# Karyotype Report

Customer sample ID: NP0134-26B
Internal sample ID: DE49DIVUKOD100200
Date of receipt: 2017-10-19

Gender
Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0134-6D-2017-10-19 / DEDIVUKO00198, NP0134-18A-2017-10-19 / DEDIVUKO00199

## 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 R07C01

Batch ID and 96 well position: WG1004253-MSA6 G02

Call rate: 0,9978808

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: 2017-10-25-1336
a
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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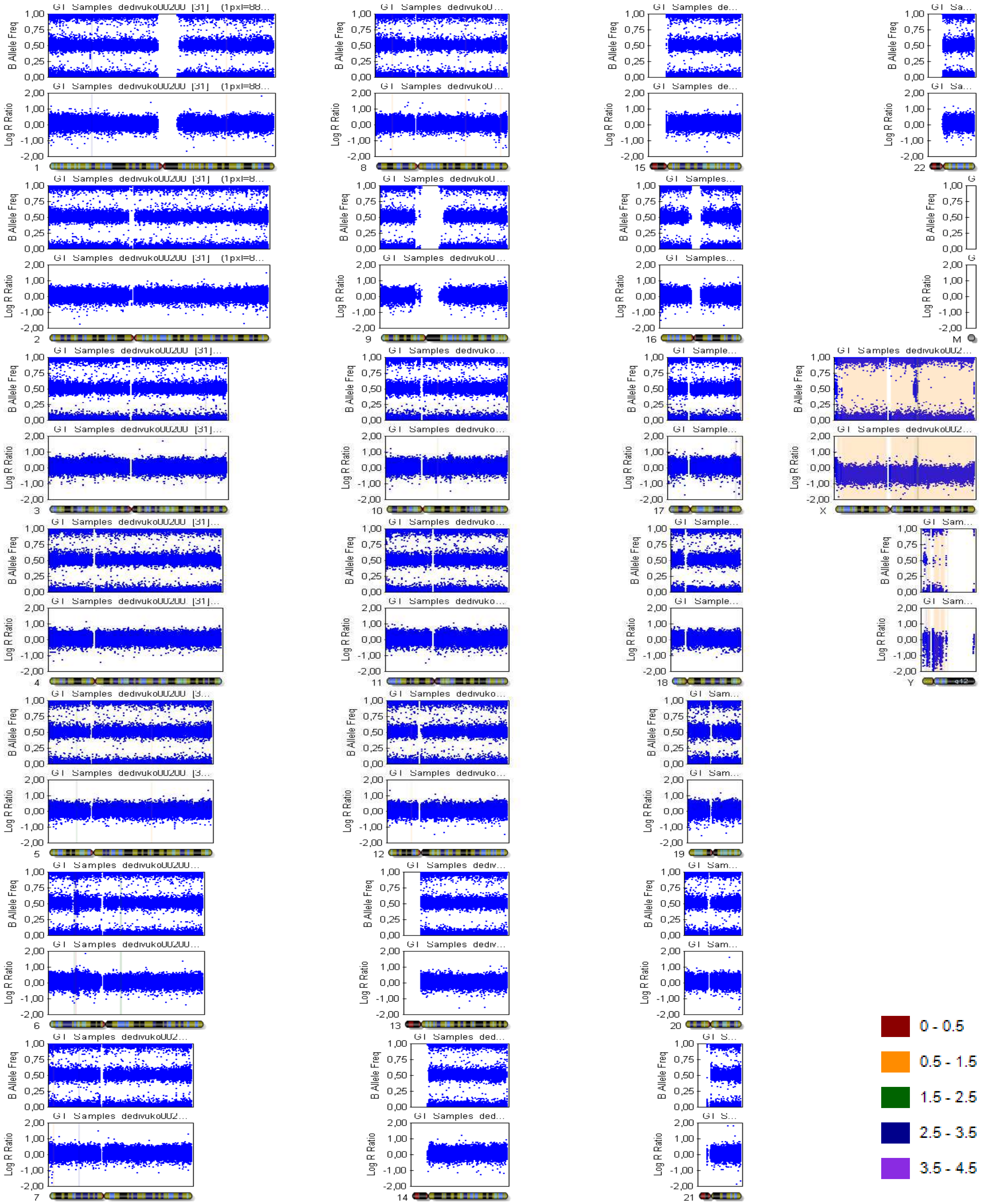
## Control Dashboard

| Sample_ID / Sentrix_Label | Category | Control (BeadType) | Section 1 X | Section 1 Y | State |
|---|---|---|---|---|---|
| DEDIVUKO00200 / 201340820116_R07C01 | Staining | DNP (High) (27630314) | 30292 | 131 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Staining | DNP (Bgnd) (29619375) | 429 | 623 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Staining | Biotin (High) (41666334) | 419 | 19566 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Staining | Biotin (Bgnd) (34648333) | 306 | 83 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Extension | Extension (A) (17616306) | 31932 | 482 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Extension | Extension (T) (14607337) | 33290 | 395 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Extension | Extension (C) (12613307) | 1283 | 23250 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Extension | Extension (G) (11603365) | 1594 | 21741 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Target Removal | Target Removal (31623323) | 865 | 197 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Hybridization | Hyb (High) (19612319) | 1728 | 22073 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Hybridization | Hyb (Medium) (20636378) | 564 | 14108 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Hybridization | Hyb (Low) (23617335) | 1320 | 4335 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Stringency | String (PM) (32629312) | 22799 | 701 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Stringency | String (MM) (33668307) | 5865 | 583 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Specific Binding | NSB (Bgnd) (26619332) | 440 | 259 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Specific Binding | NSB (Bgnd) (27624356) | 407 | 189 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Specific Binding | NSB (Bgnd) (25617343) | 415 | 377 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Specific Binding | NSB (Bgnd) (24616350) | 427 | 297 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Polymorphic | NP (A) (34633358) | 12096 | 622 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Polymorphic | NP (T) (16648324) | 14384 | 367 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Polymorphic | NP (C) (43641328) | 686 | 12935 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Non-Polymorphic | NP (G) (13642359) | 759 | 11350 | OK/OK |
| DEDIVUKO00200 / 201340820116_R07C01 | Restoration | Restore (28637363) | 370 | 464 | OK/OK |

All „Notable“ tagged probes are within specs. The karyogram can be evaluated.

# Karyogram


GT Samples dedivukoU0200 [31] (1pxl=88...
B Allele Freq
Log R Ratio
1,00
0,75
0,50
0,25
0,00
2,00
1,00
0,00
-1,00
-2,00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
G
M
X
Y
q12
0 - 0.5
0.5 - 1.5
1.5 - 2.5
2.5 - 3.5
3.5 - 4.5

## 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 |
|---|---|---|---|---|---|---|---|---|
| DEDIVUKO00200 | 5 | 30415061 | 31388158 | 2 | 973097 | 1050 | 243,1363 | |
| DEDIVUKO00200 | 6 | 27280407 | 28227860 | 2 | 947453 | 1637 | 337,7419 | |
| DEDIVUKO00200 | 6 | 78177468 | 80223453 | 2 | 2045985 | 1415 | 286,7813 | |