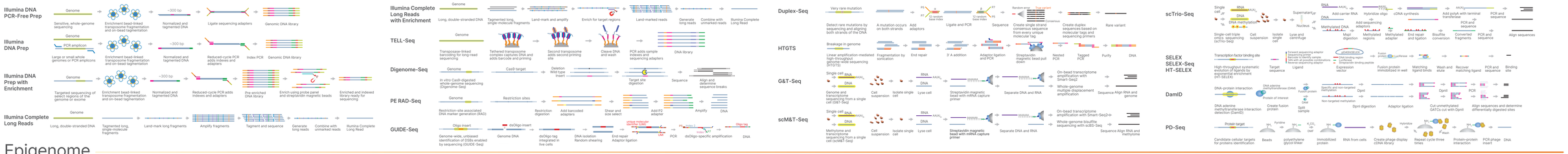
For all you seq…

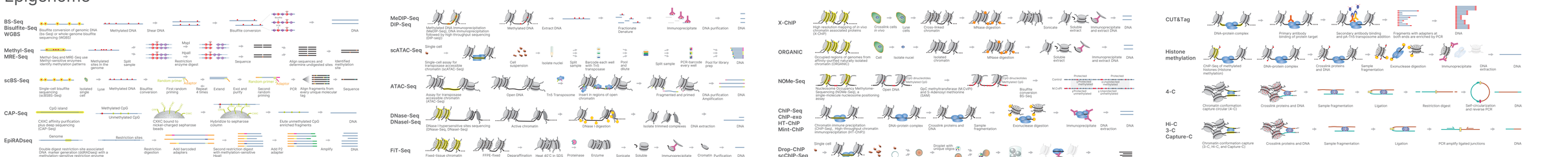
Unparalleled, comprehensive library of methods to characterize any ome, in any field of research.

illumina®

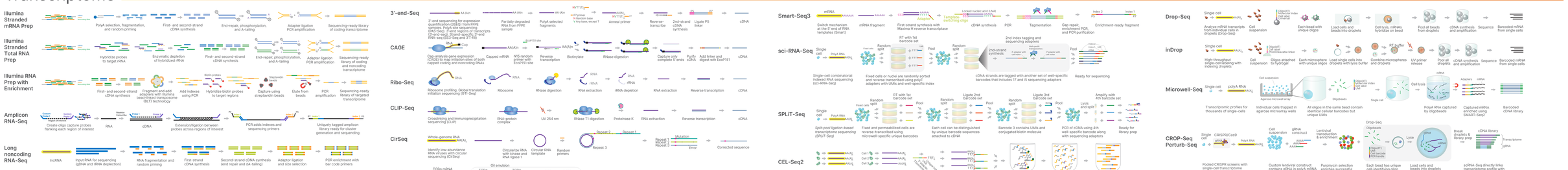
Genome



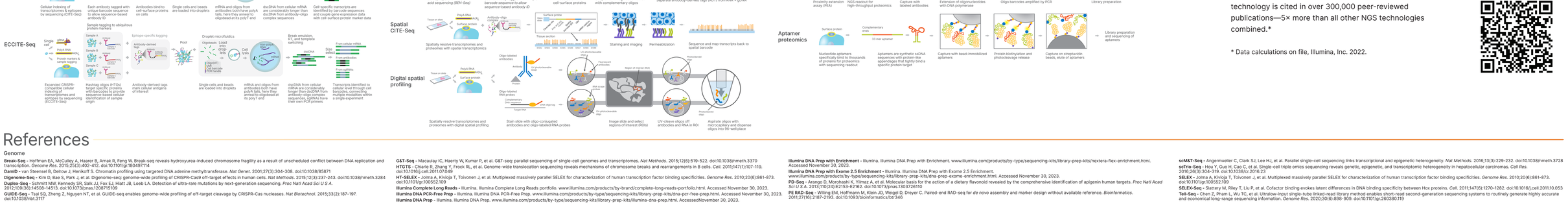
Epigenome



Transcriptome



Proteome



This is only a sample of the hundreds of next-generation sequencing (NGS) methods used today. Illumina NGS technology is cited in over 300,000 peer-reviewed publications—5× more than all other NGS technologies combined.*

* Data calculations on file, Illumina, Inc. 2022.

Learn more

References

Genome

Break-Seq - Hoffman EA, McCulley A, Haarer B, Arnak R, Feng W. Break-seq reveals hydroxyurea-induced chromosome fragility as a result of unscheduled conflict between DNA replication and transcription. *Genome Res.* 2015;25(3):402-412. doi:10.1101/gr.180497.114

DamID - van Steensel B, Delrow J, Henikoff S. Chromatin profiling using targeted DNA adenine methyltransferase. *Nat Genet.* 2001;27(3):304-308. doi:10.1038/85871

Digenome-Seq - Kim D, Bae S, Park J, et al. Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. *Nat Methods.* 2015;12(3):237-243. doi:10.1038/nmeth.3284

Duplex-Seq - Schmitt MW, Kennedy SR, Salk JJ, Fox EJ, Hiatt JB, Loeb LA. Detection of ultra-rare mutations by next-generation sequencing. *Proc Natl Acad Sci U S A.* 2012;109(36):14508-14513. doi:10.1073/pnas.1208715109

GUIDE-Seq - Tsai SQ, Zheng Z, Nguyen NT, et al. GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. *Nat Biotechnol.* 2015;33(2):187-197. doi:10.1038/nbt.3117

G&T-Seq - Macaulay IC, Haerty W, Kumar P, et al. G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. *Nat Methods.* 2015;12(6):519-522. doi:10.1038/nmeth.3370

HTGTS - Chiarle R, Zhang Y, Frock RL, et al. Genome-wide translocation sequencing reveals mechanisms of chromosome breaks and rearrangements in B cells. *Cell.* 2011;147(1):107-119. doi:10.1016/j.cell.2011.07.049

HT-SELEX - Jolma A, Kivioja T, Toivonen J, et al. Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. *Genome Res.* 2010;20(6):861-873. doi:10.1101/gr.100552.109

Illumina Complete Long Reads - Illumina. Illumina Complete Long Reads portfolio. www.illumina.com/products/by-brand/complete-long-reads-portfolio.html. Accessed November 30, 2023.

Illumina DNA PCR-Free Prep - Illumina. Illumina DNA PCR-Free Prep. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/dna-pcr-free-prep.html. Accessed November 30, 2023.

Illumina DNA Prep - Illumina. Illumina DNA Prep. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/illumina-dna-prep.html. AccessedNovember 30, 2023.

Illumina DNA Prep with Enrichment - Illumina. Illumina DNA Prep with Enrichment. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/nextera-flex-enrichment.html. Accessed November 30, 2023.

Illumina DNA Prep with Exome 2.5 Enrichment - Illumina. Illumina DNA Prep with Exome 2.5 Enrichment. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/dna-prep-exome-enrichment.html. Accessed November 30, 2023.

PD-Seq - Arango D, Morohashi K, Yilmaz A, et al. Molecular basis for the action of a dietary flavonoid revealed by the comprehensive identification of apigenin human targets. *Proc Natl Acad Sci U S A.* 2013;110(24):E2153-E2162. doi:10.1073/pnas.1303726110

PE RAD-Seq - Willing EM, Hoffmann M, Klein JD, Weigel D, Dreyer C. Paired-end RAD-seq for *de novo* assembly and marker design without available reference. *Bioinformatics.* 2011;27(16):2187-2193. doi:10.1093/bioinformatics/btr346

scM&T-Seq - Angermueller C, Clark SJ, Lee HJ, et al. Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. *Nat Methods.* 2016;13(3):229-232. doi:10.1038/nmeth.3728

scTrio-Seq - Hou Y, Guo H, Cao C, et al. Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. *Cell Res.* 2016;26(3):304-319. doi:10.1038/cr.2016.23

SELEX - Jolma A, Kivioja T, Toivonen J, et al. Multiplexed massively parallel SELEX for characterization of human transcription factor binding specificities. *Genome Res.* 2010;20(6):861-873. doi:10.1101/gr.100552.109

SELEX-Seq - Slattery M, Riley T, Liu P, et al. Cofactor binding evokes latent differences in DNA binding specificity between Hox proteins. *Cell.* 2011;147(6):1270-1282. doi:10.1016/j.cell.2011.10.053

Tell-Seq - Chen Z, Pham L, Wu TC, et al. Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. *Genome Res.* 2020;30(6):898-909. doi:10.1101/gr.260380.119

Epigenome

3C - Duan Z, Andronescu M, Schutz K, et al. A genome-wide 3C-method for characterizing the three-dimensional architectures of genomes. *Methods.* 2012;58(3):277-288. doi:10.1016/j.ymeth.2012.06.018

4-C - Zhao Z, Tavoosidana G, Sjölinder M, et al. Circular chromosome conformation capture (4C) uncovers extensive networks of epigenetically regulated intra- and interchromosomal interactions. *Nat Genet.* 2006;38(11):1341-1347. doi:10.1038/ng1891

ATAC-Seq - Buenrostro JD, Giresi PG, Zaba LC, Chang HY, Greenleaf WJ. Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. *Nat Methods.* 2013;10(12):1213-1218. doi:10.1038/nmeth.2688

Bisulfite-Seq - Lister R, Pelizzola M, Dowen RH, et al. Human DNA methylomes at base resolution show widespread epigenomic differences. *Nature.* 2009;462(7271):315-322. doi:10.1038/nature08514

BS-Seq - Berman BP, Weisenberger DJ, Aman JF, et al. Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. *Nat Genet.* 2011;44(1):40-46. doi:10.1038/ng.969

CAP-Seq - Illingworth RS, Gruenewald-Schneider U, Webb S, et al. Orphan CpG islands identify numerous conserved promoters in the mammalian genome. *PLoS Genet.* 2010;6(9):e1001134. doi:10.1371/journal.pgen.1001134

Capture-C - Hughes JR, Roberts N, McGowan S, et al. Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. *Nat Genet.* 2014;46(2):205-212. doi:10.1038/ng.2871

ChIP-exo - Yen K, Vinayachandran V, Pugh BF. SWR-C and INO80 chromatin remodelers recognize nucleosome-free regions near +1 nucleosomes. *Cell.* 2013;154(6):1246-1256. doi:10.1016/j.cell.2013.08.043

ChIP-Seq - Barski A, Cuddapah S, Cui K, et al. High-resolution profiling of histone methylations in the human genome. *Cell.* 2007;129(4):823-837. doi:10.1016/j.cell.2007.05.009

CUT&Tag - Kaya-Okur HS, Wu SJ, Codomo CA, et al. CUT&Tag for efficient epigenomic profiling of small samples and single cells. *Nat Commun.* 2019;10(1):1930. doi:10.1038/s41467-019-09982-5

DIP-Seq - Shen L, Wu H, Diep D, et al. Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. *Cell.* 2013;153(3):692-706. doi:10.1016/j.cell.2013.04.002

DNaseI-Seq - Hesselberth JR, Chen X, Zhang Z, et al. Global mapping of protein-DNA interactions *in vivo* by digital genomic footprinting. *Nat Methods.* 2009;6(4):283-289. doi:10.1038/nmeth.1313

DNase-Seq - Boyle AP, Davis S, Shulha HP, et al. High-resolution mapping and characterization of open chromatin across the genome. *Cell.* 2008;132(2):311-322. doi:10.1016/j.cell.2007.12.014

EpiRADseq - Schield DR, Walsh MR, Card DC, Andrew AL, Adams RH, Castoe TA. EpiRADseq: scalable analysis of genome-wide patterns of methylation using next-generation sequencing. *Methods in Ecology and Evolution.* 2016;7:60-69. doi: 10.1111/2041-210X.12435

FIT-Seq - Cejas P, Li L, O'Neill NK, et al. Chromatin immunoprecipitation from fixed clinical tissues reveals tumor-specific enhancer profiles. *Nat Med.* 2016;22(6):685-691. doi:10.1038/nm.4085

Hi-C - Lieberman-Aiden E, van Berkum NL, Williams L, et al. Comprehensive mapping of long-range interactions reveals folding principles of the human genome. *Science.* 2009;326(5950):289-293. doi:10.1126/science.1181369

Histone methylation - Barski A, Cuddapah S, Cui K, et al. High-resolution profiling of histone methylations in the human genome. *Cell.* 2007;129(4):823-837. doi:10.1016/j.cell.2007.05.009

HT-ChIP - Blecher-Gonen R, Barnett-Itzhaki Z, Jaitin D, Amann-Zalcenstein D, Lara-Astiaso D, Amit I. High-throughput chromatin immunoprecipitation for genome-wide mapping of *in vivo* protein-DNA interactions and epigenomic states. *Nat Protoc.* 2013;8(3):539-554. doi:10.1038/nprot.2013.023

MeDIP-Seq - Down TA, Rakyan VK, Turner DJ, et al. A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. *Nat Biotechnol.* 2008;26(7):779-785. doi:10.1038/nbt1414

Methyl-Seq - Brunner AL, Johnson DS, Kim SW, et al. Distinct DNA methylation patterns characterize differentiated human embryonic stem cells and developing human fetal liver. *Genome Res.* 2009;19(6):1044-1056. doi:10.1101/gr.088775.108

Mint-ChIP - van Galen P, Viny AD, Ram O, et al. A Multiplexed System for Quantitative Comparisons of Chromatin Landscapes. *Mol Cell.* 2016;61(1):170-180. doi:10.1016/j.molcel.2015.11.003

MRE-Seq - Maunakea AK, Nagarajan RP, Bilenky M, et al. Conserved role of intragenic DNA methylation in regulating alternative promoters. *Nature.* 2010;466(7303):253-257. doi:10.1038/nature09165

NOMe-Seq - Han H, Cortez CD, Yang X, Nichols PW, Jones PA, Liang G. DNA methylation directly silences genes with non-CpG island promoters and establishes a nucleosome-occupied promoter. *Hum Mol Genet.* 2011;20(22):4299-4310. doi:10.1093/hmg/ddr356

ORGANIC - Zentner GE, Tsukiyama T, Henikoff S. ISWI and CHD chromatin remodelers bind promoters but act in gene bodies. *PLoS Genet.* 2013;9(2):e1003317. doi:10.1371/journal.pgen.1003317

scATAC-Seq - Buenrostro JD, Wu B, Litzenburger UM, et al. Single-cell chromatin accessibility reveals principles of regulatory variation. *Nature.* 2015;523(7561):486-490. doi:10.1038/nature14590

scBS-Seq - Smallwood SA, Lee HJ, Angermueller C, et al. Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. *Nat Methods.* 2014;11(8):817-820. doi:10.1038/nmeth.3035

scChIP-Seq or Drop-ChIP - Rotem A, Ram O, Shoresh N, et al. Single-cell ChIP-seq reveals cell subpopulations defined by chromatin state. *Nat Biotechnol.* 2015;33(11):1165-1172. doi:10.1038/nbt.3383

THS-Seq - Sos BC, Fung HL, Gao DR, et al. Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. *Genome Biol.* 2016;17:20. doi:10.1186/s13059-016-0882-7

WGBS - Lister R, Pelizzola M, Dowen RH, et al. Human DNA methylomes at base resolution show widespread epigenomic differences. *Nature.* 2009;462(7271):315-322. doi:10.1038/nature08514

X-ChIP - Skene PJ, Hernandez AE, Groudine M, Henikoff S. The nucleosomal barrier to promoter escape by RNA polymerase II is overcome by the chromatin remodeler Chd1. *Elife.* 2014;3:e02042. doi:10.7554/eLife.02042

Transcriptome

3′-end-Seq - Haenni S, Ji Z, Hoque M, et al. Analysis of C. elegans intestinal gene expression and polyadenylation by fluorescence-activated nuclei sorting and 3′-end-seq. *Nucleic Acids Res.* 2012;40(13):6304-6318. doi:10.1093/nar/gks287

Amplicon RNA-Seq - Illumina. AmpliSeq for Illumina-a comprehensive targeted resequencing solution. www.illumina.com/products/by-brand/ampliseq.html. Accessed November 15, 2023.

CAGE - Takahashi H, Lassmann T, Murata M, Carninci P. 5′ end-centered expression profiling using cap-analysis gene expression and next-generation sequencing. *Nat Protoc.* 2012;7(3):542-561. doi:10.1038/nprot.2012.005

CEL-Seq2 - Hashimshony T, Senderovich N, Avital G, et al. CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. *Genome Biol.* 2016;17:77. doi:10.1186/s13059-016-0938-8

CirSeq - Acevedo A, Brodsky L, Andino R. Mutational and fitness landscapes of an RNA virus revealed through population sequencing. *Nature.* 2014;505(7483):686-690. doi:10.1038/nature12861

CLIP-Seq - Yeo GW, Coufal NG, Liang TY, Peng GE, Fu XD, Gage FH. An RNA code for the FOX2 splicing regulator revealed by mapping RNA-protein interactions in stem cells. *Nat Struct Mol Biol.* 2009;16(2):130-137. doi:10.1038/nsmb.1545

CROP-Seq - Datlinger P, Rendeiro AF, Schmidl C, et al. Pooled CRISPR screening with single-cell transcriptome readout. *Nat Methods.* 2017;14(3):297-301. doi:10.1038/nmeth.4177

Drop-Seq - Macosko EZ, Basu A, Satija R, et al. Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. *Cell.* 2015;161(5):1202-1214. doi:10.1016/j.cell.2015.05.002

Illumina RNA Prep with Enrichment - Illumina. Illumina RNA Prep with Enrichment. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/rna-prep-enrichment.html. Accessed November 15, 2023.

Illumina Stranded mRNA Prep - Illumina. Illumina Stranded mRNA Prep. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/stranded-mrna-prep.html. Accessed November 15, 2023.

Illumina Stranded Total RNA Prep - Illumina. Illumina Stranded Total RNA Prep with Ribo-Zero Plus or Ribo-Zero Plus Microbiome. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/stranded-total-rna-prep.html. Accessed November 15, 2023.

inDrop - Klein AM, Mazutis L, Akartuna I, et al. Droplet barcoding for single-cell transcriptomics applied to embryonic stem cells. *Cell.* 2015;161(5):1187-1201. doi:10.1016/j.cell.2015.04.044

Long noncoding RNA-Seq - Lai F, Blumenthal E, Shiekhattar R. Detection and Analysis of Long Noncoding RNAs. *Methods Enzymol.* 2016;573:421-444. doi:10.1016/bs.mie.2016.03.010

MARS-Seq - Jaitin DA, Keren-Shaul H, et al. Massively parallel single-cell RNA-seq for marker-free decomposition of tissues into cell types. *Science.* 2014;343(6172):776-779. doi:10.1126/science.1247651

Microwell-Seq - Han X, Wang R, Zhou Y, et al. Mapping the Mouse Cell Atlas by Microwell-Seq. *Cell.* 2018;172(5):1091-1107.e17. doi:10.1016/j.cell.2018.02.001

Perturb-Seq - Dixit A, Parnas O, Li B, et al. Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. *Cell.* 2016;167(7):1853-1866.e17. doi:10.1016/j.cell.2016.11.038

PIP-Seq - Clark IC, Fontanez KM, Meltzer RH, et al. Microfluidics-free single-cell genomics with templated emulsification. *Nat Biotechnol.* 2023;10.1038/s41587-023-01685-z. doi:10.1038/s41587-023-01685-z

Ribo-Seq - Wan J, Qian SB. TISdb: a database for alternative translation initiation in mammalian cells. *Nucleic Acids Res.* 2014;42(Database issue):D845-D850. doi:10.1093/nar/gkt1085

sci-RNA-Seq - Martin BK, Qiu C, Nichols E, et al. Optimized single-nucleus transcriptional profiling by combinatorial indexing. *Nat Protoc.* 2023;18(1):188-207. doi:10.1016/j.xnat.2011.11.016

Slide-SeqV2 - Marshall JL, Noel T, Wang QS, et al. High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways. *iScience.* 2022;25(4):104097. doi:10.1016/j.isci.2022.104097

Smal RNA-Seq - Illumina. TruSeq Small RNA Library Preparation Kits. www.illumina.com/products/by-type/sequencing-kits/library-prep-kits/truseq-small-rna.html. Accessed November 15, 2023.

Smart-Seq3 - Hagemann-Jensen M, Ziegenhain C, Chen P, et al. Single-cell RNA counting at allele and isoform resolution using Smart-seq3. *Nat Biotechnol.* 2020;38(6):708-714. doi:10.1038/s41587-020-0497-0

SPLit-Seq - Rosenberg AB, Roco CM, Muscat RA, et al. Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding. *Science.* 2018;360(6385):176-182. doi:10.1126/science.aam8999

TCR chain pairing - Turchaninova MA, Britanova OV, Bolotin DA, et al. Pairing of T-cell receptor chains via emulsion PCR. *Eur J Immunol.* 2013;43(9):2507-2515. doi:10.1002/eji.201343453

Proteome

Aptamer proteomics - Gold L, Walker JJ, Wilcox SK, Williams S. Advances in human proteomics at high scale with the SOMAscan proteomics platform. *N Biotechnol.* 2012;29(5):543-549. doi:10.1016/j.nbt.2011.11.016

BEN-Seq - Illumina. Correlated expression of protein and RNA reveals a unique molecular signature in Th1-polarized cells. www.illumina.com/content/dam/illumina-marketing/documents/products/gcs/assembled-assets/marketing-literature/biolegend-ben-seq-app-note-m-gl-00024.pdf. Published 2021. Accessed November 15, 2023.

CITE-Seq - Stoeckius M, Hafemeister C, Stephenson W, et al. Simultaneous epitope and transcriptome measurement in single cells. *Nat Methods.* 2017;14(9):865-868. doi:10.1038/nmeth.4380

Digital spatial profiling - Merritt CR, Ong GT, Church SE, et al. Multiplex digital spatial profiling of proteins and RNA in fixed tissue. *Nat Biotechnol.* 2020;38(5):586-599. doi:10.1038/s41587-020-0472-9

ECCITE-Seq - Mimitou EP, Cheng A, Montalbano A, et al. Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. *Nat Methods.* 2019;16(5):409-412. doi:10.1038/s41592-019-0392-0

PEA-Seq - Wik L, Nordberg N, Broberg J, et al. Proximity Extension Assay in Combination with Next-Generation Sequencing for High-throughput Proteome-wide Analysis. *Mol Cell Proteomics.* 2021;20:100168. doi:10.1016/j.mcpro.2021.100168

Spatial CITE-Seq - Ben-Chetrit N, Niu X, Swett AD, et al. Integration of whole transcriptome spatial profiling with protein markers. *Nat Biotechnol.* 2023;41(6):788-793. doi:10.1038/s41587-022-01536-3

© 2023 Illumina, Inc. All rights reserved. All trademarks are the property of Illumina, Inc. or their respective owners. For specific trademark information, see www.illumina.com/company/legal.html. For Research Use Only. Not for use in diagnostic procedures. | M-GL-02323 v2.0