

## Karyotype Report

Customer sample ID:iPS1B  
Internal sample ID: DE25GSAUKDD100003  
Date of receipt: 2021-08-05

### Gender

Stated: Male  
Chr. X derived: Male

Genotype identity with: FIB1-2021-08-05 / DEGSAUKD00001, IPS1A-2021-08-05 / DEGSAUKD00002, 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: 205515290187 R01C01  
Batch ID and 96 well position: WG6822774-MSA3 A10  
Call rate: 0,9924033

### 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: 2021-08-17-1931

### 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

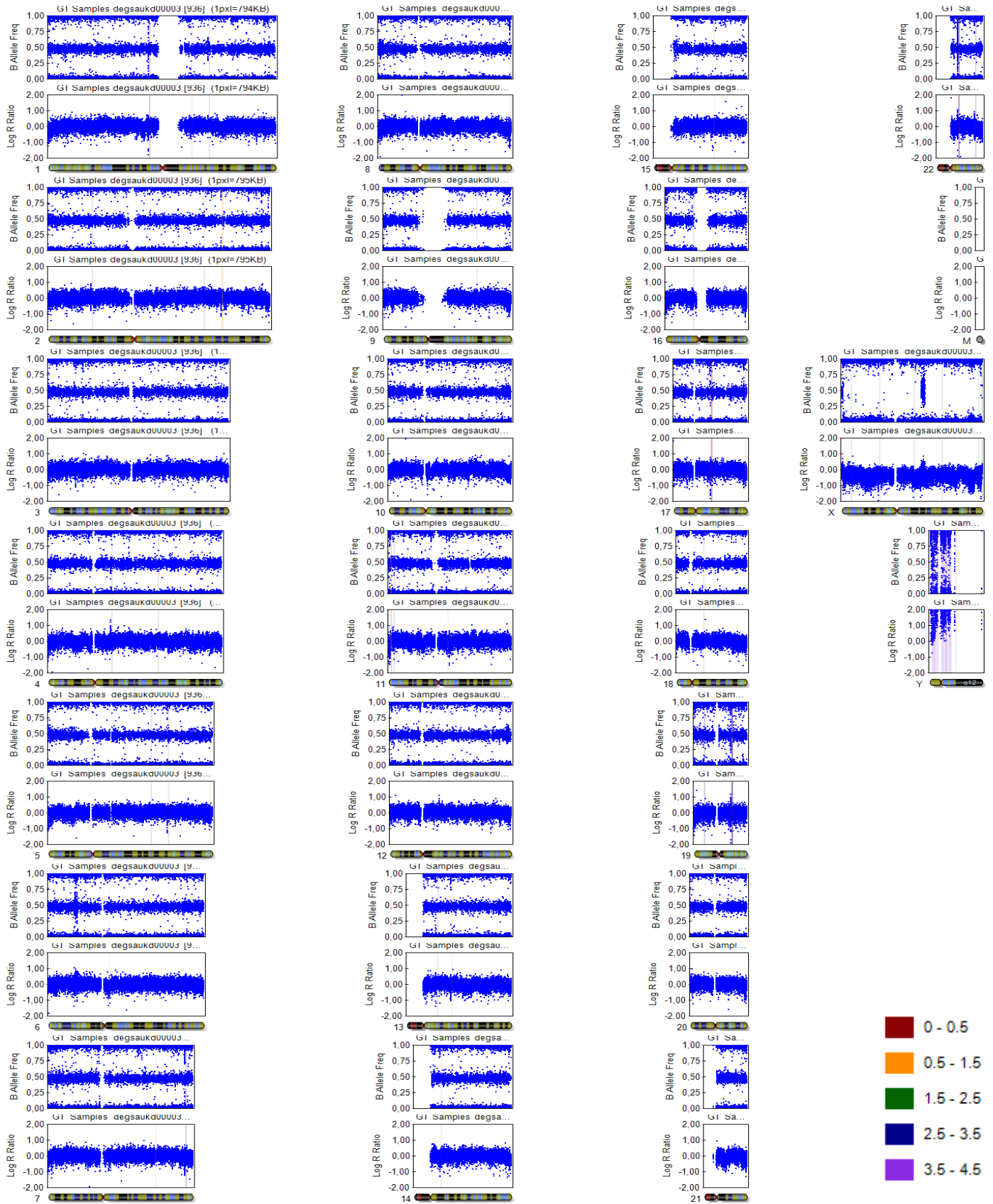
Stefan Herms  
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## Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEGSAUKD00003 / 205515290187_R01C01	Staining	DNP (High) (27630314)	56004	87	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Staining	DNP (Bgnd) (43603326)	2308	69	Notable/ Notable
DEGSAUKD00003 / 205515290187_R01C01	Staining	Biotin (High) (41666334)	2114	21405	Notable/OK
DEGSAUKD00003 / 205515290187_R01C01	Staining	Biotin (Bgnd) (34648333)	2266	74	Notable/OK
DEGSAUKD00003 / 205515290187_R01C01	Extension	Extension (A) (17616306)	34073	322	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Extension	Extension (T) (14607337)	34863	254	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Extension	Extension (C) (12613307)	1255	12316	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Extension	Extension (G) (11603365)	1321	12747	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Target Removal	Target Removal (31623323)	968	167	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Hybridization	Hyb (High) (19612319)	1591	12279	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Hybridization	Hyb (Medium) (20636378)	660	9043	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Hybridization	Hyb (Low) (23617335)	1690	2440	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Stringency	String (PM) (32629312)	25947	310	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Stringency	String (MM) (33668307)	11629	197	Notable/OK
DEGSAUKD00003 / 205515290187_R01C01	Non-Specific Binding	NSB (Bgnd) (26619332)	458	121	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non-Specific Binding	NSB (Bgnd) (27624356)	313	80	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non-Specific Binding	NSB (Bgnd) (25617343)	562	176	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non-Specific Binding	NSB (Bgnd) (24616350)	355	147	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non- Polymorphic	NP(A) (34633358)	16630	205	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non- Polymorphic	NP(T) (16648324)	19442	247	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non- Polymorphic	NP(C) (43641328)	956	7503	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Non- Polymorphic	NP(G) (13642359)	804	6597	OK/OK
DEGSAUKD00003 / 205515290187_R01C01	Restoration	Restoration (28637363)	318	122	OK/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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