**Order no.:**

**Order received:** DD/MM/YYY

**Sample type / Sample collection date:**

blood, CentoCard® / DD/MM/YYYY

**Report date:** DD/MM/YYY

**Report type:** Final Report

Patient no.: , First Name: , Last Name:
DOB: **DD/MM/YYYY**, Sex: **male**, Your ref.: **-**

**Test(s) requested: CentoGenome® Solo**

## CLINICAL INFORMATION

Autistic behavior; Behavioral abnormality; Bilateral tonic-clonic seizure; Brain atrophy; Delayed speech and language development; Global developmental delay; Growth delay; Hyperpigmentation of the skin; Intellectual disability; Motor delay; Seizure
(Clinical information indicated above follows HPO nomenclature)
Family history: No.
Siblings unaffected.
Consanguineous parents: Yes.
Rule out request(s): Angelman syndrome

> ⊕ **POSITIVE RESULT**
> **Abnormal methylation profile identified; secondary finding identified**

## INTERPRETATION

The analysis of the genome sequencing data with a specific UPD algorithm suggested uniparental disomy for chromosomal region 15q11. An abnormal methylation profile consistent with loss of methylation was detected at the 15q11 imprinting center by MS-MLPA, and no large deletions or duplications within or including this region were detected. This result is consistent with uniparental disomy of the paternal chromosome. **Thus, the genetic diagnosis of Angelman syndrome is confirmed.**

No further clinically relevant variants related to the described phenotype were detected.

As a secondary finding, a heterozygous pathogenic variant was identified in the *LDLR* gene. The result is consistent with the increased genetic risk of developing symptoms of autosomal dominant familial hypercholesterolemia type 1.

## RECOMMENDATIONS

- Microsatellite analysis for patient and parents is recommended to confirm paternal uniparental disomy.
- Additionally, chromosomal analysis (e.g., karyotype, FISH) for the patient and parents to assess the mechanism of the UPD should be considered.
- Retrospective clinical evaluation and follow-up for *LDLR*-associated symptoms is recommended. Targeted testing for affected and/or adult at-risk family members is recommended.
- Genetic counselling is recommended.

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## MAIN FINDINGS

| GENE (TRANSCRIPT, METHOD) | OUTCOME |
|---|---|
| 15q11 (NGS + MLPA) | **Aberrant methylation profile (loss of methylation)**<br>**No deletions/duplications were detected** |

### VARIANT INTERPRETATION

The analysis of the genome sequencing data with a specific UPD algorithm suggested uniparental disomy for chromosomal region 15q11. Confirmation by MS-MLPA shows an aberrant methylation pattern (loss of methylation) in the 15q11 imprinted center. No large deletion or duplication has been detected in the same region by MLPA. This finding suggests uniparental disomy of the paternal chromosome region. Paternal uniparental disomy of chromosome 15 has been reported in 3%-7% of affected individuals with Angelman syndrome (PMID: 20301323).

Angelman syndrome is characterized by severe developmental delay or intellectual disability, severe speech impairment, gait ataxia and/or tremulousness of the limbs, and unique behavior with an apparent happy demeanor that includes frequent laughing, smiling, and excitability. Microcephaly and seizures are also common. Developmental delays are first noted at around age six months; however, the unique clinical features of AS do not become manifest until after age one year. AS is caused by defects in the maternally derived imprinted domain on 15q11.13 which can arise in a variety of ways - interstitial deletion of 15q11-13mat, paternal UPD 15, an imprinting defect (2-5%), or pathogenic variants in the UBEA3A gene (PMID: 20301323).

### SECONDARY (INCIDENTAL) FINDINGS

If consent is provided, in line with ACMG recommendations for reporting of secondary (incidental) findings in clinical exome and genome sequencing (Genetics in Medicine, 2021; PMID: 34012068), we report secondary (incidental) findings, i.e., pathogenic variants (class 1) and likely pathogenic variants (class 2) in the recommended genes for the indicated phenotypes.

| SEQUENCE VARIANTS | | | | | | | |
|---|---|---|---|---|---|---|---|
| GENE | VARIANT COORDINATES | AMINO ACID CHANGE | SNP IDENTIFIER | ZYGOSITY | IN SILICO PARAMETERS* | ALLELE FREQUENCIES** | TYPE AND CLASSIFICATION*** |
| *LDLR* | NM_000527.2:c.1135T>C | p.(Cys379Arg) | rs879254803 | heterozygous | PolyPhen: -<br>Align-GVGD: C0<br>SIFT: Deleterious<br>MutationTaster: Disease causing<br>Conservation_nt: high<br>Conservation_aa: high | gnomAD: 0.000032<br>ESP: -<br>1000 G: 0.000032<br>CentoMD: - | Missense Pathogenic (class 1) |

Variant annotation based on OTFA (using VEP v94). * AlignGVD: C0: least likely to interfere with function, C65: most likely to interfere with function; splicing predictions: Ada and RF scores.
** Genome Aggregation Database (gnomAD), Exome Sequencing Project (ESP), 1000Genome project (1000G) and CentoMD (latest database available). *** based on ACMG recommendations.

### VARIANT INTERPRETATION

#### *LDLR*, c.1135T>C p.(Cys379Arg)

The *LDLR* variant c.1135T>C p.(Cys379Arg) causes an amino acid change from Cys to Arg at position 379. According to HGMD Professional 2021.3, this variant has previously been described as disease causing for hypercholesterolemia by Hobbs et al., 1992 (PMID: 1301956), Romano et al., 2011 (PMID: 21865347), Bertolini et al., 2013 (PMID: 23375686). ClinVar lists this variant (Interpretation: Pathogenic/Likely pathogenic; Variation ID: 251685). It is classified as pathogenic (class 1) according to the recommendations of CENTOGENE and ACMG (please, see additional information below).

Familial hypercholesterolemia is an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL), which promotes deposition of cholesterol in the skin (xanthelasma), tendons (xanthomas), and coronary arteries (atherosclerosis). The disorder occurs in 2 clinical forms: homozygous and heterozygous (Hobbs et al., 1992; PMID:1301956). Mode of Inheritance: Autosomal dominant (OMIM®: 143890)

## CARRIERSHIP FINDINGS

In this table we list sequence variants previously ascertained or evaluated and classified in CENTOGENE as "pathogenic" and "likely pathogenic", in selected genes associated with recessive severe and early-onset Mendelian diseases. As only in-house classified variants are presented, it should not be considered a comprehensive list of variants in these genes and does not provide a complete list of potentially relevant genetic variants in the patient. The complete gene list can be found at www.centogene.com/carriership-findings (please contact CENTOGENE customer support if the gene list has been updated after this report was issued). Orthogonal validation was not performed for these variants. Therefore, if any variant is used for clinical management of the patient, confirmation by another method needs to be considered. Furthermore, the classification of these variants may change over time, however reclassification reports for these variants will not be issued. CENTOGENE is not liable for any missing variant in this list and/or any provided classification of the variants at a certain point of time. As the identified variants may indicate (additional) genetic risks or diagnoses in the patient and/or family and/or inform about reproductive risks, we recommend discussing these findings in the context of genetic counselling.

**SEQUENCE VARIANTS**

| GENE | VARIANT COORDINATES | AMINO ACID CHANGE | SNP IDENTIFIER | ZYGOSITY | IN SILICO PARAMETERS* | ALLELE FREQUENCIES** | TYPE AND CLASSIFICATION*** |
|------|---------------------|-------------------|----------------|----------|------------------------|----------------------|----------------------------|
| *GJB2* | NM_004004.5:c.35del | p.(Gly12Valfs*2) | rs80338939 | heterozygous | PolyPhen: - Align-GVGD: N/A SIFT: N/A MutationTaster: N/A Conservation_nt: N/A Conservation_aa: N/A | gnomAD: 0.0062 ESP: 0.0074 1000 G: 0.0024 CentoMD: 0.0051 | Frameshift Pathogenic (class 1) |

Variant annotation based on OTFA (using VEP v94). * AlignGVD: C0: least likely to interfere with function, C65: most likely to interfere with function; splicing predictions: Ada and RF scores. ** Genome Aggregation Database (gnomAD), Exome Sequencing Project (ESP), 1000Genome project (1000G) and CentoMD (latest database available). *** based on ACMG recommendations.

## CENTOGENE VARIANT CLASSIFICATION (BASED ON ACMG RECOMMENDATIONS)

**Class 1** – Pathogenic

**Class 2** – Likely pathogenic

**Class 3** – Variant of uncertain significance (VUS)

**Class 4** – Likely benign

**Class 5** – Benign

Additionally, other types of clinically relevant variants can be identified (e.g., risk factors, modifiers).

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## METHODS

Genomic DNA is enzymatically fragmented and tagged with Illumina compatible adapter sequences. The libraries are paired-end sequenced on an Illumina platform to yield an average coverage depth of ~ 30x. A bioinformatics pipeline based on the DRAGEN pipeline from Illumina, as well as CENTOGENE's in-house pipeline is applied. The sequencing reads are aligned to the Genome Reference Consortium Human Build 37 (GRCh37/hg19), as well as the revised Cambridge Reference Sequence (rCRS) of the Human Mitochondrial DNA (NC_012920). Sequence variants (SNVs/indels) and copy number variations (CNVs) are called using DRAGEN, Manta and in-house algorithms. Variants with a minor allele frequency (MAF) of less than 1% in gnomAD database, or disease-causing variants reported in HGMD®, in ClinVar or in CENTOGENE's in-house Biodatabank are evaluated. Although the evaluation is focused on coding exons and flanking intronic regions, the complete gene is interrogated for candidate variants with plausible association to the phenotype. All potential modes of inheritance are considered. In addition, the provided clinical information and family history are used to evaluate identified variants with respect to their pathogenicity and disease causality. Variants are categorized into five classes (pathogenic, likely pathogenic, VUS, likely benign, and benign) according to ACMG guidelines for classification of variants in addition to ClinGen recommendations. All relevant variants related to the phenotype of the patient are reported. Likely benign and benign variants are not reported. CNVs of unknown significance with no apparent relation to the patient's phenotype are not reported. Mitochondrial variants with a heteroplasmy level of 15% or higher are reported. For detection of SNVs and indels in the regions targeted for downstream analysis a sensitivity of 99.9%, a specificity of 99.9%, and an accuracy of 99.9% is achieved. CNV detection software has a sensitivity of more than 95%. CENTOGENE has established stringent quality criteria and validation processes for variants detected by NGS. Variants with low sequencing quality and/or unclear zygosity are confirmed by orthogonal methods. Consequently, a specificity of > 99.9% for all reported variants is warranted. Screening of repeat expansions is performed by the ExpansionHunter algorithm for the following genes: *AR, ATN1, ATXN1, ATXN2, ATXN3, ATXN7, ATXN8OS, ATXN10, CACNA1A, CNBP, CSTB, C9ORF72, DMPK, FMR1, FXN, HTT, JPH3, NOP56, PABPN1, PHOX2B, PPP2R2B, PRNP* and *TBP*. The technical results of repeat expansion screenings will be correlated with the clinical information provided. Any repeat expansion called and considered relevant to the phenotype will be confirmed by an orthogonal method. *GBA1* screening is performed using Gauchian algorithm to detect recombination events affecting the region encompassing exons 9-11 (NM_000157.3), a region which has the highest homology to *GBAP1*. Any detected recombination event is reported only when considered relevant to the phenotype. Spinal muscular atrophy (SMA) screening is performed using SMN Caller algorithm to detect the copy number of the *SMN1* gene. Any detected CNV is only confirmed by an orthogonal method and reported when considered relevant to the phenotype. Screening of uniparental disomy (UPD) is performed using an in-house algorithm for Mendelian inheritance errors (MIE) to detect runs of homozygosity (ROH) for the well-known clinically relevant chromosomal regions (6q24, 7, 11p15.5, 14q32, 15q11q13, 20q13 and 20).
MLPA (multiplex ligation-dependent probe amplification) analyses were performed using SALSA MLPA probemix ME028-D1 provided by MRC-Holland to test for deletions or duplications within or including the 15q11 gene(s).

## ANALYSIS STATISTICS

**CentoGenome® Solo**

| | | |
|---|---|---|
| Targeted nucleotides covered | ≥ 10x | 98.79% |

## LIMITATIONS

The genetic results are interpreted in the context of the provided clinical findings, family history, and other laboratory data. Only variants in genes potentially related to the proband's medical condition are reported. Misinterpretation of results may occur if the provided genetic data or patient information is inaccurate and/or incomplete. If the obtained genetic results are not compatible with the clinical findings, additional testing should be considered.
Genes with mapping issues in the genome assembly used, and genomic regions that are hard to sequence by current technology and are without evidenced relevance for monogenic disorders, are excluded from this analysis. More complex genetic events not mentioned in the methods section, such as inversions and translocations, are not analyzed in this test. In addition, due to technology limitations, certain regions may be poorly covered, or not covered at all. In these regions and others encompassing repetitive, high-homology (such as pseudogene homology), and GC-rich sequences, relevant variants can be missed. Extremely low-coverage calls are expected to be artifacts based on our extensive validations and are consequently not considered during the analysis. Potential aberrant splicing is assessed with splice prediction tools. Deep intronic variants without strong prediction of aberrant splicing may not be reported, with the exception of known pathogenic splicing variants evidenced by external sources. The CNV detection sensitivity is decreased for repetitive regions, homologous regions such as pseudogenes, and for events spanning 2 or less exons. Mitochondrial variants with heteroplasmy levels below 15% may not be detected. It is expected that lower quality samples (e.g., prenatal, product of conception, blood from patients with hematologic disorders, and highly degraded DNA) may generate lower quality NGS data; in these cases, CNV analysis, mitochondrial genome analysis, and/or additional integrated screening analyses in this test may not be possible to perform. The repeat expansion algorithm used is not designed to handle complex loci that harbor multiple repeats. Repeats are only genotyped if the coverage at the locus is at least 10x. The Gauchian algorithm can only detect non-recombinant-like variants from a set of 111 known *GBA1* variants and can detect recombination events affecting exons 9-11 only. Therefore, recombinations affecting other regions are not in the scope of this screening. Silent carriers may be missed with the SMN Caller algorithm. The UPD detection is a screening method, and therefore false-positive and false-negative results may occur.

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## ADDITIONAL INFORMATION

This test was developed, and its performance was validated, by CENTOGENE. The US Food and Drug Administration (FDA) has determined that clearance or approval of this method is not necessary and thus neither have been obtained. This test has been developed for clinical purposes. All test results are reviewed, interpreted, and reported by our scientific and medical experts.

To exclude mistaken identity in your clinic, several guidelines recommend testing a second sample that is independently obtained from the proband. Please note that any further analysis will result in additional costs.

The classification of variants can change over the time. Please feel free to contact CENTOGENE (customer.support@centogene.com) in the future to determine if there have been any changes in classification of any reported variants.

## DISCLAIMER

Any preparation and processing of a sample from patient material provided to CENTOGENE by a physician, clinical institute, or a laboratory (by a "Partner") and the requested genetic and/or biochemical testing itself is based on the highest and most current scientific and analytical standards. However, in very few cases genetic or biochemical tests may not show the correct result, e.g., because of the quality of the material provided by a Partner to CENTOGENE or in cases where any test provided by CENTOGENE fails for unforeseeable or unknown reasons that cannot be influenced by CENTOGENE in advance. In such cases, CENTOGENE shall not be responsible and/or liable for the incomplete, potentially misleading, or even wrong result of any testing if such issue could not be recognized by CENTOGENE in advance.

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| Human Geneticist | Human Geneticist |  |

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