Certificate of Analysis **_NIGMS Human Genetic Cell Repository_**

Human induced Pluripotent Stem Cell (iPSC) Line: **GM28930*B**

Diagnosis	Isogenic Control, Vici Syndrome
Parental cell line mutation	EPG5 c. 1007A>G (p.Q336R) (mutation corrected with CRISPR/Cas9)
Parental cell type, cell line ID	iPSC, GM27291
Sex	Male
Reprogramming method	Sendai viral vectors containing OCT4, SOX2, KLF4 and CMYC
Passage number at freeze	P31
Culture media	mTeSR1™
Feeder or Matrix substrate	Matrigel®
Recommended passage method and split ratio	Versene; 1:7 every 5 days*
iPSC line establishment publication(s)	

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	Pass
Alkaline Phosphatase Staining	Cell staining	>80% cells with positive staining	Pass
Identity Match	STR (THO-1, D22S417, D10S526, vWA31, D5S592, and FES/FPS)	Match parental cell line	Pass
Genomic Integration of Episomal Plasmid	Genomic PCR using plasmid specific primers and endogenous FBXO1 control	No plasmid specific sequence amplified using 100 ng gDNA template	N/A
Detection of Sendai Virus Genome and Transgene	qRT-PCR using SEV specific primers	No detection of SEV genome or transgenes	Pass
Surface Antigen Expression of Stem Cell Markers	Immunostaining and flow cytometric detection	>80% expression of SSEA4	Pass
Differentiation Potential	Embryoid body (EB) formation and gene expression	Minimum of 1 gene per germ layer expressed 2 fold or higher	Pass
Cytogenomics	G-banding	46, XY[20]	Pass

*Note: Recover in 2 wells of a 6 well plate.

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Technician, Stem Cell Laboratory Date

Christine Grandizio 02/10/2023
Manager, Stem Cell Laboratory Date

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

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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 image analysis software. The average area is reported here.

Day	Average area (μm^2)
1	24,806
5	339,324

Colony area increased by 14 fold.

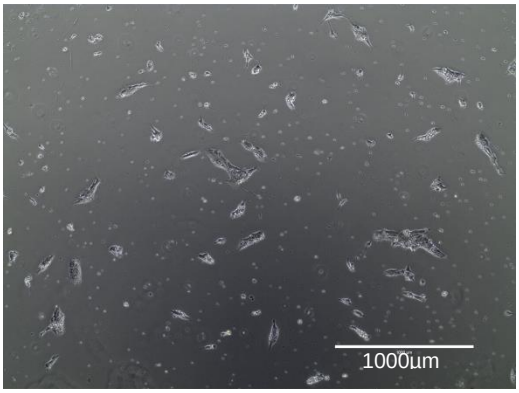

Figure 1A. Colonies post thaw (Day 1)

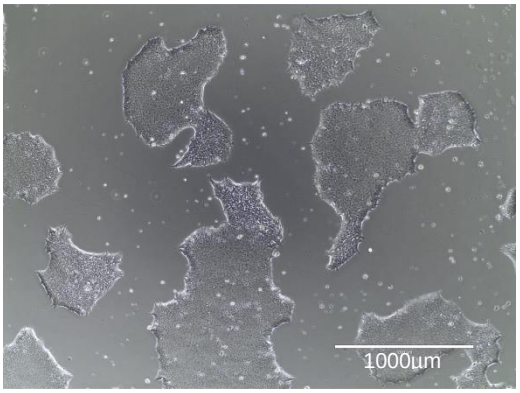

Figure 1B. Colonies 4 days after first observation (Day 5)

Alkaline Phosphatase Staining

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

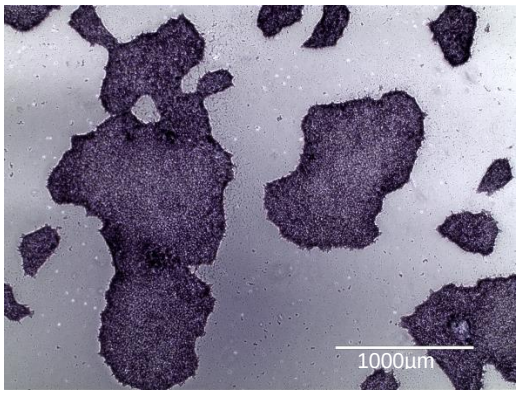

Figure 2. iPSC colonies showing alkaline phosphatase activity

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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.

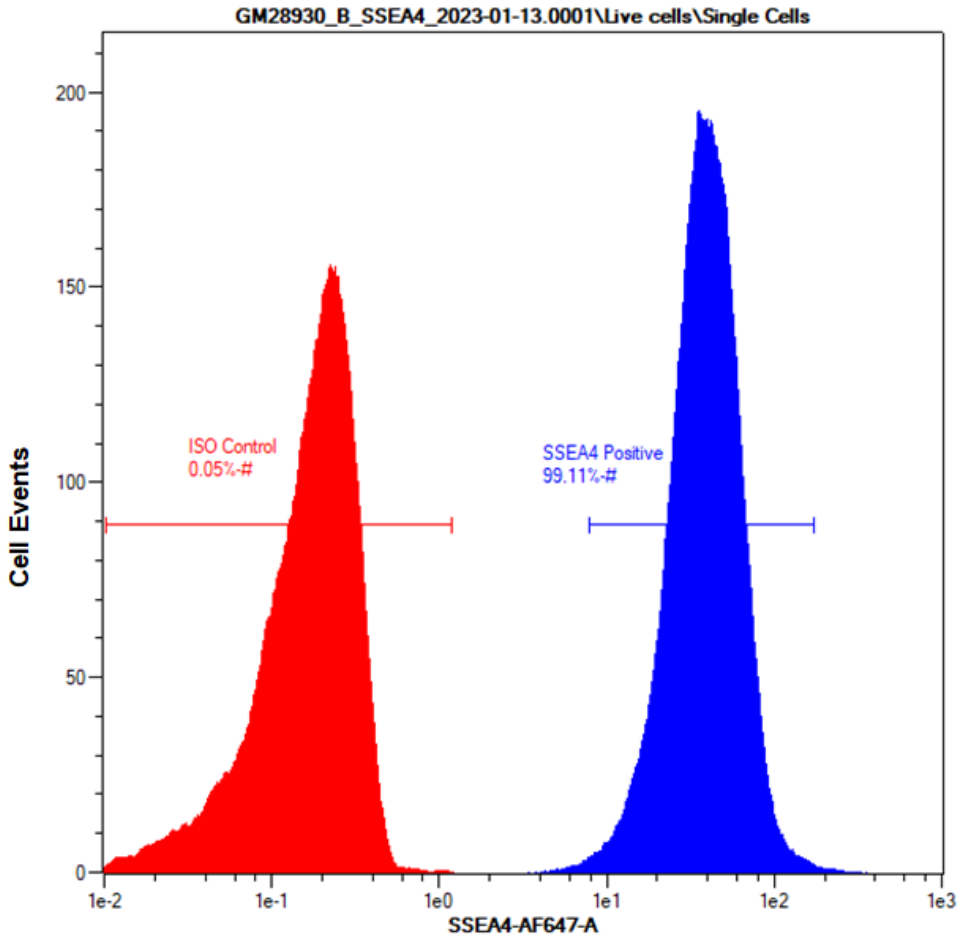

Figure 3. Representative histogram of SSEA4 positive population showing an overlay of isotype stained control (red) and SSEA4 positive population (blue)

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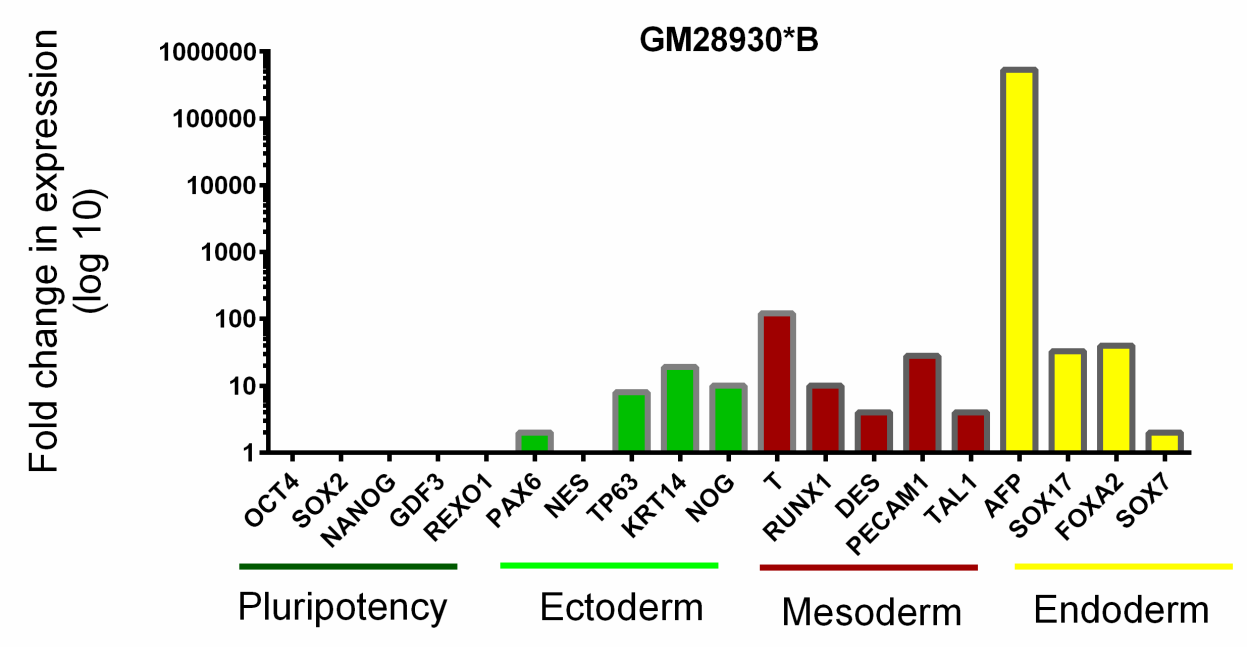
Differentiation Potential

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	2	T	121	AFP	537817
SOX2	0	NES	0	RUNX1	10	SOX17	33
NANOG	0	TP63	8	DES	4	FOXA2	40
GDF3	0	KRT14	19	PECAM1	28	SOX7	2
REXO1	1	NOG	10	TAL1	4		

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 $2^{-\Delta\Delta CT}$ method. (*Livak KJ, Schmittgen TD. Methods. 2001 Dec;25(4):402-8.PMID:11846609)*

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Cytogenomics

Cytogenetic Banding Technique	**G-banding**
Passage at Analysis	P32
Metaphase Cells Counted	20
Metaphase Cells Analyzed	5
Metaphase Cells Karyotyped	5
Short ISCN	46, XY [20]

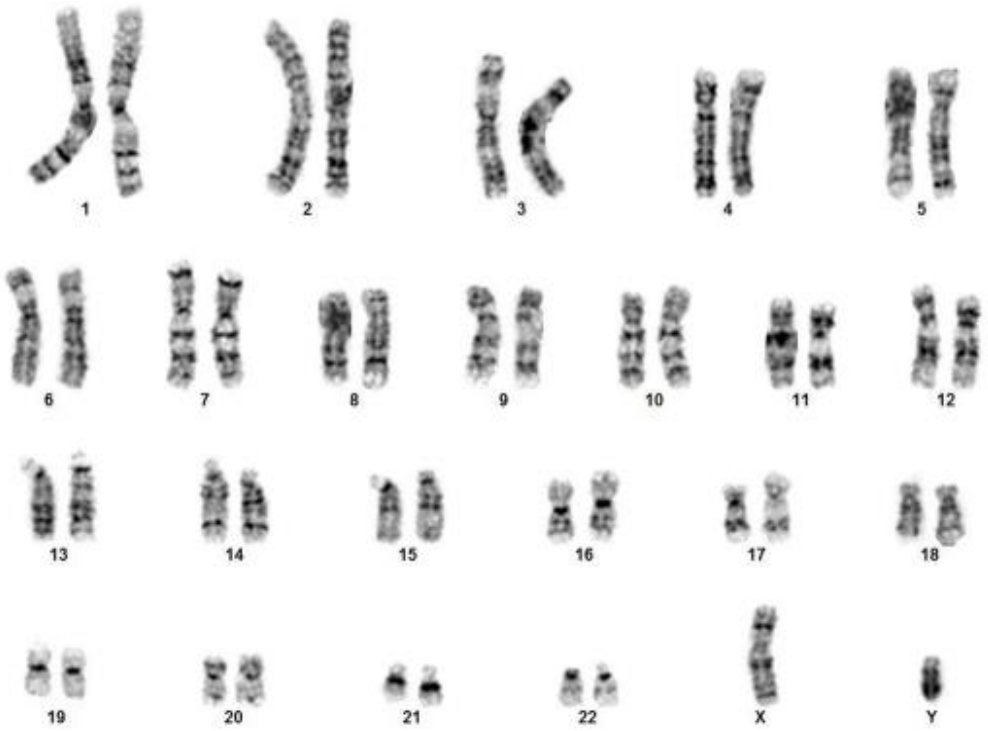

Figure 5. G-banding karyogram

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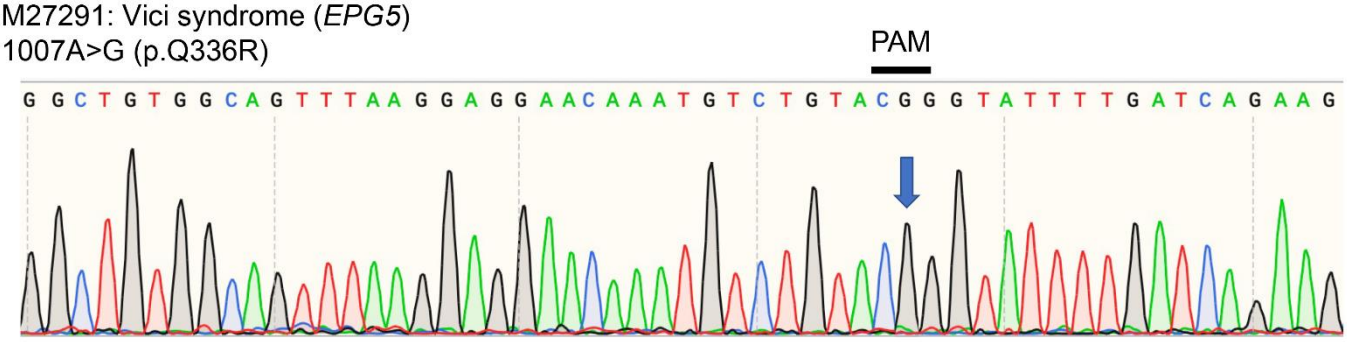
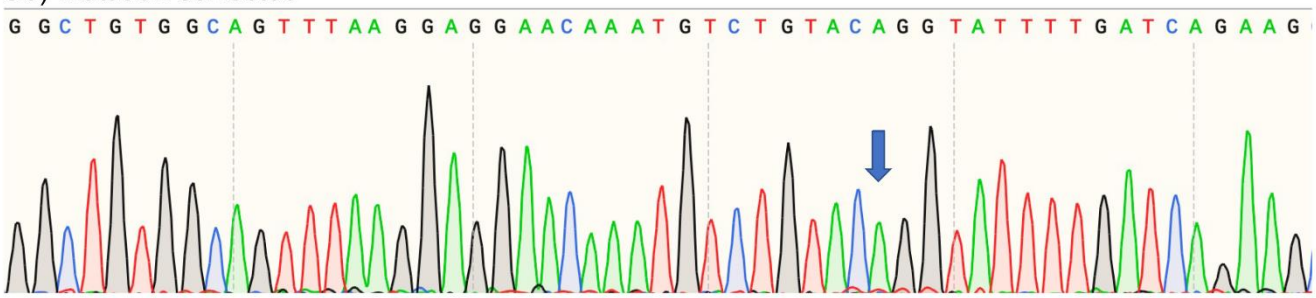
Sequence Verification

The presence of the *EPG5* c.1007A>G (p.Q336R) homozygous mutation in the patient-derived line (GM27291) was confirmed by Sanger sequencing of the *EPG5* gene. The corrected CRISPR-Cas9 gene-edited mutation was also confirmed by Sanger sequencing. The top five most likely off-target CRISPR-Cas9 cutting sites were also screened by Sanger sequencing and no off-target cutting was detected.

GM27291: Vici syndrome (*EPG5*)
c.1007A>G (p.Q336R)



GM28930: Isogenic control for Vici syndrome
(*EPG5*) Mutation corrected



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