

Karyotype Report

Customer sample ID: NP0141-31B
Internal sample ID: DE81DIVUKOD100206
Date of receipt: 2017-10-19

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0141-12C / DEDIVUKO00204, NP0141-17A /
DEDIVUKO00205

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 R06C01

Batch ID and 96 well position: WG6906607-MSA6 F02

Call rate: 0,9959649

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: 2017-12-19-1320

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

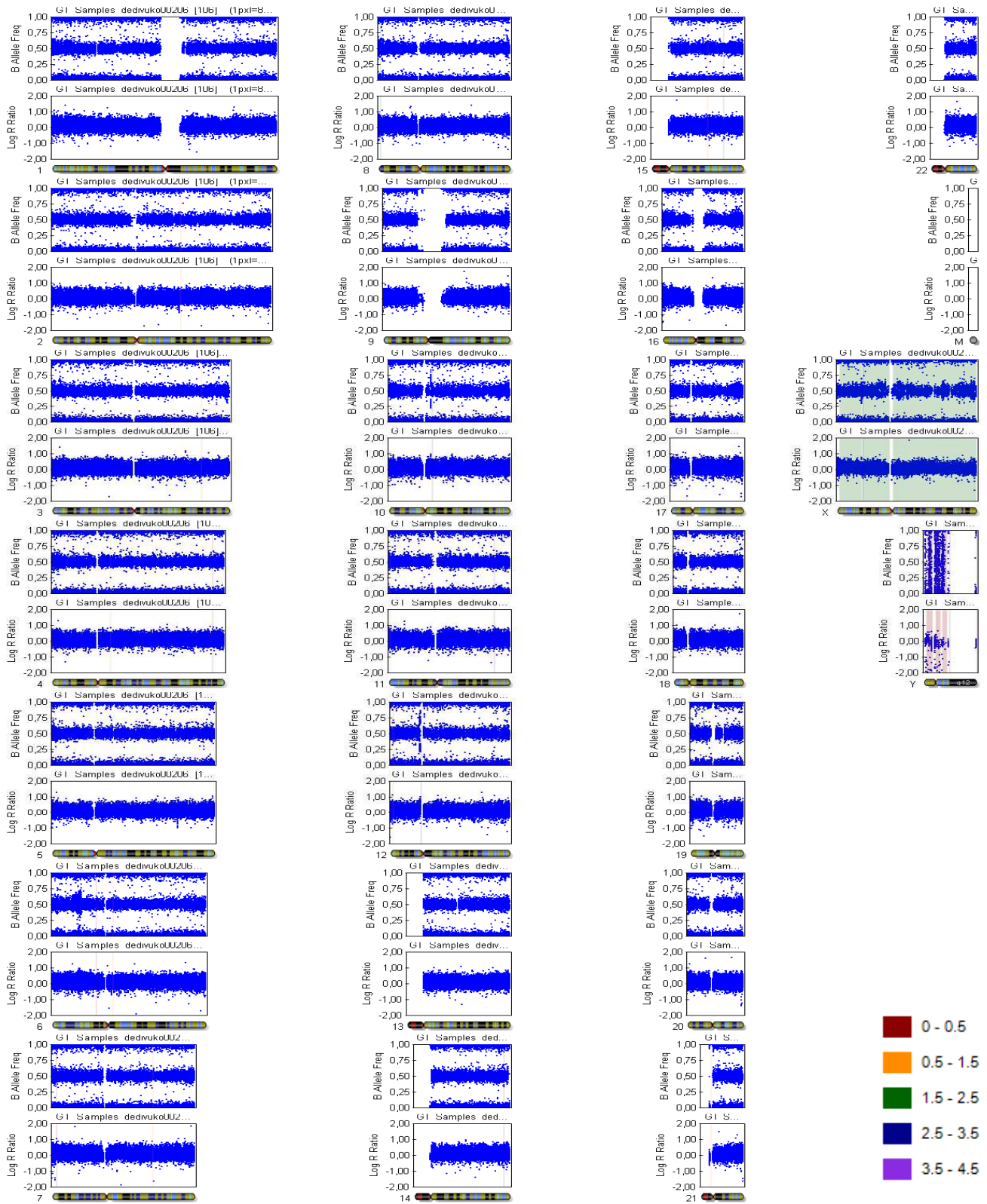
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00206 / 201334740023_R06C01	Staining	DNP (High) (27630314)	28840	107	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Staining	DNP (Bgnd) (29619375)	295	293	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Staining	Biotin (High) (41666334)	399	16485	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Staining	Biotin (Bgnd) (34648333)	277	55	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Extension	Extension (A) (17616306)	26820	341	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Extension	Extension (T) (14607337)	29498	217	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Extension	Extension (C) (12613307)	936	18565	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Extension	Extension (G) (11603365)	1161	17849	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Target Removal	Target Removal (31623323)	688	184	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Hybridization	Hyb (High) (19612319)	1580	18839	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Hybridization	Hyb (Medium) (20636378)	449	12606	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Hybridization	Hyb (Low) (23617335)	1341	3992	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Stringency	String (PM) (32629312)	19084	441	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Stringency	String (MM) (33668307)	3596	335	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non-Specific Binding	NSB (Bgnd) (26619332)	318	194	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non-Specific Binding	NSB (Bgnd) (27624356)	272	103	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non-Specific Binding	NSB (Bgnd) (25617343)	341	160	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non-Specific Binding	NSB (Bgnd) (24616350)	297	221	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non- Polymorphic	NP (A) (34633358)	9150	366	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non- Polymorphic	NP (T) (16648324)	12222	265	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non- Polymorphic	NP (C) (43641328)	567	10813	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Non- Polymorphic	NP (G) (13642359)	555	8634	OK/OK
DEDIVUKO00206 / 201334740023_R06C01	Restoration	Restore (28637363)	324	290	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
DEDIVUKO00206	12	33528281	34806478	3	1278197	667	703,078	CNV-CNV: 2, CNV-Complex: 1, CNV-Gain: 1
DEDIVUKO00206	15	79486084	81174544	2	1688460	1986	470,0727	