



**Supplementary Figure S4. Transcriptomic analysis of CDC42-knockdown stromal cells.** (A) Principal component analysis of the gene expression profile of primary endometrial stromal cells (EnSCs) which received 48 h of ad-GFP treatment (Ctr group), 48 h of ad-GFP treatment and then 72 h of 8Br-cAMP+MPA treatment (Ctr\_D group), 48 h of ad-shCDC42-GFP treatment and then 72 h of 8Br-cAMP+MPA treatment (shCDC42\_D group). (B) Volcano plot of the differential expressed genes (DEGs) between Ctr\_D EnSCs and shCDC42\_D EnSCs. (C) Gene Set Enrichment Analysis (GSEA) of 'Wnt signaling pathway' enrichment in shCDC42\_D EnSCs compared with Ctr\_D EnSCs. (D) GSEA of 'Extracellular matrix organization' enrichment in shCDC42\_D EnSCs compared with Ctr\_D EnSCs. (E) Heatmap analysis showing the expression of genes associated with extracellular matrix organization. (F) GSEA of 'Response to oxidative stress' enrichment in shCDC42\_D EnSCs compared with Ctr\_D EnSCs. (G) Representative images of ROS levels detected by Mito-SOX staining in T-EnSCs transfected with Ad-GFP or Ad-shCDC42-GFP following with 72 h of 8Br-cAMP+MPA treatment.