Quiz 3

GENOMICS

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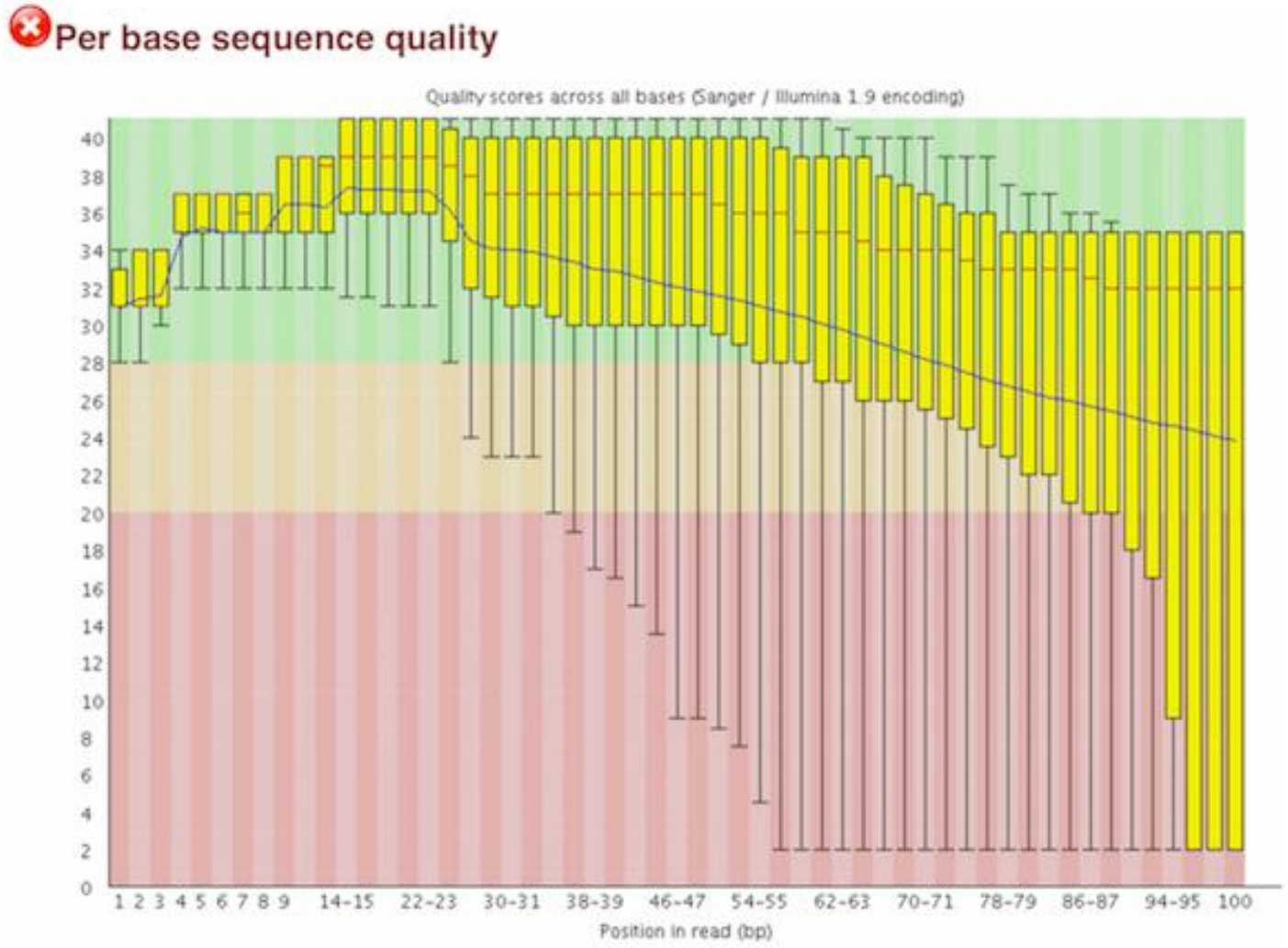
04/10/2023

Question 1

You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?



A. You sequencing is fine, we usually have a loss of quality at the end of the reads.

B. The experiment has failed, I have to redo it.

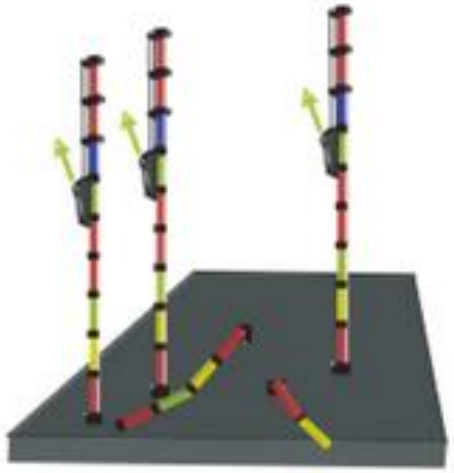
C. You have some issues, at the end of the reads, may be due a signal issue at the end of the run.

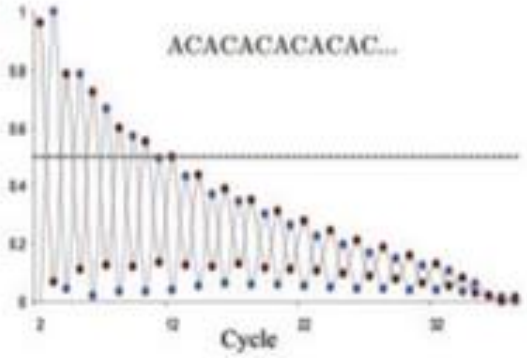
D. You have some issues, at the end of the reads, may be due phasing issues at the end of the run.

Question 1

- **Signal decay:** As sequencing proceeds, the fluorescent signal intensity decays with each cycle, yielding decreasing quality scores at the **3' end** of the read. This is due to:
    1. Degrading fluorophores
    2. A proportion of the strands in the cluster not being elongated

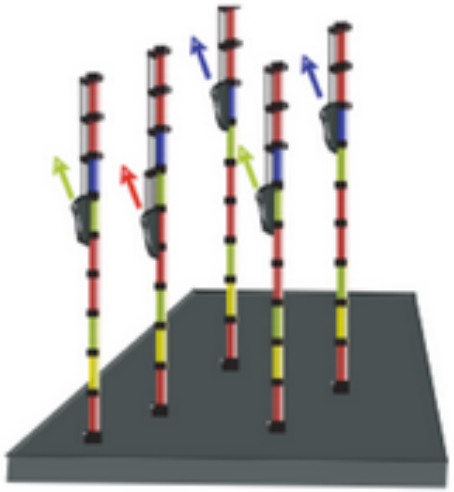
  Therefore, the proportion of signal being emitted continues to decrease with each cycle.

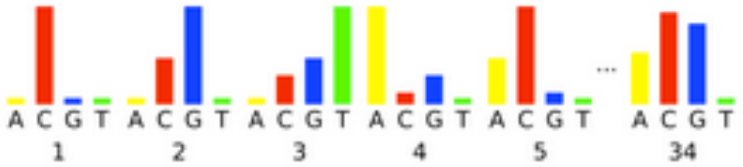




Question 1

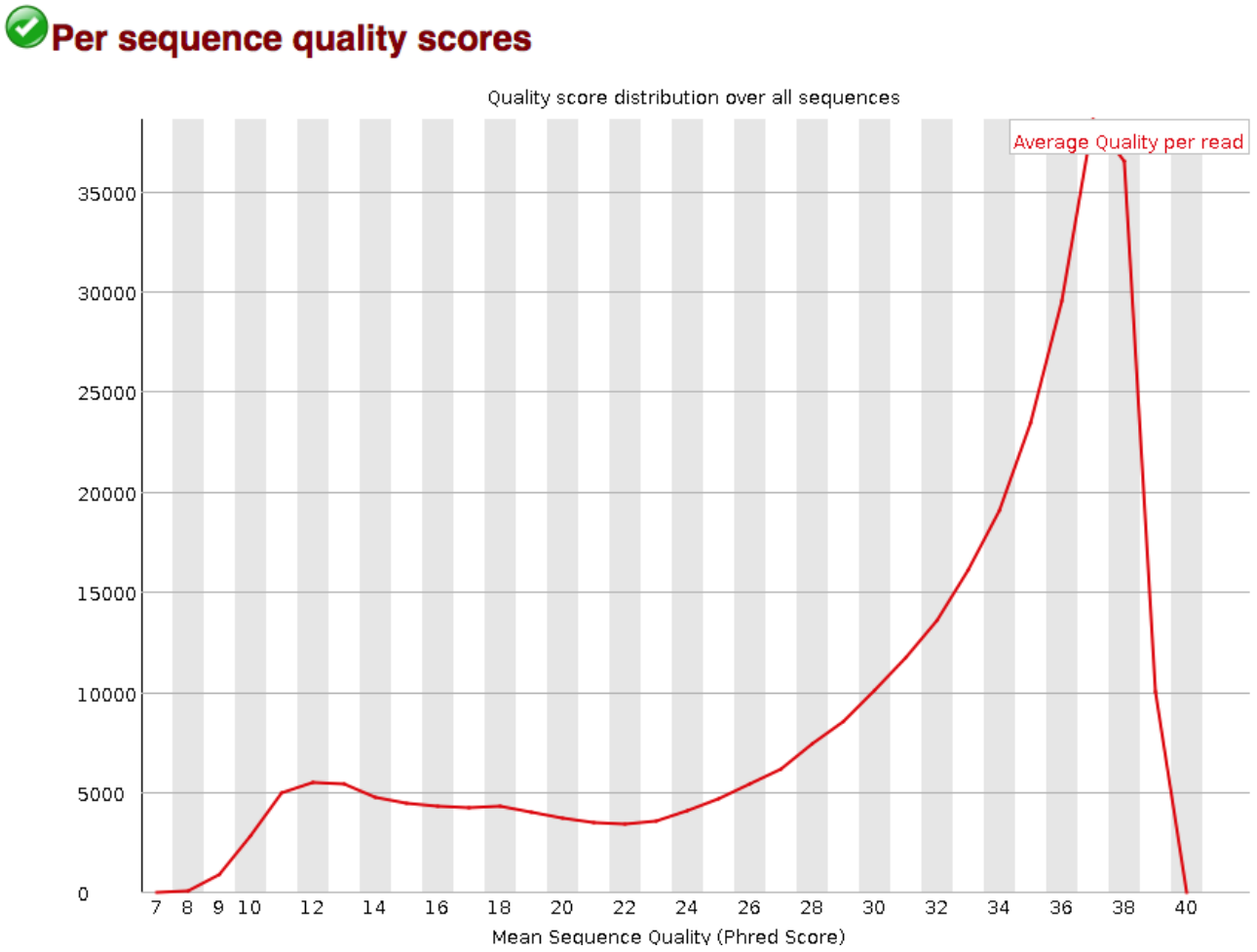
- **Phasing:** As the number of cycles increases, the signal starts to blur as the cluster loses synchronicity, also yielding a decrease in quality scores at the **3' end** of the read. As the cycles progress, some strands get random failure of nucleotides to incorporate due to:
    1. Incomplete removal of the 3' terminators and fluorophores
    2. Incorporation of nucleotides without effective 3' terminators





Question 2

You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?



A. Nothing, this plot is useless.

B. The experiment has failed, I have to redo it.

C. We have a small portion of low-quality reads that we should removed before processing.

D. We have a small portion of low-quality reads that we can keep before processing.

Question 3

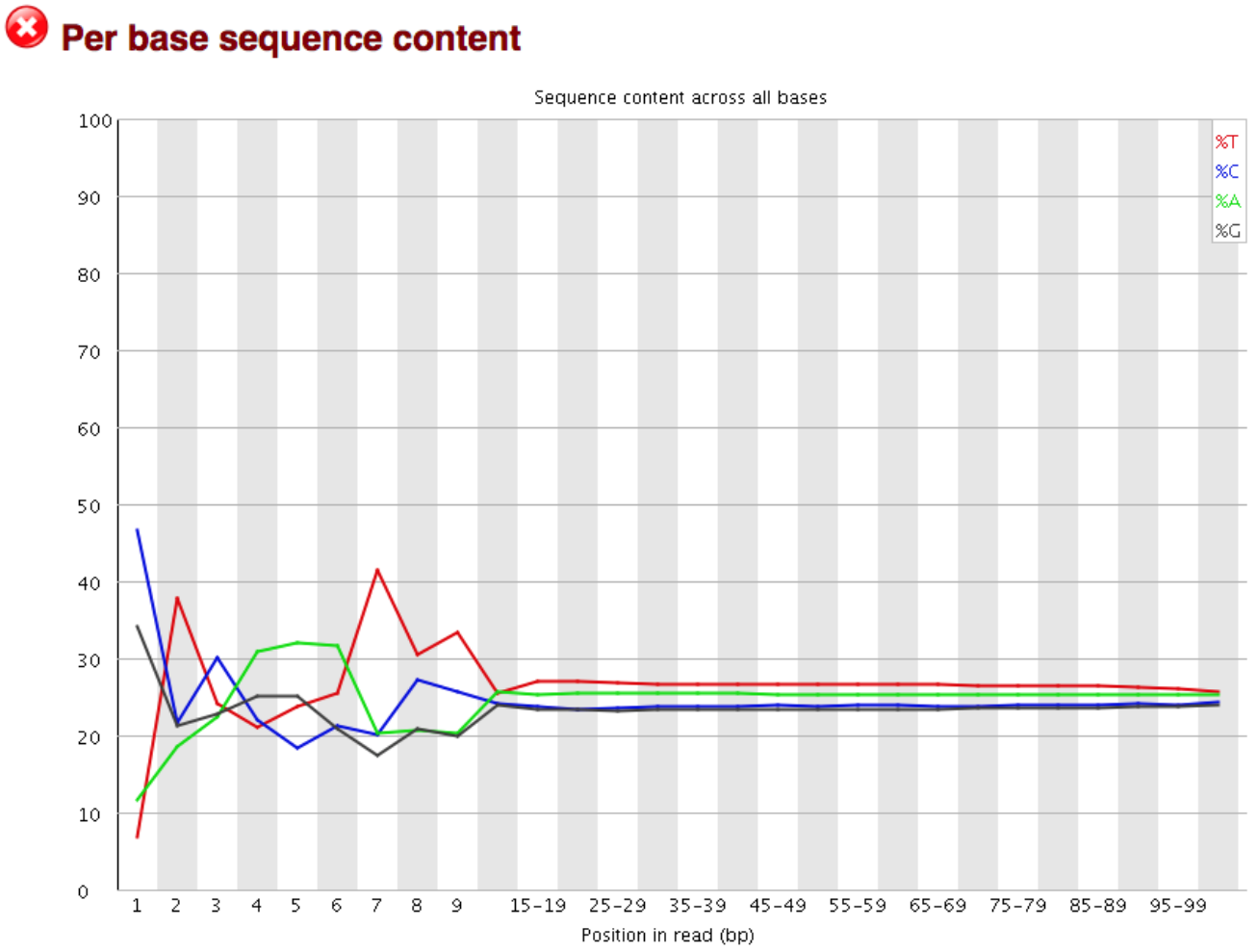
You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?

A. We have an adapters contamination.

B. It may just be an artifact due to ‘random’ hexamer which are not so random.

C. We have DNA contamination from another organism.

D. The line at the end should be all equals. I have an issue about my library.



Question 4

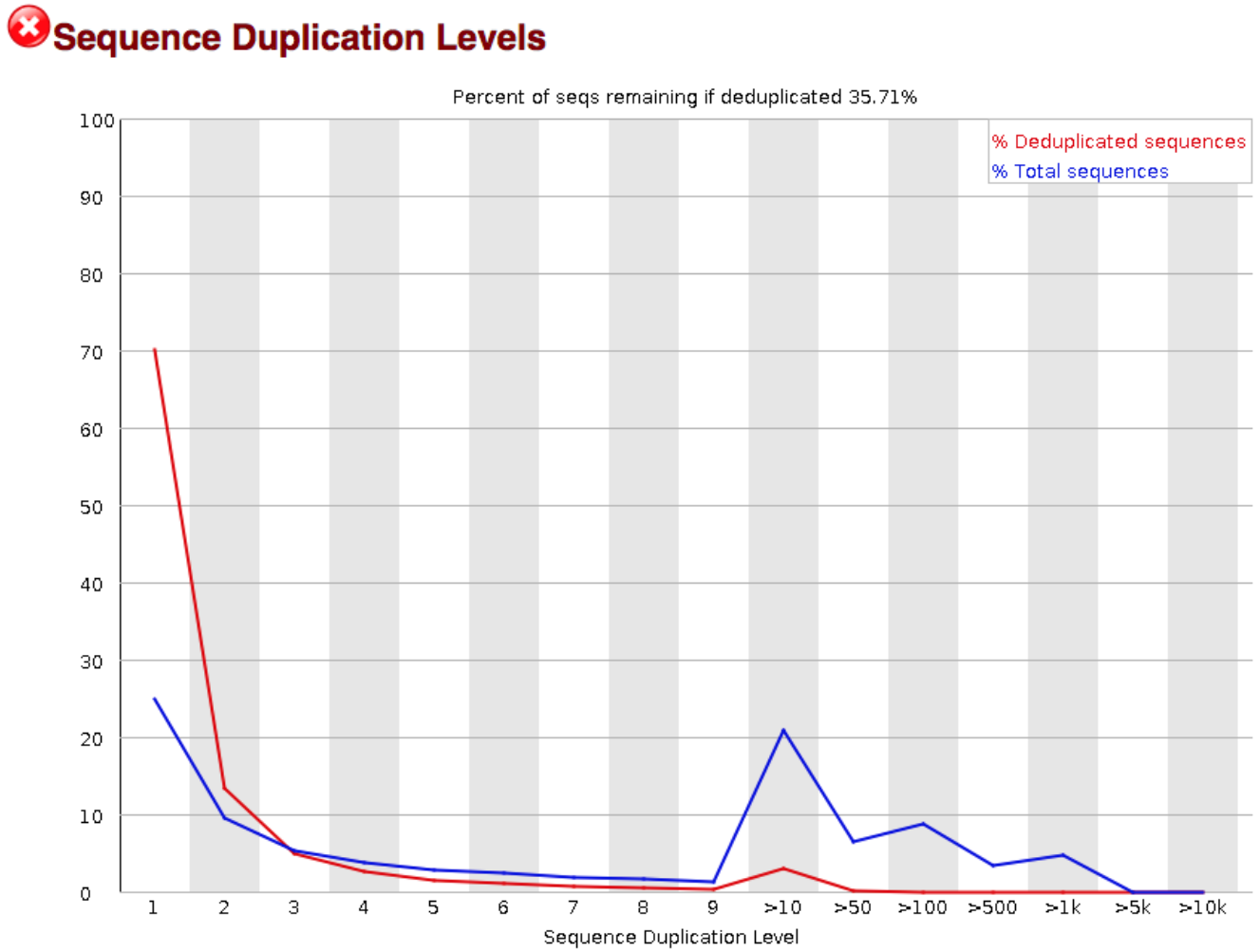
You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?

A. There are always a lot of duplication event in RNAseq experiment.

B. We have an adapters contamination.

C. We have a rDNA contamination.

D. I have a low complexity library, that I have sequence way too much.



Question 5

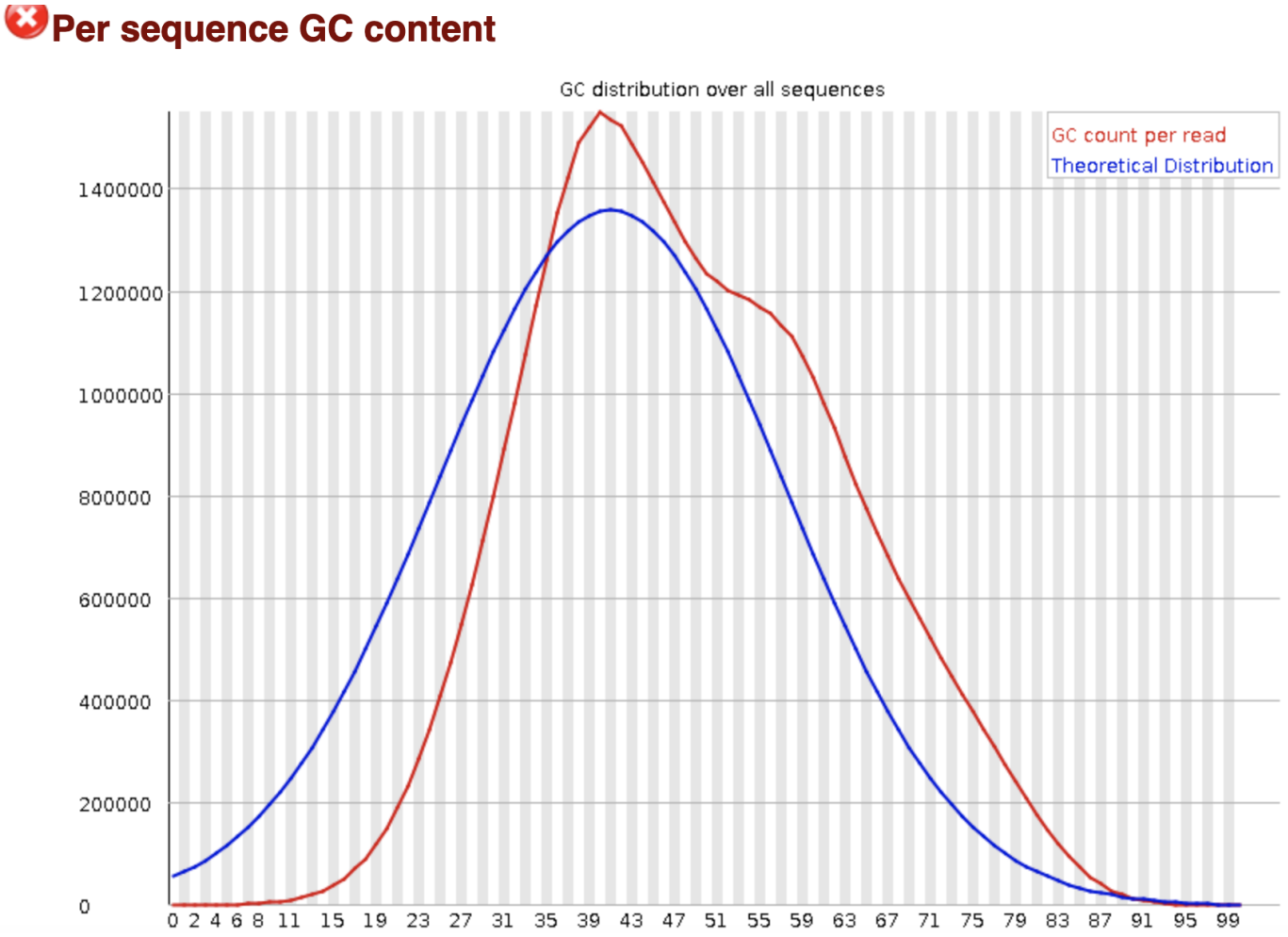
You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?

A. We have a contamination from another species.

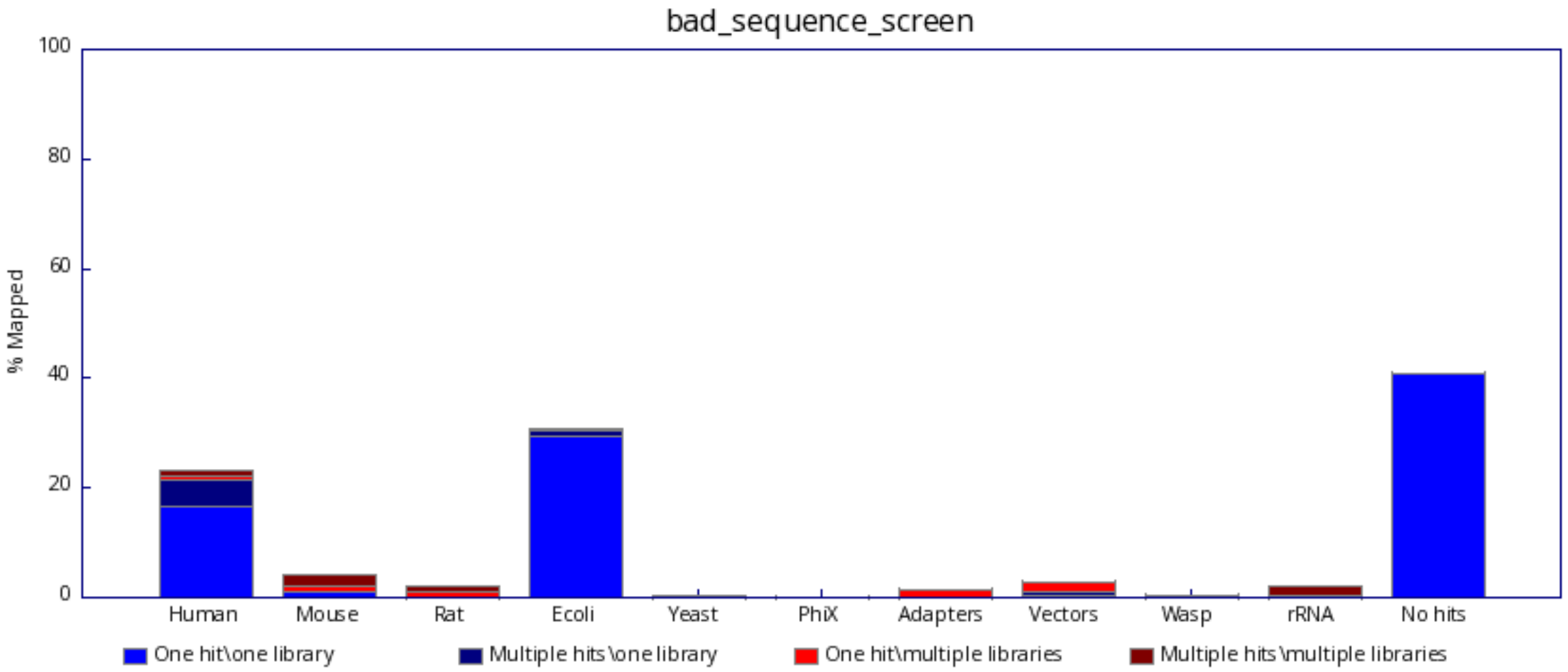
B. We have an adapters contamination.

C. We have a rDNA contamination.

D. I can't know the origin of the contamination, I will blast my reads or/and do a fastq-screen.



Question 5



Escherichia coli contamination of a human library.