Karyotype Report

Customer sample ID: NP0079-15B
Internal sample ID: DE16DIVUKOD100212
Date of receipt: 2017-12-12

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0079-79 / DEDIVUKO00211, NP0079-16H / DEDIVUKO00213

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 R03C01

Batch ID and 96 well position: WG6906606-MSA6 C12

Call rate: 0,9970548

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: 2018-01-04-0449

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; Chr12: Early mosaic in q23.1.

Analyst

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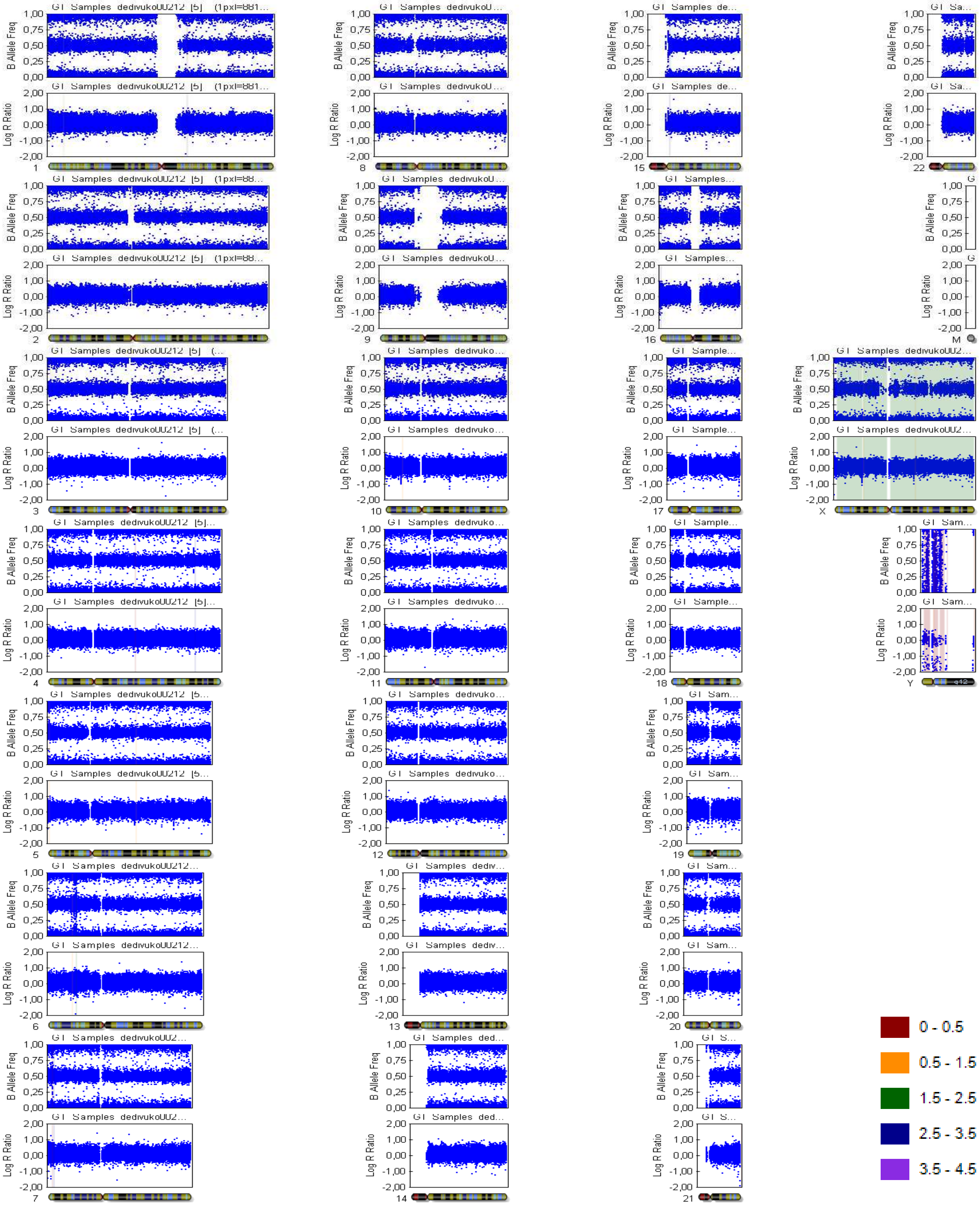
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00212 / 201353490092_R03C01	Staining	DNP (High) (27630314)	23300	66	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Staining	DNP (Bgnd) (29619375)	389	161	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Staining	Biotin (High) (41666334)	494	8811	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Staining	Biotin (Bgnd) (34648333)	429	50	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Extension	Extension (A) (17616306)	24165	251	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Extension	Extension (T) (14607337)	27089	210	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Extension	Extension (C) (12613307)	950	11023	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Extension	Extension (G) (11603365)	1189	9985	OK/Notable
DEDIVUKO00212 / 201353490092_R03C01	Target Removal	Target Removal (31623323)	663	118	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Hybridization	Hyb (High) (19612319)	1414	10798	OK/Notable
DEDIVUKO00212 / 201353490092_R03C01	Hybridization	Hyb (Medium) (20636378)	518	6957	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Hybridization	Hyb (Low) (23617335)	1217	2200	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Stringency	String (PM) (32629312)	16565	289	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Stringency	String (MM) (33668307)	4544	158	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	358	114	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	430	77	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	357	130	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	419	105	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Polymorphic	NP (A) (34633358)	8712	225	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Polymorphic	NP (T) (16648324)	11163	191	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Polymorphic	NP (C) (43641328)	662	6097	OK/OK
DEDIVUKO00212 / 201353490092_R03C01	Non-Polymorphic	NP (G) (13642359)	674	4944	OK/Notable
DEDIVUKO00212 / 201353490092_R03C01	Restoration	Restore (28637363)	393	185	OK/OK

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

Karyogram


GT Samples dedivuko00212 [5] (1pxl=881...
B Allele Freq
1,00
0,75
0,50
0,25
0,00
Log R Ratio
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
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
DEDIVUKO00212	15	22751234	23654207	3	902973	410	1585,478	