Oncology Panels

Myeloid Profiler – DNA

The Uncoded Myeloid Profiler DNA Panel is a cutting-edge tool developed to analyze **75 genes** linked to myeloid cancers. Utilizing advanced sequencing technology, this panel ensures highly efficient and precise target enrichment, offering comprehensive coverage of both DNA hotspot regions and coding sequence (CDS) regions. This extensive genomic profiling provides invaluable insights into the genetic alterations driving myeloid malignancies, enabling better understanding, diagnosis, and potential therapeutic strategies for affected individuals. The Uncoded Myeloid Profiler DNA Panel is a vital resource for researchers and clinicians seeking a deeper understanding of the genetic landscape of myeloid cancers.

➢ DNA - 75 Genes

DNA-Hot spot			
ABL1	GNAS	MYD88	SMC3
ATRX	HRAS	NOTCH1	SRSF2
BRAF	IDH1	NPM1	U2AF1
CBLB	IDH2	NRAS	WT1
CBLC	JAK3	PDGFRA	
CDKN2A	KDM6A	PTEN	
FBXW7	KIT	PTPN11	
FLT3	KMT2A	SETDB1	
GATA1	KRAS	SF3B1	
GATA2	MPL	SMC1A	

DNA-full CDS				
ANKRD26	CSF3R	IKZF1	RHOA	ZRSR2
ASXL1	CSNK1A1	JAK2	RUNX1	
BCL2	CUX1	MAP2K1	SH2B3	
BCOR	CXCR4	NF1*	SRP72	
BCORL1	DDX41	PHF6	STAG2	
BRCC3	DNMT3A	PIGA	STAT3	
CALR	ELANE	PPM1D	STAT5B	
CBL	ETNK1	PRPF8	TERT*_Promoter	
CDKN2A	ETV6	RAD21	TET2	
CEBPA	EZH2	RB1	TP53*	

- Compatible with genomic DNA (gDNA)
- *Enhanced Coverage for GC Rich Regions of CEBPA, NF1, TP53, ASXL1, TERT_Promoter
- 75 genes, including 41 genes with full CDS
- Detect SNV, INDELs and CNV

DNA Performance	
Panel Size	268Kb
Targets covered at minimum 1000×	>95%
On Target	>85%
Fold 80	<1.4
Sample type	Blood, Bone marrow

Streamlined NGS Library Preparation

Simplifies and accelerates the sequencing workflow, reducing time and effort.

Highly Sensitive and Reliable Chemistry

Ensures precise, accurate genomic analysis, even for low-abundance variants

Lower Laboratory Expenses

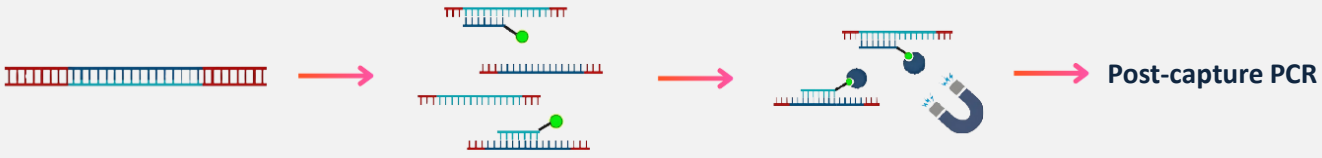
Reduces costs by optimizing reagents and simplifying procedures

Analysis Support

Expert assistance for seamless data interpretation and integration.

Workflow

DNA sample | Library preparation | Sequencing



Fragmentation End repair dA-tailing | Hybridize capture probes | Bind to Streptavidin beads

- **Hybridization:** Hybridization Buffer
- **Input DNA:** 50ng gDNA

Ordering information

Cat. No.	Reactions
UNONC/0507/024	24
UNONC/0507/048	48
UNONC/0507/096	96

For more details connect with us at:
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