



Lab resource: Stem Cell Line



## Generation of a human iPSC line GIBHi002-A-2 with a dual-reporter for NKX2-5 using TALENs

Min Zhou<sup>a,1</sup>, Rui Wei<sup>b,d,1</sup>, Yu Jiang<sup>b,1</sup>, Jian Fu<sup>a,1</sup>, Yuqing Liu<sup>a</sup>, Bo Yang<sup>a</sup>, Baorong Yu<sup>a</sup>, Yun Lin<sup>a</sup>, Xinru Ran<sup>b</sup>, Wing-Hon Lai<sup>b</sup>, Meng Chu<sup>a</sup>, Yang Hu<sup>c</sup>, Jiayin Yang<sup>a,c,\*</sup>, Hung-Fat Tse<sup>b,d,\*</sup>

<sup>a</sup> Cell Inspire Biotechnology Co., Ltd., Shenzhen 518101, China

<sup>b</sup> Department of Medicine, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China

<sup>c</sup> Cell Inspire Therapeutics Co., Ltd., Shenzhen 518101, China

<sup>d</sup> Department of Medicine, The University of Hong Kong-Shenzhen Hospital, Shenzhen 518053, China

### ABSTRACT

The human transcription factor NKX2-5 plays an important role in cardiac formation and development, and thus it can be used for isolation of cardiomyocytes (CMs) differentiated from human pluripotent stem cells (hPSCs). Here, we knocked-in enhanced GFP (eGFP) and Pac (a puromycin resistant gene; Puro<sup>R</sup>) into the exon 1 coding region of NKX2-5 from a human iPSC line iPSN0003 using TALENs. The generated GIBHi002-A-2 enables us to monitor and optimize cardiac differentiation procedures via the cardiac progenitor cells (CPCs), as well as to isolate iPSC-derived CMs for drug screening.

### Resource Table:

Unique stem cell line identifier	GIBHi002-A-2
Alternative name(s) of stem cell line	NKX2-5 <sup>GFP-Puro/wt</sup> iPSC
Institution	Cell Inspire Biotechnology (CIB), Shenzhen, China; Department of Medicine, the University of Hong Kong (HKU), Hong Kong SAR, China
Contact information of distributor	Jiayin Yang; <a href="mailto:jyyang@cib.cc">jyyang@cib.cc</a>
Type of cell line	iPSC
Origin	Human
Additional origin info	Age: 24 Sex: female Ethnicity if known: Caucasian
Cell Source	Epithelia cells from urine
Clonality	Clonal
Method of reprogramming	Retroviral Yamanaka factors
Genetic Modification	Yes
Type of Modification	Targeted knock-in
Associated disease	N/A
Gene/locus	NKX2-5, 5q35.1
Method of modification	TALENs
Name of transgene or resistance	eGFP and Pac (Puro <sup>R</sup> )

(continued on next column)

### (continued)

Inducible/constitutive system	N/A
Date archived/stock date	June 2015
Cell line repository/bank	<a href="https://hpscereg.eu/cell-line/GIBHi002-A-2">https://hpscereg.eu/cell-line/GIBHi002-A-2</a>
Ethical approval	Ethics committee: Institutional Review Board of the University of Hong Kong/Hospital Authority Hong Kong West Cluster (Approval No. UW 13-342)

### 1. Resource utility

We knocked-in a cassette containing eGFP and Pac into the NKX2-5 locus of normal human iPSCs to generate GIBHi002-A-2 by TALEN-mediated homologous recombination. GIBHi002-A-2 enables us to monitor and optimize cardiac differentiation procedures from human iPSCs, as well as to isolate CPCs and CMs by drug selection (Table 1).

### 2. Resource details

Patient-specific CMs can be differentiated from human iPSCs and are widely used in disease modeling and drug toxicity testing (Burridge

\* Corresponding authors at: Cell Inspire Therapeutics Co., Ltd., Shenzhen 518101, China (J. Yang). Department of Medicine, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China (H.-F. Tse).

E-mail addresses: [jyyang@cib.cc](mailto:jyyang@cib.cc) (J. Yang), [hftse@hku.hk](mailto:hftse@hku.hk) (H.-F. Tse).

<sup>1</sup> Co-first authors.

<https://doi.org/10.1016/j.scr.2020.102120>

Received 27 November 2020; Accepted 6 December 2020

Available online 10 December 2020

1873-5061/© 2020 The Author(s).

Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license

(<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

**Table 1**  
Characterization and validation.

Classification	Test	Result	Data
Morphology Phenotype	Photography	Normal	Fig. 1B
	Qualitative analysis	Expression of OCT4, NANOG, Tra-1-60, SSEA4	Fig. 1E
	Quantitative analysis	Relative expression to H9 hESC (set as 1): OCT4, 2.05; SOX2, 1.20; NANOG, 1.81; REX1, 1.15.	Fig. 1D
Genotype	Karyotype (G-banding) and resolution	46, XX. Resolution 320–400	Fig. 1C
Identity	Microsatellite PCR (mPCR) OR STR analysis	Not performed	N/A
		20 sites tested for engineered iPSCs and 16 sites tested for donor iPSC. All tested sites matched	Submitted in archive with journal
Mutation analysis (IF APPLICABLE)	Sequencing	N/A	N/A
	Southern Blot OR WGS	N/A	N/A
Microbiology and virology	Mycoplasma	Mycoplasma testing by luminescence: Negative	Supplementary Fig. 1F
Differentiation potential	Teratoma formation	Proof of three germ layers formation	Fig. 1F
Donor screening (OPTIONAL)	HIV 1 + 2 Hepatitis B, Hepatitis C	N/A	N/A
Genotype additional info (OPTIONAL)	Blood group genotyping	N/A	N/A
	HLA tissue typing	N/A	N/A

et al., 2016). However, the heterogeneity of the differentiated cells from hPSCs limits their applications. To facilitate the identification and isolation of the human hPSCs-derived CMs, an eGFP coding sequence was knocked into the NKX2-5 locus of a hESC line (Elliott et al., 2011). This line enables purification or monitoring the differentiation process of hESCs-derived CMs using eGFP. However, as dissociation and sorting may introduce extra stress to CMs, we aimed to generate a human iPSC line with a dual-reporter, eGFP and Pac, driven by a NKX2-5 promoter.

We designed a cassette containing eGFP and Pac, which were linked by a 2A sequence, and this cassette was then inserted into a donor plasmid containing left and right homologous arms of 700–1000 base pairs that flank the genomic site of NKX2-5 locus. A loxP-site-flanked PGK-Neo<sup>R</sup> selection cassette enables enrichment of targeted clones (Fig. 1A). Additionally, we designed a pair of TALENs to target the exon 1 of NKX2-5 to initiate a double-strand break (Supplementary Fig. 1A), which has been proved to be able to improve the homologous recombination efficiently (Hockemeyer et al., 2011). Junction PCR (F1/R1 and F2/R2) and the CEL-I PCR (F3/R3) analysis confirmed that several single cell-derived clones have targeted monoallelic integration of donor constructs (Supplementary Fig. 1B–1C). We further used Sanger sequencing to exclude clones that have non-homologous end joining event in the cutting site of the second allele (Supplementary Fig. 1D). We selected clone 18 for further experiment. To remove the drug selection cassette, we overexpressed CRE recombinase in clone C18 and identified a subclone C14 (GIBHi002-A-2) that was free of drug selection cassette (Supplementary Fig. 1E). GIBHi002-A-2 has typical hESC morphology (Fig. 1B, scale bar represents 200  $\mu$ m), a normal karyotype (Fig. 1C), and express pluripotency markers (Fig. 1D and 1E; scale bars represent 50  $\mu$ m). In addition, GIBHi002-A-2 can form teratomas containing tissues of three germ layers after subcutaneously injected into SCID mice (Fig. 1F; scale bars represent 50  $\mu$ m). Moreover, GIBHi002-A-2 was free of mycoplasma contamination (Supplementary Fig. 1F), and has the same STR

profile with its parental cells (Submitted and archived with journal).

We further differentiated GIBHi002-A-2 into the cardiac lineage (Supplementary Fig. 1G). As expected, GFP can be observed as early as day-8 of differentiation, and the expression level was stabilized at around day-11 of differentiation (Supplementary Fig. 1H, scale bars represent 200  $\mu$ m). Quantitative real-time PCR (RT-qPCR) showed that the differentiated cells expressed lineage specific markers of CPCs (ISL-1 and NKX2-5) and CMs (TNNT2; Supplementary Fig. 1I) at the indicated stages. As expected, immunofluorescent staining showed that the GFP<sup>+</sup> cells co-expressed NKX2-5, TNNT2 and ACTN2 (Fig. 1G; scale bars represent 200  $\mu$ m). After treating the day-8 differentiated CMs with puromycin for 8 days, we observed almost all cells are GFP<sup>+</sup> (Fig. 1H; scale bars represent 100  $\mu$ m), indicating GIBHi002-A-2-derived CMs can be enriched by puromycin.

### 3. Materials and methods

#### 3.1. Cell culture

Human iPSCs were cultured on Matrigel-coated plates and fed with mTeSR1 medium (STEMCELL Technologies) at 37 °C in a 5% CO<sub>2</sub> humidified incubator. When grew confluence, cells were dissociated with Accutase and seeded to a new Matrigel-coated plate with a split ratio of 1:6 in mTeSR1. Five  $\mu$ M Y27632 (Sigma-Aldrich) was used in the culture medium on the first day of passaging to promote cell survival.

#### 3.2. Genetic modification

The donor plasmids and the designed TALENs were co-delivered to human iPSCs by nucleofection using Amaxa Nucleofector II Electroporation Machine (Lonza). The transfected cells were plated on Matrigel-coated plate and cultured in mTeSR1 supplemented with 10  $\mu$ M Y27632. To enrich the targeted cells, cells were treated with 0.5 mg/mL G418 in mTeSR1 supplemented with 10  $\mu$ M Y27632 for 24 h, then medium was changed to mTeSR1 for recovery. For single cell cloning, the enriched human iPSCs were dissociated into a single cell suspension with Accutase, and seeded to feeder- or Matrigel-coated flasks at a density of 50–200 cells/cm<sup>2</sup>. Seven to 10 days later, single cell-derived colonies were picked for expansion and characterization. Genomic DNA of cells was obtained using QuickExtract™ DNA Extraction Solution 1.0 (Epicentre), and Junction PCR, CEL-I PCR and CRE-out PCR were employed to identify the targeted clones using primers listed in Table 2.

#### 3.3. Cardiac differentiation

Human iPSCs were differentiated into CMs using a PSC Cardiomyocyte Differentiation Kit (Gibco). In brief, when iPSCs grow to an optimal confluence in E8 medium (day-0), change medium with Medium A. 48 h later, change medium with Medium B and cultured for another 2 days. On day-4 and thereafter, change the medium to CMs Maintenance Medium and replace the medium every two days. To enrich CMs, day-8 differentiated cells were treated with 1.5  $\mu$ g/mL puromycin (Yeasen Biotech) for 8 days.

#### 3.4. Immunofluorescence staining

Cells were fixed with 4% paraformaldehyde solution at 4 °C overnight or room temperature for 10 min, then washed with PBST solution (PBS supplemented with 0.05% triton-X) for three times. Cells were stained with primary antibody overnight, followed by the corresponding secondary antibody for 1 h at room temperature. Finally, cell nucleus were stained with DAPI (Sigma-Aldrich). Antibodies used in this study are listed in Table 2.

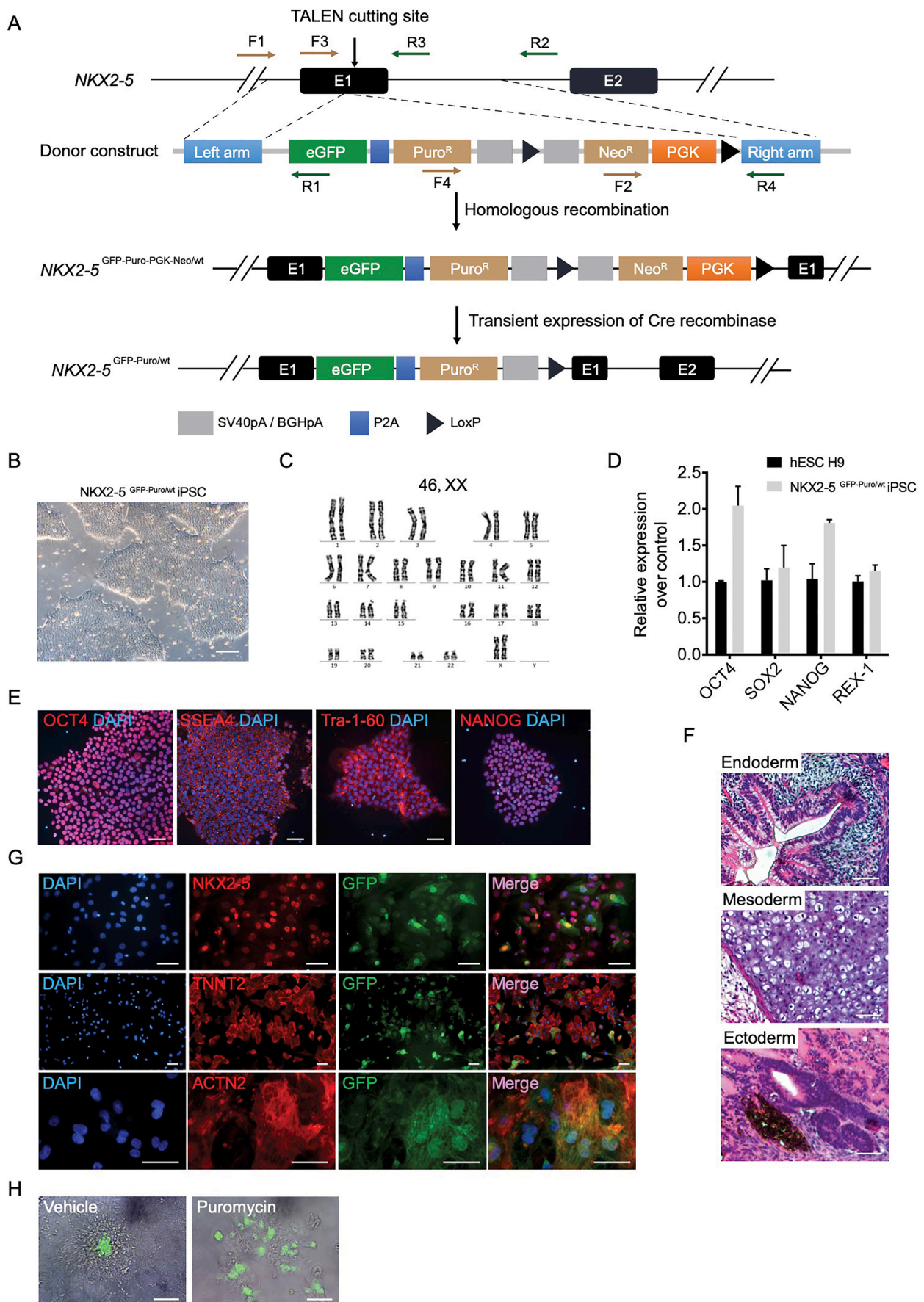


Fig. 1. Characterization and validation of GIBHi002-A-2.

**Table 2**  
Reagents details.

Antibodies used for immunocytochemistry/flow-cytometry				
	Antibody	Dilution	Company Cat # and RRID	
Pluripotency Markers	Goat anti-NANOG	1:20	R&D Systems Cat# AF1997, RRID: AB_355097	
	Rabbit anti-OCT4	1:200	Invitrogen Cat# PA5-27438 RRID: AB_2544914	
	Mouse anti-Tra-1-60	1:50	Millipore Cat# MAB4360 RRID: AB_2119183	
	Mouse anti-SSEA4	1:60	Abcam Cat# ab16287 RRID: AB_778073	
Cardiac Differentiation Markers	Rabbit anti-NKX2-5	1:50	Santa Cruz Cat# sc-14033	
	goat anti-TNNT2	1:250	Abcam Cat# ab64623, RRID: AB_1139590	
	mouse anti-ACTN2	1:250	Sigma-Aldrich Cat#A7811 RRID: AB_476766	
Secondary antibodies	NL557 Donkey Anti-Goat IgG	1:200	R&D Systems Cat# NL001 RRID: AB_663766	
	Alexa Fluor 555 Goat anti-Rabbit IgG	1:1000	Invitrogen Cat# A21428 RRID:AB_141784	
	Alexa Fluor 555 Goat anti-Mouse IgG (H + L)	1:1000	Invitrogen Cat# A21424 RRID: AB_141780	
	Alexa Fluor 594 Goat anti-Rabbit IgG (H + L)	1:1000	Invitrogen Cat# A11072	
	Alexa Fluor 594 Rabbit anti-mouse IgG (H + L)	1:1000	Invitrogen Cat# A11062	
	Alexa Fluor 594 Donkey anti-goat IgG (H + L)	1:1000	Invitrogen Cat# A11058	
Primers	<b>Target</b>	<b>Forward/Reverse primer (5'-3')</b>		
	Pluripotency Markers (qPCR)	<i>OCT4</i>	AGTTTGTGCCAGGGTTTTTG ACTTCACCTCCCTCCAACC TTTGGAAGCTGCTGGGGAAG GATGGGAGGAGGGAGAGGA AGTCTCCAAGCGACGAAAA TTTCACGTTTGCAACTGTCC AGGCCAGTCCAGAATACCAG TAGGTATCCGTCAGGGAAGC GTGGACCTGACCTGCCGTCT GGAGGAGTGGGTGTCGCTGT	
		<i>NANOG</i>	GCAGAGTGACATAGATCAGCCTG GCCTCAATAGGACTGGCTACCA CATTTTACCCGGGAGCCTAC CTTTGTCCAGCTCCACTGC CATGTCTCAGCCACTGACC TGGCCTTGCTGGGTTAT CTAACATCAAATGGGGTGAGG CGGAGATGATGACCCTTTTG TCCAACACGGGAAAACAAGGTG CGCTGAACCTGTGGCCGTTTAC GATACTTTCTCGGCAGGAGCA ACCTATGAATTTCTCCCGGC GAGCAAAGACCCCAACGAGA GGCGCAAAGAAAAGAAAGCA CCGTGGGCAGCGCCGCTTCTG GGGGGCCTGTGTTCTCCTCACC	
		<i>SOX2</i>		
		<i>REX1</i>		
		<i>GAPDH</i>		
	Cardiac Markers (qPCR)	<i>ISL-1</i>		
		<i>NKX2-5</i>		
		<i>TNNT2</i>		
		<i>GAPDH</i>		
Junction PCR	Left arm (F1/R1)	TCCAACACGGGAAAACAAGGTG CGCTGAACCTGTGGCCGTTTAC		
	Right arm (F2/R2)	GATACTTTCTCGGCAGGAGCA ACCTATGAATTTCTCCCGGC GAGCAAAGACCCCAACGAGA GGCGCAAAGAAAAGAAAGCA CCGTGGGCAGCGCCGCTTCTG GGGGGCCTGTGTTCTCCTCACC		
CRE-out PCR	F4/R4			
CEL-1 PCR	TALEN cutting region (F3/R3)			

### 3.5. RT-qPCR

Total RNA was extracted from cell lysates in TRI Reagent® (Sigma-Aldrich) using RNAPrep pure kit (TIANGEN) according to the manufacturer's protocol. A PrimeScript™ RT reagent kit with gDNA Eraser

(TaKaRa) was used for reverse transcription of 1 µg RNA to cDNA. RT-qPCR was carried out using a Real-Time PCR machine and SYBR Green Premix EX Taq™ (Takara) or a QuantiFast SYBR Green PCR Kit (Qiagen). *GAPDH* was used for normalization, and samples were measured in triplicate. The primers used are listed in Table 2.

### 3.6. Karyotype

At day-2 post passaging, human iPSCs were treated with 100 µg/mL colchicine for 10 min. Then, at least 20 metaphases were randomly selected and analyzed by 320–400 G-banding chromosome analysis.

### 3.7. Teratoma formation

Human iPSCs cultured on Matrigel were dissociated with Accutase, and cells were injected subcutaneously into the flanks, or intramuscularly into the hind legs of SCID mice. Teratomas were dissected and sectioned, and were stained with hematoxylin & eosin. The animal experiment was approved by local Institutional Review Board (CULATR 3404-14).

### 3.8. STR analysis

Genomic DNA was extracted from GIBHi002-A-2 and the donor iPSCs, and were sent to third party diagnostic labs, Genetic Testing Biotechnology or Guangzhou KingMed Centre for Clinical Laboratory, for STR analysis respectively. Fifteen or nineteen STR loci plus Amelogenin were tested.

### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

### Acknowledgement

We thank Dr. Chunmei Li for the kind advices on the manuscript. This work was supported by the Shenzhen-Hong Kong Technology Cooperation Funding Scheme (SGLH20180627143202102; GHP/130/18/SZ), the Guangdong-Hong Kong Technology Cooperation Funding Scheme (GHP/046/17GD), and the National Natural Science Foundation of China (81873521).

### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.scr.2020.102120>.

### References

- Burridge, P.W., Li, Y.F., Matsa, E., Wu, H., Ong, S.-G., Sharma, A., Holmström, A., Chang, A.C., Coronado, M.J., Ebert, A.D., Knowles, J.W., Telli, M.L., Witteles, R.M., Blau, H.M., Bernstein, D., Altman, R.B., Wu, J.C., 2016. Human induced pluripotent stem cell-derived cardiomyocytes recapitulate the predilection of breast cancer patients to doxorubicin-induced cardiotoxicity. *Nat. Med.* 22 (5), 547–556. <https://doi.org/10.1038/nm.4087>.
- Elliott, D.A., Braam, S.R., Koutsis, K., Ng, E.S., Jenny, R., Lagerqvist, E.L., Biben, C., Hatzistavrou, T., Hirst, C.E., Yu, Q.C., Skelton, R.J.P., Ward-van Oostwaard, D., Lim, S.M., Khammy, O., Li, X., Hawes, S.M., Davis, R.P., Goulburn, A.L., Passier, R., Prall, O.W.J., Haynes, J.M., Pouton, C.W., Kaye, D.M., Mummery, C.L., Elefanty, A. G., Stanley, E.G., 2011. NKX2-5eGFP/w hESCs for isolation of human cardiac progenitors and cardiomyocytes. *Nat. Methods* 8 (12), 1037–1040. <https://doi.org/10.1038/nmeth.1740>.
- Hockemeyer, D., Wang, H., Kiani, S., Lai, C.S., Gao, Q., Cassady, J.P., Cost, G.J., Zhang, L., Santiago, Y., Miller, J.C., Zeitler, B., Cherone, J.M., Meng, X., Hinkley, S. J., Rebar, E.J., Gregory, P.D., Urnov, F.D., Jaenisch, R., 2011. Genetic engineering of human pluripotent cells using TALE nucleases. *Nat. Biotechnol.* 29 (8), 731–734. <https://doi.org/10.1038/nbt.1927>.