

Methyl-Seq Overview

Raw data
fastQC

- fastqc/multiqc



Quality filter/trim

- Trim Galore



Filtered data
fastQC

- fastqc/multiqc



Read-mapping

- Bismark



Alignment QC

- Qualimap



Deduplicate
alignments*

- Bismark

*Not performed on RRBS datasets



Extract
methylation calls

- Bismark



Differential
methylation analysis

- Methykit

Generate
summary reports

- Bismark



Primary outputs:

- Alignment files (bam)
- Alignment reports (html/txt)
- Methylation calls and coverage tables
- Bismark summary files (html/txt)
- Differential methylation analysis results

Based on the Bismark workflow as
implemented by the nf-core workflow
(with modifications and additions)