Blood Cancer Sample to Insight® Series: Real-Life Experience

Maximize blood cancer clinical research with flexible NGS panels for consolidated sample to sequencing analysis

Dr. Friedel Nollet, Molecular Biologist, Department of Laboratory Medicine,
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Customer Profile

Dr. Friedel Nollet gained his first experience with next-generation sequencing (NGS) in 2014 using a MiSeq® system for HLA typing, before progressing to mutation studies using the amplicon-based QIAGEN® GeneRead™ system. In addition to the QIAseq® Human Myeloid Neoplasms Panel with 141 genes, he currently uses QIAseq DNA Custom Panels, including a 21-gene panel for myeloid malignancies, a 25-gene panel for solid tumors and a small TP53 panel. "Integrating a NextSeq® 550 instrument into our workflow in April 2020 not only increased our throughput, but enabled us to analyze more custom panels with a larger number of genes per panel," says Dr. Nollet. He is now implementing a workflow for custom lymphoid and liquid biopsy panels.

The Challenge

"Around 5 years ago, the number of genes we needed to sequence for acute myeloid leukemia increased dramatically," says Dr. Friedel Nollet. A much more efficient solution than Sanger sequencing was required to cope with the sheer volume of work. At the same time, his colleagues in the Pathology Lab were using QIAGEN Pyrosequencing® solutions to analyze solid tumors, and the number of mutations they needed to sequence was also increasing exponentially. Use of QIAseq custom NGS panels allowed them to consolidate their sequencing activities. "It very quickly became clear that switching to massively parallel sequencing would have enormous benefits for our laboratory in terms of throughput, efficiency and turnaround time. To accomplish this, we partnered with QIAGEN," Dr. Nollet explains.

"The testing workflow also needed to be compatible with GC-rich genomic regions, providing 100% coverage of genes rich in GC content such as *CEBPA*. Accurate detection of large insertions/deletions and the internal tandem duplications (ITD) of the *FLT3* gene is also a major factor for us. QIAseq panels were the optimal solution for all of these testing needs."

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Why a QIAGEN Workflow with QIAseq Panels?

Amplicon-based methods deliver high coverage for some regions, with low coverage for others. This can result in a loss of sequencing data for important regions, which means that an increased number of sequencing reads is required, with higher costs per sample. The QIAseq panels overcome this technical challenge. Dr. Nollet says, "Our lab needed a sample to sequencing solution that fulfilled a number of important criteria. Uniform horizontal coverage of genes was absolutely crucial for our testing workflow and QIAseq panels deliver this."

Dr. Nollet added, "The testing workflow also needed to be compatible with GC-rich genomic regions, providing 100% coverage of genes rich in GC content such as *CEBPA*. Accurate detection of large insertions/deletions and the internal tandem duplications (ITD) of the *FLT3* gene is also a major factor for us due to the significance of this gene as a drug target for acute myeloid leukemia (AML). QIAseq panels were the optimal solution for all of these testing needs."

Dr. Nollet's lab uses two bioinformatics tools, enabling cross-checking of results for quality purposes. One of these solutions is CLC Genomics Workbench, which enabled analysis and visualization of the vast amount of sequencing data generated.

Dr. Friedel Nollet showing QIAseq sequencing data on an Illumina sequencer to his team.

The Benefits

"QIAseq panels fulfill our requirements by providing uniform horizontal coverage of genes and enable us to successfully sequence genes rich in GC content (*CEBPA*) and very large ITD sequences (*FLT3*). A major advantage for us is that we can use the same workflow for blood, FFPE and cfDNA samples (liquid biopsies)," explains Dr. Nollet. He is currently testing the QIAseq Multimodal Leukemia Panel as he also wants to perform RNA sequencing. "QIAseq Multimodal panels have the very unique advantage that they consolidate DNA and RNA sequencing into a single workflow," says Dr. Nollet. His laboratory uses CLC Genomics Workbench to perform comprehensive NGS data analysis.

Dr. Nollet wants to expand his testing portfolio with larger panels, tests for more types of cancer, a workflow for liquid biopsy samples, and DNA and RNA sequencing for translocation detection. To further increase efficiency, he would like to implement an automated workflow to reduce hands-on time and increase throughput using the same number of lab personnel.

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The Impact of COVID-19

"COVID-19 has impacted our work as most of our highly skilled lab personnel are helping with testing for COVID-19 and will continue to do so until a high-throughput automated solution arrives in October or November. During the first phase of the pandemic, the number of samples we received dropped by about 40–50%. But, as the pandemic went on, the number of samples increased or even exceeded usual levels for a few weeks," explains Dr. Nollet.

"QIAGEN partners with us to design custom NGS panels and implement optimized sample to sequencing workflows that fulfill our testing needs."

Learnings

- "In the rapidly evolving field of blood cancer clinical research, labs like ours require optimized testing workflows, from Sample to Insight.
- QIAGEN partners with us to design custom NGS panels and implement optimized sample to sequencing workflows that fulfill our testing needs.
- We gain access to innovative NGS solutions from QIAGEN early on, enabling us to implement them promptly and maintain our competitive edge," says Dr. Nollet.

Go to **www.qiagen.com/blood-cancer-awareness** to learn about our oncohematology solutions

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QIAseq Panels are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

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