

BZ360, Sample Questions for Exam 3

Name: _____

1. Match the following genomic features with the descriptors a-f below:

- ___ Pseudogene
- ___ Transposon
- ___ mRNA
- ___ tRNA
- ___ rRNA
- ___ microRNA

- a. A gene that is able to replicate itself within a genome.
- b. A short RNA that associates with Argonaute proteins to affect gene silencing.
- c. An RNA component of the ribosome.
- d. A feature often associated with protein coding genes.
- e. An RNA that delivers amino acids to the ribosome.
- f. A feature commonly arising from gene duplications.

2. Which of the following genomic features most commonly causes mutations in the genome?

- a. Pseudogenes
- b. microRNAs
- c. rRNAs
- d. Transposons

3. In sequencing and assembling the genome of the tardigrade, which of the following features would be most difficult to assign to a unique genomic position because of associated repetitive elements?

- a. microRNA gene
- b. Pseudogene
- c. Protein coding gene
- d. long non-coding RNA gene
- e. Transposon



4. Which of the following is not considered a eukaryotic small RNA?

- a. microRNA
- b. small interfering RNA
- c. piwi-interacting RNA
- d. messenger RNA

5. _____ and _____ are two classes of non-coding RNAs that are directly involved in the synthesis of proteins.

6. When and where a gene is expressed is determined entirely by the DNA sequence of the gene.

- a. True
- b. False

7. Once a gene has been transcribed to RNA, it is no longer subjected to gene regulation.
- True
 - False
8. Which of the following is a common step during RNA-seq library preparation?
- Reverse transcription
 - PCR
 - Adapter ligation
 - RNA fragmentation
 - All of the above
9. Which of the following features is often used to enrich for mRNA during RNA-seq library preparation?
- 5' cap
 - Introns
 - Poly(A) tail
 - 5' UTR
 - 3' UTR
10. Which of the following sequencing applications is often used to identify transcription factor binding sites?
- NET-seq
 - Small RNA-seq
 - Ribosome Profiling (ribo-seq)
 - ChIP-seq
 - MethylC-seq
11. Xist is an example of what type of genomic element?
- Long non-coding RNA
 - Small RNA
 - mRNA
 - Transposon
 - All of the above
12. Match the following classes of small RNAs with the single best descriptor, a-c, below:
- ___ miRNAs
___ piRNAs
___ siRNAs
- Derive from characteristic hairpin structures and regulate mRNA expression throughout development.
 - Associate with Piwi proteins and typically regulate transposable elements.
 - Typically processed from perfectly duplexed double-stranded RNA and function during RNAi
13. The following text is in what common sequence annotation format? _____

CHROMOSOME	SOURCE	FEATURE	START	END	SCORE	STRAND	FRAME	NOTE
1	Transposon	transposable_element	127812	129834	.	+	.	TRANSPOSON ID=C2379

14. What is a UNIX command commonly used to search for patterns within a file? _____
15. You just received Next-gen sequencing data for an RNA-seq experiment that you did. Which of the following steps should be done first?
- Read mapping
 - Differential gene expression analysis
 - Quality control
 - Data visualization in a genome browser
16. Short answer: what software did we use in class for filtering poor quality reads?
17. Short answer: what software did we use in class to map reads to a reference genome sequence?
18. Short answer: what GUI-based software did we use in class for assessing read quality in a library?
19. SAM tools is software for mining Next-gen sequencing data.
- True
 - False
20. Match each program below with its function:
- ___ FastQC
 - ___ Trimmomatic
 - ___ IGV
 - ___ TopHat
 - ___ Cuffdiff
- Adapter trimming
 - Differential gene expression
 - Aligning reads across splice junctions
 - Visualizing data in a genome viewer
 - Quality control
21. In what order (1-5) would the following programs typically be run when analyzing RNA-seq data?
- ___ TopHat
 - ___ Trimmomatic
 - ___ FastQC
 - ___ Cuffdiff
 - ___ IGV

22. The following screen shot is of what common genome viewing software? _____

