

## ***An Interview with Institute of Oncology Research, Dr. Francesco Bertoni, MD***

*“The HTG EdgeSeq technology represents a nice way to combine the possibility of working with FFPE specimens and next-generation approaches. Moreover, the HTG EdgeSeq Oncology Biomarker Panel (OBP) can be applied on in vitro models and then the results can be validated on FFPE specimens from clinical studies using the same assay.”*



**Dr. Francesco Bertoni, MD**, Head, Lymphoma Genomics, Vice-Director, Institute of Oncology Research (IOR), Università della Svizzera italiana, Bellinzona, Switzerland.

Dr. Francesco Bertoni's research specialty is lymphoma. His group has two areas of interest which are interconnected. The first is the development of anti-lymphoma compounds, a topic that is linked with the Phase I and Lymphoma programs at the local Oncology Institute of Southern Switzerland. The second area of interest focuses on the identification and functional characterization of novel mechanisms underlying lymphoma pathogenesis. His team utilizes molecular profiling of both DNA and RNA, investigating copy number variations and methylation patterns. More recently, his lab is focused on the expression analysis of lymphoma cells exposed to anti-cancer drugs, looking at mechanisms of action, mechanisms of resistance, and identifying potential biomarkers using microarrays and RNASeq. In addition, his team is involved in prospective clinical trials utilizing DNA and RNA profiling.

Dr. Bertoni will be presenting a poster at the upcoming American Association of Cancer Research (AACR) 2018 Conference, (Abstract #4275, *Analysis of gene and protein expression in lymphoma cell lines using multiple platforms*). Dr. Bertoni's lab will utilize the HTG EdgeSeq OBP to study clinical specimens collected in the context of clinical studies. Dr. Bertoni provided these insights on the use of the HTG EdgeSeq OBP in advancing his lymphoma research.

### **HTG: What was the content and outcome of your recent publication with HTG EdgeSeq data?**

**Dr. Bertoni:** We have previously applied the HTG EdgeSeq Oncology Biomarker Panel to identify potential biomarkers of sensitivity to a novel dual PI3k/mTOR inhibitor (PMID: 29066507). In the poster presented at AACR 2018, we have applied the HTG EdgeSeq OBP on 51 lymphoma cell lines in parallel to microarray-based expression profiling and proteomics via mass spectrometry. The panel demonstrated a broader dynamic range and ability in detecting low abundance transcripts than microarrays. A comprehensive cell- and gene-specific analysis revealed that across cell lines showed a high correlation between mRNA and protein expression, particularly for the next-generation sequencing (NGS) panel. A low number of discordant genes (high RNA expression-low protein level or low RNA expression-high protein level) was identified and we're currently looking at these in more detail.

### **HTG: What are the next steps in your research?**

**Dr. Bertoni:** Regarding the HTG EdgeSeq technology, we would like to exploit it within prospective clinical trials aiming to identify the patients who can benefit most from specific therapeutic approaches.