Table S1. Descriptive statistics of values (%) used for proliferation analysis of iPSCs.

	hiPSC1	hiPSC2	RhiPSC1	RhiPSC2
Number of values	30	30	30	28
Minimum	39,68	43,33	36,84	42,31
Maximum	81,93	89,58	92,31	85,42
Range	42,25	46,25	55,47	43,11
Mean	63,48	62,08	66,94	62,60
Std. Deviation	11,76	12,33	15,84	12,28
Std. Error of Mean	2,148	2,251	2,891	2,321

Table S2. Percentage of cTNT-positive cells of hiPSC1 cell line after differentiation before selection. Four independent experiments were used for each group of cell seeding numbers.

Number of seeded cells/well	#1 (%)	#2 (%)	#3 (%)	#4(%)
150,000	45,43	44,42	37,22	40,32
200,000	50,25	52,93	60,82	50,21
250,000	59,26	50,73	63,56	56,56
300,000	75,89	79,02	70,46	79,39
350,000	71,06	66,28	73,99	69,16

Table S3. Percentage of cTNT-positive cells of hiPSC2 cell line after differentiation before selection. Three to four independent experiments were used for each group of cell seeding numbers.

Number of seeded cells/well	#1 (%)	#2 (%)	#3 (%)	#4(%)
40,000	23,27	26,99	30,88	26,8
50,000	31,8	30,54	36,73	
60,000	69,56	79,45	81,7	
70,000	75,48	79,07	74,51	77,03
80,000	73,72	78,32	75,12	
90,000	72,54	70,06	75,65	67,82

Table S4. Percentage of cTNT-positive cells of RhiPSC1 cell line after differentiation before selection. Three to four independent experiments were used for each group of cell seeding numbers.

Number of seeded cells/well	#1 (%)	#2 (%)	#3 (%)	#4(%)
80,000	44,56	37,71	33,54	44,04
100,000	42,74	50,57	56,5	36,13
120,000	60,69	56,96	62,9	51,23
140,000	52,68	51,24	65,88	55,38
160,000	20,28	11,65	38,4	
180,000	25,75	13,04	23,45	

Table S5. Percentage of cTNT-positive cells of RhiPSC2 cell line after differentiation before selection. Three to four independent experiments were used for each group of cell seeding numbers.

Number of seeded cells/well	#1 (%)	#2 (%)	#3 (%)	#4(%)
70,000	35,74	40,4	39,6	30,1
90,000	61,89	65,86	66,17	65,37
110,000	27,46	17,21	27,46	
130,000	4,89	5,48	8,11	
150,000	13,2	16,8	2,51	

Table S6. Percentage of cTNT-positive cells in hiPSC1, hiPSC2, RhiPSC1, and RhiPSC2 after metabolic selection. Three independent experiments were used for each group.

Cell line	#1 (%)	#2 (%)	#3 (%)
hiPSC1	97,65	97,04	97,72
hiPSC2	74,66	72,09	70,03
RhiPSC1	82,44	86,16	92,99
RhiPSC2	95,71	95,21	96,13

Figure S1

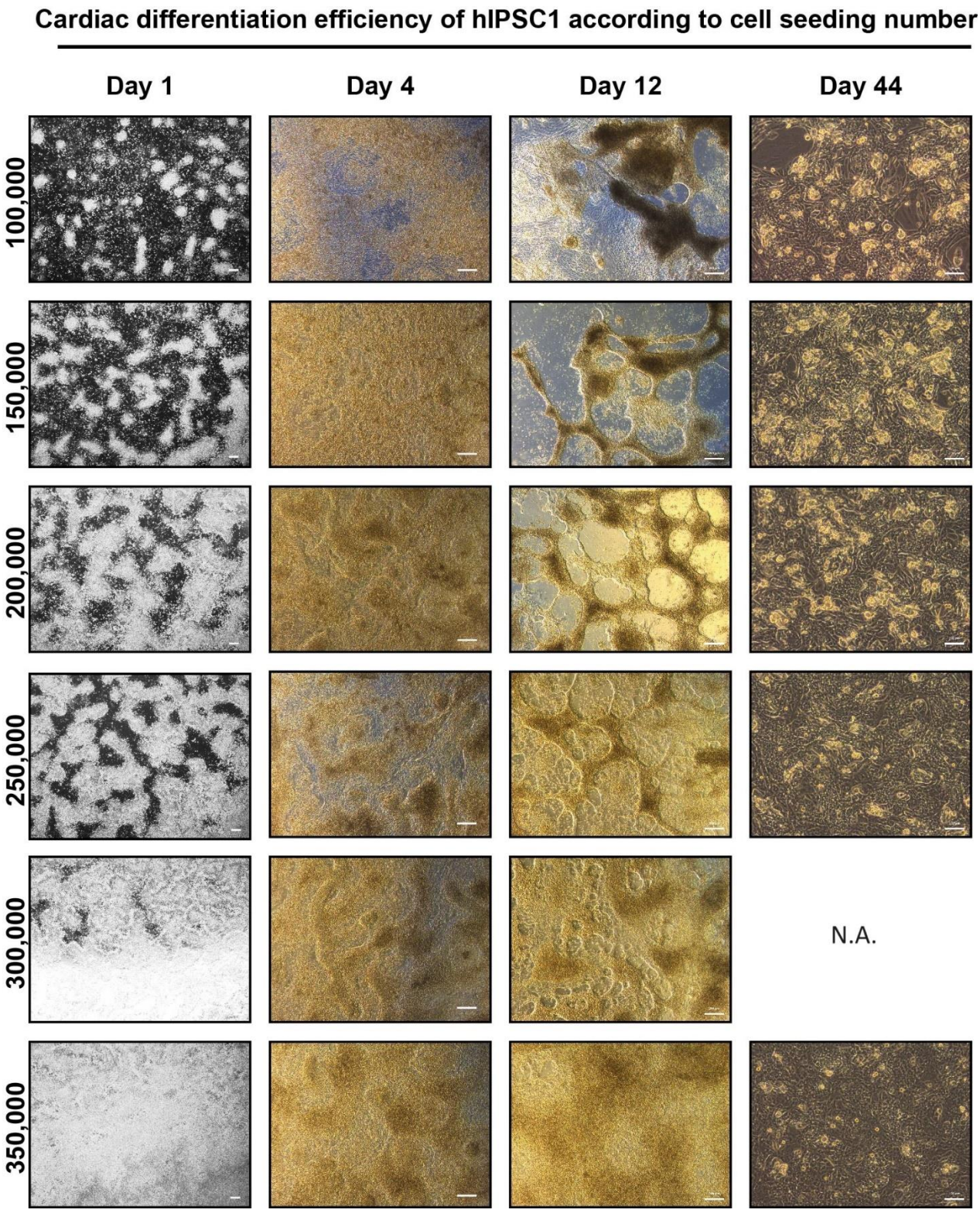

Figure S1: Overview of the morphology of the hiPSC1 line at day 1, 4, 12 and 44 of differentiation into cardiomyocytes depending on the cell seeding density. Scale bars represent X μm. N.A., no image available.

Figure S2

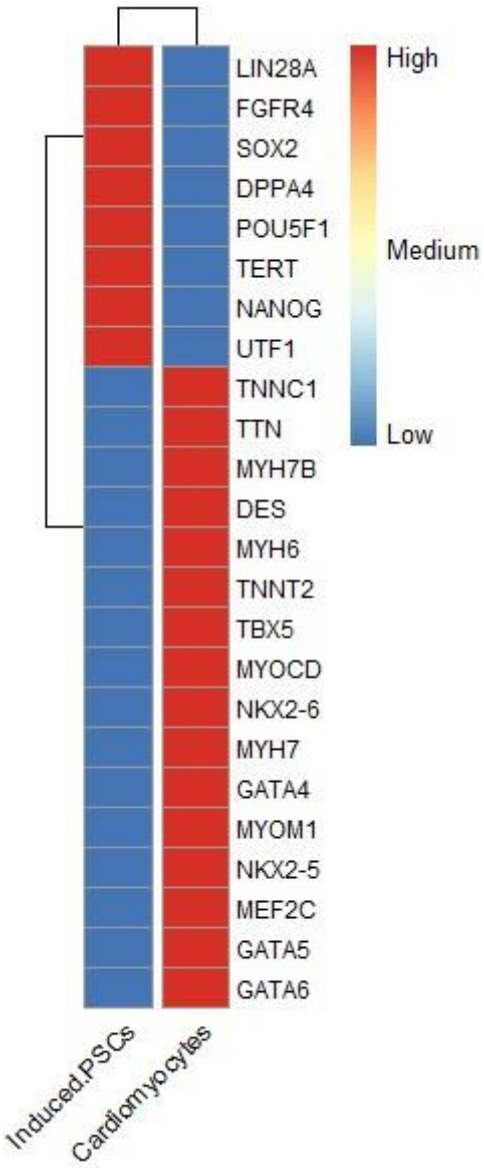

Figure S2: Expression of a selected set of pluripotent stem cell and cardiomyocyte markers in hiPSC1 and in cardiomyocytes derived from hiPSC1.