

Overview

Useful For

Diagnosis of the subset of mitochondrial diseases that results from variants in the mitochondrial genome

A second-tier test for patients in whom previous targeted gene variant analyses for specific mitochondrial disease-related genes were negative

Identifying variants within genes of the mitochondrial genome that are known to be associated with mitochondrial disease, allowing for predictive testing of at-risk family members

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
CULFB	Fibroblast Culture for Genetic Test	Yes	No

Genetics Test Information

This test includes amplification of the entire mitochondrial genome by long-range polymerase chain reaction followed by sequencing on the next-generation sequencing platform to evaluate for variants within the mitochondrial genome.

Testing Algorithm

For skin biopsy or cultured fibroblast specimens, fibroblast culture will be performed at an additional charge. If viable cells are not obtained, the client will be notified.

The following algorithms are available:

- [Epilepsy: Unexplained Refractory and/or Familial Testing Algorithm](#)
- [Neuromuscular Myopathy Testing Algorithm](#)

Special Instructions

- [Muscle Biopsy Specimen Preparation Instructions](#)
- [Molecular Genetics: Biochemical Disorders Patient Information](#)
- [Informed Consent for Genetic Testing](#)
- [Blood Spot Collection Card-Spanish Instructions](#)
- [Blood Spot Collection Card-Chinese Instructions](#)
- [Epilepsy: Unexplained Refractory and/or Familial Testing Algorithm](#)
- [Neuromuscular Myopathy Testing Algorithm](#)
- [Informed Consent for Genetic Testing \(Spanish\)](#)
- [Blood Spot Collection Instructions](#)

Highlights

Next-generation sequencing (NGS) is used to test for the presence of variants, including 13 protein coding genes, 22 transfer RNA genes, and 2 ribosomal RNA genes, within the mitochondrial genome.

# Test Definition: MITOP

Mitochondrial Full Genome Analysis,  
Next-Generation Sequencing (NGS), Varies

Large deletions within the mitochondrial genome and their locations are determined from the NGS data and confirmed by droplet digital polymerase chain reaction (ddPCR). Large deletion heteroplasmy level is determined by ddPCR.

This assay is only useful for detecting mitochondrial genomic variants. Depletion of mitochondrial DNA levels or variants in mitochondrial genes encoded by the nuclear genome is not within the scope of this assay.

### Method Name

Long-Range Polymerase Chain Reaction (LR-PCR) followed by Next-Generation Sequencing (NGS) and Droplet Digital Polymerase Chain Reaction (ddPCR) as needed

### NY State Available

Yes

## Specimen

### Specimen Type

Varies

### Ordering Guidance

If testing for variants in the mitochondrial genes encoded by the nuclear genome is requested, order NMITO / Nuclear Mitochondrial Gene Panel, Next-Generation Sequencing, Varies. Alternatively, order CMITO / Combined Mitochondrial Full Genome and Nuclear Gene Panel, Varies for both the mitochondrial genome and mitochondrial genes encoded by the nuclear genome.

### Necessary Information

[Molecular Genetics: Biochemical Disorders Patient Information](#) (T527) is available to provide information useful for accurate test interpretation. **At minimum, provide a reason for testing with each specimen.** Although testing may proceed without this information, **ordering providers are strongly encouraged** to complete the form and send it with the specimen.

### Specimen Required

**Patient Preparation:** A previous bone marrow transplant from an allogenic donor will interfere with testing. For information about testing patients who have received a bone marrow transplant, call 800-533-1710.

**Submit only 1 of the following specimens:**

**Specimen Type:** Whole blood

**Container/Tube:**

**Preferred:** Lavender top (EDTA) or yellow top (ACD)

**Acceptable:** Green top (Sodium heparin)

**Specimen Volume:** 3 mL

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**Collection Instructions:**

1. Invert several times to mix blood.
2. Send whole blood specimen in original tube. **Do not aliquot.**

**Specimen Stability Information:** Ambient 4 days/Refrigerated 4 days/Frozen 4 days

**Additional Information:**

1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA is met, the preferred volume of blood must be submitted. Testing may be canceled if DNA requirements are inadequate.

**Specimen Type:** Cultured fibroblasts

**Source:** Skin

**Container/Tube:** T-25 flask

**Specimen Volume:** 2 Flasks

**Collection Instructions:** Submit confluent cultured fibroblast cells from a skin biopsy. Cultured cells from a prenatal specimen will not be accepted.

**Specimen Stability Information:** Ambient (preferred) <24 hours/Refrigerated <24 hours

**Additional Information:**

1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks are required to culture fibroblasts before genetic testing can occur.

**Specimen Type:** Skin biopsy

**Supplies:** Fibroblast Biopsy Transport Media (T115)

**Container/Tube:** Sterile container with any standard cell culture media (eg, minimal essential media, RPMI 1640). The solution should be supplemented with 1% penicillin and streptomycin.

**Specimen Volume:** 4-mm Punch

**Specimen Stability Information:** Ambient (preferred) <24 hours/Refrigerated <24 hours

**Additional Information:**

1. Specimens are preferred to be received within 24 hours of collection. Culture and extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.
2. A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks are required to culture fibroblasts before genetic testing can occur.

**Specimen Type:** Snap frozen nerve tissue biopsy

**Collection Instructions:** Prepare snap frozen tissue biopsy per surgical procedure

**Specimen Volume:** 0.25 to 0.5 cm

**Specimen Stability Information:** Frozen

**Specimen Type:** Muscle tissue biopsy

**Supplies:** Muscle Biopsy Kit (T541)

**Specimen Volume:** 20 to 80 mg

**Collection Instructions:** Prepare and transport specimen per instructions in [Muscle Biopsy Specimen Preparation](#).

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**Specimen Stability Information:** Frozen (preferred) <24 hours/Ambient <24 hours/Refrigerated <24 hours

**Additional Information:** Specimens are preferred to be received within 24 hours of collection. Extraction will be attempted for specimens received after 24 hours and will be evaluated to determine if testing may proceed.

**Specimen Type:** Blood spot

**Supplies:** Card-Blood Spot Collection (Filter Paper) (T493)

**Container/Tube:**

**Preferred:** Collection card (Whatman Protein Saver 903 Paper)

**Acceptable:** PerkinElmer 226 filter paper or blood spot collection card

**Specimen Volume:** 2 to 5 Blood spots

**Collection Instructions:**

1. An alternative blood collection option for a patient older than 1 year is a fingerstick. For detailed instructions, see [How to Collect a Dried Blood Spot Sample](#).
2. Let blood dry on the filter paper at ambient temperature in a horizontal position for a minimum of 3 hours.
3. Do not expose specimen to heat or direct sunlight.
4. Do not stack wet specimens.
5. Keep specimen dry

**Specimen Stability Information:** Ambient (preferred)/Refrigerated

**Additional Information:**

1. Blood spot specimens are acceptable but not recommended. Multiple extractions will be required to obtain sufficient yield for supplemental analysis, and there is significant risk for test failure due to insufficient DNA.
2. Due to lower concentration of DNA yielded from blood spot, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will be noted in the report. Alternatively, additional specimen may be required to complete testing.
3. For collection instructions, see [Blood Spot Collection Instructions](#)
4. For collection instructions in Spanish, see [Blood Spot Collection Card-Spanish Instructions](#) (T777)
5. For collection instructions in Chinese, see [Blood Spot Collection Card-Chinese Instructions](#) (T800)

**Specimen Type:** Extracted DNA

**Container/Tube:**

**Preferred:** Screw Cap Micro Tube, 2 mL with skirted conical base

**Acceptable:** Matrix tube, 1 mL

**Collection Instructions:**

1. The preferred volume is at least 100 µL at a concentration of 75 ng/µL.
2. Include concentration and volume on tube.

**Specimen Stability Information:** Frozen (preferred) 1 year/Ambient/Refrigerated

**Additional Information:** DNA must be extracted in a CLIA-certified laboratory or equivalent and must be extracted from a specimen type listed as acceptable for this test (including applicable anticoagulants). Our laboratory has experience with Chemagic, Puregene, Autopure, MagnaPure, and EZ1 extraction platforms and cannot guarantee that all extraction methods are compatible with this test. If testing fails, one repeat will be attempted, and if unsuccessful, the test will be reported as failed and a charge will be applied. If applicable, specific gene regions that were unable to be interrogated due to DNA quality will be noted in the report.

## Forms

1. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file. The following documents are available:  
[-Informed Consent for Genetic Testing](#) (T576)  
[-Informed Consent for Genetic Testing-Spanish](#) (T826)
2. [Molecular Genetics: Biochemical Disorders Patient Information](#) (T527)
3. If not ordering electronically, complete, print, and send 1 of the following forms with the specimen:  
[-Neurology Specialty Testing Client Test Request](#) (T732)  
[-Biochemical Genetics Test Request](#) (T798)

**Specimen Minimum Volume**  
See Specimen Required

**Reject Due To**  
All specimens will be evaluated by at Mayo Clinic Laboratories for test suitability.

**Specimen Stability Information**

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

**Clinical & Interpretive**

**Clinical Information**

The mitochondrion occupies a unique position in eukaryotic biology. First, it is the site of energy metabolism, without which aerobic metabolism and life as we know it would not be possible. Second, it is the sole subcellular organelle that is composed of proteins derived from 2 genomes, mitochondrial and nuclear. A group of hereditary disorders due to variants in either the mitochondrial genome or nuclear mitochondrial genes have been well characterized.

The diagnosis of mitochondrial disease can be particularly challenging as the presentation can occur at any age, involve virtually any organ system, and have widely varying severity. This test utilizes massively parallel sequencing, also termed next-generation sequencing (NGS), to determine the exact sequence of the entire 16,569 base-pair mitochondrial genome. The utility of this test is to assist in the diagnosis of the subset of mitochondrial diseases that result from variants in the mitochondrial genome. This includes certain types of myopathies and neuro-ophthalmologic diseases, such as MELAS (mitochondrial encephalomyopathy, lactic acidosis, stroke-like episodes), MERRF (myoclonic epilepsy with ragged red fibers), mitochondrial myopathy, neurogenic muscle weakness, ataxia, retinitis pigmentosa, Leigh syndrome, Leber hereditary optic neuropathy, and chronic progressive external ophthalmoplegia . In addition to the detection of single base changes with these disorders, large deletions, such as those associated with Kearns-Sayre or Pearson syndromes, are also detected. Variants in mitochondrial proteins that are encoded by genes in the nucleus, such as the enzymes of fatty acid oxidation, are not detected using this test.

In contrast to variants in nuclear genes, which are present in either 0, 1, or 2 copies, mitochondrial variants can be present in any fraction of the total organelles, a phenomenon known as heteroplasmy. Typically, the severity of disease presentation is a function of the degree of heteroplasmy. Individuals with a higher fraction of altered mitochondria

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present with more severe disease than those with lower percentages of altered alleles. The sensitivity for the detection of altered alleles in a background of wild-type (or normal) mitochondrial sequences by NGS is approximately 10%.

**Reference Values**

An interpretive report will be provided.

**Interpretation**

All detected variants are evaluated according to American College of Medical Genetics and Genomics guidelines for mitochondrial DNA variant interpretation.<sup>(1)</sup> Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. The degree of heteroplasmy of each single nucleotide or delin (deletion/insertion) variant, defined as the ratio (percentage) of variant sequence reads to the total number of reads, will also be reported. Variants detected at or above 95% will be reported as homoplasmic. Heteroplasmy for large deletions will be reported and is determined by droplet digital polymerase chain reaction. Variants classified as benign or likely benign are not reported.

**Cautions**

Clinical Correlations:

A small percentage of individuals who have mitochondrial genome involvement may have a variant that is not identified by the methods performed. The absence of a variant, therefore, does not eliminate the possibility of a mitochondrial disease due to variant in the mitochondrial genome. Variants in mitochondrial genes encoded by the nuclear genome will not be detected with this assay. For predictive testing of asymptomatic individuals, it is important to first document the presence of a gene variant in an affected family member.

Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

Technical Limitations:

In some cases, DNA variants of undetermined significance may be identified.

Rare variants (ie, polymorphisms) exist that could lead to false-negative or false-positive results. If results obtained do not match the clinical findings, additional testing should be considered.

Evaluation Tools:

Multiple in-silico evaluation tools were used to assist in the interpretation of these results. These tools are updated regularly; therefore, changes to these algorithms may result in different predictions for a given variant. Additionally, the predictability of these tools for the determination of pathogenicity is currently unvalidated.

Unless reported or predicted to cause disease, variants in protein coding genes that do not result in an amino acid substitution are not reported. These and common variants identified for this patient are available upon request.

Reclassification of Variants-Policy:

Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare professionals to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time. Due to broadening genetic knowledge, it is possible

that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

**Clinical Reference**

1. McCormick EM, Lott MT, Dulik MC, et al. Specifications of the ACMG/AMP standards and guidelines for mitochondrial DNA variant interpretation. *Hum Mutat.* 2020;41(12):2028-2057
2. Munnich A, Rotig A, Cormier-Daire V, Rustin P. Clinical presentation of respiratory chain deficiency. In: Valle D, Antonarakis S, Ballabio A, Beaudet AL, Mitchell GA, eds. *The Online Metabolic and Molecular Basis of Inherited Disease*. McGraw-Hill; 2019. Accessed December 2, 2024. Available at <https://ommbid.mhmedical.com/content.aspx?bookid=2709&sectionid=225086827>
3. Wallace DC, Lott MT, Brown MD, Kerstann K. Mitochondria and neuro-ophthalmologic diseases. In: Valle D, Antonarakis S, Ballabio A, Beaudet AL, Mitchell GA, eds. *The Online Metabolic and Molecular Basis of Inherited Disease*. McGraw-Hill; 2019. Accessed December 2, 2024. Available at <https://ommbid.mhmedical.com/content.aspx?bookid=2709&sectionid=225088522>
4. Wong LJ. Molecular genetics of mitochondrial disorders. *Dev Disabil Res Rev.* 2010;16(2):154-162. doi:10.1002/ddrr.104

**Performance****Method Description**

Next-generation sequencing (NGS) is used to test for the presence of variants within the mitochondrial genome (includes 13 protein coding genes, 22 transfer RNA genes, and 2 ribosomal RNA genes) and to determine the mitochondrial haplogroup of the patient. Large deletions within the mitochondrial genome are first detected by gel electrophoresis (as size-shifted polymerase chain reaction bands), and the locations of the deletions in the mitochondrial DNA are then determined from the NGS data. Droplet digital polymerase chain reaction (ddPCR) is utilized to confirm the presence of large deletions and determine heteroplasmy level.

The haplogroup is computed using the software package HaploGrep and PhyloTree.(Weissensteiner H, Pacher D, Kloss-Brandstatter A, et al. HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. *Nucleic Acids Res.* 2016;44(W1):W58-W63. doi:10.1093/nar/gkw233; van Oven M, Kayser M. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Hum Mutat.* 2009;30(2):E386-E394. doi:10.1002/humu.20921. Available at [www.phylotree.org](http://www.phylotree.org))

**PDF Report**

No

**Day(s) Performed**

Monday

**Report Available**

28 to 42 days

**Specimen Retention Time**

Whole blood: 2 weeks (if available); Extracted DNA: 3 months

Performing Laboratory Location

Mayo Clinic Laboratories - Rochester Main Campus

Fees & Codes

Fees

- Authorized users can sign in to [Test Prices](#) for detailed fee information.
- Clients without access to Test Prices can contact [Customer Service](#) 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact [Customer Service](#).

Test Classification

This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81460-Whole Mitochondrial Genome

81465-Whole Mitochondrial Genome Large Deletion Analysis

88233-Tissue culture, skin, solid tissue biopsy (if appropriate)

88240-Cryopreservation (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
MITOP	Mitochondrial Full Genome Analysis	101152-7

Result ID	Test Result Name	Result LOINC® Value
55281	Result Summary	50397-9
55282	Result	82939-0
55283	Interpretation	69047-9
55284	Additional Information	48767-8
55285	Specimen	31208-2
55286	Source	31208-2
55287	Released By	18771-6