

## PRODUCT DATASHEET

# Single-Cell RNA Sequencing: SmartSeq2

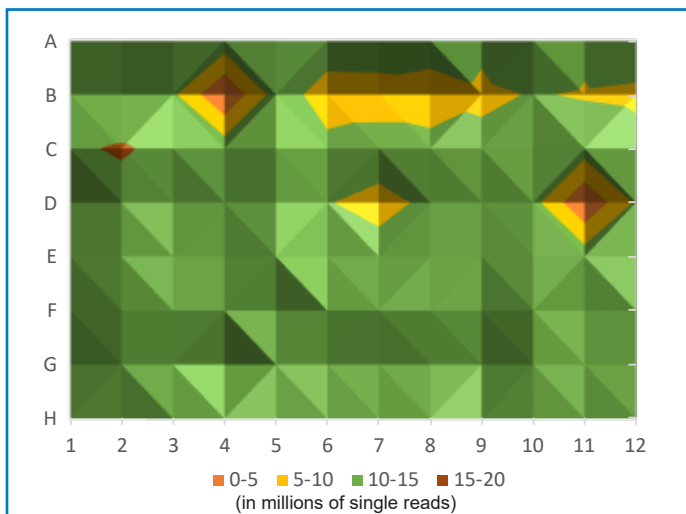
## OVERVIEW

Single-cell RNA sequencing is a powerful technique to study gene expression, cellular heterogeneity, and delineation of cell states within cell cultures, tissues, and organ systems.

As an early pioneer of single-cell sequencing, Broad Genomic Services' SmartSeq2 defines what should be expected of a scaled single-cell process. Based on the methods published by Trombetta et al.<sup>1</sup>, and used to generate data for the Human Cell Atlas, our process is ideal for applications such as; profiling gene expression in stem cell differentiation, organ development, tumor progression, and characterization of cell population responses to environmental signals and conditions. Unlike other single cell services, the SmartSeq2 process is fully compatible with frozen/archival sample types, and the sample preparation technique results in full-length transcript capture, as opposed to 3' tags.

Combining our laboratory best-practices technique with the latest in robotics, automation, and workflow design, we provide the reproducibility and quality at scale, needed for large scale collaborative projects.

<sup>1</sup> Trombetta, J. J., Gennert, D., Lu, D., Satija, R., Shalek, A. K. and Regev, A. (2014), Preparation of Single-Cell RNA-Seq Libraries for Next Generation Sequencing. *Current Protocols in Molecular Biology*, 107: 4.22.1-4.22.17. doi:10.1002/0471142727.mbo422s107



**Figure 1.** Plate heat map of the number of single reads per cell population by plate well position, illustrating evenness of coverage. Note well D11 is a negative control.



GENOMIC SERVICES

- Accurate quantification of gene expression in individual cells

- Highly reproducible and scaled version of the process used at the Klarman Cell Observatory

## WHAT'S INCLUDED

- Sample receipt and incoming visual QC
- Plating, sample preparation (LC) and QC
- 2x38bp paired sequencing
- Single cell: ~1 million reads per well\*
- Cell population: ~4 million reads per well\*
- Data delivery through a secure online portal

## INPUT REQUIREMENTS

- Cell lysate in 5 ul Buffer TCL + 1% beta-mercaptoethanol (BME)
  - Single cell = 1 cell/well
  - Cell population = ~1000 cells/well
- Very low concentration RNA (can be purified), 1-2 ng/uL in 5-10uL buffer (water, TE, etc.)
- Minimum sample data including Collaborator Participant ID and Collaborator Sample ID

This process is not compatible with nuclei or other cell components, nor purified RNA > 2ng/ul and/or 10ul.

## PERFORMANCE METRICS

|                                      | Single Cell             | Cell Population       |
|--------------------------------------|-------------------------|-----------------------|
| <b>Avg. Number of Reads:</b>         | <b>~1 million*</b>      | <b>~8-12 million*</b> |
| Avg. % Aligned:                      | ≥65%                    | ≥65%                  |
| Avg. Genes detected @ 1million reads | ~5000-6000 <sup>†</sup> | ~12000 <sup>†</sup>   |

<sup>†</sup>number of genes is cell type dependent

## DATA DELIVERABLE

- Unaligned/unmapped, non-demultiplexed FASTQ files accessible via getsite

**\* Due to the variability and nature of single cell sequencing, all samples submitted to the SmartSeq2 process are accepted "on risk" and subject to billing regardless of data quality and quantity**

## MORE INFORMATION

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