Myeloid Malignancy Mutation and Copy Number Variation Panel

The first panel of its kind to detect targeted genes, copy number variants (CNVs), and copy number-neutral loss of heterozygosity (CN-LOH) in a single assay.

FEATURED TESTS

3016621	Myeloid Malignancies Mutation and Copy Number Variation Panel by Next Generation Sequencing

A cost-effective, comprehensive, integrated analysis of the genetic abnormalities involved in tumorigenesis

- Detects and reports relevant CNVs, including gains or losses, down to 5 Mb from across the genome
- Identifies likely acquired terminal CN-LOH
- Targets more than 65 clinically relevant genes
- Provides essential information in the diagnosis, subclassification, and risk stratification of hematologic malignancies, based on updated guidelines from the World Health Organization (WHO) and the International Consensus Classification (ICC)

ADDITIONAL TESTING

2011117	Myeloid Malignancies Mutation Panel by Next Generation Sequencing

This panel covers the spectrum of clinically relevant sequence variants, including more than 65 diagnostic, prognostic, and therapeutic biomarkers in myeloid malignancies.

"This test will identify more disease-causing variants, providing patients with more conclusive results than traditional next generation sequencing (NGS) or conventional cytogenetic testing provide."

Peng Li, MD, PhD,
Hematopathologist,
ARUP Laboratories

ARUP LABORATORIES

aruplab.com/myeloid-panel

Why Choose ARUP?

Clinical Relevance

Adherence to National Comprehensive Cancer Network (NCCN) guidelines for mutation profiling in myeloid malignancies ensures accurate, industry-standard results.

Cost-Effective, Comprehensive Panels

Our comprehensive panels provide cost-effective detection of diagnostic, prognostic, and therapeutic biomarkers.

Latest Technology

Next generation sequencing enables detection of targeted gene mutations and genomewide copy number variations in a single assay.

UNLOCK THE ANSWERS THAT MATTER FOR YOUR PATIENTS.

ARUP TEST CODE AND NAME		GENES OR ALLELES ASSESSED
2011117	Myeloid Malignancies Mutation Panel by Next Generation Sequencing	*ANKRD26; ASXL1; ASXL2; BCOR; BCORL1; BRAF; CALR; CBL; CBLB; CEBPA; CSF3R; CUX1*; DDX41; DNMT1*; DNMT3A; ELANE; ETNK1; ETV6; EZH2; FBXW7; FLT3; GATA1; GATA2; GNAS; HNRNPK; IDH1; IDH2; IL7R; JAK1; JAK2; JAK3; KDM6A*; KIT; KMT2A; KRAS; LUC7L2; MPL; NOTCH1; NPM1*; NRAS; NSD1; PHF6; PIGA; PPM1D; PRPF40B; PRPF8; PTPN11; RAD21; RUNX1; SAMD9; SAMD9L; SETBP1; SF3B1; SH2B3; SMC1A; SMC3; SRSF2; STAG2; STAT3; STAT5B*; SUZ12*; TET2; TP53; U2AF1; U2AF2; UBA1; WT1; ZRSR2*
3016621	Myeloid Malignancies Mutation and Copy Number Variation Panel by Next Generation Sequencing	Includes the genes listed above, plus: • CNVs (gains or losses) in the targeted genes • Likely acquired terminal CN-LOH • CNVs ≥5 Mb across the genome Coverage of note: • Losses in *TBL1XR1, CD200, IKZF1, CDKN2A, ASMTL, ERG, ARID2, ATM* • Gains in *MYC* • Losses between *FIP1LI* and *PDGFRA* that result in a potential fusion • Any CN-LOH involving *TP53, JAK2,* and *CBL*

*One or more exons are not covered by sequencing for the indicated gene.