

scforest

A visual overview of single cell technology

Curated by Florian De Rop

Aerts Lab

October 11, 2019

Updated version on github.com/aertslab/scforest



KU Leuven/VIB

References

- Ai, S., H. Xiong, C. C. Li, Y. Luo, Q. Shi, Y. Liu, X. Yu, C. Li, and A. He
2019. Profiling chromatin states using single-cell itchip-seq. *Nature Cell Biology*, 21(9):1164–1172.
- Angermueller, C., S. J. Clark, H. J. Lee, I. C. Macaulay, M. J. Teng, T. X. Hu, F. Krueger, S. A. Smallwood, C. P. Ponting, T. Voet, and et al.
2016. Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. *Nature Methods*, 13(3):229–232.
- Bagnoli, J. W., C. Ziegenhain, A. Janjic, L. E. Wange, B. Vieth, S. Parekh, J. Geuder, I. Hellmann, and W. Enard
2018. Sensitive and powerful single-cell rna sequencing using mscrb-seq. *Nature Communications*, 9(1).
- Biočanin, M., J. Bues, R. Dainese, E. Amstad, and B. Deplancke
2019. Simplified drop-seq workflow with minimized bead loss using a bead capture and processing microfluidic chip. *Lab on a Chip*, 19(9):1610–1620.
- Buenrostro, J. D., P. G. Giresi, L. C. Zaba, H. Y. Chang, and W. J. Greenleaf
2013. Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, dna-binding proteins and nucleosome position. *Nature Methods*, 10(12):1213–1218.
- Buenrostro, J. D., B. Wu, U. M. Litzenburger, D. Ruff, M. L. Gonzales, M. P. Snyder, H. Y. Chang, and W. J. Greenleaf
2015. Single-cell chromatin accessibility reveals principles of regulatory variation. *Nature*, 523(7561):486–490.
- Cao, J., D. A. Cusanovich, V. Ramani, D. Aghamirzaie, H. A. Pliner, A. J. Hill, R. M. Daza, J. L. McFaline-Figueroa, J. S. Packer, L. Christiansen, F. J. Steemers, A. C. Adey, C. Trapnell, and J. Shendure
2018. Joint profiling of chromatin accessibility and gene expression in thousands of single cells. *Science*, 361(6409):1380–1385.
- Cao, J., J. S. Packer, V. Ramani, D. A. Cusanovich, C. Huynh, R. Daza, X. Qiu, C. Lee, S. N. Furlan, F. J. Steemers, A. Adey, R. H. Waterston, C. Trapnell, and J. Shendure
2017. Comprehensive single-cell transcriptional profiling of a multicellular organism. *Science*, 357(6352):661–667.

- Chen, C., D. Xing, L. Tan, H. Li, G. Zhou, L. Huang, and X. S. Xie
2017. Single-cell whole-genome analyses by linear amplification via transposon insertion (lianti). *Science*, 356(6334):189–194.
- Chen, K. H., A. N. Boettiger, J. R. Moffitt, S. Wang, and X. Zhuang
2015. Spatially resolved, highly multiplexed rna profiling in single cells. *Science*, 348(6233).
- Chen, S., B. B. Lake, and K. Zhang
2019. Linking transcriptome and chromatin accessibility in nanoliter droplets for single-cell sequencing. *bioRxiv*.
- Chen, X., U. M. Litzenburger, Y. Wei, A. N. Schep, E. L. Lagory, H. Choudhry, A. J. Giaccia, W. J. Greenleaf, and H. Y. Chang
2018a. Joint single-cell dna accessibility and protein epitope profiling reveals environmental regulation of epigenomic heterogeneity. *Nature Communications*, 9(1).
- Chen, X., R. J. Miragaia, K. N. Natarajan, and S. A. Teichmann
2018b. A rapid and robust method for single cell chromatin accessibility profiling. *Nature Communications*, 9(1).
- Chen, X., Y. Shen, W. Draper, J. D. Buenrostro, U. Litzenburger, S. W. Cho, A. T. Satpathy, A. C. Carter, R. P. Ghosh, A. East-Seletsky, and et al.
2016. Atac-seq reveals the accessible genome by transposase-mediated imaging and sequencing. *Nature Methods*, 13(12):1013–1020.
- Clark, S. J., R. Argelaguet, C.-A. Kapourani, T. M. Stubbs, H. J. Lee, C. Alda-Catalinas, F. Krueger, G. Sanguinetti, G. Kelsey, J. C. Marioni, and et al.
2018. scnm-seq enables joint profiling of chromatin accessibility dna methylation and transcription in single cells. *Nature Communications*, 9(1).
- Corces, M. R., A. E. Trevino, E. G. Hamilton, P. G. Greenside, N. A. Sinnott-Armstrong, S. Vesuna, A. T. Satpathy, A. J. Rubin, K. S. Montine, B. Wu, A. Kathiria, S. W. Cho, M. R. Mumbach, A. C. Carter, M. Kasowski, L. A. Orloff, V. I. Risca, A. Kundaje, P. A. Khavari, T. J. Montine, W. J. Greenleaf, and H. Y. Chang
2017. An improved atac-seq protocol reduces background and enables interrogation of frozen tissues. *Nature Methods*, 14(10):959–962. Cited By :43.
- Cusanovich, D. A., R. Daza, A. Adey, H. A. Pliner, L. Christiansen, K. L. Gunderson, F. J. Steemers, C. Trapnell, and J. Shendure
2015. Multiplex single-cell profiling of chromatin accessibility by combinatorial cellular indexing. *Science*, 348(6237):910–914.

- Datlinger, P., A. F. Rendeiro, C. Schmidl, T. Krausgruber, P. Traxler, J. Klughammer, L. C. Schuster, A. Kuchler, D. Alpar, and C. Bock
2017. Pooled crispr screening with single-cell transcriptome readout. *Nature Methods*, 14(3):297–301.
- Dey, S. S., L. Kester, B. Spanjaard, M. Bienko, and A. V. Oudenaarden
2015. Integrated genome and transcriptome sequencing of the same cell. *Nature Biotechnology*, 33(3):285–289.
- Dixit, A., O. Parnas, B. Li, J. Chen, C. P. Fulco, L. Jerby-Arnon, N. D. Marjanovic, D. Dionne, T. Burks, R. Raychowdhury, and et al.
2016. Perturb-seq: Dissecting molecular circuits with scalable single-cell rna profiling of pooled genetic screens. *Cell*, 167(7).
- Eberwine, J., H. Yeh, K. Miyashiro, Y. Cao, S. Nair, R. Finnell, M. Zettel, and P. Coleman
1992. Analysis of gene expression in single live neurons. *Proceedings of the National Academy of Sciences of the United States of America*, 89(7):3010–3014.
- Eng, C.-H. L., M. Lawson, Q. Zhu, R. Dries, N. Koulina, Y. Takei, J. Yun, C. Cronin, C. Karp, G.-C. Yuan, and et al.
2019. Transcriptome-scale super-resolved imaging in tissues by rna seqfish. *Nature*, 568(7751):235–239.
- Erhard, F., M. A. P. Baptista, T. Krammer, T. Hennig, M. Lange, P. Arampatzis, C. S. Jürges, F. J. Theis, A.-E. Saliba, L. Dölken, and et al.
2019. scslam-seq reveals core features of transcription dynamics in single cells. *Nature*, 571(7765):419–423.
- Fan, H. C., G. K. Fu, and S. P. A. Fodor
2015. Combinatorial labeling of single cells for gene expression cytometry. *Science*, 347(6222).
- Farlik, M., N. C. Sheffield, A. Nuzzo, P. Datlinger, A. Schönegger, J. Klughammer, and C. Bock
2015. Single-cell dna methylome sequencing and bioinformatic inference of epigenomic cell-state dynamics. *Cell Reports*, 10(8):1386–1397.
- Gierahn, T. M., M. H. Wadsworth, T. K. Hughes, B. D. Bryson, A. Butler, R. Satija, S. Fortune, J. Christopher Love, and A. K. Shalek
2017. Seq-well: Portable, low-cost rna sequencing of single cells at high throughput. *Nature Methods*, 14(4):395–398.

- Guo, H., P. Zhu, F. Guo, X. Li, X. Wu, X. Fan, L. Wen, and F. Tang
2015. Profiling dna methylome landscapes of mammalian cells with single-cell reduced-representation bisulfite sequencing. *Nature Protocols*, 10(5):645–659.
- Gupta, I., P. G. Collier, B. Haase, A. Mahfouz, A. Joglekar, T. Floyd, F. Koopmans, B. Barres, A. B. Smit, S. Sloan, and et al.
2018. Single-cell isoform rna sequencing (scisor-seq) across thousands of cells reveals isoforms of cerebellar cell types. *Nature Biotechnology*.
- Habib, N., I. Avraham-Davidi, A. Basu, T. Burks, K. Shekhar, M. Hofree, S. R. Choudhury, F. Aguet, E. Gelfand, K. Ardlie, and et al.
2017. Massively parallel single-nucleus rna-seq with dronc-seq. *Nature Methods*, 14(10):955–958.
- Habib, N., Y. Li, M. Heidenreich, L. Swiech, I. Avraham-Davidi, J. J. Trombetta, C. Hession, F. Zhang, and A. Regev
2016. Div-seq: Single-nucleus rna-seq reveals dynamics of rare adult newborn neurons. *Science*, 353(6302):925–928.
- Han, X., R. Wang, Y. Zhou, L. Fei, H. Sun, S. Lai, A. Saadatpour, Z. Zhou, H. Chen, F. Ye, and et al.
2018. Mapping the mouse cell atlas by microwell-seq. *Cell*, 173(5):1307.
- Hashimshony, T., N. Senderovich, G. Avital, A. Klochendler, Y. de Leeuw, L. Anavy, D. Gennert, S. Li, K. J. Livak, O. Rozenblatt-Rosen, Y. Dor, A. Regev, and I. Yanai
2016. Cel-seq2: Sensitive highly-multiplexed single-cell rna-seq. *Genome biology*, 17(1).
- Hashimshony, T., F. Wagner, N. Sher, and I. Yanai
2012. Cel-seq: Single-cell rna-seq by multiplexed linear amplification. *Cell Reports*, 2(3):666–673.
- Hayashi, T., H. Ozaki, Y. Sasagawa, M. Umeda, H. Danno, and I. Nikaido
2018. Single-cell full-length total rna sequencing uncovers dynamics of recursive splicing and enhancer rnas. *Nature Communications*, 9(1).
- Hochgerner, H., P. Lönnerberg, R. Hodge, J. Mikes, A. Heskol, H. Hubschle, P. Lin, S. Picelli, G. L. Manno, M. Ratz, and et al.
2017. Strt-seq-2i: dual-index 5' single cell and nucleus rna-seq on an addressable microwell array. *Scientific Reports*, 7(1).

- Hou, Y., H. Guo, C. Cao, X. Li, B. Hu, P. Zhu, X. Wu, L. Wen, F. Tang, Y. Huang, and J. Peng
2016. Single-cell triple omics sequencing reveals genetic, epigenetic, and transcriptomic heterogeneity in hepatocellular carcinomas. *Cell research*, 26(3):304–319.
- Islam, S., U. Kjällquist, A. Moliner, P. Zajac, J.-B. Fan, P. Lönnerberg, and S. Linnarsson
2011. Characterization of the single-cell transcriptional landscape by highly multiplex rna-seq. *Genome Research*, 21(7):1160–1167.
- Islam, S., U. Kjällquist, A. Moliner, P. Zajac, J.-B. Fan, P. Lönnerberg, and S. Linnarsson
2012. Highly multiplexed and strand-specific single-cell rna 5’ end sequencing. *Nature Protocols*, 7(5):813–828.
- Jaitin, D. A., E. Kenigsberg, H. Keren-Shaul, N. Elefant, F. Paul, I. Zaretsky, A. Mildner, N. Cohen, S. Jung, A. Tanay, and I. Amit
2014. Massively parallel single-cell rna-seq for marker-free decomposition of tissues into cell types. *Science*, 343(6172):776–779.
- Jaitin, D. A., A. Weiner, I. Yofe, D. Lara-Astiaso, H. Keren-Shaul, E. David, T. M. Salame, A. Tanay, A. V. Oudenaarden, I. Amit, and et al.
2016. Dissecting immune circuits by linking crispr-pooled screens with single-cell rna-seq. *Cell*, 167(7).
- Jin, W., Q. Tang, M. Wan, K. Cui, Y. Zhang, G. Ren, B. Ni, J. Sklar, T. M. Przytycka, R. Childs, and et al.
2015. Genome-wide detection of dnase i hypersensitive sites in single cells and fpe tissue samples. *Nature*, 528(7580):142–146.
- Keren-Shaul, H., E. Kenigsberg, D. A. Jaitin, E. David, F. Paul, A. Tanay, and I. Amit
2019. Mars-seq2.0: an experimental and analytical pipeline for indexed sorting combined with single-cell rna sequencing. *Nature Protocols*, 14(6):1841–1862.
- Kimmerling, R. J., G. Lee Szeto, J. W. Li, A. S. Genshaft, S. W. Kazer, K. R. Payer, J. De Riba Borrajo, P. C. Blainey, D. J. Irvine, A. K. Shalek, and S. R. Manalis
2016. A microfluidic platform enabling single-cell rna-seq of multigenerational lineages. *Nature Communications*, 7.

- Kind, J., L. Pagie, S. S. De Vries, L. Nahidiazar, S. S. Dey, M. Bienko, Y. Zhan, B. Lajoie, C. A. De Graaf, M. Amendola, and et al.
2015. Genome-wide maps of nuclear lamina interactions in single human cells. *Cell*, 163(1):134–147.
- Klein, A. M., L. Mazutis, I. Akartuna, N. Tallapragada, A. Veres, V. Li, L. Peshkin, D. A. Weitz, and M. W. Kirschner
2015. Droplet barcoding for single-cell transcriptomics applied to embryonic stem cells. *Cell*, 161(5):1187–1201.
- Kurimoto, K., Y. Yabuta, Y. Ohinata, Y. Ono, K. Uno, R. Yamada, H. Ueda, and M. Saitou
2006. An improved single-cell cdna amplification method for efficient high-density oligonucleotide microarray analysis. *Nucleic Acids Research*, 34(5).
- Kurimoto, K., Y. Yabuta, Y. Ohinata, and M. Saitou
2007. Global single-cell cdna amplification to provide a template for representative high-density oligonucleotide microarray analysis. *Nature Protocols*, 2(3):739–752.
- Lake, B. B., S. Chen, B. C. Sos, J. Fan, G. E. Kaeser, Y. C. Yung, T. E. Duong, D. Gao, J. Chun, P. V. Kharchenko, and et al.
2017a. Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. *Nature Biotechnology*, 36(1):7080.
- Lake, B. B., S. Codeluppi, Y. C. Yung, D. Gao, J. Chun, P. V. Kharchenko, S. Linnarsson, and K. Zhang
2017b. A comparative strategy for single-nucleus and single-cell transcriptomes confirms accuracy in predicted cell-type expression from nuclear rna. *Scientific Reports*, 7(1).
- Lan, F., B. Demaree, N. Ahmed, and A. R. Abate
2017. Single-cell genome sequencing at ultra-high-throughput with microfluidic droplet barcoding. *Nature Biotechnology*, 35(7):640–646.
- Lareau, C. A., F. M. Duarte, J. G. Chew, V. K. Kartha, Z. D. Burkett, A. S. Kohlway, D. Pokholok, M. J. Aryee, F. J. Steemers, R. Lebofsky, and J. D. Buenrostro
2019. Droplet-based combinatorial indexing for massive scale single-cell epigenomics. *bioRxiv*.
- Lee, J. H., E. R. Daugharthy, J. Scheiman, R. Kalhor, T. C. Ferrante, R. Terry,

- B. M. Turczyk, J. L. Yang, H. S. Lee, J. Aach, and et al.
2015. Fluorescent in situ sequencing (fisseq) of rna for gene expression profiling in intact cells and tissues. *Nature Protocols*, 10(3):442–458.
- Lee, J. H., E. R. Daugharthy, J. Scheiman, R. Kalhor, J. L. Yang, T. C. Ferrante, R. Terry, S. S. F. Jeanty, C. Li, R. Amamoto, and et al.
2014. Highly multiplexed subcellular rna sequencing in situ. *Science*, 343(6177):1360–1363.
- Li, G., Y. Liu, Y. Zhang, N. Kubo, M. Yu, R. Fang, M. Kellis, and B. Ren
2019. Joint profiling of dna methylation and chromatin architecture in single cells. *Nature Methods*.
- Li, W., R. B. Calder, J. C. Mar, and J. Vijg
2015. Single-cell transcriptogenomics reveals transcriptional exclusion of enu-mutated alleles. *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis*, 772:55–62.
- Liu, L., C. Liu, A. Quintero, L. Wu, Y. Yuan, M. Wang, M. Cheng, L. Leng, L. Xu, G. Dong, and et al.
2019. Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. *Nature Communications*, 10(1).
- Macaulay, I. C., W. Haerty, P. Kumar, Y. I. Li, T. X. Hu, M. J. Teng, M. Goolam, N. Saurat, P. Coupland, L. M. Shirley, and et al.
2015. G&t-seq: parallel sequencing of single-cell genomes and transcriptomes. *Nature Methods*, 12(6):519–522.
- Macaulay, I. C., M. J. Teng, W. Haerty, P. Kumar, C. P. Ponting, and T. Voet
2016. Separation and parallel sequencing of the genomes and transcriptomes of single cells using g&t-seq. *Nature Protocols*, 11(11):2081–2103.
- Macosko, E. Z., A. Basu, R. Satija, J. Nemesh, K. Shekhar, M. Goldman, I. Tirosh, A. R. Bialas, N. Kamitaki, E. M. Martersteck, J. J. Trombetta, D. A. Weitz, J. R. Sanes, A. K. Shalek, A. Regev, and S. A. McCarroll
2015. Highly parallel genome-wide expression profiling of individual cells using nanoliter droplets. *Cell*, 161(5):1202–1214.
- Mayer, A. and L. S. Churchman
2017. A detailed protocol for subcellular rna sequencing (subrna-seq). *Current Protocols in Molecular Biology*.

- Mortazavi, A., B. A. Williams, K. McCue, L. Schaeffer, and B. Wold
2008. Mapping and quantifying mammalian transcriptomes by rna-seq. *Nature Methods*, 5(7):621–628.
- Peterson, V. M., K. X. Zhang, N. Kumar, J. Wong, L. Li, D. C. Wilson, R. Moore, T. K. Mcclanahan, S. Sadekova, and J. A. Klappenbach
2017. Multiplexed quantification of proteins and transcripts in single cells. *Nature biotechnology*, 35(10):936–939.
- Picelli, S., Å. K. Björklund, O. R. Faridani, S. Sagasser, G. Winberg, and R. Sandberg
2013. Smart-seq2 for sensitive full-length transcriptome profiling in single cells. *Nature Methods*, 10(11):1096–1100.
- Picelli, S., O. R. Faridani, Å. K. Björklund, G. Winberg, S. Sagasser, and R. Sandberg
2014. Full-length rna-seq from single cells using smart-seq2. *Nature Protocols*, 9(1):171–181.
- Pollen, A. A., T. J. Nowakowski, J. Shuga, X. Wang, A. A. Leyrat, J. H. Lui, N. Li, L. Szpankowski, B. Fowler, P. Chen, and et al.
2014. Low-coverage single-cell mrna sequencing reveals cellular heterogeneity and activated signaling pathways in developing cerebral cortex. *Nature Biotechnology*, 32(10):1053–1058.
- Pott, S.
2017. Simultaneous measurement of chromatin accessibility, dna methylation, and nucleosome phasing in single cells. *eLife*, 6.
- Preissl, S., R. Fang, H. Huang, Y. Zhao, R. Raviram, D. U. Gorkin, Y. Zhang, B. C. Sos, V. Afzal, D. E. Dickel, and et al.
2018. Single-nucleus analysis of accessible chromatin in developing mouse fore-brain reveals cell-type-specific transcriptional regulation. *Nature Neuroscience*, 21(7):1015–1015.
- Ramsköld, D., S. Luo, Y. . Wang, R. Li, Q. Deng, O. R. Faridani, G. A. Daniels, I. Khrebtukova, J. F. Loring, L. C. Laurent, G. P. Schroth, and R. Sandberg
2012. Full-length mrna-seq from single-cell levels of rna and individual circulating tumor cells. *Nature biotechnology*, 30(8):777–782.
- Reyes, M., K. Billman, N. Hacohen, and P. C. Blainey
2019. Simultaneous profiling of gene expression and chromatin accessibility in single cells. *Advanced Biosystems*, P. 1900065.

- Rodrigues, S. G., R. R. Stickels, A. Goeva, C. A. Martin, E. Murray, C. R. Vanderburg, J. Welch, L. M. Chen, F. Chen, E. Z. Macosko, and et al.
2019. Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution. *Science*, 363(6434):14631467.
- Rosenberg, A. B., C. M. Roco, R. A. Muscat, A. Kuchina, P. Sample, Z. Yao, L. T. Graybuck, D. J. Peeler, S. Mukherjee, W. Chen, S. H. Pun, D. L. Sellers, B. Tasic, and G. Seelig
2018. Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding. *Science*, 360(6385):176–182.
- Rotem, A., O. Ram, N. Shores, R. A. Sperling, A. Goren, D. A. Weitz, and B. E. Bernstein
2015. Single-cell chip-seq reveals cell subpopulations defined by chromatin state. *Nature Biotechnology*, 33(11):1165–1172.
- Rubin, A. J., K. R. Parker, A. T. Satpathy, Y. Qi, B. Wu, A. J. Ong, M. R. Mumbach, A. L. Ji, D. S. Kim, S. W. Cho, and et al.
2019. Coupled single-cell crispr screening and epigenomic profiling reveals causal gene regulatory networks. *Cell*, 176(1-2).
- Sasagawa, Y., H. Danno, H. Takada, M. Ebisawa, K. Tanaka, T. Hayashi, A. Kurisaki, and I. Nikaido
2018. Quartz-seq2: a high-throughput single-cell rna-sequencing method that effectively uses limited sequence reads. *Genome Biology*, 19(1).
- Sasagawa, Y., I. Nikaido, T. Hayashi, H. Danno, K. D. Uno, T. Imai, and H. R. Ueda
2013. Quartz-seq: a highly reproducible and sensitive single-cell rna sequencing method, reveals non-genetic gene-expression heterogeneity. *Genome Biology*, 14(4).
- Satpathy, A. T., J. M. Granja, K. E. Yost, Y. Qi, F. Meschi, G. P. Mcdermott, B. N. Olsen, M. R. Mumbach, S. E. Pierce, M. R. Corces, and et al.
2019. Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral t cell exhaustion. *Nature Biotechnology*, 37(8):925936.
- Shah, S., E. Lubeck, W. Zhou, and L. Cai
2016. In situ transcription profiling of single cells reveals spatial organization of cells in the mouse hippocampus. *Neuron*, 92(2):342–357.

- Singh, M., G. Al-Eryani, S. Carswell, J. M. Ferguson, J. Blackburn, K. Barton, D. Roden, F. Luciani, T. G. Phan, S. Junankar, and et al.
2019. High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes. *Nature Communications*, 10(1).
- Smallwood, S. A., H. J. Lee, C. Angermueller, F. Krueger, H. Saadeh, J. Peat, S. R. Andrews, O. Stegle, W. Reik, and G. Kelsey
2014. Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. *Nature Methods*, 11(8):817–820.
- Soumillon, M., D. Cacchiarelli, S. Semrau, A. V. Oudenaarden, and T. S. Mikkelsen
2014. Characterization of directed differentiation by high-throughput single-cell rna-seq. *bioRxiv*.
- Stoeckius, M., C. Hafemeister, W. Stephenson, B. Houck-Loomis, P. K. Chattopadhyay, H. Swerdlow, R. Satija, and P. Smibert
2017. Simultaneous epitope and transcriptome measurement in single cells. *Nature Methods*, 14(9):865–868.
- Streets, A. M., X. Zhang, C. Cao, Y. Pang, X. Wu, L. Xiong, L. Yang, Y. Fu, L. Zhao, F. Tang, and Y. Huang
2014. Microfluidic single-cell whole-transcriptome sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, 111(19):7048–7053.
- Ståhl, P. L., F. Salmén, S. Vickovic, A. Lundmark, J. F. Navarro, J. Magnusson, S. Giacomello, M. Asp, J. O. Westholm, M. Huss, and et al.
2016. Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. *Science*, 353(6294):7882.
- Tang, F., C. Barbacioru, S. Bao, C. Lee, E. Nordman, X. Wang, K. Lao, and M. A. Surani
2010. Tracing the derivation of embryonic stem cells from the inner cell mass by single-cell rna-seq analysis. *Cell Stem Cell*, 6(5):468–478.
- Tang, F., C. Barbacioru, Y. Wang, E. Nordman, C. Lee, N. Xu, X. Wang, J. Bodeau, B. B. Tuch, A. Siddiqui, K. Lao, and M. A. Surani
2009. mrna-seq whole-transcriptome analysis of a single cell. *Nature Methods*, 6(5):377–382.

- Vickovic, S., G. Eraslan, F. Salmén, J. Klughammer, L. Stenbeck, T. Äijö, R. Bonneau, L. Bergensträhle, J. F. Navarro, J. Gould, and et al.
2019. High-density spatial transcriptomics arrays for in situ tissue profiling.
- Vickovic, S., P. L. Ståhl, F. Salmén, S. Giatrellis, J. O. Westholm, A. Mollbrink, J. F. Navarro, J. Custodio, M. Bienko, L.-A. Sutton, and et al.
2016. Massive and parallel expression profiling using microarrayed single-cell sequencing. *Nature Communications*, 7(1).
- Vitak, S. A., K. A. Torkenczy, J. L. Rosenkrantz, A. J. Fields, L. Christiansen, M. H. Wong, L. Carbone, F. J. Steemers, and A. Adey
2017. Sequencing thousands of single-cell genomes with combinatorial indexing. *Nature Methods*, 14(3):302–308.
- Wang, G., J. R. Moffitt, and X. Zhuang
2018a. Multiplexed imaging of high-density libraries of rnas with merfish and expansion microscopy. *Scientific Reports*, 8(1).
- Wang, X., W. E. Allen, M. A. Wright, E. L. Sylwestrak, N. Samusik, S. Vesuna, K. Evans, C. Liu, C. Ramakrishnan, J. Liu, and et al.
2018b. Three-dimensional intact-tissue sequencing of single-cell transcriptional states. *Science*, 361(6400).
- Wu, A. R., N. F. Neff, T. Kalisky, P. Dalerba, B. Treutlein, M. E. Rothenberg, F. M. Mburu, G. L. Mantalas, S. Sim, M. F. Clarke, and et al.
2013. Quantitative assessment of single-cell rna-sequencing methods. *Nature Methods*, 11(1):4146.
- Xia, C., H. P. Babcock, J. R. Moffitt, and X. Zhuang
2019. Multiplexed detection of rna using merfish and branched dna amplification. *Scientific Reports*, 9(1).
- Xie, S., J. Duan, B. Li, P. Zhou, and G. C. Hon
2017. Multiplexed engineering and analysis of combinatorial enhancer activity in single cells. *Molecular Cell*, 66(2).
- Yin, Y., Y. Jiang, K.-W. G. Lam, J. B. Berletch, C. M. Disteché, W. S. Noble, F. J. Steemers, R. D. Camerini-Otero, A. C. Adey, J. Shendure, and et al.
2019. High-throughput single-cell sequencing with linear amplification. *Molecular Cell*.
- Zahn, H., A. Steif, E. Laks, P. Eirew, M. Vaninsberghe, S. P. Shah, S. Aparicio, and C. L. Hansen
2017. Scalable whole-genome single-cell library preparation without preamplification. *Nature Methods*, 14(2):167–173.

- Zheng, G. X., J. M. Terry, P. Belgrader, P. Ryvkin, Z. W. Bent, R. Wilson, S. B. Ziraldo, T. D. Wheeler, G. P. McDermott, J. Zhu, M. T. Gregory, J. Shuga, L. Montesclaros, J. G. Underwood, D. A. Masquelier, S. Y. Nishimura, M. Schnall-Levin, P. W. Wyatt, C. M. Hindson, R. Bharadwaj, A. Wong, K. D. Ness, L. W. Beppu, H. J. Deeg, C. McFarland, K. R. Loeb, W. J. Valente, N. G. Ericson, E. A. Stevens, J. P. Radich, T. S. Mikkelsen, B. J. Hindson, and J. H. Bielas
2017. Massively parallel digital transcriptional profiling of single cells. *Nature Communications*, 8.
- Ziegenhain, C., B. Vieth, S. Parekh, B. Reinius, A. Guillaumet-Adkins, M. Smets, H. Leonhardt, H. Heyn, I. Hellmann, and W. Enard
2017. Comparative analysis of single-cell rna sequencing methods. *Molecular cell*, 65(4):631–643.e4.
- Žilionis, R., J. Nainys, A. Veres, V. Savova, D. Zemmour, A. M. Klein, and L. Mazutis
2017. Single-cell barcoding and sequencing using droplet microfluidics. *Nature Protocols*, 12(1):44–73.