CERTIFICATE OF ANALYSIS
AICS-0046-051:WTC-mEGFP-ATP2A2-cl51 (mono-allelic tag)

Product description	Human iPSC clonal line in which ATP2A2 has been endogenously tagged with mEGFP using CRISPR/Cas9 technology
Parental cell line	Parental hiPSC line (WTC/AICS-0 at passage 33) derived from fibroblasts reprogrammed using episomal vectors (OCT3/4, shp53, SOX2, KLF4, LMYC, and LIN28). Coriell catalog: GM25256
Publication(s) describing iPSC establishment	Kreitzer et al (2013) Am. J. Stem Cells, 30; 2(2): 119-31
Passage of gene edited iPSC reported at submission	p27[a]
Number of passages at Coriell	0
Media	mTeSR1
Feeder or matrix substrate	Matrigel
Passage method	Accutase
Thaw	1 million cells (ea vial) in 10 cm plate - ready for passaging in 3-4 days
Seeding density	400K cells/10-cm plate every 4 days or 800K cells/10-cm plate every 3 days (see culture protocol)

Test Description[b]	Method	Specification	Result
Post-Thaw Viable Cell Recovery	hiPSC culture on Matrigel	$>$ 50% confluency 3-4 days post-thaw (10 cm plate)	Pass
mEGFP insertion at genomic locus - precise editing	PCR and Sanger sequencing of recombinant and wildtype alleles	N-term insertion of mEGFP in frame with exact predicted recombinant allele junctions. No additional mutations in either allele.	Pass
Copy number	ddPCR[c] assay for mEGFP and RPP30 reference gene[d]	mEGFP/RPP30: $\sim$ 0.5 = Mono-allelic $\sim$ 1.0 = Bi-allelic	Mono-allelic (0.538)
Plasmid integration	ddPCR assay to detect plasmid integration into the genome	AmpR/RPP30: $<$ 0.1 = no plasmid integration	Pass (0.001)
Mutational analysis	Whole exome sequencing[f]	Check for acquired mutations (not detected in p8[a] parental line) that: 1) Correspond to off-target sites predicted by Cas-OFFinder[e] 2) Affect genes in Cosmic Cancer Gene Census	Sequencing planned
mEGFP localization	Spinning Disk confocal live cell imaging	Localization to the endoplasmic reticulum (ER) in hiPSCs and hiPSC-derived cardiomyocytes and sarcoplasmic reticulum (SR) in hiPSC-derived cardiomyocytes	Localization to the ER in the nuclear periphery and throughout the cytoplasm in hiPSCs and cardiomyocytes. Additional localization to sarcomeres in cardiomyocytes, consistent with localization to the longitudinal SR.

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Expression of tagged protein	Western blot	Expression of expected size product	Expected size bands for untagged and mEGFP-tagged SERCA2 protein. Semi-quantitative results show 48% of ATP2A2-encoded protein product is mEGFP labeled in cell lysates from mEGFP-tagged SERCA2 hiPSCs compared to lysates from unedited WTC hiPSCs. Western blot not performed on cardiomyocytes.
Growth rate	ATP quantitation[g]	Comparable to parental line	Pass (measured at p28)[a]
Expression of stem cell markers	Flow cytometry	Transcription factors: OCT4/SOX2/NANOG $\geq$ 85% Surface markers: SSEA3, TRA-1-60 $\geq$ 85%; SSEA1 $\leq$ 15%	Pass
Germ layer differentiation	Trilineage differentiation[h] as assayed by ddPCR gene expression analysis	Expression of endoderm (SOX17), mesoderm (Brachyury), and ectoderm (PAX6) markers upon directed differentiation to all three germ layers	Pass
Cardiomyocyte differentiation	Modified small molecule differentiation (Lian et al. 2012)[i]	Beating initiated (D7-D14) and Cardiac Troponin T expression (D12-D30) by flow cytometry	Pass
Karyotype	G-banding (30 cell analysis)	Normal karyotype, 46 XY	Pass
Mycoplasma	qPCR (IDEXX)	Negative	Pass
Sterility (bacterial, yeast and fungal testing)	Direct inoculation and incubation for 10 days	No growth after 10 days	Pass
Viral Panel Testing[j]	PCR	Negative when assayed for CMV, EBV, HepB, HepC, HIV1, and HPV	Pass
Identity of unedited parental line[k]	STR	29 allelic polymorphisms across 15 STR loci compared to donor fibroblasts	Identity matched

[a] This is the number of passages beyond the orginal parental line (WTC/AICS-0 at passage 33).
[b] All QC assays are performed on stem cells except when noted otherwise.
[c] Droplet digital PCR using Bio-Rad QX200
[d] RPP30 is a reference 2 copy gene used for normalization.
[e] Bae et al (2014) Bioinformatics. 30(10): 1473-1475
[f] Nextera rapid capture exome
[g] Promega CellTiter-Glo Luminescent Cell Viability Assay (Catalog #G7571)
[h] STEMCELL Technologies STEMdiff Trilineage Differentiation Kit (Catalog #05230)
[i] Lian et al (2012) PNAS. 109(27):E1848-E1857
[j] Viral panel testing was conducted for the parental WTC line prior to editing. Sterility (bacterial, fungal) and mycoplasma testing were conducted in both the parental and edited lines.
[k] STR tests were conducted for the WTC parental line prior to editing. WTC is the only cell line used by AICS. Edited WTC cells were not re-tested because they did not come into contact with any other cell lines.

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mEGFP tagging strategy: Used CRISPR-Cas9 methodology to introduce mEGFP at N-terminus of ATP2A2 as shown below.

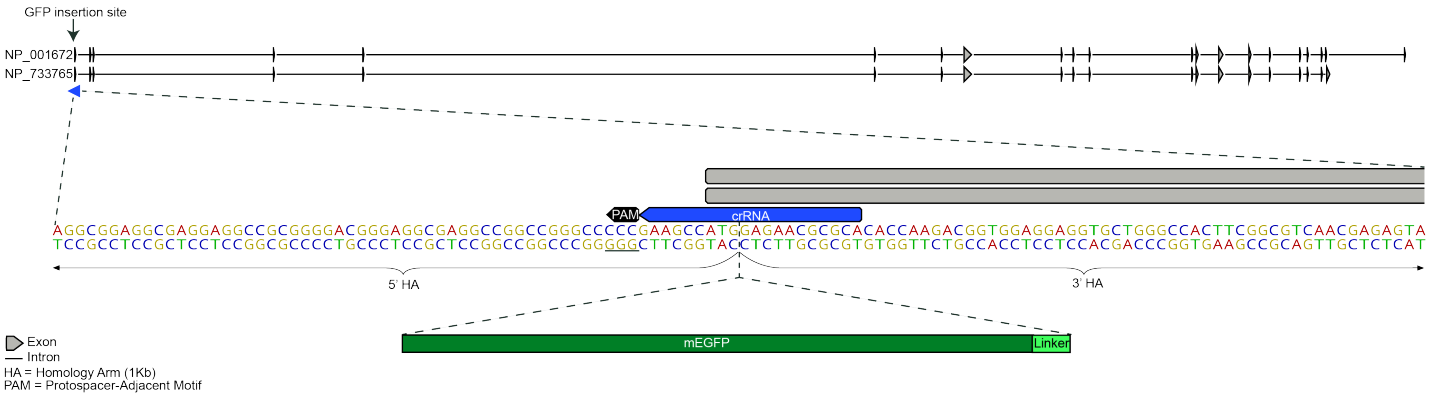

Figure 1: Top: ATP2A2 locus showing 2 ATP2A2 isoforms; Bottom: Zoom in on mEGFP insertion site at ATP2A2 N-terminal exon

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Post-thaw imaging: One vial of distribution lot was thawed (cells were treated with ROCK inhibitor for 24hrs post-thaw - refer to culture protocol). Cultures were observed daily. Colonies were photographed one and three days post-thaw[1,2] using a Leica microscope at 4X and 10x magnification.

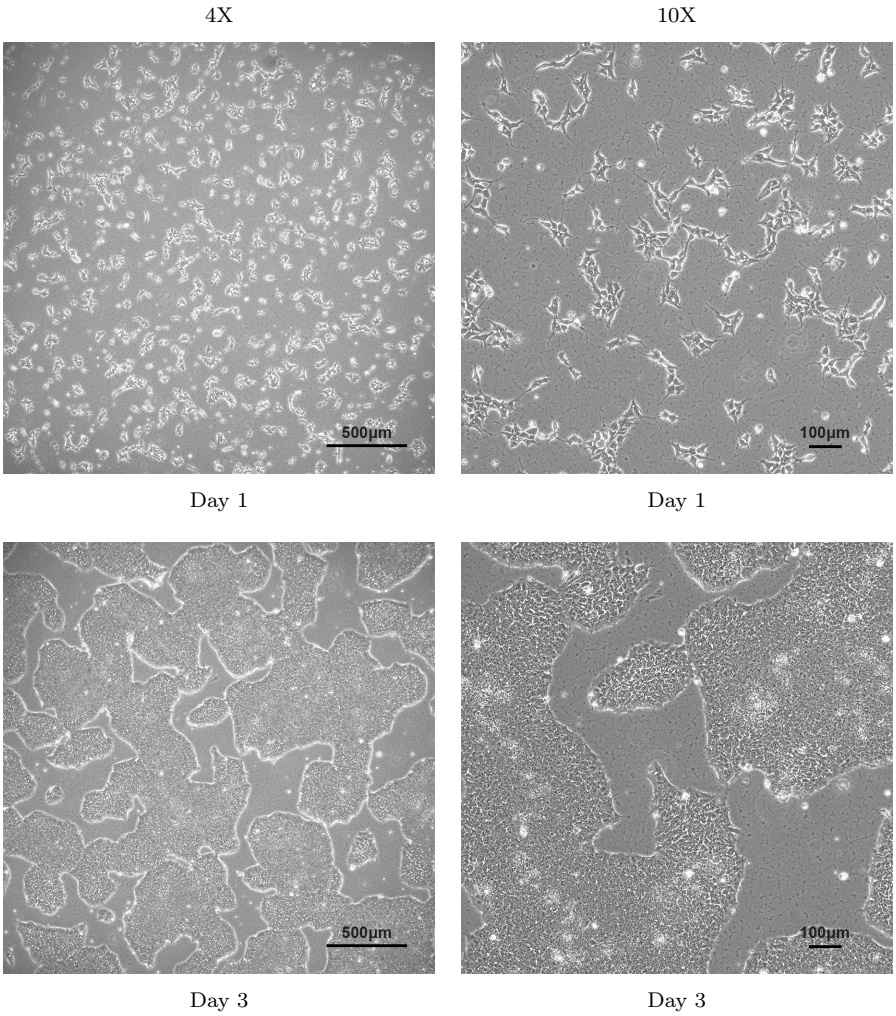

Figure 2: Viability and colony formation one day and three days post-thaw

[1]Cells may take up to 3 passages to recover after thaw
[2]Morphologies observed post-thaw are representative of cell morphologies observed post-passage

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Imaging labeled structures in endogenously tagged cells: The tagged proteins are expressed endogenously and therefore may not appear as bright as they would in an overexpressed system. hiPS cells are plated on matrigel-coated high-quality glass bottomed plates (Cellvis) and imaged in phenol red-free mTeSR media (STEMCELL Technologies). Our most common microscope configuration is a Zeiss spinning disk fluorescence microscope with a Yokogawa CSUX1 head, Hamamatsu CMOS camera, and a 488 laser (GFP). hiPS cells are imaged either with a 20x 0.8NA objective for lower magnification or 100x 1.25NA water immersion objective for higher magnification. Cardiomyocytes are plated onto high-quality glass bottomed plates (Cellvis) coated with 0.1% w/vol polyethylenimine (PEI) and 25μg/ml laminin and are imaged in phenol red-free RPMI 1640 media (Gibco) supplemented with B-27 containing insulin (Gibco). Cardiomyocytes are imaged with a 40x 1.2 NA water immersion objective on the same spinning disk confocal microscope as described for hiPSC. All live imaging is performed at 37°C and 5% CO_2 in a temperature-controlled chamber. The approximate laser power measured at the sample for our standard 100x images is ∼2.5 mW.

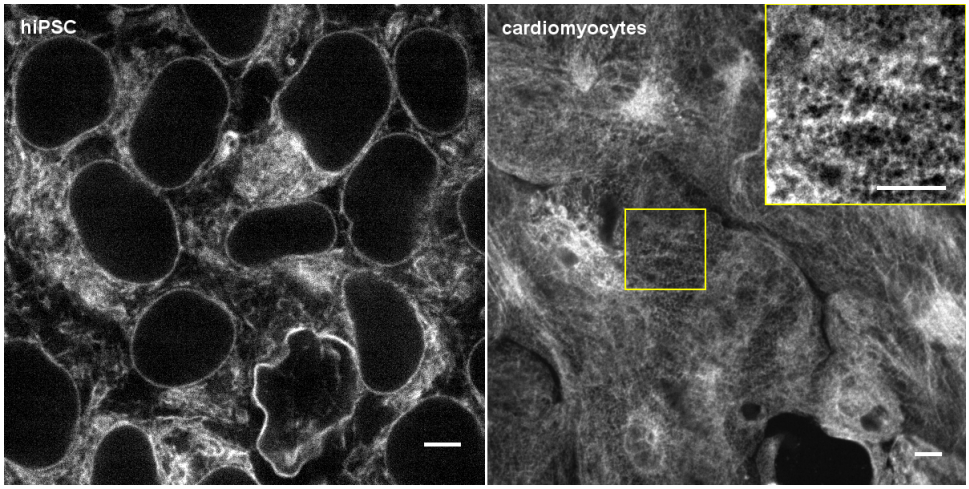

Figure 3: Left: Single, mid-level plane of cells in a live hiPS cell colony expressing mEGFP-tagged SERCA2 protein. Cells were imaged four days after plating on Matrigel-coated glass as described in methods at www.allencell.org. Scale bar, 5 μm. Right: Single, near-bottom plane of hiPSC-derived cardiomyocytes. Twelve days after the onset of differentiation, cells were plated on PEI and laminin coated glass and imaged 29 days later (41 days total after the onset of differentiation). Inset shows detail of SERCA2 in longitudinal SR. Scale bars, 10 μm. Cells were imaged in 3D on a spinning-disk confocal microscope.