

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

**TITLE: KromaTiD dGH SCREEN Whole Genome Analysis Report**

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**I. PROJECT INFORMATION**

<b>Project Quote #</b>	Q23xxxx
<b>Sample Type</b>	Cell type
<b>Sample ID</b>	S01xxxx, [sample name]
<b>Gender</b>	Female
<b>Passage number (or N/A)</b>	N/A
<b>Study Objective</b>	Assessment of genomic integrity
<b>Sample Receipt Date</b>	8/xx/23
<b>Report Date</b>	8/xx/23

**I. CHROMOSOME HARVEST**

Harvest is performed per SOP-0044.

<b>Condition</b>	<b>Result</b>
Analog incubation time:	<b>27 hrs</b>
Colcemid incubation time	<b>Performed by customer</b>
Harvest Option	<b>Standard Protocol: X</b> <b>Modified Conditions: N/A</b>

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

## II. dGH SCREEN ASSAY

<b>Assay</b>	Standard dGH SCREEN AS-0002.1 (50 Cells)
<b>Metaphase and Karyotype Qualification</b>	<p>Samples must be prepared and qualified for dGH analysis prior to running the assay.</p> <p>dGH SCREEN is designed for samples with grossly normal karyotypes and has not been qualified for highly rearranged genome analysis.</p> <p>Spread resolution of 350+ (G-band equivalent) is selected for analysis.</p>
<b>Assay Description</b>	<p>The five-color whole genome assay (5CWG or dGH SCREEN) is a dGH paint combination assay for all 24 human chromosomes.</p> <p>The assay is composed of unique sequence, high-density (HD) dGH chromosome paints in five color panels such that chromosomes painted in the same color can be differentiated by size, shape, and centromere position.</p> <p>Results include per-chromosome attribution of inter- and intra-chromosomal structural events including inversions, translocations, aneuploidy (gain and loss), insertions, centromere abnormalities and complex events across a sample.</p> <p>Prior to analysis, images of dGH SCREEN painted metaphase spreads are qualified, processed and sorted into karyograms for rapid, consistent reading of the assay.</p> <p>Per-cell event assessment is performed in an excel workbook which is built to be leveraged for population-level analysis of events ranging from random to clonal.</p>

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

### III. RESULTS

<b>Cells Analyzed</b>	50	<b>Total Karyograms</b>	50
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#### Chromosome Aberration Data:

Table 1: Structural Events

Event	Number of Events	Number Of Cells with Events
Gain	0	0
Loss	6	4
Inversion	41	32
SCE	211	49
Insertion	0	0
Size Diff	146	46
Translocations	0	0
Complex	6	5
<b>Total</b>	<b>410</b>	<b>50</b>

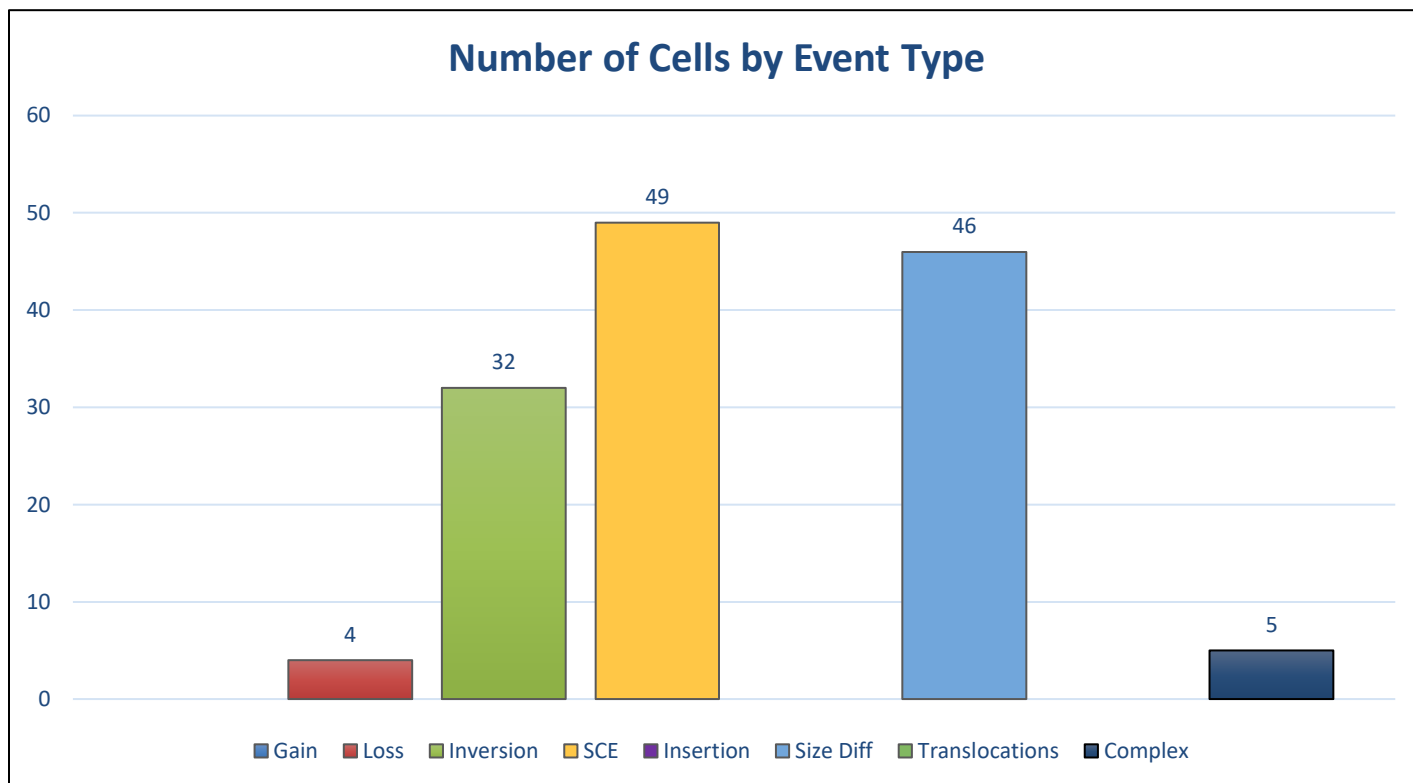
<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

**Table 2: Distribution of Events by Chromosome**

Count of Events by Chromosome																											
Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	Y	Number of Events	Number of Cells w/ Events	
Gain	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loss	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	1	1	1	0	0	6	4	
Inversion	0	2	1	1	1	0	2	27	1	2	0	0	2	0	0	0	0	1	0	0	0	0	1	0	41	32	
SCE	20	19	15	21	10	15	9	8	11	10	11	8	12	6	3	3	5	6	3	1	1	2	12	0	211	49	
Insertion	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Size Diff	16	17	11	12	10	15	9	0	10	5	7	7	1	1	3	3	3	4	3	2	0	0	7	0	146	46	
Translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Complex	1	1	1	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	6	5	
<b>Total</b>	<b>37</b>	<b>39</b>	<b>28</b>	<b>34</b>	<b>22</b>	<b>31</b>	<b>20</b>	<b>35</b>	<b>22</b>	<b>17</b>	<b>19</b>	<b>16</b>	<b>15</b>	<b>8</b>	<b>7</b>	<b>6</b>	<b>8</b>	<b>11</b>	<b>6</b>	<b>4</b>	<b>2</b>	<b>3</b>	<b>20</b>	<b>0</b>	<b>410</b>	<b>50</b>	

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

**Figure 1: Distribution of Event Rates by Number of Cells**



**Table 3: Aneuploidy Summary (whole chromosome gain and loss)**

	Number of Cells	Percentage of Cells
<b>Gain Event</b>	0	0%
<b>Loss Event</b>	4	8%

**Table 4: Aneuploidy detail, by chromosome identity and cell number.**

Location	Cell Name	Event	Gain Loss Values
Cell 16 / Chrom-12	Cell 16	Loss	-1
Cell 16 / Chrom-15	Cell 16	Loss	-1
Cell 22 / Chrom-21	Cell 22	Loss	-1
Cell 23 / Chrom-22	Cell 23	Loss	-1
Cell 33 / Chrom-11	Cell 33	Loss	-1
Cell 33 / Chrom-20	Cell 33	Loss	-1

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

**Table 5: Inversion and Sister Chromatid Exchange Event Summary**

	P-Arm								Pericentric Inversion	Q-Arm								Grand Total
	Inversion			Exchange			Terminal Inversions	Inversion			Exchange			Terminal Inversions				
	Centric Small	Mid-Arm Mid-Size	Mid-Arm Small	Large Sister Chromatid	Mid-Sized Sister Chromatid	Small Sister Chromatid		Centric Small		Mid-Arm Mid-Size	Mid-Arm Small	Large Sister Chromatid	Mid-Sized Sister Chromatid		Small Sister Chromatid			
1	0	0	0	3	8	2	0	1	0	0	0	1	5	0	0	20		
2	0	0	0	2	6	0	0	0	0	1	1	4	7	0	0	21		
3	0	0	0	0	8	1	0	0	0	1	0	2	4	0	0	16		
4	0	0	0	0	4	1	0	1	0	1	0	3	12	0	0	22		
5	1	0	0	0	5	0	0	1	0	0	0	2	2	0	0	11		
6	0	0	0	0	1	1	0	0	0	0	0	2	11	0	0	15		
7	0	1	1	0	3	0	0	0	0	0	0	2	4	0	0	11		
8	0	0	27	0	0	1	0	0	0	0	0	0	7	0	0	35		
9	0	0	1	0	4	0	0	1	0	0	0	0	4	2	0	12		
10	0	0	2	0	2	0	0	0	0	0	0	0	7	1	0	12		
11	0	0	0	0	3	1	0	0	0	0	0	2	5	0	0	11		
12	0	0	0	0	2	0	0	0	0	0	0	1	5	0	0	8		
13	0	0	0	0	0	0	0	0	1	1	0	3	9	0	0	14		
14	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	6		
15	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3		
16	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	3		
17	0	0	0	0	1	0	0	0	0	0	0	1	3	0	0	5		
18	0	0	0	0	0	0	0	0	0	0	1	1	5	0	0	7		
19	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	3		
20	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1		
21	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1		
22	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2		
X	0	0	1	0	2	2	0	1	0	0	0	2	5	0	0	13		
Y	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
<b>Grand Total</b>	<b>1</b>	<b>1</b>	<b>32</b>	<b>5</b>	<b>52</b>	<b>9</b>	<b>0</b>	<b>5</b>	<b>1</b>	<b>4</b>	<b>2</b>	<b>26</b>	<b>110</b>	<b>4</b>	<b>0</b>	<b>252</b>		
<b>Inversion Total</b>	<b>1</b>	<b>1</b>	<b>32</b>				<b>0</b>		<b>1</b>	<b>4</b>	<b>2</b>				<b>0</b>	<b>41</b>		
<b>SCE Total</b>				<b>5</b>	<b>52</b>	<b>9</b>		<b>5</b>				<b>26</b>	<b>110</b>	<b>4</b>		<b>211</b>		

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

## Recurrent SCE/Inversion Event Summary

There is a recurrent small inversion on Chr8p present in 54% of cells.

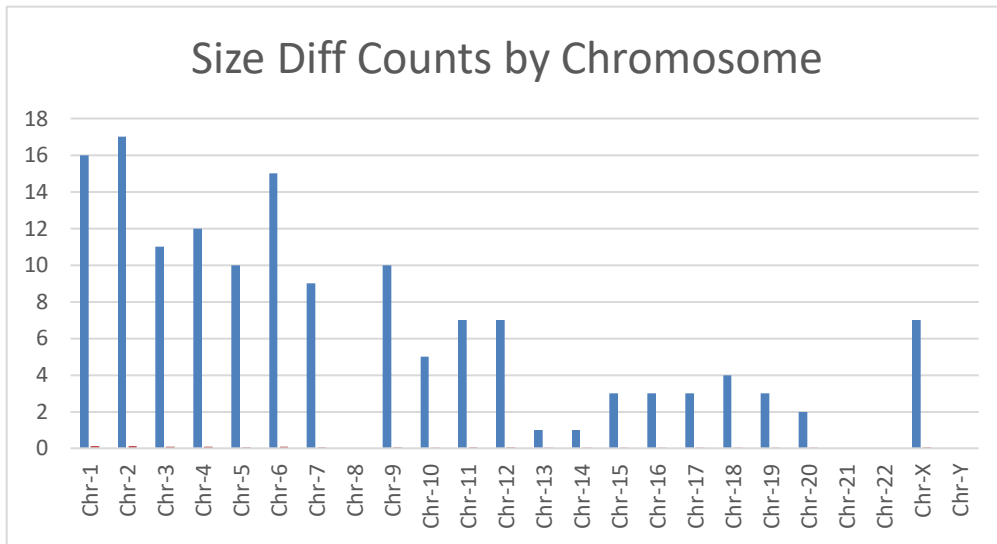
## Table 6: Insertion Event Summary

There are no insertion events in the sample.

## Table 7: Translocation Event Summary

There are no translocation events in the sample.

## Table 8: Size Difference Summary:



## Complex Events:

There were four cells that each contained a single complex event, and one cell with two events.

## Table 9: Complex Events Summary:

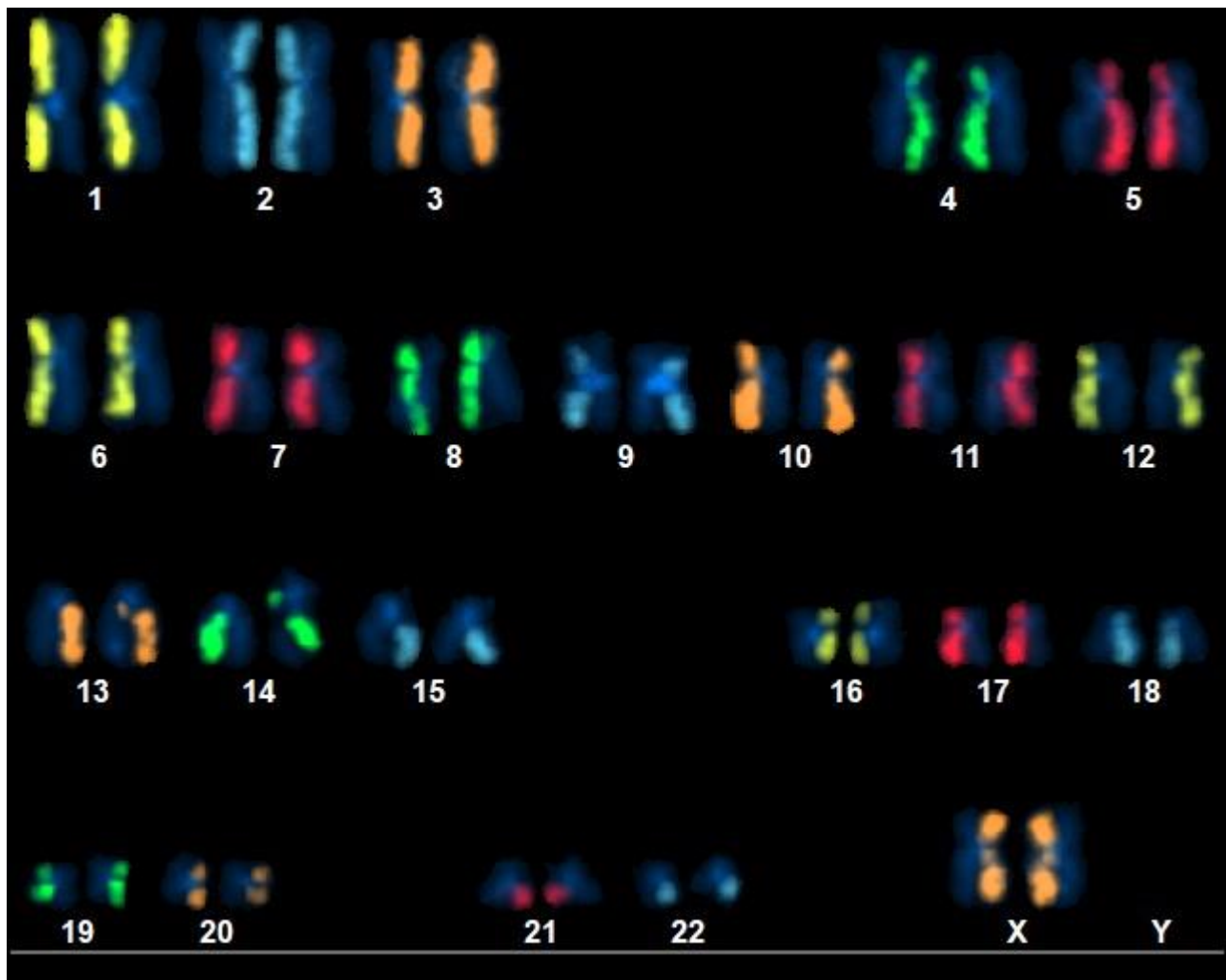
Cell	Chromosome	Complex Event	Code
4	3	Broken chromosome	C4
15	2	Broken chromosome	C4
28	1	Broken chromosome	C4
28	5	Whole arm deletion	C1
34	14	Broken chromosome	C4
43	6	Broken chromosome	C4

<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

## Interpretation / Significance:

Sample karyotype is diploid with aneuploidy observed in 8% of cells. Aneuploidy observed was loss of a single chromosome homolog. Random SCE and inversion events (events that do not appear repeatedly in over 30% of cells) were seen at the highest prevalence. The sample had no insertions or translocations. There is a recurrent small inversion on Chr8p present in 54% of the cells. There were six complex events that all involved major structural changes to the impacted chromosome.

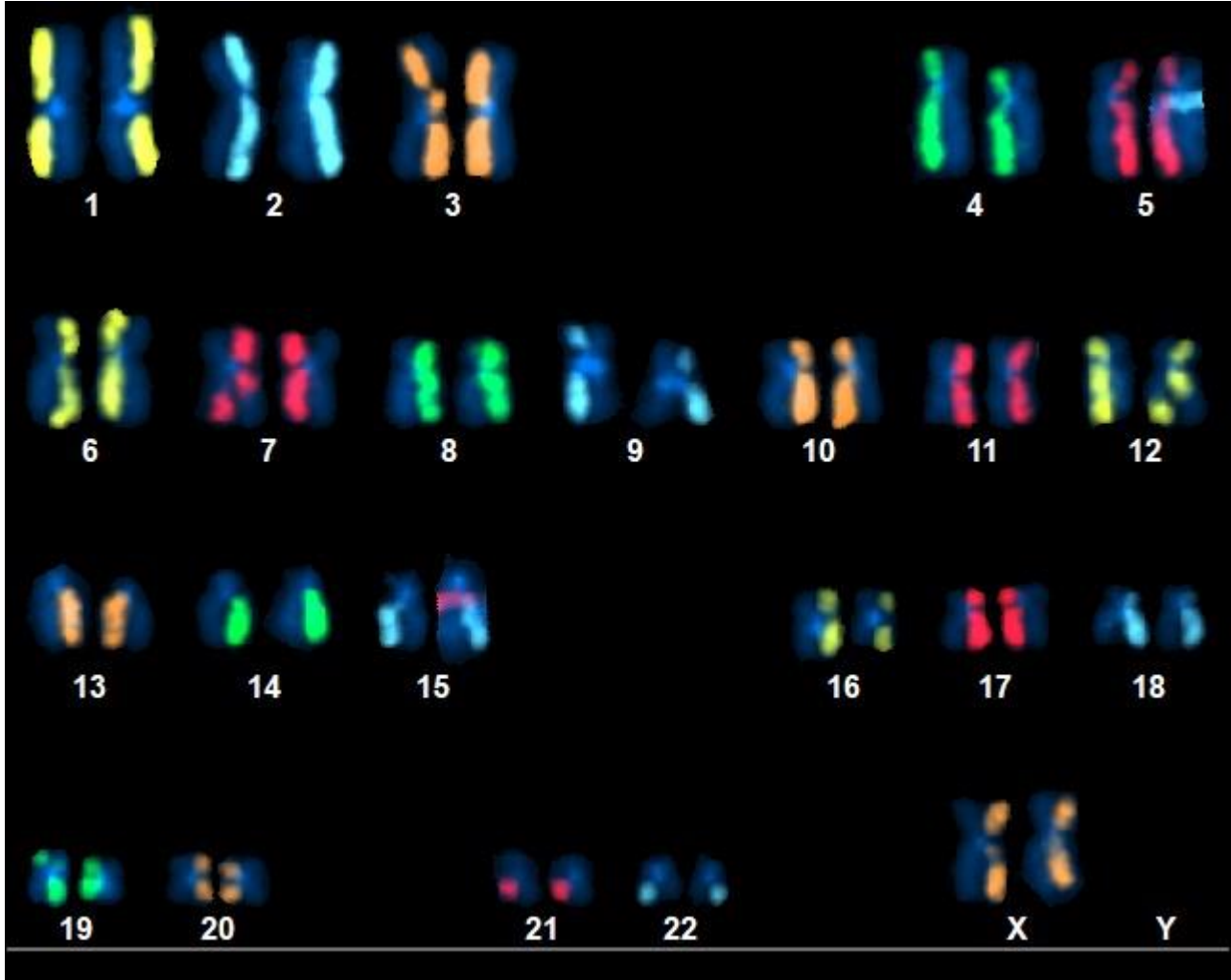
Figure 2: Example Karyogram. There are SCE events present on Chr13q and Chr14q. Chromosome 14q has a broken chromatid.





<b>Document Code:</b>	FORM-0118A	<b>Document Type:</b>	FORM
<b>Revision:</b>	1.0		
<b>Sample:</b>	[sample name]		

Figure 3: Example Karyogram. There are SCE events present on Chr3p, Chr7q, Chr12q, and Chr19p. Size difference between homologs is observed for Chr4, Chr9, Chr15, and Chr19. The recurrent small inversion on Chr8p is present. Chr3p has a broken chromatid. Note that the aqua color on Chr5 and the pink on Chr15 are due to an overlap in the metaphase spread.



dGH SCREEN 5-Color Whole Genome Assay is for research use only and is not a medical diagnostic test.