

Karyotype Report

Customer sample ID: NP0141-17A
Internal sample ID: DE11DIVUKOD100205
Date of receipt: 2017-10-19

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0141-12C / DEDIVUKO00204, NP0141-31B /
DEDIVUKO00206

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 R05C01

Batch ID and 96 well position: WG6906607-MSA6 E02

Call rate: 0,9961621

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: 2017-12-19-1316

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; Chr12: Duplication of telomeric region of short arm

Analyst

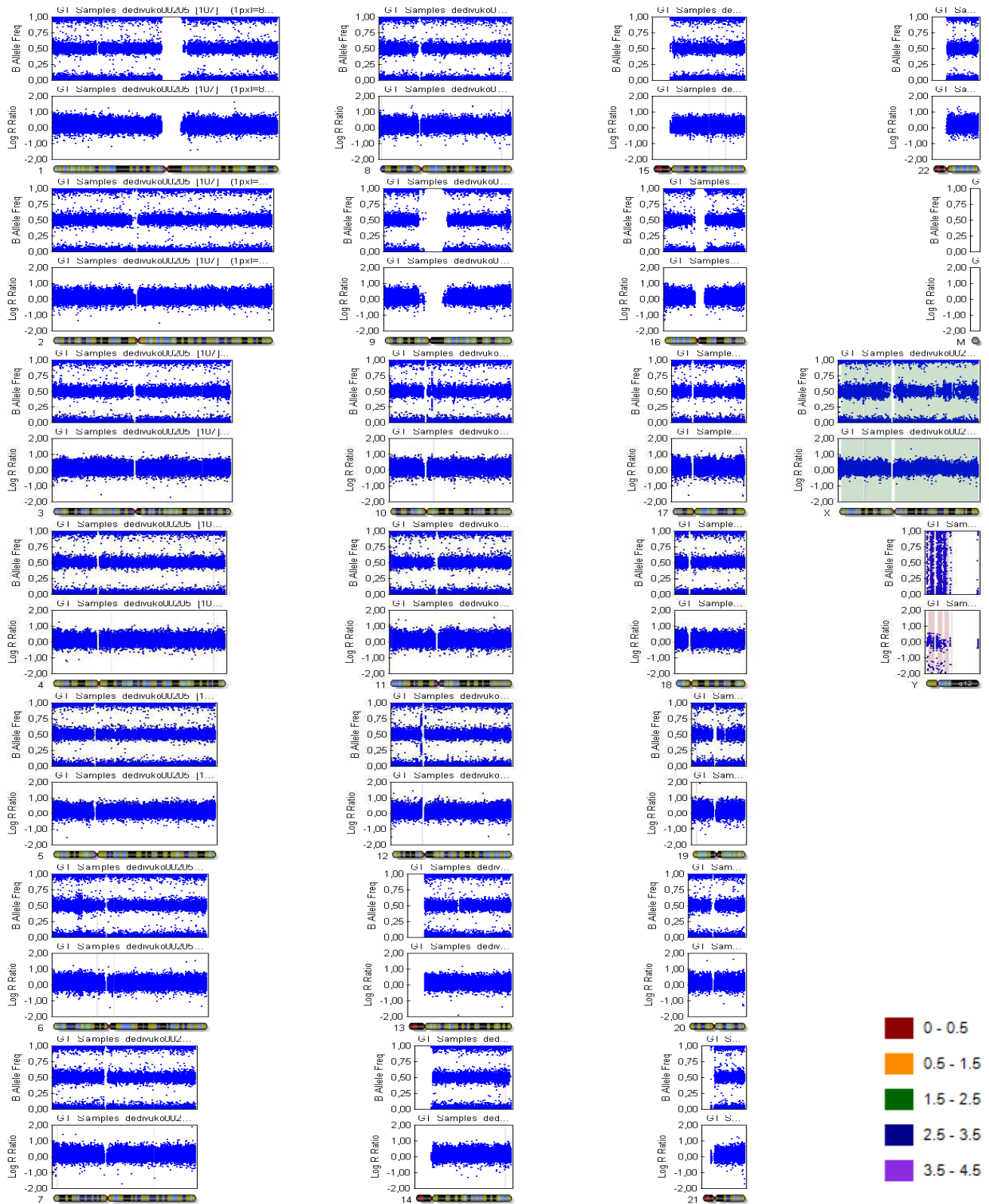
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00205 / 201334740023_R05C01	Staining	DNP (High) (27630314)	27742	99	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Staining	DNP (Bgnd) (29619375)	189	271	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Staining	Biotin (High) (41666334)	357	15106	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Staining	Biotin (Bgnd) (34648333)	244	64	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Extension	Extension (A) (17616306)	26839	302	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Extension	Extension (T) (14607337)	29334	299	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Extension	Extension (C) (12613307)	904	17718	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Extension	Extension (G) (11603365)	1131	16669	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Target Removal	Target Removal (31623323)	690	160	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Hybridization	Hyb (High) (19612319)	1628	17767	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Hybridization	Hyb (Medium) (20636378)	388	11664	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Hybridization	Hyb (Low) (23617335)	1343	3744	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Stringency	String (PM) (32629312)	18646	413	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Stringency	String (MM) (33668307)	3406	325	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non-Specific Binding	NSB (Bgnd) (26619332)	298	175	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non-Specific Binding	NSB (Bgnd) (27624356)	272	91	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non-Specific Binding	NSB (Bgnd) (25617343)	265	162	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non-Specific Binding	NSB (Bgnd) (24616350)	245	181	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non- Polymorphic	NP (A) (34633358)	9219	358	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non- Polymorphic	NP (T) (16648324)	11869	235	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non- Polymorphic	NP (C) (43641328)	511	10011	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Non- Polymorphic	NP (G) (13642359)	490	8083	OK/OK
DEDIVUKO00205 / 201334740023_R05C01	Restoration	Restore (28637363)	251	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
DEDIVUKO00205	12	33528281	34806478	3	1278197	667	1145,963	CNV-CNV: 2, CNV-Complex: 1, CNV-Gain: 1
DEDIVUKO00205	15	79486084	81174544	2	1688460	1986	470,5018	