Implementing NGS quickly and avoiding bottlenecks: One lab’s experience

Professor Kurt Zatloukal, PhD, is professor at the Institute of Pathology at the Medical University of Graz, Austria. He heads the Christian-Doppler-Laboratory, which focuses on testing new technologies for the processing of biological samples. He also works closely with the Centre for Biomarker Research in Medicine (CBmed), an Austrian competence centre developing customized solutions for biomarker research. One of the focuses of Prof Zatloukal’s lab is the development of strategies for the identification of cancer biomarkers. A highly complex and heterogeneous disease, the application of next generation sequencing technologies has the potential to provide important insights into molecular pathology of cancers.

Here Prof Zatloukal talks about his experience as an early adopter of QIAGEN’s complete sample to insight NGS workflow, the GeneReader™ NGS System, which was designed specifically with clinical cancer research labs in mind.

What is the importance of biomarker research in understanding disease?

You cannot sufficiently predict the behaviour of a cancer based on histopathological analysis alone, as the disease is influenced by so many different parameters. As such we need deeper insight into the molecular biology underlying a disease. That’s where sequencing and molecular testing comes into play.

Where does NGS play a role in this?

Thanks to next-generation sequencing we are able to get a much more comprehensive view on the variety of mechanisms underlying cancer, and identify the genetic aberrations that drive its progression.

What are the advantages of implementing NGS using an integrated solution from a single company?

If you combine different parts of the process with different products and technologies from different companies, you never know how well they will fit and function together. In order to assemble a harmonized workflow to achieve reliable results, one has to validate the whole workflow, which is not a trivial task given the inherent complexity of the NGS testing process. This process typically takes months, and requires a lot of design, testing and optimization work. This is why we favoured the approach by QIAGEN, which offers a truly complete, end-to-end solution. They have already harmonized the workflow at an industrial scale; so the workload is now minimized at the user level.

What in your opinion are the major bottlenecks to widespread implementation of NGS in labs?

People tend to largely underestimate the true cost of running NGS. Labs typically only account for the direct cost of a sample run, not considering the cost of an often lengthy and pricey validation process. With the GeneReader NGS System, I expect to see a major advantage from a concept that provides such a fully integrated workflow.

The integrated data analytics pipeline [part of the QIAGEN solution] based on the ingenuity technology is key for the proper interpretation and drawing the right conclusions. Because it is not just about producing sequencing data, but more so the right data interpretation, which is widely recognised as a major bottleneck in this field.

At the moment I am not aware of another product like the QIAGEN NGS workflow. It’s not just the GeneReader, it’s the whole workflow. Therefore I am very convinced that this is the best way to go, especially for laboratories less experienced but interested in taking advantage of the NGS technology.

See how your lab can go live with NGS in 30 days. Visit www.qiagen.com/GeneReader