

Evolution of piRNA-mediated TE Repression in *Drosophila*

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Abstract

In metazoan germlines, the piRNA pathway acts as a genomic immune system, employing small RNA-mediated silencing to defend host DNA from the harmful effects of transposable elements (TEs). Expression of genomic TEs is proposed to initiate self regulation by increasing the production of repressive piRNAs, thereby “adapting” piRNA-mediated control to the most active TE families. However, the mutational and epigenetic processes that give rise to piRNA-mediated silencing when new TEs invade the host also remain poorly understood. In addition, piRNA pathway proteins, which execute piRNA biogenesis and enforce silencing of targeted sequences, evolve rapidly and adaptively in animals. If TE silencing is ensured through piRNA biogenesis, what necessitates changes in piRNA pathway proteins? In this dissertation, we first explored forces that underlie the adaptive evolution of piRNA pathway proteins by performing interspecific complementation and examined functional differences between *Drosophila melanogaster* and *D. simulans* alleles of three adaptively evolving piRNA pathway proteins: Armitage, Aubergine and Spindle-E. We discovered that *D. simulans* alleles of *aub* and *armi* exhibit enhanced off-target effects on host transcripts in a *D. melanogaster* background, as well as modest reductions in the efficiency of piRNA biogenesis, suggesting that promiscuous binding of *D. simulans* Aub and Armi proteins to host transcripts reduces their participation in piRNA production. Avoidance of genomic auto-immunity may therefore be a critical target of selection. *P*-elements have invaded the genomes of three *Drosophila* species within the last century, providing unique opportunities to study the evolution of piRNA mediated repression. In the second part of this dissertation, we introduced *P*-elements into a naive *D. melanogaster* strain through germline transformation, and chronicled their effects on the evolution of host TE repression in 10 laboratory populations at two different temperatures. We found that populations which evolved repression are associated with accumulation of active *P*-elements within their genomes. Furthermore, our observation that repression correlates with *P*-element insertions

into multiple different piRNA clusters strongly supports the “trap” model that acquisition of TE repression is through TE insertions into piRNA clusters, and indicates that the evolution of repression occurs via simultaneous emergence of numerous different repressor alleles.

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Chapter 1 Introduction

1.1 TEs and their effects on the host

Transposable elements (TEs) were first discovered by the cytogeneticist Barbara McClintock in maize in the late 1940s [1,2]. Since their discovery, the impact and regulation of these mobile DNAs have been subjects of great interest. TEs are ubiquitous mobile genetic entities that are present in almost all organisms and can make up large fractions of the genome. For example, approximately 90% of the maize genome is comprised of TEs [3,4], as is 44% of the human genome [5].

TEs can disrupt genomic integrity and increase their copy numbers within the host genome. Based on their strategies of transposition, TEs are categorized into two classes: Class I TEs (copy and paste) and Class II TEs (cut and paste) [6]. Class I TEs, also called retrotransposons, generally function via reverse transcription. They are first transcribed from DNA to RNA intermediate, and then the RNA intermediate is reverse transcribed into a new copy of DNA, which is inserted back into the genome at a new position. Class II TEs, however, are DNA transposons and their transposition is catalyzed by transposase enzymes encoded by TEs themselves.

Although some TE insertions among the host genome can be beneficial, such as *HeT-A* and *TART* insertions into telomeres of *Drosophila* for telomere length maintenance [7], most unrestricted TE mobilization can cause deleterious effects on the host. TEs can induce gene mutations by inserting into genes' sequences, thus disrupting the integrity of genes and the biological function of their products [8–10]. Furthermore, when too many TEs exist in the same genome, they are more likely to trigger the nonhomologous recombination, which could lead to chromosome rearrangements, such as deletions, duplications, inversions, and translocations [11,12]. Moreover, TE transposition induces DNA double strand break (DSB) [13], which can trigger the DNA damage response within the cell and arrest the cell cycle.

TEs preferentially mobilize in germline cells rather than in somatic cells. TE proliferation in soma could reduce host fitness, and consequently, would hurt TEs themselves. Instead, TE proliferation in germlines will help TEs continue by infecting the offspring. On the other hand, repressing germline transposition is also critical to host fitness, because harmful mutations could be transmitted into their offspring and it will cause germline loss and sterility. Thus, it is important for the host to regulate TE activity and repress new TE invaders, especially in germline cells.

1.2 piRNA pathway and TE regulation

In the genome of many metazoans, TEs are silenced by a small RNA silencing pathway, the PIWI-interacting RNA pathway (piRNA pathway). The piRNA pathway is best understood in *Drosophila melanogaster*. The piRNA-mediated silencing system includes piRNAs (23-29nt) and many piRNA pathway proteins (Figure 1.1), and piRNAs complexed with PIWI-clade Argonaute proteins target their complementary TE sequences for transcriptional and post-transcriptional silencing [14,15].

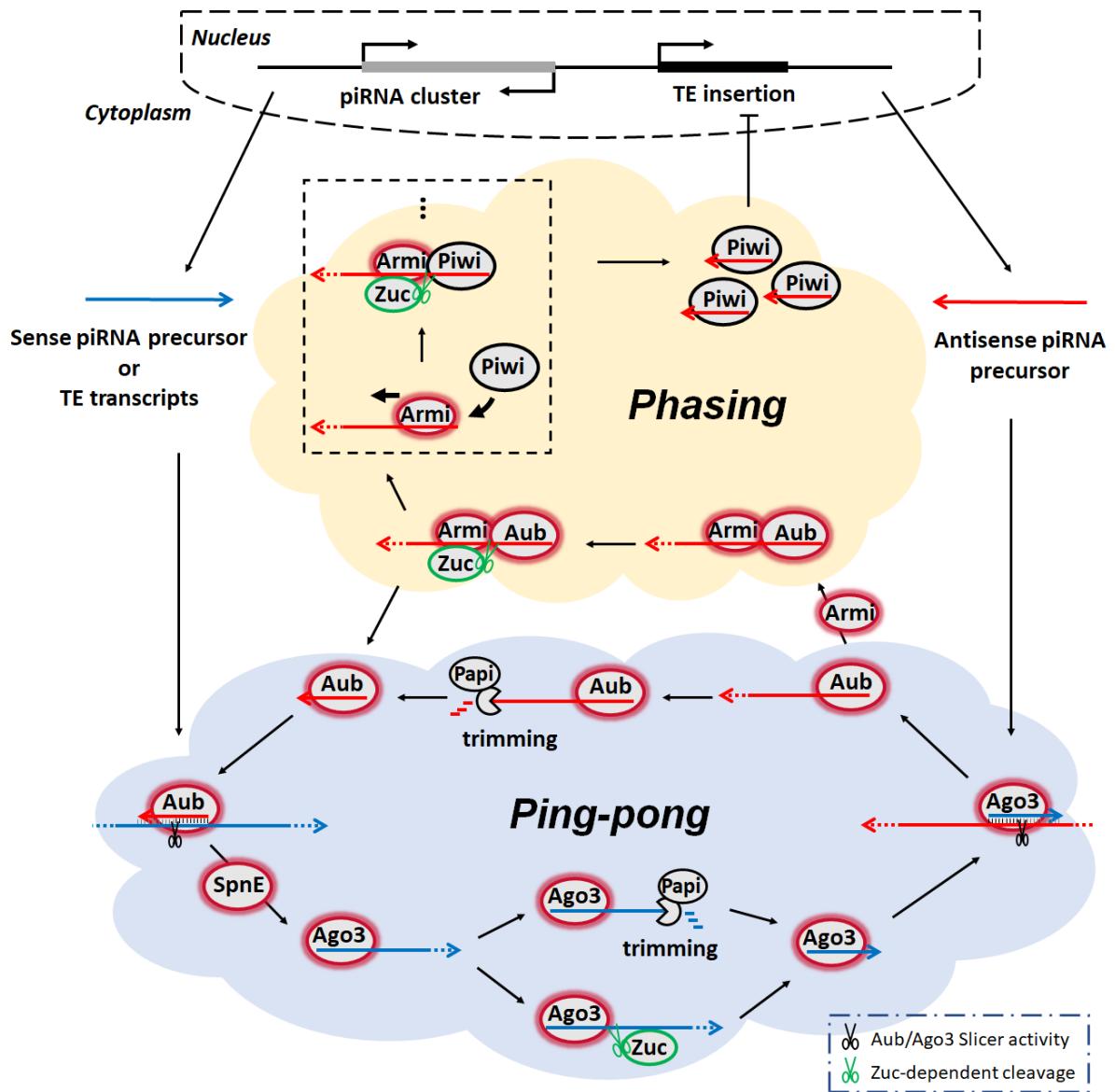


Figure 1.1 piRNA pathway in *Drosophila*. piRNA pathway proteins that are evolving adaptively are shown in red.

1.3 piRNA clusters

Computational studies using deep sequencing technology have found genomic loci in flies and mammals at which piRNA sequencing reads are clustered, indicating these loci as the source of piRNAs, thus termed as piRNA clusters [14,16–18]. In flies, the piRNA clusters are usually located in heterochromatin regions, such as the pericentromere and subtelomere [14,16,17]. piRNA clusters contain a large number of truncated TE fragments from different

TE families [14,19]. There are two types of piRNA clusters [14,16–18]. Dual-stranded piRNA clusters, such as the *42AB* cluster, produce piRNA precursors from both genomic strands in ovarian germline cells. Uni-stranded piRNA clusters, such as the *flamenco* cluster in *Drosophila* somatic follicle cells, produce piRNA precursors from only one genomic strand in both ovarian somatic and germline cells.

1.4 Ping-pong piRNA biogenesis and post-transcriptional TE silencing

There are two different mechanisms for the biogenesis of mature piRNAs from long piRNA precursors. One of them is the ping-pong amplification loop, which is germline-specific and combines piRNA biogenesis and post-transcriptional TE silencing [14,20]. It happens in perinuclear structures called ‘nuage’. In the very beginning, it is believed that maternally-deposited piRNAs trigger the ping-pong-dependent piRNA production in the primordial germline of developing embryos [21,22].

Aubergine (Aub) and Argonaute-3 (Ago-3) are two key factors of the ping-pong amplification loop. Aub predominantly associates with antisense piRNAs, whereas Ago-3 predominantly binds with sense piRNAs [14,20]. Together, these two kinds of ribonucleoproteins (RNPs) produce sense and antisense piRNAs. Guided by the complexed antisense piRNA, Aub induces slicer-dependent cleavage of sense piRNA cluster transcripts or TE-derived mRNAs, precisely 10nt downstream of the 5' end of its bound piRNA. This cleavage event produces the 5' end of sense piRNA intermediates, and simultaneously, post-transcriptionally silences TE mRNAs [14,20]. After being loaded onto Ago-3, the sense piRNA intermediates are then processed into mature sense piRNAs through two different 3' end formation mechanisms (explained below). piRNA-Ago-3 complexes in turn detect and, through Ago-3 slicer activity, cleave antisense piRNA cluster transcripts also precisely 10nt downstream of the 5' end of bound piRNA. This cleavage event generates the 5' end of

antisense piRNA intermediates, which are then loaded onto Aub and processed into mature antisense piRNAs.

Ping-pong piRNA biogenesis is facilitated by numerous additional proteins. RNA helicase Spindle-E (Spn-E) is required for the proper localization of Aub into the nuage [23]. Papi and Zucchini (Zuc) are responsible for the 3' end formation of Aub/Ago-3-bound piRNAs in the ping-pong amplification loop through mediating 3' end trimming by an unknown nuclease and Zuc-dependent 3' end cleavage, respectively [24–28]. Other proteins, such as Vasa, Krimper, Tejas, and Tapas, play accessory roles for proper ping-pong amplification [21,29,30].

1.5 Phased piRNA biogenesis and transcriptional TE silencing

The other piRNA biogenesis mechanism is Zuc-dependent phasing, which exists in both ovarian germline cells and adjacent somatic cells. Zuc is a mitochondrial outer membrane protein, thus, the Zuc-dependent phasing is believed to happen on the outer mitochondrial membrane [31]. The Zuc-dependent cleavage of Aub-bound antisense piRNA intermediates, as occurs during ping-pong amplification loop, produces not only the 3' end of Aub-bound antisense piRNAs but also initiates a series of additional continuous Zuc-dependent cleavage events along the remaining transcript, producing multiple antisense phased piRNAs that mainly bind with Piwi [26,27]. However, the mechanism that initiates the Zuc-dependent phased piRNA biogenesis in somatic cells remains unclear. Then piRNA-Piwi complexes enter the nucleus and induce transcriptional TE silencing by promoting establishment of the repressive chromatin mark H3K9me3 at euchromatic TE insertion loci [32,33].

The RNA helicase Armitage (Armi) binds to piRNA precursors, and together with Zuc is required for biogenesis of phased piRNAs in both germline and somatic cells [34–37]. Armi might facilitate the movement of the antisense piRNA intermediates produced by Ago-3 from nuage to mitochondrial cleavage sites for Zuc. A recent study has shown that Armi is

essential for proper piRNA precursor “feeding” to Zuc for cleavage in mice [38]. Moreover, Armi is found colocalizing with both mitochondrial membrane protein ATP5A and nuage-specific protein Vasa, suggesting that Armi shuttles between nuage and mitochondria [39]. In addition, an earlier study shows that the movement of Armi is under the control of Zuc and Ago-3, where Ago-3 slicer activity is required for Armi movement from nuage to mitochondria and Zuc-dependent cleavage is required for Armi movement from mitochondria to nuage [40].

1.6 Adaptive evolution of the piRNA pathway proteins

Protein components of the piRNA pathway often exhibit evidence of adaptive evolution. McDonald–Kreitman (MK) and related tests revealed that several piRNA pathway proteins such as Armi, Aub and Spn-E, exhibit elevated amino acid divergence between *D. melanogaster* and *D. simulans* as compared to polymorphism (Figure 1.1), suggesting that positive selection has altered their protein-coding sequences [41–43]. Consistent with this finding, divergence-based analyses also found that many protein components of the piRNA pathway have undergone recurrent adaptation across the *Drosophila* phylogeny [44]. In support this hypothesis, piRNA effector proteins, Rhino and Deadlock, which are components of the Rhino-Deadlock-Cutoff complex responsible the transcription of the piRNA clusters, from *D. simulans* do not function in the *D. melanogaster* genomic background because of the protein adaptive evolution along the lineage leading to *D. melanogaster* and *D. simulans* [45]. The phenomenon of adaptive evolution of piRNA pathway proteins is not likely confined to *Drosophila*, Obbard et al. observed that piRNA pathway proteins in mice also have evolved rapidly and adaptively [42].

Functional divergence among piRNA pathway proteins is also indicated by TE dysregulation among interspecific hybrids. Kelleher et al. has observed that *D. melanogaster* and *D. simulans* interspecific hybrids exhibited TE derepression and aberrant piRNA

production similar to piRNA pathway mutants [46]. Similarly, another study performed by Vela et al. also found that 33 TEs were dysregulated in *Drosophila buzzatii* and *Drosophila koepfnerae* interspecific hybrids, which also indicates that TE dysregulation among interspecific hybrids could be explained by the adaptive divergence of piRNA pathway proteins between species [47].

If the host adapts to the changes in TE content by altering piRNA production, what drives the adaptive changes among piRNA pathway proteins? Several theories have been proposed to explain this adaptive evolution [48]. (1) Mutations in TEs that allow them to escape from the host silencing system would drive the recurrent evolution among the piRNA machinery to enhance TE silencing. (2) It is also possible that TEs can directly antagonize the host piRNA machinery by encoding proteins that disrupt the piRNA biogenesis, leading to positive selection on the piRNA machinery that can evade from TE antagonism [45]. (3) The piRNA mediated silencing can also have off-target effects on protein-coding genes instead of TEs, known as a form of “genomic auto-immunity”, which could disrupt normal gene expression [48,49]. Thus, avoidance of genomic auto-immunity might be an alternative hypothesis to explain the adaptive evolution of piRNA pathway proteins. To understand the evolutionary forces that drive the adaptive evolution among the piRNA pathway proteins, in the first part of this dissertation we investigated the functional differences of three adaptively evolving piRNA proteins, Armi, Aub and Spn-E, between *D. melanogaster* and *D. simulans* via interspecific complementation.

1.7 Host response to newly invaded TEs

While TEs are transmitted vertically from parents to progeny, they are also more likely to be horizontally transferred between non-mating species [50]. Although the mechanisms of TE horizontal transfer remain elusive, TEs are more likely to integrate into the genome of a vector species, such as viruses and parasites, and also more likely to persist and spread in

the genome of a new host species [51–53]. Nearly one-third of the TE families among the *Drosophila* genome have experienced horizontal transfer [54]. However, the mechanism by which hosts adapt to and restrict new TE invaders through the piRNA pathway is poorly understood. Currently, two hypotheses have been proposed. The more prevailing mechanism is the “trap” model, among which the host acquires the ability of producing piRNAs targeting the newly invaded TEs through insertion of the invading TE into the piRNA clusters (Figure 1.2) [55–57]. Alternatively, an existing euchromatic insertion of the newly invaded TE could be converted into a novel piRNA cluster through epigenetic mutation [58].

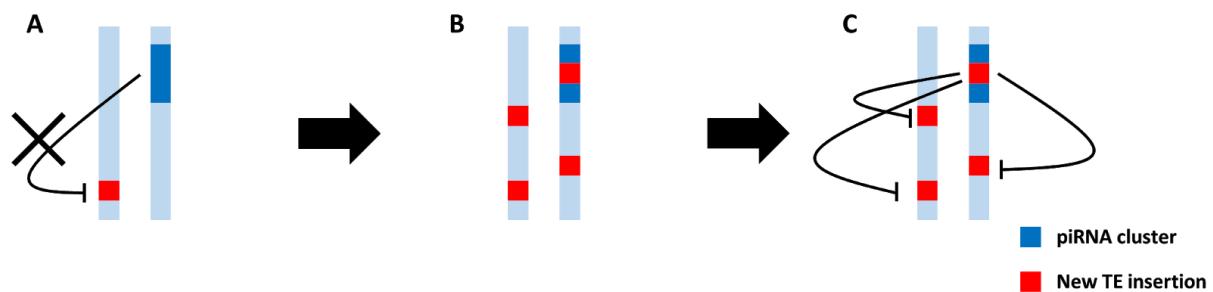


Figure 1.2 The prevailing model of the evolution of host repression on new invaded TEs. Light blue bars indicate the host genome. The new invaded TE is shown in red and the piRNA cluster is shown in dark blue. In the beginning, since the piRNA cluster does not have the sequence of the new invaded TE, the host cannot produce piRNAs targeting this new TE (A), resulting in TE mobilization and proliferation (B). When the new TE inserts into the piRNA cluster, then the host acquires the ability to produce piRNAs against this new TE species, enacting the TE silencing (C).

1.8 *P*-element and hybrid dysgenesis

P-element belongs to Class II transposon, which recently invaded into the *D. melanogaster* genome in 1950s by horizontal transfer from a distant relative, *D. willistoni* [59–61]. The spread of the *P*-elements is surprisingly fast through the species, as nearly all wild strains were infected by 1975 [60]. Meanwhile, *D. melanogaster* have rapidly evolved to suppress *P*-element activity through piRNA-mediated silencing [56,60–63], thus, providing us unique opportunities to study the evolution of the piRNA-mediated repression.

P-elements are responsible for hybrid dysgenesis, a syndrome characterized by frequent sterility, elevated mutation rates, and increased chromosome rearrangement and recombination [64–68]. *Drosophila melanogaster* strains collected after the *P*-element invasion are called P strains, while laboratory *D. melanogaster* strains that were collected before the *P*-element widespread and lack the *P*-element are called M strains. Hybrid dysgenesis happens in the offspring of a P strain father and an M strain mother (Figure 1.3A). It is caused by the unrestricted mobilization of *P*-elements derived from the P strain father while no regulatory piRNAs are transmitted from the M strain mother. However, the reciprocal crosses between a P strain mother and an M strain father produce fertile hybrid progeny due to maternal deposition of *P*-element piRNAs (Figure 1.3B). Thus, the *P*-element-induced hybrid dysgenesis makes it easy to evaluate the *P*-element repression ability of hosts under the lab conditions.

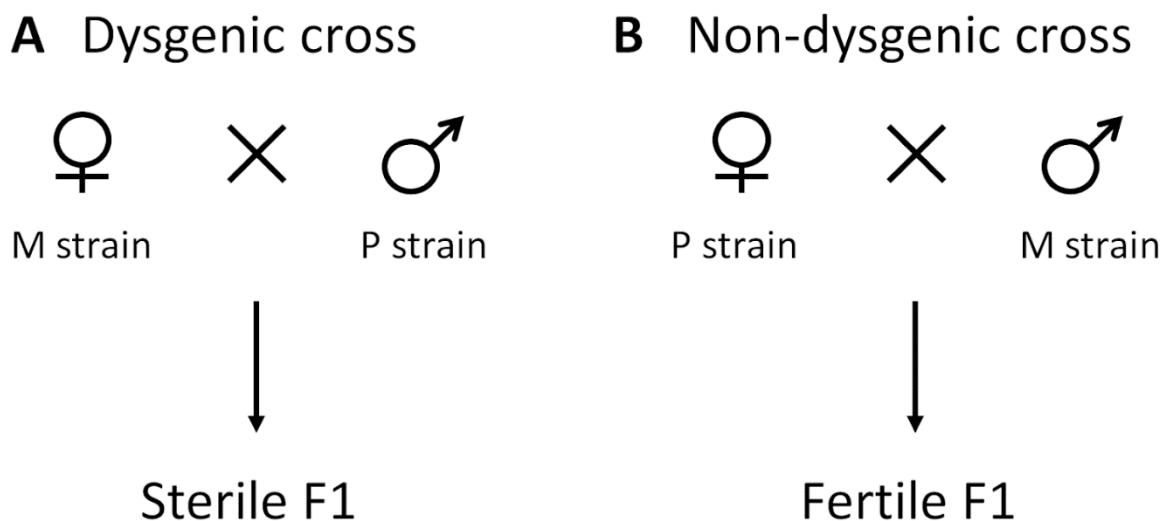


Figure 1.3 Hybrid dysgenesis in *Drosophila*. Crossing scheme of the *P*-element-induced hybrid dysgenesis (A), while the reciprocal cross generates fertile offspring (B).

In the second part of this dissertation, we recreated the TE invasion by *P*-element and reconstructed the evolutionary process of the host repression on *P*-element to better

understand the mutational and epigenetic processes that give rise to piRNA-mediated silencing when new TEs invade the host.

Chapter 2 Adaptive evolution among cytoplasmic piRNA proteins leads to decreased genomic auto-immunity¹

¹ This chapter has been previously published. Reference: Wang, Luyang, Daniel A. Barbash, and Erin S. Kelleher. "Adaptive evolution among cytoplasmic piRNA proteins leads to decreased genomic auto-immunity." Plos Genetics 16, no. 6 (2020): e1008861.

2.1 Introduction

Transposable elements (TEs) are ubiquitous mobile genetic entities, whose unrestricted propagation can cause deleterious insertional mutations and chromosome rearrangements, and are often associated with cancer and sterility [69–72]. TE regulation is therefore essential, especially in germline cells, where TE insertions and associated mutations can be transmitted to the next generation. In metazoan germlines, regulation of TE transcripts is enacted by a small RNA silencing pathway, the PIWI-interacting RNA pathway (piRNA pathway), in which piRNAs complexed with PIWI-clade Argonaute proteins target complementary TEs for post-transcriptional and transcriptional silencing [73].

Host genomes are often parasitized by multiple TE families, which change rapidly in their presence and abundance [61,74–76]. The control of TE transcripts by complementary piRNAs may facilitate adaptation to genomic TEs through changes in piRNA species [77,78]. Surprisingly, however, the protein components of the piRNA pathway that enact piRNA biogenesis and enforce TE silencing also evolve adaptively in diverse metazoan lineages [42–44,79,80]. Evidence for adaptive evolution of piRNA pathway proteins is particularly strong in *Drosophila* [42–44,79,81], which has also emerged as a work horse for uncovering the mechanisms of piRNA-mediated silencing [reviewed in 82]. For example, a recent meta analysis including both *D. melanogaster* and *D. pseudoobscura* revealed that 22 of 26 piRNA pathway proteins exhibit significant signatures of adaptive protein evolution in one or both species [79].

Adaptive evolution of piRNA effector proteins is proposed to arise from an evolutionary arms race between TEs and host silencing machinery [reviewed in 48]. In the simplest scenario, effector proteins evolve adaptively in order to restore silencing of newly invading or escaper TE families. Alternatively, if TEs “fight back” by encoding RNA or protein antagonists of host silencing machinery, piRNA pathway proteins could evolve adaptively to escape TE antagonism [45]. Finally, piRNA proteins may evolve adaptively to avoid “genomic

auto-immunity” in the form of off-target silencing of host genes [48,49]. Uncovering which of these selective forces drives the adaptive evolution of piRNA effector proteins requires elucidating the resulting functional consequences of piRNA-effector-protein divergence. For example, adaptive evolution among transcriptional silencers has led to incompatibilities between alleles of interacting proteins from different species, with dramatic consequences for piRNA production and TE control [45,83,84]. In particular, functional changes in Rhino are proposed to reflect evolutionary escape from a TE-encoded antagonist [45].

Here, we broaden our understanding of the functional consequences of adaptive evolution among *Drosophila* piRNA effector proteins by examining three additional essential piRNA pathway components that play critical roles in piRNA maturation and post-transcriptional silencing [14,20,21,23,34,39,85]: Armitage (Armi), Aubergine (Aub) and Spindle-E (Spn-E). This work significantly extends a preliminary analysis of Aub divergence [46]. Aub is a Piwi-clade Argonaute protein which, guided by piRNAs, enacts post-transcriptional silencing of sense TE-derived mRNAs [20]. Aub cleavage also feeds forward the ping-pong amplification cycle, a core mechanism for the maturation of both sense and antisense piRNAs that also requires Spn-E [14,21,23,86]. Distinct from both Aub and Spn-E, Armi binds to antisense piRNA precursors to facilitate their sequential cleavage by the nuclease Zucchini in an alternate biogenesis mechanism referred to as “phasing” [24,26,38,85,87,88]. The loci encoding Aub, Spn-E and Armi all exhibit adaptive evolution along the lineage leading to *D. melanogaster*, *D. simulans* or both, yet the underlying evolutionary force(s) remain unknown [42,43].

To isolate diverged functions of these adaptively evolving proteins, we performed interspecific complementation, in which we compared the ability of *D. melanogaster* and *D. simulans* wild-type alleles to complement a *D. melanogaster* mutant background. While nuclear transcriptional silencers were previously demonstrated to exhibit dramatic interspecific divergence in TE regulation and piRNA production [45,84], we observed only

minor allelic differences in both of these functions. Rather, we uncovered idiosyncratic differences in the regulation of a small handful of TEs, suggesting potential element-specific adaptations. We also observed that *D. simulans* alleles of *aub* and *armi* exhibit reduced efficiency of piRNA maturation in association with increased off-target regulation of host mRNAs. We propose that in contrast to nuclear transcriptional silencers, selection acts on cytoplasmic piRNA proteins to maximize their specificity to piRNA production and TE transcripts, while minimizing non-functional or deleterious interactions with host mRNA.

2.2 Results

2.2.1 Identifying functional divergence through interspecific complementation

Previous divergence-based analyses of Aub and Spn-E suggest that adaptive evolution is not confined to a particular functional domain but is dispersed throughout the proteins [43,44]. Consistent with these findings, we identified abundant amino-acid differences between *D. melanogaster* and *D. simulans* throughout Aub and Spn-E (Figure 2.1A). Armi does not exhibit strong evidence of positive selection in divergence-based tests, however, an excess of amino acid substitutions exists between *D. melanogaster* and *D. simulans*, which have likely arisen by positive selection in one or both lineages [43]. Similar to Aub and Spn-E, we observe that these amino acid differences are scattered throughout the protein, both inside and outside of functional domains (Figure 2.1A).

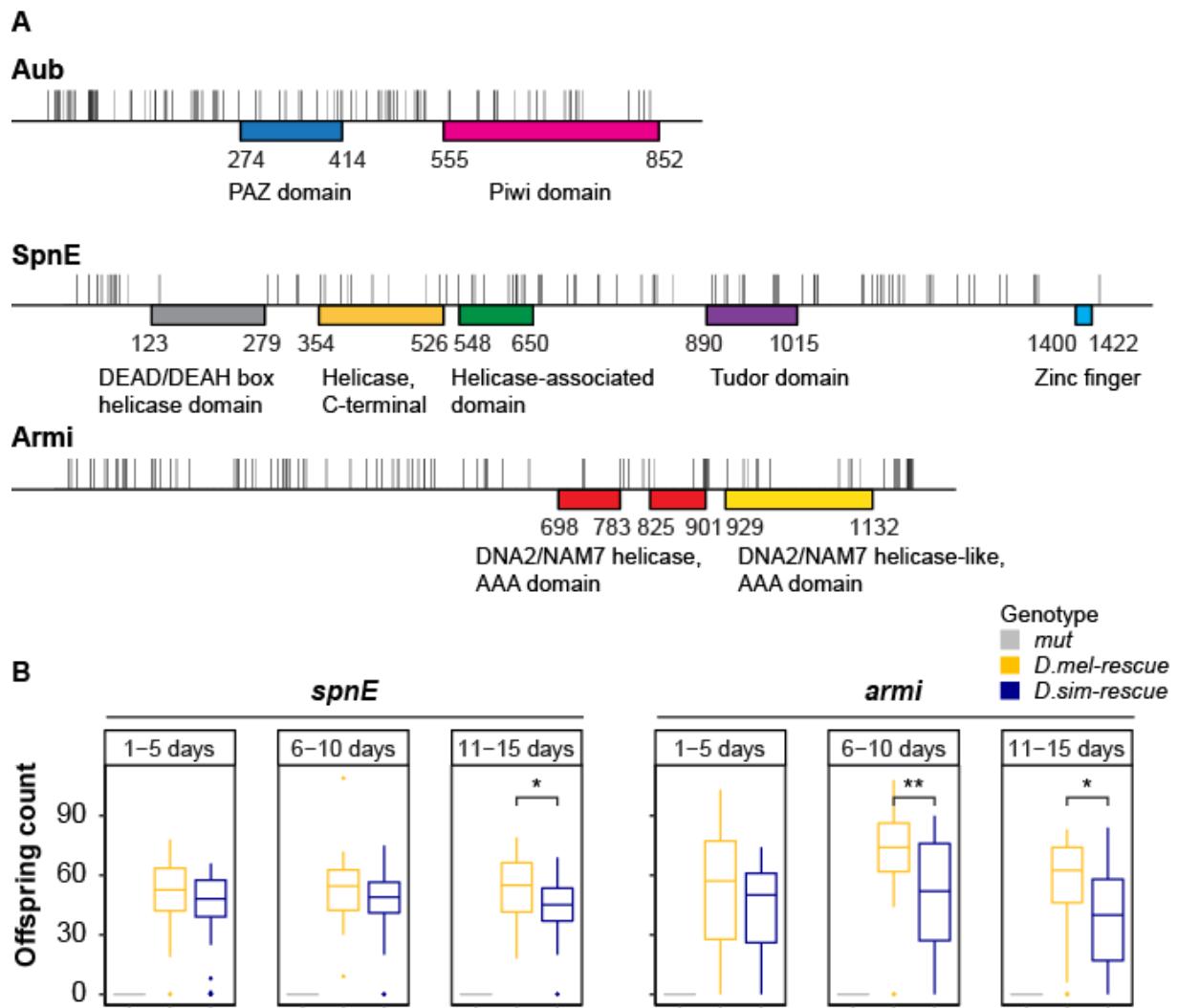


Figure 2.1 Functional and sequence divergence in piRNA pathway proteins. (A) Amino acid substitutions between *D. melanogaster* [89] and *D. simulans* [90] reference alleles are indicated as grey tick marks. Starting and ending amino acids for InterPro [91] annotated functional domains are indicated. (B) Female fertility for *D. melanogaster* and *D. simulans* transgenic rescues are compared for three different age classes. Females with the *D. simulans* *spn-E* transgene are significantly less fertile across the experiment (Repeated measures ANOVA, $F_{1,172} = 4.043$, $p < 0.05$) and at the third time point we measured (11-15 days, $t_{56} = 2.304$, $p < 0.05$). Females with the *D. simulans* *armi* transgene are significantly less fertile across the experiment (Repeated measures ANOVA, $F_{1,175} = 8.824$, $p < 0.01$) and at the second(06-10 days, $t_{57} = 3.0718$, $p < 0.01$) and the third time points (11-15 days, $t_{57} = 2.5915$, $p < 0.05$). Sample sizes are 25-35 females. * denotes $p \leq 0.05$. ** denotes $p \leq 0.01$.

To isolate phenotypic differences between *D. melanogaster* and *D. simulans* alleles that result from adaptive evolution, we employed interspecific complementation, in which we compared the ability of *D. melanogaster* and *D. simulans* wild-type alleles to complement a

D. melanogaster mutant background. For each selected piRNA protein, we generated and compared three genotypes: 1) a trans-heterozygous loss-of-function mutant, 2) the same mutant with a *D. melanogaster* genomic transgene rescue, and 3) the same mutant with a *D. simulans* genomic transgene rescue (Figure A2.1). The transgenes include the complete genomic region from either *D. melanogaster* or *D. simulans*, including upstream and downstream sequences containing potential cis-regulatory elements. Transgenes were inserted into matched *attP* sites by Φ C31 integrase [92], in order to avoid variable position effects. Phenotypes for which the *D. simulans* alleles fail to fully complement the mutant, or otherwise differ between the alleles of the two species, point to diverged functions that are potential targets of adaptive evolution.

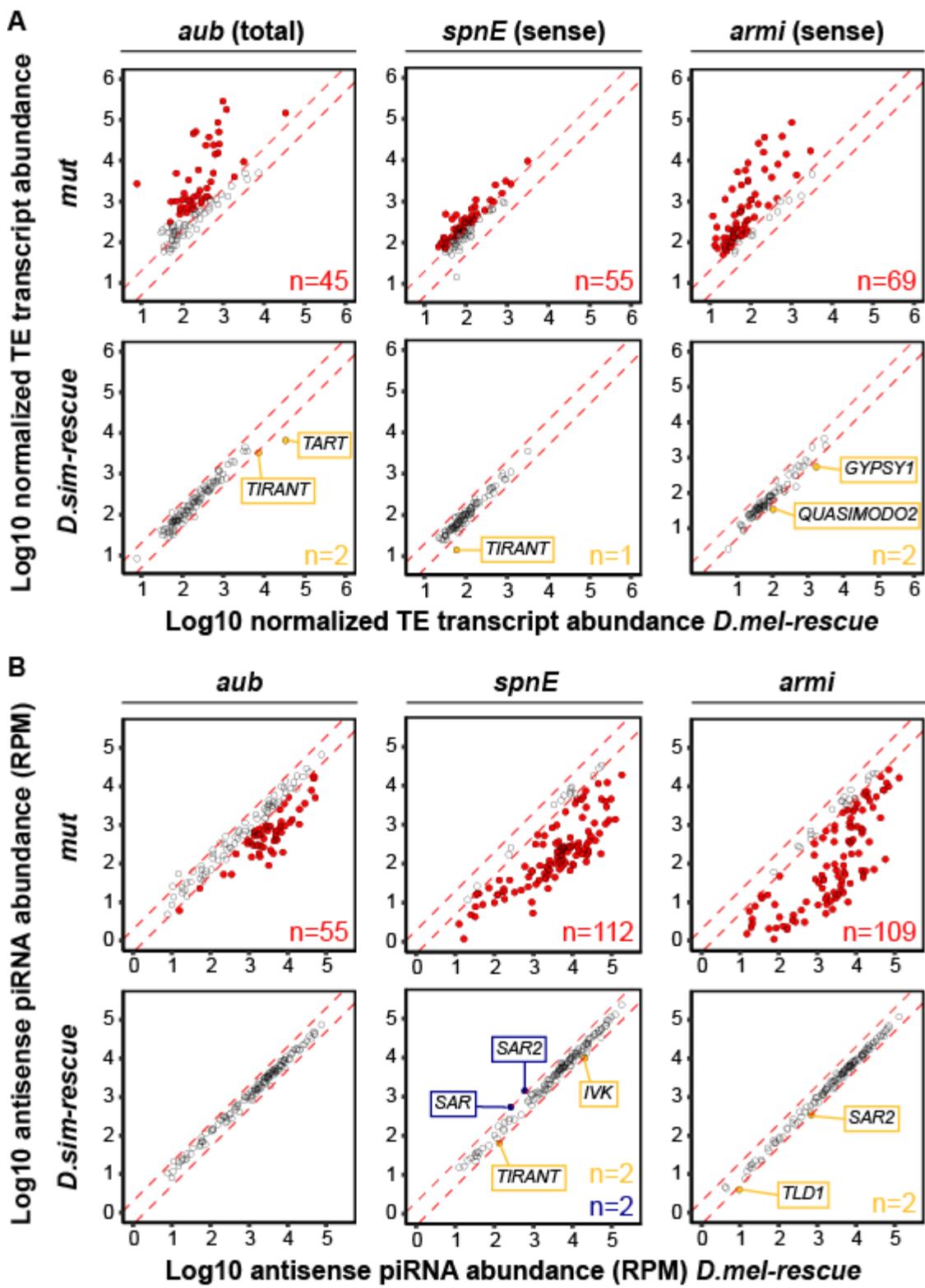
We first considered the effect of transgenic rescue on female fertility. Homozygosity or trans-heterozygosity for loss of function alleles in all three genes causes complete female sterility (Figure 2.1B, Table A2.1), while heterozygotes are fertile [93]. For all three proteins, fertility is restored by transgenic rescues from the two species to different degrees, with *D. melanogaster* transgenes conferring higher fertility than their *D. simulans* counterparts (Figure 2.1B, Table A2.1) [46]. *Drosophila simulans* transgenes do not exhibit significantly reduced expression when compared to *D. melanogaster*, in fact for *spn-E* the *D. simulans* transgene exhibits a modest 22% increase in expression (Figure A2.2). Therefore, reduced fertility effects in the presence of *D. simulans* transgenes most likely reflect amino acid sequence divergence in the encoded proteins.

2.2.2 Idiosyncratic differences in TE regulation

To uncover molecular phenotypes that relate to fertility differences, we first examined whether *D. melanogaster* and *D. simulans* alleles differed with respect to TE transcriptional control and associated piRNA production using RNA-seq and small RNA-seq (Figure A2.3, Table A2.2). Notably, our *D. melanogaster* transgenic rescues down-regulated TE transcripts

and up-regulated piRNA production similarly to heterozygotes, which are generally considered wild-type with respect to piRNA production and TE silencing (Figure 2.2, Figure A2.4, Table A2.3 and Table A2.4). Transgenically expressed *D. melanogaster* proteins are therefore fully functional with respect to TE silencing and piRNA biogenesis.

Figure 2.2 Minimal differences in TE regulation and piRNA production between alleles. TE transcript abundance (A) and TE-derived antisense piRNA abundance (B) is compared between *D. melanogaster* rescues and either trans-heterozygous mutants ("mut", upper row) or *D. simulans* rescues (lower row) for *aub*, *spn-E* and *armi*. Red dashed lines indicate the two-fold-change threshold. TE families whose abundance differs substantially between mutants and *D. melanogaster* rescues are indicated in red ($p < 0.05$ for TE transcripts; >2 -fold for piRNA abundance). P -values were not considered for small RNA analysis because the small number of TE families in the analysis (<130 families, Table A2.4) is unlikely to provide a sufficiently large sample size for the statistical model implemented in DESeq2 [94]. TE families whose abundance is more than two-fold higher in *D. melanogaster* rescues than in *D. simulans* rescues are in yellow, whereas the reciprocal is in blue. Total mRNA abundance is from unstranded mRNA sequencing of one biological replicate (*aub*), sense RNA abundance is from stranded RNA sequencing of three biological replicates (*spn-E* and *armi*). TE-derived piRNA abundance is based on two biological replicates for *aub* and three biological replicates for *spn-E* and *armi*, and was normalized to the total number of sequenced miRNAs in the same library.



Enhanced piRNA-mediated negative regulation of TEs is an obvious target of positive selection acting on piRNA pathway proteins. However, sense transcripts for the majority of TEs are not differentially expressed between the transgenic rescues for *armi* and *spn-E*, implying that negative regulation of TEs is largely conserved between species (Figure 2.2A). Similarly, the majority of TEs are not differentially expressed between *aub* transgenic rescues (non-stranded RNA-seq, Figure 2.2A). Nevertheless, despite an overall conservation of TE repression, we discovered idiosyncratic differences in regulation, in which individual TE families are more robustly silenced by the *D. melanogaster* or *D. simulans* allele. Unexpectedly, 5 out of 5 TE families whose transcript abundance differs between transgenic rescues for one of the three proteins are more robustly silenced by the *D. simulans* allele. While differences in TE copy number could arise between transgenes through backcrossing, thereby creating the appearance of differential regulation, this would be equally likely to result in increased or decreased expression in the *D. simulans* rescue for any given TE. Thus, the bias towards enhanced negative regulation by *D. simulans* is not consistent with the random segregation of polymorphic TE insertion alleles during backcrossing, but rather suggests a true increase in negative regulation by the *D. simulans* allele. In particular, the *tirant* LTR retrotransposon is more robustly silenced by the *D. simulans* allele of both *aub* and *spn-E*. Furthermore, we did not observe any systematic differences in expression for germline or soma-specific protein-coding genes between the transgenic rescues, strongly suggesting that the germline-to-soma ratio is equivalent between transgenic genotypes (Figure A2.2). Differences in silencing of individual TE families therefore suggest lineage-specific coevolution with the host-regulatory machinery.

Divergence in TE regulation between *D. melanogaster* and *D. simulans* alleles could arise from differential production of complementary antisense piRNAs. Of 5 TE families that are differentially regulated between transgenic rescues for one of the proteins (Figure 2.2A), only *tirant* differential expression between *spn-E* transgenes is associated with a

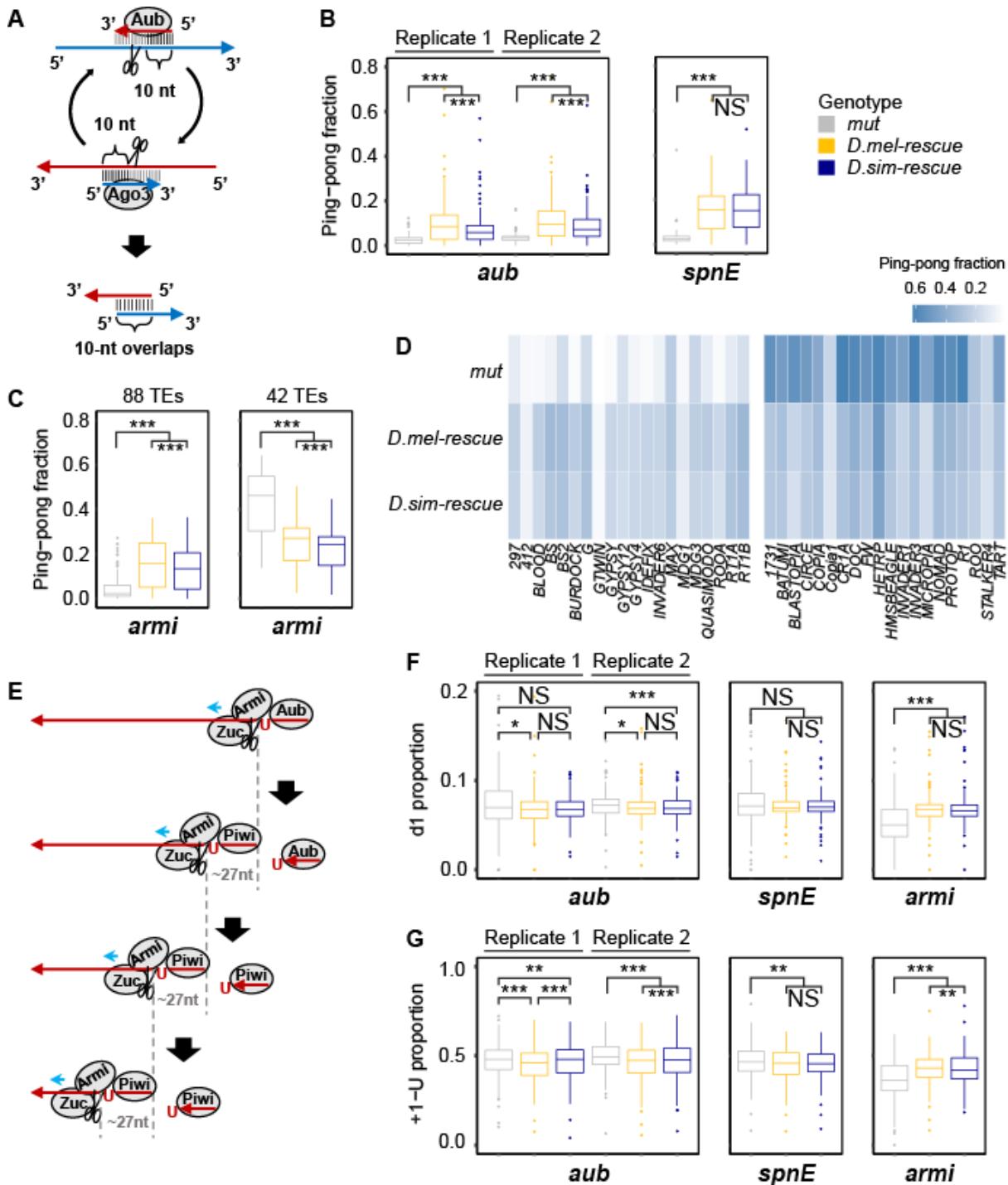
corresponding change in antisense piRNA abundance (Figure A2.5). Furthermore, *tirant* antisense piRNAs were increased in the *D. melanogaster* transgene, which is not consistent with piRNA loss as the cause of increased TE expression. Similar to their antisense counterparts, the abundances of sense piRNAs, which are produced during post-transcriptional silencing of TE-derived mRNAs, are not systematically different between transgenic rescues for differentially regulated TEs (Figure A2.5). Differences in TE negative regulation between alleles therefore occur independently of piRNA production. Furthermore, *D. simulans* and *D. melanogaster* alleles have very similar effects on the overall pool of TE-derived piRNAs, with only 10 repeat classes differentially abundant for sense or antisense piRNAs for any of the three pairs of transgenic rescues, four of which are satellite repeats (*HETRP*, *HMR1*, *SAR* and *SAR2*, Figure 2.2B, Figure A2.5 and Figure A2.6). Interspecific divergence in piRNA production is therefore modest between alleles, with no detectable impact on the regulation of genomic TEs.

2.2.3 *Drosophila simulans* alleles exhibit reduced piRNA biogenesis

Despite the absence of large-scale interspecific differences in antisense piRNAs that regulate TEs (Figure 2.2B), we interrogated piRNA pools associated with each of the transgenic rescues for evidence of underlying differences in piRNA biogenesis. We examined molecular signatures of the two major mechanisms of piRNA biogenesis: ping-pong and phasing. Ping-pong biogenesis produces piRNAs through reciprocal cleavage of complementary precursors (Figure 2.3A) [14,20]. The frequency of ping-pong amplification is therefore estimated by the fraction of piRNAs occurring on opposite strands of the TE consensus whose sequences overlap by 10 bp, a reflection of the cleavage-site preference of the key ping-pong cycle factors Aub and Argonaute-3 (Ago-3, Figure 2.3A-D, Table A2.5) [14,20,21]. In contrast, phasing biogenesis occurs through sequential cleavage of a single RNA strand, which is usually antisense [26,87]. Phasing is detected from the fraction of

piRNAs whose 3' ends are immediately followed by a uracil residue (+1-U), as well as the frequency of piRNAs from the same strand that are separated by a distance of a single nucleotide (d1), both of which are diagnostic of cleavage by the phasing nuclease Zucchini (Figure 2.3E-G, Table A2.6 and Table A2.7) [26,87]. In general, ping-pong and phasing are inversely correlated in mutant piRNA pools, because reducing the frequency of one leads to a proportional increase in the other [26,87].

Figure 2.3 *Drosophila simulans* alleles reduce ping-pong biogenesis and phasing biogenesis. (A) Simplified diagram of ping-pong amplification loop. (B) Ping-pong fractions of TE-derived piRNAs from 142 TE families are compared between trans-heterozygous mutants and transgenic rescues for *aub* and *spn-E*. (C) Ping-pong fractions of TE-derived piRNAs are compared between trans-heterozygous mutants and transgenic rescues for *armi*. Comparison for 88 and 42 TE families whose ping-pong fractions are decreased (left) or increased (right), respectively, in *armi* mutants as compared to the *D. melanogaster* transgenic rescue. (D) Left: ping-pong fraction heat map for the 20 most piRNA-abundant TE families from panel C left. Right: ping-pong fraction heat map for 20 most piRNA-abundant TE families from panel C right. (E) Diagram of Zucchini-dependent phased piRNA biogenesis. (F) Proportions of 1 nt distance between adjacent piRNAs (d1) mapped to the TE consensus sequences are compared between each genotype of each gene. (G) Proportions of uridine residues immediately after the 3' ends of piRNAs (+1-U) mapped to the TE consensus sequences are compared between each genotype of each gene. Statistical significance was assessed by the Wilcoxon signed-rank test. In all panels, for *aub*, two biological replicates of each genotype generated at different times are shown separately. For *spn-E* and *armi*, the average of three biological replicates of each genotype generated at the same time are shown. NS denotes $p > 0.05$. *, **, and *** denote $p \leq 0.05$, $p \leq 0.01$, $p \leq 0.001$, respectively.



Aub plays a direct role in ping-pong amplification by cleaving piRNA precursors (Figure 2.3A) [14,20,21], and *spn-E* is required for the localization of Aub into the perinuclear nuage, where ping-pong occurs [23]. Mutations in either gene therefore cause a complete

collapse of ping-pong amplification (Figure 2.3B, Figure A2.7A and B, Table A2.5) [21,86]. Both *D. melanogaster* and *D. simulans* *aub* and *spn-E* alleles exhibited a dramatic increase in the ping-pong fraction, indicating a conserved role in ping-pong biogenesis (Figure 2.3B, Figure A2.7A and B). However in the case of *aub*, ping-pong fractions associated with the *D. simulans* transgenic rescue were modestly yet significantly lower than *D. melanogaster*, and there was a corresponding proportional increase in phased piRNA biogenesis (Figure 2.3B, F and G, Figure A2.8, Table A2.6 and Table A2.7), suggesting reduced efficiency of ping-pong. By contrast, *D. simulans* *spn-E* allele did not reduce ping-pong (Figure 2.3B, Figure A2.7B, Table A2.5), yet there was a modest but significant increase in the d1 proportion with the *D. simulans* *spn-E* rescue (Figure 2.3F, Table A2.6), potentially suggesting increased phasing.

Armi promotes the production of phased piRNAs by binding to antisense piRNA intermediates and facilitating their cleavage by the nuclease Zucchini (Figure 2.3E) [26,85,87]. Both d1 and +1-U are therefore significantly reduced in *armi* mutants (Figure 2.3F and G, Figure A2.8, S6 and Table A2.7). While Armi is not involved in ping-pong, phasing produces Aub-bound antisense piRNAs, which are required for ping-pong biogenesis for some TE families [21,95]. Ping-pong fractions are therefore decreased in *armi* mutants for some TE families (Figure 2.3C and D, Figure A2.7C, Table A2.5). By contrast, for TE families that do not rely on phased piRNA production for ping-pong, ping-pong-derived piRNAs proportionally increase in *armi* mutants, owing to the loss of phased piRNAs (Figure 2.3C and D, Figure A2.7C, Table A2.5). Although exhibiting piRNA production similar to the *D. melanogaster* allele (Figure 2.2B), the *D. simulans* *armi* rescue exhibited modestly but significantly reduced +1-U proportion, indicating reduced phasing (Figure 2.3G, Figure A2.8B, Table A2.7). However, the more dramatic and statistically significant allelic effect is on ping-pong biogenesis, which is reduced for most TE families by the *D. simulans* *armi* rescue when compared to *D. melanogaster* (Figure 2.3C and D, Figure A2.7C, Table A2.5). Importantly, this reduction occurs regardless of whether *armi* function enhances or represses

ping-pong biogenesis, revealing a global inhibitory effect imposed by *D. simulans armi*. Indeed, although the differential abundance of TE and repeat-derived piRNAs between transgenic rescues rarely exceeded two-fold, significantly more TE families were more abundant in the presence of the *D. melanogaster armi* rescue compared to the *D. simulans armi* rescue (118 out of 131 TE families, Sign-test, *P*-value < 10⁻¹⁵). Therefore, the modest reductions in ping-pong and phasing biogenesis exhibited by the *D. simulans armi* allele lead to a similarly modest reduction in the abundance of TE and repeat-derived piRNAs.

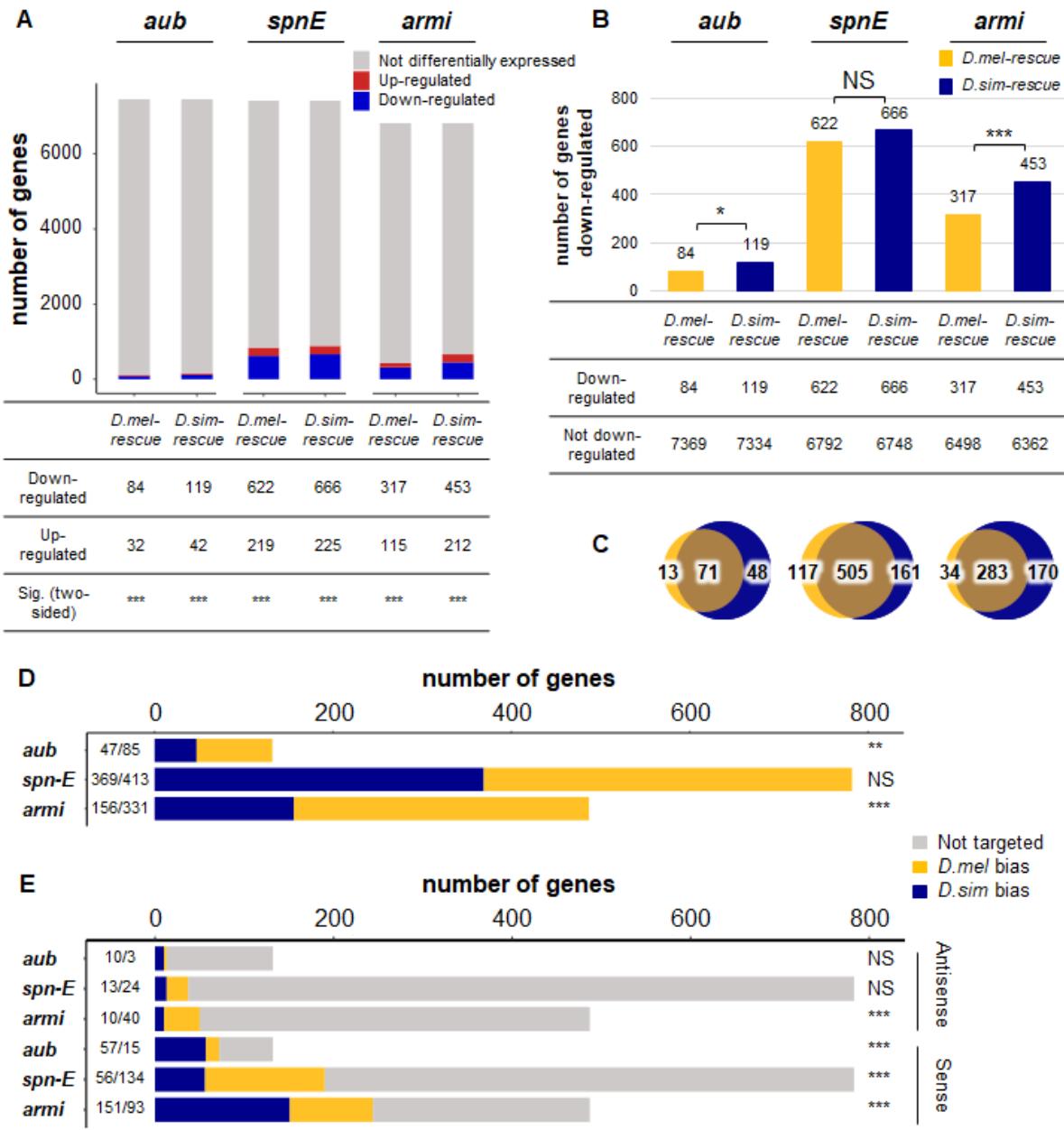
2.2.4 Increased off-target effects of *D. simulans* alleles suggest increased genomic auto-immunity

While effective negative regulation of TE transcripts is a critical function of piRNA pathway proteins, it is equally important that they avoid off-target effects that interfere with the function of host genes [48,49]. Aub, Spn-E and Armi are all RNA binding proteins that must specifically interact with piRNAs, piRNA precursors, and target transcripts, while avoiding interactions with cytoplasmic mRNAs. We therefore considered whether off-target effects differ between *D. melanogaster* and *D. simulans* alleles, predicting that *D. simulans* alleles may produce more off-target effects as they are not adapted to avoid interactions with *D. melanogaster* transcripts.

To test this prediction, we first identified protein-coding genes that are negatively regulated by piRNA pathway proteins by comparing their expression levels between mutants and transgenic rescues (Table A2.8). Protein-coding genes whose expression is significantly reduced in transgenic rescues (>1.5 fold) are candidates for off-target effects of piRNA-mediated silencing. We observed that for all three proteins, significantly more genes decreased than increased in expression in transgenic rescues compared to mutants (Figure 2.4A), suggesting that piRNA pathway proteins tend to reduce the expression of protein-coding genes. Furthermore, the majority of protein-coding genes that are negatively

regulated by *D. melanogaster* rescues are also repressed by *D. simulans* rescues, suggesting a shared impact on the expression of many protein-coding genes (Figure 2.4B and C). Indeed, protein-coding genes that are down-regulated by *aub* alleles from either species are enriched among mRNAs bound by Aub (Pearson's Chi-squared test, *P*-value = 0.04) [96].

Figure 2.4 Negative regulation of protein-coding genes suggests increased genomic auto-immunity of *D. simulans* alleles. (A) The number of genes whose expression levels are decreased/increased (>1.5 fold, blue/red) in the presence of each transgene as compared to the corresponding mutant. Statistical significance was assessed by the binomial test evaluating the probability of the observed proportion of down-regulated genes as compared to up-regulated genes under the null hypothesis that the two probabilities are equal. (B) The number of genes whose expression levels are decreased (>1.5 fold) in the presence of each transgene as compared to the corresponding mutant. Contingency tables are shown below. Statistical significance was assessed by the Pearson's Chi-squared Test of Independence. (C) Overlap of genes whose expression levels are decreased (>1.5 fold) in the presence of each transgene as compared to the corresponding mutant for *aub* (left Venn diagram), *spn-E* (middle Venn diagram) and *armi* (right Venn diagram). (D) For genes whose expression levels are down-regulated by alleles from either species, the number of those whose transcripts are more abundant in *D. melanogaster* rescues than in *D. simulans* rescues is in yellow (\log_2 fold-change between *D. mel* and *D. sim* > 0), whereas the reciprocal is in blue. \log_2 fold-change values of gene expression are based on one biological replicate for *aub* and three biological replicates for *spn-E* and *armi*, and are obtained from a DESeq analysis for *aub* and a DESeq2 analysis for *spn-E* and *armi* (adjusted *p* < 0.05 for Figure 2.4A-C). (E) For genes whose expression levels are down-regulated by alleles from either species, the number of those whose antisense/sense piRNAs are more abundant in *D. melanogaster* rescues than in *D. simulans* rescues is in yellow (\log_2 fold-change between *D. mel* and *D. sim* > 0), whereas the reciprocal is in blue. Genes whose piRNA abundance is too low to estimate the differential expression (< 50 piRNAs on average in at least one genotype) are represented in gray. Genic piRNA abundance is based on two biological replicates for *aub* and three biological replicates for *spn-E* and *armi*, and was normalized to the total number of sequenced miRNAs in the same library. The number of genes corresponding to the blue or yellow part of the bar graph is indicated in Figure 2.4D and E. NS denotes *p* > 0.05. * denotes *p* ≤ 0.05. ** denotes *p* ≤ 0.01. *** denotes *p* ≤ 0.001.



Consistent with the auto-immunity hypothesis, we observed expanded negative regulation of protein coding genes by *D. simulans* alleles of both *aub* and *armi*. While both *D. melanogaster* and *D. simulans* alleles tend to decrease expression of host genes, significantly more genes exhibit reduced expression when the *D. simulans* transgenic rescue is compared to the mutant (Pearson's Chi-squared test, *P*-value = 0.01338 for *aub*;

Pearson's Chi-squared test, P -value = 4.519×10^{-7} for *armi*) (Figure 2.4B). Furthermore, among those protein-coding genes down-regulated by either transgene, there is a systematic bias towards lower expression in the presence of the *D. simulans* alleles (One-sample Sign-Test, P -value = 0.001195 for *aub*; One-sample Sign-Test, P -value = 1.332×10^{-15} for *armi*). However, the majority of these genes are not significantly differentially expressed between transgenic rescues (127 out of 132 genes for *aub*, 481 out of 487 genes for *armi*) (Figure 2.4D, Table A2.9), indicating that expanded negative regulation by *D. simulans* alleles exhibits only a subtle effect on host gene expression.

Increased off-target effects of *D. simulans* alleles could be explained by increased production of antisense genic piRNAs that target host transcripts, or by piRNA-independent interactions between proteins and mRNAs. Recent analyses of off-target interactions between host mRNAs and Piwi (closely related to Aub) or Armi support the latter scenario, suggesting that while the binding of host mRNAs by piRNA proteins reduces mRNA abundance, it does not result from enhanced antisense genic piRNA production [39,97,98]. We therefore compared the abundance of antisense genic piRNAs that target the silencing of sense transcripts between transgenic rescues (Table A2.9). Of 132 and 487 protein-coding genes that are negatively regulated by either allele of *aub* and *armi*, only 13 and 50 are meaningfully targeted by antisense piRNAs, respectively (i.e. >50 antisense piRNAs on average are observed in at least one genotype, Figure 2.4E). Furthermore, no significant bias towards increased antisense piRNA production in the *D. simulans* allele was observed for either gene; indeed *D. simulans armi* even exhibits decreased, not increased, antisense piRNA abundance when compared to *D. melanogaster* (One-sample Sign-Test, P -value = 0.09229 for *aub*; One-sample Sign-Test, P -value = 2.386×10^{-5} for *armi*) (Figure 2.4E). Finally, *D. simulans* transgenic rescues do not exhibit expanded production of genic piRNAs for any of the three proteins (Figure A2.9). Therefore, enhanced negative regulation of host mRNAs by *D. simulans* Aub and Armi appears to be independent of antisense piRNA

production, and may arise through more frequent binding of *D. simulans* proteins to *D. melanogaster* transcripts.

If *D. simulans* Aub and Armi proteins exhibit enhanced binding to *D. melanogaster* mRNAs independently of antisense piRNAs, they could introduce them into the piRNA pool by treating them as substrates for piRNA maturation. Consistent with this model, we observed that sense piRNAs derived from genic transcripts that are negatively regulated by either transgene are significantly more likely to be more abundant in the presence of *D. simulans* alleles of *aub* and *armi* when compared to *D. melanogaster* (One-sample Sign-Test, *P*-value = 6.54×10^{-7} for *aub*; One-sample Sign-Test, *P*-value = 0.0002476 for *armi*). However, as with host mRNAs, these increases in sense piRNA abundance are subtle and predominantly not significant for individual genes (71 out of 72 genes in *aub* comparison, and 236 out of 244 genes in *armi* comparison are not significantly different) (Figure 2.4E, Table A2.9). While these modest increases in sense piRNA abundance are consistent with the use of host mRNAs as substrates for piRNA biogenesis, it is also possible that host mRNAs bound by piRNA proteins may be eliminated by the mRNA degradation machinery [99,100].

2.3 Discussion

Despite pervasive adaptive evolution and gene duplication among piRNA pathway proteins in both insect and vertebrate lineages [42–44,79,101,102], the underlying forces that drive these evolutionary dynamics remain unclear. By performing interspecific complementation on three adaptively evolving piRNA pathway genes, we revealed diverged functions that may have arisen through positive selection. For all three proteins we observed idiosyncratic differences in TE regulation between *D. melanogaster* and *D. simulans* alleles, which is consistent with genetic conflict between host and parasite. However, we also revealed more extensive off-target effects and reduced efficiency of piRNA maturation associated with *D. simulans* alleles of both *aub* and *armi*, suggesting that selection acts to maximize biogenesis

function while minimizing friendly fire on host transcripts. Taken together, our results suggest that positive selection acts at multiple molecular and functional interfaces within the piRNA pathway.

The simplest explanation for the adaptive evolution of piRNA proteins is that selection acts to maximize host control of TE transposition. At face value, TEs that are differentially expressed between transgenes from the two species seem to support this model (Figure 2.2A). However, all 5 of these TE families were more robustly silenced by the heterospecific *D. simulans* proteins. This suggests that rather than conspecific piRNA proteins being well-adapted to silence their genomic TEs, active genomic TEs may be well-adapted to evade silencing by their host regulators. Indeed the *tirant* element, which is more robustly regulated by *D. simulans* alleles of both *armi* and *spn-E*, is unusually active in *D. melanogaster* but is being actively lost from *D. simulans* [103–105]. We propose that the differential evolutionary dynamics of *tirant* in these two lineages may in part reflect the differences in host-control that we have uncovered.

Genomic auto-immunity was recently proposed as an additional target of positive selection among piRNA proteins [48]. The deliberate non-specificity of piRNA pathway proteins that allows them to target any sequence represented among piRNAs for silencing presents a huge liability for host-gene regulation: how can piRNA proteins avoid deleterious interactions with host transcripts? Furthermore, RNA-immunoprecipitation (RIP) and cross-linking immunoprecipitation (CLIP) of Piwi suggest that piRNA proteins may also negatively regulate host mRNAs by binding them directly in a piRNA-independent manner [97,98]. Similar observations have been made with Armi protein, with the ATP-ase domain being required to disassociate Armi from host mRNAs in the cytoplasm [39]. We observed that *D. simulans armi* and *aub* alleles are characterized by expanded negative regulation of host genes (Figure 2.4A-C), which is accompanied by reduced efficiency of TE-derived piRNA production (Figure 2.3). Importantly, this observation is not consistent with a subtle difference

in protein abundance between transgenic rescues, since this would reduce both piRNA biogenesis and off-target effects. Rather our observations suggest that *D. simulans* alleles bind more frequently to host mRNAs (Figure 2.4), thereby reducing host-gene expression and depleting the pool of protein available to enact piRNA maturation. Nevertheless, we cannot discount an equally intriguing alternative explanation: that *D. simulans* alleles have decreased affinity for interacting protein partners that mediate piRNA biogenesis, which liberates them to bind more frequently to host mRNAs. Future comparisons of molecular interactions involving *D. melanogaster* and *D. simulans* proteins could differentiate between these alternatives.

Our observations considerably expand our understanding of the enigmatic forces that drive adaptive evolution across the piRNA pathway. The three proteins we studied here, which are cytoplasmic factors involved in piRNA maturation and post-transcriptional silencing, provide an informative contrast to similar studies of three adaptively evolving nuclear transcriptional silencing factors: Rhino, Deadlock and Cutoff [45,83,106]. In comparison to the modest functional differences we observed between *D. melanogaster* and *D. simulans* alleles, nuclear factors are characterized by dramatic interspecific divergence, with *D. simulans* alleles behaving similarly to loss of function or dominant negative mutations [45,83,106]. Furthermore, adaptive evolution among transcriptional silencers has resulted in interspecific incompatibilities between interacting proteins, as opposed to the divergence in protein-RNA interactions that our data suggest. These observations logically reflect differences in the molecular functions of the two classes of proteins, with transcriptional regulation relying on suites of proteins that modify chromatin or regulate RNA-polymerase, while piRNA maturation and post-transcriptional silencing relies more on interactions between proteins and RNA.

Interestingly, a recent meta-analysis of piRNA protein evolution in insects revealed that while positive selection is pervasive throughout the piRNA pathway, signatures of

adaptive evolution are significantly stronger among nuclear transcriptional regulators, as compared to the cytoplasmic factors we studied here [79]. Thus, our functional analysis recapitulates an evolutionary signature in sequence data. Why might nuclear transcriptional regulators diverge more rapidly or dramatically than their cytoplasmic counterparts? Enhanced positive selection on nuclear factors may reflect their greater potential to fully suppress the expression of host genes through disrupted chromatin state, as opposed to depleting host transcripts through non-productive binding [48]. We therefore propose that off-target effects may play an under-appreciated role in the evolution of both nuclear and cytoplasmic piRNA proteins, with the strength and consequences of positive selection depending on the mechanisms of—and costs to—host gene regulation.

2.4 Materials and methods

2.4.1 Fly strains and crosses

All *Drosophila* strains were reared at room temperature on standard cornmeal media.

For the studies of *aubergine* (*aub*), the following *D. melanogaster* strains were used: *w; aub^{N11} bw¹/CyO, y w; aub^{HN} bw¹/CyO, y w; aub^{HN} bw¹/CyO; $\Phi P\{D. melanogaster aub\}$, and y w; aub^{HN} bw¹/CyO; $\Phi P\{D. simulans aub\}$.* *w; aub^{N11} bw¹/CyO*, was a gift from Paul MacDonald. *y w; aub^{HN} bw¹/CyO* was obtained by extracting *y w* into *aub^{HN} bw¹/CyO* (Bloomington *Drosophila* Stock Center #8517). *y w; aub^{HN} bw¹/CyO; $\Phi P\{D. melanogaster aub\}$* and *y w; aub^{HN} bw¹/CyO; $\Phi P\{D. simulans aub\}$* , originally generated in [46], were backcrossed for 6 generations in *y w; aub^{HN} bw¹/CyO* to minimize background effects that could lead to differences between transgenic stocks that are unrelated to the transgenes.

For the studies of *spindle-E* (*spn-E*), the following *D. melanogaster* strains were used: *y w; spn-E¹/TM6, y w; spn-E^{hls-03987}/TM6, y w; spn-E^{hls-03987}/TM6; $\Phi P\{D. melanogaster spn-E\}$, and y w; spn-E^{hls-03987}/TM6; $\Phi P\{D. simulans spn-E\}$.* *y w; spn-E¹/TM6* and *y w; spn-E^{hls-03987}/TM6* were obtained by crossing *spn-E¹/TM3* and *spn-E^{hls-03987}/TM3* (gifts from Celeste

Berg) to $y\ w; TM3/TM6$. To generate $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. melanogaster spn-E\}$ and $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. simulans spn-E\}, w^{1118}; \Phi P\{D. melanogaster spn-E\}$ and $w^{1118}; \Phi P\{D. simulans spn-E\}$ were first crossed to $y\ w; TM3/TM6. +/TM6; \Phi P\{D. melanogaster spn-E\}/+$ and $+/TM6; \Phi P\{D. simulans spn-E\}/+$ offspring were then crossed to $y\ w; spn-E^{hls-03987}/TM3$. Finally, $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. melanogaster spn-E\}/+$ and $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. simulans spn-E\}/+$ offspring were backcrossed into $y\ w; spn-E^{hls-03987}/TM6$ for 6 generations, and subsequently homozygosed for the transgene, to minimize background effects.

For the studies of *armite* (*armi*), the following *D. melanogaster* strains were used: $y\ w; armi^1/TM6, w; armi^{72.1}/TM6, w; armi^{72.1}/TM6; \Phi P\{D. melanogaster armi\}$, and $w; armi^{72.1}/TM6; \Phi P\{D. simulans armi\}$. $y\ w; armi^1/TM6$ was obtained by crossing $y\ w; armi^1/TM3$ (Bloomington *Drosophila* Stock Center #8513) to $y\ w; TM3/TM6$. $w; armi^{72.1}/TM6$ was obtained from Bloomington *Drosophila* Stock Center (#8544). To generate $w; armi^{72.1}/TM6; \Phi P\{D. melanogaster armi\}$ and $w; armi^{72.1}/TM6; \Phi P\{D. simulans armi\}, w^{1118}; \Phi P\{D. melanogaster armi\}$ and $w^{1118}; \Phi P\{D. simulans armi\}$ were first crossed to $y\ w; TM3/TM6. +/TM3; \Phi P\{D. melanogaster armi\}/+$ and $+/TM3; \Phi P\{D. simulans armi\}/+$ offspring were then crossed to $w; armi^{72.1}/TM6$. Finally, $w; armi^{72.1}/TM3; \Phi P\{D. melanogaster armi\}/+$ and $w; armi^{72.1}/TM3; \Phi P\{D. simulans armi\}/+$ were backcrossed into $w; armi^{72.1}/TM6$ for 6 generations, and subsequently homozygosed for the transgene, to minimize background effects.

Experimental genotypes were obtained from the following crosses. For studies of *aub*, virgin females $w; aub^{N11} bw^1/CyO$ were crossed to (1) $y\ w; aub^{HN} bw^1/CyO$, (2) $y\ w; aub^{HN} bw^1/CyO; \Phi P\{D. melanogaster aub\}$ or (3) $y\ w; aub^{HN} bw^1/CyO; \Phi P\{D. simulans aub\}$ males. For studies of *spn-E*, virgin females $y\ w; spn-E^1/TM6$ were crossed to (1) $y\ w; spn-E^{hls-03987}/TM6$, (2) $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. melanogaster spn-E\}$ or (3) $y\ w; spn-E^{hls-03987}/TM6; \Phi P\{D. simulans spn-E\}$ males. For studies of *armi*, virgin females $y\ w; armi^1/TM6$

were crossed to (1) *w; armi*^{72.1}/*TM6*, (2) *w; armi*^{72.1}/*TM6;* Φ*P{D. melanogaster armi}* or (3) *w; armi*^{72.1}/*TM6;* Φ*P{D. simulans armi}* males. Crosses were maintained at 25°C on standard cornmeal media.

2.4.2 Generation of transgenic lines

To introduce *D. melanogaster* and *D. simulans* alleles into *D. melanogaster*, we used ΦC31 integrase-mediated transgenesis system [92], which allows for site-specific integration. To generate transgenes, the gene and flanking regulatory regions of *spn-E* (~9.7 Kb, *D. melanogaster* Release 6, 3R:15835349..15845065; *D. simulans* Release 2, 3R:9575537..9585081) [107,108] and *armi* (~6 Kb, *D. melanogaster* Release 6, 3L:3460305..3466368; *D. simulans* Release 2, 3L:3357002..3363099) [107,108] were PCR-amplified by using corresponding primers (below) and iProof high-fidelity taq DNA polymerase (Bio-Rad).

D.mel/D.sim-spn-E forward primer: ATTGAACGCCGTCTATGCCAAGC

D.mel/D.sim-spn-E reverse primer: ACTGTTGCCATTGCCACAGATTG

D.mel/D.sim-armi forward primer: CACCGCTGAAAGATAACGCACACG

D.mel-armi reverse primer: GCTAGCCTGCGCTTGGGAGTGTTACCATTG

D.sim-armi reverse primer: GCTAGCCTGACCTGGGAGTGTTACCACCTC

The PCR products were cloned into pCR-Blunt-II-Topo according to manufacturer instructions (Invitrogen). Mutation-free clones were verified by sequencing.

attB-containing constructs used for site-specific integration were generated by subcloning the *NotI/BamHI* fragment of each *spn-E* TOPO plasmid, and the *NotI/NheI* fragment of each *armi* TOPO plasmid into *NotI/BamHI* and *NotI/XbaI*-linearized *pCasper4/attB* [109], respectively. *spn-E* and *armi* transgenic constructs were introduced into *D. melanogaster* at the *P{CaryP}attP40* site, and site-specific integration of transgenes was

confirmed by PCR [110]. The resulting transgenes were made homozygous in *D. melanogaster* *w¹¹¹⁸*. Transgenes are indicated as $\phi P\{$ in genotypes.

2.4.3 Female fertility

25-35 individual virgin females of each experimental genotype were crossed to two *y w* males on standard cornmeal media at 25°C. Fresh media and new males were provided every 5 days. The number of progeny from each 5-day period was quantified.

2.4.4 Small RNA-seq

3-6-day old female ovaries were dissected from each experimental genotype and placed directly in Trizol reagent (Invitrogen), and homogenized. For *aub* genotypes, Illumina small RNA libraries were prepared by Fasteris according to a proprietary protocol that depletes for 2S-RNA. Because the two biological replicates were prepared at different time points (5/13 and 7/13), they were analyzed separately. Small RNA libraries for *spn-E* and *armi* genotypes were prepared as described in [111]. In brief, total RNAs were extracted according to the manufacturer's instructions, and size fractionated on a 12% polyacrylamide/urea gel to select for 18-30 nt small RNAs. Small RNAs were treated with 2S Block oligo (5'-TAC AAC CCT CAA CCA TAT GTA GTC CAA GCA/3SpC3'-3'), and were subsequently ligated to 3' and 5' adaptors, reverse transcribed and PCR amplified using NEBNext Multiplex Small RNA Library Prep Set for Illumina. Small RNA libraries were further purified from a 2% agarose gel and sequenced on a Illumina NextSeq 500 at the University of Houston Seq-N-Edit Core.

2.4.5 RNA-seq

RNA-seq libraries for the studies of *aub* were generated by Weill Cornell Epigenomics Core according to the protocol of [112]. Briefly, total RNA was extracted from the same ovaries as above, and mRNAs were isolated using poly-T Dynabeads (Invitrogen) according to the

manufacturer's instructions. Isolated mRNAs were further fragmented using fragmentation buffer (Ambion), ethanol precipitated, and reverse transcribed using Superscript II (Invitrogen) and random hexamer primers. Second-strand synthesis was performed using DNA polymerase I (Promega). cDNA was purified on a MinElute column (Qiagen), repaired with End-IT DNA repair kit (Epicentre), A-tailed with Klenow enzyme (New England Biolabs), and ligated to Illumina adaptors. Ligated cDNA was gel purified with the MinElute gel purification kit (Qiagen), PCR amplified, and gel purified again to make libraries.

RNA-seq libraries for the studies of *spn-E* and *armi* were prepared by using TruSeq Stranded Total RNA Library Preparation Kit for Illumina. 50 bp reads from each library were sequenced on a HiSeq 2000 (Aub and Spn-E) and a HiSeq 2500 (Armi) by the Weill-Cornell Epigenomics Core. RNA-seq and small RNA-seq data sets are deposited under PRJNA494103.

2.4.6 Bioinformatic analysis of small RNA-seq libraries

3' Illumina adaptors were removed from sequencing reads by Cutadapt [113]. Sequence alignments were made by Bowtie [114]. Contaminating ribosomal RNAs were identified and removed by mapping sequencing reads to annotated ribosomal RNAs from flybase [115]. TE-derived piRNAs and genic piRNAs were identified by aligning sequencing reads ranging from 23-30 nucleotides (nt) to Repbase [116] or protein-coding gene reference sequence from Flybase [115], respectively, allowing for up to two mismatches. The number of reads mapped to each TE family or gene were counted using a Linux shell script. Redundant TE families in Repbase were identified by checking sequence identity (those consensus sequences that were >90% identical across >90% of their length were categorized as the same TE family), and reads mapped to multiple redundant TE families were counted only once. Reads mapped to multiple non-redundant TE families were discarded. To identify miRNAs sequencing reads ranging from 18-22 nt were aligned to a miRNA reference

sequence from Flybase [115]. TE families or genes with low read count (< 50 on average) in every genotype library were discarded. piRNA counts for each TE family or gene were normalized to the total number of sequenced miRNAs from each library. Normalized values were used for comparisons of the abundance of piRNAs between libraries.

2.4.7 Bioinformatic analysis of RNA-seq libraries

Removal of ribosomal RNAs, and identification of TE-derived reads was performed as for small RNA libraries (above) except that three mismatches were permitted between sequencing reads and TE consensus sequences. Non TE-derived reads were aligned to flybase annotated transcripts in the *D. melanogaster* reference genome (*D. melanogaster* Release 6) [107,115] by TopHat [117], requiring unique mapping. The number of reads from each protein-coding gene were counted using HTseq-count [118]. TE families or genes with low read count (< 50 on average) in every genotype were discarded. Differential expression was estimated concurrently for TEs and protein-coding genes by DESeq for *aub* [119] and DESeq2 for *spn-E* and *armi* [94]. TEs or protein-coding genes were considered differentially expressed if they exhibited an adjusted *P*-value < 0.05 and a fold-change > 2 for TEs and > 1.5 for protein-coding genes.

2.4.8 Ping-pong fraction

Ping-pong fraction was calculated as described in [62]. In brief, small RNA sequencing reads ranging from 23-30 nt were aligned to TE consensus sequences from Repbase [116], and redundant TE families in Repbase were identified as described above. For each piRNA, the proportion of overlapping antisense binding partners whose 5' end occurs on the 10th nucleotide was determined. This fraction was subsequently summed across all piRNAs from a given TE family, while incorporating the difference in sampling frequency between individual piRNAs. Finally, this sum was divided by the total number of piRNAs aligned to the

TE family of interest. For multi-mappers, reads were apportioned by the number of times they can be aligned to the reference.

2.4.9 Phasing analysis

Small RNA sequencing reads ranging from 23-30 nt were aligned to the Repbase [116], and redundant TE families in Repbase were identified as described above. To calculate the d1 proportion [87], the number of piRNAs whose 5' end was 1-22 nt downstream piRNA was determined for every TE-derived piRNA. The fraction of distances corresponding to 1 nt was then calculated. To calculate the +1-U proportion [87], the nucleotide after the 3' end of each piRNA was determined based on alignment to the Repbase [116]. The frequency of each nucleotide at the +1 position was subsequently summed across all piRNAs from a given TE family, and the proportion of uridine was calculated. For both analyses, multiply-mapping reads were apportioned by the number of times they aligned to the reference.

Chapter 3 Host response to an invading TE: repression vs. extinction

3.1 Introduction

Transposable elements (TEs) are genomic parasites that can increase their genomic copy numbers and change their genomic locations through replication and mobilization. Unrestricted TE transposition can impose a severe mutation load on their hosts by inserting into gene coding sequences [8–10], and mediating ectopic recombination leading to chromosome rearrangements [11,12]. In addition, TE mobilization can trigger the DNA damage response within cells [13], which is associated with germline loss and sterility. Thus, TEs must be strictly regulated in host genomes, especially in germline cells where TE-induced mutations could be transmitted to offspring. In the germline of most organisms, TEs are regulated by a conserved small RNA silencing pathway, the piRNA pathway, in which piRNAs bind to and guide PIWI-clade Argonaute proteins to their complementary target TEs, and then silencing is induced by Argonaute proteins transcriptionally and post-transcriptionally [14,15].

TEs can frequently invade new hosts through horizontal transfer between non-mating species [50]. In *Drosophila* genomes nearly one-third of TE families have experienced horizontal transfer [54]. Thus, host genomes are often challenged to suppress the new TE invaders, which can potentially drive adaptive evolution of the piRNA pathway [122,123]. Although endogenous TEs are regulated by the host piRNA silencing system, it is not clear how the host evolves the repression against a newly invaded TE. Currently, the prevailing hypothesis is the “trap” model, in which repressor alleles are proposed to arise through transpositional insertions into piRNA producing loci referred to as piRNA clusters [55–57].

The recent invasion of the *Drosophila melanogaster* genome by *P*-element DNA transposons provides a great opportunity to study the genetic dynamics among the evolution process of piRNA mediated host TE repression. *P*-elements invaded the *D. melanogaster* genome by horizontal transfer from *D. willistoni* around 1950 [59–61]. In response, many

natural populations of *D. melanogaster* evolved piRNA-mediated repression almost concurrently with its invasion, in less than 50 years [56,60–63].

P-element transposition causes hybrid dysgenesis, a sterility syndrome characterized by elevated mutation rates, and increased chromosome rearrangement and recombination, and germline loss [64–68] among offspring of fathers with genomic *P*-elements and mothers without genomic *P*-elements, as no *P*-element piRNAs are maternally transmitted to the offspring. Thus, the ability of a strain to induce hybrid dysgenesis among their offspring provides an estimate of *P*-element transposition, while the ability of a strain to reduce hybrid dysgenesis among their offspring can be used to estimate the host repression against *P*-elements.

Hybrid dysgenesis further presents a major fitness cost of *P*-elements to their host. Therefore, the severity of hybrid dysgenesis is predicted to increase positive selection for repression, as well as negative selection against *P*-element accumulation. In addition, the severity of hybrid dysgenesis phenotype is positively correlated with temperature [67]. We therefore hypothesize that at different temperatures the effects of natural selection on the evolution of *P*-element repression would be different.

P-element insertions in piRNA clusters are ubiquitous in natural populations of *D. melanogaster*, and played a critical role in the evolution of host repression against *P*-elements [124,125]. *P*-element insertions in subtelomeric piRNA clusters located in telomeric associated sequence (TAS) have been demonstrated to confer maternal repression of *P*-element by producing *P*-element-derived piRNAs [62,126–128]. In addition, *P*-element insertions into non-TAS piRNA clusters can also establish repression [56,129], supporting a general role for piRNA clusters in regulating *P*-elements.

Here, we introduced *P*-elements into a naïve *D. melanogaster* strain through germline transformation, and recreated the process of *P*-element invasion and the evolution of the host repression. To determine whether different fitness costs of hybrid dysgenesis by *P*-

element pose different effects on the evolution of host repression we also contrasted the evolution between populations under two different temperature conditions. Consistent with previous studies [56,62,124,126–129], most populations evolved repression as *P*-elements accumulated, through the transposition of *P*-elements into multiple different piRNA clusters. Our results support the “trap” model that host TE repression evolves through *de novo* insertions into existing piRNA clusters, and indicate that repression evolves via the concurrent emergence of multiple different repressor alleles.

3.2 Results

3.2.1 Evolved populations exhibit increasing *P*-element activity, and also increasing repression

To explore details of the evolution of host TE repression, we recreated the process of TE invasion using *P*-elements, and reconstructed the evolution of host TE repression (Figure 3.1). *P*-elements were introduced into a naive *D. melanogaster* strain through 10 independent germline transformations, which established 10 populations with unrepresed genomic *P*-elements. Successful transformations were confirmed by PCR.

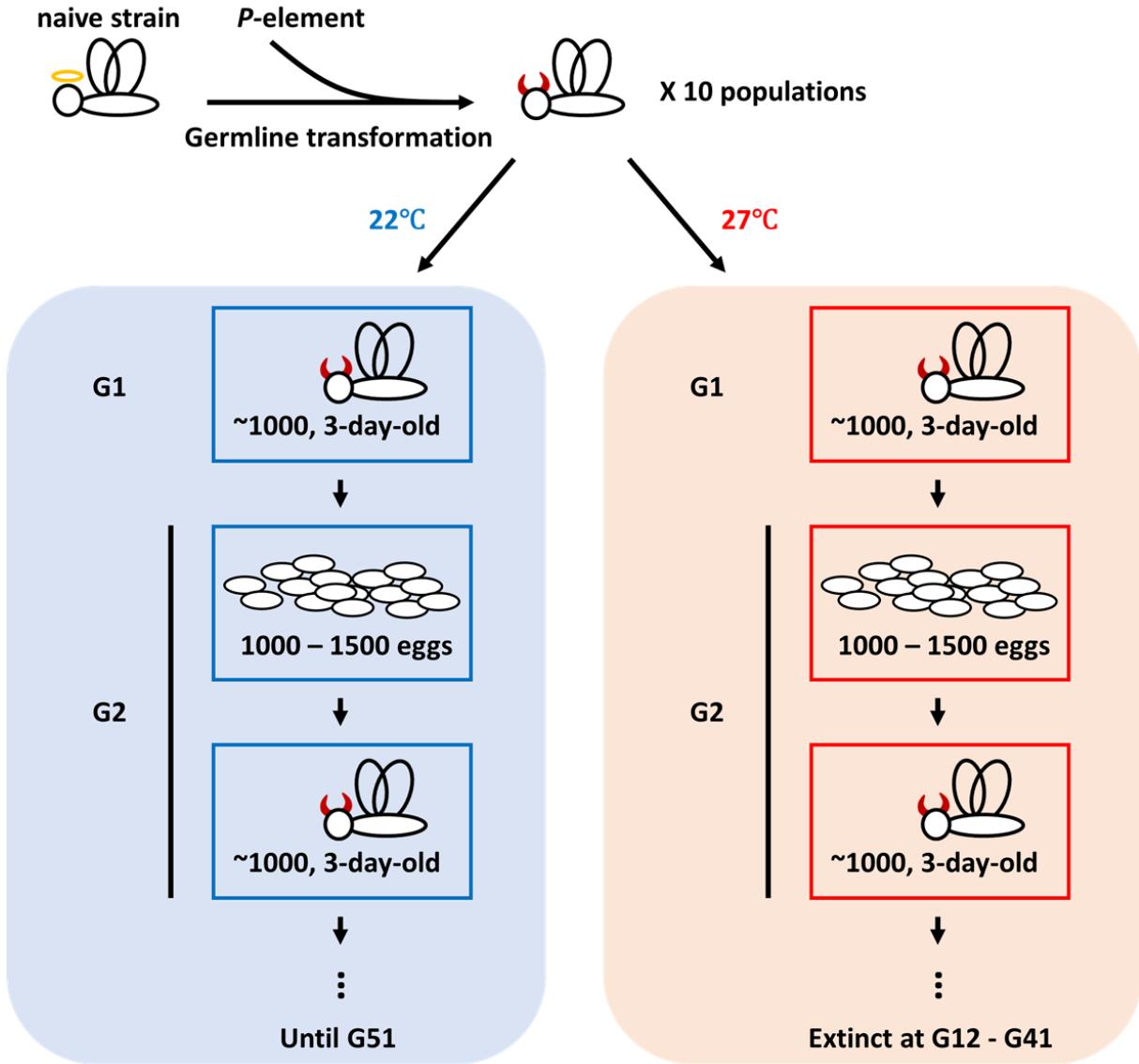


Figure 3.1 Experiment design for recreating *P*-element invasion and evolution of host TE repression.

To evaluate whether different fitness costs of hybrid dysgenesis by *P*-element pose different effects on the evolution of host repression, we separated each population into two different temperature conditions, 22 °C and 27 °C. All populations were maintained for three years (51 generations for 22 °C populations; 27 °C populations went extinct between generation 12 and 41) to allow the evolution of repression. To track the accumulation of genomic *P*-elements and the evolution of *P*-element repression in all populations, we

crossed experimental flies to P and M strains every 5 generations. piRNA-mediated repression is detected from crosses between experimental females and P strain males (Harwich) (Figure 3.2A). A higher proportion of fertile F1 females indicates higher quantity of maternally transmitted piRNAs [62]. Induction ability, which is related to the accumulation of *P*-element copies, was tested by crosses between experimental males and M strain females (Canton-S) (Figure 3.2B). A higher proportion of fertile F1 females indicates lower ability of induction, i.e. fewer *P*-element copies.

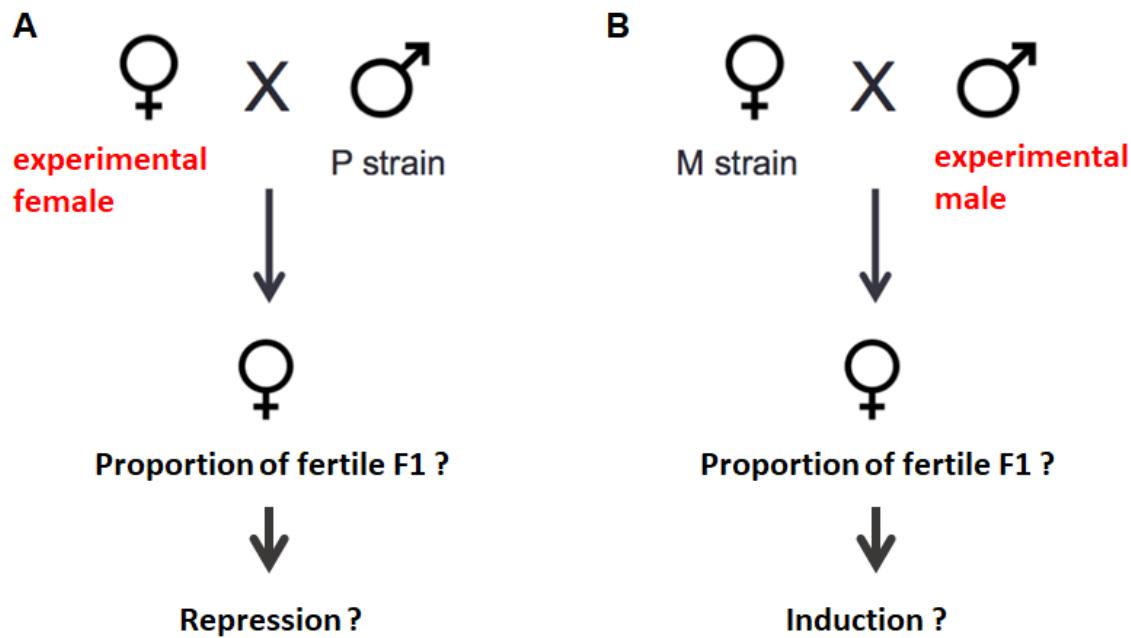


Figure 3.2 Cross design for phenotype checking. Cross scheme for checking the ability of host *P*-element repression (A) and *P*-element activities (B) in each population.

In our experiment, all 22 °C populations successfully survived for 51 generations. Most 22 °C populations (9 out of 10) exhibited elevated induction of hybrid dysgenesis as generation increases (mixed effects logistic regression, $p < 0.05$), suggesting accumulation of active *P*-elements (Figure 3.3A, solid lines). Correspondingly, maternal repression of *P*-elements also increased in most populations (mixed effects logistic regression, $p < 0.05$) (Figure 3.3A, dashed lines). Population 21, however, did not evolve repression, and induction

remained low throughout the experiment. Together, these results indicate that the accumulation of genomic *P*-elements is accompanied by the evolution of host repression.

The 27 °C populations all went extinct between generation 12 and generation 41. Furthermore, most 27 °C populations did not exhibit significantly increased abilities of *P*-element repression and induction (Figure 3.3B). There was one population, population 8, that survived longer than others, which showed an increased repression (mixed effects logistic regression, $p > 0.05$) as well as elevated induction (mixed effects logistic regression, $p < 0.05$) as compared to the other 27 °C populations (Figure 3.3B).

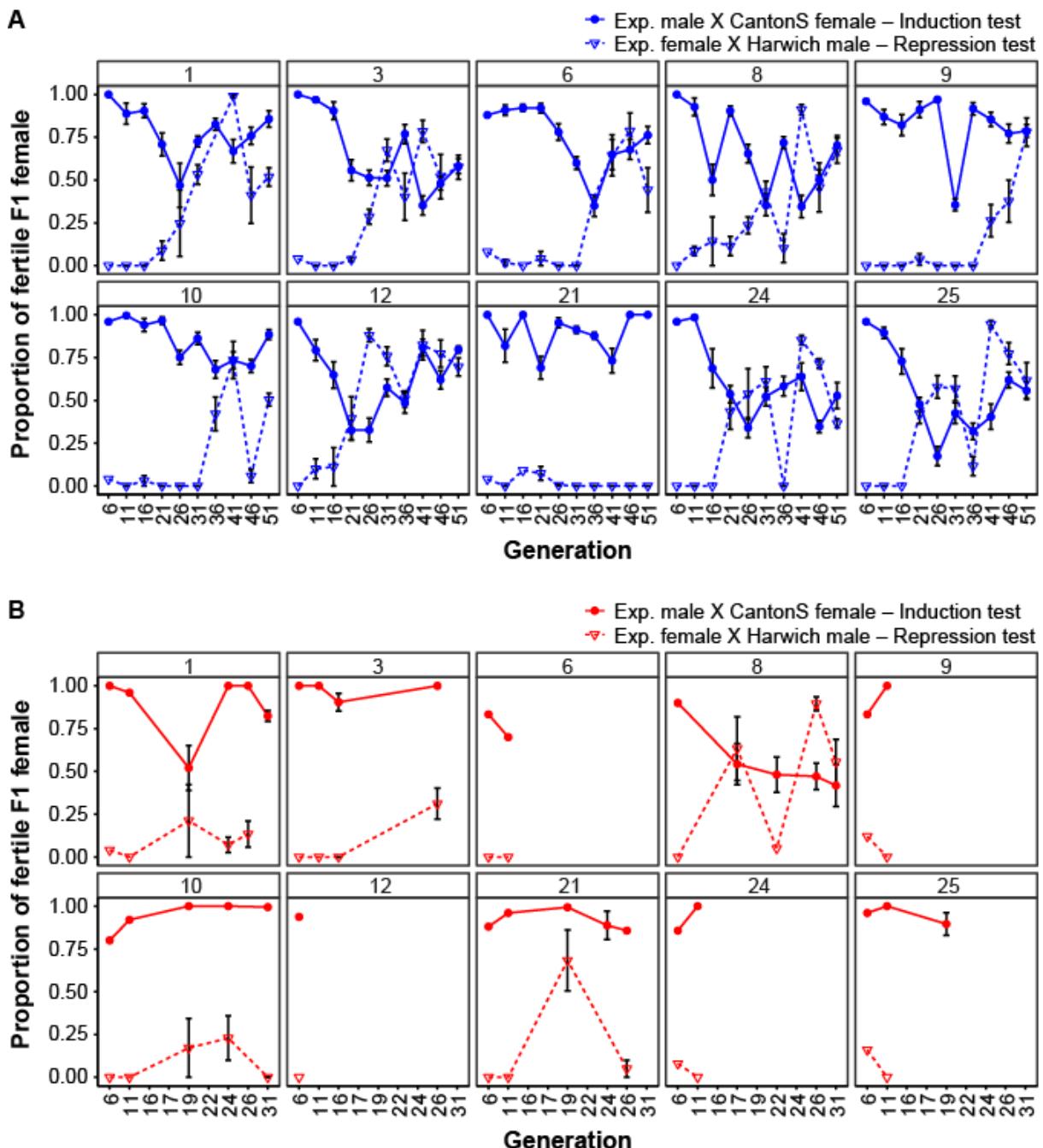


Figure 3.3 P-element accumulation correlates with repression. Most 22 °C populations exhibit increasing *P*-element activity and repression. Changes of repression and induction ability of 22 °C populations (A) and 27 °C populations (B) over time are shown. Dashed lines and triangles indicate repression crosses (experimental female X Harwich male), higher proportion of fertile F1 females means higher repression ability. Solid lines and dots indicate induction crosses (experimental male X Canton-S female), higher proportion of fertile F1 females means lower induction ability.

3.2.2 Whole genome sequencing data support evolved repression

To investigate the genetic basis of the increased *P*-element activity, we performed the whole genome sequencing on all the populations to determine the number of genomic *P*-elements. In addition, we detect the presence of insertions in piRNA clusters, which is a prerequisite of host piRNA-mediated repression. Subtelomeric piRNA clusters located in telomeric associated sequence (TAS) have a well-documented role in *P*-element repression in *D. melanogaster* [56,62,124,126–129] and *D. simulans* [130]. However, annotating *P*-element insertions to a specific location in the repeat-rich TAS regions through unique read alignment is difficult. Thus, we divided our reference genome into TAS-excluded regions and TAS regions, and detected *P*-element insertions in TAS separately. We predict that the induction ability correlates with the number of *P*-element insertions and the repression correlates with insertions in piRNA clusters.

For 22 °C populations, consistent with our phenotypic observations, a great number of *P*-element insertions exist in the genomes of all the populations that exhibited increasing induction of hybrid dysgenesis (Figure 3.4). Similarly, for populations that exhibited *P*-element repression, corresponding *P*-element insertions were detected in multiple non-TAS piRNA clusters (Figure 3.4). We also detected *P*-element insertions in multiple TAS piRNA clusters, most of which occur in X-TAS, in agreement with previous study that *P*-elements preferentially insert into X-TAS (Table 3.1) [131]. On the contrary, population 21, which did not exhibit increasing induction or repression of *P*-elements, showed a correspondingly dramatically fewer *P*-element insertions in its genome and none in piRNA clusters (Figure 3.4, Table 3.1). Together, our sequencing results from the 22 °C populations suggest the evolution of host TE repression occurred simultaneously with insertions into multiple different piRNA clusters.

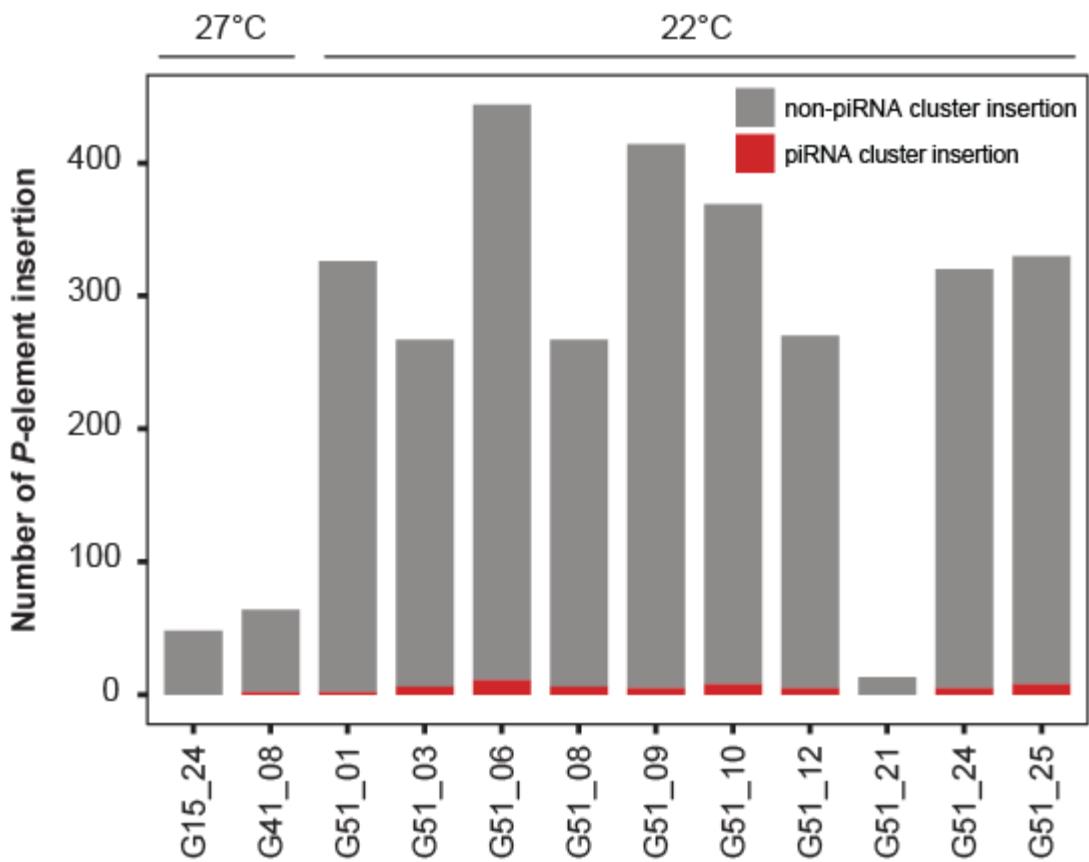


Figure 3.4 Genomic insertions of *P*-elements in each population examined. The number of *P*-element insertions within the host genome (TAS-excluded) as a whole and in non-TAS piRNA clusters specifically correlates to the phenotypic observation across populations from two different temperature conditions. *P*-element insertions into non-TAS piRNA clusters are shown in red, non-piRNA cluster insertions within the genomes are shown in grey.

Table 3.1 The number of whole genome sequencing reads supporting *P*-element insertions into each TAS region in each population genome Equal TAS indicates sequencing reads that have the same mapping quality when aligned to each TAS region.

strain ID	total TAS	2R TAS	3R TAS	X TAS	equal TAS
G15_24	0	0	0	0	0
G41_08	0	0	0	0	0
G51_01	868	3	0	456	409
G51_03	606	22	0	176	408
G51_06	667	13	0	491	163
G51_08	766	28	0	128	610

Table 3.1 continued

G51_09	416	17	0	119	280
G51_10	552	8	0	221	323
G51_12	237	6	0	55	176
G51_21	1	0	0	0	1
G51_24	727	4	0	228	495
G51_25	330	2	0	115	213

3.2.3 Extinction in 27 °C populations is not due to *P*-element accumulation

27 °C populations all went extinct before generation 41. One possible reason for their extinction is the accumulation of a lot of deleterious mutations by *P*-element insertions. In order to test this hypothesis, we also sequenced two 27 °C populations, population 8 and 24. So we expected that their genomes were loaded with more *P*-elements than those 22 °C populations that were not extinct.

Population 8, which survived for 41 generations, exhibited more *P*-element insertions at its last generation 41 as compared to the short-lived population 24 at its generation 15 (Figure 3.4). Notably, most 22 °C populations, which have survived for 51 generations and never went extinct at the end of our experiment, exhibited even more *P*-element insertions than 27 °C populations that were extinct earlier (Figure 3.4), indicating that load of *P*-element copies might not be the reason for the 27 °C population extinction. Interestingly, population 8, which exhibited repression at its last generation (Figure 3.3), also contained *P*-element insertions into piRNA clusters (Figure 3.4). The observations are therefore overall in agreement with the hypothesis that host repression evolves via TE insertions into piRNA clusters.

3.3 Discussion

TEs burden their host genome with deleterious mutations and incite genome instability [8–13]. To avoid these costs, host genomes control the mobilization of TEs through piRNA-mediated silencing. However, the mutational and epigenetic processes that give rise to piRNA-mediated silencing when new TEs invade the host remain poorly understood. By introducing *P*-elements into a naive *D. melanogaster* strain through germline transformation, and chronicling the evolution of host TE repression in 10 laboratory populations at two different temperatures, we observed that although the higher temperature drove population extinction before the evolution of repression, at the lower temperature repression evolved in most populations (Figure 3.3). From the whole genome sequencing data, all the populations that evolved repression contained *P*-element insertion within piRNA clusters (Figure 3.4), supporting the “trap” model that the host TE repression evolves through TE insertions into multiple piRNA clusters and novel piRNA production [55–57,124]. Taken together, our results suggest that after invasion, host TE repression evolved via the concurrent emergence of multiple different repressor alleles, which is very similar to what we see in natural populations [124].

The severity of hybrid dysgenesis induced by *P*-elements differs under different temperatures [67]. It is possible that the transposition rate of *P*-elements increases as temperature goes up, resulting in more *P*-element insertions within the host genome. From our observation, however, 27 °C populations that went extinct have fewer, not more *P*-element insertions in their genomes as compared to 22 °C populations, the latter of which survived for the entire 3-year experiment. At this moment, we cannot rule out the possibility that the 27 °C populations went extinct because of the accumulation of more deleterious *P*-element insertions, which impact the function of host genes. However, the comparatively modest number of *P*-element insertions suggests that mutation load induced by *P*-elements might not be the cause of the 27 °C population extinction.

Alternatively, the extinction of 27 °C populations might be caused by a higher germline sensitivity to hybrid dysgenesis induced by *P*-element activity. At higher temperature, there could be more germline loss as the consequence of the *P*-element transposition [129]. Thus, it is possible that the 27 °C population went extinct not because of the high load of *P*-elements *per se*, but because the sterility imposed by *P*-element transposition is more severe. By modeling the effect of different extent of sterility costs induced by TEs on the evolution of the host repression, Kelleher et al. showed that a higher fitness cost of hybrid dysgenesis results in a lower TE copy number through purifying selection [123]. Furthermore, under this regime, repression does not evolve deterministically. Reduced *P*-element copy number, and the absence of repression in 27 °C populations are therefore potentially explained by fitness costs of hybrid dysgenesis.

Finally, lab populations of *Drosophila* that have been raised in a constant thermal environment for multiple generations can exhibit a reduced fitness when transferred to a different thermal condition [132,133]. Thus, another explanation for the 27 °C population extinction might be that the fly strain we used was kept under a thermal environment similar to 22 °C before being separated into the two evolution temperatures, resulting in poor survival in the 27 °C populations.

The predominant mechanism by which hosts adapt to and restrict new TE invaders is the “trap” model, among which the host acquires the ability of producing piRNAs targeting the newly invaded TEs through insertion of the invading TE into pre-existing piRNA clusters [55–57]. Our observations strongly support the “trap” model since all populations that evolved repression contained *P*-element insertions into multiple piRNA clusters. In conclusion, our results indicate that host TE repression evolves via the concurrent emergence of multiple different repressor alleles, rather than through a single piRNA cluster insertion that gets fixed within the population.

3.4 Materials and methods

3.4.1 Establishment and maintenance of populations with *P*-element invasion

We introduced *P*-elements into the A4 founder strain (naive M strain) of the *Drosophila* Synthetic Population Resource (DSPR) [134] using germline transformation. Ten independent transformations established 10 populations of flies with genomic *P*-elements, which were identified by PCR. Each population was then split into two populations under different experimental treatments: one was maintained at a lower temperature (22 °C). The other was maintained at a higher temperature (27 °C).

Every generation, about one thousand 3-6-day old flies were placed in a population cage and used for producing eggs for the next generation. Two days before the egg collection, grape juice agar plates along with a drop of yeast paste were provided to make sure that the flies were well nourished. One day before the egg collection, new grape juice agar plates covered with yeast paste were provided to allow flies to lay eggs on the yeast for 24 hours. Then eggs were collected by flushing the yeast paste along with the eggs into a collection container with a filter net. Collected eggs were rinsed and about one thousand eggs were transferred into bottles with standard cornmeal media and kept until they developed into 3-6-day old adults, which would comprise the next generation.

3.4.2 *P*-element germline transformation

Founder A4 strain of The *Drosophila* Synthetic Population Resource (DSPR) [134] was transformed using a full-length *P*-element p(pi)25.1 in a pUC13 plasmid at 300 ng/uL. The embryonic injection was performed by The Best Gene inc (Chino Hills, CA). Founder A4 was provided by Tony Long. Plasmid was provided by Michael Simmons.

3.4.3 Phenotypic measurements

Every 5 generations, we measured the induction of hybrid dysgenesis associated with the *P*-element for each population at each temperature by evaluating the ability of experimental males to cause dysgenesis among their F1 offspring females when crossed to M strain females (Canton-S). We similarly measured repression, by evaluating the ability of experimental females to repress hybrid dysgenesis in their F1 offspring females when crossed to P strain males (Harwich). Dysgenic crosses were maintained at 29 °C. The ability of induction and repression are measured by the proportion of F1 females that have atrophied ovaries. We collected 20 experimental males/females from each population under each temperature, set 20 individual crosses with 1-2 Canton-S females/Harwich males, respectively, and assayed 20 3-day-old F1 females from each cross.

The change of repression or induction over generations was modeled with a mixed effects logistic regression model in the R package lme4 [135]. The model had fertility of F1 offspring females from either the induction or repression crosses as a response variable, generation as a fixed effect and individual experimental fly as a random effect.

3.4.4 Whole genome sequencing

Flies from the last generation of two 27 °C populations (9 females for population 8 and 8 females for population 24) and from generation 51 of all the 22 °C populations (20 females/population) were used to build the whole genomic sequencing libraries by using the Nextera DNA Flex Library Preparation Kit. In brief, DNA was extracted from whole flies using QIAGEN DNeasy Blood & Tissue Kits. Then genomic DNAs were fragmented and tagged with adapter sequences by Bead-Linked Transposomes (BLT). Adapter-tagged DNAs were washed and amplified by PCR. Final libraries were sent for whole genome sequencing on an Illumina NovaSeq 6000 by Genomic and RNA Profiling Core in Baylor College of Medicine.

3.4.5 Detecting *P*-element insertions in A4 genomes

P-element insertions were detected as described in [124,136]. Briefly, whole genome sequencing reads were locally aligned to full-length *P*-element consensus sequence [137] using Bowtie 2 [138] to identify reads that include *P*-element sequence. *P*-element sequences were then trimmed from aligned reads. Since TAS are repeat-rich regions, which prevent the unique alignments of sequencing reads for precise *P*-element annotation, we generated a TAS-excluded A4 reference genome and detected TAS insertions separately (described below). Trimmed reads were aligned to the TAS-excluded A4 reference using Bowtie 2. Alignments with mapping quality greater than 20 and edit distance, the minimal number of one-nucleotide edits (substitutions, insertions and deletions) needed to convert the read sequence to the reference, less than four were kept. The *P*-element insertion sites were then determined by those qualified reads with one segment aligned to the *P*-element consensus sequence and the remainder aligned to the A4 genome.

3.4.6 Detecting *P*-element Insertions in TAS

TAS regions from the dm6 reference genome [107]: 2R-TAS (Chr2R: 25258060..25261551, 3492 bp) and 3R-TAS (Chr3R: 32073015..32079331, 6317 bp) [139], 2L-TAS (Chr2L: 1..5041, 5041 bp) and 3L-TAS (Chr3L: 1..19608, 19608 bp) [140], as well as X-TAS (9872 bp, L03284) [131], were used to build the TAS reference. *P*-derived trimmed reads not aligned to TAS-excluded A4 reference genome were subsequently aligned to the TAS reference using Bowtie 2 outputting all valid alignments (-a). A read was considered aligned to TAS if the edit distance was fewer than 4.

3.4.7 Detecting *P*-element Insertions in non-TAS piRNA clusters

The coordinates of *P*-element insertions within the TAS-excluded A4 genome were transferred into dm6 coordinates by BLAST [141]. Non-TAS piRNA clusters described by [124] were used to identify *P*-element insertions in non-TAS piRNA clusters.

Chapter 4 Discussion

4.1 Components of piRNA pathway evolve adaptively

TEs are selfish elements that can pose a significant threat to their hosts by inducing deleterious mutations, chromosome rearrangements and DNA damage [69–72]. In germlines of many eukaryotes, TE activity is controlled by a conserved defense mechanism, the piRNA pathway, which comprises piRNAs and piRNA pathway proteins [14,15]. TEs can vary in their number, composition, and expression pattern in the host genomes, thus imposing evolutionary pressures onto the host piRNA silencing system. It has been reported that a number of piRNA pathway proteins are evolving adaptively [42–44,80,81,142–145]. In response to changes in genomic TE content, the host piRNA pool changes rapidly to maintain the host control over TE activities [77,78]. For example, TEs represented in the *flamenco* piRNA cluster differs between close species, suggesting that this piRNA cluster evolves to repress the changing TE threat in each species [21]. In addition, proteins in the piRNA pathway, which enact piRNA biogenesis and silence target TEs, also show signatures of positive selection [42–44,79,80].

Many questions about the evolution of the host piRNA silencing machinery remain unanswered. For instance, the forces that drive the adaptive evolution of piRNA pathway proteins are poorly understood. It is also not clear about the mutational and epigenetic processes that give rise to piRNA-mediated silencing when new TEs invade the host. To answer these questions, in this dissertation, we explored the mechanisms responsible for the positive selection among piRNA pathway proteins by examining functional divergence between *D. melanogaster* and *D. simulans* for three adaptively evolving piRNA pathway proteins. We also investigated the precise process of the evolution of the host piRNA-mediated TE repression by recreating the *P*-element invasion into a naive strain of *D. melanogaster*.

4.2 The role of TEs in adaptive evolution of piRNA pathway proteins

It has been proposed by multiple studies that piRNA pathway proteins evolve adaptively to efficiently silence genomic TEs and/or to evade antagonists encoded by TEs [45,48]. Both hypotheses predict dramatic divergence in TE regulation and/or piRNA biogenesis, respectively, between different species. We observed minor differences in abundance of TE transcripts and TE-derived piRNAs between *D. melanogaster* and *D. simulans* piRNA proteins, which is not consistent with either of these hypotheses. Nevertheless, we cannot disregard the power of TEs in driving the adaptive evolution among piRNA pathway proteins. Indeed, an important caveat of our work is that horizontal transfer of TEs has occurred between *D. melanogaster* and *D. simulans* [54], such that both sets of piRNA pathway proteins are effectively adapting to the same TE pool. As a result, incompatibilities between piRNA proteins and the TEs they regulate might not arise.

4.3 Auto-immunity in adaptive evolution of piRNA pathway proteins

Genomic auto-immunity has been recently proposed as an additional target of positive selection among piRNA pathway proteins [48]. Our finding that *D. simulans* alleles of three cytoplasmic piRNA pathway proteins exhibited enhanced negative regulation of host mRNAs under the *D. melanogaster* background is the first concrete evidence that piRNA proteins may experience positive selection against their effect of auto-immunity. Selection against genomic auto-immunity may not be limited to the cytoplasmic piRNA proteins involved in piRNA maturation and post-transcriptional silencing. It has been reported that genes close to TE insertions are more likely to be silenced, caused by the spreading of H3K9me3 by the piRNA-mediated transcriptional silencing on the TE insertions [10,146]. Thus, piRNA pathway proteins responsible for the TE transcriptional silencing may also be under the positive selection for their off-target effects on host genes. Indeed, it is proposed that the adaptive evolution of the nuclear transcriptional silencing factors Rhino, Deadlock and Cutoff

might be driven by strong selection against transcriptional TE silencing that spreads into flanking host genes [48]. Future studies investigating the functional divergence of Rhino, Deadlock and Cutoff in down-regulating host gene expression between species could further validate the auto-immunity hypothesis.

4.4 Our data support the “trap” model of the evolution of host resistance to new TE invaders

The predominant mechanism by which hosts adapt to and restrict new TE invaders is the “trap” model, in which host repression evolves via random transposition of novel TEs into pre-existing piRNA clusters [55–57,124]. In addition, *P*-element insertions in TAS piRNA clusters have been demonstrated to confer repression of *P*-element by producing *P*-element-derived piRNAs [126–128]. Our observation that *P*-element repression correlates with the insertions of *P*-elements into pre-existing TAS and non-TAS piRNA clusters supports the “trap” model, and is in agreement with the significance of the TAS regions in *P*-element regulation [126–128].

4.5 Mutation load induced by *P*-elements may not drive population extinction

The severity of hybrid dysgenesis induced by *P*-elements differs under different temperatures [67]. We intended to determine whether different fitness costs of hybrid dysgenesis by *P*-element create different regimes for the evolution of host repression by contrasting populations under two different temperature conditions. However, all populations from our 27 °C experiment went extinct. To our surprise, the number of *P*-element insertions from two examined 27 °C populations is less than those of the 22 °C populations which have survived much longer, indicating that the mutation load imposed by *P*-element transposition may not be the reason for the extinction of 27 °C populations. It is also possible that their extinction is because there are more deleterious mutations caused by *P*-elements in their genomes. We

have not tested on this possibility at this moment yet, which is another caveat for this study. Future work on examining the frequency of *P*-element insertions might provide insights on if there are more deleterious *P*-element insertions into host genes in those 27 °C populations.

Another explanation for the extinction of 27 °C populations might be that germlines of 27 °C populations are more sensitive to hybrid dysgenesis by *P*-element transposition. As a consequence, there could be more germline loss and more severe sterility in those 27 °C populations. At higher temperature, hybrid dysgenesis could impose strong negative selection against *P*-element accumulation in the host genome [123], which in turn limits the emergence of new repressor alleles (*P*-element insertions into piRNA clusters) through random transposition, resulting in reduced *P*-element copy number, and the absence of repression in 27 °C populations.

It has been reported that lab populations of *Drosophila* that have been raised at a constant thermal environment for generations exhibit a reduced fitness when put into a different thermal condition [132,133]. Thus, it is possible that the fly strain we used was kept in a thermal environment similar to 22 °C before being separated into the two evolution temperatures, resulting in better survival in the 22 °C populations than the 27 °C populations.

Appendix

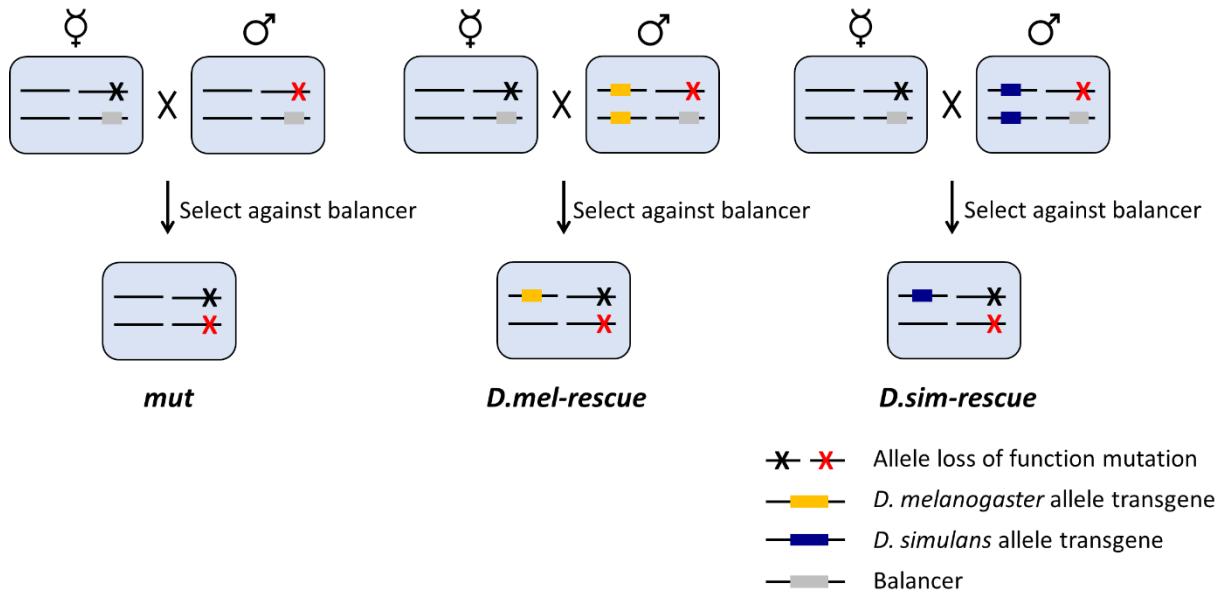


Figure A2.1 *Drosophila melanogaster* genotypes and crossing scheme.

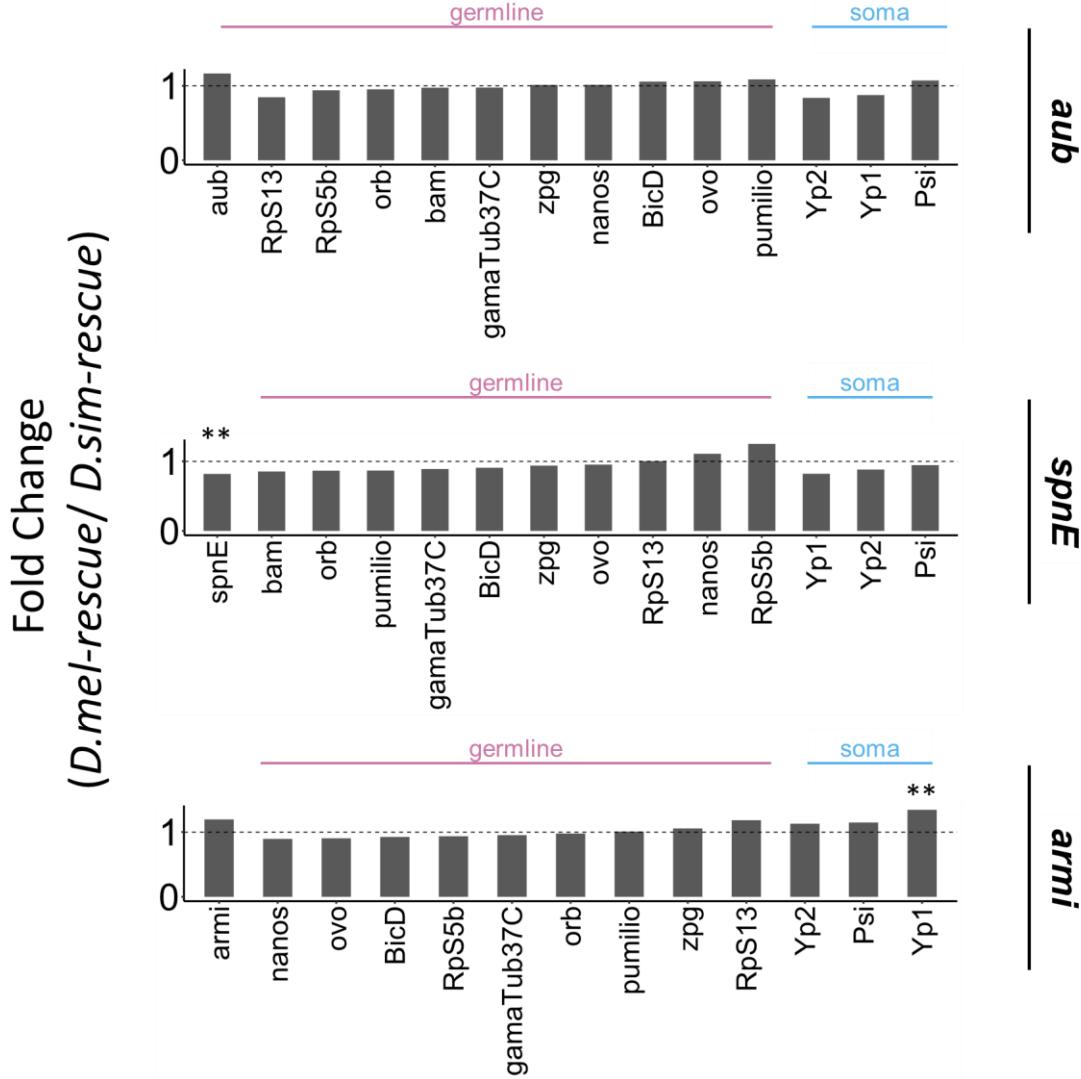


Figure A2.2 Similar expression level of *aub*, *spn-E* and *armi* transgenes, as well as germline and soma specific genes between *D. melanogaster* transgenic rescue and *D. simulans* transgenic rescue. Fold-change of expression level of *aub*, *spn-E*, *armi*, germline-specific genes and soma-specific genes between *D. melanogaster* transgenic rescue and *D. simulans* transgenic rescue are shown. Fold-change values are based on one biological replicate for *aub* and three biological replicates for *spn-E* and *armi*, and were obtained from a DESeq analysis for *aub* and a DESeq2 analysis for *spn-E* and *armi*. ** denotes $p \leq 0.01$. NS if not labeled.

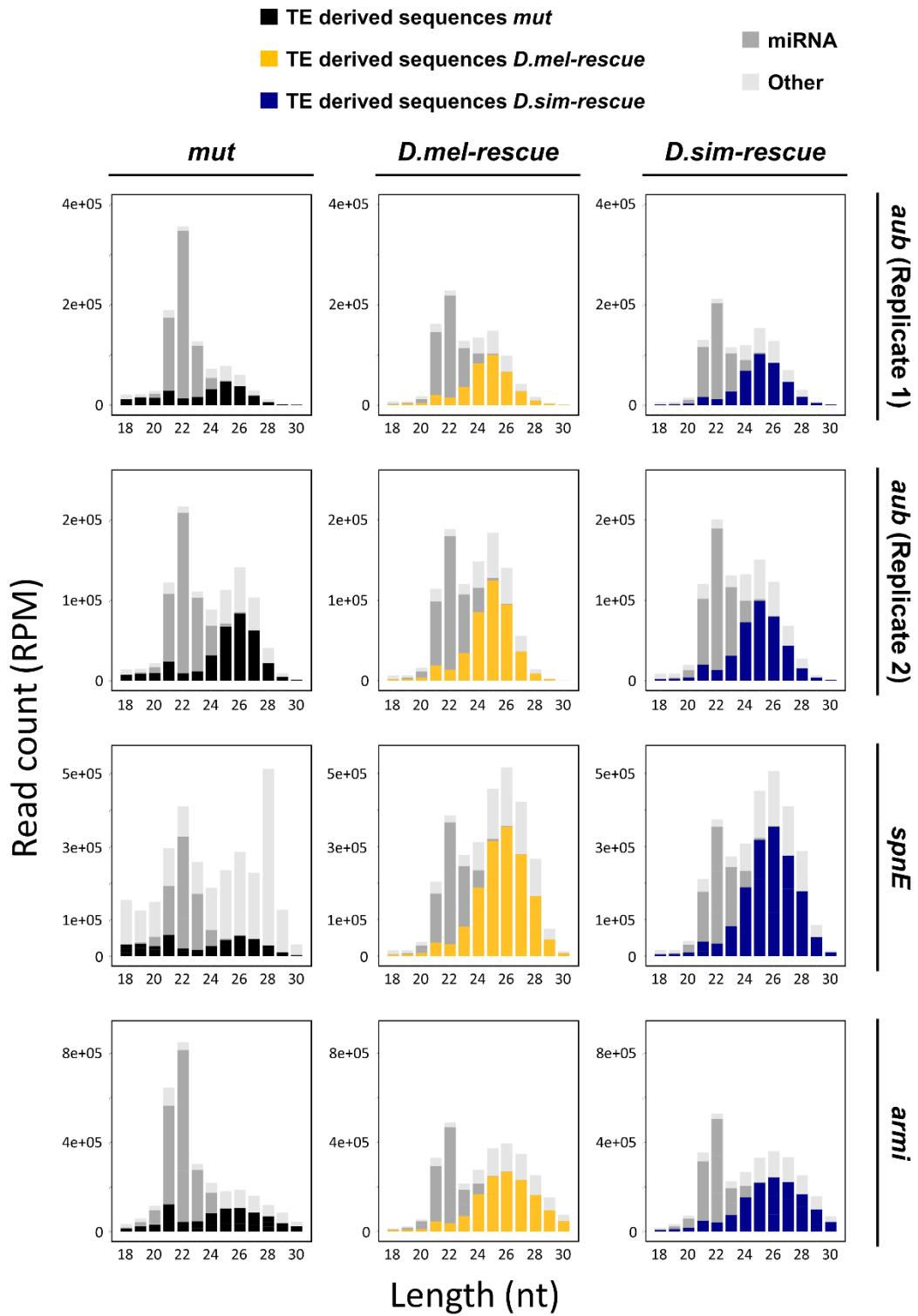
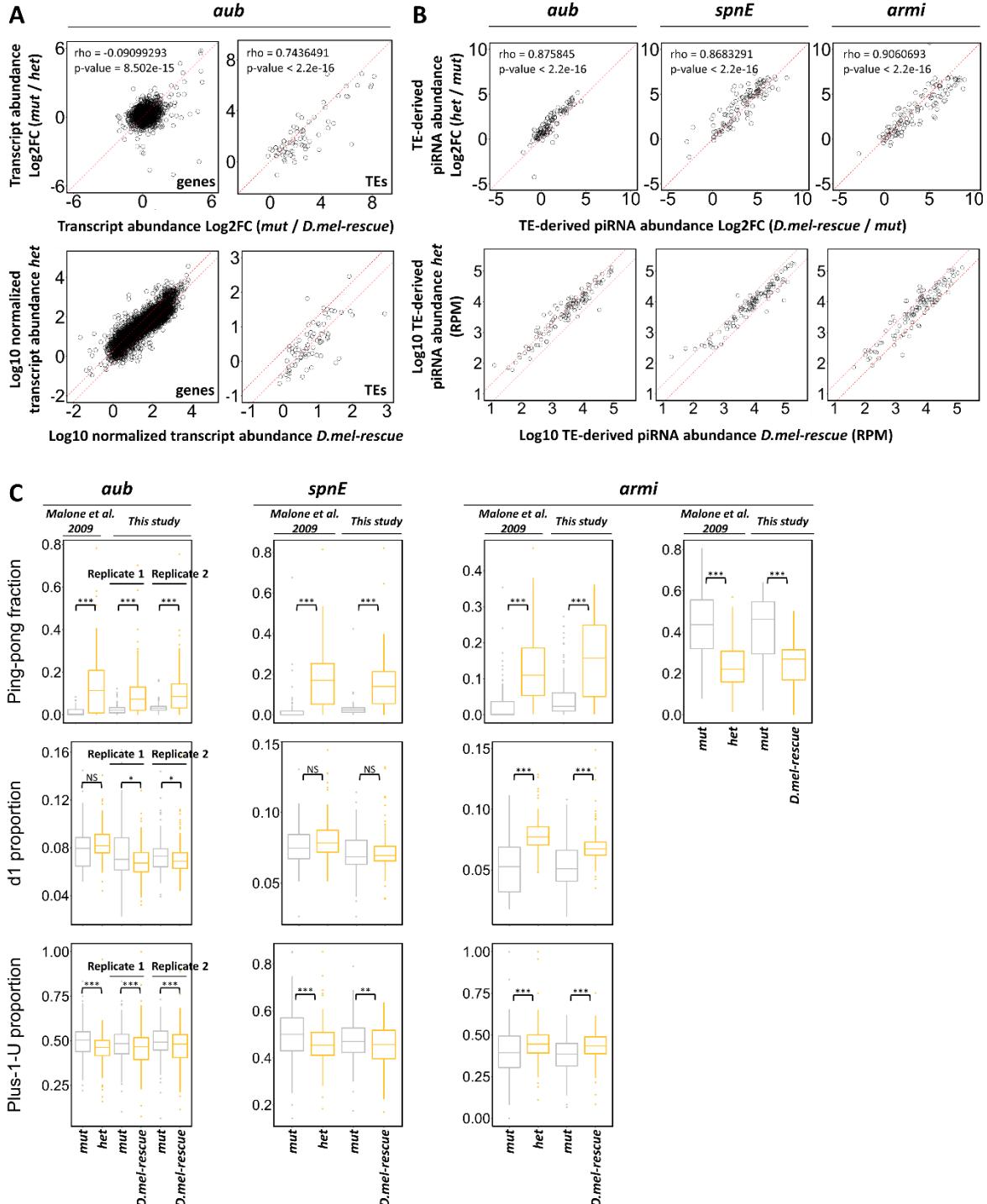


Figure A2.3 Size distribution and composition of the small RNA pool for each genotype.

Figure A2.4 *Drosophila melanogaster* transgenes exhibit similar profiles of piRNA biogenesis to heterozygotes. *Drosophila melanogaster* transgenes and heterozygotes are compared to trans-heterozygous mutants with respect to transcript abundance (A), TE-derived piRNA abundance (B), ping-pong and phasing biogenesis (C). RNA-seq data comparing *aub* heterozygotes and trans-heterozygous mutants is from [120]. Transcript abundance was normalized to the total number of mapped reads of that library. The small RNA-seq data comparing heterozygotes and mutants for *aub*, *spn-E* and *armi* are from [121]. TE-derived piRNA abundance was normalized to the total number of sequenced miRNAs in the same library. Statistical significance was assessed by the Wilcoxon signed-rank test. For *aub*, two biological replicates of each genotype generated at different times are shown separately. For *spn-E* and *armi*, averages of three biological replicates of each genotype generated at the same time are shown. NS denotes $p > 0.05$. *, **, and *** denote $p \leq 0.05$, $p \leq 0.01$, $p \leq 0.001$, respectively.



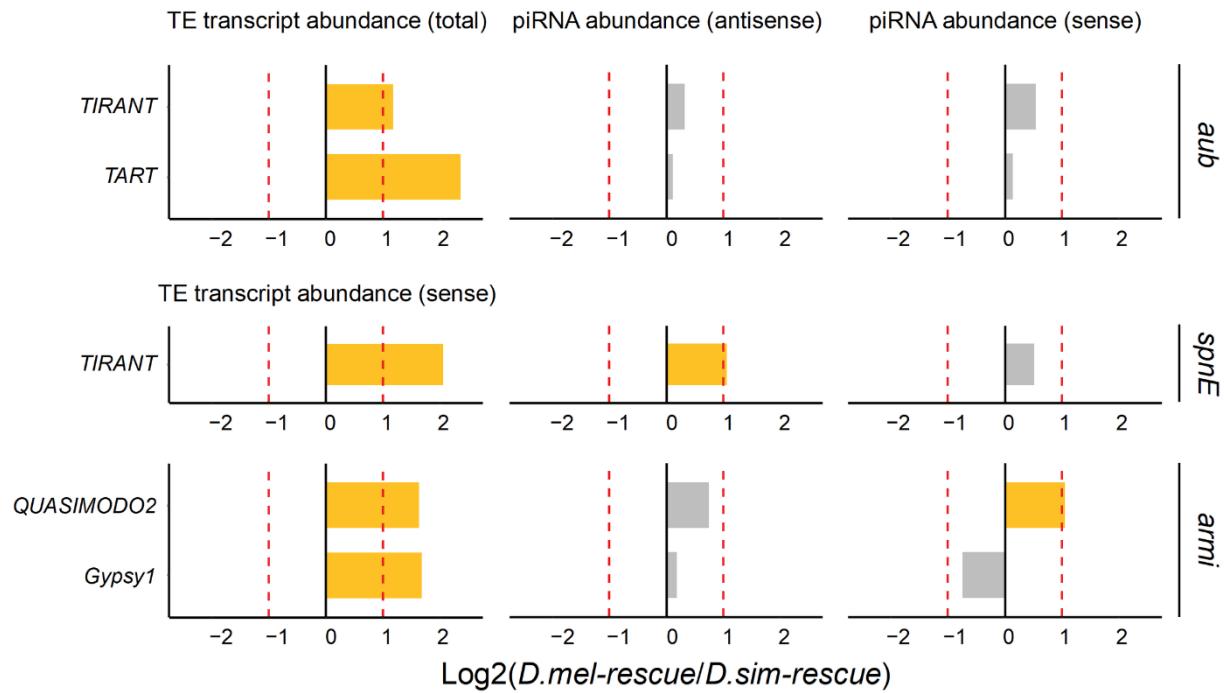


Figure A2.5 Decoupling between changes in TE transcript abundance and changes in TE-derived piRNA abundance. Log2 fold-change TE transcript abundance and TE-derived sense/antisense piRNA abundance between two transgenic rescues for the TE families whose TE transcript abundance is substantively different (> 2 fold) between two rescues from Fig 2A. Red dashed lines indicate the 2 fold-change threshold.

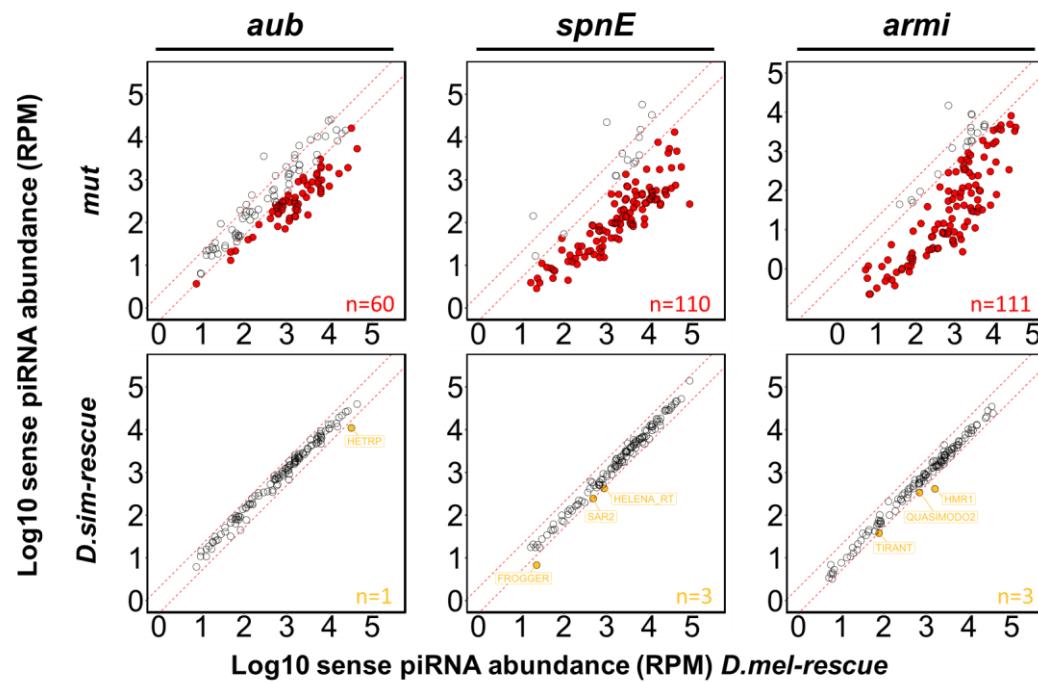


Figure A2.6 Minimal differences in sense piRNA production between alleles.

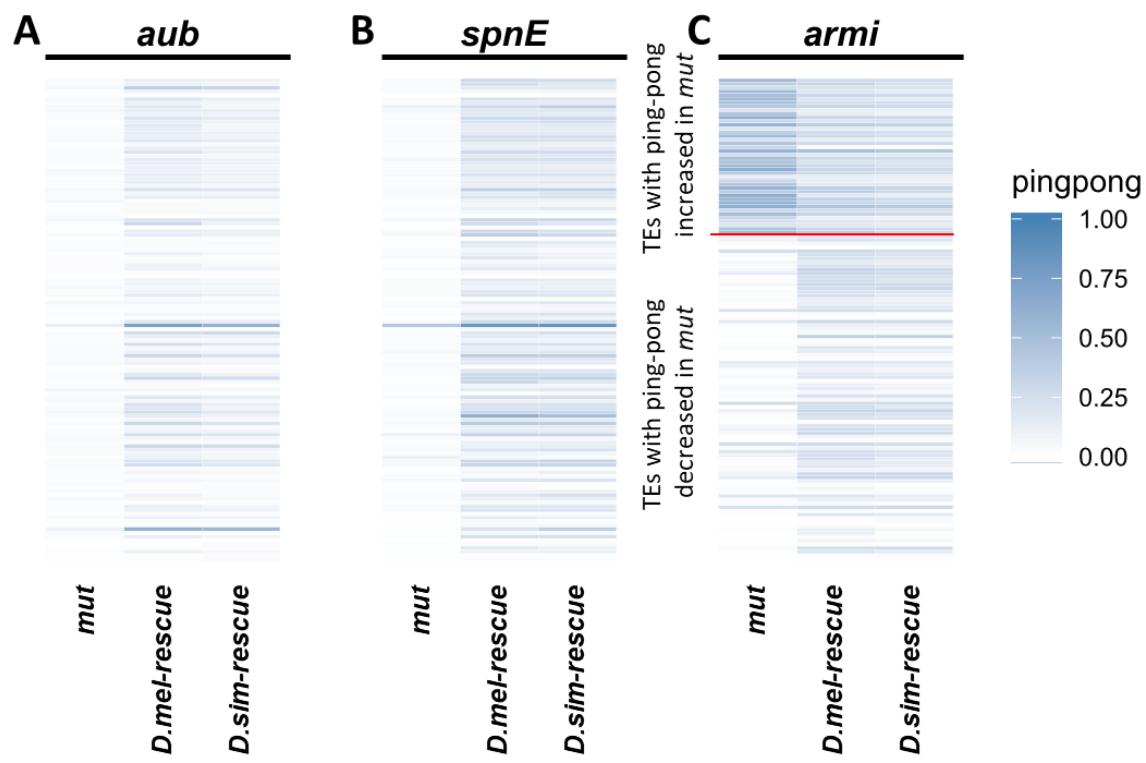


Figure A2.7 Ping-pong fraction heat map for each protein studied. (A) *aub*, (B) *spn-E* and (C) *armi*. Among (C), 88 and 42 TE families whose ping-pong fractions are decreased (below red line) or increased (above red line), respectively, in *armi* mutant as compared to those in *D. melanogaster* transgenic rescue are shown.

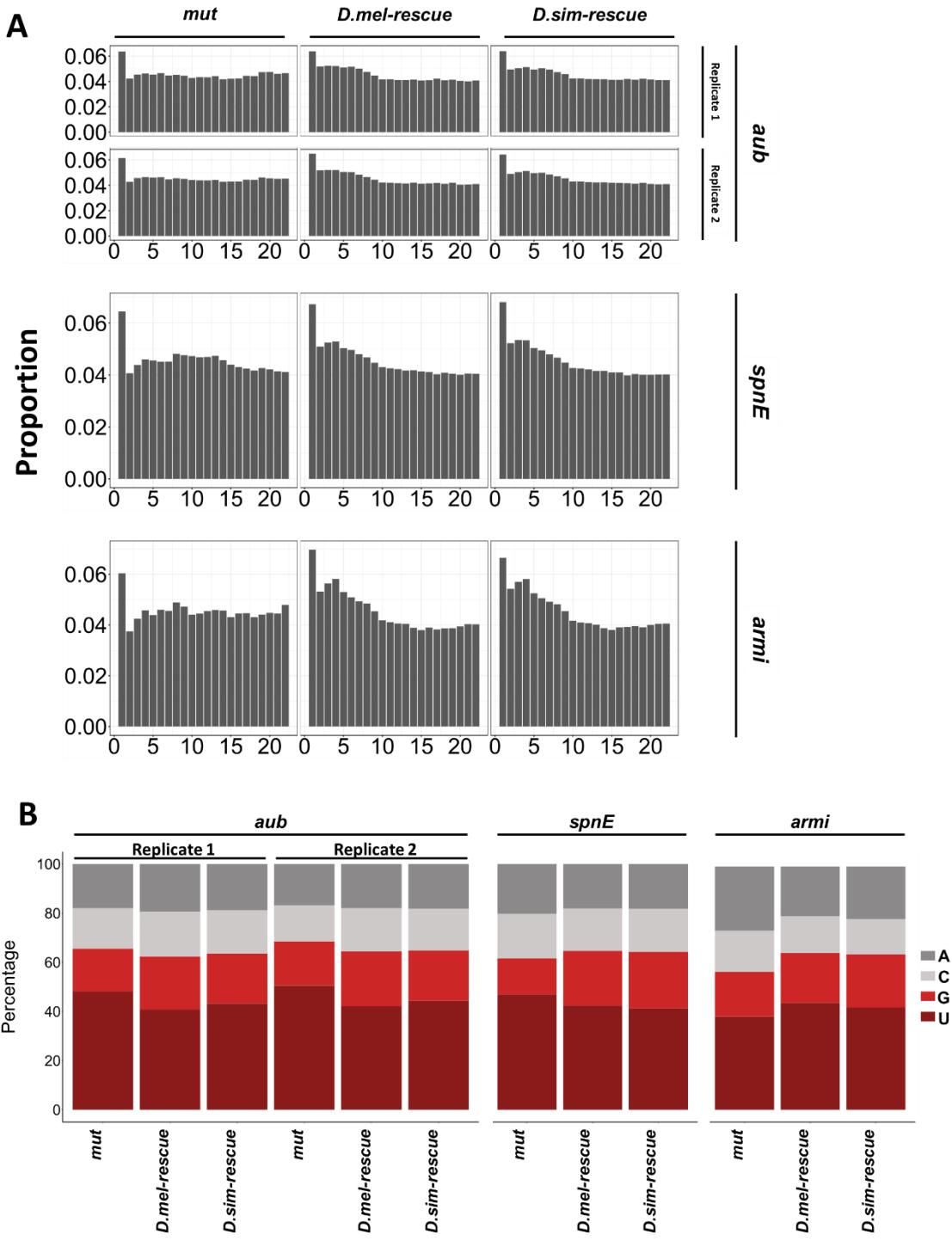


Figure A2.8 Observed peaks of 1nt distance (A) and +1-U bias (B) among each genotype for each protein studied.

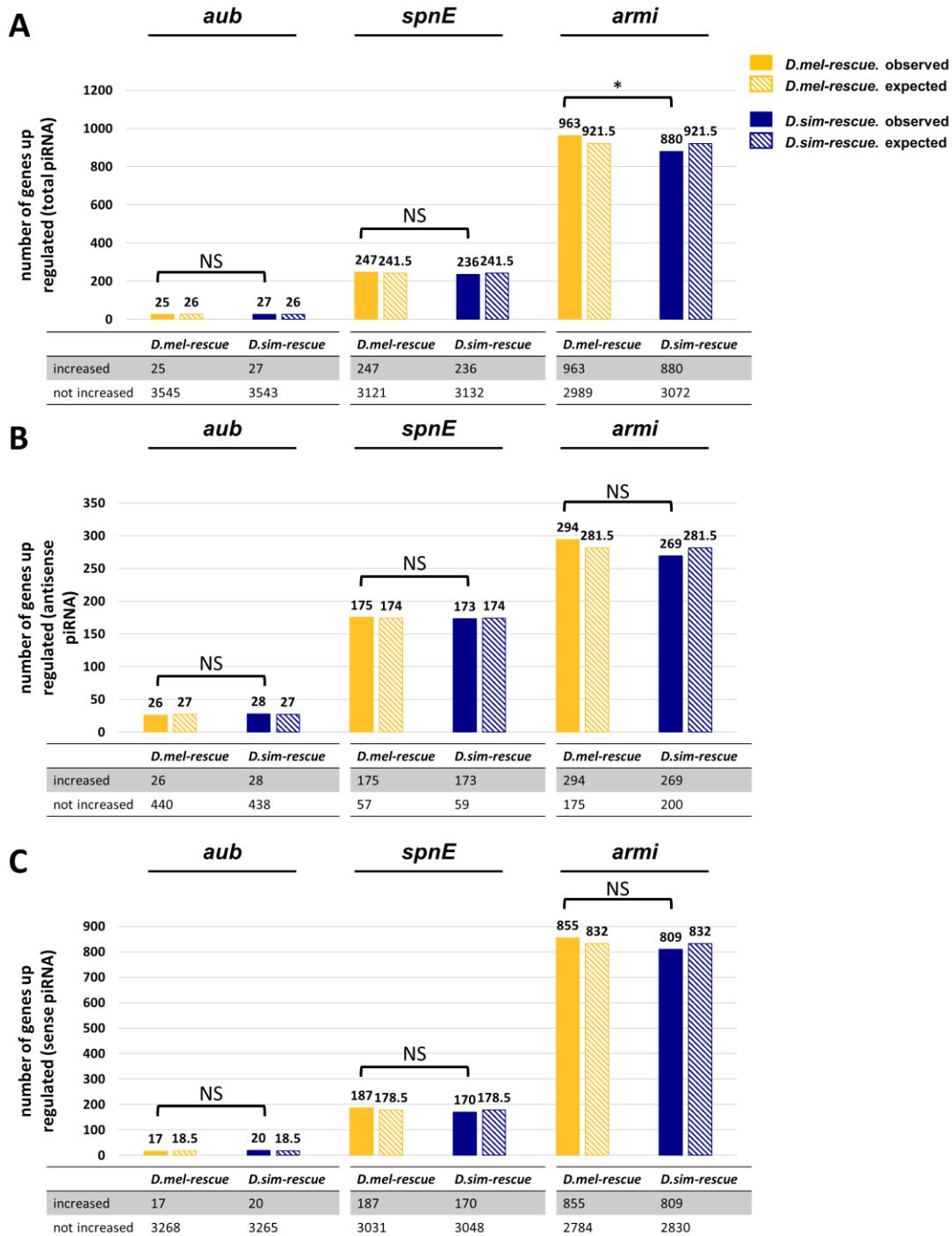


Figure A2.9 Auto-immunity analysis for the genic piRNA profile. The number of genes whose corresponding total (A) / anti-sense (B) / sense (C) piRNA abundance is increased (>1.5 fold) in the presence of each transgene as compared to the mutant. Contingency tables are shown below. Log2 fold-change values were based on two biological replicates for *aub* and three biological replicates for *spn-E* and *armi*, and were obtained from a DESeq2 analysis (adjusted $p < 0.05$). Statistical significance was assessed by the Pearson's Chi-squared test. NS denotes $p > 0.05$. * denotes $p \leq 0.05$.

Table A2.1 Offspring count from the female fertility test.

<i>spn-E</i>												
<i>D. melanogaster</i> rescue				<i>D. simulans</i> rescue				mut				
Female #	Day 1 -5	Day 6 - 10	Day 11 - 15	Female #	Day 1 -5	Day 6 - 10	Day 11 - 15	Female #	Day 1 - 5	Day 6 - 10	Day 11 - 15	
1	48	65	46	1	48	43	41	1	0	0	0	
2	47	54	56	2	51	46	42	2	0	0	0	
3	41	62	40	3	41	39	45	3	0	0	0	
4	68	58	51	4	65	38	38	4	0	0	0	
5	78	42	39	5	8	59	32	5	0	0	0	
6	71	57	30	6	61	46	37	6	0	0	0	
7	0	62	42	7	50	52	54	7	0	0	0	
8	45	55	44	8	1	58	25	8	0	0	0	
9	67	33	18	9	57	28	20	9	0	0	0	
10	0	9	NA	10	37	39	56	10	0	0	0	
11	54	43	61	11	62	45	37					
12	21	30	69	12	55	75	46					
13	58	55	54	13	47	55	28					
14	46	72	60	14	55	52	50					
15	36	40	35	15	0	56	31					
16	62	54	71	16	58	63	NA					
17	19	51	68	17	60	48	45					
18	47	45	24	18	43	57	48					
19	65	42	66	19	44	51	55					
20	32	35	49	20	42	49	52					
21	56	68	72	21	0	0	0					
22	51	51	65	22	52	71	42					
23	54	72	79	23	47	39	52					
24	64	64	67	24	0	51	54					

25	55	63	64	25	49	63	46				
26	67	109	NA	26	NA	NA	NA				
				27	44	20	59				
				28	63	46	63				
				29	0	0	0				
				30	25	52	43				
				31	62	48	67				
				32	66	61	69				

Table A2.1 continued

<i>armi</i>											
<i>D. melanogaster</i> rescue				<i>D. simulans</i> rescue				mut			
Female #	Day 1 -5	Day 6 -10	Day 11 -15	Female #	Day 1 -5	Day 6 -10	Day 11 -15	Female #	Day 1 -5	Day 6 -10	Day 11 -15
1	37	44	37	1	31	90	72	1	0	0	0
2	67	59	46	2	0	58	74	2	0	0	0
3	79	54	0	3	0	52	37	3	0	0	0
4	61	74	57	4	51	70	30	4	0	0	0
5	90	80	67	5	55	76	53	5	0	0	0
6	56	57	47	6	60	76	61	6	0	0	0
7	37	84	51	7	37	45	48	7	0	0	0
8	78	78	75	8	0	0	8	8	0	0	0
9	0	71	0	9	21	0	0	9	0	0	0
10	0	68	46	10	70	88	16	10	0	0	0
11	0	0	19	11	53	47	10				
12	90	100	78	12	62	7	84				
13	0	71	83	13	46	67	40				
14	57	57	78	14	59	27	31				
15	57	61	54	15	37	20	0				

16	80	95	59	16	74	86	48				
17	33	74	66	17	63	86	72				
18	15	0	47	18	61	83	43				
19	0	93	82	19	62	52	39				
20	79	73	83	20	26	36	17				
21	75	82	45	21	67	65	67				
22	0	95	74	22	20	0	0				
23	95	87	74	23	0	27	40				
24	0	79	6	24	26	37	42				
25	41	73	51	25	50	55	58				
26	26	102	33								
27	75	108	74								
28	103	90	68								
29	69	76	71								
30	45	73	65								
31	79	52	66								
32	67	93	62								
33	62	81	80								
34	53	64	63								

Table A2.2 RNA-seq and small RNA-seq library statistics.

RNA seq						
protein	genotype	replicate	total number of reads	number of reads mapped to the rRNA	number of reads mapped to the genome	number of reads mapped to the repbase
Aub	<i>mut</i>	1	47810791	2543899	37497437	987798
Aub	<i>D.mel-rescue</i>	1	61437786	4321529	48059195	92964
Aub	<i>D.sim-rescue</i>	1	50137268	3761238	38897060	48939
Spn-E	<i>mut</i>	1	23820895	3214448	18558984	1386271
Spn-E	<i>mut</i>	2	26015710	2856910	20837090	1692058
Spn-E	<i>mut</i>	3	23300741	3045803	18257248	1380190
Spn-E	<i>D.mel-rescue</i>	1	27651089	2100788	22958185	114617
Spn-E	<i>D.mel-rescue</i>	2	24792297	1518132	20903454	46285
Spn-E	<i>D.mel-rescue</i>	3	25296375	1480031	21319672	62568
Spn-E	<i>D.sim-rescue</i>	1	24403984	1108831	20825645	60113
Spn-E	<i>D.sim-rescue</i>	2	25470279	1420912	21492747	62520
Spn-E	<i>D.sim-rescue</i>	3	25362128	1236761	21490386	66223
Armi	<i>mut</i>	1	8231924	712990	5881337	185557
Armi	<i>mut</i>	2	11445456	897182	8314959	365642
Armi	<i>mut</i>	3	13991801	882511	10446980	512377
Armi	<i>D.mel-rescue</i>	1	9105135	834175	6530522	23849
Armi	<i>D.mel-rescue</i>	2	11390689	1178249	7979924	27373

Armi	<i>D.mel-rescue</i>	3	10932588	1317328	7578183	22992
Armi	<i>D.sim-rescue</i>	1	11220177	1281188	7799510	24671
Armi	<i>D.sim-rescue</i>	2	9699112	934004	6861548	18512
Armi	<i>D.sim-rescue</i>	3	12418860	1233058	8749302	25778

Table A2.2 continued

small RNA seq							
protein	genotype	replicate	total number of reads	number of reads mapped to the rRNA	number of reads mapped to the miRNA	number of reads mapped to the genome	number of reads mapped to the repbase
Aub	<i>mut</i>	1	32740568	3398142	13039864	26574824	6443637
Aub	<i>mut</i>	2	54266213	3410059	13656353	46511782	16058895
Aub	<i>D.mel-rescue</i>	1	36614858	2196722	11052511	32603308	12244735
Aub	<i>D.mel-rescue</i>	2	55256621	2775522	12458643	48883533	20992091
Aub	<i>D.sim-rescue</i>	1	30670974	1854996	8172544	27197333	10594669
Aub	<i>D.sim-rescue</i>	2	49086275	3151282	11394105	42313960	16514744
Spn-E	<i>mut</i>	1	20899999	4437687	2323540	15686701	1981000
Spn-E	<i>mut</i>	2	17603761	3694992	2085693	13273840	1905636
Spn-E	<i>mut</i>	3	17973523	3769116	2255063	13587119	1892794
Spn-E	<i>D.mel-rescue</i>	1	26400250	589228	4222149	24984066	12565045

Sp-n-E	<i>D.mel-rescue</i>	2	22742105	418857	3151183	21530656	11274055
Sp-n-E	<i>D.mel-rescue</i>	3	23398135	598692	3836220	22015361	11120772
Sp-n-E	<i>D.sim-rescue</i>	1	27047613	586134	4159179	25562780	13243466
Sp-n-E	<i>D.sim-rescue</i>	2	24189297	578975	3447397	22730793	11898886
Sp-n-E	<i>D.sim-rescue</i>	3	22125008	664645	3445068	20729394	10727966
Ar-mi	<i>mut</i>	1	73538658	9467718	25034916	58097614	15772233
Ar-mi	<i>mut</i>	2	36075719	5014915	12635398	28474148	6993374
Ar-mi	<i>mut</i>	3	24519555	3422474	8230568	19304494	5394553
Ar-mi	<i>D.mel-rescue</i>	1	67582282	3638247	13802601	59086995	28590698
Ar-mi	<i>D.mel-rescue</i>	2	74402243	5866958	15066382	63862400	30644648
Ar-mi	<i>D.mel-rescue</i>	3	69993616	4603941	15486035	61233449	28153391
Ar-mi	<i>D.sim-rescue</i>	1	78632316	19573325	14962815	54855137	24169005
Ar-mi	<i>D.sim-rescue</i>	2	47347859	4684127	10094698	39686618	18503290
Ar-mi	<i>D.sim-rescue</i>	3	21474320	1539245	4783745	18620920	8641505

Table A2.3 Normalized abundance and differential expression of TE transcripts.

aub_total_mRNA_normalized							
TE	mutant	mel	sim	L2FC(mut/D.mel)	padj	L2FC(D.mel/D.sim)	padj
1731	2102.46	405.04	402.36	2.38	0.00	0.01	1.00
176	1063.02	302.49	322.10	1.81	0.00	-0.09	1.00
297	902.50	288.70	359.62	1.64	0.00	-0.32	1.00
412	25546.08	808.36	1151.83	4.98	0.00	-0.51	1.00
ACCORD	1574.88	111.17	96.94	3.82	0.00	0.20	1.00
ACCORD2	150.42	69.81	76.09	1.11	1.00	-0.12	1.00
BAGGINS1	264.91	115.48	74.01	1.20	0.76	0.64	1.00
BARI	233.48	55.15	111.53	2.08	0.10	-1.02	1.00
BATUMI	3351.81	143.06	109.45	4.55	0.00	0.39	1.00
BEL	285376.82	991.06	989.22	8.17	0.00	0.00	1.00
Bica	528.70	127.54	121.96	2.05	0.00	0.06	1.00
BLASTOPIA	23869.05	379.19	444.06	5.98	0.00	-0.23	1.00
BLOOD	14378.23	641.17	594.16	4.49	0.00	0.11	1.00
BS	1001.28	151.68	160.53	2.72	0.00	-0.08	1.00
BS2	712.79	126.68	126.13	2.49	0.00	0.01	1.00
BS3	87.56	44.81	27.10	0.97	1.00	0.73	1.00
BURDOCK	51181.96	214.59	259.55	7.90	0.00	-0.27	1.00
Chimpo	1095.57	99.97	59.42	3.45	0.00	0.75	1.00
Chouto	179.60	100.83	81.31	0.83	1.00	0.31	1.00
CIRCE	236.85	41.37	45.86	2.52	0.05	-0.15	1.00
COPIA	9457.15	3222.23	3625.41	1.55	0.00	-0.17	1.00
Copia1	1120.26	135.30	156.36	3.05	0.00	-0.21	1.00
COPIA2	172.87	47.40	34.40	1.87	0.52	0.46	1.00
CR1A	560.13	259.40	203.26	1.11	0.27	0.35	1.00
DIVER	178811.34	1213.40	774.49	7.20	0.00	0.65	0.09
DIVER2	255.93	62.05	74.01	2.04	0.12	-0.25	1.00

DNAREP1	512.99	349.89	499.30	0.55	1.00	-0.51	1.00
DOC	4928.94	3458.36	4447.85	0.51	0.24	-0.36	1.00
DOC2	370.43	272.33	230.37	0.44	1.00	0.24	1.00
DOC3	1283.03	370.57	399.23	1.79	0.00	-0.11	1.00
DOC5	141.44	104.28	123.00	0.44	1.00	-0.24	1.00
DOC6	847.49	181.84	117.79	2.22	0.00	0.63	1.00
FB4	1501.92	921.25	700.48	0.71	0.28	0.40	1.00
FW	617.38	447.27	414.87	0.47	1.00	0.11	1.00
G	169.50	31.02	40.65	2.45	0.19	-0.39	1.00
G2	307.57	50.85	48.99	2.60	0.01	0.05	1.00
G4	215.52	111.17	160.53	0.96	1.00	-0.53	1.00
G5	185.21	60.33	71.92	1.62	0.57	-0.25	1.00
G5A	206.54	225.79	231.41	-0.13	1.00	-0.04	1.00
G6	195.32	32.75	31.27	2.58	0.11	0.07	1.00
GTWIN	1106.79	484.33	607.71	1.19	0.01	-0.33	1.00
GYPSY	473.70	196.49	86.52	1.27	0.27	1.18	1.00
Gypsy1	1304.36	423.14	366.92	1.62	0.00	0.21	1.00
GYPSY10	106.64	68.94	71.92	0.63	1.00	-0.06	1.00
GYPSY12	730.75	93.07	120.92	2.97	0.00	-0.38	1.00
Gypsy2	646.57	169.77	151.15	1.93	0.00	0.17	1.00
GYPSY2	145.93	80.15	72.97	0.86	1.00	0.14	1.00
GYPSY3	59.49	35.33	38.57	0.75	1.00	-0.13	1.00
GYPSY4	654.42	196.49	260.60	1.74	0.00	-0.41	1.00
GYPSY6	115.62	56.88	67.75	1.02	1.00	-0.25	1.00
GYPSY7	59.49	49.12	30.23	0.28	1.00	0.70	1.00
GYPSY8	166.13	62.05	64.63	1.42	0.86	-0.06	1.00
HETA	45961.17	187.01	195.97	7.94	0.00	-0.07	1.00
HMR2	2708.62	7.76	8.34	8.45	0.00	-0.10	1.00
HMSBEAGLE	86477.04	743.72	1235.22	6.86	0.00	-0.73	0.02

HOBO	2379.72	1617.58	2014.93	0.56	0.35	-0.32	1.00
I	5934.71	249.92	238.71	4.57	0.00	0.07	1.00
IDEFIX	508.50	215.45	160.53	1.24	0.21	0.42	1.00
INVADER1	180.72	70.67	66.71	1.35	0.87	0.08	1.00
INVADER2	1413.24	237.85	209.52	2.57	0.00	0.18	1.00
INVADER3	1271.80	191.32	202.22	2.73	0.00	-0.08	1.00
INVADER4	145.93	58.60	38.57	1.32	1.00	0.60	1.00
INVADER6	443.39	202.52	212.65	1.13	0.36	-0.07	1.00
IVK	1015.87	70.67	71.92	3.85	0.00	-0.03	1.00
Jockey	3010.57	502.42	492.00	2.58	0.00	0.03	1.00
M4DM	67.35	49.12	38.57	0.46	1.00	0.35	1.00
MAX	4948.02	579.12	606.67	3.09	0.00	-0.07	1.00
MDG1	837.39	743.72	793.25	0.17	1.00	-0.09	1.00
MDG3	15431.14	758.38	660.87	4.35	0.00	0.20	1.00
MICROPIA	982.20	53.43	66.71	4.20	0.00	-0.32	1.00
NOMAD	956.38	496.39	428.42	0.95	0.15	0.21	1.00
PEN1	3521.31	3915.97	3554.53	-0.15	1.00	0.14	1.00
PEN2	84.19	69.81	39.61	0.27	1.00	0.82	1.00
PLACW	68.47	56.88	64.63	0.27	1.00	-0.18	1.00
POGO	1857.75	270.60	395.06	2.78	0.00	-0.55	1.00
PROTOP	1149.45	689.43	660.87	0.74	0.34	0.06	1.00
QUASIMODO	620.75	289.56	257.47	1.10	0.21	0.17	1.00
QUASIMODO2	4891.90	71.53	84.43	6.10	0.00	-0.24	1.00
R1	729.63	452.44	373.17	0.69	0.76	0.28	1.00
R2	81.94	59.46	32.31	0.46	1.00	0.88	1.00
ROO	4001.75	1889.04	1945.09	1.08	0.00	-0.04	1.00
ROOA	1322.32	1318.54	1700.13	0.00	1.00	-0.37	1.00
ROVER	50515.19	789.40	1243.56	6.00	0.00	-0.66	0.10
RT1A	483.80	87.04	100.07	2.47	0.00	-0.20	1.00

RT1B	614.01	88.76	86.52	2.79	0.00	0.04	1.00
RT1C	76.33	35.33	43.78	1.11	1.00	-0.31	1.00
S	181.85	66.36	65.67	1.45	0.76	0.02	1.00
STALKER2	237.97	59.46	43.78	2.00	0.20	0.44	1.00
STALKER4	260.42	114.62	107.37	1.18	0.75	0.09	1.00
TABOR	286.24	84.46	93.81	1.76	0.17	-0.15	1.00
TAHRE	37901.55	451.58	386.72	6.39	0.00	0.22	1.00
TART	147703.22	34096.73	6614.96	2.11	0.00	2.37	0.00
TC1	260.42	148.23	124.04	0.81	1.00	0.26	1.00
TC1-2	305.32	178.39	236.62	0.78	1.00	-0.41	1.00
TIRANT	4992.92	7421.74	3276.21	-0.57	0.09	1.18	0.00
TOM1	152.66	144.78	169.91	0.08	1.00	-0.23	1.00
TRANSIB2	189.70	81.87	71.92	1.21	0.93	0.19	1.00
TRANSIB3	116.74	73.25	64.63	0.67	1.00	0.18	1.00
TRANSPAC	24133.96	587.74	680.68	5.36	0.00	-0.21	1.00
ZAM	115.62	56.02	56.29	1.05	1.00	-0.01	1.00

Table A2.3 continued

spn-E_sense_mRNA_normalized														
TE	mutant 1	mutant 2	mutant 3	mel1	mel2	mel3	sim1	sim2	sim3	L2FC(mut/D. mel)	padj	L2FC(D.mel/ D.sim)	padj	
1731	94.97	136.83	140.66	32.47	31.41	29.21	39.11	33.74	47.78	2.00	0.00	-0.37	0.63	
176	664.77	662.67	637.98	188.32	96.33	121.56	163.27	126.53	152.36	2.27	0.00	-0.11	0.88	
297	942.88	892.23	891.67	1247.64	546.56	816.98	707.83	703.85	769.90	0.06	0.92	0.26	0.66	
412	599.19	688.68	624.17	587.70	309.93	446.65	442.88	467.67	491.33	0.51	0.06	-0.06	0.94	
ACCO RD	367.43	443.29	359.18	107.96	95.28	85.75	116.34	107.78	101.87	2.01	0.00	-0.17	0.75	
ACCO RD2	185.41	210.33	179.59	110.40	75.39	75.38	105.59	98.41	104.58	1.13	0.00	-0.23	0.70	

BAGGI NS1	395.69	493.04	418.20	185.89	196.84	182.81	198.47	209.94	185.71	1.21	0.00	-0.07	0.90
BARI	119.84	166.23	118.05	33.28	16.75	37.69	19.55	23.43	30.65	2.19	0.00	0.26	0.80
BATU MI	686.25	831.16	749.75	181.83	164.39	155.48	175.00	167.76	148.75	2.17	0.00	0.03	0.97
BEL	187.67	144.75	123.08	60.88	70.15	78.21	54.75	47.80	74.83	1.13	0.00	0.23	0.75
Bica	396.82	538.28	477.23	56.01	59.68	59.37	48.88	63.73	62.21	3.01	0.00	0.00	1.00
BLAST OPIA	179.76	201.29	173.31	71.43	40.83	63.13	83.10	74.98	100.97	1.65	0.00	-0.55	0.31
BLOO D	563.02	348.30	400.62	153.42	114.13	142.29	99.72	105.91	116.30	1.68	0.00	0.35	0.51
BS	215.94	226.17	233.59	69.81	64.92	56.54	61.59	65.61	70.32	1.82	0.00	-0.04	0.97
BS2	264.55	346.03	283.83	115.27	128.79	106.48	109.50	106.84	81.14	1.35	0.00	0.24	0.67
BURD OCK	78.01	88.20	74.10	35.72	29.32	38.63	25.42	21.56	30.65	1.21	0.00	0.42	0.59
Chimp o	82.53	70.11	81.63	46.27	42.93	47.12	47.91	47.80	39.67	0.78	0.02	0.01	0.99
Chouto	88.18	135.70	116.80	45.46	42.93	57.48	40.08	61.86	50.49	1.22	0.00	-0.06	0.97
CIRCE	178.63	214.86	175.82	83.61	92.14	94.23	82.12	85.29	73.93	1.08	0.00	0.16	0.79
COPIA	166.19	162.84	177.08	114.46	60.73	64.08	65.50	80.60	80.24	1.07	0.00	0.09	0.93
Copia1	318.82	320.03	287.59	107.96	86.90	92.35	107.54	100.28	105.48	1.68	0.00	-0.12	0.83
COPIA 2	68.96	87.07	82.89	21.92	19.89	23.56	22.49	31.87	30.65	1.87	0.00	-0.38	0.68
CR1A	991.50	1167.02	1059.95	439.15	308.88	433.46	461.46	469.55	448.06	1.44	0.00	-0.22	0.57
DIVER	89.31	76.90	76.61	60.07	46.07	56.54	66.48	103.09	93.76	0.57	0.14	-0.69	0.19
DIVER 2	200.11	256.70	228.57	86.04	81.67	88.58	93.86	97.47	104.58	1.42	0.00	-0.21	0.70
DNAR EP1	109.66	122.13	97.96	69.81	50.26	65.96	63.55	58.11	54.99	0.82	0.00	0.08	0.93
DOC	1355.54	1909.98	1451.78	791.44	696.28	763.27	879.90	861.31	880.79	1.07	0.00	-0.22	0.52

DOC2	224.98	257.83	251.17	151.79	104.70	140.40	145.67	136.83	167.68	0.88	0.00	-0.18	0.74
DOC3	327.86	389.01	331.55	168.03	144.49	132.87	184.78	206.19	190.22	1.23	0.00	-0.38	0.31
DOC5	59.92	82.55	62.79	62.50	32.46	23.56	43.02	46.86	45.98	0.78	0.14	-0.18	0.88
DOC6	127.75	111.95	133.12	125.01	67.01	99.88	54.75	70.29	64.91	0.34	0.47	0.63	0.27
FROG GER	35.05	71.24	47.72	52.76	31.41	52.77	49.86	55.30	53.19	0.16	0.85	-0.20	0.84
FW	2448.7 8	2853.0 9	2234.1 9	541.43	491.06	519.21	515.23	543.59	496.74	2.28	0.00	0.00	0.99
G	59.92	75.77	54.00	47.89	92.14	65.02	44.97	59.05	36.06	-0.10	0.90	0.54	0.48
G2	106.27	119.87	128.10	76.30	107.85	70.67	62.57	78.73	56.80	0.48	0.21	0.36	0.57
G4	58.79	87.07	64.05	42.21	20.94	32.04	41.06	21.56	35.16	1.13	0.01	-0.02	0.99
G5	59.92	74.63	51.49	39.78	35.60	41.46	43.99	46.86	30.65	0.67	0.13	-0.05	0.97
G6	49.74	71.24	55.26	31.66	26.18	37.69	34.22	33.74	25.24	0.88	0.04	0.04	0.98
GTWI N	547.19	740.70	596.54	413.99	412.54	455.13	404.75	446.12	487.73	0.56	0.00	-0.06	0.91
GYPS Y	249.85	248.78	227.31	73.87	77.48	65.96	65.50	72.17	82.94	1.74	0.00	-0.02	0.98
Gypsy 1	90.44	139.09	120.56	48.70	68.06	51.83	56.70	55.30	55.89	1.06	0.00	0.00	1.00
GYPS Y10	76.88	121.00	128.10	54.39	41.88	60.31	36.17	55.30	50.49	1.05	0.00	0.14	0.89
GYPS Y12	179.76	217.12	205.96	78.74	56.54	62.19	82.12	98.41	99.17	1.60	0.00	-0.49	0.31
Gypsy 2	257.77	301.93	270.01	139.62	147.63	133.81	149.58	163.08	154.16	0.98	0.00	-0.15	0.75
GYPS Y2	998.28	1259.7 5	1048.6 5	198.06	160.20	166.79	183.80	182.76	215.46	2.65	0.00	-0.15	0.75
GYPS Y4	475.96	555.24	501.09	201.31	162.29	185.63	158.38	214.62	221.78	1.48	0.00	-0.11	0.83
GYPS Y5	169.58	189.98	162.01	77.12	54.45	72.56	80.17	73.10	70.32	1.35	0.00	-0.12	0.87
GYPS Y6	118.71	174.15	148.19	93.35	105.75	85.75	119.28	140.58	112.69	0.63	0.02	-0.39	0.44

HETA	187.67	158.32	195.92	94.97	96.33	78.21	68.44	90.91	71.22	1.01	0.00	0.22	0.71
HMSB EAGL E	477.09	487.39	507.37	34.90	32.46	30.15	32.26	40.30	22.54	3.91	0.00	0.04	0.97
I	209.15	204.68	184.61	114.46	57.59	80.10	94.83	95.60	96.46	1.24	0.00	-0.18	0.81
IDEFIX	316.56	304.19	307.69	139.62	75.39	81.98	94.83	104.03	107.28	1.63	0.00	-0.03	0.97
INVAD ER1	137.93	203.55	170.80	61.69	53.40	69.73	51.82	58.11	60.40	1.47	0.00	0.12	0.89
INVAD ER2	96.10	92.73	108.00	39.78	28.27	28.27	40.08	27.18	32.45	1.61	0.00	-0.04	0.98
INVAD ER3	96.10	94.99	89.17	32.47	23.03	18.85	27.37	29.05	24.34	1.90	0.00	-0.11	0.94
INVAD ER4	169.58	257.83	214.75	51.14	42.93	61.25	42.04	54.36	52.29	2.04	0.00	0.06	0.96
INVAD ER6	126.62	156.05	128.10	120.95	142.40	127.21	159.36	142.46	132.52	0.08	0.88	-0.16	0.77
IVK	133.41	183.19	140.66	62.50	61.78	65.02	64.53	73.10	61.30	1.27	0.00	-0.07	0.94
Jockey	171.84	173.02	153.22	133.12	89.00	120.62	125.14	125.59	119.00	0.53	0.05	-0.10	0.88
JOCK EY2	61.05	124.39	89.17	58.45	51.31	59.37	48.88	63.73	60.40	0.70	0.09	-0.03	0.98
M4DM	61.05	82.55	79.12	43.83	21.99	28.27	37.15	38.43	42.37	1.23	0.00	-0.31	0.74
MARIN ER2	87.05	126.65	125.59	45.46	41.88	43.35	45.95	44.05	45.98	1.37	0.00	-0.06	0.97
MAX	582.24	757.66	665.61	347.42	409.39	330.75	294.28	332.71	272.26	0.88	0.00	0.27	0.46
MDG1	548.32	612.91	587.75	435.09	299.45	391.06	371.51	386.14	474.20	0.63	0.00	-0.13	0.79
MDG3	422.83	295.15	322.76	125.82	45.02	72.56	99.72	87.16	100.97	2.09	0.00	-0.23	0.79
MICR OPIA	82.53	118.74	110.52	29.22	17.80	32.98	24.44	32.80	18.93	1.95	0.00	0.08	0.97
NOMA D	332.38	409.36	345.36	169.65	140.30	186.58	267.88	243.68	238.90	1.13	0.00	-0.59	0.08
POGO	203.50	201.29	172.05	164.78	98.42	121.56	119.28	133.09	140.64	0.58	0.04	-0.02	0.98
PROT OP	3157.6 4	2862.1 4	3305.4 5	1082.8 6	836.59	850.90	773.33	795.70	682.45	1.75	0.00	0.30	0.31

QUASI MODO	364.04	341.51	360.43	177.77	73.29	111.19	84.08	116.22	110.89	1.55	0.00	0.23	0.77
QUASI MODO 2	89.31	82.55	99.21	70.62	48.16	53.71	44.97	55.30	49.58	0.64	0.07	0.21	0.79
R1	327.86	409.36	350.39	184.26	252.34	212.02	187.71	245.55	173.09	0.75	0.00	0.09	0.88
ROO	2680.5 5	2661.9 8	2564.4 8	1602.3 7	860.67	1225.0 0	1078.3 6	1086.2 4	1162.9 7	1.10	0.00	0.15	0.77
ROOA	884.09	1030.1 9	1043.6 3	772.77	662.78	927.23	910.21	973.77	1153.0 5	0.32	0.16	-0.36	0.28
ROVE R	165.06	171.89	162.01	124.20	76.43	109.31	85.06	97.47	122.61	0.68	0.02	0.03	0.98
RT1A	280.38	334.73	295.13	117.70	156.01	132.87	113.41	134.96	91.96	1.17	0.00	0.25	0.62
RT1B	525.71	709.03	586.49	253.26	329.82	278.92	287.43	283.98	226.28	1.08	0.00	0.11	0.83
S	63.31	92.73	71.58	71.43	68.06	63.13	35.20	38.43	36.96	0.17	0.80	0.87	0.10
STALK ER2	122.10	132.31	155.73	58.45	32.46	43.35	48.88	52.48	38.77	1.60	0.00	-0.05	0.97
STALK ER4	1012.9 8	954.42	945.67	666.44	317.25	431.58	298.19	356.14	381.35	1.04	0.00	0.45	0.35
TABO R	133.41	175.28	143.17	134.75	127.74	130.04	53.77	82.48	119.00	0.20	0.74	0.62	0.28
TAHR E	185.41	217.12	192.15	132.31	115.17	141.35	131.01	142.46	96.46	0.61	0.02	0.08	0.92
TART	7908.2 3	10628. 70	9883.6 9	3034.2 8	3188.2 5	3226.4 6	3789.4 3	3490.2 2	3333.8 4	1.59	0.00	-0.17	0.57
TC1	128.88	137.96	101.73	81.99	56.54	84.81	82.12	84.35	87.45	0.72	0.02	-0.18	0.80
TIRAN T	12.44	12.44	18.84	51.14	71.20	55.60	10.75	12.18	19.83	-2.03	0.00	2.05	0.00
TRAN SIB2	153.76	135.70	144.42	94.97	60.73	66.90	62.57	65.61	66.71	0.95	0.00	0.20	0.77
TRAN SPAC	428.48	369.78	327.78	69.81	31.41	38.63	39.11	48.74	41.47	2.99	0.00	0.13	0.90
ZAM	80.27	117.61	95.45	49.52	47.12	52.77	53.77	50.61	52.29	0.97	0.00	-0.07	0.96

Table A2.3 continued

armi_sense_mRNA_normalized													
TE	mutant 1	mutant 2	mutant 3	mel1	mel2	mel3	sim1	sim2	sim3	L2FC(mut/D. mel)	padj	L2FC(D.mel/ D.sim)	padj
1731	149.61	179.61	239.64	98.31	129.98	94.27	67.18	58.19	57.05	0.83	0.00	0.83	0.03
176	741.38	1063.18	1433.77	100.60	111.00	84.45	101.26	52.70	60.41	3.45	0.00	0.46	0.38
297	153.62	179.61	188.29	89.17	82.54	64.81	83.73	61.49	85.58	1.15	0.00	0.02	0.97
412	1331.81	1474.55	1678.31	137.18	127.13	122.75	222.97	250.33	206.40	3.54	0.00	-0.81	0.00
ACCO RD	320.60	570.70	725.45	50.30	59.77	54.99	54.52	31.84	28.53	3.29	0.00	0.53	0.40
ACCO RD2	26.72	53.11	69.28	28.58	15.18	19.64	24.34	19.76	27.69	1.27	0.01	-0.20	0.84
BAGGI NS1	50.76	85.94	70.91	29.72	24.67	15.71	18.50	19.76	19.30	1.59	0.00	0.28	0.73
BATU MI	1409.28	2303.08	2288.82	33.15	36.05	37.32	41.87	46.11	28.53	5.81	0.00	-0.11	0.87
BEL	16984.86	27637.90	34955.09	171.47	182.16	117.84	143.13	127.36	104.04	7.40	0.00	0.33	0.50
Bica	148.28	248.17	304.85	13.72	13.28	17.68	11.68	6.59	8.39	3.98	0.00	0.74	0.40
BLAST OPIA	695.96	984.96	885.21	176.04	167.92	116.86	143.13	139.44	149.34	2.48	0.00	0.09	0.84
BLOO D	69563.80	92627.20	96214.53	1194.59	966.75	905.38	955.16	612.66	650.23	6.40	0.00	0.47	0.17
BS	150.95	196.03	268.99	52.58	63.56	57.94	46.74	40.62	29.37	1.83	0.00	0.59	0.28
BS2	179.00	191.20	245.35	48.01	40.80	38.30	36.03	41.72	26.01	2.29	0.00	0.30	0.59
BURD OCK	4874.38	5705.07	6699.37	98.31	59.77	65.79	47.71	38.43	36.08	6.28	0.00	0.86	0.01
Chimp o	188.35	311.91	317.08	68.59	79.69	64.81	48.68	53.80	41.11	1.95	0.00	0.58	0.23

CIRCE	148.28	116.84	111.67	33.15	34.15	15.71	14.60	40.62	21.81	2.18	0.00	0.12	0.90
COPIA	16744. 42	19340. 06	16073. 11	2880.7 3	2975.2 0	2921.3 8	3265.6 6	3022.6 5	4002.9 2	2.57	0.00	-0.23	0.34
Copia1	94.84	144.85	141.83	28.58	17.08	21.60	24.34	27.45	23.49	2.53	0.00	-0.17	0.82
COPIA 2	78.81	92.70	91.29	18.29	30.36	17.68	21.42	25.25	20.14	1.98	0.00	0.01	0.99
CR1A	187.01	190.23	187.47	28.58	45.54	34.37	41.87	39.53	34.40	2.37	0.00	-0.08	0.91
DIVER	8927.2 4	14707. 83	19509. 61	831.07	795.03	616.68	674.75	524.82	468.17	4.27	0.00	0.43	0.50
DIVER 2	53.43	67.60	60.32	28.58	29.41	20.62	24.34	19.76	15.94	1.21	0.00	0.39	0.57
DOC	2647.5 8	4888.1 3	6278.7 8	3780.3 9	3145.0 2	2748.5 6	2677.5 7	1790.7 5	2008.5 9	0.51	0.37	0.58	0.39
DOC2	205.72	317.70	468.69	84.59	89.18	63.83	66.21	57.09	46.98	2.07	0.00	0.48	0.40
DOC3	590.43	789.90	996.88	321.22	249.51	246.48	203.49	187.75	145.99	1.55	0.00	0.61	0.09
DOC5	66.79	100.43	130.42	38.87	30.36	33.39	25.32	17.57	21.81	1.56	0.00	0.65	0.33
DOC6	1092.7 0	1246.6 6	1030.3 0	19.43	27.51	24.55	20.45	26.35	26.01	5.55	0.00	-0.01	0.99
FW	818.85	1182.9 2	1486.7 6	553.28	435.46	346.64	358.31	262.41	325.54	1.39	0.00	0.49	0.24
G	164.31	236.58	322.78	38.87	47.44	45.17	39.92	27.45	52.02	2.46	0.00	0.13	0.87
G2	136.25	163.20	210.30	32.01	41.74	39.28	38.95	42.82	21.81	2.18	0.00	0.15	0.83
G4	56.10	77.25	87.22	42.30	24.67	30.44	40.89	24.15	29.37	1.20	0.00	0.03	0.98
G5	140.26	200.86	302.41	32.01	30.36	21.60	18.50	28.55	15.10	2.95	0.00	0.45	0.55
G6	100.19	163.20	204.59	51.44	44.59	21.60	20.45	20.86	26.01	2.01	0.00	0.79	0.26
GYPS Y	2924.0 9	4103.0 5	6291.8 2	1454.0 8	1344.3 4	1215.6 9	2123.5 5	1765.5 0	2101.7 2	1.73	0.00	-0.58	0.13
Gypsy 1	931.06	1331.6 3	1837.2 5	1870.1 9	1814.9 1	1548.5 8	862.66	367.81	401.05	-0.35	0.68	1.68	0.01
GYPS Y12	2773.1 5	3454.1 3	3048.5 0	74.30	104.36	79.54	74.97	102.11	62.09	5.16	0.00	0.13	0.77
Gypsy	256.48	425.85	529.82	304.08	319.72	246.48	346.62	284.37	343.16	0.48	0.13	-0.16	0.74

2													
GYPS Y4	133.58	149.68	160.58	64.02	52.18	57.94	50.63	32.94	49.50	1.36	0.00	0.37	0.44
GYPS Y6	74.81	117.81	113.30	35.44	33.21	37.32	29.21	35.13	28.53	1.54	0.00	0.20	0.77
HETA	23273. 87	36639. 70	52453. 01	243.49	219.16	193.45	103.21	117.48	109.91	7.42	0.00	0.99	0.01
HMR2	543.68	1277.5 6	1726.4 0	5.72	7.59	3.93	3.89	2.20	1.68	7.68	0.00	1.17	0.41
HMSB EAGL E	1834.0 7	3115.1 9	2628.7 2	61.73	66.41	50.08	52.58	28.55	50.34	5.41	0.00	0.42	0.40
HOBO	49.43	74.36	64.39	52.58	38.90	34.37	46.74	25.25	42.79	0.60	0.18	0.11	0.88
I	3212.6 3	7759.0 1	13522. 64	514.42	496.18	394.76	180.13	136.15	128.37	4.12	0.00	1.66	0.05
IDEFIX	68.13	118.78	180.14	18.29	13.28	10.80	14.60	9.88	9.23	3.14	0.00	0.32	0.76
INVAD ER1	98.85	110.08	93.74	29.72	34.15	27.50	24.34	37.33	26.01	1.73	0.00	0.08	0.92
INVAD ER2	579.74	867.15	867.27	112.03	87.28	68.74	96.39	63.68	88.10	3.12	0.00	0.10	0.86
INVAD ER3	313.92	334.12	226.60	49.16	47.44	36.33	45.76	52.70	62.09	2.72	0.00	-0.28	0.59
INVAD ER4	426.12	477.03	413.26	8.00	18.97	8.84	14.60	15.37	8.39	5.17	0.00	-0.04	0.97
INVAD ER6	651.88	579.39	473.58	54.87	59.77	54.99	57.45	63.68	61.25	3.32	0.00	-0.10	0.84
IVK	402.08	753.21	999.32	58.30	62.62	54.99	51.60	21.96	27.69	3.62	0.00	0.80	0.39
Jockey	2185.3 9	3622.1 6	4125.2 6	99.45	83.49	75.61	86.66	43.92	50.34	5.27	0.00	0.51	0.47
M4DM	77.48	62.77	89.66	35.44	30.36	28.48	35.05	36.23	35.24	1.30	0.00	-0.18	0.79
MAX	3551.9 3	4117.5 4	3967.9 5	330.37	372.85	284.77	511.17	480.90	551.23	3.56	0.00	-0.64	0.00
MDG1	96.18	143.88	110.85	45.73	59.77	41.24	53.55	43.92	36.08	1.26	0.00	0.15	0.82

MDG3	4354.75	7362.12	4228.78	45.73	56.92	41.24	37.00	31.84	36.08	6.79	0.00	0.45	0.40
MICR OPIA	353.99	566.84	454.02	30.86	47.44	42.23	39.92	30.74	31.88	3.50	0.00	0.24	0.68
NOMAD	327.27	366.95	376.58	89.17	102.46	74.63	83.73	64.78	83.06	2.01	0.00	0.20	0.63
PEN1	968.46	998.48	1211.25	919.09	805.47	879.85	833.45	841.03	822.23	0.29	0.07	0.06	0.82
PEN2	149.61	138.09	155.69	124.60	116.69	102.13	95.42	114.19	106.55	0.37	0.15	0.12	0.77
PEN4	42.75	49.25	73.36	48.01	34.15	41.24	25.32	34.04	43.63	0.45	0.40	0.25	0.73
POGO	84.16	78.22	88.85	19.43	9.49	10.80	11.68	13.18	11.75	2.69	0.00	0.10	0.93
PROT OP	133.58	162.23	185.03	81.16	87.28	58.92	59.39	56.00	63.76	1.09	0.00	0.34	0.45
QUASI MODO	362.01	650.85	746.64	78.88	55.03	42.23	76.92	42.82	45.31	3.33	0.00	0.09	0.94
QUASI MODO 2	626.50	1130.78	1507.13	124.60	105.31	87.40	42.84	26.35	32.72	3.37	0.00	1.63	0.01
R1	1095.37	1008.14	856.68	467.55	629.95	518.48	582.25	720.25	479.08	0.87	0.00	-0.14	0.71
R2	141.60	182.51	123.08	96.02	118.59	87.40	74.97	86.74	87.26	0.56	0.04	0.28	0.52
ROO	382.04	429.71	420.60	142.89	118.59	109.98	119.76	92.23	93.97	1.74	0.00	0.27	0.43
ROOA	45.42	86.91	106.78	27.44	18.03	29.46	25.32	23.06	26.85	1.70	0.00	-0.01	0.99
ROVER	2981.53	5875.99	9419.39	292.65	183.10	191.49	143.13	95.52	98.16	4.78	0.00	0.99	0.26
RT1A	92.17	159.33	183.40	60.59	59.77	62.85	53.55	37.33	50.34	1.26	0.00	0.37	0.52
RT1B	187.01	205.68	202.15	92.59	77.80	72.67	86.66	69.17	67.12	1.30	0.00	0.12	0.79
STALK ER2	106.87	166.09	136.12	38.87	45.54	28.48	28.24	34.04	13.42	1.86	0.00	0.60	0.36
STALK ER4	126.90	111.05	149.98	37.72	43.64	40.26	60.37	27.45	46.98	1.67	0.00	-0.16	0.82
TABOR	48.09	65.66	97.00	20.58	14.23	11.78	9.74	6.59	9.23	2.21	0.00	0.84	0.36

TAHR E	7806.49	15527.67	24784.99	251.49	210.62	160.06	148.00	113.09	133.40	6.27	0.00	0.66	0.43
TART	27515.08	39906.50	50867.63	600.15	628.06	546.96	583.22	544.58	518.51	6.06	0.00	0.11	0.80
TC1-2	101.52	84.01	111.67	46.87	54.08	52.04	50.63	50.51	35.24	0.96	0.00	0.18	0.75
TIRAN T	378.04	408.47	891.73	587.58	478.16	320.12	432.31	220.69	272.68	0.28	0.79	0.58	0.54
TRAN SPAC	8215.25	9134.09	8926.25	89.17	74.95	95.25	88.60	75.76	93.97	6.67	0.00	-0.01	0.99

Table A2.4 Normalized abundance and differential expression of TE-derived piRNAs.

aub_antisense_normalized (RPM)								
TE	mutant1	mutant2	mel1	mel2	sim1	sim2	L2FC(mut/D.mel)	L2FC(D.mel/D.sim)
1731	81.60	220.26	1473.87	2349.77	1866.74	2323.75	-3.66	-0.13
176	1228.77	5914.76	6981.22	9473.26	5410.56	6052.08	-1.20	0.52
297	2987.07	14406.41	12913.72	20244.90	16487.52	18285.77	-0.93	-0.07
412	4965.93	20796.47	10219.58	18839.61	14050.09	20010.08	-0.17	-0.23
ACCORD	57.98	238.35	839.54	1494.71	1203.42	1612.59	-2.98	-0.27
ACCORD2	289.27	1277.21	1224.97	2393.20	2296.59	2945.73	-1.21	-0.53
ARS406	97.47	367.37	201.67	339.12	212.79	258.20	-0.22	0.20
BAGGINS1	2657.08	7871.87	8996.60	12242.51	10168.56	9279.80	-1.01	0.13
BARI	1961.68	5854.71	3901.29	7460.12	4839.86	5917.71	-0.54	0.08
BATUMI	7525.62	24502.00	38432.71	57373.99	41241.01	45652.82	-1.58	0.14
BEL	113.57	278.04	5721.32	9308.64	8494.78	8842.55	-5.26	-0.21
Bica	249.62	631.28	2065.14	2752.31	2361.20	2667.08	-2.45	-0.06
BLASTOPIA	66.10	302.50	1395.34	2241.42	1656.52	1939.69	-3.30	0.02
BLOOD	8886.06	37947.98	29159.35	45158.05	38035.16	38284.18	-0.67	-0.04
BS	559.52	1873.27	5343.58	8336.94	6011.22	6530.57	-2.49	0.13
BS2	684.06	1417.51	17095.21	22792.53	17120.50	15439.39	-4.25	0.29
BS3	300.39	422.66	778.19	1352.96	925.29	1092.76	-1.56	0.08
BURDOCK	199.47	328.78	1811.08	2895.10	2190.75	2560.80	-3.16	-0.01
Chimpo	263.65	598.62	3925.62	5722.21	4391.90	4641.44	-3.48	0.09
Chouto	93.25	261.71	374.49	550.38	539.86	631.20	-1.38	-0.34
CIRCE	234.67	1623.79	4459.71	8472.11	5690.03	7714.95	-2.80	-0.05
COPIA	473.16	3299.34	1040.40	1956.63	1362.61	1830.24	0.33	-0.09
Copia1	238.35	902.51	1480.30	2702.14	1670.96	2053.61	-1.87	0.17
COPIA2	1579.46	5567.67	2522.96	4126.77	3879.58	4458.45	0.10	-0.33
CR1A	8977.93	28548.54	13643.42	20988.72	17168.34	18553.45	0.12	-0.04
DIVER	43.79	136.27	2496.27	3989.52	3077.01	3570.36	-5.17	-0.04

DIVER2	438.58	979.54	2238.04	3909.74	2898.73	3617.40	-2.12	-0.08
DNAREP1	172.39	433.42	983.03	1532.27	1065.15	1238.45	-2.05	0.13
DOC	9467.43	26794.20	21638.79	28133.24	24210.21	20794.79	-0.46	0.15
DOC2	700.08	2230.54	2095.45	3198.98	2961.50	3211.75	-0.85	-0.22
DOC3	1279.54	3750.34	4847.59	7703.25	6856.25	6807.47	-1.32	-0.12
DOC4	37.35	138.62	43.43	71.60	81.98	93.29	0.61	-0.61
DOC5	169.48	485.85	320.29	521.41	508.41	572.84	-0.36	-0.36
DOC6	139.04	447.56	1087.45	1925.81	1204.77	1314.63	-2.36	0.26
FB4	26.92	54.99	46.41	61.56	58.12	61.26	-0.40	-0.14
FROGGER	10.66	40.42	8.78	12.44	10.03	13.16	1.27	-0.13
FW	15323.63	43614.43	25162.52	36933.08	28029.22	28301.13	-0.08	0.14
FW2	63.57	214.99	85.86	142.07	137.90	156.92	0.29	-0.37
FW3	32.44	91.68	23.98	46.55	42.58	52.31	0.82	-0.43
G	304.37	1091.65	3784.66	5933.39	4711.63	4879.54	-2.80	0.02
G2	311.28	972.59	5820.76	8004.56	6066.90	6657.57	-3.43	0.12
G3	34.51	105.81	81.61	129.79	120.65	146.13	-0.59	-0.34
G4	194.86	711.68	413.93	621.42	631.99	713.79	-0.19	-0.38
G5	112.81	210.23	178.24	255.89	349.22	314.55	-0.43	-0.61
G5A	39.65	84.87	63.79	88.61	102.66	125.59	-0.29	-0.58
G6	368.64	1090.04	5197.46	6067.84	5120.68	4274.58	-2.95	0.26
G7	8.67	8.42	8.41	11.48	9.67	6.14	-0.22	0.33
GTWIN	1636.37	5074.20	2722.19	3872.65	3447.40	3684.62	0.03	-0.11
GYPSY	1439.20	4732.82	3178.92	4650.43	3857.92	4099.40	-0.34	-0.02
Gypsy1	1293.11	4786.42	3008.73	5018.28	4229.89	5045.77	-0.40	-0.21
GYPSY10	2416.28	9478.81	3424.83	5597.64	4935.67	5696.81	0.40	-0.24
GYPSY11	18.33	43.86	21.90	27.61	33.04	33.79	0.33	-0.43
GYPSY12	521.02	2607.72	1889.80	3363.05	2967.37	3525.07	-0.75	-0.31
Gypsy2	3912.16	14330.69	9627.31	14832.19	12522.66	13670.58	-0.42	-0.10
GYPSY2	1764.82	5930.35	3057.31	5542.82	4468.38	5849.16	-0.16	-0.26

GYPSY3	1146.64	4086.23	1843.02	3102.67	2958.69	3276.34	0.08	-0.33
GYPSY4	2170.19	7521.77	6437.18	9786.62	8626.08	9557.92	-0.74	-0.16
GYPSY5	290.34	1040.83	393.67	642.85	547.69	624.09	0.36	-0.18
GYPSY6	3197.35	10869.74	7283.23	10526.51	10288.96	11056.95	-0.34	-0.26
GYPSY6A	324.85	785.42	652.16	833.56	816.39	803.22	-0.42	-0.12
GYPSY7	293.79	678.07	392.22	497.81	495.07	461.29	0.13	-0.10
GYPSY8	662.81	1185.75	2879.26	4277.99	4258.04	4081.94	-1.95	-0.22
GYPSY9	30.22	70.74	56.82	65.66	71.70	65.12	-0.28	-0.16
HELENA_RT	127.61	504.53	176.88	297.62	265.03	345.62	0.41	-0.36
HETA	1011.74	1764.53	11598.45	14571.81	15124.05	12340.07	-3.24	-0.07
HETRP	358.44	1262.64	905.13	1410.03	842.70	1045.01	-0.51	0.29
HMR1	3.68	8.42	13.21	18.22	17.62	22.47	-1.38	-0.35
HMR2	24.62	80.04	219.95	488.42	212.42	337.98	-2.76	0.36
HMSBEAGLE	175.54	441.99	1267.68	2103.04	1435.66	1574.15	-2.45	0.16
HOBO	223.01	926.09	1331.37	2106.25	1984.45	2411.07	-1.58	-0.35
I	92.41	273.72	3642.07	4820.03	3760.89	3829.70	-4.53	0.16
IDEFIX	1206.15	4798.57	2383.62	3523.26	3378.26	3757.21	0.02	-0.27
INVADER1	877.16	3871.68	1997.01	3681.06	2758.87	3676.55	-0.26	-0.18
INVADER2	383.67	1276.04	1853.52	3257.90	2166.64	2798.38	-1.62	0.04
INVADER3	272.32	1014.55	1019.59	1714.31	1494.64	1814.71	-1.09	-0.28
INVADER4	858.37	2046.08	1282.69	1956.87	1576.74	1597.76	-0.16	0.03
INVADER5	8.97	19.26	21.71	26.97	23.86	25.80	-0.79	-0.03
INVADER6	133.21	645.71	3186.88	5637.77	4210.56	5404.72	-3.50	-0.12
IVK	288.27	771.14	4457.54	5329.87	4227.94	4173.04	-3.21	0.22
Jockey	213.19	612.10	4852.74	5859.79	5216.74	4963.27	-3.70	0.07
JOCKEY2	57.44	186.07	124.77	194.24	178.04	212.30	-0.39	-0.29
LOOPER1	123.93	564.79	134.54	231.00	223.55	275.05	0.91	-0.45
M4DM	56.29	202.03	188.74	317.77	249.86	302.61	-0.97	-0.13
MARINER2	10.28	24.60	15.65	21.91	26.43	23.43	-0.11	-0.41

MAX	11688.85	25159.50	40827.92	54982.55	54044.74	46736.45	-1.38	-0.07
MDG1	757.29	3411.09	2310.79	3799.69	2985.85	3669.35	-0.55	-0.12
MDG3	398.93	1423.51	2720.29	3527.27	2832.78	2960.83	-1.78	0.11
MICROPIA	202.61	876.88	1347.39	2040.75	1516.79	1780.75	-1.65	0.04
NOMAD	2604.55	2542.33	16002.43	24547.62	15936.29	17750.67	-2.98	0.27
NTS	238.96	1037.61	943.86	1381.05	675.55	957.16	-0.86	0.51
POGO	100.08	482.93	1925.44	2134.42	1761.14	1599.60	-2.80	0.27
PROTOP	7812.12	19858.45	7186.96	10360.92	9398.42	9317.01	0.66	-0.09
QUASIMODO	1619.88	5404.08	4319.74	5717.16	5826.95	5497.84	-0.51	-0.17
QUASIMODO2	187.58	612.46	711.87	1151.65	1095.13	1180.35	-1.22	-0.29
R1	4716.38	11207.24	31307.27	51379.99	31505.73	34528.56	-2.38	0.32
R1-2	24.39	43.50	46.41	80.67	63.02	75.92	-0.90	-0.13
R2	113.42	397.18	261.93	411.60	344.57	406.09	-0.40	-0.16
ROO	28165.78	106089.23	60941.81	89497.95	72923.19	77595.39	-0.16	0.00
ROOA	503.92	1843.10	8460.70	14709.23	8787.47	10763.90	-3.30	0.24
ROVER	342.49	1048.08	1190.77	1623.45	1450.59	1472.08	-1.02	-0.05
RSP	315.49	1143.28	508.30	621.58	443.56	370.37	0.37	0.47
RT1A	2484.46	4778.22	22961.48	33071.42	24339.91	22411.94	-2.95	0.26
RT1B	3863.69	6397.24	44151.42	59802.58	45285.90	40762.31	-3.34	0.27
RT1C	215.57	451.22	718.57	1079.33	967.51	961.20	-1.43	-0.10
S	431.75	1512.12	2387.69	3122.89	2223.54	2202.45	-1.50	0.32
S2	9.59	32.15	15.11	26.57	23.37	23.96	0.00	-0.18
SAR	69.33	284.12	77.72	158.93	116.12	164.82	0.58	-0.25
SAR2	241.41	772.68	149.29	344.42	154.42	283.22	1.04	0.17
STALKER2	3178.25	16614.68	4382.99	9277.74	6928.56	10241.61	0.53	-0.33
STALKER3	120.40	407.21	246.28	384.55	325.60	366.94	-0.26	-0.13
STALKER4	3854.79	14254.61	5938.38	9848.83	8081.45	9450.06	0.20	-0.15
TABOR	1787.83	6891.74	2509.20	3963.51	3643.05	4147.58	0.42	-0.27
TAHRE	113.73	329.66	2668.08	4574.17	1831.50	2059.31	-4.03	0.90

TART	513.04	1344.65	5639.80	11052.41	6891.12	8538.27	-3.17	0.11
TC1	18.56	47.96	25.42	35.80	30.10	35.90	0.12	-0.11
TC1-2	29.14	75.72	185.93	251.95	283.51	319.29	-2.06	-0.46
TIRANT	21.32	82.38	60.17	87.89	54.70	63.89	-0.51	0.32
TLD2	7.44	38.15	34.56	71.12	41.97	60.73	-1.21	0.04
TOM1	2.45	7.10	5.70	9.71	9.91	11.15	-0.69	-0.45
Transib1	29.52	111.01	48.50	69.03	69.01	77.50	0.26	-0.32
TRANSIB2	151.54	906.17	1031.71	1658.53	1266.68	1561.86	-1.35	-0.07
TRANSIB3	10.28	36.83	16.01	20.71	19.82	24.49	0.36	-0.27
Transib4	5.14	21.97	10.04	12.28	22.02	20.01	0.28	-0.91
Transib5	96.40	349.00	94.64	134.04	135.94	148.06	0.96	-0.31
TRANSPAC	244.40	1153.68	573.17	1007.97	796.20	1254.51	-0.18	-0.38
XDMR	43.41	65.02	12.21	17.34	14.81	16.68	1.88	-0.09
ZAM	452.77	1825.60	598.51	981.17	933.49	1043.70	0.53	-0.32

spnE_antisense_normalized (RPM)											
TE	mutant1	mutant2	mutant3	mel1	mel2	mel3	sim1	sim2	sim3	L2FC(mut/D.mel)	L2FC(D.mel/D.sim)
1731	355.06	377.81	301.99	14107.74	16098.08	13011.25	11762.18	13338.18	11703.11	-5.38	0.23
176	1475.77	1617.69	1515.26	15683.72	22153.58	16155.75	11135.85	11709.41	11842.15	-3.55	0.64
297	11065.87	12153.27	10911.89	44202.37	51505.42	41334.96	40829.93	45501.87	40008.79	-2.01	0.12
412	27677.60	30686.68	26688.39	45084.15	54233.92	43761.05	46716.43	51689.72	48170.31	-0.75	-0.03
ACCORD	478.15	513.50	417.28	7860.93	10428.15	8040.73	5692.71	6697.81	6223.10	-4.22	0.50
ACCORD2	266.40	285.76	256.31	7301.02	8652.31	7080.93	7534.90	8087.84	7450.36	-4.83	0.00

ARS406	69.72	64.25	56.76	805.99	992.33	920.96	1161.77	1257.47	1017.11	-3.83	-0.34
BAGGIN S1	2862.44	3008.59	2550.26	21397.63	26002.62	19909.18	22346.00	25498.95	21056.19	-3.00	-0.03
BARI	112.33	114.59	109.09	19599.73	29412.76	18805.75	13144.18	14300.64	12329.51	-7.66	0.77
BATUMI	1022.58	1159.33	970.70	64122.09	82163.75	64692.59	64236.48	70728.44	65251.83	-6.06	0.08
BEL	178.18	181.71	135.69	22294.81	26470.38	20703.71	20947.16	23132.82	20280.59	-7.13	0.11
Bica	231.11	267.06	249.66	4693.34	5577.91	4420.50	5203.67	5636.72	5024.86	-4.30	-0.11
BLASTO PIA	205.29	248.36	191.57	5351.78	5734.67	5086.26	7144.68	7979.35	6843.70	-4.65	-0.44
BLOOD	6740.15	8082.69	7366.98	20949.52	24579.02	20025.18	21624.70	23936.61	20794.65	-1.56	-0.02
BS	220.35	249.32	189.35	14301.25	15703.31	13127.77	16818.70	18423.76	16454.83	-6.03	-0.26
BS2	384.33	434.39	371.61	36251.92	43655.03	35552.71	39206.30	42278.57	40359.73	-6.60	-0.08
BS3	38.73	54.66	39.02	1800.98	2233.76	1851.82	2032.37	2086.79	1931.17	-5.47	-0.04
BURDO CK	37.87	50.34	46.56	3127.79	4099.41	3432.02	3685.34	3739.05	3666.40	-6.31	-0.06
Chimpo	94.68	104.04	73.61	9939.01	12049.76	9530.48	8156.66	9159.37	8304.63	-6.85	0.30
Chouto	86.51	85.34	90.46	5402.23	6065.02	5161.85	5748.01	6173.35	5399.89	-5.99	-0.06
CIRCE	280.61	342.81	298.44	21820.88	25462.18	21114.27	22232.27	24341.26	22904.05	-6.21	-0.02
COPIA	201.85	224.87	183.14	3804.22	4634.45	3675.49	3720.21	4060.45	3145.95	-4.31	0.15
Copia1	233.70	231.58	204.43	5574.41	5761.96	5153.25	5746.33	5935.49	5089.89	-4.62	-0.02
COPIA2	247.04	283.36	261.19	5574.65	6811.73	5562.51	5688.14	6115.05	5462.30	-4.50	0.06
CR1A	482.45	589.73	455.42	28114.59	32897.17	27159.55	30597.63	33397.08	29082.74	-5.85	-0.08
DIVER	70.58	78.15	68.29	4268.68	5181.23	4564.13	5206.08	5988.29	5154.62	-6.01	-0.22
DIVER2	158.38	174.04	152.99	4522.58	5498.25	4430.66	4652.84	5201.61	4669.86	-4.90	-0.01

DNARE P1	77.90	89.18	82.48	2052.04	2284.54	2094.25	1486.35	1631.09	1310.86	-4.69	0.54
DOC	4327.45	5168.55	4195.00	50147.45	64641.44	49642.10	52683.23	58244.52	51453.85	-3.59	0.02
DOC2	265.97	283.36	269.17	5635.52	6955.17	5381.34	6372.65	6843.13	6371.14	-4.46	-0.12
DOC3	278.02	297.74	255.87	12990.30	14955.34	12699.48	14851.25	15490.82	14575.04	-5.61	-0.14
DOC4	19.37	19.66	16.85	298.43	375.41	312.29	268.80	250.62	250.21	-4.14	0.36
DOC5	85.21	93.49	89.13	1338.42	1757.44	1297.11	1223.08	1294.89	1240.61	-4.04	0.23
DOC6	101.14	137.12	113.52	5407.91	4917.52	5221.55	7026.15	8056.22	6687.24	-5.47	-0.49
FB4	11.19	8.15	7.54	48.55	55.22	47.44	48.57	46.99	47.31	-2.49	0.08
FROGGER	6.03	10.55	7.10	28.66	36.81	32.84	22.36	20.02	23.80	-2.05	0.57
FW	3833.81	4551.96	3691.69	64046.06	81640.13	64217.12	63741.67	69418.75	63826.32	-4.12	0.09
FW2	16.35	12.47	8.43	173.37	185.64	186.64	214.22	233.80	212.77	-3.87	-0.28
FW3	15.49	17.74	14.19	99.71	139.95	114.44	86.32	85.28	82.15	-2.90	0.48
G	182.91	202.81	147.22	15964.38	21913.36	15580.44	13474.05	15452.24	13814.24	-6.65	0.32
G2	197.11	202.33	141.46	47742.99	66354.13	46602.38	31330.46	36629.96	31651.92	-8.21	0.69
G3	15.49	26.37	15.52	148.27	193.26	180.13	148.11	150.55	150.65	-3.18	0.22
G4	69.29	68.08	65.19	2502.04	2974.76	2398.72	2054.73	2175.26	2002.86	-5.28	0.34
G5	43.04	44.11	35.48	1892.64	2367.68	1897.96	1570.50	1848.35	1646.12	-5.65	0.28
G5A	24.10	17.26	21.73	465.88	539.16	457.48	315.21	386.67	329.75	-4.53	0.50
G6	337.85	418.57	359.64	4385.92	5140.61	3972.92	4428.52	4979.70	4430.39	-3.60	-0.04
G7	0.86	0.48	2.22	12.08	18.41	19.03	17.55	17.40	13.35	-3.80	0.04
GTWIN	31381.00	36533.18	30954.35	51930.66	66483.92	49682.50	51277.91	58054.24	53496.19	-0.77	0.05
GYPSY	2062.37	2352.22	2021.23	6233.79	7629.83	6090.37	6096.88	6864.31	6432.67	-1.63	0.04
Gypsy1	926.60	1064.87	938.78	3560.98	4472.61	3841.02	3851.24	4474.68	4069.59	-2.02	-0.06

GYPSY10	7959.84	9367.63	8158.53	8732.76	9907.71	7995.11	8541.35	9737.49	9479.93	-0.06	-0.06
GYPSY11	16.78	17.74	15.96	34.58	41.25	32.58	36.31	44.38	34.54	-1.10	-0.09
GYPSY12	288.35	313.56	308.64	10105.28	10327.23	9168.92	12636.39	13770.97	12996.84	-5.02	-0.41
Gypsy2	4212.54	4846.35	4050.88	15977.17	17898.99	15664.38	14885.63	15844.42	14507.12	-1.92	0.13
GYPSY2	4644.64	5050.12	4367.51	11983.94	15044.19	12060.83	12637.59	14286.43	13287.98	-1.47	-0.04
GYPSY3	804.81	899.94	787.56	2823.21	3427.28	2800.41	2737.56	3139.76	2959.59	-1.86	0.03
GYPSY4	4834.86	5849.85	4973.25	17548.41	22247.84	17503.17	18634.69	21235.73	19108.77	-1.87	-0.04
GYPSY5	5149.47	6070.40	5627.34	5724.10	6870.44	5583.62	5597.74	6327.09	6292.76	-0.11	0.00
GYPSY6	3230.85	3924.36	3388.82	11329.06	13294.05	10905.53	12479.63	14020.14	12475.23	-1.75	-0.13
GYPSY6A	551.74	615.62	481.58	1231.84	1466.12	1169.12	1244.00	1386.26	1336.40	-1.23	-0.04
GYPSY7	58.53	65.21	70.06	833.94	1032.95	903.75	1065.11	1157.10	1105.64	-3.84	-0.26
GYPSY8	252.20	290.55	265.18	7937.43	8739.89	7986.77	8810.87	9182.87	8443.66	-4.93	-0.10
GYPSY9	32.28	34.04	47.89	239.21	257.36	241.64	258.70	302.55	256.89	-2.69	-0.15
HELENA_RT	483.74	554.25	540.12	1741.06	2299.45	1709.23	1422.88	1609.04	1505.92	-1.87	0.34
HETA	209.16	230.62	205.76	24987.75	28588.95	23751.51	22122.64	26048.93	24000.40	-6.90	0.10
HETRP	21.52	28.77	18.62	2328.91	2560.94	2189.92	1687.11	1644.14	1462.09	-6.68	0.56
HMR1	6.46	4.79	37.69	117.00	142.49	117.30	138.73	252.07	132.36	-2.94	-0.47
HMR2	6.46	5.75	3.99	921.09	1045.00	945.98	747.74	849.92	905.35	-7.49	0.22
HMSBEAGLE	301.69	389.80	313.96	3470.27	4208.26	3540.72	3852.44	4036.67	3585.42	-3.48	-0.03
HOBO	144.61	157.74	142.35	4005.07	4712.52	3539.68	3780.79	4065.39	3781.06	-4.78	0.08
I	187.64	215.28	205.76	7063.46	8744.65	6865.35	7426.95	7677.97	6975.77	-5.22	0.04

IDEFIX	5759.32	6734.45	5879.21	8306.91	9820.76	7996.67	8486.05	9976.80	9046.85	-0.51	-0.07
INVADE R1	256.07	289.59	248.33	8829.63	10326.92	8320.69	6235.85	6761.62	5855.33	-5.11	0.54
INVADE R2	137.72	140.48	127.27	5186.22	6515.97	5107.37	5220.74	5727.51	5158.68	-5.37	0.06
INVADE R3	191.09	216.71	217.29	4342.34	5327.84	4058.42	3590.85	4273.66	3542.17	-4.46	0.27
INVADE R4	72.73	78.15	67.85	2345.25	2496.84	2286.37	2758.24	2999.65	2565.12	-5.03	-0.22
INVADE R5	3.87	4.79	6.21	30.08	30.15	15.38	28.61	30.17	21.19	-2.35	-0.08
INVADE R6	192.38	198.02	172.94	25648.55	26309.80	23767.93	26554.04	28682.22	26139.98	-7.07	-0.10
IVK	209.16	281.92	214.63	17386.17	26244.75	17630.38	9398.73	10840.06	8932.77	-6.44	1.07
Jockey	95.11	111.71	88.25	9327.71	11633.73	9397.01	10621.57	12027.34	10074.11	-6.68	-0.11
JOCKEY 2	292.23	346.17	301.99	1590.90	2185.21	1460.81	1062.71	1335.79	1155.86	-2.48	0.56
LOOPE R1	10.76	10.55	9.76	879.17	1059.60	782.54	597.71	564.19	649.62	-6.45	0.59
M4DM	24.96	37.88	26.61	1061.78	1339.81	1123.76	880.94	1001.34	895.77	-5.30	0.34
MARINE R2	13.34	11.99	10.64	18.00	26.97	17.20	19.96	25.82	24.38	-0.79	-0.17
MAX	1315.66	1400.97	1185.33	78832.13	102764.90	78406.35	86011.93	97792.91	85984.66	-6.06	-0.05
MDG1	16914.28	19874.45	17092.21	32745.17	37800.72	31924.39	34411.60	37004.15	35099.74	-0.93	-0.06
MDG3	250.05	252.19	263.85	5349.17	6329.69	5257.00	5257.29	5624.24	4987.13	-4.47	0.09
MICROP IA	160.10	175.00	157.42	5268.64	6192.59	4913.17	6254.84	6954.52	6132.83	-5.06	-0.24
NOMAD	376.58	403.22	346.33	24276.97	30365.74	25480.03	32002.95	34554.19	29988.09	-6.15	-0.27
NTS	65.42	57.06	47.01	1722.35	2414.01	1718.62	1744.82	2099.27	1721.30	-5.11	0.07

POGO	43.04	61.37	50.11	2232.28	2725.33	2148.47	1997.27	2291.58	1988.93	-5.52	0.18
PROTO P	661.06	651.10	706.85	23090.61	30156.61	22817.77	20030.88	22314.81	18828.37	-5.24	0.31
QUASIMODO	5585.87	6719.11	5950.61	11236.93	13071.92	10790.57	11735.49	13425.20	11989.31	-0.94	-0.08
QUASIMODO2	94.25	118.43	94.01	3348.06	4582.09	3267.28	2502.90	2783.55	2273.69	-5.19	0.57
R1	5035.42	4921.15	3740.92	94218.84	112593.59	85534.20	108437.27	117293.42	107016.47	-4.42	-0.19
R1-2	6.89	14.38	8.87	99.48	114.88	86.54	96.41	102.98	107.40	-3.32	-0.03
R2	115.77	128.49	108.20	4267.26	5133.63	3821.99	4572.06	4841.62	4402.53	-5.23	-0.06
ROO	18491.18	20321.30	18079.76	183589.21	192618.77	171446.11	224727.76	236285.23	215308.38	-3.27	-0.30
ROOA	1094.45	1190.97	1037.67	36995.62	38614.07	34198.51	39798.96	42311.34	38123.20	-5.05	-0.13
ROVER	6590.38	7678.50	6675.20	8685.39	10493.20	8456.76	8829.39	9898.19	9596.04	-0.40	-0.04
RSP	40.89	43.15	52.77	739.67	882.53	651.94	810.50	868.77	777.92	-4.06	-0.11
RT1A	620.60	634.80	556.08	46273.83	55310.97	45806.55	48901.48	52499.32	48149.99	-6.35	-0.02
RT1B	1364.73	1512.21	1229.23	118327.42	142106.31	115246.26	125059.06	135323.84	121896.87	-6.52	-0.03
RT1C	95.97	106.92	86.47	2664.05	2833.86	2474.83	2531.51	2808.50	2291.68	-4.78	0.06
S	62.40	70.00	67.40	7822.79	10164.75	7974.52	7859.48	9486.00	8948.15	-7.02	-0.02
S2	29.70	23.01	27.05	36.71	38.08	33.37	30.29	31.62	26.12	-0.44	0.30
SAR	253.49	281.44	235.03	246.79	308.46	234.35	517.41	574.06	532.94	-0.04	-1.04
SAR2	93.39	81.51	80.26	565.35	696.88	547.41	1465.43	1556.54	1230.74	-2.83	-1.23
STALKE R2	3970.67	4621.01	4079.27	4985.38	5813.05	4673.87	5009.40	5579.86	5406.57	-0.29	-0.05
STALKE R3	291.37	364.87	294.45	1127.62	1177.97	1077.88	1218.03	1360.16	1182.56	-1.83	-0.15
STALKE	11163.1	13091.0	11913.6	76918.1	82496.3	73926.4	90223.3	99694.9	85933.8	-2.69	-0.24

R4	4	9	4	8	2	2	3	3	6		
TABOR	8515.89	10090.17	8926.14	9195.08	10902.89	8891.30	9425.90	10667.76	10560.60	-0.07	-0.08
TAHRE	161.39	178.84	146.78	11672.02	13149.98	12341.58	10108.00	11410.64	11316.18	-6.25	0.18
TART	2493.18	3269.90	2854.47	63115.96	90619.62	70431.31	79608.50	76257.25	76524.76	-4.70	-0.05
TC1	25.82	25.41	20.84	65.13	85.68	66.99	60.83	51.92	55.44	-1.60	0.37
TC1-2	27.11	26.85	23.50	718.12	813.03	681.40	710.24	795.38	690.26	-4.84	0.01
TIRANT	41.32	38.36	34.15	116.77	161.21	121.73	58.42	65.27	68.21	-1.81	1.06
TLD2	154.94	195.14	163.63	222.87	256.09	222.61	231.78	261.07	224.38	-0.45	-0.03
TOM1	2.58	4.32	6.21	25.58	41.89	28.67	32.22	32.49	28.45	-2.87	0.05
Transib1	20.66	25.41	21.29	179.53	184.06	156.93	132.72	143.30	124.53	-2.95	0.38
TRANSIB2	105.87	122.74	88.69	6244.45	7612.70	5868.80	5174.58	6018.16	5518.90	-5.96	0.24
TRANSIB3	14.63	17.26	16.41	29.37	41.25	31.28	37.27	32.49	38.03	-1.08	-0.08
Transib4	14.63	20.14	16.85	36.00	49.19	34.15	36.31	37.13	35.41	-1.21	0.13
Transib5	33.14	45.55	33.26	1271.15	1599.72	1239.76	1093.49	1333.47	1026.69	-5.20	0.25
TRANS PAC	108.02	134.73	122.83	2432.65	3002.36	2315.56	2872.44	3020.83	2575.57	-4.41	-0.13
XDMR	3.44	3.36	1.77	13.03	13.01	11.47	13.22	16.24	16.26	-2.13	-0.29
ZAM	2967.45	3599.76	3131.18	3196.95	3766.84	3084.29	3210.97	3558.34	3544.78	-0.05	-0.04

armi_antisense_normalized (RPM)											
TE	mutant1	mutant2	mutant3	mel1	mel2	mel3	sim1	sim2	sim3	L2FC(mut/D.mel)	L2FC(D.mel/D.sim)
1731	195.97	132.96	204.48	8378.28	7360.63	7162.91	5625.75	6748.89	6042.34	-5.42	0.31
176	1070.35	1024.11	1335.51	7363.32	7097.26	6104.47	5874.90	6718.28	6694.55	-2.58	0.09
297	7851.55	7093.56	8916.76	53804.06	53717.48	52143.24	34300.36	38245.32	38460.03	-2.74	0.52

412	21689.5 1	20008.4 7	24736.0 8	29677.0 9	30808.8 6	24078.8 6	24535.2 2	25735.5 9	26125.1 4	-0.35	0.15
ACCORD	92.67	72.42	103.03	4914.22	5121.53	4315.24	4027.45	4930.21	4862.09	-5.74	0.05
ACCORD2	13.30	16.38	23.45	4816.99	4969.94	4365.80	3841.52	4530.40	4585.95	-8.06	0.13
ARS406	683.61	692.66	753.65	684.07	624.70	706.57	369.52	390.60	440.87	0.08	0.75
BAGGIN S1	865.79	848.17	1019.74	11829.6 5	11039.8 1	9693.77	8729.84	10020.4 1	9809.05	-3.57	0.19
BARI	1892.88	1944.46	2460.58	4955.88	4851.99	3948.85	3425.69	3931.47	4213.85	-1.13	0.25
BATUMI	19640.1 7	16026.3 3	17579.4 7	46280.3 4	45760.4 2	40832.2 7	33940.3 4	39535.4 1	38255.5 9	-1.32	0.25
BEL	33.07	31.97	41.31	4682.60	4382.94	3940.84	3514.98	4388.94	4257.96	-6.93	0.10
Bica	12.38	14.96	16.52	1842.12	1956.48	1575.94	1665.60	1902.78	2015.16	-6.94	-0.06
BLASTO PIA	5981.57	4417.19	5811.26	22149.5 9	20410.0 1	17472.4 5	16633.1 0	18574.0 1	18540.2 9	-1.89	0.16
BLOOD	7265.17	6684.71	7851.46	17700.7 2	18052.6 4	15818.7 0	14578.8 1	16164.0 3	17185.7 0	-1.24	0.11
BS	53.65	52.47	85.41	19333.4 6	17691.9 1	16126.2 7	12671.6 8	14626.4 9	13480.8 6	-8.12	0.38
BS2	40.18	47.01	70.96	16855.5 2	15865.5 9	14137.9 6	12142.9 7	14144.5 5	13716.2 4	-8.21	0.23
BS3	3.24	4.12	7.78	1751.41	1799.70	1422.77	1425.00	1711.10	1650.59	-8.36	0.06
BURDO CK	25.84	28.41	37.66	7815.85	7099.71	6318.73	6553.98	7409.63	7524.44	-7.85	-0.02
Chimpo	5.43	8.71	16.04	6210.28	6834.22	5632.17	5392.57	6312.42	6965.46	-9.27	0.00
Chouto	11.26	11.08	15.67	3328.79	3139.17	2602.60	2703.03	3032.38	3137.92	-7.90	0.03
CIRCE	763.45	599.74	801.28	15704.7 2	14934.5 7	13157.6 6	10899.3 5	12778.0 9	12237.4 8	-4.34	0.29
COPIA	2593.42	1844.82	2877.20	15777.6 1	14286.5 8	13917.5 1	12053.7 5	13017.1 3	13450.7 6	-2.59	0.19
Copia1	754.91	724.55	900.42	15335.7 3	14779.9 3	13093.0 9	11002.7 4	11202.7 1	11787.2 1	-4.18	0.35

COPIA2	704.74	718.38	790.10	2817.58	2848.53	2668.08	1782.22	1887.03	1899.56	-1.91	0.58
CR1A	5396.86	4837.84	5947.46	33576.21	34932.74	32246.28	29387.99	31620.26	34143.54	-2.64	0.08
DIVER	14.06	15.20	17.37	3717.99	3654.96	3181.64	2398.61	3138.88	2997.02	-7.82	0.31
DIVER2	34.55	32.21	46.78	1586.15	1518.21	1317.45	1192.49	1432.53	1362.32	-5.28	0.15
DNARE P1	22.85	26.28	32.80	4741.28	4126.60	3373.68	3174.34	3995.86	3851.79	-7.22	0.15
DOC	22227.52	19271.89	22707.67	35493.67	35685.94	32174.73	24775.02	28854.26	29130.32	-0.69	0.32
DOC2	98.82	84.76	104.00	2754.63	2993.82	2638.57	2375.69	2598.79	2724.02	-4.87	0.12
DOC3	874.22	762.86	1049.62	8322.05	8430.09	7399.31	7395.27	8364.29	8454.88	-3.17	0.00
DOC4	1.00	2.14	2.67	153.38	186.18	149.94	148.30	157.90	160.33	-6.40	0.07
DOC5	7.79	8.47	8.99	1089.29	1118.18	933.42	879.91	1086.11	1051.27	-6.96	0.06
DOC6	35.15	35.77	45.68	1573.25	1454.23	1322.74	1119.44	1250.26	1107.92	-5.22	0.32
FB4	13.90	11.08	12.64	38.98	37.77	32.09	21.19	21.99	21.11	-1.53	0.76
FROGGER	1.52	1.19	1.82	15.21	16.59	12.98	12.16	10.20	12.96	-3.31	0.34
FW	26840.03	25613.99	29841.93	71932.31	74671.54	64615.44	56855.14	66097.97	63994.21	-1.36	0.18
FW2	2.32	2.22	2.19	171.71	174.56	154.20	122.04	155.82	153.65	-6.22	0.21
FW3	7.35	8.39	10.21	87.01	75.93	74.45	63.49	61.32	64.80	-3.19	0.32
G	54.72	55.48	88.33	14362.29	14666.76	12972.40	11595.28	13289.55	13658.75	-7.72	0.12
G2	49.53	45.67	59.66	5490.85	5352.71	4908.49	3882.76	4654.62	4325.69	-6.67	0.29
G3	2.16	3.09	1.82	139.25	129.36	118.82	88.49	97.77	77.97	-5.78	0.55
G4	12.90	14.32	18.95	3162.37	3072.34	2694.56	2193.04	2482.00	2565.56	-7.60	0.30
G5	7.83	9.10	13.36	524.54	519.50	505.36	555.71	592.69	516.96	-5.68	-0.10
G5A	3.95	3.40	2.79	225.32	243.72	208.70	187.60	232.30	213.01	-6.06	0.10
G6	317.16	330.82	363.64	7692.83	7339.39	6355.86	6262.79	6920.27	7912.21	-4.40	0.02
GTWIN	17821.91	16975.56	20169.93	22830.91	23825.10	18466.06	20491.40	22150.14	23355.34	-0.24	-0.02

GYPSY	2506.70	2031.04	2302.27	9027.94	9042.65	7525.17	7429.08	8116.54	8768.65	-1.90	0.07
Gypsy1	879.41	842.16	1001.51	7257.91	7107.35	6278.37	5499.90	6137.97	6550.52	-2.92	0.18
GYPSY10	3968.66	3872.30	4765.77	4698.90	4795.38	3757.32	3759.79	4019.54	4054.98	-0.07	0.16
GYPSY11	16.66	13.22	16.28	52.53	55.62	46.56	40.43	49.63	52.68	-1.74	0.12
GYPSY12	186.70	155.28	210.92	12700.79	12441.47	10385.49	8028.30	9520.74	9126.53	-6.01	0.41
Gypsy2	3272.59	3358.42	3929.13	5710.30	5793.23	4580.45	4577.68	5254.74	5378.84	-0.61	0.08
GYPSY2	2987.87	2809.80	3360.89	6660.99	6381.36	5208.69	5500.90	6226.83	6368.44	-0.99	0.01
GYPSY3	664.95	703.42	727.77	1732.79	1797.18	1465.45	1442.04	1580.04	1668.36	-1.25	0.09
GYPSY4	3371.81	3373.70	3926.34	11279.47	11408.78	9516.77	8761.72	10182.18	10367.61	-1.59	0.14
GYPSY5	5108.55	5025.64	5853.30	5375.94	5295.63	4272.11	4465.14	4964.39	5065.49	0.10	0.04
GYPSY6	2386.31	2313.74	2671.50	6297.80	6420.79	5614.80	5271.13	5938.86	6218.98	-1.31	0.07
GYPSY6A	478.41	399.51	410.42	673.21	699.11	647.49	568.68	580.60	641.13	-0.65	0.17
GYPSY7	2.92	2.37	3.89	289.66	284.81	233.24	172.83	210.41	199.22	-6.46	0.47
GYPSY8	3.20	6.41	9.96	2657.90	2593.06	2184.23	2538.29	2745.60	2487.80	-8.57	-0.06
GYPSY9	2.12	2.30	1.94	90.49	84.16	81.82	62.42	73.21	61.25	-5.33	0.38
HELENA_RT	455.76	471.61	596.92	1004.09	994.47	812.86	859.66	975.07	981.45	-0.88	0.00
HETA	54.92	35.85	49.94	3517.96	3549.56	3321.96	3397.22	3945.14	4131.49	-6.21	-0.14
HETRP	1971.89	1068.90	1521.16	7854.82	6937.17	7416.17	5581.17	6802.48	6974.87	-2.28	0.20
HMR1	1.72	0.71	0.85	70.93	97.10	57.08	59.41	66.97	70.45	-6.10	0.19
HMR2	6.59	4.67	7.29	401.08	380.32	367.82	262.32	316.21	313.56	-5.95	0.37
HMSBEAGLE	7321.57	5900.33	8305.62	20121.71	20580.26	17871.52	17883.80	19306.17	19455.89	-1.44	0.05
HOBO	44.50	48.59	56.74	1404.59	1303.96	1205.09	995.53	1239.36	1103.53	-4.71	0.23
I	146.24	144.59	167.30	4930.66	4999.81	4520.20	3749.70	4883.85	4960.55	-4.98	0.09
IDEFIX	4508.86	4477.03	5184.58	10125.4	10200.0	8491.13	8135.23	8905.86	9448.46	-1.02	0.12

				8	6						
INVADE R1	419.01	361.76	473.84	9046.34	8512.79	7650.44	6566.08	6897.28	6802.41	-4.33	0.31
INVADE R2	371.08	325.04	410.06	3019.14	2763.57	2373.17	2406.90	2712.81	2674.26	-2.88	0.07
INVADE R3	2830.53	2337.96	3028.59	9993.99	9926.60	8801.22	7759.30	8282.76	8389.45	-1.81	0.23
INVADE R4	345.48	340.87	472.39	6406.11	6362.31	6432.51	4439.20	4309.69	5111.69	-4.05	0.47
INVADE R5	0.52	0.40	0.61	14.56	13.27	12.40	8.09	8.02	6.48	-4.72	0.83
INVADE R6	30.76	39.10	61.11	16720.33	15784.21	13517.15	10015.96	11922.69	10563.06	-8.46	0.50
IVK	57.60	57.70	67.55	4992.03	5063.06	4515.68	2893.24	3714.03	3460.89	-6.32	0.53
Jockey	16.34	18.76	27.22	4411.27	4030.89	3693.00	2679.64	3425.07	3235.75	-7.61	0.38
JOCKEY 2	177.03	146.02	174.71	853.32	860.13	778.44	758.21	810.92	662.45	-2.32	0.16
LOOPE R1	2.36	3.32	3.40	527.07	464.81	409.92	370.92	433.79	440.03	-7.27	0.17
M4DM	38.91	33.16	45.68	962.43	863.78	818.09	910.12	937.32	1056.70	-4.49	-0.14
MARINE R2	2.96	4.67	3.28	19.34	22.97	18.98	14.30	13.47	14.84	-2.49	0.52
MAX	1751.39	1109.26	1750.67	43506.08	45799.58	40982.73	38265.86	41030.15	41618.44	-4.82	0.11
MDG1	15151.28	12940.07	15414.33	21301.13	21617.47	18385.73	16129.65	17199.33	18208.12	-0.49	0.25
MDG3	5039.96	4053.14	5682.84	9671.80	9518.28	8794.83	7407.70	8382.42	8759.25	-0.92	0.19
MICROP IA	624.33	482.53	731.18	14938.13	14464.99	13482.73	11193.21	11883.66	12018.62	-4.54	0.29
NOMAD	3139.26	2199.85	3301.47	26674.68	26253.28	29547.59	19543.65	21642.25	21458.71	-3.25	0.40
NTS	536.89	366.51	479.31	1512.90	1374.45	1283.22	914.33	1211.63	1108.96	-1.59	0.37
POGO	961.10	833.21	1097.74	2971.40	2726.20	2683.19	1727.01	1999.37	1982.34	-1.53	0.55

PROTO P	6236.25	5665.12	7055.53	17403.10	16348.25	14705.96	12135.82	13405.25	13889.12	-1.35	0.30
QUASIMODO	4227.26	3896.28	4725.68	23350.82	23455.27	20833.54	19570.92	20319.18	21190.93	-2.40	0.15
QUASIMODO2	16.26	16.15	21.38	2825.99	2929.97	2281.60	1422.13	1661.86	1713.09	-7.22	0.74
R1	8186.49	6918.82	9161.21	54531.32	51981.76	45332.07	41702.98	45419.19	44355.21	-2.65	0.21
R1-2	1.48	2.22	2.43	62.52	57.28	46.56	38.03	41.11	40.14	-4.76	0.48
R2	9.11	8.39	14.58	2254.72	2458.92	1988.57	2197.11	2378.38	2760.60	-7.71	-0.13
ROO	17636.25	14031.30	18442.23	141223.53	129425.50	122688.80	111510.70	125981.58	122654.53	-2.97	0.13
ROOA	334.57	333.82	429.98	24236.95	22048.76	19963.60	15413.54	18011.24	16955.75	-5.91	0.40
ROVER	4745.05	4143.28	4992.73	6912.18	7067.79	5951.88	5535.59	6223.27	6358.20	-0.52	0.14
RSP	49.37	37.75	54.43	110.41	108.12	98.15	77.66	75.68	85.08	-1.16	0.41
RT1A	46.97	57.46	106.07	31591.07	30196.04	26375.38	24765.53	27862.75	26366.16	-8.71	0.16
RT1B	91.59	111.59	184.56	60093.75	59794.58	53196.06	48522.69	53519.28	53176.96	-8.80	0.16
RT1C	6.59	9.18	10.69	1937.03	1844.04	1452.34	1585.33	1756.07	1746.75	-7.63	0.04
S	94.19	58.09	105.22	1857.91	1743.15	1593.05	1411.83	1635.51	1547.53	-4.33	0.18
S2	3.00	3.72	1.58	19.85	22.23	19.95	16.24	18.72	19.44	-2.90	0.19
SAR	261.71	311.03	291.84	308.06	324.30	312.73	193.21	234.08	221.79	-0.13	0.54
SAR2	706.41	531.68	475.42	618.51	693.27	761.98	282.83	380.40	363.73	-0.28	1.01
SAT6	0.20	0.63	0.36	3.98	4.12	4.13	4.68	4.06	5.23	-3.35	-0.19
STALKE R2	3925.80	3929.52	4556.79	4511.98	4453.29	3654.13	3583.42	4215.48	4042.02	-0.02	0.09
STALKE R3	274.66	291.09	410.30	823.32	898.22	816.54	667.92	708.69	702.59	-1.38	0.29
STALKE R4	12560.46	11007.17	13343.92	62822.65	64891.36	59666.27	54340.18	58701.01	57636.85	-2.34	0.13

TABOR	7789.00	7702.01	9076.89	7628.49	7946.63	6300.39	6381.02	6927.60	7032.57	0.17	0.10
TAHRE	64.23	65.37	72.17	3001.10	3226.12	3092.27	3628.93	4367.24	4272.18	-5.53	-0.40
TART	10194.00	8593.48	11014.43	74114.07	73439.46	63644.50	61262.07	75796.72	74531.36	-2.83	0.00
TC1	6.59	8.63	8.26	25.29	26.08	21.18	20.12	24.07	21.53	-1.63	0.14
TC1-2	10.86	12.19	13.36	1686.42	1733.00	1384.21	1430.21	1391.52	1354.38	-7.04	0.20
TIRANT	62.11	55.08	64.39	74.84	78.52	68.84	64.09	74.10	86.54	-0.29	-0.02
TLD1	0.12	0.16	0.00	12.10	8.76	7.43	3.81	4.85	3.14	-6.67	1.26
TLD2	198.44	248.90	336.31	414.78	373.35	259.33	371.86	446.17	422.89	-0.42	-0.24
TOM1	1.60	3.09	1.94	19.63	21.04	16.79	16.11	15.75	19.86	-3.12	0.15
Transib1	4.99	4.27	4.62	250.60	249.96	216.65	269.33	271.73	259.84	-5.69	-0.16
TRANSIB2	413.58	275.97	410.30	8030.66	7729.00	6664.84	5023.39	6065.86	5696.79	-4.35	0.42
TRANSIB3	3.32	2.77	6.20	115.05	106.66	92.99	75.85	94.21	98.25	-4.68	0.23
Transib4	6.07	4.75	6.68	19.92	16.33	15.63	13.30	15.95	16.51	-1.57	0.18
Transib5	30.92	28.33	35.96	1114.14	1128.47	1003.61	676.41	702.35	772.83	-5.09	0.59
TRANS PAC	18.81	22.63	27.22	1542.39	1381.82	1114.42	1124.32	1342.78	1302.54	-5.88	0.10
XDMR	14.14	14.64	15.67	36.59	31.93	35.71	19.38	27.54	23.62	-1.23	0.56
ZAM	2495.00	2407.44	2769.19	2558.72	2630.49	2085.81	2029.23	2426.32	2394.57	0.08	0.09
G7	0.00	0.16	0.00	5.29	4.18	3.49	3.74	3.96	5.23	-6.36	0.00

Table A2.5 piRNA ping-pong biogenesis signature for TE-derived piRNAs.

aub_pingpong	mutant1_pingpong	mutant2_pingpong	mel1_pingpong	mel2_pingpong	sim1_pingpong	sim2_pingpong
TE						
1731	0.019555	0.040135	0.114668	0.136492	0.100658	0.117645
176	0.025694	0.042434	0.10276	0.097913	0.066172	0.08638
297	0.063903	0.046386	0.400804	0.372083	0.328894	0.314767
412	0.016387	0.022717	0.077832	0.09393	0.067459	0.085119
5S	0.0112	0.003429	0	0	0	0
ACCORD	0.057044	0.062276	0.192582	0.227682	0.105843	0.172574
ACCORD2	0.019827	0.04001	0.103227	0.109687	0.05775	0.066971
ARS406	0.04696	0.072165	0.1545	0.175758	0.069271	0.071703
BAGGINS1	0.046686	0.081796	0.084774	0.17495	0.150619	0.121999
BARI	0.020426	0.041822	0.094986	0.094159	0.093183	0.109661
BATUMI	0.032981	0.039987	0.204494	0.203514	0.126032	0.187991
BEL	0.008042	0.018934	0.133464	0.126601	0.082885	0.119282
Bica	0.017824	0.027345	0.169398	0.16075	0.061723	0.064528
BLASTOPIA	0.020767	0.034088	0.124903	0.153587	0.084945	0.073623
BLOOD	0.026627	0.032432	0.134731	0.134148	0.116455	0.104102
BS	0.021276	0.035289	0.113705	0.125799	0.069392	0.085249
BS2	0.034704	0.038642	0.198303	0.202883	0.139215	0.168579
BS3	0.010082	0.021164	0.032373	0.055316	0.031876	0.048128
BURDOCK	0.010321	0.032232	0.135772	0.127995	0.116502	0.108587
Chimpo	0.031598	0.038741	0.211371	0.21304	0.088382	0.140408
Chouto	0.016035	0.024778	0.048263	0.067712	0.043623	0.055154
CIRCE	0.034919	0.039766	0.119786	0.176314	0.081532	0.114641
COPIA	0.026004	0.040367	0.12188	0.134255	0.086524	0.108702
Copia1	0.005294	0.023707	0.109903	0.121626	0.052683	0.078887
COPIA2	0.095865	0.042204	0.10866	0.101993	0.077551	0.100785
CR1A	0.046088	0.047859	0.137058	0.145242	0.104386	0.11489

DIVER	0.017518	0.027287	0.099355	0.117918	0.068355	0.094245
DIVER2	0.026982	0.033229	0.125251	0.138748	0.083136	0.112992
DNAREP1	0.023468	0.025807	0.05105	0.063636	0.049794	0.054322
DOC	0.058983	0.066245	0.228105	0.214105	0.188576	0.212562
DOC2	0.030009	0.043095	0.060986	0.07696	0.054572	0.071371
DOC3	0.036887	0.037476	0.146865	0.156469	0.124614	0.141193
DOC4	0.083855	0.050998	0.021028	0.026445	0.030488	0.028374
DOC5	0.011431	0.022174	0.049283	0.053792	0.027165	0.047463
DOC6	0.002587	0.038882	0.044704	0.049889	0.02585	0.03829
FB4	0.020881	0.024232	0.02437	0.056174	0.038852	0.060706
FROGGER	0	0.07787	0	0.010135	0	0.03076
FW	0.065619	0.068167	0.185135	0.234059	0.142942	0.201132
FW2	0.031913	0.025935	0.230276	0.396625	0.008067	0.187017
FW3	0.00214	0.006856	0.004536	0.006485	0.0033	0.00913
G	0.025321	0.041545	0.131591	0.15252	0.115698	0.122482
G2	0.031475	0.038784	0.124689	0.145372	0.093549	0.122145
G3	0.0051	0.01847	0.017331	0.039632	0.009379	0.019961
G4	0.023677	0.024811	0.027449	0.043239	0.036067	0.04683
G5	0.018153	0.026164	0.024314	0.043957	0.02455	0.040722
G5A	0.027918	0.02551	0.01701	0.035864	0.022645	0.021738
G6	0.015367	0.020978	0.120523	0.107849	0.057845	0.081645
G7	0.043864	0.003994	0.007618	0.02963	0.001961	0.04245
GTWIN	0.003614	0.034251	0.017261	0.045199	0.021899	0.034106
GYPSY	0.012314	0.025496	0.127535	0.079038	0.043791	0.06154
Gypsy1	0.021258	0.03495	0.099757	0.095603	0.079686	0.08928
GYPSY10	0.01119	0.019899	0.011753	0.033456	0.024859	0.01459
GYPSY11	0.00332	0.013753	0.001789	0.007611	0.020279	0.005696
GYPSY12	0.029233	0.049065	0.073375	0.089585	0.048333	0.073195
Gypsy2	0.031354	0.034945	0.093072	0.085765	0.076851	0.074658

GYPSY2	0.062561	0.073187	0.062578	0.063547	0.045497	0.070698
GYPSY3	0.022011	0.038265	0.089614	0.092678	0.071711	0.080851
GYPSY4	0.059832	0.037041	0.16349	0.170746	0.104512	0.122468
GYPSY5	0	0.011272	0.003397	0.080411	0.009801	0.02979
GYPSY6	0.103765	0.031787	0.074824	0.081944	0.068294	0.070834
GYPSY6A	0.024396	0.035032	0.0122	0.029376	0.016223	0.027032
GYPSY7	0.011441	0.021099	0.021357	0.029949	0.015127	0.040122
GYPSY8	0.018921	0.021509	0.074085	0.086033	0.054385	0.077149
GYPSY9	0.002746	0.034785	0.013116	0.03773	0.009866	0.020266
HETA	0.029979	0.036893	0.178271	0.221702	0.127767	0.172265
HETRP	0.092876	0.157766	0.702099	0.754216	0.570183	0.628209
HMR1	0	0.001016	0.011123	0.011072	0.009473	0.008518
HMR2	0.048363	0.041291	0.290875	0.207664	0.308542	0.253553
HMSBEAGLE	0.032537	0.032141	0.137724	0.138981	0.100269	0.120904
HOBO	0.010886	0.017978	0.038339	0.045355	0.046483	0.048447
I	0.026665	0.039034	0.297569	0.207598	0.20954	0.163067
IDEFIX	0.021566	0.036827	0.049002	0.054292	0.038956	0.045173
INVADER1	0.021077	0.033711	0.087073	0.113491	0.075344	0.096326
INVADER2	0.030963	0.047975	0.294054	0.313153	0.232042	0.239481
INVADER3	0.017104	0.031792	0.077836	0.083072	0.052698	0.071331
INVADER4	0.044392	0.054014	0.083275	0.125776	0.064223	0.111024
INVADER5	0	0.021486	0.015622	0.008781	0.025053	0.009295
INVADER6	0.017438	0.02177	0.053256	0.043331	0.046005	0.051272
IVK	0.028344	0.044504	0.163182	0.180512	0.07059	0.116744
Jockey	0.020252	0.043154	0.342197	0.263828	0.298542	0.244364
JOCKEY2	0.02373	0.021388	0.060029	0.04254	0.034591	0.042793
LOOPER1	0.016191	0.030956	0.02503	0.034273	0.021777	0.027426
M4DM	0.122738	0.030831	0.047229	0.086595	0.065318	0.071193
MARINER2	0	0.036328	0.018406	0.031305	0.026251	0.017703

MAX	0.053393	0.038526	0.167899	0.174668	0.130159	0.150047
MDG1	0.034772	0.050936	0.088225	0.065712	0.040836	0.070516
MDG3	0.014942	0.021333	0.230203	0.223427	0.088252	0.16301
MICROPIA	0.03515	0.034716	0.204005	0.170683	0.083805	0.093021
NOMAD	0.065741	0.061564	0.267458	0.252183	0.168893	0.193863
NTS	0.034591	0.025172	0.210701	0.095836	0.124313	0.070514
POGO	0.008376	0.023644	0.036209	0.10052	0.019255	0.093869
PROTOP	0.035986	0.056723	0.246789	0.328535	0.149631	0.26817
QUASIMODO	0.012854	0.02358	0.052557	0.059589	0.034676	0.060541
QUASIMODO2	0.012191	0.025613	0.063425	0.096171	0.064997	0.079006
R1	0.033014	0.043919	0.229151	0.285937	0.168356	0.221788
R1-2	0.039391	0.059754	0.048829	0.076955	0.079783	0.067101
R2	0.043681	0.02304	0.013563	0.032388	0.033178	0.037692
ROO	0.051568	0.032766	0.308776	0.287121	0.269335	0.251731
ROOA	0.024	0.040355	0.106259	0.142902	0.084928	0.09498
ROVER	0.023541	0.032144	0.087138	0.086754	0.051824	0.075106
RSP	0.008373	0.012431	0.055558	0.170972	0.02665	0.101946
RT1A	0.030349	0.038016	0.197943	0.237144	0.144548	0.215468
RT1B	0.037958	0.037791	0.260042	0.256875	0.162524	0.211426
RT1C	0.024533	0.028974	0.050091	0.03585	0.031674	0.040824
S	0.019879	0.032878	0.076901	0.079576	0.05922	0.058681
S2	0.015859	0.024165	0.027444	0.024102	0.017587	0.021649
SAR	0.020114	0.022916	0.06552	0.082563	0.049318	0.063133
SAR2	0.038448	0.035439	0.02465	0.028468	0.017445	0.022594
SAT6	0.009818	0.015982	0	0.015258	0.051887	0.029063
STALKER2	0.048767	0.024941	0.025622	0.030105	0.023365	0.033032
STALKER3	0.011377	0.015488	0.080833	0.117344	0.015023	0.064894
STALKER4	0.061328	0.038869	0.057907	0.05984	0.046309	0.056045
TABOR	0.005203	0.042859	0.016956	0.019615	0.016739	0.018862

TAHRE	0.017773	0.026534	0.115608	0.142706	0.064336	0.087891
TART	0.02387	0.038034	0.098961	0.135006	0.081555	0.126466
TC1	0.01185	0.018452	0.042157	0.018242	0.020407	0.023607
TC1-2	0.034535	0.039187	0.097323	0.111865	0.073931	0.118384
TIRANT	0.014235	0.013839	0.025604	0.04102	0.032983	0.039764
TLD2	0	0	0	0.029849	0	0.019042
TOM1	0.026897	0.163844	0.584933	0.643899	0.472475	0.654638
Transib1	0.044598	0.029363	0.02547	0.022402	0.016755	0.023253
TRANSIB2	0.030125	0.036137	0.115029	0.134353	0.059633	0.095352
TRANSIB3	0	0.026614	0.011173	0.022531	0	0.013894
Transib4	0	0.016239	0	0.004091	0.047015	0.03354
Transib5	0.009191	0.028513	0.034851	0.017474	0.026977	0.0177
TRANSPAC	0.007722	0.034787	0.08898	0.119674	0.057169	0.07155
XDMR	0.008695	0.009892	0.019295	0.0066	0.06127	0.012364
ZAM	0.007437	0.030589	0.019029	0.031996	0.05073	0.028746

spn-E_pingpong									
TE	mutant1_pingpong	mutant2_pingpong	mutant3_pingpong	mel1_pingpong	mel2_pingpong	mel3_pingpong	sim1_pingpong	sim2_pingpong	sim3_pingpong
1731	0.043287	0.057	0.037267	0.296462	0.290101	0.306482	0.275581	0.271968	0.295168
176	0.019911	0.034841	0.026712	0.254871	0.248052	0.25193	0.19666	0.161112	0.215442
297	0.036162	0.029161	0.038147	0.169544	0.163657	0.179338	0.179895	0.173715	0.178539
412	0.029533	0.021788	0.02841	0.073316	0.074011	0.073617	0.078777	0.0819	0.075084
5S	0.003069	0	0.006191	0	0	0	0	0	0
ACCORD	0.027243	0.030334	0.026779	0.23964	0.228692	0.251332	0.217144	0.189347	0.200907
ACCORD 2	0.018146	0.035482	0.033468	0.162907	0.153539	0.164904	0.144782	0.138612	0.158604
ARS406	0.109205	0.137131	0.083732	0.297015	0.270708	0.295183	0.384226	0.379364	0.363714
BAGGINS 1	0.06456	0.051645	0.066638	0.179717	0.174523	0.172514	0.185152	0.174563	0.191287

BARI	0.014654	0.056344	0.012669	0.182346	0.19412	0.179375	0.148542	0.15888	0.149658
BATUMI	0.04922	0.041972	0.03853	0.247639	0.283246	0.300499	0.28239	0.301741	0.309847
BEL	0.019373	0.010248	0.011154	0.206161	0.202772	0.240641	0.255953	0.250667	0.244987
Bica	0.025234	0.02841	0.027488	0.129949	0.158886	0.178456	0.156157	0.166893	0.161806
BLASTOP IA	0.030144	0.030152	0.030238	0.137066	0.128379	0.137337	0.143358	0.153437	0.144327
BLOOD	0.031426	0.034445	0.033882	0.155533	0.158294	0.170208	0.174633	0.177794	0.158556
BS	0.030746	0.037326	0.023884	0.246894	0.242008	0.242705	0.261196	0.258599	0.235193
BS2	0.035857	0.043495	0.031562	0.237174	0.229243	0.248867	0.243135	0.235593	0.241706
BS3	0.014528	0.040651	0.021869	0.117597	0.118296	0.118199	0.109755	0.125617	0.092747
BURDOC K	0.023813	0.02103	0.006079	0.131375	0.139472	0.133955	0.162177	0.162139	0.171624
Chimpo	0.020434	0.029134	0.026893	0.268555	0.278873	0.289696	0.245367	0.261981	0.290963
Chouto	0.030678	0.004713	0.010422	0.185505	0.179984	0.175952	0.205125	0.183064	0.186462
CIRCE	0.066333	0.067204	0.053936	0.23969	0.239154	0.241193	0.238229	0.241608	0.24146
COPIA	0.040842	0.022108	0.023806	0.171949	0.179569	0.178916	0.190665	0.180816	0.167172
Copia1	0.030846	0.013597	0.026771	0.130715	0.14314	0.143307	0.135446	0.13107	0.114098
COPIA2	0.059568	0.020352	0.04318	0.147375	0.157317	0.158929	0.173523	0.157826	0.163531
CR1A	0.033417	0.03772	0.036288	0.227349	0.227674	0.231851	0.227947	0.225813	0.22553
DIVER	0.01374	0.018376	0.011287	0.121646	0.104222	0.126382	0.12221	0.123428	0.128229
DIVER2	0.031198	0.024069	0.022693	0.155257	0.148784	0.148122	0.176925	0.16705	0.181241
DNAREP 1	0.017567	0.0301	0.019332	0.119881	0.107561	0.124884	0.100521	0.105785	0.094393
DOC	0.049052	0.053262	0.057437	0.381254	0.38684	0.382642	0.364162	0.376636	0.365591
DOC2	0.027807	0.026106	0.062639	0.120831	0.141484	0.152254	0.201683	0.17711	0.210295
DOC3	0.030918	0.038125	0.020981	0.224979	0.20973	0.213327	0.238198	0.230121	0.242889
DOC4	0.019825	0	0.012195	0.071717	0.109402	0.098762	0.066939	0.103883	0.079633
DOC5	0.014881	0.002841	0.032244	0.068756	0.087109	0.079965	0.061406	0.063959	0.057945
DOC6	0.031034	0.036894	0.01277	0.141401	0.110006	0.123645	0.156423	0.186477	0.129162
FB4	0.017644	0.009305	0.028241	0.045154	0.03195	0.110278	0.047026	0.071465	0.027549

FROGGE R	0	0.045977	0	0.00381	0.00787	0.011348	0	0	0
FW	0.051582	0.051226	0.051393	0.294233	0.314922	0.301666	0.314046	0.307261	0.309796
FW2	0	0	0	0.209035	0.232098	0.390306	0.204051	0.134382	0.223795
FW3	0.009456	0.010274	0.006494	0.012804	0.012457	0.020263	0.014263	0.017844	0.011776
G	0.050032	0.036041	0.033332	0.258668	0.285843	0.276485	0.226302	0.225663	0.221884
G2	0.043819	0.052693	0.049057	0.36023	0.389737	0.369576	0.281975	0.293652	0.286157
G3	0	0.003342	0	0.02448	0.017293	0.012121	0.024683	0.054433	0.017985
G4	0.009705	0.011604	0.024972	0.217031	0.144944	0.167148	0.151274	0.133097	0.17101
G5	0.010824	0.003963	0.006808	0.122	0.152492	0.146762	0.130229	0.121981	0.119013
G5A	0.00455	0.080247	0.017767	0.064749	0.051908	0.051206	0.038797	0.037308	0.044729
G6	0.031521	0.026063	0.033762	0.096602	0.118007	0.105811	0.106382	0.091474	0.111564
G7	0	0	0.130435	0.236248	0.132788	0.197285	0.106745	0.10529	0.091367
GTWIN	0.01024	0.007	0.005443	0.056928	0.048508	0.04472	0.038073	0.049415	0.056602
GYPSY	0.022366	0.023264	0.026222	0.091755	0.102427	0.091821	0.112594	0.098613	0.101811
Gypsy1	0.045548	0.03956	0.031972	0.165413	0.180808	0.152598	0.171896	0.17409	0.178257
GYPSY10	0.01233	0.009334	0.022761	0.048918	0.043652	0.042072	0.040749	0.048917	0.053539
GYPSY11	0	0	0	0.01319	0.004835	0.001423	0.004811	0.000857	0.002338
GYPSY12	0.032255	0.029522	0.022154	0.186888	0.141818	0.181563	0.152909	0.154467	0.153253
Gypsy2	0.027311	0.029601	0.027583	0.128357	0.126617	0.142215	0.111373	0.116663	0.111769
GYPSY2	0.036135	0.01905	0.047005	0.096741	0.101779	0.101607	0.125125	0.127377	0.123629
GYPSY3	0.025084	0.023159	0.02105	0.158868	0.161678	0.169337	0.155919	0.156856	0.159292
GYPSY4	0.032528	0.026727	0.042835	0.217183	0.228732	0.224349	0.223214	0.225224	0.209167
GYPSY5	0.001289	0.001512	0.001798	0.013193	0.01422	0.013153	0.009831	0.027207	0.017228
GYPSY6	0.034015	0.030243	0.033649	0.14173	0.141926	0.153103	0.174952	0.168959	0.173677
GYPSY6A	0.041726	0.051554	0.009032	0.056098	0.042317	0.05211	0.077855	0.071644	0.077437
GYPSY7	0.020956	0	0.004994	0.07835	0.054774	0.052126	0.06725	0.058756	0.074065
GYPSY8	0.022889	0.031909	0.023572	0.197373	0.183397	0.195643	0.218262	0.207995	0.220146
GYPSY9	0	0.007207	0	0.124008	0.112041	0.112803	0.071099	0.10144	0.075517

HETA	0.047867	0.055981	0.047136	0.277571	0.275188	0.298594	0.288075	0.282021	0.287132
HETRP	0.351633	0.242315	0.675522	0.823995	0.814091	0.82371	0.864973	0.858451	0.827953
HMR1	0	0.004403	0.007718	0.073004	0.048297	0.051965	0.048346	0.07071	0.057935
HMR2	0.015819	0.028267	0.023347	0.183423	0.167851	0.194624	0.248564	0.226275	0.250636
HMSBEA GLE	0.0245	0.043383	0.029098	0.170216	0.169062	0.182592	0.138503	0.131193	0.13779
HOBO	0.014283	0.004546	0.020593	0.105591	0.072634	0.080596	0.090191	0.07697	0.063366
I	0.021397	0.031355	0.034056	0.215242	0.236744	0.230754	0.238354	0.231046	0.238768
IDEFIX	0.043443	0.015837	0.045154	0.129859	0.130949	0.132255	0.113789	0.102476	0.107862
INVADER 1	0.066652	0.086521	0.043049	0.164243	0.165757	0.178064	0.190855	0.180339	0.173803
INVADER 2	0.035969	0.024442	0.013076	0.372958	0.386823	0.386565	0.366918	0.397309	0.36697
INVADER 3	0.005749	0.025737	0.022054	0.187457	0.18547	0.193351	0.172257	0.177557	0.16556
INVADER 4	0.041898	0.033721	0.029186	0.155044	0.165449	0.177598	0.151729	0.148593	0.152084
INVADER 5	0	0	0.130435	0.008134	0.018556	0.005237	0.0061	0.009211	0.005634
INVADER 6	0.021504	0.047071	0.021093	0.223858	0.185259	0.213044	0.21453	0.189985	0.209046
IVK	0.024207	0.027738	0.015334	0.275219	0.300469	0.306225	0.248877	0.263186	0.247297
Jockey	0.023096	0.010839	0.017675	0.310684	0.315989	0.32734	0.365517	0.369514	0.354029
JOCKEY2	0.021933	0.010514	0.015614	0.275753	0.335987	0.301296	0.183936	0.187556	0.177105
LOOPER 1	0.074405	0	0	0.08765	0.078964	0.067268	0.072689	0.087197	0.08939
M4DM	0.030088	0.015255	0.01982	0.153794	0.164473	0.17124	0.211191	0.170407	0.173744
MARINER 2	0.045185	0	0	0.008606	0	0.01769	0.015012	0.034703	0.048934
MAX	0.036736	0.039184	0.039355	0.216362	0.238104	0.253691	0.225067	0.25686	0.244703
MDG1	0.014448	0.012897	0.017297	0.10709	0.102255	0.105808	0.110611	0.098915	0.104803
MDG3	0.012807	0.025005	0.012828	0.208197	0.264283	0.269983	0.25419	0.259358	0.248575

MICROPIA	0.016943	0.050556	0.016076	0.207803	0.21206	0.221725	0.23531	0.210531	0.242333
NOMAD	0.047213	0.034646	0.031605	0.312881	0.307006	0.322372	0.327738	0.307643	0.334002
NTS	0.040423	0.034891	0.054377	0.588932	0.704091	0.645451	0.513278	0.476459	0.558848
POGO	0.019387	0.01465	0.022871	0.139197	0.167774	0.186406	0.127109	0.161421	0.151457
PROTOP	0.046315	0.049985	0.037472	0.371359	0.415837	0.407563	0.367603	0.384954	0.346279
QUASIMODO	0.014967	0.028436	0.034068	0.120662	0.124349	0.144201	0.130968	0.171972	0.151158
QUASIMODO2	0.017454	0.011791	0.011384	0.146198	0.145914	0.154896	0.139812	0.141437	0.136911
R1	0.109643	0.097799	0.104619	0.342295	0.350704	0.330101	0.32914	0.335586	0.333574
R1-2	0.090364	0	0.013245	0.040287	0.043909	0.037763	0.048012	0.056771	0.04743
R2	0.037814	0.008499	0.008681	0.110947	0.103463	0.131648	0.123254	0.126194	0.121247
ROO	0.02853	0.015822	0.023846	0.125346	0.123358	0.12599	0.142413	0.121985	0.168345
ROOA	0.030682	0.082199	0.02547	0.210056	0.196567	0.204567	0.221205	0.229768	0.212471
ROVER	0.035577	0.036571	0.041261	0.068574	0.05801	0.07249	0.071841	0.072713	0.076871
RSP	0.0681	0.111329	0.14151	0.068681	0.033358	0.072739	0.033822	0.028327	0.01949
RT1A	0.064278	0.037628	0.032463	0.307101	0.30403	0.303435	0.326174	0.319998	0.345837
RT1B	0.049892	0.049326	0.054268	0.320528	0.319478	0.328765	0.313606	0.313849	0.327181
RT1C	0.008146	0.012567	0.002315	0.035114	0.033371	0.034893	0.027313	0.031457	0.029697
S	0.002701	0.022621	0.005682	0.055787	0.053206	0.088074	0.128673	0.08983	0.126654
S2	0.076518	0.031215	0	0.014101	0.009936	0.074184	0.058445	0.016763	0.017339
SAR	0.055779	0.054457	0.040902	0.191887	0.205483	0.196593	0.210915	0.204066	0.207077
SAR2	0.008201	0.019149	0.037753	0.016017	0.013394	0.013811	0.011046	0.0096	0.007683
SAT6	0	0.047265	0	0.02309	0.02945	0.031079	0.007853	0.010684	0.004251
STALKER2	0.018515	0.020512	0.032321	0.095466	0.079248	0.09223	0.103659	0.099159	0.096324
STALKER3	0.009163	0.002972	0.081391	0.173105	0.151745	0.165571	0.242885	0.232985	0.20903
STALKER4	0.020451	0.050431	0.019843	0.109939	0.097368	0.112631	0.134967	0.130627	0.123032

TABOR	0.004002	0.023929	0.013651	0.039166	0.049269	0.031175	0.029531	0.03546	0.040606
TAHRE	0.047571	0.04724	0.040576	0.182041	0.182265	0.19168	0.180204	0.175609	0.190579
TART	0.051064	0.04447	0.03941	0.21346	0.212162	0.21995	0.217435	0.200272	0.225633
TC1	0	0	0.021164	0.040304	0.021186	0.015722	0.024284	0.05026	0.017698
TC1-2	0.05008	0	0.00401	0.132683	0.144156	0.161612	0.116385	0.122227	0.119662
TIRANT	0.005168	0	0.023542	0.047623	0.045717	0.046771	0.01803	0.016394	0.032789
TLD2	0	0.007514	0	0.050089	0.082771	0.001529	0.080687	0.053443	0.053721
TOM1	0.017105	0.027903	0.003704	0.223456	0.153477	0.251342	0.43584	0.313214	0.383052
Transib1	0.006667	0	0.046429	0.065319	0.055616	0.042891	0.044644	0.058761	0.03859
TRANSIB 2	0.02525	0.026377	0.015221	0.238942	0.263645	0.241246	0.241053	0.252928	0.222974
TRANSIB 3	0	0	0	0.006068	0.008862	0.02139	0.010909	0	0.012306
Transib4	0.030303	0	0	0.027788	0.034995	0.021697	0.041895	0.015811	0.031172
Transib5	0.011278	0	0	0.160019	0.209986	0.143612	0.119948	0.109105	0.093264
TRANSP AC	0.01677	0.006723	0.012245	0.093926	0.0797	0.109267	0.109112	0.118003	0.112972
XDMR	0	0.010802	0	0.014632	0.018914	0.022329	0.004547	0	0.021544
ZAM	0.010369	0.022627	0.01882	0.026362	0.03754	0.027475	0.036327	0.025748	0.027014

armi_pingpong									
TE	mutant1_pingpong	mutant2_pingpong	mutant3_pingpong	mel1_pingpong	mel2_pingpong	mel3_pingpong	sim1_pingpong	sim2_pingpong	sim3_pingpong
1731	0.58943	0.515764	0.52751	0.259213	0.304572	0.264743	0.272115	0.253252	0.278284
176	0.154305	0.105193	0.132268	0.179256	0.208778	0.180152	0.194109	0.184084	0.21079
297	0.093318	0.074573	0.106882	0.215016	0.219694	0.230989	0.208811	0.191697	0.224759
412	0.032591	0.046129	0.024626	0.061251	0.065689	0.067022	0.062077	0.064317	0.056317
5S	0	0.000218	0	0	0.001772	0.005815	0.002259	0.002559	0.001217
ACCORD	0.338921	0.161957	0.23733	0.263145	0.267734	0.330445	0.21713	0.24409	0.281238
ACCORD 2	0.070351	0.027865	0.032667	0.224702	0.267698	0.253743	0.225479	0.216185	0.210768

ARS406	0.34401	0.346792	0.412294	0.349187	0.331374	0.343089	0.254325	0.223419	0.246562
BAGGINS 1	0.301936	0.235581	0.21765	0.223999	0.226213	0.209412	0.216121	0.206956	0.219676
BARI	0.542215	0.523764	0.553327	0.193843	0.202886	0.208236	0.169538	0.115845	0.156387
BATUMI	0.447905	0.51379	0.496545	0.318497	0.305988	0.298365	0.273885	0.266644	0.274497
BEL	0.018966	0.019951	0.017064	0.219932	0.216398	0.215892	0.190939	0.196737	0.212296
Bica	0.061178	0.069924	0.055305	0.146022	0.137988	0.150789	0.128512	0.122891	0.131296
BLASTOP IA	0.542498	0.531255	0.542972	0.197729	0.200358	0.212756	0.163006	0.147952	0.147471
BLOOD	0.038559	0.03435	0.033107	0.231344	0.239232	0.249543	0.186213	0.186469	0.180464
BS	0.053545	0.03784	0.090818	0.348088	0.333331	0.327744	0.275595	0.283487	0.279212
BS2	0.177617	0.143023	0.161369	0.324692	0.332827	0.318849	0.3017	0.290382	0.291022
BS3	0.036285	0	0	0.247469	0.257567	0.257419	0.237312	0.232403	0.22598
BURDOC K	0.043557	0.016524	0.007709	0.265978	0.241539	0.243623	0.216842	0.194015	0.189055
Chimpo	0.026427	0.075126	0.082373	0.304892	0.324391	0.332188	0.297392	0.284141	0.317928
Chouto	0.012137	0.009563	0.011111	0.248838	0.268159	0.246589	0.292981	0.270457	0.299795
CIRCE	0.491609	0.4304	0.56662	0.27346	0.250937	0.251919	0.265838	0.246178	0.276434
COPIA	0.45719	0.378707	0.437108	0.324657	0.316944	0.318492	0.279028	0.265094	0.290296
Copia1	0.180583	0.20844	0.225141	0.139987	0.143573	0.126149	0.129404	0.116533	0.129114
COPIA2	0.475338	0.473303	0.441784	0.126955	0.131633	0.131157	0.094072	0.089517	0.102773
CR1A	0.616921	0.627407	0.626237	0.312289	0.326249	0.328653	0.293153	0.277664	0.313896
DIVER	0.031117	0.026758	0.024499	0.225803	0.223281	0.209808	0.200062	0.21151	0.202763
DIVER2	0.331603	0.231803	0.305237	0.19761	0.213563	0.197297	0.203733	0.19624	0.212894
DNAREP 1	0.032344	0.021885	0.02471	0.236589	0.228855	0.261888	0.170387	0.155592	0.167945
DOC	0.593734	0.594283	0.580005	0.395794	0.393288	0.385885	0.339362	0.34903	0.347566
DOC2	0.179953	0.266153	0.123093	0.138823	0.159579	0.179375	0.109247	0.130675	0.130733
DOC3	0.362715	0.370272	0.355339	0.263073	0.258113	0.252734	0.24597	0.246519	0.247353
DOC4	0.047847	0.029361	0.008488	0.126694	0.114577	0.127686	0.098491	0.085378	0.113228

DOC5	0.036214	0	0	0.148176	0.148723	0.146676	0.135632	0.140461	0.138201
DOC6	0.004389	0.007351	0.0131	0.17144	0.174294	0.190817	0.142397	0.129373	0.154833
FB4	0.27092	0.163434	0.246587	0.245125	0.230024	0.283378	0.263398	0.218662	0.245989
FROGGE R	0	0	0	0.013437	0.022445	0.084923	0.015271	0.034031	0
FW	0.560502	0.514516	0.524724	0.284402	0.29805	0.314396	0.266532	0.253702	0.24572
FW2	0.265731	0.200049	0.183327	0.117963	0.122061	0.162267	0.103315	0.109308	0.108765
FW3	0.000967	0.046166	0.001051	0.011724	0.019585	0.01957	0.02375	0.036099	0.018512
G	0.202982	0.131253	0.16448	0.287208	0.321761	0.307874	0.286812	0.301472	0.299593
G2	0.472359	0.40837	0.465219	0.28289	0.271041	0.26618	0.270539	0.271609	0.277825
G3	0.509811	0.134089	0.305923	0.028038	0.028473	0.025171	0.01803	0.021403	0.015656
G4	0.027808	0.018825	0.007554	0.122374	0.09677	0.139762	0.124204	0.13995	0.085559
G5	0.014616	0.014631	0.014652	0.067489	0.075518	0.106882	0.072209	0.081025	0.074221
G5A	0.010892	0.002352	0	0.056785	0.052352	0.047584	0.04587	0.047673	0.053628
G6	0.014399	0.021731	0.041036	0.356076	0.367544	0.362047	0.36911	0.318314	0.40533
G7	0	0	0	0.0068	0.044466	0.025106	0.007831	0	0.026132
GTWIN	0.007709	0.001757	0.001644	0.031834	0.044504	0.040057	0.035576	0.034488	0.026349
GYPSY	0.020704	0.025321	0.024165	0.207004	0.209434	0.187633	0.202391	0.17513	0.206932
Gypsy1	0.026892	0.022267	0.020079	0.147364	0.155967	0.155368	0.126598	0.119005	0.126111
GYPSY10	0.018992	0.005772	0.006974	0.055492	0.045153	0.052151	0.049303	0.044689	0.035514
GYPSY11	3.36E-05	0.012195	0.037105	0.05603	0.011678	0.006904	0.009828	0.018147	0.012788
GYPSY12	0.170703	0.107807	0.155597	0.179901	0.200545	0.174422	0.16878	0.139535	0.1789
Gypsy2	0.134671	0.103995	0.118402	0.151206	0.137486	0.1387	0.130719	0.123302	0.137446
GYPSY2	0.020826	0.003594	0.035471	0.0823	0.087467	0.089364	0.07517	0.066965	0.07106
GYPSY3	0.01464	0.011326	0.010501	0.17369	0.177516	0.167401	0.140769	0.129095	0.164932
GYPSY4	0.060866	0.041557	0.049401	0.19329	0.192593	0.197844	0.19022	0.193929	0.210985
GYPSY5	0.000338	3.16E-05	9.06E-05	0.014928	0.023809	0.016216	0.012674	0.018527	0.014716
GYPSY6	0.034066	0.031316	0.038226	0.105127	0.110539	0.101266	0.094161	0.099165	0.094687
GYPSY6A	0.073514	0.074532	0.059626	0.127682	0.137982	0.189643	0.10189	0.07712	0.085353

GYPSY7	0.01303	0.022959	0	0.033157	0.056338	0.037602	0.028487	0.033232	0.069594
GYPSY8	0.016576	0.038732	0.057802	0.236516	0.208723	0.227532	0.20421	0.219021	0.244947
GYPSY9	0.011667	0	0	0.048723	0.036033	0.064288	0.095267	0.077623	0.051691
HETA	0.338721	0.205721	0.273514	0.284709	0.28105	0.279536	0.266855	0.266699	0.283497
HETRP	0.593848	0.605297	0.608464	0.516229	0.497421	0.496319	0.447226	0.467539	0.422524
HMR1	0	0.021858	0	0.206419	0.314838	0.257788	0.194532	0.137398	0.156915
HMR2	0.281689	0.232896	0.307278	0.170731	0.169365	0.171064	0.174274	0.166908	0.17878
HMSBEA GLE	0.501719	0.4936	0.515477	0.292033	0.300247	0.304924	0.283842	0.25075	0.291183
HOBO	0.111294	0.117915	0.132096	0.343042	0.314295	0.275281	0.345475	0.374141	0.293981
I	0.040242	0.028389	0.013079	0.24489	0.262856	0.282928	0.227134	0.224799	0.203425
IDEFIX	0.035726	0.026821	0.020087	0.212272	0.214069	0.214246	0.216329	0.19011	0.192346
INVADER 1	0.469892	0.40849	0.509439	0.206095	0.222565	0.198647	0.2179	0.202622	0.21162
INVADER 2	0.624082	0.526344	0.517405	0.296403	0.296846	0.298096	0.246142	0.229525	0.240783
INVADER 3	0.620616	0.605872	0.622933	0.292555	0.309026	0.305755	0.296269	0.268091	0.296136
INVADER 4	0.413292	0.408084	0.425515	0.275774	0.293912	0.279537	0.228844	0.27115	0.261889
INVADER 5	0	0	0	0.003275	0.011468	0.01124	0.018372	0.011538	0
INVADER 6	0.055967	0.065382	0.077865	0.202627	0.208431	0.20463	0.184417	0.180291	0.207163
IVK	0.083868	0.10152	0.127037	0.259575	0.286028	0.26509	0.223674	0.219293	0.221661
Jockey	0.036762	0.030427	0.067754	0.289263	0.31056	0.282396	0.257146	0.259849	0.265336
JOCKEY2	0.155392	0.165087	0.096885	0.162027	0.105143	0.121521	0.080702	0.234056	0.05109
LOOPER 1	0	0.023148	0	0.085995	0.085125	0.070844	0.054932	0.0493	0.059799
M4DM	0.372352	0.263109	0.266913	0.117109	0.118697	0.137942	0.112363	0.093461	0.104881
MARINER 2	0.030172	0	0	0.010872	0.056716	0.016966	0.071647	0.049834	0

MAX	0.283393	0.172959	0.278692	0.279471	0.276133	0.282985	0.251064	0.236581	0.257102
MDG1	0.043636	0.035043	0.031915	0.097519	0.112652	0.123664	0.079336	0.080571	0.08575
MDG3	0.199891	0.161672	0.235405	0.233727	0.237689	0.235726	0.198286	0.188129	0.230565
MICROPIA	0.466819	0.429329	0.444744	0.165811	0.176579	0.157196	0.171086	0.152496	0.188698
NOMAD	0.585886	0.57658	0.604798	0.352305	0.370151	0.372151	0.324273	0.314758	0.311577
NTS	0.435491	0.283889	0.474483	0.33312	0.365961	0.403092	0.308206	0.255987	0.310388
POGO	0.649046	0.623941	0.654256	0.195219	0.156612	0.140422	0.134084	0.118991	0.115977
PROTOP	0.580777	0.553295	0.559869	0.340054	0.358503	0.362683	0.281127	0.278981	0.283211
QUASIMODO	0.104564	0.085004	0.09072	0.261197	0.231827	0.255011	0.205847	0.196113	0.207566
QUASIMODO2	0.032368	0.026011	0.054635	0.289916	0.201219	0.283573	0.124228	0.133655	0.135893
R1	0.627352	0.609651	0.615201	0.309384	0.311442	0.305674	0.282238	0.274907	0.268898
R1-2	0.571979	0.659712	0.652206	0.422262	0.490035	0.448233	0.377172	0.486876	0.353173
R2	0.038363	0.012459	0.003181	0.16492	0.153672	0.165889	0.14308	0.149326	0.142221
ROO	0.316926	0.260837	0.287106	0.263082	0.2632	0.281456	0.23714	0.219226	0.242562
ROOA	0.042216	0.016606	0.02458	0.186735	0.193266	0.199997	0.162479	0.143297	0.148574
ROVER	0.041637	0.03594	0.036532	0.081495	0.081356	0.085137	0.072685	0.082088	0.073294
RSP	0.539079	0.549824	0.501629	0.313217	0.35297	0.345954	0.344843	0.27844	0.220622
RT1A	0.117146	0.085609	0.083858	0.290207	0.289073	0.276462	0.284993	0.298957	0.285694
RT1B	0.151446	0.128181	0.170953	0.325312	0.360276	0.363365	0.334307	0.297639	0.319085
RT1C	0.015732	0.002949	0.010482	0.090646	0.101543	0.090718	0.103587	0.08261	0.101967
S	0.347649	0.329416	0.271149	0.106063	0.115246	0.106868	0.084673	0.094662	0.081058
S2	0.035935	0	0	0.022151	0.027922	0.030451	0.025239	0.001357	0.00751
SAR	0.211222	0.255919	0.25369	0.182636	0.190933	0.177205	0.174284	0.160033	0.193541
SAR2	0.048967	0.035685	0.033799	0.062453	0.053076	0.068092	0.023819	0.032439	0.024004
SAT6	0.029356	0.044057	0	0.029649	0.019012	0.028145	0.030662	0.024602	0.031877
STALKER2	0.201568	0.194729	0.192267	0.201033	0.208335	0.194402	0.146137	0.142651	0.138069

STALKER 3	0.024074	0.027485	0.019579	0.102419	0.131388	0.135627	0.113807	0.130255	0.1169
STALKER 4	0.205644	0.183182	0.209512	0.181512	0.185026	0.167633	0.14547	0.134096	0.146237
TABOR	0.01211	0.0071	0.026084	0.040569	0.019078	0.029055	0.022239	0.016822	0.014028
TAHRE	0.283734	0.150068	0.207976	0.256137	0.270356	0.271851	0.267212	0.26151	0.295543
TART	0.461205	0.440885	0.495817	0.289942	0.314054	0.282277	0.289998	0.259514	0.279008
TC1	0.012234	0.026173	0.015504	0.008879	0.044954	0.048959	0.029916	0.009251	0.007962
TC1-2	0.013155	0.018265	0.010859	0.250546	0.153979	0.176031	0.12379	0.223302	0.13366
TIRANT	0.001801	0	0.001241	0.027403	0.006777	0.015546	0.0406	0.030827	0.038018
TLD1	0	0	0	0.003596	0.001775	0.017791	0.002769	0.034341	0.065215
TLD2	0.008922	0.001725	0.004746	0.033183	0.027714	0.027347	0.019311	0.013712	0.010287
TOM1	0.070909	0	0	0.112078	0.090497	0.190996	0.037905	0.046951	0.116684
Transib- N1	0	0	0	0	0.392481	0	0	0	0
Transib1	0.010363	0.03592	0	0.016295	0.018016	0.030708	0.016758	0.036138	0.011194
TRANSIB 2	0.591057	0.571524	0.488916	0.367446	0.408878	0.377982	0.325468	0.266979	0.307673
TRANSIB 3	0	0	0	0.097437	0.087643	0.10104	0.060896	0.064781	0.057474
Transib4	0	0.042254	0	0.01879	0.01553	0.019938	0.020437	0.00418	0
Transib5	0.036866	0.084667	0.019406	0.236297	0.269158	0.283508	0.284371	0.283666	0.256094
TRANSP AC	0.020979	0.011227	0.022562	0.203484	0.224665	0.186654	0.161612	0.134512	0.145765
XDMR	0.000804	0.002701	0	0.033101	0.027405	0.01591	0.041807	0.022498	0.027727
ZAM	0.015814	0.008712	0.000117	0.011608	0.01685	0.019355	0.017851	0.018191	0.010663

Table A2.6 piRNA phasing biogenesis signature (d1 proportion) for TE-derived piRNAs.

aub_d1	TE	d1_mut1	d1_mut2	d1_mel1	d1_mel2	d1_sim1	d1_sim2
TE	0.028638	0.074548	0.056614	0.061093	0.058105	0.065305	
1731							
176	0.068546	0.064405	0.081513	0.080104	0.080165	0.072873	
297	0.050037	0.057722	0.047505	0.053516	0.050166	0.05367	
412	0.088631	0.068018	0.082725	0.076425	0.084446	0.074925	
5S	0.029757	0.002657	0.028796	0.019193	0.014862	0.018684	
ACCORD	0.04995	0.073051	0.066755	0.066515	0.068326	0.06993	
ACCORD2	0.065789	0.078211	0.075574	0.080602	0.075421	0.076212	
ARS406	0.039488	0.039052	0.041904	0.043983	0.044488	0.043186	
BAGGINS1	0.064482	0.066219	0.067051	0.070295	0.067991	0.069537	
BARI	0.056819	0.056461	0.052555	0.054433	0.048189	0.060982	
BATUMI	0.070158	0.06753	0.071012	0.071133	0.072611	0.073075	
BEL	0.075787	0.076439	0.063973	0.065151	0.063592	0.066946	
Bica	0.022433	0.0602	0.042982	0.058363	0.048989	0.056122	
BLASTOPIA	0.065388	0.078871	0.068067	0.070317	0.067015	0.066901	
BLOOD	0.078632	0.061512	0.061053	0.063018	0.062102	0.060194	
BS	0.095547	0.083313	0.078132	0.071182	0.079061	0.07209	
BS2	0.080358	0.068183	0.064976	0.065283	0.063306	0.062629	
BS3	0.058048	0.073668	0.070765	0.069179	0.066193	0.065391	
BURDOCK	0.10691	0.081767	0.064982	0.062709	0.064753	0.062381	
Chimpo	0.075926	0.076861	0.06105	0.062385	0.061747	0.063655	
Chouto	0.087709	0.096345	0.076405	0.077902	0.071363	0.077791	
CIRCE	0.060026	0.066681	0.067763	0.066629	0.063645	0.064959	
COPIA	0.094594	0.067171	0.069947	0.075607	0.074034	0.073828	
Copia1	0.08185	0.078687	0.062751	0.069094	0.063735	0.068993	
COPIA2	0.062167	0.060338	0.067109	0.068434	0.06216	0.069279	
CR1A	0.054759	0.057937	0.051957	0.055895	0.052798	0.056334	

DIVER	0.083256	0.111237	0.076598	0.072604	0.081931	0.073083
DIVER2	0.083504	0.077476	0.06931	0.070999	0.073027	0.07102
DNAREP1	0.066202	0.066589	0.063571	0.059105	0.070464	0.060021
DOC	0.052829	0.054434	0.06128	0.061531	0.066317	0.064938
DOC2	0.104418	0.091982	0.092312	0.080022	0.09489	0.080042
DOC3	0.06255	0.065796	0.079854	0.07709	0.073351	0.077249
DOC4	0.092683	0.109451	0.073619	0.083361	0.084584	0.091376
DOC5	0.090827	0.078866	0.07615	0.075753	0.069977	0.067213
DOC6	0.128559	0.085709	0.082737	0.071792	0.081411	0.077489
FB4	0.033089	0.040779	0.048246	0.04876	0.058486	0.051352
FROGGER	0.075843	0.044597	0	0.044898	0.109307	0.071429
FW	0.0618	0.060239	0.063853	0.064887	0.064345	0.063524
FW2	0.04971	0.073517	0.048953	0.062462	0.065434	0.054686
FW3	0.049423	0.062863	0.058411	0.06386	0.060055	0.050875
G	0.064013	0.066493	0.057967	0.057422	0.057892	0.058181
G2	0.08401	0.066738	0.07605	0.07389	0.073016	0.071982
G3	0.194716	0.143952	0.082766	0.110673	0.097526	0.10926
G4	0.068912	0.06509	0.060757	0.06424	0.056649	0.062046
G5	0.089579	0.068513	0.072177	0.064796	0.075528	0.059828
G5A	0.082507	0.076481	0.079533	0.069651	0.072054	0.061627
G6	0.109864	0.098358	0.081141	0.082189	0.080542	0.080376
G7	0.015314	0.052588	0.098131	0.049061	0.084567	0.014501
GTWIN	0.117251	0.077686	0.090861	0.074478	0.078493	0.077427
GYPSY	0.094667	0.070067	0.073164	0.071373	0.077468	0.07071
Gypsy1	0.069571	0.079903	0.067217	0.068805	0.065207	0.065139
GYPSY10	0.078583	0.06124	0.071495	0.082179	0.102409	0.077291
GYPSY11	0.048927	0.076278	0.043163	0.083758	0.064213	0.103875
GYPSY12	0.069843	0.070007	0.068749	0.068422	0.07117	0.06932
Gypsy2	0.06842	0.072635	0.061239	0.063233	0.060139	0.063375

GYPSY2	0.081782	0.079313	0.075893	0.07237	0.079321	0.070494
GYPSY3	0.069744	0.07124	0.06353	0.065086	0.062534	0.063519
GYPSY4	0.060259	0.064117	0.056544	0.059185	0.059975	0.060499
GYPSY5	0.038866	0.07172	0.091692	0.153928	0.038224	0.084983
GYPSY6	0.072648	0.076873	0.069473	0.065976	0.069138	0.067996
GYPSY6A	0.072012	0.077219	0.075372	0.073682	0.067875	0.06859
GYPSY7	0.057589	0.07863	0.10237	0.072883	0.062023	0.067111
GYPSY8	0.057402	0.056429	0.05391	0.057246	0.054212	0.05709
GYPSY9	0.045886	0.065951	0.033536	0.053838	0.068751	0.069009
HELENA_RT	0.017283	0.086544	0.065415	0.048985	0.050214	0.058952
HETA	0.10183	0.070308	0.067867	0.063582	0.073223	0.066537
HETRP	0.062878	0.056525	0.088117	0.092285	0.077415	0.069732
HMR1	0	0.050319	0.053851	0.054817	0.058253	0.047326
HMR2	0.046316	0.059112	0.049781	0.053485	0.051848	0.053863
HMSBEAGLE	0.068666	0.07651	0.054395	0.062688	0.057049	0.062702
HOBO	0.065008	0.066554	0.061503	0.063528	0.062936	0.05951
I	0.116427	0.076724	0.104426	0.095873	0.106195	0.093136
IDEFIX	0.070438	0.075271	0.057456	0.071404	0.067247	0.070681
INVADER1	0.066136	0.063742	0.064907	0.064631	0.066576	0.063279
INVADER2	0.065857	0.073363	0.065495	0.06918	0.069382	0.069896
INVADER3	0.085026	0.076274	0.077217	0.076053	0.07662	0.076539
INVADER4	0.073662	0.061764	0.091253	0.083314	0.089119	0.07675
INVADER5	0	0.065748	0.193517	0.200778	0.052941	0.084653
INVADER6	0.041507	0.073763	0.063531	0.060767	0.064497	0.065259
IVK	0.16199	0.093912	0.108841	0.091157	0.096683	0.090478
Jockey	0.058336	0.061495	0.055291	0.05995	0.051961	0.055065
JOCKEY2	0.07706	0.076122	0.072208	0.073938	0.068755	0.087674
LOOPER1	0.106181	0.085631	0.096955	0.088008	0.087843	0.085896
MARINER2	0.078604	0.089501	0.040786	0.103187	0.073269	0.081056

MAX	0.06775	0.05981	0.067051	0.067104	0.064938	0.06425
MDG1	0.069806	0.063977	0.060391	0.066482	0.062515	0.067866
MDG3	0.080268	0.06293	0.096053	0.074289	0.085057	0.073737
MICROPIA	0.093883	0.089418	0.074853	0.074046	0.079264	0.078828
NOMAD	0.057154	0.065729	0.065801	0.067732	0.068739	0.067652
NTS	0.099009	0.076395	0.03539	0.046329	0.036232	0.050847
POGO	0.059889	0.085329	0.080222	0.065069	0.097701	0.073637
PROTOP	0.047503	0.052281	0.045711	0.0479	0.048439	0.04878
QUASIMODO	0.066167	0.064584	0.066196	0.059841	0.063988	0.062329
QUASIMODO2	0.093221	0.069247	0.060332	0.068906	0.065322	0.064461
R1	0.064055	0.063425	0.062814	0.064169	0.062199	0.063838
R1-2	0.03392	0.109595	0.044232	0.064666	0.059111	0.059868
R2	0.047009	0.079937	0.063257	0.069103	0.069451	0.078315
ROO	0.07274	0.063508	0.067315	0.066272	0.068617	0.070014
ROOA	0.075297	0.073646	0.064288	0.069618	0.068028	0.068571
ROVER	0.084122	0.08361	0.073199	0.070078	0.073254	0.072242
RSP	0.191152	0.108078	0.253358	0.158175	0.064593	0.108194
RT1A	0.055278	0.058483	0.050662	0.055715	0.052247	0.053811
RT1B	0.067017	0.065377	0.058237	0.058375	0.058158	0.057379
RT1C	0.090363	0.077061	0.057822	0.065462	0.057854	0.062828
S	0.151167	0.090746	0.128042	0.108177	0.106414	0.10115
S2	0.083922	0.086189	0.031983	0.076839	0.080969	0.077533
SAR	0.065632	0.057143	0.070768	0.068266	0.065999	0.064626
SAR2	0.052411	0.089718	0.078334	0.099854	0.069846	0.082671
SAT6	0.020742	0.052907	0.029747	0.030403	0.225961	0.078874
STALKER2	0.078029	0.065712	0.069306	0.066485	0.073375	0.06873
STALKER3	0.060838	0.103498	0.149722	0.111921	0.045588	0.077792
STALKER4	0.07194	0.067067	0.070337	0.070743	0.071557	0.068874
TABOR	0.054582	0.06331	0.069546	0.078145	0.061325	0.083545

TAHRE	0.132583	0.087444	0.081241	0.072772	0.089204	0.080739
TART	0.092357	0.071973	0.069497	0.068776	0.071855	0.068159
TC1	0.072485	0.093344	0.043858	0.07544	0.058206	0.067137
TC1-2	0.125843	0.121623	0.075547	0.097162	0.09334	0.099846
TIRANT	0.107427	0.061798	0.048119	0.055	0.044412	0.059464
TLD2	0	0.021352	0.027778	0.004785	0.019608	0.032847
TOM1	0	0.085475	0.048765	0.049671	0.037799	0.048888
Transib1	0.103664	0.07852	0.095407	0.089022	0.106863	0.089072
TRANSIB2	0.088299	0.077007	0.059757	0.067209	0.0732	0.071527
TRANSIB3	0.026667	0.079991	0.095085	0.090805	0.04539	0.055889
Transib4	0.176471	0.092743	0	0.118182	0.080645	0.083969
Transib5	0.0312	0.07291	0.038489	0.05916	0.048394	0.064624
TRANSPAC	0.111446	0.091927	0.097403	0.083092	0.093966	0.085274
ZAM	0.146485	0.07419	0.079204	0.090465	0.100283	0.087467

spn-E_d1									
TE	d1_mut1	d1_mut2	d1_mut3	d1_mel1	d1_mel2	d1_mel3	d1_sim1	d1_sim2	d1_sim3
1731	0.060449	0.074593	0.062753	0.064715	0.071316	0.066511	0.071902	0.068785	0.07138
176	0.069387	0.063188	0.058776	0.072821	0.069633	0.071165	0.065062	0.064711	0.064943
297	0.056052	0.053028	0.068733	0.058844	0.055666	0.057017	0.057444	0.054809	0.054828
412	0.08632	0.088004	0.091238	0.072143	0.071955	0.072717	0.070873	0.07156	0.071729
5S	0.005572	0.005665	0.00698	0.029321	0.013889	0	0.016467	0.008333	0.005
ACCORD	0.058113	0.063934	0.069644	0.064672	0.065113	0.066564	0.069199	0.071987	0.069588
ACCORD2	0.106159	0.093673	0.073898	0.075087	0.076022	0.075328	0.077069	0.078482	0.074294
ARS406	0.058408	0.047021	0.053209	0.035552	0.039053	0.041676	0.047068	0.046527	0.047723
BAGGINS1	0.086105	0.07702	0.079659	0.073973	0.074259	0.074058	0.075124	0.074282	0.075102
BARI	0.059274	0.139929	0.067367	0.057204	0.053285	0.05511	0.056404	0.057852	0.058345
BATUMI	0.067673	0.066861	0.069769	0.075066	0.075157	0.075387	0.073476	0.076015	0.075853
BEL	0.055723	0.052256	0.078881	0.067895	0.066649	0.067823	0.065572	0.06946	0.067989

Bica	0.070453	0.05271	0.062098	0.06624	0.071459	0.06619	0.071437	0.075376	0.071663
BLASTOPIA	0.067879	0.09148	0.078511	0.071994	0.074835	0.077462	0.075349	0.078256	0.077278
BLOOD	0.072923	0.070236	0.070384	0.064518	0.065906	0.066984	0.066785	0.067289	0.066877
BS	0.079454	0.084644	0.083759	0.08003	0.079733	0.080587	0.081194	0.079229	0.07979
BS2	0.070591	0.070666	0.076067	0.06441	0.063397	0.064883	0.063591	0.064092	0.06372
BS3	0.080471	0.098621	0.083624	0.075304	0.078489	0.076534	0.078311	0.076798	0.073737
BURDOCK	0.064774	0.073746	0.075008	0.06749	0.067782	0.069297	0.068274	0.071755	0.069632
Chimpo	0.064516	0.073226	0.051986	0.070537	0.067896	0.072483	0.067834	0.071462	0.070796
Chouto	0.091732	0.090771	0.106595	0.07788	0.083572	0.083784	0.079407	0.081106	0.079462
CIRCE	0.07079	0.067712	0.057261	0.07015	0.071	0.070819	0.07067	0.069217	0.07051
COPIA	0.080012	0.081081	0.071215	0.081072	0.079418	0.078125	0.079151	0.081459	0.074944
Copia1	0.088413	0.086328	0.08307	0.075109	0.073752	0.073435	0.075742	0.075398	0.077374
COPIA2	0.086286	0.046328	0.072969	0.067152	0.068729	0.065171	0.070744	0.069818	0.070341
CR1A	0.06562	0.064559	0.071893	0.063968	0.062401	0.063513	0.066384	0.066901	0.066577
DIVER	0.076506	0.064217	0.072667	0.080154	0.079135	0.078175	0.081645	0.078802	0.078527
DIVER2	0.072411	0.09179	0.070269	0.068047	0.070483	0.070364	0.072698	0.068579	0.072908
DNAREP1	0.069995	0.063365	0.08079	0.062288	0.06338	0.061828	0.062112	0.066538	0.067505
DOC	0.05753	0.059965	0.058918	0.061701	0.060737	0.062377	0.060301	0.062633	0.063658
DOC2	0.108232	0.120798	0.113521	0.084757	0.090839	0.086458	0.083002	0.089422	0.08832
DOC3	0.065876	0.065646	0.058986	0.079933	0.077764	0.079082	0.081735	0.081592	0.08042
DOC4	0.153571	0.029412	0.159113	0.113742	0.110912	0.108771	0.121123	0.102746	0.118775
DOC5	0.034806	0.049422	0.03719	0.073684	0.065813	0.064159	0.062493	0.064449	0.069238
DOC6	0.080864	0.086523	0.088651	0.074773	0.075614	0.081363	0.074672	0.076074	0.07516
FB4	0.051733	0.051243	0.052425	0.038865	0.051236	0.053317	0.031464	0.078689	0.055542
FROGGER	0	0	0	0.042604	0.081513	0.039942	0.008772	0.037037	0.036364
FW	0.059371	0.05729	0.057885	0.067258	0.068274	0.067063	0.068068	0.067824	0.068015
FW2	0.103175	0	0.2	0.06317	0.052359	0.06241	0.054737	0.05675	0.061939
FW3	0.082784	0.060606	0.058475	0.058652	0.069066	0.074197	0.061637	0.070705	0.076247
G	0.072584	0.065784	0.074627	0.070962	0.068987	0.073076	0.069429	0.071573	0.069907

G2	0.092016	0.085646	0.086975	0.078325	0.077137	0.079792	0.074779	0.07743	0.075993
G3	0.333333	0.2	0.074074	0.082192	0.117079	0.115486	0.124439	0.136959	0.110177
G4	0.071121	0.07189	0.077795	0.072192	0.068963	0.063158	0.06683	0.074696	0.070105
G5	0.137268	0.032353	0.046746	0.065536	0.064987	0.065091	0.064293	0.061307	0.066085
G5A	0.034783	0.020478	0.024954	0.067292	0.068893	0.069673	0.06608	0.075462	0.071504
G6	0.106123	0.106048	0.093537	0.081906	0.081763	0.07804	0.08245	0.085901	0.085055
G7	0.5	0	0	0.088664	0.057474	0.061637	0.031114	0.095655	0.027508
GTWIN	0.073642	0.111854	0.036713	0.081744	0.080297	0.07688	0.081625	0.090737	0.080934
GYPSY	0.090089	0.09504	0.088727	0.064097	0.063977	0.065951	0.066025	0.065902	0.065494
Gypsy1	0.071159	0.082163	0.087604	0.06866	0.069572	0.070084	0.070695	0.071426	0.069426
GYPSY10	0.051993	0.066996	0.060967	0.064678	0.070942	0.080408	0.065415	0.072988	0.066167
GYPSY11	0.118644	0.1875	0.05854	0.052985	0.097141	0.086586	0.058851	0.059147	0.147234
GYPSY12	0.060892	0.059357	0.072148	0.06927	0.068372	0.070292	0.068761	0.071104	0.07072
Gypsy2	0.07767	0.076382	0.074968	0.065739	0.066303	0.065283	0.065449	0.063868	0.064394
GYPSY2	0.067722	0.082326	0.063738	0.065525	0.068591	0.069835	0.068859	0.065536	0.065884
GYPSY3	0.071237	0.073831	0.069011	0.069688	0.070475	0.0702	0.073229	0.070362	0.071309
GYPSY4	0.076473	0.09302	0.071333	0.065744	0.068158	0.065906	0.066056	0.067124	0.065722
GYPSY5	0.032234	0.033684	0.032675	0.078799	0.063086	0.081716	0.074754	0.095767	0.03378
GYPSY6	0.057308	0.064037	0.06379	0.068609	0.067739	0.06745	0.068292	0.070243	0.069019
GYPSY6A	0.07856	0.065448	0.060785	0.070443	0.073818	0.072389	0.063682	0.065262	0.073846
GYPSY7	0.109524	0.021739	0.102041	0.095926	0.075543	0.10121	0.083474	0.090136	0.100607
GYPSY8	0.05766	0.052437	0.077971	0.068909	0.069864	0.066779	0.066551	0.065935	0.065117
GYPSY9	0.5	0.111111	0.008772	0.063028	0.067263	0.079439	0.057745	0.062349	0.076438
HELENA_RT	0.02406	0.125864	0.019029	0.059078	0.059033	0.064167	0.056216	0.055232	0.054541
HETA	0.062759	0.054604	0.071731	0.063267	0.066133	0.063616	0.064245	0.063318	0.063271
HETRP	0.081805	0.114365	0.108037	0.111797	0.108207	0.111485	0.117853	0.118489	0.110917
HMR1	0.085355	0.071429	0.069274	0.075971	0.05668	0.078903	0.065378	0.092714	0.071928
HMR2	0.040929	0.039319	0.089222	0.064805	0.065691	0.064324	0.065108	0.067674	0.064294
HMSBEAGLE	0.067575	0.066532	0.064197	0.064742	0.063677	0.063677	0.066737	0.066703	0.064899

HOBO	0.073853	0.076751	0.074425	0.056863	0.055086	0.053775	0.054519	0.057581	0.056615
I	0.092542	0.08748	0.080751	0.092784	0.091989	0.095968	0.088073	0.090306	0.086599
IDEFIX	0.075012	0.07304	0.095098	0.070313	0.066816	0.068073	0.073635	0.078009	0.072353
INVADER1	0.07301	0.068246	0.071329	0.066743	0.068969	0.069949	0.067241	0.067532	0.068569
INVADER2	0.061764	0.056361	0.06086	0.071717	0.071097	0.07149	0.073582	0.071077	0.073276
INVADER3	0.073142	0.064246	0.065411	0.079268	0.081821	0.077084	0.074746	0.077627	0.075336
INVADER4	0.074831	0.07106	0.072358	0.080277	0.081707	0.077874	0.081951	0.093692	0.079742
INVADER5	0	0	0	0.04223	0.007353	0.037975	0.045455	0.03125	0.12672
INVADER6	0.063867	0.07555	0.044606	0.070443	0.068875	0.068801	0.07103	0.067224	0.066112
IVK	0.111306	0.117822	0.092221	0.068781	0.07065	0.071612	0.072424	0.072658	0.074058
Jockey	0.05449	0.060362	0.052142	0.062372	0.06085	0.059938	0.060502	0.063512	0.062115
JOCKEY2	0.139387	0.146839	0.163186	0.141858	0.122834	0.127952	0.121337	0.137608	0.116151
LOOPER1	0	0	0.125	0.071992	0.075378	0.074813	0.080771	0.080515	0.077168
MARINER2	0.027778	0.1	0	0.064825	0.079261	0.07055	0.089841	0.059442	0.059729
MAX	0.068432	0.066143	0.067449	0.06346	0.063746	0.064185	0.065474	0.067483	0.066459
MDG1	0.06253	0.060333	0.055161	0.070799	0.072153	0.07444	0.077057	0.07469	0.074397
MDG3	0.052989	0.0729	0.069426	0.069708	0.080006	0.078621	0.079184	0.077326	0.07739
MICROPIA	0.106675	0.079788	0.091093	0.072513	0.076958	0.0756	0.073363	0.074635	0.074876
NOMAD	0.080441	0.057747	0.059172	0.075393	0.073274	0.071505	0.074516	0.073009	0.074279
NTS	0.089887	0.072834	0.063551	0.041473	0.028717	0.047917	0.035543	0.034985	0.04667
POGO	0.04036	0.139103	0.176268	0.074517	0.077291	0.081433	0.079162	0.07419	0.075215
PROTOP	0.044314	0.039527	0.055409	0.050695	0.050681	0.053011	0.052061	0.052079	0.051937
QUASIMODO	0.083048	0.076402	0.082038	0.06422	0.066812	0.066495	0.063406	0.062061	0.06054
QUASIMODO2	0.062938	0.058037	0.068938	0.066013	0.066016	0.065974	0.065494	0.063937	0.062935
R1	0.070202	0.068828	0.073457	0.063315	0.063523	0.062018	0.062404	0.062941	0.061817
R1-2	0.020833	0.036364	0.196779	0.05898	0.087357	0.072778	0.064041	0.066924	0.067512
R2	0.099332	0.09979	0.119519	0.074935	0.072704	0.078098	0.07613	0.077208	0.075036
ROO	0.065718	0.071297	0.065995	0.065419	0.065094	0.066314	0.065802	0.0648	0.064877
ROOA	0.095357	0.070882	0.089133	0.06838	0.06706	0.070151	0.068961	0.072913	0.070793

ROVER	0.088937	0.077688	0.082323	0.073147	0.070158	0.072918	0.070064	0.068381	0.070514
RSP	0	0	0.232143	0.168225	0.056014	0.621447	0.154497	0.086305	0.573297
RT1A	0.055905	0.059347	0.065527	0.062043	0.061374	0.060947	0.061043	0.061131	0.061845
RT1B	0.069196	0.073984	0.060438	0.061507	0.06108	0.061447	0.058286	0.059427	0.059179
RT1C	0.111975	0.084083	0.102173	0.067189	0.070798	0.070291	0.06663	0.066159	0.062909
S	0.165337	0.219383	0.136853	0.085484	0.089132	0.086212	0.088304	0.09457	0.082417
S2	0.045455	0.078947	0.058824	0.090638	0.090532	0.093222	0.076743	0.084883	0.069564
SAR	0.029344	0.041471	0.041088	0.045622	0.057388	0.053549	0.052303	0.050676	0.053346
SAR2	0.032382	0.014765	0.032011	0.055741	0.076346	0.060242	0.075202	0.079361	0.075613
SAT6	0.037127	0.016542	0.004843	0.034573	0.079337	0.033993	0.028352	0.032459	0.036262
STALKER2	0.075966	0.071469	0.065236	0.065988	0.066536	0.065423	0.069566	0.067913	0.065925
STALKER3	0.088898	0.033288	0.062335	0.155282	0.117376	0.123863	0.14595	0.147898	0.136291
STALKER4	0.064636	0.071231	0.066984	0.065912	0.067114	0.068598	0.069458	0.069786	0.069671
TABOR	0.121709	0.052787	0.126928	0.076727	0.078486	0.072678	0.074365	0.082843	0.074746
TAHRE	0.030879	0.05758	0.032789	0.074004	0.075673	0.073556	0.074721	0.072198	0.074577
TART	0.049859	0.048783	0.04627	0.067385	0.0688	0.068814	0.06837	0.070024	0.069492
TC1	0.02381	0.216667	0	0.087535	0.035186	0.045843	0.045288	0.077668	0.069551
TC1-2	0	0.15	0.145614	0.097434	0.10286	0.093632	0.104973	0.099808	0.100622
TIRANT	0.258013	0.062315	0.142104	0.039743	0.064678	0.096539	0.031655	0.066957	0.039123
TLD2	0	0.03125	0	0.061738	0.058059	0.055732	0.08351	0.056497	0.040665
TOM1	0.025641	0	0.200152	0.103759	0.083245	0.167046	0.089828	0.101106	0.088998
Transib1	0.219697	0.1	0.086806	0.087886	0.080108	0.0769	0.106096	0.066097	0.074898
TRANSIB2	0.1625	0.109758	0.091548	0.060812	0.062431	0.061201	0.068414	0.06565	0.06224
TRANSIB3	0.03125	0	0.05	0.076569	0.081223	0.124445	0.044335	0.025801	0.040122
Transib4	0.055556	0	0.2	0.207754	0.068868	0.224359	0.143145	0.221631	0.145833
Transib5	0.162428	0.087387	0.027778	0.068222	0.070002	0.065138	0.065525	0.062333	0.069256
TRANSPAC	0.110101	0.121682	0.101233	0.08898	0.095803	0.087355	0.096564	0.086623	0.088304
ZAM	0.086658	0.039809	0.040324	0.091001	0.064194	0.074026	0.077646	0.085089	0.079805

armi_d1									
TE	d1_mut1	d1_mut2	d1_mut3	d1_mel1	d1_mel2	d1_mel3	d1_sim1	d1_sim2	d1_sim3
1731	0.036398	0.041692	0.032192	0.068905	0.071244	0.071879	0.069404	0.068896	0.07356
176	0.048696	0.05183	0.052153	0.073557	0.069495	0.070264	0.067662	0.073548	0.068222
297	0.046164	0.044916	0.042893	0.055215	0.053428	0.055162	0.05434	0.05602	0.052773
412	0.072778	0.069576	0.055384	0.111287	0.11093	0.09868	0.092134	0.089203	0.090248
5S	0.011129	0.009373	0.010571	0.031084	0.026336	0.023688	0.031188	0.029273	0.019613
ACCORD	0.058327	0.036153	0.027754	0.05791	0.057758	0.058959	0.05571	0.057866	0.055939
ACCORD2	0.041247	0.011483	0.016639	0.075025	0.074423	0.074833	0.070176	0.068676	0.068408
ARS406	0.010293	0.010345	0.014167	0.033892	0.035152	0.035822	0.038939	0.041746	0.033758
BAGGINS1	0.039138	0.029847	0.035029	0.056075	0.054428	0.056251	0.052279	0.051986	0.050196
BARI	0.059741	0.072749	0.071497	0.099566	0.100219	0.095547	0.117355	0.121694	0.123078
BATUMI	0.030168	0.033457	0.033093	0.069968	0.071842	0.072274	0.066916	0.063917	0.067117
BEL	0.063448	0.062321	0.073749	0.064159	0.063001	0.063905	0.063072	0.061382	0.063403
Bica	0.030422	0.037697	0.076685	0.07772	0.077507	0.078646	0.075844	0.075986	0.077066
BLASTOPIA	0.065952	0.072747	0.063272	0.068905	0.07056	0.070484	0.065688	0.066074	0.065812
BLOOD	0.089054	0.093669	0.094034	0.068113	0.06556	0.068554	0.066327	0.070154	0.06719
BS	0.055408	0.052664	0.048662	0.074924	0.072704	0.071539	0.067442	0.065913	0.067932
BS2	0.058797	0.060198	0.045796	0.06843	0.065947	0.069415	0.06061	0.05922	0.059743
BS3	0.083404	0.07929	0.036005	0.066025	0.069446	0.062769	0.064953	0.064561	0.069107
BURDOCK	0.071266	0.067656	0.076934	0.073678	0.079929	0.079126	0.073312	0.071061	0.071099
Chimpo	0.026013	0.019231	0.044004	0.080489	0.080611	0.084343	0.073574	0.074295	0.074379
Chouto	0.070457	0.088326	0.028422	0.067298	0.068765	0.069058	0.072815	0.069905	0.07485
CIRCE	0.043261	0.041391	0.047216	0.063948	0.062869	0.064192	0.058896	0.058411	0.059244
COPIA	0.046355	0.045965	0.045463	0.081825	0.078205	0.077322	0.079861	0.081771	0.080471
Copia1	0.105591	0.115035	0.103378	0.065531	0.066142	0.068729	0.064942	0.059009	0.063171
COPIA2	0.057062	0.057993	0.056534	0.060935	0.060483	0.056019	0.059641	0.058616	0.062587
CR1A	0.067084	0.071623	0.069805	0.065277	0.065359	0.065185	0.060833	0.059935	0.058734
DIVER	0.066704	0.047188	0.095734	0.06435	0.061565	0.064273	0.062022	0.06045	0.061886

DIVER2	0.050429	0.070292	0.055254	0.068542	0.068592	0.065205	0.065842	0.066483	0.069701
DNAREP1	0.04753	0.051584	0.039902	0.065291	0.060138	0.065894	0.056573	0.063498	0.056615
DOC	0.049562	0.051877	0.051039	0.067638	0.067449	0.06698	0.065328	0.064604	0.064315
DOC2	0.042972	0.044057	0.060396	0.064715	0.064147	0.06265	0.062341	0.063475	0.060572
DOC3	0.025652	0.02298	0.023025	0.068938	0.066778	0.069771	0.069834	0.068878	0.069723
DOC4	0	0	0.125	0.085147	0.087049	0.086902	0.091838	0.083075	0.101497
DOC5	0.054885	0.096774	0.145833	0.072346	0.072157	0.072945	0.072356	0.069263	0.076136
DOC6	0.066669	0.088123	0.028846	0.070834	0.070911	0.07047	0.06807	0.066741	0.068592
FB4	0.045613	0.040558	0.034136	0.048109	0.045083	0.040318	0.045622	0.068226	0.03293
FROGGER	0	0	0	0.026901	0.065629	0.047308	0.130559	0	0.068217
FW	0.044219	0.043901	0.044744	0.072903	0.073523	0.073356	0.068961	0.067071	0.068564
FW2	0.041562	0.015986	0.004717	0.071052	0.067234	0.075239	0.067882	0.061024	0.058166
FW3	0.045393	0.097633	0.045961	0.053899	0.048585	0.056819	0.064718	0.053412	0.067161
G	0.05359	0.055104	0.046472	0.069816	0.070468	0.071042	0.070172	0.069793	0.070726
G2	0.053079	0.051197	0.062938	0.071591	0.074788	0.073036	0.079552	0.075017	0.085784
G3	0.117647	0	0	0.072417	0.070235	0.059223	0.063972	0.077489	0.056259
G4	0.079017	0.063547	0.063333	0.066724	0.064708	0.066285	0.068993	0.070873	0.07429
G5	0.037075	0.043749	0.084366	0.060698	0.056439	0.055659	0.052332	0.054536	0.054685
G5A	0.11402	0.115966	0.06	0.070621	0.068152	0.066388	0.062063	0.064844	0.068803
G6	0.055288	0.051022	0.065335	0.091748	0.089472	0.093168	0.088865	0.083202	0.086804
G7	0	0	0	0.05211	0.058172	0.05826	0.128651	0.0784	0
GTWIN	0.120965	0.130049	0.157232	0.068484	0.067607	0.06896	0.070085	0.065431	0.072831
GYPSY	0.093138	0.101355	0.106498	0.0672	0.068043	0.067678	0.066506	0.062667	0.064286
Gypsy1	0.072012	0.074311	0.075262	0.069137	0.069635	0.071267	0.07284	0.073114	0.080559
GYPSY10	0.072532	0.046477	0.03164	0.060169	0.068414	0.073111	0.060757	0.052434	0.06293
GYPSY11	0.084337	0.113047	0.106329	0.094529	0.100433	0.087945	0.157199	0.111012	0.132053
GYPSY12	0.052766	0.042016	0.047741	0.064094	0.065307	0.065426	0.060753	0.059973	0.059521
Gypsy2	0.070599	0.076625	0.072278	0.059315	0.060748	0.060215	0.061976	0.059976	0.061867
GYPSY2	0.091861	0.085387	0.122606	0.062215	0.062677	0.063598	0.061383	0.064101	0.061423

GYPSY3	0.055248	0.060544	0.055592	0.060329	0.05914	0.060042	0.059818	0.059226	0.061857
GYPSY4	0.054085	0.053806	0.065397	0.066167	0.064472	0.065798	0.064416	0.063663	0.064162
GYPSY5	0.028684	0.028902	0.028981	0.061078	0.042521	0.050294	0.073534	0.056185	0.043254
GYPSY6	0.062926	0.061709	0.05856	0.070263	0.071142	0.068872	0.074965	0.074677	0.077756
GYPSY6A	0.068963	0.091195	0.093835	0.100254	0.094343	0.093409	0.102422	0.101151	0.094688
GYPSY7	0.12372	0	0.025	0.067957	0.063321	0.072832	0.070703	0.079804	0.064095
GYPSY8	0.009091	0.058462	0.034483	0.063311	0.067057	0.069428	0.066231	0.071403	0.066941
GYPSY9	0.014085	0.044118	0	0.060777	0.068873	0.082237	0.084545	0.06397	0.090062
HELENA_RT	0.032423	0.03575	0.039513	0.071931	0.066867	0.06684	0.06222	0.063169	0.060835
HETA	0.025496	0.02195	0.026127	0.057123	0.056885	0.057812	0.053208	0.053119	0.052113
HETRP	0.053931	0.054713	0.057998	0.150323	0.133682	0.117809	0.133989	0.129173	0.139714
HMR1	0.026786	0	0.027027	0.0718	0.071399	0.064135	0.0602	0.061865	0.050953
HMR2	0.018305	0.030182	0.040242	0.054591	0.055861	0.056741	0.048963	0.04814	0.050271
HMSBEAGLE	0.035685	0.038751	0.037218	0.077648	0.077006	0.075675	0.07104	0.071509	0.074849
HOBO	0.041038	0.039993	0.045094	0.052115	0.049887	0.047524	0.049532	0.04998	0.047779
I	0.089092	0.0919	0.085673	0.083852	0.08461	0.084305	0.084572	0.081119	0.083525
IDEFIX	0.054045	0.059175	0.067991	0.062355	0.062359	0.060287	0.063315	0.067151	0.066353
INVADER1	0.023784	0.020894	0.01827	0.068054	0.06704	0.066785	0.067444	0.069456	0.06832
INVADER2	0.030089	0.036026	0.037838	0.06492	0.064805	0.061514	0.073992	0.069315	0.071994
INVADER3	0.084965	0.110481	0.116068	0.077739	0.076555	0.077507	0.076599	0.078176	0.076516
INVADER4	0.031969	0.020712	0.029516	0.074664	0.071581	0.07672	0.067981	0.066974	0.061722
INVADER5	0	0	0	0.08875	0.139456	0.038323	0.105731	0.019663	0
INVADER6	0.054899	0.049097	0.048662	0.063589	0.061805	0.062373	0.062248	0.061882	0.062522
IVK	0.034475	0.041254	0.018987	0.060982	0.060996	0.064726	0.0543	0.058839	0.055885
Jockey	0.049769	0.029495	0.061661	0.053517	0.055288	0.055676	0.05658	0.055687	0.055315
JOCKEY2	0.101795	0.092943	0.207064	0.147087	0.147769	0.151922	0.13406	0.126924	0.150398
LOOPER1	0.070272	0.027778	0	0.059138	0.065357	0.067032	0.066934	0.062106	0.069897
MARINER2	0.193548	0.166667	0	0.096287	0.08007	0.10071	0.101911	0.149576	0.214686
MAX	0.040487	0.043123	0.030184	0.055102	0.054719	0.053665	0.053076	0.054262	0.054861

MDG1	0.053327	0.058907	0.061007	0.071951	0.071368	0.071248	0.073364	0.071401	0.073802
MDG3	0.045046	0.043375	0.043157	0.087987	0.093385	0.093574	0.087854	0.080803	0.089754
MICROPIA	0.046423	0.042703	0.037044	0.072694	0.072908	0.072835	0.072096	0.071971	0.075751
NOMAD	0.028505	0.028124	0.035505	0.081011	0.082406	0.08248	0.080054	0.077168	0.073304
NTS	0.042528	0.040808	0.039159	0.035049	0.043514	0.047778	0.052455	0.043548	0.042591
POGO	0.031238	0.029727	0.025702	0.058913	0.057915	0.058914	0.056886	0.052458	0.05626
PROTOP	0.048329	0.050832	0.053237	0.063841	0.063728	0.060436	0.058581	0.056763	0.055105
QUASIMODO	0.060724	0.054416	0.064968	0.063755	0.068123	0.065789	0.05878	0.062913	0.060926
QUASIMODO2	0.077231	0.067582	0.066197	0.063683	0.059317	0.057347	0.063568	0.063243	0.065719
R1	0.040142	0.045463	0.046394	0.067538	0.066969	0.065389	0.067102	0.067109	0.067876
R1-2	0.181116	0	0.128906	0.058001	0.054849	0.036289	0.044804	0.036652	0.040985
R2	0.047486	0.036797	0.031339	0.076688	0.07547	0.072071	0.074434	0.074904	0.077268
ROO	0.051535	0.050968	0.046505	0.069324	0.07004	0.068942	0.065029	0.065732	0.066521
ROOA	0.049338	0.089546	0.072282	0.079988	0.07541	0.076427	0.077703	0.078053	0.085853
ROVER	0.086383	0.083172	0.082593	0.075466	0.074216	0.076727	0.081901	0.07562	0.086864
RSP	0.451268	0.429424	0.152278	0.037884	0.057746	0.073544	0.015352	0.021222	0.170996
RT1A	0.041121	0.044728	0.053857	0.066273	0.065591	0.067761	0.059898	0.059519	0.059631
RT1B	0.055855	0.0476	0.043342	0.060575	0.058658	0.060585	0.055713	0.055107	0.056623
RT1C	0.058954	0.058218	0.078409	0.059663	0.060602	0.060413	0.059077	0.058965	0.056692
S	0.034334	0.034143	0.02965	0.079156	0.075605	0.076573	0.074512	0.070857	0.075139
S2	0.019608	0.098039	0	0.043042	0.051432	0.051555	0.063713	0.059951	0.077164
SAR	0.064172	0.064604	0.074447	0.071645	0.075542	0.068349	0.076939	0.074355	0.073277
SAR2	0.057151	0.054381	0.047393	0.072783	0.075255	0.070867	0.063376	0.07379	0.062373
SAT6	0.066667	0.561728	0	0.052178	0.081571	0.06393	0.05423	0.095537	0.058938
STALKER2	0.059085	0.056749	0.057081	0.07068	0.070993	0.070766	0.066041	0.069029	0.067325
STALKER3	0.081015	0.043293	0.047203	0.072993	0.069434	0.071374	0.080004	0.07472	0.079416
STALKER4	0.05627	0.054712	0.055345	0.065194	0.066911	0.069281	0.064161	0.066611	0.063843
TABOR	0.125301	0.062022	0.076279	0.081036	0.078832	0.079018	0.072364	0.062683	0.058243
TAHRE	0.034181	0.028682	0.024627	0.063233	0.063246	0.062783	0.059495	0.057956	0.057873

TART	0.042183	0.041112	0.035152	0.066634	0.067166	0.067157	0.060471	0.06067	0.059945
TC1	0.161725	0.109467	0.040541	0.067576	0.053341	0.056734	0.078179	0.067244	0.06253
TC1-2	0.04381	0.031457	0.070301	0.052571	0.051581	0.055697	0.046773	0.052917	0.05617
TIRANT	0.075289	0.172474	0.05625	0.04702	0.042856	0.053854	0.13603	0.080146	0
TLD1	0	0	0	0.037088	0.15035	0.276119	0.5	0.013575	0
TLD2	0.027162	0.089006	0.012117	0.014427	0.014837	0.018867	0.008297	0.131133	0.002457
TOM1	0.021583	0.610599	0	0.147964	0.126614	0.111451	0.048881	0.044513	0.140411
Transib-N1	0	0	0	0	0	0	0	0	0
Transib1	0.018519	0.152174	0.1	0.073215	0.065687	0.077128	0.082902	0.066804	0.066567
TRANSIB2	0.07795	0.07823	0.081265	0.054683	0.055783	0.054567	0.058765	0.057451	0.057364
TRANSIB3	0.0625	0	0.0375	0.08257	0.077674	0.084316	0.077218	0.082552	0.079166
Transib4	0.014563	0.0625	0	0.055556	0.074348	0.035978	0.04878	0.057637	0.027397
Transib5	0.032508	0.05042	0.045952	0.058065	0.057893	0.061139	0.060547	0.065822	0.058743
TRANSPAC	0.093662	0.078801	0.075633	0.065035	0.060092	0.061093	0.065336	0.064956	0.0634
ZAM	0.062668	0.029124	0.029047	0.059795	0.063917	0.062687	0.055461	0.064609	0.07903

Table A2.7 piRNA phasing biogenesis signature (+1-U proportion) for TE-derived piRNAs.

aub_plus1u	p1u_mut1	p1u_mut2	p1u_mel1	p1u_mel2	p1u_sim1	p1u_sim2
TE						
1731	0.406441	0.478292	0.438262	0.465162	0.451032	0.455123
176	0.514638	0.604138	0.441332	0.524757	0.522424	0.543263
297	0.562709	0.598509	0.587527	0.598513	0.62375	0.635104
412	0.606125	0.655469	0.512854	0.515961	0.540646	0.537632
5S	0.101399	0.065217	0.075472	0.055556	0.039855	0.078035
ACCORD	0.520248	0.514746	0.572751	0.534649	0.577589	0.541711
ACCORD2	0.49767	0.485842	0.485568	0.456469	0.491681	0.45635
ARS406	0.529929	0.42486	0.546091	0.508191	0.508204	0.477533
BAGGINS1	0.464893	0.465674	0.392547	0.415489	0.413045	0.436354
BARI	0.579045	0.571285	0.54631	0.591358	0.568952	0.5743
BATUMI	0.448702	0.456569	0.426276	0.409612	0.456125	0.422325
BEL	0.383158	0.402359	0.360407	0.382129	0.371553	0.380749
Bica	0.466889	0.529231	0.445599	0.494967	0.462492	0.509301
BLASTOPIA	0.448019	0.427158	0.421507	0.458776	0.441319	0.457246
BLOOD	0.520867	0.536332	0.473508	0.499847	0.531924	0.538702
BS	0.498944	0.508392	0.460621	0.451217	0.491721	0.480283
BS2	0.441086	0.450195	0.347467	0.334289	0.369596	0.344626
BS3	0.604008	0.516852	0.44725	0.384506	0.484591	0.395956
BURDOCK	0.502536	0.485636	0.531608	0.535656	0.538203	0.537537
Chimpo	0.490074	0.507289	0.390157	0.39709	0.427973	0.394855
Chouto	0.424076	0.453711	0.430613	0.441892	0.426764	0.455733
CIRCE	0.580469	0.594164	0.513771	0.516348	0.549559	0.540624
COPIA	0.605198	0.617266	0.552689	0.570948	0.556253	0.564622
Copia1	0.625388	0.605312	0.504864	0.536292	0.548116	0.558395
COPIA2	0.567809	0.56773	0.4909	0.486639	0.485833	0.488975
CR1A	0.54052	0.558822	0.46054	0.475471	0.470934	0.471244

DIVER	0.430241	0.454985	0.439096	0.446499	0.467301	0.469233
DIVER2	0.439153	0.485549	0.521844	0.501861	0.493667	0.502704
DNAREP1	0.489616	0.550187	0.482454	0.511128	0.535169	0.567869
DOC	0.479271	0.491745	0.487411	0.472034	0.49039	0.444885
DOC2	0.527814	0.546134	0.557186	0.527715	0.548035	0.524509
DOC3	0.47955	0.524262	0.45129	0.467792	0.463229	0.459426
DOC4	0.486087	0.56545	0.39629	0.489783	0.463389	0.497982
DOC5	0.595047	0.50772	0.502848	0.489593	0.509099	0.47612
DOC6	0.519904	0.525654	0.528563	0.561061	0.529464	0.556159
FB4	0.463631	0.509375	0.499816	0.630697	0.546558	0.726648
FROGGER	0.482909	0.577709	0.500696	0.572363	0.54466	0.499123
FW	0.443684	0.430499	0.341204	0.36527	0.342057	0.360786
FW2	0.436546	0.504111	0.467324	0.568068	0.407384	0.548054
FW3	0.318564	0.412766	0.610468	0.581184	0.569588	0.586628
G	0.421074	0.468244	0.449161	0.456335	0.486293	0.477082
G2	0.343437	0.431261	0.324284	0.351298	0.359164	0.378622
G3	0.350247	0.404856	0.29563	0.332633	0.289029	0.340313
G4	0.479861	0.534709	0.471692	0.501942	0.485914	0.542382
G5	0.509101	0.500883	0.481601	0.478533	0.511291	0.48804
G5A	0.383557	0.462244	0.362449	0.408985	0.344337	0.398146
G6	0.448176	0.451871	0.259064	0.293201	0.254931	0.291524
G7	0.460061	0.480386	0.437897	0.405339	0.470923	0.48065
GTWIN	0.413505	0.468684	0.488215	0.475395	0.473007	0.47847
GYPSY	0.536802	0.522806	0.518717	0.513965	0.545093	0.518998
Gypsy1	0.464052	0.47557	0.398452	0.399809	0.400913	0.414702
GYPSY10	0.457887	0.535727	0.49042	0.510033	0.531708	0.546725
GYPSY11	0.700285	0.577525	0.459925	0.53185	0.551342	0.497001
GYPSY12	0.451146	0.485644	0.420827	0.418792	0.471121	0.453735
Gypsy2	0.418809	0.434118	0.454358	0.474687	0.453398	0.480648

GYPSY2	0.422451	0.471579	0.448486	0.465617	0.452678	0.469127
GYPSY3	0.492503	0.492407	0.418075	0.428871	0.440746	0.428233
GYPSY4	0.538079	0.531274	0.432597	0.433452	0.482683	0.469392
GYPSY5	0.532599	0.57691	0.485545	0.443399	0.412946	0.454402
GYPSY6	0.523789	0.508849	0.517576	0.497475	0.509919	0.510104
GYPSY6A	0.445368	0.446006	0.432999	0.457263	0.385641	0.407816
GYPSY7	0.457737	0.47038	0.481579	0.486905	0.479887	0.47967
GYPSY8	0.2581	0.287253	0.275013	0.292281	0.277835	0.29568
GYPSY9	0.578876	0.579903	0.562334	0.520366	0.567763	0.587165
HELENA_RT	0.483292	0.557357	0.543808	0.561554	0.520622	0.556669
HETA	0.449389	0.433303	0.294365	0.325993	0.327834	0.371394
HETRP	0.348204	0.387574	0.227368	0.219918	0.231506	0.222338
HMR1	0.215812	0.26586	0.314184	0.219681	0.286839	0.285352
HMR2	0.398211	0.400383	0.307598	0.346633	0.324736	0.347359
HMSBEAGLE	0.380137	0.4155	0.46845	0.48978	0.482793	0.492368
HOBO	0.486803	0.503333	0.516146	0.528924	0.457332	0.482577
I	0.514978	0.537605	0.425374	0.408982	0.504755	0.468093
IDEFIX	0.56893	0.584795	0.534297	0.542222	0.533614	0.54655
INVADER1	0.485041	0.443108	0.404692	0.404714	0.452683	0.430925
INVADER2	0.598191	0.618814	0.57755	0.566539	0.585373	0.586806
INVADER3	0.527775	0.554198	0.456919	0.492635	0.489608	0.51696
INVADER4	0.256718	0.311298	0.339253	0.371544	0.331841	0.375954
INVADER5	0.57638	0.488831	0.538314	0.541316	0.528033	0.560225
INVADER6	0.454991	0.445691	0.375928	0.386222	0.398752	0.417048
IVK	0.537582	0.539778	0.46564	0.443002	0.507969	0.48906
Jockey	0.528058	0.542505	0.436843	0.451544	0.476508	0.468157
JOCKEY2	0.480416	0.492357	0.502107	0.496887	0.512989	0.540304
LOOPER1	0.722775	0.689872	0.699929	0.662602	0.69046	0.678226
MARINER2	0.384522	0.490634	0.304707	0.445947	0.330816	0.428208

MAX	0.458676	0.488886	0.390367	0.41166	0.378067	0.407609
MDG1	0.525826	0.545026	0.576528	0.582958	0.556955	0.556681
MDG3	0.390716	0.465893	0.450382	0.471932	0.450304	0.469434
MICROPIA	0.514654	0.579373	0.514945	0.518844	0.538769	0.529962
NOMAD	0.439275	0.4621	0.38216	0.386805	0.416288	0.3947
NTS	0.442658	0.45924	0.31833	0.348618	0.28467	0.358472
POGO	0.355866	0.485709	0.277861	0.354926	0.294375	0.389151
PROTOP	0.425628	0.460755	0.29569	0.343133	0.341459	0.408589
QUASIMODO	0.57177	0.616998	0.515092	0.547271	0.558282	0.55611
QUASIMODO2	0.502251	0.513484	0.57078	0.550411	0.599852	0.568814
R1	0.314264	0.361743	0.28966	0.340959	0.289782	0.329983
R1-2	0.420176	0.362793	0.391127	0.33763	0.402061	0.323479
R2	0.394777	0.440208	0.415199	0.436352	0.413773	0.44921
ROO	0.583271	0.587363	0.51909	0.520854	0.52349	0.525235
ROOA	0.506488	0.507314	0.479861	0.491258	0.476954	0.492899
ROVER	0.419155	0.477667	0.486375	0.503017	0.508736	0.510543
RSP	0.59266	0.612347	0.490851	0.642146	0.535557	0.606718
RT1A	0.377349	0.393508	0.287397	0.29002	0.310012	0.294465
RT1B	0.360216	0.394812	0.262767	0.294412	0.295449	0.318555
RT1C	0.384101	0.401213	0.377745	0.388625	0.387901	0.405782
S	0.418551	0.469383	0.352716	0.411842	0.411286	0.449562
S2	0.476297	0.48322	0.3834	0.396285	0.434094	0.469697
SAR	0.432835	0.385583	0.228497	0.211102	0.286324	0.284318
SAR2	0.492422	0.408391	0.401297	0.372271	0.281682	0.267346
SAT6	0.318282	0.474146	0.515237	0.256782	0.236769	0.380842
STALKER2	0.674662	0.668233	0.585235	0.599515	0.603685	0.613848
STALKER3	0.507294	0.647669	0.617698	0.684112	0.575364	0.645971
STALKER4	0.533517	0.577479	0.492256	0.533975	0.501305	0.543907
TABOR	0.439498	0.422383	0.604442	0.593408	0.603282	0.573206

TAHRE	0.415713	0.404635	0.447794	0.45156	0.440899	0.441589
TART	0.537076	0.556145	0.453869	0.460235	0.467696	0.478394
TC1	0.53981	0.55365	0.512798	0.542508	0.548211	0.538545
TC1-2	0.661826	0.649798	0.552615	0.557314	0.605805	0.580703
TIRANT	0.495373	0.452774	0.407434	0.406973	0.463871	0.397487
TLD2	0.123711	0.308906	0.136055	0.116006	0.141217	0.196476
TOM1	0.473754	0.330161	0.316764	0.188762	0.248398	0.194175
Transib1	0.514911	0.524965	0.550141	0.576325	0.593377	0.590311
TRANSIB2	0.511209	0.569928	0.518112	0.507369	0.483068	0.523803
TRANSIB3	0.648396	0.645535	0.495193	0.544183	0.569256	0.56362
Transib4	0.265458	0.519367	0.332432	0.530588	0.494444	0.529252
Transib5	0.625123	0.640406	0.608137	0.606544	0.661596	0.640123
TRANSPAC	0.544744	0.509927	0.647097	0.641387	0.651163	0.641057
ZAM	0.558308	0.548213	0.542548	0.569842	0.508835	0.549323

spn-E_plus1u									
TE	p1u_mut1	p1u_mut2	p1u_mut3	p1u_mel1	p1u_mel2	p1u_mel3	p1u_sim1	p1u_sim2	p1u_sim3
1731	0.481925	0.498935	0.464073	0.464385	0.4418	0.459586	0.481046	0.471214	0.478624
176	0.549929	0.550957	0.566227	0.541585	0.534525	0.53579	0.509319	0.510841	0.505302
297	0.604442	0.5587	0.5714	0.625	0.630171	0.629837	0.630977	0.635885	0.629501
412	0.52371	0.502753	0.513928	0.538068	0.536064	0.536346	0.547006	0.553431	0.531859
5S	0.085546	0.078292	0.077844	0.060811	0.125	0.045455	0.091549	0.095588	0.085227
ACCORD	0.524933	0.508821	0.535641	0.483924	0.490884	0.479791	0.512954	0.496762	0.501693
ACCORD2	0.463205	0.494205	0.458974	0.447409	0.442176	0.439613	0.435154	0.438079	0.447228
ARS406	0.415013	0.446547	0.412414	0.360624	0.374601	0.42795	0.319423	0.338113	0.338694
BAGGINS1	0.500744	0.510782	0.519939	0.432411	0.435909	0.432322	0.449269	0.451501	0.45803
BARI	0.573824	0.580603	0.563008	0.636408	0.63745	0.633714	0.573728	0.578372	0.565939
BATUMI	0.396654	0.38995	0.397556	0.439889	0.446963	0.444958	0.443883	0.447173	0.440099
BEL	0.395632	0.382451	0.350425	0.401479	0.388204	0.404018	0.420728	0.421084	0.423102

Bica	0.527812	0.543277	0.526683	0.503486	0.508559	0.515078	0.495653	0.508197	0.491501
BLASTOPIA	0.427228	0.436919	0.426481	0.465304	0.466737	0.473363	0.48443	0.473805	0.487656
BLOOD	0.551106	0.553107	0.54598	0.54428	0.552483	0.553858	0.504375	0.504884	0.501348
BS	0.537419	0.523133	0.54337	0.408508	0.411197	0.412722	0.409645	0.419081	0.409117
BS2	0.414337	0.430269	0.445921	0.373446	0.368246	0.364257	0.367856	0.371519	0.361634
BS3	0.435613	0.444999	0.466392	0.380961	0.372344	0.364763	0.364945	0.367111	0.375986
BURDOCK	0.484299	0.434033	0.535725	0.491028	0.496165	0.490879	0.47495	0.50064	0.476426
Chimpo	0.529723	0.517318	0.507548	0.437664	0.428333	0.430322	0.429393	0.428417	0.418443
Chouto	0.473649	0.493579	0.522686	0.421338	0.431582	0.429949	0.426735	0.431062	0.419306
CIRCE	0.508395	0.532118	0.552665	0.487461	0.497861	0.490921	0.47701	0.482471	0.481612
COPIA	0.606832	0.580541	0.601272	0.563576	0.558262	0.551723	0.535378	0.530969	0.5423
Copia1	0.56654	0.557387	0.529347	0.479042	0.480223	0.470636	0.485412	0.482256	0.473326
COPIA2	0.446741	0.413598	0.484785	0.367452	0.368862	0.380536	0.395111	0.393936	0.377828
CR1A	0.526659	0.533002	0.528478	0.458117	0.445904	0.446184	0.453017	0.451282	0.453239
DIVER	0.395696	0.390996	0.37788	0.457742	0.459779	0.452971	0.458345	0.464359	0.446893
DIVER2	0.455581	0.476625	0.446728	0.497149	0.499813	0.49536	0.500702	0.499346	0.503649
DNAREP1	0.501925	0.525516	0.489078	0.518521	0.52052	0.512751	0.515304	0.502949	0.510381
DOC	0.508248	0.516779	0.515661	0.460351	0.452085	0.459928	0.451015	0.45571	0.461993
DOC2	0.517577	0.538003	0.521839	0.536839	0.546799	0.535594	0.520771	0.524641	0.527423
DOC3	0.467345	0.478746	0.468368	0.454187	0.452206	0.444715	0.457707	0.45573	0.456073
DOC4	0.413931	0.474485	0.372414	0.458794	0.462841	0.426928	0.451625	0.444353	0.445133
DOC5	0.489242	0.466336	0.441702	0.522746	0.524783	0.519908	0.52431	0.50943	0.529168
DOC6	0.517694	0.515511	0.532185	0.503861	0.527873	0.523604	0.503625	0.484776	0.49168
FB4	0.411683	0.504435	0.534774	0.552725	0.54321	0.588816	0.557339	0.565175	0.461352
FROGGER	0.492857	0.484848	0.375	0.646075	0.515406	0.525142	0.462034	0.467748	0.581149
FW	0.427854	0.425589	0.434287	0.378264	0.377962	0.367913	0.357919	0.355833	0.352984
FW2	0.491988	0.47619	0.482735	0.484637	0.485089	0.491341	0.466915	0.475526	0.471944
FW3	0.410066	0.396396	0.422922	0.536884	0.534687	0.555306	0.516079	0.536169	0.531112
G	0.437105	0.452425	0.437187	0.46747	0.468076	0.465927	0.473015	0.471025	0.467464

G2	0.450881	0.432728	0.47146	0.409625	0.411583	0.405573	0.414007	0.424781	0.414986
G3	0.432558	0.400522	0.380719	0.379836	0.362801	0.376218	0.347495	0.40208	0.373482
G4	0.620205	0.604766	0.656463	0.520525	0.521155	0.500433	0.534447	0.537342	0.526696
G5	0.437627	0.449917	0.395578	0.454055	0.454828	0.447796	0.452671	0.446637	0.443446
G5A	0.404783	0.392475	0.41093	0.33299	0.339166	0.351643	0.342912	0.352459	0.342682
G6	0.39958	0.372222	0.370218	0.327132	0.331329	0.323595	0.325075	0.321851	0.333964
G7	0.333333	0.75	0.3	0.408645	0.417903	0.463594	0.379501	0.452151	0.443305
GTWIN	0.407712	0.451874	0.421248	0.469712	0.480768	0.466758	0.459731	0.458648	0.456947
GYPSY	0.426205	0.435756	0.421857	0.441987	0.442869	0.442394	0.441275	0.440131	0.435896
Gypsy1	0.434425	0.450581	0.458948	0.367307	0.366453	0.371788	0.359857	0.36054	0.359566
GYPSY10	0.529094	0.582795	0.520187	0.495523	0.496867	0.511366	0.516223	0.51605	0.512526
GYPSY11	0.598551	0.546296	0.567234	0.455215	0.50791	0.519347	0.478827	0.490108	0.463435
GYPSY12	0.457956	0.436658	0.437259	0.509604	0.504065	0.511606	0.50557	0.511564	0.511432
Gypsy2	0.364021	0.369627	0.370704	0.440585	0.447731	0.436491	0.433519	0.431019	0.432908
GYPSY2	0.441094	0.46652	0.461639	0.424561	0.430351	0.434801	0.414425	0.415079	0.417682
GYPSY3	0.508286	0.486241	0.503888	0.420746	0.41055	0.422526	0.415741	0.411367	0.419002
GYPSY4	0.538824	0.539995	0.523437	0.457519	0.455471	0.459177	0.484014	0.488704	0.48661
GYPSY5	0.440158	0.588142	0.496574	0.459582	0.457841	0.475005	0.456062	0.452003	0.427322
GYPSY6	0.425454	0.44223	0.434942	0.455262	0.456567	0.458598	0.453733	0.456698	0.456904
GYPSY6A	0.428603	0.477405	0.43146	0.315491	0.324514	0.31398	0.334239	0.323432	0.305755
GYPSY7	0.484843	0.434359	0.49091	0.500994	0.49086	0.520724	0.489638	0.471005	0.496258
GYPSY8	0.312387	0.362082	0.319874	0.306344	0.303103	0.304574	0.300863	0.302594	0.2974
GYPSY9	0.613769	0.488445	0.587383	0.612781	0.630167	0.570915	0.578615	0.5822	0.591572
HELENA_RT	0.397736	0.453008	0.417488	0.378114	0.382546	0.386803	0.413738	0.414498	0.40428
HETA	0.408435	0.421747	0.439087	0.328006	0.310535	0.324809	0.335002	0.333567	0.356741
HETRP	0.131407	0.229839	0.162113	0.166666	0.170466	0.170906	0.167663	0.170923	0.168101
HMR1	0.447917	0.5	0.418605	0.282578	0.269318	0.312782	0.313395	0.359603	0.307534
HMR2	0.296207	0.307947	0.296237	0.316261	0.300064	0.313681	0.288712	0.288384	0.308304
HMSBEAGLE	0.387963	0.373012	0.374623	0.446149	0.454522	0.446017	0.45517	0.451795	0.454334

HOBO	0.513346	0.53272	0.49011	0.492386	0.534103	0.506235	0.517268	0.506247	0.500074
I	0.535658	0.520066	0.517822	0.484125	0.470615	0.480906	0.491782	0.513175	0.484601
IDEFIX	0.555816	0.573268	0.555294	0.490092	0.494987	0.484859	0.490159	0.48485	0.492013
INVADER1	0.45495	0.486114	0.467012	0.429692	0.424724	0.43035	0.436548	0.439468	0.435546
INVADER2	0.510222	0.502325	0.521615	0.524543	0.526251	0.54162	0.528515	0.527449	0.534594
INVADER3	0.4573	0.500573	0.529873	0.471418	0.475405	0.467707	0.4666	0.47152	0.470598
INVADER4	0.427244	0.375	0.426735	0.409446	0.416735	0.426098	0.43757	0.440112	0.433418
INVADER5	0.416667	0.578571	0.464286	0.468931	0.525794	0.508971	0.610559	0.532258	0.476471
INVADER6	0.366854	0.416966	0.383251	0.378472	0.377392	0.387528	0.402644	0.396271	0.404179
IVK	0.499498	0.522936	0.52814	0.43373	0.421226	0.436536	0.43567	0.438403	0.443225
Jockey	0.480817	0.494899	0.494434	0.41555	0.417353	0.40962	0.415323	0.41501	0.403024
JOCKEY2	0.519041	0.536077	0.533846	0.52739	0.507301	0.514947	0.517899	0.532293	0.530062
LOOPER1	0.670323	0.602273	0.7189	0.59577	0.606257	0.586134	0.522026	0.545637	0.511102
MARINER2	0.488479	0.29	0.5625	0.409946	0.349118	0.363163	0.402782	0.32339	0.340281
MAX	0.35977	0.369581	0.367534	0.369657	0.362034	0.366587	0.366677	0.367883	0.372703
MDG1	0.792981	0.795541	0.784291	0.630698	0.631927	0.633387	0.612646	0.617312	0.61477
MDG3	0.367815	0.370422	0.395268	0.464148	0.489207	0.484334	0.49842	0.503621	0.502038
MICROPIA	0.553273	0.502186	0.534285	0.512272	0.527763	0.520411	0.525386	0.523467	0.523285
NOMAD	0.446758	0.441016	0.464268	0.401846	0.406241	0.398112	0.417193	0.418046	0.410427
NTS	0.323999	0.326954	0.289595	0.313167	0.226174	0.33371	0.304609	0.317005	0.29355
POGO	0.422278	0.483964	0.442586	0.403411	0.39455	0.387708	0.383579	0.384938	0.394753
PROTOP	0.422326	0.41966	0.441646	0.350022	0.362388	0.345328	0.345204	0.354722	0.34348
QUASIMODO	0.573259	0.547704	0.59848	0.565757	0.58085	0.575685	0.570168	0.575364	0.571028
QUASIMODO2	0.50609	0.553559	0.580154	0.557358	0.542531	0.545283	0.549882	0.55575	0.539337
R1	0.327355	0.33448	0.332084	0.295239	0.295253	0.295781	0.293662	0.30166	0.29591
R1-2	0.311831	0.447778	0.52193	0.422129	0.409764	0.440024	0.435338	0.399393	0.417023
R2	0.373806	0.443141	0.420492	0.443613	0.438798	0.441137	0.441932	0.438854	0.430965
ROO	0.560606	0.586818	0.576625	0.528357	0.528264	0.526998	0.516492	0.506044	0.518143
ROOA	0.526644	0.538217	0.544375	0.516015	0.504362	0.511383	0.500792	0.500431	0.505028

ROVER	0.513438	0.519159	0.518596	0.567916	0.564442	0.571692	0.559979	0.555382	0.569445
RSP	0.702256	0.627992	0.726496	0.479288	0.459374	0.459799	0.435405	0.457517	0.41316
RT1A	0.361665	0.391307	0.38223	0.321685	0.313471	0.314252	0.302855	0.308273	0.311368
RT1B	0.357288	0.373222	0.387715	0.28606	0.284478	0.28504	0.281015	0.278076	0.280098
RT1C	0.410434	0.397014	0.418182	0.460563	0.449393	0.447204	0.461301	0.435691	0.446604
S	0.379968	0.439738	0.456783	0.378106	0.377837	0.386894	0.352964	0.330097	0.331244
S2	0.396832	0.459936	0.352151	0.447212	0.449311	0.478584	0.484459	0.451011	0.350773
SAR	0.358758	0.326526	0.38839	0.356222	0.31282	0.342798	0.375933	0.366863	0.372686
SAR2	0.340262	0.317493	0.324153	0.341438	0.36132	0.36385	0.369135	0.360409	0.359111
SAT6	0.318182	0.357143	0.25	0.297203	0.256272	0.254545	0.206597	0.338685	0.497748
STALKER2	0.551876	0.562237	0.571834	0.417636	0.427608	0.414938	0.425717	0.437642	0.430312
STALKER3	0.596383	0.607639	0.538644	0.609254	0.613906	0.607377	0.558666	0.53774	0.57092
STALKER4	0.490824	0.482432	0.496657	0.472357	0.481794	0.47385	0.468059	0.457716	0.471543
TABOR	0.344366	0.332766	0.336191	0.52554	0.547162	0.544804	0.524881	0.526499	0.529753
TAHRE	0.250185	0.254593	0.265113	0.42589	0.423614	0.429818	0.421947	0.426322	0.43094
TART	0.447735	0.442231	0.440428	0.475031	0.478651	0.477492	0.467368	0.473693	0.47367
TC1	0.379545	0.476415	0.379433	0.522807	0.458868	0.479744	0.496981	0.543391	0.475885
TC1-2	0.605885	0.741071	0.700809	0.549576	0.553391	0.534305	0.56763	0.558392	0.552468
TIRANT	0.527174	0.48445	0.523082	0.549831	0.529099	0.518143	0.496846	0.530349	0.506577
TLD2	0.271229	0.453818	0.403986	0.2458	0.276398	0.150738	0.255996	0.27	0.152706
TOM1	0.330357	0.376068	0.404762	0.356201	0.364035	0.322464	0.341998	0.389898	0.367589
Transib1	0.511574	0.326415	0.520833	0.60359	0.574138	0.573162	0.580429	0.574327	0.564289
TRANSIB2	0.510902	0.537773	0.494682	0.553167	0.537344	0.545651	0.550264	0.562538	0.54846
TRANSIB3	0.634314	0.588384	0.626843	0.592294	0.616794	0.619318	0.532412	0.62757	0.555556
Transib4	0.361765	0.52381	0.583333	0.588431	0.544199	0.479528	0.569631	0.5906	0.638815
Transib5	0.650162	0.546749	0.629474	0.614259	0.61507	0.616533	0.618477	0.618454	0.615584
TRANSPAC	0.494911	0.506196	0.482939	0.455641	0.521561	0.528996	0.484546	0.49505	0.528275
ZAM	0.536764	0.509422	0.582565	0.543447	0.53237	0.517828	0.526415	0.530006	0.521099

armi_plus1u									
TE	p1u_mut1	p1u_mut2	p1u_mut3	p1u_mel1	p1u_mel2	p1u_mel3	p1u_sim1	p1u_sim2	p1u_sim3
1731	0.31989	0.30756	0.298657	0.419534	0.417079	0.388909	0.369537	0.380557	0.362013
176	0.411052	0.436855	0.414617	0.54443	0.542681	0.533055	0.544419	0.544117	0.537423
297	0.444893	0.476667	0.532632	0.532494	0.509027	0.480519	0.4991	0.499326	0.496463
412	0.475167	0.452194	0.446	0.562203	0.548741	0.536443	0.555533	0.533582	0.542561
5S	0.047923	0.205846	0.050398	0.078962	0.078512	0.09034	0.10131	0.086262	0.590633
ACCORD	0.350124	0.376192	0.349754	0.511664	0.523417	0.5258	0.504656	0.486924	0.496144
ACCORD2	0.426977	0.367738	0.421007	0.3845	0.37816	0.378437	0.38271	0.38772	0.382257
ARS406	0.086564	0.076905	0.080076	0.144563	0.145489	0.133222	0.168921	0.20045	0.18139
BAGGINS1	0.221383	0.221362	0.207978	0.316646	0.317771	0.319968	0.312475	0.307469	0.303752
BARI	0.463238	0.469914	0.442058	0.507128	0.500706	0.508349	0.506282	0.515189	0.515677
BATUMI	0.124333	0.136163	0.145839	0.35979	0.367331	0.367354	0.349708	0.344162	0.351026
BEL	0.264644	0.262327	0.289494	0.371155	0.373948	0.37065	0.364476	0.357343	0.354432
Bica	0.326324	0.307487	0.340028	0.429757	0.429543	0.436105	0.431821	0.421393	0.432866
BLASTOPIA	0.32188	0.344317	0.343875	0.470703	0.47993	0.475694	0.48632	0.464436	0.46476
BLOOD	0.50365	0.500015	0.499849	0.460493	0.455297	0.450583	0.476741	0.479995	0.468882
BS	0.335272	0.374088	0.351258	0.517711	0.5193	0.524454	0.490618	0.467069	0.468228
BS2	0.276771	0.298004	0.321535	0.349291	0.338349	0.3396	0.306552	0.293797	0.290422
BS3	0.279762	0.211034	0.198834	0.310388	0.313122	0.329244	0.324496	0.312768	0.336276
BURDOCK	0.419508	0.430329	0.457936	0.488391	0.480376	0.461444	0.498442	0.486973	0.47937
Chimpo	0.346784	0.243939	0.366269	0.395609	0.39953	0.394276	0.381022	0.370439	0.368708
Chouto	0.283776	0.27708	0.331212	0.408612	0.408292	0.407163	0.374595	0.377671	0.37043
CIRCE	0.427545	0.42333	0.454108	0.457181	0.479537	0.487601	0.434336	0.444873	0.431491
COPIA	0.464286	0.493729	0.498515	0.609368	0.605364	0.606772	0.60279	0.587058	0.592883
Copia1	0.481092	0.478637	0.474585	0.42601	0.43687	0.442855	0.44675	0.42608	0.447229
COPIA2	0.253431	0.240973	0.247473	0.385527	0.366588	0.359414	0.39409	0.392145	0.392043
CR1A	0.331028	0.342989	0.3419	0.415717	0.399165	0.391704	0.370343	0.377559	0.367365
DIVER	0.39005	0.337996	0.328146	0.413343	0.41665	0.409511	0.397814	0.402373	0.402777

DIVER2	0.446099	0.422104	0.44437	0.393685	0.391186	0.386507	0.394431	0.379942	0.382935
DNAREP1	0.450029	0.410639	0.454082	0.532627	0.531112	0.525599	0.505657	0.5032	0.503426
DOC	0.305395	0.32097	0.31142	0.355094	0.352069	0.34047	0.330528	0.336758	0.332972
DOC2	0.355285	0.356311	0.37246	0.439185	0.444749	0.429006	0.435606	0.446557	0.439733
DOC3	0.332568	0.334575	0.308977	0.425739	0.42702	0.430329	0.414587	0.405074	0.403734
DOC4	0.456919	0.431588	0.399609	0.349346	0.330078	0.339297	0.333133	0.360785	0.357105
DOC5	0.318054	0.361857	0.40045	0.423536	0.419705	0.424667	0.425628	0.428902	0.431352
DOC6	0.498	0.380188	0.472566	0.46411	0.480799	0.477887	0.496734	0.499362	0.497186
FB4	0.190366	0.196097	0.246418	0.259924	0.243507	0.225611	0.300643	0.289868	0.220127
FROGGER	0.513158	0.6	0.6	0.521867	0.556953	0.54387	0.539855	0.465072	0.605556
FW	0.309909	0.317467	0.313096	0.382633	0.390056	0.385335	0.384124	0.379319	0.368504
FW2	0.373109	0.398591	0.307248	0.481993	0.490208	0.489423	0.491046	0.496323	0.485421
FW3	0.332751	0.383537	0.427849	0.425133	0.444943	0.431333	0.4633	0.440321	0.505652
G	0.244835	0.230724	0.25863	0.315715	0.307913	0.304231	0.294987	0.300876	0.298005
G2	0.193583	0.224997	0.222068	0.312533	0.31671	0.309129	0.310937	0.305273	0.306203
G3	0.359238	0.48627	0.493356	0.40894	0.417178	0.397247	0.384774	0.354547	0.392148
G4	0.509718	0.402817	0.465361	0.480356	0.481867	0.463327	0.486497	0.482733	0.497014
G5	0.357251	0.417229	0.372378	0.399318	0.404917	0.408625	0.363752	0.345467	0.360243
G5A	0.512753	0.469489	0.556194	0.391582	0.397143	0.407468	0.381529	0.353803	0.344882
G6	0.401597	0.402497	0.440856	0.35153	0.341741	0.353288	0.311032	0.303868	0.315907
G7	0	0.25	0.5	0.485059	0.46981	0.459443	0.537634	0.43047	0.595238
GTWIN	0.355705	0.346711	0.339805	0.45116	0.451979	0.453017	0.445785	0.438719	0.43661
GYPSY	0.529042	0.511364	0.508874	0.443184	0.447256	0.444027	0.43131	0.421924	0.41853
Gypsy1	0.631501	0.603072	0.617154	0.393217	0.38813	0.387671	0.433506	0.438835	0.451228
GYPSY10	0.397472	0.433107	0.477453	0.563234	0.564511	0.57082	0.605896	0.595156	0.612575
GYPSY11	0.481503	0.514367	0.598344	0.574743	0.555079	0.527459	0.508021	0.518679	0.515935
GYPSY12	0.251854	0.230068	0.268047	0.442844	0.436011	0.429717	0.41161	0.406521	0.397384
Gypsy2	0.349155	0.351119	0.354614	0.417113	0.411489	0.405186	0.392208	0.39904	0.398795
GYPSY2	0.424443	0.418499	0.441679	0.410834	0.410301	0.402499	0.403547	0.394388	0.397401

GYPSY3	0.576972	0.567676	0.563557	0.394668	0.392376	0.38057	0.398863	0.380956	0.396719
GYPSY4	0.434224	0.452842	0.420882	0.416726	0.41452	0.421162	0.412225	0.420026	0.425559
GYPSY5	0.435841	0.386918	0.400385	0.484451	0.480501	0.473577	0.501426	0.499819	0.49016
GYPSY6	0.51412	0.520431	0.517497	0.43392	0.434913	0.426128	0.447981	0.462141	0.474313
GYPSY6A	0.530642	0.474211	0.494699	0.510104	0.529654	0.548252	0.511438	0.487398	0.492408
GYPSY7	0.421128	0.403345	0.431579	0.514571	0.488476	0.501612	0.489794	0.515032	0.51939
GYPSY8	0.218627	0.182959	0.338735	0.29219	0.306082	0.305509	0.256823	0.266388	0.272863
GYPSY9	0.484653	0.376289	0.43617	0.411693	0.420144	0.423228	0.429261	0.456313	0.470677
HELENA_RT	0.470153	0.41385	0.568656	0.491187	0.511314	0.504545	0.516709	0.516671	0.532949
HETA	0.301795	0.302181	0.31473	0.32097	0.319533	0.312002	0.298093	0.296248	0.292601
HETRP	0.274025	0.276231	0.285565	0.333701	0.341193	0.321313	0.341043	0.332449	0.341562
HMR1	0.271994	0.282051	0.179167	0.341247	0.301545	0.324535	0.355073	0.358559	0.339845
HMR2	0.295049	0.307632	0.341761	0.327241	0.325695	0.304892	0.324512	0.318241	0.31519
HMSBEAGLE	0.207562	0.231229	0.227755	0.448813	0.443584	0.449216	0.388501	0.398419	0.391968
HOBO	0.466609	0.392292	0.420124	0.420673	0.417531	0.400893	0.43011	0.452864	0.441598
I	0.421421	0.455832	0.474222	0.481599	0.483593	0.47827	0.475011	0.453668	0.454345
IDEFIX	0.446631	0.439637	0.454643	0.432142	0.43294	0.435514	0.424461	0.431117	0.435092
INVADER1	0.179351	0.185697	0.191761	0.381936	0.384306	0.378556	0.379548	0.381941	0.3836
INVADER2	0.419086	0.414413	0.40937	0.5383	0.549152	0.55048	0.548197	0.537794	0.547038
INVADER3	0.330237	0.337445	0.339976	0.432574	0.416567	0.404736	0.397942	0.421705	0.404049
INVADER4	0.497713	0.500735	0.512347	0.439159	0.427183	0.425638	0.437984	0.425799	0.403482
INVADER5	0.453846	0.366667	0.1	0.519388	0.481644	0.518972	0.496515	0.307618	0.346041
INVADER6	0.379729	0.404598	0.462647	0.533084	0.522702	0.525203	0.520519	0.499634	0.495567
IVK	0.404608	0.352597	0.425236	0.436574	0.432929	0.448499	0.405278	0.411586	0.413651
Jockey	0.3065	0.307672	0.379726	0.438545	0.430839	0.430748	0.38812	0.375251	0.366036
JOCKEY2	0.355265	0.33275	0.407946	0.41903	0.431947	0.427353	0.430104	0.38231	0.42753
LOOPER1	0.372378	0.364618	0.263547	0.399091	0.406985	0.42906	0.370182	0.391203	0.366442
MARINER2	0.563929	0.305085	0.296296	0.495977	0.505196	0.515543	0.451718	0.547915	0.532081
MAX	0.277296	0.265481	0.268097	0.329454	0.330696	0.325175	0.31868	0.311635	0.317549

MDG1	0.480134	0.497213	0.490006	0.476887	0.474448	0.473247	0.467719	0.475182	0.48383
MDG3	0.325901	0.315064	0.353151	0.47325	0.477766	0.476876	0.457039	0.457188	0.439287
MICROPIA	0.269393	0.281395	0.285543	0.432967	0.433378	0.428973	0.445502	0.444655	0.448565
NOMAD	0.380208	0.39906	0.413403	0.460419	0.475566	0.472146	0.4633	0.440332	0.43494
NTS	0.237829	0.276168	0.262375	0.287193	0.293101	0.308211	0.343676	0.32481	0.319664
POGO	0.385195	0.346515	0.362554	0.45462	0.470702	0.46213	0.452467	0.456845	0.4566
PROTOP	0.228561	0.225238	0.238951	0.350085	0.336677	0.338929	0.341315	0.338185	0.32898
QUASIMODO	0.444345	0.466857	0.480696	0.5613	0.546155	0.538492	0.528952	0.525992	0.51876
QUASIMODO2	0.467909	0.459672	0.462483	0.447575	0.440532	0.438939	0.449834	0.45087	0.445309
R1	0.345591	0.340612	0.349833	0.340443	0.348294	0.349121	0.353858	0.339431	0.341548
R1-2	0.253695	0.239519	0.242402	0.255029	0.24586	0.248013	0.232682	0.232603	0.261943
R2	0.308838	0.346613	0.382021	0.400584	0.416468	0.381589	0.40168	0.415615	0.407711
ROO	0.395041	0.409099	0.402789	0.44458	0.446428	0.458027	0.42445	0.424073	0.418087
ROOA	0.363771	0.324309	0.359461	0.405309	0.410732	0.417895	0.415054	0.419228	0.419373
ROVER	0.470193	0.4493	0.454769	0.509546	0.514032	0.528039	0.513095	0.495744	0.515254
RSP	0.070098	0.055717	0.072522	0.205745	0.22379	0.213771	0.222462	0.209095	0.178463
RT1A	0.239643	0.275022	0.287042	0.363185	0.359831	0.361536	0.333544	0.323923	0.315591
RT1B	0.276497	0.274963	0.28756	0.28031	0.277558	0.28109	0.258487	0.258914	0.249307
RT1C	0.24536	0.259297	0.240877	0.323713	0.325912	0.346917	0.286631	0.282986	0.267923
S	0.342025	0.304437	0.323069	0.437192	0.420919	0.411377	0.377451	0.376886	0.358782
S2	0.457317	0.469188	0.348739	0.468902	0.468607	0.466171	0.521116	0.459419	0.518707
SAR	0.308638	0.353204	0.363621	0.409314	0.43091	0.385884	0.43157	0.410932	0.374405
SAR2	0.436159	0.446437	0.44143	0.579369	0.593585	0.588983	0.541771	0.522371	0.54535
SAT6	0	0	0	0.332895	0.344949	0.403689	0.246173	0.314815	0.399123
STALKER2	0.498648	0.490705	0.491025	0.477131	0.492374	0.474832	0.44156	0.463508	0.44063
STALKER3	0.445564	0.438544	0.528292	0.393484	0.406477	0.402811	0.37396	0.414626	0.384794
STALKER4	0.483009	0.48275	0.478884	0.528956	0.53143	0.530771	0.493936	0.497613	0.500887
TABOR	0.343079	0.326347	0.329359	0.492382	0.500986	0.481149	0.47108	0.483445	0.535789
TAHRE	0.193913	0.181045	0.196982	0.366454	0.369805	0.370169	0.356276	0.357399	0.353796

TART	0.340557	0.347222	0.339485	0.481521	0.491863	0.495783	0.491953	0.464059	0.469406
TC1	0.345563	0.371009	0.487132	0.433416	0.404501	0.397724	0.417635	0.391192	0.426106
TC1-2	0.569227	0.455478	0.414695	0.42141	0.394947	0.413171	0.392776	0.404334	0.408895
TIRANT	0.244879	0.204184	0.163883	0.279061	0.273055	0.298561	0.289611	0.361192	0.322244
TLD1	0.166667	0.5	0	0.7378	0.77044	0.74561	0.715909	0.803697	0.819444
TLD2	0.618429	0.719187	0.525332	0.397735	0.41075	0.511801	0.465471	0.464167	0.390276
TOM1	0.358766	0.457265	0.472222	0.5745	0.562145	0.52032	0.62077	0.551106	0.660027
Transib-N1	0.5	0	0.5	0.369919	0.769048	0.47318	0.865591	0.852459	0.35
Transib1	0.377231	0.275463	0.520243	0.583996	0.586949	0.572017	0.611971	0.602874	0.605962
TRANSIB2	0.409377	0.403318	0.410378	0.471768	0.471329	0.469677	0.458132	0.479011	0.463011
TRANSIB3	0.497992	0.444444	0.540441	0.534258	0.54385	0.52984	0.526194	0.546766	0.511817
Transib4	0.469831	0.366667	0.492063	0.473858	0.433735	0.436812	0.498205	0.32958	0.46875
Transib5	0.472579	0.435658	0.466583	0.449357	0.440148	0.455026	0.403647	0.403576	0.412483
TRANSPAC	0.393716	0.410866	0.403481	0.458661	0.454503	0.455867	0.449934	0.446367	0.447981
ZAM	0.461862	0.424111	0.467724	0.538772	0.533897	0.526565	0.543054	0.516228	0.54258

Table A2.8 Protein-coding genes that are differentially regulated by transgenes as compared to the mutant.

genes that are differentially regulated by <i>D. mel aub</i> as compared to <i>mut</i>			genes that are down regulated by <i>D. mel aub</i> as compared to <i>mut</i>			genes that are differentially regulated by <i>D. sim aub</i> as compared to <i>mut</i>			genes that are down regulated by <i>D. sim aub</i> as compared to <i>mut</i>		
gene	log2FoldC hange	padj	gene	log2Fold Change	padj	gene	log2FoldC hange	padj	gene	log2Fold Change	padj
FBgn000 0003	2.026451	1.57E- 09	FBgn00 00044	-1.38415	3.05E -06	FBgn000 0044	-1.26411	2.61E- 05	FBgn00 00044	-1.26411	2.61E -05
FBgn000 0044	-1.38415	3.05E- 06	FBgn00 00100	-0.86636	4.02E -05	FBgn000 0100	-0.67974	0.003 522	FBgn00 00100	-0.67974	0.003 522
FBgn000 0100	-0.86636	4.02E- 05	FBgn00 00299	-1.39985	7.06E -10	aub	1.340624	4.79E- 09	FBgn00 00299	-1.52698	5.07E -12
aub	1.562345	4.96E- 12	FBgn00 00355	-1.31478	4.96E -12	FBgn000 0299	-1.52698	5.07E- 12	FBgn00 00355	-1.32307	2.04E -12
FBgn000 0299	-1.39985	7.06E- 10	FBgn00 00356	-1.61131	2.65E -12	FBgn000 0355	-1.32307	2.04E- 12	FBgn00 00356	-1.6161	1.30E -12
FBgn000 0355	-1.31478	4.96E- 12	FBgn00 00357	-0.87318	0.000 175	FBgn000 0356	-1.6161	1.30E- 12	FBgn00 00357	-1.01131	3.80E -06
FBgn000 0356	-1.61131	2.65E- 12	FBgn00 00358	-1.72375	1.54E -18	FBgn000 0357	-1.01131	3.80E- 06	FBgn00 00358	-1.98891	3.56E -25
FBgn000 0357	-0.87318	0.000 175	FBgn00 00359	-0.87334	3.55E -05	FBgn000 0358	-1.98891	3.56E- 25	FBgn00 00360	-0.77663	0.000 293
FBgn000 0358	-1.72375	1.54E- 18	FBgn00 00360	-0.93021	5.10E -06	FBgn000 0360	-0.77663	0.000 293	FBgn00 02526	-0.72992	0.009 689
FBgn000 0359	-0.87334	3.55E- 05	FBgn00 02590	-0.66594	0.014 425	FBgn000 2526	-0.72992	0.009 689	FBgn00 02590	-0.63332	0.018 189
FBgn000 0360	-0.93021	5.10E- 06	FBgn00 02773	-1.78088	0.000 204	FBgn000 2590	-0.63332	0.018 189	FBgn00 02773	-1.39182	0.009 136
FBgn000 2590	-0.66594	0.014 425	FBgn00 02868	-1.33129	0.028 34	FBgn000 2773	-1.39182	0.009 136	FBgn00 03053	-0.84148	0.022 337
FBgn000 2773	-1.78088	0.000 204	FBgn00 03137	-1.65899	4.58E -05	FBgn000 2791	0.840797	0.003 735	FBgn00 03137	-2.02079	2.01E -07
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FBgn000 3137	-1.65899	4.58E- 05	FBgn00 03517	-1.08734	4.90E -08	FBgn000 3149	-1.50412	0.011 949	FBgn00 03285	-3.24747	6.78E -22
FBgn000 3274	-0.63996	0.013 315	FBgn00 03979	-1.01923	2.13E -06	FBgn000 3279	-0.6521	0.005 449	FBgn00 03517	-0.98384	9.80E -07
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FBgn000 3979	-1.01923	2.13E- 06	FBgn00 04169	-1.35489	0.016 63	FBgn000 3979	-1.13038	4.44E- 08	FBgn00 03983	-1.09684	4.36E -07
FBgn000 3980	-1.16322	2.78E- 07	FBgn00 04647	-0.60038	0.043 874	FBgn000 3980	-1.27784	4.83E- 09	FBgn00 03997	-1.10991	0.014 354
FBgn000 3983	-0.96252	2.29E- 05	FBgn00 04867	-0.92983	5.37E -06	FBgn000 3983	-1.09684	4.36E- 07	FBgn00 04117	-1.56712	0.021 204
FBgn000 4169	-1.35489	0.016 63	FBgn00 05666	-1.23245	5.39E -05	FBgn000 3997	-1.10991	0.014 354	FBgn00 04169	-1.35135	0.012 984
FBgn000 4647	-0.60038	0.043 874	FBgn00 10051	-0.63912	0.033 073	FBgn000 4117	-1.56712	0.021 204	FBgn00 04647	-0.6135	0.024 436
FBgn000 4867	-0.92983	5.37E- 06	FBgn00 11828	-2.28666	0.001 494	FBgn000 4169	-1.35135	0.012 984	FBgn00 04654	-0.72601	0.016 891
FBgn000 5666	-1.23245	5.39E- 05	FBgn00 13275	-1.96712	3.00E -14	FBgn000 4647	-0.6135	0.024 436	FBgn00 04867	-0.82134	9.21E -05
FBgn001 0051	-0.63912	0.033 073	FBgn00 13276	-1.98272	2.44E -14	FBgn000 4654	-0.72601	0.016 891	FBgn00 05666	-1.62245	1.18E -08
FBgn001 1642	0.980912	0.000 441	FBgn00 13277	-2.31643	8.87E -06	FBgn000 4867	-0.82134	9.21E- 05	FBgn00 10051	-1.17284	5.06E -08
FBgn001 1828	-2.28666	0.001 494	FBgn00 13278	-2.32676	3.80E -05	FBgn000 5666	-1.62245	1.18E- 08	FBgn00 11828	-2.46234	0.000 419
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FBgn001 3276	-1.98272	2.44E- 14	FBgn00 13680	-1.02004	0.000 285	FBgn001 1642	1.252305	8.11E- 07	FBgn00 13276	-1.3018	1.48E -06

FBgn001 3277	-2.31643	8.87E- 06	FBgn00 13681	-0.90217	0.000 453	FBgn001 1828	-2.46234	0.000 419	FBgn00 13277	-1.8461	0.000 806
FBgn001 3278	-2.32676	3.80E- 05	FBgn00 14076	-1.20272	2.06E -05	FBgn001 3275	-1.30251	1.47E- 06	FBgn00 13278	-1.83391	0.002 614
FBgn001 3279	-2.25745	7.00E- 05	FBgn00 15288	-0.65729	0.037 966	FBgn001 3276	-1.3018	1.48E- 06	FBgn00 13279	-1.76328	0.004 566
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FBgn001 4466	0.940476	0.000 579	FBgn00 26255	-3.18407	0.006 799	FBgn001 3680	-0.93236	0.001 289	FBgn00 14464	-0.88248	0.000 958
FBgn001 5288	-0.65729	0.037 966	FBgn00 26372	-0.5925	0.028 34	FBgn001 3688	0.820201	0.001 928	FBgn00 15245	-0.61359	0.015 539
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FBgn001 7448	0.789235	0.035 604	FBgn00 28490	-0.79802	0.028 34	FBgn001 4076	-1.04088	0.000 419	FBgn00 16123	-0.94033	0.001 111
FBgn002 4183	-0.87452	0.001 839	FBgn00 30040	-1.51183	0.012 938	FBgn001 4464	-0.88248	0.000 958	FBgn00 21906	-0.6855	0.047 261
FBgn002 5777	-0.6943	0.023 115	FBgn00 31913	-0.80661	0.032 042	FBgn001 4466	1.626338	4.23E- 12	FBgn00 24183	-0.74972	0.013 275
FBgn002 6255	-3.18407	0.006 799	FBgn00 32788	-1.1157	1.27E -05	FBgn001 5245	-0.61359	0.015 539	FBgn00 26255	-3.2018	0.005 554
FBgn002 6372	-0.5925	0.028 34	FBgn00 32789	-0.93018	0.000 211	FBgn001 5568	0.947693	0.029 278	FBgn00 26372	-0.75825	0.000 547
FBgn002 7341	-3.6084	6.31E- 05	FBgn00 33188	-1.59699	0.000 214	FBgn001 6075	-1.37478	3.27E- 09	FBgn00 27341	-3.33662	0.000 268
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FBgn002 8743	1.757225	1.23E- 05	FBgn00 33958	-2.5651	2.00E -11	FBgn002 4183	-0.74972	0.013 275	FBgn00 28490	-0.86882	0.007 226
FBgn003 0040	-1.51183	0.012 938	FBgn00 35422	-0.6919	0.004 501	FBgn002 6255	-3.2018	0.005 554	FBgn00 29840	-0.71257	0.006 16
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FBgn003 3926	-1.22071	1.98E- 06	FBgn00 38290	-3.67576	0.006 57	FBgn002 8743	1.594633	9.97E- 05	FBgn00 32789	-1.1281	1.37E -06
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FBgn003 3958	-2.5651	2.00E- 11	FBgn00 41709	-0.94348	0.001 797	FBgn003 0040	-1.29604	0.047 392	FBgn00 33926	-1.24373	8.08E -07
FBgn003 4075	0.979308	0.047 776	FBgn00 50345	-4.24696	5.48E -38	FBgn003 0174	-0.80887	0.008 378	FBgn00 33927	-1.14265	0.001 202
FBgn003 4999	0.733052	0.041 025	FBgn00 51202	-5.52048	0.000 251	FBgn003 0266	-0.60057	0.033 747	FBgn00 33958	-2.23692	4.83E -09
FBgn003 5422	-0.6919	0.004 501	FBgn00 51354	-2.43535	2.37E -05	FBgn003 1913	-0.80195	0.023 684	FBgn00 34479	-6.57063	0.025 312
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FBgn003 5880	-2.4639	5.60E- 05	FBgn00 51926	-1.56999	8.17E -05	FBgn003 2788	-1.43267	2.47E- 09	FBgn00 35542	-1.11264	0.000 861
FBgn003 6213	-0.7906	0.000 264	FBgn00 51928	-1.3887	2.88E -07	FBgn003 2789	-1.1281	1.37E- 06	FBgn00 36279	-0.70819	0.025 617

FBgn003 7229	-5.19033	0.025 776	FBgn00 51988	-6.66838	0.047 463	FBgn003 2889	1.005175	0.029 908	FBgn00 36652	-7.50352	6.60E -07
FBgn003 7351	-0.82838	0.000 172	FBgn00 52602	-1.13318	1.24E -08	FBgn003 3000	1.768356	3.99E- 14	FBgn00 36663	-0.66323	0.015 993
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FBgn003 9936	0.67688	0.004 596	FBgn00 86265	-0.97605	0.001 452	FBgn003 3926	-1.24373	8.08E- 07	FBgn00 37351	-1.08904	5.52E -08
FBgn003 9959	0.691636	0.002 801	FBgn00 86408	-1.15233	0.038 635	FBgn003 3927	-1.14265	0.001 202	FBgn00 37409	-4.04194	0.000 861
FBgn003 9993	0.747731	0.014 425	FBgn00 86906	-1.22241	0.002 025	FBgn003 3958	-2.23692	4.83E- 09	FBgn00 37645	-4.58693	0.000 806
FBgn004 1252	-1.05221	0.000 579	FBgn02 50907	-2.47594	1.27E -05	FBgn003 4479	-6.57063	0.025 312	FBgn00 38290	-4.02547	0.002 081
FBgn004 1709	-0.94348	0.001 797	FBgn02 61258	-1.06955	0.006 633	FBgn003 4999	0.885202	0.002 755	FBgn00 38881	-1.47694	0.018 842
FBgn004 4510	1.013972	1.26E- 05	FBgn02 61563	-1.42686	0.016 564	FBgn003 5422	-0.59792	0.021 226	FBgn00 39155	-1.4966	0.021 959
FBgn005 0345	-4.24696	5.48E- 38	FBgn02 62608	-0.97934	4.28E -06	FBgn003 5542	-1.11264	0.000 861	FBgn00 39257	-2.68057	0.031 158
FBgn005 0440	0.853025	0.001 669	FBgn02 63219	-0.82235	0.028 34	FBgn003 5642	0.722019	0.039 654	FBgn00 39635	-0.66828	0.042 028
FBgn005 1202	-5.52048	0.000 251	FBgn02 64695	-1.83992	6.90E -10	FBgn003 5976	1.896763	2.58E- 05	FBgn00 39713	-0.59106	0.018 907
FBgn005 1354	-2.43535	2.37E- 05	FBgn02 64894	-1.16575	0.021 36	FBgn003 5999	1.065582	0.009 689	FBgn00 39776	-1.13809	0.015 675
FBgn005 1661	-1.65193	2.77E- 06	FBgn02 67001	-2.36758	1.01E -07	FBgn003 6279	-0.70819	0.025 617	FBgn00 41180	-0.93403	0.023 684
FBgn005 1926	-1.56999	8.17E- 05	FBgn02 67033	-0.79395	0.033 925	FBgn003 6652	-7.50352	6.60E- 07	FBgn00 41252	-1.17159	5.51E -05

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FBgn005 1988	-6.66838	0.047 463	FBgn02 84408	-0.95807	1.45E -05	FBgn003 6734	-0.91692	0.002 755	FBgn00 51202	-5.57063	0.000 293
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FBgn008 5362	-1.00652	2.20E- 06				FBgn003 7351	-1.08904	5.52E- 08	FBgn00 51928	-1.25867	3.85E -06
FBgn008 5753	0.873945	2.39E- 05				FBgn003 7409	-4.04194	0.000 861	FBgn00 52311	-1.44295	0.039 654
FBgn008 5771	0.985944	7.98E- 07				FBgn003 7645	-4.58693	0.000 806	FBgn00 52602	-1.30894	7.91E -12
FBgn008 5810	0.969227	0.010 603				FBgn003 8290	-4.02547	0.002 081	FBgn00 53196	-2.2029	0.006 113
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FBgn008 6265	-0.97605	0.001 452				FBgn003 9257	-2.68057	0.031 158	FBgn00 85362	-0.91978	1.89E -05
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FBgn008 6906	-1.22241	0.002 025				FBgn003 9635	-0.66828	0.042 028	FBgn00 86355	-0.61623	0.024 436
FBgn025 0907	-2.47594	1.27E- 05				FBgn003 9713	-0.59106	0.018 907	FBgn00 86708	-1.6525	0.007 237
FBgn026 1258	-1.06955	0.006 633				FBgn003 9776	-1.13809	0.015 675	FBgn00 86906	-1.94893	1.20E -08
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FBgn026 1563	-1.42686	0.016 564					FBgn003 9936	0.63754	0.008 054	FBgn02 61258	-1.03058	0.008 378
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FBgn026 2608	-0.97934	4.28E- 06					FBgn004 1180	-0.93403	0.023 684	FBgn02 61617	-0.61709	0.010 301
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FBgn026 4894	-1.16575	0.021 36					FBgn005 0345	-4.18836	5.78E- 37	FBgn02 62109	-0.61549	0.013 738
FBgn026 7001	-2.36758	1.01E- 07					FBgn005 0440	0.979732	9.02E- 05	FBgn02 62160	-0.92426	0.000 806
FBgn026 7033	-0.79395	0.033 925					FBgn005 1202	-5.57063	0.000 293	FBgn02 62608	-0.89468	3.45E -05
FBgn026 7508	1.007752	7.70E- 07					FBgn005 1354	-1.95577	0.001 355	FBgn02 63219	-1.25444	1.30E -05
FBgn026 7511	0.968464	9.86E- 07					FBgn005 1661	-1.5473	1.29E- 05	FBgn02 63705	-0.97054	0.006 342
FBgn026 7515	0.680117	0.030 386					FBgn005 1926	-1.2926	0.002 666	FBgn02 64695	-1.81929	7.35E -10
FBgn026 7519	0.842001	6.60E- 05					FBgn005 1928	-1.25867	3.85E- 06	FBgn02 65045	-1.36222	0.046 375
FBgn026 7520	1.001239	1.56E- 06					FBgn005 2311	-1.44295	0.039 654	FBgn02 65991	-0.87474	0.017 178
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FBgn028 3427	-0.62891	0.028 34					FBgn005 3196	-2.2029	0.006 113	FBgn02 67033	-0.88928	0.006 342
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						FBgn005 8160	0.734234	0.018 251	FBgn02 84408	-1.24703	1.55E -09
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						FBgn005 8263	0.694645	0.028 128			
						FBgn008 5362	-0.91978	1.89E- 05			
						FBgn008 5753	0.607786	0.013 453			
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						FBgn008 5810	1.214209	0.000 171			
						FBgn008 5813	0.855167	2.58E- 05			
						FBgn008 5819	0.845477	4.12E- 05			
						FBgn008 6265	-0.84262	0.010 069			
						FBgn008 6355	-0.61623	0.024 436			
						FBgn008 6708	-1.6525	0.007 237			
						FBgn008 6906	-1.94893	1.20E- 08			
						FBgn025 0830	0.626723	0.032 859			
						FBgn025 0907	-2.91636	1.61E- 07			
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						FBgn026 1563	-1.52555	0.005 526				
						FBgn026 1617	-0.61709	0.010 301				
						FBgn026 1639	1.239297	0.000 456				
						FBgn026 1640	1.272997	0.000 469				
						FBgn026 1797	-0.7422	0.000 74				
						FBgn026 1836	-0.96739	0.000 182				
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						FBgn026 2608	-0.89468	3.45E- 05				
						FBgn026 3219	-1.25444	1.30E- 05				
						FBgn026 3705	-0.97054	0.006 342				
						FBgn026 4695	-1.81929	7.35E- 10				
						FBgn026 5045	-1.36222	0.046 375				
						FBgn026 5991	-0.87474	0.017 178				
						FBgn026 6347	0.992316	0.003 129				

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							FBgn026 7033	-0.88928	0.006 342				
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							FBgn026 7508	0.845208	6.03E- 05				
							FBgn026 7511	0.819984	6.03E- 05				
							FBgn026 7519	0.586614	0.021 226				
							FBgn026 7520	0.836799	0.000 113				
							FBgn026 7861	1.161361	2.38E- 06				
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							FBgn028 4408	-1.24703	1.55E- 09				
							FBgn028 5955	-0.92857	0.022 37				

genes that are differentially regulated by <i>D. mel</i> <i>spnE</i> as compared to <i>mut</i>			genes that are down regulated by <i>D. mel</i> <i>spnE</i> as compared to <i>mut</i>			genes that are differentially regulated by <i>D. sim</i> <i>spnE</i> as compared to <i>mut</i>			genes that are down regulated by <i>D. sim</i> <i>spnE</i> as compared to <i>mut</i>		
gene	log2FoldC hange	padj	gene	log2Fold Change	padj	gene	log2FoldC hange	padj	gene	log2Fold Change	padj
FBgn00 00075	0.769284	0.006 797	FBgn00 00246	-0.60719	0.00 2737	FBgn00 00003	-0.60197	0.005 254	FBgn00 00003	-0.60197	0.005 254
FBgn00 00166	0.687668	1.39E -16	FBgn00 00274	-0.69676	0.00 9695	FBgn00 00018	0.598351	9.53E -09	FBgn00 00083	-0.60882	6.66E -16
FBgn00 00246	-0.60719	0.002 737	FBgn00 00395	-0.93531	0.00 0778	FBgn00 00075	0.842524	0.002 509	FBgn00 00320	-0.88008	9.79E -08

FBgn00 00274	-0.69676	0.009 695		FBgn00 00416	-0.60485	8.86 E-07	FBgn00 00083	-0.60882	6.66E -16		FBgn00 00395	-1.11917	4.91E -05
FBgn00 00351	0.765515	5.94E -09		FBgn00 00427	-0.65705	0.00 032	FBgn00 00166	0.814611	3.80E -23		FBgn00 00490	-0.72981	0.009 515
FBgn00 00395	-0.93531	0.000 778		FBgn00 00489	-0.58819	0.00 133	FBgn00 00320	-0.88008	9.79E -08		FBgn00 00504	-0.97848	0.000 694
FBgn00 00416	-0.60485	8.86E -07		FBgn00 00490	-1.04236	0.00 0204	FBgn00 00395	-1.11917	4.91E -05		FBgn00 00592	-1.7683	2.08E -08
FBgn00 00427	-0.65705	0.000 32		FBgn00 00504	-0.86987	0.00 2911	FBgn00 00490	-0.72981	0.009 515		FBgn00 00633	-1.69724	0.000 262
FBgn00 00489	-0.58819	0.001 33		FBgn00 00567	-0.6003	0.00 226	FBgn00 00504	-0.97848	0.000 694		FBgn00 00636	-1.71103	1.33E -54
FBgn00 00490	-1.04236	0.000 204		FBgn00 00592	-1.25049	4.86 E-05	FBgn00 00592	-1.7683	2.08E -08		FBgn00 00928	-1.06815	1.71E -05
FBgn00 00504	-0.86987	0.002 911		FBgn00 00633	-1.77165	0.00 0142	FBgn00 00633	-1.69724	0.000 262		FBgn00 01123	-0.63678	0.000 332
FBgn00 00567	-0.6003	0.002 26		FBgn00 00635	-0.78749	7.04 E-11	FBgn00 00636	-1.71103	1.33E -54		FBgn00 01145	-0.97077	2.13E -05
FBgn00 00592	-1.25049	4.86E -05		FBgn00 00636	-1.72751	1.31 E-55	FBgn00 00928	-1.06815	1.71E -05		FBgn00 01168	-0.66935	0.000 511
FBgn00 00633	-1.77165	0.000 142		FBgn00 01123	-0.87485	4.15 E-07	FBgn00 01123	-0.63678	0.000 332		FBgn00 01217	-0.75712	0.001 194
FBgn00 00635	-0.78749	7.04E -11		FBgn00 01145	-0.94349	3.98 E-05	FBgn00 01145	-0.97077	2.13E -05		FBgn00 01224	-1.4948	1.68E -11
FBgn00 00636	-1.72751	1.31E -55		FBgn00 01168	-0.84822	7.21 E-06	FBgn00 01168	-0.66935	0.000 511		FBgn00 01230	-1.00107	0.000 17
FBgn00 00826	0.784652	1.06E -07		FBgn00 01217	-0.59036	0.01 3949	FBgn00 01217	-0.75712	0.001 194		FBgn00 01257	-0.66908	0.000 234
FBgn00 00927	0.616568	9.46E -06		FBgn00 01224	-1.32439	2.87 E-09	FBgn00 01224	-1.4948	1.68E -11		FBgn00 01296	-0.64902	1.28E -07
FBgn00 01123	-0.87485	4.15E -07		FBgn00 01230	-1.0388	0.00 0102	FBgn00 01230	-1.00107	0.000 17		FBgn00 02609	-1.45957	1.44E -12
FBgn00 01145	-0.94349	3.98E -05		FBgn00 01257	-0.99074	1.59 E-08	FBgn00 01257	-0.66908	0.000 234		FBgn00 02716	-1.95965	1.15E -13

FBgn00 01168	-0.84822	7.21E -06		FBgn00 01296	-0.59342	1.75 E-06	FBgn00 01296	-0.64902	1.28E -07	FBgn00 02733	-1.58435	2.71E -10
FBgn00 01217	-0.59036	0.013 949		FBgn00 01297	-0.77108	4.33 E-10	FBgn00 01301	0.623056	9.34E -10	FBgn00 02772	-0.59452	0.008 254
FBgn00 01224	-1.32439	2.87E -09		FBgn00 01624	-0.59329	6.32 E-07	FBgn00 02466	0.612194	3.85E -10	FBgn00 02773	-0.9757	4.68E -17
FBgn00 01225	0.65163	4.21E -06		FBgn00 01987	-0.6108	6.72 E-08	FBgn00 02609	-1.45957	1.44E -12	FBgn00 02789	-0.97903	4.89E -09
FBgn00 01230	-1.0388	0.000 102		FBgn00 02609	-1.2342	1.43 E-09	FBgn00 02716	-1.95965	1.15E -13	FBgn00 02868	-1.86794	2.27E -46
FBgn00 01257	-0.99074	1.59E -08		FBgn00 02716	-1.98198	7.66 E-14	FBgn00 02733	-1.58435	2.71E -10	FBgn00 03053	-0.63774	3.34E -07
FBgn00 01296	-0.59342	1.75E -06		FBgn00 02733	-1.62416	1.34 E-10	FBgn00 02772	-0.59452	0.008 254	FBgn00 03089	-1.39135	2.07E -13
FBgn00 01297	-0.77108	4.33E -10		FBgn00 02772	-0.67059	0.00 2863	FBgn00 02773	-0.9757	4.68E -17	FBgn00 03137	-1.16017	4.45E -16
FBgn00 01624	-0.59329	6.32E -07		FBgn00 02773	-0.71438	1.05 E-09	FBgn00 02789	-0.97903	4.89E -09	FBgn00 03285	-0.65233	1.69E -08
FBgn00 01987	-0.6108	6.72E -08		FBgn00 02789	-0.76814	6.33 E-06	FBgn00 02868	-1.86794	2.27E -46	FBgn00 03301	-0.81619	1.69E -06
FBgn00 02609	-1.2342	1.43E -09		FBgn00 02868	-1.64326	2.07 E-36	FBgn00 03053	-0.63774	3.34E -07	FBgn00 03308	-0.99345	4.12E -07
FBgn00 02716	-1.98198	7.66E -14		FBgn00 03053	-0.67441	6.20 E-08	FBgn00 03089	-1.39135	2.07E -13	FBgn00 03328	-1.16689	2.27E -22
FBgn00 02733	-1.62416	1.34E -10		FBgn00 03089	-1.86365	2.84 E-21	FBgn00 03137	-1.16017	4.45E -16	FBgn00 03366	-1.18529	2.04E -23
FBgn00 02772	-0.67059	0.002 863		FBgn00 03137	-0.70471	1.43 E-06	FBgn00 03209	0.600207	1.65E -06	FBgn00 03388	-1.68906	2.87E -06
FBgn00 02773	-0.71438	1.05E -09		FBgn00 03285	-0.74411	9.25 E-11	FBgn00 03285	-0.65233	1.69E -08	FBgn00 03731	-0.76519	2.40E -06
FBgn00 02789	-0.76814	6.33E -06		FBgn00 03308	-0.66045	0.00 099	FBgn00 03292	0.807177	6.94E -21	FBgn00 03867	-0.59315	0.027 53
FBgn00 02868	-1.64326	2.07E -36		FBgn00 03328	-1.39725	1.12 E-31	FBgn00 03301	-0.81619	1.69E -06	FBgn00 03888	-0.98591	2.39E -15

FBgn00 03053	-0.67441	6.20E -08		FBgn00 03366	-1.02003	8.79 E-18	FBgn00 03308	-0.99345	4.12E -07	FBgn00 03916	-0.70899	0.001 435
FBgn00 03089	-1.86365	2.84E -21		FBgn00 03388	-1.42311	7.88 E-05	FBgn00 03328	-1.16689	2.27E -22	FBgn00 03996	-2.337	1.52E -12
FBgn00 03137	-0.70471	1.43E -06		FBgn00 03486	-0.75019	0.00 0326	FBgn00 03353	0.645272	8.80E -06	FBgn00 03997	-0.62434	0.002 29
FBgn00 03285	-0.74411	9.25E -11		FBgn00 03731	-0.91172	1.22 E-08	FBgn00 03366	-1.18529	2.04E -23	FBgn00 04117	-0.8266	3.59E -08
FBgn00 03292	0.759678	1.56E -18		FBgn00 03867	-0.65206	0.01 6239	FBgn00 03388	-1.68906	2.87E -06	FBgn00 04133	-0.80998	8.24E -13
FBgn00 03308	-0.66045	0.000 99		FBgn00 03888	-1.24917	6.05 E-24	FBgn00 03450	0.714693	2.51E -05	FBgn00 04169	-0.74805	3.79E -06
FBgn00 03328	-1.39725	1.12E -31		FBgn00 03996	-2.01639	3.83 E-10	spnE	3.468795	0	FBgn00 04183	-0.99194	3.46E -06
FBgn00 03366	-1.02003	8.79E -18		FBgn00 03997	-0.91028	4.52 E-06	FBgn00 03731	-0.76519	2.40E -06	FBgn00 04185	-0.71535	0.028 03
FBgn00 03388	-1.42311	7.88E -05		FBgn00 04055	-0.75142	4.79 E-09	FBgn00 03867	-0.59315	0.027 53	FBgn00 04186	-0.74792	0.018 615
FBgn00 03450	0.875137	1.19E -07		FBgn00 04117	-0.80603	8.40 E-08	FBgn00 03888	-0.98591	2.39E -15	FBgn00 04191	-0.71886	0.000 822
FBgn00 03464	0.619236	1.39E -05		FBgn00 04169	-0.62255	0.00 0158	FBgn00 03916	-0.70899	0.001 435	FBgn00 04456	-0.73465	4.25E -08
FBgn00 03480	0.71978	0.000 651		FBgn00 04456	-0.84578	2.17 E-10	FBgn00 03950	0.992519	0.001 084	FBgn00 04512	-1.12955	0.003 157
spnE	3.179953	3.55E -280		FBgn00 04512	-1.41811	0.00 0211	FBgn00 03996	-2.337	1.52E -12	FBgn00 04852	-0.82421	0.001 054
FBgn00 03486	-0.75019	0.000 326		FBgn00 04646	-0.80634	7.88 E-08	FBgn00 03997	-0.62434	0.002 29	FBgn00 04858	-0.61308	0.005 27
FBgn00 03567	0.663092	3.89E -18		FBgn00 04666	-0.59209	0.00 0245	FBgn00 04034	1.050404	0.002 919	FBgn00 04870	-1.70285	3.19E -15
FBgn00 03731	-0.91172	1.22E -08		FBgn00 04852	-0.98461	8.76 E-05	FBgn00 04117	-0.8266	3.59E -08	FBgn00 04893	-0.63244	0.000 296
FBgn00 03866	0.822739	0.001 572		FBgn00 04858	-1.00605	2.67 E-06	FBgn00 04133	-0.80998	8.24E -13	FBgn00 04919	-1.08336	0.000 247

FBgn00 03867	-0.65206	0.016 239		FBgn00 04870	-2.07181	1.72 E-20	FBgn00 04169	-0.74805	3.79E -06	FBgn00 05612	-0.79026	7.63E -08
FBgn00 03888	-1.24917	6.05E -24		FBgn00 04885	-0.75023	0.01 1429	FBgn00 04183	-0.99194	3.46E -06	FBgn00 05631	-0.69974	0.008 378
FBgn00 03950	1.025085	0.000 724		FBgn00 04893	-0.62622	0.00 0366	FBgn00 04185	-0.71535	0.028 03	FBgn00 05666	-0.58573	7.04E -05
FBgn00 03996	-2.01639	3.83E -10		FBgn00 04919	-1.53433	3.43 E-07	FBgn00 04186	-0.74792	0.018 615	FBgn00 05771	-0.88584	9.79E -08
FBgn00 03997	-0.91028	4.52E -06		FBgn00 05612	-1.13811	3.73 E-15	FBgn00 04191	-0.71886	0.000 822	FBgn00 10038	-1.17032	0.005 028
FBgn00 04055	-0.75142	4.79E -09		FBgn00 05631	-0.8043	0.00 2413	FBgn00 04456	-0.73465	4.25E -08	FBgn00 10039	-1.13868	6.39E -15
FBgn00 04117	-0.80603	8.40E -08		FBgn00 05666	-0.86896	1.05 E-09	FBgn00 04512	-1.12955	0.003 157	FBgn00 10052	-1.55161	2.94E -08
FBgn00 04169	-0.62255	0.000 158		FBgn00 05771	-0.95549	9.66 E-09	FBgn00 04852	-0.82421	0.001 054	FBgn00 10225	-0.71957	3.32E -05
FBgn00 04191	0.612225	0.005 48		FBgn00 10038	-1.70043	2.69 E-05	FBgn00 04858	-0.61308	0.005 27	FBgn00 10228	-0.86675	4.30E -18
FBgn00 04456	-0.84578	2.17E -10		FBgn00 10039	-0.93056	2.92 E-10	FBgn00 04870	-1.70285	3.19E -15	FBgn00 10241	-10.1762	3.38E -06
FBgn00 04512	-1.41811	0.000 211		FBgn00 10052	-2.61244	1.36 E-18	FBgn00 04893	-0.63244	0.000 296	FBgn00 10246	-1.09438	5.35E -36
FBgn00 04646	-0.80634	7.88E -08		FBgn00 10228	-0.62532	6.99 E-10	FBgn00 04919	-1.08336	0.000 247	FBgn00 10263	-0.72801	2.72E -05
FBgn00 04666	-0.59209	0.000 245		FBgn00 10241	-7.23653	0.00 0525	FBgn00 05612	-0.79026	7.63E -08	FBgn00 10383	-0.74469	1.00E -08
FBgn00 04852	-0.98461	8.76E -05		FBgn00 10246	-1.048	4.07 E-33	FBgn00 05631	-0.69974	0.008 378	FBgn00 10388	-1.14684	0.016 393
FBgn00 04858	-1.00605	2.67E -06		FBgn00 10263	-0.79153	4.96 E-06	FBgn00 05666	-0.58573	7.04E -05	FBgn00 10389	-0.72248	0.002 268
FBgn00 04870	-2.07181	1.72E -20		FBgn00 10383	-0.839	8.98 E-11	FBgn00 05771	-0.88584	9.79E -08	FBgn00 10395	-1.55127	1.83E -19
FBgn00 04885	-0.75023	0.011 429		FBgn00 10388	-3.26557	4.38 E-10	FBgn00 10038	-1.17032	0.005 028	FBgn00 10424	-1.0166	0.000 728

FBgn00 04893	-0.62622	0.000 366		FBgn00 10389	-0.58669	0.01 5881	FBgn00 10039	-1.13868	6.39E -15		FBgn00 10434	-0.74336	3.77E -25
FBgn00 04919	-1.53433	3.43E -07		FBgn00 10395	-1.67809	3.04 E-22	FBgn00 10052	-1.55161	2.94E -08		FBgn00 10435	-0.58988	0.001 514
FBgn00 05612	-1.13811	3.73E -15		FBgn00 10424	-0.85845	0.00 4982	FBgn00 10053	0.73168	4.68E -08		FBgn00 10482	-1.0433	2.68E -05
FBgn00 05631	-0.8043	0.002 413		FBgn00 10434	-0.90979	4.83 E-37	FBgn00 10194	0.612087	1.60E -07		FBgn00 11274	-0.91692	2.30E -05
FBgn00 05666	-0.86896	1.05E -09		FBgn00 10435	-0.85015	2.20 E-06	FBgn00 10223	1.025642	3.81E -05		FBgn00 11591	-0.75455	1.03E -06
FBgn00 05771	-0.95549	9.66E -09		FBgn00 10482	-1.18457	1.96 E-06	FBgn00 10225	-0.71957	3.32E -05		FBgn00 11676	-2.42249	1.18E -11
FBgn00 10038	-1.70043	2.69E -05		FBgn00 11206	-0.69629	0.00 5466	FBgn00 10226	1.503772	3.85E -45		FBgn00 11695	-3.29149	1.22E -94
FBgn00 10039	-0.93056	2.92E -10		FBgn00 11274	-1.06269	8.86 E-07	FBgn00 10228	-0.86675	4.30E -18		FBgn00 11706	-2.72708	3.44E -10
FBgn00 10052	-2.61244	1.36E -18		FBgn00 11591	-1.06854	2.58 E-12	FBgn00 10241	-10.1762	3.38E -06		FBgn00 11828	-1.38404	1.25E -05
FBgn00 10053	1.081627	3.79E -17		FBgn00 11676	-2.45802	8.12 E-12	FBgn00 10246	-1.09438	5.35E -36		FBgn00 12037	-0.91371	4.62E -07
FBgn00 10223	1.060404	2.01E -05		FBgn00 11695	-3.33855	1.47 E-95	FBgn00 10263	-0.72801	2.72E -05		FBgn00 13272	-0.76583	4.17E -08
FBgn00 10226	1.645765	3.35E -54		FBgn00 11706	-2.8693	1.11 E-10	FBgn00 10383	-0.74469	1.00E -08		FBgn00 13275	-3.08679	5.74E -82
FBgn00 10228	-0.62532	6.99E -10		FBgn00 12037	-0.92616	3.33 E-07	FBgn00 10388	-1.14684	0.016 393		FBgn00 13276	-2.99185	2.11E -47
FBgn00 10241	-7.23653	0.000 525		FBgn00 13272	-1.06089	7.08 E-15	FBgn00 10389	-0.72248	0.002 268		FBgn00 13277	-2.87248	4.28E -33
FBgn00 10246	-1.048	4.07E -33		FBgn00 13275	-2.70629	9.70 E-65	FBgn00 10395	-1.55127	1.83E -19		FBgn00 13278	-3.01897	7.30E -44
FBgn00 10263	-0.79153	4.96E -06		FBgn00 13276	-2.68691	9.58 E-39	FBgn00 10424	-1.0166	0.000 728		FBgn00 13279	-2.96356	7.00E -31
FBgn00 10383	-0.839	8.98E -11		FBgn00 13277	-2.46775	2.67 E-26	FBgn00 10434	-0.74336	3.77E -25		FBgn00 13469	-1.04107	0.002 743

FBgn00 10388	-3.26557	4.38E -10		FBgn00 13278	-2.60302	1.14 E-36	FBgn00 10435	-0.58988	0.001 514		FBgn00 13680	-1.43051	0.020 095
FBgn00 10389	-0.58669	0.015 881		FBgn00 13279	-2.64494	2.20 E-26	FBgn00 10482	-1.0433	2.68E -05		FBgn00 13813	-2.29191	3.43E -49
FBgn00 10395	-1.67809	3.04E -22		FBgn00 13469	-1.36302	8.35 E-05	FBgn00 11274	-0.91692	2.30E -05		FBgn00 13953	-0.62589	5.54E -10
FBgn00 10424	-0.85845	0.004 982		FBgn00 13771	-0.99981	1.63 E-09	FBgn00 11591	-0.75455	1.03E -06		FBgn00 13954	-1.05865	4.03E -19
FBgn00 10434	-0.90979	4.83E -37		FBgn00 13813	-3.18083	1.74 E-78	FBgn00 11642	1.165829	1.17E -12		FBgn00 14073	-0.86774	1.14E -08
FBgn00 10435	-0.85015	2.20E -06		FBgn00 13953	-0.67289	2.64 E-11	FBgn00 11676	-2.42249	1.18E -11		FBgn00 14076	-0.79024	4.47E -08
FBgn00 10482	-1.18457	1.96E -06		FBgn00 14073	-1.36011	3.84 E-19	FBgn00 11695	-3.29149	1.22E -94		FBgn00 14380	-0.7655	7.92E -05
FBgn00 11206	-0.69629	0.005 466		FBgn00 14076	-1.00577	1.45 E-12	FBgn00 11706	-2.72708	3.44E -10		FBgn00 14469	-0.846	6.19E -15
FBgn00 11274	-1.06269	8.86E -07		FBgn00 14469	-1.19846	4.94 E-29	FBgn00 11828	-1.38404	1.25E -05		FBgn00 14863	-0.76477	0.000 65
FBgn00 11591	-1.06854	2.58E -12		FBgn00 15033	-1.51951	1.24 E-11	FBgn00 12034	0.781267	9.57E -30		FBgn00 15033	-1.61347	7.25E -13
FBgn00 11642	0.970799	6.11E -09		FBgn00 15037	-3.55936	9.87 E-53	FBgn00 12037	-0.91371	4.62E -07		FBgn00 15037	-3.35233	2.61E -50
FBgn00 11659	0.645891	2.86E -05		FBgn00 15039	-0.94832	1.55 E-10	FBgn00 13272	-0.76583	4.17E -08		FBgn00 15039	-1.06376	5.78E -13
FBgn00 11676	-2.45802	8.12E -12		FBgn00 15221	-0.70804	6.81 E-14	FBgn00 13275	-3.08679	5.74E -82		FBgn00 15399	-2.11808	1.00E -75
FBgn00 11695	-3.33855	1.47E -95		FBgn00 15399	-2.11532	1.82 E-75	FBgn00 13276	-2.99185	2.11E -47		FBgn00 15569	-1.23072	1.90E -21
FBgn00 11706	-2.8693	1.11E -10		FBgn00 15569	-1.16586	2.01 E-19	FBgn00 13277	-2.87248	4.28E -33		FBgn00 15575	-1.03107	1.13E -05
FBgn00 12034	0.704475	3.56E -24		FBgn00 15575	-0.91911	9.97 E-05	FBgn00 13278	-3.01897	7.30E -44		FBgn00 15576	-0.71232	0.019 046
FBgn00 12037	-0.92616	3.33E -07		FBgn00 15576	-0.9802	0.00 1012	FBgn00 13279	-2.96356	7.00E -31		FBgn00 15773	-0.9243	0.001 559

FBgn00 13272	-1.06089	7.08E -15		FBgn00 15766	-0.65876	0.00 0167	FBgn00 13469	-1.04107	0.002 743		FBgn00 15774	-0.93607	0.001 778
FBgn00 13275	-2.70629	9.70E -65		FBgn00 15773	-0.75436	0.01 1703	FBgn00 13680	-1.43051	0.020 095		FBgn00 15777	-1.14614	5.25E -13
FBgn00 13276	-2.68691	9.58E -39		FBgn00 15774	-0.83903	0.00 5619	FBgn00 13813	-2.29191	3.43E -49		FBgn00 15872	-0.75319	0.000 704
FBgn00 13277	-2.46775	2.67E -26		FBgn00 15777	-1.05576	3.71 E-11	FBgn00 13953	-0.62589	5.54E -10		FBgn00 16053	-0.59343	2.49E -06
FBgn00 13278	-2.60302	1.14E -36		FBgn00 15872	-0.60363	0.00 8337	FBgn00 13954	-1.05865	4.03E -19		FBgn00 16075	-1.08094	6.17E -10
FBgn00 13279	-2.64494	2.20E -26		FBgn00 16075	-0.90254	3.79 E-07	FBgn00 14073	-0.86774	1.14E -08		FBgn00 16080	-0.9668	7.74E -05
FBgn00 13469	-1.36302	8.35E -05		FBgn00 16080	-0.94086	0.00 013	FBgn00 14076	-0.79024	4.47E -08		FBgn00 16684	-1.14736	0.009 237
FBgn00 13771	-0.99981	1.63E -09		FBgn00 16684	-0.969	0.03 2387	FBgn00 14380	-0.7655	7.92E -05		FBgn00 17482	-0.97832	2.98E -06
FBgn00 13813	-3.18083	1.74E -78		FBgn00 17482	-0.82711	9.06 E-05	FBgn00 14395	1.141733	0.000 656		FBgn00 20257	-0.88754	0.007 448
FBgn00 13953	-0.67289	2.64E -11		FBgn00 20255	-0.71327	4.91 E-19	FBgn00 14417	0.638086	3.63E -07		FBgn00 20294	-1.42348	1.15E -18
FBgn00 14073	-1.36011	3.84E -19		FBgn00 20257	-0.74412	0.02 83	FBgn00 14469	-0.846	6.19E -15		FBgn00 20299	-0.61615	0.012 689
FBgn00 14076	-1.00577	1.45E -12		FBgn00 20294	-1.61966	2.46 E-23	FBgn00 14863	-0.76477	0.000 65		FBgn00 20414	-0.87911	2.21E -07
FBgn00 14395	0.739718	0.043 309		FBgn00 20299	-0.71299	0.00 3941	FBgn00 15033	-1.61347	7.25E -13		FBgn00 20415	-0.84086	1.99E -13
FBgn00 14417	0.640256	3.37E -07		FBgn00 20414	-0.96543	1.35 E-08	FBgn00 15037	-3.35233	2.61E -50		FBgn00 20521	-1.28619	2.64E -05
FBgn00 14469	-1.19846	4.94E -29		FBgn00 20415	-0.99044	3.10 E-18	FBgn00 15039	-1.06376	5.78E -13		FBgn00 20762	-1.16751	1.70E -14
FBgn00 15033	-1.51951	1.24E -11		FBgn00 20521	-1.05988	0.00 0598	FBgn00 15399	-2.11808	1.00E -75		FBgn00 22160	-0.94174	1.08E -06
FBgn00 15037	-3.55936	9.87E -53		FBgn00 20762	-1.45374	7.08 E-22	FBgn00 15569	-1.23072	1.90E -21		FBgn00 22774	-0.84616	7.21E -13

FBgn00 15039	-0.94832	1.55E -10		FBgn00 22984	-0.91737	2.87 E-22	FBgn00 15575	-1.03107	1.13E -05	FBgn00 22984	-0.72358	2.83E -14
FBgn00 15221	-0.70804	6.81E -14		FBgn00 22986	-1.18958	8.83 E-31	FBgn00 15576	-0.71232	0.019 046	FBgn00 22986	-0.91083	9.39E -19
FBgn00 15399	-2.11532	1.82E -75		FBgn00 23076	-0.94531	0.00 1588	FBgn00 15663	1.140955	1.46E -08	FBgn00 23023	-0.68473	0.006 935
FBgn00 15568	0.852581	3.43E -09		FBgn00 23095	-0.64487	7.29 E-10	FBgn00 15773	-0.9243	0.001 559	FBgn00 23076	-0.62442	0.041 457
FBgn00 15569	-1.16586	2.01E -19		FBgn00 23214	-0.77607	0.00 3368	FBgn00 15774	-0.93607	0.001 778	FBgn00 23095	-0.64063	8.43E -10
FBgn00 15575	-0.91911	9.97E -05		FBgn00 23479	-1.85017	1.06 E-08	FBgn00 15777	-1.14614	5.25E -13	FBgn00 23479	-1.71058	8.91E -08
FBgn00 15576	-0.9802	0.001 012		FBgn00 23520	-0.83036	8.58 E-11	FBgn00 15872	-0.75319	0.000 704	FBgn00 23520	-1.37347	6.87E -26
FBgn00 15663	0.655931	0.003 123		FBgn00 23549	-0.82825	8.06 E-09	FBgn00 16053	-0.59343	2.49E -06	FBgn00 23549	-0.78615	4.64E -08
FBgn00 15714	1.198872	4.54E -15		FBgn00 24189	-8.65185	0.00 0324	FBgn00 16054	0.714346	1.62E -06	FBgn00 24189	-8.66403	0.000 302
FBgn00 15766	-0.65876	0.000 167		FBgn00 24321	-0.72515	0.00 1318	FBgn00 16075	-1.08094	6.17E -10	FBgn00 24234	-0.74135	1.39E -05
FBgn00 15773	-0.75436	0.011 703		FBgn00 24989	-0.69316	0.03 7726	FBgn00 16080	-0.9668	7.74E -05	FBgn00 24321	-0.63169	0.005 531
FBgn00 15774	-0.83903	0.005 619		FBgn00 25111	-0.62914	0.04 5114	FBgn00 16684	-1.14736	0.009 237	FBgn00 24989	-0.72082	0.027 651
FBgn00 15777	-1.05576	3.71E -11		FBgn00 25391	-1.50871	1.75 E-07	FBgn00 17448	3.047112	1.21E -67	FBgn00 25111	-1.05192	0.000 486
FBgn00 15872	-0.60363	0.008 337		FBgn00 25631	-1.31697	6.88 E-18	FBgn00 17482	-0.97832	2.98E -06	FBgn00 25391	-1.09898	0.000 118
FBgn00 16054	1.347521	1.04E -21		FBgn00 26061	-0.67904	8.57 E-09	FBgn00 20257	-0.88754	0.007 448	FBgn00 25631	-1.02622	8.93E -12
FBgn00 16075	-0.90254	3.79E -07		FBgn00 26160	-0.60504	0.02 8882	FBgn00 20294	-1.42348	1.15E -18	FBgn00 25680	-1.01819	2.19E -10
FBgn00 16080	-0.94086	0.000 13		FBgn00 26319	-1.18974	2.50 E-09	FBgn00 20299	-0.61615	0.012 689	FBgn00 26061	-0.85486	2.40E -13

FBgn00 16684	-0.969	0.032 387		FBgn00 27106	-1.00452	2.13 E-10	FBgn00 20414	-0.87911	2.21E -07	FBgn00 26079	-0.76247	6.19E -19
FBgn00 17448	2.800903	1.18E -56		FBgn00 27339	-0.63533	0.00 0807	FBgn00 20415	-0.84086	1.99E -13	FBgn00 26160	-0.59449	0.029 659
FBgn00 17482	-0.82711	9.06E -05		FBgn00 27341	-4.037	2.88 E-72	FBgn00 20521	-1.28619	2.64E -05	FBgn00 26319	-0.94711	2.22E -06
FBgn00 20255	-0.71327	4.91E -19		FBgn00 27364	-1.05367	1.47 E-13	FBgn00 20762	-1.16751	1.70E -14	FBgn00 26562	-0.81851	8.50E -06
FBgn00 20257	-0.74412	0.028 3		FBgn00 27556	-1.38573	0.00 881	FBgn00 22160	-0.94174	1.08E -06	FBgn00 27106	-1.26234	1.90E -15
FBgn00 20294	-1.61966	2.46E -23		FBgn00 27585	-1.00387	8.42 E-08	FBgn00 22359	0.921145	0.009 216	FBgn00 27341	-3.88007	4.45E -69
FBgn00 20299	-0.71299	0.003 941		FBgn00 27596	-0.98821	1.25 E-15	FBgn00 22702	0.932532	1.13E -09	FBgn00 27364	-1.40818	3.74E -23
FBgn00 20312	0.635632	1.06E -11		FBgn00 27601	-1.18791	2.54 E-28	FBgn00 22774	-0.84616	7.21E -13	FBgn00 27556	-1.6499	0.001 514
FBgn00 20385	0.908339	2.69E -07		FBgn00 27611	-0.60107	2.53 E-06	FBgn00 22984	-0.72358	2.83E -14	FBgn00 27560	-1.05529	0.000 417
FBgn00 20414	-0.96543	1.35E -08		FBgn00 27843	-1.17233	1.68 E-14	FBgn00 22986	-0.91083	9.39E -19	FBgn00 27585	-0.92878	7.32E -07
FBgn00 20415	-0.99044	3.10E -18		FBgn00 28341	-0.59141	0.00 1189	FBgn00 23023	-0.68473	0.006 935	FBgn00 27586	-0.72894	0.005 318
FBgn00 20521	-1.05988	0.000 598		FBgn00 28369	-0.77286	0.00 0621	FBgn00 23076	-0.62442	0.041 457	FBgn00 27596	-1.13008	6.02E -20
FBgn00 20762	-1.45374	7.08E -22		FBgn00 28550	-0.74129	0.00 0297	FBgn00 23095	-0.64063	8.43E -10	FBgn00 27601	-1.32127	1.73E -34
FBgn00 22359	1.549789	1.49E -06		FBgn00 28886	-1.5682	2.59 E-23	FBgn00 23479	-1.71058	8.91E -08	FBgn00 27843	-1.47152	4.34E -22
FBgn00 22702	1.282964	9.35E -18		FBgn00 28956	-0.90166	3.33 E-09	FBgn00 23520	-1.37347	6.87E -26	FBgn00 28341	-1.19848	1.50E -12
FBgn00 22772	0.607326	2.61E -15		FBgn00 28988	-1.26502	5.15 E-05	FBgn00 23540	0.703844	1.31E -10	FBgn00 28369	-0.90853	4.13E -05
FBgn00 22984	-0.91737	2.87E -22		FBgn00 29002	-0.65464	1.72 E-07	FBgn00 23549	-0.78615	4.64E -08	FBgn00 28394	-0.66505	8.21E -10

FBgn00 22986	-1.18958	8.83E -31		FBgn00 29082	-4.04552	1.49 E-27	FBgn00 24179	0.785536	1.78E -06	FBgn00 28527	-0.67817	1.45E -05
FBgn00 23076	-0.94531	0.001 588		FBgn00 29148	-0.60278	8.41 E-11	FBgn00 24189	-8.66403	0.000 302	FBgn00 28572	-0.7392	1.53E -07
FBgn00 23095	-0.64487	7.29E -10		FBgn00 29167	-0.72759	0.02 3446	FBgn00 24234	-0.74135	1.39E -05	FBgn00 28622	-0.71973	1.27E -05
FBgn00 23214	-0.77607	0.003 368		FBgn00 29506	-0.60057	1.05 E-08	FBgn00 24321	-0.63169	0.005 531	FBgn00 28886	-1.07729	6.30E -12
FBgn00 23479	-1.85017	1.06E -08		FBgn00 29507	-1.68646	2.54 E-09	FBgn00 24728	0.769902	5.41E -07	FBgn00 28956	-0.66675	1.55E -05
FBgn00 23507	0.789905	0.000 116		FBgn00 29608	-1.35263	1.59 E-05	FBgn00 24912	0.801094	1.00E -05	FBgn00 28988	-1.13368	0.000 273
FBgn00 23520	-0.83036	8.58E -11		FBgn00 29723	-1.68374	1.02 E-21	FBgn00 24989	-0.72082	0.027 651	FBgn00 29082	-5.68065	3.27E -27
FBgn00 23549	-0.82825	8.06E -09		FBgn00 29766	-0.94481	4.60 E-08	FBgn00 25111	-1.05192	0.000 486	FBgn00 29148	-0.60253	7.34E -11
FBgn00 24189	-8.65185	0.000 324		FBgn00 29771	-0.90329	0.00 0581	FBgn00 25382	0.885944	0.014 646	FBgn00 29167	-0.92486	0.002 945
FBgn00 24321	-0.72515	0.001 318		FBgn00 29838	-0.66385	3.19 E-05	FBgn00 25387	0.588136	9.42E -06	FBgn00 29507	-1.40019	4.80E -07
FBgn00 24754	0.599068	0.000 261		FBgn00 29843	-2.39785	3.09 E-28	FBgn00 25391	-1.09898	0.000 118	FBgn00 29608	-1.58744	4.78E -07
FBgn00 24912	0.992967	1.87E -08		FBgn00 29878	-0.61168	5.57 E-12	FBgn00 25631	-1.02622	8.93E -12	FBgn00 29723	-1.75928	2.33E -23
FBgn00 24989	-0.69316	0.037 726		FBgn00 29932	-1.07282	0.00 6497	FBgn00 25632	0.91927	0.000 218	FBgn00 29771	-0.95924	0.000 234
FBgn00 25111	-0.62914	0.045 114		FBgn00 29939	-0.82058	8.10 E-07	FBgn00 25680	-1.01819	2.19E -10	FBgn00 29843	-2.39776	2.53E -28
FBgn00 25382	0.864	0.019 168		FBgn00 29966	-0.86813	7.68 E-07	FBgn00 25726	1.619667	3.57E -25	FBgn00 29932	-1.16875	0.002 696
FBgn00 25391	-1.50871	1.75E -07		FBgn00 30017	-1.43899	4.32 E-05	FBgn00 25739	0.599326	1.16E -05	FBgn00 29939	-1.08477	5.13E -11
FBgn00 25630	0.704526	2.39E -06		FBgn00 30040	-2.22626	1.64 E-111	FBgn00 25740	1.500536	1.91E -17	FBgn00 29966	-0.65839	0.000 258

FBgn00 25631	-1.31697	6.88E -18		FBgn00 30041	-0.65806	0.01 8597	FBgn00 25836	0.658827	8.53E -13		FBgn00 30017	-0.93365	0.008 22
FBgn00 25632	0.773729	0.002 639		FBgn00 30174	-0.71829	2.20 E-13	FBgn00 26061	-0.85486	2.40E -13		FBgn00 30040	-2.31846	2.73E -119
FBgn00 25726	1.195453	6.36E -14		FBgn00 30234	-1.38854	0.00 0109	FBgn00 26079	-0.76247	6.19E -19		FBgn00 30091	-0.63261	1.85E -16
FBgn00 25739	0.739236	3.13E -08		FBgn00 30237	-1.49117	5.55 E-05	FBgn00 26160	-0.59449	0.029 659		FBgn00 30218	-0.61195	0.001 006
FBgn00 25740	1.10583	1.02E -09		FBgn00 30300	-1.53011	1.16 E-10	FBgn00 26315	1.563617	9.12E -32		FBgn00 30234	-1.69341	2.88E -06
FBgn00 26061	-0.67904	8.57E -09		FBgn00 30309	-1.42362	1.16 E-16	FBgn00 26319	-0.94711	2.22E -06		FBgn00 30237	-1.41887	0.000 114
FBgn00 26160	-0.60504	0.028 882		FBgn00 30349	-1.07523	5.52 E-34	FBgn00 26323	0.945177	4.02E -39		FBgn00 30266	-0.63892	0.002 485
FBgn00 26315	1.163162	2.69E -17		FBgn00 30438	-2.09672	4.21 E-33	FBgn00 26562	-0.81851	8.50E -06		FBgn00 30300	-1.7623	1.84E -13
FBgn00 26319	-1.18974	2.50E -09		FBgn00 30479	-0.74791	3.08 E-09	FBgn00 26602	0.679568	2.36E -06		FBgn00 30309	-1.25795	2.22E -13
FBgn00 26323	0.824783	1.07E -29		FBgn00 30485	-1.27969	1.10 E-07	FBgn00 27070	1.30245	5.42E -34		FBgn00 30331	-0.61789	0.002 963
FBgn00 26439	1.111647	0.000 406		FBgn00 30596	-0.68877	1.19 E-08	FBgn00 27101	0.608994	0.000 275		FBgn00 30349	-0.82431	1.19E -20
FBgn00 26602	1.151349	4.46E -17		FBgn00 30600	-5.62098	1.66 E- 166	FBgn00 27106	-1.26234	1.90E -15		FBgn00 30360	-0.7531	0.042 836
FBgn00 27070	0.589879	2.39E -07		FBgn00 30662	-0.68094	0.00 018	FBgn00 27341	-3.88007	4.45E -69		FBgn00 30438	-1.62151	4.59E -20
FBgn00 27106	-1.00452	2.13E -10		FBgn00 30796	-0.91904	0.00 0289	FBgn00 27364	-1.40818	3.74E -23		FBgn00 30479	-0.93528	8.12E -14
FBgn00 27339	-0.63533	0.000 807		FBgn00 30816	-1.08503	1.02 E-25	FBgn00 27556	-1.6499	0.001 514		FBgn00 30485	-1.00243	3.05E -05
FBgn00 27341	-4.037	2.88E -72		FBgn00 30847	-0.61381	0.00 0531	FBgn00 27560	-1.05529	0.000 417		FBgn00 30594	-1.74155	0.000 205
FBgn00 27364	-1.05367	1.47E -13		FBgn00 30884	-0.80757	2.86 E-07	FBgn00 27585	-0.92878	7.32E -07		FBgn00 30596	-0.86188	5.10E -13

FBgn00 27556	-1.38573	0.008 81		FBgn00 30899	-2.39155	1.50 E-06	FBgn00 27586	-0.72894	0.005 318		FBgn00 30600	-6.29712	2.89E -181
FBgn00 27585	-1.00387	8.42E -08		FBgn00 30955	-1.04363	1.22 E-20	FBgn00 27596	-1.13008	6.02E -20		FBgn00 30662	-0.82317	4.20E -06
FBgn00 27596	-0.98821	1.25E -15		FBgn00 30976	-0.76644	0.00 3695	FBgn00 27601	-1.32127	1.73E -34		FBgn00 30796	-0.69122	0.006 723
FBgn00 27601	-1.18791	2.54E -28		FBgn00 31220	-2.07178	9.24 E-20	FBgn00 27843	-1.47152	4.34E -22		FBgn00 30816	-0.97862	4.63E -21
FBgn00 27611	-0.60107	2.53E -06		FBgn00 31275	-2.58882	6.10 E-12	FBgn00 28341	-1.19848	1.50E -12		FBgn00 30839	-0.66476	2.87E -06
FBgn00 27791	0.641441	0.001 775		FBgn00 31305	-0.62704	3.06 E-06	FBgn00 28369	-0.90853	4.13E -05		FBgn00 30884	-0.9162	4.78E -09
FBgn00 27843	-1.17233	1.68E -14		FBgn00 31327	-0.97783	0.00 234	FBgn00 28394	-0.66505	8.21E -10		FBgn00 30899	-2.10556	1.91E -05
FBgn00 27903	0.608003	2.10E -06		FBgn00 31343	-1.36718	0.00 0219	FBgn00 28491	0.890259	3.40E -06		FBgn00 30955	-1.32177	3.33E -32
FBgn00 28341	-0.59141	0.001 189		FBgn00 31414	-2.83115	3.38 E-19	FBgn00 28499	0.944285	1.91E -06		FBgn00 30976	-0.70592	0.007 395
FBgn00 28369	-0.77286	0.000 621		FBgn00 31461	-1.01345	0.00 9004	FBgn00 28523	0.772096	0.000 522		FBgn00 30999	-1.75966	0.033 074
FBgn00 28491	1.192692	1.08E -10		FBgn00 31571	-1.06323	1.96 E-11	FBgn00 28525	1.016456	9.16E -11		FBgn00 31220	-1.93564	1.39E -17
FBgn00 28499	1.267108	3.94E -11		FBgn00 31628	-0.91615	1.05 E-05	FBgn00 28527	-0.67817	1.45E -05		FBgn00 31275	-2.14439	5.77E -09
FBgn00 28550	-0.74129	0.000 297		FBgn00 31717	-0.83985	5.23 E-07	FBgn00 28572	-0.7392	1.53E -07		FBgn00 31327	-1.36223	1.75E -05
FBgn00 28743	1.36777	5.56E -16		FBgn00 31756	-0.73746	2.40 E-06	FBgn00 28622	-0.71973	1.27E -05		FBgn00 31343	-1.45436	7.47E -05
FBgn00 28886	-1.5682	2.59E -23		FBgn00 31888	-2.84364	2.83 E-11	FBgn00 28743	1.442948	7.55E -18		FBgn00 31414	-3.15018	9.32E -22
FBgn00 28956	-0.90166	3.33E -09		FBgn00 31894	-0.69343	8.65 E-10	FBgn00 28886	-1.07729	6.30E -12		FBgn00 31571	-0.78383	1.26E -06
FBgn00 28988	-1.26502	5.15E -05		FBgn00 31907	-2.12824	4.70 E-12	FBgn00 28956	-0.66675	1.55E -05		FBgn00 31628	-0.69137	0.000 985

FBgn00 29002	-0.65464	1.72E -07		FBgn00 31908	-0.94922	0.00 0817	FBgn00 28988	-1.13368	0.000 273	FBgn00 31717	-0.94621	1.41E -08
FBgn00 29082	-4.04552	1.49E -27		FBgn00 31913	-1.20054	3.34 E-21	FBgn00 29082	-5.68065	3.27E -27	FBgn00 31756	-0.83177	7.43E -08
FBgn00 29148	-0.60278	8.41E -11		FBgn00 31914	-0.7069	0.00 1309	FBgn00 29114	0.884333	5.70E -14	FBgn00 31777	-0.63246	0.001 038
FBgn00 29167	-0.72759	0.023 446		FBgn00 31948	-0.6673	8.88 E-06	FBgn00 29148	-0.60253	7.34E -11	FBgn00 31816	-0.80483	2.88E -05
FBgn00 29506	-0.60057	1.05E -08		FBgn00 31961	-0.75497	0.00 0724	FBgn00 29167	-0.92486	0.002 945	FBgn00 31888	-3.20052	1.14E -12
FBgn00 29507	-1.68646	2.54E -09		FBgn00 32006	-0.80791	1.56 E-13	FBgn00 29172	1.109967	0.031 749	FBgn00 31894	-0.61592	5.49E -08
FBgn00 29608	-1.35263	1.59E -05		FBgn00 32021	-0.75536	0.04 7795	FBgn00 29507	-1.40019	4.80E -07	FBgn00 31907	-2.71513	1.52E -16
FBgn00 29723	-1.68374	1.02E -21		FBgn00 32022	-0.94953	0.00 0359	FBgn00 29608	-1.58744	4.78E -07	FBgn00 31908	-1.02789	0.000 263
FBgn00 29766	-0.94481	4.60E -08		FBgn00 32025	-1.00346	0.00 0834	FBgn00 29686	0.66003	3.13E -11	FBgn00 31913	-1.21036	1.62E -21
FBgn00 29771	-0.90329	0.000 581		FBgn00 32075	-1.15482	0.00 0277	FBgn00 29723	-1.75928	2.33E -23	FBgn00 31961	-1.05787	1.28E -06
FBgn00 29831	0.860266	4.14E -26		FBgn00 32126	-0.88813	1.26 E-13	FBgn00 29771	-0.95924	0.000 234	FBgn00 31974	-1.09834	3.49E -20
FBgn00 29838	-0.66385	3.19E -05		FBgn00 32129	-0.72821	0.02 7264	FBgn00 29831	0.950306	6.99E -32	FBgn00 31975	-0.91917	8.10E -15
FBgn00 29843	-2.39785	3.09E -28		FBgn00 32140	-0.98532	2.00 E-07	FBgn00 29843	-2.39776	2.53E -28	FBgn00 32006	-0.61668	2.64E -08
FBgn00 29854	0.676493	1.41E -07		FBgn00 32156	-1.1532	2.65 E-12	FBgn00 29879	0.724488	1.82E -18	FBgn00 32022	-1.29387	9.41E -07
FBgn00 29866	0.619308	3.34E -07		FBgn00 32167	-1.56971	4.86 E-20	FBgn00 29932	-1.16875	0.002 696	FBgn00 32025	-1.17991	6.62E -05
FBgn00 29878	-0.61168	5.57E -12		FBgn00 32211	-1.06732	0.01 0991	FBgn00 29939	-1.08477	5.13E -11	FBgn00 32075	-1.16794	0.000 22
FBgn00 29879	0.884565	2.51E -27		FBgn00 32218	-1.08521	4.62 E-11	FBgn00 29966	-0.65839	0.000 258	FBgn00 32126	-1.15489	2.86E -22

FBgn00 29924	0.800306	7.26E -07		FBgn00 32235	-0.60182	0.03 8577	FBgn00 30017	-0.93365	0.008 22	FBgn00 32129	-0.68748	0.034 811
FBgn00 29932	-1.07282	0.006 497		FBgn00 32264	-1.33435	6.96 E-22	FBgn00 30040	-2.31846	2.73E -119	FBgn00 32140	-1.22219	6.81E -11
FBgn00 29939	-0.82058	8.10E -07		FBgn00 32297	-1.18516	1.12 E-08	FBgn00 30091	-0.63261	1.85E -16	FBgn00 32149	-0.59436	0.000 368
FBgn00 29942	0.809404	5.12E -12		FBgn00 32405	-2.17937	8.79 E-11	FBgn00 30100	0.752429	6.97E -05	FBgn00 32156	-0.85704	2.20E -07
FBgn00 29966	-0.86813	7.68E -07		FBgn00 32470	-5.097	3.91 E-23	FBgn00 30187	1.737653	1.11E -12	FBgn00 32167	-1.41873	8.10E -17
FBgn00 30017	-1.43899	4.32E -05		FBgn00 32666	-1.34264	8.19 E-12	FBgn00 30189	0.585204	0.002 456	FBgn00 32187	-1.07541	8.27E -05
FBgn00 30040	-2.22626	1.64E -111		FBgn00 32669	-2.15935	6.18 E-07	FBgn00 30218	-0.61195	0.001 006	FBgn00 32211	-1.71333	2.21E -05
FBgn00 30041	-0.65806	0.018 597		FBgn00 32670	-2.27453	5.78 E-10	FBgn00 30234	-1.69341	2.88E -06	FBgn00 32218	-0.73768	1.02E -05
FBgn00 30100	0.800187	2.13E -05		FBgn00 32671	-0.59648	2.85 E-08	FBgn00 30237	-1.41887	0.000 114	FBgn00 32253	-1.05833	0.001 576
FBgn00 30174	-0.71829	2.20E -13		FBgn00 32683	-1.21027	5.15 E-10	FBgn00 30266	-0.63892	0.002 485	FBgn00 32264	-1.15708	8.10E -17
FBgn00 30187	2.161668	1.40E -19		FBgn00 32684	-1.98037	6.60 E-44	FBgn00 30300	-1.7623	1.84E -13	FBgn00 32297	-1.16664	1.84E -08
FBgn00 30234	-1.38854	0.000 109		FBgn00 32694	-0.66422	7.83 E-11	FBgn00 30309	-1.25795	2.22E -13	FBgn00 32311	-1.0846	2.03E -08
FBgn00 30237	-1.49117	5.55E -05		FBgn00 32713	-0.7073	2.58 E-05	FBgn00 30331	-0.61789	0.002 963	FBgn00 32405	-2.11264	1.93E -10
FBgn00 30300	-1.53011	1.16E -10		FBgn00 32731	-0.66117	3.83 E-15	FBgn00 30349	-0.82431	1.19E -20	FBgn00 32422	-0.63609	2.18E -06
FBgn00 30309	-1.42362	1.16E -16		FBgn00 32897	-0.95312	2.20 E-29	FBgn00 30357	0.965596	1.57E -08	FBgn00 32470	-6.24342	4.13E -18
FBgn00 30349	-1.07523	5.52E -34		FBgn00 32899	-1.23606	2.28 E-08	FBgn00 30360	-0.7531	0.042 836	FBgn00 32524	-0.76452	4.16E -07
FBgn00 30357	0.724043	4.93E -05		FBgn00 32946	-1.76888	3.71 E-15	FBgn00 30438	-1.62151	4.59E -20	FBgn00 32666	-0.96205	1.08E -06

FBgn00 30432	0.69144	4.03E -11		FBgn00 33108	-7.22433	3.08 E-15	FBgn00 30439	1.059999	8.75E -08	FBgn00 32669	-3.50847	2.80E -12
FBgn00 30438	-2.09672	4.21E -33		FBgn00 33128	-1.04377	5.26 E-05	FBgn00 30479	-0.93528	8.12E -14	FBgn00 32670	-1.78402	2.83E -07
FBgn00 30439	1.09964	2.62E -08		FBgn00 33134	-1.51201	2.95 E-10	FBgn00 30485	-1.00243	3.05E -05	FBgn00 32683	-0.77519	9.59E -05
FBgn00 30479	-0.74791	3.08E -09		FBgn00 33153	-0.8189	1.50 E-08	FBgn00 30594	-1.74155	0.000 205	FBgn00 32684	-1.66779	1.44E -31
FBgn00 30485	-1.27969	1.10E -07		FBgn00 33159	-1.42335	3.67 E-05	FBgn00 30596	-0.86188	5.10E -13	FBgn00 32694	-0.91302	1.23E -19
FBgn00 30596	-0.68877	1.19E -08		FBgn00 33188	-2.10813	8.36 E-41	FBgn00 30600	-6.29712	2.89E -181	FBgn00 32713	-0.73876	9.85E -06
FBgn00 30600	-5.62098	1.66E -166		FBgn00 33214	-1.43922	3.71 E-14	FBgn00 30662	-0.82317	4.20E -06	FBgn00 32787	-1.02926	5.23E -12
FBgn00 30662	-0.68094	0.000 18		FBgn00 33302	-1.49371	1.74 E-05	FBgn00 30666	2.180735	9.04E -06	FBgn00 32891	-1.89632	0.000 128
FBgn00 30666	3.607176	1.95E -15		FBgn00 33369	-5.58575	3.60 E-10	FBgn00 30701	0.636788	2.00E -12	FBgn00 32897	-1.07025	1.06E -36
FBgn00 30793	0.589761	0.000 448		FBgn00 33387	-2.20785	5.86 E-19	FBgn00 30796	-0.69122	0.006 723	FBgn00 32899	-1.01244	4.24E -06
FBgn00 30796	-0.91904	0.000 289		FBgn00 33388	-5.14577	2.74 E- 118	FBgn00 30816	-0.97862	4.63E -21	FBgn00 32946	-1.29773	2.07E -09
FBgn00 30799	0.616844	0.000 554		FBgn00 33395	-2.84959	0	FBgn00 30839	-0.66476	2.87E -06	FBgn00 33093	-0.8501	0.015 538
FBgn00 30816	-1.08503	1.02E -25		FBgn00 33438	-1.59986	3.84 E-31	FBgn00 30884	-0.9162	4.78E -09	FBgn00 33108	-8.71524	1.03E -11
FBgn00 30847	-0.61381	0.000 531		FBgn00 33483	-1.2461	1.47 E-06	FBgn00 30899	-2.10556	1.91E -05	FBgn00 33128	-1.1399	9.19E -06
FBgn00 30884	-0.80757	2.86E -07		FBgn00 33494	-2.1566	3.32 E-31	FBgn00 30955	-1.32177	3.33E -32	FBgn00 33132	-1.11523	0.000 113
FBgn00 30899	-2.39155	1.50E -06		FBgn00 33519	-0.71461	0.00 3663	FBgn00 30968	0.925914	4.28E -05	FBgn00 33134	-2.28742	1.79E -19
FBgn00 30955	-1.04363	1.22E -20		FBgn00 33520	-0.62989	0.01 5073	FBgn00 30976	-0.70592	0.007 395	FBgn00 33153	-0.8385	6.25E -09

FBgn00 30968	1.253112	8.45E -09		FBgn00 33521	-0.78752	7.92 E-05	FBgn00 30999	-1.75966	0.033 074	FBgn00 33159	-1.20492	0.000 436
FBgn00 30976	-0.76644	0.003 695		FBgn00 33584	-0.76508	9.62 E-16	FBgn00 31053	1.100567	5.09E -05	FBgn00 33188	-1.93844	7.70E -35
FBgn00 31053	1.473482	1.37E -08		FBgn00 33652	-0.92558	0.00 0843	FBgn00 31157	0.754421	0.000 803	FBgn00 33214	-1.59385	1.00E -16
FBgn00 31157	1.032801	1.43E -06		FBgn00 33654	-0.69102	0.00 3859	FBgn00 31182	0.724441	3.44E -09	FBgn00 33274	-0.81729	0.007 942
FBgn00 31184	1.884407	1.07E -21		FBgn00 33782	-2.06449	2.70 E-09	FBgn00 31184	1.704824	9.65E -18	FBgn00 33302	-1.24031	0.000 42
FBgn00 31191	0.646	1.75E -09		FBgn00 33787	-1.98794	1.77 E-28	FBgn00 31220	-1.93564	1.39E -17	FBgn00 33369	-6.01636	1.68E -09
FBgn00 31220	-2.07178	9.24E -20		FBgn00 33817	-1.31277	2.08 E-06	FBgn00 31275	-2.14439	5.77E -09	FBgn00 33387	-2.71773	4.64E -26
FBgn00 31275	-2.58882	6.10E -12		FBgn00 33855	-4.28273	3.95 E-08	FBgn00 31322	1.342029	2.69E -12	FBgn00 33388	-5.67721	6.99E -118
FBgn00 31305	-0.62704	3.06E -06		FBgn00 33875	-0.70741	8.15 E-09	FBgn00 31327	-1.36223	1.75E -05	FBgn00 33395	-2.89439	0
FBgn00 31313	1.145217	0.000 178		FBgn00 33887	-0.77877	9.90 E-09	FBgn00 31343	-1.45436	7.47E -05	FBgn00 33438	-1.44406	8.67E -26
FBgn00 31321	0.633411	0.001 405		FBgn00 33919	-0.71898	0.00 2185	FBgn00 31414	-3.15018	9.32E -22	FBgn00 33446	-0.81652	0.000 436
FBgn00 31322	1.522032	8.23E -16		FBgn00 33926	-2.7403	0	FBgn00 31483	1.052809	7.76E -42	FBgn00 33483	-1.05914	4.73E -05
FBgn00 31327	-0.97783	0.002 34		FBgn00 33927	-2.75708	5.83 E- 166	FBgn00 31571	-0.78383	1.26E -06	FBgn00 33494	-1.91423	3.64E -26
FBgn00 31343	-1.36718	0.000 219		FBgn00 33958	-2.92268	8.15 E-09	FBgn00 31628	-0.69137	0.000 985	FBgn00 33540	-0.6096	2.20E -09
FBgn00 31414	-2.83115	3.38E -19		FBgn00 33978	-0.71314	0.00 7995	FBgn00 31678	0.801187	1.75E -10	FBgn00 33654	-0.70953	0.002 741
FBgn00 31461	-1.01345	0.009 004		FBgn00 33980	-0.88275	0.02 82	FBgn00 31717	-0.94621	1.41E -08	FBgn00 33782	-1.71475	2.97E -07
FBgn00 31483	1.166177	1.84E -51		FBgn00 33982	-0.68099	0.00 5725	FBgn00 31756	-0.83177	7.43E -08	FBgn00 33787	-1.42559	1.56E -15

FBgn00 31571	-1.06323	1.96E -11		FBgn00 34005	-1.58644	3.67 E-05	FBgn00 31777	-0.63246	0.001 038		FBgn00 33810	-0.92512	1.05E -07
FBgn00 31628	-0.91615	1.05E -05		FBgn00 34075	-0.87662	2.47 E-06	FBgn00 31805	1.22373	1.62E -05		FBgn00 33817	-1.81405	1.65E -10
FBgn00 31678	0.794446	2.98E -10		FBgn00 34085	-1.89692	4.88 E-09	FBgn00 31816	-0.80483	2.88E -05		FBgn00 33855	-4.45388	1.27E -08
FBgn00 31717	-0.83985	5.23E -07		FBgn00 34142	-0.83533	6.85 E-07	FBgn00 31888	-3.20052	1.14E -12		FBgn00 33926	-1.9382	2.16E -183
FBgn00 31756	-0.73746	2.40E -06		FBgn00 34143	-0.66388	2.19 E-08	FBgn00 31894	-0.61592	5.49E -08		FBgn00 33927	-2.10274	1.76E -104
FBgn00 31805	1.684032	4.60E -10		FBgn00 34145	-0.66535	0.00 398	FBgn00 31907	-2.71513	1.52E -16		FBgn00 34005	-1.19014	0.002 064
FBgn00 31888	-2.84364	2.83E -11		FBgn00 34219	-0.81353	0.01 5276	FBgn00 31908	-1.02789	0.000 263		FBgn00 34075	-0.76416	4.61E -05
FBgn00 31894	-0.69343	8.65E -10		FBgn00 34253	-0.59487	0.00 4302	FBgn00 31913	-1.21036	1.62E -21		FBgn00 34085	-0.79408	0.016 986
FBgn00 31907	-2.12824	4.70E -12		FBgn00 34264	-5.20019	3.75 E-56	FBgn00 31961	-1.05787	1.28E -06		FBgn00 34142	-0.60158	0.000 454
FBgn00 31908	-0.94922	0.000 817		FBgn00 34312	-1.05678	6.23 E-10	FBgn00 31971	0.844126	1.52E -10		FBgn00 34143	-0.77506	3.56E -11
FBgn00 31913	-1.20054	3.34E -21		FBgn00 34406	-1.48559	4.13 E-45	FBgn00 31974	-1.09834	3.49E -20		FBgn00 34194	-0.76536	3.17E -08
FBgn00 31914	-0.7069	0.001 309		FBgn00 34436	-0.59242	5.30 E-06	FBgn00 31975	-0.91917	8.10E -15		FBgn00 34264	-5.91421	1.47E -51
FBgn00 31948	-0.6673	8.88E -06		FBgn00 34438	-0.77755	0.00 0105	FBgn00 31999	0.91778	0.010 715		FBgn00 34275	-0.84851	0.004 452
FBgn00 31961	-0.75497	0.000 724		FBgn00 34493	-2.1668	4.43 E-30	FBgn00 32006	-0.61668	2.64E -08		FBgn00 34312	-1.21942	1.03E -12
FBgn00 31999	1.132522	0.001 138		FBgn00 34501	-0.9671	6.26 E-24	FBgn00 32022	-1.29387	9.41E -07		FBgn00 34406	-2.04444	3.98E -82
FBgn00 32006	-0.80791	1.56E -13		FBgn00 34512	-1.5839	2.14 E-07	FBgn00 32025	-1.17991	6.62E -05		FBgn00 34438	-1.25262	2.15E -10
FBgn00 32021	-0.75536	0.047 795		FBgn00 34602	-1.44181	4.91 E-16	FBgn00 32075	-1.16794	0.000 22		FBgn00 34439	-2.01709	8.35E -11

FBgn00 32022	-0.94953	0.000 359		FBgn00 34638	-0.94755	9.36 E-07	FBgn00 32126	-1.15489	2.86E -22	FBgn00 34443	-0.60248	3.23E -06
FBgn00 32025	-1.00346	0.000 834		FBgn00 34639	-1.85282	1.92 E-08	FBgn00 32129	-0.68748	0.034 811	FBgn00 34493	-2.22031	2.57E -31
FBgn00 32075	-1.15482	0.000 277		FBgn00 34659	-6.25665	9.72 E-13	FBgn00 32140	-1.22219	6.81E -11	FBgn00 34500	-0.71699	1.35E -10
FBgn00 32126	-0.88813	1.26E -13		FBgn00 34709	-0.88239	6.92 E-13	FBgn00 32149	-0.59436	0.000 368	FBgn00 34501	-0.87351	7.41E -20
FBgn00 32129	-0.72821	0.027 264		FBgn00 34718	-0.76209	9.97 E-05	FBgn00 32156	-0.85704	2.20E -07	FBgn00 34512	-1.59313	1.68E -07
FBgn00 32140	-0.98532	2.00E -07		FBgn00 34761	-0.70343	8.98 E-05	FBgn00 32161	0.726201	2.55E -13	FBgn00 34602	-0.98363	3.24E -08
FBgn00 32156	-1.1532	2.65E -12		FBgn00 34861	-1.14806	7.94 E-05	FBgn00 32167	-1.41873	8.10E -17	FBgn00 34638	-0.89244	3.87E -06
FBgn00 32167	-1.56971	4.86E -20		FBgn00 34903	-0.69799	0.00 3785	FBgn00 32187	-1.07541	8.27E -05	FBgn00 34639	-1.64748	4.59E -07
FBgn00 32211	-1.06732	0.010 991		FBgn00 35023	-0.73652	0.02 1232	FBgn00 32211	-1.71333	2.21E -05	FBgn00 34659	-8.2434	8.80E -19
FBgn00 32213	0.602449	0.007 554		FBgn00 35049	-1.83814	3.23 E-08	FBgn00 32218	-0.73768	1.02E -05	FBgn00 34709	-0.8128	3.94E -11
FBgn00 32218	-1.08521	4.62E -11		FBgn00 35099	-0.62551	0.01 868	FBgn00 32253	-1.05833	0.001 576	FBgn00 34761	-1.12902	1.31E -10
FBgn00 32235	-0.60182	0.038 577		FBgn00 35131	-1.29378	0.00 0317	FBgn00 32256	0.597193	6.54E -07	FBgn00 34861	-1.56207	1.04E -07
FBgn00 32264	-1.33435	6.96E -22		FBgn00 35132	-0.8827	2.57 E-09	FBgn00 32264	-1.15708	8.10E -17	FBgn00 35049	-1.50853	4.13E -06
FBgn00 32297	-1.18516	1.12E -08		FBgn00 35160	-0.58864	1.65 E-05	FBgn00 32297	-1.16664	1.84E -08	FBgn00 35131	-0.94515	0.008 55
FBgn00 32343	0.636212	4.19E -06		FBgn00 35262	-0.94324	0.00 0433	FBgn00 32311	-1.0846	2.03E -08	FBgn00 35160	-0.67859	4.71E -07
FBgn00 32382	0.713208	7.90E -07		FBgn00 35290	-0.68046	0.00 5869	FBgn00 32343	0.64328	3.07E -06	FBgn00 35262	-0.91602	0.000 613
FBgn00 32405	-2.17937	8.79E -11		FBgn00 35308	-0.65577	5.57 E-05	FBgn00 32405	-2.11264	1.93E -10	FBgn00 35308	-0.60346	0.000 216

FBgn00 32449	0.900262	1.42E -10		FBgn00 35490	-0.82081	0.01 4595	FBgn00 32422	-0.63609	2.18E -06	FBgn00 35542	-0.67263	1.41E -08
FBgn00 32470	-5.097	3.91E -23		FBgn00 35497	-0.76573	2.47 E-06	FBgn00 32449	0.770229	6.56E -08	FBgn00 35574	-0.69467	0.000 17
FBgn00 32666	-1.34264	8.19E -12		FBgn00 35542	-0.75381	1.89 E-10	FBgn00 32470	-6.24342	4.13E -18	FBgn00 35656	-1.08244	0.003 93
FBgn00 32669	-2.15935	6.18E -07		FBgn00 35574	-0.79251	1.61 E-05	FBgn00 32512	0.677849	5.70E -05	FBgn00 35695	-0.74701	0.001 807
FBgn00 32670	-2.27453	5.78E -10		FBgn00 35656	-0.98636	0.00 9472	FBgn00 32524	-0.76452	4.16E -07	FBgn00 35710	-0.82423	7.57E -15
FBgn00 32671	-0.59648	2.85E -08		FBgn00 35695	-0.83638	0.00 0462	FBgn00 32666	-0.96205	1.08E -06	FBgn00 35767	-0.77939	3.03E -05
FBgn00 32683	-1.21027	5.15E -10		FBgn00 35710	-0.75893	1.03 E-12	FBgn00 32669	-3.50847	2.80E -12	FBgn00 35770	-0.86512	7.30E -14
FBgn00 32684	-1.98037	6.60E -44		FBgn00 35763	-0.65819	3.76 E-15	FBgn00 32670	-1.78402	2.83E -07	FBgn00 35844	-0.89825	0.002 821
FBgn00 32694	-0.66422	7.83E -11		FBgn00 35767	-0.79213	2.42 E-05	FBgn00 32683	-0.77519	9.59E -05	FBgn00 35917	-0.88319	3.73E -05
FBgn00 32698	0.632368	6.73E -16		FBgn00 35770	-0.62414	1.04 E-07	FBgn00 32684	-1.66779	1.44E -31	FBgn00 35975	-0.92894	0.001 641
FBgn00 32713	-0.7073	2.58E -05		FBgn00 35791	-0.66353	0.00 2662	FBgn00 32694	-0.91302	1.23E -19	FBgn00 35976	-0.94805	0.003 672
FBgn00 32731	-0.66117	3.83E -15		FBgn00 35844	-1.02895	0.00 0609	FBgn00 32713	-0.73876	9.85E -06	FBgn00 36091	-2.08845	3.62E -14
FBgn00 32752	0.726394	1.20E -17		FBgn00 35868	-0.80007	5.34 E-05	FBgn00 32730	0.640968	9.09E -08	FBgn00 36101	-0.86918	0.008 428
FBgn00 32775	1.089029	1.95E -32		FBgn00 35917	-0.64199	0.00 3652	FBgn00 32752	0.70915	7.33E -17	FBgn00 36155	-0.63867	6.94E -06
FBgn00 32889	2.22772	1.43E -59		FBgn00 35975	-1.4809	5.61 E-07	FBgn00 32775	1.104013	2.33E -33	FBgn00 36205	-0.75095	2.53E -05
FBgn00 32891	2.178423	9.36E -10		FBgn00 35976	-0.96517	0.00 3325	FBgn00 32787	-1.02926	5.23E -12	FBgn00 36288	-1.37239	1.43E -05
FBgn00 32897	-0.95312	2.20E -29		FBgn00 36091	-1.52397	3.09 E-08	FBgn00 32869	1.871066	7.12E -05	FBgn00 36381	-1.46222	3.87E -11

FBgn00 32899	-1.23606	2.28E -08		FBgn00 36101	-1.3439	3.92 E-05	FBgn00 32889	2.072069	3.38E -51	FBgn00 36382	-0.6199	0.031 298
FBgn00 32946	-1.76888	3.71E -15		FBgn00 36205	-0.84928	1.67 E-06	FBgn00 32891	-1.89632	0.000 128	FBgn00 36454	-1.11372	6.23E -07
FBgn00 33051	1.257244	1.40E -19		FBgn00 36288	-0.87882	0.00 6021	FBgn00 32897	-1.07025	1.06E -36	FBgn00 36640	-0.65027	1.64E -10
FBgn00 33108	-7.22433	3.08E -15		FBgn00 36381	-1.50191	1.54 E-11	FBgn00 32899	-1.01244	4.24E -06	FBgn00 36714	-0.82555	8.75E -14
FBgn00 33128	-1.04377	5.26E -05		FBgn00 36433	-0.68846	5.73 E-06	FBgn00 32946	-1.29773	2.07E -09	FBgn00 36732	-0.64037	1.02E -05
FBgn00 33134	-1.51201	2.95E -10		FBgn00 36454	-1.32143	3.61 E-09	FBgn00 32997	0.774756	1.40E -06	FBgn00 36734	-0.6594	2.03E -14
FBgn00 33153	-0.8189	1.50E -08		FBgn00 36640	-0.77274	1.77 E-14	FBgn00 33051	1.282396	2.23E -20	FBgn00 36752	-0.7833	5.62E -11
FBgn00 33159	-1.42335	3.67E -05		FBgn00 36714	-1.34133	4.26 E-35	FBgn00 33075	0.620912	1.08E -08	FBgn00 36756	-1.6212	1.48E -17
FBgn00 33174	0.807377	4.36E -06		FBgn00 36732	-0.74875	2.03 E-07	FBgn00 33093	-0.8501	0.015 538	FBgn00 36926	-0.7801	0.005 576
FBgn00 33188	-2.10813	8.36E -41		FBgn00 36734	-0.67442	5.19 E-15	FBgn00 33108	-8.71524	1.03E -11	FBgn00 36945	-1.67586	0.000 193
FBgn00 33214	-1.43922	3.71E -14		FBgn00 36752	-0.92388	7.93 E-15	FBgn00 33128	-1.1399	9.19E -06	FBgn00 37012	-0.8434	2.93E -06
FBgn00 33234	1.178506	1.63E -13		FBgn00 36756	-1.58535	7.92 E-17	FBgn00 33132	-1.11523	0.000 113	FBgn00 37166	-1.59857	6.78E -07
FBgn00 33302	-1.49371	1.74E -05		FBgn00 36834	-0.65495	0.03 5161	FBgn00 33134	-2.28742	1.79E -19	FBgn00 37186	-1.26189	0.001 19
FBgn00 33304	0.644132	0.029 372		FBgn00 36882	-0.75894	0.01 5276	FBgn00 33153	-0.8385	6.25E -09	FBgn00 37290	-0.88958	0.014 827
FBgn00 33315	0.76736	8.26E -08		FBgn00 36926	-0.7261	0.01 0941	FBgn00 33159	-1.20492	0.000 436	FBgn00 37447	-0.89525	0.001 29
FBgn00 33369	-5.58575	3.60E -10		FBgn00 36945	-0.94641	0.04 2113	FBgn00 33174	1.117118	3.04E -11	FBgn00 37519	-0.96087	0.002 754
FBgn00 33373	1.0549	1.69E -21		FBgn00 37007	-0.62649	2.39 E-07	FBgn00 33188	-1.93844	7.70E -35	FBgn00 37520	-1.07269	0.000 399

FBgn00 33381	0.756316	4.06E -05		FBgn00 37012	-1.06024	2.77 E-09	FBgn00 33214	-1.59385	1.00E -16	FBgn00 37521	-1.26535	2.51E -05
FBgn00 33387	-2.20785	5.86E -19		FBgn00 37166	-1.57956	9.42 E-07	FBgn00 33234	0.940938	9.52E -09	FBgn00 37525	-0.67628	3.55E -08
FBgn00 33388	-5.14577	2.74E -118		FBgn00 37186	-1.05916	0.00 7548	FBgn00 33274	-0.81729	0.007 942	FBgn00 37548	-1.31921	2.83E -17
FBgn00 33392	1.437513	1.04E -45		FBgn00 37409	-1.0569	0.00 0426	FBgn00 33302	-1.24031	0.000 42	FBgn00 37577	-1.38555	2.94E -07
FBgn00 33395	-2.84959	0		FBgn00 37447	-0.76453	0.00 6872	FBgn00 33304	0.782552	0.005 714	FBgn00 37730	-2.06432	0.001 653
FBgn00 33431	0.762501	2.94E -07		FBgn00 37519	-0.91562	0.00 4699	FBgn00 33315	0.59459	5.49E -05	FBgn00 37796	-0.97966	0.000 275
FBgn00 33438	-1.59986	3.84E -31		FBgn00 37520	-1.21942	5.64 E-05	FBgn00 33369	-6.01636	1.68E -09	FBgn00 37836	-2.38327	2.73E -22
FBgn00 33483	-1.2461	1.47E -06		FBgn00 37521	-1.0585	0.00 0448	FBgn00 33373	0.992031	5.08E -19	FBgn00 37898	-0.63814	0.008 327
FBgn00 33494	-2.1566	3.32E -31		FBgn00 37525	-0.72226	3.67 E-09	FBgn00 33387	-2.71773	4.64E -26	FBgn00 37934	-1.39741	6.99E -18
FBgn00 33519	-0.71461	0.003 663		FBgn00 37548	-1.05251	1.31 E-11	FBgn00 33388	-5.67721	6.99E -118	FBgn00 37936	-1.56585	1.15E -16
FBgn00 33520	-0.62989	0.015 073		FBgn00 37552	-0.77656	7.91 E-09	FBgn00 33392	1.506011	2.21E -50	FBgn00 37956	-0.92561	1.66E -08
FBgn00 33521	-0.78752	7.92E -05		FBgn00 37577	-0.60509	0.03 6132	FBgn00 33395	-2.89439	0	FBgn00 37989	-0.8476	1.33E -05
FBgn00 33549	0.670703	1.59E -05		FBgn00 37730	-2.80326	1.90 E-05	FBgn00 33431	0.693199	4.22E -06	FBgn00 38088	-2.10863	2.06E -28
FBgn00 33584	-0.76508	9.62E -16		FBgn00 37796	-1.32108	1.06 E-06	FBgn00 33438	-1.44406	8.67E -26	FBgn00 38207	-1.26696	2.85E -05
FBgn00 33627	0.668133	0.006 405		FBgn00 37836	-2.38587	2.64 E-22	FBgn00 33446	-0.81652	0.000 436	FBgn00 38243	-0.62002	6.47E -08
FBgn00 33652	-0.92558	0.000 843		FBgn00 37934	-1.59811	1.27 E-22	FBgn00 33453	0.794428	1.16E -13	FBgn00 38260	-1.22811	1.39E -12
FBgn00 33654	-0.69102	0.003 859		FBgn00 37936	-1.82501	1.88 E-21	FBgn00 33483	-1.05914	4.73E -05	FBgn00 38294	-0.75522	9.19E -07

FBgn00 33769	2.106456	3.05E -30		FBgn00 37956	-0.85495	2.11 E-07	FBgn00 33494	-1.91423	3.64E -26		FBgn00 38321	-0.69817	1.45E -05
FBgn00 33782	-2.06449	2.70E -09		FBgn00 37989	-1.01754	1.50 E-07	FBgn00 33540	-0.6096	2.20E -09		FBgn00 38460	-0.65356	0.000 21
FBgn00 33787	-1.98794	1.77E -28		FBgn00 38088	-2.51593	1.96 E-36	FBgn00 33654	-0.70953	0.002 741		FBgn00 38465	-0.90842	9.30E -32
FBgn00 33799	1.486589	1.38E -20		FBgn00 38207	-1.55007	4.27 E-07	FBgn00 33769	1.863054	2.17E -23		FBgn00 38610	-0.69265	1.29E -05
FBgn00 33817	-1.31277	2.08E -06		FBgn00 38260	-0.99614	7.53 E-09	FBgn00 33777	0.662867	2.31E -11		FBgn00 38681	-3.26648	9.31E -65
FBgn00 33855	-4.28273	3.95E -08		FBgn00 38321	-0.61759	0.00 0158	FBgn00 33782	-1.71475	2.97E -07		FBgn00 38682	-0.8975	0.000 369
FBgn00 33875	-0.70741	8.15E -09		FBgn00 38460	-0.70543	6.17 E-05	FBgn00 33787	-1.42559	1.56E -15		FBgn00 38720	-1.30181	1.40E -12
FBgn00 33887	-0.77877	9.90E -09		FBgn00 38465	-0.8458	1.13 E-27	FBgn00 33799	1.820543	4.30E -31		FBgn00 38774	-1.2812	3.65E -05
FBgn00 33917	0.840553	8.13E -12		FBgn00 38638	-0.62544	0.00 2631	FBgn00 33810	-0.92512	1.05E -07		FBgn00 38799	-9.93713	3.77E -15
FBgn00 33919	-0.71898	0.002 185		FBgn00 38681	-3.57364	3.79 E-70	FBgn00 33817	-1.81405	1.65E -10		FBgn00 38842	-0.87542	2.89E -11
FBgn00 33926	-2.7403	0		FBgn00 38682	-0.93036	0.00 0227	FBgn00 33855	-4.45388	1.27E -08		FBgn00 38881	-0.75979	1.08E -06
FBgn00 33927	-2.75708	5.83E -166		FBgn00 38720	-1.31455	9.59 E-13	FBgn00 33926	-1.9382	2.16E -183		FBgn00 38938	-1.78658	0.000 483
FBgn00 33958	-2.92268	8.15E -09		FBgn00 38774	-0.71286	0.02 5394	FBgn00 33927	-2.10274	1.76E -104		FBgn00 38981	-1.05024	2.86E -11
FBgn00 33978	-0.71314	0.007 995		FBgn00 38799	-6.26441	9.14 E-25	FBgn00 33979	0.639021	6.26E -20		FBgn00 38986	-4.84203	2.66E -98
FBgn00 33980	-0.88275	0.028 2		FBgn00 38826	-0.85168	0.00 025	FBgn00 33993	0.825591	1.47E -07		FBgn00 39039	-7.67581	4.82E -09
FBgn00 33982	-0.68099	0.005 725		FBgn00 38842	-0.69607	1.48 E-07	FBgn00 34005	-1.19014	0.002 064		FBgn00 39075	-1.01437	8.96E -05
FBgn00 33994	0.637531	8.77E -10		FBgn00 38881	-0.85978	3.14 E-08	FBgn00 34063	0.903718	1.49E -25		FBgn00 39084	-1.22507	5.70E -05

FBgn00 34005	-1.58644	3.67E -05		FBgn00 38981	-0.9029	1.26 E-08	FBgn00 34075	-0.76416	4.61E -05	FBgn00 39114	-1.29336	4.37E -16
FBgn00 34075	-0.87662	2.47E -06		FBgn00 38986	-4.83551	8.05 E-98	FBgn00 34085	-0.79408	0.016 986	FBgn00 39155	-1.31019	5.65E -22
FBgn00 34085	-1.89692	4.88E -09		FBgn00 39039	-5.76873	4.80 E-12	FBgn00 34142	-0.60158	0.000 454	FBgn00 39266	-0.66944	8.24E -07
FBgn00 34141	0.656262	6.49E -08		FBgn00 39075	-1.24312	1.57 E-06	FBgn00 34143	-0.77506	3.56E -11	FBgn00 39312	-2.14068	1.65E -06
FBgn00 34142	-0.83533	6.85E -07		FBgn00 39084	-1.40052	4.47 E-06	FBgn00 34194	-0.76536	3.17E -08	FBgn00 39313	-2.01788	2.68E -13
FBgn00 34143	-0.66388	2.19E -08		FBgn00 39114	-1.41046	1.11 E-18	FBgn00 34261	0.587495	5.40E -10	FBgn00 39328	-1.33281	6.66E -05
FBgn00 34145	-0.66535	0.003 98		FBgn00 39155	-1.23443	9.96 E-20	FBgn00 34264	-5.91421	1.47E -51	FBgn00 39419	-0.93555	4.87E -08
FBgn00 34219	-0.81353	0.015 276		FBgn00 39266	-1.02867	1.01 E-14	FBgn00 34275	-0.84851	0.004 452	FBgn00 39486	-1.26283	7.37E -06
FBgn00 34253	-0.59487	0.004 302		FBgn00 39312	-1.22445	0.00 8567	FBgn00 34312	-1.21942	1.03E -12	FBgn00 39529	-1.1226	2.18E -09
FBgn00 34264	-5.20019	3.75E -56		FBgn00 39313	-1.19122	2.52 E-05	FBgn00 34335	1.602258	2.09E -24	FBgn00 39620	-0.67551	0.046 732
FBgn00 34312	-1.05678	6.23E -10		FBgn00 39328	-1.30625	0.00 0101	FBgn00 34354	0.794452	1.40E -05	FBgn00 39678	-0.76733	0.005 089
FBgn00 34335	1.698269	1.87E -27		FBgn00 39419	-1.23723	6.04 E-13	FBgn00 34389	0.597452	1.68E -10	FBgn00 39738	-0.60124	0.000 182
FBgn00 34354	1.240682	1.24E -12		FBgn00 39431	-0.62893	3.03 E-07	FBgn00 34406	-2.04444	3.98E -82	FBgn00 39748	-0.93197	0.000 403
FBgn00 34406	-1.48559	4.13E -45		FBgn00 39486	-0.72483	0.01 1516	FBgn00 34438	-1.25262	2.15E -10	FBgn00 39756	-0.88838	0.001 291
FBgn00 34436	-0.59242	5.30E -06		FBgn00 39529	-0.61435	0.00 1557	FBgn00 34439	-2.01709	8.35E -11	FBgn00 39776	-1.29231	1.20E -24
FBgn00 34438	-0.77755	0.000 105		FBgn00 39633	-0.59884	2.90 E-06	FBgn00 34443	-0.60248	3.23E -06	FBgn00 39809	-1.00748	5.73E -05
FBgn00 34493	-2.1668	4.43E -30		FBgn00 39678	-0.6182	0.02 8092	FBgn00 34493	-2.22031	2.57E -31	FBgn00 39827	-1.54025	2.67E -10

FBgn00 34501	-0.9671	6.26E -24		FBgn00 39756	-1.12724	3.63 E-05	FBgn00 34500	-0.71699	1.35E -10		FBgn00 39836	-1.18473	3.43E -08
FBgn00 34512	-1.5839	2.14E -07		FBgn00 39776	-0.89053	3.30 E-12	FBgn00 34501	-0.87351	7.41E -20		FBgn00 39872	-1.49648	0.008 222
FBgn00 34564	0.602703	4.49E -08		FBgn00 39809	-1.17582	2.97 E-06	FBgn00 34512	-1.59313	1.68E -07		FBgn00 39883	-1.19502	0.004 066
FBgn00 34578	0.701628	0.000 275		FBgn00 39827	-1.45155	2.70 E-09	FBgn00 34602	-0.98363	3.24E -08		FBgn00 39925	-1.40045	7.68E -06
FBgn00 34602	-1.44181	4.91E -16		FBgn00 39836	-1.18529	3.61 E-08	FBgn00 34638	-0.89244	3.87E -06		FBgn00 40038	-5.51187	1.04E -30
FBgn00 34638	-0.94755	9.36E -07		FBgn00 39862	-0.73902	0.00 0859	FBgn00 34639	-1.64748	4.59E -07		FBgn00 40089	-0.73261	0.000 374
FBgn00 34639	-1.85282	1.92E -08		FBgn00 39872	-1.23986	0.03 3009	FBgn00 34659	-8.2434	8.80E -19		FBgn00 40299	-3.1716	1.46E -08
FBgn00 34659	-6.25665	9.72E -13		FBgn00 39883	-1.2694	0.00 23	FBgn00 34709	-0.8128	3.94E -11		FBgn00 40351	-3.16301	3.56E -14
FBgn00 34709	-0.88239	6.92E -13		FBgn00 39925	-1.6068	3.53 E-07	FBgn00 34761	-1.12902	1.31E -10		FBgn00 40364	-1.73077	4.74E -25
FBgn00 34718	-0.76209	9.97E -05		FBgn00 40038	-4.91738	2.24 E-33	FBgn00 34796	0.826153	5.80E -12		FBgn00 40370	-1.44523	2.63E -10
FBgn00 34761	-0.70343	8.98E -05		FBgn00 40089	-0.84335	3.69 E-05	FBgn00 34861	-1.56207	1.04E -07		FBgn00 40398	-1.27015	1.95E -07
FBgn00 34796	0.750478	6.69E -10		FBgn00 40299	-3.3663	4.38 E-09	FBgn00 34924	0.723054	7.94E -12		FBgn00 40491	-0.73531	0.000 79
FBgn00 34861	-1.14806	7.94E -05		FBgn00 40351	-3.02252	1.93 E-13	FBgn00 34997	0.658123	3.55E -20		FBgn00 40551	-1.0075	0.000 803
FBgn00 34903	-0.69799	0.003 785		FBgn00 40364	-1.69113	5.27 E-24	FBgn00 34999	1.130643	3.45E -19		FBgn00 40609	-2.0946	3.49E -15
FBgn00 34997	0.6552	5.39E -20		FBgn00 40370	-1.29987	1.39 E-08	FBgn00 35035	1.190584	1.48E -16		FBgn00 40765	-1.25212	6.23E -11
FBgn00 34999	1.48945	2.64E -33		FBgn00 40398	-1.28385	1.53 E-07	FBgn00 35049	-1.50853	4.13E -06		FBgn00 40823	-0.77745	1.96E -07
FBgn00 35023	-0.73652	0.021 232		FBgn00 40514	-0.70253	0.04 2503	FBgn00 35085	0.715613	0.000 429		FBgn00 40827	-1.63953	0.000 52

FBgn00 35035	1.343603	4.37E -21		FBgn00 40609	-2.07349	6.76 E-15	FBgn00 35131	-0.94515	0.008 55	FBgn00 40832	-0.64611	0.042 688
FBgn00 35049	-1.83814	3.23E -08		FBgn00 40765	-1.23353	1.39 E-10	FBgn00 35160	-0.67859	4.71E -07	FBgn00 40850	-1.32138	7.76E -12
FBgn00 35084	0.712443	0.004 095		FBgn00 40823	-1.17901	9.62 E-16	FBgn00 35262	-0.91602	0.000 613	FBgn00 41180	-1.30854	7.31E -33
FBgn00 35085	0.976273	5.28E -07		FBgn00 40827	-1.95213	3.49 E-05	FBgn00 35308	-0.60346	0.000 216	FBgn00 41182	-1.46565	0.000 2
FBgn00 35099	-0.62551	0.018 68		FBgn00 40850	-0.96865	4.70 E-07	FBgn00 35542	-0.67263	1.41E -08	FBgn00 41184	-1.39161	1.63E -18
FBgn00 35131	-1.29378	0.000 317		FBgn00 41180	-1.3545	4.93 E-35	FBgn00 35574	-0.69467	0.000 17	FBgn00 41721	-1.10131	0.031 385
FBgn00 35132	-0.8827	2.57E -09		FBgn00 41184	-1.28926	4.41 E-16	FBgn00 35656	-1.08244	0.003 93	FBgn00 42094	-0.58522	1.34E -07
FBgn00 35160	-0.58864	1.65E -05		FBgn00 41712	-0.95177	0.02 705	FBgn00 35695	-0.74701	0.001 807	FBgn00 43841	-0.62418	6.30E -08
FBgn00 35189	0.757964	0.018 352		FBgn00 43364	-0.66046	5.94 E-09	FBgn00 35710	-0.82423	7.57E -15	FBgn00 44047	-1.20727	1.22E -10
FBgn00 35209	1.010811	5.31E -08		FBgn00 43783	-1.023	0.02 3468	FBgn00 35767	-0.77939	3.03E -05	FBgn00 44510	-0.86665	1.74E -11
FBgn00 35210	0.598842	0.000 845		FBgn00 43841	-0.65953	1.07 E-08	FBgn00 35770	-0.86512	7.30E -14	FBgn00 45064	-1.07029	8.30E -24
FBgn00 35262	-0.94324	0.000 433		FBgn00 44047	-1.54735	2.44 E-16	FBgn00 35844	-0.89825	0.002 821	FBgn00 45479	-4.62446	9.84E -14
FBgn00 35290	-0.68046	0.005 869		FBgn00 44510	-0.72079	3.67 E-08	FBgn00 35917	-0.88319	3.73E -05	FBgn00 46887	-0.81995	0.020 687
FBgn00 35308	-0.65577	5.57E -05		FBgn00 45064	-0.98411	1.95 E-20	FBgn00 35975	-0.92894	0.001 641	FBgn00 50089	-1.32828	4.21E -09
FBgn00 35490	-0.82081	0.014 595		FBgn00 45479	-4.61264	1.23 E-13	FBgn00 35976	-0.94805	0.003 672	FBgn00 50104	-1.41224	1.42E -20
FBgn00 35497	-0.76573	2.47E -06		FBgn00 50015	-0.78926	3.28 E-05	FBgn00 36091	-2.08845	3.62E -14	FBgn00 50115	-1.1836	1.51E -22
FBgn00 35542	-0.75381	1.89E -10		FBgn00 50069	-0.68294	7.05 E-05	FBgn00 36101	-0.86918	0.008 428	FBgn00 50197	-1.49861	7.27E -12

FBgn00 35574	-0.79251	1.61E -05		FBgn00 50089	-1.31957	5.71 E-09	FBgn00 36155	-0.63867	6.94E -06		FBgn00 50345	-3.30831	1.77E -211
FBgn00 35656	-0.98636	0.009 472		FBgn00 50104	-1.46311	6.56 E-22	FBgn00 36205	-0.75095	2.53E -05		FBgn00 50401	-1.91816	5.17E -05
FBgn00 35695	-0.83638	0.000 462		FBgn00 50115	-1.0482	4.20 E-18	FBgn00 36288	-1.37239	1.43E -05		FBgn00 50418	-0.66119	0.041 739
FBgn00 35710	-0.75893	1.03E -12		FBgn00 50197	-1.45113	3.67 E-11	FBgn00 36324	1.714493	5.10E -09		FBgn00 50428	-1.60816	1.37E -19
FBgn00 35761	0.59215	3.64E -10		FBgn00 50345	-3.28309	7.47 E- 209	FBgn00 36330	0.670829	1.81E -09		FBgn00 51004	-3.63387	1.68E -26
FBgn00 35763	-0.65819	3.76E -15		FBgn00 50401	-1.03479	0.03 4038	FBgn00 36381	-1.46222	3.87E -11		FBgn00 51029	-2.0001	4.85E -24
FBgn00 35767	-0.79213	2.42E -05		FBgn00 50428	-1.52524	7.74 E-18	FBgn00 36382	-0.6199	0.031 298		FBgn00 51053	-0.75742	8.21E -06
FBgn00 35770	-0.62414	1.04E -07		FBgn00 50460	-0.77724	0.00 0224	FBgn00 36454	-1.11372	6.23E -07		FBgn00 51116	-0.95585	5.53E -08
FBgn00 35791	-0.66353	0.002 662		FBgn00 50466	-0.70458	3.25 E-05	FBgn00 36565	0.645802	1.35E -10		FBgn00 51279	-0.88136	0.005 148
FBgn00 35844	-1.02895	0.000 609		FBgn00 51004	-3.77878	3.60 E-27	FBgn00 36640	-0.65027	1.64E -10		FBgn00 51313	-2.06681	6.18E -13
FBgn00 35868	-0.80007	5.34E -05		FBgn00 51029	-2.07497	2.29 E-25	FBgn00 36648	0.866244	7.90E -13		FBgn00 51324	-1.35265	5.08E -19
FBgn00 35917	-0.64199	0.003 652		FBgn00 51053	-0.74613	1.20 E-05	FBgn00 36710	0.587384	2.34E -09		FBgn00 51354	-3.24734	1.12E -39
FBgn00 35975	-1.4809	5.61E -07		FBgn00 51116	-1.15274	5.88 E-11	FBgn00 36714	-0.82555	8.75E -14		FBgn00 51514	-1.05925	0.001 188
FBgn00 35976	-0.96517	0.003 325		FBgn00 51313	-2.35355	2.32 E-15	FBgn00 36732	-0.64037	1.02E -05		FBgn00 51525	-0.61517	0.042 196
FBgn00 36091	-1.52397	3.09E -08		FBgn00 51324	-1.2167	1.13 E-15	FBgn00 36734	-0.6594	2.03E -14		FBgn00 51617	-0.75552	4.54E -11
FBgn00 36101	-1.3439	3.92E -05		FBgn00 51354	-2.46996	1.07 E-27	FBgn00 36752	-0.7833	5.62E -11		FBgn00 51661	-0.65966	0.000 415
FBgn00 36205	-0.84928	1.67E -06		FBgn00 51514	-0.68605	0.04 2024	FBgn00 36756	-1.6212	1.48E -17		FBgn00 51781	-1.36095	1.13E -06

FBgn00 36288	-0.87882	0.006 021		FBgn00 51525	-0.9851	0.00 0959	FBgn00 36765	0.841804	0.001 329		FBgn00 51807	-0.87691	0.003 123
FBgn00 36324	1.650343	2.40E -08		FBgn00 51612	-0.63146	0.00 0362	FBgn00 36926	-0.7801	0.005 576		FBgn00 51869	-0.64566	0.001 482
FBgn00 36381	-1.50191	1.54E -11		FBgn00 51614	-0.63096	0.00 3589	FBgn00 36945	-1.67586	0.000 193		FBgn00 51973	-0.94812	0.001 548
FBgn00 36433	-0.68846	5.73E -06		FBgn00 51661	-0.70778	0.00 0141	FBgn00 36991	0.609193	2.18E -05		FBgn00 52091	-1.31955	1.17E -23
FBgn00 36454	-1.32143	3.61E -09		FBgn00 51710	-0.67327	0.00 6485	FBgn00 37012	-0.8434	2.93E -06		FBgn00 52099	-0.63998	1.10E -05
FBgn00 36640	-0.77274	1.77E -14		FBgn00 51781	-0.65296	0.02 2927	FBgn00 37071	0.59733	4.14E -07		FBgn00 52195	-0.68925	0.000 699
FBgn00 36648	0.844484	3.85E -12		FBgn00 51807	-0.97363	0.00 1024	FBgn00 37166	-1.59857	6.78E -07		FBgn00 52280	-0.64195	0.023 167
FBgn00 36714	-1.34133	4.26E -35		FBgn00 51869	-0.66476	0.00 1064	FBgn00 37186	-1.26189	0.001 19		FBgn00 52311	-0.90018	1.67E -06
FBgn00 36732	-0.74875	2.03E -07		FBgn00 51973	-1.51847	6.40 E-07	FBgn00 37290	-0.88958	0.014 827		FBgn00 52364	-1.27713	2.22E -11
FBgn00 36734	-0.67442	5.19E -15		FBgn00 52091	-1.42173	2.68 E-27	FBgn00 37447	-0.89525	0.001 29		FBgn00 52369	-0.72446	0.000 391
FBgn00 36752	-0.92388	7.93E -15		FBgn00 52099	-0.85157	3.55 E-09	FBgn00 37515	1.631174	5.90E -31		FBgn00 52448	-0.63469	0.028 479
FBgn00 36756	-1.58535	7.92E -17		FBgn00 52137	-0.80279	3.37 E-10	FBgn00 37519	-0.96087	0.002 754		FBgn00 52476	-1.40893	1.22E -05
FBgn00 36765	1.166553	2.54E -06		FBgn00 52195	-0.98144	9.54 E-07	FBgn00 37520	-1.07269	0.000 399		FBgn00 52625	-0.7131	7.28E -09
FBgn00 36834	-0.65495	0.035 161		FBgn00 52218	-0.68244	0.00 0948	FBgn00 37521	-1.26535	2.51E -05		FBgn00 52687	-0.99362	1.66E -12
FBgn00 36882	-0.75894	0.015 276		FBgn00 52311	-0.65895	0.00 0598	FBgn00 37525	-0.67628	3.55E -08		FBgn00 52702	-0.91742	1.00E -09
FBgn00 36926	-0.7261	0.010 941		FBgn00 52364	-0.66342	0.00 0643	FBgn00 37548	-1.31921	2.83E -17		FBgn00 52773	-1.36701	1.43E -06
FBgn00 36945	-0.94641	0.042 113		FBgn00 52369	-0.91494	5.01 E-06	FBgn00 37577	-1.38555	2.94E -07		FBgn00 52816	-0.84143	4.52E -09

FBgn00 37007	-0.62649	2.39E -07		FBgn00 52476	-1.66447	3.04 E-07	FBgn00 37581	1.294857	1.83E -07	FBgn00 52850	-0.64797	3.23E -09
FBgn00 37012	-1.06024	2.77E -09		FBgn00 52687	-1.10909	3.40 E-15	FBgn00 37646	0.746304	1.75E -05	FBgn00 53080	-1.01319	2.64E -10
FBgn00 37028	0.589883	1.03E -09		FBgn00 52702	-0.90975	1.55 E-09	FBgn00 37664	1.059644	1.75E -25	FBgn00 53099	-1.01868	1.77E -05
FBgn00 37166	-1.57956	9.42E -07		FBgn00 52773	-1.34325	2.25 E-06	FBgn00 37730	-2.06432	0.001 653	FBgn00 53196	-0.7704	0.019 419
FBgn00 37186	-1.05916	0.007 548		FBgn00 52816	-1.29025	7.73 E-20	FBgn00 37773	0.931989	3.09E -15	FBgn00 53207	-2.28268	2.63E -21
FBgn00 37409	-1.0569	0.000 426		FBgn00 53080	-0.8547	1.17 E-07	FBgn00 37779	0.591684	3.26E -08	FBgn00 53508	-7.23722	6.93E -20
FBgn00 37447	-0.76453	0.006 872		FBgn00 53099	-0.93713	8.91 E-05	FBgn00 37796	-0.97966	0.000 275	FBgn00 53519	-0.70668	0.030 865
FBgn00 37515	1.950649	1.44E -44		FBgn00 53108	-0.64811	0.04 442	FBgn00 37836	-2.38327	2.73E -22	FBgn00 53810	-0.7616	1.27E -08
FBgn00 37519	-0.91562	0.004 699		FBgn00 53207	-1.22343	4.30 E-08	FBgn00 37879	1.448264	5.14E -11	FBgn00 53813	-0.71348	5.21E -14
FBgn00 37520	-1.21942	5.64E -05		FBgn00 53508	-5.76894	1.14 E-29	FBgn00 37898	-0.63814	0.008 327	FBgn00 53816	-0.68902	1.91E -13
FBgn00 37521	-1.0585	0.000 448		FBgn00 53810	-0.58534	1.95 E-05	FBgn00 37934	-1.39741	6.99E -18	FBgn00 53819	-0.78233	8.05E -14
FBgn00 37525	-0.72226	3.67E -09		FBgn00 53816	-0.59286	3.52 E-10	FBgn00 37936	-1.56585	1.15E -16	FBgn00 53822	-0.81888	5.74E -17
FBgn00 37535	0.610487	7.95E -06		FBgn00 53825	-0.68267	3.13 E-08	FBgn00 37956	-0.92561	1.66E -08	FBgn00 53825	-0.88785	2.75E -13
FBgn00 37548	-1.05251	1.31E -11		FBgn00 53828	-0.60927	2.30 E-10	FBgn00 37973	1.318196	1.33E -08	FBgn00 53828	-0.8315	2.12E -18
FBgn00 37552	-0.77656	7.91E -09		FBgn00 53831	-0.68617	6.28 E-12	FBgn00 37989	-0.8476	1.33E -05	FBgn00 53831	-0.90138	8.62E -20
FBgn00 37577	-0.60509	0.036 132		FBgn00 53855	-0.87871	1.24 E-09	FBgn00 38011	0.70523	0.002 573	FBgn00 53855	-1.0306	8.29E -13
FBgn00 37581	1.556838	1.37E -10		FBgn00 53858	-0.85947	3.75 E-11	FBgn00 38038	0.590439	0.001 516	FBgn00 53858	-0.89223	5.40E -12

FBgn00 37617	0.697911	4.10E -05		FBgn00 53861	-0.9394	7.91 E-13	FBgn00 38047	0.63394	0.000 156	FBgn00 53861	-0.77788	3.22E -09
FBgn00 37664	1.172143	3.31E -31		FBgn00 53926	-0.73426	0.02 2834	FBgn00 38088	-2.10863	2.06E -28	FBgn00 53868	-1.28788	7.77E -16
FBgn00 37730	-2.80326	1.90E -05		FBgn00 53970	-0.64631	0.00 0865	FBgn00 38115	0.900188	4.72E -21	FBgn00 53926	-0.89542	0.004 521
FBgn00 37773	0.687664	2.09E -08		FBgn00 58160	-0.64272	3.39 E-06	FBgn00 38207	-1.26696	2.85E -05	FBgn00 58178	-0.74476	8.07E -05
FBgn00 37796	-1.32108	1.06E -06		FBgn00 60296	-0.67149	8.86 E-07	FBgn00 38243	-0.62002	6.47E -08	FBgn00 58469	-1.08367	0.000 977
FBgn00 37836	-2.38587	2.64E -22		FBgn00 62449	-0.88995	2.23 E-19	FBgn00 38260	-1.22811	1.39E -12	FBgn00 60296	-0.72906	7.69E -08
FBgn00 37844	0.796226	1.06E -06		FBgn00 62978	-1.03042	9.84 E-05	FBgn00 38273	0.78862	0.000 193	FBgn00 62978	-0.69339	0.010 39
FBgn00 37879	1.495647	1.14E -11		FBgn00 63497	-1.02335	1.73 E-05	FBgn00 38294	-0.75522	9.19E -07	FBgn00 63497	-0.97028	4.31E -05
FBgn00 37934	-1.59811	1.27E -22		FBgn00 63499	-2.80447	6.51 E-83	FBgn00 38321	-0.69817	1.45E -05	FBgn00 63499	-2.71123	3.21E -79
FBgn00 37936	-1.82501	1.88E -21		FBgn00 65055	-0.63279	0.00 1728	FBgn00 38450	1.597504	0.002 836	FBgn00 65046	-0.62554	0.004 367
FBgn00 37956	-0.85495	2.11E -07		FBgn00 69938	-3.73774	2.02 E-16	FBgn00 38460	-0.65356	0.000 21	FBgn00 65047	-0.67471	0.000 123
FBgn00 37973	1.709858	3.05E -14		FBgn00 82947	-2.04981	5.29 E-15	FBgn00 38465	-0.90842	9.30E -32	FBgn00 65048	-0.70845	2.55E -05
FBgn00 37975	1.42062	1.00E -04		FBgn00 82981	-0.63159	0.00 5176	FBgn00 38547	0.595628	0.010 665	FBgn00 65055	-1.37124	3.20E -13
FBgn00 37989	-1.01754	1.50E -07		FBgn00 83940	-1.54213	3.86 E-20	FBgn00 38610	-0.69265	1.29E -05	FBgn00 65098	-0.60762	0.003 015
FBgn00 37999	0.632062	0.000 761		FBgn00 83949	-7.15159	4.27 E-10	FBgn00 38681	-3.26648	9.31E -65	FBgn00 69923	-0.6552	0.014 012
FBgn00 38038	0.901245	3.39E -07		FBgn00 85354	-1.13146	6.42 E-08	FBgn00 38682	-0.8975	0.000 369	FBgn00 69938	-4.82515	1.39E -16
FBgn00 38088	-2.51593	1.96E -36		FBgn00 85362	-0.68498	0.00 3336	FBgn00 38720	-1.30181	1.40E -12	FBgn00 82925	-0.97014	0.001 229

FBgn00 38115	0.815837	2.65E -17		FBgn00 85376	-1.0317	9.05 E-18	FBgn00 38740	0.633273	7.44E -12	FBgn00 82947	-2.35176	1.21E -18
FBgn00 38207	-1.55007	4.27E -07		FBgn00 85382	-5.13155	1.12 E-47	FBgn00 38744	0.685771	0.001 76	FBgn00 82958	-0.80972	0.008 901
FBgn00 38260	-0.99614	7.53E -09		FBgn00 85383	-7.05084	2.10 E-28	FBgn00 38774	-1.2812	3.65E -05	FBgn00 82959	-0.67203	0.038 153
FBgn00 38273	0.799103	0.000 162		FBgn00 85407	-2.28584	8.61 E-10	FBgn00 38799	-9.93713	3.77E -15	FBgn00 82966	-0.67087	0.002 644
FBgn00 38321	-0.61759	0.000 158		FBgn00 85408	-0.92276	1.50 E-08	FBgn00 38804	0.947781	1.09E -07	FBgn00 82971	-0.71189	0.002 349
FBgn00 38460	-0.70543	6.17E -05		FBgn00 85410	-1.18475	0.00 1626	FBgn00 38828	0.604683	2.70E -08	FBgn00 82974	-0.99055	0.000 126
FBgn00 38465	-0.8458	1.13E -27		FBgn00 85412	-0.73306	1.72 E-07	FBgn00 38842	-0.87542	2.89E -11	FBgn00 82980	-0.87406	0.003 876
FBgn00 38490	0.609585	0.002 607		FBgn00 85413	-1.59975	5.01 E-06	FBgn00 38881	-0.75979	1.08E -06	FBgn00 82981	-1.11689	1.61E -07
FBgn00 38638	-0.62544	0.002 631		FBgn00 85446	-0.9198	2.52 E-11	FBgn00 38938	-1.78658	0.000 483	FBgn00 83001	-0.73462	0.006 92
FBgn00 38681	-3.57364	3.79E -70		FBgn00 85450	-0.6361	1.23 E-07	FBgn00 38981	-1.05024	2.86E -11	FBgn00 83003	-1.44052	0.006 612
FBgn00 38682	-0.93036	0.000 227		FBgn00 85638	-0.90847	2.19 E-17	FBgn00 38986	-4.84203	2.66E -98	FBgn00 83005	-0.89816	0.000 837
FBgn00 38720	-1.31455	9.59E -13		FBgn00 85732	-2.62458	7.95 E- 162	FBgn00 39006	2.406167	6.56E -86	FBgn00 83007	-0.60626	0.011 844
FBgn00 38774	-0.71286	0.025 394		FBgn00 85753	-1.23495	1.86 E-23	FBgn00 39039	-7.67581	4.82E -09	FBgn00 83010	-0.89203	5.69E -06
FBgn00 38799	-6.26441	9.14E -25		FBgn00 85771	-2.00266	4.92 E-10	FBgn00 39073	0.754792	1.82E -18	FBgn00 83011	-0.66039	0.002 963
FBgn00 38804	0.729497	9.00E -05		FBgn00 85810	-0.89254	1.49 E-11	FBgn00 39075	-1.01437	8.96E -05	FBgn00 83039	-0.71147	0.002 072
FBgn00 38826	-0.85168	0.000 25		FBgn00 85819	-2.01159	1.34 E-10	FBgn00 39084	-1.22507	5.70E -05	FBgn00 83040	-0.8249	0.011 137
FBgn00 38828	0.621664	1.03E -08		FBgn00 86265	-0.82242	2.84 E-07	FBgn00 39098	0.739582	2.69E -07	FBgn00 83041	-0.69551	0.002 007

FBgn00 38842	-0.69607	1.48E -07		FBgn00 86365	-0.63073	0.00 3091	FBgn00 39114	-1.29336	4.37E -16		FBgn00 83042	-1.06248	2.57E -06
FBgn00 38881	-0.85978	3.14E -08		FBgn00 86408	-0.98371	3.67 E-09	FBgn00 39118	1.508534	7.60E -14		FBgn00 83048	-0.75667	8.40E -05
FBgn00 38981	-0.9029	1.26E -08		FBgn00 86447	-0.72979	1.53 E-07	FBgn00 39137	0.605897	4.88E -08		FBgn00 83049	-1.09013	3.78E -05
FBgn00 38986	-4.83551	8.05E -98		FBgn00 86450	-0.84437	0.00 0113	FBgn00 39155	-1.31019	5.65E -22		FBgn00 83050	-0.85806	8.00E -08
FBgn00 39006	2.307964	1.44E -78		FBgn00 86659	-0.61214	0.00 4062	FBgn00 39250	0.607563	5.47E -08		FBgn00 83940	-1.48844	5.15E -19
FBgn00 39039	-5.76873	4.80E -12		FBgn00 86698	-0.98864	4.84 E-16	FBgn00 39260	0.883204	2.74E -30		FBgn00 83949	-8.96075	2.12E -14
FBgn00 39073	0.857065	1.09E -23		FBgn00 86708	-0.96312	0.00 013	FBgn00 39266	-0.66944	8.24E -07		FBgn00 85279	-0.66583	0.000 279
FBgn00 39075	-1.24312	1.57E -06		FBgn00 86758	-1.20622	0.00 0975	FBgn00 39312	-2.14068	1.65E -06		FBgn00 85354	-0.8582	4.85E -05
FBgn00 39084	-1.40052	4.47E -06		FBgn00 86917	-5.85073	0.00 0505	FBgn00 39313	-2.01788	2.68E -13		FBgn00 85376	-0.94437	3.53E -15
FBgn00 39098	1.066284	1.82E -14		FBgn00 87012	-3.31548	2.18 E-26	FBgn00 39328	-1.33281	6.66E -05		FBgn00 85382	-5.81805	1.17E -42
FBgn00 39099	0.637944	3.70E -06		FBgn00 87035	-0.65453	3.01 E-09	FBgn00 39419	-0.93555	4.87E -08		FBgn00 85383	-10.5021	5.04E -17
FBgn00 39114	-1.41046	1.11E -18		FBgn02 50835	-3.31037	4.47 E-48	FBgn00 39486	-1.26283	7.37E -06		FBgn00 85407	-1.86231	1.53E -07
FBgn00 39118	1.756433	6.97E -19		FBgn02 50871	-1.54194	4.72 E-13	FBgn00 39529	-1.1226	2.18E -09		FBgn00 85410	-1.21899	0.001 108
FBgn00 39155	-1.23443	9.96E -20		FBgn02 59163	-0.6793	5.17 E-05	FBgn00 39620	-0.67551	0.046 732		FBgn00 85412	-0.63781	6.69E -06
FBgn00 39258	0.804164	3.42E -08		FBgn02 59173	-1.1713	9.78 E-06	FBgn00 39678	-0.76733	0.005 089		FBgn00 85413	-2.31299	4.29E -10
FBgn00 39260	0.635567	8.94E -16		FBgn02 59229	-5.50803	3.34 E-06	FBgn00 39738	-0.60124	0.000 182		FBgn00 85638	-0.71689	2.90E -11
FBgn00 39266	-1.02867	1.01E -14		FBgn02 59244	-2.31601	5.07 E-11	FBgn00 39748	-0.93197	0.000 403		FBgn00 85732	-2.38058	3.54E -136

FBgn00 39312	-1.22445	0.008 567		FBgn02 59736	-1.64004	3.01 E-12	FBgn00 39756	-0.88838	0.001 291		FBgn00 85753	-1.57112	1.03E -37
FBgn00 39313	-1.19122	2.52E -05		FBgn02 59878	-1.09577	2.32 E-23	FBgn00 39776	-1.29231	1.20E -24		FBgn00 85771	-2.47951	4.49E -15
FBgn00 39328	-1.30625	0.000 101		FBgn02 60004	-0.89078	0.00 0376	FBgn00 39809	-1.00748	5.73E -05		FBgn00 85810	-0.89295	1.25E -11
FBgn00 39419	-1.23723	6.04E -13		FBgn02 60400	-0.80397	0.01 2629	FBgn00 39827	-1.54025	2.67E -10		FBgn00 85813	-3.67608	1.15E -05
FBgn00 39431	-0.62893	3.03E -07		FBgn02 60660	-1.05349	9.79 E-11	FBgn00 39836	-1.18473	3.43E -08		FBgn00 85819	-2.46789	1.10E -15
FBgn00 39486	-0.72483	0.011 516		FBgn02 60768	-0.9968	4.53 E-06	FBgn00 39856	1.517089	1.04E -37		FBgn00 86365	-0.86185	2.84E -05
FBgn00 39529	-0.61435	0.001 557		FBgn02 60964	-1.03833	5.19 E-05	FBgn00 39872	-1.49648	0.008 222		FBgn00 86408	-0.95147	1.19E -08
FBgn00 39633	-0.59884	2.90E -06		FBgn02 61113	-1.32902	1.92 E-27	FBgn00 39883	-1.19502	0.004 066		FBgn00 86447	-0.75419	5.28E -08
FBgn00 39678	-0.6182	0.028 092		FBgn02 61258	-1.00976	1.87 E-12	FBgn00 39890	0.638918	4.96E -05		FBgn00 86450	-1.59059	2.19E -13
FBgn00 39756	-1.12724	3.63E -05		FBgn02 61461	-0.61001	6.74 E-15	FBgn00 39914	1.606217	1.33E -15		FBgn00 86600	-0.95615	0.000 62
FBgn00 39776	-0.89053	3.30E -12		FBgn02 61505	-1.91995	1.43 E-76	FBgn00 39920	0.737738	4.77E -07		FBgn00 86602	-0.60487	0.017 085
FBgn00 39809	-1.17582	2.97E -06		FBgn02 61552	-0.59279	0.00 0977	FBgn00 39925	-1.40045	7.68E -06		FBgn00 86658	-0.93921	0.001 539
FBgn00 39827	-1.45155	2.70E -09		FBgn02 61555	-1.64199	5.58 E-31	FBgn00 39972	0.71072	4.55E -06		FBgn00 86659	-1.21502	5.77E -10
FBgn00 39836	-1.18529	3.61E -08		FBgn02 61563	-0.65765	1.38 E-05	FBgn00 40001	1.109092	2.25E -05		FBgn00 86661	-0.72288	0.026 03
FBgn00 39856	1.727784	1.73E -49		FBgn02 61612	-4.33392	2.10 E-32	FBgn00 40022	0.807526	6.00E -06		FBgn00 86665	-0.68875	0.000 159
FBgn00 39862	-0.73902	0.000 859		FBgn02 61639	-0.95294	1.36 E-15	FBgn00 40038	-5.51187	1.04E -30		FBgn00 86666	-0.6744	0.025 005
FBgn00 39872	-1.23986	0.033 009		FBgn02 61640	-0.82076	2.23 E-14	FBgn00 40089	-0.73261	0.000 374		FBgn00 86667	-1.15307	3.27E -08

FBgn00 39881	0.817959	7.89E -05		FBgn02 61788	-0.88075	0.00 3212	FBgn00 40299	-3.1716	1.46E -08	FBgn00 86669	-0.77478	0.000 844
FBgn00 39883	-1.2694	0.002 3		FBgn02 61799	-1.72317	5.44 E-07	FBgn00 40351	-3.16301	3.56E -14	FBgn00 86671	-1.03275	1.41E -08
FBgn00 39914	1.246847	1.26E -09		FBgn02 61822	-1.09111	1.07 E-13	FBgn00 40364	-1.73077	4.74E -25	FBgn00 86698	-1.07799	6.10E -19
FBgn00 39925	-1.6068	3.53E -07		FBgn02 62003	-2.13814	2.13 E-10	FBgn00 40370	-1.44523	2.63E -10	FBgn00 86708	-0.85063	0.000 748
FBgn00 40038	-4.91738	2.24E -33		FBgn02 62004	-1.84697	7.13 E-19	FBgn00 40398	-1.27015	1.95E -07	FBgn00 86758	-1.3351	0.000 247
FBgn00 40089	-0.84335	3.69E -05		FBgn02 62104	-0.95522	0.00 1036	FBgn00 40491	-0.73531	0.000 79	FBgn00 86917	-6.2889	0.000 227
FBgn00 40299	-3.3663	4.38E -09		FBgn02 62123	-3.04257	5.59 E- 123	FBgn00 40551	-1.0075	0.000 803	FBgn00 87012	-3.97648	3.52E -29
FBgn00 40351	-3.02252	1.93E -13		FBgn02 62160	-0.63285	8.91 E-05	FBgn00 40609	-2.0946	3.49E -15	FBgn02 50757	-2.26848	0.004 193
FBgn00 40364	-1.69113	5.27E -24		FBgn02 62475	-0.63692	0.00 1481	FBgn00 40765	-1.25212	6.23E -11	FBgn02 50835	-3.25796	2.70E -47
FBgn00 40370	-1.29987	1.39E -08		FBgn02 62508	-0.73859	6.17 E-05	FBgn00 40780	0.844494	0.000 837	FBgn02 50871	-1.32164	3.48E -10
FBgn00 40398	-1.28385	1.53E -07		FBgn02 62509	-0.8667	0.00 0847	FBgn00 40823	-0.77745	1.96E -07	FBgn02 59163	-0.61107	0.000 281
FBgn00 40514	-0.70253	0.042 503		FBgn02 62686	-0.90292	0.03 2265	FBgn00 40827	-1.63953	0.000 52	FBgn02 59173	-1.2827	1.28E -06
FBgn00 40600	0.664559	0.021 2		FBgn02 62867	-1.23991	0.00 018	FBgn00 40832	-0.64611	0.042 688	FBgn02 59209	-0.92691	7.36E -07
FBgn00 40609	-2.07349	6.76E -15		FBgn02 63019	-1.18717	2.61 E-07	FBgn00 40850	-1.32138	7.76E -12	FBgn02 59229	-7.51729	3.77E -10
FBgn00 40765	-1.23353	1.39E -10		FBgn02 63111	-0.75043	0.00 2537	FBgn00 41180	-1.30854	7.31E -33	FBgn02 59244	-2.62185	8.69E -13
FBgn00 40780	0.710311	0.006 706		FBgn02 63316	-1.00214	2.08 E-09	FBgn00 41182	-1.46565	0.000 2	FBgn02 59736	-1.51914	6.42E -11
FBgn00 40823	-1.17901	9.62E -16		FBgn02 63413	-0.77035	0.01 8231	FBgn00 41184	-1.39161	1.63E -18	FBgn02 59878	-1.06244	4.12E -22

FBgn00 40827	-1.95213	3.49E -05		FBgn02 63492	-0.96811	0.00 4355	FBgn00 41629	0.586276	4.65E -05	FBgn02 59977	-0.84335	0.003 579
FBgn00 40850	-0.96865	4.70E -07		FBgn02 63772	-0.76371	1.68 E-06	FBgn00 41721	-1.10131	0.031 385	FBgn02 59993	-0.82716	9.19E -07
FBgn00 41180	-1.3545	4.93E -35		FBgn02 63873	-0.89472	3.34 E-06	FBgn00 42094	-0.58522	1.34E -07	FBgn02 60004	-0.8417	0.000 756
FBgn00 41184	-1.28926	4.41E -16		FBgn02 63930	-0.69042	0.00 0589	FBgn00 43069	1.510054	3.52E -21	FBgn02 60400	-0.74701	0.019 738
FBgn00 41629	0.873865	2.05E -10		FBgn02 63973	-1.21364	5.21 E-08	FBgn00 43841	-0.62418	6.30E -08	FBgn02 60660	-0.71561	1.50E -05
FBgn00 41712	-0.95177	0.027 05		FBgn02 63995	-0.84748	0.00 2062	FBgn00 43854	0.810759	2.19E -32	FBgn02 60768	-0.87162	6.07E -05
FBgn00 43069	1.580127	3.14E -23		FBgn02 64089	-0.75403	2.72 E-05	FBgn00 44047	-1.20727	1.22E -10	FBgn02 60942	-0.61142	5.80E -06
FBgn00 43364	-0.66046	5.94E -09		FBgn02 64273	-0.88129	0.00 0417	FBgn00 44510	-0.86665	1.74E -11	FBgn02 60964	-1.39046	4.11E -08
FBgn00 43783	-1.023	0.023 468		FBgn02 64385	-0.72983	1.38 E-06	FBgn00 45064	-1.07029	8.30E -24	FBgn02 61113	-0.95555	9.39E -15
FBgn00 43841	-0.65953	1.07E -08		FBgn02 64439	-0.81342	3.44 E-05	FBgn00 45479	-4.62446	9.84E -14	FBgn02 61258	-0.72822	6.00E -07
FBgn00 44047	-1.54735	2.44E -16		FBgn02 64489	-1.02195	0.00 0651	FBgn00 46887	-0.81995	0.020 687	FBgn02 61504	-0.60604	0.005 005
FBgn00 44510	-0.72079	3.67E -08		FBgn02 64490	-0.96726	1.70 E-09	FBgn00 50046	0.725171	0.002 126	FBgn02 61505	-1.70812	6.14E -62
FBgn00 45064	-0.98411	1.95E -20		FBgn02 64542	-0.76044	4.29 E-10	FBgn00 50054	0.701266	4.61E -05	FBgn02 61555	-1.24392	1.34E -18
FBgn00 45479	-4.61264	1.23E -13		FBgn02 64556	-0.92211	0.00 1221	FBgn00 50089	-1.32828	4.21E -09	FBgn02 61563	-0.80872	5.89E -08
FBgn00 47199	0.664342	2.48E -07		FBgn02 64834	-1.9938	2.13 E-10	FBgn00 50104	-1.41224	1.42E -20	FBgn02 61612	-5.11089	4.09E -32
FBgn00 50015	-0.78926	3.28E -05		FBgn02 64894	-1.53704	3.60 E-22	FBgn00 50115	-1.1836	1.51E -22	FBgn02 61639	-0.88402	1.32E -13
FBgn00 50046	0.855544	0.000 215		FBgn02 64975	-1.04538	1.52 E-25	FBgn00 50184	1.310193	0.000 685	FBgn02 61640	-0.94462	1.06E -18

FBgn00 50069	-0.68294	7.05E -05		FBgn02 65002	-1.63374	0.00 0443	FBgn00 50197	-1.49861	7.27E -12		FBgn02 61788	-1.2915	1.03E -05
FBgn00 50089	-1.31957	5.71E -09		FBgn02 65082	-0.63581	2.11 E-07	FBgn00 50345	-3.30831	1.77E -211		FBgn02 61799	-1.30672	9.82E -05
FBgn00 50104	-1.46311	6.56E -22		FBgn02 65180	-1.27621	0.00 0317	FBgn00 50401	-1.91816	5.17E -05		FBgn02 61801	-0.88173	0.000 901
FBgn00 50115	-1.0482	4.20E -18		FBgn02 65185	-1.34299	6.55 E-05	FBgn00 50418	-0.66119	0.041 739		FBgn02 61822	-0.74646	8.03E -07
FBgn00 50184	1.17795	0.002 918		FBgn02 65274	-1.22843	8.83 E-21	FBgn00 50428	-1.60816	1.37E -19		FBgn02 62003	-2.26596	1.99E -11
FBgn00 50197	-1.45113	3.67E -11		FBgn02 65276	-0.59733	0.00 0614	FBgn00 50438	1.102767	0.000 13		FBgn02 62004	-1.93278	2.21E -20
FBgn00 50345	-3.28309	7.47E -209		FBgn02 65296	-5.98655	2.10 E-97	FBgn00 50440	0.64993	0.003 634		FBgn02 62104	-0.79876	0.006 247
FBgn00 50401	-1.03479	0.034 038		FBgn02 65316	-0.63716	0.00 7292	FBgn00 50460	0.904751	3.99E -06		FBgn02 62123	-2.79043	1.05E -107
FBgn00 50428	-1.52524	7.74E -18		FBgn02 65413	-1.24368	8.22 E-30	FBgn00 50489	0.810587	7.38E -10		FBgn02 62160	-0.59568	0.000 24
FBgn00 50438	1.68453	3.94E -10		FBgn02 65434	-0.67112	2.90 E-09	FBgn00 51004	-3.63387	1.68E -26		FBgn02 62508	-0.79925	1.24E -05
FBgn00 50460	-0.77724	0.000 224		FBgn02 65457	-3.53254	1.76 E-32	FBgn00 51029	-2.0001	4.85E -24		FBgn02 62509	-0.72083	0.005 887
FBgn00 50466	-0.70458	3.25E -05		FBgn02 65487	-1.28138	1.81 E-15	FBgn00 51032	1.06823	4.01E -06		FBgn02 62608	-0.89519	8.29E -13
FBgn00 51004	-3.77878	3.60E -27		FBgn02 65548	-6.39337	0.00 2501	FBgn00 51053	-0.75742	8.21E -06		FBgn02 62686	-1.67056	4.23E -05
FBgn00 51029	-2.07497	2.29E -25		FBgn02 65669	-1.15931	0.00 026	FBgn00 51116	-0.95585	5.53E -08		FBgn02 62867	-0.98471	0.002 996
FBgn00 51032	0.921113	0.000 109		FBgn02 65726	-1.06883	2.49 E-07	FBgn00 51119	2.270146	1.33E -14		FBgn02 63018	-1.00557	1.95E -07
FBgn00 51053	-0.74613	1.20E -05		FBgn02 65767	-1.66477	2.54 E-13	FBgn00 51274	2.129394	1.04E -10		FBgn02 63019	-1.12412	1.07E -06
FBgn00 51075	0.865764	9.05E -07		FBgn02 65977	-0.73855	0.00 3859	FBgn00 51279	-0.88136	0.005 148		FBgn02 63316	-1.07077	1.32E -10

FBgn00 51116	-1.15274	5.88E -11		FBgn02 65991	-0.85207	1.10 E-07	FBgn00 51313	-2.06681	6.18E -13	FBgn02 63397	-0.80054	0.004 066
FBgn00 51119	2.365312	7.56E -16		FBgn02 66000	-0.71223	1.14 E-09	FBgn00 51324	-1.35265	5.08E -19	FBgn02 63459	-0.91952	0.000 881
FBgn00 51274	2.150887	7.51E -11		FBgn02 66377	-0.65349	6.96 E-05	FBgn00 51354	-3.24734	1.12E -39	FBgn02 63468	-0.82967	1.15E -05
FBgn00 51313	-2.35355	2.32E -15		FBgn02 66414	-0.66658	0.00 9723	FBgn00 51388	1.38081	1.32E -17	FBgn02 63481	-0.72254	0.027 95
FBgn00 51324	-1.2167	1.13E -15		FBgn02 66418	-0.60197	1.82 E-13	FBgn00 51441	0.59943	0.000 598	FBgn02 63489	-0.96288	0.002 912
FBgn00 51354	-2.46996	1.07E -27		FBgn02 66758	-1.10962	2.99 E-09	FBgn00 51514	-1.05925	0.001 188	FBgn02 63492	-1.04779	0.001 807
FBgn00 51388	1.185553	7.25E -13		FBgn02 67033	-0.6129	0.00 2685	FBgn00 51525	-0.61517	0.042 196	FBgn02 63510	-0.77901	1.77E -12
FBgn00 51514	-0.68605	0.042 024		FBgn02 67191	-1.13068	0.00 2051	FBgn00 51617	-0.75552	4.54E -11	FBgn02 63705	-0.71945	8.46E -05
FBgn00 51525	-0.9851	0.000 959		FBgn02 67336	-0.58893	0.00 0259	FBgn00 51661	-0.65966	0.000 415	FBgn02 63772	-0.78039	9.27E -07
FBgn00 51612	-0.63146	0.000 362		FBgn02 67348	-0.60787	0.00 0177	FBgn00 51674	0.828989	1.21E -05	FBgn02 63873	-1.02785	7.15E -08
FBgn00 51614	-0.63096	0.003 589		FBgn02 67428	-2.23537	2.80 E-35	FBgn00 51781	-1.36095	1.13E -06	FBgn02 63973	-1.00112	8.15E -06
FBgn00 51661	-0.70778	0.000 141		FBgn02 67511	-1.75465	7.95 E-09	FBgn00 51793	0.635055	3.20E -15	FBgn02 63995	-0.63203	0.023 855
FBgn00 51674	1.183402	5.35E -11		FBgn02 67515	-1.56269	1.31 E-28	FBgn00 51807	-0.87691	0.003 123	FBgn02 64089	-0.93575	1.26E -07
FBgn00 51710	-0.67327	0.006 485		FBgn02 67519	-1.21731	5.87 E-23	FBgn00 51869	-0.64566	0.001 482	FBgn02 64273	-0.64091	0.012 323
FBgn00 51781	-0.65296	0.022 927		FBgn02 67668	-0.74597	0.04 0118	FBgn00 51897	0.603702	0.040 206	FBgn02 64385	-0.82012	4.56E -08
FBgn00 51807	-0.97363	0.001 024		FBgn02 67704	-2.20166	3.08 E-21	FBgn00 51898	0.636562	1.93E -06	FBgn02 64439	-0.68302	0.000 562
FBgn00 51869	-0.66476	0.001 064		FBgn02 67798	-1.1346	1.81 E-05	FBgn00 51973	-0.94812	0.001 548	FBgn02 64489	-0.9033	0.002 631

FBgn00 51973	-1.51847	6.40E -07		FBgn02 67826	-0.93894	0.00 1494	FBgn00 51999	1.059815	1.13E -07		FBgn02 64490	-0.77829	1.55E -06
FBgn00 51989	0.807565	1.68E -17		FBgn02 83451	-0.85578	3.93 E-05	FBgn00 52009	1.426275	2.88E -11		FBgn02 64502	-0.62635	0.025 659
FBgn00 51999	1.033435	2.69E -07		FBgn02 83471	-0.88073	4.54 E-08	FBgn00 52010	1.522098	6.92E -18		FBgn02 64542	-0.76422	2.99E -10
FBgn00 52009	1.136504	2.36E -07		FBgn02 83680	-0.64376	0.02 5898	FBgn00 52011	1.411173	1.21E -14		FBgn02 64695	-0.69924	1.55E -07
FBgn00 52010	1.052801	8.38E -09		FBgn02 84408	-0.78134	4.50 E-08	FBgn00 52027	0.94447	2.83E -19		FBgn02 64834	-1.6751	3.56E -08
FBgn00 52011	1.006171	9.94E -08		FBgn02 85955	-0.96052	1.85 E-10	FBgn00 52091	-1.31955	1.17E -23		FBgn02 64894	-1.12368	1.13E -12
FBgn00 52027	0.743929	5.66E -12		FBgn02 85991	-0.66425	2.34 E-05	FBgn00 52099	-0.63998	1.10E -05		FBgn02 64975	-0.80223	2.36E -15
FBgn00 52091	-1.42173	2.68E -27					FBgn00 52195	-0.68925	0.000 699		FBgn02 65002	-2.7196	1.32E -08
FBgn00 52099	-0.85157	3.55E -09					FBgn00 52280	-0.64195	0.023 167		FBgn02 65045	-0.63075	8.79E -05
FBgn00 52137	-0.80279	3.37E -10					FBgn00 52311	-0.90018	1.67E -06		FBgn02 65082	-0.60089	9.85E -07
FBgn00 52195	-0.98144	9.54E -07					FBgn00 52350	1.086408	0.008 748		FBgn02 65180	-1.02982	0.003 672
FBgn00 52218	-0.68244	0.000 948					FBgn00 52364	-1.27713	2.22E -11		FBgn02 65185	-0.95257	0.005 246
FBgn00 52311	-0.65895	0.000 598					FBgn00 52369	-0.72446	0.000 391		FBgn02 65274	-1.09576	9.48E -17
FBgn00 52350	1.09891	0.008 44					FBgn00 52412	0.646931	3.03E -07		FBgn02 65296	-7.4969	2.96E -63
FBgn00 52364	-0.66342	0.000 643					FBgn00 52448	-0.63469	0.028 479		FBgn02 65316	-0.87326	0.000 135
FBgn00 52369	-0.91494	5.01E -06					FBgn00 52476	-1.40893	1.22E -05		FBgn02 65356	-0.78922	0.005 011
FBgn00 52412	0.76881	6.57E -10					FBgn00 52625	-0.7131	7.28E -09		FBgn02 65413	-1.23603	1.53E -29

FBgn00 52476	-1.66447	3.04E -07					FBgn00 52687	-0.99362	1.66E -12		FBgn02 65457	-3.75251	1.02E -33
FBgn00 52687	-1.10909	3.40E -15					FBgn00 52702	-0.91742	1.00E -09		FBgn02 65487	-1.21637	3.97E -14
FBgn00 52702	-0.90975	1.55E -09					FBgn00 52773	-1.36701	1.43E -06		FBgn02 65508	-1.42196	0.002 185
FBgn00 52773	-1.34325	2.25E -06					FBgn00 52816	-0.84143	4.52E -09		FBgn02 65548	-9.93278	2.76E -05
FBgn00 52816	-1.29025	7.73E -20					FBgn00 52850	-0.64797	3.23E -09		FBgn02 65669	-1.72986	6.17E -08
FBgn00 53080	-0.8547	1.17E -07					FBgn00 53080	-1.01319	2.64E -10		FBgn02 65726	-1.16172	1.99E -08
FBgn00 53099	-0.93713	8.91E -05					FBgn00 53099	-1.01868	1.77E -05		FBgn02 65767	-2.20597	6.35E -20
FBgn00 53108	-0.64811	0.044 42					FBgn00 53126	0.633502	0.010 432		FBgn02 65977	-0.75228	0.002 972
FBgn00 53170	0.831584	2.58E -10					FBgn00 53196	-0.7704	0.019 419		FBgn02 65991	-0.72668	7.55E -06
FBgn00 53207	-1.22343	4.30E -08					FBgn00 53207	-2.28268	2.63E -21		FBgn02 66758	-1.04701	2.07E -08
FBgn00 53508	-5.76894	1.14E -29					FBgn00 53213	0.605852	9.48E -11		FBgn02 67191	-1.23952	0.000 616
FBgn00 53653	0.88065	0.006 977					FBgn00 53508	-7.23722	6.93E -20		FBgn02 67348	-0.62072	0.000 117
FBgn00 53810	-0.58534	1.95E -05					FBgn00 53519	-0.70668	0.030 865		FBgn02 67428	-1.60077	4.18E -21
FBgn00 53816	-0.59286	3.52E -10					FBgn00 53653	0.742995	0.025 315		FBgn02 67505	-1.79761	0.013 72
FBgn00 53825	-0.68267	3.13E -08					FBgn00 53810	-0.7616	1.27E -08		FBgn02 67506	-1.80078	0.022 699
FBgn00 53828	-0.60927	2.30E -10					FBgn00 53813	-0.71348	5.21E -14		FBgn02 67507	-1.86231	0.011 211
FBgn00 53831	-0.68617	6.28E -12					FBgn00 53816	-0.68902	1.91E -13		FBgn02 67508	-2.32266	0.015 524

FBgn00 53855	-0.87871	1.24E -09					FBgn00 53819	-0.78233	8.05E -14		FBgn02 67511	-2.19475	1.92E -13
FBgn00 53858	-0.85947	3.75E -11					FBgn00 53822	-0.81888	5.74E -17		FBgn02 67515	-1.86709	1.03E -40
FBgn00 53861	-0.9394	7.91E -13					FBgn00 53825	-0.88785	2.75E -13		FBgn02 67516	-1.60373	0.007 373
FBgn00 53926	-0.73426	0.022 834					FBgn00 53828	-0.8315	2.12E -18		FBgn02 67519	-1.52799	6.48E -36
FBgn00 53970	-0.64631	0.000 865					FBgn00 53831	-0.90138	8.62E -20		FBgn02 67520	-3.07673	0.030 731
FBgn00 58160	-0.64272	3.39E -06					FBgn00 53855	-1.0306	8.29E -13		FBgn02 67668	-0.91107	0.009 869
FBgn00 58470	1.281557	6.77E -05					FBgn00 53858	-0.89223	5.40E -12		FBgn02 67704	-2.48521	1.80E -25
FBgn00 60296	-0.67149	8.86E -07					FBgn00 53861	-0.77788	3.22E -09		FBgn02 67728	-0.70631	0.000 696
FBgn00 62449	-0.88995	2.23E -19					FBgn00 53868	-1.28788	7.77E -16		FBgn02 67798	-2.18726	1.81E -14
FBgn00 62978	-1.03042	9.84E -05					FBgn00 53877	1.132182	1.99E -13		FBgn02 67826	-0.99118	0.000 736
FBgn00 63491	0.615701	0.004 62					FBgn00 53879	0.995871	8.42E -10		FBgn02 67910	-1.09362	0.001 591
FBgn00 63492	0.966752	1.91E -06					FBgn00 53881	1.12437	2.04E -17		FBgn02 83471	-0.90351	1.89E -08
FBgn00 63493	0.80949	1.77E -05					FBgn00 53926	-0.89542	0.004 521		FBgn02 83680	-0.59899	0.036 145
FBgn00 63497	-1.02335	1.73E -05					FBgn00 58006	0.607927	6.44E -16		FBgn02 84256	-0.61319	1.62E -18
FBgn00 63499	-2.80447	6.51E -83					FBgn00 58178	-0.74476	8.07E -05		FBgn02 84408	-0.72918	3.81E -07
FBgn00 65055	-0.63279	0.001 728					FBgn00 58469	-1.08367	0.000 977		FBgn02 85955	-0.94738	2.89E -10
FBgn00 69938	-3.73774	2.02E -16					FBgn00 58470	1.072694	0.001 196		FBgn02 85991	-1.68951	1.33E -30

FBgn00 82947	-2.04981	5.29E -15					FBgn00 60296	-0.72906	7.69E -08					
FBgn00 82981	-0.63159	0.005 176					FBgn00 62978	-0.69339	0.010 39					
FBgn00 83012	0.68721	0.012 473					FBgn00 63493	0.787244	2.99E -05					
FBgn00 83940	-1.54213	3.86E -20					FBgn00 63497	-0.97028	4.31E -05					
FBgn00 83949	-7.15159	4.27E -10					FBgn00 63499	-2.71123	3.21E -79					
FBgn00 85245	0.676887	1.87E -05					FBgn00 65046	-0.62554	0.004 367					
FBgn00 85354	-1.13146	6.42E -08					FBgn00 65047	-0.67471	0.000 123					
FBgn00 85362	-0.68498	0.003 336					FBgn00 65048	-0.70845	2.55E -05					
FBgn00 85376	-1.0317	9.05E -18					FBgn00 65055	-1.37124	3.20E -13					
FBgn00 85382	-5.13155	1.12E -47					FBgn00 65098	-0.60762	0.003 015					
FBgn00 85383	-7.05084	2.10E -28					FBgn00 69923	-0.6552	0.014 012					
FBgn00 85407	-2.28584	8.61E -10					FBgn00 69938	-4.82515	1.39E -16					
FBgn00 85408	-0.92276	1.50E -08					FBgn00 82925	-0.97014	0.001 229					
FBgn00 85410	-1.18475	0.001 626					FBgn00 82947	-2.35176	1.21E -18					
FBgn00 85412	-0.73306	1.72E -07					FBgn00 82958	-0.80972	0.008 901					
FBgn00 85413	-1.59975	5.01E -06					FBgn00 82959	-0.67203	0.038 153					
FBgn00 85433	0.613019	0.000 234					FBgn00 82966	-0.67087	0.002 644					

FBgn00 85446	-0.9198	2.52E -11					FBgn00 82971	-0.71189	0.002 349				
FBgn00 85450	-0.6361	1.23E -07					FBgn00 82974	-0.99055	0.000 126				
FBgn00 85453	0.864645	0.000 257					FBgn00 82980	-0.87406	0.003 876				
FBgn00 85599	0.841861	8.88E -06					FBgn00 82981	-1.11689	1.61E -07				
FBgn00 85638	-0.90847	2.19E -17					FBgn00 83001	-0.73462	0.006 92				
FBgn00 85732	-2.62458	7.95E -162					FBgn00 83003	-1.44052	0.006 612				
FBgn00 85753	-1.23495	1.86E -23					FBgn00 83005	-0.89816	0.000 837				
FBgn00 85771	-2.00266	4.92E -10					FBgn00 83007	-0.60626	0.011 844				
FBgn00 85810	-0.89254	1.49E -11					FBgn00 83010	-0.89203	5.69E -06				
FBgn00 85819	-2.01159	1.34E -10					FBgn00 83011	-0.66039	0.002 963				
FBgn00 86265	-0.82242	2.84E -07					FBgn00 83039	-0.71147	0.002 072				
FBgn00 86365	-0.63073	0.003 091					FBgn00 83040	-0.8249	0.011 137				
FBgn00 86408	-0.98371	3.67E -09					FBgn00 83041	-0.69551	0.002 007				
FBgn00 86447	-0.72979	1.53E -07					FBgn00 83042	-1.06248	2.57E -06				
FBgn00 86450	-0.84437	0.000 113					FBgn00 83048	-0.75667	8.40E -05				
FBgn00 86659	-0.61214	0.004 062					FBgn00 83049	-1.09013	3.78E -05				
FBgn00 86695	0.614152	3.84E -06					FBgn00 83050	-0.85806	8.00E -08				

FBgn00 86698	-0.98864	4.84E -16					FBgn00 83940	-1.48844	5.15E -19					
FBgn00 86704	1.004535	0.001 721					FBgn00 83949	-8.96075	2.12E -14					
FBgn00 86708	-0.96312	0.000 13					FBgn00 83977	2.358941	1.09E -07					
FBgn00 86758	-1.20622	0.000 975					FBgn00 85279	-0.66583	0.000 279					
FBgn00 86917	-5.85073	0.000 505					FBgn00 85354	-0.8582	4.85E -05					
FBgn00 87012	-3.31548	2.18E -26					FBgn00 85376	-0.94437	3.53E -15					
FBgn00 87035	-0.65453	3.01E -09					FBgn00 85382	-5.81805	1.17E -42					
FBgn02 50835	-3.31037	4.47E -48					FBgn00 85383	-10.5021	5.04E -17					
FBgn02 50871	-1.54194	4.72E -13					FBgn00 85400	0.634381	0.005 536					
FBgn02 50907	1.535399	2.10E -06					FBgn00 85407	-1.86231	1.53E -07					
FBgn02 59111	1.289118	9.22E -05					FBgn00 85410	-1.21899	0.001 108					
FBgn02 59112	1.349928	6.18E -11					FBgn00 85412	-0.63781	6.69E -06					
FBgn02 59163	-0.6793	5.17E -05					FBgn00 85413	-2.31299	4.29E -10					
FBgn02 59173	-1.1713	9.78E -06					FBgn00 85453	0.750324	0.001 841					
FBgn02 59229	-5.50803	3.34E -06					FBgn00 85599	0.829341	1.21E -05					
FBgn02 59244	-2.31601	5.07E -11					FBgn00 85638	-0.71689	2.90E -11					
FBgn02 59736	-1.64004	3.01E -12					FBgn00 85732	-2.38058	3.54E -136					

FBgn02 59818	0.625698	0.001 549					FBgn00 85753	-1.57112	1.03E -37				
FBgn02 59822	0.669252	0.034 855					FBgn00 85771	-2.47951	4.49E -15				
FBgn02 59878	-1.09577	2.32E -23					FBgn00 85810	-0.89295	1.25E -11				
FBgn02 59936	0.906792	1.76E -08					FBgn00 85813	-3.67608	1.15E -05				
FBgn02 60004	-0.89078	0.000 376					FBgn00 85819	-2.46789	1.10E -15				
FBgn02 60388	0.913303	6.43E -11					FBgn00 86251	0.636908	6.69E -06				
FBgn02 60400	-0.80397	0.012 629					FBgn00 86365	-0.86185	2.84E -05				
FBgn02 60435	2.768286	2.18E -19					FBgn00 86408	-0.95147	1.19E -08				
FBgn02 60469	0.635583	2.04E -05					FBgn00 86447	-0.75419	5.28E -08				
FBgn02 60660	-1.05349	9.79E -11					FBgn00 86450	-1.59059	2.19E -13				
FBgn02 60768	-0.9968	4.53E -06					FBgn00 86600	-0.95615	0.000 62				
FBgn02 60964	-1.03833	5.19E -05					FBgn00 86602	-0.60487	0.017 085				
FBgn02 60986	0.598791	1.21E -07					FBgn00 86658	-0.93921	0.001 539				
FBgn02 60997	0.752188	5.17E -05					FBgn00 86659	-1.21502	5.77E -10				
FBgn02 61113	-1.32902	1.92E -27					FBgn00 86661	-0.72288	0.026 03				
FBgn02 61258	-1.00976	1.87E -12					FBgn00 86665	-0.68875	0.000 159				
FBgn02 61393	0.834678	3.03E -15					FBgn00 86666	-0.6744	0.025 005				

FBgn02 61397	0.624273	1.23E -10					FBgn00 86667	-1.15307	3.27E -08					
FBgn02 61461	-0.61001	6.74E -15					FBgn00 86669	-0.77478	0.000 844					
FBgn02 61505	-1.91995	1.43E -76					FBgn00 86671	-1.03275	1.41E -08					
FBgn02 61552	-0.59279	0.000 977					FBgn00 86698	-1.07799	6.10E -19					
FBgn02 61555	-1.64199	5.58E -31					FBgn00 86704	0.807829	0.014 458					
FBgn02 61563	-0.65765	1.38E -05					FBgn00 86708	-0.85063	0.000 748					
FBgn02 61612	-4.33392	2.10E -32					FBgn00 86758	-1.3351	0.000 247					
FBgn02 61639	-0.95294	1.36E -15					FBgn00 86917	-6.2889	0.000 227					
FBgn02 61640	-0.82076	2.23E -14					FBgn00 87012	-3.97648	3.52E -29					
FBgn02 61788	-0.88075	0.003 212					FBgn02 50757	-2.26848	0.004 193					
FBgn02 61799	-1.72317	5.44E -07					FBgn02 50816	0.676398	0.001 48					
FBgn02 61808	0.609764	1.93E -06					FBgn02 50835	-3.25796	2.70E -47					
FBgn02 61822	-1.09111	1.07E -13					FBgn02 50871	-1.32164	3.48E -10					
FBgn02 61963	1.061803	0.000 929					FBgn02 50907	3.112868	3.20E -25					
FBgn02 62003	-2.13814	2.13E -10					FBgn02 59112	0.855891	0.000 105					
FBgn02 62004	-1.84697	7.13E -19					FBgn02 59163	-0.61107	0.000 281					
FBgn02 62104	-0.95522	0.001 036					FBgn02 59173	-1.2827	1.28E -06					

FBgn02 62108	0.601191	0.000 661					FBgn02 59175	0.688003	0.009 697				
FBgn02 62123	-3.04257	5.59E -123					FBgn02 59209	-0.92691	7.36E -07				
FBgn02 62160	-0.63285	8.91E -05					FBgn02 59229	-7.51729	3.77E -10				
FBgn02 62475	-0.63692	0.001 481					FBgn02 59244	-2.62185	8.69E -13				
FBgn02 62508	-0.73859	6.17E -05					FBgn02 59736	-1.51914	6.42E -11				
FBgn02 62509	-0.86667	0.000 847					FBgn02 59818	0.679849	0.000 459				
FBgn02 62686	-0.90292	0.032 265					FBgn02 59878	-1.06244	4.12E -22				
FBgn02 62867	-1.23991	0.000 18					FBgn02 59936	1.0658	1.68E -11				
FBgn02 62887	1.491048	8.80E -10					FBgn02 59977	-0.84335	0.003 579				
FBgn02 63019	-1.18717	2.61E -07					FBgn02 59985	0.639796	9.12E -11				
FBgn02 63048	1.115847	3.23E -17					FBgn02 59993	-0.82716	9.19E -07				
FBgn02 63111	-0.75043	0.002 537					FBgn02 60004	-0.8417	0.000 756				
FBgn02 63316	-1.00214	2.08E -09					FBgn02 60388	0.651453	6.97E -06				
FBgn02 63413	-0.77035	0.018 231					FBgn02 60400	-0.74701	0.019 738				
FBgn02 63484	0.628075	0.030 958					FBgn02 60435	2.724579	8.80E -19				
FBgn02 63485	0.842212	0.016 96					FBgn02 60469	0.808237	2.03E -08				
FBgn02 63492	-0.96811	0.004 355					FBgn02 60660	-0.71561	1.50E -05				

FBgn02 63745	0.841515	1.51E -09					FBgn02 60768	-0.87162	6.07E -05				
FBgn02 63772	-0.76371	1.68E -06					FBgn02 60942	-0.61142	5.80E -06				
FBgn02 63782	0.793056	2.07E -27					FBgn02 60964	-1.39046	4.11E -08				
FBgn02 63873	-0.89472	3.34E -06					FBgn02 60997	0.73172	8.18E -05				
FBgn02 63930	-0.69042	0.000 589					FBgn02 61113	-0.95555	9.39E -15				
FBgn02 63973	-1.21364	5.21E -08					FBgn02 61258	-0.72822	6.00E -07				
FBgn02 63995	-0.84748	0.002 062					FBgn02 61393	0.846801	1.02E -15				
FBgn02 64089	-0.75403	2.72E -05					FBgn02 61397	0.8729	2.67E -20				
FBgn02 64273	-0.88129	0.000 417					FBgn02 61504	-0.60604	0.005 005				
FBgn02 64305	0.621508	3.25E -13					FBgn02 61505	-1.70812	6.14E -62				
FBgn02 64385	-0.72983	1.38E -06					FBgn02 61555	-1.24392	1.34E -18				
FBgn02 64439	-0.81342	3.44E -05					FBgn02 61563	-0.80872	5.89E -08				
FBgn02 64489	-1.02195	0.000 651					FBgn02 61612	-5.11089	4.09E -32				
FBgn02 64490	-0.96726	1.70E -09					FBgn02 61639	-0.88402	1.32E -13				
FBgn02 64542	-0.76044	4.29E -10					FBgn02 61640	-0.94462	1.06E -18				
FBgn02 64556	-0.92211	0.001 221					FBgn02 61788	-1.2915	1.03E -05				
FBgn02 64607	0.610753	5.06E -08					FBgn02 61799	-1.30672	9.82E -05				

FBgn02 64834	-1.9938	2.13E -10					FBgn02 61801	-0.88173	0.000 901				
FBgn02 64894	-1.53704	3.60E -22					FBgn02 61822	-0.74646	8.03E -07				
FBgn02 64975	-1.04538	1.52E -25					FBgn02 61963	1.467482	1.39E -06				
FBgn02 64979	1.111252	2.28E -10					FBgn02 62003	-2.26596	1.99E -11				
FBgn02 65002	-1.63374	0.000 443					FBgn02 62004	-1.93278	2.21E -20				
FBgn02 65082	-0.63581	2.11E -07					FBgn02 62104	-0.79876	0.006 247				
FBgn02 65102	0.644103	1.17E -14					FBgn02 62123	-2.79043	1.05E -107				
FBgn02 65180	-1.27621	0.000 317					FBgn02 62160	-0.59568	0.000 24				
FBgn02 65184	0.78529	0.004 243					FBgn02 62508	-0.79925	1.24E -05				
FBgn02 65185	-1.34299	6.55E -05					FBgn02 62509	-0.72083	0.005 887				
FBgn02 65274	-1.22843	8.83E -21					FBgn02 62608	-0.89519	8.29E -13				
FBgn02 65276	-0.59733	0.000 614					FBgn02 62686	-1.67056	4.23E -05				
FBgn02 65296	-5.98655	2.10E -97					FBgn02 62867	-0.98471	0.002 996				
FBgn02 65316	-0.63716	0.007 292					FBgn02 62887	1.626491	1.10E -11				
FBgn02 65413	-1.24368	8.22E -30					FBgn02 63018	-1.00557	1.95E -07				
FBgn02 65434	-0.67112	2.90E -09					FBgn02 63019	-1.12412	1.07E -06				
FBgn02 65457	-3.53254	1.76E -32					FBgn02 63048	1.508158	1.12E -31				

FBgn02 65487	-1.28138	1.81E -15					FBgn02 63316	-1.07077	1.32E -10				
FBgn02 65512	0.873491	2.93E -27					FBgn02 63397	-0.80054	0.004 066				
FBgn02 65548	-6.39337	0.002 501					FBgn02 63459	-0.91952	0.000 881				
FBgn02 65669	-1.15931	0.000 26					FBgn02 63468	-0.82967	1.15E -05				
FBgn02 65726	-1.06883	2.49E -07					FBgn02 63481	-0.72254	0.027 95				
FBgn02 65767	-1.66477	2.54E -13					FBgn02 63489	-0.96288	0.002 912				
FBgn02 65977	-0.73855	0.003 859					FBgn02 63492	-1.04779	0.001 807				
FBgn02 65991	-0.85207	1.10E -07					FBgn02 63510	-0.77901	1.77E -12				
FBgn02 66000	-0.71223	1.14E -09					FBgn02 63705	-0.71945	8.46E -05				
FBgn02 66129	0.721127	0.006 183					FBgn02 63745	1.218863	1.14E -19				
FBgn02 66347	1.371227	4.54E -10					FBgn02 63772	-0.78039	9.27E -07				
FBgn02 66377	-0.65349	6.96E -05					FBgn02 63782	0.735208	1.67E -23				
FBgn02 66414	-0.66658	0.009 723					FBgn02 63873	-1.02785	7.15E -08				
FBgn02 66418	-0.60197	1.82E -13					FBgn02 63973	-1.00112	8.15E -06				
FBgn02 66457	1.696545	4.91E -10					FBgn02 63975	0.791504	0.002 533				
FBgn02 66569	0.94831	5.31E -08					FBgn02 63995	-0.63203	0.023 855				
FBgn02 66758	-1.10962	2.99E -09					FBgn02 64089	-0.93575	1.26E -07				

FBgn02 66958	0.817733	0.007 65					FBgn02 64273	-0.64091	0.012 323				
FBgn02 67033	-0.6129	0.002 685					FBgn02 64385	-0.82012	4.56E -08				
FBgn02 67191	-1.13068	0.002 051					FBgn02 64439	-0.68302	0.000 562				
FBgn02 67336	-0.58893	0.000 259					FBgn02 64489	-0.9033	0.002 631				
FBgn02 67348	-0.60787	0.000 177					FBgn02 64490	-0.77829	1.55E -06				
FBgn02 67428	-2.23537	2.80E -35					FBgn02 64502	-0.62635	0.025 659				
FBgn02 67511	-1.75465	7.95E -09					FBgn02 64542	-0.76422	2.99E -10				
FBgn02 67514	0.881241	0.024 084					FBgn02 64607	0.807343	1.52E -13				
FBgn02 67515	-1.56269	1.31E -28					FBgn02 64676	0.621096	0.005 445				
FBgn02 67519	-1.21731	5.87E -23					FBgn02 64695	-0.69924	1.55E -07				
FBgn02 67668	-0.74597	0.040 118					FBgn02 64704	0.592601	0.001 47				
FBgn02 67704	-2.20166	3.08E -21					FBgn02 64821	0.814492	0.043 892				
FBgn02 67798	-1.1346	1.81E -05					FBgn02 64834	-1.6751	3.56E -08				
FBgn02 67826	-0.93894	0.001 494					FBgn02 64894	-1.12368	1.13E -12				
FBgn02 83451	-0.85578	3.93E -05					FBgn02 64942	0.646156	0.000 264				
FBgn02 83471	-0.88073	4.54E -08					FBgn02 64975	-0.80223	2.36E -15				
FBgn02 83494	1.750437	9.68E -06					FBgn02 64979	0.685396	0.000 2				

FBgn02 83680	-0.64376	0.025 898					FBgn02 65002	-2.7196	1.32E -08				
FBgn02 84408	-0.78134	4.50E -08					FBgn02 65045	-0.63075	8.79E -05				
FBgn02 84442	0.615221	1.03E -06					FBgn02 65082	-0.60089	9.85E -07				
FBgn02 85955	-0.96052	1.85E -10					FBgn02 65102	0.799863	1.77E -22				
FBgn02 85991	-0.66425	2.34E -05					FBgn02 65180	-1.02982	0.003 672				
							FBgn02 65184	0.995074	0.000 142				
							FBgn02 65185	-0.95257	0.005 246				
							FBgn02 65274	-1.09576	9.48E -17				
							FBgn02 65296	-7.4969	2.96E -63				
							FBgn02 65316	-0.87326	0.000 135				
							FBgn02 65356	-0.78922	0.005 011				
							FBgn02 65413	-1.23603	1.53E -29				
							FBgn02 65457	-3.75251	1.02E -33				
							FBgn02 65487	-1.21637	3.97E -14				
							FBgn02 65508	-1.42196	0.002 185				
							FBgn02 65512	0.786031	4.75E -22				
							FBgn02 65548	-9.93278	2.76E -05				

							FBgn02 65623	0.657342	7.37E -06					
							FBgn02 65669	-1.72986	6.17E -08					
							FBgn02 65726	-1.16172	1.99E -08					
							FBgn02 65767	-2.20597	6.35E -20					
							FBgn02 65977	-0.75228	0.002 972					
							FBgn02 65991	-0.72668	7.55E -06					
							FBgn02 66129	0.846103	0.000 881					
							FBgn02 66347	1.839643	9.52E -18					
							FBgn02 66457	1.304578	4.18E -06					
							FBgn02 66758	-1.04701	2.07E -08					
							FBgn02 66958	0.675742	0.030 304					
							FBgn02 67191	-1.23952	0.000 616					
							FBgn02 67348	-0.62072	0.000 117					
							FBgn02 67428	-1.60077	4.18E -21					
							FBgn02 67505	-1.79761	0.013 72					
							FBgn02 67506	-1.80078	0.022 699					
							FBgn02 67507	-1.86231	0.011 211					

							FBgn02 67508	-2.32266	0.015 524					
							FBgn02 67511	-2.19475	1.92E -13					
							FBgn02 67515	-1.86709	1.03E -40					
							FBgn02 67516	-1.60373	0.007 373					
							FBgn02 67519	-1.52799	6.48E -36					
							FBgn02 67520	-3.07673	0.030 731					
							FBgn02 67585	0.982695	0.000 348					
							FBgn02 67668	-0.91107	0.009 869					
							FBgn02 67704	-2.48521	1.80E -25					
							FBgn02 67728	-0.70631	0.000 696					
							FBgn02 67798	-2.18726	1.81E -14					
							FBgn02 67826	-0.99118	0.000 736					
							FBgn02 67910	-1.09362	0.001 591					
							FBgn02 78598	0.594003	0.027 53					
							FBgn02 83471	-0.90351	1.89E -08					
							FBgn02 83494	1.145629	0.006 917					
							FBgn02 83680	-0.59899	0.036 145					

							FBgn02 84256	-0.61319	1.62E -18					
							FBgn02 84408	-0.72918	3.81E -07					
							FBgn02 85955	-0.94738	2.89E -10					
							FBgn02 85991	-1.68951	1.33E -30					

genes that are differentially regulated by <i>D. mel armi</i> as compared to <i>mut</i>				genes that are down regulated by <i>D. mel armi</i> as compared to <i>mut</i>				genes that are differentially regulated by <i>D. sim armi</i> as compared to <i>mut</i>				genes that are down regulated by <i>D. sim armi</i> as compared to <i>mut</i>			
gene	log2FoldC hange	padj		gene	log2Fold Change	padj		gene	log2FoldC hange	padj		gene	log2Fold Change	padj	
FBgn000 0044	-0.68984	8.00E -07		FBgn00 00044	-0.68984	8.00 E-07		FBgn00 00044	-1.08466	3.76E -16		FBgn00 00044	-1.08466	3.76E -16	
FBgn000 0139	-2.34951	9.69E -73		FBgn00 00139	-2.34951	9.69 E-73		FBgn00 00046	-0.89025	0.004 751		FBgn00 00046	-0.89025	0.004 751	
FBgn000 0180	-1.56032	0.002 226		FBgn00 00180	-1.56032	0.00 2226		FBgn00 00139	-2.45725	3.44E -79		FBgn00 00139	-2.45725	3.44E -79	
FBgn000 0246	-0.61237	0.018 077		FBgn00 00246	-0.61237	0.01 8077		FBgn00 00180	-1.12277	0.020 772		FBgn00 00180	-1.12277	0.020 772	
FBgn000 0299	-1.4842	6.36E -27		FBgn00 00299	-1.4842	6.36 E-27		FBgn00 00246	-0.99995	7.75E -06		FBgn00 00246	-0.99995	7.75E -06	
FBgn000 0320	-1.09954	7.35E -12		FBgn00 00320	-1.09954	7.35 E-12		FBgn00 00299	-1.52408	1.78E -28		FBgn00 00299	-1.52408	1.78E -28	
FBgn000 0394	0.637765	0.016 416		FBgn00 00635	-0.6989	0.00 1957		FBgn00 00320	-1.09789	5.05E -12		FBgn00 00320	-1.09789	5.05E -12	
FBgn000 0635	-0.6989	0.001 957		FBgn00 00636	-1.33196	9.24 E-18		FBgn00 00394	1.007293	7.30E -06		FBgn00 00416	-0.74498	0.001 15	
FBgn000 0636	-1.33196	9.24E -18		FBgn00 01123	-1.01194	0.01 8898		FBgn00 00416	-0.74498	0.001 15		FBgn00 00427	-0.58616	0.001 982	
FBgn000 0826	0.71477	1.22E -06		FBgn00 01145	-0.87419	0.00 1143		FBgn00 00427	-0.58616	0.001 982		FBgn00 00463	-0.59444	5.67E -06	

FBgn000 1123	-1.01194	0.018 898		FBgn00 01168	-1.23951	3.96 E-08	FBgn00 00463	-0.59444	5.67E -06	FBgn00 00542	-0.68302	0.009 566
FBgn000 1145	-0.87419	0.001 143		FBgn00 01297	-0.84162	5.05 E-12	FBgn00 00542	-0.68302	0.009 566	FBgn00 00635	-0.87588	2.54E -05
FBgn000 1168	-1.23951	3.96E -08		FBgn00 02609	-1.25201	2.39 E-05	FBgn00 00635	-0.87588	2.54E -05	FBgn00 00636	-1.47501	9.12E -22
FBgn000 1225	0.74583	8.89E -09		FBgn00 02773	-0.83309	2.37 E-06	FBgn00 00636	-1.47501	9.12E -22	FBgn00 01098	-0.59961	2.88E -06
FBgn000 1297	-0.84162	5.05E -12		FBgn00 02868	-2.00474	2.03 E-33	FBgn00 00808	0.722871	0.001 991	FBgn00 01123	-0.84122	0.032 286
FBgn000 2609	-1.25201	2.39E -05		FBgn00 03053	-0.71526	5.31 E-05	FBgn00 00826	0.693866	2.07E -06	FBgn00 01145	-1.29714	2.64E -07
FBgn000 2773	-0.83309	2.37E -06		FBgn00 03089	-1.35191	0.00 0316	FBgn00 01092	0.677727	3.28E -12	FBgn00 01168	-1.26901	1.20E -08
FBgn000 2868	-2.00474	2.03E -33		FBgn00 03090	-1.41261	0.00 0525	FBgn00 01098	-0.59961	2.88E -06	FBgn00 01297	-0.7126	6.05E -09
FBgn000 3053	-0.71526	5.31E -05		FBgn00 03137	-0.82936	0.00 4713	FBgn00 01123	-0.84122	0.032 286	FBgn00 02431	-0.76156	0.029 024
FBgn000 3089	-1.35191	0.000 316		FBgn00 03285	-3.71734	3.35 E-29	FBgn00 01145	-1.29714	2.64E -07	FBgn00 02526	-1.23057	0.012 928
FBgn000 3090	-1.41261	0.000 525		FBgn00 03328	-1.26551	6.45 E-17	FBgn00 01168	-1.26901	1.20E -08	FBgn00 02609	-1.28942	7.40E -06
FBgn000 3137	-0.82936	0.004 713		FBgn00 03366	-1.3615	1.50 E-11	FBgn00 01225	0.786046	7.80E -10	FBgn00 02773	-0.88708	2.64E -07
FBgn000 3285	-3.71734	3.35E -29		FBgn00 03731	-1.05255	3.05 E-07	FBgn00 01297	-0.7126	6.05E -09	FBgn00 02868	-1.58153	3.83E -21
FBgn000 3328	-1.26551	6.45E -17		FBgn00 03888	-0.86491	4.25 E-08	FBgn00 02431	-0.76156	0.029 024	FBgn00 02926	-1.03144	0.023 722
FBgn000 3366	-1.3615	1.50E -11		FBgn00 03890	-1.06196	3.07 E-07	FBgn00 02526	-1.23057	0.012 928	FBgn00 03053	-0.81246	1.77E -06
FBgn000 3480	0.58987	0.015 734		FBgn00 03931	-1.16904	0.00 0314	FBgn00 02609	-1.28942	7.40E -06	FBgn00 03089	-1.34639	0.000 192
FBgn000 3567	0.597111	2.77E -07		FBgn00 03997	-1.46365	1.73 E-25	FBgn00 02773	-0.88708	2.64E -07	FBgn00 03090	-1.40957	0.000 292

FBgn000 3731	-1.05255	3.05E -07		FBgn00 04003	-0.96526	0.00 2796	FBgn00 02868	-1.58153	3.83E -21	FBgn00 03137	-1.52256	5.90E -09
FBgn000 3888	-0.86491	4.25E -08		FBgn00 04117	-0.7475	0.04 2024	FBgn00 02926	-1.03144	0.023 722	FBgn00 03285	-3.92869	5.66E -31
FBgn000 3890	-1.06196	3.07E -07		FBgn00 04133	-0.64676	0.00 053	FBgn00 03053	-0.81246	1.77E -06	FBgn00 03301	-0.74665	1.26E -06
FBgn000 3931	-1.16904	0.000 314		FBgn00 04456	-0.73635	0.00 0144	FBgn00 03089	-1.34639	0.000 192	FBgn00 03312	-0.81686	0.034 261
FBgn000 3996	5.010132	3.32E -94		FBgn00 04569	-1.07653	4.96 E-05	FBgn00 03090	-1.40957	0.000 292	FBgn00 03328	-1.19429	2.64E -15
FBgn000 3997	-1.46365	1.73E -25		FBgn00 04859	-0.64063	0.04 9268	FBgn00 03137	-1.52256	5.90E -09	FBgn00 03366	-0.86634	1.98E -05
FBgn000 4003	-0.96526	0.002 796		FBgn00 05612	-1.16485	2.87 E-07	FBgn00 03285	-3.92869	5.66E -31	FBgn00 03396	-0.97224	0.042 393
FBgn000 4117	-0.7475	0.042 024		FBgn00 05666	-1.12247	0.00 0476	FBgn00 03301	-0.74665	1.26E -06	FBgn00 03486	-1.05471	0.010 6
FBgn000 4133	-0.64676	0.000 53		FBgn00 05771	-0.95932	1.57 E-05	FBgn00 03312	-0.81686	0.034 261	FBgn00 03731	-1.04827	2.46E -07
FBgn000 4456	-0.73635	0.000 144		FBgn00 10019	-0.80224	0.00 0949	FBgn00 03328	-1.19429	2.64E -15	FBgn00 03862	-0.99645	0.044 738
FBgn000 4569	-1.07653	4.96E -05		FBgn00 10228	-0.90208	2.61 E-18	FBgn00 03366	-0.86634	1.98E -05	FBgn00 03888	-0.96895	3.56E -10
FBgn000 4859	-0.64063	0.049 268		FBgn00 10246	-0.82798	4.47 E-08	FBgn00 03396	-0.97224	0.042 393	FBgn00 03890	-1.3435	4.22E -11
FBgn000 5612	-1.16485	2.87E -07		FBgn00 10388	-1.52828	3.09 E-11	FBgn00 03480	0.734094	0.000 64	FBgn00 03931	-1.07087	0.000 597
FBgn000 5666	-1.12247	0.000 476		FBgn00 10424	-0.95019	3.47 E-05	FBgn00 03486	-1.05471	0.010 6	FBgn00 03963	-0.70098	0.003 627
FBgn000 5771	-0.95932	1.57E -05		FBgn00 10651	-1.17678	2.24 E-07	FBgn00 03567	0.947255	2.62E -18	FBgn00 03980	-0.77656	0.047 158
FBgn001 0019	-0.80224	0.000 949		FBgn00 11591	-0.62395	0.03 2687	FBgn00 03731	-1.04827	2.46E -07	FBgn00 03997	-1.303	7.19E -21
FBgn001 0194	0.823166	2.72E -10		FBgn00 11695	-3.97869	1.84 E-23	FBgn00 03862	-0.99645	0.044 738	FBgn00 04045	-0.59567	0.004 291

FBgn001 0228	-0.90208	2.61E -18		FBgn00 11828	-0.86984	0.03 9847	FBgn00 03888	-0.96895	3.56E -10	FBgn00 04117	-0.8519	0.007 941
FBgn001 0246	-0.82798	4.47E -08		FBgn00 12037	-1.04682	0.00 3078	FBgn00 03890	-1.3435	4.22E -11	FBgn00 04167	-0.86693	0.030 503
FBgn001 0388	-1.52828	3.09E -11		FBgn00 13275	-1.31382	1.81 E-17	FBgn00 03931	-1.07087	0.000 597	FBgn00 04169	-0.98528	3.93E -06
FBgn001 0424	-0.95019	3.47E -05		FBgn00 13276	-1.25629	1.91 E-10	FBgn00 03963	-0.70098	0.003 627	FBgn00 04449	-0.62952	0.004 643
FBgn001 0651	-1.17678	2.24E -07		FBgn00 13277	-1.91445	2.11 E-10	FBgn00 03980	-0.77656	0.047 158	FBgn00 04456	-0.58799	0.002 184
FBgn001 1591	-0.62395	0.032 687		FBgn00 13278	-1.90905	6.02 E-08	FBgn00 03996	4.619302	2.16E -79	FBgn00 04569	-1.25753	9.86E -07
FBgn001 1642	0.799238	1.78E -09		FBgn00 13279	-2.42789	2.54 E-13	FBgn00 03997	-1.303	7.19E -21	FBgn00 04606	-0.65824	0.000 881
FBgn001 1695	-3.97869	1.84E -23		FBgn00 13469	-1.48417	3.32 E-05	FBgn00 04045	-0.59567	0.004 291	FBgn00 04859	-0.95581	0.000 558
FBgn001 1761	0.706206	9.15E -09		FBgn00 13953	-0.67975	0.00 0601	FBgn00 04117	-0.8519	0.007 941	FBgn00 04861	-0.65028	0.007 338
FBgn001 1828	-0.86984	0.039 847		FBgn00 14022	-1.47047	2.68 E-28	FBgn00 04167	-0.86693	0.030 503	FBgn00 05612	-1.21299	5.44E -08
FBgn001 2037	-1.04682	0.003 078		FBgn00 14076	-0.61775	0.00 6812	FBgn00 04169	-0.98528	3.93E -06	FBgn00 05631	-1.0035	0.010 667
FBgn001 3275	-1.31382	1.81E -17		FBgn00 14141	-0.68453	6.20 E-12	FBgn00 04449	-0.62952	0.004 643	FBgn00 05666	-1.9914	2.24E -11
FBgn001 3276	-1.25629	1.91E -10		FBgn00 14380	-0.77885	0.03 578	FBgn00 04456	-0.58799	0.002 184	FBgn00 05771	-1.01176	2.82E -06
FBgn001 3277	-1.91445	2.11E -10		FBgn00 14396	-0.63888	3.27 E-05	FBgn00 04569	-1.25753	9.86E -07	FBgn00 10019	-1.09042	1.16E -06
FBgn001 3278	-1.90905	6.02E -08		FBgn00 15399	-0.80506	2.06 E-05	FBgn00 04606	-0.65824	0.000 881	FBgn00 10228	-0.76836	1.36E -13
FBgn001 3279	-2.42789	2.54E -13		FBgn00 15558	-1.13012	0.01 7202	FBgn00 04797	0.761533	8.73E -06	FBgn00 10246	-0.75383	6.15E -07
FBgn001 3469	-1.48417	3.32E -05		FBgn00 15609	-2.49935	4.27 E-17	FBgn00 04859	-0.95581	0.000 558	FBgn00 10317	-0.692	9.59E -06

FBgn001 3953	-0.67975	0.000 601		FBgn00 15872	-1.00193	3.59 E-05	FBgn00 04861	-0.65028	0.007 338		FBgn00 10383	-0.66624	0.002 644
FBgn001 4022	-1.47047	2.68E -28		FBgn00 16075	-1.55957	5.28 E-22	FBgn00 05612	-1.21299	5.44E -08		FBgn00 10387	-0.71459	0.049 35
FBgn001 4076	-0.61775	0.006 812		FBgn00 16076	-0.79436	5.71 E-06	FBgn00 05631	-1.0035	0.010 667		FBgn00 10388	-1.24042	4.74E -08
FBgn001 4141	-0.68453	6.20E -12		FBgn00 16080	-1.67746	3.48 E-07	FBgn00 05666	-1.9914	2.24E -11		FBgn00 10424	-1.43094	1.23E -10
FBgn001 4380	-0.77885	0.035 78		FBgn00 16797	-0.65941	9.50 E-05	FBgn00 05771	-1.01176	2.82E -06		FBgn00 10435	-0.58693	0.026 696
FBgn001 4396	-0.63888	3.27E -05		FBgn00 20257	-1.122	1.82 E-05	FBgn00 10019	-1.09042	1.16E -06		FBgn00 10473	-0.79625	0.049 12
FBgn001 4466	0.716503	0.000 604		FBgn00 20762	-1.78785	3.46 E-19	FBgn00 10039	0.641284	0.002 622		FBgn00 10651	-0.81035	0.000 4
FBgn001 5399	-0.80506	2.06E -05		FBgn00 22160	-0.66197	0.00 056	FBgn00 10194	0.890417	3.61E -12		FBgn00 11206	-0.81317	0.005 494
FBgn001 5558	-1.13012	0.017 202		FBgn00 22355	-0.60633	0.02 0956	FBgn00 10225	0.866292	0.000 16		FBgn00 11259	-0.5914	0.003 428
FBgn001 5568	0.889579	8.05E -07		FBgn00 22774	-0.64051	0.00 0222	FBgn00 10228	-0.76836	1.36E -13		FBgn00 11591	-0.90998	0.000 298
FBgn001 5609	-2.49935	4.27E -17		FBgn00 22986	-1.05093	1.68 E-21	FBgn00 10246	-0.75383	6.15E -07		FBgn00 11695	-3.60731	2.59E -22
FBgn001 5714	1.170129	0.001 852		FBgn00 23001	-1.96124	3.53 E-19	FBgn00 10317	-0.692	9.59E -06		FBgn00 11828	-1.02112	0.005 833
FBgn001 5872	-1.00193	3.59E -05		FBgn00 23479	-2.44735	1.99 E-15	FBgn00 10383	-0.66624	0.002 644		FBgn00 12051	-0.7273	0.020 173
FBgn001 6075	-1.55957	5.28E -22		FBgn00 23520	-1.54326	7.53 E-13	FBgn00 10387	-0.71459	0.049 35		FBgn00 13272	-1.13703	0.001 488
FBgn001 6076	-0.79436	5.71E -06		FBgn00 23549	-1.46264	1.06 E-17	FBgn00 10388	-1.24042	4.74E -08		FBgn00 13275	-1.71049	1.20E -28
FBgn001 6080	-1.67746	3.48E -07		FBgn00 24234	-0.58861	0.03 9898	FBgn00 10424	-1.43094	1.23E -10		FBgn00 13276	-1.5297	2.66E -15
FBgn001 6797	-0.65941	9.50E -05		FBgn00 24289	-0.96514	0.01 0272	FBgn00 10435	-0.58693	0.026 696		FBgn00 13277	-2.10632	3.19E -12

FBgn001 7448	2.788613	1.09E -24		FBgn00 24321	-1.41736	2.18 E-09	FBgn00 10473	-0.79625	0.049 12	FBgn00 13278	-1.787	1.92E -07
FBgn002 0257	-1.122	1.82E -05		FBgn00 24366	-1.12129	3.84 E-06	FBgn00 10651	-0.81035	0.000 4	FBgn00 13279	-1.93233	4.11E -10
FBgn002 0415	2.027264	2.04E -14		FBgn00 24732	-0.59536	0.00 045	FBgn00 11206	-0.81317	0.005 494	FBgn00 13343	-0.62369	0.000 52
FBgn002 0762	-1.78785	3.46E -19		FBgn00 25391	-2.54538	2.74 E-08	FBgn00 11259	-0.5914	0.003 428	FBgn00 13469	-1.91348	3.23E -08
FBgn002 2160	-0.66197	0.000 56		FBgn00 25456	-0.66491	0.03 4488	FBgn00 11591	-0.90998	0.000 298	FBgn00 13733	-0.96738	0.019 182
FBgn002 2355	-0.60633	0.020 956		FBgn00 25631	-0.83016	0.02 6349	FBgn00 11642	1.414589	2.39E -30	FBgn00 14022	-1.58132	1.31E -32
FBgn002 2702	1.521323	1.68E -21		FBgn00 26061	-0.88669	6.03 E-09	FBgn00 11695	-3.60731	2.59E -22	FBgn00 14076	-0.72631	0.000 478
FBgn002 2774	-0.64051	0.000 222		FBgn00 26319	-0.97484	0.00 4068	FBgn00 11761	1.035291	1.12E -18	FBgn00 14343	-0.63527	0.036 538
FBgn002 2986	-1.05093	1.68E -21		FBgn00 26562	-1.35595	2.14 E-08	FBgn00 11828	-1.02112	0.005 833	FBgn00 14380	-0.76102	0.020 173
FBgn002 3001	-1.96124	3.53E -19		FBgn00 26872	-0.82485	0.02 1886	FBgn00 12051	-0.7273	0.020 173	FBgn00 14396	-0.63619	2.19E -05
FBgn002 3479	-2.44735	1.99E -15		FBgn00 27106	-1.16656	0.00 1935	FBgn00 13272	-1.13703	0.001 488	FBgn00 15031	-0.61726	0.000 176
FBgn002 3520	-1.54326	7.53E -13		FBgn00 27341	-4.47027	4.51 E-50	FBgn00 13275	-1.71049	1.20E -28	FBgn00 15399	-0.68519	0.000 259
FBgn002 3549	-1.46264	1.06E -17		FBgn00 27364	-1.37152	6.20 E-12	FBgn00 13276	-1.5297	2.66E -15	FBgn00 15513	-0.7493	0.002 171
FBgn002 4234	-0.58861	0.039 898		FBgn00 27560	-0.76969	0.02 0861	FBgn00 13277	-2.10632	3.19E -12	FBgn00 15558	-1.07553	0.012 627
FBgn002 4289	-0.96514	0.010 272		FBgn00 27578	-1.68638	7.48 E-07	FBgn00 13278	-1.787	1.92E -07	FBgn00 15609	-3.13404	1.26E -24
FBgn002 4321	-1.41736	2.18E -09		FBgn00 27596	-0.85641	0.00 3073	FBgn00 13279	-1.93233	4.11E -10	FBgn00 15795	-0.68476	9.59E -08
FBgn002 4366	-1.12129	3.84E -06		FBgn00 28888	-9.17436	1.56 E-12	FBgn00 13303	1.112612	5.21E -06	FBgn00 15872	-0.90638	0.000 141

FBgn002 4732	-0.59536	0.000 45		FBgn00 29172	-0.90936	0.04 8393		FBgn00 13343	-0.62369	0.000 52		FBgn00 16075	-1.62831	5.32E -24
FBgn002 4754	0.698884	0.002 535		FBgn00 29723	-0.62962	0.00 5468		FBgn00 13469	-1.91348	3.23E -08		FBgn00 16080	-1.66582	2.45E -07
FBgn002 4804	0.616245	6.50E -06		FBgn00 29766	-0.76494	0.00 7076		FBgn00 13733	-0.96738	0.019 182		FBgn00 16131	-0.9174	3.12E -07
FBgn002 4912	0.803241	0.011 249		FBgn00 29843	-1.59182	5.05 E-09		FBgn00 14022	-1.58132	1.31E -32		FBgn00 16797	-0.80968	4.68E -07
FBgn002 5391	-2.54538	2.74E -08		FBgn00 29895	-0.58606	0.00 6844		FBgn00 14076	-0.72631	0.000 478		FBgn00 16977	-1.12881	0.042 078
FBgn002 5456	-0.66491	0.034 488		FBgn00 30017	-0.88819	0.03 9735		FBgn00 14343	-0.63527	0.036 538		FBgn00 20257	-0.75513	0.003 652
FBgn002 5631	-0.83016	0.026 349		FBgn00 30040	-2.26448	1.01 E-26		FBgn00 14380	-0.76102	0.020 173		FBgn00 20294	-0.95143	0.006 335
FBgn002 5726	0.591667	0.042 883		FBgn00 30091	-0.79784	2.14 E-08		FBgn00 14396	-0.63619	2.19E -05		FBgn00 20306	-0.75122	0.000 293
FBgn002 5739	0.971487	7.19E -11		FBgn00 30218	-0.75034	0.04 3837		FBgn00 14466	0.823572	2.89E -05		FBgn00 20762	-1.8021	9.81E -20
FBgn002 6061	-0.88669	6.03E -09		FBgn00 30309	-0.74669	0.00 7367		FBgn00 15031	-0.61726	0.000 176		FBgn00 21764	-0.66982	4.01E -06
FBgn002 6315	1.571999	4.85E -08		FBgn00 30349	-0.74024	2.76 E-06		FBgn00 15399	-0.68519	0.000 259		FBgn00 22355	-0.64862	0.005 932
FBgn002 6319	-0.97484	0.004 068		FBgn00 30485	-0.8813	0.00 1798		FBgn00 15513	-0.7493	0.002 171		FBgn00 22986	-1.20254	5.19E -28
FBgn002 6323	0.637003	4.58E -09		FBgn00 30600	-4.15253	1.38 E-51		FBgn00 15558	-1.07553	0.012 627		FBgn00 23001	-2.051	4.99E -21
FBgn002 6562	-1.35595	2.14E -08		FBgn00 30662	-0.81229	0.04 7173		FBgn00 15568	1.143926	1.76E -11		FBgn00 23083	-0.61487	0.005 735
FBgn002 6570	0.80159	0.006 013		FBgn00 30665	-4.74997	5.96 E-37		FBgn00 15609	-3.13404	1.26E -24		FBgn00 23479	-2.45865	5.75E -16
FBgn002 6872	-0.82485	0.021 886		FBgn00 30666	-3.64135	4.04 E-78		FBgn00 15714	0.934007	0.011 843		FBgn00 23520	-1.64107	1.48E -14
FBgn002 7070	0.84163	0.009 63		FBgn00 30816	-0.69144	0.00 9506		FBgn00 15754	0.807303	2.07E -09		FBgn00 23549	-1.13156	4.97E -11

FBgn002 7106	-1.16656	0.001 935		FBgn00 30941	-0.63852	0.01 7181	FBgn00 15795	-0.68476	9.59E -08	FBgn00 24289	-1.27871	0.000 182
FBgn002 7341	-4.47027	4.51E -50		FBgn00 30955	-1.22384	1.05 E-11	FBgn00 15872	-0.90638	0.000 141	FBgn00 24321	-1.1139	3.10E -06
FBgn002 7364	-1.37152	6.20E -12		FBgn00 31220	-2.30101	5.17 E-11	FBgn00 16075	-1.62831	5.32E -24	FBgn00 24366	-1.19587	4.58E -07
FBgn002 7560	-0.76969	0.020 861		FBgn00 31275	-1.72575	0.00 1713	FBgn00 16080	-1.66582	2.45E -07	FBgn00 25391	-2.23219	2.64E -07
FBgn002 7578	-1.68638	7.48E -07		FBgn00 31322	-0.78235	0.02 7482	FBgn00 16131	-0.9174	3.12E -07	FBgn00 25456	-0.67709	0.014 964
FBgn002 7596	-0.85641	0.003 073		FBgn00 31571	-0.75671	0.01 7663	FBgn00 16797	-0.80968	4.68E -07	FBgn00 25631	-0.92372	0.005 434
FBgn002 7843	0.61507	2.31E -05		FBgn00 31645	-0.61819	0.00 1257	FBgn00 16977	-1.12881	0.042 078	FBgn00 26061	-0.73657	1.39E -06
FBgn002 7865	0.686613	3.31E -09		FBgn00 31689	-4.88012	0.00 0241	FBgn00 17414	0.778358	0.000 377	FBgn00 26160	-0.70021	0.001 971
FBgn002 8525	0.836691	0.000 306		FBgn00 31741	-1.11621	1.22 E-06	FBgn00 17448	3.066284	2.39E -30	FBgn00 26319	-1.33	1.98E -05
FBgn002 8888	-9.17436	1.56E -12		FBgn00 31745	-0.71559	0.01 1148	FBgn00 20257	-0.75513	0.003 652	FBgn00 26562	-1.10665	3.93E -06
FBgn002 9114	0.685669	0.007 277		FBgn00 31834	-0.65172	0.00 9544	FBgn00 20294	-0.95143	0.006 335	FBgn00 26577	-0.70382	0.000 495
FBgn002 9172	-0.90936	0.048 393		FBgn00 31913	-1.43563	6.41 E-23	FBgn00 20306	-0.75122	0.000 293	FBgn00 26630	-0.65867	0.002 648
FBgn002 9723	-0.62962	0.005 468		FBgn00 31981	-0.66829	9.85 E-05	FBgn00 20388	0.585595	2.10E -06	FBgn00 27106	-1.27433	0.000 321
FBgn002 9766	-0.76494	0.007 076		FBgn00 32006	-0.80877	3.90 E-06	FBgn00 20415	1.683741	6.44E -10	FBgn00 27339	-0.62923	0.004 123
FBgn002 9831	0.820347	4.74E -11		FBgn00 32025	-0.75339	0.02 9707	FBgn00 20762	-1.8021	9.81E -20	FBgn00 27341	-4.91376	8.49E -51
FBgn002 9843	-1.59182	5.05E -09		FBgn00 32129	-0.97182	0.00 1696	FBgn00 21764	-0.66982	4.01E -06	FBgn00 27364	-1.21037	8.10E -10
FBgn002 9879	0.770688	6.05E -12		FBgn00 32156	-0.90623	0.00 3776	FBgn00 21895	0.709943	3.21E -05	FBgn00 27499	-0.61397	0.014 839

FBgn002 9895	-0.58606	0.006 844		FBgn00 32167	-1.80221	7.42 E-10	FBgn00 21967	0.59944	0.002 528		FBgn00 27560	-0.74205	0.013 643
FBgn003 0017	-0.88819	0.039 735		FBgn00 32187	-0.95474	0.00 2875	FBgn00 22338	0.603354	4.08E -06		FBgn00 27578	-1.61959	1.20E -06
FBgn003 0040	-2.26448	1.01E -26		FBgn00 32218	-0.87512	0.01 1923	FBgn00 22355	-0.64862	0.005 932		FBgn00 27596	-0.64351	0.019 737
FBgn003 0091	-0.79784	2.14E -08		FBgn00 32264	-2.16876	4.93 E-11	FBgn00 22702	1.549183	2.08E -22		FBgn00 28690	-0.62859	0.000 385
FBgn003 0137	1.171736	0.000 157		FBgn00 32297	-0.97733	1.49 E-05	FBgn00 22893	0.62286	8.57E -05		FBgn00 28888	-9.25792	8.12E -13
FBgn003 0187	0.880869	0.046 723		FBgn00 32330	-0.69939	1.81 E-10	FBgn00 22986	-1.20254	5.19E -28		FBgn00 29148	-0.6402	0.000 296
FBgn003 0218	-0.75034	0.043 837		FBgn00 32666	-1.1228	0.00 0371	FBgn00 22987	0.648898	1.18E -06		FBgn00 29172	-0.95765	0.017 134
FBgn003 0309	-0.74669	0.007 367		FBgn00 32713	-0.86888	0.00 9105	FBgn00 23001	-2.051	4.99E -21		FBgn00 29835	-0.78576	0.017 617
FBgn003 0349	-0.74024	2.76E -06		FBgn00 32864	-1.43566	4.35 E-24	FBgn00 23083	-0.61487	0.005 735		FBgn00 29843	-1.02456	0.000 148
FBgn003 0439	1.224505	0.009 327		FBgn00 33033	-2.20477	1.69 E-10	FBgn00 23479	-2.45865	5.75E -16		FBgn00 29939	-0.85487	0.000 103
FBgn003 0485	-0.8813	0.001 798		FBgn00 33108	-4.27251	5.18 E-15	FBgn00 23517	0.617323	1.19E -06		FBgn00 30017	-1.15434	0.002 214
FBgn003 0600	-4.15253	1.38E -51		FBgn00 33153	-0.60614	0.00 1333	FBgn00 23520	-1.64107	1.48E -14		FBgn00 30040	-2.08876	1.25E -23
FBgn003 0660	0.648969	4.48E -05		FBgn00 33188	-2.62077	2.63 E-54	FBgn00 23549	-1.13156	4.97E -11		FBgn00 30091	-0.62868	1.34E -05
FBgn003 0662	-0.81229	0.047 173		FBgn00 33274	-0.6167	0.04 5899	FBgn00 24289	-1.27871	0.000 182		FBgn00 30349	-0.67107	1.82E -05
FBgn003 0665	-4.74997	5.96E -37		FBgn00 33356	-0.7169	0.00 0275	FBgn00 24321	-1.1139	3.10E -06		FBgn00 30485	-0.77167	0.003 943
FBgn003 0666	-3.64135	4.04E -78		FBgn00 33388	-4.92888	1.43 E-09	FBgn00 24366	-1.19587	4.58E -07		FBgn00 30600	-4.40301	1.04E -54
FBgn003 0799	1.237053	0.000 164		FBgn00 33395	-1.85389	4.33 E-25	FBgn00 24754	0.933059	5.86E -06		FBgn00 30653	-0.85888	0.002 434

FBgn003 0816	-0.69144	0.009 506		FBgn00 33438	-1.32122	1.20 E-14	FBgn00 24912	1.119688	4.04E -05	FBgn00 30662	-0.90255	0.011 389
FBgn003 0941	-0.63852	0.017 181		FBgn00 33494	-1.00327	0.00 5731	FBgn00 24944	0.589915	3.93E -05	FBgn00 30665	-5.27864	1.54E -36
FBgn003 0955	-1.22384	1.05E -11		FBgn00 33518	-0.72091	0.00 8118	FBgn00 25391	-2.23219	2.64E -07	FBgn00 30666	-3.54047	3.60E -75
FBgn003 0968	0.624517	0.013 19		FBgn00 33654	-0.93522	0.00 1704	FBgn00 25456	-0.67709	0.014 964	FBgn00 30828	-0.79018	0.020 917
FBgn003 1117	0.841206	3.06E -08		FBgn00 33782	-2.30625	1.14 E-09	FBgn00 25631	-0.92372	0.005 434	FBgn00 30955	-1.28908	5.07E -13
FBgn003 1157	1.547339	1.21E -14		FBgn00 33787	-1.99292	4.78 E-11	FBgn00 25739	0.980151	3.59E -11	FBgn00 31118	-0.59863	0.002 593
FBgn003 1184	1.518877	1.64E -09		FBgn00 33926	-1.6164	9.34 E-32	FBgn00 25820	0.613342	0.001 494	FBgn00 31220	-2.18374	1.55E -10
FBgn003 1220	-2.30101	5.17E -11		FBgn00 33927	-1.47212	1.98 E-15	FBgn00 26061	-0.73657	1.39E -06	FBgn00 31258	-0.63448	0.013 671
FBgn003 1275	-1.72575	0.001 713		FBgn00 34075	-1.61033	2.94 E-18	FBgn00 26088	0.635768	0.000 4	FBgn00 31275	-2.20886	2.68E -05
FBgn003 1313	0.85625	0.005 889		FBgn00 34194	-0.96842	0.02 1068	FBgn00 26144	0.618737	5.71E -07	FBgn00 31322	-0.67262	0.033 976
FBgn003 1322	-0.78235	0.027 482		FBgn00 34312	-0.93918	0.00 7068	FBgn00 26160	-0.70021	0.001 971	FBgn00 31571	-1.34074	1.10E -06
FBgn003 1571	-0.75671	0.017 663		FBgn00 34406	-1.83895	1.27 E-11	FBgn00 26199	0.752543	1.09E -10	FBgn00 31574	-0.7592	0.028 121
FBgn003 1633	0.725838	1.40E -07		FBgn00 34436	-0.68303	0.04 9037	FBgn00 26315	1.259003	2.60E -05	FBgn00 31628	-0.91284	0.007 961
FBgn003 1645	-0.61819	0.001 257		FBgn00 34500	-0.60206	0.00 271	FBgn00 26319	-1.33	1.98E -05	FBgn00 31645	-0.96037	4.68E -08
FBgn003 1678	0.989151	2.80E -08		FBgn00 34501	-0.63187	0.00 6079	FBgn00 26323	0.644601	1.96E -09	FBgn00 31689	-6.47362	6.97E -07
FBgn003 1689	-4.88012	0.000 241		FBgn00 34602	-1.14445	4.24 E-05	FBgn00 26433	0.608026	4.08E -05	FBgn00 31690	-11.0207	2.49E -05
FBgn003 1741	-1.11621	1.22E -06		FBgn00 34611	-0.65619	1.33 E-06	FBgn00 26562	-1.10665	3.93E -06	FBgn00 31698	-0.67067	0.000 52

FBgn003 1745	-0.71559	0.011 148		FBgn00 34638	-0.61522	0.01 2647	FBgn00 26577	-0.70382	0.000 495	FBgn00 31741	-1.05452	3.28E -06
FBgn003 1834	-0.65172	0.009 544		FBgn00 34639	-1.45904	2.84 E-05	FBgn00 26630	-0.65867	0.002 648	FBgn00 31745	-0.6604	0.010 948
FBgn003 1913	-1.43563	6.41E -23		FBgn00 34709	-1.06812	7.05 E-11	FBgn00 27070	0.645466	0.038 987	FBgn00 31756	-0.73348	1.60E -06
FBgn003 1979	0.614693	0.015 091		FBgn00 34718	-0.69973	0.00 6139	FBgn00 27106	-1.27433	0.000 321	FBgn00 31913	-1.41321	2.56E -22
FBgn003 1981	-0.66829	9.85E -05		FBgn00 34723	-0.66333	0.04 3838	FBgn00 27339	-0.62923	0.004 123	FBgn00 31990	-0.87619	0.048 029
FBgn003 2006	-0.80877	3.90E -06		FBgn00 34761	-1.18914	7.21 E-12	FBgn00 27341	-4.91376	8.49E -51	FBgn00 32006	-0.84213	8.71E -07
FBgn003 2025	-0.75339	0.029 707		FBgn00 35094	-3.76687	2.26 E-30	FBgn00 27364	-1.21037	8.10E -10	FBgn00 32101	-0.59651	1.00E -04
FBgn003 2079	1.396325	1.74E -09		FBgn00 35308	-0.81847	0.01 3907	FBgn00 27499	-0.61397	0.014 839	FBgn00 32129	-0.79639	0.006 784
FBgn003 2127	0.761085	0.000 296		FBgn00 35490	-1.46323	8.62 E-05	FBgn00 27560	-0.74205	0.013 643	FBgn00 32156	-0.71856	0.015 434
FBgn003 2129	-0.97182	0.001 696		FBgn00 35763	-0.65959	5.83 E-09	FBgn00 27578	-1.61959	1.20E -06	FBgn00 32167	-2.27478	4.11E -15
FBgn003 2156	-0.90623	0.003 776		FBgn00 35767	-0.90625	0.00 9755	FBgn00 27596	-0.64351	0.019 737	FBgn00 32187	-0.63559	0.039 886
FBgn003 2167	-1.80221	7.42E -10		FBgn00 35975	-1.1124	0.00 1096	FBgn00 27784	0.633058	0.000 244	FBgn00 32218	-1.15171	0.000 226
FBgn003 2187	-0.95474	0.002 875		FBgn00 36144	-0.64702	2.74 E-08	FBgn00 27843	0.615074	1.53E -05	FBgn00 32264	-1.92467	1.82E -09
FBgn003 2218	-0.87512	0.011 923		FBgn00 36147	-0.59556	2.01 E-05	FBgn00 27864	0.601916	0.000 74	FBgn00 32297	-0.82459	0.000 224
FBgn003 2249	0.85146	0.019 889		FBgn00 36155	-0.73297	9.54 E-06	FBgn00 27865	0.599504	3.46E -07	FBgn00 32330	-0.62405	1.22E -08
FBgn003 2264	-2.16876	4.93E -11		FBgn00 36205	-0.73746	0.02 2619	FBgn00 28499	0.714905	0.000 303	FBgn00 32363	-0.61786	0.000 143
FBgn003 2290	0.695587	0.000 171		FBgn00 36287	-3.23292	1.23 E-11	FBgn00 28690	-0.62859	0.000 385	FBgn00 32666	-1.45256	1.51E -06

FBgn003 2297	-0.97733	1.49E -05		FBgn00 36381	-1.48295	0.00 0152	FBgn00 28888	-9.25792	8.12E -13	FBgn00 32681	-0.63195	0.006 994
FBgn003 2330	-0.69939	1.81E -10		FBgn00 36589	-0.75703	0.01 055	FBgn00 28897	0.769718	0.000 538	FBgn00 32713	-0.61828	0.047 397
FBgn003 2382	0.624922	0.029 905		FBgn00 36732	-0.65063	0.02 1146	FBgn00 29148	-0.6402	0.000 296	FBgn00 32720	-0.76799	0.000 851
FBgn003 2666	-1.1228	0.000 371		FBgn00 36752	-1.24862	5.36 E-08	FBgn00 29172	-0.95765	0.017 134	FBgn00 32833	-0.61761	1.26E -06
FBgn003 2713	-0.86888	0.009 105		FBgn00 36789	-5.24	5.33 E-76	FBgn00 29508	0.807041	0.000 33	FBgn00 32864	-1.47655	1.45E -25
FBgn003 2864	-1.43566	4.35E -24		FBgn00 37007	-0.62231	0.00 4732	FBgn00 29648	0.761419	0.008 783	FBgn00 33033	-2.86326	2.03E -15
FBgn003 2889	1.541053	4.14E -17		FBgn00 37016	-0.84623	4.65 E-06	FBgn00 29821	0.813395	0.029 024	FBgn00 33108	-1.63249	4.37E -06
FBgn003 3033	-2.20477	1.69E -10		FBgn00 37525	-1.22881	1.87 E-14	FBgn00 29831	0.941493	1.02E -14	FBgn00 33153	-0.71145	5.56E -05
FBgn003 3051	0.890798	3.13E -06		FBgn00 37577	-0.70639	0.01 2033	FBgn00 29835	-0.78576	0.017 617	FBgn00 33188	-2.56799	6.10E -53
FBgn003 3079	1.175878	0.006 429		FBgn00 37659	-0.70519	1.46 E-06	FBgn00 29843	-1.02456	0.000 148	FBgn00 33274	-0.59118	0.029 077
FBgn003 3108	-4.27251	5.18E -15		FBgn00 37856	-1.85791	2.09 E-51	FBgn00 29849	0.739696	3.28E -06	FBgn00 33356	-1.11048	1.41E -09
FBgn003 3153	-0.60614	0.001 333		FBgn00 37956	-1.04	4.58 E-06	FBgn00 29879	1.025728	1.38E -21	FBgn00 33388	-5.02013	5.11E -10
FBgn003 3188	-2.62077	2.63E -54		FBgn00 38294	-0.6715	1.16 E-05	FBgn00 29892	0.71704	0.030 503	FBgn00 33395	-1.86503	9.50E -26
FBgn003 3274	-0.6167	0.045 899		FBgn00 38341	-0.65703	0.00 0993	FBgn00 29924	0.901352	1.60E -10	FBgn00 33438	-1.2402	4.34E -13
FBgn003 3356	-0.7169	0.000 275		FBgn00 38353	-3.17698	7.00 E-09	FBgn00 29939	-0.85487	0.000 103	FBgn00 33459	-0.60225	0.000 192
FBgn003 3381	0.618966	1.92E -05		FBgn00 38720	-1.06597	1.75 E-08	FBgn00 29942	0.693688	1.79E -05	FBgn00 33494	-0.92401	0.005 969
FBgn003 3388	-4.92888	1.43E -09		FBgn00 38774	-0.93518	0.00 4348	FBgn00 30017	-1.15434	0.002 214	FBgn00 33518	-1.19285	1.26E -06

FBgn003 3395	-1.85389	4.33E -25		FBgn00 38826	-0.74437	0.00 6416	FBgn00 30040	-2.08876	1.25E -23	FBgn00 33548	-0.78608	0.000 222
FBgn003 3438	-1.32122	1.20E -14		FBgn00 38842	-0.88954	0.00 0164	FBgn00 30091	-0.62868	1.34E -05	FBgn00 33649	-0.5927	0.040 389
FBgn003 3453	0.608411	0.000 907		FBgn00 38881	-0.8305	0.00 0128	FBgn00 30137	1.232252	3.16E -05	FBgn00 33654	-0.72435	0.010 724
FBgn003 3494	-1.00327	0.005 731		FBgn00 39075	-0.91918	0.02 1886	FBgn00 30187	1.259141	0.000 56	FBgn00 33661	-1.2998	0.011 085
FBgn003 3518	-0.72091	0.008 118		FBgn00 39109	-0.61507	5.14 E-05	FBgn00 30349	-0.67107	1.82E -05	FBgn00 33782	-2.65333	3.61E -12
FBgn003 3519	0.663917	0.000 254		FBgn00 39114	-2.20304	7.08 E-23	FBgn00 30432	0.73122	3.76E -10	FBgn00 33787	-2.04248	1.10E -11
FBgn003 3654	-0.93522	0.001 704		FBgn00 39155	-1.51647	1.70 E-09	FBgn00 30439	1.401233	0.001 076	FBgn00 33816	-0.62346	0.000 606
FBgn003 3777	0.8104	4.25E -08		FBgn00 39251	-0.93034	1.09 E-09	FBgn00 30484	0.585944	0.000 68	FBgn00 33926	-0.95909	1.18E -11
FBgn003 3782	-2.30625	1.14E -09		FBgn00 39419	-1.84999	3.53 E-18	FBgn00 30485	-0.77167	0.003 943	FBgn00 33927	-0.86543	4.27E -06
FBgn003 3787	-1.99292	4.78E -11		FBgn00 39430	-0.84468	0.00 674	FBgn00 30600	-4.40301	1.04E -54	FBgn00 34075	-1.30218	5.49E -13
FBgn003 3799	0.768092	0.000 333		FBgn00 39431	-0.71302	0.00 3567	FBgn00 30615	0.831107	1.54E -05	FBgn00 34194	-0.83596	0.027 483
FBgn003 3917	0.703684	2.18E -06		FBgn00 39678	-0.95654	7.38 E-06	FBgn00 30653	-0.85888	0.002 434	FBgn00 34240	-0.82672	0.045 799
FBgn003 3926	-1.6164	9.34E -32		FBgn00 39776	-0.91372	2.96 E-07	FBgn00 30660	1.116979	5.71E -15	FBgn00 34253	-0.76136	0.031 503
FBgn003 3927	-1.47212	1.98E -15		FBgn00 39883	-1.32478	9.07 E-13	FBgn00 30662	-0.90255	0.011 389	FBgn00 34300	-0.7594	0.001 939
FBgn003 4075	-1.61033	2.94E -18		FBgn00 40351	-2.85444	1.02 E-10	FBgn00 30665	-5.27864	1.54E -36	FBgn00 34406	-1.19551	6.20E -06
FBgn003 4194	-0.96842	0.021 068		FBgn00 40364	-1.8758	2.54 E-24	FBgn00 30666	-3.54047	3.60E -75	FBgn00 34408	-0.84809	0.034 491
FBgn003 4312	-0.93918	0.007 068		FBgn00 40398	-1.24664	3.97 E-05	FBgn00 30683	0.98626	3.04E -07	FBgn00 34436	-0.71845	0.017 404

FBgn003 4406	-1.83895	1.27E -11		FBgn00 40609	-1.00812	0.00 4925	FBgn00 30799	1.330585	1.98E -05	FBgn00 34500	-0.8143	8.73E -06
FBgn003 4436	-0.68303	0.049 037		FBgn00 40765	-0.94638	6.24 E-06	FBgn00 30828	-0.79018	0.020 917	FBgn00 34501	-0.61463	0.004 177
FBgn003 4500	-0.60206	0.002 71		FBgn00 40823	-1.38727	5.05 E-12	FBgn00 30955	-1.28908	5.07E -13	FBgn00 34504	-0.61492	3.81E -08
FBgn003 4501	-0.63187	0.006 079		FBgn00 40827	-2.10192	1.27 E-17	FBgn00 30968	0.601646	0.009 632	FBgn00 34602	-0.84532	0.002 294
FBgn003 4602	-1.14445	4.24E -05		FBgn00 40949	-0.73276	0.03 7254	FBgn00 31001	0.68363	0.034 552	FBgn00 34638	-0.98447	6.99E -06
FBgn003 4611	-0.65619	1.33E -06		FBgn00 41180	-0.87449	6.50 E-05	FBgn00 31118	-0.59863	0.002 593	FBgn00 34639	-2.02075	2.27E -09
FBgn003 4638	-0.61522	0.012 647		FBgn00 41184	-1.41782	3.17 E-15	FBgn00 31148	0.663846	4.22E -11	FBgn00 34718	-1.00956	8.45E -06
FBgn003 4639	-1.45904	2.84E -05		FBgn00 42083	-0.86729	1.16 E-05	FBgn00 31157	1.534443	1.63E -14	FBgn00 34761	-1.19238	4.28E -12
FBgn003 4709	-1.06812	7.05E -11		FBgn00 42132	-0.61691	7.40 E-06	FBgn00 31184	1.673598	1.10E -11	FBgn00 35023	-0.92691	0.006 2
FBgn003 4718	-0.69973	0.006 139		FBgn00 44047	-1.73065	1.11 E-09	FBgn00 31220	-2.18374	1.55E -10	FBgn00 35049	-1.22994	0.004 114
FBgn003 4723	-0.66333	0.043 838		FBgn00 45064	-1.21703	5.29 E-11	FBgn00 31252	0.607316	0.000 255	FBgn00 35094	-2.82864	4.66E -25
FBgn003 4733	0.653314	0.000 852		FBgn00 47000	-1.44326	0.00 0258	FBgn00 31258	-0.63448	0.013 671	FBgn00 35308	-1.04889	0.000 444
FBgn003 4761	-1.18914	7.21E -12		FBgn00 50015	-0.62061	0.02 7147	FBgn00 31268	0.59955	0.000 312	FBgn00 35490	-1.61066	8.28E -06
FBgn003 4999	0.792075	3.37E -07		FBgn00 50021	-0.74543	0.00 0807	FBgn00 31275	-2.20886	2.68E -05	FBgn00 35574	-0.71611	0.001 402
FBgn003 5094	-3.76687	2.26E -30		FBgn00 50089	-0.95105	0.00 0531	FBgn00 31313	0.877713	0.002 231	FBgn00 35617	-0.71004	0.002 13
FBgn003 5109	0.682887	0.007 152		FBgn00 50104	-1.39777	0.00 0316	FBgn00 31322	-0.67262	0.033 976	FBgn00 35763	-0.71722	1.20E -10
FBgn003 5308	-0.81847	0.013 907		FBgn00 50115	-1.02404	0.00 025	FBgn00 31453	0.59882	2.00E -08	FBgn00 35767	-0.92466	0.004 039

FBgn003 5312	1.123913	0.000 185		FBgn00 50197	-1.5498	3.90 E-09	FBgn00 31571	-1.34074	1.10E -06	FBgn00 35975	-0.86315	0.007 922
FBgn003 5490	-1.46323	8.62E -05		FBgn00 50345	-3.54447	2.75 E- 104	FBgn00 31574	-0.7592	0.028 121	FBgn00 36091	-1.61047	0.008 227
FBgn003 5641	0.81439	4.30E -10		FBgn00 50428	-2.05829	6.83 E-13	FBgn00 31628	-0.91284	0.007 961	FBgn00 36144	-0.59385	3.55E -07
FBgn003 5642	0.83144	1.23E -05		FBgn00 51176	-1.3912	0.00 2039	FBgn00 31645	-0.96037	4.68E -08	FBgn00 36147	-0.77144	5.91E -09
FBgn003 5691	0.652264	0.025 299		FBgn00 51202	-9.34469	7.55 E-13	FBgn00 31678	1.090728	3.10E -10	FBgn00 36155	-0.60699	0.000 226
FBgn003 5763	-0.65959	5.83E -09		FBgn00 51354	-2.06166	9.56 E-09	FBgn00 31689	-6.47362	6.97E -07	FBgn00 36196	-0.76305	0.021 136
FBgn003 5767	-0.90625	0.009 755		FBgn00 51661	-0.6167	0.03 7422	FBgn00 31690	-11.0207	2.49E -05	FBgn00 36205	-0.88457	0.002 138
FBgn003 5975	-1.1124	0.001 096		FBgn00 51869	-0.5975	0.00 4203	FBgn00 31698	-0.67067	0.000 52	FBgn00 36287	-4.63122	3.45E -13
FBgn003 5976	1.192642	7.55E -13		FBgn00 51997	-1.69472	1.72 E-05	FBgn00 31741	-1.05452	3.28E -06	FBgn00 36381	-1.34921	0.000 322
FBgn003 6144	-0.64702	2.74E -08		FBgn00 52091	-1.30925	1.53 E-17	FBgn00 31745	-0.6604	0.010 948	FBgn00 36454	-0.73347	0.023 048
FBgn003 6147	-0.59556	2.01E -05		FBgn00 52137	-0.66229	0.00 781	FBgn00 31756	-0.73348	1.60E -06	FBgn00 36589	-0.9327	0.000 52
FBgn003 6155	-0.73297	9.54E -06		FBgn00 52625	-0.82946	1.95 E-07	FBgn00 31824	0.636046	0.001 823	FBgn00 36752	-1.51084	2.31E -11
FBgn003 6205	-0.73746	0.022 619		FBgn00 52687	-1.48787	1.70 E-17	FBgn00 31848	0.744216	2.96E -06	FBgn00 36789	-6.7969	7.18E -55
FBgn003 6287	-3.23292	1.23E -11		FBgn00 52702	-1.15938	6.59 E-05	FBgn00 31865	0.674214	0.000 115	FBgn00 36814	-0.64195	0.007 794
FBgn003 6381	-1.48295	0.000 152		FBgn00 52816	-0.60349	0.00 9072	FBgn00 31913	-1.41321	2.56E -22	FBgn00 37012	-0.78797	0.012 6
FBgn003 6589	-0.75703	0.010 55		FBgn00 52865	-2.11798	1.20 E-05	FBgn00 31990	-0.87619	0.048 029	FBgn00 37016	-0.76678	2.73E -05
FBgn003 6620	0.851792	4.22E -05		FBgn00 60296	-1.1994	6.76 E-05	FBgn00 32006	-0.84213	8.71E -07	FBgn00 37137	-0.65403	0.000 532

FBgn003 6648	0.712645	0.000 223		FBgn00 63499	-1.78431	1.38 E-09	FBgn00 32047	0.755785	0.000 379	FBgn00 37344	-0.59403	0.006 904
FBgn003 6732	-0.65063	0.021 146		FBgn00 83940	-1.1978	5.02 E-05	FBgn00 32079	1.103931	4.73E -06	FBgn00 37525	-1.39499	1.58E -18
FBgn003 6752	-1.24862	5.36E -08		FBgn00 85376	-1.78823	2.83 E-27	FBgn00 32101	-0.59651	1.00E -04	FBgn00 37577	-0.66199	0.010 607
FBgn003 6789	-5.24	5.33E -76		FBgn00 85408	-0.62914	0.00 4713	FBgn00 32127	0.643345	0.002 066	FBgn00 37659	-0.85612	1.31E -09
FBgn003 6806	1.350108	2.96E -07		FBgn00 85412	-0.69467	0.02 134	FBgn00 32129	-0.79639	0.006 784	FBgn00 37856	-1.73487	2.73E -46
FBgn003 7007	-0.62231	0.004 732		FBgn00 85427	-1.35222	0.00 057	FBgn00 32156	-0.71856	0.015 434	FBgn00 37944	-0.68334	0.001 591
FBgn003 7016	-0.84623	4.65E -06		FBgn00 85732	-2.00399	4.34 E-28	FBgn00 32162	0.659234	0.003 834	FBgn00 37956	-0.80856	0.000 312
FBgn003 7092	0.672827	0.047 173		FBgn00 86365	-0.87763	0.00 3356	FBgn00 32167	-2.27478	4.11E -15	FBgn00 38047	-0.72404	0.038 315
FBgn003 7525	-1.22881	1.87E -14		FBgn00 86408	-1.16884	4.62 E-12	FBgn00 32187	-0.63559	0.039 886	FBgn00 38294	-0.65999	1.05E -05
FBgn003 7577	-0.70639	0.012 033		FBgn00 86447	-0.59534	0.00 034	FBgn00 32218	-1.15171	0.000 226	FBgn00 38353	-3.1967	2.77E -09
FBgn003 7659	-0.70519	1.46E -06		FBgn00 86659	-0.83116	0.00 0308	FBgn00 32231	0.633449	0.000 276	FBgn00 38679	-0.67898	0.003
FBgn003 7664	0.896962	3.17E -06		FBgn00 86667	-0.89975	6.40 E-05	FBgn00 32264	-1.92467	1.82E -09	FBgn00 38720	-0.91668	1.40E -06
FBgn003 7696	0.828546	0.000 237		FBgn00 86708	-1.18571	1.76 E-07	FBgn00 32290	0.741061	2.73E -05	FBgn00 38774	-1.00353	0.000 982
FBgn003 7838	0.69431	0.040 507		FBgn00 87002	-0.62519	0.01 3308	FBgn00 32297	-0.82459	0.000 224	FBgn00 38826	-1.0452	1.92E -05
FBgn003 7856	-1.85791	2.09E -51		FBgn02 50871	-0.70446	0.04 6667	FBgn00 32330	-0.62405	1.22E -08	FBgn00 38842	-0.67122	0.003 729
FBgn003 7879	1.507491	9.02E -08		FBgn02 59171	-0.72164	0.02 3488	FBgn00 32363	-0.61786	0.000 143	FBgn00 38881	-0.75788	0.000 336
FBgn003 7956	-1.04	4.58E -06		FBgn02 59993	-0.64361	0.00 3598	FBgn00 32382	0.887985	0.000 232	FBgn00 39075	-1.10147	0.002 179

FBgn003 7973	0.858954	0.013 826		FBgn02 60660	-0.99985	0.00 0719	FBgn00 32422	0.720107	1.91E -05	FBgn00 39114	-2.07985	4.73E -21
FBgn003 8011	0.975812	0.000 226		FBgn02 60768	-1.07619	2.77 E-07	FBgn00 32474	0.601557	1.92E -05	FBgn00 39155	-1.79849	6.26E -13
FBgn003 8294	-0.6715	1.16E -05		FBgn02 60964	-0.95626	0.00 0955	FBgn00 32666	-1.45256	1.51E -06	FBgn00 39214	-0.7003	0.048 099
FBgn003 8341	-0.65703	0.000 993		FBgn02 61113	-1.03522	3.80 E-06	FBgn00 32681	-0.63195	0.006 994	FBgn00 39251	-1.00186	2.62E -11
FBgn003 8353	-3.17698	7.00E -09		FBgn02 61258	-1.02269	8.24 E-07	FBgn00 32713	-0.61828	0.047 397	FBgn00 39266	-0.75587	0.000 193
FBgn003 8720	-1.06597	1.75E -08		FBgn02 61505	-2.23344	6.12 E-27	FBgn00 32720	-0.76799	0.000 851	FBgn00 39419	-1.53361	1.39E -13
FBgn003 8774	-0.93518	0.004 348		FBgn02 61555	-1.88579	9.90 E-06	FBgn00 32822	0.70226	0.008 581	FBgn00 39430	-0.78112	0.007 03
FBgn003 8826	-0.74437	0.006 416		FBgn02 61563	-0.94528	0.00 0614	FBgn00 32833	-0.61761	1.26E -06	FBgn00 39431	-0.81874	0.000 303
FBgn003 8842	-0.88954	0.000 164		FBgn02 61800	-0.81756	0.00 0149	FBgn00 32864	-1.47655	1.45E -25	FBgn00 39590	-0.80588	1.21E -06
FBgn003 8881	-0.8305	0.000 128		FBgn02 61835	-7.11587	2.63 E-54	FBgn00 32889	1.29804	4.84E -12	FBgn00 39678	-0.95884	4.16E -06
FBgn003 8966	0.924123	3.49E -07		FBgn02 62003	-1.89931	4.47 E-12	FBgn00 32979	0.604947	1.43E -05	FBgn00 39714	-0.60402	1.53E -07
FBgn003 9006	2.487017	1.09E -08		FBgn02 62004	-1.2121	6.40 E-05	FBgn00 33033	-2.86326	2.03E -15	FBgn00 39776	-0.78994	8.21E -06
FBgn003 9075	-0.91918	0.021 886		FBgn02 62123	-4.48279	8.32 E- 108	FBgn00 33051	0.862264	4.93E -06	FBgn00 39863	-0.64175	0.001 083
FBgn003 9098	2.628443	3.17E -15		FBgn02 62508	-1.21794	0.00 3937	FBgn00 33079	1.357384	0.000 489	FBgn00 39883	-1.23795	1.78E -11
FBgn003 9099	1.131224	1.43E -05		FBgn02 63019	-0.88826	0.00 1127	FBgn00 33108	-1.63249	4.37E -06	FBgn00 39928	-0.82861	0.000 318
FBgn003 9109	-0.61507	5.14E -05		FBgn02 63109	-1.61921	0.00 1127	FBgn00 33153	-0.71145	5.56E -05	FBgn00 40351	-2.80919	6.23E -11
FBgn003 9114	-2.20304	7.08E -23		FBgn02 63219	-0.81464	2.03 E-06	FBgn00 33188	-2.56799	6.10E -53	FBgn00 40364	-1.67651	2.91E -20

FBgn003 9118	0.938353	0.020 673		FBgn02 63397	-0.8778	0.02 8503	FBgn00 33234	0.885465	0.002 697	FBgn00 40398	-1.55955	1.06E -07
FBgn003 9155	-1.51647	1.70E -09		FBgn02 63462	-0.93648	0.03 2242	FBgn00 33274	-0.59118	0.029 077	FBgn00 40609	-1.41045	2.05E -05
FBgn003 9251	-0.93034	1.09E -09		FBgn02 63499	-1.24558	0.00 0903	FBgn00 33315	0.64983	0.000 124	FBgn00 40765	-1.08075	1.04E -07
FBgn003 9258	0.620196	0.000 204		FBgn02 63510	-0.61191	1.08 E-06	FBgn00 33356	-1.11048	1.41E -09	FBgn00 40813	-0.80195	0.000 117
FBgn003 9419	-1.84999	3.53E -18		FBgn02 63659	-0.9734	0.00 2002	FBgn00 33373	0.615789	0.008 344	FBgn00 40823	-1.84512	2.67E -20
FBgn003 9430	-0.84468	0.006 74		FBgn02 63772	-0.58657	0.04 3837	FBgn00 33381	0.795766	4.80E -09	FBgn00 40827	-2.27331	3.18E -20
FBgn003 9431	-0.71302	0.003 567		FBgn02 63873	-1.85632	2.55 E-36	FBgn00 33388	-5.02013	5.11E -10	FBgn00 40949	-0.65076	0.037 127
FBgn003 9538	0.680119	0.015 609		FBgn02 63930	-0.86253	2.12 E-05	FBgn00 33395	-1.86503	9.50E -26	FBgn00 41092	-0.58882	1.69E -08
FBgn003 9678	-0.95654	7.38E -06		FBgn02 64089	-1.4337	2.81 E-07	FBgn00 33438	-1.2402	4.34E -13	FBgn00 41180	-0.82826	0.000 106
FBgn003 9776	-0.91372	2.96E -07		FBgn02 64385	-1.18246	2.12 E-05	FBgn00 33459	-0.60225	0.000 192	FBgn00 41184	-1.17853	3.49E -11
FBgn003 9856	1.38813	3.73E -09		FBgn02 64489	-1.21877	0.00 0287	FBgn00 33494	-0.92401	0.005 969	FBgn00 42083	-0.86946	6.54E -06
FBgn003 9883	-1.32478	9.07E -13		FBgn02 64490	-0.73396	0.00 0129	FBgn00 33518	-1.19285	1.26E -06	FBgn00 42132	-0.79153	1.71E -09
FBgn003 9914	0.624032	0.011 817		FBgn02 64617	-0.91714	0.02 0364	FBgn00 33519	0.963547	4.04E -09	FBgn00 43364	-0.71925	7.77E -07
FBgn003 9955	0.630083	7.36E -09		FBgn02 64695	-0.89727	0.00 0249	FBgn00 33548	-0.78608	0.000 222	FBgn00 43799	-0.59907	0.019 944
FBgn004 0351	-2.85444	1.02E -10		FBgn02 64835	-3.53342	3.14 E-10	FBgn00 33649	-0.5927	0.040 389	FBgn00 43884	-0.78908	0.024 59
FBgn004 0364	-1.8758	2.54E -24		FBgn02 64894	-1.92031	1.09 E-14	FBgn00 33654	-0.72435	0.010 724	FBgn00 44047	-1.82867	7.16E -11
FBgn004 0398	-1.24664	3.97E -05		FBgn02 65082	-0.7097	0.00 3016	FBgn00 33661	-1.2998	0.011 085	FBgn00 45064	-1.28083	3.22E -12

FBgn004 0609	-1.00812	0.004 925		FBgn02 65274	-0.83271	7.44 E-06	FBgn00 33716	0.599723	3.28E -07	FBgn00 46776	-0.68442	0.000 529
FBgn004 0765	-0.94638	6.24E -06		FBgn02 65296	-10.9575	5.39 E-18	FBgn00 33782	-2.65333	3.61E -12	FBgn00 47000	-1.49348	8.69E -05
FBgn004 0823	-1.38727	5.05E -12		FBgn02 65487	-1.03757	0.00 1854	FBgn00 33787	-2.04248	1.10E -11	FBgn00 50015	-0.79947	0.001 119
FBgn004 0827	-2.10192	1.27E -17		FBgn02 65669	-0.96537	0.00 6139	FBgn00 33799	0.808726	7.73E -05	FBgn00 50026	-0.95521	0.005 558
FBgn004 0949	-0.73276	0.037 254		FBgn02 65726	-0.72824	0.00 5903	FBgn00 33810	0.649121	8.99E -07	FBgn00 50089	-0.89416	0.000 736
armi	1.796296	1.37E -26		FBgn02 65991	-0.60061	0.03 421	FBgn00 33816	-0.62346	0.000 606	FBgn00 50104	-1.06961	0.003 943
FBgn004 1180	-0.87449	6.50E -05		FBgn02 66084	-1.23937	1.40 E-08	FBgn00 33917	0.737289	3.70E -07	FBgn00 50115	-1.21533	4.92E -06
FBgn004 1184	-1.41782	3.17E -15		FBgn02 66129	-3.11051	1.56 E-15	FBgn00 33926	-0.95909	1.18E -11	FBgn00 50197	-1.40717	4.68E -08
FBgn004 1629	0.802132	0.003 211		FBgn02 66758	-1.33219	1.24 E-06	FBgn00 33927	-0.86543	4.27E -06	FBgn00 50345	-3.85626	1.66E -115
FBgn004 2083	-0.86729	1.16E -05		FBgn02 66801	-2.76367	2.77 E-21	FBgn00 33979	0.588416	1.95E -11	FBgn00 50428	-1.58652	5.28E -09
FBgn004 2132	-0.61691	7.40E -06		FBgn02 67001	-0.69259	0.04 1337	FBgn00 34075	-1.30218	5.49E -13	FBgn00 50456	-0.69725	0.001 285
FBgn004 3069	1.174314	3.38E -07		FBgn02 67348	-1.04848	6.73 E-07	FBgn00 34081	0.821746	1.81E -05	FBgn00 50460	-1.42978	0.000 529
FBgn004 4047	-1.73065	1.11E -09		FBgn02 67689	-5.29999	1.42 E-18	FBgn00 34194	-0.83596	0.027 483	FBgn00 51015	-0.62623	0.010 667
FBgn004 5064	-1.21703	5.29E -11		FBgn02 67764	-2.87535	2.73 E-08	FBgn00 34240	-0.82672	0.045 799	FBgn00 51116	-0.81052	0.007 443
FBgn004 7000	-1.44326	0.000 258		FBgn02 67796	-2.43526	7.55 E-13	FBgn00 34253	-0.76136	0.031 503	FBgn00 51176	-2.08289	1.40E -06
FBgn004 7199	0.888828	2.36E -10		FBgn02 67986	-1.49841	5.60 E-05	FBgn00 34300	-0.7594	0.001 939	FBgn00 51202	-7.5764	2.86E -11
FBgn005 0005	0.847706	0.017 055		FBgn02 83471	-0.73559	0.02 714	FBgn00 34314	0.741393	2.27E -06	FBgn00 51279	-0.72967	0.029 668

FBgn005 0015	-0.62061	0.027 147		FBgn02 84408	-1.24483	0.00 5412	FBgn00 34354	0.877376	0.006 108		FBgn00 51352	-0.59567	0.000 528
FBgn005 0021	-0.74543	0.000 807					FBgn00 34402	0.599287	0.027 401		FBgn00 51354	-2.47232	2.11E -11
FBgn005 0046	1.39162	0.000 749					FBgn00 34406	-1.19551	6.20E -06		FBgn00 51612	-0.79993	0.027 257
FBgn005 0089	-0.95105	0.000 531					FBgn00 34408	-0.84809	0.034 491		FBgn00 51755	-0.75656	0.005 859
FBgn005 0104	-1.39777	0.000 316					FBgn00 34436	-0.71845	0.017 404		FBgn00 51869	-0.63075	0.001 183
FBgn005 0115	-1.02404	0.000 25					FBgn00 34500	-0.8143	8.73E -06		FBgn00 51997	-1.03069	0.006 388
FBgn005 0197	-1.5498	3.90E -09					FBgn00 34501	-0.61463	0.004 177		FBgn00 52091	-1.10402	8.03E -13
FBgn005 0345	-3.54447	2.75E -104					FBgn00 34504	-0.61492	3.81E -08		FBgn00 52311	-1.04128	0.001 259
FBgn005 0428	-2.05829	6.83E -13					FBgn00 34588	0.697284	0.014 448		FBgn00 52625	-1.0433	1.54E -11
FBgn005 0440	1.091102	5.50E -07					FBgn00 34602	-0.84532	0.002 294		FBgn00 52687	-1.41642	2.87E -16
FBgn005 1075	0.762312	1.03E -06					FBgn00 34638	-0.98447	6.99E -06		FBgn00 52702	-1.06378	0.000 192
FBgn005 1176	-1.3912	0.002 039					FBgn00 34639	-2.02075	2.27E -09		FBgn00 52865	-1.87687	5.56E -05
FBgn005 1202	-9.34469	7.55E -13					FBgn00 34718	-1.00956	8.45E -06		FBgn00 53087	-0.75146	0.000 489
FBgn005 1354	-2.06166	9.56E -09					FBgn00 34733	1.060529	4.86E -10		FBgn00 60296	-1.08441	0.000 212
FBgn005 1388	0.708337	0.004 761					FBgn00 34761	-1.19238	4.28E -12		FBgn00 61200	-0.67754	0.000 998
FBgn005 1661	-0.6167	0.037 422					FBgn00 34800	0.803496	0.000 965		FBgn00 63499	-2.03376	5.38E -12
FBgn005 1869	-0.5975	0.004 203					FBgn00 34999	0.931831	4.11E -10		FBgn00 65047	-0.90966	0.000 893

FBgn005 1997	-1.69472	1.72E -05					FBgn00 35023	-0.92691	0.006 2		FBgn00 65048	-0.92064	0.000 497
FBgn005 2091	-1.30925	1.53E -17					FBgn00 35049	-1.22994	0.004 114		FBgn00 82974	-2.15784	5.96E -05
FBgn005 2137	-0.66229	0.007 81					FBgn00 35094	-2.82864	4.66E -25		FBgn00 82983	-0.86323	9.25E -05
FBgn005 2350	0.744034	1.31E -06					FBgn00 35109	0.663234	0.004 947		FBgn00 83003	-0.80533	0.028 97
FBgn005 2625	-0.82946	1.95E -07					FBgn00 35308	-1.04889	0.000 444		FBgn00 83004	-0.83886	0.020 231
FBgn005 2687	-1.48787	1.70E -17					FBgn00 35312	1.674201	3.25E -10		FBgn00 83005	-0.78255	0.027 153
FBgn005 2702	-1.15938	6.59E -05					FBgn00 35356	0.637181	0.042 501		FBgn00 83027	-0.65577	0.009 769
FBgn005 2816	-0.60349	0.009 072					FBgn00 35392	0.631071	0.037 364		FBgn00 83045	-1.77204	2.19E -05
FBgn005 2865	-2.11798	1.20E -05					FBgn00 35407	0.621018	0.001 203		FBgn00 83940	-1.02289	0.000 376
FBgn005 8006	0.866054	4.58E -09					FBgn00 35490	-1.61066	8.28E -06		FBgn00 85195	-0.6835	0.020 307
FBgn005 8439	0.588682	0.001 918					FBgn00 35515	0.895933	0.000 312		FBgn00 85249	-2.02159	0.002 593
FBgn006 0296	-1.1994	6.76E -05					FBgn00 35574	-0.71611	0.001 402		FBgn00 85362	-1.3716	0.025 245
FBgn006 3499	-1.78431	1.38E -09					FBgn00 35617	-0.71004	0.002 13		FBgn00 85376	-1.96082	1.81E -32
FBgn008 3940	-1.1978	5.02E -05					FBgn00 35642	1.129916	1.17E -10		FBgn00 85408	-1.19647	5.62E -10
FBgn008 5376	-1.78823	2.83E -27					FBgn00 35725	0.710554	0.000 715		FBgn00 85410	-0.79001	0.026 117
FBgn008 5408	-0.62914	0.004 713					FBgn00 35763	-0.71722	1.20E -10		FBgn00 85412	-1.05415	5.38E -05
FBgn008 5412	-0.69467	0.021 34					FBgn00 35767	-0.92466	0.004 039		FBgn00 85427	-1.59742	1.93E -05

FBgn008 5427	-1.35222	0.000 57					FBgn00 35959	0.633668	4.06E -06		FBgn00 85434	-1.24705	0.000 311
FBgn008 5732	-2.00399	4.34E -28					FBgn00 35975	-0.86315	0.007 922		FBgn00 85732	-2.40904	3.21E -39
FBgn008 5753	0.674292	2.12E -05					FBgn00 35976	1.10629	3.49E -11		FBgn00 86265	-0.72274	0.000 113
FBgn008 5819	0.640403	0.000 237					FBgn00 36091	-1.61047	0.008 227		FBgn00 86365	-0.63962	0.023 777
FBgn008 6365	-0.87763	0.003 356					FBgn00 36144	-0.59385	3.55E -07		FBgn00 86408	-1.46367	1.58E -18
FBgn008 6408	-1.16884	4.62E -12					FBgn00 36147	-0.77144	5.91E -09		FBgn00 86447	-0.7692	8.59E -07
FBgn008 6447	-0.59534	0.000 34					FBgn00 36155	-0.60699	0.000 226		FBgn00 86655	-0.80318	5.13E -06
FBgn008 6659	-0.83116	0.000 308					FBgn00 36196	-0.76305	0.021 136		FBgn00 86659	-1.26239	1.92E -09
FBgn008 6667	-0.89975	6.40E -05					FBgn00 36205	-0.88457	0.002 138		FBgn00 86661	-0.66343	0.019 39
FBgn008 6708	-1.18571	1.76E -07					FBgn00 36248	0.60904	0.000 192		FBgn00 86665	-0.72487	0.006 388
FBgn008 7002	-0.62519	0.013 308					FBgn00 36271	0.724215	0.009 523		FBgn00 86667	-0.77001	0.000 563
FBgn025 0871	-0.70446	0.046 667					FBgn00 36287	-4.63122	3.45E -13		FBgn00 86708	-1.11162	7.37E -07
FBgn025 0907	1.377147	5.50E -07					FBgn00 36381	-1.34921	0.000 322		FBgn00 86906	-1.51933	0.030 785
FBgn025 9171	-0.72164	0.023 488					FBgn00 36423	0.762328	0.002 156		FBgn00 87002	-0.81029	0.000 326
FBgn025 9936	0.759697	0.000 158					FBgn00 36454	-0.73347	0.023 048		FBgn02 43516	-0.63471	0.002 197
FBgn025 9993	-0.64361	0.003 598					FBgn00 36589	-0.9327	0.000 52		FBgn02 50871	-0.92656	0.002 482
FBgn026 0660	-0.99985	0.000 719					FBgn00 36620	0.750085	0.000 309		FBgn02 59171	-0.93672	0.000 881

FBgn026 0768	-1.07619	2.77E -07					FBgn00 36690	0.759185	1.16E -08		FBgn02 59927	-0.60547	0.049 246
FBgn026 0964	-0.95626	0.000 955					FBgn00 36752	-1.51084	2.31E -11		FBgn02 59993	-0.71933	0.000 451
FBgn026 1113	-1.03522	3.80E -06					FBgn00 36789	-6.7969	7.18E -55		FBgn02 60400	-0.70887	0.027 58
FBgn026 1258	-1.02269	8.24E -07					FBgn00 36806	1.354637	1.82E -07		FBgn02 60634	-0.62991	0.002 622
FBgn026 1393	0.629074	0.002 164					FBgn00 36814	-0.64195	0.007 794		FBgn02 60660	-0.58841	0.046 283
FBgn026 1505	-2.23344	6.12E -27					FBgn00 37011	0.678723	0.012 306		FBgn02 60745	-0.66779	0.000 64
FBgn026 1555	-1.88579	9.90E -06					FBgn00 37012	-0.78797	0.012 6		FBgn02 60768	-0.71829	0.000 827
FBgn026 1563	-0.94528	0.000 614					FBgn00 37016	-0.76678	2.73E -05		FBgn02 60932	-0.72107	0.027 227
FBgn026 1625	0.76404	9.57E -06					FBgn00 37045	0.764312	0.001 213		FBgn02 60964	-0.63159	0.024 44
FBgn026 1800	-0.81756	0.000 149					FBgn00 37092	0.632341	0.034 866		FBgn02 61053	-1.10922	0.003 515
FBgn026 1835	-7.11587	2.63E -54					FBgn00 37137	-0.65403	0.000 532		FBgn02 61113	-1.22708	1.28E -08
FBgn026 1963	0.7404	0.019 688					FBgn00 37244	0.640492	0.000 134		FBgn02 61258	-1.14465	1.47E -08
FBgn026 2003	-1.89931	4.47E -12					FBgn00 37261	0.609197	7.73E -06		FBgn02 61505	-2.45325	9.53E -32
FBgn026 2004	-1.2121	6.40E -05					FBgn00 37344	-0.59403	0.006 904		FBgn02 61549	-0.59985	0.005 057
FBgn026 2108	0.77072	0.000 647					FBgn00 37347	0.91666	0.000 149		FBgn02 61555	-2.18984	1.05E -07
FBgn026 2123	-4.48279	8.32E -108					FBgn00 37515	0.592762	0.010 394		FBgn02 61563	-0.82327	0.001 974
FBgn026 2508	-1.21794	0.003 937					FBgn00 37525	-1.39499	1.58E -18		FBgn02 61617	-0.65988	0.000 314

FBgn026 2620	1.513257	2.20E -11					FBgn00 37577	-0.66199	0.010 607		FBgn02 61790	-0.65736	1.19E -08
FBgn026 2895	0.907983	0.001 089					FBgn00 37617	0.770266	0.007 364		FBgn02 61797	-0.67615	0.002 714
FBgn026 3019	-0.88826	0.001 127					FBgn00 37659	-0.85612	1.31E -09		FBgn02 61800	-0.77121	0.000 248
FBgn026 3048	0.978504	0.008 658					FBgn00 37664	1.05379	9.36E -09		FBgn02 61835	-7.20067	1.38E -55
FBgn026 3109	-1.61921	0.001 127					FBgn00 37696	0.791163	0.000 312		FBgn02 61955	-0.71006	4.97E -10
FBgn026 3219	-0.81464	2.03E -06					FBgn00 37844	0.720561	7.95E -06		FBgn02 62003	-1.80644	2.61E -11
FBgn026 3397	-0.8778	0.028 503					FBgn00 37856	-1.73487	2.73E -46		FBgn02 62004	-1.7001	1.23E -08
FBgn026 3462	-0.93648	0.032 242					FBgn00 37879	1.563123	1.53E -08		FBgn02 62109	-1.05422	0.008 783
FBgn026 3499	-1.24558	0.000 903					FBgn00 37944	-0.68334	0.001 591		FBgn02 62123	-3.90914	1.06E -107
FBgn026 3510	-0.61191	1.08E -06					FBgn00 37956	-0.80856	0.000 312		FBgn02 62127	-0.82888	0.001 183
FBgn026 3659	-0.9734	0.002 002					FBgn00 37973	0.997097	0.001 286		FBgn02 62160	-0.58807	0.001 517
FBgn026 3745	0.697822	0.004 79					FBgn00 37999	0.631053	0.043 876		FBgn02 62508	-1.36654	0.000 52
FBgn026 3772	-0.58657	0.043 837					FBgn00 38011	0.963454	0.000 179		FBgn02 62945	-0.76161	0.004 56
FBgn026 3873	-1.85632	2.55E -36					FBgn00 38020	0.679968	5.83E -08		FBgn02 63006	-0.60401	0.010 654
FBgn026 3930	-0.86253	2.12E -05					FBgn00 38037	0.711441	0.047 158		FBgn02 63019	-1.21213	2.29E -06
FBgn026 4089	-1.4337	2.81E -07					FBgn00 38047	-0.72404	0.038 315		FBgn02 63109	-2.35509	7.03E -07
FBgn026 4385	-1.18246	2.12E -05					FBgn00 38252	0.84228	7.94E -12		FBgn02 63110	-0.72767	0.004 341

FBgn026 4489	-1.21877	0.000 287					FBgn00 38294	-0.65999	1.05E -05		FBgn02 63132	-0.78315	0.031 458
FBgn026 4490	-0.73396	0.000 129					FBgn00 38353	-3.1967	2.77E -09		FBgn02 63200	-0.69157	0.001 944
FBgn026 4617	-0.91714	0.020 364					FBgn00 38679	-0.67898	0.003		FBgn02 63219	-1.27468	1.59E -14
FBgn026 4695	-0.89727	0.000 249					FBgn00 38720	-0.91668	1.40E -06		FBgn02 63397	-0.92482	0.009 441
FBgn026 4704	0.731057	0.008 224					FBgn00 38774	-1.00353	0.000 982		FBgn02 63413	-1.09851	0.002 18
FBgn026 4835	-3.53342	3.14E -10					FBgn00 38826	-1.0452	1.92E -05		FBgn02 63462	-1.13131	0.003 325
FBgn026 4894	-1.92031	1.09E -14					FBgn00 38842	-0.67122	0.003 729		FBgn02 63499	-1.22122	0.000 618
FBgn026 4979	0.724987	3.32E -05					FBgn00 38881	-0.75788	0.000 336		FBgn02 63659	-1.05211	0.000 376
FBgn026 5042	0.718537	0.008 348					FBgn00 38943	1.374052	1.61E -05		FBgn02 63768	-0.61285	0.026 289
FBgn026 5082	-0.7097	0.003 016					FBgn00 38966	0.825267	6.40E -06		FBgn02 63772	-0.64555	0.010 945
FBgn026 5274	-0.83271	7.44E -06					FBgn00 39006	2.813532	2.31E -11		FBgn02 63873	-1.72556	7.11E -32
FBgn026 5296	-10.9575	5.39E -18					FBgn00 39043	0.663951	0.015 436		FBgn02 63930	-1.08803	1.89E -08
FBgn026 5487	-1.03757	0.001 854					FBgn00 39075	-1.10147	0.002 179		FBgn02 63973	-1.08962	0.007 576
FBgn026 5669	-0.96537	0.006 139					FBgn00 39098	2.749223	6.85E -17		FBgn02 63995	-0.89294	0.039 113
FBgn026 5726	-0.72824	0.005 903					FBgn00 39099	1.574202	4.18E -11		FBgn02 64089	-1.35637	8.87E -07
FBgn026 5991	-0.60061	0.034 21					FBgn00 39114	-2.07985	4.73E -21		FBgn02 64385	-1.64086	1.87E -09
FBgn026 6084	-1.23937	1.40E -08					FBgn00 39118	1.104319	0.001 887		FBgn02 64489	-1.16449	0.000 311

FBgn026 6129	-3.11051	1.56E -15					FBgn00 39155	-1.79849	6.26E -13		FBgn02 64490	-0.63179	0.000 86
FBgn026 6347	1.528003	9.34E -13					FBgn00 39214	-0.7003	0.048 099		FBgn02 64617	-0.9725	0.006 2
FBgn026 6569	0.609533	0.003 567					FBgn00 39251	-1.00186	2.62E -11		FBgn02 64695	-1.28933	1.78E -08
FBgn026 6666	0.782992	9.57E -13					FBgn00 39258	0.63399	8.14E -05		FBgn02 64835	-4.74493	2.03E -11
FBgn026 6758	-1.33219	1.24E -06					FBgn00 39266	-0.75587	0.000 193		FBgn02 64894	-2.02076	2.77E -16
FBgn026 6801	-2.76367	2.77E -21					FBgn00 39272	0.732263	3.10E -06		FBgn02 65082	-0.64892	0.004 33
FBgn026 7001	-0.69259	0.041 337					FBgn00 39419	-1.53361	1.39E -13		FBgn02 65140	-0.59513	0.000 429
FBgn026 7348	-1.04848	6.73E -07					FBgn00 39430	-0.78112	0.007 03		FBgn02 65274	-0.83641	4.45E -06
FBgn026 7689	-5.29999	1.42E -18					FBgn00 39431	-0.81874	0.000 303		FBgn02 65296	-8.19199	6.32E -26
FBgn026 7764	-2.87535	2.73E -08					FBgn00 39464	0.775599	2.63E -07		FBgn02 65316	-0.61546	0.010 145
FBgn026 7796	-2.43526	7.55E -13					FBgn00 39590	-0.80588	1.21E -06		FBgn02 65434	-0.614	0.000 195
FBgn026 7986	-1.49841	5.60E -05					FBgn00 39678	-0.95884	4.16E -06		FBgn02 65487	-1.73669	7.08E -09
FBgn028 3471	-0.73559	0.027 14					FBgn00 39714	-0.60402	1.53E -07		FBgn02 65669	-1.38031	2.04E -05
FBgn028 4408	-1.24483	0.005 412					FBgn00 39776	-0.78994	8.21E -06		FBgn02 65726	-0.79297	0.001 132
							FBgn00 39856	1.535449	1.95E -11		FBgn02 65991	-0.94258	7.83E -05
							FBgn00 39863	-0.64175	0.001 083		FBgn02 66084	-1.29213	2.03E -09
							FBgn00 39883	-1.23795	1.78E -11		FBgn02 66129	-3.6414	4.36E -18

						FBgn00 39890	1.081712	8.69E -14	FBgn02 66717	-0.59103	0.014 435
						FBgn00 39928	-0.82861	0.000 318	FBgn02 66756	-0.62169	0.002 482
						FBgn00 39955	0.971013	4.55E -21	FBgn02 66758	-1.03532	0.000 135
						FBgn00 39958	0.856169	2.75E -13	FBgn02 66801	-2.86785	8.65E -23
						FBgn00 40056	0.737194	2.24E -05	FBgn02 67001	-0.88042	0.002 753
						FBgn00 40351	-2.80919	6.23E -11	FBgn02 67033	-0.59035	0.006 905
						FBgn00 40364	-1.67651	2.91E -20	FBgn02 67348	-1.12561	4.96E -08
						FBgn00 40384	0.644973	9.28E -06	FBgn02 67506	-0.64271	0.015 23
						FBgn00 40398	-1.55955	1.06E -07	FBgn02 67689	-9.23222	1.38E -12
						FBgn00 40609	-1.41045	2.05E -05	FBgn02 67764	-4.08612	5.35E -11
						FBgn00 40765	-1.08075	1.04E -07	FBgn02 67796	-2.2773	4.13E -12
						FBgn00 40813	-0.80195	0.000 117	FBgn02 67986	-1.56015	1.50E -05
						FBgn00 40823	-1.84512	2.67E -20	FBgn02 83427	-0.95384	0.004 238
						FBgn00 40827	-2.27331	3.18E -20	FBgn02 83451	-1.05065	0.005 54
						FBgn00 40928	0.608925	0.001 08	FBgn02 83471	-0.9275	0.001 591
						FBgn00 40949	-0.65076	0.037 127	FBgn02 84221	-0.67484	0.000 145
						FBgn00 41004	0.776096	9.10E -09	FBgn02 84408	-1.69256	2.38E -05

							FBgn00 41092	-0.58882	1.69E -08		FBgn02 85925	-0.70356	0.001 613
						armi	1.540239	1.72E -19					
						FBgn00 41180	-0.82826	0.000 106					
						FBgn00 41184	-1.17853	3.49E -11					
						FBgn00 41629	1.054141	1.42E -05					
						FBgn00 41630	0.616966	0.004 492					
						FBgn00 42083	-0.86946	6.54E -06					
						FBgn00 42111	0.615747	0.000 454					
						FBgn00 42132	-0.79153	1.71E -09					
						FBgn00 43069	1.552203	5.61E -13					
						FBgn00 43364	-0.71925	7.77E -07					
						FBgn00 43799	-0.59907	0.019 944					
						FBgn00 43884	-0.78908	0.024 59					
						FBgn00 44046	1.172158	0.003 63					
						FBgn00 44047	-1.82867	7.16E -11					
						FBgn00 45064	-1.28083	3.22E -12					
						FBgn00 46692	0.789117	3.60E -05					

							FBgn00 46776	-0.68442	0.000 529					
							FBgn00 47000	-1.49348	8.69E -05					
							FBgn00 47199	0.669878	4.54E -06					
							FBgn00 50005	0.715495	0.030 831					
							FBgn00 50015	-0.79947	0.001 119					
							FBgn00 50026	-0.95521	0.005 558					
							FBgn00 50046	1.467208	0.000 181					
							FBgn00 50089	-0.89416	0.000 736					
							FBgn00 50096	0.596431	0.032 893					
							FBgn00 50104	-1.06961	0.003 943					
							FBgn00 50115	-1.21533	4.92E -06					
							FBgn00 50197	-1.40717	4.68E -08					
							FBgn00 50345	-3.85626	1.66E -115					
							FBgn00 50428	-1.58652	5.28E -09					
							FBgn00 50440	0.81238	0.000 334					
							FBgn00 50456	-0.69725	0.001 285					
							FBgn00 50460	-1.42978	0.000 529					

							FBgn00 51015	-0.62623	0.010 667					
							FBgn00 51075	0.957012	1.31E -10					
							FBgn00 51116	-0.81052	0.007 443					
							FBgn00 51176	-2.08289	1.40E -06					
							FBgn00 51202	-7.5764	2.86E -11					
							FBgn00 51262	1.011513	0.003 236					
							FBgn00 51279	-0.72967	0.029 668					
							FBgn00 51344	0.609273	0.005 8					
							FBgn00 51352	-0.59567	0.000 528					
							FBgn00 51354	-2.47232	2.11E -11					
							FBgn00 51388	0.63185	0.008 076					
							FBgn00 51612	-0.79993	0.027 257					
							FBgn00 51755	-0.75656	0.005 859					
							FBgn00 51869	-0.63075	0.001 183					
							FBgn00 51875	0.713794	0.025 245					
							FBgn00 51997	-1.03069	0.006 388					
							FBgn00 52091	-1.10402	8.03E -13					

							FBgn00 52207	0.800175	2.02E -06					
							FBgn00 52311	-1.04128	0.001 259					
							FBgn00 52350	1.238561	9.24E -19					
							FBgn00 52625	-1.0433	1.54E -11					
							FBgn00 52642	0.764768	5.13E -05					
							FBgn00 52687	-1.41642	2.87E -16					
							FBgn00 52702	-1.06378	0.000 192					
							FBgn00 52865	-1.87687	5.56E -05					
							FBgn00 53062	0.758306	0.016 698					
							FBgn00 53087	-0.75146	0.000 489					
							FBgn00 53816	0.626706	0.009 069					
							FBgn00 58006	0.926482	1.45E -10					
							FBgn00 58439	1.035294	2.10E -10					
							FBgn00 60296	-1.08441	0.000 212					
							FBgn00 61200	-0.67754	0.000 998					
							FBgn00 63499	-2.03376	5.38E -12					
							FBgn00 65047	-0.90966	0.000 893					

							FBgn00 65048	-0.92064	0.000 497					
							FBgn00 82974	-2.15784	5.96E -05					
							FBgn00 82983	-0.86323	9.25E -05					
							FBgn00 83003	-0.80533	0.028 97					
							FBgn00 83004	-0.83886	0.020 231					
							FBgn00 83005	-0.78255	0.027 153					
							FBgn00 83027	-0.65577	0.009 769					
							FBgn00 83045	-1.77204	2.19E -05					
							FBgn00 83940	-1.02289	0.000 376					
							FBgn00 85195	-0.6835	0.020 307					
							FBgn00 85249	-2.02159	0.002 593					
							FBgn00 85362	-1.3716	0.025 245					
							FBgn00 85376	-1.96082	1.81E -32					
							FBgn00 85408	-1.19647	5.62E -10					
							FBgn00 85410	-0.79001	0.026 117					
							FBgn00 85412	-1.05415	5.38E -05					
							FBgn00 85427	-1.59742	1.93E -05					

							FBgn00 85434	-1.24705	0.000 311					
							FBgn00 85732	-2.40904	3.21E -39					
							FBgn00 85813	0.611825	0.000 64					
							FBgn00 86265	-0.72274	0.000 113					
							FBgn00 86365	-0.63962	0.023 777					
							FBgn00 86408	-1.46367	1.58E -18					
							FBgn00 86447	-0.7692	8.59E -07					
							FBgn00 86655	-0.80318	5.13E -06					
							FBgn00 86659	-1.26239	1.92E -09					
							FBgn00 86661	-0.66343	0.019 39					
							FBgn00 86665	-0.72487	0.006 388					
							FBgn00 86667	-0.77001	0.000 563					
							FBgn00 86708	-1.11162	7.37E -07					
							FBgn00 86906	-1.51933	0.030 785					
							FBgn00 87002	-0.81029	0.000 326					
							FBgn02 43516	-0.63471	0.002 197					
							FBgn02 50816	0.655184	5.43E -07					

							FBgn02 50871	-0.92656	0.002 482					
							FBgn02 50907	1.217972	1.19E -05					
							FBgn02 59111	1.121237	0.000 462					
							FBgn02 59171	-0.93672	0.000 881					
							FBgn02 59927	-0.60547	0.049 246					
							FBgn02 59936	0.925366	8.08E -07					
							FBgn02 59993	-0.71933	0.000 451					
							FBgn02 60005	0.637639	0.004 435					
							FBgn02 60400	-0.70887	0.027 58					
							FBgn02 60634	-0.62991	0.002 622					
							FBgn02 60660	-0.58841	0.046 283					
							FBgn02 60745	-0.66779	0.000 64					
							FBgn02 60768	-0.71829	0.000 827					
							FBgn02 60798	0.700853	5.39E -06					
							FBgn02 60859	0.851713	0.049 872					
							FBgn02 60932	-0.72107	0.027 227					
							FBgn02 60964	-0.63159	0.024 44					

							FBgn02 60986	0.641747	9.02E -06					
							FBgn02 61053	-1.10922	0.003 515					
							FBgn02 61113	-1.22708	1.28E -08					
							FBgn02 61258	-1.14465	1.47E -08					
							FBgn02 61393	0.770709	3.66E -05					
							FBgn02 61505	-2.45325	9.53E -32					
							FBgn02 61549	-0.59985	0.005 057					
							FBgn02 61555	-2.18984	1.05E -07					
							FBgn02 61563	-0.82327	0.001 974					
							FBgn02 61617	-0.65988	0.000 314					
							FBgn02 61625	0.899123	4.74E -08					
							FBgn02 61790	-0.65736	1.19E -08					
							FBgn02 61797	-0.67615	0.002 714					
							FBgn02 61800	-0.77121	0.000 248					
							FBgn02 61808	0.588205	0.012 223					
							FBgn02 61835	-7.20067	1.38E -55					
							FBgn02 61955	-0.71006	4.97E -10					

							FBgn02 62003	-1.80644	2.61E -11					
							FBgn02 62004	-1.7001	1.23E -08					
							FBgn02 62108	0.882798	2.85E -05					
							FBgn02 62109	-1.05422	0.008 783					
							FBgn02 62123	-3.90914	1.06E -107					
							FBgn02 62124	0.648297	5.11E -10					
							FBgn02 62127	-0.82888	0.001 183					
							FBgn02 62160	-0.58807	0.001 517					
							FBgn02 62508	-1.36654	0.000 52					
							FBgn02 62620	1.767919	7.31E -16					
							FBgn02 62731	0.608728	0.000 816					
							FBgn02 62895	0.682033	0.014 281					
							FBgn02 62945	-0.76161	0.004 56					
							FBgn02 62987	0.597734	0.048 768					
							FBgn02 63006	-0.60401	0.010 654					
							FBgn02 63019	-1.21213	2.29E -06					
							FBgn02 63109	-2.35509	7.03E -07					

							FBgn02 63110	-0.72767	0.004 341					
							FBgn02 63132	-0.78315	0.031 458					
							FBgn02 63200	-0.69157	0.001 944					
							FBgn02 63219	-1.27468	1.59E -14					
							FBgn02 63397	-0.92482	0.009 441					
							FBgn02 63413	-1.09851	0.002 18					
							FBgn02 63462	-1.13131	0.003 325					
							FBgn02 63499	-1.22122	0.000 618					
							FBgn02 63659	-1.05211	0.000 376					
							FBgn02 63745	0.651116	0.005 3					
							FBgn02 63768	-0.61285	0.026 289					
							FBgn02 63772	-0.64555	0.010 945					
							FBgn02 63873	-1.72556	7.11E -32					
							FBgn02 63930	-1.08803	1.89E -08					
							FBgn02 63973	-1.08962	0.007 576					
							FBgn02 63995	-0.89294	0.039 113					
							FBgn02 64089	-1.35637	8.87E -07					

							FBgn02 64385	-1.64086	1.87E -09					
							FBgn02 64489	-1.16449	0.000 311					
							FBgn02 64490	-0.63179	0.000 86					
							FBgn02 64617	-0.9725	0.006 2					
							FBgn02 64695	-1.28933	1.78E -08					
							FBgn02 64704	0.967343	6.55E -05					
							FBgn02 64835	-4.74493	2.03E -11					
							FBgn02 64894	-2.02076	2.77E -16					
							FBgn02 64979	1.000835	4.97E -10					
							FBgn02 65082	-0.64892	0.004 33					
							FBgn02 65140	-0.59513	0.000 429					
							FBgn02 65274	-0.83641	4.45E -06					
							FBgn02 65296	-8.19199	6.32E -26					
							FBgn02 65316	-0.61546	0.010 145					
							FBgn02 65434	-0.614	0.000 195					
							FBgn02 65487	-1.73669	7.08E -09					
							FBgn02 65669	-1.38031	2.04E -05					

							FBgn02 65726	-0.79297	0.001 132					
							FBgn02 65991	-0.94258	7.83E -05					
							FBgn02 66084	-1.29213	2.03E -09					
							FBgn02 66129	-3.6414	4.36E -18					
							FBgn02 66347	1.751262	3.80E -17					
							FBgn02 66569	0.856612	3.78E -06					
							FBgn02 66666	0.977383	4.80E -20					
							FBgn02 66717	-0.59103	0.014 435					
							FBgn02 66756	-0.62169	0.002 482					
							FBgn02 66758	-1.03532	0.000 135					
							FBgn02 66768	0.713264	0.014 67					
							FBgn02 66801	-2.86785	8.65E -23					
							FBgn02 67001	-0.88042	0.002 753					
							FBgn02 67033	-0.59035	0.006 905					
							FBgn02 67348	-1.12561	4.96E -08					
							FBgn02 67506	-0.64271	0.015 23					
							FBgn02 67689	-9.23222	1.38E -12					

							FBgn02 67764	-4.08612	5.35E -11					
							FBgn02 67796	-2.2773	4.13E -12					
							FBgn02 67986	-1.56015	1.50E -05					
							FBgn02 83427	-0.95384	0.004 238					
							FBgn02 83451	-1.05065	0.005 54					
							FBgn02 83471	-0.9275	0.001 591					
							FBgn02 84221	-0.67484	0.000 145					
							FBgn02 84408	-1.69256	2.38E -05					
							FBgn02 85925	-0.70356	0.001 613					

Table A2.9 Log2 fold-change of transcript/piRNA abundance between *D. mel* rescue and *D. sim* rescue, for protein-coding genes whose expression levels are down-regulated by alleles from either *D. melanogaster* or *D. simulans*.

aub						
gene	Transcript abundance		Antisense piRNA abundance		Sense piRNA abundance	
	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj
FBgn0000044	-0.120034707	1	NA	NA	NA	NA
FBgn0000100	-0.186612927	1	NA	NA	-0.585796147	0.99963829
FBgn0000299	0.127125086	1	NA	NA	0.080130559	0.99963829
FBgn0000355	8.29E-03	1	NA	NA	-0.543001848	0.99963829
FBgn0000356	4.79E-03	1	NA	NA	NA	NA
FBgn0000357	0.138128117	1	NA	NA	-0.457458287	0.99963829
FBgn0000358	0.265160229	1	NA	NA	0.348770436	0.99963829
FBgn0000359	-0.360486835	1	NA	NA	NA	NA
FBgn0000360	-0.153581849	1	NA	NA	NA	NA
FBgn0002526	0.292490725	1	NA	NA	-0.356797557	0.99963829
FBgn0002590	-3.26E-02	1	NA	NA	-0.810301853	0.99963829
FBgn0002773	-0.38906112	1	NA	NA	NA	NA
FBgn0002868	-0.469174466	1	NA	NA	NA	NA
FBgn0003053	0.148996271	1	-0.351236513	0.998144804	-0.676538504	0.99963829
FBgn0003137	0.361794847	1	NA	NA	NA	NA
FBgn0003149	0.321524204	1	NA	NA	NA	NA
FBgn0003274	-0.276820452	1	NA	NA	-0.215739241	0.99963829
FBgn0003279	8.38E-02	1	NA	NA	-0.434398579	0.99963829
FBgn0003285	1.306363637	0.01281927	NA	NA	NA	NA
FBgn0003517	-0.103495798	1	NA	NA	0.463867141	0.99963829
FBgn0003979	0.111144178	1	NA	NA	0.109002464	0.99963829
FBgn0003980	0.114619853	1	NA	NA	-0.268364578	0.99963829
FBgn0003983	0.134321506	1	NA	NA	NA	NA
FBgn0003997	9.94E-02	1	NA	NA	-0.21034211	0.99963829

FBgn0004117	0.129695174	1	NA	NA	NA	NA
FBgn0004169	-3.54E-03	1	NA	NA	NA	NA
FBgn0004647	1.31E-02	1	NA	NA	-0.279108307	0.99963829
FBgn0004654	0.107409826	1	NA	NA	0.035311611	0.99963829
FBgn0004867	-0.108489425	1	NA	NA	-0.310526282	0.99963829
FBgn0005666	0.389992495	1	-0.501312868	0.998144804	-0.064829634	0.99963829
FBgn0010051	0.533724517	1	NA	NA	-0.849975205	0.99963829
FBgn0011828	0.175681379	1	NA	NA	NA	NA
FBgn0013275	-0.664619351	1	NA	NA	NA	NA
FBgn0013276	-0.68092084	1	NA	NA	NA	NA
FBgn0013277	-0.470323277	1	NA	NA	NA	NA
FBgn0013278	-0.492856687	1	NA	NA	NA	NA
FBgn0013279	-0.494170019	1	NA	NA	NA	NA
FBgn0013680	-8.77E-02	1	NA	NA	-0.108186057	0.99963829
FBgn0013681	-0.347527018	1	NA	NA	NA	NA
FBgn0013733	0.437883631	1	NA	NA	-1.418911696	0.99963829
FBgn0014076	-0.161838564	1	NA	NA	NA	NA
FBgn0014464	0.234764262	1	NA	NA	NA	NA
FBgn0015245	0.102909638	1	NA	NA	-0.496991287	0.99963829
FBgn0015288	-0.23323819	1	NA	NA	-0.422788185	0.99963829
FBgn0016075	6.59E-02	1	NA	NA	-0.104739567	0.99963829
FBgn0016123	0.360903317	1	NA	NA	NA	NA
FBgn0021906	6.15E-02	1	NA	NA	-0.440686573	0.99963829
FBgn0024183	-0.124799939	1	NA	NA	NA	NA
FBgn0025777	-0.143107572	1	NA	NA	-0.370444338	0.99963829
FBgn0026255	1.77E-02	1	NA	NA	-0.282583001	0.99963829
FBgn0026372	0.165742914	1	NA	NA	-0.175403315	0.99963829
FBgn0027341	-0.271777598	1	-0.098490681	0.998144804	0.052812621	0.99963829
FBgn0028369	0.85723946	1	-0.010966065	0.998144804	0.273888212	0.99963829

FBgn0028400	Inf	3.62E-11	NA	NA	NA	NA
FBgn0028490	7.08E-02	1	NA	NA	-0.533984495	0.99963829
FBgn0029840	0.332048539	1	NA	NA	NA	NA
FBgn0030040	-0.215792988	1	NA	NA	NA	NA
FBgn0030174	0.309656667	1	NA	NA	NA	NA
FBgn0030266	0.516476016	1	NA	NA	-0.508106547	0.99963829
FBgn0031913	-4.66E-03	1	NA	NA	-0.225986729	0.99963829
FBgn0032084	0.411963057	1	NA	NA	NA	NA
FBgn0032788	0.31697449	1	NA	NA	NA	NA
FBgn0032789	0.197917486	1	NA	NA	NA	NA
FBgn0033188	-0.113986352	1	NA	NA	0.899947999	0.99963829
FBgn0033926	2.30E-02	1	NA	NA	-1.761098333	0.99963829
FBgn0033927	-3.75E-02	1	NA	NA	NA	NA
FBgn0033958	-0.328176768	1	NA	NA	-0.656718222	0.99963829
FBgn0034479	1.728222402	1	NA	NA	NA	NA
FBgn0035422	-9.40E-02	1	NA	NA	-0.138798553	0.99963829
FBgn0035542	7.95E-04	1	NA	NA	NA	NA
FBgn0035880	-1.045269068	1	NA	NA	2.285095248	0.594145786
FBgn0036213	-0.255770267	1	NA	NA	-0.275909967	0.99963829
FBgn0036279	8.14E-02	1	NA	NA	-0.612437083	0.99963829
FBgn0036652	6.509582116	0.000443918	NA	NA	NA	NA
FBgn0036663	0.128695274	1	0.742628993	0.998144804	-0.471398273	0.99963829
FBgn0036734	0.212642903	1	NA	NA	-0.271585425	0.99963829
FBgn0037229	Inf	1	4.23034132	0.005936013	5.646493336	0.032541237
FBgn0037328	0.133540707	1	NA	NA	-0.275628725	0.99963829
FBgn0037351	0.260659297	1	NA	NA	-0.229955877	0.99963829
FBgn0037409	4.328135244	0.00222917	NA	NA	NA	NA
FBgn0037645	1.772616522	1	NA	NA	NA	NA
FBgn0038277	-8.95E-02	1	NA	NA	-0.040386569	0.99963829

FBgn0038290	0.349710779	1	NA	NA	NA	NA
FBgn0038881	0.10134626	1	NA	NA	-0.253193928	0.99963829
FBgn0039155	0.190788272	1	NA	NA	NA	NA
FBgn0039257	1.373938934	1	NA	NA	NA	NA
FBgn0039635	9.36E-02	1	NA	NA	0.486674943	0.99963829
FBgn0039713	7.95E-02	1	NA	NA	-0.483312861	0.99963829
FBgn0039776	0.107832385	1	NA	NA	0.393898569	0.99963829
FBgn0041180	0.124423259	1	NA	NA	NA	NA
FBgn0041252	0.119385627	1	NA	NA	NA	NA
FBgn0041709	-0.541299401	1	NA	NA	NA	NA
FBgn0050345	-5.86E-02	1	NA	NA	NA	NA
FBgn0051202	5.02E-02	1	NA	NA	NA	NA
FBgn0051354	-0.479582483	1	NA	NA	NA	NA
FBgn0051661	-0.104628612	1	NA	NA	NA	NA
FBgn0051926	-0.277391204	1	NA	NA	NA	NA
FBgn0051928	-0.13003241	1	NA	NA	NA	NA
FBgn0051988	-2.593705693	1	NA	NA	NA	NA
FBgn0052311	0.130891344	1	NA	NA	NA	NA
FBgn0052602	0.175764733	1	NA	NA	NA	NA
FBgn0053196	0.865725926	1	NA	NA	NA	NA
FBgn0053508	NA	1	NA	NA	NA	NA
FBgn0053531	1.313184903	1	-0.734117495	0.998144804	-0.436718228	0.99963829
FBgn0085362	-8.67E-02	1	NA	NA	NA	NA
FBgn0086265	-0.133435054	1	NA	NA	NA	NA
FBgn0086355	0.122621787	1	NA	NA	-0.246621716	0.99963829
FBgn0086408	-7.23E-02	1	NA	NA	NA	NA
FBgn0086708	2.265488161	0.000190732	NA	NA	NA	NA
FBgn0086906	0.72651608	1	NA	NA	0.037502891	0.99963829
FBgn0250907	0.440420091	1	-0.725549049	0.998144804	-0.527942083	0.99963829

FBgn0261258	-3.90E-02	1	NA	NA	-0.195933523	0.99963829
FBgn0261260	0.209176569	1	-0.061907031	0.998144804	-0.558847624	0.99963829
FBgn0261563	9.87E-02	1	-0.419003944	0.998144804	-0.930019158	0.99963829
FBgn0261617	0.466734962	1	NA	NA	-0.418044298	0.99963829
FBgn0261797	0.292750125	1	NA	NA	-0.249564428	0.99963829
FBgn0261836	0.657786833	0.49131821	-0.4248939	0.998144804	-0.715520977	0.99963829
FBgn0262109	0.291798643	1	NA	NA	-0.621732451	0.99963829
FBgn0262160	0.343095506	1	NA	NA	-0.406103288	0.99963829
FBgn0262608	-8.47E-02	1	NA	NA	NA	NA
FBgn0263219	0.432090308	1	NA	NA	0.23743242	0.99963829
FBgn0263705	0.33822749	1	NA	NA	-0.586383902	0.99963829
FBgn0264695	-2.06E-02	1	0.00752432	0.998144804	0.82832644	0.99963829
FBgn0264894	-0.240413427	1	NA	NA	NA	NA
FBgn0265045	0.44016573	1	NA	NA	NA	NA
FBgn0265991	8.22E-02	1	NA	NA	-0.088216665	0.99963829
FBgn0267001	0.327178175	1	NA	NA	-0.453763434	0.99963829
FBgn0267033	9.53E-02	1	-0.836707705	0.998144804	-0.439604944	0.99963829
FBgn0267336	0.23499855	1	NA	NA	-0.533948472	0.99963829
FBgn0283427	2.36E-02	1	NA	NA	-0.118117267	0.99963829
FBgn0284408	0.288958203	1	NA	NA	-0.325945612	0.99963829
FBgn0285955	0.370911613	1	NA	NA	-1.716455326	0.99963829

spnE

gene	Transcript abundance		Antisense piRNA abundance		Sense piRNA abundance	
	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj
FBgn0000003	0.581286238	0.03215389	NA	NA	NA	NA
FBgn0000083	0.130363982	0.172634607	NA	NA	-0.145794959	0.999426936
FBgn0000246	-0.43917778	0.066801207	NA	NA	0.947390195	0.26381259
FBgn0000274	-0.187942728	0.568546578	NA	NA	0.383027881	0.999426936

FBgn0000320	0.415873465	0.052145042	NA	NA	0.333017284	0.999426936
FBgn0000395	0.183860492	0.617939326	NA	NA	NA	NA
FBgn0000416	-0.30905836	0.050449284	NA	NA	0.275044903	0.999426936
FBgn0000427	-0.265385215	0.217028754	NA	NA	0.094678271	0.999426936
FBgn0000489	-0.308490747	0.147110061	NA	NA	NA	NA
FBgn0000490	-0.312553895	0.371990252	NA	NA	NA	NA
FBgn0000504	0.108609186	0.784924611	NA	NA	-0.047049678	0.999426936
FBgn0000567	-0.270459678	0.232306137	NA	NA	NA	NA
FBgn0000592	0.517815355	0.208172641	NA	NA	NA	NA
FBgn0000633	-0.074411515	0.914434183	NA	NA	0.021428641	0.999426936
FBgn0000635	-0.231050255	0.128141321	NA	NA	-0.001365467	0.999426936
FBgn0000636	-0.0164799	0.927633643	NA	NA	0.002060683	0.999426936
FBgn0000928	0.545586864	0.078255504	NA	NA	0.01923395	0.999426936
FBgn0001123	-0.238066549	0.266042929	NA	NA	NA	NA
FBgn0001145	0.027280727	0.938021066	NA	NA	NA	NA
FBgn0001168	-0.178875232	0.456513188	NA	NA	NA	NA
FBgn0001217	0.166759999	0.574093365	NA	NA	NA	NA
FBgn0001224	0.170413699	0.578415648	NA	NA	NA	NA
FBgn0001230	-0.037728748	0.927496869	NA	NA	NA	NA
FBgn0001257	-0.321661258	0.139691908	NA	NA	-0.446152051	0.999426936
FBgn0001296	0.055593625	0.744320535	NA	NA	0.350815069	0.999426936
FBgn0001297	-0.192053947	0.214246418	NA	NA	0.074626886	0.999426936
FBgn0001624	-0.221960454	0.128271967	NA	NA	-0.007195819	0.999426936
FBgn0001987	-0.128842049	0.370127479	NA	NA	NA	NA
FBgn0002609	0.225375169	0.431800054	NA	NA	NA	NA
FBgn0002716	-0.022331899	0.961278363	NA	NA	NA	NA
FBgn0002733	-0.039811915	0.925096869	NA	NA	NA	NA
FBgn0002772	-0.076068474	0.801609955	NA	NA	NA	NA
FBgn0002773	0.261321055	0.0861713	NA	NA	NA	NA

FBgn0002789	0.21088765	0.322872722	NA	NA	NA	NA
FBgn0002868	0.224675408	0.196882247	NA	NA	NA	NA
FBgn0003053	-0.036671385	0.840243614	NA	NA	NA	NA
FBgn0003089	-0.472305947	0.082648012	NA	NA	NA	NA
FBgn0003137	0.455458963	0.025772065	NA	NA	NA	NA
FBgn0003285	-0.09177516	0.549569374	NA	NA	NA	NA
FBgn0003301	0.287651802	0.168021962	NA	NA	NA	NA
FBgn0003308	0.333001658	0.173540225	0.301927881	0.834700374	0.000848777	0.999426936
FBgn0003328	-0.230362448	0.138773434	NA	NA	NA	NA
FBgn0003366	0.165260251	0.295534433	-0.018534836	0.975064512	0.002542417	0.999426936
FBgn0003388	0.265953343	0.591440295	NA	NA	NA	NA
FBgn0003486	-0.279887614	0.257668304	NA	NA	NA	NA
FBgn0003731	-0.146532332	0.481593911	NA	NA	0.304896218	0.999426936
FBgn0003867	-0.058916276	0.871418769	NA	NA	NA	NA
FBgn0003888	-0.263255947	0.102655199	NA	NA	NA	NA
FBgn0003916	0.658361185	0.022799162	NA	NA	NA	NA
FBgn0003996	0.320601912	0.504258331	NA	NA	NA	NA
FBgn0003997	-0.285944194	0.238580791	NA	NA	0.259794043	0.999426936
FBgn0004055	-0.264539521	0.099920536	NA	NA	NA	NA
FBgn0004117	0.020574701	0.929925804	NA	NA	NA	NA
FBgn0004133	0.241126029	0.096924022	NA	NA	NA	NA
FBgn0004169	0.125501263	0.553130512	NA	NA	NA	NA
FBgn0004183	0.677076943	0.019113662	NA	NA	NA	NA
FBgn0004185	0.653398417	0.079447178	NA	NA	NA	NA
FBgn0004186	0.67481633	0.067352001	NA	NA	NA	NA
FBgn0004191	1.331081722	8.25E-10	NA	NA	NA	NA
FBgn0004456	-0.111128577	0.531880357	NA	NA	0.235778779	0.999426936
FBgn0004512	-0.288557551	0.566046725	NA	NA	NA	NA
FBgn0004646	-0.225074991	0.223521069	NA	NA	0.052527922	0.999426936

FBgn0004666	-0.169044723	0.390000944	NA	NA	NA	NA
FBgn0004852	-0.16040032	0.629135097	NA	NA	NA	NA
FBgn0004858	-0.392972428	0.137693719	NA	NA	NA	NA
FBgn0004870	-0.368954584	0.230695323	NA	NA	NA	NA
FBgn0004885	-0.351150376	0.298883727	NA	NA	NA	NA
FBgn0004893	0.006225183	0.982141021	NA	NA	-0.666416671	0.999426936
FBgn0004919	-0.450968168	0.244151678	NA	NA	NA	NA
FBgn0005612	-0.347852649	0.067230898	NA	NA	NA	NA
FBgn0005631	-0.104566741	0.768120123	NA	NA	NA	NA
FBgn0005666	-0.283236173	0.111531119	0.531926403	0.121942524	0.189013085	0.999426936
FBgn0005771	-0.069645749	0.774737644	NA	NA	NA	NA
FBgn0010038	-0.53010577	0.283514454	NA	NA	NA	NA
FBgn0010039	0.208119327	0.26859909	NA	NA	-0.195742015	0.999426936
FBgn0010052	-1.060834715	0.015153664	NA	NA	NA	NA
FBgn0010225	0.139769203	0.529424623	NA	NA	-0.433166525	0.999426936
FBgn0010228	0.241434756	0.067352001	NA	NA	NA	NA
FBgn0010241	2.939678435	0.276915741	NA	NA	-2.697924785	0.10566477
FBgn0010246	0.046375282	0.71835511	NA	NA	NA	NA
FBgn0010263	-0.063514774	0.796196955	NA	NA	NA	NA
FBgn0010383	-0.094309274	0.588386852	NA	NA	NA	NA
FBgn0010388	-2.118736805	0.002094185	NA	NA	NA	NA
FBgn0010389	0.135795765	0.653119851	NA	NA	NA	NA
FBgn0010395	-0.126815081	0.612750457	NA	NA	NA	NA
FBgn0010424	0.1581521	0.690737412	NA	NA	NA	NA
FBgn0010434	-0.166424756	0.081349189	NA	NA	-0.527112143	0.999426936
FBgn0010435	-0.260267259	0.235193833	NA	NA	NA	NA
FBgn0010482	-0.141264806	0.682547491	NA	NA	NA	NA
FBgn0011206	-0.121283084	0.704787536	NA	NA	NA	NA
FBgn0011274	-0.145775818	0.617939326	NA	NA	NA	NA

FBgn0011591	-0.313991248	0.106966966	NA	NA	0.03045936	0.999426936
FBgn0011676	-0.035530511	0.954139229	NA	NA	NA	NA
FBgn0011695	-0.047061002	0.873807702	NA	NA	NA	NA
FBgn0011706	-0.142217293	0.849344911	NA	NA	NA	NA
FBgn0011828	0.940442839	0.02669338	NA	NA	NA	NA
FBgn0012037	-0.012453706	0.965296963	NA	NA	NA	NA
FBgn0013272	-0.295067892	0.090290911	NA	NA	0.089469857	0.999426936
FBgn0013275	0.38049744	0.086582197	NA	NA	NA	NA
FBgn0013276	0.30493985	0.271317531	NA	NA	NA	NA
FBgn0013277	0.404729164	0.225571082	NA	NA	NA	NA
FBgn0013278	0.415941564	0.190645189	NA	NA	NA	NA
FBgn0013279	0.318621201	0.397055869	NA	NA	NA	NA
FBgn0013469	-0.321955568	0.469448606	NA	NA	NA	NA
FBgn0013680	0.688778525	0.329714808	0.632935427	0.834700374	0.147459485	0.999426936
FBgn0013771	-1.537690376	7.26E-22	NA	NA	NA	NA
FBgn0013813	-0.88892067	0.000115913	NA	NA	0.109319705	0.999426936
FBgn0013953	-0.047005654	0.742083152	NA	NA	NA	NA
FBgn0013954	1.096776148	4.94E-19	NA	NA	0.249967307	0.999426936
FBgn0014073	-0.492366517	0.025772065	NA	NA	NA	NA
FBgn0014076	-0.215535675	0.227312216	NA	NA	NA	NA
FBgn0014380	0.212782029	0.377847267	NA	NA	NA	NA
FBgn0014469	-0.352461718	0.022863963	NA	NA	0.35393362	0.999426936
FBgn0014863	0.60929581	0.03215389	NA	NA	NA	NA
FBgn0015033	0.093960678	0.788937042	NA	NA	NA	NA
FBgn0015037	-0.207037077	0.588058526	NA	NA	NA	NA
FBgn0015039	0.11544236	0.573306778	NA	NA	NA	NA
FBgn0015221	-0.281838319	0.031546271	NA	NA	0.149847936	0.999426936
FBgn0015399	0.002762285	0.99025207	NA	NA	-0.609452729	0.999426936
FBgn0015569	0.064858957	0.734319037	NA	NA	NA	NA

FBgn0015575	0.111960118	0.734319037	NA	NA	NA	NA
FBgn0015576	-0.267886309	0.466267948	NA	NA	NA	NA
FBgn0015766	-0.172704157	0.421135031	NA	NA	NA	NA
FBgn0015773	0.169942235	0.651758868	NA	NA	NA	NA
FBgn0015774	0.097044091	0.816313415	NA	NA	NA	NA
FBgn0015777	0.09038007	0.688032696	NA	NA	NA	NA
FBgn0015872	0.149554774	0.595554703	NA	NA	NA	NA
FBgn0016053	0.139796192	0.374334971	NA	NA	-0.017216212	0.999426936
FBgn0016075	0.178401288	0.430995413	NA	NA	NA	NA
FBgn0016080	0.02594283	0.946166098	NA	NA	0.352376518	0.999426936
FBgn0016684	0.178358939	0.758224594	NA	NA	NA	NA
FBgn0017482	0.151206818	0.590437514	NA	NA	NA	NA
FBgn0020255	-0.140716035	0.167422634	NA	NA	-0.097162424	0.999426936
FBgn0020257	0.143421753	0.742360667	NA	NA	NA	NA
FBgn0020294	-0.196182465	0.38131368	NA	NA	0.118330512	0.999426936
FBgn0020299	-0.096831971	0.768800794	NA	NA	NA	NA
FBgn0020414	-0.086320111	0.721016247	NA	NA	NA	NA
FBgn0020415	-0.149572337	0.313014975	NA	NA	NA	NA
FBgn0020521	0.226316066	0.581696179	NA	NA	NA	NA
FBgn0020762	-0.286224697	0.144591678	NA	NA	NA	NA
FBgn0022160	0.6178686	0.018457281	NA	NA	NA	NA
FBgn0022774	0.262937588	0.082613983	NA	NA	NA	NA
FBgn0022984	-0.19378836	0.114142759	NA	NA	NA	NA
FBgn0022986	-0.278750188	0.05075566	NA	NA	NA	NA
FBgn0023023	0.494386813	0.090174402	NA	NA	0.161335922	0.999426936
FBgn0023076	-0.320896034	0.374067548	NA	NA	NA	NA
FBgn0023095	-0.004232901	0.980169223	NA	NA	-0.260184003	0.999426936
FBgn0023214	-0.296052047	0.343194839	NA	NA	NA	NA
FBgn0023479	-0.139586185	0.777877034	NA	NA	NA	NA

FBgn0023520	0.543106212	0.002571651	NA	NA	NA	NA
FBgn0023549	-0.042100817	0.843018745	NA	NA	NA	NA
FBgn0024189	0	1	NA	NA	-1.235348147	0.999426936
FBgn0024234	0.389774365	0.066026066	NA	NA	NA	NA
FBgn0024321	-0.093462671	0.755195946	NA	NA	0.050224004	0.999426936
FBgn0024989	0.027651263	0.95308517	NA	NA	NA	NA
FBgn0025111	0.422774902	0.24228536	NA	NA	0.361296687	0.999426936
FBgn0025391	-0.409735241	0.270774578	NA	NA	NA	NA
FBgn0025631	-0.290753791	0.152639789	NA	NA	NA	NA
FBgn0025680	0.61924344	0.003394149	NA	NA	NA	NA
FBgn0026061	0.17582415	0.238753856	NA	NA	NA	NA
FBgn0026079	0.202621188	0.07260093	NA	NA	-0.108813954	0.999426936
FBgn0026160	-0.0105577	0.979635986	NA	NA	NA	NA
FBgn0026319	-0.242633386	0.348303989	NA	NA	NA	NA
FBgn0026562	0.342892297	0.125225976	NA	NA	NA	NA
FBgn0027106	0.257823616	0.218063446	NA	NA	NA	NA
FBgn0027339	-0.381270133	0.088802935	NA	NA	0.175361993	0.999426936
FBgn0027341	-0.15693071	0.662224166	0.156085501	0.940560234	0.358970793	0.999426936
FBgn0027364	0.354510904	0.064891042	NA	NA	NA	NA
FBgn0027556	0.264170557	0.700963404	NA	NA	NA	NA
FBgn0027560	0.491907042	0.164566048	NA	NA	NA	NA
FBgn0027585	-0.075088073	0.781809016	NA	NA	NA	NA
FBgn0027586	0.252649286	0.41910682	NA	NA	NA	NA
FBgn0027596	0.141869188	0.39646959	NA	NA	0.287637084	0.999426936
FBgn0027601	0.13335465	0.365930369	0.071302553	0.949085382	NA	NA
FBgn0027611	-0.503731912	0.001627178	NA	NA	NA	NA
FBgn0027843	0.299192338	0.133161576	NA	NA	0.268600232	0.999426936
FBgn0028341	0.607067165	0.008622493	-0.883564512	0.747464626	0.062321165	0.999426936
FBgn0028369	0.135673616	0.642513776	-0.053365337	0.949085382	0.299023115	0.999426936

FBgn0028394	0.400740798	0.004845319	NA	NA	NA	NA
FBgn0028527	0.093282442	0.653534577	NA	NA	NA	NA
FBgn0028550	-0.310253309	0.198525302	NA	NA	0.13880402	0.999426936
FBgn0028572	0.231368444	0.183612004	NA	NA	NA	NA
FBgn0028622	0.389957476	0.060161295	NA	NA	NA	NA
FBgn0028886	-0.490916264	0.031546271	NA	NA	2.165406203	0.999426936
FBgn0028956	-0.234909137	0.220262223	NA	NA	NA	NA
FBgn0028988	-0.131342642	0.767948085	NA	NA	NA	NA
FBgn0029002	-0.166404603	0.28495984	NA	NA	NA	NA
FBgn0029082	1.635130368	0.041791302	NA	NA	1.230754534	0.999426936
FBgn0029148	-0.000248514	0.999470726	NA	NA	-0.019393433	0.999426936
FBgn0029167	0.197265355	0.615601107	NA	NA	NA	NA
FBgn0029506	-0.11908781	0.371164948	NA	NA	-0.032149083	0.999426936
FBgn0029507	-0.286268208	0.460872555	NA	NA	NA	NA
FBgn0029608	0.234811119	0.594998378	NA	NA	NA	NA
FBgn0029723	0.075534854	0.787474353	NA	NA	NA	NA
FBgn0029766	-0.373249872	0.085947807	NA	NA	0.031954731	0.999426936
FBgn0029771	0.055951977	0.88386535	NA	NA	NA	NA
FBgn0029838	-0.125456187	0.542837182	NA	NA	NA	NA
FBgn0029843	-8.47E-05	0.999917253	NA	NA	NA	NA
FBgn0029878	-0.037012985	0.772065933	NA	NA	-0.033218898	0.999426936
FBgn0029932	0.095925792	0.861165367	NA	NA	NA	NA
FBgn0029939	0.264186023	0.211781124	NA	NA	NA	NA
FBgn0029966	-0.209740484	0.33984466	NA	NA	NA	NA
FBgn0030017	-0.505343046	0.243732774	NA	NA	0.180249692	0.999426936
FBgn0030040	0.09219561	0.542999751	-1.384068704	0.119205215	NA	NA
FBgn0030041	-0.399390003	0.196021923	NA	NA	NA	NA
FBgn0030091	0.148130994	0.131892446	NA	NA	-0.012652972	0.999426936
FBgn0030174	-0.226379788	0.073984413	NA	NA	0.280859658	0.999426936

FBgn0030218	0.380778585	0.083374521	NA	NA	NA	NA
FBgn0030234	0.304874158	0.541242816	NA	NA	NA	NA
FBgn0030237	-0.072302743	0.898124099	NA	NA	NA	NA
FBgn0030266	0.326397425	0.181204141	NA	NA	0.217444211	0.999426936
FBgn0030300	0.232186561	0.490987976	NA	NA	NA	NA
FBgn0030309	-0.165677188	0.480615313	NA	NA	NA	NA
FBgn0030331	0.193281142	0.441790841	NA	NA	NA	NA
FBgn0030349	-0.250921727	0.043774849	-0.496835632	0.834700374	0.070185928	0.999426936
FBgn0030360	0.318822097	0.460607187	NA	NA	NA	NA
FBgn0030438	-0.475209174	0.047772271	NA	NA	NA	NA
FBgn0030479	0.187365345	0.244621103	NA	NA	NA	NA
FBgn0030485	-0.277257722	0.379786616	NA	NA	NA	NA
FBgn0030594	0.79846754	0.153746411	NA	NA	NA	NA
FBgn0030596	0.173105391	0.25574639	NA	NA	NA	NA
FBgn0030600	0.676139428	0.047474683	-0.051900937	0.949085382	-0.518080047	0.999426936
FBgn0030662	0.142228612	0.545908799	NA	NA	NA	NA
FBgn0030796	-0.227825892	0.477404782	0.367820077	0.834700374	NA	NA
FBgn0030816	-0.106413123	0.445429792	NA	NA	NA	NA
FBgn0030839	0.297584508	0.088819406	NA	NA	NA	NA
FBgn0030847	-0.13991875	0.527370415	NA	NA	NA	NA
FBgn0030884	0.108632712	0.6114816	NA	NA	NA	NA
FBgn0030899	-0.285991832	0.682781847	NA	NA	NA	NA
FBgn0030955	0.278133889	0.066226493	NA	NA	NA	NA
FBgn0030976	-0.060512864	0.867708777	NA	NA	NA	NA
FBgn0030999	0.607022858	0.537550136	NA	NA	-1.847187923	0.999426936
FBgn0031220	-0.13613938	0.681900897	NA	NA	NA	NA
FBgn0031275	-0.444435539	0.386389936	NA	NA	0.745082457	0.999426936
FBgn0031305	-0.043902164	0.817057162	NA	NA	NA	NA
FBgn0031327	0.384402527	0.340600071	NA	NA	NA	NA

FBgn0031343	0.087183822	0.870987403	NA	NA	NA	NA
FBgn0031414	0.319038352	0.526729348	NA	NA	NA	NA
FBgn0031461	-1.097284915	0.022583123	NA	NA	NA	NA
FBgn0031571	-0.27939649	0.159687915	NA	NA	NA	NA
FBgn0031628	-0.22478591	0.394205639	NA	NA	NA	NA
FBgn0031717	0.1063651	0.645029804	NA	NA	NA	NA
FBgn0031756	0.09431536	0.650522657	NA	NA	NA	NA
FBgn0031777	0.60132454	0.014063803	NA	NA	NA	NA
FBgn0031816	0.224678697	0.3480223	NA	NA	NA	NA
FBgn0031888	0.356884116	0.61245308	NA	NA	NA	NA
FBgn0031894	-0.077517405	0.612583247	NA	NA	NA	NA
FBgn0031907	0.586886778	0.201032006	NA	NA	NA	NA
FBgn0031908	0.078669535	0.847699489	NA	NA	NA	NA
FBgn0031913	0.009827708	0.961745425	NA	NA	NA	NA
FBgn0031914	-0.397435911	0.120463409	NA	NA	NA	NA
FBgn0031948	-0.457972968	0.022799162	NA	NA	NA	NA
FBgn0031961	0.30289509	0.267088364	NA	NA	-0.133197157	0.999426936
FBgn0031974	0.856724608	3.54E-11	NA	NA	-6.075048428	3.20E-25
FBgn0031975	0.465361745	0.003200814	NA	NA	NA	NA
FBgn0032006	-0.191230227	0.167973024	NA	NA	NA	NA
FBgn0032021	-0.284605425	0.519347144	NA	NA	NA	NA
FBgn0032022	0.344342112	0.307366511	NA	NA	NA	NA
FBgn0032025	0.176454711	0.654301714	NA	NA	NA	NA
FBgn0032075	0.013124288	0.979700192	NA	NA	NA	NA
FBgn0032126	0.266756551	0.088167842	NA	NA	NA	NA
FBgn0032129	-0.040734055	0.929624765	NA	NA	NA	NA
FBgn0032140	0.236866404	0.327595793	NA	NA	NA	NA
FBgn0032149	0.35345137	0.07767062	NA	NA	NA	NA
FBgn0032156	-0.296151453	0.160003267	NA	NA	NA	NA

FBgn0032167	-0.150976371	0.53330243	NA	NA	NA	NA
FBgn0032187	0.589978065	0.078240193	NA	NA	NA	NA
FBgn0032211	0.646017617	0.190047598	NA	NA	NA	NA
FBgn0032218	-0.347536034	0.098064043	NA	NA	NA	NA
FBgn0032235	-0.240221547	0.472125089	NA	NA	-1.61105921	0.016425781
FBgn0032253	0.471681467	0.232315864	NA	NA	2.442069495	0.002999089
FBgn0032264	-0.177274514	0.336029058	NA	NA	NA	NA
FBgn0032297	-0.018514827	0.95485081	NA	NA	-0.112375388	0.999426936
FBgn0032311	0.594362998	0.026510134	NA	NA	NA	NA
FBgn0032405	-0.066730508	0.90757016	NA	NA	NA	NA
FBgn0032422	0.093636129	0.596106928	NA	NA	NA	NA
FBgn0032470	1.146425081	0.292498337	NA	NA	NA	NA
FBgn0032524	0.401159402	0.04335272	NA	NA	NA	NA
FBgn0032666	-0.380599145	0.130996454	NA	NA	NA	NA
FBgn0032669	1.349121582	0.056004757	NA	NA	NA	NA
FBgn0032670	-0.4905136	0.333256722	NA	NA	NA	NA
FBgn0032671	-0.161562363	0.223254234	NA	NA	NA	NA
FBgn0032683	-0.435076388	0.081943544	NA	NA	NA	NA
FBgn0032684	-0.312579983	0.098518862	NA	NA	NA	NA
FBgn0032694	0.248791168	0.064080527	NA	NA	-0.22609426	0.999426936
FBgn0032713	0.031464233	0.898769707	NA	NA	NA	NA
FBgn0032731	-0.240586765	0.036902692	NA	NA	NA	NA
FBgn0032787	0.899412821	3.58E-08	NA	NA	NA	NA
FBgn0032891	4.07474502	8.72E-20	NA	NA	NA	NA
FBgn0032897	0.11713353	0.296464749	NA	NA	NA	NA
FBgn0032899	-0.223617059	0.450635246	NA	NA	NA	NA
FBgn0032946	-0.471158142	0.119485243	NA	NA	NA	NA
FBgn0033093	0.19077195	0.665167175	NA	NA	NA	NA
FBgn0033108	1.490905983	0.463587105	NA	NA	NA	NA

FBgn0033128	0.096123062	0.796196955	NA	NA	NA	NA
FBgn0033132	0.751977572	0.042157632	NA	NA	NA	NA
FBgn0033134	0.775401943	0.036234343	NA	NA	NA	NA
FBgn0033153	0.019592738	0.931024791	-0.156581248	0.949085382	NA	NA
FBgn0033159	-0.218433593	0.642771328	NA	NA	NA	NA
FBgn0033188	-0.169686776	0.435483014	NA	NA	NA	NA
FBgn0033214	0.154628903	0.583993851	NA	NA	NA	NA
FBgn0033274	0.401038566	0.257953421	NA	NA	NA	NA
FBgn0033302	-0.253401987	0.577996982	NA	NA	NA	NA
FBgn0033369	0.430618143	0.81158112	NA	NA	0.033726109	0.999426936
FBgn0033387	0.509880785	0.150377537	0.798576468	0.747464626	0.857538443	0.999426936
FBgn0033388	0.531444468	0.166057073	-1.122541726	0.439073913	-0.393045969	0.999426936
FBgn0033395	0.044806441	0.679852834	NA	NA	NA	NA
FBgn0033438	-0.155796647	0.409684997	NA	NA	NA	NA
FBgn0033446	0.413969633	0.131892446	NA	NA	NA	NA
FBgn0033483	-0.186957845	0.588157745	NA	NA	NA	NA
FBgn0033494	-0.242369222	0.368171399	NA	NA	-1.071478233	0.734918195
FBgn0033519	-0.810421785	0.006561217	NA	NA	NA	NA
FBgn0033520	-0.604422637	0.047479887	NA	NA	NA	NA
FBgn0033521	-0.681641001	0.006561237	NA	NA	NA	NA
FBgn0033540	0.140721408	0.270774578	NA	NA	NA	NA
FBgn0033584	-0.767086939	1.05E-14	NA	NA	2.719040289	6.02E-06
FBgn0033652	-0.540302936	0.097886844	NA	NA	NA	NA
FBgn0033654	0.018505488	0.957197253	NA	NA	NA	NA
FBgn0033782	-0.349740651	0.476611557	NA	NA	NA	NA
FBgn0033787	-0.562342414	0.031441586	NA	NA	NA	NA
FBgn0033810	1.182670164	5.61E-11	NA	NA	NA	NA
FBgn0033817	0.501274986	0.180589809	NA	NA	NA	NA
FBgn0033855	0.171158963	0.88848899	NA	NA	NA	NA

FBgn0033875	-0.157882389	0.304454441	NA	NA	NA	NA
FBgn0033887	-0.506132822	0.004151813	NA	NA	NA	NA
FBgn0033919	-0.146858933	0.6174187	NA	NA	0.284000379	0.999426936
FBgn0033926	-0.802105747	2.84E-25	NA	NA	-1.300661324	0.208020554
FBgn0033927	-0.654347038	1.11E-07	NA	NA	NA	NA
FBgn0033958	-3.46886348	2.77E-11	NA	NA	NA	NA
FBgn0033978	-1.282647755	1.02E-06	NA	NA	1.604178649	1.95E-05
FBgn0033980	-1.437795495	0.000757961	NA	NA	NA	NA
FBgn0033982	-0.22906563	0.435764595	NA	NA	NA	NA
FBgn0034005	-0.396297878	0.418405872	NA	NA	NA	NA
FBgn0034075	-0.112455223	0.652409858	NA	NA	NA	NA
FBgn0034085	-1.102844061	0.014250818	NA	NA	NA	NA
FBgn0034142	-0.233749916	0.262780144	NA	NA	NA	NA
FBgn0034143	0.111179731	0.468756287	NA	NA	NA	NA
FBgn0034145	-0.257922156	0.33984466	NA	NA	NA	NA
FBgn0034194	0.191002857	0.271506902	NA	NA	NA	NA
FBgn0034219	-0.26839348	0.500209662	NA	NA	NA	NA
FBgn0034253	-0.302802562	0.201072287	NA	NA	-0.044614841	0.999426936
FBgn0034264	0.714018233	0.245166755	NA	NA	NA	NA
FBgn0034275	0.451534877	0.188325297	NA	NA	NA	NA
FBgn0034312	0.162638854	0.491618528	NA	NA	NA	NA
FBgn0034406	0.558855835	3.89E-05	0.249581047	0.947321862	NA	NA
FBgn0034436	-0.178678791	0.25906139	NA	NA	-0.195236513	0.999426936
FBgn0034438	0.475078548	0.066603937	NA	NA	0.62007292	0.999426936
FBgn0034439	1.907408443	1.57E-08	NA	NA	NA	NA
FBgn0034443	0.050609796	0.78081938	NA	NA	NA	NA
FBgn0034493	0.053516937	0.867312325	NA	NA	0.897550338	0.999426936
FBgn0034500	0.152261201	0.281274632	NA	NA	NA	NA
FBgn0034501	-0.093590369	0.477348373	NA	NA	NA	NA

FBgn0034512	0.009227936	0.986202198	NA	NA	NA	NA
FBgn0034602	-0.45818639	0.057731001	NA	NA	NA	NA
FBgn0034638	-0.055113743	0.848274947	NA	NA	NA	NA
FBgn0034639	-0.205343733	0.662405095	NA	NA	NA	NA
FBgn0034659	1.98674879	0.102971311	NA	NA	1.768351536	0.84128059
FBgn0034709	-0.069594326	0.683321474	NA	NA	0.078868724	0.999426936
FBgn0034718	-0.229527136	0.334408057	NA	NA	NA	NA
FBgn0034761	0.425591483	0.064985035	NA	NA	NA	NA
FBgn0034861	0.414010768	0.278655672	NA	NA	NA	NA
FBgn0034903	-0.34977361	0.203705727	NA	NA	NA	NA
FBgn0035023	-0.164311974	0.677279754	NA	NA	NA	NA
FBgn0035049	-0.329615582	0.467179743	NA	NA	NA	NA
FBgn0035099	-0.210284857	0.502197775	NA	NA	0.17256667	0.999426936
FBgn0035131	-0.348629707	0.443642799	NA	NA	NA	NA
FBgn0035132	-0.308224233	0.098518862	NA	NA	NA	NA
FBgn0035160	0.08994925	0.615679641	NA	NA	NA	NA
FBgn0035262	-0.027220509	0.946786886	NA	NA	NA	NA
FBgn0035290	-0.214128444	0.46768579	NA	NA	NA	NA
FBgn0035308	-0.052307692	0.818837906	NA	NA	0.006738131	0.999426936
FBgn0035490	-0.485283628	0.195868639	NA	NA	NA	NA
FBgn0035497	-0.332563208	0.095218571	NA	NA	NA	NA
FBgn0035542	-0.081183623	0.613283386	NA	NA	NA	NA
FBgn0035574	-0.09784028	0.691336566	NA	NA	NA	NA
FBgn0035656	0.096080112	0.854725633	NA	NA	NA	NA
FBgn0035695	-0.089368876	0.785559788	NA	NA	NA	NA
FBgn0035710	0.065293318	0.661271357	NA	NA	NA	NA
FBgn0035763	-0.130413596	0.218466803	NA	NA	0.177686386	0.999426936
FBgn0035767	-0.012742838	0.964795146	NA	NA	NA	NA
FBgn0035770	0.240979171	0.103537525	NA	NA	NA	NA

FBgn0035791	-0.275183907	0.28282709	NA	NA	NA	NA
FBgn0035844	-0.130699908	0.748379924	0.199813925	0.947321862	NA	NA
FBgn0035868	-0.395531029	0.097209873	NA	NA	NA	NA
FBgn0035917	0.241206632	0.367780994	NA	NA	NA	NA
FBgn0035975	-0.551966786	0.140241366	NA	NA	NA	NA
FBgn0035976	-0.017120602	0.972920708	NA	NA	NA	NA
FBgn0036091	0.564472141	0.116596023	NA	NA	NA	NA
FBgn0036101	-0.474720739	0.236236005	NA	NA	NA	NA
FBgn0036155	0.156982942	0.377603178	NA	NA	NA	NA
FBgn0036205	-0.098331811	0.682547491	NA	NA	NA	NA
FBgn0036288	0.493579168	0.2089952	NA	NA	NA	NA
FBgn0036381	-0.039695905	0.912275296	NA	NA	NA	NA
FBgn0036382	0.508706628	0.111531119	NA	NA	NA	NA
FBgn0036433	-0.126779153	0.515922409	NA	NA	NA	NA
FBgn0036454	-0.207703498	0.491606254	NA	NA	NA	NA
FBgn0036640	-0.122467946	0.346622099	NA	NA	0.642079565	0.33728489
FBgn0036714	-0.515784692	0.000176097	NA	NA	-0.493747253	0.84128059
FBgn0036732	-0.108375558	0.57199688	NA	NA	NA	NA
FBgn0036734	-0.01501568	0.911191741	NA	NA	NA	NA
FBgn0036752	-0.14058236	0.367780994	NA	NA	NA	NA
FBgn0036756	0.035846847	0.907940469	NA	NA	NA	NA
FBgn0036834	-0.1705311	0.649242345	NA	NA	NA	NA
FBgn0036882	-0.194373276	0.61124375	NA	NA	0.313249618	0.999426936
FBgn0036926	0.054007247	0.891559454	NA	NA	NA	NA
FBgn0036945	0.729448192	0.17969097	NA	NA	NA	NA
FBgn0037007	-0.227917333	0.126335123	NA	NA	NA	NA
FBgn0037012	-0.216836158	0.342920939	NA	NA	-0.152214212	0.999426936
FBgn0037166	0.019011985	0.972442855	NA	NA	NA	NA
FBgn0037186	0.202730738	0.693054767	NA	NA	NA	NA

FBgn0037290	0.187810843	0.682547491	NA	NA	NA	NA
FBgn0037409	-0.867724143	0.026450187	NA	NA	NA	NA
FBgn0037447	0.130716925	0.724605166	NA	NA	NA	NA
FBgn0037519	0.045244163	0.924365051	NA	NA	NA	NA
FBgn0037520	-0.146736435	0.725172993	NA	NA	NA	NA
FBgn0037521	0.206852628	0.611795227	NA	NA	NA	NA
FBgn0037525	-0.045985761	0.794680626	NA	NA	0.214195926	0.999426936
FBgn0037548	0.266701853	0.19483837	NA	NA	0.328092812	0.999426936
FBgn0037552	-0.218569778	0.191038513	NA	NA	-0.243667448	0.999426936
FBgn0037577	0.780455839	0.032482415	NA	NA	NA	NA
FBgn0037730	-0.73893736	0.374740334	NA	NA	-1.369980505	0.999426936
FBgn0037796	-0.3414268	0.328221308	NA	NA	NA	NA
FBgn0037836	-0.002604029	0.996474358	NA	NA	NA	NA
FBgn0037898	0.333869967	0.225540162	NA	NA	NA	NA
FBgn0037934	-0.200691675	0.368171399	NA	NA	NA	NA
FBgn0037936	-0.259165497	0.325768989	NA	NA	NA	NA
FBgn0037956	0.070667724	0.764591294	NA	NA	NA	NA
FBgn0037989	-0.169940937	0.507067174	NA	NA	NA	NA
FBgn0038088	-0.407296949	0.15022867	NA	NA	NA	NA
FBgn0038207	-0.283114787	0.496508171	NA	NA	NA	NA
FBgn0038243	0.10205368	0.496119195	NA	NA	NA	NA
FBgn0038260	0.231973245	0.31627828	NA	NA	NA	NA
FBgn0038294	0.188408353	0.327595793	NA	NA	NA	NA
FBgn0038321	0.080574192	0.71100136	NA	NA	NA	NA
FBgn0038460	-0.051874955	0.83661631	NA	NA	NA	NA
FBgn0038465	0.062615708	0.564182327	NA	NA	NA	NA
FBgn0038610	0.241580943	0.206883834	NA	NA	NA	NA
FBgn0038638	-0.066923361	0.811777926	NA	NA	0.309622277	0.999426936
FBgn0038681	-0.307155949	0.322536748	NA	NA	NA	NA

FBgn0038682	-0.032860865	0.930352401	NA	NA	NA	NA
FBgn0038720	-0.012740161	0.965296963	NA	NA	NA	NA
FBgn0038774	0.56833894	0.136604688	NA	NA	NA	NA
FBgn0038799	3.672727997	0.047856689	NA	NA	2.493678377	0.999426936
FBgn0038826	-0.277660286	0.319677454	NA	NA	0.321569048	0.999426936
FBgn0038842	0.17935455	0.292109285	NA	NA	NA	NA
FBgn0038881	-0.099988475	0.637029625	NA	NA	0.305353354	0.999426936
FBgn0038938	1.059323388	0.085431861	NA	NA	NA	NA
FBgn0038981	0.147340151	0.488758907	NA	NA	NA	NA
FBgn0038986	0.006521152	0.990457842	NA	NA	0.938979633	0.999426936
FBgn0039039	1.907075926	0.317771207	NA	NA	3.300994483	0.999426936
FBgn0039075	-0.228752557	0.504821752	NA	NA	NA	NA
FBgn0039084	-0.175445877	0.678057788	NA	NA	NA	NA
FBgn0039114	-0.117103458	0.609021003	NA	NA	NA	NA
FBgn0039155	0.075764966	0.704593665	NA	NA	NA	NA
FBgn0039266	-0.359229606	0.046332361	NA	NA	NA	NA
FBgn0039312	0.916230082	0.099058867	NA	NA	NA	NA
FBgn0039313	0.826659059	0.03215389	NA	NA	NA	NA
FBgn0039328	0.026553753	0.959928709	NA	NA	NA	NA
FBgn0039419	-0.301686081	0.173540225	NA	NA	NA	NA
FBgn0039431	-0.263305361	0.084599631	NA	NA	0.145858483	0.999426936
FBgn0039486	0.537994823	0.12457883	NA	NA	NA	NA
FBgn0039529	0.508250182	0.043872829	NA	NA	NA	NA
FBgn0039620	0.077444649	0.862986905	NA	NA	NA	NA
FBgn0039633	-0.190004282	0.221583841	NA	NA	0.125814328	0.999426936
FBgn0039678	0.149132157	0.668956109	NA	NA	NA	NA
FBgn0039738	0.184506544	0.344777881	NA	NA	NA	NA
FBgn0039748	0.38365813	0.222186938	NA	NA	NA	NA
FBgn0039756	-0.238865977	0.494747512	NA	NA	NA	NA

FBgn0039776	0.401770601	0.026510134	NA	NA	NA	NA
FBgn0039809	-0.168334888	0.625077719	NA	NA	0.221286332	0.999426936
FBgn0039827	0.088695791	0.811777926	NA	NA	NA	NA
FBgn0039836	-0.000557481	0.999491377	NA	NA	NA	NA
FBgn0039862	-0.330651283	0.201400625	NA	NA	0.268813732	0.999426936
FBgn0039872	0.256619804	0.726885468	NA	NA	NA	NA
FBgn0039883	-0.074381467	0.898588338	0.185406791	0.915266824	NA	NA
FBgn0039925	-0.20634646	0.642461426	NA	NA	NA	NA
FBgn0040038	0.594491621	0.453437235	0.220299641	0.834700374	0.102346633	0.999426936
FBgn0040089	-0.110740465	0.683872337	NA	NA	NA	NA
FBgn0040299	-0.194692634	0.837217739	NA	NA	NA	NA
FBgn0040351	0.140485238	0.845844547	NA	NA	NA	NA
FBgn0040364	0.039636048	0.881894134	NA	NA	NA	NA
FBgn0040370	0.145360987	0.652409858	NA	NA	NA	NA
FBgn0040398	-0.01369991	0.972920708	NA	NA	NA	NA
FBgn0040491	0.439587285	0.089652318	NA	NA	NA	NA
FBgn0040514	-0.187492867	0.651755305	NA	NA	NA	NA
FBgn0040551	0.617993066	0.084676627	NA	NA	NA	NA
FBgn0040609	0.0211029	0.963219271	NA	NA	NA	NA
FBgn0040765	0.018592522	0.952628021	NA	NA	NA	NA
FBgn0040823	-0.401562015	0.04511587	NA	NA	0.5373791	0.999426936
FBgn0040827	-0.312598626	0.617939326	NA	NA	NA	NA
FBgn0040832	0.108117135	0.792340345	NA	NA	NA	NA
FBgn0040850	0.352729116	0.160245029	NA	NA	NA	NA
FBgn0041180	-0.045959139	0.782557589	NA	NA	NA	NA
FBgn0041182	1.595198336	0.000458984	NA	NA	NA	NA
FBgn0041184	0.102343737	0.653117046	NA	NA	0.215447361	0.999426936
FBgn0041712	-0.19606077	0.715993209	NA	NA	NA	NA
FBgn0041721	0.737740242	0.196188801	NA	NA	NA	NA

FBgn0042094	0.021011845	0.898673883	NA	NA	NA	NA
FBgn0043364	-0.443616617	0.002373874	NA	NA	NA	NA
FBgn0043783	-0.160058919	0.783802768	NA	NA	NA	NA
FBgn0043841	-0.035344814	0.835603871	NA	NA	NA	NA
FBgn0044047	-0.340084713	0.168042624	NA	NA	NA	NA
FBgn0044510	0.145862027	0.380138686	0.196184926	0.915266824	0.276151272	0.999426936
FBgn0045064	0.086175792	0.568168613	NA	NA	NA	NA
FBgn0045479	0.011817801	0.994007618	NA	NA	1.208906807	0.3798911
FBgn0046887	1.08133849	0.009522565	NA	NA	NA	NA
FBgn0050015	-0.263780296	0.249738669	NA	NA	-0.15979708	0.999426936
FBgn0050069	-0.378407112	0.071624423	NA	NA	NA	NA
FBgn0050089	0.008709229	0.982270556	NA	NA	NA	NA
FBgn0050104	-0.050861319	0.829616717	NA	NA	NA	NA
FBgn0050115	0.13540523	0.41371869	1.075834836	0.244111875	-0.034643156	0.999426936
FBgn0050197	0.047485428	0.891768871	NA	NA	NA	NA
FBgn0050345	0.025223487	0.893014756	NA	NA	NA	NA
FBgn0050401	0.883371249	0.129384938	NA	NA	NA	NA
FBgn0050418	0.227349055	0.557511751	NA	NA	0.422096244	0.999426936
FBgn0050428	0.082921815	0.758743954	NA	NA	NA	NA
FBgn0050460	-1.681986982	2.32E-17	NA	NA	0.515900411	0.999426936
FBgn0050466	-0.423304968	0.047772271	NA	NA	NA	NA
FBgn0051004	-0.144915427	0.81549763	NA	NA	NA	NA
FBgn0051029	-0.074874312	0.819709791	NA	NA	0.497973867	0.999426936
FBgn0051053	0.011283495	0.965707824	NA	NA	NA	NA
FBgn0051116	-0.196887771	0.396030324	NA	NA	NA	NA
FBgn0051279	0.298039193	0.434262396	NA	NA	NA	NA
FBgn0051313	-0.286735665	0.512522624	NA	NA	NA	NA
FBgn0051324	0.135950224	0.519963221	NA	NA	-0.029797909	0.999426936
FBgn0051354	0.777378241	0.038070033	NA	NA	NA	NA

FBgn0051514	0.373202181	0.3480223	NA	NA	NA	NA
FBgn0051525	-0.369931627	0.300224171	NA	NA	NA	NA
FBgn0051612	-0.493278417	0.03105779	NA	NA	-1.846121689	0.000359195
FBgn0051614	-0.158040136	0.555389335	NA	NA	NA	NA
FBgn0051617	0.281829428	0.060610726	NA	NA	NA	NA
FBgn0051661	-0.048118274	0.85338848	NA	NA	NA	NA
FBgn0051710	-0.421685573	0.132732592	NA	NA	NA	NA
FBgn0051781	0.707991822	0.052145042	NA	NA	NA	NA
FBgn0051807	-0.096713437	0.814154289	NA	NA	NA	NA
FBgn0051869	-0.019100979	0.948700313	NA	NA	NA	NA
FBgn0051973	-0.570354379	0.14159127	0.1511307	0.947321862	NA	NA
FBgn0052091	-0.102179888	0.579039417	NA	NA	NA	NA
FBgn0052099	-0.211586328	0.245053449	NA	NA	NA	NA
FBgn0052137	-0.279146167	0.084845643	NA	NA	NA	NA
FBgn0052195	-0.292190159	0.241391087	NA	NA	NA	NA
FBgn0052218	-0.280846306	0.245594706	NA	NA	NA	NA
FBgn0052280	0.194415631	0.570122782	NA	NA	NA	NA
FBgn0052311	0.241233353	0.306773088	NA	NA	NA	NA
FBgn0052364	0.613710679	0.023439721	NA	NA	NA	NA
FBgn0052369	-0.190478552	0.455967797	NA	NA	0.301932699	0.999426936
FBgn0052448	0.637544538	0.055883253	NA	NA	NA	NA
FBgn0052476	-0.255538305	0.570091661	NA	NA	NA	NA
FBgn0052625	0.151997902	0.333524232	NA	NA	NA	NA
FBgn0052687	-0.115466804	0.553109161	NA	NA	NA	NA
FBgn0052702	0.007673913	0.975497578	NA	NA	0.183217478	0.999426936
FBgn0052773	0.023757164	0.958886797	NA	NA	NA	NA
FBgn0052816	-0.448815012	0.026510134	NA	NA	NA	NA
FBgn0052850	0.115252276	0.415254803	NA	NA	0.296216559	0.999426936
FBgn0053080	0.158482855	0.459292279	NA	NA	NA	NA

FBgn0053099	0.081550065	0.81153195	NA	NA	NA	NA
FBgn0053108	-0.06968489	0.869130629	NA	NA	NA	NA
FBgn0053196	0.344787024	0.368943906	NA	NA	NA	NA
FBgn0053207	1.059254775	0.001274166	NA	NA	0.718894587	0.999426936
FBgn0053508	1.46827275	0.205484136	NA	NA	3.23144373	0.75578525
FBgn0053519	0.121604053	0.774320104	NA	NA	NA	NA
FBgn0053810	0.176259064	0.294178024	NA	NA	NA	NA
FBgn0053813	0.252316903	0.047633044	NA	NA	NA	NA
FBgn0053816	0.096159078	0.438135727	NA	NA	NA	NA
FBgn0053819	0.200793761	0.133161576	NA	NA	NA	NA
FBgn0053822	0.244417388	0.061446202	NA	NA	NA	NA
FBgn0053825	0.20518197	0.183612004	NA	NA	NA	NA
FBgn0053828	0.222235677	0.076644165	NA	NA	NA	NA
FBgn0053831	0.215212659	0.096062221	NA	NA	NA	NA
FBgn0053855	0.15189046	0.431504777	NA	NA	NA	NA
FBgn0053858	0.032756482	0.868487802	NA	NA	NA	NA
FBgn0053861	-0.161519441	0.345483667	NA	NA	NA	NA
FBgn0053868	0.839963387	8.10E-06	NA	NA	NA	NA
FBgn0053926	0.161158358	0.6935851	NA	NA	NA	NA
FBgn0053970	-0.115661084	0.639801586	NA	NA	NA	NA
FBgn0058160	-0.41703542	0.025772065	0.120278666	0.947321862	-0.009642003	0.999426936
FBgn0058178	0.241264588	0.289905404	-0.101558743	0.834700374	0.228658294	0.999426936
FBgn0058469	0.583500226	0.130453769	NA	NA	0.472698383	0.999426936
FBgn0060296	0.05757669	0.764609423	NA	NA	0.01435985	0.999426936
FBgn0062449	-0.585355816	1.70E-07	NA	NA	NA	NA
FBgn0062978	-0.337027395	0.295534433	NA	NA	0.049457812	0.999426936
FBgn0063497	-0.053070807	0.880899474	NA	NA	NA	NA
FBgn0063499	-0.093241815	0.688470346	NA	NA	NA	NA
FBgn0065046	0.765182878	0.004149984	NA	NA	-0.049848642	0.999426936

FBgn0065047	0.799989777	6.49E-05	NA	NA	NA	NA
FBgn0065048	0.829158941	1.06E-05	NA	NA	NA	NA
FBgn0065055	0.738450148	0.003146061	NA	NA	NA	NA
FBgn0065098	0.6092995	0.021528642	NA	NA	NA	NA
FBgn0069923	0.614045759	0.052414432	NA	NA	NA	NA
FBgn0069938	1.087415882	0.200625527	0.715646497	0.747464626	NA	NA
FBgn0082925	0.735308489	0.046961846	NA	NA	NA	NA
FBgn0082947	0.301945628	0.425659329	NA	NA	NA	NA
FBgn0082958	0.719858591	0.050393972	NA	NA	NA	NA
FBgn0082959	0.514488017	0.15279047	NA	NA	NA	NA
FBgn0082966	0.256243663	0.329714808	NA	NA	NA	NA
FBgn0082971	0.478718629	0.081714949	NA	NA	NA	NA
FBgn0082974	0.599742341	0.061385663	NA	NA	NA	NA
FBgn0082980	0.657773084	0.066026066	NA	NA	NA	NA
FBgn0082981	0.485297532	0.072893163	NA	NA	NA	NA
FBgn0083001	0.789394184	0.022583123	NA	NA	NA	NA
FBgn0083003	0.728235318	0.23087748	NA	NA	NA	NA
FBgn0083005	0.911762751	0.005496068	NA	NA	NA	NA
FBgn0083007	0.705747324	0.018605549	NA	NA	NA	NA
FBgn0083010	0.411055227	0.088167842	NA	NA	NA	NA
FBgn0083011	0.190505234	0.481606986	NA	NA	NA	NA
FBgn0083039	0.788313481	0.004586818	NA	NA	0.173152788	0.999426936
FBgn0083040	0.732056921	0.05855777	NA	NA	NA	NA
FBgn0083041	0.82210625	0.002469948	NA	NA	NA	NA
FBgn0083042	0.724772424	0.017617551	NA	NA	NA	NA
FBgn0083048	0.493677312	0.044096055	NA	NA	NA	NA
FBgn0083049	0.718000082	0.036755697	NA	NA	NA	NA
FBgn0083050	0.473984181	0.029689915	NA	NA	NA	NA
FBgn0083940	-0.053688597	0.841722941	NA	NA	0.256331008	0.999426936

FBgn0083949	1.809161529	0.228353502	NA	NA	0.962193462	0.999426936
FBgn0085279	0.165093901	0.469558087	NA	NA	NA	NA
FBgn0085354	-0.273260454	0.303829264	NA	NA	NA	NA
FBgn0085362	-0.281346728	0.298322113	NA	NA	NA	NA
FBgn0085376	-0.08733175	0.606152335	NA	NA	0.125223349	0.999426936
FBgn0085382	0.686503704	0.315407566	NA	NA	0.798745811	0.517997178
FBgn0085383	3.451269399	0.061446202	NA	NA	0.411935987	0.999426936
FBgn0085407	-0.423530616	0.420437425	NA	NA	NA	NA
FBgn0085408	-0.350676443	0.088819406	NA	NA	-0.384465322	0.999426936
FBgn0085410	0.034244771	0.952628021	NA	NA	NA	NA
FBgn0085412	-0.09525236	0.609796235	NA	NA	0.155088182	0.999426936
FBgn0085413	0.713231471	0.149538251	0.267149603	0.915266824	NA	NA
FBgn0085446	-0.395873181	0.034457863	-0.12685389	0.949085382	-0.344803838	0.999426936
FBgn0085450	-0.516058397	0.000329043	NA	NA	0.650822978	0.26412514
FBgn0085638	-0.191586899	0.163548818	0.240928506	0.834700374	0.134347749	0.999426936
FBgn0085732	-0.244005229	0.07516471	NA	NA	NA	NA
FBgn0085753	0.336168002	0.046379487	-0.463761752	0.876543431	NA	NA
FBgn0085771	0.47684701	0.233156194	NA	NA	NA	NA
FBgn0085810	0.000417866	0.999341632	NA	NA	0.389248195	0.999426936
FBgn0085813	1.951861125	0.063276481	NA	NA	NA	NA
FBgn0085819	0.456298222	0.242602486	NA	NA	NA	NA
FBgn0086265	-0.410929911	0.047772271	NA	NA	NA	NA
FBgn0086365	0.23112314	0.368171399	NA	NA	NA	NA
FBgn0086408	-0.032245339	0.898124099	NA	NA	NA	NA
FBgn0086447	0.02440126	0.909071003	NA	NA	NA	NA
FBgn0086450	0.746215863	0.015785586	NA	NA	NA	NA
FBgn0086600	0.773328725	0.031447118	NA	NA	NA	NA
FBgn0086602	0.163886354	0.595554703	NA	NA	NA	NA
FBgn0086658	0.722905371	0.047474683	NA	NA	NA	NA

FBgn0086659	0.602883678	0.026510134	NA	NA	0.067012966	0.999426936
FBgn0086661	0.618926829	0.092843803	NA	NA	NA	NA
FBgn0086665	0.734443873	0.000744776	NA	NA	NA	NA
FBgn0086666	0.955259646	0.008823774	NA	NA	NA	NA
FBgn0086667	0.722288648	0.0102125	NA	NA	0.05050347	0.999426936
FBgn0086669	0.780301436	0.006922142	NA	NA	NA	NA
FBgn0086671	0.535934535	0.031447118	NA	NA	NA	NA
FBgn0086698	0.089346393	0.594260798	NA	NA	NA	NA
FBgn0086708	-0.112489868	0.745398656	NA	NA	NA	NA
FBgn0086758	0.128875996	0.805554706	NA	NA	NA	NA
FBgn0086917	0.438173757	0.862263614	-0.048577234	0.949085382	-0.17165177	0.999426936
FBgn0087012	0.660998873	0.213590367	NA	NA	0.184885887	0.999426936
FBgn0087035	-0.269283843	0.059371261	NA	NA	0.067361975	0.999426936
FBgn0250757	1.243896042	0.174081515	NA	NA	NA	NA
FBgn0250835	-0.052409093	0.89727144	NA	NA	NA	NA
FBgn0250871	-0.220302573	0.453437235	NA	NA	NA	NA
FBgn0259163	-0.068223766	0.769049	NA	NA	NA	NA
FBgn0259173	0.1114018	0.777357012	NA	NA	NA	NA
FBgn0259209	0.362723664	0.118815261	NA	NA	NA	NA
FBgn0259229	2.009262176	0.183612004	NA	NA	0.880446722	0.999426936
FBgn0259244	0.30583818	0.58768577	NA	NA	NA	NA
FBgn0259736	-0.120904436	0.73116205	NA	NA	NA	NA
FBgn0259878	-0.033330014	0.846938796	NA	NA	NA	NA
FBgn0259977	0.312817549	0.368171399	NA	NA	NA	NA
FBgn0259993	0.378684183	0.073507179	NA	NA	NA	NA
FBgn0260004	-0.049071892	0.893302457	NA	NA	NA	NA
FBgn0260400	-0.056959485	0.897960739	NA	NA	NA	NA
FBgn0260660	-0.337884439	0.101869191	NA	NA	NA	NA
FBgn0260768	-0.125186643	0.674814072	NA	NA	-0.069009494	0.999426936

FBgn0260942	0.153826957	0.357808971	NA	NA	NA	NA
FBgn0260964	0.35213036	0.275260746	NA	NA	NA	NA
FBgn0261113	-0.373467907	0.03215389	NA	NA	0.035506387	0.999426936
FBgn0261258	-0.281540791	0.120554697	NA	NA	0.080138784	0.999426936
FBgn0261461	-0.144936444	0.145498836	NA	NA	0.009019468	0.999426936
FBgn0261504	0.583056234	0.03215389	NA	NA	NA	NA
FBgn0261505	-0.211833119	0.1354372	NA	NA	NA	NA
FBgn0261552	-0.182873038	0.397055869	NA	NA	0.090876182	0.999426936
FBgn0261555	-0.398065647	0.045968761	NA	NA	NA	NA
FBgn0261563	0.151072013	0.435956383	NA	NA	NA	NA
FBgn0261612	0.77697133	0.238412688	NA	NA	NA	NA
FBgn0261639	-0.068916051	0.682024784	NA	NA	NA	NA
FBgn0261640	0.123862912	0.386442875	NA	NA	NA	NA
FBgn0261788	0.410749537	0.259016091	NA	NA	NA	NA
FBgn0261799	-0.416456591	0.362437483	NA	NA	NA	NA
FBgn0261801	0.424003043	0.174097921	0.312902004	0.915266824	0.063514117	0.999426936
FBgn0261822	-0.344645997	0.069526016	NA	NA	0.273895503	0.999426936
FBgn0262003	0.127819006	0.809042553	NA	NA	NA	NA
FBgn0262004	0.085815678	0.791375419	NA	NA	NA	NA
FBgn0262104	-0.156456706	0.682547491	NA	NA	NA	NA
FBgn0262123	-0.252141501	0.169482169	0.044182388	0.949085382	0.603203962	0.082880035
FBgn0262160	-0.037174959	0.870083727	NA	NA	-0.234652854	0.999426936
FBgn0262475	-0.170300368	0.487335356	NA	NA	-0.117628694	0.999426936
FBgn0262508	0.060658867	0.816900863	NA	NA	NA	NA
FBgn0262509	-0.145877714	0.666064824	0.063042827	0.949085382	NA	NA
FBgn0262608	0.336509974	0.04511587	NA	NA	-0.285205463	0.999426936
FBgn0262686	0.76764119	0.125761226	NA	NA	NA	NA
FBgn0262867	-0.255208204	0.555445408	NA	NA	NA	NA
FBgn0263018	0.526829553	0.039713568	NA	NA	NA	NA

FBgn0263019	-0.063050365	0.854290795	NA	NA	NA	NA
FBgn0263111	-0.301658405	0.299113533	NA	NA	0.373884315	0.999426936
FBgn0263316	0.068628698	0.780896999	NA	NA	NA	NA
FBgn0263397	0.381003656	0.238110884	NA	NA	NA	NA
FBgn0263413	-0.258794235	0.50182957	NA	NA	NA	NA
FBgn0263459	0.461585501	0.156949877	NA	NA	0.987353271	0.223539504
FBgn0263468	0.535113603	0.03215389	NA	NA	NA	NA
FBgn0263481	0.288475372	0.454379396	NA	NA	NA	NA
FBgn0263489	0.979130536	0.016633874	NA	NA	NA	NA
FBgn0263492	0.07967432	0.867708777	NA	NA	NA	NA
FBgn0263510	0.30857589	0.039109226	NA	NA	NA	NA
FBgn0263705	0.380002521	0.085781786	NA	NA	NA	NA
FBgn0263772	0.016676935	0.946786886	NA	NA	0.463407906	0.999426936
FBgn0263873	0.133126545	0.606352201	NA	NA	0.077997479	0.999426936
FBgn0263930	-0.278185251	0.23800856	NA	NA	0.09977363	0.999426936
FBgn0263973	-0.212514923	0.46880206	NA	NA	NA	NA
FBgn0263995	-0.215456948	0.52660148	NA	NA	0.133977987	0.999426936
FBgn0264089	0.181723129	0.430612545	NA	NA	-0.733624403	0.830029579
FBgn0264273	-0.240382357	0.433570367	NA	NA	NA	NA
FBgn0264385	0.090293486	0.65964607	NA	NA	NA	NA
FBgn0264439	-0.130400575	0.611928419	NA	NA	NA	NA
FBgn0264489	-0.118650464	0.774165838	NA	NA	NA	NA
FBgn0264490	-0.188970117	0.361711983	NA	NA	0.195575909	0.999426936
FBgn0264502	0.194982451	0.565726104	NA	NA	NA	NA
FBgn0264542	0.003774404	0.98519705	NA	NA	0.573886967	0.296760299
FBgn0264556	-0.401954305	0.230596835	NA	NA	NA	NA
FBgn0264695	0.11733601	0.496860026	NA	NA	-0.073379048	0.999426936
FBgn0264834	-0.318703026	0.472912746	NA	NA	0.160371663	0.999426936
FBgn0264894	-0.413352844	0.058432627	1.437660926	0.057277863	1.299251098	0.001994718

FBgn0264975	-0.243147657	0.067228755	NA	NA	-0.064598703	0.999426936
FBgn0265002	1.08586691	0.08241133	NA	NA	NA	NA
FBgn0265045	0.253983852	0.185424046	NA	NA	NA	NA
FBgn0265082	-0.034916808	0.845999208	-0.376847599	0.867079825	NA	NA
FBgn0265180	-0.246387472	0.59564586	NA	NA	0.616412556	0.343792576
FBgn0265185	-0.39041975	0.350511595	NA	NA	NA	NA
FBgn0265274	-0.132663095	0.452282232	NA	NA	NA	NA
FBgn0265276	-0.345625107	0.092618525	NA	NA	0.229072011	0.999426936
FBgn0265296	1.510350429	0.037364684	NA	NA	0.741767915	0.999426936
FBgn0265316	0.236106101	0.404002175	NA	NA	NA	NA
FBgn0265356	0.39760713	0.219969429	NA	NA	NA	NA
FBgn0265413	-0.007650008	0.966865265	NA	NA	NA	NA
FBgn0265434	-0.171161984	0.221584722	NA	NA	-0.240441516	0.999426936
FBgn0265457	0.219974425	0.677810503	NA	NA	NA	NA
FBgn0265487	-0.065008567	0.786978335	NA	NA	0.074676698	0.999426936
FBgn0265508	0.505955845	0.365656281	NA	NA	NA	NA
FBgn0265548	3.539402842	0.221887522	NA	NA	NA	NA
FBgn0265669	0.570556261	0.163548818	NA	NA	NA	NA
FBgn0265726	0.092889518	0.758647687	NA	NA	NA	NA
FBgn0265767	0.541198026	0.107693003	NA	NA	NA	NA
FBgn0265977	0.013730542	0.9713988	NA	NA	NA	NA
FBgn0265991	-0.125399651	0.555389335	NA	NA	-0.029416027	0.999426936
FBgn0266000	-0.283643156	0.061157763	NA	NA	-0.203067744	0.999426936
FBgn0266377	-0.180050037	0.374334971	NA	NA	NA	NA
FBgn0266414	-0.295924735	0.31734676	NA	NA	NA	NA
FBgn0266418	-0.067711969	0.54017937	NA	NA	0.219387212	0.999426936
FBgn0266758	-0.062607519	0.822687826	NA	NA	NA	NA
FBgn0267033	-0.116061074	0.650317245	NA	NA	0.125226038	0.999426936
FBgn0267191	0.108837619	0.829883857	NA	NA	NA	NA

FBgn0267336	-0.193493905	0.3159949	NA	NA	0.084552965	0.999426936
FBgn0267348	0.012846651	0.957105502	NA	NA	0.283099979	0.999426936
FBgn0267428	-0.634604713	0.022583123	0.311261773	0.243517763	0.340756262	0.84128059
FBgn0267505	1.156788744	0.161548647	NA	NA	NA	NA
FBgn0267506	1.19854545	0.176997482	NA	NA	NA	NA
FBgn0267507	1.236435494	0.139964785	NA	NA	NA	NA
FBgn0267508	1.513282406	0.163285369	NA	NA	NA	NA
FBgn0267511	0.440092928	0.24228536	NA	NA	NA	NA
FBgn0267515	0.304395122	0.096284689	NA	NA	NA	NA
FBgn0267516	1.029674359	0.133666147	NA	NA	NA	NA
FBgn0267519	0.310681227	0.059801265	NA	NA	NA	NA
FBgn0267520	2.102399636	0.185911625	NA	NA	NA	NA
FBgn0267668	0.165108589	0.718005397	NA	NA	NA	NA
FBgn0267704	0.28355238	0.410260716	0.121717868	0.887925971	0.029630298	0.999426936
FBgn0267728	1.030218493	1.96E-06	NA	NA	0.143376255	0.999426936
FBgn0267798	1.052658813	0.010495299	NA	NA	NA	NA
FBgn0267826	0.052237453	0.903104634	NA	NA	NA	NA
FBgn0267910	0.692144512	0.089800717	NA	NA	NA	NA
FBgn0283451	-0.443890424	0.081166998	NA	NA	NA	NA
FBgn0283471	0.022779694	0.927633643	NA	NA	NA	NA
FBgn0283680	-0.04476714	0.910483757	NA	NA	NA	NA
FBgn0284256	0.080498912	0.379734163	NA	NA	0.104409115	0.999426936
FBgn0284408	-0.052164873	0.796196955	NA	NA	0.189357318	0.999426936
FBgn0285955	-0.01314026	0.955624241	NA	NA	-0.140751798	0.999426936
FBgn0285991	1.025261765	3.12E-10	NA	NA	0.160611001	0.999426936
armi						
gene	Transcript abundance		Antisense piRNA abundance		Sense piRNA abundance	
	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj	L2FC(D.mel/D.sim)	padj

FBgn0000044	0.394819004	0.085465502	NA	NA	NA	NA
FBgn0000046	0.725575198	0.16050111	NA	NA	NA	NA
FBgn0000139	0.107741803	0.736156794	NA	NA	0.345303079	0.999894467
FBgn0000180	-0.437544414	0.635212011	0.156544958	0.999650967	NA	NA
FBgn0000246	0.387579812	0.339952175	NA	NA	0.504797518	0.999894467
FBgn0000299	0.039879945	0.910389436	NA	NA	-0.76705295	0.999894467
FBgn0000320	-0.001649984	0.995909175	NA	NA	0.052980422	0.999894467
FBgn0000416	0.324168951	0.410659833	NA	NA	-0.314501967	0.999894467
FBgn0000427	0.335627131	0.305875566	NA	NA	0.06697754	0.999894467
FBgn0000463	0.132155202	0.59673795	NA	NA	-0.358993894	0.999894467
FBgn0000542	0.161009863	0.751556273	NA	NA	0.67013434	0.943052266
FBgn0000635	0.176981058	0.663356226	0.370212099	0.999650967	-0.253312116	0.999894467
FBgn0000636	0.143047249	0.662075873	NA	NA	0.658715599	0.999894467
FBgn0001098	0.050712369	0.863505918	NA	NA	-0.010978016	0.999894467
FBgn0001123	-0.170720187	0.838704462	NA	NA	NA	NA
FBgn0001145	0.42294885	0.38080136	NA	NA	NA	NA
FBgn0001168	0.029502223	0.958682359	NA	NA	0.158318607	0.999894467
FBgn0001297	-0.129022808	0.598857564	NA	NA	-0.227761907	0.999894467
FBgn0002431	0.443570044	0.442101121	NA	NA	0.045595572	0.999894467
FBgn0002526	0.429807364	0.628014293	NA	NA	-0.229078146	0.999894467
FBgn0002609	0.037402473	0.959454938	NA	NA	NA	NA
FBgn0002773	0.053990785	0.90001117	NA	NA	-3.460446795	1.66E-03
FBgn0002868	-0.423213864	0.183675059	NA	NA	NA	NA
FBgn0002926	0.671351722	0.37248912	NA	NA	0.869850653	4.07E-02
FBgn0003053	0.097198675	0.795506494	0.743334855	0.999650967	0.201169414	0.999894467
FBgn0003089	-0.005522727	0.994390607	NA	NA	NA	NA
FBgn0003090	-0.003042594	0.997072713	NA	NA	-0.432554513	0.999894467
FBgn0003137	0.693193945	0.131147141	NA	NA	-0.662433329	0.999894467
FBgn0003285	0.211344288	0.835513622	NA	NA	NA	NA

FBgn0003301	0.292243718	0.308324184	NA	NA	-0.264904005	0.999894467
FBgn0003312	0.172255916	0.831433163	NA	NA	NA	NA
FBgn0003328	-0.071227791	0.850276865	-0.413747023	0.999650967	NA	NA
FBgn0003366	-0.495152559	0.193736034	NA	NA	NA	NA
FBgn0003396	0.555144475	0.486598767	NA	NA	0.123857762	0.999894467
FBgn0003486	0.166288285	0.854506462	NA	NA	NA	NA
FBgn0003731	-0.004278765	0.993546975	NA	NA	-0.436455516	0.999894467
FBgn0003862	0.734769232	0.366942914	NA	NA	-0.384505606	0.999894467
FBgn0003888	0.104042707	0.752279191	NA	NA	-0.484627774	0.999894467
FBgn0003890	0.281533465	0.498779853	NA	NA	-0.186481857	0.999894467
FBgn0003931	-0.098172641	0.897214749	NA	NA	NA	NA
FBgn0003963	0.25346291	0.546422419	0.631951511	0.999650967	0.092575689	0.999894467
FBgn0003980	0.496199078	0.440638724	NA	NA	0.447483563	0.999894467
FBgn0003997	-0.160646641	0.591499696	NA	NA	-0.022840323	0.999894467
FBgn0004003	-0.427248353	0.427454763	NA	NA	NA	NA
FBgn0004045	0.424215698	0.221317526	NA	NA	-0.27403304	0.999894467
FBgn0004117	0.104400003	0.884952899	NA	NA	-4.528895158	4.41E-02
FBgn0004133	-0.105395885	0.781048489	NA	NA	NA	NA
FBgn0004167	0.530444319	0.419903631	NA	NA	-0.328714484	0.999894467
FBgn0004169	0.41221891	0.304829809	NA	NA	-2.566141636	0.639681139
FBgn0004449	0.395037387	0.302300185	NA	NA	-0.570256187	0.999894467
FBgn0004456	-0.148361415	0.691082084	NA	NA	0.102871298	0.999894467
FBgn0004569	0.180992326	0.748428098	NA	NA	NA	NA
FBgn0004606	0.341527047	0.319870311	NA	NA	NA	NA
FBgn0004859	0.315182293	0.534012099	NA	NA	0.074275361	0.999894467
FBgn0004861	0.229666604	0.596140451	NA	NA	NA	NA
FBgn0005612	0.048146133	0.924658764	NA	NA	NA	NA
FBgn0005631	0.138499574	0.872989306	NA	NA	NA	NA
FBgn0005666	0.868923548	0.085465502	-0.121332496	0.999650967	-0.662822501	0.999894467

FBgn0005771	0.052443942	0.918320054	NA	NA	0.560060068	0.999894467
FBgn0010019	0.288176829	0.491281494	NA	NA	NA	NA
FBgn0010228	-0.13371565	0.518041552	NA	NA	-0.427853464	0.999894467
FBgn0010246	-0.074147279	0.831433163	NA	NA	-0.353542458	0.999894467
FBgn0010317	0.365831669	0.180319563	NA	NA	0.962624295	0.999894467
FBgn0010383	0.107356003	0.81859255	NA	NA	NA	NA
FBgn0010387	0.014088081	0.987445168	NA	NA	NA	NA
FBgn0010388	-0.287859765	0.534216209	NA	NA	NA	NA
FBgn0010424	0.480745947	0.276261639	NA	NA	NA	NA
FBgn0010435	0.39042768	0.372404509	NA	NA	NA	NA
FBgn0010473	-0.085640122	0.919856864	NA	NA	-0.658290563	0.999894467
FBgn0010651	-0.366427644	0.387540816	NA	NA	0.185775949	0.999894467
FBgn0011206	0.456056915	0.360636806	NA	NA	-1.223933949	0.999894467
FBgn0011259	0.108459218	0.796090408	0.004261816	0.999650967	-0.186036795	0.999894467
FBgn0011591	0.286027616	0.534148187	NA	NA	-0.154413578	0.999894467
FBgn0011695	-0.371378786	0.708717689	NA	NA	NA	NA
FBgn0011828	0.151276314	0.853789354	NA	NA	NA	NA
FBgn0012037	-0.904229543	0.074294239	NA	NA	NA	NA
FBgn0012051	0.277324119	0.628014293	NA	NA	NA	NA
FBgn0013272	0.33408026	0.610438215	NA	NA	-0.673689361	0.999894467
FBgn0013275	0.396665195	0.191093118	NA	NA	NA	NA
FBgn0013276	0.273409647	0.47122683	NA	NA	NA	NA
FBgn0013277	0.1918712	0.803842625	NA	NA	NA	NA
FBgn0013278	-0.122056459	0.894470774	NA	NA	NA	NA
FBgn0013279	-0.495562197	0.480066256	NA	NA	NA	NA
FBgn0013343	0.298822433	0.338005691	NA	NA	NA	NA
FBgn0013469	0.42931058	0.532551501	NA	NA	0.095207261	0.999894467
FBgn0013733	0.496284563	0.473979274	NA	NA	-0.932669383	0.999894467
FBgn0013953	-0.200159564	0.564454859	NA	NA	NA	NA

FBgn0014022	0.110843369	0.720199101	NA	NA	0.728042591	0.999894467
FBgn0014076	0.1085677	0.803481553	NA	NA	NA	NA
FBgn0014141	-0.393881085	0.007587895	1.16105471	0.72221555	-0.16640229	0.999894467
FBgn0014343	0.40251825	0.419903631	NA	NA	-0.144823353	0.999894467
FBgn0014380	-0.017826352	0.982674327	NA	NA	NA	NA
FBgn0014396	-0.002692875	0.994239288	NA	NA	-0.657320718	0.999894467
FBgn0015031	0.278726384	0.333162358	NA	NA	-0.02759136	0.999894467
FBgn0015399	-0.119873291	0.757198442	NA	NA	NA	NA
FBgn0015513	0.432774596	0.306439259	NA	NA	-0.091981358	0.999894467
FBgn0015558	-0.054589373	0.956220483	NA	NA	NA	NA
FBgn0015609	0.634686548	0.320164335	NA	NA	-0.111188196	0.999894467
FBgn0015795	0.285054461	0.220426091	NA	NA	-0.735819997	0.999894467
FBgn0015872	-0.095549432	0.864098931	NA	NA	0.073489343	0.999894467
FBgn0016075	0.06873881	0.864098931	NA	NA	-0.588774009	0.999894467
FBgn0016076	-0.311682836	0.322494958	NA	NA	-0.310626759	0.999894467
FBgn0016080	-0.011639256	0.989560731	NA	NA	NA	NA
FBgn0016131	0.392206072	0.234824676	NA	NA	-0.187574658	0.999894467
FBgn0016797	0.150270016	0.641880916	NA	NA	-0.221257795	0.999894467
FBgn0016977	0.751389993	0.409486156	-0.098340652	0.999650967	-0.248943084	0.999894467
FBgn0020257	-0.366867303	0.442101121	NA	NA	NA	NA
FBgn0020294	0.475069025	0.431115263	NA	NA	-0.095074663	0.999894467
FBgn0020306	0.426342467	0.23107148	NA	NA	0.318953527	0.999894467
FBgn0020762	0.014244258	0.980067155	NA	NA	NA	NA
FBgn0021764	0.264507133	0.314525048	NA	NA	-0.122815065	0.999894467
FBgn0022160	-0.177386211	0.610438215	NA	NA	0.098675965	0.999894467
FBgn0022355	0.042296493	0.93436926	NA	NA	-0.702215992	0.999894467
FBgn0022774	-0.126312113	0.702888893	NA	NA	NA	NA
FBgn0022986	0.151613035	0.500634638	NA	NA	NA	NA
FBgn0023001	0.08976166	0.879263356	NA	NA	0.85797794	0.999894467

FBgn0023083	0.592883422	0.074294239	NA	NA	NA	NA
FBgn0023479	0.01130364	0.990141194	NA	NA	NA	NA
FBgn0023520	0.097813184	0.863273805	0.315324409	0.999650967	NA	NA
FBgn0023549	-0.331071194	0.323536158	0.450073888	0.999650967	0.188353055	0.999894467
FBgn0024234	-0.293627381	0.500383541	NA	NA	NA	NA
FBgn0024289	0.313568994	0.639138588	NA	NA	NA	NA
FBgn0024321	-0.303463958	0.505725589	NA	NA	-1.668019113	2.02E-04
FBgn0024366	0.074587408	0.90001117	NA	NA	NA	NA
FBgn0024732	-0.074383624	0.835289197	NA	NA	NA	NA
FBgn0025391	-0.313197187	0.78096813	NA	NA	NA	NA
FBgn0025456	0.012178017	0.986195009	NA	NA	NA	NA
FBgn0025631	0.093565814	0.901780499	NA	NA	NA	NA
FBgn0026061	-0.150113162	0.628488051	NA	NA	-0.052195239	0.999894467
FBgn0026160	0.280750816	0.480690893	NA	NA	NA	NA
FBgn0026319	0.355157576	0.548128982	NA	NA	NA	NA
FBgn0026562	-0.249306016	0.617434228	NA	NA	NA	NA
FBgn0026577	0.45941683	0.171084957	NA	NA	-0.138913145	0.999894467
FBgn0026630	0.074561471	0.8792552	NA	NA	0.00638443	0.999894467
FBgn0026872	-0.280818759	0.641792383	NA	NA	NA	NA
FBgn0027106	0.107771738	0.901327622	NA	NA	NA	NA
FBgn0027339	0.241442078	0.529131071	NA	NA	-0.046904768	0.999894467
FBgn0027341	0.443486497	0.605475193	0.830479443	0.999650967	0.907041959	0.999894467
FBgn0027364	-0.161153564	0.712503958	NA	NA	-0.302941104	0.999894467
FBgn0027499	0.513057232	0.213722277	NA	NA	0.277335959	0.999894467
FBgn0027560	-0.027640225	0.968795634	NA	NA	-0.892698758	0.999894467
FBgn0027578	-0.066791009	0.934835488	NA	NA	NA	NA
FBgn0027596	-0.212897093	0.687442146	NA	NA	-0.262937619	0.999894467
FBgn0028690	0.457826998	0.097446389	NA	NA	-0.148414774	0.999894467
FBgn0028888	0.083558398	0.986890779	NA	NA	NA	NA

FBgn0029148	0.211806053	0.502867561	NA	NA	-0.187877382	0.999894467
FBgn0029172	0.048290628	0.958795246	NA	NA	NA	NA
FBgn0029723	-0.261978193	0.481577662	NA	NA	NA	NA
FBgn0029766	-0.329607039	0.473979274	NA	NA	0.306946509	0.999894467
FBgn0029835	0.532529201	0.337625288	NA	NA	NA	NA
FBgn0029843	-0.56725925	0.280771502	NA	NA	NA	NA
FBgn0029895	-0.103652112	0.803729949	NA	NA	-0.106513849	0.999894467
FBgn0029939	0.326768391	0.409486156	NA	NA	NA	NA
FBgn0030017	0.266147347	0.72508518	NA	NA	0.243569017	0.999894467
FBgn0030040	-0.175716963	0.720199101	NA	NA	NA	NA
FBgn0030091	-0.16915576	0.534216209	NA	NA	NA	NA
FBgn0030218	-0.233836428	0.702933435	NA	NA	NA	NA
FBgn0030309	-0.464493381	0.298510404	NA	NA	NA	NA
FBgn0030349	-0.069168639	0.848806963	0.767842514	0.999650967	0.192872479	0.999894467
FBgn0030485	-0.109628656	0.855111216	NA	NA	NA	NA
FBgn0030600	0.250478745	0.742162812	0.815251963	0.999650967	0.423057933	0.999894467
FBgn0030653	0.247842028	0.649573634	NA	NA	NA	NA
FBgn0030662	0.090259159	0.911143406	NA	NA	-0.104864075	0.999894467
FBgn0030665	0.528672649	0.628261483	NA	NA	NA	NA
FBgn0030666	-0.100881283	0.843556831	NA	NA	NA	NA
FBgn0030816	-0.172667667	0.718348603	NA	NA	NA	NA
FBgn0030828	0.243476644	0.709832219	NA	NA	NA	NA
FBgn0030941	-0.310994297	0.458555812	NA	NA	NA	NA
FBgn0030955	0.065241782	0.884952899	NA	NA	-0.321873558	0.999894467
FBgn0031118	0.344597664	0.310921089	NA	NA	-0.542072399	0.999894467
FBgn0031220	-0.117266936	0.902334613	NA	NA	NA	NA
FBgn0031258	0.157960296	0.748669563	NA	NA	NA	NA
FBgn0031275	0.48311262	0.657096239	NA	NA	NA	NA
FBgn0031322	-0.109731101	0.877671831	NA	NA	NA	NA

FBgn0031571	0.584029748	0.247887336	NA	NA	NA	NA
FBgn0031574	0.081096208	0.916032941	NA	NA	NA	NA
FBgn0031628	0.262724627	0.694818502	NA	NA	NA	NA
FBgn0031645	0.342171707	0.309018069	NA	NA	-0.287769574	0.999894467
FBgn0031689	1.593503977	0.518608765	NA	NA	NA	NA
FBgn0031690	5.795132281	0.207731188	NA	NA	2.888308907	NA
FBgn0031698	0.421766629	0.195935276	NA	NA	0.041879715	0.999894467
FBgn0031741	-0.061684637	0.912639817	NA	NA	NA	NA
FBgn0031745	-0.055190869	0.921615476	NA	NA	0.076240038	0.999894467
FBgn0031756	0.173968591	0.540619252	NA	NA	NA	NA
FBgn0031834	-0.289212663	0.47343322	NA	NA	NA	NA
FBgn0031913	-0.022413736	0.951984942	NA	NA	-0.2689411	0.999894467
FBgn0031981	-0.210798744	0.488567256	NA	NA	-0.093805357	0.999894467
FBgn0031990	0.441852444	0.54975452	NA	NA	0.084315905	0.999894467
FBgn0032006	0.033364157	0.93436926	NA	NA	-0.284383904	0.999894467
FBgn0032025	-0.222484724	0.702933435	NA	NA	NA	NA
FBgn0032101	0.28540647	0.302300185	NA	NA	NA	NA
FBgn0032129	-0.175434074	0.782055089	NA	NA	NA	NA
FBgn0032156	-0.187666667	0.748428098	NA	NA	NA	NA
FBgn0032167	0.472567313	0.409486156	NA	NA	NA	NA
FBgn0032187	-0.319140763	0.557404864	NA	NA	NA	NA
FBgn0032218	0.276594116	0.646148938	NA	NA	NA	NA
FBgn0032264	-0.244090521	0.74826721	NA	NA	NA	NA
FBgn0032297	-0.152743221	0.74097193	NA	NA	-0.103132662	0.999894467
FBgn0032330	-0.075345723	0.748925519	NA	NA	-0.169826832	0.999894467
FBgn0032363	0.209786248	0.468288187	NA	NA	0.077667651	0.999894467
FBgn0032666	0.329755023	0.587723775	NA	NA	-0.213248674	0.999894467
FBgn0032681	0.306448425	0.442101121	NA	NA	NA	NA
FBgn0032713	-0.250596591	0.665806921	NA	NA	NA	NA

FBgn0032720	0.51286922	0.189459345	NA	NA	NA	NA
FBgn0032833	0.204341955	0.377849931	NA	NA	-0.420087961	0.999894467
FBgn0032864	0.040894034	0.912288103	NA	NA	0.527988283	0.999894467
FBgn0033033	0.658493555	0.381389374	0.593944351	0.999650967	0.533019768	0.999894467
FBgn0033108	-2.640024381	0.000611301	-0.901703075	0.854315825	-0.499047838	0.999894467
FBgn0033153	0.105308913	0.783580947	0.706826963	0.999650967	0.396534392	0.999894467
FBgn0033188	-0.052776555	0.908817904	NA	NA	-0.886166172	0.999894467
FBgn0033274	-0.025526139	0.966549994	NA	NA	NA	NA
FBgn0033356	0.393575906	0.264359373	NA	NA	NA	NA
FBgn0033388	0.091252051	0.973539828	0.408407025	0.999650967	-0.013846291	0.999894467
FBgn0033395	0.011148408	0.983259123	NA	NA	NA	NA
FBgn0033438	-0.081020641	0.846062213	NA	NA	NA	NA
FBgn0033459	0.234006639	0.412274493	NA	NA	0.303664438	0.999894467
FBgn0033494	-0.079265386	0.916854419	0.35299552	0.999650967	0.152844209	0.999894467
FBgn0033518	0.471945135	0.310975492	NA	NA	NA	NA
FBgn0033548	0.361072139	0.334844342	NA	NA	NA	NA
FBgn0033649	0.233865558	0.651505999	NA	NA	NA	NA
FBgn0033654	-0.210873516	0.709683812	NA	NA	0.328378967	0.999894467
FBgn0033661	0.746529033	0.382557325	NA	NA	0.141202067	0.999894467
FBgn0033782	0.347080609	0.686960068	NA	NA	NA	NA
FBgn0033787	0.049558176	0.948778316	NA	NA	NA	NA
FBgn0033816	0.204907666	0.528279217	NA	NA	NA	NA
FBgn0033926	-0.657313864	0.00078591	NA	NA	-0.728054682	0.999894467
FBgn0033927	-0.606687798	0.056724971	NA	NA	NA	NA
FBgn0034075	-0.30815577	0.414008648	NA	NA	-0.370539774	0.999894467
FBgn0034194	-0.132453075	0.876537736	NA	NA	-0.164376254	0.999894467
FBgn0034240	0.679835646	0.317784993	NA	NA	0.200530532	0.999894467
FBgn0034253	0.411540248	0.491281494	NA	NA	0.423605605	0.999894467
FBgn0034300	0.523398179	0.201147158	NA	NA	0.091776913	0.999894467

FBgn0034312	-0.314402976	0.601265051	NA	NA	-0.047700765	0.999894467
FBgn0034406	-0.64343838	0.220426091	0.928353211	0.999650967	0.548584122	0.999894467
FBgn0034408	0.092857735	0.916032941	0.899313781	0.999650967	0.419549859	0.999894467
FBgn0034436	0.035415309	0.959441238	NA	NA	0.101499415	0.999894467
FBgn0034500	0.212245416	0.538541454	NA	NA	NA	NA
FBgn0034501	-0.017238765	0.973339996	NA	NA	-0.696702172	0.999894467
FBgn0034504	0.274649662	0.164223581	NA	NA	NA	NA
FBgn0034602	-0.29912947	0.563900724	NA	NA	NA	NA
FBgn0034611	-0.074393269	0.802397872	NA	NA	-0.017019556	0.999894467
FBgn0034638	0.369247793	0.366190582	NA	NA	NA	NA
FBgn0034639	0.561707388	0.39515859	NA	NA	NA	NA
FBgn0034709	-0.502883025	0.068745898	NA	NA	-0.423113449	0.999894467
FBgn0034718	0.309833441	0.450342604	NA	NA	-0.300845617	0.999894467
FBgn0034723	-0.266043153	0.610438215	-0.447289197	0.999650967	NA	NA
FBgn0034761	0.003236063	0.994239288	NA	NA	0.274236658	0.999894467
FBgn0035023	0.429167724	0.468288187	NA	NA	NA	NA
FBgn0035049	0.375824644	0.646148938	NA	NA	NA	NA
FBgn0035094	-0.938232044	0.176093614	0.862989946	0.999650967	0.910169696	0.354150799
FBgn0035308	0.230414721	0.696127778	NA	NA	0.109801725	0.999894467
FBgn0035490	0.147427972	0.870686472	NA	NA	NA	NA
FBgn0035574	0.15360931	0.725224925	NA	NA	NA	NA
FBgn0035617	0.487778851	0.208787868	NA	NA	0.251019819	0.999894467
FBgn0035763	0.057635737	0.823396549	NA	NA	-0.254266657	0.999894467
FBgn0035767	0.018415517	0.982674327	NA	NA	NA	NA
FBgn0035975	-0.249256261	0.703370027	NA	NA	NA	NA
FBgn0036091	0.3141677	0.801725697	NA	NA	NA	NA
FBgn0036144	-0.053173215	0.84231552	NA	NA	0.122292889	0.999894467
FBgn0036147	0.175873176	0.48860798	NA	NA	0.053624746	0.999894467
FBgn0036155	-0.125979505	0.703804017	NA	NA	NA	NA

FBgn0036196	0.24214097	0.699389864	NA	NA	NA	NA
FBgn0036205	0.147104338	0.810905466	NA	NA	NA	NA
FBgn0036287	1.398296172	0.307570015	NA	NA	NA	NA
FBgn0036381	-0.133741504	0.884952899	-0.245733393	0.999650967	NA	NA
FBgn0036454	0.031892697	0.964893487	NA	NA	-0.3611678	0.999894467
FBgn0036589	0.175670701	0.748428098	NA	NA	NA	NA
FBgn0036732	-0.286857897	0.517318714	NA	NA	0.316529177	0.999894467
FBgn0036752	0.262219704	0.569898951	NA	NA	NA	NA
FBgn0036789	1.556899208	0.076018512	3.695816929	0.999650967	0.499940374	0.999894467
FBgn0036814	0.31201681	0.442101121	NA	NA	NA	NA
FBgn0037007	-0.288692489	0.414061742	NA	NA	NA	NA
FBgn0037012	0.205861758	0.736862009	NA	NA	-0.124749448	0.999894467
FBgn0037016	-0.079451514	0.851134098	NA	NA	-0.172292265	0.999894467
FBgn0037137	0.448083034	0.147119102	NA	NA	0.225606688	0.999894467
FBgn0037344	0.372567191	0.315391602	NA	NA	-0.197344215	0.999894467
FBgn0037525	0.166184435	0.624610154	NA	NA	0.122517663	0.999894467
FBgn0037577	-0.044398662	0.936305899	NA	NA	NA	NA
FBgn0037659	0.150932257	0.588595452	NA	NA	0.218856715	0.999894467
FBgn0037856	-0.123040374	0.664263855	NA	NA	0.921513666	0.672404816
FBgn0037944	0.477432387	0.182443697	NA	NA	0.132386114	0.999894467
FBgn0037956	-0.231434988	0.604583238	NA	NA	-0.171879189	0.999894467
FBgn0038047	0.271486499	0.670831156	NA	NA	NA	NA
FBgn0038294	-0.011504355	0.976101241	NA	NA	NA	NA
FBgn0038341	-0.155888579	0.66865975	NA	NA	NA	NA
FBgn0038353	0.019719614	0.990141194	NA	NA	NA	NA
FBgn0038679	0.207766349	0.622351979	NA	NA	-0.368482449	0.999894467
FBgn0038720	-0.149287144	0.702999041	NA	NA	NA	NA
FBgn0038774	0.068349685	0.919856864	NA	NA	NA	NA
FBgn0038826	0.300822917	0.504078529	NA	NA	-0.446352915	0.999894467

FBgn0038842	-0.218317293	0.626222435	NA	NA	NA	NA
FBgn0038881	-0.072619949	0.881119929	NA	NA	-0.307272285	0.999894467
FBgn0039075	0.182282395	0.81646719	NA	NA	NA	NA
FBgn0039109	-0.355065367	0.161021986	NA	NA	NA	NA
FBgn0039114	-0.12319024	0.829030553	NA	NA	NA	NA
FBgn0039155	0.282023018	0.591775072	NA	NA	NA	NA
FBgn0039214	0.465149918	0.419903631	NA	NA	-0.419950783	0.999894467
FBgn0039251	0.071513915	0.84571595	NA	NA	NA	NA
FBgn0039266	0.290928557	0.414197179	NA	NA	NA	NA
FBgn0039419	-0.316377911	0.474577091	NA	NA	NA	NA
FBgn0039430	-0.063562365	0.919856864	NA	NA	NA	NA
FBgn0039431	0.105721359	0.831719617	NA	NA	-0.009080139	0.999894467
FBgn0039590	0.44947007	0.098112924	NA	NA	NA	NA
FBgn0039678	0.002305156	0.995840361	NA	NA	NA	NA
FBgn0039714	0.046046683	0.864428175	NA	NA	-0.025955914	0.999894467
FBgn0039776	-0.123786079	0.742212797	NA	NA	-0.045255349	0.999894467
FBgn0039863	0.427609287	0.193736034	NA	NA	-0.151351378	0.999894467
FBgn0039883	-0.086834192	0.849895884	-0.244072928	0.999650967	-0.337893517	0.999894467
FBgn0039928	0.416733977	0.308143998	0.57361394	0.999650967	0.045797205	0.999894467
FBgn0040351	-0.045246282	0.973339996	NA	NA	NA	NA
FBgn0040364	-0.199292237	0.62328826	NA	NA	NA	NA
FBgn0040398	0.312909227	0.602123348	NA	NA	NA	NA
FBgn0040609	0.402334342	0.528909476	NA	NA	NA	NA
FBgn0040765	0.134364063	0.764139339	NA	NA	NA	NA
FBgn0040813	0.244760978	0.520106459	NA	NA	NA	NA
FBgn0040823	0.457855451	0.256199394	NA	NA	0.000962209	0.999894467
FBgn0040827	0.171387721	0.790570249	NA	NA	-0.986966833	0.999894467
FBgn0040949	-0.082005543	0.907109648	NA	NA	NA	NA
FBgn0041092	0.119783012	0.548162933	1.579662007	0.999650967	0.602951348	0.187179744

FBgn0041180	-0.046237551	0.924155484	NA	NA	NA	NA
FBgn0041184	-0.239289885	0.513542389	NA	NA	0.036578288	0.999894467
FBgn0042083	0.002175081	0.995802895	NA	NA	NA	NA
FBgn0042132	0.17461482	0.493657997	NA	NA	NA	NA
FBgn0043364	0.136616214	0.630424599	NA	NA	NA	NA
FBgn0043799	0.21027391	0.658401417	NA	NA	NA	NA
FBgn0043884	0.495238681	0.392800864	NA	NA	0.00059782	0.999894467
FBgn0044047	0.098019415	0.89044198	NA	NA	NA	NA
FBgn0045064	0.063798602	0.892268326	NA	NA	NA	NA
FBgn0046776	0.654321979	0.022383155	NA	NA	NA	NA
FBgn0047000	0.050218134	0.956698944	NA	NA	NA	NA
FBgn0050015	0.178862339	0.707607732	NA	NA	-0.065347377	0.999894467
FBgn0050021	-0.197709924	0.628261483	NA	NA	-0.563139457	0.999894467
FBgn0050026	0.260790196	0.696745871	NA	NA	NA	NA
FBgn0050089	-0.056886666	0.922709048	NA	NA	NA	NA
FBgn0050104	-0.328159641	0.664230575	NA	NA	NA	NA
FBgn0050115	0.191287237	0.729403683	0.340075925	0.999650967	0.060128248	0.999894467
FBgn0050197	-0.142630299	0.824194946	NA	NA	NA	NA
FBgn0050345	0.311785716	0.427389718	0.43047154	0.999650967	NA	NA
FBgn0050428	-0.471774351	0.418523638	NA	NA	NA	NA
FBgn0050456	0.215862759	0.59068308	NA	NA	-0.02025546	0.999894467
FBgn0050460	0.697146674	0.331484915	NA	NA	NA	NA
FBgn0051015	0.145968791	0.757661474	NA	NA	0.474546409	0.999894467
FBgn0051116	0.153084052	0.809459871	NA	NA	NA	NA
FBgn0051176	0.691690808	0.405191826	NA	NA	0.290305772	0.999894467
FBgn0051202	-1.768289029	0.603955458	NA	NA	NA	NA
FBgn0051279	0.201670965	0.756296468	NA	NA	0.707608608	0.999894467
FBgn0051352	0.061762299	0.875352906	NA	NA	NA	NA
FBgn0051354	0.410666275	0.623817003	NA	NA	NA	NA

FBgn0051612	0.418294803	0.500816714	0.050810896	0.999650967	0.424919696	0.999894467
FBgn0051661	-0.208808481	0.662042403	NA	NA	NA	NA
FBgn0051755	0.463626883	0.322494958	NA	NA	NA	NA
FBgn0051869	0.033245636	0.936196785	NA	NA	0.132829053	0.999894467
FBgn0051997	-0.664030575	0.360636806	NA	NA	NA	NA
FBgn0052091	-0.205229567	0.503732079	NA	NA	-0.491116434	0.999894467
FBgn0052137	-0.436745217	0.270596601	NA	NA	NA	NA
FBgn0052311	0.46105839	0.416568656	NA	NA	-1.338654919	0.999894467
FBgn0052625	0.213845368	0.480217108	NA	NA	NA	NA
FBgn0052687	-0.071447043	0.875199565	NA	NA	0.220314374	0.999894467
FBgn0052702	-0.095599044	0.884952899	NA	NA	1.260284739	1.80E-04
FBgn0052816	-0.129438419	0.756457399	NA	NA	-0.536079623	0.999894467
FBgn0052865	-0.241104982	0.83282915	1.164660966	0.000331748	0.970855723	6.81E-02
FBgn0053087	0.287151007	0.446473213	NA	NA	-0.496237359	0.999894467
FBgn0060296	-0.114990933	0.869536483	NA	NA	-0.212103977	0.999894467
FBgn0061200	0.355258128	0.31831874	NA	NA	0.409090437	0.999894467
FBgn0063499	0.249441085	0.71409869	NA	NA	NA	NA
FBgn0065047	0.622084075	0.168585285	NA	NA	NA	NA
FBgn0065048	0.709440363	0.077920418	NA	NA	NA	NA
FBgn0082974	1.51268482	0.074294239	NA	NA	NA	NA
FBgn0082983	0.579331953	0.097446389	NA	NA	NA	NA
FBgn0083003	0.391473146	0.530485491	NA	NA	NA	NA
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FBgn0083005	0.484846672	0.409941067	NA	NA	NA	NA
FBgn0083027	0.262875741	0.546683446	NA	NA	NA	NA
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FBgn0083940	-0.174911752	0.786573908	0.915040915	0.999650967	0.447164104	0.999894467
FBgn0085195	0.367521719	0.46337004	NA	NA	NA	NA
FBgn0085249	0.798277012	0.500218641	NA	NA	NA	NA

FBgn0085362	0.956569591	0.342481431	NA	NA	NA	NA
FBgn0085376	0.172595087	0.639138588	NA	NA	-0.077704228	0.999894467
FBgn0085408	0.567327911	0.07704703	NA	NA	-0.253422743	0.999894467
FBgn0085410	0.190365048	0.794872224	0.952177319	0.999650967	NA	NA
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FBgn0086265	0.324953286	0.324336472	NA	NA	NA	NA
FBgn0086365	-0.238016383	0.661518174	NA	NA	NA	NA
FBgn0086408	0.294828833	0.375809685	NA	NA	-0.195017242	0.999894467
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FBgn0086655	0.265707004	0.403627329	0.639832214	0.999650967	0.387497942	0.999894467
FBgn0086659	0.431228294	0.270993316	NA	NA	0.348238404	0.999894467
FBgn0086661	0.293469329	0.544371967	NA	NA	NA	NA
FBgn0086665	0.411035473	0.360755337	NA	NA	NA	NA
FBgn0086667	-0.129743418	0.783580947	NA	NA	-0.379409759	0.999894467
FBgn0086708	-0.074091244	0.893767684	NA	NA	NA	NA
FBgn0086906	0.727482892	0.540044238	NA	NA	-2.311684666	2.42E-02
FBgn0087002	0.185097083	0.669383124	NA	NA	-0.39278416	0.999894467
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FBgn0259993	0.075713069	0.869536483	NA	NA	NA	NA
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FBgn0262109	0.557330825	0.409486156	NA	NA	-0.190733698	0.999894467
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FBgn0263413	0.609921312	0.329124957	NA	NA	-1.024267545	0.999894467
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FBgn0264489	-0.054281313	0.944156494	NA	NA	-3.158591862	0.231334535
FBgn0264490	-0.102170893	0.798470577	NA	NA	-0.411356478	0.999894467
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FBgn0264695	0.392064929	0.366942914	0.725798942	0.999650967	-4.639155815	3.60E-03
FBgn0264835	1.211503133	0.421338107	NA	NA	NA	NA
FBgn0264894	0.100446745	0.869536483	0.576856484	0.999650967	NA	NA
FBgn0265082	-0.060775101	0.906406692	-1.63951	6.86E-05	-2.378207785	6.98E-11
FBgn0265140	0.2463142	0.403968992	NA	NA	-0.09714429	0.999894467
FBgn0265274	0.00369798	0.993546975	NA	NA	NA	NA
FBgn0265296	-2.765523521	0.33009258	NA	NA	NA	NA
FBgn0265316	0.119291566	0.809459871	NA	NA	NA	NA
FBgn0265434	0.219199276	0.449169823	NA	NA	-0.169916168	0.999894467
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FBgn0265669	0.414931149	0.504078529	NA	NA	NA	NA
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FBgn0265991	0.341970898	0.416568656	NA	NA	-1.569903501	0.96979896
FBgn0266084	0.052760367	0.916032941	NA	NA	-0.475112306	0.999894467
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FBgn0283471	0.191908934	0.747201921	NA	NA	NA	NA
FBgn0284221	0.422615708	0.161021986	NA	NA	0.299090096	0.999894467
FBgn0284408	0.447729887	0.539583481	NA	NA	-0.143691271	0.999894467
FBgn0285925	0.332366985	0.384138436	NA	NA	-0.477397153	0.999894467

Bibliography

1. McClintock B. The origin and behavior of mutable loci in maize. *Proc Natl Acad Sci U S A.* 1950;36: 344–355.
2. McClintock B. Induction of instability at selected loci in maize. *Genetics.* 1953;38: 579–599.
3. SanMiguel P, Tikhonov A, Jin YK, Motchoulskaia N, Zakharov D, Melake-Berhan A, et al. Nested retrotransposons in the intergenic regions of the maize genome. *Science.* 1996;274: 765–768.
4. Jiao Y, Peluso P, Shi J, Liang T, Stitzer MC, Wang B, et al. Improved maize reference genome with single-molecule technologies. *Nature.* 2017;546: 524–527.
5. Mills RE, Andrew Bennett E, Iskow RC, Devine SE. Which transposable elements are active in the human genome? *Trends in Genetics.* 2007. pp. 183–191. doi:10.1016/j.tig.2007.02.006
6. Wicker T, Sabot F, Hua-Van A, Bennetzen JL, Capy P, Chalhoub B, et al. A unified classification system for eukaryotic transposable elements. *Nat Rev Genet.* 2007;8: 973–982.
7. Pardue M-L, DeBaryshe PG. Retrotransposons provide an evolutionarily robust non-telomerase mechanism to maintain telomeres. *Annu Rev Genet.* 2003;37: 485–511.
8. Levis R, O'Hare K, Rubin GM. Effects of transposable element insertions on RNA encoded by the white gene of *Drosophila*. *Cell.* 1984. pp. 471–481. doi:10.1016/0092-8674(84)90502-6
9. McGinnis W, Shermoen AW, Beckendorf SK. A transposable element inserted just 5' to a *Drosophila* glue protein gene alters gene expression and chromatin structure. *Cell.* 1983. pp. 75–84. doi:10.1016/0092-8674(83)90137-x

10. Lee YCG. The role of piRNA-mediated epigenetic silencing in the population dynamics of transposable elements in *Drosophila melanogaster*. *PLoS Genet.* 2015;11: e1005269.
11. Lim JK. Intrachromosomal rearrangements mediated by hobo transposons in *Drosophila melanogaster*. *Proc Natl Acad Sci U S A.* 1988;85: 9153–9157.
12. Hedges DJ, Deininger PL. Inviting instability: Transposable elements, double-strand breaks, and the maintenance of genome integrity. *Mutat Res.* 2007;616: 46–59.
13. Gasior SL, Wakeman TP, Xu B, Deininger PL. The human LINE-1 retrotransposon creates DNA double-strand breaks. *J Mol Biol.* 2006;357: 1383–1393.
14. Brennecke J, Aravin AA, Stark A, Dus M, Kellis M, Sachidanandam R, et al. Discrete small RNA-generating loci as master regulators of transposon activity in *Drosophila*. *Cell.* 2007;128: 1089–1103.
15. Le Thomas A, Rogers AK, Webster A, Marinov GK, Liao SE, Perkins EM, et al. Piwi induces piRNA-guided transcriptional silencing and establishment of a repressive chromatin state. *Genes Dev.* 2013;27: 390–399.
16. Aravin A, Gaidatzis D, Pfeffer S, Lagos-Quintana M, Landgraf P, Iovino N, et al. A novel class of small RNAs bind to MILI protein in mouse testes. *Nature.* 2006;442: 203–207.
17. Girard A, Sachidanandam R, Hannon GJ, Carmell MA. A germline-specific class of small RNAs binds mammalian Piwi proteins. *Nature.* 2006;442: 199–202.
18. Lau NC, Seto AG, Kim J, Kuramochi-Miyagawa S, Nakano T, Bartel DP, et al. Characterization of the piRNA complex from rat testes. *Science.* 2006;313: 363–367.
19. Zanni V, Eymery A, Coiffet M, Zytnicki M, Luyten I, Quesneville H, et al. Distribution, evolution, and diversity of retrotransposons at the flamenco locus reflect the regulatory properties of piRNA clusters. *Proc Natl Acad Sci U S A.* 2013;110: 19842–19847.

20. Gunawardane LS, Saito K, Nishida KM, Miyoshi K, Kawamura Y, Nagami T, et al. A slicer-mediated mechanism for repeat-associated siRNA 5' end formation in *Drosophila*. *Science*. 2007;315: 1587–1590.
21. Malone CD, Brennecke J, Dus M, Stark A, McCombie WR, Sachidanandam R, et al. Specialized piRNA pathways act in germline and somatic tissues of the *Drosophila* ovary. *Cell*. 2009;137: 522–535.
22. Le Thomas A, Stuwe E, Li S, Du J, Marinov G, Rozhkov N, et al. Transgenerationally inherited piRNAs trigger piRNA biogenesis by changing the chromatin of piRNA clusters and inducing precursor processing. *Genes Dev*. 2014;28: 1667–1680.
23. Andress A, Bei Y, Fonslow BR, Giri R, Wu Y, Yates JR 3rd, et al. Spindle-E cycling between nuage and cytoplasm is controlled by Qin and PIWI proteins. *J Cell Biol*. 2016;213: 201–211.
24. Wang W, Han BW, Tipping C, Ge DT, Zhang Z, Weng Z, et al. Slicing and binding by Ago3 or Aub trigger Piwi-bound piRNA production by distinct mechanisms. *Mol Cell*. 2015;59: 819–830.
25. Senti K-A, Jurczak D, Sachidanandam R, Brennecke J. piRNA-guided slicing of transposon transcripts enforces their transcriptional silencing via specifying the nuclear piRNA repertoire. *Genes Dev*. 2015;29: 1747–1762.
26. Mohn F, Handler D, Brennecke J. piRNA-guided slicing specifies transcripts for Zucchini-dependent, phased piRNA biogenesis. *Science*. 2015;348: 812–817.
27. Han BW, Wang W, Li C, Weng Z, Zamore PD. piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. *Science*. 2015. pp. 817–821.
doi:10.1126/science.aaa1264
28. Kawaoka S, Izumi N, Katsuma S, Tomari Y. 3' end formation of PIWI-interacting RNAs in vitro. *Mol Cell*. 2011;43: 1015–1022.

29. Lim AK, Kai T. Unique germ-line organelle, nuage, functions to repress selfish genetic elements in *Drosophila melanogaster*. *Proc Natl Acad Sci U S A*. 2007;104: 6714–6719.
30. Patil VS, Kai T. Repression of retroelements in *Drosophila* germline via piRNA pathway by the Tudor domain protein Tejas. *Curr Biol*. 2010;20: 724–730.
31. Czech B, Hannon GJ. One Loop to Rule Them All: The Ping-Pong Cycle and piRNA-Guided Silencing. *Trends Biochem Sci*. 2016;41: 324–337.
32. Klenov MS, Sokolova OA, Yakushev EY, Stolyarenko AD, Mikhaleva EA, Lavrov SA, et al. Separation of stem cell maintenance and transposon silencing functions of Piwi protein. *Proc Natl Acad Sci U S A*. 2011;108: 18760–18765.
33. Rozhkov NV, Hammell M, Hannon GJ. Multiple roles for Piwi in silencing *Drosophila* transposons. *Genes Dev*. 2013;27: 400–412.
34. Haase AD, Fenoglio S, Muerdter F, Guzzardo PM, Czech B, Pappin DJ, et al. Probing the initiation and effector phases of the somatic piRNA pathway in *Drosophila*. *Genes Dev*. 2010;24: 2499–2504.
35. Olivieri D, Sykora MM, Sachidanandam R, Mechtler K, Brennecke J. An in vivo RNAi assay identifies major genetic and cellular requirements for primary piRNA biogenesis in *Drosophila*. *EMBO J*. 2010;29: 3301–3317.
36. Saito K, Ishizu H, Komai M, Kotani H, Kawamura Y, Nishida KM, et al. Roles for the Yb body components Armitage and Yb in primary piRNA biogenesis in *Drosophila*. *Genes Dev*. 2010;24: 2493–2498.
37. Handler D, Meixner K, Pizka M, Lauss K, Schmied C, Gruber FS, et al. The genetic makeup of the *Drosophila* piRNA pathway. *Mol Cell*. 2013;50: 762–777.
38. Vourekas A, Zheng K, Fu Q, Maragkakis M, Alexiou P, Ma J, et al. The RNA helicase MOV10L1 binds piRNA precursors to initiate piRNA processing. *Genes Dev*. 2015;29: 617–629.

39. Ge DT, Wang W, Tipping C, Gainetdinov I, Weng Z, Zamore PD. The RNA-binding ATPase, Armitage, couples piRNA amplification in nuage to phased piRNA production on mitochondria. *Mol Cell*. 2019;74: 982–995.e6.
40. Huang H, Li Y, Szulwach KE, Zhang G, Jin P, Chen D. AGO3 Slicer activity regulates mitochondria–nuage localization of Armitage and piRNA amplification. *Journal of Cell Biology*. 2014. pp. 217–230. doi:10.1083/jcb.201401002
41. McDonald JH, Kreitman M. Adaptive protein evolution at the Adh locus in *Drosophila*. *Nature*. 1991;351: 652–654.
42. Obbard DJ, Gordon KHJ, Buck AH, Jiggins FM. The evolution of RNAi as a defence against viruses and transposable elements. *Philos Trans R Soc Lond B Biol Sci*. 2009;364: 99–115.
43. Simkin A, Wong A, Poh Y-P, Theurkauf WE, Jensen JD. Recurrent and recent selective sweeps in the piRNA pathway. *Evolution*. 2013;67: 1081–1090.
44. Kolaczkowski B, Hupalo DN, Kern AD. Recurrent adaptation in RNA interference genes across the *Drosophila* phylogeny. *Mol Biol Evol*. 2011;28: 1033–1042.
45. Parhad SS, Tu S, Weng Z, Theurkauf WE. Adaptive evolution leads to cross-species incompatibility in the piRNA transposon silencing machinery. *Dev Cell*. 2017;43: 60–70.e5.
46. Kelleher ES, Edelman NB, Barbash DA. *Drosophila* interspecific hybrids phenocopy piRNA-pathway mutants. *PLoS Biol*. 2012;10: e1001428.
47. Vela D, Fontdevila A, Vieira C, García Guerreiro MP. A genome-wide survey of genetic instability by transposition in *Drosophila* hybrids. *PLoS One*. 2014;9: e88992.
48. Blumenstiel JP, Erwin AA, Hemmer LW. What drives positive selection in the *Drosophila* piRNA machinery? The Genomic Autoimmunity Hypothesis. *Yale J Biol Med*. 2016;89: 499–512.

49. Castillo DM, Mell JC, Box KS, Blumenstiel JP. Molecular evolution under increasing transposable element burden in *Drosophila*: a speed limit on the evolutionary arms race. *BMC Evol Biol.* 2011;11: 258.
50. Dotto BR, Carvalho EL, Silva AF, Duarte Silva LF, Pinto PM, Ortiz MF, et al. HTT-DB: horizontally transferred transposable elements database. *Bioinformatics.* 2015;31: 2915–2917.
51. Houck MA, Clark JB, Peterson KR, Kidwell MG. Possible horizontal transfer of *Drosophila* genes by the mite *Proctolaelaps regalis*. *Science.* 1991;253: 1125–1128.
52. Gilbert C, Schaack S, Pace JK 2nd, Brindley PJ, Feschotte C. A role for host-parasite interactions in the horizontal transfer of transposons across phyla. *Nature.* 2010;464: 1347–1350.
53. Gilbert C, Peccoud J, Chateigner A, Moumen B, Cordaux R, Herniou EA. Continuous influx of genetic material from host to virus populations. *PLoS Genet.* 2016;12: e1005838.
54. Bartolomé C, Bello X, Maside X. Widespread evidence for horizontal transfer of transposable elements across *Drosophila* genomes. *Genome Biol.* 2009;10: R22.
55. Bergman CM, Quesneville H, Anxolabéhère D, Ashburner M. Recurrent insertion and duplication generate networks of transposable element sequences in the *Drosophila melanogaster* genome. *Genome Biol.* 2006;7: R112.
56. Khurana JS, Wang J, Xu J, Koppetsch BS, Thomson TC, Nowosielska A, et al. Adaptation to P element transposon invasion in *Drosophila melanogaster*. *Cell.* 2011;147: 1551–1563.
57. Girard A, Hannon GJ. Conserved themes in small-RNA-mediated transposon control. *Trends Cell Biol.* 2008;18: 136–148.
58. de Vanssay A, Bougé A-L, Boivin A, Hermant C, Teysset L, Delmarre V, et al. Paramutation in *Drosophila* linked to emergence of a piRNA-producing locus. *Nature.* 2012;490: 112–115.

59. Daniels SB, Peterson KR, Strausbaugh LD, Kidwell MG, Chovnick A. Evidence for horizontal transmission of the P transposable element between *Drosophila* species. *Genetics*. 1990;124: 339–355.
60. Kidwell MG. Evolution of hybrid dysgenesis determinants in *Drosophila melanogaster*. *Proc Natl Acad Sci U S A*. 1983;80: 1655–1659.
61. Anxolabéhère D, Kidwell MG, Periquet G. Molecular characteristics of diverse populations are consistent with the hypothesis of a recent invasion of *Drosophila melanogaster* by mobile P elements. *Mol Biol Evol*. 1988;5: 252–269.
62. Brennecke J, Malone CD, Aravin AA, Sachidanandam R, Stark A, Hannon GJ. An epigenetic role for maternally inherited piRNAs in transposon silencing. *Science*. 2008;322: 1387–1392.
63. Jensen PA, Stuart JR, Goodpaster MP, Goodman JW, Simmons MJ. Cytotype regulation of P transposable elements in *Drosophila melanogaster*: repressor polypeptides or piRNAs? *Genetics*. 2008;179: 1785–1793.
64. Kidwell MG, Kidwell JF. Cytoplasm–chromosome interactions in *Drosophila melanogaster*. *Nature*. 1975. pp. 755–756. doi:10.1038/253755a0
65. Sved JA. Hybrid dysgenesis in *Drosophila melanogaster*: a possible explanation in terms of spatial organization of chromosomes. *Aust J Biol Sci*. 1976;29: 375–388.
66. Kidwell MG, Kidwell JF, Sved JA. Hybrid dysgenesis in *Drosophila melanogaster*: a syndrome of aberrant traits including mutation, sterility and male recombination. *Genetics*. 1977;86: 813–833.
67. Engels WR, Preston CR. Hybrid dysgenesis in *Drosophila melanogaster*: the biology of female and male sterility. *Genetics*. 1979;92: 161–174.
68. Schaefer RE, Kidwell MG, Fausto-Sterling A. Hybrid dysgenesis in *Drosophila melanogaster*: morphological and cytological studies of ovarian dysgenesis. *Genetics*. 1979;92: 1141–1152.

69. Chalitchagorn K, Shuangshoti S, Hourpai N, Kongruttanachok N, Tangkijvanich P, Thong-ngam D, et al. Distinctive pattern of LINE-1 methylation level in normal tissues and the association with carcinogenesis. *Oncogene*. 2004;23: 8841–8846.
70. Howard G, Eiges R, Gaudet F, Jaenisch R, Eden A. Activation and transposition of endogenous retroviral elements in hypomethylation induced tumors in mice. *Oncogene*. 2008;27: 404–408.
71. Kidwell MG, Novy JB. Hybrid dysgenesis in *Drosophila melanogaster*: sterility resulting from gonadal dysgenesis in the P-M system. *Genetics*. 1979;92: 1127–1140.
72. Vilà MR, Gelpí C, Nicolás A, Morote J, Schwartz S, Schwartz S, et al. Higher processing rates of Alu-containing sequences in kidney tumors and cell lines with overexpressed Alu-mRNAs. *Oncol Rep*. 2003;10: 1903–1909.
73. Czech B, Hannon GJ. One loop to rule them all: the ping-pong cycle and piRNA-guided silencing. *Trends Biochem Sci*. 2016;41: 324–337.
74. Yang H-P, Barbash DA. Abundant and species-specific DINE-1 transposable elements in 12 *Drosophila* genomes. *Genome Biol*. 2008;9: R39.
75. de la Chaux N, Wagner A. BEL/Pao retrotransposons in metazoan genomes. *BMC Evol Biol*. 2011;11: 154.
76. Lu C, Chen J, Zhang Y, Hu Q, Su W, Kuang H. Miniature inverted-repeat transposable elements (MITEs) have been accumulated through amplification bursts and play important roles in gene expression and species diversity in *Oryza sativa*. *Mol Biol Evol*. 2012;29: 1005–1017.
77. Lu J, Clark AG. Population dynamics of PIWI-interacting RNAs (piRNAs) and their targets in *Drosophila*. *Genome Res*. 2010;20: 212–227.
78. Malone CD, Hannon GJ. Molecular evolution of piRNA and transposon control pathways in *Drosophila*. *Cold Spring Harb Symp Quant Biol*. 2009;74: 225–234.

79. Palmer WH, Hadfield JD, Obbard DJ. RNA-Interference Pathways Display High Rates of Adaptive Protein Evolution in Multiple Invertebrates. *Genetics*. 2018;208: 1585–1599.
80. Yi M, Chen F, Luo M, Cheng Y, Zhao H, Cheng H, et al. Rapid evolution of piRNA pathway in the teleost fish: implication for an adaptation to transposon diversity. *Genome Biol Evol*. 2014;6: 1393–1407.
81. Vermaak D, Henikoff S, Malik HS. Positive selection drives the evolution of rhino, a member of the heterochromatin protein 1 family in *Drosophila*. *PLoS Genet*. 2005;1: 96–108.
82. Senti K-A, Brennecke J. The piRNA pathway: a fly's perspective on the guardian of the genome. *Trends Genet*. 2010;26: 499–509.
83. Yu B, Lin YA, Parhad SS, Jin Z, Ma J, Theurkauf WE, et al. Structural insights into Rhino-Deadlock complex for germline piRNA cluster specification. *EMBO Rep*. 2018;19. doi:10.15252/embr.201745418
84. Parhad SS, Yu T, Zhang G, Rice NP, Weng Z, Theurkauf WE. Adaptive evolution targets a piRNA precursor transcription network. *bioRxiv*. 2019. p. 678227. doi:10.1101/678227
85. Pandey RR, Homolka D, Chen K-M, Sachidanandam R, Fauvarque M-O, Pillai RS. Recruitment of Armitage and Yb to a transcript triggers its phased processing into primary piRNAs in *Drosophila* ovaries. *PLoS Genet*. 2017;13: e1006956.
86. Li C, Vagin VV, Lee S, Xu J, Ma S, Xi H, et al. Collapse of germline piRNAs in the absence of Argonaute3 reveals somatic piRNAs in flies. *Cell*. 2009;137: 509–521.
87. Han BW, Wang W, Li C, Weng Z, Zamore PD. Noncoding RNA. piRNA-guided transposon cleavage initiates Zucchini-dependent, phased piRNA production. *Science*. 2015;348: 817–821.
88. Ishizu H, Kinoshita T, Hirakata S, Komatsuzaki C, Siomi MC. Distinct and collaborative functions of Yb and Armitage in transposon-targeting piRNA biogenesis. *Cell Rep*. 2019;27: 1822–1835.e8.

89. Adams MD, Celtniker SE, Holt RA, Evans CA, Gocayne JD, Amanatides PG, et al. The genome sequence of *Drosophila melanogaster*. *Science*. 2000;287: 2185–2195.
90. Clark AG, Eisen MB, Smith DR, Bergman CM, Oliver B, Markow TA, et al. Evolution of genes and genomes on the *Drosophila* phylogeny. *Nature*. 2007;450: 203–218.
91. Mitchell AL, Attwood TK, Babbitt PC, Blum M, Bork P, Bridge A, et al. InterPro in 2019: improving coverage, classification and access to protein sequence annotations. *Nucleic Acids Res*. 2019;47: D351–D360.
92. Groth AC, Fish M, Nusse R, Calos MP. Construction of transgenic *Drosophila* by using the site-specific integrase from phage phiC31. *Genetics*. 2004;166: 1775–1782.
93. Schüpbach T, Wieschaus E. Female sterile mutations on the second chromosome of *Drosophila melanogaster*. II. Mutations blocking oogenesis or altering egg morphology. *Genetics*. 1991;129: 1119–1136.
94. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol*. 2014;15: 550.
95. Olivieri D, Senti K-A, Subramanian S, Sachidanandam R, Brennecke J. The cochaperone shutdown defines a group of biogenesis factors essential for all piRNA populations in *Drosophila*. *Mol Cell*. 2012. doi:10.1016/j.molcel.2012.07.021
96. Barckmann B, Pierson S, Dufourt J, Papin C, Armenise C, Port F, et al. Aubergine iCLIP reveals piRNA-dependent decay of mRNAs involved in germ cell development in the early embryo. *Cell Rep*. 2015;12: 1205–1216.
97. Post C, Clark JP, Sytnikova YA, Chirn G-W, Lau NC. The capacity of target silencing by *Drosophila* PIWI and piRNAs. *RNA*. 2014. pp. 1977–1986. doi:10.1261/rna.046300.114
98. Sytnikova YA, Rahman R, Chirn G-W, Clark JP, Lau NC. Transposable element dynamics and PIWI regulation impacts lncRNA and gene expression diversity in *Drosophila* ovarian cell cultures. *Genome Res*. 2014;24: 1977–1990.

99. Lim AK, Tao L, Kai T. piRNAs mediate posttranscriptional retroelement silencing and localization to pi-bodies in the *Drosophila* germline. *J Cell Biol.* 2009;186: 333–342.
100. Rouget C, Papin C, Boureux A, Meunier A-C, Franco B, Robine N, et al. Maternal mRNA deadenylation and decay by the piRNA pathway in the early *Drosophila* embryo. *Nature.* 2010;467: 1128–1132.
101. Levine MT, McCoy C, Vermaak D, Lee YCG, Hiatt MA, Matsen FA, et al. Phylogenomic analysis reveals dynamic evolutionary history of the *Drosophila* heterochromatin protein 1 (HP1) gene family. *PLoS Genet.* 2012;8: e1002729.
102. Levine MT, Vander Wende HM, Hsieh E, Baker EP, Malik HS. Recurrent gene duplication diversifies genome defense repertoire in *Drosophila*. *Mol Biol Evol.* 2016;33: 1641–1653.
103. Cañizares J, Grau M, Paricio N, Moltó MD. Tirant is a new member of the gypsy family of retrotransposons in *Drosophila melanogaster*. *Genome.* 2000;43: 9–14.
104. Fablet M, McDonald JF, Biémont C, Vieira C. Ongoing loss of the tirant transposable element in natural populations of *Drosophila simulans*. *Gene.* 2006;375: 54–62.
105. Kofler R, Nolte V, Schlötterer C. Tempo and mode of transposable element activity in *Drosophila*. *PLoS Genet.* 2015;11: e1005406.
106. Parhad SS, Yu T, Zhang G, Rice NP, Weng Z, Theurkauf WE. Adaptive evolution targets a piRNA precursor transcription network. *Cell Rep.* 2020;30: 2672–2685.e5.
107. Hoskins RA, Carlson JW, Wan KH, Park S, Mendez I, Galle SE, et al. The Release 6 reference sequence of the *Drosophila melanogaster* genome. *Genome Res.* 2015;25: 445–458.
108. Hu TT, Eisen MB, Thornton KR, Andolfatto P. A second-generation assembly of the *Drosophila simulans* genome provides new insights into patterns of lineage-specific divergence. *Genome Res.* 2013;23: 89–98.

109. Maheshwari S, Barbash DA. Cis-by-Trans regulatory divergence causes the asymmetric lethal effects of an ancestral hybrid incompatibility gene. *PLoS Genet.* 2012;8: e1002597.
110. Venken KJT, He Y, Hoskins RA, Bellen HJ. P[acman]: a BAC transgenic platform for targeted insertion of large DNA fragments in *D. melanogaster*. *Science.* 2006;314: 1747–1751.
111. Wickersheim ML, Blumenstiel JP. Terminator oligo blocking efficiently eliminates rRNA from *Drosophila* small RNA sequencing libraries. *Biotechniques.* 2013;55: 269–272.
112. Marioni JC, Mason CE, Mane SM, Stephens M, Gilad Y. RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. *Genome Res.* 2008;18: 1509–1517.
113. Martin M. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.journal.* 2011;17: 10–12.
114. Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol.* 2009;10: R25.
115. Gramates LS, Marygold SJ, Santos G dos, Urbano J-M, Antonazzo G, Matthews BB, et al. FlyBase at 25: looking to the future. *Nucleic Acids Res.* 2017;45: D663–D671.
116. Bao W, Kojima KK, Kohany O. Repbase Update, a database of repetitive elements in eukaryotic genomes. *Mob DNA.* 2015;6: 11.
117. Trapnell C, Pachter L, Salzberg SL. TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics.* 2009;25: 1105–1111.
118. Anders S, Pyl PT, Huber W. HTSeq - A Python framework to work with high-throughput sequencing data. *bioRxiv.* 2014. p. 002824. doi:10.1101/002824
119. Anders S, Huber W. Differential expression analysis for sequence count data. *Genome Biol.* 2010;11: R106.

120. Teixeira FK, Okuniewska M, Malone CD, Coux R-X, Rio DC, Lehmann R. piRNA-mediated regulation of transposon alternative splicing in the soma and germ line. *Nature*. 2017;552: 268–272.
121. Malone CD, Hannon GJ. Molecular evolution of piRNA and transposon control pathways in *Drosophila*. *Cold Spring Harb Symp Quant Biol*. 2009;74: 225–234.
122. Kofler R. Dynamics of Transposable Element Invasions with piRNA Clusters. *Mol Biol Evol*. 2019;36: 1457–1472.
123. Kelleher ES, Azevedo RBR, Zheng Y. The evolution of small-RNA-mediated silencing of an invading transposable element. *Genome Biol Evol*. 2018;10: 3038–3057.
124. Zhang S, Pointer B, Kelleher ES. Rapid evolution of piRNA-mediated silencing of an invading transposable element was driven by abundant de novo mutations. *Genome Res*. 2020;30: 566–575.
125. Kelleher ES. Reexamining the P-Element Invasion of *Drosophila melanogaster* Through the Lens of piRNA Silencing. *Genetics*. 2016;203: 1513–1531.
126. Ronsseray S, Lehmann M, Anxolabéhère D. The maternally inherited regulation of P elements in *Drosophila melanogaster* can be elicited by two P copies at cytological site 1A on the X chromosome. *Genetics*. 1991;129: 501–512.
127. Marin L, Lehmann M, Nouaud D, Izaabel H, Anxolabéhère D, Ronsseray S. P-Element repression in *Drosophila melanogaster* by a naturally occurring defective telomeric P copy. *Genetics*. 2000;155: 1841–1854.
128. Stuart JR, Haley KJ, Swedzinski D, Lockner S, Kocian PE, Merriman PJ, et al. Telomeric P elements associated with cytotype regulation of the P transposon family in *Drosophila melanogaster*. *Genetics*. 2002;162: 1641–1654.
129. Moon S, Cassani M, Lin YA, Wang L, Dou K, Zhang ZZZ. A Robust Transposon-Endogenizing Response from Germline Stem Cells. *Developmental Cell*. 2018. pp. 660–671.e3. doi:10.1016/j.devcel.2018.10.011

130. Kofler R, Senti K-A, Nolte V, Tobler R, Schlötterer C. Molecular dissection of a natural transposable element invasion. *Genome Res.* 2018;28: 824–835.
131. Karpen GH, Spradling AC. Analysis of subtelomeric heterochromatin in the *Drosophila* minichromosome Dp1187 by single P element insertional mutagenesis. *Genetics*. 1992;132: 737–753.
132. Thuy JLV, Le Vinh Thuy J, VandenBrooks JM, Angilletta MJ. Developmental plasticity evolved according to specialist–generalist trade-offs in experimental populations of *Drosophila melanogaster*. *Biology Letters*. 2016. p. 20160379. doi:10.1098/rsbl.2016.0379
133. Tobler R, Hermission J, Schlötterer C. Parallel trait adaptation across opposing thermal environments in experimental *Drosophila melanogaster* populations. *Evolution*. 2015;69: 1745–1759.
134. King EG, Merkes CM, McNeil CL, Hoofer SR, Sen S, Broman KW, et al. Genetic dissection of a model complex trait using the *Drosophila Synthetic Population Resource*. *Genome Research*. 2012. pp. 1558–1566. doi:10.1101/gr.134031.111
135. Bates D, Mächler M, Bolker B, Walker S. Fitting linear mixed-effects models using lme4. *Journal of Statistical Software*. 2015. doi:10.18637/jss.v067.i01
136. Zhang S, Kelleher ES. Targeted identification of TE insertions in a *Drosophila* genome through hemi-specific PCR. *Mobile DNA*. 2017. doi:10.1186/s13100-017-0092-1
137. O'Hare K, Rubin GM. Structures of P transposable elements and their sites of insertion and excision in the *Drosophila melanogaster* genome. *Cell*. 1983;34: 25–35.
138. Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. *Nat Methods*. 2012;9: 357–359.
139. Yin H, Lin H. An epigenetic activation role of Piwi and a Piwi-associated piRNA in *Drosophila melanogaster*. *Nature*. 2007;450: 304–308.

140. Walter MF, Jang C, Kasravi B, Donath J, Mechler BM, Mason JM, et al. DNA organization and polymorphism of a wild-type *Drosophila* telomere region. *Chromosoma*. 1995;104: 229–241.
141. Johnson M, Zaretskaya I, Raytselis Y, Merezhuk Y, McGinnis S, Madden TL. NCBI BLAST: a better web interface. *Nucleic Acids Research*. 2008. pp. W5–W9. doi:10.1093/nar/gkn201
142. Lee YCG, Langley CH. Long-term and short-term evolutionary impacts of transposable elements on *Drosophila*. *Genetics*. 2012;192: 1411–1432.
143. Lewis SH, Salmela H, Obbard DJ. Duplication and diversification of dipteran Argonaute genes, and the evolutionary divergence of Piwi and Aubergine. *Genome Biol Evol*. 2016;8: 507–518.
144. Heger A, Ponting CP. Evolutionary rate analyses of orthologs and paralogs from 12 *Drosophila* genomes. *Genome Res*. 2007;17: 1837–1849.
145. Obbard DJ, Welch JJ, Kim K-W, Jiggins FM. Quantifying adaptive evolution in the *Drosophila* immune system. *PLoS Genet*. 2009;5: e1000698.
146. Shpiz S, Ryazansky S, Olovnikov I, Abramov Y, Kalmykova A. Euchromatic transposon insertions trigger production of novel Pi- and endo-siRNAs at the target sites in the drosophila germline. *PLoS Genet*. 2014;10: e1004138.