BS-Seq Data Delivery Specifications

Output data info

- FASTQ.GZ files containing raw sequences.

  Reads will be provided with adapter sequences masked. No quality clipping is provided with raw reads delivery.

BS-Seq standard bioinformatics analysis

- Alignments in BAM format.
- Alignment and methylation summary metrics for each sample in PDF format.
- Coverage and methylation information at single base resolution in tabular format
- Differential methylation analysis results in tabular format.
- A REPORT file describing the library preparation and analysis flow.

FAQ

Do reads contain adapters?

Unless differently agreed, reads are provided with masking of adapters read-through. When a minimum of 5bp read-through is found with respect to sample-specific (barcode included) adapters, bases are masked with N character. Thus, read length is maintained to its original size. No quality clipping is applied on raw reads delivery, while regularly used in our standard bioinformatic pipelines.

Are reads quality trimmed?

Delivered raw data are not quality trimmed. However, our internal analysis pipelines always rely on a quality trimming and adapter filtering steps which are described in the delivery REPORT.