

## Karyotype Report

Customer sample ID: NP0134-18A  
Internal sample ID: DE76DIVUKOD100199  
Date of receipt: 2017-10-19

### Gender

Stated: Unknown  
Chr. X derived: Male

Genotype identity with: NP0134-6D-2017-10-19 / DEDIVUKO00198, 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 R06C01

Batch ID and 96 well position: WG1004253-MSA6 F02

Call rate: 0,9975114

### 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: 2017-10-25-1333

### 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

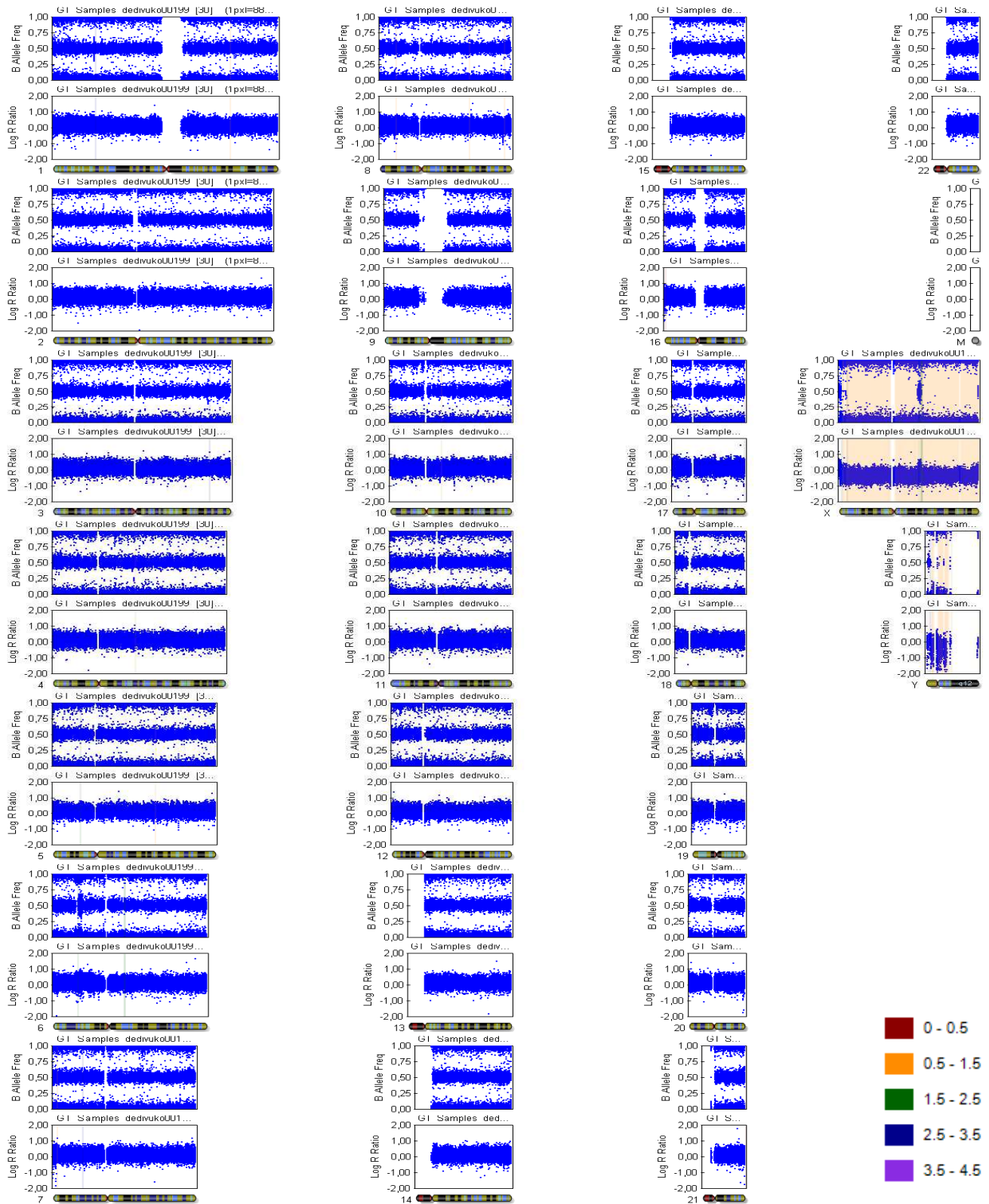
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**Control Dashboard**

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00199 / 201340820116_R06C01	Staining	DNP (High) (27630314)	27888	119	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Staining	DNP (Bgnd) (29619375)	306	477	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Staining	Biotin (High) (41666334)	335	17538	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Staining	Biotin (Bgnd) (34648333)	247	101	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Extension	Extension (A) (17616306)	29622	445	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Extension	Extension (T) (14607337)	30925	346	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Extension	Extension (C) (12613307)	1103	20323	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Extension	Extension (G) (11603365)	1501	19481	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Target Removal	Target Removal (31623323)	814	199	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Hybridization	Hyb (High) (19612319)	1593	19258	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Hybridization	Hyb (Medium) (20636378)	428	12174	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Hybridization	Hyb (Low) (23617335)	1258	4020	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Stringency	String (PM) (32629312)	21235	643	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Stringency	String (MM) (33668307)	6468	537	Notable/OK
DEDIVUKO00199 / 201340820116_R06C01	Non-Specific Binding	NSB (Bgnd) (26619332)	298	212	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non-Specific Binding	NSB (Bgnd) (27624356)	331	154	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non-Specific Binding	NSB (Bgnd) (25617343)	375	295	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non-Specific Binding	NSB (Bgnd) (24616350)	365	213	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non- Polymorphic	NP (A) (34633358)	11681	554	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non- Polymorphic	NP (T) (16648324)	13660	319	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non- Polymorphic	NP (C) (43641328)	606	11414	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Non- Polymorphic	NP (G) (13642359)	656	9923	OK/OK
DEDIVUKO00199 / 201340820116_R06C01	Restoration	Restore (28637363)	375	421	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
DEDIVUKO00199	5	30415061	31388158	2	973097	1050	241,7892	
DEDIVUKO00199	6	27280407	28227860	2	947453	1637	337,677	
DEDIVUKO00199	6	78177468	80223453	2	2045985	1415	287,323	