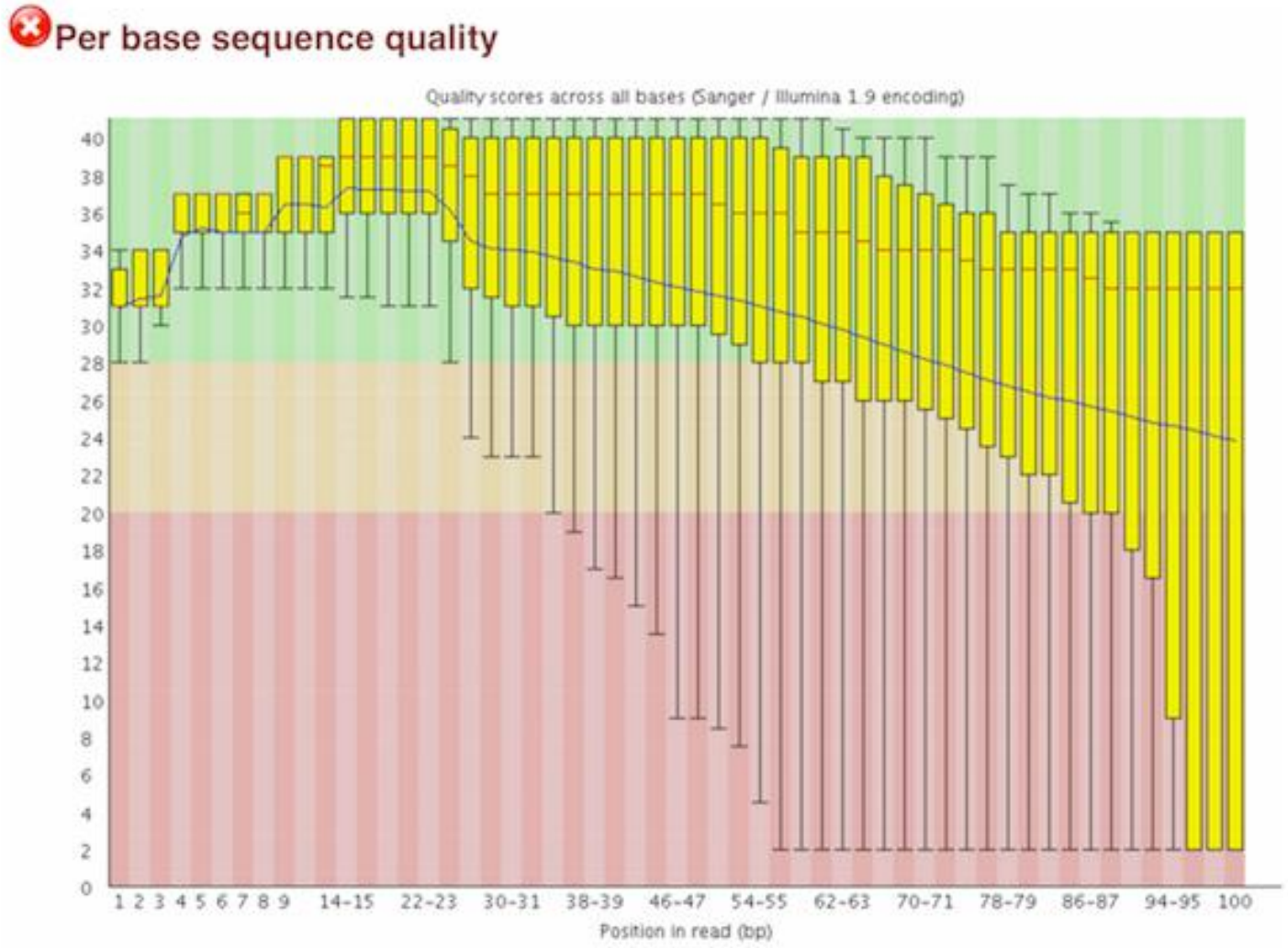
Quiz 3

GENOMICS

BIGNAUD AMAURY
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.

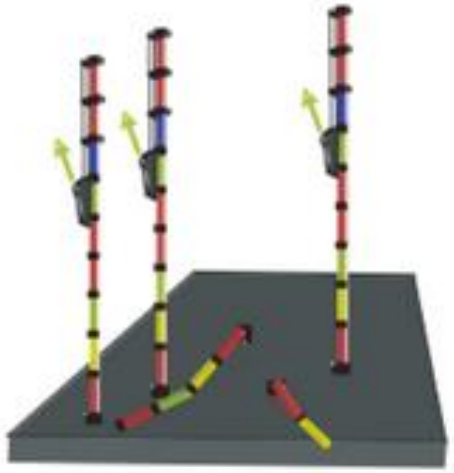
C. **You have some issues, at the end of the reads, may be due a signal issue at the end of the run.**

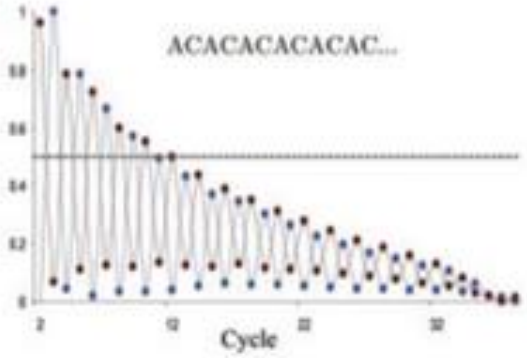
D. **You have some issues, at the end of the reads, may be due phasing issues at the end of the run.**

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

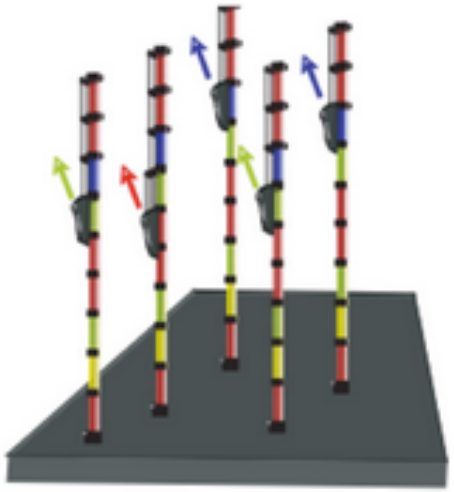
  Therefore, the proportion of signal being emitted continues to decrease with each cycle.

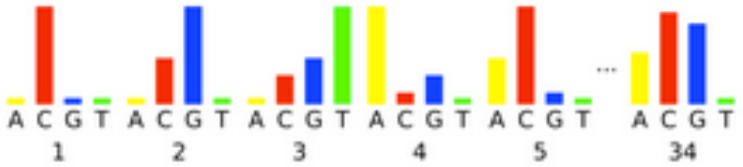




Question 1

- **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

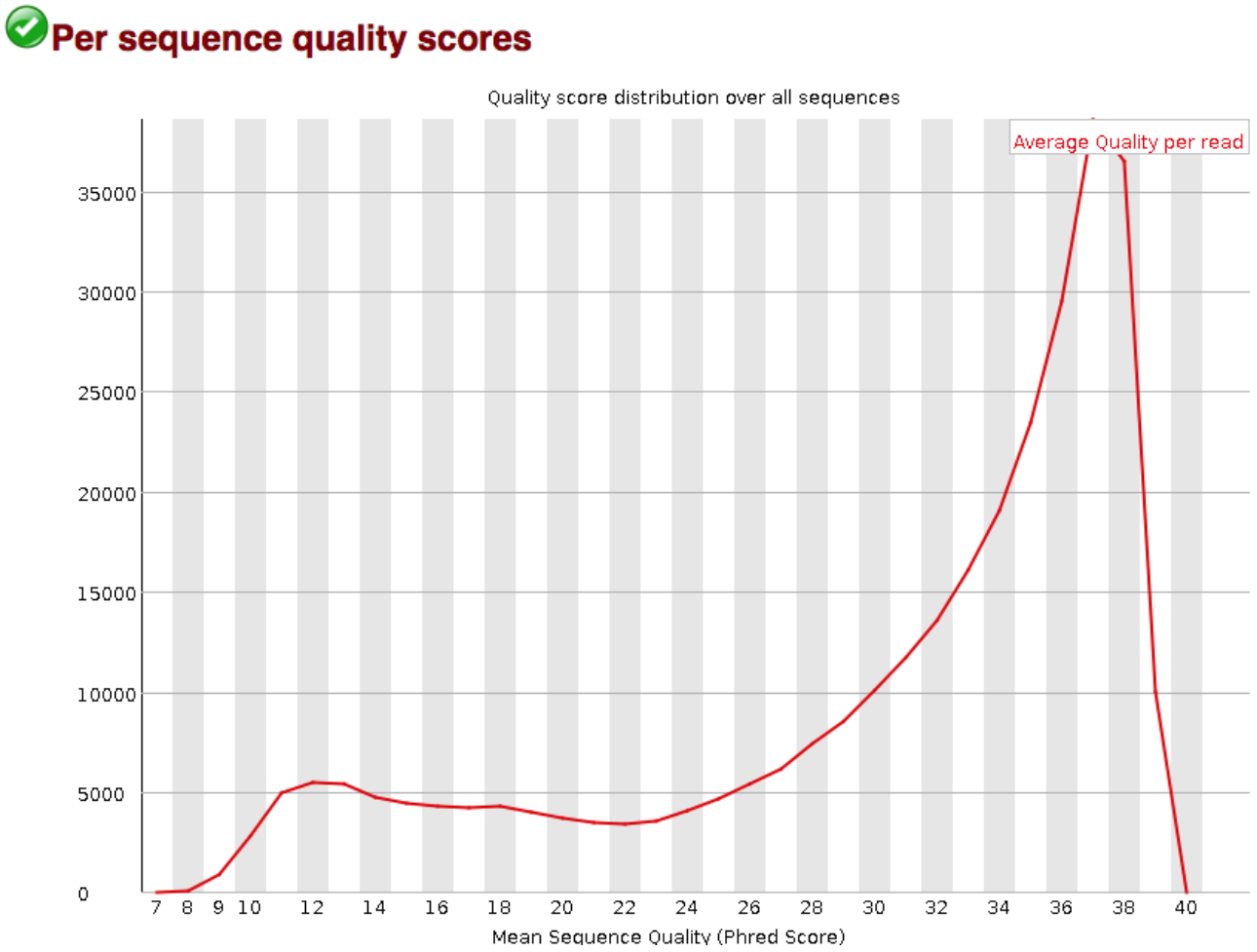
You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?

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

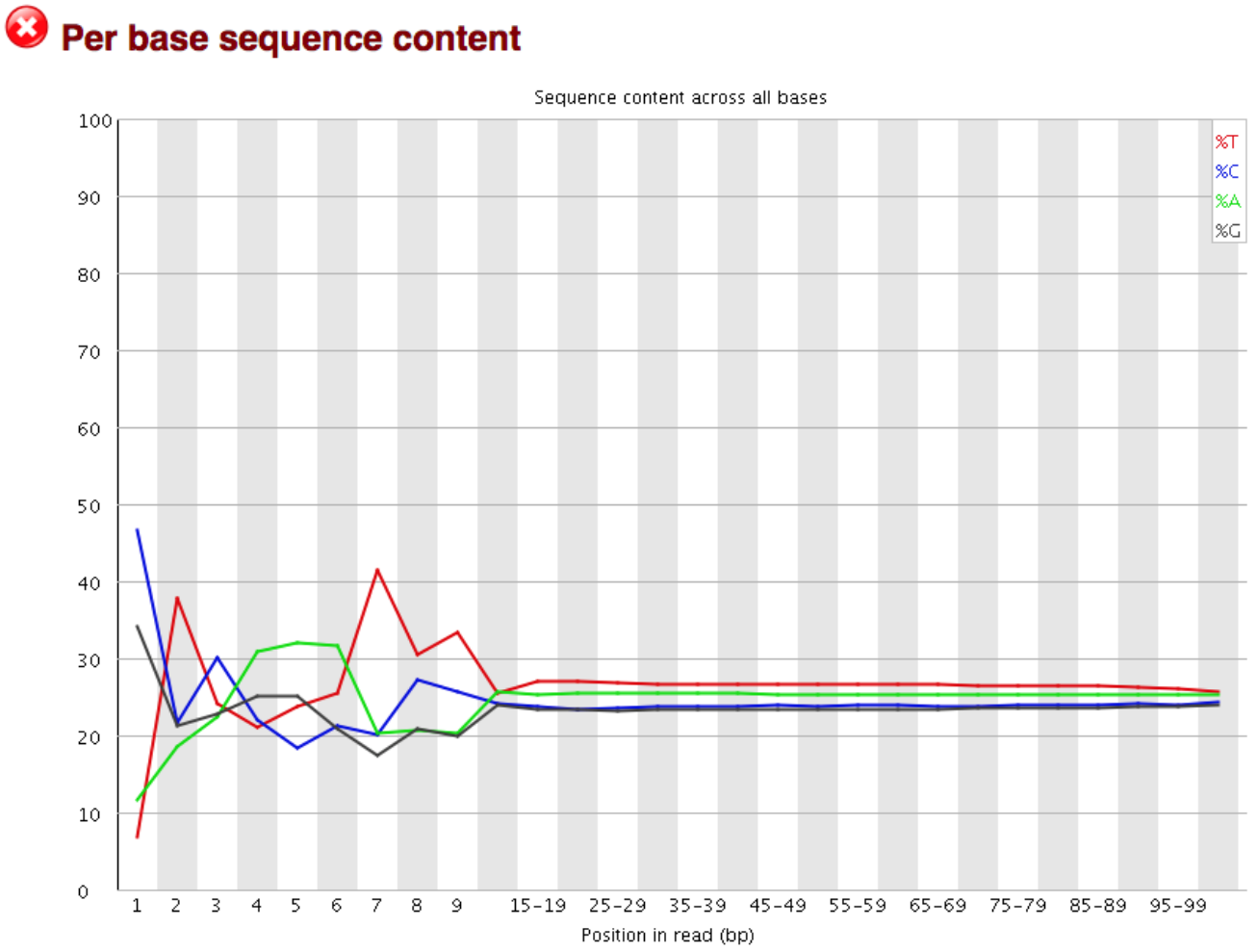
You did your fastqc on a RNAseq illumina library, you observed this plot. What do you deduce ?

A. We have an adapters contamination.

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

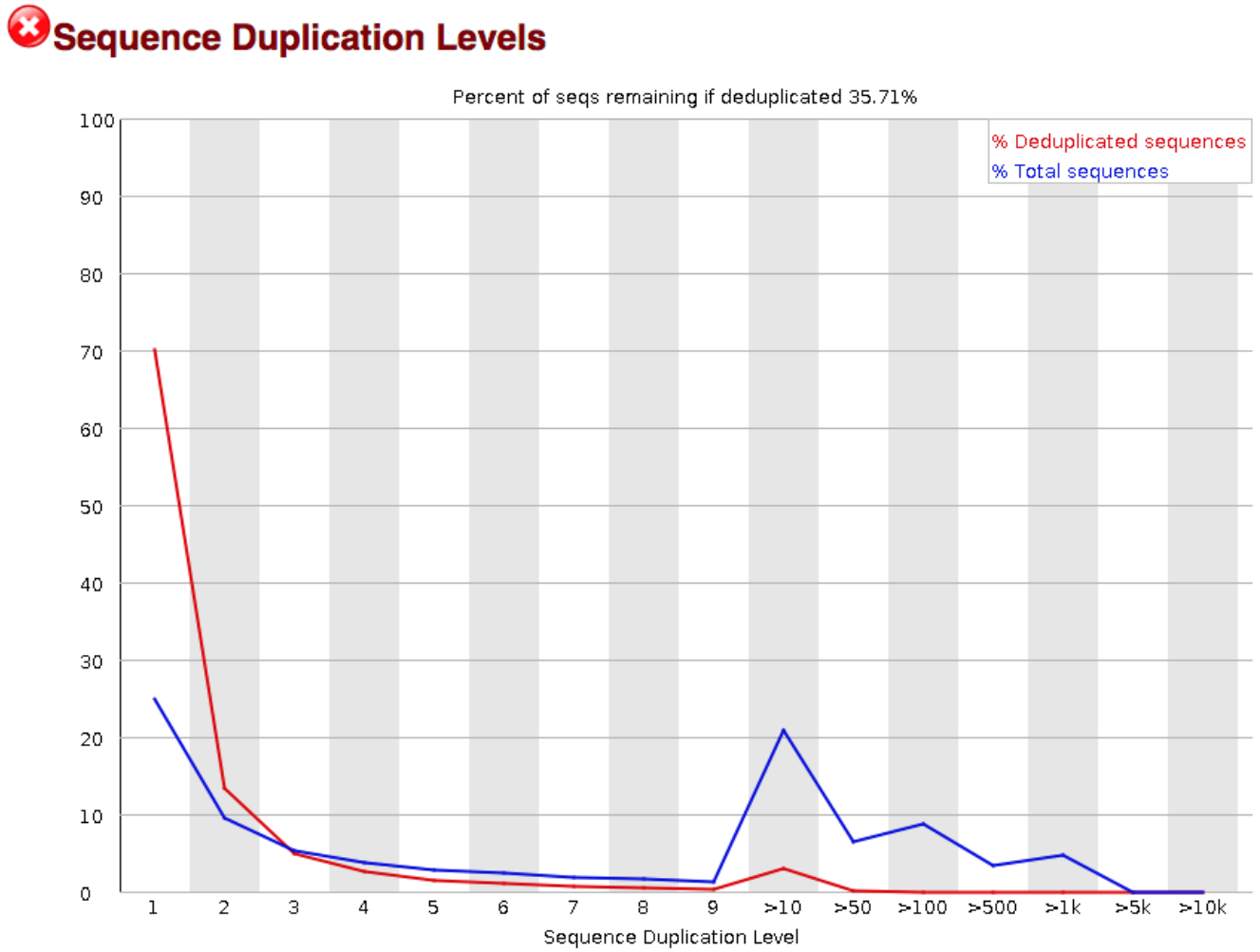
C. We have DNA contamination from another organism.

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.

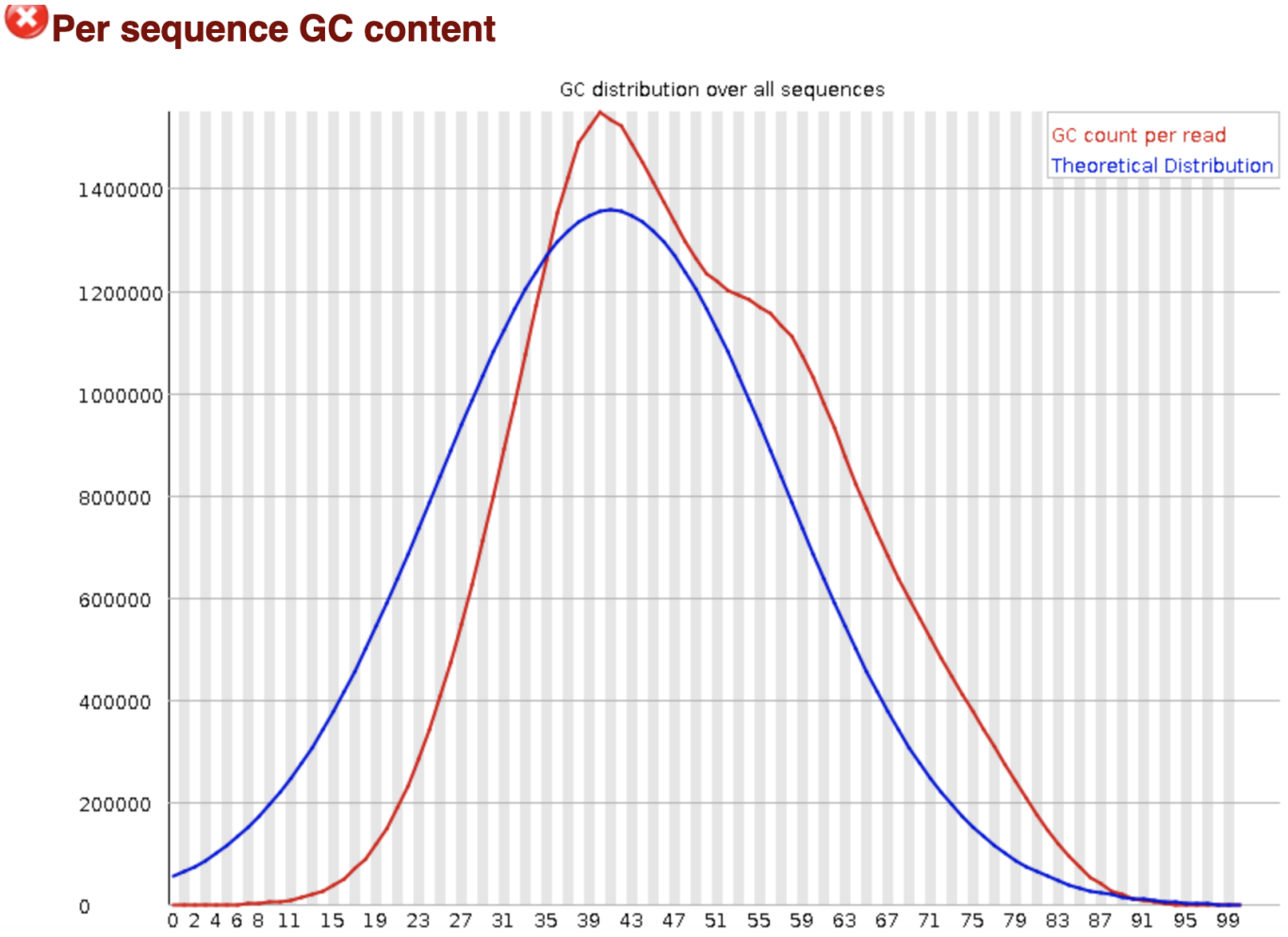
B. We have an adapters contamination.

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 ?



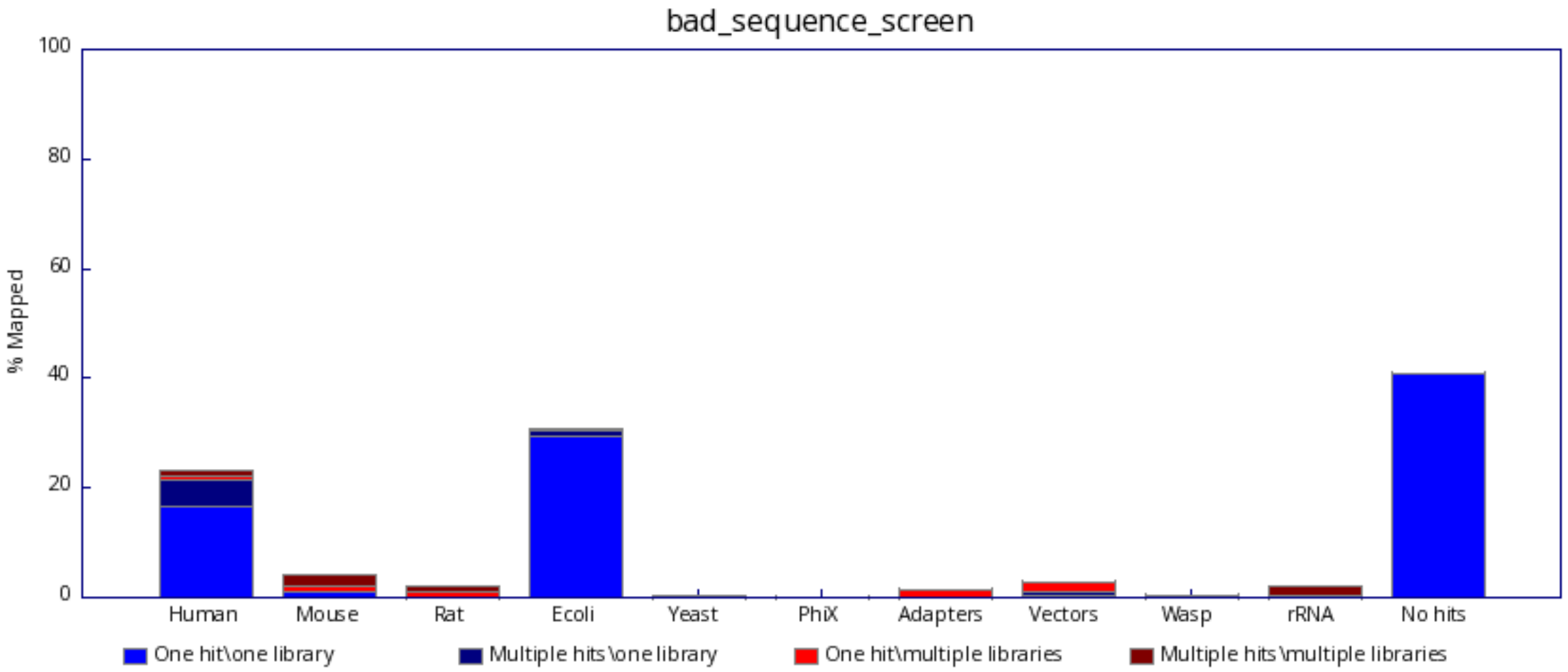
A. We have a contamination from another species.

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.