

MEDICAL POLICY

Medical Policy Title	Molecular Testing of Tumor Tissue to Identify Targeted Therapies for Cancers
Policy Number	2.02.51
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Next Review Date	February 2027

Our medical policies are guides to evaluate technologies or services for medical necessity. Criteria are established through the assessment of evidence based, peer-reviewed scientific literature, and national professional guidelines. Federal and state law(s), regulatory mandates and the member's subscriber contract language are considered first in the determination of a covered service. (Link to [Product Disclaimer](#))

POLICY STATEMENT(S)

- I. Molecular testing of tumor tissue is considered **medically appropriate** when **ALL** the following criteria are met:
 - A. To direct targeted therapy;
 - B. The results will be used to guide management of the patient;

AND

 - C. In the treatment of **ANY** of the following: (CPT code examples not all inclusive)
 1. **Metastatic colorectal cancer** for the following targeted genes:
 - a. Kirsten rat sarcoma viral oncogene (KRAS) (CPT: 81275, 81276);
 - b. Neuroblastoma RAS viral oncogene (NRAS) (CPT: 81311);
 - c. B-Raf proto-oncogene (BRAF) (CPT: 81210);
 - d. Human epidermal growth factor receptor 2 (HER2) amplification;
 - e. Neurotrophic tyrosine receptor kinase (NTRK) gene fusions (CPT: 81191-81193, 81194);
 - f. POLE/POLD1;
 - g. Rearranged during transfection (RET);
 - h. MSI/MMR status (if not previously done);
 2. **Non-small-cell lung cancer (NSCLC)** including adenocarcinoma, large cell, squamous cell, and NSCLC not otherwise specified for the following targeted genes:
 - a. Epidermal Growth Factor Receptor (EGFR) gene mutations (CPT: 81235);
 - b. Anaplastic lymphoma kinase (ALK) gene rearrangement;
 - c. KRAS (CPT: 81275, 81276);
 - d. NTRK 1/2/3 gene fusion (CPT: 81191-81193, or 81194);

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- e. ROS proto-oncogene 1 (ROS-1) gene rearrangement;
 - f. BRAF point mutations (CPT: 81210);
 - g. Mesenchymal-epithelial transition MET exon 14 skipping variants;
 - h. High-level MET amplification;
 - i. RET gene rearrangements;
 - j. Erb-B2 Receptor Tyrosine Kinase 2 (ERBB2)/(HER2) gene mutation;
 - k. NRG1;
3. Stage III **melanoma** at high risk of recurrence, stage IV melanoma, or clinical recurrence for the following targeted gene mutations:
- a. BRAF (CPT: 81210);
 - b. KIT (CPT: 81272);
4. Newly diagnosed **metastatic pancreatic cancer** or metastatic pancreatic cancer that is progressing on or after chemotherapy or immunotherapy, and have never been tested for molecular biomarker analysis for the following targeted gene mutations:
- a. Anaplastic lymphoma kinase (ALK) gene fusions;
 - b. NRG1 gene fusions;
 - c. NTRK 1/2/3 gene fusion (CPT: 81191-81193, or 81194);
 - d. ROS-1 gene fusion;
 - e. BRAF gene mutation (CPT: 81210);
 - f. BRCA 1/2 gene mutation (CPT 81162);
 - g. KRAS gene mutation (CPT: 81275, 81276);
 - h. PALB2 gene mutation (CPT: 81307);
 - i. HER2 amplifications;
 - j. FGFR2 gene fusion;
 - k. RET gene fusion;
 - l. Microsatellite instability (MSI)/ DNA mismatch repair (MMR);
 - m. TMB;
5. Recently diagnosed or recurrent **ovarian cancer** for the following targeted gene mutations:
- a. BRCA 1/2 (CPT 81162);
 - b. Homologous recombination deficiency (HRD) status;

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- c. MSI/MMR;
 - d. TMB;
 - e. NTRK (CPT: 81191-81193, or 81194);
 - f. BRAF (CPT: 81210);
 - g. FRα (FOLR1);
 - h. RET;
 - i. HER2;
6. **Metastatic prostate cancer** for the following targeted gene mutations:
- a. BRCA 1/2 (CPT 81162);
 - b. ATM;
 - c. PALB2 (CPT 81307);
 - d. FANCA;
 - e. RAD51D;
 - f. CHEK2;
 - g. CDK12;
 - h. MSI/MMR;
 - i. TMB;
7. **Breast cancer** (note specific classifications by genes below) for the following targeted gene mutations:
- a. PIK3CA mutation (HR-positive/HER2-negative breast cancer) (CPT 81309);
 - b. NTRK fusion (all breast cancers) (CPT: 81191-81193, or 81194);
 - c. MSI/MMR (all breast cancers);
 - d. TMB (all breast cancers);
 - e. Estrogen Receptor 1 (ESRI) (HR-positive/HER2-negative breast cancer) at progression following prior lines of endocrine therapy;
 - f. RET (all breast cancers);
8. **Primary brain tumors** for the following targeted gene mutations:
- a. Isocitrate dehydrogenase 1 (IDH1) and IDH2 (CPT: 81120, 81121);
 - b. 1p19q codeletion;
 - c. 6 -methylguanine-DNA methyl-transferase (MGMT) (CPT: 81287);

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- d. ATRX;
- e. Telomerase reverse transcriptase (TERT) (CPT: 81345);
- f. BRAF V600 (CPT: 81210);
- g. H3-3A;
- h. NTRK;

9. **Ependyomas** for the following targeted gene mutations:

- a. ZFTA;
- b. YAP1;
- c. MYCN;

10. **Medulloblastoma** for the following targeted gene mutations:

- a. CTNNB1;
- b. GAB1;
- c. YAP1;
- d. TP53.

D. Testing for genetic alterations in any other genes than those listed above is considered **investigational**.

Other Cancers

II. Gene mutational analysis of tumor tissue to predict response to targeted therapies and to direct targeted therapy, is considered **medically appropriate** when **ALL** the following criteria are met:

- A. Testing is recommended (2A or 1) by the current NCCN Guidelines for the cancer indication;
- B. Testing should include only the number of genes necessary for therapeutic decision making;
- C. The results will be used to guide management of the patient;

AND

D. Diagnosed with **EITHER** of the following:

- 1. Who have previous biopsy-confirmed, newly diagnosed advanced stage III or IV or metastatic cancer; **or**
- 2. Advanced stage III or IV or metastatic cancer that is progressing on or after chemotherapy or immunotherapy, and who have never been tested for molecular and biomarker analysis.

III. Programmed death receptor 1 (PD-1) or its ligand (PDL-1) expression analysis is considered **medically appropriate** as a technique to predict treatment response to drug therapy.

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- IV. Tumor tissue testing to identify targeted cancer treatment with a comprehensive genomic profiling test (e.g., FoundationOne CDx, CARIS Life Sciences MI Tumor Seek Hybrid, MSK-IMPACT, TEMPUS xT) is considered **investigational**.

RELATED POLICIES

Corporate Medical Policy

- 2.02.53 JAK2, MPL, and CALR Molecular Testing for Myeloproliferative Neoplasm
- 2.02.54 Measurable Residual Disease Assessment Testing
- 2.02.56 Circulating Tumor DNA for Management of Cancer (Liquid Biopsy)
- 11.01.03 Experimental or Investigational Services

POLICY GUIDELINE(S)

- I. Smaller targeted panels with actionable gene mutations and drug therapies based on the presence of a specific mutation may be approvable.
- II. A negative liquid biopsy test result should be followed by reflex testing to a formalin-fixed paraffin-embedded tissue test.
- III. A liquid biopsy and formalin-fixed paraffin-embedded tissue test should not be tested simultaneously.
- IV. The Health Plan and its employees adhere to all State and Federal laws concerning the confidentiality of genetic testing and the results of genetic testing. All records, findings and results of any genetic test performed on any person shall be deemed confidential and shall not be disclosed without the written informed consent of the person to whom such genetic test relates. This information shall not be released to any person or organization not specifically authorized by the individual subject of the test or in compliance with applicable law.
- V. Genetic testing is appropriate only when performed by a qualified laboratory certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) and offered in a setting with adequately trained health care professionals who are qualified to provide appropriate pre- and post-test counseling.
- VI. Genetic testing is contract dependent. Coverage only applies to members with a valid contract; coverage is not provided for family members without a valid contract.
- VII. Supporting documentation required - for other cancers not listed in the policy:

The purpose of tumor tissue testing is to provide information that will assist in predicting response to targeted therapies or to direct targeted therapy. Documentation that must be submitted for review includes all of the following documentation:

 - A. The purpose of the test;
 - B. The gene mutation(s) to be tested;

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- C. The drug therapy plan based on results of the testing; and
- D. Supportive evidence demonstrating efficacy of the proposed drug therapy for the gene mutation in patient's cancer.

DESCRIPTION

According to the Precision Medicine Initiative, precision medicine is an emerging approach for disease treatment and prevention that considers individual variability in genes, environment, and lifestyle for each person. Research has been directed to understanding molecular variations in tumors from different cancer types so that drugs used to treat the tumors are "targeted" or directed to inhibit the function of the molecular alteration. The goal of precision medicine is to maximize efficiency and minimize side effects of therapy.

Multigene Panel Testing

Comprehensive Genomic Profiling tests evaluate between 140-300 genes in tumor tissue for which there are only a small number of FDA-approved targeted therapy options. Large panel tests contain many genes that have no actionable gene mutations, thus no targeted therapy. Molecular panel testing has been used to determine off-label drug therapy or whether or not a patient may be eligible for a clinical trial. Of those patients tested, only a small number will experience clinical utility (have a targeted therapy identified), and an even smaller number will experience clinical benefit.

SUPPORTIVE LITERATURE

Comprehensive Genomic Profiling Tests

It is difficult to determine the clinical validity of the molecular panels because of the different mutations and the large number of potential cancers for which they can be used. Testing each gene in the panel for each of the cancer types would require extensive research potentially taking many years to complete. Consequently, the evidence on clinical validity of the molecular panels is insufficient to make any recommendations.

The evidence for clinical utility of molecular panel testing to direct targeted therapies in cancer patients has been conflicting. The SHIVA study, a randomized, open-label phase 2 trial, randomized patients with any kind of metastatic solid tumor refractory to standard of care (Le Tourneau 2015) to matched molecularly targeted treatment based on one of three molecular pathways; hormone receptor, PI3K/AKT/mTOR, and RAF/MEK (the experimental group) or physician's choice treatment (the control group). At median follow-up of 11.3 months, median progression-free survival was similar for both groups. Grade 3 to 4 adverse events were slightly higher in the experimental group. The authors concluded that progression-free survival was not improved with the use of molecularly targeted agents outside their indications, compared with the physician's choice treatment in heavily pretreated patients with cancer. Off-label use of molecularly targeted agents should be encouraged in clinical trials to assess predictive biomarkers of efficacy.

The IMPACT study (Tsimberidou 2017), a phase I study at the University of Texas, MD Anderson Cancer Center, assessed whether molecular analysis of advanced cancer and targeted therapy was

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associated with improved clinical outcomes. Of the 1,144 patients analyzed, 40.2% had one or more molecular aberration in their tumor. The patients with one aberration and matched therapy had a higher overall response rate (27%) compared to those patients without matched therapy (5%). Patients with matched therapy had longer time-to-treatment failure (5.2 months) and longer survival (13.4 months) compared to those patients without matched therapy (2.2 months and 9.0 months, respectively).

PROFESSIONAL GUIDELINE(S)

Colorectal Cancer

The Molecular Biomarkers for the Evaluation of Colorectal Cancer Guidelines from the American Society for Clinical Pathology, College of American Pathologists, Association for Molecular Pathology, and the American society of Clinical Oncology (Sepulveda 2017) recommend RAS mutational testing for colorectal carcinoma patients being considered for anti-EGFR therapy. Mutational analysis should include KRAS and NRAS codons 12, 13 of exon 2; 59, 61 of exon 3; and 117 and 146 of exon 4 ("expanded" or "extended" RAS) (Strength of evidence: convincing/adequate. Quality of evidence: high/intermediate). BRAF p.V600 (BRAF c. 1799 (p.V600) mutational analysis should be performed in colorectal cancer tissue in patients with colorectal carcinoma for prognostic stratification. (Strength of evidence: adequate/inadequate. Quality of evidence: intermediate/low).

The NCCN guidelines for Colon Cancer (V.5.2025) have expanded recommendations regarding biomarker testing as the role of targeted therapy for treatment of advanced or metastatic colorectal cancer (mCRC) and recommend testing should be done as part of broad molecular profiling. Currently, determination of tumor gene status for KRAS/NRAS and BRAF mutations, as well as HER2 amplifications and MSI/MMR status (if not previously done), are recommended for patients with mCRC. The testing can be performed on formalin-fixed paraffin-embedded tissue (preferred) or blood-based assay and may be carried out for individual genes or as part of an NGS panel, although no specific methodology is recommended. NGS panels have the advantage of being able to pick up rare and actionable genetic alterations, such as neurotrophic tyrosine receptor kinase (NTRK) fusions. Based on the limited data in the colorectal cancer population, the NCCN Panel does not currently recommend TMB biomarker testing, unless measured as part of a clinical trial. Patients with known KRAS mutation (exon 2, 3, 4) or NRAS mutation (exon 2, 3, 4) should not be treated with either cetuximab or panitumumab. BRAF V600E mutation makes response to panitumumab or cetuximab highly unlikely unless given with a BRAF inhibitor. HER2-targeted therapies are now recommended as subsequent therapy options in patients with tumors that have HER2 overexpression. Testing for HER2 amplifications for patients with metastatic colorectal cancer is recommended. If the tumor is already known to have a KRAS/NRAS or BRAF mutation, HER2 testing is not required. However, HER2-targeted therapies are still under investigation, enrollment in a clinical trial is encouraged. Anti-HER2 therapy is only indicated in HER2-amplified tumors that are also RAS and BRAF wild type. NTRK fusions were limited to cancer that were wild type for KRAS, NRAS, and BRAF. A majority of the CRCs harboring NTRK fusions were also MMR-deficient. NTRK fusion testing may be limited to those patients with wild-type KRAS, NRAS, and BRAF. There are two targeted therapies (larotrectinib and entrectinib) that have been FDA-approved for the treatment of patients with metastatic, unresectable

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solid tumors that have an NTRK gene fusion and no satisfactory alternative treatment options, regardless of the location of the primary tumor. These treatment options are not appropriate for most patients due to the rarity of the NTRK fusion in CRC.

Non-Small Cell Lung Cancer

The NCCN guidelines for Non-Small Cell Lung Cancer (NSCLC) (V.3.2026) strongly advises broader molecular profiling with the goal of identifying rare driver mutations for which effective drugs may already be available, or to appropriately counsel patients regarding the availability of clinical trials. Broad molecular profiling is a key component of the improvement of care of patients with NSCLC. Complete biomarker testing including molecular assessment of EGFR, ALK, ROS1, BRAF, ERBB2 (HER2), KRAS, NTRK 1/2/3, MET, NRG1, and RET, repeat biopsy and/or plasma testing should be done. If these are not feasible, treatment is guided by available results, and, if unknown, these patients are treated as though they do not have driver oncogenes. Erlotinib is recommended, with or without chemotherapy, as first-line therapy for advanced or metastatic NSCLC in patients with known activated EGFR mutation or gene amplification. EGFR mutations were predictive of a better response in patients receiving erlotinib (53% in patients with mutations versus 18% in those without mutations). KRAS mutations are associated with intrinsic TKI resistance and KRAS gene sequencing could be useful for the selection of patients as candidates for TKI therapy. Overlapping EGFR and KRAS mutations occur in less than 1% of patients with lung cancer. Other TKIs such as, Afatinib and Osimertinib have been recommended by NCCN in patients with EGFR mutations and metastatic NSCLC. Afatinib has been recommended and FDA approved for first-line therapy in patients with metastatic non-squamous NSCLC who have sensitizing EGFR mutations. Osimertinib has been approved by the FDA for patients with metastatic EGFR T790M mutation-positive NSCLC, who have progressed on or after EGFR TKI therapy. NCCN recommends Osimertinib for individuals with stage IB NSCLC with EGFR exon 19 deletion or L858R. ROS1 gene rearrangements occur more frequently in younger women with adenocarcinoma who are never smokers and in those who are negative for EGFR mutations, KRAS mutations, and ALK gene rearrangements (also known as triple negative). Crizotinib is very effective for patients with ROS1 rearrangement with response rates of about 70% including complete responses. The FDA has approved crizotinib for patients with ROS1 rearrangements.

Other genetic alterations such as, BRAF V600E and HER2 mutations, MET amplification, and RET rearrangements have been associated with emerging targeted therapies. Targeted agents are available for patients with NSCLC who have these other genetic alterations, although they are FDA approved for other indications.

As a primary immunosuppressive driver, PD-L1 overexpression may be an important facilitator for tumor growth and metastasis. PD-L1 has been detected in up to 50% of human cancers, making the PD-L1 pathway a focus of cancer research. NCCN recommends IHC testing for PD-L1 expression before first-line treatment in patients with metastatic NSCLC with negative or unknown test results for EGFR mutations, ALK rearrangements, and ROS1 rearrangements. Although it is not an optimal biomarker, PD-L1 expression is currently the best available biomarker to assess whether patients are candidates for pembrolizumab. PD-L1 expression is continuously variable and dynamic; thus, a cutoff

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value for a positive result is artificial. Patients with PD-L1 expression levels just below and just above 50% will probably have similar responses. The definition of a positive PD-L1 test result varies depending on which biomarker assay is used. For the 2022 update, the NCCN NSCLC Panel recommends testing for ERBB2 (HER2) mutations in eligible patients with metastatic NSCLC based on clinical trial data and the FDA approval of fam-trastuzumab deruxtecan-nxki. ERBB2 (HER2) exon 20 mutations occur in approximately 3% of patients (median age, 62 years) with advanced nonsquamous NSCLC. Patients tend to be females who do not smoke cigarettes; they have a higher incidence of brain metastases than those with other actionable mutations. Emerging predictive molecular biomarkers include high-level MET amplifications. Targeted agents are available for patients with NSCLC who have high-level MET amplifications. However, there is less data to support using these agents and they may not be FDA approved for NSCLC; therefore, they are referred to as emerging biomarkers.

Melanoma

The NCCN guidelines for Cutaneous Melanoma (V.2.2025) state emerging molecular technologies for cutaneous melanoma diagnosis and prognostication indications include that BRAF or next-generation sequencing (NGS) for resected stage I-II cutaneous melanoma is not recommended unless it will inform clinical trial participation. BRAF mutation is recommended for patients with stage III at high risk for recurrence for whom future BRAF-directed therapy may be an option. For initial presentation with stage IV disease or clinical recurrence, obtain tissue to ascertain alterations in BRAF, and in the appropriate clinical setting, KIT from either biopsy of the metastasis (preferred) or archival material if the patient is being considered for targeted therapy. Broader genomic profiling (e.g., larger NGS panels, BRAF non-V600 mutations) is recommended if feasible, especially if the test results might guide future treatment decisions or eligibility for participation in a clinical trial. If BRAF single-gene testing was the initial test performed, and is negative, clinicians should strongly consider larger NGS panels to identify other potential genetic targets (e.g., KIT, NRAS, BRAF non-V600).

BRAF and KIT mutations appear to be early genetic driver events in melanoma. Thus, repeat molecular testing upon recurrence or metastases is likely to be of low yield. Repeat testing following progression on targeted therapy (BRAF- or KIT-directed therapy) does not appear to have clinical utility, since the mechanisms of resistance are diverse and do not have prognostic or therapeutic relevance.

Pancreatic Cancer

The NCCN guidelines for Pancreatic Adenocarcinoma (V.2.2025) recommend gene profiling of tumor tissue as clinically indicated for individuals with locally advanced/metastatic disease who are candidates for anti-cancer therapy to identify uncommon mutations using comprehensive genomic profiling via an FDA-approved and/or validated NGS-based assay. Consider specifically testing for actionable somatic findings including, but not limited to fusions (ALK, NRG1, NTRK, ROS1, FGFR2, RET), mutations (BRAF, BRCA 1/2, KRAS, PALB2), amplifications (HER2), microsatellite instability (MSI), and/or mismatch repair (MMR) deficiency and tumor mutational burden (TMB). Testing on tumor tissue is preferred and may be performed if recurrence after resection if not previously performed.

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Ovarian Cancer

The NCCN guidelines for Ovarian Cancer/Fallopian Tube Cancer/ Primary Peritoneal Cancer (V.3.2025) state comprehensive tumor testing may not be necessary for certain patients in the upfront setting, specifically those with a germline mutation in BRCA1/2 or other homologous recombination/DNA repair pathway genes. Initially molecular analysis should include BRCA1/2 status, loss of heterozygosity, or homologous recombination status, in the absence of a germline BRCA mutation. However, some patients (such as those who lack a BRCA1/2 mutation or experience disease recurrence) may benefit from a more thorough tumor molecular analysis to inform additional targeted therapy options. In the recurrence setting, tumor molecular analysis is recommended to include, at a minimum, tests to identify potential benefit from targeted therapeutics that have tumor-specific or tumor-agnostic benefit including, but not limited to, HER2 status, BRCA1/2, HRD status, MSI, MMR, TMB, BRAF, FR α (FOLR1), RET, and NTRK if prior testing did not include these markers. Additional somatic tumor testing can be considered at the physician's discretion to identify genetic alterations for which FDA-approved tumor-specific or tumor-agnostic targeted therapy options exist. These additional tests may be particularly useful for patients who recurrence therapy options are limited.

Prostate Cancer

The NCCN guidelines for Prostate Cancer (V.4.2026) state that tumor molecular and biomarker analysis may be used for treatment decision-making, including understanding eligibility for biomarker-directed treatments, genetic counseling, early use of platinum chemotherapy, and eligibility for clinical trials. Clinical trials may include established and/or candidate molecular biomarkers for eligibility. Tumor molecular profiles may change with subsequent treatments and re-evaluation may be considered at time of cancer progression for treatment decision-making. Tumor testing for alterations in homologous recombination DNA repair genes, such as BRCA1, BRCA2, ATM, PALB2, FANCA, RAD51D, CHEK2, and CDK12, is recommended for individuals with metastatic prostate cancer and can be considered in individuals with regional (N1) prostate cancer. Tumor testing for MSI-H or dMMR is also recommended in patients with metastatic castration-resistant prostate cancer and may be considered in patients with regional or castration-sensitive metastatic prostate cancer. Early studies suggest germline and somatic mutations in these genes may be predictive of the clinical benefit of poly-ADP ribose polymerase (PARP) inhibitors. PARP inhibitors that have been approved by the FDA for use in prostate cancer are Olaparib and Rucaparib.

Breast Cancer

The NCCN guidelines for Breast Cancer (V.5.2025) state for recurrent unresectable (local or regional) or stage IV disease, for HR-positive/HER2-negative breast cancer, assess for PIK3CA mutations to identify candidates for Inavolisib plus palbociclib plus fulvestrant (Category 1 Evidence) or alpelisib plus fulvestrant. (Category 1 Evidence). Additionally in HR-positive/HER2-negative breast cancer, assess for PIK3CA OR AKT1 activating mutations OR PTEN alterations for Capivasertib plus fulvestrant (Category 1 Evidence). At progression in HR-positive/HER2-negative breast cancer, assess for ESR1 mutations for treatment with Elecestrant or Imlunestrant (Category 2A Evidence). In triple negative breast cancer, PD-L1 can be assessed by IHC (Category 1 Evidence). In all types of breast

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cancer NTRK fusions/MMR tumor mutational burden (TMB) and RET fusion can be assessed by NGS (Category 2A Evidence). Larotrectinib, Entrectinib, and Repotrectinib are indicated for the treatment of solid tumors that have an NTRK gene fusion without a known acquired resistance mutation and have no satisfactory alternative treatments or that have progressed following treatment. Pembrolizumab is indicated for the treatment of patients with unresectable or metastatic, microsatellite instability-high (MSI-H) or mismatch repair deficient (dMMR) solid tumors, or TMB-H tumors that have progressed following prior treatment and who have no satisfactory alternative treatment options. Dostarlimab-gxly is indicated for adult patients with MSI-H/dMMR unresectable or metastatic tumors that have progressed on or following prior treatment and who have no satisfactory alternative treatment options. Selpercatinib is indicated for locally advanced or metastatic tumors with a RET gene fusion that have progressed on or following prior systemic treatment or who have no satisfactory alternative treatment options.

Central Nervous System Cancers

The NCCN guidelines for Central Nervous System Cancers (V.3.2025) state with the use of genetic and molecular testing, histologically similar CNS neoplasms can be differentiated more accurately in terms of prognosis and response to different therapies. The fifth edition of the WHO classification of CNS tumors was published in 2021. In this newest classification, adult diffuse gliomas are subsumed within a super category of gliomas and glioneuronal tumors and are split into three subtypes: 1) IDH-mutant astrocytoma; 2) oligodendroglioma, 1p/19q-codeleted and IDH-mutant; and 3) glioblastoma, IDH wild-type. The panel recommends IDH mutation testing in patients with glioma. Testing for 1p/19q codeletion is essential for the diagnosis of oligodendroglioma. Mutation testing for ATRX and TERT promoter are also recommended, given the diagnostic value of these mutations. Grade 3–4 gliomas should undergo testing for MGMT promoter methylation, since MGMT promoter-methylated tumors typically respond better to alkylating chemotherapy, compared to unmethylated tumors. Molecular testing of glioblastomas is encouraged by the panel, as patients with a detected driver mutation (e.g., BRAF V600E mutation or NTRK fusion) may be treated with a targeted therapy on a compassionate use basis, and these tests improve diagnostic accuracy and prognostic stratification. Recurrent or progressive disease of glioblastoma patients should be enrolled in clinical trials evaluating systemic therapy options.

Ependymomas arising in the supratentorium often contain activating fusions of ZFTA. This leads to increased NF-kappa-B signaling and more aggressive behavior. This event is more common in children than in adults, and occurs only in the supratentorium, not the posterior fossa or spine. A subset of spinal cord ependymomas show MYCN amplification. Such tumors tend to behave more aggressively and are therefore now codified as SP-EPN-MYCN. As is often the case in other tumor types (e.g., medulloblastoma), MYCN amplification is strongly associated with more aggressive behavior and worse prognosis.

Medulloblastomas are WHO grade 4 tumors that predominantly arise from the cerebellum in pediatric patients but can also occur in adults. The WHO committee on CNS tumors now recommends subclassification of these tumors into four distinct groups: i) WNT-activated; ii) Sonic hedgehog (SHH)-activated and TP53-mutant; iii) SHH-activated and TP53- wild type; and iv) non-WNT/non-

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SHH. Differentiating between WNT-activated, SHH-activated, and non-WNT/ non-SHH tumors is best classified by expression arrays, DNA methylation arrays, or an IHC panel composed of beta-catenin, GAB1, and YAP1. Because there are a variety of hotspots in TP53, gene sequencing is recommended in SHH-activated medulloblastomas. SHH-pathway inhibitors that have been evaluated in phase II trials including adults with recurrent medulloblastoma include vismodegib²⁹⁶ and sonidegib.²⁹⁷ Patients in these trials with SHH-activated disease were more likely to respond than patients with non-SHH disease.

Multigene Panel Testing

The NCCN guidelines contain specific genetic testing guidelines for individual cancers, based on situations in which there is a known mutation-drug combination that has demonstrated benefits for that specific tumor type (e.g., NSCLC, ovarian cancer, colorectal cancer, and melanoma). The NCCN NSCLC Panel (V.3.2026) recommends molecular testing based on clinical trial data, but strongly advises broader molecular profiling, to identify these and other rare driver mutations for which targeted therapies may be available to ensure that patients receive the most appropriate treatment; patients may be eligible for clinical trials for some of these targeted agents. The panel defines broad molecular profiling for NSCLC as molecular testing that identifies all of the classic actionable biomarkers described in the algorithm using either a single assay or a combination of a limited number of assays—and optimally also identifies the emerging biomarkers.

The American Society of Clinical Oncology (ASCO) (Chakravarty 2022) published a clinical opinion paper regarding somatic genetic testing for metastatic or advanced solid tumor cancers. They state genomic testing should be performed when there are genomic biomarker-linked therapies approved by regulatory agencies for the type of cancer and when considering a treatment for which there is a specific genomic biomarker-based contraindication (strength of recommendation: strong). For patients with metastatic or advanced solid tumors, genomic testing using multigene genomic sequencing is preferred whenever patients are eligible for a genomic biomarker-linked therapy that a regulatory agency has approved (strength of recommendation: moderate). Multigene panel-based genomic testing should be used whenever more than one genomic biomarker is linked to a regulatory agency-approved therapy (strength of recommendation: strong). For tumors with actionable genomic alterations without approved genomic biomarker-linked targeted therapies, patient participation in clinical trials is encouraged after considering the expected efficacy of available standard-of-care options (strength of recommendation: strong). Off-label and off-study use of genomic biomarker-linked therapies approved in other diseases is not recommended when a clinical trial is available or without clinical evidence of meaningful efficacy (strength of recommendation: strong).

REGULATORY STATUS

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service. Laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments (CLIA).

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Laboratories that offer laboratory-developed tests must be licensed by CLIA for high-complexity testing. More information is available at: [Clinical Laboratory Improvement Amendments \(CLIA\) | FDA](#) [accessed 2026 Jan 20]

[List of Cleared or Approved Companion Diagnostic Devices \(In Vitro and Imaging Tools\) | FDA](#) [accessed 2026 Jan 20]

[FDA Cleared-Approved-CDx.](#) [accessed 2026 Jan 20]

CODE(S)

- Codes may not be covered under all circumstances.
- Code list may not be all inclusive (AMA and CMS code updates may occur more frequently than policy updates).
- (E/I)=Experimental/Investigational
- (NMN)=Not medically necessary/appropriate

CPT Codes

Code	Description
81120	IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (e.g., glioma), common variants (e.g., R132H, R132C)
81121	IDH2 (isocitrate dehydrogenase 2 [NADP+], mitochondrial) (e.g., glioma), common variants (e.g., R140W, R172M)
81162	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (i.e., detection of large gene rearrangements)
81175	ASXL1 (additional sex combs like 1, transcriptional regulator) (e.g., myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; full gene sequence
81191	NTRK1 (Neurotrophic Receptor Tyrosine Kinase 1) (e.g., solid tumors) translocation analysis
81192	NTRK2 (Neurotrophic Receptor Tyrosine Kinase 2) (e.g., solid tumors) translocation analysis
81193	NTRK3 (Neurotrophic Receptor Tyrosine Kinase 3) (e.g., solid tumors) translocation analysis

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Code	Description
81194	NTRK (neurotrophic receptor tyrosine kinase 1, 2, and 3) (e.g., solid tumors) translocation analysis
81210	BRAF (B-Raf proto-oncogene, serine/threonine kinase) (e.g., colon cancer, melanoma), gene analysis, V600 variant(s)
81235	EGFR (epidermal growth factor receptor) (e.g., non-small cell lung cancer) gene analysis, common variants (e.g., exon 19 LREA deletion, L858R, T790M, G719A, G719S, L861Q)
81272	KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (e.g., gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (e.g., exons 8, 11, 13, 17, 18)
81275	KRAS (Kirsten rat sarcoma viral oncogene homolog) (e.g., carcinoma) gene analysis; variants in exon 2 (e.g., codons 12 and 13)
81276	KRAS (Kirsten rat sarcoma viral oncogene homolog) (e.g., carcinoma) gene analysis; additional variant(s) (e.g., codon 61, codon 146)
81287	MGMT (O-6-methylguanine-DNA methyltransferase) (e.g., glioblastoma multiforme) promoter methylation analysis
81307	PALB2 (partner and localizer of BRCA2) (e.g., breast and pancreatic cancer) gene analysis; full gene sequence
81309	PIK3CA (Phosphatidylinositol-4, 5-biphosphate 3-kinase, catalytic subunit alpha) (e.g., colorectal and breast cancer) gene analysis, targeted sequence analysis (e.g., exons 7, 9, 20)
81311	NRAS (neuroblastoma RAS viral [v-ras] oncogene homolog) (e.g., colorectal carcinoma), gene analysis, variants in exon 2 (e.g., codons 12 and 13) and exon 3 (e.g., codon 61)
81345	TERT (telomerase reverse transcriptase) (e.g., thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (e.g., promoter region)
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])

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Code	Description
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)
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
81449	Solid organ neoplasm, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants and copy number variants or rearrangements, if performed; RNA analysis
81455 (E/I)	Solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes, genomic sequence analysis panel, interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis

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Code	Description
81456 (E/I)	Solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes, genomic sequence analysis panel, interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis
81457	Solid organ neoplasm, genomic analysis panel; DNA analysis, microsatellite instability
81458	Solid organ neoplasm, genomic analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability
81459	Solid organ neoplasm, genomic analysis panel, interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements
81479	Unlisted molecular pathology procedure
88363	Examination and selection of retrieved archival (i.e., previously diagnosed) tissue(s) for molecular analysis (e.g., KRAS mutational analysis)
0037U (E/I)	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 (e.g., FoundationOne CDx (F1CDx), Foundation Medicine Inc)
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 (e.g.; theascreen FGFR RGQ RT-PCR Kit, QIAGEN, QIAGEN GmbH)
0155U	Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4,5-bisphosphate 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 (e.g., theascreen PIK3CA RGQ PCR Kit, QIAGEN, QIAGEN GmbH)

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Code	Description
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 (myChoice CDx, Myriad Genetics Laboratories, Inc)
0211U (E/I)	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 (MI Cancer Seek NGS Analysis, Caris MPI d/b/a Caris Life Sciences)
0244U (E/I)	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 (Oncotype MAPTM Pan-Cancer Tissue Test, Paradigm Diagnostics, Inc, Paradigm Diagnostics, Inc)
0249U (E/I)	Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report (Theralink Reverse Phase Protein Array (RPPA), Theralink Technologies, Inc,)
0250U (E/I)	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 (PGDx elio tissue complete, Personal Genome Diagnostics, Inc)
0329U (E/I)	Oncology (neoplasia), exome and transcriptome sequence analysis for sequence variants, gene copy number amplifications and deletions, gene rearrangements, microsatellite instability and tumor mutational burden utilizing DNA and RNA from tumor with DNA from normal blood or saliva for subtraction, report of clinically significant mutation(s) with therapy associations (Oncomap ExTra, Exact Sciences, Inc, Genomic Health Inc)

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Code	Description
0334U (E/I)	Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin embedded (FFPE) tumor tissue, DNA analysis, 84 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden (Guardant360 TissueNext, Guardant Health, Inc)
0379U (E/I)	Targeted genomic sequence analysis panel, solid organ neoplasm, DNA (523 genes) and RNA (55 genes) by next-generation sequencing, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutational burden (Solid Tumor Expanded Panel, Quest Diagnostics)
0391U (E/I)	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 (Strata Select, Strata Oncology, Inc)
0414U (E/I)	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 (LungOI, Imagene)
0444U (E/I)	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) (Aventa FusionPlus, Aventa Genomics, LLC)
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)
0473U (E/I)	Oncology (solid tumor), next-generation sequencing (NGS) of DNA from formalin-fixed paraffin-embedded (FFPE) tissue with comparative sequence analysis from a matched normal specimen (blood or saliva), 648 genes, interrogation for sequence variants, insertion and deletion alterations, copy number variants, rearrangements, microsatellite instability, and tumor-mutation burden (xT CDx, Tempus AI, Inc)

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Code	Description
0478U	Oncology (non-small cell lung cancer), DNA and RNA, digital PCR analysis of 9 genes (EGFR, KRAS, BRAF, ALK, ROS1, RET, NTRK 1/2/3, ERBB2, and MET) in formalin-fixed paraffin-embedded (FFPE) tissue, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements, and reported as actionable detected variants for therapy selection (Lung HDPCR, Protean BioDiagnostics)
0481U	IDH1 (isocitrate dehydrogenase 1 [NADP+]), IDH2 (isocitrate dehydrogenase 2 [NADP+]), and TERT (telomerase reverse transcriptase) promoter (e.g., central nervous system [CNS] tumors), next-generation sequencing (single-nucleotide variants [SNV], deletions, and insertions) (IDH1, IDH2, and TERT Mutation Analysis, Next-Generation Sequencing, Tumor (IDTRT), Mayo Clinic, Laboratory Developed Test)
0498U (E/I)	Oncology (colorectal), next-generation sequencing for mutation detection in 43 genes and methylation pattern in 45 genes, blood, and formalin-fixed paraffin-embedded (FFPE) tissue, report of variants and methylation pattern with interpretation (OptiSeq Colorectal Cancer NGS Panel, DiaCarta, Inc)
0499U	Oncology (colorectal and lung), DNA from formalin-fixed paraffin-embedded (FFPE) tissue, next-generation sequencing of 8 genes (NRAS, EGFR, CTNNB1, PIK3CA, APC, BRAF, KRAS, and TP53), mutation detection (OptiSeq Dual Cancer Panel Kit, DiaCarta, Inc)
0523U (E/I)	Oncology (solid tumor), DNA, qualitative, next-generation sequencing (NGS) of single-nucleotide variants (SNV) and insertion/deletions in 22 genes utilizing formalin-fixed paraffin-embedded tissue, reported as presence or absence of mutation(s), location of mutation(s), nucleotide change, and amino acid change (oncoReveal CDx, Pillar Biosciences, Inc)
0538U (E/I)	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 (PredicineATLAS Assay, Predicine Inc) (Effective 04/01/25)

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Code	Description
0543U (E/I)	Oncology (solid tumor), next- generation sequencing of DNA from formalin fixed paraffin embedded (FFPE) tissue of 517 genes, interrogation for single nucleotide variants, multi nucleotide variants, insertions and deletions from DNA, fusions in 24 genes and splice variants in 1 gene from RNA, and tumor mutation burden (TruSight Oncology Comprehensive, Illumina, Inc) (Effective 04/01/25)
0586U (E/I)	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 (RNA Salah Targeted Expression Panel, Moffitt Cancer Center Advanced Diagnostics Laboratory, Laboratory Developed Test) (Effective 10/01/25)

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HCPCS Codes

Code	Description
Not Applicable	

ICD10 Codes

Code	Description
C18.0-C21.8	Malignant neoplasm of colon, rectosigmoid junction, rectum, and anus and anal canal (code range)
C25.0-C25.9	Malignant neoplasm of pancreas (code range)
C34.10-C34.92	Malignant neoplasm of lobe, bronchus, or lung (code range)
C43.0-C43.9	Malignant melanoma of skin (code range)
C50.011-C50.929	Malignant neoplasm of breast (code range)
C56.1-C56.9	Malignant neoplasm of ovary (code range)
C61	Malignant neoplasm of prostate
C71.0-C71.9	Malignant neoplasm of brain (code range)

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Code	Description
C78.5	Secondary malignant neoplasm of large intestine and rectum
C79.60- C79.63	Secondary malignant neoplasm of ovary (code range)
C79.81	Secondary malignant neoplasm of breast
D05.00- D05.02	Lobular carcinoma in situ of breast (code range)
D05.10- D05.12	Intraductal carcinoma in situ of breast (code range)
D05.80- D05.92	Carcinoma in situ of breast, specified, unspecified (code range)
D07.30- D07.39	Carcinoma in situ of other and unspecified female genital organs (code range)
D40.0	Neoplasm of uncertain behavior of prostate

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SEARCH TERMS

Foundation One, Caris Life Sciences, OmniSeq, PyroSeq

CENTERS FOR MEDICARE AND MEDICAID SERVICES (CMS)

[Next Generation Sequencing \(NGS\) \(NCD 90.2\)](#) [accessed 2026 Jan 15]

[Molecular Pathology Procedures \(LCD L35000\)](#) [accessed 2026 Jan 15]

[Molecular Pathology Procedures \(Article-Billing and Coding A56199\)](#) [accessed 2026 Jan 15]

[Genomic Sequence Analysis Panels in the Treatment of Solid Organ Neoplasms \(LCD L37810\)](#) [accessed 2026 Jan 15]

[Genomic Sequence Analysis Panels in the Treatment of Solid Organ Neoplasms \(Article- Billing and Coding A56867\)](#) [accessed 2026 Jan 15]

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- If a Medicare HMO-Dual Special Needs Program (DSNP) product DOES NOT cover a specific service, please refer to the Medicaid Product coverage line.

POLICY HISTORY/REVISION

Committee Approval Dates

12/21/17, 12/21/18, 10/17/19, 12/17/20, 12/16/21, 01/19/23, 01/18/24, 02/20/25, 02/19/26

Date

Summary of Changes

02/19/26

- Annual review, policy intent unchanged.

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09/30/25	<ul style="list-style-type: none">Off-cycle policy review, code edit, added CPT code 0586U. Policy intent unchanged.
02/20/25	<ul style="list-style-type: none">Annual review, policy statements revised with recommended genes, intent unchanged.
01/01/25	<ul style="list-style-type: none">Summary of changes tracking implemented.
12/21/17	<ul style="list-style-type: none">Original effective date