TITLE: KromaTiD Genomic Integrity G-Band Report

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I. PROJECT INFORMATION

Project Quote #	QYYMMDD
Sample Type	Edited Cells
Sample ID	S######, Treated Z
Gender	Male
Passage number (or N/A)	N/A
Study Objective	Assessment of genomic integrity
Project Start Date	DDMonYYYY
Project Completion Date	DDMonYYYY

I. G-BAND ASSAY

Assay	Standard G-BAND **SOP-0068.3 (100 Cells)**
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 are used to score events (ISCN 2020: An International System for Human Cytogenomic Nomenclature). Events for this report are listed by type and prevalence. Appendix A contains a list of all events that were scored and abbreviations.

II. RESULTS

Cells Analyzed	100

Table 1: Summary of cell ploidy results

Category	% of Cells
Diploid	100

Table 2: Summary of cells with chromosomal rearrangements (Note: Total % can be greater than 100 because there can be more than one event per cell)

Category	% of Cells
No Events	74
chromosome aneuploidy	20
acentric fragments	0
additional material of unknown origin	0
constitutional anomaly	0
chromosome breaks	0
chromatid breaks	0
chromothripsis	0
deletions	2
derivative chromosomes	0
dicentrics	0
double minutes	0
duplications	0
endoreduplications	0
fragile sites	0
heterochromatin, constitutive	0
homogeneously staining regions	0
isochromosomes	0
isodicentrics	0
insertions	0
inversions	1
marker chromosomes	2
losses	0
multiple copies of same abnormality	0
gains	0
quadriradials	0
ring chromosomes	0
translocations	2
triradials	0

Table 3: Rearrangement event rates

Category	Event	# of Cells	% of Cells
Chromosome Aneuploidy	−X	1	1
	−2	4	4
	−3	1	1
	−5	2	2
	−9	1	1
	−15	2	2
	−16	1	1
	−18	1	1
	−21	6	6
	+9	1	1
Marker Chromosomes	+M	2	2
Deletions	del(9)(q15)	1	1
	del(21)(q25)	1	1
Inversions	inv(7)(p13)	1	1
Translocation	t(2;9)(p15.3;q22)	1	1
	t(8;12)(q15;q12)	1	1

Table 4: Event rates for Edit Target Chromosomes

S#######	# Events	# of Cells	% of Cells
Chr 9 Events	4	4	4
Chr 21 Events	7	7	7

Summary of Results:

Sample karyotype is 100% diploid, with aneuploidy observed in 20% of cells.

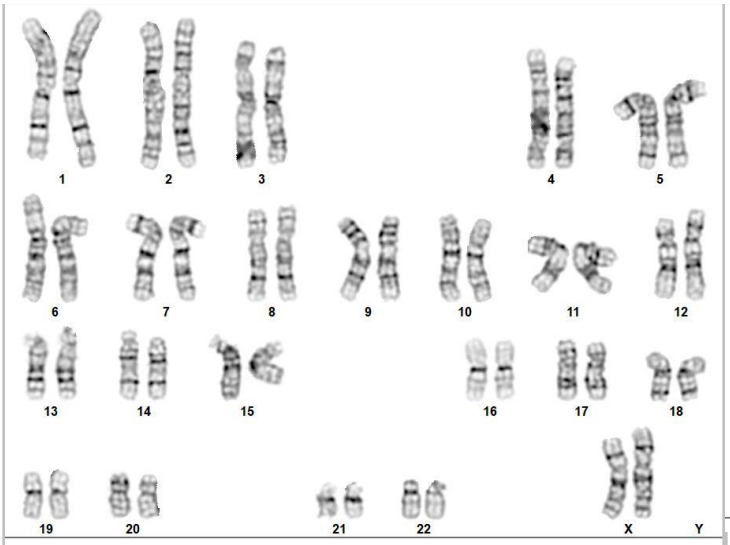
Loss of chromosome 2 (four cells) and chromosome 21 (six cells) would be considered recurrent in standard g-band karyotyping. The remaining aneuploidy observed should be regarded as random loss/gain of a chromosome.

A small percentage (7%) of cells with structurally rearranged chromosomes were detected, however none of these events was recurrent.

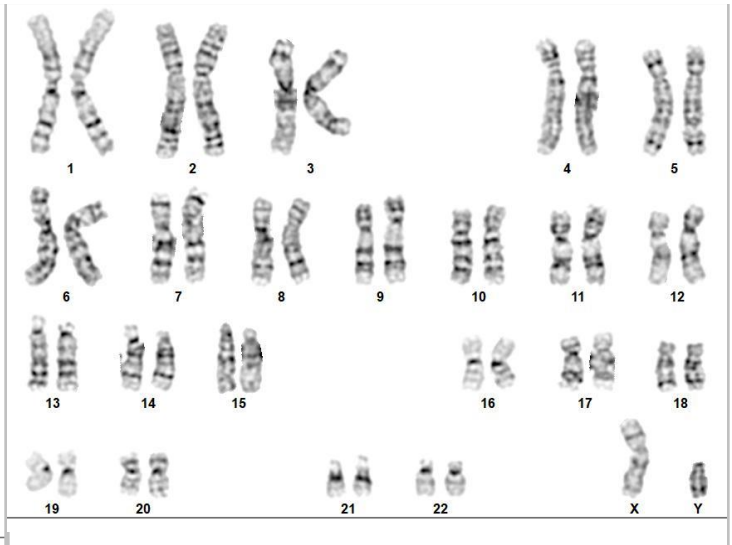
A summary of observed karyotypes is included in Appendix B.

Example Karyograms (Two normal representative Images; if there are recurrent structural events, then additional images will be included):

Karyotyped: 46,XY Slide#-Cell#



Karyotyped: 46,XY Slide#-Cell#



KromaTiD Genomic Integrity G-Band Assay is for research use only and is not a medical diagnostic test.

Appendix A. Table of karyotyping abbreviations

Abbreviation	Definition
ace	acentric fragment
add	additional material of unknown origin
c	constitutional anomaly
chrb	chromosome break
chtb	chromatid break
cth	chromothripsis
del	deletion
der	derivative chromosome
dic	dicentric
dmin	double minute
dup	duplication
end	endoreduplication
fra	fragile site
h	heterochromatin, constitutive
hsr	homogeneously staining region
i	isochromosome
idic	isodicentric
ins	insertion
inv	inversion
mar or M	marker chromosome
minus sign (-)	loss
multiplication sign (x)	multiple copies of same abnormality
plus sign (+)	gain
qr	quadriradial
r	ring chromosome
t	translocation
tr	triradial

Appendix B. Table of cell karyotypes.

Karyotype:	# Cells
46,XY	74
45,Y, −X	1
45,XY, −2	4
45,XY, −3	1
45,XY, −5	2
45,XY, −9	1
45,XY, −15	1
45,XY, −16	1
45,XY, −18	1
45,XY, −21	6
45,XY,del(21)(q25), −15	1
46,XY,del(9)(q15)	1
46,XY, inv(7)(p13)	1
46,XY,t(2;9)(p15.3;q22)	1
46,XY,t(8;12)(q15;q12)	1
47,XY, +9	1
47,XY, +M	2