Karyotype Report

Customer sample ID: NP0143-5
Internal sample ID: DE85DIVUKOD100231
Date of receipt: 2018-05-15

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0143-15*-2018-05-15 / DEDIVUKO00232, NP0143-18-2018-05-15 / DEDIVUKO00233

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 R01C01

Batch ID and 96 well position: WG6902506-MSA6 A04

Call rate: 0,9955978

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: 2018-06-11-0801

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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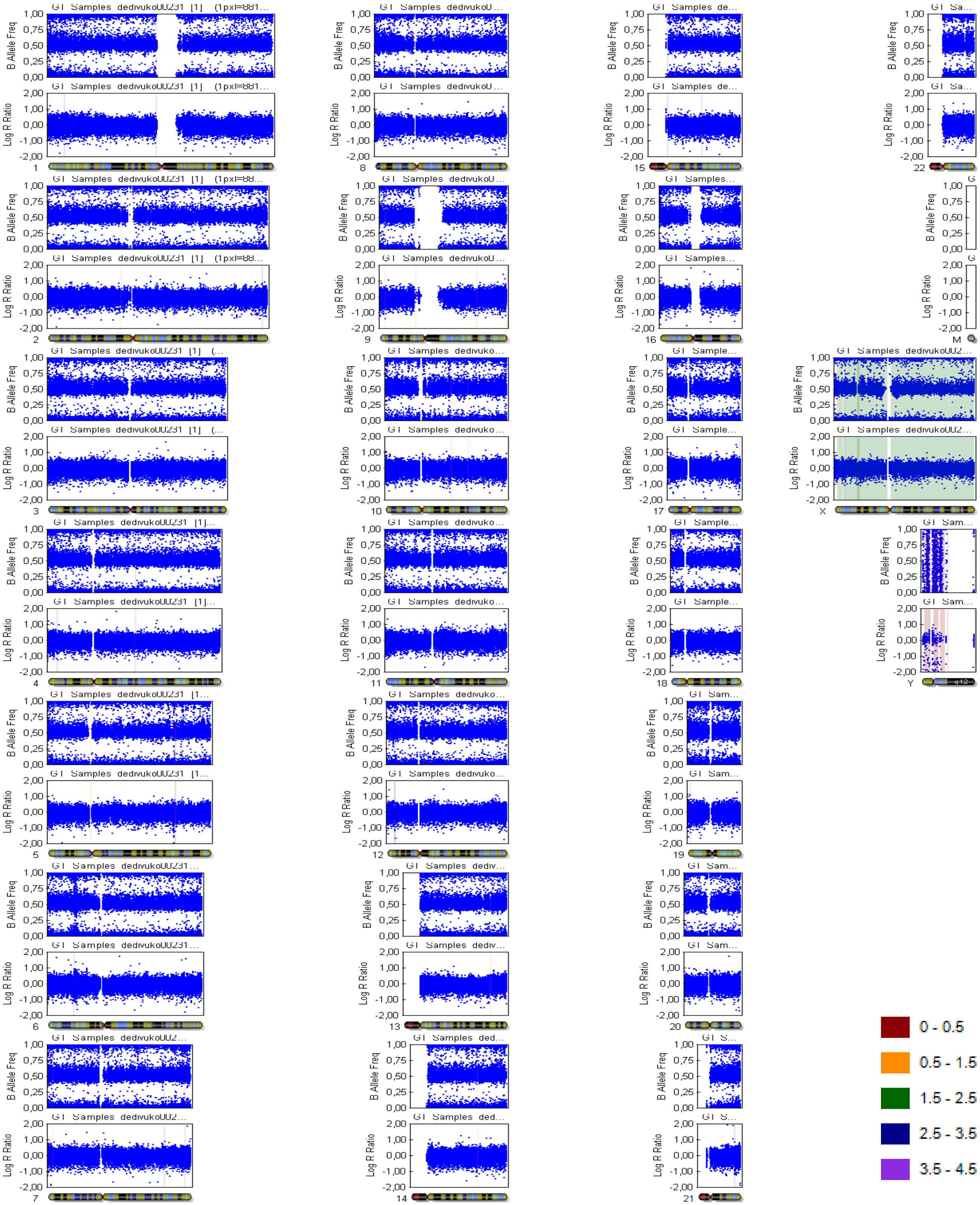
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00231 / 201375320086_R01C01	Staining	DNP (High) (27630314)	28312	131	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Staining	DNP (Bgnd) (29619375)	250	167	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Staining	Biotin (High) (41666334)	368	14120	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Staining	Biotin (Bgnd) (34648333)	316	128	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Extension	Extension (A) (17616306)	23596	318	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Extension	Extension (T) (14607337)	29419	203	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Extension	Extension (C) (12613307)	798	14279	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Extension	Extension (G) (11603365)	863	12999	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Target Removal	Target Removal (31623323)	427	96	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Hybridization	Hyb (High) (19612319)	1024	12825	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Hybridization	Hyb (Medium) (20636378)	341	7956	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Hybridization	Hyb (Low) (23617335)	728	2261	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Stringency	String (PM) (32629312)	18107	247	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Stringency	String (MM) (33668307)	5442	151	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Specific Binding	NSB (Bgnd) (26619332)	239	108	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Specific Binding	NSB (Bgnd) (27624356)	241	105	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Specific Binding	NSB (Bgnd) (25617343)	238	149	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Specific Binding	NSB (Bgnd) (24616350)	261	112	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Polymorphic	NP (A) (34633358)	8289	202	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Polymorphic	NP (T) (16648324)	11037	184	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Polymorphic	NP (C) (43641328)	473	6788	OK/OK
DEDIVUKO00231 / 201375320086_R01C01	Non-Polymorphic	NP (G) (13642359)	392	5593	OK/Notable
DEDIVUKO00231 / 201375320086_R01C01	Restoration	Restore (28637363)	257	194	OK/OK

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

Karyogram


GT Samples dedivukoU0231 [1] (1pxl=881…
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
X
Y
M
G
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