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Research Publications Featuring Sony Cell Sorter Technology in Single Cell RNA Sequencing Studies

Single-cell transcriptomic technologies have emerged as powerful tools used for in-depth analysis of cellular heterogeneity at a single cell level. Advances in single cell RNA sequencing (scRNAseq) have enabled researchers to interrogate previously unexplored rare cell types. Due to the high sensitivity of scRNAseq, cells should be carefully processed to ensure that the expression profile is preserved. Individual steps of a typical single cell analysis workflow include obtaining the tissue, optimizing cell prep, performing RNA sequencing on single cells, and analyzing and visualizing data.

Flow cytometry is a widely used technique for isolating viable target subsets or purifying intact nuclei and cells for single cell sequencing workflows. The following table highlights the use of Sony cell sorters for isolation of viable cells of different origin for RNA sequencing analysis.

Research Area	Featured Publication	Experiment
Epigenomics	Large-scale simultaneous measurement of epitopes and transcriptomes in single cells. *Nat Methods.* 2017;14(9):865-868	Used the SH800 cell sorter to sort CD4+ and CD8a. Cells expressing different levels of CD8 were used for CITESeq to simultaneously perform epigenetic and transcriptome analysis.
Developmental Biology	Neonatal transplantation confers maturation of PSC-derived cardiomyocytes conducive to modeling cardiomyopathy. *Cell Rep.* 2017;18(2):571-582	Used the SH800 to sort cardiomyocytes with 100-µm and 130-µm sorting chips. Post-sort assays for viability, organoid formation, and sc-RNA sequencing (NextSeq 500) were performed.
Cell Atlas	Single-cell transcriptomics of 20 mouse organs creates a Tabula Muris. *Nature.* 2018;562(7727):367-372	Cells dissociated from 17 organs were either stained with viability dye (PI) or surface antibodies (CD31, endomucin, CD45, PDGFR, Epcam, Thbs1 Sdc4-A) and sorted with the SH800. FACS-based full length transcript analysis provided higher sensitivity and coverage using SMART-seq2.
Disease Progression	An immune-cell signature of bacterial sepsis. *Nat Med.* 2020;26:333-340	Donor blood from people with sepsis was sorted using the SH800 for viable PBMCs and myeloid cell states with CD14+, CD16+ markers, and dendritic cells. Gene expression profiling using the 10X Chromium platform was used to define 16 immune states, epigenomics, and functional phenotypes in sepsis conditions.
Immunology	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity *Cell.* 2019;176(6):1265-1281.e24	Frozen aspirates from normal and AML donors were stained with viability dye (PI) and sorted for mononuclear cells using the SH800. Fresh samples from healthy BM donors were stained and sorted for DAPI– (viable), CD34+, and CD34+CD38– populations using the SH800. Post sorting, 96% pure fractions of CD34+ and CD34+ CD38- cells (10,000 cells) were used for the Seq-Well scRNA-seq protocol.
Neurobiology	Single-Cell RNA-Seq Analysis of Infiltrating Neoplastic Cells at the Migrating Front of Human Glioblastoma *Cell Rep.* 2017;21(5):1399-1410	Individual cells infiltrating in glioblastomas were sorted on 96-well plates using the SH800 to isolate CD45+ (myeloid), GalC+ (oligodendrocytes), BSL+ (endothelial), Thy1+ (neurons), and HepaCAM+ (astrocytes) for deep single cell RNA seq using the Illumina NextSeq 500.
Methods Development	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. *Nat Neurosci.* 2018;21(3):432-439	Intact nuclei from flash frozen primary tissue samples were sorted on 96-well plates using the SH800 cell sorter to develop single-nucleus ATAC-seq, a combinatorial barcoding-assisted single-cell assay.

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Sony Cell Sorter Technology in Single Cell RNA
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Selected Additional Publications

Epigenomics
Takahashi S, Miura H, Shibata T, et al. Genome-wide stability of the DNA replication program in single mammalian cells. *Nat Genet.* 2019;51(3):529-540. PubMed

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Yao Z, Liu H, Xie F, et al. An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types. 2020 doi: https://doi.org/10.1101/2020.02.29.970558

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Pisco AO, McGeever A, Schaum N, et al. A Single Cell Transcriptomic Atlas Characterizes Aging Tissues in the Mouse. 2019. doi: https://doi.org/10.1101/661728

Disease Progression
Zanini F, Robinson ML, Croote D, et al. Virus-inclusive single-cell RNA sequencing reveals the molecular signature of progression to severe dengue. *Proc Natl Acad Sci U S A.* 2018;115(52):E12363-E12369. PubMed

Knott SRV, Wagenblast E, Khan S, et al. Asparagine bioavailability governs metastasis in a model of breast cancer. *Nature.* 2018;554(7692):378-381. PubMed

Lenos KJ, Miedema DM, Lodestijn SC, et al. Stem cell functionality is microenvironmentally defined during tumour expansion and therapy response in colon cancer. *Nat Cell Biol.* 2018;20(10):1193-1202. PubMed

Neurobiology
MacKay H, Scott CA, Duryea JD, et al. DNA methylation in AgRP neurons regulates voluntary exercise behavior in mice. *Nat Commun.* 2019;10:5364. PubMed

Sun S, Babola T, Pregernig G, et al. Hair Cell Mechanotransduction Regulates Spontaneous Activity and Spiral Ganglion Subtype Specification in the Auditory System. *Cell.* 2018;174(5):1247-1263.e15. PubMed

Trujillo CA, Gao R, Negraes PD, et al. Complex Oscillatory Waves Emerging from Cortical Organoids Model Early Human Brain Network Development. *Cell Stem Cell.* 2019;25(4):558-569.e7. PubMed

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Immunology

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