

Robust and sensitive detection of gene fusions using high-throughput SMART-Seq chemistry on the ICELL8 cx system

Genomics

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Isolating single cells at high-throughput levels and obtaining their full-length transcript information has become critical to the scientific community to generate rich single-cell datasets. We automated SMART-Seq chemistry on the ICELL8cx Single-Cell System to address this need and show this workflow provides useful information that end-capture technologies cannot. We present performance data showing that capturing junction and spanning reads with this automated, full-length mRNA-seq method enables confident and robust identification of gene fusions in a breast cancer tumor cell line.