MAYO CLINIC LABORATORIES

Test Definition: CMAPT

Chromosomal Microarray, Tumor, Formalin-Fixed Paraffin-Embedded

Overview

Useful For

Genomic characterization of tumor for copy number imbalances and loss of heterozygosity

Assisting in the diagnosis and classification of malignant neoplasms

Evaluating the prognosis for patients with malignant tumors

Testing Algorithm

This test does not include a pathology consult. If a pathology consultation is requested, PATHC / Pathology Consultation should be ordered, and the appropriate fluorescence in situ hybridization (FISH) test will be ordered and performed at an additional charge.

Hematoxylin and eosin stain review of the paraffin-embedded sample is performed to identify the area of invasive tumor prior to DNA extraction and microarray analysis. If additional FISH testing is requested, it will be performed at an additional charge.

For more information see Aggressive B-cell Lymphoma Diagnostic Algorithm.

Special Instructions

- Aggressive B-cell Lymphoma Diagnostic Algorithm
- Primary Central Nervous System Tumor Genetic Testing Guide

Method Name

Chromosomal Microarray (CMA)

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

This test is **not performed** on fresh tissue specimens. If testing is needed for fresh tissue specimens, order CMAT / Chromosomal Microarray, Tumor, Fresh or Frozen.

If a fresh tissue specimen is submitted, this test will be canceled and CMAT will be performed and charged.

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For test selection guidance for primary CNS tumors see Primary Central Nervous System Tumor Genetic Testing Guide.

Necessary Information

A reason for testing and pathology report are required for testing to be performed. Send information with specimen. Acceptable pathology reports include working drafts, preliminary pathology or surgical pathology reports.

Specimen Required

Submit only 1 of the following specimens:

Specimen Type: Tissue
Container/Tube: Formalin-fixed, paraffin-embedded tumor tissue block

Specimen Type: Slides
Specimen Volume: 10 Consecutive, unstained, 5-micron-thick sections placed on positively charged slides and 1 hematoxylin and eosin-stained slide
Additional Information: Broken or cracked unstained slides will be rejected. Stained slides that were broken and repaired (ie, double mounted) at the client site will not be rejected, as, in most cases, they can still be reviewed under the microscope. However, due to the double mounting, digital scanning cannot be performed.

Forms

If not ordering electronically, complete, print, and send 1 of the following forms with the specimen:
-Hematopathology/Cytogenetics Test Request (T726)
-Children's Oncology Group Test Request (T829)

Specimen Minimum Volume

See Specimen Required

Reject Due To

Broken or cracked unstained slides	Reject
Broken or cracked stained slides that cannot be repaired	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Ambient (preferred)		
	Refrigerated		

Clinical & Interpretive

Clinical Information

The importance of identifying chromosome abnormalities in malignant neoplasms is well established, and often provides important diagnostic, prognostic, and therapeutic information critical to proper patient management. Although many chromosomal abnormalities are large enough to be detected with conventional chromosome analysis, many others are below its limits of resolution, and conventional chromosome analysis does not detect copy-neutral loss of heterozygosity.

Chromosomal microarray (CMA) improves the diagnostic yield to identify genetic changes that are not detected by conventional chromosome analysis or fluorescence in situ hybridization (FISH) studies. CMA utilizes copy number probes and single nucleotide polymorphism probes to detect copy number changes and regions of copy-neutral loss of heterozygosity.

Chromosomal microarray analysis is appropriate to identify gain or loss of chromosome material throughout the genome at a resolution of 50 to 100 kilobases. CMA can:
-Define the size, precise breakpoints, and gene content of copy number changes to demonstrate the complexity of abnormalities
-Characterize unidentified chromosome material, marker chromosomes, and DNA amplification detected by conventional chromosome and FISH studies
-Determine if apparently balanced chromosome rearrangements identified by conventional chromosome studies have cryptic imbalances
-Assess regions of copy-neutral loss of heterozygosity, which is common in neoplasia and often masks homozygous mutations involving tumor suppressor genes

The limit of detection is dependent on size of the abnormality, type of abnormality (deletion or duplication) and DNA quality. When a deletion or duplication exceeds the reporting limits, mosaicism can confidently be detected as low as 25% and may be lower if the abnormality is large and DNA quality is good.

Reference Values

An interpretive report will be provided.

Interpretation

The interpretive report describes copy number changes and any loss of heterozygosity that may be associated with the neoplastic process. Abnormal clones with subclonal cytogenetic evolution will be discussed if identified.

The continual discovery of novel copy number variation and published clinical reports means that the interpretation of any given copy number change may evolve with increased scientific understanding.

Although the presence of a clonal abnormality usually indicates a neoplasia, in some situations it may reflect a benign or constitutional genetic change. If a genetic change is identified that is likely constitutional and clearly disease-associated (eg, XYY), follow-up with a medical genetic consultation may be suggested.

The absence of an abnormal clone may be the result of specimen collection from a site that is not involved in the neoplasm or may indicate that the disorder is caused by a point mutation that is not detectable by chromosomal microarray.

Chromosomal microarray, fluorescence in situ hybridization (FISH), and conventional cytogenetics are to some extent complementary methods. In some instances, additional FISH or conventional cytogenetic studies will be recommended to clarify interpretive uncertainties.

For more information and frequently asked questions, see Clarity on Reason for and Benefits of Chromosomal Microarray.

Cautions

This test is not approved by the US Food and Drug Administration, and it is best used as an adjunct to existing clinical and pathologic information.

This test does not detect balanced chromosome rearrangements such as reciprocal translocations, inversions, or balanced insertions.

This test does not detect point mutations, small deletions or insertions below the resolution of the assay, or other types of mutations such as epigenetic changes.

This test may not detect mosaic abnormalities in a minor proportion of cells, as such it is not recommended for minimal residual disease monitoring or for specimens with tumor proportions less than approximately 20% of sample.

The results of this test may reveal incidental findings unrelated to the original reason for referral.

Broken or cracked unstained slides are not compatible with the instrumentation used in our performing laboratories and will be rejected. Additional material may be requested.

Attempts will be made to repair broken or cracked stained slides; however, if they are unable to be repaired (ie, shattered in transit), they will be rejected and discarded due to safety concerns.

Supportive Data

The chromosomal microarray was validated on the Affymetrix OncoScan platform in a study of 50 specimens from a variety of tumors including glioma, breast, and melanoma. Results were correlated with the pathology report, fluorescence in situ hybridization, or other results.

Clinical Reference

1. Mikhail FM, Biegel JA, Cooley LD, et al. Technical laboratory standards for interpretation and reporting of acquired copy-number abnormalities and copy-neutral loss of heterozygosity in neoplastic disorders: a joint consensus recommendation from the American College of Medical Genetics and Genomics (ACMG) and the Cancer Genomics Consortium (CGC). Genet Med. 2019;21(9):1903-1916
2. Chun K, Wenger GD, Chaubey A, et al. Assessing copy number aberrations and copy-neutral loss-of-heterozygosity across the genome as best practice: An evidence-based review from the Cancer Genomics Consortium (CGC) working group for chronic lymphocytic leukemia. Cancer Genet. 2018;228-229:236-250

3. Shao L, Akkari Y, Cooley LD, et al. Chromosomal microarray analysis, including constitutional and neoplastic disease applications, 2021 revision: a technical standard of the American College of Medical Genetics and Genomics (ACMG). Genet Med. 2021;23(10):1818-1829
4. Wang Y, Cottman M, Schiffman JD. Molecular inversion probes: a novel microarray technology and its application in cancer research. Cancer Genet. 2012;205(7-8):341-355

Performance

Method Description
The selection of tissue and the identification of invasive tumor on the hematoxylin and eosin (H and E)-stained slide are performed by a pathologist. Using the H and E slide as a reference, the target areas are marked on the unstained slide, the DNA is extracted from the tumor is labeled and hybridized to the microarray. Following hybridization, the microarray is scanned, and the intensity of signals is measured and compared to a reference data set. These data are used to determine copy number changes and regions with loss of heterozygosity. Chromosomal microarray data alone does not provide information about the structural nature of an imbalance. Thus, it may be of benefit to utilize fluorescence in situ hybridization or additional techniques to further characterize a patient sample.(Unpublished Mayo method)

PDF Report
No

Day(s) Performed
Monday through Sunday

Report Available
10 to 21 days

Specimen Retention Time
Slides and hematoxylin and eosin used for analysis are retained by the lab indefinitely. Client provided paraffin blocks and extra unstained slides (if provided) will be returned after testing is complete.

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

Test Classification

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This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81277

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
CMAPT	Chromosomal Microarray, Tumor, FFPE	94087-4

Result ID	Test Result Name	Result LOINC® Value
54735	Result Summary	50397-9
54736	Result	62356-1
54737	Nomenclature	62378-5
54738	Interpretation	69965-2
CG908	Reason for Referral	42349-1
54744	Specimen	31208-2
54739	Source	31208-2
54740	Tissue ID	80398-1
54741	Method	85069-3
53425	Additional Information	48767-8
54742	Released By	18771-6