



Medical Coverage Policy

Effective Date12/3/2023

Next Review Date7/15/2024

Coverage Policy Number..... 0520

Molecular and Proteomic Diagnostic Testing for Hematology and Oncology Indications

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Related Coverage Resources

- [Genetics](#)
- [Genetic Testing Collateral File](#)

INSTRUCTIONS FOR USE

The following Coverage Policy applies to health benefit plans administered by Cigna Companies. Certain Cigna Companies and/or lines of business only provide utilization review services to clients and do not make coverage determinations. References to standard benefit plan language and coverage determinations do not apply to those clients. Coverage Policies are intended to provide guidance in interpreting certain standard benefit plans administered by Cigna Companies. Please note, the terms of a customer's particular benefit plan document [Group Service Agreement, Evidence of Coverage, Certificate of Coverage, Summary Plan Description (SPD) or similar plan document] may differ significantly from the standard benefit plans upon which these Coverage Policies are based. For example, a customer's benefit plan document may contain a specific exclusion related to a topic addressed in a Coverage Policy. In the event of a conflict, a customer's benefit plan document always supersedes the information in the Coverage Policies. In the absence of a controlling federal or state coverage mandate, benefits are ultimately determined by the terms of the applicable benefit plan document. Coverage determinations in each specific instance require consideration of 1) the terms of the applicable benefit plan document in effect on the date of service; 2) any applicable laws/regulations; 3) any relevant collateral source materials including Coverage Policies and; 4) the specific facts of the particular situation. Each coverage request should be reviewed on its own merits. Medical directors are expected to exercise clinical judgment where appropriate and have discretion in making individual coverage determinations. Where coverage for care or services does not depend on specific circumstances, reimbursement will only be provided if a requested service(s) is submitted in accordance with the relevant criteria outlined in the applicable Coverage Policy, including covered diagnosis and/or procedure code(s). Reimbursement is not allowed for services when billed for conditions or diagnoses that are not covered under this Coverage Policy (see "Coding Information" below). When billing, providers must use the most appropriate codes as of the effective date of the submission. Claims submitted for services that are not accompanied by covered code(s) under the applicable Coverage Policy will be denied as not covered. Coverage Policies relate exclusively to the administration of health benefit plans. Coverage Policies are not recommendations for treatment and should never be used as treatment guidelines. In certain markets, delegated vendor guidelines may be used to support medical necessity and other coverage determinations.

Overview

This Coverage Policy addresses testing for harmful or likely harmful changes in the genetic information of cells that occur after conception, for selected cancers and blood disorders. These changes, also called variants, are referred to as acquired or somatic. They are not inherited or passed down by blood relatives. The changes may occur in any cell of the human body except the egg or sperm cell. They may increase a person's risk or tendency to have a certain disease or disorder.

Several types of testing are discussed in this Coverage Policy, including testing for a single change in a gene or part of a gene and testing for multiple changes in a gene or genes. Also discussed are tests that measure how a gene is turned on or off, which is referred to as gene expression. Test results can help determine how advanced a disease is and the chance of it coming back. Results can also help decide on a treatment and how well the disease may respond, or is responding to treatment.

Coverage Policy

Coverage for Genetic Testing and Counseling varies across plans. Refer to the customer's benefit plan document for coverage details.

For additional information regarding coverage for specific genetic tests please refer to the [Genetic Testing Collateral: Molecular Tests and Biomarkers](#).

General Criteria for Somatic Pathogenic or Likely Pathogenic Variant Genetic Testing

Medically Necessary

A tissue-based molecular tumor biomarker, broad molecular profile panel or gene expression classifier (GEC) testing is considered medically necessary when ALL of the following criteria are met:

- the individual is a candidate for a targeted therapy associated with a specific tumor biomarker(s) or disease site
- results of testing will directly impact clinical decision making
- the testing method is considered to be scientifically valid and proven to have clinical utility based on prospective evidence
- no other tumor biomarker, broad molecular profile panel or gene expression classifier test has been performed on this tumor sample for the same indication
- disease-specific criteria are not described elsewhere in the Coverage Policy
- ANY of the following:
 - identification of the specific biomarker or risk assessment using a GEC has been validated by the National Comprehensive Cancer Network™ (NCCN Guidelines™) as a category 1, 2A or 2B recommendation for the individual's tumor type of disease
 - identification of the specific biomarker or use of a GEC has been demonstrated in published peer-reviewed literature to improve diagnosis, management or clinical outcomes for the individual's condition being addressed
 - biomarker confirmation is required by a US_Federal Drug Administration (FDA)-approved or cleared test as described within the section heading "Indications and Usage" of the FDA-approved prescribing label prior to initiating therapy
 - broad molecular profile panel testing for EITHER of the following:
 - advanced, metastatic solid tumors
 - ANY of the following hematologic malignancies:
 - acute myeloid leukemia
 - myelodysplastic disease
 - myeloproliferative disease
 - multiple myeloma
 - systemic mastocytosis

Targeted somatic testing for PIK3CA is considered medically necessary when the following criteria are met:

- Post-menopausal female or male with advanced or metastatic, ER/PR positive and HER2 negative breast cancer
- Patient has progressed on endocrine therapy

Targeted molecular testing for NTRK fusions (NTRK1/2/3 fusions) is considered medically necessary when the individual has a solid tumor known to respond to treatment with an FDA approved drug therapy targeting NTRK gene fusions.

Liquid biopsy by cell-free DNA laboratory testing methods (e.g., cDNA, ctDNA) is considered medically necessary when tissue testing is not available or contraindicated for EITHER of the following:

- advanced or metastatic solid tumors
- biomarker confirmation is required by an FDA-approved or cleared test as described within the section heading "Indications and Usage" of the US FDA-approved prescribing label prior to initiating therapy

Testing of bone marrow samples for minimal residual disease (MRD) using high-throughput immunosequencing (e.g., Clonoseq) is considered medically necessary for ANY of the following indications or when designated by NCCN as a category 1, 2A or 2B recommendation:

- multiple myeloma (MM)
- B-cell acute lymphoblastic leukemia (ALL)
- chronic lymphoblastic leukemia (CLL)
- peripheral and cutaneous T-cell lymphoma (TCL)

Other testing (e.g., non-high-throughput immunosequencing) for MRD using a validated technology when recommended by NCCN Guidelines™ as a Category 1, 2A, or 2B recommendation is considered medically necessary.

Not Covered or Reimbursable

Molecular testing for hematology and oncology indications is not covered or reimbursable if the criteria described above are not met.

[Tumor Profile/Gene Expression Classifier Testing](#)

Medically Necessary

Gene expression classifier testing (GEC) is considered medically necessary when ALL of the following criteria are met:

- individual is a candidate for chemotherapy (i.e., chemotherapy not excluded due to other factors)
- adjuvant chemotherapy is being considered and this testing is being ordered to assess recurrence risk
- no other GEC has been performed on this tumor sample for the same indication

and the associated criteria are met for ANY of the following indications:

Test Name	Cancer Type and Indication																
MammaPrint® 70-Gene Breast Cancer Recurrence Assay (CPT code 81521)	<p>For a woman with anatomic stage I or stage 2 invasive breast cancer when ALL of the following criteria are met:</p> <table border="1"> <thead> <tr> <th data-bbox="402 625 646 655">Tumor Grade</th> <th data-bbox="669 625 760 655">Nodes</th> <th data-bbox="782 625 945 655">Tumor Size</th> <th data-bbox="993 646 1448 760"></th> </tr> </thead> <tbody> <tr> <td data-bbox="402 655 646 760">Well differentiated</td> <td data-bbox="669 709 760 760">None 1-3</td> <td data-bbox="782 709 945 760">3.1-5 cm 2.1-5 cm</td> <td data-bbox="993 646 1448 760"> <ul style="list-style-type: none"> • histologic type is ductal/No Special Type (NST), lobular, mixed (ductal/lobular), or micropapillary • high clinical risk of recurrence* </td> </tr> <tr> <td data-bbox="402 760 646 865">Moderately differentiated</td> <td data-bbox="669 823 760 865">None 1-3</td> <td data-bbox="782 823 945 865">2.1-5 cm Any size</td> <td data-bbox="993 793 1448 865"> <ul style="list-style-type: none"> • estrogen receptor (ER)-positive/progesterone receptor (PR)-positive </td> </tr> <tr> <td data-bbox="402 865 646 970">Poorly differentiated or undifferentiated</td> <td data-bbox="669 970 760 1012">None 1-3</td> <td data-bbox="782 970 945 1012">1.1-5 cm Any size</td> <td data-bbox="993 865 1448 970"> <ul style="list-style-type: none"> • human epidermal growth factor receptor 2 (HER2)-negative • up to three positive nodes </td> </tr> </tbody> </table>	Tumor Grade	Nodes	Tumor Size		Well differentiated	None 1-3	3.1-5 cm 2.1-5 cm	<ul style="list-style-type: none"> • histologic type is ductal/No Special Type (NST), lobular, mixed (ductal/lobular), or micropapillary • high clinical risk of recurrence* 	Moderately differentiated	None 1-3	2.1-5 cm Any size	<ul style="list-style-type: none"> • estrogen receptor (ER)-positive/progesterone receptor (PR)-positive 	Poorly differentiated or undifferentiated	None 1-3	1.1-5 cm Any size	<ul style="list-style-type: none"> • human epidermal growth factor receptor 2 (HER2)-negative • up to three positive nodes
Tumor Grade	Nodes	Tumor Size															
Well differentiated	None 1-3	3.1-5 cm 2.1-5 cm	<ul style="list-style-type: none"> • histologic type is ductal/No Special Type (NST), lobular, mixed (ductal/lobular), or micropapillary • high clinical risk of recurrence* 														
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Poorly differentiated or undifferentiated	None 1-3	1.1-5 cm Any size	<ul style="list-style-type: none"> • human epidermal growth factor receptor 2 (HER2)-negative • up to three positive nodes 														
Oncotype DX® for Early- Stage, Invasive Breast Cancer Assay (CPT code 81519)	<p>For recently diagnosed anatomic stage 1 or stage 2 infiltrating breast cancer when ALL of the following criteria are met:</p> <ul style="list-style-type: none"> • histologic type is ductal/NST, lobular, mixed (ductal/lobular), or micropapillary • tumor size 0.6-1.0cm and intermediate or high grade (Grade 2 or 3) OR tumor size 1.1-5.0 cm any grade • estrogen receptor positive and/or progesterone receptor positive • HER2 receptor negative • No evidence of distant metastasis • EITHER of the following criteria: <ul style="list-style-type: none"> ➢ axillary node status is negative (micrometastasis is no greater than 2.0 millimeters) ➢ up to three positive axillary nodes in a post-menopausal woman or a man 																
Prosigna® Breast Cancer Prognostic Gene Signature Assay (PAM50) (CPT Code 81520) EndoPredict® Risk Score (CPT code 81599)	<p>For recently diagnosed anatomic stage 1 or stage 2 breast cancer breast cancer when ALL of the following criteria are met:</p> <ul style="list-style-type: none"> • histologic type is ductal/NST, lobular, mixed (ductal/lobular), or micropapillary • tumor size 0.6-1.0cm and intermediate or high grade (Grade 2 or 3) OR tumor size 1.1-5.0cm any grade • estrogen receptor positive and/or progesterone receptor positive • HER2 receptor negative • Postmenopausal • No evidence of distant metastasis • Axillary node status is negative (micrometastasis is no greater than 2.0 mm) 																

Test Name	Cancer Type and Indication
Breast Cancer Index (BCI) Risk of Recurrence and Extended Endocrine Benefit Test (CPT code 81518)	

Breast Cancer Index (BCI) Risk of Recurrence and Extended Endocrine Benefit Test (CPT code 81518) is considered medically necessary for a woman with early stage T1-T3 breast cancer diagnosed within the last five years when ALL of the following criteria are met:

- estrogen receptor (ER) positive
- human epidermal growth factor receptor 2 (HER2) negative
- no evidence of distant metastasis
- EITHER of the following:
 - axillary node status is negative (micrometastasis no greater than 2.0 mm)
 - axillary node status is positive (LN+ with 1-3 positive nodes)
- no evidence of cancer at the time of testing
- test results will be used to determine treatment management of the individual for extended endocrine therapy after completion of at least four years of endocrine therapy

Experimental/Investigational/Unproven

Gene expression testing for breast cancer is considered experimental, investigational or unproven if the criteria described above are not met.

OncotypeDx Breast DCIS Score test is considered experimental, investigational or unproven.

Proteomic Testing

Proteomic testing is considered medically necessary when ALL of the following criteria are met:

- **results of testing will directly impact clinical decision making**
- **the testing method is considered to be scientifically valid and proven to have clinical utility based on prospective evidence**
- **testing has been validated by the National Comprehensive Cancer Network™ (NCCN Guidelines) as a category 1, 2A or 2B recommendation for the individual's tumor type or disease**
- **disease-specific criteria are not described elsewhere in the Coverage Policy**

Veristat is considered medically necessary for advanced non-small cell lung cancer to determine second-line treatment when ALL of the following criteria are met:

- EGFR variant mutation status is wild-type (i.e., no pathogenic or likely pathogenic variant detected) or unknown
- individual has failed first-line systemic chemotherapy
- test results will be used to decide whether to proceed with erlotinib (Tarceva®) therapy

Proteomic testing is considered experimental, investigational or unproven if the criteria described above are not met.

Circulating Tumor Cells Testing

Medically Necessary

AR-V7 testing from circulating tumor cells is considered medically necessary for a male with metastatic castrate resistant prostate cancer (mCRPC) considering second line therapy when BOTH of the following criteria are met:

- progression on androgen receptor–signaling inhibitor (ARSi) therapy (i.e., enzalutamide (Xtandi), abiraterone (Zytiga))
- nuclear expression of AR-V7 will be assessed to guide subsequent therapeutic decision making

Experimental, Investigational or Unproven

Detection of circulating whole tumor cells for any other indication is considered experimental, investigational or unproven.

Screening and Prognostic Tests for Early Detection of Prostate Cancer

Medically Necessary

The following prostate cancer screening and prognostic genetic tests are considered medically necessary for the early detection of prostate cancer when results will impact medical management and the associated criteria are met:

Name	Cancer Type and Indication
Percent free PSA Prostate Health Index (PHI)™	<ul style="list-style-type: none"> PSA >3.0ng/mL
ExoDX	When EITHER of the following criteria is met: <ul style="list-style-type: none"> PSA >3.0 ng/mL with or without previous benign prostate biopsy suspicious digital rectal exam (DRE)
ProgenSA® PCA3 Assay	When BOTH of the following criteria are met: <ul style="list-style-type: none"> PSA >3.0 ng/mL previous benign prostate biopsy or focal high grade prostatic intraepithelial neoplasia (PIN)

The miR Sentinel™ Prostate Cancer Test (CPT 0343U) (miR Scientific, LLC, New York, NY) for prostate cancer early detection prior to biopsy is not covered or reimbursable.

mRNA gene expression profiling and algorithmic analysis (i.e., 12 genes) (CPT 0011M) to predict high-grade prostate cancer risk score is considered experimental, investigational or unproven.

[Tumor Tissue-Based Molecular and Proteomic Assays for Prostate Cancer](#)

Medically Necessary

The following tumor-based assays for detection of prostate cancer are considered medically necessary when the associated criteria are met:

Test Name	Cancer Type and Indication
Decipher® Prostate Cancer Classifier Assay	ANY of the following: <ul style="list-style-type: none"> PSA persistence after radical prostatectomy (i.e., failure of PSA to fall to undetectable levels after radical prostatectomy) PSA recurrence after radical prostatectomy (i.e., undetectable PSA after radical prostatectomy with a subsequent detectable PSA that increases on two or more determinations) Post-prostate biopsy when the individual is a candidate for active surveillance or definitive therapy for ANY of the following prostate cancer risk types: <ul style="list-style-type: none"> low-risk* favorable intermediate-risk* unfavorable intermediate-risk* high-risk*
Prolaris® Prostate Cancer Test	Post prostate biopsy when the individual is a candidate for active surveillance or definitive therapy for ANY of the following risk types:

Test Name	Cancer Type and Indication
OncotypeDX® Genomic Prostate Score	<ul style="list-style-type: none"> ➤ low-risk* ➤ favorable intermediate-risk* ➤ unfavorable intermediate-risk* ➤ high-risk*
ProMark® Proteomic Prognostic Test	Post prostate biopsy for low risk* or favorable intermediate-risk* prostate cancer when the individual is a candidate for active surveillance or definitive therapy

***Low-risk:** T1-T2a disease AND Gleason score ≤6/grade group 1 AND PSA <10ng/mL
Favorable intermediate-risk: T2b-T2c disease OR Gleason score 3+4=7/grade group 2 OR PSA 10-20 ng/mL AND percentage of positive biopsy cores <50%
Unfavorable intermediate-risk: One or more of the following: 2 or 3 intermediate risk factors, grade group 3, ≥50% biopsy cores positive (e.g., ≥6/12 cores)
High-risk: no very-high-risk features and has exactly one high-risk feature: • cT3a OR • Grade Group 4 or Grade Group 5 OR • PSA >20 ng/mL

Not Medically Necessary

Tumor-based molecular assays for prostate cancer are considered not medically necessary if the criteria described above are not met.

Myeloproliferative Neoplasms

Medically Necessary

Polycythemia Vera (PV)

Genetic testing for JAK2 common variants (CPT code 81270, 81279), MPL common variants (CPT code 81338, 81339), and CALR exon 9 common variants (CPT code 81219) is considered medically necessary for the diagnosis of polycythemia vera (PV) when BOTH of the following criteria are met:

- genetic testing would impact medical management of the individual being tested
- ONE of the following:
 - hemoglobin >16.5 g/dL in men, >16.0 g/dL in women
 - hematocrit >49% in men, >48% in women
 - increased red cell mass (RCM) more than 25% above mean normal predicted value

Essential Thrombocythemia

Genetic testing for JAK2 common variants (CPT code 81270, 81279), MPL common variants (CPT code 81338, 81339), and CALR exon 9 common variants (CPT code

81219) is considered medically necessary for the diagnosis of essential thrombocythemia or thrombocytosis (ET) when BOTH of the following criteria are met:

- results will impact medical management
 - EITHER of the following criteria are met:
 - platelet count $\geq 450 \times 10^9/L$
 - bone marrow biopsy showing proliferation mainly of the megakaryocyte lineage with increased numbers of enlarged, mature megakaryocytes with hyperlobulated nuclei. No significant increase or left shift in neutrophil granulopoiesis or erythropoiesis and very rarely minor (grade 1) increase in reticulin fibers
-

Primary Myelofibrosis (PMF)

Genetic testing for JAK2 common variants (CPT code 81270, 81279), MPL common variants (CPT code 81338, 81339), and CALR exon 9 common variants (CPT code 81219) is considered medically necessary for the diagnosis of primary myelofibrosis (PMF) when BOTH of the following criteria are met:

- results will impact medical management
- primary myelofibrosis is suspected but not confirmed, based on results of conventional testing

ASXL1, EZH2, TET2, IDH1/IDH2, SRSF2, and SF3B1 testing is considered medically necessary for the diagnosis of primary myelofibrosis (PMF) when ALL of the following criteria are met:

- primary myelofibrosis is confirmed or suspected
 - based on clinical findings above criteria are met
 - results will impact medical management.
 - bone marrow findings of megakaryocytic proliferation and atypia, without reticulin fibrosis >grade 1, accompanied by increased age-adjusted bone marrow cellularity, granulocytic proliferation, and often, decreased erythropoiesis
 - testing will be completed on bone marrow sample JAK2, CALR and MPL mutation analysis was previously completed and was negative
-

Chronic Myelogenous Leukemia (CML) and Philadelphia Chromosome Positive (PH+) Acute Lymphoblastic Leukemia (ALL)

BCR-ABL T315-I mutation testing (81401, 81170) is considered medically necessary in individuals with chronic myelogenous leukemia (CML) or Philadelphia chromosome positive (Ph+) acute lymphoblastic leukemia (ALL) when ANY of the following are met:

- inadequate initial response to tyrosine kinase inhibitor therapy (i.e., failure to achieve complete hematological response at 3 months, minimal cytogenetic response at 6 months or major cytogenetic response at 12 months)
- loss of response to tyrosine kinase inhibitor therapy (i.e., hematologic relapse, cytogenetic relapse, loss of major molecular response [MMR])

- progression to accelerated or blast phase CML while on tyrosine kinase inhibitor therapy
-

Occult Neoplasms

Medically Necessary

The following paraneoplastic (onconeural) antibodies are considered medically necessary for the evaluation of neurological symptoms when the diagnosis remains uncertain following conventional work-up and an occult neoplasm is suspected:

- anti-Hu (ANNA-1 [antineuronal nuclear autoantibodies-1])
 - anti-Yo (PCA-1 [Purkinje cell antibody-1])
 - anti-CV2 (CRMP5 [collapsing mediator response protein5])
 - anti-Ri (ANNA-2)
 - anti-MA2 (Ta)
-

Other Tumor Profile Testing

Experimental/Investigational/Unproven

Topographic genotyping for any indication is considered experimental, investigational or unproven.

Adhesive patch gene expression assay for pigmented skin lesions is considered experimental, investigational or unproven.

General Background

For additional information regarding specific genetic tests please refer to the [Genetic Testing Collateral: Molecular Tests and Biomarkers](#).

General Criteria for Somatic Mutation Genetic Testing

Somatic mutations are changes in the DNA of a cell that may occur in any cell of the body except the germ cells (i.e., egg and sperm). Somatic mutations differ from germline mutations, which are passed down by blood relatives; somatic mutations are not inherited. The genetic tests described in this Coverage Policy are used to identify disease-causing somatic mutations or the biological activity of genes originating in a tumor or hematologic malignancy.

Tumor markers, also known as biomarkers, are substances that are produced by certain cells of the body in response to cancer or some noncancerous conditions. Although most tumor markers are made by normal cells as well as by cancer cells, they are produced at much higher levels in cancerous conditions. They can be found in the blood, urine, stool, tumor tissue, or other tissues or bodily fluids of some patients with cancer (National Cancer Institute [NCI], 2022. Tumor marker levels may be useful in determining the extent or stage of disease or recurrence, determining the most effective treatment for a specific disease and how well the disease will respond to treatment.

Published peer-reviewed evidence and professional society/organizational consensus guidelines support testing for certain tumor markers for the screening, staging, diagnosis and management of some types of cancer. However, for other tumor markers there is insufficient evidence to establish clinical utility for informing on improvement of health outcomes.

To have clinical utility the specific gene or gene biomarker for which testing has been requested, or gene expression classifier assay should be demonstrated in the published, peer-reviewed scientific literature in the form of prospective clinical trial data to improve the diagnosis, management, or clinical outcomes for the individual's tumor type or disease when the individual is a candidate for a related therapy. The identification of the gene or biomarker should also be required to initiate a related therapy that has been validated by the NCCN as a Category 1, 2A or 2B Level of Evidence and Consensus recommendation as a standard of care. The NCCN recommendations are defined as: Category 1: Based upon high-level evidence there is uniform NCCN consensus that the intervention is appropriate, Category 2A: Based upon lower-level evidence there is uniform NCCN consensus that the intervention is appropriate, Category 2B: Based upon lower-level evidence there is NCCN consensus that the intervention is appropriate and Category 3: Based upon any level of evidence, there is major NCCN disagreement that the intervention is appropriate.

Multigene panels may also provide important information regarding an individual's tumor type to direct proven therapy or support management changes for hematology-oncology indications. These tests may be clinically useful when sequential testing of individual genes or biomarkers is not feasible because of limited tissue availability, or when urgent treatment decisions are pending and sequential testing would result in a prolonged testing schedule.

There is insufficient evidence in the published, peer-reviewed scientific literature to support molecular testing when the requested gene(s) or biomarker(s) is(are) correlated with a known therapy, but that therapy has not been validated in prospective clinical trials for the specific tumor type or disease site.

Broad Molecular Profile Testing

Broad molecular profile tests, also known as molecular profiling and comprehensive genome profiling panels are large multigene tests which assess multiple genetic alterations simultaneously in a solid tumor. Several laboratory methods may be used to assess the tumor; however, next generation sequencing techniques are most commonly used. Broad molecular tests can identify alterations to base substitutions (substitution of an amino acid), insertions and deletions (amino acids are added or removed from DNA), copy number alterations (sections of DNA are repeated) and rearrangements (amino acids are rearranged in a different order). Broad molecular profile testing may be used with the goal of identifying mutations of interest for which drug therapy may be available or for enrollment in a clinical trial. Limitations to testing include testing for more alterations than have been identified for a specific type of cancer and the identification of variations of unknown significance. Nonetheless, such testing is supported by published professional society guidelines, including from the NCCN as a key component of care for a number of advanced, metastatic, refractory and recurrent cancers.

Biopsy Testing Methods

A biopsy is used as a diagnostic and monitoring tool to identify abnormalities in tissue or blood. A traditional tissue biopsy is used to sample and analyze a solid biological specimen. Tissue biopsy remains the gold standard for the confirmation and diagnosis of disease, including various

cancers. Limitations include patient risk due the invasive nature of the test and limited availability of the tissue sample.

There is increasing use of plasma cell-free DNA testing, also known as a liquid biopsy, which is used to sample and analyze nucleic acids in peripheral circulation, most commonly in plasma. At present there are no standards for analytical performance and no guidelines exist for regarding the recommended performance characteristics. Cell-free DNA testing has a high specificity rate but limitations include a compromised sensitivity with up to a 30% false-negative rate. Such testing may also identify alterations that are unrelated to a lesion of interest. Nonetheless, the use of cell-free DNA testing may be considered appropriate when a patient is medically unfit for invasive tissue sampling or there is insufficient material for analysis in advanced (III or IV), metastatic, recurrent or refractory solid cancers.

Testing for Minimal Residual Disease

Minimal residual disease refers to the presence of leukemic cells below the threshold of detection by conventional morphologic methods. Patients who achieve complete response by morphologic assessment alone can harbor leukemic cells in the bone marrow. Methods frequently utilized include a multiparameter (i.e., at least 6-color) flow cytometry to detect abnormal phenotypes, real-time quantitative polymerase chain reaction (RQ-PCT) assays to detect fusion genes and high-throughput next generation sequencing (NGS)-based assays to detect clonal arrangements (NCCN, 2022). An assay for minimal residual disease by high throughput sequencing methods is currently recommended as clinically useful for multiple myeloma, B-cell acute lymphoblastic leukemia, chronic lymphoblastic leukemia and peripheral and cutaneous T-cell lymphoma (NCCN, 2023; 2022; 2023; 2023).

U.S. Food and Drug Administration (FDA)

FDA approval is not required for the development or marketing of specific gene tumor markers profiling tests, multigene panel tests or gene classifier tests. Many high-complexity tests are laboratory-developed in a Clinical Laboratory Improvement Amendment (CLIA)-certified laboratory. However, a number of devices with reagents that are used to “qualitatively or quantitatively measure, by immunochemical techniques, tumor-associated antigens in serum, plasma, urine, or other body fluids” and intended as an aid in monitoring patients for disease progress or response to therapy or for the detection of recurrent or residual disease” are approved by the FDA 510(k) process (FDA, 2009).

Tumor Profile/Gene Expression Classifier Testing

Gene expression classifier assays identify genetic alterations or biological activity of several genes in a tumor. Such tests may provide a more complete picture of a tumor’s molecular signature and enable a better estimate of the risk of distant recurrence when considered along with other molecular signatures and clinical characteristics (Marrone, 2014). They have been proposed as an adjuvant tool to assist in determining overall survival (OS), recurrence probability, appropriate treatment options and responsiveness to chemotherapy and are not advocated as stand-alone tools. Numerous gene profiling assays are currently marketed for use in the U.S..

Breast Cancer Index (BCI) Risk of Recurrence & Extended Endocrine Benefit Test

BCI (BioTheranostics, Inc, San Diego, CA) is a quantitative molecular assessment of estrogen signaling pathways. According to the manufacturer, BCI is intended for use in an individual diagnosed with estrogen receptor-positive (ER+), lymph node-negative (LN-) or lymph node positive (LN+; with 1-3 positive nodes) early-stage, invasive breast cancer, who are distant recurrence-free. BCI provides a quantitative assessment of the likelihood of both late (post-5

years) and overall (0-10 year) distant recurrence following an initial 5 years of endocrine therapy (LN- patients) or 5 years of endocrine therapy plus adjuvant chemotherapy (LN+ patients), and prediction of likelihood of benefit from extended (>5 year) endocrine therapy. BCI results require correlation with other clinical findings. The NCCN (2023) notes BCI is predictive of benefit of extended adjuvant endocrine therapy and is also prognostic for an individual with node negative or node positive breast cancer. (Category of Evidence 2A).

U.S. Food and Drug Administration (FDA)

BCI has not received U.S. Food and Drug Administration (FDA) approval.

EndoPredict Risk Score

According to the manufacturer, the EndoPredict Risk Score (Myriad Genetics Laboratory, Inc., Salt Lake City, UT), is a 12 gene next-generation breast cancer recurrence test that integrates biology and pathology to accurately predict early and late (5-15 years) recurrence with an individualized absolute chemotherapy benefit. The test is intended for use for patients diagnosed with ER+, HER2- early-stage breast cancer with either node-negative or node-positive disease (1- 3 nodes). The NCCN (2019) notes that EndoPredict is a prognostic assay for consideration for addition of adjuvant systemic chemotherapy to adjuvant endocrine therapy; however, predictive value has not yet been determined (Category of Evidence 2A). The NCCN (2023) noted EndoPredict is a prognostic assay; however, predictive value has not yet been determined (Category of Evidence 2A).

U.S. Food and Drug Administration (FDA)

EndoPredict has not received U.S. FDA approval.

MammaPrint® 70-Gene Breast Cancer Recurrence Assay

The MammaPrint® 70-Gene Breast Cancer Recurrence Assay (Agendia, Inc. USA, Irvine, CA) utilizes a deoxyribonucleic acid (DNA) microarray assay to perform 70-gene profiling of breast cancer tissue to assess risk of recurrence. The assay is designed to determine the expression of specific genes in a tissue sample. The result is an expression profile, or “fingerprint”, of the sample. The MammaPrint Index is calculated from fresh, frozen or formalin-fixed paraffin embedded (FFPE) breast cancer tissue and the molecular prognosis profile of the sample is determined (i.e., Low Risk, High Risk) (FDA, 2015).

The test has been validated in an individual being considered for adjuvant systemic therapy with Stage I or Stage 2 invasive breast cancer who has estrogen receptor (ER) positive/progesterone receptor (PR) positive, human epidermal growth factor receptor 2 (HER2)-negative disease, and up to three positive lymph nodes, when there is a high clinical risk of recurrence:

Tumor Grade	Nodes	Tumor Size
Well differentiated	None	3.1-5 cm
	1-3	2.1-5 cm
Moderately differentiated	None	2.1-5 cm
	1-3	Any size
Poorly differentiated or undifferentiated	None	1.1-5 cm
	1-3	Any size

The NCCN (2023) notes that Mammoprint is a prognostic assay for consideration for addition of adjuvant systemic chemotherapy to adjuvant endocrine therapy; however, predictive value has not yet been determined (Category of Evidence 2A). There is consensus support in the form of

published guidelines by the American Society of Clinical Oncology ([ASCO], 2017) for the use of MammaPrint to inform decisions on withholding adjuvant systemic chemotherapy due to its ability to identify a good prognosis population with potentially limited chemotherapy benefit.

U.S. Food and Drug Administration (FDA)

MammaPrint® 70-Gene Breast Cancer Recurrence Assay (Agendia, Inc. USA, Irvine, CA) received a 510K approval for an individual with Stage I or Stage II lymph node negative breast cancer with a tumor size ≤ 5.0 cm. According to the FDA approval summary, MammaPrint FFPE is not indicated as a standalone test to determine the outcome of disease, nor to suggest or infer an individual's likely response to therapy. Results should be taken in the context of other relevant clinicopathological factors and standard practice of medicine (2015).

Oncotype DX® for Early-Stage, Invasive Breast Cancer Assay

According to the manufacturer (Genomic Health, Inc., Redwood City, CA), this test is recommended for use after the original breast cancer surgery and is proposed for a newly diagnosed individual with node-negative or node-positive, ER-positive, HER2-negative invasive breast cancer. The purpose of the Oncotype DX Breast Cancer Assay is to quantify the likelihood of distant recurrence (i.e., within 10 years) in a woman or a man with breast cancer, and is used as one factor in determining whether or not a patient is a candidate for chemotherapy. This assay is not proposed for or used as a test to monitor the response of a specific chemotherapy drug.

Using tumor tissue, ribonucleic acid (RNA) is extracted, purified and analyzed for expression of a panel of 21 genes using quantitative reverse transcription polymerase chain reaction (RT-PCR) on formalin-fixed, paraffin-embedded (FFPE) tumor tissue. A Recurrence Score™ (RS) is calculated from the gene expression results using a proprietary Oncotype DX algorithm. The RS is based on a scale of 0–100. A score of less than 18 is considered low-risk; 18-31 is intermediate-risk; and a score over 31 is designated as high-risk. Each RS correlates with a specific likelihood of distant recurrence at 10 years. This test is recommended by the American Society of Clinical Oncology (ASCO) (2016) and NCCN (2023) for use in a select population of women with breast cancer. NCCN notes OncotypeDx is both a predictive and prognostic assay for consideration of addition of adjuvant systemic chemotherapy to adjuvant endocrine therapy for node negative disease (Category of Evidence 1). For node positive disease NCCN notes the test is prognostic but predictive value has not yet been determined (Category of Evidence 2A).

US Food and Drug Administration (FDA)

Oncotype DX has not received U.S. Food and Drug Administration (FDA) approval. The assay is performed in the licensed Genomic Health laboratory where the assay was developed.

Prosigna® Breast Cancer Prognostic Gene Signature Assay: Prosigna® (NanoString Technologies, Seattle, WA) is an in vitro diagnostic assay which is performed on the NanoString nCounter® Dx Analysis System using formalin-fixed paraffin embedded (FFPE) breast tumor tissue previously diagnosed as invasive breast carcinoma. It is designed to identify intrinsic breast cancer subtypes (i.e., luminal A/B, HER2 enriched, basal like) and generate a Risk of Recurrence (ROR) score, expressed as a numerical value (0-100 scale) which correlates with the probability of distant recurrence within 10 years. The Prosigna Risk of Recurrence (ROR) score is generated by Prediction Analysis of Microarray (PAM50) proprietary algorithm (NanoString Technologies, 2014-2019).

The NCCN (2023) notes that Prosigna is a prognostic assay for consideration of the addition of adjuvant systemic chemotherapy to adjuvant endocrine therapy. The predictive value has not yet been determined (Category of Evidence 2A).

U.S. Food and Drug Administration (FDA)

Prosigna received FDA 501K approval in September, 2013. According to the FDA, the Prosigna Breast Cancer Prognostic Gene Signature Assay is indicated in female breast cancer patients who have undergone surgery in conjunction with locoregional treatment consistent with standard of care, either as:

- A prognostic indicator for distant recurrence-free survival at 10 years in postmenopausal women with Hormone Receptor-Positive (HR+), lymph node-negative, Stage I or II breast cancer to be treated with adjuvant endocrine therapy alone, when used in conjunction with other clinicopathological factors.
- A prognostic indicator for distant recurrence-free survival at 10 years in postmenopausal women with Hormone Receptor-Positive (HR+), lymph node-positive (1-3 positive nodes), Stage III breast cancer to be treated with adjuvant endocrine therapy alone, when used in conjunction with other clinicopathological factors.

Prosigna is not intended for diagnosis, to predict or detect response to therapy, or to help select the optimal therapy for patients. The device is not intended for patients with four or more positive nodes. The role of Prosigna for women with node positive disease has not yet been established.

Proteomic Testing

Proteomics involves the quantitative and qualitative study of proteins, including the function, composition and structure and the way they interact inside cells. Protein expression may be changed by environmental conditions.

Proteomics can identify and monitor biomarkers by analyzing the proteins in body fluids such as urine, serum, exhaled breath and spinal fluid. Proteomics can also facilitate drug development by providing a comprehensive map of protein interactions associated with disease pathways. A proteomic profile may be used to find and diagnose a disease or condition and to see how well the body responds to treatment (National Cancer Institute [NCI], 2023).

To be clinically useful the testing method must be scientifically and clinically validated and proven to have clinical utility based on prospective evidence, testing must be validated by the National Comprehensive Cancer Network™ (NCCN Guidelines) as a category 1, 2A or 2B recommendation for the individual's tumor type or disease and results of testing must directly impact clinical decision making.

VeriStrat® Proteomic Testing

VeriStrat® (Biodesix, Boulder, CO) is not an EGFR mutation test. It is a serum protein analysis for advanced non-small cell lung cancer (NSCLC) and has been proposed as a means to identify individuals who should receive treatment with erlotinib (Tarceva®, Genentech, San Francisco, CA), an epidermal growth factor inhibitor (EGFRI). According to the Biodesix website, the test stratifies individuals who are likely to have good or poor outcomes with EGFRI treatment (2015). The analysis utilizes matrix-assisted laser desorption/ionization mass spectrometry to analyze serum for eight discriminating features. The test has an established prediction algorithm which was validated in two separate populations. Classifications based on spectra acquired at the two institutions had a concordance of 97.1%. (Taguchi, 2007). According to the manufacturer, results are predictive of outcomes, independent of ECOG performance status, PD-L1 expression, mutation status, and treatment choice.

The clinical utility of VeriStrat has been validated in both retrospective and prospective trials as a means to identify an individual who should receive treatment with erlotinib (Tarceva[®], Genentech, San Francisco, CA), an epidermal growth factor inhibitor (EGFRI).

US Food and Drug Administration

VeriStrat has not received U.S. Food and Drug Administration (FDA) approval.

Literature Review

The clinical utility of VeriStrat is supported by prospective and retrospective clinical trial evidence in the published, peer-review scientific literature. The utility of VeriStrat as compared to standard KRAS and EGFR mutation analysis was performed on 102 samples by Amann et al (2010). VeriStrat classification identified 64 of 88 (73%) as predicted to have "good" and 24 of 88 (27%) predicted to have "poor" outcomes. Statistically significant correlation to VeriStrat status and clinical survival outcome was demonstrated ($p < 0.001$).

Cost utility analysis of applying VeriStrat to guide treatment for NSCLC patients was compared to all patients receiving treatment with EGFRI, all patients receiving chemotherapy; and treatment determined by performance status. Patients where treatment was guided by VeriStrat showed the second best survival outcome (9.6 months) when compared to chemotherapy only (10.1 months); Performance status indicated (9.2 months) and EGFRI only (8.2 months) (Nelson, 2013).

Carbone et al. (2012) reported results of a retrospective analysis of 436 patient samples with NSCLC that were tested in patients treated with erlotinib and those on placebo. VeriStrat status was prognostic for overall survival and progression free survival, independent of clinical features ($p = 0.002$); however, it was not predictive of differential survival from erlotinib over placebo ($p = 0.48$). Similar results were found for progression-free survival. Data suggest a predictive effect of VeriStrat for response to erlotinib.

Subsequent studies have also sought to determine the predictive value of VeriStrat testing. Sun et al (2014) conducted a meta-analysis of current relevant publications. Eleven cohorts involving 706 patients collected from seven studies were subjected to final analysis. The statistical analysis of these articles found that the test's "good" status predicted better clinical outcome for overall and progression free survival ($p < 0.001$ for both overall and progression-free survival).

A blinded randomized clinical trial by Gregorc et al. (2014) analyzed data collected through PROSE, a biomarker-stratified randomized phase III trial of 285 patients with stage IIIB or IV NSCLC from 14 centers across Italy. The proteomic test classification was masked for patients and investigators who gave treatments, and treatment allocation was masked for investigators who generated the proteomic classification. The primary endpoint was overall survival and the primary hypothesis was the existence of a significant interaction between the serum protein test classification and treatment. A significant interaction between treatment and proteomic classification was noted. Patients who were classified as "poor" in regards to their serum protein test status (30% of participants) were more likely to have better outcomes on chemotherapy than on erlotinib ($p = 0.022$). The data suggests that this subset of patients should not receive erlotinib. This supports the use of a multivariate serum protein test in predicting overall survival for erlotinib versus chemotherapy in second-line therapy. However, there was no difference in treatment observed for patients with the classification of "good" ($p = 0.714$). Although the study demonstrates which patients will not benefit from treatment with erlotinib ("poor" status), additional studies are needed to determine the best treatment option for patients with "good" status.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding gene expression classifier tests please click [here](#).

Circulating Whole Tumor Cell Testing

Circulating whole tumor cells (CTCs) have been found in the peripheral blood circulation of individuals with various forms of metastatic cancer. CTCs are whole cells that have been shed by the tumor. The detection and testing of these tumor cells has been proposed as a method to stratify risk, monitor progression and monitor response to treatment.

The use of circulating whole tumor cell testing has not been proven to impact meaningful health outcomes for most cancers. There is limited evidence to establish the clinical significance of circulating whole tumor cells and how identification can improve health outcomes. Pilot studies suggest that the identification of whole tumor cells may have a role in risk stratification and monitoring responses to treatment.

However, the National Comprehensive Cancer Network® (NCCN®) recommends testing for the androgen receptor splice variant 7 (AR-V7)(2022) in circulating tumor cells. Lack of response of men with metastatic castrate-resistant prostate cancer is associated with detection of this biomarker. NCCN notes that testing in circulating tumor cells can be considered to help guide selection of therapy considering second line therapy when there is progression on androgen receptor–signaling inhibitor (ARSi) therapy (2A: Based upon lower-level evidence there is uniform NCCN consensus that the intervention is appropriate).

With the exception of testing for the AR-V7 variant in metastatic castrate-resistant prostate cancer the role of this testing in patient management is not yet known. Larger longitudinal studies with standard techniques in clearly-defined populations of patients are needed to establish the role of such testing.

Literature Review

Breast Cancer

Smerage et al. (2014) reported on a randomized trial of patients with persistent increase in CTCs that were tested to determine whether changing chemotherapy after one cycle of first-line chemotherapy would improve the primary outcome of overall survival (OS). Five hundred ninety-five Female patients were included with histologically confirmed breast cancer and clinical and/or radiographic evidence of metastatic disease. Patients who underwent chemotherapy had evaluation for CTCs at baseline and then after one cycle. Women whose CTCs remained elevated after the first cycle of therapy (arm C) (n=123) were randomly assigned to either maintain the initial treatment plan (n=64) or to change of chemotherapy (n=59). Changing to an alternate regimen had no difference in OS compared with continuation of the initial regimen (median 12.5 versus 10.7 months, respectively, P= .98). The CTCs did appear to have prognostic value: the median OS for arms A, B, and C were 35 months, 23 months, and 13 months, respectively). While it appears that there is prognostic value of CTCs, the role in clinical management is has not been demonstrated.

Zhang et al. (2012) reported on a meta-analysis of published literature on the prognostic relevance of CTC, including patients with early and advanced disease. Forty-nine eligible studies with 6,825 patients were identified. The main outcomes analyzed were overall survival (OS) and disease-free survival (DFS) in early-stage breast cancer patients, as well as progression-free survival (PFS) and OS in metastatic breast cancer patients. Pooled hazard ratio (HR) and 95% confidence intervals (CIs) were calculated using the random and the fixed-effects models. The presence of CTC was significantly associated with shorter survival in the total population. The

prognostic value of CTC was significant in both early (DFS: HR, 2.86; 95% CI, 2.19–3.75; OS: HR, 2.78; 95% CI, 2.22–3.48) and metastatic breast cancer (PFS: HR, 1.78; 95% CI, 1.52–2.09; OS: HR, 2.33; 95% CI, 2.09–2.60). Subgroup analyses showed that our results were stable irrespective of the CTC detection method and time point of blood withdrawal. The authors conclude that the meta-analysis indicates that the detection of CTC is a stable prognosticator in patients with early-stage and metastatic breast cancer; however further studies are required to explore the clinical utility of CTC in breast cancer.

A prospective observational study that compared serum marker levels with CTC in 267 metastatic breast cancer patients (Bidard, et al., 2012). The secondary pre-planned endpoint a study that previously reported on CTC as prognostic factor (Pierga, et al., 2011), compared prospectively the positivity rates and the value of CTC (CellSearch), of serum tumor markers (carcinoembryonic antigen (CEA), cancer antigen 15.3 (CA 15-3), CYFRA 21-1), and of serum non-tumor markers (lactate dehydrogenase (LDH), alkaline phosphatase (ALP)) at baseline and under treatment for PFS prediction, independently from the other known prognostic factors, using univariate analyses and concordance indexes. The study reported that a total of 90% of the patients had at least one elevated blood marker. The blood markers were correlated with poor performance status, high number of metastatic sites and with each other. CYFRA 21-1, a marker usually used in lung cancer, was elevated in 65% of patients. A total of 86% of patients had either CA 15-3 and/or CYFRA 21-1 elevated at baseline. Each serum marker was associated, when elevated at baseline, with a significantly shorter PFS. Serum marker changes during treatment, assessed either between baseline and the third week or between baseline and weeks six-nine, were significantly associated with PFS, as reported for CTC. Concordance indexes comparison showed no clear superiority of any of the serum marker or CTC for PFS prediction. The authors concluded that for the purpose of PFS prediction by measuring blood marker changes during treatment, currently available blood-derived markers (CTC and serum markers) had globally similar performances. There was no clear superiority found of CTC over the other serum markers.

Liu et al. (2009) conducted on a prospective study that examined the correlation of CTCs with radiographic findings for disease progression. Serial CTC levels were obtained in patients (n=68) that were starting a new treatment regimen for progressive, radiographically measurable metastatic breast cancer. Blood was collected at baseline and three to four week intervals and radiographic studies were performed in nine to twelve week intervals. Median follow-up was 13.3 months. Patients who had five or more CTCs had 6.3 times the odds of radiographic disease progression when compared with patients who had less than five CTCs. Shorter progression-free survival was observed for patients with five or more CTCs at three to five weeks and at seven to nine weeks after the start of treatment. The CTC result was statistically significantly associated with disease progression for all patients ($p < .001$). The association was noted to remain strong in patients treated with either chemotherapy or endocrine therapy. Potential limitations of the study include that the study included patients receiving various lines and types of therapy. The subgroup analysis for CTC-imaging correlation was performed by including biologic agents with either chemotherapy or endocrine therapy—it was noted that each group was too small to be analyzed alone.

Nole et al. (2007) conducted a prospective study to evaluate the prognostic significance of CTCs detection in advanced breast cancer patients. The study included 80 patients with inclusion criteria: women with histological diagnosis of breast cancer, evidence of metastatic disease from imaging studies, starting a new line of therapy and/or treated for the advanced disease with a maximum two lines of therapy. The CellSearch system was used to test for circulating tumor cell levels before starting a new treatment and after four, eight weeks and the first clinical evaluation and every two months thereafter. At baseline, 49 patients were found to have ≥ 5 CTCs. The baseline number of CTCs were associated with progression-free survival (hazard ratio [HR] 2.5; 95% confidence interval [CI] 1.2–5.4). The risk of progression for patients with CTCs ≥ 5 at the

last available blood draw was five times the risk of patients with 0–4 CTCs at the same time point (HR 5.3; 95% CI 2.8–10.4). At the last available blood draw, patients with rising or persistent CTCs ≥ 5 demonstrated a statistically significant higher risk of progression with respect to patients with CTCs < 5 at both blood draws (HR 6.4; 95% CI 2.8–14.6). The authors noted that these results indicate that elevated CTCs levels measured at any time in the clinical course of a patient with metastatic breast cancer predict an imminent progression and that this analysis represents an additional step in the process of validating this method. There are still unanswered questions regarding the treatment of a patient with low or high levels of CTCs in breast cancer.

Prostate Cancer

Folkersma et al. (2012) reported on a prospective study that analyzed the correlation between circulating tumor cell (CTC) levels and clinicopathologic parameters (prostate-specific antigen [PSA] level, Gleason score, and TNM stage) in patients with metastatic hormone-sensitive prostate cancer (PCa) and to establish its prognostic value in overall survival (OS) and progression-free survival (PFS). The study included three arms: 30 patients with localized PCa; 30 patients with metastatic PCa; and, 30 healthy volunteers. The median follow-up was 42.9 months. A significant positive correlation was demonstrated between the CTC level and all tumor burden markers (PSA and T, N, and M stage; $P < .001$), except for Gleason score ($\text{tau} = 0.16$). A cutoff of ≥ 4 CTCs/7.5 mL was chosen to distinguish patients with a poor prognosis. These patients had a significantly shorter median OS and PFS (24 compared to 45 months and 7 compared to 44 months, respectively; $P < .001$). As the CTC level increased, the OS and PFS were noted to decrease. The risk of mortality and progression for the patients with ≥ 4 CTCs was 4.1 ($P = .029$) and 8.5 ($P < .001$) times greater. Multivariate analyses indicated that a CTC of ≥ 4 was an independent prognostic factor for PFS (hazard ratio 5.9, $P < .005$).

Several observational studies have been published that correlate CTC with disease status and progression in prostate cancer (Goodman, et al. 2009; Okegawa, et al., 2009; Okegawa, et al., 2008; Scher, et al., 2009; Olmos, et al., 2009; Danila, et al., 2007; and Shaffer, et al., 2007; Moreno, et al., 2005).

Colorectal Cancer

Groot Koerkamp et al. (2013) reported on systematic review of studies that investigated the prognostic value of tumor cells in blood (CTCs) or bone marrow (BM) (disseminated tumor cells [DTC]) of patients with resectable colorectal liver metastases or widespread metastatic colorectal cancer (CRC). A total of 16 studies with 1,491 patients were included in the review and the results of 12 studies (1,329 patients) included in the meta-analysis. Eight studies used RT-PCR methodology to detect tumor cells, nine studies applied immunocytochemistry (five with CellSearch) and one study applied both methods. The overall survival (hazard ratio [HR], 2.47; 95 % CI 1.74–3.51) and progression-free survival (PFS) (HR, 2.07; 95 % CI 1.44–2.98) were worse in patients with CTCs. The subgroup of studies with more than 35% CTC-positive patients was the only subgroup with a statistically significant worse PFS. The eight studies that had multivariable analysis identified the detection of CTCs as an independent prognostic factor for survival. Limitations of the study included a considerable degree of interstudy heterogeneity. The study does not demonstrate the clinical utility of CTC detection, or that the detection of CTCs is a predictive factor, or identify patients that may benefit from a specific treatment. Further studies are needed to investigate the clinical utility of detection of CTCs in metastatic colorectal cancer.

Sastre et al. (2012) reported on an ancillary study of 180 patients that was a subset of a phase III study (The Maintenance in Colorectal Cancer trial) that assessed maintenance therapy with single-agent bevacizumab versus bevacizumab plus chemotherapy in patients with metastatic colorectal cancer. The ancillary study was conducted to evaluate CTC count as a prognostic and/or predictive marker for efficacy endpoints. Blood samples were obtained at baseline and after three cycles.

CTC enumeration was performed with CellSearch System. The study found that the median progression-free survival (PFS) interval for patients with a CTC count ≥ 3 at baseline was 7.8 months, as compared to 12.0 months found in patients with a CTC count < 3 ($p=.0002$). The median overall survival (OS) time was 17.7 months for patients with a CTC count > 3 , compared with 25.1 months for patients with a lower count ($p=.0059$). After three cycles, the median PFS interval for patients with a low CTC count was 10.8 months, which was noted to be longer than the 7.5 months for patients with a high CTC count ($p=.005$). The median OS time for patients with a CTC count < 3 was significantly longer than for patients with a CTC count ≥ 3 , 25.1 months compared to 16.2 months, respectively ($p=.0095$). Further studies are needed to identify the role of CTC in treatment of metastatic colorectal cancer.

Thorsteinsson et al. (2011) conducted a review of studies of CTCs in colorectal cancer (CRC). Nine studies were included in the review. Detection rates of CTC in peripheral blood of patients with non-metastatic CRC varied from 4% to 57%. Inclusion criteria included: patients diagnosed with non-metastatic colorectal cancer; CTC detected in peripheral blood samples; pre- and/or post-operative blood samples; and, samples size of more than 99 patients. Seven studies applied RT-PCR and two studies used immunocytochemical methods. Seven studies found the presence of CTC to be a prognostic marker of poor disease-free survival. The authors concluded that the presence of CTC in peripheral blood is a potential marker of poor disease-free survival in patients with non-metastatic CRC and that the low abundance of CTC in non-metastatic CRC needs very sensitive and specific detection methods. They also noted that an international consensus on choice of detection method and markers is warranted before incorporating CTC into risk stratification in the clinical setting.

Rahbari et al. (2010) reported on a meta-analysis of studies to assess whether the detection of tumor cells in blood and bone marrow of patients diagnosed with colorectal cancer (CRC) can be used as a prognostic factor. Thirty-six studies were included in the review that examined the detection of free blood or bone marrow tumor cells with patients prognosis and included various methods of techniques (e.g., reverse transcriptase-PCR [RT-PCR]) and immunologic). The review indicated that the presence of CTCs detected in peripheral blood is of strong prognostic significance in patients with CRC. There was considerable interstudy heterogeneity noted in regards to differences in the detection methods, types and numbers of target genes or antigens, sampling site and time, and in demographic or clinicopathologic status of patients.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding circulating tumor cells please click [here](#).

Screening and Prognostic Tests for Early Detection of Prostate Cancer

Prostate specific antigen (PSA), an organ-specific marker, is often used as a tumor marker. The higher the level of PSA at baseline, the higher is the risk for metastatic disease or subsequent disease progression. However, it is an imprecise marker of risk. Various approaches aimed at improving the performance of PSA in early cancer detection have been tested, including the measurement of prostate biomarkers. None are clearly more accurate than total serum PSA levels (National Cancer Institute [NCI], 2023). According to the National Comprehensive Cancer Network Guideline (NCCN Guidelines™) for Prostate Cancer Early Detection (2023), tests that have been shown to increase specificity in the post-biopsy state are percent free PSA (%fPSA), 4Kscore (OPKO Health, Inc., Miami, FL), Prostate Health Index (PHI), (Beckman Coulter, Atlanta, GA) , prostate cancer gene 3 (PCA3, Progenesa® PCA3, Gen-Probe, Inc., San Diego, CA), ConfirmMDx for

Prostate Cancer (MDX Health, Irvine, CA), Select MDx (MDx Health, Irvine, CA) and the ExoDx (Bio-Techne, Waltham, MA) tests.

The NCCN also notes that biomarkers that improve the specificity of detection are for use in those individuals who wish to further define the probability of high-grade cancer. Improved specificity post biopsy has been demonstrated in the published-peer-reviewed scientific literature.

The 4Kscore, percent free PSA, Prostate Health Index (PHI), Select MDx and ExoDx tests are considered clinically useful when results of the tests will impact management and there is a PSA >3 ng/mL with or without a previous benign biopsy and a suspicious digital rectal exam. Along with the 4K Score test, %free PSA and Prostate Health Index, ProgenSA PCA3, ConfirmMDx tests may be clinically useful when results of testing will impact management, the PSA >3 ng/mL and previous biopsy results are benign or indicate focal high-grade prostatic intraepithelial neoplasia (PIN). The role of these tests for any other indication or clinical scenario has not been established.

Percent Free PSA (% free PSA): Serum PSA exists in both free form and complexed to a number of protease inhibitors. Assays for total PSA measure both free and complexed forms. Percent-free PSA may be related to biologic activity of the tumor. The NCCN (2023) notes that unbound or free PSA, expressed as a ratio of total PSA is clinically useful with the potential to improve early detection, staging and monitoring of prostate cancer. According to the NCCN, this test has received widespread clinical acceptance, specifically for patients with suspicious digital rectal exams who have previously undergone prostate biopsy because they had a total PSA (tPSA) level within the diagnostic gray zone. % free PSA may also be clinically useful to detect prostate cancer when the PSA is >3.0 ng/mL and a previous biopsy is benign or reflects PIN.

4Kscore: This test combines four prostate-specific kallikrein assay results with clinical information in an algorithm that calculates the individual patient's percent risk for aggressive prostate cancer. It also considers age, digital rectal exam results and prior biopsy status. According to the manufacturer's website, the 4Kscore is not indicated for men who have a diagnosis of prostate cancer, are taking or have taken 5-alpha reductase inhibitors within the last 6 months or have recently undergone a prostate procedure within the last 6 months. This test is a laboratory developed test and is not FDA approved. According to the NCCN Guidelines™ (2023), the test can be considered for patients prior to biopsy and for those with prior negative biopsy for those thought to be at higher risk for clinically significant prostate cancer, such as an individual with a suspicious digital rectal exam. No cut-off threshold has been established for the 4Kscore. The 4K Score test may also be clinically useful to detect prostate cancer when the PSA is >3.0 ng/mL and a previous biopsy is benign or reflects PIN.

ConfirmMDx® for Prostate Cancer: This test is a tissue-based epigenetic assay which aids in the stratification of men being considered for repeat prostate biopsy. The test uses DNA methylation to assess the presence of cancer biomarkers (i.e., GSTP1, APC, RASSF1) in core biopsy tissue samples. ConfirmMDx is a laboratory developed test and is not FDA approved.

ExoDx: According to the manufacturer, this test is a urine-based, liquid biopsy test indicated for men 50 years of age and older with a prostate-specific antigen (PSA) 2-10ng/mL, or PSA in the "gray zone", considering an initial biopsy. The ExoDx Prostate test returns a risk score that

determines a patient's risk of clinically significant prostate cancer (Gleason Score ≥ 7) on prostate biopsy. A score above the validated cut-point of 15.6 is associated with an increased likelihood of $GS \geq 7$ PCa on a biopsy and a score below the cut-point of 15.6 is associated with a decreased likelihood of $GS \geq 7$ PCa. NCCN Guidelines (2023) note this test may be clinically useful if the individual has a PSA >3.0 ng/mL with or without previous benign prostate biopsy and a suspicious DRE result.

Progenesa® PCA3: Progenesa PCA3 is an in vitro nucleic acid amplification test. The assay measures the concentration of prostate cancer gene 3 (PCA3) and prostate-specific antigen (PSA) RNA (RNA) molecules and calculates the ratio of PCA3 RNA molecules to PSA RNA molecules (PCA3 Score) in post digital rectal exam (DRE) first catch male urine specimens. U.S. Food and Drug Administration (FDA): According to the U.S. Food and Drug Administration ([FDA], 2012) it is intended for use in conjunction with other patient information to aid in the decision for repeat biopsy in men 50 years of age or older who have had one or more previous negative prostate biopsies and for whom a repeat biopsy would be recommended by a urologist based on current standard of care, before consideration of Progenesa PCA3 Assay results.

Prostate Health Index (PHI)™: This test is a combination of existing tests (Access Hybritech PSA, Access Hybritech free PSA, and Access Hybritech p2PSA, Beckman Coulter, Atlanta, GA) for total PSA, free PSA and proPSA. According to the manufacturer's website, a proprietary algorithm provides a probability of prostate cancer. PHI results are intended to be used as an aid in distinguishing prostate cancer from benign prostatic conditions in men 50 years of age and older with total PSA results in the 4 – 10 ng/mL range and suspicious digital rectal examination (DRE) findings. The three assays that make up this test have received FDA approval with numerous supplements. The NCCN (2023) also notes this test may be clinically useful to detect prostate cancer when the PSA is >3.0 ng/mL and a previous biopsy is benign or reflects PIN.

Select MDx: According to the manufacturer website, this test is a non-invasive urine test ("liquid biopsy"). SelectMDx measures the expression of two mRNA cancer-related biomarkers (HOXC6 and DLX1). The test provides binary results that, when combined with the patient's clinical risk factors, help the physician determine whether the patient may benefit from a biopsy or can return to routine screening. NCCN (2023) notes this test may be clinically useful if the individual has a PSA >3.0 ng/mL with or without previous benign prostate biopsy and a suspicious DRE result.

Professional Society/Organizations

Each of these tests is specifically mentioned in the NCCN Guideline for Prostate Cancer Early Detection as a category 2A recommendation. For additional information regarding professional society recommendations please click [here](#).

[Tumor Tissue-Based Molecular and Proteomic Assays for Detection of Prostate Cancer](#)

The NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines™) for Prostate Cancer (2022) notes that although risk groups, life expectancy estimates and nomograms help inform treatment decisions, there remains uncertainty regarding the risk of disease progression. Several tumor tissue-based molecular assays have been included in the guideline for prostate cancer (2022). The

guideline notes that men with low or favorable intermediate risk may consider the use of certain molecular tests (i.e., Decipher[®], OncotypeDx Genomic Prostate Score[®], Prolaris[®] Prostate Cancer Test, ProMark Proteomic Prostate Test), which are briefly reviewed in this section of the Coverage Policy.

Although these tests have not been validated by prospective, randomized clinical trial data, retrospective case cohort studies demonstrate that these tests provide prognostic information independent of NCCN risk groups for men with low or favorable intermediate risk disease, including likelihood of death with conservative management, likelihood of biochemical recurrence after radical prostatectomy or radiotherapy and likelihood of developing metastasis after operation or salvage radiotherapy (NCCN, 2019).

Decipher[®] Prostate Cancer Classifier Assay (GenomeDx, San Diego, CA): This test is a 22 biomarker genomic expression classifier assay which uses formalin-fixed paraffin embedded (FFPE) tissue from a radical prostatectomy specimen to predict the probability of metastasis and tumor aggressiveness. Decipher is listed as a Category 2B recommendation in the NCCN Practice Guidelines in Oncology for Prostate Cancer (2022) as an option following radical prostatectomy with PSA persistence/recurrence defined as failure of PSA to fall to undetectable levels (PSA persistence) or undetectable PSA after radical prostatectomy with a subsequent PSA that increases on two or more determinations (PSA recurrence). The Guideline also notes that Decipher may be used in men with low-risk prostate cancer, defined as T1-T2a disease, Gleason score ≤6/grade group 1 and a PSA <10ng/mL and those with favorable intermediate-risk disease, defined as T2b-Tc disease, Gleason score 3+4=7/grade group 2, PSA 10-20 ng/mL and percentage of positive biopsy cores <50%. It may also be clinically useful for an individual with unfavorable intermediate-risk, defined as one or more of the following: two or three risk factors, grade 3 Gleason group, ≥50% biopsy cores positive (e.g., ≥6/12 cores) or with high-risk type, defined as an individual with no very-high-risk features and has exactly one high-risk feature: cTA3a OR Gleason group 4 or 5 OR PSA >20 ng/mL.

OncotypeDx[®] Genomic Prostate Score (Genomic Health[®], Redwood City, CA): This test is a genomic classifier test measuring the activity of 17 genes to predict clinical risk and tumor aggressiveness. OncotypeDx Prostate uses FFPE tissue from a prostate biopsy specimen. NCCN (2022) notes that men with low or favorable intermediate risk prostate cancer may consider the use of this test after prostate biopsy for low or favorable intermediate risk prostate cancer when there is a ≥ 10 years life expectancy and the individual is a candidate for active surveillance or definitive therapy.

Prolaris[®] Prostate Cancer Test (Myriad Genetic Laboratories, Inc., Salt Lake City, UT): This test is a gene expression classifier risk stratification tool designed to measure the expression level of 31 genes in a prostate cancer tumor biopsy tissue, in conjunction with clinical parameters such as the Gleason score and PSA. The NCCN Practice Guidelines in Oncology for Prostate Cancer notes that men with low or favorable intermediate risk prostate cancer may consider the use of this test post prostate biopsy for low or favorable intermediate risk prostate cancer when there is a ≥ 10 years life expectancy and the individual is a candidate for active surveillance or definitive therapy. According to NCCN (2022), the test may also be clinically useful for an individual with unfavorable intermediate risk or high-risk type prostate cancer.

ProMark® Proteomic Prognostic Test (Metamark, Waltham, MA): This test is a prognostic assay that measures the signal intensity of eight protein biomarkers in FFPE prostate biopsy tissue. Using a proprietary algorithm the test generates a risk score indicating the likelihood of having high-risk disease.

Myeloproliferative Neoplasms

Polycythemia Vera (PV), Essential Thrombocythemia (ET) and Primary Myelofibrosis (PMF)

Identification of the JAK2, MPL and CALR exon 9 common variants in individuals with polycythemia vera (PV), essential thrombocythemia (ET) and primary myelofibrosis (PMF) may aid in diagnosis based on diagnostic criteria for each of these diseases. For some individuals with PV, JAK2 exon 12 mutation testing may also be of benefit in disease management. Likewise genetic testing for MPL common variants and targeted mutation analysis of CALR exon 9 may be appropriate to aid in the diagnosis and management of ET and PMF. According to 2016 World Health Organization (WHO) criteria (Arber, 2016), ASXL1, EZH2, TET2, IDH1/IDH2, SRSF2 and SF3B1 mutation analysis may aid in diagnosis of PMF.

Chronic Myelogenous Leukemia and Philadelphia Chromosome Positive (PH+) Acute Lymphoblastic Leukemia Mutation Testing

Specific mutations in the Breakpoint Cluster Region-Abelson (BCR-ABL) gene have been shown to confer resistance to imatinib both in vitro and in vivo, by affecting the binding of the drug to the tyrosine kinase enzyme (AHRQ, 2010). Of interest is the T315-I mutation which is thought to be resistant to all current TKI therapy. The mutation frequency in imatinib resistant patients with CML ranges between 2% and 20%, with variability related to detection methods as well as patient cohort characteristics and treatment. T315I mutation frequency appears to be greater in patients with Philadelphia chromosome-positive (Ph⁺) ALL and likely increases with the continuation of TKI treatment (Nicolini, 2009). The detection of mutations of the BCR-ABL gene has been proposed with potential impact on diagnosis and management decisions (Agency for Healthcare Research and Quality [AHRQ], 2010; National Cancer Institute [NCI], 2015; Najfeld, 2012; National Institute for Clinical Excellence [NICE], 2002). Evidence in the published, peer-reviewed scientific literature also supports the usefulness of testing for BCR-ABL resistance or inhibition.

Real-time quantitative PCR (RQ-PCR) is by far the most sensitive method. It provides an accurate measure of the total leukemia cell mass and the degree to which breakpoint cluster region-Abelson (BCR-ABL) transcripts are reduced by therapy, and correlates with progression-free survival. Current international recommendations for optimal molecular monitoring of patients receiving imatinib treatment include an RQ-PCR assay expressing the BCR-ABL transcript levels, which is predictive of prognosis (Bhatia, 2012; Najfeld, 2012). Molecular responses at 12 and 18 months are also predictive of long-term outcome (Bhatia, 2012). In acute lymphocytic leukemia (ALL), because many patients have a different fusion protein from the one found in chronic myelogenous leukemia (CML), the BCR-ABL gene may be detectable only by pulsed-field gel electrophoresis or reverse-transcriptase polymerase chain reaction (RT-PCR). These tests should be performed whenever possible in patients with ALL, especially those with B-cell lineage disease (NCI, 2015a).

Although certain BCR-ABL mutations may be associated with TKI therapy resistance, sensitivity and specificity values in outcome studies are not suggestive of strong predictive ability, with the exception of the T315-I mutation. Early identification of this mutation may allow for alternative

treatment regimens including increased dose scheduling and drug selection. Data in the published peer-reviewed scientific literature supports the clinical utility of testing for the presence of the T315-I mutation. The clinical utility of testing for other mutations to determine TKI resistance has not been established.

Literature Review

Several studies have reported associations between variations of BCR-ABL and response to drug therapy. AHRQ (2010) performed a systematic review of the published literature regarding variations of the BCR-ABL1 fusion gene and response to imatinib, dasatinib, and nilotinib in CML. Thirty-one studies were analyzed for outcomes of interest including overall survival and cancer specific survival; progression-free or event-free survival (as defined by each study); and treatment failure. Typically, treatment failure is defined as absence of hematologic, cytogenetic, or molecular response to treatment, according to various criteria. Data was analyzed for first-, second-, and third- line TKI therapy. Second-line TKI therapy studies (four publications) demonstrated sensitivity and specificity ranges of 0.35 to 0.83 and from 0.58 to 1.00, respectively, for high-dose imatinib and imatinib-based combination. These studies were small, the calculated sensitivity and specificity values have wide confidence intervals, and a range of different mutations was identified in each of them. No robust conclusions could be made. Eight studies (nine publications) pertained to dasatinib; some had overlapping populations. Sensitivities and specificities ranged from 0.27 to 0.90 and from 0.14 to 0.87, respectively. A lack of predictive ability is suggested. For nilotinib, three studies had relevant data. Sensitivity ranged from 0.56 to 0.71 and specificity ranged from 0.42 to 0.56 for all identified mutations. Only one included study reviewed overall survival (OS). No statistically significant differences in the time-to-death among patients with, versus without mutations were found. When any breakpoint cluster region- Abelson (BCR-ABL1) mutation was considered, almost all studies reported sensitivity and specificity values that are not suggestive of strong predictive ability. The Agency for Healthcare Research and Quality (AHRQ) notes that no study explicitly reported details on changes in treatment plans before or after testing.

AHRQ determined that the presence of any BCR-ABL mutation does not appear to differentiate response to tyrosine kinase inhibitor (TKI) treatment (i.e., imatinib, dasatinib, nilotinib). AHRQ also notes that the majority of evidence pertains to the short term surrogate outcomes of hematologic, cytogenetic or molecular response. Data on overall or progression-free survival are sparse. There is consistent evidence that presence of the relatively rare T315-I mutation can predict TKI treatment failure, mainly in terms of hematologic and cytogenetic response.

Jabbour et al. (2009) studied 169 patients with chronic myelogenous leukemia (CML) after imatinib failure. The goals of the study were to investigate whether in vitro sensitivity of kinase domain mutations could be used to predict the response to therapy as well as the long-term outcome of patients receiving second-generation TKIs after imatinib failure. Treatment failure was defined as loss of a cytogenetic, or complete hematologic response (CHP), or failure to achieve a CHR or any hematologic response (for patients in accelerated phase or blast phase after 3 months of therapy, or persistence of 100% Philadelphia chromosome (Ph)-positive metaphases after 6 months of therapy, or more than or equal to 35% after 12 months). Fifty-seven patients (66%) had received prior therapy with interferon-alpha before the start of imatinib; 29 (34%) had received imatinib as their first-line therapy for CML. Mutations were detected by cDNA sequencing for mutations in the kinase domain of BCR-ABL before a change to dasatinib or nilotinib in 86 patients. Ninety-four mutations were identified in 86 patients with imatinib failure. Seven patients harbored more than 1 mutation. There was no difference in patient characteristics between those with mutations at the time of imatinib failure versus those with no mutations. Forty-one patients received dasatinib and 45 received nilotinib after developing failure to imatinib therapy. Hematologic and cytogenetic response rates were similar for patients without or with KD

mutations. After a median follow-up of 23 months, 48 (58%) of patients without baseline mutations were alive compared with 52 (60%) with any mutation.

Nicolini et al. (2009) reported the results of a retrospective observational study of 222 patients with CML in chronic-phase, accelerated-phase, or blastic-phase and Philadelphia chromosome-positive (Ph⁺) ALL patients with the BCR-ABL T315I mutation. After T315I mutation detection, second-generation TKIs were used in 56% of cases, hydroxyurea in 39%, imatinib in 35%, cytarabine in 26%, MK-0457 in 11%, stem cell transplantation in 17%, and interferon-alpha in 6% of cases. Median overall survival from T315I mutation detection was 22.4, 28.4, 4.0, and 4.9 months, and median progression-free survival was 11.5, 22.2, 1.8, and 2.5 months, respectively, for chronic phase, accelerated phase, blastic phase, and Ph(+) ALL patients. These results suggest that survival of patients harboring a T315I mutation is dependent on disease phase at the time of mutation detection.

In an earlier study by Jabbour et al. (2006) 171 patients were screened for mutations after failing TKI therapy with a median follow-up of 38 months from start of therapy. Sixty-six mutations impacting 23 amino acids in the BCR-ABL oncogene were identified in 62 (36%) patients. Factors associated with the development of mutations were older age, previous interferon therapy and accelerated or blast phase at the start of TKI therapy. By multivariate analysis, factors associated with a worse survival were development of clonal evolution and a higher percentage of peripheral blood basophils. The presence of a BCR-ABL kinase domain mutation had no impact on survival. When survival was measured from the time therapy started, non-P-loop mutations were associated with a shorter survival than P-loop mutations. The authors concluded that BCR-ABL P-loop mutations were not associated with a worse outcome. This study suggests that outcomes of individuals who fail TKI therapy may be influenced by multiple factors.

Nicolini and colleagues (2006) retrospectively analyzed the predictive impact of 94 breakpoint cluster region (BCR) - Abelson (ABL) kinase domain mutations found in 89 protein tyrosine kinase inhibitor (TKI) resistant chronic myelogenous leukemia (CML) individuals. With a median follow-up of 39 months, overall survival was worse for P-loop and another point mutation (T315-I), but not for other BCR-ABL mutations. For individuals in chronic phase only, analysis demonstrated a worse overall survival for P-loop and worse progression free survival for T315-I mutations.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding BCR-ABL mutation analysis please click [here](#).

Occult Neoplasms

While the supporting published evidence is limited, certain paraneoplastic/onconeural antibodies (i.e., anti-Hu, anti-Yo, anti-CV2, anti-RI, anti-MA1 and anti amphiphysin), are established markers used to aid in the diagnosis of paraneoplastic syndromes and occult neoplasms (i.e., cancers of unknown origin).

If initial diagnostic studies (e.g., laboratory, radiography, cerebral spinal fluid analysis, and/or electromyography) are negative, testing for paraneoplastic antibodies may be warranted. If the test is positive for a paraneoplastic antibody, it may help to focus the search for the neoplasm and establish the diagnosis of cancer. Continued testing (e.g., computed tomography, ultrasound) and early diagnosis for an underlying neoplasm would allow for early treatment of the cancer and could also improve the symptoms of PNS. In 90% of patients with paraneoplastic antibodies, the underlying tumor is diagnosed within the first year of PNS symptoms (Dalmau and Rosenfeld, 2008; Spiro et al., 2007; Bataller and Dalmau, 2005). The specificity of paraneoplastic antibodies

reported to be greater than 90% for paraneoplastic neurologic syndromes or some types of cancer makes them useful diagnostic tools. However, not all paraneoplastic antibodies have the same sensitivity and specificity. Hu antibodies, most often associated with subacute sensory neuropathy (SSN) and small cell lung cancer, have an estimated specificity of 99% and a sensitivity of 82% (Dalmau and Rosenfeld, 2008; Honnorat and Antoine, 2007; Vedeler, et al., 2006).

Well-characterized, antibodies are reactive with molecularly defined onconeural antigens, prove the paraneoplastic etiology of the neurological syndrome, and are strongly associated with cancer. The well-characterized paraneoplastic antibodies include: anti-Hu (antineuronal nuclear autoantibodies-1 [ANNA-1]), anti-Yo (PCA-1 [Purkinje cell antibody-1]), anti-CV2 (CRMP5 [collapsing mediator response protein]), anti-Ri (ANNA-2), anti-MA2 (Ta), and anti-amphiphysin. Partially-characterized antibodies are antibodies with an unidentified target antigen and have only been found in a few patients. The partially-characterized antibodies (i.e., antibodies with an unidentified target antigen) include anti-Tr (PCA-Tr), ANNA-3, PCA-2, anti-recoverin, anti-Zic4 and anti-mGluR1. The detection of partially-characterized antibodies is considered of limited diagnostic value. Antibodies that can be detected in paraneoplastic and nonparaneoplastic form and can occur with and without cancer include: anti-VGCC (voltage-gated calcium channel), anti-AchR (acetylcholine receptor), anti-nAChR (nicotine acetylcholine receptor), and anti-VGKC (voltage-gated potassium channels) (Monstad, et al., 2009; De Graaf and Smitt, 2008; deBeukelaar and Smitt, 2006; Vedeler, et al., 2006; Battler and Dalmau, 2005; Karim, et al., 2005; Vincent, 2005; Graus, et al., 2004).

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding molecular testing for solid tumor cancers please click [here](#).

Other Tumor Profile Testing

Topographic Genotyping

Topographic genotyping refers to a method of mutational analysis that incorporates minute tumor samples selected according to histopathologic considerations, polymerase chain reaction (PCR) amplification and direct sequencing. The mutational alterations that are found are then correlated with the histology of the tumor. It has been proposed that the results of this testing will provide predictive information that will influence the management of certain cancers.

Studies comparing topographic genotyping with established testing methods are lacking. There do not appear to be prospective studies published in the peer-reviewed medical literature that focus on the clinical validity, the clinical utility of the test or the impact of the test on clinical outcomes.

Literature Review

High-quality prospective controlled studies informing the clinical validity and clinical utility of topographic genotyping tests are lacking in the published, peer-reviewed scientific literature. Studies generally focus on the association of the topographic genotyping results with tumor characteristics (Al-Haddad, et al., 2014; Al-Haddad et al., 2013; Malhotra et al, 2014; Panarelli et al., 2012; Khalid, et al., 2009).

A technology assessment and systematic review regarding topographic genotyping with PathFinderTG was commissioned by Centers for Medicare and Medicaid Services (CMS) and conducted by the Tufts Evidence-based Practice Center for the Agency for Healthcare Research and Quality (AHRQ) (Trikalinos TA, et al., 2010). The review included studies evaluating the patented technology, specifically those using loss of heterozygosity (LOH) analysis. LOH is a frequent genetic alteration that is found in many cancers. It is thought that LOH alterations may

have prognostic significance. Fifteen studies were included—these pertained to: lung cancer (n=4); pancreatic and biliary tree tumors (n=4); hepatocellular carcinoma (n=4); gliomas, thyroid tumors, lacrimal gland tumors and mucinous tumors of the appendix (n=1 for each). The sample size in the studies ranged from 11 to 103. The review identified no studies regarding the analytic validity of LOH based topographic genotyping with PathFinderTG. The studies were retrospective in design and utilized available archival tissue blocks. One study, molecular profiles of gliomas and reactive gliosis were determined retrospectively and they were used prospectively on 16 diagnostically challenging cases of reactive gliosis versus glial tumors. There were no studies found that evaluated whether the use of LOH based topographic genotyping with PathFinderTG affects patient outcomes. There were no studies identified that compared LOH based topographic genotyping with PathFinderTG with conventional pathology. The review found that all studies are small, they have important methodological limitations, and they do not address patient-relevant outcomes.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding topographic genotyping please click [here](#).

Adhesive Patch Gene Expression Assay for Pigmented Skin Lesions

Adhesive patch gene expression assay (e.g., Pigmented Lesion Assay, Dermtech, LaJolla, CA) has been proposed as a tool to improve the differentiation between pigmented skin lesions that may be biopsied and those that may be monitored. At present there is insufficient evidence to support improved morbidity and mortality with the use of this technology.

Cutaneous melanoma (CM) is skin cancer originating from melanocytes. CM is more common in certain ethnic groups and is more common in males. The risk increases with age. It is more than 20 times more common in whites than in African Americans. Overall, the lifetime risk of getting melanoma is about 2.6% (1 in 38) for whites, 0.1% (1 in 1,000) for Blacks and 0.6% (1 in 167) for Hispanics (American Cancer Society [ACS], 2021). Melanoma is less common than basal cell or squamous cell skin cancer, but can be much more aggressive. Prognosis is directly correlated to stage at diagnosis.

The origin of the increase in diagnosis of CM is unclear; it cannot be fully attributed to environmental factors (e.g. sun exposure) instead increased scrutiny appears to be the largest driver behind the increase (Welch et al, 2021). While the diagnosis of melanoma has risen dramatically, this has not translated into a commensurate decrease in melanoma related mortality. As the mortality secondary to melanoma is largely static, the recent increase in melanoma diagnosis is largely understood to represent over diagnosis (Welch et al., 2021; Ferris 2021; Rubin 2020).

The current standard of care is to biopsy all lesions suspicious for melanoma (Kim et al., 2015). Multiple criteria, including the Asymmetry, Border, Color, Diameter, Evolving (ABCD(E) criteria and Glasgow 7-point criteria, as well as use of dermoscopy imaging and total body photography are used in clinical practice to help monitor and guide clinical decision making regarding biopsy. These criteria have individual sensitivities ranging from 57% to 90% and specificities of 59% to 90%. When multiple ABCDE criteria are used the sensitivity and specificity are improved with 89.3% and 65.3% for two criteria, and 65.5% and 81% for three criteria (American Academy of Dermatology, 2015).

No screening protocol has been sufficiently established to be the method of choice for biopsy decision making. Guidelines remain silent on this issue and discuss only what to do once the decision to biopsy has been reached. Perhaps most importantly, in the current era, more work is needed to understand how to specifically identify lesions associated with high-risk melanoma for

biopsy to make improvements to overall morbidity and mortality (Ferris 2021). The NCCN Guidelines™ for Cutaneous Melanoma (2022) includes many clinical risk factors for the development of melanoma which should also be considered in biopsy decision making. These include gender, age, family history, phenotype, personal history including genetic predisposition, and environmental factors.

The Pigmented Lesion Assay (PLA) is a non-invasive gene expression profile test to assess an atypical primary melanocytic (pigmented) skin lesion suspicious for melanoma, prior to the decision to biopsy. According to the manufacturer, the test is used to help guide decision-making regarding the need for biopsy and is not a diagnostic test for melanoma. Using an adhesive patch a stratum corneum skin tissue sample is collected from the surface of the lesion. Ribonucleic acid (RNA) is extracted from the from skin tissue sample and tested for the expression of LINC00518 (LINC) and preferentially expressed antigen in melanoma (PRAME). The test has not been validated in patients with Fitzpatrick skin type IV-VI (i.e., light brown, brown, dark brown or black), in the presence of other non-cancerous skin disorders, non-melanocytic lesions, or in pediatric patients.

Literature review

Gerami et al. (2017) reported results of a clinical validation study involving pigmented lesions (157 training and 398 validation samples) obtained noninvasively via adhesive patch biopsy. Assay results for PRAME and LINC00518 were compared to histopathologic assessment by a three-person dermatopathology panel. Using the expression of PRAME and/or LINC00518 in 398 samples (87 melanomas and 311 nonmelanomas), the test differentiated melanoma from nonmelanoma samples with a sensitivity of 91% and a specificity of 69%. Study limitations which limit use in routine clinical practice include exclusion of cases where multi-expert pathology reviews were not unanimous (11%) and cases excluded due to test failure (14%). Additionally there is a lack of validation Fitzpatrick skin types IV-VI, use on mucous membranes, palms of hands and soles of feet, and for an individual less than 18 years.

Brouha et al. (2020) reported utility findings and up to 12 month follow-up for a registry study based in the United States. Results of PLA testing of 3418 lesions from 53 dermatology practices, including 90 providers were uploaded to a web portal. Biopsy decision, biopsy type, lesion location, biological sex and three, six or 12-month follow-up was also requested. Clinical impact on management and clinical monitoring of a lesion based on PLA test results were assessed. Of 3418 lesions submitted, 324 lesions were PLA positive and 3,094 were negative. PLA positive lesions were biopsied in 97.53% of patients and PLA negative lesions were clinically monitored and not biopsied in 99.94% of patients. Study limitations which limit the ability to translate results to routine clinical practice include inclusion criteria (e.g., lesion selection).

Medicare Coverage Determinations

	Contractor	Determination Name/Number	Revision Effective Date
NCD	National	National Coverage Determination (NCD) for Next Generation Sequencing (NGS) (90.2)	1/27/2020
LCD	Local	Multiple LCDs for molecular diagnostic testing for hematology and oncology indications	

Note: Please review the current Medicare Policy for the most up-to-date information. (NCD = National Coverage Determination; LCD = Local Coverage Determination)

Appendix A

PROFESSIONAL SOCIETY/ORGANIZATION RECOMMENDATIONS/GUIDELINES

TUMOR PROFILING

Sepulveda et al. (2017) published a guideline on behalf of the American Society for Clinical Pathology, College of American Pathologists, Association for Molecular Pathology, and the American Society of Clinical Oncology regarding molecular biomarkers testing for the evaluation of colorectal cancer. The guideline notes evidence supports mutational testing for genes in the EGFR signaling pathway, since they provide clinically actionable information as negative predictors of benefit to anti-EGFR monoclonal antibody therapies for targeted therapy of CRC. Mutations in several of the biomarkers have clear prognostic value.

GENE EXPRESSION CLASSIFIER TESTS

American Society of Clinical Oncology ([ASCO], 2016, updated 2019): Regarding an individual who presents with a hormone receptor–positive, human epidermal growth factor receptor not overexpressed, axillary node–negative early breast cancer, ASCO notes the following updated recommendations:

- 1.1.1. For patients older than 50 years and whose tumors have Oncotype DX recurrence scores of less than 26, and for patients age 50 years or younger whose tumors have Oncotype DX recurrence scores of less than 16, there is little to no benefit from chemotherapy. Clinicians may offer endocrine therapy alone (Type of recommendation: evidence based, benefits outweigh harms; Evidence quality: high; Strength of recommendation: strong).
- 1.1.2. For patients age 50 years or younger with Oncotype DX recurrence scores of 16 to 25, clinicians may offer chemoendocrine therapy (Type of recommendation: evidence based, benefits outweigh harms; Evidence quality: intermediate; Strength of recommendation: moderate).
- 1.1.3. Patients with Oncotype DX recurrence scores of greater than 30 should be considered candidates for chemoendocrine therapy (Type of recommendation: evidence based, benefits outweigh harms; Evidence quality: high; Strength of recommendation: strong).
- 1.1.4. Based on Expert Panel consensus, oncologists may offer chemoendocrine therapy to patients with Oncotype DX scores of 26 to 30 (Type of recommendation: informal consensus; Evidence quality: insufficient; Strength of recommendation: moderate).

No biomarker except for estrogen receptor, progesterone receptor, and human epidermal growth factor receptor 2 was found to guide choices of specific treatment regimens. Treatment decisions should also consider disease stage, comorbidities, and patient preferences.

National Comprehensive Cancer Network™ (NCCN™)

According to assessment by the NCCN (2023), some gene expression classifier tests predict recurrence risk; others are prognostic of clinical outcome:

Test	NCCN Category of Evidence	Prognostic	Predictive
Breast Cancer Index (BCI) Risk of Recurrence & Extended Endocrine Benefit Test	2A	Yes	Predictive of benefit of extended adjuvant endocrine therapy
EndoPredict® Risk Score Node negative (pN0), 1-3 positive nodes (pN1)	2A	Yes	Not determined

Test	NCCN Category of Evidence	Prognostic	Predictive
MammaPrint test pN0, pN1	1	Yes	Not determined
OncotypeDx [®] , for Early-Stage, Invasive Breast Cancer pN0	1	Yes	Yes
OncotypeDx [®] , for Early-Stage, Invasive Breast Cancer pN1	Postmenopausal: 1 Premenopausal: 2A	Yes	Yes
Prosigna [®] , Breast Cancer Prognostic Gene Signature Assay (PAM50) Node negative (pN0), 1-3 positive nodes (pN1)	2A	Yes	Not determined

The NCCN (2023) does not provide guidance related to use of a specific gene expression assay for pigmented skin lesions using adhesive patch technology. Regarding common follow-up recommendations for all patients the Guideline notes that available, pre-biopsy imaging and molecular technologies have not been prospectively compared for diagnostic accuracy. The Guideline also notes pre-diagnostic noninvasive genomic patch testing may be helpful to guide biopsy decisions.

National Institute for Health and Clinical Excellence (NICE), United Kingdom: A guidance document on the diagnosis and management of carcinomas of unknown primary (CUP) recommends against the use of gene-expression-based profiling to identify primary tumors in patients with provisional CUP. (2010, updated 2016).

A NICE guidance (2018) document titled Tumour Profiling Tests to Guide Adjuvant Chemotherapy Decisions in Early Breast Cancer notes that EndoPredict (EPclin score), Oncotype DX Breast Recurrence Score and Prosigna are recommended as options for guiding adjuvant chemotherapy decisions for people with oestrogen receptor (ER)-positive, human epidermal growth factor receptor 2 (HER2)-negative and lymph node (LN)-negative (including micrometastatic disease for certain populations of individuals with early breast cancer.

The guidance also notes:

- MammaPrint is not recommended for guiding adjuvant chemotherapy decisions for people with ER-positive, HER2-negative and LN-negative early breast cancer because it is not cost effective.
- IHC4+C is not recommended for guiding adjuvant chemotherapy decisions for people with ER-positive, HER2-negative and LN-negative early breast cancer because the analytical validity of the test is uncertain.

MammaPrint[®] 70-Gene Breast Cancer Recurrence Assay

American Society of Clinical Oncology (ASCO, 2017): On behalf of ASCO, Krop et al. published a focused update: Use of Biomarkers to Guide Decisions on Adjuvant Systemic Therapy for Women With Early-Stage Invasive Breast Cancer which addressed the use of MammaPrint to guide decisions on the use of adjuvant systemic therapy. ASCO recommends the following:

- If a patient has ER/PgR-positive, HER2-negative, node-negative, breast cancer, the MammaPrint assay may be used in those with high clinical risk per MINDACT categorization to inform decisions on withholding adjuvant systemic chemotherapy due to its ability to identify a good prognosis population with potentially limited chemotherapy benefit (Type: evidence based; Evidence quality: high; Strength of recommendation: strong).
- If a patient has ER/PgR-positive, HER2-negative, node-negative, breast cancer, the MammaPrint assay should not be used in those with low clinical risk per MINDACT categorization to inform decisions on withholding adjuvant systemic chemotherapy, because women in the low clinical risk category had excellent outcomes and did not appear to benefit from chemotherapy even with a genomic high-risk cancer (Type: evidence based; Evidence quality: high; Strength of recommendation: strong).
- If a patient has ER/PgR-positive, HER2-negative, node-positive, breast cancer, the MammaPrint assay may be used in patients with one to three positive nodes and at high clinical risk per MINDACT categorization to inform decisions on withholding adjuvant systemic chemotherapy due to its ability to identify a good prognosis population with potentially limited chemotherapy benefit. However, such patients should be informed that a benefit of chemotherapy cannot be excluded, particularly in patients with greater than one involved lymph node (Type: evidence based; Evidence quality: high; Strength of recommendation: moderate).
- Recommendation 1.2.2: (update of 2016 recommendation 1.7): If a patient has ER/PgR-positive, HER2-negative, node-positive, breast cancer, the MammaPrint assay should not be used in patients with one to three positive nodes and at low clinical risk per MINDACT categorization to inform decisions on withholding adjuvant systemic chemotherapy. There are insufficient data on the clinical utility of MammaPrint in this specific patient population (Type: informal consensus; Evidence quality: low; Strength of recommendation: moderate).
- Recommendation 1.3: (update of 2016 recommendation 1.8): If a patient has HER2-positive breast cancer, the clinician should not use the MammaPrint assay to guide decisions on adjuvant systemic therapy. Additional studies are required to address the role of MammaPrint in patients with this tumor subtype who are also receiving HER2-targeted therapy (Type: informal consensus; Evidence quality: low; Strength of recommendation: moderate).
- Recommendation 1.4: (update of 2016 recommendation 1.9): If a patient has ER/PgR negative and HER2-negative (triple negative) breast cancer, the clinician should not use the MammaPrint assay to guide decisions on adjuvant systemic chemotherapy (Type: informal consensus; Evidence quality: insufficient; Strength of recommendation: strong).

Oncotype DX® Assay

Spanish Society of Pathology (SEAP) and the Spanish Society of Medical Oncology

(SEOM): In a joint guideline for biomarker testing in colon cancer published by Garcia-Alfonso on behalf of SEAP/SEOM, the authors noted although Oncotype DX gene expression signature has been shown to have prognostic value, no consensus yet exists on its use in clinical practice. The authors noted that the clinical usefulness of the test was compromised because the predictive value of Oncotype DX could not be validated (2012).

Prediction Analysis of Microarray 50 (PAM50) Prosigna® Breast Cancer Prognostic Gene Signature Assay

American Society of Clinical Oncology ([ASCO], 2016): On behalf of ASCO, Harris et al. published recommendations titled Use of Biomarkers to Guide Decisions on Adjuvant Systemic Therapy for Women With Early-Stage Invasive Breast Cancer: American Society of Clinical Oncology Clinical Practice Guideline Summary. Regarding the PAM50 risk of recurrence score, ASCO notes that if a patient has ER/PgR-positive, HER2 negative node negative breast cancer a

clinician may use this assay in conjunction with other clinicopathologic variables to guide decisions on adjuvant systemic therapy. (High Quality Evidence; Strong Recommendation)

CIRCULATING WHOLE TUMOR CELL MARKERS

American Society of Clinical Oncology (ASCO, 2016): A Guideline on the Use of Biomarkers to Guide Decisions on Systemic Therapy for Women With Metastatic Breast Cancer notes for patients already receiving systemic therapy for metastatic breast cancer, decisions on changing to a new drug or regimen or discontinuing treatment should be based on clinical evaluation, judgment of disease progression or response, and the patient's goals for care. The Guideline also notes there is no evidence at this time that changing therapy based solely on circulating biomarker results improves health outcomes, quality of life, or cost effectiveness.

American Society of Clinical Oncologists (ASCO)/College of American Pathologists (CAP) (2018): In collaboration with CAP, ASCO published a joint review regarding Circulating Tumor DNA Analysis in Patients With Cancer (2018). This review notes some circulating DNA (ctDNA) assays have demonstrated clinical validity and utility with certain types of advanced cancer; however, there is insufficient evidence of clinical validity and utility for the majority of ctDNA assays in advanced cancer. Evidence shows discordance between the results of ctDNA assays and genotyping tumor specimens and supports tumor tissue genotyping to confirm undetected results from ctDNA tests. There is no evidence of clinical utility and little evidence of clinical validity of ctDNA assays in early-stage cancer, treatment monitoring, or residual disease detection. There is no evidence of clinical validity and clinical utility to suggest that ctDNA assays are useful for cancer screening, outside of a clinical trial.

National Comprehensive Cancer Network™ (NCCN™) (2022): The NCCN guideline for Prostate Cancer notes that AR-V7 testing in circulating tumor cells can be considered to help guide election of therapy in the post-abiraterone/enzalutamide metastatic CRPC setting.

PROSTATE CANCER SCREENING AND PROGNOSTIC TESTS

American Urological Association (2013): In the guideline for "Early Detection of Prostate Cancer", Carter et al. (2013) note that the literature supporting the efficacy of DRE, PSA derivatives and isoforms (e.g. free PSA, -2proPSA, prostate health index, hK2, PSA velocity or PSA doubling time) and novel urinary markers and biomarkers (e.g. PCA3) for screening with the goal of reducing prostate cancer mortality provide limited evidence to draw conclusions. While some data suggest use of these secondary screening tools may reduce unnecessary biopsies (i.e. reduce harms) while maintaining the ability to detect aggressive prostate cancer (i.e. maintain the benefits of PSA screening), more research is needed to confirm this. However, the likelihood of a future population-level screening study using these secondary screening approaches is highly unlikely at least in the near future. The authors further note that the Guideline focuses only on the efficacy of PSA screening for the early detection of prostate cancer and not secondary tests often used after screening to determine the need for a prostate biopsy or a repeat prostate biopsy (e.g., PSA isoforms, PCA3, imaging).

National Comprehensive Cancer Network (NCCN Guidelines™): The Guideline for Prostate Cancer Early Detection (2023) notes that PSA derivatives and other assays potentially improve the specificity of testing and may diminish the probability of unnecessary biopsies. Several biomarker tests have the goals of refining selection for biopsies, decreasing unnecessary biopsies and increasing the specificity of cancer detection, without missing a substantial number of higher-grade (Gleason \geq 7) cancers. These tests may be especially useful in men with PSA levels between 3 and 10 ng/mL.

BCR-ABL MUTATION ANALYSIS

National Cancer Institute (NCI): Regarding BCR-ABL mutation analysis in individuals with chronic myelogenous leukemia (CML), the NCI notes “In case of treatment failure or suboptimal response, patients should undergo BCR/ABL kinase domain mutation analysis to help guide therapy with the newer tyrosine kinase inhibitors or with allogeneic transplantation.” (2022)

National Comprehensive Cancer Network™ (NCCN™): Regarding kinase domain mutation testing, the NCCN Guideline for Chronic Myeloid Leukemia notes kinase domain mutation analysis is recommended in chronic phase CML if there is inadequate initial response at three and six months or less than complete cytogenetic response at 12-18 months, any sign of loss of response, increase in BCR-ABL transcript levels and loss of minimal molecular response (MMR), and disease progression to accelerated or blast phase (2022).

The NCCN Guideline for Ductal Carcinoma in Situ does not support routine CYP2D6 genotype testing for women being considered for tamoxifen therapy (2023).

TOPOGRAPHIC GENOTYPING

American Gastroenterological Association Institute: A Guideline on the Diagnosis and Management of Asymptomatic Neoplastic Pancreatic Cysts notes, that molecular techniques to evaluate pancreatic cysts remain an emerging area of research and the diagnostic utility of these tests is uncertain (Vege, et al., 2015).

Coding Information

- Note:** 1) This list of codes may not be all-inclusive.
 2) Deleted codes and codes which are not effective at the time the service is rendered may not be eligible for reimbursement.

General Criteria for Somatic Pathogenic or Likely Pathogenic Variant Genetic Testing

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81120	IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (eg, glioma), common variants (eg, R132H, R132C)
81121	IDH2 (isocitrate dehydrogenase 2 [NADP+], mitochondrial) (eg, glioma), common variants (eg, R140W, R172M)
81162	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (ie, detection of large gene rearrangements)
81168	CCND1/IGH (t(11;14)) (eg, mantle cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performed
81191	NTRK1 (neurotrophic receptor tyrosine kinase 1) (eg, solid tumors) translocation analysis
81192	NTRK2 (neurotrophic receptor tyrosine kinase 2) (eg, solid tumors) translocation analysis
81193	NTRK3 (neurotrophic receptor tyrosine kinase 3) (eg, solid tumors) translocation analysis
81194	NTRK (neurotrophic receptor tyrosine kinase 1, 2, and 3) (eg, solid tumors) translocation analysis

CPT®* Codes	Description
81202	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; known familial variants
81203	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants
81206	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; major breakpoint, qualitative or quantitative
81207	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; minor breakpoint, qualitative or quantitative)
81208	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; other breakpoint, qualitative or quantitative
81210	BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)
81218	CEBPA (CCAAT/enhancer binding protein [C/EBP], alpha) (eg, acute myeloid leukemia), gene analysis, full gene sequence
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
81232	DPYD (dihydropyrimidine dehydrogenase) (eg, 5-fluorouracil/5-FU and capecitabine drug metabolism), gene analysis, common variant(s) (eg, *2A, *4, *5, *6)
81233	BTK (Bruton's tyrosine kinase) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, C481S, C481R, C481F)
81235	EGFR (epidermal growth factor receptor) (eg, non-small cell lung cancer) gene analysis, common variants (eg, exon 19 LREA deletion, L858R, T790M, G719A, G719S, L861Q)
81237	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, diffuse large B-cell lymphoma) gene analysis, common variant(s) (eg, codon 646)
81242	FANCC (Fanconi anemia, complementation group C) (eg, Fanconi anemia, type C) gene analysis, common variant (eg, IVS4+4A>T)
81245	FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; internal tandem duplication (ITD) variants (ie, exons 14, 15)
81246	FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; tyrosine kinase domain (TKD) variants (eg, D835, I836)
81261	IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); amplified methodology (eg, polymerase chain reaction)
81262	IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); direct probe methodology (eg, Southern blot)
81263	IGH@ (Immunoglobulin heavy chain locus) (eg, leukemia and lymphoma, B-cell), variable region somatic mutation analysis
81264	IGK@ (Immunoglobulin kappa light chain locus) (eg, leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)
81272	KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18)

CPT®* Codes	Description
81273	KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, mastocytosis), gene analysis, D816 variants(s)
81275	KRAS (Kirsten rat sarcoma viral oncogene homolog) (eg, carcinoma) gene analysis; variants in exon 2 (eg, codons 12 and 13)
81276	KRAS (Kirsten rat sarcoma viral oncogene homolog) (eg, carcinoma) gene analysis; additional variant(s) (eg, codon 61, codon 146)
81277	Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number and loss-of-heterozygosity variants for chromosomal abnormalities
81278	IGH@/BCL2 (t(14;18)) (eg, follicular lymphoma) translocation analysis, major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative
81287	MGMT (0-6-methylguanine-DNA methyltransferase) (eg, glioblastoma multiforme), promoter methylation analysis
81288	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; promoter methylation analysis
81292	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81293	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81294	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81295	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81298	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81299	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary nonpolyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81301	Microsatellite instability analysis (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) of markers for mismatch repair deficiency (eg, BAT25, BAT26), includes comparison of neoplastic and normal tissue, if performed
81305	MYD88 (myeloid differentiation primary response 88) (eg, Waldenstrom's macroglobulinemia, lymphoplasmacytic leukemia) gene analysis, p.Leu265Pro (L265P) variant
81310	NPM1 (nucleophosmin) (eg, acute myeloid leukemia) gene analysis, exon 12 variants
81311	NRAS (neuroblastoma RAS viral [v-ras] oncogene homolog) (eg, colorectal carcinoma), gene analysis, variants in exon 2 (eg, codons 12 and 13) and exon 3 (eg, codon 61)
81314	PDGFRA (platelet-derived growth factor receptor, alpha polypeptide) (eg, gastrointestinal stromal tumor [GIST]), gene analysis, targeted sequence analysis (eg, exons 12, 18)

CPT®* Codes	Description
81315	PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor alpha) (eg, promyelocytic leukemia) translocation analysis; common breakpoints (eg, intron 3 and intron 6), qualitative or quantitative
81316	PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor alpha) (eg, promyelocytic leukemia) translocation analysis; single breakpoint (eg, intron 3, intron 6 or exon 6), qualitative or quantitative
81320	PLCG2 (phospholipase C gamma 2) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, R665W, S707F, L845F)
81340	TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using amplification methodology (eg, polymerase chain reaction)
81341	TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using direct probe methodology (eg, Southern blot)
81342	TRG@ (T cell antigen receptor, gamma) (eg, leukemia and lymphoma), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)
81345	TERT (telomerase reverse transcriptase) (eg, thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (eg, promoter region)
81346	TYMS (thymidylate synthetase) (eg, 5-fluorouracil/5-FU drug metabolism), gene analysis, common variant(s) (eg, tandem repeat variant)
81351	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; full gene sequence
81352	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; targeted sequence analysis (eg, 4 oncology)
81353	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; known familial variant
81401 [†]	Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)
81406	Molecular pathology procedure, Level 7 (eg, analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons)
81407	Molecular pathology procedure, Level 8 (eg, analysis of 26-50 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of >50 exons, sequence analysis of multiple genes on one platform)
81449	Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, MET, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; RNA analysis
81450	Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NOTCH1, NPM1, NRAS), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis
81451	Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2,

CPT®* Codes	Description
	JAK2, KIT, KRAS, MLL, NOTCH1, NPM1, NRAS), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis
81455	Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis
81456	Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis
81457	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability (Code effective 01/01/2024)
81458	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability (Code effective 01/01/2024)
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 (Code effective 01/01/2024)
81462	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements (Code effective 01/01/2024)
81463	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis, copy number variants, and microsatellite instability (Code effective 01/01/2024)
81464	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements (Code effective 01/01/2024)
81500	Oncology (ovarian), biochemical assays of two proteins (CA-125 and HE-4), utilizing serum, with menopausal status, algorithm reported as a risk score
81503	Oncology (ovarian), biochemical assays of five proteins (CA-125, apolipoprotein A1, beta-2 microglobulin, transferrin, and pre-albumin), utilizing serum, algorithm reported as a risk score
81546	Oncology (thyroid) mRNA, gene expression analysis of 10,196 genes, utilizing fine needle aspirate, algorithm reported as a categorical result (eg, benign or suspicious)
81552	Oncology (uveal melanoma), mRNA, gene expression profiling by real-time RT-PCR of 15 genes (12 content and 3 housekeeping), utilizing fine needle

CPT®* Codes	Description
	aspirate or formalin-fixed paraffin-embedded tissue, algorithm reported as risk of metastasis
82105	Alpha-fetoprotein (AFP); serum
82232	Beta-2 microglobulin
82308	Calcitonin
82378	Carcinoembryonic antigen (CEA)
83497	Hydroxyindolacetic acid, 5-(HIAA)
83876	Myeloperoxidase (MPO)
83950	Oncoprotein; HER-2/neu
84432	Thyroglobulin
84702	Gonadotropin, chorionic (hCG); quantitative
84703	Gonadotropin, chorionic (hCG); qualitative
84704	Gonadotropin, chorionic (hCG); free beta chain
86294	Immunoassay for tumor antigen, qualitative or semiquantitative (eg, bladder tumor antigen)
86300	Immunoassay for tumor antigen, quantitative; CA 15-3 (27.29)
86301	Immunoassay for tumor antigen, quantitative; CA 19-9
86304	Immunoassay for tumor antigen, quantitative; CA 125
86386	Nuclear Matrix Protein 22 (NMP22), qualitative
88120	Cytopathology, in situ hybridization (eg, FISH), urinary tract specimen with morphometric analysis, 3-5 molecular probes, each specimen; manual
88121	Cytopathology, in situ hybridization (eg, FISH), urinary tract specimen with morphometric analysis, 3-5 molecular probes, each specimen; using computer-assisted technology
88271	Molecular cytogenetics; DNA probe, each (eg, FISH)
88272	Molecular cytogenetics; chromosomal in situ hybridization, analyze 3-5 cells (eg, for derivatives and markers)
88273	Molecular cytogenetics; chromosomal in situ hybridization, analyze 10-30 cells (eg, for microdeletions)
88274	Molecular cytogenetics; interphase in situ hybridization, analyze 25-99 cells
88275	Molecular cytogenetics; interphase in situ hybridization, analyze 100-300 cells
88342	Immunohistochemistry or immunocytochemistry, per specimen; initial single antibody stain procedure
88360	Morphometric analysis, tumor immunohistochemistry (eg, Her-2/neu, estrogen receptor/progesterone receptor), quantitative or semiquantitative, per specimen, each single antibody stain procedure; manual
88361	Morphometric analysis, tumor immunohistochemistry (eg, Her-2/neu, estrogen receptor/progesterone receptor), quantitative or semiquantitative, per specimen, each single antibody stain procedure; using computer-assisted technology
0006M	Oncology (hepatic), mRNA expression levels of 161 genes, utilizing fresh hepatocellular carcinoma tumor tissue, with alpha-fetoprotein level, algorithm reported as a risk classifier
0018U	Oncology (thyroid), microRNA profiling by RT-PCR of 10 microRNA sequences, utilizing fine needle aspirate, algorithm reported as a positive or negative result for moderate to high risk of malignancy
0034U	TPMT (thiopurine S-methyltransferase), NUDT15 (nudix hydroxylase 15)(eg, thiopurine metabolism) gene analysis, common variants (ie, TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5)

CPT®* Codes	Description
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
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)
0154U	Oncology (urothelial cancer), RNA, analysis by real-time RT-PCR of the FGFR3 (fibroblast growth factor receptor 3) gene analysis (ie, p.R248C [c.742C>T], p.S249C [c.746C>G], p.G370C [c.1108G>T], p.Y373C [c.1118A>G], FGFR3-TACC3v1, and FGFR3-TACC3v3) utilizing formalin-fixed paraffin-embedded urothelial cancer tumor tissue, reported as FGFR gene alteration status
0155U	Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha) (eg, breast cancer) gene analysis (ie, p.C420R, p.E542K, p.E545A, p.E545D [g.1635G>T only], p.E545G, p.E545K, p.Q546E, p.Q546R, p.H1047L, p.H1047R, p.H1047Y), utilizing formalin-fixed paraffin-embedded breast tumor tissue, reported as PIK3CA gene mutation status
0169U	NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (eg, drug metabolism) gene analysis, common variants
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
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
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
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
0329U	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

CPT®* Codes	Description
0364U	Oncology (hematolymphoid neoplasm), genomic sequence analysis using multiplex (PCR) and next-generation sequencing with algorithm, quantification of dominant clonal sequence(s), reported as presence or absence of minimal residual disease (MRD) with quantitation of disease burden, when appropriate
0375U	Oncology (ovarian), biochemical assays of 7 proteins (follicle stimulating hormone, human epididymis protein 4, apolipoprotein A-1, transferrin, beta-2 macroglobulin, prealbumin [ie, transthyretin], and cancer antigen 125), algorithm reported as ovarian cancer risk score
0388U	Oncology (non-small cell lung cancer), next-generation sequencing with identification of single nucleotide variants, copy number variants, insertions and deletions, and structural variants in 37 cancer-related genes, plasma, with report for alteration detection
0397U	Oncology (non-small cell lung cancer), cell-free DNA from plasma, targeted sequence analysis of at least 109 genes, including sequence variants, substitutions, insertions, deletions, select rearrangements, and copy number variations

†Note: Considered Not Medically Necessary when used to report:

- **LINC00518 (long intergenic non-protein coding RNA 518) (eg, melanoma), expression analysis**
- **PRAME (preferentially expressed antigen in melanoma) (eg, melanoma), expression analysis**

Not Covered or Reimbursable:

CPT®* Codes	Description
81327	SEPT9 (Septin9) (eg, colorectal cancer) promoter methylation analysis
81350	UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg, drug metabolism, hereditary unconjugated hyperbilirubinemia [Gilbert syndrome], gene analysis, common variants (eg, *28, *36, *37))
81404 [†]	Molecular pathology procedure, Level 5 (eg, analysis of 2-5 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by Southern blot analysis)
0015M	Adrenal cortical tumor, biochemical assay of 25 steroid markers, utilizing 24-hour urine specimen and clinical parameters, prognostic algorithm reported as a clinical risk and integrated clinical steroid risk for adrenal cortical carcinoma, adenoma, or other adrenal malignancy
0036U	Exome (ie, somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses
0037U ^{††}	Targeted genomic sequence analysis, solid organ neoplasm, DNA analysis of 324 genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden
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

CPT®* Codes	Description
0229U	BCAT1 (Branched chain amino acid transaminase 1) and IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis
0285U	Oncology, response to radiation, cell-free DNA, quantitative branched chain DNA amplification, plasma, reported as a radiation toxicity score
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 and oncoprotein des-gamma-carboxy-prothrombin (DCP), algorithm reported as normal or abnormal result
0334U	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
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
0368U	Oncology (colorectal cancer), evaluation for mutations of APC, BRAF, CTNNB1, KRAS, NRAS, PIK3CA, SMAD4, and TP53, and methylation markers (MYO1G, KCNQ5, C9ORF50, FLI1, CLIP4, ZNF132 and TWIST1), multiplex quantitative polymerase chain reaction (qPCR), circulating cell-free DNA (cfDNA), plasma, report of risk score for advanced adenoma or colorectal cancer
0379U	Targeted genomic sequence analysis panel, solid organ neoplasm, DNA (523 genes) and RNA (55 genes) by next-generation sequencing, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutational burden
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 (Code effective 01/01/2024)
0436U	Oncology (lung), plasma analysis of 388 proteins, using aptamer-based proteomics technology, predictive algorithm reported as clinical benefit from immune checkpoint inhibitor therapy (Code effective 01/01/2024)

†Note: Considered Medically Necessary when used to report:

- **NRAS (neuroblastoma RAS viral oncogene homolog) (eg, colorectal carcinoma), exon 1 and exon 2 sequences**
- **KIT (C-kit) (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, GIST, acute myeloid leukemia, melanoma), targeted gene analysis (eg, exons 8, 11, 13, 17, 18)**

††Note: Considered Medically Necessary when used for companion diagnostic testing to determine appropriate drug therapy

Considered Experimental/Investigational/Unproven:

CPT®* Codes	Description
81445 [†]	Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; DNA analysis or combined DNA and RNA analysis
81479 ^{††}	Unlisted molecular pathology procedure
81504	Oncology (tissue of origin), microarray gene expression profiling of > 2000 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as tissue similarity scores
81525	Oncology (colon), mRNA, gene expression profiling by real-time RT-PCR of 12 genes (7 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a recurrence score
81529	Oncology (cutaneous melanoma), mRNA, gene expression profiling by real-time RT-PCR of 31 genes (28 content and 3 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk, including likelihood of sentinel lymph node metastasis
81540	Oncology (tumor of unknown origin), mRNA, gene expression profiling by real-time RT-PCR of 92 genes (87 content and 5 housekeeping) to classify tumor into main cancer type and subtype, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a probability of predicted main cancer type and subtype
81599 ^{††}	Unlisted multianalyte assay with algorithmic analysis
82387	Cathepsin-D
83520 ^{††}	Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; quantitative, not otherwise specified
83951	Oncoprotein; des-gamma-carboxy-prothrombin (DCP)
84275	Sialic acid
84999 ^{††}	Unlisted chemistry procedure
88358	Morphometric analysis; tumor (eg, DNA ploidy)
0012M	Oncology (urothelial), mRNA, gene expression profiling by real-time quantitative PCR of five genes (MDK, HOXA13, CDC2 [CDK1], IGFBP5, and CXCR2), utilizing urine, algorithm reported as a risk score for having urothelial carcinoma
0017M	Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-embedded tissue, algorithm reported as cell of origin
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
0089U	Oncology (melanoma), gene expression profiling by RTqPCR, PRAME and LINC00518, superficial collection using adhesive patch(es)
0356U	Oncology (oropharyngeal), evaluation of 17 DNA biomarkers using droplet digital PCR (ddPCR), cell-free DNA, algorithm reported as a prognostic risk score for cancer recurrence
0360U	Oncology (lung), enzyme-linked immunosorbent assay (ELISA) of 7 autoantibodies (p53, NY-ESO-1, CAGE, GBU4-5, SOX2, MAGE A4, and HuD), plasma, algorithm reported as a categorical result for risk of malignancy

CPT®* Codes	Description
0362U	Oncology (papillary thyroid cancer), gene-expression profiling via targeted hybrid capture–enrichment RNA sequencing of 82 content genes and 10 housekeeping genes, 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
0386U	Gastroenterology (Barrett’s esophagus), P16, RUNX3, HPP1, and FBN1 methylation analysis, prognostic and predictive algorithm reported as a risk score for progression to high-grade dysplasia or esophageal cancer
0391U	Oncology (solid tumor), DNA and RNA by next-generation sequencing, utilizing formalin-fixed paraffin-embedded (FFPE) tissue, 437 genes, interpretive report for single nucleotide variants, splice-site variants, insertions/deletions, copy number alterations, gene fusions, tumor mutational burden, and microsatellite instability, with algorithm quantifying immunotherapy response score
0395U	Oncology (lung), multi-omics (microbial DNA by shotgun next-generation sequencing and carcinoembryonic antigen and osteopontin by immunoassay), plasma, algorithm reported as malignancy risk for lung nodules in early-stage disease
0405U	Oncology (pancreatic), 59 methylation haplotype block markers, next-generation sequencing, plasma, reported as cancer signal detected or not detected
0409U	Oncology (solid tumor), DNA (80 genes) and RNA (36 genes), by next-generation sequencing from plasma, including single nucleotide variants, insertions/deletions, copy number alterations, microsatellite instability, and fusions, report showing identified mutations with clinical actionability
0410U	Oncology (pancreatic), DNA, whole genome sequencing with 5-hydroxymethylcytosine enrichment, whole blood or plasma, algorithm reported as cancer detected or not detected
0413U	Oncology (hematolymphoid neoplasm), optical genome mapping for copy number alterations, aneuploidy, and balanced/complex structural rearrangements, DNA from blood or bone marrow, report of clinically significant alterations
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 (Code effective 01/01/2024)
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 (Code effective 01/01/2024)

†Note: Considered Medically Necessary when used to report ThyGeNext®

†† Note: Considered Experimental/Investigational/Unproven when used to report any non-covered genetic test for somatic mutations that do not have an assigned CPT/HCPCS code

Tumor Profile/Gene Expression Classifier Testing

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81518	Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 11 genes (7 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithms reported as percentage risk for metastatic recurrence and likelihood of benefit from extended endocrine therapy
81519	Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 21 genes, utilizing formalin-fixed paraffin embedded tissue, algorithm reported as recurrence risk score
81520	Oncology (breast), mRNA gene expression profiling by hybrid capture of 58 genes (50 content and 8 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a recurrence risk score
81521	Oncology (breast), mRNA, microarray gene expression profiling of 70 content genes and 465 housekeeping genes, utilizing fresh frozen or formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk of distant metastasis
81538	Oncology (lung), mass spectrometric 8-protein signature, including amyloid A, utilizing serum, prognostic and predictive algorithm reported as good versus poor overall survival
81599 [†]	Unlisted multianalyte assay with algorithmic analysis
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")

† Note: Considered Medically Necessary when used to report EndoPredict® Risk Score

HCPCS Codes	Description
S3854	Gene expression profiling panel for use in the management of breast cancer treatment

Considered Experimental/Investigational/Unproven:

CPT®* Codes	Description
0016M	Oncology (bladder), mRNA, microarray gene expression profiling of 219 genes, utilizing formalin fixed paraffin-embedded tissue, algorithm reported as molecular subtype (luminal, luminal infiltrated, basal, basal claudin-low, neuroendocrine-like)
0009U	Oncology (breast cancer), ERBB2 (HER2) copy number by FISH, tumor cells from formalin fixed paraffin embedded tissue isolated using image-based

CPT®* Codes	Description
	dielectrophoresis (DEP) sorting, reported as ERBB2 gene amplified or non-amplified
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
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

Circulating Tumor Cells Testing

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
86152	Cell enumeration using immunologic selection and identification in fluid specimen (eg, circulating tumor cells in blood);
86153	Cell enumeration using immunologic selection and identification in fluid specimen (eg, circulating tumor cells in blood); physician interpretation and report, when required

ICD-10-CM Codes	Description
C61	Malignant neoplasm of prostate
C79.82	Secondary malignant neoplasm of genital organs
D40.0	Neoplasm of uncertain behavior of prostate

Screening and Prognostic Tests for Early Detection of Prostate Cancer

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81313	PCA/KLK3 (prostate cancer antigen 3 [non-protein coding]/kallikrein-related peptidase 3 [prostate specific antigen]) ratio (eg, prostate cancer)
0005U	Oncology (prostate) gene expression profile by real-time RT-PCR of 3 genes (ERG, PCA3, and SPDEF), urine, algorithm reported as risk score

Not Covered or Reimbursable:

CPT®* Codes	Description
0343U	Oncology (prostate), exosome-based analysis of 442 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RT-qPCR), urine, reported as molecular evidence of no-, low-, intermediate- or high-risk of prostate cancer

0403U	Oncology (prostate), mRNA, gene expression profiling of 18 genes, first-catch post-digital rectal examination urine (or processed first-catch urine), algorithm reported as percentage of likelihood of detecting clinically significant prostate cancer
0424U	Oncology (prostate), exosomebased analysis of 53 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RTqPCR), urine, reported as no molecular evidence, low-, moderate- or elevated-risk of prostate cancer (Code effective 01/01/2024)
0433U	Oncology (prostate), 5 DNA regulatory markers by quantitative PCR, whole blood, algorithm, including prostate-specific antigen, reported as likelihood of cancer (Code effective 01/01/2024)

Considered Experimental/Investigational/Unproven:

CPT®* Codes	Description
0011M	Oncology, prostate cancer, mRNA expression assay of 12 genes (10 content and 2 housekeeping), RT-PCR test utilizing blood plasma and/or urine, algorithms to predict high-grade prostate cancer risk

Tumor Tissue-Based Molecular and Proteomic Assays for Prostate Cancer

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81479 [†]	Unlisted molecular pathology procedure
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
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

[†]Note: Considered Medically Necessary when used to report Decipher® Prostate Cancer Classifier Assay or ProMark® Proteomic Prognostic Test

Myeloproliferative Neoplasms

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81120	IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (eg, glioma), common variants (eg, R132H, R132C)

CPT®* Codes	Description
81121	IDH2 (isocitrate dehydrogenase 2 [NADP+], mitochondrial) (eg, glioma), common variants (eg, R140W, R172M)
81170	ABL1 (ABL proto-oncogene 1, non-receptor tyrosine kinase) (eg, acquired imatinib tyrosine kinase inhibitor resistance), gene analysis, variants in the kinase domain
81175	ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; full gene sequence
81176	ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; targeted sequence analysis (eg, exon 12)
81219	CALR (calreticulin) (eg, myeloproliferative disorders), gene analysis, common variants in exon 9
81236	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, myelodysplastic syndrome, myeloproliferative neoplasms) gene analysis, full gene sequence
81270	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, p.Val617Phe (V617F) variant
81279	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)
81334	RUNX1 (runt related transcription factor 1) (eg, acute myeloid leukemia, familial platelet disorder with associated myeloid malignancy), gene analysis, targeted sequence analysis (eg, exons 3-8)
81338	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)
81339	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10
81347	SF3B1 (splicing factor [3b] subunit B1) (eg, myelodysplastic syndrome/acute myeloid leukemia) gene analysis, common variants (eg, A672T, E622D, L833F, R625C, R625L)
81348	SRSF2 (serine and arginine-rich splicing factor 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, P95H, P95L)
81357	U2AF1 (U2 small nuclear RNA auxiliary factor 1) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, S34F, S34Y, Q157R, Q157P)
81360	ZRSR2 (zinc finger CCCH-type, RNA binding motif and serine/arginine-rich 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variant(s) (eg, E65fs, E122fs, R448fs)
81401	Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)
81402	Molecular pathology procedure, Level 3 (eg, >10 SNPs, 2-10 methylated variants, or 2-10 somatic variants [typically using non-sequencing target variant analysis], immunoglobulin and T-cell receptor gene rearrangements, duplication/deletion variants of 1 exon, loss of heterozygosity [LOH], uniparental disomy [UPD])

CPT®* Codes	Description
81403	Molecular pathology procedure, Level 4 (eg, 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)
81479 [†]	Unlisted molecular pathology procedure
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
0027U	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, targeted sequence analysis exons 12-15
0040U	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis, major breakpoint, quantitative

†Note: Considered Medically Necessary when used to report TET2, SRSF2, or SF3B1 gene mutation analysis testing

Occult Neoplasms

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
83516	Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; qualitative or semiquantitative, multiple step method
83520 [†]	Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; quantitative, not otherwise specified
84181	Protein; Western Blot, with interpretation and report, blood or other body fluid
84182	Protein; Western Blot, with interpretation and report, blood or other body fluid, immunological probe for band identification, each
86255	Fluorescent noninfectious agent antibody; screen, each antibody
86256	Fluorescent noninfectious agent antibody; titer, each antibody

†Note: Considered Medically Necessary when used to report anti-CV2 (CRMP5 [collapsing mediator response protein5]) or anti-MA2 (Ta)

Other Tumor Profile Testing

Considered Experimental/Investigational/Unproven when used to report topographic genotyping:

CPT®* Codes	Description
81479	Unlisted molecular pathology procedure
81599	Unlisted multianalyte assay with algorithmic analysis
84999	Unlisted chemistry procedure

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Revision Details

Type of Revision	Summary of Changes	Date
Annual Review	Updated to new template and formatting standards	12/3/2023

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