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Laboratory Bulletin

NGS TESTING FOR MYELOID MALIGNANCY

Effective immediately, the hematopathology department will reflex all bone marrows with a new diagnosis of acute myeloid leukemia or a new diagnosis of myelodysplasia for a myeloid panel by next generation sequencing (NGS). Additional testing will continue to follow the DMT guidelines below.

Due to the required turn-around time for FLT3 this test will continue to be sent out as a single gene test to University of Michigan, in addition to the myeloid panel by NGS. Repeat testing for positive markers will also be performed as individual gene tests.

B Lymphoblastic Leukemia/Lymphoma	• Karyotype • ALL FISH Panel [4,10 trisomy, t(9;22), 11q23 rearrangement, t(12;21), t(1;19), IGH/IL3 for t(5;14), iAMP21, ABL1, ABL2, PDGFRB per Children's Oncology Group protocol] • RT-PCR for BCR-ABL1 • Send out for Phil-like ALL FISH Panel testing (MAYO), at ordering physician request only
Acute Myeloid Leukemia, including evolving AML	• Karyotype • Limited AML FISH Panel [CBFB gene rearrangement for inv16/t(16;16), p53, t(15;17), MLL, t(9;22), NUP98] on all • Expanded FISH panel upon request to also include t(8;21) and 3q26 rearrangement • Next Generation Sequencing - Myeloid Panel • FLT3
Myelodysplastic Syndrome	• Karyotype • Next Generation Sequencing - Myeloid Panel • FISH only upon request or at discretion of pathologist or if traditional karyotype obtained <20 metaphases [MDS FISH Panel: trisomy 8,del(20q),monosomy 5/del(5q),monosomy 7/del(7q),3q26 rearrangement, monosomy 13/del(13q), MLL,p53]
Myeloproliferative Neoplasms	• Karyotype • FISH or RT-PCR for BCR-ABL1 • JAK2 V617F, if negative CALR, MPL (ET and MF) and JAK2 Exon 12 (PV)
Myelodysplastic/Myeloproliferative Neoplasms including Chronic Myelomonocytic Leukemia	• Karyotype • FISH or RT-PCR for BCR-ABL1 • JAK2 V617F, if negative CALR and MPL • Eosinophilia FISH Panel [FIP1L1/PDGFRA, PDGFRB, FGFR1 and JAK2 rearrangements]

	• MDS FISH only upon request or at discretion of pathologist or if traditional karyotype obtained <20 metaphases [MDS FISH Panel: trisomy 8,del(20q),monosomy 5/del(5q),monosomy 7/del(7q),3q26 rearrangement, monosomy 13/del(13q), MLL,p53]
Eosinophilia associated with myeloid/lymphoid neoplasms	• Eosinophilia FISH Panel [FIP1L1/PDGFRA, PDGFRB, FGFR1 and JAK2 rearrangements]
Plasma Cell Myeloma	• Karyotype • Myeloma FISH Panel [CDKN2C/CKS1B for chromosome 1q rearrangement, CEP3/7 for hyperdiploidy, monosomy 13/del(13q), p53, IGH/CCND1 with reflex to IGH/FGFR3, IGH/MAF, and IGH/MAFB]
Chronic Lymphocytic Leukemia/ Small Lymphocytic Lymphoma	• CLL FISH Panel [MYB/CEP6, trisomy 12, p53, ATM,monosomy 13/del(13q), IGH/CCND1] • Karyotype
Diffuse Large B-cell Lymphoma	• FISH for double hit lymphoma all cases [MYC and IGH/MYC; Reflex to BCL2 and BCL6 if MYC rearranged] • Karyotype optional
Burkitt Lymphoma	• [FISH for IGH/MYC with reflex to IGK/MYC and IGL/MYC]
Hairy Cell Leukemia	• BRAF V600E (send out)
Lymphoplasmacytic Lymphoma	• MYD88 L265P • CXCR4 at request of ordering physician for patient's being considered for ibrutinib
Gastric Malt Lymphoma	• H. pylori testing (also should be performed in gastric DLBCL) • If positive for H. pylori; FISH for t(11;18) will be performed
T-cell leukemia/lymphoma including T-cell Prolymphocytic Leukemia	• Karyotype • T-cell leukemia/lymphoma FISH Panel [TCL1 (14q32),TCRAD (14q11), TCRB (7q434), and TLX3 (5q32) rearrangements; chromosome 8 abnormalities; del(9p)]
Peripheral T-cell Lymphoma and Primary Cutaneous CD30 Positive T-cell Lymphoproliferative Disorders	• FISH for DUSP22 if ALK negative ALCL consideration (paraffin only)
Other lymphomas	• Additional cytogenetic and molecular testing is useful under certain circumstances and will be performed at discretion of pathologist; nothing routinely performed or required

	• NHL FISH Panel (IGH/CCND1, IGH/BCL2, MALT1, MYC, BCL6)

NGS Test Information:

The Myeloid Neoplasm NGS Panel (42 genes) is designed for sequencing both DNA and RNA for the detection of single nucleotide variants (SNV), insertion/deletion mutations (indels), gene copy number changes (CNV), and gene fusions in the following genes:

ABL1, ABL2, ASXL1, BCR, BCOR, BRAF, CALR, CBL, CEBPA, CSF3R, DNMT3A, ETV6, EZH2, FLT3, GATA1, GATA2, GNAS, HRAS, IDH1, IDH2, JAK2, KIT, KRAS, MLL, MYD88, MPL, NPM1, NRAS, PHF6, PTEN, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SRSF2, SMC3, STAG2, TET2, TP53, WT1, ZRSR2

Synonyms:

TSO500, TruSight Oncology 500, next generation sequencing, NGS, myeloid panel

Test Code:

Soft code-5 character: MMYLD
EPIC code: LAB7971

CPT Code(s):

81450, G0452

Specimen Collection Criteria:

Bone Marrow:

- 1.0 mL bone marrow aspirate in a Lavender-top EDTA tube. (Minimum: 0.5 mL).
- The specimen must be accompanied by a completed requisition and must contain the patient name, date of birth, collection date, ordering physician, clinical diagnosis, and source of specimen.

Specimen Preparation for Courier Transport:

- Transport all bone marrow at room temperature (20-26°C or 68-78.8°F).

Rejection Criteria

- Specimens collected in heparin (Green-top), clot tubes (Red-top), ACD anti-coagulant tubes, or SST tubes.
- Improper labeling or inadequate information.
- Poor quality and/or quantity of extracted genomic DNA.

- Frozen specimens.
- Unlabeled tubes or samples.

Testing will be cancelled on specimens meeting the above criteria with client notification. Under certain circumstances (i.e., lack of alternative specimens), testing may proceed with approval from the medical director or designee.

Performed

Once or twice per week, dependent upon test volume. Results available in 10-15 business days.

Reference Range

No variants detected or likely benign variants detected.

Test Methodology

RNA, DNA or both are isolated from the sample and quantified. Recovered nucleic acid extracts are prepared for sequencing with the Illumina TruSight Oncology 500 library preparation kit and sequenced on the Illumina NextSeq instrument with the Illumina TruSight Oncology 500 sequencing kit. Analysis is performed using PierianDx Clinical Genomics Workspace (CGW) software.

A personalized interpretive report is generated for each sample that lists the variants detected in each gene, classifies these based on a standardized classification scheme for somatic variants, and provides interpretative comments for each variant of known significance.

Interpretation

Test results should be interpreted in the context of clinical findings, tumor sampling, and other laboratory data. If results obtained do not match other clinical or laboratory findings, please contact the laboratory director.

Date submitted: **May 11, 2021**
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