

Karyotype Report

Customer sample ID: iPS2C
Internal sample ID: DE84GSAUKDD100008
Date of receipt: 2021-08-05

Gender

Stated: Female
Chr. X derived: Female

Genotype identity with: FIB1-2021-08-05 / DEGSAUKD000001, IPS1A-2021-08-05 / DEGSAUKD000002, IPS1B-2021-08-05 / DEGSAUKD000003, IPS1C-2021-08-05 / DEGSAUKD000004, FIB2-2021-08-05 / DEGSAUKD000005, IPS2A-2021-08-05 / DEGSAUKD000006, IPS2B-2021-08-05 / DEGSAUKD000007

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 R11C01
Batch ID and 96 well position: WG6822774-MSA3 F10
Call rate: 0,9919021

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: 2021-08-17-1939

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

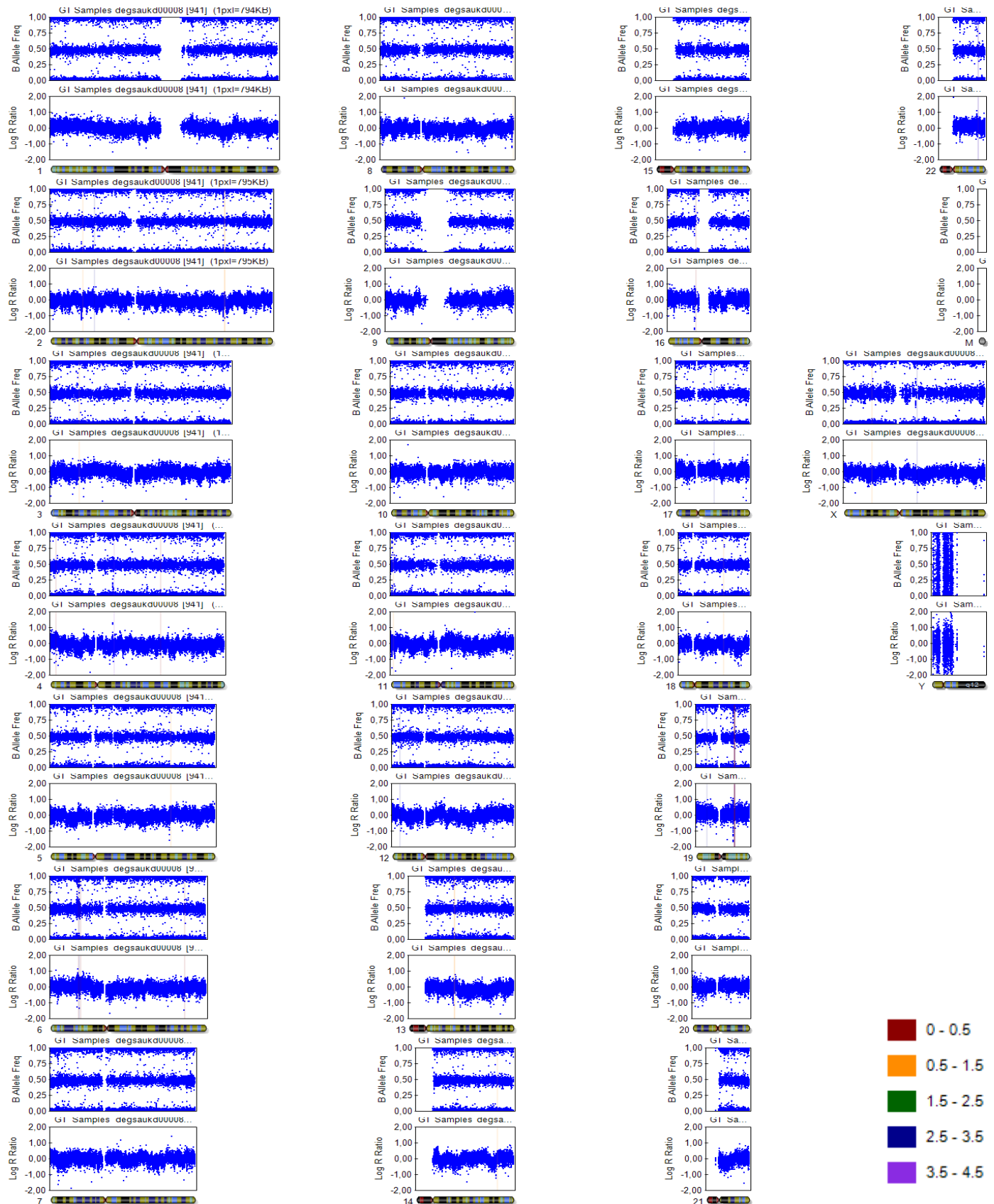
Stefan Herms
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Control Dashboard

Sample_ID / Sentry Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEGSAUKD00008 / 205515290187_R11C01	Staining	DNP (High) (27630314)	60073	110	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Staining	DNP (Bgnd) (43603326)	2902	107	Notable/ Notable
DEGSAUKD00008 / 205515290187_R11C01	Staining	Biotin (High) (41666334)	3043	43480	Notable/OK
DEGSAUKD00008 / 205515290187_R11C01	Staining	Biotin (Bgnd) (34648333)	3107	95	Notable/OK
DEGSAUKD00008 / 205515290187_R11C01	Extension	Extension (A) (17616306)	37638	482	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Extension	Extension (T) (14607337)	38114	351	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Extension	Extension (C) (12613307)	1352	22283	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Extension	Extension (G) (11603365)	1471	21877	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Target Removal	Target Removal (31623323)	868	350	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Hybridization	Hyb (High) (19612319)	2006	23905	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Hybridization	Hyb (Medium) (20636378)	735	16770	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Hybridization	Hyb (Low) (23617335)	1655	4448	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Stringency	String (PM) (32629312)	28902	533	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Stringency	String (MM) (33668307)	12742	322	Notable/OK
DEGSAUKD00008 / 205515290187_R11C01	Non-Specific Binding	NSB (Bgnd) (26619332)	409	208	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non-Specific Binding	NSB (Bgnd) (27624356)	415	247	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non-Specific Binding	NSB (Bgnd) (25617343)	530	201	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non-Specific Binding	NSB (Bgnd) (24616350)	435	301	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non- Polymorphic	NP(A) (34633358)	19869	394	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non- Polymorphic	NP(T) (16648324)	19460	308	OK/OK
DEGSAUKD00008 / 205515290187_R11C01	Non- Polymorphic	NP(C) (43641328)	1139	14670	Notable/OK
DEGSAUKD00008 / 205515290187_R11C01	Non- Polymorphic	NP(G) (13642359)	1080	12357	Notable/OK
DEGSAUKD00008 / 205515290187_R11C01	Restoration	Restoration (28637363)	634	319	Notable/OK

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

Karyogram



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
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