

# Quiz 1

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TRANSCRIPTOMICS

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09/03/2023

# Question 1

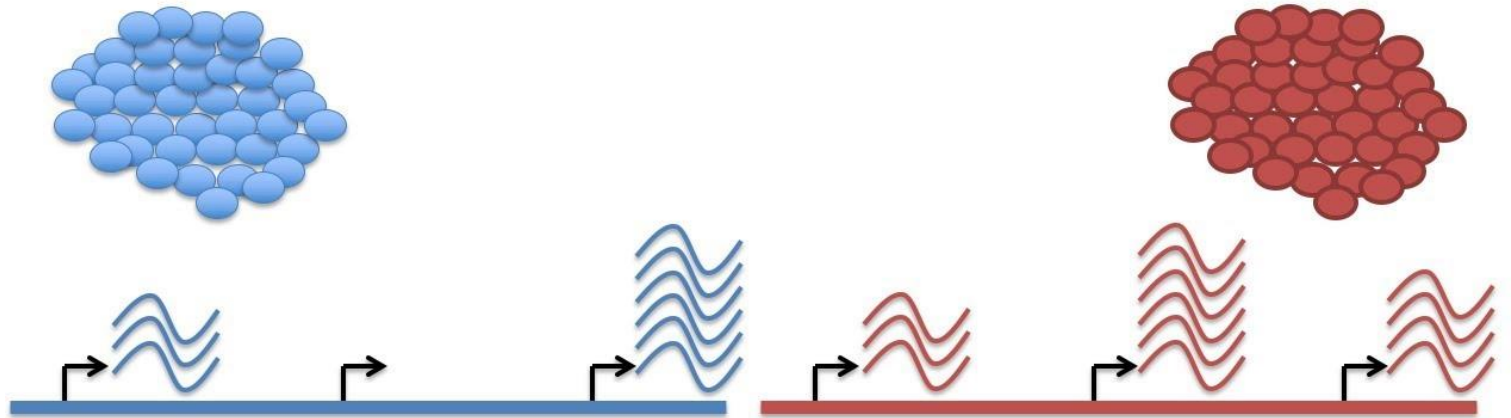
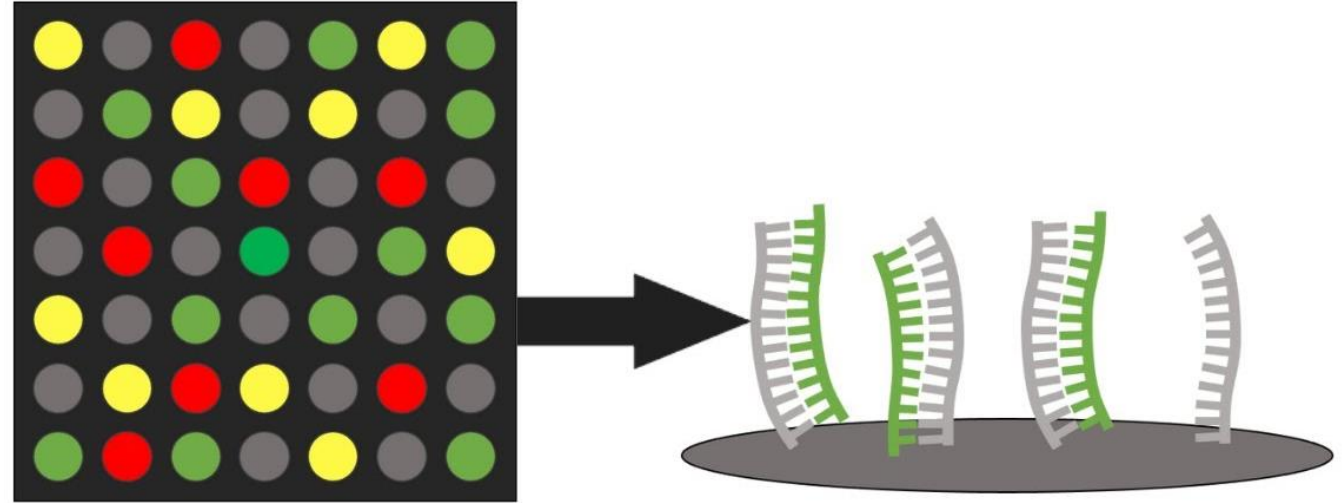
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- A.** Microarrays and ChIP
- B.** Shotgun DNA sequencing and HiC
- C.** Microarrays and RNA sequencing
- D.** ATAC-seq and whole exome sequencing

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## Question 2:

Which are the limitations of microarrays ?

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- B. Frequent contamination
- C. Complicated and long experiments
- D. Measurements errors

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- A. Adaptors to hybrid the reads to the flow cell adaptors.
- B. Barcode to trace from which sample the read came from.
- C. Primer for the cluster amplification process.
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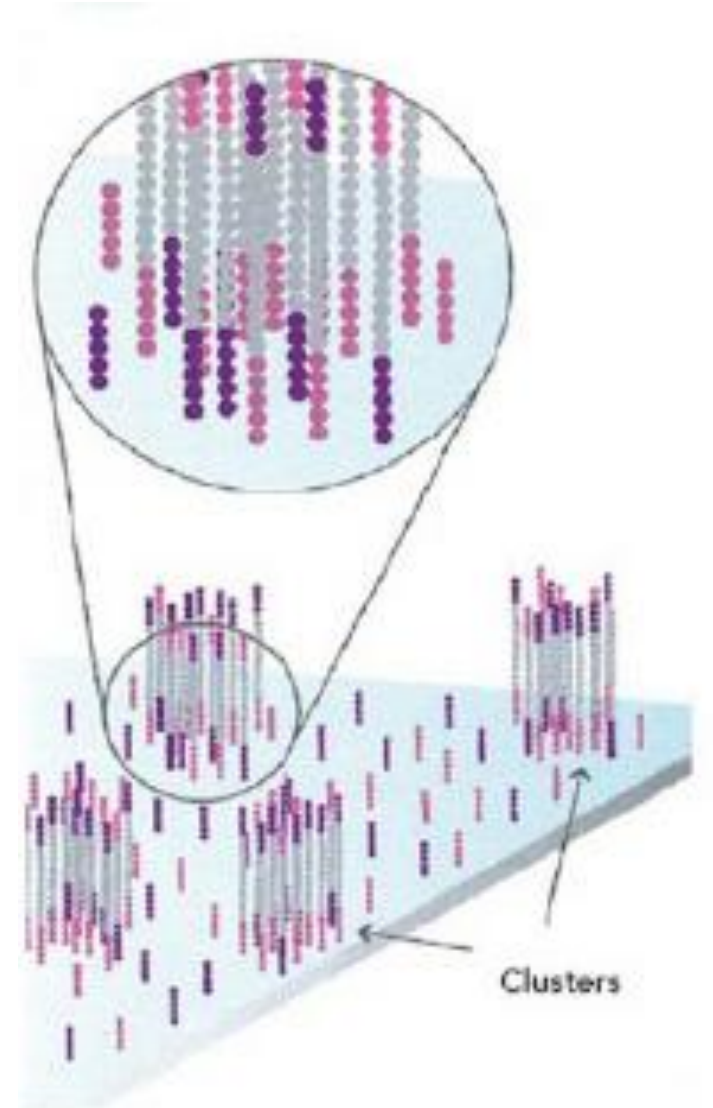
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# Question 4

What's the goal of the cluster amplification in the illumina sequencing ?

- A. Increase the number of reads to sequencing of billions of reads in low amount sample.
- B. Increase the optical signal on one spot for the detection of the base pair.
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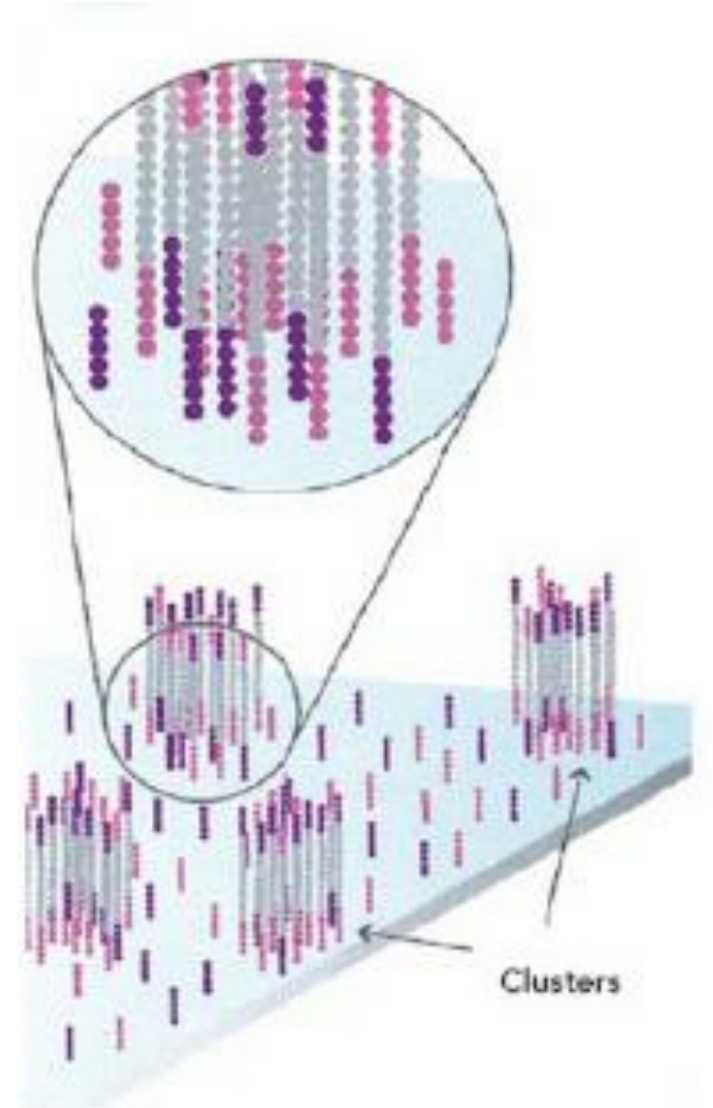




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# Question 5

Which are the four lines of an entry in a fastq file ?

- A. Read Id, sequence, a '+' and sequence quality
- B. There are only three lines.
- C. Read Id, sequence, sequence quality and a '@'
- D. Read Id, sequence, a '@' and sequence quality

# Question 5

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	Sequence ID
DNA sequence	@NS500150:681:HWJNLBGXK:1:11101:20163:1075 1:N:0:CGGCTATG+NTTCGCCT
	GATCCCATACGTACCTCAAGTGGTTTAGCAGTGTA
A useless plus	+
	AAAAEEEEEEEEEEEEEEEEEEEE/EEEEEEEEEEEEEEEE
	A quality score