

# Characterization of Late-Onset Parkinson's Disease Human iPSC Line, Female, SCTi017-A

Catalog # 200-1070  
Lot # 2512415002

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## Product Information

<b>Product</b>	Late-Onset Parkinson's Disease Human iPSC Line, Female, SCTi017-A
<b>Catalog #</b>	200-1070
<b>Lot #</b>	2512415002
<b>Format</b>	~1 million viable cells per vial
<b>Date Viald</b>	2025-12-15
<b>Country of Manufacture</b>	US
<b>Stability, Storage, and Use Information</b>	<p>Product stable at -135°C or colder for 12 months from date of receipt. Thawed samples must be used immediately.</p> <p>Product is derived from cells or tissues that are collected using consent forms and protocols approved by either an Institutional Review Board, the Food and Drug Administration, the U.S. Department of Health and Human Services, and/or an equivalent regulatory authority.</p> <p>FOR IN VITRO RESEARCH USE ONLY. NOT APPROVED FOR DIAGNOSTIC, THERAPEUTIC, OR CLINICAL APPLICATIONS.</p> <p>NOT APPROVED FOR HUMAN OR VETERINARY USE IN VIVO.</p>

## Cell Line Information

<b>Cell Line Name</b>	SCTi017-A
<b>Parent Material</b>	SCTi017-A
<b>Disease Associated Mutations</b>	None detected (sporadic)
<b>Cell Type</b>	Human Induced Pluripotent Stem Cell (hiPSC)
<b>Passage Number of Cell Banks*</b>	<p><b>Working Cell Bank:</b> Passage 18  <b>Commercial Cell Bank:</b> Passage 21</p> <p>*This vial is from a SCTi017-A commercial cell bank and was cultured for 20 passages prior to cryopreservation. +1 is added to the passage number on the vial to best represent the overall passage number of the cells at thaw.</p>
<b>Source Cell Tissue</b>	Blood
<b>Source Cell Type</b>	Peripheral Blood Mononuclear Cell (PBMC); T Cell
<b>Reprogramming Vector</b>	Non-Integrating

## Recommended Culture Conditions

<b>Maintenance Medium</b>	mTeSR™ Plus (Cat # 100-0276)
<b>Culture Type</b>	Adherent
<b>Supplement</b>	Not Required
<b>Substrate</b>	Corning® Matrigel® hESC-Qualified Matrix
<b>Dissociation Reagent</b>	ReLeSR™ (Cat # 100-0484)
<b>Dissociation Method</b>	Non-enzymatic aggregate dissociation
<b>Split Ratio</b>	1:60 - 1:100 every 6 - 8 days
<b>Incubator Atmosphere</b>	37°C, 5% CO <sub>2</sub> , and 95% humidity
<b>Cryopreservation Reagent</b>	CryoStor® CS10 (Cat # 07930/100-1061)
<b>Thaw Recommendation</b>	After thaw, pellet cells and resuspend in 1 mL mTeSR™ Plus. Aliquot into a pre-prepared six-well plate at six different densities: 150 µL, 100 µL, 75 µL, 50 µL, 25 µL, and 15 µL. Select the well with optimal colony density for passaging at Day 6 - 8.

Culture conditions are reflective of how the cell line was maintained prior to cryopreservation.

## Donor Information

<b>Age*</b>	60	
<b>Sex†</b>	Female	
<b>Ethnicity and/or Race*</b>	Caucasian	
<b>Ancestry†</b>	0% African 100% European	0% East Asian 0% South Asian
<b>Diagnosis‡</b>	Late-Onset Parkinson's Disease	
<b>Age at Symptom Onset‡</b>	60	
<b>Height†</b>	183 cm	
<b>Weight†</b>	91.6 kg	
<b>BMI†</b>	27.4 kg/m <sup>2</sup>	
<b>Blood Type†</b>	A+	
<b>Tobacco Use*</b>	Non-Smoker	
<b>HLA Haplotype†</b>	HLA Class I:  A*02:01:01G, 25:01:01G B*07:02:01G, 18:01:01G C*07:02:01G, 12:03:01G E*01:01:01G, 01:03:02G F*01:01:01G, - G*01:01:01G, 01:01:02G	HLA Class II:  DRB1*01:01:01G, 15:01:01G DRB3*, - DRB4*, - DQA1*01:01:01G, 01:02:01G DQB1*05:01:01G, 05:02:01G DPA1*01:03:01G, - DPB1*04:01:01G, 09:01:01

\* Self-declared

† Calculated

‡ Clinically documented

## Results Summary

Assessment	Analytical Method	Acceptance Criteria	Result
<b>Viability</b> <sup>CCB</sup>	Viability assessment performed on thawed cells using the NucleoCounter® NC-250™ by ChemoMetec	≥ 60% viable	Pass
<b>Recovery</b> <sup>CCB</sup>	Cells recovered using specified thaw and culture recommendations	Recoverable attachment 24 hr. after plating and cells grow to confluency	Pass
<b>Cell Line Identity</b> <sup>CCB</sup>	STR amplification performed using the Powerplex 16 HS System by Promega	Match	Pass
<b>Sterility</b> <sup>CCB</sup>	Presence or absence of bacterial and fungal organisms by incubation in TSB and FTB for 14 days	Negative	Pass
<b>Mycoplasma</b> <sup>CCB</sup>	Presence or absence of mycoplasma using the EZ-PCR™ Mycoplasma Detection Kit by Sartorius	Negative	Pass
<b>Viral Screen</b> <sup>PMB</sup>	Human Comprehensive CLEAR PCR Panel	Negative	Pass
<b>Parental Cell Lineage</b> <sup>PMB</sup>	Presence or absence of TCR Gene Rearrangements using the T cell clonality assay	No specification	Reported
<b>Residual Vector</b> <sup>PMB</sup>	Genomic DNA analyzed by PCR	Negative	Pass
<b>Karyotype</b> <sup>CCB</sup>	GTL Banding performed on 20 metaphase cells	Normal	Pass
<b>20q Amplification</b> <sup>CCB</sup>	Fluorescence in situ hybridization (FISH)	Negative	Pass
<b>Copy Number Variants</b> <sup>CCB</sup>	Genomic DNA analyzed using Illumina Global Diversity Array with Cytogenetics-8 (GDACyto)	No Specification	Reported
<b>Ancestry</b> <sup>WCB</sup>	Whole exome and whole genome sequencing data analyzed using EthSeq	No specification	Reported
<b>Genetic Variants</b> <sup>WCB</sup>	Whole exome and whole genome sequencing data analyzed using ClinVar	No Specification	Reported
<b>TP53 and BCOR Status</b> <sup>WCB</sup>	Whole exome and whole genome sequencing data analyzed using ClinVar	No Specification	Reported
<b>Undifferentiated Status</b> <sup>CCB</sup>	Three-passage assay and flow cytometry for undifferentiated cell markers	OCT4+, TRA-1-60+ ≥ 80%	Pass
<b>Pluripotency</b> <sup>WCB</sup>	Flow cytometry performed on cells differentiated into endoderm, mesoderm, and ectoderm germ layers	<b>Endoderm:</b> CXCR4+, SOX17+ ≥ 70% <b>Mesoderm:</b> T+, NCAM+ ≥ 70% <b>Ectoderm:</b> PAX6+, NESTIN+ ≥ 70%	Pass

<sup>CCB</sup>Assessment performed on the Commercial Cell Bank

<sup>WCB</sup>Assessment performed on the Working Cell Bank

<sup>MCB</sup>Assessment performed on the Master Cell Bank

<sup>PMB</sup>Assessment performed prior to the Master Cell Bank

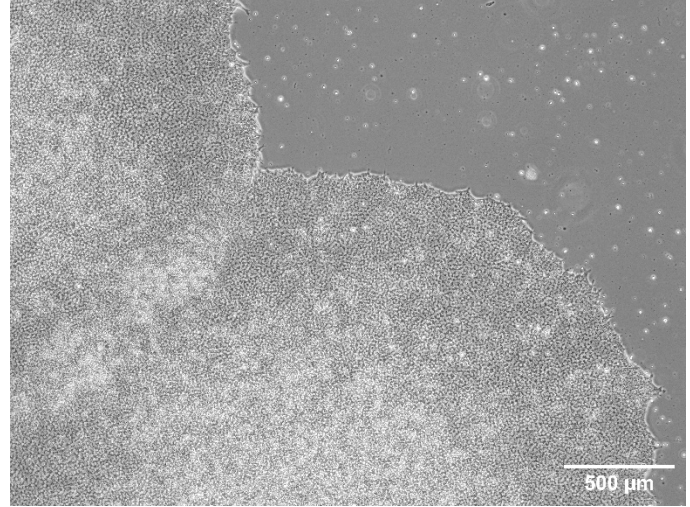
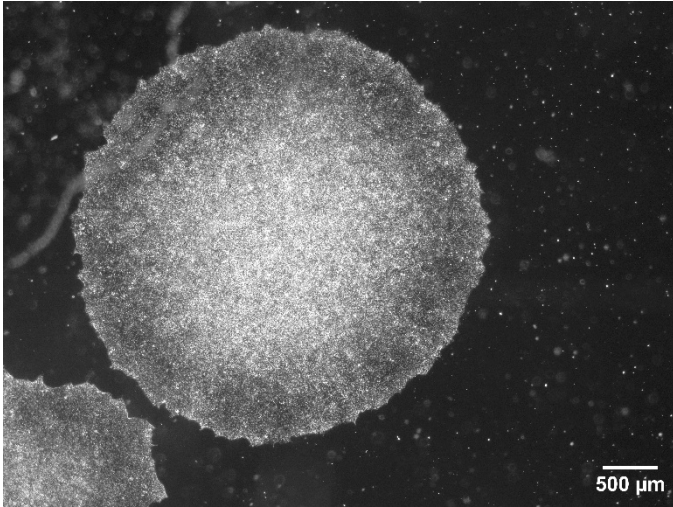
X VM 2026-06-05

Approved by Initial & Date

# Morphology Report

Sample	SCTi017-A Lot # 2512415002
Submitted Passage #	24
Analysis Date	2026-02-18

## Results:



## Interpretation:

Sample demonstrated round colonies containing tightly packed cells with a high nucleus-to-cytoplasm ratio and prominent nucleoli. Colony centers were dense and appeared bright under a phase contrast microscope. This morphology is consistent with the undifferentiated state.

## Assay Description:

Sample is thawed as described in the Product Information Sheet and cultured in mTeSR™ Plus (#100-0276) on Corning® Matrigel® hESC-Qualified Matrix for three passages using ReLeSR™ (#100-0484). Images are captured at 20X and 40X magnification on Day 7 of Passage 3.

# Viability and Recovery Report

<b>Sample</b>	SCTi017-A Lot # 2512415002
<b>Viability Platform</b>	NucleoCounter® NC-250™
<b>Viability Protocol</b>	Viability and Cell Count - A100 and B Assay
<b>Viability Analysis Date</b>	2026-01-21
<b>Recovery Completion Date</b>	2026-01-28

## Results:

<b>Viability</b>	88.4%
<b>Recovery after 24h</b>	<input checked="" type="checkbox"/>
<b>Cells Grow to Confluence</b>	<input checked="" type="checkbox"/>

## Assay Description:

**Viability:** iPSC aggregates are analyzed at thaw using the NucleoCounter® NC-250™ Viability and Cell Count - A100 and B Assay. Cell aggregates are disaggregated, singularized, and stained with DAPI. Viability % represents the mean of two counts.

**Recovery:** Sample is thawed and recovered as described in the Product Information Sheet. At 24 h after thaw, the culture is assessed for the number of adherent cellular aggregates. Cells are expanded until the culture reaches an optimal density consisting of large, multilayered colonies that have begun to merge.

# Cell Line Identity Report

	SCTi017-A Lot # 2512415002	SCTi017-A Pre-Master Cell Bank
Samples Received Date	2026-01-07	2026-01-07
STR Amplification Date	2026-01-20	2026-01-13

## Short Tandem Repeat (STR) Analysis

Sample Name	SCTi017-A Lot # 2512415002	SCTi017-A Pre-Master Cell Bank
CTR No. †	110276	110267
FGA	22, 23	22, 23
TPOX	8, 9	8, 9
D8S1179	12, 13	12, 13
vWA	17, 18	17, 18
Amelogenin	X, X	X, X
Penta_D	8, 12	8, 12
CSF1PO	9, 12	9, 12
D16S539	12, 13	12, 13
D7S820	10, 12	10, 12
D13S317	10, 11	10, 11
D5S818	11, 13	11, 13
Penta_E	13, 14	13, 14
D18S51	13, 17	13, 17
D21S11	30, 33.2	30, 33.2
TH01	6, 7	6, 7
D3S1358	17, 18	17, 18
Allelic Polymorphisms	30	30
Matches*	110267	110276
Comments		

†CTR No.: Characterization Test Request Number; also known as a laboratory accessioning number.

\*Note: The STR profile of the following sample is a 100% match for the given sample/samples.

## Cell Line Identity Report (cont.)

### Assay Description:

STR Analysis is performed using the PowerPlex 16 HS System by Promega™. Results are reported as 13 CODIS STR markers, Amelogenin for sex determination and two low-stutter, highly discriminating pentanucleotide STR markers.

### Results:

The genotypic profiles comprise a range of 30 allelic polymorphisms across the 15 STR loci analyzed.

### Interpretation:

The concentration of DNA required to achieve an acceptable STR genotype (signal/noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. These results suggest that the cells submitted correspond to the cell lines as named and were not contaminated with any other human cells or a significant amount of mouse feeder layer cells.

### Sensitivity:

Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2 - 4%.

# Sterility Report

Collection Date	2025-12-18
Approval Date	2026-01-02

## Diagnostic Summary

Test	Colony	Tested	+	+/-	?	PDG
All results NEGATIVE						

+ = Positive; +/- = Equivocal; ? = Indeterminate; PDG = Pending

## Bacteriology – Sterility Test – Broth Cultures: 2 Samples

	SCTi017-A Lot # 2512415002 Cryovial 1	SCTi017-A Lot # 2512415002 Cryovial 2
<b>Sterility Test (TSB, FTM)</b>	-	-

### Remarks:

- = Negative/No Growth as determined by culture conditions; + = Positive/Growth Present

NE = Not Evaluated: Samples evaluated on scheduled business days; NI = Not Interpreted: Culture could not be interpreted due to overgrowth of Proteus; NT = Not Tested; TSB = Tryptic soy broth; FTM = Fluid thioglycollate media.

# Mycoplasma Report

<b>Date Reported</b>	2026-01-24
<b>Assay Description</b>	Sample is tested for presence of mycoplasma using EZ-PCR™ Mycoplasma Detection Kit (Sartorius).

Sample Name	Result	Interpretation
<b>SCTi017-A Lot # 2512415002</b>	Negative	Band was not seen at 270bp, indicating the absence of mycoplasma
<b>Positive (+) Control</b>	Positive	
<b>Negative (-) Control</b>	Negative	

# Viral Screen Report

Collection Date	2025-11-20
Approval Date	2025-11-24

## Molecular Diagnostics – Infectious Disease PCR Human Comprehensive CLEAR Panel

	SCTi017-A Pre-Master Cell Bank
<i>AAV2 (Adeno-Associated Virus 2)</i>	-
<i>BK Virus</i>	-
<i>Epstein-Barr Virus</i>	-
<i>Hantaan PCR</i>	-
<i>Hepatitis A Virus</i>	-
<i>Hepatitis B Virus</i>	-
<i>Hepatitis C Virus</i>	-
<i>Herpes Simplex Virus 1 PCR</i>	-
<i>Herpes Simplex Virus 2 PCR</i>	-
<i>Herpes Virus Type 6</i>	-
<i>Herpes Virus Type 7</i>	-
<i>Herpes Virus Type 8</i>	-
<i>HIV-1</i>	-
<i>HIV-2</i>	-

	SCTi017-A Pre-Master Cell Bank
<i>HPV-16</i>	-
<i>HPV-18</i>	-
<i>Human Adenovirus PCR</i>	-
<i>Human Cytomegalovirus</i>	-
<i>Human Foamy Virus</i>	-
<i>Human T-Lymphotropic Virus</i>	-
<i>John Cunningham Virus</i>	-
<i>LCMV PCR</i>	-
<i>Parvovirus B19</i>	-
<i>Sarbecovirus (SARs Virus) PCR</i>	-
<i>Seoul Virus PCR</i>	-
<i>C. bovis PCR</i>	-
<i>Mycoplasma Genus PCR</i>	-

### Remarks:

- = Negative; +/- = Equivocal; + = Positive; I = Inconclusive

An equivocal result indicates inconsistent amplification detected by real-time PCR.

Inconclusive indicates failure of control result.

Nucleic Acid Recovery Control (NRC)/Inhibition Control: A low copy exogenous nucleic acid was added to sample lysis prior to nucleic acid isolation to serve as both a control to monitor for nucleic acid recovery and PCR inhibition. An RNA NRC also monitors reverse transcription for RNA virus assays. Nucleic acid recovery and PCR inhibition is monitored by a PCR assay specific for the NRC template. Unless otherwise stated, control results passed for this order.

Any samples reported as equivocal or positive result in this report has been confirmed by re-extracting nucleic acid and repeating real-time PCR amplification to confirm the initial testing result.

# Parent Cell Lineage Determination Report

## T-Cell Receptor (TCR) Gene Rearrangement Analysis (Blood-derived cell lines only)

	TCR- $\alpha\beta$		TCR- $\gamma\delta$	
<b>T Cell Clonality Assay:</b>	<input checked="" type="checkbox"/> Positive	<input type="checkbox"/> Negative	<input checked="" type="checkbox"/> Positive	<input type="checkbox"/> Negative
<b>Final Result:</b>	<input checked="" type="checkbox"/> T Cell Derived	<input type="checkbox"/> Non-T Cell Derived	<input type="checkbox"/> TBD	<input type="checkbox"/> N/A

### Assay Description:

Genomic DNA is extracted using the KingFisher Duo Prime Purification System (Thermo Scientific) and isolated using the MagMAX DNA Multi-Sample Ultra 2.0 Kit (Applied Biosystems), then resuspended to a final concentration of 100  $\mu\text{g}/\text{mL}$  – 400  $\mu\text{g}/\text{mL}$  in elution buffer. Using the TCRB + TCRG T-Cell Clonality Assay for Gel Detection (Invivoscribe), PCR is then carried out as per the manufacturer's protocol. The T-Cell Clonality Assay uses multiple consensus DNA primers which target conserved regions within the T-cell receptor  $\beta$  chain and  $\gamma$  chain genes, including the conserved framework, diversity, and joining regions. PCR products are analyzed using 6% Tris-borate-EDTA (TBE) gel electrophoresis with a 100bp ladder and gel red staining. Clonality is indicated as positive if any of the master mixes generate clonal band(s), and negative if no clonal band(s) are generated. For further details regarding clonal band product size, please refer to the TCRB + TCRG T-Cell Clonality Assay manual.

### Reference:

Invivoscribe (2019) Instructions for Use TCRB + TCRG T-Cell Clonality Assay. Rev. G:3-15.

# Chromosome Analysis Report

## GTL-Banded Karyotype Analysis

Date Reported	2025-12-23
Sample	SCTi017-A Lot # 2512415002
Cell Line Sex	Female
Submitted Passage #	21
Date of Sample	2025-12-18
Specimen	Human iPSC
Results	46,XX



Cell	40
Slide	1
Slide Type	Karyotype
Total Counted	20
Total Analyzed	20
Total Karyogrammed	20
Band Resolution	475

### Interpretation:

This is a normal karyotype; no clonal abnormalities were detected at the stated band level of resolution.

### Limitations:

This assay allows for microscopic visualization of numerical and structural chromosome abnormalities. The size of structural abnormality that can be detected is > 3 - 10Mb, dependent upon the G-band resolution obtained from this specimen. For the purposes of this report, band level is defined as the number of G-bands per haploid genome. It is documented here as "band level", i.e., the range of bands determined from the twenty karyograms in this assay. Detection of heterogeneity of clonal cell populations in this specimen (i.e., mosaicism) is limited by the number of metaphase cells examined, documented here as "# of cells counted".

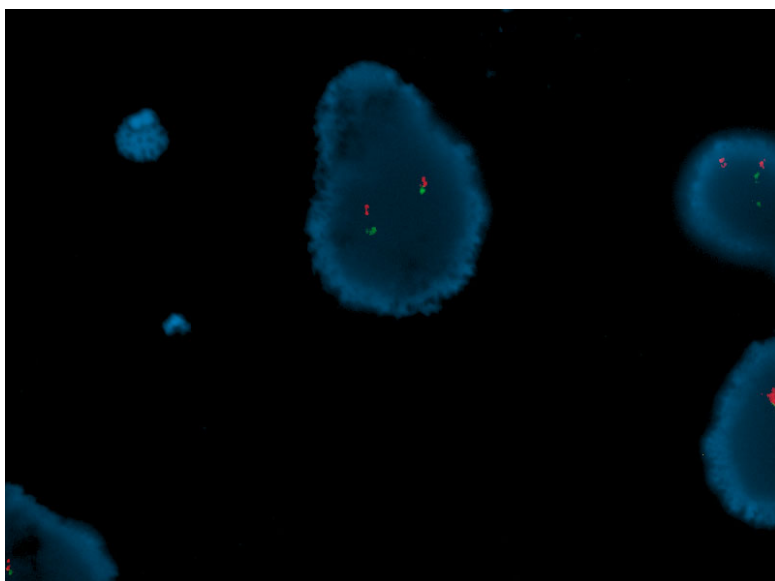
# 20q Status Report

## Fluorescence In-Situ Hybridization (FISH) Analysis

Date Reported	2025-12-23
Sample	SCTi017-A Lot # 2512415002
Cell Line Sex	Female
Submitted Passage #	21
Date of Sample	2025-12-18
Specimen	Human iPSC

Probe	# of cells with 2R2G pattern	# of cells with 1R2G pattern	# of cells with 1R1G pattern	# of cells with 2R1G pattern	# of cells with $\geq 3R2G$ pattern
20p11 (G) / BCL2L1 (R)	189 / 200 (94.5%)	4 / 200 (2.0%)	4 / 200 (2.0%)	2 / 200 (1.0%)	1 / 200 (0.5%)
Cutoff	N/A	4%	4%	4%	5%

Probe: 20p11 (G) / 20q11.21 (R)



### Interpretation:

There is no evidence for aneusomy of chromosome 20. Two probe signals were observed in 94.5% of two hundred interphase cells examined for the 20p11.21 and 20q11.21 (BCL2L1) regions.

# Copy Number Variants (CNV) Report

## Microarray Analysis

<b>Date Reported</b>	2026-02-16
<b>Sample</b>	SCTi017-A Lot # 2512415002
<b>Cell Line Sex</b>	Female
<b>Submitted Passage #</b>	21
<b>Date of Sample</b>	2026-01-07
<b>Specimen</b>	Human iPSC

Microarray Results arr(X,1-22)x2

### Call Table:

Chr	Cytoband	Event (% Mosaic)	Estimated Copy Number	Start	End	Length (Base Pairs)	Gene Count
2	2q37.3	Loss	1	242,853,745	243,062,047	208,303	4
4	4q31.21	Loss	1	145,770,167	145,899,524	129,358	0
5	5p15.31	Loss	1	8,702,852	8,749,689	46,838	0
6	6q26	Gain	3	163,159,187	163,224,089	64,903	1
7	7p14.1	Homozygous Loss	0	38,293,984	38,368,834	74,851	1
7	7q34	Loss	1	142,335,526	142,494,569	159,044	1
9	9q33.1	Loss	1	118,466,402	118,596,253	129,852	1
10	10q26.3	Gain	3	135,241,711	135,381,199	139,489	4
12	12q21.31	Loss	1	85,490,167	85,516,243	26,077	1
14	14q11.2	Loss	1	22,568,723	22,631,766	63,044	0
14	14q11.2	Homozygous Loss	0	22,632,184	22,966,662	334,479	1
14	14q11.2	Loss	1	22,966,701	22,989,426	22,726	0

## Copy Number Variants (CNV) Report (cont.)

### Call Table (cont.):

Chr	Cytoband	Event (% Mosaic)	Estimated Copy Number	Start	End	Length (Base Pairs)	Gene Count
14	14q31.3	Loss	1	86,285,503	86,311,276	25,774	0
X	Xp22.33	Gain	3	1,011,976	1,321,404	309,429	1
X	Xq28	Gain	3	153,495,572	153,582,737	87,166	3

### Interpretation:

There were 0 reportable copy number changes as well as 0 reportable regions of LOH identified:

# Copy Number Variants (CNV) Report (cont.)

## Specifications:

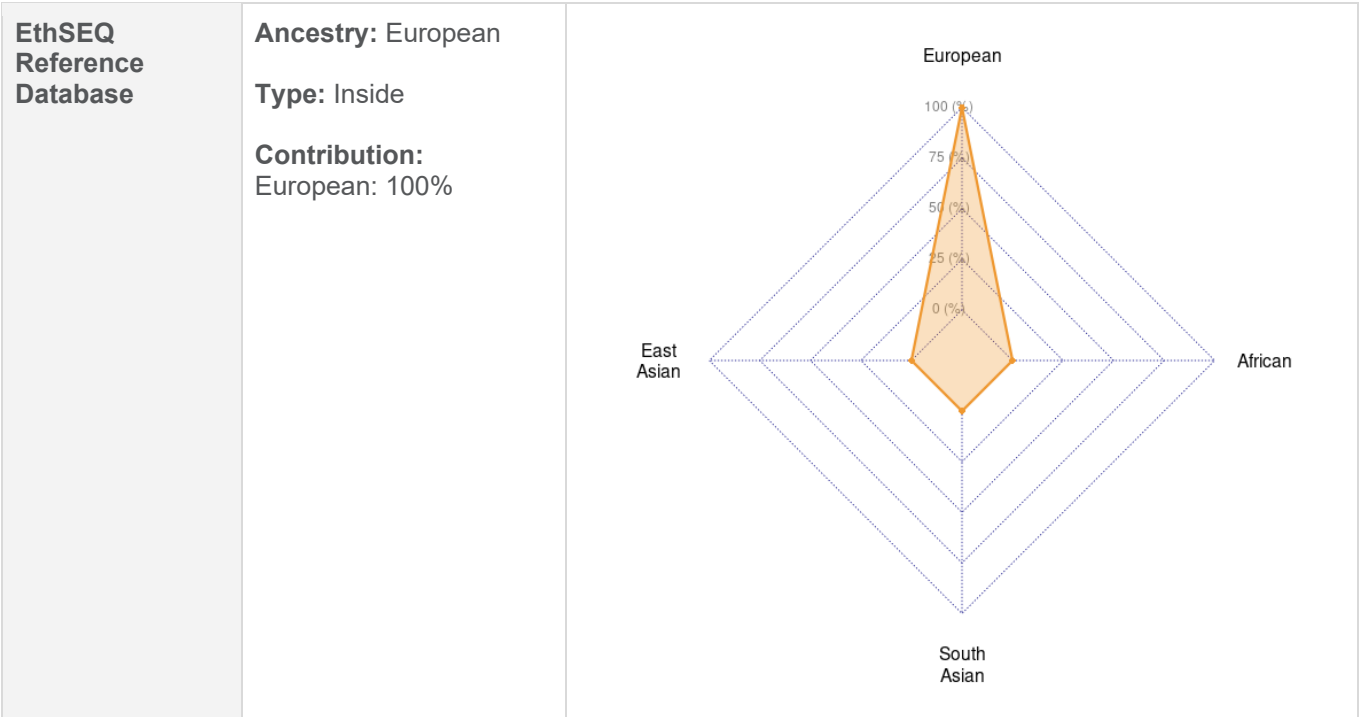
- Platform: Illumina: Global Diversity Array with Cytogenetics-8 (GDACyto)
- Marker coverage: 1,825,277 spanning whole human genome
- Analysis software: Bionano: Via™ Software
- Array design, genomic position, genes and chromosome banding are based on genome build GRCh37/hg19.
- Aberrant copy number genomic regions are identified by log R ratio (LRR) and B allele frequency (BAF). LRR is the log ratio of observed probe intensity to expected intensity, deviations from zero are evidence for copy number change. BAF is the proportion of hybridized sample that carries the B allele: 0.0, 0.5, and 1.0 are expected for each locus in a normal sample. Deviations from this expectation are indicative of aberrant copy number.
- Quality assurance monitors: 1) Call Rate; 2) Confidence Threshold; 3) LogRDev; 4) Illumina sample dependent/independent QC measures.
- Reportable copy number changes are gains or losses greater than 400kb. Reportable regions of LOH are greater than 5Mb. See Interpretation for copy number changes and regions of LOH that meet these criteria. See Call Table for all copy number changes identified by the analysis software. If mosaicism is detected, the approximate percentage of mosaicism is listed in the 'Event (% Mosaic)' column.
- Copy number changes and regions of LOH are reported at greater than 10% and 20% mosaicism respectively.
- The assay is currently validated for the detection of copy number losses greater than 20kb in size and copy number gains 50kb in size (smaller changes may be detected depending on gene content and probe number but will not be included in the Call Table). From validation studies, abnormalities present in a mosaic state are reliably detected if the mosaicism level (percentage of abnormal cells) is 20% or higher.
- Fluorescence type and intensity of each probe is compared to a custom cluster file using Illumina's Beeline or iScan control software.

## Limitations:

This assay will detect aneuploidy, deletions, and duplications of represented loci, and regions of loss/absence of heterozygosity (LOH), but will not detect balanced alterations (reciprocal translocations, Robertsonian translocations, inversions, and insertions), or point mutations. Based on the results of internal validation studies, abnormalities present in a mosaic state are reliably detected if the mosaicism level (percentage of abnormal cells) is 20% or higher. The failure to detect an alteration at any locus does not exclude all anomalies at that locus. Significance of the number of probes used to detect an aberration has not been determined and confirmational testing may be informative. Actual chromosomal localization of copy number change is not determined by this assay. Other mapping procedures are required for determining chromosomal localization.

# Ancestry Report

Sample	SCTi017-A Working Cell Bank
Whole Exome and Whole Genome Sequencing Report Date	2026-02-24



# Ancestry Report (cont.)

## Analysis Description:

### Sequencing and Analysis Workflow:

Genomic DNA from the sample underwent whole-genome sequencing (WGS) using the NovaSeq X Plus System (Illumina), generating paired-end 150 bp reads at an average coverage of 50x across the genome. Prior to sequencing, DNA was randomly fragmented, end-repaired, A-tailed, and ligated with Illumina adapters. The adapter-ligated fragments were size-selected, PCR-amplified, and purified to generate the final sequencing libraries. To further enhance variant detection in coding regions, whole-exome capture was performed using the SureSelect Human All Exon V6 kit (Agilent Technologies), enriching for ~60 Mb of exonic and splice junction regions across approximately 20,000 human genes. Sequencing reads were aligned to the GRCh38 human reference genome, and single nucleotide variants (SNVs) and insertions/deletions (indels) were identified following the GATK best practices (v4.6.1.0).

Ancestry was calculated using the EthSEQ R package (v3.0.2) and a reference model described by Romanel et al. (2017). The reference model included genotype data from 233,887 loci representing individuals with known ancestries, categorized into four major populations: African, European, South Asian, and East Asian. If a sample's ancestry fell within one of these ancestral groups, it was reported as "Inside." If the sample's ancestry lay outside the predefined groups, the nearest ancestry was reported as "Closest."

## Reference:

Romanel, A. et al. (2017) EthSEQ: ethnicity annotation from whole exome sequencing data. *Bioinformatics*. 33(15):2402-04.

# Genetic Variants Report

Sample	SCTi017-A Working Cell Bank
Whole Exome and Whole Genome Sequencing Report Date	2026-02-24
ClinVar Version Date	2024-02-15

## Pathogenic or Likely Pathogenic Variants:

Gene	ClinVar ID	Coordinates	Molecular Consequence	Nucleotide Change	Protein Change
<i>ADAR</i>	2228217	chr1:154585811	Frameshift variant	c.3255_3256del	D1087fs
<i>AMPD1</i>	92338	chr1:114679616	Missense variant	c.860A>T	K287I
<i>APOE</i>	17864	chr19:44908684	Missense variant	c.388T>C	C112R
<i>ATP7B</i>	35716	chr13:51946299	Synonymous variant	c.3045G>A	L1015=
<i>BCHE</i>	13220	chr3:165773492	Missense variant	c.1699G>A	A567T
<i>CFTR,CFTR-AS1</i>	242535	chr7:117548628	Intron variant	c.1210-12T[5]	
<i>COL4A4</i>	191312	chr2:227028004	Missense variant	c.3979G>A	V1327M
<i>DCAF17</i>	191260	chr2:171448667	Intron variant	c.322-14C>T	
<i>GJB3</i>	6490	chr1:34784955	Inframe deletion	c.196_198del	D66del
<i>HNF1A</i>	14937	chr12:120978847	Missense variant	c.79A>C	I27L
<i>ITPKB</i>	1705897	chr1:226735804	Missense variant	c.1655C>A	P552Q
<i>ITPKB</i>	1705899	chr1:226736237	Missense variant	c.1222T>G	S408A
<i>ITPKB,LOC129932672</i>	1705896	chr1:226737174	Inframe deletion	c.267CAGCG GCAG[1]	p.91GSS[1]
<i>MBL2</i>	14352	chr10:52771482	Missense variant	c.154C>T	R52C
<i>PADI3</i>	374868	chr1:17262194	Missense variant	c.335T>A	L112H
<i>PRODH</i>	4011	chr22:18918451	Missense variant	c.1292G>A	R323H
<i>PRSS1,TRB</i>	38363	chr7:142750561	Missense variant	c.47C>T	A16V
<i>SERPINA1</i>	17969	chr14:94380925	Missense variant	c.863A>T	E288V
<i>SLC3A1,PREPL</i>	336214	chr2:44320435	Missense variant	c.1854G>A	M618I

## Genetic Variants Report (cont.)

### Pathogenic or Likely Pathogenic Variants (cont.):

Gene	ClinVar ID	Coordinates	Molecular Consequence	Nucleotide Change	Protein Change
<i>SPTA1</i>	258954	chr1:158618068	Intron variant	c.6531-12C>T	
<i>SPTA1</i>	258948	chr1:158627717	Missense variant	c.5572C>G	L1858V
<i>TYR</i>	3778	chr11:89178528	Missense variant	c.575C>A	S192Y
<i>UGT1A, UGT1A10, UGT1A8, UGT1A7, UGT1A6, UGT1A5, UGT1A9, UGT1A4, UGT1A1, UGT1A3</i>	12288	chr2:233757013	Intron variant	c.862-10021T>G	
<i>UGT1A, UGT1A10, UGT1A8, UGT1A7, UGT1A6, UGT1A5, UGT1A9, UGT1A4, UGT1A1, UGT1A3</i>	12275	chr2:233760233	Intron variant		
<i>VDR</i>	308887	chr12:47879112	Initiator codon variant	c.2T>C	M1T

# Genetic Variants Report (cont.)

## Analysis Description:

### Sequencing and Analysis Workflow:

Genomic DNA from the sample underwent whole-genome sequencing (WGS) using the NovaSeq X Plus System (Illumina), generating paired-end 150 bp reads at an average coverage of 50x across the genome. Prior to sequencing, DNA was randomly fragmented, end-repaired, A-tailed, and ligated with Illumina adapters. The adapter-ligated fragments were size-selected, PCR-amplified, and purified to generate the final sequencing libraries. To further enhance variant detection in coding regions, whole-exome capture was performed using the SureSelect Human All Exon V6 kit (Agilent Technologies), enriching for ~60 Mb of exonic and splice junction regions across approximately 20,000 human genes. Sequencing reads were aligned to the GRCh38 human reference genome, and single nucleotide variants (SNVs) and insertions/deletions (indels) were identified following GATK best practices (v4.6.1.0).

### Variant Filtering and Classification:

Single nucleotide variants (SNVs) and insertions/deletions (indels) were retained if they met the convolutional neural network (CNN) filtering threshold and were supported by a minimum of two sequencing reads. All retained variants were cross-referenced against ClinVar (version 2024-02), a publicly available database curated by the NCBI that links human genetic variants to associated phenotypes. Only variants classified by ClinVar as *pathogenic* or *likely pathogenic* were included in this report.

### Disclaimer:

Pathogenicity classifications are based solely on ClinVar annotations and have not been independently validated by STEMCELL. Classifications reflect the state of knowledge at the time of reporting and may be subject to change as new evidence emerges.

# TP53 and BCOR Status Report

Sample	SCTi017-A Working Cell Bank
Whole Exome and Whole Genome Sequencing Report Date	2026-02-24
ClinVar Version Date	2024-02-15

## Overview:

Gene	% Exon Covered by 15+ Reads	Average Exonic Read Depth	# Exonic or Impact Variants Detected
TP53	100.00%	106.19 (sd:46.91)	1
BCOR	100.00%	107.85 (sd:65.01)	1

## TP53:

Locus	ClinVar ID	Nucleotide Change	Protein Change	Variant Type	# Ref Reads	# Alt Reads	Inferred Inheritance
chr17:7676154	12351	c.215C>G	p.Pro72Arg	Missense variant	0	145	Germline homozygous

## BCOR:

Locus	ClinVar ID	Nucleotide Change	Protein Change	Variant Type	# Ref Reads	# Alt Reads	Inferred Inheritance
chrX:40074086	95764	c.1260T>C	p.Asp420Asp	Synonymous variant	0	202	Germline homozygous

## ***TP53* and *BCOR* Status Report (cont.)**

### **Interpretation:**

No pathogenic or likely pathogenic variants were identified in *TP53* and *BCOR*. No variants were identified in *TP53* that were previously reported as common recurring mutations in human pluripotent stem cell cultures by Merkle et al. (2017).

### **Analysis Description:**

#### Sequencing and Analysis Workflow:

Genomic DNA from the sample underwent whole-genome sequencing (WGS) using the NovaSeq X Plus System (Illumina), generating paired-end 150 bp reads at an average coverage of 50x across the genome. Prior to sequencing, DNA was randomly fragmented, end-repaired, A-tailed, and ligated with Illumina adapters. The adapter-ligated fragments were size-selected, PCR-amplified, and purified to generate the final sequencing libraries. To further enhance variant detection in coding regions, whole-exome capture was performed using the SureSelect Human All Exon V6 kit (Agilent Technologies), enriching for ~60 Mb of exonic and splice junction regions across approximately 20,000 human genes. Sequencing reads were aligned to the GRCh38 human reference genome, and single nucleotide variants (SNVs) and insertions/deletions (indels) were identified following GATK best practices (v4.6.1.0).

#### Variant Filtering and Classification:

Single nucleotide variants (SNVs) and insertions/deletions (indels) were retained if they met the convolutional neural network (CNN) filtering threshold and were supported by a minimum of two sequencing reads. All retained variants were cross-referenced against ClinVar (version 2024-02), a publicly available database curated by the NCBI that links human genetic variants to associated phenotypes. All exonic variants in the *TP53* and *BCOR* genes that meet these criteria and result in amino acid changes are reported. For *TP53*, variants are further cross-referenced with those described by Merkle et al. (2017).

#### Disclaimer:

Pathogenicity classifications are based solely on ClinVar annotations and have not been independently validated by STEMCELL. Classifications reflect the state of knowledge at the time of reporting and may be subject to change as new evidence emerges.

### **Reference:**

Merkle, FT. et al. (2017) Human pluripotent stem cells recurrently acquire and expand dominant negative P53 mutations. *Nature*. 545(7653):229-233.

# Undifferentiated Status Report

## Flow Cytometric Analysis

<b>Sample</b>	SCTi017-A Lot # 2512415002
<b>Submitted Passage #</b>	24
<b>Analysis Date</b>	2026-02-18
<b># of Events Analyzed</b>	10,000

### Results:

<b>Marker</b>	<b>Expression</b>
OCT4	94.8%
TRA-1-60	99.2%

### Interpretation:

Upon examination, a high percentage of cells exhibited OCT4 and TRA-1-60 markers of the undifferentiated status, indicative of a primarily undifferentiated cell culture.

### Assay Description:

Sample is thawed and cultured for three consecutive passages, then singularized for undifferentiated marker expression analysis by flow cytometry at the end of passage 3. Results are analyzed using FlowJo™ software. Results are presented as the mean marker expression of two technical replicates.

# Pluripotency Report

## In Vitro Directed Trilineage Differentiation Analysis

<b>Sample</b>	SCTi017-A Working Cell Bank
<b>Submitted Passage #</b>	20
<b>Analysis Date</b>	2026-02-11

### Results:

Lineage	Marker	Expression
Endoderm	SOX17	95.1%
	CXCR4	98.0%
Mesoderm	BRACHYURY (T)	97.9%
	NCAM	97.5%
Ectoderm	PAX6	92.2%
	NESTIN	92.1%

### Interpretation:

Following directed differentiation, expression was observed for markers specific to each lineage: endoderm, mesoderm, and ectoderm. This result is consistent with the pluripotent state.

### Assay Description:

Sample undergoes directed differentiation using the STEMdiff™ Definitive Endoderm Kit (Cat # 05110), STEMdiff™ Mesoderm Induction Medium (Cat # 05221), and the STEMdiff™ SMADi Neural Induction Kit (Cat # 08581). Expression of lineage-specific markers is assessed by flow cytometry following five days of culture for endoderm and mesoderm lineages, and following seven days of culture for the ectoderm lineage. Results are reported as the percent of total cells with positive expression for each individual lineage-specific marker. Results are presented as the mean marker expression of two technical replicates.

