



Lab resource: Stem cell line

## Generation of an isogenic, gene-corrected control cell line of the spinocerebellar ataxia type 2 patient-derived iPSC line H271



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### ABSTRACT

Spinocerebellar ataxia type 2 (SCA2) is a neurodegenerative disease primarily affecting the cerebellum. Very little is known about the molecular mechanisms underlying the disease and, to date, no cure or treatment is available. We have successfully generated *bona fide* induced pluripotent stem cell (iPSC) lines of SCA2 patients in order to study a disease-specific phenotype. Here, we demonstrate the gene correction of the iPSC line H271 clone 1 where we have exchanged the expanded CAG repeat of the *ATXN2* gene with the normal length found in healthy alleles. This gene corrected cell line will provide the ideal control to model SCA2 by iPSC technology.

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### Resource table

Name of Stem Cell construct	H271 clone1 GC
Institution	University of Copenhagen and Bioneer A/S
Person who created resource	Adele G. Marthaler, Benjamin Schmid
Contact person and email	Adele G. Marthaler, <a href="mailto:adele.marthaler@sund.ku.dk">adele.marthaler@sund.ku.dk</a>
Date archived/stock date	April 2015
Origin	Human induced pluripotent stem cell line H271 clone 1
Type of resource	Gene-corrected induced pluripotent stem cells; originally derived from skin fibroblasts of patient with spinocerebellar ataxia type 2
Sub-type	Cell line
Key transcription factors	Episomal plasmids containing <i>hOCT4</i> , <i>hSOX2</i> , <i>hL-MYC</i> , <i>hKLF4</i> , <i>hLIN28</i> , and <i>shP53</i> (Addgene plasmids 27077, 27078 and 27080; Okita et al. 2011)

(continued)

Authentication	Identity and purity of stem cell line confirmed (Fig. 1)
Link to related literature (direct URL links and full references)	
Information in public databases	

### Resource details

An induced pluripotent stem cell (iPSC) line had been generated from human skin fibroblasts of a male, symptomatic 33-year-old spinocerebellar type 2 (SCA2) patient (anonymized as H271) using episomal vectors carrying transcripts for human *OCT4*, *SOX2*, *KLF4*, *L-MYC*, *LIN28*, and small hairpin RNA for *TP53* (Okita et al., 2011). This cell line, H271 clone (c) 1, has been described as a *bona fide* iPSC line with a normal karyotype (Marthaler et al., submitted to Stem Cell Research).

We have generated a gene-corrected clone of H271 c1 using the CRISPRs/Cas9 system (Ran et al., 2013), where the expanded 44 CAG region in the *ATXN2* gene has been replaced with a wildtype 22 CAG repeat (Fig. 1A). Successful exchange was validated by sequencing (Fig. 1B). We have furthermore confirmed that the DNA sequence stayed intact and no frameshift or other mutation had been introduced into the gene edited site, by analyzing the region around the CRISPR cutting site (nucleotide 121–143 in Fig. 1A).

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Subsequently, we confirmed that the gene corrected clone of H271 c1, termed H271 c1 GC, remained truly pluripotent. This was demonstrated by the expression of key pluripotency markers on RNA, as well as protein level (Fig. 1C and D). Additionally, H271 c1 GC retained the potential to differentiate into cell types of the three germ layers upon embryoid body formation (Fig. 1E). More importantly, no genetic chromosomal aberrations were introduced by the gene editing process and the cells still exhibit a normal karyotype (Fig. 1F).

In summary, we have generated an isogenic, gene-corrected iPSC line of an existing SCA2 iPSC line. Together with two more SCA2 patient-derived iPSC lines and their corresponding isogenic, gene-corrected controls (Marthaler et al., submitted to Stem Cell Research), they will serve as an ideal study tool for *in vitro* disease modeling of SCA2.

## Materials and methods

### CRISPR design

Isogenic gene-corrected controls were obtained using the CRISPRs/Cas9 system in combination with a homologous construct in the pEay Flox II vector. CRISPRs targeting each site of the CAG repeat of the *ATXN2* locus were designed at <http://crispr.mit.edu/>. The CRISPRs were generated following the protocol from Ran et al. (Ran et al. 2013) in a single plasmid containing both sgRNA and the Cas9 (Addgene plasmid ID 48139).

### Nucleofection

iPSCs growing on dishes coated with matrigel (Corning Bioscience) in E8 medium (Gibco) were detached using Accutase (Gibco).  $10^6$  cells were co-nucleofected with 2  $\mu$ g of each CRISPR/Cas9 plasmid and 1  $\mu$ g of the resistance marker using the Amaxa 4D Nucleofector (program CA167) and P3 Primary Cell Kit according to the manufacturer's instructions (Lonza). iPSCs were subsequently transferred back to a matrigel-coated dish in E8 medium supplemented with 1 mM ROCK inhibitor (Sigma). 24 h postnucleofection, cells were subjected to neomycin selection and allowed to recover for a week. Resistant colonies were then picked and expanded for genotyping.

### Genotyping

DNA for genotyping was extracted using the FlexiGene Kit (Qiagen). PCR genotyping was performed using TEMPase Hot Start DNA Polymerase (Ampliqon) according to the manufacturer's instructions at an annealing temperature of 58 °C. The following primers were designed 300 base pairs up- and downstream of the CRISPR cutting site to ensure detection of insertion at homologous site: SCA2 long1 forward 5'-CAGACCCGCTTGAGGAAG-3' and SCA2 long1 reverse 5'-GAGGAGACCGAGGACGAGG-3'. Clones where the expanded SCA2 allele was successfully replaced with the *ATXN2* wildtype construct were subjected to sequencing to exclude introduction of frameshifts or other mutations.

### Sequencing

Sanger sequencing of a 300 base pair region around the CAG repeat region of the *ATXN2* gene was carried out in an ABI PRISM 310 Genetic Analyzer using the primers SCA2 seq2 forward 5'-CTTG GTCTCGGCGGC-3' and SCA2 seq2 reverse 5'-GAGGAGACCGAGGA CGAGG-3'.

### RNA extraction, cDNA synthesis, and quantitative real-time PCR (qRT-PCR)

RNA was extracted using RNeasy Mini (QIAGEN) and cDNA synthesis was performed using Revert Aid First Strand cDNA synthesis kit (Thermo Scientific) according to the manufacturers' protocols. qRT-PCR was carried out using LightCycler 480 SYBR Green I Master (Roche). Data was plotted using the delta delta Ct algorithm,  $2^{(-\Delta\Delta Ct)}$ . The following primers were used:

OCT4 for	5'-CCCCAGGGCCCCATTTTGGTACC-3'
OCT4 rev	5'-ACCTCAGTTTGAATGCATGGGAGAGC-3'
SOX2 for	5'-TTCACATGTCCAGCACTACCAGA-3'
SOX2 rev	5'-TCACATGTGTGAGAGGGGCGATGTGC-3'
NANOG for	5'-AAAGAATCTTCACATATGCC-3'
NANOG rev	5'-GAAGGAAGAGGAGAGACAGT-3'
REX1 for	5'-TTTCTGAGTACGTGCCAGGCAA-3'
REX1 rev	5'-CTCTGAGAAAGCATCTCTCTCTC-3'
LIN28 for	5'-AGCCATATGGTAGCCTCATGTCCGC-3'
LIN28 rev	5'-TCAATTCTGTGCTCCGGGAGCAGGGTAGG-3'
ACTB for	5'-TCAAGATCATTGCTCCTCTGAG-3'
ACTB rev	5'-ACATCTGCTGGAAGGTGGACA-3'
RPL13A for	5'-TTCCAAGCGGCTGCCGAAGA-3'
RPL13A rev	5'-TCCCGCCAGCAGTACCTGT-3'
HSP90AB1 for	5'-TCCCGCCAGTGTGGGAC-3'
HSP90AB1 rev	5'-TCCATGGTGCACTTCTCAGGC-3'
GAPDH for	5'-CTGGTAAAGTGGATATTGTGCCAT-3'
GAPDH rev	5'-TGGAATCATATTGGAACATGTAACC-3'

### Immunocytochemistry

Immunocytochemistry was performed as previously described (Marthaler et al., 2013). The following primary antibodies were used: Anti-OCT4 (Santa Cruz, sc 8628); anti-NANOG (Peprotech, 500P236); anti-TRA1-60 (BioLegend, 330602); anti-SSEA4 (BioLegend, 330,402); anti-TUBB3 (Millipore, MAB1637); anti-SMA (Dako, M0851), anti-AFP (Dako, A0008); all 1:500. Secondary antibodies used were: Alexa Fluor 488 donkey anti-rabbit (A21206), donkey anti-goat (A11055), and goat anti-mouse (A11017), all 1:2000 (Invitrogen).

### Embryoid body differentiation

iPSCs growing in E8 medium (Gibco) on matrigel (Corning Bioscience) were dissociated with EDTA (Gibco) and allowed to form aggregates in none-coated cell culture dishes. On day 3, aggregates were transferred to matrigel-coated dishes and medium was switched to differentiation medium: DMEM/F12 containing 20% FBS, L-glutamine, and non-essential amino acids (all Gibco) for meso- and endoderm induction, or DMEM/F12 containing 50% neurobasal medium, B27, N2, and L-glutamine (all Gibco) for ectoderm induction. Cells were fixed for immunocytochemistry on day 14.

### Verification and authentication

An intact genome was demonstrated by karyotyping using G-banding (Fig. 1F). Analysis was performed at the Institute of Medical Genetics and Applied Genomics, University of Tübingen, Tübingen, Germany.

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