Karyotype Report

Customer sample ID: 3A, iPSC-3A-DNA
Internal sample ID: DE95SCRHIHD100033
Date of receipt: 2021-12-06

Gender
Stated: Male
Chr. X derived: Male

Genotype identity: DESCRHIH00032 3 Fibroblast control_3_DNA
DESCRHIH00034 3B iPSC-3B-DNA

Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmni2.5Exome-8 BeadChip v1.5
Manifest file: InfiniumOmni2-5Exome-8v1-5_A1.bpm
Cluster file: InfiniumOmni2-5Exome-8v1-5_A1-Cluster-File.egt

Chip barcode and segment: 204372050076 R08C01

Batch ID and 96 well position: WG6926597-MSA6 H11

Call rate: 0,991304

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: 2021-12-15-2230

Genotype Analysis
Genome Studio: GenomeStudio V2.0.5
Genotyping module: Ver. 2.0.5

Copy Number Analysis
Algorithm applied: CNV-Partition
Version: 3.2.0
Software producer: Illumina, Inc., San Diego, United States of America

Noteworthy findings

No larger chromosomal aberrations observed.

Analyst

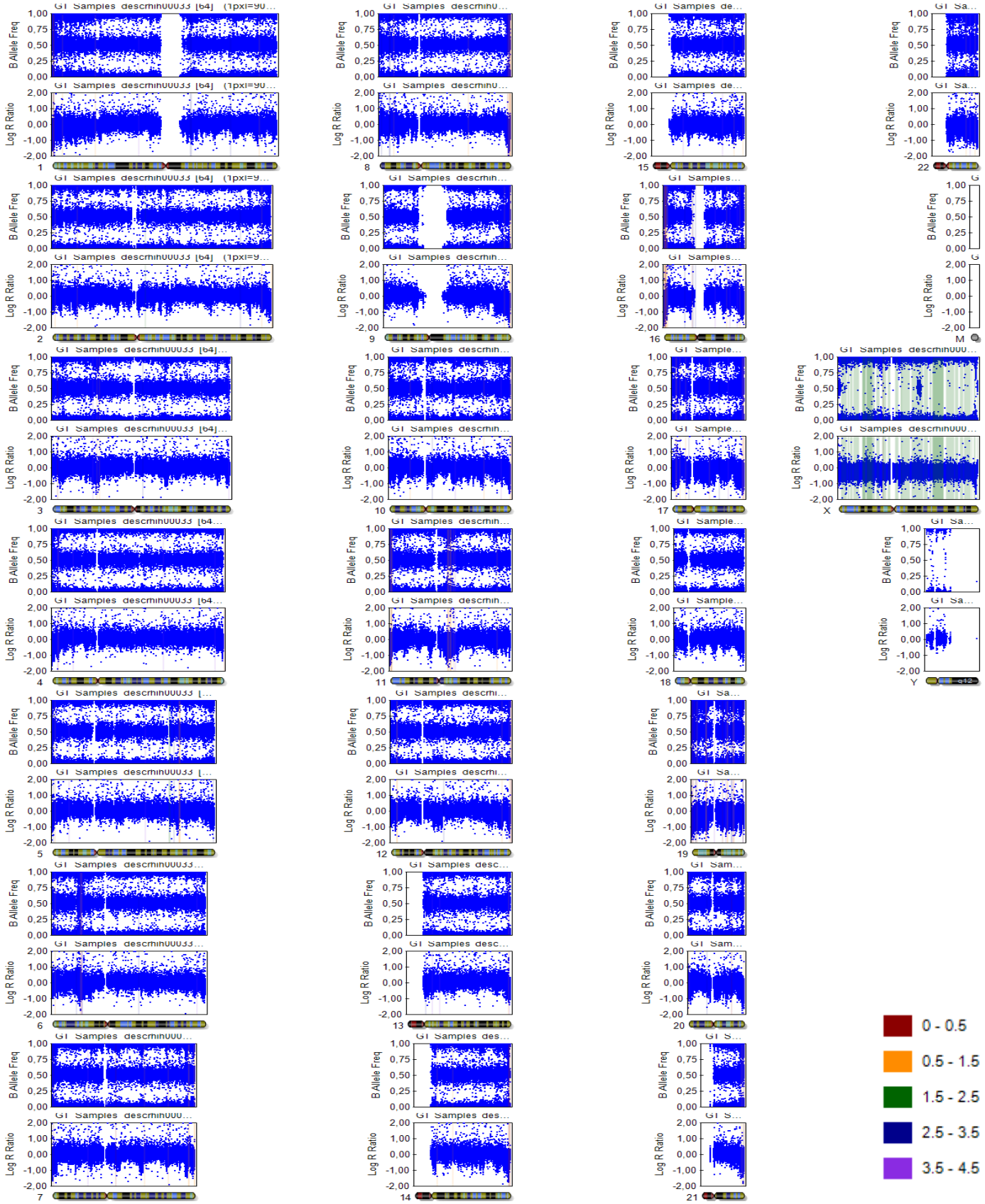
Stefan Herms
sherms@lifeandbrain.com
Tel.: +49 228 6885 411

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRHIH00033 / 204372050076_R08C01	Staining	DNP (High) (27630314)	35931	87	OK/ OK
DESCRHIH00033 / 204372050076_R08C01	Staining	DNP (Bgnd) (43603326)	572	297	Notable/ Notable
DESCRHIH00033 / 204372050076_R08C01	Staining	Biotin (High) (41666334)	692	22260	OK/ OK
DESCRHIH00033 / 204372050076_R08C01	Staining	Biotin (Bgnd) (34648333)	517	89	Notable/ OK
DESCRHIH00033 / 204372050076_R08C01	Extension	Extension (A) (17616306)	31545	447	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Extension	Extension (T) (14607337)	33553	400	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Extension	Extension (C) (12613307)	1530	21584	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Extension	Extension (G) (11603365)	1867	21340	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Target Removal	Target Removal (31623323)	965	191	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Hybridization	Hyb (High) (19612319)	1596	21043	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Hybridization	Hyb (Medium) (20636378)	725	13957	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Hybridization	Hyb (Low) (23617335)	1539	4240	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Stringency	String (PM) (32629312)	23749	469	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Stringency	String (MM) (33668307)	10741	286	Notable/ OK
DESCRHIH00033 / 204372050076_R08C01	Non-Specific Binding	NSB (Bgnd) (28637363)	544	256	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Specific Binding	NSB (Bgnd) (27624356)	487	168	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Specific Binding	NSB (Bgnd) (25617343)	480	187	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Specific Binding	NSB (Bgnd) (24616350)	512	158	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Polymorphic	NP(A) (34633358)	9877	254	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Polymorphic	NP(T) (16648324)	16367	347	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Polymorphic	NP(C) (43641328)	882	10909	OK/OK
DESCRHIH00033 / 204372050076_R08C01	Non-Polymorphic	NP(G) (13642359)	821	9964	OK/OK

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

Karyogram



DESCRHIH00033
3A - iPSC-3A-DNA

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
DESCRHIH00033	2	102235949	103309025	2	1073076	1038	238,1352	
DESCRHIH00033	4	190156968	190731392	1	574424	496	470,1957	CNV-Gain: 1, CNV-Gain+Loss: 1, CNV-Loss: 2
DESCRHIH00033	5	129297802	131894046	2	2596244	1634	310,8454	
DESCRHIH00033	16	32379046	33052685	3	673639	73	88,9427	CNV-: 1, CNV-CNV: 42, CNV-Complex: 4, CNV-Gain: 61, CNV-Gain+Loss: 2, CNV-Loss: 9