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Supplementary Figure 1

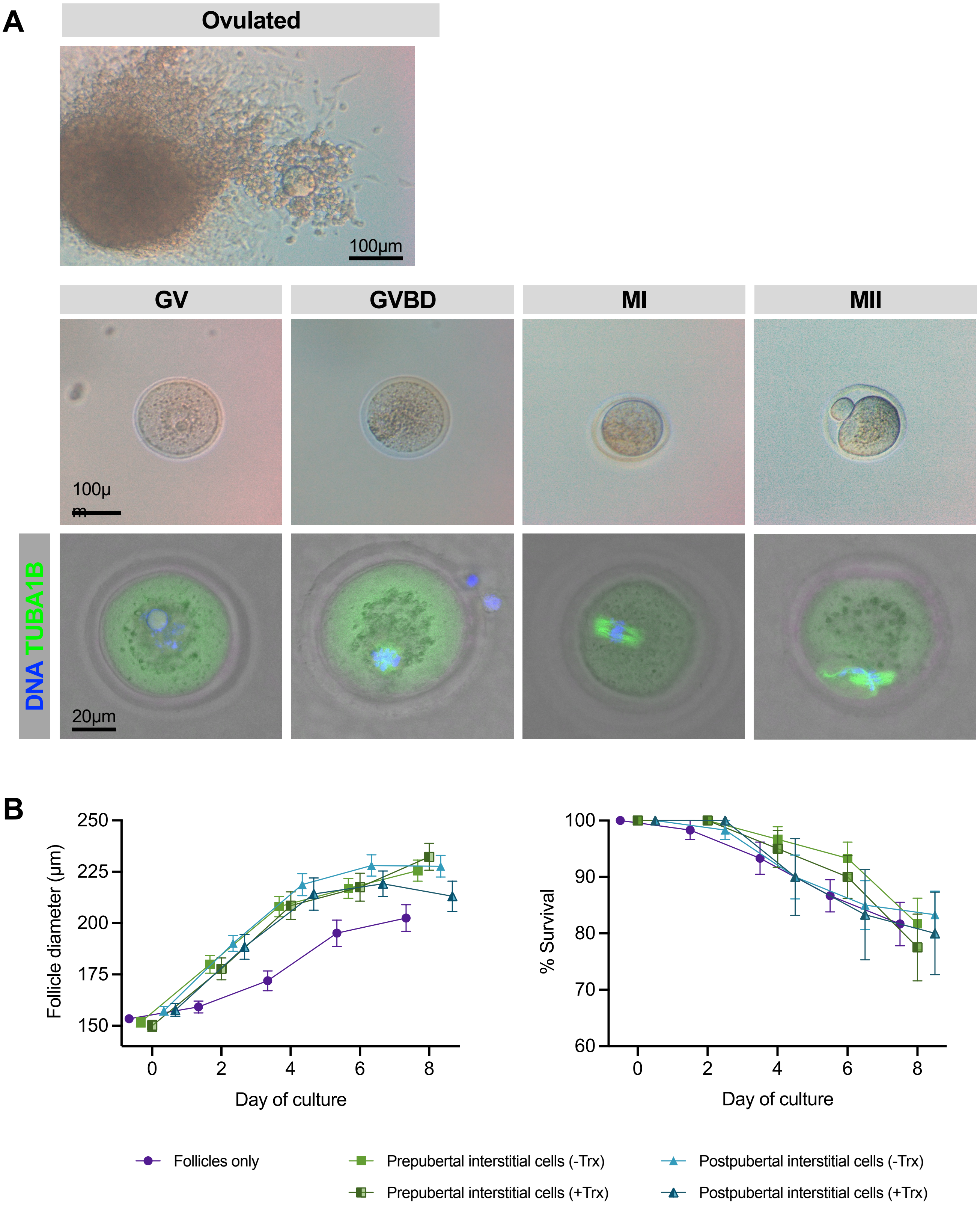

Figure S1. Representative oocyte staging by brightfield and fluorescence microscopy and stratification of follicle growth and survival by participant chemotherapy status. (A) Examples of maturation outcomes shown in **Figure 1E**. GV, germinal vesicle; GVBD, germinal vesicle breakdown; MI, metaphase I oocyte; MII, metaphase II oocyte. (B) Follicle diameter and survival (mean ± SEM) stratified by previous chemotherapy treatment. Trx, history of previous cyclophosphamide equivalent dose.

Supplementary Figure 2

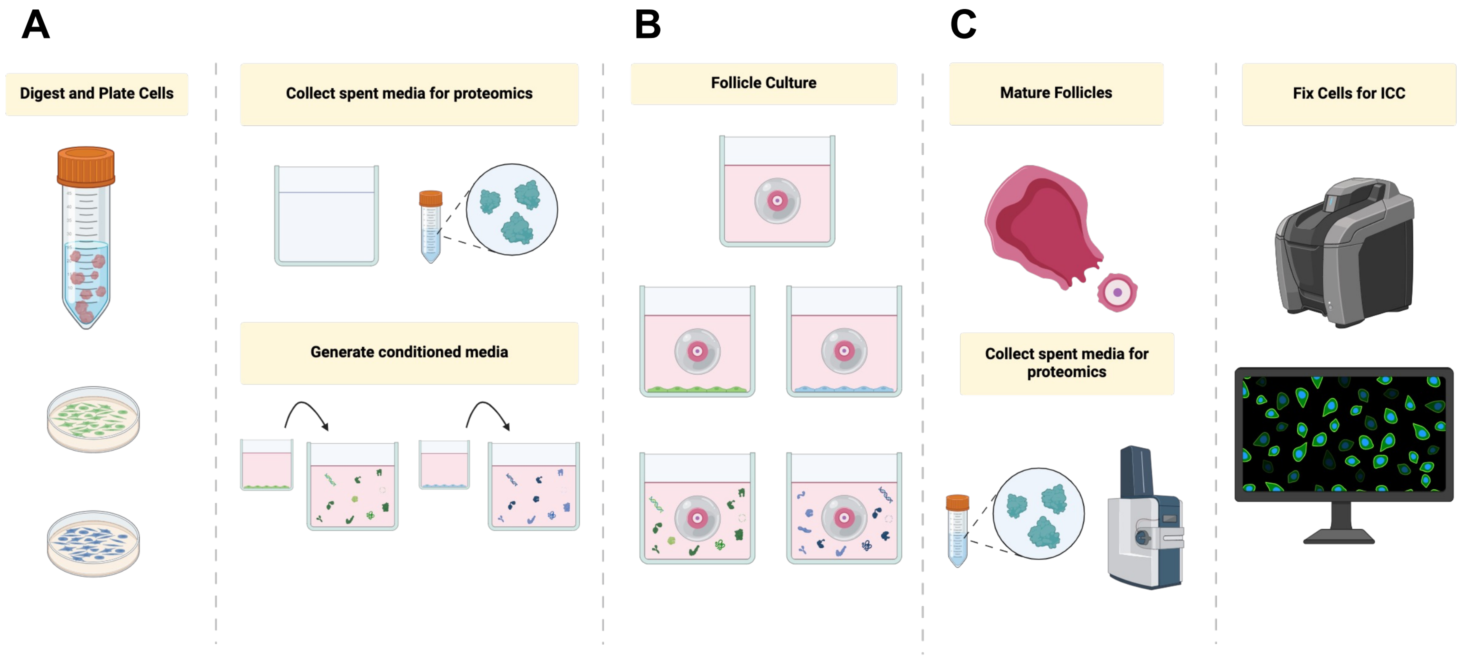

Figure S2. Experimental schematic of co-culture and conditioned media experiments. (A) Ovarian interstitial cells isolated from human ovary tissue were seeded and allowed to reach confluence, then treated with mitomycin C to pause proliferation and allowed to recover overnight. For interstitial cell conditioned media groups, cells were incubated in DMEM for 18-24 hours before media was collected and added to alginate-encapsulated secondary murine follicles. (B) Encapsulated follicles were cultured in control groups, with interstitial cells (co-culture, CC), or with conditioned media (CM). Follicles were monitored by brightfield microscopy and evaluated for diameter and survival, with half media changes performed every other day of culture beginning at culture day 2. (C) At end of culture (day 8 or day 6), cultured follicles were lyased, matured, and classified by brightfield or immunofluorescence microscopy using established morphologic criteria. Cells from CC groups were fixed in paraformaldehyde for ICC and spent media from CC and CM conditions was collected and stored at -80ºC until lyophilization.

Supplementary Figure 3

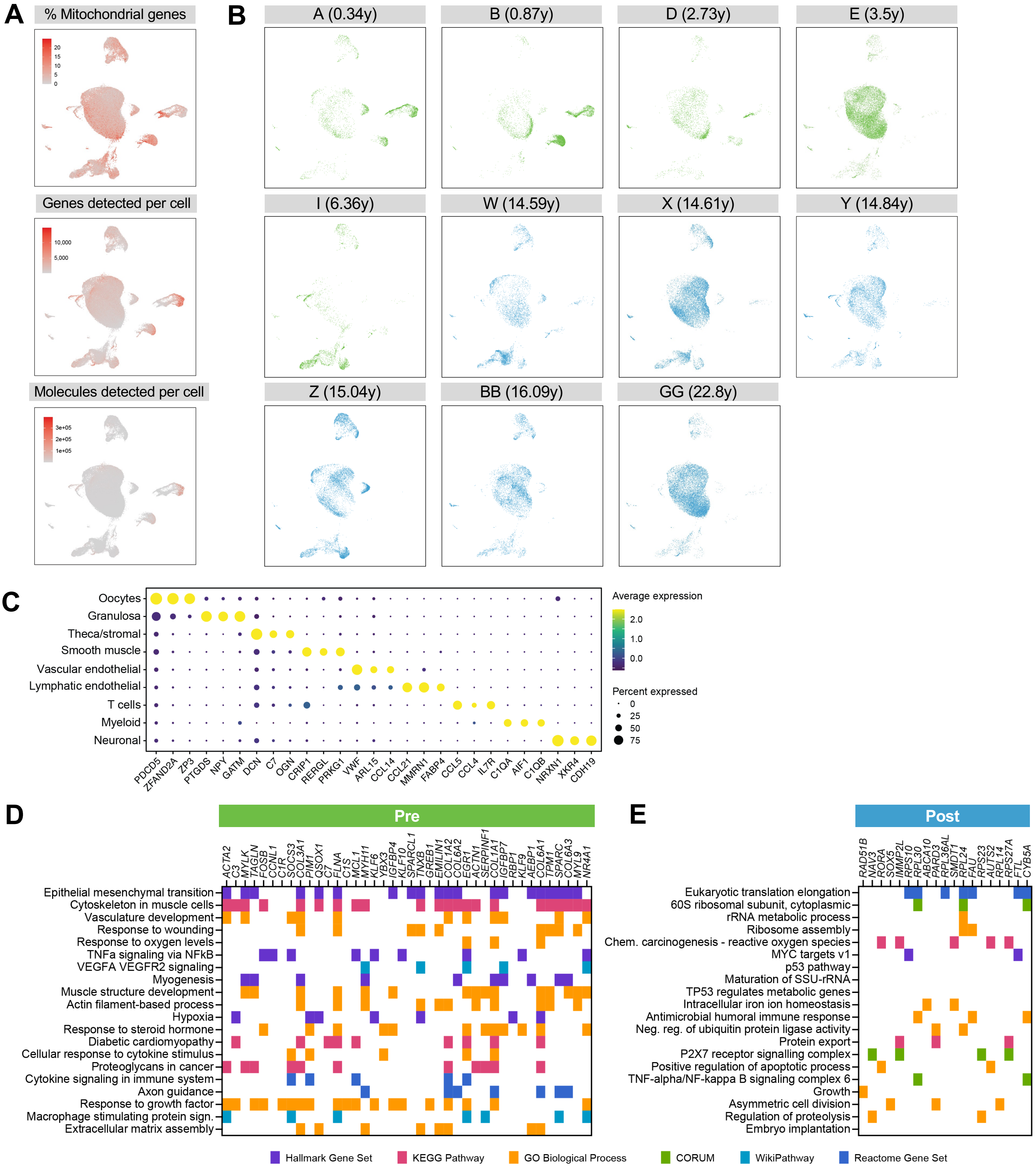

Figure S3. Single cell RNA-sequencing of human ovarian tissue from pediatric and adolescent individuals. (A) Uniform Manifold Approximation Projection (UMAP) of all analyzed cells, colored by quality control metrics. (B) UMAP of cells analyzed per individual sample, listed by age (green, prepubertal; blue, postpubertal). (C) Dot plot of selected top differentially expressed genes per cluster. (D-E) Member genes of selected enriched pathways for prepubertal (D) and postpubertal (E) theca/stromal cells; rows are colored by ontology database and ordered by enrichment p-value (most significant at top). Neg., negative; Reg., regulation; Sig., signaling.

Supplementary Figure 4

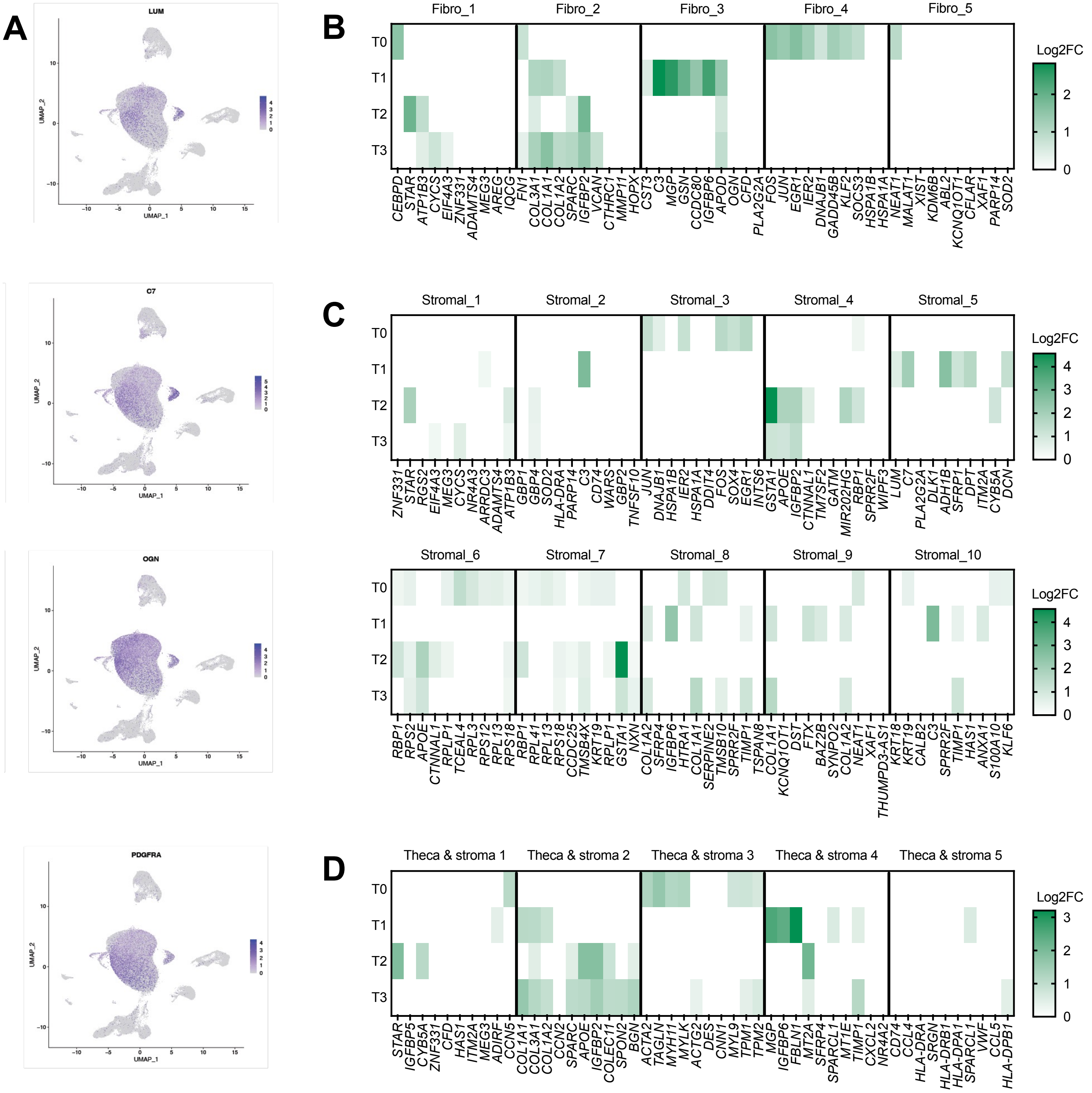

Figure S4. Comparison of theca/stromal subpopulations to previously published datasets. (A) UMAP showing gene expression of stromal cell markers *LUM*, *C7*, *OGN*, and *PDGFRA*. (B-D) Enrichment in each theca/stromal subpopulation of top 10 enriched genes in annotated stromal populations in previously published datasets: Deng 2022 (B; n=6 samples, ages 47-70)[60], Lengyel 2022 (C; n=6 samples, ages 55-65)[40], and Wu 2024 (D; n=9 samples, ages 18-49)[33].

Supplementary Figure 5

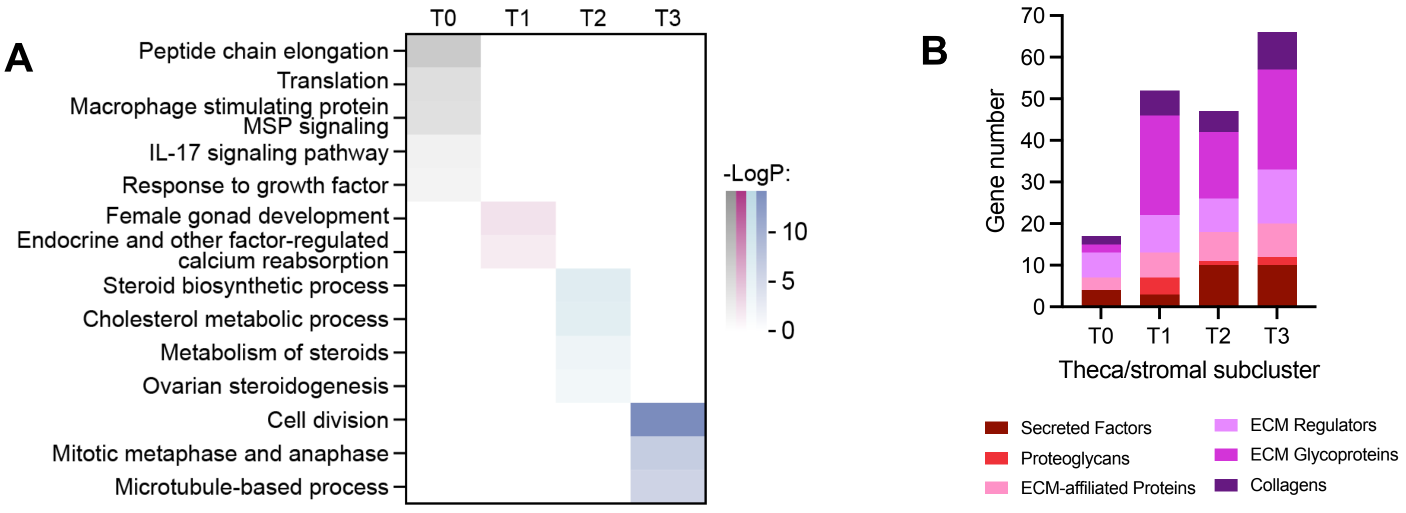

Figure S5. Theca/stromal subpopulations reflect variable biological functions. (A) Pathway enrichment for top 50 genes upregulated in each theca/stromal subpopulation. Adjusted p-values are expressed as negative $\log_{10}$. (B) Matrisome-annotated[50] significantly enriched genes in each theca/stromal subpopulation. SMC, smooth muscle cell; V. endothelial, vascular endothelial.

Supplementary Figure 6

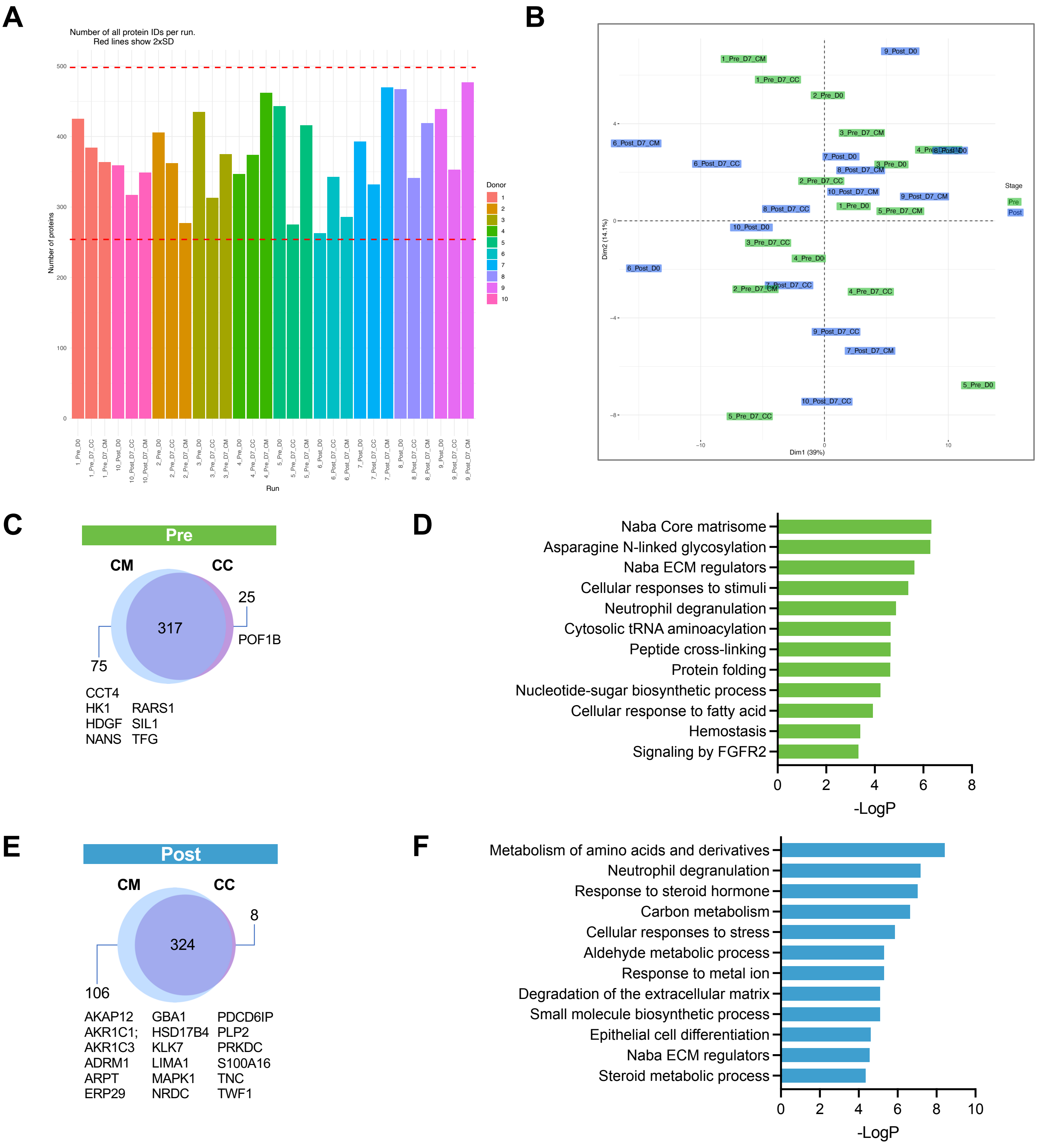

Figure S6. Proteomics analysis of parallel experiments utilizing murine follicles co-cultured with human ovarian tissue-derived interstitial cell-condition media or co-culture. (A) Unique human proteins detected per sample. (B) Principal component analysis (PCA) of samples colored by age group. (C) Number of proteins detected in Pre-CC and Pre-CM that were present in n≥3 of 5 samples per group. Proteins listed are detected in zero samples of other group. (D) Selected enriched pathways for 75 proteins unique to Pre-CM compared to Pre-CC, as shown in panel C. (E) Number of proteins detected in Post-CC and Post-CM that were present in n≥3 of 5 samples per group. Proteins listed are detected in zero samples of other group. (F) Selected enriched pathways for 106 proteins unique to Post-CM compared to Post-CC, as shown in panel E.

Supplementary Figure 7

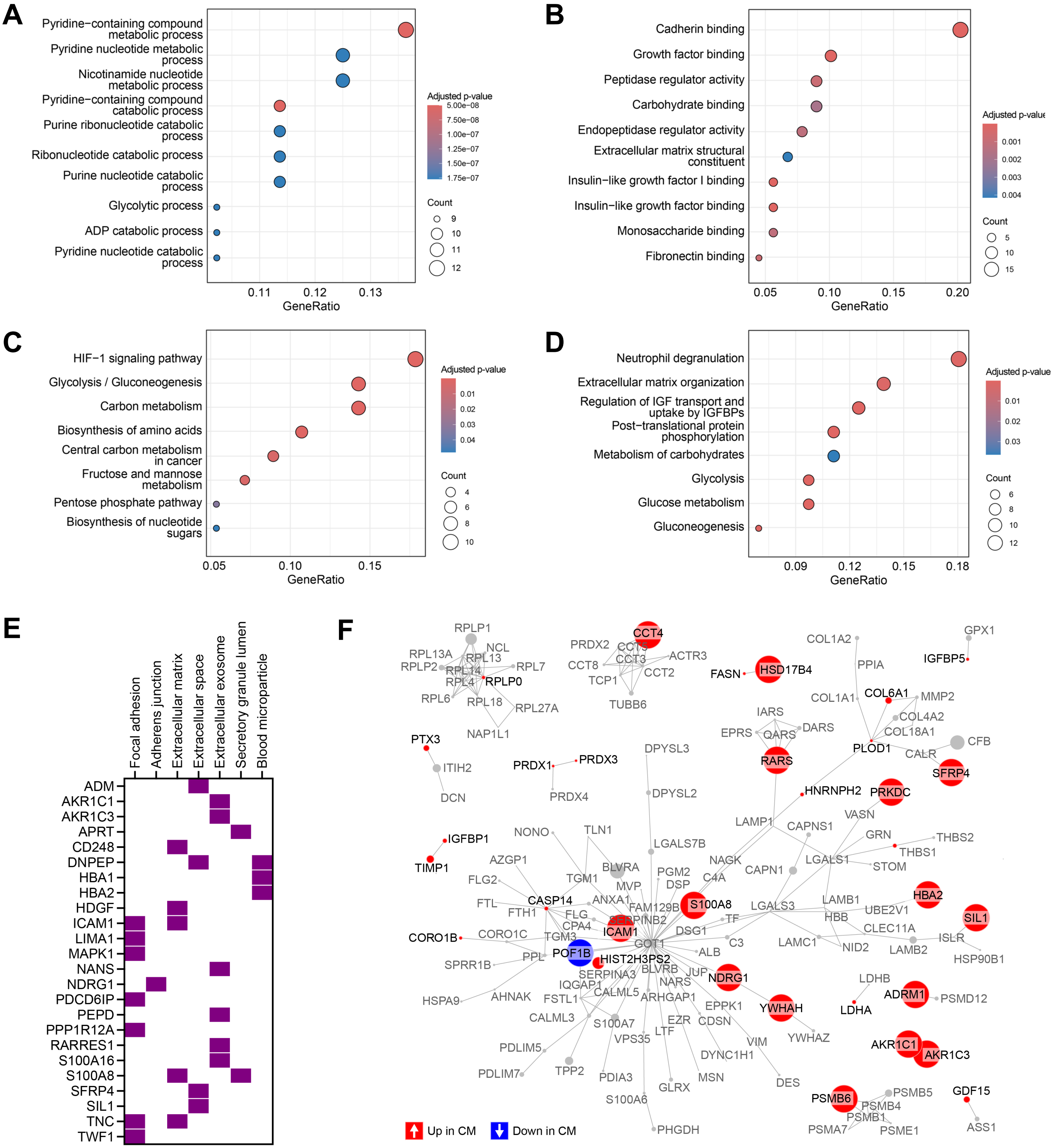

Figure S7. Proteins enriched in conditioned media culture compared to co-culture. (A-D) Enriched pathways (GO Biological Process, A; GO Molecular Function, B; KEGG, C; Reactome, D) for genes specifically upregulated or only present in CM compared to CC, Pre and Post combined (n=10 samples per condition). (E) Proteins with vesicle-related gene ontology (GO) cellular component (CC) annotations enriched or uniquely present in CM compared to CC, Pre and Post combined. (F) Protein-protein interaction diagram showing proteins upregulated or downregulated in CM, Pre and Post combined. Dot size indicates degree of enrichment; only statistically significant (padj<0.01) are colored. Lines connecting proteins represent predicted or experimentally validated interactions.

Supplementary Table 1. Participant demographic and clinical information for samples utilized in this study.

Abbreviations: CC, co-culture; CM, conditioned media; N, no; Y, yes.

								Experiments				
Deidentified ID	Anon-ymized	Age (years)	Tanner Stage	Group	Diagnosis category	Previous treatment	Sample type	8-day CC (Fig 1, S1)	CM (Fig 2)	CM (Fig 3)	scRNA-seq (Fig 4, 5)	s (Fig 6, 7)
MLAR-Ov-0168	A	0.34	1	Prepubertal	Other	N	Punch biopsy				X	
MLAR-Ov-0112	B	0.87	1	Prepubertal	Rhabdoid/sarcoma	N	Punch biopsy				X	
MLAR-Ov-0175	C	2.20	1	Prepubertal	Wilm's/neuroblastoma	N	Tissue fragments	X				
MLAR-Ov-0113	D	2.73	1	Prepubertal	Brain/spine tumor	N	Punch biopsy				X	
MLAR-Ov-0063	E	3.50	1	Prepubertal	Rhabdoid/sarcoma	N	Cortical strip				X	
MLAR-Ov-0164	F	3.94	1	Prepubertal	Wilm's/neuroblastoma	Y	Tissue fragments	X				
MLAR-Ov-0142	G	4.46	1	Prepubertal	Leukemia	Y	Tissue fragments	X				
MLAR-Ov-0234	H	4.51	1	Prepubertal	Rhabdoid/sarcoma	N	Tissue fragments		X	X		X
MLAR-Ov-0188	I	6.36	1	Prepubertal	Rhabdoid/sarcoma	N	Punch biopsy				X	
MLAR-Ov-0214	J	6.84	1	Prepubertal	Wilm's/neuroblastoma	Y	Tissue fragments	X				
MLAR-Ov-0243	K	7.73	1	Prepubertal	Wilm's/neuroblastoma	Y	Tissue fragments			X		X
MLAR-Ov-0180	L	8.41	1	Prepubertal	Rhabdoid/sarcoma	N	Tissue fragments	X				
MLAR-Ov-0225	M	8.87	1	Prepubertal	Rhabdoid/sarcoma	N	Tissue fragments		X	X		X
MLAR-Ov-0206	T	12.30	1	Prepubertal	Brain/spine tumor	Y	Tissue fragments	X				
MLAR-Ov-0199	N	10.28	1	Prepubertal	Rhabdoid/sarcoma	N	Tissue fragments		X	X		X
MLAR-Ov-0223	O	10.63	2	Postpubertal	Rhabdoid/sarcoma	N	Tissue fragments		X			
MLAR-Ov-0208	P	10.70	2	Postpubertal	Other	Y	Tissue fragments	X				
MLAR-Ov-0219	Q	11.51	2	Postpubertal	Brain/spine tumor	N	Tissue fragments		X			
MLAR-Ov-0212	V	13.57	2	Postpubertal	Leukemia	Y	Tissue fragments	X				
MLAR-Ov-0182	R	12.14	5	Postpubertal	Rhabdoid/sarcoma	N	Tissue fragments	X	X			
MLAR-Ov-0238	S	12.29	5	Postpubertal	Non-oncologic	N	Tissue fragments		X			
MLAR-Ov-0183	U	13.40	5	Postpubertal	Leukemia	N	Tissue fragments	X		X		X
MLAR-Ov-0129	W	14.59	5	Postpubertal	Leukemia	N	Punch biopsy				X	
MLAR-Ov-0104	X	14.61	5	Postpubertal	Brain/spine tumor	N	Punch biopsy				X	
MLAR-Ov-0100	Y	14.84	5	Postpubertal	Brain/spine tumor	N	Punch biopsy				X	
MLAR-Ov-0165	Z	15.04	5	Postpubertal	Rhabdoid/sarcoma	N	Punch biopsy				X	
MLAR-Ov-0207	AA	15.18	5	Postpubertal	Rhabdoid/sarcoma	Y	Tissue fragments	X		X		X
MLAR-Ov-0110	BB	16.09	5	Postpubertal	Non-oncologic	N	Punch biopsy				X	
MLAR-Ov-0244	CC	17.81	5	Postpubertal	Other	N	Tissue fragments			X		X
MLAR-Ov-0213	DD	18.34	5	Postpubertal	Other	N	Tissue fragments	X	X			
MLAR-Ov-0250	EE	19.93	5	Postpubertal	Other	N	Tissue fragments			X		X
MLAR-Ov-0150	FF	21.17	5	Postpubertal	Leukemia	N	Tissue fragments			X		X
MLAR-Ov-0089	GG	22.80	5	Postpubertal	Rhabdoid/sarcoma	N	Cortical strip				X	

Supplementary Table 2A. Quality control and sample metrics for scRNA-seq.
Abbreviations: UMI, unique molecular identifier.

Participant ID	**A**	**B**	**D**	**E**	**I**	**W**	**X**	**Y**	**Z**	**BB**	**GG**
Age (years)	0.34	0.87	2.73	3.5	6.36	14.59	14.61	14.84	15.04	16.09	22.8
Cells sequenced	4,857	8,547	4,160	14,184	3,704	6,207	14,037	9,854	11,164	8,852	15,446
Median genes/cell	1,701	1,439	1,148	1,206	1,900	787	1,261	2,471	1,598	1,753	1,191
Median UMI/cell	3,230	2,933	2,264	2,489	3,922	1,290	2,590	6,523	3,584	4,764	2,406
Total pass-QC cells	4,394	5,789	3,571	12,628	5,794	5,908	12,624	6,573	10,270	7,139	13,544
Oocytes	1,693	1,502	89	17	14	90	75	43	0	0	24
Granulosa	469	3,565	211	0	113	157	0	0	0	0	0
Theca/stromal	1,610	554	2,815	11,537	705	2,803	9,714	4,862	6,041	5,134	12,237
Smooth muscle cells (SMC)	353	89	148	330	422	579	931	414	1,770	955	432
Vascular endothelial	200	35	207	495	2,263	2,188	1,596	948	2,181	894	716
Lymphatic endothelial	0	0	95	76	2,263	41	147	203	0	133	21
T cells	0	0	0	14	14	0	8	55	5	5	8
Myeloid	0	0	0	93	0	0	0	14	0	0	45
Neuronal	69	44	6	66	0	50	153	34	273	18	61

Supplementary Table 2B. Top 10 differentially expressed genes for each cell cluster.

Abbreviations: Avg_log2FC, average log2fold change; Pct.1, percentage of cells where the gene is detected in the identified cluster; Pct. 2, percentage of cells where the genes is dectected on average in other clusters; p_val_adj, p-value adjusted for multiple comparisons; SMC, smooth muscle cell.

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster
VWF	0	4.15974195	0.862	0.046	0	Vascular endothelial
ARL15	0	3.74669237	0.526	0.08	0	Vascular endothelial
CCL14	0	3.67954294	0.543	0.022	0	Vascular endothelial
LDB2	0	3.62239558	0.745	0.119	0	Vascular endothelial
MECOM	0	3.3386846	0.586	0.009	0	Vascular endothelial
LIFR	0	3.25224451	0.718	0.154	0	Vascular endothelial
EGFL7	0	3.09872998	0.766	0.058	0	Vascular endothelial
CD74	0	3.04698774	0.699	0.118	0	Vascular endothelial
CLDN5	0	3.00114909	0.622	0.025	0	Vascular endothelial
A2M	0	2.97484808	0.819	0.156	0	Vascular endothelial
PTGDS	0	3.99176301	0.887	0.059	0	Granulosa
NPY	0	3.64580157	0.793	0.01	0	Granulosa
GATM	0	2.64069706	0.888	0.163	0	Granulosa
PRXL2A	0	2.48966418	0.829	0.13	0	Granulosa
ISYNA1	0	2.40823311	0.873	0.181	0	Granulosa
BEX1	0	2.31711768	0.74	0.029	0	Granulosa
WNT6	0	2.26772914	0.737	0.019	0	Granulosa
KRT18	0	2.26363216	0.73	0.045	0	Granulosa
MIR202HG	0	2.22228511	0.716	0.053	0	Granulosa
ANGPTL6	0	2.21130907	0.7	0.009	0	Granulosa
CCL21	0	5.31388092	0.79	0.015	0	Lymphatic endothelial
MMRN1	0	4.6073703	0.839	0.033	0	Lymphatic endothelial
FABP4	0	4.50759595	0.603	0.015	0	Lymphatic endothelial
TFPI	0	4.00489829	0.876	0.166	0	Lymphatic endothelial
TFF3	0	4.00385137	0.728	0.018	0	Lymphatic endothelial
FABP5	0	3.68693085	0.629	0.108	0	Lymphatic endothelial
PKHD1L1	0	3.33971719	0.523	0.003	0	Lymphatic endothelial
PROX1	0	3.24766356	0.68	0.052	0	Lymphatic endothelial
RELN	0	3.04206909	0.554	0.034	0	Lymphatic endothelial
ANGPT2	0	2.95239642	0.512	0.067	0	Lymphatic endothelial
C1QA	0	4.23281782	0.599	0.004	0	Myeloid
AIF1	0	3.80795624	0.572	0.003	0	Myeloid
C1QB	0	3.72667595	0.559	0.003	0	Myeloid
F13A1	0	3.70857434	0.546	0.014	0	Myeloid
TYROBP	0	3.24886059	0.513	0.002	0	Myeloid
C1QC	0	2.97621974	0.408	0.001	0	Myeloid
FCER1G	0	2.73184139	0.395	0.002	0	Myeloid
MS4A6A	0	2.51241947	0.362	0.002	0	Myeloid
FOLR2	0	2.40153811	0.342	0.001	0	Myeloid

CYBB	0	2.26663336	0.342	0.001	0	Myeloid
NRXN1	0	6.22239552	0.951	0.021	0	Neuronal
XKR4	0	4.7691508	0.714	0.003	0	Neuronal
CDH19	0	4.71857185	0.853	0.004	0	Neuronal
CRYAB	0	4.20241887	0.779	0.137	0	Neuronal
ADGRB3	0	4.15332905	0.63	0.033	0	Neuronal
GPM6B	0	4.15249444	0.848	0.071	0	Neuronal
CADM2	0	4.14915242	0.601	0.015	0	Neuronal
S100B	0	4.09979543	0.695	0.012	0	Neuronal
NRXN3	0	3.99088693	0.583	0.016	0	Neuronal
GRIK2	0	3.58527583	0.491	0.034	0	Neuronal
PDCD5	0	4.71335143	0.988	0.332	0	Oocytes
ZFAND2A	0	4.60272967	0.95	0.092	0	Oocytes
ZP3	0	4.306322	0.888	0.032	0	Oocytes
TUBB8	0	4.3015879	0.899	0.032	0	Oocytes
UCHL1	0	3.84847749	0.914	0.125	0	Oocytes
FIGLA	0	3.75616846	0.855	0.02	0	Oocytes
AL033523.1	0	3.68872196	0.659	0.019	0	Oocytes
STAG3	0	3.51864585	0.862	0.037	0	Oocytes
PADI6	0	3.47785927	0.885	0.029	0	Oocytes
KCNQ1-AS1	0	3.4304321	0.855	0.022	0	Oocytes
CRIP1	0	3.97735855	0.754	0.04	0	SMC
RERGL	0	3.4724509	0.585	0.021	0	SMC
PRKG1	0	3.44072141	0.7	0.12	0	SMC
MUSTN1	0	3.24937905	0.65	0.018	0	SMC
ADIRF	0	3.02732635	0.887	0.456	0	SMC
RGS5	0	2.89586104	0.475	0.032	0	SMC
TAGLN	0	2.73665842	0.891	0.432	0	SMC
PLN	0	2.72092289	0.586	0.023	0	SMC
ACTA2	0	2.64337332	0.885	0.354	0	SMC
S100A4	0	2.51040575	0.455	0.023	0	SMC
CCL5	0	4.25255375	0.725	0.002	0	T cells
CCL4	0	4.23910239	0.33	0.001	0	T cells
IL7R	0	4.07631438	0.651	0.002	0	T cells
CD69	0	3.87248766	0.651	0	0	T cells
PTPRC	0	3.60417512	0.743	0.001	0	T cells
CD2	0	3.39402755	0.725	0	0	T cells
KLRB1	0	3.20402288	0.532	0	0	T cells
CXCR4	0	3.17882046	0.688	0.011	0	T cells
CD52	0	3.14045787	0.596	0.003	0	T cells
LTB	0	2.81969127	0.404	0.001	0	T cells
DCN	0	3.22981512	0.942	0.312	0	Theca/stromal
C7	0	2.45033861	0.585	0.128	0	Theca/stromal
OGN	0	2.38401287	0.642	0.085	0	Theca/stromal
MEG3	0	2.31269255	0.5	0.114	0	Theca/stromal

COL1A1	0	2.27813066	0.673	0.19	0	Theca/stromal
PDGFRA	0	2.17947888	0.591	0.066	0	Theca/stromal
COL1A2	0	2.14401641	0.724	0.236	0	Theca/stromal
C1R	0	2.01957833	0.628	0.171	0	Theca/stromal
C1S	0	2.00597846	0.622	0.156	0	Theca/stromal
PEG3	0	1.97103131	0.711	0.229	0	Theca/stromal

Supplementary Table 4C. Predicted source for CM- and CC-enriched or unique proteins for all samples (Pre and Post combined).

Abbreviations: CC, co-culture; CM, conditioned media; D0, [experimental] day 0; D7, [experimental] day 7; Pre, prepubertal; Post, postpubertal; SMC, smooth muscle cell.

'N/A' in 'Predicted source' column indicates the corresponding transcript was detected at extremely low levels in all interstitial cell types.

ProtName	Gene symbol(s)	Classification	Predicted source
ADML	ADM	Only in CM	Lymphatic endothelial
AKA12	AKAP12	Only in CM	Lymphatic endothelial
BGAL	GLB1	Up in CM	Lymphatic endothelial
MK01	MAPK1	Only in CM	Lymphatic endothelial
EFNMT	METTL13	Up in CC	Lymphatic endothelial
NDRG1	NDRG1	Only in CM	Lymphatic endothelial
NNMT	NNMT	Only in CM	Lymphatic endothelial
PDC6I	PDCD6IP	Only in CM	Lymphatic endothelial
PEPD	PEPD	Only in CM	Lymphatic endothelial
PTX3	PTX3	Up in CM	Lymphatic endothelial
PXDN	PXDN	Up in CM	Lymphatic endothelial
S10AG	S100A16	Only in CM	Lymphatic endothelial
SEPT9	SEPTIN9	Only in CM	Lymphatic endothelial
TPD54	TPD52L2	Only in CM	Lymphatic endothelial
ACPH	APEH	Up in CM	Myeloid
FRIH	FTH1	Up in CM	Myeloid
S10AB	S100A11	Up in CM	Myeloid
S10A8	S100A8	Only in CM	Myeloid
DDTL	DDTL	Up in CM	N/A
GDF15	GDF15	Up in CM	N/A
IBP1	IGFBP1	Up in CM	N/A
K22O	KRT76	Only in CC	N/A
MXRA5	MXRA5	Up in CM	N/A
POF1B	POF1B	Only in CC	N/A
S10A7	S100A7	Up in CM	N/A
SBSN	SBSN	Up in CM	N/A
SPB12	SERPINB12	Up in CC	N/A
STC2	STC2	Up in CM	N/A
PDLI4	PDLIM4	Only in CM	Neuronal
PRIO	PRNP	Up in CM	Neuronal
TIG1	RARRES1	Only in CM	Neuronal
ALDOA	ALDOA	Up in CM	SMC
THOC4	ALYREF	Up in CM	SMC
RHG01	ARHGAP1	Up in CC	SMC
PUR9	ATIC	Up in CM	SMC
BMP1	BMP1	Up in CM	SMC

CBR1	CBR1	Up in CM	SMC
TCPD	CCT4	Only in CM	SMC
CD248	CD248	Only in CM	SMC
CLIC1	CLIC1	Up in CM	SMC
DCTN2	DCTN2	Only in CM	SMC
DNPEP	DNPEP	Only in CM	SMC
G3P	GAPDH	Up in CM	SMC
G6PI	GPI	Up in CM	SMC
HDGF	HDGF	Only in CM	SMC
HNRH2	HNRNPH2	Up in CM	SMC
KTN1	KTN1	Only in CM	SMC
MIF	MIF	Up in CM	SMC
MT2	MT2A	Up in CM	SMC
MYPT1	PPP1R12A	Only in CM	SMC
PRDX1	PRDX1	Up in CM	SMC
PRDX3	PRDX3	Up in CM	SMC
PSB6	PSMB6	Only in CM	SMC
SARNP	SARNP	Only in CM	SMC
TSP1	THBS1	Up in CM	SMC
TENA	TNC	Only in CM	SMC
TPIS	TPI1	Up in CM	SMC
1433F	YWHAH	Only in CM	SMC
COR1B	CORO1B	Up in CM	T cells
PNPH	PNP	Up in CM	T cells
CO6A1	COL6A1	Up in CM	Theca/stromal
EF2	EEF2	Up in CM	Theca/stromal
ENOA	ENO1	Up in CM	Theca/stromal
FBLN1	FBLN1	Up in CM	Theca/stromal
H37	H3-7	Up in CM	Theca/stromal
HBA	HBA1; HBA2	Only in CM	Theca/stromal
IDHC	IDH1	Up in CM	Theca/stromal
IBP2	IGFBP2	Up in CM	Theca/stromal
IBP5	IGFBP5	Up in CM	Theca/stromal
P4HA1	P4HA1	Only in CM	Theca/stromal
PA2GA	PLA2G2A	Only in CM	Theca/stromal
PLIN3	PLIN3	Only in CM	Theca/stromal
PLOD1	PLOD1	Up in CM	Theca/stromal
RLA0	RPLP0	Up in CM	Theca/stromal
PAI1	SERPINE1	Up in CM	Theca/stromal
SFRP4	SFRP4	Only in CM	Theca/stromal
TFR1	TFRC	Up in CM	Theca/stromal
TIMP1	TIMP1	Up in CM	Theca/stromal
ADRM1	ADRM1	Only in CM	Vascular endothelial
AK1C1	AKR1C1	Only in CM	Vascular endothelial
APT	APRT	Only in CM	Vascular endothelial

GDIR1	ARHGDIA	Up in CM	Vascular endothelial
AT1A1	ATP1A1	Only in CM	Vascular endothelial
B2MG	B2M	Up in CM	Vascular endothelial
CLUS	CLU	Up in CM	Vascular endothelial
COPA	COPA	Up in CM	Vascular endothelial
DHX9	DHX9	Only in CM	Vascular endothelial
FAS	FASN	Up in CM	Vascular endothelial
GLGB	GBE1	Up in CM	Vascular endothelial
GDIB	GDI2	Up in CM	Vascular endothelial
HXK1	HK1	Only in CM	Vascular endothelial
DHB4	HSD17B4	Only in CM	Vascular endothelial
ICAM1	ICAM1	Only in CM	Vascular endothelial
IBP3	IGFBP3	Up in CM	Vascular endothelial
IBP4	IGFBP4	Up in CM	Vascular endothelial
ISG15	ISG15	Up in CM	Vascular endothelial
LDHA	LDHA	Up in CM	Vascular endothelial
LIMA1	LIMA1	Only in CM	Vascular endothelial
MACF1	MACF1	Only in CM	Vascular endothelial
MGP	MGP	Up in CM	Vascular endothelial
SIAS	NANS	Only in CM	Vascular endothelial
NRDC	NRDC	Only in CM	Vascular endothelial
PFKAP	PFKP	Up in CM	Vascular endothelial
PRKDC	PRKDC	Only in CM	Vascular endothelial
SYRC	RARS1	Only in CM	Vascular endothelial
SIL1	SIL1	Only in CM	Vascular endothelial
TFG	TFG	Only in CM	Vascular endothelial
TWF1	TWF1	Only in CM	Vascular endothelial

Supplementary Table 5. Antibodies used for immunocytochemistry.

Target	Supplier	Catalog Number	RRID	Dilution
ACTA2 (SMA)	Sigma-Aldrich	A5228	AB_262054	1:200
APOC1	Abcam	ab198288	AB_3698448	1:200
DDX4	Abcam	ab27591	AB_11139638	1:200
FOXL2	Abcam	ab246511	AB_2895602	1:200
HMGB1	Abcam	ab18256	AB_444360	1:200
NR2F2 (COUPTFII)	R&D Systems	PPH714700	AB_2155627	1:200
SERPINE2	Proteintech	66203-1-IG	AB_2881594	1:400
TUBA1B (α-tubulin)	Cell Signaling Technology	8058S	AB_10860077	1:50
VWF	Abcam	ab154193	AB_3094475	1:200
Mouse IgG-AF488	Thermo Fisher	A21202	AB_141607	1:500
Rabbit IgG-AF488	Thermo Fisher	A21206	AB_2535792	1:500
Mouse IgG-AF568	Thermo Fisher	A10037	AB_11180865	1:500
Rabbit IgG-AF568	Thermo Fisher	A10042	AB_2534017	1:500