

Reanalysis of Acute Myeloid Leukemia 4- or 11- Gene Panels, Additional Genes

Test ID: NGSFX

Explanation: Changes to the following will occur on the above effective date: naming convention, genes evaluated, report available time, days performed, and reorganization of the method description.

Current Reporting Name	New Reporting Name
Reflex Analysis, NGSHEM	Reanalysis, AML 4 or 11 Gene Panel
Current Published Name	New Published Name
Next-Generation Sequencing, Reflex from Acute Myeloid Leukemia 4- or 11-Gene Panels, Varies	Reanalysis of Acute Myeloid Leukemia 4- or 11- Gene Panels, Additional Genes
Current Genetics Information	New Genetics Information
This test includes next-generation sequencing to evaluate for 42 genes and select intronic regions.	This test includes next-generation sequencing to evaluate for 47 genes and select intronic regions. Genes added: BCORL1, BRAF, NF1, PPM1D STAT3, UBA1 Gene removed: SRP72
Current Report Available	New Report Available
14 to 21 days	16 to 21 days
Current Days Performed	New Days Performed
Monday, Wednesday, Friday	Monday through Friday

Current Method Description	New Method Description
<p>This analysis requires a next-generation sequencing panel be previously performed at Mayo Clinic Laboratories within the last 6 months (NGAMT / Next-Generation Sequencing Acute Myeloid Leukemia, Therapeutic Gene Mutation Panel [FLT3, IDH1, IDH2, TP53], Varies or NGAML / Next-Generation Sequencing, Acute Myeloid Leukemia, 11-Gene Panel, Varies). An extended bioinformatics analysis is performed on the original data by a bioinformatics pipeline and a variant call file is generated for final analysis and reporting of any additional pathogenic variants within genomic target regions present in the larger NGS HM / OncoHeme Next-Generation Sequencing for Myeloid Neoplasms, Varies.(Unpublished Mayo method)</p>	<p>This analysis requires either NGAMT / Acute Myeloid Leukemia, Therapeutic Gene Mutation Panel (FLT3, IDH1, IDH2, TP53), Next-Generation Sequencing Varies or NGAML / Acute Myeloid Leukemia, 11-Gene Panel, Varies to have been previously performed at Mayo Clinic Laboratories within the last 6 months. An extended bioinformatics analysis is performed on the original data by a bioinformatics pipeline, and a variant call file is generated for final analysis and reporting of any additional disease-causing variants within genomic target regions present in the larger NGS HM / Myeloid Neoplasms, Comprehensive OncoHeme Next-Generation, Varies.(Unpublished Mayo method)</p>

Questions

Contact Connie Penz, Laboratory Technologist Resource Coordinator at 800-533-1710.