# Karyotype Report

Customer sample ID: NP0114-2C_(E2), 24
Internal sample ID: DE39DIVUKOD2190_1
Date of receipt: 2017-06-21

Gender
Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0114-1A_(E2)-2017-06-21 / DEDIVUKO00189, NP0114-5E_(E1)-2017-06-21 / DEDIVUKO00191

## 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: 201340960012 R01C01

Batch ID and 96 well position: WG1004252-MSA6 A01

Call rate: 0,9969135

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: 2017-10-12-1324

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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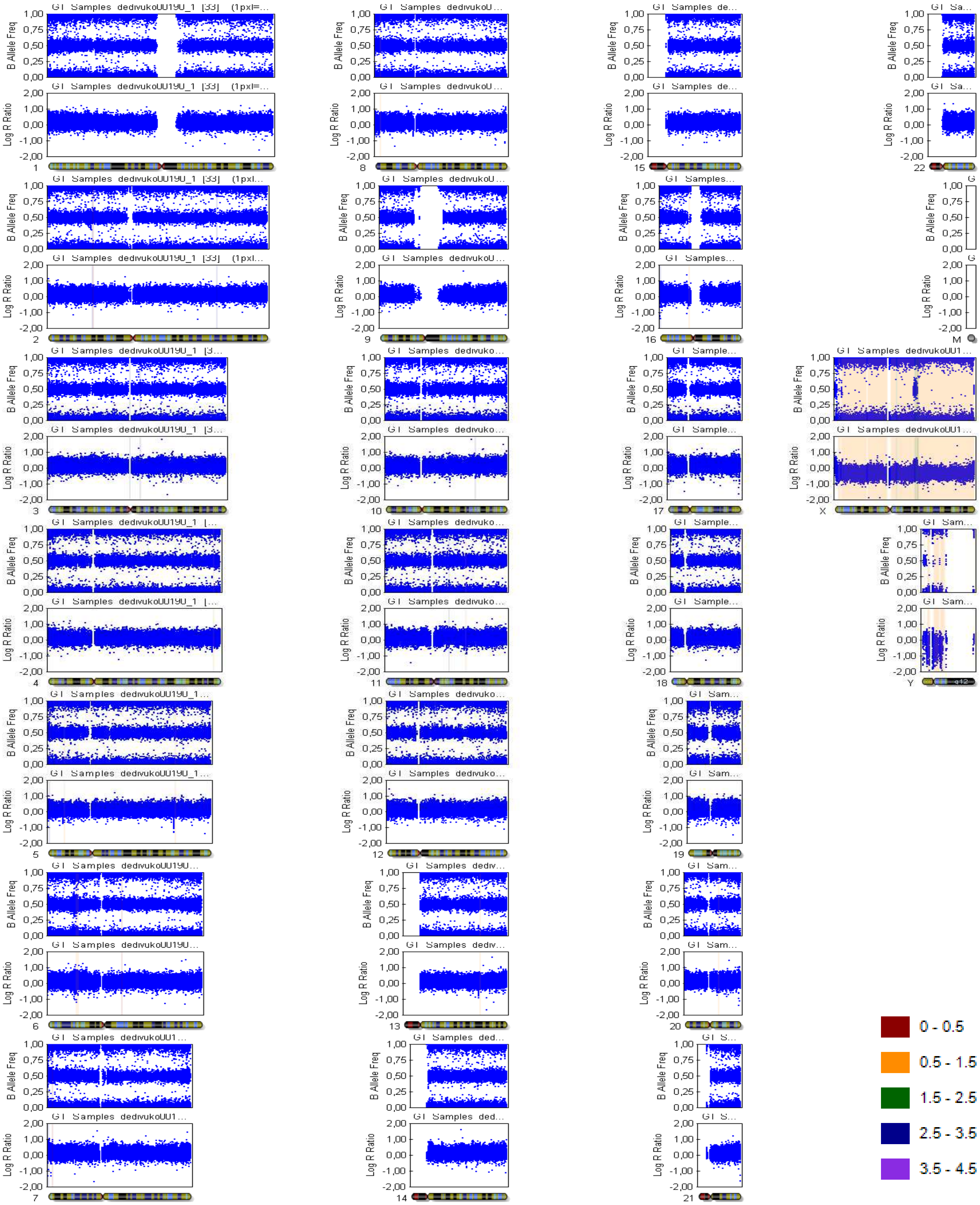
## Control Dashboard

| Sample_ID / Sentrix_Label | Category | Control (BeadType) | Section 1 X | Section 1 Y | State |
|---|---|---|---|---|---|
| DEDIVUKO00190_1 / 201340960012_R01C01 | Staining | DNP (High) (27630314) | 20785 | 65 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Staining | DNP (Bgnd) (29619375) | 321 | 221 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Staining | Biotin (High) (41666334) | 314 | 7251 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Staining | Biotin (Bgnd) (34648333) | 258 | 36 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Extension | Extension (A) (17616306) | 22656 | 252 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Extension | Extension (T) (14607337) | 25774 | 208 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Extension | Extension (C) (12613307) | 1137 | 10072 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Extension | Extension (G) (11603365) | 1298 | 9432 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Target Removal | Target Removal (31623323) | 662 | 156 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Hybridization | Hyb (High) (19612319) | 1310 | 8020 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Hybridization | Hyb (Medium) (20636378) | 420 | 5066 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Hybridization | Hyb (Low) (23617335) | 1075 | 1670 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Stringency | String (PM) (32629312) | 14268 | 275 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Stringency | String (MM) (33668307) | 3488 | 216 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Specific Binding | NSB (Bgnd) (26619332) | 317 | 156 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Specific Binding | NSB (Bgnd) (27624356) | 305 | 136 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Specific Binding | NSB (Bgnd) (25617343) | 367 | 171 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Specific Binding | NSB (Bgnd) (24616350) | 365 | 144 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Polymorphic | NP (A) (34633358) | 7717 | 246 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Polymorphic | NP (T) (16648324) | 9166 | 180 | OK/OK |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Polymorphic | NP (C) (43641328) | 501 | 4677 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Non-Polymorphic | NP (G) (13642359) | 552 | 3972 | OK/Notable |
| DEDIVUKO00190_1 / 201340960012_R01C01 | Restoration | Restore (28637363) | 379 | 237 | OK/OK |

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

## Karyogram


B Allele Freq
Log R Ratio
GT Samples dedivuko00190_1 [33] (1pxl=...
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
M
X
Y
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 |
|---|---|---|---|---|---|---|---|---|
| DEDIVUKO00190_1 | 16 | 32257633 | 32821530 | 1 | 563897 | 57 | 88,2682 | CNV-: 1, CNV-CNV: 46, CNV-Complex: 4, CNV-Gain: 65, CNV-Gain+Loss: 2, CNV-Insertion: 1, CNV-Loss: 13, OTHER-Inversion: 2 |