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# Next generation tools for gene expression profiling and gene fusion detection in tumor samples

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Next generation RNA sequencing is an ideal platform to leverage archival formalin-fixed paraffin-embedded (FFPE) tissue samples for cancer research, as it offers extensive functional genomic information including transcriptome expression profiling, differential expression analysis and fusion detection. However, both RNA degradation from the formalin fixation process as well as limited sample material, pose major challenges for RNA sequencing of FFPE samples. In this talk, we will detail a novel method for generating whole-transcriptome RNA sequencing libraries from moderate to poor quality FFPE samples starting with as low as 20 ng total RNA. This approach provides increased transcriptome coverage and robust measurement of gene expression levels compared to established FFPE RNA sequencing methods. Furthermore, we demonstrate that we can detect both known and novel gene fusions in clinical tumor samples that are potential drivers of disease. We anticipate this new technology, called TruSeq RNA Access, will enable functional genomic studies on numerous FFPE tumor samples that would not previously be possible, providing invaluable information for developing cancer diagnostics and therapeutics.

## Biography

Gary P Schroth is currently a Distinguished Scientist at Illumina where he directs the Genomic Applications Group based in San Diego. He obtained his PhD in Biochemistry from the University of California at Davis. He has been working in the field of next-generation sequencing for over 9 years as part of Illumina (and Solexa). His main research interests today are in the use of NGS to study gene structure and expression, epigenetics, and cancer genomics. Over the course of this career, he has published more than 75 peer reviewed research papers and holds 17 U.S. patents.

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