Read Alignment
Trim adaptor and low quality end

Quality Control
Adjust amplification bias, end-repair bias, and short fragment bias
Estimate bisulfite conversion rate

Single Sample Analysis
Call methylation ratio at each cytosine
Report confidence interval
Generate descriptive figures, tables, and browser visualization
Detect CpGs with strand bias of methylation
Detect hypo- or hyper- methylated regions

Multiple Sample Analysis
Identify de novo of differential methylated cytosines and regions
Examine differential methylation levels of pre-defined regions
Report correlation between multiple samples

Scale chr11:
10 kb
69,390,000
mm9

Wrp53 Trp53

Methylation Ratio

Hypermethylated Region

Distribution of CpG Count (%)

0% meth: 78.8%
1%–25% meth: 12.6%
75%–99% meth: 3%
100% meth: 2.6%

Average of local CpG density (%)