Sequencing cancer genomes, rather than testing specific genes is future of treatment

In the march toward personalized medicine, genotyping cancers has become more and more complex. Panels that pick up variations in hundreds of potentially important genes can help physicians determine how a particular tumor operates and the best course of treatment. Whole-exome sequencing—the analysis of all the coding regions of the genome—has been somewhat of a pipe dream for clinical oncology, but a study published May 19 in Nature Medicine introduces a platform for analyzing the entire exome of cancer patients' tumors.

"It's fantastic," said Sameek Roychowdhury, an oncology genomics researcher at Ohio State University who did not participate in the study. "It's what everybody needs to see happening for this field."

The new whole-exome platform extracts DNA from a preserved tumor sample, sequences all of the coding regions in the genome, and runs the data through an algorithm that can make sense of the variations uncovered and pick out those for which an available treatment might be appropriate.

Read the full, original story: Making Sense of the Tumor Exome