Karyotype Report

Customer sample ID: NP0139-24
Internal sample ID: DE59DIVUKOD100214
Date of receipt: 2017-12-12

Gender
Stated: Unknown
Chr. X derived: Male

No genotype identities found.

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: 201353490092 R05C01

Batch ID and 96 well position: WG6906606-MSA6 E12

Call rate: 0,9976718

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: 2018-01-04-0505

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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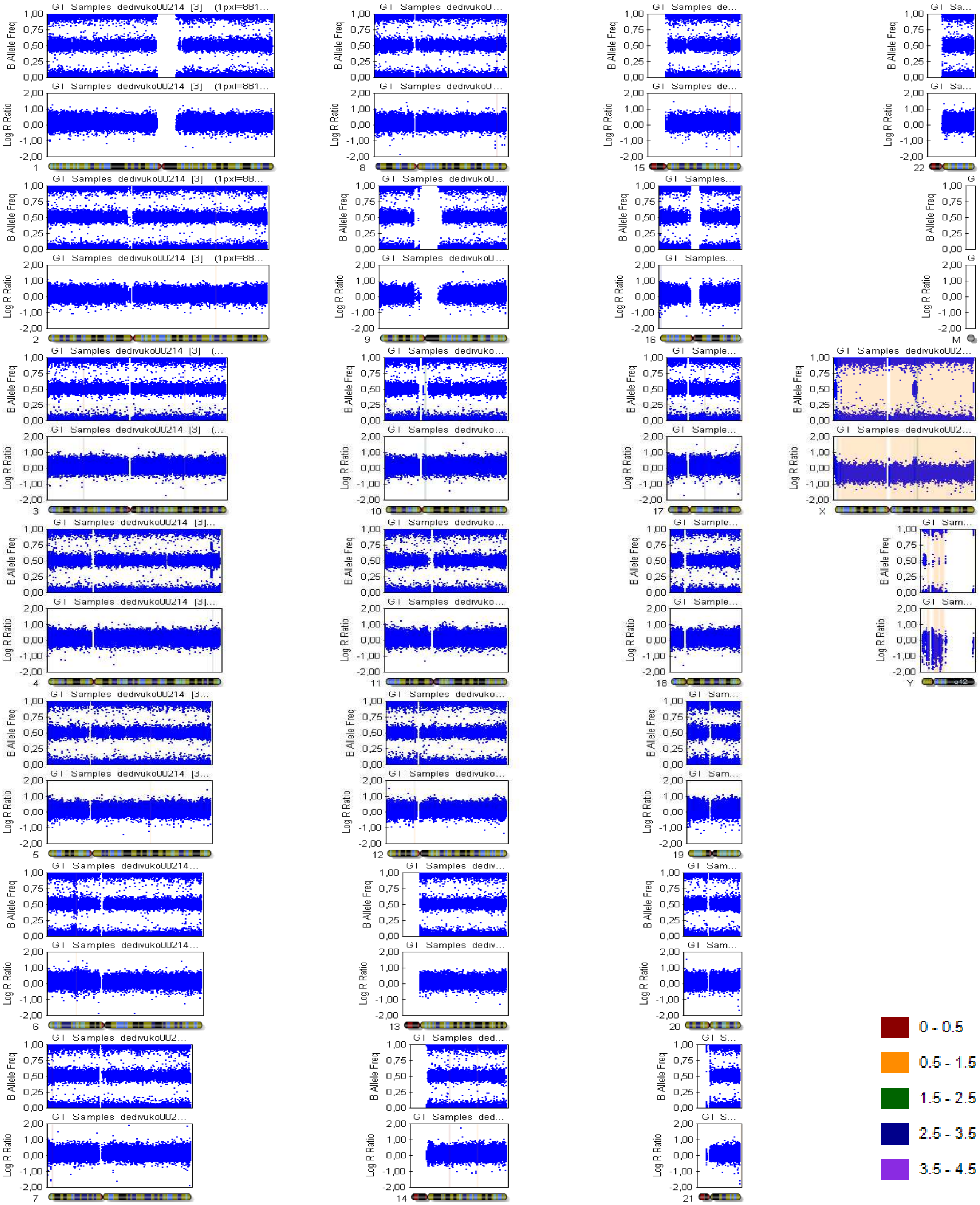
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00214 / 201353490092_R05C01	Staining	DNP (High) (27630314)	24664	93	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Staining	DNP (Bgnd) (29619375)	491	203	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Staining	Biotin (High) (41666334)	483	10847	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Staining	Biotin (Bgnd) (34648333)	480	56	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Extension	Extension (A) (17616306)	26150	359	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Extension	Extension (T) (14607337)	29171	292	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Extension	Extension (C) (12613307)	1080	13375	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Extension	Extension (G) (11603365)	1340	12924	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Target Removal	Target Removal (31623323)	851	159	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Hybridization	Hyb (High) (19612319)	1642	13491	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Hybridization	Hyb (Medium) (20636378)	665	8720	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Hybridization	Hyb (Low) (23617335)	1387	2705	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Stringency	String (PM) (32629312)	18383	410	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Stringency	String (MM) (33668307)	5468	275	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Specific Binding	NSB (Bgnd) (26619332)	518	72	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Specific Binding	NSB (Bgnd) (27624356)	402	136	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Specific Binding	NSB (Bgnd) (25617343)	429	141	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Specific Binding	NSB (Bgnd) (24616350)	496	96	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Polymorphic	NP (A) (34633358)	9820	277	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Polymorphic	NP (T) (16648324)	12542	234	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Polymorphic	NP (C) (43641328)	770	7904	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Non-Polymorphic	NP (G) (13642359)	707	6381	OK/OK
DEDIVUKO00214 / 201353490092_R05C01	Restoration	Restore (28637363)	496	175	OK/OK

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

Karyogram


GT Samples dedivukoUU214 [3] (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
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
DEDIVUKO00214	10	43547646	45809267	2	2261621	2098	437,7878	