TITLE: KromaTiD Genomic Integrity G-Band Report

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I. PROJECT INFORMATION

Project Quote #	240328
Sample Type	T-Cells
Sample ID	S019000 , GTX CAR Insert 1
Passage number (or N/A)	N/A
Study Objective	G-Banding
Project Start Date	04/15/2024
Report Date	04/26/2024

I. G-BAND ASSAY

Assay	**Standard G-banding SOP-0068.4**
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 event types evaluated. Appendix B contains a list of all unique events with their observed counts.

II. RESULTS

Cells Analyzed	100

Table 1: Summary of cell ploidy results

Category	% of Cells
Haploid	0.0
Diploid	97.0
Triploid	1.0
Tetraploid	2.0
>4n Ploidy	0.0

Table 2: Summary of cells with chromosomal events

Category	% of Cells with > 0 Events in Category
No Events	35.0
Chromosome aneuploidy	35.0
Acentric fragments	0.0
Additional material of unknown origin	5.0
Constitutional anomaly	0.0
Chromosome breaks	1.0
Chromatid breaks	4.0
Chromothripsis	0.0
Deletions	24.0
Derivative chromosomes	6.0
Dicentrics	1.0
Double minutes	0.0
Duplications	1.0
Endoreduplications	0.0
Fragile sites	0.0
Heterochromatin, constitutive	0.0
Homogeneously staining regions	0.0
Isochromosomes	0.0
Isodicentrics	0.0
Insertions	0.0
Inversions	0.0
Marker chromosomes	6.0
Quadriradials	0.0
Ring chromosomes	0.0
Translocations	14.0
Triradials	0.0

Table 3: Chromosomal aneuploidy event rates

Category	Event	# of Cells	% of Cells
Chromosome Aneuploidy (Loss)	-1	0	0.0
	-2	1	1.0
	-3	1	1.0
	-4	1	1.0
	-5	0	0.0
	-6	2	2.0
	-7	0	0.0
	-8	0	0.0
	-9	1	1.0
	-10	0	0.0
	-11	2	2.0
	-12	0	0.0
	-13	1	1.0
	-14	3	3.0
	-15	1	1.0
	-16	2	2.0
	-17	0	0.0
	-18	2	2.0
	-19	2	2.0
	-20	2	2.0
	-21	2	2.0
	-22	0	0.0
	-X	13	13.0
	-Y	0	0.0

Category	Event	# of Cells	% of Cells
Chromosome Aneuploidy (gain)	+1	0	0.0
	+2	2	2.0
	+3	0	0.0
	+4	0	0.0
	+5	0	0.0
	+6	0	0.0
	+7	1	1.0
	+8	0	0.0
	+9	0	0.0
	+10	0	0.0
	+11	0	0.0
	+12	0	0.0
	+13	0	0.0
	+14	0	0.0
	+15	0	0.0
	+16	0	0.0
	+17	0	0.0
	+18	0	0.0
	+19	0	0.0
	+20	0	0.0
	+21	0	0.0
	+22	0	0.0
	+X	1	1.0
	+Y	0	0.0

Table 4: Event rates for Project-specific chromosomes

Chromosome	# Events	# of Cells	% of Cells
16	38	37	37

Summary of Results:

Sample karyotype is 97.0% diploid, with non-recurrent aneuploidy observed in 35.0% of cells.

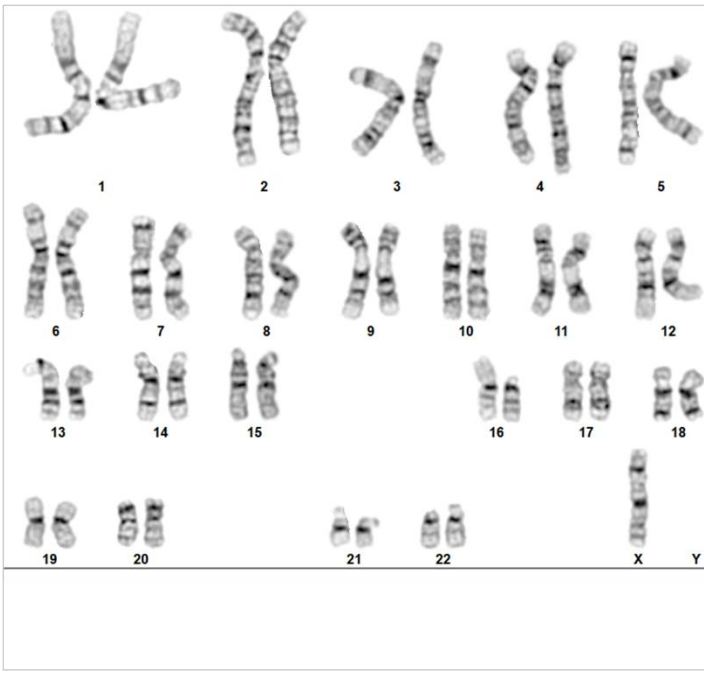
Non-recurrent aneuploidy observed should be regarded as random loss/gain of a chromosome.

Structurally rearranged chromosomes were detected in 49.0% of cells. Events with occurrence in over 15% of cells are considered recurrent.

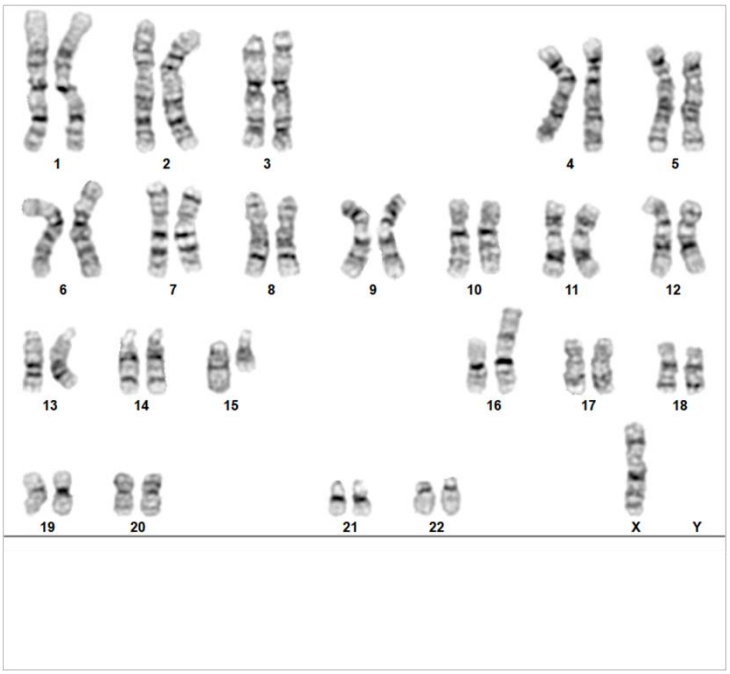
A summary of observed events is included in Appendix B.

Example Karyograms:

Karyotyped: 45,X,-X,del(16)(p12) 1 - 16



Karyotyped: 45,X,-X,t(15;16)(q21;p13.3) 1 - 34



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 individual karyotypic events

Karyotype	Category	# of Events	# of Cells	% of Cells
add(16)(p13.3)	additional_material_unknown_origin	5	5	5.0
chtb(1)(p)	chromatid_break	1	1	1.0
chtb(10)(q)	chromatid_break	1	1	1.0
chtb(16)(p)	chromatid_break	1	1	1.0
chtb(4)(q)	chromatid_break	1	1	1.0
chrb(3)(p)	chromosome_break	1	1	1.0
del(14)(q11.2)	deletion	5	5	5.0
del(15)(q21)	deletion	1	1	1.0
del(16)(p12)	deletion	12	12	12.0
del(16)(p12)x2	deletion	2	1	1.0
del(16)(p13.2)	deletion	3	3	3.0
del(19)(p13.2)	deletion	1	1	1.0
del(3)(p10)	deletion	1	1	1.0
del(3)(p25)	deletion	1	1	1.0
der(11)t(11;17)(p11.2;q21)	derivative_chromosome	1	1	1.0
der(14;16)(p11.2;p13.2)	derivative_chromosome	4	4	4.0
der(3;6)(p21.3;p21)	derivative_chromosome	1	1	1.0
dic(6;11)(p25;p15)	dicentric	1	1	1.0
dup(9)(q21q31)	duplication	1	1	1.0
+2	gain	2	2	2.0
+7	gain	1	1	1.0
+X	gain	1	1	1.0
-2	loss	1	1	1.0
-3	loss	1	1	1.0
-4	loss	1	1	1.0
-6	loss	2	2	2.0
-9	loss	1	1	1.0
-11	loss	2	2	2.0
-13	loss	1	1	1.0
-14	loss	3	3	3.0
-15	loss	1	1	1.0
-16	loss	2	2	2.0
-18	loss	2	2	2.0
-19	loss	2	2	2.0
-20	loss	2	2	2.0
-21	loss	2	2	2.0
-X	loss	15	13	13.0
+4M	marker_chromosome	4	1	1.0
+M	marker_chromosome	5	5	5.0
t(15;16)(q21;p13.3)	translocation	9	9	9.0
t(3;11)(p24;p11.2)	translocation	4	4	4.0