

Figure S1

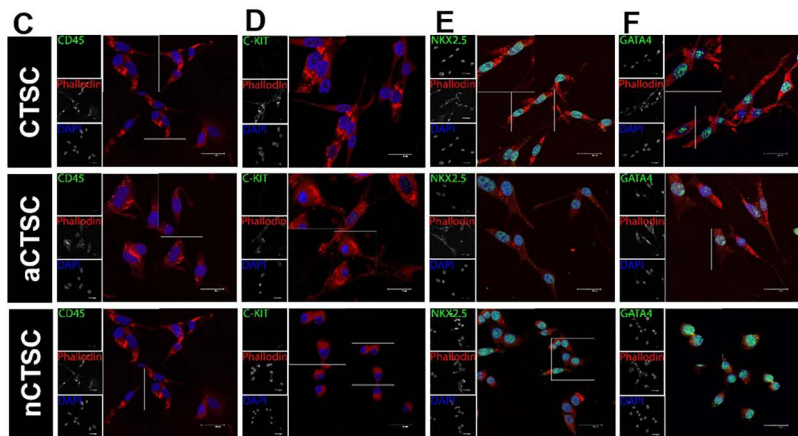
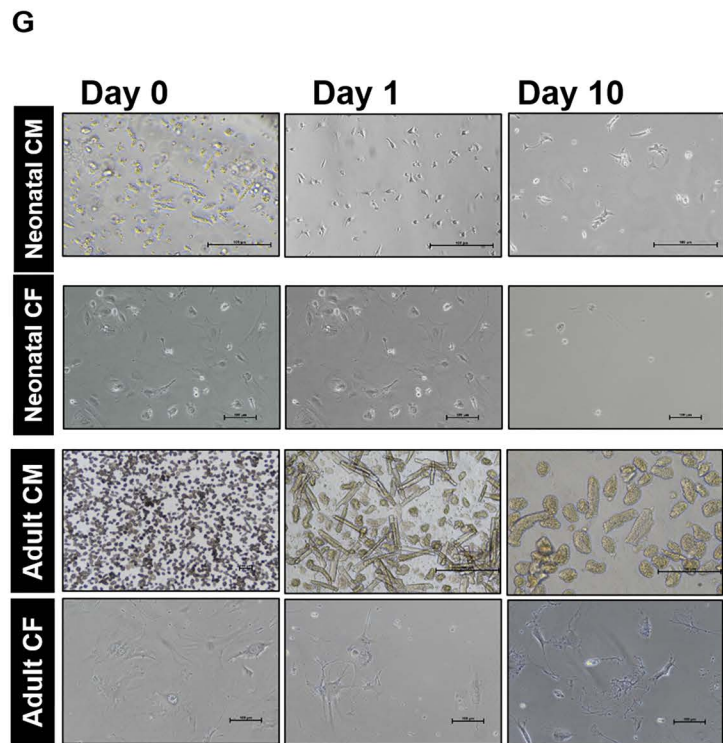
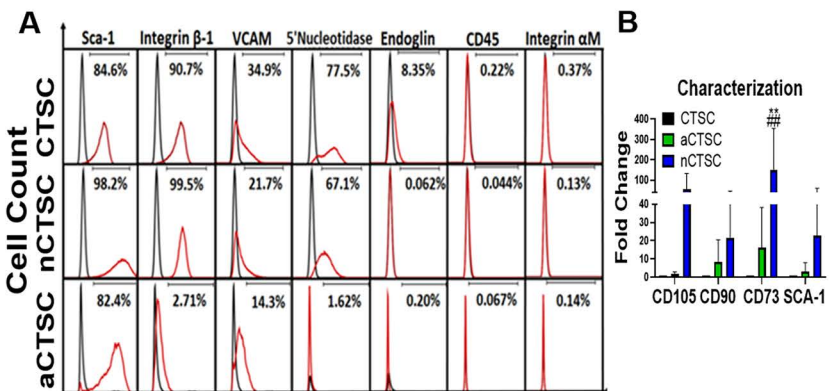


Figure S2

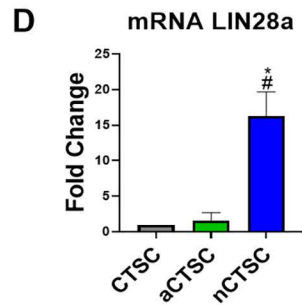
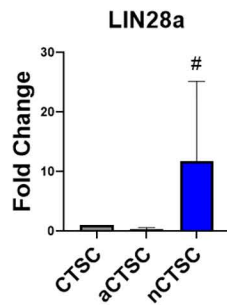
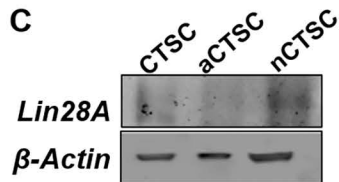
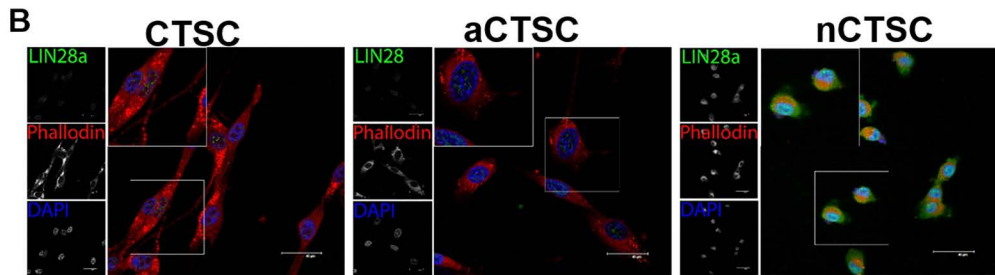
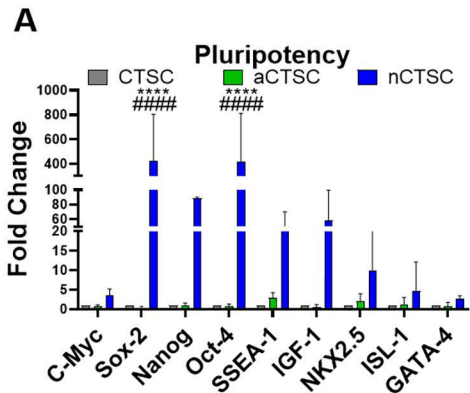
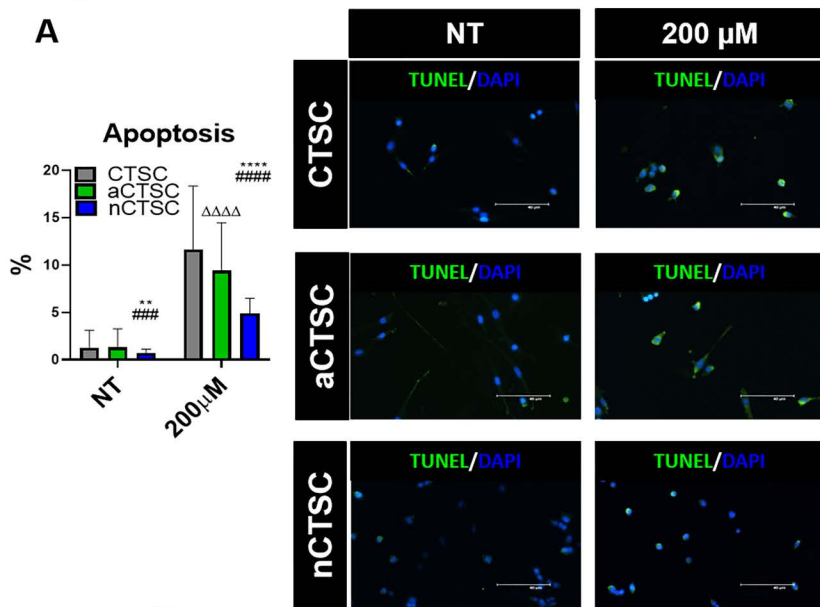
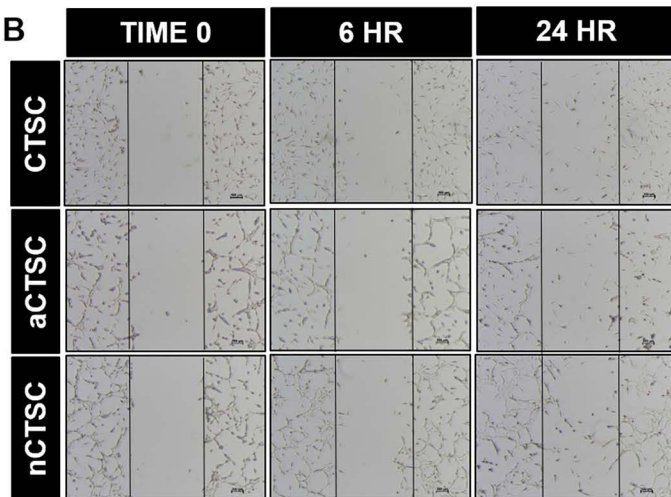


Figure S3

A



B



C

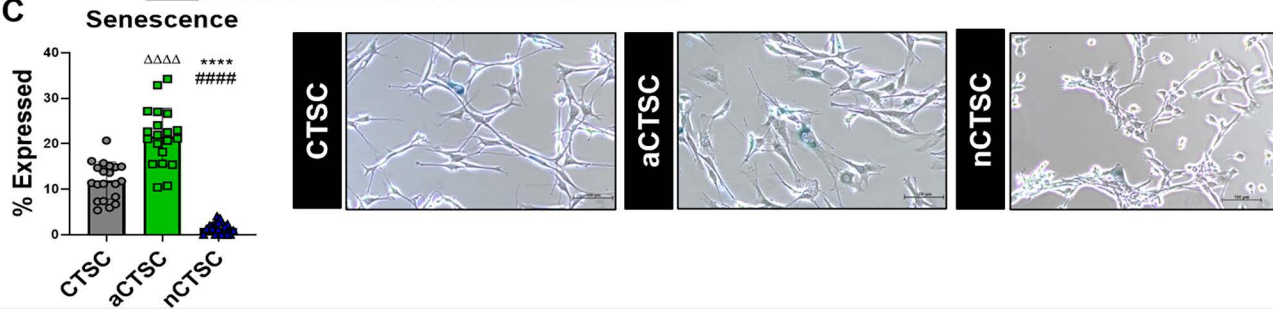
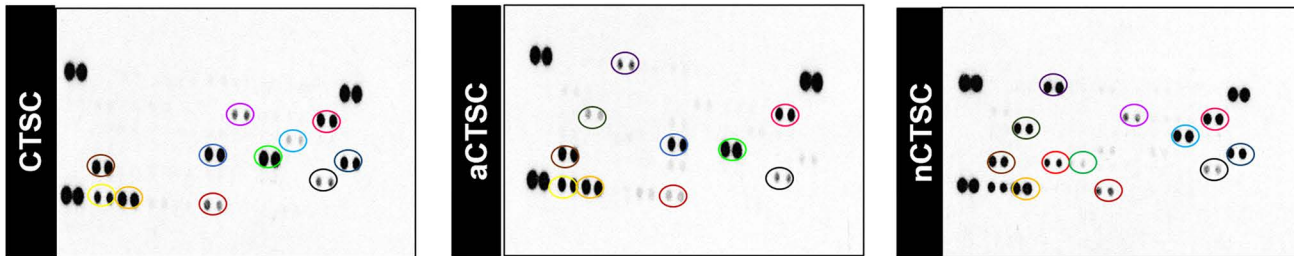


Figure S4

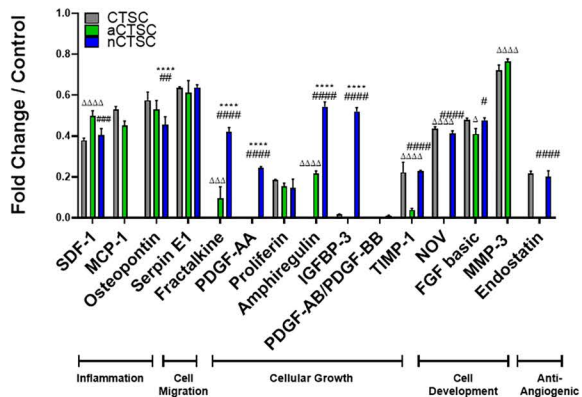
A

Proteome Profiler

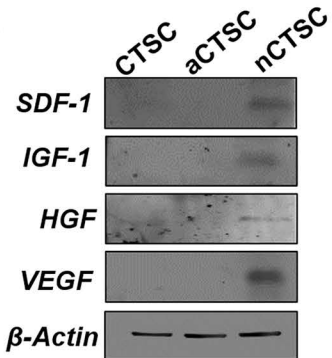


Identifier	Protein
Yellow circle	SDF-1
Light blue circle	MCP-1
Brown circle	Osteopontin
Orange circle	Serpin E1
Light green circle	Fractalkine
Red circle	PDGF-AA
White circle	Proliferin
Purple circle	Amphiregulin
Light blue circle	IGFBP-3
Light green circle	PDGF-AB/PDGF-BB
Red circle	TIMP-1
Light blue circle	NOV
Pink circle	FGF basic
Light green circle	MMP-3
Purple circle	Endostatin

Angiogenesis Markers



B



C

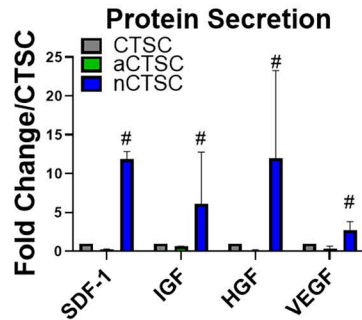
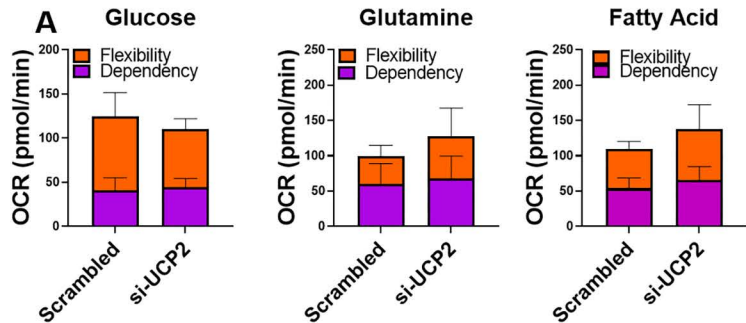
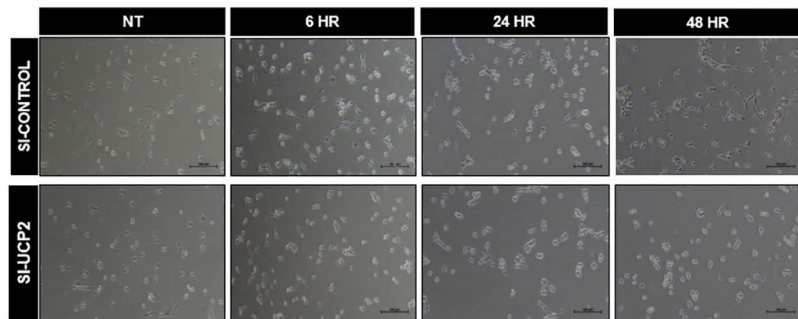


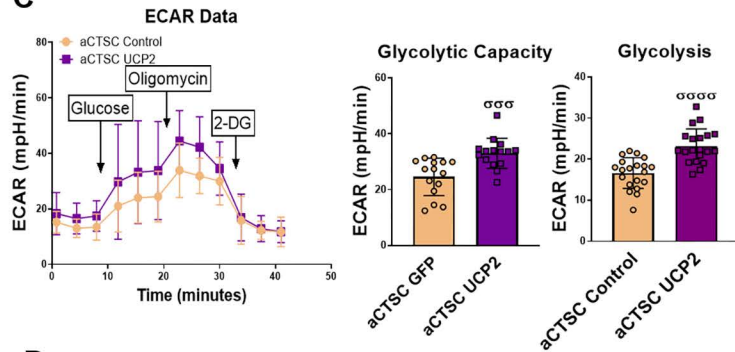
Figure S6



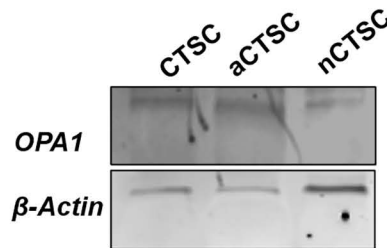
B



C



D



Supplemental Methods

Supplemental Methods

Morphological Analysis

All 3 cell types were plated in 6 well plate with 50,000 cells/well followed by acquisition of brightfield images of the cells using Nikon Eclipse Ts2 microscope. Morphological analysis was conducted using ImageJ software by outlining each cell's structure. For each cell line a total of 100 cells were assessed from 3 separate experiments and data was cumulated.

Wound Healing Assay

Cells were plated as 100,000 cells/ well of a 6-well plate (BD Falcon). Serum-free media (DMEM/F12 + PSG) was added to cells and kept overnight. Once 95% confluency was achieved in each well, wound was performed by creating a single scrape onto the well using a p200 tip. Images were taken at time 0, 6 hours, and 24 hours using Nikon Eclipse Ts2 microscope.

Flow cytometry

Cell characterization and cell cycle analysis was done on CTSCs lines by flow cytometry assays as described previously[1]. For cell cycle measurements, CTSCs were serum starved overnight for synchronization and then release by addition of full medium for 6 hrs followed by staining with propidium iodide (BD Biosciences) and assessed on flow cytometer.

Senescence-Associated β -Galactosidase Staining

Cellular senescence was assessed by staining the cells with senescence associated β -galactosidase kit (Abcam) as described previously[2,3]. Images were taken on Nikon Eclipse Ts2 microscope, 10 images were taken per CTSC slide for 3 independent experiments.

Cell Apoptosis

For measurement of cell apoptosis, 50,000 cells /wells were plated into 6-well plate. CTSCs growth medium with 2.5% FBS media (12.5mL CTSC Media + 37.5mL F12/DMEM) was added along with 100 μ M of H₂O₂ for assessing cell death in response to stress. Cells were fixed in 4% paraformaldehyde and stained TUNEL cell apoptosis kit (Invitrogen) according to manufacturer's instruction.

Reverse Transcriptase Polymerase Chain Reaction

CTSCs RNA extraction and purification were done using manufacturer's instruction (Qiagen). After RNA quantification (Nanodrop) cDNA was created using iScript cDNA Synthesis Kit (Bio-Rad). Amplification was conducted using SimpliAmp thermocycler (Applied Biosystems). Real-time polymerase chain reaction (RT-PCR) was done by running samples on StepOnePlus RT-PCR System (Applied Biosystems). Primers were created from Life Technologies and sequences are included in the Table SI.

Mitochondrial DNA Content Determination

For assessment of Mitochondrial DNA content, cells were centrifuged into a pellet, supernatant was aspirated and DNA lysis buffer (0.5% SDS, 0.1M NaCl, 0.05M Tris (pH 8.0), 3mM EDTA, and ddH₂O) was added to cells. Proteinase K is added at 100 μ g/mL to digest any contaminating proteins. Samples were incubated at 60°C overnight and then mixed with 8M Potassium Acetate. Chloroform was added to sample followed by centrifugation for 5 minutes at 9500rpm. Aqueous phase was isolated and 100% EtOH was added and stored in -20°C freezer for 15 minutes. After centrifugation for 5 minutes at 13000 rpm, supernatant was removed and pellet was washed with 75% EtOH. Samples were centrifuged for 2 minutes at 1300 rpm and supernatant was removed. Once air-dried, samples were resuspended in 100 μ L ddH₂O. DNA

samples were normalized to 100ng/ μ l. qPCR was performed with primers for β -globin representing nuclear genome and COXII for mitochondrial genome. Mitochondrial genome content was measured after normalizing CTSCs samples.

Citrate Synthase Activity

Citrate synthase activity in CTSCs was measured using citrate synthase kit (Biovision) according to manufacturer's protocol. Briefly, CTSCs were grown to confluency followed by lyses using ice-cold CS Assay Buffer. Lysate was kept on ice for 10 minutes then centrifuged at 10,000 RPM for 5 minutes. Once supernatant was collected, samples were added to a 96-well flat bottom plate. Total volume of 50 μ L was achieved by adding appropriate amount of CS Assay Buffer. Diluted CS Positive Control was added in specific wells and adjusted to total 50 μ L with CS Assay Buffer. Standard curve preparation involved diluting GSH Standard and adding to wells. Reaction mix consisting of CS Assay Buffer, CS Developer, and CS Substrate Mix was then added to each well containing either sample, Positive Control, or Standards. Absorbance (OD 412 nm) was measured in kinetic mode at 25°C for 20-40 minutes. Calculation of citrate synthase activity was done using manufacturer's equation.

Measurement of mitochondrial membrane potential by TMRM

For measurement of mitochondrial membrane potential, 50,000 cells/wells were plated into 2-chamber slide for each CTSC line. Final concentration of 50nM TMRM (Invitrogen) prepared in CTSC growth medium, was added to samples and incubated for 30 minutes at 37°C. Live nuclear dye (Invitrogen) was added to chambers 10 minutes prior to scanning on the microscope. Images were taken on Leica SP8 Confocal Microscope. TMRM intensity quantifications were done through ImageJ.

Lentivirus Transduction

nCTSC and aCTSCs were transfected with Lv-CMV-UCP2-GFP (Cyagen) lentivirus while control cells were infected with Lv-GFP to create stable cell lines as described previously [1].

References

- 1 Khan M, Mohsin S, Avitabile D et al. beta-Adrenergic regulation of cardiac progenitor cell death versus survival and proliferation. *Circ Res* 2013;112(3):476-486.
- 2 Choudhery MS, Khan M, Mahmood R et al. Mesenchymal stem cells conditioned with glucose depletion augments their ability to repair-infarcted myocardium. *J Cell Mol Med* 2012;16(10):2518-2529.
- 3 Khan M, Mohsin S, Khan SN et al. Repair of senescent myocardium by mesenchymal stem cells is dependent on the age of donor mice. *J Cell Mol Med* 2011;15(7):1515-1527.

Table S1 – List of primers and antibodies

Primer Name	Forward/Reverse	Product size	Sequence
<i>Wee1</i>	Forward	363	TCTTACCGTAGTCCGGAGGCA
<i>Wee1</i>	Reverse		GCACATGACATTTCTGTTGCGA
<i>Lin28a</i>	Forward	78	TTTGCCTCCGGACTTCTCTG
<i>Lin28a</i>	Reverse		CCCATGGTCGTCTGCTGAG
<i>Cyclin B1</i>	Forward	134	GGTGAACGACTGTTGGTCT
<i>Cyclin B1</i>	Reverse		TTTCGTGTTCTGGTGACCC
<i>Cyclin A2</i>	Forward	77	AGGACAAAGCTGGCCTGAATC
<i>Cyclin A2</i>	Reverse		GGTCCATGAGGCAAGGCTTA
<i>Cyclin D1</i>	Forward	145	ATTTCCAACCCGCCTTCCAT
<i>Cyclin D1</i>	Reverse		GACAGTCCGCGTCACACTTG
<i>Cyclin D2</i>	Forward	165	GCTCTGTGTGCTACCGACTT
<i>Cyclin D2</i>	Reverse		CACATCGGTGTGGGTGATCT
<i>Cyclin E1</i>	Forward	243	TCCAGGAAAAGAAAGGCAAATGT
<i>Cyclin E1</i>	Reverse		TGCCAGTTCAGTATAGGCAG
<i>CDK1</i>	Forward	78	CCTCTAAGCTCCCGGAGTCCG
<i>CDK1</i>	Reverse		CAACGGACCCTCTCTGTTCC
<i>E2F1</i>	Forward	178	GCCTCGAATAGGCAACCTGA
<i>E2F1</i>	Reverse		ACCCTCCTCGAGACCAAAGT
<i>c-myc</i>	Forward	187	ACTCGGTGCAGCCCTATTTTC
<i>c-myc</i>	Reverse		GTAGCGACCGCAACATAGGA
<i>CDK2</i>	Forward	84	CTTTGCCGAAATGGTGACCC
<i>CDK2</i>	Reverse		CCCAGAGTCCGAAAGATCCG
<i>HK1</i>	Forward	75	GATCGTTGGAGCAGACCACA
<i>HK1</i>	Reverse		TGTACAAACACCCCGAGACG
<i>ALDO1</i>	Forward	80	CCTTAGTCCTTTTCGCCTACCC
<i>ALDO1</i>	Reverse		CGTTGCCATGGGTACACTTG
<i>TPI1</i>	Forward	61	GAGAGCCGTGCGTTTGTACT
<i>TPI1</i>	Reverse		CTGGTAGGCGCCATTGTACC
<i>ENO1</i>	Forward	61	TCCTTAAGGCTCTCCTCGGT
<i>ENO1</i>	Reverse		AGTAGGATCGCTGCAAAGCA
<i>PGAM</i>	Forward	56	TTGCCAGTGGTCAGGACTTG
<i>PGAM</i>	Reverse		CCTGTCAGACCGCCATAGTG
<i>PKM2</i>	Forward	135	CGCCTGGACATTGACTCTG
<i>PKM2</i>	Reverse		GAAATTCAGCCGAGCCACATT
<i>PDK4</i>	Forward	80	ACGTCCTTTGCTTTTCTGCG
<i>PDK4</i>	Reverse		CGGTCAGGCAGGATGTCAAT
<i>GAPDH</i>	Forward	267	GAAGCTCATTTCCTGGTATGACA
<i>GAPDH</i>	Reverse		TATTGATGGTATTCGAGAGAAGGG

Application	Antibody	Dilution	Cat No.	Company
Western Blot	Wee1	1:300	Ab137377	Abcam
Western Blot	Lin28a	1:500	SC-6216	Santa Cruz
Western Blot	Cyclin B1	1:1000	4138	Cell Signaling
Western Blot	Cyclin D1	1:3000	2922S	Cell Signaling
Western Blot	CDK1	1:500	ab18	Abcam
Western Blot	p-CDK tyr15	1:500	9114	Cell signaling
Western Blot	β actin	1:1000	9664S	Cell Signaling
Western Blot	p-AKT S473	1:500	4060	Cell Signaling
Western Blot	AKT	1:500	9272	Cell Signaling
ICC	BrdU	1:100	Ab6326	Abcam
ICC	Sarcomeric Actin	1:100	A2172	Sigma Aldrich
ICC	Aurora B	1:50	Ab2254	Abcam
ICC	Phospho Histone 3	1:100	441190G	Life technologies
ICC	Ki67	1:100	Ab15580	Abcam
ICC	SMA		A2547	Sigma Aldrich
IHC	WGA-488	1:200	W11261	Life technologies

TABLE S2**A. Comparison Cardiomyocytes (CM) to nCTSC**

No.	Gene	CM	nCTSC
1.	alpha-Sarcoglycan	++++	
2.	Atrial Natriuretic Peptide/ANP	+++	
3.	beta-Sarcoglycan	++++	++
4.	BMP-4	+++	+
5.	Connexin 37/GJA4	+++	
6.	Connexin 40/GJA5	++	
7.	Cripto		
8.	Desmin	+++++	
9.	epsilon-Sarcoglycan	+++	++
10.	FABP3/H-FABP	+++++	+
11.	GATA-4	++++	
12.	GATA-6	+++	+
13.	HCN4	+++	
14.	Kir2.1	+++	+
15.	LRG1	+++	
16.	MEF2C	+++	++
17.	MYH6	+++++	
18.	MYH7	+++++	
19.	TBX5	+++	
20.	Troponin T	+++	
21.	Troponin T2	+++++	++

Quality Score	Normalized read count
+	10s
++	100s
++++	1000s
+++++	10000s
+++++	100000s

TABLE S2**B. Comparison of Cardiac fibroblast (CF) to nCTSC**

No.	Gene	CF	nCTSC
1.	WT1	++	
2.	Tcf21	+++	
3.	Prolyl-4-hydroxylase	+	+
4.	Vimentin	++++	+++++
5.	aSMA	++	+
6.	PDGFR?	+++	+++
7.	DDR2	+++	+++
8.	CD90	+++	
9.	Sca1	+++	
10.	Periostin	+++	
11.	Fibronectin	+++	
12.	Collagen type I	++++	++
13.	Collagen type III	++++	++
14.	FAP	++	

TABLE S2**C. Comparison of Endothelial Cells (ECs) to nCTSCs**

No.	Gene	EC	nCTSC
1.	ACE/CD143	++	+
2.	C1qR1/CD93	++++	+
3.	VE-Cadherin	++	
4.	CC Chemokine Receptor D6	+	
5.	CD31/PECAM-1	++++	
6.	CD34	++++	++++
7.	CD36/SR-B3	++++	
8.	CD151	++	++++
9.	CD160	+	
10.	CD300g/Nepmucin	++++	
11.	CL-K1/COLEC11	+	
12.	CL-P1/COLEC12	++	++
13.	Coagulation Factor III/Tissue Factor		++
14.	DCBLD2/ESDN	++	++++
15.	ECSCR	++	
16.	EMMPRIN/CD147	++	++++
17.	Endoglin/CD105	++	++
18.	Endomucin	++++	
19.	Endosialin/CD248		++++
20.	EPCR	+	++
21.	Erythropoietin R		+
22.	ESAM	++	
23.	FABP5/E-FABP	++	++
24.	ICAM-1/CD54	++	
25.	ICAM-2/CD102	++	
26.	IL-13 R alpha 1	+	++++
27.	Integrin beta 2/CD18	+	
28.	KLF4	++	++++
29.	LYVE-1	++	
30.	MCAM/CD146	++	++
31.	Nectin-2/CD112	+	++
32.	PD-ECGF/Thymidine Phosphorylase	+	+
33.	Podocalyxin	++++	++
34.	Podoplanin	+	+
35.	S1P1/EDG-1	++++	++

36.	S1P2/EDG-5	+	++++
37.	S1P3/EDG-3	+	+
38.	S1P4/EDG-6	+	
39.	E-Selectin/CD62E	+	++++
40.	P-Selectin/CD62P	+	++++
41.	SLAM/CD150	+	
42.	Stabilin-1	++++	+
43.	TEM7/PLXDC1	+	
44.	TEM8/ANTXR1	+	++++
45.	Thrombomodulin/BDCA-3	++++	++++
46.	THSD1	++	+
47.	THSD7A	++	++
48.	Tie-2	++++	
49.	TNF RI/TNFRSF1A	++	++++
50.	TNF RII/TNFRSF1B	++	++
51.	TRAIL R2/TNFRSF10B	++	++++
52.	TRAILR1/TNFRSF10A	+	++
53.	VCAM-1/CD106	++	++
54.	VE-Statin	++++	+
55.	VEGFR1/Flt-1	++++	++++
56.	VEGFR2/KDR/Flk-1	++++	+
57.	VEGFR3/Flt-4	++++	+
58.	VG5Q	++	++
59.	vWF-A2	++++	+

TABLE S2**D. Embryonic stem cell (ESC) comparison to nCTSC**

No.	Gene	ESC	nCTSC
1.	E-Cadherin	++++	
2.	Cbx2	++	++
3.	CD9	+++	+++
4.	CD30/TNFRSF8	+	
5.	CD117/c-kit	+++	
6.	CHD1	+++	+++
7.	Cripto	++++	
8.	DNMT3B	++	+
9.	DPPA2	++	
10.	DPPA4	++	
11.	DPPA5/ESG1	++++	
12.	EpCAM/TROP1	++	
13.	F-box protein 15/FBXO15	+++	
14.	FGF-4	+++	
15.	FGF-5	+	
16.	FoxD3	+	
17.	GBX2	+	
18.	GCNF/NR6A1	++	+
19.	GDF-3	++	
20.	Integrin alpha 6/CD49f	+++	++++
21.	Integrin beta 1/CD29	+++	++++
22.	KLF4	+++	+++
23.	KLF5	+++	++
24.	L1TD1	+++	
25.	Lefty-1		+
26.	Lefty-A	++	
27.	LIN-28A	++	
28.	LIN-28B	++	
29.	LIN-41	+++	
30.	c-Maf	+++	+++
31.	Nanog	++++	
32.	Oct-4.	+++	
33.	Podocalyxin	++	++
34.	Rex-1/ZFP42	+++	

35.	Smad2	++	+++
36.	SOX2	+++	+++
37.	SSEA-1		+
38.	STAT3	+++	+++
39.	Stella/Dppa3	+	
40.	SUZ12	+++	+++
41.	TBX3	+++	+++
42.	TBX5	+	
43.	TEX19.1	++	
44.	THAP11	++	++
45.	UTF1	++	
46.	VISTA/B7-H5/PD-1H		+
47.	ZIC3	++	

TABLE S2**E. Cardiac progenitor Cell (CPC) comparison to nCTSC**

No.	Gene	CPC	nCTSC
1.	ABCG2	++	++
2.	CD34	++	+++
3.	CD117/c-kit	++	
4.	ETV2/ER71	+	
5.	GATA-4	+++	
6.	Integrin beta 1/CD29	+++	++++
7.	Islet-1	++	+
8.	NKX2.5	+++	
9.	Sca-1/Ly6		++
10.	SCF/c-kit Ligand	++	++
11.	SSEA-1	+	+
12.	TBX18	+	+
13.	WT1	+	

TABLE S2**F. Comparison of nCTSC to Mesenchymal Stem Cell (MSCs)**

No.	Gene	MSCs	nCTSC
1.	5'-Nucleotidase/CD73	+	+++
2.	ALCAM/CD166	++	+++
3.	Aminopeptidase N/CD13	++	+
4.	BMPR-IA/ALK-3	+++	+++
5.	BMPR-IB/ALK-6	++	+
6.	BMPR-II	++++	++++
7.	N-Cadherin	+++	+++
8.	CD44	++++	++++
9.	CD45	++	
10.	CD90/Thy1	+++	
11.	Endoglin/CD105	++	++
12.	Fibronectin	+	
13.	Anastellin	++++	++++
14.	ICAM-1/CD54	+	
15.	Integrin alpha 1/CD49a	++	+
16.	Integrin alpha 5/CD49e	++++	+++
17.	Integrin alpha V/CD51	++++	+++
18.	Integrin beta 1/CD29	++++	++++
19.	NCAM-1/CD56	+++	+++
20.	Nucleostemin	++	+++
21.	Sca-1/Ly6	+++	++
22.	SUSD2	+	
23.	TfR (Transferrin R)	++	
24.	VCAM-1/CD106	+++	++
25.	Vimentin	++++	++++

TABLE S3

Comparison of nCTSC to embryonic CPC populations

Quality Score	Normalized read count
+	10s
++	100s
++++	1000s
++++	10000s
++++	100000s

Origin	Subpopulation	Marker	CTSC	aCTSC	nCTSC
pSHF	A	Foxf1	++	+	++
pSHF	A	Lefty2			
pSHF	A	Pitx2			
pSHF	B	Aldh1a2		+	
pSHF	B	Pbx1	+++	+++	+++
pSHF	C	Gata6	++	+	+
pSHF	C	Wnt2			
pSHF	C	Nr2f2	+++	+++	+++
pSHF	C	Tnnt2		+	++
pSHF	C	Myl7	+	++	+++
pSHF	C	Sfrp5			
pSHF	C	Actc1			
pSHF	C	Upp1			
<i>FHF</i>	D	Phlda2			
<i>FHF</i>	D	Mab21/2		++	++
<i>FHF</i>	D	Msx1	++	++	++
<i>FHF</i>	D	Krt8			
<i>FHF</i>	D	Hand1			
<i>FHF</i>	D	Irx4			
AHF	E	Schip1	+	+	++
AHF	E	Fhl1		+	+
	E	Bambi	++	++	+
AHF	E	Nkx2-5			
AHF	E	Mef2c	++	++	++
AHF	E	Dkk1			
AHF	F	Bmp4			+
AHF	F	Dlk1	+++	++	+
AHF	F	Myh10	+++	+++	+++
AHF	F	Prrx1	+++	+++	+++
AHF	F	Rgs5	+	++	++
AHF	H	Crabp2		++	
AHF	H	Vamp8	++	++	++
AHF	H	Pdcd4	++	+++	++
AHF	H	Fgf10	+++	+++	+++
AHF	H	Mpped2			
AHF	H	Igfbp1			
AHF	H	Nkx2-6			
AHF	I	Isl1	+		+
AHF	I	Lefty1		+	+
AHF	I	Fst	++	+++	+++
AHF	I	Irx5	+	++	++
AHF	I	Tbx1			

AHF	I	Fgf8			
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