Agilent SureSelect CD HMH Myeloid Cancer Panel

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"This new sensitive and cost-efficient NGS method allowed integrated analysis of resistant chronic myeloid leukemia and thus will be of interest to elucidate the mutational landscape and clonal architecture of myeloid malignancies driven by these fusion genes."

Targeted next-generation sequencing for leukaemia investigation

Agilent Community Designs for next-generation sequencing (NGS) are targeted sequencing panels established in collaboration with subject matter experts in different research fields. These NGS designs are available as custom, made-to-order panels that provide you with robust and cost-effective sequencing results that focus only on your genes of interest.

The Agilent SureSelect CD HMH myeloid cancer panel has been developed in association with Dr. Ivan Sloma, Associate Professor at the Department of Hematology and Immunology, Henri Mondor University Hospital. The onco-hematology laboratory at Henri Mondor is dedicated to molecular diagnostics and translational research on myeloproliferative neoplasms, myelodysplastic syndromes, acute leukemia, and hematopoietic stem cell transplantation.

This targeted enrichment panel has been designed for the research of hematological disease.

The identification by NGS of well-characterized fusion genes, such as BCR::ABL1, FIP1L1::PDGFRA, or PML::RARA, is essential for a more accurate estimation of the clonal architecture of these malignancies and to track their clonal evolution. The detection and quantification of these fusions by NGS technology remains technically challenging.
Gricourt et al.[1] have developed an asymmetric capture sequencing strategy (aCAP-Seq) built on SureSelect technology. Fusion detection by aCAP-Seq was determined to be of both high sensitivity and specificity, with a low limit of detection. In addition to probes designed to detect these fusions, this panel also contains 43 genes to detect single nucleotide changes, indels, and copy number variants (CNVs) within a key set of hematological genes (Figure 1).

Breakpoint locations and sequences identified by NGS were concordant with results obtained by Sanger sequencing.

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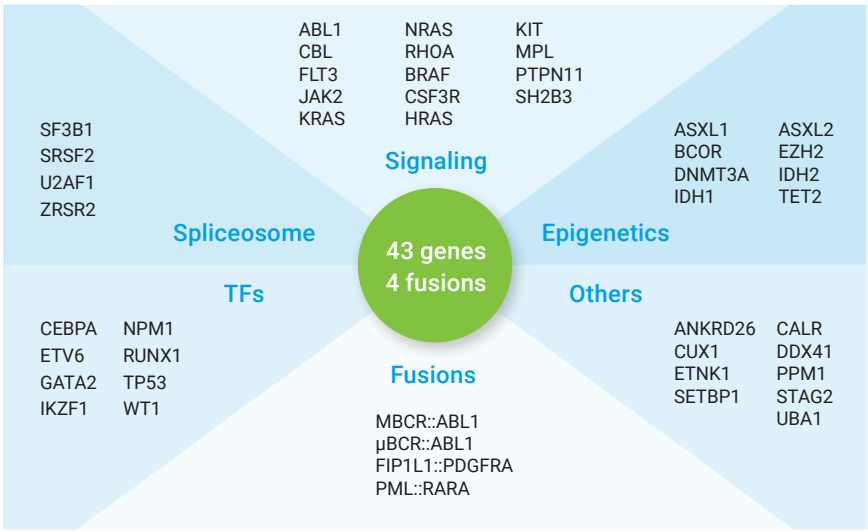
Features of the Gene Panel Design

- A 43-gene panel specifically selected to identify mutations in myeloid malignancies
- An asymmetric capture design unique for coverage of the most frequent breakpoint regions involved in BCR::ABL1, FIP1L1::PDGFRA, and PML::RARA fusions
- A 104.7Kb total footprint
- Agilent SureSelect XT HS library preparation application
- Optimization with Illumina chemistry, with 16 libraries per MiSeq run (v3 2 × 300 bp flow cell)
- A bioinformatic pipeline, HmnFusion, designed for fusion detection and quantification, available through Conda and Docker. Documentation and support can be found at https://github.com/guillaume-gricourt/HmnFusion

HMH Myloid Cancer



Diagnosis, prognosis, relapse

- Size: 105kb
- 16 samples on Mi-SeqV3 2x300bp
- Myeloid malignancies
  - AML
  - CML
  - ET, PV, PMF, MPN-Eo
  - aCML
  - CNL
  - CMML/JMML
  - MDS + predisposition
- Clonal hematopoiesis
- AITL
- VEXAS syndrome

Figure 1. Coverage by the SureSelect CD HMH myeloid cancer panel

Product	Part Number
SureSelect CD HMH Myeloid Cancer 16	5282-0013
SureSelect CD HMH Myeloid Cancer 96	5282-0014
SureSelect CD HMH Myeloid Cancer 96A	5282-0015

Table 1. Ordering information for the Agilent SureSelect CD HMH myeloid cancer panel. *Note: part numbers cover the capture probe libraries only. Library prep and target enrichment kits must be purchased separately.*

References

1. Gricourt et al. Fusion Gene Detection and Quantification by Asymmetric Capture Sequencing (ACAP-Seq). The Journal of molecular diagnostics: JMD **2022**, 24 (11), 1113-1127. https://doi.org/10.1016/j.jmoldx.2022.07.004.
2. Tran Quang et al. TET2 mutational status affects myelodysplastic syndrome evolution to chronic myelomonocytic leukemia. Haematologica **2023**. https://doi.org/10.3324/haematol.2022.282528

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