Karyotype Report

Customer sample ID: NP0106-10, 12+5
Internal sample ID: DE50DIVUKOD100182
Date of receipt: 2017-02-01

Gender
Stated: Unknown
Chr. X derived: Female

Genotype identity with: NP0106 HDF*-17.10.2016 / DEDIVUKO00148, NP0106-34-17.10.2016 / DEDIVUKO00149, NP0106-12-01.02.2017 / DEDIVUKO00183, NP0106-5-01.03.2017 / DEDIVUKO00185

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 R04C01

Batch ID and 96 well position: WG0086079-MSA1 D01

Call rate: 0,998

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: 2017-02-09-0434

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

Chr10: 3Mbp large duplication mosaicism on short arm.

Analyst

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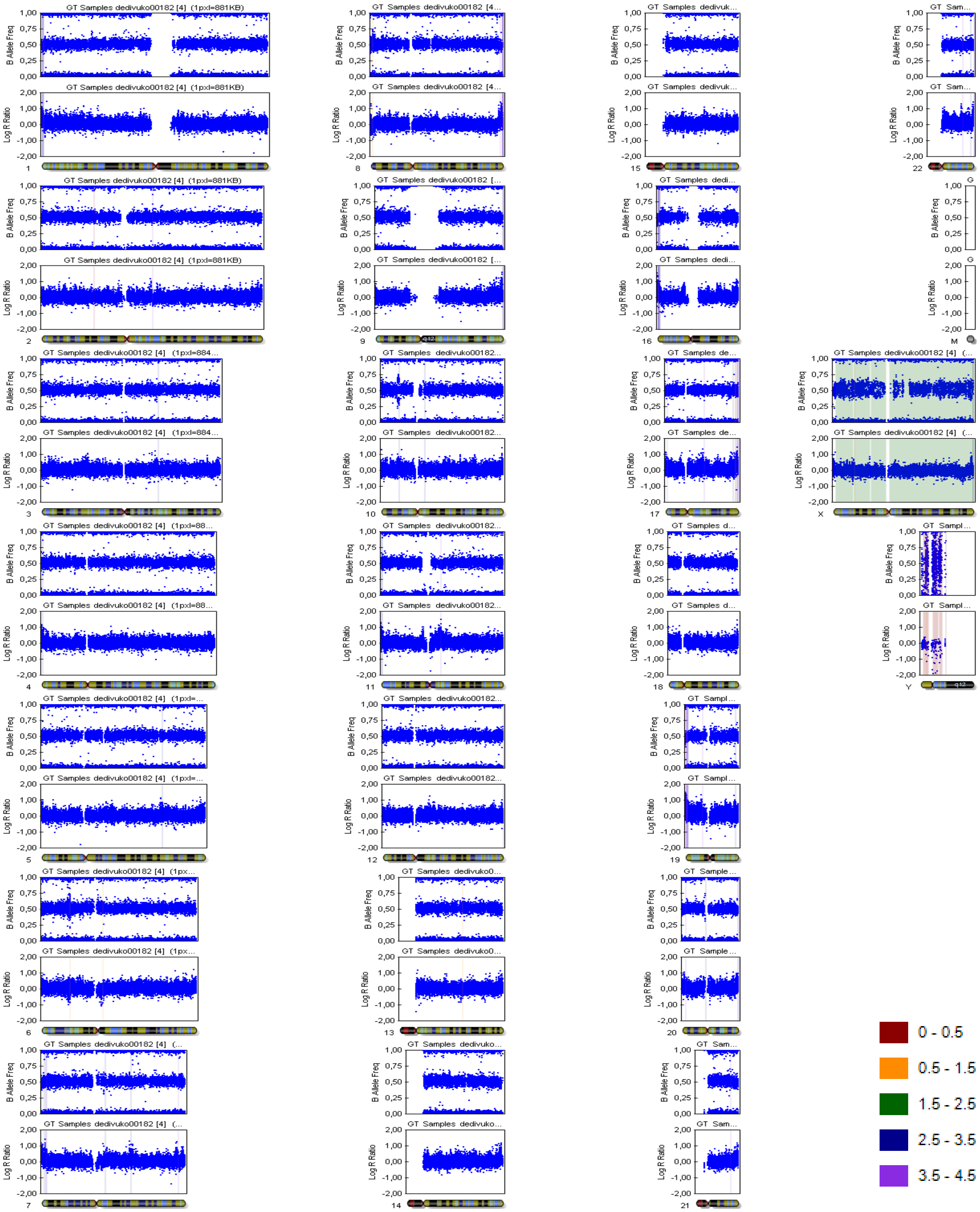
Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00182 / 200729680112_R04C01	Staining	DNP (High) (27630314)	14795	274	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Staining	DNP (Bgnd) (29619375)	392	252	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Staining	Biotin (High) (41666334)	334	7240	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Staining	Biotin (Bgnd) (34648333)	282	262	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Extension	Extension (A) (17616306)	31060	390	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Extension	Extension (T) (14607337)	33058	354	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Extension	Extension (C) (12613307)	1102	19466	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Extension	Extension (G) (11603365)	1422	18883	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Target Removal	Target Removal (31623323)	1045	248	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Hybridization	Hyb (High) (19612319)	1372	18106	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Hybridization	Hyb (Medium) (20636378)	528	11246	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Hybridization	Hyb (Low) (23617335)	1664	3395	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Stringency	String (PM) (32629312)	19191	525	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Stringency	String (MM) (33668307)	3582	241	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Specific Binding	NSB (Bgnd) (26619332)	300	185	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Specific Binding	NSB (Bgnd) (27624356)	312	230	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Specific Binding	NSB (Bgnd) (25617343)	285	311	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Specific Binding	NSB (Bgnd) (24616350)	298	231	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Polymorphic	NP (A) (34633358)	11352	414	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Polymorphic	NP (T) (16648324)	11229	305	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Polymorphic	NP (C) (43641328)	521	9931	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Non-Polymorphic	NP (G) (13642359)	577	10406	OK/OK
DEDIVUKO00182 / 200729680112_R04C01	Restoration	Restore (28637363)	308	429	OK/OK

All „Notable“ tagged probes are within specs. The karyogram can be evaluated.

Karyogram


GT Samples dedivuko00182 [4] (1pxl=881KB)
B Allele Freq
Log R Ratio
1,00
0,75
0,50
0,25
0,00
2,00
1,00
0,00
-1,00
-2,00
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y
M
G
q12
🟥 0 - 0.5
🟧 0.5 - 1.5
🟩 1.5 - 2.5
🟦 2.5 - 3.5
🟪 3.5 - 4.5

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
DEDIVUKO00182	10	19724287	21157652	3	1433365	581	1907,086	