NeuraCell Contract Research Update – TAU Project G389R donor

April 12th, 2017

Steve Lotz

G389R (MHF-102) Reprogramming Status Report

MHF-102-SeV-hiPSC Clones 1, 2 and 3

- Reprogramming summary:
  - Expand Fibroblast and Tested for Myco (negative)
  - Length = ~7 weeks

  - All lines were derived using Sendai Virus 2.0 (Transgenic free system)
  - Length = 5 weeks; Split at Day 10 onto MG (Corning)
  - Format: 25K and 50K; 12w plate

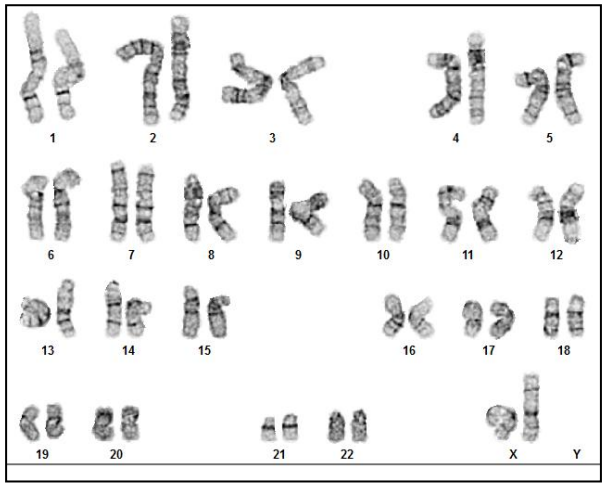
- 3 lines were obtained for MHF-102. Each has been expanded and banked. Three clones from the patient's fibroblasts will be fully characterized

G389R (MHF-102) Characterization Summary

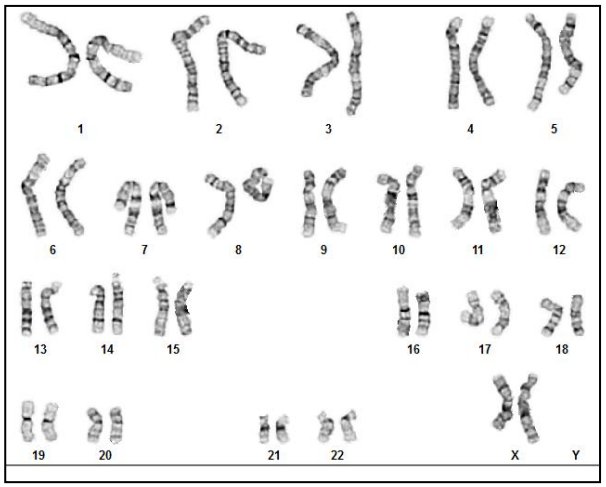
KT and FP confirms genomic integrity and identification

MHF102-SeV-hiPSC

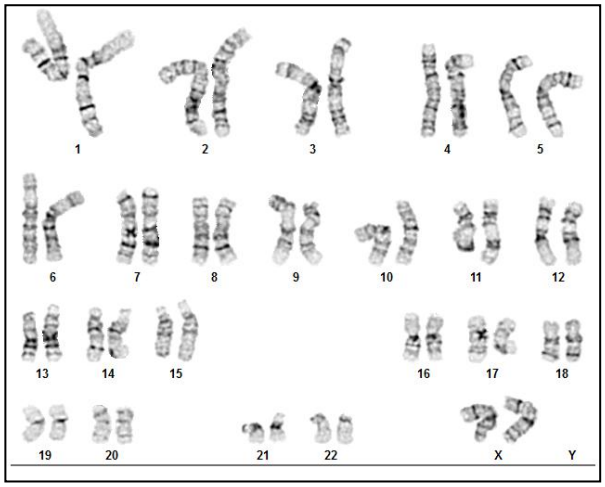
Clone 1 (p2)



Clone 2 (p2)



Clone 3 (p2)



MHF-102 -SeV-hiPSC clones 1, 2 and 3 have been assayed by WiCell to confirm a normal karyotype and no clonal abnormalities are detected at the stated band level of resolution.

G389R (MHF-102) -SeV-hiPSC Characterization Summary

KT and FP confirms genomic integrity and identification

Label on tube	MHF-102 C1 p3 (70883)	MHF-102 C2 p3 (70884)	MHF-102 C3 p3 (70885)
Label on Report	MHF-102 C1 p3 (70883)	MHF-102 C2 p3 (70884)	MHF-102 C3 p3 (70885)
conc (ng/µL)	28.0	39.7	65.2
A260/280	1.58	1.57	1.61
Assay Date	3/21/2018	3/21/2018	3/21/2018
File Name	STR 180322 wmr	STR 180322 wmr	STR 180322 wmr
Report Date	3/27/2018	3/27/2018	3/27/2018
FGA	22,23	22,23	22,23
TPOX	8,8	8,8	8,8
D8S1179	10,15	10,15	10,15
vWA	14,17	14,17	14,17
Amelogenin	X,X	X,X	X,X
Penta_D	12,13	12,13	12,13
CSF1PO	10,10	10,10	10,10
D16S539	9,13	9,13	9,13
D7S820	9,12	9,12	9,12
D13S317	11,13	11,13	11,13
D5S818	13,13	13,13	13,13
Penta_E	5,11	5,11	5,11
D18S51	15,17	15,17	15,17
D21S11	28,29	28,29	28,29
TH01	8,9.3	8,9.3	8,9.3
D3S1358	15,16	15,16	15,16
Allelic Polymorphisms	27	27	27
Matches**	70884, 70885, 70913	70883, 70885, 70913	70883, 70884, 70913

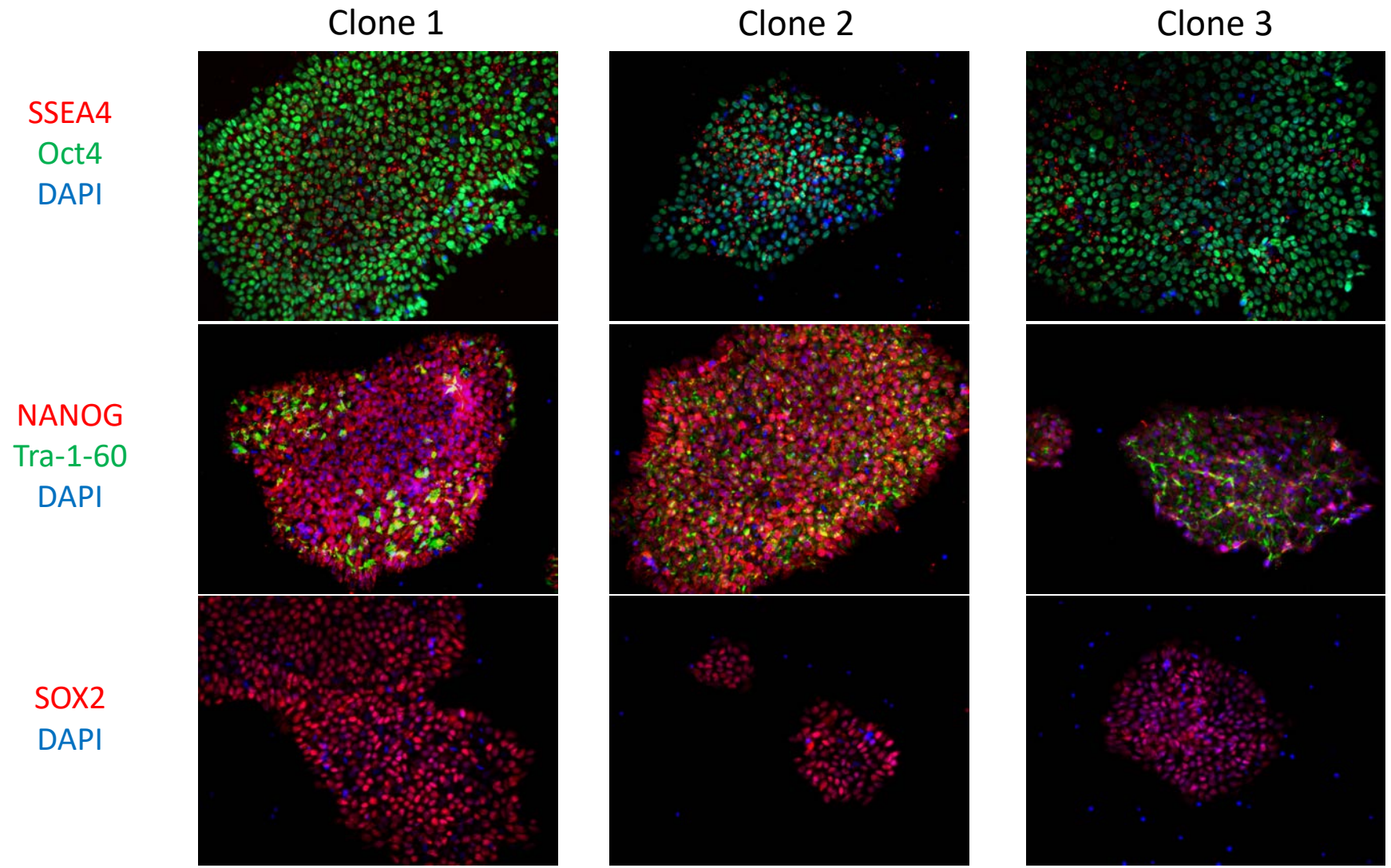
Results: Based on the cells submitted by WiCell Cytogenetics for Neural Stem Cell Institute dated and received on 03/26/18, these samples define the STR profiles of the human stem cell lines as indicated by name. The genotypic profiles comprising a range of 26-27 allelic polymorphisms across the 15 STR 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 suggests that the stem cells submitted correspond to the cell lines as named and were not contaminated with any other human stem 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 stem cell lines is ~2-5%.

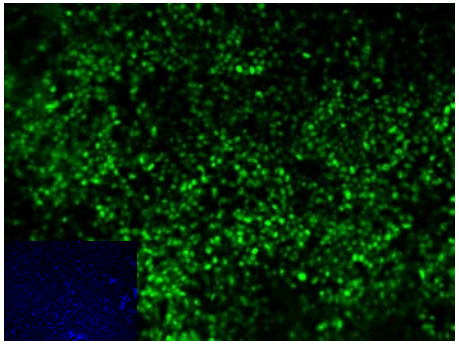
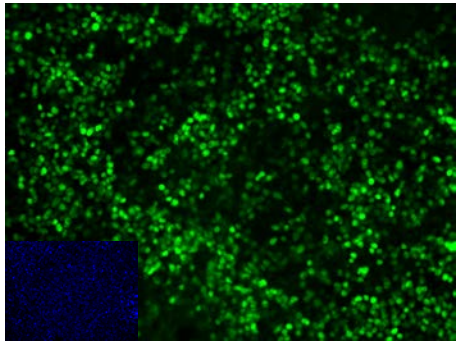
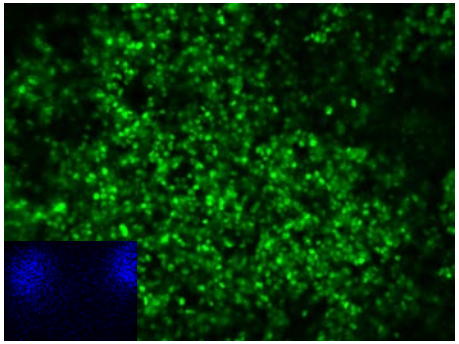
G389R (MHF-102) -SeV-hiPSC Characterization Summary

Pluripotency expression confirmed via immunoflorescence



G389R (MHF-102) -hiPSC Characterization Summary

Differentiation potential confirmed via directed tri-lineage

	Clone 1	Clone 2	Clone 3
Ectoderm PAX6			
Mesoderm Brachyury			
Endoderm SOX17			