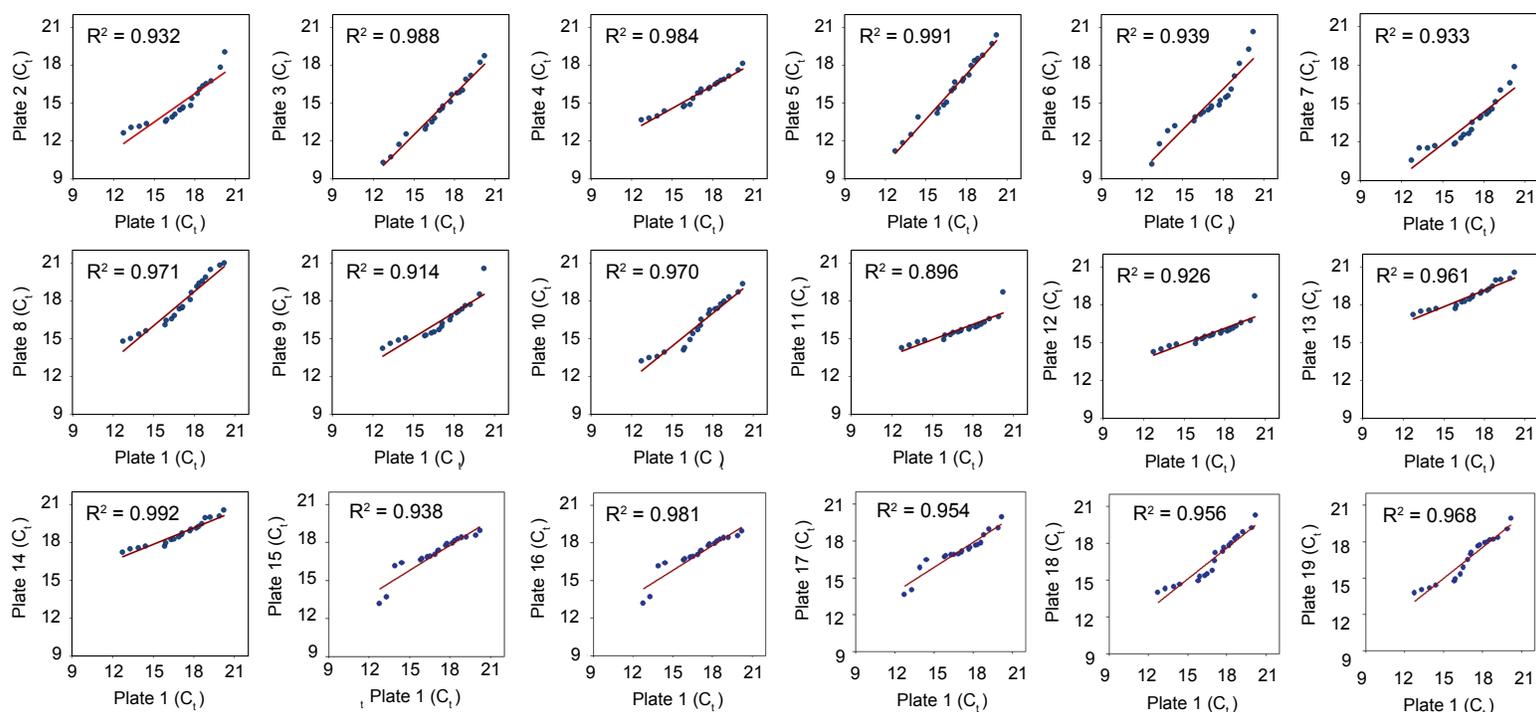


**Figure S1 - Relative expression of lineage markers in single ES cell and cardiomyocyte by real-time quantitative PCR analysis.** Single ES cell (red) and cardiomyocyte (blue) were lysed and reverse transcribed into cDNA and then PCR amplified using primers for the indicated ES cell (Pou5f1) and cardiomyocyte (Nkx2-5, Tnni3) genes. GAPDH expression in each single cell served as a control for cell quality and RNA input. Data represents two independent experiments performed in three replicates.

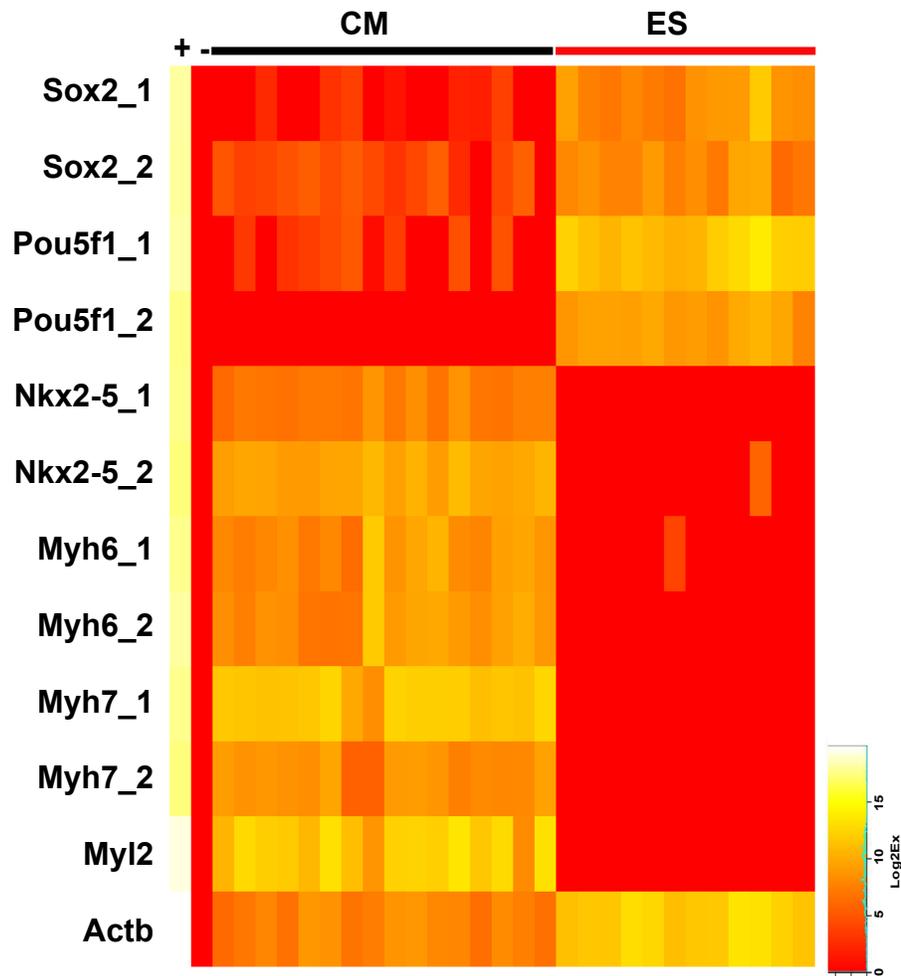
**A**



**B**

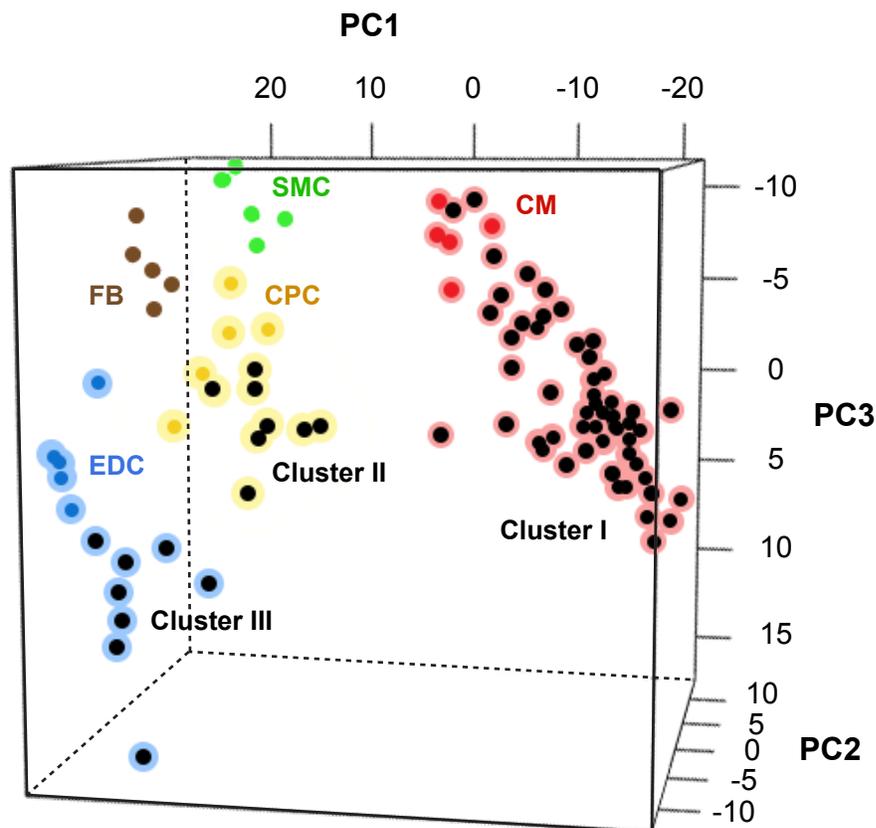
Plate	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
1	1	0.932	0.988	0.984	0.991	0.939	0.933	0.971	0.914	0.970	0.896	0.926	0.961	0.992	0.938	0.981	0.954	0.956	0.968	
2		1	0.962	0.966	0.953	0.967	0.990	0.972	0.990	0.959	0.958	0.953	0.979	0.951	0.82	0.941	0.9	0.973	0.95	
3			1	0.990	0.994	0.968	0.965	0.982	0.948	0.979	0.927	0.946	0.980	0.995	0.927	0.978	0.964	0.972	0.974	
4				1	0.992	0.948	0.966	0.984	0.951	0.991	0.929	0.956	0.982	0.990	0.895	0.975	0.93	0.984	0.991	
5					1	0.950	0.953	0.979	0.937	0.980	0.914	0.946	0.976	0.994	0.93	0.983	0.954	0.974	0.978	
6						1	0.975	0.941	0.964	0.924	0.958	0.901	0.957	0.955	0.877	0.919	0.961	0.934	0.912	
7							1	0.969	0.984	0.964	0.957	0.962	0.984	0.956	0.828	0.94	0.909	0.977	0.952	
8								1	0.945	0.986	0.901	0.975	0.988	0.981	0.876	0.988	0.914	0.986	0.974	
9									1	0.942	0.982	0.937	0.962	0.932	0.817	0.918	0.9	0.962	0.939	
10										1	0.907	0.977	0.986	0.980	0.873	0.979	0.899	0.991	0.995	
11											1	0.877	0.932	0.914	0.812	0.874	0.906	0.923	0.909	
12												1	0.970	0.940	0.83	0.968	0.86	0.987	0.963	
13													1	0.978	0.862	0.973	0.917	0.989	0.973	
14														1	0.921	0.98	0.956	0.97	0.973	
15															1	0.914	0.965	0.858	0.874	
16																1	0.926	0.976	0.968	
17																	1	0.898	0.892	
18																		1	0.984	
19																				1

**Figure S2 - Quality control of single cell expression data among different Fluidigm® arrays.** (A) Quantile-Quantile plots of the housekeeping gene Beta-Actin between plate 1 and the other 18 plates. (B) A table of Pearson correlation coefficient for Beta-actin expression among the nineteen plates.



**Figure S3 - Confirmation of single ES cell and cardiomyocyte gene expression using independent primers.** Single ES cells (ES) or embryo derived cardiomyocytes (CM) were isolated and reverse transcribed into cDNA and amplified on the Fluidigm platform using primers targeting ES cell genes (Sox2 and Pou5f1) and cardiomyocytes genes (Nkx2-5, Myh6, Myh7). Note the selective expression of Sox2 and Pou5f1 in single ES cells and Nkx2-5, Myh6, Myh7 in cardiomyocytes. Data represents the results from two independent experiments.

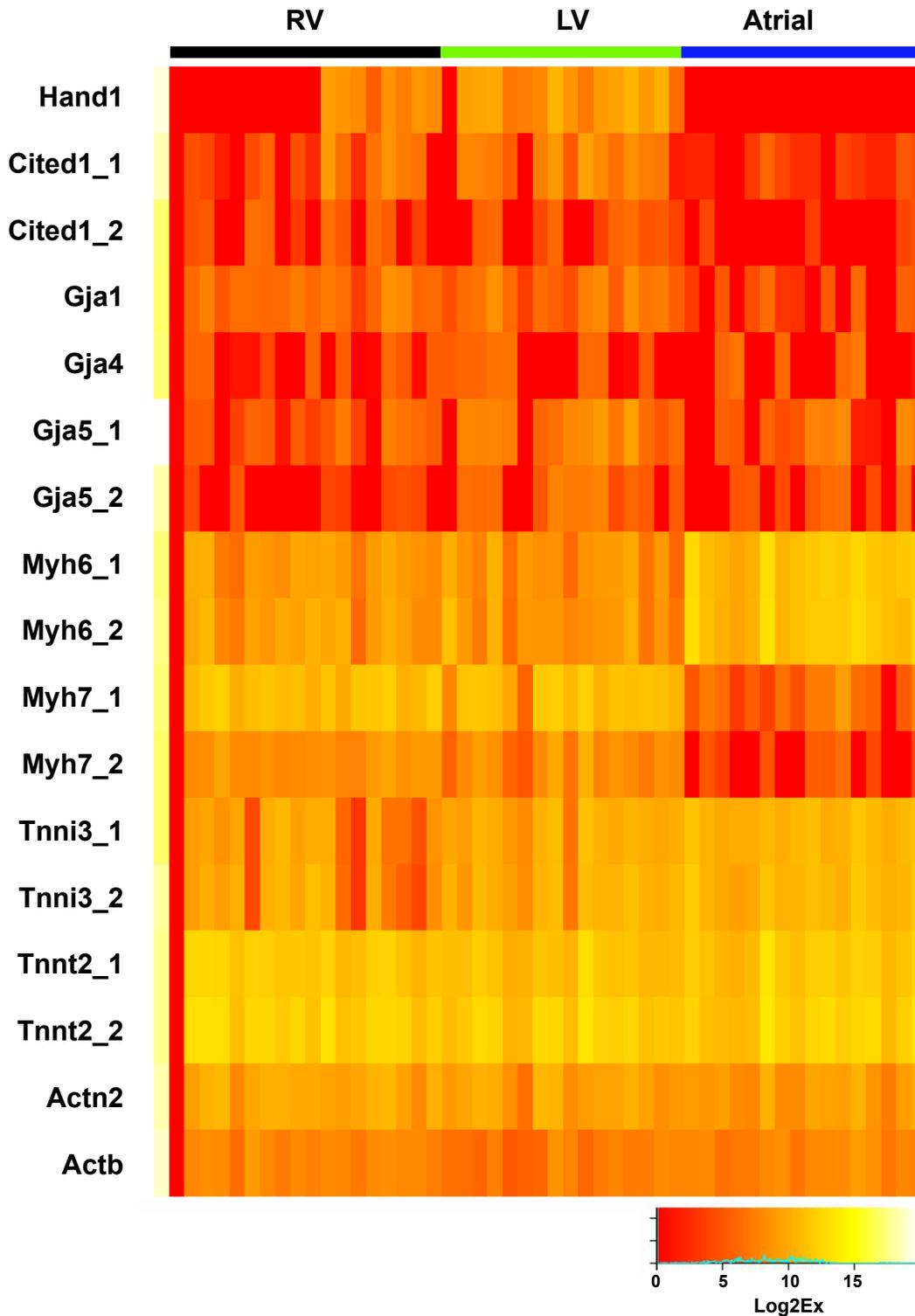
A



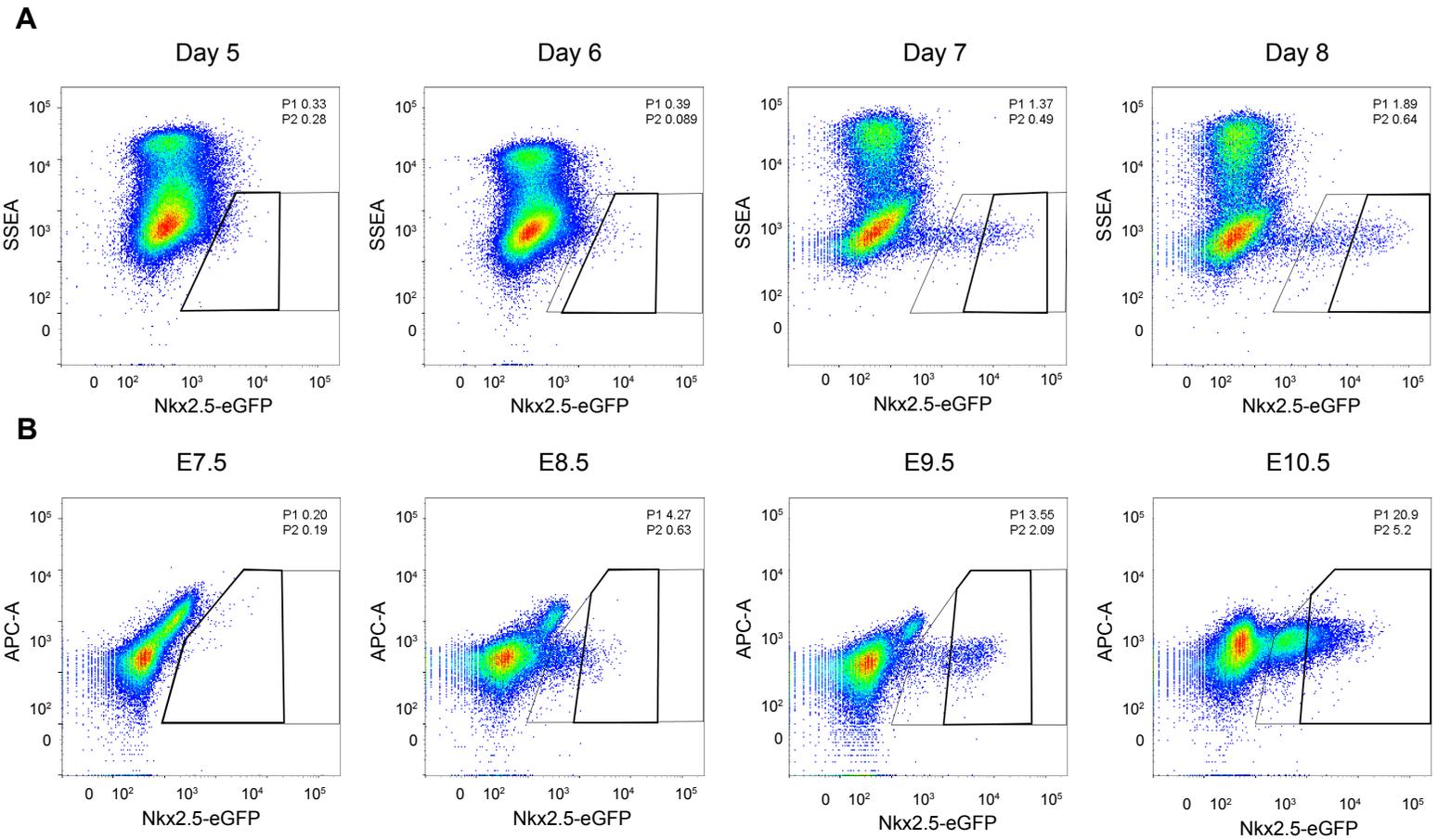
B

	Cluster I	CM	Cluster II	CPC	SMC	Cluster III	EDC	FB
Cluster I	0.839	0.737	0.297	0.024	0.147	-0.028	-0.119	0.156
CM		0.928	0.098	-0.109	-0.116	-0.127	-0.181	0.016
Cluster II			0.844	0.576	0.512	0.531	0.428	0.676
CPC				0.868	0.544	0.436	0.435	0.632
SMC					0.913	0.325	0.372	0.637
Cluster III						0.785	0.786	0.584
EDC							0.941	0.617
FB								0.895

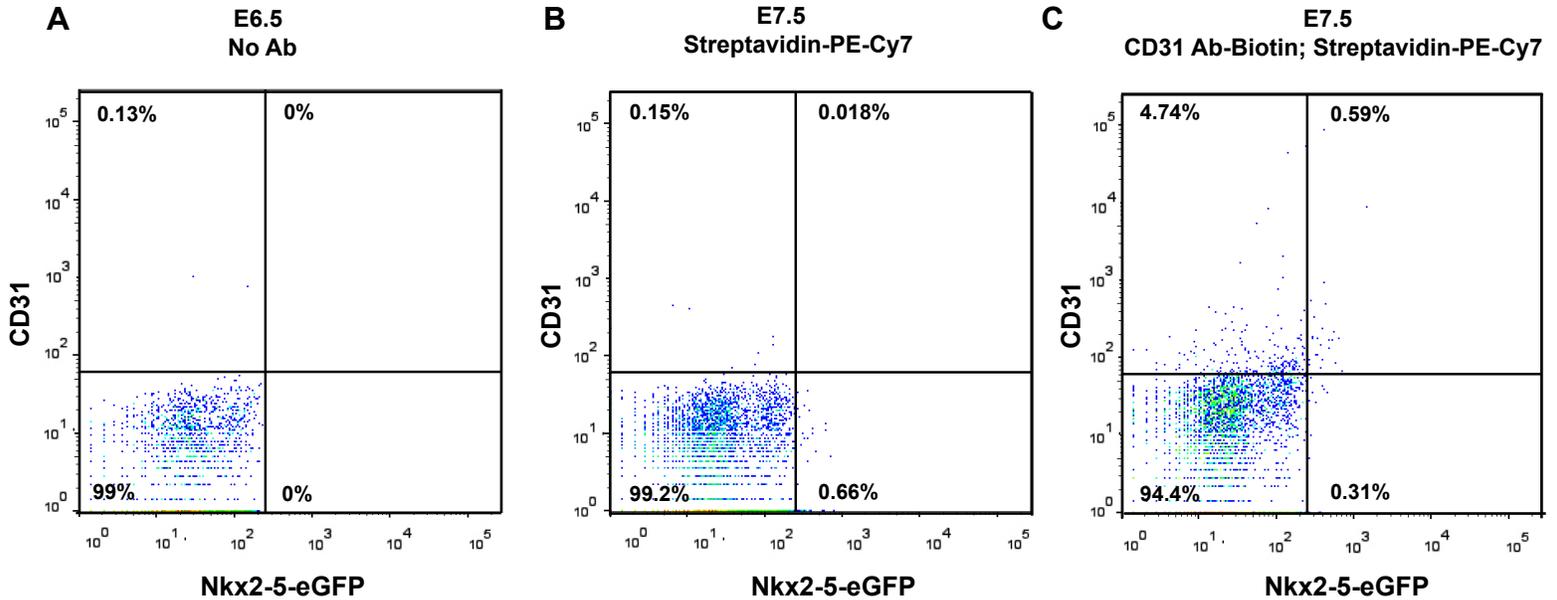
**Figure S4 - Bioinformatic analysis of single cells from day 10.5 embryonic mouse heart.** (A) A three-dimensional PCA plot of all single cells derived from a day 10.5 embryonic mouse heart (black dot) along with standard cardiomyocytes (CM) (red dot), smooth muscle cells (SMC) (green dot), cardiac progenitor cells (CPC) (yellow dot), fibroblasts (FB) (brown dot), and endothelial cells (EDC) (blue dot). Note that cells in Cluster I associates closest with CM and Cluster III with EDC. Cluster II appears to sit between CPC and CM. (B) A table of Pearson correlation coefficients of gene expression between each cell cluster in day 10.5 embryonic heart and standard cells. Data represents combined results from two independent experiments.



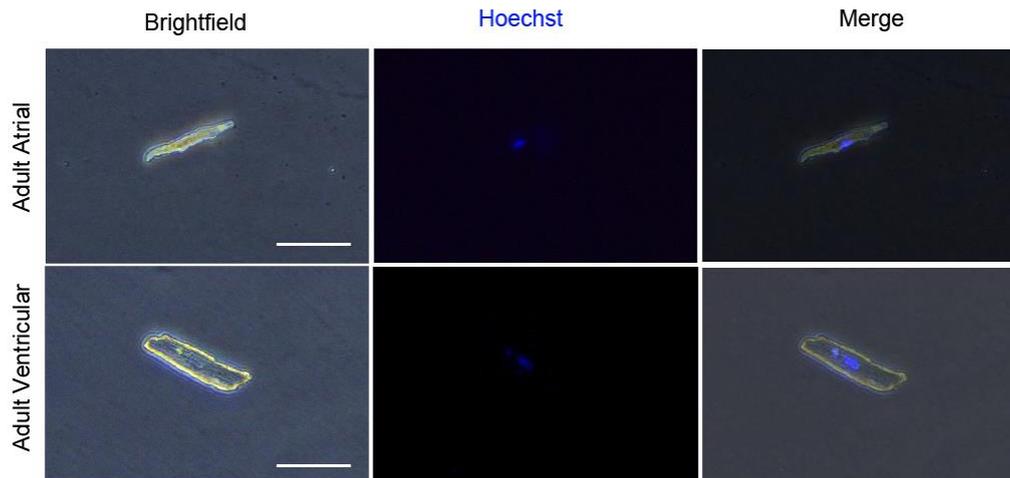
**Figure S5 - Analysis of chamber-specific cardiomyocyte gene expression by single cell Fluidigm assays.** Atrial, right, and left ventricular cardiomyocytes from e10.5 embryonic hearts were isolated as single cells and the mRNA in cell lysate was reverse transcribed using primers targeting the indicated genes. The heatmap shown represents expression of each indicated gene following amplification on the Fluidigm platform. Data represents the results from two independent experiments.



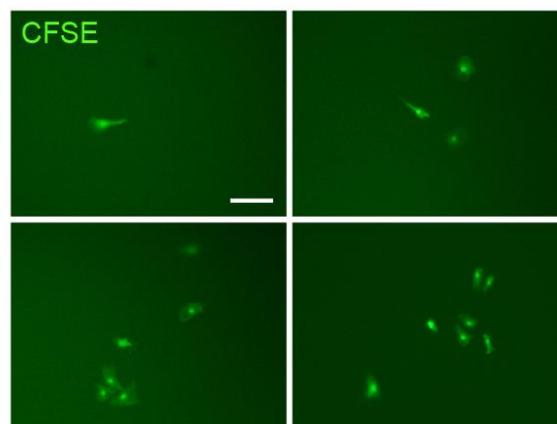
**Figure S6 - Representative FACS plots used to isolate single eGFP+ cells from in vitro differentiated Nkx2-5-eGFP ES cells and transgenic embryos.** Gate 1 (P1) represents fixed gates for the analysis of the percentage of all eGFP+ cells and Gate 2 (P2) represents dynamic gates for sorting the most mature eGFP+ cells at the indicated time point of ES cell in vitro differentiation (A) or transgenic embryo development (B).



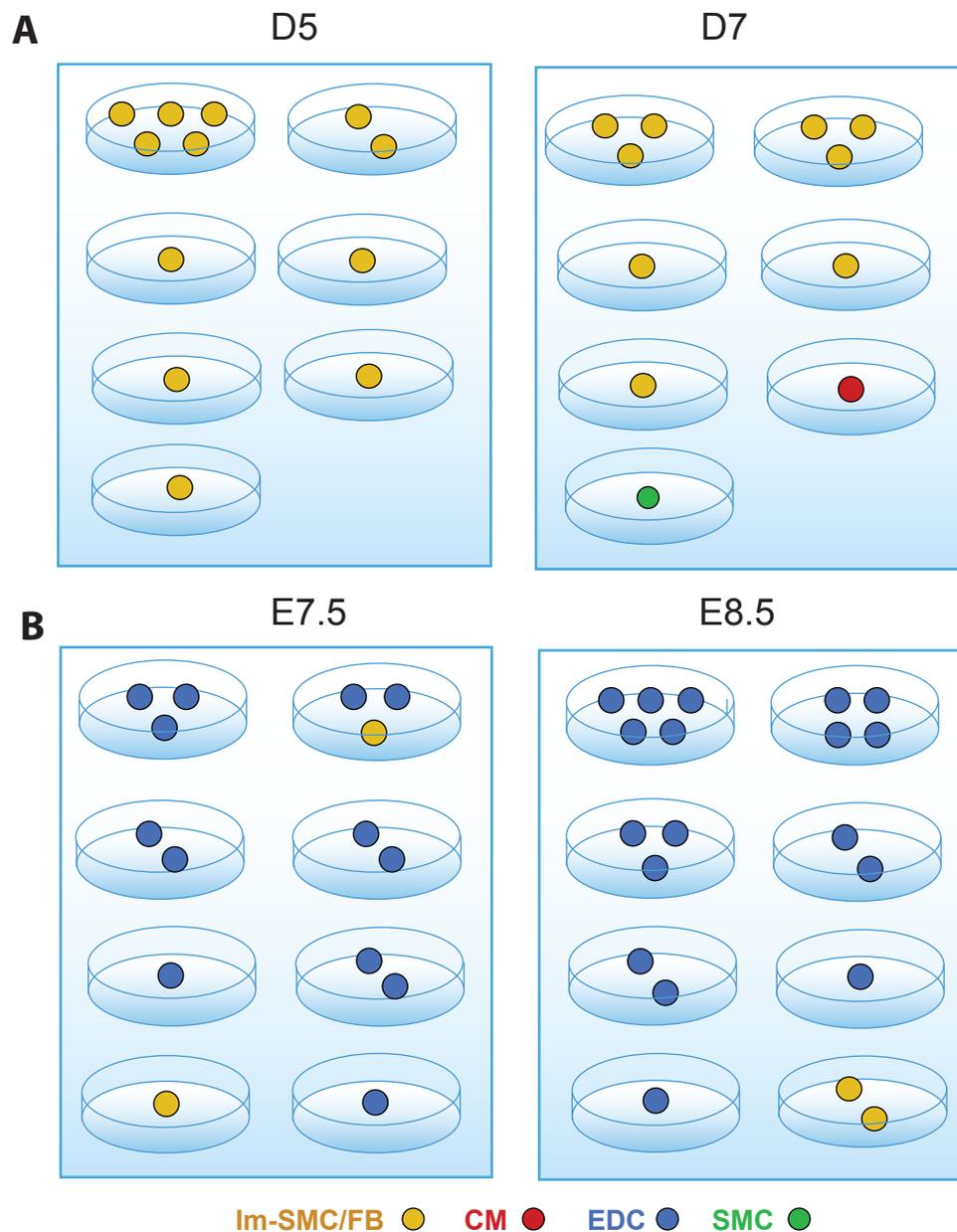
**Figure S7 - Flow cytometric analysis of endothelial marker PECAM/CD31 expression in Nkx2-5-eGFP transgenic mouse embryos.** (A) Cells from day 6.5 Nkx2-5-eGFP transgenic mouse embryos without antibody staining. Note the absence of eGFP+ cells. (B) Cells from day 7.5 Nkx2-5-eGFP transgenic mouse embryos stained with Streptavidin conjugated with PE-Cy7. (C) Same cells as (B) except that biotin conjugated anti-CD31 antibody was used. Note the expression of CD31 in a significant proportion of eGFP+ cells at embryonic day 7.5. Data represents the results of two independent experiments.



**Figure S8 - Single adult atrial and ventricular cardiomyocytes derived from 3-months old mouse hearts.** Representative bright field (left panel), fluorescence (middle panel), and merged (right panel) images of single cardiomyocytes from atria (upper panels) and ventricles (lower panels) stained with Hoechst 33342 are shown. Bar =200  $\mu$ M.



**Figure S9 - CFSE-stained progenies derived from single CPC after 5 days of in vitro culturing.** Cells in each well of a 96-well plate were treated with CFSE and imaged in 510 nm bandpass filter to highlight the location of the progenies from each single CPC after 5 days of in vitro culturing. Bar=200  $\mu$ m.



**Figure S10 - Determination of lineage decisions by single CPCs during in vitro differentiation in endothelial cell (EDC) medium.** Single eGFP<sup>+</sup> cell isolated by FACS from in vitro differentiated Nkx2.5-eGFP ES cells (A) or transgenic embryo (B) at the indicated day of differentiation or development is cultured in each well of 96-well plate in EDC medium for 5 days. After culturing, cell progenies are isolated and profiled on the Fluidigm assay to determine the exact cell identity. The color of each circle presents the identity of each progeny cell and number of circles represents the number of progeny cells from each starting single cell. The data shown represents all surviving cells from two independent experiments.

**Table S1.** TaqMan primers used for single-cell real-time qPCR

Gene	TaqMan primer
Gapdh	Mm99999915_g1
Pou5f1	Mm03053917_g1
Nkx2.5_2	Mm00657783_m1
Tnni3_1	Mm00437164_m1

**Table S2.** Fluidigm array TaqMan primers

Gene	TaqMan primer	Gene	TaqMan primer
Actb	Mm01205647_g1	Myh6_1	Mm00440354_m1
Actn2	Mm00473657_m1	Myh7_2	Mm01319006_g1
Cdh5	Mm00486938_m1	Myh7_1	Mm00600555_m1
Calponin-1	Mm00487032_m1	Myl2	Mm00440384_m1
Calponin-2	Mm01169510_m1	Nkx2.5_2	Mm00657783_m1
Fn1	Mm01256744_m1	Nkx2.5_1	Mm01309813_s1
Gata4_2	Mm00484689_m1	Pdgfra	Mm00440701_m1
Gata4_1	Mm01310447_m1	Pecam1	Mm00476702_m1
Hand1	Mm00433931_m1	Pou5f1	Mm03053917_g1
Hand2	Mm00439247_m1	Sarcolipin	Mm00481536_m1
Hcn4	Mm01176086_m1	Sox2	Mm03053810_s1
Isl1_1	Mm00627860_m1	Sm22a	Mm00441661_g1
Isl1_2	Mm00517585_m1	Tbx1	Mm00448948_m1
Flk1	Mm01222421_m1	Tbx5	Mm00803518_m1
Kit_2	Mm00442972_m1	Tnni3_1	Mm00437164_m1
Kit_1	Mm00445212_m1	Tnni3_2	Mm01330976_m1
Mef2C_2	Mm01340839_m1	Tnnt2_2	Mm01290256_m1
Mef2C_1	Mm01340842_m1	Tnnt2_1	Mm00441920_m1
Mesp1	Mm00801883_g1	Vcam1	Mm01320970_m1
Myh11	Mm00443013_m1	Vim	Mm01333430_m1
Myh6_2	Mm00440359_m1	Vwf	Mm00550376_m1

**Table S3.** Independent TaqMan primers used for confirmation of single ESC gene expression.

Gene	TaqMan primer	Gene	TaqMan primer
Pou5f1_1	Mm03053917_g1	Sox2_1	Mm03053810_s1
Pou5f1_1	Mm00658129_gH	Sox2_2	Mm00488369_s1

**Table S4.** Pearson correlation values for standard cells in reference panel (Figure 1)

	CPC	CM	SMC	FB	EDC	ES
CPC	0.868	-0.109	0.544	0.632	0.435	0.511
CM		0.928	-0.116	0.016	-0.181	-0.053
SMC			0.913	0.637	0.372	0.435
FB				0.895	0.617	0.718
EDC					0.941	0.579
ES						0.925

**Table S5.** TaqMan primers used for characterizing specific chamber derived cardiomyocytes

Gene	TaqMan primer	Gene	TaqMan primer
Cited1_1	Mm01235642_g1	Gja4	Mm00433610_s1
Cited1_2	Mm04207352_m1	Gja5_1	Mm00433619_s1
Gja1	Mm01179639_s1	Gja5_2	Mm01265686_m1

**Table S6.** TaqMan primers used for characterizing cardiomyocyte populations

Gene	TaqMan primer	Gene	TaqMan primer
Hand2	Mm00439247_m1	Tnni3_2	Mm01330976_m1
Mef2C_1	Mm01340842_m1	Tnnt2_2	Mm01290256_m1
Myh6_1	Mm00440354_m1	Gata4_1	Mm01310447_m1
Myh7_1	Mm00600555_m1	Myl2	Mm00440384_m1
Sarcolipin	Mm00481536_m1		

**Table S7.** Number of cells analyzed in each single cell experiment

**A.** Standard cells reference panel (Figure 1)

Cell Type	Count
CPC	26
CM	23
SMC	25
FB	25
EDC	25
ES	27

**B.** Comparison of mESC and embryo-derived eGFP<sup>+</sup> cells (Figure 3)

Source	Time Point	Count
EB	D5	26
	D6	30
	D7	21
	D8	22
Embryo	E7.5	27
	E8.5	15
	E9.5	12
	E10.5	31

**C.** Comparison of *in vivo* neonatal and adult CMs and *in vitro* mESC-derived CMs (Figure 4)

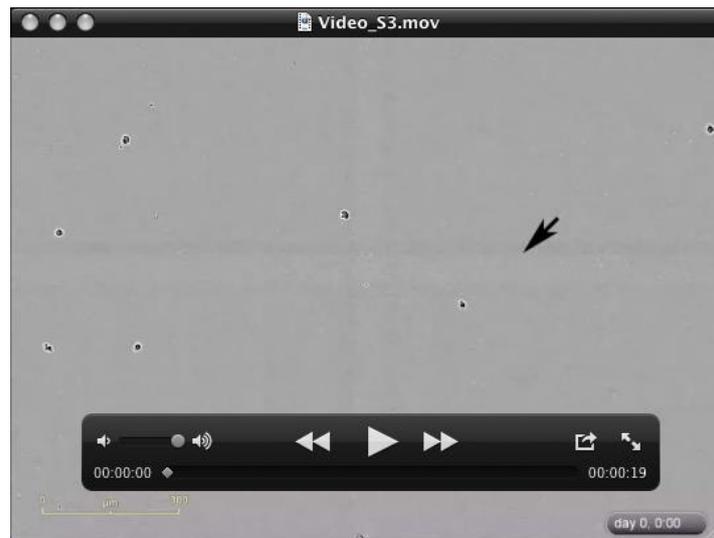
Source	Time Point	Count
mESC	D23	20
	D29	21
Mouse heart	Neonatal Atrial	16
	Neonatal Ventricular	17
	Adult Atrial	20
	Adult Ventricular	19



**Supplementary Movie 1** - Beating single atrial cardiomyocyte from 3 month old adult mouse.



**Supplementary Movie 2** - Beating single ventricular cardiomyocyte from 3 month old adult mouse.



**Supplementary Movie 3** – Time-lapse video microscopy of Nkx2-5-eGFP+ CPCs from day 6 in vitro differentiated mESCs. FACS-purified eGFP+ cells were imaged every hour with incuCyte system (Essen BioScience) for 5 days.