Exam 3 (100 pts)

Name:_____

1. The majority of RNA in most cells is mRNA.
    a. True
    b. False

2. Match the following genomic features with the attributes a-f below:
    ___Pseudogene
    ___Transposon
    ___mRNA
    ___tRNA
    ___rRNA
    ___lncRNA

    a. Long non-coding RNAs
    b. A component of the ribosome
    c. Mobile elements
    d. Protein coding
    e. Lost the ability to encode a protein
    f. Carry amino acids to the ribosome

3. Which of the following genomic features commonly causes mutations in the genome?
    a. tRNAs
    b. Pseudogenes
    c. lncRNAs
    d. Transposons
    e. rRNAs

4. In sequencing and assembling the genome of the naked mole rat, high-throughput sequencing reads from which of the following features would likely be most difficult to assign to a unique genomic position because of associated repetitive elements?
    a. Transposon
    b. Pseudogene
    c. Protein coding mRNA
    d. lncRNA

5. _____ and _____ and _____ are three classes of small non-coding RNAs that are directly involved in gene regulation.

6. tRNAs are typically >1 kb in length
    a. True
    b. False

7. Which of the following features is NOT used to classify lncRNAs:
    a. Length >200 nt
    b. Inability to code for a protein
    c. Lack of known known protein domains
    d. Lack of a polyA tail
    e. Lack of sequence similarity to protein coding genes

8. What is the role of the Xist lncRNA?
    a. Dosage compensation
    b. Translation
    c. Y chromosome activation
    d. RNAi
    e. DNA methylation

9. Order the following 3 steps in small RNA-seq library preparation:
    ____PCR
    ____Adapter ligation
    ____Reverse transcription

10. Which of the following is commonly used to align small RNA-seq reads to a reference genome?
    a. Excel
    b. SamTools
    c. IGV
    d. FastQC
    e. Bowtie

11. Which of the following features is often used to enrich for mRNA during RNA-seq library preparation?
    a. 5’ cap
    b. Introns
    c. 5’ UTR
    d. 3’ UTR
    e. Poly(A) tail

12. Which of the following features necessitates special read mapping software when analyzing RNA-seq data?
    a. 5’ cap
    b. Introns
    c. 5’ UTR
    d. 3’ UTR
    e. Poly(A) tail

13. Which of the following best describes what RNA-seq is commonly used to measure?
    a. Rates of transcription
    b. mRNA decay
    c. Steady state mRNA levels
    d. Translation
    e. DNA methylation

14. You just received high-throughput sequencing data for an RNA-seq experiment that you did. Which of the following steps should be done first?
    a. Read mapping
    b. Quality control
    c. Differential gene expression analysis
    d. Data visualization in a genome browser

15. Order the following 5 steps in RNA-seq library preparation:
    ____PCR
    ____mRNA enrichment
    ____Adapter ligation
    ____Reverse transcription
    ____RNA fragmentation

16. Match each program below with its function:
    ___FastQC
    ___IGV
    ___TopHat
    ___Trimmomatic
    ___Cuffdiff

    a. Adapter trimming
    b. Quality control
    c. Differential gene expression
    d. Aligning reads across splice junctions
    e. Visualizing data in a genome viewer

17. In what order (1-5) would the following programs typically be run when analyzing RNA-seq data?
    ___TopHat
    ___Trimmomatic
    ___FastQC
    ___Cuffdiff
    ___IGV

18. What file format is commonly used for raw high-throughput sequence data?

19. What file format is commonly used for gene annotations?

20. What file format is commonly used for genome sequences?

21. What does the RNA-seq expression unit fpkm stand for?