

TITLE: KROMATID CHROMOSOME ANALYSIS REPORT

I. ASSAY INFORMATION

Project Quote #	Q200401
Specimen Type	iPSC
Body Site	N/A
Sample ID	120 AB (S005961)
Cell Line Gender	Male
Passage number (or N/A)	N/A
Study Objective	The purpose of this study is to characterize iPS cells grown <i>in vitro</i> , designated for cytogenetic analysis.

II. CELL MAINTENANCE

Culture vessel	N/A
Media	N/A
Density (estimated)	N/A
Culture atmosphere	N/A
Culture maintenance	N/A

DocuSign Envelope ID: AEFF5DA2-ECD6-4F3A-9EF0-3037	FCA1F37D		
KromaliD	Document Code:	FORM-0068A	Docum
NUIIAIID			
	D * *		D

Date Effective:08-27-21

 Culture
Maintenance
Process
Description
 N/A

 Maintenance
Process
Description
 N/A

Revision: 3.0

III. CULTURE HARVEST

Culture Harvest Process Description	N/A
	Analyst Initial/Date: N/A

Material	Usage information
Harvest materials (trypsin, EDTA, etc.)	Type: N/a LN/ Exp. Date: N/a
Colcemid	LN/ Exp. Date: N/a Concentration: 0.1 µg/ml (10 µl/ml) Incubation time: N/a
Hypotonic	LN/ Exp. Date: N/a Solution: N/a Incubation time:
Fixative	Prepared Fresh, day-of-use



IV. STAINING

Solution Type	Lot#	Exp. Date	Solution Type	Lot#	Exp. Date
Isoton II Diluent	4710610	07/12/22	Wright Stain	210817-Wright	08/17/22
Pancreatin	SLCD9444	01/11/23	Gurr Buffer	211007-Gurr	11/7/21
FBS	19J079	11/4/22	Permount	210201-01	02/1/23

Process Description	A sample of fixed cells labeled 120 AB (KromaTiD Sample ID S005961) was received at KromaTiD on 10-20-21. The fixed cells were washed twice with fixative (prepared fresh day-of-use) and the O.D. was adjusted. Drops of the final cell suspension were placed on clean slides and aged for 60 minutes at 90°C. Slides were digested in a pancreatin solution with Isoton II diluent. The enzymatic reaction was then stopped by rinsing with FBS, followed by application of a stain solution (3:1 Wright/Gurr buffer) which was poured on the slides so that it covered the entire surface. After staining for up to 1 minute, slides were washed with de- ionized water for 1-5 seconds and air dried. The mounting medium Permount was applied to the slides, a coverslip was placed on the slide and the slides were scanned on the microscope.
	Analyst Initial/Date: MV 10-26-21 through 10-29-21

TEST DESCRIPTION:

G-banding with trypsin treatment and Giemsa stain (GTG-banding) is used in cytogenetics to produce a visible karyotype by staining metaphase chromosomes. This technique allows each chromosome to be distinguished by its characteristic banding pattern. G-banding is useful in assessing structural abnormalities in individual chromosomes, as well as extra or missing chromosomes within a cell. Industry-standard protocols for scoring and describing results were used (ISCN 2016: An International System for Human Cytogenomic Nomenclature).

KromaliD

V. **RESULTS**

Cells Counted	20	Total Karyograms	2
Cells Analyzed	20	Average Band Resolution	375
Image File Location		Jax Gbanding_S005961	

5.1 Chromosome Count per 20 Metaphases

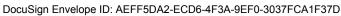
Of the 20 cells counted, 19 contained 46 chromosomes (95%). *Cells containing greater than* 57 *chromosomes are recorded as polyploid*. The polyploid frequency was 0%, based on the metaphases counted.

5.2 CHROMOSOME ABERRATION DATA

The chromosome aberration data via G-band for the 20 metaphases examined is summarized in attached case report cell list. 0 chromosome aberrations were found in the 20 cells analyzed with 0% of the cells aberrant.

*Note: Cells with an euploidy gain/loss were found to be non-clonal, and therefore not included in the aberration data below.

	Tech Summary	Additional Comments		
Karyotype 46,XY[20]		Normal Male Karyotype		
Cells Analyzed	20			
Normal Cells	20	Random loss/gain cells normalized		
Abnormal Cells	0			
Aberration	n/a			
Туре				
Aberration %	0%			





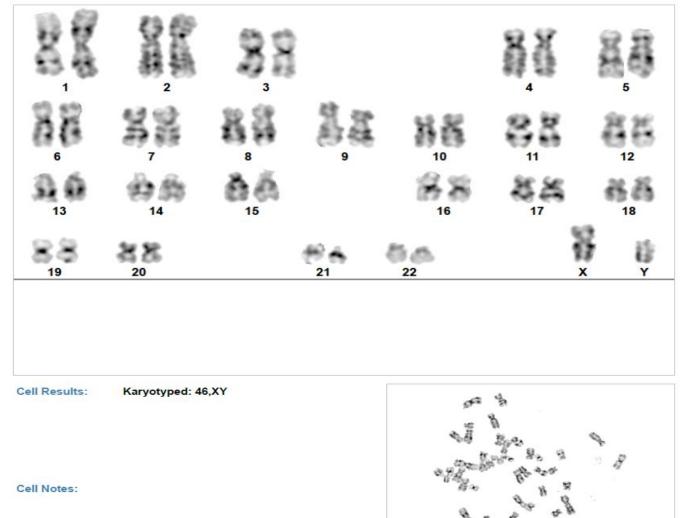
501	I CATI 37D			
	Document Code:	FORM-0068A	Document Type:	FORM
	Revision:	3.0	Date Effective:	08-27-21

5.3. INTERPRETATION/ SIGNIFICANCE:

G-banded chromosome analysis of metaphase cells designated as 120 AB (KromaTiD Sample ID S005961) show a normal male karyotype 46,XY[20].

The other abnormalities/aberrations detected were non-clonal, and were designated as low level mosaicism or random gain/loss.





Label - Slide/Cell: S005961 - 1/21

X,Y: 16.9 , 24.0

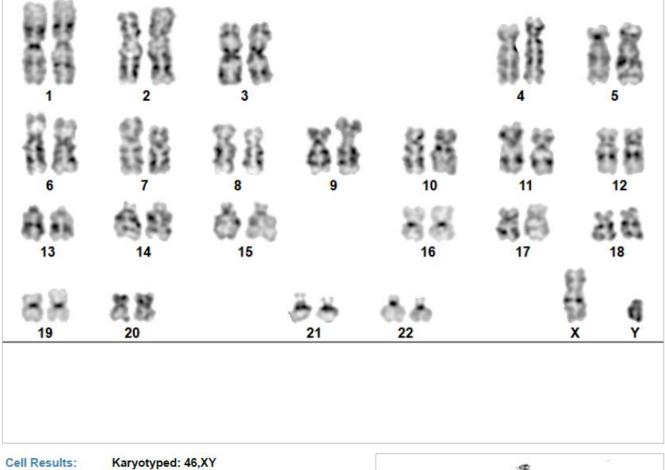
Report Date: Wednesday, November 3, 2021

DocuSign Envelope ID: AEFF5DA2-ECD6	-4F3A-9	9EF0-3037FCA1F37D		
Kroma		Document Code:	FORM-0068A	Document Type:
NUIIA				

Revision: 3.0

Date Effective: 08-27-21

FORM



Cell Notes:

1 100 6% 2012

Label - Slide/Cell: S005961 - 1/26

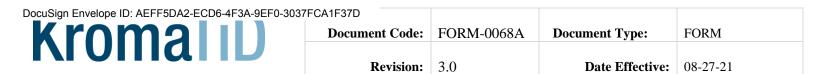
17.8, 29.2 X,Y:

DocuSign Envelope ID: AEFF5DA2-ECD6-4F3A-9EF0-3037FCA1F37D					
KromaliD	Document Code:	FORM-0068A	Document Type:	FORM	
NUIIAID					
	Revision:	3.0	Date Effective:	08-27-21	

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. Detection of heterogeneity of clonal cell populations in this specimen is limited by the number of metaphase cells analyzed, documented above as "number of cells counted". Results are for Research Use Only, and should not be used for clinical purposes.

DocuSigned by: 11/11/2021 **Completed By/Date:** rel Vernich -B510035B47034EE.. **Michael Vernich Cytogenetics Associate** DocuSigned by: 11/11/2021 wan Peres **Reviewed By/ Date:** 78884964FB9848A. Ivan Perez **Cytogenetics Technologist III** DocuSianed by: **Approved By/Date:** Maussa Badrigues /11/2021 5FAF272CE1894D0.

Marissa Rodrigues QA Manager



APPENDIX A: CASE REPORT FOR SAMPLE S005961

DeauCian Envilone	ID: AEFF5DA2-ECD6-4F3A	
	10. AEFF30AZ-E000-4F3A	1-9EFU-3U3/FUAIF3/D

USIGN Envelope ID: AEFF5DA2-ECD6-4F3A-9EF0-303	/FCA1F3/D				
(romal ID	Document Code:	FORM-0068A	Document Type:	FORM	
VUIIAID					
	Revision:	3.0	Date Effective:	08-27-21	

 Table A-1: Chromosome Analysis for sample 120 AB (S005961).
 20 cells were analyzed.

#	Slide	Cell	Coordinates	Results	Analysis State	State By
Slide: Nam	ne: 1 Label	: S005961	l			
1	1	8	13.00 X 19.87	Karyotyped: 46,XY	Karyotyped	mvernich
2	1	12	16.32 X 21.08	Karyotyped: 46,XY	Karyotyped	mvernich
3	1	13	13.22 X 21.03	Karyotyped: 46,XY	Karyotyped	mvernich
4	1	15	12.18 X 21.47	Karyotyped: 46,XY	Karyotyped	mvernich
5	1	16	11.09 X 22.90	Karyotyped: 46,XY	Karyotyped	mvernich
6	1	18	13.25 X 22.12	Karyotyped: 46,XY	Karyotyped	mvernich
7	1	21	16.86 X 23.96	Karyotyped: 46,XY	Karyotyped	mvernich
8	1	23	15.91 X 26.23	Karyotyped: 46,XY	Karyotyped	mvernich
9	1	24	7.43 X 27.22	Karyotyped: 46,XY	Karyotyped	mvernich
10	1	25	17.51 X 28.09	Karyotyped: 46,XY	Karyotyped	mvernich
11	1	26	17.81 X 29.17	Karyotyped: 46,XY	Karyotyped	mvernich
12	1	27	14.68 X 29.39	Karyotyped: 46,XY	Karyotyped	mvernich
13	1	29	9.45 X 31.14	Karyotyped: 46,XY	Karyotyped	mvernich
14	1	33	16.85 X 30.98	Karyotyped: 46,XY	Karyotyped	mvernich
15	1	35	11.52 X 33.78	Karyotyped: 46,XY	Karyotyped	mvernich
16	1	37	16.04 X 34.56	Karyotyped: 45,XY, -20	Karyotyped	mvernich
17	1	42	17.11 X 38.05	45,X1, -20 Karyotyped: 46,XY	Karyotyped	mvernich
18	1	48	16.17 X 43.26	Karyotyped: 46,XY	Karyotyped	mvernich
19	1	50	16.19 X 43.92	Karyotyped: 46,XY	Karyotyped	mvernich
Slide: Nam	ne: 2 Label	: S005961	L			
20	2	8	12.14 X 19.01	Karyotyped: 46,XY	Karyotyped	mvernich