

Karyotype Report

Customer sample ID: NP0105-19, 11+4
Internal sample ID: DE77DIVUKOD100181
Date of receipt: 2017-02-01

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0105-2-08.12.2016 / DEDIVUKO00172

Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmniExpressExome-8 BeadChip v1.3
Manifest file: HumanOmniExpressExome-8v1-3_A.bpm
Cluster file: HumanOmniExpressExome-8v1-3_A.egt

Chip barcode and segment: 200729680112 R03C01

Batch ID and 96 well position: WG0086079-MSA1 C01

Call rate: 0,999

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: 2017-02-09-0430

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

Chr07: Larger duplication (20Mbp) mosaic (80%) on long arm.

Analyst

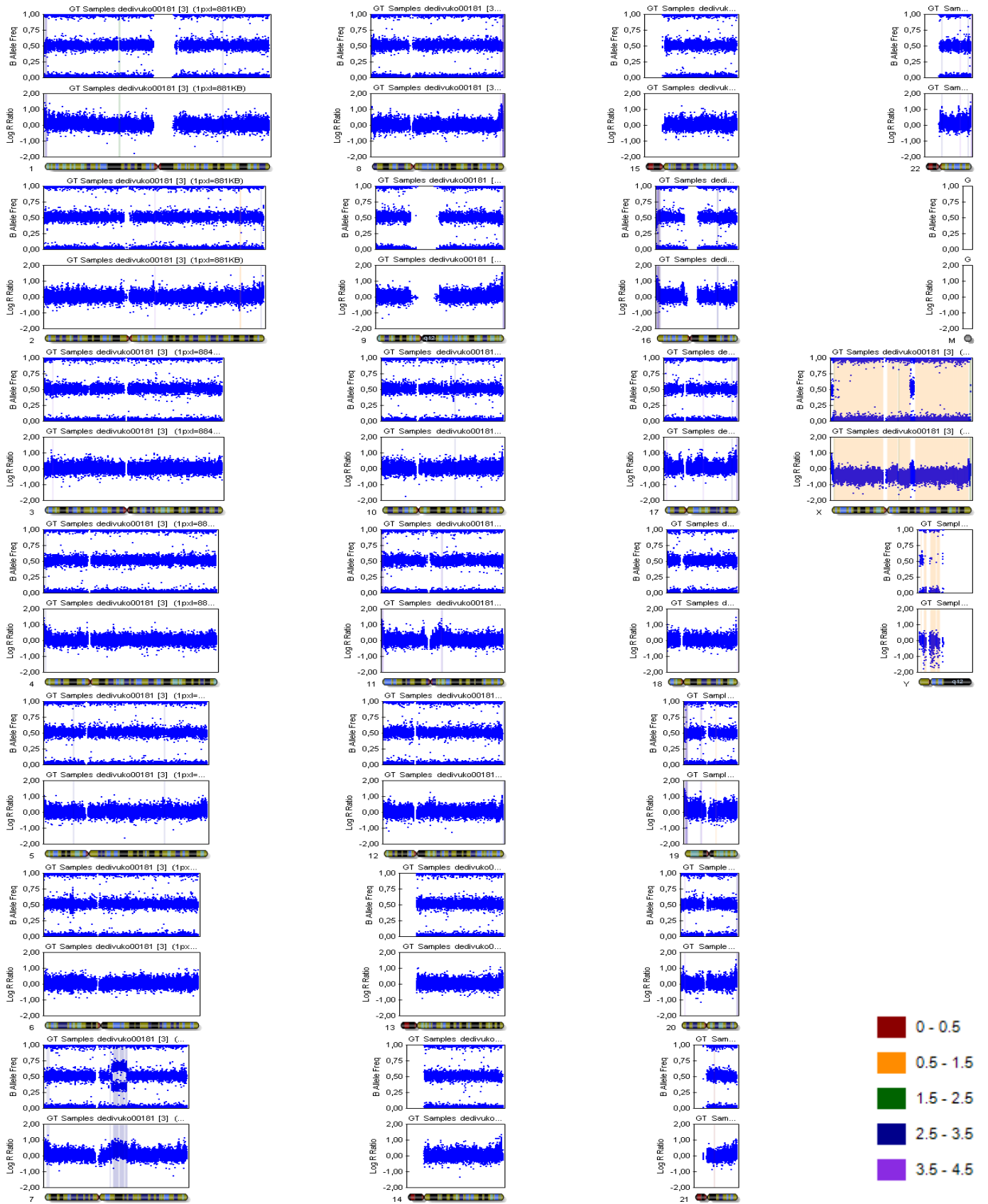
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Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00181 / 200729680112_R03C01	Staining	DNP (High) (27630314)	14354	225	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Staining	DNP (Bgnd) (29619375)	328	213	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Staining	Biotin (High) (41666334)	309	6396	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Staining	Biotin (Bgnd) (34648333)	279	248	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Extension	Extension (A) (17616306)	29627	385	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Extension	Extension (T) (14607337)	30043	286	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Extension	Extension (C) (12613307)	1102	17513	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Extension	Extension (G) (11603365)	1427	18756	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Target Removal	Target Removal (31623323)	905	188	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Hybridization	Hyb (High) (19612319)	1322	16908	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Hybridization	Hyb (Medium) (20636378)	418	10450	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Hybridization	Hyb (Low) (23617335)	1489	3238	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Stringency	String (PM) (32629312)	17727	437	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Stringency	String (MM) (33668307)	3147	224	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	285	195	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	302	202	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	251	235	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	296	148	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non- Polymorphic	NP (A) (34633358)	11528	380	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non- Polymorphic	NP (T) (16648324)	10662	256	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non- Polymorphic	NP (C) (43641328)	484	9326	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Non- Polymorphic	NP (G) (13642359)	493	9565	OK/OK
DEDIVUKO00181 / 200729680112_R03C01	Restoration	Restore (28637363)	325	393	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.

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
DEDIVUKO00181	1	81872593	84310193	2	2437600	690	260,919	
DEDIVUKO00181	7	75931160	82783846	3	6852686	1995	2957,132	
DEDIVUKO00181	7	82789419	88956699	3	6167280	1660	3908,85	
DEDIVUKO00181	7	88974907	92236829	3	3261922	933	4438,917	