PRESBYTERIAN

# Medical Policy

**Subject:** Genetic, Biomarker and Genomic Testing

**Medical Policy:** 7.1 **Original Effective Date:** 12/17/2008

**Status:** Reviewed **Last Review Date:** 05-28-2025

## Disclaimer

**Refer to the member's specific benefit plan and Schedule of Benefits to determine coverage. This may not be a benefit on all plans, or the plan may have broader or more limited benefits than those listed in this Medical Policy.**

## Description

Genetic testing (Biomarkers) may be covered when, either because of symptomatology and/or family history. Genetic testing is the use of specific assays to determine the genetic status of individuals already suspected to be at high risk for a particular inherited condition. High risk means that the individual has a known family history or classic symptoms of the disorder. Genetic testing includes a variety of techniques that test genetic diseases and analyzes genetic risk factors that may contribute to disease. Techniques involve the examination of a blood sample, or other body fluid, or tissue to indicate the presence, absence, or alteration (mutation) of genes linked to specific diseases or conditions.

The main difference between genetic and genomic tests is that genetic tests look at sequence variants in single genes while genomic tests look at the expression of multiple genes in a single assay. Genetic testing typically refers to inherited disorders. Genomic testing usually refers to tests that look at expression profiles of multiple genes in a particular tissue affected by an acquired disease (e.g., a tumor), and in many cases, are cancer tests.

Recognizing the differences as described above, for the purposes of this Medical Policy, the term "genetic testing" is considered interchangeable with "genomic testing" and "Biomarkers" is used throughout.

**Note**: the following definitions are provided by the state, which also meet the PHP definitions for Genetic Testing, above:

**Other related medical policies:**

- Genetic Testing: Colorectal Cancer (CRC) Screening, MPM 7.4
- Genetic Testing for Breast Cancer Recurrence and Predictive, MPM 33.0
- Genetic Testing for Cutaneous Melanoma, MPM 7.7
- Genetic Testing for Lynch Syndrome, MPM 7.5
- Genetic Testing: Hypercoagulability/Thrombophilia, 7.11
- Genetic Testing: Next Generation Sequencing, MPM 29.0
- Genetic Testing for Non-Invasive Prenatal Testing (NIPT), MPM 20.15
- Genetic Testing for Pancreatic Cyst (PathfinderTG/PancraGen), MPM 7.6
- Genetic Testing for Prostate Cancer, MPM 7.8
- Genetic Testing for Uveal Melanoma, MPM 7.9
- Genetic Testing: InvisionFirst Liquid Biopsy for Lung Cancer, MPM 39.1
- Genetic Testing: Plasma-Based Genomic Profiling in Solid Tumor, MPM 39.0
- Genetic Testing for Whole Exome Sequencing, MPM 7.12
- Genetic Testing for Circulating Tumor DNA Tests for Management of Cancer, MPM 54.0
- Genetic Testing for Multi-biomarker (Vectra™ DA) test for Rheumatoid Arthritis, MPM 42.0
- Genetic Testing for Carrier Testing and Prenatal Diagnosis, MPM 7.13

## Coverage Determination

**All newly released genetic codes will require prior authorization until further research is completed.**

**Prior Authorization may or may not be required. Logon to Pres Online to submit a request:** https://ds.phs.org/preslogin/index.jsp

**Genetic testing may not be a benefit on all plans. Refer to the member's specific benefit plan and *Schedule of Benefits* to determine coverage.**

**Biomarker testing is covered, unless otherwise indicated for Medicare, Medicaid on a case-by-case basis.**

**Exclusions:**

- Biomarkers and Genomic testing are non-covered when it is considered investigational or experimental.
- General population screening using genetic testing is not covered

**Nationally recognized clinical practice guidelines**: Evidence-based clinical practice guidelines that are developed by independent organizations or medical professional societies using a transparent methodology and reporting structure with a conflict-of-interest policy.

**Coverage Criteria for Biomarkers:**
Biomarker testing is covered when used for the purposes of diagnosis, treatment, appropriate management, or ongoing monitoring of a member's disease or condition when the test is supported by medical and scientific evidence.

**Additional Genetic/ Genomic tests:**
Ongoing assessment of genetic tests will be evaluated for medical necessity by reviewing the following:

- Medicare/Medicaid coverage updates and other State/Federal research/recommendations, statutes, regulations or coverage determinations.
- Review of evidence-based guidelines provided by organizations such as, National Comprehensive Cancer Network (NCCN), specialty societies, Knowledge Center/Hayes (a Division of Tract Manager), MCG Health, part of the Hearst Health network, and Up-to Date.
- Review of medical literature(s).

**Example**: Hereditary Cancer Genetic Testing criteria for High-Penetrance Breast Cancer Genes: BRCA1, BRC2, CDH1, PALB2, PTEN, and TP53:

- For Medicaid and Commercial members: PHP follows the current version NCCN guidelines.
- For Medicare members: PHP follows either of the following:
  - BRCA1, BRCA2, and High-Penetrance Breast Cancer Gene Genetic Testing: by Novitas (L36715), with related Article (A56542).
  - NCCN risk evaluation that is performed must be applied to patients with the diagnosis confirmed of cancer of ovarian or breast origin.
- These testing limited to once-in-a-lifetime.

**The following basic guidelines apply:**
General population screening using genetic testing is not covered.

Metabolic disease/Genetic inborn errors of metabolism testing are covered for newborn screening for genetic disorders as mandated by state guidelines.[1]

Biomarkers are covered as mandated by state guidelines when appropriate medical necessity is provided in accordance with the criteria above.[5] Genetic testing is covered for when **all** of the following criteria have been met. Genetic testing should be ordered by specialized physicians and/or certified genetic counselors qualified to interpret the testing results. Appropriate documentation of patient consent should be obtained.

- After physical examination and routine testing, the diagnosis remains uncertain. The member is at risk for a genetic disease, either with a direct risk factor for the development of an inheritable disease (known family history) or demonstrating signs/symptoms of a genetic disease.
- The genetic test result has potential to affect the course of treatment for the member.
- Pharmacogenetics is a type of genetic testing that may help determine what medication and dosage will be most effective and beneficial for a particular health condition or disease. See also Pharmacogenomics Testing for Behavioral Health for Medicare, MPM 30.0.
- Consultations with qualified genetic counselors and physicians should be part of the treatment plan in order for the patient to receive the appropriate interpretation of the genetic testing. Unless otherwise stated, a printed three generation pedigree should be part of the genetic consultation and should be available for review.
- The genetic test is considered a proven method to
  - identify or rule out an inheritable disease, **or**
  - to detect an inherited or acquired disease-related genotype, mutation, phenotype or karyotype for clinical purposes.
- Genetic testing for germ-line mutation of specific disease is only covered **once in a person's lifetime**, for identification purposes and does not include genetic testing monitoring related drug therapy.
- Carrier and predictive testing are covered for certain genetic diseases when there is an affected family member of first or second-degree relation who has an identified mutation or genetic disease, and the

information will help with medical or reproductive decision-making. In some circumstances, testing may also be covered when the patient is the reproductive partner of a person with a positive genetic test and the couple intends to have a baby.

- Prenatal or preimplantation genetic testing is covered for certain genetic diseases if there is an increased risk (known family history) that an offspring will have a genetic or chromosomal disorder. (Please note: Preimplantation genetic testing, as part of assisted reproductive techniques such as in-vitro fertilization, may not be a covered benefit. Refer to the member's specific benefit plan to determine coverage).

**Background**

**Biomarkers:**

- Biomarkers are a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a specific therapeutic intervention, including known gene-drug interactions for medications being considered for use or already being administered. "Biomarker" includes gene mutations, characteristics of genes or protein expression.
- Biomarker testing analysis of a patient's tissue, blood, or other biospecimen for the presence of a biomarker and includes single-analyte tests, multi-plex panel tests, protein expression and whole exome, whole genome, and whole transcriptome sequencing.
- Biomarkers for oncology can be generally classified into four functional types:
    1. **Diagnostic** biomarkers detect or confirm the presence of a disease or condition.
    2. **Prognostic** biomarkers provide information about the likely course of a disease process and potential patient outcomes if left untreated.
    3. **Predictive** biomarkers forecast a patient's response and/or benefit to a specific treatment.
    4. **Therapeutic** biomarkers identify potential targets for medical intervention. (e.g., targeted drug therapy)

**Genetic/Genome:**

- **Genetics** refers to the study of genes and their role in inheritance – the way certain traits or conditions are passed down from one generation to another. Genetics involves scientific studies of single genes and their effects. Genes (units of heredity) carry the instructions for making proteins, which direct the activities of cells and functions of the body. Genes influence traits such as hair and eye color as well as health and disease development. Genetics determines much (but not all) of a person's health status; environmental differences also play a part.
- A **genome** is defined as all the genetic material in the chromosomes of a particular organism. **Genomics** is a relatively new term describing the study of multiple genes from the same person, including interactions of those genes with each other and the person's environment. Genomics involves scientific study of complex diseases such as heart disease, asthma, diabetes and cancer because they are caused more by a combination of genetic and environmental factors. Genomics is offering new possibilities for therapies and treatment of some diseases, as well as new diagnostic methods. The major tools and methods related to genomics studies are bioinformatics, genetic analysis, measurement of gene expression, and determination of gene function.

**Types of Tests:**

- Newborn screening: Used just after birth to identify genetic disorders that can be treated early in life.
- Diagnostic testing: Used to identify or rule out a specific genetic or chromosomal condition. In many cases, genetic testing is used to confirm a diagnosis when a particular condition is suspected based on physical signs and symptoms. Diagnostic testing can be performed before birth or at any time during a person's life but is not available for all genes or all genetic conditions. The results of a diagnostic test can influence a person's choices about health care and the management of the disorder.
- Carrier testing: Used to identify people who carry one copy of a gene mutation that, when present in two copies, causes a genetic disorder. This type of testing is offered to individuals who have a family history of a genetic disorder and to people in certain ethnic groups with an increased risk of specific genetic conditions. If both parents are tested, the test can provide information about a couple's risk of having a child with a genetic condition.
- Prenatal testing: Used to detect changes in a fetus' genes or chromosomes before birth. This type of testing is offered during pregnancy if there is an increased risk that the baby will have a genetic or chromosomal disorder. In some cases, prenatal testing can lessen a couple's uncertainty or help them make decisions about pregnancy. It cannot identify all possible inherited disorders and birth defects. See also Genetic Testing for Non-Invasive Prenatal Testing (NIPT), MPM 20.15.

- Preimplantation testing: A specialized technique that can reduce the risk of having a child with a genetic or chromosomal disorder. It is used to detect genetic changes in embryos created using assisted reproductive techniques such as in-vitro fertilization. Only embryos without certain genetic changes are implanted in the uterus to initiate a pregnancy.
- Predictive and presymptomatic testing: Used to detect gene mutations associated with disorders that appear after birth, often later in life. These tests can be helpful to people who have a family member with a genetic disorder, but who have no features of the disorder themselves at the time of testing. The results of the testing can provide information about a person's risk of developing a specific disorder and help with making decisions about medical care.

**Medical Terms:**

- Assay: A laboratory test to find and measure the amount of a specific substance.
- First-degree relative: Parents, children, siblings (blood relatives).
- Gene expression: The process by which proteins are made from the instructions encoded in DNA.
- Second-degree relative: Grandparents, aunts and uncles, nieces and nephews, grandchildren, half-sibling (blood relatives)
- Third-degree relative: Great-grandparents, great-aunts, great-uncles, and first cousins (blood relatives)
- Three-Generation Pedigree: A pictorial representation of diseases within a family to assess hereditary influences on disease or to help identify relatively rare conditions that may not be considered in a differential diagnosis.

**Mechanism by which to determine coverage for Medicare, Medicaid and Commercial:**

When a specific policy is not in place for genetic/biomarker criteria at phs.org then the service determination will fall to this policy.

1. Coverage determination within this policy will be determined by the following considerations:
    a. If a National Coverage Determination (NCD) exists with explicit instructions, we will follow the NCD.
    b. If an NCD does not exist, or instructions are unclear, or do not specifically outline the specific genetic/biomarker test, we will look for more specific guidance from a Local Coverage Determination (LCD).
        i. For LCD, we consider New Mexico Medicare Administrative Contractor either Novitas or Wisconsin Physician Services (WPS) first for our local area coverage determination and will follow their guidance.
            1. In the instance that Novitas and WPS are stating separate coverage guidance, Novitas will take priority over WPS.
            2. If Novitas and WPS are silent, we will utilize the MolDX® Program (Administered by Palmetto GBA), Dex Z-code® for verification of covered services.

    **OR**

    c. If all the above is silent, the review will be on a case-by-case basis for the following:
        i. A review of national guidelines that recommends the use of the biomarker for diagnosis, treatment, appropriate management or ongoing monitoring of an insured's disease or condition when the test is supported by medical and scientific evidence.
        ii. A review of package inserts for medication that recommends the use of biomarker for therapeutic monitoring of the medication

## Coding

**The coding listed in this medical policy is for reference only. Covered and non-covered codes are within this list. Please visit the prior authorization for consideration of other test(s) which may not be listed in this table. Not all test(s) meet coverage and test(s) will be considered on a case-by-case basis.**

| Codes | Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)* |
|---|---|
| 81441 | Inherited bone marrow failure syndromes (IBMFS) (eg, Fanconi anemia, dyskeratosis congenita, Diamond-Blackfan anemia, Shwachman-Diamond syndrome, GATA2 deficiency syndrome, congenital amegakaryocytic thrombocytopenia) sequence analysis panel, must include sequencing of at least 30 genes, including BRCA2, BRIP1, DKC1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, GATA1, GATA2, MPL, NHP2, NOP10, PALB2, RAD51C, RPL11, RPL35A, RPL5, RPS10, RPS19, RPS24, RPS26, RPS7, SBDS, TERT, and TINF2 |
| 81457 | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability |
| 81458 | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability |
| 81459 | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements |
| 81462 | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements |
| 81463 | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis, copy number variants, and microsatellite instability |
| 81464 | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements |
| 81517 | Liver disease, analysis of 3 biomarkers (hyaluronic acid [HA], procollagen III amino terminal peptide [PIIINP], tissue inhibitor of metalloproteinase 1 [TIMP-1]), using immunoassays, utilizing serum, prognostic algorithm reported as a risk score and risk of liver fibrosis and liver-related clinical events within 5 years |
| 0012U | Germline disorders, gene rearrangement detection by whole genome next-generation sequencing, DNA, whole blood, report of specific gene rearrangement(s) |
| 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) |
| 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) |
| 0056U | Hematology (acute myelogenous leukemia), DNA, whole genome next-generation sequencing to detect gene rearrangement(s), blood or bone marrow, report of specific gene rearrangement(s) |
| 0080U | Oncology (lung), mass spectrometric analysis of galectin-3-binding protein and scavenger receptor cysteine-rich type 1 protein M130, with five clinical risk factors (age, smoking status, nodule diameter, nodule-spiculation status and nodule location), utilizing plasma, algorithm reported as a categorical probability of malignancy |
| 0091U | Oncology (colorectal) screening, cell enumeration of circulating tumor cells, utilizing whole blood, algorithm, for the presence of adenoma or cancer, reported as a positive or negative result |
| 0108U | Gastroenterology (Barrett's esophagus), whole slide-digital imaging, including morphometric analysis, computer-assisted quantitative immunolabeling of 9 protein biomarkers (p16, AMACR, p53, CD68, COX-2, CD45RO, HIF1a, HER-2, K20) and morphology, formalin-fixed paraffin-embedded tissue, algorithm reported as risk of progression to high-grade dysplasia or cancer.<br>Includes: TissueCypher® Barrett's Esophagus Assay, Cernostics, Cernostics |

| Codes | Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)* |
|---|---|
| 0204U | Oncology (thyroid), mRNA, gene expression analysis of 593 genes (including BRAF, RAS, RET, PAX8, and NTRK) for sequence variants and rearrangements, utilizing fine needle aspirate, reported as detected or not detected |
| 0208U | Oncology (medullary thyroid carcinoma), mRNA, gene expression analysis of 108 genes, utilizing fine needle aspirate, algorithm reported as positive or negative for medullary thyroid carcinoma |
| 0246U | Red blood cell antigen typing, DNA, genotyping of at least 16 blood groups with phenotype prediction of at least 51 red blood cell antigens |
| 0295U | Oncology (breast ductal carcinoma in situ), protein expression profiling by immunohistochemistry of 7 proteins (COX2, FOXA1, HER2, Ki-67, p16, PR, SIAH2), with 4 clinicopathologic factors (size, age, margin status, palpability), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a recurrence risk score |
| 0317U | Oncology (lung cancer), four-probe FISH (3q29, 3p22.1, 10q22.3, 10cen) assay, whole blood, predictive algorithm-generated evaluation reported as decreased or increased risk for lung cancer |
| 0318U | Pediatrics (congenital epigenetic disorders), whole genome methylation analysis by microarray for 50 or more genes, blood. |
| 0319U | Nephrology (renal transplant), RNA expression by select transcriptome sequencing, using pretransplant peripheral blood, algorithm reported as a risk score for early acute rejection |
| 0337U | Oncology (plasma cell disorders and myeloma), circulating plasma cell immunologic selection, identification, morphological characterization, and enumeration of plasma cells based on differential CD138, CD38, CD19, and CD45 protein biomarker expression, peripheral blood |
| 0338U | Oncology (solid tumor), circulating tumor cell selection, identification, morphological characterization, detection and enumeration based on differential EpCAM, cytokeratins 8, 18, and 19, and CD45 protein biomarkers, and quantification of HER2 protein biomarker expressing cells, peripheral blood |
| 0347U | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 16 gene report, with variant analysis and reported phenotypes. (Effective 10/1/2022) |
| 0348U | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes. (Effective 10/1/2022) |
| 0350U | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes. (Effective 10/1/2022) |
| 0356U | Oncology (oropharyngeal), evaluation of 17 DNA biomarkers using droplet digital PCR (ddPCR), cell-free DNA, algorithm reported as a prognostic risk score for cancer recurrence |
| 0359U | Oncology (prostate cancer), analysis of all prostate-specific antigen (PSA) structural isoforms by phase separation and immunoassay, plasma, algorithm reports risk of cancer |
| 0395U | Oncology (lung), multi-omics (microbial DNA by shotgun next- generation sequencing and carcinoembryonic antigen and osteopontin by immunoassay), plasma, algorithm reported as malignancy risk for lung nodules in early-stage disease |
| 0401U | Cardiology (coronary heart disease [CAHD]), 9 genes (12 variants), targeted variant genotyping, blood, saliva, or buccal swab, algorithm reported as a genetic risk score for a coronary event |
| 0414U | Oncology (lung), augmentative algorithmic analysis of digitized whole slide imaging for 8 genes (ALK, BRAF, EGFR, ERBB2, MET, NTRK1-3, RET, ROS1), and KRAS G12C and PD-L1, if performed, formalin-fixed paraffin- embedded (FFPE) tissue, reported as positive or negative for each biomarker |
| 0422U | Oncology (pan-solid tumor), analysis of DNA biomarker response to anti-cancer therapy using cell-free circulating DNA, biomarker comparison to a previous baseline pre-treatment cell-free circulating DNA analysis using next-generation sequencing, algorithm reported as a quantitative change from baseline, including specific alterations, if appropriate |

| Codes | Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)* |
|---|---|
| 0425U | Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis, each comparator genome (eg, parents, siblings) |
| 0426U | Genome (eg, unexplained constitutional or heritable disorder or syndrome), ultra-rapid sequence analysis |
| 0434U | Drug metabolism (adverse drug reactions and drug response), genomic analysis panel, variant analysis of 25 genes with reported phenotypes |
| 0437U | Psychiatry (anxiety disorders), mRNA, gene expression profiling by RNA sequencing of 15 biomarkers, whole blood, algorithm reported as predictive risk score |
| 0438U | Drug metabolism (adverse drug reactions and drug response), buccal specimen, gene-drug interactions, variant analysis of 33 genes, including deletion/duplication analysis of CYP2D6, including reported phenotypes and impacted gene-drug interactions |
| 0439U | Cardiology (coronary heart disease [CHD]), DNA, analysis of 5 single-nucleotide polymorphisms (SNPs) (rs11716050 [LOC105376934], rs6560711 [WDR37], rs3735222 [SCIN/LOC107986769], rs6820447 [intergenic], and rs9638144 [ESYT2]) and 3 DNA methylation markers (cg00300879 [transcription start site {TSS200} of CNKSR1], cg09552548 [intergenic], and cg14789911 [body of SPATC1L]), qPCR and digital PCR, whole blood, algorithm reported as a 4-tiered risk score for a 3-year risk of symptomatic CHD |
| 0448U | Oncology (lung and colon cancer), DNA, qualitative, next-generation sequencing detection of single-nucleotide variants and deletions in EGFR and KRAS genes, formalin-fixed paraffin-embedded (FFPE) solid tumor samples, reported as presence or absence of targeted mutation(s), with recommended therapeutic options |
| G9143 | Warfarin responsiveness testing by genetic technique using any method, any number of specimen(s) |
| S0265 | Genetic counseling, under physician supervision, each 15 minutes |
| S3800 | Genetic testing for amyotrophic lateral sclerosis |
| S3840 | DNA analysis for germline mutations of the RET proto-oncogene for susceptibility to multiple endocrine neoplasia type 2 |
| S3841 | Genetic testing for retinoblastoma |
| S3842 | Genetic testing for Von Hippel-Lindau disease |
| S3844 | DNA analysis of the connexin 26 gene (GJB2) for susceptibility to congenital, profound deafness |
| S3845 | Genetic testing for alpha-thalassemia |
| S3846 | Genetic testing for hemoglobulin E beta-thalassemia |
| S3849 | Genetic testing for Niemann-Pick disease |
| S3850 | Genetic testing for sickle cell anemia |
| S3852 | DNA analysis for APOE epsilon 4 allele for susceptibility to Alzheimer's disease |
| S3853 | Genetic testing for myotonic muscular dystrophy |
| S3854 | Gene expression profiling panel for use in the management of breast cancer treatment |
| S3861 | Genetic testing, sodium channel, voltage-gated, type V, alpha subunit (SCN5A) and variants for suspected Brugada Syndrome |
| S3865 | Comprehensive gene sequence analysis for hypertrophic cardiomyopathy |
| S3866 | Genetic analysis for a specific gene mutation for hypertrophic cardiomyopathy (HCM) in an individual with a known HCM mutation in the family |
| S3870 | Comparative Genomic Hybridization (CGH) Microarray Testing for Developmental Delay, Autism Spectrum Disorder and/or Intellectual Disability |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 0264U | RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), IDENTIFICATION OF COPY NUMBER VARIATIONS, INVERSIONS, INSERTIONS, TRANSLOCATIONS, AND OTHER STRUCTURAL VARIANTS BY OPTICAL GENOME MAPPING |
| 0265U | RARE CONSTITUTIONAL AND OTHER HERITABLE DISORDERS, WHOLE GENOME AND MITOCHONDRIAL DNA SEQUENCE ANALYSIS, BLOOD, FROZEN AND FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE, SALIVA, BUCCAL SWABS OR CELL LINES, IDENTIFICATION OF SINGLE NUCLEOTIDE AND COPY |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | NUMBER VARIANTS |
| 0266U | UNEXPLAINED CONSTITUTIONAL OR OTHER HERITABLE DISORDERS OR SYNDROMES, TISSUE-SPECIFIC GENE EXPRESSION BY WHOLE-TRANSCRIPTOME AND NEXT-GENERATION SEQUENCING, BLOOD, FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE) TISSUE OR FRESH FROZEN TISSUE, REPORTED AS PRESENCE OR ABSENCE OF SPLICING OR EXPRESSION CHANGES |
| 0267U | RARE CONSTITUTIONAL AND OTHER HERITABLE DISORDERS, IDENTIFICATION OF COPY NUMBER VARIATIONS, INVERSIONS, INSERTIONS, TRANSLOCATIONS, AND OTHER STRUCTURAL VARIANTS BY OPTICAL GENOME MAPPING AND WHOLE GENOME SEQUENCING |
| 0273U | HEMATOLOGY (GENETIC HYPERFIBRINOLYSIS, DELAYED BLEEDING), ANALYSIS OF 9 GENES (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINE1, SERPINF2 BY NEXT-GENERATION SEQUENCING, AND PLAU BY ARRAY COMPARATIVE GENOMIC HYBRIDIZATION), BLOOD, BUCCAL SWAB, OR AMNIOTIC FLUID |
| 0282U | RED BLOOD CELL ANTIGEN TYPING, DNA, GENOTYPING OF 12 BLOOD GROUP SYSTEM GENES TO PREDICT 44 RED BLOOD CELL ANTIGEN PHENOTYPES |
| 0424U | ONCOLOGY (PROSTATE), EXOSOME-BASED ANALYSIS OF 53 SMALL NONCODING RNAS (SNCRNAS) BY QUANTITATIVE REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION (RT-QPCR), URINE, REPORTED AS NO MOLECULAR EVIDENCE, LOW-, MODERATE- OR ELEVATED-RISK OF PROSTATE CANCER<br><br>MIR SENTINEL™ PROSTATE CANCER TEST, MIR SCIENTIFIC®, LLC, MIR SCIENTIFIC®, LLC |
| 0433U | ONCOLOGY (PROSTATE), 5 DNA REGULATORY MARKERS BY QUANTITATIVE PCR, WHOLE BLOOD, ALGORITHM, INCLUDING PROSTATE-SPECIFIC ANTIGEN, REPORTED AS LIKELIHOOD OF CANCER<br><br>EPISWITCH® PROSTATE SCREENING TEST (PSE), OXFORD BIODYNAMICS INC, OXFORD BIODYNAMICS PLC |
| 0460U | ONCOLOGY, WHOLE BLOOD OR BUCCAL, DNA SINGLE-NUCLEOTIDE POLYMORPHISM (SNP) GENOTYPING BY REAL-TIME PCR OF 24 GENES, WITH VARIANT ANALYSIS AND REPORTED PHENOTYPES<br><br>RIGHTMED® ONCOLOGY GENE REPORT, ONEOME® LLC, ONEOME® LLC |
| 0461U | ONCOLOGY, PHARMACOGENOMIC ANALYSIS OF SINGLE-NUCLEOTIDE POLYMORPHISM (SNP) GENOTYPING BY REAL-TIME PCR OF 24 GENES, WHOLE BLOOD OR BUCCAL SWAB, WITH VARIANT ANALYSIS, INCLUDING IMPACTED GENE-DRUG INTERACTIONS AND REPORTED PHENOTYPES<br><br>RIGHTMED® ONCOLOGY MEDICATION REPORT, ONEOME® LLC, ONEOME® LLC |
| 0466U | CARDIOLOGY (CORONARY ARTERY DISEASE [CAD]), DNA, GENOME-WIDE ASSOCIATION STUDIES (564856 SINGLE-NUCLEOTIDE POLYMORPHISMS [SNPS], TARGETED VARIANT GENOTYPING), PATIENT LIFESTYLE AND CLINICAL DATA, BUCCAL SWAB, ALGORITHM REPORTED AS POLYGENIC RISK TO ACQUIRED HEART DISEASE<br><br>CARDIORISK+, GENE BY GENE, LTD, OPENDNA, LTD |
| 0467U | ONCOLOGY (BLADDER), DNA, NEXT-GENERATION SEQUENCING (NGS) OF 60 GENES AND WHOLE GENOME ANEUPLOIDY, URINE, ALGORITHMS REPORTED AS MINIMAL RESIDUAL DISEASE (MRD) STATUS POSITIVE OR NEGATIVE AND QUANTITATIVE DISEASE BURDEN |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | UROAMP MRD, CONVERGENT GENOMICS, INC, CONVERGENT GENOMICS, INC |
| 0469U | RARE DISEASES (CONSTITUTIONAL/HERITABLE DISORDERS), WHOLE GENOME SEQUENCE ANALYSIS FOR CHROMOSOMAL ABNORMALITIES, COPY NUMBER VARIANTS, DUPLICATIONS/DELETIONS, INVERSIONS, UNBALANCED TRANSLOCATIONS, REGIONS OF HOMOZYGOSITY (ROH), INHERITANCE PATTERN THAT INDICATE UNIPARENTAL DISOMY (UPD), AND ANEUPLOIDY, FETAL SAMPLE (AMNIOTIC FLUID, CHORIONIC VILLUS SAMPLE, OR PRODUCTS OF CONCEPTION), IDENTIFICATION AND CATEGORIZATION OF GENETIC VARIANTS, DIAGNOSTIC REPORT OF FETAL RESULTS BASED ON PHENOTYPE WITH MATERNAL SAMPLE AND PATERNAL SAMPLE, IF PERFORMED, AS COMPARATORS AND/OR MATERNAL CELL CONTAMINATION<br><br>IRISIGHT™ CNV ANALYSIS, VARIANTYX INC, VARIANTYX INC |
| 0470U | ONCOLOGY (OROPHARYNGEAL), DETECTION OF MINIMAL RESIDUAL DISEASE BY NEXT-GENERATION SEQUENCING (NGS) BASED QUANTITATIVE EVALUATION OF 8 DNA TARGETS, CELL-FREE HPV 16 AND 18 DNA FROM PLASMA<br>HPV-SEQ TEST, SYSMEX INOSTICS, INC, SYSMEX INOSTICS, INC |
| 0471U | ONCOLOGY (COLORECTAL CANCER), QUALITATIVE REAL-TIME PCR OF 35 VARIANTS OF KRAS AND NRAS GENES (EXONS 2, 3, 4), FORMALIN-FIXED PARAFFIN-EMBEDDED (FFPE), PREDICTIVE, IDENTIFICATION OF DETECTED MUTATIONS<br>CRCDX® RAS MUTATION DETECTION KIT, ENTROGEN, INC, ENTROGEN, INC |
| 0474U | HEREDITARY PAN-CANCER (EG, HEREDITARY SARCOMAS, HEREDITARY ENDOCRINE TUMORS, HEREDITARY NEUROENDOCRINE TUMORS, HEREDITARY CUTANEOUS MELANOMA), GENOMIC SEQUENCE ANALYSIS PANEL OF 88 GENES WITH 20 DUPLICATIONS/DELETIONS USING NEXT-GENERATION SEQUENCING (NGS), SANGER SEQUENCING, BLOOD OR SALIVA, REPORTED AS POSITIVE OR NEGATIVE FOR GERMLINE VARIANTS, EACH GENE<br><br>GENETICSNOW® COMPREHENSIVE GERMLINE PANEL, GOPATH DIAGNOSTICS, INC, GOPATH DIAGNOSTICS, INC |
| 0475U | HEREDITARY PROSTATE CANCER-RELATED DISORDERS, GENOMIC SEQUENCE ANALYSIS PANEL USING NEXT-GENERATION SEQUENCING (NGS), SANGER SEQUENCING, MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION (MLPA), AND ARRAY COMPARATIVE GENOMIC HYBRIDIZATION (CGH), EVALUATION OF 23 GENES AND DUPLICATIONS/DELETIONS WHEN INDICATED, PATHOLOGIC MUTATIONS REPORTED WITH A GENETIC RISK SCORE FOR PROSTATE CANCER<br><br>PROSTATENOW™ PROSTATE GERMLINE PANEL, GOPATH DIAGNOSTICS, INC, GOPATH DIAGNOSTICS, INC |
| 0486U | ONCOLOGY (PAN-SOLID TUMOR), NEXT-GENERATION SEQUENCING ANALYSIS OF TUMOR METHYLATION MARKERS PRESENT IN CELL-FREE CIRCULATING TUMOR DNA, ALGORITHM REPORTED AS QUANTITATIVE MEASUREMENT OF METHYLATION AS A CORRELATE OF TUMOR FRACTION<br>NORTHSTAR RESPONSE™, BILLIONTOONE LABORATORY, BILLIONTOONE, INC |
| 0487U | ONCOLOGY (SOLID TUMOR), CELL-FREE CIRCULATING DNA, TARGETED GENOMIC SEQUENCE ANALYSIS PANEL OF 84 GENES, INTERROGATION FOR SEQUENCE VARIANTS, ANEUPLOIDY-CORRECTED GENE COPY NUMBER AMPLIFICATIONS AND LOSSES, GENE REARRANGEMENTS, AND MICROSATELLITE INSTABILITY<br>NORTHSTAR SELECT™, BILLIONTOONE LABORATORY, BILLIONTOONE, INC |
| 0488U | OBSTETRICS (FETAL ANTIGEN NONINVASIVE PRENATAL TEST), CELL-FREE |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | DNA SEQUENCE ANALYSIS FOR DETECTION OF FETAL PRESENCE OR ABSENCE OF 1 OR MORE OF THE RH, C, C, D, E, DUFFY (FYA), OR KELL (K) ANTIGEN IN ALLOIMMUNIZED PREGNANCIES, REPORTED AS SELECTED ANTIGEN(S) DETECTED OR NOT DETECTED<br>UNITY FETAL ANTIGEN™ NIPT, BILLIONTOONE LABORATORY, BILLIONTOONE, INC |
| 0489U | OBSTETRICS (SINGLE-GENE NONINVASIVE PRENATAL TEST), CELL-FREE DNA SEQUENCE ANALYSIS OF 1 OR MORE TARGETS (EG, CFTR, SMN1, HBB, HBA1, HBA2) TO IDENTIFY PATERNALLY INHERITED PATHOGENIC VARIANTS, AND RELATIVE MUTATION-DOSAGE ANALYSIS BASED ON MOLECULAR COUNTS TO DETERMINE FETAL INHERITANCE OF MATERNAL MUTATION, ALGORITHM REPORTED AS A FETAL RISK SCORE FOR THE CONDITION (EG, CYSTIC FIBROSIS, SPINAL MUSCULAR ATROPHY, BETA HEMOGLOBINOPATHIES [INCLUDING SICKLE CELL DISEASE], ALPHA THALASSEMIA)<br>UNITY FETAL RISK SCREEN™, BILLIONTOONE LABORATORY, BILLIONTOONE, INC |
| 81277 | CYTOGENOMIC NEOPLASIA (GENOME-WIDE) MICROARRAY ANALYSIS, INTERROGATION OF GENOMIC REGIONS FOR COPY NUMBER AND LOSS-OF-HETEROZYGOSITY VARIANTS FOR CHROMOSOMAL ABNORMALITIES |
| 81105 | Human Platelet Antigen 1 genotyping (HPA-1), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa], antigen CD61 [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-1a/b (L33P) |
| 81106 | Human Platelet Antigen 2 genotyping (HPA-2), GP1BA (glycoprotein Ib [platelet], alpha polypeptide [GPIba]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-2a/b (T145M) |
| 81107 | Human Platelet Antigen 3 genotyping (HPA-3), ITGA2B (integrin, alpha 2b [platelet glycoprotein IIb of IIb/IIIa complex], antigen CD41 [GPIIb]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-3a/b (I843S) |
| 81108 | Human Platelet Antigen 4 genotyping (HPA-4), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa], antigen CD61 [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-4a/b (R143Q) |
| 81109 | Human Platelet Antigen 5 genotyping (HPA-5), ITGA2 (integrin, alpha 2 [CD49B, alpha 2 subunit of VLA-2 receptor] [GPIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant (eg, HPA-5a/b (K505E)) |
| 81110 | Human Platelet Antigen 6 genotyping (HPA-6w), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa, antigen CD61] [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-6a/b (R489Q) |
| 81111 | Human Platelet Antigen 9 genotyping (HPA-9w), ITGA2B (integrin, alpha 2b [platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41] [GPIIb]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-9a/b (V837M) |
| 81112 | Human Platelet Antigen 15 genotyping (HPA-15), CD109 (CD109 molecule) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-15a/b (S682Y) |
| 81120 | IDH1 (ISOCITRATE DEHYDROGENASE 1 [NADP+], SOLUBLE) (EG, GLIOMA), COMMON VARIANTS (EG, R132H, R132C) |
| 81121 | IDH2 (ISOCITRATE DEHYDROGENASE 2 [NADP+], MITOCHONDRIAL) (EG, GLIOMA), COMMON VARIANTS (EG, R140W, R172M) |
| 81161 | DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy) deletion analysis, and duplication analysis, if performed |
| 81162 | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (ie, detection of large gene rearrangements) |
| 81163 | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81164 | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements) |
| 81165 | BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis |
| 81166 | BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements) |
| 81167 | BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements) |
| 81168 | CCND1/IGH (t(11;14)) (eg, mantle cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performed |
| 81170 | ABL1 (ABL proto-oncogene 1, non-receptor tyrosine kinase) (eg, acquired imatinib tyrosine kinase inhibitor resistance), gene analysis, variants in the kinase domain |
| 81173 | AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; full gene sequence |
| 81174 | AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; known familial variant |
| 81175 | ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; full gene sequence |
| 81176 | ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; targeted sequence analysis (eg, exon 12) |
| 81177 | ATN1 (atrophin 1) (eg, dentatorubral-pallidoluysian atrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81178 | ATXN1 (ataxin 1) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81179 | ATXN2 (ataxin 2) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81180 | ATXN3 (ataxin 3) (eg, spinocerebellar ataxia, Machado-Joseph disease) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81181 | ATXN7 (ataxin 7) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81182 | ATXN8OS (ATXN8 opposite strand [non-protein coding]) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81183 | ATXN10 (ataxin 10) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81184 | CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; evaluation to detect abnormal (eg, expanded) alleles |
| 81185 | CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; full gene sequence |
| 81186 | CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; known familial variant |
| 81187 | CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81188 | CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles |
| 81189 | CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; full gene sequence |
| 81190 | CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; known familial variant(s) |
| 81191 | NTRK1 (neurotrophic receptor tyrosine kinase 1) (eg, solid tumors) translocation analysis |
| 81192 | NTRK2 (neurotrophic receptor tyrosine kinase 2) (eg, solid tumors) translocation analysis |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81193 | NTRK3 (neurotrophic receptor tyrosine kinase 3) (eg, solid tumors) translocation analysis |
| 81194 | NTRK (neurotrophic-tropomyosin receptor tyrosine kinase 1, 2, and 3) (eg, solid tumors) translocation analysis |
| 81200 | ASPA (ASPARTOACYLASE) (EG, CANAVAN DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, E285A, Y231X) |
| 81201 | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; full gene sequence |
| 81202 | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; known familial variants |
| 81203 | APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants |
| 81204 | AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; characterization of alleles (eg, expanded size or methylation status) |
| 81205 | BCKDHB (BRANCHED-CHAIN KETO ACID DEHYDROGENASE E1, BETA POLYPEPTIDE) (EG, MAPLE SYRUP URINE DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, R183P, G278S, E422X) |
| 81206 | BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; MAJOR BREAKPOINT, QUALITATIVE OR QUANTITATIVE |
| 81207 | BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; MINOR BREAKPOINT, QUALITATIVE OR QUANTITATIVE |
| 81208 | BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS; OTHER BREAKPOINT, QUALITATIVE OR QUANTITATIVE |
| 81209 | BLM (BLOOM SYNDROME, RECQ HELICASE-LIKE) (EG, BLOOM SYNDROME) GENE ANALYSIS, 2281DEL6INS7 VARIANT |
| 81210 | BRAF (B-RAF PROTO-ONCOGENE, SERINE/THREONINE KINASE) (EG, COLON CANCER, MELANOMA), GENE ANALYSIS, V600 VARIANT(S) |
| 81212 | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; 185delAG, 5385insC, 6174delT variants |
| 81215 | RCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; known familial variant |
| 81216 | BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis |
| 81217 | BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; known familial variant |
| 81218 | CEBPA (CCAAT/enhancer binding protein [C/EBP], alpha) (eg, acute myeloid leukemia), gene analysis, full gene sequence |
| 81219 | CALR (calreticulin) (eg, myeloproliferative disorders), gene analysis, common variants in exon 9 |
| 81228 | Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, bacterial artificial chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis) |
| 81229 | Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities |
| 81233 | BTK (Bruton's tyrosine kinase) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, C481S, C481R, C481F) |
| 81234 | CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; evaluation to detect abnormal (eg, expanded) alleles |
| 81235 | EGFR (EPIDERMAL GROWTH FACTOR RECEPTOR) (EG, NON-SMALL CELL LUNG CANCER) GENE ANALYSIS, COMMON VARIANTS (EG, EXON 19 LREA DELETION, L858R, T790M, G719A, G719S, L861Q) |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81236 | EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, myelodysplastic syndrome, myeloproliferative neoplasms) gene analysis, full gene sequence |
| 81237 | EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, diffuse large B-cell lymphoma) gene analysis, common variant(s) (eg, codon 646) |
| 81238 | F9 (coagulation factor IX) (eg, hemophilia B), full gene sequence |
| 81239 | DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size) |
| 81242 | ASHKENAZI JEWISH ASSOCIATED DISORDERS (EG, BLOOM SYNDROME, CANAVAN DISEASE, CYSTIC FIBROSIS, FAMILIAL DYSAUTONOMIA, FANCONI ANEMIA GROUP C, GAUCHER DISEASE, TAY-SACHS DISEASE), GENOMIC SEQUENCE ANALYSIS PANEL, MUST INCLUDE SEQUENCING OF AT LEAST 9 GENES, INCLUDING ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, AND SMPD1 |
| 81245 | FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; internal tandem duplication (ITD) variants (ie, exons 14, 15) |
| 81246 | FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; tyrosine kinase domain (TKD) variants (eg, D835, I836) |
| 81248 | G6PD (glucose-6-phosphate dehydrogenase) (eg, hemolytic anemia, jaundice), gene analysis; known familial variant(s) |
| 81249 | G6PD (glucose-6-phosphate dehydrogenase) (eg, hemolytic anemia, jaundice), gene analysis; full gene sequence |
| 81250 | G6PC (glucose-6-phosphatase, catalytic subunit) (eg, Glycogen storage disease, type 1a, von Gierke disease) gene analysis, common variants (eg, R83C, Q347X) |
| 81251 | GBA (GLUCOSIDASE, BETA, ACID) (EG, GAUCHER DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, N370S, 84GG, L444P, IVS2+1G>A) |
| 81252 | GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; full gene sequence |
| 81253 | GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; known familial variants |
| 81254 | GJB6 (gap junction protein, beta 6, 30kDa, connexin 30) (eg, nonsyndromic hearing loss) gene analysis, common variants (eg, 309kb [del(GJB6-D13S1830)] and 232kb [del(GJB6-D13S1854)]) |
| 81255 | HEXA (HEXOSAMINIDASE A [ALPHA POLYPEPTIDE]) (EG, TAY-SACHS DISEASE) GENE ANALYSIS, COMMON VARIANTS (EG, 1278INSTATC, 1421+1G>C, G269S) |
| 81256 | HFE (hemochromatosis) (eg, hereditary hemochromatosis) gene analysis, common variants (eg, C282Y, H63D) |
| 81258 | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known familial variant |
| 81259 | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; full gene sequence |
| 81260 | IKBKAP (INHIBITOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS, KINASE COMPLEX-ASSOCIATED PROTEIN) (EG, FAMILIAL DYSAUTONOMIA) GENE ANALYSIS, COMMON VARIANTS (EG, 2507+6T>C, R696P) |
| 81261 | IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); amplified methodology (eg, polymerase chain reaction) |
| 81262 | IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); direct probe methodology (eg, Southern blot) |
| 81263 | IGH@ (Immunoglobulin heavy chain locus) (eg, leukemia and lymphoma, B-cell), variable region somatic mutation analysis |
| 81264 | IGK@ (Immunoglobulin kappa light chain locus) (eg, leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s) |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81265 | Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (eg, pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [eg, 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 (eg, 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 (eg, hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection |
| 81268 | Chimerism (engraftment) analysis, post transplantation specimen (eg, hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (eg, CD3, CD33), each cell type |
| 81269 | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; duplication/deletion variants |
| 81270 | JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, p.Val617Phe (V617F) variant |
| 81271 | HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles |
| 81272 | KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18) |
| 81273 | KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, mastocytosis), gene analysis, D816 variant(s) |
| 81274 | HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size) |
| 81275 | KRAS (KIRSTEN RAT SARCOMA VIRAL ONCOGENE HOMOLOG) (EG, CARCINOMA) GENE ANALYSIS; VARIANTS IN EXON 2 (EG, CODONS 12 AND 13) |
| 81276 | KRAS (Kirsten rat sarcoma viral oncogene homolog) (eg, carcinoma) gene analysis; additional variant(s) (eg, codon 61, codon 146) |
| 81278 | IGH@/BCL2 (t(14;18)) (eg, follicular lymphoma) translocation analysis, major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative |
| 81279 | JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13) |
| 81284 | FXN (frataxin) (eg, Friedreich ataxia) gene analysis; evaluation to detect abnormal (expanded) alleles |
| 81285 | FXN (frataxin) (eg, Friedreich ataxia) gene analysis; characterization of alleles (eg, expanded size) |
| 81286 | FXN (frataxin) (eg, Friedreich ataxia) gene analysis; full gene sequence |
| 81287 | MGMT (O-6-methylguanine-DNA methyltransferase) (eg, glioblastoma multiforme) promoter methylation analysis |
| 81289 | FXN (frataxin) (eg, Friedreich ataxia) gene analysis; known familial variant(s) |
| 81290 | MCOLN1 (MUCOLIPIN 1) (EG, MUCOLIPIDOSIS, TYPE IV) GENE ANALYSIS, COMMON VARIANTS (EG, IVS3-2A>G, DEL6.4KB) |
| 81302 | MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; FULL SEQUENCE ANALYSIS |
| 81303 | MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; KNOWN FAMILIAL VARIANT |
| 81304 | MECP2 (METHYL CPG BINDING PROTEIN 2) (EG, RETT SYNDROME) GENE ANALYSIS; DUPLICATION/DELETION VARIANTS |
| 81305 | MYD88 (myeloid differentiation primary response 88) (eg, Waldenstrom's macroglobulinemia, lymphoplasmacytic leukemia) gene analysis, p.Leu265Pro (L265P) variant |
| 81307 | PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | analysis; full gene sequence |
| 81308 | PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; known familial variant |
| 81309 | PIK3CA (phosphatidylinositol-4, 5-biphosphate 3-kinase, catalytic subunit alpha) (eg, colorectal and breast cancer) gene analysis, targeted sequence analysis (eg, exons 7, 9, 20) |
| 81310 | NPM1 (nucleophosmin)(eg. acute myeloid leukemia) gene analysis, exon 12 variants |
| 81311 | NRAS (neuroblastoma RAS viral [v-ras] oncogene homolog)(eg. colorectal carcinoma), gnee analysis, variants in exon 2 (eg. codons 12 and 13) and exon 3 (eg. codon 61) |
| 81312 | PABPN1 (poly[A] binding protein nuclear 1) (eg, oculopharyngeal muscular dystrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81314 | PDGFRA (platelet-derived growth factor receptor, alpha polypeptide)(eg. gastrointestinal stromal tumor [GIST]), gene analysis, targeted sequence analysis (eg. exons 12, 18) |
| 81315 | PML/RARalpha, (t[15:17]), (promyelocytic leukemia/retinoic acid receptor alpha)(eg. promyelocytic leukemia) translocation analysis; common breakpoints (eg. intron 3 and intron 6), qualitative or quantitative |
| 81316 | PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor alpha) (eg, promyelocytic leukemia) translocation analysis; single breakpoint (eg, intron 3, intron 6 or exon 6), qualitative or quantitative |
| 81320 | PLCG2 (phospholipase C gamma 2) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, R665W, S707F, L845F) |
| 81321 | PTEN (phosphatase and tensin homolog)(eg. Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis |
| 81322 | PTEN (phosphatase and tensin homolog)(eg. Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variants |
| 81323 | PTEN (phosphatase and tensin homolog)(eg. Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication /deletion variants |
| 81324 | PMP22 (peripheral mylin protein 22)(eg Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; duplication/deletion analysis |
| 81325 | PMP22 (peripheral mylin protein 22)(eg Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; |
| 81326 | PMP22 (peripheral myelin protein 22) (eg, Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; known familial variant |
| 81330 | SMPD1(sphingomyelin phosphodiesterase 1, acid lysosomal) (eg, Niemann-Pick disease, Type A) gene analysis, common variants (eg, R496L, L302P, fsP330) |
| 81331 | SNRPN/UBE3A (small nuclear ribonucleoprotein polypeptide N and ubiquitin protein ligase E3A)(eg. Prader-Willi syndrome and/or Angelman syndrome), methylation analysis |
| 81333 | TGFBI (transforming growth factor beta-induced) (eg, corneal dystrophy) gene analysis, common variants (eg, R124H, R124C, R124L, R555W, R555Q) |
| 81334 | RUNX1 (runt related transcription factor 1) (eg, acute myeloid leukemia, familial platelet disorder with associated myeloid malignancy), gene analysis, targeted sequence analysis (eg, exons 3-8) |
| 81338 | MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R) |
| 81339 | MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10 |
| 81340 | TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using amplification methodology (eg, polymerase chain reaction) |
| 81341 | TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using direct probe methodology (eg, Southern blot) |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81342 | TRG@ (T cell antigen receptor, gamma) (eg, leukemia and lymphoma), gene rearrangement analysis, evaluation to detect abnormal clonal population(s) |
| 81343 | PPP2R2B (protein phosphatase 2 regulatory subunit Bbeta) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81344 | TBP (TATA box binding protein) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles |
| 81345 | TERT (telomerase reverse transcriptase) (eg, thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (eg, promoter region) |
| 81347 | SF3B1 (splicing factor [3b] subunit B1) (eg, myelodysplastic syndrome/acute myeloid leukemia) gene analysis, common variants (eg, A672T, E622D, L833F, R625C, R625L) |
| 81348 | SRSF2 (serine and arginine-rich splicing factor 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, P95H, P95L) |
| 81349 | Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis |
| 81351 | TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; full gene sequence |
| 81352 | TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; targeted sequence analysis (eg, 4 oncology) |
| 81353 | TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; known familial variant |
| 81357 | U2AF1 (U2 small nuclear RNA auxiliary factor 1) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, S34F, S34Y, Q157R, Q157P) |
| 81360 | ZRSR2 (zinc finger CCCH-type, RNA binding motif and serine/arginine-rich 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variant(s) (eg, E65fs, E122fs, R448fs) |
| 81361 | HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); COMMON VARIANT(S) (EG, HBS, HBC, HBE) |
| 81362 | HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); KNOWN FAMILIAL VARIANT(S) |
| 81363 | HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); DUPLICATION/DELETION VARIANT(S) |
| 81364 | HBB (HEMOGLOBIN, SUBUNIT BETA) (EG, SICKLE CELL ANEMIA, BETA THALASSEMIA, HEMOGLOBINOPATHY); FULL GENE SEQUENCE |
| 81370 | HLA Class I and II typing, low resolution (eg. antigen equivalents); HLA-A -B, -C, -DRB1/3/4/5, and -DQB1 |
| 81371 | HLA Class I and II typing, low resoultion (eg. antigen equivalents); HLA-A, -B, and -DQB1 (eg. verification typing) |
| 81372 | HLA Class I typing, low resolution (eg. antigen equivalents); complete (ie. HLA-A, -B, and -C) |
| 81373 | HLA Class I typing, low resolution (eg. antigen equivalents); one locus (ie. HLA-A, -B, and -C), each |
| 81375 | HLA Class II typing, low resolution (eg. antigen equivalents); HLA-DRB1/3/4/5 and -DQB1 |
| 81378 | HLA-Class I and II typing, high resolution (ie. alleles or allele groups), HLA-A, -B, -C, and -DRB1 |
| 81379 | HLA-Class I typing, high resolution (ie. alleles or allele groups), complete (ie. HLA-A, -B, -C)HLA-A, -B, -C, and -DRB1 |
| 81380 | HLA-Class I typing, high resolution (ie. alleles or allele groups), one locus (eg. HLA-A, -B, -C), each |
| 81400 | Molecular pathology procedure, Level 1 (eg. identification of single germline variant (eg. SNP) by techniques such as restriction enzyme digestion or melt curve analysis |
| 81401 | MOLECULAR PATHOLOGY PROCEDURE, LEVEL 2 (EG, 2-10 SNPS, 1 METHYLATED VARIANT, OR 1 SOMATIC VARIANT [TYPICALLY USING NONSEQUENCING TARGET VARIANT ANALYSIS], OR DETECTION OF A |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | DYNAMIC MUTATION DISORDER/TRIPLET REPEAT) |
| 81402 | Molecular pathology procedure, Level 3 (eg. >10 SNPs, 2-10 methylated variants, or 2-10 somatic variants ]typically using non-sequencing target variant analysis]j, immunoglobulin and T-cell receptor gene rearrangements, duplication/deletion variants of 1 exon, loss of heterozygosity [LOH]. uniparnetal disomy [UPD]) |
| 81403 | Molecular pathology procedure, Level 4 (eg. analysis of single exon by DNA sequence analysis, analysis of >10 amlicons using multiplex PCR in 2 or more independent reactions, mutation scanning or duplication/deletion variants of 2-5 exons) |
| 81404 | Molecular pathology procedure, Level 5 (eg. analysis of 2-5 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by Southern blot analysis |
| 81405 | Molecular pathology procedure, Level 6 (eg. analysis of 6-10 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 11-25 exons), regionally targeted cytogenomic analysis |
| 81406 | Molecular pathology procedure, Level 7 (eg. analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons, cytogenomic array analysis for neoplasia) |
| 81407 | Molecular pathology procedure, Level 8 (eg. analysis of 26-50 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of >50 exons, sequence analysis of multiple genes on one platform) |
| 81408 | Molecular pathology procedure, Level 9 (eg, analysis of > 50 exons in a single gene by DNA sequence analysis) |
| 81410 | Aortic dysfunction or dilitation (eg. Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); genomic sequence analysis panel, must include sequencing of at least 9 genes, including FBN1, TGFBR1, TGFBR2, COL3A1, MYH11, ACTA2, SLC2A10, SMAD3, and MYLK |
| 81411 | Aortic dysfunction or dilitation (eg. Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); duplication/deletion analysis panel, must include TGFBR1, TGFBR2, MYH11, COL3A1 |
| 81412 | Ashkenazi Jewish associated disorders (eg, Bloom syndrome, Canavan disease, cystic fibrosis, familial dysautonomia, Fanconi anemia group C, Gaucher disease, Tay-Sachs disease), genomic sequence analysis panel, must include sequencing of at least 9 genes, including ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, and SMPD1 |
| 81413 | Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia); genomic sequence analysis panel, must include sequencing of at least 10 genes, including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A |
| 81414 | Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia); duplication/deletion gene analysis panel, must include analysis of at least 2 genes, including KCNH2 and KCNQ1 |
| 81419 | Epilepsy genomic sequence analysis panel, must include analyses for ALDH7A1, CACNA1A, CDKL5, CHD2, GABRG2, GRIN2A, KCNQ2, MECP2, PCDH19, POLG, PRRT2, SCN1A, SCN1B, SCN2A, SCN8A, SLC2A1, SLC9A6, STXBP1, SYNGAP1, TCF4, TPP1, TSC1, TSC2, and ZEB2 |
| 81427 | Genome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (eg, updated knowledge or unrelated condition/syndrome) |
| 81430 | Hearing loss (eg. nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); genomic sequence analysis panel, must include sequencing of at least 60 genes, including CDH23, CLRN1, GJB2, GPR98, MTRNR1, MY07A, MY015A, PCDH15, 0T0F, SLC26A4, TMC1, TMPRSS3, USH1G, USH2A, and WFS1 |
| 81431 | Hearing loss (eg. nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); duplication/deletion gene analysis panel, must include copy number analyses for STRC |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | and DFNB1 deletions in GJB2 asnd GJB6 genes |
| 81432 | Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer, hereditary pancreatic cancer, hereditary prostate cancer), genomic sequence analysis panel, 5 or more genes, interrogation for sequence variants and copy number variants |
| 81433 | Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); duplication/deletion analysis panel, must include analyses for BRCA1, BRCA2, MLH1, MSH2, and STK11 |
| 81434 | Hereditary retinal disorders (eg, retinitis pigmentosa, Leber congenital amaurosis, cone-rod dystrophy), genomic sequence analysis panel, must include sequencing of at least 15 genes, including ABCA4, CNGA1, CRB1, EYS, PDE6A, PDE6B, PRPF31, PRPH2, RDH12, RHO, RP1, RP2, RPE65, RPGR, and USH2 |
| 81437 | Hereditary neuroendocrine tumor disorders (eg. medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); genomic sequence analysis panel, must include sequencing of at least 6 genes, including MAX, SDHB, SDHC, SDHD, and VHL |
| 81438 | Hereditary neuroendocrine tumor disorders (eg. medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); duplication/deletion analysis panel, must include analyses for SDHB, SDHC, SDHD, and VHL |
| 81439 | Inherited cardiomyopathy (eg, hypertrophic cardiomyopathy, dilated cardiomyopathy, arrhythmogenic right ventricular cardiomyopathy) genomic sequence analysis panel, must include sequencing of at least 5 genes, including DSG2, MYBPC3, MYH7, PKP2, and TTN |
| 81440 | Nuclear encoded mitochondiral genes (eg. neurologic or myopathic phenotypes), genomic sequence panel, must include analysis of at least 100 genes, including BCS1L, C10orf2, COQ2, COX10, DGU0K, MRP17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, and TYMP |
| 81442 | Noonan spectrum disorders (eg. Noonan syndrome, cardio-facio-cutaneous syndrome, Costello syndrome, LEOPARD syndrome, Noonan-like syndrome), genomic sequence analysis panel, must include sequencing of at least 12 genes, including BRAF, CBL, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RIT1, SHOC2, and SOS1 |
| 81443 | Genetic testing for severe inherited conditions (eg, cystic fibrosis, ashkenazi jewish-associated disorders [eg, bloom syndrome, canavan disease, fanconi anemia type C, mucolipidosis type VI, gaucher disease, tay-sachs disease], beta hemoglobinopathies, phenylketonuria, galactosemia), genomic sequence analysis panel, must include sequencing of at least 15 genes (EG, ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH) |
| 81445 | Solid organ neoplasm, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants and copy number variants or rearrangements, if performed; DNA analysis<br>or combined DNA and RNA analysis |
| 81448 | ONC PRST8 MRNA GENE XPRSN PRFL RT-PCR 46 GENES |
| 81450 | Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, DNA analysis, and RNA analysis when performed, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KRAS, KIT, MLL, NRAS, NPM1, NOTCH1), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed |
| 81451 | Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NOTCH1, NPM1, NRAS), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 81455 | Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm, DNA analysis, and RNA analysis when performed, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NPM1, NRAS, MET, NOTCH1, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed |
| 81456 | Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis |
| 81460 | Whole mitochondrial genome (eg, Leigh syndrome, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes [MELAS], myoclonic epilepsy with ragged-red fibers [MERFF], neuropathy, ataxia, and retinitis pigmentosa [NARP], Leber hereditary optic neuropathy [LHON]), genomic sequence, must include sequence analysis of entire mitochondrial genome with heteroplasmy detection |
| 81465 | Whole mitochondrial genome large deletion analysis panel (eg, Kearns-Sayre syndrome, chronic progressive external ophthalmoplegia), including heteroplasmy detection, if performed |
| 81479 | Unlisted molecular pathology procedure |
| 81493 | Coronary artery disease, mRNA, gene expression profiling by real-time RT-PCR of 23 genes, utilizing whole peripheral blood, algorithm reported as a risk score |
| 81504 | Oncology (tissue of origin), microarray gene expression profiling of > 2000 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as tissue similarity scores |
| 81506 | Endocrinology (type 2 diabetes), biochemical assays of seven analytes (glucose, HbA1c, insulin, hs-CRP, adiponectin, ferritin, interleukin 2-receptor alpha), utilizing serum or plasma, algorithm reporting a risk score |
| 81509 | Fetal congenital abnormalities, biochemical assays of three proteins (PAPP-A, hCG [any form], DIA), utilizing maternal serum, algorithm reported as a risk score |
| 81510 | Fetal congenital abnormalities, biochemical assays of three analytes (AFP, uE3, hCG [any form]), utilizing maternal serum, algorithm reported as a risk score |
| 81519 | Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 21 genes, utilizing formalin-fixed paraffin embedded tissue, algorithm reported as recurrence score |
| 81525 | Oncology (colon), mRNA, gene expression profiling by real-time RT-PCR of 12 genes (7 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a recurrence score |
| 81540 | Oncology (tumor of unknown origin), mRNA, gene expression profiling by real-time RT-PCR of 92 genes (87 content and 5 housekeeping) to classify tumor into main cancer type and subtype, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a probability of a predicted main cancer type and subtype |
| 81546 | Oncology (thyroid), mRNA, gene expression analysis of 10,196 genes, utilizing fine needle aspirate, algorithm reported as a categorical result (eg, benign or suspicious) |
| 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]) |
| 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 |
| 81599 | Unlisted multianalyte assay with algorithmic analysis |
| 0001U | Red blood cell antigen typing, DNA, human erythrocyte antigen gene analysis of 35 antigens from 11 blood groups, utilizing whole blood, common RBC alleles reported |
| 0004M | Scoliosis, DNA analysis of 53 single nucleotide polymorphisms (SNPs), using saliva, prognostic algorithm reported as a risk score |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 0010U | Infectious disease (bacterial), strain typing by whole genome sequencing, phylogenetic-based report of strain relatedness, per submitted isolate |
| 0011M | Oncology, prostate cancer, mRNA expression assay of 12 genes (10 content and 2 housekeeping), RT-PCR test utilizing blood plasma and/or urine, algorithms to predict high-grade prostate cancer risk |
| 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 |
| 0018U | Oncology (thyroid), microRNA profiling by RT-PCR of 10 microRNA sequences, utilizing fine needle aspirate, algorithm reported as a positive or negative result for moderate to high risk of malignancy |
| 0019U | Oncology, RNA, gene expression by whole transcriptome sequencing, formalin-fixed paraffin embedded tissue or fresh frozen tissue, predictive algorithm reported as potential targets for therapeutic agents. Includes OncoTarget/OncoTreat, Columbia University Department of Pathology and Cell Biology, Darwin Health |
| 0022U | Targeted genomic sequence analysis panel, cholangiocarcinoma and cholangiocarcinoma and non-small cell lung neoplasia, DNA and RNA analysis, 23 genes, interrogation for sequence variants and rearrangements, reported as presence/absence of variants and associated therapy(ies) to consider |
| 0023U | Oncology (acute myelogenous leukemia), DNA, genotyping of internal tandem duplication, p.D835, p.I836, using mononuclear cells, reported as detection or non-detection of FLT3 mutation and indication for or against the use of midostaurin |
| 0026U | Oncology (thyroid), DNA and mRNA of 112 genes, next-generation sequencing, fine needle aspirate of thyroid nodule, algorithmic analysis reported as a categorical result ("Positive, high probability of malignancy" or "Negative, low probability of malignancy") |
| 0027U | JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, targeted sequence analysis exons 12-15 |
| 0030U | Drug metabolism (warfarin drug response), targeted sequence analysis (ie, CYP2C9, CYP4F2, VKORC1, rs12777823) |
| 0034U | TPMT (thiopurine S-methyltransferase), NUDT15 (nudix hydroxylase 15) (eg, thiopurine metabolism) gene analysis, common variants (ie, TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5) |
| 0036U | Exome (ie, somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses |
| 0037U | Targeted genomic sequence analysis, solid organ neoplasm, DNA analysis of 324 genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden |
| 0040U | BCR/ABL1 (T(9;22)) (EG, CHRONIC MYELOGENOUS LEUKEMIA) TRANSLOCATION ANALYSIS, MAJOR BREAKPOINT, QUANTITATIVE |
| 0046U | FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia) internal tandem duplication (ITD) variants, quantitative |
| 0048U | Oncology (solid organ neoplasia), DNA, targeted sequencing of protein-coding exons of 468 cancer-associated genes, including interrogation for somatic mutations and microsatellite instability, matched with normal specimens, utilizing formalin-fixed paraffin-embedded tumor tissue, report of clinically significant mutation(s) |
| 0049U | NPM1 (nucleophosmin) (eg, acute myeloid leukemia) gene analysis, quantitative |
| 0055U | Cardiology (heart transplant), cell-free DNA, PCR assay of 96 DNA target sequences (94 single nucleotide polymorphism targets and two control targets), plasma |
| 0084U | Red blood cell antigen typing, DNA, genotyping of 10 blood groups with phenotype prediction of 37 red blood cell antigens |
| 0094U | Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 0102U | Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with mRNA analytics to resolve variants of unknown significance when indicated (17 genes [sequencing and deletion/duplication]) |
| 0103U | Hereditary ovarian cancer (eg, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with mRNA analytics to resolve variants of unknown significance when indicated (24 genes [sequencing and deletion/duplication], EPCAM [deletion/duplication only]) |
| 0111U | Oncology (colon cancer), targeted KRAS (codons 12, 13, and 61) and NRAS (codons 12, 13, and 61) gene analysis utilizing formalin-fixed paraffin-embedded tissue |
| 0114U | Gastroenterology (Barrett's esophagus), VIM and CCNA1 methylation analysis, esophageal cells, algorithm reported as likelihood for Barrett's esophagus |
| 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 |
| 0129U | Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis and deletion/duplication analysis panel (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, and TP53) |
| 0130U | Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure) |
| 0138U | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| 0153U | Oncology (breast), mRNA, gene expression profiling by next-generation sequencing of 101 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a triple negative breast cancer clinical subtype(s) with information on immune cell involvement, |
| 0155U | Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha) (eg, breast cancer) gene analysis (ie, p.C420R, p.E542K, p.E545A, p.E545D [g.1635G>T only], p.E545G, p.E545K, p.Q546E, p.Q546R, p.H1047L, p.H1047R, p.H1047Y), utilizing formalin-fixed paraffin-embedded breast tumor tissue, reported as PIK3CA gene mutation status |
| 0169U | NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (eg, drug metabolism) gene analysis, common variants |
| 0171U | Targeted genomic sequence analysis panel, acute myeloid leukemia, myelodysplastic syndrome, and myeloproliferative neoplasms, DNA analysis, 23 genes, interrogation for sequence variants, rearrangements and minimal residual disease, reported as presence/absence |
| 0172U | Oncology (solid tumor as indicated by the label), somatic mutation analysis of BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) and analysis of homologous recombination deficiency pathways, DNA, formalin-fixed paraffin-embedded tissue, algorithm quantifying tumor genomic instability score |
| 0177U | Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha) gene analysis of 11 gene variants utilizing plasma, reported as PIK3CA gene mutation status |
| 0179U | Oncology (non-small cell lung cancer), cell-free DNA, targeted sequence analysis of 23 genes (single nucleotide variations, insertions and deletions, fusions without prior knowledge of partner/breakpoint, copy number variations), with report of significant mutation(s) |
| 0180U | Red cell antigen (ABO blood group) genotyping (ABO), gene analysis Sanger/chain termination/conventional sequencing, ABO (ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase) gene, including subtyping, 7 exons |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 0181U | Red cell antigen (Colton blood group) genotyping (CO), gene analysis, AQP1 (aquaporin 1 [Colton blood group]) exon 1 |
| 0182U | Red cell antigen (Cromer blood group) genotyping (CROM), gene analysis, CD55 (CD55 molecule [Cromer blood group]) exons 1-10 |
| 0183U | Red cell antigen (Diego blood group) genotyping (DI), gene analysis, SLC4A1 (solute carrier family 4 member 1 [Diego blood group]) exon 19 |
| 0184U | Red cell antigen (Dombrock blood group) genotyping (DO), gene analysis, ART4 (ADP-ribosyltransferase 4 [Dombrock blood group]) exon 2 |
| 0185U | Red cell antigen (H blood group) genotyping (FUT1), gene analysis, FUT1 (fucosyltransferase 1 [H blood group]) exon 4 |
| 0186U | Red cell antigen (H blood group) genotyping (FUT2), gene analysis, FUT2 (fucosyltransferase 2) exon 2 |
| 0187U | Red cell antigen (Duffy blood group) genotyping (FY), gene analysis, ACKR1 (atypical chemokine receptor 1 [Duffy blood group]) exons 1-2 |
| 0188U | Red cell antigen (Gerbich blood group) genotyping (GE), gene analysis, GYPC (glycophorin C [Gerbich blood group]) exons 1-4 |
| 0189U | Red cell antigen (MNS blood group) genotyping (GYPA), gene analysis, GYPA (glycophorin A [MNS blood group]) introns 1, 5, exon 2 |
| 0190U | Red cell antigen (MNS blood group) genotyping (GYPB), gene analysis, GYPB (glycophorin B [MNS blood group]) introns 1, 5, pseudoexon 3 |
| 0191U | Red cell antigen (Indian blood group) genotyping (IN), gene analysis, CD44 (CD44 molecule [Indian blood group]) exons 2, 3, 6 |
| 0192U | Red cell antigen (Kidd blood group) genotyping (JK), gene analysis, SLC14A1 (solute carrier family 14 member 1 [Kidd blood group]) gene promoter, exon 9 |
| 0194U | Red cell antigen (Kell blood group) genotyping (KEL), gene analysis, KEL (Kell metallo-endopeptidase [Kell blood group]) exon 8 |
| 0195U | KLF1 (Kruppel-like factor 1), targeted sequencing (ie, exon 13) |
| 0196U | Red cell antigen (Lutheran blood group) genotyping (LU), gene analysis, BCAM (basal cell adhesion molecule [Lutheran blood group]) exon 3 |
| 0197U | Red cell antigen (Landsteiner-Wiener blood group) genotyping (LW), gene analysis, ICAM4 (intercellular adhesion molecule 4 [Landsteiner-Wiener blood group]) exon 1 |
| 0198U | Red cell antigen (RH blood group) genotyping (RHD and RHCE), gene analysis Sanger/chain termination/conventional sequencing, RHD (Rh blood group D antigen) exons 1-10 and RHCE (Rh blood group CcEe antigens) exon 5 |
| 0199U | Red cell antigen (Scianna blood group) genotyping (SC), gene analysis, ERMAP (erythroblast membrane associated protein [Scianna blood group]) exons 4, 12 |
| 0200U | Red cell antigen (Kx blood group) genotyping (XK), gene analysis, XK (X-linked Kx blood group) exons 1-3 |
| 0201U | Red cell antigen (Yt blood group) genotyping (YT), gene analysis, ACHE (acetylcholinesterase [Cartwright blood group]) exon 2 |
| 0209U | Cytogenomic constitutional (genome-wide) analysis, interrogation of genomic regions for copy number, structural changes and areas of homozygosity for chromosomal abnormalities |
| 0211U | Oncology (pan-tumor), DNA and RNA by next-generation sequencing, utilizing formalin-fixed paraffin-embedded tissue, interpretative report for single nucleotide variants, copy number alterations, tumor mutational burden, and microsatellite instability, with therapy association |
| 0212U | Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband |
| 0213U | Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, each comparator genome (eg, parent, sibling) (Do not report 0213U in conjunction with 81426) |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| 0214U | Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband |
| 0215U | Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, each comparator exome (eg, parent, sibling) |
| 0221U | Red cell antigen (ABO blood group) genotyping (ABO), gene analysis, next-generation sequencing, ABO (ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase) gene |
| 0222U | Red cell antigen (RH blood group) genotyping (RHD and RHCE), gene analysis, next-generation sequencing, RH proximal promoter, exons 1-10, portions of introns 2-3 |
| 0229U | BCAT1 (Branched chain amino acid transaminase 1) and IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis<br>Includes: Colvera®, Clinical Genomics Pathology Inc |
| 0230U | AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation), full sequence analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions |
| 0231U | CACNA1A (calcium voltage-gated channel subunit alpha 1A) (eg, spinocerebellar ataxia), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) gene expansions, mobile element insertions, and variants in non-uniquely mappable regions |
| 0232U | CSTB (cystatin B) (eg, progressive myoclonic epilepsy type 1A, Unverricht-Lundborg disease), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions |
| 0233U | FXN (frataxin) (eg, Friedreich ataxia), gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions |
| 0234U | MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions |
| 0235U | PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions |
| 0236U | SMN1 (survival of motor neuron 1, telomeric) and SMN2 (survival of motor neuron 2, centromeric) (eg, spinal muscular atrophy) full gene analysis, including small sequence changes in exonic and intronic regions, duplications and deletions, and mobile element insertions |
| 0237U | Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia), genomic sequence analysis panel including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions |
| 0239U | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free DNA, analysis of 311 or more genes, interrogation for sequence variants, including substitutions, insertions, deletions, select rearrangements, and copy number variations |
| 0242U | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 55-74 genes, interrogation for sequence variants, gene copy number amplifications, and gene rearrangements |
| 0245U | Oncology (thyroid), mutation analysis of 10 genes and 37 RNA fusions and expression of 4 mRNA markers using next-generation sequencing, fine needle aspirate, report |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | includes associated risk of malignancy expressed as a percentage |
| 0260U | Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping |
| 0262U | Oncology (solid tumor), gene expression profiling by real-time RT-PCR of 7 gene pathways (ER, AR, PI3K, MAPK, HH, TGFB, Notch), formalin-fixed paraffin-embedded (FFPE), algorithm reported as gene pathway activity 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 22 genes, blood, buccal swab, or amniotic fluid |
| 0270U | Hematology (congenital coagulation disorders), genomic sequence analysis of 20 genes, blood, buccal swab, or amniotic fluid |
| 0271U | Hematology (congenital neutropenia), genomic sequence analysis of 24 genes, blood, buccal swab, or amniotic fluid |
| 0272U | Hematology (genetic bleeding disorders), genomic sequence analysis of 60 genes, and duplication/deletion of PLAU blood, buccal swab, or amniotic fluid, comprehensive |
| 0274U | Hematology (genetic platelet disorders), genomic sequence analysis of 62 genes, and duplication/deletion of PLAU 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 40 genes, |
| 0287U | Oncology (thyroid), DNA and mRNA, next-generation sequencing analysis of 112 genes, fine needle aspirate or formalin-fixed paraffin-embedded (FFPE) tissue, algorithmic prediction of cancer recurrence, reported as a categorical risk result (low, intermediate, high) |
| 0290U | Pain management, mRNA, gene expression profiling by RNA sequencing of 36 genes, whole blood, algorithm reported as predictive risk score |
| 0291U | Psychiatry (mood disorders), mRNA, gene expression profiling by RNA sequencing of 144 genes, whole blood, algorithm reported as predictive risk score |
| 0292U | Psychiatry (stress disorders), mRNA, gene expression profiling by RNA sequencing of 72 genes, whole blood, algorithm reported as predictive risk score |
| 0293U | Psychiatry (suicidal ideation), mRNA, gene expression profiling by RNA sequencing of 54 genes, whole blood, algorithm reported as predictive risk score |
| 0294U | Longevity and mortality risk, mRNA, gene expression profiling by RNA sequencing of 18 genes, whole blood, algorithm reported as predictive risk score |
| 0297U | Oncology (pan tumor), whole genome sequencing of paired malignant and normal DNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and variant identification |
| 0298U | Oncology (pan tumor), whole transcriptome sequencing of paired malignant and normal RNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and expression level and chimeric transcript identification |
| 0299U | Oncology (pan tumor), whole genome optical genome mapping of paired malignant and normal DNA specimens, fresh frozen tissue, blood, or bone marrow, comparative structural variant identification |
| 0300U | Oncology (pan tumor), whole genome sequencing and optical genome mapping of paired malignant and normal DNA specimens, fresh tissue, blood, or bone marrow, comparative sequence analyses and variant identification |
| 0306U | Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis, cell-free DNA, initial (baseline) assessment to determine a patient specific panel for future comparisons to evaluate for MRD |
| 0307U | Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis of a patient-specific panel, cell-free DNA, subsequent assessment with |

| Codes | Cpt Code Description for Codes listed on LOD#42 |
|---|---|
| | comparison to previously analyzed patient specimens to evaluate for MRD |
| 0313U | Oncology (pancreas), DNA and mRNA next-generation sequencing analysis of 74 genes and analysis of CEA (CEACAM5) gene expression, pancreatic cyst fluid, algorithm reported as a categorical result (ie, negative, low probability of neoplasia or positive, high probability of neoplasia) |
| 0332U | Oncology (pan-tumor), genetic profiling of 8 DNA-regulatory (epigenetic) markers by quantitative polymerase chain reaction (qPCR), whole blood, reported as a high or low probability of responding to immune checkpoint–inhibitor therapy. |
| 0333U | Oncology (liver), surveillance for hepatocellular carcinoma (HCC) in highrisk patients, analysis of methylation patterns on circulating cell-free DNA (cfDNA) plus measurement of serum of AFP/AFP-L3 and oncoprotein des-gammacarboxyprothrombin (DCP), algorithm reported as normal or abnormal result. |
| 0335U | Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, fetal sample, identification and categorization of genetic variants (Do not report 0335U in conjunction with |
| 0336U | Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, blood or saliva, identification and categorization of genetic variants, each comparator genome (eg, parent) (Do not report 0336U in conjunction with 81426, 0213U). |
| 0343U | Oncology (prostate), exosome-based analysis of 442 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RTqPCR), urine, reported as molecular evidence of no-, low-, intermediate- or highrisk of prostate cancer. |
| 0356U | Oncology (oropharyngeal), evaluation of 17 DNA biomarkers using droplet digital PCR (ddPCR), cell-free DNA, algorithm reported as a prognostic risk score for cancer recurrence |
| 0364U | Oncology (hematolymphoid neoplasm), genomic sequence analysis using multiplex (PCR) and next-generation sequencing with algorithm, quantification of dominant clonal sequence(s), reported as presence or absence of minimal residual disease (MRD) with quantitation of disease burden, when appropriate |
| 0368U | Oncology (colorectal cancer), evaluation for mutations of APC, BRAF, CTNNB1, KRAS, NRAS, PIK3CA, SMAD4, and TP53, and methylation markers (MYO1G, KCNQ5, C9ORF50, FLI1, CLIP4, ZNF132 and TWIST1), multiplex quantitative polymerase chain reaction (qPCR), circulating cell- free DNA (cfDNA), plasma, report of risk score for advanced adenoma or colorectal cancer |
| 0379U | Targeted genomic sequence analysis panel, solid organ neoplasm, DNA (523 genes) and RNA (55 genes) by next-generation sequencing, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutational burden |
| 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 |
| 0391U | Oncology (solid tumor), DNA and RNA by next-generation sequencing, utilizing formalin- fixed paraffin-embedded (FFPE) tissue, 437 genes, interpretive report for single nucleotide variants, splice-site variants, insertions/deletions, copy number alterations, gene fusions, tumor mutational burden, and microsatellite instability, with algorithm quantifying immunotherapy response score |
| 0444U | Oncology (solid organ neoplasia), targeted genomic sequence analysis panel of 361 genes, interrogation for gene fusions, translocations, or other rearrangements, using DNA from formalin-fixed paraffin-embedded (FFPE) tumor tissue, report of clinically significant variant(s) |

| CPT | Cytogenic Studies and surgical pathology (Codes on HB-73) |
|---|---|

| | |
|---|---|
| 88245 | Chromosome analysis for breakage syndromes; baseline Sister Chromatid Exchange (SCE), 20-25 cells |
| 88248 | Chromosome analysis for breakage syndromes; baseline breakage, score 50-100 cells, count 20 cells, 2 karyotypes (eg, for ataxia telangiectasia, Fanconi anemia, fragile X) |
| 88249 | Chromosome analysis for breakage syndromes; score 100 cells, clastogen stress (eg, diepoxybutane, mitomycin C, ionizing radiation, UV radiation) |
| 88261 | Chromosome analysis; count 5 cells, 1 karyotype, with banding |
| 88262 | Chromosome analysis; count 15-20 cells, 2 karyotypes, with banding |
| 88263 | Chromosome analysis; count 45 cells for mosaicism, 2 karyotypes, with banding |
| 88264 | Chromosome analysis; analyze 20-25 cells |
| 88267 | Chromosome analysis, amniotic fluid or chorionic villus, count 15 cells, 1 karyotype, with banding |
| 88269 | Chromosome analysis, in situ for amniotic fluid cells, count cells from 6-12 colonies, 1 karyotype, with banding |
| 88271 | Molecular cytogenetics; DNA probe, each (eg, FISH) |
| 88272 | Molecular cytogenetics; chromosomal in situ hybridization, analyze 3-5 cells (eg, for derivatives and markers) |
| 88273 | Molecular cytogenetics; chromosomal in situ hybridization, analyze 10-30 cells (eg, for microdeletions) |
| 88274 | Molecular cytogenetics; interphase in situ hybridization, analyze 25-99 cells |
| 88275 | Molecular cytogenetics; interphase in situ hybridization, analyze 100-300 cells |
| 88280 | Chromosome analysis; additional karyotypes, each study |
| 88283 | Chromosome analysis; additional specialized banding technique (eg, NOR, C-banding) |
| 88285 | Chromosome analysis; additional cells counted, each study |
| 88289 | Chromosome analysis; additional high resolution study |
| 88371 | Protein analysis of tissue by Western Blot, with interpretation and report; |
| 88372 | Protein analysis of tissue by Western Blot, with interpretation and report; immunological probe for band identification, each |

## Reviewed by / Approval Signatures

**Population Health & Clinical Quality Committee (PHCQC):** Clinton White, MD
**Senior Medical Director:** Jim Romero, MD
**Medical Director:** Kresta Antillon, MD
**Date Approved:** 05-28-2025

## References


1. National Comprehensive Cancer Network, NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®). [Cited 02/19/2025]
2. U.S. Food & Drug Administration (FDA), Medical Devices. [Accessed 04/15/2025]
3. CMS, Novitas, Wisconsin Physician Services (WPS), Local Coverage Determination (LCD) and/or Local Coverage Articles (LCA) see the Medicare Coverage Database to search for guidelines that apply to New Mexico for a specific genetic tests. [Cited 04/15/2025]
4. New Mexico HealthCare Authority Letter of Direction (LOD) #42 Biomarker Coverage, 12/20/2024, effective 11/1/2024, [Cited 02/19/2025]
5. Palmetto GBA DEX Registry (MolDX Program) LCD - MolDX: Molecular Diagnostic Tests (MDT) (L35025) effective 5/4/2023, R29 [Cited on 02/19/2025]


## Publication History

12-17-08: Original Effective Date

03-25-09: Review and Revision
01-27-10: Review and Revision
01-19-11: Annual Review & Revision
02-22-12: Revision Updated BRCA1/BRCA2 guidelines
11-28-12: Revised BRCA1/BRCA2, BART guidelines
03-27-13: Revised added Decision Dx-UM for Uveal Melanoma, Mammaprint and Chromosomal Microarray Analysis are not covered.
02-24-16: Language added re: Non-coverage of multigene panels.
03-22-17: Annual Review. Removed repetitive language re: Chromosomal Microarray Analysis and corrected page number from 8 to 10 for this testing.
02-11-19: Update on CPT codes and references links to BRCA1 & BRCA2 test for breast **only**
05-20-20 Annual review. Updated references. Noted in policy to see the newly created MPMs:

- Breast Cancer Recurrent Predictive Genetic Testing, MPM 33.0
- Genetic Testing for Lynch Syndrome, MPM 7.5
- Genetic Testing, InvisionFirst Liquid Biopsy for Lung Cancer, MPM 37.0
- Genetic Testing for Pancreatic Cyst (PathfinderTG/PancraGen), MPM 7.6
- Genetic Testing for Cutaneous Melanoma, MPM 7.7
- Genetic Testing for Prostate Cancer, MPM 7.8
- Coverage diagnosis added are: Interstitial lung disease, Envisia/Veracyte, (diagnostic) and thyroid nodules, Afirma Thyroid FNA Analysis (Veracyte) (diagnostic).

05-26-21 Annual review. Reviewed by PHP Medical Policy Committee on 07/30/2021. The policy was revamped to be general. CMS references were listed, applicable to genetic testing. Prior authorization will continue for those genetic codes already on the PA grid. There is currently a total of 466 genetic codes and 183 of those are new codes added to the policy which may be duplicative to other Genetic MPMs. Of the 183 new codes added to the policy, only those CPT codes ending in "U" or "M" will be placed on the PA grid on this review: 0014M, 0016M, 0017M, 0001U, 0008U, 0010U, 0016U, 0017U, 0018U, 0019U, 0022U, 0023U, 0048U, 0049U, 0055U, 0056U, 0060U, 0069U, 0070U, 0071U, 0072U, 0073U, 0074U, 0075U, 0076U, 0078U, 0079U, 0080U, 0084U, 0087U, 0088U, 0089U, 0090U, 0091U, 0092U, 0094U, 0101U, 0105U, 0111U, 0113U, 0114U, 0118U, 0120U, 0130U, 0152U, 0153U, 0154U, 0155U, 0156U, 0172U, 0173U, 0174U, 0175U, 0177U, 0179U, 0180U, 0181U, 0182U, 0183U, 0184U, 0185U, 0186U, 0187U, 0188U, 0189U, 0190U, 0191U, 0192U, 0193U, 0194U, 0195U, 0196U, 0197U, 0198U, 0199U, 0200U, 0201U, 0203U, 0204U, 0205U, 0208U, 0209U, 0211U, 0212U, 0213U, 0214U, 0215U, 0216U, 0217U, 0218U, 0219U, 0220U, 0221U, 0222U, 0229U, 0230U, 0231U, 0232U, 0233U, 0234U, 0235U, 0236U, 0237U, 0238U, 0239U, 0242U, 0244U, 0245U, 0250U, 0252U, 0253U and 0254U. Removed the unrelated genetic codes from the genetic policy: 0002M, 0003M, 83520, 84311, 86152, 86153, 88245, 88248, 88249, 88261, 88262, 88263, 88264, 88271, 88272, 88273, 88274, 88275, 88280, 88283, 88285, 88289, 88291, 88299, 88380. Removed the deleted codes from policy: 81211, 81213, 81280 81281, 81282, 81545. These are not related to genetic but are assigned a PA towards the genetic related policies: 0002M, 0003M, 0035U, 0038U, 0039U, 0041U, 0042U, 0043U, 0044U, 84999. The following are deleted codes that are on the PA grid: 81211, 81213, 81214, 81281, 81282, 81545, 0005M, 0008M, 0009M, 0010M, 0028U which will be removed.

05-25-22 Annual review. Reviewed by PHP Medical Policy Committee on 04/13/2022. Title of policy changed to remove "Disease Specific" from the title. Language added regarding the evaluation to determine medical coverage, "*Assessment of genetic tests will be evaluated for medical necessity by review of the following: Medicare/Medicaid coverage updates and other State/Federal research/recommendations, statutes, regulations or coverage determinations. Review of evidence-based guidelines provided by organization such as, National Comprehensive Cancer Network (NCCN), specialty societies, Knowledge Center/Hayes (a Division of Tract Manager), Milliman Care Guidelines (MCG), and Up-to Date. Review of medical literature(s).*"
CPT codes updated:
Removed codes related to Pharmacogenomics Testing for BH and moved them to MPM 30.0: 81225, 81226, 81227, 81230, 81231, 81232, 81247, 81283, 81306, 81328, 81335, 81346, 81350, 81355, 81374, 81377, 81381, 81383, 0029U, 0031U, 0032U, 0033U, 0070U, 0071U, 0072U, 0073U, 0074U, 0075U, 0076U, 0173U and 0175U.
Removed fetal aneuploidy related to NIPT and moved them to MPM 20.15: 81420, 81422, 81507, 0252U & 0254U.Code 0168U was deleted in 2021 which will be removed from PA grid.
Removed codes related to WES and moved them to MPM 7.12: 81415, 81416 and 81417.

**CPT codes added to policy**: Codes effective 02/27/2021 thru 04/01/2022: 0012U, 0013U, 0014U, 81349,81523, 0246U, 0258U, 0260U, 0262U, 0268U, 0269U, 0270U, 0271U, 0272U, 0274U, 0276U, 0277U, 0278U, 0285U, 0287U, 0288U, 0289U, 0290U, 0294U, 0295U, 0296U, 0297U, 0298U, 0299U, 0300U, 0306U, 0307U, 0308U, 0309U, 0310U, 0313U, 0314U, 0315U, 0318U, 0319U and 0320U. Codes effective 07/01/2022 :0323U, 0324U, 0325U, 0326U, 0328U, 0329U and 0331U per AMA, Proprietary Laboratory Analyses. All these added codes will require prior authorization including 0060U.

**Continue no PA requirement for CPT codes determined in 2021 to not require PA:** 81105, 81106, 81107, 81108, 81109, 81110, 81111, 81112, 81171, 81172, 81173, 81174, 81220, 81221, 81222, 81223, 81224, 81243, 81244, 81306, 81308, 81329, 81336, 81337, 81508, 81509, 81510 and 81511.

**Continue no PA requirement for CPT codes recommended to require PA CY 2021**, but we only included the "U" and "M" codes to be added. 81168, 81177, 81178, 81179, 81180, 81181, 81182, 81183, 81184, 81185, 81186, 81188, 81189, 81190, 81191, 81192, 81193, 81194, 81204, 81233, 81234, 81236, 81237, 81239, 81269, 81274, 81278, 81284, 81285, 81286, 81289, 81305, 81307, 81309, 81312, 81320, 81333, 81343, 81344, 81345, 81347, 81348, 81351, 81352, 81353, 81357, 81360, 81419, 81546 and 81554.

For all LOBs the following codes 81279, 81338 and 81339 will be configured to allow Hematology and Oncology to by-pass PA requirement and all other specialties will now require PA. For all LOBs the following codes 81219 and 81270 will be configured to allow Hematology and Oncology to by-pass PA requirement and all other specialties will continue to require PA. For all LOBs the following code 81335 will be configured to allow Rheumatology and Gastroenterologist to by-pass PA requirement and all other specialties will continue to require PA. On 06-10-2022, Medical Policy Committee decision to remove previous ICD-10 configuration for CPT: 81206, 81207, 81208, 81170, 0016U and 0040U and instead configure to not require PA **for Onc/Hem** and all others will now require PA for all LOB.

**Update on 01-25-2023**:

PHP Medical Policy Committee approved on 11-11-22 to add these codes to policy and to require PA (0332U, 0333U, 0334U, 0335U, 0336U, 0339U, 0340U, 0343U, 0345U, 0347U, 0348U, 0349U, and 0350U). MPC also approved on 01-13-23 the Jan 2023 newly released codes: 0355U, 0356U, 0357U, 0358U, 0359U, 0360U, 0361U, 0362U, 0363U, 81418, 81441, 81449, 81451, and 81456 and have these codes all require PA.

On-going clean-up of CPT codes: Code 81529 removed, see MPM 7.7. Code 81539, 0005U, 81541, 81542, 0047U removed, see MPM 7.8. Removed 81490 see MPM 42.0. Removed 0045U, 81522, 81521, 81523, 81520, 81518 see MPM 33.0. Removed 81528, and 81327 see MPM 7.4. Removed 81288, 81292, 81293, 81294, 81295, 81296, 81297, 81298, 81299, 81300, 81317, 81318, 81319, 0101U, 81301, 81435, 81436, 0238U see MPM 7.5. Removed 81552, see MPM 7.9. Removed 0326U, see MPM 39.0. Removed 0329U, 0244U, 0250U, see MPM 29.0. Removed 81240, 81241, see MPM 7.11. Removed 81291, see MPM 36.0

**Update on 03-22-2023:**

Removed 0340U, see MPM 54.0. PHP Medical Policy Committee approved on 03-03-2023 and 04/12/2023. Codes 0337U, 0338U, 0342U will be added to policy and will also require PA. Removed 0334U and 81449, see MPM 29.0. Removed 0089U, see MPM 36.0. Removed 81418 and 0193U, see MPM 30.0. Added the newly released codes on April 1, 2023, which will also require PA: 0364U, 0365U, 0366U, 0367U, 0368U, 0369U, 0370U, 0371U, 0372U, 0373U, 0374U, 0375U, 0376U, 0378U, 0379U, 0380U, and 0386U.

05-24-23 Annual review. Reviewed by PHP Medical Policy Committee on 04-05-2023 and 04-12-2023. No change, the policy will remain generalized. The individual listing of CMS LCDs has been removed in the reference section. Deleted Codes 0324U and 0325U.

**Updated 07/26/2023**: Language added to policy to say, "*All newly released genetic codes will require prior authorization until further research is completed*." Added new genetic codes for effective July 01, 2023: 0388U, 0391U, 0392U, 0395U, 0396U, 0398U, 0400U, and 0401U which will require PA for all lines of business. The following genetic codes are for effective date Oct 01, 2023: Add codes 0403U, 0405U, 0409U, 0410U, 0411U, 0413U, 0414U, 0417U, and 0419U which will require PA; removed deleted codes from PA grid and/or from policy 0357U and 0386U; and updated the revised codes: 0269U, 0271U, 0272U, 0274U, 0277U, 0278U, and 0362U. Removed code 0373U and moved to MPM 43.0.

**Update on 02/07/2024:** Reviewed by PHP Medical Policy Committee on 01/19/2024.

- **DecisionDX SCC:** (code 0315U) is considered investigational for ALOB and will be configured as such then code will be removed from PA grid. Novitas LCD (L39365)/LCA(A59125) says DecisionDX-SCC is not medical reasonable and necessary. Also, NCCN does not mention the 40 GEP test within their guidelines.
- **TissueCypher:** (code 0108U) was added to policy and is considered investigational for ALOB and will be configured as investigational. No LCD/NCD found and NCCN does not mention the use of test.
- **IDgenetix:** (code 0411U) removed from policy and moved code to MPM 30.0.
- Reviewed by PHP Medical Policy Committee on 02/07/2024: Added the newly released 2024 Q1 CPT codes effective on 01/01/2024: 0420U, 0422U, 0423U, 0425U, 0426U, 0428U, 0434U, 0437U, 0438U, 81457, 81458, 81459, 81462, 81463, 81464, and 81517. These codes will require PA for ALOB.
- Removed 0060U and moved to MPM 20.15

05-22-24 Reviewed by PHP Medical Policy Committee on 04/17/2024 for newly released codes and annual review completed by MPC on 05/01/2024. .

- No change. Policy will remain generalized. Coding update are as follow:
- Add codes (0440U, 0444U, 0448U), effective 04-01-2024 and request to require PA for ALOB.
- Add codes 0291U, 0292U, 0293U, which were moved from MPM 30.0, (already requires PA).
- Remove codes 0392U, 0423U, 0345U to be listed in MPM 30.0. Remove code 0388U to be listed in MPM 39.1; Remove codes 81257, 81171, 81172, 81243, 81244, 81329, 81336, 81337, 81220, 81221, 81222, 81223, 81224 to be listed in MPM 7.13; removed code 0314U to be listed in MPM 7.7; removed code 0089U, since it is listed in MPM 36.0.
- Code 81220 (cystic fibrosis) will continue to not require PA as per our response to HSD May 2023.
- Correction to 05-25-22 annual review, code 81269, 81170, and 0040U does require PA.
- Continue no PA requirement for CPT codes 81168, 81177, 81178, 81179, 81180, 81181, 81182, 81183, 81184, 81185, 81186, 81188, 81189, 81190, 81191, 81192, 81193, 81194, 81204, 81233, 81234, 81236, 81237, 81239, 81274, 81278, 81284, 81285, 81286, 81289, 81305, 81307, 81309, 81312, 81320, 81333, 81343, 81344, 81345, 81347, 81348, 81351, 81352, 81353, 81357, 81360, 81419, 81546, 81554, 81105, 81106, 81107, 81108, 81109, 81110, 81111, 81112, 81171, 81172, 81173, 81174, 81220, 81221, 81222, 81223, 81224, 81243, 81244, 81306, 81308, 81329, 81336, 81337, 81508, 81509, 81510 and 81511.
- Continue no PA requirement **for Onc/Hem** 81206, 81207, 81208, 81219, 81225, 81240,81241,81256, 81270, 81279, 81338, 81339, 0016U, 0017U and 0027U; Code 81335 for Rheumo/Gastro.

**Update 08/21/2024**: MPC meeting on 07-26-2024, determined that prior auth requirement will be removed for ALOB when Laboratory Benefit Management (LBM), Routine Testing Management (RTM) product becomes effective for policies which includes Q1 and 07/01/2024 updates. The following CPT codes previously required PA as part of this policy, are now listed in the Laboratory Benefit Management (LBM) Program policy which can be found in the PHP Administrative Claims Edits Guide under Appendix A, LBM Program Policy. The policy can be found at this weblink: CORRECT CODING MEDICAL REVIEW GUIDES/ Administrative Claims Edits Guide. CPT code(s) include: 81332, 81376, 81382, 81425, 81426, 81500, 81503, 81535, 81536, 81538, 0006M, 0007M, 0012M, 0013M, 0069U, 0131U, 0132U, 0133U, 0134U, 0135U, 0136U, 0137U, 0157U, 0158U, 0159U, 0160U, 0161U, 0162U, 0163U, 0164U, 0166U, 0258U, 0278U, 0285U, 0288U, 0289U, 0296U, 0308U, 0309U, 0310U, 0315U, 0320U, 0323U, 0328U, 0331U, 0342U, 0355U, 0358U, 0360U, 0361U, 0362U, 0363U, 0365U, 0366U, 0367U, 0369U, 0370U, 0371U, 0372U, 0374U, 0375U, 0376U, 0378U. 81408, 81470, 81471, 0170U and 0420U. Other codes that LBM will manage that do not require PA will be removed from the policy: 0008U, 0014M, 0016M, 0017M, 0050U, 0078U, 0079U, 0087U, 0088U, 0092U, 0105U, 0120U, 0152U, 0154U, 0156U, 0167U, 0174U, 0203U, 0205U, 0216U, 0217U, 0219U, 0220U and 0253U.

Additional PA requirement will be removed for ALOB for codes: 85300, 85303, 0024U, 0025U, 0002M, 0003M, 0035U, 0038U, 0039U, 0041U, 0042U, 0043U, and 0044U. Note: These codes were never assigned to an MPM. The codes are assigned to the following MPMs per PA grid: • MPM 7.1 • MPM 7.12 • MPM 7.4 • MPM 7.5 • MPM 7.6 • MPM 7.7 • MPM 7.8 • MPM 7.9 • MPM 20.15 • MPM 29.0 • MPM 30.0 • MPM 33.0 • MPM 39 • MPM 39.1 • MPM 54.0

Codes clean-up: Removed 81508, 81511 and 81512, since these codes reside in MPM 20.15

**03-26-2025 AD HOC REVIEW:** Reviewed by PHP Medical Policy Committee on 02/19/2025 to review LOD #42 for biomarkers. Based on s large amount of the LOD #42 falling on our MPM 7.1, decision to move remaining codes (44) not previously on any MPM policies to this policy. Criteria to meet the Medicaid definition was added, providing clarify and definitions for biomarkers. An additional 129 codes were identified on this policy that are also on LOD 42 that did not currently have specific coverage criteria or PA. Decision to add PA to ensure criteria for coverage is met following first our local LCD, then Palmetto, last by reference to national guidelines of drug insert, as indicated in the LOD, was made to all 129 codes and the added 44 codes, (173 total). A hierarchy was also added to provide guidance for determining coverage vs. I & E when a more specific genetic policy is not found.
Added PA for CPT Codes: 0317U, 0245U, 0237U, 0236U, 0235U, 0234U, 0233U, 0232U, 0231U, 0230U, 0229U, 0222U, 0221U, 0215U, 0214U, 0213U, 0212U, 0211U, 0209U, 0201U, 0200U, 0199U, 0198U, 0197U, 0196U, 0195U, 0194U, 0192U, 0191U, 0190U, 0189U, 0188U, 0187U, 0186U, 0185U, 0184U, 0183U, 0182U, 0181U, 0177U, 0155U, 0153U, 0118U, 0114U, 0094U, 0084U, 0055U, 0049U, 0048U, 0046U, 0023U, 0019U, 0018U, 0010U, 0001U, 81554, 81546, 81519, 81511, 81510, 81509, 81508, 81419, 81360, 81357, 81353, 81352, 81351, 81348, 81347, 81345, 81344, 81343, 81337, 81336, 81333, 81329, 81320, 81312, 81309, 81308, 81307, 81305, 81289, 81286, 81285, 81284, 81278, 81274, 81244, 81243, 81239, 81237, 81236, 81234, 81233, 81224, 81223, 81222, 81221, 81220, 81204, 81194, 81193, 81192, 81191, 81190, 81189, 81188, 81186, 81185, 81184, 81183, 81182, 81181, 81180, 81179, 81178, 81177, 81174, 81173, 81112, 81111, 81110, 81109, 81108, 81107, 81106, 81105

Added codes with PA: 0489U, 0488U, 0487U, 0486U, 0475U, 0474U, 0473U, 0471U, 0470U, 0469U, 0467U, 0466U, 0461U, 0460U, 0433U, 0424U, 0282U, 0273U, 0267U, 0266U, 0265U, 0264U, 88372, 88371, 88289, 88285, 88283, 88280, 88275, 88274, 88273, 88272, 88271, 88269, 88267, 88264, 88263, 88262, 88261, 88249, 88248, 88245, 81277, G0452.

05-28-25 Annual review by PHP Medical Policy Committee on 04/16/2025. Continue PA on codes listed for this policy, and continue criteria identified in recent Ad Hoc. A coding cleanup will be made during this annual review to identify codes with specific policies.
The following are listed on multiple MPMs:
Also listed in **MPM 30.0**: 81401, 81406
Also listed in **MPM 7.9**: 81403
Also listed in **MPM 29.0**: 0022U, 0037U, 0111U, 81445, 81450, 0239U, 0242U, 0172U
Also listed in **MPM 7.13:** 81187, 81200, 81205, 81209, 81242, 81234, 81239, 81251, 81252, 81253, 81254, 81255, 81256, 81258, 81259, 81260, 81269, 81271, 81274, 81290, 81302, 81303, 81304, 81312, 81321, 81322, 81323, 81324, 81325, 81330, 81331, 81361, 81362, 81363, 81364, 81400, 81401, 81403, 81404, 81405, 81406, 81408, 81412, 81430, 81431, 81437, 81438, 81440, 81443, 0236U, 0335U, 0336U, 81161
Also listed in **MPM 54.0**: 0040U, 81261, 81263
Also listed in **MPM 39.**0: 81445, 0179U, 0487U
Also listed on **MPM 54.0**: 81207, 81208, 81261, 81263, 81264, 81310, 81315, 81316, 81334, 81340, 81342, 81401, 0356U, 0422U, 81450, 81445
The following were removed from this policy as they are specifically for the named MPMs:
Removed code 0090U listed in **MPM 7.7**
Removed codes listed in **MPM 7.8**: 81313, 0339U, 0113U, 81551
Removed code listed in **MPM 29.0**: 0473U
Removed code listed in **MPM 30.0**: 0349U
The following codes were reviewed on 03-26-2025 as AD HOC REVIEW but were not updated to be included in the code Table: 0317U, 0229U, 0222U, 0221U, 0215U, 88372, 88371, 88289, 88285, 88283, 88280, 88275, 88274, 88273, 88272, 88271, 88269, 88267, 88264, 88263, 88262, 88261, 88249, 88248, 88245

**Ad-hoc 08-27-2025 –** Correction to ad-hoc 03-26-2025 to apply PA has been corrected for codes: 81220, 81221, 81222, 81223, 81224, 81234, 81239, 81243, 81244, 81274, 81312, 81329, 81336, and 81337. These codes apply to MPM 7.13

*This Medical Policy is intended to represent clinical guidelines describing medical appropriateness and is developed to assist Presbyterian Health Plan and Presbyterian Insurance Company, Inc. (Presbyterian) Health*

*Services staff and Presbyterian medical directors in determination of coverage. The Medical Policy is not a treatment guide and should not be used as such.*

*For those instances where a member does not meet the criteria described in these guidelines, additional information supporting medical necessity is welcome and may be utilized by the medical director in reviewing the case. Please note that all Presbyterian Medical Policies are available online at:* ***Click here for Medical Policies***

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*When PHP follows a particular guideline such as LCDs, NCDs, MCG, NCCN etc., for the purposes of determining coverage; it is expected providers maintain or have access to appropriate documentation when requested to support coverage. See the References section to view the source materials used to develop this resource document.*