

## Karyotype Report

Customer sample ID: NP0139-3E  
Internal sample ID: DE20DIVUKOD100237  
Date of receipt: 2018-05-15

### Gender

Stated: Unknown  
Chr. X derived: Male

Genotype identity with: NP0139-6C\*-2018-05-15 / DEDIVUKO00238

## 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: 201375320086 R07C01

Batch ID and 96 well position: WG6902506-MSA6 G04

Call rate: 0,996902

### 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: 2018-06-11-0822

### 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

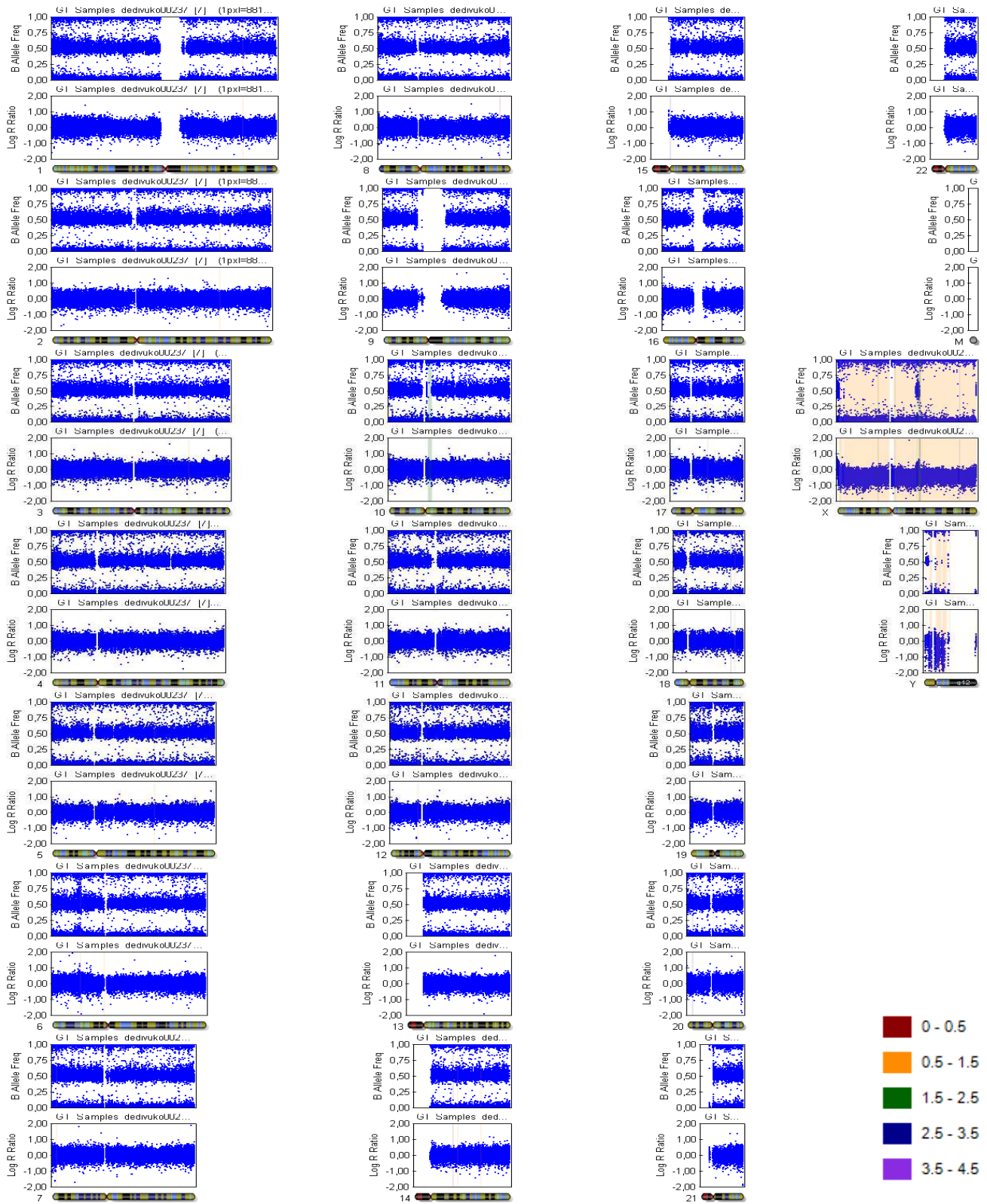
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**Control Dashboard**

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00237 / 201375320086_R07C01	Staining	DNP (High) (27630314)	33771	121	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Staining	DNP (Bgnd) (29619375)	298	311	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Staining	Biotin (High) (41666334)	431	23586	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Staining	Biotin (Bgnd) (34648333)	311	115	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Extension	Extension (A) (17616306)	27474	587	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Extension	Extension (T) (14607337)	30765	343	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Extension	Extension (C) (12613307)	868	22406	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Extension	Extension (G) (11603365)	1014	21728	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Target Removal	Target Removal (31623323)	480	264	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Hybridization	Hyb (High) (19612319)	1210	22484	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Hybridization	Hyb (Medium) (20636378)	408	13532	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Hybridization	Hyb (Low) (23617335)	966	3900	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Stringency	String (PM) (32629312)	21141	531	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Stringency	String (MM) (33668307)	6766	319	Notable/OK
DEDIVUKO00237 / 201375320086_R07C01	Non-Specific Binding	NSB (Bgnd) (26619332)	277	242	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non-Specific Binding	NSB (Bgnd) (27624356)	339	213	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non-Specific Binding	NSB (Bgnd) (25617343)	309	255	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non-Specific Binding	NSB (Bgnd) (24616350)	326	265	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non- Polymorphic	NP (A) (34633358)	10319	389	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non- Polymorphic	NP (T) (16648324)	12562	314	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non- Polymorphic	NP (C) (43641328)	550	12033	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Non- Polymorphic	NP (G) (13642359)	502	9987	OK/OK
DEDIVUKO00237 / 201375320086_R07C01	Restoration	Restore (28637363)	309	337	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
DEDIVUKO00237	10	43547646	47703946	2	4156300	2641	529,5054	