# Molina Clinical Policy
# Genetic Testing: Policy No. 051

**Last Approval: 2/14/2024**
**Next Review Due By: February 2025**

## DISCLAIMER

This Molina Clinical Policy (MCP) is intended to facilitate the Utilization Management process. Policies are not a supplementation or recommendation for treatment; Providers are solely responsible for the diagnosis, treatment, and clinical recommendations for the Member. It expresses Molina's determination as to whether certain services or supplies are medically necessary, experimental, investigational, or cosmetic for purposes of determining appropriateness of payment. The conclusion that a particular service or supply is medically necessary does not constitute a representation or warranty that this service or supply is covered (e.g., will be paid for by Molina) for a particular Member. The Member's benefit plan determines coverage – each benefit plan defines which services are covered, which are excluded, and which are subject to dollar caps or other limits. Members and their Providers will need to consult the Member's benefit plan to determine if there are any exclusion(s) or other benefit limitations applicable to this service or supply. If there is a discrepancy between this policy and a Member's plan of benefits, the benefits plan will govern. In addition, coverage may be mandated by applicable legal requirements of a State, the Federal government or CMS for Medicare and Medicaid Members. CMS's Coverage Database can be found on the CMS website. The coverage directive(s) and criteria from an existing National Coverage Determination (NCD) or Local Coverage Determination (LCD) will supersede the contents of this MCP and provide the directive for all Medicare members. References included were accurate at the time of policy approval and publication.

## OVERVIEW

Genetic testing is defined by the National Human Genome Research Institute (NHGRI) as an array of laboratory techniques to examine an individual's DNA (**D**eoxyribo**N**ucleic **A**cid). There are 4 "types" or letters of DNA. The sequence of these letters "code" for information required for health. These letters are repeated in long sequences. These long sequences are packaged into chromosomes much like books of information. The total number of DNA letters making up a complete set of instructions is about 6.4 billion letters (3.2 billion form the mother and 3.2 from the father). The complete set of genetic instructions for a person is called the genome. The genetic code or genome is a type of blueprint that tells cells when to grow and when not to grow and how to function to maintain health. A copy of the genome is in just about every cell in the human body. The genetic code is also linked to clinical appearances of a trait or disease (phenotype).

Genetic testing determines a person's genotype (the order and number of DNA letters of a small part of the genome). Genotyping can help diagnose certain conditions and provide information about certain treatments. Genotyping does this by comparing a portion of the person's genetic code or genotype to a reference code. The reference code is what is thought to be a "healthy" code or typical genetic code. When there are differences between a person's genetic code and the reference code an interpretation is required to determine if the change (variant) is meaningful or not. Most changes from the reference genetic code do not affect health (benign variants), but when variants are potentially disease causing, we call them pathogenic variants.

Genotyping can be determined for germline cells (cells that contain the genetic information inherited form our parents and copied to all the cells we are born with) or for certain somatic cells (cells that may or may not represent the original genetic information inherited from our parents because of changes to the genetic code since birth). For example, cells that "acquire" genetic changes after we are born that alter or remove instructions for stopping cell growth may be considered tumor cells.

Germline variants are changes in the DNA letters (nucleotide sequence) you are born with. Genetic changes that occur to a person's DNA after they are born are called somatic variants or changes. Somatic changes can happen because of exposure to certain chemicals or ultraviolet radiation from the sun or just changes to DNA that sometimes occur as we grow and become older.

Genetic tests are used as a health care tool to detect gene variants associated with a specific disease or condition, as well as for non-clinical uses such as paternity testing and forensics. In the clinical setting, genetic tests can be performed to determine the genetic cause of a disease, confirm a suspected diagnosis, predict future illness, detect when an individual might pass a genetic mutation to his or her children, and predict response to therapy. They can be used to screen newborns and fetuses which may help diagnose and treat disease before symptoms develop. Genetic testing of embryos can also occur as part of the in vitro fertilization process (NHGRI 2020; NHGRI 2019).

There are many types of genetic tests. A very brief look at the types of genetic tests is as follows:

- **Whole genome sequence**: the broadest genetic test examining all the letters of the genome.
- **Whole exome sequence**: a broad test that looks at just the important coding portions of the genome.

- **Karyotype**: a test that looks at a low level of resolution of all the chromosomes.
- **Chromosomal microarray**: a test that looks at chromosomes in greater detail (multiple types of microarrays).
- **Panel**: a genetic test that looks at a smaller number of genes focused on 1 or multiple conditions.
- **Single gene test**: a genetic test of just one gene.
- **Targeted testing**: a genetic test that looks at a few DNA letters (or small subsets of other genetic segments).
- **Pharmacogenomic test**: a type of targeted testing looking at genes involved in drug metabolism.
- **Tumor marker genotyping**: a panel test looking for genes that drive tumor growth &/or identify a tumor type.

Genetic testing also has ethical, legal, and psychosocial implications. These include psychosocial consequences of testing; disclosure to family members; testing children; undisclosed familial relationships; and genetic discrimination. Protections for discrimination are covered under the Americans with Disabilities Act, the Genetic Information Nondiscrimination Act, and the Affordable Care Act (Kohlmann & Slavotinek 2022).

### Genetic Counseling

The National Society of Genetic Counselors defines genetic counseling as the process of aiding individuals to understand and acclimate to the medical, psychological, and familial implications of genetic contributions to disease. Genetic counseling includes the compilation of a detailed family history; interpretation of the family history with the medical history to assess the chance of disease occurrence or recurrence; patient and family education about the inheritance, testing, management, risk reduction, resources, and research regarding the individual's specific condition; and counseling to help the individual make informed choices to provide appropriate interventions. Indications for referral can include, but are not limited to, personal or family history of a confirmed clinical diagnosis with a known genetic etiology (e.g., hemophilia, neurofibromatosis, Marfan syndrome). Genetic testing may also be warranted when an individual has an increased risk due to genetic or environmental factors or uncertainty about genetic risks (Raby & Kohlmann 2022).

Federal regulation of genetic tests is conducted by the Food and Drug Administration (FDA), the Centers for Medicare and Medicaid Services (CMS), and the Federal Trade Commission (NHGRI 2020). The FDA regulates medical products and devices while the CMS Clinical Laboratory Improvement Amendments of 1988 (CLIA) provides regulation of clinical laboratories and testing services. Additional regulation exists for laboratories that develop laboratory-developed tests – this includes tests developed for use only in one laboratory. While largely federally regulated, some laboratories are also regulated at the State-level (AACC 2021; AACC 2020; HHS 2008).

### Access to Genetic Testing Information

The Genetic Testing Registry (GTR) provides a central location for voluntary submission of genetic test information by providers. This includes the purpose of a given test, laboratory contact information and credentials, as well as the test's methodology, validity, and evidence of usefulness. Overall, the aim of the GTR is to advance the public health and research into the genetic basis of health and disease (National Center for Biotechnology Information, n.d.).

GeneReviews is a searchable database of summaries of genetic disorders, their diagnosis, management, and key points in genetic counseling. Experts on the specific condition write the individual chapters; GeneReviews contains over 800 chapters. Chapters are reviewed every four to five years or as necessary (Adam et al. 2022).

## COVERAGE POLICY

For ALL requests, Molina uses this clinical policy as a baseline overarching policy where specific criteria do not exist. Where specific MCG criteria exist those criteria explicit to the test should be followed. Please note mandatory biomarker coverage and state legal requirements may supersede this policy.

Genetic testing **is considered medically necessary and may be authorized** when the following criteria are met:

1. The genetic test is ordered by a practitioner within the scope of their practice or a medical geneticist.

2. One of the following applies based on the **type of genetic testing** (broad vs narrow scope, non-cancer vs cancer, carrier screening, predictive testing or pharmacogenomics) requested:

    a. For **inherited conditions with a broad scope of testing** (e.g., whole exome, chromosomal microarray or karyotype) not related to carrier screening or cancer, documentation of the following is a necessary first step. If condition specific guidelines are available in MCG, please see the more specific guideline for a complete list of criteria.
        i. Clinical history, physical examination, pedigree analysis and completion of conventional diagnostic testing AND a definitive diagnosis remains uncertain AND an inherited condition is suspected based on the presence of documented key risk factors, for example:
            (1) Major congenital anomalies unexplained by teratogenic or environmental exposures
            (2) Three or more minor anomalies
            (3) Autism
            (4) Intellectual disability not explained by trauma, teratogen or environmental exposures (including maternal exposures)
            (5) Global developmental delay
            (6) Developmental regression not related to autism or epilepsy;
            (7) Severe psychological disturbances such as self-injurious behavior, sleep-wake cycle reversal, schizophrenia, bipolar disorder, Tourette Syndrome
            (8) Complex neurodevelopmental disorders (ataxia, dystonia, alternating hemiplegia, neuromuscular disorder)
            (9) Evidence of a metabolic disorder
            (10) Unexplained growth retardation or failure to thrive or asymmetry
            (11) History of 3 or more miscarriages or still-births
            (12) Epilepsy with a suspected genetic cause (not due to tumor, trauma, teratogen or other environmental exposures)

    b. For **inherited conditions with a narrow scope of testing** (condition specific panels), documentation of a major feature or multiple minor features of the syndrome is required (e.g., neurofibromatosis-1: neurofibroma or multiple café au lait macules and inguinal freckling).

    c. For **inherited cancer risk syndromes** (for example Lynch syndrome, Hereditary Breast Ovarian Cancer syndrome and others) documentation of relevant personal history (e.g., early onset cancer, multiple colon polyps or rare pathologic findings), and/or family history (inheritance pattern of early onset cancers – pedigree), as well as relevant ethnic background is required.

    d. For **cancer marker testing** (somatic or tumor marker testing), **carrier screening and pharmacogenomics**: At a minimum such testing should have:
        i. Analytical and clinical validity (validation that the test measures what it says it measures and that measurement is linked to clinical disease or drug metabolism).
        ii. Clinical utility (results of the test can meaningfully change clinical management e.g., surgery, the extent of surgery, a change in surveillance, hormonal manipulation, or a change from standard therapeutic or adjuvant chemotherapy)
        iii. Please note guidelines specific to diagnose or monitor cancer conditions, carrier screening, or tests to determine drug metabolism (pharmacogenomics) may be available.

    e. For **predictive testing**, documentation confirming a causative genetic change has been identified in an affected **family** member and that genetic change is actionable for the member e.g., could change medical management (see also special considerations below regarding minors not being tested for adult-onset conditions).

3. Pre-test genetic counseling must be performed by a board-certified medical geneticist, certified genetic counselor, or provider experienced in delivering genetic information (e.g., OB/GYN, neuro-geneticist) when a genetic condition is suspected. **Exception**: genetic counseling is not necessary for genetic tests aimed at understanding drug metabolism for medication choice, dosing, or non-inherited cancers (“acquired” cancers)

4. Clinical documentation supports the validity and clinical utility of test results. The results have the potential to significantly alter the management or treatment of disease.

5. The testing ordered is reasonable in scope, and risks of testing do not outweigh its benefits. For example, it is not reasonable to order a whole exome sequence (looks at the coding sequences for approximately 20,000 genes) when looking for a single point mutation in one gene.

6. The clinical testing laboratory must be accredited by the Clinical Laboratory Improvement Amendments (CLIA) or a CLIA waiver is in place or accredited by the State and/or other applicable accrediting agencies.

## Limitations and Exclusions

**Frequency Limitations:**

1. Testing is allowed once during the member's lifetime per disease for diagnostic purposes.
2. A second genetic test may be authorized in one of the following circumstances:
   a. The genetic test identifies other mutations not previously tested and is different from the original test;
   b. The genetic test measures gene expressions or identifies somatic mutations which can vary over time, when clinically appropriate.

Genetic testing **is considered not medically necessary** under the following circumstances:

1. Criteria other than those outlined under the "Coverage Criteria" section above.
2. Testing for conditions or purposes where the test results would not directly influence the management or treatment of the disease or condition (e.g., disease without known treatment). Refer to the Corporate / Health Plan experimental and investigational policy as appropriate.
3. Testing for informational purposes or management of a member's family member.
4. For cases of carrier testing when there is no meaningful impact on health outcomes.
5. Minors under the age of 18 for adult-onset conditions that have no preventative or therapeutic options.
6. Population screening in individuals without a personal or family history (except for State mandated or required newborn screening or prenatal screening for certain conditions).
7. More than one lifetime test for each disease or condition except as defined above.
8. Whole Genome Sequencing (WGS).

**DOCUMENTATION REQUIREMENTS.** Molina Healthcare reserves the right to require that additional documentation be made available as part of its coverage determination; quality improvement; and fraud; waste and abuse prevention processes. Documentation required may include, but is not limited to, patient records, test results and credentials of the provider ordering or performing a drug or service. Molina Healthcare may deny reimbursement or take additional appropriate action if the documentation provided does not support the initial determination that the drugs or services were medically necessary, not investigational, or experimental, and otherwise within the scope of benefits afforded to the member.

## NATIONAL AND PROFESSIONAL ORGANIZATIONS

Please find below a listing on policy statements and committee opinions from the following national and professional organizations (links are below in the Reference section):

**American Association for Clinical Chemistry (AACC)**
- *Modernization of CLIA: Laboratory Developed Tests*
- *Oversight of Laboratory Developed Tests*

**American Academy of Pediatrics (AAP) & American College of Medical Genetics and Genomics (ACMG)**
- *Ethical and Policy Issues in Genetic Testing and Screening of Children*
- *Technical Report: Ethical and Policy Issues in Genetic Testing and Screening of Children*

**American College of Medical Genetics and Genomics (ACMG)**
- *ACMG Clinical Laboratory Standards for Next-Generation Sequencing*

- *ACMG SF v3. List for Reporting of Secondary Findings in Clinical Exome and Genome Sequencing*
- *Points to Consider in the Clinical Application of Genomic Sequencing*
- *Policy Statement: Recommendations for Reporting of Incidental Findings in Clinical Exome and Genome Sequencing*
- *A Practice Guideline from the American College of Medical Genetics and Genomics and the National Society of Genetic Counselors: Referral Indications for Cancer Predisposition Assessment*
- *Addendum: A Practice Guideline from the American College of Medical Genetics and Genomics and the National Society of Genetic Counselors: Referral Indications for Cancer Predisposition Assessment*

**American College of Obstetricians and Gynecologists (ACOG)**

- *Carrier Screening in the Age of Genomic Medicine (No. 690)*
- *Consumer Testing for Disease Risk (No. 816)*
- *Ethical Issues in Genetic Testing (No. 410)*
- *Personalized Genomic Testing for Disease Risk (No. 527)*

**American Society of Clinical Oncology (ASCO)**

- *Genetic and Genomic Testing for Cancer Susceptibility*

**National Society of Genetic Counselors**

- *Various Practice Guidelines*

## CODING & BILLING INFORMATION

**CPT (Current Procedural Terminology) Codes**

| Code | Description |
|---|---|
| **81161** | DMD (dystrophin) (e.g., Duchenne/Becker muscular dystrophy) deletion analysis, and duplication analysis, if performed |
| **81171** | AFF2 (ALF transcription elongation factor 2 [FMR2]) (e.g., fragile X intellectual disability 2 [FRAXE]) gene analysis; evaluation to detect abnormal (e.g., expanded) alleles |
| **81172** | AFF2 (ALF transcription elongation factor 2 [FMR2]) (e.g., fragile X intellectual disability 2 [FRAXE]) gene analysis; characterization of alleles (e.g., expanded size and methylation status) |
| **81173** | AR (androgen receptor) (e.g., spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; full gene sequence |
| **81174** | AR (androgen receptor) (e.g., spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; known familial variant |
| **81200** | ASPA (aspartoacylase) (e.g., Canavan disease) gene analysis, common variants (e.g., E285A, Y231X) |
| **81204** | AR (androgen receptor) (e.g., spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; characterization of alleles (e.g., expanded size or methylation status) |
| **81205** | BCKDHB (branched-chain keto acid dehydrogenase E1, beta polypeptide) (e.g., Maple syrup urine disease) gene analysis, common variants (e.g., R183P, G278S, E422X) |
| **81209** | BLM (Bloom syndrome, RecQ helicase-like) (e.g., Bloom syndrome) gene analysis, 2281del6ins7 variant |
| **81218** | CEBPA (CCAAT/enhancer binding protein [C/EBP], alpha) (e.g., acute myeloid leukemia), gene analysis, full gene sequence |
| **81220** | CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic fibrosis) gene analysis; common variants (e.g., ACMG/ACOG guidelines) |
| **81221** | CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic fibrosis) gene analysis; known familial variants |
| **81222** | CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic fibrosis) gene analysis; duplication/deletion variants |
| **81223** | CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic fibrosis) gene analysis; full gene sequence |
| **81224** | CFTR (cystic fibrosis transmembrane conductance regulator) (e.g., cystic fibrosis) gene analysis; intron 8 poly-T analysis (e.g., male infertility) |

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| **81225** | CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (e.g., drug metabolism), gene analysis, common variants (e.g., *2, *3, *4, *8, *17) |
| **81226** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism), gene analysis, common variants (e.g., *2, *3, *4, *5, *6, *9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN) |
| **81227** | CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9) (e.g., drug metabolism), gene analysis, common variants (e.g., *2, *3, *5, *6) |
| **81228** | Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number variants, comparative genomic hybridization (CGH) microarray analysis |
| **81229** | Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants, comparative genomic hybridization (CGH) microarray analysis |
| **81230** | CYP3A4 (cytochrome P450 family 3 subfamily A member 4) (e.g., drug metabolism) gene analysis, common variant(s) (e.g., *2, *22) |
| **81231** | CYP3A5 (cytochrome P450 family 3 subfamily A member 5) (e.g., drug metabolism) gene analysis, common variants (e.g., *2, *3, *4, *5 *6, *7) |
| **81232** | DPYD (dihydropyrimidine dehydrogenase) (e.g., 5-fluorouracil/5-FU and capecitabine drug metabolism) gene analysis, common variant(s) (e.g., *2A, *4, *5, *6) |
| **81240** | F2 (prothrombin, coagulation factor II) (e.g., hereditary hypercoagulability) gene analysis, 20210G>A variant |
| **81241** | F5 (coagulation Factor V) (e.g., hereditary hypercoagulability) gene analysis, Leiden variant |
| **81242** | FANCC (Fanconi anemia, complementation group C) (e.g., Fanconi anemia, type C) gene analysis, common variant (e.g., IVS4+4A>T) |
| **81243** | FMR1 (fragile X messenger ribonucleoprotein 1) (e.g., fragile X syndrome, X-linked intellectual disability [XLID]) gene analysis; evaluation to detect abnormal (e.g., expanded) alleles |
| **81244** | FMR1 (fragile X messenger ribonucleoprotein 1) (e.g., fragile X syndrome, X-linked intellectual disability [XLID]) gene analysis; characterization of alleles (e.g., expanded size and promoter methylation status) |
| **81245** | FLT3 (FMS-related tyrosine kinase 3) (e.g., acute myeloid leukemia), gene analysis, internal tandem duplication (ITD) variants (i.e., exons 14, 15) |
| **81246** | FLT3 (FMS-related tyrosine kinase 3) (e.g., acute myeloid leukemia), gene analysis; tyrosine kinase domain (TKD) variants (e.g., D835, I836) |
| **81250** | G6PC (glucose-6-phosphatase, catalytic subunit) (e.g., Glycogen storage disease, Type 1a, von Gierke disease) gene analysis, common variants (e.g., R83C, Q347X) |
| **81251** | GBA (glucosidase, beta, acid) (e.g., Gaucher disease) gene analysis, common variants (e.g., N370S, 84GG, L444P, IVS2+1G>A) |
| **81255** | HEXA (hexosaminidase A [alpha polypeptide]) (e.g., Tay-Sachs disease) gene analysis, common variants (e.g., 1278insTATC, 1421+1G>C, G269S) |
| **81256** | HFE (hemochromatosis) (e.g., hereditary hemochromatosis) gene analysis, common variants (e.g., C282Y, H63D) |
| **81257** | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis, for common deletions or variant (e.g., Southeast Asian, Thai, Filipino, Mediterranean, alpha3.7, alpha4.2, alpha20.5, Constant Spring) |
| **81258** | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known familial variant |
| **81259** | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., 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) (e.g., familial dysautonomia) gene analysis, common variants (e.g., 2507+6T>C, R696P) |
| **81265** | Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (e.g., pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [e.g., buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells) |
| **81266** | Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (e.g., additional 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) |

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| **81269** | HBA1/HBA2 (alpha globin 1 and alpha globin 2) (e.g., alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; duplication/deletion variants |
| **81277** | Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number and loss-of-heterozygosity variants for chromosomal abnormalities |
| **81290** | MCOLN1 (mucolipin 1) (e.g., Mucolipidosis, type IV) gene analysis, common variants (e.g., IVS3-2A>G, del6.4kb) |
| **81291** | MTHFR (5,10-methylenetetrahydrofolate reductase) (e.g., hereditary hypercoagulability) gene analysis, common variants (e.g., 677T, 1298C) |
| **81302** | MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene analysis; full sequence analysis |
| **81303** | MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene analysis; known familial variant |
| **81304** | MECP2 (methyl CpG binding protein 2) (e.g., Rett syndrome) gene analysis; duplication/deletion variants |
| **81310** | NPM1 (nucleophosmin) (e.g., acute myeloid leukemia) gene analysis, exon 12 variants |
| **81313** | PCA3/KLK3 (prostate cancer antigen 3 [non-protein coding]/kallikrein-related peptidase 3 [prostate specific antigen]) ratio (e.g., prostate cancer) |
| **81321** | PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis |
| **81322** | PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variant |
| **81323** | PTEN (phosphatase and tensin homolog) (e.g., Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/deletion variant |
| **81324** | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; duplication/deletion analysis |
| **81325** | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; full sequence analysis |
| **81326** | PMP22 (peripheral myelin protein 22) (e.g., Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; known familial variant |
| **81328** | SLCO1B1 (solute carrier organic anion transporter family, member 1B1) (e.g., adverse drug reaction) gene analysis, common variant(s) (e.g., *5) |
| **81331** | SNRPN/UBE3A (small nuclear ribonucleoprotein polypeptide N and ubiquitin protein ligase E3A) (e.g., Prader-Willi syndrome and/or Angelman syndrome), methylation analysis |
| **81332** | SERPINA1 (serpin peptidase inhibitor, clade A, alpha-1 antiproteinase, antitrypsin, member 1) (e.g., alpha-1-antitrypsin deficiency), gene analysis, common variants (e.g., *S and *Z) |
| **81346** | TYMS (thymidylate synthetase) (e.g., 5-fluorouracil/5-FU drug metabolism) gene analysis, common variant(s) (e.g., tandem repeat variant) |
| **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 |
| **81355** | VKORC1 (vitamin K epoxide reductase complex, subunit 1) (e.g., warfarin metabolism), gene analysis, common variants (e.g., -1639G>A, c.173+1000C>T) |
| **81370** | HLA Class I and II typing, low resolution (e.g., antigen equivalents); HLA-A, -B, -C, -DRB1/3/4/5, and DQB1 |
| **81371** | HLA Class I and II typing, low resolution (e.g., antigen equivalents); HLA-A, -B, and DRB1 (e.g., verification typing) |
| **81372** | HLA Class I typing, low resolution (e.g., antigen equivalents); complete (i.e., HLA-A, -B, and C) |
| **81373** | HLA Class I typing, low resolution (e.g., antigen equivalents); 1 locus (e.g., HLA-A, -B, or C), each |
| **81374** | HLA Class I typing, low resolution (e.g., antigen equivalents); 1 antigen equivalent (e.g., B*27), each |
| **81375** | HLA Class II typing, low resolution (e.g., antigen equivalents); HLA-DRB1/3/4/5 and DQB1 |
| **81376** | HLA Class II typing, low resolution (e.g., antigen equivalents); 1 locus (e.g., HLA-DRB1, DRB3/4/5, -DQB1, -DQA1, -DPB1, or DPA1), each |
| **81377** | HLA Class II typing, low resolution (e.g., antigen equivalents); 1 antigen equivalent, each |
| **81378** | HLA Class I and II typing, high resolution (i.e., alleles or allele groups), HLA-A, -B, -C, and DRB1 |

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| **81379** | HLA Class I typing, high resolution (i.e., alleles or allele groups); complete (i.e., HLA-A, -B, and C) |
| **81380** | HLA Class I typing, high resolution (i.e., alleles or allele groups); 1 locus (e.g., HLA-A, -B, or C), each |
| **81381** | HLA Class I typing, high resolution (i.e., alleles or allele groups); 1 allele or allele group (e.g., B*57:01P), each |
| **81382** | HLA Class II typing, high resolution (i.e., alleles or allele groups); 1 locus (e.g., HLA-DRB1, -DRB3, -DRB4, -DRB5, -DQB1, -DQA1, -DPB1, or DPA1), each |
| **81383** | HLA Class II typing, high resolution (i.e., alleles or allele groups); 1 allele or allele group (e.g., HLA-DQB1*06:02P), each |
| **81400** | Molecular pathology procedure, Level 1 (e.g., identification of single germline variant [e.g., SNP] by techniques such as restriction enzyme digestion or melt curve analysis) |
| **81401** | Molecular pathology procedure, Level 2 (e.g., 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 (e.g., >10 SNPs, 2-10 methylated variants, or 2-10 somatic variants [typically using non-sequencing target variant analysis], immunoglobulin and T-cell receptor gene rearrangements, duplication/deletion variants of 1 exon, loss of heterozygosity [LOH], uniparental disomy [UPD]) |
| **81403** | Molecular pathology procedure, Level 4 (e.g., analysis of single exon by DNA sequence analysis, analysis of >10 amplicons 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 (e.g., analysis of 2-5 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by Southern blot analysis) |
| **81405** | Molecular pathology procedure, Level 6 (e.g., analysis of 6-10 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 11-25 exons, regionally targeted cytogenomic array analysis) |
| **81406** | Molecular pathology procedure, Level 7 (e.g., analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons) |
| **81407** | Molecular pathology procedure, Level 8 (e.g., 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 (e.g., analysis of >50 exons in a single gene by DNA sequence analysis) |
| **81410** | Aortic dysfunction or dilation (e.g., Marfan syndrome, Loeys Dietz syndrome, Ehler Danlossyndrome 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 dilation (e.g., Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); duplication/deletion analysis, panel must include analyses for TGFBR1, TGFBR2, MYH11, and COL3A1 |
| **81412** | Ashkenazi Jewish associated disorders (e.g., 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 (e.g., 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 (e.g., 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 |
| **81415** | Exome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis |
| **81416** | Exome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator exome (e.g., parents, siblings) (List separately in addition to code for primary procedure) |

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| **81417** | Exome (e.g., unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained exome sequence (e.g., updated knowledge or unrelated condition/syndrome) |
| **81418** | Drug metabolism (e.g., pharmacogenomics) genomic sequence analysis panel, must include testing of at least 6 genes, including CYP2C19, CYP2D6, and CYP2D6 duplication/deletion analysis |
| **81425** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis |
| **81426** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator genome (e.g., parents, siblings) (List separately in addition to code for primary procedure) |
| **81427** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (e.g., updated knowledge or unrelated condition/syndrome) |
| **81432** | Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); genomic sequence analysis panel, must include sequencing of at least 10 genes, always including BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, TP53 |
| **81433** | Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); duplication/deletion analysis panel, must include analyses for BRCA1, BRCA2, MLH1, MSH2, and STK11 |
| **81435** | Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); genomic sequence analysis panel, must include sequencing of at least 10 genes, including APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, and STK11 |
| **81436** | Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); duplication/deletion analysis panel, must include analysis of at least 5 genes, including MLH1, MSH2, EPCAM, SMAD4 |
| **81437** | Hereditary neuroendocrine tumor disorders (e.g., 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, TMEM127, and VHL |
| **81438** | Hereditary neuroendocrine tumor disorders (e.g., medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); duplication/deletion analysis panel, must include analyses for SDHB, SDHC, SDHD, and VHL |
| **81439** | Hereditary cardiomyopathy (e.g., hypertrophic cardiomyopathy, dilated cardiomyopathy, arrhythmogenic right ventricular cardiomyopathy), genomic sequence analysis panel, must include sequencing of at least 5 cardiomyopathy-related genes (e.g., DSG2, MYBPC3, MYH7, PKP2, TTN) |
| **81440** | Nuclear encoded mitochondrial genes (e.g., neurologic or myopathic phenotypes), genomic sequence panel, must include analysis of at least 100 genes, including BCS1L, C10orf2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, and TYMP |
| **81443** | Genetic testing for severe inherited conditions (e.g., cystic fibrosis, Ashkenazi Jewish-associated disorders [e.g., 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 (e.g., ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH) |
| **81448** | Hereditary peripheral neuropathies panel (e.g., Charcot-Marie-Tooth, spastic paraplegia), genomic sequence analysis panel, must include sequencing of at least 5 peripheral neuropathy-related genes (e.g., BSCL2, GJB1, MFN2, MPZ, REEP1, SPAST, SPG11, and SPTLC1) |
| **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 (e.g., plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements |

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| **81463** | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (e.g., 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 (e.g., plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements |
| **81460** | Whole mitochondrial genome (e.g., Leigh syndrome, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes [MELAS], myoclonic epilepsy with ragged-red fibers [MERFF], neuropathy, ataxia, and retinitis pigmentosa [NARP], Leber hereditary optic neuropathy [LHON]), genomic sequence, must include sequence analysis of entire mitochondrial genome with heteroplasmy detection |
| **81465** | Whole mitochondrial genome large deletion analysis panel (e.g., Kearns-Sayre syndrome, chronic progressive external ophthalmoplegia), including heteroplasmy detection, if performed |
| **81470** | X-linked intellectual disability (XLID) (e.g., syndromic and non-syndromic XLID); genomic sequence analysis panel, must include sequencing of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2 |
| **81471** | X-linked intellectual disability (XLID) (e.g., syndromic and non-syndromic XLID); duplication/deletion gene analysis, must include analysis of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2 |
| **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 |
| **81539** | Oncology (high-grade prostate cancer), biochemical assay of four proteins (Total PSA, Free PSA, Intact PSA, and human kallikrein-2 [hK2]), utilizing plasma or serum, prognostic algorithm reported as a probability score |
| **81541** | Oncology (prostate), mRNA gene expression profiling by real-time RT-PCR of 46 genes (31 content and 15 housekeeping), utilizing formalin-fixed paraffin embedded tissue, algorithm reported as a disease-specific mortality risk score |
| **81542** | Oncology (prostate), mRNA, microarray gene expression profiling of 22 content genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as metastasis risk score |
| **81551** | Oncology (prostate), promoter methylation profiling by real-time PCR of 3 genes (GSTP1, APC, RASSF1), utilizing formalin-fixed paraffin embedded tissue, algorithm reported as a likelihood of prostate cancer detection on repeat biopsy |
| **0005U** | Oncology (prostate) gene expression profile by real-time RT-PCR of 3 genes (ERG, PCA3, and SPDEF), urine, algorithm reported as risk score |
| **0008U** | Helicobacter pylori detection and antibiotic resistance, DNA, 16S and 23S rRNA, gyrA, pbp1, rdxA and rpoB, next generation sequencing, formalin-fixed paraffin embedded or fresh tissue or fecal sample, predictive, reported as positive or negative for resistance to clarithromycin, fluoroquinolones, metronidazole, amoxicillin, tetracycline, and rifabutin |
| **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 |
| **0029U** | Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis (i.e., CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 and rs12777823) |
| **0030U** | Drug metabolism (warfarin drug response), targeted sequence analysis (i.e., CYP2C9, CYP4F2, VKORC1, rs12777823) |
| **0031U** | CYP1A2 (cytochrome P450 family 1, subfamily A, member 2) (e.g., drug metabolism) gene analysis, common variants (i.e., *1F, *1K, *6, *7) |
| **0032U** | COMT (catechol-O-methyltransferase) (drug metabolism) gene analysis, c.472G>A (rs4680) variant |
| **0033U** | HTR2A (5-hydroxytryptamine receptor 2A), HTR2C (5-hydroxytryptamine receptor 2C) (e.g., citalopram metabolism) gene analysis, common variants (i.e., HTR2A rs7997012 [c.614-2211T>C], HTR2C rs3813929 [c.-759C>T] and rs1414334 [c.551-3008C>G]) |
| **0036U** | Exome (i.e., somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses |
| **0046U** | FLT3 (FMS-related tyrosine kinase 3) (e.g., acute myeloid leukemia) internal tandem duplication (ITD) variants, quantitative |

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| **0047U** | Oncology (prostate), mRNA, gene expression profiling by real-time RT-PCR of 17 genes (12 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a risk score |
| **0049U** | NPM1 (nucleophosmin) (e.g., acute myeloid leukemia) gene analysis, quantitative |
| **0050U** | Targeted genomic sequence analysis panel, acute myelogenous leukemia, DNA analysis, 194 genes, interrogation for sequence variants, copy number variants or rearrangements |
| **0053U** | Oncology (prostate cancer), FISH analysis of 4 genes (ASAP1, HDAC9, CHD1 and PTEN), needle biopsy specimen, algorithm reported as probability of higher tumor grade |
| **0070U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, common and select rare variants (i.e., *2, *3, *4, *4N, *5, *6, *7, *8, *9, *10, *11, *12, *13, *14A, *14B, *15, *17, *29, *35, *36, *41, *57, *61, *63, *68, *83, *xN) |
| **0071U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, full gene sequence (List separately in addition to code for primary procedure) |
| **0072U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, targeted sequence analysis (i.e., CYP2D6-2D7 hybrid gene) (List separately in addition to code for primary procedure) |
| **0073U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, targeted sequence analysis (i.e., CYP2D7-2D6 hybrid gene) (List separately in addition to code for primary procedure) |
| **0074U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, targeted sequence analysis (i.e., non-duplicated gene when duplication/multiplication is trans) (List separately in addition to code for primary procedure) |
| **0075U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, targeted sequence analysis (i.e., 5' gene duplication/multiplication) (List separately in addition to code for primary procedure) |
| **0076U** | CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (e.g., drug metabolism) gene analysis, targeted sequence analysis (i.e., 3' gene duplication/ multiplication) (List separately in addition to code for primary procedure) |
| **0078U** | Pain management (opioid-use disorder) genotyping panel, 16 common variants (i.e., ABCB1, COMT, DAT1, DBH, DOR, DRD1, DRD2, DRD4, GABA, GAL, HTR2A, HTTLPR, MTHFR, MUOR, OPRK1, OPRM1), buccal swab or other germline tissue sample, algorithm reported as positive or negative risk of opioid-use disorder |
| **0094U** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis |
| **0101U** | Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), 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 (15 genes [sequencing and deletion/duplication], EPCAM and GREM1 [deletion/duplication only]) |
| **0102U** | Hereditary breast cancer-related disorders (e.g., 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 (e.g., 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)] |
| **0113U** | Oncology (prostate), measurement of PCA3 and TMPRSS2-ERG in urine and PSA in serum following prostatic massage, by RNA amplification and fluorescence-based detection, algorithm reported as risk score |
| **0129U** | Hereditary breast cancer–related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis and deletion/duplication analysis panel (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, and TP53) |
| **0130U** | Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, |

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| | CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure) |
| **0131U** | Hereditary breast cancer–related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (13 genes) (List separately in addition to code for primary procedure) |
| **0132U** | Hereditary ovarian cancer–related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (17 genes) (List separately in addition to code for primary procedure) |
| **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 (e.g., 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) |
| **0135U** | Hereditary gynecological cancer (e.g., hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (12 genes) (List separately in addition to code for primary procedure) |
| **0136U** | ATM (ataxia telangiectasia mutated) (e.g., ataxia telangiectasia) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0137U** | PALB2 (partner and localizer of BRCA2) (e.g., breast and pancreatic cancer) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0138U** | BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0156U** | Copy number (e.g., intellectual disability, dysmorphology), sequence analysis |
| **0157U** | APC (APC regulator of WNT signaling pathway) (e.g., familial adenomatosis polyposis [FAP]) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0158U** | MLH1 (mutL homolog 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0159U** | MSH2 (mutS homolog 2) (e.g., hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) |
| **0160U** | MSH6 (mutS homolog 6) (e.g., 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) (e.g., hereditary nonpolyposis 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) |
| **0170U** | Neurology (autism spectrum disorder [ASD]), RNA, next-generation sequencing, saliva, algorithmic analysis, and results reported as predictive probability of ASD diagnosis |
| **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 |
| **0173U** | Psychiatry (i.e., depression, anxiety), genomic analysis panel, includes variant analysis of 14 genes |
| **0175U** | Psychiatry (e.g., depression, anxiety); genomic analysis panel, variant analysis of 15 genes |
| **0203U** | Autoimmune (inflammatory bowel disease), mRNA, gene expression profiling by quantitative RT-PCR, 17 genes (15 target and 2 reference genes), whole blood, reported as a continuous risk score and classification of inflammatory bowel disease aggressiveness |
| **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 |
| **0209U** | Cytogenomic constitutional (genome-wide) analysis, interrogation of genomic regions for copy number, structural changes, and areas of homozygosity for chromosomal abnormalities |
| **0214U** | Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene |

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| | 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 (e.g., parent, sibling) |
| **0218U** | Neurology (muscular dystrophy), DMD gene sequence analysis, including small sequence changes, deletions, duplications, and variants in non-uniquely mappable regions, blood or saliva, identification, and characterization of genetic variants |
| **0235U** | PTEN (phosphatase and tensin homolog) (e.g., 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 |
| **0237U** | Cardiac ion channelopathies (e.g., 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 |
| **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 |
| **0326U** | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 83 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden |
| **0327U** | Fetal aneuploidy (trisomy 13, 18, and 21), DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy, includes sex reporting, if performed |
| **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 |
| **0007U** | Drug test(s), presumptive, with definitive confirmation of positive results, any number of drug classes, urine, includes specimen verification including DNA authentication in comparison to buccal DNA, per date of service |
| **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 |
| **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), micro-RNA profiling by rt-PCR of 10 micro RNA 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 |
| **0022U** | Targeted genomic sequence analysis panel, non-small cell lung neoplasia, DNA and RNA analysis, 23 genes, interrogation for sequence variants and rearrangements, reported as presence or absence of variants and associated therapy(ies) to consider |
| **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) (e.g., myeloproliferative disorder) gene analysis, targeted sequence analysis exons 12-15 |

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| **0034U** | TPMT (thiopurine S-methyltransferase), NUDT15 (nudix hydroxylase 15) (e.g., thiopurine metabolism) gene analysis, common variants (i.e., TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5) |
| **0037U** | Targeted genomic sequence analysis, solid organ neoplasm, dna analysis of 324 genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden |
| **0040U** | BCR/ABL1 (t(9;22)) (e.g., chronic myelogenous leukemia) translocation analysis, major breakpoint, quantitative |
| **0045U** | Oncology (breast ductal carcinoma in situ), 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 recurrence score |
| **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) |
| **0055U** | Cardiology (heart transplant), cell-free DNA, PCR assay of 96 DNA target sequences (94 single nucleotide polymorphism targets and two control targets), plasma |
| **0060U** | Twin zygosity, genomic targeted sequence analysis of chromosome 2, using circulating cell-free fetal DNA in maternal blood |
| **0069U** | Oncology (colorectal), micro-RNA, rt-PCR expression profiling of mir-31-3p, formalin-fixed paraffin-embedded tissue, algorithm reported as an expression sco |
| **0079U** | Comparative DNA analysis using multiple selected single-nucleotide polymorphisms (SNPs), urine and buccal DNA, for specimen identity verification |
| **0084U** | Red blood cell antigen typing, DNA, genotyping of 10 blood groups with phenotype prediction of 37 red blood cell antigens |
| **0087U** | Cardiology (heart transplant), mRNA gene expression profiling by microarray of 1283 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 1494 genes, utilizing transplant biopsy tissue, algorithm reported as a probability score for rejection |
| **0089U** | Oncology (melanoma), gene expression profiling by rtqPCR, prame and linc00518, superficial collection using adhesive patch(es) |
| **0090U** | Oncology (cutaneous melanoma), mRNA gene expression profiling by rt-PCR of 23 genes (14 content and 9 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical result (i.e., benign, intermediate, malignant) |
| **0105U** | Nephrology (chronic kidney disease), multiplex electrochemiluminescent immunoassay (ECLIA) of tumor necrosis factor receptor 1A, receptor superfamily 2 (TNFR1, TNFR2), and kidney injury molecule-1 (KIM-1) combined with longitudinal clinical data, including APOL1 genotype if available, and plasma (isolated fresh or frozen), algorithm reported as probability score for rapid kidney function decline (RKFD) |
| **0111U** | Oncology (colon cancer), targeted KRAS (codons 12, 13, and 61) and NRAS (codons 12, 13, and 61) gene analysis utilizing formalin-fixed paraffin-embedded tissue |
| **0112U** | Infectious agent detection and identification, targeted sequence analysis (16S and 18S rRNA genes) with drug-resistance gene |
| **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 |
| **0140U** | Infectious disease (fungi), fungal pathogen identification, DNA (15 fungal targets), blood culture, amplified probe technique, each target reported as detected or not detected |
| **0141U** | Infectious disease (bacteria and fungi), gram-positive organism identification and drug resistance element detection, DNA (20 gram-positive bacterial targets, 4 resistance genes, 1 pan gram-negative bacterial target, 1 pan Candida target), blood culture, amplified probe technique, each target reported as detected or not detected |
| **0142U** | Infectious disease (bacteria and fungi), gram-negative bacterial identification and drug resistance element detection, DNA (21 gram-negative bacterial targets, 6 resistance genes, 1 pan gram-positive |

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| | bacterial target, 1 pan Candida target), amplified probe technique, each target reported as detected or not detected |
| **0152U** | Infectious disease (bacteria, fungi, parasites, and DNA viruses), microbial cell-free DNA, plasma, untargeted next-generation sequencing, report for significant positive pathogens |
| **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 |
| **0154U** | Oncology (urothelial cancer), RNA, analysis by real-time rt-PCR of the fgfr3 (fibroblast growth factor receptor 3) gene analysis (i.e., 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 |
| **0155U** | Oncology (breast cancer), DNA, pik3ca (phosphatidylinositol-4,5bisphosphate 3-kinase, catalytic subunit alpha) (e.g., breast cancer) gene analysis (i.e., p.c420r, p.e542k, p.e545a, p.e545d [g.1635g>t only], p.e545g, p.e545k, p.q546e, p.q546r, p.h1047l, p.h1047r, p.h1047y), utilizing formalin-fixed paraffin-embedded breast tumor tissue, reported as pik3ca gene mutation status |
| **0169U** | NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (e.g., drug metabolism) gene analysis, common variants |
| **0172U** | Oncology (solid tumor as indicated by the label), somatic mutation analysis of BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, dna repair associated) and analysis of homologous recombination deficiency pathways, DNA, formalin-fixed paraffin-embedded tissue, algorithm quantifying tumor genomic instability score |
| **0177U** | Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha) gene analysis of 11 gene variants utilizing plasma, reported as pik3ca gene mutation status |
| **0179U** | Oncology (non-small cell lung cancer), cell-free DNA, targeted sequence analysis of 23 genes (single nucleotide variations, insertions and deletions, fusions without prior knowledge of partner/breakpoint, copy number variations), with report of significant mutation(s) |
| **0180U** | Red cell antigen (ABO blood group) genotyping (ABO), gene analysis Sanger/chain termination/conventional sequencing, ABO (ABO, alpha 1-3-N-acetylgalactosaminyltransferase and alpha 1-3-galactosyltransferase) gene, including subtyping, 7 exons |
| **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 |

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| **0193U** | Red cell antigen (JR blood group) genotyping (JR), gene analysis, ABCG2 (ATP binding cassette subfamily G member 2 [Junior blood group]) exons 2-26 |
| **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 (i.e., exon 13) |
| **0196U** | Red cell antigen (Lutheran blood group) genotyping (LU), gene analysis, BCAM (basal cell adhesion molecule [Lutheran blood group]) exon 3 |
| **0197U** | Red cell antigen (Landsteiner-Wiener blood group) genotyping (LW), gene analysis, ICAM4 (intercellular adhesion molecule 4 [Landsteiner-Wiener blood group]) exon 1 |
| **0198U** | Red cell antigen (RH blood group) genotyping (RHD and RHCE), gene analysis Sanger/chain termination/conventional sequencing, RHD (Rh blood group D antigen) exons 1-10 and RHCE (Rh blood group CcEe antigens) exon 5 |
| **0199U** | Red cell antigen (Scianna blood group) genotyping (SC), gene analysis, ERMAP (erythroblast membrane associated protein [Scianna blood group]) exons 4, 12 |
| **0200U** | Red cell antigen (Kx blood group) genotyping (XK), gene analysis, XK (X-linked Kx blood group) exons 1-3 |
| **0201U** | Red cell antigen (Yt blood group) genotyping (YT), gene analysis, ACHE (acetylcholinesterase [Cartwright blood group]) exon 2 |
| **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 |
| **0211U** | Oncology (pan-tumor), DNA and RNA by next-generation sequencing, utilizing formalin-fixed paraffin-embedded tissue, interpretative report for single nucleotide variants, copy number alterations, tumor mutational burden, and microsatellite instability, with therapy association |
| **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 |
| **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) (e.g., colorectal cancer) promoter methylation analysis |
| **0230U** | AR (androgen receptor) (e.g., 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) (e.g., 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) (e.g., 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) (e.g., 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) (e.g., 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 |

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| **0236U** | SMN1 (survival of motor neuron 1, telomeric) and SMN2 (survival of motor neuron 2, centromeric) (e.g., spinal muscular atrophy) full gene analysis, including small sequence changes in exonic and intronic regions, duplications, deletions, and mobile element insertions |
| **0238U** | Oncology (lynch syndrome), genomic DNA sequence analysis of mlh1, msh2, msh6, pms2, and epcam, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions |
| **0239U** | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free DNA, analysis of 311 or more genes, interrogation for sequence variants, including substitutions, insertions, deletions, select rearrangements, and copy number variations |
| **0242U** | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 55-74 genes, interrogation for sequence variants, gene copy number amplifications, and gene rearrangements |
| **0244U** | Oncology (solid organ), DNA, comprehensive genomic profiling, 257 genes, interrogation for single-nucleotide variants, insertions/deletions, copy number alterations, gene rearrangements, tumor-mutational burden, and microsatellite instability, utilizing formalin-fixed paraffin-embedded tumor tissue |
| **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 |
| **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 |
| **0250U** | Oncology (solid organ neoplasm), targeted genomic sequence DNA analysis of 505 genes, interrogation for somatic alterations (SNVS [single nucleotide variant], small insertions and deletions, one amplification, and four translocations), microsatellite instability and tumor-mutation burden |
| **0252U** | Fetal aneuploidy short tandem-repeat comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplication, mosaicism, and segmental aneuploidy |
| **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 (e.g., pre-receptive, receptive, post-receptive) |
| **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/duplication, mosaicism, and segmental aneuploidy, per embryo tested |
| **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 |
| **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 |
| **0264U** | Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping |
| **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 |
| **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 |

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| **0272U** | Hematology (genetic bleeding disorders), genomic sequence analysis of 60 genes and duplication/deletion of PLAU, blood, buccal swab, or amniotic fluid, comprehensive |
| **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 |
| **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 42 genes, blood, buccal swab, or amniotic fluid |
| **0277U** | Hematology (genetic platelet function disorder), genomic sequence analysis of 40 genes and duplication/deletion of PLAU, blood, buccal swab, or amniotic fluid |
| **0278U** | Hematology (genetic thrombosis), genomic sequence analysis of 14 genes, 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 |
| **0285U** | Oncology, response to radiation, cell-free DNA, quantitative branched chain DNA amplification, plasma, reported as a radiation toxicity score |
| **0286U** | CEP72 (centrosomal protein, 72-KDa), NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (e.g., drug metabolism) gene analysis, common variants |
| **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) |
| **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 |
| **0289U** | Neurology (Alzheimer disease), mRNA, gene expression profiling by RNA sequencing of 24 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 |
| **0296U** | Oncology (oral and/or oropharyngeal cancer), gene expression profiling by RNA sequencing of at least 20 molecular features (e.g., human and/or microbial mRNA), saliva, algorithm reported as positive or negative for signature associated with malignancy |
| **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 |
| **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 enhancement |
| **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 (i.e., negative, low probability of neoplasia or positive, high probability of neoplasia) |
| **0314U** | Oncology (cutaneous melanoma), mRNA gene expression profiling by rt-PCR of 35 genes (32 content and 3 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical result (i.e., benign, intermediate, malignant) |
| **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 (i.e., class 1, class 2a, class 2b) |
| **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 high-risk patients, analysis of methylation patterns on circulating cell-free DNA (cfDNA) plus measurement of serum of AFP/AFP-l3 |

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| | and oncoprotein des-gammacarboxy-prothrombin (DCP), algorithm reported as normal or abnormal result |
| **0340U** | Oncology (pan-cancer), analysis of minimal residual disease (MRD) from plasma, with assays personalized to each patient based on prior next-generation sequencing of the patient's tumor and germline DNA, reported as absence or presence of MRD, with disease-burden correlation, if appropriate |
| **0341U** | Fetal aneuploidy DNA sequencing comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplication, mosaicism, and segmental aneuploid |
| **0355U** | APOL1 (apolipoprotein L1) (e.g., chronic kidney disease), risk variants (G1, G2) |
| **0356U** | Oncology (oropharyngeal or anal), evaluation of 17 DNA biomarkers using droplet digital PCR (ddPCR), cell-free DNA, algorithm reported as a prognostic risk score for cancer recurrence |
| **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 |
| **0363U** | Oncology (urothelial), mRNA, gene-expression profiling by real-time quantitative PCR of 5 genes (MDK, HOXA13, CDC2 [CDK1], IGFBP5, and CXCR2), utilizing urine, algorithm incorporates age, sex, smoking history, and macrohematuria frequency, reported as a risk score for having urothelial carcinoma |
| **0420U** | Oncology (urothelial), mRNA expression profiling by real-time quantitative PCR of MDK, HOXA13, CDC2, IGFBP5, and CXCR2 in combination with droplet digital PCR (ddPCR) analysis of 6 single-nucleotide polymorphisms (SNPs) genes TERT and FGFR3, urine, algorithm reported as a risk score for urothelial carcinoma |
| **0421U** | Oncology (colorectal) screening, quantitative real-time target and signal amplification of 8 RNA markers (GAPDH, SMAD4, ACY1, AREG, CDH1, KRAS, TNFRSF10B, EGLN2) and fecal hemoglobin, algorithm reported as a positive or negative for colorectal cancer risk |
| **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 |
| **0423U** | Psychiatry (e.g., depression, anxiety), genomic analysis panel, including variant analysis of 26 genes, buccal swab, report including metabolizer status and risk of drug toxicity by condition |
| **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 |
| **0425U** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis, each comparator genome (e.g., parents, siblings) |
| **0426U** | Genome (e.g., unexplained constitutional or heritable disorder or syndrome), ultra-rapid sequence analysis |
| **0428U** | Oncology (breast), targeted hybrid-capture genomic sequence analysis panel, circulating tumor DNA (ctDNA) analysis of 56 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutation burden |
| **0433U** | Oncology (prostate), 5 DNA regulatory markers by quantitative PCR, whole blood, algorithm, including prostate-specific antigen, reported as likelihood of cancer |
| **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 |

## APPROVAL HISTORY

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| **2/14/2024** | Coverage policy revised to clarify requirements unique to different types of genetic testing.Added key features of genetic conditions. Removed published study requirements and removed need for genetic counseling in non-genetic conditions. |
| **4/13/2023** | Policy reviewed, clarified hierarchy of policy utilization, change in coverage requirements to allow practitioners within their scope practice and to allow two published studies (instead of three) to establish phenotype/genotypic alignment. Clarification of verbiage and coding. |
| **2/9/2022** | Policy reviewed; no changes to criteria; updated Overview, Summary of Medical Evidence and Reference sections. |
| **2/8/2021** | Policy reviewed; no criteria changes; added that Molina utilizes MCG and eviCore for genetic testing criteria. |
| **4/23/2020** | Policy reviewed, no changes. |
| **9/18/2019** | Policy reviewed, no changes. |
| **7/10/2018** | Policy reviewed; clinical criteria updated to remove exclusions for: whole exome sequencing (WES) and carrier testing in children < age 18 years; criteria updated to allow a MD specialist to perform pre/post genetic counseling; updated Summary of Medical Evidence and Reference sections. |
| **6/22/2017** | New policy. |

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