

iBio - MYELOID TUMOR PANEL



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- Mutations of 59 genes involved in myeloid neoplasia are investigated.
- ▶ Based on national collaboration.
- Genes required for diagnosis, relevant for prognosis and indentifying myeloid neoplasm with germline predisposition are included.
- Mutations relevant in myeloproliferative neoplasms are included.

Mininum diagnostic requirement

ASXLI, CEBPA, FLT3, NPMI, RUNXI, TP53

Important prognostic markers or potential targets of therapy

BRAF, DNMT3A, EZH2, IDH1, IDH2, KIT, MT2A, NRAS, STAG2, PTPN11, RAD21, SF3B1, SRSF2, U2AF1, WT1, ZRSR2

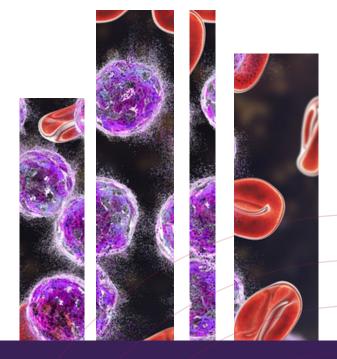
Predisposition identifiers

ANKRD26, ATG28, DDX41, ETV6, GATA2, SRP72, TERT

Myeloproliferative neoplasia genes CALR, CSF3R, JAK2, MPL, SH2B3

ACUTE MYELOID LEUKEMIA

- Acute myeloid leukemia (AML) is a multitude of diseases with distinct genetic background and prognosis.
- Only 25% of patients are expected to survive 5 or more years after diagnosis.
- ➤ >90% of cases show translocations or mutations.
- Besides translocations, ELN recommends routine testing for mutations of 6 genes, over 20 are recognized as relevant for prognosis or identifying myeloid neoplasm with germline predisposition category.



MÓDSZER

- Isolated genomic DNA or bone marrow aspirate/peripheral blood sample in EDTA.
- ► Recommended tumor cell ratio: ≥20%
- Bioinformatic identification of single nucleotide variants (SNV), short insertions and deletions as well as copy number variations (CNV).
- ► Variant classification and annotation (e.g., ClinVar, COSMIC, HGMD, etc.).

LIST OF INVESTIGATED GENES

FULL CODING REGION:

ASXLI, BCOR, CEBPA, DNMT3A, ETV6, EZH2, GATAI, GATA2, IKZFI, PHF6, RAD21, RUNX1, SETD2, SRSF2, STAG2, TET2, TP53, ZRSR2, DDX41, TERC

нотѕротѕ:

ABLI, ACD, ANKRD26, BRAF, CALR, CBL, CSF3R, CUXI, ERCC6L2, ETNKI, FLT3, GNAS, GNBI, IDHI, IDH2, JAK2, KDM6A, KIT, KRAS, MPL, MYC, NFI, NPMI, NRAS, PDGFRA, PRPF8, PTPNII, SAMD9, SAMD9L, SETBPI, SF3BI, SH2B3, SMC1A, SMC3, SRP72, TERT, TINF2, U2AF1, WT1

COVERAGE: >95% (>500×)

AVERAGE SEQUENCING DEPTH: >1000×

turnaround time: 2-3 weeks



WORKFLOW

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CONTACT

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SAMPLE DISPATCH

DNA, bone marrow aspirate or peripheral blood



\$ 63

SAMPLE PROCESSING

microscopical control of tumor cell ratio, DNA isolation



GENETIC ANALYSIS

bioinformatic analysis, variant identification and annotation

REFERENCES

Mims AS et al. J Hematol Oncol. 2021;14(1):96. Döhner H et al. Blood. 2017;129(4):424-447. Hou HA et al. J Biomed Sci. 2020;27(1):81. Leisch M et al. Cancers (Basel). 2019;11(2):252. Döhner H et al. Nat Rev Clin Oncol. 2021 May 18. PMID: 34162404 PMID: 27895058 PMID: 32690020 PMID: 30795628 PMID: 34006997



REPORT

categorization of variants based on guidelines (pathogenic, likely pathogenic, VUS etc.)

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