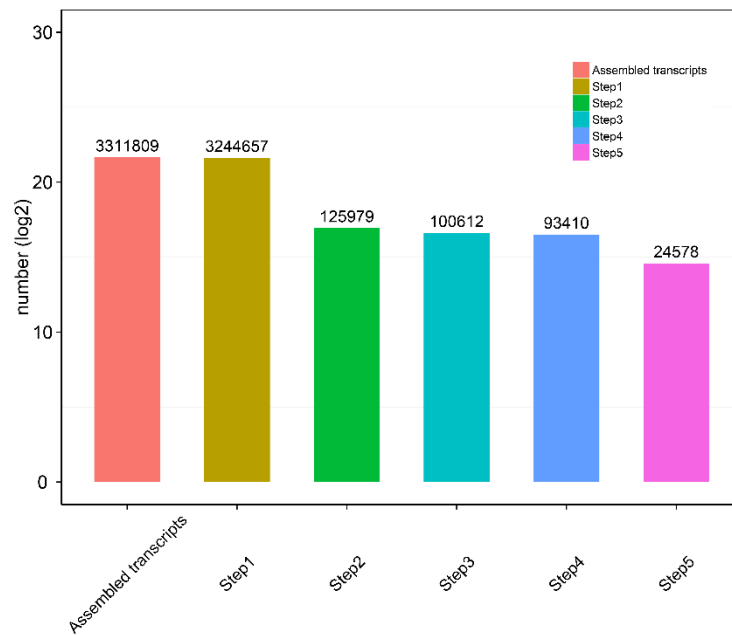
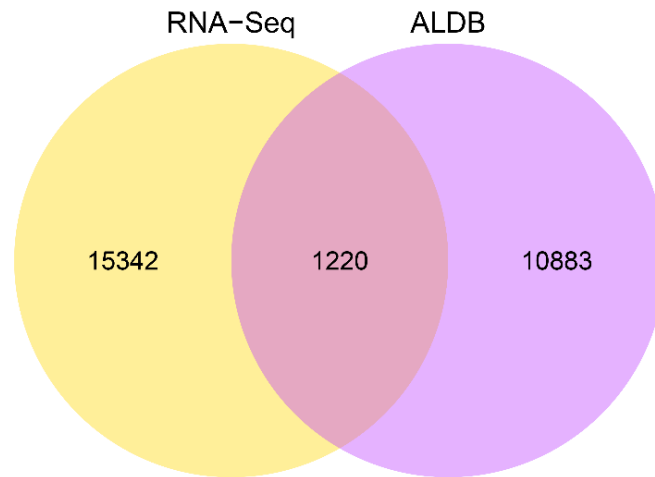


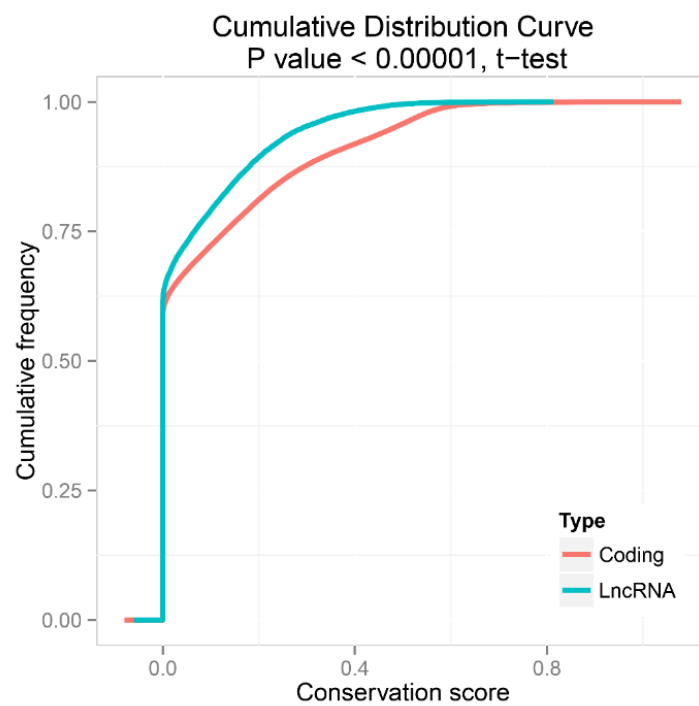
**Figure S1** Transcripts expression level distribution of each placenta sample. (A) A box plot of FPKM distribution with different gestation stage on the horizontal axis and  $\log_{10}(\text{FPKM}+1)$  on the vertical axis. (B) Density plot of expression distribution with  $\log_{10}(\text{FPKM} + 1)$  on the horizontal axis and density on the vertical axis.



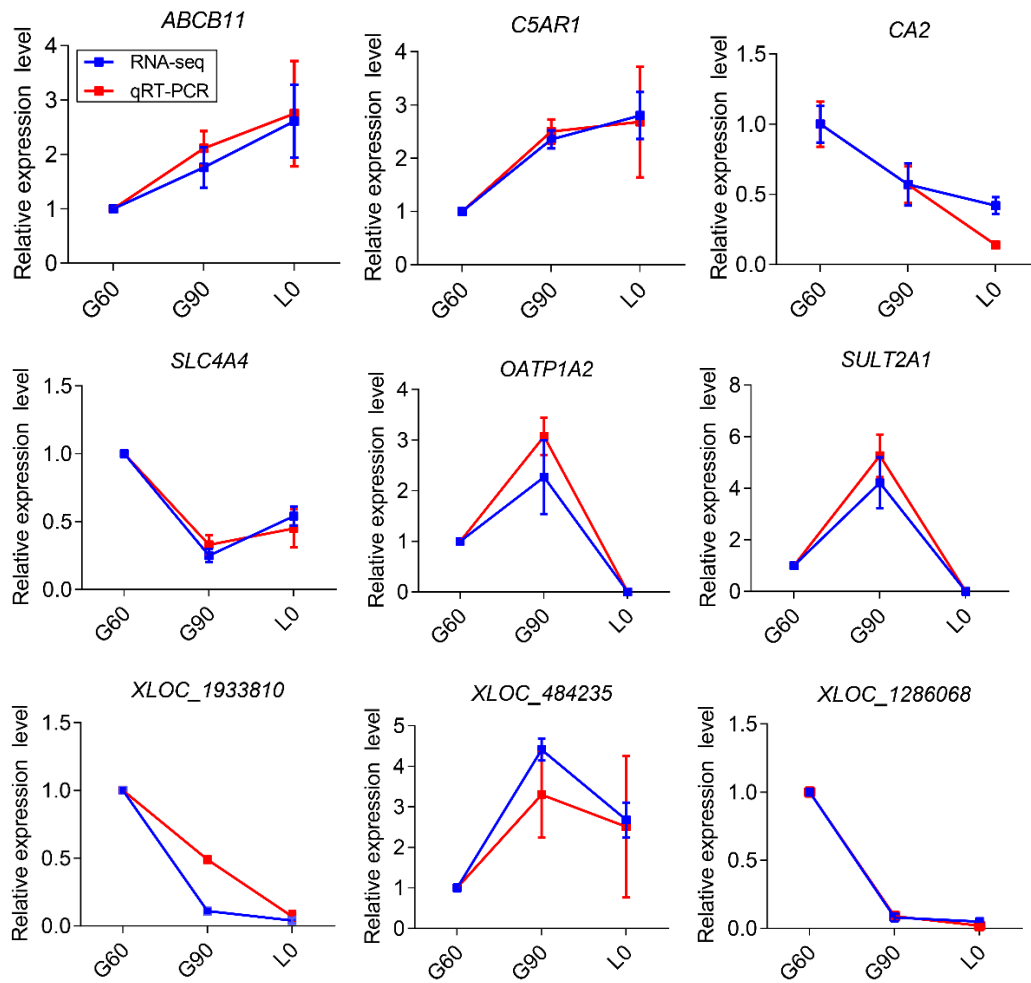
**Figure S2** 24,578 non-coding lncRNAs were selected by using Cufflinks and Scripture.



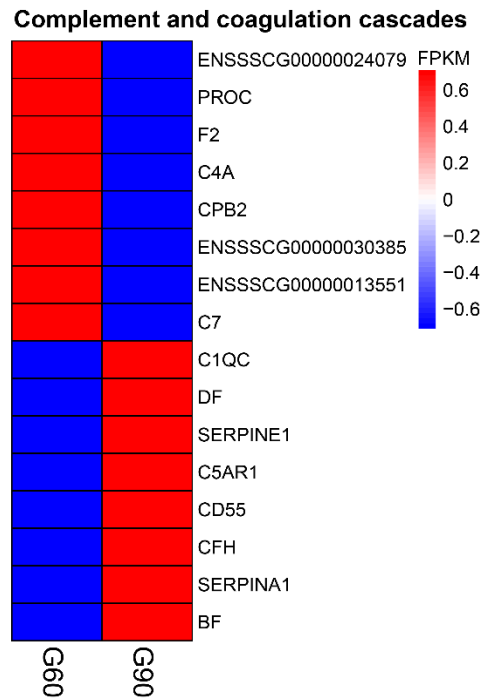
**Figure S3** Screening of the known and novel lncRNAs in placenta transcriptome. Identification known and novel lncRNAs from ALDB.



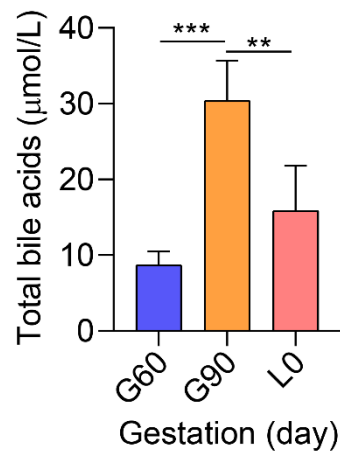
**Figure S4** The conservation of the sequence in mRNAs and LncRNAs were evaluated using phyloP (<http://compugen.bscb.cornell.edu/phast/>).



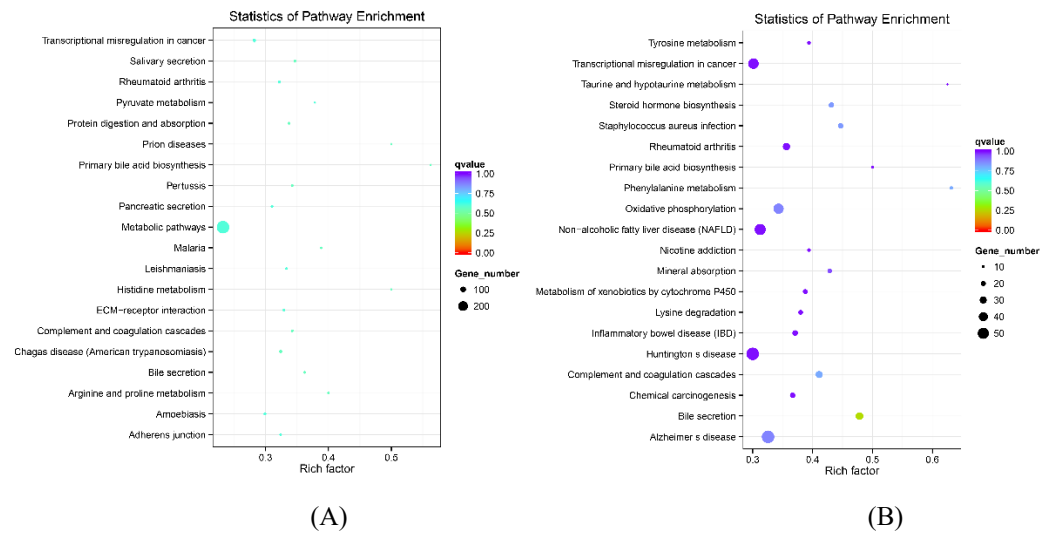
**Figure S5** Confirmation of the expression patterns of mRNAs and lncRNAs using qRT-PCR. Six mRNA and three novel lncRNA were chosen for quantitative RT-PCR to confirm the reliability of RNA-Seq. Data are shown as means  $\pm$  SE.



**Figure S6** Unsupervised hierarchical clustering of the expression profile of significant genes enriched in bile secretion between G60 and G90.



**Figure S7** The dynamic change of TBA in maternal serum at G60, G90 and L0, respectively (n=10/group). Data are shown as means  $\pm$  SE, \* $P$  < 0.05, \*\* $P$  < 0.01, \*\*\* $P$  < 0.001.



**Figure S8** The KEGG pathway analysis of dysregulated mRNAs and predicted trans-regulated targeted mRNAs of differentially expressed lncRNAs. (A) The top 20 over-represented KEGG pathways of dysregulated mRNAs, and (B) predicted trans-regulated targeted mRNAs of differentially expressed lncRNAs between G60 and L0.