Karyotype Report

Customer sample ID: NP0077-18C
Internal sample ID: DE33DIVUKOD100197
Date of receipt: 2017-10-19

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0077-6D-2017-10-19 / DEDIVUKO00195, NP0077-16E-2017-10-19 / DEDIVUKO00196

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: 201340820116 R04C01

Batch ID and 96 well position: WG1004253-MSA6 D02

Call rate: 0,9972106

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: 2017-10-25-1326

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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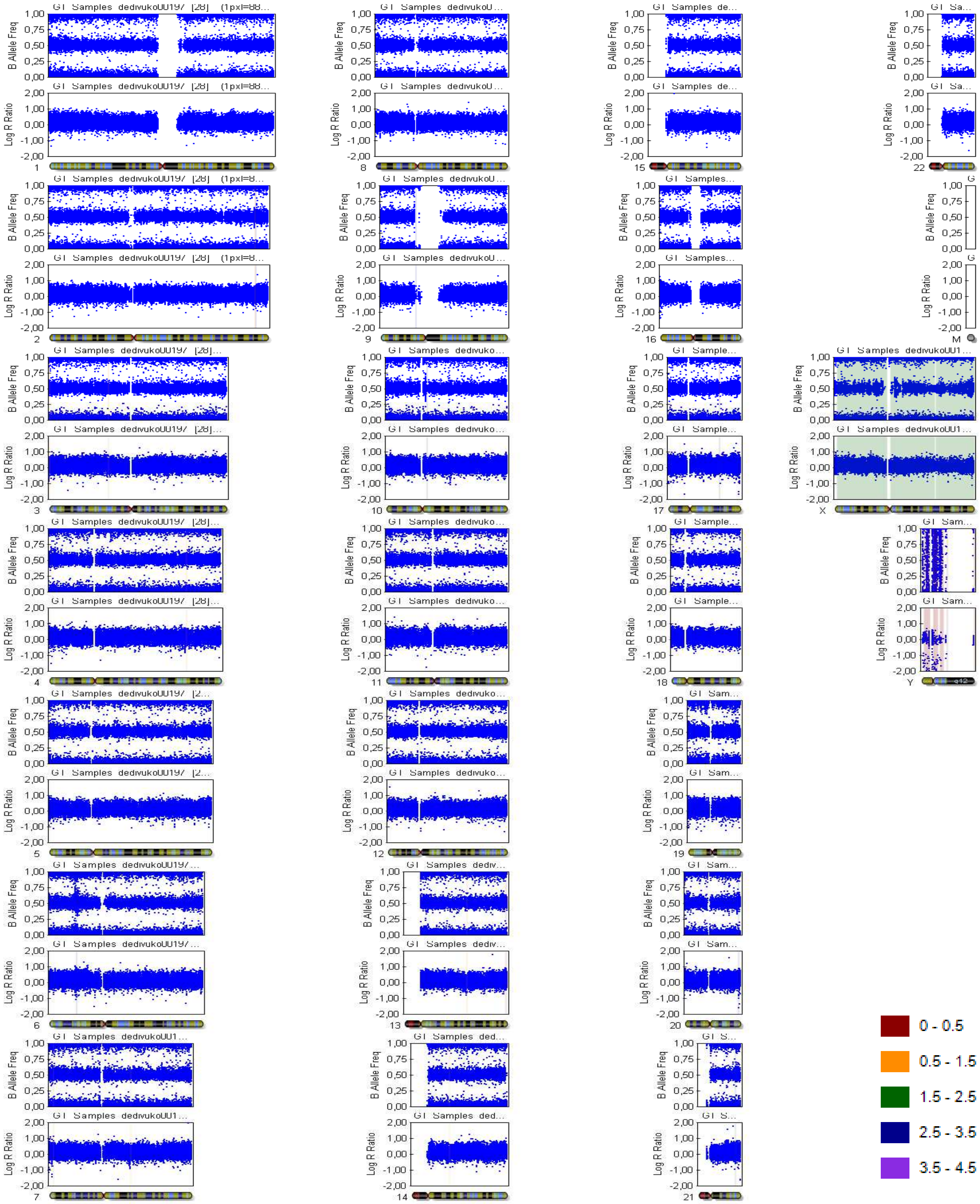
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00197 / 201340820116_R04C01	Staining	DNP (High) (27630314)	28679	86	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Staining	DNP (Bgnd) (29619375)	280	459	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Staining	Biotin (High) (41666334)	326	15564	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Staining	Biotin (Bgnd) (34648333)	203	51	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Extension	Extension (A) (17616306)	27290	378	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Extension	Extension (T) (14607337)	29378	309	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Extension	Extension (C) (12613307)	1019	17199	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Extension	Extension (G) (11603365)	1315	16170	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Target Removal	Target Removal (31623323)	661	179	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Hybridization	Hyb (High) (19612319)	1453	16067	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Hybridization	Hyb (Medium) (20636378)	358	10068	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Hybridization	Hyb (Low) (23617335)	1127	3388	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Stringency	String (PM) (32629312)	19124	525	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Stringency	String (MM) (33668307)	5437	435	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Specific Binding	NSB (Bgnd) (26619332)	209	232	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Specific Binding	NSB (Bgnd) (27624356)	247	172	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Specific Binding	NSB (Bgnd) (25617343)	253	290	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Specific Binding	NSB (Bgnd) (24616350)	332	214	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Polymorphic	NP (A) (34633358)	9556	422	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Polymorphic	NP (T) (16648324)	12098	274	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Polymorphic	NP (C) (43641328)	517	9460	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Non-Polymorphic	NP (G) (13642359)	552	7622	OK/OK
DEDIVUKO00197 / 201340820116_R04C01	Restoration	Restore (28637363)	266	334	OK/OK

Karyogram


GT Samples dedivuko00197 [28] (1pxl=88...
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
G
M
X
Y
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
DEDIVUKO00197	21	41390179	42497492	2	1107313	1423	367,5198	