Quiz 2

TRANSCRIPTOMICS

BIGNAUD AMAURY
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Question 1

What are the difference between genetics and genomics

A. There are none

B. Genetics is the old name for genomics

C. Genetics studies heredity whereas genomics studies the genome of an organism

D. Genetics focuses on genes whereas genomics focuses on the whole genome of an organism

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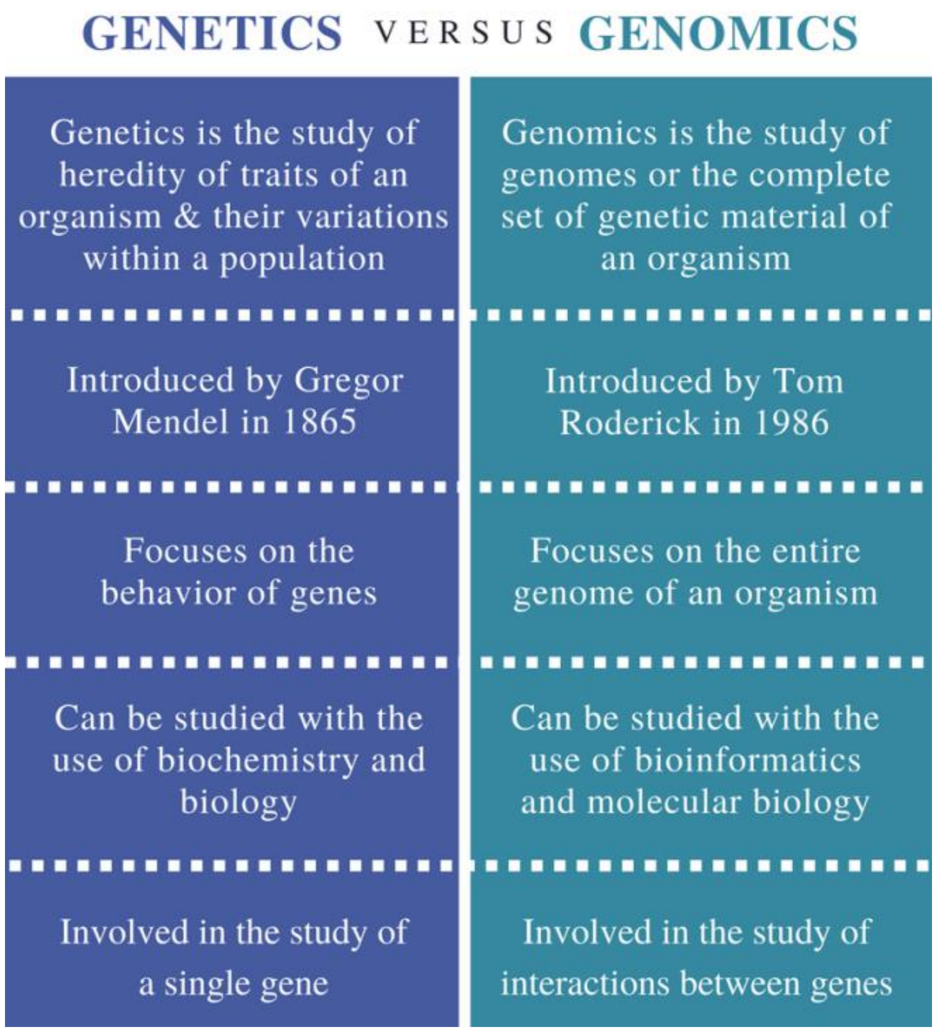


GENETICS	GENOMICS
Genetics is the study of heredity of traits of an organism & their variations within a population	Genomics is the study of genomes or the complete set of genetic material of an organism
Introduced by Gregor Mendel in 1865	Introduced by Tom Roderick in 1986
Focuses on the behavior of genes	Focuses on the entire genome of an organism
Can be studied with the use of biochemistry and biology	Can be studied with the use of bioinformatics and molecular biology
Involved in the study of a single gene	Involved in the study of interactions between genes

Question 2:

Which of this experiment is not a genomics experiment ?

A. GWAS (Genome-wide association studies)
B. ChIP-seq
C. DNA mutation of one gene
D. Hi-C

Question 3

Which are the roles of the i5 and i7 part of the illumine adaptors ?

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.

D. Primer for the sequencing process.

Question 4

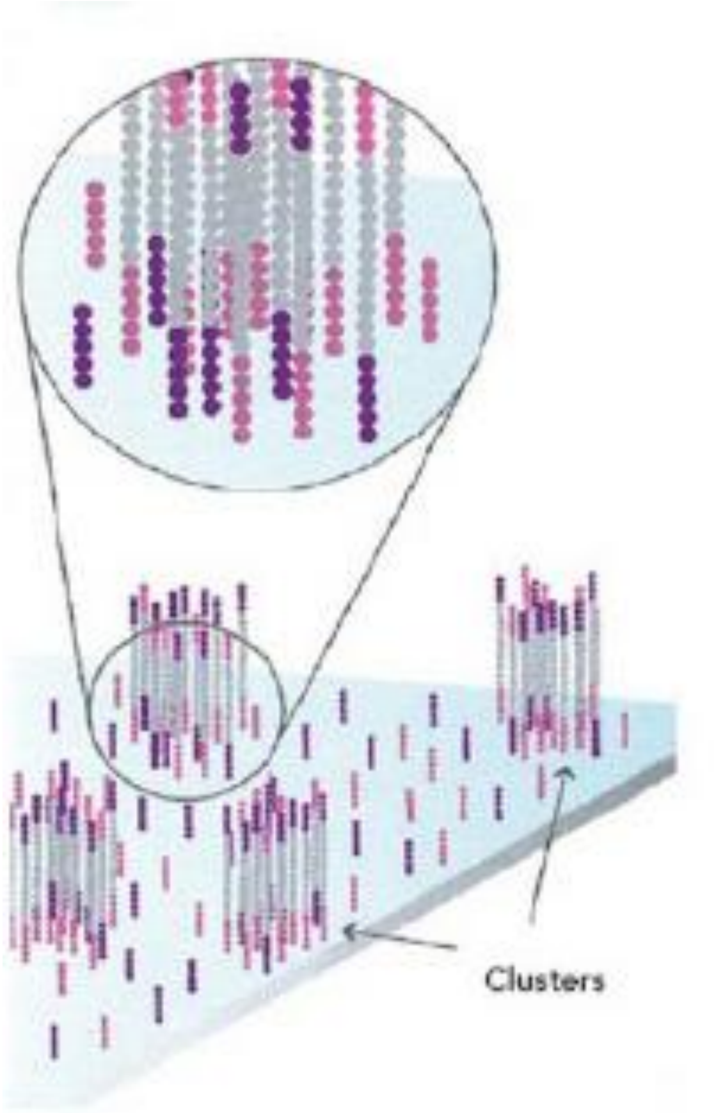
What's the goal of the cluster amplification in the Illumina sequencing ?

A. Increase the number of reads to sequence billions of reads in low amount sample.

B. Increase the optical signal on one spot for the detection of the base pair.

C. Put the DNA on the flow cell.

D. There is no cluster amplification during Illumina sequencing.



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

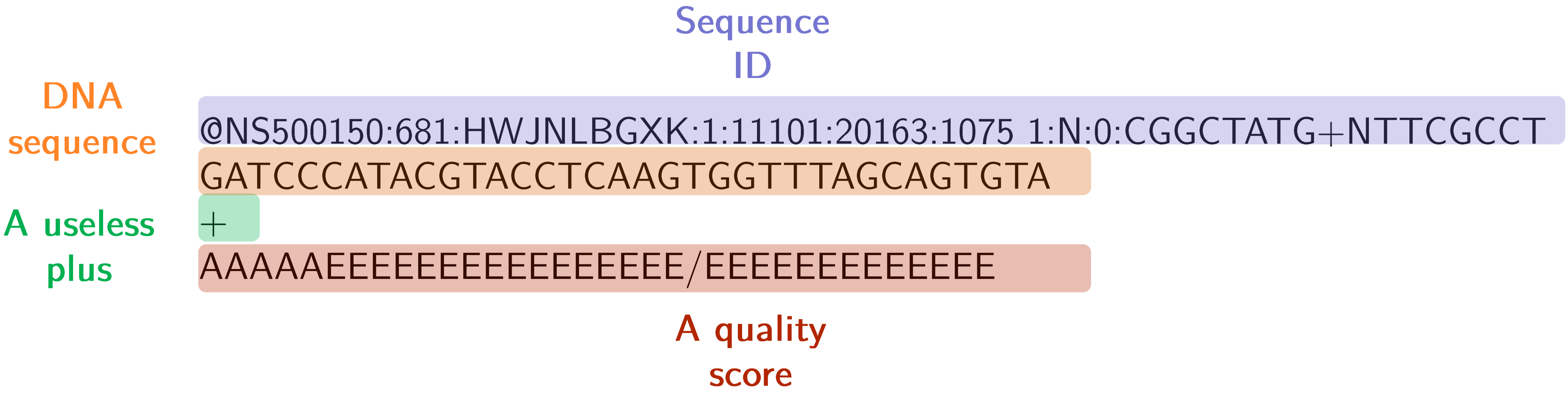
Which are the four lines of an entry in a fastq file ?

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



Sequence ID

DNA sequence

```
@NS500150:681:HWJNLBGXK:1:11101:20163:1075 1:N:0:CGGCTATG+NTTCGCCT
GATCCCATACGTACCTCAAGTGGTTTAGCAGTGTA
+
AAAAAEEEEEEEEEEEEEEEEEE/EEEEEEEEEEEEE
```

A useless plus

A quality score