Table S1 : Statistics for RNA-sequencing libraries.

Poly(A) Library	Oocyte	Stage 6	Stage 9	Stage 12	Stage 16	Stage 30
Total reads	31523769	50019507	16649345	30313122	18261070	19901121
Mapped reads	19659282	16003974	10756981	14999462	11076320	13606315
% mapped	62.4	32.0	64.6	49.5	60.6	68.3

Ribozero Library	Oocyte	Stage 6	Stage 9
Total reads	30420177	31831783	30896600
Mapped reads	15064112	13836284	15960698
% mapped	49.5	43.5	51.7

Table S2 : Pearson correlation coefficients for polyA$^+$ vs. total RNA (RZ) libraries.

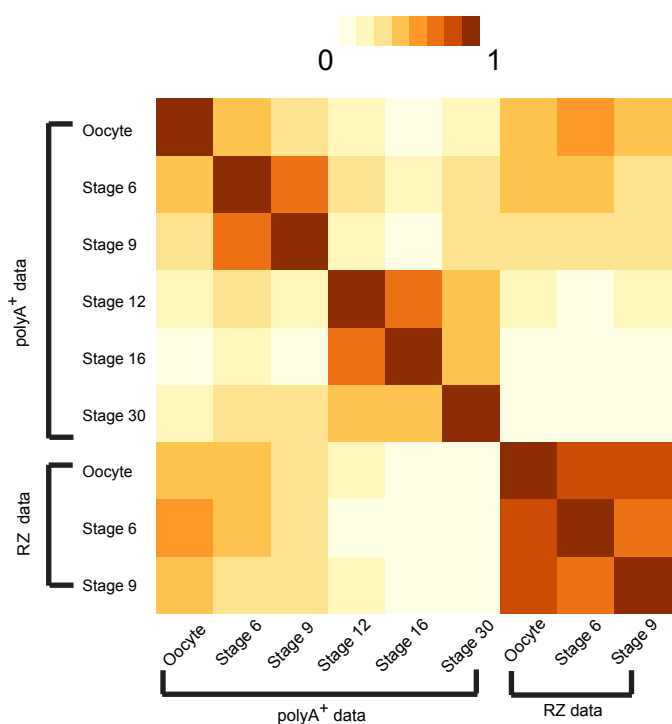| Library	Oocyte(RZ)	Stage 6(RZ)	Stage 9(RZ)
Oocyte(PolyA)	0.66	0.67	0.60
Stage 6(PolyA)	0.65	0.67	0.57
Stage 9(PolyA)	0.56	0.55	0.55
Stage 12(PolyA)	0.40	0.35	0.43
Stage 16(PolyA)	0.36	0.35	0.37
Stage 30(PolyA)	0.35	0.35	0.30

Figure S1

(a) Barplots showing RT-qPCR validation in biological replicates.

(b) Heatmap showing Pearson correlation between RNA-seq libraries.
Filter : Max [Oocyte polyA$^+$, RZ] RPKM > 1

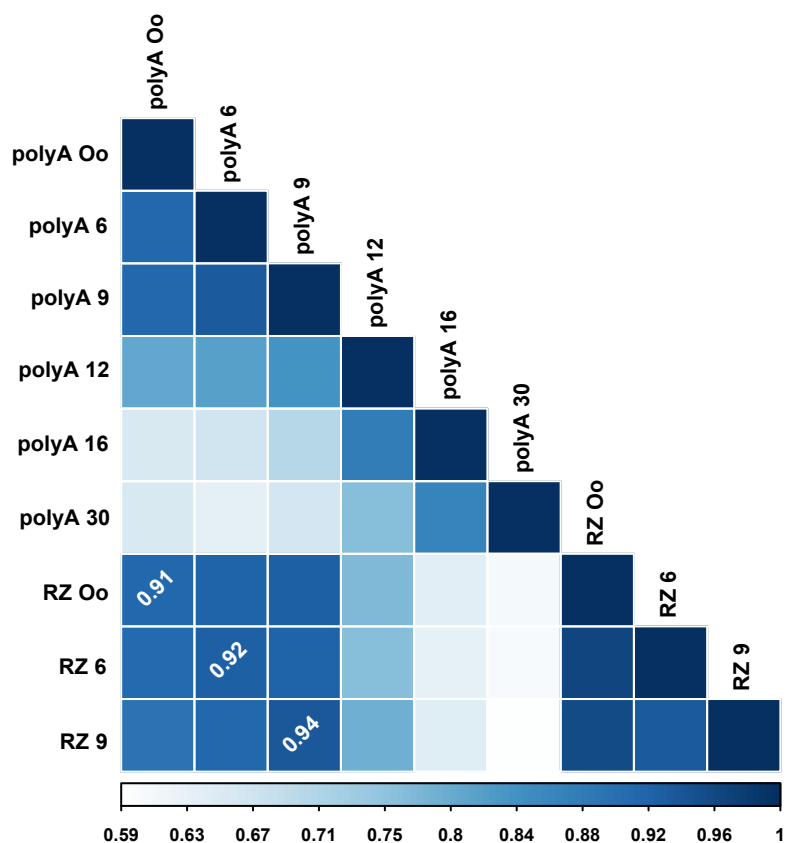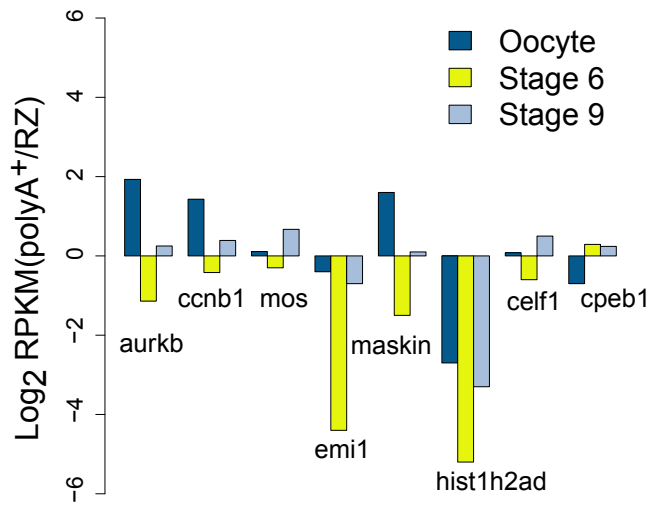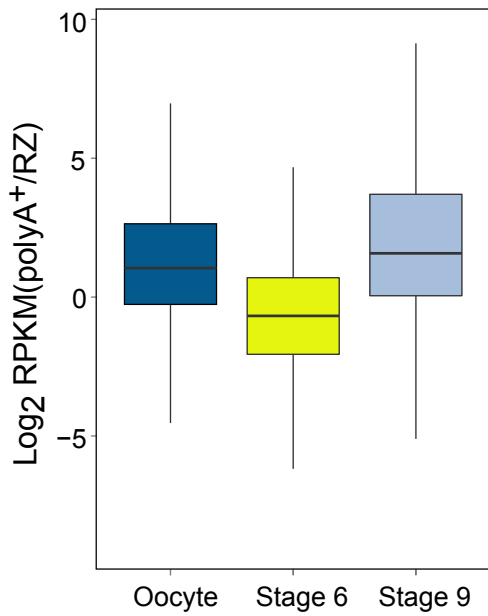(c) Spearman's rank correlation heatmap.

Figure S2

(a) Spearman's rank correlation with published data : Tan MH et al., Genome Res. 2013

(b) Heatmap to visualize Spearman's rank correlation with published data.

Figure S3

(a) Gene-specific RPKM ratios.

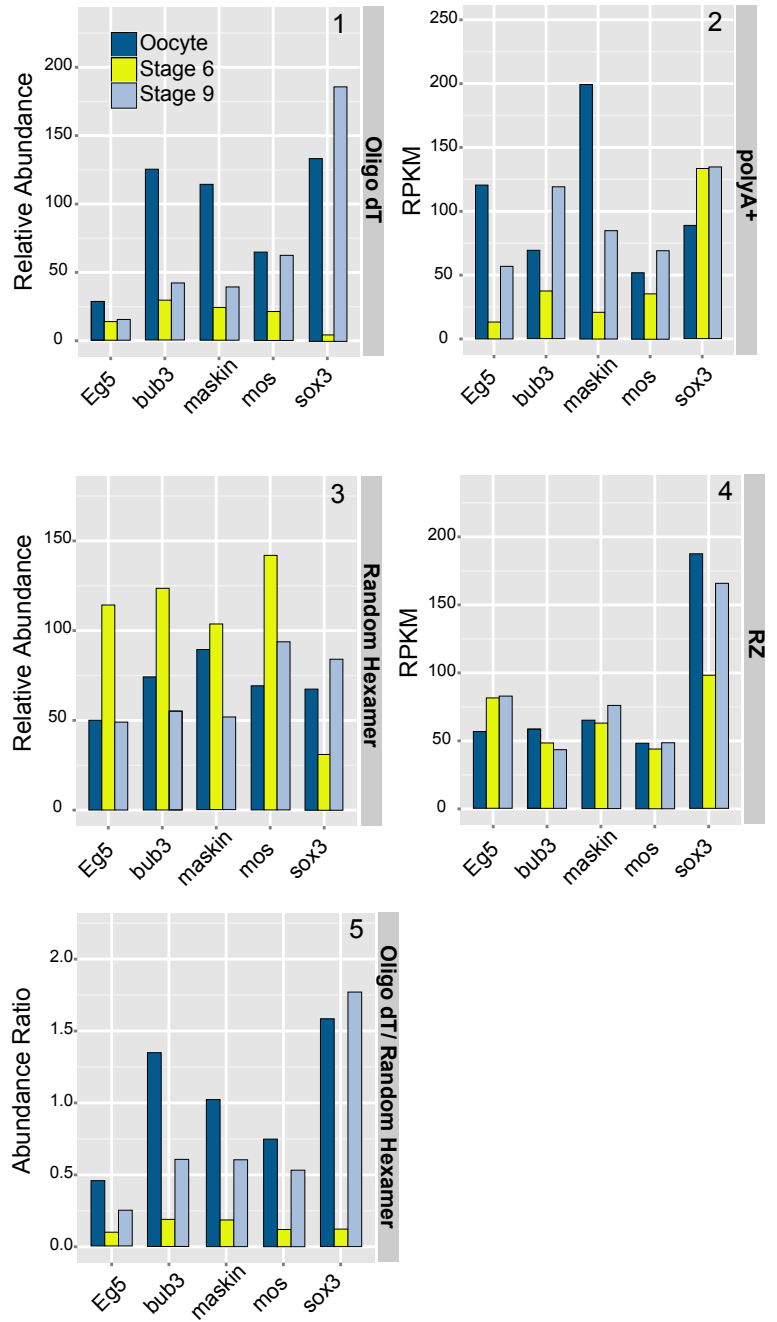## (b) Genome-wide average RPKM ratios.

(c) Validation Experiments.

Figure S3

(d) Comparison of DAVID-derived GO terms for RZ-enriched genes in Oocyte, Stage 6 and Stage 9 respectively.
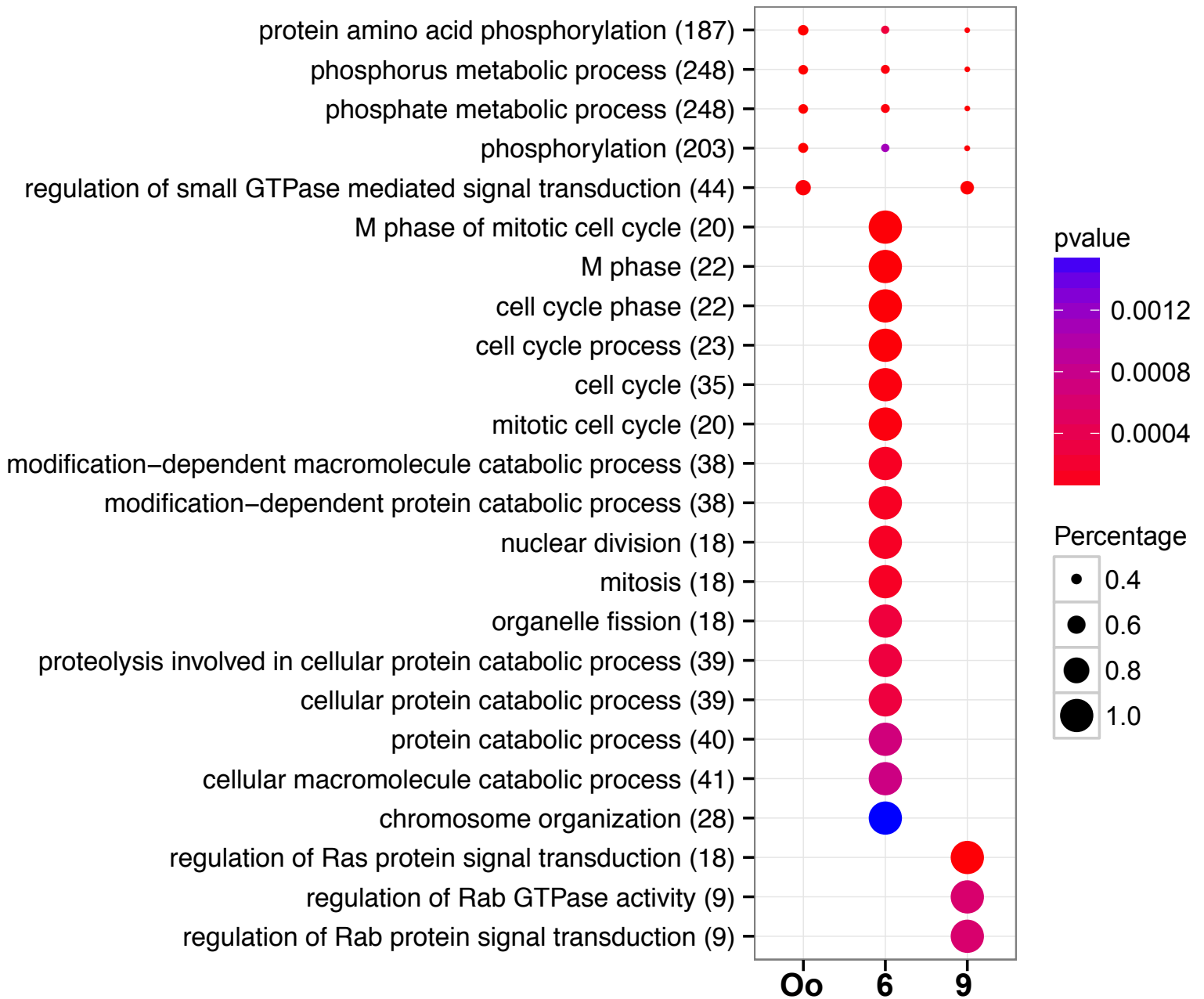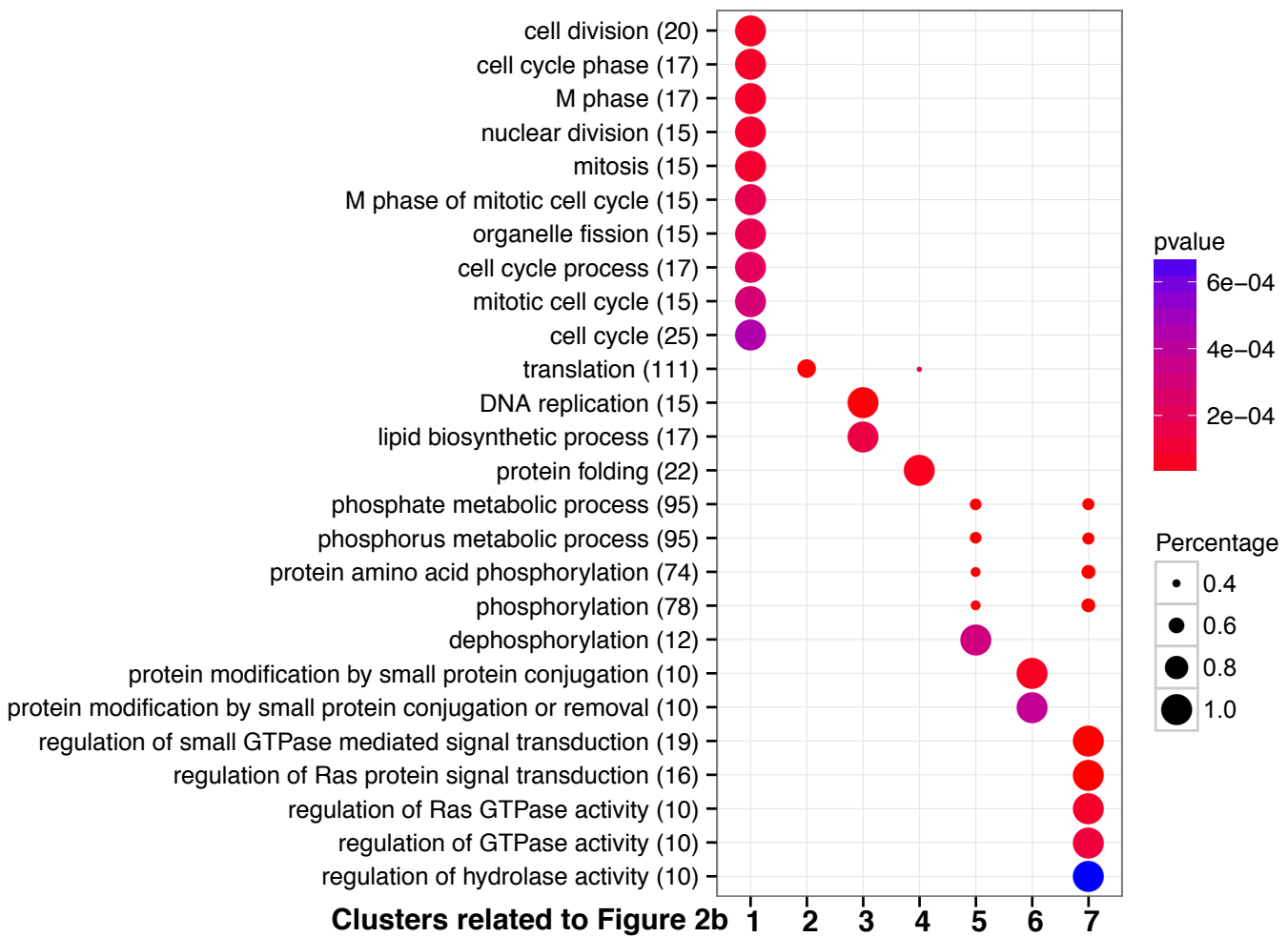
Figure S4

(a) Comparison of DAVID-derived GO terms for clusters 1-7 related to Figure 2b.

(b) A heatmap to visualize adenylation motif enrichment in clusters 1-7 related to Figure 2b.
(ARE : A-U rich elements, CPE : Cytoplasmic polyadenylation element,
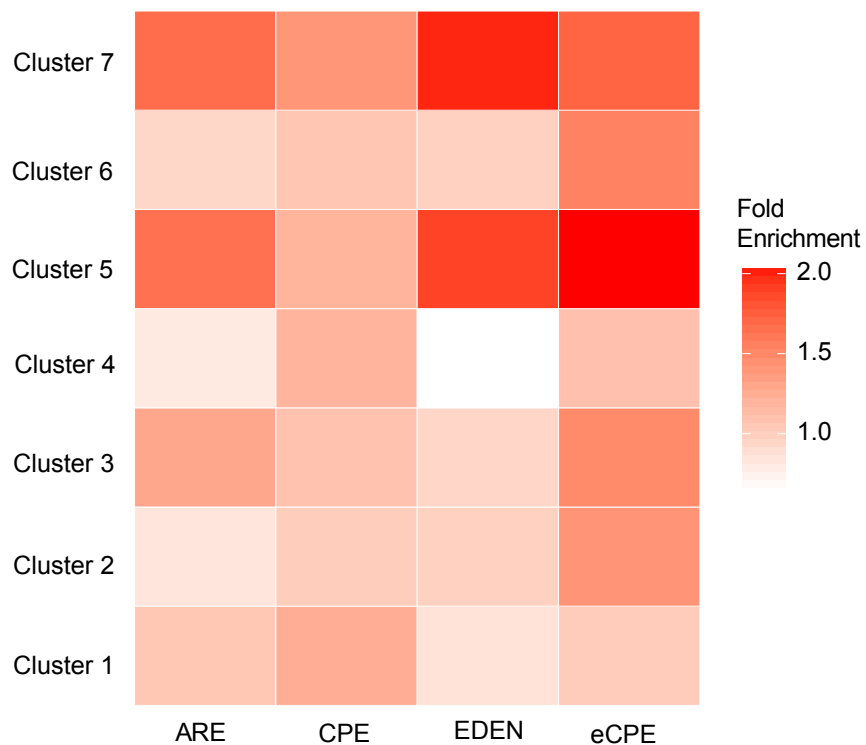EDEN : Embryonic deadenylation element, eCPE : Embryonic -CPE)

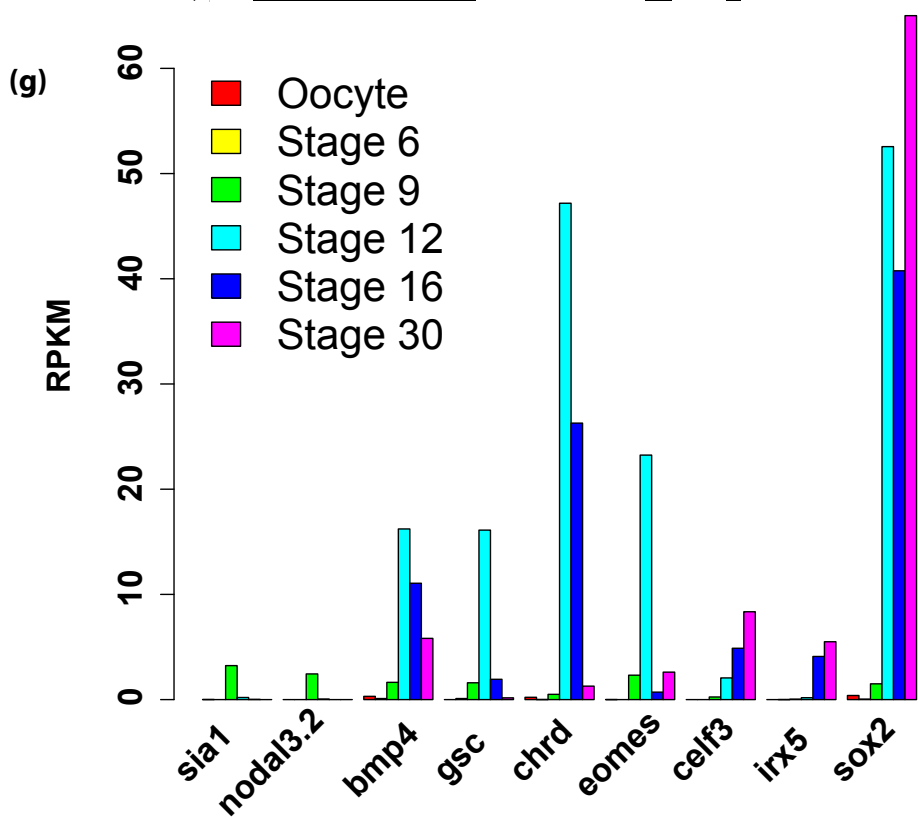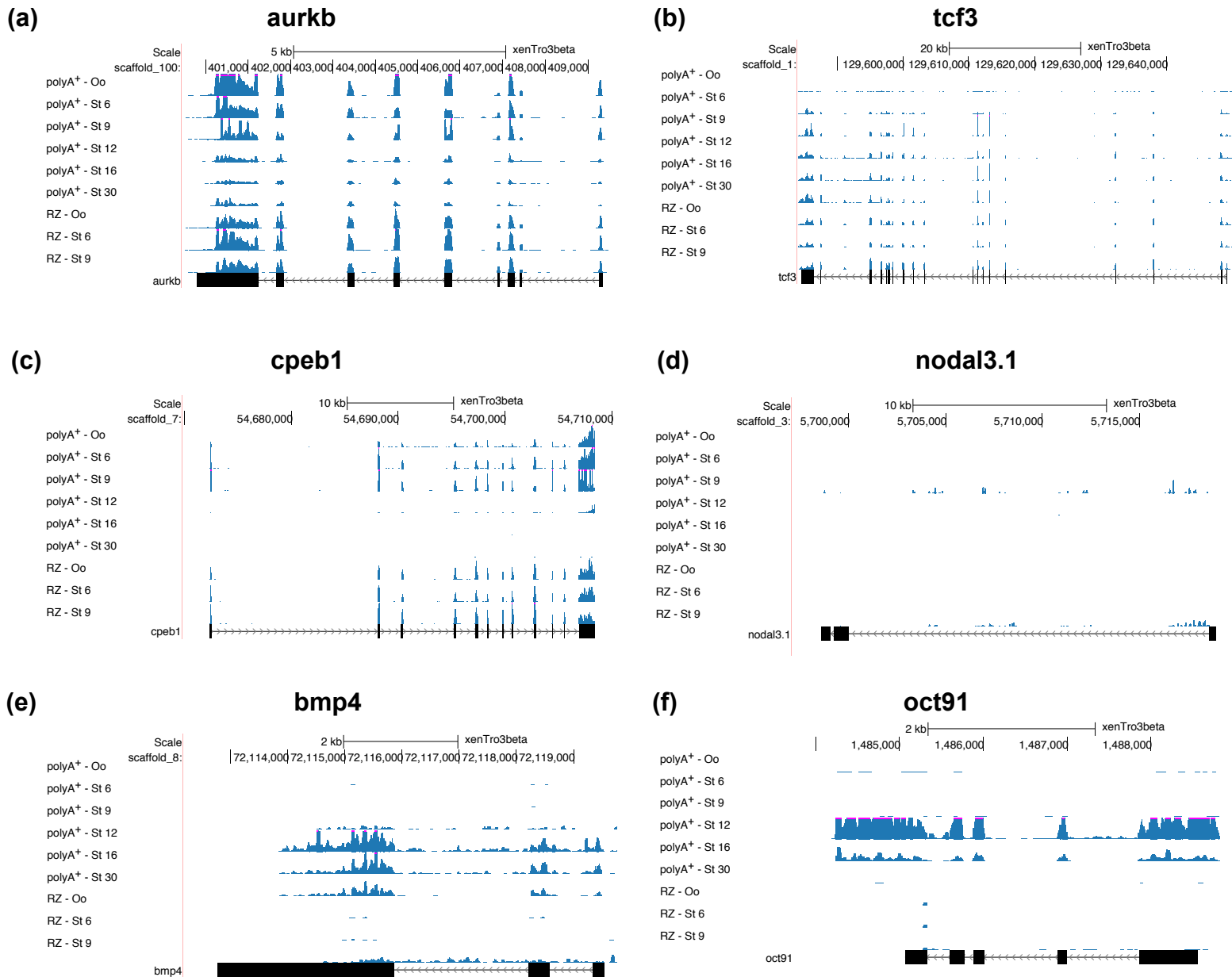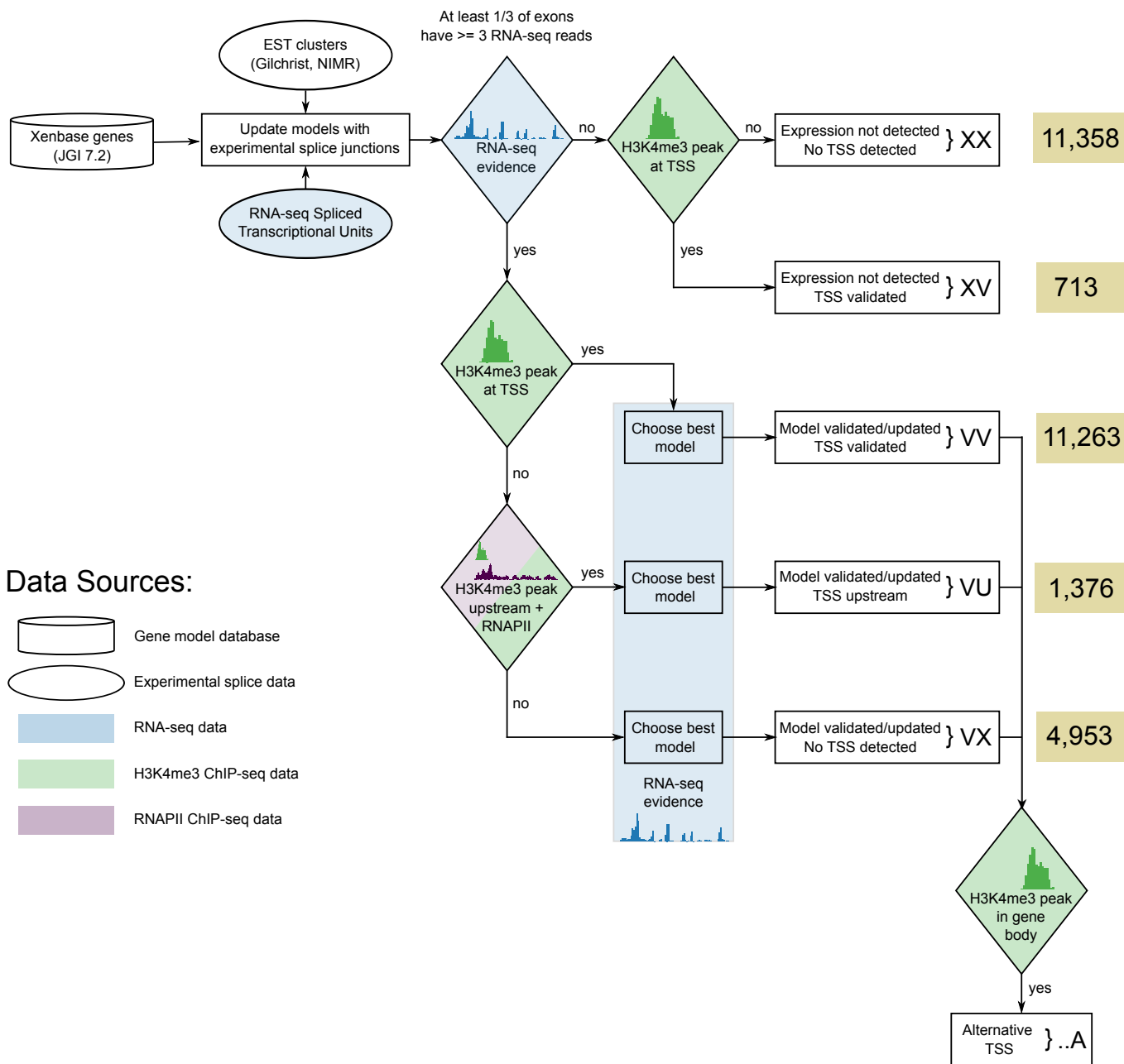# Figure S5. UCSC Genome browser shots of developmentally regulated genes

Xenopus tropicalis Experimentally Validated Genes annotation pipeline

Data Sources:

- Gene model database
- Experimental splice data
- RNA-seq data
- H3K4me3 ChIP-seq data
- RNAPII ChIP-seq data

Gene Model Code:

V Validated, gene model with RNA-seq evidence
X No RNA-seq evidence, expression not detected
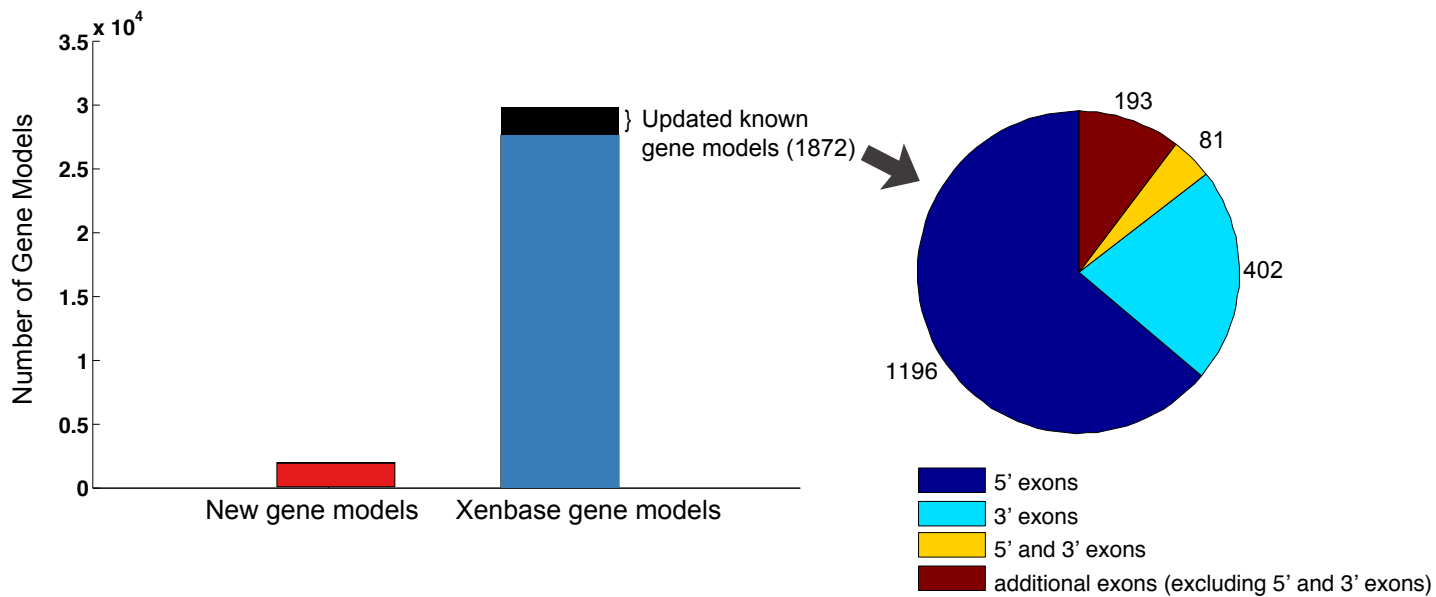
Xtev_2.198.3_VV(A) → (Optional) H3K4me3 peak in gene body, putative Alternative TSS

V Validated, H3K4me3 peak at TSS
U H3K4me3 peak Upstream, with RNAPII evidence
X No TSS evidence found

Figure S7.

(a) Statistics on updated Xtev(v3.4) gene models.

(b) MALAT1 : Highly conserved lncRNA from unspliced single exon gene models (CUFF.28619.1).
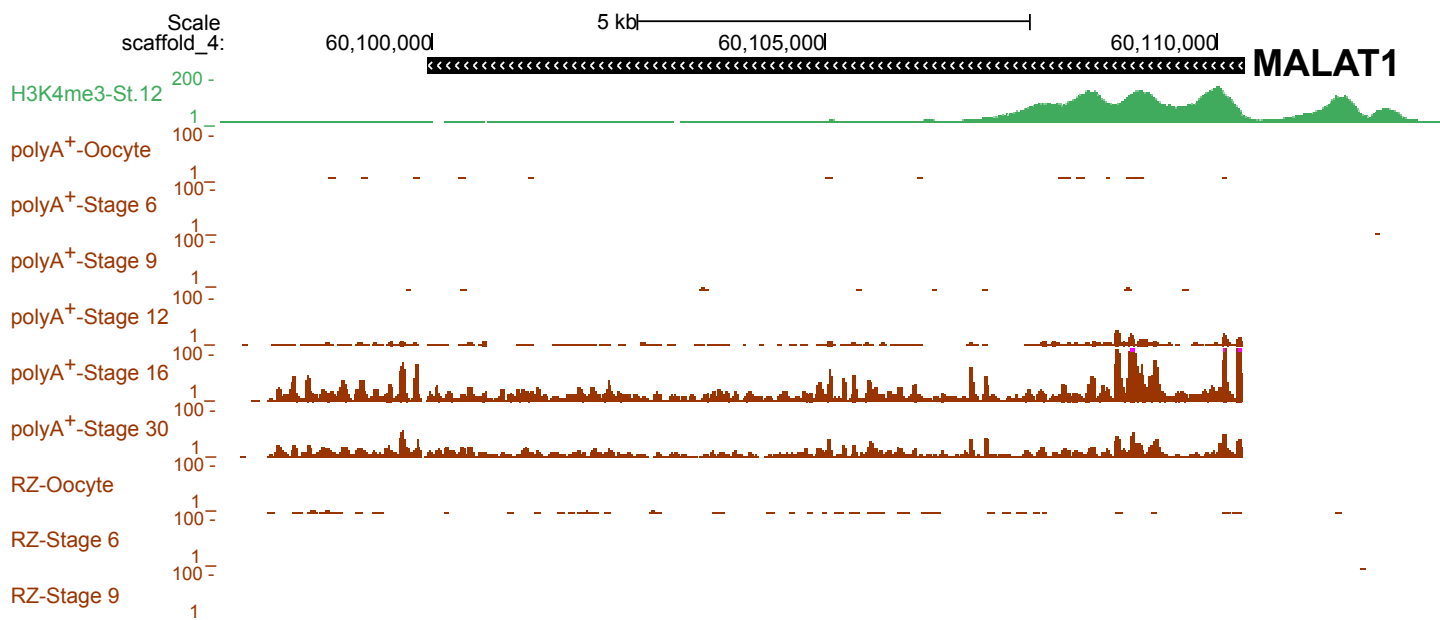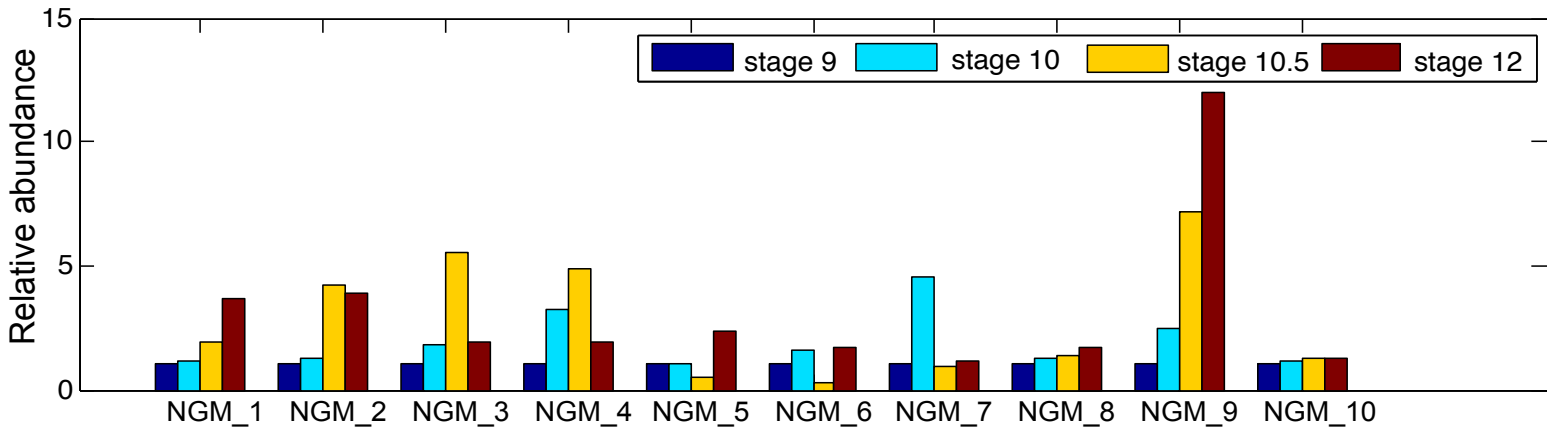(for complete list of single exon gene models see Additional file 3)

Figure S8

(a) Real-time qPCR validation of new gene models (NGM subset).

(b) Average polyA$^+$ expression (RPKM, GM subset) profiles during embryogenesis.
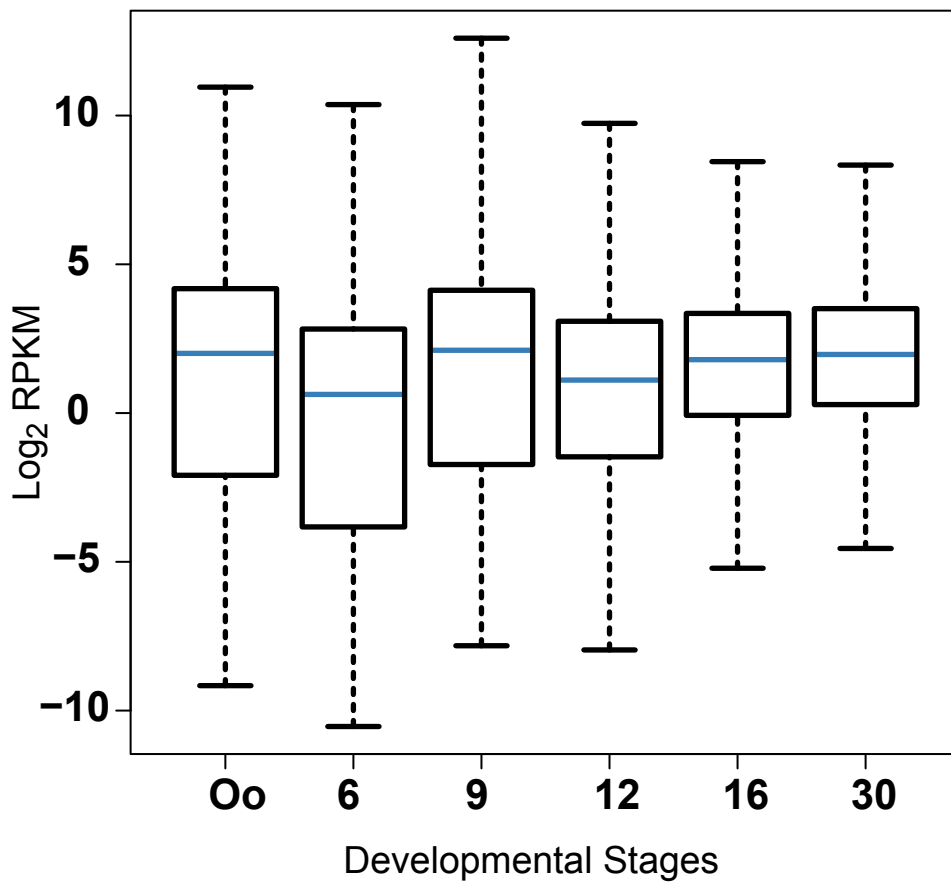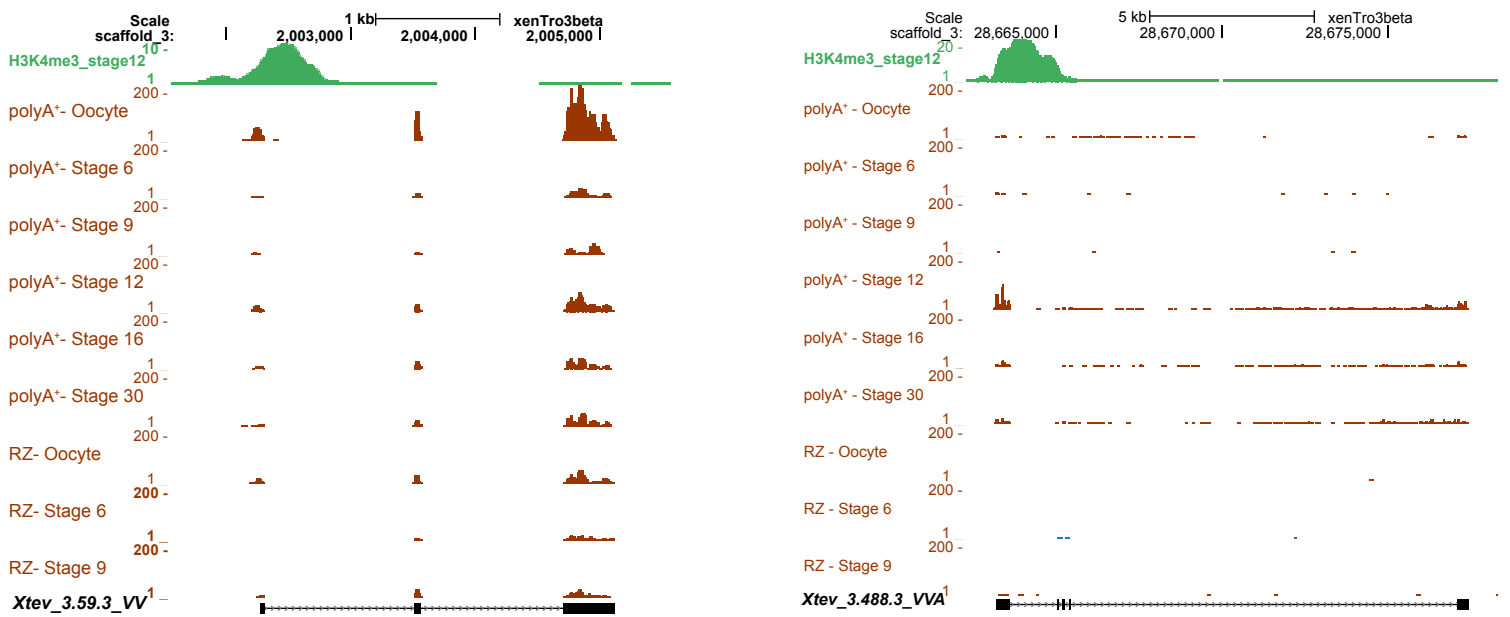
Figure S9

(a) Examples of lncRNAs from NGM$_{VVO}$ subset.

(b) Stage-specific polyA$^+$expression (RPKM) of high-confidence lncRNAs (NGM$_{VVO}$ subset).

lncRNAs	NGM$_{VVO}$ subset ID	Stage of peak expression
1	Xtev_9.872.3_VV	Oocyte
2	Xtev_2.453.3_VV	Stage 6
3	Xtev_3.488.3_VVA	Stage 12
4	Xtev_9.642.3_VV	Stage 16
5	Xtev_3.895.3_VV	Stage 30