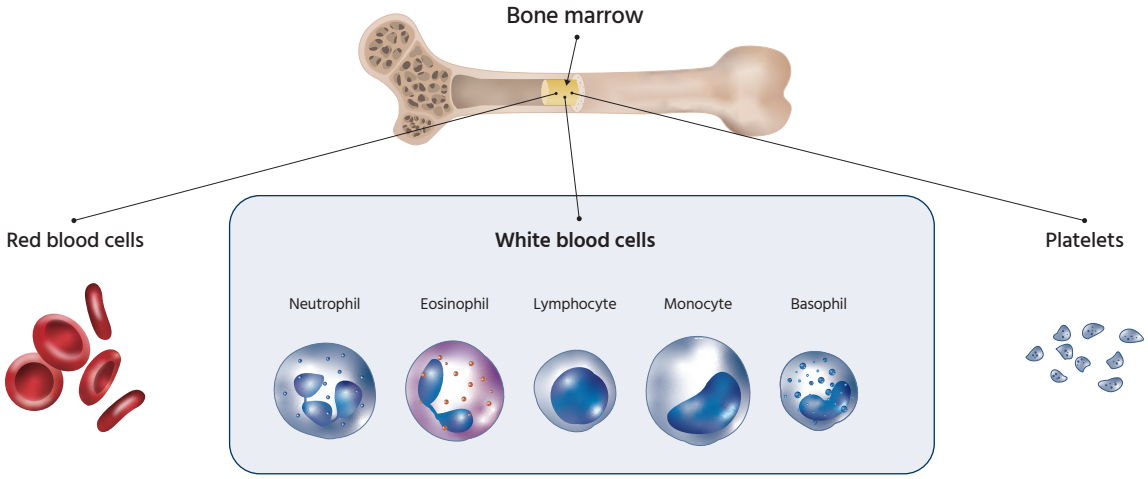
Versatile Solution for
Genomic Profiling of Hematologic Cancers

Hematologic Cancer Panel

What is Hematologic Cancer?



A hematologic cancer is a cancer involving the blood. This begins in the cells of the immune system or in blood-forming tissue, such as the bone marrow. This occurs when cells in the blood grow abnormally, interfering with the ways they are supposed to work. Common types of hematologic cancer are lymphoma, myeloma, and leukemia.

Classification of Hematologic Cancer

Test item	Target region	Gene list
Acute Lymphoblastic Leukemia (ALL)	50 genes	*ABL1, BRAF, BTG1, CDKN2A, CREBBP, DNM2, DNMT3A, EP300, ETV6, EZH2, FBXW7, FLT3, GATA3, IDH1, IDH2, IKZF1, IL7R, JAK1, JAK2, JAK3, KDM6A, KMT2A, KMT2D, KRAS, LEF1, LMO1, MAPK1, NF1, NOTCH1, MSD2, NRAS, NT5C2, NUDT15, PAX5, PDGFRB, PHF6, PTEN, PTPN11, RB1, RUNX1, SETD2, SH2B3, STAG2, STAT3, STAT5B, TBL1XR1, TCF3, TP53, TPMT, WT1*
Acute Myeloid Leukemia (AML)	49 genes	*ANKRD26, ASXL1, ATRX, BCOR, BCORL1, BRAF, CALR, CBL, CBLB, CEBPA, CSF3R, DDX41, DNMT3A, ETV6, EZH2, FLT3, GATA1, GATA2, HRAS, IDH1, IDH2, JAK2, JAK3, KDM6A, KIT, KRAS, MPL, NOTCH1, NPM1, NRAS, PDGFRA, PHF6, PPM1D, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG1, STAG2, STAT3, TET2, TP53, U2AF1, WT1, ZRSR2*
Myelodysplastic / Myeloproliferative neoplasm (MDS/MPN)	49 genes	*ANKRD26, ASXL1, ATRX, BCOR, BCORL1, BRAF, CALR, CBL, CBLB, CEBPA, CSF3R, DDX41, DNMT3A, ETV6, EZH2, FLT3, GATA1, GATA2, HRAS, IDH1, IDH2, JAK2, JAK3, KDM6A, KIT, KRAS, MPL, NOTCH1, NPM1, NRAS, PDGFRA, PHF6, PPM1D, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG1, STAG2, STAT3, TET2, TP53, U2AF1, WT1, ZRSR2*
Lymphoma	66 genes	*ALK, ATM, B2M, BCL10, BCL2, BCL6, BIRC3, BRAF, BTG2, BTK, CARD11, CCND3, CD79A, CD79B, CD83, CDKN2A, CREBBP, CXCR4, DDX3X, EGR2, EP300, ETV6, EZH2, FAS, FAT4, FBXO11, HIST1H1E, ID3, IDH2, IKBKB, IKZF1, JAK3, KLF2, KLHL6, KMT2D, MEF2B, MYC, MYD88, NFKBIA, NFKBIE, NOTCH1, NOTCH2, PIM1, PLCG1, PLCG2, POT1, PRDM1, RHOA, RPS15, RRAGC, SF3B1, SGK1, SOCS1, SPEN, STAT3, STAT5B, TBL1XR1, TCF3, TET2, TNFAIP3, TNFRSF14, TP53, TP63, TRAF3, UBR5, XPO1*
Multiple Myeloma (MM)	34 genes	*ATM, ATR, BRAF, CARD11, CCND1, CDK4, CDKN1B, CRBN, CUL4A, CUL4B, CXCR4, CYLD, DIS3, EGR1, FGFR3, IDH2, IKZF1, IRF4, KRAS, MAX, MYD88, NFKBIA, NR3C1, NRAS, PSMB5, PSMD1, TENT5C, PSMG2, RB1, TENT5C, TP53, TRAF2, TRAF3, XBP1*

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Hematologic Cancer Panel

Advantage of GC Genome's hematologic cancer panel

1. High-quality analysis using advanced bioinformatics pipeline
2. The most up-to-date panel gene with the latest medical and in-house findings
3. Accurate clinical interpretation from specialized medical doctors

Service features

Test	Hematologic Cancer Panel_ALL (ON082) Hematologic Cancer Panel_AML (ON064) Hematologic Cancer Panel_MDS/ MPN (ON065) Hematologic Cancer Panel_Lymphoma (ON083) Hematologic Cancer Panel_MM (ON104)		
Specimen	EDTA WB 3 ml or EDTA BM 3 ml	**TAT**	14 days
Method	NGS (Next Generation Sequencing)	**Sample Storage**	Room temperature (Refrigerated is recommended.)
Test description	This test is for diagnosing hematologic cancer (ALL, AML, MDS/MPN, Lymphoma, and MM), evaluating the prognosis, and determining the treatment policy. DNA is extracted from bone marrow or blood and mutation information of related genes is analyzed. It can detect SNV and small indel mutations, and the detection sensitivity of mutations is about 5%. For ALL panel, thiopurine toxicity-related gene mutations are analyzed together. For AML panel and MDS/MPN panel, FLT-ITD mutations with low allele burden can be detected sensitively.		
Caution & Limitation	• This test was performed using sequencing analysis. It can detect SNP and small-indel variants within the analyzed region, but not structural variations such as copy number variation (CNV) and gene rearrangement. • The limit of detection for SNV and small-indel variants is approximately 5%. • The detected variants in this test are not re-confirmed by Sanger sequencing, ddPCR or other confirmation methods. • This test does not distinguish between germline and somatic variants. If the variant allele frequency of the mutation is close to 50% or 100%, the possibility of a germline variant cannot be excluded. • The variants detected in this test are classified into four (tier 1~4) according to the 2017 JMD guideline (J Mol Diagn 2017;19:313-327), and tier 4 variants are not reported.		

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