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Dynamic regulation of alternative splicing and chromatin structure in *Drosophila* gonads revealed by RNA-seq

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Abstract

Both transcription and post-transcriptional processes, such as alternative splicing, play crucial roles in controlling developmental programs in metazoans. Recently emerged RNA-seq method has brought our understandings of eukaryotic transcriptomes to a new level, because it can resolve both gene expression level and alternative splicing events simultaneously.

To gain a better understanding of cellular differentiation in gonads, we analyzed mRNA profiles from *Drosophila* testes and ovaries using RNA-seq. We identified a set of genes that have sex-specific isoforms in *wild-type* (*wt*) gonads, including several transcription factors. We found that differentiation of sperms from undifferentiated germ cells induced a dramatic down-regulation of RNA splicing factors. Our data confirmed that RNA splicing events are significantly more frequent in the undifferentiated-cell enriched *bag of marbles* (*bam*) mutant testis, but down-regulated upon differentiation in *wt* testis. Consistent with this, we showed that genes required for meiosis and terminal differentiation in *wt* testis were mainly regulated at the transcriptional level, but not by alternative splicing. Unexpectedly, we observed an increase in expression of all families of chromatin remodeling factors and histone modifying enzymes in the undifferentiated cell-enriched *bam* testis. More interestingly, chromatin regulators and histone modifying enzymes with opposite enzymatic activities are co-enriched in undifferentiated cells in testis, suggesting these cells may possess dynamic chromatin architecture. Finally, our data revealed many new features of the *Drosophila* gonadal transcriptomes, and will lead to a more comprehensive understanding of how differential gene expression and splicing regulate gametogenesis in *Drosophila*. Our data provided a foundation for the systematic study of gene expression and alternative splicing in many interesting areas of germ cell biology in *Drosophila*, such as the molecular basis for sexual dimorphism and the regulation of the proliferation vs. terminal differentiation programs in germline stem cell lineages. The GEO accession number for the raw and analyzed RNA-seq data is GSE16960.

Keywords

Transcription; alternative splicing; differentiation; testis; ovary; *Drosophila*

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Introduction

Drosophila melanogaster is an excellent model organism for studying the molecular mechanisms underlying cellular differentiation. Of all cell types, germ cells are unique in their ability to produce the next generation of an organism upon fertilization¹. The *Drosophila* male and female germlines are stereotypical adult stem cell lineages that provide powerful model systems for studying the molecular mechanisms that regulate stem cell maintenance vs. differentiation²⁻⁷. Recent studies using loss-of-function assays for individual genes indicate that a unique chromatin structure in germline stem cells (GSCs) is critical for their self-renewal^{8,9}. Previous microarray analysis also demonstrated that GSCs express specific isoforms of genes, which encode components distinct from those in canonical transcriptional or translational machinery¹⁰. These data implicate alternative splicing in the regulation of GSC's maintenance.

Alternative splicing, through which a single pre-mRNA gives rise to different mature mRNAs, significantly increases protein diversity in higher eukaryotes^{11,12}. Several well-known examples of how splicing regulates cellular differentiation during *Drosophila* development come from studying sexual development of somatic tissues, where the X chromosome to autosome ratio is fundamental in the establishment of somatic sexual identity through sex-specific gene splicing¹³⁻¹⁷. Previous microarray studies of gene expression in whole flies reveal a broad spectrum of sex-specific expression of alternatively spliced isoforms¹⁸. However, those studies cannot resolve the difference between somatic tissues and gonads. Recent exon-specific microarray studies have demonstrated a handful of genes that are sex-specifically spliced in *Drosophila* gonads, demonstrating that alternative splicing may also contribute to sex determination of gonads¹⁹. On the other hand, the unequal dosage of X chromosomes between males and females necessitates compensatory mechanisms for X chromosomal gene expression. Through a process known as dosage compensation, the transcription level of genes on the single X chromosome in males is doubled to match the level of their expression in females²⁰. Previous microarray analysis of gene expression has shown that male-biased genes are depleted on the X chromosome²¹⁻²³. However, it is not clear whether such a preferential gene distribution applies to other groups of differentially expressed genes, such as stage-specific genes during gametogenesis.

Extensive global gene expression studies over the past decade, which have relied primarily on hybridization-based (e.g., microarray²⁴) and Sanger sequencing-based (e.g., serial analysis of gene expression (SAGE)²⁵) techniques, have described transcriptomes in a variety of cell types and developmental stages. However, these techniques are not optimal to resolve different isoforms of genes. Previous studies of alternative splicing mainly relied on expression sequence tag sequencing (EST) data, which is very difficult to reach genome-wide coverage. Recently developed massively parallel signature DNA sequencing technologies have been applied to profile transcriptomes in yeast^{26,27}, plant²⁸, and mammalian cells²⁹⁻³¹. The single-nucleotide resolution data from RNA-seq simultaneously provides information about mRNA levels and alternatively spliced isoforms (reviewed in³²).

To obtain a comprehensive understanding of gene expression and splicing events during sexual and cellular differentiation of *Drosophila* gonads, we used the RNA-seq technique to profile mRNAs in *wt* gonads and mutant gonads enriched with undifferentiated cells, from both male and female adult flies. Our high-resolution, genome-wide transcriptome data revealed the existence of a large number of genes that exhibit differential splicing in male and female gonads, suggesting that alternative splicing may also be a critical mechanism underlying sexual dimorphism in gonads. A dramatic increase in the expression of all families of chromatin modifying enzymes, including both ATP-dependent chromatin

remodeling factors [Brahma associated proteins (BAPs) and ATP-dependent nucleosome remodeling factor (NURF)] and histone modifying enzymes [histone methyltransferases (HMTs), histone demethylases (HDMTs), histone acetyltransferases (HATs), and histone deacetylases (HDACs)], was detected in the undifferentiated cell-enriched testis, indicating a need for the dynamic regulation of chromatin structure in those cells. At the same time, splicing factors were expressed at high levels in the undifferentiated cell-enriched testis, suggesting that alternative splicing is important in maintaining the undifferentiated status of those cells in testis. In contrast, genes required for meiosis and terminal differentiation were mainly regulated at the transcriptional level, and not by alternative splicing, in the differentiated cells of testis. Interestingly, we found that the differentiation genes in testis have a significantly biased distribution on the 2L autosomal arm. In contrast, these genes are the most under-represented on the X chromosome, indicating a potential mechanism for them to escape the X-inactivation, which is thought to occur during late spermatocyte stage. In summary, our high resolution and genome-wide RNA-seq data provided a platform to study sexual and cellular differentiation of *Drosophila* gonads at a molecular level.

Results

Generation of sex- and stage-specific gonadal transcriptomes using RNA-seq

To characterize the molecular signatures of sexual and cellular differentiation during gametogenesis, we isolated female and male gonadal poly(A) RNAs from two different adult flies (Fig. 1A): ovaries and testes from the *bam* mutant flies; ovaries and testes from *wt* flies. In *bam* mutant gonads, the transition from undifferentiated cells to differentiating cells is abolished and the tissues are enriched with over-proliferative undifferentiated cells, including GSCs, transit-amplifying spermatogonial cells, as well as somatic cells^{33, 34}. Although the *bam* mutant gonads have some abnormal features, they are highly enriched with early-staged germ cells, and thus, have been used in previous microarray analysis to study molecular characteristics of undifferentiated cells in gonads^{10, 35}.

Using these gonadal samples, we performed RNA-seq analysis using the Illumina/Solexa genome analyzer, as described in the Methods and Figure S1A. We retrieved about ten million non-redundant unique reads per sample to reach a sequencing depth sufficient to cover the entire predicted fly transcriptome approximately ten times (Table 1). We normalized transcript abundance for all expressed genes as sequencing reads/per kilobase merged exonic region/per million mapped reads (RPKM value²⁹, see Fig. S1B and Methods). To evaluate how well the RPKM value reflects transcriptional activity of genes, we used ChIP-seq (chromatin immunoprecipitation followed by high-throughput sequencing) to plot the enrichment of RNA Pol II at the transcription start sites (TSSs) for five groups of genes in the *bam* testis sample, classified according to their RPKM values^(30, Fig. 1B). The Pol II occupancy at TSSs positively correlated with genes' RPKM values. The silent group (RPKM=0) showed no Pol II enrichment.

Using the RPKM values of individual genes (Table S1), we performed four pair-wise comparisons between different samples in two categories (Fig. 1A): (1) sex-biased genes in *bam* mutant and *wt* gonads, respectively, to examine key regulators for sexual dimorphism in gonads; (2) genes that are expressed in a stage-specific manner in male and female gonads, to study stem cell or undifferentiated cell-enriched factors, as well as genes required for cellular differentiation of gametes.

The *wt* gonads demonstrated an outstanding sex-biased gene expression pattern, shown as a low correlation coefficient ($r=0.182$ for *wt* ovary vs. *wt* testis comparison). The sexual difference in undifferentiated cell-enriched *bam* gonads was much smaller ($r=0.716$ for *bam* ovary vs. *bam* testis comparison). In addition, more differential gene expression was

observed in testes than in ovaries when comparing gonads with different-staged germline and somatic cells: testis samples showed much higher variation ($r=0.242$ for *bam* vs. *wt* testis) than ovary samples ($r=0.865$ for *bam* vs. *wt* ovary). A possible explanation for such a difference is that we used flies that were within one day post-eclosion, which is sufficient for testis to reach full-term spermatogenesis but may be too early for ovary to have mature eggs^{36, 37}.

In order to further evaluate the data quality, we compared our RNA-seq results with the existing gene expression profiling data using microarray. We found that our data were largely consistent with the microarray data (²² and <http://www.flyatlas.org/>). For example, in the *wt* testis vs. *wt* ovary comparison (Fig. S2), greater than 77% (in most cases, greater than 89%) of the sex-biased genes identified by microarrays overlapped with the same category of genes identified by RNA-seq, indicating that the RNA-seq method largely recapitulated the microarray results and will be useful to identify possibly other differentially expressed genes in gonads. Our data also showed that approximately 56% of all genes in *wt* gonads and 21% in *bam* mutant gonads showed sex-biased expression patterns (≥ 2 -fold difference between sexes). These data were consistent with the previous work that indicates approximately half of the *Drosophila* genes have sex-biased expression pattern¹⁸ and *wt* gonads contain most of them^{38–40}.

Enrichment of chromatin regulators in undifferentiated cell-enriched *bam* testis

The differentiation of germ cells, especially in testis, is characterized by a dramatic morphological change and genome-wide chromatin condensation with replacement of histones by protamines⁴¹. To probe the molecular circuitries regulating gametes differentiation programs, gene expression profiles between *wt* and *bam* mutant gonads were compared in both male and female.

These comparisons indicated that spermatogenesis has a distinct gene expression profile switch from undifferentiated cell-enriched *bam* testis to fully differentiated *wt* testis: We found that 501 and 1,894 genes were uniquely expressed in *bam* and *wt* testis, respectively (Fig. 2A). These results were consistent with the thought that a large pool of meiotic and terminal differentiation genes are transcribed in spermatocytes (⁴², Fuller, M.T. and White-Cooper, H. personal communications). Examples of such genes included the testis-specific TAF homologs (tTAFs) and components of a testis-specific version of the MIP/DREAM complex (tMAC), which are remarkably up-regulated in *wt* testis (Fig. 2B)^{42–45}.

Previous studies have suggested that the undifferentiated status of female GSCs is maintained by a unique chromatin structure^{8, 9, 46}. To examine the potential epigenetic mechanisms that maintain the undifferentiated status of male GSCs and spermatogonia, we compared the expression levels of all families of chromatin remodeling factors and histone modifying enzymes in *bam* testis vs. *wt* testis: We found that 62.5% (20 out of 32) of chromatin remodeling factors and 70.2% (40 out of 57) of histone modifying enzymes are highly enriched in the undifferentiated cells of *bam* testis (Table 2). For example, BAP60 and BAP55, components of the ATP-dependent SWI/SNF family of chromatin remodeling BAP complexes^{47, 48}, were elevated 6.1-fold and 5.8-fold, respectively, in *bam* testis compared to *wt* testis. Nurf-38, a subunit of the NURF complexes^{49, 50} was elevated 3.4-fold in *bam* testis compared to *wt* testis (Table 2). The Polycomb group (PcG) and Trithorax group (TrxG) complexes, as well as other histone modifying enzymes, including HMTs, HDMTs, HATs, and HDACs, were also remarkably elevated in undifferentiated cells in *bam* testis. Interestingly, chromatin modifying enzymes that have antagonizing functions were co-enriched in *bam* testis. For example, the activities of the PcG and TrxG protein complexes counteract with each other in the determination of cell fate^{51, 52}. We detected a 4.1-fold enrichment of a key PcG component *Enhancer of zeste* [*E(z)*] and a 3.3-fold

enrichment of a critical TrxG component *trithorax* (*trx*) in *bam* testis, compared to *wt* testis (Fig. 2B and Table 2). In addition, genes encoding histone modifying enzymes that have opposite biochemical activities, such as the H3K4me3 HMT (e.g. *trx*)⁵³ and HDMT (e.g. *little imaginal disc* or *lid*: 5.6-fold enrichment)^{54–56}; as well as HATs (e.g., *Pcaf*: 4.9-fold enrichment)⁵⁷ and HDACs (e.g., *Rpd3*: 15.4-fold enrichment)⁵⁸, were both highly expressed in *bam* testis compared to *wt* testis. Interestingly, the *lid* gene was genetically identified as a TrxG gene⁵⁹, indicating that it may act with *trx* in a coordinated manner to antagonize PcG activities and regulate male germ cell differentiation. Recent studies have also demonstrated that the HAT and HDAC enzymes act together to regulate gene transcription⁶⁰, and different histone enzymes associate with each other and affect their respective enzymatic activities⁶¹. Consistent with those findings, here our data demonstrated that chromatin modifying enzymes with opposite activities were co-enriched and may act cooperatively to regulate the undifferentiated status of male germ cells.

To further validate these RNA-seq results, we performed *in situ* hybridization using gene-specific antisense riboprobes for a number of chromatin regulators. Indeed, we found co-enrichment of the *trx* and *lid* transcripts in undifferentiated cells located at the tip of the *wt* testis (Fig. 2C). The same co-enrichment pattern was also obtained for the antagonizing *Pcaf* and *Rpd3* genes (Fig. 2D). These data confirmed the RNA-seq results and implicated that the chromatin status of undifferentiated cells in testis may be dynamically regulated by balanced activities of counteracting chromatin regulators and histone modifying enzymes. In contrast, among the 925 genes that are uniquely expressed in *bam* ovary (Fig. 2A), only two chromatin regulator genes (*tma* and *Iswi*) were enriched in the *bam* ovary compared to *wt* ovary. These observations were consistent with previous reports that female GSCs have a relatively repressed transcriptome^{10, 62} and possibly a repressive chromatin landscape.

In summary, our data suggest that the status of undifferentiated cells in *bam* testis is associated with high expression level of a cohort of chromatin regulators, which may be critical for the maintenance of the unique molecular identities and cellular behavior of undifferentiated male GSCs and spermatogonial cells, which have been shown to retain the plasticity to de-differentiate to become GSC-like cells^{7, 63, 64}.

RNA-splicing factors are highly enriched in undifferentiated cell-enriched *bam* testis

Interestingly, we found significant enrichment of splicing factors in the *bam* testis: Approximately 56.9% of genes that encode characterized or putative splicing factors were enriched at least 2-fold in *bam* testis relative to *wt* testis (177 out of 311, Fig. 3A and Table S2), which was significantly higher than random distribution ($P < 10^{-15}$). The *bam* testis-enriched splicing factors included seven genes encoding SR proteins, which regulate splice site selection (Table S2). In contrast, only 8.4% of splicing factors were enriched in *wt* testis compared to *bam* testis (26 out of 311, Fig. 3A and Table S2), which was significantly lower than random distribution ($P < 10^{-8}$). These data suggested that the undifferentiated cells in testis may be associated with a genome-wide increase of splicing activities.

Enhanced alternative splicing activities in undifferentiated cell-enriched *bam* testis

To test the above hypothesis, we used gene entropy (*S*) as a measure of overall splicing complexity at any given splicing locus (Methods and⁶⁵). We computed gene entropy using the formula $S = - \sum p_k \log_2 p_k$. The p_k is the frequency of a particular transcribed isoform *k*, which is estimated from the RNA-seq data (Methods and Table S3). We then used normalized genes' entropy to plot a "Cumulative Distribution Function (CDF)" for each sample (Methods).

We first examined alternative splicing activities in *bam* gonads and compared the results with those in *wt* gonads. Indeed, we found that there were 23% more alternatively spliced genes in *bam* testis compared to *wt* testis (Table 1). Consistently, the CDF plot of *bam* testis shifted to the right side of *wt* testis, indicating an overall higher complexity of transcripts in *bam* testis ($P < 0.001$, Fig. 3B). Similarly but less significantly, results were obtained from the *bam* ovary vs. *wt* ovary comparison ($P < 0.02$, data not shown).

The significantly decreased expression of splicing factors in *wt* testis (Fig. 3A) implicated that single-transcript genes may be popular for terminal differentiation genes in testis ($\text{RPKM} < 0.5$ in *bam* testis and $\text{RPKM} \geq 1$ in *wt* testis). Indeed, we found that the percentage of multi-isoform genes is significantly ($P < 10^{-15}$) under-represented among terminal differentiation genes in testis (Fig. 3C): Only 13% of testis differentiation genes are multi-isoform genes; whereas 23% of all Ensembl annotated genes are multi-isoform genes. In addition, when we computed the ratio (percentage) of the intronic region size relative to the total gene size, we found a unique feature for testis differentiation genes: The mean of the intron size to the entire gene size ratio for all *Drosophila* genes is approximately 25%. However, for the terminal differentiation genes in testis, this ratio was significantly reduced to 19.3% ($P < 10^{-16}$). These intriguing results indicated that this particular group of genes might have evolved to become the simplest single-isoform ones, which could be the molecular mechanism that ensures efficient and coordinated transcription of a cohort of genes required for meiosis and spermiogenesis. However, this finding appeared to be in contrast with previous studies in mammals, which have suggested that alternative splicing is prevalent in testis^{66, 67}. This apparent discrepancy could be due to mixed staged germ cells in the mammalian studies, incomplete coverage of the mammalian EST libraries, or a difference between mammals and flies during evolution.

Sex-specific isoforms in *bam* and *wt* gonads

Alternative splicing is well known to play a critical role for sexual differentiation in *Drosophila* somatic tissues^{17, 68}. However, sex determination of germ cells in gonads is not as well-understood, but is thought to take a different route and rely on signals emanating from surrounding somatic cells^{69, 70}. Interestingly, recent studies have demonstrated that alternative splicing may also contribute to sexual differentiation of gonads, with a set of representative examples¹⁹. Here we used the RNA-seq data to identify sex-specific isoforms genome-wide in gonads. We analyzed uniquely detectable isoforms of each alternatively spliced gene in all four samples (Methods and Table S3). We then plotted each alternatively spliced gene for the presence or absence of sex-specific isoforms in both *bam* testis vs. *bam* ovary, and *wt* testis vs. *wt* ovary comparisons, respectively. Our analysis revealed 462 genes with sex-specific isoforms in *bam* testis vs. *bam* ovary comparison (Fig. 4A and Table S4-1). We also identified 614 genes that have sex-specific isoforms in *wt* testis and *wt* ovary (Fig. 4B and Table S4-2). Surprisingly, *p53* was among these genes with different isoforms in *wt* male and female gonads (Table 3 and Table S4-2). Using real-time PCR assays with isoform-specific primers, we found that the *p53-RA* isoform was 2-fold more enriched in *wt* ovary than in *wt* testis; whereas the *p53-RB* isoform was 14.6-fold more enriched in *wt* testis than in *wt* ovary (Fig. 4C–D). The *p53* gene is well known for its regulation of cell cycle and programmed cell death in response to cellular stresses^{71, 72}. The *Drosophila* *p53* was also known to regulate primordial germ cell development in embryos⁷³. Our discovery that there are distinct *p53* isoforms in *wt* testis and ovary implicated potentially dimorphic roles of *p53* in regulating apoptosis, which could contribute to distinct cellular differentiation pathways of male and female gametes.

Another interesting example is the *Rab14* gene (Table 3 and Table S4-2). Our real-time PCR analyses revealed that the two *Rab14* isoforms demonstrated the opposite enrichment in *wt* ovary (*Rab14-RA*, with 13.9-fold enrichment in ovary) and *wt* testis (*Rab14-RB*, with 171.4-

fold enrichment in testis, Fig. 4E–F). The *Rab* genes encode small guanosine triphosphatases (GTPases), which have important roles in regulating vesicle trafficking and actin filament assembly in flies^{74, 75}. Interestingly, certain *Rab* gene, such as the *Rab11*, has been shown to maintain the identities of female GSCs⁷⁶. It will be intriguing to explore whether *Rab14* may regulate germ cell dimorphism or have dimorphic functions through its distinct isoforms. More examples of genes that exhibit sex-specific (biased) isoforms are shown in Figure S3. In summary, our data indicated that sex-specific isoforms may contribute to sex-specific gametogenesis, and provide a splicing atlas for further studies.

Splicing factors (or putative splicing factors) themselves exhibit sex- and stage-specific isoforms in gonads

It has been reported that splicing factors themselves are regulated by alternative splicing during *C. elegans* development⁷⁷. To obtain a comprehensive understanding of this phenomenon in *Drosophila* gonads, we searched all 311 genes that encode characterized or putative splicing factors (Table S2) for distinct isoforms in both *bam* and *wt* gonads. Indeed, we found that 21 of them have differential isoforms in at least one of the four pair-wise comparisons (Table S4-1 to Table S4-4). One interesting example is the *exuperantia* (*exu*) gene (Table 3), which regulates RNA localization^{78, 79} and possibly splicing as well (Table S2). The *exu* gene exhibits germline-specific expression pattern in adult flies⁸⁰ and has been demonstrated to have male germ cell-specific splicing under the control of the Transformer 2 (Tra2) splicing factor⁸¹. Our RNA-seq data confirmed previous reports that the *exu-RC* is a testis-specific isoform. In addition, using real-time PCR assays, we found that the *exu-RA* is a testis-biased isoform (with 4.9-fold enrichment in *wt* testis) and the *exu-RB* is an ovary-biased isoform (with 94.3-fold enrichment in *wt* ovary, Fig. 5A–B). The differences of all *exu* transcripts are located at the untranslated regions (UTRs), which may lead to different Exu protein levels in male and female germ cells. It will be interesting to examine whether such a difference may allow Exu to execute sex-specific functions, such as splicing, in germ cells.

Another interesting example showed that a splicing factor had stage-specific isoforms (Table S4-3 and Table S5). The IGF-II mRNA-binding protein (Imp) is a component of the *Drosophila* spliceosomal complex⁸². The *Imp* gene is expressed in both undifferentiated spermatogonia and differentiating spermatids⁸³. Our RNA-seq data and real-time PCR validation experiments revealed both *bam* testis-specific isoforms (*imp-RA*, *imp-RB* and/or *imp-RC* with 40.2-fold enrichment in *bam* testis) and *wt* testis-specific isoforms (*imp-RG* and/or *imp-RH* with 1,966-fold enrichment in *wt* testis, Fig. 5C–D), indicating that it may regulate splicing in both staged cells using distinct isoforms. Overall, our results suggested that a subset of splicing factors (or putative splicing factors) may regulate cell type-specific splicing through their own sex- or stage-specific isoforms.

Biased distribution of testis terminal differentiation genes on the 2L chromosomal arm

We next investigated whether and how chromosomal territories affect gene expression by studying chromosomal distribution of stage-specific genes during spermatogenesis. In mammals, it has been reported that the spermatogonial genes are over-represented on the X chromosome^{84–86}. Here, we mapped spermatogonia-enriched genes based on the comparison of *bam* testis vs. *wt* testis (Fig. 6A). We found that the *bam* testis (thus spermatogonia)-enriched genes were significantly enriched on the X chromosome ($P < 10^{-15}$), consistent with what has been reported from mammalian studies. Interestingly, this biased gene distribution on the X chromosome was reversed on the 2L arm, where the spermatogonia-enriched genes were the least frequent ($P < 10^{-7}$). In contrast, terminal differentiation genes that are highly expressed in *wt* testis were significantly under-represented on the X chromosome ($P < 10^{-5}$), and were found mostly enriched on the 2L arm

($P < 10^{-5}$) (Fig. 6B). The X-inactivation is thought to occur during the late spermatocyte stage⁸⁷, which could have provided the selective pressure for differentiation genes to translocate from the X chromosome to autosomes, where they could avoid inactivation. These data suggested that in addition to the X chromosome, the 2L arm is critical in the determination of proper gene expression during spermatogenesis. And the fact that the X chromosome and 2L chromosomal arm were reciprocally favored or avoided suggested that the gene distribution on these two chromosomes may have been subjected to selective pressures during evolution.

New features of the *Drosophila* gonadal transcriptomes

Our RNA-seq data revealed many new features of the *Drosophila* gonadal transcriptomes, including thousands of transcribed regions that are not included in current Flybase. We called them Complementary-to-Flybase Transcribed Regions or CFTRs. In each sample, we identified ~1,500–2,500 CFTRs (Methods). The average size of the CFTRs was approximately 400 bp (Table 1). Most of the CFTRs were located in the intergenic regions (Fig. 7A). On average, the expression level of CFTRs was approximately 30–43% of that of the annotated genes (Fig. 7B). To test whether the CFTRs have been predicted or identified, we compared them to the N-SCAN, CONTRAST, mRNA and EST databases. We found that about 47–83% of the identified CFTRs in each sample were supported by the mRNA or EST databases, and about 15–20% of the identified CFTRs in each sample were present in predicted gene datasets (Table S6 and Methods). Using an extensive BLAST search, we found that only 8.9–15.4% of the CFTRs contain known protein coding sequences (Table 1, Table S6 and Methods). The remaining approximately 85% of the CFTRs could encode novel peptides or non-coding RNAs. Interestingly, analysis of the tissue specificity of the CFTRs revealed hundreds of specific ones in each pair-wise comparison (Fig. S4). This result indicated that CFTRs are another source of differentially expressed transcripts in gonads.

In summary, our data revealed many new features of the *Drosophila* gonadal transcriptomes, which will lead to a more comprehensive understanding of how differential gene expression and splicing regulate sexual and cellular differentiation of the fly gonads^{88–90}.

Discussion

Epigenetic regulation in male gonads

Emerging evidence indicates that embryonic stem cells maintain their identities by a unique transcription network and chromatin structure (reviewed by^{91, 92}). However, it is not well understood whether adult stem cells, such as GSCs, maintain their unique features using a particular chromatin structure; and if so, how developmental programs change such a structure and regulate terminal differentiation (reviewed by^{93, 94}). Previous studies in male germline lineage revealed that the cell type-specific tTAFs counteract Polycomb functions upon differentiation⁴⁴, which indicate that the chromatin structure in germ cells may switch upon the transition from undifferentiated to differentiating status. Here our RNA-seq data demonstrated a remarkable enrichment of nearly all families of chromatin modifying enzymes, including both ATP-dependent chromatin remodeling factors and histone modifying enzymes in the undifferentiated cell-enriched testis, compared with fully differentiated testis. These data demonstrated that a dynamically regulated chromatin structure may be required for maintaining the undifferentiated status of male GSCs and transit-amplifying spermatogonial cells. In addition, developmentally programmed mechanisms are required for switching such a chromatin landscape in order to initiate the terminal differentiation gene expression program.

Enhanced splicing factors in undifferentiated-cell enriched testis may contribute to stage-specific splicing events in testis

Differential gene expression and alternative splicing contribute significantly to pleiotropic phenotypic and behavioral features^{10, 22, 35}. In addition to the dynamic chromatin structure, our studies revealed enrichment of the majority of the splicing factors in the undifferentiated cell-enriched testis. The significantly higher splicing activities may collaborate with the highly expressed chromatin remodeling factors and histone modifying enzymes to maintain an intricate but sensitive transcription network through post-transcriptional mechanisms. Upon differentiation, the developmental program switches the gene network from undifferentiated to differentiating status in a unidirectional mode. The terminal differentiation genes that are turned on in differentiating cells are less dependent on splicing factors. The lower transcript complexity of this group of genes may contribute to the higher degree of transcriptional efficiency, in order to coordinate the co-expression of a large number of genes in spermatocytes⁴². It is not clear how these stage-specific features of transcriptomes are regulated. However, these phenomena are amenable to further genetic and molecular studies.

Sex-specific isoforms in gonads

Among all the phenotypic traits of *Drosophila*, sexual dimorphism is undoubtedly one of the most distinct features, and gonads are the most sexually distinguishable tissues. Despite a wealth of knowledge about sexual differentiation of soma, sexual differentiation of germ cells is not well understood. Our data demonstrate that *wt* gonads are not only the major tissues with sex-specifically expressed genes, but also the tissues with prevalent sex-specific isoforms of genes (Fig. 4B). Studying these genes, especially those with regulatory roles such as transcription factors or splicing factors will undoubtedly shed light on how sexual dimorphism is established and maintained during gametogenesis. And our work has provided much needed information to address these intriguing biological questions at a molecular level in gonads.

In summary, we have discovered that the dynamic regulation of chromatin remodeling factors and histone modifying enzymes is characteristic of undifferentiated cell-enriched *Drosophila* testis. The sex-specific isoforms of critical transcription factors and splicing factors may contribute to the sexual differentiation of gonads. Our single base-pair resolution, genome-wide RNA-seq data provide a foundation for the systematic study of many interesting areas in *Drosophila* reproductive biology and stem cell biology, such as the molecular basis for sexual dimorphism of gonads, and the regulation of proliferation *vs.* terminal differentiation programs in GSC lineages.

Materials and Methods

Fly strains and tissue preparation

All fly stocks were grown at 25°C incubator with standard medium. The *bam[1]/TM3* stock were obtained from Bloomington *Drosophila* Stock Centers. The *bam[delta86]/TM3* strain was a gift from Dr. Allan C. Spradling. The *bam[114-97]/TM6B* strain was a gift from Dr. Margaret Fuller. Testes from *bam[1]/bam[114-97]* mutant males and ovaries from *bam[1]/bam[delta86]* females were dissected in DEPC-treated 1× PBS buffer in 20mins interval, followed by immediate snap freezing in liquid nitrogen. The *wt* testes and ovaries were dissected from *y, w* flies using the same method. All flies were less than one day post-eclosion. Noticeably, we found some accessory gland genes (e.g. *Acp* genes) in our *bam* testis RNA-seq dataset (Table S1), which may be caused by technical difficulties to completely isolate testes from accessory glands from *bam* mutant males. In fact, we found

the same issue with previous microarray data using a similar fly strain³⁵, shown as high deviation among different biological replicates.

Library preparation for RNA-seq

Total RNA was extracted using TRIzol (Invitrogen, #15596-018) following the manufacturer's instructions. Samples used for total RNA extraction were from ~200 pairs of *bam* testes (8.5 µg), ~200 pairs of *bam* ovaries (6.9 µg), ~200 pairs of *wt* testes (19 µg) and 45 pairs of *wt* ovaries (15 µg). DNA was degraded using 2 Units of DNase I (Fermentas, #EN0521) at 37°C for 20 mins. The integrity of RNA was checked by gel electrophoresis (1% agarose).

From ~10 µg total RNA for each sample, we performed two rounds of mRNA isolation using Dynabeads mRNA purification kit (Invitrogen, #610-06), according to the manufacturer's instructions. The final mRNAs were eluted in 13.5 µl 10 mM Tris-HCl (pH=7.5) and immediately used to generate the first strand cDNA, using 4 µl random hexamers (ABI, #N8080127) and SuperScript II Reverse Transcription Kit (Invitrogen, #18064-014) in a 30 µl final volume, following the manufacturer's instructions. The second strand cDNA was generated with the following recipe: 10 µl 5× second strand buffer (500 mM Tris-HCl pH7.8, 50 mM MgCl₂, 10 mM DTT), 30 nmol dNTPs (Invitrogen, #18427-013), 2 Units of RNase H (Invitrogen, #18021-014) and 50 Units of DNA Pol I (Invitrogen, #18010-025). The entire reaction mix was incubated at 16°C for 2.5 hours. The double-stranded DNA (dsDNA) was purified with QIAquick PCR purification kit (Qiagen, #28106) and the concentration was quantified by a Qubit fluorometer (Invitrogen).

For generating libraries for sequencing, about 300 ng dsDNA of each sample was fragmented by sonication using Bioruptor (Diagenode, UCD-200-TM-EX) under the following conditions: medium power output for 30 mins in ice water. The resulting DNA fragments were analyzed by agarose gel to verify a ~100–300 bp size range. Sequencing libraries were prepared as follows: end-repair (DNA end-repair kit from Epicenter, #ER0720); A-tailing (300 ng dsDNA, 5 µl Thermo buffer, 10 nmol dATP, 15 Units of Taq polymerase, at 70°C for 30mins); Solexa adaptor ligation (300 ng dsDNA, 4 µl DNA Ligase buffer, 1 µl Solexa adaptor mix, 3 µl DNA Ligase, at 70°C overnight.); PCR (98°C 10 sec, 65°C 30 sec, 72°C 30 sec for 16 cycles; then additional 72°C for 5 mins) amplification with adaptor primers and size selection (200–400 bp). Then the library dsDNA for each sample was used on Solexa 1G sequencer at a concentration of 10ng per lane.

Primary annotation information

Drosophila exon annotation information was downloaded using BioMart from the *Drosophila* BDGP5.4, Ensembl database (release 50).

Preliminary analysis of short read data

Short reads alignment and filtering—The quality-filtered 30 bp short sequence reads were aligned to the reference sequence consisting of dm3 *Drosophila melanogaster* genome plus a library of synthetic exon junction sequences using ELAND (Efficient Local Alignment of Nucleotide Data) software, allowing up to two mismatches with the reference sequence (Fig. S1B). The library of exon junction sequences was created as follows. *Drosophila* exon sequences were retrieved from Ensembl database (release 50). All possible pairs of exons that belonged to the same transcript were joined such that the genomic order of exons is aligned. A junction sequence is consisted of the last 26 bp of 5' exon and the first 26 bp of 3' exon. Redundant sequences were removed from the resulting set of 52 bp exon junction sequences. The numbers of reads that aligned uniquely to the genome and exon junctions are shown in Table 1. In order to remove possible PCR amplification artifacts and

to reduce confounding effects of systematically bad sequencing cycles in short sequence reads, we retained a single copy of each unique read. This filtering procedure yields the set of non-redundant unique reads.

Generating an in-silico fly transcriptome—As described above we created a library of exon junction sequences by joining pairs of exons that belong to the same transcript such that the genomic order of exons is retained. Not all junctions in the resulting library are present in the annotated Ensembl transcripts. Junctions of neighboring exons in a transcript belong to annotated transcripts, whereas junctions of non-neighbor exons potentially belong to novel transcripts.

Sequencing depths in different samples—There was some variability in sequencing depths in different tissue samples. At least two technical replicates were used and 10–13 million 30 bp sequencing reads were obtained per sample (Table 1). In order to characterize splicing and gene expression differences between samples in an unbiased way, we used the following procedure to equate the sequencing depths of different samples. We randomly sub-sampled approximately 10 million non-redundant unique reads (300 million bp) in each of the four samples and used these reads for all downstream analyses, which was sufficient to cover the entire predicted fly transcriptome 10 times (~30 million bp transcribed sequences according to Ensembl database release 50).

Calculation of gene expression level

For each tissue sample, we used the following procedure to compute a single number that summarizes overall expression level of a gene. All exon regions belonging to a gene are merged and the total number of non-redundant unique reads in the resulting merged exonic region is counted. The resulting number of reads is normalized with respect to the total size of merged exonic region of the gene and the total number of genomic unique and non-redundant reads in the particular sample, and RPKM value is computed. The use of merged regions to compute read counts avoids the problem of double-counting in regions where exons overlap with each other.

Using the RPKM values, the correlation coefficient (r) among the technical replicates for each sample was calculated, and this coefficient showed very little variation ($r > 0.983$) in all samples, consistent with the idea that the RNA-seq method is highly reproducible. Thus, data from all technical replicates for each sample were combined for further analysis.

ChIP-seq procedure

We dissected 200 pairs of *bam* testes in cold PBS and grouped in 200 μ l PBS which contained protease inhibitor (Roche complete mini, # 11836153001) and 0.5 mM PMSF (MP Biomedicals, #195381); We then added 5.5 μ l 37% fresh formaldehyde (Supelco, # 47083-U) and incubated at 37°C for 15mins. The testes were spin at 2k for 2 mins and washed 2 times with 450 μ l cold 1 \times PBS (with inhibitors and PMSF). Then 200 μ l lysis buffer (50 mM Tris-HCl, pH7.6, 1 mM CaCl₂, 0.2% Triton X-100, 5 mM butyrate, 1 \times proteinase inhibitor cocktail, and 0.5 mM fresh PMSF) was added and the tissues were homogenized thoroughly followed by incubation at RT for 10mins. We then did sonication with Microtip (Misonix, Inc, Microson XL-2000) under the following procedure: 5'' at power 20, rest for 50'', 3–4 times, followed by spinning at 14k rpm for 10' at 4°C. The chromatin was diluted 10 \times with RIPA buffer (10 mM Tris, pH7.6, 1 mM EDTA, 0.1% SDS, 0.1% Na-Deoxycholate, 1% Triton X-100, with protease inhibitors and PMSF) and 50 μ l of this dilution was taken out as input.

We washed 40 μ l of Dynabeads Protein A (DynaL Biotech ASA, Oslo, Norway) once with 1 \times PBS. We then added 4 μ g anti-RNA Pol II antibody (Abcam, ab5408) to the Dynabeads and incubated at RT for 40mins, followed by washing with 1 \times PBS. Next 1ml of the chromatin extract was added to the beads and the mixture was rotated at 4°C overnight. Subsequent washing was performed per the manufacturer's instructions. The beads were suspended in 100 μ l 1 \times TE containing 3 μ l 10% SDS and 5 μ l 20 mg/ml proteinase K. After overnight incubation at 65°C, the supernatant was transferred to a new tube using a magnet (DynaL MPC-S) to precipitate the Dynabeads. Samples were treated by Phenol/Chloroform extraction, salt/EtOH precipitation, and resuspended in 50 μ l 1 \times TE. The products were processed for Solexa sequencing according to the established protocol⁹⁵.

Comparison of RNA-seq with ChIP-seq

All *Drosophila* Ensembl genes were classified into five groups according to their RPKM value: 8,943 genes that have at least one RPKM were classified into high (2,981 genes, 41.07<RPKM<5307), moderate (2,981 genes, 15.36<RPKM<41.06) or low (2,981 genes, 1.00<RPKM<15.36). 2,294 genes whose RPKM between 0.01 to 1.00 was considered as uncertain group, and the rest 1,902 genes were classified as a silent group (RPKM=0). The genes in each group were aligned to their transcription start site (TSS), using UCSC annotation (<ftp://hgdownload.cse.ucsc.edu/goldenPath/dm3/database/>). The read density was calculated in 5 bp windows.

Comparison of RNA-seq data with published microarray data

We first downloaded the CEL files generated by Parisi et al²² and Chintapalli et al⁹⁶ from NCBI GEO database. We then extracted and normalized microarray signals with RMA function embedded in the limma package [downloaded from Bioconductor R packages (<http://www.bioconductor.org>)]. Genes with multiple probes were filtered out if different probes give out inconsistent Present (P) or Absent (A) calls. Genes with at least three P calls or three A calls from four independent biological replicates for each sample were retained for further analysis. Differentially expressed genes were identified using the combination of P-value ($P \leq 0.05$) and fold change (≥ 2) cutoffs, followed by comparison with their expression level using the RNA-seq data.

Heat map analyses

To visualize gene expression across different samples, heat map was generated using the TIGR software MeV v4.3.01 (<http://www.tm4.org/mev.html>). The hierarchical clustering was made using parameters of Euclidean distance and average linkage clustering. The sample columns were fixed and the genes were clustered with the optimized gene leaf order.

In situ hybridization

PCR primers were appended with a T7 RNA polymerase binding site at their 5' ends (5'-AAGGATCCTAATACGACTCACTATAGGGAGA-3'). For each of the following genes, we design two sets of primers to synthesize both sense (S) and antisense (AS) riboprobes. The primers' sequences are:

T7_AS_trx:
AAGGATCCTAATACGACTCACTATAGGGAGAAGGTCTCCTTGCCAAGCTTC
AGAT;

S_trx: TAGAAACGTGCTGGAGACAAGCGA;

T7_S_trx:
AAGGATCCTAATACGACTCACTATAGGGAGATAGAAACGTGCTGGAGACAA
GCGA;

AS_trx: AGGTCTCCTTGCCAAGCTTCAGAT;

T7_AS_lid:
AAGGATCCTAATACGACTCACTATAGGGAGACGCCACTATTGCTGTTGCTAT
TGG;

S_lid: TCAAGAAGCGATTATGGCGCAGCA;

T7_S_lid:
AAGGATCCTAATACGACTCACTATAGGGAGATCAAGAAGCGATTATGGCGC
AGCA;

AS_lid: CGCCACTATTGCTGTTGCTATTGG;

T7_AS_rpd3:
AAGGATCCTAATACGACTCACTATAGGGAGATGCGTTATTCGCCACATTGG
ATCG;

S_rpd3: ACAGCAACAAGGCATCCTCAGAGA;

T7_S_rpd3:
AAGGATCCTAATACGACTCACTATAGGGAGAACAGCAACAAGGCATCCTCA
GAGA;

AS_rpd3: TCGTTATTCGCCACATTGGATCG;

T7_AS_Pcaf:
AAGGATCCTAATACGACTCACTATAGGGAGAACGTTCTCATCCC GCGACAC
ATTA;

S_Pcaf: AAGGATGATTGCCCCATCTGGGAT;

T7_S_Pcaf:
AAGGATCCTAATACGACTCACTATAGGGAGAAAGGATGATTGCCCCATCTG
GGAT;

AS_Pcaf: ACGTTCTCATCCC GCGACACATTA.

After the PCR amplification (Fermentas PCR purification Kit, #K0702), we synthesize the RNA probes using DIG-labeled NTPs (Roche #11277073910) and the T7 RNA polymerase (Roche #10881767001) at 37°C for 2 hours, followed by hydrolysis with carbonate buffer (120 mM Na₂CO₃; 80 mM NaHCO₃; pH=10.2) at 65°C for 10 min. Whole mount testes *in situ* hybridization was carried out as previously described⁹⁷ with the following modifications: For each reaction, ~15 pairs of testes were dissected from the y,w males that were less than one day post-eclosion. RNA hybridization to DIG-labeled probes was carried out in RNase-Free tubes at 65°C for 16–18 hours. And the testes were subsequently washed 6 times (15 minutes each time) with 500 µL Hybe B [10.75 ml DEPC H₂O, 25 ml Formamide (Fermentas #BP227500), 12.5ml 20X SSC, 1ml sheared herring sperm DNA (5mg/ml, Sigma #D3159-10G), 250 µL heparin (10mg/ml, Sigma #H3393-100KU), 500 µL Tween 20 (Promega #H5151)] in a 65 C water bath; followed by 15min with each of the following solutions at room temperature (RT): Hybe B: PBST (4:1); Hybe B: PBST (3:2); Hybe B: PBST (2:3); Hybe B: PBST (1:4); and 2× 15min with 500 µL PBST (1× PBS plus 0.1% Tween-20).

The results were next developed using anti-Digoxigenin antibody (Roche #11093274910, at a 1:2000 dilution) in RNase-Free tubes at 4°C overnight. The testes was then washed 4× 20 min with 500 µL PBST at RT; followed by 3× 5min washes in freshly made NMTT (for 10 ml NMTT: 8.3 ml DEPC H₂O, 1 ml Tri-HCl (pH 9.0), 200 µL 5M NaCl, 500 µL 1M MgCl₂, 10 µL Tween 20) at RT. The testes were then transferred from the tubes into the

wells of dissecting dish. The NMTT buffer in each well was replaced by 300 μL NBT (4-Nitro blue tetrazolium chloride) staining solution [298 μL NMTT, 1.35 μL NBT (Roche #11383213001) and 1.05 μL X-phosphatase (Roche #11383221001)]. The color reaction was allowed until differential staining signal could be detected in testes stained with antisense probe vs. sense probe. The reaction was then stopped by 3 \times quick washes using PBST; 1 \times quick wash using 100% EtOH: PBST (1:1); 2 \times quick washes using 100% EtOH; and 2 \times quick washes using 100% EtOH: Methyl salicylate (1:1). Approximately 300 μL GMM [3 ml Methyl Salicylate (Fermentas #03695-500), and 12 ml Canada Balsam (Fermentas #B10-100)] were added to the testes followed by overnight shaking at RT. Finally, the testes were mounted on slides and visualized using the CCD camera. The images were processed by Adobe Photoshop.

Transcript isoform expression from RNA-seq data

Since many transcripts overlap with each other, not all isoforms are unambiguously detectable using RNA-seq short reads. In order to facilitate transcript isoform detection, we introduce the following natural ID system for transcripts. For each transcript T, let R_T be the union of its exonic region that does not overlap with the rest of Ensembl transcripts. R_T uniquely identifies transcript T. We then called a transcript T with a non-empty R_T a uniquely detectable isoform. However, not all transcripts possess a non-empty R_T , because some are fully overlapped with other transcripts. We estimate the expression level of each uniquely detectable transcript isoform T by counting the number of unique and non-redundant reads in the R_T region, followed by using the total size of R_T as the normalization factor to compute the RPKM value. We used $\text{RPKM} \geq 1$ as the cutoff for positive transcription.

We did not use exon-exon junction reads data to estimate the expression levels of alternatively spliced isoforms. The estimates of expression level using exon-exon junction read counts are not reliable due to a high level of sampling noise present at the small junctions. The relative sampling noise level is of the order $n^{-1/2}$. The n is the expected number of reads at an exon-exon junction, dependent on the expression level of the corresponding transcript.

Entropy as a measure of alternatively spliced gene complexity

We set T_1, T_2, \dots, T_n to be the set of uniquely detectable isoforms of a gene; and x_1, x_2, \dots, x_n to be the corresponding RPKM values estimated as described above. If only a few isoforms of a multi-isoform gene are expressed, the gene has low AS complexity. If majority of isoforms are expressed, the gene has high AS complexity. As a measure of AS complexity, we used gene entropy (or “S” in abbreviation)⁶⁵. The probability p_k of isoform T_k is estimated as the frequency $p_k = x_k/N$, where N is the sum $x_1+x_2+\dots+x_n$ of isoforms’ RPKM values of the corresponding gene. We added a pseudo-count $\epsilon = 0.001$ to each x_k to avoid zeroes. Using the pseudo-count-adjusted probability estimates, we computed the entropy of the gene as $S = -\sum p_k \log_2 p_k$.

By definition, the entropy is non-negative ($S \geq 0$). It is zero if and only if all p_k , except one, are zero. This is a desired property because if only one isoform of a multi-isoform gene is expressed, then the AS complexity of the gene should be zero. Another property of entropy is that it only depends on the probabilities (estimated as frequencies), but not on absolute RPKM values, as long as these values are large enough for a reliable estimate of frequencies. Thus, for a sufficiently expressed gene, entropy does not depend on the overall expression level of the gene. Therefore, it is meaningful to compare gene entropies across different samples. Entropy estimates for genes expressed at very low levels are less reliable. But, since we are mainly interested in the comparison of the overall AS complexity of a

large number of genes across different samples, the effect of unreliable entropy estimates for a small subset of genes is insignificant.

The largest possible entropy $\log_2 k$ for a gene with k uniquely detectable isoforms will be achieved when the frequencies of all isoforms are equal to $1/k$. We normalized gene entropy by dividing it with $\log_2 k$. Therefore, the normalized entropy S_{norm} is always within the range from zero to one ($0 \leq S_{\text{norm}} \leq 1$).

Cumulative Distribution Function (CDF)

For each normalized entropy value x , the function $\text{CDF}(x)$ gave out the fraction of genes whose normalized entropies are smaller than x . For example, $\text{CDF}(0.1) = 0.9$ means that 90% of genes have normalized entropy less than 0.1. To statistically test if normalized entropies of AS loci in one sample is significantly larger than those in another sample, we used one-sided Kolmogorov-Smirnov test, which gave out P values shown in Fig.3B.

Differential splicing analysis

In Ensembl 50 database, 3,463 *Drosophila* genes (approximately 23%) have multiple isoforms. Among them, 2,094 were identified in our dataset that have more than one uniquely detectable isoform.

In order to visually display differential splicing of genes in two samples, we used the following method. For each gene, we asked the following questions:

1. Does it have transcript isoforms expressed both in samples 1 and 2?
2. Does it have transcript isoforms expressed only in sample 1?
3. Does it have transcript isoforms expressed only in sample 2?

The answer to each of these questions is yes (Y) or no (N). Thus, for each gene, there can be 8 combinations of answers: YYY, YNY, NYY, YYN, NNY, YNN, NYN, NNN. In Fig. 4A and Fig. 4D, Y is denoted by red color and N is denoted by blue color (The NNN category for each comparisons were not shown.).

We generated the list of candidate genes that undergo alternative splicing in a sex-specific or sex-biased manner in Table 3 as follows. The number of observed RNA-seq reads from a small exonic region is subjected to large sampling noise. The relative sampling noise level is of the order $n^{-1/2}$. The n is the expected number of reads at the exonic region, which is dependent on the expression level of the corresponding transcript. In order to avoid the noise and thus false positive differentially spliced genes, we removed all uniquely detectable transcript isoforms with the ID region R of a total size smaller than 100bp. Only genes with two or more uniquely detectable long R isoforms (UDLRI) were retained for further analysis. A differentially spliced gene must be: (1) sufficiently expressed in both samples (i.e. most expressed UDLRI isoforms have $\text{RPKM} \geq 10$), (2) contain at least one UDLRI isoform which is not expressed ($\text{RPKM} < 2$) in one sample but highly expressed (≥ 10 RPKM) in another one. The differentially spliced genes identified using the above procedure were then manually inspected on the UCSC genome browser to remove false positives and listed in Table 3 and Table S5.

Chromosomal mapping assay

Chromosomal mapping was done with Pearson's chi-squared test in R programming environment (R version 2.5.0, download from <http://www.r-project.org>). For *bam* testis vs. *wt* testis comparison in Figure 6, we calculated the P-value in a 2x2 tables with the gene numbers of the following categories: differentially expressed genes (≥ 2 fold change

between *bam* testis and *wt* testis) on a certain chromosome arm (e.g. chrX), non-differentially expressed genes on a certain chromosome arm (e.g. chrX), differentially expressed genes on the other four chromosome arms (e.g. chr2L, chr2R, chr3L and chr3R in together), non-differentially expressed genes on the other four chromosome arms. And the $P < 0.01$ was used to evaluate the significance of differential chromosomal distribution.

Identification of Complementary-to-Flybase Transcribed Regions (CFTRs)

The identification of CFTRs was modified from ⁹⁵. Reads which can be mapped to known exons were all removed. Known exons were obtained from Ensembl database (<http://www.ensembl.org/index.html>) and the newest Flybase version (r5.19) (<http://flybase.org/>). The remaining reads were analyzed to discover CFTRs. For this purpose, CFTRs were defined for each sample by first calculating the number of reads aligning to each 40-bp window across the genome, and windows passing a P-value threshold (Poisson) of 0.05 were retained. Consecutive windows were grouped to form a large region allowing a gap of two windows that did not satisfy the p-value cutoff. Finally, all CFTRs smaller than 100 bp (to reduce false positive caused by non-specific PCR amplification in some small regions that have high density of sequencing reads), or contain fewer than 10 reads were eliminated. The RPKM for a CFTR was calculated according to their reads, sizes and the total unique sequencing reads in each sample.

CFTRs were mapped to intergenic or intronic regions according to their mapped genomic loci (Ensembl). To eliminate possible contamination by pre-mRNA, intronic CFTRs were removed if their RPKM value was less than 10% of the RPKM of neighboring gene(s).

To validate the CFTRs, we compared them with the EST and mRNA sequences retrieved from UCSC or NCBI database, and genes predicted by N-SCAN (<http://mblab.wustl.edu/predictions/Drosophila/dm3/>) or CONTRAST (<http://contra.stanford.edu/contrast/dm3.html>). We found approximately 14–23% CFTRs in each sample overlapped with these predicted genes (≥ 20 bp) at their corresponding genomic loci.

BLAST search

To determine potential products encoded by CFTR transcripts (e.g. protein coding sequences or non-coding RNA sequences), all CFTR sequences were extracted with a Perl script based on BDGP v5.0 and analyzed by BLASTX search against all non-redundant protein sequence with entries from GenPept, Swissprot, PIR, PDF, PDB and NCBI RefSeq (4-Oct-2007) downloaded from <ftp://ftp.ncbi.nih.gov/blast/db> (Dec, 24th, 2008). BLASTX were performed with local Linux system and the cutoffs were as following: minimum score = 50, e-value $\leq 10^{-6}$, percent identity $\geq 50\%$, and have a minimum match of 30 amino acids.

Box plot analysis

The distribution of gene expression level was analyzed using boxplot in the R programming environment (R version 2.5.0, downloaded from <http://www.r-project.org>). The box represents the 25th and 75th percentiles, with the 50th percentile as a black bar. The whiskers refer to the outliers which are at least 1.5x IQR (interquartile range) from the box. The Y axis represents the \log_2 RPKM value.

Real time RT-PCR validation

Real time RT-PCR was used to validate sample-specific isoforms in all four pair-wise comparisons. In each experiment, two biological samples were prepared independently to carry out the real time PCR experiments. For each PCR reaction, we run duplicates using SYBR Green PCR Master Mix (Fermentas #K0221) in an ABI 7300 system. The following

primers were used to validate corresponding genes for the their common regions (c) and isoform-specific regions:

p53.cF: GGAGAAGCAAAGGAACACACGCAA;
 p53.cR: ACTCGATTCCGCTGAACAAGCTCT;
 p53.RA-F: ATTCCGATCCCGATACCTCCACC;
 p53.RA-R: CAGCCAATGTCGTGGCACAAAGAA;
 p53.RB-F: CTCTGCAGAACTTCGTTGCCGAT;
 p53.RB-R: GCGGACACAAATCGCAACTGCTAA;
 rab14.cF: TCTGGAGACCGCACGCAAGATTTA;
 rab14.cR: TTTAGCACGAGCACTGATCCTTGG;
 rab14.RA-F: ATTGCAATCGAATTCCGCACAGCC;
 rab14.RA-R: TTTAGTCCACCTTAGGGAGCGAAC;
 rab14.RB-F: TAAGCAGCGACTACGGTTGGACAT;
 rab14.RB-R: TGCGCACTTTGCTCATCTTGACAC.
 exu.cF: ACTTGTCACCTCCTGCTCCAAACT;
 exu.cR: TGCTCGAGCTTCTGGACAGCTATT;
 exu.RA-F: ACGCCCACCAGGATATAATTACCG;
 exu.RA-R: AAAGCGAAAGAGCCCATCGAAACC;
 exu.RB-F: ACGCCCACCAGGATATAATTACCG;
 exu.RB-R: ATCTAGTGAAAGCGGTTGCGGT;
 imp.cF: CATTTCGCTCTGCACAAGAATGCG;
 imp.cR: TGTTGGTCTGAACGGTGTGAGTT;
 imp.RA/RC/RB-F: CTGGCCGACTGTTGAGTTTCTTTC;
 imp.RA/RC/RB-R: GCAATAACTACAACAACACACGGCT;
 imp.RG/RH-F: AACTTGGTTGTGCGTTGCGA;
 imp.RG/RH-R: AAGGCCAAAGGAAAGGCCGAAAGAC;

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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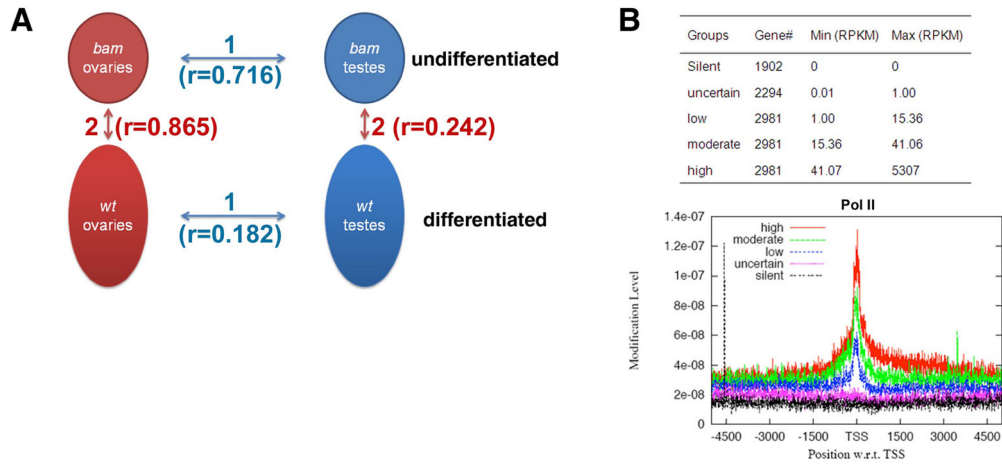


Figure 1. Generation of gonadal transcriptomes using RNA-seq

(A) The four samples used for RNA-seq and four pair-wise comparisons in two categories to investigate: 1. sex-biased; 2. stage-specific patterns of gene expression and alternative splicing; (B) The anti-RNA Pol II ChIP-seq results using the *bam* testis sample. The five gene groups were classified according to their RPKM value based on RNA-seq results. The thresholds for low, moderate and high expression level were set up to reach the same number of genes in each group.

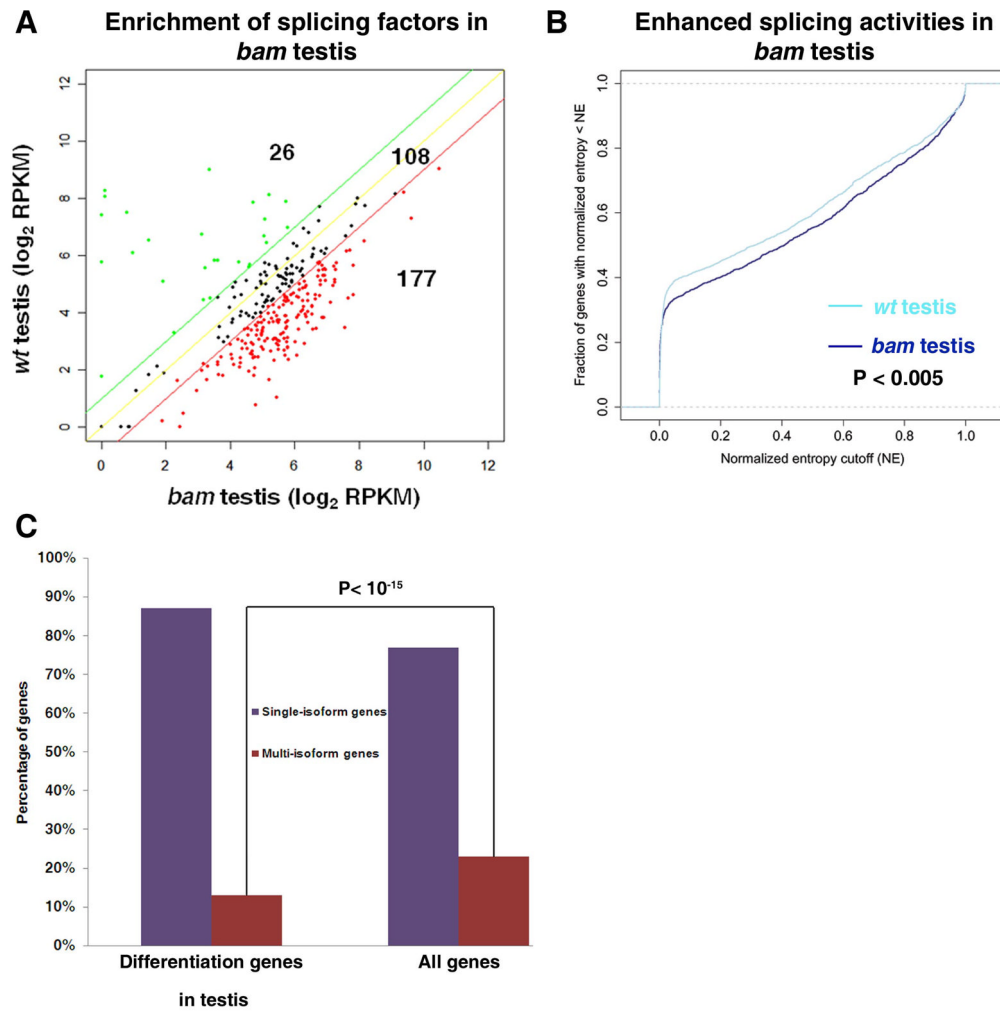


Figure 3. Enhanced splicing activities in undifferentiated cell-enriched *bam* testis

(A) Expression of splicing factors is up-regulated in *bam* testis compared to *wt* testis. The red and green lines are the 2-fold cutoff lines. 177 splicing factors are 2-fold more enriched in *bam* testis relative to *wt* testis; while 26 splicing factors are 2-fold more enriched in *wt* testis relative to *bam* testis. The enrichment of splicing factors in *bam* testis is significant ($P < 10^{-15}$). P-value was calculated using the chi-square test. (B) Enhanced overall splicing activities in *bam* testis compared to *wt* testis, shown by the CDF plot. P-value was calculated using one-sided Kolmogorov-Smirnov test. (C) Percentage of differentiation genes as single-isoform vs. multi-isoform genes [Differentiation genes are defined as silent in *bam* testis (RPKM in *bam* testis < 0.5); but are expressed in *wt* testis (RPKM in *wt* testis ≥ 1).]. Only 13% of the differentiation genes are multi-isoform genes, which is significantly ($P < 10^{-15}$) lower than the 23% genome-wide proportion of multi-isoform genes, based on the Ensembl annotation. The P value was calculated using one-sided Fisher exact test.

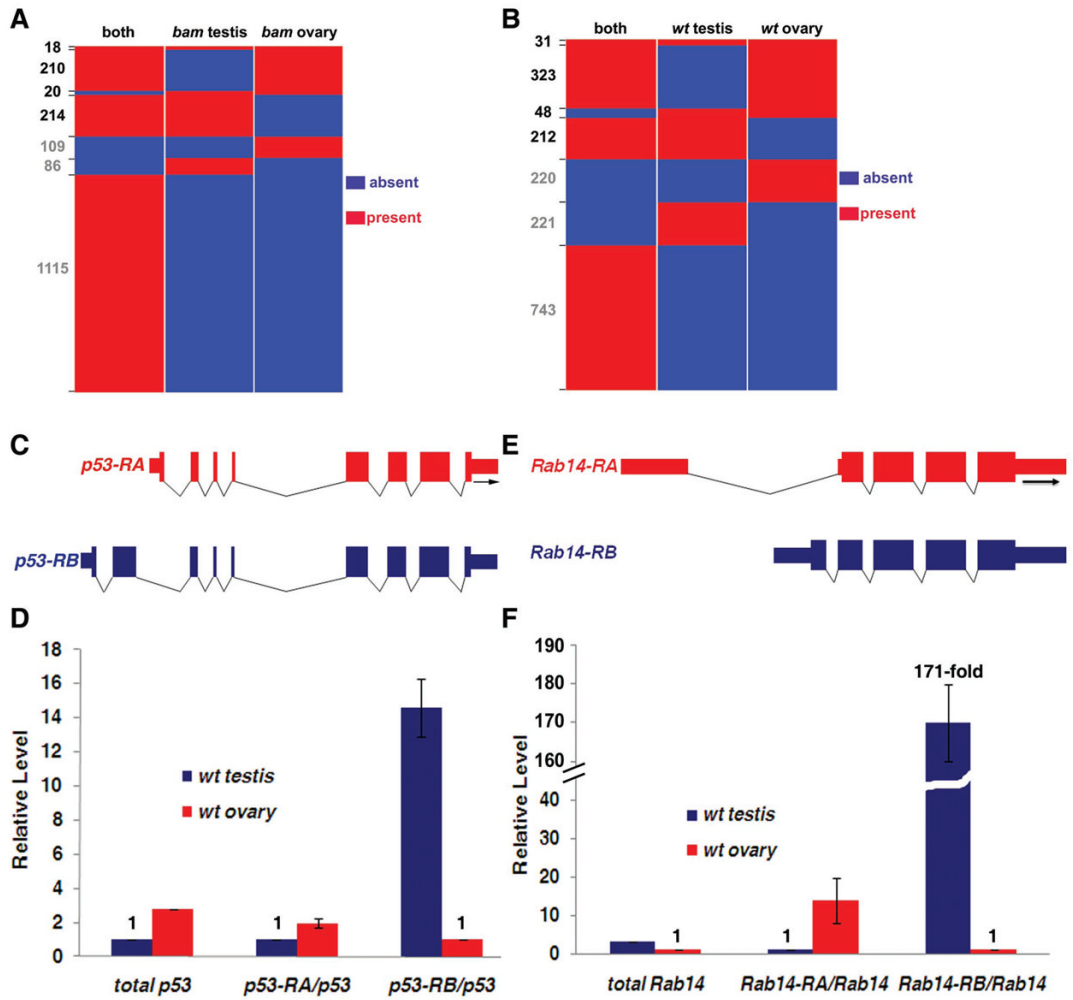


Figure 4. Visualization of sex-specific isoforms of individual genes in *bam* and *wt* testis vs. ovary comparisons

(A) Genes with sex-specific isoforms in *bam* testis vs. *bam* ovary. All genes with ≥ 2 uniquely detectable isoforms (Methods) were analyzed for the presence (red) and absence (blue) of sex-specific isoforms. Presence (red) in “both” category indicated that the corresponding gene has at least one isoform expressed in both *bam* testis and *bam* ovary samples. The gene numbers of each class were labeled on the Y-axis of the panel. The RRR, RBR, BRR and RRB classes had at least one sex-specific isoform, therefore were labeled as black numbers (see Table S4-1 for details.). (B) Genes with sex-specific isoforms in *wt* testis vs. *wt* ovary. The presence (red) and absence (blue) of sex-specific isoforms for each individual gene were analyzed in *wt* testis and *wt* ovary samples; the presence (red) in both somatic samples indicated a lack of sex specificity for a particular isoform(s) of an individual gene (Table S4-2). (C) The *wt* ovary-biased *p53* isoform is *CG33336-RA* or *FBtr0084359*. The *wt* testis-biased *p53* isoform is *CG33336-RB* or *FBtr0084360*. (D) Real-time RT-PCR using isoform-specific primer sets showed that *p53-RA* is about 2-fold more enriched in *wt* ovary compared to *wt* testis; while *p53-RB* is approximately 14.6-fold more enriched in *wt* testis compared to *wt* ovary. The level of both *p53-RA* and *p53-RB* were normalized to the total *p53* level, using a primer set that amplifies a common region of both isoforms (Methods). The total *p53* level in *wt* ovary and *wt* testis was also shown, which has been normalized to the sample with a smaller RPKM (*wt* testis in this case, Table S1). (E)

The *wt* ovary-biased *Rab14* isoform is *CG4212-RA* or FBtr0080626. The *wt* testis-biased *Rab14* isoform is *CG4212-RB* or FBtr0080627. (F) Real-time RT-PCR using isoform-specific primer sets showed that *Rab14-RA* is about 13.9-fold more enriched in *wt* ovary compared to *wt* testis; while *Rab14-RB* is approximately 171.4-fold more enriched in *wt* testis compared to *wt* ovary. The level of both *Rab14-RA* and *Rab14-RB* were normalized to the total *Rab14* level, using a primer set that amplifies a common region of both isoforms (Methods). The total *Rab14* level in *wt* ovary and *wt* testis was also shown, which has been normalized to the sample with a smaller RPKM (*wt* ovary in this case, Table S1).

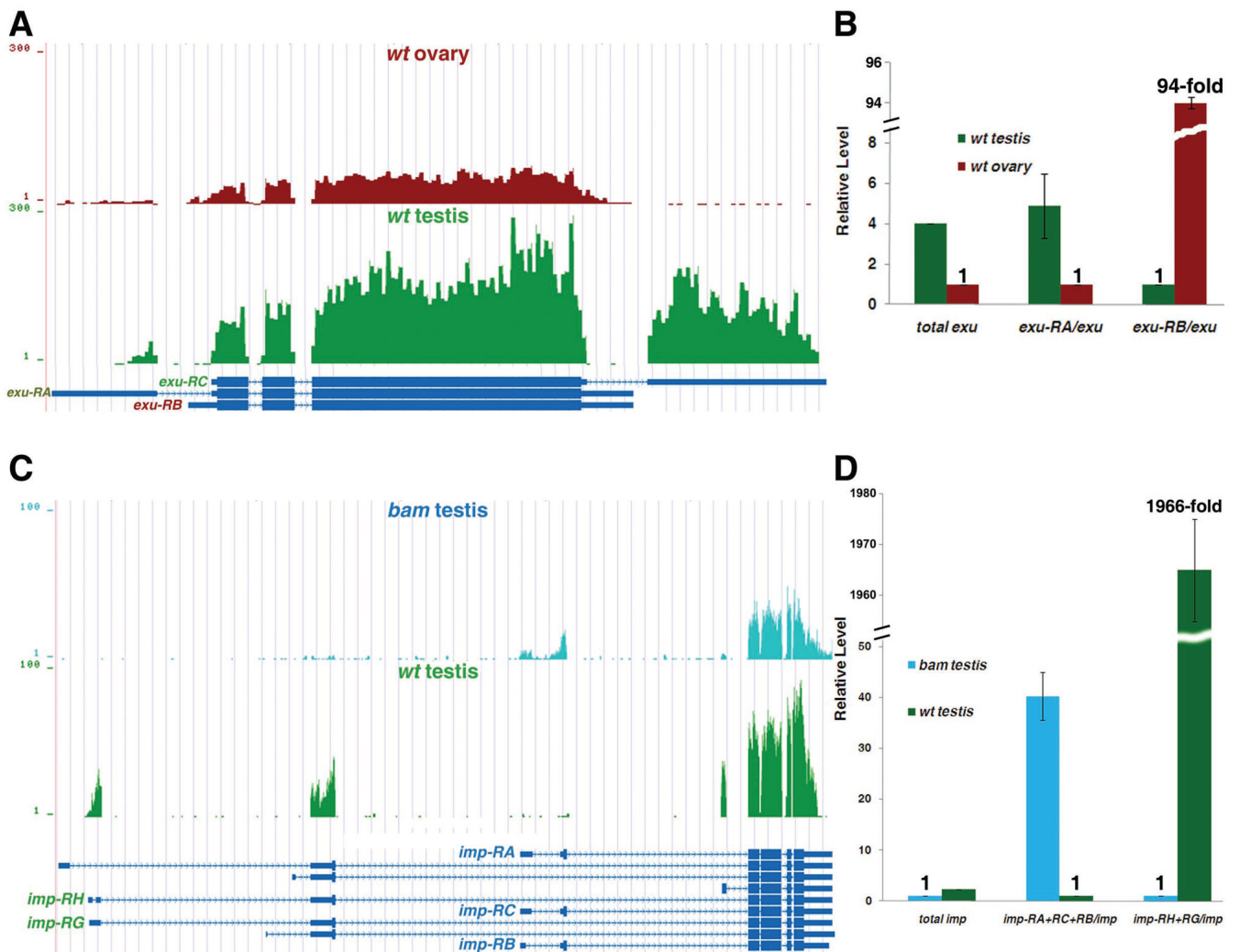


Figure 5. Examples of characterized or putative splicing factors that have sex- or stage-specific isoforms

(A) UCSC snapshots show that the *exu* gene has sex-specific and sex-biased isoforms: *exu-RC* is *wt testis*-specific, *exu-RA* is *wt testis*-biased and *exu-RB* is *wt ovary*-biased isoforms, respectively. (B) Real-time RT-PCR results showed that *exu-RA* is 4.9-fold more enriched in *wt testis* compared to *wt ovary*; while *exu-RB* is approximately 94.3-fold more enriched in *wt ovary* compared to *wt testis*. The level of both *exu-RA* and *exu-RB* were normalized to the total *exu* level, using a primer set that amplifies a common region of all three isoforms (Methods). The total *exu* level in *wt ovary* and *wt testis* was also shown, which has been normalized to the sample with a smaller RPKM (*wt ovary* in this case, Table S1). (C) UCSC snapshots show that the *imp* gene is expressed in both undifferentiated spermatogonia-enriched *bam testis* and differentiating spermatids-containing *wt testis*. The *imp* gene has stage-specific isoforms: *imp-RA/RB/RC* are *bam testis*-specific, and *imp-RG/RH* are *wt testis*-specific. (D) Real-time RT-PCR results showed that *imp-RA/RB/RC* are 40.2-fold more enriched in *bam testis* compared to *wt testis*; while *imp-RG/RH* are approximately 1,966-fold more enriched in *wt testis* compared to *bam testis*. The level of both subsets of *imp* isoforms were normalized to the total *imp* level, using a primer set that amplifies a common region of all isoforms (Methods). The total *imp* level in *bam testis* and *wt testis* was

also shown, which has been normalized to the sample with a smaller RPKM (*bam* testis in this case, Table S1).

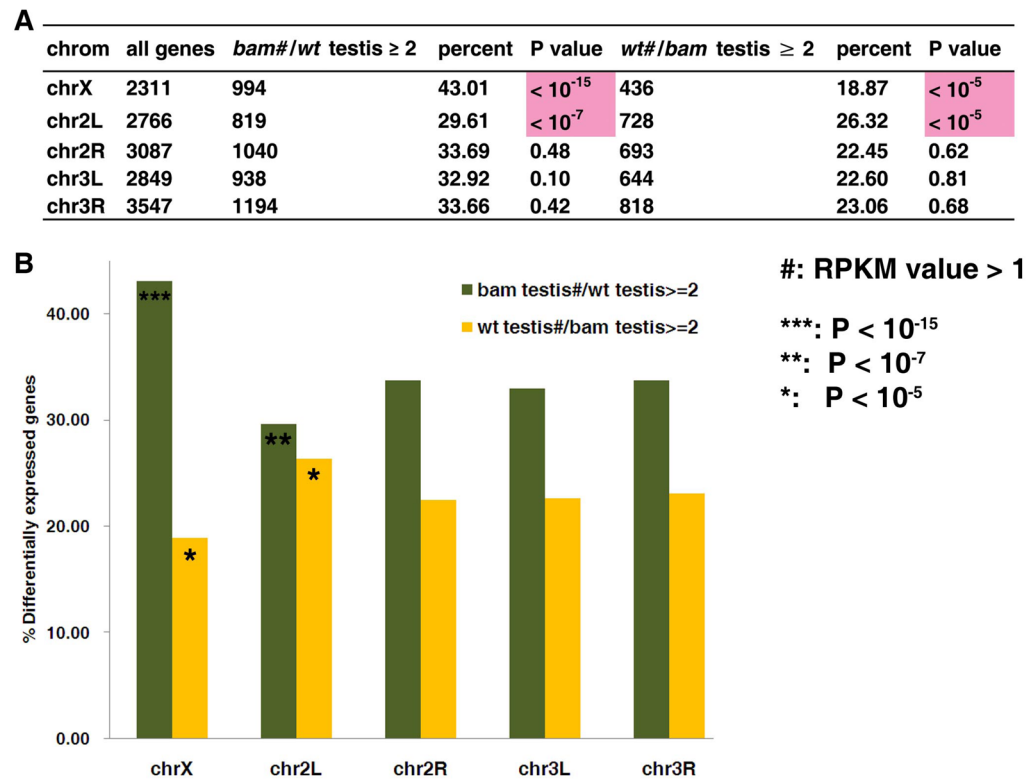


Figure 6. Preferential gene distribution of testis terminal differentiation genes on the 2L chromosomal arm

Preferential chromosomal distribution of stage-biased genes in testis on the X chromosome and the 2L chromosomal arm: Percentage was calculated as the differentially expressed genes (≥ 2 -fold change)/ total genes on a particular chromosome arm (X, 2L, 2R, 3L and 3R). To calculate the ratio of RPKM of *bam* testis/ *wt* testis or *wt* testis/ *bam* testis, the RPKM value was set to 0.5 if it less than 0.5. P-value was calculated with the Pearson's chi-squared test (Method).

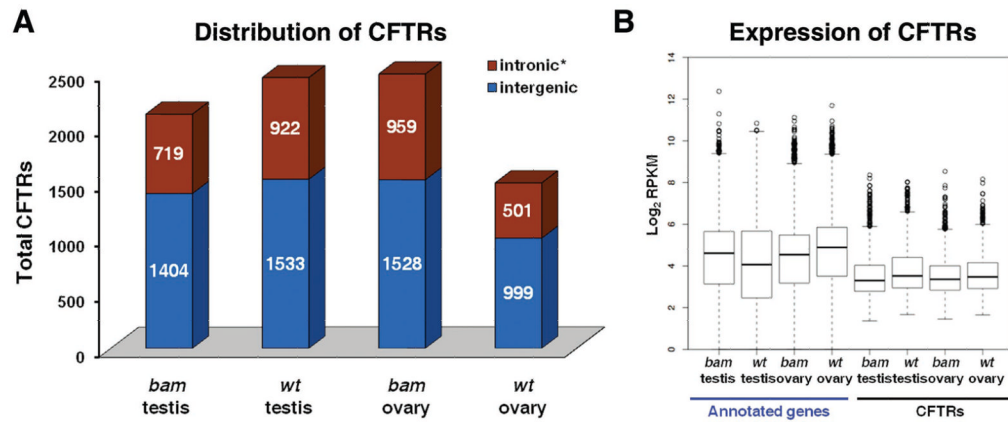


Figure 7. New features of the *Drosophila* gonadal transcriptome

(A) Distribution of identified CFTRs at the intronic and intergenic regions, based on the Ensembl annotation (<http://www.ensembl.org/index.html>) and the most update Flybase version (r5.19). *: Retained intronic CFTR must have a RPKM value greater than 10% of the RPKM(s) of the neighboring gene(s), to avoid contamination from pre-mRNAs. (B) Box plot of the expression level (\log_2 RPKM) of annotated expressed genes and CFTRs in all four samples.

Table 1Summary of the *Drosophila* RNA-seq results.

Mapping summary	<i>bam testis</i>	<i>wt testis</i>	<i>bam ovary</i>	<i>wt ovary</i>
Total reads	41730579	30013546	32806238	29736261
Low-quality and no matched reads	14736702	8645118	14287662	8220597
Reads with multiple matches (>1 hits)	6952842	2667877	1862272	1094363
Uniquely mapped reads (genomic+junction)	20041035	18700551	16656304	20421301
Uniquely mapped non-redundant reads (genomic+junction)	13028364	10853191	11765719	11206968
Uniquely mapped non-redundant reads (genomic+junction) subsample	10163916	10163916	10163916	10163916
Uniquely mapped non-redundant reads (genomic)	9780037	9827900	9763089	9774561
Uniquely mapped non-redundant reads (junction)	383879	336016	400827	389355
Unique and non-redundant reads mapping to annotated exons	9311716	9416811	9216015	9444989
Unique and non-redundant reads mapping to annotated introns	208725	174567	274958	152291
Unique and non-redundant reads mapping to intergenic region	259596	236522	272116	177281
ENSEMBL genes with at least 1RPKM	9383	10735	9486	8434
ENSEMBL genes with at least 5RPKM	7777	8233	7828	7147
Alternatively spliced genes	989	805	988	879
Total CFTRs	2123	2455	2487	1500
CFTRs in intron *	719	922	959	501
CFTRs in intergenic regions	1404	1533	1528	999
CFTRs supported by mRNA or EST	1402	1149	1727	1241
CFTRs predicted by N-SCAN or CONTRAST	332	370	408	304
CFTRs hit to NCBI non-redundant protein sequence	227	378	223	150
Average length of CFTRs (bp)	419	348	417	415

* The RPKM of intronic CFTRs are $\geq 10\%$ of neighboring gene's (or genes') RPKM.

Table 2

Chromatin regulators are enriched in *bam* testis compared to *wt* testis

The chromatin remodeling factors were retrieved from http://web.wi.mit.edu/young/pub/chromatin_remodeling.html; the histone modifying enzymes were from ⁹⁹⁻¹⁰⁷ (All chromatin remodeling factors and histone modifying enzymes listed here are supported by published research papers.). For each chromatin regulator, the fold change in *bam/wt* gonads is listed, as well as the RPKM values in *bam* and *wt* gonads, respectively. Red numbers indicate enrichment in *bam* gonads, and blue numbers indicate enrichment in *wt* gonads. Most of the chromatin regulators have high expression in *bam* testis (RPKM > 10), therefore the down-regulation in *wt* testis is significant.

Gene Name	<i>bam/wt</i> testis (RPKM)	<i>bam</i> testis (RPKM)	<i>wt</i> testis (RPKM)	Gene Name	<i>bam/wt</i> testis (RPKM)	<i>bam</i> testis (RPKM)	<i>wt</i> testis (RPKM)	Gene Name	<i>bam/wt</i> ovary (RPKM)	<i>bam</i> ovary (RPKM)	<i>wt</i> ovary (RPKM)			
Rpd3	15.35	158.02	10.29	CG11033	4.70	43.67	9.30	trr	3.05	26.58	8.72	2.81	48.70	17.31
ph-p	13.46	17.27	1.28	Suv4-20	4.56	78.75	17.25	mof	2.90	34.20	11.80	2.29	122.00	53.20
Art4	11.92	43.10	3.62	kis	4.45	120.73	27.16	tlk	2.89	80.46	27.86	0.29	8.37	28.63
CG3654	8.45	48.74	5.77	Mi-2	4.30	138.92	32.32	Snr1	2.82	59.58	21.12	0.36	26.46	73.45
tara	8.38	17.31	2.07	osa	4.20	174.52	41.54	Su(var)3-9	2.74	85.46	31.20	0.37	28.12	75.50
mod	8.24	127.82	15.52	CG13902	4.19	22.48	5.36	Su(var)2-HP2	2.58	37.82	14.65	0.48	14.46	30.38
egg	6.77	76.40	11.29	ial	4.11	56.06	13.62	CG2982	2.52	72.24	28.65	0.48	28.40	59.37
MED21	6.53	14.72	2.25	E(z)	4.06	51.80	12.75	wda	2.48	18.39	7.42	0.50	22.94	46.21
Psc	6.31	15.90	2.52	not	4.02	66.83	16.62	Hcf	2.32	43.82	18.91	0.49	23.64	48.50
Rpb4	6.19	20.81	3.36	Bre1	3.96	52.01	13.13	Su(var)3-3	2.27	28.13	12.39	0.50	29.84	60.13
BAP60	6.12	69.93	11.43	CG12879	3.90	15.40	3.95	See	2.17	47.07	21.73	0.50	29.84	60.13
esc	6.03	51.57	8.55	CG8165	3.87	10.56	2.73	Invadolysin	2.14	50.45	23.56	0.50	29.84	60.13
BAP55	5.77	87.57	15.17	phol	3.77	68.00	18.03	Su(var)205	2.14	101.00	47.23	0.50	29.84	60.13
lid	5.56	149.49	26.87	pr-set7	3.52	44.45	12.64	TafI	2.05	46.89	22.86	0.50	29.84	60.13
Hdac3	5.56	68.80	12.38	Nurf-38	3.39	191.34	56.43	ash1	0.49	18.95	38.48	0.50	29.84	60.13
Art1	5.53	140.78	25.47	Sir2	3.37	39.03	11.58	Ms35Ba	0.49	0.00	84.60	0.50	29.84	60.13
mor	5.39	103.02	19.12	trx	3.28	29.73	9.07	Kdm4B	0.49	54.43	111.24	0.50	29.84	60.13
Dpl	5.37	157.07	29.24	Pc	3.28	12.13	3.70	tna	0.21	42.48	205.15	0.50	29.84	60.13
Elp3	5.30	57.39	10.83	Nurf55	3.21	123.73	38.50	Ms35Bb	0.01	0.00	135.32	0.50	29.84	60.13
Acf1	4.97	55.55	11.17	HDAC4	3.16	31.95	10.12	CG31281	0.00	0.00	282.35	0.50	29.84	60.13
Peaf	4.86	50.72	10.44	Su(z)12	3.10	75.43	24.30							

Table 3
Genes that exhibit sex-specific or sex-biased isoforms in *bam* and *wt* gonads

Genes that encode transcription factors or putative transcription factors were highlighted in red. Genes that encode splicing factors or putative splicing factors were highlighted in yellow.

<i>bam</i> testis vs. <i>bam</i> ovary	<i>wt</i> testis vs. <i>wt</i> ovary	<i>wt</i> testis vs. <i>wt</i> ovary
CG18812 (unknown)	CG6151 (unknown)	mge (transmembrane transporter activit)
Jbug (actin binding)	CG6767 (ribose phosphate diphosphokinase activity)	Mlf (unknown)
ltd (GTPase activity)	CG6921 (unknown)	mud (protein binding)
Mctp (unknown)	CG8709 (unknown)	Pabp (mRNA 3'-UTR binding)
PRL-1 tyrosine phosphatase activity)	cnn (microtubule binding)	Pfk (6-phosphofructokinase ac)
<i>wt</i> testis vs. <i>wt</i> ovary	CoRest (chromatin binding)	PhKgamma (phosphorylase kinase activity)
Alh (transcription factor activity)	Cpr (NADPH-hemoprotein reductase activity)	Picot (high affinity inorganic phosphate:sodium symporter activity)
aop (protein binding)	CycB (cyclin-dependent protein kinase regulator activity)	qua (actin binding)
aret (RNA binding)	eIF-4E (translation initiation factor activity)	Rab14 (GTPase activity)
BicC (protein binding)	exu (RNA localization)	rdx (protein binding)
bun (protein homodimerization activity)	fs(2)ltoPP43 (unknown)	Rpn6 (endopeptidase activity)
capu (microtubule binding)	garz (guanyl-nucleotide exchange factor activity)	Rtn1 (unknown)
Cbl (ligase activity)	granny-smith (aminopeptidase activity)	sgg (protein kinase activity)
CG12360 (unknown)	Hmgcr (NADPH activity)	sle (unknown)
CG1244 (ATPase activity)	I-2 (phosphoprotein phosphatase inhibitor activity)	smg (translation repressor activity)
CG14619 (ubiquitin-specific protease)	Imp (mRNA bindin)	SPoCk (manganese-transporting ATPase activity)
CG1640 (L-alanine:2-oxoglutarate aminotransferase activity)	p53 (transcription factor activity)	SRPK (protein kinase activity)
CG17034 (ATPase activity)	jog (unknown)	ssh (protein phosphatase activity)
CG18135 (protein binding)	kdn (citrate synthase activity)	tamo (protein binding)
CG1882 (catalytic activity)	kis (ATP-dependent helicase activity)	toc (protein kinase binding)
CG3074 (endopeptidase activity)	klar (protein binding)	Tpi (triose-phosphate isomerase activity)
CG33523 (structural molecule activity)	Lk6 (protein kinase activity)	Tpr2 (heat shock protein binding)
CG3994 (zinc ion transmembrane transporter activity)	lola (transcription factor activity)	vig (mRNA binding)
CG4238 (ubiquitin-protein ligase activity)	ltd (GTPase activity)	CG5315 (hormone binding)