

Regenerative and non-regenerative transcriptional states of the human epicardium: from foetus to adult and back again: Supplementary Tables

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Supplementary Table 1. Sample information including sample labels, age, number of cells called by cellranger, and number of cells retained after quality control (QC) steps. Ages of foetal samples are approximate.

Sample	Alt name	Age	# cells raw	# cells after QC
F1	BRC2252	58 days	7038	3753
F2	BRC2262	61 days	5487	1470
F3	BRC2251	64 days	3540	1731
F4	BRC2263	66 days	2729	663
F5	alexsc	67 days	2486	1813
F6	BRC2256	69 days	3265	515
F7	BRC2260	80 days	10787	4109
A1	D3	55-60 years	3856	3743
A2	D4	70-75 years	1523	881
A3	D5	65-70 years	6105	4721
A4	D6	65-70 years	20889	19439
A5	D7	60-65 years	5089	4318

Supplementary Table 2. Typical mean results from one 6-fold cross-validation run of the foetal sample F5. A sample of 36 cells was taken from each cluster of the total dataset in this run of 6-fold cross validation. Data points can be observed in the UMAP in Supplementary figure 2.

Cell type	Recall	Precision	Balanced Accuracy
Unknown / Noise	0.306	NA	0.645
Atrial CMs	1.000	1.000	1.000
RBCs	0.944	1.000	0.972
Ventricular CMs	1.000	1.000	1.000
Immune cells	0.972	0.976	0.985
Endothelial	0.944	0.935	0.968
Endocardial	0.944	0.925	0.968
Epicardial	1.000	0.976	0.999
Fibroblast-like	0.944	0.877	0.966
Cardiac Fibroblast	0.944	0.866	0.965
SMCs / Pericytes	0.917	0.858	0.951
Cycling cells	0.972	0.817	0.975

Supplementary Table 3. The top 100 differentially upregulated genes of epicardial cluster 15 compared with all other clusters identified using Wilcoxon rank-sum tests on the adult and foetal integrated dataset. Genes are ranked according to their log 2 fold change against the overall dataset excluding those with log2 fold-change lower than 0.5 or a p value greater than 1×10^{-10} . Epicardial genes in only cluster 15 are shown in blue.

Gene	Log2 FC	Adj pvalue	cluster %	dataset %	Epi_cluster
ITLN1	5.12	1.26E-158	100	50.4	Both
HP	5.11	5.06E-160	100	56.6	Mesothelial
PRG4	3.78	1.90E-156	99.6	61.6	Both
SLPI	3.76	1.23E-158	100	69.3	Both
PLA2G2A	3.12	1.51E-150	100	70.4	Both
KRT18	2.88	1.15E-154	99.6	50	Both
KRT19	2.75	1.37E-159	99.2	41	Both
KRT8	2.42	6.33E-153	99.2	47.4	Both
UPK3B	2.38	1.14E-165	99.2	28.8	Both
TIMP1	2.15	1.58E-143	100	86.9	Both
C3	2.14	2.15E-143	100	70.4	Both
CCDC80	2.05	3.43E-137	99.6	66.5	Both
SAT1	2.02	2.82E-133	100	90.7	Mesothelial
SGK1	1.80	3.77E-148	100	75	Both
CYSTM1	1.72	3.30E-139	100	85.2	Both
HAS1	1.54	1.02E-158	99.6	54.5	Both
SYT4	1.52	1.55E-176	99.2	26.6	Both
RARRES2	1.46	5.36E-126	99.2	68.6	Both
INMT	1.45	1.76E-129	99.6	77.3	Both
WFDC2	1.45	4.56E-156	99.6	55.5	Mesothelial
SLC39A8	1.45	1.00E-149	99.6	66.3	Both
FOS	1.43	2.21E-109	100	86	Mesothelial
TM4SF1	1.41	8.44E-107	100	80.8	Mesothelial
CALB2	1.39	8.55E-144	96	30.4	Both
EFEMP1	1.38	1.35E-118	99.6	71.5	Both
MSLN	1.37	2.53E-138	95.2	35.6	Both
CFI	1.36	1.30E-130	98.4	78.1	Both
NNMT	1.35	1.76E-114	99.6	78.5	Both
UPK1B	1.34	4.18E-150	98	37.9	Both
AQP1	1.32	3.66E-104	100	84.7	Mesothelial
CEBPB	1.32	1.25E-116	100	87.2	Mesothelial
PROCR	1.30	8.97E-114	96.8	73.4	Both
CXADR	1.29	1.32E-149	98.4	46.6	Both
CLDN15	1.27	7.75E-142	98.4	59.1	Both
CHI3L1	1.24	4.12E-142	96.8	56.6	Both
LINC01133	1.22	1.26E-140	97.6	46.8	Both
MGST1	1.21	2.23E-98	100	76.8	Both
S100A10	1.16	1.11E-119	100	94.5	Both
PTGIS	1.14	1.31E-123	99.6	67.5	Both
FLRT3	1.09	2.16E-155	99.2	54.2	Both
TGM1	1.06	2.63E-143	96.4	38.9	Both
SELENBP1	1.05	5.14E-117	99.6	67.3	Mesothelial
RPL22L1	1.04	3.02E-101	99.2	76.6	Mesothelial
ZFAS1	1.04	6.86E-99	100	86.3	Mesothelial
PDPN	1.03	1.64E-137	99.2	60.4	Both
GCHFR	1.03	3.34E-134	98.8	73.9	Mesothelial
CD200	1.03	1.71E-141	98.8	62	Mesothelial
RARRES1	1.02	6.03E-86	98.4	70.8	Both
ID2	1.02	1.38E-90	99.2	86.4	Mesothelial
CFH	1.01	2.54E-94	100	73.7	Both

KLF6	1.00	2.63E-100	100	93.1	Mesothelial
HILPDA	0.98	1.32E-126	97.2	65.3	Both
ALOX15	0.98	1.01E-173	98.8	29	Mesothelial
MT1E	0.96	1.20E-92	98.8	82.5	Both
TPT1	0.94	2.73E-127	100	99.6	Mesothelial
PTPRF	0.93	5.40E-118	93.6	51.7	Mesothelial
DUSP1	0.93	6.11E-81	100	94.4	Mesothelial
ERRF1	0.89	2.07E-139	98.4	76.5	Mesothelial
PHYHIP	0.88	8.89E-140	98	65.1	Both
LAMA4	0.87	7.58E-109	98.8	65.7	Mesothelial
PRR15	0.86	6.99E-156	98.4	46	Mesothelial
RPS8	0.85	6.11E-128	100	99.1	Mesothelial
EPHB6	0.85	9.80E-104	92	66.8	Both
SNCA	0.83	4.52E-124	98	52.7	Mesothelial
KRT7	0.83	2.25E-82	86.5	58.6	Mesothelial
RBP4	0.82	1.77E-112	91.2	38.5	Mesothelial
TMEM176A	0.82	1.79E-78	93.2	74.9	Both
LDHA	0.82	1.37E-70	99.6	93	Both
DMKN	0.81	7.83E-88	89.2	53.2	Mesothelial
RPS12	0.78	8.67E-113	100	99.2	Mesothelial
JUN	0.76	8.52E-52	98.8	88.9	Mesothelial
RHOB	0.74	6.86E-68	100	91.1	Mesothelial
PLIN2	0.74	9.88E-101	98.8	77.2	Both
KCNT2	0.74	2.68E-145	98.4	64.2	Mesothelial
SLC16A1	0.73	1.11E-110	95.6	68.8	Mesothelial
RPL12	0.72	2.97E-109	100	98.7	Mesothelial
MEDAG	0.71	2.82E-85	91.2	69.5	Both
PDLIM4	0.71	1.25E-116	98	53.5	Mesothelial
MT2A	0.71	1.03E-61	99.2	92.5	Mesothelial
GFPT2	0.71	5.52E-111	97.2	61.6	Both
SLC4A4	0.70	2.33E-139	98.4	55.6	Mesothelial
LY6E	0.68	3.92E-57	96.4	88.6	Mesothelial
PIM1	0.67	7.41E-125	98.8	69.2	Mesothelial
NDN	0.67	4.78E-72	96	62.6	Mesothelial
MYRF	0.67	5.80E-70	82.9	39.1	Mesothelial
RPS4X	0.67	4.22E-103	100	98.1	Mesothelial
VSIG2	0.67	4.32E-153	98.8	56.5	Mesothelial
COBLL1	0.67	3.57E-88	98.4	80.3	Mesothelial
CTNNA1	0.66	9.37E-47	98.4	86.7	Mesothelial
RPL7A	0.66	2.30E-84	100	98.8	Mesothelial
PRDM6	0.65	4.86E-153	98.4	45	Mesothelial
CDH3	0.65	6.75E-131	94	37.5	Mesothelial
PKHD1L1	0.65	7.75E-121	97.6	64.8	Mesothelial
RPL3	0.64	1.36E-88	100	98.9	Mesothelial
MT-ND4	0.63	1.46E-92	100	100	Mesothelial
ZNF593	0.63	1.45E-97	98.8	77.1	Mesothelial
SERPING1	0.62	4.07E-54	99.2	86.6	Both
NAMPT	0.62	9.27E-104	100	88.2	Mesothelial
RBP1	0.61	2.33E-48	92	69.3	Both
ATP1B1	0.61	2.25E-69	96	72.4	Mesothelial

Supplementary Table 4. The top 88 differentially upregulated genes of epicardial cluster 17 compared with all other clusters identified using Wilcoxon rank sum tests on the adult and foetal integrated dataset. Genes are ranked according to their log 2 fold change against the overall dataset excluding those with log2 fold-change lower than 0.5 or a p value greater than 1×10^{-10} . Epicardial genes in only cluster 17 are shown in red.

Gene	Log2 FC	Adj pvalue	cluster %	dataset %	Epi_cluster
PLA2G2A	0.85	1.06E-65	100	70.6	Both
CCDC80	0.84	5.77E-60	97.9	66.8	Both
TIMP1	0.83	6.52E-44	100	87	Both
C3	0.73	2.02E-58	99.5	70.6	Both
EFEMP1	0.65	1.48E-52	99.5	71.7	Both
SLPI	0.63	2.60E-98	98.9	69.5	Both
NNMT	0.60	1.23E-42	98.4	78.7	Both
MGST1	0.59	5.26E-46	100	76.9	Both
C1R	0.56	2.23E-33	98.4	77	FB-like
RARRES1	0.55	5.42E-49	98.9	70.9	Both
KRT19	0.53	1.39E-70	89.9	41.5	Both
CFH	0.51	2.57E-44	100	73.8	Both
PTGIS	0.51	4.36E-50	98.4	67.7	Both
RARRES2	0.48	4.25E-46	96.8	68.8	Both
LDHA	0.47	1.89E-21	100	93	Both
KRT18	0.46	2.37E-35	84.1	50.5	Both
MT1X	0.45	1.77E-21	99.5	87.6	FB-like
S100A6	0.44	3.88E-22	100	98.3	Both
C1S	0.44	3.50E-34	98.4	76.1	FB-like
KRT8	0.43	2.12E-26	77.8	48.1	Both
CYSTM1	0.42	2.86E-30	98.4	85.3	Both
LGALS3BP	0.42	9.21E-20	93.1	75.3	Both
ITLN1	0.41	3.30E-84	95.8	50.7	Both
MFAP4	0.41	2.92E-36	92.6	57.6	FB-like
IGFBP6	0.41	2.88E-39	96.3	70.8	FB-like
LINC01133	0.40	1.67E-37	81.5	47.4	Both
CHI3L1	0.40	2.82E-93	97.4	56.8	Both
COL6A2	0.40	7.74E-21	98.9	84.5	FB-like
SERPING1	0.39	9.71E-22	98.9	86.7	Both
FSTL1	0.39	1.10E-23	93.1	73.9	FB-like
UPK3B	0.39	1.70E-40	78.8	29.6	Both
NUPR1	0.39	2.85E-21	97.9	81.8	Both
CLDN15	0.38	1.04E-34	82	59.6	Both
MEDAG	0.38	2.46E-20	79.4	69.8	Both
HTRA1	0.37	1.86E-21	93.1	77.7	Both
ID4	0.37	3.54E-25	92.6	71.8	Both
PRG4	0.37	1.25E-91	97.4	61.8	Both
PLAC9	0.37	5.17E-17	98.4	82.3	FB-like
INMT	0.36	2.15E-51	97.4	77.4	Both
S100A10	0.36	5.23E-17	99.5	94.6	Both
MSLN	0.35	9.16E-37	78.8	36.2	Both
CXADR	0.34	6.62E-25	74.6	47.3	Both
CST3	0.34	5.89E-12	99.5	94.6	FB-like
HILPDA	0.33	4.50E-35	91.5	65.6	Both
SGK1	0.33	5.50E-36	95.8	75.2	Both
RPLP0	0.33	2.02E-21	99.5	96.7	Both
ARL4D	0.33	1.37E-26	88.4	69.3	Both
FLRT3	0.33	1.88E-33	78.8	54.8	Both
COL1A2	0.33	2.87E-20	94.2	66.1	FB-like

FBLN2	0.33	1.81E-27	95.8	77.8	FB-like
SYT4	0.33	8.79E-101	94.2	27.1	Both
RBP1	0.30	3.59E-22	90.5	69.5	Both
UAP1	0.30	3.45E-34	95.2	71.5	FB-like
TMEM176A	0.30	1.22E-27	93.1	75	Both
TGM1	0.29	2.21E-27	74.6	39.6	Both
PROCR	0.29	2.76E-17	85.7	73.7	Both
CYBRD1	0.29	4.95E-31	97.4	78.5	Both
COL1A1	0.29	2.85E-20	85.7	53.6	FB-like
PLIN2	0.29	9.68E-32	96.8	77.3	Both
GFPT2	0.29	2.07E-57	97.4	61.9	Both
COL6A1	0.29	8.09E-18	94.7	75.9	FB-like
MT1E	0.29	1.27E-20	97.9	82.6	Both
FBLN1	0.29	1.01E-37	97.9	60.9	FB-like
DPT	0.29	5.15E-44	98.4	74.2	FB-like
PKDCC	0.28	7.23E-35	91.5	66.9	Both
OGN	0.28	1.89E-13	80.4	62.5	FB-like
PHYHIP	0.28	1.06E-62	91.5	65.4	Both
CFI	0.28	1.41E-34	90.5	78.4	Both
HAS1	0.28	3.10E-32	79.4	55.1	Both
UPK1B	0.28	1.32E-82	92.6	38.3	Both
CALB2	0.28	4.88E-17	69.3	31.2	Both
AEBP1	0.27	5.27E-25	93.1	75.5	FB-like
PCOLCE2	0.27	3.81E-46	97.9	68.5	FB-like
SLC39A8	0.27	5.95E-41	87.8	66.7	Both
GXYLT2	0.27	2.07E-42	88.9	55.3	Both
PTN	0.27	6.03E-16	85.2	65.4	FB-like
EPHB6	0.27	1.03E-15	73.5	67.3	Both
RERG	0.27	1.56E-37	95.8	67.6	Both
FBN1	0.26	1.49E-37	98.4	68.2	FB-like
ADGRD1	0.26	1.27E-40	94.7	73.2	Both
TNXB	0.26	1.12E-28	97.9	81.7	FB-like
FN1	0.26	2.10E-23	98.9	78.8	FB-like
VASN	0.26	3.16E-17	87.3	69	FB-like
ACKR3	0.26	3.48E-22	96.8	79	FB-like
GPC3	0.26	1.74E-15	75.7	49.5	FB-like
GAS1	0.25	7.03E-14	83.1	73.7	FB-like
TCF21	0.25	1.51E-30	90.5	60.2	FB-like
PDPN	0.25	3.72E-14	75.1	61	Both

Additional table legends (actual tables are in located separate excel sheets for ease of sharing).

Supplementary Tables 5a to i. Listed gene module genes and the fraction of cells in each of the seven transcriptional states expressing each gene.

Supplementary Tables 6a to c. Raw expressions of Foetal, Intersect and Adult markers respectively in either foetal or adult mesothelial epicardial cell clusters (15) after parallel differential expression analysis using Wilcoxon rank-sum tests between clusters. Foetal and Adult sub-tables include log fold and p value columns of these markers within Foetal and Adult epicardium respectively for reference.