BROAD CLINICAL LABS

PRODUCT DATASHEET

SmartSeq2 Single Cell Sequencing

Product 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. 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 single cells, starting with multiple potential input types, and 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 most single cell methods, 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
- Plating, library construction, and QC
- 2x38bp paired-end sequencing
- Expected output: ~1M reads per well for single cell; ~4M reads per well for cell population
- Data delivery to Terra Workspace

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)
- Single cells should be 1-100 cells per well, and 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.
- Volume should be 5- 10µL per well, and all wells should have the same volume.
- Minimum sample data including collaborator participant ID and collaborator sample ID

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

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

†number of genes is cell type dependent

** 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/