

Supplementary Table 20. The basic statistics of methylome data

	CTL-1	CTL-2	bDKO-1	bDKO-2
Summary of mapping				
Total number of read 1	391,428,791	391,671,069	401,983,185	387,465,279
Rate for uniquely mapread read 1	87.0%	87.0%	87.2%	87.4%
Rate for unmapread read 1	9.4%	9.4%	9.2%	9.1%
Total number of read 2	391,428,790	391,671,068	401,983,185	387,465,280
Rate for uniquely mapread read 2	84.7%	84.6%	84.8%	83.1%
Rate for unmapread read 2	11.7%	11.8%	11.6%	13.4%
Mean read depth				
Top strand	12.7	12.7	13.2	12.8
Bottom strand	12.7	12.6	13.1	12.7
Both strands	25.4	25.4	26.3	25.4
All nucleotides	12.7	12.7	13.1	12.7
All cytosines	13.5	13.4	14.0	13.4
Cytosines in CpG context	19.1	18.8	20.0	19.0
Cytosines in CHG context	15.0	15.0	15.7	15.0
Cytosines in CHH context	13.3	13.3	13.8	13.3
Median read depth				
All nucleotides	12	12	12	12
All Cs	13	12	13	13
Cs in CpG context	15	15	15	15
Cs in CHG context	14	14	15	14
Cs in CHH context	13	13	13	13
Methylation level				
All chromosomes (all Cs)	4.4%	4.4%	4.3%	4.4%
All chromosomes (Cs in CpG context)	77.6%	77.5%	76.4%	77.8%
All chromosomes (Cs in CHG context)	1.3%	1.3%	1.3%	1.2%
All chromosomes (Cs in CHH context)	1.2%	1.2%	1.2%	1.2%
Lambda (all Cs)	1.1%	1.1%	1.1%	1.0%
Lambda (Cs in CpG context)	1.0%	1.0%	1.0%	0.9%
Lambda (Cs in CHG context)	1.2%	1.2%	1.2%	1.1%
Lambda (Cs in CHH context)	1.0%	1.1%	1.1%	1.0%
Percentage of genomic regions covered with indicated read number				
1 read or more	86.6%	86.7%	86.7%	86.6%
3 reads or more	81.9%	82.0%	82.0%	81.8%
5 reads or more	75.6%	75.6%	75.9%	75.4%
10 reads or more	55.7%	55.4%	56.6%	55.4%