (11478)	7.57	0.01
(((Nucleus and Zinc Ion Binding) and Nucleic Acid Binding) not RNA Polymerase II Transcription Factor Activity)	8 (148)	82 (11478)	7.57	0.01

Gene Ontology Category	I^A	I^B	Odds Ratio	P-value
Zinc Finger, AD-Type	8 (148)	94 (10649)	6.12	0.01

Table 6.S25 Continued

Gene Ontology Category

Nucleic Acid Binding
<i>KH1, CG9247, CG17181, CG10274, ZC3H3, CG3808, CG11762, CG8159, CG8319, CG4820, CG14906, CG31224, CG4424, CG10669</i>
Zinc Ion Binding
<i>CG8974, DBR, CG16863, CG8677, HR39, CG17181, CG10274, CG8539, ZC3H3, AEF1, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669, CG32121, CG31053</i>
Nucleus
<i>DM, DBR, PROSALPHA6T, SU(H), CG8677, HR39, CG12104, CG10274, LDBR, AEF1, PROSBETA7, SYM, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669, NET, CG18806, CG32006</i>

Gene Ontology Category

Nucleus and Zinc Ion Binding
<i>DBR, CG8677, HR39, CG10274, AEF1, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
Nucleic Acid Binding and Nucleus
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
Nucleic Acid Binding and Zinc Ion Binding
<i>CG17181, CG10274, ZC3H3, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>

Gene Ontology Category

((Nucleus and Zinc Ion Binding) and Nucleic Acid Binding)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
((Nucleic Acid Binding and Nucleus) and Zinc Ion Binding)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
((Nucleic Acid Binding and Zinc Ion Binding) and Nucleus)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>

Gene Ontology Category

((((Nucleic Acid Binding and Zinc Ion Binding) and Nucleus) not RNA Polymerase II Transcription Factor Activity)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
((((Nucleic Acid Binding and Nucleus) and Zinc Ion Binding) not RNA Polymerase II Transcription Factor Activity)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>
((((Nucleus and Zinc Ion Binding) and Nucleic Acid Binding) not RNA Polymerase II Transcription Factor Activity)
<i>CG10274, CG11762, CG8159, CG8319, CG4820, CG31224, CG4424, CG10669</i>

Gene Ontology Category

Zinc Finger, AD-Type
<i>DBR, CG10274, CG11762, CG8159, CG8319, CG4820, CG4424, CG10669</i>

CHAPTER 7. CONCLUSIONS AND FUTURE DIRECTIONS

CONCLUSIONS

During meiosis, homologous chromosomes exchange genetic material in a process known as meiotic recombination. This process helps ensure proper chromosome segregation. Defects in this process can lead to severe decreases in fitness, including aneuploid gametes and cell mortality. This process is also a pivotal evolutionary force, creating new allelic combinations for selection to act upon in future generations. Despite this crucial function, rates of recombination are highly variable within and between taxa and vary due to both environmental and genetic factors. The preceding work has aimed to decipher the environmental and genetic determinants of that variation using the model organism, *Drosophila melanogaster*.

In CHAPTER 2, I employed classical genetics to address how female and male genetic backgrounds individually and jointly affect crossover rates. I measured rates of crossing over in a 33 cM region of the X chromosome using a two-step crossing scheme exploiting visible markers. In total, I measured crossover rates of 10 inbred lines in a full diallel cross. The experimental design facilitates measuring the contributions of female genetic background, male genetic background, and female by male genetic background interaction effects on rates of crossing over in females. My results indicate that although female genetic background significantly affects female meiotic crossover rates in *Drosophila*, male genetic background and the interaction of female and male genetic backgrounds have no significant effect. These findings thus suggest that male-mediated effects are unlikely to contribute greatly to variation in recombination rates in natural populations of *Drosophila*.

In CHAPTER 3, I tested the hypothesis that maternal age influences rates of crossing over in a genotypic-specific manner. Using classical genetic techniques, I estimated rates of crossing over for individual *D. melanogaster* females from several strains as a function of maternal age. I find that both age and genetic background significantly contribute to observed variation in recombination frequency, as do genotype-age interactions. Further, I observe differences in the effect of age on recombination in the two genomic regions surveyed. These results highlight the complexity of recombination rate variation and reveal a new role of genotype by environment interactions in mediating recombination rate.

In CHAPTER 4, I exploit the natural variation in the inbred, sequenced lines of the *D. melanogaster* Genetic Reference Panel (DGRP) (Mackay et al. 2012; Huang et al. 2014) to map genetic variants affecting recombination rate. I used a two-step crossing scheme and visible markers to measure rates of recombination in a 33 cM interval on the X chromosome and in a 20.4 cM interval on chromosome 3R for 205 DGRP lines. I find ~2-fold variation in recombination rates among lines. Interestingly, I further find that recombination rates are uncorrelated between the two chromosomal regions. I performed a genome-wide association study to identify genetic variants associated with recombination rate in each of the two intervals surveyed. I refined the list of candidate variants and genes associated with recombination rate variation and selected twenty genes for functional variation. I present strong evidence that four genes are likely to contribute to natural variation in recombination rate in *D. melanogaster* and lie outside of the canonical meiotic recombination pathway. Further, I find a weak effect of Wolbachia infection on recombination rate and I confirm the interchromosomal effect of polymorphic inversions in both regions. My results highlight the magnitude of population variation in recombination rate present in *D. melanogaster* and implicate new genetic factors mediating natural variation in this quantitative trait.

In CHAPTER 5, I hypothesized that the connection between hybrid sterility and meiotic recombination of PRDM9 in mammals was not coincidental and that in fact, the hybrid sterility is a consequence of recombination defects. To test this hypothesis, I used *Drosophila* as a model system. Specifically, I asked whether genes involved in hybrid incompatibilities in *Drosophila* also have yet unknown roles in meiotic recombination. My results suggest that two genes with clear roles in hybrid incompatibility, *JYalpha* and *Lhr*, mediate rates of recombination. Future work is aimed at exploring the molecular mechanisms of *JYalpha* and *Lhr* in meiotic recombination.

In CHAPTER 6, I utilized a method entitled evolutionary rate covariation (ERC) (Clark et al. 2012) to identify genetic factors playing a role in mediating recombination rate variation. This method is based on the idea that members of a given biological pathway are likely to experience similar evolutionary pressures, which could result in correlated changes in rates of coding sequence evolution. ERC identifies genes that experience similar rates of evolution by analyzing phylogenetic trends; genes with highly correlated rates of evolution may be functionally connected in gene or biological networks. I attempted to identify genes that modulate rates of recombination by analyzing evolutionary rate covariation of 21 genes with known function in *Drosophila* meiotic recombination. My results confirm elevated ERC among meiotic recombination genes within *Drosophila*. I also identify thirteen candidate

genes that have statistically significant ERC with at least eight meiotic recombination genes. A majority of these candidate genes have no known function though two have been previously implicated in mitotic chromosome segregation. Functional validation highlights two genes, *CG31898* and *CG2975*, that when disrupted significantly alter rates of recombination rate in an interval on chromosome 3R. My results thus contribute two genetic factors involved in possibly mediating recombination rate in *Drosophila*. My findings also demonstrate the potential of the ERC method in predicting new members of existing biological pathways.

FUTURE DIRECTIONS

My work has opened the door for many future possible experiments in regards to deciphering the environmental and genetic determinants of recombination rate variation. I will highlight a subset of possible future directions for each chapter.

For CHAPTER 2, I highlight discrepancies between my study and the original study that suggested male-mediated effects on recombination (Stevison 2012). Some of these discrepancies include the population of flies used (a North American population versus an African population), the markers used to estimate recombination (visible markers versus molecular markers), the temperature used in the study (25°C versus 21°C) and the age of the virgin females used for the crossing scheme (1 day versus 4 days). In order to identify the source of the difference between the two studies, it would be ideal to repeat the diallel cross testing specifically for each of these variables. Similar results controlling for these different variables would confirm my conclusions that male-mediated effects are unlikely to contribute greatly to variation in recombination rates in natural populations of *Drosophila*. Different results from an altering a certain variable would give evidence of what (if anything) is driving possible male-mediated effects.

For CHAPTER 3, my work regarding advancing maternal age and recombination rate variation highlighted that there are both genetic background by maternal age effects as well as differential effects based on genomic location. First, it remains unknown what are the genetic factors that cause differential changes in rates of recombination over time. One could address this problem by using a mapping approach like in CHAPTER 4. Second, it will be important to test how rates of recombination change in other genomic locations of varying genetic sizes. This can be easily done using different morphological markers that span the length of entire chromosomes and repeating my experimental design. Finally, another question that still remains unanswered is how levels of nondisjunction change with

advancing maternal age. It will be interesting to correlate how rates of recombination and levels of nondisjunction change over time.

For CHAPTER 4, my analysis of recombination rate variation in the DGRP yielded several key results. While there are similar degrees of population-level variation in recombination rate in both regions that were assayed, I do observe a rather large discrepancy in the broad-sense heritability estimates. Moreover, these rates of recombination are not correlated between the two regions, evidenced in part by differences in the genetic variants associating with rates of recombination. It will be important to assay rates of recombination in other genomic regions (on other chromosomes and other locations on the same chromosome). This would provide evidence of whether there are simply differences between autosomes and the sex chromosome or if there are chromosome specific modifiers. Additionally, I would be able to test if these modifiers are limited to specific genomic regions or entire chromosomes.

We observe significant effects of both chromosomal inversions and Wolbachia infection on rates of crossing over. While it has long been known that chromosomal inversions influence rates of recombination (Schultz and Redfield 1951; Lucchesi and Suzuki 1968), it remains unclear how other chromosomal rearrangements such as large deletions affects rates of recombination. This would be easily testable with the large collection of chromosomal aberrations available from the DrosDel Collection (Ryder et al. 2004, 2007). Would large deletions also cause increases of recombination elsewhere in the genome? Additionally, I see a significant association with Wolbachia infection in crossover rates in the *y v* region yet not in the *e ro* region. Future work includes testing to see if infecting DGRP lines with Wolbachia causes an increase of crossover rates and if curing DGRP lines via tetracycline yields a decrease in crossover rates.

Finally, my results highlight 5 genes (*CG10864*, *CG33970*, *Eip75B*, *Iola*, and *Ptp61F*) that play putative roles in modulating recombination rate variation in *Drosophila* through both gene-level and expression-level validation. Future work is aimed at determining the role of these candidate genes in the molecular process of recombination.

For CHAPTER 5, my results suggest that two genes with clear functions in hybrid incompatibility, *JYalpha* and *Lhr*, mediate rates of recombination. As stated in the text, a clear link between *JYalpha* and meiotic recombination does not emerge from these results. Additional experiments to further validate *JYalpha*'s role in modulating recombination rate include analyzing expression in ovaries and whole females using quantitative RT-PCR. Meiotic recombination occurs only in the ovaries and *JYalpha* has only been detected in the

testes of flies. Therefore, if expression of *JYalpha* can be detected in the ovaries (even at a low level), this would indicate a secondary unexplored function of *JYalpha*. A second experiment involves analyzing mutants of *JYalpha* with respect to their sensitivity to DNA damaging agents such as the oxidizing agent paraquat (methyl viologen dichloride). Meiotic recombination is initiated by programmed double-strand breaks and further resolved by DNA repair proteins. If *JYalpha* also has an unexplored role in DNA damage repair, I would expect to see increased sensitivity of flies possessing only one functional copy of *JYalpha*. Finally, I can repeat the above experiments in hybrids using a cross between *D. simulans* females and *D. melanogaster* males (with and without the *JYalpha* P-element). Often, phenotypes from hybrid incompatibility genes are masked in non-hybrids. Perhaps, phenotypes will be exaggerated in hybrids, which would provide additional support for a role of *JYalpha* in recombination. These experiments can also be repeated similarly for *Lhr* and even its known interactor *Hmr*.

For CHAPTER 6, I identified thirteen candidate genes that have statistically significant ERC with at least eight meiotic recombination genes. While only two of these candidate genes functionally validated in my recombination rate assays, it remains untested what role these thirteen candidate genes have in meiosis. A great first step in deciphering these roles is testing protein-protein interactions using yeast two-hybrid assays. Further work can take advantage of the well-studied process of oogenesis in *Drosophila* to look for possible defects when these thirteen candidate genes are perturbed.

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