

Table S3. Enriched Gene-Ontology Biological Processes of genes that were both downregulated in *Yap1/Taz* deficient GCs and downregulated in *Erk1/2*-deficient GCs isolated 2.5 hours after hCG stimulation.

	GO Biological Process	# genes	% of GO BP	P-value
Metascape				
	vasculature development	10	31.25	1.78E-07
	regulation of cell adhesion	9	28.12	1.70E-06
	transmembrane receptor protein tyrosine kinase signaling pathway	8	25	2.63E-06
	negative regulation of cell population proliferation	8	25	1.51E-05
	positive regulation of cell migration	7	21.88	2.04E-05
	regulation of cell-substrate adhesion	5	15.62	2.24E-05
DAVID				
	ovulation	3	9.4	1.50E-04
	positive regulation of protein catabolic process	3	9.4	4.40E-03
	positive regulation of cell migration	4	12.5	4.50E-03
	angiogenesis	4	12.5	7.10E-03
	positive regulation of smooth muscle cell proliferation	3	9.4	7.80E-03
	pulmonary artery morphogenesis	2	6.2	8.30E-03

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.