# oncology

# Solutions for your hematological cancer research

# Hematological malignancies are known to have a multitude of aberrations across the genome, including:

- Fusion genes
- Somatic mutations (SMs) such as single nucleotide variants (SNVs) and insertions/deletions (indels)
- Copy number (CN) changes such as duplications, deletions, loss of heterozygosity (LOH), copy neutral (cn) LOH, ploidy, and more

No matter the type of aberration you are interested in analyzing, we offer a wide range of tools for comprehensive sample profiling and confirmation of results.

## Applied Biosystems<sup>™</sup> CytoScan<sup>™</sup> HD Suite

- Identify whole-genome CN changes
- Increase detection rate of abnormalities compared to karyotyping, FISH, SNP arrays, and array CGH
- Identify new abnormalities

Detect CN gains and losses, LOH, cnLOH, mosaicism, and clonal heterogeneity in one assay

• Process one to tens of samples per day

## Ion Torrent<sup>™</sup> Oncomine<sup>™</sup> Myeloid Research Assay

Obtain a comprehensive view of DNA mutations (SNVs, indels) and all major gene fusions for myeloid malignancies

 Analyze and detect even challenging genes like CEBPA and and the internal tandem duplications of FLT3 (FLT3-ITDs)

Easily assess all disorders and mutation types in a single, standardized run

Process one to twelve samples per chip



CytoScan HD Suite includes arrays, reagents, and software-runs on the Applied Biosystems" GeneChip" Scanner 3000 7G System

Runs on Ion GeneStudio<sup>™</sup> S5 instrument

# Applied Biosystems<sup>™</sup> Sanger sequencing technology

#### Identify known cancer-specific SMs

- Clearly identify somatic mosaicism down to 5%
- Ideal for low- to medium-throughput needs

#### Detect known CN changes using MLPA analysis

- Obtain CN data for known target genes
- Ideal for detecting known genomic deletions and insertions

Runs on Applied Biosystems<sup>™</sup> SeqStudio<sup>™</sup> Genetic Analyzer

## Applied Biosystems<sup>™</sup> TaqMan<sup>®</sup> Assays

Accurately detect known SMs, CN changes, and fusion genes

- Quickly and easily detect known targets
- Ideal for identifying known abnormalities

#### Cover known abnormalities with targeted analysis

- Verify microarray and next-generation sequencing results
- One abnormality per assay



Runs on Applied Biosystems" QuantStudio" family of real-time PCR instruments



# Find out more at thermofisher.com/hemeonc

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