TABLES
Supplemental Table 1. Antibodies.

Reagent	Manufacturer	Catalog No.	Туре	Dilution	
Primary Antibodies					
Anti-Vimentin	Abcam	ab92547	Rabbit	1:500	
antibody			monoclonal		
Anti-Fibroblasts	Millipore	CBL271	Mouse	1:100	
Antibody, clone			monoclonal		
TE-7					
Anti-Tra-1-60	Abcam	ab16288	Mouse	1:100	
antibody			monoclonal		
	R&D Systems	BBA10	Mouse	1:100	
Pan Specific			monoclonal		
Antibody					
Anti-Oct4	Abcam	ab19857	Rabbit	1:100	
antibody			monoclonal		
Anti-Nanog	Abcam	ab109250	Rabbit	1:100	
antibody			monoclonal		
Anti-SOX2	Abcam	ab97959	Rabbit	1:100	
antibody			monoclonal		
Anti-SSEA4	Abcam	ab16287	Mouse	1:100	
antibody			monoclonal		
Secondary Antibodies					
Cy3 AffiniPure		711-165-152	Donkey	1:200	
•	ImmunoResearch		monoclonal		
Rabbit IgG					
Cy5 AffiniPure		715-175-150	Donkey	1:200	
•	ImmunoResearch		monoclonal		
Mouse IgG					
Fluorescein	Jackson	715-095-150	Donkey	1:200	
•	ImmunoResearch		monoclonal		
Donkey Anti-					
Mouse IgG		705 005 000		4.000	
	Jackson	705-095-003	Donkey	1:200	
` ,	ImmunoResearch		monoclonal		
Donkey Anti-Goat					
IgG	la alsa sa	705 545 000	Danila	1.000	
Alexa Fluor 488	Jackson	705-545-003	Donkey	1:200	
AffiniPure Donkey	ImmunoResearch		monoclonal		
Anti-Goat IgG					

**Supplemental Table 2. Primers for quantitative RT-PCR.** 

Standard	Forward 5'-3'	Reverse 5'-3'
gene		
name		
OCT4	CAGTGCCCGAAACCCACAC	GGAGACCCAGCAGCCTCAAA
Nanog	TACCTCAGCCTCCAGCAGAT	CTTCTGCGTCACACCATTGC
SOX2	TGGACAGTTACGCGCACAT	CGAGTAGGACATGCTGTAGG T
Brachyury	TGCTTCCCTGAGACCCAGT T	GATCACTTCTTTCCTTTGCAT CAAG
MESP1	GAAGTGGTTCCTTGGCAGA C	TCCTGCTTGCCTCAAAGTGT
GATA4	TGCCGTTCATCTTGTGGTA G	CCGACACCCCAATCTCG
NKX2.5	CAAGTGTGCGTCTGCCTTT	CAGCTCTTTCTTTTCGGCTCT A

**Supplemental Table 3.** The mapping quality of bulk-RNAseq data (12 samples of AiPSC, ViPSC, AiPSC-CM, and ViPSC-CM groups) was reported by the STAR pipeline.

**Supplemental Table 4:** the data origin and characteristics of the iPSC and iPSC-CM cell lines, in which Bulk-RNAseq data were integrated and analyzed.

**Supplemental Table 5**: The statistics of 1081 differentially expressed genes comparing between cardiac-tissue-derived iPSC-CM (AiPSC-CM/ViPSC-CM) and skin-tissue-derived iPSC-CM (S-D30iPSC-CM/S-D90iPSC-CM). Deseq2 pipeline was used to normalize gene expression. For statistical significance, the fold-change and non-parametric tests were applied.

**Supplemental Table 6**: The statistics of 124 differentially expressed genes comparing between AiPSC-CM and ViPSC-CM. The gene expression was normalized using Deseq2 pipeline, then fold-change and non-parametric tests was applied for statistical significance.