Karyotype Report

Customer sample ID: iPS2B
Internal sample ID: DE14GSAUKDD100007
Date of receipt: 2021-08-05

Gender
Stated: Female
Chr. X derived: Female

Genotype identity with: FIB1-2021-08-05 / DEGSAUKD00001, 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, 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: 205515290187 R09C01

Batch ID and 96 well position: WG6822774-MSA3 E10

Call rate: 0,9924718

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: 2021-08-17-1937

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

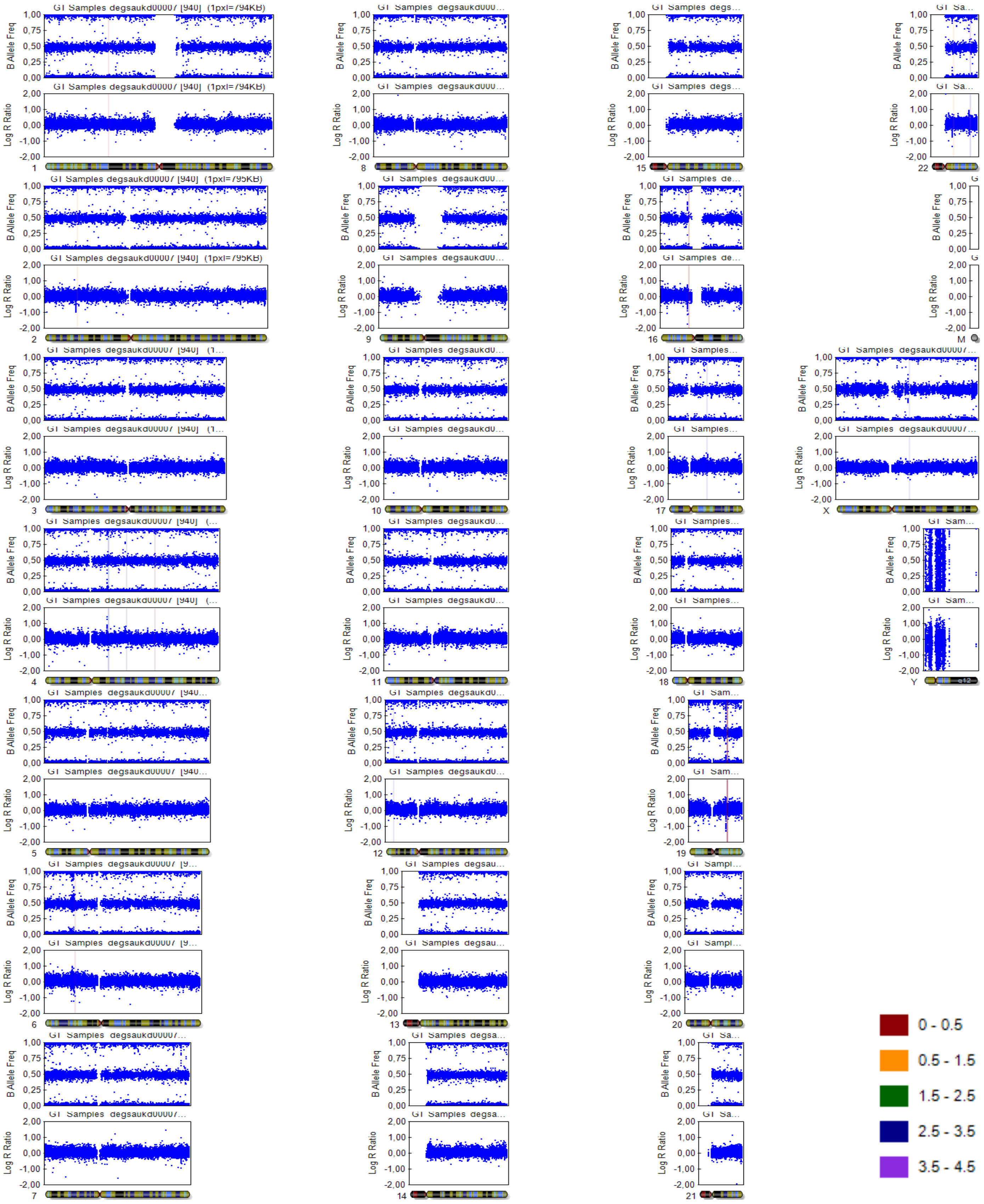
Stefan Herms
sherms@lifeandbrain.com
Tel.: +49 228 6885 411

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEGSAUKD00007 / 205515290187_R09C01	Staining	DNP (High) (27630314)	61913	78	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Staining	DNP (Bgnd) (43603326)	1935	131	Notable/ Notable
DEGSAUKD00007 / 205515290187_R09C01	Staining	Biotin (High) (41666334)	1727	37287	Notable/OK
DEGSAUKD00007 / 205515290187_R09C01	Staining	Biotin (Bgnd) (34648333)	1847	148	Notable/OK
DEGSAUKD00007 / 205515290187_R09C01	Extension	Extension (A) (17616306)	37080	503	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Extension	Extension (T) (14607337)	38375	343	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Extension	Extension (C) (12613307)	1405	19729	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Extension	Extension (G) (11603365)	1748	19631	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Target Removal	Target Removal (31623323)	1064	196	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Hybridization	Hyb (High) (19612319)	2083	20212	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Hybridization	Hyb (Medium) (20636378)	697	14351	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Hybridization	Hyb (Low) (23617335)	1697	4162	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Stringency	String (PM) (32629312)	29194	583	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Stringency	String (MM) (33668307)	13559	326	Notable/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Specific Binding	NSB (Bgnd) (26619332)	441	151	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Specific Binding	NSB (Bgnd) (27624356)	373	181	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Specific Binding	NSB (Bgnd) (25617343)	507	190	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Specific Binding	NSB (Bgnd) (24616350)	401	238	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Polymorphic	NP(A) (34633358)	20489	340	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Polymorphic	NP(T) (16648324)	20557	312	OK/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Polymorphic	NP(C) (43641328)	1066	12709	Notable/OK
DEGSAUKD00007 / 205515290187_R09C01	Non-Polymorphic	NP(G) (13642359)	1131	11281	Notable/OK
DEGSAUKD00007 / 205515290187_R09C01	Restoration	Restoration (28637363)	541	321	OK/OK

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

Karyogram


GT Samples degsaukd00007 [940] (1pxl=794KB)
GT Samples degsaukd00007 [940] (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