

FastQC Quality Control Report: Pre- and Post-Trimming

Which file is of better quality?

SRR957824_trimmed.fastq is of better quality. This is evident from the increase in green checks [PASS] and decrease in red crosses [FAIL] in the FastQC report after trimming.

What improvements are visible after trimming?

- Per base sequence quality: Improved from Fail to Pass (trimming removed low-quality ends).
- Per base sequence content: Improved from Fail to Warning (still slightly biased but better).
- Overrepresented sequences: Improved from Fail to Pass (adapters removed).
- Sequence Length Distribution: Now shows variation due to trimming.
- Adapter Content: Remained Pass.

What should you pay attention to in a FastQC report?

- Per base sequence quality
- Adapter content
- Sequence duplication levels
- Overrepresented sequences
- Per sequence GC content

What are the potential consequences of skipping QC in a diagnostic lab?

- False-positive variant calls
- Incorrect genome assemblies
- Misclassification in metagenomics
- Reduced reproducibility
- Wasted resources and potential misdiagnosis

Summary Comparison

Before Trimming: Moderate-poor quality, adapters and low-quality ends present

After Trimming: Good quality, adapters removed, ready for downstream analysis