Karyotype Report

Customer sample ID: NP0106-5, 20
Internal sample ID: DE66DIVUKOD100185
Date of receipt: 2017-03-01

Gender
Stated: Unstated
Chr. X derived: Female

Genotype identity with: NP0106 HDF*-17.10.2016 / DEDIVUKO00148, NP0106-34-17.10.2016 / DEDIVUKO00149, NP0106-10-01.02.2017 / DEDIVUKO00182, NP0106-12-01.02.2017 / DEDIVUKO00183

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: 200729680034 R06C01

Batch ID and 96 well position: WG1001271-MSA1 F06

Call rate: 0,997

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: 2017-03-22-2327

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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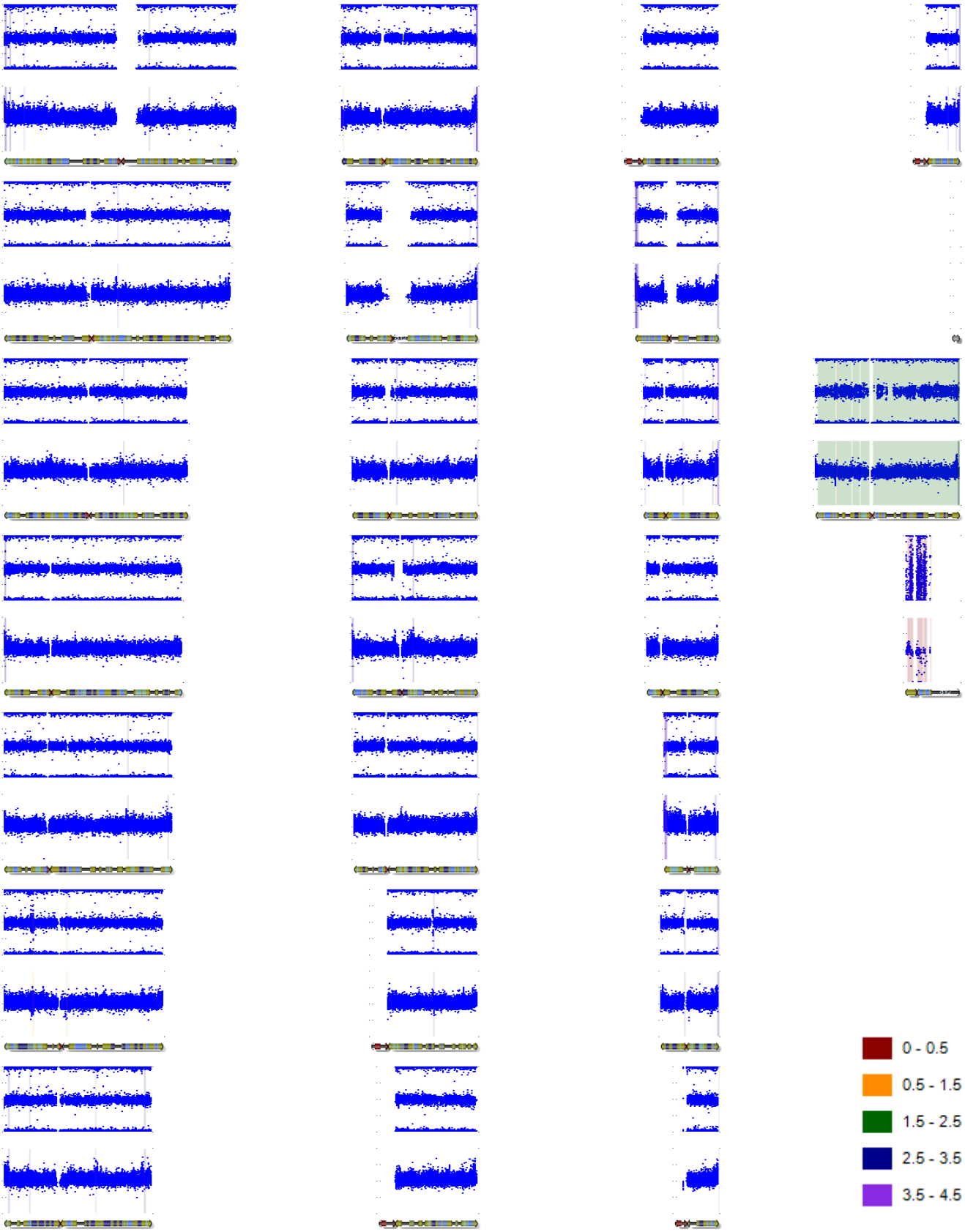
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00185 / 200729680034_R06C01	Staining	DNP (High) (27630314)	32197	288	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Staining	DNP (Bgnd) (29619375)	404	197	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Staining	Biotin (High) (41666334)	470	15595	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Staining	Biotin (Bgnd) (34648333)	266	336	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Extension	Extension (A) (17616306)	38922	370	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Extension	Extension (T) (14607337)	41762	254	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Extension	Extension (C) (12613307)	1515	25924	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Extension	Extension (G) (11603365)	2175	25677	Notable/OK
DEDIVUKO00185 / 200729680034_R06C01	Target Removal	Target Removal (31623323)	1008	180	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Hybridization	Hyb (High) (19612319)	1937	24613	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Hybridization	Hyb (Medium) (20636378)	498	15824	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Hybridization	Hyb (Low) (23617335)	2111	4871	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Stringency	String (PM) (32629312)	25350	443	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Stringency	String (MM) (33668307)	4630	155	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Specific Binding	NSB (Bgnd) (26619332)	400	157	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Specific Binding	NSB (Bgnd) (27624356)	374	179	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Specific Binding	NSB (Bgnd) (25617343)	402	244	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Specific Binding	NSB (Bgnd) (24616350)	316	99	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Polymorphic	NP (A) (34633358)	17322	331	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Polymorphic	NP (T) (16648324)	16192	287	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Polymorphic	NP (C) (43641328)	711	15310	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Non-Polymorphic	NP (G) (13642359)	783	14849	OK/OK
DEDIVUKO00185 / 200729680034_R06C01	Restoration	Restore (28637363)	381	371	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
DEDIVUKO00185	13	67141362	68471414	3	1330052	318	897,5023	