

# METHYLATOR

BiBs

sample1\_merged.bam  
sample2\_merged.bam

sample1\_R1.fastq.gz  
sample1\_R2.fastq.gz

raw FASTQ

download  
public data

FASTQ dump

FastQC

MultiQC

quality control

sample plan

metadata.tsv

nanopore  
data

bam to bed

modbam2bed

reference  
genome  
mm39.fa

Bismark

MultiQC

genome  
alignment

QualiMap

preprocessing

MethylKit

CpG  
annotation

cpgIslandExt.mm39.bed

gene  
annotation

gencode.vM27.annotation.gtf

annotations

annotatr

custom  
annotations

personal  
annotation

enhancers\_mm39.bed

exploratory methylation analysis

Tiles

CpG

MethylKit

differential methylation analysis

Tiles

CpG

Regions

MethylKit

DMRICH

visualization  
reporting

RMarkdown