Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	6/8/1988
Sex:	Unknown
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

Acute Myeloid Leukemia Mutation Panel by Next Generation Sequencing

ARUP test code 3002714

Acute Myeloid Leukemia Specimen	Whole Blood
Acute Myeloid Leukemia Interp	See Note

Section 79-1 of New York State Civil Rights Law requires informed consent be obtained from patients (or their legal guardians) prior to pursuing genetic testing. These forms must be kept on file by the ordering physician. Consent forms for genetic testing are available at www.aruplab.com. Incidental findings are not reported unless clinically significant but are available upon request.

Submitted diagnosis or diagnosis under consideration for variant interpretation:
Acute myeloid leukemia (AML)

Result:
I. Tier 1 Variants (Variants of known significance in myeloid malignancies):

NONE DETECTED

II. Tier 2 Variants (Variants of unknown significance in myeloid malignancies):

NONE DETECTED

Low coverage regions:
This list contains exons where the average sequencing depth (number of times a particular position is sequenced) for 20% or more of the region is below our stringent cutoff of 300. Sensitivity for detection of low allelic frequency mutations may be reduced in areas with low depth of coverage. The sequencing reads from these exons were manually reviewed. If high quality variants are detected in these regions, they will be listed above in Tier 1 or Tier 2.

NONE

BACKGROUND INFORMATION: Acute Myeloid Leukemia Panel by NGS

CHARACTERISTICS: Acute myeloid leukemia (AML) is a genetically heterogeneous hematologic malignancy characterized by the clonal expansion of myeloid blasts (e.g. undifferentiated myeloid precursors) in the peripheral blood, bone marrow, and/or other

tissues, which results in impaired hematopoiesis and bone marrow failure. AML is the most common acute leukemia in adults (approximately 80 percent of leukemia cases) and accounts for the largest number of annual deaths from leukemia in the United States. The median age at diagnosis is 67 years, and 54 percent of patients are diagnosed at 65 years of age or older. Advances in the treatment of AML have led to significant improvement in outcomes for younger patients; however, prognosis in the elderly, in whom the majority of new cases occur, remains poor. Recent studies have identified recurrently mutated genes with diagnostic and/or prognostic impact in AML. The presence of certain mutations may inform clinical management. This multi-gene panel by massively parallel sequencing (next generation sequencing) is a more cost-effective approach when compared to the cost of multiple single gene tests. This test can be used to complement the morphologic and cytogenetic workup of myeloid malignancies.

GENES TESTED: ANKRD26, ASXL1, CEBPA, DDX41, DNMT3A, ETV6, FLT3, GATA2, IDH1, IDH2, KIT, KRAS, NPM1*, NRAS, RUNX1, TP53, WT1
* - One or more exons are not covered by sequencing for the indicated gene; see limitations section below.

METHODOLOGY: Genomic DNA was isolated from peripheral blood or bone marrow and then enriched for the targeted exonic regions of the tested genes. The variant status of the targeted genes was determined by massively parallel sequencing. The hg19 (GRCh37) human genome assembly was used as a reference for identifying genetic variants.

LIMITATIONS: Variants outside the targeted regions or below the limit of detection are not identified. Variants in regions that are not included in the preferred transcript for the targeted genes are not detected. In some cases, variants may not be identified due to technical limitations in the presence of pseudogenes or in repetitive or homologous regions. It is also possible some insertion/deletion variants may not be identified. The following region was not sequenced due to technical limitations of the assay:
NPM1 (NM_002520) exon 1

LIMIT OF DETECTION (LOD): 5 percent variant allele fraction (VAF) for single nucleotide variants (SNV) and small variants less than 24 base pairs (bp). Variants greater than 24bp may be detected at LOD, but the analytical sensitivity may be reduced.

ANALYTICAL SENSITIVITY: The positive percent agreement (PPA) estimate for the respective variant classes (with 95 percent credibility region) are listed below. Genes included on this test are a subset of a larger methods-based validation from which the PPA values are derived.
Single nucleotide variants (SNVs): 96.9 percent (95.1 - 98.1 percent)
Insertions/Duplications (1-24bp): 98.1 percent (95.5 - 99.3 percent)
Insertions/Duplications (greater than 24bp): > 99 percent (92.9 - 100.0 percent)
Deletions (1-24bp): 96.7 percent (92.8 - 98.7 percent)
Deletions (greater than 24bp): 90 percent (79.5 - 96.1 percent)
Multi-nucleotide variants (MNVs): 97 percent (93.0 - 99.0 percent)
FLT3 ITDs: Greater than 99 percent (97.1 - 100.0 percent)

CLINICAL DISCLAIMER: Results of this test must always be interpreted within the context of clinical findings and other relevant data and should not be used alone for a diagnosis of malignancy. This test is not intended to detect minimal residual disease.

This test was developed and its performance characteristics

determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

EER, AML Panel by NGS	See Note

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Acute Myeloid Leukemia Specimen	21-048-118412	2/17/2021 3:36:00 PM	2/17/2021 3:47:17 PM	2/17/2021 4:05:00 PM
Acute Myeloid Leukemia Interp	21-048-118412	2/17/2021 3:36:00 PM	2/17/2021 3:47:17 PM	2/17/2021 4:05:00 PM
EER, AML Panel by NGS	21-048-118412	2/17/2021 3:36:00 PM	2/17/2021 3:47:17 PM	2/17/2021 4:05:00 PM

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical