Karyotype Report

Customer sample ID: NP0077-6D
Internal sample ID: DE87DIVUKOD100195
Date of receipt: 2017-10-19

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0077-16E-2017-10-19 / DEDIVUKO00196, NP0077-18C-2017-10-19 / DEDIVUKO00197

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 R02C01

Batch ID and 96 well position: WG1004253-MSA6 B02

Call rate: 0,9973909

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: 2017-10-25-1319

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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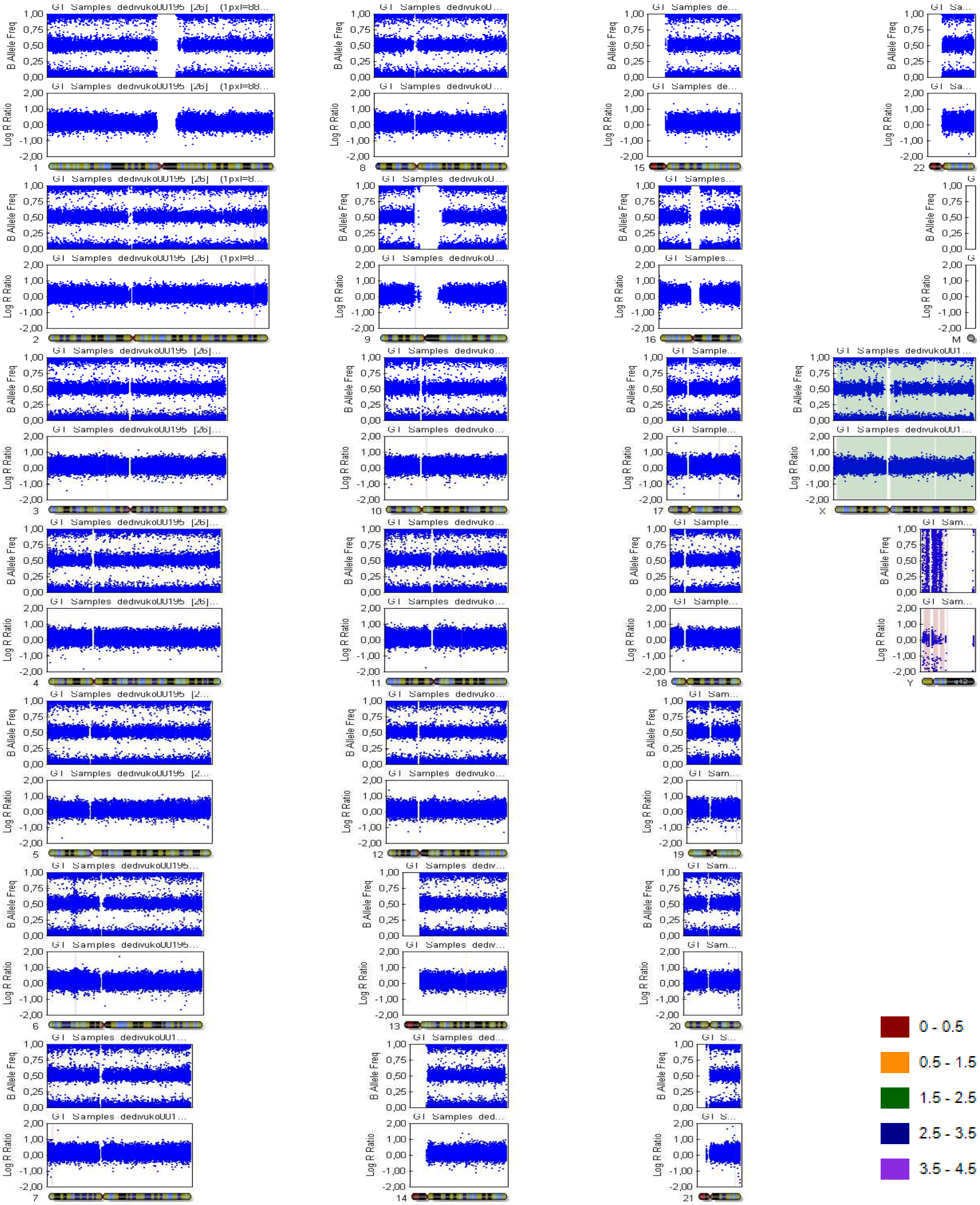
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00195 / 201340820116_R02C01	Staining	DNP (High) (27630314)	23958	95	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Staining	DNP (Bgnd) (29619375)	377	410	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Staining	Biotin (High) (41666334)	337	10963	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Staining	Biotin (Bgnd) (34648333)	253	53	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Extension	Extension (A) (17616306)	26340	405	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Extension	Extension (T) (14607337)	29685	320	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Extension	Extension (C) (12613307)	1049	14180	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Extension	Extension (G) (11603365)	1285	12942	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Target Removal	Target Removal (31623323)	726	209	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Hybridization	Hyb (High) (19612319)	1474	13200	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Hybridization	Hyb (Medium) (20636378)	505	8162	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Hybridization	Hyb (Low) (23617335)	1184	2706	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Stringency	String (PM) (32629312)	18159	509	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Stringency	String (MM) (33668307)	4735	391	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Specific Binding	NSB (Bgnd) (26619332)	350	224	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	315	191	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	378	248	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	399	229	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Polymorphic	NP (A) (34633358)	8942	419	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Polymorphic	NP (T) (16648324)	11356	277	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Polymorphic	NP (C) (43641328)	600	7600	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Non-Polymorphic	NP (G) (13642359)	631	6186	OK/OK
DEDIVUKO00195 / 201340820116_R02C01	Restoration	Restore (28637363)	356	330	OK/OK

Karyogram


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
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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
DEDIVUKO00195	21	41390179	42497492	2	1107313	1423	367,3701	