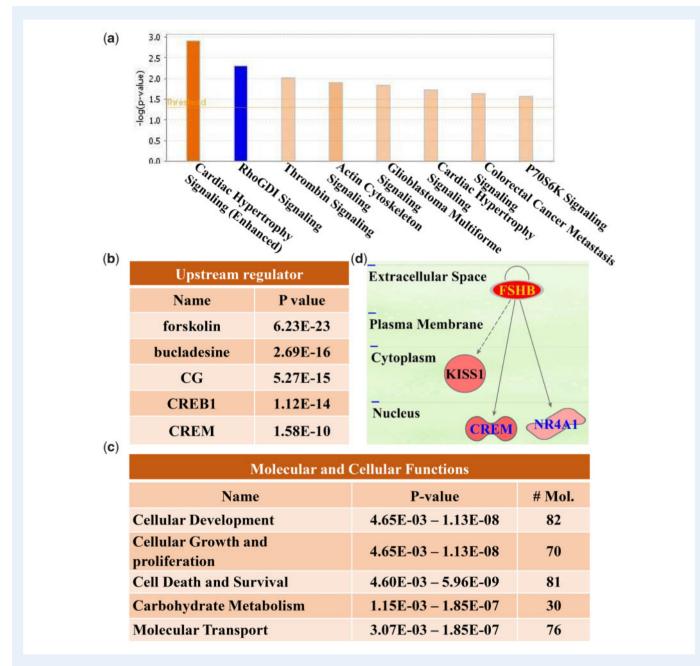
Human Reproduction, pp. 1-1, 2021

doi:10.1093/humrep/deab135

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SUPPLEMENTARY DATA



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).