

Karyotype Report

Customer sample ID: NP0100-10, 10+4
Internal sample ID: DE34DIVUKOD100179
Date of receipt: 2017-02-01

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0100 HDF-17.10.2016 / DEDIVUKO00146, NP0100-4*-17.10.2016 / DEDIVUKO00147, NP0100-8-08.12.2016 / DEDIVUKO00171, NP0100-11-01.02.2017 / DEDIVUKO00180

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 R01C01

Batch ID and 96 well position: WG0086079-MSA1 A01

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: 2017-02-09-0424

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

Chr20: Duplication in 20q11.21

Analyst

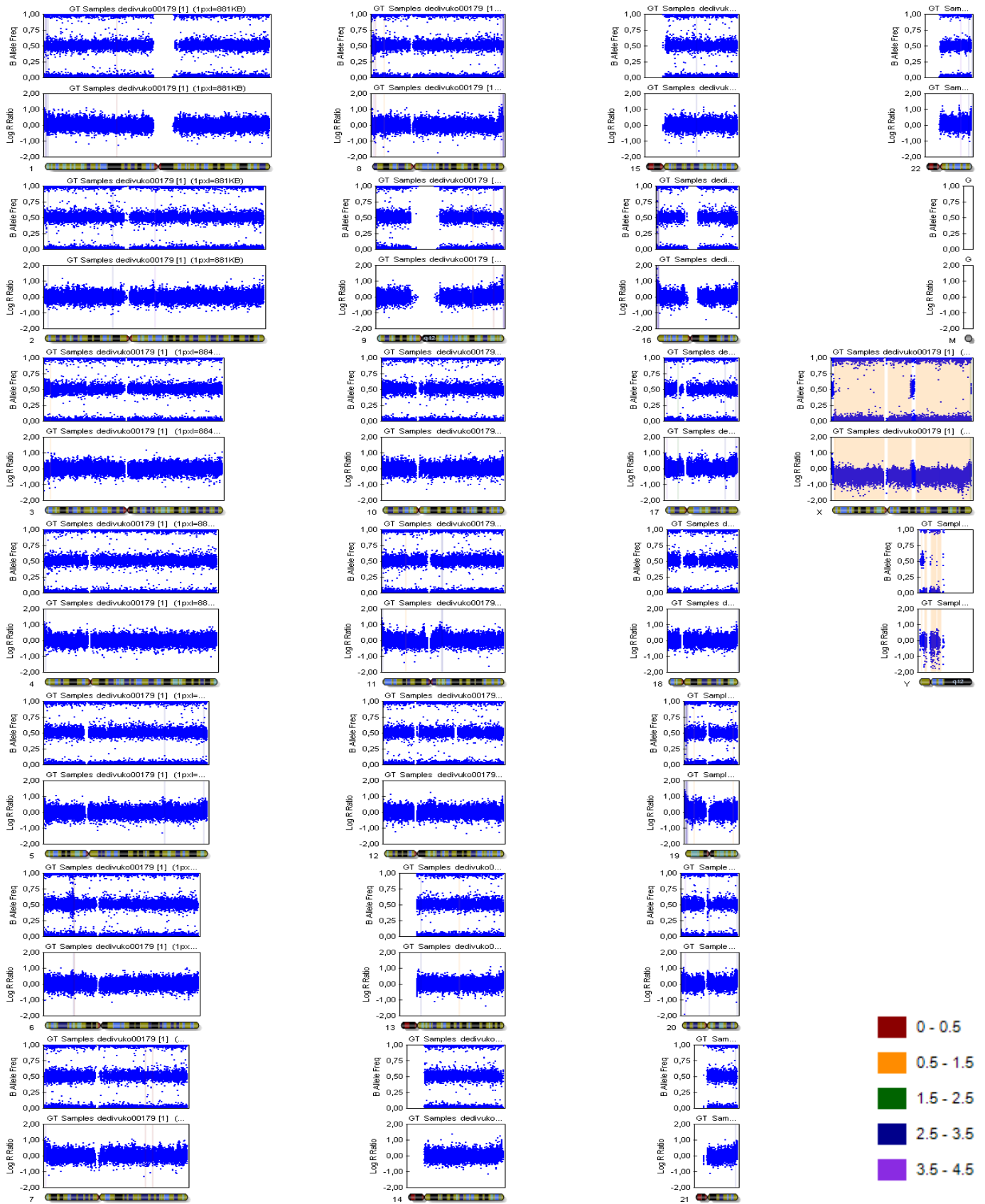
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00179 / 200729680112_R01C01	Staining	DNP (High) (27630314)	14198	183	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Staining	DNP (Bgnd) (29619375)	286	182	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Staining	Biotin (High) (41666334)	299	6294	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Staining	Biotin (Bgnd) (34648333)	222	195	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Extension	Extension (A) (17616306)	28448	342	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Extension	Extension (T) (14607337)	28784	276	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Extension	Extension (C) (12613307)	902	15056	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Extension	Extension (G) (11603365)	1232	15145	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Target Removal	Target Removal (31623323)	785	169	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Hybridization	Hyb (High) (19612319)	1119	14052	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Hybridization	Hyb (Medium) (20636378)	337	8755	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Hybridization	Hyb (Low) (23617335)	1190	2586	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Stringency	String (PM) (32629312)	16372	345	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Stringency	String (MM) (33668307)	2471	167	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non-Specific Binding	NSB (Bgnd) (26619332)	236	170	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non-Specific Binding	NSB (Bgnd) (27624356)	208	124	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non-Specific Binding	NSB (Bgnd) (25617343)	237	211	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non-Specific Binding	NSB (Bgnd) (24616350)	236	132	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non- Polymorphic	NP (A) (34633358)	10081	289	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non- Polymorphic	NP (T) (16648324)	9003	236	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non- Polymorphic	NP (C) (43641328)	422	7686	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Non- Polymorphic	NP (G) (13642359)	490	7919	OK/OK
DEDIVUKO00179 / 200729680112_R01C01	Restoration	Restore (28637363)	247	309	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
DEDIVUKO00179	17	14290540	15592762	2	1302222	614	254,016	
DEDIVUKO00179	20	29942695	30419954	3	477259	136	437,9913	