

**Patient**
Legal Name **Sample Patient**
Sex Assigned at Birth **Male**
Birthdate **01/01/1970**
MRN **000000**
Indication **Diagnostic**

**Provider**
Ordering Provider **Sample Doctor**
Client **Sample Facility**

Additional Recipients
Sample Genetic Counselor

**Test Information**
Accession # **00-000000**
Family # **000000**
Specimen **Blood EDTA (Purple top)**
Portal Order # **000000**
Collected **07/01/2026**
Received **07/01/2026**
Test Started **07/01/2026**

 Uncertain

Variant(s) of Uncertain Clinical Relevance Detected

Results
Sequence Variants

Gene(s) (RefSeq ID)	Relevant Associated Condition (Mode of Inheritance)	Variant (Zygosity)	Genomic Coordinates (GRCh38)	Variant Classification
CSF1R (NM_001288705.3) Characterized	CSF1R-related diffuse leukoencephalopathy with spheroids (Autosomal dominant)	c.2442+5G>A (Heterozygous)	chr5:g.150056214C>T	Uncertain Significance

Indication for Testing:
Memory decline, motor impairment, seizures

Interpretation

- **Overall, the evidence suggests it is uncertain if the identified *CSF1R* alteration is the cause of the patient's clinical symptoms.**
- Clinical correlation is recommended, and genetic testing results should be interpreted in the context of the patient's clinical and family history.
- RNA analysis of the *CSF1R* c.2442+5G>A variant is in progress. When this analysis is completed, an additional report will be issued.

Considerations

- If secondary findings were requested, results were issued in a separate report.
- Genetic counseling is a recommended option for all patients undergoing genetic testing.
- Any tests on hold, previously reported, and those that have been cancelled (including reflex testing steps cancelled due to a positive result in a preceding test) have not been included in this report. For additional information, please contact Ambry Genetics.

All content hereafter is supplemental information to the preceding report.

General Gene-Disease Information

Gene(s) (RefSeq ID)	Genomic Coordinates (GRCh38)	Genomic Size (bp)	Total Exons	Coding Exons	Number of Amino Acids
CSF1R (NM_001288705.3)	chr5:150053295-150086554	33260	21	21	973

The *CSF1R* gene is located on chromosome 5q32 and encodes the macrophage colony-stimulating factor 1 receptor. Pathogenic variants in this gene are known to cause *CSF1R*-related diffuse leukoencephalopathy with spheroids, which is inherited in an autosomal dominant fashion, and *CSF1R*-related brain abnormalities, neurodegeneration, and dysosteosclerosis, which is inherited in an autosomal recessive fashion. *CSF1R*-related diffuse leukoencephalopathy with spheroids is an adult-onset leukoencephalopathy characterized by axonal spheroids and pigmented glia, executive dysfunction, memory decline, personality changes, motor impairments, and seizures. The mean age of onset is 47 years of age (range 18-78) and variable expressivity has been observed (Rademakers, 2012). The mechanism of disease is unclear for *CSF1R*-related diffuse leukoencephalopathy with spheroids. *CSF1R*-related brain abnormalities, neurodegeneration, and dysosteosclerosis is an early-onset, progressive disorder characterized by cognitive impairment, brain MRI showing multiple calcifications and/or white matter abnormalities, and skeletal dysplasia in the dysosteosclerosis-Pyle disease spectrum. While neurologic regression is generally present, onset and severity of symptoms range from infantile-onset and rapidly progressing disease to late-onset symptoms with slower progression (Guo, 2019; Kindiş, 2021). Biallelic loss of function has been reported as the mechanism of disease for *CSF1R*-related brain abnormalities, neurodegeneration, and dysosteosclerosis.

Variant Details

Uncertain Significance c.2442+5G>A variant in the *CSF1R* gene

Alteration description: The c.2442+5G>A variant in the *CSF1R* gene is a nucleotide substitution in the intron.

Affected individuals: This variant was reported in individual(s) with features consistent with *CSF1R*-related diffuse leukoencephalopathy with spheroids (Konno, 2017).

Population frequency: This variant was not reported in population-based cohorts in the Genome Aggregation Database (gnomAD).

In silico: In silico splice site analysis predicts that this variant will not have any significant effect on splicing.

Based on the available evidence, the clinical significance of this variant is uncertain.

Report References

- Konno T *et al.* | Eur. J. Neurol. | 2016 | [PMID: 27680516](#)
Clinical and genetic characterization of adult-onset leukoencephalopathy with axonal spheroids and pigmented glia associated with CSF1R mutation.
- Kindiş E *et al.* | Am J Med Genet A | 2021 | [PMID: 33749994](#)
Further expanding the mutational spectrum of brain abnormalities, neurodegeneration, and dysosteosclerosis: A rare disorder with neurologic regression and skeletal features.
- Guo L *et al.* | Am J Hum Genet | 2019 | [PMID: 30982609](#)
Bi-allelic CSF1R Mutations Cause Skeletal Dysplasia of Dysosteosclerosis-Pyle Disease Spectrum and Degenerative Encephalopathy with Brain Malformation.
- Rademakers R *et al.* | Nat Genet | 2011 | [PMID: 22197934](#)
Mutations in the colony stimulating factor 1 receptor (CSF1R) gene cause hereditary diffuse leukoencephalopathy with spheroids.

Samples Received, Metrics, and Coverage

Family Member (Accession #)	Affected	Depth of Coverage	
		% Bases ≥ 10x	% Bases ≥ 20x
Proband* (00-000000)	AFFECTED	98.7	98

*Genome sequencing performed.
All family members with samples received are represented in this table. Complete coverage data for the proband can be e-mailed or made available for download through AmbryPort by request.

Analyses Performed

- Genome sequencing, bioinformatics, filtering and manual review based on dominant and recessive inheritance models was performed. Medical review of characterized genetic etiologies revealed an alteration with possible clinical relevance.
- Medical review of uncharacterized genes* and gene-disease relationships for potential candidate gene findings was not performed because both parents were not available for sequencing and a characterized finding was identified.
- Additional analyses were performed as described in the methodology. Clinically significant variants with relevance to the patient phenotype, if identified by these analyses, are included on this report.

*Uncharacterized genes are not currently established to underlie Mendelian genetic conditions. An uncharacterized gene will be classified as a "candidate" when sufficient evidence, based on Ambry's comprehensive, rule-based scoring criteria, is available (Farwell Hagman, 2017).

Raw Data

A list of variants prioritized by our filtering pipeline is available upon request via this form (www.ambrygen.com/file/material/view/1262/Raw_Sequence_Data_Consent_0619_final.pdf). This list includes variants in characterized and uncharacterized genes that were determined not to be clinically relevant. Additional variant filtering details are provided. These variants are not systematically confirmed via orthogonal methods.

Assay Information

General Information	Ambry's GenomeNext™ is a comprehensive genome sequencing assay designed to increase diagnostic yield for suspected genetic disorders that have remained unsolved using traditional approaches. The genome includes both protein-coding and non-coding regions, and genome sequencing has been successfully applied to identify inherited and de novo variants across autosomal dominant, autosomal recessive, and X-linked disorders. This assay includes analysis of single nucleotide variants (SNVs); small insertions and deletions (indels); copy number variants (CNVs); mitochondrial genome SNVs and indels; repeat expansions in the <i>DMPK</i> , <i>FMR1</i> , and <i>PHOX2B</i> genes; <i>SMN1</i> deletions; uniparental disomy (UPD); and aneuploidy. In addition to the primary analysis focused on the patient's reported clinical presentation, genome testing may also detect secondary findings (pathogenic/likely pathogenic variants in select genes) unrelated to the indication for testing.
Methodology	Genomic DNA is isolated from the patient's specimen using standardized technology. PCR-free libraries are prepared and sequenced on Illumina platforms using paired-end sequencing chemistry with an average mean sequencing coverage of at least 30x. Initial data processing (base calling, alignment, and variant calling) is performed using validated bioinformatics tools and aligned to the GRCh38/hg38 human reference genome assembly. Variants are annotated and prioritized using the clinical and family information provided by the ordering provider, population databases, published literature, sequence level quality metrics, and established variant classification guidelines. Copy number changes are assessed using coverage and/or breakpoint evidence from NGS data. Reportable findings not satisfying established quality metrics are verified with an appropriate orthogonal method as needed. Screening for repeat expansions in <i>DMPK</i>, <i>FMR1</i>, and <i>PHOX2B</i> is performed via sequencing. For reported <i>DMPK</i> and <i>FMR1</i> expansions, repeat size is determined by repeat-primed PCR. <i>SMN1</i> deletions are assessed by sequencing and are confirmed by multiplex ligation-dependent probe amplification (MLPA) prior to reporting. Co-segregation studies may be performed when family members are available. If ordered, ribonucleic acid (RNA) is isolated from the patient's whole blood. RNA is converted to complementary DNA (cDNA) by reverse transcriptase polymerase chain reaction (RT-PCR). RNA analysis is performed for reportable germline DNA variants expected to affect splicing, provided such studies are likely to meaningfully inform variant classification.
Result Reports	A primary clinical report is generated only for the proband; family member information will be reported if applicable. Only variants relevant to the proband's current phenotype are included in the primary report. Relevant pathogenic and likely pathogenic variants are routinely reported; selected variants of uncertain significance may also be reported. Variants that increase a statistical risk for disease are not routinely reported. Incidental findings, as well as benign or likely benign variants, are not reported. Pathogenic and likely pathogenic secondary findings within the ACMG-recommended gene list are reported separately unless opted out.
Test Limitations and Disclaimers	This test was developed and its performance characteristics determined by Ambry Genetics. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) to perform high-complexity clinical laboratory testing. Results should be interpreted in the context of the patient's clinical and family history and do not constitute medical advice; a negative result does not rule out a genetic condition. Detectable variant types include nucleotide substitutions and small insertions/deletions <50 bp, copy number variants and select structural variants, and mitochondrial variants with ≥5% heteroplasmy. Sensitivity may be reduced for copy number variants between 1kb and 10kb. Uniparental disomy of clinically relevant regions will only be reported when testing is run as a trio analysis. Trinucleotide repeat screening by this assay is limited to the <i>DMPK</i> , <i>FMR1</i> , and <i>PHOX2B</i> genes. Repeat

sizes are reported with an accuracy of +/- 2 repeats for alleles with 1-54 repeats and an accuracy of +/- 5 repeats for alleles with 55-200 repeats. Exact repeat size cannot be determined for alleles with >200 repeats.

The overall coverage of each genomic region varies and each individual may have slightly different coverage yield; regions with shared homology/repetitive sequence and other sequence-context limitations may reduce sensitivity and specificity (including for CNVs/structural variation). This test is not intended to analyze certain variant types, including but not limited to: gross/balanced rearrangements, portions of genes with highly homologous pseudogenes, mitochondrial genome deletions/duplications, epigenetic effects, oligogenic inheritance, X-linked recessive variants in females who manifest disease due to skewed X-inactivation, or variants involved in tri-allelic inheritance. Some variants may not be detected due to technical limitations such as but not limited to low coverage, repetitive/highly homologous regions, certain structural rearrangements, or low-level mosaicism. Although molecular tests are highly accurate, rare diagnostic errors may occur (e.g., sample mix-up, erroneous paternity identification, technical, clerical, or genotyping errors; trace contamination; rare variants that may interfere with analysis; or other sources of error).

Resources Used for Bioinformatics, Medical Review Filtering, and Reporting

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4. Castellana S, et al. (2020) Nucleic Acids Res. 49(D1):D1282-D1288 PMID: 33300029. MitImpact 3D: <https://mitimpact.mcb2lab.org>
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Understanding Your Uncertain Exome or Genome Sequencing Test Result

INFORMATION FOR PATIENTS WITH ONE OR MORE UNCERTAIN RESULTS

Chromosomes and Genes	Chromosomes are packages of DNA. They are made up of genes that provide instructions for how our bodies develop. Almost everyone has two copies of each chromosome, one from each parent. Variants in our genes or chromosomes can cause genetic conditions. These genetic variants may be passed down in families or occur for the first time in the person who has a genetic condition. Even if there is no history of the specific condition in your family, it can still be caused by a variant in a person’s genes or chromosomes.
Exome and Genome Sequencing	Exome and genome sequencing tests are designed to look for genetic variants in genes that may be the cause of an existing medical condition. Exome sequencing is a test that analyzes all genes known to cause medical conditions. Genome sequencing is another test that analyzes all genes known to cause medical conditions; it can also detect rare types of genetic variants that can not be detected by exome sequencing.
Result	This testing found one or more variants in one or more genes, but it is not clear if this test result is the cause for your existing medical condition.
Diagnosis	This test result does not change your diagnosis. If you have been diagnosed with a specific condition, that remains the same.
Reclassification	Collecting information about an uncertain result is an ongoing process. It is possible that your result may be better understood in the future. The healthcare provider that ordered your test will be notified if new information becomes available about your uncertain result.
Patient for Life	As part of Ambry’s Patient for Life™ program, we keep your results on file. While we did not find a genetic cause of your medical condition today, future genetic discoveries may provide enough information to update your result. We will notify your healthcare provider if any clinically significant results are identified in the future.
Family Members	Your report will indicate if testing family members may help us learn more about your specific result.
Management Options	Management options vary by condition and other factors. Talk to your healthcare provider about which may be right for you.

Please discuss this information with your healthcare provider. The field of genetics is continuously changing, so updates related to your genetic testing result, medical recommendations, and/or potential treatments may be available over time. This information is not meant to replace a discussion with a healthcare provider, and should not be considered or interpreted as medical advice.

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