

INDEX

A

Acetylation 210
 Adaptor/adapter 141, 142, 144, 146–148,
 151, 152, 166, 167, 181, 198, 206, 219, 226,
 234, 235, 240, 243, 248, 254, 259
 Adaptor ligation 142, 147, 152, 166
 Adenine 57, 148
 Affymetrix 271
 Agarose 4, 5, 19, 24, 25, 161, 164, 167,
 242, 246, 292, 296, 318
 Agilent 144, 145, 149, 150, 162,
 202, 214, 217–219, 259, 271, 277, 279
 Aging 57, 83, 141, 143, 175
 Algorithm 32, 35, 50, 116, 168,
 204, 258, 271, 280,
 282, 304
 Alignment 85, 98, 106, 124, 158,
 160, 167–169, 182, 183, 203, 204, 219, 220,
 226, 250, 251, 254, 258, 271, 278
 Allele-specific
 expression 50, 109
 methylation 53, 56
 Alternative splicing 52–54, 60
 Amplicon 110, 113, 117, 142, 144, 148,
 306, 307, 327, 330
 Amplification 84, 89, 93, 95, 103, 109–120,
 138–154, 166, 201, 204, 206, 236, 237, 254,
 258, 278, 299, 300, 305–307, 318
 Annotations 129, 132, 168, 172, 204, 252, 253
 Antibodies 98, 158, 211, 221, 231, 233,
 234, 240, 241, 244, 246, 254
 Arrays 93, 97, 98, 103, 105, 106, 116,
 119, 124, 134, 138, 140, 142, 144, 146,
 149–152, 154, 176, 177, 307
 Assay for Transposase Accessible Chromatin
 (ATAC-seq) 197–206, 212
 Assembly 33–35, 40, 41, 43, 46, 91, 92, 98, 134
 Azacitidine 175
 5-Aza-2'-deoxycytidine 53

B

Bacteria 20, 27, 34, 39, 40, 111, 139,
 159, 285, 288, 292–294, 297, 304
 BAM files 219, 220

Barcodes 97, 98, 106, 125, 199,
 201, 219, 226, 259, 272, 274, 278, 280,
 305–307, 326
 Beads 16, 18, 19, 21, 22, 24, 25, 36,
 95, 97, 98, 105, 106, 161, 165, 166, 172, 199,
 201, 214, 219, 234–237, 240–244, 246–249,
 254, 259, 271, 275, 276, 278, 327
 BED file 33, 43, 44, 221, 251, 252
 Beta values 124, 125, 127, 129, 132, 133
 Bias 17, 32, 39, 103, 146, 167, 172, 179,
 183, 184, 203, 204, 212, 227, 240, 250, 255, 278
 Binary 124, 204
 BioCAP-seq 15–27
 Bioinformatics v, 32, 175–189, 258
 Biotinylated 16, 17, 22, 24, 159, 239
 Biotinylated CxxC affinity purification
 (BioCAP) 15–27
 Biotinylation 19, 22, 27, 240, 241, 244
 Bisulfite
 conversion 90–92, 101, 110, 188, 214, 226
 converted DNA 95, 176, 218
 sequencing 139, 176, 177, 179, 185,
 187, 219, 226
 Blacklist 172, 204
 BOWTIE 162, 167, 182, 203
 Brain 5, 53, 55, 126, 182

C

Caenorhabditis elegans (*C. elegans*) 34, 38–40
 Calibration 26, 27, 327
 The Cancer Genome Atlas (TCGA) 123–134
 5-Carboxycytosine (5caC) 53
 Cas 285, 286, 289, 298
 Cas9 286–290, 292, 293, 295–299
 Cell culture 160, 163, 221, 233, 240, 289,
 291, 295, 296, 309, 311, 328
 Cell line 7, 60, 65, 159, 165, 171,
 198, 199, 222, 280, 289, 298–300
 Cell lysis 222, 224
 Cell types 8, 36, 49, 66, 138, 171,
 180, 182, 183, 186, 188, 189, 197, 198, 213,
 222, 225, 227, 258, 277, 280–282, 328, 329
 CEL-Seq2 258
 Centrifugation 17, 20, 21, 23–25, 85–87,
 89, 91–97, 101, 104, 105, 114, 148, 149, 160,

- 166, 200, 201, 215–217, 234, 235, 259, 269,
 272–276, 299, 309, 311, 314–316, 318, 319, 324
- Chromatin v, 8, 15, 32, 49–51, 53,
 57, 59, 60, 63, 65, 138, 158–161, 163–165, 167,
 169, 171, 172, 176, 188, 197, 202, 210–212,
 227, 232, 239–255, 286, 331
- Chromatin architecture 199
- Chromatin associated 158, 172
- Chromatin immunoprecipitation
 (ChIP) 53, 158–161, 163, 165, 166,
 168, 172, 202, 231, 233, 234, 236, 237, 240,
 242, 246, 247
- Chromatin immunoprecipitation sequencing
 (ChIP-seq) 158, 203, 204, 206,
 211, 221, 224, 227, 232, 253
- Chromosome 4, 7, 33, 35–39, 41–43, 50,
 53, 55, 132, 133, 220, 239, 250, 252, 255, 329
- Chromosome instability 53, 59
- Click chemistry 232–234, 236, 237
- Clustering 31–46, 140, 169, 170,
 222, 223, 280, 282
- CNON cells 221, 222, 224
- Column 3, 18, 21, 22, 24, 26, 43–45,
 84, 85, 87, 93, 94, 98, 101, 103, 144, 148, 149,
 164, 217, 225, 250–252, 255, 259, 272–274,
 281, 293, 309, 319
- Computational v, 9, 32, 139, 142,
 146, 151, 176, 188, 198, 203, 240, 282, 327
- Conformation capture 239
- Correlation 51, 65, 67, 124, 178,
 187, 188, 282, 301
- CpG island (CGI) v, 3–9, 15, 31–46, 49–53,
 55–67, 124, 130–134, 138–140, 160, 168–170,
 176, 177, 183, 186, 220, 227, 287, 288, 290, 291
- CpG island shores 186
- CRISPR 285–301
- Cross-link 158, 160, 163–165, 171,
 222, 232, 240, 243, 247
- CTCF 52–54, 60, 63, 65, 210,
 221, 222, 224, 227, 232–234
- CxxC 8, 15–22, 24–27
- CxxC affinity purification (CAP) 17–22, 26
- Cytogenetic 109, 113, 304
- Cytosine methylation 31, 39, 42, 44, 45,
 59, 83, 90, 189
- D**
- Damage 141, 143, 226
- Data analysis 116, 117, 119, 146,
 150, 170, 178, 201, 203, 204, 240, 249–251,
 258, 280, 281
- Data visualization 124, 127–130, 167
- Database 33, 44, 134, 327
- Degraded DNAs 87
- Development v, 4, 6, 7, 9, 16, 49, 51–53,
 55, 56, 59, 141, 154, 187, 189, 197, 240, 257,
 258, 304, 306
- 3D-FISH 312, 322, 323, 328, 331
- Diagnosis 58, 66, 67, 84
- Diagnostic 109, 111, 133, 304
- Differential
 expression 51, 280
 methylation 33, 44–46, 51–53, 58, 60,
 62, 130, 132, 133, 176, 179, 183–187, 189
- Differentiation v, 49, 53, 55–57, 175, 180, 258
- Digestion 4, 5, 8, 9, 110, 114, 115,
 119, 141, 142, 146–148, 152, 199, 240, 280,
 293, 294, 298
- Dinucleotide v, 3, 6, 15–17, 31, 33, 35,
 39, 50, 51, 53, 56, 57, 62, 120, 138, 139, 157,
 186, 210, 212, 227
- Distribution 3, 4, 32, 36–39, 41, 44, 50,
 52, 98, 103, 124, 127, 128, 132, 139, 140, 142,
 163, 169, 170, 183, 185, 186, 189, 199–201,
 205, 218, 226, 232, 277, 279, 281, 326
- DNA
 concentration 16, 26, 27, 87, 88, 113,
 166, 180, 202, 318
 demethylase 16
 digestion 141, 146, 240
 elution 16, 26, 103, 160, 161, 164, 165
 fluorescence in situ hybridization
 (DNA FISH) 303–327
 fragmentation 95, 164, 212, 214, 217
 looping 53, 65, 240
 methylation analysis 176, 186, 187, 189
 methyltransferase (DNMT) 8, 42, 55, 59,
 64, 157, 170
 methyltransferase 1 (DNMT1) 55, 56, 59,
 65, 157
 methyltransferase 3A (DNMT3A) 55–57,
 65, 157, 170
 methyltransferase 3B (DNMT3B) 55, 61,
 65, 157
- Deoxyribonuclease I (DNase I) 8, 198
- Domains 4, 8, 15–17, 20, 21, 27,
 51, 62, 124, 188, 212, 286
- Dosage quotient (DQ) 117, 119
- Double-strand break repair 286–288
- Doublets 273
- Drosophila* 4, 53, 232, 240
- Drug 53, 54, 58, 66, 67, 83, 180,
 187, 287, 288, 296, 297, 300
- Duplicates 167, 181, 204, 219,
 220, 226, 227, 254
- Dynabeads 161, 233
- Dynamic 7, 51, 56, 57, 66, 177, 180, 186,
 187, 197, 236, 258

E

EdU231–234, 236
 Efficiencies154, 164, 171, 182, 199,
 202, 232, 237, 244, 286, 290, 298–300, 329
 Electrophoresis110, 111, 113–117,
 142, 161, 164, 292, 296, 318
 Elongation52, 53, 147, 278
 ENCODE.....172, 176, 204
 Endogenous retrovirus50
 Endonucleases6, 111, 286
 Enhancers7, 51, 53, 56, 59, 64, 66,
 138, 166, 176, 177, 188, 210, 213, 221, 224, 227
 Enzymatic3, 17, 92, 95, 115, 158, 198
 Epigeneticsv, 8, 15, 49–51, 53, 55–59, 62,
 66, 67, 83, 109, 124, 133, 138, 157, 169, 175,
 178, 180, 185, 187, 188
 Epigenetic variation187
 Epigenomics123, 177, 179, 187, 189
 Epimutations119
Escherichia coli (E. coli).....19, 20, 34, 38, 149,
 271, 274, 309
 Euchromatin.....286
 Eukaryotic31–46, 53, 197
 Evolution9, 50, 180
 Evolutionary9, 43, 57, 124
 Exons6, 50, 52–54, 56, 60, 170, 287, 300
 Experiment planning176
 Exposures.....103, 175, 180, 329, 331
 Expression4, 7, 18–22, 27, 49–53,
 55–57, 59, 60, 62, 64–66, 83, 109, 124, 133, 150,
 185, 188, 213, 258, 271, 278, 280, 282, 286,
 288, 289

F

False positive.....41, 42, 172, 185, 212, 221, 280
 FASTA33–35, 250
 FASTQ.....203, 219, 249, 254, 278
 FASTQC.....180, 181, 203, 219, 226, 271, 278
 Fingerprinting139, 141–143, 151
 Fluorescence26, 27, 101, 105, 106, 257,
 297, 300, 301, 304, 305
 Fluorescence in situ hybridization
 (FISH).....304, 306–308, 326, 327, 329, 330
 Fluorescent87, 111, 115–117, 143,
 146, 149, 299, 304–307, 324, 326, 329, 330
 Fluorophore98, 144, 177, 288, 306, 326, 331
 Formalin-fixed paraffin-embedded (FFPE).....84, 90
 Fragments.....5, 6, 16, 17, 33, 84, 88,
 92, 95, 104, 115, 116, 139, 141–143, 148, 151,
 152, 167, 171, 172, 177, 181, 182, 198, 199,
 201, 205, 217, 218, 225–227, 233, 235,
 239–241, 245, 251, 254, 255, 277, 293–295,
 298, 304, 307, 327

G

Gene expression4, 7, 49–51, 55, 56,
 83, 133, 186, 188, 197, 198, 213, 257, 286, 288
 Genome architecture304, 328, 331
 Genome browser124, 130, 134, 204, 205,
 220, 224, 231
 Genome engineering286, 289
 Genomestudio.....101
 Genome-wide7, 9, 18, 37, 42, 50, 51,
 54, 56, 57, 59, 66, 83, 123, 138, 139, 157–173,
 176, 179, 198, 202–205, 210, 231–237, 239
 Genome wide association study (GWAS)205, 213
 Genomic sequencing.....109, 140, 142, 210,
 286, 305
 Global4, 31, 33, 35, 38, 40, 59, 66, 138
 Green fluorescent protein (GFP)299

H

H3K27ac210, 212, 213, 221, 224
 H3K4me3.....8, 210, 221, 224, 232–234
 H3K9me3.....53
 Heat map169, 170, 220–223
 Hemimethylated.....56, 132
 HEPES.....19, 160, 171, 292
 Hi-chromatin immunoprecipitation
 (HiChIP)239, 240, 253, 255
 High-definition DNA FISH (HD FISH).....306, 307,
 313, 314, 317–323, 326–331
 High-resolution.....54, 101, 141, 239, 304
 High-throughput9, 92, 158–160, 198,
 231, 236, 249, 257–282
 Histone
 demethylase8
 methylation.....8, 50, 53, 55–57,
 169, 210, 212, 224
 modification.....8, 50, 57, 169, 210, 212,
 213, 224, 232
 octamer197
 HP1.....53, 55
 Hpa II4–6, 9
 HPLC144
 Human.....v, 4, 7, 17, 20, 34, 38–40, 50–53,
 55, 56, 59, 67, 132–134, 138, 176, 177, 181,
 197, 210, 232, 280, 288, 289, 292, 305, 309,
 317, 327
 Hybridization4, 6, 9, 85, 93, 96–98,
 105, 110, 114, 115, 120, 146, 150, 152, 257,
 259, 293, 304, 305, 307, 311, 313–316,
 320–324, 326, 330, 331
 5-Hydroxymethylcytosine (5hmC).....53, 56,
 66, 187
 Hypermethylated50, 52, 130,
 133, 153

Hypermethylation 51, 53, 55, 57, 58, 60,
 64–67, 124, 127, 132, 133, 141, 143, 152, 154
 Hypomethylated..... 3, 26, 50, 58, 60, 61, 63, 213

I

Igepal 240, 242
 Illumina
 methylation array EPIC 84, 176
 methylation array 27K 83, 176, 186
 methylation array 450K 83, 132, 176, 186
 methylation arrays 138, 144, 176, 177, 186
 methylation beadChip 85
 sequencing 167, 219, 240, 248, 249
 Immunoprecipitation (IP) 158, 159, 161, 165,
 171, 233, 234, 240–242, 245–247, 251
 Imprinting 7, 50, 53, 55, 62, 109–120,
 125, 132, 183, 212
 In situ
 Hi-C 239
 hybridization 257
 In vitro
 biotinylation 16
 transcription 271, 273–277
 Inactivation 7, 50, 53, 55, 64, 87,
 115, 147, 216, 244, 274, 291
 Inhibition 27, 51, 53, 54, 60, 63, 65,
 286, 295, 329
 Insulator 59, 64, 65, 198, 210, 224,
 287–289, 291
 Intracellular 288
 Intron 52, 53, 56, 59, 62, 65, 170, 300
 Invasion 59
 Isolation 6, 17, 26, 120, 172,
 177, 198–201, 210, 212–215, 218, 222, 225,
 231, 232, 277, 280, 282, 327

K

Kcnq1ot1 53, 112, 280, 282
 KDM2B 8, 19, 24, 27
 Kinase 243
 Klenow 149, 233, 235, 241, 243
 K-mer 32, 36, 42

L

Ladder 162, 202, 242
 Library preparation 16, 26,
 162, 166, 167, 181, 219, 226, 233, 235, 236,
 271, 274, 277, 278
 Ligase 22, 111, 114, 144, 147, 151,
 159, 166, 233, 235, 241, 243, 248, 271, 274
 Ligation-mediated 6
 Linux 32, 33, 146, 249
 Long non-coding RNAs 280

Low salt 16, 17, 242, 246
 Lysis buffer 18, 21, 160, 163, 199–201,
 213, 215, 224, 240, 241, 244, 245

M

M.CviPI 210, 212, 214–218, 224, 225
 Mammalian 3, 6, 31, 36, 50, 51, 55, 157,
 203, 289, 298
 Mappability 134, 182
 Massively parallel sequencing 16–18
 McCP2 8, 52, 53
 Melanoma 62, 126
 Melting 324
 Metabolic 83, 175, 292, 297, 301
 Methylated 3–9, 16, 17, 31,
 33, 37, 42, 45, 50–55, 58–60, 62, 90, 93, 110,
 124, 125, 127, 132, 133, 138, 139, 152, 154,
 170, 176, 177, 179, 182, 183, 185–187, 189,
 210, 212, 217–219, 226
 Methylated DNA binding domain (MBD) 8, 51
 Methylation-sensitive
 amplification fragment length polymorphism
 (MS-AFLP) 138
 multiplex ligation-dependent probe amplification
 (MS-MLPA) 109–120
 restriction enzyme (MSRE) 17, 139
 Methylation-specific 139
 5-Methyl-cytosine (5mC) 3, 6, 31, 44,
 45, 50, 66, 138, 187
 Methylome 8, 9, 56, 59, 67,
 177–179, 188, 210
 Methyltransferase, *see* DNA methyltransferase
 Microarray 83–106, 138, 176, 185, 189, 257
 Microscopy 171, 200, 215, 299, 304,
 305, 309, 312, 320, 322, 324, 326, 331
 Mitotic 55, 329
 Monoallelic 7, 109
 Motifs 53, 54, 169,
 212, 221, 222, 227, 286
 Mouse v, 6–8, 16, 26, 34, 40, 53,
 55, 56, 163, 170, 277, 280, 282, 327
MseI 141, 142, 144, 146–148, 177
MspI 177, 181, 186
 Multi drug resistance protein 1
 (MDR1) 287–289, 296
 Mutation 31, 50, 53, 57, 59, 64, 66, 109,
 120, 143, 179, 183, 298

N

Nascent chromatin 232
 NasChIP-seq 232
 Native 198, 199, 222
 Network 34, 53

Next-generation sequencing6, 177, 202, 226, 304

Non-methylated
DNA 15–27

Normalization 36, 38, 88, 116, 118, 134, 144, 150, 152, 153, 167–169, 173, 232, 250, 255, 258, 280, 297, 300

NotI 139–144, 146–148, 150–152, 154

Nuclear lysis 239

Nuclease 3, 8, 162, 166, 214–218, 286, 293, 298, 309, 314–319, 330

Nucleosome 8, 31, 51, 53, 58, 59, 188, 197, 199, 210, 213

Nucleosome-depleted region (NDR) 59, 210–213, 219, 221, 223, 224, 227

Nucleosome Occupancy and Methylome Sequencing (NOME-seq) 210, 211, 213, 218, 222, 223

O

Oligonucleotide97, 110, 111, 144, 146, 150, 152, 202, 304–307, 324, 326, 330, 331

Omics176, 187–189

Oncogene 62

Orthologous 9

P

Pancancer 124, 127, 128, 130–134

Pathway 64, 144

Phusion 271, 274, 289, 292, 293, 296

Picogreen 19, 26, 27, 87

Plasmid 19, 27, 288–290, 292–299

Pluripotency 56, 175

Pluripotent 57

Polycomb 65, 132

Polymerase 53, 103, 111, 115, 144, 147–149, 151, 177, 241, 243, 271, 274, 286, 289, 292, 293, 296

Prediction 9, 31–46, 50, 66

Predictive 67, 180

Program 32, 33, 35, 36, 114, 115, 147, 151, 185, 201, 203, 204, 219–221, 226, 250, 286, 294, 299, 300

Protease 18, 20, 21, 160, 161, 241, 244

Protein interaction 240

Proteinase K 19, 20, 24, 27, 84, 86, 161, 165, 199, 201, 214, 216, 241, 242, 245, 247

Purification 17–24, 26, 27, 92, 94, 95, 111, 144, 146, 148, 149, 159, 162, 164–167, 180, 199, 201, 216, 232, 292–294, 307, 318, 319

Q

Quality control (QC) 88–90, 115, 167, 176, 180–184, 189, 201, 203, 271

Quantification 19, 26, 27, 32, 87, 109–120, 138, 142, 176, 201, 216, 217, 247, 249, 258, 271, 278, 280, 281, 300

Quantitative PCR (qPCR) 16, 26, 88–90, 103, 231, 233, 236, 243, 248, 249, 254, 257

R

Radioactive 142

Randomized 33–35, 38–40, 42, 103, 146

Reads 9, 44, 45, 158, 160, 167–170, 172, 173, 177, 180–185, 187, 202–204, 206, 212, 219–221, 226, 227, 232, 249, 251, 258, 278, 281, 282, 297

Reads per million (rpm) 24, 25, 84, 93, 95, 97, 165, 232, 235

Real-time 26, 88, 236, 249, 307, 309, 317

Recombinant 16, 17, 19, 21, 241, 242, 271, 273

Reduced Representation Bisulfite Sequencing (RRBS) 177, 181–183, 186, 189

Regulation v, 4, 9, 49, 51–53, 55–60, 62, 65, 124, 132, 134, 157, 160, 178, 185, 187, 197, 288

Regulatory 9, 15, 49–51, 53, 56–59, 62, 66, 132, 158, 176, 177, 186, 188, 189, 197, 205, 210–227, 288

Remodeling 198

Renewal 49

Repair 49, 64, 67, 147, 148, 151, 166, 219, 233, 235, 240, 241, 243, 244, 248, 254, 286, 287, 289, 291, 294–296, 299

Repetitive 3
elements 132, 134, 138, 143, 151, 170, 172
sequences (*see* Repetitive elements)

Replication 7, 9, 49, 56, 57, 89, 168, 176, 178, 179, 185, 189, 231, 236, 255

Repression v, 4, 7, 50, 51, 55, 57, 59, 60, 62–65, 67, 133

Response 58, 66, 67, 83, 175, 178, 180, 184, 187, 285

Restoration 84, 88, 90, 92–94, 101, 104, 232

Restriction enzyme 4, 17, 139, 140, 144, 151, 177, 181, 186, 241, 250, 290, 293

Resuspension 23, 96, 103, 104, 330

Retrotransposon 7, 59

Reverse transcription PCR (RT-PCR) 287–289, 292, 296, 300

Ribonuclease (RNase) 117, 241, 259, 269, 271–276, 278

RNA polymerase 53, 286

S

S-adenosylmethionine 50
 Saline 160, 198, 200, 213,
 233, 291, 295, 308, 309
 SAMTOOLS 204, 219
 Score 125, 129, 203, 220, 222, 223,
 252, 280, 293, 298
 Sensitivity 17, 18, 67, 166, 185,
 199, 214, 217–219, 271, 279, 303, 304, 327
 Sequencing depth 17, 167, 206, 212
 Shearing 16, 17, 231, 240, 241, 245, 254
 Silencing v, 7, 16, 51, 53,
 55, 58–60, 65–67, 133, 138
 Single cell RNA sequencing (scRNA-seq) 258
 Single guide RNA (sgRNA) 286–290,
 293–296, 298
 Single molecule real time (SMRT) 177, 178
 Single nucleotide polymorphism (SNP) 93, 119,
 120, 183, 212, 220, 221
 Sliding window 32, 185
 Somatic 138, 141, 143, 144
 Sonication 16, 17, 21, 25, 26,
 159, 161, 163–165, 171, 172, 217, 225, 240,
 245, 254
 Southern blot 4, 9
 Spectrophotometer 23, 24, 26, 214, 217, 247, 249
 Sperm 5, 6, 19, 20, 27, 309
 Statistical significance 32, 33, 39, 41, 46, 133, 186
 Stem cells 37, 56, 57, 163, 164,
 176, 232, 257, 282
 Stress 175, 199, 200, 280, 282
 Super-resolution microscopy 305

T

Telomere length 49
 Tet1 56
 Tet2 56, 66
 Tet3 56, 57
 Theory 32, 33, 42, 105, 124,
 142, 154, 288, 300
 Tissue-culture 198, 200, 295
 Tissue-specific 7, 51, 53, 55, 62
 Tn5 transposase 198–201, 206, 254
 Toxicity 288, 298, 300
 Transcription 4, 7–9, 16, 31, 49,
 51–60, 62, 65–67, 132, 138, 159, 168, 169, 177,
 180, 186–188, 197, 198, 205, 206, 210, 221,
 227, 232, 259, 271, 273–277, 286–288, 300
 Transcription factor (TF) 9, 16, 49, 51, 54,
 59, 159, 169, 170, 177, 187, 197, 198, 205, 206,
 210, 212
 Transcription initiation 7, 8, 31, 186
 Transcription start site (TSS) 49–52, 54, 66,
 132, 168, 170, 198, 221, 227, 232, 287
 Transcriptional repression 57, 59
 Transcriptomics 52, 188, 258
 Transfer 20–23, 53, 87, 91–94, 114, 149,
 163, 166, 200, 215, 217, 245, 248, 254,
 273–278, 309, 311–313, 319–321
 Translational 52
 Transposase 197, 212, 254
 Transposition 198, 201, 205
 Transposon 206, 212
 Treatment 6, 53, 67, 141, 175, 177,
 187, 210, 212, 214–218, 222, 224, 226, 276,
 287, 296, 297, 300

U

UniFISH 305–307, 315, 316,
 323–326, 328, 330, 331
 Uniparental disomy 113, 117, 119
 Unique molecular identifiers (UMIs) 259, 278
 University of California Santa Cruz
 (UCSC) 33–35, 124, 127, 131,
 132, 134, 168, 204, 205, 220
 Unmethylated, *see* Non-methylated

V

Vertebrate 4–6, 9, 15, 17, 18
 Virtual machine 32, 33, 46

W

Whole Genome Bisulfite Sequencing
 (WGBS) 139, 176, 177, 181
 Word, *see* K-mer

X

X-chromosome 4, 7, 50, 53, 55

Z

Zebrafish 34, 40, 280