

## Karyotype Report

Customer sample ID: NP0075-8D, 36  
Internal sample ID: DE93DIVUKOD100184  
Date of receipt: 2017-02-01

### Gender

Stated: Unknown  
Chr. X derived: Female

Genotype identity with: NP0075-8 F-08.12.2016 / DEDIVUKO00161, NP0075-10 K-08.12.2016 / DEDIVUKO00162, NP0075-11 B-08.12.2016 / DEDIVUKO00163

## Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmniExpressExome-8 BeadChip v1.3  
Manifest file: HumanOmniExpressExome-8v1-3\_A.bpm  
Cluster file: HumanOmniExpressExome-8v1-3\_A.egt

Chip barcode and segment: 200729680112 R06C01

Batch ID and 96 well position: WG0086079-MSA1 F01

Call rate: 0,998

### 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: 2017-02-09-0440

### 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

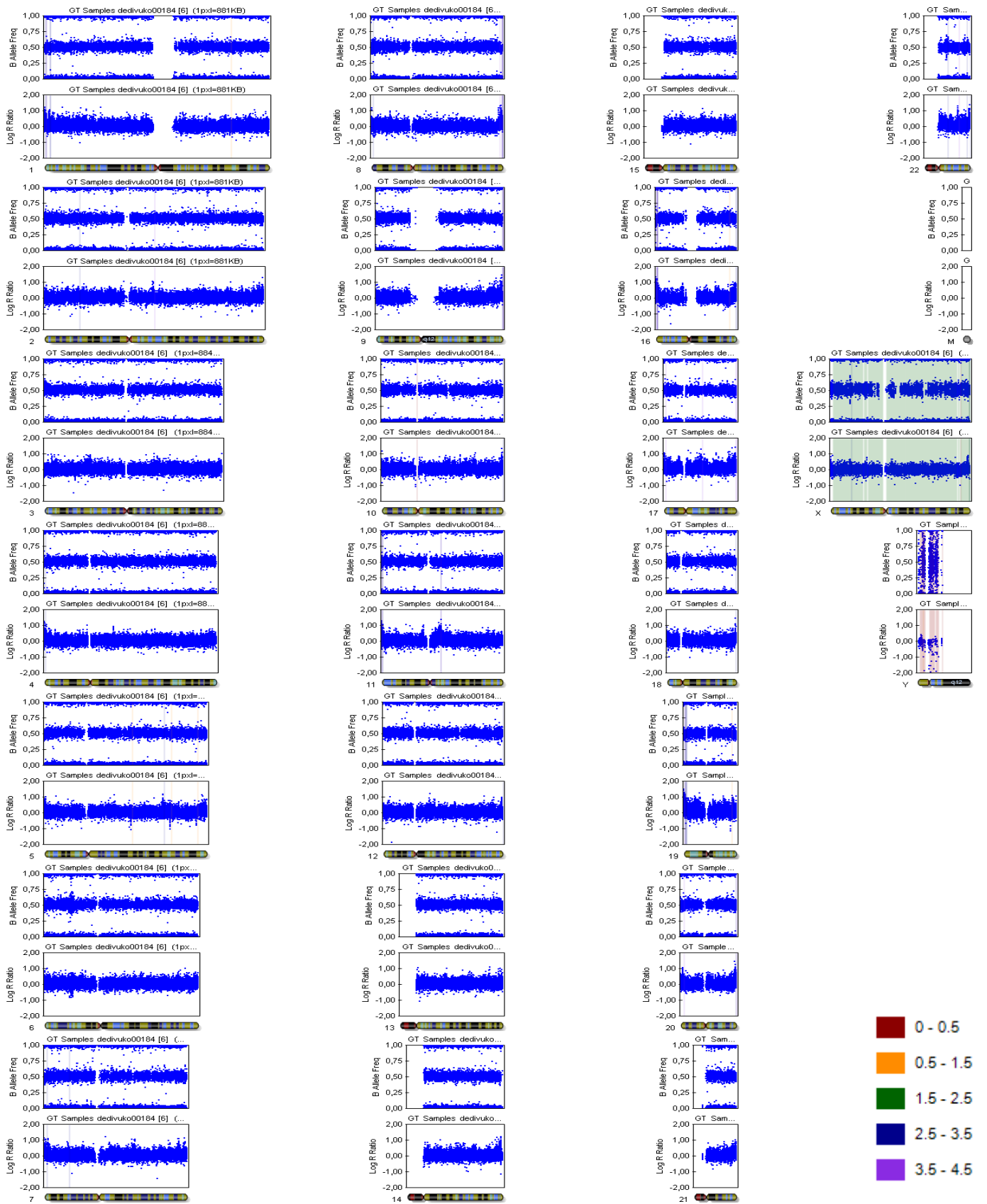
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## Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00184 / 200729680112_R06C01	Staining	DNP (High) (27630314)	15369	329	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Staining	DNP (Bgnd) (29619375)	341	259	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Staining	Biotin (High) (41666334)	247	8181	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Staining	Biotin (Bgnd) (34648333)	230	271	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Extension	Extension (A) (17616306)	31965	411	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Extension	Extension (T) (14607337)	33181	372	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Extension	Extension (C) (12613307)	1263	21110	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Extension	Extension (G) (11603365)	1692	21247	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Target Removal	Target Removal (31623323)	1108	254	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Hybridization	Hyb (High) (19612319)	1549	20035	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Hybridization	Hyb (Medium) (20636378)	480	12445	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Hybridization	Hyb (Low) (23617335)	1870	3698	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Stringency	String (PM) (32629312)	20780	551	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Stringency	String (MM) (33668307)	3863	274	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non-Specific Binding	NSB (Bgnd) (26619332)	318	202	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non-Specific Binding	NSB (Bgnd) (27624356)	318	217	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non-Specific Binding	NSB (Bgnd) (25617343)	342	291	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non-Specific Binding	NSB (Bgnd) (24616350)	298	218	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non- Polymorphic	NP (A) (34633358)	12521	458	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non- Polymorphic	NP (T) (16648324)	11887	349	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non- Polymorphic	NP (C) (43641328)	519	11003	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Non- Polymorphic	NP (G) (13642359)	608	11798	OK/OK
DEDIVUKO00184 / 200729680112_R06C01	Restoration	Restore (28637363)	340	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.

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
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