

## Nuclear Mitochondrial Gene Panel, Next-Generation Sequencing, Varies

**Test ID:** NMITO

### Useful for:

- Diagnosing the subset of mitochondrial disease that results from variants in the nuclear-encoded genes
- 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 nuclear 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

### Methods:

Sequence Capture and Targeted Next-Generation Sequencing followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing

### Reference Values:

An interpretive report will be provided

### Shipping Instructions:

Specimen preferred to arrive within 96 hours of collection.

### Specimen Requirements:

**Patient Preparation:** A previous bone marrow transplant from an allogenic donor will interfere with whole blood or dried blood spot testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

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

<b>Specimen Type:</b>	<b>Whole blood</b>
<b>Preferred:</b>	Lavender top (EDTA) or yellow top (ACD)
<b>Acceptable:</b>	Any anticoagulant
<b>Specimen Volume:</b>	3 mL
<b>Collection Instructions:</b>	1. Invert several times to mix blood. 2. Send whole specimen in original tube. <b>Do not aliquot.</b>
<b>Specimen Stability Information:</b>	Ambient (preferred) 4 days/Refrigerated 4 days
<b>Minimum Volume:</b>	1 mL

<b>Specimen Type:</b>	<b>Skin biopsy</b>
<b>Supplies:</b>	Fibroblast Biopsy Transport Media (T115)
<b>Container/Tube:</b>	Sterile container with any standard cell culture media (eg, minimal essential media, RPMI 1640). The solution should be supplemented with 1% penicillin and streptomycin.
<b>Specimen Volume:</b>	4-mm punch
<b>Specimen Stability Information:</b>	Refrigerated (preferred)/Ambient
<b>Additional Information:</b>	A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks is required to culture fibroblasts before genetic testing can occur

<b>Specimen Type:</b>	<b>Cultured fibroblast</b>
<b>Container/Tube:</b>	T-25 flask
<b>Specimen Volume:</b>	2 Flasks
<b>Collection Instructions:</b>	Submit confluent cultured fibroblast cells from a skin biopsy from another laboratory. Cultured cells from a prenatal specimen will not be accepted.
<b>Specimen Stability Information:</b>	Ambient (preferred)/Refrigerated (<24 hours)
<b>Additional Information:</b>	A separate culture charge will be assessed under CULFB / Fibroblast Culture for Biochemical or Molecular Testing. An additional 3 to 4 weeks is required to culture fibroblasts before genetic testing can occur.

### Ordering Guidance:

- The diagnostic workup for a mitochondrial disorder may include testing to demonstrate elevations of the lactate-to-pyruvate ratio and an elevated growth differentiation factor 15 concentration. Consider LAPYP / Lactate Pyruvate Panel, Plasma and GDF15 / Growth Differentiation Factor 15, Plasma.
- Customization of this panel and single gene analysis for any gene present on this panel are available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies.
- Targeted testing for familial variants (also called site-specific or known variants testing) is available for the genes on this panel. See FMTT / Familial Mutation, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

## Specimen Stability Information:

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

## Cautions:

### Clinical Correlations:

- 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.
- If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.
- To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact a Mayo Clinic Laboratories genetic counselor at 800-533-1710.

### Technical Limitations:

- Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.
- There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.
- This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

### Deletion/Duplication Analysis:

- This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.
- This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.
- Genes may be added or removed based on updated clinical relevance. Refer to the [Targeted Genes and Methodology Details for Nuclear Mitochondrial Gene Panel, Next-Generation Sequencing, Varies](#) for the most up to date list of genes included in this test. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.
- If the patient has had an allogeneic hematopoietic stem cell transplant or a recent heterologous blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

### Reclassification of Variants:

- At this time, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare providers 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.

### Variant Evaluation:

- Evaluation and categorization of variants is performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(1) 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. Variants classified as benign or likely benign are not reported.

- Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.
- Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. These findings will be carefully reviewed to determine whether they will be reported.

**CPT Code:**

81440

**Day(s) Performed:** Varies

**Report Available:** 28 to 42 days

**Questions**

Contact Michelle Rath, Laboratory Technologist Resource Coordinator at 800-533-1710.