CENTOGENE
THE RARE DISEASE COMPANY

# Myeloid Tumor Panel

## The Targeted Approach to Detecting Myeloid Malignancies

PRODUCT SHEET

# Myeloid Tumor Panel Somatic Mutation Testing

Myeloid tumors represent the fourth most frequently diagnosed cancer in economically developed countries. The majority of myeloid tumors contain high numbers of somatic mutations, which significantly contribute to the pathogenesis, progression, and prognosis of myeloid malignancies. Sequencing and identification of the genetic variants can provide valuable information for diagnostic decisions, prognosis, therapeutic approaches and patient counseling.

CENTOGENE's Myeloid Tumor Panel has been designed to target important regions within 35 genes that are frequently mutated in myeloid malignancies. Our panel helps physicians identify patients who are less likely to respond well to conventional treatment, enables the identification of patients who will benefit from biomarker targeted therapies, supports in determining the intensity of treatment each patient should receive, and enables rapid eligibility identification and patient stratification for clinical trials.

## The CENTOGENE Advantage

Coverage of **all relevant disease-causing genes** and non-coding and coding pathogenic variants

Powered by CENTOGENE's Biodatabank, **the world's largest real-world data repository** for rare and neurodegenerative diseases

GATTCGA
ACGTTCG
GGACACT

The most **up-to-date panel gene content** with the latest medical and in-house findings

**High-quality analysis for precise clinical interpretation** using advanced bioinformatics and artificial intelligence-powered tools

## Diseases Covered

Acute myeloid leukemia (AML), Chronic myeloid leukemia (CML), Myelodysplastic syndrome (MDS), Myeloproliferative neoplasms (MPN), Chronic myelomonocytic leukemia (CMML), and Juvenile myelomonocytic leukemia (JMML)

# Key Features and Performance

| | |
|---|---|
| **COVERAGE** | ≥ 97.0 % targeted regions covered at ≥ 200 x |
| **VARIANT TYPES** | • Sensitivity<br>SNVs and InDels (≤ 50 bp) > 99.7 %<br>• Accuracy of > 99.7 %<br>• Specificity of ≥ 99.9 % guaranteed for all reported variant. Variants with low quality and/or unclear zygosity are confirmed by orthogonal methods* |
| **REPORTING** | Pathogenic and likely pathogenic variants are reported following ACMG classification guidelines recommendations. Additionally, these variants are reported according to their actionability into Tier 1 (strong clinical significance) or Tier 2 (potential clinical significance), following the standards and guidelines for the Interpretation and reporting of sequence variants in cancer.** |
| **REQUESTED MATERIAL** | ≥ 1 µg DNA or 1 ml bone marrow or 1 ml blood or 1 filtercard (CentoCard®) |
| **TAT** | 10 business days |

SNVs: single nucleotide variants; InDels: small insertions/deletions
* Variants with low quality and/or unclear zygosity are confirmed by orthogonal methods, i.e.: SNVs and InDels by Sanger sequencing
** Li et al. 2017, PMID: 27993330

| GENE | ASSOCIATED SOMATIC PHENOTYPES | RELEVANCE [1–3] | Percentange of acute myeloid leukemia patients with ALTERED GENE [4] |
|---|---|---|---|
| *ASXL1* | Myelodysplastic syndrome | Related with poor prognosis in AML (Predictive biomarker) | 18.18% |
| *ATM* | B-cell non-Hodgkin Lymphoma, Mantle cell lymphoma, T-cell prolymphocytic leukemia | (Predictive biomarker) | 2.66% |
| *CBL* | Juvenile myelomonocytic leukemia | Eligibility criterion for clinical trials | 2.32% |
| *CDKN2A* | Multiple myeloma, Acute lymphoblastic leukemia | Eligibility criterion for clinical trials | 6.70% |
| *CEBPA* | Acute myeloid leukemia | Biallelic mutations related with favourable prognosis (Predictive biomarker) | 4.03% |
| *CREBBP* | Lung adenocarcinomas, Colon adenocarcinomas, Acute myeloid leukemia | Eligibility criterion for clinical trials | 3.19% |
| *DNMT3A* | Somatic acute myeloid leukemia | related with adverse prognosis (Predictive biomarker) | 19.73% |
| *ETV6* | Acute myeloid leukemia | Eligibility criterion for clinical trials | 16.81% |
| *EZH2* | Myelodysplastic syndromes, Lymphoma, Colorectal cancer, Endometrial cancer | Eligibility criterion for clinical trials | 4.22% |
| *FLT3* | Acute lymphoblastic leukemia, Acute myeloid leukemia | Related with reduced survival in Acute lymphoblastic leukemia, (Predictive biomarker), biomarker-directed therapy available | 11.13% |
| *GATA2* | Acute myeloid leukemia | related with adverse prognosis (Predictive biomarker) | 5.33% |
| *HRAS* | Follicular thyroid carcinoma | (Predictive biomarker) | 2.28% |
| *IDH1* | Glioma | biomarker-directed therapy available (Predictive biomarker) | 7.95% |
| *IDH2* | Acute myeloid leukemia, Breast cancer, Colon adenocarcinoma, Lung adenocarcinoma, Myelodysplasic syndromes | biomarker-directed therapy available (Predictive biomarker) | 10.50% |
| *JAK2* | Acute myeloid leukemia, Myelofibrosis, Polycythemia vera | Eligibility criterion for clinical trials | 3.04% |
| *KIT* | Acute myeloid leukemia, Germ cell tumors | (Predictive biomarker) | 2.14% |
| *KRAS* | Acute myeloid leukemia, Bladder cancer, Breast cancer, Gastric cancer, Lung cancer, Pancreatic carcinoma | (Predictive biomarker) | 3.87% |
| *NF1* | Juvenile myelomonocytic leukemia | (Predictive biomarker) | 7.45% |
| *NOTCH1* | Colon adenocarcinoma, Lung adenocarcinoma, Breast cancer | Eligibility criterion for clinical trials | 2.79% |
| *NPM1* | Acute myeloid leukemia | (Predictive biomarker) related with favourable prognosis | 16.38% |
| *NRAS* | Colorectal cancer, Follicular thyroid carcinoma | Eligibility criterion for clinical trials | 9.68% |
| *PDGFRB* | Myeloproliferative disorder | Eligibility criterion for clinical trials | 2.13% |
| *PHF6* | Acute myeloid leukemia, Lung adenocarcinoma, Myelodysplastic syndromes, Endometrial endometrioid adenocarcinoma | Eligibility criterion for clinical trials | 4.21% |
| *PTPN11* | Juvenile myelomonocytic leukemia | Eligibility criterion for clinical trials | 4.84% |
| *RAD21* | Breast cancer, Lung adenocarcinoma, Prostate adenocarcinoma, Colon adenocarcinoma, Acute myeloid leukemia | Eligibility criterion for clinical trials | 2.65% |
| *RUNX1* | Acute myeloid leukemia | (Predictive biomarker) related with adverse prognosis | 14.75% |
| *SF3B1* | Myelodysplastic syndrome | Eligibility criterion for clinical trials | 3.34% |
| *SMC1A* | Lung adenocarcinoma, Endometrial adenocarcinoma, Colon adenocarcinoma, Acute myeloid leukemia | Eligibility criterion for clinical trials | 1.02% |
| *SMC3* | Lung adenocarcinoma, Colon adenocarcinoma, Acute myeloid leukemia | Eligibility criterion for clinical trials | 1.27% |
| *SRSF2* | Acute myeloid leukemia, Myelodysplastic syndromes, Breast cancer, Chronic myelomonocytic leukemia | Eligibility criterion for clinical trials | 10.38% |
| *STAG2* | Lung adenocarcinoma, Bladder urothelial carcinoma, Colon adenocarcinoma, Acute myeloid leukemia | Eligibility criterion for clinical trials | 5.88% |
| *TET2* | Myelodysplastic syndrome | (Predictive biomarker) | 16.98% |
| *TP53* | Breast cancer, Hepatocellular carcinoma, Nasopharyngeal carcinoma, Pancreatic cancer, Osteosarcoma, Glioma | (Predictive biomarker) related with adverse prognosis | 12.30% |
| *U2AF1* | Lung adenocarcinoma, Myelodysplastic syndromes, Acute myeloid leukemia | Eligibility criterion for clinical trials | 4.63% |
| *WT1* | Mesothelioma, Wilms tumor | (Predictive biomarker) related with adverse prognosis | 4.29% |

1 https://www.mycancergenome.org/content/disease/acute-myeloid-leukemia/
2 World Health Organization classification of myeloid neoplasms and acute leukemia (2016)
3 ELN recommendations from an international expert panel (2017)
4 The AACR Project GENIE Consortium. AACR Project GENIE: powering precision medicine through an international consortium. Cancer Discovery. 2017;7(8):818-831. Dataset Version 8. This dataset does not represent the totality of the genetic landscape; see paper for more information.