

Exam 3 (100 pts)

Name: _____

- The majority of RNA in most cells is mRNA.
 - True
 - False
- Match the following genomic features with the attributes a-f below:
 - Pseudogene
 - Transposon
 - mRNA
 - tRNA
 - rRNA
 - lncRNA
 - Long non-coding RNAs
 - A component of the ribosome
 - Mobile elements
 - Protein coding
 - Lost the ability to encode a protein
 - Carry amino acids to the ribosome
- Which of the following genomic features commonly causes mutations in the genome?
 - tRNAs
 - Pseudogenes
 - lncRNAs
 - Transposons
 - rRNAs
- 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?
 - Transposon
 - Pseudogene
 - Protein coding mRNA
 - lncRNA
- ____ miRNAs ____ and ____ piRNAs ____ and ____ siRNAs ____ are three classes of small non-coding RNAs that are directly involved in gene regulation.
- tRNAs are typically >1 kb in length
 - True
 - False

7. Which of the following features is NOT used to classify lncRNAs:
- Length >200 nt
 - Inability to code for a protein
 - Lack of known known protein domains
 - Lack of a polyA tail
 - Lack of sequence similarity to protein coding genes
8. What is the role of the Xist lncRNA?
- Dosage compensation
 - Translation
 - Y chromosome activation
 - RNAi
 - DNA methylation
9. Order the following 3 steps in small RNA-seq library preparation:
- 3_PCR
 - 1_Adapter ligation
 - 2_Reverse transcription
10. Which of the following is commonly used to align small RNA-seq reads to a reference genome?
- Excel
 - SamTools
 - IGV
 - FastQC
 - Bowtie
11. Which of the following features is often used to enrich for mRNA during RNA-seq library preparation?
- 5' cap
 - Introns
 - 5' UTR
 - 3' UTR
 - Poly(A) tail
12. Which of the following features necessitates special read mapping software when analyzing RNA-seq data?
- 5' cap
 - Introns
 - 5' UTR
 - 3' UTR
 - Poly(A) tail
13. Which of the following best describes what RNA-seq is commonly used to measure?
- Rates of transcription
 - mRNA decay
 - Steady state mRNA levels
 - Translation
 - 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?
- Read mapping
 - Quality control
 - Differential gene expression analysis
 - 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
- Adapter trimming
 - Quality control
 - Differential gene expression
 - Aligning reads across splice junctions
 - 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?
- fastq
19. What file format is commonly used for gene annotations?
- gff or gtf
20. What file format is commonly used for genome sequences?
- fasta

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

Fragments per kilobase transcript per million mapped reads/framgents