



✓ **Congratulations! You passed!**  
TO PASS 70% or higher

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GRADE  
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## Module 3 Quiz

LATEST SUBMISSION GRADE  
100%

1. How many lines make up each record contained in a FASTQ file?

1 / 1 point

- ☐ Three
- ☒ Four
- ☐ One
- ☐ Two

✓ **Correct**

2. Which of the following are components of the FASTQ format?

1 / 1 point

- ☐ Sequence
- ☐ Quality score
- ☐ Sequence identifier
- ☒ All of these options

✓ **Correct**

3. Which of the following is NOT a type of encoding of sequence quality scores in a FASTQ file?

1 / 1 point

- ☒ Ion torrent
- ☐ Solexa
- ☐ Sanger
- ☐ Illumina 1.3+

✓ **Correct**

4. Which of the following operations of quality control can be performed with Galaxy's NGS: QC and manipulation?

1 / 1 point

- ☐ FastQC: Read Quality reports
- ☒ All of these options
- ☐ Trim Sequences
- ☐ FASTA to FASTQ, and FASTQ to FASTA format conversion, Manipulate FASTQ

✓ **Correct**

5. Which of the following is NOT part of the FastQC report?

1 / 1 point

- ☐ Per sequence quality score
- ☒ Per sequence base quality
- ☐ Sequence Length distribution
- ☐ Per base sequence quality

✓ **Correct**

6. When do we filter and trim reads? Choose the correct option.

1 / 1 point

- ☐ Always trim the reads. We want only equal length reads in our data.
- ☐ Always filter and trim reads, we want high quality equal length reads to gain flexibility of using any tool of choice

during downstream analysis.

- ☐ Always filter reads. We want only high quality reads in our data.
- ☒ Depends on tools used during downstream analysis.

✓ Correct

7. What is ChIP sequencing most commonly used to measure?

1 / 1 point

- ☒ The locations of protein to DNA interaction
- ☐ Expression levels of particular proteins
- ☐ Ratios of miRNA to DNA
- ☐ Methylation of bases

✓ Correct

8. What is MACS used for?

1 / 1 point

- ☐ Detect sequence variants using both qPCR and ChIP-seq data
- ☐ Genome assembly using suffix trees and ChIP-seq data
- ☐ Measure RNA levels
- ☒ Peak calling/reconstruction from ChIP-seq data

✓ Correct

9. What is the advantage of using a control in a ChIP sequencing experiment?

1 / 1 point

- ☐ Neither option
- ☐ Determine background expectation of the number of peaks detected.
- ☒ Both options
- ☐ Allow MACS to calculate FDR.

✓ Correct