BROAD CLINICAL LABS

PRODUCT DATASHEET

SmartSeq2 Single Cell Sequencing

Product Overview

RNA sequencing is a powerful technique to study gene expression within cell cultures, tissues, and organ systems. However, high input requirements for standard mRNA or total RNA processes can exclude valuable specimens. Our SmartSeq2 service was developed based on the methods published by Trombetta et al.[1], and used to generate data for the Human Cell Atlas[2]. SmartSeq2 accurately profiles gene expression in cell populations and from low-input specimens, starting with multiple potential input types, and is ideal for applications such as profiling gene expression and characterization of cell population responses to environmental signals and conditions.

SmartSeq2 is compatible with frozen/archival sample types, and the sample preparation method results in full-length transcript capture, as opposed to 3' tags. Combining our laboratory best practices with the latest in automation and workflow design, we provide the reproducibility and quality at scale needed for large scale projects.

What's Included

- Sample receipt and incoming visual QC
- Library construction and QC
- 2x38bp paired-end sequencing
- Expected output: ~80M reads per well
- Data delivery to customer-provided GCP or AWS S3

Input Requirements

- Very low concentration RNA (can be purified), 1-2 ng/µL in 5-10µL buffer (water, TE, etc.); or
- Cell lysate in 5µL TCL or RLT Buffer + 1% beta-mercaptoethanol (BME)
- Cell populations should be 100-1000 cells per well
- Samples must be in 96 well Eppendorf twin.tec® PCR LoBind or 96 well Eppendorf twin.tec® PCR plates, sealed with Bio-Rad Microseal "F" foil; please ensure a tight seal seal around the edges as well as in between rows and columns.
    - Improper sealing risks sample contamination or sample loss
- Volume should be 5- 10µL per well, and all wells should have the same volume.
- Minimum sample data including collaborator participant ID,collaborator sample ID, and expected number of cells per well.

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

Avg. Number of Reads	>80 Million
Avg. % Aligned	>80%
Avg. Genes Detected	~17000*

** These numbers are expected averages and dependent on cell type; results for individual wells may vary due to variability in sample inputs.*

Data Deliverable

- FASTQ files

[1] 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.mb0422s107

[2] https://www.humancellatlas.org/