## Cell Line Information Sheet

<table>
<thead>
<tr>
<th>Test Description</th>
<th>Method</th>
<th>Expected Result</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Expression of pluripotency-associated proteins</strong></td>
<td>Flow cytometry</td>
<td>≥ 80% of population is positive for expression of surface markers (SSEA4, Tra-1-60), and intracellular marker (OCT4).</td>
<td><strong>Antigen</strong>&lt;br&gt;SSEA4&lt;br&gt;Tra-1-60&lt;br&gt;OCT4&lt;br&gt;SOX2</td>
</tr>
<tr>
<td><strong>Gene expression of pluripotency markers</strong></td>
<td>qRT-PCR</td>
<td>≥ 80% expression measured in hESCs reference standard (HE82 hESCs on Matrigel).</td>
<td><strong>Gene</strong>&lt;br&gt;OCT4&lt;br&gt;NANOG&lt;br&gt;DNMT3B</td>
</tr>
<tr>
<td><strong>Germ layer differentiation</strong></td>
<td>Directed Differentiation Followed by qPCR</td>
<td>Increased expression of germ lineage-specific marker relative to starting pluripotent cell population</td>
<td><strong>Germ Layer</strong>&lt;br&gt;Endoderm&lt;br&gt;Mesoderm&lt;br&gt;Ectoderm</td>
</tr>
<tr>
<td><strong>Definitive endoderm differentiation – gene expression</strong></td>
<td>Directed Differentiation Followed by qPCR</td>
<td>Increased expression of additional endoderm lineage-specific marker relative to starting pluripotent cell population</td>
<td><strong>Gene</strong>&lt;br&gt;GATA 6&lt;br&gt;GATA 4&lt;br&gt;FOXA2</td>
</tr>
<tr>
<td><strong>Definitive endoderm differentiation – protein expression</strong></td>
<td>Directed Differentiation Followed by Flow cytometry</td>
<td>≥ 80% of population is double positive for expression of DE markers (cKIT and CXCR4)</td>
<td><strong>% Expressing-cells</strong>&lt;br&gt;91.8%&lt;br&gt;(Histograms shown in Figure 2)</td>
</tr>
<tr>
<td><strong>Mycoplasma</strong></td>
<td>Lonza MycoAlert Plus kit</td>
<td>None detected</td>
<td>None detected</td>
</tr>
<tr>
<td><strong>Identity</strong></td>
<td>STR: PCR profiling of 9 STR regions plus Amelogenin for gender determination.</td>
<td>Consistent with expected¹</td>
<td>Consistent with parental - Amel: XX&lt;br&gt;CSF1PO:10:10&lt;br&gt;D21S11:32.2,33.2&lt;br&gt;D1S13517:8,12&lt;br&gt;D5S818:11,12&lt;br&gt;D7S820:9,13&lt;br&gt;THO1:9,9.3&lt;br&gt;TPOX: 8,9&lt;br&gt;D16S539:8,12&lt;br&gt;D1S13517:8,12&lt;br&gt;D5S818:11,12&lt;br&gt;D7S820:9,13&lt;br&gt;vWA:15,17</td>
</tr>
<tr>
<td><strong>Karyotype</strong></td>
<td>G-banding analysis detecting structural abnormality of size ≥3-10Mb</td>
<td>Normal karyotype, 46 XX or 46 XY 19/20 cells normal²</td>
<td>Normal karyotype, 46 XX at passage 3+5</td>
</tr>
<tr>
<td><strong>Post-Thaw Viability</strong></td>
<td>Cell count and viability using Nucleocounter</td>
<td>Viable cell count and viability within 7 days post thaw</td>
<td>Viable cell count&lt;br&gt;Viability</td>
</tr>
<tr>
<td><strong>Residual Sendai</strong></td>
<td>RT-PCR against Sendai viral elements</td>
<td>None detected in PCR amplification</td>
<td>None detected</td>
</tr>
</tbody>
</table>

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

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

Laboratory No: O16/0324

Date of Receipt: 19/08/2016  Analysed By: Frankie Shaw
Date of Report: 06/09/2016  Checked By: Rachel Newby
Clinical details: Stem cells for karyotyping

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