Karyotype Report

Customer sample ID: NP0143-15
Internal sample ID: DE58DIVUKOD100232
Date of receipt: 2018-05-15

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0143-5*-2018-05-15 / DEDIVUKO00231, NP0143-18-2018-05-15 / DEDIVUKO00233

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 R02C01

Batch ID and 96 well position: WG6902506-MSA6 B04

Call rate: 0,9956679

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: 2018-06-11-0804

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. Chr20: Early mosaicism of whole chromosome visible (~20%).

Analyst

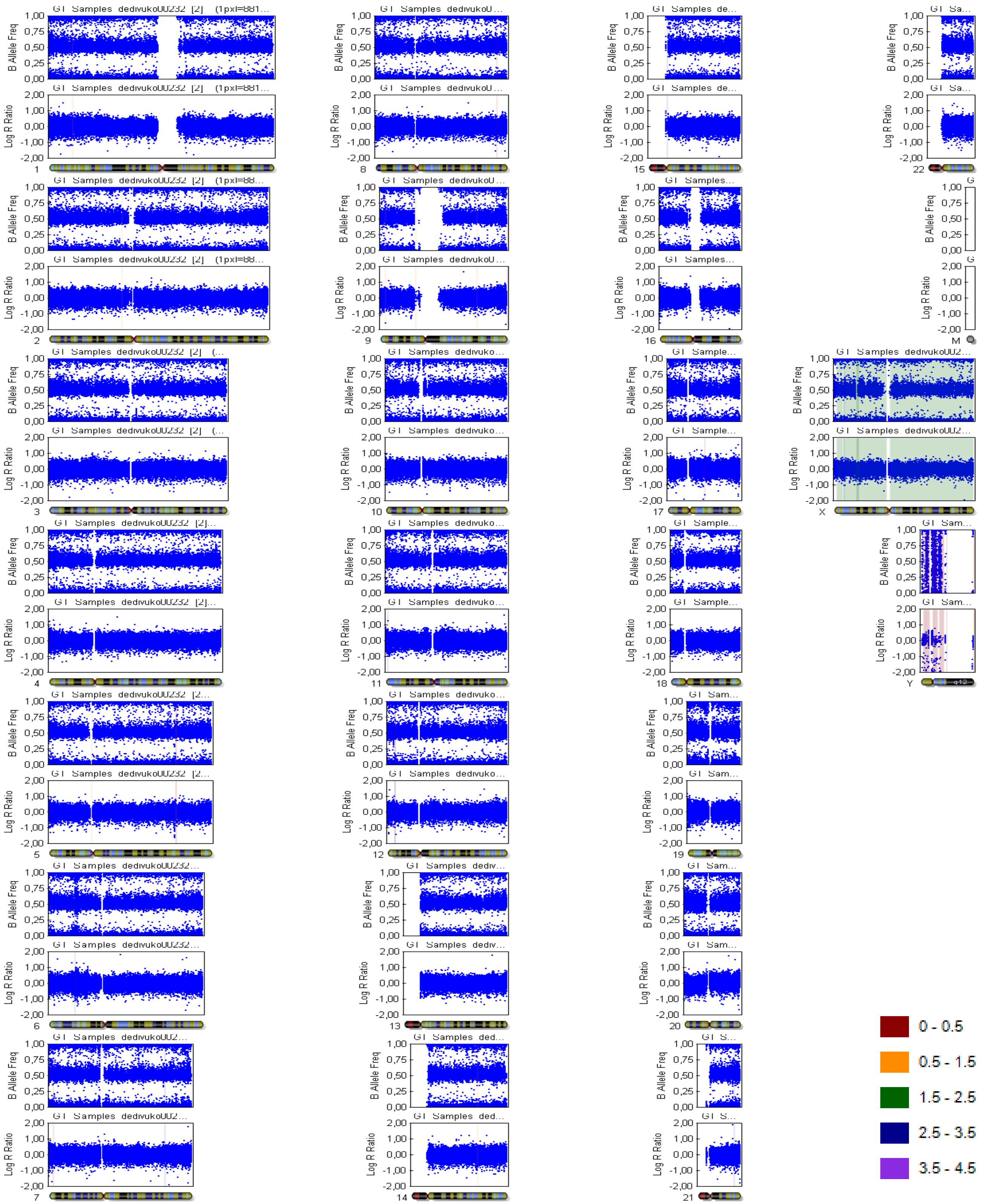
Stefan Herms
Stefan.Herms@unibas.ch
Tel.: +41 61 328 50 19

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00232 / 201375320086_R02C01	Staining	DNP (High) (27630314)	28552	99	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Staining	DNP (Bgnd) (29619375)	235	192	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Staining	Biotin (High) (41666334)	377	14751	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Staining	Biotin (Bgnd) (34648333)	334	112	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Extension	Extension (A) (17616306)	24104	317	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Extension	Extension (T) (14607337)	29068	206	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Extension	Extension (C) (12613307)	680	14740	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Extension	Extension (G) (11603365)	913	13819	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Target Removal	Target Removal (31623323)	441	144	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Hybridization	Hyb (High) (19612319)	1061	14155	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Hybridization	Hyb (Medium) (20636378)	399	8479	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Hybridization	Hyb (Low) (23617335)	797	2377	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Stringency	String (PM) (32629312)	18157	308	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Stringency	String (MM) (33668307)	5483	212	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Specific Binding	NSB (Bgnd) (26619332)	244	147	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	294	79	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	269	180	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	298	127	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Polymorphic	NP (A) (34633358)	8924	205	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Polymorphic	NP (T) (16648324)	11266	225	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Polymorphic	NP (C) (43641328)	479	7646	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Non-Polymorphic	NP (G) (13642359)	409	6265	OK/OK
DEDIVUKO00232 / 201375320086_R02C01	Restoration	Restore (28637363)	261	200	OK/OK

All control probes are within specs. The karyogram can be evaluated.

Karyogram


GT Samples dedivukoUU232 [2] (1pxl=881…
B Allele Freq
Log R Ratio
1,00
0,75
0,50
0,25
0,00
2,00
1,00
0,00
-1,00
-2,00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
M
G
q12
🟥 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