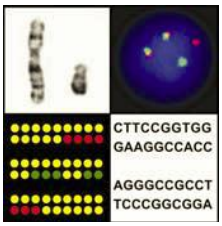
Wisconsin State Laboratory of Hygiene
UNIVERSITY OF WISCONSIN–MADISON



UW Cytogenetic Services and Molecular Genetics

Information for Medical Providers

Chromosomal microarray analysis (CMA) for hematological malignancies

CMA analysis provides a high resolution, genome-wide assessment of copy number variants (gains and losses) and copy neutral loss of heterozygosity (cn-LOH) recurrent in hematological malignancies. CMA is recommended for individuals with a new diagnosis or suspected diagnosis of a hematological disease, or individuals with relapsed disease. The results are intended for use by the physician to **further refine diagnoses**, **offer more accurate prognostic assessments** and **select optimal treatments**. CMA can reveal additional genomic imbalances not detectable by chromosomes or FISH and increase the diagnostic yield for a clonal marker from 50% to approximately 80% in myeloid malignancies.

Technique	Resolution	Sensitivity (mosaicism)	Cell culture	Whole genome	Unbalanced rearrangements	Balanced rearrangements	cn-LOH
G-banded chromosomes	10-20 Mb (400 bands)	10%	Yes	Yes	Yes	Yes	No
Interphase FISH	150-900 kb	3-10%	No	No	Yes	Yes	No
SNP array	50 kb	15-20%	No	Yes	Yes	No	Yes

Table 1. Comparison of Cytogenetic Methods. Mb=Megabases, kb=kilobases

Test Information

Test name: Illumina Microarray Analysis – Oncology

CPT code: 81406

Specimen Requirements: 1-3 mL bone marrow collected in sodium heparin OR 3-5 mL whole blood collected in sodium heparin or EDTA.

Turnaround time: 4-8 days

Limitations: Not recommended for minimal residual disease monitoring or for individuals with expected lower levels of malignant cells. This assay will not detect point mutations or balanced alterations (reciprocal translocations, Robertsonian translocations, inversions and insertions), imbalances smaller than the resolution of this array, or low level mosaicism (less than 20%).

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