

Karyotype Report

Customer sample ID: NP0079-16H
Internal sample ID: DE86DIVUKOD100213
Date of receipt: 2017-12-12

Gender

Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0079-79 / DEDIVUKO00211, NP0079-15B / DEDIVUKO00212

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: 201353490092 R04C01

Batch ID and 96 well position: WG6906606-MSA6 D12

Call rate: 0,9972894

Typing

Scanner: Illumina iScan, S/N: N234
Site of processing: Life&Brain GENOMICS, Bonn, Germany
Manufacturer: Illumina, Inc., San Diego, United States of America
Date of scan: 2018-01-04-0457

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; Chr15: Duplication in q11.2 on long arm.

Analyst

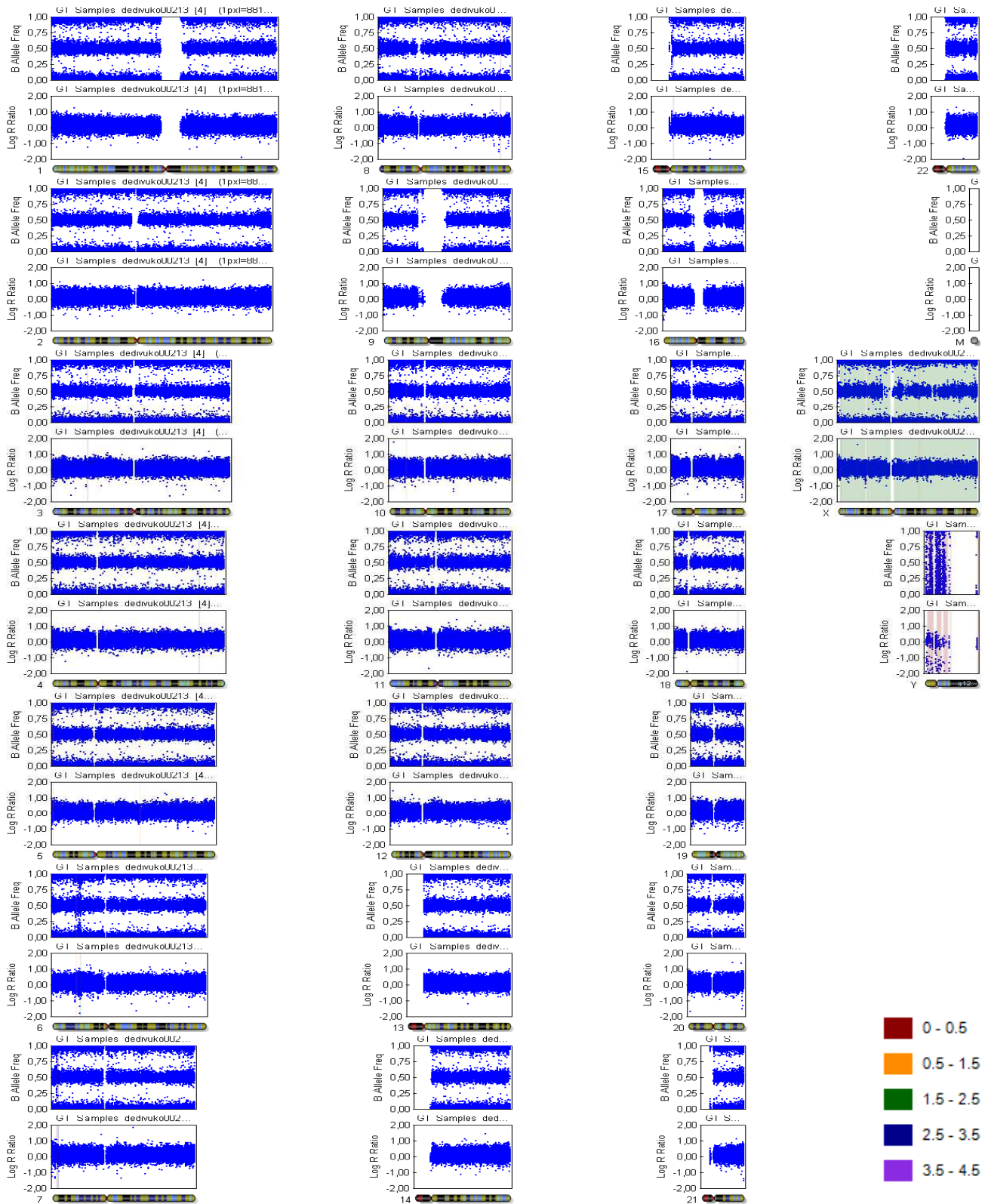
Stefan Herms
Stefan.Herms@unibas.ch
Tel.: +41 61 328 50 19

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00213 / 201353490092_R04C01	Staining	DNP (High) (27630314)	24270	83	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Staining	DNP (Bgnd) (29619375)	454	203	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Staining	Biotin (High) (41666334)	518	9873	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Staining	Biotin (Bgnd) (34648333)	394	81	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Extension	Extension (A) (17616306)	25827	314	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Extension	Extension (T) (14607337)	28518	265	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Extension	Extension (C) (12613307)	1049	12244	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Extension	Extension (G) (11603365)	1366	11830	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Target Removal	Target Removal (31623323)	865	176	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Hybridization	Hyb (High) (19612319)	1565	12359	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Hybridization	Hyb (Medium) (20636378)	527	7856	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Hybridization	Hyb (Low) (23617335)	1423	2489	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Stringency	String (PM) (32629312)	17985	397	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Stringency	String (MM) (33668307)	5070	235	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non-Specific Binding	NSB (Bgnd) (26619332)	496	117	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non-Specific Binding	NSB (Bgnd) (27624356)	485	111	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non-Specific Binding	NSB (Bgnd) (25617343)	532	143	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non-Specific Binding	NSB (Bgnd) (24616350)	468	101	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non- Polymorphic	NP (A) (34633358)	9040	303	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non- Polymorphic	NP (T) (16648324)	12036	227	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non- Polymorphic	NP (C) (43641328)	706	7089	OK/OK
DEDIVUKO00213 / 201353490092_R04C01	Non- Polymorphic	NP (G) (13642359)	747	5935	OK/Notable
DEDIVUKO00213 / 201353490092_R04C01	Restoration	Restore (28637363)	516	208	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
DEDIVUKO00213	15	22751234	23654207	3	902973	410	1630,878	