



Supplementary Fig. 1. RNA-Seq analysis of differentially expressed mRNAs. (A) Principle component analysis of differentially expressed genes (DEGs) from RNA-seq of WT-PPs and *FOXA2*^{-/-} PPs. (B) Analysis for all differentially expressed miRNAs (DEmiRs) from miRNA-seq of WT-PPs and *FOXA2*^{-/-} PPs. KEGG pathway enrichment analysis of differentially expressed genes (DEGs) showing the associated enriched pathways in downregulated DEGs (B) and upregulated DEGs (C) in *FOXA2*^{-/-} PPs using the DAVID function annotation tool. Enriched pathways were plotted against -Log10 (P-value).