

Karyotype Report

Customer sample ID: NP0139-6C
Internal sample ID: DE90DIVUKOD100238
Date of receipt: 2018-05-15

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0139-3E*-2018-05-15 / DEDIVUKO00237

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 R08C01

Batch ID and 96 well position: WG6902506-MSA6 H04

Call rate: 0,9967344

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: 2018-06-11-0825

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

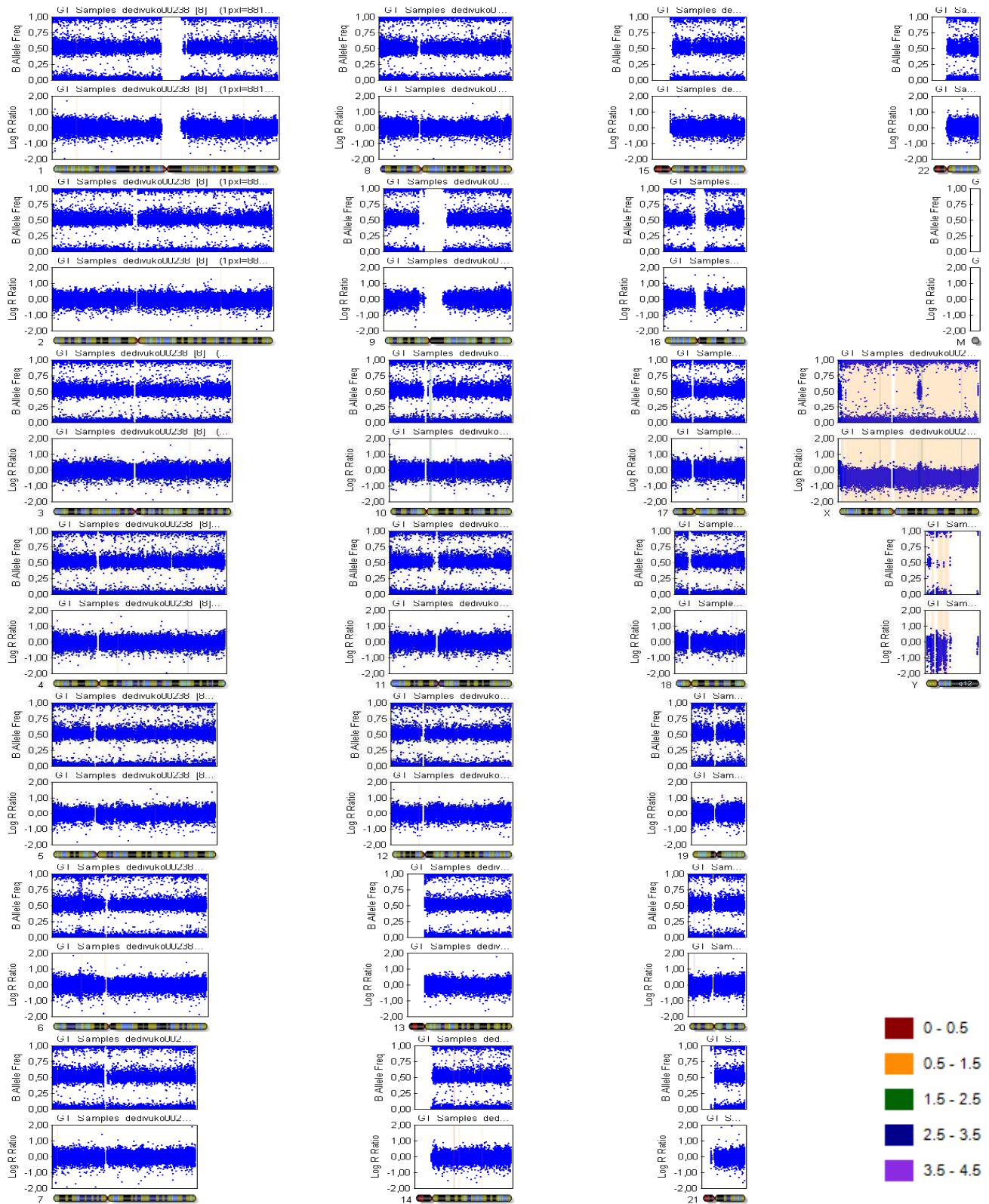
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00238 / 201375320086_R08C01	Staining	DNP (High) (27630314)	37052	260	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Staining	DNP (Bgnd) (29619375)	315	327	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Staining	Biotin (High) (41666334)	559	28169	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Staining	Biotin (Bgnd) (34648333)	365	229	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Extension	Extension (A) (17616306)	30541	615	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Extension	Extension (T) (14607337)	33762	456	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Extension	Extension (C) (12613307)	989	26170	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Extension	Extension (G) (11603365)	1117	24891	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Target Removal	Target Removal (31623323)	537	271	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Hybridization	Hyb (High) (19612319)	1285	25087	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Hybridization	Hyb (Medium) (20636378)	504	15663	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Hybridization	Hyb (Low) (23617335)	1019	4218	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Stringency	String (PM) (32629312)	23065	583	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Stringency	String (MM) (33668307)	6968	382	Notable/OK
DEDIVUKO00238 / 201375320086_R08C01	Non-Specific Binding	NSB (Bgnd) (26619332)	312	321	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non-Specific Binding	NSB (Bgnd) (27624356)	313	308	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non-Specific Binding	NSB (Bgnd) (25617343)	328	300	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non-Specific Binding	NSB (Bgnd) (24616350)	351	275	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non- Polymorphic	NP (A) (34633358)	11907	430	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non- Polymorphic	NP (T) (16648324)	13754	351	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non- Polymorphic	NP (C) (43641328)	556	13449	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Non- Polymorphic	NP (G) (13642359)	508	11260	OK/OK
DEDIVUKO00238 / 201375320086_R08C01	Restoration	Restore (28637363)	346	346	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
DEDIVUKO00238	10	43659093	46997563	2	3338470	2224	448,9951	