

Certificate of Analysis

NIGMS Human Genetic Cell Repository

Human induced Pluripotent Stem Cell (iPSC) Line: GM24675*C

Diagnosis	Alzheimer Disease, Familial	
Parental cell line mutation	APP duplication, APOE E3	
Parental cell type, cell line ID	Fibroblast, N/A	
Sex	Female	
Reprogramming method	Retroviral vectors containing OCT4, SOX2, KLF4, and MYC	
Passage number at freeze	P26	
Culture media	DMEM/F12 + 20% KOSR + 10ng/ml bFGF	
Feeder or Matrix substrate	CF1 MEFs on 0.1% Gelatin	
Recommended passage method and split ratio	Tryple Express; 1:6 every 5-7 days	
iPSC line establishment publication(s)	Israel, PMID: 22278060	

The following testing specifications have been met for this product lot:

Test Description	Test Method	Test Specification	Result
Post-Thaw Cell Viability	Colony doubling Colony formation and diameter doubling within 5 days		Pass
Sterility	Growth on agar and broth Negative		Pass
Mycoplasma	qRT-PCR	Negative	
Alkaline Phosphatase Staining	Cell staining	>80% cells with positive staining	
Identity Match	STR (THO-1, D22S417, D10S526, vWA31, D5S592, and FES/FPS)	Match parental cell line	
Genomic Integration of Episomal Plasmid	Genomic PCR using plasmid specific primers and endogenous FBXO1 control	orimers No plasmid specific sequence amplified using 100 ng gDNA template	
Detection of Sendai Virus Genome and Transgene	qRT-PCR using SEV specific primers	No detection of SEV genome or transgenes	
Surface Antigen Expression of Stem Cell Markers	Immunostaining and flow cytometric detection	n >80% expression of SSEA4	
Differentiation Potential	Embryoid body (EB) formation and gene expression Minimum of 1 gene per germ layer expressed 2 fold or higher Pass		Pass
Cytogenomics	G-banding, Affymetrix Human SNP Array 6.0	46,XX[24].arr 21q21.3(27,061,345- 27,824,478)x3 Pass ³	

*Note: Array finding: 763kb copy number gain at 21q21.3, encompassing the entire APP gene, as expected.

Edward Bell	11/25/20019	Christine Grandizio	12/02/2019
Technician, Stem Cell Laboratory	/ Date	Manager, Stem Cell Laboratory	Date

Disclaimer: iPSC lines distributed by Coriell Institute for Medical Research may differ from one passage or expansion to another.

Form 1701-07 Rev P-110519: NIGMS HGCR Certificate of Analysis GM24675*C

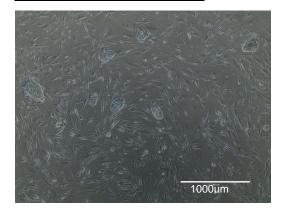


Post-Thaw Cell Viability

One distribution lot vial of the cell line was thawed and placed in culture. Cultures were observed daily. Colonies were photographed upon first appearance, then 4 days later. Colonies must double in diameter within 5 days. The area for 5 colonies was measured using CellSens software on the Olympus IX50 microscope at 40x magnification. The average area is reported here.

Day	Average area (µm²)		
1	16,294		
5	374,730		

Colony area increased by 23 fold.



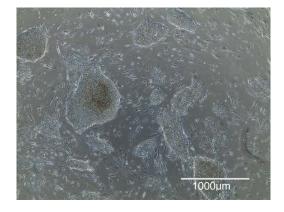


Figure 1A. Colonies post thaw (Day 1)

Figure 1B. Colonies 4 days after first observation (Day 5)

Alkaline Phosphatase Staining

Cells were stained using the StemTAG[™] Alkaline Phosphatase Staining Kit from CellBiolabs, Inc.

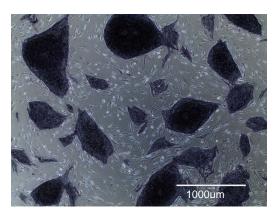


Figure 2. iPSC colonies showing alkaline phosphatase activity

Form 1701-07 Rev P-110519: NIGMS HGCR Certificate of Analysis GM24675*C



Surface Antigen Expression of Stem Cell Markers

Undifferentiated cells are stained for stage specific embryonic antigen 4 (SSEA4) which is expressed on the surface of undifferentiated human pluripotent stem cells. Cells were analyzed using the MACSQuant Flow Cytometer by Miltyeni Biotec. More than 80% of cells should stain with antibodies specific for SSEA4.

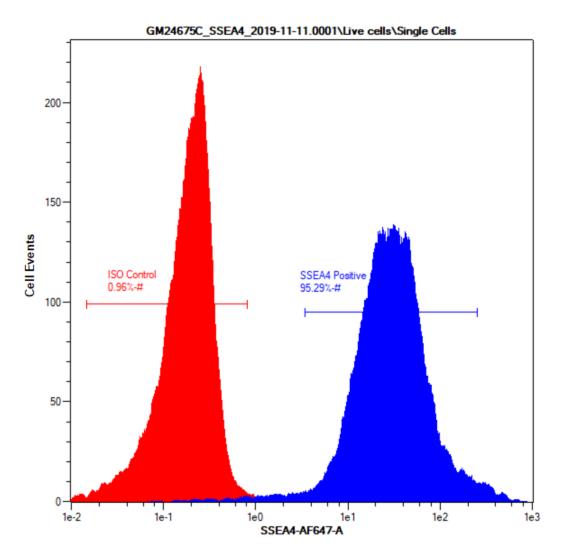
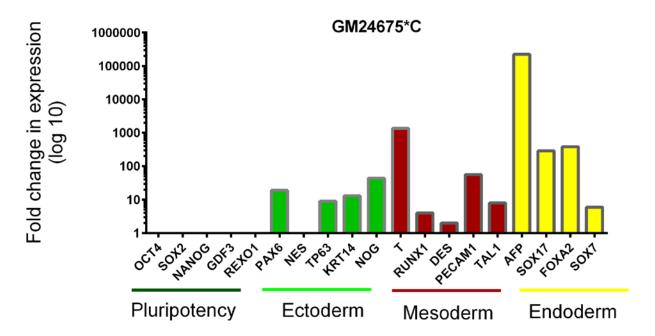


Figure 3. Representative histogram of SSEA4 positive population showing an overlay of isotype stained control (red) and SSEA4 positive population (blue)



Differentiation Potential

Cells are differentiated by embryoid body (EB) formation to assess pluripotency. RNA is extracted and gene expression is measured by quantitative RT-PCR. Ct values are adjusted to the endogenous housekeeping gene GAPDH. Relative gene expression is shown as the fold difference in expression compared to undifferentiated cells. Expression of at least one gene per germ layer should increase by 2 fold or higher.



Gene	Fold change	Gene	Fold change	Gene	Fold change	Gene	Fold change
OCT4	0	PAX6	19	Т	1358	AFP	223478
SOX2	0	NES	0	RUNX1	4	SOX17	291
NANOG	0	TP63	9	DES	2	FOXA2	384
GDF3	0	KRT14	13	PECAM1	56	SOX7	6
REXO1	0	NOG	44	TAL1	8		

Figure 4. Fold change in expression of pluripotency genes and tri-lineage specific genes

Note: Negative values are set as 0. Calculations are performed using the 2^{- ΔΔCT} method. (*Livak KJ*, *Schmittgen TD. Methods. 2001 Dec;25(4):402-8.PMID:11846609*)



Cytogenomics

Microarray	Affymetrix Human SNP Array 6.0
Cytogenetic Banding Technique	G-banding
Passage at Analysis	P31
Metaphase Cells Counted	25
Metaphase Cells Analyzed	25
Metaphase Cells Karyotyped	5
Short ISCN	46,XX[24].arr 21q21.3(27,061,345- 27,824,478)x3

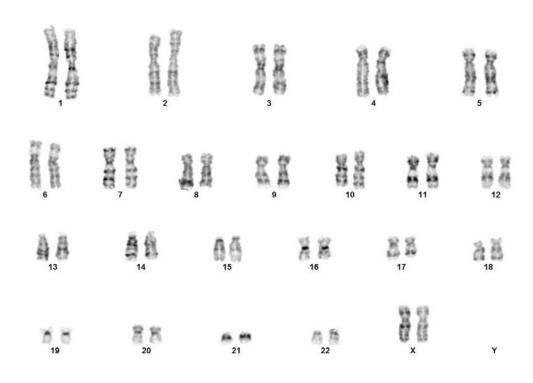


Figure 5. G-banding karyogram