Each instrument will be able to produce 300 gigabases of sequence per run. This equates to three genomes, 40 exomes or 20 transcriptomes. For targeted resequencing and microRNAs, we can use 96 barcodes to multiplex samples for high-throughput projects. Advances in sequencing chemistry and base-calling algorithms have pushed the read length to 75 bases the accuracy to 99.99 percent. This will allow us to produce twice as much data of a higher quality in half the time. To put this in perspective, sequencing the first human genome took 13 years and cost $3 billion. This technology enables us to do that in two weeks for less than $10,000.

What will this contribute to our battle against cancer? Our researchers and physicians will be able to unravel the complexities of each cancer and come to a deeper understanding of how different cancers initiate and progress. Better understanding will lead to the development of new and better therapies. In the near future, this technology will eventually be used in the clinic to diagnose the unique genetic signature of each cancer and customize each patient's therapy. This technology is creating a paradigm shift in medicine and will lead to the development of *personalized medicine*. Our goal is to make each cancer curable.

For more information, email Timothy.Wise@osumc.edu or visit http://cancer.osu.edu/research/cancerresearch/sharedresources/microarray/pages/index.aspx