Single-Cell

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RNA Low-Level Detection







Integrated Techniques

References												
Act-Seq Wu Y. E. et al. (2017) Neuron 96(2): 313-329	DroNC-seq	Habib N. et al. (2017) Nat Methods 14(10): 955-958	IMS-MDA	Seth-Smith H. M. et al. (2013) Nat Protoc 8: 2404-2412	Nanogrid		scATAC-Seq	Cusanovich D. A. et al. (2015) Science 348: 910-4 (Cell Index)	SCRB-Seq	Soumillon M. et al. (2014) bioRxiv: 003236	snmC-Seq	Luo C. et al. (2017) Science 357(6351): 600
CEL-Seq Hashimshony T. et al. (2012) Cell Rep 2: 666-673	Drop-Seq	Macosko E. Z. et al. (2015) Cell 161: 1202-1214	inDrop	Klein A. M. et al. (2015) Cell 161: 1187-201	SNRS	Gao R. et al. (2017) Nat Commun 8(1): 228	scChip-seq	Rotem A. et al. (2015) Nat Biotechnol 33: 1165-72	scTHS-seq	Lake B. B. et al. (2018) Nature Biotechnology 36(1): 70-80	snRNA-seq	Grindberg R. V. et al. (2013) Proc Natl Acad Sci USA 110:
CirSeq Acevedo A. et al. (2014) Nature 505: 686-690	DR-Seq	Dey S. S. et al. (2015) Nat Biotechnol 33: 285-9	LIANTI	Chen C. et al. (2017) Science 356(6334): 189-194	nuc-seq	Wang Y. et al. (2014) Nature 512: 155-160	scCool-seq	Li L. et al. (2018) Nature Cell Biology 20(7): 847-858	scTrio-seq	Hou Y. et al. (2016) Cell Res 26: 304-19		19802-7
CITE-Seq Stoeckius M., et al. (2017) Nat Methods 14(9): 865-868	Drop-ChIP	Rotem A. et al. (2015) Nat Biotechnol 33: 1165-72	MALBAC	Zong C. et al. (2012) Science 338: 1622-1626	Nuc-Seq/SNES	Leung M. L. et al. (2015) Genome Biology 16(1): 55	sciHi-C	Ramani V. et al. (2017) Nature Methods 14: 263	scTrio-seq2	Bian S. et al. (2018) Science 362(6418): 1060	SPLIT-seq	Rosenberg A. B. et al. (2018) Science 360(6385): 176
CLaP Binan L. et al. (2016) Nat Commun 7: 11636	Duplex-Seq	Schmitt M. W. et al. (2012) Proc Natl Acad Sci USA 109:	MARS-seq	Jaitin D. A. et al. (2014) Science 343:776-9	OS-Seq	Myllykangas S. et al. (2011) Nat Biotechnol 29: 1024-1027	sci-CAR	Cao J. et al. (2018) Science 361(6409): 1380	Seq-Well	Gierahn T. M., et al. (2017). Nat Methods 14(4): 395-398	SIRI	Islam S. et al. (2011) Genome Res 21: 1160-1167
CRISPR-UMI Michlits G. et al. (2017) Nat Methods 14(12): 1191-1197		14508-14513	MATQ-seq	Sheng K. et al. (2017) Nat Methods 14(3): 267-270	PAIR	Bell T. J. et al. (2015) Methods Mol Biol 1324: 457-68	sci-DNA-seq	Rosenberg A. B. et al. (2018) Science 360: 176-182	SIDR	Han K. Y. et al. (2018) Genome Research 28(1): 75-87	SUPER-seq	Fan X. et al. (2015) Genome Blol 16: 148
CROP-Seq Datlinger P. et al. (2017) Nat Methods 14(3): 297-301	ECCITE-seq	Mimitou E. P. et al. (2019) Nat Methods 16(5): 409-412	MDA	Dean F. B. et al. (2001) Genome Res 11: 1095-1099	Quartz-Seq	Sasagawa Y. et al. (2013) Genome Biol 14: R31	sci-MET	Mulqueen R. M. et al. (2018) Nature Biotechnology 36: 428	SINC-seq	Abdelmoez M. N. et al. (2018) Genome Biology 19(1): 66	Deiring	Turchaninova M. A. et al. (2012) Eur J Immunol 42:
CytoSeq Fan H. C. et al. (2015) Science 347: 1258367	FREQ-Seq	Chubiz L. M. et al. (2012) PLoS One 7: e47959	Microwell-seq	Han X. et al. (2018) Cell 172(5): 1091-1107.e1017	Quartz-Seq2	Sasagawa Y. et al. (2018) Genome Biology 19(1): 29	sci-RNA-seq	Cao J. et al. (2017) Science 357(6352): 661	Smart-Seq	Ramskold D. et al. (2012) Nat Biotechnol 30: 777-782	Pairing	2507-2515
Digital RNA Shiroguchi K. et al. (2012) Proc Natl Acad Sci USA	FRISCR	Thomsen E. R. et al. (2016) Nat Methods 13: 87-93	MIDAS	Gole J. et al. (2013) Nat Biotechnol 31:1126-32	RamDA-seq	Hayashi T. et al. (2018) Nature Communications 9(1): 619	SCMDA	Dong X. et al. (2017) Nature Methods 14: 491	Smart-seq2	Picelli S. et al. (2013) Nat Methods 10: 1096-1098v	TCR-LA-MC-PC	R Ruggiero E. et al. (2015) Nat Commun 6: 8081
109:1347-1352	G&T-seq	Macaulay I. C. et al. (2015) Nat Methods 12: 519-522	MIPSTR	Carlson K. D. et al. (2015) Genome Res 25: 750-761	RNAtag-Seq	Shishkin A. A. et al. (2015) Nat Methods 12: 323-325	scM&T-seq	Angermueller C. et al. (2016) Nature Methods 13: 229	SMDB	Lan F. et al. (2016) Nat Commun 7: 11784	TIVA	Lovatt D. et al. (2014) Nat Methods 11: 190-196
Dip-C Tan L., et al. (2018) Science 361(6405): 924-928	HiRes-Seq	Imashimizu M. et al. (2013) Nucleic Acids Res 41:	Mosaic-seq	Han X. et al. (2018) Cell 172(5): 1091-1107 e1017	Safe-SeqS	Kinde I. et al. (2011) Proc Natl Acad Sci USA 108: 9530-5	scNMT-seq	Clark S. J. et al. (2018) Nature Communications 9(1): 781	smMIP	Hiatt J. B. et al. (2013) Genome Res 23: 843-854	TSCS	Casasent A. K. et al. (2018) Cell 172(1): 205-217.e212
Div-Seq Habib N. et al. (2016) Science 353(6302): 925-928		9090-9104	MULTI-seq	McGinnis C. S. et al. (2019) Nat Methods 16(7): 619-626	scABA-seq	Mooijman D. et al. (2016) Nature Biotechnology 34: 852	scRC-Seq	Upton K. R. et al. (2015) Cell 161: 228-39	snDrop-seq	Lake B. B. et al. (2018) Nature Biotechnology 36(1): 70-80	UMI Method	Kivioja T. et al. (2012) Nat Methods 9: 72-74
DP-Seq Bhargava V. et al. (2013) Sci Rep 3: 1740	HI-SCL	Rotem A. et al. (2015) PLoS One 10: e0116328	NanoCAGE	Plessy C. et al. (2010) Nat Methods 7: 528-534	scATAC-seq	Buenrostro J. D. et al. (2015) Nature 523: 486-490 (Microfluidics)	scRNA-seq	Tang F. et al. (2009) Nat Methods 6: 377-82	SNES	Leung M. L. et al. (2015) Genome Biol 16: 55	viscRNA-seq	Zanini F. et al. (2018) Elife 7: e32942

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