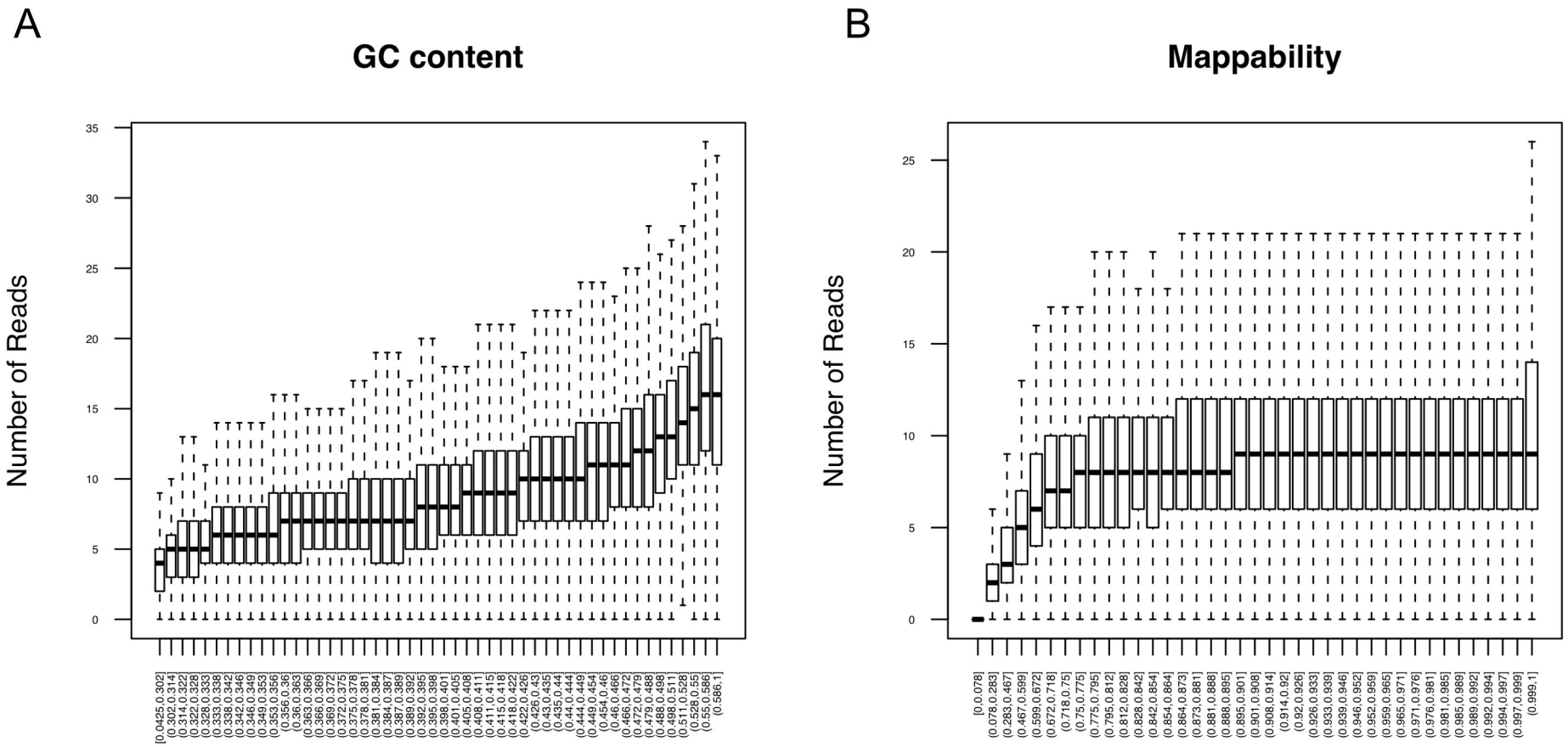
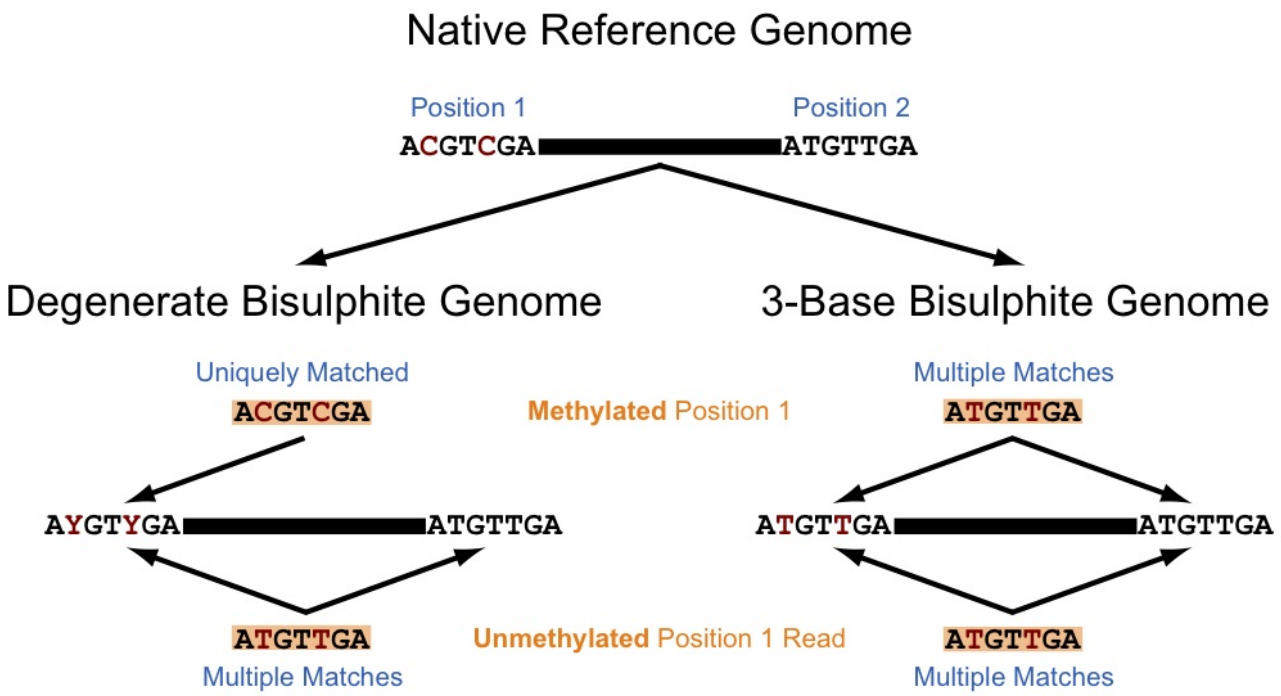
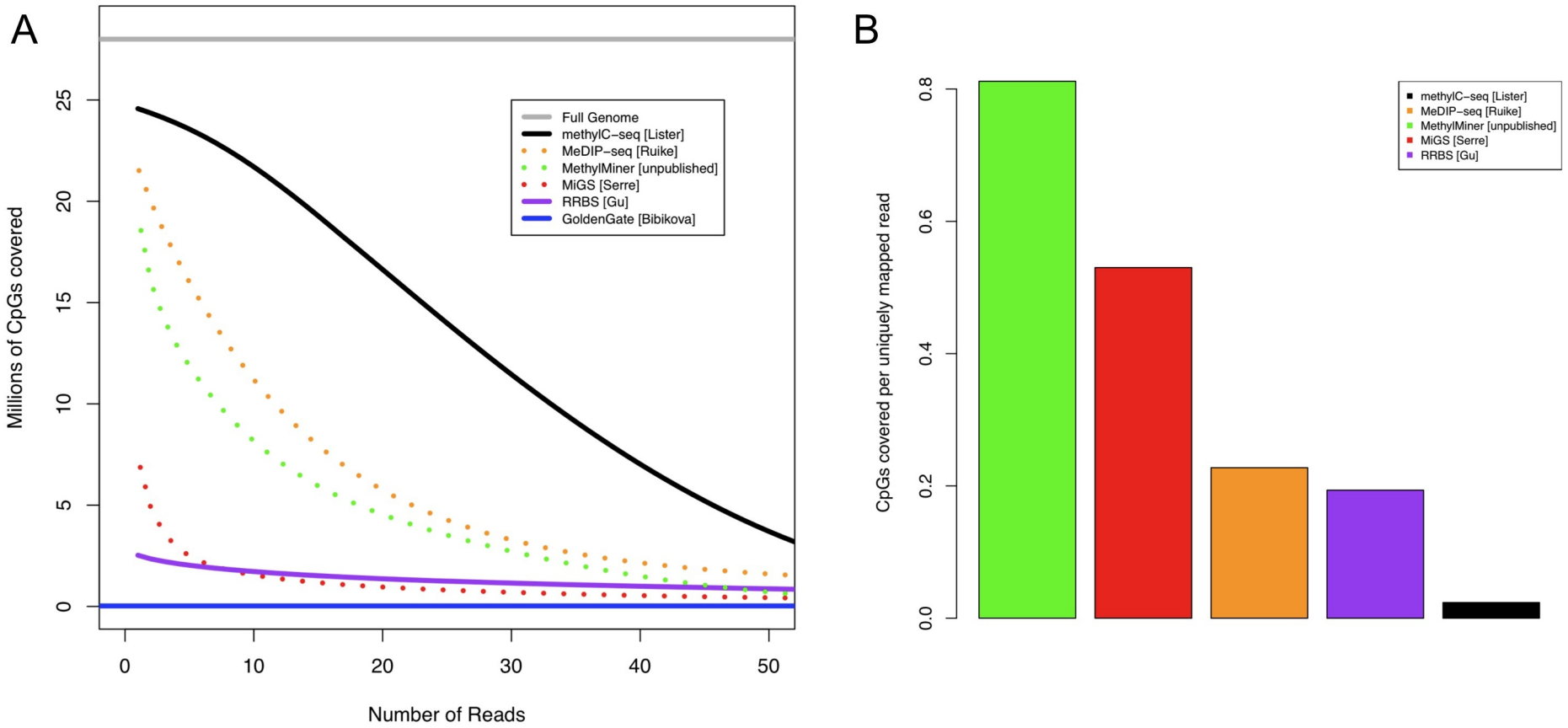
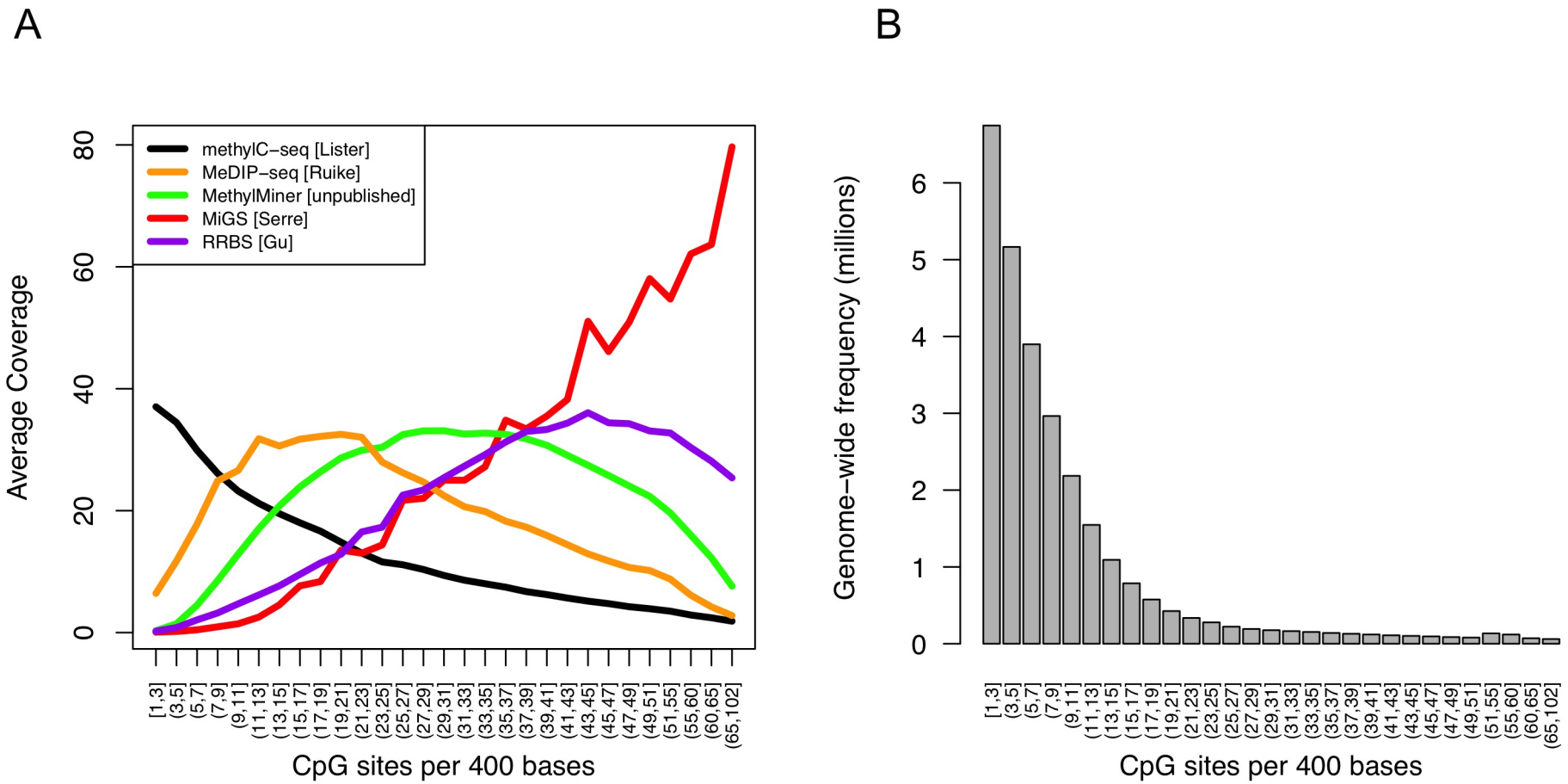
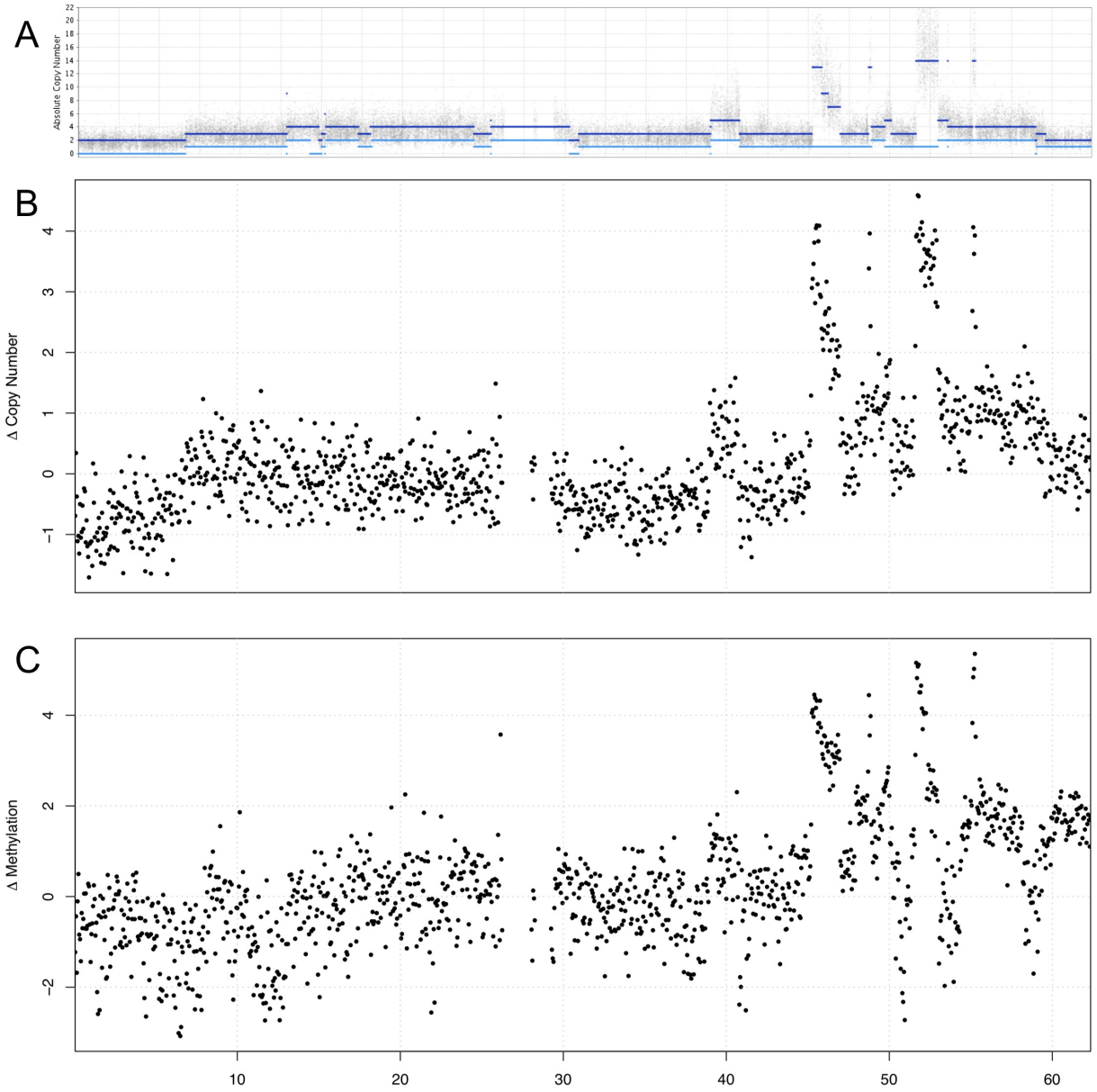

A
GC content
Number of Reads
0
5
10
15
20
25
30
35
[0.0425,0.302]
(0.302,0.314]
(0.314,0.322]
(0.322,0.328]
(0.328,0.333]
(0.333,0.338]
(0.338,0.342]
(0.342,0.346]
(0.346,0.349]
(0.349,0.353]
(0.353,0.356]
(0.356,0.36]
(0.36,0.363]
(0.363,0.366]
(0.366,0.369]
(0.369,0.372]
(0.372,0.375]
(0.375,0.378]
(0.378,0.381]
(0.381,0.384]
(0.384,0.387]
(0.387,0.389]
(0.389,0.392]
(0.392,0.395]
(0.395,0.398]
(0.398,0.401]
(0.401,0.405]
(0.405,0.408]
(0.408,0.411]
(0.411,0.415]
(0.415,0.418]
(0.418,0.422]
(0.422,0.426]
(0.426,0.43]
(0.43,0.435]
(0.435,0.44]
(0.44,0.444]
(0.444,0.449]
(0.449,0.454]
(0.454,0.46]
(0.46,0.466]
(0.466,0.472]
(0.472,0.479]
(0.479,0.488]
(0.488,0.498]
(0.498,0.511]
(0.511,0.528]
(0.528,0.55]
(0.55,0.586]
(0.586,1]
B
Mappability
Number of Reads
0
5
10
15
20
25
[0,0.078]
(0.078,0.283]
(0.283,0.467]
(0.467,0.599]
(0.599,0.672]
(0.672,0.718]
(0.718,0.75]
(0.75,0.775]
(0.775,0.795]
(0.795,0.812]
(0.812,0.828]
(0.828,0.842]
(0.842,0.854]
(0.854,0.864]
(0.864,0.873]
(0.873,0.881]
(0.881,0.888]
(0.888,0.895]
(0.895,0.901]
(0.901,0.908]
(0.908,0.914]
(0.914,0.92]
(0.92,0.926]
(0.926,0.933]
(0.933,0.939]
(0.939,0.946]
(0.946,0.952]
(0.952,0.959]
(0.959,0.965]
(0.965,0.971]
(0.971,0.976]
(0.976,0.981]
(0.981,0.985]
(0.985,0.989]
(0.989,0.992]
(0.992,0.994]
(0.994,0.997]
(0.997,0.999]
(0.999,1]


Native Reference Genome
Position 1
Position 2
ACGTCGA
ATGTTGA
Degenerate Bisulphite Genome
3-Base Bisulphite Genome
Uniquely Matched
ACGTCGA
Methylated Position 1
Multiple Matches
ATGTTGA
AYGTYGA
ATGTTGA
ATGTTGA
ATGTTGA
ATGTTGA
Unmethylated Position 1 Read
ATGTTGA
Multiple Matches
Multiple Matches


A
Millions of CpGs covered
0
5
10
15
20
25
0
10
20
30
40
50
Number of Reads
Full Genome
methylC−seq [Lister]
MeDIP−seq [Ruike]
MethylMiner [unpublished]
MiGS [Serre]
RRBS [Gu]
GoldenGate [Bibikova]
B
CpGs covered per uniquely mapped read
0.0
0.2
0.4
0.6
0.8
methylC−seq [Lister]
MeDIP−seq [Ruike]
MethylMiner [unpublished]
MiGS [Serre]
RRBS [Gu]


A
B
methylC−seq [Lister]
MeDIP−seq [Ruike]
MethylMiner [unpublished]
MiGS [Serre]
RRBS [Gu]
Average Coverage
0
20
40
60
80
Genome−wide frequency (millions)
0
1
2
3
4
5
6
[1,3]
(3,5]
(5,7]
(7,9]
(9,11]
(11,13]
(13,15]
(15,17]
(17,19]
(19,21]
(21,23]
(23,25]
(25,27]
(27,29]
(29,31]
(31,33]
(33,35]
(35,37]
(37,39]
(39,41]
(41,43]
(43,45]
(45,47]
(47,49]
(49,51]
(51,55]
(55,60]
(60,65]
(65,102]
CpG sites per 400 bases
CpG sites per 400 bases


A
Absolute Copy Number
B
Δ Copy Number
C
Δ Methylation
10
20
30
40
50
60