



Supplementary Figure S6. Bioinformatics analysis of overlapped differentially expressed genes (DEGs) (n = 301) between FSH18/21 versus Ctrl and FSH24 versus Ctrl groups. Gene expression data was derived from RNA-Sequencing analysis described in [Supplementary Fig. S3](#). (a) Top canonical pathways (absolute Z score > 1.0, -log P-value < 1.3) of overlapped DEGs. (b) Top activated upstream regulators of the overlapped DEGs analyzed by Ingenuity pathway analysis (IPA). (c) Analysis of top 5 molecular and cellular functions determined by IPA. (d) Overlapping of DEGs and genes known to be affected by FSHB database (IPA).