Supplemental Table Legends

Table S1. Primer sequences used in this study.

Tables S2. Gene abbreviation symbols, ID (accession numbers) and related references used in this study.

Table S3. Statistical data of transcriptome analyses in each sample of three replicate WT and mutants.

Table S4. DEGs between *foxl2a*$^{-/-}$ or *foxl2b*$^{-/-}$ mutant ovaries VS control WT ovaries at 150 dpf revealed by transcriptome analyses. Compared to control WT ovaries, the DEGs (relative change $\geq$ 2) were divided into commonly up-regulated (S4.1), commonly down-regulated (S4.2) both in *foxl2a*$^{-/-}$ and *foxl2b*$^{-/-}$ mutant ovaries, specifically up-regulated in *foxl2a*$^{-/-}$ (S4.3) or *foxl2b*$^{-/-}$ (S4.4) mutant ovaries, and specifically down-regulated in *foxl2a*$^{-/-}$ (S4.5) or *foxl2b*$^{-/-}$ (S4.6) mutant ovaries and were showed in an single sheet, respectively. List of DEGs includes FPKM, log$_2$ fold change, up- or down-regulation and annotation.

Table S5. Enriched KEGG pathways of DEGs between *foxl2a*$^{-/-}$ or *foxl2b*$^{-/-}$ mutant ovaries VS control WT ovaries at 150 dpf. The DEGs were divided into commonly up-regulated (S5.1), commonly down-regulated (S5.2) both in *foxl2a*$^{-/-}$ and *foxl2b*$^{-/-}$ mutant ovaries, specifically up-regulated in *foxl2a*$^{-/-}$ (S5.3) or *foxl2b*$^{-/-}$ (S5.4) mutant ovaries, and specifically down-regulated DEGs in *foxl2a*$^{-/-}$

(S5.5) or *foxl2b*$^{-/-}$ (S5.6) mutant ovaries respectively to perform KEGG analysis. KEGG pathway description, number of DEGs assigned to the corresponding pathway, P value, Q value, Pathway ID, KEGG function classification, unigene ID assigned to the corresponding pathway and annotated KO ID of DEGs are shown.