

# For all you seq...

# Single-Cell

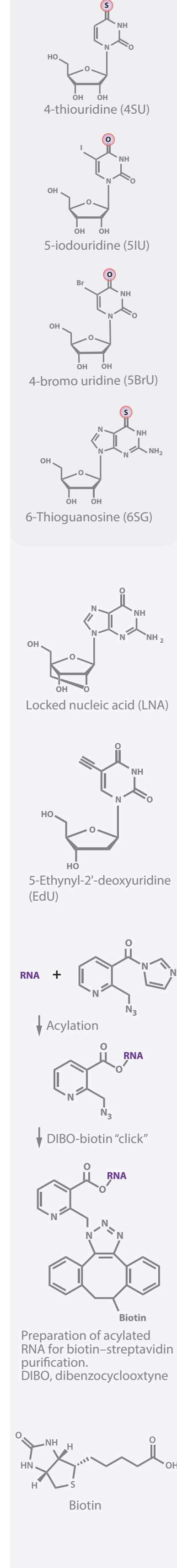
## RNA Low-Level Detection



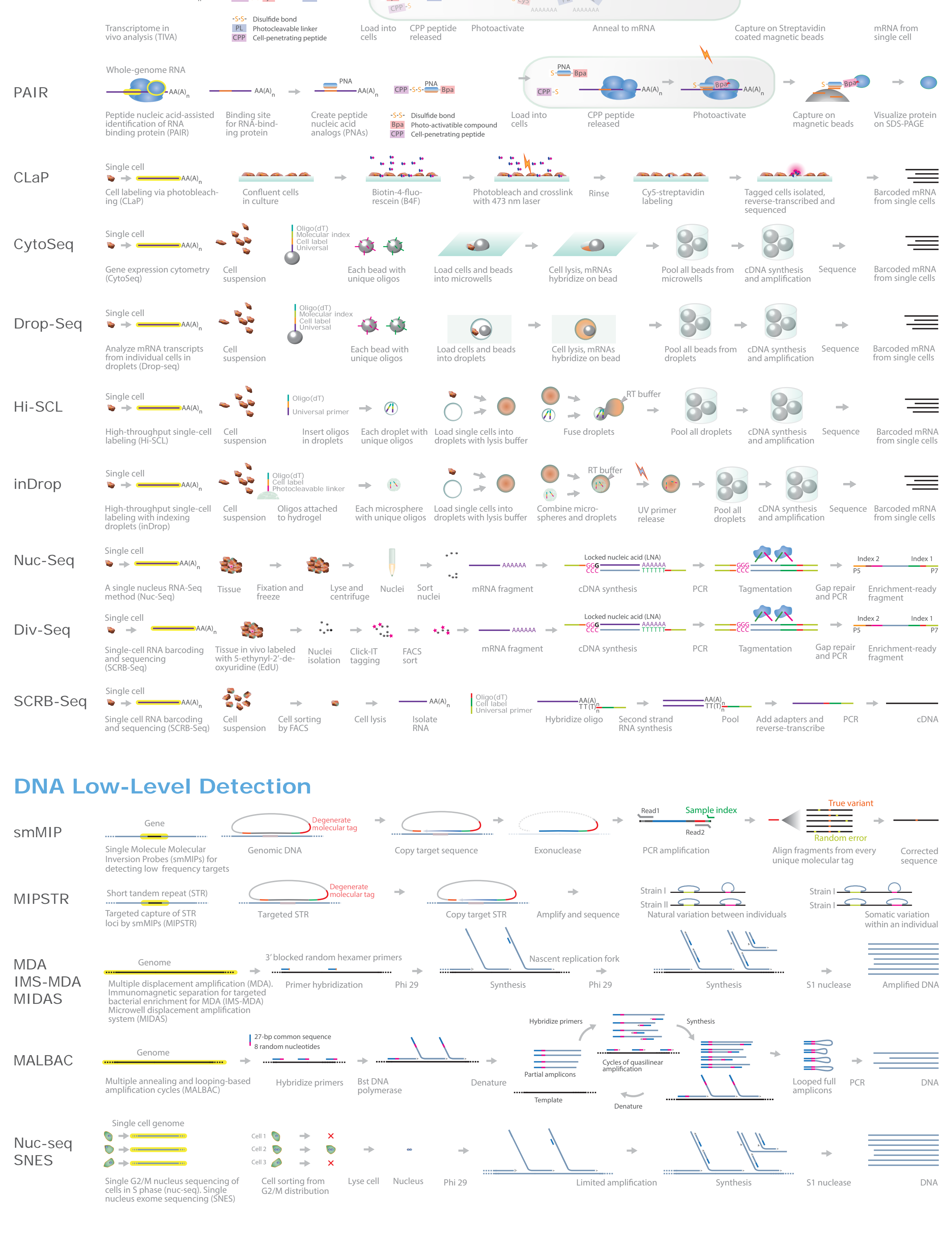
**References**

CAGEscan Plessy C. et al. (2010) Nat Methods 7: 528-534  
 CEL-Seq Hashimshony T. et al. (2012) Cell Rep 2: 666-673  
 Cir-Seq Acvedo A. et al. (2014) Nature 505: 686-690  
 Cytoseq Bin H. C. et al. (2013) Science 341: 12656-7  
 Digital RNA Shiroguchi K. et al. (2012) Proc Natl Acad Sci U S A 109: 13471-1352  
 Div-Seq Habibi H. et al. (2016) bioRxiv  
 DP-Seq Bhargava V. et al. (2013) Sci Rep 3: 1740  
 Drop-Seq Maccosco E. Z. et al. (2015) Cell 161: 1202-1214  
 DR-Seq Day SS et al. (2015) Nat Biotechnol 33: 285-9  
 Duplex-Seq Rotem A. et al. (2015) Nat Biotechnol 33: 1165-72  
 Cytoseq Bin H. C. et al. (2013) Science 341: 12656-7  
 FREQ-Seq Chubiz L. M. et al. (2012) PLoS One 7: e47959  
 FRISCR Thomsen ER et al. (2016) Nat Methods 13: 87-93  
 G&T-Seq Macaulay I. C. et al. (2015) Nat Methods 12: 519-522  
 HiRes-Seq Imashimizu M. et al. (2013) Nucleic Acids Res 41: 9090-9104  
 Hi-SCL Rotem A. et al. (2015) PLoS One 10: e0116328  
 HiDrop Smith-Smith H. M. et al. (2013) Nat Protoc 8: 2404-2412  
 MALBAC Klein AM et al. (2015) Cell 161: 1187-201  
 MARS-Seq Zong C. et al. (2012) Science 338: 1622-1626  
 MDA Justin DA et al. (2014) Science 343: 774-9  
 MIDAS Dean F. B. et al. (2001) Genome Res 11: 1099-1099  
 MIPSTR Gole J. et al. (2013) Nat Biotechnol 31: 1126-32  
 NanoCAGE Carlson K. D. et al. (2015) Genome Res 25: 750-761  
 Plessy C. et al. (2010) Nat Methods 7: 528-534  
 nuc-seq Wang Y. et al. (2014) Nature 512: 155-160  
 Nuc-Seq Habib N. et al. (2016) bioRxiv  
 OS-Seq Mylykangas S. et al. (2011) Nat Biotechnol 29: 1024-1027  
 PAIR Bell T J et al. (2015) Methods Mol Biol 1324: 457-68  
 Quant-Seq Sanagawa Y. et al. (2013) Genome Biol 14: R31  
 RNAtag-Seq Shikhan A. A. et al. (2015) Nat Methods 12: 323-325  
 Safe-Seq5 Kindel I et al. (2011) Proc Natl Acad Sci U S A 108: 9530-5  
 scABA-seq Moajim D et al. (2016) Nat Biotechnol advance online publication  
 scATAC-Seq (Cell Index) Buenrostro J. D. et al. (2015) Nature 523: 486-490  
 scATAC-Seq (Microfluidics) Cusanovich DA et al. (2015) Science 348: 910-4  
 scATAC-Seq (Nucleofection) Rotem A. et al. (2015) Nat Biotechnol 33: 1165-72  
 scATAC-Seq (Nucleofection) Angermuller C. et al. (2016) Nat Methods advance online publication  
 scChIP-Seq Upton KR et al. (2015) Cell 161: 228-39  
 scChIP-Seq Tang F. et al. (2009) Nat Methods 6: 377-82  
 scCRB-Seq Soumillion M. et al. (2014) bioRxiv  
 scCRB-Seq Hou Y. et al. (2016) Cell Res 26: 304-19  
 scCRB-Seq Rasmikh D. et al. (2012) Nat Biotechnol 30: 777-782  
 scCRB-Seq Paoletti S. et al. (2013) Nat Methods 10: 1096-1098  
 scCRB-Seq Lan F. et al. (2014) Nat Commun 5: 3714  
 scCRB-Seq Hatt J. B. et al. (2013) Genome Res 23: 843-854  
 scCRB-Seq Luong M. L. et al. (2015) Genome Biol 16: 55  
 scCRB-Seq Grindberg RV et al. (2013) Proc Natl Acad Sci U S A 110: 19802-7  
 scCRB-Seq Islam S. et al. (2011) Genome Res 21: 1160-1167  
 scCRB-Seq Fan X. et al. (2015) Genome Biol 16: 148  
 scCRB-Seq Turchaninova M. A. et al. (2013) Eur J Immunol 43: 2507-2515  
 scCRB-Seq Ruggiero E. et al. (2015) Nat Commun 6: 8081  
 scCRB-Seq Lovatt D. et al. (2014) Nat Methods 11: 190-196  
 scCRB-Seq Kivits T. et al. (2012) Nat Methods 9: 72-74

## Photoactivatable Nucleosides



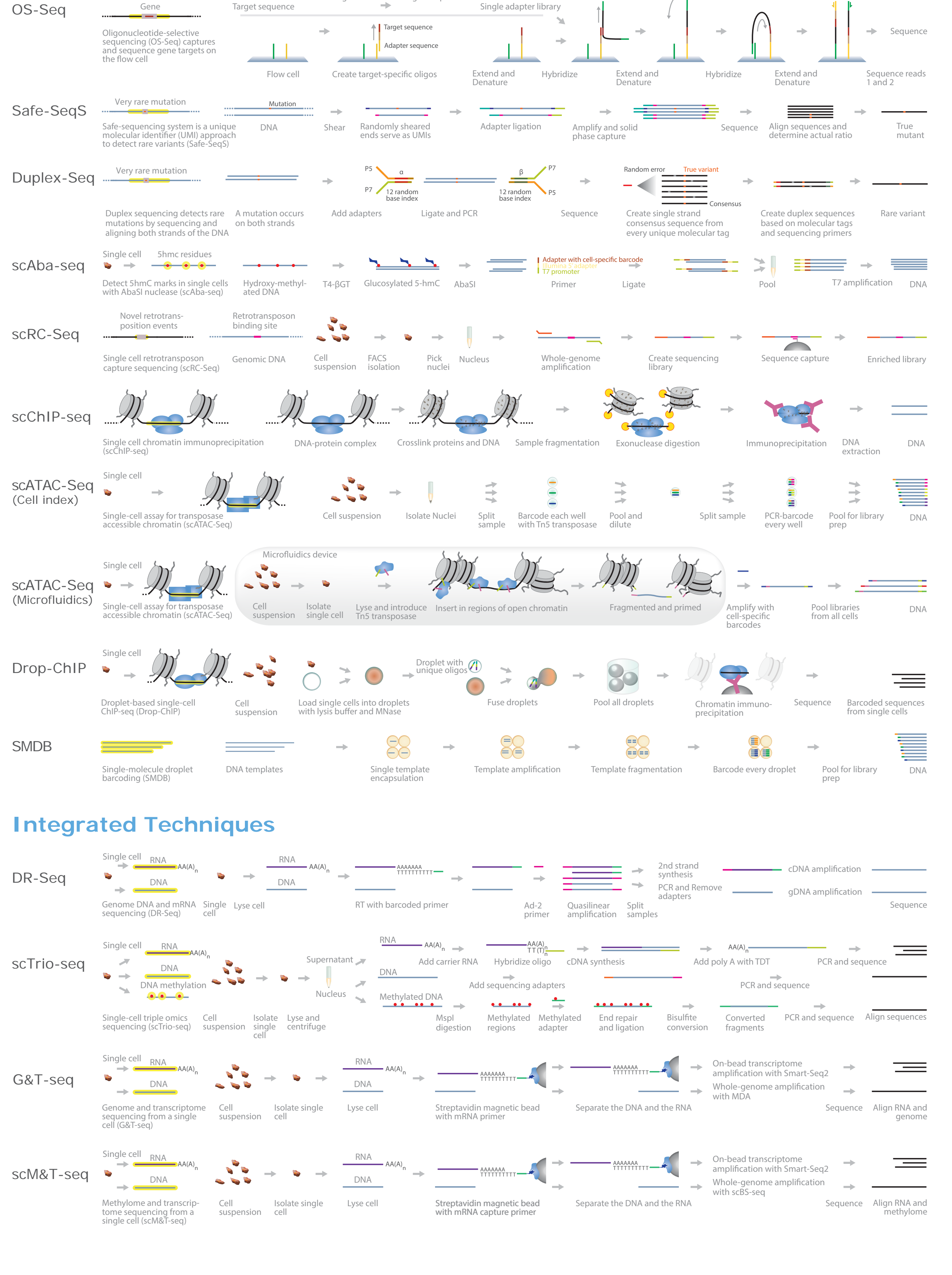
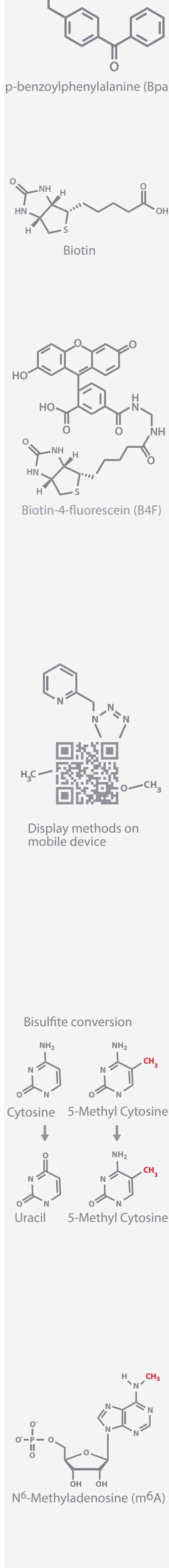
## TIVA



**References**

Wang Y. et al. (2014) Nature 512: 155-160  
 Habib N. et al. (2016) bioRxiv  
 Mylykangas S. et al. (2011) Nat Biotechnol 29: 1024-1027  
 Bell T J et al. (2015) Methods Mol Biol 1324: 457-68  
 Sanagawa Y. et al. (2013) Genome Biol 14: R31  
 Shikhan A. A. et al. (2015) Nat Methods 12: 323-325  
 Kindel I et al. (2011) Proc Natl Acad Sci U S A 108: 9530-5  
 Moajim D et al. (2016) Nat Biotechnol advance online publication  
 Buenrostro J. D. et al. (2015) Nature 523: 486-490  
 Cusanovich DA et al. (2015) Science 348: 910-4  
 Rotem A. et al. (2015) Nat Biotechnol 33: 1165-72  
 Angermuller C. et al. (2016) Nat Methods advance online publication  
 Upton KR et al. (2015) Cell 161: 228-39  
 Tang F. et al. (2009) Nat Methods 6: 377-82  
 Soumillion M. et al. (2014) bioRxiv  
 Hou Y. et al. (2016) Cell Res 26: 304-19  
 Rasmikh D. et al. (2012) Nat Biotechnol 30: 777-782  
 Paoletti S. et al. (2013) Nat Methods 10: 1096-1098  
 Lan F. et al. (2014) Nat Commun 5: 3714  
 Hatt J. B. et al. (2013) Genome Res 23: 843-854  
 Luong M. L. et al. (2015) Genome Biol 16: 55  
 Grindberg RV et al. (2013) Proc Natl Acad Sci U S A 110: 19802-7  
 Islam S. et al. (2011) Genome Res 21: 1160-1167  
 Fan X. et al. (2015) Genome Biol 16: 148  
 Turchaninova M. A. et al. (2013) Eur J Immunol 43: 2507-2515  
 Ruggiero E. et al. (2015) Nat Commun 6: 8081  
 Lovatt D. et al. (2014) Nat Methods 11: 190-196  
 Kivits T. et al. (2012) Nat Methods 9: 72-74

## OS-Seq



**References**

Oligonucleotide selective sequencing (OS-Seq) captures and sequence gene targets on the flow cell  
 Safe sequencing system is a unique molecular identifier (UMI) approach to detect rare variants (Safe-Seq5)  
 Duplex sequencing detects rare mutations by sequencing and aligning both strands of the DNA  
 Single cell Aba sequencing  
 Single cell chromatin resequencing (scCR-Seq)  
 Single cell chromatin immunoprecipitation (scChIP-Seq)  
 Single cell assay for transposase accessible chromatin (scATAC-Seq)  
 Drop-based single-cell ChIP (Drop-ChIP)  
 Single molecule droplet barcoding (SMDB)  
 Genome DNA and mRNA  
 Single cell tripartite sequencing (scTrio-seq)  
 Genome and transcriptome sequencing from a single cell (G&T-Seq)  
 Methylation and transcriptome sequencing from a single cell (scM&T-Seq)

