

Karyotype Report

Customer sample ID: iPS-CO-22_2.1
Internal sample ID: DE04SCRHIHD100022
Date of receipt: 2020-02-26

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: DESCRHIH00023

Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmni2.5Exome-8 BeadChip v1.4
Manifest file: HumanOmni2-5Exome-8v1-4_A1.bpm
Cluster file: HumanOmni2-5Exome-8v1-4_A1.egt

Chip barcode and segment: 203730650093 R02C01

Batch ID and 96 well position: WG6911135-MSA6 B05

Call rate: 0,9976248

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: 2020-03-31-1456

Genotype Analysis

Genome Studio: GenomeStudio V2.0.4
Genotyping module: Ver. 2.0.4

Copy Number Analysis

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

Noteworthy findings

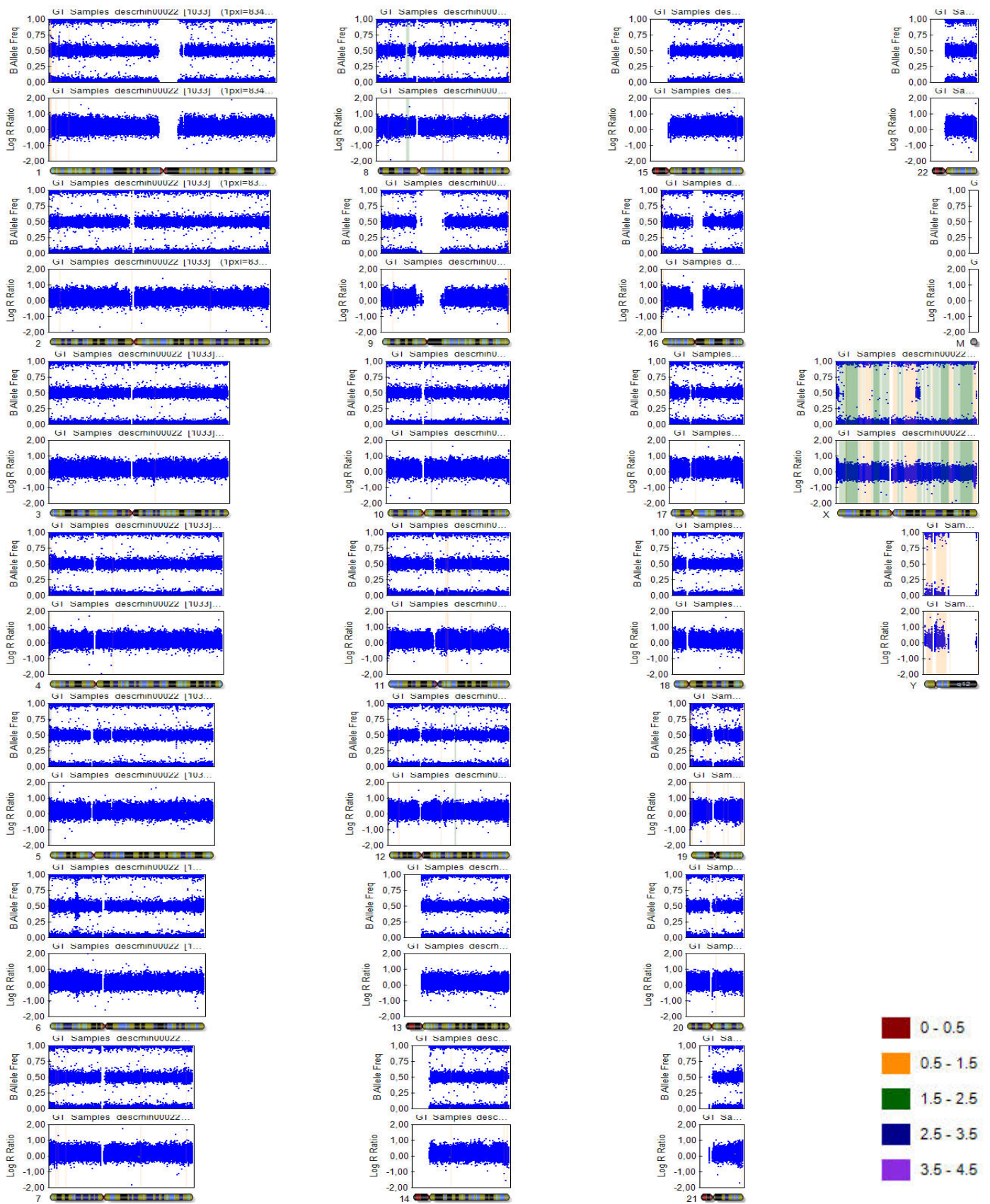
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRHIH00022 / 203730650093_R02C01	Staining	DNP (High) (27630314)	20239	110	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Staining	DNP (Bgnd) (29619375)	261	211	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Staining	Biotin (High) (41666334)	287	9696	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Staining	Biotin (Bgnd) (34648333)	220	84	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Extension	Extension (A) (17616306)	17544	294	Notable/OK
DESCRHIH00022 / 203730650093_R02C01	Extension	Extension (T) (14607337)	19510	257	Notable/OK
DESCRHIH00022 / 203730650093_R02C01	Extension	Extension (C) (12613307)	731	10601	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Extension	Extension (G) (11603365)	821	9764	OK/Notable
DESCRHIH00022 / 203730650093_R02C01	Target Removal	Target Removal (31623323)	486	206	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Hybridization	Hyb (High) (19612319)	1167	10813	OK/Notable
DESCRHIH00022 / 203730650093_R02C01	Hybridization	Hyb (Medium) (20636378)	349	6851	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Hybridization	Hyb (Low) (23617335)	982	2204	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Stringency	String (PM) (32629312)	12362	284	Notable/OK
DESCRHIH00022 / 203730650093_R02C01	Stringency	String (MM) (33668307)	2315	182	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non-Specific Binding	NSB (Bgnd) (26619332)	240	190	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	223	186	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	241	192	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	264	190	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non- Polymorphic	NP (A) (34633358)	6289	247	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non- Polymorphic	NP (T) (16648324)	8394	246	OK/OK
DESCRHIH00022 / 203730650093_R02C01	Non- Polymorphic	NP (C) (43641328)	448	5688	OK/Notable
DESCRHIH00022 / 203730650093_R02C01	Non- Polymorphic	NP (G) (13642359)	472	5285	OK/Notable
DESCRHIH00022 / 203730650093_R02C01	Restoration	Restore (28637363)	273	212	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
DESCRHIH00022	8	31781189	35324420	2	3543231	2334	455,1505	
DESCRHIH00022	12	72825139	74758965	2	1933826	1162	235,608	

Karyotype Report

Customer sample ID: 27_iPS-CO-57cl.B.1
Internal sample ID: DE86SCRDZND100143
Date of receipt: 26.07.2018

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: 28_F-CO-57-2018-07-26 / DESCRDZN00144

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: 201364830139 R03C01

Batch ID and 96 well position: WG6906661-MSA6 C04

Call rate: 0,9981163

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: 2018-08-01-2310

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

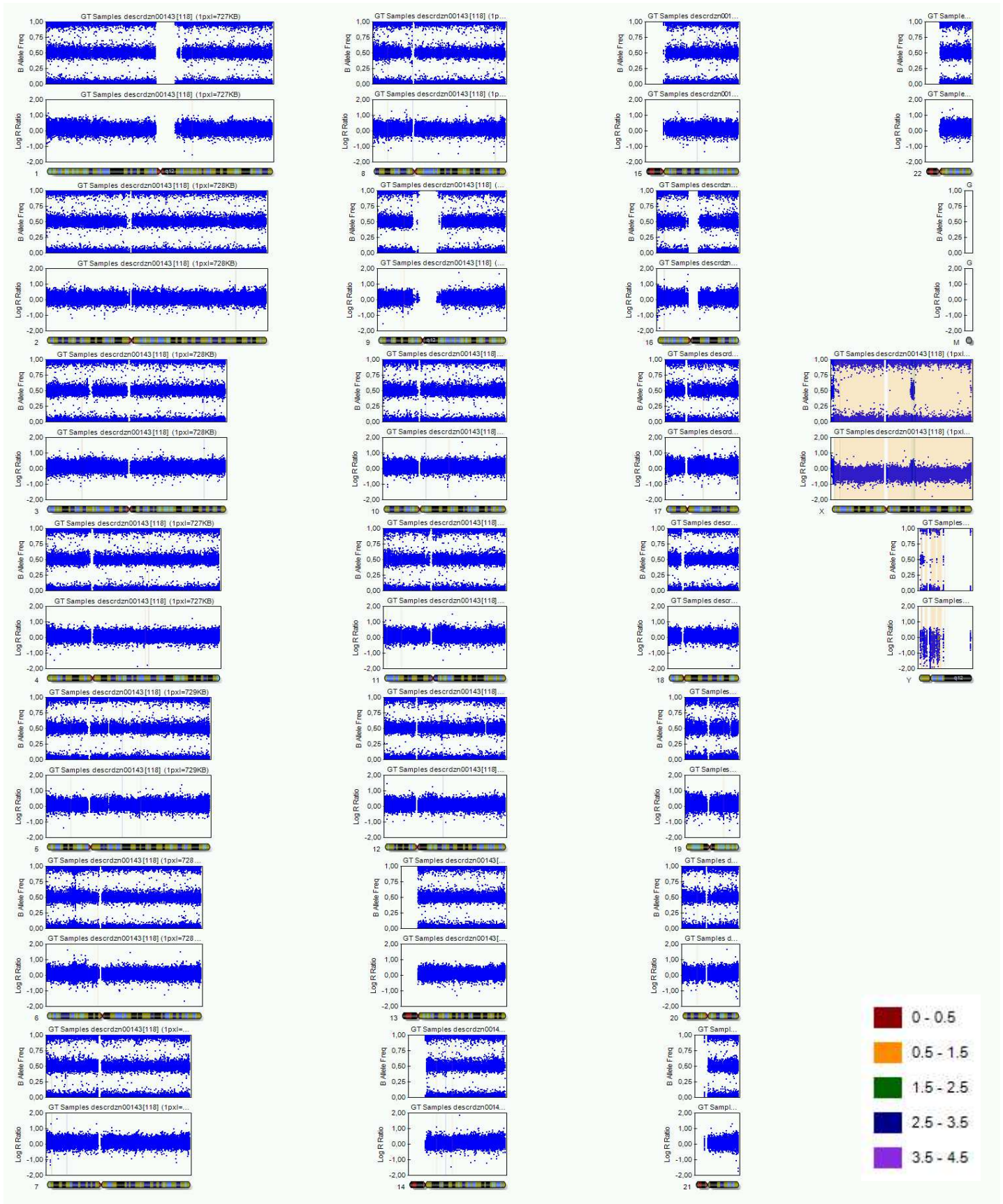
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRDZN00143 / 201364830139_R03C01	Staining	DNP (High) (27630314)	27305	137	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Staining	DNP (Bgnd) (29619375)	387	223	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Staining	Biotin (High) (41666334)	486	12740	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Staining	Biotin (Bgnd) (34648333)	374	100	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Extension	Extension (A) (17616306)	27672	396	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Extension	Extension (T) (14607337)	30291	315	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Extension	Extension (C) (12613307)	1063	13549	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Extension	Extension (G) (11603365)	1345	13010	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Target Removal	Target Removal (31623323)	677	179	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Hybridization	Hyb (High) (19612319)	1329	12828	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Hybridization	Hyb (Medium) (20636378)	550	7772	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Hybridization	Hyb (Low) (23617335)	1251	2588	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Stringency	String (PM) (32629312)	17938	361	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Stringency	String (MM) (33668307)	4743	270	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non-Specific Binding	NSB (Bgnd) (26619332)	365	166	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non-Specific Binding	NSB (Bgnd) (27624356)	350	164	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non-Specific Binding	NSB (Bgnd) (25617343)	347	185	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non-Specific Binding	NSB (Bgnd) (24616350)	380	156	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non- Polymorphic	NP (A) (34633358)	9101	296	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non- Polymorphic	NP (T) (16648324)	11388	240	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non- Polymorphic	NP (C) (43641328)	619	6573	OK/OK
DESCRDZN00143 / 201364830139_R03C01	Non- Polymorphic	NP (G) (13642359)	517	5944	OK/Notable
DESCRDZN00143 / 201364830139_R03C01	Restoration	Restore (28637363)	371	197	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
DESCRDZN00143	8	43057452	43806224	3	748772	361	427,1952	

Karyotype Report

Customer sample ID: iPS-CO-60_4.3
Internal sample ID: DE47SCRHIHD100024
Date of receipt: 2020-02-26

Gender

Stated: Unknown
Chr. X derived: Male

Genotype identity with: DESCRHIH00025

Karyotyping

Technology used: Illumina BeadArray

Product: HumanOmni2.5Exome-8 BeadChip v1.4
Manifest file: HumanOmni2-5Exome-8v1-4_A1.bpm
Cluster file: HumanOmni2-5Exome-8v1-4_A1.egt

Chip barcode and segment: 203730650093 R04C01

Batch ID and 96 well position: WG6911135-MSA6 D05

Call rate: 0,997606

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: 2020-03-31-1503

Genotype Analysis

Genome Studio: GenomeStudio V2.0.4
Genotyping module: Ver. 2.0.4

Copy Number Analysis

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

Noteworthy findings

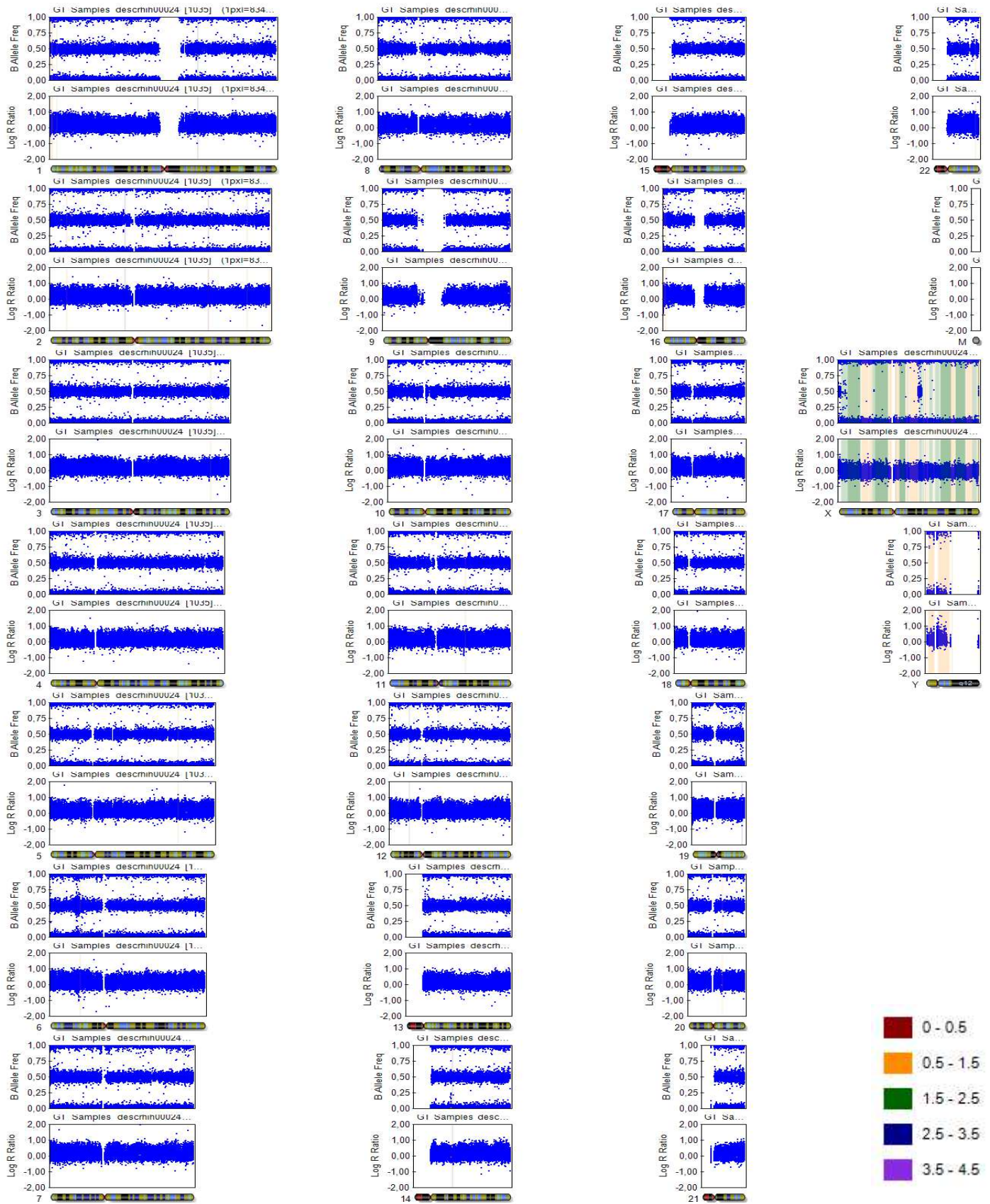
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentrix_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRHIH00024 / 203730650093_R04C01	Staining	DNP (High) (27630314)	21958	137	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Staining	DNP (Bgnd) (29619375)	344	203	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Staining	Biotin (High) (41666334)	321	12082	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Staining	Biotin (Bgnd) (34648333)	247	110	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Extension	Extension (A) (17616306)	20971	373	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Extension	Extension (T) (14607337)	23411	283	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Extension	Extension (C) (12613307)	878	12869	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Extension	Extension (G) (11603365)	959	12222	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Target Removal	Target Removal (31623323)	598	252	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Hybridization	Hyb (High) (19612319)	1366	13100	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Hybridization	Hyb (Medium) (20636378)	384	8349	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Hybridization	Hyb (Low) (23617335)	1176	2737	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Stringency	String (PM) (32629312)	14996	379	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Stringency	String (MM) (33668307)	3141	269	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non-Specific Binding	NSB (Bgnd) (26619332)	313	201	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non-Specific Binding	NSB (Bgnd) (27624356)	324	197	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non-Specific Binding	NSB (Bgnd) (25617343)	299	228	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non-Specific Binding	NSB (Bgnd) (24616350)	296	226	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non- Polymorphic	NP (A) (34633358)	7804	266	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non- Polymorphic	NP (T) (16648324)	9916	297	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non- Polymorphic	NP (C) (43641328)	522	7149	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Non- Polymorphic	NP (G) (13642359)	537	6188	OK/OK
DESCRHIH00024 / 203730650093_R04C01	Restoration	Restore (28637363)	363	206	OK/OK

All 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
DESCRHIH00024	12	20522796	21680693	2	1157897	1493	342,3974	
DESCRHIH00024	23	2700157	24993887	2	22293730	11958	1481,305	
DESCRHIH00024	23	25000842	33074340	1	8073498	4676	676,9131	
DESCRHIH00024	23	33112111	37029338	1	3917227	1767	289,3273	
DESCRHIH00024	23	37033484	54733713	2	17700229	7686	1490,719	
DESCRHIH00024	23	54736227	58563509	1	3827282	990	70,9988	
DESCRHIH00024	23	61686465	62573853	1	887388	185	146,1671	
DESCRHIH00024	23	63400883	67085251	1	3684368	976	271,2258	CNV-Gain: 1, OTHER-Inversion: 2
DESCRHIH00024	23	67097144	74027649	2	6930505	2957	2351,022	
DESCRHIH00024	23	74031648	76230687	1	2199039	618	66,9812	
DESCRHIH00024	23	76237943	77787620	2	1549677	293	678,5046	
DESCRHIH00024	23	77804801	88440097	1	10635296	4446	1318,529	
DESCRHIH00024	23	88442047	92374313	2	3932266	1160	248,2036	
DESCRHIH00024	23	92547980	94025957	2	1477977	831	1801,044	
DESCRHIH00024	23	94027807	95538643	1	1510836	738	313,9972	
DESCRHIH00024	23	95544051	97068109	2	1524058	763	1833,992	
DESCRHIH00024	23	97074770	99554768	1	2479998	903	165,7551	
DESCRHIH00024	23	99557421	104463794	2	4906373	1423	3124,86	

DESCRHIH00024	23	104464069	106109204	1	1645135	428	164,2652	
DESCRHIH00024	23	106112751	111616869	2	5504118	1301	963,7	
DESCRHIH00024	23	111650324	123584863	2	11934539	2763	1477,011	
DESCRHIH00024	23	123588245	128397152	1	4808907	897	251,0483	
DESCRHIH00024	23	128398819	140002446	2	11603627	2758	1564,544	
DESCRHIH00024	23	140010139	147122830	1	7112691	1731	612,3635	
DESCRHIH00024	23	147158718	152213311	2	5054593	1464	1059,053	
DESCRHIH00024	23	152222116	153282028	1	1059912	385	427,3397	
DESCRHIH00024	23	153698458	154916845	2	1218387	380	825,4448	CNV-Gain: 1, CNV-Gain+Loss: 1
DESCRHIH00024	24	2657176	10082095	1	7424919	728	3551,399	
DESCRHIH00024	24	13133499	24891486	1	11757987	1499	7184,58	

Karyotype Report

Customer sample ID: iPS-PCH-01_3.1_p11
Internal sample ID: DE34SCRDZND100206
Date of receipt: 2021-03-09

Gender

Stated: Unstated
Chr. X derived: Male

Genotype identity with: F-PCH-01_P3-2021-03-09 / DESCRDZN00202,
IPS-PCH-01_2.1_P11-2021-03-09 / DESCRDZN00205

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: 204372050103 R07C01

Batch ID and 96 well position: WG6917121-MSA6 G02

Call rate: 0,9986958

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: 2021-03-17-1200

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

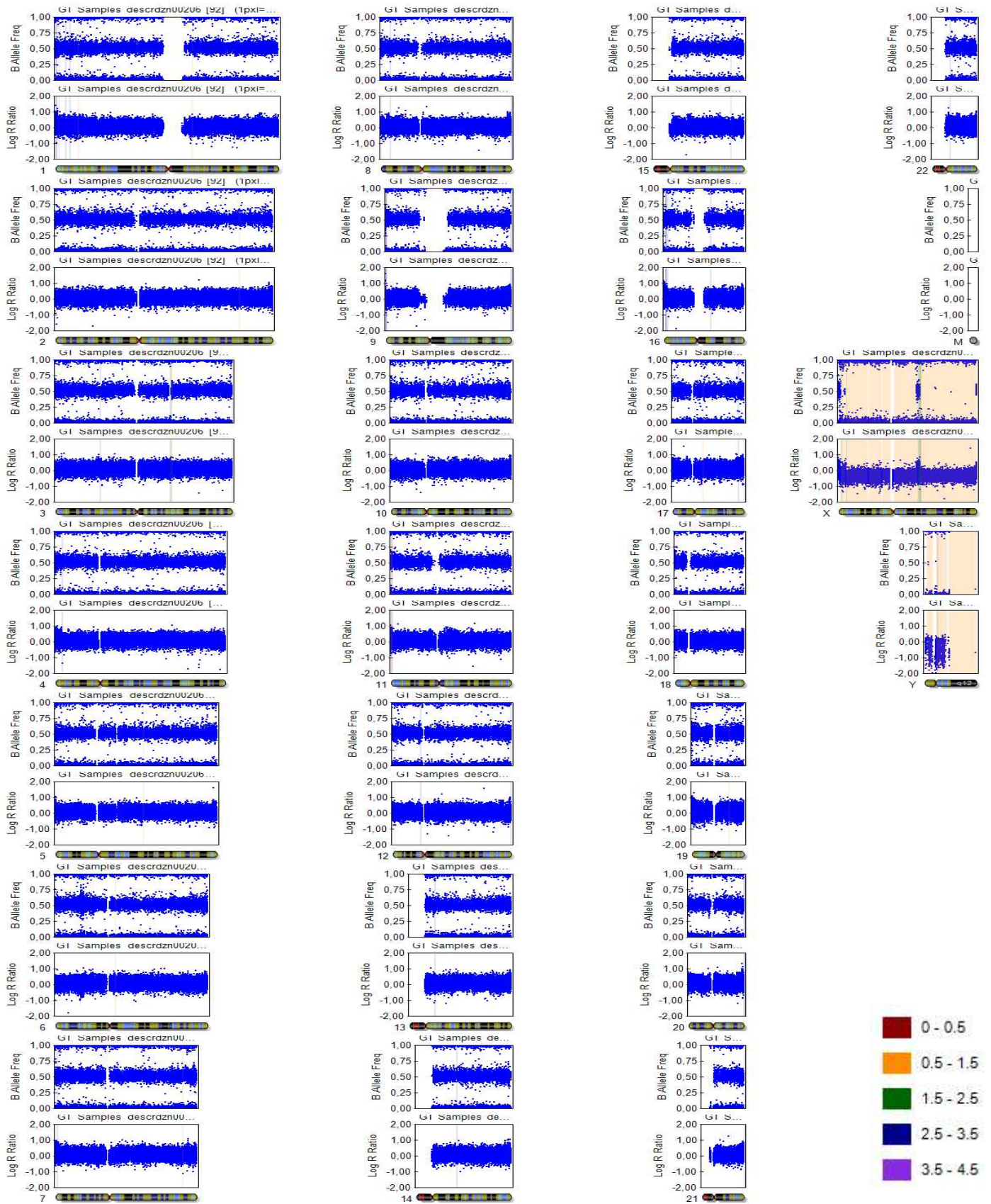
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRDZN00206 / 204372050103_R07C01	Staining	DNP (High) (27630314)	37630	369	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Staining	DNP (Bgnd) (43603326)	710	450	Notable/ Notable
DESCRDZN00206 / 204372050103_R07C01	Staining	Biotin (High) (41666334)	792	20828	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Staining	Biotin (Bgnd) (34648333)	582	355	Notable/OK
DESCRDZN00206 / 204372050103_R07C01	Extension	Extension (A) (17616306)	36574	466	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Extension	Extension (T) (14607337)	37520	410	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Extension	Extension (C) (12613307)	1845	21676	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Extension	Extension (G) (11603365)	2118	21803	Notable/OK
DESCRDZN00206 / 204372050103_R07C01	Target Removal	Target Removal (31623323)	1220	256	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Hybridization	Hyb (High) (19612319)	1778	22924	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Hybridization	Hyb (Medium) (20636378)	771	15775	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Hybridization	Hyb (Low) (23617335)	1949	4464	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Stringency	String (PM) (32629312)	26788	516	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Stringency	String (MM) (33668307)	9148	380	Notable/OK
DESCRDZN00206 / 204372050103_R07C01	Non-Specific Binding	NSB (Bgnd) (28637363)	528	370	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non-Specific Binding	NSB (Bgnd) (27624356)	596	283	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non-Specific Binding	NSB (Bgnd) (25617343)	1828	287	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non-Specific Binding	NSB (Bgnd) (24616350)	558	1113	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non- Polymorphic	NP(A) (34633358)	13152	391	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non- Polymorphic	NP(T) (16648324)	19273	444	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non- Polymorphic	NP(C) (43641328)	901	11699	OK/OK
DESCRDZN00206 / 204372050103_R07C01	Non- Polymorphic	NP(G) (13642359)	932	11048	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
DESCRDZN00206	3	127465894	129762545	2	2296651	1816	283,233	

Karyotype Report

Customer sample ID: iPS-PCH-02_1.7_p10
Internal sample ID: DE07SCRDZND100207
Date of receipt: 2021-03-09

Gender

Stated: Unstated
Chr. X derived: Male

Genotype identity with: F-PCH-02_P5-2021-03-09 / DESCRDZN00203,
IPS-PCH-02_4.1_P11-2021-03-09 / DESCRDZN00208

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: 204372050103 R08C01

Batch ID and 96 well position: WG6917121-MSA6 H02

Call rate: 0,9970004

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: 2021-03-17-1200

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

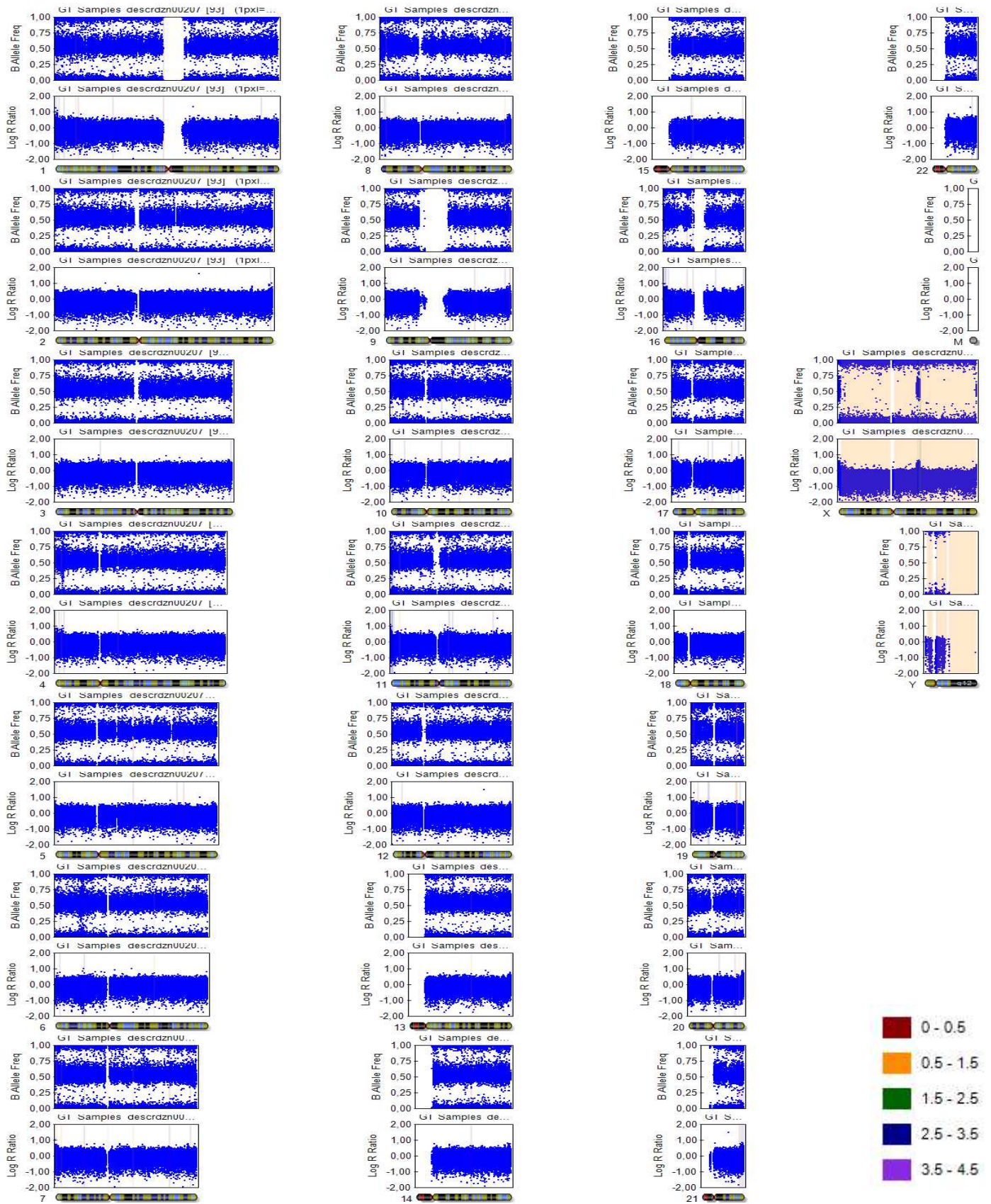
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRDZN00207 / 204372050103_R08C01	Staining	DNP (High) (27630314)	43484	373	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Staining	DNP (Bgnd) (43603326)	813	392	Notable/ Notable
DESCRDZN00207 / 204372050103_R08C01	Staining	Biotin (High) (41666334)	1013	24996	Notable/OK
DESCRDZN00207 / 204372050103_R08C01	Staining	Biotin (Bgnd) (34648333)	743	362	Notable/OK
DESCRDZN00207 / 204372050103_R08C01	Extension	Extension (A) (17616306)	39698	614	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Extension	Extension (T) (14607337)	40283	498	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Extension	Extension (C) (12613307)	1959	25122	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Extension	Extension (G) (11603365)	2321	25291	Notable/OK
DESCRDZN00207 / 204372050103_R08C01	Target Removal	Target Removal (31623323)	1360	398	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Hybridization	Hyb (High) (19612319)	1643	25731	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Hybridization	Hyb (Medium) (20636378)	876	17961	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Hybridization	Hyb (Low) (23617335)	1879	4195	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Stringency	String (PM) (32629312)	28809	621	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Stringency	String (MM) (33668307)	6714	417	Notable/OK
DESCRDZN00207 / 204372050103_R08C01	Non-Specific Binding	NSB (Bgnd) (28637363)	719	402	Notable/OK
DESCRDZN00207 / 204372050103_R08C01	Non-Specific Binding	NSB (Bgnd) (27624356)	691	344	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non-Specific Binding	NSB (Bgnd) (25617343)	661	380	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non-Specific Binding	NSB (Bgnd) (24616350)	699	357	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non- Polymorphic	NP(A) (34633358)	12123	492	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non- Polymorphic	NP(T) (16648324)	19309	448	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non- Polymorphic	NP(C) (43641328)	951	13059	OK/OK
DESCRDZN00207 / 204372050103_R08C01	Non- Polymorphic	NP(G) (13642359)	961	12365	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
DESCRDZN00207	4	9558683	10407505	3	848822	710	2740,706	

Karyotype Report

Customer sample ID: iPS-PCH-03_4.2_p10
Internal sample ID: DE50SCRDZND100209
Date of receipt: 2021-03-09

Gender

Stated: Unstated
Chr. X derived: Male

Genotype identity with: F-PCH-03_P2-2021-03-09 / DESCRDZN00204,
IPS-PCH-03_6.1_P11-2021-03-09 / DESCRDZN00210

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: 204372060010 R02C01

Batch ID and 96 well position: WG6917121-MSA6 B03

Call rate: 0,9982454

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: 2021-03-17-1200

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

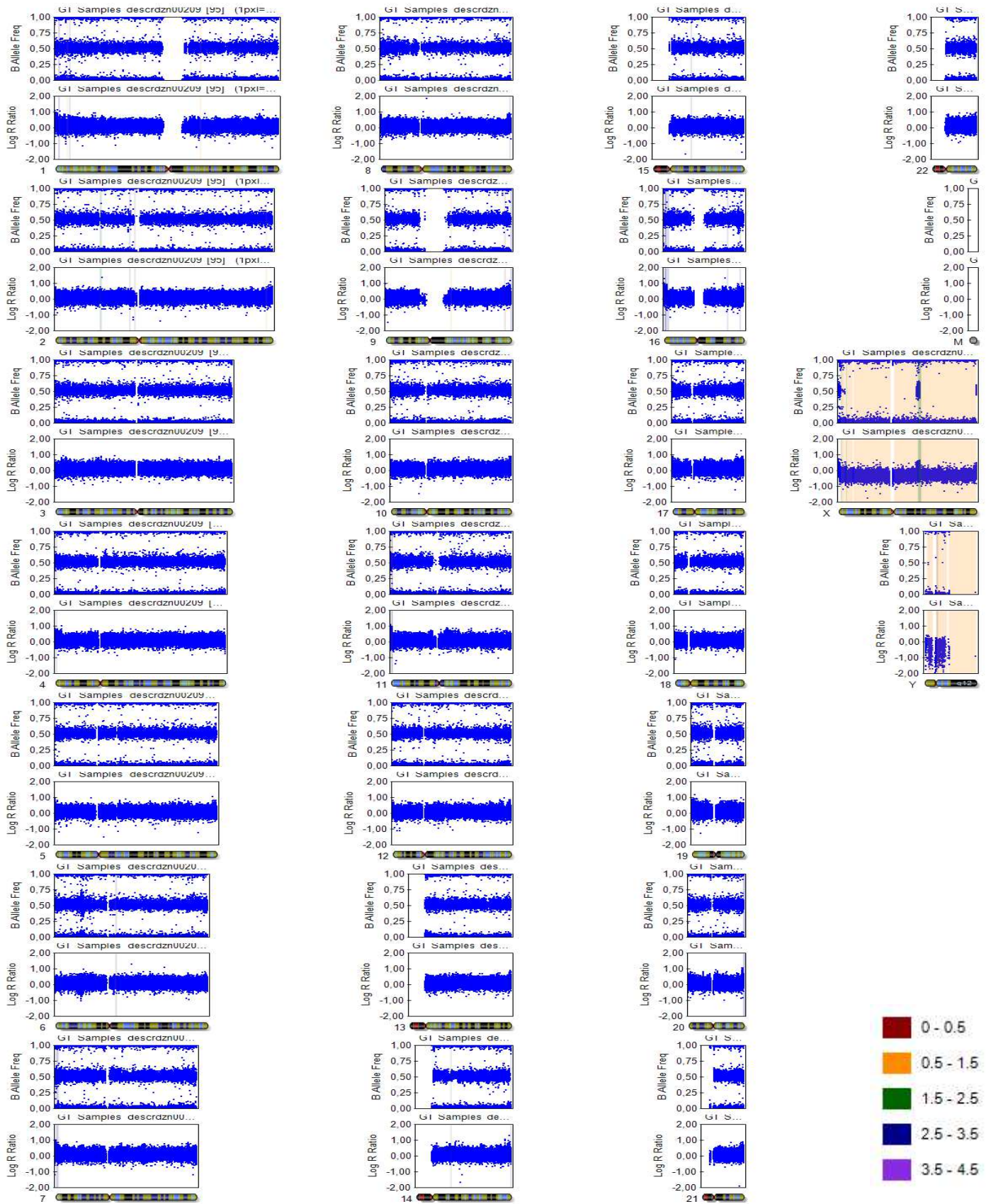
No larger chromosomal aberrations to be reported.

Control Dashboard

Sample_ID / Sentry_Label	Category	Control (BeadType)	Section 1 X	Section 1 Y	State
DESCRDZN00209 / 204372060010_R02C01	Staining	DNP (High) (27630314)	30251	86	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Staining	DNP (Bgnd) (43603326)	339	156	Notable/ Notable
DESCRDZN00209 / 204372060010_R02C01	Staining	Biotin (High) (41666334)	465	11921	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Staining	Biotin (Bgnd) (34648333)	363	141	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Extension	Extension (A) (17616306)	26250	248	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Extension	Extension (T) (14607337)	27511	254	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Extension	Extension (C) (12613307)	1074	12240	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Extension	Extension (G) (11603365)	1331	11312	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Target Removal	Target Removal (31623323)	643	156	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Hybridization	Hyb (High) (19612319)	1131	12010	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Hybridization	Hyb (Medium) (20636378)	414	8273	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Hybridization	Hyb (Low) (23617335)	998	2530	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Stringency	String (PM) (32629312)	18022	296	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Stringency	String (MM) (33668307)	5625	182	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non-Specific Binding	NSB (Bgnd) (28637363)	358	156	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non-Specific Binding	NSB (Bgnd) (27624356)	336	162	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non-Specific Binding	NSB (Bgnd) (25617343)	347	184	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non-Specific Binding	NSB (Bgnd) (24616350)	286	178	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non- Polymorphic	NP(A) (34633358)	8841	256	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non- Polymorphic	NP(T) (16648324)	12595	230	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non- Polymorphic	NP(C) (43641328)	549	6457	OK/OK
DESCRDZN00209 / 204372060010_R02C01	Non- Polymorphic	NP(G) (13642359)	644	6025	OK/OK

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

Karyogram



Copy Number Analysis

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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
DESCRDZN00209	2	49977093	52048553	2	2071460	1910	481,6987	
DESCRDZN00209	14	38487404	40341185	2	1853781	1534	333,2639	