CANCER GENETICS®
Empowering Personalized Cancer Treatment

MatBA FL
INFORM PREDICT DECIDE
Mature B-Cell Neoplasm Array

FL

# MatBA®-FL Array-CGH Assay

## Overview

Follicular lymphoma (FL) is considered to be the malignant counterpart of normal germinal center B-cells, characterized by typical morphology and the presence of the chromosomal translocation t(14;18)(q32;q21). In spite of its indolent clinical course and a median survival time reaching over 10 years, accurate prognostication for treatment options is highly desirable in FL, as patients display clinical heterogeneity in the course of their disease.

While low stage FL patients are often put under watch-and-wait surveillance, a significant portion of follicular lymphoma cases are not discovered until they are at advanced stages. These cases often require treatment, most often immunochemotherapy. Over time, up to 45% of FL undergoes transformation into an aggressive form of lymphoma, usually diffuse large B-cell lymphoma (DLBCL) which is associated with poorer outcomes. Thus, biomarkers of transformation and overall patient outcome are highly desirable to assist in patient management.

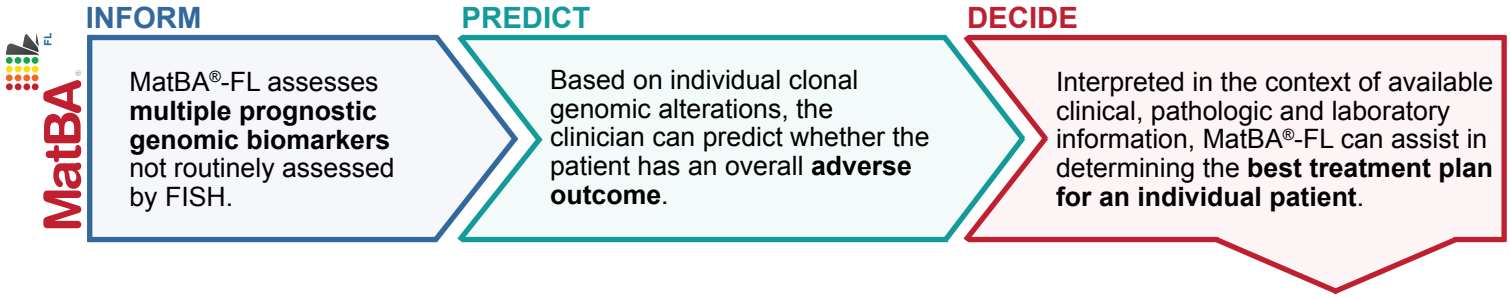
MatBA®-FL Array-CGH detects the gain of 2p, 3q, 8q (*MYC*), 7p, 12q and chromosome 18 and loss of 1p, 6q (*TNFAIP3*), 9p (*CDKN2A*), and 17p (*TP53*), as well as others, and can assist in the prognosis of FL. The results of the assay should be interpreted in the context of available clinical, pathologic, and laboratory information.

## Clinical Indications

MatBA®-FL assists in the prognosis of FL.

## Methodology and Interpretation

DNA is extracted and fluorescently labeled by enzymatic procedures. Genomic gains and losses in the labeled DNA are detected by hybridization to a custom oligonucleotide array in the presence of labeled normal DNA. Quantitative PCR is used to confirm the detected genomic gains and losses. Results are reported as positive or negative for the gain or loss of each respective alteration.




## Assay Specifications

### Sensitivity

Limit is 50-60 cells in 100 cells.

### Reporting

Results are reported as positive or negative for the gain or loss of each respective alteration. Identification of genomic gain/loss should not be used alone for the prognosis of FL and a negative finding cannot exclude the possibility of a diagnosis of FL.

**TAT:** 10-14 days

**CPT Code:** 81479

### Specimen Requirements

- FFPE block: containing ≥ 60% tumor. Minimum size: 2 mm x 2 mm tumor area, shipped at room temperature.
- Fresh-Frozen tissue: 0.2 $cm^3$ minimum (in OCT is acceptable) containing ≥50% tumor. Stored at -80°C /-20°C, shipped on dry ice.
- FFPE block or fresh-frozen specimen from incisional or excisional biopsy.

### CGI Laboratory Licensure

CAP (Laboratory #: 7191582, AU-ID: 1434060), CLIA (Certificate #: 31D1038733), New Jersey (CLIS ID #: 0002299), New York State (PFI: 8192), Pennsylvania (031978), Florida (800018142), Maryland (1395).

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| | | | |
|---|---|---|---|
| Patient Name: | | Accession Number: | |
| Sex: | ❑ Male ❑ Female | CGI ID No: | |
| Date of Birth: | | Ordering Physician: | |
| Specimen: | | Client: | |
| Collected: | | Client Account No: | |
| Received: | | Client ID No: | |
| Reported: | | Client Address: | |
| Clinical Hx: | | Telephone: | |

# MatBA®-FL Array-CGH Sample Report

**Results:**

| *Genomic Aberration* | *Result* | *Genomic Aberration* | *Result* |
|---|---|---|---|
| Loss of 1p (1p36.33-p36.22) | NEGATIVE | Loss of 9p21 (9p21.3; *CDKN2A*) | NEGATIVE |
| Gain of 2p (2p16.1-p15; *REL*) | NEGATIVE | Gain of 11q (11q12-q25) | NEGATIVE |
| Gain of 3q (3q21.2-q27.3) | NEGATIVE | Gain of 12q (12q12-q15) | **POSITIVE** |
| Loss of 6q (6q12-q16.3) | NEGATIVE | Loss of 15q (15q21.1) | NEGATIVE |
| Loss 6q (6q23.3-q24.1; *TNFAIP3*) | NEGATIVE | Loss of 17p (17p13.2-p13.1; *TP53*) | NEGATIVE |
| Gain of 7p (7p22.3-p21.2) | **POSITIVE** | Gain of 17q (17q22-q25.1) | NEGATIVE |
| Gain of 8q (8q24.13-q24.21; *MYC*) | NEGATIVE | Gain of chr18 | **POSITIVE** |

**Interpretation**: ***Positive for gain of 7p22.3-p21.2, 12q12-q15 and chr18.***

**Description:** Follicular lymphoma (FL) is generally considered an indolent mature B-cell neoplasm though about 40% will undergo transformation associated with poorer outcome. FL is mostly characterized by the presence of the t(14;18)(q32;q21) translocation, but other cytogenomic studies have identified recurrent genomic gains and losses with prognostic significance. Gains in chromosome 2p (*REL*), 3q, 7p, 8q24 (*MYC*), 11q, 12q, 17q and chr18 have been shown to associate with an adverse outcome and/or transformation, as have deletions of 1p36, 6q21-q24.3 (*TNFAIP3/A20*), 6q12-q16.3, 9p21 (*CDKN2A*) and 17p (*TP53*) [1-6]. Deletion of the 15q arm in FL has been shown to be a marker for transformation [1, 3-6].

This assay utilizes microarray-based comparative genomic hybridization (array-CGH) to simultaneously detect the gain and loss of multiple loci in specimen DNA. The sensitivity of the assay is 50-60% for formalin-fixed paraffin-embedded and fresh frozen specimens. Aberrations may not be detected in samples in which the tumor percentage is less than the assay sensitivity. The test results should be interpreted in the context of other clinical and laboratory findings.

**References:**


*1. Schwaenen, C., et al., Microarray-based genomic profiling reveals novel genomic aberrations in follicular lymphoma which associate with patient survival and gene expression status. Genes, chromosomes & cancer, 2009. 48(1): p. 39-54.*

*2. Martinez-Climent, J.A., et al., Transformation of follicular lymphoma to diffuse large cell lymphoma is associated with a heterogeneous set of DNA copy number and gene expression alterations. Blood, 2003. 101(8): p. 3109-17.*

*3. Bouska, A., et al., Genome-wide copy number analyses reveal genomic abnormalities involved in transformation of follicular lymphoma. Blood, 2013.*

*4. Cheung, K.J., et al., Genome-wide profiling of follicular lymphoma by array comparative genomic hybridization reveals prognostically significant DNA copy number imbalances. Blood, 2009. 113(1): p. 137-48.*

*5. Berglund, M., et al., Genomic imbalances during transformation from follicular lymphoma to diffuse large B-cell lymphoma. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 2007. 20(1): p. 63-75.*

*6. Eide, M.B., et al., Genomic alterations reveal potential for higher grade transformation in follicular lymphoma and confirm parallel evolution of tumor cell clones. Blood, 2010. 116(9): p. 1489-97.*


End of Report




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