



Cell Line Information Sheet

Cell Line Name and Description:	Example; Human Induced Pluripotent Stem Cells
Consent status:	Research only; Not consented for distribution
Depositor Name and Institution:	Dr. Christine Bear; The Hospital for Sick Children
Parental Name and Description:	Example; Peripheral Blood
Disease:	Cystic Fibrosis; F508del-CFTR
Donor Information:	Female; XX yrs
Reprogramming Method:	Sendai viral expression of Oct4, Sox2, Klf4, and Myc genes
Culture Format:	Culture medium: E8 (Life Technologies #A1517001); Subst rate: Matrigel (Corning #354277)
Incubation Conditions:	37°C, 5% CO ₂ , >95% RH, Subculture: single cell passaging using GCDR (StemCell Technologies #07174)
Passage No:	P3+7
Thaw Recommendations:	1 vial should be thawed into 2 wells of a 6 well plate

Test Description	Method	Expected Result	Result												
Expression of pluripotency-associated proteins	Flow cytometry	≥ 80% of population is positive for expression of surface markers (SSEA4, Tra-1-60), and intracellular marker (OCT4).	<table> <thead> <tr> <th>Antigen</th> <th>% Expressing-cells</th> </tr> </thead> <tbody> <tr> <td>SSEA4</td> <td>94.1%</td> </tr> <tr> <td>Tra-1-60</td> <td>98.0%</td> </tr> <tr> <td>OCT4</td> <td>98.0%</td> </tr> <tr> <td>SOX2</td> <td>98.1%</td> </tr> </tbody> </table> (Histograms shown in Figure 1)	Antigen	% Expressing-cells	SSEA4	94.1%	Tra-1-60	98.0%	OCT4	98.0%	SOX2	98.1%		
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Gene expression of pluripotency markers	qRT-PCR	≥ 80% expression measured in hESC reference standard (HES2 hESCs on Matrigel).	<table> <thead> <tr> <th>Gene</th> <th>Relative Expression</th> </tr> </thead> <tbody> <tr> <td>OCT4</td> <td>203%</td> </tr> <tr> <td>NANOG</td> <td>159%</td> </tr> <tr> <td>DNMT3B</td> <td>157%</td> </tr> </tbody> </table>	Gene	Relative Expression	OCT4	203%	NANOG	159%	DNMT3B	157%				
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Germ layer differentiation	Directed Differentiation Followed by qPCR	Increased expression of germ lineage-specific marker relative to starting pluripotent cell population	<table> <thead> <tr> <th>Germ Layer</th> <th>Gene</th> <th>Fold Induction</th> </tr> </thead> <tbody> <tr> <td>Endoderm</td> <td>SOX17</td> <td>4,300</td> </tr> <tr> <td>Mesoderm</td> <td>HAND1</td> <td>91,800</td> </tr> <tr> <td>Ectoderm</td> <td>SOX1</td> <td>67</td> </tr> </tbody> </table>	Germ Layer	Gene	Fold Induction	Endoderm	SOX17	4,300	Mesoderm	HAND1	91,800	Ectoderm	SOX1	67
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Definitive endoderm differentiation – gene expression	Directed Differentiation Followed by qPCR	Increased expression of additional endoderm lineage-specific marker relative to starting pluripotent cell population	<table> <thead> <tr> <th>Gene</th> <th>Fold Induction</th> </tr> </thead> <tbody> <tr> <td>GATA 6</td> <td>12,000</td> </tr> <tr> <td>GATA 4</td> <td>7,000</td> </tr> <tr> <td>FOXA2</td> <td>2,700</td> </tr> </tbody> </table>	Gene	Fold Induction	GATA 6	12,000	GATA 4	7,000	FOXA2	2,700				
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Definitive endoderm differentiation – protein expression	Directed Differentiation Followed by Flow cytometry	≥ 80% of population is double positive for expression of DE markers (cKIT and CXCR4)	<table> <thead> <tr> <th>% Expressing-cells</th> </tr> </thead> <tbody> <tr> <td>91.8%</td> </tr> </tbody> </table> (Histograms shown in Figure 2)	% Expressing-cells	91.8%										
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Mycoplasma	Lonza MycoAlert Plus kit	None detected	None detected												
Identity	STR: PCR profiling of 9 STR regions plus Amelogenin for gender determination.	Consistent with expected ¹	Consistent with parental - Amel: XX CSF1PO:10,10 D21S11:32.2,33.2 TH01:9,9,3 D13S317:8,12 D5S818:11,12 TPOX: 8,9 D16S539:8,12 D7S820:9,13 vWA:15,17												
Karyotype	G-banding analysis detecting structural abnormality of size >3-10Mb	Normal karyotype, 46 XX or 46 XY 19/20 cells normal ²	Normal karyotype, 46 XX at passage 3+5												
Post-Thaw Viability	Cell count and viability using Nucleocounter	Viable cell count and viability within 7 days post thaw	<table> <tbody> <tr> <td>Viable cell count</td> <td>1.1E+06</td> </tr> <tr> <td>Viability</td> <td>87.0%</td> </tr> </tbody> </table>	Viable cell count	1.1E+06	Viability	87.0%								
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Residual Sendai	RT-PCR against Sendai viral elements	None detected in PCR amplification	None detected												

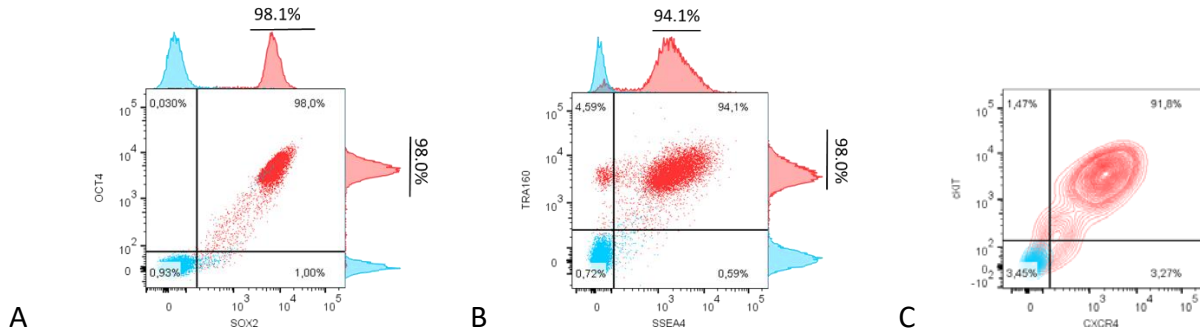
¹ STR results are compared to the STR profile of the parental cells.

² ISCI standards (Stem Cell Rev and Rep (2009) 5:301-314)

Cells distributed by CCRM are intended for research purposes only and are not intended for use in humans.

Appropriate biosafety precautions should be followed when working with these cells. The end user is responsible for ensuring that the cells are handled and stored in an appropriate manner. CCRM is not responsible for damages or injuries that may result from the use of these cells.

Supplemental Figure 1: Expression proteins by flow cytometry. A. Pluripotency associated proteins OCT4 and SOX2. B. Pluripotency associated proteins TRA160 and SSEA4. C. DE associated proteins after DE differentiation.



Approval Signature:

Lise Munsie, Ph.D
 Development Scientist

 Date

Emily Titus, Ph.D
 Director, Technology Development

 Date

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Karyotype on fixed cells of P3+5 iSv.PB.CF.G

Laboratory No: O16/0324

Date of Receipt: 19/08/2016

Date of Report: 06/09/2016

Clinical details: Stem cells for karyotyping

Analysed By: Frankie Shaw

Checked By: Rachel Newby

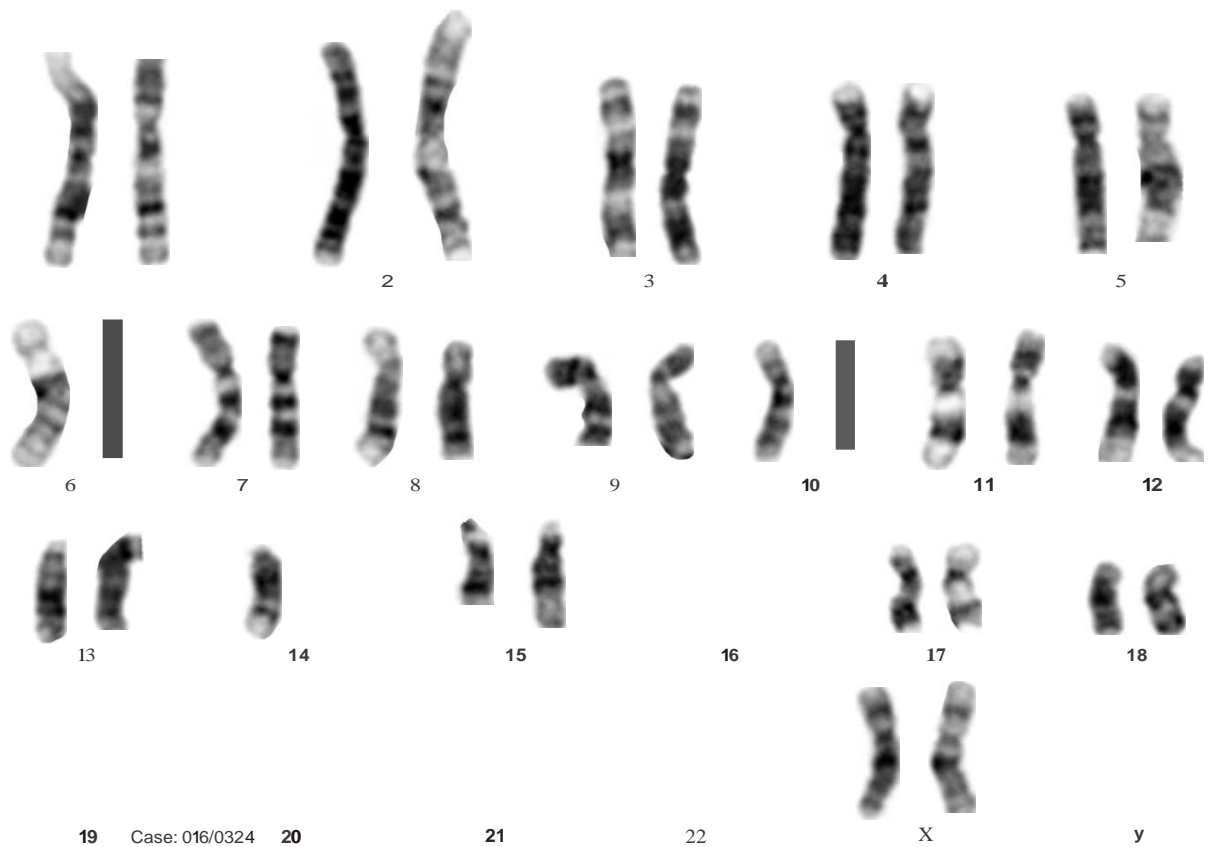
Karyotype: 46,XX

Chromosome analysis of the fixed cell suspension from this stem cell line, P3+5 iSv.PB.CF3.G, has shown an apparently normal female karyotype in 20 cells examined.

The preparations obtained from this sample were of sufficient quality to detect numerical and large structural abnormalities.

Authorised by: *AJ Clarkson*

Amanda Clarkson, Lead Clinical Scientist



19 Case: 016/0324 20
Name: iSv.PB.CF3.G,P3+5
Date: 06/09/2016
Result: 46,XX