Figure 1. Sun et al.
SampleA_rep1  SampleA_rep2  SampleB_rep1  SampleB_rep2

**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

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**Figure 2. Sun et al.**
Figure 3: Sun et al.

% true DMCs predicted at 5% FDR

Average sequencing depth

MOABS
FETP
Figure 4. Sun et al.

(a) ROC-like curve for method evaluation

(b) Sensitivity with 5% FDR cutoff at different sequencing depth
Figure 5. Sun et al.
Figure 6. Sun et al.