

Clinical Appropriateness Guidelines

Genetic Testing for Single-Gene and Multifactorial Conditions

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Scope

This document addresses the general principles of clinical appropriateness for genetic testing, including diagnostic testing for Mendelian disorders and susceptibility testing for multifactorial conditions. It also addresses genetic testing to predict risk of thrombosis. See separate clinical appropriateness guidelines for more specific criteria related to reproductive genetics, hereditary cancer, hereditary cardiac conditions, pharmacogenomics, somatic tumor testing, and chromosomal microarray analysis/whole exome sequencing/whole genome sequencing. All tests listed in these guidelines may not require prior authorization; please refer to the health plan.

Appropriate Use Criteria

Germline Genetic Testing

Genetic testing is medically necessary when all of the following criteria are met:

- The test is clinically reasonable:
 - Symptoms and presentation are consistent with the suspected condition
 - Results are expected to lead to a change in medical management
 - If testing guidelines exist, the clinical scenario falls within those recommendations
 - The test is customarily recognized as clinically and technically appropriate in the diagnosis and/or treatment of the suspected condition
- The clinical benefit of testing outweighs the potential risk of psychological or medical harm to the individual being tested
- The test is as targeted as possible for the clinical situation (e.g., familial pathogenic or likely pathogenic (P/LP) variant testing, common variants, genes related to phenotype)
- The clinical presentation warrants testing of multiple genes when a multi-gene panel is requested
- The testing methodology* has been clinically validated and is the most accurate method unless technical limitations (e.g., poor sample quality) necessitate the need for alternate testing strategies

*The testing methodology may target DNA and/or RNA.

Thrombophilia Testing

Testing for common variants in Factor V Leiden (F5) and prothrombin (F2) is medically necessary for any of the following indications (*for additional genes related to thrombophilia see germline genetic testing criteria above*):

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- Pregnant woman who has a personal history of a venous thromboembolism (VTE)
- In an individual with an unprovoked VTE (e.g., not associated with fracture, surgery, prolonged immobilization, cancer) when test results will impact long term medication management and at least one of the following:
 - There is concern for homozygous F2 or F5 or compound heterozygous F2/F5
 - The annual risk of recurrent VTE is estimated to be between 5% and 10%
- Individual who has a first-degree relative with F5 or F2 thrombophilia and one of the following:
 - Surgery is planned
 - Patient is pregnant
 - Females considering estrogen contraception or hormone replacement therapy if results would influence decision to use estrogen

Multifactorial (Non-Mendelian) Genetic Testing

Tests which fall into this category of testing include those which are intended to determine risk or susceptibility to conditions and are not diagnostic. A multifactorial disease is defined as a condition caused by the interaction of multiple genes and/or environmental factors, e.g., cancer, diabetes, and heart disease.

Genetic testing such as gene expression classifiers or polygenic risk scores are considered medically necessary when all of the following are met:

- Patient is at risk for the suspected condition based on personal or family history
- Presence of the genetic variant(s) is highly predictive for the development of the multifactorial condition
- Treatment exists for the multifactorial condition and has been shown to improve outcomes through published, prospective peer-reviewed studies
- Results will directly impact clinical decision-making and/or clinical outcome for the individual being tested

Testing for multifactorial conditions in the general population is not medically necessary.

HLA Histocompatibility Testing

Note: HLA typing for the purpose of matching organ and tissue transplant recipients to compatible donors may not be in scope for all health plans referencing these guidelines.

For criteria regarding HLA genotyping for disease diagnosis or susceptibility testing, please refer to general genetic testing guidelines for multifactorial diseases above. For criteria related to drug

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metabolism or risk of adverse reaction, see Clinical Appropriateness Guidelines for Pharmacogenomic Testing.

CPT Codes

The following codes are associated with the guidelines outlined in this document. This list is not all inclusive. Medical plans may have additional coverage policies that supersede these guidelines.

Covered when medical necessity criteria are met:

- 81240 F2 (prothrombin, coagulation factor II) (eg, hereditary hypercoagulability) gene analysis, 20210G>A variant
- 81241 F5 (coagulation factor V) (eg, hereditary hypercoagulability) gene analysis, Leiden variant
- 81595 Cardiology (heart transplant), mRNA, gene expression profiling by real-time quantitative PCR of 20 genes (11 content and 9 housekeeping), utilizing subfraction of peripheral blood, algorithm reported as a rejection risk score
- 0268U Hematology (atypical hemolytic uremic syndrome [aHUS]), genomic sequence analysis of 15 genes, blood, buccal swab, or amniotic fluid
- 0269U Hematology (autosomal dominant congenital thrombocytopenia), genomic sequence analysis of 14 genes, blood, buccal swab, or amniotic fluid
- 0271U Hematology (congenital neutropenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid
- 0273U Hematology (genetic hyperfibrinolysis, delayed bleeding), genomic sequence analysis of 8 genes (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINE1, SERPINF2, PLAU), blood, buccal swab, or amniotic fluid
- 0274U Hematology (genetic platelet disorders), genomic sequence analysis of 43 genes, blood, buccal swab, or amniotic fluid
- 0276U Hematology (inherited thrombocytopenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid
- 0277U Hematology (genetic platelet function disorder), genomic sequence analysis of 31 genes, blood, buccal swab, or amniotic fluid

Codes that do not meet medical necessity criteria:

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81291	MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis, common variants (eg, 677T, 1298C)
81554	Pulmonary disease (idiopathic pulmonary fibrosis [IPF]), mRNA, gene expression analysis of 190 genes, utilizing transbronchial biopsies, diagnostic algorithm reported as categorical result (eg, positive or negative for high probability of usual interstitial pneumonia [UIP])
0087U	Tissue rejection (allograft organ heart), mRNA gene expression analysis of 1,283 genes utilizing microarray, measuring mRNA transcript levels in transplant heart biopsy tissue, with allograft rejection and injury algorithm reported as a probability score
0088U	Tissue rejection (allograft organ kidney), mRNA gene expression analysis of 1,494 genes utilizing microarray, measuring mRNA transcript levels in transplant kidney biopsy tissue, with allograft rejection and injury algorithm reported as a probability score
0118U	Transplantation medicine, quantification of donor-derived cell-free DNA using whole genome next-generation sequencing, plasma, reported as percentage of donor derived cell-free DNA in the total cell-free DNA
0270U	Hematology (congenital coagulation disorders), genomic sequence analysis of 20 genes, blood, buccal swab, or amniotic fluid
0272U	Hematology (genetic bleeding disorders), genomic sequence analysis of 51 genes, blood, buccal swab, or amniotic fluid, comprehensive
0278U	Hematology (genetic thrombosis), genomic sequence analysis of 12 genes, blood, buccal swab, or amniotic fluid
ANY	TruGraf [®] , Transplant Genomics [™]
ANY	AlloSure [®] , CareDx [®]
ANY	Prospera, Natera

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Background

Genetic Testing

The number of commercially available genetic tests is increasing rapidly, with over 75,000 tests on the market today (Phillips et al. 2018). Rather than individually addressing every possible test and indication, these guidelines describe our general approach to evaluating the medical necessity of genetic tests. Genetic testing may be performed for a variety of reasons, including, but not limited to: establishing a diagnosis, confirming a clinical diagnosis, predictive testing in an asymptomatic patient, reproductive carrier screening, prenatal diagnosis and preimplantation genetic testing, drug response prediction, and clinical research.

The recommendations put forth in this document were created in consideration of national guidelines concerning the safety, clinical validity and clinical utility of genetic tests. In its narrowest definition, clinical utility refers to the demonstrated ability of a test to improve health outcomes across a large population. However, due to the rare nature of most genetic disorders, it is often difficult to meet this definition of clinical utility. Groups such as the American College of Medical Genetics and Genomics (ACMG) have urged payers to expand this narrow definition to include evaluation of psychosocial benefit, enabling testing of family members, and broader benefits to society and science. While it is true that genetic testing does not always easily fit into the traditional model of proven clinical utility, medical benefit must still be the primary factor in determining coverage. However, “improved health outcome” for genetic conditions may also include considerations such as avoiding unnecessary, unpleasant or multiple interventions and providing guidance in medical management.

The National Human Genome Research Institute Task Force on Genetic Testing ([NHGRI] 1995; Holtzman 1999) recommended the following underlying principles to ensure the safety and effectiveness of genetic tests:

- The genotypes to be detected by a genetic test must be shown by scientifically valid methods to be associated with the occurrence of a disease, independently replicated and subject to peer review.
- Analytical sensitivity and specificity of a genetic test must be determined before it is made available in clinical practice.
- Data to establish the clinical validity of genetic tests (clinical sensitivity, specificity, and predictive value) must be collected under investigative protocols. In clinical validation, the study sample must be drawn from a group of subjects representative of the population for whom the test is intended. Formal validation for each intended use of a genetic test is needed.
- Before a genetic test can be generally accepted in clinical practice, data must be collected to demonstrate the benefits and risks that accrue from both positive and negative results.

NGS Multi-Gene Panels

Multi-gene testing panels rapidly sequence several to many genes. Panels target testing to genes that have been associated with a certain phenotype, or encompass a set of genes associated with heterogeneous and overlapping phenotypes. While multi-gene panels are typically more cost-effective

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than stepwise testing of multiple single genes, large panels may include genes of uncertain clinical utility. Unexpected or unclear results can potentially lead to patient distress and downstream healthcare costs. A benefit of targeting testing to a smaller subset of genes is the lower risk of incidental or uncertain findings, as the genes on the panel are expected to correlate with the patient's phenotype. The risk of incidental findings is lowest with highly targeted gene testing, and increases as the number and type of genes on the panel increases.

Organ Transplant (Donor-Derived Cell-free DNA (dd-cfDNA) and RNA Gene Expression Profiles (GEP))

Organ transplant recipients are at risk for allograft rejection, even with modern immunosuppressive therapies. Traditionally, diagnosis of allograft rejection has relied on nonspecific biochemical markers and histologic examination of the grafted tissue. As this requires an invasive tissue biopsy, there is great interest among those in the field of transplantation medicine to develop a noninvasive method of detecting organ transplant rejection (Verhoeven et al. 2018). Non-invasive methods have been proposed for both rejection surveillance of stable post-transplant patients, as well as in aiding biopsy decision-making for patients experiencing symptoms of active rejection. Two general classes of molecular tests have emerged as having the potential to fill this need: donor-derived cell-free DNA (dd-cfDNA) monitoring and RNA gene expression profiles (GEP).

Cell-free DNA is an indicator of dying cells, therefore it has been hypothesized that transplant patients experiencing organ injury associated with acute rejection will have higher levels of donor-derived cell free DNA (dd-cfDNA) than patients without rejection. Elevated dd-cfDNA in plasma has been associated with transplant rejection in heart, liver, lung, kidney, and bone marrow recipients (Synder et al. 2011; Grskovic et al. 2016; Sharon et al. 2017; Jordan et al. 2018; Sayah et al. 2020). It has been proposed that these tests be used for serial monitoring in order to detect new onset injury or rejection prior to clinical symptoms, however the optimal time interval has yet to be established (Bloom et al. 2017; Knight et al. 2019). Furthermore, the ability of dd-cfDNA technology to accurately predict rejection may be different depending on the type of organ rejection; the data is more robust in the setting of antibody mediated rejection versus T-cell mediated rejection (Wijtvliet et al. 2020). In addition, dd-cfDNA testing may be able to be used to guide immunosuppressive treatment of rejection by helping to determine the minimum effective dose, although larger studies to validate this use have not been published (Oellerich et al. 2014). The evaluation of donor-derived cell free DNA has not yet been addressed by professional societies such as the American Society of Transplantation, European Society for Organ Transplantation, or the British Transplantation Society.

Gene expression profiles analyze RNA expression levels of certain genes associated with acute cellular rejection with the end goal to distinguish between rejection and the absence of rejection (Pham et al. 2010). This testing methodology has been most studied in the setting of post-cardiac transplantation monitoring, although it has been explored in other allografts (e.g., kidney). In low risk (stable) heart transplant patients, those who underwent transplant monitoring via gene expression profiling (specifically Allomap) had no worse outcomes than those who were monitored via the conventional method of endomyocardial biopsy (Pham et al. 2010). The GEP group also had six-fold fewer biopsies during the study period (Pham et al. 2010). While the current International Society of Heart and Lung Transplantation guidelines do state that GEPs (specifically Allomap) can be used to rule out the presence of acute heart rejection (grade 2R or greater) in low risk patients between 6 months and 5 years post-transplant, the use of GEPs is not universally accepted (Costanzo et al. 2010; Crespo-Leiro

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et al. 2017). This may be due to the test's limited sensitivity for detection of acute rejection and its inability to detect antibody-mediated rejection (Crespo-Leiro et al. 2017).

The use of noninvasive transplant monitoring methodologies to evaluate transplant rejection is a promising new development in the field of transplant medicine, however the clinical utility of these technologies has yet to be uniformly established (Knight et al. 2019; Dengu 2020). It is not clear if results of these tests will ultimately preclude the need for invasive biopsy in the majority of patients. Additional information from prospective trials as well as interventional studies are needed to demonstrate the clinical utility (Menon et al. 2017; Crespo-Leiro et al. 2017; Verhoeven et al. 2018; Filippone and Farber 2020; Preka et al. 2020; Puliyaanda et al. 2020). Additionally, further research is needed to determine if these molecular biomarkers can be used as a proxy for tolerance of and adequate immunosuppression (O'Callaghan and Knight 2019).

Thrombophilia Testing

Thrombophilia describes a state of hypercoagulability that leads to an increased risk of thrombotic events. Venous thromboembolism (VTE) is a common, complex disease associated with both environmental and genetic risk factors. Risk factors for VTE include advancing age, travel, surgery, injury, family history of VTE, and certain genetic polymorphisms leading to excessive clotting. In women, pregnancy, hormonal contraceptive use, selective estrogen receptor modulators, and hormone replacement therapy are additional risk factors for VTE (Montagnana et al. 2017; Pruthi 2017).

Genetic factors that have been associated with thrombophilia include pathogenic or likely pathogenic (P/LP) variants in several genes including: F5, F2, PROC, PROS1 and SERPINC1 as well as others.

While standard of care for work up of VTE or DVT is to perform protein activity and antigen studies, Factor V and Prothrombin studies are easiest to perform as molecular genotyping given that these conditions are almost always caused by a common variant. There have been conflicting recommendations as to how to approach genetic testing for thrombophilias. ACMG and ACOG have recommended testing for F2 and F5 in certain scenarios, while the Evaluation of Genomic Applications and Prevention Working Group (EGAPP) found insufficient evidence to perform this testing for any indication. Because standard of care for evaluation of thrombophilias includes protein assays for common anticoagulants and single-site P/LP variant studies, large NGS panels are not considered medically necessary. Genetic panel testing for thrombophilia also frequently includes additional genes with limited evidence of association and unclear management implications, such as PAI-1 and MTHFR (Carroll and Piazza 2018; Franchini et al. 2016)

It has been suggested that genetic testing for inherited thrombophilias may allow for prophylactic treatment of individuals at risk for VTE or enhance the prediction of recurrence risk for patients who have already had a VTE. However, the clinical utility of such genetic testing is controversial, and testing is often ordered inappropriately in scenarios where results do not have clinical utility (Shen et al. 2016; Gava et al. 2017; Pruthi et al. 2017; Gaddh et al. 2020).

In all cases, the clinical utility of genetic testing for thrombophilias depends on whether test results will impact the initiation or duration of anticoagulation therapy. It is important to consider the risk of harm from inappropriate prolonged treatment with anticoagulants, as well as the fact that genetic testing does not detect all inherited risk factors for hypercoagulation. In addition, the presence of an inherited thrombophilia variant itself does not always require prophylactic treatment with anticoagulants, and other risk factors should be considered when assessing a patient's individual risk of VTE and the need

for anticoagulation therapy (ACOG 2018; Carroll and Piazza 2018; Ashraf et al. 2019; Stem et al. 2019). For example, genetic test results may have direct implications for treatment in pregnant women with a previous history of VTE, thus testing in this population would be appropriate (ACOG 2018). There may also be a benefit to screening pregnant women with a family history of VTE due to a known familial variant, as those women found to have a high-risk genotype would be offered antenatal prophylactic anticoagulant therapy even in the absence of a personal history of VTE (ACOG 2018).

Factor V Leiden

The Factor V Leiden (FVL) variant (1691G>A; R506Q) in the F5 gene is the most common known inherited risk factor for thrombosis. This P/LP variant leads to reduced inactivation of clotting factor V by activated protein C (ie. APC resistance), which causes increased thrombin generation. Heterozygous carriers of the FVL variant have an approximately 3-fold to 8-fold increased risk of VTE compared to non-carriers (Kujovich 2018). However, the absolute risk of VTE in heterozygotes remains low, with only ~5% of carriers developing a VTE by age 65 (Rodeghiero and Tosetto 1999; Heit et al. 2005). Individuals who are homozygous for the FVL variant have a much higher increased risk of VTE, approximately 9-fold to 80-fold (Rosendaal 2009, EGAPP 2011; Carroll and Piazza 2018). This increased risk corresponds to an absolute incidence of 15 VTE events/1,000 persons/year (Juul et al. 2004).

The prevalence of FVL P/LP variants varies according to population. Approximately 3-8% of the general US and European population carry a heterozygous FVL P/LP variant, while it is rarely identified in individuals from Asian and African populations (Kujovich 2018). Homozygosity of the FVL P/LP variants is seen in approximately 1/5,000 individuals in the general US and European population (Kujovich 2018).

Prothrombin (F2)

The second most common inherited risk factor for VTE is the 20210G>A (G20210A) variant in the F2 gene, which is also called the prothrombin variant. This activating P/LP variant leads to higher circulating levels of prothrombin, which results in an increased risk for clot formation. Heterozygous carriers of the F2 variant have a 2-fold to 4-fold increased risk of VTE compared to non-carriers (Rosendaal and Reitsma 2009; Kujovich 2021). However, the absolute risk of a VTE in heterozygotes again remains quite low: 0.19%/year to 0.41%/year in asymptomatic carriers (Lijfering et al. 2009; Kujovich 2021).

The prevalence of F2 heterozygosity varies by population. Approximately 2-3% of the general US and European population are carriers of the F2 variant, while individuals from African and Asian populations have a much lower prevalence (Kujovich 2021). F2 homozygotes are very rare, approximately 1/10,000 in the general US and European population, and the increased risk associated with this genotype is not well-defined, but may be up to 7 times higher than that of the general population (Kujovich 2021; Carroll and Piazza 2018). Patients with compound heterozygosity for Factor V Leiden and prothrombin mutations may have up to a 20-fold increased risk for VTE. Neither of these mutations exhibit a strongly increased risk for VTE recurrence (Carroll and Piazza 2018).

Professional Society Guidelines

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American College of Medical Genetics and Genomics (ACMG)

ACMG Points to Consider Statement. DNA-Based Screening and Population Health.

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Chao EC, Astbury C, Deignan JL, et al. Genet Med. 2021 Apr 16. PubMed PMID: 33864022.

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ACMG Practice Resource. Genetic Evaluation of Short Stature, Focused Revision.

Mintz C, Seaver L, Irons M, et al. Genet Med. 2021 Jan 29. PubMed PMID: 33514815.

International Society of Heart and Lung Transplantation (ISHLT)

ISHLT Guidelines. Care of Heart Transplant Recipients.

Costanzo MR, Dipchand A, Starling R, et al. J Heart Lung Transplant. 2010 Aug;29(8):914-956. PubMed PMID: 20643330.

Joint Statements

Technical Standards for the Interpretation and Reporting of Constitutional Copy-Number Variants. ACMG and Clinical Genome Resource (ClinGen).

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Standards and Guidelines for the Interpretation of Sequence Variants. ACMG and Association for Molecular Pathology (AMP). Joint Consensus Recommendation.

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Thrombophilia Testing

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ACMG Technical Standards. Venous Thromboembolism Laboratory Testing (Factor V Leiden and Factor II c.*97G>A)

Genet Med. 2018 Dec;20(12):1489-1498. PubMed PMID: 30297698.

American College of Obstetricians and Gynecologists (ACOG)

ACOG Practice Bulletin No. 197. Inherited Thrombophilias in Pregnancy.

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American College of Chest Physicians (ACCP)

ACCP Guideline. VTE, Thrombophilia, Antithrombotic Therapy, and Pregnancy: Antithrombotic Therapy and Prevention of Thrombosis.

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Kearon C, Akl EA, Ornelas J, et al. *Chest*. 2016;149(2):315-52. PubMed PMID: 26867832.

American Society for Reproductive Medicine (ASRM)

ASRM Guideline. Combined Hormonal Contraception and the Risk of Venous Thromboembolism.

Fertil Steril. 2017 Jan;107(1):43-51. PubMed PMID: 27793376.

Veterans Health Administration (VHA)

VHA Policy Recommendation. Pharmacogenetic Testing in the Veterans Health Administration.

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Thrombophilias

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Revision History

Medical Advisory Review Board Review:

- v1.2022 09/20/2021: Approved
- v2.2021 03/12/2021: Approved
- v1.2021 11/13/2020: Approved
- v2.2020 05/08/2020: Reviewed
- v1.2020 11/04/2019: Reviewed
- v2.2019 05/23/2019: No Criteria Changes
- v1.2019 11/07/2018: Reviewed
- v1.2018 03/31/2018: Reviewed

Clinical Steering Committee Review:

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v1.2022 08/23/2021: Approved

v2.2021 02/22/2021: Approved

v1.2021 10/13/2020: Approved

v2.2020 04/06/2020: Approved

v1.2020 10/11/2019: Approved

v2.2019 04/03/2019: Approved

v1.2019 10/03/2018: Approved

v1.2018 02/28/2018: Approved

v1.2017 01/25/2017: Approved

Revisions:

Version	Date	Editor	Description
v1.2022 GEN01-0322.1	8/16/2021	Carrie Langbo, MS, CGC	Semi-annual review. No criteria changes. Thrombophilia testing criteria was moved from the Pharmacogenomic guideline. CMA criteria and content was moved to the Whole Exome and Whole Genome Sequencing guideline. Updated CPT codes, background, professional society guidelines and references (<i>including the addition of applicable thrombophilia information</i>).
v2.2021 GEN01-0921.1	2/15/2021	Carrie Langbo, MS, CGC	Semi-annual review. No criteria changes. Chromosomal Microarray Analysis criteria was clarified to reflect new terminology for developmental and epileptic encephalopathies. Updated CPT codes, background, professional society guidelines and references.
v1.2021	9/11/2020	Carrie Langbo, MS, CGC	Semi-annual review. No criteria changes. Chromosomal Microarray Analysis criteria was

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			clarified. Updated CPT codes, background, professional society guidelines and references.
v2.2020	3/13/2020	Carrie Langbo, MS, CGC	Semi-annual review. Updated text in Genetic Testing for Germline Conditions and Multi-factorial (Non-Mendelian) Genetic Testing. Updated CPT codes, background (added organ transplant and RNA gene expression profiles section) and references.
v1.2020	9/10/2019	Carrie Langbo, MS, CGC	Semi-annual review. No criteria changes. Updated background and references.
v2.2019	4/03/2019	Karen Buser, MS, CGC	Semi-annual review. No criteria changes. Reformatted single and multi-gene criteria. Updated references.
v1.2019	10/03/2018	Kate Charyk, MS, CGC	Semi-annual review. Added CMA criteria for early-onset epilepsy. Updated background. Renumbered to 2019. Reformatted CPT code list. PMID added.
v1.2018	3/31/2018	Gwen Fraley, MS, CGC	Semi-annual review. Removed criteria related to evaluation by a specialty physician for multi-gene panels. Added disclaimer sentence to Scope.
v1.2017	10/27/2017	Gwen Fraley, MS, CGC	Quarterly review. No criteria changes.
v1.2017	09/18//2017	Megan Czarniecki, MS, CGC	Formatted references to NLM style. Moved methodological considerations to appropriate use criteria and background. Updated associated CPT codes. Approved by Policy Lead.
v1.2017	07/03/2017	Gwen Fraley, MS, CGC	Quarterly review. No criteria changes. Updated references.

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v1.2017	04/25/2017	Gwen Fraley, MS, CGC	Quarterly review. No criteria changes. Updated references.
v1.2017	01/23/2017	Gwen Fraley, MS, CGC	Quarterly review. No criteria changes. Added “prospective” to clarify scientific validation criteria for Multifactorial (Non-Mendelian) Conditions. Updated references. Renumbered to 2017 version.
v2.2016	10/06/2016	Gwen Fraley, MS, CGC	Added HLA and transplant criteria. Updated references.
v1.2016	06/17/2016	Gwen Fraley, MS, CGC	Revised medical necessity criteria for single gene and panel testing. Updated references.
v1.2015	06/04/2015	Gwen Fraley, MS, CGC	Original version

Original Effective Date: 06/04/2015

Primary Author: Gwen Fraley, MS, CGC

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