How do we perform molecular characterization of a patient's tumor? Well, most of us today will use Next-Generation Sequencing. It's fast, cost-effective, and requires less tissue. Also, it allows us to see many genes, mutations, and much more. I'll come back to that during my talk.

Previously, we used other platforms, like FISH, immunohistochemistry, or PCR, where we did single studies for single abnormalities. But with Next-Generation Sequencing, we can capture a lot of abnormalities at the same time using a relatively small amount of tissue.

“Next-Generation Sequencing” is a broad term. Within that term, we have small panels, larger panels, and the type of panel differs from institution to institution or, let's say, vendor to vendor. Some use smaller panels, others use larger ones. But Comprehensive Genomic Profiling covers a large number of genes and mutations.

Do we know if Next-Generation Sequencing leads to changes? Well, we learned that many years ago. This data goes back to 2014. A study showed that 28% of patients received different therapy than initially recommended before Next-Generation Sequencing was performed. So, in other words, Next-Generation Sequencing, or NGS as we often call it, can truly change the way we are treating lung cancer patients today.