2.04.117	Genetic Testing for Mitochondrial Disorders		
Original Policy Date:	August 1, 2016	**Effective Date:**	November 1, 2021
Section:	2.0 Medicine	**Page:**	Page 1 of 22

Policy Statement

Genetic testing to establish a genetic diagnosis of a mitochondrial disorder may be considered **medically necessary** when signs and symptoms of a mitochondrial disorder are present and genetic testing may eliminate the need for muscle biopsy.

Targeted genetic testing for a known familial variant in at-risk relatives may be considered **medically necessary** as preconceptional carrier testing under **both** of the following conditions (see Benefit Application section):

I. There is a defined mitochondrial disorder in the family of sufficient severity to cause impairment of quality of life or functional status
II. A variant that is known to be pathogenic for that specific mitochondrial disorder has been identified in the index case

Genetic testing for mitochondrial disorders is considered **investigational** in **all** other situations when the criteria for medical necessity are not met.

NOTE: Refer to Appendix A to see the policy statement changes (if any) from the previous version.

Policy Guidelines

Mitochondrial disorders can be caused by variants in mitochondrial DNA (mtDNA) or nuclear DNA (nDNA). A 3-generation family history may suggest a mode of inheritance. A family history in which affected women transmit the disease to male and female children and affected men do not transmit the disease to their children suggests the familial variant(s) is in the mtDNA. A family history consistent with Mendelian autosomal dominant or autosomal recessive inheritance or with X-linked inheritance suggests the familial variant(s) is in the nDNA. De novo pathogenic variants are also possible.

Carrier screening for mitochondrial disorders associated with autosomal recessive inheritance of nDNA variants is addressed in Blue Shield of California Medical Policy: Genetic Testing for Mitochondrial Disorders

Testing Strategy

Individuals With a Suspected Mitochondrial Disorder

If the phenotype is highly suggestive of a specific disorder that is supported by the inheritance pattern noted in the family history, it would be reasonable to begin genetic testing with single genes or targeted multigene panels that test for pathogenic variants specific for that disorder.

If a mitochondrial disorder is suspected, but the phenotype is nonspecific, broader genetic testing is appropriate under the guidance of a clinical geneticist and genetics counselor. For patients in whom the family history is suggestive of a disorder due to pathogenic variant(s) in mtDNA, multigene panels or sequencing of the mitochondrial genome may be appropriate. If multiple mtDNA deletions are noted, or the family history is suggestive of a disorder due to variants in nDNA, then multigene panels covering known nuclear genes associated with mitochondrial disease may be appropriate. Testing using whole exome sequencing is reviewed in Blue Shield of California Medical Policy: Whole Exome and Whole Genome Sequencing for Diagnosis of Genetic Disorders.

Individuals With a Family Member With a Mitochondrial Disorder and Known Familial Variant

Targeted testing of the parents of a proband with a mitochondrial disorder and a confirmed pathogenic/likely pathogenic gene variant is done to identify mode of transmission [germline (autosomal recessive, autosomal dominant, X-linked, mitochondrial) vs. *de novo*] thereby indicating risk for future offspring and other family members.
Targeted testing for a known familial variant in parents and other at-risk relatives as part of preconceptional carrier testing is appropriate. At-risk relatives include only female relatives if the familial pathogenic variant is in the mtDNA but includes both male and female relatives if the familial pathogenic variant is in the nDNA.

Genetics Nomenclature Update

The Human Genome Variation Society nomenclature is used to report information on variants found in DNA and serves as an international standard in DNA diagnostics. It is being implemented for genetic testing medical evidence review updates starting in 2017 (see Table PG1). The Society's nomenclature is recommended by the Human Variome Project, the Human Genome Organization, and by the Human Genome Variation Society itself.

The American College of Medical Genetics and Genomics and the Association for Molecular Pathology standards and guidelines for interpretation of sequence variants represent expert opinion from both organizations, in addition to the College of American Pathologists. These recommendations primarily apply to genetic tests used in clinical laboratories, including genotyping, single genes, panels, exomes, and genomes. Table PG2 shows the recommended standard terminology - "pathogenic," "likely pathogenic," "uncertain significance," "likely benign," and "benign"-to describe variants identified that cause Mendelian disorders.

Table PG1. Nomenclature to Report on Variants Found in DNA

Previous	Updated	Definition
Mutation	Disease-associated variant	Disease-associated change in the DNA sequence
	Variant	Change in the DNA sequence
	Familial variant	Disease-associated variant identified in a proband for use in subsequent targeted genetic testing in first-degree relatives

Table PG2. ACMG-AMP Standards and Guidelines for Variant Classification

Variant Classification	Definition
Pathogenic	Disease-causing change in the DNA sequence
Likely pathogenic	Likely disease-causing change in the DNA sequence
Variant of uncertain significance	Change in DNA sequence with uncertain effects on disease
Likely benign	Likely benign change in the DNA sequence
Benign	Benign change in the DNA sequence

ACMG: American College of Medical Genetics and Genomics; AMP: Association for Molecular Pathology.

Genetic Counseling

Experts recommend formal genetic counseling for patients who are at risk for inherited disorders and who wish to undergo genetic testing. Interpreting the results of genetic tests and understanding risk factors can be difficult for some patients; genetic counseling helps individuals understand the impact of genetic testing, including the possible effects the test results could have on the individual or their family members. It should be noted that genetic counseling may alter the utilization of genetic testing substantially and may reduce inappropriate testing; further, genetic counseling should be performed by an individual with experience and expertise in genetic medicine and genetic testing methods.

Coding

There are CPT codes for genomic sequencing procedures (or next-generation sequencing panels) for mitochondrial diseases. If the panel complies with the requirements in the code descriptor, these codes may be used:

- **81440:** Nuclear encoded mitochondrial genes (e.g., neurologic or myopathic phenotypes), genomic sequence panel, must include analysis of at least 100 genes, including BCS1L, C10orf2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, and TYMP
- **81460:** Whole mitochondrial genome (e.g., Leigh syndrome, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes [MELAS], myoclonic epilepsy with ragged-red fibers [MERFF], neuropathy, ataxia, and retinitis pigmentosa [NARP], Leber hereditary optic neuropathy [LHON]), genomic sequence, must include sequence analysis of entire mitochondrial genome with heteroplasmy detection
- **81465:** Whole mitochondrial genome large deletion analysis panel (e.g., Kearns-Sayre syndrome, chronic progressive external ophthalmoplegia), including heteroplasmy detection, if performed

If the panel does not meet the requirements in the codes above or the test is not a panel, there are several mitochondrial tests listed in the CPT tier 2 molecular pathology codes.

Effective January 1, 2021, the following CPT code has been **revised**: Code 81401 includes:

- *MT-ATP6 (mitochondrially encoded ATP synthase 6)* (e.g., neuropathy with ataxia and retinitis pigmentosa [NARP], Leigh syndrome), common variants (e.g., m.8993T>G, m.8993T>C)
- *MT-ND4, MT-ND6 (mitochondrially encoded NADH dehydrogenase 4, mitochondrially encoded NADH dehydrogenase 6)* (e.g., Leber hereditary optic neuropathy [LHON]), common variants (e.g., m.11778G>A, m.3460G>A, m.14484T>C)
- *MT-TK (mitochondrially encoded tRNA lysine)* (e.g., myoclonic epilepsy with ragged-red fibers [MERRF]), common variants (e.g., m.8344A>G, m.8356T>C)
- *MT-ND5 (mitochondrially encoded tRNA leucine 1 [UUA/G], mitochondrially encoded NADH dehydrogenase 5)* (e.g., mitochondrial encephalopathy with lactic acidosis and stroke-like episodes [MELAS]), common variants (e.g., m.3243A>G, m.3271T>C, m.3252A>G, m.13513G>A)
- *MT-TL1 (mitochondrially encoded tRNA leucine 1 [UUA/G])* (e.g., diabetes and hearing loss), common variants (e.g., m.3243A>G, m.14709 T>C)
- *MT-TS1, MT-RNR1 (mitochondrially encoded tRNA serine 1 [UCN], mitochondrially encoded 12S RNA)* (e.g., nonsyndromic sensorineural deafness [including aminoglycoside-induced nonsyndromic deafness]), common variants (e.g., m.7445A>G, m.1555A>G)

Effective January 1, 2021, the following CPT code has been **revised**: Code 81403 includes:

- *MT-RNR1 (mitochondrially encoded 12S RNA)* (e.g., nonsyndromic hearing loss), full gene sequence
- *MT-TS1 (mitochondrially encoded tRNA serine 1)* (e.g., nonsyndromic hearing loss), full gene sequence

Effective January 1, 2021, the following CPT code has been **revised**: Code 81404 includes:

- *C10orf2 (chromosome 10 open reading frame 2)* (e.g., mitochondrial DNA depletion syndrome), full gene sequence
- *MPV17 (MpV17 mitochondrial inner membrane protein)*(e.g., mitochondrial DNA depletion syndrome), duplication/deletion analysis
- *NDUFA1 (NADH dehydrogenase [ubiquinone] 1 alpha subcomplex, 1, 7.5kDa)* (e.g., Leigh syndrome, mitochondrial complex I deficiency), full gene sequence
- *NDUFAF2 (NADH dehydrogenase [ubiquinone] 1 alpha subcomplex, assembly factor 2)* (e.g., Leigh syndrome, mitochondrial complex I deficiency), full gene sequence
- *NDUFS4 (NADH dehydrogenase [ubiquinone] Fe-S protein 4, 18kDa [NADH-coenzyme Q reductase])* (e.g., Leigh syndrome, mitochondrial complex I deficiency), full gene sequence
- *SCO2 (SCO cytochrome oxidase deficient homolog 2 [SCO1L])* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence

- *SLC25A4 (solute carrier family 25 [mitochondrial carrier; adenine nucleotide translocator], member 4)* (e.g., progressive external ophthalmoplegia), full gene sequence
- *TACO1 (translational activator of mitochondrial encoded cytochrome c oxidase I)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence

Effective January 1, 2021, the following CPT code has been **revised**: Code 81405 includes:

- *BCS1L (BCS1-like [S. cerevisiae])* (e.g., Leigh syndrome, mitochondrial complex III deficiency, GRACILE syndrome), full gene sequence
- *COX10 (COX10 homolog, cytochrome c oxidase assembly protein)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence
- *COX15 (COX15 homolog, cytochrome c oxidase assembly protein)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence
- *DGUOK (deoxyguanosine kinase)* (e.g., hepatocerebral mitochondrial DNA depletion syndrome), full gene sequence
- *MPV17 (MpV17 mitochondrial inner membrane protein)*(e.g., mitochondrial DNA depletion syndrome), full gene sequence
- *NDUFV1 (NADH dehydrogenase [ubiquinone] flavoprotein 1, 51kDa)* (e.g., Leigh syndrome, mitochondrial complex I deficiency), full gene sequence
- *RRM2B (ribonucleotide reductase M2 B [TP53 inducible])* (e.g., mitochondrial DNA depletion), full gene sequence
- *SCO1 (SCO cytochrome oxidase deficient homolog 1)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence
- *SURF1 (surfeit 1)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence
- *TK2 (thymidine kinase 2, mitochondrial)* (e.g., mitochondrial DNA depletion syndrome), full gene sequence
- *TYMP (thymidine phosphorylase)*(e.g., mitochondrial DNA depletion syndrome), full gene sequence

Effective January 1, 2021, the following CPT code has been **revised**: Code 81406 includes:

- *FASTKD2 (FAST kinase domains 2)* (e.g., mitochondrial respiratory chain complex IV deficiency), full gene sequence
- *NDUFS1 (NADH dehydrogenase [ubiquinone] Fe-S protein 1, 75kDa [NADH-coenzyme Q reductase])* (e.g., Leigh syndrome, mitochondrial complex I deficiency), full gene sequence
- *SDHA (succinate dehydrogenase complex, subunit A, flavoprotein [Fp])* (e.g., Leigh syndrome, mitochondrial complex II deficiency), full gene sequence

If there is no specific listing in the CPT molecular pathology code list for the mitochondrial DNA test that is performed, the unlisted molecular pathology code 81479 may be reported. If multiple unlisted mitochondrial DNA tests are performed, the unlisted code is only reported once for all of the unlisted tests.

Description

Mitochondrial diseases are multisystem diseases that arise from dysfunction in the mitochondrial protein complexes involved in oxidative metabolism. There are many related but distinct syndromes and some patients have overlapping syndromes. As a result, these disorders can be difficult to diagnose. Genetic testing has the potential to improve the accuracy of diagnosis for mitochondrial diseases. Genetic testing also has the potential to determine future risk of disease in individuals who have a close relative with a pathogenic variant.

Related Policies

- Whole Exome and Whole Genome Sequencing for Diagnosis of Genetic Disorders

Benefit Application

Benefit determinations should be based in all cases on the applicable contract language. To the extent there are any conflicts between these guidelines and the contract language, the contract language will control. Please refer to the member's contract benefits in effect at the time of service to determine coverage or non-coverage of these services as it applies to an individual member.

Some state or federal mandates (e.g., Federal Employee Program [FEP]) prohibits plans from denying Food and Drug Administration (FDA)-approved technologies as investigational. In these instances, plans may have to consider the coverage eligibility of FDA-approved technologies on the basis of medical necessity alone.

Regulatory Status

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments. Genetic testing for mitochondrial diseases is under the auspices of Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by Clinical Laboratory Improvement Amendments for high-complexity testing. To date, the U.S. Food and Drug Administration has chosen not to require any regulatory review of this test.

Rationale

Background
Mitochondrial DNA
Mitochondria are organelles within each cell that contain their own set of DNA, distinct from the nuclear DNA that makes up most of the human genome. Human mitochondrial DNA (mtDNA) consists of 37 genes. Thirteen genes code for protein subunits of the mitochondrial oxidative phosphorylation complex and the remaining 24 genes are responsible for proteins involved in the translation and/or assembly of the mitochondrial complex.[1,] Additionally, there are over 1000 nuclear genes coding for proteins that support mitochondrial function.[2,] The protein products from these genes are produced in the nucleus and later migrate to the mitochondria.

Mitochondrial DNA differs from nuclear DNA (nDNA) in several important ways. Inheritance of mtDNA does not follow traditional Mendelian patterns. Rather, mtDNA is inherited only from maternal DNA so disorders that result from variants in mtDNA can only be passed on by the mother. Also, there are thousands of copies of each mtDNA gene in each cell, as opposed to nDNA, which contains only 1 copy per cell. Because there are many copies of each gene, variants may be present in some copies of the gene but not others. This phenomenon is called heteroplasmy. Heteroplasmy can be expressed as a percentage of genes that have the variant ranging from 0% to 100%. Clinical expression of the variant will generally depend on a threshold effect (i.e., clinical symptoms will begin to appear when the percentage of mutated genes exceeds a threshold amount).[3,]

Mitochondrial Diseases
Primary mitochondrial diseases arise from dysfunction of the mitochondrial respiratory chain. The mitochondrial respiratory chain is responsible for aerobic metabolism, and dysfunction, therefore, affects a wide variety of physiologic pathways dependent on aerobic metabolism. Organs with a high-energy requirement, such as the central nervous system, cardiovascular system, and skeletal muscle, are preferentially affected by mitochondrial dysfunction.

The prevalence of these disorders has risen over the last 2 decades as the pathophysiology and clinical manifestations have been better characterized. It is currently estimated that the minimum prevalence of primary mitochondrial diseases is at least 1 in 5000.[1,4]

Some specific mitochondrial diseases are listed next:

- Mitochondrial encephalopathy with lactic acidosis and stroke-like episodes syndrome;
- Myoclonic epilepsy with ragged red fibers syndrome;
- Kearns-Sayre syndrome;
- Leigh syndrome;
- Chronic progressive external ophthalmoplegia;
- Leber hereditary optic neuropathy;
- Neurogenic weakness with ataxia and retinitis pigmentosa.

Most of these disorders are characterized by multisystem dysfunction, which generally includes myopathies and neurologic dysfunction and may involve multiple other organs. Each defined mitochondrial disease has a characteristic set of signs or symptoms. The severity of illness is heterogeneous and can vary markedly. Some patients will have only mild symptoms for which they never require medical care, while other patients have severe symptoms, a large burden of morbidity, and a shortened life expectancy.

Diagnosis

The diagnosis of mitochondrial diseases can be difficult. The individual symptoms are nonspecific, and symptom patterns can overlap considerably. As a result, a patient often cannot be easily classified into 1 particular syndrome.[5] Biochemical testing is indicated for patients who do not have a clear clinical picture of 1 specific disorder. Measurement of serum lactic acid is often used as a screening test but the test is neither sensitive nor specific for mitochondrial diseases.[2]

A muscle biopsy can be performed if the diagnosis is uncertain after biochemical workup. However, this invasive test is not definitive in all cases. The presence of "ragged red fibers" on histologic analysis is consistent with a mitochondrial disease. Ragged red fibers represent a proliferation of defective mitochondria.[1] This characteristic finding may not be present in all types of mitochondrial diseases and also may be absent early in the course of disease.[2]

Treatment

Treatment of mitochondrial disease is largely supportive because there are no specific therapies that impact the natural history of the disorder.[5] Identification of complications such as diabetes and cardiac dysfunction is important for early treatment of these conditions. A number of vitamins and cofactors (e.g., coenzyme Q, riboflavin) have been used but empirical evidence of benefit is lacking.[6] Exercise therapy for myopathy is often prescribed but the effect on clinical outcomes is uncertain.[5] The possibility of gene transfer therapy is under consideration but is at an early stage of development and untested in clinical trials.

Genetic Testing

Mitochondrial diseases can be caused by pathogenic variants in the maternally inherited mtDNA or 1 of many nDNA genes. Genetic testing for mitochondrial diseases may involve testing for point mutations, deletion and duplication analysis, and/or whole exome sequencing of nuclear or mtDNA. The type of testing done depends on the specific disorder being considered. For some primary mitochondrial diseases such as mitochondrial encephalopathy with lactic acidosis and stroke-like episodes and myoclonic epilepsy with ragged red fibers, most variants are point mutations, and there is a finite number of variants associated with the disorder. When testing for one of these disorders, known pathogenic variants can be tested for with polymerase chain reaction, or sequence analysis can be performed on the particular gene. For other mitochondrial diseases, such as chronic progressive external ophthalmoplegia and Kearns-Sayre syndrome, the most common variants are deletions, and therefore duplication and deletion analysis would be the first test when these disorders are suspected. Table 1 provides examples of

clinical symptoms and particular genetic variants in mtDNA or nDNA associated with particular mitochondrial syndromes.[5,7,] A repository of published and unpublished data on variants in human mtDNA is available in the MITOMAP database.[8,] Lists of mtDNA and nDNA genes that may lead to mitochondrial diseases and testing laboratories in the U.S. are provided at Genetic Testing Registry of the National Center for Biotechnology Information website.[9,]

Table 1. Examples of Mitochondrial Diseases, Clinical Manifestations, and Associated Pathogenic Genes

Syndrome	Main Clinical Manifestations	Major Genes Involved
MELAS	• Stroke-like episodes at age <40 y • Seizures and/or dementia • Pigmentary retinopathy • Lactic acidosis	• *MT-TL1*, *MT-ND5* (>95%) • *MT-TF*, *MT-TH*, *MT-TK*, *MT-TQ*, *MT-TS1*, *MT-TS2*, *MT-ND1*, *MT-ND6* (rare)
MERFF	• Myoclonus • Seizures • Cerebellar ataxia • Myopathy	• *MT-TK* (>80%) • *MT-TF*, *MT-TP* (rare)
CPEO	• External ophthalmoplegia • Bilateral ptosis	• Various deletions of mitochondrial DNA
Kearns-Sayre syndrome	• External ophthalmoplegia at age <20 y • Pigmentary retinopathy • Cerebellar ataxia • Heart block	• Various deletions of mitochondrial DNA
Leigh syndrome	• Subacute relapsing encephalopathy • Infantile-onset • Cerebellar/brainstem dysfunction	• *MT-ATP6*, *MT-TL1*, *MT-TK*, *MT-TW*, *MT-TV*, *MT-ND1*, *MT-ND2*, *MT-ND3*, *MT-ND4*, *MT-ND5*, *MT-ND6*, *MT-CO3* • Mitochondrial DNA deletions (rare) • *SUCLA2*, *NDUSFx*, *NDFVx*, *SDHA*, *BCS 1L*, *SURF1*, *SCO2*, *COX15*
LHON	• Painless bilateral visual failure • Male predominance • Dystonia • Cardiac pre-excitation syndromes	• *MT-ND1*, *MT-ND4*, *MT-ND6*
NARP	• Peripheral neuropathy • Ataxia • Pigmentary retinopathy	• *MT-ATP6*
MNGIE	• Intestinal malabsorption • Cachexia • External ophthalmoplegia • Neuropathy	• *TP*
IOSCA	• Ataxia • Hypotonia • Athetosis • Ophthalmoplegia • Seizures	• *TWINKLE*
SANDO	• Ataxic neuropathy • Dysarthria • Ophthalmoparesis	• *POLG*
Alpers syndrome	• Intractable epilepsy • Psychomotor regression • Liver disease	• *POLG*, *DGUOK*, *MPV17*
GRACILE	• Growth retardation • Aminoaciduria • Cholestasis • Iron overload	• *NDUSFx*

Syndrome	Main Clinical Manifestations	Major Genes Involved
	• Lactic acidosis	
Coenzyme Q_{10} deficiency	• Encephalopathy • Steroid-resistant nephrotic syndrome • Hypertrophic cardiomyopathy • Retinopathy • Hearing loss	• *COQ2* • *COQ9* • *CABC1* • *ETFDH*

Adapted from Chinnery et al (2014)[5] and Angelini et al (2009).[7]
CPEO: chronic progressive external ophthalmoplegia; GRACILE: growth retardation, aminoaciduria, cholestasis, iron overload, early death; IOSCA: infantile onset spinal cerebellar atrophy; LHON: Leber hereditary optic neuropathy; MELAS: mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes; MERFF: myoclonic epilepsy with ragged-red fibers; MNGIE: mitochondrial neurogastrointestinal encephalopathy; NARP: neuropathy, ataxia, and retinitis pigmentosa; SANDO: sensory ataxia, neuropathy, dysarthria and ophthalmoplegia.

Literature Review
Evidence reviews assess whether a medical test is clinically useful. A useful test provides information to make a clinical management decision that improves the net health outcome. That is, the balance of benefits and harms is better when the test is used to manage the condition than when another test or no test is used to manage the condition.

The first step in assessing a medical test is to formulate the clinical context and purpose of the test. The test must be technically reliable, clinically valid, and clinically useful for that purpose. Evidence reviews assess the evidence on whether a test is clinically valid and clinically useful. Technical reliability is outside the scope of these reviews, and credible information on technical reliability is available from other sources.

Mitochondrial Diseases
The clinical validity and utility of testing for mitochondrial diseases for both indications are presented together, focusing discretely on each indication when evaluating clinical usefulness.

Clinical Context and Test Purpose
The purpose of genetic testing in patients who have signs and symptoms of mitochondrial diseases is to confirm the diagnosis. Diagnosis of a specific mitochondrial disease is complex due to the phenotypic heterogeneity and general lack of genotype-phenotype associations, particularly in infants and children. Identifying a disease-causing variant can end the diagnostic odyssey for families, help to avoid muscle biopsy for patients, and provide the information needed for testing asymptomatic family members. While the current treatment for most patients with mitochondrial disease is primarily supportive, potential treatments exist for patients with coenzyme Q10 deficiency and mitochondrial neurogastrointestinal encephalopathy (MNGIE), although evidence for their effectiveness is not conclusive.

The 2 questions addressed in this evidence review are: (1) Does genetic testing for mitochondrial diseases improve the net health outcome in individuals with signs and symptoms of a mitochondrial disease, and (2) Does genetic testing for mitochondrial diseases improve the net health outcome in asymptomatic relatives of an individual with a mitochondrial disease?
The following PICO was used to select literature to inform this review.

Populations
The relevant populations of interest for both indications are individuals with signs and symptoms of a mitochondrial disease and individuals who are asymptomatic with a close relative who has a mitochondrial disease and a known pathogenic variant.

Interventions
The tests being considered are genetic testing and targeted familial variant testing. Testing for the individual variants associated with mitochondrial diseases is offered by numerous labs.

Genetic panel testing is also available, with numerous panels available. Some are disease-specific panels that include only a small number of genes associated with a particular mitochondrial disease.

Several labs currently offer panel testing for mitochondrial and nuclear genes associated with multiple mitochondrial diseases by next-generation sequencing (NGS). The number of genes included in these panels varies widely.

Comparators
The following practice is currently being used for patients with signs and/or symptoms of a mitochondrial disorder: standard clinical workup for diagnosis without genetic testing, which might include measurements of lactate and pyruvate in plasma and cerebrospinal fluid; plasma, urine, and cerebrospinal fluid amino acids; plasma acylcarnitines; and urine organic acids. Additionally, a muscle biopsy has been traditionally considered the criterion standard for the diagnosis of mitochondrial diseases. For individuals who are asymptomatic with a close relative who has a mitochondrial disease and a known pathogenic variant, the following practice is currently being used: standard risk assessment without genetic testing.

Outcomes
The general outcomes of interest include test validity, other test performance measures, symptoms, functional outcomes, changes in reproductive decision making, health status measures, and quality of life.

The beneficial outcomes resulting from a true test result are establishing a diagnosis and avoiding muscle biopsy. The harmful outcomes resulting from a false test result are a delay in diagnosis and additional testing.

Genetic testing for variants associated with mitochondrial disease is complex. Referral for genetic counseling is important for the explanation of the genetic disease, heritability, genetic risk, test performance, and possible outcomes.

The time frame of interest is the time to establish a diagnosis for those who are asymptomatic or to perform preconceptional carrier testing for those with a close relative who has a mitochondrial disease and a known pathogenic variant.

Study Selection Criteria
For the evaluation of clinical validity of genetic testing for mitochondrial disorders, methodologically credible studies were selected using the following principles:

- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described
- Included a validation cohort separate from development cohort.

Clinically Valid
A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

Review of Evidence
The evidence on the clinical sensitivity and specificity of genetic testing for mitochondrial diseases is limited. There are some small case series of patients with a well-defined syndrome such as mitochondrial encephalomyopathy, lactic acidosis, and stroke-likesymptoms (MELAS) syndrome, and some studies include larger numbers of patients with less specific clinical diagnoses. There are wide variations in reported testing yields, probably reflecting the selection

process used to evaluate patients for testing. Some representative information pertinent to clinical validity is reviewed here.

Clinical Sensitivity

Several series of patients with mixed diagnoses or suspected mitochondrial diseases have been published. In these studies, the variant detection rate (or yield) may or may not be an accurate estimate of clinical sensitivity, because the proportion of patients with a mitochondrial disease is uncertain (see Table 2).

Table 2. Studies Reporting Diagnostic Yield in Patient With Suspected Mitochondrial Diseases

Study	Population	N	Genetic Test	Design	Yield, n (%)
Riley et al (2020)[10]	Australian cohort of children with suspected mitochondrial disease	40	Trio GS	• Prospective enrollment • Selection method not reported	• 22 (67.5%) with "causal" variants • 22 (50%) with a "definitive molecular diagnosis" per modified Nijmegen mitochondrial disease severity scale
Nogueira et al (2019)[11]	Children and adults suspected of having mitochondrial disease	146 (including 110 children)	Custom NGS panel of 209 genes followed by Sanger sequencing	• Prospective/retrospective not reported • Selection method not reported	• 16 (11%) with "causative" variants • 20 (14%) with VUS • 54/107 (50%) with defects identified on muscle biopsy
Fang et al (2017)[12]	Children and young adults suspected of having mitochondrial disease	141	Targeted NGS	• Prospective enrollment • Selection method not reported	• 40 (28%) with "causative" variants
Legati et al (2016)[13]	Patients clinically diagnosed with mitochondrial disease	NGS=125 WES=10	Custom NGS panel of 132 genes followed by WES for those negative after NGS	• Prospective/retrospective not reported • Selection method not reported	*NGS:* • 19 (15%) with "causative" variants • 27 (22%) with possible pathoge

						nic variants
					WES: • 6 (60%) with "causative" variants	
Pronicka et al (2016)[14]	Patients referred for possible or probable mitochondrial disease	113 (including 47 neonates)	WES followed by Sanger sequencing	• Prospective/retrospective samples included; consecutive patients included in prospective sample • Selection method for retrospective samples not reported	• 67 (59%) with likely pathogenic variants • 30 (64%) of neonates with likely pathogenic variants	
Kohda et al (2016)[15]	Children with early-onset respiratory chain disease	142	NGS of the entire mtDNA plus WES of the nDNA	• Prospective enrollment • Selection method not reported	• 29 (20%) with known pathogenic variants • 53 (37%) inconclusive but possibly pathogenic variants	
Wortmann et al (2015)[16]	Children and young adults with a suspected mitochondrial disease	109	Panel of 238 genes associated with mitochondrial disease followed by WES	• Prospective enrollment • Selection method not reported	• 42 (39%) with pathogenic variants	
Ohtake et al (2014)[17]	Patients with mitochondrial respiratory chain diseases	104	NGS of exome of nDNA	• Prospective/retrospective not reported • Selection method not reported	• 18 (17%) with known pathogenic variants • 27 (26%) with likely pathogenic variants	
Taylor et al (2014)[18]	Patients with suspected mitochondrial disease and multiple respiratory chain complex defects	53	WES validated with Sanger sequencing	• Prospective/retrospective not reported; selection method not reported but only included patients with multiple respiratory chain complex defects	• 28 (53%) with known pathogenic variants • 4 (8%) with likely pathoge	

					nic variants
Lieber et al (2013)[19]	Patients with suspected mitochondrial diseases and heterogeneous clinical symptoms	102	NGS of entire mitochondrial genome and 1598 nuclear genes	• Prospective/retrospective not reported • Patients in a repository having highest clinical suspicion of disease selected	• 22 (22%) with likely pathogenic variants • 26 (25%) VUS
DaRe et al (2013)[20]	Patients with diagnosed or suspected mitochondrial diseases	148	NGS panel of 447 genes (Transgenomic)	• Prospective/retrospective not reported; consecutive patients	• 13 (9%) possible pathogenic variants • 67 (45%) with VUS
McCormick et al (2013)[21]	Patients with suspected mitochondrial disease	152	mtDNA genome sequencing, genome-wide SNV microarray, and step-wise individual sequencing of select nuclear genes	• Retrospective chart review; consecutive patients included	• 25 (16%) with "definite" mitochondrial disease • 46 (30%) with "probable" or "possible" mitochondrial disease
Calvo et al (2012)[22]	Infants with clinical and biochemical evidence of oxidative phosphorylation disease	42	NGS of entire mitochondrial genome and 1034 nuclear genes	• Prospective/retrospective not reported • Selection method not reported	• 10 (24%) with known pathogenic variants • 13 (31%) possible pathogenic variants
Qi et al (2007)[23]	Patients with mitochondrial encephalopathies (MELAS, MERRF, Leigh syndrome, LHON, or an overlap syndrome)	552	PCR-RFLP analysis, site-specific PCR, and PCR-sequencing methods of common mitochondrial pathogenic variants	• Prospective/retrospective not reported • Selection method not reported	• 64 (12%) with pathogenic variants

GS: genome sequencing; LHON: Leber hereditary optic neuropathy; MELAS: mitochondrial encephalopathy, lactic acidosis, and stroke-like symptoms; MERRF: myoclonus epilepsy with ragged red fibers; mtDNA: mitochondrial DNA; nDNA: nuclear DNA: NGS: next-generation sequencing; PCR: polymerase chain reaction; RFLP: restriction fragment length polymorphism; SNV: single nucleotide variant; VUS: variant of uncertain significance; WES: whole-exome sequencing.

Clinical Specificity

The clinical specificity of genetic testing for mitochondrial diseases is largely unknown, but false-positive results have been reported.[24] Some epidemiologic evidence is available on the population prevalence of pathogenic variants, which provides some indirect evidence on the potential for false-positive results.

A study of population-based testing reported that the prevalence of pathogenic variants is higher than the prevalence of clinical disease. In this study by Elliott et al (2008), 3168 consecutive newborns were tested for the presence of 1 or more of the 10 most common mitochondrial DNA (mtDNA) variants thought to be associated with clinical disease.[25] At least 1 pathogenic variant was identified in 15 (0.54%) of 3168 people (95% confidence interval [CI], 0.30% to 0.89%). This finding implies that there are many more people with a variant who are asymptomatic than there are people with clinical disease, and this raises the possibility of false-positive results on genetic testing.

An earlier population-based study by Majamaa et al (1998) evaluated the prevalence of the nucleotide 3243 variant associated with MELAS syndrome.[26] This study included 245201 subjects from Finland. Participants were screened for common symptoms associated with MELAS, and screen-positive patients were tested for the variant. The population prevalence was estimated at 16.3 (0.16%) in 100000. This study might have underestimated the prevalence because patients who screened negative were not tested for the variant.

In addition to false-positive results, there are variants of uncertain significance (VUS) detected in substantial numbers of patients. The number of variants increases when NGS methods are used to examine a larger portion of the genome. In the study by DaRe et al (2013), which used targeted exome sequencing, VUS were far more common than definite pathogenic variants.[20] In that study, 148 patients with suspected or confirmed mitochondrial diseases were tested using a genetic panel that included 447 genes. Thirteen patients were found to have pathogenic variants. In contrast, VUS were very common, occurring at a rate of 6.5 per patient.

A further consideration is the clinical heterogeneity of variants known to be pathogenic. Some variants associated with mitochondrial diseases can result in heterogeneous clinical phenotypes, and this may cause uncertainty about the pathogenicity of the variant detected. For example, the nucleotide 3243 variant in the *MT-TL1* gene is found in most patients with clinically defined MELAS syndrome.[27] This same variant has also been associated with chronic progressive external ophthalmoplegia (CPEO) and Leigh syndrome.[28] Therefore, the more closely the clinical syndrome matches MELAS, the more likely a positive genetic test will represent a pathogenic variant.

Section Summary: Clinically Valid

Case series and cohort studies have provided information on the diagnostic testing yield. For patients with signs and symptoms of mitochondrial diseases, but without a well-defined clinical syndrome, the variant detection rates differ by the population included, testing strategy, and outcome reported. Studies reporting a yield of known pathogenic variants for NGS panels tend to report rates in the 15% to 25% range. There is very little evidence on clinical specificity, but there have been false-positive tests reported.

Clinically Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, or more effective therapy, or avoid unnecessary therapy, or avoid unnecessary testing.

Review of Evidence

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from randomized controlled trials.
No direct evidence on clinical utility was identified.

Chain of Evidence

Indirect evidence on clinical utility rests on clinical validity. If the evidence is insufficient to demonstrate test performance, no inferences can be made about clinical utility.

There are 2 ways that clinical utility might be demonstrated from a chain of evidence. First, confirmation of the diagnosis may have benefits in ending the need for further clinical workup and eliminating the need for a muscle biopsy. Second, knowledge of pathogenic variant status may have benefits for family members in determining their risk of developing the disease.

Confirmation of Diagnosis in Individuals With Signs and/or Symptoms of a Mitochondrial Disease
For patients with signs and symptoms consistent with a defined mitochondrial syndrome, testing can be targeted to those pathogenic variants associated with that particular syndrome. In the presence of a clinical picture consistent with the syndrome, the presence of a known pathogenic variant will confirm the diagnosis with a high degree of certainty. Confirmation of the diagnosis by genetic testing can result in a reduced need for further testing, especially a muscle biopsy. However, a negative genetic test in the blood does not rule out a mitochondrial disease and should be reflexed to testing in the affected tissue to avoid the possibility of missing tissue-specific variants or low levels of heteroplasmy in blood.

There is no specific therapy for mitochondrial diseases. Treatment is largely supportive management for complications of the disease. It is possible that confirmation of the diagnosis by genetic testing would lead to management changes, such as increased surveillance for complications of the disease and/or the prescription of exercise therapy or antioxidants. However, the impact of these management changes on health outcomes is not known. A Cochrane review updated in 2012 by Pfeffer and coworkers did not find any clear evidence supporting the use of any intervention for the treatment of mitochondrial disorders.[29.]

Testing of Asymptomatic Individuals With a Close Relative Who Has a Mitochondrial Disease and a Known Pathogenic Variant
Confirmation of a pathogenic variant has implications for family members of the affected person. Knowledge of variant status will clarify the inheritance pattern of the variant, thus clarifying risk to family members. For example, for a male patient with MELAS syndrome, confirmation of a pathogenic variant in the mtDNA would indicate that his offspring are not at risk for inheriting the variant, because the inheritance of the mitochondrial variant could only occur through the mother. In contrast, identification of a pathogenic variant in nuclear DNA (nDNA) would indicate that his offspring are at risk for inheriting the variant.

Reproductive Testing
When there is a disease of moderate severity or higher, it is reasonable to assume that many patients will consider the results of testing in reproductive decision-making. For purposes of informing family planning, when a pathogenic variant is detected in the nDNA of a prospective parent or in the mtDNA of a prospective mother, the prospective parent can choose to refrain from having children. If the variant is in the nDNA, the prospective parent could also choose medically-assisted reproduction during which pre-implantation testing would permit a choice to avoid an affected offspring. The use of pre-implantation testing when a pathogenic variant is identified in the mtDNA of an affected mother is complicated by issues of heteroplasmy of the mtDNA variant, threshold levels, and phenotypic expression leading.

Section Summary: Clinically Useful

For diagnostic testing, clinical utility is relatively high when a definite diagnosis cannot be made without genetic testing. In this situation, a positive test for a pathogenic variant will confirm the diagnosis and may avoid further testing, including invasive tests (e.g., muscle biopsy). It is likely that confirmation of the diagnosis will lead to management changes, including referral to a specialist in mitochondrial disease. However, it is not known whether these management changes improve outcomes because of the lack of research on treatment interventions for mitochondrial diseases.

For testing at-risk relatives, clinical utility can also be demonstrated. When a disease phenotype displays moderate-to-severe disease, it is likely that knowledge of variant status will affect reproductive decision-making. When a pathogenic variant is detected in a prospective parent, the prospective parent can choose to refrain from having children or may be able to choose medically-assisted reproduction.

Summary of Evidence

For individuals with signs and/or symptoms of a mitochondrial disease who receive genetic testing, the evidence includes case series and cohort studies. Relevant outcomes are test validity, other test performance measures, symptoms, functional outcomes, health status measures, and quality of life. There is some evidence on clinical validity that varies by the patient population and testing strategy. Studies reporting diagnostic yield for known pathogenic variants using NGS panels tend to report rates ranging from 15% to 25%. Clinical specificity is unknown, but population-based studies have indicated that the prevalence of certain variants exceeds the prevalence of clinical disease, suggesting that the variant will be found in some people without the clinical disease (false-positives). Clinical utility is relatively high for confirming the diagnosis of mitochondrial diseases in people who have signs and symptoms of the disease. In these patients, a positive result in genetic testing can avoid a muscle biopsy and eliminate the need for further clinical workup. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who are asymptomatic with a close relative with a mitochondrial disease and a known pathogenic variant and who receive targeted familial variant testing, the evidence includes case series and cohort studies. Relevant outcomes are test validity, other test performance measures, changes in reproductive decision-making, symptoms, functional outcomes, health status measures, and quality of life. Clinical validity is expected to be high for targeted testing of a known familial variant, assuming sufficient analytic validity. Clinical utility can be demonstrated by testing at-risk family members who have a close relative with a pathogenic variant. When a specific mitochondrial disease is present in the family that is severe enough to cause impairment and/or disability, genetic testing may impact reproductive decision-making. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

Supplemental Information

The purpose of the following information is to provide reference material. Inclusion does not imply endorsement or alignment with the evidence review conclusions.

Practice Guidelines and Position Statements

Guidelines or position statements will be considered for inclusion in 'Supplemental Information' if they were issued by, or jointly by, a US professional society, an international society with US representation, or National Institute for Health and Care Excellence (NICE). Priority will be given to guidelines that are informed by a systematic review, include strength of evidence ratings, and include a description of management of conflict of interest.

Mitochondrial Medicine Society

The Mitochondrial Medicine Society (2015) published a consensus statement on the diagnosis and management of mitochondrial disease.[30.] Most evidence was grade III or less (case-control,

low-quality cohort studies, or expert opinion without an explicit critical appraisal) using the Oxford Centre for Evidence-Based Medicine criteria. Consensus recommendations were reported using the Delphi method. A subset of the consensus recommendations for DNA testing are as follows:

1. "Massively parallel sequencing/NGS [next-generation sequencing] of the mtDNA [mitochondrial DNA] genome is the preferred methodology when testing mtDNA and should be performed in cases of suspected mitochondrial disease instead of testing for a limited number of pathogenic point mutations.
2. mtDNA deletion and duplication testing should be performed in cases of suspected mitochondrial disease via NGS of the mtDNA genome, especially in all patients undergoing a diagnostic tissue biopsy.
    a. If a single small deletion is identified using polymerase chain reaction-based analysis, then one should be cautious in associating these findings with a primary mitochondrial disorder.
    b. When multiple mtDNA deletions are noted, sequencing of nuclear genes involved in mtDNA biosynthesis is recommended.
3. When considering nuclear gene testing in patients with likely primary mitochondrial disease, NGS methodologies providing complete coverage of known mitochondrial disease genes is preferred. Single-gene testing should usually be avoided because mutations in different genes can produce the same phenotype. If no known mutation is identified via known NGS gene panels, then whole exome sequencing should be considered."

U.S. Preventive Services Task Force Recommendations

Not applicable.

Medicare National Coverage

There is no national coverage determination. In the absence of a national coverage determination, coverage decisions are left to the discretion of local Medicare carriers.

Ongoing and Unpublished Clinical Trials

Some currently unpublished trials that might influence this review are listed in Table 3.

Table 3. Summary of Key Trials

NCT No.	Trial Name	Planned Enrollment	Completion Date
NCT04912843[a]	A Phase 1/2/3, Single-arm, Multi-center, Two-stage Clinical Trial to Evaluate the Safety and Efficacy of Gene Therapy for Leber Hereditary Optic Neuropathy (LHON) Associated With ND4 Mutation	55	Apr 2027 (recruiting)
NCT03747328[a]	A Phase 2a, Open-label Study to Evaluate the Safety, Tolerability, and Clinical Activity of ABI-009 (Nab-sirolimus) in Patients With Genetically-confirmed Leigh or Leigh-like Syndrome	32	Mar 202 5 (not yet recruiting)
NCT03153293	Safety and Efficacy Study of Gene Therapy for The Treatment of Leber's Hereditary Optic Neuropathy	159	Jan 202 5
NCT03293524[a]	Efficacy and Safety of Bilateral Intravitreal Injection of GS010: A Randomized, Double-Masked, Placebo-Controlled Trial in Subjects Affected With G11778A ND4 Leber Hereditary Optic Neuropathy for Up to One Year (REFLECT)	90	Jun 2024
NCT02161380	An Open-label Dose Escalation Study of an Adeno-associated Virus Vector (scAAV2-P1ND4v2) for Gene Therapy of Leber's Hereditary Optic Neuropathy (LHON) Caused by the G11778A Mutation in Mitochondrial DNA	28	Mar 2023
NCT03406104[a]	Long-term Follow-up of ND4 LHON Subjects Treated With GS010 Ocular Gene Therapy in the RESCUE or REVERSE Phase III Clinical Trials	61	Aug 2022
NCT04165239[a]	A Phase IIb Double-blind, Randomised, Placebo-controlled, Multi-centre, Confirmative Three-way Cross-over Study on	27	Mar 2022 (recruiting)

	Cognitive Function With Two Doses of KH176 in Subjects With a Genetically Confirmed Mitochondrial DNA tRNALeu(UUR) m.3243A>G Mutation (KHENERGYZE)		
NCT04102501[a]	A Randomized, Double-Blind, Controlled, Phase 2/3 Study to Assess Efficacy, Long Term Safety and Tolerability of RT001 in Subjects With Friedreich's Ataxia	65	Dec 2021
NCT02774005[a]	External Natural History Controlled, Open-Label Intervention Study to Assess the Efficacy and Safety of Long-Term Treatment With Raxone® in Leber's Hereditary Optic Neuropathy (LHON) (LEROS)	199	March 2021
NCT03428178	Efficacy Study of Gene Therapy for The Treatment of Acute LHON Onset Within Three Months	120	Dec 2020
NCT03917225[a]	A Double-Blind, Placebo-controlled Study on the Effects of MIN-102 on Biochemical, Imaging, Neurophisyiological, and Clinical Markers in Patients With Friedreich's Ataxia (FRAMES)	36	Sep 2020

NCT: national clinical trial.
[a] Denotes industry-sponsored or cosponsored trial.

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Documentation for Clinical Review

Please provide the following documentation:

- History and physical and/or consultation notes including:
  - Clinical findings (i.e., pertinent symptoms and duration)
  - Comorbidities
  - Activity and functional limitations
  - Family history if applicable
  - Reason for procedure/test/device, when applicable
  - Pertinent past procedural and surgical history

  - Past and present diagnostic testing and results as applicable
  - Prior conservative treatments, duration, and response
  - Treatment plan (i.e., surgical intervention) if applicable
- Consultation and medical clearance report(s), when applicable
- Radiology report(s) and interpretation (i.e., MRI, CT, discogram)
- Laboratory results
- Other pertinent multidisciplinary notes/reports: (e.g., psychological or psychiatric evaluation, physical therapy, multidisciplinary pain management) when applicable

Post Service (in addition to the above, please include the following):
- Results/reports of tests performed
- Procedure report(s)

Coding

This Policy relates only to the services or supplies described herein. Benefits may vary according to product design; therefore, contract language should be reviewed before applying the terms of the Policy.

The following codes are included below for informational purposes. Inclusion or exclusion of a code(s) does not constitute or imply member coverage or provider reimbursement policy. Policy Statements are intended to provide member coverage information and may include the use of some codes for clarity. The Policy Guidelines section may also provide additional information for how to interpret the Policy Statements and to provide coding guidance in some cases.

Type	Code	Description
CPT®	81401	Molecular Pathology Procedure Level 2 ***(Code revision effective 1/1/2021)***
	81403	Molecular Pathology Procedure Level 4 ***(Code revision effective 1/1/2021)***
	81404	Molecular Pathology Procedure Level 5 ***(Code revision effective 1/1/2021)***
	81405	Molecular Pathology Procedure Level 6 ***(Code revision effective 1/1/2021)***
	81406	Molecular Pathology Procedure Level 7 ***(Code revision effective 1/1/2021)***
	81440	Nuclear encoded mitochondrial genes (e.g., neurologic or myopathic phenotypes), genomic sequence panel, must include analysis of at least 100 genes, including BCS1L, C10orf2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, and TYMP
	81460	Whole mitochondrial genome (e.g., Leigh syndrome, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes [MELAS], myoclonic epilepsy with ragged-red fibers [MERFF], neuropathy, ataxia, and retinitis pigmentosa [NARP], Leber hereditary optic neuropathy [LHON]), genomic sequence, must include sequence analysis of entire mitochondrial genome with heteroplasmy detection
	81465	Whole mitochondrial genome large deletion analysis panel (e.g., Kearns-Sayre syndrome, chronic progressive external ophthalmoplegia), including heteroplasmy detection, if performed
	81479	Unlisted molecular pathology procedure
HCPCS	None	

Policy History

This section provides a chronological history of the activities, updates and changes that have occurred with this Medical Policy.

Effective Date	Action
08/01/2016	BCBSA Medical Policy adoption
08/01/2017	Policy revision with position change
08/01/2018	Policy revision without position change
08/01/2019	Policy revision without position change
08/01/2020	Annual review. No change to policy statement.
12/01/2020	No change to policy statement. Policy guidelines and literature updated.
01/01/2021	Coding Update
11/01/2021	Annual review. No change to policy statement. Policy guidelines and literature review updated.

Definitions of Decision Determinations

Medically Necessary: Services that are Medically Necessary include only those which have been established as safe and effective, are furnished under generally accepted professional standards to treat illness, injury or medical condition, and which, as determined by Blue Shield, are: (a) consistent with Blue Shield medical policy; (b) consistent with the symptoms or diagnosis; (c) not furnished primarily for the convenience of the patient, the attending Physician or other provider; (d) furnished at the most appropriate level which can be provided safely and effectively to the patient; and (e) not more costly than an alternative service or sequence of services at least as likely to produce equivalent therapeutic or diagnostic results as to the diagnosis or treatment of the Member's illness, injury, or disease.

Investigational/Experimental: A treatment, procedure, or drug is investigational when it has not been recognized as safe and effective for use in treating the particular condition in accordance with generally accepted professional medical standards. This includes services where approval by the federal or state governmental is required prior to use, but has not yet been granted.

Split Evaluation: Blue Shield of California/Blue Shield of California Life & Health Insurance Company (Blue Shield) policy review can result in a split evaluation, where a treatment, procedure, or drug will be considered to be investigational for certain indications or conditions, but will be deemed safe and effective for other indications or conditions, and therefore potentially medically necessary in those instances.

Prior Authorization Requirements (as applicable to your plan)

Within five days before the actual date of service, the provider must confirm with Blue Shield that the member's health plan coverage is still in effect. Blue Shield reserves the right to revoke an authorization prior to services being rendered based on cancellation of the member's eligibility. Final determination of benefits will be made after review of the claim for limitations or exclusions.

Questions regarding the applicability of this policy should be directed to the Prior Authorization Department at (800) 541-6652, or the Transplant Case Management Department at (800) 637-2066 ext. 3507708 or visit the provider portal at www.blueshieldca.com/provider.

Disclaimer: This medical policy is a guide in evaluating the medical necessity of a particular service or treatment. Blue Shield of California may consider published peer-reviewed scientific literature, national guidelines, and local standards of practice in developing its medical policy. Federal and state law, as well as contract language, including definitions and specific contract provisions/exclusions, take precedence

over medical policy and must be considered first in determining covered services. Member contracts may differ in their benefits. Blue Shield reserves the right to review and update policies as appropriate.

Appendix A

POLICY STATEMENT (No changes)	
BEFORE	**AFTER**
Genetic Testing for Mitochondrial Disorders 2.04.117 **Policy Statement:** Genetic testing to establish a genetic diagnosis of a mitochondrial disorder may be considered **medically necessary** when signs and symptoms of a mitochondrial disorder are present and genetic testing may eliminate the need for muscle biopsy. Targeted genetic testing for a known familial variant in at-risk relatives may be considered **medically necessary** as preconceptional carrier testing under **both** of the following conditions (see Benefit Application section): I. There is a defined mitochondrial disorder in the family of sufficient severity to cause impairment of quality of life or functional status II. A variant that is known to be pathogenic for that specific mitochondrial disorder has been identified in the index case Genetic testing for mitochondrial disorders is considered **investigational** in **all** other situations when the criteria for medical necessity are not met.	**Genetic Testing for Mitochondrial Disorders 2.04.117** **Policy Statement:** Genetic testing to establish a genetic diagnosis of a mitochondrial disorder may be considered **medically necessary** when signs and symptoms of a mitochondrial disorder are present and genetic testing may eliminate the need for muscle biopsy. Targeted genetic testing for a known familial variant in at-risk relatives may be considered **medically necessary** as preconceptional carrier testing under **both** of the following conditions (see Benefit Application section): I. There is a defined mitochondrial disorder in the family of sufficient severity to cause impairment of quality of life or functional status II. A variant that is known to be pathogenic for that specific mitochondrial disorder has been identified in the index case Genetic testing for mitochondrial disorders is considered **investigational** in **all** other situations when the criteria for medical necessity are not met.