

Karyotype Report

Customer sample ID: NP0138-31B
Internal sample ID: DE65DIVUKOD100203
Date of receipt: 2017-10-19

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0138-8B / DEDIVUKO00201, NP0138-19E / DEDIVUKO00202

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 R03C01

Batch ID and 96 well position: WG6906607-MSA6 C02

Call rate: 0,9965947

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: 2017-12-19-1309

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: Duplication in q11.21

Analyst

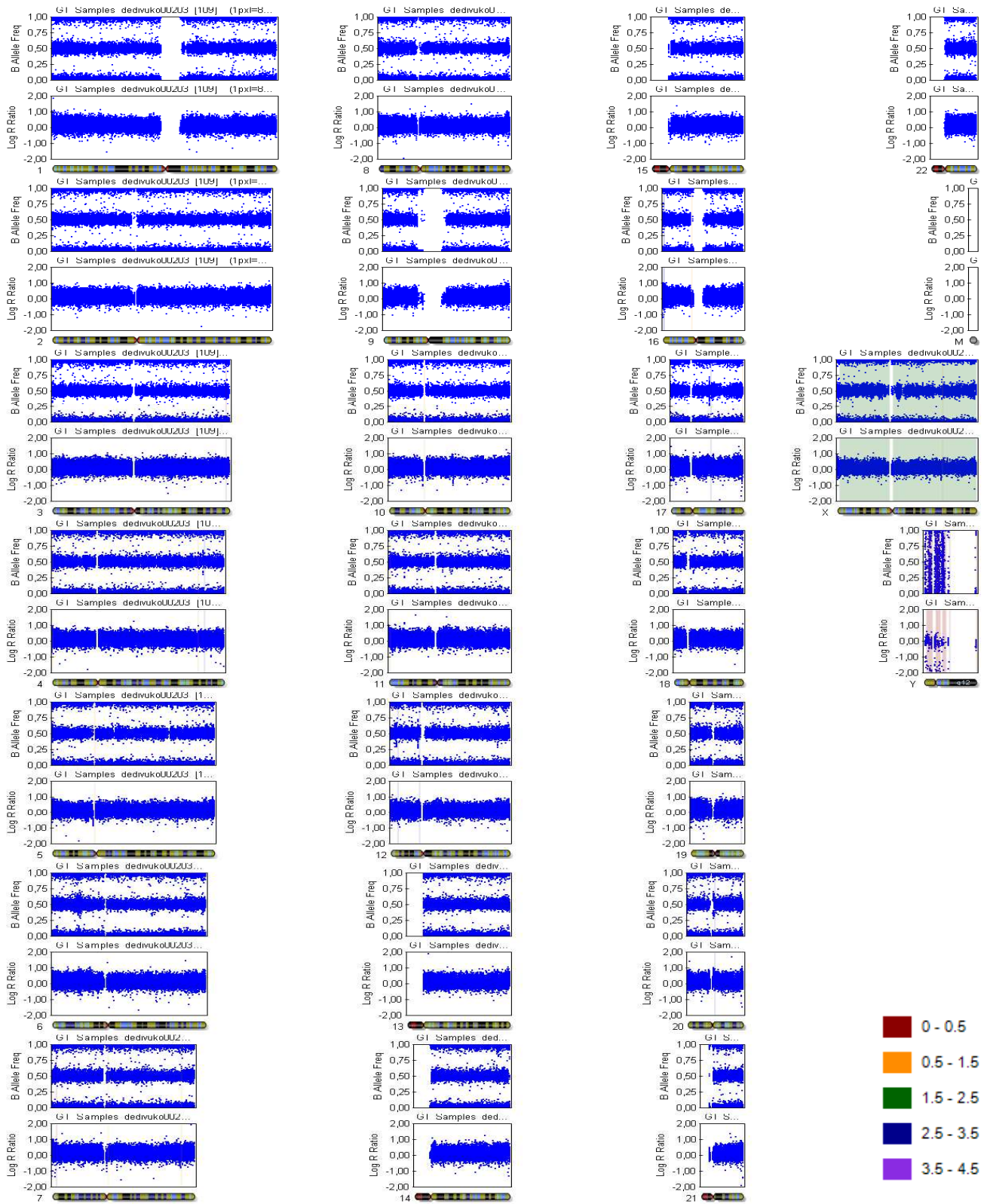
Stefan Herms
Stefan.Herms@unibas.ch
Tel.: +41 61 328 50 19

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00203 / 201334740023_R03C01	Staining	DNP (High) (27630314)	25829	91	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Staining	DNP (Bgnd) (29619375)	261	238	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Staining	Biotin (High) (41666334)	346	11775	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Staining	Biotin (Bgnd) (34648333)	249	39	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Extension	Extension (A) (17616306)	24625	300	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Extension	Extension (T) (14607337)	27319	206	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Extension	Extension (C) (12613307)	905	13567	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Extension	Extension (G) (11603365)	1201	12931	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Target Removal	Target Removal (31623323)	738	117	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Hybridization	Hyb (High) (19612319)	1533	13364	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Hybridization	Hyb (Medium) (20636378)	390	8571	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Hybridization	Hyb (Low) (23617335)	1341	2713	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Stringency	String (PM) (32629312)	16786	330	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Stringency	String (MM) (33668307)	2869	248	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	342	149	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	307	111	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	319	151	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	310	131	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non- Polymorphic	NP (A) (34633358)	8699	259	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non- Polymorphic	NP (T) (16648324)	11129	191	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non- Polymorphic	NP (C) (43641328)	476	7564	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Non- Polymorphic	NP (G) (13642359)	558	6239	OK/OK
DEDIVUKO00203 / 201334740023_R03C01	Restoration	Restore (28637363)	325	219	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
DEDIVUKO00203	16	32257633	33614448	1	1356815	119	73,5286	CNV-CNV: 32, CNV-Complex: 2, CNV-Gain: 55, CNV-Gain+Loss: 2, CNV-Loss: 7
DEDIVUKO00203	20	29804073	30829991	3	1025918	807	149,2048	