

# Measuring Functional Heterogeneity Among Single Cells

#### Product

Enzymatic Screening

#### Indication

Cancer Biology

#### **Value Propositions**

- Extends the utility of singlecell assays
- Compatible with existing platforms measuring gene expression

#### Market

- \$168 billion—
  Global cancer diagnostics market (2020)
   (6.9% CAGR 2018-2028)
- Precision medicine emerging in the global market and expected to reach \$216B by 2028

#### **Intellectual Property**

- US and EP national stage patent applications\*
- Available for Exclusive & Non-Exclusive Licensing

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## Background on CU4163H

New methods to study heterogeneity at cellular resolution in complex tissues are rapidly transforming our understanding of cellular heterogeneity in human tissues and disease. These methods measure differences in gene expression, chromatin accessibility, and protein levels across thousands of cells to understand developmental trajectories of tissues, tumors, and whole organisms. However, their reliance on measurements of the steady-state abundance of DNA, RNA, and protein limits our ability to extract dynamic information from single cells. These processes can vary widely from cell to cell, making any consequences or mutagenic effects vary depending on genetic background and physiological phase. Tools that can measure such enzymatic activities will be valuable in understanding functional heterogeneity in single cells for insight into changes that occur during chemotherapy and more accurate and effective prognoses for cancer patients.

### **Technical Innovation**

Dr. Jay Hesselberth and Dr. Amanda Richer at the University of Colorado have developed a novel method for measuring enzymatic activities simultaneously in thousands of single cells — a scale that has not been previously achievable. Rather than measuring the abundance of molecules, they can directly measure enzymatic activities present in single cells by analyzing the conversion of substrates to products by single cell extracts in a high-throughput DNA sequencing approach. This technology is compatible with existing platforms (e.g., from 10X Genomics) that measure gene expression in 10<sup>3</sup>-10<sup>6</sup> cells and can be many different enzymatic activities simultaneously. One assay measures DNA repair capacity of cells by examining repair products exposure to a single cell extract. This method has high potential for understanding how cells repair DNA under normal conditions and during chemotherapy. The method also complements existing approaches to measure static levels of biomolecules in single cells, providing a dynamic view of cellular function that will allow for many new types of experimental approaches. In contrast to existing methods, this method can be applied to primary human cells and tissues, and researchers are focusing on expanding its utility to understand fundamental aspects of cancer biology by measuring additional activities, including proteases, protein kinases, and protein phosphatases.



**Figure:** Overview of single-cell measurement of biochemical activities (e.g. DNA repair) in single-cell mRNA sequencing experiments