

Karyotype Report

Customer sample ID: [REDACTED]
Internal sample ID: [REDACTED]
Date of receipt: [REDACTED]

Gender

Stated: Male
Chr. X derived: Male

Karyotyping

Technology used: Illumina BeadArray

Product: Global Screening Array + Multi Disease content 24 v3

BeadChip

Manifest file: [REDACTED]
Cluster file: [REDACTED]

Chip barcode and segment: 208069790068 R11C02

Batch ID and 96 well position: WG4514941-MSA3 B09

Call rate: 0,9857491

Typing

Scanner: Illumina iScan, S/N: N263
Site of processing: Life&Brain GENOMICS, Bonn, Germany
Manufacturer: Illumina, Inc., San Diego, United States of America
Date of scan: 2023-12-29-1833

Genotype Analysis

Genome Studio: GenomeStudio V2.0.5
Genotyping module: Ver. 2.0.5

Copy Number Analysis

Algorithm applied: cnvPartition
Version: 3.2
Software producer: Illumina, Inc., San Diego, United States of America

Noteworthy findings

Analyst

[REDACTED]

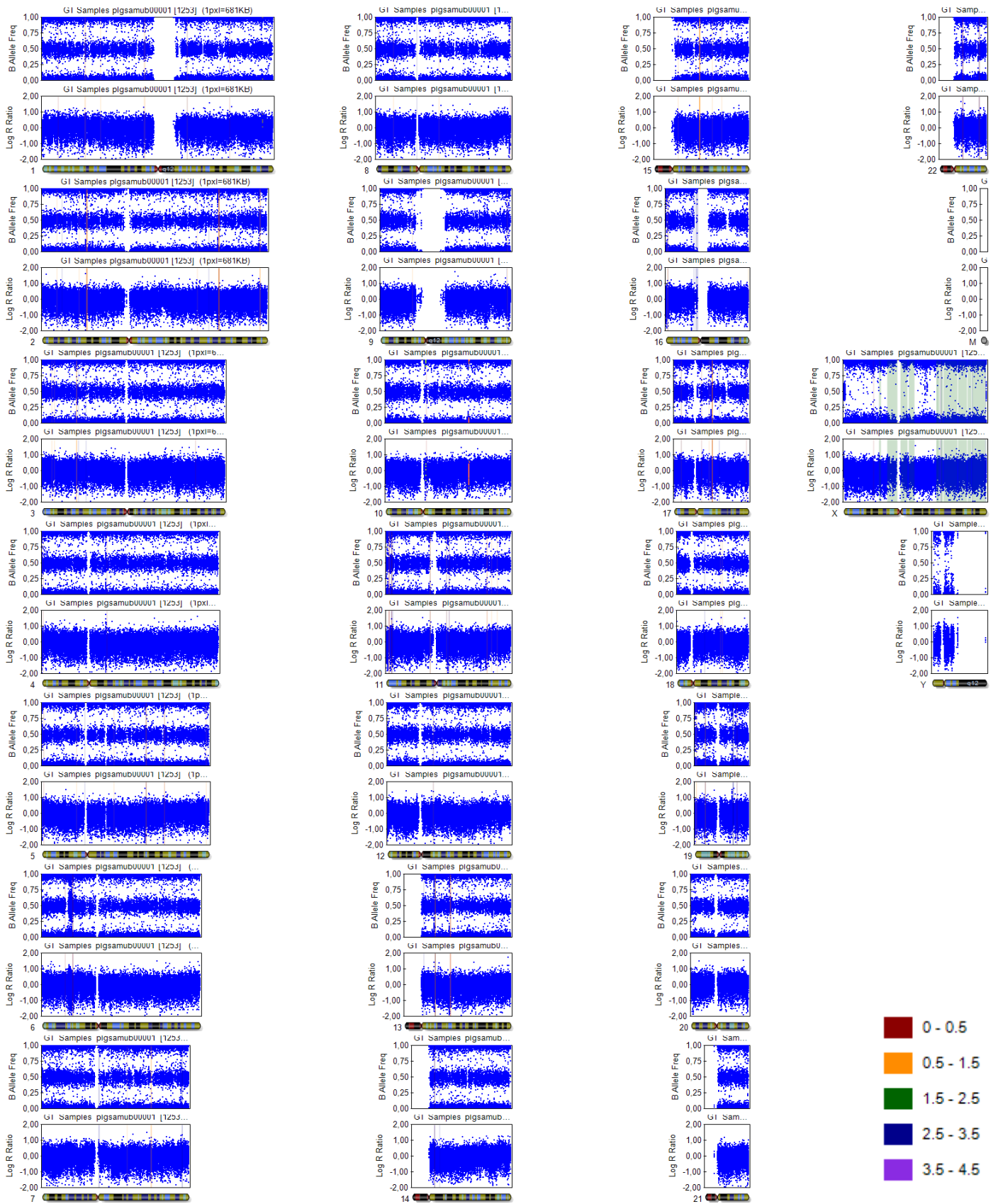
[REDACTED]

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
PLGSAMUB00001 / 208069790068_R11C02	Staining	DNP (High) (27630314)	40560	267	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Staining	DNP (Bgnd) (43603326)	656	285	Notable / Notable
PLGSAMUB00001 / 208069790068_R11C02	Staining	Biotin (High) (41666334)	668	30692	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Staining	Biotin (Bgnd) (34648333)	681	157	Notable / OK
PLGSAMUB00001 / 208069790068_R11C02	Extension	Extension (A) (17616306)	35947	777	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Extension	Extension (T) (14607337)	37073	557	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Extension	Extension (C) (12613307)	1565	28304	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Extension	Extension (G) (11603365)	1656	28843	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Target Removal	Target Removal (31623323)	1046	284	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Hybridization	Hyb (High) (19612319)	1841	28174	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Hybridization	Hyb (Medium) (20636378)	561	20371	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Hybridization	Hyb (Low) (23617335)	2028	6142	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Stringency	String (PM) (32629312)	29552	782	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Stringency	String (MM) (33668307)	10940	303	Notable / OK
PLGSAMUB00001 / 208069790068_R11C02	Non-Specific Binding	NSB (Bgnd) (26619332)	408	331	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non-Specific Binding	NSB (Bgnd) (27624356)	313	378	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non-Specific Binding	NSB (Bgnd) (25617343)	489	368	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non-Specific Binding	NSB (Bgnd) (24616350)	466	332	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non- Polymorphic	NP(A) (34633358)	20158	549	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non- Polymorphic	NP(T) (16648324)	15934	345	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Non- Polymorphic	NP(C) (43641328)	1175	19120	Notable / OK
PLGSAMUB00001 / 208069790068_R11C02	Non- Polymorphic	NP(G) (13642359)	777	13559	OK / OK
PLGSAMUB00001 / 208069790068_R11C02	Restoration	Restoration (28637363)	427	627	OK / Notable

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: cnvPartition

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
PLGSAMUB00001	1	45976147	46602294	1	626147	110	37,7577	
PLGSAMUB00001	2	39216456	39583446	1	366990	106	269,0386	
PLGSAMUB00001	5	36986241	37351168	1	364927	216	605,0994	CNV-Gain: 1, CNV-Loss: 2
PLGSAMUB00001	5	45887984	46393481	3	505497	48	76,0911	
PLGSAMUB00001	7	61075297	62535226	3	1459929	58	141,3228	
PLGSAMUB00001	8	67778964	68163686	1	384722	74	48,8967	
PLGSAMUB00001	9	33954299	34324338	1	370039	51	46,0088	
PLGSAMUB00001	16	1549333	1961866	1	412533	139	269,4233	CNV-Duplication: 2, CNV-Gain: 1
PLGSAMUB00001	16	32096969	35257255	3	3160286	183	52,0435	
PLGSAMUB00001	18	46617871	46971732	1	353861	60	90,3583	

Comment: Sub-optimal gDNA quantity or quality caused a noisy signal, and as a result, the software identified many CNVs that were likely false positives.