Karyotype Report

Customer sample ID: NP0143-18
Internal sample ID: DE31DIVUKOD100233
Date of receipt: 2018-05-15

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0143-5*-2018-05-15 / DEDIVUKO00231, NP0143-15*-2018-05-15 / DEDIVUKO00232

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 R03C01

Batch ID and 96 well position: WG6902506-MSA6 C04

Call rate: 0,9956468

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: 2018-06-11-0808

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

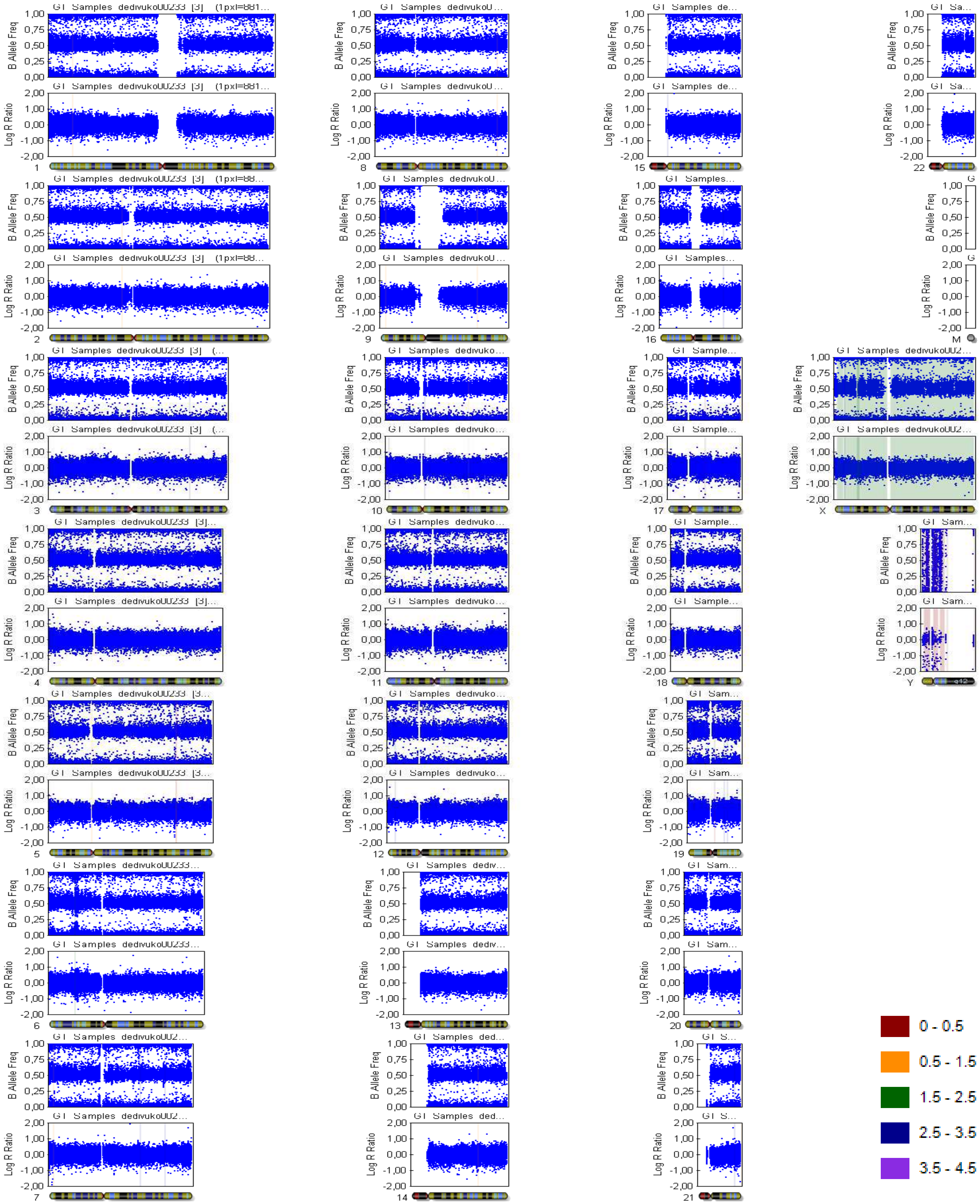
Stefan Herms
Stefan.Herms@unibas.ch
Tel.: +41 61 328 50 19

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00233 / 201375320086_R03C01	Staining	DNP (High) (27630314)	29390	104	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Staining	DNP (Bgnd) (29619375)	282	238	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Staining	Biotin (High) (41666334)	394	16158	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Staining	Biotin (Bgnd) (34648333)	319	117	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Extension	Extension (A) (17616306)	26040	359	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Extension	Extension (T) (14607337)	30560	279	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Extension	Extension (C) (12613307)	845	16539	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Extension	Extension (G) (11603365)	926	16038	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Target Removal	Target Removal (31623323)	438	134	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Hybridization	Hyb (High) (19612319)	1127	16012	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Hybridization	Hyb (Medium) (20636378)	416	9739	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Hybridization	Hyb (Low) (23617335)	775	2788	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Stringency	String (PM) (32629312)	20110	373	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Stringency	String (MM) (33668307)	7153	266	Notable/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	228	149	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	289	117	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	295	193	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	283	181	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Polymorphic	NP (A) (34633358)	9763	254	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Polymorphic	NP (T) (16648324)	12145	219	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Polymorphic	NP (C) (43641328)	534	8570	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Non-Polymorphic	NP (G) (13642359)	506	7228	OK/OK
DEDIVUKO00233 / 201375320086_R03C01	Restoration	Restore (28637363)	344	249	OK/OK

All „Notable“ tagged probes are within specs. The karyogram can be evaluated.

Karyogram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22
X
Y
G
M
🟥 0 - 0.5
🟧 0.5 - 1.5
🟩 1.5 - 2.5
🟦 2.5 - 3.5
🟪 3.5 - 4.5

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