Test Definition: CMAT

Chromosomal Microarray, Tumor, Fresh or Frozen

Overview

Useful For

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

Assisting in the diagnosis and classification of malignant neoplasms, including hematolymphoid malignancies

Evaluating the prognosis for patients with malignant tumors

Testing Algorithm

DNA is extracted from the specimen prior to hybridization to the microarray.

Method Name

Chromosomal Microarray (CMA)

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

This test is **not performed** on formalin-fixed, paraffin-embedded (FFPE) specimens. If testing is needed for FFPE specimens, order CMAPT / Chromosomal Microarray, Tumor, Formalin-Fixed Paraffin-Embedded.

If an FFPE specimen is submitted, this test will be canceled and CMAPT / Chromosomal Microarray, Tumor, Formalin-Fixed Paraffin-Embedded will be added and performed as the appropriate test.

Shipping Instructions

Advise Express Mail or equivalent if not on courier service.

Necessary Information

1. **A reason for testing must be provided for testing to be performed.**
2. A pathology report should accompany the specimen. If this information is not available at the time of order, submit as soon as possible for appropriateness of testing and to aid in interpretation of results.

Specimen Required

Submit only 1 of the following specimens:

Supplies: Hank's Solution (T132)

Specimen Type: Tumor biopsy
Container/Tube: Sterile container with sterile Hank's balanced salt solution, Ringer's solution, or normal saline
Specimen Volume: 0.5-3 cm(3) or larger

Specimen Type: Lymph node
Container/Tube: Sterile container with sterile Hank's balanced salt solution, Ringer's solution, or normal saline.
Specimen Volume: 1 cm(3)

Specimen Type: Skin biopsy
Container/Tube: Sterile container with sterile Hank's balanced salt solution, Ringer's solution, or normal saline.
Specimen Volume: 4-mm diameter
Collection Instructions:
1. Wash biopsy site with an antiseptic soap.
2. Thoroughly rinse area with sterile water.
3. **Do not use alcohol or iodine preparations**.
4. A local anesthetic may be used.
5. Biopsy specimens are best taken by punch biopsy to include full thickness of dermis.

Specimen Minimum Volume
Tumor biopsy: 3 cm(3); Lymph node: 1 cm(3); Skin biopsy: 4 mm diameter

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 greater than 2 million copy number probes and approximately 750,000 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 30 to 60 kilobases.
CMA can:
-Define the size, 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 loss of heterozygosity that may be associated with the neoplastic process being evaluated. Abnormal clones with subclonal abnormalities will be discussed if identified.

The continual discovery and publication of novel copy number abnormalities and losses of heterozygosity associated with neoplastic processes means that the interpretation of any given detected abnormality may change with increased scientific understanding.

Although the presence of a clonal abnormality is usually associated with 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 or likely pathogenic and/or related to the clinical reason for referral, this will be included in the report and 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.

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/pathogenic variants, small insertions or deletions, trinucleotide repeat expansions, or other copy number abnormalities below the resolution of the assay, or other types of variants such as epigenetic changes.

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

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

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. doi:10.1038/s41436-019-0545-7
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. doi:10.1016/j.cancergen.2018.07.004
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. doi:10.1038/s41436-021-01214-w

Performance

Method Description

DNA 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

Four weeks

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

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
CMAT	Chromosomal Microarray, Tumor	94087-4

Result ID	Test Result Name	Result LOINC® Value
54728	Result Summary	50397-9
54729	Result	62356-1
54730	Nomenclature	62356-1
54731	Interpretation	69965-2
CG905	Reason for Referral	42349-1
54743	Specimen	31208-2
54732	Source	31208-2
54733	Method	85069-3
53424	Additional Information	48767-8
54734	Released By	18771-6