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.

If a fresh tissue specimen is submitted, this test will be cancelled and CMAT / Chromosomal Microarray, Tumor will be performed.

See Aggressive B-cell Lymphoma Diagnostic Algorithm in Special Instructions.

Special Instructions

- Cytogenetic Analysis of Glioma
- Aggressive B-cell Lymphoma Diagnostic Algorithm

Method Name

Chromosomal Microarray (CMA) using Applied Biosystems (Affymetrix) Oncoscan

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 using Affymetrix Cytoscan HD.

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

Forms

If not ordering electronically, complete, print, and send an Oncology Test Request (T729) with the specimen.

Specimen Minimum Volume

See Specimen Required

Reject Due To

All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

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.

CMA 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 pathogenic (eg, XYY), follow-up with a medical genetics 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 (CMA).

CMA, 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.

See Cytogenetic Analysis of Glioma in Special Instructions for common questions and answers.

Cautions
This test is not approved by the FDA 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.

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. Cooley L, Lebo M, Li M, et al: American College of Medical Genetics and Genomics technical standards and guidelines: microarray analysis for chromosome abnormalities in neoplastic disorders. Genet Med. 2013;15:484-494. doi: 10.1038/gim.2013.49
2. Ciriello G, Miller ML, Aksoy BA, Senbabaoglu Y, Schultz N, Sander C: Emerging landscape of oncogenic signatures across human cancers. Nat Genet. 2013 Sep 26;45(10):1127-1133. doi: 10.1038/ng.2762
3. Wang Y, Cottman M, Schiffman JD: Molecular inversion probes: a novel microarray technology and its application in cancer research. Cancer Genet. 2012 Jul-Aug;205(7-8):341-355. doi: 10.1016/j.cancergen.2012.06.005

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 Friday

Report Available

10 to 21 days

Specimen Retention Time

Slides and H and E 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

Rochester

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

This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test 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