Widespread gene duplication and adaptive evolution in the RNA interference pathways of the *Drosophila obscura* group

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ABSTRACT

Background: RNA interference (RNAi) related pathways provide defense against viruses and transposable elements, and have been implicated in the suppression of meiotic drive elements. Genes in these pathways often exhibit high levels of adaptive substitution, and over longer timescales show frequent gene duplication and loss—most likely as a consequence of their role in mediating conflict with these parasites. This is particularly striking for *Argonaute 2* (*Ago2*), which is ancestrally the key effector of antiviral RNAi in insects, but has repeatedly formed new testis-specific duplicates in the recent history of the *Drosophila obscura* group.

Results: Here we take advantage of publicly available genomic and transcriptomic data to identify six further RNAi-pathway genes that have duplicated in this clade of *Drosophila*, and examine their evolutionary history. As seen for *Ago2*, we observe high levels of adaptive amino-acid substitution and changes in sex-biased expression in many of the paralogs. However, our phylogenetic analysis suggests that co-duplications of the RNAi machinery were not synchronous, and our expression analysis fails to identify consistent male-specific expression.

Conclusions: These results confirm that RNAi genes, including genes of the antiviral and piRNA pathways, undergo frequent independent duplications and that their history has been particularly labile within the *Drosophila obscura* group. However, they also suggest that the selective pressures driving these changes have not been consistent, implying that more than one selective agent may be responsible.

Keywords: gene duplication, RNAi, RNA interference, adaptive evolution, neofunctionalization

Introduction

Gene duplication is an important process in molecular evolution, providing raw genetic material for evolutionary innovation. The subsequent evolutionary dynamics following gene duplication are often described in terms of two alternative models, 'neofunctionalization' and 'sub-functionalization' [1]. Under neofunctionalization, the functional redundancy following duplication provides relaxed selective constraint, and allows new mutations to accumulate through genetic drift. Most such mutations will reduce the functionality of the gene (resulting in pseudogenization), but some paralogs can be selected for novel or derived functions. Under sub-functionalization, the duplicates independently accumulate mutations that allow them to specialise in a subset of ancestral functions of a pleiotropic gene. Neo-functionalization leads to asymmetrical evolutionary rates among paralogs (with faster evolution in paralogs that gain derived function), whereas equal rates are expected for the latter [2]. It has been suggested that both processes have played an important role in the rapid evolution of RNA interference-related pathways, including the long- and short-term evolutionary history of the Argonautes, the effectors of RNAi [3–5].

The RNAi-related pathways comprise a range of small-RNA mechanisms best known for their roles in mediating the control of gene expression, antiviral responses, and defence against mobile genetic elements (respectively: the miRNA pathway; Dicer-1 and Argonaute-1 in insects [6]; the siRNA pathway; Dcr-2 and Argounate 2 in insects [7]; and the piRNA pathway; piwi-family Argonaute AGO3 and Piwi/Aub in insects [8, 9]). In addition, RNAi-related pathways have been implicated in a variety of biological processes, such as the control of dosage compensation [10–12] and the suppression of genetic drive [13–18], among others. Several genes involved in the defensive piRNA

and siRNA pathways, but not the miRNA pathway, display elevated rates of adaptive protein evolution. This is best studied in *Drosophila* [19–21], but is also detectable in other insects [22]. It has been hypothesised that this is a consequence of parasite-mediated 'arms-race' coevolution [20, 23], either through conflict with parasite-encoded immune suppressors—as widely seen in RNA viruses [24]— or in the case of the piRNA pathway, through selection for 're-tuning' suppression mechanisms [25].

Adaptive evolution of RNAi pathways is also partly reflected in the gain, loss, and functional divergence of Argonaute-family duplications [26]. For example, within the Drosophilidae—an important model for RNAi-related pathways of animals—Piwi has been duplicated in the lineages leading to *Phortica variegata* and *Scaptodrosophila deflexa* [3], and *Ago2* has been duplicated in those leading to *S. deflexa*, *D. willistoni*, *D. melanogaster* (where only one paralog remains – the canonical *Ago2*) and *D. pseudoobscura* [4]. This is particularly striking in the *Drosophila obscura* species group, which has experienced at least 6 independent duplications of *Ago2* over the last 20 million years, with all but one of the resulting duplicates becoming testis-specific, and most displaying evidence of recent and/or ongoing positive selection [4].

Very recently it has been noted that several accessory components of the siRNA and piRNA pathways have also been duplicated in *D. pseudoobscura*, including *armitage*, *asterix*, *cutoff*, *maelstrom*, *tejas* and *vreteno* [22]. In *D. melanogaster*, these proteins are engaged in a number of roles in the piRNA pathway (**Table 1**). Here we use publicly available data to reconfirm the history and expression of *Ago2* in the obscura group, and to test whether duplications in the other genes also show male-specific expression, whether they are contemporaneous with those of *Ago2*, and whether they too show strong signatures of adaptive protein evolution. We find no clear pattern of these duplications being coincident with *Ago2* duplications, but both

asterix and *cutoff* duplications display increased sexual dimorphism relative to their ancestral copies, through decreased female expression. In addition, several of the gene duplicates show evidence of adaptive protein evolution in *D. pseudoobscura*, including both copies of *cutoff*, the ancestral copy of *asterix*, and the new duplicates of *tejas*, *maelstrom* and *vreteno*.

RESULTS

Obscura group *Argonaute 2* are duplicated and show male-biased expression

The *Drosophila obscura* group has experienced multiple duplications of *Ago2* and it has previously been shown that these are associated with positive selection and testis-specific expression [4]. Here we reanalyzed the expression patterns and evolutionary history of these genes using publicly available RNAseq and genomic data, additionally including newly available genomic sequences from *D. algonquin*, *D. athabasca*, *D. bifasciata* and *D. miranda*. In contrast to the previous qPCR analysis that failed to identify strong expression of the ancestral copy in *D. pseudoobscura* (*Ago2d* [4]), we found that all the *Ago2* homologs in *D. pseudoobscura* were detectable at a high level in RNAseq data, and that that all show significant male-bias (**Figure 1**). The *Ago2d* expression detected here is unlikely to be an artefact of cross-mapping between paralogs as we observed the reads that mapped uniquely across the gene. The male bias was largest for *Ago2e*, where expression in males is approximately 1000-fold higher than females (pMCMC<0.001; **Figure 1**), and smallest in *Ago2c* and the ancestral copy *Ago2d*, consistent with the *ca.* two-fold enrichment of the single copy of *Ago2* in male *D. melanogaster*. We also confirmed that *D. miranda*, a close relative of *D. pseudoobscura* that has not previously been analyzed, displayed a qualitatively similar pattern among those paralogs represented (**Figure 1**). In *D. obscura* and we

found the ancestral copy (*Ago2a*) again showed slightly, but marginally significantly, higher expression in males (pMCMC=-0.014), but that other *Ago2* proteins showed a strong male biased expression, with the largest effect for *Ago2f*, where male expression was 2000-fold higher (**Figure 1**; pMCMC<0.001).

Six piRNA pathway genes are duplicated, and *asterix* and *cutoff* duplicates show increased male-bias in their expression

Palmer *et al.* [22] recently identified six accessory piRNA pathway genes that have also experienced duplication in the obscura group (**Additional file 1 Table S1**). We could locate the duplicates for all genes in *D. pseudoobscura*, except for *armitage* where we instead identified a duplicate in the affinis subgroup but not in the obscura or subobscura subgroups. Where new chromosomal locations could be determined by synteny in *D. pseudoobscura*, we found that *cutoff*, *maelstrom* and *vreteno* were duplicated from an autosome to the X chromosome, *asterix* duplicated from the X chromosome to an autosome, and *tejas* duplicated between autosomal locations. Two duplicates (*asterix* and *tejas*) lack introns, suggesting they are retro-transcribed copies created through an mRNA intermediate.

Using public RNAseq data from *D. pseudoobscura*, *D. miranda*, and *D. obscura*, we found that all of the gene duplicates were expressed (**Figure 2**). *Armitage*, which was not duplicated within the newly examined lineages for which RNAseq data were available, did not show strong sex-biased expression. Similarly, *tejas*, *maelstrom*, and *vreteno* were not strongly differentially expressed between the sexes, and nor were their duplicates in *D. pseudoobscura* and *D. miranda*. In contrast, both *asterix* and *cutoff* duplicates displayed substantially reduced expression in females and slightly increased expression in males (**Figure 2**). For example, as previously reported from

qPCR analysis [27] the paralog of *asterix* in *D. pseudoobscura* displays ca. 1000-fold higher expression in males than females. In both *D. pseudoobscura* and *D. miranda*, those genes with overall strongly increased male-biased expression (*Argonaute 2*, *asterix*, *cutoff,* and their paralogs) had the highest expression in testis, and had reduced their expression in ovaries (**Additional file 2 Figure S1**).

Adaptive amino-acid substitutions are generally more common in the duplicates

Using population genetic data from *D. pseudoobscura*, and *D. miranda a*s an outgroup, we used the McDonald-Kreitman framework and a maximum-likelihood extension to estimate the rate of adaptive substitution in protein sequences, and to test whether this was different between the ancestral and duplicated copies [28, 29]. Treating genes individually, we found evidence for positive selection acting on at least one paralog for each of the genes except *asterix* and *Ago2c* ($p < 0.05$; **Additional file 3 Table S2**). Among the ancestral copies, only *cutoff* displayed evidence of positive selection. We then tested whether the paralogs generally showed a different pattern of selection to the ancestral copies by dividing the genes into two classes (6 ancestral copies and 8 paralogs) and comparing the likelihood of models that allowed the classes to differ in the adaptive rate α (**Table 2**) [29]. The best supported model allowed α to differ between ancestral and duplicate copies (Akaike weight: 0.81), and the second best supported model was that in which α=0 for the ancestral copies (Akaike weight: 0.19), providing overall evidence that the paralogs have experienced more adaptive protein evolution. In the best-supported model, the α was estimated to be 0.68 for the duplicate group, which more than three times larger than the ancestral group (0.20). In case segregating weakly-deleterious variants had led to a downward bias in estimates of α, we repeated this analysis excluding all alleles with a minor allele

174 frequency <0.125 [30], although this reduced power to the extent that few genes
175 remained individually significant (**Additional file 6 Table S3**). We also repeated the
176 analysis with a larger dataset PRJNA326536 [31] (**Additional file 6 Table S3**), and
177 obtained qualitatively similar results (R^2=0.946 for α estimate between the analyses;
178 the second dataset, while larger, is less suitable for analysis as only the third
179 chromosome is a direct sample from a wild population).

180 Gene duplications were unlikely to be contemporaneous

181 Given the multiple duplications of *Ago2* and the piRNA pathway components in the
182 obscura group, we hypothesized that some duplications may have occurred near-
183 simultaneously, duplicating whole components of a pathway together. We therefore
184 used relaxed-clock phylogenetic methods to estimate the relative timings of each
185 duplication. In agreement with the previous analysis of Ago2 [4], we found that the
186 duplications giving rise to *Ago2e* and *Ago2f* predated the split between the obscura
187 and pseudoobscura subgroups, with a subsequent loss of *Ago2f* from the
188 pseudoobscura subgroup (**Figure 3**). In contrast, we found that duplications in five of
189 the other six genes unambiguously occurred after the obscura/pseudoobscura split,
190 with the timing of duplication in *maelstrom* being uncertain. Briefly, *armitage* displayed
191 a single duplication shared by members of the affinis subgroup, *asterix* and *tejas* a
192 single duplication each in the lineage leading to *D. pseudoobscura* (which were
193 subsequently lost in the affinis subgroup), *cutoff* a single duplication recently in the
194 pseudoobscura subgroup, and *vreteno* a single duplication at the base of the obscura
195 group (**Figure 4**). For *maelstrom*, the maximum clade credibility tree suggests
196 duplication occurred very slightly prior to this split, followed by subsequent loss of one
197 paralog the obscura subgroup (**Figure 4**). However, this was poorly supported, and
198 similar pattern to the others genes may be more parsimonious. We used the posterior

distributions of split times, relative to the divergence time of the obscura and pseudoobscura subgroups, to infer whether or not duplications occurred at approximately the same time (**Figure 5**). Although the small amount of information available from single genes made relative timings highly uncertain, it is clear that few of the *Ago2* duplications could have been concurrent with the piRNA-pathway duplications (**Additional file 5 Figure S2**). However, the recent and rapid duplications within the piRNA could have been concurrent, with *vreteno*, *tejas, maelstrom* and *asterix* not differing significantly, all having duplicated very close to the split between *D. obscura* and *D. pseudoobscura* (posterior overlap >0.1 in each case; **Additional file 5 Figure S2**).

DISCUSSION

Although four of the six piRNA pathway duplicates did not display altered tissue specificity compared to the ancestral copy, *asterix* and *cutoff* both became significantly more male biased, as did each of the *Ago2* duplicates [4]; **Figure 1**, **Figure 2**). In each case, this was due to higher (or exclusive) expression in the testis. The duplicated genes also showed higher rates of adaptive amino acid substitution, together and individually, whereas only two (*asterix* and *armitage*) displayed evidence of positive selection when single-copy in *D. melanogaster* (**Additional file 6 Table S3**).

This new tissue specificity and the rapid evolution of duplicated copies broadly suggest that gene duplication in these pathways may be associated with functional diversification through neofunctionalization, for example by testis-specific selective pressure. Three main selective pressures seem likely candidates to have driven this. First, given the role of *Ago2* in antiviral defense in *Drosophila* [7], and the role of the piRNA pathway in antiviral defense in mosquitoes [32], it is possible that these

duplications have specialized to a virus that is active in the male germline, such as *D. obscura* and *D. affinis* Sigmaviruses [33]. Second, given the role of all of these genes in the suppression of transposable elements (TEs), their evolution may have been shaped by the invasion of TEs that are more active in testis, as seen for Penelope [34] and copia [35]. Such a 'duplication arms-race' in response to TE invasion is thought to occur in mammals, where repeated duplications of KRAB-ZNF family are selected following the invasion of novel TEs, and subsequently provide defence [36, 37]. Alternatively, duplicates may quantitatively enhance the pre-existing response to TEs, as suggested for another rapidly-evolving piRNA-pathway component, Rhino [38].

The third, and arguably most compelling hypothesis, is that selection is mediated by conflict with meiotic drive elements, such as sex ratio distorting X-chromosomes [39, 40]. Most directly, meiotic drive elements are common in *Drosophila*, and RNAi-related pathways have been widely implicated in their action and suppression [15, 16, 18]. In addition, sex-chromosome drive is widespread in the *Drosophila obscura* group. X chromosome drive was first described in *D. obscura*, and has also been reported in *pseudoobscura*, *persimilis*, *affinis*, *azteca*, *subobscura* and *athabasca* [39] and is mediated through a testis-specific function (Y-bearing sperm have reduced function). Finally, a testis-specific class of hairpin (endo) siRNAs is required for male fertility in *D. melanogaster* [41], testes-restricted clustered miRNAs show rapid evolutionary turnover and are represented in large numbers in *D. pseudoobscura* [42], and suppression of sex-specific duplicates of S-Lap1 via a small-RNA mechanism has very recently been implicated in the meiotic drive mechanism of *D. pseudoobscura* [17]. In this context, it is also interesting to note that *Ago2* is involved in directing heterochromatin formation in *Drosophila* dosage compensation [10–12], and that in *D.*

247 *melanogaster* the sex-ratio distorting *Spiroplasma* achieves male-killing through the
248 disruption of dosage compensation, although this acts at the embryonic stage [43].

249 Nevertheless, in the absence of mechanistic studies, this remains highly speculative.
250 Testis is generally more permissive to gene expression and testis-specific expression
251 may be a transient state (i.e. the "Out of Testis Hypothesis" [44]). In addition, the
252 application of MK-like analyses to paralogs is inherently flawed [1], as the MK
253 framework implicitly assumes that the selective regime has been consistent across all
254 (group and outgroup) sequences analyzed. If gene duplicates experience an early but
255 transient period of relaxed constraint, a high proportion of the amino-acid fixations may
256 have occurred as a result of genetic drift that is no longer detectable from current
257 patterns of polymorphism.

258 Methods

259 Sequence collation and paralog identification

260 The full-length sequences for 7 RNA inteference genes; *armitage* (*armi*), *asterix* (*arx*),
261 *cutoff* (*cuff*), *tejas (tej)*, *vreteno* (*vret*), *maelstrom* (*mael*), and *Argonaute 2* (*Ago2*) from
262 12 obscura group species were identified using tBLASTn (BLAST+ 2.6.0) [45] with a
263 local BLAST database (see below for the details of the construction of local genomic
264 database). Known gene sequences from *D. pseudoobscura* and *D. melanogaster*
265 were used as a query with a stringent e-value threshold (1e-40). Genes were inferred
266 to have been duplicated when BLAST indicated that there were multiple full-length hits
267 located in different genomic regions. The sequences were manually inspected, introns
268 removed and the coding frame identified using Bioedit v 7.2 [46]. Genes in *D.*
269 *pseudoobscura* were classified as ancestral or duplicate copies based on the syntenic

orthology with *D. melanogaster* using Flybase Genome Browser [47]. High quality genomes are not available for other members of the obscura groups, and in those cases ancestral/derived status was assigned based on homology with *D. pseudoobscura*. To provide a comprehensive overview of the evolution of the RNAi paralogs, we included 24 *Drosophila* species outside of *obscura* group with assembled genomes already available in public databases. The Flybase and NCBI tblastn online portal were used to identify the target genes with queries from *D. melanogaster* or closely related species.

Five obscura group species had assembled genomes at the time of this study: *D. pseudoobscura* (assembly Dpse_3.0 [48]), *D. miranda* (assembly DroMir_2.2 [49] [50]), *D. persimilis* (assembly dper_caf1 [51]), *D. affinis* (Drosophila affinis Genome Release 1.0 [52]) and *D. lowei* (Drosophila lowei Genome Release 1.0 [52, 53]) and in these cases the genome was directly used for local BLAST database. For four species (*D. obscura*, *D. subobscura*, *D. subsilvestris*, *D. tristis*) we used de novo assembled transcriptomes based on paired RNA-seq reads data from wild-collected males [54] (Accession: PRJNA312496). Assembly was performed using Trinity [55] with '--trimmomatric' and otherwise default parameters, and the assembled transcriptome was searched locally using BLAST. For three other species: *D. athabasca*, *D. Algonquin* [56] (Accession: PRJNA274695) and *D. bifasciata* (Accession: PRJDB4817), only unassembled genomic reads were available. For these species we applied a targeted assembly approach as follows: (i) reads that had local similarity with all known duplicated RNAi proteins were identified using Diamond [57] with relaxed e-value of 1; (ii) hits from Diamond were then retained and used for assembly using Spades v3.10.1 [58]; and (iii) scaffolds produced by Spades were then used as references in local BLAST database.

Phylogenetic analysis and the relative timing of duplications

Bayesian relaxed clock trees were used to infer the evolutionary relationship among paralogs. First, the sequences were aligned as translated nucleotide in Clustal W [59] with default parameters. Regions with ambiguous alignment were identified and removed manually by eye. A total of 7 gene trees were then inferred using Beast v1.7.0 [60]. Inference used a relaxed clock model with an uncorrelated lognormal distribution among branches, and an HKY substitution model with empirical base frequencies and rate variation among sites was modelled as a gamma distribution with four categories. The site model allowed for third codon position to have different substitution model from the other positions.

The trees were scaled by setting the time to most recent common ancestor of the *D. obscura* group to have lognormal distribution with a data-scale mean of 1, and a very small standard deviation of 0.01. This had the advantage of scaling all duplications to the same relative timescale, while allowing different genes and different paralogs to vary in their rate. To record the posterior ages of duplication, we specified the ancestral and duplicated genes as a distinct taxon set. The Monte Carlo Markov Chain analysis was run for at least 100 million states and posterior sample was recorded every 10000 states. Log files were then inspected in Tracer v1.6 [61] for parameter stationarity, and adequate sampling as indicated by an effective sample size over 200. Finally, 25% of initial trees were discarded as burn-in, and maximum clade credibility trees were summarized using Tree Annotator. Parameter MCMC files were processed using a custom R script [62] to infer the posterior distribution the age of duplication for each gene and to quantify the degree overlapping between these age distributions.

Differential expression analysis of the duplicated RNAi genes

For this analysis, we used obscura group transcriptome datasets available in EBI ENA (European Nucleotide Archive, http://www.ebi.ac.uk/ena) and DDBJ (DNA DataBank of Japan, http://www.ddbj.nig.ac.jp/) that included the sex and tissue annotation. The datasets comprised 163, 42 and 34 RNA-seqs datasets of *D. pseudoobscura, D. miranda* and *D. obscura* respectively; Bioproject: DRA004463, PRJEB1227 [63], PRJNA226598, PRJNA219224 [64], PRJNA326536 [31], PRJNA74723, PRJNA321079, PRJNA291085 [65], PRJNA268967 [66]. Since our main interest was the comparison expression between sex, but not its absolute expression value, we a performed a simple read-counting analysis. In outline, each RNA-seq dataset was mapped to the full-length CDS using Bowtie2 v2.3.2 [67] with mode '--very sensitive' and otherwise default parameters. The reads mapped to reference were counted using combination of SAMtools view flag -F 4 and SAMtools idxstats v1.4 [68]. The count data were then normalized by gene length and read depth, where it was then scaled relative to the expression of RpL32. To determine the statistical significance of difference gene expression, generalised linear mixed models were fitted using R package MCMCglmm [69] with sex as fixed effect and tissue as a random effect, and log-transformed normalised expression as the response variable. The natural logarithm transformation ($\log_e$) was used to reduce the skewness of the distributions. To allow for zero value for non-expressed genes, the genes with read count 0 was replaced with 1.

$$\mathbf{Y} \sim \boldsymbol{\mu} + \mathbf{sex} + \mathbf{tissue}\ (\mathbf{random}) + \boldsymbol{\varepsilon}$$

Where Y is $\log_e$ transformed normalized expression data (response variable), μ is mean of $\log_e$ transformed expression and ε is residual error. The random effects

(tissue) and the residual were assumed to be distributed multivariate normal with mean 0 and uncorrelated covariance matrix MVN (0, $\mathbf{I}\sigma^2$). Sex was modelled as a factor with 2 variables (male-female) and tissue contained 13 variables of different tissue.

Population Genetic Analysis of the RNAi Duplicated Genes

We used the McDonald-Krietman test [28] to compare the rate of adaptive evolution between ancestral and duplicate genes using polymorphism data from publicly-available sequencing datasets: Pseudobase (12 strains of *pseudoobscura*, Accession list: SRP007802 [53]) and 12 strains *D. miranda* (Bioproject: PRJNA277849 [70]).

Genomic reads for each strain were mapped to the genomic reference using Bowtie2 with '--very-sensitive' mode and otherwise default parameters and reads mapped to the genes of interest were extracted using SAMtools view (flag -F 4). Duplicate reads were marked using MarkDuplicates (Picard Tools [71]). To reduce the excessive variants surrounding indel, we then applied GATK IndelRealigner [71], which discards the original mapping and performs local-realignment around indel. The output was then sorted and indexed and the BAM file was used for 'mpileup' variant calling (SAMtools v1.4 [72]). The output VCF files were then filtered to only include SNP (GATK SelectVariants [71]), and variants that were covered by less than five reads were masked with 'N' (undetermined bases, --snpmask GATK v3.5 [71]). The variant files were then converted to FASTA format using GATK FastaAlternateReferenceMaker, which replaced genomic reference with variants defined in VCF files [73] and output the heterozygous calls with IUPAC ambiguous code. Finally, FastPHASE [74] was used to generate pseudo-haplotypes, although haplotype information was not utilized by the analysis.

MK tests were performed for each gene on *D. pseudoobscura-D miranda.* DNAsp v5.0 [75] was used to estimate the statistics for the MK test and Fisher's exact test was used to calculate the statistical significance for single-gene analyses. Genes were then grouped into ancestral and duplicate genes, and a cross-gene analysis was performed using a maximum likelihood extension of the MK test [29]. Five different models were fitted that differed in the constraint of α (proportion of non-synonymous subtitutions estimated to be adaptive), and the relative support between models was compared using Akaike Weights.

List of Abbreviations

Ago2: Agronaute 2 **armi**: armitage **arx**: asterix **BAM**: Binary Alignment Map **BLAST**: Basic Alignment Search Tool **cuff**: cutoff **GATK**: Genome Analysis Toolkit **HKY**: Hasegawa, Kishino and Yano model **mael**: maelstrom **MCMC**: Monte Carlo Markov Chain **MK:** McDonald-Kreitman test **RNAi**: RNA interference **SNP**: Single Nucleotide Polymorphism **TE:** Transposable Elements **tej**: tejas **VCF**: Variant Call Format **vret**: vreteno

Declarations

Ethics approval and consent to participate

Not applicable

Consent to publication

Not applicable

Availability of data and material

Fasta alignment (both for phylogenetic and MK analysis) and raw expression data are available via Figshare (DOI: 10.6084/m9.figshare.7145720).

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

DJO and DC conceived the study and designed the analysis, DC analyzed the data and wrote the first draft of the manuscript. Both authors read and approved the final manuscript.

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Figures

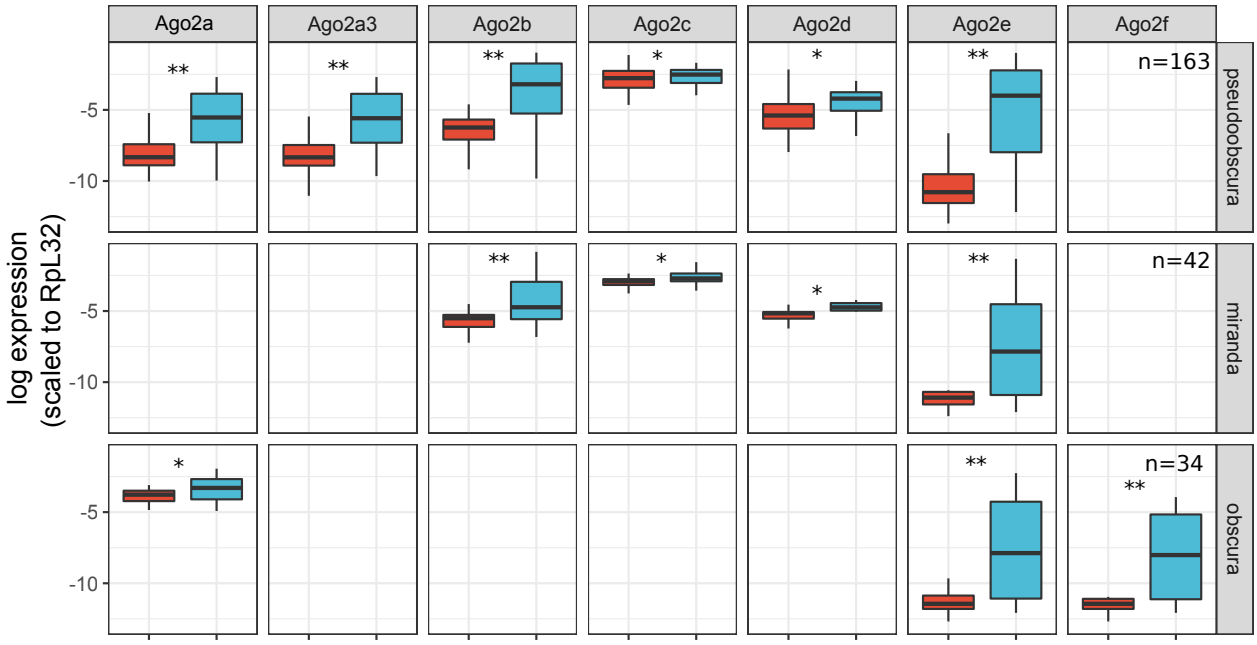


Figure 1 Expression Profile of Argonaute 2

Plots show the difference in expression between female (red) and male (blue) flies, based on public RNAseq data, normalized to rpL32 and plotted on a natural log scale. The significance of differences between the sexes was assessed using a linear model fitted with MCMCglmm and is denoted by asterisks: * 0.001 < pMCMC < 0.05; ** pMCMC <= 0.001). Sample size (n) represents the number of RNAseq datasets used (combined across tissues). *Ago2d* is the ancestral copy in Dpse and Dmir, *Ago2a* is the ancestral copy in *D. obscura* and *Ago2a* is recently duplicated in Dpse become *Ago2a1* (*Ago2a*) and *Ago2a3*.

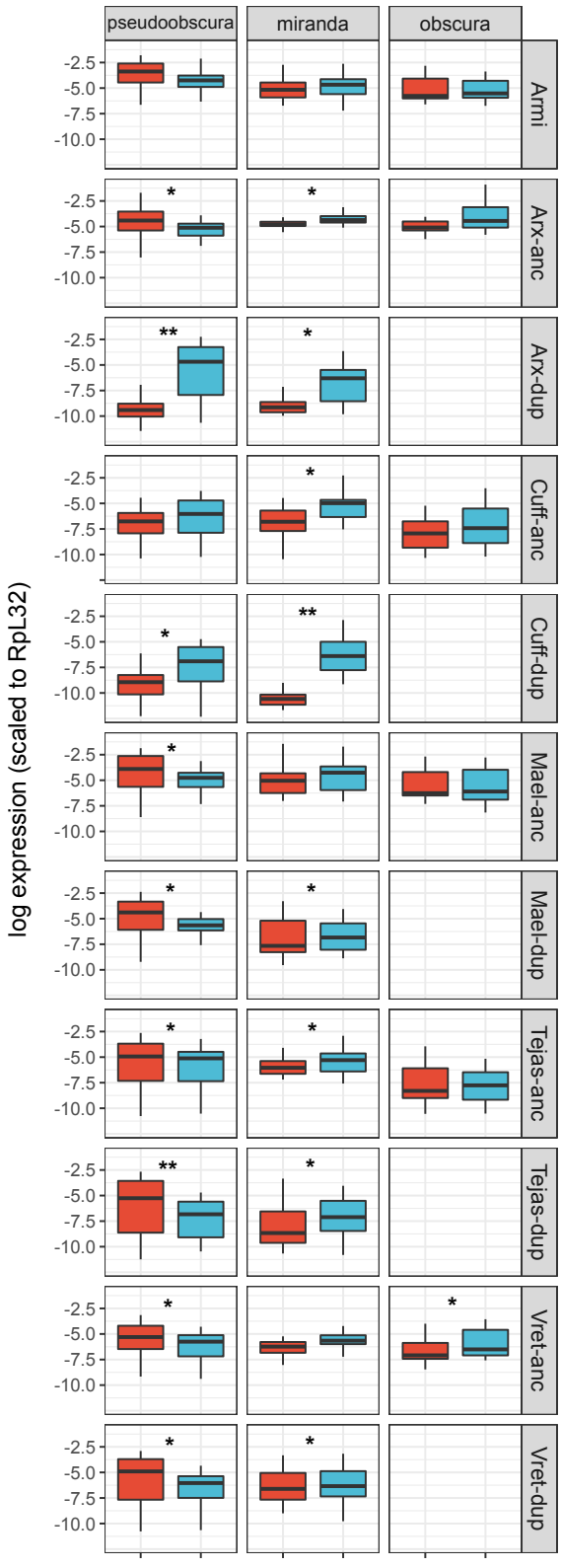


Figure 2 The expression profile of RNAi-accessory protein genes

Plots show the expression pattern between sex (male: blue, female:red) for genes other than *Ago2*; 'anc' ancestral copy, 'dup' duplicate copy as inferred by synteny. The y-axis is the natural log of normalized expression. The significance between sexes is denoted by * (0.001 < pMCMC < 0.05) and ** (pMCMC < 0.001). Sample sizes are the same as **Figure 1**.

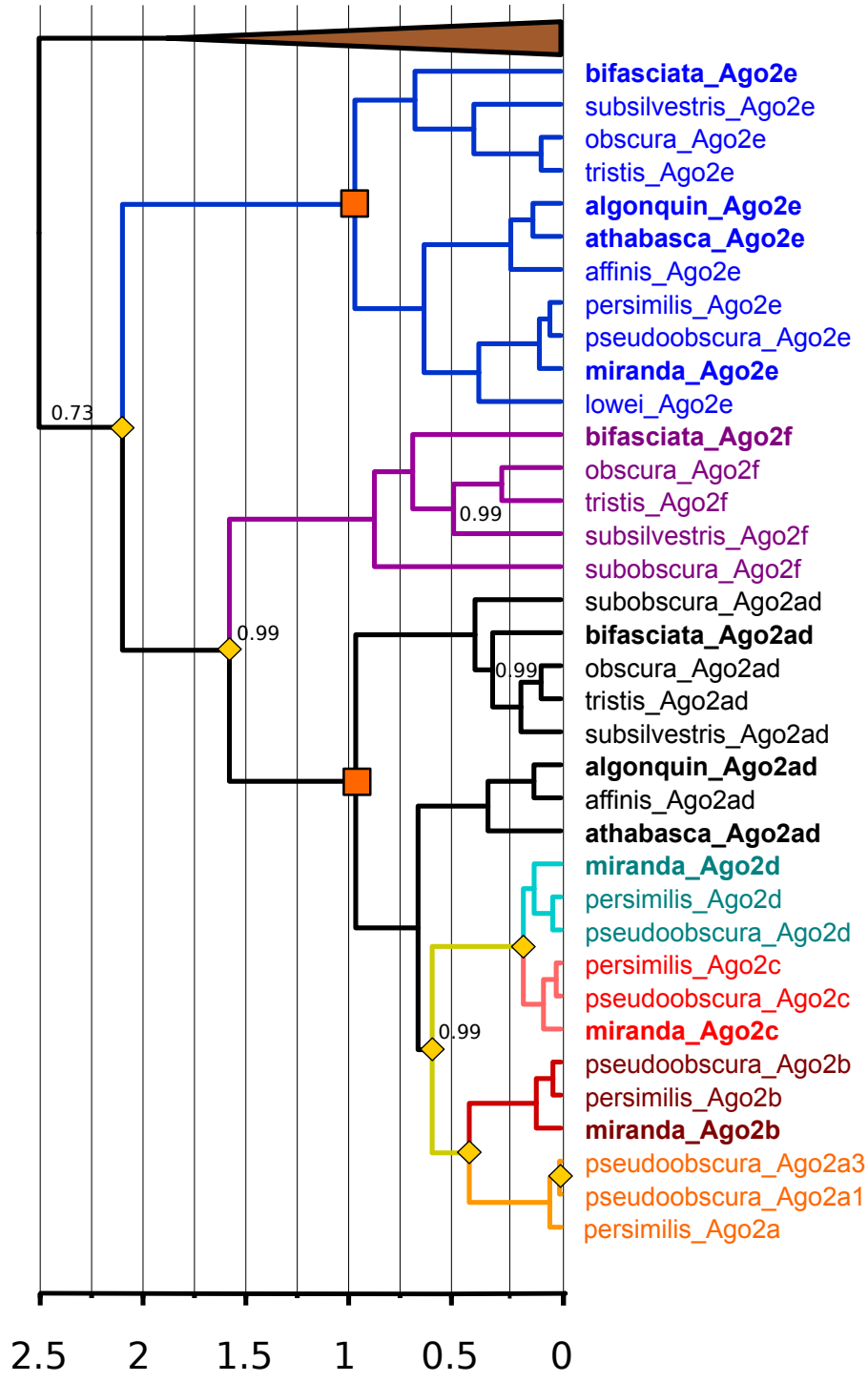
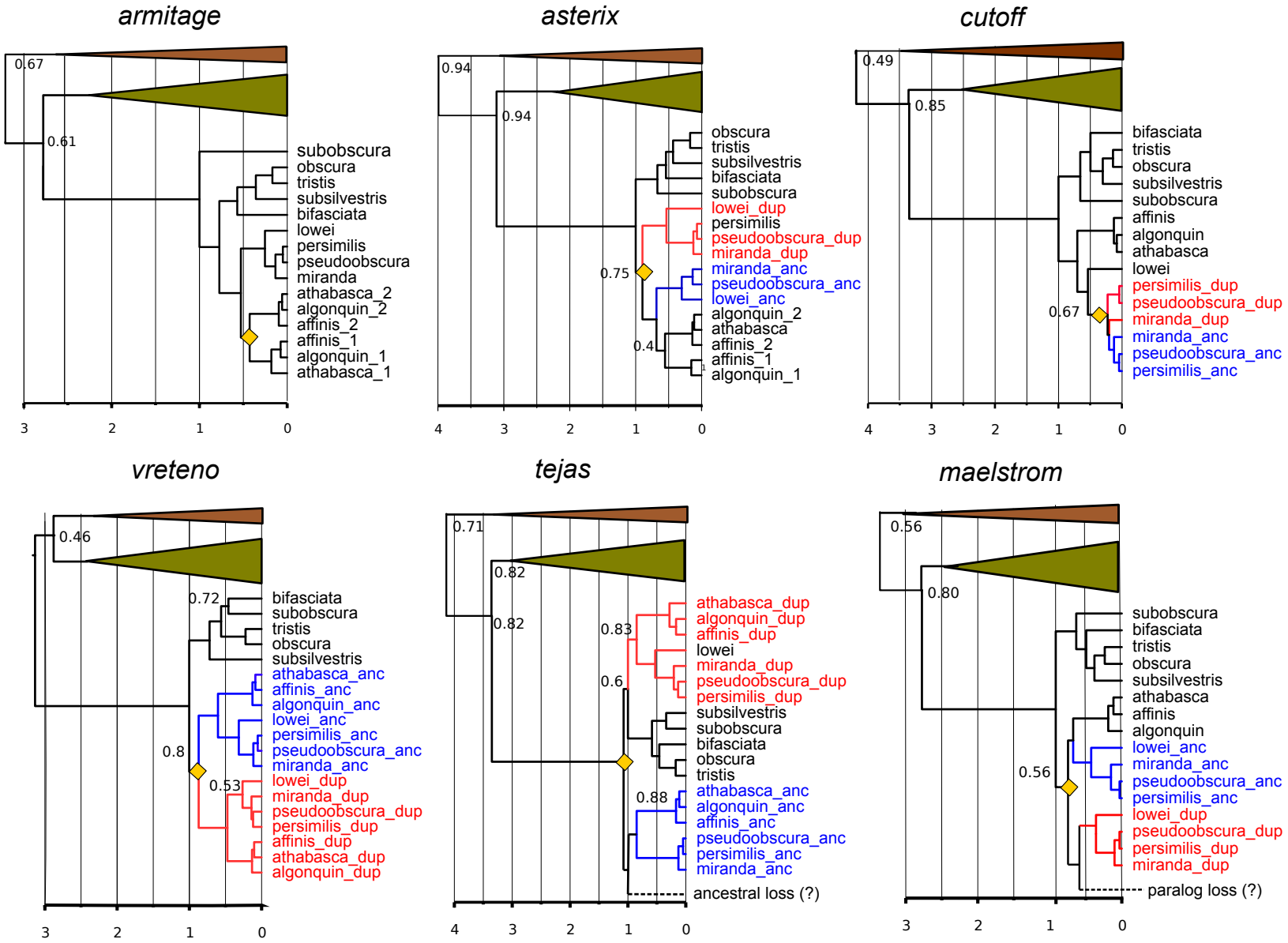


Figure 3 Bayesian Relaxed Clock Gene Tree for Argonaute2

The duplication events are marked by yellow diamonds, species other than the obscura group are collapsed (brown triangle), and paralog clades are colored. Bayesian posterior supports are only shown for the nodes with support less than 1. Genes not previously included in the analysis of [4] are marked in bold. Time is expressed relative to the split between the obscura and subobscura subgroups (orange boxes), which was constrained to be 1 using a strongly informative prior.

Figure 4 Bayesian Relaxed Clock Trees for 6 RNAi accessory protein genes
Ancestral genes are marked by bold blue, duplicates in bold red. Yellow diamonds indicate duplication events. Species other than *obscura* group are collapsed (green triangle; melanogaster group and brown triangle: other *Drosophila* species). Posterior Bayesian Supports are only shown in the nodes with support less than 1. Duplicated genes which could not be assigned as ancestral or duplicate is marked by _1 or _2. Scale axis is in the time relative to the *obscura* speciation, which was set to 1.


armitage
0.67
0.61
subobscura
obscura
tristis
subsilvestris
bifasciata
lowei
persimilis
pseudoobscura
miranda
athabasca_2
algonquin_2
affinis_2
affinis_1
algonquin_1
athabasca_1
3
2
1
0
asterix
0.94
0.94
obscura
tristis
subsilvestris
bifasciata
subobscura
lowei_dup
persimilis
pseudoobscura_dup
miranda_dup
0.75
miranda_anc
pseudoobscura_anc
lowei_anc
algonquin_2
athabasca
affinis_2
0.4
affinis_1
algonquin_1
4
3
2
1
0
cutoff
0.49
0.85
bifasciata
tristis
obscura
subsilvestris
subobscura
affinis
algonquin
athabasca
lowei
persimilis_dup
pseudoobscura_dup
0.67
miranda_dup
miranda_anc
pseudoobscura_anc
persimilis_anc
4
3
2
1
0
vreteno
0.46
0.72
bifasciata
subobscura
tristis
obscura
subsilvestris
athabasca_anc
affinis_anc
algonquin_anc
lowei_anc
persimilis_anc
0.8
pseudoobscura_anc
miranda_anc
0.53
lowei_dup
miranda_dup
pseudoobscura_dup
persimilis_dup
affinis_dup
athabasca_dup
algonquin_dup
3
2
1
0
tejas
0.71
0.82
0.82
0.83
athabasca_dup
algonquin_dup
affinis_dup
lowei
miranda_dup
0.6
pseudoobscura_dup
persimilis_dup
subsilvestris
subobscura
bifasciata
obscura
tristis
0.88
athabasca_anc
algonquin_anc
affinis_anc
pseudoobscura_anc
persimilis_anc
miranda_anc
ancestral loss (?)
4
3
2
1
0
maelstrom
0.56
0.80
subobscura
bifasciata
tristis
obscura
subsilvestris
athabasca
affinis
algonquin
lowei_anc
miranda_anc
0.56
pseudoobscura_anc
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miranda_dup
paralog loss (?)
3
2
1
0

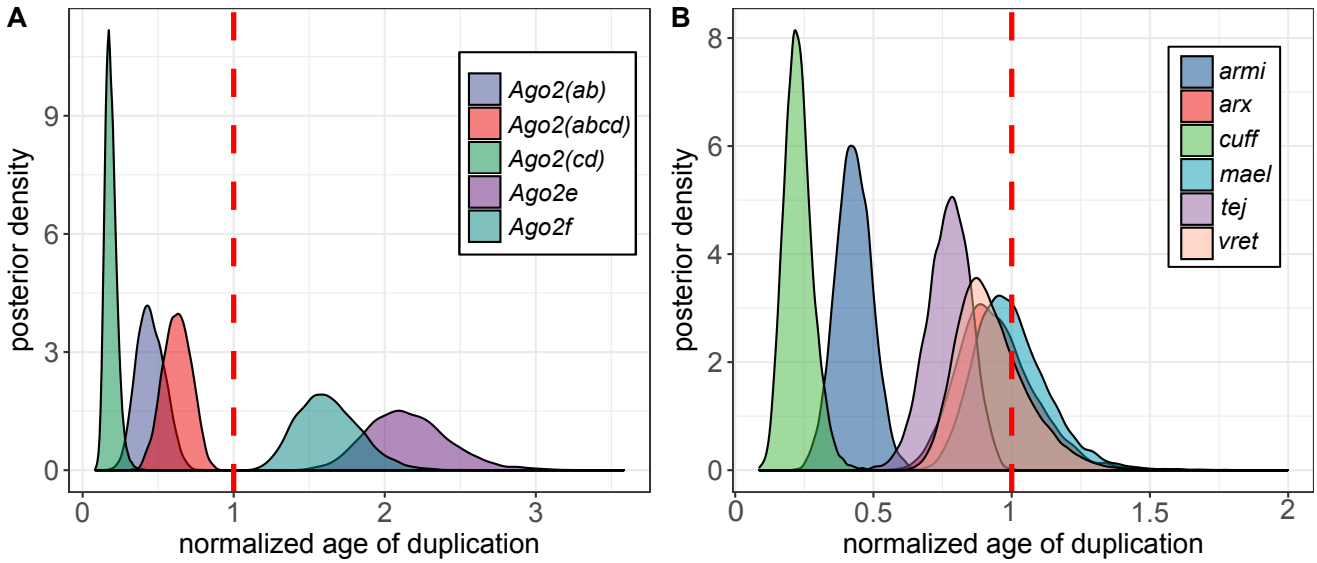


Figure 5 Density plot for posterior distributions of the duplication age

The MCMC posterior of the age of duplication node after 25% burn-in. (**A**) *Argounate 2* and (**B**) RNAi accessory proteins. The broken red line denotes speciation event in *obscura* group which was normalised to be 1.

Tables

Table 1 The details of RNAi accessory genes duplicated in the obscura group as reported by Palmer *et al.* [22]
*The tissue gene expression in *Dmel* is based on the FlyAtlas2 [76]. We report tissues with enrichment > 0.4.

Gene	Involvement in piRNA pathway	Function of the protein product	Tissue expression in *Dmel*	Reference
cutoff (*cuff*)	piRNA transcription	Forms a complex with Rhino-Deadlock-Cutoff (Rhi-Del-Cuff) to protect uncapped non-canonical (dual-strand cluster) piRNA transcript from degradation, splicing and transcription termination	testis	[77]
vreteno (*vret*)	piRNA biogenesis	A Tudor-domain protein which essential for an early primary piRNA processing	larval brain, adult female salivary gland, ovary, testis	[78]
armitage (*armi*)	piRNA biogenesis	A RNA helicase which unwinds the piRNA intermediates before loading into Piwi	ubiquitously expressed	[79] [80]
tejas *(tej)*	Secondary piRNA production (Ping-pong cycle)	A Tudor-domain protein which physically interact with *Vas*, *Spn-E* and *Aub* for a proper ping-pong cycle in the *nuage*	testis, accessory glands, adult female salivary gland, ovary	[81]
asterix (*arx*)	TGS (Transcriptional Gene Silencing)	A zinc-finger protein which directly interacts with Piwi to scan and identify the transposon transcriptions as target for histone modifications	ubiquitously expressed	[82] [83]
maelstrom (*mael*)	TGS	Act downstream of Piwi to establish histone modification and prevent the spreading of the silencing marker to the surrounding genes	brain, testis, adult female salivary gland, ovary	[84]

Table 2 Joint estimates of adaptive evolution across genes

Maximum-likelihood extension of MK test model fitted with different constraints on α [29]. LnL is the log likelihood of the model, AIC is the Akaike Information Criterion with corresponding relative probability as Akaike Weight (w_i). The most supported model is in bold.

Model	Model description	LnL	AICc	Akaike weight(w_i)	Maximum likelihood α estimate	
					ancestral	duplicate
M0	α-anc=0, α-dup=0	-300.61	633.2207	4.00×10^{-12}	0	0
M1	α-anc > 0, α-dup>0 α-anc = α-dup	-284.105	602.2092	2.6×10^{-05}	0.539	0.539
M2	α-anc>0, α-dup=0	-301.857	637.7133	5.10×10^{-13}	0.047	0
M3	α-anc=0, α-dup>0	-275.249	584.4975	0.186	0	0.618
M4	**α-anc > 0, α-dup>0 α-anc ≠ α-dup**	**-272.774**	**581.5471**	**0.813**	**0.2**	**0.676**

Additional files

Additional file 1 Table S1

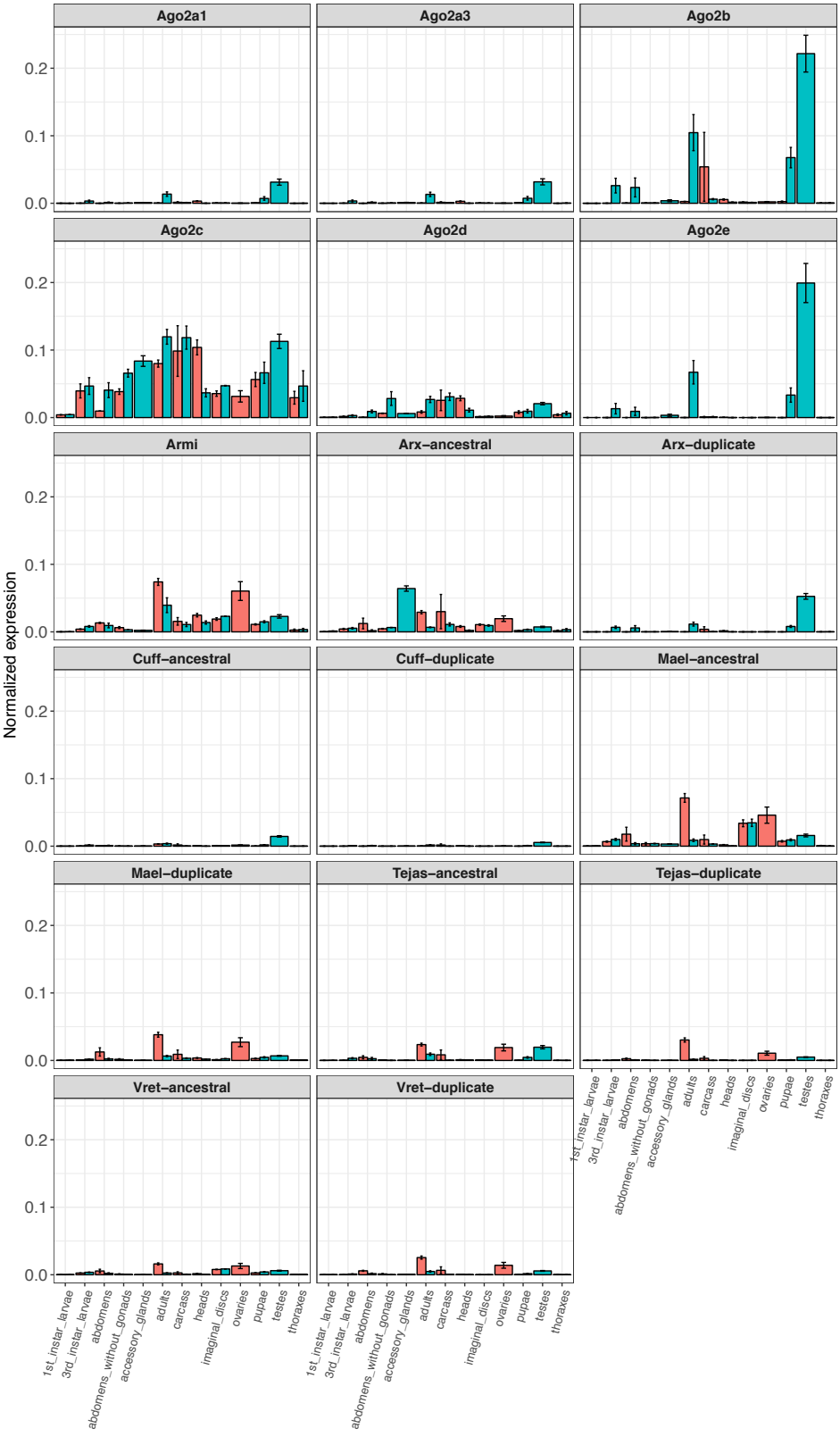
File format: xlsx
Title: **The detailed RNAi genes and its duplicate in** *D. pseudoobscura*
Description: The genomic position is based on the D. pseudoobscura assembly 3.0

Gene	Flybase ID	Locus Tag	Chromosomal location	Muller Element	Start Position	Gene length	Duplication mechanism
Armi	FBgn0246685	GA25304	4_group1	D	981803	3507	
Arx-ancestral	FBgn0077765	GA17756	XR_group8	D	6958861	495	
Arx-duplicate	FBgn0247462	GA26086	4_group3	B	10387204	501	Retrotransposition
Cuff-ancestral	FBgn0246456	GA25073	3	C	17023607	1113	
Cuff-duplicate	FBgn0244163	GA22760	XL_group1a	A	3011154	1119	Direct DNA duplication
Tejas-ancestral	FBgn0081173	GA21185	3	C	17440474	1782	
Tejas-duplicate	FBgn0248235	GA26863	2	E	1079477	1413	Retrotransposition
Vret-ancestral	FBgn0078422	GA18420	2	E	6266048	2085	
Vret-duplicate	FBgn0244928	GA23527	XL_group1e	A	10126307	2110	
Mael-ancestral	FBgn0248264	GA26892	2	E	54104	1314	
Mael-duplicate	FBgn0249827	GA28467	XR_group8	D	396866	1113	Direct DNA duplication
Ago2a	FBgn0249477	GA28114	Unknown_group_265		16703	2008	Direct DNA duplication
Ago2b	FBgn0248821	GA27454	2	E	23856171	2940	Direct DNA duplication
Ago2c	FBgn0248778	GA27411	2	E	21862037	2915	Direct DNA duplication
Ago2d(ancestral)	FBgn0245029	GA23629	XR_group6	D	200896	2839	
Ago2e	FBgn0247385	GA23629	4_group3	B	6716295	2285	Direct DNA duplication

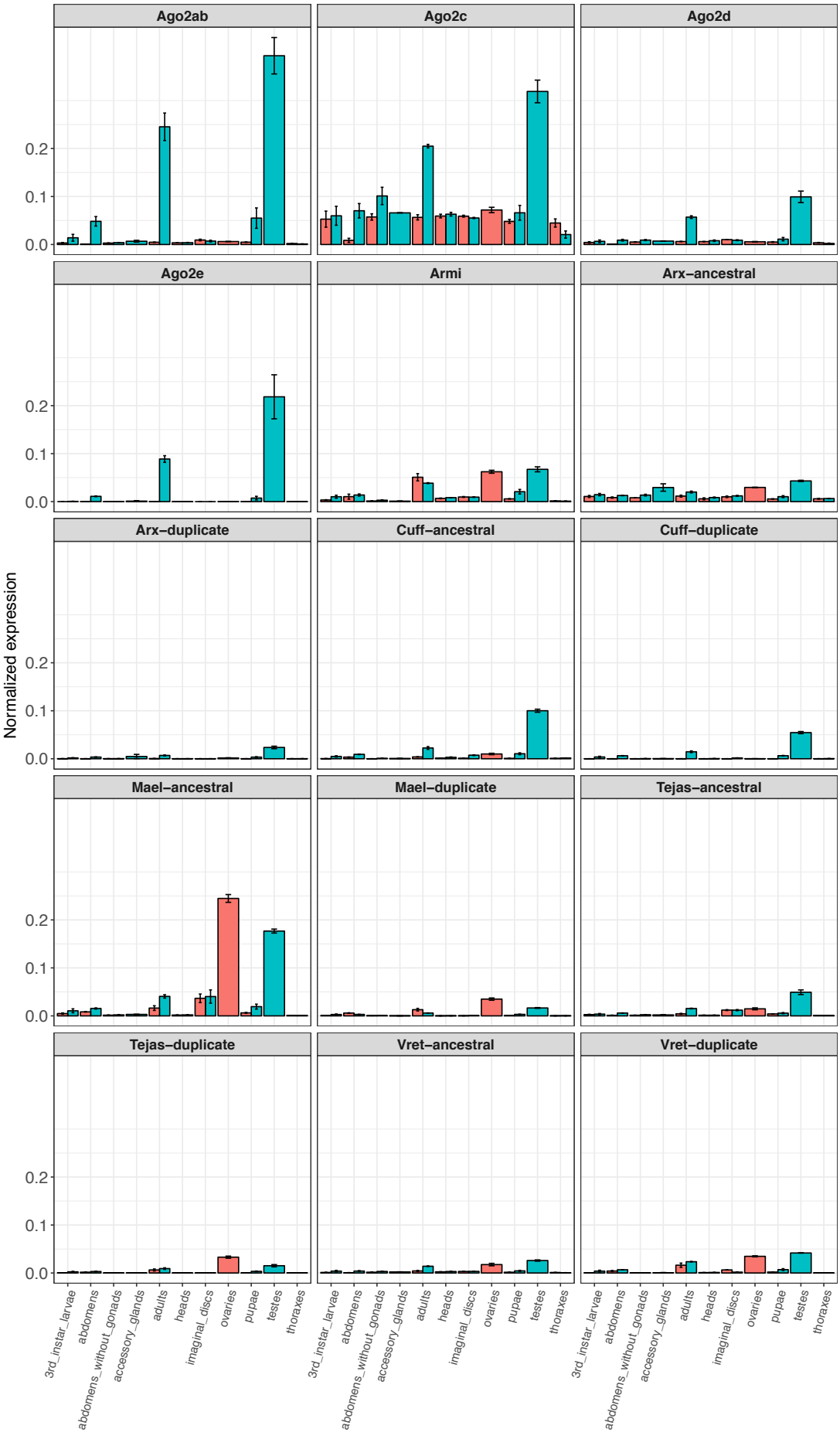
Additional file 2 Figure S1

File format: pdf
Title: **The expression profile of RNAi across tissue**
Description: The normalized expression plotted across tissues. The error bars denote the standard error for the given tissue. Blue bar indicates male and female is indicated by red bar. The plot is shown for *D. pseudoobscura* (n=163), *D. miranda* (n=42) and *D. obscura* (n=34), respectively.

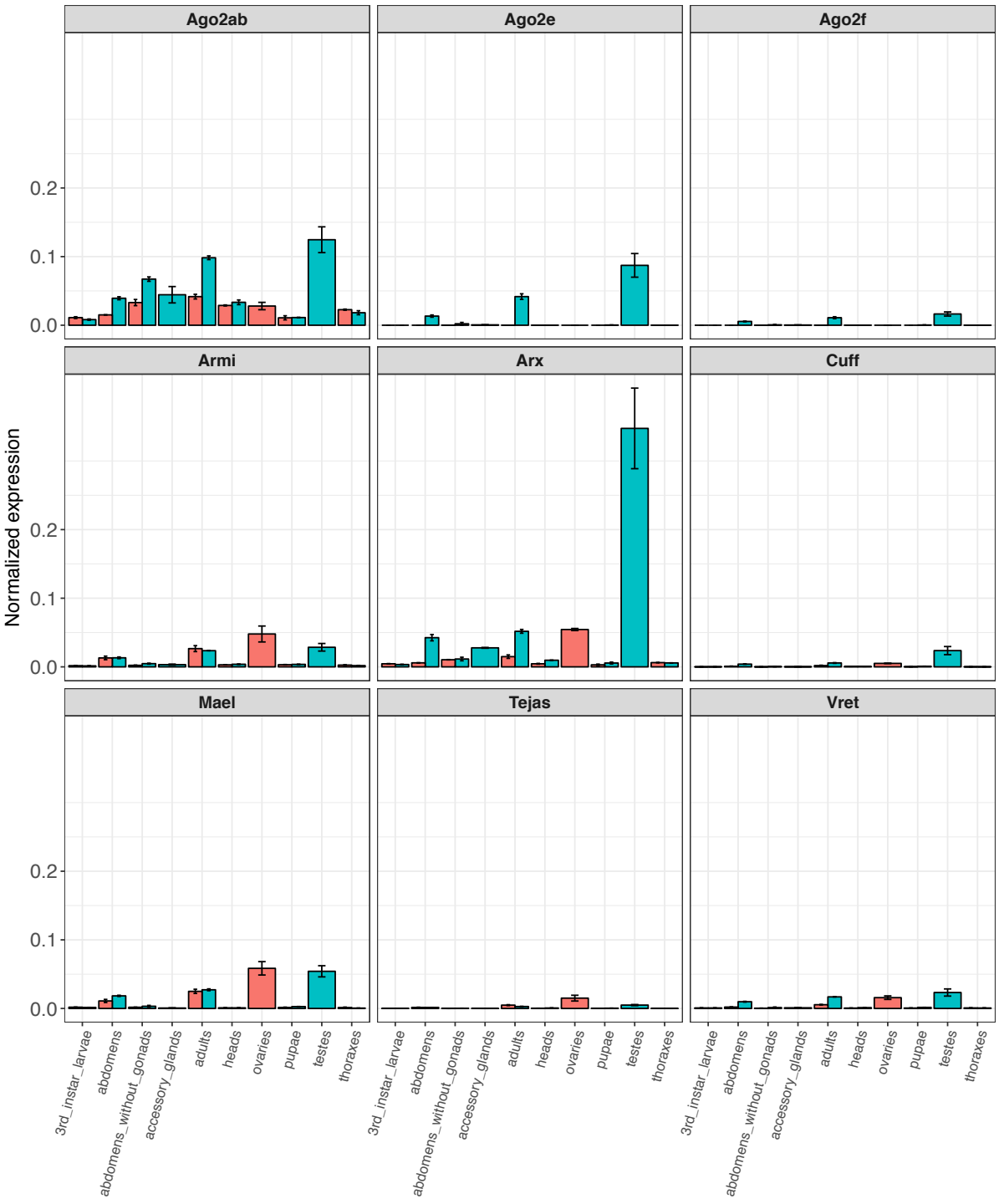
D. pseudoobscura



D. miranda



D. obscura



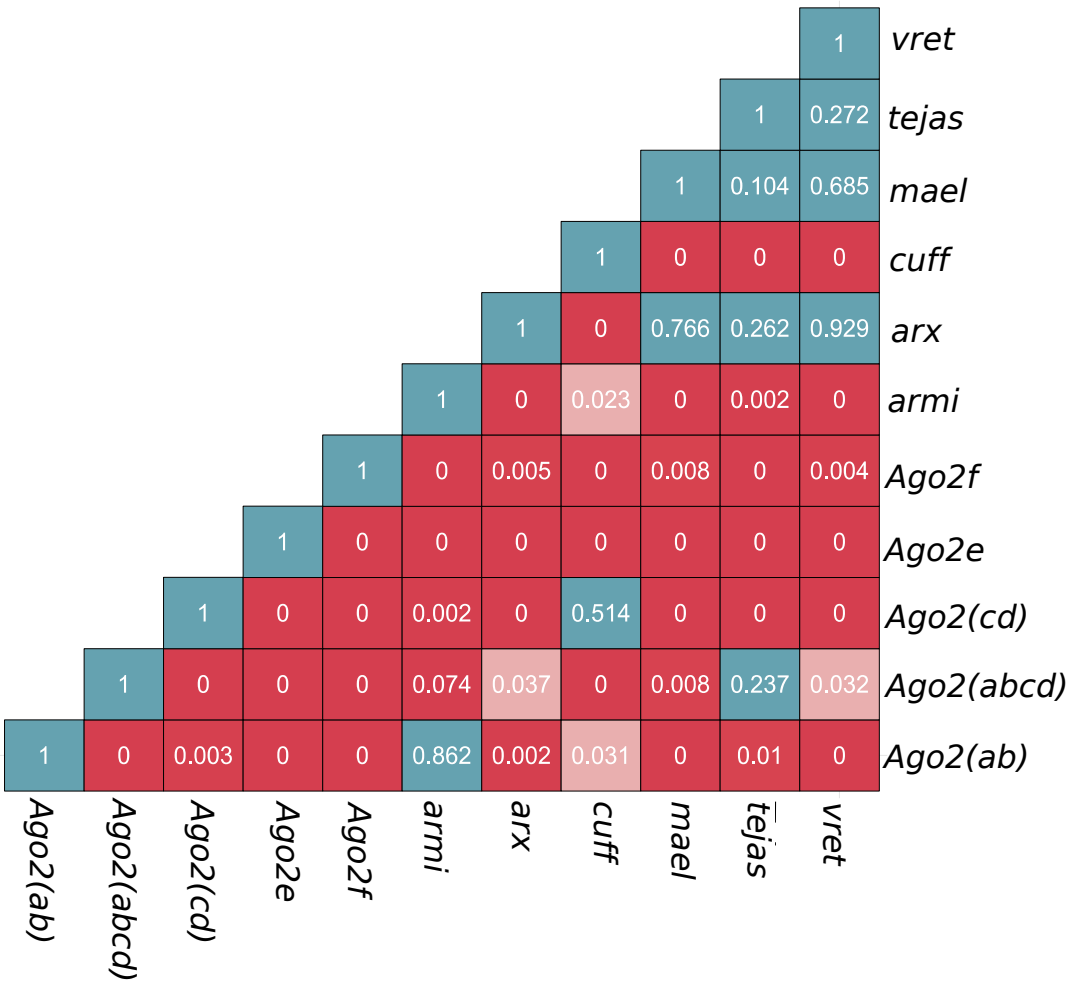
Additional file 3 Table S2

File format: xlsx
Title: **MK test of duplicated RNAi genes in** *D. pseudoobscura-D. miranda*
Description: Ds is synonymous divergence, Dn is non-synonomous divergence, Pn is the non-synonomous polymorphisms, Ps is the synonymous polymorphisms, α represents proportion of substitutions that are adaptive, a is the absolute number of adaptive substitution. Ln is the number of non-synonymous sites, Ls is the number of synonymous sites. Ka is the number of non-synonymous mutations per non-synonymous sites and Ks the number of synonymous mutations per synonymous sites from single randomly chosen strain for each species (Li, 1993 [85] calculated using R package seqinr). Parameter ω_a is identical to Ka/Ks ratio except that the numerator only takes adaptive divergence (α * Dn)/Ln)/(Ds/Ls).

Gene	Ds	Dn	Ps	Pn	alpha(α)	Fisher p-value	A	Ln	Ls	Ka	Ks	Ka/Ks	ω_a
Armi	34	72	22	30	0.356	0.220	26	2639.83	810.17	0.0380	0.0538	0.707	0.252
Arx-ancestral	2	9	7	4	**0.905**	**0.017**	8	383.67	102.33	0.0246	0.0232	**1.059**	**0.958**
Arx-duplicate	3	5	10	10	0.400	0.680	2	386.67	105.33	0.0204	0.0400	0.509	0.204
Cuff-ancestral	5	29	10	10	**0.828**	**0.010**	24	863.67	255.33	0.0352	0.0275	**1.281**	**1.060**
Cuff-duplicate	6	39	14	17	**0.813**	**0.003**	32	856.83	250.17	0.0297	0.0417	**0.714**	**0.580**
Tejas-ancestral	11	24	10	23	-0.054	1.000	0	1082.17	312.83	0.0312	0.0293	1.067	0.000
Tejas-duplicate	16	68	9	13	**0.660**	**0.046**	45	1264.83	379.17	0.0222	0.0352	**0.631**	**0.416**
Mael-ancestral	8	27	9	22	0.276	0.586	7	1001.67	303.33	0.0312	0.0293	1.067	0.294
Mael-duplicate	4	28	11	13	**0.831**	**0.007**	23	865.67	247.33	0.0323	0.0162	**2.000**	**1.662**
Vret-ancestral	17	34	37	70	0.054	1.000	2	1610.33	471.67	0.0211	0.0360	0.586	0.032
Vret-duplicate	25	65	23	26	**0.565**	**0.027**	37	1582.83	466.17	0.0517	0.0617	**0.838**	**0.473**
Ago2b	41	52	3	12	**-2.154**	**0.097**	0	882.00	264.00	0.0590	0.1553	**0.380**	**0.000**
Ago2c	2	34	2	22	0.353	1.000	12	1571.83	483.17	0.0216	0.0041	5.226	1.845
Ago2d	27	44	5	16	-0.964	0.300	0	1228.83	367.17	0.0358	0.0735	0.487	0.000
Ago2e	3	18	54	16	**0.951**	**0.000**	17	1410.17	464.83	0.0128	0.0065	**1.978**	**1.881**

Additional file 5 Figure S2

File format: pdf
Title: **The heat-map p-value of the difference between pairwise posterior distributions**
Description: Large p-value (>0.05) indicates the overlapping distribution and the duplication time might be shared (blue box). Red boxes denote comparison with p-value < 0.05 which indicate non-overlapping posterior distribution and an asynchronous duplication events . Pink colored box indicates the marginally significant (0.01 < p-value <0.05).



Additional file 6 Table S3

File format: multiple-tab xlsx
Title: **Additional MK test analysis**
Description: Table the results of additional MK test analysis where minor allele frequency is removed, repetition with larger dataset and results in *D. melanogaster*

Table 1 MK test result in *D. pseudoobscura* with MAF < 12.5% removed

Gene	Ds	Dn	Ps	Pn	α	Fisher p-value
Armi	38	74	7	11	0.193	0.79
Arx-ancestral	**2**	**9**	**3**	**0**	**1**	**0.0274**
Arx-duplicate	3	5	1	1	0.4	1
Cuff-ancestral	5	29	2	8	0.31	1
Cuff-duplicate	**6**	**41**	**5**	**4**	**0.883**	**0.0099**
Tejas-ancestral	11	24	5	11	-0.008	1
Tejas-duplicate	17	69	1	2	0.507	0.496
Mael-ancestral	8	28	4	4	0.714	0.1846
Mael-duplicate	**4**	**31**	**2**	**1**	**0.935**	**0.0592**
Vret-ancestral	18	35	16	27	0.132	0.831
Vret-duplicate	**25**	**68**	**8**	**7**	**0.665**	**0.069**
Ago2b	41	53	2	6	-1.321	0.4621
Ago2c	2	34	0	5	0	0
Ago2d	27	44	2	8	-1.455	0.318
Ago2e	**4**	**19**	**13**	**2**	**0.968**	**0.000037**

Table 2 MK test result for larger pseudoobscura dataset Fuller *et. al* [31]

Gene	Ds	Dn	Ps	Pn	NI	α	Fisher p-value
Armi	**33**	**71**	**36**	**38**	**0.491**	**0.509**	**0.02259**
Arx-ancestral	**2**	**7**	**14**	**4**	**0.082**	**0.918**	**0.011**
Arx-duplicate	3	5	14	11	0.471	0.529	0.438
Cuff-ancestral	**4**	**29**	**18**	**16**	**0.123**	**0.877**	**0.000569**
Cuff-duplicate	**6**	**39**	**15**	**18**	**0.185**	**0.815**	**0.002**
Tejas-ancestral	12	23	11	28	1.328	-0.328	0.62
Tejas-duplicate	**14**	**67**	**16**	**23**	**0.3**	**0.7**	**0.0069**
Mael-ancestral	8	27	7	22	0.724	0.276	0.568
Mael-duplicate	**4**	**28**	**11**	**15**	**0.195**	**0.805**	**0.015**
Vret-ancestral	17	33	44	85	0.995	0.005	1
Vret-duplicate	**25**	**65**	**25**	**27**	**0.415**	**0.585**	**0.018**

Table 3 MK test from DGRP Freeze 1 Dataset (*D. melanogaster* - *D. simulans*)

Gene	Ds	Dn	Ps	Pn	NI	α	Fisher p-value
Arx	**9**	**3**	**3**	**3**	**0**	**0.333**	**0.04**
Ago2	53	100	1	4	2.12	-1.12	0.66
Tejas	35	87	4	20	2.011	-1.011	0.314
Mael	22	36	4	5	0.764	0.236	0.72
Armi	**54**	**64**	**17**	**6**	**0.298**	**0.702**	**0.02**
Vret	45	30	13	17	1.962	-0.962	0.134
Cuff	33	62	5	5	0.532	0.468	0.49