



Lab Resource: Single Cell Line

# Generation and cardiac differentiation of a human induced pluripotent stem cell line UALGi002-A from a female patient with Left-Ventricular Noncompaction Cardiomyopathy

Sofia M. Calado<sup>a,b,c</sup>, Dina Bento<sup>d</sup>, Nuno Marques<sup>b,c,d</sup>, José Bragança<sup>a,b,c,e,\*</sup><sup>a</sup> CBMR, Centre for Biomedical Research, Universidade do Algarve, 8005-139 Faro, Portugal<sup>b</sup> Faculdade de Medicina e Ciências Biomédicas (FMCB), Universidade do Algarve, Campus de Gambelas, 8005-139 Faro, Portugal<sup>c</sup> ABC-RI, Algarve Biomedical Center Research Institute, 8005-139 Faro, Portugal<sup>d</sup> Centro Hospitalar e Universitário do Algarve, Department of Cardiology, Faro, Portugal<sup>e</sup> Champalimaud Research Program, Champalimaud Center for the Unknown, 1400-038 Lisbon, Portugal

## ABSTRACT

Left Ventricular Noncompaction Cardiomyopathy (LVNC) is characterized by abnormal number and prominence of trabeculations of the left ventricle of the heart. Although LVNC has been associated with mutations in several genes encoding for transcriptional regulators, ion channels, sarcomeric and mitochondrial proteins, approximately 60% of LVNC patients do not present these genetic alterations. Here, we describe an induced pluripotent stem cell (hiPSC) line (UALGi002-A) originated from a LVNC female patient (LVNC-hiPSC) who does not present any previously known mutations associated to LVNC. The LVNC-hiPSC exhibited full pluripotency and differentiation potential and retained a normal karyotype after reprogramming. Moreover, the LVNC-hiPSC differentiated into contracting cardiomyocytes. This cellular model will be useful to study the molecular, genetic and functional aspects of LVNC *in vitro*.

## 1. Resource Table

Unique stem cell line identifier	UALGi002-A
Alternative name(s) of stem cell line	VITAL8
Institution	Universidade do Algarve, Faro, Portugal Algarve Biomedical Center Research Institute (ABC-RI), Faro, Portugal
Contact information of distributor	jebaganca@ualg.pt
Type of cell line	iPSC
Origin	Human
Additional origin info required for human ESC or iPSC	Age: 51 Sex: Female Ethnicity: Caucasian/Portuguese
Cell Source	Peripheral blood mononuclear cells
Clonality	Clonal
Method of reprogramming	Non-integrating, Sendai Virus expressing hOCT3/4, hSOX2, hKLF4 and hC-MYC
Genetic Modification	NO
Type of Modification	N/A
Associated disease	Left Ventricular Non-Compaction Cardiomyopathy (LVNC)
Gene/locus	N/A
Date archived/stock date	June 2019

(continued on next column)

(continued)

Unique stem cell line identifier	UALGi002-A
Cell line repository/bank	<a href="https://hpscereg.eu/cell-line/UALGi002-A">https://hpscereg.eu/cell-line/UALGi002-A</a>
Ethical approval	Approval ID: 78/19 by Ethics Committee for Health, Centro Hospital e Universitário do Algarve, Faro, Portugal

## 2. Resource utility

Left Ventricular Noncompaction Cardiomyopathy (LVNC) is a heart disorder characterized by endomyocardial noncompaction. The UALGi002-A cell line, derived from a female patient with LVNC offers a useful tool for molecular, cellular and physiological analysis to study mechanisms involved in this cardiomyopathy.

## 3. Resource details

Mononucleated cells were collected from 4 mL of peripheral blood sample from a 51-year-old female. The patient has a history of palpitations and was clinically diagnosed with left ventricular trabeculations located in the middle and apical segments, with a diastolic ratio of >2.3,

\* Corresponding author at: CBMR, Centre for Biomedical Research, Universidade do Algarve, 8005-139 Faro, Portugal.

E-mail address: [jebaganca@ualg.pt](mailto:jebaganca@ualg.pt) (J. Bragança).

compatible with Left Ventricular Noncompaction Cardiomyopathy (LVNC). A genetic study of this patient showed no clinically relevant mutations in LDB3, TAZ, LMNA/C, MYH7, MYBPC3, TNNT2, ACTC1, TPM1, CSRP3, TCAP, SGCD, and PLN genes that have been previously associated with LVNC. LVNC is characterized by the presence of vast trabeculations likely due to endomyocardial morphogenesis arrest during embryogenesis. Clinical manifestations and their onset are variable, and may include heart failure, thromboembolism, ventricular arrhythmias, and ultimately sudden cardiac death (Finsterer et al., 2017). The human induced pluripotent stem cell (hiPSC) line UALGi002-A was generated using the CytoTune® iPSC-Reprogramming kit (Thermo Fisher Scientific, Invitrogen), encoding for the reprogramming factors hOCT3/4, hc-MYC, hKLF4, and hSOX2 (Takahashi and Yamanaka, 2006), according to manufacturer's instructions. Clonal hiPSC lines were established and further characterized (Table 1), formed colonies with a standard stem-like morphology visible by phase contrast (Fig. 1A) and were positive for Alkaline Phosphatase (AP) activity (Fig. 1B). The expression of pluripotency markers was demonstrated by immunofluorescence staining of NANOG, SOX2, OCT4 and SSEA4 proteins (Fig. 1C), as well as by detection of NANOG expressing hiPSCs by flow cytometry (Fig. 1D), and by detection of NANOG, OCT4, SOX2 and REX1 transcripts expression by RT-PCR (Supplementary Fig. S1A). Viral clearance was confirmed at passage 11 (Fig. 1E).

Genomic integrity was assessed by karyotype analysis, showing that

**Table 1**  
Characterization and validation.

Classification	Test	Result	Data
<b>Morphology</b>	Photography Bright field	Normal	Fig. 1A
<b>Phenotype</b>	Qualitative analysis (Immunocytochemistry)	Positive pluripotency markers: Alkaline Phosphatase, Oct3/4, Nanog, Sox2, and SSEA-4	Fig. 1B and C
	Quantitative analysis (Flow cytometry)	Percentage of NANOG positive cells: 95%; SSEA-4 positive cells: 93,3%	Fig. 1D
<b>Genotype</b>	Karyotype (G-banding) and resolution	46XY, Resolution 400–500	Fig. 1E
<b>Identity</b>	Microsatellite PCR (mPCR)	Not performed	N/A
	STR analysis	16 loci analyzed, all matched	Supplementary table 1
<b>Mutation analysis (IF APPLICABLE)</b>	Sequencing	N/A	N/A
	Southern Blot OR WGS	N/A	N/A
<b>Microbiology and virology</b>	Mycoplasma	Mycoplasma testing by RT-PCR: Negative	Supplementary Fig. 1
<b>Differentiation potential</b>	e.g. Embryoid body formation	Positive staining for $\alpha$ -fetoprotein (AFP), $\beta$ III-tubulin (TUBB3), $\alpha$ -smooth muscle actin (SMA).	Fig. 1F
<b>Donor screening (OPTIONAL)</b>	HIV 1 + 2 Hepatitis B, Hepatitis C	Not performed	N/A
<b>Genotype additional info (OPTIONAL)</b>	Blood group genotyping	Not performed	N/A
	HLA tissue typing	Not performed	N/A

UALGi002-A, at passage 22, presented a normal diploid (46, XX) chromosomal content (Fig. 1F). The capacity of hiPSCs to differentiate into three germ layers was confirmed by embryoid body (EB) differentiation assay, and by the detection of ectoderm (TUJ1), mesoderm ( $\alpha$ -SMA) and endoderm (AFP) markers expression (Fig. 1G). In addition, hiPSC were differentiated into contracting cardiomyocytes as previously described (Lian et al., 2013), and expressed the sarcomeric protein  $\alpha$ -actinin (Figure H). DNA fingerprinting was used to prove the genetic identity between hiPSCs and parental mononucleated blood cells (archived with journal). Mycoplasma was regularly tested negative throughout cell culture indicating that UALGi002-A line is mycoplasma-free (Supplementary Fig. S1B).

## 4. Materials and methods

### 4.1. Reprogramming of PBMCs

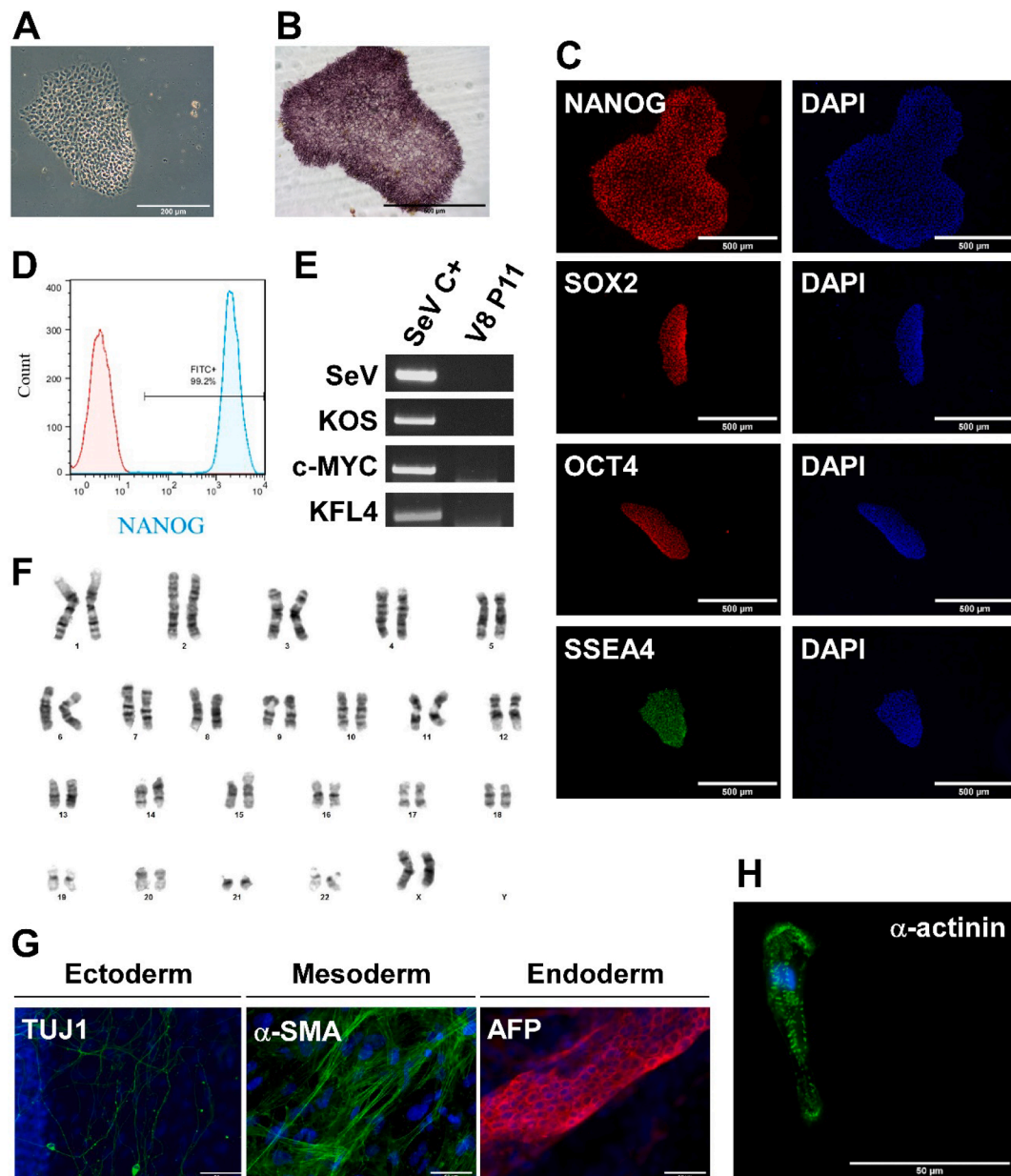
The collection of blood samples was performed as we previously reported (Calado et al., 2021). In brief, PBMCs were isolated using the Vacutainer® CPT™ tubes (BD Biosciences). PBMCs were cultured ( $1.0 \times 10^6$  cells) in PBMCs Medium (StemPro-34 SFM medium; 1% GlutaMAX; 1% Pen/Strep, 100 ng/mL SCF, 100 ng/mL FLT-3; 20 ng/mL IL-3, 20 ng/mL 20 ng/mL IL-6), for one week before transduction with CytoTune®-iPS 2.0 Sendai Reprogramming Kit. Briefly,  $0.25 \times 10^5$  cells were transduced using MOI of 5–5.3 (hKOS, hc-MYC, hKLF4, respectively). After 24 h of incubation, cells were collected, centrifuged, and seeded in a 24-well plate containing PBMCs Medium. Two days later, reprogrammed cells were transferred onto a 6-well plate covered with irradiated mouse embryonic fibroblasts (Gibco) and cultured in hiPSC medium (Knockout-DMEM, KSR 20%, Glutamax 2 mM, non-essential amino acids 0.1 mM,  $\beta$ -mercaptoethanol 0.23 mM, bFGF 10 ng/ml, penicillin/streptomycin, Gibco). Individual colonies with stem-like morphology were manually picked and expanded for 14 to 21 days post-transduction. hiPSC were adapted to feeder-free cell culture on plates coated with Geltrex LDEV-Free Reduced Growth Factor Basement Membrane Matrix (Gibco) using mTeSR1 medium (StemCell Technologies). Passages were performed using ReLeSR (StemCell Technologies), using a split ratio of 1:5 and cells were maintained at 37 °C in humidified atmosphere containing 5% CO<sub>2</sub>.

### 4.2. Immunocytochemistry

Cells were grown in glass coverslips coated with Geltrex LDEV-Free Reduced Growth Factor Basement Membrane Matrix and washed in ice-cold PBS before fixation in 4% PFA, for 15 min. Fixed cells were washed twice with PBS and placed in blocking solution (2% bovine serum albumin in 0.2% Triton X100/PBS) for 1 h, at room temperature. Next, cells were incubated for 1 h at room temperature with the primary antibody (Table 2). After incubation, samples were washed 3 times with 0.2% Triton X100/PBS, and incubated with the secondary antibodies for 1 h, at room temperature (Table 2). After 3 washes, sections were mounted with Fluoromount G mounting medium (Thermo Fisher Scientific) containing 4,6-diamidino-2-phenylindole (DAPI) and analyzed on a Axioimager Z2 fluorescence microscope (Carl Zeiss).

### 4.3. In vitro differentiation assay

Three germ layers differentiation *in vitro* was performed by EB formation. hiPSC colonies were lifted manually and cultured in non-adherent conditions in mTeSR1 medium, containing 0.4% of polyvinyl alcohol, for 48 h. Next, EBs were seeded on glass coverslips coated with Geltrex LDEV-Free Reduced Growth Factor Basement Membrane Matrix and cultured for 3 weeks in differentiation medium (DMEM, 10% FBS, 1% Pen/Strep, 1% GlutaMAX, 1% MEM-NEAA). Directed cardiomyocyte differentiation was performed following the GiWi protocol, as described by Lian and co-workers (Lian et al., 2013). The coverslips were fixed



**Fig. 1.** Characterisation of the induced pluripotent stem cell line (UALGi002-A) from a patient with LVNC. (A) Phase contrast micrograph of UALGi002-A colony cultured in feeder-free conditions. (B) Alkaline phosphatase positive staining. (C) Immunofluorescence for pluripotency markers NANOG, SOX2, OCT4 and SSEA4. Nuclei were counterstained with DAPI (blue). (D) Flow cytometry of nuclear NANOG pluripotency marker. (E) RT-PCR analysis of Sendai virus and reprogramming transgenes at day 7 after transduction (SeV C+) and at passage 11 in UALGi002-A line (V8 P11). (F) Representative metaphase showing normal diploid 46, XY karyotype. (G) Immunocytochemistry for ectodermal (TUJ1), mesodermal ( $\alpha$ -SMA) and endodermal (AFP) markers. Nuclei were counterstained with DAPI (blue). (H) Detection by immunofluorescence of the sarcomeric protein  $\alpha$ -actinin (green) and staining of the nuclei by DAPI (blue). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

with 4% paraformaldehyde (PFA) for 15 min and analyzed by immunofluorescence (Table 2) on Axioimager Z2/Apotome fluorescence microscope (Carl Zeiss).

#### 4.4. Flow cytometry

hiPSCs were dissociated using TrypLE Select (Gibco) for 3 min at RT, centrifuged at 300 g for 5 min and 100,000 cells resuspended in 200  $\mu$ l of ice-cold 0.5% PFA in PBS, for 20 min. Fixed cells were washed twice in PBS/0.5% BSA/0.1% Triton X100 and incubated with the primary antibody for 1 h at 4  $^{\circ}$ C (Table 2). After incubation, samples were washed 3 times with PBS/0.5% BSA/0.1% Triton X100, and incubated with the secondary antibodies for 1 h, at 4  $^{\circ}$ C (Table 2), protected from

light. The cells were analyzed using a FACScalibur cell analyzer (BD Biosciences) and data was analyzed by CytExpert 2.0 software.

#### 4.5. Alkaline phosphatase activity

Alkaline phosphatase staining was carried out using Alkaline Phosphatase Staining Kit II (Stemgent, MA).

#### 4.6. RT-PCR for detection of viral clearance

Total RNA was isolated from cultured hiPSC with RNeasy Mini Kit (Qiagen). 1  $\mu$ g of total RNA was used as template to obtain cDNA, using NZY First-Strand cDNA Synthesis Kit (nzytech). Viral clearance was

**Table 2**  
Reagents details.

Antibodies used for immunocytochemistry/flow-cytometry				
	Antibody	Dilution	Company Cat #	RRID
Pluripotency Markers (immunofluorescence and flow cytometry)	Rabbit anti-OCT4	1:400	Cell Signaling Technology Cat# 2840	RRID: AB_2167691
	Rabbit anti-NANOG	1:400	Cell Signaling Technology Cat# 4903	RRID: AB_10559205
	Rabbit anti-SOX2	1:400	Cell Signaling Technology Cat# 3579	RRID: AB_2195767
	Mouse anti-SSEA-4	1:200	BD Biosciences Cat# 560073	RRID: AB_1645601
Differentiation Markers	Mouse anti-TUBB3	1:500	BioLegend Cat#801213	RRID: AB_2728521
	Mouse anti-ASM	1:500	Sigma-Aldrich Cat#A5228	RRID: AB_262054
	Rabbit anti-AFP	1:100	Dako Cat# A0008	RRID: AB_2650473
	Donkey anti-Mouse 488	1:500	Molecular Probes Cat# A-21202	RRID: AB_141607
Secondary antibodies for immunofluorescence	Donkey anti-Rabbit 594	1:500	Molecular Probes Cat# A-21207	RRID: AB_141637
	Donkey anti-Rabbit 488	1:200	Molecular Probes Cat# A-21206	RRID: AB_2535792
Primers				
	Target	Size of band	Forward/Reverse primer (5'-3')	
Episomal Plasmids (RT-PCR)	SeV Plasmid	181 bp	GGATCACTAGGTGATATCGAGC/	
	hKLF4 Plasmid	410 bp	ACCAGACAAGAGTTTAAAGATATGTATC	
	hKOS Plasmid	528 bp	TTCCTGTCATGCCAGAGGAGCCC/	
	hC-MYC Plasmid	532 bp	AATGTATCGAAGGTGCTCAA	
Mycoplasma (PCR)			ATGCACCGCTACGACGTGAGCGC/	
			ACCTTGACAATCCTGATGTGG	
			TAACTGACTAGCAGGCTTGTGCG/	
			TCCACATACAGTCTGGATGATGATG	
			<b>Forward primers:</b>	
	<i>M. arginine</i>	500 bp	CGC CTG AGT AGT ACG TTC GC	
	<i>M. boris</i>		CGC CTG AGT AGT ACG TAC GC	
	<i>M. fermentans</i>		TGC CTG AGT AGT ACA TTC GC	
	<i>M. hominis</i>		CGC CTG GGT AGT ACA TTC GC	
	<i>M. hyorhinis</i>		CGC CTG AGT AGT ATG CTC GC	
	<i>M. orale</i>		TGC CTG GGT AGT ACA TTC GC	
			<b>Reverse primers:</b>	
			GCG GTG TGT ACA AGA CCC GA	
			GCG GTG TGT ACA AAA CCC GA	
			GCG GTG TGT ACA AAC CCC GA	

analyzed using the primers described in Table 2. RT-PCR reaction was performed using DreamTaq DNA Polymerase (Thermo Scientific) and PCR products were visualized on a 2% agarose gel.

#### 4.7. Karyotype analyses

Genome integrity of the hiPSC was evaluated by G-banding at 400–550 band resolution, with a minimum of 20 metaphase spreads analyzed (Genomed, Lisbon, Portugal).

#### 4.8. Fingerprinting

Genomic DNA from PBMC and hiPSC was extracted using QIAamp DNA Blood mini kit (Qiagen). Fingerprinting analyses was performed using Promega's PowerPlex 16 kit and analyzed on ABI PRISM 3100 using GeneMapper (Thermo Fisher) by STABVida, Lisbon, Portugal.

#### 4.9. Mycoplasma detection

The presence of mycoplasma was tested regularly by PCR (Uphoff and Drexler, 2001) using the Primers listed in Table 2.

#### Funding

This work was supported by Fundação para a Ciência e Tecnologia (FCT) and the Comissão de Coordenação e Desenvolvimento Regional do Algarve (CCDR Algarve) for the project ALG-01-0145-FEDER-28044 "VITAL", PTDC/BTM-TEC/28044/2017 and with individual grant to S. M. Calado (2020.01532.CEECIND). We acknowledge the Light Microscopy Unit of CBMR-UAlg. The Microscopy Unit was partially supported by national Portuguese funding FCT: PPBI-POCI-01-0145-FEDER-

022122.

#### Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Jose Braganca reports financial support, article publishing charges, equipment, drugs, or supplies, and travel were provided by Fundação para a Ciência e Tecnologia (FCT).

#### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.scr.2021.102462>.

#### References

- Calado, S.M., Bento, D., Justino, D., Mendes-Silva, L., Marques, N., Bragança, J., 2021. Generation of a human induced pluripotent stem cell line (UALGi001-A) from a patient with Left-Ventricular Noncompaction Cardiomyopathy. *Stem Cell Res.* 53, 102302.
- Finsterer, J., Stöllberger, C., Towbin, J.A., 2017. Left ventricular noncompaction cardiomyopathy: cardiac, neuromuscular, and genetic factors. *Nature Rev. Cardiology* 14 (4), 224–237. <https://doi.org/10.1038/nrcardio.2016.207>.
- Takahashi, K., Yamanaka, S., 2006. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. *Cell* 126 (4), 663–676. <https://doi.org/10.1016/j.cell.2006.07.024>.
- Lian, X., Zhang, J., Azarin, S.M., Zhu, K., Hazeltine, L.B., Bao, X., Hsiao, C., Kamp, T.J., Palecek, S.P., 2013. Directed cardiomyocyte differentiation from human pluripotent stem cells by modulating Wnt/beta-catenin signaling under fully defined conditions. *Nat. Protoc.* 8, 162–175. <https://doi.org/10.1038/nprot.2012.150>.
- Uphoff, C.C., Drexler, H.G., 2001. Prevention of mycoplasma contamination in leukemia-lymphoma cell lines. *Hum. Cell* 14, 244–247.