

NeuraCell Contract Research Update

– TAU Project

G389R Donor

April 12th, 2017

Steve Lotz

G389R (MHF-100) Reprogramming Status Report

MHF-100-SeV-hiPSC Clones 1, 2 and 3

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

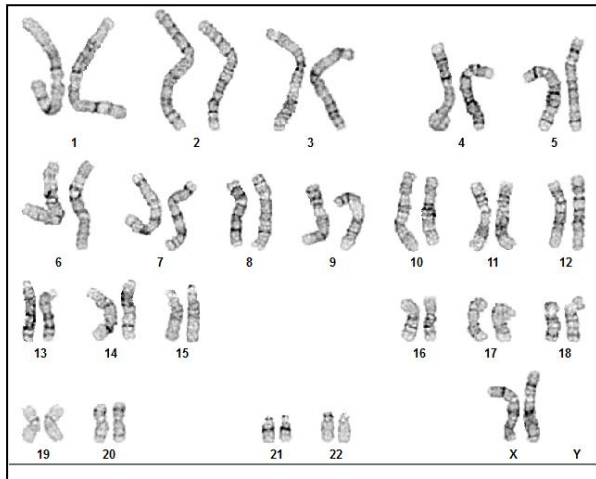
 - All lines were derived using Sendai Virus 2.0 (Transgenic free system)
 - Length = 5 weeks; Split at Day 10 onto MG (Corning)
 - Format: 25K and 50K; 12w plate
- 3 lines were obtained for MHF-100. Each has been expanded and banked. Three clones from the patient's fibroblasts will be fully characterized

G389R (MHF-100) Characterization Summary

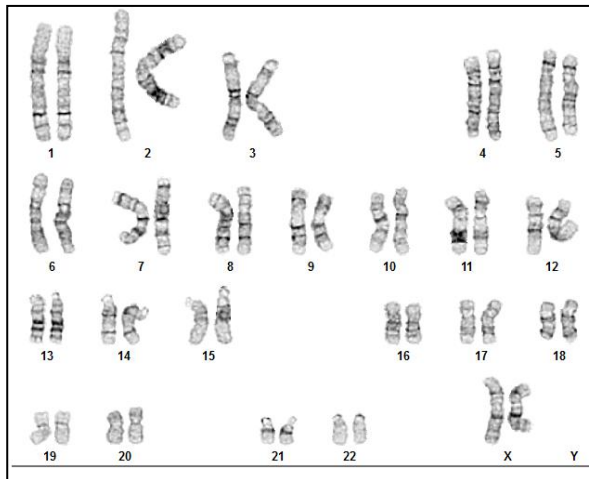
KT and FP confirms genomic integrity and identification

MHF-100-SeV-hiPSC

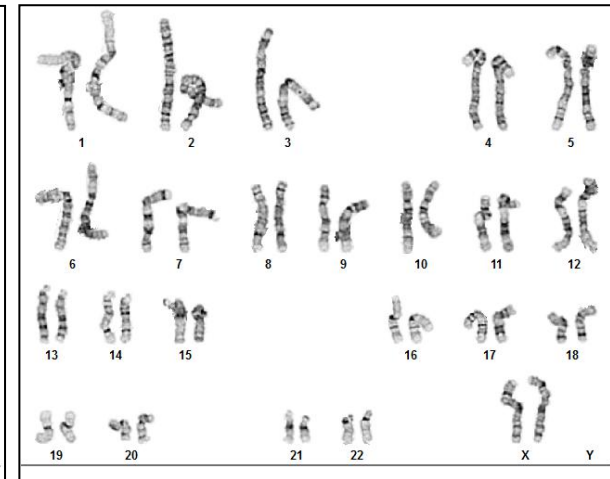
Clone 1 (p3)



Clone 2 (p3)



Clone 3 (p3)



MHF-100 -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-100) -SeV-hiPSC Characterization Summary

KT and FP confirms genomic integrity and identification

Label on tube	MHF-100 p8 (70911)	MHF-100 C1 p3 (70912)	MHF-100 C2 p3 (70886)	MHF-100 C3 p3 (70887)
Label on Report	MHF-100 p8 (70911)	MHF-100 C1 p3 (70912)	MHF-100 C2 p3 (70886)	MHF-100 C3 p3 (70887)
conc (ng/μL)	29.8	104.9	42.2	21.6
A260/280	1.44	1.79	1.59	1.51
Assay Date	3/21/2018	3/21/2018	3/21/2018	3/21/2018
File Name	STR 180322 wmr	STR 180322 wmr	STR 180322 wmr	STR 180322 wmr
Report Date	3/27/2018	3/27/2018	3/27/2018	3/27/2018
FGA	22,23	22,23	22,23	22,23
TPOX	8,12	8,12	8,12	8,12
D8S1179	13,15	13,15	13,15	13,15
vWA	14,18	14,18	14,18	14,18
Amelogenin	X,X	X,X	X,X	X,X
Penta_D	11,12	11,12	11,12	11,12
CSF1PO	10,12	10,12	10,12	10,12
D16S539	9,13	9,13	9,13	9,13
D7S820	9,11	9,11	9,11	9,11
D13S317	11,13	11,13	11,13	11,13
D5S818	13,13	13,13	13,13	13,13
Penta_E	5,12	5,12	5,12	5,12
D18S51	17,19	17,19	17,19	17,20
D21S11	29,29	29,29	29,29	29,29
TH01	6,9.3	6,9.3	6,9.3	6,9.3
D3S1358	14,16	14,16	14,16	14,16
Allelic Polymorphisms	28	28	28	28
Matches**	70886, 70912	70886, 70911	70911, 70912	>80% match criteria
			>80% match criteria	>80% match criteria

Results: Based on the cells submitted by WiCell Cytogenetics for Neural Stem Cell Institute dated and received on 03/19/18, these samples define the STR profiles of the human stem cell lines as indicated by name. The genotypic profiles comprising a range of 25-29 allelic polymorphisms across the 15 STR loci analyzed.

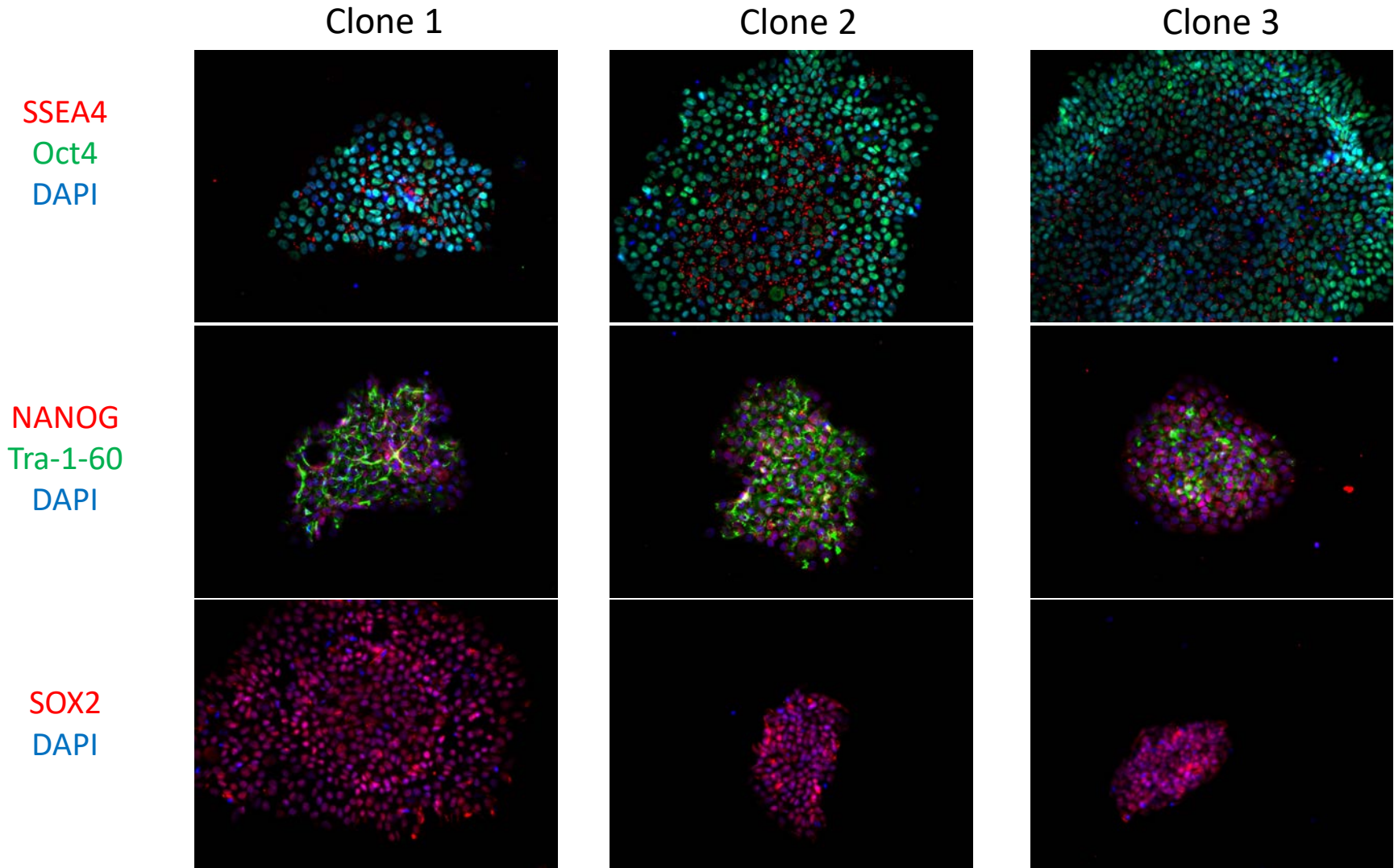
Interpretation: The concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. These results suggests that the stem cells submitted correspond to the cell lines as 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%.

** Note: The STR profile of the following sample is an exact match for the given sample/samples. Sample 70886 is a match to sample 70887 with the exception of the D18S51 loci (17,19) where in sample 70887 17,20 is observed. Standards for cell line authentication have been promoted with suggested algorithms to determine degrees of “relatedness” and have been recommended as a simple and effective way to interpret results from STR profiling of human cell lines. In general, >80% match is common between related samples, whereas < 50% match is unrelated (Int. J. Cancer: 132, 2510-2519. 2013). Using this criteria, across the 15 microsatellite STR loci, determined the 70886 sample displays a 29/30 allelic match (97% match), thus we would call this sample a match to sample 70887.

G389R (MHF-100) -SeV-hiPSC Characterization Summary

Pluripotency expression confirmed via immunoflorescence



G389R (MHF-100) -hiPSC Characterization Summary

Differentiation potential confirmed via directed tri-lineage

