

Karyotype Report

Customer sample ID: NP0078-10
Internal sample ID: DE27DIVUKOD100208
Date of receipt: 2017-12-12

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0078-12 / DEDIVUKO00209, NP0078-13 /
DEDIVUKO00210

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: 201334740023 R07C01

Batch ID and 96 well position: WG6906607-MSA6 G02

Call rate: 0,9969637

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: 2017-12-19-1323

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

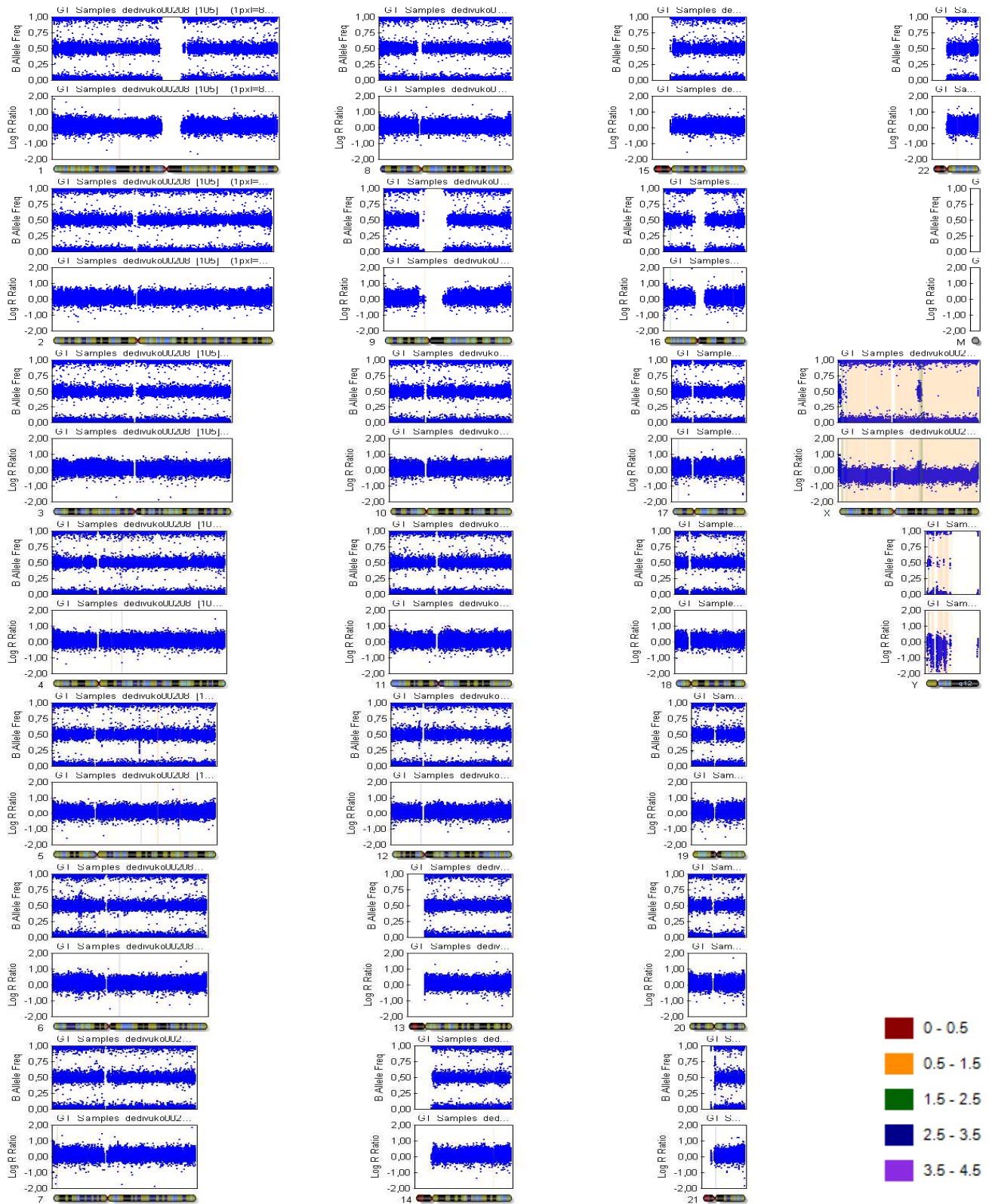
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00208 / 201334740023_R07C01	Staining	DNP (High) (27630314)	29615	141	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Staining	DNP (Bgnd) (29619375)	247	306	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Staining	Biotin (High) (41666334)	363	17986	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Staining	Biotin (Bgnd) (34648333)	257	95	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Extension	Extension (A) (17616306)	28719	416	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Extension	Extension (T) (14607337)	30861	252	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Extension	Extension (C) (12613307)	948	20393	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Extension	Extension (G) (11603365)	1294	19167	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Target Removal	Target Removal (31623323)	803	237	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Hybridization	Hyb (High) (19612319)	1601	20593	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Hybridization	Hyb (Medium) (20636378)	482	13493	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Hybridization	Hyb (Low) (23617335)	1498	4181	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Stringency	String (PM) (32629312)	20076	529	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Stringency	String (MM) (33668307)	3421	403	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non-Specific Binding	NSB (Bgnd) (26619332)	287	212	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non-Specific Binding	NSB (Bgnd) (27624356)	325	175	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non-Specific Binding	NSB (Bgnd) (25617343)	317	295	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non-Specific Binding	NSB (Bgnd) (24616350)	325	212	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non- Polymorphic	NP (A) (34633358)	9688	408	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non- Polymorphic	NP (T) (16648324)	13317	291	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non- Polymorphic	NP (C) (43641328)	544	11712	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Non- Polymorphic	NP (G) (13642359)	604	10140	OK/OK
DEDIVUKO00208 / 201334740023_R07C01	Restoration	Restore (28637363)	295	302	OK/OK

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

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

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
DEDIVUKO00208	9	44401981	44841930	1	439949	18	37,8885	CNV-CNV: 4, CNV-Complex: 1, CNV-Gain: 22, CNV-Loss: 11
DEDIVUKO00208	21	14613203	15153902	3	540699	110	342,0715	CNV-CNV: 4, CNV-Complex: 1, CNV-Gain: 1