

## Karyotype Report

Customer sample ID: NP0078-13  
Internal sample ID: DE70DIVUKOD100210  
Date of receipt: 2017-12-12

### Gender

Stated: Unknown  
Chr. X derived: Male

Genotype identity with: NP0078-10 / DEDIVUKO00208, NP0078-12 / DEDIVUKO00209

## 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: 201353490092 R01C01

Batch ID and 96 well position: WG6906606-MSA6 A12

Call rate: 0,9976447

### Typing

Scanner: Illumina iScan, S/N: N234  
Site of processing: Life&Brain GENOMICS, Bonn, Germany  
Manufacturer: Illumina, Inc., San Diego, United States of America  
Date of scan: 2018-01-04-0434

### 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; Chr21: Duplication in telomeric region of long arm

## Analyst

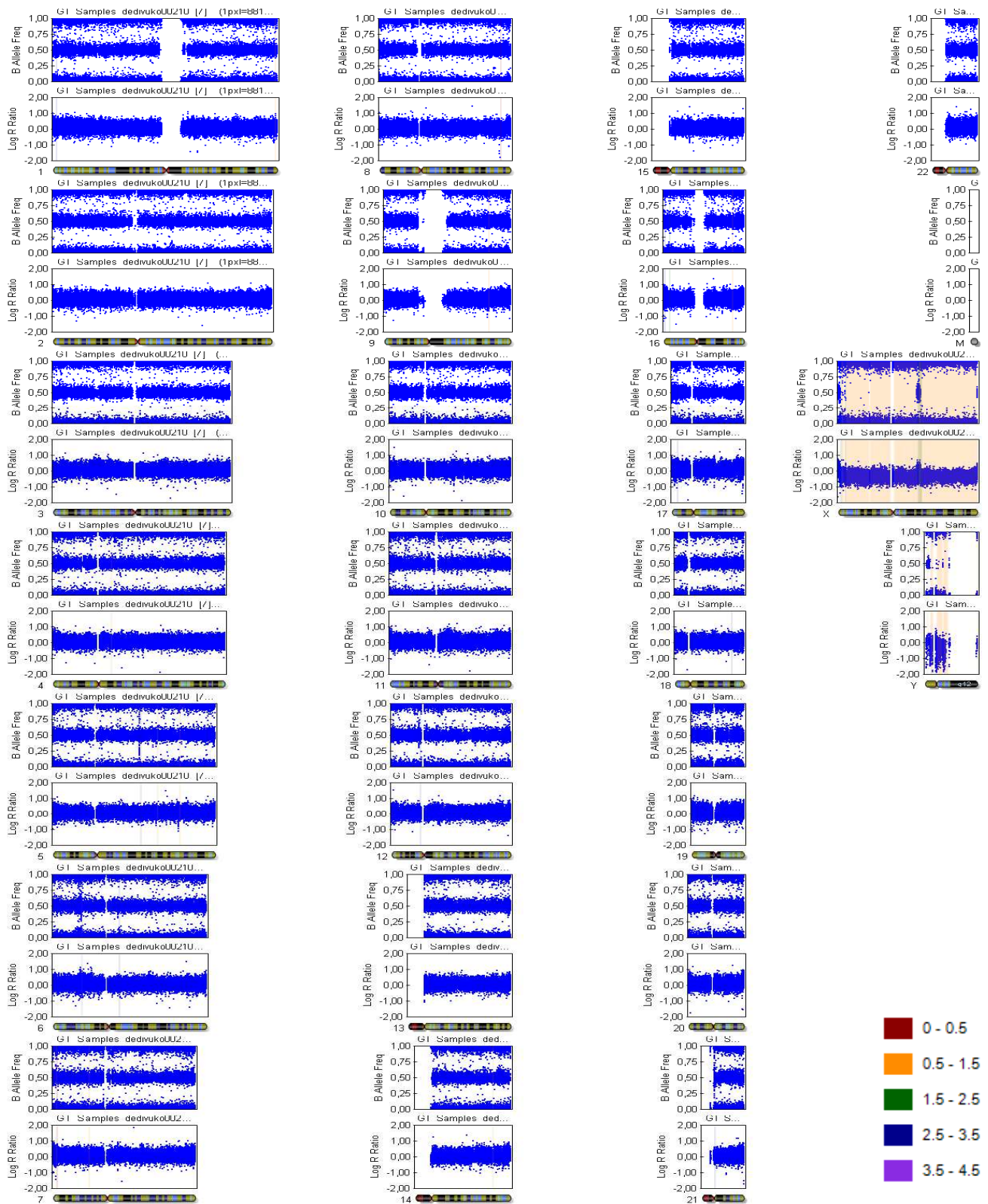
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**Control Dashboard**

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00210 / 201353490092_R01C01	Staining	DNP (High) (27630314)	22105	95	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Staining	DNP (Bgnd) (29619375)	384	161	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Staining	Biotin (High) (41666334)	460	7534	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Staining	Biotin (Bgnd) (34648333)	397	75	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Extension	Extension (A) (17616306)	22738	258	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Extension	Extension (T) (14607337)	26077	156	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Extension	Extension (C) (12613307)	887	9400	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Extension	Extension (G) (11603365)	1067	8718	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Target Removal	Target Removal (31623323)	677	126	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Hybridization	Hyb (High) (19612319)	1290	8946	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Hybridization	Hyb (Medium) (20636378)	493	5763	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Hybridization	Hyb (Low) (23617335)	994	1816	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Stringency	String (PM) (32629312)	15521	259	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Stringency	String (MM) (33668307)	4060	167	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non-Specific Binding	NSB (Bgnd) (26619332)	394	129	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non-Specific Binding	NSB (Bgnd) (27624356)	360	81	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non-Specific Binding	NSB (Bgnd) (25617343)	375	118	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non-Specific Binding	NSB (Bgnd) (24616350)	386	80	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non- Polymorphic	NP (A) (34633358)	7418	215	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non- Polymorphic	NP (T) (16648324)	10617	167	OK/OK
DEDIVUKO00210 / 201353490092_R01C01	Non- Polymorphic	NP (C) (43641328)	594	4988	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Non- Polymorphic	NP (G) (13642359)	597	4239	OK/Notable
DEDIVUKO00210 / 201353490092_R01C01	Restoration	Restore (28637363)	361	182	OK/OK

All „Notable“ tagged control 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
DEDIVUKO00210	21	14342006	15154357	3	812351	133	217,0011	