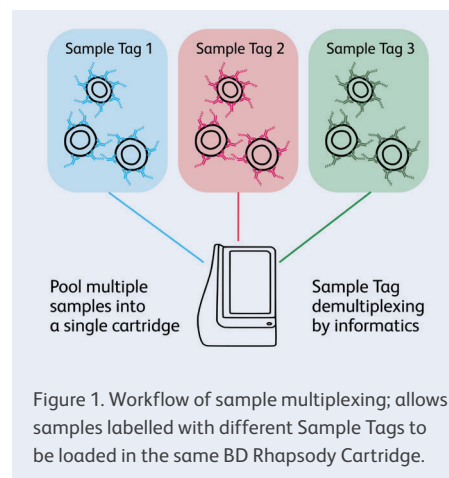# BD™ Single-Cell Multiplexing Kit

## Reduce single-cell sequencing reagent cost and improve data quality in single-cell sequencing analysis

Single-cell RNA-seq library preparation can be an expensive and time consuming process. Using the BD Sample Multiplexing kit, one can add more samples from a study on a single run for a more controlled experiment.

As a leader in antibody and single-cell analysis, BD has developed a method by which users can multiplex samples on a single run of a BD Rhapsody™ Single-Cell Analysis System, 10X Chromium™ or other 3' RNA-seq platform. By conjugating a polyadenylated DNA barcode to a universal antibody, a single-cell sequencing workflow can be multiplexed with up to 12 human samples to reduce reagent cost (Figure 1). Addition of the antibody tags does not affect sequencing data and improves data quality by reducing noise. The BD Single-Cell

Multiplexing Kit identifies inter-sample multiplets in downstream data analysis, which are unwanted artifacts during single cell capture. By identifying and eliminating these artifacts in the data analysis, researchers can expect much cleaner and defined cell populations.



Figure 1. Workflow of sample multiplexing; allows samples labelled with different Sample Tags to be loaded in the same BD Rhapsody Cartridge.

## Product features:

- **Reduces cost:** Reduce single-cell library preparation reagent cost by adding more samples to each run
- **Better data:** Lower technical errors between samples for a controlled experiment
- **Decreases noise:** Identify multiplets that have >1 associated Sample Tag
- **Easy workflow:** Simple upstream antibody-labelling step
- **Validated on a BD system:** Compatible with the BD Rhapsody Single-Cell Analysis System
- **Compatible with 10X Chromium system:** User-demonstrated protocol and open source demultiplexing informatics tool available for 10X Chromium Single Cell 3' Solution

| Save significant time and reagent cost per sample by using the BD Sample Multiplexing Kit | | | |
|---|---|---|---|
| Sample # | Standard 10X Chromium 3' run | Using the BD Sample Multiplexing Kit on a 10X Chromium 3' run | |
| | Runs required | Runs required | Approximate savings using BD's Sample Multiplexing Kit* |
| 8 | 1 | 1 | 0 |
| 16 | 2 | 1 | 50% |
| 48 | 6 | 1 | 83% |
| 96 | 12 | 1 | 92% |

*Does not include the price of BD Sample Tags
Number of loaded cells per sample will vary and decrease for larger sample numbers

**BD**

# Multiplet identification for cleaner single-cell sequencing analysis

To determine the ability of using Sample Tags for multiplet identification, ~20,000 cells of 4 different cell types—peripheral blood mononuclear cells (PBMCs), T47D breast cancer cells, Jurkat T cells, and Ramos B cells with 3 Sample Tags, (ST) each—were loaded in a single BD Rhapsody Cartridge (Figure 2). Sequencing data from BD analysis software revealed 4.9% of the cells were inter-sample multiplets, many of which were located in unique multiplet clusters. Removal of multiplets allows for more representative data analysis of multiple biological samples (Figure 3).
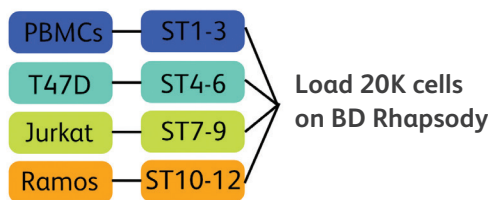


Figure 2. Demonstration of multiplet and sample identification.

**BD Single-Cell Multiplexing Kit on BD Rhapsody system dataset available for download at www.sbgenomics.com/bdgenomics.**

| Catalog number | Product |
|---|---|
| 633781 | BD™ Single-Cell Multiplexing Kit |
| 633782 | BD™ Single-Cell Multiplexing Amplification Component |



**A** — Highlighted by Sample Tags

- Multiplet (4.9 %)
- SampleTag01_hs (4.7 %)
- SampleTag02_hs (4.6 %)
- SampleTag03_hs (5.9 %)
- SampleTag04_hs (7.8 %)
- SampleTag05_hs (8.3 %)
- SampleTag06_hs (9.3 %)
- SampleTag07_hs (8.8 %)
- SampleTag08_hs (9.2 %)
- SampleTag09_hs (9.0 %)
- SampleTag10_hs (10.1 %)
- SampleTag11_hs (9.3 %)
- SampleTag12_hs (7.4 %)
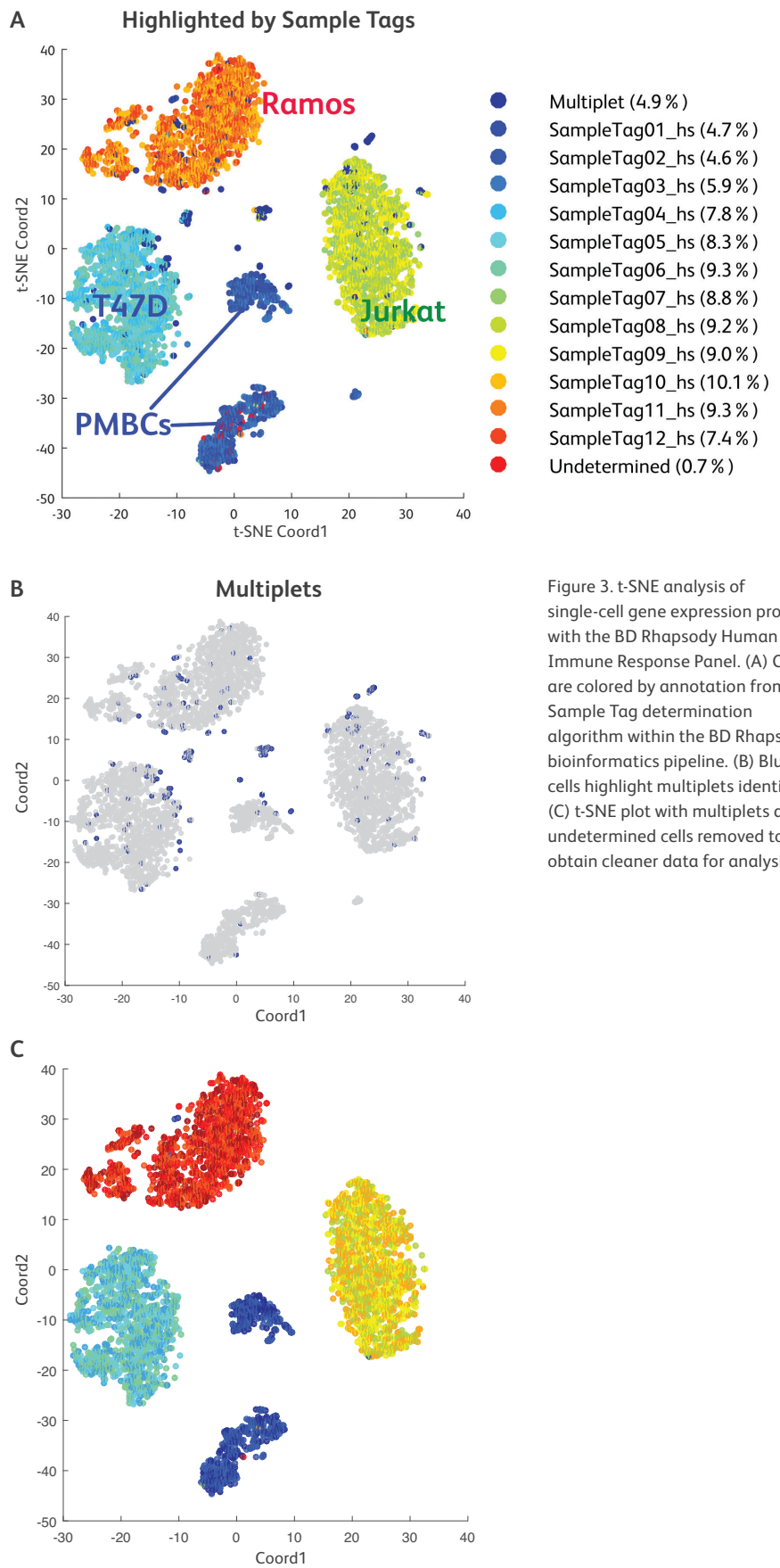- Undetermined (0.7 %)

**B** — Multiplets

Figure 3. t-SNE analysis of single-cell gene expression profile with the BD Rhapsody Human Immune Response Panel. (A) Cells are colored by annotation from the Sample Tag determination algorithm within the BD Rhapsody bioinformatics pipeline. (B) Blue cells highlight multiplets identified. (C) t-SNE plot with multiplets and undetermined cells removed to obtain cleaner data for analysis.

**C**

## www.bd.com/genomics

BD