

Karyotype Report

Customer sample ID: NP0144-32
Internal sample ID: DE04DIVUKOD100234
Date of receipt: 2018-05-15

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: NP0144-33-2018-05-15 / DEDIVUKO00235, NP0144-41-2018-05-15 / DEDIVUKO00236

Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmni2.5Exome-8 BeadChip v1.3
Manifest file: HumanOmni2-5Exome-8v1-3_A1.bpm
Cluster file: HumanOmni2-5Exome-8v1-3_A1.egt

Chip barcode and segment: 201375320086 R04C01

Batch ID and 96 well position: WG6902506-MSA6 D04

Call rate: 0,9966513

Typing

Scanner: Illumina iScan, S/N: N263
Site of processing: Life&Brain GENOMICS, Bonn, Germany
Manufacturer: Illumina, Inc., San Diego, United States of America
Date of scan: 2018-06-11-0811

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

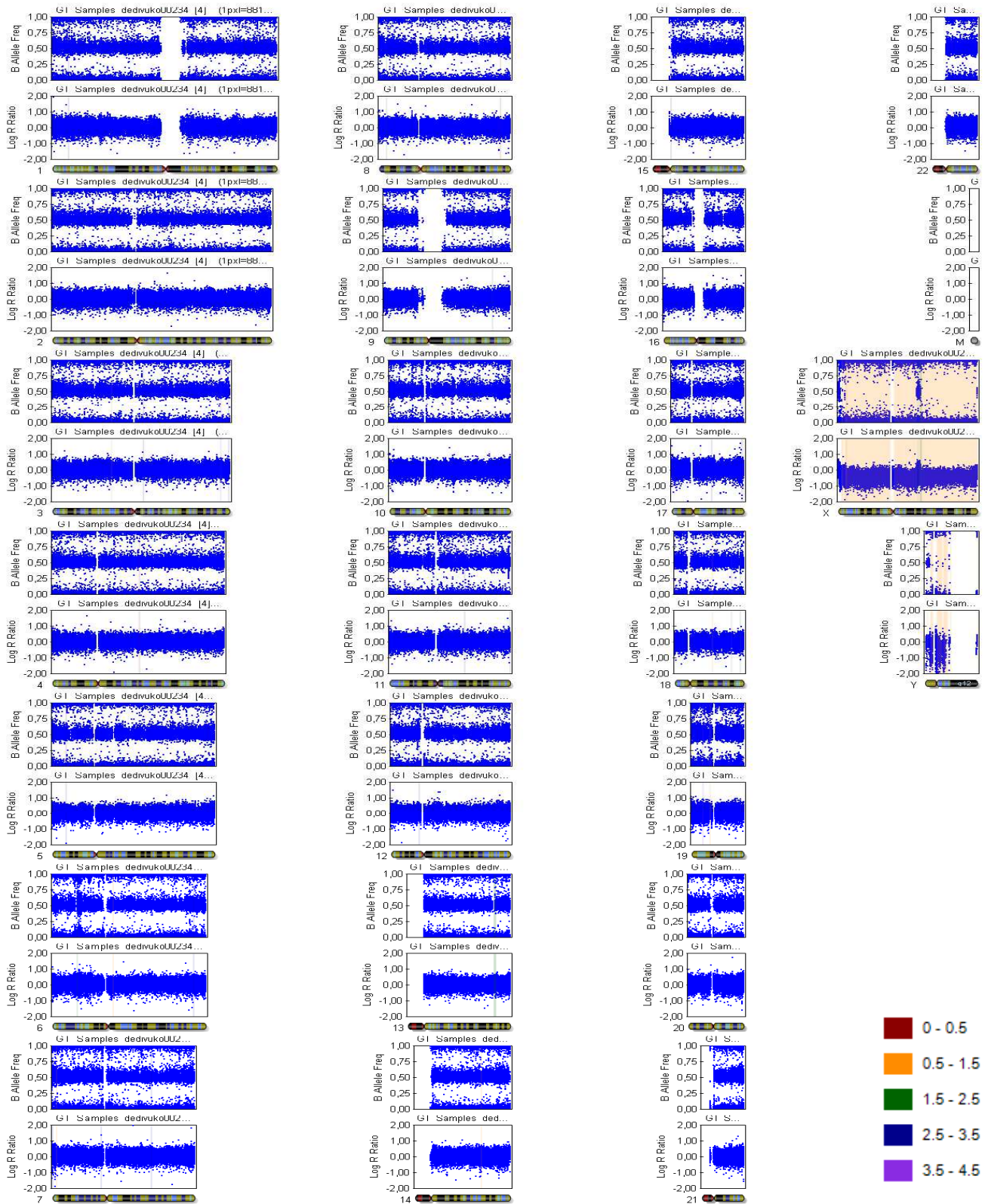
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Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DEDIVUKO00234 / 201375320086_R04C01	Staining	DNP (High) (27630314)	31775	124	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Staining	DNP (Bgnd) (29619375)	284	266	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Staining	Biotin (High) (41666334)	398	17958	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Staining	Biotin (Bgnd) (34648333)	326	104	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Extension	Extension (A) (17616306)	27729	406	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Extension	Extension (T) (14607337)	33040	257	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Extension	Extension (C) (12613307)	861	18853	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Extension	Extension (G) (11603365)	1119	17708	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Target Removal	Target Removal (31623323)	534	182	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Hybridization	Hyb (High) (19612319)	1282	17491	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Hybridization	Hyb (Medium) (20636378)	405	10800	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Hybridization	Hyb (Low) (23617335)	954	3171	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Stringency	String (PM) (32629312)	21086	397	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Stringency	String (MM) (33668307)	7574	265	Notable/OK
DEDIVUKO00234 / 201375320086_R04C01	Non-Specific Binding	NSB (Bgnd) (26619332)	256	156	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non-Specific Binding	NSB (Bgnd) (27624356)	291	190	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non-Specific Binding	NSB (Bgnd) (25617343)	310	207	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non-Specific Binding	NSB (Bgnd) (24616350)	308	177	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non- Polymorphic	NP (A) (34633358)	11105	260	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non- Polymorphic	NP (T) (16648324)	13313	255	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non- Polymorphic	NP (C) (43641328)	568	9731	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Non- Polymorphic	NP (G) (13642359)	550	8565	OK/OK
DEDIVUKO00234 / 201375320086_R04C01	Restoration	Restore (28637363)	255	267	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, 1Mbp for loss of heterozygosity regions.

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
DEDIVUKO00234	6	27011650	28147385	2	1135735	1834	359,4485	
DEDIVUKO00234	11	132897653	133368176	3	470523	570	2056,673	
DEDIVUKO00234	13	95535368	98311810	2	2776442	2583	546,7808	
DEDIVUKO00234	17	44168225	44580136	3	411911	75	81,6752	CNV-CNV: 37, CNV-Complex: 3, CNV-Gain: 14, CNV-Gain+Loss: 4, OTHER-Inversion: 1