

Gene Expression Test

Diagnostic Accuracy & Confidence in Site-Specific Treatment Decisions

The Tissue of Origin® Test is an Innovation in Molecular Diagnostics

Tissue of Origin® (TOO®) is a gene expression test that relies on genomic information to help identify the origin in cases that are metastatic and/or poorly differentiated. TOO® assesses 2,000 genes, covering 15 of the most common tumor types and 90% of all solid tumors.¹ These tumors include thyroid, breast, non-small cell lung, pancreas, gastric, colorectal, liver, bladder, kidney, non-Hodgkin's lymphoma, melanoma, ovarian, sarcoma, testicular germ cell and prostate.

TOO® is FDA-cleared, Medicare-approved, and provides extensive analytical and clinical validation for statistically significant improvement in accuracy over other methods, including IHC.² TOO® leads to a change in patient treatment 65% of the time and in challenging cancers that require a second round of IHC, TOO® increases diagnostic accuracy and confidence in site-specific treatment decisions¹.

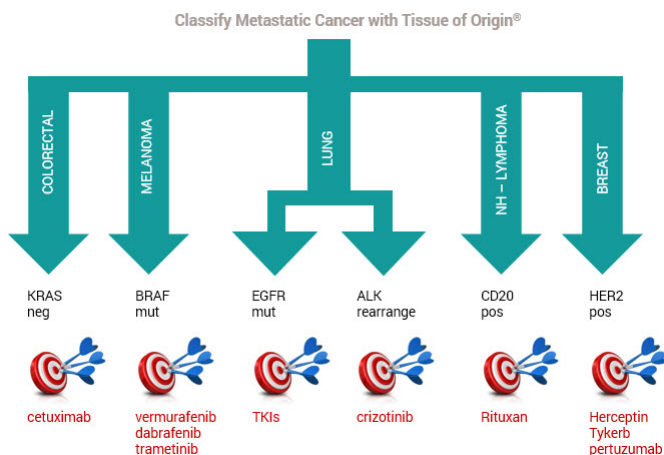
Clinical Indications

Thyroid cancer, breast cancer, non-small cell lung cancer, pancreatic cancer, gastric cancer, colorectal cancer, liver cancer, bladder cancer, kidney cancer, non-hodgkin's lymphoma, melanoma, ovarian cancer, sarcoma, testicular germ cell cancer, and prostate cancer.

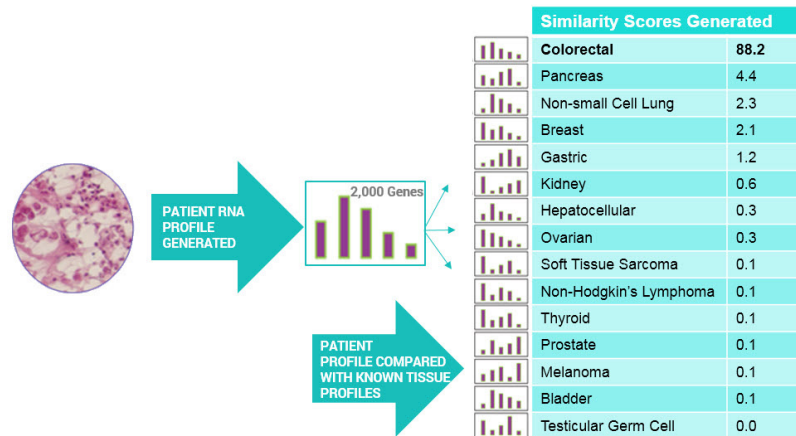
Clinical Utility

Tissue of Origin® is supported by extensive analytical and clinical validation data from robust, multi-centered clinical studies. In a reproducibility analysis, the Tissue of Origin® test demonstrated an average of 89% overall concordance across 3 laboratories in a cross-laboratory comparison study of 149 metastatic and poorly differentiated and undifferentiated tissue specimens.³ A majority of the oncologists identified the Tissue of Origin® test results as influencing the decision to make a change in therapy.⁴

Cascade of Testing to Targeted Therapy



How the Test Works



Tissue of Origin®

Identifying the Primary Tissue Type Helps Physicians Choose the Most Appropriate Treatment

With metastatic tumors or primary tumors that are undifferentiated or poorly differentiated, the Tissue of Origin® test can fill the information gap with accurate, objective, actionable information.

When to Order TOO®

- The tumor is poorly differentiated or undifferentiated.
- There is an unresolved differential diagnosis of 2 or more cancer types
- The specimen is small, constraining the diagnostic work up and limiting prognostic studies
- The patient has a history of multiple cancers
- IHC are inconclusive or conflicting after the first round
- Clinical history and histology differ on the diagnosis
- There is atypical distribution of metastases
- Oncology and Pathology differ on the diagnosis
- The diagnosis is questioned when the patient fails to respond to treatment

Patient Benefits

- Reduced need for repeated testing, examinations, imaging / biopsy procedures.
- Opportunity to enter appropriate clinical trials.
- Important information in assessing one's familial risks for cancer.
- Knowing the primary tissue type with greater certainty helps physicians choose the most appropriate treatment regimens.

Reporting

For each tumor specimen, the Tissue of Origin® test report provides Similarity Scores (SS) that are graphically represented. SS measure the similarity of the RNA expression pattern of the specimen to the RNA expression pattern of the indicated tissue. SS range from 0 (low) to 100 (high) and sum of 100 across 15 tumor types on the panel: bladder, breast, colorectal, gastric, hepatocellular, kidney, non-small cell lung, non-Hodgkin's lymphoma, melanoma, ovarian, pancreatic, prostate, soft tissue sarcoma, testicular germ cell and thyroid. The test provides an accurate, objective result with the ability to rule in or rule out tissues to increase the accuracy of the diagnosis. Tissue of Origin® test clinical report is interpreted and signed by a CGI staff pathologist.

Specimen Requirements

FFPE block containing at least 1 mm² of tumor tissue by area and an H&E stained slide if possible. Unstained slides of at least 5 µm thickness (10 µm thickness preferred) that contain no less than 1 mm² of tumor tissue. A study published in the peer-reviewed journal (*Cancer Cytopathology*) demonstrated the capability of the Tissue of Origin® test to be performed on a variety of body fluid cytology specimens preserved in FFPE. The test successfully yielded results in 89% of the specimens examined, and correctly identified the available diagnosis with a 94.1% agreement.⁵

TAT 5-11 days

CPT Codes 81504

CGI Laboratory Licensure

CAP (Laboratory #: 7191582 AU-ID: 1434060 (NJ); 8033768 AU-ID: 1636028 (NC); 7209131(CA)), CLIA (Certificate #: 31D1038733 (NJ); 34D1009209 (NC); 05D1066073 (CA)), New Jersey (CLIS ID #: 0002299), New York State (PFI: 8192), Pennsylvania (031978), Florida (800018142), Maryland (1395), California (COS00800558) (CA)

References:

1. Validation and Reproducibility of a Microarray-based Gene Expression Test for Identifying the Primary Site of Tumors in Formalin-Fixed Paraffin-Embedded Specimens. R Pillai, R Deeter, CT Rigl, JS Nystrom, M Halks Miller, L Buturovic, WD Henner. *J Molec Diag* 13 2011;13:48-56 1
2. Gene Expression Profiling from Formalin-Fixed, Paraffin-Embedded Tissue for Tumor Diagnosis. JP Grenert, A Smith, W Ruan, R Pillai, AH Wu. *Clin Chim Acta*. 2011 Jul 15;412(15-16):1462-4. Epub 2011 Apr 7
3. A Gene Expression Profile Test for the Differential Diagnosis of Ovarian Versus Endometrial Cancers. A Lal, R Panos, M Marjanovic, M Walker, E Fuentes, DS Kapp, WD Henner, L Buturovic, and M Halks Miller. *Oncotarget*, Vol. 3, No. 2, February 2012
4. A Gene Expression Profile Test to Differentiate Head & Neck Squamous Versus Lung Squamous Cancers. A Lal, R Panos, M Marianovic, M Walker, E Fuentes, GJ Kubicek, WD Henner, LJ Buturovic, M Halks-Miller. *Diagn Pathol*. 2013 Mar 11;8:44.
5. Identification of Tissue of Origin in Body Fluid Specimens with a Gene Expression Microarray Assay. GA Stancel, D Coffey, K Alvarez, M Halks-Miller, A Lal, D Mody, T Koen, T Fairley, FA Monzon. *Cancer Cytopathology*, 2011 Jun 29
6. Clinical Utility of Gene-Expression Profiling for Tumor-Site Origin in patients with Metastatic or Poorly Differentiated Cancer: Impact on Diagnosis, Treatment, and Survival. JS Nystrom, J Hornberger, G Varadhachary, R Hornberger, H Gutierrez, WD Henner, S Becker, M Amin, M Walker. *Oncotarget* 2012 Jun;3(6):620-8
7. A Multicenter Study Directly Comparing the Diagnostic Accuracy of Gene Expression Profiling and Immunohistochemistry for Primary Site Identification in Metastatic Tumors. CR Handorf, A Kulkarni, JP Grenert, L Weiss, W Rogers, O Kim, F Monzon, M Halks-Miller, G Anderson, M Walker, R Pillai, WD Henner. *Am J Surg Pathol* 2013;37:1067

For more information, contact:

CGI Laboratories™
1640 Marengo Street
Los Angeles, California 90033
Tel: 888.700.7110
www.cancergenetics.com

