



# 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

**De Rop FV et al. (2023).**

Systematic benchmarking of single-cell ATAC-sequencing protocols.  
Nat Biotechnol [online ahead of print Aug 3, 2023]. Accessed March 27, 2024.

**Miyata K et al. (2023).**

Chromatin conformational changes at human satellite II contribute to the senescence phenotype in the tumor microenvironment.  
Proc Natl Acad Sci USA 120, e2305046120.

**Suen HC et al. (2023).**

The single-cell chromatin accessibility landscape in mouse perinatal testis development.  
eLife 12, e75624.

**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-Salineró JM et al. (2022).**

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

**Gómez-Salineró JM et al. (2022).**

Specification of fetal liver endothelial progenitors to functional zoned 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 $\beta$  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<sup>+</sup> 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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