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Tan *et al.* - *Xenopus* transcriptome

RNA sequencing reveals diverse and dynamic repertoire of the *Xenopus tropicalis* transcriptome over development

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ABSTRACT

The *Xenopus* embryo has provided key insights into fate specification, the cell cycle, and other fundamental developmental and cellular processes, yet a comprehensive understanding of its transcriptome is lacking. Here, we used paired end RNA sequencing (RNA-seq) to explore the transcriptome of *Xenopus tropicalis* in 23 distinct developmental stages. We determined expression levels of all genes annotated in RefSeq and Ensembl and showed for the first time on a genome-wide scale that, despite a general state of transcriptional silence in the earliest stages of development, ~150 genes are transcribed prior to the midblastula transition. In addition, our splicing analysis uncovered more than 10,000 novel splice junctions at each stage and revealed that many known genes have additional unannotated isoforms. Furthermore, we used Cufflinks to reconstruct transcripts from our RNA-seq data and found that ~13.5% of the final contigs are derived from novel transcribed regions, both within introns and in intergenic regions. We then developed a filtering pipeline to separate protein-coding transcripts from non-coding RNAs and identified a confident set of 6,686 non-coding transcripts in 3,859 genomic loci. Since the current reference genome, XenTro3, consists of hundreds of scaffolds instead of full chromosomes, we also performed *de novo* reconstruction of the transcriptome using Trinity and uncovered hundreds of transcripts that are missing from the genome. Collectively, our data will not only aid in completing the assembly of the *Xenopus tropicalis* genome but will also serve as a valuable resource for gene discovery and for unraveling the fundamental mechanisms of vertebrate embryogenesis.

INTRODUCTION

Xenopus is one of the major model systems for the study of vertebrate embryogenesis and basic cell biological processes. There are multiple advantages to the use of *Xenopus* as an experimental system, such as the availability of large abundant eggs that are easily manipulated, ready accessibility to any developmental stage, and conservation of cellular pathways between *Xenopus* and mammals. In the past 50 years, landmark studies on *Xenopus* have been critical towards our understanding of nuclear reprogramming (Gurdon, et al, 1958), embryonic patterning (Harland, et al, 1997, De Robertis, 2006), membrane channels and receptors (Kusano, et al, 1977), and cell cycle control (Murray, et al, 1989a, Murray, et al, 1989b, Glotzer, et al, 1991).

Genomics resources for *Xenopus* research have emerged in the past 10-15 years. During the early days of the genomics era, several cDNA sequencing efforts, such as EST (expressed sequence tag) projects, have allowed the construction of full length cDNA clones and identification of *Xenopus* open reading frames (ORFs) (Gilchrist, et al, 2004, Morin, et al, 2006, Fierro, et al, 2007). Microarrays have also been used to investigate the expression levels of annotated genes and gave some insights into transcriptome changes over development as well as expression differences between two closely-related frog species, *Xenopus laevis* and *Xenopus tropicalis* (Yanai, et al, 2011). In addition, forward and reverse genetic screens have uncovered mutations that affect a myriad of organogenesis and differentiation processes in *Xenopus* (Goda, et al, 2006), while a genetic map based on simple sequence length polymorphism (SSLP) markers, which can be used to clone genes identified by mutation, has recently been generated (Wells, et al, 2011).

Notably, while early developmental and molecular studies have been performed on *Xenopus laevis*, its closely-related cousin *Xenopus tropicalis* has proven to be more widely used for genetic and genomic research. This is mainly because *Xenopus laevis* has a more complex pseudotetraploid genome, while *Xenopus tropicalis* has a smaller and more amenable diploid genome. Hence, the initial genome sequencing effort has been directed mostly at *Xenopus tropicalis*, whose genome has recently been published (Hellsten, et al, 2010). Strikingly, the frog genome is highly syntenic with the human genome, with regions of synteny frequently spanning

Tan *et al.* - *Xenopus* transcriptome

more than a hundred genes. Nevertheless, while it is largely assembled into multiple scaffolds, the *Xenopus tropicalis* genome is yet to be sequenced at the same depth and annotated at the same level of details and accuracy as the genomes of human and mouse. Importantly, annotations of protein-coding and non-coding genes are strikingly incomplete, including the widely used RefSeq and Ensembl annotations.

The advent of high-throughput sequencing technologies has had an enormous impact on genomics. In particular, such technologies have revolutionized studies of the transcriptome in many species from yeast to humans and have revealed tremendous amounts of complexities and gaps in our understanding of any transcriptome (Wang, et al, 2009). Not only does RNA sequencing (RNA-seq) provide a more accurate measurement of expression levels, it provides single nucleotide resolution and has the ability to reveal novel splice junctions, unannotated transcripts, and allele-specific expression. Here, we present the first comprehensive study of the transcriptome of *Xenopus tropicalis* using RNA-seq over development from a two-cell fertilized embryo to a feeding tadpole. We report evidence for transcription of more than a hundred genes prior to the midblastula transition, when the embryonic genome is generally believed to be transcriptionally silent. We also discovered thousands of novel splicing events, including exon skipping in annotated genes, as well as thousands of unannotated, potentially non-coding transcripts. Hence, our data serve as a valuable resource for developmental biologists and the general genomics community. Furthermore, to extend the reach of our work, we have created an interactive website (<http://hci.stanford.edu/~jcchuang/frog-genes/latest/>) that allows users to not only browse the heatmaps in this manuscript but to also query the expression profile of any RefSeq or Ensembl annotated gene with ease.

RESULTS

Mapping and analysis of RNA-seq reads

To systematically examine the dynamics of the *Xenopus* transcriptome over development, we generated RNA-seq libraries for 23 distinct groups of stages (Figure 1A). As biological replicates, we collected embryos from two different clutches (see Methods for detailed descriptions of the stages) and made libraries for each replicate independently. We first mapped the reads to the XenTro3 genome (JGI assembly v4.2) using SeqMap (Jiang, et al, 2008) and calculated the RPKMs (Reads Per Kilobase per Million mapped reads) for each replicate separately using RSeq (Jiang, et al, 2009). A comparison of the two replicates showed that the expression values between identical stages were highly correlated (average $R^2 = 0.916$) (Figure S1). Hence, for the same group of stages, we pooled all the reads together to improve statistical power, resulting in 20 to 70 million reads for each group, and re-calculated all the RPKMs. Out of all the reads, about 46.9% were mappable to RefSeq annotations, while about 60.5% were mappable to Ensembl annotations (Figure 1B). Overall, we detected 97.3% of the RefSeq genes that are annotated in the genome (or 8211 out of 8437 genes) at any time of development and 80.5% of the annotated Ensembl genes (or 16012 out of 19884 genes) (Figure 1C). Furthermore, our RNA-seq results are in reasonable agreement with previously published microarray data (Yanai, et al, 2011) (Figures S2-S3 and Supplemental Information). The expression levels based on the RefSeq annotation and the Ensembl annotation are given in Supplementary Files S1 and S2 respectively, while the distribution of the RPKM values over all developmental stages is displayed as a box-and-whisker plot in Figure S4.

We asked if the *Xenopus* transcriptome can be categorized into group defining patterns. K-means clustering across all stages revealed that the majority of the annotated genes are temporally regulated over development and may be broadly classified into eight distinct clusters (Figure 1D and Figure S5). To gain insights into the functional significance of the eight clusters, we performed Gene Ontology (GO) analysis using the Panther classification system (Thomas, et al, 2006). The first cluster is enriched for genes associated with protein phosphorylation, meiosis, and DNA repair, including genes encoding MAPK signaling proteins and serine/threonine kinases. Notably, the second cluster is enriched for genes associated with RNA processing, in

Tan *et al.* - *Xenopus* transcriptome

particular splicing, which indicates an important role for post-transcriptional regulation during the early developmental stages. The third cluster is associated with protein localization, signal transduction, and transcription from the RNA polymerase II promoter, which correlates well with activation of the embryonic genome. Strikingly, the fourth and fifth clusters are enriched for genes associated with multiple developmental processes, including anterior-posterior axis specification, segment specification, ectoderm development, and mesoderm development. In addition, the sixth cluster is strongly enriched for genes associated with translation and contains dozens of genes encoding ribosomal proteins. As evidence has recently emerged to show that ribosomes can function as regulators of key tissue patterning events during vertebrate embryogenesis (Kondrashov, et al, 2011), our analysis hints at potential tissue-specific roles for the ribosome during *Xenopus* organogenesis. Finally, the seventh cluster is associated with steroid or lipid metabolism, response to external stimulus, and respiration, while the eighth cluster is associated with coenzyme or fatty acid metabolism and mitochondrion-related processes. The full list of GO terms for each cluster ($p < 0.1$) is provided in Supplementary File S3.

Identification of genes transcribed prior to the midblastula transition

Following fertilization, the beginning stages of development in many organisms are thought to be transcriptionally silent until the midblastula transition when large scale activation of zygotic genes occurs. This period of transcriptional quiescence lasts until the twelfth cell division in *Xenopus* embryos (approximately Stage 8.5). However, despite the general state of transcriptional repression in the earliest stages, a few genes, including the nodal-related genes *xnr5* and *xnr6*, have been found to be activated prior to the midblastula transition (Yang, et al, 2002). Here, we sought to identify genome-wide all the genes that are transcribed before the transition.

From our datasets corresponding to the pre-midblastula transition stages (2-cell to Stage 8), we detected a total of 7,187 RefSeq genes. Clustering analysis reveals that these genes can be broadly divided into four clusters (Figure 2A). The first cluster contains the set of genes whose RNAs are rapidly degraded after fertilization and the genes may be expressed again at the

Tan *et al.* - *Xenopus* transcriptome

approach of the transition. The second cluster corresponds to the transcripts that appear to be degraded more slowly and hence persist for a longer period of time but are nevertheless absent by Stage 8. The third cluster represents the set of genes whose transcript levels gradually increase over development. Finally, the fourth cluster contains the genes whose expression is more sharply activated closer to the midblastula transition compared to the previous cluster. Importantly, the last two clusters appear to contain numerous genes that are transcribed prior to the transition despite the general state of transcriptional silence.

To confidently identify a set of genes whose transcription is activated before the midblastula transition, we imposed three criteria. First, we require that the RPKM at Stage 6 is at least two-fold higher than the RPKM at the 2-cell stage. We chose Stage 6 instead of Stage 8 because even though embryonic genome activation occurs at Stage 8.5, the time of its onset can vary on factors like temperature changes and we wanted to be certain that we are examining timepoints significantly prior to the transition. Second, we require an average RPKM of at least 1 for each gene. Third, we require that the expression level is monotonically increasing. A total of 150 genes passed all the three filters. GO analysis of these genes reveals that they are associated with the cell cycle, apoptosis, signal transduction, and phosphorylation (Figure 2B). In addition, we found that 24% of them (or 36 genes) are also transcribed prior to the midblastula transition in zebrafish (Aanes, et al, 2011). The list of 150 genes, together with their expression profiles and associated GO terms are provided in Supplementary File S4.

We used quantitative real-time PCR (RT-qPCR) to validate the expression patterns observed from RNA-seq (Figure 2C). In the validation experiments, we focused on the genes with an average RPKM of at least 20 and sorted them by fold change. Out of the top ten genes (fold change ranging from 2.82 to 4.26 according to RNA-seq), we were able to validate eight of them (*cdc14b*, *dpp8*, *btbd17*, *cdk5r2*, *arih2*, *slc9a3r1*, *loc100170544*, and *mtx1*). Out of the bottom ten genes (fold change ranging from 2.00 to 2.04), we were able to validate five of them (*slain2*, *lrrcc1*, *gart*, *oct25*, and *ets2*). Hence, we estimate the true positive rate to be between 50% and 80%.

We recognize that our three criteria above for identifying early-transcribed genes are somewhat arbitrary and may even be too stringent. In particular, our requirement for a monotonic increase in expression level may filter out *bona fide* genes whose RPKM values contain some

measurement error. When we loosened this criterion to allow for a decrease by 1 RPKM or a 20% drop in expression level between two consecutive developmental stages while maintaining the other two filters, we obtained a total of 313 genes (Supplementary File S5). GO analysis showed that this larger gene set is still associated with phosphorylation, the cell cycle, signal transduction, and apoptosis (Figure S6A). We further selected 8 genes for validation by RT-qPCR and were able to confirm 6 of them (Figure S6B). Taken together, our analysis showed that even though the embryonic genome is generally repressed prior to the midblastula transition, the transcripts of dozens, if not hundreds, of *Xenopus* genes actually increase in abundance even before the onset of widespread zygotic transcription. These findings are in good agreement with a similar observation in zebrafish, where hundreds of genes have been determined to be transcribed before the midblastula transition (Aanes, et al, 2011).

Detection and classification of novel splice junctions

Alternative splicing is a prevalent post-transcriptional mechanism in many higher eukaryotes to diversify the proteome. RNA-seq studies have revealed that more than 90% of multi-exon human genes undergo alternative splicing (Wang, et al, 2008, Pan, et al, 2008), while 60%, 50%, and 25% of genes in *Drosophila*, zebrafish, and *C. elegans* respectively can be alternatively spliced (Aanes, et al, 2011, Graveley, et al, 2011, Ramani, et al, 2011, Gerstein, et al, 2010). Here, we sought to understand splicing regulation in *Xenopus tropicalis* on a genome-wide scale.

To detect splice junctions, we applied SpliceMap (Au, et al, 2010) to our paired end RNA-seq datasets. We identified between 100,000 to 170,000 junctions at each developmental stage (Figure 3A). The varying number of junctions detected is largely due to different sequencing coverage between the various stages (Figure S7A). Importantly, we were able to detect a significant number of novel splicing events at every stage (red and blue colored portions in Figure 3A). On average, 27.4% of the total junctions identified at each developmental stage are absent from both the RefSeq and the Ensembl annotations, while 15.2% of the total detected junctions are not only novel but are also well-supported by at least two non-redundant reads

(nNR > 1) (Figure S7B). Furthermore, the majority of the novel junctions supported by at least two reads have additional backing from existing ESTs (Figure S8).

Next, we asked if annotated junctions are more likely to belong to isoforms that are either constitutively or more widely-expressed, while the novel junctions tend to belong to transcripts that are expressed only at specific stages of development and hence are more difficult to discover. To address this hypothesis, we divided our non-redundant set of splice junctions into three groups, namely annotated junctions, novel but weakly-supported junctions (nNR = 1), and novel but strongly-supported junctions (nNR > 1) and counted the number of stages that each junction can be detected in (Figure 3B). We found that the distribution of the annotated junctions is clearly different from the distribution of the novel junctions. Specifically, 21.1% of the annotated junctions were detected in all the 23 stages, while 0% (nNR = 1) or 8.5% (nNR > 1) of the novel junctions were detected in all the stages. In contrast, 12.5% of the annotated junctions were detected in only one developmental stage, while 54.2% (nNR = 1) or 27.2% (nNR > 1) of the novel junctions were detected in only a single stage. Furthermore, we found that despite our deep sequencing efforts, we have not saturated the discovery of novel splicing events that occur in only one developmental stage (Figure S9 and Supplemental Information). Hence, our data support the hypothesis that many transcripts or isoforms are currently unannotated because they are hard to detect as a result of their low or temporally restricted expression.

It is possible that some of the novel junctions that we uncovered are a result of inexact splicing. The splice site signals are short and considerably degenerate (Stamm, et al, 2006) and the splicing machinery is not error-free (Hsu, et al, 2009), thereby generating debate over the likelihood that stochastic noise contributes to much of the observed mRNA diversity arising from alternative splicing (Melamud, et al, 2009). To obtain an estimate of the percentage of novel junctions that may be products of inexact splicing, we calculated the number of novel junctions that are within 3 basepairs of annotated junctions. Out of the 229,848 novel splicing events that we detected using SpliceMap, we found that 11,240 of them (4.89%) are shifted by 3 bases in either direction of annotated junctions. Although we cannot discern true functional transcripts from erroneously spliced ones, the small percentage lends support to the hypothesis that the majority of the novel junctions may have some biological impact during *Xenopus* development.

To gain additional insights into the novel junctions, we categorized them based on their genomic location and how they modify existing annotations (Figure 3C and Supplemental Table S1). While about a quarter of the novel junctions lie in intergenic regions, most of them occur within annotated genes. We found that the predominant way in which existing annotations may be modified is in the creation of novel 5' or 3' splice sites, which together account for 37.25% of the novel junctions. This may be due to non-canonical splice sites, incorrect demarcations of splice junctions in current databases, or the presence of extra exons. Furthermore, we discovered thousands of new exon skipping events and extensions of the 5'UTR or the 3'UTR. Using reverse transcription PCR, we went on to validate the existence of novel splice junctions in nine out of ten different transcripts (Figure 4, Figure S10-S14, and Supplemental Information). Taken together, our results indicate the existence of new isoforms for many known genes and also highlight the inadequacies of the present RefSeq and Ensembl annotations.

Novel transcribed regions of the genome

Numerous transcriptome studies have discovered that multicellular eukaryotic genomes are replete with unannotated transcripts that originate from intronic or intergenic regions (Manak, et al, 2006, Rinn, et al, 2007, Bertone, et al, 2004, Guttman, et al, 2009). In agreement with these previous studies, our splicing analysis of the frog transcriptome has uncovered thousands of novel splice junctions that do not simply modify existing gene structures but instead appear to belong to unknown gene models (Figure 3C, Figure 4F, and Figure S13). Hence, we sought to assemble transcripts from our RNA-seq data in order to identify novel transcribed regions of the *Xenopus* genome. We also developed a filtering pipeline aimed at separating the novel transcripts into two groups, namely the protein-coding transcripts and the non-coding RNAs (Figure 5A and Supplemental Information).

After transcript assembly using Cufflinks (Trapnell, et al, 2010), we asked how the reconstructed contigs compare with known genes annotated in the reference genome (XenTro3) (Figure 5B). As expected, essentially all the Cufflinks transcripts (> 99.9%) can be aligned to the genome. In addition, between 74.3% to 79.7% of the transcripts assembled by Cufflinks at each developmental stage matches a gene annotated in either RefSeq or Ensembl. When we applied

CuffMerge to all the individual contigs reconstructed at each stage, we obtained an overall set of 167,386 unique transcripts, of which 86.5% match a RefSeq or Ensembl gene. This higher percentage is likely a result of CuffMerge combining some shorter contigs with another transcript that already aligns to a known gene. In subsequent steps, we focused our attention on the set of merged transcripts.

Next, we examined the unannotated Cufflinks contigs (13.5% of the merged transcripts or 22,520 transcripts) for protein-coding potential. We searched existing protein databases and found 8,997 matches in the Pfam database and 8,252 matches in the Uniprot database (Figure S15A). In addition, we translated the contigs in all three forward frames and found that 8,887 of them may encode peptides that are at least 100 amino acids long. We further checked the *Xenopus* Cufflinks transcripts against annotated human and mouse protein-coding genes and uncovered 182 transcripts that showed at least 10% identity to a human or mouse protein-coding gene. Hence, our filters identified a total of 12,991 unannotated *Xenopus* Cufflinks transcripts as protein-coding (Figure 5C and Supplementary File S6), leaving 9,529 transcripts as potential non-coding RNAs.

In order to determine how many of the putative non-coding RNAs may actually correspond to known non-coding genes, we searched the Rfam and NONCODE databases for matches to the 9,529 Cufflinks transcripts that passed through the protein-coding filters (Figure S15B). For Rfam, we utilized the Infernal software package (Nawrocki, et al, 2009) to search for matches and identified 112 contigs that have hits to one of the database's secondary structure-based covariance models (score ≥ 40). Using BLASTN, we also found 200 contigs that could align to entries in NONCODE by sequence similarity. In addition, since many long intergenic non-coding RNAs (lincRNAs) are poorly conserved by sequence but instead share conserved genomic locations (Ulitsky, et al, 2011), we further searched the NONCODE database for matches by synteny and uncovered 812 intergenic contigs that shared the same neighboring genes as known non-coding RNAs. Besides the databases, we separately checked the *Xenopus* transcripts against annotated human and mouse non-coding genes and discovered 22 transcripts that showed at least 10% sequence identity to a known mammalian non-coding gene (Figure S15C). Hence, we identified a total of 1,046 *Xenopus* Cufflinks transcripts that matched known non-coding genes in other species and so, we consider this set of 1,046 transcripts to be

Tan *et al.* - *Xenopus* transcriptome

definitely non-coding (Figure 5C). Of these, we noted a contig that originates from the genomic locus between *hoxc11* and *hoxc12*, where a long intergenic non-coding RNA (lincRNA), *HOTAIR*, is known to be present in mammals (Rinn, et al, 2007). We further examined the mappings and observed that there are clusters of reads in the intergenic region between the two *hox* genes (Figure S16), which suggests that the putative *Xenopus HOTAIR* may be spliced. To validate the lincRNA, we performed reverse transcription PCR and obtained a product whose size is between 2,000 to 3,000bp (Figure 5D), which is similar to the length of *HOTAIR* in mammals. These results suggest that a *HOTAIR* ortholog exists beyond the mammalian lineage and can be found in the *Xenopus* genome.

To further analyze the non-coding RNAs, we categorized all the 9,529 potential non-coding Cufflinks contigs based on their genomic locations (Figure 5E). 79.6% of the contigs (or 7,585 transcripts) are intergenic, while the remainder overlap with annotated RefSeq or Ensembl genes. In addition, we note that intergenic contigs that are on the same strand as one of its neighboring genes may simply be an extension of the neighboring gene and therefore are not true independent non-coding RNAs. Similarly, intronic contigs that are on the same strand as the host gene may in fact represent additional exons of that gene. Hence, we also examined the strand of the non-coding Cufflinks contigs relative to their immediate neighboring or overlapping genes. 4,271 Cufflinks contigs are intergenic and on the same strand as one or both of their neighboring genes, while 3,314 contigs are intergenic and on the opposite strand. Furthermore, of the 1,944 contigs that are intragenic, 72.0% of them (or 1,400 contigs) are antisense transcripts. In summary, a total of 4,714 putative non-coding Cufflinks contigs originate from a different strand and they certainly represent novel transcripts.

Not all intergenic contigs that derive from the same strand as one of its immediate neighboring genes are extensions of their annotated neighbors; a portion of these intergenic contigs may be genuine independent transcripts. We rationalized that the further the contig is from its nearest same strand neighbor, the more likely the intergenic contig represents a novel standalone gene. Hence, we determined the distance between each intergenic Cufflinks contig and its nearest same strand neighbor and binned the contigs by their distance from the annotated neighboring gene (Figure 5F). The mean distance of an intergenic contig from its same strand neighbor is 37,250bp and the median distance is 10,605bp. Since more than 95% of *Xenopus*

Tan *et al.* - *Xenopus* transcriptome

introns annotated in RefSeq (Figure S17A) and approximately 95% of introns present in the extensively-annotated human genome (hg19) (Figure S17B) are shorter than 25kb, we reasoned that an intergenic transcript that is more than 25kb away from its nearest neighboring gene is unlikely to be part of that gene. Therefore, we estimate, with a false discovery rate (FDR) of 5%, that 1,359 intergenic *Xenopus* contigs that have a same strand neighbor are likely to originate from separate independent genes and represent genuine non-coding RNAs.

Collectively, our analysis has uncovered with confidence a total of 6,686 unannotated non-coding transcripts in 3,859 genomic loci (Supplementary File S6). Not only do they lack protein-coding potential, they also 1) match entries in NONCODE or Rfam based on sequence, syntenicity, or structure similarity, 2) are on a different strand from its neighboring or overlapping gene, or 3) are far away from a known protein-coding gene. We observed that the majority of these non-coding RNAs appear to be lowly expressed, with 67.6% of them (or 4,519 contigs) having a maximum FPKM (Fragments Per Kilobase per Million mapped fragments) of less than 5 (Figure S18A), thereby suggesting that even deeper sequencing is required to reveal the full repertoire of non-coding RNAs in *Xenopus*. In addition, the non-coding transcripts that we found in this study appear to be developmentally regulated (Figure S18B), which indicates that they may perform stage-specific functions during embryogenesis. In summary, our results have demonstrated the diversity and the dynamic regulation of the *Xenopus* transcriptome.

Assembly of transcripts beyond the current *Xenopus tropicalis* genome

Cufflinks is a mapping-first approach and uses the reference genome as a guide to build the transcripts. Conceptually, such mapping-first methods offer superior sensitivity than *de novo* assemblers. However, the current version of the *Xenopus tropicalis* genome is still incomplete and consists of hundreds of scaffolds with scattered gaps, which may cause Cufflinks to discard unaligned reads and miss some novel transcripts. Thus, besides Cufflinks, we also assembled transcripts *de novo* without a reference genome by applying Trinity (Grabherr, et al, 2011) to our RNA-seq data (Figure 5A).

We compared the assembled Trinity contigs with the RefSeq and Ensembl annotations as well as the *Xenopus tropicalis* genome. At every developmental stage, between 47.9% and

Tan *et al.* - *Xenopus* transcriptome

65.8% of the contigs match either annotation (E-value $< 1 \times 10^{-10}$) (Figure S19). Interestingly, we note that a small but substantial fraction of contigs (from 1.3% to 2.4%) have sequences that could not be aligned to any part of the genome. We asked if there are any *Xenopus* ESTs that support these unaligned Trinity contigs. At every stage, we found between 400 and 900 contigs that contained matches in the collection of ESTs (E-value $< 1 \times 10^{-10}$) but are missing from the genome (Figure 6A, grey portions). Next, we wondered if the remaining unaligned contigs with no EST support might be derived from contaminating sources. Hence, we used BLAST to remove all possible heterologous sequences from bacteria and fungi (Figure S20). In addition, we also discarded all contigs that matched cloning vectors or plasmids in the NCBI nucleotide collection database as another source of DNA contamination. Out of all the unaligned Trinity contigs with no EST evidence, 25.2% (or 2448 out of 9733 contigs) contain matches in bacteria genomes, 0.1% (or 8 contigs) may be attributed to fungal contamination, while 3.7% (359 contigs) match cloning vectors in the NCBI database. The sequences that passed through the filters are then deemed to be non-contaminating and to represent genuine *Xenopus* transcripts, even though they are not supported by ESTs (Figure 6A, unshaded portions). We checked these transcripts for protein-coding potential by the same filters used for analyzing the Cufflinks sequences and found that on average, 13.1% of them may encode proteins (Figure S21). In addition, we discovered that a small percentage of the non-contaminating unaligned Trinity contigs (from 0.3% to 7.8%) are conserved between *Xenopus* and humans, mice, or zebrafish (Supplementary File S7), which suggests that they might be functionally important.

Since the discovery of novel transcripts is often a function of sequencing depth, we asked whether we have uncovered most of the transcribed sequences that are yet to be incorporated into the genome. To address this question, we plotted the number of unaligned (non-contaminating) contigs found at each stage against the corresponding number of sequencing reads (Figure 6B). The graph showed a linearly increasing trend, suggesting that despite our efforts, many more novel transcripts may be discovered with an even higher sequencing depth. When we further divided the set of unaligned contigs into those with EST support and those without EST evidence and plotted them separately against the number of reads, we observed that, while the number of EST-supported contigs is beginning to saturate, the number of novel undocumented contigs is still increasing linearly (Figure S22). Taken together, our results indicate that numerous *Xenopus*

Tan *et al.* - *Xenopus* transcriptome

transcripts remain to be detected and strongly suggest that even though the *Xenopus tropicalis* genome is close to being finished, it is still missing hundreds of transcribed sequences.

To determine if the Trinity contigs that could not be aligned to the genome are true transcripts or are simply spurious assemblies, we sought to validate some of them by reverse transcription PCR. We first picked five contigs that had matches to *Xenopus* ESTs and performed PCRs using cDNA templates from multiple developmental stages. PCRs for four of the contigs yielded products of the expected size (Figure 6C). We also observed that these validated contigs are generally strongly expressed in all the stages tested, which is unsurprising since Sanger sequencing of ESTs and cDNA clones in the past covers only a small fraction of the entire transcriptome and thus the EST collection would be biased towards genes that are more highly or constitutively transcribed. Next, we selected another four contigs without EST matches for validations and found that PCRs for three of them yielded products of the correct size (Figure 6D). Interestingly, all the three validated contigs that had never been observed before appeared to be developmentally regulated. In summary, we were able to confirm seven out of nine Trinity contigs that could not be aligned to the *Xenopus* genome and hence, we estimate that 75-80% of them are likely to be accurate assemblies.

Comparison of transcripts assembled with and without a reference genome

Since Cufflinks and Trinity utilize fundamentally different algorithms to reconstruct transcripts from RNA-seq reads, we wanted to compare the contigs assembled by both programs and to determine how reliable each transcript assembly may be. In almost all developmental stages, Trinity reconstructed more contigs than Cufflinks (Figure 7A). However, while an average of 76.3% of Cufflinks transcripts matches RefSeq or Ensembl annotated genes in the *Xenopus* genome ($E\text{-value} < 1 \times 10^{-10}$) at each developmental stage (Figure 5B), only 57.1% of Trinity contigs contain matches in either annotation (Figure S19). In addition, the mean length of a contig assembled by Trinity is shorter than the mean length of a transcript assembled by Cufflinks at all developmental stages (Figure 7B and Figure S23). On average, a Cufflinks transcript is 1.72 times as long as a Trinity contig. Furthermore, at each stage, 71.3% to 78.6% of the Trinity contigs, but only 42.5% to 49.3% of the Cufflinks transcripts, are less than or equal to

Tan *et al.* - *Xenopus* transcriptome

1000bp (Figure S24). Hence, even though more contigs are reconstructed by Trinity, they are generally shorter and a smaller percentage of them can be aligned to RefSeq or Ensembl annotated genes.

Since it utilizes the reference genome as a guide, a possible reason why Cufflinks reconstructs fewer but longer transcripts than Trinity is that Cufflinks can merge several shorter sequences that are mapped close together into a single long transcript and it may also be able to detect splice junctions more sensitively. As examples, we examined transcripts originating from the *ccnK* locus (Figure 7C) and the intergenic region between *sox10* and *baiap2l2* (Figure S25). In each case, our PCR results showed that the single long transcript reported by Cufflinks is more accurate than the multiple short contigs generated by Trinity (see Supplemental Information). Hence, Cufflinks outperforms Trinity at piecing together longer or spliced transcripts. However, as Trinity reconstructs contigs without a reference genome, it can discover novel genes that are absent from an incomplete genome. Collectively, our results indicate that both *ab initio* transcript assembly using Cufflinks and *de novo* transcript assembly using Trinity are required to obtain a more comprehensive understanding of the *Xenopus* transcriptome.

DISCUSSION

We have generated the first extensive map of the *Xenopus tropicalis* transcriptome at single-base resolution using paired end RNA-seq. By sampling 23 distinct stages, we acquired a broad understanding of the dynamic changes in the transcriptome during development from a 2-cell embryo to a feeding tadpole. We obtained at least 20 million reads for each stage and over 900 million reads in total. The deep coverage allowed us to examine the *Xenopus* transcriptome in unprecedented detail and to identify a large number of novel splice junctions and novel transcribed regions.

The initial stages of vertebrate development rely predominantly on maternal factors deposited in the egg and there is minimal zygotic transcription until the embryonic genome gets activated. While this activation occurs at the late 2-cell stage in mice and between the 4-cell and 8-cell stage in humans, transcription is believed to be repressed in *Xenopus* embryos all the way until the twelfth cell division, when the midblastula transition takes place. Prior to our study, less than 10 genes were known to be transcribed in the beginning stages following fertilization (Yang, et al, 2002, Skirkanich, et al, 2011). We examined the expression of thousands of annotated genes and found that ~150 genes are clearly transcribed prior to the midblastula transition according to our RNA-seq data. This large collection of genes provides a rich resource for future functional studies, which will greatly enhance our understanding of the role of transcription in early development. In particular, 36 of these genes have also recently been determined to be transcribed before the midblastula transition in zebrafish (Aanes, et al, 2011). Strikingly, 8 of the genes that are common between *Xenopus* and zebrafish, including the histone acetyltransferase *hat1* and the DNA methyltransferase-associated protein *dmap1*, perform functions that are related to transcriptional regulation, while another 3 genes, namely *wdr36*, *taf5l*, and *pik3r4*, encode proteins that contain WD repeats. It has previously been shown that the WD repeat-containing protein *wdr5* plays an essential role in epigenetic regulation of vertebrate development by interacting with dimethylated histone3-lysine4 (H3K4me2) and mediating its transition to a trimethylated stage (H3K4me3) (Wysocka, et al, 2005). Hence, *wdr36*, *taf5l*, and *pik3r4*, together with *hat1* and *dmap1*, may potentially perform important epigenetic functions to prime the embryonic genome for large-scale activation at the midblastula transition in

vertebrates. Future studies directed at mapping changes in histone modifications and DNA methylation marks during the earliest stages of development will serve to deepen our understanding of the interplay between chromatin architecture and transcription and will eventually allow us to decipher how a generally quiescent genome may become fully activated in order to drive further developmental events.

Surprisingly, none of the genes that have been previously reported to be transcribed before the midblastula transition (Skirkanich, et al, 2011) showed up in our lists of early transcribed genes (Supplementary Files S4 and S5). We examined our RNA-seq data to determine the reasons for their absence. The nodal-related gene *xnr5* is duplicated in the *Xenopus* genome and the corresponding short reads cannot be uniquely or reliably mapped. The homeobox-containing gene *bix4* is not demarcated in the XenTro3 genome; it is absent from both the RefSeq and the Ensembl annotations. In addition, the expression levels of *xnr6*, *mixer*, and *sox17a* did not meet the criterion of a 2-fold increase between the 2-cell stage and stage 6 (Figure S26). Finally, while the expression of *derrière* did increase by more than two-fold from the 2-cell to the 16-cell stage, it showed a sudden decline at stage 6 (Figure S26). It is possible that the decline might be due to a measurement error as the RPKM at stage 8 continued the increasing trend. We further note that in contrast to the report by Skirkanich *et al.* (2011), we did not observe a gradual increase in expression levels for any of these genes. Instead, the general trend appears to be exponential, that is, there is at most a modest degree of transcription in the beginning stages of development followed by a strong burst of transcription upon activation of the embryonic genome. Although the disparity may be due to the different species used (*Xenopus tropicalis* versus *Xenopus laevis*), further work is needed to fully understand the discrepancies.

Alternative splicing plays a widespread and important role during the development of many multicellular eukaryotes, including *C.elegans* (Barberan-Soler, et al, 2008), *Xenopus* (Fletcher, et al, 2006), and mice (Revil, et al, 2010). Our global splicing analysis uncovered between 23,000 to 54,000 novel splice junctions at every developmental stage in the frog, most of which are supported by at least two non-redundant reads. Interestingly, we found that the majority of these novel splicing events are stage-specific and result in new unannotated isoforms of known genes. For example, exon skipping events in the fibronectin gene, *fn1*, result in two new transcript isoforms, one of which is most highly expressed from stage 11 to stage 28 (Figure

Tan *et al.* - *Xenopus* transcriptome

4A), while the other is most strongly expressed from stage 33 to stage 45 (Figure 4B). Even though some of the novel junctions might be a result of inexact splicing and may not have any biological relevance, we observed during our validation experiments that the expression of the novel isoform often does not vary together with that of the canonical isoform over development. Hence, we propose that many of the novel isoforms that we discovered here perform particular roles during certain developmental timepoints and future studies are needed to unravel their specific functions.

Our extensive RNA-seq data allowed us to identify novel transcripts that are protein-coding, non-coding, or even non-existent in the current version of the genome assembly of *Xenopus tropicalis*. We reconstructed transcripts from the reads using two distinct assemblers, Cufflinks and Trinity, and generated a catalog of novel transcribed regions. To discover new non-coding RNAs, we developed a series of filtering steps to remove contigs with protein-coding potential and identified a total of 9,529 putative non-coding transcripts. We have higher confidence in 70.2% of them (6,686 transcripts in 3,859 genomic loci) as genuine non-coding genes because they contain matches in the NONCODE or Rfam databases, align to human or mouse non-coding genes, are on a different strand from its neighboring genes, encode antisense transcripts, or are located at a remote distance away from an annotated protein-coding gene. Besides uncovering new non-coding RNAs, we also found hundreds of *de novo* assembled contigs that could not be aligned to the current reference genome (XenTro3), which indicates that the *Xenopus tropicalis* genome is still unfinished. Our study will aid in the future completion and full annotation of the genome.

In summary, we used paired end RNA-seq to examine in detail the transcriptome of an important model organism, *Xenopus tropicalis*. We have uncovered a large number of novel transcribed regions, which will support the full assembly and annotation of the reference genome. In addition, our work has laid the foundation for the discovery and analysis of new protein-coding and non-coding genes in *Xenopus* and will serve as a valuable resource to be integrated into future genomic and developmental studies.

METHODS

Xenopus tropicalis embryo culture and collection

The animals used in this study are out-bred Nigerian frogs from a stock maintained by the University of Virginia and were purchased directly from Nasco (Fort Atkinson, Wisconsin, USA). Embryos were obtained by natural mating as follows. Adult female *Xenopus tropicalis* were injected 20-24 hours before embryo collection with 10U human chorionic gonadotropin (HCG) (Sigma). 4-5 hours before embryo collection, male and female frogs were injected with 100U and 400U HCG respectively and amplexus is allowed to begin. 45 minutes after the onset of egg laying, embryos were collected and dejellied in 1/9 MR+ 3% cysteine. Embryos were then cultured in 1/9 MR at room temperature and were staged according to Niewkoop and Faber 1994. Embryos from two separate clutches were harvested and frozen at -80°C until RNA isolation. For the first clutch, embryos were collected at stage 9, stage 10, stage 11, stage 12, stage 15, stage 16, stage 19, stages 20-21, stages 22-23, stages 24-26, stage 28, stages 31-32, stages 33-34, stage 40, and stages 41-42. For the second clutch, embryos were collected at 2-cell stage, 4-cell stage, 8-cell stage, 16-cell stage, stage 6, stage 8, stage 9, stage 10, stages 11-12, stages 13-14, stages 16-18, stage 19, stages 20-21, stages 22-23, stages 24-26, stage 28, stages 31-32, stages 33-34, stages 38-39, stage 40, stage 41-42, and stages 44-45. For each clutch, approximately 10-15 embryos or 5-10 tadpoles were collected at every stage.

RNA isolation and RNA-seq library preparation

Total RNA was extracted from whole embryos using either the RNeasy Mini Kit (Qiagen) or the RNeasy Lipid Tissue Mini Kit (Qiagen) according to manufacturer's instructions, including the on-column DNase I treatment. The concentrations of all the RNA samples were measured using the NanoDrop (Thermo Scientific) and their integrity was determined using an Agilent 2100 Bioanalyzer. RNA-seq libraries were made from samples with a RNA Integrity Number (RIN) of at least 8.0.

Tan *et al.* - *Xenopus* transcriptome

The general Illumina mRNA-seq library preparation workflow was followed with some modifications. First, polyA-containing RNAs were selected using two rounds of Dynal Oligo(dT) beads (Invitrogen). The RNAs were then fragmented in 5X First-Strand Buffer (Invitrogen) at 85°C for 7-8 minutes. Random hexamers and SuperScript III (Invitrogen) were used to synthesize the first strand cDNA. Next, second strand cDNA synthesis was performed with dUTP in place of dTTP to mark the second strand (Parkhomchuk, et al, 2009). After polishing the ends with End-It DNA End Repair Kit (Epicentre) and adding adenosine to the 3' ends using Klenow fragment (New England Biolabs), standard Illumina adapters were ligated. DNA fragments in the size range of 300 to 600bp were gel extracted and treated with uracil-DNA glycosylase (New England Biolabs) before each library was amplified using Phusion DNA polymerase (Finnzymes). Libraries were quantified using the Qubit dsDNA High Sensitivity Assay Kit (Invitrogen) and sequenced on HiSeq 2000 (Illumina) to produce paired 100bp reads.

Quantitative real-time PCR

Several genes that showed an increase in transcript levels prior to the midblastula transition according to our RNA-seq data were further tested. Reverse transcription was performed using the SuperScript III First-Strand Synthesis System (Invitrogen). Real-time PCR was performed using iQ SYBR Green Supermix (Bio-Rad) on the ABI 7900HT machine (see Supplemental Table S2 for the primer sequences). The cycling parameters are as follows: 95°C for 3 minutes followed by 40 cycles of 95°C for 15 seconds, 57°C for 30 seconds, and 72°C for 15 seconds. With the 2-cell stage as reference, fold change was calculated by normalizing Ct values in each developmental stage against the ODC gene using the $2^{-\Delta\Delta Ct}$ method (Livak, et al, 2001). In order for a gene to be considered as validated, its normalized expression level must increase by at least 2-fold in three out of four biological replicates. Each of the two clutches of embryos used for constructing the RNA-seq libraries constitutes a biological replicate, while embryos for the remaining two replicates were obtained from additional independent matings.

Non-quantitative reverse transcription PCR

Tan *et al.* - *Xenopus* transcriptome

Multiple novel splice junctions and unannotated transcripts assembled by Cufflinks or Trinity were selected for further validation. The RNA samples used to construct the RNA-seq libraries were reverse transcribed using the SuperScript III First-Strand Synthesis System (Invitrogen) to generate cDNA templates for the subsequent PCRs. For transcripts shorter than 1000bp, the iQ SYBR Green Supermix (Bio-Rad) was used together with the following cycling parameters: 95°C for 3 minutes followed by 35 cycles of 95°C for 15 seconds, 60°C for 30 seconds, and 72°C for 30 seconds and then followed by 72°C for 2 minutes. The primer sequences are given in Supplemental Table S3. For transcripts longer than 1000bp, the Herculase II Fusion DNA Polymerase (Agilent) was used according to manufacturer's instructions for cDNA. The primer sequences and the corresponding annealing temperatures are given in Supplemental Table S4.

Expression analysis of annotated genes

The annotation-dependent expression analysis was performed using rSeq (version 0.0.7) (Jiang, et al, 2009). Two mismatches were allowed and either RefSeq or Ensembl was used as the reference annotation. To compare the transcript levels estimated by RNA-seq and microarrays, the microarray dataset GSE27227 (Yanai, et al, 2011) was downloaded from the Gene Expression Omnibus (GEO) database. For each gene tiled on the microarray, the transcript level was calculated as the average of the corresponding probes from all the three biological replicates in the dataset.

Cluster analysis

K-means clustering was performed using the software Cluster and the results were displayed using the program Java TreeView (Eisen, et al, 1998). The number of clusters, K, was varied in order to find the maximum number of distinct clusters, i.e. K was chosen such that all the unique patterns were revealed and no two clusters appeared nearly identical to one another.

RNA-seq data alignment and junction detection

SpliceMap (version 3.3.5.2) (Au, et al, 2010) was used to map our RNA-seq data to the genome and to detect exon junctions. The maximum and minimum intron lengths were set as 40,000bp and 20,000bp respectively. 10 hits were allowed for the 25-mer seed mapping with up to 2 mismatches and 4 mismatches were allowed for the full read. Bowtie (version 0.12.7) (Langmead, et al, 2009) was employed for the 25-mer seed mapping and the "try hard" option was used. Since the *Xenopus* genome (XenTro3) consists of too many individual scaffolds, which increases computing intensity of Bowtie mapping, all the scaffolds were merged into a single sequence for this mapping and the results were then post-processed to have the correct scaffolds and coordinates assignments. We define novel junctions as the ones that are not reported in RefSeq, KnownGene, and Ensembl annotation libraries. The number of non-redundant reads (nNR, reported from SpliceMap) was used to define the reliability of the junction detections, as discussed in Au *et al.* 2010.

Ab initio transcript assembly and quantification.

The Tophat-Cufflinks pipeline was used to predict gene isoforms from our RNA-seq data. In Tophat (version 1.2.0) (Trapnell, et al, 2009), the option "min-isoform-fraction" was disabled, while "coverage-search", "butterfly-search", and "microexon-search" were used. The option "multi-read-correct" and "min-isoform-fraction" were enabled in Cufflinks (version 1.1.0) (Trapnell, et al, 2010). The expected fragment length was set to 350bp and the "small-anchor-fraction" was set to 0.08, which requires at least 8bp on each side of an exon junction for our 100bp RNA-seq data. In order to compare and merge the reference annotation and the isoform predictions, an in-house script was written to convert the UCSC RefSeq annotation from genephed format to GTF format in a correct sorted order. All isoform predictions from the 23 stages and the reference annotations were merged for differential analysis by Cuffdiff. In Cuffdiff, "multi-read-correct" and "time-series" analysis were enabled. The expected fragment length was set to 350bp and the "min-alignment-count" was set to 5.

Tan *et al.* - *Xenopus* transcriptome

***De novo* transcript assembly**

Trinity (trinityrnaseq_r2011-10-29) (Grabherr, et al, 2011) was used to perform *de novo* transcriptome assembly from the RNA-seq data. The options included were “--seqType fq”, “--SS_lib_type RF”, “--CPU 10”, and “--no_run_butterfly”. Due to cluster limitations, all Butterfly commands were run in parallel after Chrysalis has finished. The Trinity pipeline was performed for reads from each of the 23 stages as well as pooled reads from the second biological replicate.

Identification of unannotated or unassembled transcripts

Each of the output Trinity and Cufflinks fasta files served as input for BLASTN (version 2.2.25) against the following databases: 1) XenTro3 reference genome, 2) XenTro3 reference genome and *Xenopus* ESTs, 3) RefSeq, 4) Ensembl, and 5) RefSeq and Ensembl. An E-value threshold of 1×10^{-10} was used to determine the significant hits. The fraction of BLAST matches for a stage is calculated as the number of contigs in that stage with a significant BLAST match divided by the total number of contigs in that stage.

Identification of novel non-coding RNAs

The merged Cufflinks transcripts and the Trinity contigs assembled from pool reads were used to identify novel non-coding RNAs. To eliminate potential protein-coding genes, contigs that did not have a significant BLASTN match to either RefSeq or Ensembl were processed through the following filters: 1) Hmmer (version 3.0) against PfamA and PfamB (Punta, et al, 2012), with the contig sequences translated in all three forward frames ($E\text{-value} \leq 1 \times 10^{-10}$), 2) BLASTX (version 2.2.25) against PfamA and PfamB ($E\text{-value} \leq 1 \times 10^{-10}$), 3) BLASTX against UniProtKB/Swiss-Prot (UniProt Consortium, 2012) ($E\text{-value} \leq 1 \times 10^{-10}$), 4) BLAT against human and mouse protein coding genes in RefSeq (at least 10% identity), and 5) any sequence that may encode an open reading frame of at least 100 amino acids in any of the three translated forward frames (START to STOP, from the beginning of the contig to the first STOP, or from the first START after the last STOP until the end of the contig). All contigs that did not fulfill any of the above criteria were considered to be potential non-coding RNAs.

Tan *et al.* - *Xenopus* transcriptome

To curate a confident set of non-coding transcripts, we sought to identify the contigs that match known non-coding RNAs in other species, are on a different strand from an annotated gene, or are far away (greater than 25kb) from a known *Xenopus* gene. The following steps were taken to identify the transcripts that match non-coding RNAs in other species: 1) BLAT against human and mouse non-coding RNAs in RefSeq (at least 10% identity), 2) searched the Rfam database (Gardner, et al, 2011) with Infernal (Nawrocki, et al, 2009) (score ≥ 40), 3) BLASTN against the NONCODE database (Bu, et al, 2012) (E-value $\leq 1 \times 10^{-10}$), and 4) determined if the neighboring genes of an intergenic contig match the neighboring genes of a NONCODE-annotated non-coding RNA (i.e. contig is present in NONCODE by synteny). In addition, since contigs that are located close to one another may actually be part of the same transcript, we divided the *Xenopus* scaffolds into 50kb segments and grouped the confident non-coding contigs into these segments or genomic loci.

Tan *et al.* - *Xenopus* transcriptome

DATA ACCESS

All the raw RNA-seq data can be accessed from the Gene Expression Omnibus (GEO) database (accession number GSE37452).

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AUTHOR CONTRIBUTIONS

MHT and JBL conceived the study. MHT performed experiments with guidance from AEW. KFA, MHT, and ALY analyzed the data with help from JBL. JC designed the interactive website. JCB, WHW, and JBL provided overall supervision for the project. MHT wrote the manuscript with inputs from the other authors.

FIGURE LEGENDS

Figure 1. Deep RNA-seq covers the majority of annotated genes and reveals dynamic temporal regulation over development.

(A) The developmental stages (adapted from Nieuwkoop and Faber 2004) investigated in this study. For each stage, the approximate time of occurrence after fertilization is given in brackets and is estimated from (Khokha, et al, 2002) or Xenbase. The beginnings of four major developmental events – embryonic genome activation (EGA), gastrulation, neurulation, and organogenesis – are also indicated in the schematic.

(B) Number of sequencing reads for each of the stages. In blue: the total number of reads; in red: the number of reads that mapped to RefSeq genes; in green: the number of reads that mapped to Ensembl genes.

(C) Number of annotated genes that were detected at each of the stages. In red: RefSeq genes; in green: Ensembl genes.

(D) Clustered expression profiles for all detected RefSeq genes are organized by time of expression. The RPKM values were mean-centered and normalized, with each row representing a different gene. The key developmental events, namely the midblastula transition (MBT), gastrulation (Gast), neurulation, and organogenesis, are also labeled below the heatmap. The first cluster contains the set of genes whose RNAs are present at high levels in the earliest stages of development until after the embryonic genome is activated. The second cluster contains the set of transcripts that are present not only before the midblastula transition but remain expressed until the end of gastrulation. The third cluster corresponds to the early response genes that are first transcribed around the midblastula transition. The fourth cluster represents the cohort of genes that are expressed during gastrulation and neurulation, while the fifth cluster represents genes that are expressed not only during neurulation but also during early organogenesis. The sixth cluster contains the set of genes that are first transcribed at the onset of organogenesis and whose expression remains on throughout all the tadpole stages. The seventh cluster represents genes that are transcribed only at later tadpole stages. Finally, the eighth cluster contains genes that are expressed in the earliest developmental stages, repressed after the midblastula transition, and transcribed again in the late tadpole stages. Taken together, clustering analysis reveals interesting dynamics of transcript levels during *Xenopus* development.

Figure 2. Many genes are transcribed before the midblastula transition, despite a general state of transcriptional repression.

(A) Heatmap showing distinct expression profiles of all RefSeq genes that were detected before the midblastula transition in our RNA-seq experiments. In order to focus on the stages before embryonic genome activation, only the RPKM values from the 2-cell stage to stage 8 were used for mean-centering, normalization, and clustering. Each row in the heatmap represents a different gene.

(B) GO analysis of the 150 early-transcribed genes that passed the following 3 criteria: (i) the transcript level at Stage 6 is at least two-fold higher than that at the 2-cell stage; (ii) the average RPKM at each developmental stage is at least 1; (iii) the expression profile is monotonically increasing.

(C) Validations of the RNA-seq results. The RT-qPCR expression profiles (blue bars) matches the RNA-seq data (red lines) closely for 13 out of the 20 genes we tested. The nodal-related gene *xnr5* serves as a positive control (its expression is activated before EGA), while *xbra* serves as a negative control (its expression is activated after EGA). There is no RNA-seq data for *xnr5* because it is duplicated in the *Xenopus* genome and the corresponding reads cannot be uniquely mapped. We also note that for the majority of the validated genes, the fold changes obtained from our RT-qPCR experiments are relatively small (2- to 3-fold) compared to the fold changes observed for *xnr5* and *xbra* (greater than 100-fold).

Figure 3. Novel splice junctions of different types can be detected at all developmental stages.

(A) Total number of splicing events identified at every stage. While the majority of the junctions detected at each stage are annotated in either RefSeq or Ensembl (white portions), a sizeable number of junctions are novel (colored portions). In red: there are two or more non-redundant reads supporting the novel junction ($nNR > 1$). In blue: there is only one non-redundant read supporting the novel junction ($nNR = 1$).

(B) Plots showing the number of stages that each splice junction is detected in. Compared to the novel junctions, a greater fraction of annotated junctions is constitutively expressed. On average, each annotated junction was detected in 11.0 stages, while each strongly-supported novel junction ($nNR > 1$) was detected in 7.7 stages and each weakly-supported novel junction ($nNR =$

Tan *et al.* - *Xenopus* transcriptome

1) was detected in 2.2 stages. The red dotted line indicates the height of the bar for single-occurrence junctions, while the blue dotted line indicates the height of the bar for constitutive junctions.

(C) Pie chart showing the different types of novel splice junctions identified, with the number of junctions (percentage in brackets) given next to each segment. Only 27.93% of the novel junctions occur in intergenic regions (in green), while the majority of them (72.07%) occur within annotated genes.

Figure 4. Most of the novel splice junctions supported by at least two non-redundant reads can be validated by reverse transcription PCR.

(A) Skipping of exon 19 in the fibronectin gene, *fn1*. Upper panel: a schematic of the splicing events between exons 18 to 21 inclusive. Black boxes indicate the individual exons, while the bent lines indicate the splicing events (black – annotated; red – novel). The arrows indicate the primers used for PCR. Lower panel: gel image of the PCR, showing two products. The upper stronger band is present in all stages and represents the annotated isoform, while the lower band represents the exon skipping event and shows a peak expression between stages 20 to 23.

(B) Skipping of exon 24 in *fn1*. Upper panel: a schematic of the splicing events between exons 23 to 25 inclusive. The arrows indicate the PCR primers. Lower panel: gel image showing the results of the PCR. The upper stronger band is present in all stages and corresponds to the annotated isoform, while the lower band represents the exon skipping event. Interestingly, the product lacking exon 24 is only clearly expressed from Stage 33 onwards.

(C) Splicing of a facultative intron in the metabolic gene, *hpd1*. Upper panel: a schematic of the gene structure of *hpd1*. The arrows indicate the PCR primers, while the red bent line indicates a novel splicing event detected within the coding exon of the gene. Middle panel: gel image showing the PCR results. The upper stronger bands represent the annotated gene product, while the lower weaker bands correspond to the novel transcript, which is present in the beginning stages of development. Lower panel: a schematic showing that the novel splice junction creates a premature STOP codon.

(D) Intron retention in the *gata3* transcription factor. Upper panel: a schematic showing the location of the novel splice junction (red bent line) and the location of the PCR primers (arrows). The newly detected splicing event removes the annotated STOP codon (shown in asterisk).

Tan *et al.* - *Xenopus* transcriptome

Middle panel: Gel image of the PCR results. Both the annotated isoform (upper stronger bands) and the novel isoform (lower weaker bands) are not expressed from the 2-cell stage to stage 9 inclusive. Lower panel: a schematic showing that the novel splice junction extends the C-terminus of the protein by 17 amino acids.

(E) Extra exon in the myosin gene, *myl6*. Upper panel: A schematic showing novel splicing events (red bent lines) between exons 2 and 3. Middle panel: Gel image of the PCR results. While the annotated isoform is strongly expressed in all the stages tested, the novel isoform containing the additional exon is only expressed after neurulation. Lower panel: a schematic showing the location of the newly discovered exon in *myl6*.

(F) A novel intergenic transcript between *tmtc2* and *slc6a15*. Upper panel: A snapshot of the UCSC Genome Browser showing the genomic locus of a splicing event detected between GL172641: 2808467 and GL172641: 2808964. Several ESTs support the detected splicing event. Lower panel: Gel image showing the results of a PCR using primers flanking the novel splice junction. The expression of the corresponding transcript is highest at the 2-cell stage and stage 8 and it then decreases over development.

Figure 5. Reconstruction of transcripts from RNA-seq data reveals novel transcribed regions.

(A) Overview of our pipeline that defined a set of unannotated protein-coding genes and a set of novel non-coding RNAs.

(B) Comparison of transcripts assembled by Cufflinks with the RefSeq (purple crosses) and Ensembl (green triangles) annotations as well as the reference genome (XenTro3, red diamonds). The blue squares correspond to Cufflinks transcripts that can be found in either the RefSeq or the Ensembl annotation.

(C) A breakdown of the unannotated Cufflinks contigs into protein-coding transcripts and non-coding transcripts.

(D) By reverse transcription PCR, we detected a gene product in the intergenic region between *hoxc11* and *hoxc12*, where a long non-coding RNA, *HOTAIR*, is known to exist in mammals. The PCR product was further sequenced to confirm that it matched the correct genomic locus.

(E) We classified the putative non-coding RNAs based on their genomic locations relative to annotated RefSeq or Ensembl genes.

Tan *et al.* - *Xenopus* transcriptome

(F) For intergenic contigs that are on the same strand as one or both of their neighboring genes, we determined the distance of each Cufflinks transcript from its closest same strand neighbor and binned the transcripts by this distance. In the histogram, “10kb” means that the transcripts are between 9,001 to 10,000bp (inclusive) away from their same strand neighbors and so on.

Figure 6. Hundreds of transcripts assembled *de novo* do not align to the reference genome.

(A) Number of unaligned contigs assembled by Trinity at every developmental stage. The portions shaded in gray represent the contigs that have EST support, while the unshaded portions correspond to the contigs that do not match any existing *Xenopus* EST and are not derived from contaminating sources.

(B) Number of unaligned Trinity contigs plotted against sequencing coverage. A linearly increasing trend is observed, indicating that deeper sequencing is required to discover even more transcribed sequences that are missing from the reference genome.

(C) Validations of unaligned Trinity contigs with EST support. All the PCR products were sequenced to confirm that they were indeed the relevant contigs. The names in brackets correspond to the matching ESTs or cDNA clones, which were previously sequenced as part of either the NIH *Xenopus* Initiative (Klein, et al, 2002, Gerhard, et al, 2004) or the Sanger *Xenopus tropicalis* EST/cDNA project (Gilchrist, et al, 2004, Carruthers, et al, 2006).

(D) Validations of unaligned Trinity contigs that have never been detected prior to this study. All the PCR products were sequenced as confirmation. The name of each contig was arbitrarily given by the program. One contig, comp29928, was most highly transcribed from stages 13 to 28, while the expression of the other two contigs, comp697 and comp39806, showed a general increase over development and remained strong even in the feeding tadpole stages.

Figure 7. *Ab initio* transcript assembly with a reference genome (Cufflinks) results in fewer but longer contigs than *de novo* transcript assembly without a reference genome (Trinity).

(A) Number of contigs assembled by Cufflinks (blue diamonds) and Trinity (red triangles) at every developmental stage. Trinity almost always reconstructs a larger number of transcripts than Cufflinks.

Tan *et al.* - *Xenopus* transcriptome

(B) The mean length of Cufflinks transcripts (blue diamonds) and Trinity contigs (red triangles) at each stage. On average, a transcript reconstructed by Cufflinks is 628bp longer than a contig assembled by Trinity.

(C) The Cufflinks transcript for the *ccnK* gene is more accurate than the corresponding Trinity contig. Left panel: a schematic of the genomic locus of *ccnK* at the 3' end. Right panel: a gel image showing the result of a PCR performed with the primers depicted in pink at the left. The PCR product shown was further sequenced to confirm that it was indeed the intended target.

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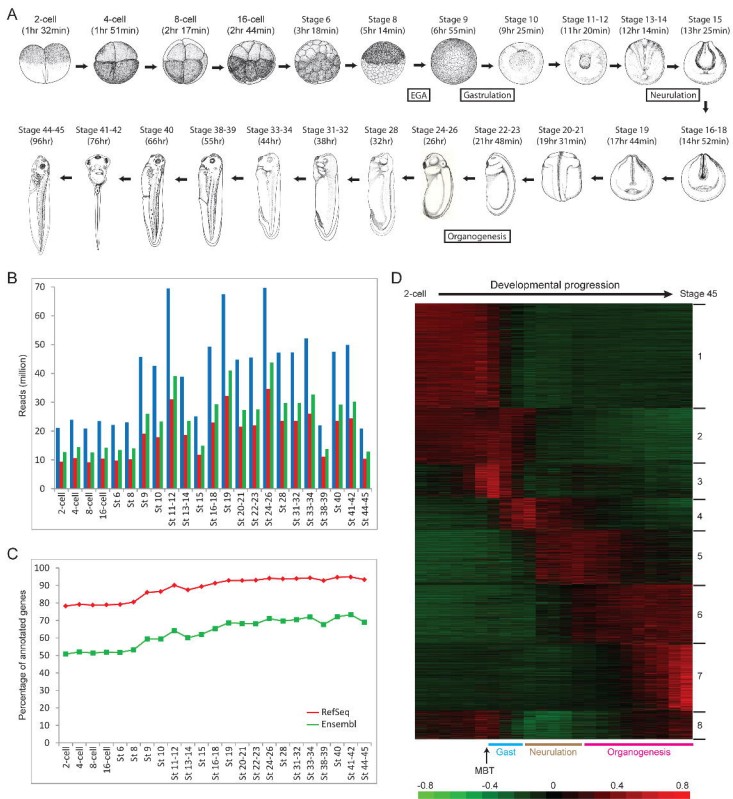


Figure 1

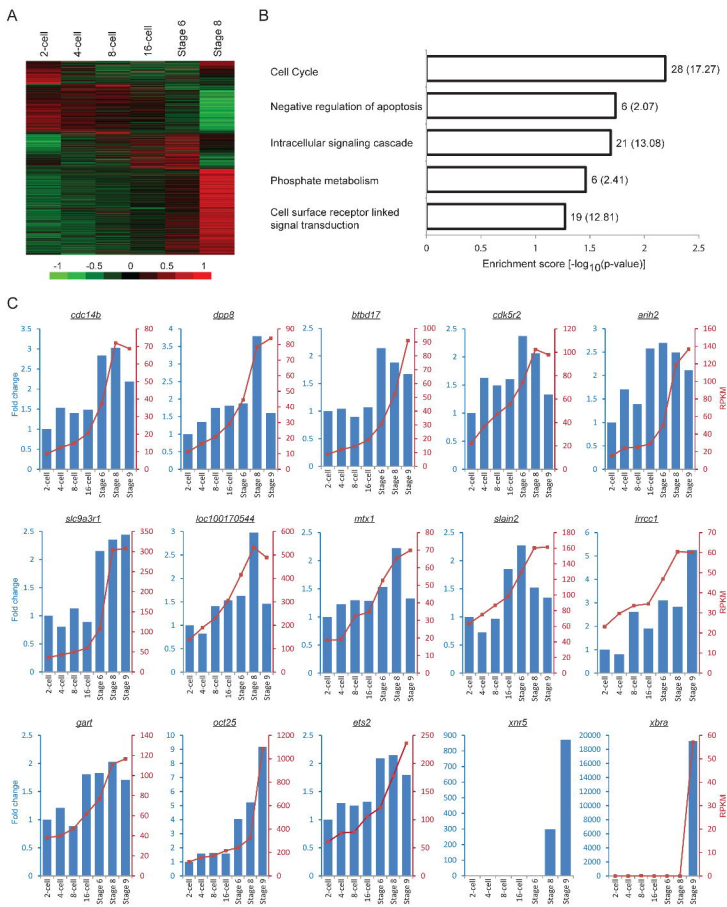


Figure 2

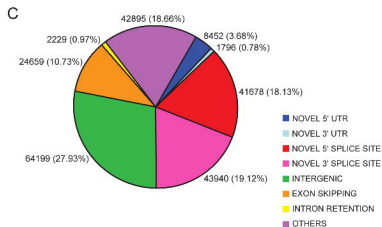
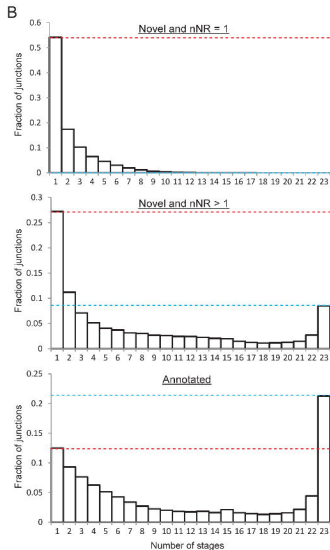
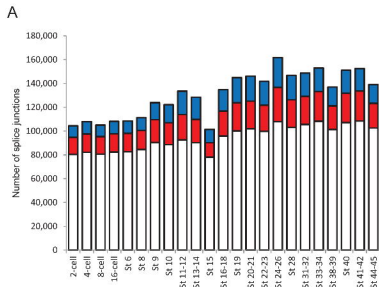


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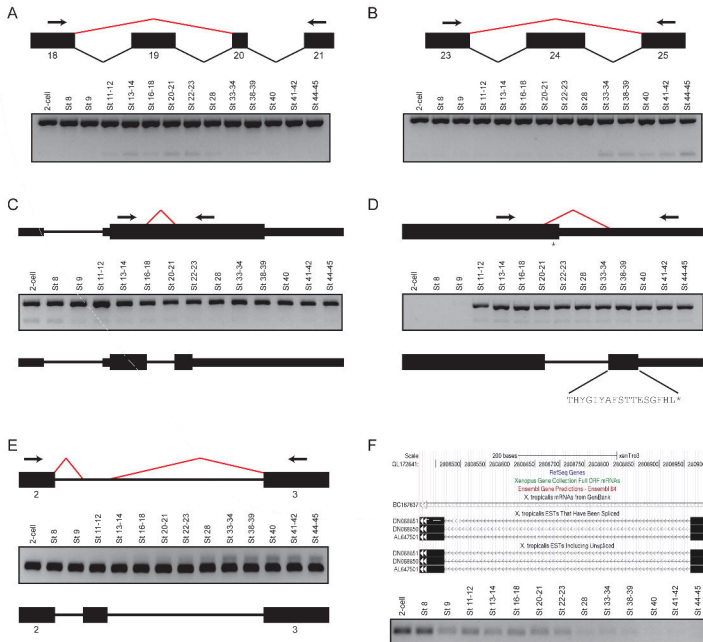


Figure 4

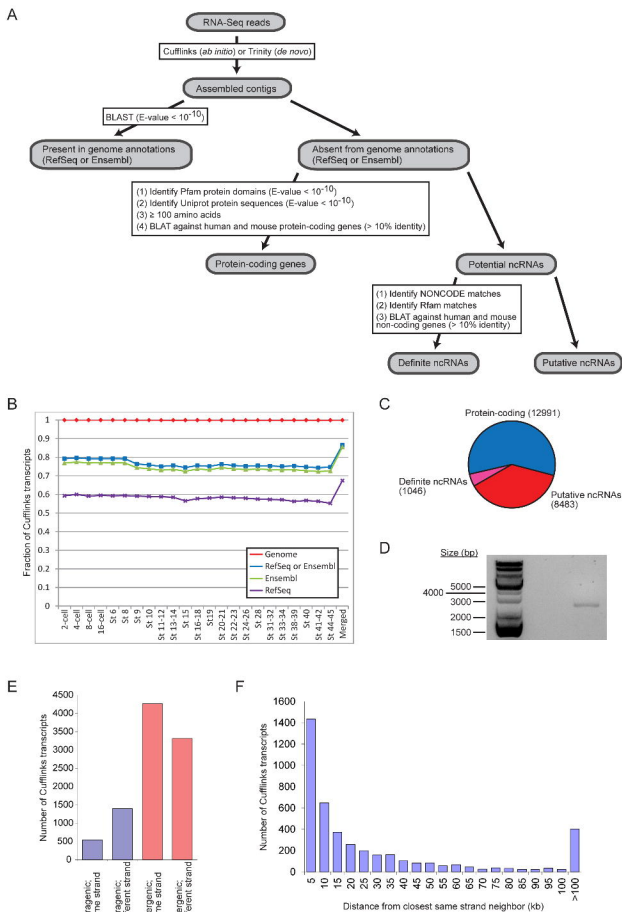
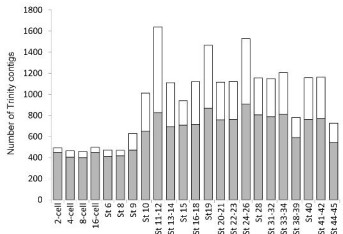
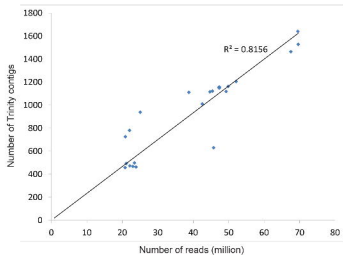
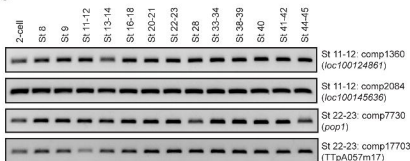
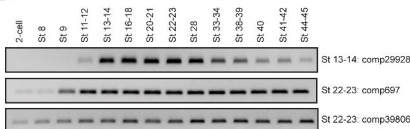
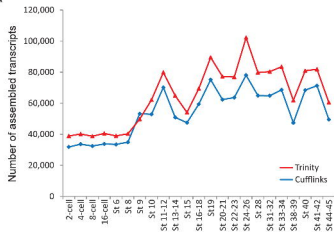


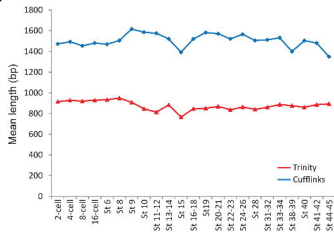
Figure 5

A**B****C****D****Figure 6**

A



B



C

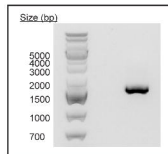


Figure 7