Figure S1. mTomato gene was targeted into the *MESP1* gene locus correctly in H9 cells

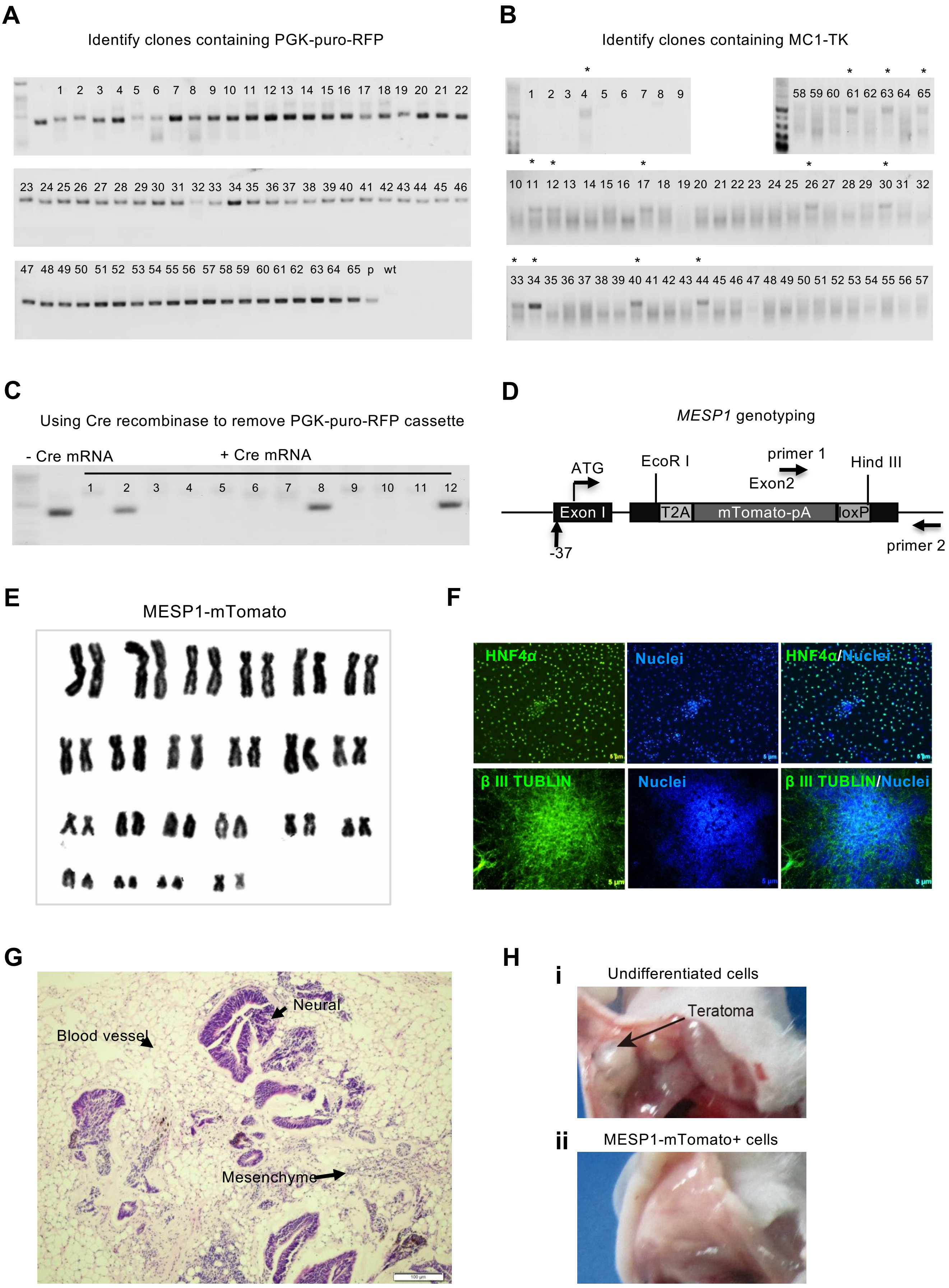

Figure S1. mTomato gene was targeted into the *MESP1* gene locus correctly in H9 cells.
(A) After transfection and selection, 65 puromycin resistant hESC clones all contained the PGK-puroRFP cassette. pc, plasmid positive control; wt, wild-type genomic DNA. (B) Genomic DNA PCR to analyze random insertion. Out of 65 clones, 13 clones had MC1-TK sequence, indicating random insertion "*". The rest clones did not contain MC1-TK cassette, suggesting correct targeting. (C) PGK-puroRFP cassette removal. Of the 12 clones examined, PGK-puroRFP was removed from 9 clones. (D) Positions of genomic DNA PCR primer pair used in A-C. The forward primer is within T2A-mTomato sequence; the reverse primer is on the 3′ homologous arm. (E) MESP1-mTomato reporter cells had a normal 46 XX diploid karyotype. (F) MESP1-mTomato cells can differentiate into endoderm and neuroectoderm derivatives. Upper panels, immunostaining of endoderm transcription factor HNF4a (green); lower panels, immunostaining of neural marker gene βIII Tubulin (green), DNA (blue). (G) Undifferentiated MESP1-mTomato H9 can form well-differentiated teratoma upon transplantation into nude mice. Arrows indicate neural, vascular and mesenchyme tissues (HE staining). (H) MESP1-mTomato$^+$ cells do not have tumorigenicity. i. well-differentiated teratoma formed by undifferentiated MESP1 reporter cells ($n = 4$). ii. No tumor was detected in mTomato$^+$ cells injected mice ($n = 4$).

Figure S2. Heatmap of marker gene expression in MESP1-mTomato$^+$ cells.

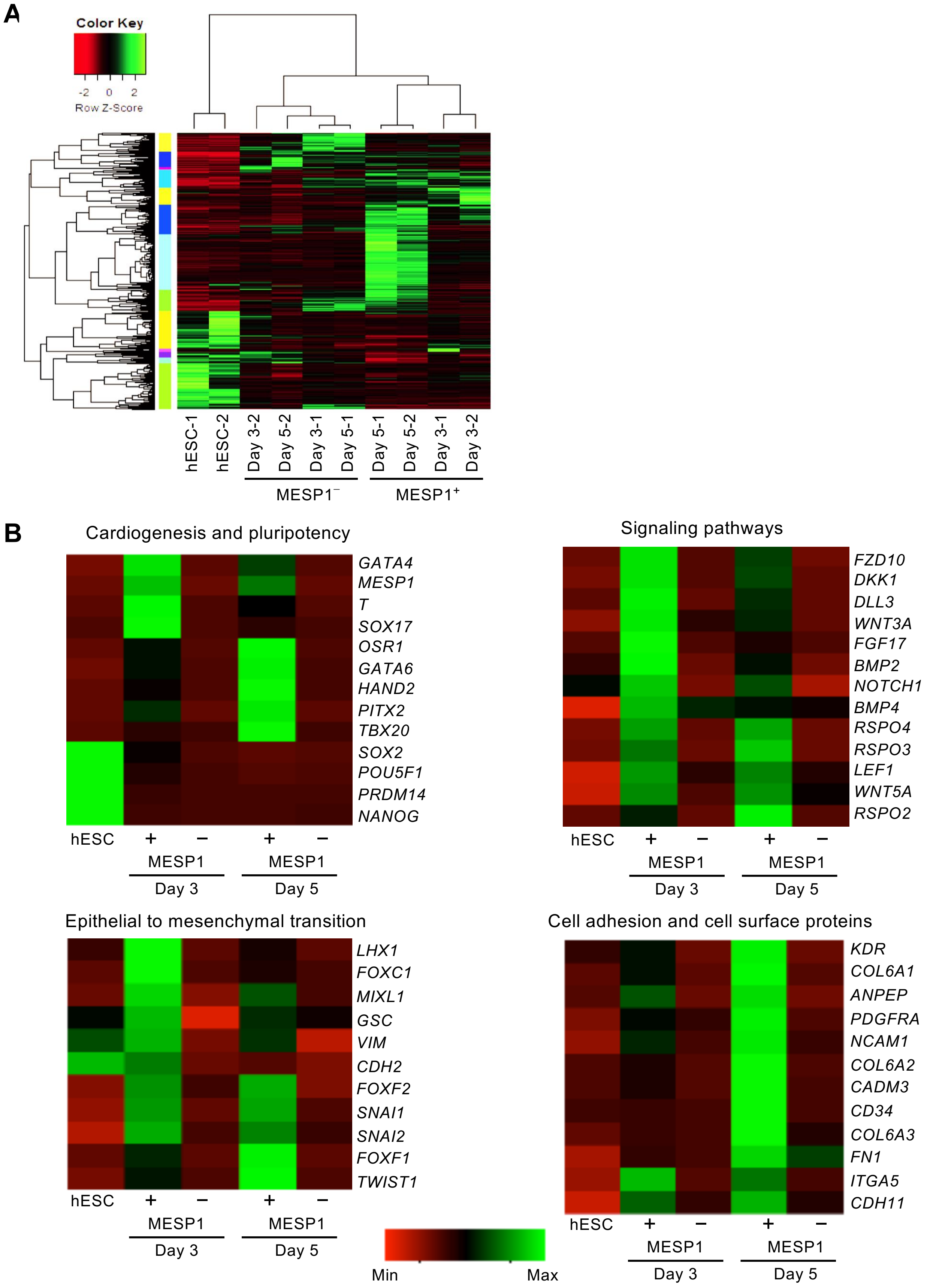

Figure S2. Heatmap of marker gene expression in MESP1-mTomato$^+$ cells.
(A) Heatmap clustering of the transcriptome of undifferentiated H9, day 3 and 5 MESP1$^+$ and MESP1$^-$ cells. (B) Heatmap of selective gene expression in undifferentiated hESCs, differentiation day 3 and day 5 mTomato$^+$ and mTomato$^-$ cells. mTomato$^+$ cells enriched genes include transcription factors involved in cardiogenesis, signaling pathway ligands and receptors, epithelial to mesenchymal transition-related genes, specific cell surface proteins. Selected genes with a fold change ≥ 1.5 in mTomato$^+$ cells versus mTomato$^-$ cells are shown.

Figure S3. Cell death related gene expression in MESP1-mTomato^{+} cells.

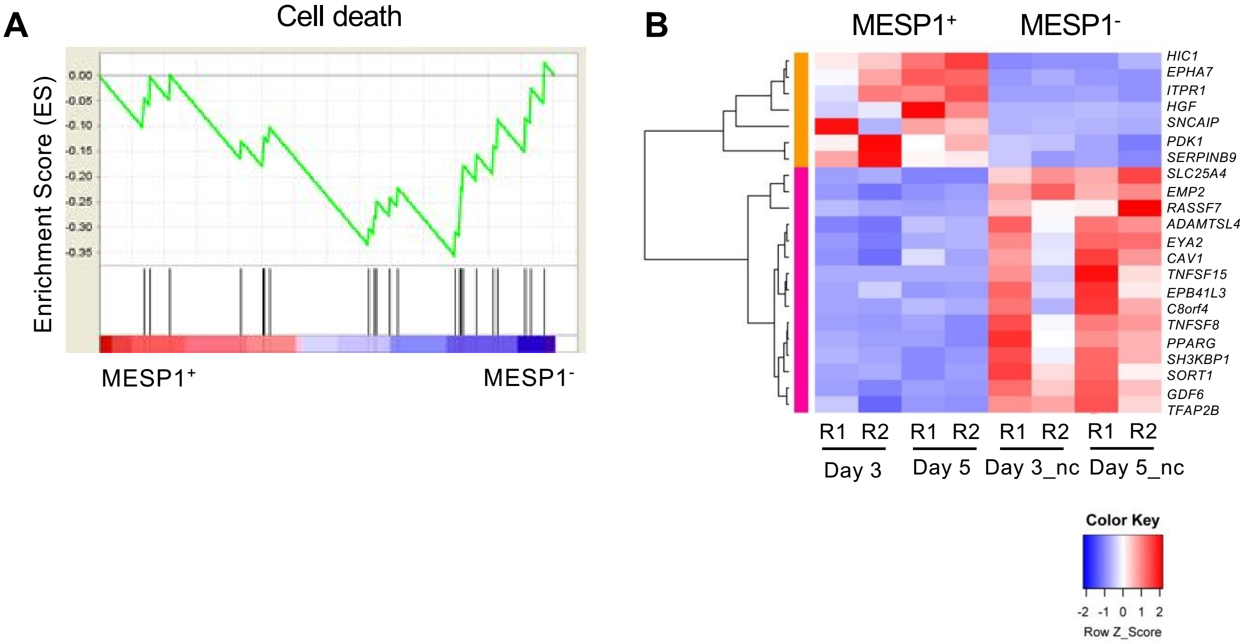

Figure S3. Cell death gene expression in MESP1-mTomato^{+} cells.
(A) GSEA analysis of cell-death related genes in MESP1^{+} cells and MESP1^{-} cells. (B) Heatmap of selective cell-death related gene expression in differentiation day 3 and day 5 MESP1^{+} and MESP1^{-} cells.

Figure S4. Quantification of western blot in Figure 4.

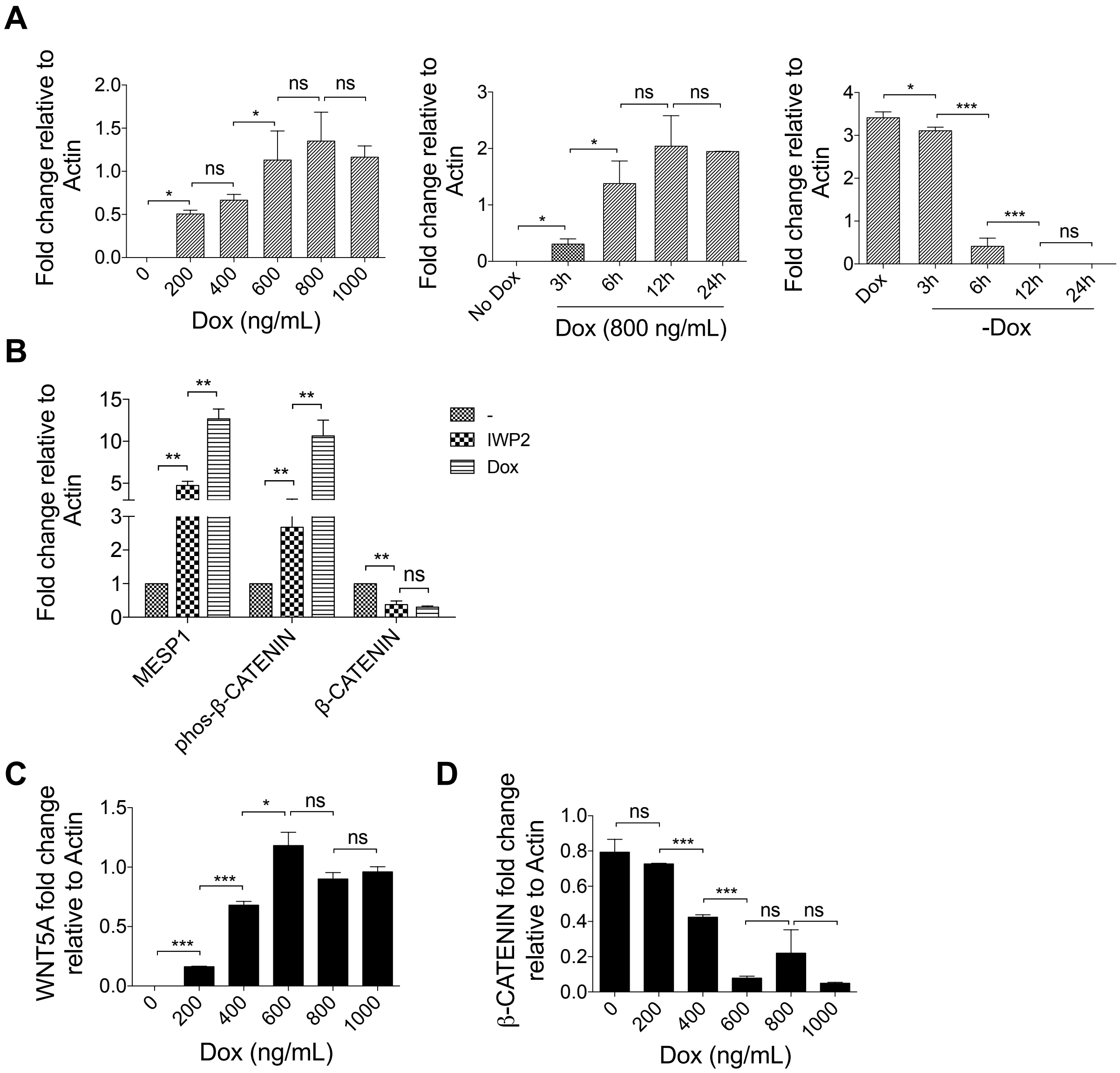

Figure S4. Quantification of western blots in Figure 4.

(A) Quantification of the MESP1-Flag bands in Figure 4A, the relative levels were normalized to ACTIN. (B) Quantification of MESP1, b-CATENIN, Phos-b-CATENIN proteins in Figure 4E, the relative levels were all normalized to ACTIN. None, IWP2, or Dox treatment was as indicated. (C) Quantification of WNT5A and β-CATENIN proteins in Figure 4J, the relative levels were all normalized to ACTIN.

Figure S5. Larger blood vessels formed in MESP1 cells engrafted rat MI hearts.

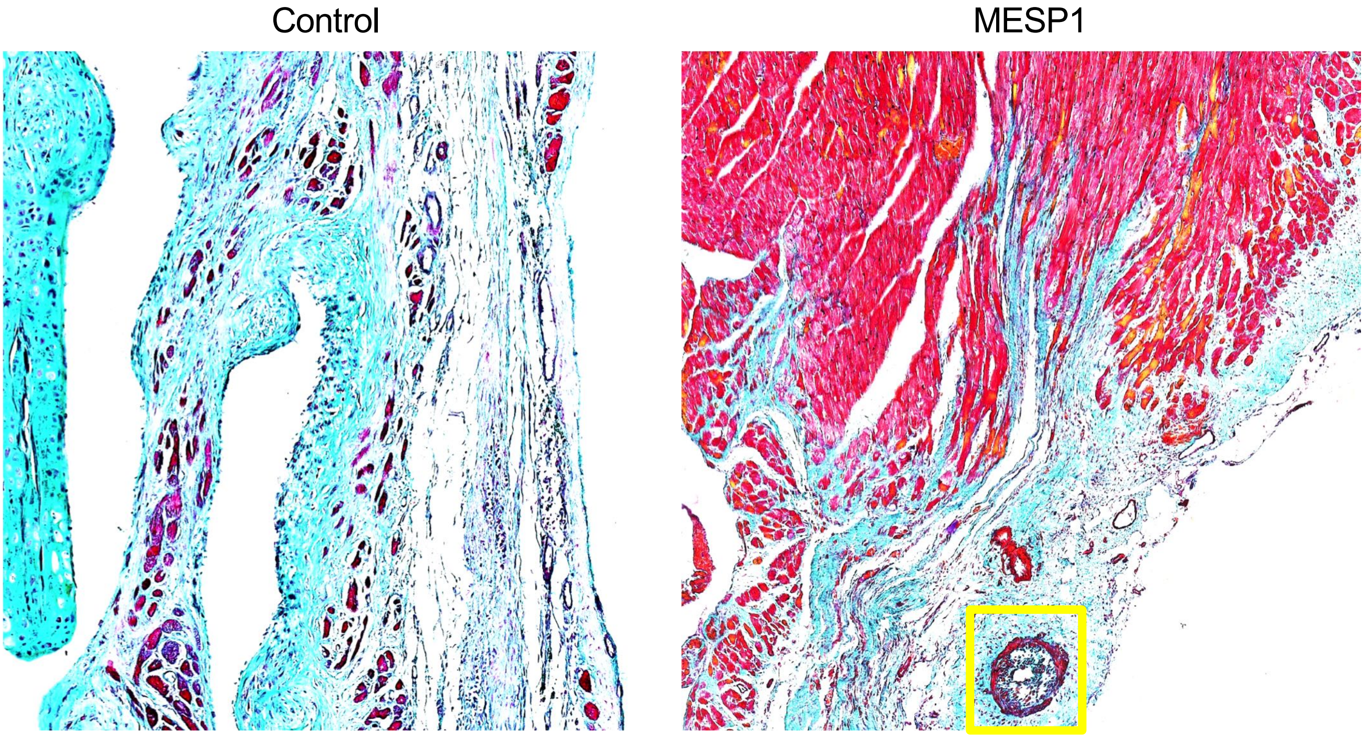

Figure S5. Blood vessels in MESP1 cells engrafted rat MI hearts.
Enlarged histological section and Masson’s trichrome staining of control and MESP1 cells transplanted hearts. Yellow square highlights a large blood vessel, and black arrows pointing to smaller blood vessels in the MESP1 group.

Figure S6. Immunostaining and quantification of β-CATENIN expression in rat heart 28 days after transplantation.

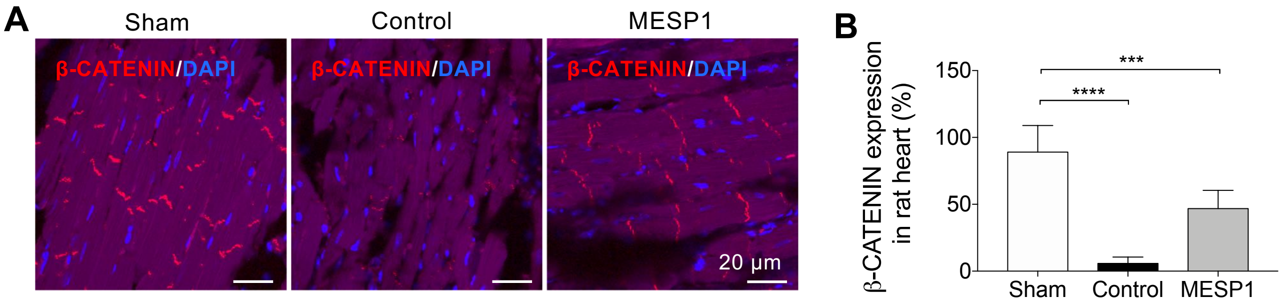

Figure S6. Immunostaining analysis and quantification of β-CATENIN expression (percent area) in rat heart 28 days after transplantation.

(A) Immunostaining of β-CATENIN (red) on histological sections of rat hearts 28 days post engraftment. DNA (blue). (B) Quantification of β-CATENIN fluorescence signal (*n* = 5 or 6 animals per group). Data are mean ± SEM, ***$p < 0.001$, ****$p < 0.0005$.

Supplemental Information

Homozygous MESP1 knock-in reporter hESCs facilitated cardiovascular cell differentiation and myocardial infarction repair

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Supplemental Materials and Methods

Verification of MESP1-mTomato knocking-in reporter cell line

Genomic DNA of individual MESP1-mTomato clones was extracted. PCR was performed to detect correct *MESP1* gene targeting and Cre mediated PGK-Puro cassette removal. The primer sequences were listed in Table S4 and the results were shown in Figure S1. The identity of the PCR products was verified by Hind III and EcoR I digestion. PCR primers used to verify mTomato knock-in were listed in Table S4.

Teratoma formation assay

All animal experiments were conducted following the Guide for the Care and Use of Animals for Research Purposes. The protocol for teratoma formation in nude mice was approved by the Institutional Animal Care and Use Committee and Internal Review Board of Tsinghua University. For teratoma assay, 5 × 10^6 undifferentiated MESP1-mTomato hESC or purified mTomato$^+$ cells in 100 μL medium were mixed with 100 μL Matrigel and injected subcutaneously into nude mice. 4 weeks later, mice were sacrificed, hESC formed teratomas were dissected, fixed in 4% paraformaldehyde, embedded in paraffin, sectioned and stained with hematoxylin and eosin (HE) dye.

WNT5A promoter luciferase reporter assay

Plasmids were constructed using Seamless Assembly Cloning Kit (Taihe Biotechnology, Co LTD). Wild-type *WNT5A* promoter containing E-box regulatory elements was cloned from hESC genomic DNA and inserted between Nhe I and Bgl II sites of the Firefly luciferase reporter plasmid (PGL-basic vector). Reporter plasmids containing mutated E-box motif was constructed by PCR. For Mut E-box A, the E-box motif “CATCTG” was mutated to “TGTCTG” through primer design and overlapping PCR. Primers used to generate luciferase reporters were list in Table S5.

Luciferase reporter assay was performed in 293FT cells. Cells were seeded in 24-well plates and transfected with CAG-HA-MESP1 (0.8 μg), pRL-TK (0.1 μg), and WNT5A E-box plasmids (0.8 μg) using Lipofectamin2000 (Invitrogen). 48 h after transfection, cells were harvest and luciferase activity was analyzed using Dual Luciferase Reporter Gene Assay Kit (Beyotime). Renilla luciferase activity was used to normalize the test reporter activity. The value of the empty pGL vector activity was set as “1”. Luciferase activity was measured in a FLASH microplate reader SP-Max 1800L.

Supplementary Tables

Table S1. Primers for Q-PCR

Gene	**Accession No.**	**Forward primer**	**Reverse primer**	$\mathbf{T_m}$
KDR/FLK1	NM_002253	tgagcaaagggtggaggtgact	cttgcacaaagtgacacgttgag	60
GAPDH	NM_002046	tgatgacatcaagaaggtggtgaag	tccttggaggccatgtgggccat	60
GATA4	NM_002052	gaaaacggaagcccaagaacct	ccagacatcgcactgactgag	60
HAND1	NM_004821	gcgagtgcatccccaacgtg	gaggaaaaccttcgtgctgct	60
HAND2	NM_021973	tcagaagaccgacgtgaaa	gttgctgctcactgtgcttt	60
ISL1	NM_002202	ctgcacaccttgcggacctg	caccgtcgtgtctctctggac	60
MEF2C	NM_001131005	cagtct ccatcccagtgtcca	gcctgcaccagacgtgaggt	60
MESP1	NM_018670	cgctgtgccccgacgact	ggcatccaggtctccaacag	60
NKX2.5	NM_004387	aaggaccctagagccgaaaag	gccgctccagctcatagacc	60
PAX6	NM_000280	aattcgtggcaaagcttgtt	actggggaaggaatggactt	60
PDGFR A	NM_006206	acaggttggtgtgggtccat	ctgcatcttccaaagcatca	60
TBX5	NM_000192	aggcggatgtttcccagttac	aatgggtccaggtggttgttg	60

WNT5A	NM_001256105	cggcatctctctttcaccat	aatgcaaataggcacgaagg	60
WNT3A	NM_033131	acgggacgagaggcttctat	ccacaccgtcaggtactcct	60
AXIN2	NM_004655	aacccccaaaatgttgatga	ggagtgcgttcatggtttct	60
DKK1	NM_012242	ggagtgcggcactgatgagt	ggtttcctcaatttctcctcgg	60

Table S2. Primers for ChIP-Q-PCR

Coverage regions of primers and conserved E-box sites are indicated relative to the ATG for *WNT5A* gene.

Fragment	**Primers**	**Region 5′/ 3′**	**Ebox position 5′/ 3′**
WNT5A-A	Forward: aattatctgagaggcaataaacat Reverse: ctaggaagaacttggaagacatt	36 / -86	-60 / -65
WNT5A-B	Forward: tccttctcccctccctagtct Reverse: ggaaatgcagctccgaattaac	-654 / -793	-648 / -653 -726 / -731
WNT5A-C	Forward: aaccccagatcaggaccaag Reverse: cccaaattctgatttttcactct	-995 / -1107	-1031 / -1036 -1038 / -1043
WNT5A-D	Forward: ccaactcctacccctgaaattc Reverse: agagcccttgcagatgagtcc	-1241 / -1376	-1251 / -1256 -1294 / -1299 -1421 / -1426
Unrelated region	Forward: cgtgccccatttcccgtgcg Reverse: gaagcctggtgcgtaagccg	Genomic fragment	-

Table S3. Genes in cluster I-II-III

Figure 2E cluster I genes

Genes	hESC		Day 3 MESP1$^+$		Day 3 MESP1$^-$		Day 5 MESP1$^+$		Day 5 MESP1$^-$	
	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2
ACOXL	5.74	5.52	0.78	0.18	0.39	0.27	0.28	0.25	0.33	0.30
ACTG2	39.90	5.23	1.30	0.31	4.01	3.73	1.22	0.54	3.91	5.83
ADD2	47.42	26.42	9.61	18.24	4.99	5.29	11.23	15.35	3.27	1.90
ADM	95.83	10.32	10.49	4.25	15.59	17.61	3.59	5.87	16.05	25.07
AK4	30.68	6.47	3.21	3.19	2.20	2.63	7.38	7.80	1.70	1.09
AKNA	7.53	8.11	1.93	2.78	7.70	1.64	2.22	3.20	8.78	5.74
ALDH3A2	31.58	27.13	10.83	10.32	10.05	16.33	13.88	13.46	8.83	6.96
ANO5	1.66	1.32	0.32	0.29	0.67	0.70	0.51	0.35	0.65	0.18

AP1S2	54.33	53.57	19.00	19.55	27.33	27.23	36.71	29.83	25.85	11.35
ARHGAP23	15.94	6.78	4.83	3.19	8.17	5.91	7.06	6.73	9.73	7.60
ARNTL2	5.12	3.53	0.89	1.20	0.99	1.12	0.57	0.67	0.87	0.45
ATP8A2	1.90	2.37	0.16	0.30	0.36	0.11	0.22	0.07	0.17	0.09
ATPAF1	33.92	41.02	14.09	12.66	18.43	29.29	20.18	20.33	19.38	17.45
AUTS2	30.34	22.02	9.72	7.73	10.69	6.31	5.92	7.46	10.50	3.69
B3GALT5	4.37	0.47	0.32	0.30	0.99	0.09	0.96	0.41	1.59	0.18
BCOR	35.91	14.34	9.51	8.23	6.63	5.20	9.56	11.15	6.65	1.28
BEND3	20.78	12.04	3.11	5.11	3.29	3.47	2.25	2.77	3.03	1.61
BEND4	4.62	5.13	0.81	0.76	0.88	0.70	0.38	0.36	0.30	0.10
C1orf94	6.85	3.47	0.49	0.42	0.29	0.06	0.87	0.06	0.07	0.15
C21orf88	11.47	3.72	0.54	0.56	2.60	0.98	2.85	1.02	2.81	1.09
CALN1	1.02	0.93	0.08	0.19	0.06	0.08	0.10	0.08	0.06	0.02
CAV1	22.31	2.37	1.72	0.38	10.95	5.91	5.28	2.62	15.53	11.42
CD200	28.04	19.74	8.23	8.92	4.60	6.71	5.34	5.24	3.03	1.89
CD24	1353.00	1136.71	273.03	344.86	537.84	463.48	249.03	303.48	505.26	368.14
CDCA7L	40.80	34.40	6.84	5.83	5.41	6.93	3.23	3.66	4.48	4.39
CELF2	7.25	5.85	3.05	1.42	3.04	2.37	1.11	1.08	3.24	0.95
CHODL	7.33	2.85	0.57	0.34	0.30	0.20	0.62	0.14	0.26	0.24
CHRDL1	3.90	3.73	0.91	0.20	0.61	0.59	0.26	0.10	0.40	0.06
CHST7	13.59	7.30	2.69	2.32	1.96	3.22	1.66	2.04	1.27	1.44
CNTNAP3	3.95	4.34	0.74	0.24	0.89	0.49	0.40	0.50	0.50	0.18
COBL	8.27	4.26	1.87	1.25	3.84	2.11	2.71	2.45	2.41	1.12
COL7A1	12.51	8.85	3.48	1.83	4.52	2.47	2.74	3.34	4.62	3.76
CPT1A	11.35	1.43	0.47	1.16	0.33	0.15	0.82	0.35	0.26	0.16
CSMD2	1.23	1.13	0.24	0.23	0.23	0.07	0.39	0.10	0.07	0.03
CUZD1	11.36	12.20	1.81	1.81	0.63	0.00	0.88	0.35	0.80	0.48
CYP2S1	56.90	43.08	9.28	3.45	10.97	4.42	4.64	4.06	10.40	9.74
CYP2U1	4.30	3.63	1.28	1.12	1.11	1.35	1.84	1.33	1.09	0.48
D21S2088E	13.75	1.46	0.15	0.62	0.16	0.07	0.39	0.15	0.11	0.04
DBC1	17.80	3.33	1.68	1.54	1.56	0.97	1.91	0.71	1.68	0.98
DBNDD1	26.94	29.32	3.91	1.41	5.30	6.16	1.01	1.15	2.27	3.38
DNAJB5	32.16	30.50	11.56	11.56	9.95	12.43	10.71	10.52	7.65	6.41
DNMT3B	316.16	180.52	28.72	54.35	27.24	18.64	19.14	30.45	19.68	12.00
DPPA4	235.28	108.76	33.03	43.17	35.45	36.73	26.34	29.68	31.98	17.99
DPYSL3	204.77	248.61	75.43	45.02	84.87	44.95	25.22	29.97	111.69	68.55
ERBB2	130.42	68.36	18.41	22.81	35.85	41.03	21.78	27.14	29.56	29.81
ESRG	350.14	164.32	20.33	11.13	12.46	3.73	2.78	4.19	8.22	3.98
ESYT3	2.05	0.95	0.12	0.21	0.50	0.14	0.42	0.12	0.39	0.12
ETV1	16.09	5.88	1.52	2.23	0.73	1.30	1.21	1.64	0.75	0.22
ETV4	43.25	8.22	7.69	4.38	2.87	6.53	2.30	3.22	3.28	5.52
FAM124A	10.38	11.40	0.97	1.56	0.56	0.48	1.10	0.65	0.45	0.31

FAM129A	4.80	2.31	0.93	0.63	2.57	0.13	1.00	0.46	5.42	2.01
FAM155B	4.97	5.96	1.23	1.24	0.73	0.55	0.34	0.34	0.54	0.40
FAT3	2.87	0.97	0.36	0.61	3.36	0.71	1.29	0.41	2.19	0.29
FERMT1	5.34	4.33	0.79	0.85	5.44	1.98	1.20	1.01	3.91	1.69
FGD4	7.89	3.75	1.17	0.60	1.76	0.89	1.57	1.19	1.46	0.75
FHDC1	10.55	4.13	2.36	1.49	4.26	1.79	0.94	0.74	3.28	1.47
FKBP5	29.76	28.70	6.55	9.86	5.81	6.65	5.54	8.17	4.59	2.40
FOXO1	14.66	6.32	4.33	2.03	8.40	4.26	3.49	3.95	11.23	4.37
FST	112.13	119.93	18.39	15.25	32.43	34.80	24.69	17.96	29.28	46.19
FZD5	14.49	18.32	2.39	0.56	1.94	0.62	0.74	0.53	1.49	0.70
GABRA5	4.77	3.37	0.29	0.29	0.68	0.27	0.39	0.16	1.10	0.81
GABRB3	46.54	16.47	6.61	7.21	4.56	2.04	1.26	1.45	3.12	1.59
GATM	5.84	5.89	1.45	0.69	2.95	3.49	2.56	2.17	1.52	0.57
GLDC	33.93	31.59	8.66	9.05	8.65	5.34	2.20	3.63	7.13	5.79
GPC4	127.78	52.50	18.42	25.57	15.60	8.13	5.31	7.48	14.55	7.98
GPM6B	46.73	36.30	15.37	10.26	8.11	16.42	15.15	12.94	5.18	2.71
GPR176	23.46	12.05	3.03	2.56	1.36	0.78	1.90	1.73	1.55	0.97
GPR98	2.78	2.44	0.93	0.75	0.78	0.82	1.22	0.70	0.57	0.27
GRID2	6.17	1.73	0.55	1.06	0.52	0.16	2.81	1.28	0.32	0.04
GRIK5	12.31	21.32	3.91	1.66	3.33	9.14	1.63	1.67	1.40	2.12
GRTP1	13.08	13.96	2.68	2.44	5.08	5.38	1.95	2.28	4.27	4.17
HDAC9	4.50	3.36	0.75	0.39	0.60	1.10	1.08	0.38	0.51	0.14
HOMER2	6.44	7.06	1.77	1.52	3.06	2.00	1.31	1.35	2.45	1.50
HOOK1	5.07	2.95	0.56	0.49	4.36	2.25	0.90	0.63	4.46	1.16
HSD11B2	7.04	6.71	1.14	1.16	0.48	1.19	1.50	1.00	0.73	0.74
HTR3A	2.22	2.77	0.14	0.04	0.05	0.18	0.61	0.04	0.07	0.12
IQGAP2	15.22	9.69	2.60	2.69	20.25	11.60	8.32	6.58	22.64	6.69
IRF2BPL	19.35	14.06	4.66	4.67	8.55	11.48	13.53	13.02	7.98	8.17
ITGA6	53.85	32.23	7.99	6.84	11.58	6.08	14.24	9.63	11.96	3.95
ITGA7	11.78	16.45	3.29	1.70	3.60	6.06	1.73	1.90	1.86	2.31
JARID2	70.32	29.21	14.46	20.13	8.66	6.32	9.40	14.23	6.24	3.38
KAL1	30.58	10.06	2.98	6.85	1.36	0.63	2.12	3.52	1.86	0.52
KIAA1244	1.46	1.19	0.35	0.16	0.24	0.04	0.46	0.12	0.30	0.06
KIAA1644	3.89	1.89	0.64	0.57	0.28	0.17	1.36	1.17	0.26	0.07
KIF1A	42.93	34.03	7.67	3.16	10.26	3.17	1.32	1.83	5.00	3.06
KIF21A	11.04	8.68	3.31	2.82	5.98	5.05	4.92	3.37	4.57	2.87
KLHDC7A	4.51	1.89	0.35	0.42	1.89	0.61	1.00	0.19	0.57	0.52
L1TD1	274.69	41.35	29.65	43.25	66.54	25.25	7.14	8.32	59.34	39.85
LARGE	17.06	19.48	5.52	7.07	8.24	4.91	6.12	6.74	7.38	4.62
LCK	14.78	5.02	1.10	1.47	0.37	0.17	0.64	0.44	0.47	0.66
LECT1	102.16	89.62	3.59	1.31	2.93	4.51	2.02	1.68	1.25	1.26
LEFTY1	28.46	1.30	0.32	0.78	0.58	0.19	0.47	0.37	1.07	1.84
LIMCH1	9.20	5.70	1.85	3.06	7.76	3.50	6.04	5.48	9.03	4.24

LINC-ROR	5.65	0.18	0.23	0.18	0.12	0.02	0.05	0.06	0.20	0.09
LINC00707	9.61	2.70	0.19	0.10	0.35	0.11	0.03	0.07	0.10	0.19
LOC100506013	96.62	29.47	4.07	1.30	3.65	7.15	1.25	1.01	1.51	0.99
LRAT	42.49	4.37	2.69	0.83	0.22	2.05	1.77	1.15	0.31	0.24
LRIG1	48.96	47.48	7.96	5.47	3.64	12.06	3.58	4.59	2.04	1.16
LRRC8B	7.04	4.52	1.67	2.34	2.49	2.02	1.92	1.61	1.97	0.63
MAGI1	16.43	10.25	2.57	4.12	5.65	2.82	3.78	3.90	4.59	1.59
MAP7	8.16	6.54	2.19	1.98	8.89	4.53	1.01	0.88	5.79	3.28
MEGF10	5.96	4.37	1.20	2.20	0.31	0.26	0.98	0.91	0.88	0.20
MRGPRF	8.76	6.81	1.23	0.83	0.45	1.77	1.46	1.07	0.37	1.00
MTA3	66.66	71.68	23.47	32.44	33.15	37.69	28.81	29.06	25.41	24.31
MTM1	5.50	6.13	1.53	1.88	2.48	2.02	1.82	1.79	2.68	0.62
MYEF2	14.00	14.67	3.97	3.17	8.37	9.40	3.66	3.49	8.02	3.31
MYO5C	4.27	4.19	0.85	0.81	3.19	1.21	0.77	0.57	2.29	0.72
N4BP3	12.50	8.68	3.73	2.80	3.15	3.16	2.22	2.42	2.16	3.10
NANOG	77.79	6.26	2.77	2.13	1.66	0.37	0.47	0.10	2.03	1.86
NEFL	5.03	7.59	1.35	0.94	0.96	2.36	0.91	0.81	0.55	0.54
NFASC	3.73	2.07	0.50	0.14	0.76	0.51	0.93	0.36	0.59	0.26
NFE2L3	22.96	4.74	3.80	1.67	3.66	2.15	1.31	1.15	3.16	1.32
NLRP12	3.52	0.86	0.08	0.11	0.25	0.06	0.93	0.07	0.07	0.10
NMRK2	38.01	27.08	2.84	2.54	4.47	6.66	0.30	0.45	2.53	6.58
NPTX1	7.46	8.07	0.40	0.01	0.05	0.16	0.11	0.04	0.06	0.05
NUP210	29.92	26.31	4.42	2.60	10.47	7.21	2.18	2.96	7.94	3.22
OAZ2	128.93	120.80	53.44	39.34	57.15	82.83	53.40	50.66	49.56	61.75
PAR5	19.22	1.55	1.12	5.38	2.99	0.80	1.95	3.64	3.28	0.19
PCDH1	62.64	36.16	6.51	1.53	12.96	11.01	2.24	1.43	9.67	7.65
PCDH11X	3.15	0.99	0.30	0.58	1.80	1.00	0.57	0.60	1.03	0.28
PCNXL2	5.74	3.99	1.62	1.80	2.82	1.00	2.25	2.16	2.43	0.83
PDGFA	19.25	9.42	6.06	3.39	7.43	9.43	3.22	3.75	5.46	9.20
PDGFD	2.13	2.28	0.42	0.39	1.07	0.56	0.91	0.76	1.57	0.59
PDZD4	43.49	24.19	8.15	11.68	3.56	5.73	4.53	6.04	3.25	4.62
PGBD5	8.48	6.82	1.29	1.99	1.32	1.75	1.27	1.10	0.95	0.76
PHF15	13.89	5.51	1.59	2.96	2.17	0.72	3.39	2.59	2.30	1.43
PIM2	54.70	24.53	6.32	8.76	3.18	4.38	2.17	2.76	3.28	4.26
PLA2G3	3.60	4.21	0.64	0.66	1.15	1.89	0.83	0.58	0.93	0.85
PLAUR	8.40	7.75	1.52	1.55	2.79	3.75	1.90	1.91	2.05	3.81
PLCH1	7.98	6.65	1.32	1.44	0.94	1.09	1.40	0.92	0.78	0.26
PLS3	127.58	98.18	44.33	39.97	81.07	49.07	33.68	30.48	73.59	39.20
PODXL	373.08	261.69	55.49	75.71	188.79	119.48	208.61	193.35	181.61	58.35
POLR3G	64.84	18.65	2.42	5.13	2.83	2.59	1.73	2.68	2.47	1.36
POU5F1	202.33	108.92	28.83	30.64	11.74	9.80	3.57	5.77	7.22	14.53

PPM1B	65.71	30.25	16.82	15.58	21.98	22.59	9.17	9.39	17.69	7.86
PPP1R16B	3.61	0.89	0.52	0.14	0.07	0.05	1.16	1.21	0.15	0.04
PPP2R2B	12.95	10.66	1.62	0.35	1.95	2.89	0.79	0.29	2.47	2.37
PPP2R2C	1.93	1.76	0.30	0.35	0.17	0.21	0.25	0.12	0.09	0.06
PRDM14	96.42	48.19	3.23	1.31	0.64	0.23	0.79	0.57	0.34	0.30
PREX2	8.50	2.63	1.36	2.15	1.82	0.55	2.03	2.20	0.96	0.08
PRKAA2	1.20	1.45	0.39	0.17	2.19	1.22	0.82	0.61	1.54	0.44
PRKCA	4.40	6.22	0.98	1.48	1.84	1.41	1.07	1.27	1.57	0.40
PRKCQ	4.96	3.08	0.80	0.66	1.44	1.30	0.81	0.88	1.64	1.52
PRKCQ-AS1	4.75	3.56	0.68	0.71	1.34	2.69	0.66	1.37	1.68	1.93
PRRT3	5.77	7.86	1.56	0.79	2.03	3.68	1.60	1.71	1.33	1.56
PTPRZ1	47.97	25.63	7.08	3.18	5.08	8.41	3.98	4.28	4.50	0.97
PVRL3	26.52	13.20	7.46	7.33	12.65	10.98	8.75	9.26	13.22	4.36
RABGAP1L	28.12	10.57	2.52	3.86	5.08	0.98	5.33	4.19	3.78	1.29
RAP1GAP2	5.14	3.51	1.22	0.84	3.93	0.86	0.46	0.69	3.95	1.78
RBM47	15.45	1.71	3.04	2.33	14.68	7.40	6.63	4.61	12.58	7.43
RRAGD	6.18	6.03	1.20	0.65	1.56	1.33	0.82	0.85	0.93	1.11
SALL2	83.53	69.24	22.91	13.60	15.25	19.39	13.39	15.27	10.57	5.17
SAMHD1	8.10	8.86	1.85	2.13	0.87	1.01	1.72	1.71	0.97	0.25
SBK1	18.24	29.17	6.01	4.99	10.64	10.14	3.37	5.26	7.39	6.58
SCAMP5	18.04	26.41	6.37	6.51	10.01	9.09	5.68	6.06	7.89	9.01
SCGB3A2	64.54	58.29	10.21	3.77	10.12	9.38	1.67	1.16	4.37	10.09
SCNN1A	14.12	11.33	2.21	0.99	4.69	2.61	1.03	0.58	2.84	2.52
SEMA4D	8.02	12.32	2.09	2.23	5.00	5.50	2.40	2.43	3.47	2.54
SEPHS1	224.88	88.51	49.08	73.88	38.59	40.27	30.61	39.28	39.72	39.15
SERPINE1	64.14	3.23	12.95	1.12	13.87	8.39	3.97	2.94	24.74	12.57
SFRP2	212.62	130.93	28.30	15.34	15.69	39.78	8.40	8.30	19.87	18.67
SFTA1P	5.84	0.54	0.00	0.00	0.09	0.00	0.00	0.00	0.41	0.97
SHANK2	2.25	2.21	0.52	0.42	2.88	0.66	1.20	0.80	2.38	0.53
SHC3	2.32	0.38	0.28	0.15	0.17	0.15	0.28	0.26	0.09	0.07
SHISA3	32.52	43.82	8.60	3.07	0.24	0.64	0.97	0.52	0.36	0.18
SLAIN1	9.11	8.33	1.99	0.68	3.54	6.61	1.53	0.72	2.65	1.20
SLC12A8	4.28	4.55	0.89	0.93	1.05	0.50	0.99	0.84	0.95	1.04
SLC16A9	16.18	18.87	4.29	6.01	23.18	12.19	4.80	5.28	18.31	6.71
SLC29A1	76.69	83.21	17.79	8.79	21.34	31.52	13.87	14.54	14.50	21.81
SLC38A5	25.35	13.18	6.17	5.76	0.89	2.48	13.47	10.90	1.16	1.46
SMIM3	43.85	41.69	2.94	1.77	4.33	5.39	4.72	4.69	2.89	3.61
SNTB1	4.24	3.57	0.78	0.20	1.63	0.57	0.98	0.46	1.82	0.72
SORBS2	7.00	3.95	0.96	0.39	0.57	0.84	1.14	0.37	1.04	0.52
ST8SIA3	1.68	1.94	0.31	0.36	0.20	0.44	0.24	0.24	0.03	0.03
STAT3	30.92	25.12	8.06	12.19	10.01	9.87	13.50	15.07	9.71	6.14
STK33	6.50	7.36	2.49	1.26	1.45	1.90	2.00	1.85	1.17	0.89
SYT13	1.61	2.78	0.43	0.49	0.78	0.40	0.54	0.50	0.51	0.25

SYT6	15.86	12.85	4.81	3.59	2.48	1.30	1.48	1.63	0.97	0.48
SYTL2	8.27	5.28	1.71	0.18	1.12	1.50	1.33	0.42	0.88	0.45
TCF7L1	64.60	59.03	17.23	11.92	21.57	17.11	13.92	16.09	21.70	27.06
TDGF1	209.83	16.55	11.75	22.37	3.93	0.70	3.34	4.40	4.50	3.60
TERF1	166.58	63.38	26.83	44.25	18.69	21.64	16.37	20.86	18.38	11.91
TFDP2	8.15	9.84	3.67	3.26	4.22	5.07	4.33	5.01	3.80	2.38
THBS2	6.17	3.79	0.52	0.13	0.49	0.22	0.62	0.14	0.25	0.16
THY1	132.29	49.69	38.62	15.85	18.41	20.23	32.58	35.40	16.23	23.02
TLL2	1.26	1.28	0.24	0.15	0.06	0.07	0.22	0.08	0.01	0.02
TM4SF18	11.21	1.08	0.21	0.10	0.04	0.19	1.95	1.58	0.14	0.03
TM7SF3	15.44	19.08	5.79	4.61	7.38	10.17	4.52	4.80	7.01	4.72
TMEM132B	6.91	5.13	1.43	1.09	2.78	1.25	0.86	0.55	2.15	0.69
TMEM132D	3.39	1.86	0.43	0.55	0.14	0.19	0.82	0.44	0.13	0.05
TMEM178B	1.90	1.76	0.45	0.20	1.07	0.41	0.43	0.32	1.04	0.42
TNFRSF8	11.80	4.30	0.15	0.31	0.24	0.10	0.30	0.14	0.32	0.48
TOX	10.98	5.95	0.47	0.31	2.85	1.37	0.55	0.45	2.84	0.97
TOX3	7.48	10.77	2.44	0.89	1.36	1.46	1.95	1.54	1.05	0.35
TRERF1	6.49	6.50	1.22	1.13	3.41	1.46	3.66	3.19	3.20	1.03
TRIM2	19.16	15.66	7.51	5.88	5.37	5.85	5.58	5.72	4.27	1.05
TRIM22	8.47	9.11	0.36	0.24	0.49	0.28	0.99	0.25	0.27	0.09
TRIM24	104.98	94.79	27.97	51.11	46.07	25.43	34.68	40.62	55.34	27.79
TRIM71	95.58	32.67	14.04	31.25	21.32	3.16	10.30	20.19	15.51	1.11
TRNP1	12.64	11.69	4.15	2.91	3.98	6.02	4.23	4.66	3.96	6.98
TRPC4	14.76	16.82	2.74	1.75	1.33	1.72	2.11	1.03	0.76	0.52
TTC9	5.96	2.77	1.44	1.33	2.67	1.55	0.85	0.80	1.91	1.24
UNC13A	4.20	2.57	0.31	0.95	0.25	0.08	0.26	0.15	0.26	0.06
UNC5D	7.22	3.28	0.64	0.75	0.95	0.37	0.96	0.57	0.95	0.11
USP44	66.82	27.30	0.95	1.04	0.73	0.95	1.20	0.57	0.60	0.22
USP9X	58.49	42.56	10.38	14.48	12.19	5.97	11.40	13.34	12.56	4.80
VASH2	35.51	16.66	3.30	5.94	2.43	3.45	4.14	4.75	1.90	0.50
VAT1L	91.49	109.50	12.93	6.44	13.94	9.18	14.41	10.98	6.34	2.87
VLDLR	13.17	7.14	2.60	3.57	18.64	4.69	8.49	7.37	18.16	7.25
VRTN	93.31	69.94	12.23	36.47	4.37	6.03	4.74	8.81	2.78	3.11
VSNL1	15.51	5.72	4.04	0.99	1.41	0.96	1.54	0.76	0.82	0.45
WNK2	6.83	8.40	1.68	1.85	1.12	1.39	1.34	1.66	0.87	0.42
WSCD1	9.28	14.31	1.58	0.17	0.79	3.76	1.32	0.97	0.53	0.43
ZDHHC22	4.50	2.44	0.70	0.66	0.25	0.47	0.91	0.55	0.24	0.22
ZNF589	31.23	24.70	11.56	9.76	8.82	3.87	7.07	7.96	5.77	3.52
ZSCAN10	61.29	32.93	8.89	7.97	5.58	4.32	2.35	3.90	2.75	5.57
AASS	34.85	26.29	12.61	16.26	11.88	9.17	10.39	12.51	12.04	4.40
ADAMTS16	3.44	1.31	0.94	0.11	0.37	0.20	0.47	0.12	0.31	0.15
ADCY2	5.96	2.53	1.55	3.19	0.74	0.78	1.34	1.40	0.39	0.27
AKAP1	26.44	26.71	8.12	12.88	8.29	6.36	6.61	8.28	7.30	4.58

AP1S3	2.52	1.61	0.43	0.50	0.82	1.04	0.23	0.33	1.01	0.50
ARC	5.41	2.32	1.03	0.24	0.88	1.75	0.53	0.88	1.49	2.43
AZIN1	123.91	74.39	51.50	63.73	71.24	66.43	34.95	39.63	65.21	26.56
BUB1	96.55	69.11	30.24	39.66	24.77	19.89	19.58	26.23	26.37	11.86
CABLES1	7.15	3.49	1.98	2.66	0.76	1.27	1.56	1.74	0.77	0.94
CDC42EP3	17.00	4.32	11.41	5.95	9.06	8.82	2.74	3.78	9.89	7.91
CDC6	69.47	44.67	23.23	31.94	26.88	34.00	12.90	16.70	24.17	19.02
CEBPZ	121.85	61.09	35.87	43.68	24.66	25.04	19.30	21.16	22.96	15.26
CNTNAP3B	1.59	2.39	0.40	0.13	0.55	0.44	0.24	0.29	0.40	0.10
CST1	113.18	14.65	39.71	27.12	6.30	18.14	12.27	13.49	16.69	52.08
CTSC	216.98	143.86	66.19	90.90	48.99	51.92	57.28	64.41	36.34	26.04
CUX2	1.66	2.33	0.48	0.69	0.93	0.82	0.58	0.41	0.56	0.20
DAB1	5.12	5.14	1.12	1.75	0.97	0.18	1.15	1.16	0.47	0.21
DOCK3	1.60	2.30	0.80	0.26	2.62	0.42	0.43	0.21	2.25	0.73
ECT2	38.61	32.00	15.70	26.09	18.26	19.82	11.66	16.28	19.24	6.94
EMB	11.81	8.72	3.99	4.55	6.64	4.88	2.52	2.62	5.28	1.88
EPB41L4B	4.95	3.38	1.31	2.04	3.14	1.13	0.78	0.75	2.68	1.67
ESRP1	15.58	5.93	7.24	5.79	20.85	8.42	2.59	1.92	17.13	8.66
FAM111B	14.34	9.74	4.10	5.27	8.52	5.87	3.99	3.04	8.91	3.63
FAM189A2	8.55	1.38	1.82	0.69	1.09	0.28	0.69	0.32	1.12	1.17
FANCD2	28.36	26.98	12.72	18.44	12.88	13.09	7.42	12.05	11.36	7.83
FAT1	27.49	16.08	11.93	8.48	16.94	4.02	5.43	7.92	15.83	2.44
FGF2	16.14	8.81	3.69	5.84	4.30	2.81	3.53	4.71	2.50	1.21
GAL	131.65	28.43	51.84	59.87	8.67	5.34	7.62	16.29	10.76	22.62
GDAP1	11.32	8.63	4.78	6.73	6.06	4.65	2.84	2.55	5.65	2.75
GPRC5B	61.39	37.93	18.26	22.32	6.17	7.39	8.51	12.30	3.94	2.82
GSPT2	20.74	22.78	11.68	10.66	10.58	12.80	6.23	6.88	8.42	5.81
HELLS	36.03	20.96	13.52	17.27	13.39	19.11	7.35	9.57	10.98	6.45
HHLA1	5.00	0.23	0.56	0.91	0.47	0.11	0.40	0.32	0.70	0.43
ICMT	52.32	53.82	27.37	33.51	31.12	35.40	17.11	23.88	28.35	22.74
IDO1	13.13	7.01	0.28	0.10	0.17	0.14	0.71	0.11	0.25	1.06
IL17RD	20.57	2.41	4.49	10.80	4.16	6.05	3.41	4.46	3.61	1.51
IPW	30.57	20.36	13.90	11.38	12.07	9.63	4.27	5.95	9.22	5.89
ITPR3	9.08	6.15	2.79	3.96	6.31	1.09	2.46	3.20	7.10	2.31
KIAA1804	3.29	2.79	0.79	1.20	0.63	0.55	1.04	0.76	0.63	0.19
KLKB1	7.05	2.17	1.30	2.21	0.41	0.29	1.06	0.58	0.27	0.21
LOC653653	14.50	8.73	3.15	3.92	3.88	2.03	3.03	2.44	2.53	0.22
LRRN1	91.80	65.01	41.53	32.67	142.75	52.66	16.86	22.56	107.86	30.81
MAL2	9.92	7.99	4.48	1.68	9.19	5.71	1.55	1.47	6.65	3.92
MCM3	144.93	156.77	83.62	83.11	82.65	86.48	47.19	66.21	72.15	66.08
MCM4	120.75	107.01	69.84	80.09	62.38	73.78	36.72	51.18	55.67	38.88
MGC45800	4.58	2.96	2.67	1.32	5.30	3.08	1.01	1.17	5.71	3.39

MLF1IP	58.38	46.83	25.45	32.49	25.89	29.19	16.52	20.39	24.93	19.95
MOCOS	5.96	4.33	1.36	2.18	1.87	1.11	1.20	1.23	1.49	1.46
MSH2	115.36	63.37	34.65	51.38	44.45	36.38	27.30	30.95	40.25	17.61
MTHFD1	80.31	49.31	40.04	59.67	34.58	31.66	19.65	29.88	32.28	22.18
MYO10	26.84	22.89	16.06	18.60	14.99	6.53	8.31	11.22	13.94	6.22
MYO1E	10.36	8.24	3.98	3.63	5.27	1.78	2.65	2.72	4.19	1.76
NAA50	51.26	35.73	25.76	38.28	26.55	33.07	15.67	19.87	23.33	13.59
NLN	26.15	15.98	7.95	15.50	10.62	7.42	5.44	7.66	9.29	4.83
NLRP2	39.72	31.20	15.19	18.32	27.80	21.04	10.84	12.51	23.71	19.74
NQO2	47.13	34.34	13.44	19.78	9.37	13.99	10.70	11.42	7.59	12.52
NR6A1	45.05	32.10	9.50	22.03	12.54	2.94	10.22	17.17	6.12	1.21
ORC1	40.19	31.17	15.71	17.93	13.18	10.23	7.48	10.49	12.20	9.38
PAK1	59.96	33.02	20.15	26.61	21.92	18.21	15.50	17.86	19.69	15.60
PARP1	186.95	176.62	84.24	77.31	89.92	105.14	57.25	70.68	76.11	54.18
PAWR	26.63	15.59	7.29	10.44	29.22	18.20	5.44	8.77	24.31	11.65
PCSK9	10.54	3.38	2.44	3.40	0.94	0.22	1.49	2.56	0.80	0.79
PCYT1B	5.22	7.09	2.15	2.23	3.17	2.69	1.67	2.51	1.80	1.20
PKI55	7.03	4.79	4.80	2.94	3.68	4.04	1.39	1.80	4.67	4.07
PLCB3	24.97	23.36	7.38	12.81	10.30	10.83	7.98	11.09	9.24	9.88
PLS1	5.93	5.87	1.44	3.00	3.70	3.34	1.47	1.80	2.48	0.90
PMAIP1	47.57	12.61	21.77	23.14	7.61	2.61	4.48	10.04	7.24	2.87
PPP1R3B	24.21	11.12	9.45	15.78	7.94	5.51	6.35	6.83	6.24	2.75
PSAT1	224.43	175.31	129.92	126.54	170.76	76.27	41.84	73.34	177.71	116.31
PSIP1	240.90	186.49	85.51	80.78	77.05	93.51	75.10	76.14	62.60	46.75
RAB39B	3.93	4.37	1.70	2.46	1.89	1.04	0.90	0.97	1.11	0.55
RFWD3	41.15	26.36	20.22	28.29	19.91	14.78	10.49	14.83	17.49	7.83
RNF138	35.36	24.34	15.32	20.55	14.70	22.21	10.24	12.94	14.71	7.50
ROR1	34.90	25.69	14.41	24.23	15.19	8.75	10.21	12.08	17.66	5.62
RTN3	93.59	121.11	52.25	32.47	52.13	77.34	29.06	29.85	44.92	43.16
RTN4IP1	10.57	10.01	2.53	4.72	3.10	3.79	2.95	2.81	2.91	3.48
SCG3	14.93	6.36	4.11	4.89	6.25	2.99	1.28	1.55	4.71	3.24
SELRC1	32.01	20.00	12.47	21.69	10.75	7.14	8.23	9.77	9.58	5.30
SEMA6A	111.47	45.04	42.13	41.20	53.08	16.08	14.69	18.24	34.94	14.74
SHISA9	11.05	4.92	4.55	4.33	5.81	3.12	2.56	2.76	5.89	4.39
SLC16A1	204.29	162.83	89.68	144.59	104.44	88.99	54.61	73.81	73.06	40.23
SLC7A1	33.51	14.88	18.50	14.27	25.21	7.84	5.09	8.76	24.72	8.08
SLC7A11	11.26	3.84	7.02	3.15	11.85	2.98	1.53	2.14	11.52	4.54
SLC7A3	41.84	39.82	20.85	13.56	23.47	17.34	6.96	11.34	24.11	20.52
STEAP3	8.09	6.29	2.76	4.25	3.10	1.53	1.45	1.45	1.96	1.99
TAF4B	11.07	3.11	3.56	3.73	1.43	0.70	1.95	2.42	1.22	0.38

TJP2	24.69	9.18	8.20	5.43	30.20	8.82	5.15	4.75	34.16	19.13
TMEM178A	7.10	4.86	1.12	0.27	2.12	1.89	1.20	0.54	1.73	1.89
TUBB2A	568.21	293.19	233.55	187.28	196.57	193.07	60.56	95.15	169.78	300.55
TXLNG	24.16	12.16	10.11	13.60	10.04	6.86	6.67	7.43	9.42	4.06
TXNRD1	63.03	42.39	29.88	38.92	39.26	32.91	19.09	21.36	42.32	22.31
WWC1	4.74	6.63	3.20	1.65	7.71	3.09	1.54	1.59	7.54	4.92
YEATS4	42.47	48.56	15.54	26.15	28.22	42.46	15.35	18.77	24.30	18.06

Figure 2E. Cluster II genes

Genes	hESC		Day 3 MESP1$^+$		Day 3 MESP1$^-$		Day 5 MESP1$^+$		Day 5 MESP1$^-$	
	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2
ACE	0.34	0.23	1.32	3.15	0.36	0.30	2.06	2.40	0.22	0.30
ACSL6	0.05	0.04	0.25	0.80	0.02	0.02	0.25	0.21	0.01	0.00
ADRA2C	3.37	7.97	15.01	20.64	4.65	8.73	5.15	10.70	3.65	10.12
ALDH2	28.89	28.70	71.21	106.09	35.24	32.88	62.40	83.76	44.69	52.13
ALPK2	0.40	0.10	10.19	22.68	7.46	1.29	8.95	14.49	11.96	4.09
ALPK3	5.12	2.59	10.62	19.09	9.19	1.49	7.25	11.39	6.68	1.93
AMER3	0.03	0.09	0.20	3.06	0.34	0.67	0.67	0.49	0.10	0.05
AMIGO2	2.56	1.40	35.79	58.39	2.87	6.68	41.22	45.46	2.64	1.53
ANKRD55	0.00	0.00	0.16	1.17	0.00	0.09	0.61	0.45	0.04	0.00
APLNR	2.14	1.01	184.27	385.56	5.69	14.26	81.18	156.43	3.28	3.78
APOBEC3B	5.37	5.04	12.00	21.79	7.71	8.02	7.01	8.99	5.95	7.11
APOBEC3G	0.59	0.84	3.66	11.96	0.89	1.09	4.06	5.85	1.23	0.85
ATP12A	0.12	0.10	6.99	18.46	3.83	0.25	2.16	3.29	1.07	0.33
ATP8B3	0.60	1.48	2.44	4.58	0.58	0.30	2.30	2.38	0.38	0.25
BAALC	0.75	1.94	4.74	6.65	1.04	2.59	4.21	5.87	0.24	0.23
BCAR3	4.43	3.44	19.78	26.02	8.37	8.47	13.73	17.07	8.49	6.16
BMP2	6.60	5.38	31.60	24.72	1.97	3.02	11.54	19.44	1.41	0.96
BMPER	0.36	0.11	14.42	34.40	3.32	3.29	5.20	11.10	2.48	1.18
C8orf31	0.21	0.19	3.39	6.66	1.23	0.58	3.70	5.07	0.84	0.71
CA12	1.05	1.84	4.39	13.29	6.63	1.99	6.27	7.78	3.30	2.28
CA2	5.85	5.88	51.20	45.40	14.27	17.54	6.02	12.65	11.18	10.79
CALCB	0.92	1.96	25.01	17.49	3.07	2.60	2.28	4.47	4.57	5.57
CD1D	0.34	0.36	3.61	8.57	0.38	0.54	1.88	2.72	0.35	0.21
CER1	15.08	0.62	28.86	55.54	2.97	0.54	6.61	12.42	2.26	0.86
CGNL1	7.79	3.87	21.17	32.44	18.84	6.86	17.41	27.91	15.27	6.82
CLSTN2	0.41	1.10	3.17	9.74	8.23	2.64	3.50	4.03	3.17	1.23
COL13A1	2.47	9.21	13.17	26.91	2.29	5.83	15.43	21.60	1.32	1.52
COL9A2	2.33	5.86	35.95	54.97	7.25	12.95	12.73	25.96	4.43	7.42
CRLF1	0.89	1.32	4.17	8.19	0.50	0.71	1.19	2.24	0.45	0.71
CYP27C1	1.52	2.39	6.49	5.05	2.62	2.35	2.34	3.29	1.63	1.24
DENND2C	0.73	0.58	1.79	3.71	0.36	0.08	1.34	1.13	0.34	0.10

DLL3	1.07	3.04	26.31	76.37	0.26	6.23	11.26	21.76	0.47	1.13
DUSP10	2.01	1.25	7.50	5.58	1.33	1.95	2.73	4.38	3.11	2.88
EGF	0.80	0.38	1.84	2.99	0.43	0.36	0.90	1.01	0.20	0.12
ELN	1.25	2.34	4.45	9.48	0.82	3.11	2.66	6.32	0.24	0.55
EOMES	8.96	0.12	10.82	27.55	1.30	0.28	2.56	4.07	2.31	1.29
FAM222A	1.97	2.02	6.09	6.36	0.88	4.00	2.33	4.00	1.05	1.07
FBN2	12.14	8.44	34.52	86.51	31.00	9.22	27.73	44.55	21.81	3.30
FGF19	3.08	1.22	8.52	36.37	0.97	5.69	7.86	22.40	0.40	0.45
FGFRL1	4.70	4.51	9.03	20.01	4.07	6.53	10.46	15.74	6.69	3.86
FNIP2	2.75	1.79	10.72	9.29	5.40	1.08	6.66	7.19	4.50	0.53
GATA4	1.21	0.11	17.47	29.17	2.81	6.99	9.42	14.17	3.11	2.53
GATA6	1.47	0.18	16.98	53.61	5.84	18.03	45.23	56.04	6.72	4.35
GYPB	0.00	0.00	0.44	1.21	0.00	0.00	0.00	0.00	0.00	0.00
GYPE	0.00	0.00	0.67	1.25	0.03	0.00	0.36	0.12	0.00	0.00
HAS2	11.97	1.81	84.49	155.97	13.15	13.28	35.82	61.11	14.80	5.11
HHIPL2	0.08	0.33	4.17	7.03	2.88	3.21	4.57	5.43	1.22	1.14
HLA-DQB1	4.54	2.56	20.10	34.52	6.19	10.30	6.58	10.14	3.98	7.71
HOXD13	0.00	0.00	1.73	4.25	0.04	0.61	2.59	2.25	0.08	0.10
HS3ST3A1	1.97	3.32	9.31	21.71	1.48	3.06	3.99	8.74	1.05	1.72
IKZF1	0.09	0.17	0.45	1.20	0.32	0.04	0.28	0.27	0.60	0.31
IL13RA1	6.77	2.90	10.53	18.06	6.46	4.03	10.14	9.64	7.03	4.33
ITGB8	0.49	0.94	2.93	2.93	0.24	0.52	1.37	1.85	0.27	0.10
JAKMIP1	0.40	1.09	1.01	9.48	0.26	0.07	1.46	2.06	0.29	0.23
JHDM1D	1.58	1.24	1.95	7.89	3.52	1.59	3.26	4.30	2.74	0.74
KEL	1.75	0.44	6.47	4.58	0.70	0.44	2.62	2.42	0.87	1.16
KIAA1024	0.06	0.12	1.80	5.60	0.44	0.11	2.00	2.17	0.58	0.16
KIAA1551	21.63	7.93	53.04	83.00	59.02	19.43	40.98	51.66	39.14	9.25
LGR5	0.48	0.04	9.80	14.75	1.13	0.24	3.13	5.41	0.48	0.06
LHX1	0.89	0.34	6.47	7.03	0.18	0.43	1.40	3.94	0.11	0.12
LINC00261	1.41	0.24	5.02	2.98	0.47	1.52	1.19	1.05	0.56	0.35
LPGAT1	3.29	2.35	6.93	10.09	5.27	2.50	5.43	5.89	6.21	2.15
LRRC37BP1	6.10	6.39	13.46	19.66	13.84	11.29	7.51	8.84	8.18	5.57
LZTS1	8.55	1.43	11.68	35.90	0.61	0.76	5.51	9.17	0.84	0.56
MALT1	5.89	6.26	12.89	24.58	10.20	5.93	9.07	11.29	10.26	4.63
MESP2	0.25	0.36	4.77	9.99	0.03	0.08	1.69	3.36	0.12	0.12
MIXL1	2.43	0.23	6.38	50.10	1.47	1.95	5.31	10.97	2.62	1.60
MSGN1	0.00	0.00	8.46	43.72	0.00	0.57	9.59	16.73	0.00	0.00
MYC	20.43	4.92	55.25	34.89	16.45	12.12	24.15	34.18	22.01	21.76
MYLK3	0.10	0.05	1.45	2.79	2.23	1.36	1.53	1.86	1.10	0.63
NAV2	20.25	10.37	23.95	71.28	26.51	8.03	28.42	46.46	24.41	5.90
NRG2	0.09	0.24	3.62	3.98	0.14	0.37	1.62	2.66	0.10	0.16
ODAM	0.00	0.00	3.57	4.69	0.86	0.70	2.74	3.92	0.73	0.35
PCED1B	2.00	0.69	6.68	9.38	0.38	0.66	4.00	5.23	0.54	0.58

PCSK2	0.10	1.63	4.59	8.74	0.51	0.55	1.09	1.19	0.36	0.42
PELI2	2.98	4.37	8.63	10.09	1.43	2.16	4.60	6.78	1.30	0.58
PENK	0.19	0.38	6.50	12.61	0.37	2.49	7.10	6.83	0.13	0.43
PLEKHA6	1.69	1.72	5.30	9.90	5.11	1.95	3.32	5.22	3.73	2.80
PLXNA2	0.69	1.12	15.49	33.59	11.07	4.28	15.91	22.32	15.41	4.71
PRDM1	0.66	0.27	3.48	3.68	0.91	0.79	1.68	0.82	0.41	0.35
PVR	6.17	4.70	19.19	16.72	9.79	6.51	11.83	13.06	9.33	7.72
RASGRP3	0.10	0.03	2.06	7.73	0.09	0.08	3.50	4.70	0.08	0.01
RGS13	0.00	0.00	8.45	23.14	0.11	0.56	4.99	6.90	0.19	0.12
RGS2	11.06	14.59	51.02	43.24	4.63	10.90	25.25	37.97	5.61	4.65
SEMA6D	6.91	3.22	16.84	29.27	3.74	3.76	21.12	21.07	3.59	0.86
SERPINB9	13.20	1.79	62.49	104.14	24.83	11.69	40.54	44.55	15.85	8.16
SERPINE2	122.55	43.96	212.02	337.10	37.67	36.62	55.71	96.78	68.52	58.64
SEZ6L	0.16	0.28	1.08	2.73	0.92	0.59	1.29	1.38	0.45	0.13
SHISA6	1.04	1.37	1.84	8.37	0.40	0.24	1.62	3.34	0.29	0.09
SLC39A8	8.22	3.40	14.62	18.24	13.00	10.99	15.43	12.82	9.27	5.92
SLPI	0.00	0.00	1.54	1.43	0.11	0.27	0.54	0.28	0.00	0.13
SMAD9	0.15	0.34	3.78	4.57	2.81	2.76	3.00	3.04	2.74	0.77
SNAI1	3.98	5.25	19.43	49.39	6.30	8.14	20.45	57.65	7.57	9.32
SOX17	1.30	0.35	24.78	16.72	1.40	2.79	3.69	4.59	1.51	3.21
ST3GAL6	1.24	2.77	6.52	10.24	3.25	4.95	6.09	8.85	3.58	2.62
SYNJ1	1.00	0.56	2.55	4.37	2.20	1.19	2.74	2.78	1.78	0.39
SYNM	0.74	0.74	3.20	2.37	1.59	0.78	1.57	1.05	1.34	0.62
T	0.78	0.21	19.85	29.72	1.55	1.25	5.98	10.22	1.19	0.84
TBX6	0.36	1.17	8.98	16.93	0.70	0.81	4.80	10.03	0.48	0.78
TERF2IP	8.09	10.60	19.87	42.25	13.40	21.52	28.63	34.89	13.64	15.56
TMEM185A	6.88	8.32	34.29	51.09	7.18	8.05	23.85	34.10	6.93	6.94
TP53INP1	1.62	3.28	6.16	9.43	7.65	5.68	7.29	7.58	7.05	2.89
TSLP	0.23	0.20	2.07	2.59	0.34	0.46	1.36	1.35	0.23	0.02
WNT3	3.16	1.36	5.89	14.54	5.93	2.92	5.19	5.66	5.15	2.34
WNT5A	1.56	2.46	29.28	90.82	12.25	10.01	29.46	54.23	17.23	6.95
WNT8A	0.65	7.95	20.14	35.16	1.37	1.79	12.54	18.18	0.59	0.04
ZNF516	3.25	5.71	7.28	16.20	4.99	4.59	8.78	14.36	4.24	2.01
ZNF611	3.52	1.87	12.65	10.65	4.81	2.10	5.89	6.72	4.62	1.38
ANXA6	57.80	56.37	96.70	145.01	60.23	92.30	124.40	140.42	56.56	68.86
IGFBP4	39.78	39.15	68.91	115.27	13.69	50.99	85.51	111.63	15.93	38.58
ABTB2	6.45	1.94	10.32	10.61	2.29	2.66	2.87	4.47	1.99	1.46
ALDH1A3	3.32	0.84	3.63	10.17	0.30	0.05	0.92	2.03	0.58	0.21
CALB1	3.63	1.33	5.17	3.79	0.67	0.23	0.47	0.33	0.66	0.19
CHCHD2	0.31	0.00	0.59	0.69	0.15	0.00	0.00	0.00	0.00	0.00
FABP5	320.75	174.97	365.73	559.21	95.07	258.41	159.07	214.01	90.35	139.23
HSPH1	55.13	34.56	56.96	74.81	38.45	38.43	18.07	29.62	34.81	20.34
LEPREL1	20.19	19.13	22.14	40.07	20.70	13.81	8.08	14.97	16.65	10.95

NTS	152.48	4.31	151.64	307.42	12.26	7.28	29.97	46.88	6.27	4.68

Figure 2E. Cluster III genes

Genes	hESC		Day 3 MESP1$^+$		Day 3 MESP1$^-$		Day 5 MESP1$^+$		Day 5 MESP1$^-$	
	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2
COL3A1	0.84	1.40	224.29	151.47	345.37	292.56	5035.29	3197.53	686.05	301.08
COL1A1	36.82	20.91	113.15	110.68	184.26	278.01	1506.58	1289.41	298.52	248.63
SPARC	156.34	103.46	262.77	282.76	262.71	211.91	1275.25	847.71	377.40	337.25
IGF2	0.50	3.08	159.84	101.79	73.38	262.40	1265.50	1056.50	194.96	277.47
COL6A2	64.31	28.08	190.38	218.69	41.38	75.77	1109.28	986.89	64.78	106.72
POSTN	1.99	0.35	9.47	5.81	3.45	10.13	965.83	535.86	15.13	6.27
COL6A1	56.98	25.72	279.97	405.71	45.87	58.49	848.43	841.83	57.14	50.17
COL1A2	17.33	10.55	21.56	26.16	72.22	113.17	537.01	394.29	138.65	81.49
COL5A1	11.42	8.73	71.65	103.96	92.02	38.66	379.67	334.28	142.49	82.35
FOS	74.01	68.77	17.61	10.67	110.34	192.27	370.42	225.20	211.62	140.59
MEST	72.82	82.87	192.11	159.78	125.97	179.05	309.12	325.50	175.09	113.31
COL6A3	0.55	0.32	29.98	39.41	21.46	4.18	306.29	300.77	48.21	12.32
NID2	2.47	5.72	91.71	90.27	16.44	24.63	301.12	300.12	38.71	11.78
SST	0.44	1.23	13.35	4.66	0.95	7.15	251.15	154.94	2.91	14.63
VCAN	86.14	38.27	43.21	52.84	16.44	23.72	240.88	191.28	16.23	8.20
SLC9A3R1	32.36	54.89	126.68	104.30	130.68	317.08	240.64	251.57	108.59	184.11
COL4A2	47.99	43.39	89.40	91.77	63.56	34.83	233.53	210.37	81.28	49.92
PCOLCE	9.47	12.79	23.65	19.85	26.88	58.09	214.43	178.07	27.30	65.09
B2M	60.46	71.60	108.61	109.99	84.25	91.12	211.82	175.18	66.20	76.60
COL4A1	50.20	34.77	84.25	85.53	54.92	21.20	195.82	172.19	80.15	24.26
FKBP10	76.99	100.98	67.03	69.10	59.88	79.44	192.70	172.28	66.11	75.90
COL5A2	14.50	2.04	28.45	49.28	46.49	26.47	192.23	143.17	63.28	20.41
FRZB	3.78	14.50	6.49	2.28	0.85	9.66	188.56	112.58	2.10	2.90
BST2	31.43	104.47	33.94	13.38	11.78	50.65	166.17	172.75	6.75	16.94

MFAP4	4.08	2.82	28.18	44.93	3.16	4.75	154.54	139.82	4.22	3.58
PLTP	44.17	53.30	44.67	40.86	22.06	35.84	152.42	118.83	18.49	28.94
TMEM98	46.54	59.15	59.87	71.45	46.52	104.66	151.14	142.68	49.45	63.84
PITX2	2.68	1.64	56.15	64.33	2.45	15.02	139.37	115.90	5.53	5.55
TFPI	5.52	7.01	28.70	19.32	15.60	27.11	135.50	98.76	12.84	8.26
FGFR2	39.28	38.90	34.37	42.17	40.73	35.72	135.22	109.30	42.58	19.40
AQP1	0.05	0.18	21.70	16.96	1.39	15.38	103.58	73.02	8.56	9.02
PEG10	35.44	31.20	44.94	34.78	36.59	23.87	98.92	82.29	48.07	15.11
GNG11	12.84	6.42	7.35	4.90	3.13	6.81	92.53	59.37	6.18	9.34
CRHBP	0.00	0.07	16.28	8.00	0.34	1.72	91.15	63.54	1.66	1.42
IL6ST	2.33	1.23	16.29	25.60	8.04	7.80	88.58	69.83	13.36	3.19
MRC2	9.66	13.16	23.23	31.53	12.37	15.69	83.85	79.76	12.62	12.86
SERPINF1	14.83	26.55	6.23	1.83	3.87	9.61	81.61	57.60	3.81	3.78
GABARAPL1	22.80	25.99	45.33	39.71	27.09	13.64	80.30	57.35	27.90	28.17
FMOD	0.01	0.03	4.25	6.85	1.05	1.51	77.35	48.96	1.63	1.25
ADAMTS1	9.86	3.23	27.98	38.69	23.67	16.61	75.59	66.18	28.62	11.47
CHN1	27.60	33.96	15.38	24.37	13.82	15.85	74.32	49.90	14.36	11.24
IMPAD1	10.29	6.36	29.31	40.74	11.54	11.21	73.99	61.48	12.69	6.49
CHSY1	31.93	11.48	26.35	41.75	13.59	11.71	71.36	58.51	11.91	5.60
MAN1A1	1.69	1.09	9.72	16.72	6.64	5.62	71.07	51.32	14.32	3.18
SLN	0.00	0.14	9.30	3.31	1.30	4.80	68.32	44.01	3.95	8.46
PPIC	9.07	5.00	21.67	23.14	17.47	15.44	66.52	51.16	20.28	19.02
MYRF	2.43	3.34	14.46	13.03	18.71	12.64	66.49	59.31	31.74	17.24
ATP7B	0.97	1.61	8.31	13.42	6.08	4.37	64.88	54.90	7.79	2.34
LEPRE1	22.57	23.20	23.17	32.63	18.90	22.60	63.33	56.73	18.79	23.44
HGF	0.00	0.10	5.37	10.28	0.18	0.28	59.30	36.10	0.85	0.30
P4HA1	9.98	19.15	17.82	25.37	14.33	18.69	56.34	45.77	12.77	9.83
ADAMTS9	2.32	2.08	21.48	23.32	15.87	4.71	55.91	47.21	22.50	6.44
PAMR1	2.80	18.63	26.70	20.80	5.48	9.50	54.47	54.42	3.69	3.27
SPON1	1.95	2.53	14.97	15.17	2.10	4.17	51.08	47.46	1.68	0.89
TGFBR3	1.77	2.36	4.43	3.48	1.18	1.35	50.80	34.26	1.65	0.80
TPST1	4.92	7.10	23.11	23.84	9.05	10.68	50.73	43.68	10.22	6.60
S1PR3	2.76	2.22	22.58	23.74	8.18	4.71	50.66	52.69	7.84	3.90
NID1	17.12	7.39	10.99	13.98	3.36	4.39	50.49	44.54	5.49	1.26
PNRC1	7.44	21.33	18.56	16.59	25.37	34.88	50.42	43.98	28.61	28.78
CHST2	9.23	4.73	4.86	4.22	0.71	2.76	50.41	40.65	1.02	1.23
EGFL7	14.69	38.82	19.87	19.39	11.74	28.50	49.96	54.83	8.78	32.08
REN	0.00	0.03	1.07	0.09	0.04	0.26	49.55	31.02	0.07	0.17
AEBP1	9.28	13.05	17.81	24.41	11.44	15.72	48.33	43.59	11.99	13.28
ENPP2	1.22	4.00	8.91	4.58	1.39	4.17	46.28	28.43	1.58	0.87
VEGFA	7.27	8.92	16.32	19.41	13.84	6.79	45.96	55.98	14.46	10.49
JUNB	2.66	12.47	6.69	6.73	4.68	12.60	44.64	39.48	9.58	21.50

SOCS3	3.92	3.15	10.95	12.15	24.53	36.57	44.61	40.04	20.13	19.73
SLIT2	1.93	0.85	7.37	14.85	6.92	3.94	44.50	41.75	11.74	1.70
CREB3L1	3.03	4.39	27.22	13.22	9.74	9.16	44.21	37.33	12.67	15.84
EGFL6	0.24	0.30	0.93	0.31	0.21	0.29	43.31	25.65	1.28	0.93
RAMP2	10.39	14.44	10.35	11.43	3.29	11.36	42.93	35.03	2.74	8.22
GPR124	0.59	1.19	17.97	21.56	6.95	4.03	41.50	48.33	9.92	5.25
CD248	3.82	2.49	6.68	4.28	6.44	6.05	41.43	33.70	8.68	13.71
SEPP1	5.80	7.58	13.88	6.81	16.46	21.35	41.21	26.28	11.75	7.41
ST6GALNAC3	7.14	12.24	13.86	19.69	16.11	18.21	41.00	34.29	15.78	7.92
SLC40A1	0.36	0.15	8.99	6.94	4.67	4.14	40.68	26.77	6.02	3.05
BGN	3.23	2.17	5.93	5.56	2.54	2.74	38.60	33.52	3.32	4.60
EGFLAM	0.38	0.36	13.27	12.50	0.93	2.04	37.15	27.47	1.01	1.17
EMILIN1	2.59	4.69	4.64	7.38	5.06	12.08	37.11	35.39	5.33	9.55
THBD	0.38	0.05	0.62	1.00	1.15	2.38	37.01	27.12	2.40	1.65
STRA6	8.69	10.45	21.27	10.11	14.17	27.42	36.92	36.87	11.91	15.56
STMN2	0.79	2.08	2.97	0.90	2.91	2.43	36.21	19.18	4.79	6.82
P4HA2	2.70	8.44	9.87	12.90	8.11	7.54	35.17	30.39	9.04	9.79
TCF21	0.07	0.00	7.90	9.88	2.44	6.67	34.66	28.09	2.24	3.38
GPX7	8.75	13.86	16.98	19.73	11.11	21.75	33.77	30.56	11.31	17.62
TXNIP	5.43	23.01	12.33	16.99	7.50	15.51	33.66	43.29	6.28	3.93
PCMTD2	12.40	14.96	15.28	19.29	17.62	15.48	33.58	29.63	17.09	7.30
C12orf23	4.54	4.64	7.83	11.98	10.44	10.17	33.11	22.71	13.90	7.54
FREM1	0.25	0.48	7.53	9.96	6.14	4.46	32.69	31.70	5.66	3.11
COL15A1	0.02	0.06	0.39	0.18	0.10	0.09	32.31	21.62	0.53	0.15
COL21A1	0.62	0.47	0.86	0.68	1.27	0.38	32.11	19.41	1.79	0.73
EFNB3	4.56	12.51	12.59	9.97	10.03	17.58	30.26	33.92	10.08	8.65
TMEM200A	4.16	4.43	12.93	14.87	11.31	13.23	29.83	22.81	9.20	3.09
MAGEH1	6.91	10.06	10.15	11.30	12.43	17.90	29.76	23.78	13.95	16.59
FAM110B	0.77	1.65	5.30	3.80	6.68	6.67	29.56	22.16	4.68	5.96
TEK	8.17	8.63	13.41	9.38	3.79	3.83	29.43	24.04	3.69	1.18
NR4A1	5.41	8.87	12.56	10.97	8.31	10.56	28.55	22.87	11.13	17.08
ADAM12	0.07	0.38	2.28	3.84	0.37	0.27	28.35	22.29	1.14	0.25
ADAMTS15	0.46	0.34	9.28	1.83	1.51	2.16	28.29	24.17	1.93	1.35
ZEB2	4.10	10.37	13.49	15.43	6.00	5.40	28.00	21.79	7.95	1.88
NDRG2	5.89	11.12	11.10	13.09	6.85	20.57	27.80	23.61	6.60	8.86
NPNT	0.10	0.04	1.74	1.37	2.63	0.97	27.80	16.44	5.67	2.55
DIO3	1.10	1.36	16.57	11.89	16.36	32.95	27.64	21.22	8.92	14.41
KCNN2	9.87	9.00	5.20	5.37	7.35	12.18	27.21	20.32	4.79	4.69
COBLL1	0.92	0.56	8.37	8.62	4.18	3.00	26.23	17.39	6.08	1.38
PDCD4	3.99	7.00	13.16	8.35	10.02	13.43	26.03	20.71	10.66	6.81
TBX20	0.07	0.00	3.40	13.04	2.07	0.50	25.58	25.24	1.72	0.10
ZNF503	0.29	6.05	10.04	19.27	7.39	41.92	25.19	36.26	9.16	11.18
RPP25	10.96	19.03	8.67	8.56	3.71	7.32	25.14	24.19	3.51	6.64

TSPAN5	5.86	11.24	17.06	15.19	10.36	8.16	25.08	23.33	9.37	6.60
ECM1	1.77	0.73	3.19	2.63	1.26	1.00	24.41	18.36	1.57	2.65
IFI16	1.30	1.88	8.48	7.18	8.14	6.25	23.97	19.40	5.64	3.32
TSHZ1	0.27	0.51	5.94	5.90	2.44	4.97	23.76	22.13	2.28	0.66
VTN	0.60	0.87	6.32	4.44	2.80	6.88	23.72	16.26	2.98	5.54
CLIP3	4.02	20.63	11.05	6.33	5.68	9.22	23.45	21.67	5.73	3.67
SLC22A17	8.47	25.05	10.94	6.66	8.12	19.35	22.94	25.76	5.91	10.69
STC1	8.34	6.78	2.99	0.81	2.48	1.75	22.80	13.97	0.91	0.38
DSC3	0.35	0.63	2.96	3.86	0.57	1.88	22.74	15.79	1.78	0.55
ISLR	1.12	0.34	4.09	2.78	0.86	7.24	22.46	17.97	1.23	2.31
COL14A1	1.62	2.35	1.33	0.74	0.80	1.01	22.38	14.63	0.62	0.19
DRD2	0.48	2.14	4.67	4.15	0.15	1.16	21.71	19.26	0.50	0.81
ENTPD3	0.04	0.12	2.22	2.38	0.09	0.48	21.14	13.76	0.38	0.27
NTRK3	1.51	2.43	2.45	2.84	0.68	1.08	21.04	15.88	1.22	0.64
ANXA8L2	0.05	0.00	0.96	0.44	0.95	1.36	21.02	11.92	2.61	2.78
CADM3	0.89	2.47	2.67	1.85	0.75	1.16	20.04	15.00	1.19	0.91
CHPF2	6.63	5.50	9.73	8.63	10.10	8.94	19.94	18.93	10.79	9.65
RAB37	1.03	2.34	3.59	2.99	3.38	4.68	19.52	16.92	2.28	3.17
PARM1	1.56	1.20	0.68	0.31	0.34	1.25	19.39	11.46	0.29	0.24
HOXC8	0.04	0.04	6.00	4.83	0.52	7.61	18.69	17.80	1.71	1.35
STON1	1.84	5.07	2.87	5.40	5.90	3.93	18.67	14.89	4.14	1.24
MGP	0.00	0.00	0.12	0.06	0.04	0.14	18.41	9.52	0.07	0.23
PLVAP	0.07	0.09	0.89	0.08	0.14	0.60	18.41	16.02	0.10	0.21
RHPN2	9.81	13.79	6.31	3.36	6.64	5.66	18.29	13.68	5.72	4.00
TNS1	1.17	0.55	5.57	7.63	2.09	1.07	18.06	18.53	3.62	1.18
ABO	0.06	0.09	3.60	1.01	0.14	0.00	17.92	12.89	0.25	0.08
CD34	0.25	0.23	0.52	0.06	0.06	0.96	17.73	15.11	0.16	0.36
VEGFC	0.31	0.67	3.04	6.79	0.48	1.84	17.54	17.07	0.93	0.61
SPON2	0.35	2.81	2.52	1.28	0.73	1.36	17.46	13.83	0.56	1.96
LRFN5	2.22	0.41	4.25	9.83	1.55	1.47	17.09	15.66	2.46	1.23
PTGIS	6.42	9.96	5.67	3.13	11.24	10.79	16.55	15.55	7.95	6.07
PKIA	4.42	6.18	3.98	3.05	3.85	3.81	16.44	10.32	3.37	1.44
OSBPL10	5.90	3.06	5.33	4.53	2.74	2.09	16.40	13.08	3.19	1.94
DOK5	1.94	5.47	5.90	5.40	3.22	3.14	16.22	11.53	3.38	3.29
GRK5	0.84	2.20	5.99	5.06	5.00	3.96	16.00	13.93	6.95	6.36
RAB38	5.39	6.02	2.13	1.17	3.86	8.62	15.86	10.70	3.89	4.68
TBX2	0.01	0.00	1.38	2.36	0.76	6.35	15.70	12.85	1.06	1.73
ZFPM2	0.03	0.15	0.99	2.11	0.14	1.20	15.18	10.93	0.95	0.28
S1PR1	0.41	1.01	5.70	5.45	0.17	1.63	14.95	14.20	0.82	0.40
TBC1D4	6.13	5.30	2.24	4.68	1.87	2.41	14.82	12.92	1.74	0.50
HTRA3	1.87	3.47	4.00	4.80	1.89	3.83	14.41	13.23	2.89	5.42
MORC4	0.98	0.63	6.33	2.57	3.88	1.96	14.23	8.68	5.91	3.85
ZADH2	1.06	1.74	5.33	4.76	3.19	4.30	13.99	13.68	2.68	1.67

FLRT2	1.64	1.57	7.22	5.66	3.22	1.39	13.76	11.02	4.19	1.03
KISS1	0.00	0.00	0.35	0.00	0.36	0.32	13.75	7.74	0.24	0.73
CLEC1B	0.00	0.00	3.66	2.61	0.12	0.64	13.71	9.47	1.17	1.45
CDH5	0.46	0.13	0.42	0.11	1.12	0.92	13.55	11.32	0.92	0.62
PGM5	0.01	0.01	0.91	1.24	1.73	2.12	13.41	12.64	2.36	1.28
RGL1	2.21	1.57	6.43	4.35	1.90	1.91	13.32	10.42	2.74	1.06
RHOBTB1	4.29	3.76	7.26	6.06	5.66	3.98	13.28	10.94	6.13	2.92
NFATC4	3.30	14.02	3.01	3.80	7.75	6.60	13.28	12.87	7.56	10.46
IL11RA	1.68	4.28	4.13	3.27	3.64	4.71	13.15	11.11	3.63	5.59
SRPX	3.00	4.94	2.63	1.67	2.10	2.73	12.86	10.21	1.66	1.58
F10	0.78	3.42	2.20	2.82	1.26	3.15	12.66	10.38	0.85	1.58
MGAT3	1.45	4.27	5.16	6.85	5.65	4.78	12.64	12.82	5.55	4.88
ESAM	1.18	0.40	2.12	0.28	0.25	0.58	12.42	10.12	0.46	0.65
PLAGL1	1.09	3.19	8.65	5.20	5.41	5.41	12.38	14.44	4.36	1.70
GATA5	0.11	0.30	1.09	3.42	4.21	17.95	12.38	11.09	3.29	5.08
SOX6	0.03	0.02	1.09	1.60	0.84	1.20	12.08	10.78	1.82	0.71
FCGRT	2.22	6.72	3.28	2.21	4.23	6.39	11.96	9.38	4.25	10.09
P2RY1	5.76	1.23	2.50	3.68	0.68	0.32	11.83	9.58	0.87	0.11
EPOR	1.95	6.28	2.34	5.11	3.00	3.59	11.73	11.62	2.67	3.32
BMP5	0.14	0.72	4.24	2.37	1.94	3.18	11.40	12.67	1.51	0.50
JAZF1	3.85	1.90	1.96	3.71	1.01	0.99	11.40	7.25	1.08	0.62
IGDCC4	4.28	6.49	3.77	4.63	1.70	1.36	11.09	10.23	2.14	0.56
CYGB	0.71	0.80	2.30	4.59	0.12	0.58	10.95	9.22	0.28	0.50
GREM2	0.03	0.01	0.57	1.21	0.88	0.45	10.90	6.55	0.69	0.53
UAP1L1	1.74	2.13	4.40	4.92	2.94	0.94	10.89	9.61	2.96	2.70
TSHZ3	0.78	0.52	3.00	4.59	2.10	2.18	10.80	10.38	3.40	1.24
FMO4	0.82	1.66	1.33	1.38	1.63	0.47	10.75	7.02	1.34	0.81
PROS1	1.24	1.41	3.41	2.62	4.57	5.58	10.75	7.28	4.80	1.88
CALB2	0.88	4.92	1.94	1.56	3.91	3.71	10.66	5.98	4.39	8.22
ICAM2	0.29	0.33	0.31	0.29	0.10	0.58	10.59	8.44	0.00	0.23
CLIP4	0.03	0.14	0.49	0.80	0.49	0.62	10.53	7.08	0.69	0.21
PRPH	0.33	1.01	3.76	5.40	1.99	18.53	10.51	8.91	2.91	5.01
LAMC3	4.61	1.82	2.97	5.39	0.29	0.16	10.50	10.19	0.39	0.41
PID1	0.68	0.75	1.98	2.30	0.67	0.27	10.38	6.49	1.04	0.61
ORAI3	3.26	7.86	2.80	3.54	4.55	3.78	10.26	10.01	4.15	4.29
ITGA8	0.04	0.06	1.65	3.25	1.39	0.39	9.97	9.68	1.29	0.25
MMP1	0.00	0.00	1.19	0.96	0.03	0.48	9.95	7.03	0.92	0.67
C2orf72	0.30	1.49	1.53	1.88	2.73	1.65	9.95	9.67	1.93	1.93
PROK1	0.00	0.00	1.63	0.73	0.00	0.18	9.91	7.19	0.00	0.05
ANGPT1	0.92	1.17	0.51	0.66	0.49	1.21	9.71	6.21	0.27	0.13
C1S	3.41	1.45	0.78	0.71	0.65	0.34	9.62	5.71	2.73	1.83
PXK	1.80	1.95	3.55	4.05	2.70	2.01	9.57	7.63	2.79	1.07
TIE1	1.75	0.43	0.28	0.18	0.19	0.53	9.50	7.30	0.25	0.42

KYNU	0.13	0.27	2.25	0.79	0.45	0.55	9.18	4.88	0.29	0.40
CLDN5	0.23	1.12	0.17	0.23	0.16	0.97	9.17	7.18	0.20	0.54
HTR7	3.04	0.40	1.24	2.43	1.16	0.39	9.16	5.49	0.90	0.37
CYSLTR2	0.00	0.00	0.30	0.07	0.12	0.02	9.14	5.17	0.33	0.00
CD93	0.03	0.00	0.07	0.05	0.01	0.07	8.97	6.56	0.07	0.03
C5orf4	0.44	3.59	1.54	1.49	2.01	1.00	8.86	6.24	1.33	1.03
SLC26A2	3.33	2.77	4.38	4.90	2.57	2.29	8.76	7.77	2.54	0.91
CPED1	0.04	0.03	1.15	0.90	0.17	0.24	8.73	6.52	0.32	0.04
AKR1B15	0.00	0.00	0.95	0.22	0.07	0.25	8.69	6.47	0.30	0.34
COL8A2	0.41	0.58	0.15	0.13	0.07	0.25	8.49	5.08	0.35	0.36
SH3RF2	0.49	0.22	2.58	2.51	2.08	2.15	8.18	8.12	3.31	2.85
MMP16	2.70	1.09	0.86	2.53	1.00	0.55	8.14	6.71	0.81	0.16
MMRN2	0.59	0.32	0.26	0.16	0.15	0.26	8.11	7.16	0.12	0.18
CHST9	2.30	1.28	0.97	1.13	0.30	1.15	8.10	5.72	0.65	0.19
PLCB2	2.52	1.36	1.68	1.89	3.32	2.64	8.06	7.01	3.26	3.44
SLC2A10	2.69	3.27	1.88	2.56	2.62	1.73	7.79	7.06	2.50	0.92
KLF2	0.27	0.14	2.00	1.10	1.04	2.57	7.65	8.95	1.23	3.59
ADAMTS20	0.56	0.78	1.32	0.59	0.99	0.20	7.64	4.90	2.18	0.18
GJA4	0.68	0.17	2.20	3.00	0.10	1.10	7.37	5.30	0.36	1.22
FLI1	1.71	0.15	3.55	2.17	0.69	0.27	7.35	7.73	1.44	0.81
WNT2	0.01	0.01	1.43	0.55	0.59	0.56	7.29	3.73	0.77	0.74
MPPED2	2.79	0.58	2.51	4.22	0.67	0.77	7.24	6.39	0.75	0.41
SLC34A2	0.39	0.39	0.49	0.22	2.01	0.48	7.14	3.51	0.55	0.32
CDK20	0.99	2.37	1.94	2.22	1.83	2.65	6.96	5.46	3.00	2.30
EBF4	0.36	1.58	1.31	1.22	0.61	1.49	6.94	7.09	0.68	1.30
C12orf68	0.11	1.50	0.65	0.47	0.22	0.71	6.87	5.73	0.12	0.63
PDE4B	2.44	1.00	0.86	1.40	0.55	0.63	6.84	5.10	0.67	0.25
MASP1	0.50	0.62	2.42	1.09	0.71	0.37	6.76	4.23	0.41	0.36
PRR16	0.27	0.38	0.87	0.75	0.21	0.14	6.75	3.53	0.24	0.24
CNTN5	0.00	0.01	0.09	0.09	0.08	0.17	6.75	4.22	0.22	0.07
DEPTOR	0.49	0.70	1.44	2.42	0.27	0.49	6.74	5.15	0.23	0.07
SHANK3	1.84	5.05	2.68	3.11	3.84	3.35	6.68	8.60	4.01	2.35
LMO2	0.30	0.90	1.11	0.92	0.40	0.58	6.41	6.59	0.59	0.58
AKAP4	0.00	0.01	0.79	1.59	0.12	0.34	6.37	5.68	0.37	0.25
LOC100506190	0.42	0.76	0.92	1.64	1.69	1.69	6.36	5.15	2.50	2.35
CNTNAP1	2.25	5.94	1.55	3.04	1.35	1.25	6.35	5.98	1.44	0.71
LMO3	0.35	0.29	0.51	0.62	0.09	1.02	6.35	5.80	0.19	0.08
SH2D3C	0.36	1.91	1.49	0.30	0.52	0.67	6.31	4.91	0.69	1.41
FAM65C	0.20	0.60	1.66	2.06	0.36	0.49	6.26	7.29	0.68	0.44
IL2RB	1.27	0.67	2.08	2.44	1.37	0.35	6.23	4.90	2.23	1.22
EDN3	0.19	0.44	0.38	0.27	0.33	0.98	6.22	5.71	0.88	0.65
LOX	0.22	0.21	2.14	1.42	1.10	0.65	6.19	4.63	1.71	0.72

FIBIN	0.00	0.03	0.43	0.82	0.12	0.31	6.17	4.22	0.15	0.12
NT5E	1.64	0.31	0.28	0.18	0.08	0.06	6.03	3.83	0.13	0.07
ZNF467	0.28	1.59	0.44	0.30	1.79	2.86	5.94	4.76	1.58	2.51
C1R	2.72	2.70	1.16	0.43	0.68	1.18	5.92	3.27	0.70	0.92
CSPG4	1.53	1.15	1.56	1.62	0.66	0.50	5.91	5.40	0.87	0.51
ADAMTS10	1.45	1.39	1.26	1.52	1.42	1.00	5.71	5.52	1.37	1.47
PYGM	1.12	3.31	1.53	0.25	0.71	1.83	5.69	4.26	1.60	2.12
ALOX15	0.20	0.55	0.56	0.24	0.64	0.55	5.67	4.71	0.84	0.59
SRPX2	0.14	0.02	0.61	0.41	0.21	0.05	5.61	3.58	0.71	0.63
CHSY3	0.20	0.10	0.52	1.11	0.69	0.39	5.55	3.47	1.00	0.30
RERG	0.11	0.06	1.20	0.64	1.58	2.29	5.50	2.87	1.87	0.92
GLT8D2	2.56	2.43	0.79	0.86	1.77	1.58	5.50	4.27	1.77	1.36
RNF112	0.30	0.81	0.54	0.55	0.19	0.29	5.46	4.61	0.21	0.23
PAG1	0.48	0.11	2.49	1.91	0.25	0.26	5.41	4.32	0.55	0.24
BCL6B	0.41	1.59	0.68	1.63	0.20	0.34	5.39	5.42	0.12	0.10
LAPTM5	0.36	0.12	0.79	0.84	0.18	0.24	5.39	4.98	0.31	0.37
SLC47A1	2.25	1.91	1.26	1.19	0.28	0.40	5.38	4.08	0.31	0.23
GHR	0.21	0.29	1.27	1.54	1.41	0.93	5.37	4.02	1.72	0.69
SEMA3E	0.63	1.13	1.36	1.06	0.77	1.00	5.31	3.09	0.40	0.85
PLCE1	0.16	0.22	1.83	2.19	1.84	0.47	5.19	4.46	1.41	0.57
LOXL4	0.42	0.29	2.03	0.89	1.49	1.58	5.08	3.39	1.25	1.07
RPS6KA5	0.81	0.98	0.37	0.84	1.06	0.93	5.06	3.13	0.90	0.09
FLT4	2.76	4.86	1.02	1.29	0.95	2.42	5.06	6.09	0.89	0.97
HSPA12B	1.11	1.56	0.79	1.92	0.42	0.75	4.96	4.77	0.52	0.52
CALCRL	0.13	0.18	0.24	0.15	0.15	0.16	4.95	3.29	0.27	0.08
COL22A1	1.33	0.98	0.70	0.58	2.14	2.50	4.85	4.87	1.96	1.05
OIT3	0.00	0.00	0.20	0.18	0.00	0.10	4.78	2.98	0.08	0.05
PLXNA4	0.47	0.21	0.49	0.47	0.42	0.17	4.77	3.40	0.49	0.10
RASIP1	0.44	1.35	0.83	0.68	0.55	0.94	4.74	6.37	0.48	0.86
ABCA2	1.62	4.39	1.76	1.12	0.90	1.50	4.68	5.58	0.96	0.54
ABCA8	0.00	0.00	0.14	0.20	0.01	0.09	4.66	2.42	0.02	0.00
PABPC4L	0.53	0.31	0.90	1.11	0.72	1.56	4.62	3.95	1.09	0.23
GFRA2	0.72	0.98	2.64	2.66	1.36	1.50	4.56	4.38	1.42	2.15
HPSE2	0.17	0.35	0.24	0.22	0.13	0.08	4.54	3.47	0.09	0.07
OTUD1	0.60	1.33	2.38	1.81	2.19	2.71	4.53	4.56	2.45	2.09
IFIT1	0.53	1.31	1.13	0.42	0.46	0.71	4.44	3.12	0.89	0.57
TRANK1	0.45	0.94	0.49	0.76	0.78	0.72	4.42	4.14	0.77	0.26
GBP4	0.06	0.05	0.89	0.36	0.06	0.23	4.38	3.78	0.13	0.24
TRABD2B	0.98	1.23	1.53	1.33	0.29	1.15	4.38	3.56	0.59	0.61
DES	0.53	0.79	1.67	1.71	0.46	0.53	4.36	3.54	0.42	0.56
DARC	0.13	0.35	0.86	0.47	0.13	0.36	4.24	2.73	0.28	0.52
SCARF1	0.96	0.49	0.15	0.18	0.28	0.22	4.18	3.54	0.27	0.32
ALOX5	0.10	0.19	1.19	1.77	0.17	0.37	4.15	3.43	0.25	0.36

CPA1	0.00	0.00	2.15	1.64	0.11	0.53	3.89	3.14	0.41	0.70
LSAMP	1.29	2.47	1.42	0.74	0.95	1.47	3.85	3.22	0.98	0.41
CARD16	0.00	0.00	0.44	0.00	0.00	0.10	3.84	1.28	0.00	0.11
SLC19A3	0.50	0.42	0.41	0.53	1.88	2.35	3.84	2.22	1.30	1.11
ERG	0.04	0.09	0.48	0.15	0.42	0.13	3.71	3.30	0.14	0.07
LRRC4C	0.13	0.27	0.66	0.83	0.66	0.47	3.67	1.68	0.73	0.38
GRIN2D	0.56	0.45	1.05	2.15	1.04	0.75	3.66	3.37	0.69	0.89
CLEC12A	0.00	0.00	0.54	0.44	0.00	0.04	3.63	2.58	0.03	0.18
PLD1	0.37	0.15	0.91	0.67	0.50	0.33	3.58	2.31	1.04	0.31
ART4	0.00	0.00	2.22	0.50	1.08	0.28	3.56	2.02	1.12	0.55
EPHA6	0.15	0.08	0.15	0.18	0.11	0.12	3.52	1.48	0.17	0.06
ASXL3	0.08	0.29	0.68	1.20	0.61	0.45	3.51	2.33	0.85	0.27
ZFHX4	0.48	0.89	1.52	0.29	0.71	0.83	3.51	2.41	1.15	0.42
SCUBE1	0.56	0.82	1.45	0.54	0.77	1.68	3.48	3.07	1.33	0.93
CLMN	0.51	0.88	0.62	0.73	0.98	0.54	3.46	3.48	1.21	0.70
DKK2	0.53	0.18	0.29	0.34	0.21	0.09	3.46	2.53	0.40	0.21
ZNF469	0.19	0.11	1.24	0.33	0.15	0.08	3.39	3.02	0.31	0.10
CD109	1.39	0.56	0.91	1.86	0.37	0.15	3.29	2.70	0.37	0.08
FAM179A	0.09	0.24	0.51	0.29	0.07	0.24	3.29	2.42	0.13	0.11
C9orf172	0.36	0.62	2.31	0.84	0.61	1.09	3.27	4.28	1.20	0.74
PLB1	0.01	0.02	0.33	0.14	0.13	0.07	3.25	2.41	0.10	0.04
IL6R	0.76	0.30	0.72	0.90	0.37	0.12	3.16	2.42	0.59	0.47
PDZRN4	0.00	0.04	0.09	0.08	0.44	0.53	3.13	1.26	0.14	0.07
PRHOXNB	0.00	0.00	0.78	1.98	0.00	2.86	3.13	4.35	0.12	0.49
PCDH12	0.03	0.02	0.11	0.05	0.06	0.04	3.11	2.24	0.10	0.07
SOBP	0.95	2.00	1.01	0.78	0.60	1.18	3.06	2.70	0.50	0.41
OSBP2	0.84	0.82	0.26	0.35	0.23	0.17	2.89	1.61	0.24	0.16
PCDH20	0.17	0.23	0.48	0.44	0.56	0.81	2.77	1.21	0.35	0.08
SUCNR1	0.00	0.00	0.00	0.03	0.00	0.04	2.72	0.90	0.00	0.00
CAMK2A	0.01	0.09	0.53	0.18	0.32	0.34	2.71	2.59	0.88	0.63
TNFRSF1B	0.43	0.76	0.33	0.38	0.19	0.20	2.71	2.41	0.27	0.27
FAM78A	0.48	1.59	0.43	0.45	0.29	0.48	2.69	2.00	0.23	0.32
ATP8B4	0.03	0.49	0.51	0.96	0.62	0.25	2.67	1.87	1.01	0.42
TAL1	0.43	0.99	0.82	0.28	0.01	0.19	2.67	3.94	0.03	0.03
ERBB4	0.09	0.02	0.07	0.22	0.22	0.39	2.67	1.56	0.49	0.11
ARHGEF15	0.29	0.37	0.23	0.26	0.08	0.16	2.60	1.94	0.04	0.06
NDST3	0.03	0.08	0.39	0.76	0.31	0.17	2.47	1.50	0.47	0.14
HOXA11-AS	0.00	0.00	0.54	1.29	0.00	0.20	2.46	2.24	0.09	0.32
PTPRH	0.19	0.30	0.10	0.32	0.08	0.24	2.44	1.26	0.14	0.15
MLC1	0.01	0.03	0.11	0.06	0.11	0.02	2.36	1.73	0.05	0.19
SLITRK3	0.31	0.94	0.17	0.09	0.01	0.09	2.33	0.81	0.02	0.01
SYNE1	0.13	0.15	0.76	0.81	0.36	0.12	2.27	1.95	0.72	0.14
MS4A4A	0.00	0.00	0.00	0.00	0.07	0.07	2.26	0.96	0.00	0.08

SHE	0.05	0.18	0.14	0.28	0.06	0.08	2.17	1.98	0.06	0.04
MITF	0.17	0.06	0.63	0.81	0.49	0.63	2.13	1.39	0.64	0.29
GLYAT	0.00	0.00	0.48	0.21	0.13	0.17	2.12	1.72	0.18	0.12
DNASE1L3	0.00	0.00	0.29	0.13	0.00	0.07	2.01	0.87	0.11	0.00
PTGFR	0.02	0.08	0.11	0.18	0.03	0.00	1.99	0.99	0.11	0.04
MAST4	0.49	0.37	1.27	1.12	0.91	0.37	1.92	1.50	1.00	0.96
DCC	0.22	0.16	0.46	0.26	0.30	0.15	1.90	1.30	0.31	0.08
CACNA1A	0.79	1.89	0.46	0.18	0.76	0.98	1.87	1.54	0.70	0.39
AADAC	0.00	0.00	0.08	0.00	0.00	0.00	1.77	0.43	0.00	0.00
ADAMTSL1	0.59	0.74	0.06	0.05	0.03	0.07	1.76	0.77	0.08	0.03
SLCO2B1	0.00	0.00	0.17	0.13	0.14	0.15	1.67	0.97	0.15	0.21
OSR2	0.00	0.00	0.47	0.12	0.15	0.20	1.64	0.74	0.37	0.27
RALYL	0.00	0.00	0.39	0.63	0.37	0.67	1.61	0.84	0.48	0.34
MECOM	0.09	0.18	0.34	0.21	0.67	0.88	1.58	0.81	0.48	0.20
SLC8A3	0.02	0.21	0.15	0.34	0.15	0.09	1.57	1.69	0.06	0.12
CLEC12B	0.00	0.00	0.18	0.16	0.00	0.00	1.57	0.50	0.00	0.05
BCO2	0.05	0.03	0.50	0.42	0.20	0.41	1.55	0.97	0.35	0.17
NLRP1	0.06	0.02	0.12	0.07	0.23	0.06	1.54	0.48	0.37	0.20
CCRL2	0.00	0.00	0.05	0.03	0.00	0.00	1.46	0.52	0.00	0.00
PLEK2	0.00	0.00	0.20	0.03	0.07	0.43	1.43	1.12	0.23	0.21
TECRL	0.00	0.00	0.56	0.49	0.58	0.93	1.41	2.22	0.57	0.42
TBX5	0.03	0.00	0.00	0.00	0.29	1.27	1.41	0.72	0.50	0.22
ADAMTSL3	0.14	0.19	0.26	0.25	0.24	0.13	1.36	0.70	0.40	0.05
GRIA1	0.23	0.38	0.15	0.05	0.15	0.24	1.35	0.64	0.09	0.04
HOXD3	0.00	0.00	0.26	0.22	0.09	2.34	1.34	0.80	0.04	0.05
KRT24	0.00	0.00	0.00	0.00	0.00	0.00	1.31	0.27	0.00	0.00
IFIT2	0.00	0.00	0.19	0.36	0.00	0.03	1.28	0.40	0.05	0.03
CETP	0.00	0.00	0.00	0.00	0.00	0.00	1.23	0.38	0.00	0.04
PTPRB	0.21	0.03	0.19	0.10	0.06	0.02	1.17	0.61	0.07	0.01
RNASE13	0.00	0.00	0.24	0.19	0.00	0.00	1.10	0.35	0.09	0.04
LYST	0.02	0.04	0.18	0.35	0.24	0.08	1.09	0.45	0.37	0.08
MYBPH	0.00	0.00	0.27	0.27	0.06	0.37	1.04	0.79	0.05	0.07
GDF2	0.00	0.00	0.17	0.09	0.00	0.00	1.02	0.46	0.00	0.00
PRL	0.00	0.00	0.22	0.19	0.00	0.06	0.98	0.21	0.00	0.00
VAV1	0.16	0.12	0.00	0.00	0.00	0.02	0.93	0.70	0.02	0.02
LOC100505495	0.00	0.00	0.02	0.00	0.00	0.02	0.86	0.41	0.01	0.02
ABCG1	0.07	0.07	0.20	0.21	0.07	0.14	0.86	0.32	0.09	0.02
CYP2E1	0.00	0.00	0.23	0.08	0.13	0.29	0.85	0.21	0.20	0.15
TSHZ2	0.03	0.13	0.09	0.04	0.46	0.74	0.83	0.32	0.40	0.31
CIDEC	0.00	0.00	0.32	0.08	0.05	0.20	0.79	0.23	0.04	0.11
CSF2RB	0.00	0.00	0.03	0.04	0.13	0.02	0.78	0.33	0.14	0.08
GIMAP6	0.00	0.00	0.07	0.16	0.01	0.00	0.75	0.29	0.00	0.00

EVX2	0.00	0.00	0.16	0.22	0.00	0.15	0.70	0.35	0.03	0.04
BANK1	0.04	0.00	0.00	0.00	0.00	0.02	0.69	0.28	0.06	0.02
TYROBP	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.71	0.11	0.14
GRIA2	0.00	0.00	0.01	0.00	0.00	0.00	0.67	0.21	0.04	0.00
EMCN	0.00	0.00	0.01	0.00	0.04	0.10	0.65	0.34	0.06	0.03
CD69	0.10	0.00	0.00	0.00	0.03	0.00	0.64	0.49	0.00	0.00
CSMD1	0.00	0.01	0.05	0.05	0.02	0.01	0.63	0.33	0.05	0.01
HOXD-AS2	0.00	0.00	0.15	0.15	0.00	1.32	0.60	0.99	0.17	0.43
IL1RN	0.00	0.00	0.12	0.00	0.00	0.00	0.59	0.25	0.00	0.07

Table S4. Primers for Genomic DNA PCR to confirm 2A-mTomato knock-in.

Aim	**Forward primer**	**Reverse primer**	T_m
Test positive integration	gctccagactgccttgggaaa	gaagaagaaattgccaactgaca	60
Test random integration	cgagcggctggacctggcta	gtctccttccgtgtttcagttag	60
Confirmation of PGK-puro removal	gggcgacgtgctggctctgt	catgaactctttgatgacctcct	60
Confirmation of homozygote	cccgccgtggattcaaagggt	tccatagagggtaaaggacgctt	60

Table S5. Primers for WNT5A promoter cloning and E-box A motif mutation.

Primer name	**Purpose**	**Forward primer**	**Reverse primer**	T_m
WNT5A-promoter	WNT5A promoter cloning	ccgagctcttacgcgtgcaggggctatgggcgatgca	ccaagcttacttagatcgcagcaactcctgggcttaatattc	60
WNT5A-ΔE-box A	WNT5A E-box A deletion	ccgagctcttacgcgtgcaggggctatgggcgatgca	ccaagcttacttagatcgcacgtgagttttttgatggcaagat	60
Overlap-1	WNT5A E-box A point mutation	ccgagctcttacgcgtgcaggggctatgggcgatgca	tctggagagggaagaaaggagtggatgtttattgcctctc	60
Overlap-2	WNT5A E-box A point mutation	gagaggcaataaacatccactcctttcttccctctccaga	ccaagcttacttagatcgcagcaactcctgggcttaatattc	60

Supplementary Videos

Movie S1. MESP1-mTomato cells emerging and migrating together.

MESP1-mTomato$^+$ cells first appeared in a scattered manner, then migrated actively, displayed stronger red fluorescence, and converged together to form bigger cell clumps.

Movie S2. Beating cardiac tissues differentiated from MESP1-mTomato reporter cells.

MESP1-mTomato reporter cells were induced with 12 μmol/L CHIR for 24 h. 48 h after CHIR removal, 5 μmol/L IWP2 was added for 48 h. After IWP2 removal, cells were cultured in RPMI-1640 / B-27 minus insulin medium for another 2 days before switching to RPMI-1640 / B-27 medium until day 12. Time-lapse movie of beating cardiomyocytes was recorded on day 12.

Movie S3. Calcium transient in beating foci from MESP1-mTomato reporter cells.

After 12 days of differentiation, MESP1-mTomato reporter cells derived cardiomyocytes were incubated with 10 μmol/L Fluo-4 AM. Calcium transients were recorded by time-lapse imaging.

Movie S4. Calcium transient after Isoproterenol treatment.

Isoproterenol (5 μmol/L) was added to MESP1-mTomato reporter cells derived cardiomyocytes filmed above, Calcium transients were recorded by time-lapse imaging.