Epigenetics and Chromatin State Homework

BMSC8203, Spring 2020

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Please send me your answers in either a word document or a PDF with your LAST NAME in the file name and NO SPACEs. If you need any clarification on the assignment, please email me at kelsey.h.keith@gmail.com.

Multiple Choice

Please indicate your choice by changing the color of the answer or making it bold.

1. Which of the following describes the epigenetic landscape as originally described in the 1940s by C.H. Waddington?
    a. Each cell has a different DNA sequence that determines its cellular identity.
    b. A non-nuclear heritability of long-term cell memory.
    c. Specific patterns of DNA methylation that determine cell fate during development.
    d. Cell fates are irreversibly determined during development; like a marble rolling down a slope, cells come to rest at the lowest local elevation.
2. Which is **NOT** an epigenetic modification?
    a. DNA methylation
    b. DNA mutations
    c. Histone modifications
    d. Chromatin rearrangement
3. DNA methylation does which of the following?
    a. Silences repetitive elements
    b. Signals for spatial rearrangement of chromatin.
    c. Translates mRNA into proteins
    d. Signals that DNA repair is needed
4. What is the correct order of DNA structure from smallest to largest?
    a. chromosome, chromatin, nucleosomes, DNA
    b. DNA, chromosome, nucleosomes, chromatin
    c. DNA, nucleosomes, chromatin, chromosome
    d. Chromosome, chromatin, DNA, nuclesomes
5. What 3 factors do you need to consider when doing NGS sequencing?
    a. Sequencing depth, sequencing adaptor type, and whether to sequence single or paired-end
    b. Read length, DNA repetitiveness, and whether to sequence single or paired-end
    c. Sequencing depth, read length, and whether to sequence single or paired-end
    d. Sequencing depth, read length, and the species of the sample

6. Why would you prefer reduced representation bisulfite sequencing (RRBS) over whole genome bisulfite sequencing?
    a. There is never any reason to prefer RRBS over WGBS.
    b. RRBS detects more CpG sites than WGS.
    c. Only cytosines in the CCGG context can be methylated, so doing RRBS only gives you the possible methylated cytosines.
    d. Cost savings. RRBS samples a representative fraction of the genome for much less sequencing than WGBS requires.
7. Why are the results of BS-seq reported as methylation percents?
    a. Because we are sequencing a population of cells and are getting a population average, we report that as percent methylation, what percentage of the cells in the population sequenced were methylated at that position.
    b. Cytosines can only be methylated (100%) or unmethylated (0%) so it is incorrect to report their methylation status as a percent.
    c. Methylation percents tell you what percent of the samples sequenced were methylated at that position.
    d. Blah, blah
8. What is a unique feature of processing BS-seq data?
    a. Counting genes.
    b. Aligning to a reference genome.
    c. Trimming to remove poor quality reads and adapters.
    d. You must align to two genomes: the normal reference genome and a bisulfite-converted version of the reference genome.
9. What extra control MUST you have when doing ChIP-seq?
    a. Control sample in triplicate
    b. IgG
    c. PhiX spike-in
    d. Spike in cells from another organism, ex: when doing ChIP-seq on human cells, add mouse cells as control
10. What does peak calling do?
    a. Identify enriched regions that are not present in the IgG control.
    b. Single cell RNA-seq is cheaper than bulk RNA-seq.
    c. Single cell RNA-seq is cheaper than bulk RNA-seq.
    d. You can measure different cell types simultaneously in single cell RNA-seq; in bulk RNA-seq you get an average expression from all cell types sequenced.
11. How can you test for a change in ChIP-seq peaks between treatment and control?
    a. t-test
    b. linear model
    c. chi-square test
    d. permutation test

12. What is used to fragment DNA for ATAC-seq?
    a. A hyperactive, mutant Tn5 transposase
    b. Sonication
    c. Micrococcal nuclease (MNase)
    d. The DNA doesn't need to be fragmented.
13. Which of the following types of sequences is overrepresented in ATAC-seq, more so than in other NGS assays, and must be removed?
    a. mitochondrial sequences
    b. repetitive sequences
    c. ribosomal sequences
    d. sequencing adapters
14. What is an advantage of single cell ATAC-seq over single cell RNA-seq?
    a. You can measure changes in gene expression in single cell ATAC-seq, but not single cell RNA-seq.
    b. Single cell ATAC-seq data quality is better for frozen samples than single cell RNA-seq data.
    c. You can measure changes in chromatin accessibility in single cell RNA-seq, but not in single cell ATAC-seq.
    d. Single cell ATAC-seq data quality is better in mouse cells than single cell RNA-seq data.
15. Which is **NOT** a reason to combine NGS datasets?
    a. To understand how the openness of the promoters of expressed genes changes before and after drug treatment.
    b. To understand what changes in methylation are actually associated with changes in gene expression.
    c. To understand how DNA methylation changes with age.
    d. To understand what histone modifications are associated with expressed vs silenced genes.