Single Nucleotide Polymorphism (SNP)- Karyotype

	Reference			clone			Clone			clone		
Sample (cell type, ID)	PBMCs	CN01		iPSCs	CN01-cl.1		iPSCs	CN01-cl.2		iPSCs	CN01-cl.3	
Passage No.				3			3			3		
DNA sample ID	D0508			D0534			D0533			D0535		
Chip-ID and Position	206735420118 R05C01			206764550040 R09C02			206764550040 R07C02			206764550040 R11C02		
Date of testing	11.10.2022			09.11.2022			09.11.2022			09.11.2022		
Call Rate	0.9924544		√	0.9924294		√	0.9922350		√	0.9923964		√
Gender (provided/estimated chip data)	Female	Female	√	Female	Female	√	Female	Female	√	Female	Female	√

Patient Disease: Nasu-Hakola-Erkrankung, PLO

Technology: Illumina BeadArray
Product: Illumina Infinium Global Screening Array-24 BeadChip
Manifest: GSAMD-24v3-0-EA_20034606_A1
Clusterfile: GSA-24v3-0_A1_ClusterFile

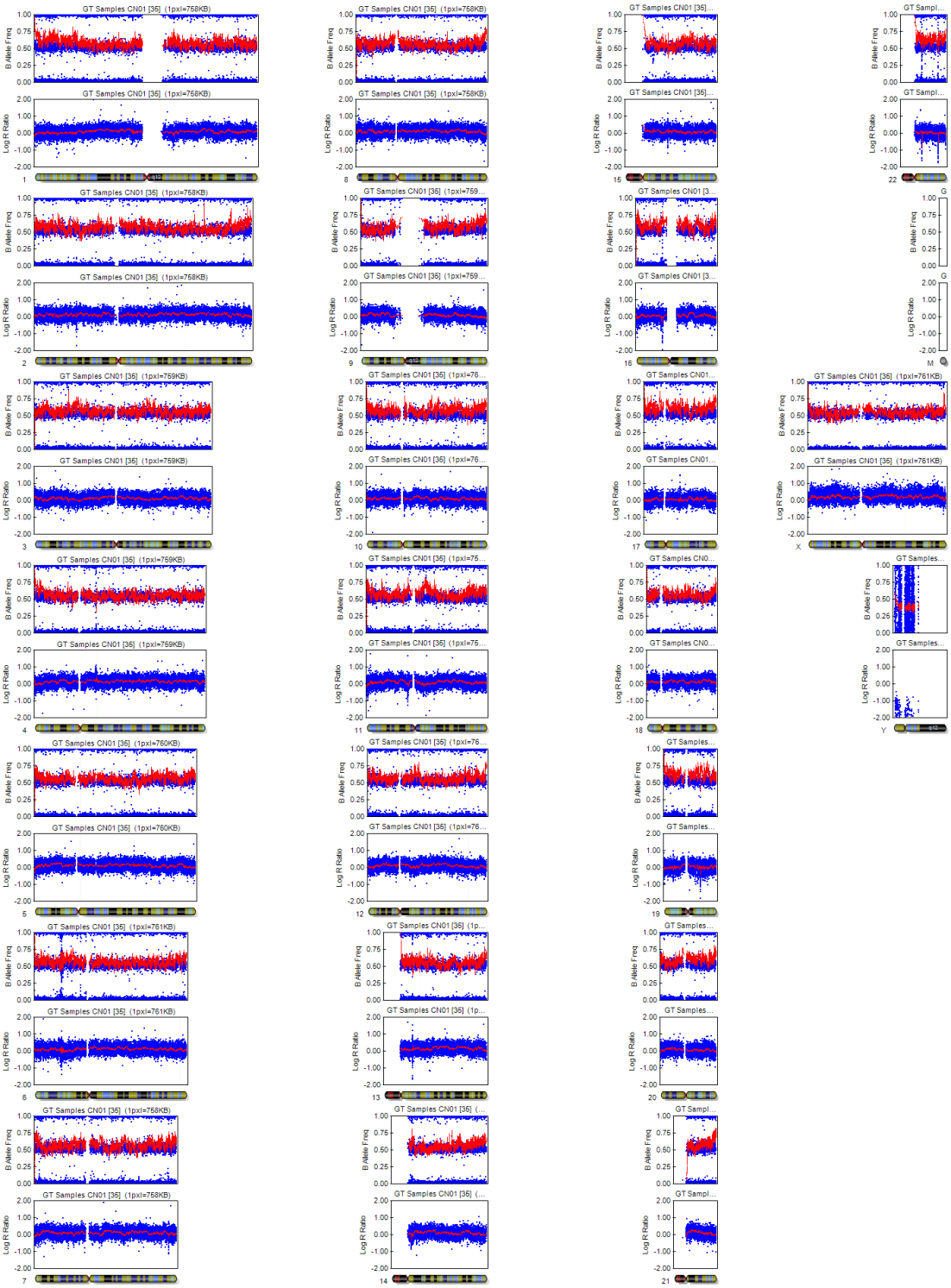
Genotype Analysis
GenomeStudio: GenomeStudio V2.0.5
Genotyping Module: V2.0.5

CNV Analysis
Algorithm: CNV-Partition
Version: 3.2.0

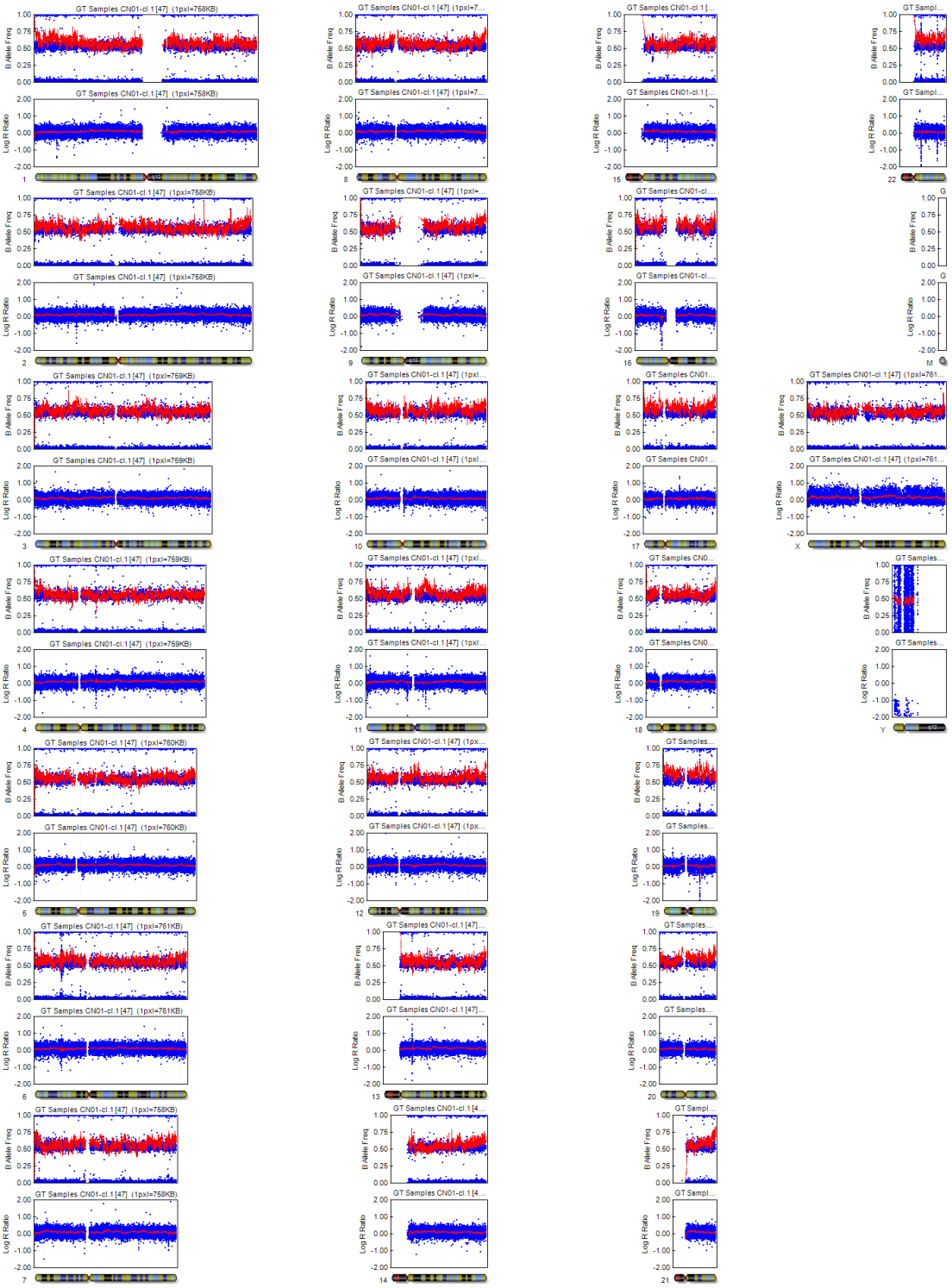
Parameters are set to detect copy number variations (CNVs) ≥ 45 kb and loss of heterozygosity (LOH) regions > 1 Mb with a confidence value > 35. Balanced translocations and inversions cannot be detected with this method. Aberrant copy number regions are identified by log R ratio and B allele frequency. Copy number changes (gains and losses) greater than **0.4 Mb** and regions of LOH above **5 Mb** are considered reportable and taken into account for interpretation. Genomic positions are based on genome build GRCh37/hg19.

If in the tested cell line (compared to the reference) new CNVs greater than **2 Mb** and/or LOH greater than **5 Mb** are detected the CNV QC test has "failed" regarding the internal QC criteria of CUSCO. We recommend not to use a "failed" cell line for further research or only after careful consideration.

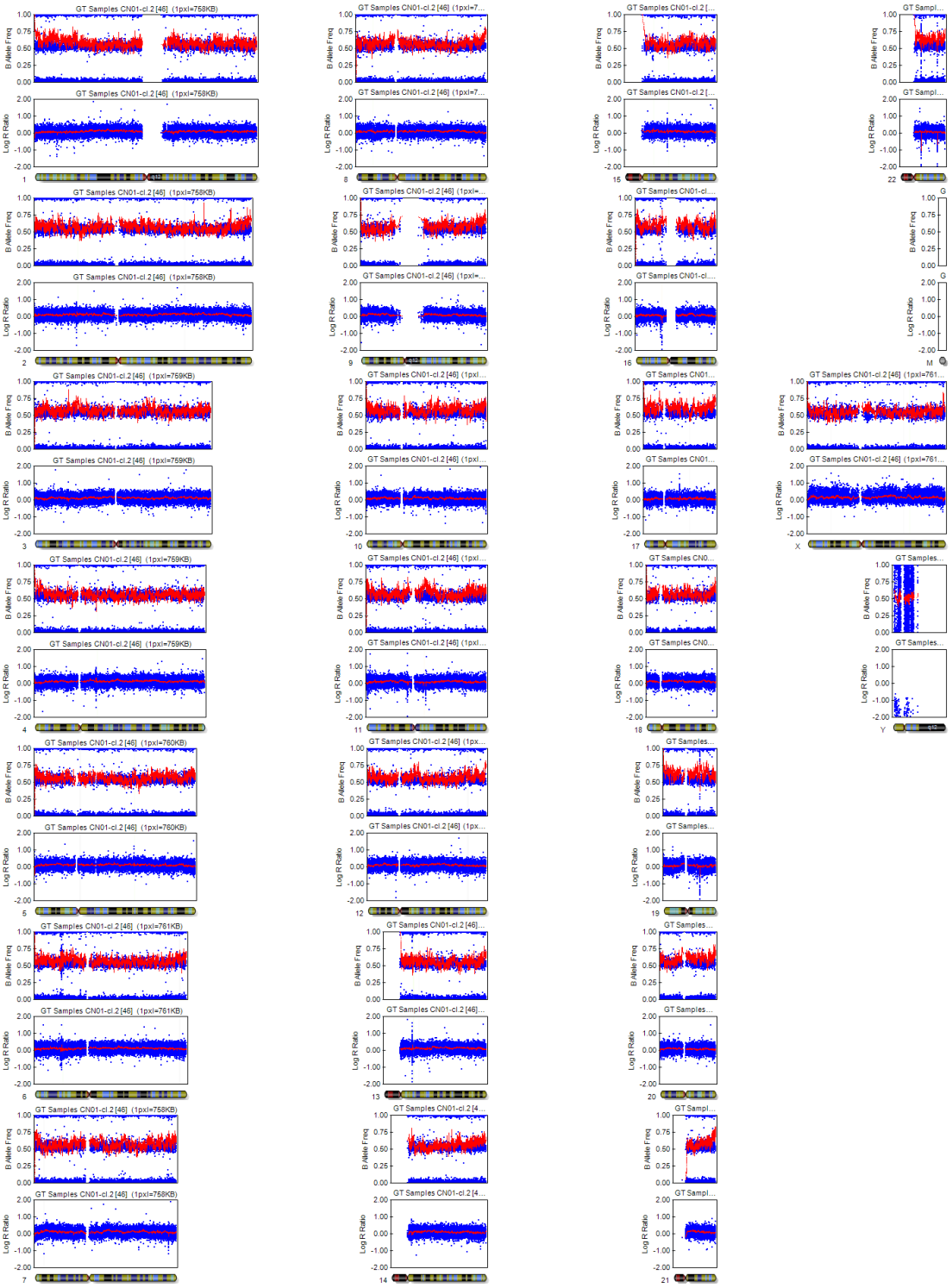
Virtual Karyotype: *CN01*



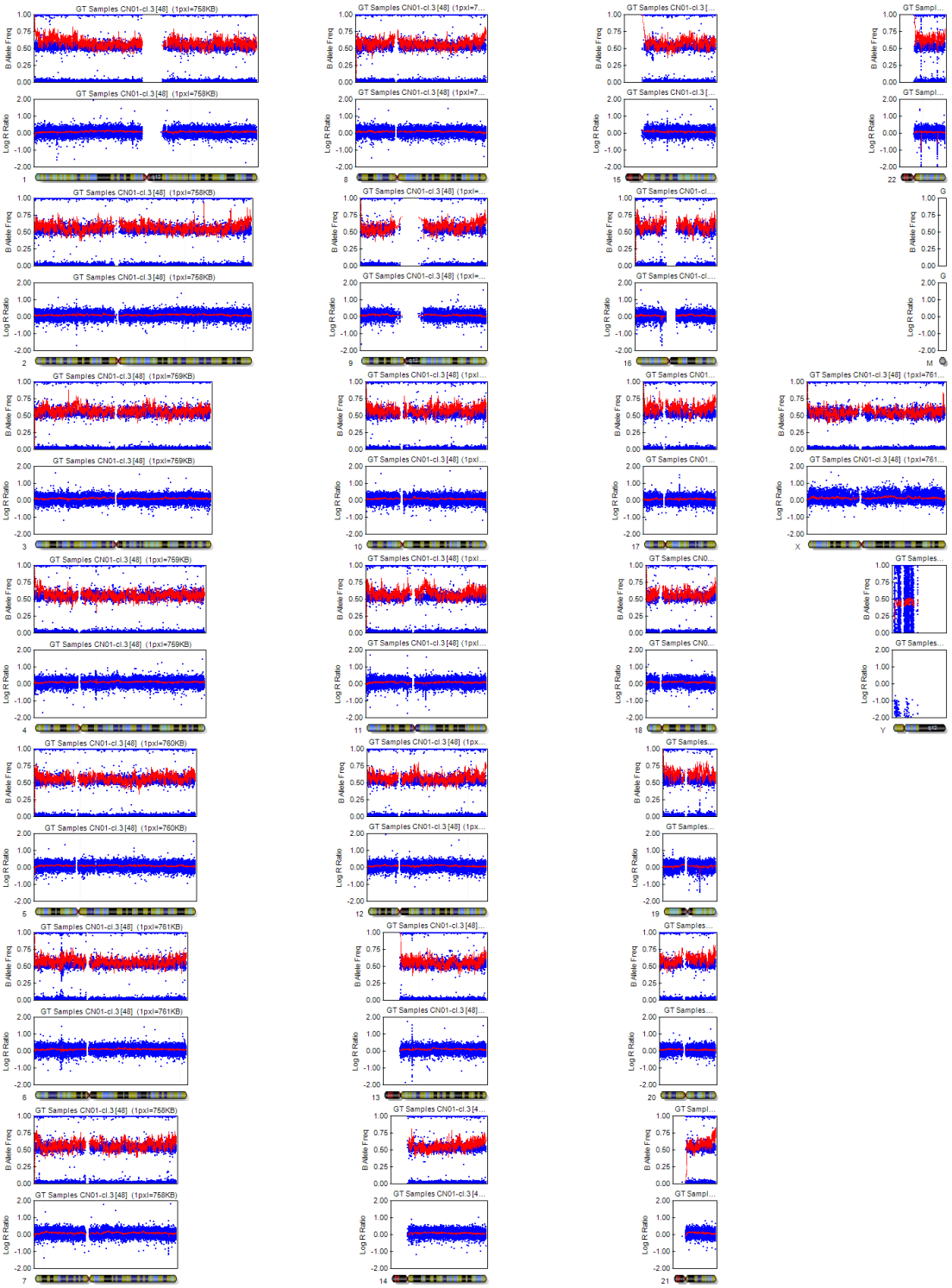
Virtual Karyotype: *CN01-cl.1*



Virtual Karyotype: *CN01-cl.2*



Virtual Karyotype: *CN01-cl.3*



Call Tables

CNV regions common to ***CN01 and cl.1, cl.2 and cl.3***

Chr	Start	End	Size (bp)	CNV Value	Variant Type	Number of Genes*
2	167218502	168530575	1312073	2	LOH	
5	50100563	51877988	1777425	2	LOH	
6	31360255	31451680	91425	3	gain	
6	161778405	164008408	2230003	2	LOH	
7	10188571	11225216	1036645	2	LOH	
12	111553880	113261782	1707902	2	LOH	
13	38290614	39358846	1068232	2	LOH	
15	32029447	32515100	485653	3	gain	1
17	51092674	52140367	1047693	2	LOH	
X	26127446	27160333	1032887	2	LOH	
X	107406648	108724046	1317398	2	LOH	

CNV regions only found in ***CN01-cl.1***

Chr	Start	End	Size (bp)	CNV Value	Variant Type	Number of Genes*
15	32145735	32515100	369365	3	gain	1

CNV regions only found in ***CN01-cl.2***

Chr	Start	End	Size (bp)	CNV Value	Variant Type	Number of Genes*
5	112102898	112164675	61777	3	gain	

*Number of genes in CNV/LOH regions given only for **reportable** calls (see Appendix for details on genes in reported regions).

Interpretation

- There was 1 reportable copy number change identified in the ***CN01 and cl.1, cl.2 and cl.3***.
  > A 0.487 Mb (0,369 Mb in CN01-cl.1) gain on the chromosome 15 was observed. 1 gene was found in this genomic region.

The CNV analysis result suggests that the iPSC line contains neither CNVs > 2 Mb nor regions of LOH > 5 Mb. Further information about genes in the detected regions and linked known diseases may be provided by the UCSC Genome Browser (https://genome.ucsc.edu) and Decipher (https://decipher.sanger.ac.uk/search).

Appendix

Gene located in the reportable CNV region found in ***CN01 and cl.1, cl.2 and cl.3***

Gene	Chr	Transcription Start	Transcription End	Strand	Description
CHRNA7	15	32,322,726	32,461,234	+	cholinergic receptor, nicotinic, alpha 7

References:

1. LaFramboise, T. (1 July 2009). "Single nucleotide polymorphism arrays: a decade of biological, computational and technological advances". Nucleic Acids Research. 37 (13): 4181–4193.

2. Arsham, M. S., Barch, M. J., & Lawce, H. J. (Eds.) (2017). The AGT Cytogenetics Laboratory Manual (4th Ed.). Hoboken, NJ: John Wiley & Sons, Inc.

3. Haraksingh RR, Abyzov A, Urban AE. Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans. BMC Genomics. 2017 Apr 24;18(1):321. doi: 10.1186/s12864-017-3658-x.

4. Wicell: https://www.wicell.org/home/characterization/cytogenetics/snp-microarray/single-nucleotide-polymorphism-snp-mircroarray-.cmsx