

Karyotype Report

Customer sample ID: NP0100-11, 10+5
Internal sample ID: DE07DIVUKOD100180
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, NP0100-10-01.02.2017 / DEDIVUKO00179

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 R02C01

Batch ID and 96 well position: WG0086079-MSA1 B01

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: 2017-02-09-0427

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.

Analyst

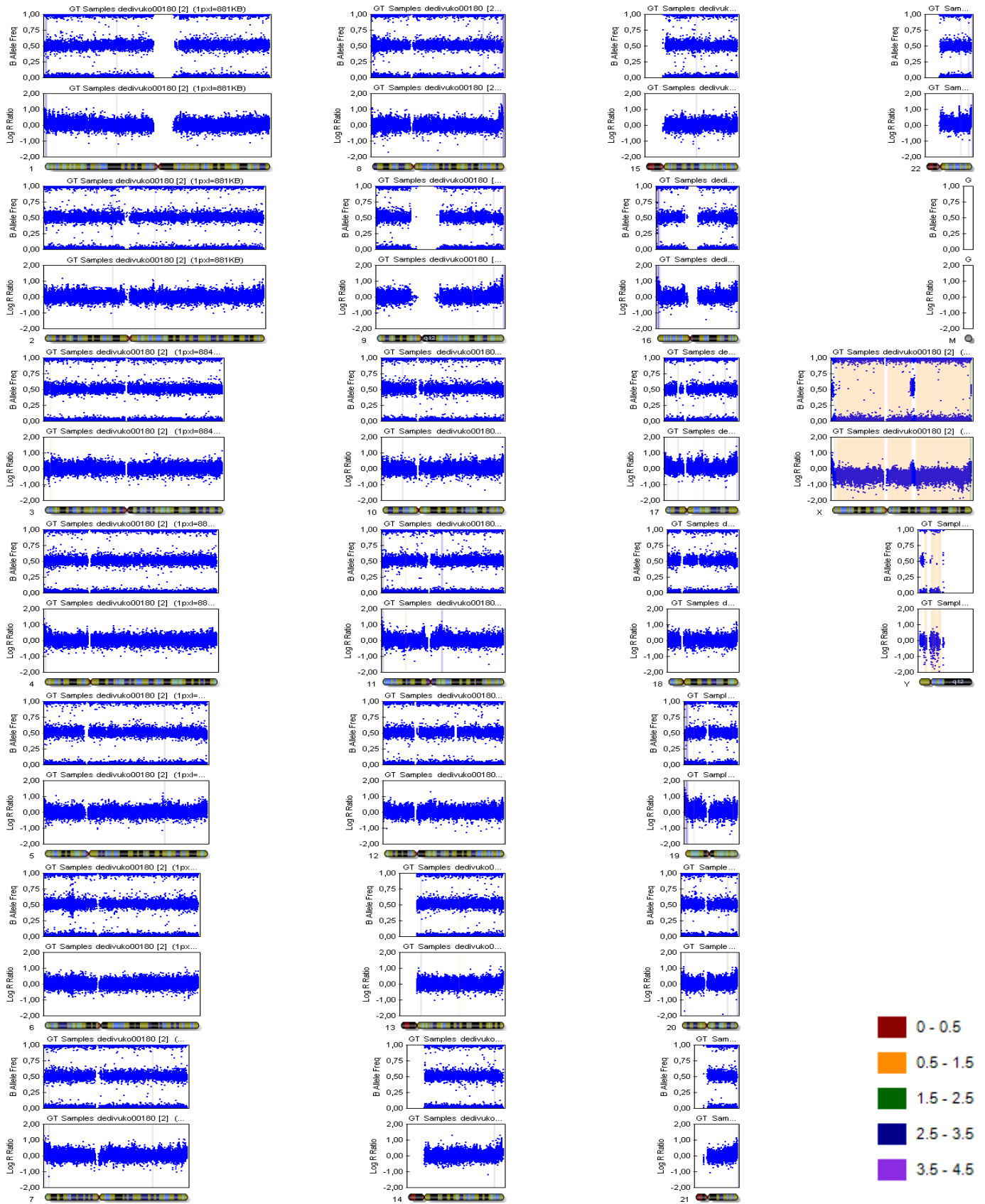
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00180 / 200729680112_R02C01	Staining	DNP (High) (27630314)	14331	197	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Staining	DNP (Bgnd) (29619375)	253	170	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Staining	Biotin (High) (41666334)	286	6434	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Staining	Biotin (Bgnd) (34648333)	205	173	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Extension	Extension (A) (17616306)	28057	351	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Extension	Extension (T) (14607337)	30368	279	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Extension	Extension (C) (12613307)	983	16131	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Extension	Extension (G) (11603365)	1285	16481	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Target Removal	Target Removal (31623323)	877	156	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Hybridization	Hyb (High) (19612319)	1135	15070	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Hybridization	Hyb (Medium) (20636378)	370	9167	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Hybridization	Hyb (Low) (23617335)	1253	2988	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Stringency	String (PM) (32629312)	17170	382	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Stringency	String (MM) (33668307)	2895	136	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non-Specific Binding	NSB (Bgnd) (26619332)	232	183	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	232	133	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	225	194	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	199	130	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non- Polymorphic	NP (A) (34633358)	10640	340	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non- Polymorphic	NP (T) (16648324)	9599	234	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non- Polymorphic	NP (C) (43641328)	434	7995	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Non- Polymorphic	NP (G) (13642359)	427	8767	OK/OK
DEDIVUKO00180 / 200729680112_R02C01	Restoration	Restore (28637363)	256	356	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
DEDIVUKO00180	17	14290540	15592762	2	1302222	614	254,016	