



Droplet Digital™ Sequencing (ddSEQ™) Solution

Publications List

The ddSEQ workflow utilizes a droplet-based single-cell partitioning technology, enabling rapid, accurate, and economical single-cell research in various fields.

This selection of research articles highlights the advantages and applications of the ddSEQ Single-Cell Isolator, which helps researchers assess epigenomic and transcriptomic profiles associated with disease, development, and immunity.

Single-Cell ATAC Sequencing

Zhang H et al. (2023).

Targeting WDxR motif reprograms immune microenvironment and inhibits hepatocellular carcinoma progression.
EMBO Mol Med 15, e15924.

Kartha VK et al. (2022).

Functional inference of gene regulation using single-cell multi-omics.
Cell Genom 2, 100166.

Kumegawa K et al. (2022).

GRHL2 motif is associated with intratumor heterogeneity of cis-regulatory elements in luminal breast cancer.
NPJ Breast Cancer 8, 70.

Suen HC et al. (2022).

scATAC-Seq reveals heterogeneity associated with spermatogonial differentiation in cultured male germline stem cells.
Sci Rep 12, 21482.

Adey AC (2021).

Tagmentation-based single-cell genomics.
Genome Res 31, 1,693–1,705.

de la Fuente LR et al. (2021).

Tumor dissociation of highly viable cell suspensions for single-cell omic analyses in mouse models of breast cancer.
STAR Protoc 2, 100841.

Lal A et al. (2021).

Deep learning-based enhancement of epigenomics data with AtacWorks.
Nat Commun 12, 1,507.

Rebboah E et al. (2021).

Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. *Genome Biol* 22, 286.

Sinha S et al. (2021).

Profiling chromatin accessibility at single-cell resolution. *Genomics Proteomics Bioinformatics* 19, 172–190.

LaFave LM et al. (2020).

Epigenomic state transitions characterize tumor progression in mouse lung adenocarcinoma. *Cancer Cell* 38, 212–228.

Lareau CA et al. (2020).

Inference and effects of barcode multiplets in droplet-based single-cell assays. *Nat Commun* 11, 866.

Malkani S et al. (2020).

Circulating miRNA spaceflight signature reveals targets for countermeasure development. *Cell Rep* 33, 108448.

Lareau CA et al. (2019).

Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. *Nat Biotechnol* 37, 916–924.

Single-Cell RNA Sequencing

Paul I et al. (2023).

Parallelized multidimensional analytic framework applied to mammary epithelial cells uncovers regulatory principles in EMT. *Nat Commun* 14, 688.

Salam R et al. (2023).

Cellular senescence in malignant cells promotes tumor progression in mouse and patient glioblastoma. *Nat Commun* 14, 441.

Torres-Flores U et al. (2023).

Spermiogenesis alterations in the absence of CTCF revealed by single cell RNA sequencing. *Front Cell Dev Biol* 11, 1119514.

Abe S et al. (2022).

Combination of ultrasound-based mechanical disruption of tumor with immune checkpoint blockade modifies tumor microenvironment and augments systemic antitumor immunity. *J Immunother Cancer* 10, e003717.

Cho YE et al. (2022).

Circulating immune cell landscape in patients who had mild ischaemic stroke. *Stroke Vasc Neurol* 7, 319–327.

Gómez-Arboledas A et al. (2022).

C5aR1 antagonism alters microglial polarization and mitigates disease progression in a mouse model of Alzheimer's disease. *Acta Neuropathol Commun* 10, 116.

Gómez-Salinero JM et al. (2022).

Cooperative ETS transcription factors enforce adult endothelial cell fate and cardiovascular homeostasis. Nat Cardiovasc Res 1, 882–899.

Gómez-Salinero JM et al. (2022).

Specification of fetal liver endothelial progenitors to functional zonated adult sinusoids requires c-Maf induction. Cell Stem Cell 29, 593–609.

Raabe FJ et al. (2022).

Expression of lineage transcription factors identifies differences in transition states of induced human oligodendrocyte differentiation. Cells 11, 241.

Salmani BY et al. (2022).

Selective requirement for polycomb repressor complex 2 in the generation of specific hypothalamic neuronal subtypes. Development 149, dev200076.

De Biasi S et al. (2021).

Circulating mucosal-associated invariant T cells identify patients responding to anti-PD-1 therapy. Nat Commun 12, 1,669.

Egedal JH et al. (2021).

Hyaluronic acid is a negative regulator of mucosal fibroblast-mediated enhancement of HIV infection. Mucosal Immunol 14, 1,203–1,213.

Ginzel JD et al. (2021).

HER2 isoforms uniquely program intratumor heterogeneity and predetermine breast cancer trajectories during the occult tumorigenic phase. Mol Cancer Res 19, 1,699–1,711.

Ho R et al. (2021).

Cross-comparison of human iPSC motor neuron models of familial and sporadic ALS reveals early and convergent transcriptomic disease signatures. Cell Syst 12, 159–175.

Hoek A et al. (2021).

WASP: A versatile, web-accessible single cell RNA-Seq processing platform. BMC Genomics 22, 195.

Kim KP et al. (2021).

Donor cell memory confers a metastable state of directly converted cells. Cell Stem Cell 28, 1,291–1,306.

Yamawaki TM et al. (2021).

Systematic comparison of high-throughput single-cell RNA-seq methods for immune cell profiling. BMC Genomics 22, 66.

Björn N et al. (2020).

Single-cell RNA sequencing of hematopoietic stem and progenitor cells treated with gemcitabine and carboplatin. Genes (Basel) 11, 549.

Fernandes LM et al. (2020).

Single-cell RNA-seq identifies unique transcriptional landscapes of human nucleus pulposus and annulus fibrosus cells. *Sci Rep* 10, 15263.

Ha CWY et al. (2020).

Translocation of viable gut microbiota to mesenteric adipose drives formation of creeping fat in humans. *Cell* 183, 666–683.

Hoffman JA et al. (2020).

Single-cell RNA sequencing reveals a heterogeneous response to glucocorticoids in breast cancer cells. *Commun Biol* 3, 126.

Jiang S et al. (2020).

Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. *PLoS Genet* 16, e1008754.

Mereu E et al. (2020).

Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. *Nat Biotechnol* 38, 747–755.

Muciño-Olmos EA et al. (2020).

Unveiling functional heterogeneity in breast cancer multicellular tumor spheroids through single-cell RNA-seq. *Sci Rep* 10, 12728.

Sen P et al. (2020).

Linking indirect effects of cytomegalovirus in transplantation to modulation of monocyte innate immune function. *Sci Adv* 6, eaax9856.

Vobořil M et al. (2020).

Toll-like receptor signaling in thymic epithelium controls monocyte-derived dendritic cell recruitment and Treg generation. *Nat Commun* 11, 2,361.

Aarreberg LD et al. (2019).

Interleukin-1 β induces mtDNA release to activate innate immune signaling via cGAS-STING. *Mol Cell* 74, 801–815.

Barry DM et al. (2019).

Molecular determinants of nephron vascular specialization in the kidney. *Nat Commun* 10, 5,705.

Bernard V et al. (2019).

Single-cell transcriptomics of pancreatic cancer precursors demonstrates epithelial and microenvironmental heterogeneity as an early event in neoplastic progression. *Clin Cancer Res* 25, 2,194–2,205.

Boone PG et al. (2019).

A cancer rainbow mouse for visualizing the functional genomics of oncogenic clonal expansion. *Nat Commun* 10, 5,490.

Kato Y et al. (2019).

Lenvatinib plus anti-PD-1 antibody combination treatment activates CD8⁺ T cells through reduction of tumor-associated macrophage and activation of the interferon pathway. *PLoS One* 14, e0212513.

Khan S et al. (2019).

Single-cell RNA-sequencing of peripheral blood mononuclear cells with ddSEQ.
Methods Mol Biol 1979, 155–176.

Kusnadi A et al. (2019).

The cytokine TNF promotes transcription factor SREBP activity and binding to inflammatory genes to activate macrophages and limit tissue repair.
Immunity 51, 241–257.

Lam M et al. (2019).

Single-cell study of neural stem cells derived from human iPSCs reveals distinct progenitor populations with neurogenic and gliogenic potential.
Genes Cells 24, 836–847.

Sakamoto S et al. (2019).

Dissecting early development of the kidney by single cell transcriptomics (article in Japanese).
Nihon Yakurigaku Zasshi 153, 61–66.

Tran KA et al. (2019).

Defining reprogramming checkpoints from single-cell analyses of induced pluripotency.
Cell Rep 27, 1,726–1,741.

Romagnoli D et al. (2018).

ddSeeker: A tool for processing Bio-Rad ddSEQ single cell RNA-seq data.
BMC Genomics 19, 960.

Valihrach L et al. (2018).

Platforms for single-cell collection and analysis.
Int J Mol Sci 19, 807.

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