Karyotype Report

Customer sample ID: Fib1
Internal sample ID: DE79GSAUKDD100001
Date of receipt: 2021-08-05

Gender
Stated: Male
Chr. X derived: Male

Genotype identity with: IPS1A-2021-08-05 / DEGSAUKD00002, IPS1B-2021-08-05 / DEGSAUKD00003, IPS1C-2021-08-05 / DEGSAUKD00004, FIB2-2021-08-05 / DEGSAUKD00005, IPS2A-2021-08-05 / DEGSAUKD00006, IPS2B-2021-08-05 / DEGSAUKD00007, IPS2C-2021-08-05 / DEGSAUKD00008

Karyotyping

Technology used: Illumina BeadArray

Product: Global Screening Array + Multi Disease content 24 v3 BeadChip
Manifest file: GSAMD-24v3-0-EA_20034606_A1.bpm
Cluster file: GSAMD24v3-0-EA_20034606_A1.egt

Chip barcode and segment: 205515290056 R10C02

Batch ID and 96 well position: WG6822774-MSA3 G09

Call rate: 0,9930622

Typing
Scanner: Illumina iScan, S/N:
Site of processing: Life&Brain GENOMICS, Bonn, Germany
Manufacturer: Illumina, Inc., San Diego, United States of America
Date of scan: 2021-08-17-1926

Genotype Analysis
Genome Studio: GenomeStudio V2.0.2
Genotyping module: Ver. 2.0.2

Copy Number Analysis
Algorithm applied: CNV-Partition
Version: 3.2
Software producer: Illumina, Inc., San Diego, United States of America

Noteworthy findings

No larger chromosomal aberrations were found.;

Analyst

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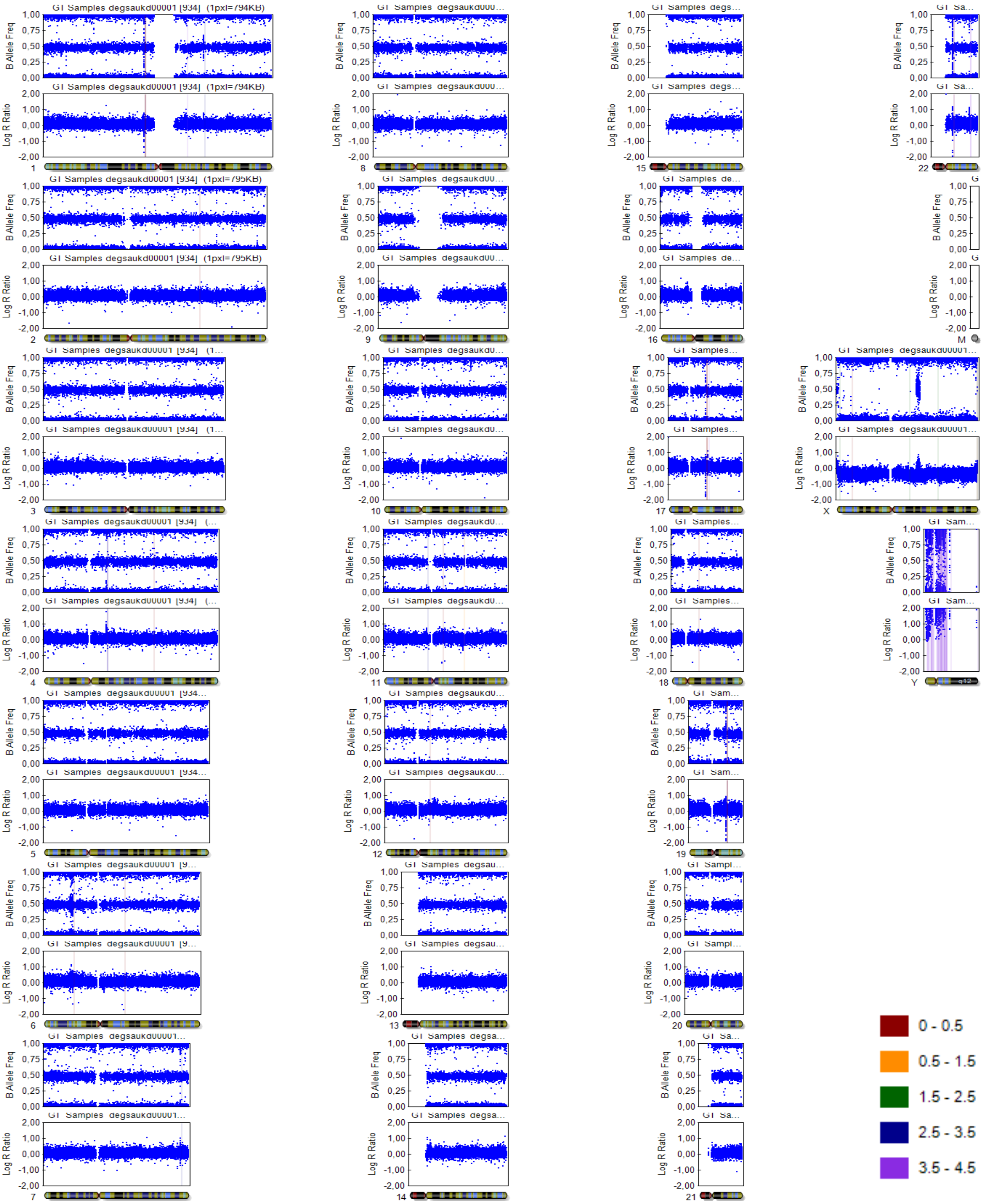
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEGSAUKD00001 / 205515290056_R10C02	Staining	DNP (High) (27630314)	49586	150	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Staining	DNP (Bgnd) (43603326)	1761	290	Notable/ Notable
DEGSAUKD00001 / 205515290056_R10C02	Staining	Biotin (High) (41666334)	1720	23796	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Staining	Biotin (Bgnd) (34648333)	1509	93	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Extension	Extension (A) (17616306)	45306	632	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Extension	Extension (T) (14607337)	46521	508	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Extension	Extension (C) (12613307)	1980	22627	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Extension	Extension (G) (11603365)	2394	22354	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Target Removal	Target Removal (31623323)	2508	369	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Hybridization	Hyb (High) (19612319)	3248	22474	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Hybridization	Hyb (Medium) (20636378)	1216	16223	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Hybridization	Hyb (Low) (23617335)	3278	4611	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Stringency	String (PM) (32629312)	35369	721	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Stringency	String (MM) (33668307)	17228	467	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Specific Binding	NSB (Bgnd) (26619332)	869	264	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Specific Binding	NSB (Bgnd) (27624356)	822	303	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Specific Binding	NSB (Bgnd) (25617343)	846	338	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Specific Binding	NSB (Bgnd) (24616350)	840	299	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Polymorphic	NP(A) (34633358)	24593	589	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Polymorphic	NP(T) (16648324)	26386	541	OK/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Polymorphic	NP(C) (43641328)	1643	14425	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Non-Polymorphic	NP(G) (13642359)	1633	12350	Notable/OK
DEGSAUKD00001 / 205515290056_R10C02	Restoration	Restoration (28637363)	868	451	Notable/OK

All „Notable“ tagged probes are within specs. The karyogram can be evaluated.

Karyogram


GI Samples degsaukd00001 [934] (1pxl=794KB)
GI Samples degsaukd00001 [934] (1pxl=795KB)
B Allele Freq
Log R Ratio
1,00
0,75
0,50
0,25
0,00
2,00
1,00
0,00
-1,00
-2,00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
M
q12
0 - 0.5
0.5 - 1.5
1.5 - 2.5
2.5 - 3.5
3.5 - 4.5

Copy Number Analysis

Copy number events will be reported if larger than 350'000 base pairs, 1Mbp for loss of heterozygosity regions.
Database of Genomic Variants comparison: Number stated represent population based copy number variants that span the reported event completely.

Copy number analysis
Algorithm applied: CNV-Partition
Version: 3.2
Software producer: Illumina, Inc., San Diego, United States of America

Sample ID	Chr	Start	End	Type	Length	Marker count	CN Confidence	DGV Comparison