Mitochondrial Diseases - Nuclear Genes Only Panel: Sequencing and CNV Analysis

**Test Code:** MM300  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81406 x1, 81404 x1, 81405 x1

### Condition Description

Mitochondrial diseases are a group of disorders caused by mutations in either mitochondrial DNA (mtDNA) or nuclear genes (nDNA). Production of energy in mitochondria, by means of oxidative phosphorylation, strictly depends upon factors which are encoded both by the mtDNA and the nDNA. Respiratory chain complexes are formed, for the most part by subunits of nuclear origin, as are several indispensable complex-assembling proteins. Accurate replication and efficient maintenance of mtDNA are also essential for the respiratory chain to function properly.

Many metabolic processes, distinct from ATP production, are fulfilled in mitochondria: for instance, important steps of metal cation metabolism take place in the mitochondrial matrix. Furthermore, mitochondria actively fuse and divide, and move interacting with the cytoskeleton. All these functions require the expression of nDNA. Mitochondrial disorders caused by nDNA defects have been the object of increasing attention in the past few years, establishing themselves as an important and relatively prevalent group of pathologies, and challenging the relevance of disease caused by inherited mutations of mtDNA itself.

In addition to mtDNA genome sequencing (see related tests), EGL Genetics offers this complementary panel that sequences 44 nuclear mitochondria genes through next generation sequencing technology. This technology is an excellent tool for obtaining gene sequences rapidly and accurately since it allows deep coverage of the genome through multiple independent sequence reads.

### References:

- OMIM.
- GeneReviews.

### Genes

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### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of mitochondrial diseases.

### Methodology

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

**Copy Number Analysis:** Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

### Detection

**Next Generation Sequencing:** Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient’s clinical/biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

**Copy Number Analysis:** The sensitivity and specificity of this method for CNV detection is highly dependent on the size of the event, sequence context and depth of coverage for the region involved. The assay is highly sensitive for CNVs of 500 base pairs or larger and those containing at least 3 exons. Smaller (< 500 base pairs) CNVs and those that involving only 1 or 2 exons may or may not be detected depending on the sequence context, size of exon(s) involved and depth of coverage.

### Specimen Requirements

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Submit only 1 of the following specimen types

Type: Saliva

**Specimen Requirements:**
Oragene™ Saliva Collection Kit
Oragene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

**Specimen Collection and Shipping:**
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

Type: DNA, Isolated

**Specimen Requirements:**
Microtainer
8µg
Isolation using the Perkin Elmer™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

**Specimen Collection and Shipping:**
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Type: Whole Blood (EDTA)

**Specimen Requirements:**
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

**Specimen Collection and Shipping:**
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

**Related Tests**

- Mitochondrial Genome: Sequencing
- Mitochondrial Diseases - Nuclear Genes Only: Deletion/Duplication Panel