

Supplementary Table 2. Differentially expressed genes in the top 6 canonical pathways found by IPA analysis for theca interna versus stroma (interstitial stroma and pre-theca).

Gene symbol	Entrez Gene Name	p-value	Fold change*
Hepatic Fibrosis / Hepatic Stellate Cell Activation			
<i>VEGFD</i>	vascular endothelial growth factor D	0.000000188	6.3
<i>COL21A1</i>	collagen type XXI alpha 1 chain	0.0000013	6.0
<i>COL1A2</i>	collagen type I alpha 2 chain	0.0000978	5.0
<i>VEGFC</i>	vascular endothelial growth factor C	0.00122	3.8
<i>COL4A1</i>	collagen type IV alpha 1 chain	0.000000377	3.3
<i>COL15A1</i>	collagen type XV alpha 1 chain	0.0151	3.1
<i>BCL2</i>	BCL2, apoptosis regulator	0.000000294	-7.0
<i>HGF</i>	hepatocyte growth factor	0.0106	-6.7
<i>MET</i>	MET proto-oncogene, receptor tyrosine kinase	0.0205	-5.4
<i>IGFBP5</i>	insulin like growth factor binding protein 5	0.00221	-5.4
<i>MYH11</i>	myosin heavy chain 11	0.00000738	-5.1
<i>BAMBI</i>	BMP and activin membrane bound inhibitor	0.00000577	-4.8
<i>VEGFB</i>	vascular endothelial growth factor B	0.000000252	-4.2
<i>PDGFD</i>	platelet derived growth factor D	0.00000125	-4.2
<i>TGFB2</i>	transforming growth factor beta 2	0.0000305	-4.0
<i>A2M</i>	alpha-2-macroglobulin	0.0329	-3.1
<i>TGFB3</i>	transforming growth factor beta 3	0.0194	-3.0
Androgen Biosynthesis			
<i>HSD3B2</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	2.73E-12	71.9
<i>CYP17A1</i>	cytochrome P450 family 17 subfamily A member 1	0.00000516	49.8
<i>EBP</i>	emopamil binding protein (sterol isomerase)	0.0151	5.4
<i>AKR1C3</i>	aldo-keto reductase family 1 member C3	0.000335	-4.8
TGF-β Signaling			
<i>INHBA</i>	inhibin beta A subunit	0.000416	9.4
<i>INHA</i>	inhibin alpha subunit	0.0000577	6.8
<i>NRAS</i>	NRAS proto-oncogene, GTPase	0.000384	3.3
<i>BCL2</i>	BCL2, apoptosis regulator	0.000000294	-7.0
<i>PMEPA1</i>	prostate transmembrane protein, androgen induced 1	0.00000159	-4.4
<i>TGFB2</i>	transforming growth factor beta 2	0.0000305	-4.0
<i>JUN</i>	Jun proto-oncogene, AP-1 transcription factor subunit	0.00244	-3.5

<i>SMAD9</i>	SMAD family member 9	0.0000899	-3.4
<i>TGIF1</i>	TGFB induced factor homeobox 1	0.000194	-3.4
<i>TGFB3</i>	transforming growth factor beta 3	0.0194	-3.0
Regulation of the Epithelial-Mesenchymal Transition Pathway			
<i>PIK3R3</i>	phosphoinositide-3-kinase regulatory subunit 3	0.000000423	-13.4
<i>LOX</i>	lysyl oxidase	0.000869	-6.2
<i>JAK3</i>	Janus kinase 3	0.00103	-6.1
<i>JAG1</i>	jagged 1	0.000675	-3.9
<i>NRAS</i>	NRAS proto-oncogene, GTPase	0.000384	-3.3
<i>EGR1</i>	early growth response 1	0.0214	7.1
<i>ID2</i>	inhibitor of DNA binding 2, HLH protein	0.0000156	6.7
<i>HGF</i>	hepatocyte growth factor	0.0106	6.7
<i>WNT5A</i>	Wnt family member 5A	0.000309	6.6
<i>MET</i>	MET proto-oncogene, receptor tyrosine kinase	0.0205	5.4
<i>PDGFD</i>	platelet derived growth factor D	0.00000125	4.2
<i>TGFB2</i>	transforming growth factor beta 2	0.0000305	4.0
<i>WNT4</i>	Wnt family member 4	0.000156	3.1
<i>ZEB1</i>	zinc finger E-box binding homeobox 1	0.00000737	3.0
<i>TGFB3</i>	transforming growth factor beta 3	0.0194	3.0
Glucocorticoid Biosynthesis			
<i>HSD3B2</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	2.73E-12	71.9
<i>CYP17A1</i>	cytochrome P450 family 17 subfamily A member 1	0.00000516	49.8
<i>EBP</i>	emopamil binding protein (sterol isomerase)	0.0151	5.4
Cholesterol Biosynthesis			
<i>DHCR24</i>	24-dehydrocholesterol reductase	0.000208	11.7
<i>EBP</i>	emopamil binding protein (sterol isomerase)	0.0151	5.4
<i>NSDHL</i>	NAD(P) dependent steroid dehydrogenase-like	0.0499	4.0
<i>HMGCR</i>	3-hydroxy-3-methylglutaryl-CoA reductase	0.0216	3.6
<i>ACAT2</i>	acetyl-CoA acetyltransferase 2	0.00877	3.3

*A positive value indicates upregulation and a negative value indicates downregulation in the theca interna.