PRESBYTERIAN

Medical Policy

Subject: Genetic, Biomarker and Genomic Testing

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

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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.

Other related medical policies:

- 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 Prostate Cancer, MPM 7.8
- 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 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

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

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. 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
0530U	Oncology (pan-solid tumor), ctDNA, utilizing plasma, next-generation sequencing (NGS) of 77 genes, 8 fusions, microsatellite instability, and tumor mutation burden, interpretative report for single-nucleotide variants, copy-number alterations, with therapy association
0532U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome and mitochondrial DNA sequencing for single-nucleotide variants, insertions/deletions, copy number variations, peripheral blood, buffy coat, saliva, buccal or tissue sample, results reported as positive or negative
0533U	Drug metabolism (adverse drug reactions and drug response), genotyping of 16 genes (ie, ABCG2, CYP2B6, CYP2C9, CYP2C19, CYP2C, CYP2D6, CYP3A5, CYP4F2, DPYD, G6PD, GGCX, NUDT15, SLCO1B1, TPMT, UGT1A1, VKORC1), reported as metabolizer status and transporter function

Codes	Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)*
0534U	Oncology (prostate), microRNA, single-nucleotide polymorphisms (SNPs) analysis by RT-PCR of 32 variants, using buccal swab, algorithm reported as a risk score
0538U	Oncology (solid tumor), next-generation targeted sequencing analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, DNA analysis of 600 genes, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements, and copy number alterations, microsatellite instability, tumor mutation burden, reported as actionable variant
0539U	Oncology (solid tumor), cell-free circulating tumor DNA (ctDNA), 152 genes, next-generation sequencing, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements, copy number alterations, and microsatellite instability, using whole-blood samples, mutations with clinical actionability reported as actionable variant
0544U	Nephrology (transplant monitoring), 48 variants by digital PCR, using cell-free DNA from plasma, donor-derived cell-free DNA, percentage reported as risk for rejection
0550U	Oncology (prostate), enzyme-linked immunosorbent assays (ELISA) for total prostate-specific antigen (PSA) and free PSA, serum, combined with age, previous negative prostate biopsy status, digital rectal examination findings, prostate volume, and image and data reporting of the prostate, algorithm reported as a risk score for the presence of high-grade prostate cancer
0552U	Reproductive medicine (preimplantation genetic assessment), analysis for known genetic disorders from trophectoderm biopsy, linkage analysis of disease-causing locus, and when possible, targeted mutation analysis for known familial variant, reported as low-risk or high-risk for familial genetic disorder
0553U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from embryonic trophectoderm for structural rearrangements, aneuploidy, and a mitochondrial DNA score, results reported as normal/balanced (euploidy/balanced), unbalanced structural rearrangement, monosomy, trisomy, segmental aneuploidy, or mosaic, per embryo tested
0554U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from trophectoderm biopsy for aneuploidy, ploidy, a mitochondrial DNA score, and embryo quality control, results reported as normal (euploidy), monosomy, trisomy, segmental aneuploidy, triploid, haploid, or mosaic, with quality control results reported as contamination detected or inconsistent cohort when applicable, per embryo tested
0555U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from embryonic trophectoderm for structural rearrangements, aneuploidy, ploidy, a mitochondrial DNA score, and embryo quality control, results reported as normal/balanced (euploidy/balanced), unbalanced structural rearrangement, monosomy, trisomy, segmental aneuploidy, triploid, haploid, or mosaic, with quality control results reported as contamination detected or inconsistent cohort when applicable, per embryo tested
0560U	Oncology (minimal residual disease [MRD]), genomic sequence analysis, cell-free DNA, whole blood and tumor tissue, baseline assessment for design and construction of a personalized variant panel to evaluate current MRD and for comparison to subsequent MRD assessments
0561U	Oncology (minimal residual disease [MRD]), genomic sequence analysis, cell-free DNA, whole blood, subsequent assessment with comparison to initial assessment to evaluate for MRD
0562U	Oncology (solid tumor), targeted genomic sequence analysis, 33 genes, detection of single-nucleotide variants (SNVs), insertions and deletions, copy-number amplifications, and translocations in human genomic circulating cell-free DNA, plasma, reported as presence of actionable variants
0565U	Oncology (hepatocellular carcinoma), next-generation sequencing methylation pattern assay to detect 6626 epigenetic alterations, cell-free DNA, plasma, algorithm reported as cancer signal detected or not detected

Codes	Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)*
0566U	Oncology (lung), qPCR-based analysis of 13 differentially methylated regions (CCDC181, HOXA7, LRRC8A, MARCHF11, MIR129-2, NCOR2, PANTR1, PRKCB, SLC9A3, TBR1_2, TRAP1, VWC2, ZNF781), pleural fluid, algorithm reported as a qualitative result
0567U	Rare diseases (constitutional/heritable disorders), whole-genome sequence analysis combination of short and long reads, for single-nucleotide variants, insertions/deletions and characterized intronic variants, copy-number variants, duplications/deletions, mobile element insertions, runs of homozygosity, aneuploidy, and inversions, mitochondrial DNA sequence and deletions, short tandem repeat genes, methylation status of selected regions, blood, saliva, amniocentesis, chorionic villus sample or tissue, identification and categorization of genetic variants
0572U	Oncology (prostate), high-throughput telomere length quantification by FISH, whole blood, diagnostic algorithm reported as risk of prostate cancer
0573U	Oncology (pancreas), 3 biomarkers (glucose, carcinoembryonic antigen, and gastricsin), pancreatic cyst lesion fluid, algorithm reported as categorical mucinous or non-mucinous
0575U	Transplantation medicine (liver allograft rejection), miRNA gene expression profiling by RT-PCR of 4 genes (miR-122, miR-885, miR-23a housekeeping, spike-in control), serum, algorithm reported as risk of liver allograft rejection
0576U	Transplantation medicine (liver allograft rejection), quantitative donor-derived cell-free DNA (cfDNA) by whole genome next-generation sequencing, plasma and mRNA gene expression profiling by multiplex real-time PCR of 56 genes, whole blood, combined algorithm reported as a rejection risk score
0577U	Oncology (ovarian), serum, analysis of 39 glycoproteins by liquid chromatography with tandem mass spectrometry (LC-MS/MS) in multiple reaction monitoring mode, reported as likelihood of malignancy
0578U	Oncology (cutaneous melanoma), RNA, gene expression profiling by real-time qPCR of 10 genes (8 content and 2 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reports a binary result, either low-risk or high-risk for sentinel lymph node metastasis and recurrence
0582U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome DNA sequencing for single-nucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported
0583U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome comparator DNA sequencing for single-nucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported with proband results (List separately in addition to code for primary procedure)
0585U	Targeted genomic sequence analysis panel, solid organ neoplasm, circulating cell-free DNA (cfDNA) analysis from plasma of 521 genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, and microsatellite instability, report shows identified mutations, including variants with clinical actionability
0586U	Oncology, mRNA, gene expression profiling of 216 genes (204 targeted and 12 housekeeping genes), RNA expression analysis, formalin-fixed paraffin-embedded (FFPE) tissue, quantitative, reported as log2 ratio per gene
0591U	Oncology (prostate cancer), biochemical analysis of 3 proteins (total PSA, free PSA, and HE4), plasma, serum, prognostic algorithm incorporating 3 proteins and digital rectal examination, results reported as a probability score for clinically significant prostate cancer
0592U	Oncology (hematolymphoid neoplasms), DNA, targeted genomic sequence of 417 genes, interrogation for gene fusions, translocations, rearrangements, utilizing formalin-fixed paraffin-embedded (FFPE) tumor tissue, results report clinically significant variant(s)
0597U	Oncology (breast), RNA expression profiling of 329 genes by targeted next-generation sequencing and 20 proteins by multiplex immunofluorescence, formalin-fixed paraffin-embedded (FFPE) tissue, algorithmic analyses to determine tumor-recurrence risk score
81195	Cytogenomic (genome-wide) analysis, hematologic malignancy, structural variants and copy number variants, optical genome mapping (OGM)

Codes	Description of Genetic and Genomic Testing Codes *(Not currently identified by Medicaid as a Biomarker)*
81558	Transplantation medicine (allograft rejection, kidney), mRNA, gene expression profiling by quantitative polymerase chain reaction (qPCR) of 139 genes, utilizing whole blood, algorithm reported as a binary categorization as transplant excellence, which indicates immune quiescence, or not transplant excellence, indicating subclinical rejection
0605U	Allergy and immunology (hereditary alpha tryptasemia), DNA, analysis of TPSAB1 gene copy number variation using digital PCR, whole blood, results reported with genotype-specific interpretation of alpha-tryptase copy number and algorithmic classification as normal or abnormal
0609U	Oncology (prostate), immunoassay for total prostate-specific antigen (PSA) and free PSA, serum or plasma, combined with clinical features, algorithm reported as a probability score for clinically significant prostate cancer
81354	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of structural and copy number variants, optical genome mapping (OGM)
81524	Oncology (central nervous system tumor), DNA methylation analysis of at least 10,000 methylation sites, utilizing DNA extracted from formalin-fixed tumor tissue, algorithm(s) reported as probability of matching a reference tumor family and class, and MGMT (O-6-methylguanine-DNA methyltransferase) promoter methylation status, if performed
87494	Infectious agent detection by nucleic acid (DNA or RNA); Chlamydia trachomatis and Neisseria gonorrhoeae, multiplex amplified probe technique
87627	Infectious agent detection by nucleic acid (DNA or RNA); joint space pathogens and drug resistance genes, multiplex amplified probe technique, 26 or more targets
0256U	Trimethylamine/trimethylamine N-oxide (TMA/TMAO) profile, liquid chromatography tandem mass spectrometry (LC-MS/MS), urine, with algorithmic analysis and interpretive report
0580U	Borrelia burgdorferi (Lyme disease), antibody detection of 2431 recombinant protein groups, by immunoassay, IgG
0614U	Inborn error of metabolism (primary mitochondrial disease), mitochondrial analysis of 4 enzyme complexes by stained blue native polyacrylamide gel electrophoresis (PAGE), frozen tissue (muscle, liver, heart, cultured skin fibroblasts), diagnostic qualitative result
0615U	Borrelia burgdorferi (Lyme disease), antibody detection of 26 recombinant protein groups, by immunoassay, IgM
0618U	Psychiatry (bipolar disorder), DNA methylation analysis of more than 10,000 sites, whole blood, algorithm reported as positive or negative risk
0619U	Pulmonary (chronic obstructive pulmonary disease [COPD]), DNA methylation analysis of more than 18,000 sites, whole blood, algorithm reported as positive or negative risk
0622U	Psychiatry (major depressive disorder), DNA methylation analysis of more than 20,000 sites, whole blood, algorithm reported as positive or negative risk
0623U	Autoimmune (multiple sclerosis), DNA methylation analysis of more than 5,000 sites, whole blood, algorithm reported as positive or negative risk
0624U	Hepatology (nonalcoholic steatohepatitis [NASH]), DNA methylation analysis of 5,000 sites, whole blood, algorithm reported as positive or negative risk
0625U	Endocrinology (osteoporosis), DNA methylation analysis of more than 5,000 sites, whole blood, algorithm reported as positive or negative risk
0626U	Neurology (Parkinson disease), DNA methylation analysis of more than 20,000 sites, whole blood, algorithm reported as positive or negative risk
0627U	Psychiatry (schizophrenia), DNA methylation analysis of more than 15,000 sites, whole blood, algorithm reported as positive or negative risk
0629U	Infectious disease (tuberculosis), DNA, analysis of 1 target by PCR with clustered regularly interspaced short palindromic repeat (CRISPR)-based probe detection, plasma or serum, qualitative report as detected or not detected

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

Codes	Cpt Code Description for Codes listed on LOD#42
	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 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 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 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 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 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

Codes	Cpt Code Description for Codes listed on LOD#42
	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 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 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 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 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 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 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 NORTHSTAR RESPONSE™, BILLIONTOONE LABORATORY, BILLIONTOONE, INC
0487U	ONCOLOGY (SOLID TUMOR), CELL-FREE CIRCULATING DNA, TARGETED GENOMIC SEQUENCE ANALYSIS PANEL OF 84 GENES, INTERROGATION FOR

Codes	Cpt Code Description for Codes listed on LOD#42
	SEQUENCE VARIANTS, ANEUPLOIDY-CORRECTED GENE COPY NUMBER AMPLIFICATIONS AND LOSSES, GENE REARRANGEMENTS, AND MICROSATELLITE INSTABILITY NORTHSTAR SELECT™, 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
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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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

Codes	Cpt Code Description for Codes listed on LOD#42
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)
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

Codes	Cpt Code Description for Codes listed on LOD#42
	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)
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

Codes	Cpt Code Description for Codes listed on LOD#42
	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 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)

Codes	Cpt Code Description for Codes listed on LOD#42
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)
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)

Codes	Cpt Code Description for Codes listed on LOD#42
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 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

Codes	Cpt Code Description for Codes listed on LOD#42
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 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

Codes	Cpt Code Description for Codes listed on LOD#42
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 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
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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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
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
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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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
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])
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)
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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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
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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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)
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 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

Codes	Cpt Code Description for Codes listed on LOD#42
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
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 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

Codes	Cpt Code Description for Codes listed on LOD#42
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 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
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
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)

Codes	Cpt Code Description for Codes listed on LOD#42
0016M	Oncology (bladder), mRNA, microarray gene expression profiling of 219 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as molecular subtype (luminal, luminal infiltrated, basal, basal claudin-low, neuroendocrine-like)
0017M	Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-embedded tissue, algorithm reported as cell of origin (Do not report 0017 M in conjunction with 0120U)
0050U	Targeted genomic sequence analysis panel, acute myelogenous leukemia, DNA analysis, 194 genes, interrogation for sequence variants, copy number variants or rearrangements
0069U	Oncology (colorectal), microRNA, RT-PCR expression profiling of miR-31-3p, formalin-fixed paraffin-embedded tissue, algorithm reported as an expression score
0087U	Cardiology (heart transplant), mRNA gene expression profiling by microarray of 1,283 genes, transplant biopsy tissue, allograft rejection and injury algorithm reported as a probability score
0088U	Transplantation medicine (kidney allograft rejection), microarray gene expression profiling of 1,494 genes, utilizing transplant biopsy tissue, algorithm reported as a probability score for rejection
0120U	Oncology (B-cell lymphoma classification), mRNA, gene expression profiling by fluorescent probe hybridization of 58 genes (45 content and 13 housekeeping genes), formalin-fixed paraffin-embedded tissue, algorithm reported as likelihood for primary mediastinal B-cell lymphoma (PMBCL) and diffuse large B-cell lymphoma (DLBCL) with cell of origin subtyping in the latter
0154U	Oncology (urothelial cancer), RNA, analysis by real-time RT-PCR of the FGFR3 (fibroblast growth factor receptor 3) gene analysis (ie, p.R248C [c.742C>T], p.S249C [c.746C>G], p.G370C [c.1108G>T], p.Y373C [c.1118A>G], FGFR3-TACC3v1, and FGFR3-TACC3v3), utilizing formalin-fixed paraffin-embedded urothelial cancer tumor tissue, reported as FGFR gene alteration status
0156U	Copy number (eg, intellectual disability, dysmorphology), sequence analysis
0205U	Ophthalmology (age-related macular degeneration), analysis of 3 gene variants (2 CFH gene, 1 ARMS2 gene), using PCR and MALDI-TOF, buccal swab, reported as positive or negative for neovascular age-related macular-degeneration risk associated with zinc supplements
0216U	Neurology (inherited ataxias), genomic DNA sequence analysis of 12 common genes 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
0217U	Neurology (inherited ataxias), genomic DNA sequence analysis of 51 genes 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
0253U	Reproductive medicine (endometrial receptivity analysis), RNA gene expression profile, 238 genes by next-generation sequencing, endometrial tissue, predictive algorithm reported as endometrial window of implantation (eg, pre-receptive, receptive, post-receptive)
0006M	Oncology (hepatic), mRNA expression levels of 161 genes, utilizing fresh hepatocellular carcinoma tumor tissue, with alpha-fetoprotein level, algorithm reported as a risk classifier
0007M	Oncology (gastrointestinal neuroendocrine tumors), real-time PCR expression analysis of 51 genes, utilizing whole peripheral blood, algorithm reported as a nomogram of tumor disease index

Codes	Cpt Code Description for Codes listed on LOD#42
0133U	Hereditary prostate cancer-related disorders, targeted mRNA sequence analysis panel (11 genes) (List separately in addition to code for primary procedure)
0134U	Hereditary pan cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (18 genes) (List separately in addition to code for primary procedure)
0137U	PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)
0157U	APC (APC regulator of WNT signaling pathway) (eg, familial adenomatosis polyposis [FAP]) mRNA sequence analysis (List separately in addition to code for primary procedure)
0158U	MLH1 (mutL homolog 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
0159U	MSH2 (mutS homolog 2) (eg, hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
0160U	MSH6 (mutS homolog 6) (eg, hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
0161U	PMS2 (PMS1 homolog 2, mismatch repair system component) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
0162U	Hereditary colon cancer (Lynch syndrome), targeted mRNA sequence analysis panel (MLH1, MSH2, MSH6, PMS2) (List separately in addition to code for primary procedure)
0258U	Autoimmune (psoriasis), mRNA, next-generation sequencing, gene expression profiling of 50-100 genes, skin-surface collection using adhesive patch, algorithm reported as likelihood of response to psoriasis biologics
0288U	Oncology (lung), mRNA, quantitative PCR analysis of 11 genes (BAG1, BRCA1, CDC6, CDK2AP1, ERBB3, FUT3, IL11, LCK, RND3, SH3BGR, WNT3A) and 3 reference genes (ESD, TBP, YAP1), formalin-fixed paraffin-embedded (FFPE) tumor tissue, algorithmic interpretation reported as a recurrence risk score
0315U	Oncology (cutaneous squamous cell carcinoma), mRNA gene expression profiling by RT-PCR of 40 genes (34 content and 6 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical risk result (ie, Class 1, Class 2A, Class 2B)
0331U	Oncology (hematolymphoid neoplasia), optical genome mapping for copy number alterations and gene rearrangements utilizing DNA from blood or bone marrow, report of clinically significant alterations
0362U	Oncology (papillary thyroid cancer), gene-expression profiling via targeted hybrid capture-enrichment RNA sequencing of 82 content genes and 10 housekeeping genes, fine needle aspirate or formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as one of three molecular subtypes
0372U	Infectious disease (genitourinary pathogens), antibiotic-resistance gene detection, multiplex amplified probe technique, urine, reported as an antimicrobial stewardship risk score
0378U	RFC1 (replication factor C subunit 1), repeat expansion variant analysis by traditional and repeat-primed PCR, blood, saliva, or buccal swab
0457U	Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 9 PFAS compounds by LC-MS/MS, plasma or serum, quantitative

Codes	Cpt Code Description for Codes listed on LOD#42
0458U	Oncology (breast cancer), S100A8 and S100A9, by enzyme-linked immunosorbent assay (ELISA), tear fluid with age, algorithm reported as a risk score
0472U	Carbonic anhydrase VI (CA VI), parotid specific/secretory protein (PSP) and salivary protein (SP1) IgG, IgM, and IgA antibodies, enzyme-linked immunosorbent assay (ELISA), semiqualitative, blood, reported as predictive evidence of early Sjogren syndrome
0009U	Oncology (breast cancer), ERBB2 (HER2) copy number by FISH, tumor cells from formalin fixed paraffin embedded tissue isolated using image-based dielectrophoresis (DEP) sorting, reported as ERBB2 gene amplified or non amplified
0020M	Oncology (central nervous system), analysis of 30000 DNA methylation loci by methylation array, utilizing DNA extracted from tumor tissue, diagnostic algorithm reported as probability of matching a reference tumor subclass
0301U	Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR);
0302U	Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR); following liquid enrichment
0389U	Pediatric febrile illness (Kawasaki disease [KD]), interferon alpha-inducible protein 27 (IFI27) and mast cell-expressed membrane protein 1 (MCEMP1), RNA, using reverse transcription polymerase chain reaction (RT-qPCR), blood, reported as a risk score for KD

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
0252U	Fetal aneuploidy short tandem–repeat comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy
0254U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using embryonic DNA genomic sequence analysis for aneuploidy, and a mitochondrial DNA score in euploid embryos, results reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy, per embryo tested

Reviewed by / Approval Signatures

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Date Approved: 05/20/2026

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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 on **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 should not require PA per MPM 7.13

Ad-hoc 11-19-2025: Reviewed by PHP Medical Policy Committee (MPC) on 09-12-2025. Code (0229U) – Colvera® has been added to the code table. Codes (0287U) – ThyroSeq® CRC and (0313U) – PancreaSeq® already exist in the policy. All three tests are considered investigational and experimental (I&E) due to insufficient evidence of clinical validity and utility. These codes will be configured as I&E for ALOB and PA requirement will be removed.

The outdated test PathfinderTG® has been replaced by PancraGEN® (81479), which will also be considered I&E. According to LCD L39365, PancraGEN™ (formerly PathfinderTG®) is no longer covered. The newer version includes the genetic marker GNAS, but current society and expert guidelines do not recommend PancraGEN (81479) for pancreatic cyst evaluation. This lack of endorsement further demonstrates insufficient evidence supporting PancraGEN's clinical utility. As of this review, there is no specific CPT code for the new version.

Removed BillionToOne Laboratory (prenatal)- plasma (cell-free fetal DNA) codes 0488U & 0489U- moved to MPM 7.13.

MPC on 09-12-2025 - Code 0130U- moved to MPM 7.5. MPC on 10-03-2025 - Interpretation of a molecular test, HCPCS G0452 removed from prior authorization for ALOB.

Ad-hoc 03-25-2026:
Reviewed by PHP Medical Policy Committee (MPC) on 03-04-2026.

- Added codes (0252U and 0254U) that were moved from MPM 20.15 because codes are not related to Non-Invasive Prenatal Testing. There is no utilization. Continue PA requirements for both codes.
- Removed codes (81509, 81510) and moved to MPM 20.15 as they are related to non-invasive Prenatal Testing. No utilization for 2024-2025. PA is required as of current.
- Added newly released CPT codes for 2025 that will require Prior Auth for ALOB: 0530U, 0532U, 0533U, 0534U, 0538U, 0539U, 0544U, 0550U, 0552U, 0553U, 0554U, 0555U, 0560U, 0561U, 0562U, 0565U, 0566U, 0567U, 0572U, 0573U, 0575U, 0576U, 0577U, 0578U, 0582U, 0583U, 0585U, 0586U, 0591U, 0592U, 0597U, 81195, 81558.
- Added newly released CPT codes for Jan 2026 that will require PA for ALOB: 0605U, 0609U, 81354, 81524, **87494**, 87627.
- Added newly released CPT codes for April 2026: 0256U, 0580U, 0614U, 0615U, 0618U, 0619U, 0622U, 0623U, 0624U, 0625U, 0626U, 0627U, 0629U.
- Removed code 0364U and moved to MPM 54.0.

05-20-2026 The PHP Medical Policy Committee completed its annual review on May 6, 2026, and approved maintaining the policy without changes.

In addition, the Committee conducted an ad hoc review on April 10, 2026, to evaluate the transition of certain codes back to this policy. These codes had previously been managed by an external vendor due to coverage discrepancies involving PLA codes. The affected codes are identified in HB73 and LOD42.

The codes listed below are being removed from LBM policy R2162, which currently applies to an automatic denial and is not compliant with HB73 and LOD42 criteria. These codes were previously included in this policy and were removed when LBM assumed management.

Policy Updates:

Codes 0010U and 0486U are removed from LBM policy R2162 and will continue to require prior authorization (PA) under this policy, as they are already listed herein.

The following codes are removed from LBM policy R2162 and reinstated in this policy: 0006M, 0007M, 0016M, 0017M, 0050U, 0069U, 0087U, 0088U, 0120U, 0154U, 0156U, 0205U, 0216U, 0217U, 0253U, 0133U, 0134U, 0137U, 0157U, 0158U, 0159U, 0160U, 0161U, 0162U, 0258U, 0288U, 0315U, 0331U, 0362U, 0372U, 0378U. 0457U, 0458U, 0472U, 0009U, 0020M, 0301U, 0302U, 0389U. These codes will be designated to require prior authorization for ALOB.

Minor formatting revisions: Removed references to related medical policies (MPM 7.6 and MPM 7.9) from the Description section, as these policies have been retired. Additionally, the note stating, *"The following definitions are provided by the state, which also align with PHP's definitions for Genetic Testing above,"* has now been appropriately repositioned, as it was inadvertently left unchanged during the previous review.

Codes: 0037U, 0022U, 0111U, 0172U, 0211U, 0239U, 0242U, 0379U were removed from this policy and to be management in Next Generation Sequencing, MPM 29.0.

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***

Web links:
At any time during your visit to this policy and find the source material web links has been updated, retired or superseded, PHP is not responsible for the continued viability of websites listed in this policy.

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.