

## Karyotype Report

Customer sample ID: NP0134-6D  
Internal sample ID: DE06DIVUKOD100198  
Date of receipt: 2017-10-19

### Gender

Stated: Unknown  
Chr. X derived: Male

Genotype identity with: NP0134-18A-2017-10-19 / DEDIVUKO00199, NP0134-26B-2017-10-19 / DEDIVUKO00200

## Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmni2.5Exome-8 BeadChip v1.3  
Manifest file: HumanOmni2-5Exome-8v1-3\_A1.bpm  
Cluster file: HumanOmni2-5Exome-8v1-3\_A1.egt

Chip barcode and segment: 201340820116 R05C01

Batch ID and 96 well position: WG1004253-MSA6 E02

Call rate: 0,9975811

### 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: 2017-10-25-1330

### 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 to be reported.

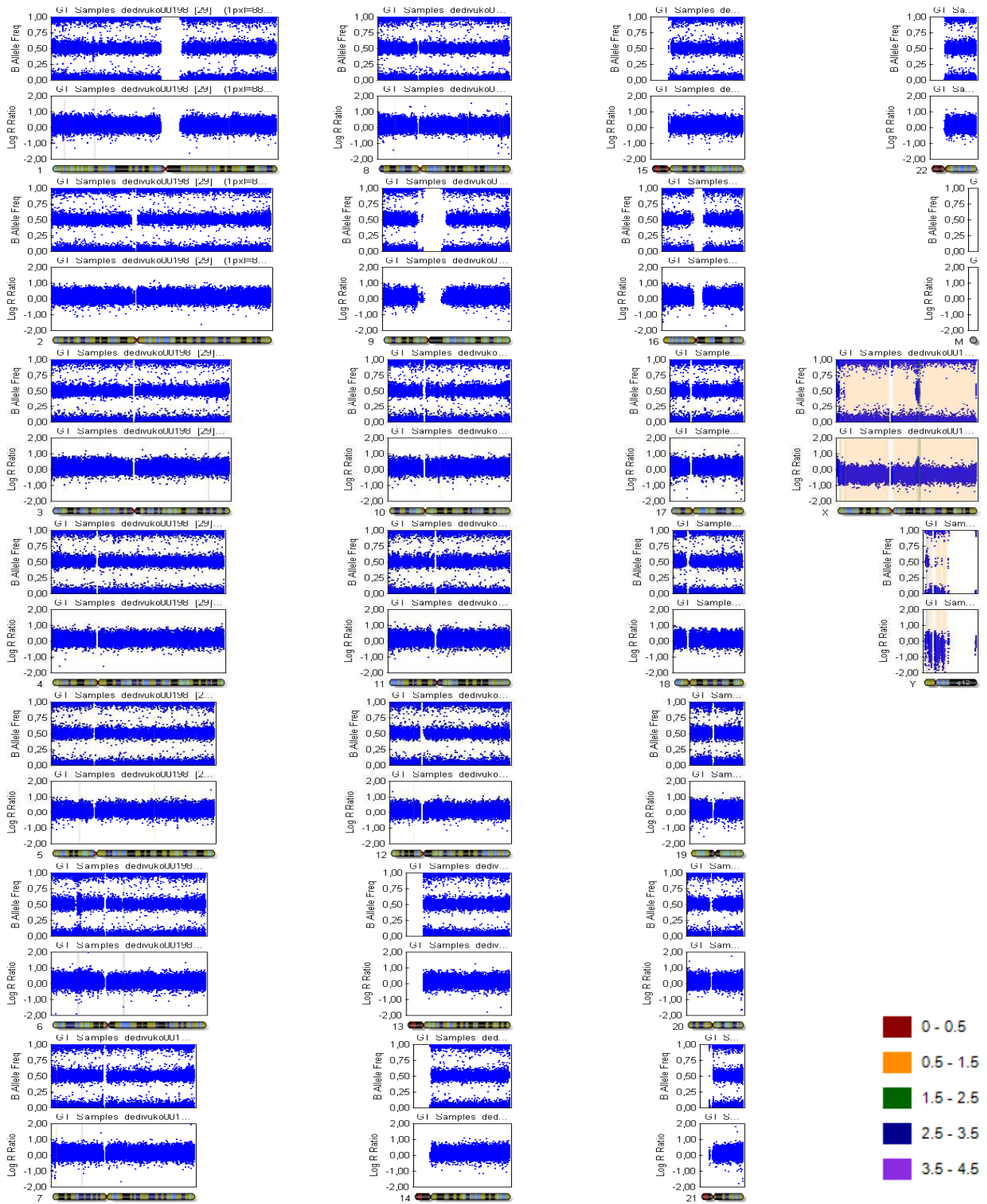
## Analyst

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## Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00198 / 201340820116_R05C01	Staining	DNP (High) (27630314)	28474	156	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Staining	DNP (Bgnd) (29619375)	338	471	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Staining	Biotin (High) (41666334)	359	17437	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Staining	Biotin (Bgnd) (34648333)	263	108	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Extension	Extension (A) (17616306)	28275	428	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Extension	Extension (T) (14607337)	29781	305	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Extension	Extension (C) (12613307)	992	18193	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Extension	Extension (G) (11603365)	1368	17446	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Target Removal	Target Removal (31623323)	706	130	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Hybridization	Hyb (High) (19612319)	1497	17203	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Hybridization	Hyb (Medium) (20636378)	418	11051	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Hybridization	Hyb (Low) (23617335)	1205	3562	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Stringency	String (PM) (32629312)	19955	583	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Stringency	String (MM) (33668307)	5760	487	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non-Specific Binding	NSB (Bgnd) (26619332)	288	209	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non-Specific Binding	NSB (Bgnd) (27624356)	268	139	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non-Specific Binding	NSB (Bgnd) (25617343)	328	290	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non-Specific Binding	NSB (Bgnd) (24616350)	294	197	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non- Polymorphic	NP (A) (34633358)	10646	482	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non- Polymorphic	NP (T) (16648324)	12181	316	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non- Polymorphic	NP (C) (43641328)	557	10085	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Non- Polymorphic	NP (G) (13642359)	589	8791	OK/OK
DEDIVUKO00198 / 201340820116_R05C01	Restoration	Restore (28637363)	302	330	OK/OK

# 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
DEDIVUKO00198	5	30415061	31388158	2	973097	1050	243,3781	
DEDIVUKO00198	6	27280407	28227860	2	947453	1637	338,0942	
DEDIVUKO00198	6	78177468	80223453	2	2045985	1415	286,2641	