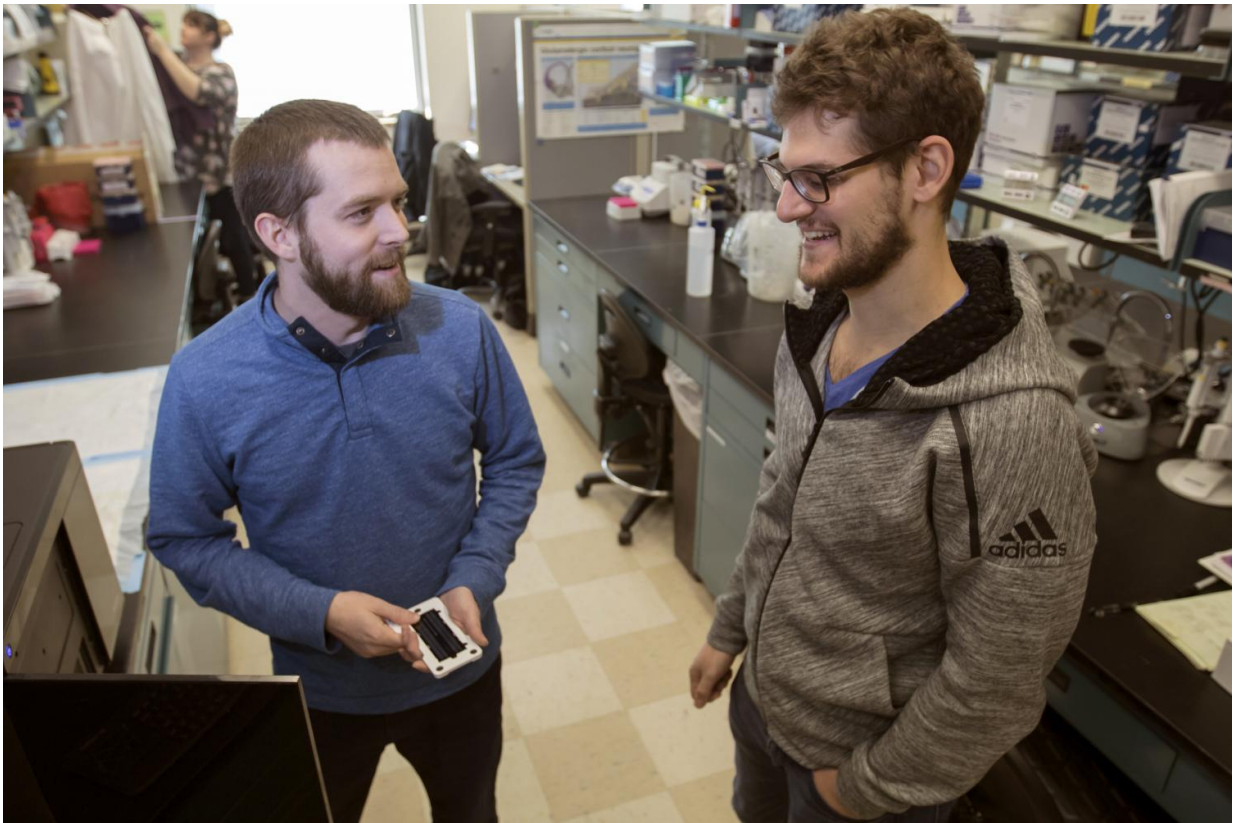


New genome-mapping technique opens new avenues for precision medicine

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Andrew Adey and Kristof A. Torkenczy work in their research laboratory at Oregon Health & Science University in Portland. Credit: OHSU/Kristyna Wentz-Graff

OHSU scientists have uncovered a method for quickly and efficiently

mapping the genome of single cells within the body. Their findings, to be published Jan. 30 in the journal *Nature Methods*, clears the way for a significant advance in precision medicine, including cancer, and many other disease areas.

Single-cell genome sequencing has proved valuable for detecting variations within cells, particularly within tumors. However, the lack of an efficient, cost-effective method to map the genome of large numbers of [single cells](#) has made it difficult to conduct the kind of robust analysis necessary to characterize the specific genetic makeup of [cancerous tumors](#) affecting individuals, or other [cell types](#) in the body.

The study demonstrates a method of barcoding cells multiple times and then sequencing them. The method greatly expands the number of single cells that can be mapped.

"A tumor is constantly evolving and constantly changing," said senior author Andrew Adey, Ph.D., an assistant professor of molecular and medical genetics in the OHSU School of Medicine. "If we're able to break down the distinct cellular components of a tumor, we can target the cancer much more precisely."

Using their cell indexing [method](#), researchers constructed genomic libraries for 16,698 single cells - approximately two orders of magnitude beyond what could be achieved using conventional methods. In the next phase of work, Adey hopes to expand on the types of information that can be accessed in single [cells](#), including epigenetic properties that vary greatly between different cell types in the body.

"This will enable big advances," Adey said. "Through collaboration with other researchers at OHSU, we hope to begin using this tool fairly quickly in a clinical research setting."

More information: Sequencing thousands of single-cell genomes with combinatorial indexing, *Nature Methods*, [nature.com/articles/doi:10.1038/nmeth.4154](https://doi.org/10.1038/nmeth.4154)

Provided by Oregon Health & Science University

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