

# Quiz 3

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TRANSCRIPTOMICS

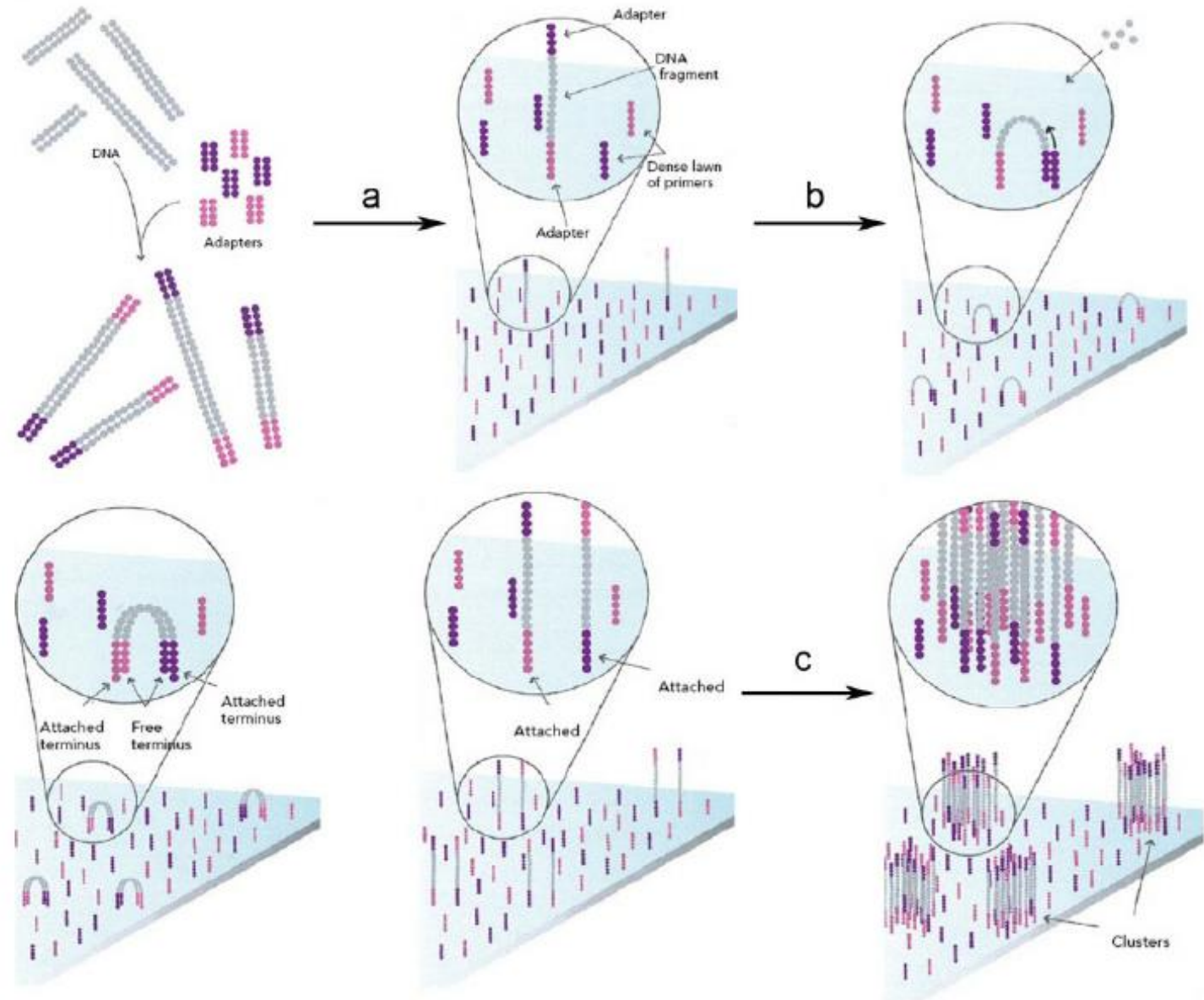
BIGNAUD AMAURY

12/04/2023

# Question 1

What is paired-end sequencing ?

- A. A method to sequence two samples at the same time.
- B. A method to sequence the read twice to reduce sequencing errors.
- C. A method to sequence both ends of a fragment.
- D. A method to sequence only double stranded DNA.



# Question 1

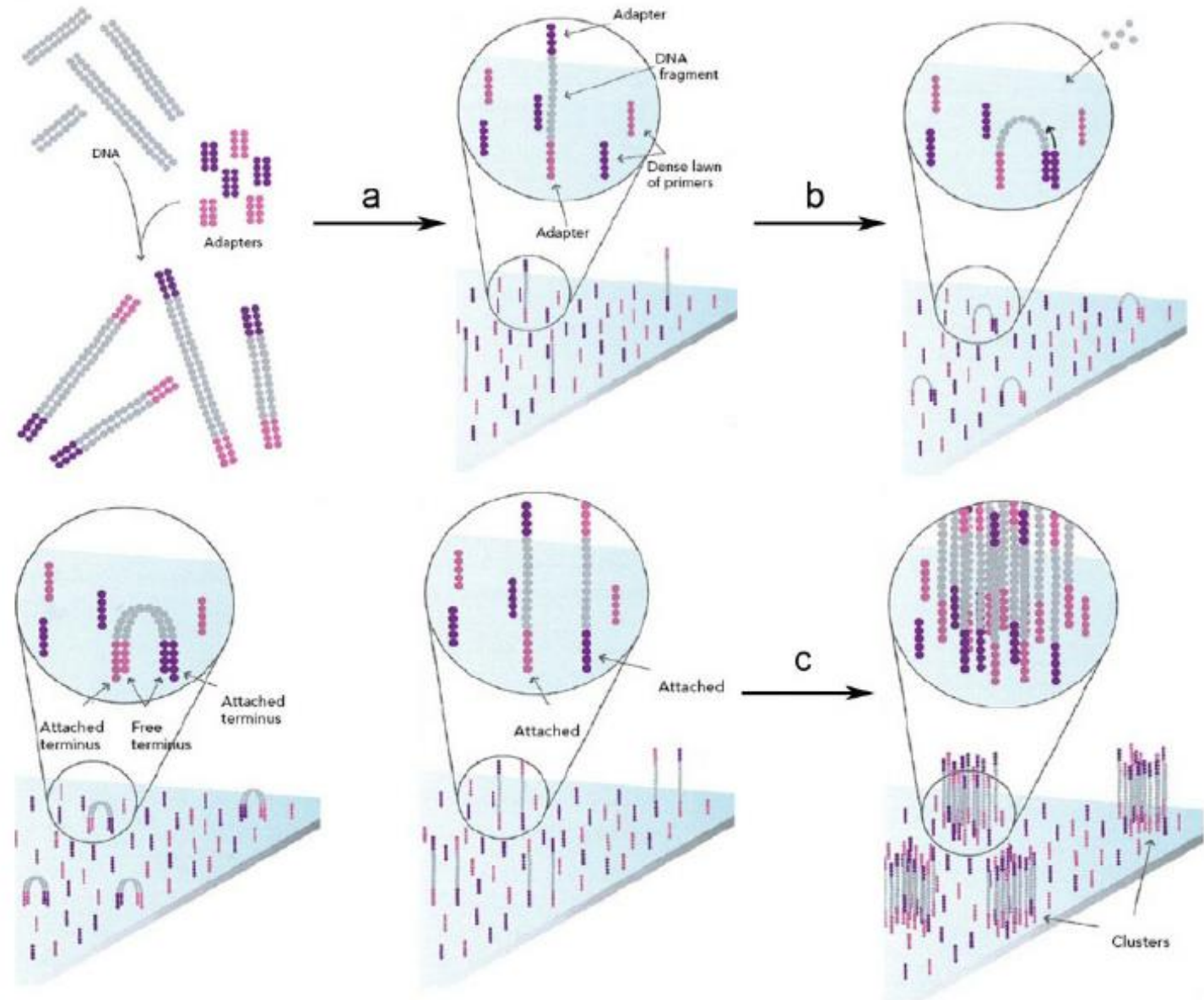
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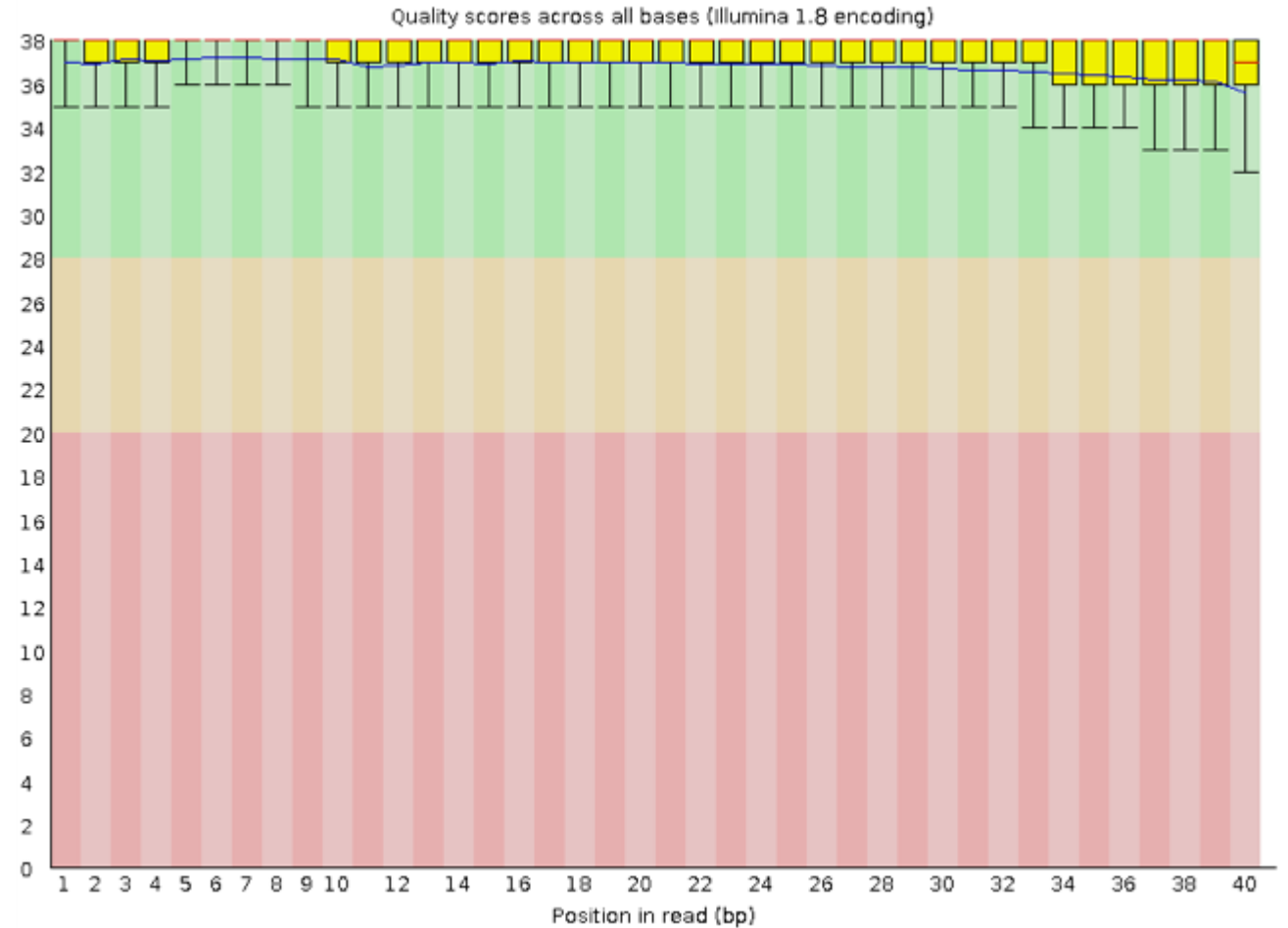
☒ D. A method to sequence only double stranded DNA.



# Question 2

A fail in fastqc can be ignore ?

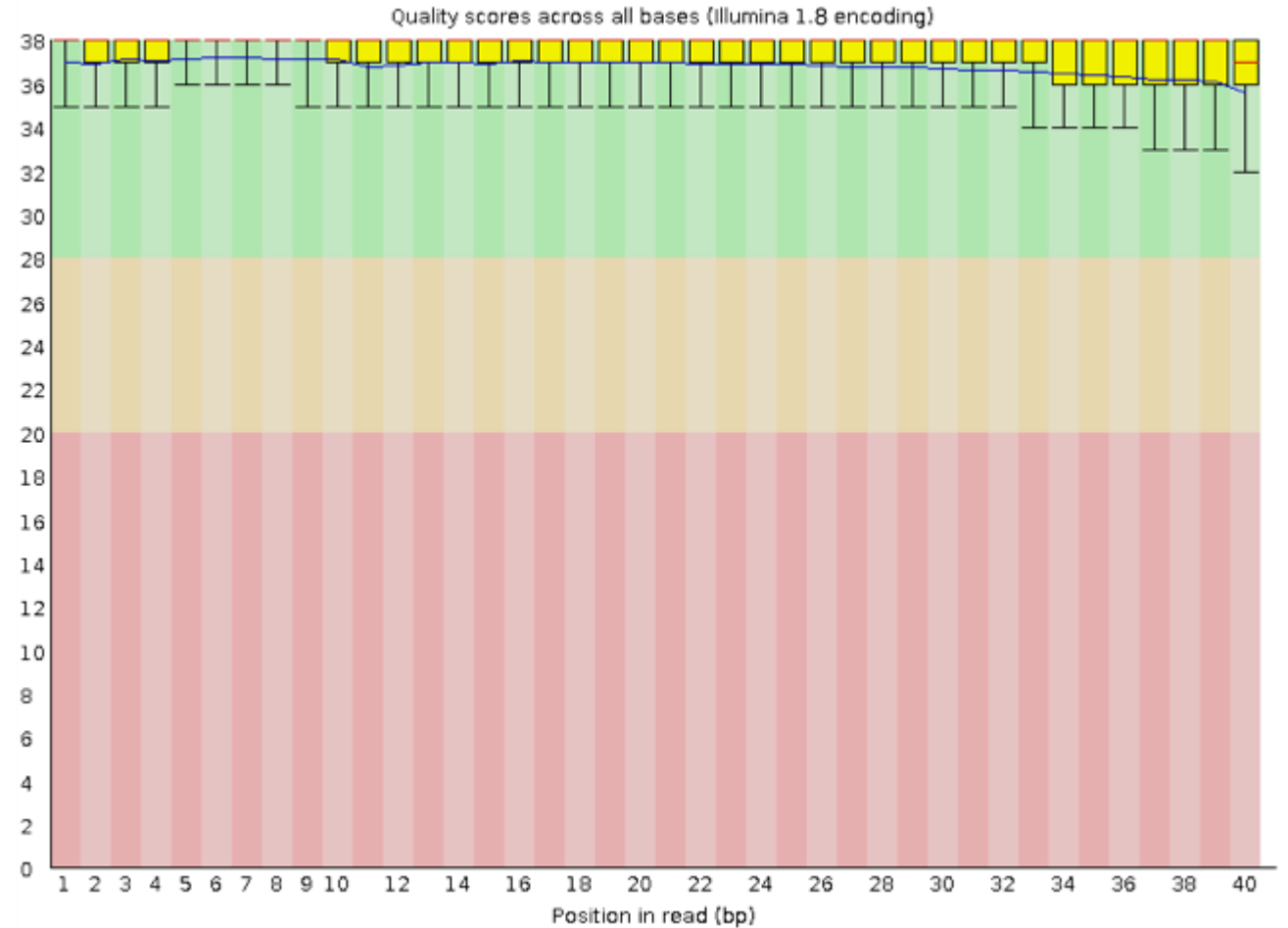
- A. Yes
- B. No
- C. Could be, it needs to be explored.
- D. I shouldn't have done the fastqc.



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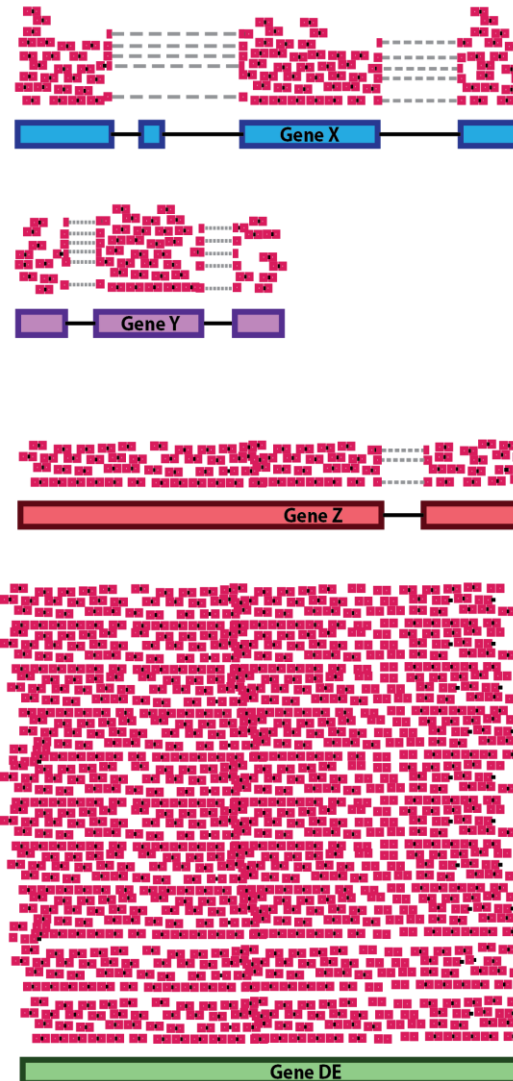


# Question 3

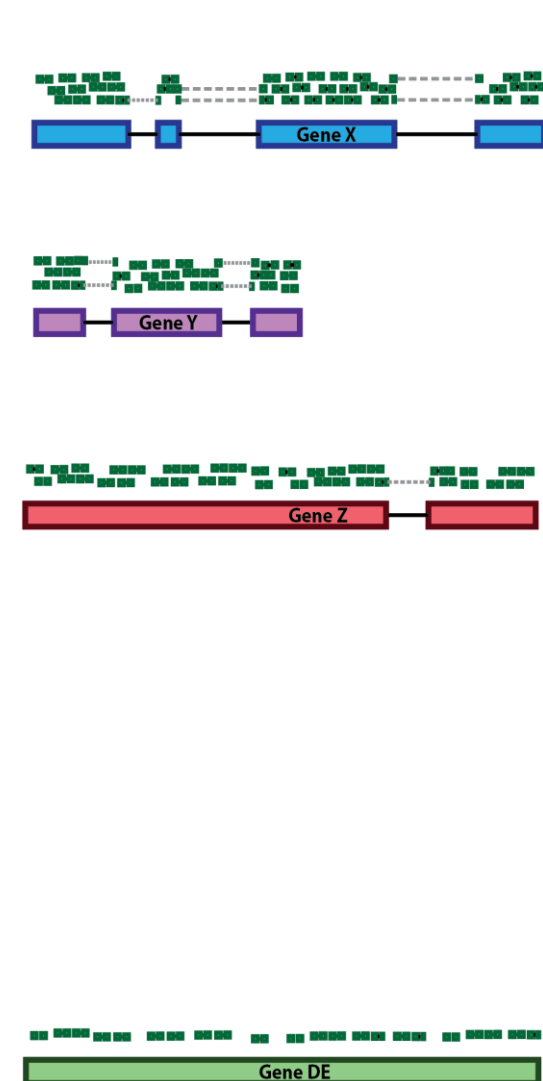
Why the RPKM (Read Per Kilobase per Million) normalization cannot be used between samples ?

- A. The sum of the RPKM values can be different between two samples.
- B. Because it doesn't consider the number of reads in the sample.
- C. Because it doesn't consider the number of reads in the sample.
- D. None of the above.

Sample A Reads



Sample B Reads



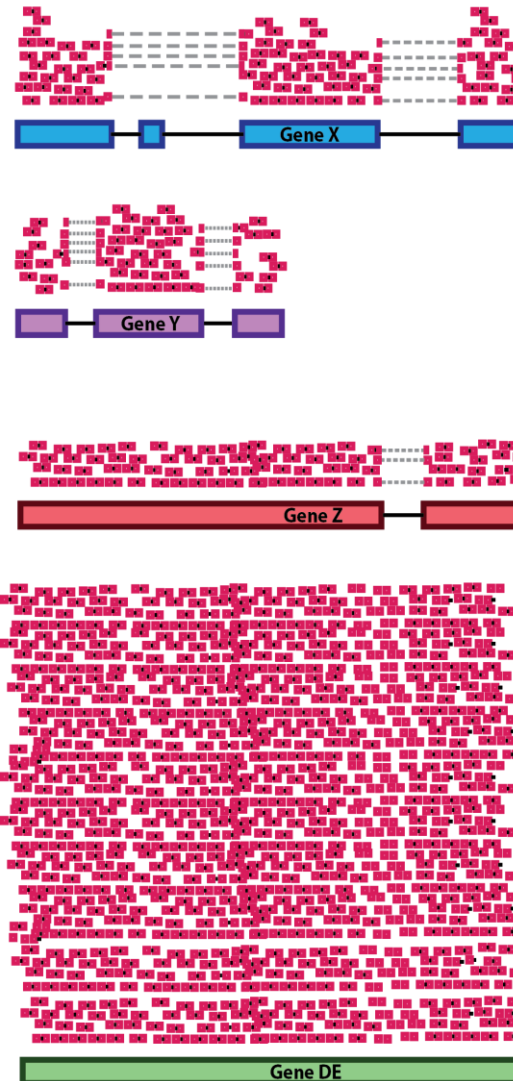


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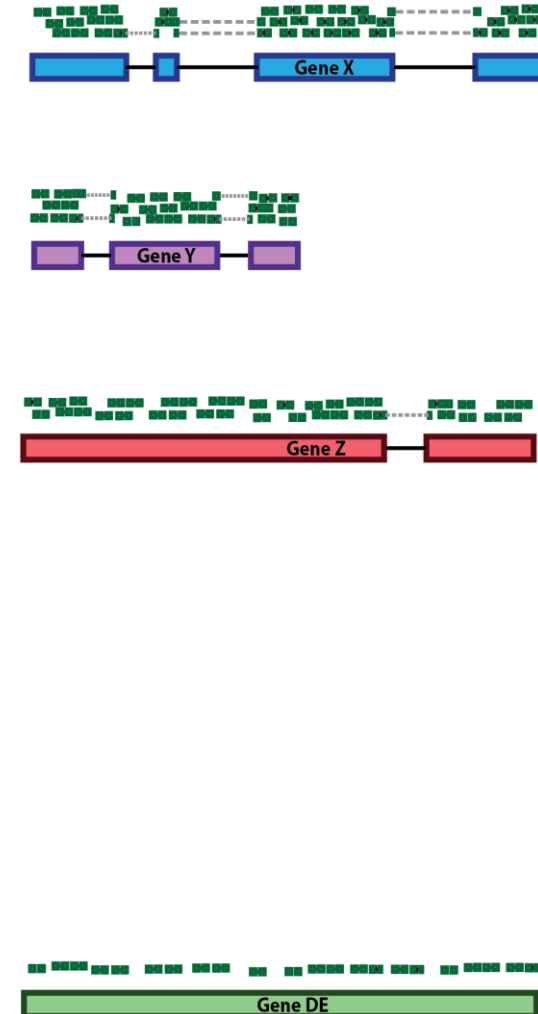
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Sample A Reads



Sample B Reads



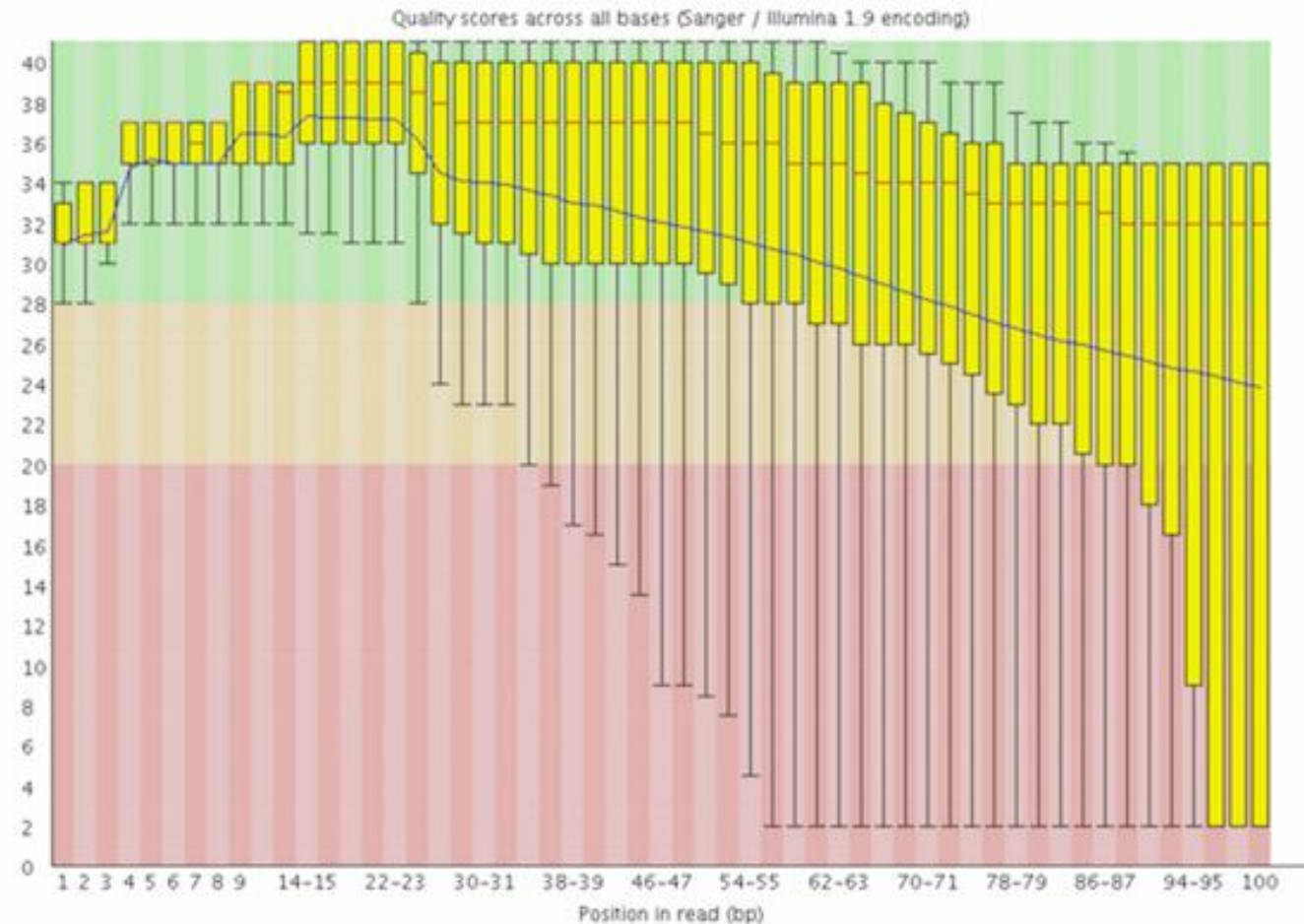
# Question 4

What can be the reason for a loose of signal at the end of the sequencing cycle ?

- A. Signal decay due to a degradation of the fluorophores.
- B. Phasing issues.
- C. Signal decay due an issue of elongation of some reads.
- D. Some reads are too short and have not been amplified.



## Per base sequence quality





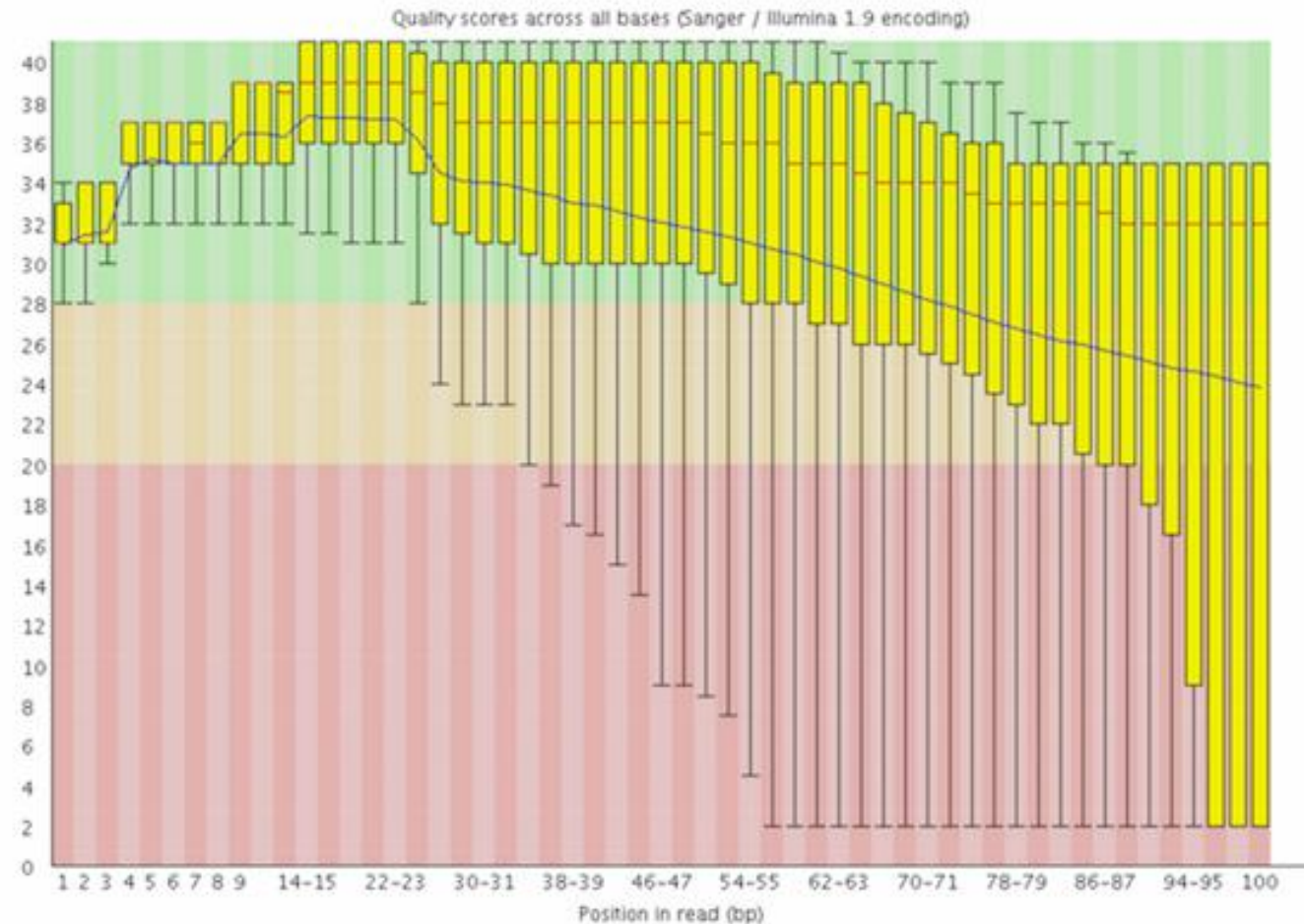
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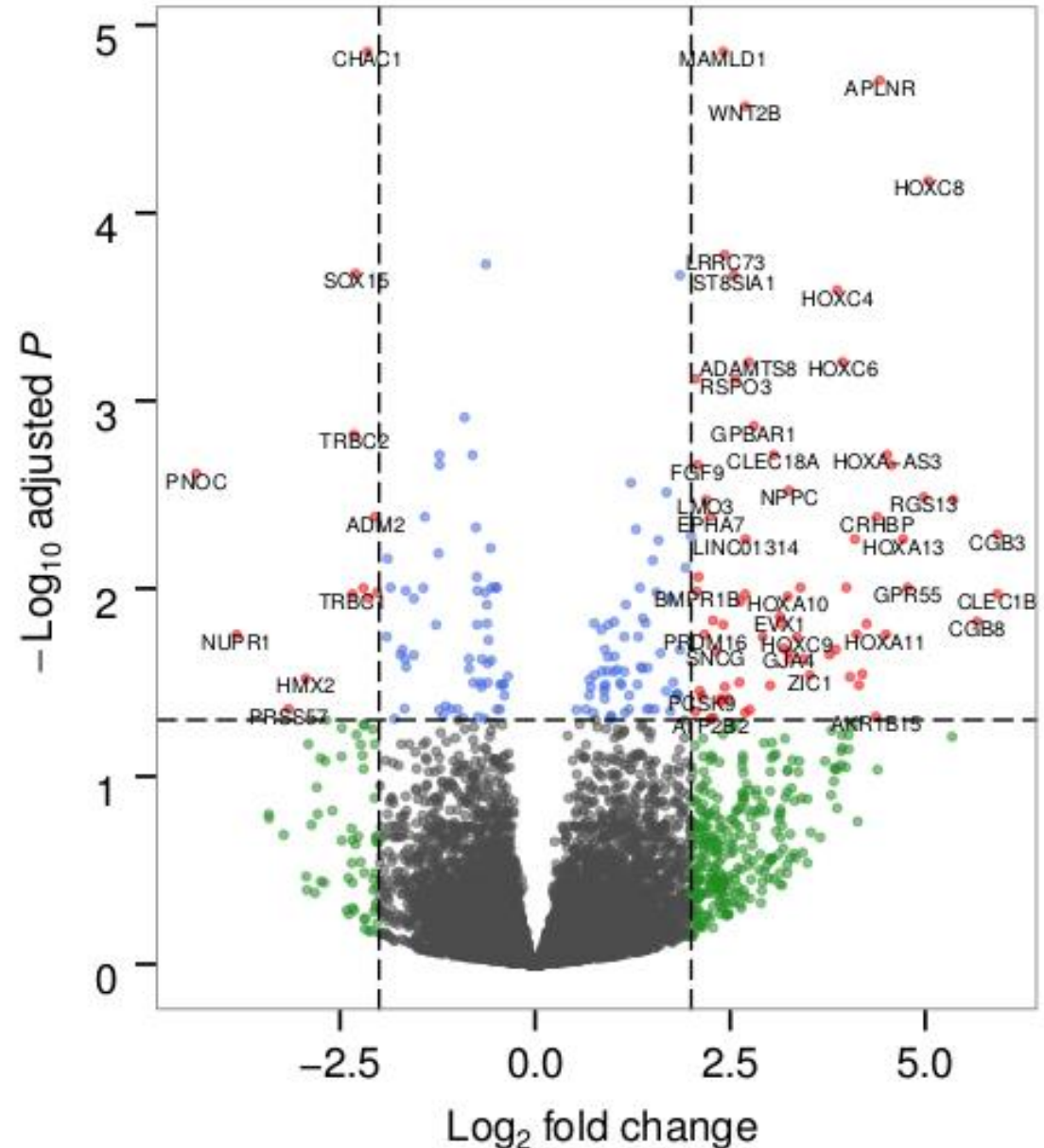
## Per base sequence quality



# Question 5

What is the color of the genes which are **NOT** significantly differentially expressed.

- A. blue
- B. red
- C. grey
- D. green



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