

SampleA_rep1

SampleA_rep2

SampleB_rep1

SampleB_rep2



Read alignment

Align to reference and spike-in genomes, and filter common reads
Estimate size factors for sample replicates
Remove PCR duplication



CMS measurement construction

Build genome scan windows
Tabulate read counts and mean WIG sums



DHMR detection

Filter low-depth windows
Negative binomial, *t*-test, Chi-squared, and *G*-test
Independent filtering
Merge detected adjacent differential hydroxymethylation regions