

T1D iPSC cell line 1018A

- Age of onset: 10

Quality controls



Cell Line Characterization

Cell Line ID: 1018A
 Passage #: p18
 Specimen Type: Human PSC Culture
 Indication for Study: Routine Culture QC

Lab #: CLG-40154
 PI: Dieter Egli
 Contact Person: Morgan Smith
 Email: ms6040@cumc.columbia.edu
 Address:
 Columbia University
 1150 St Nicholas Avenue, Room 605
 New York, New York 10032

Test Code: 100
 Account #: NA
 PO #: 08172020

Date Received: 9/3/2020
 Date Reported: 9/16/2020
 Time in Culture: 1 Day

Additional copies sent to:

Banding Technique: GTL
 Metaphases Counted: 20
 Analyzed: 7
 Karyotyped: 2

Band Resolution: Fair

RESULTS: 46,XX[19] Apparently NORMAL Human Female Karyotype

Non-clonal Aberrations: 43,XX,-8,-10,-20(one cell)

INTERPRETATION:

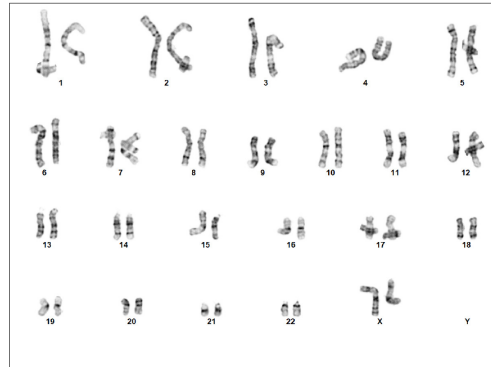
Cytogenetic analysis was performed on twenty G-banded metaphase cells from human cell line 1018A p18. Nineteen cells demonstrated an apparently normal female karyotype, and one cell demonstrated non-clonal chromosome aberrations (listed above), which are most likely artifacts of culture.



Case name: CLG-40154
 Cell Line Name: 1018A p18



Result: 46,XX



Case: CLG-40154 Slide: 40154-2_9 Cell: M38/0_cell 652



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Cell Line DNA Fingerprint Report

Contact Person: Ryan Viola
 PI: Dieter Egli
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 Email: nw2399@cumc.columbia.edu
 Tel: 212-851-4890
 Columbia University

Lab #: CLG-32566
 Cell Line ID: 1018A
 Passage: 13
 Species: Human
 Cell Type: iPSC
 Feeders: None

Date Received: 6/5/2018
 Date Reported: 6/21/2018
 Sample Type: Frozen Cells
 Reason for Study: Cell Line DNA STR profile

PO: nw053118
 Test Code: 321

Amelogenin	X	D18S51	13	15
WVA	16	Penta E	12	14
D8S1179	10	D5S818	11	13
TPOX	8	D13S317	9	11
FGA	25	D7S820	9	10
D3S1358	15	D16S539	11	13
TH01	9,3	CSF1PO	10	12
D21S11	28	Penta D	9	13

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Data availability & Publications

- Methylome [GSE61657](#)
- RNA seq and Methylome. Biosample [GSM1510138](#)

- Johannesson, B., Sagi, I., Gore, A., Paull, D., Yamada, M., Golav-Lev, T., LeDuc, C., Shen, Y., Stern, S., Xu, N., Ma, H., Kang, E., Mitalipov, S., Sauer, M., Zhang, K., Benvenisty, N., Egli, D* ., Comparable frequencies of coding mutations and loss-of-imprinting in human pluripotent stem cells derived by nuclear transfer and defined factors. Cell Stem Cell, 2014, (15), pp. 1-9. [doi:10.1016/j.stem.2014.10.002](https://doi.org/10.1016/j.stem.2014.10.002). [PMID: 25517467](https://pubmed.ncbi.nlm.nih.gov/25517467/)

Functional analysis and publications

- Beta cell differentiation

Sui L, Danzl N, Campbell SR, Viola R, Williams D, Xing Y, Wang Y, Phillips N, Poffenberger G, Johannesson B, Oberholzer J, Powers AC, Leibel RL, Chen X, Sykes M, **Egli D***. [Beta Cell Replacement in Mice Using Human Type 1 Diabetes Nuclear Transfer Embryonic Stem Cells](#). Diabetes. 2018 Jan;67(1):26-35. doi: 10.2337/db17-0120. [PMID: 28931519](#)

Other analysis

HLA genotype info

LabID			DRB_1	DQA_1	DQB_1	DRB_2	DQA_2	DQB_2	HLA A1	HLA A2	HLA B1	HLA B2
1018			402	301	302	405	301	201	1	31	18	73