**Table S1. Methodologies for epigenetic analyses1**

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|  | **Method** | **Discrimination principle** | **Detection technique** | **Resolution**  | **References** |
| ***DNA Methylation*** | ***Quantification of global 5-methylcytosines*** |
| HPLC, HPCE | Chromatography | Absorbance | 5-mC genomic content | [[1](#_ENREF_1),[2](#_ENREF_2)] |
| HPLC/EI-MS | Chromatography  | EI-MS | 5-mC genomic content | [[3](#_ENREF_3)] |
| LUMA | Methylation-sensitive RE | Pyrosequencing | RE recognition sites within the genome | [[4](#_ENREF_4)] |
| ***Sequence specific analyses*** |
| Southern blot | Methylation-sensitive RE  | Hybridization | Single RE recognition site  | [[5](#_ENREF_5)] |
| PCR amplification | Methylation-sensitive RE  | PCR | Single RE recognition site  | [[6](#_ENREF_6)] |
| Bisulphite sequencing | Bisulphite conversion | Sanger sequencing | Single nucleotide within the amplicon | [[7](#_ENREF_7),[8](#_ENREF_8)] |
| PyroMeth | Bisulphite conversion | Pyrosequencing | Single nucleotide within the amplicon | [[9](#_ENREF_9)] |
| MSP | Bisulphite conversion | PCR | Few CpGs inside the primers | [[10](#_ENREF_10)] |
| MethyLight | Bisulphite conversion | Fluorescence real-time PCR | Few CpGs inside the primers | [[11](#_ENREF_11)] |
| Headloop-PCR | Bisulphite conversion | PCR | Few CpGs inside the primers | [[12](#_ENREF_12)] |
| In-tube melting curves analysis | Bisulphite conversion | Fluorescence real-time PCR | Average methylation of amplicon | [[13](#_ENREF_13)] |
| COBRA | Bisulphite conversion + Methylation-sensitive RE | PCR | Single RE recognition site within the amplicon | [[14](#_ENREF_14)] |
| Bisulphite-Sequenom | Bisulphite conversion | MALDITOF-MS | Single nucleotide within the amplicon | [[15](#_ENREF_15)] |
| MS-SnuPE | Bisulphite conversion | SnuPE | Few CpGs within the amplicon | [[16](#_ENREF_16)] |
| MS-SSCA | Bisulphite conversion | SSCA | Relative average methylation of amplicon | [[17](#_ENREF_17)] |
| ***Genome-wide analyses*** |
| RLGS | Methylation-sensitive RE | 2D-electrophoresis | RE recognition sites within the genome | [[18](#_ENREF_18)] |
| AP-MS-PCR | Methylation sensitive RE | Southern blot | RE recognition sites within the genome | [[19](#_ENREF_19)] |
| MS-AFLP | Methylation sensitive RE | Fingerprinting | RE recognition sites within the genome | [[20](#_ENREF_20)] |
| MCA | Methylation sensitive RE | RDA | RE recognition sites within the genome | [[21](#_ENREF_21)] |
| AIMS | Methylation sensitive RE  | Fingerprinting | RE recognition sites within the genome | [[22](#_ENREF_22)] |
| MeDIP-chip | 5mC antibody | Microarray | Relative average methylation of the immunoprecipitated sequences that hybridize to microarrayed probes | [[23](#_ENREF_23)] |
| MeDIP-seq | 5mC antibody | NGS | Relative average methylation of the immunoprecipitated sequences | [[24](#_ENREF_24)] |
| Bisulphite-chip | Bisulphite conversion | Microarray | Few CpGs within the probes of the microarray | [[25](#_ENREF_25)] |
| Bisulphite-seq | Bisulphite conversion | NGS | Single nucleotide within the genome | [[26](#_ENREF_26)] |
| Nanopore sequencing | Conductivity changes in grapheme nanopores when DNA strands pass through | NGS | Single nucleotide within the genome | [[27](#_ENREF_27)] |
| SMRT | SMRT | NGS | Single nucleotide within the genome | [[28](#_ENREF_28)] |

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| ***Histone modifications*** ***and variants*** | ***Quantification of histone modifications/variants*** |  |
| Mass spectrometry | Mass spectrometry | Mass spectrometry | Global content of a specific histone mark/variant | [[29](#_ENREF_29)] |
| Western Blot | Antibody | Western Blot | Global content of a specific histone mark/variant | [[30](#_ENREF_30)] |
| ***Sequence specific analyses*** |
| ChIP-PCR | Antibody | Conventional PCR or fluorescence real-time PCR | Relative average of the histone mark/variant content within the amplicon | [[31](#_ENREF_31)] |
| ***Genome-wide analyses*** |
| ChIP-on-chip | Antibody | Microarray | Relative average of the histone mark/variant content of the immunoprecipitated sequences that hybridize on the microarray | [[32](#_ENREF_32)] |
| ChIP-seq | Antibody | NGS | Relative average of the histone mark/variant content of the immunoprecipitated sequences | [[33](#_ENREF_33)] |
| ***Both2*** | ChIP-BS-seq | Antibody + Bisulphite conversion | NGS | Single nucleotide within the immunoprecipitated sequences | [[34](#_ENREF_34),[35](#_ENREF_35)] |

1 Abbreviations: HPLC, High Performance Liquid Chromatography; EI, Electrospray Ionization; MS, Mass Spectrometry; HPCE, High Performance Capillary Electrophoresis; LUMA, LUminometric Methylation Assay; RE, restriction enzyme; 5mC, 5-methylcytosine; PCR, Polymerase Chain Reaction; MSP: Methylation Specific PCR; COBRA, COmbined Bisulphite Restriction Analysis; MS-SnuPE, Methylation Sensitive-Single nucleotide Primer Extension; MS-SSCA, Methylation Sensitive-Single Conformational Analysis; RLGS, Restriction Landmark Genomic Scanning; AP-MS-PCR, Arbitrarily Primed Methylation Sensitive-PCR; MS-AFLP, Methylation-Sensitive Amplified Fragment Length Polymorphism; MCA, Methylated CpG island Amplification; AIMS, Amplification of Inter-Methylated Sites; chip, microarray; MeDIP, Methyl-DNA Immunoprecipitation; RDA, Representational Difference Analysis; SPM, Segregation of Partially Melted molecules; NGS, Next Generation Sequencing; SMRT, Single Molecule Real Time; ChIP: Chromatin ImmunoPrecipitation.

2 DNA methylation + Histone modifications and variants

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