

Karyotype Report

Customer sample ID: NP0079-79
Internal sample ID: DE43DIVUKOD100211
Date of receipt: 2017-12-12

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0079-15B / DEDIVUKO00212, 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 R02C01

Batch ID and 96 well position: WG6906606-MSA6 B12

Call rate: 0,9969751

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: 2018-01-04-0440

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; Chr15: Duplication in q11.2 on long arm.

Analyst

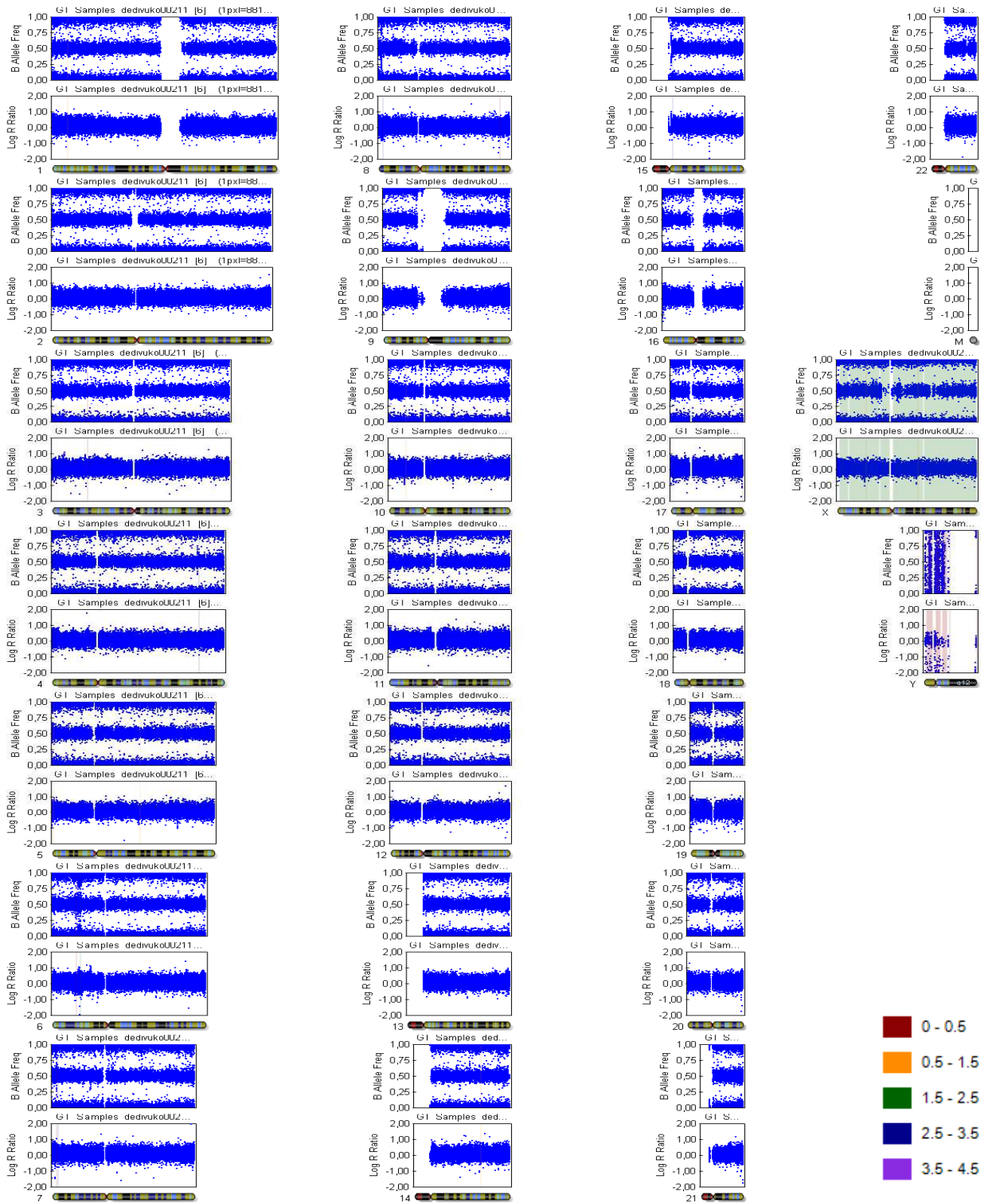
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00211 / 201353490092_R02C01	Staining	DNP (High) (27630314)	22614	86	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Staining	DNP (Bgnd) (29619375)	402	177	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Staining	Biotin (High) (41666334)	465	8144	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Staining	Biotin (Bgnd) (34648333)	365	57	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Extension	Extension (A) (17616306)	24757	294	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Extension	Extension (T) (14607337)	27633	216	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Extension	Extension (C) (12613307)	1050	10587	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Extension	Extension (G) (11603365)	1316	9847	OK/Notable
DEDIVUKO00211 / 201353490092_R02C01	Target Removal	Target Removal (31623323)	870	177	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Hybridization	Hyb (High) (19612319)	1534	10166	OK/Notable
DEDIVUKO00211 / 201353490092_R02C01	Hybridization	Hyb (Medium) (20636378)	551	6324	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Hybridization	Hyb (Low) (23617335)	1322	2058	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Stringency	String (PM) (32629312)	16835	292	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Stringency	String (MM) (33668307)	4791	196	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non-Specific Binding	NSB (Bgnd) (26619332)	492	147	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	453	127	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	542	153	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	512	149	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non- Polymorphic	NP (A) (34633358)	8742	246	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non- Polymorphic	NP (T) (16648324)	11187	189	OK/OK
DEDIVUKO00211 / 201353490092_R02C01	Non- Polymorphic	NP (C) (43641328)	751	5843	OK/Notable
DEDIVUKO00211 / 201353490092_R02C01	Non- Polymorphic	NP (G) (13642359)	650	4675	OK/Notable
DEDIVUKO00211 / 201353490092_R02C01	Restoration	Restore (28637363)	526	213	OK/OK

All „Notable“ tagged 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
DEDIVUKO00211	8	4198480	4655995	3	457515	1152	460,0918	CNV-: 1, CNV-CNV: 8, CNV-Complex: 1, CNV-Gain: 11, CNV-Gain+Loss: 1
DEDIVUKO00211	15	22751234	23654207	3	902973	410	1673,723	