For all you seq...

DNA

DNA Rearrangements and Markers

RAD
PE RAD-Seq
ddRADseq
2b-RAD
SLAF-seq
hyRAD
Rapture
Dige-nome-seq
HydEn-seq
Ribose-seq
G4-seq
CAP-seq
CPT-Seq
RC-Seq
TN-Seq
INSeq
TC-Seq
Ig-seq
Rep-Seq
MAF
SSB-Seq
BLESS
DSB-Seq
GUIDE-seq
EC-seq
Bubble-Seq
NSCR
Repli Seq
NS-seq

DNA Low-Level Detection

smMIP
MIPSTR
MDA
IMS-MDA
MIDAS
MALBAC
nuc-seq
SNES
OS-Seq
Safe-SeqS
Duplex-Seq
DR-Seq
G&T-seq

Key

Yellow highlights indicate the target of the protocol

Bisulfite conversion

Display methods on mobile device

Pyridostatin (PDS)

Digoxigenin

Al-mediated cyclization labeling in fC-CET

EDTA

scM&T-seq
scMT-seq
scTrio-seq
scBS-seq
scAba-seq
scRC-Seq
scATAC-Seq (Cell index)
scATAC-Seq (Microfluidics)
Drop-ChIP
scChIP-seq
SMDB

Epigenetics

BS-Seq
Bisulfite-seq
WGBS
EpiGnome™ HELP-Seq
PBAT
BSPP
RRBS
scRRBS
BSAS
Methyl-Seq
MRE-Seq
EpiRADseq
T-WGBS
JBP1-seq
Aba-seq
TAmC-Seq
fC-Seal
fC-CET
CAB-Seq
oxBS-Seq
RedBS-Seq
caMAB-seq
fCAB-Seq
MAB-seq
RRMAB-seq
TAB-Seq
MIRA
MeDIP-Seq
DIP-seq
hMeDIP-Seq
MBDCap-seq
Methyl-Cap-seq
MBD-Seq
MiGS
BisChIP-Seq
ChIP-BS-seq

Methidiumpro-pyl-EDTA (MPE)

Preparation of acylated RNA for biotin–streptavidin purification. DIBO, dibenzocyclooctyne

Uridine diphosphate glucose (UDP-Glu)

Glucosylated 5hmc

Biotin

N3-5GMC

Pyridine

Display methods on mobile device

DNA-Protein Interactions

ChIP-Seq
ChIP-exo
HT-ChIP
Mint-ChIP
DNase-Seq
DNaseI-Seq
DNaseI-SIM
MAINE-Seq
MNase-Seq
Nucleo-Seq
FiT-seq
PAT-ChIP
X-ChIP
ORGANIC
ATAC-Seq
THS-seq
CATCH-IT
MINCE-seq
FAIRE-seq
Sono-Seq
NOMe-Seq
Histone methylation
ChIPmenta-tion
Chia-PET
Hi-C
3-C
Capture-C
NG Cap-ture-C
4-C
UMI-4C
5-C
PB-seq
Pu-seq
Break-seq
LAM-HTGTS
HTGTS
SELEX
SELEX-seq
HT-SELEX
HiTS-FLIP
DamID
MPE-seq
Chem-seq

Protein-Protein Interactions

PD-Seq
ProP-PD
PDZ-Seq

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3C Duan Z. et al. (2012) Methods 58: 277-288
4-C Zhao Z. et al. (2006) Nat Genet 38: 1341-1347
5-C Dostie J. et al. (2007) Nat Protoc 2: 988-1002
Aba-seq Sun Z. et al. (2013) Cell Rep 3: 567-576
ATAC-Seq Buenrostro J. D. et al. (2013) Nat Methods 10: 1213-1218
BisChIP-Seq Statham A. L. et al. (2012) Genome Res 22: 1120-1127
Bisulfite-seq Berman B. P. et al. (2012) Nat Genet 44: 40-46
BLESS Crosetto, N. et al. Nat. Methods 10, 361–365 (2013).
Break-seq Hoffman E.A. et al. (2015) Genome Res 25: 402-412
BSAS Masser D. R. et al. (2013) Epigenetics Chromatin 6: 33
BSPP Deng J. et al. (2009) Nat Biotechnol 27: 353-360
BS-Seq Lister R. et al. (2009) Nature 462: 315-322
Bubble-Seq Mesner L. D. et al. (2013) Genome Res 23: 1774-1788
CAB-Seq Lu X. et al. (2013) J Am Chem Soc 135: 9315-9317
caMAB-seq Wu H et al. (2016) Nat Protoc 11:1081-100
CAP-seq Illingworth R. S. et al. (2010) PLoS Genet 6: e1001134
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ChIP-exo Yen K. et al. (2013) Cell 154: 1246-1256
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ChIP-Seq Barski A. et al. (2007) Cell 129: 823-837
CPT-seq Amini S. et al. (2014) Nat Genet 46: 1343-1349
DamID Vogel M. J. et al. (2007) Nat Protoc 2: 1467-1478
ddRADseq Peterson B. K. et al. (2012) PLoS One 7: e37135
Digenome-seq Kim D et al. (2015) Nat Methods 12:237-43
DIP-seq Shen L. et al. (2013) Cell 153: 692-706
Dnase I SIM Cumbie JS et al. (2015) Plant Methods 11:42
DNaseI-Seq Hesselberth J. R. et al. (2009) Nat Methods 6: 283-289
DNase-Seq Boyle A. P. et al. (2008) Cell 132: 311-322
Drop-ChIP Rotem A et al. (2015) Nat Biotechnol 33:1165-72
DR-Seq Dey SS et al. (2015) Nat Biotechnol 33:285-9
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Duplex-Seq Schmitt M. W. et al. (2012) Proc Natl Acad Sci U S A 109: 14508-14513
EC-seq Parkinson N. J. et al. (2015) Genome Res 25: 226-234
EpiRADSeq Schield DR et al. (2016) Methods in Ecology and Evolution 7:60-69
FAIRE-Seq Gaulton K. J. et al. (2010) Nat Genet 42: 255-259
fCAB-Seq Song C. X. et al. (2013) Cell 153: 678-691
fC-CET Xia B et al. (2015) Nat Methods 12:1047-50
fC-Seal Song C. X. et al. (2013) Cell 153: 678-691
FIT-Seq Cejas P et al. (2016) Nat Med
G&T-seq Macaulay I. C. et al. (2015) Nat Methods 12: 519-522
G4-seq Chambers V. S. et al. (2015) Nat Biotechnol 33: 877-881
GUIDE-seq Tsai SQ et al. (2015) Nat Biotechnol 33:187-97
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HiTS-Flip Nutiu R. et al. (2011) Nat Biotechnol 29: 659-664
hMeDIP-seq Xu Y et al. (2011) Mol Cell 42:451-64
HT-ChIP Blecher-Gonen R. et al. (2013) Nat Protoc 8: 539-554
HTGTS Chiarle, R. et al. (2011) Cell 147, 107–119
HT-SELEX Jolma A. et al. (2010) Genome Res 20: 861-873
HydEn-seq Clausen A. R. et al. (2015) Nat Struct Mol Biol 22: 185-191
hyRAD Suchan T et al. (2016) PLoS One 11:e0151651
Ip-Seq Volmers C. et al. (2013) Proc Natl Acad Sci U S A 110: 13463-13468
IMS-MDA Seth-Smith H. M. et al. (2013) Nat Protoc 8: 2404-2412
INSeq Goodman AL et al. (2009) Cell Host Microbe 6:279-89
JBP1-seq Cui L. et al. (2014) Genomics
LAM-HTGTS Hu J et al. (2016) Nat. Protocols 11:853-871
MAB-seq Wu H. et al. (2014) Nat Biotechnol
MAF Khan TA et al. (2016) Sci Adv 2:e1501371
MAINE-Seq Ponts N. et al. (2010) Genome Res 20: 228-238
MALBAC Zong C. et al. (2012) Science 338: 1622-1626
MBDCap-Seq de Assis S. et al. (2012) Nat Commun 3: 1053
MBD-Seq Nair S. S. et al. (2011) Epigenetics 6: 34-44
MDA Dean F. B. et al. (2001) Genome Res 11: 1095-1099
MeDIP-Seq Down T. A. et al. (2008) Nat Biotechnol 26: 779-785
MethylCap-Seq Brinkman A. B. et al. (2010) Methods 52: 232-236
Methyl-seq Brunner A. L. et al. (2009) Genome Res 19: 1044-1056
MIDAS Gole J et al. (2013) Nat Biotechnol 31:1126-32
MiGS Serre D. et al. (2010) Nucleic Acids Res 38: 391-399
MINCE-seq Ramachandran S et al. (2016) Cell 165:580-92
Mint-ChIP van Galen P et al. (2016) Mol Cell 61:170-80
MIPSTR Carlson K. D. et al. (2015) Genome Res 25: 750-761
MIRA Rauch T. A. et al. (2010) Methods 52: 213-217
MNase-Seq Schones D. E. et al. (2008) Cell 132: 887-898
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OS-Seq Mylykangas S. et al. (2011) Nat Biotechnol 29: 1024-1027
oxBS-Seq Booth M. J. et al. (2012) Science 336: 934-937
PAT–ChIP Fanelli M et al. (2011) Nat Protoc 6:1905-19
PBAT Miura F. et al. (2012) Nucleic Acids Res 40: e136
PB-seq Guertin M. J. et al. (2012) PLoS Genet 8: e1002610
PD-Seq Arango D. et al. (2013) Proc Natl Acad Sci U S A 110: E2153-2162
PDZ-Seq Ernst A. et al. (2010) Mol Biosyst 6: 1782-1790
PE RAD-Seq Willing E. M. et al. (2011) Bioinformatics 27: 2187-2193
ProP-PD Ivarsson Y. et al. (2014) Proc Natl Acad Sci U S A 111: 2542-2547
Pu-seq Daigaku Y. et al. (2015) Nat Struct Mol Biol 22: 192-198
RAD Baird N. A. et al. (2008) PLoS One 3: e3376
Rapture Ali OA et al. (2016) Genetics 202:389-400
RBBS Meissner A et al. (2008) Nature 454:766-70
RC-Seq Baillie J. K. et al. (2011) Nature 479: 534-537
RedBS-Seq Booth M. J. et al. (2014) Nat Chem 6: 435-440
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RRBS Meissner A. et al. (2008) Nature 454: 766-770
RRMAB-seq Neri F. et al. (2015) Cell Rep 10: 674-683
SELEX Kinde I et al. (2011) Proc Natl Acad Sci U S A 108:9530-5
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scRC-Seq
scRRBS
scTrio-seq
SELEX
SELEX-seq
SLAF-Seq
SMDB
smMIP
SNES
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THS-seq Sos BC et al. (2016) Genome Biol 17:20
TN-Seq van Opijnen T. et al. (2013) Nat Rev Microbiol 11: 435-442
T-WGBS Wang Q. et al. (2013) Nat Protoc 8: 2022-2032
UMI-4C Schwartzman O et al. (2016) Nat Methods advance online publication
WGBS Lister R. et al. (2009) Nature 462: 315-322
X-ChIP-seq Skene P. J. et al. (2014) Elife 3: e02042

TruSeq PCR Free

Double-stranded DNA → Fractionate Size select → End repair Phosphorylate → A-overhang → Add Adaptors → Adaptor ligation → Product ready for cluster generation

TruSeq Nano

Double-stranded DNA → Fractionate Size select → End repair Phosphorylate → A-overhang → Add Adaptors → Adaptor ligation → Denature and amplify → Product ready for cluster generation

TruSeq Custom Amplicon

Double-stranded DNA → Region of interest → Custom Probe 1, Custom Probe 2 → Add custom probes → Extension and ligation → Add sequencing primers → PCR → Product ready for cluster generation

TruSeq RNA

AAAAA mRNA → polyA select → Fragment → Random hexamer → First and second strand synthesis

TruSeq Small RNA

5' → 3' Small RNA fragment → Ligate adaptors (5' Adapter, 3' Adapter) → Add primer → Reverse transcription → Denature and amplify → Product ready for cluster generation

TruSeq RNA Stranded

RNA → Random primer → Create cDNA → Create second strand cDNA → End repair Phosphorylate A-overhang → Adaptor ligation → Denature and amplify → Product ready for cluster generation

TruSeq RNA Access

Target → Pool stranded RNA-Seq libraries → Biotinylated target probe → Hybridize probes to targets → Capture on streptavidin magnetic beads → Elute → Product ready for cluster generation

TruSeq Targeted RNA Expression

Target → Total RNA → cDNA → Add custom primers → Hybridization → Extension-Ligation → Denature and amplify → Product ready for cluster generation

Nextera Library Preparation

Transposase → DNA → ~300bp → Tagmentation → Amplification → Product ready for cluster generation

Nextera Rapid Capture

Target → Denatured and pooled fragments from Nextera library → Biotinylated target probe → Hybridize probes to targets → Capture on magnetic beads → Elute → Product ready for cluster generation

Nextera Mate Pair

Transposase (biotinylated junction adapter) → DNA → Tagmentation → Circularize → Fragment → Isolate biotinylated fragment → Adaptor ligation → Denature and amplify → Product ready for cluster generation

Sequencing by Synthesis

Adapter hybridizes to flowcell; Reverse strand synteis; Forward strand; Reverse strand; Remove forward strand; Fold over and hybridize to second primer; Synthesize second strand; Bridge amplification; Thousands of molecules are amplified in parallel; The reverse strand is cleaved and washed away; Sequence primer; With each cycle, four fluorescently tagged nucleotides compete for addition to the growing chain. Only one is incorporated based on the sequence of the template.; The read product is washed away; Index 1 primer; Sequence Index1; The read product is washed away; Fold over and hybridize to first primer; Deblock P5 primer and add unlabeled bases; Sequence Index2; Synthesize second strand; The forward-strand is cleaved and washed away; Read 2 primer; The second read is sequenced

Moleculo

~10kb Sheared genomic DNA → End repair → Adapter ligation → Generate clonal pools Amplify → Transposase → Tagmentation → ~600bp → Add indices → Prepared fragments → Pool and purify

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This poster was compiled by the Illumina Scientific Affairs. Additional information, the latest version of the poster, and a comprehensive list of *seq methods, are available at http://www.illumina.com/libraryprepmethods. Please contact Scientific Affairs with any questions, comments, or suggestions.

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