FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per tile sequence quality

✅ Per sequence quality scores

❌ Per base sequence content

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⚠️ Per base N content

✅ Sequence Length Distribution

⚠️ Sequence Duplication Levels

✅ Overrepresented sequences

❌ Adapter Content

✅ **Basic Statistics**

Measure	Value
Filename	DdiaME23.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	481396760
Sequences flagged as poor quality	0
Sequence length	151
%GC	54

✅ **Per base sequence quality**

Quality scores across all bases (Sanger / Illumina 1.9 encoding)