

Karyotype Report

Customer sample ID: NP0077-16E
Internal sample ID: DE60DIVUKOD100196
Date of receipt: 2017-10-19

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0077-6D-2017-10-19 / DEDIVUKO00195, 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 R03C01

Batch ID and 96 well position: WG1004253-MSA6 C02

Call rate: 0,99717

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: 2017-10-25-1323

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.

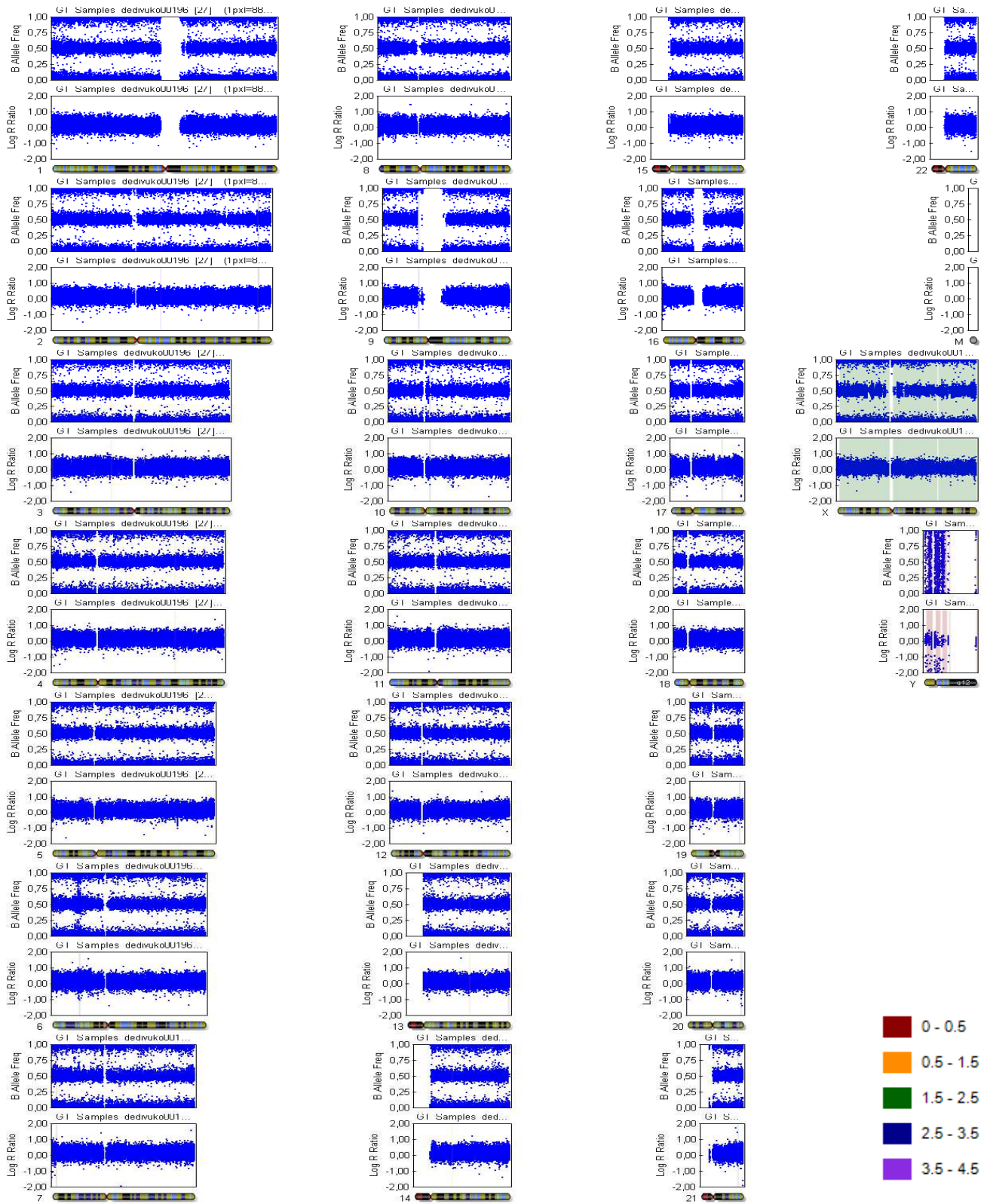
Analyst

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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00196 / 201340820116_R03C01	Staining	DNP (High) (27630314)	24766	73	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Staining	DNP (Bgnd) (29619375)	252	398	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Staining	Biotin (High) (41666334)	253	12371	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Staining	Biotin (Bgnd) (34648333)	159	38	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Extension	Extension (A) (17616306)	26157	332	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Extension	Extension (T) (14607337)	28222	267	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Extension	Extension (C) (12613307)	961	15526	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Extension	Extension (G) (11603365)	1318	14544	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Target Removal	Target Removal (31623323)	655	158	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Hybridization	Hyb (High) (19612319)	1417	14325	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Hybridization	Hyb (Medium) (20636378)	335	8789	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Hybridization	Hyb (Low) (23617335)	1076	3010	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Stringency	String (PM) (32629312)	17788	460	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Stringency	String (MM) (33668307)	5143	378	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	269	170	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	250	164	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	252	230	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	304	213	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non- Polymorphic	NP (A) (34633358)	9065	396	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non- Polymorphic	NP (T) (16648324)	11358	267	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non- Polymorphic	NP (C) (43641328)	524	8263	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Non- Polymorphic	NP (G) (13642359)	524	6891	OK/OK
DEDIVUKO00196 / 201340820116_R03C01	Restoration	Restore (28637363)	288	317	OK/OK

Karyogram





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

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Sample ID	Chr	Start	End	Type	Length	Marker count	CN Confidence	DGV Comparison
DEDIVUKO00196	9	39021035	40599590	3	1578555	35	109,2153	
DEDIVUKO00196	21	41390179	42497492	2	1107313	1423	367,2024	