

Karyotype Report

Customer sample ID: NP0144-41
Internal sample ID: DE47DIVUKOD100236
Date of receipt: 2018-05-15

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0144-32-2018-05-15 / DEDIVUKO00234, NP0144-33-2018-05-15 / DEDIVUKO00235

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: 201375320086 R06C01

Batch ID and 96 well position: WG6902506-MSA6 F04

Call rate: 0,9967462

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: 2018-06-11-0818

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

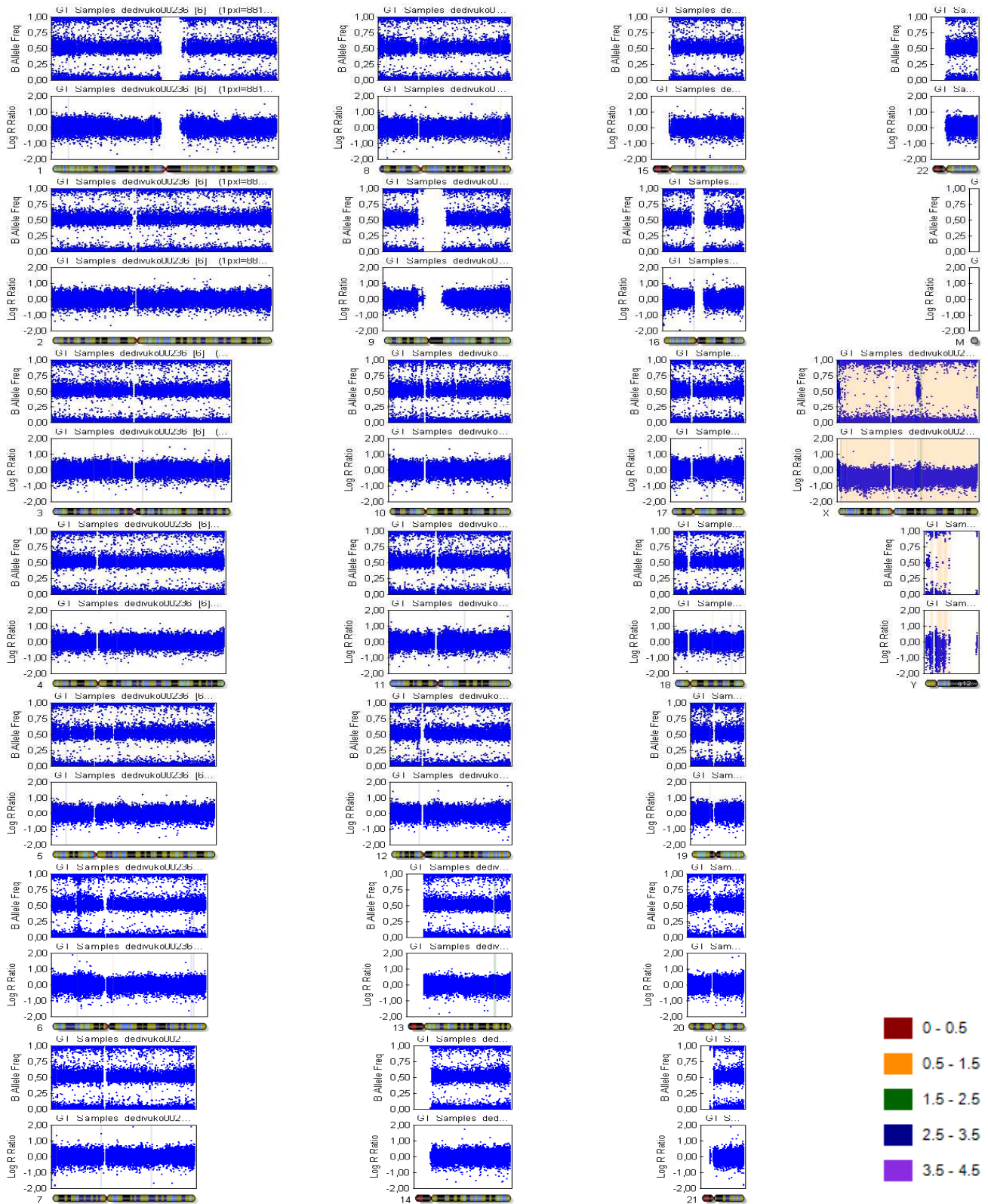
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00236 / 201375320086_R06C01	Staining	DNP (High) (27630314)	32061	152	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Staining	DNP (Bgnd) (29619375)	278	315	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Staining	Biotin (High) (41666334)	396	21978	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Staining	Biotin (Bgnd) (34648333)	323	180	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Extension	Extension (A) (17616306)	27695	534	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Extension	Extension (T) (14607337)	31394	369	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Extension	Extension (C) (12613307)	826	20848	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Extension	Extension (G) (11603365)	984	19808	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Target Removal	Target Removal (31623323)	491	289	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Hybridization	Hyb (High) (19612319)	1204	20481	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Hybridization	Hyb (Medium) (20636378)	398	12595	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Hybridization	Hyb (Low) (23617335)	913	3669	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Stringency	String (PM) (32629312)	20902	503	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Stringency	String (MM) (33668307)	7443	341	Notable/OK
DEDIVUKO00236 / 201375320086_R06C01	Non-Specific Binding	NSB (Bgnd) (26619332)	305	220	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non-Specific Binding	NSB (Bgnd) (27624356)	284	205	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non-Specific Binding	NSB (Bgnd) (25617343)	306	250	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non-Specific Binding	NSB (Bgnd) (24616350)	344	206	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non- Polymorphic	NP (A) (34633358)	11074	336	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non- Polymorphic	NP (T) (16648324)	12642	306	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non- Polymorphic	NP (C) (43641328)	591	11414	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Non- Polymorphic	NP (G) (13642359)	585	9909	OK/OK
DEDIVUKO00236 / 201375320086_R06C01	Restoration	Restore (28637363)	301	280	OK/OK

All „Notable“ tagged 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
DEDIVUKO00236	6	27011650	28147385	2	1135735	1834	357,9399	
DEDIVUKO00236	11	132897653	133368885	3	471232	573	2171,023	
DEDIVUKO00236	13	95535368	98311810	2	2776442	2583	546,3029	
DEDIVUKO00236	17	44168225	44580136	3	411911	75	102,1551	CNV-CNV: 37, CNV-Complex: 3, CNV-Gain: 14, CNV-Gain+Loss: 4, OTHER-Inversion: 1