CentraCare™

CentraCare Laboratory Services

MEMO

TO: **Medical staff**

FROM: **CCLS – Specimen Referral Center**

DATE: **November 10, 2022**

SUBJECT: **NGS for Myeloid Neoplasms (NGSHM)**

Effective October 24, Mayo made changes to the following test:

NGS FOR MYELOID NEOPLASMS, MAYO CODE NGSHM (LAB0233816)

will be updated as shown below

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
NGS for Myeloid Neoplasms (NGSHM)	Myeloid Neoplasms, NGS, V

Current Published Name	New Published Name
OncoHeme Next-Generation Sequencing for Myeloid Neoplasms, Varies	MayoComplete Myeloid Neoplasms, Comprehensive OncoHeme Next-Generation Sequencing, Varies

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

CentraCare™

CentraCare Laboratory Services

Current Method Description	New Method Description
Next-generation sequencing is performed for the presence of a mutation in targeted regions of the following 42 genes: ANKRD26, ASXL1, BCOR, CALR, CBL, CEBPA, CSF3R, DDX41, DNMT3A, ELANE, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, IDH1, IDH2, JAK2, KDM6A, KIT, KRAS, MPL, NPM1, NRAS, PHF6, PTPN11, RAD21, RUNX1, SETBP1, SH2B3, SF3B1, SRP72, SMC3, SRSF2, STAG2, TERT, TET2, TP53, U2AF1, WT1, and ZRSR2. See Targeted Gene Regions Interrogated by OncoHeme Next-Generation Sequencing for details regarding the targeted gene regions identified in this test. This is a laboratory-developed test using research use only reagents. Extracted DNA from the clinical specimen is fragmented, adapter ligated, and a sequence library of fragments is prepared using a custom capture hybridization method. Individual patient samples are indexed ("bar-coded") for identification and the library is sequenced on an Illumina platform. Sequence data are processed through a bioinformatics pipeline and a variant call file is generated for final analysis and reporting.(Unpublished Mayo method)	Next-generation sequencing is performed for the presence of a mutation in targeted regions of 47 genes. This is a laboratory-developed test using research use only reagents. Extracted DNA from the clinical specimen is fragmented, adapter ligated, and a sequence library of fragments is prepared using a custom capture hybridization method. Individual patient samples are indexed ("bar-coded") for identification and the library is sequenced on an Illumina platform. Sequence data are processed through a bioinformatics pipeline and a variant call file is generated for final analysis and reporting.(Unpublished Mayo method) Genes analyzed: ANKRD26, ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, DDX41, DNMT3A, ELANE, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, IDH1, IDH2, JAK2, KDM6A, KIT, KRAS, MPL, NF1, NPM1, NRAS, PHF6, PPM1D, PTPN11, RAD21, RUNX1, SETBP1, SH2B3, SF3B1, SMC3, SRSF2, STAG2, STAT3, TERT, TET2, TP53, U2AF1, UBA1, WT1, and ZRSR2.

Please feel free to contact the Specimen Referrals Center with any questions at 320-251-2700 Ext. 57320