Karyotype Report

Customer sample ID: NP0078-12
Internal sample ID: DE97DIVUKOD100209
Date of receipt: 2017-12-12

Gender
Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0078-10 / DEDIVUKO00208, NP0078-13 / DEDIVUKO00210

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: 201334740023 R08C01

Batch ID and 96 well position: WG6906607-MSA6 H02

Call rate: 0,993863

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: 2017-12-19-1327

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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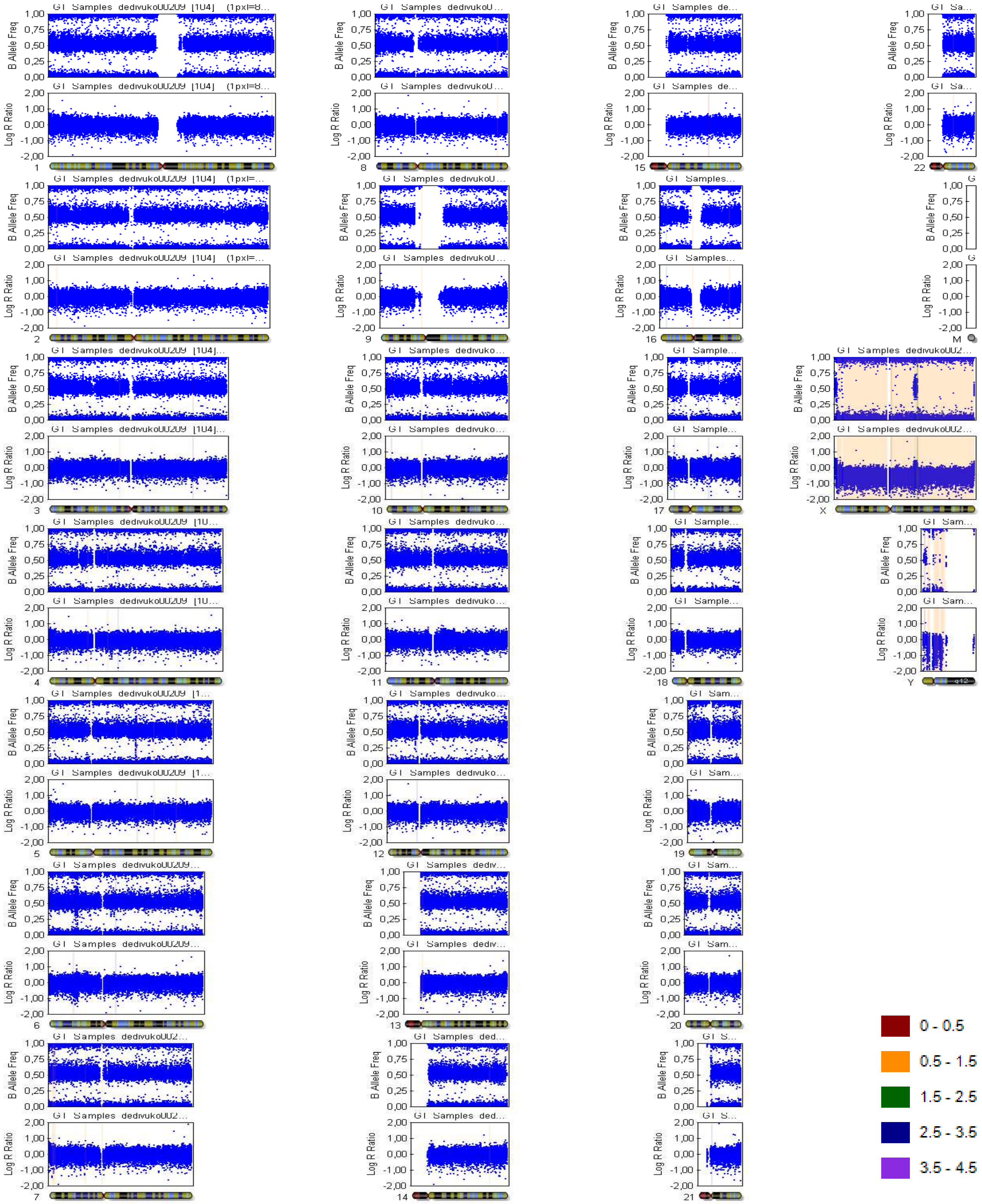
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00209 / 201334740023_R08C01	Staining	DNP (High) (27630314)	32973	235	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Staining	DNP (Bgnd) (29619375)	353	375	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Staining	Biotin (High) (41666334)	464	21634	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Staining	Biotin (Bgnd) (34648333)	427	183	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Extension	Extension (A) (17616306)	32249	513	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Extension	Extension (T) (14607337)	34603	367	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Extension	Extension (C) (12613307)	1249	24312	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Extension	Extension (G) (11603365)	1557	22918	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Target Removal	Target Removal (31623323)	1043	258	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Hybridization	Hyb (High) (19612319)	1887	23752	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Hybridization	Hyb (Medium) (20636378)	658	15732	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Hybridization	Hyb (Low) (23617335)	1552	4326	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Stringency	String (PM) (32629312)	23188	607	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Stringency	String (MM) (33668307)	2652	458	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Specific Binding	NSB (Bgnd) (26619332)	347	308	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Specific Binding	NSB (Bgnd) (27624356)	397	242	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Specific Binding	NSB (Bgnd) (25617343)	445	346	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Specific Binding	NSB (Bgnd) (24616350)	434	270	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Polymorphic	NP (A) (34633358)	9570	487	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Polymorphic	NP (T) (16648324)	14556	303	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Polymorphic	NP (C) (43641328)	627	13426	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Non-Polymorphic	NP (G) (13642359)	713	11562	OK/OK
DEDIVUKO00209 / 201334740023_R08C01	Restoration	Restore (28637363)	409	421	OK/OK

All control probes are within specs. The karyogram can be evaluated.

Karyogram


GT Samples dedivuko00209 [104] (1pxl=8...
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
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11
12
13
14
15
16
17
18
19
20
21
22
X
Y
M
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
DEDIVUKO00209	17	44168225	44787713	3	619488	79	54,1994	CNV-CNV: 34, CNV-Complex: 2, CNV-Gain: 5, CNV-Gain+Loss: 1
DEDIVUKO00209	21	14388926	15154357	3	765431	121	347,1442	