

Karyotype Report

Customer sample ID: 2A, iPSC-2A-DNA
Internal sample ID: DE79SCRHIHD100030
Date of receipt: 2021-12-06

Gender

Stated: Male
Chr. X derived: Male

Genotype identity: DESCRHIH00029 2 Fibroblast control_2_DNA
DESCRHIH00031 2B iPSC-2B-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 R05C01

Batch ID and 96 well position: WG6926597-MSA6 E11

Call rate: 0,9927381

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: 2021-12-15-2221

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

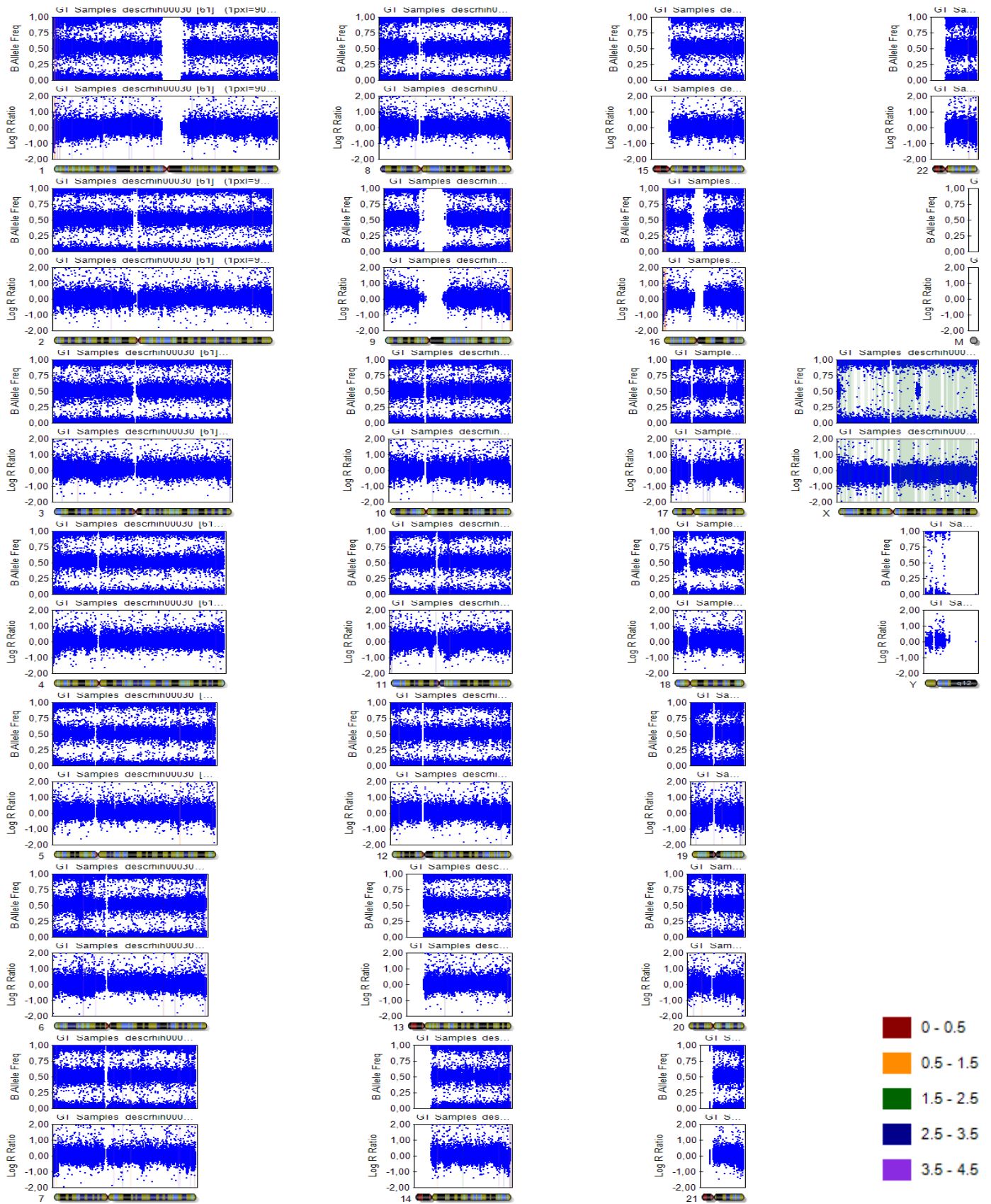
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Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRHH00030 / 204372050076_R05C01	Staining	DNP (High) (27630314)	31846	55	OK/OK
DESCRHH00030 / 204372050076_R05C01	Staining	DNP (Bgnd) (43603326)	369	106	Notable/ Notable
DESCRHH00030 / 204372050076_R05C01	Staining	Biotin (High) (41666334)	567	15537	OK/OK
DESCRHH00030 / 204372050076_R05C01	Staining	Biotin (Bgnd) (34648333)	317	69	OK/OK
DESCRHH00030 / 204372050076_R05C01	Extension	Extension (A) (17616306)	30393	382	OK/OK
DESCRHH00030 / 204372050076_R05C01	Extension	Extension (T) (14607337)	31488	279	OK/OK
DESCRHH00030 / 204372050076_R05C01	Extension	Extension (C) (12613307)	1462	15963	OK/OK
DESCRHH00030 / 204372050076_R05C01	Extension	Extension (G) (11603365)	1776	16210	OK/OK
DESCRHH00030 / 204372050076_R05C01	Target Removal	Target Removal (31623323)	925	144	OK/OK
DESCRHH00030 / 204372050076_R05C01	Hybridization	Hyb (High) (19612319)	1554	15096	OK/OK
DESCRHH00030 / 204372050076_R05C01	Hybridization	Hyb (Medium) (20636378)	719	9857	OK/OK
DESCRHH00030 / 204372050076_R05C01	Hybridization	Hyb (Low) (23617335)	1333	3334	OK/OK
DESCRHH00030 / 204372050076_R05C01	Stringency	String (PM) (32629312)	21336	396	OK/OK
DESCRHH00030 / 204372050076_R05C01	Stringency	String (MM) (33668307)	10647	230	Notable/ OK
DESCRHH00030 / 204372050076_R05C01	Non-Specific Binding	NSB (Bgnd) (28637363)	484	245	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non-Specific Binding	NSB (Bgnd) (27624356)	552	113	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non-Specific Binding	NSB (Bgnd) (25617343)	532	139	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non-Specific Binding	NSB (Bgnd) (24616350)	552	178	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non- Polymorphic	NP(A) (34633358)	11318	272	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non- Polymorphic	NP(T) (16648324)	14365	299	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non- Polymorphic	NP(C) (43641328)	850	8213	OK/OK
DESCRHH00030 / 204372050076_R05C01	Non- Polymorphic	NP(G) (13642359)	810	7384	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
DESCRHIH00030	10	47000426	47375657	3	375231	76	72,6489	CNV-CNV: 241, CNV-Complex: 6, CNV-Deletion: 1, CNV-Gain: 159, CNV-Gain+Loss: 3, CNV-Loss: 156, OTHER-: 1, OTHER-Inversion: 5
DESCRHIH00030	11	50152718	50780580	3	627862	227	1024,775	CNV-Gain: 1, CNV-Gain+Loss: 1
DESCRHIH00030	14	52756283	54162101	2	1405818	1080	291,0912	