

Karyotype Report

Customer sample ID: hvs554a
Internal sample ID: NL08GSAUMCD100040

Gender
Stated by customer: Male
According to array data: Male

Copy Number Analysis

Copy number events are reported when they exceed 50 kb in size, have a confidence value greater than 50, and are confirmed by visual inspection of the B-allele frequency (BAF) and log R ratio profiles. CNVs located in known hot spot regions of recurrent mutations in hPSCs are additionally highlighted in the summary table. Loss of heterozygosity (LOH) are reported for regions larger than 1 Mbp.

The reported CNVs can be checked against the [Database of Genomic Variants](#) which provides a comprehensive summary of structural variation in the human genome. The content of the database only includes structural variations identified in healthy control samples.

Affected genes can be monitored by using a genome browser such as the NCBI [Genome Data Viewer](#), [Ensembl Genome Browser](#) or the [UCSC Genome Browser](#).

SampleID	Chr	Start	End	Size	Value	Hotspot region	LOH region
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Conclusion: The sample does not show any copy number events that fall under any of the criteria listed above.

Karyogram



NL08GSAUMCD100040
hvs554a

Karyotyping

Technical annex

Technology used:	Illumina BeadArray		
Product:	Global Screening Array + Multi Disease content 24		
v3 BeadChip			
Manifest file:	GSAMD-24v3-0-EA_20034606_A1.bpm		
Cluster file:	GSAMD24v3-0-EA_20034606_A1.egt		
Chip barcode and segment:	209838860171	R01C02	
Batch ID and 96 well position:	WG7941481-MSA3	E05	
Call rate:	0.9955894		
Typing			
Scanner:	Illumina iScan, S/N: N263		
Site of processing:	Life&Brain GENOMICS, Bonn, Germany		
Manufacturer:	Illumina, Inc., San Diego, United States of America		
Genotype Analysis			
Genome Studio:	GenomeStudio V2.0.5		
Genotyping module:	Vers. 2.0.5		
Copy Number Analysis			
Algorithm applied:	cnvPartition		
Version:	3.2		
Software producer:	Illumina, Inc., San Diego, United States of America		

Analyst

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