

Table S2. Enriched Gene-Ontology Biological Processes of genes that were both downregulated in *Yap1/Taz* deficient GCs and upregulated in WT GCs in response to LH.

	GO Biological Process	# genes	% of GO BP	P-value
Metascape				
	ovulation	5	11.11	1.91E-09
	cell migration involved in sprouting angiogenesis	4	8.89	5.13E-06
	surfactant homeostasis	3	6.67	2.63E-05
	female gonad development	4	8.89	1.20E-04
	platelet-derived growth factor receptor signaling pathway	3	6.67	3.55E-04
	regulation of cell-matrix adhesion	3	6.67	2.63E-03
DAVID				
	positive regulation of ovulation	3	6	3.00E-05
	ovulation	3	6	2.70E-04
	multicellular organism development	9	18	1.90E-03
	angiogenesis	5	10	2.10E-03
	positive regulation of cell migration	4	8	1.10E-02
	smooth muscle cell migration	2	4	1.80E-02

The top 6 (based on P-value) biological processes identified with both the Metascape and DAVID bioinformatic software are listed. For each biological process, the number of corresponding genes in the analysis, the percentage of the biological process that these genes represent and the P-value of the enrichment are indicated. GO = Gene-Ontology. BP = Biological Process.