blue 🗑 of california

2.04.91	General Approach to Genetic Testing						
Original Policy Date:	December 18, 2009	Effective Date:	August 1, 2023				
Section:	2.0 Medicine	Page:	Page 1 of 33				

Policy Statement

Note: Starting on July 1, 2022 (per CA law SB 535) for commercial plans regulated by the California Department of Managed Healthcare and California Department of Insurance (PPO and HMO), health care service plans and insurers shall not require prior authorization for biomarker testing, including biomarker testing for cancer progression and recurrence, if a member has stage 3 or 4 cancer. Health care service plans and insurers can still do a medical necessity review of a biomarker test and possibly deny coverage after biomarker testing has been completed and a claim is submitted (post service review).

- I. Genetic testing classified in one of the categories below may be considered **medically necessary** when **all** criteria are met for each category, as outlined in the Rationale section:
 - A. Testing of an affected (symptomatic) individual's germline DNA to benefit the individual (excluding reproductive testing)
 - 1. Diagnostic
 - 2. Prognostic
 - 3. Therapeutic
 - B. Testing cancer cells of an affected individual to benefit the individual
 - 1. Diagnostic
 - 2. Prognostic
 - 3. Therapeutic
 - C. Testing an asymptomatic individual to determine future risk of disease
- II. Genetic testing that does not meet the criteria for a specific category is considered **investigational** or **not medically necessary**, according to the standard definitions used for these terms (see Policy Guidelines section).
- III. Genetic testing is considered **not medically necessary** when **any** of the following situations exist:
 - A. Testing is not considered standard of care, such as when the clinical diagnosis can be made without the use of a genetic test
 - B. Testing is not clinically appropriate for the patient's condition (e.g., when it would not change diagnosis and/or management). Other situations where testing is not clinically appropriate include, but are not limited to:
 - 1. Testing performed entirely for nonmedical (e.g., social) reasons
 - 2. Testing not expected to provide a definitive diagnosis that would obviate the need for further testing
 - C. Testing is performed primarily for the convenience of the patient, physician, or other health care provider
 - D. Testing would result in outcomes that are equivalent to outcomes using an alternative strategy, and the genetic test is more costly

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

Policy Guidelines

For the following category of testing, the benefit of testing is for a family member rather than the individual being tested. In this category, the decision would be based on the clinical utility of the information obtained.

Blue Shield of California 601 12th Street, Oakland, CA 94607

Page 2 of 33

I. Testing of an affected individual's germline to benefit family member(s).

This policy addresses testing of one to a few individual genes. For panel testing, see Blue Shield of California Medical Policy: General Approach to Evaluating the Utility of Genetic Panels.

Genetics Nomenclature Update

The Human Genome Variation Society (HGVS) 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 PGI). The Society's nomenclature is recommended by the Human Variome Project, the HUman Genome Organization (HUGO), and by the Human Genome Variation Society itself.

The American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP) 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 V	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
ACNAC, Association Callered of Marilian	Constinue and Conservices AND: Association for Malesular Dath down

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.

General Information

Claims for molecular genetic testing should clearly identify the test type and the indications for testing. Appropriate HCPCS codes or CPT code modifiers should be utilized when available.

This policy applies only if there is not a separate Blue Shield Medical Policy that outlines specific criteria for testing. If a separate medical policy does exist, then the criteria for medical necessity in that policy supersede the guidelines in this policy.

Page 3 of 33

This policy does not include cytogenetic testing (karyotyping), biochemical testing, or molecular testing for infectious disease.

This policy does not address prenatal testing.

The following Web sites may provide additional information on specific genetic tests and genetic testing laboratories:

- A. Agency for Healthcare Research and Quality: Genetic Testing
 a. <u>https://effectivehealthcare.ahrq.gov/health-topics/genetic-testing</u>
- B. American College of Medical Genetics (ACMG): Translating Genes Into Health[®]
 a. <u>https://www.acmg.net/</u>
- C. Centers for Disease Control and Prevention: Public Health Genomics a. <u>http://www.cdc.gov/genomics/default.htm</u>
- D. Evaluation of Genomic Applications in Practice and Prevention (EGAPP)
 - a. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2743609/
- E. Hayes, Inc.a. <u>https://evidence.hayesinc.com/</u>
- F. Mayo Clinic Mayo Medical Laboratories: Lab-Specific Test Indexes a. <u>https://www.mayocliniclabs.com/test-catalog</u>
- G. National Center for Biotechnology Information: Genetic Testing Registry
 a. <u>http://www.ncbi.nlm.nih.gov/sites/genetests/</u>
- H. National Human Genome Research Institute
 - a. http://www.genome.gov/1000006

Coding

If the specific analyte is listed in codes 81200-81355 or 81400-81408, that CPT code would be reported. If the specific analyte is not listed in the more specific CPT codes, unlisted code 81479 would be reported.

The following CPT codes has been **revised**:

- **81228**: Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number variants, comparative genomic hybridization [CGH] microarray analysis
- **81229**: Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants, comparative genomic hybridization (CGH) microarray analysis

Effective April 1, 2023, there is a new CPT PLA code for PersonalisedRX, Lab Genomics LLC, Agena Bioscience, Inc. Per the manufacturer, this is a drug metabolism test that predicts adverse drug reactions and drug response:

• **0380U:** Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis, 20 gene variants and CYP2D6 deletion or duplication analysis with reported genotype and phenotype

Description

Commercially available genetic tests can perform a host of functions, such as providing a guided intervention in both symptomatic or asymptomatic people, identifying people at risk for future disorders, predicting the prognosis of a diagnosed disease, and predicting the appropriate treatment response.

Related Policies

- a. Carrier Screening for Genetic Diseases
- b. General Approach to Evaluating the Utility of Genetic Panels
- c. Invasive Prenatal (Fetal) Diagnostic Testing
- d. Preimplantation Genetic Testing

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. Most genetic tests are lab tests available under the auspices of the Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by the 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

The purpose of this conceptual framework is to assist evaluation of the utility of genetic tests. In providing a framework for evaluating genetic tests, this review will not determine the clinical utility of genetic testing for specific disorders. Rather, it provides guidelines that can be applied to a wide range of tests.

This conceptual framework applies only if there is not a separate evidence review that outlines specific criteria for testing. If a separate review exists, then the criteria for medical necessity in that evidence review supersede the guidelines herein.

This conceptual framework does not include cytogenetic testing (karyotyping), biochemical testing, or molecular testing for infectious disease.

This conceptual framework also does not address reproductive genetic testing. There are separate evidence reviews for genetic testing in the reproductive setting, addressing, e.g., carrier testing for genetic diseases is addressed in Blue Shield of California Medical Policy: Carrier Screening for Genetic Diseases, invasive prenatal (fetal) diagnostic testing is addressed in Blue Shield of California Medical Policy: Invasive Prenatal (Fetal) Diagnostic Testing, and preimplantation genetic testing is addressed in Blue Shield of California Medical Policy: Preimplantation Genetic Testing.

The following categories of genetic testing are addressed herein (see Appendix 1):

Page 5 of 33

- 1. Testing of an affected (symptomatic) individual's germline to benefit the individual
 - a. Diagnostic
 - b. Prognostic
 - c. Therapeutic
- 2. Testing cancer cells of an affected individual to benefit the individual
 - a. Diagnostic
 - b. Prognostic
 - c. Therapeutic
- 3. Testing an asymptomatic individual to determine future risk of disease
- 4. Testing of an affected individual's germline to benefit family members.

Blue Cross Blue Shield Association genetic testing category 5 (Reproductive testing) is not addressed herein.

Definitions

Genetic Testing

Genetic testing involves the analysis of chromosomes, DNA, RNA, genes, or gene products to detect inherited (germline) or noninherited (somatic) genetic variants related to disease or health.

Carrier Testing

A carrier of a genetic disorder has 1 abnormal allele for a disorder. When associated with an autosomal recessive or X-linked disorder, carriers of the causative variant are typically unaffected. When associated with an autosomal dominant disorder, the person has 1 normal copy of the gene and 1 mutated copy of the gene; such a person may be affected with the disorder, may be unaffected but at high risk of developing the disease later in life, or may remain unaffected because of the sex-limited nature of the disease.

Carrier testing may be offered to people: (a) who have family members with a genetic condition; (b) who have family members who are identified carriers; and (c) who are members of ethnic or racial groups known to have a higher carrier rate for a particular condition.

Germline Variants

Germline variants are present in the DNA of every cell of the body, from the moment of conception. They include cells in the gonads (testes or ova) and could, therefore, be passed on to offspring.

Somatic Variants

Somatic variations occur with the passage of time and are restricted to a specific cell or cells derived from it. If these variants are limited to cells that are not in the gonads, they will not be passed on to offspring.

Pharmacogenomics

Pharmacogenomics studies how a person's genetic makeup affects his or her body's response to drugs.

Literature Review

General Principles of Genetic Tests

A test should be cleared or approved by the U.S. Food and Drug Administration or performed in a Clinical Laboratory Improvement Amendments–certified laboratory.

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 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.

Page 6 of 33

The following rubric outlines the steps in assessing a medical test. The first step is to formulate the clinical context and purpose of the test. Then the evidence is reviewed to determine whether the test is technically reliable, clinically valid, and clinically useful. However, as noted below, technical reliability is outside the scope of evidence reviews.^{1,2}

Types of Genetic Tests Addressed in this Conceptual Framework

- 1. Testing of an affected (symptomatic) individual's germline to benefit the individual (excluding reproductive testing)
 - a. Diagnostic: To confirm or exclude genetic or heritable variants in a symptomatic person. This refers to a molecular diagnosis supported by the presence of a known pathogenic variant. For genetic testing, a symptomatic person is defined as an individual with a clinical phenotype correlated with a known pathogenic variant.
 - b. Prognostic: To determine or refine estimates of disease natural history or recurrence in patients already diagnosed with disease in order to predict natural disease course (e.g., aggressiveness, recurrence, risk of death). This type of testing may use gene expression of affected tissue to predict the course of disease (e.g., testing breast cancer tissue with Oncotype DX).
 - c. Therapeutic: To determine that a particular therapeutic intervention is effective (or ineffective) for an individual. To determine the probability of favorable or adverse response to medications. To detect genetic variants that alter risk of treatment response, adverse events, drug metabolism, drug effectiveness, etc. (e.g., cytochrome P450 testing). To detect genetic variants that adversely affect response to exposures in the environment that are ordinarily tolerated (e.g., *G6PD* deficiency, genetic disorders of immune function, aminoacidopathies).
- 2. Testing cancer cells of an affected individual to benefit the individual
 - a. Diagnostic: To determine the origin of a cancer or to determine a clinically relevant subgroup into which a cancer is classified.
 - b. Prognostic: To determine the risk of progression, recurrence, or mortality for a cancer that is already diagnosed.
 - c. Therapeutic: To determine the likelihood that a patient will respond to a targeted cancer therapy that is based on the presence or absence of a specific variant.
- 3. Testing an asymptomatic individual to determine future risk of disease. To detect genetic variants associated with disorders that appear after birth, usually later in life. Such testing is intended for individuals with a family history of a genetic disorder, but who themselves have no features of the disorder, at the time of testing, in order to determine their risk for developing the disorder.
- 4. Testing of an affected individual's germline to benefit family member(s). To focus and direct family testing of asymptomatic relatives, by testing an individual with known disease but in whom the presence or absence of a pathogenic variant has not been determined.

Medical Necessity Criteria

The criteria listed below for medical necessity represent minimum criteria that must be met in each category to conclude that a test is medically necessary. Alternative approaches to grouping these factors are presented in Appendix 2. The tables in Appendix 2 list all factors considered for clinical utility, and the figures in Appendix 2 group the factors into a branching logic schematic that facilitates a decision whether the test does or does not meet clinical utility.

Genetic testing is considered **medically necessary** for a genetic or heritable disorder when the following are met.

For ALL genetic testing, the condition being tested for must have either:

- Reduced life expectancy OR
- At least moderate-to-severe morbidity.³

Page 7 of 33

For the specific categories of testing, the following criteria must also be met:

- 1. Testing of an affected (symptomatic) individual's germline to benefit the individual (excluding reproductive testing)
 - a. Diagnostic
 - i. An association between the marker and the disorder has been established AND
 - ii. Symptoms of the disease are present AND
 - iii. A definitive diagnosis cannot be made based on history, physical examination, pedigree analysis, and standard diagnostic studies/tests AND
 - iv. The clinical utility of identifying the variant has been established (see Appendix 2):
 - 1) Leads to changes in clinical management of the condition that improve outcomes OR
 - 2) Eliminates the need for further clinical workup or invasive testing OR
 - 3) Leads to discontinuation of interventions that are unnecessary and/or ineffective
 - b. Prognostic
 - i. An association between the marker and the natural history of the disease has been established AND
 - ii. Clinical utility of identifying the variant has been established (see Appendix 2):
 - 1) Provides incremental prognostic information above that of standard testing AND
 - 2) Reclassifies patients into clinically relevant prognostic categories for which there are different treatment strategies AND
 - 3) Reclassification leads to changes in management that improve outcomes
 - c. Therapeutic
 - i. Genetic testing identifies variants of a phenotype/metabolic state that relate to different pharmacokinetics, drug efficacy, or adverse drug reactions AND
 - ii. Clinical utility of identifying the variant has been established (see Appendix 2):
 - 1) Leads to initiation of effective medication(s) OR
 - 2) Leads to discontinuation of medications that are ineffective or harmful OR
 - 3) Leads to clinical meaningful change in dosing of medication that is likely to improve outcomes
- 2. Testing cancer cells of an affected individual to benefit the individual
 - a. Diagnostic
 - i. Genetic testing can establish the cell origin of a cancer when the origin is uncertain following standard workup AND
 - ii. Clinical utility of identifying the variant has been established (see Appendix 2):
 - 1) Start effective treatment OR
 - 2) Discontinue ineffective or harmful treatment
 - b. Prognostic

ii.

- i. An association between the marker and the natural history of the disease has been established AND
 - Clinical utility of identifying the variant has been established (see Appendix 2):
 - 1) Provides incremental prognostic information above that of standard testing AND
 - 2) Reclassifies patients into clinically relevant prognostic categories for which there are different treatment strategies AND
 - 3) Reclassification leads to changes in management that improve outcomes
- c. Therapeutic
 - i. Association between a variant and treatment response to a particular drug has been established AND
 - ii. Clinical utility has been established (see Appendix 2):
 - 1) The patient is a candidate for targeted drug therapy associated with a specific variant AND
 - 2) There is a clinically meaningful improvement in outcomes when targeted therapy is given for the condition
- 3. Testing an asymptomatic individual to determine future risk of disease
 - i. An association between the marker and future disorder has been established AND

Page 8 of 33

- ii. Clinical utility has been established (see Appendix 2):
 - 1) There is a presymptomatic phase for this disorder and interventions or surveillance are available AND
 - 2) Interventions in the presymptomatic phase are likely to improve outcomes: a. Prevent or delay onset of disease OR
 - b. Detect disease at an earlier stage during which treatment is more effective OR
 - c. Discontinuation of ineffective or unnecessary interventions

Clinical Utility Criteria

For the following category, focusing on the benefit of testing for another individual, the definition of medical necessity may not apply. When an individual is tested to benefit a family member, and there is no benefit for the individual being tested, eligibility for coverage depends on individual plan benefit language. Individual plans may differ whether benefit structure allows testing of an individual to benefit an unaffected family member.

For these reasons, the following criteria are considered for clinical utility of testing and not for medical necessity.

- 4. Testing of an affected individual's germline to benefit family members
 - i. An association between the genetic variant and clinical disease has been established AND
 - ii. Family members are available who may be at risk for the disorder AND
 - iii. The individual tested has a clinical diagnosis of the condition (or represents the family member who is most likely to harbor the pathogenic variant), but genetic testing has not been performed AND
 - iv. There is a presymptomatic phase for the disorder in which interventions are available AND
 - v. Interventions in the presymptomatic phase are likely to improve outcomes in one of the following ways:
 - 1) Prevent or delay onset of disease
 - 2) Detect disease at an earlier stage during which treatment is more effective
 - 3) Discontinuation of interventions that are ineffective or unneeded

Limitations of Genetic Testing

- The testing methods may not detect all variants that may occur in a gene
- Genetic testing may identify variants of uncertain significance
- Genetic testing may not necessarily determine the clinical outcome
- Different genes can cause the same disease (genetic heterogeneity)
- A variant in a gene may cause different phenotypes (phenotypic heterogeneity)
- Some disease-causing genes may not yet be identified
- Genetic testing is subject to laboratory error

Summary of Evidence

This conceptual framework addresses genetic testing in nonreproductive settings. Genetic testing in reproductive settings is addressed separately in Blue Shield of California Medical Policies (e.g., Carrier Screening for Genetic Diseases, Invasive Prenatal (Fetal) Diagnostic Testing, Preimplantation Genetic Testing). For categories of genetic testing for which the benefit of testing is the individual, criteria for medical necessity apply. When the benefit of testing is not for the individual, but for a family member, medical necessity criteria may not apply, and the criteria are developed for clinical utility.

Supplemental Information Practice Guidelines and Position Statements No guidelines or statements were identified. 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

A search of ClinicalTrials.gov in November 2017 did not identify any ongoing or unpublished trials that would likely influence this review.

Appendix 1 - 8

Category	Addressed
1. Testing of an affected individual's germline to benefit the individual	
la. Diagnostic	
1b. Prognostic	
Ic. Therapeutic	
2. Testing cancer cells from an affected individual to benefit the individual	
2a. Diagnostic	
2b. Prognostic	
2c. Therapeutic	
3. Testing an asymptomatic individual to determine future risk of disease	
4. Testing of an affected individual's germline to benefit family members	
5. Reproductive testing	
5a. Carrier testing: preconception	
5b. Carrier testing: prenatal	
5c. In utero testing: aneuploidy	
5d. In utero testing: variants	
5e. In utero testing: other	
5f. Preimplantation testing with in vitro fertilization	

Appendix 2. Approach to Determining Clinical Utility for Genetic Testing Direct Evidence

If direct evidence is available on the impact of testing on outcomes, this evidence takes precedence. Examples of direct evidence are:

- Trial comparing outcomes with and without use of the test versus
- Associational study of genetic testing with outcomes

Indirect Evidence

When direct evidence is not available, indirect evidence should be evaluated. Indirect evidence addresses 1 or more components of a chain of evidence, but does not itself connect the intervention with the outcome.

An example of indirect evidence is the accuracy of the genetic test for diagnosing the clinical condition (i.e., clinical sensitivity and specificity). If improved accuracy leads to improved diagnosis of the disorder, and if more accurate diagnosis leads to management changes that improve outcomes, then clinical utility has been established.

Many disorders are rare, and high-quality evidence on the efficacy of treatment is often lacking. This is particularly true for aspects of management such as increased surveillance for complications, ancillary treatments (e.g., physical therapy, occupational therapy), and referrals to specialists. When

Page 10 of 33

evidence on outcomes is lacking, consideration may be given to whether these aspects of care are considered standard of care for that disorder, especially when they are part of guidelines by authoritative bodies.

A number of factors influence the strength of indirect evidence that is needed to determine whether health outcomes are improved. None by itself is determinative of whether genetic testing should be performed, but the factors may be important determinants of the potential clinical utility of testing. We enumerate below 4 factors, each with an accompanying table (see Appendix Tables 1-4).

Factors impacting the strength of indirect evidence for diagnostic testing (categories 1a, 2a)

Disease Characteristics

- Is life expectancy reduced with this disorder?
- What is the level of physical and/or psychosocial morbidity (disability) associated with the disorder?
 - o Severe morbidity/disability
 - o Moderate morbidity/disability
 - Minor or no morbidity/disability

Impact of Genetic Testing on Diagnosis

- Can genetic testing confirm the suspected diagnosis?
- Can the diagnosis be confirmed by alternative methods without genetic testing?
 - Disorder is defined by the presence of genetic variant
 - Genetic testing is one of several factors contributing to diagnosis
 - o Unable to make diagnosis without genetic testing in some patients
- Can genetic testing rule out the disorder?
- Can genetic testing eliminate further clinical workup?
 - Is this a disorder for which a diagnosis can be difficult, and the patient may be subjected to long and complicated workups?

Impact of Genetic Testing on Clinical Management

- Does confirmation of diagnosis by genetic testing lead to improved outcomes?
 - o Initiation of effective treatment
 - o Discontinuation of ineffective treatment
- Does confirmation of diagnosis by genetic testing lead to initiation of other management changes with uncertain impact on outcomes (e.g., referrals to specialists and/or ancillary care, initiate screening)?
- Does confirmation of diagnosis by genetic testing lead to initiation of other management changes that are considered "standard of care" treatment for disorder?

Impact on Health Outcomes

- Is there a definite improvement in health outcomes with genetic testing? For example:
 - Diagnosis cannot be made without genetic testing, and confirmation of diagnosis leads to initiation of effective treatment
- Is there a possible, but not definite, improvement in health outcomes with genetic testing? For example:
 - Diagnosis cannot be made without genetic testing, and confirmation of diagnosis leads to management changes with uncertain impact on outcomes
- Are there significant barriers to research, such as rarity of the disorder?
- What is the impact of genetic testing on lifestyle factors?
 - Employment/occupational decision making
 - o Leisure activities

o Reproductive decision-maker

Appendix Table 1. Factors Influencing the Strength of an Indirect Chain of Evidence on Clinical Utility: Categories 1a, 2a

2. Factors impacting the strength of indirect evidence for assessing risk of future disease in asymptomatic individuals (category 3)

Disease Characteristics

- Is life expectancy reduced with this disorder?
- What is the level of physical and/or psychosocial morbidity (disability) associated with the disorder?
 - Severe morbidity/disability
 - Moderate morbidity/disability
 - o Minor or no morbidity/disability
- Is there a presymptomatic phase during which a clinical diagnosis cannot be made?

Impact of Genetic Testing on Defining Risk of Disease

- Can genetic testing determine the risk of subsequent disease in at least a substantial proportion of the population tested?
- Is there a known variant in the family?
- Is the penetrance of the genetic variant known?
- Are there other factors that impact the clinical expression of disease?

Impact of Genetic Testing on Management

- Does confirmation of risk lead to interventions that are indicated for this condition in the presymptomatic phase?
 - Interventions that prevent or delay disease onset
 - o Surveillance for manifestations or complications of disease
- Does confirmation of risk by a positive genetic testing result lead to the initiation of other management changes that may or may not lead to improved outcomes (e.g., referrals to specialists and/or ancillary care, initiate screening)?
- Does a negative test confirm a lack of risk for the disease, and does this lead to discontinuation of interventions (e.g., surveillance) that would otherwise be performed?
- Is it likely that knowledge of variant status will lead to alterations in reproductive decision making?

Page 12 of 33

Impact on Health Outcomes

- Is there a definite improvement in health outcomes with genetic testing? For example:
 - Risk assessment cannot be made without genetic testing, and confirmation of risk leads to initiation of effective preventive interventions that delay onset of disease
- Is there a possible, but not definite, improvement in health outcomes with genetic testing? For example:
 - Risk assessment cannot be made without genetic testing, and confirmation of risk leads to management changes with uncertain impact on outcomes
- Are there significant barriers to research, such as rarity of the disorder?
 - What is the impact of genetic testing on lifestyle factors?
 - o Employment/occupational decision making
 - o Leisure activities
 - o Reproductive decision-maker

Appendix Table 2. Factors Influencing the Strength of Indirect Evidence for Risk Assessment Testing: Category 3

Factors influencing the strength of indirect evidence for prognosis testing (categories lb, 2b)

Disease Characteristics

- Is life expectancy reduced with this disorder?
- What is the level of physical and/or psychosocial morbidity (disability) associated with the disorder?
 - Severe morbidity/disability
 - o Moderate morbidity/disability
 - Minor or no morbidity/disability

Impact of Genetic Testing on Prognosis

- Does the genetic test have an association with prognosis of disease?
- Does genetic testing lead to an incremental improvement in prognosis above that which can be done by usual testing?
- Does the genetic testing allow classification of patients into clinically credible prognostic groups?
 - Have these prognostic groups been defined clinically a priori?

Page 13 of 33

Impact of Genetic Testing on Management

- Are different prognostic groups associated with different treatment interventions?
 - Type of intervention
 - Timing of intervention
- Has treatment according to risk category been demonstrated to improve outcomes?
- Is treatment according to risk category considered standard of care for this disorder?

Impact on Health Outcomes

- Is there a definite improvement in health outcomes with genetic testing? For example:
 - Reclassification by prognosis leads to change in management that is known to be effective for the condition
- Is there a possible, but not definite, improvement in health outcomes with genetic testing? For example:
 - Reclassification by prognosis leads to changes in management with uncertain impact on outcomes
- Are there significant barriers to research, such as rarity of the disorder?
- What is the impact of testing on lifestyle factors?
 - o Employment/occupational decision making
 - o Leisure activities
 - o Reproductive decision-maker

Appendix Table 3. Factors Influencing the Strength of Indirect Evidence: Categories 1b, 2b

Disorder	Disea	Disease Characteristics			Impact on Prognosis			Impact on Management				Impact on Outcomes			
	Shortened life expectancy	Severe morbidity/disability	Moderate morbidity/disability	Minor or no morbidity/disability	Variant associated with prognosis	cren	tributes to ab Jnosis	Clinically credible prognostic groups	Prognostic groups have different treatment	Treatment by prognostic groups improve outcomes	Treatment by prognostic group is standard of care	Definite improved health outcomes	Possible impact on outcomes, data lacking	Barriers to research	Impact on lifestyle factors

4. Factors influencing the strength of indirect evidence for genetic variants that alter response to treatment (categories 1c, 2c)

Disease Characteristics

- Is life expectancy reduced with this disorder?
- What is the level of physical and/or psychosocial morbidity (disability) associated with the disorder?
 - Severe morbidity/disability
 - Moderate morbidity/disability
 - o Minor or no morbidity/disability
- Is there effective pharmacologic therapy for this disorder?

Impact of Genetic Testing on Assessing Response to Treatment

- Can genetic testing define variants associated with different pharmacokinetics of drug metabolism?
- Are these changes in drug metabolism clinically important?

Page 14 of 33

- Variants have been associated with clinically significant differences in outcomes of treatment
- Are there genetic variants associated with increased risk for adverse effects?

Impact of Genetic Testing on Pharmacologic Management

- Does identification of genetic variants lead to changes in pharmacologic management?
 - o Initiation of alternate agents
 - o Discontinuation ineffective agents
 - o Changes in dosing

Impact on Health Outcomes

- Is there a definite improvement in health outcomes with genetic testing? For example:
 - \circ ~ Identification of variants leads to initiation of medications known to be effective
- Is there a possible, but not definite, improvement in health outcomes with genetic testing? For example:
 - Identification of variants leads to change in pharmacologic management with uncertain impact on outcomes
- Are there significant barriers to research, such as rarity of the disorder?

Appendix Table 4. Factors Influencing the Strength of Indirect Evidence: Genetic Variants That Alter Response to Treatment (Categories 1c, 2c)

Shortened life expectancy Shortened life expectancy Severe morbidity/disability Moderate morbidity/disability Minor or no morbidity/disability Define variants with different Nariants lead to differences in Outcomes Variants with increased risk for Initiation of alternate agents Discontinue ineffective treatment Discontinue ineffective treatment Discontinue ineffective treatment Descible improved health Descible improved health Descible improved health Mata lacking Barriers to research	Disorder	1	Disease Characteristics				Impact on Response to Treatment				Impact on Management			Impact on Outcomes		
		tened life			or no	pharmacologic	다	: pharmacokinetics important	to differences i	: with increased risk effects	of alternate	ineffective	.L S		ossible impact on ata lacking	ę

Appendix Figure 1. Diagnostic Testing Schematic of an Affected Individual's Germline to Benefit the Individual (category 1a)



Appendix Figure 2. Prognostic Testing of an Affected Individual's Germline to Benefit the Individual (category 1b)



Appendix Figure 3. Therapeutic Testing of an Affected Individual's Germline to Benefit the Individual (category 1c)



Appendix Figure 4. Diagnostic Testing of DNA Cells from Cancer Cells of an Affected Individual to Benefit the Individual (category 2a)





Appendix Figure 5. Prognostic Testing of DNA from Cancer Cells of an Affected Individual to Benefit the Individual (category 2b)



Appendix Figure 6. Therapeutic Testing of Cancer Cells of an Affected Individual to Benefit the Individual (category 2c)



Appendix Figure 7. Testing an Asymptomatic Individual to Determine Future Risk of Disease (category 3)



3. Testing an asymptomatic individual to determine future risk of disease

Appendix Figure 8. Testing an Affected Individual's Determine DNA to Benefit Family Members (category 4)



CU: clinical utility.

References

- ACMG Board of Directors. Clinical utility of genetic and genomic services: a position statement of the American College of Medical Genetics and Genomics. Genet Med. Jun 2015;17(6):505-507. PMID 25764213
- 2. Teutsch SM, Bradley LA, Palomaki GE, et al. The Evaluation of Genomic Applications in Practice and Prevention (EGAPP) Initiative: methods of the EGAPP Working Group. Genet Med. Jan 2009;11(1):3-14. PMID 18813139
- Beltran-Sanchez H, Razak F, Subramanian SV. Going beyond the disability-based morbidity definition in the compression of morbidity framework. Glob Health Action. 2014;7:24766. PMID 25261699

Documentation for Clinical Review

Please provide the following documentation:

- Provider order for genetic test
- Name and description of genetic test
- Name of laboratory performing the test
- Any available evidence supporting the clinical validity/utility of the specific test
- CPT codes to be billed for the particular genetic test
- History and physical and/or consultation notes including:
 - Reason for performing test
 - o Signs/symptoms/test results related to reason for genetic testing
 - o Family history if applicable
 - o How test result will impact clinical decision making

Post Service (in addition to the above, please include the following):

• Results/reports of tests performed

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.

Туре	Code	Description
	0009U	Oncology (breast cancer), ERBB2 (HER2) copy number by FISH, tumor cells from formalin fixed paraffin embedded tissue isolated using image-based dielectrophoresis (DEP) sorting, reported as ERBB2 gene amplified or non-amplified
	0013U	Oncology (solid organ neoplasia), gene rearrangement detection by whole genome next-generation sequencing, DNA, fresh or frozen tissue or cells, report of specific gene rearrangement(s) <i>(Deleted code</i> <i>effective 10/1/2022)</i>
CPT [®]	0014U	Hematology (hematolymphoid neoplasia), gene rearrangement detection by whole genome next-generation sequencing, DNA, whole blood or bone marrow, report of specific gene rearrangement(s) <i>(Deleted code effective 10/1/2022)</i>
	0015U	Drug metabolism (adverse drug reactions), DNA, 22 drug metabolism and transporter genes, real-time PCR, blood or buccal swab, genotype and metabolizer status for therapeutic decision support
	0016U	Oncology (hematolymphoid neoplasia), RNA, BCR/ABL1 major and minor breakpoint fusion transcripts, quantitative PCR amplification, blood or bone marrow, report of fusion not detected or detected with quantitation
	0017U	Oncology (hematolymphoid neoplasia), JAK2 mutation, DNA, PCR amplification of exons 12-14 and sequence analysis, blood or bone marrow, report of JAK2 mutation not detected or detected

Туре	Code	Description
		Drug metabolism (adverse drug reactions and drug response), targeted
	0380U	sequence analysis, 20 gene variants and CYP2D6 deletion or duplication
		analysis with reported genotype and phenotype (Code effective
		4/1/2023)
		Gastroenterology (Barrett esophagus), P16, RUNX3, HPP1, and FBN1
		DNA methylation analysis using PCR, formalin-fixed paraffin-
	0398U	embedded (FFPE) tissue, algorithm reported as risk score for
		progression to high-grade dysplasia or cancer <i>(Code effective</i>
		7/1/2023)
		Patient-specific, assistive, rules-based algorithm for ranking pharmaco-
		oncologic treatment options based on the patient's tumor-specific
	070/7	cancer marker information obtained from prior molecular pathology,
	0794T	immunohistochemical, or other pathology results which have been
		previously interpreted and reported separately <i>(Code effective</i>
		7/1/2023)
		BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair
	81163	associated) (e.g., hereditary breast and ovarian cancer) gene analysis;
		full sequence analysis
		BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair
		associated) (e.g., hereditary breast and ovarian cancer) gene analysis;
	81164	full duplication/deletion analysis (i.e., detection of large gene
		rearrangements)
	81165	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and
		ovarian cancer) gene analysis; full sequence analysis
	-	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and
	81166	ovarian cancer) gene analysis; full duplication/deletion analysis (i.e.,
		detection of large gene rearrangements)
	-	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and
	81167	ovarian cancer) gene analysis; full duplication/deletion analysis (i.e.,
		detection of large gene rearrangements)
	01200	ASPA (aspartoacylase) (e.g., Canavan disease) gene analysis, common
	81200	variants (e.g., E285A, Y231X)
		APC (adenomatous polyposis coli) (e.g., familial adenomatosis polyposis
	81201	[FAP], attenuated FAP) gene analysis; full gene sequence
		APC (adenomatous polyposis coli) (e.g., familial adenomatosis polyposis
	81202	[FAP], attenuated FAP) gene analysis; known familial variants
		APC (adenomatous polyposis coli) (e.g., familial adenomatosis polyposis
	81203	[FAP], attenuated FAP) gene analysis; duplication/deletion variants
		BCKDHB (branched-chain keto acid dehydrogenase E1, beta
	81205	polypeptide) (e.g., maple syrup urine disease) gene analysis, common
		variants (e.g., R183P, G278S, E422X)
	01206	BCR/ABL1 (t(9;22)) (e.g., chronic myelogenous leukemia) translocation
	81206	analysis; major breakpoint, qualitative or quantitative
	01207	BCR/ABL1 (t(9;22)) (e.g., chronic myelogenous leukemia) translocation
	81207	analysis; minor breakpoint, qualitative or quantitative
		BCR/ABL1 (t(9;22)) (e.g., chronic myelogenous leukemia) translocation
	81208	analysis; other breakpoint, qualitative or quantitative
	01200	BLM (Bloom syndrome, RecQ helicase-like) (e.g., Bloom syndrome) gene
	81209	analysis, 2281del6ins7 variant
	01010	BRAF (B-Raf proto-oncogene, serine/threonine kinase) (e.g., colon
	81210	cancer, melanoma), gene analysis, V600 variant(s)

Туре	Code	Description
		BRCA1, BRCA2 (breast cancer 1 and 2) (e.g., hereditary breast and
	81211	ovarian cancer) gene analysis; full sequence analysis and common
	01211	duplication/deletion variants in BRCA1 (i.e., exon 13 del 3.835kb, exon 13
		dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb)
		BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair
	81212	associated) (e.g., hereditary breast and ovarian cancer) gene analysis;
		185delAG, 5385insC, 6174delT variants
	01217	BRCA1, BRCA2 (breast cancer 1 and 2) (e.g., hereditary breast and
	81213	ovarian cancer) gene analysis; uncommon duplication/deletion variants
		BRCA1 (breast cancer 1) (e.g., hereditary breast and ovarian cancer) gene
	0121/	analysis; full sequence analysis and common duplication/deletion
	81214	variants (i.e., exon 13 del 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb,
		exon 22 del 510bp, exon 8-9 del 7.1kb)
	01215	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and
	81215	ovarian cancer) gene analysis; known familial variant
	01016	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and
	81216	ovarian cancer) gene analysis; full sequence analysis
	01017	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and
	81217	ovarian cancer) gene analysis; known familial variant
	01000	CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic
	81220	fibrosis) gene analysis; common variants (e.g., ACMG/ACOG guidelines)
		CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic
	81221	fibrosis) gene analysis; known familial variants
		CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic
	81222	fibrosis) gene analysis; duplication/deletion variants
		CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic
	81223	fibrosis) gene analysis; full gene sequence
		CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic
	81224	fibrosis) gene analysis; intron 8 poly-T analysis (e.g., male infertility)
		CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (e.g.,
	81225	drug metabolism), gene analysis, common variants (e.g., *2, *3, *4, *8,
		*17)
		CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g.,
	81226	drug metabolism), gene analysis, common variants (e.g., *2, *3, *4, *5, *6,
		*9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN)
	01007	CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9) (e.g.,
	81227	drug metabolism), gene analysis, common variants (e.g., *2, *3, *5, *6)
		Cytogenomic (genome-wide) analysis for constitutional chromosomal
	81228	abnormalities; interrogation of genomic regions for copy number
		variants, comparative genomic hybridization [CGH] microarray analysis
		Cytogenomic (genome-wide) analysis for constitutional chromosomal
	01220	abnormalities; interrogation of genomic regions for copy number and
	81229	single nucleotide polymorphism (SNP) variants, comparative genomic
		hybridization (CGH) microarray analysis
		EGFR (epidermal growth factor receptor) (e.g., non-small cell lung
	81235	cancer) gene analysis, common variants (e.g., exon 19 LREA deletion,
		L858R, T790M, G719A, G719S, L861Q)
	81238	F9 (coagulation factor IX) (e.g., hemophilia B), full gene sequence
	012/0	F2 (prothrombin, coagulation factor II) (e.g., hereditary
	81240	hypercoagulability) gene analysis, 20210G>A variant
	012/1	F5 (coagulation factor V) (e.g., hereditary hypercoagulability) gene
	81241	analysis, Leiden variant
		1 -

Туре	Code	Description
		FANCC (Fanconi anemia, complementation group C) (e.g., Fanconi
	81242	anemia, type C) gene analysis, common variant (e.g., IVS4+4A>T)
	010/7	FMR1 (fragile X mental retardation 1) (e.g., fragile X mental retardation)
	81243	gene analysis; evaluation to detect abnormal (e.g., expanded) alleles
		FMR1 (fragile X mental retardation 1) (e.g., fragile X mental retardation)
	81244	gene analysis; characterization of alleles (e.g., expanded size and
		promoter methylation status)
		FLT3 (fms-related tyrosine kinase 3) (e.g., acute myeloid leukemia), gene
	81245	analysis; internal tandem duplication (ITD) variants (i.e., exons 14, 15)
	012/ 6	FLT3 (fms-related tyrosine kinase 3) (e.g., acute myeloid leukemia), gene
	81246	analysis; tyrosine kinase domain (TKD) variants (e.g., D835, I836)
	012/7	G6PD (glucose-6-phosphate dehydrogenase) (e.g., hemolytic anemia,
	81247	jaundice), gene analysis; common variant(s) (e.g., A, A-)
	012/0	G6PD (glucose-6-phosphate dehydrogenase) (e.g., hemolytic anemia,
	81248	jaundice), gene analysis; known familial variant(s)
	012/0	G6PD (glucose-6-phosphate dehydrogenase) (e.g., hemolytic anemia,
	81249	jaundice), gene analysis; full gene sequence
		G6PC (glucose-6-phosphatase, catalytic subunit) (e.g., Glycogen storage
	81250	disease, type 1a, von Gierke disease) gene analysis, common variants
		(e.g., R83C, Q347X)
		GBA (glucosidase, beta, acid) (e.g., Gaucher disease) gene analysis,
	81251	common variants (e.g., N370S, 84GG, L444P, IVS2+1G>A)
		GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (e.g.,
	81252	nonsyndromic hearing loss) gene analysis; full gene sequence
		GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (e.g.,
	81253	nonsyndromic hearing loss) gene analysis; known familial variants
		GJB6 (gap junction protein, beta 6, 30kDa, connexin 30) (e.g.,
	81254	nonsyndromic hearing loss) gene analysis, common variants (e.g., 309kb
		[del(GJB6-D13S1830)] and 232kb [del(GJB6-D13S1854)])
	01255	HEXA (hexosaminidase A [alpha polypeptide]) (e.g., Tay-Sachs disease)
	81255	gene analysis, common variants (e.g., 1278insTATC, 1421+1G>C, G269S)
	01256	HFE (hemochromatosis) (e.g., hereditary hemochromatosis) gene
	81256	analysis, common variants (e.g., C282Y, H63D)
		HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
	81257	Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis;
		common deletions or variant (e.g., Southeast Asian, Thai, Filipino,
		Mediterranean, alpha3.7, alpha4.2, alpha20.5, Constant Spring)
		HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
	81258	Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known
		familial variant
		HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
	81259	Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; full gene
		sequence
		IKBKAP (inhibitor of kappa light polypeptide gene enhancer in B-cells,
	81260	kinase complex-associated protein) (e.g., familial dysautonomia) gene
		analysis, common variants (e.g., 2507+6T>C, R696P)
		IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemias and
	81261	lymphomas, B-cell), gene rearrangement analysis to detect abnormal
	01201	clonal population(s); amplified methodology (e.g., polymerase chain
		reaction)

Type Code Description IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); direct probe methodology (e.g., Southern blot) 81263 IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemia and lymphoma, B-cell), variable region somatic mutation analysis 81264 IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s) 81265 Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells) 81266 Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure) 81267 Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection 81268 Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection 81269 HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease)
81262 lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); direct probe methodology (e.g., Southern blot) 81263 IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemia and lymphoma, B-cell), variable region somatic mutation analysis 81264 IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s) 81264 Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells) 81266 Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure) 81267 Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection 81268 Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection 81268 Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection
clonal population(s); direct probe methodology (e.g., Southern blot)81263IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemia and lymphoma, B-cell), variable region somatic mutation analysis81264IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81264IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81263IGH@ (Immunoglobulin heavy chain locus) (e.g., leukemia and lymphoma, B-cell), variable region somatic mutation analysis81264IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection
81263lymphoma, B-cell), variable region somatic mutation analysis81264IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81264IGK@ (Immunoglobulin kappa light chain locus) (e.g., leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81264lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81265Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81265patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81265patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81265donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81265germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
testing, twin zygosity testing, or maternal cell contamination of fetal cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268Hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268Hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
cells)81266Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection81268HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81266additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Hantopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81266additional specimen (e.g., additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Hantopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81266samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Hantopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
pregnancies) (List separately in addition to code for primary procedure)81267Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell typeHBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81267hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell typeHBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81267hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell typeHBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
baseline analyses; without cell selection Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81268Chimerism (engraftment) analysis, post transplantation specimen (e.g., hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
81268hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (e.g., CD3, CD33), each cell typeHBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
baseline analyses; with cell selection (e.g., CD3, CD33), each cell type HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia,
duplication/deletion variants
B1270 JAK2 (Janus kinase 2) (e.g., myeloproliferative disorder) gene analysis,
p.Val617Phe (V617F) variant
KRAS (Kirsten rat sarcoma viral oncogene homolog) (e.g., carcinoma)
gene analysis; variants in exon 2 (e.g., codons 12 and 13)
81287 MGMT (O-6-methylguanine-DNA methyltransferase) (e.g., glioblastoma
multiforme) promoter methylation analysis
MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g.,
81288 hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
analysis; promoter methylation analysis
81290 MCOLN1 (mucolipin 1) (e.g., Mucolipidosis, type IV) gene analysis,
common variants (e.g., IVS3-2A>G, del6.4kb)
81291 MTHFR (5,10-methylenetetrahydrofolate reductase) (e.g., hereditary
hypercoagulability) gene analysis, common variants (e.g., 6/71, 1298C)
MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g.,
81292 hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
analysis; full sequence analysis
MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g.,
81293 hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
analysis; known familial variants
MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g.,
81294 hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
analysis; duplication/deletion variants
MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g.,
81295 hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
analysis; full sequence analysis

Туре	Code	Description
		MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g.,
	81296	hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
		analysis; known familial variants
		MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g.,
	81297	hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
		analysis; duplication/deletion variants
	01200	MSH6 (mutS homolog 6 [E. coli]) (e.g., hereditary non-polyposis
	81298	colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
		MSH6 (mutS homolog 6 [E. coli]) (e.g., hereditary non-polyposis
	81299	colorectal cancer, Lynch syndrome) gene analysis; known familial
		variants
		MSH6 (mutS homolog 6 [E. coli]) (e.g., hereditary non-polyposis
	81300	colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion
		variants
		Microsatellite instability analysis (e.g., hereditary non-polyposis
	01701	colorectal cancer, Lynch syndrome) of markers for mismatch repair
	81301	deficiency (e.g., BAT25, BAT26), includes comparison of neoplastic and
		normal tissue, if performed
	017.00	MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene
	81302	analysis; full sequence analysis
	017.07	MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene
	81303	analysis; known familial variant
		MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene
	81304	analysis; duplication/deletion variants
		NPM1 (nucleophosmin) (e.g., acute myeloid leukemia) gene analysis,
	81310	exon 12 variants
		PCA3/KLK3 (prostate cancer antigen 3 [non-protein coding]/kallikrein-
	81313	related peptidase 3 [prostate specific antigen]) ratio (e.g., prostate
		cancer)
	81315	PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor
		alpha) (e.g., promyelocytic leukemia) translocation analysis; common
		breakpoints (e.g., intron 3 and intron 6), qualitative or quantitative
		PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor
	81316	alpha) (e.g., promyelocytic leukemia) translocation analysis; single
		breakpoint (e.g., intron 3, intron 6 or exon 6), qualitative or quantitative
		PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (e.g.,
	81317	hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
		analysis; full sequence analysis
		PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (e.g.,
	81318	hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
		analysis; known familial variants
		PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (e.g.,
	81319	hereditary non-polyposis colorectal cancer, Lynch syndrome) gene
		analysis; duplication/deletion variants
	81321	PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN
		hamartoma tumor syndrome) gene analysis; full sequence analysis
	01700	PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN
	81322	hamartoma tumor syndrome) gene analysis; known familial variant
		PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN
	81323	hamartoma tumor syndrome) gene analysis; duplication/deletion
		variant

Туре	Code	Description
		PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth,
	81324	hereditary neuropathy with liability to pressure palsies) gene analysis;
		duplication/deletion analysis
		PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth,
	81325	hereditary neuropathy with liability to pressure palsies) gene analysis;
		full sequence analysis
		PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth,
	81326	hereditary neuropathy with liability to pressure palsies) gene analysis;
		known familial variant
		SMPD1(sphingomyelin phosphodiesterase 1, acid lysosomal) (e.g.,
	81330	Niemann-Pick disease, Type A) gene analysis, common variants (e.g.,
		R496L, L302P, fsP330)
		SNRPN/UBE3A (small nuclear ribonucleoprotein polypeptide N and
	81331	ubiquitin protein ligase E3A) (e.g., Prader-Willi syndrome and/or
		Angelman syndrome), methylation analysis
		SERPINA1 (serpin peptidase inhibitor, clade A, alpha-1 antiproteinase,
	81332	antitrypsin, member 1) (e.g., alpha-1-antitrypsin deficiency), gene
		analysis, common variants (e.g., *S and *Z)
		TRB@ (T cell antigen receptor, beta) (e.g., leukemia and lymphoma),
	81340	gene rearrangement analysis to detect abnormal clonal population(s);
		using amplification methodology (e.g., polymerase chain reaction)
		TRB@ (T cell antigen receptor, beta) (e.g., leukemia and lymphoma),
	81341	gene rearrangement analysis to detect abnormal clonal population(s);
		using direct probe methodology (e.g., Southern blot)
		TRG@ (T cell antigen receptor, gamma) (e.g., leukemia and lymphoma),
	81342	gene rearrangement analysis, evaluation to detect abnormal clonal
		population(s)
		UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (e.g.,
	81350	irinotecan metabolism), gene analysis, common variants (e.g., *28, *36,
		*37)
		VKORC1 (vitamin K epoxide reductase complex, subunit 1) (e.g., warfarin
	81355	metabolism), gene analysis, common variant(s) (e.g., -1639G>A,
		c.173+1000C>T)
		HBB (hemoglobin, subunit beta) (e.g., sickle cell anemia, beta
	81361	thalassemia, hemoglobinopathy); common variant(s) (e.g., HbS, HbC,
		HbE)
	81362	HBB (hemoglobin, subunit beta) (e.g., sickle cell anemia, beta
		thalassemia, hemoglobinopathy); known familial variant(s)
	81363	HBB (hemoglobin, subunit beta) (e.g., sickle cell anemia, beta
		thalassemia, hemoglobinopathy); duplication/deletion variant(s)
	81364	HBB (hemoglobin, subunit beta) (e.g., sickle cell anemia, beta
		thalassemia, hemoglobinopathy); full gene sequence
	81400	Molecular Pathology Procedure Level 1
	81401	Molecular Pathology Procedure Level 2
	81402	Molecular Pathology Procedure Level 3
	81403	Molecular Pathology Procedure Level 4
	81404	Molecular Pathology Procedure Level 5
	81405	Molecular Pathology Procedure Level 6
	81406	Molecular Pathology Procedure Level 7
	81407	Molecular Pathology Procedure Level 8
	81408	Molecular Pathology Procedure Level 9
	1	

Туре	Code	Description
	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	
12/18/2009	New Policy Adoption	
01/25/2010	Coding Update	
09/27/2013	Policy revision with position change	
07/31/2015	Coding Update	
07/31/2013	Policy revision without position change	
02/01/2016	Coding update	
05/01/2016	Policy revision without position change	
02/01/2017	Coding update	
06/01/2017	Policy revision without position change	
08/01/2017	Coding update	
02/01/2018	Policy revision without position change	
02/01/2018	Coding update	
01/01/2019	Coding update	
07/01/2019	Policy revision without position change	
07/01/2019	Coding Update	
04/01/2020	Annual review. No change to policy statement.	
01/01/2021	Coding update.	
04/01/2021	Annual review. No change to policy statement.	
02/01/2022	Coding update.	
04/01/2022	Annual review. Policy guidelines updated.	
10/01/2022	Administrative update.	
11/01/2022	Coding update.	
06/01/2023	Coding update.	
08/01/2023	Coding update.	

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.

2.04.91 General Approach to Genetic Testing Page 31 of 33

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 and Feedback (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 <u>www.blueshieldca.com/provider</u>.

We are interested in receiving feedback relative to developing, adopting, and reviewing criteria for medical policy. Any licensed practitioner who is contracted with Blue Shield of California or Blue Shield of California Promise Health Plan is welcome to provide comments, suggestions, or concerns. Our internal policy committees will receive and take your comments into consideration.

For utilization and medical policy feedback, please send comments to: <u>MedPolicy@blueshieldca.com</u>

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

	TATEMENT langes)
BEFORE	AFTER
General Approach to Genetic Testing 2.04.91	General Approach to Genetic Testing 2.04.91
Policy Statement: Note: Starting on July 1, 2022 (per CA law SB 535) for commercial plans regulated by the California Department of Managed Healthcare and California Department of Insurance (PPO and HMO), health care service plans and insurers shall not require prior authorization for biomarker testing, including biomarker testing for cancer progression and recurrence, if a member has stage 3 or 4 cancer. Health care service plans and insurers can still do a medical necessity review of a biomarker test and possibly deny coverage after biomarker testing has been completed and a claim is submitted (post service review).	Policy Statement: Note: Starting on July 1, 2022 (per CA law SB 535) for commercial plans regulated by the California Department of Managed Healthcare and California Department of Insurance (PPO and HMO), health care service plans and insurers shall not require prior authorization for biomarker testing, including biomarker testing for cancer progression and recurrence, if a member has stage 3 or 4 cancer. Health care service plans and insurers can still do a medical necessity review of a biomarker test and possibly deny coverage after biomarker testing has been completed and a claim is submitted (post service review).
 Genetic testing classified in one of the categories below may be considered medically necessary when all criteria are met for each category, as outlined in the Rationale section: Testing of an affected (symptomatic) individual's germline DNA to benefit the individual (excluding reproductive testing) Diagnostic Prognostic Therapeutic Testing cancer cells of an affected individual to benefit the individual	 I. Genetic testing classified in one of the categories below may be considered medically necessary when all criteria are met for each category, as outlined in the Rationale section: A. Testing of an affected (symptomatic) individual's germline DNA to benefit the individual (excluding reproductive testing) 1. Diagnostic 2. Prognostic 3. Therapeutic B. Testing cancer cells of an affected individual to benefit the individual 1. Diagnostic 2. Prognostic 3. Therapeutic B. Testing cancer cells of an affected individual to benefit the individual 1. Diagnostic 2. Prognostic 3. Therapeutic C. Testing an asymptomatic individual to determine future risk of disease
II. Genetic testing that does not meet the criteria for a specific category is considered investigational or not medically necessary, according to the standard definitions used for these terms (see Policy Guidelines section).	II. Genetic testing that does not meet the criteria for a specific category is considered investigational or not medically necessary , according to the standard definitions used for these terms (see Policy Guidelines section).

POLICY STATEMENT (No changes)			
BEFORE	AFTER		
 III. Genetic testing is considered not medically necessary when any of the following situations exist: A. Testing is not considered standard of care, such as when the clinical diagnosis can be made without the use of a genetic test B. Testing is not clinically appropriate for the patient's condition (e.g., when it would not change diagnosis and/or management). Other situations where testing is not clinically appropriate include, but are not limited to: Testing performed entirely for nonmedical (e.g., social) reasons Testing not expected to provide a definitive diagnosis that would obviate the need for further testing Testing is performed primarily for the convenience of the patient, physician, or other health care provider Testing would result in outcomes that are equivalent to outcomes using an alternative strategy, and the genetic test is more costly 	 III. Genetic testing is considered not medically necessary when any of the following situations exist: A. Testing is not considered standard of care, such as when the clinical diagnosis can be made without the use of a genetic test B. Testing is not clinically appropriate for the patient's condition (e.g., when it would not change diagnosis and/or management). Other situations where testing is not clinically appropriate include, but are not limited to: 1. Testing performed entirely for nonmedical (e.g., social) reasons 2. Testing not expected to provide a definitive diagnosis that would obviate the need for further testing C. Testing is performed primarily for the convenience of the patient, physician, or other health care provider D. Testing would result in outcomes that are equivalent to outcomes using an alternative strategy, and the genetic test is more costly 		