Exam #2 (Ch 7-10)

This is a preview of the published version of the quiz

Started: Oct 16 at 8:20pm

Quiz Instructions

This is Exam #2 for Biology 366 (Fall 2024). It covers the material from the lectures covering Chapters 7-10.

You will have 75 minutes to complete the exam. Students registered with SDS will receive approved accommodations. The format is 25 questions worth 4 points each for a total of 100 points.

Although this exam is open book and notes, it must be completed independently and without assistance from another individual or ChatGPT.

Good luck!

Dr. Ellis

Question 1 4 pts

Shown below is the **coding strand** for a section of DNA that is about to undergo transcription. What would the correct sequence of transcribed mRNA be for this section?

5' AATCGTTCCA **3'**

○ **5'** ACCUUGCUAA **3'**

○ **3'** AATCGTTCCA **5'**

○ **3'** TTACGAACCT **5'**

○ **5'** UUAGCAAGGU **3'**

Question 2 4 pts

Which of the following is FALSE about the differences between DNA and RNA?

DNA is missing an oxygen at the 2' position that is present in RNA.

Just like with DNA, when RNA engages in base pairing with itself, it will always bind U to A and C to G, and never other combinations.

An easy way to differentiate RNA from DNA is that RNA utilizes the nitrogenous base uracil, while DNA utilizes thymine.

As RNA is single stranded, it can fold into complex 3D geometries that can convey catalytic function.

Question 3 4 pts

Which of the following is TRUE about mRNA processing?

The mature, fully processed mRNA will contain nucleotides which will ultimately not be translated into amino acids by the ribosome.

The 5' cap is a universal mRNA processing feature in eukaryotes and prokaryotes alike, helping facilitate export of processed mRNA from the nucleus.

A shorter poly(A) tail is typical for highly stable transcripts the cell wants to translate over a longer period of time.

RNA processing events only begin to occur after the precursor mRNA has been fully transcribed.

Question 4 4 pts

Reverse transcriptase is an enzyme that synthesizes complementary DNA (cDNA) from a fully processed mRNA. You perform an experiment using reverse transcriptase on mRNA for gene X to produce cDNA for gene X.

When comparing the DNA for gene X and the cDNA for gene X, which of the following is TRUE?

The cDNA will be significantly shorter than the DNA, as splicing will have removed introns during mRNA processing.

If you were to align the nucleotide sequences of the DNA and cDNA, there would be perfect alignment from the 5' end to the 3' end with no gaps.

The DNA and cDNA will be the same length because they are from the same gene, and are both DNA.

The DNA will be significantly shorter than the cDNA, due to the poly(A) tail added during mRNA processing.

Question 5 4 pts

Which of the following is an accurate description of eukaryotic transcription?

○ RNA polymerase requires a DNA primer to perform transcription, similarly to how DNA polymerase requires an RNA primer for DNA replication.

○ Of the two strands of DNA, only one can ever be used for transcription, with the other serving only as a coding strand that will reflect the mRNA sequence.

○ The TATA box is a specific nucleotide motif involved in the termination of transcription.

○ Due to tightly regulated control of gene expression, RNA polymerase cannot often bind directly to DNA and requires a series of general transcription factors to facilitate this process.

Question 6 4 pts

Why would it be efficient for the genetic code to be redundant and unambiguous?

○ This allows the cell to differentiate between coding (e.g., mRNA) and non-coding RNAs (e.g., tRNA, rRNA, lncRNA).

○ This allows the ribosome to recognize each codon and send out a specific signal to recruit the respective tRNA.

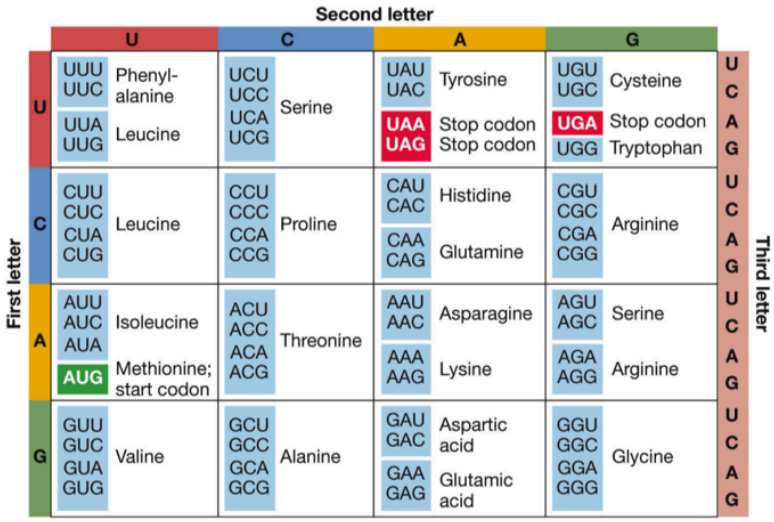
○ This allows a single tRNA to recognize multiple codons for the same amino acid, instead of needing a separate tRNA for every codon.

○ This allows the same codon to be used by multiple tRNAs to code for multiple different amino acids.

Question 7 4 pts

Given the genetic code chart below, and assuming that *the first nucleotide shown was the start site for transcription*, what would the *translated* sequence of amino acids be for the following mRNA?

5' AGCCAUGCGUGAA **3'**



Methionine - Arginine - Glutamic Acid

Methionine - Leucine - Glycine

Serine - Histidine - Alanine - STOP

Serine - Leucine - Glutamic Acid - STOP

Question 8 4 pts

Which of the following is FALSE about translation initiation?

In eukaryotes, the small ribosomal subunit recognizes the 5' cap of mRNA and scans along the nucleotide sequence until it locates the AUG start codon.

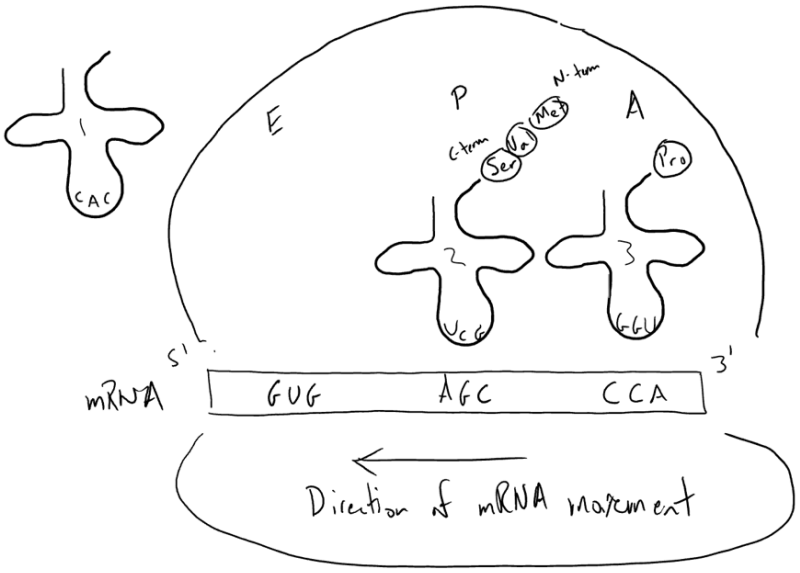
A second ribosome can bind to the 5' cap in eukaryotes and begin translation while the first ribosome is still actively translating the same mRNA molecule.

In prokaryotes, the ribosomes recognize internal sites within the mRNA allowing for the possibility for multiple different proteins to be encoded from a single mRNA.

When the tRNA charged with methionine base pairs with the start codon, it will be located in the rightmost A site of the ribosome to facilitate peptide chain elongation.

Question 9 4 pts

Given the image below, which is an accurate description of how the next step in translation elongation will occur?



○
The tRNA labeled "1" will be charged with the amino acid corresponding to the anticodon CAC, which will then be catalytically added to the growing chain on the tRNA labeled "2." This new amino acid will form the new N-terminus of the peptide.

○
The proline (Pro) on the tRNA labeled "3" will be catalytically removed from this tRNA and added onto the growing peptide chain on the tRNA labeled "2." Proline will form the new C-terminus of the peptide.

○
The proline (Pro) on the tRNA labeled "3" will be catalytically removed from this tRNA and added onto the growing peptide chain on the tRNA labeled "2." Proline will form the new N-terminus of the peptide.

○
The tRNA labeled "2" will have the growing peptide chain catalytically removed and added onto the proline (Pro) on the tRNA labeled "3." Proline will form the new C-terminus of the peptide.

Question 10 4 pts

Cycloheximide is an antibiotic that blocks the translocation step in translation, where the large ribosomal subunit shifts to move the newly uncharged tRNA from the P to the E site to facilitate continued elongation.

Which of the following would you expect to occur in the presence of cycloheximide?

○
The peptidyl transferase reaction would not be able to occur, and so the growing peptide chain would remain on the tRNA in the P site indefinitely.

○
The final product of translation would be missing several amino acids as the drug will prevent certain codons from being accessible, but a modified peptide will ultimately be produced once the ribosome locates a STOP codon.

○
The ribosome would be stalled with an uncharged tRNA in the P site and the growing peptide chain attached to the tRNA in the A site, not allowing the old tRNA to be ejected nor new tRNAs to enter.

This would dramatically slow down translation for a given ribosome, but not fully prevent it, as now only 2 of the three ribosomal sites can be used.

Question 11 4 pts

Which of the following is TRUE of the RNA molecules that make up the ribosome and the spliceosome?

The RNAs in these complexes serve as structural binding sites for tRNAs and premature mRNA, respectively, but have no catalytic role themselves.

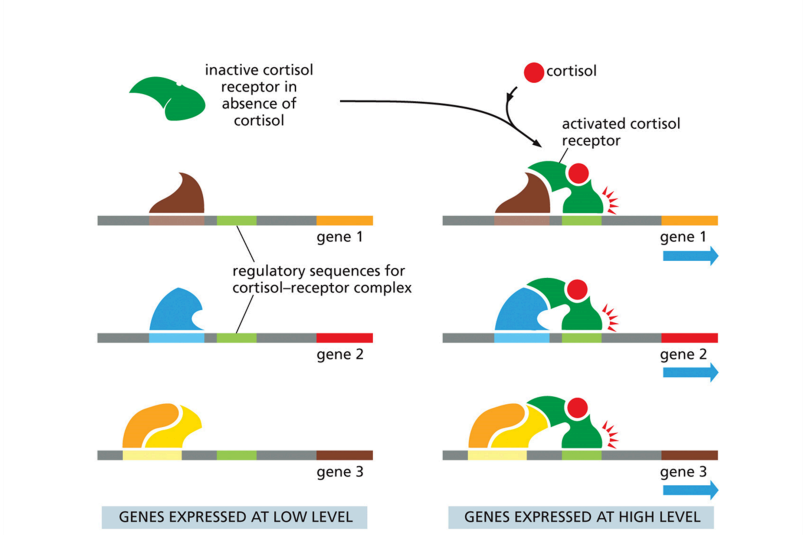
The RNAs is these complexes perform both structural and catalytic roles in translation and splicing, respectively.

The ribosome and spliceosome are made up only of proteins, and the only time RNAs are involved are in their interactions with tRNAs and mRNAs.

The primary role of these RNAs is to base pair with target mRNAs, and serve as scaffolds for protein catalysts.

Question 12 4 pts

What would be a correct interpretation of the image below:



The promoters for genes 1, 2, and 3 are likely highly similar in nucleotide sequence, allowing them to have their gene expression each regulated by a single cortisol receptor.

There is likely no change in the overall 3D shape of the cortisol receptor following cortisol binding.

○ The cortisol receptor that increases transcription of gene 1 is likely to be structurally distinct from the cortisol receptor that regulates expression of gene 2.

○ The cortisol receptor recognizes a regulatory sequence present in several distinct genes and can upregulate gene expression across all of these genes in response to cortisol binding.

Question 13 4 pts

Which of the following is FALSE regarding the concept that each of our cells can contain the same DNA but appear highly dissimilar and carry out completely different, specialized functions?

○ Patterns of chromosomal accessibility, such as via histone modifications or DNA methylation, can affect whether gene promoters and regulatory sequences are accessible in different cell types, which would alter gene expression.

○ In some cells, the nucleotide sequence of certain transcriptional regulatory sequences is different for the same gene, altering binding activity of regulators and subsequently gene expression patterns.

○ Certain promoters are only active in specific tissues/environments, and so the genes under those promoters would only be expressed in those tissues/environments and not others.

○ Gene expression is a highly complex interplay of transcriptional regulators and the overall combination of activators and repressors will vary between highly dissimilar cells.

Question 14 4 pts

Which of the following is TRUE of long non-coding RNAs (lncRNAs)?

○ lncRNAs can regulate gene expression by simultaneously base-pairing with a complementary target DNA sequence while serving as a scaffold for a transcriptional regulatory protein.

○ lncRNAs primarily regulate gene expression by complementary base-pairing with target mRNAs, leading to their degradation by the RISC complex.

○ Some, but not all, lncRNAs will be translated by the ribosome into protein.

○ lncRNAs are highly common in germ line cells, but relatively uncommon in somatic cells.

Question 15 4 pts

von Hippel-Lindau (VHL) is a ubiquitin-E3 ligase that binds to the hypoxia inducible factor (HIF) in high oxygen environments, leading to its degradation.

You are interested in developing a tool that can selectively degrade endogenous Protein Z within a cell. Which of the following tools would allow you to do this?

- A PROTAC that has HIF at one end and Protein Z on the other end.
- A PROTAC that has VHL at one end and HIF on the other end.
- A PROTAC that has HIF at one end and a specific ligand for Protein Z on the other end.
- A PROTAC that has VHL at one end and Protein Z on the other end.

Question 16 4 pts

In a famine, where food is scarce, which of the following mutations would you expect to NOT display a selective advantage?

- A mutation that allowed a bear to go into hibernation for extended periods of time compared to other species.
- A mutation that increased an organism's basal metabolic rate, causing them to break down food more rapidly.
- A mutation that increased the efficiency of fast twitch muscle fiber firing, allowing a gazelle to run more quickly.
- A mutation that led to birds with differently shaped beaks, so they can newly access otherwise inaccessible locations.

Question 17 4 pts

A spontaneous mutation occurs in a *germ line cell* of a parent that is then passed onto its offspring as a gamete.

Which of the following is TRUE?

- Only the somatic cells of the offspring will contain this mutation.
- The somatic cells of the parent will contain this mutation.
- All somatic and germ line cells of the offspring will contain this mutation.
- Only some of the somatic cells in the offspring will contain the mutation, while all of the germ line cells in the offspring will contain the mutation.

Question 18 4 pts

A child appears to have albinism, as they produce noticeably less melanin than their parents. An analysis of gene expression in genes critical to melanin production reveals Gene X is no longer being transcribed into mRNA. However, the introns, exons and length of the gene appear to be *completely unchanged* from the parent's genes.

Which of the following could explain this outcome?

A mobile genetic element existed within Gene X that was recognized by transposase, which removed a key part of the gene.

A LINE integrated into Gene X, somehow altering transcriptional efficiency.

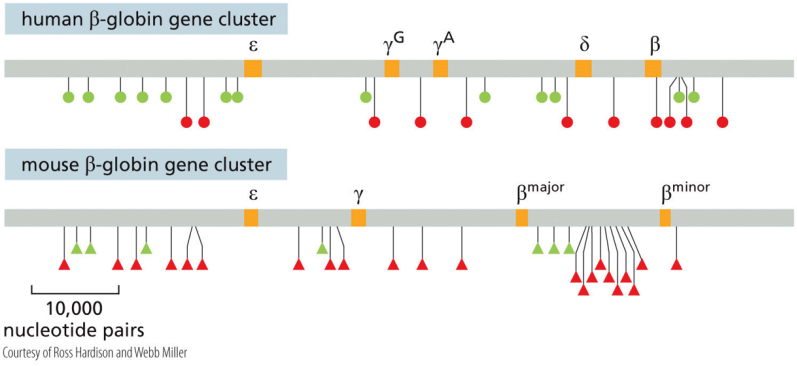
Repetitive DNA sequences flanking Gene X led to unequal crossing over and a genetic duplication event.

The mutation occurred in a regulatory DNA sequence, blocking the binding of transcriptional regulators to activate the gene.

Question 19 4 pts

In the image below, the green circles/triangles are a short interspersed nuclear element (SINE) and the red circles/triangles are a long interspersed nuclear element (LINE). The grey sections of the gene indicate introns, while the orange sections indicate exons.

Which of the following is a correct interpretation of the figure?



The pattern of SINEs and LINEs is remarkably similar between mice and humans.

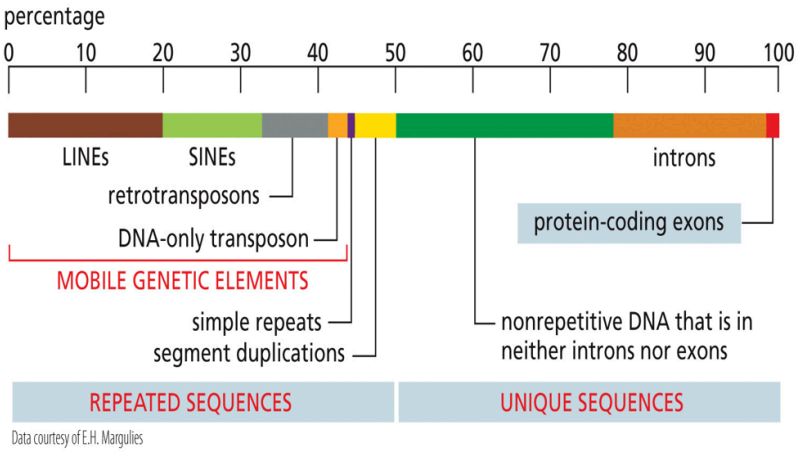
Because LINEs or SINEs only exist within intronic sections of the gene, they likely have had no effect of the speciation that differentiates mice and humans.

Purifying selection likely accounts for the lack of mobile genetic elements within exons.

LINEs are probably more critical to human identity and SINEs are more critical to mouse identity.

Question 20 4 pts

Considering the breakdown of the human genome into its core components in the image below, which of the following is FALSE?



The vast amount of non-repetitive DNA that is in neither introns nor exons highlights the complexity of regulatory control of gene expression.

Nearly half of the human genome consists of mobile genetic elements, highlighting its intrinsically dynamic nature, and accounting for evolutionary diversity.

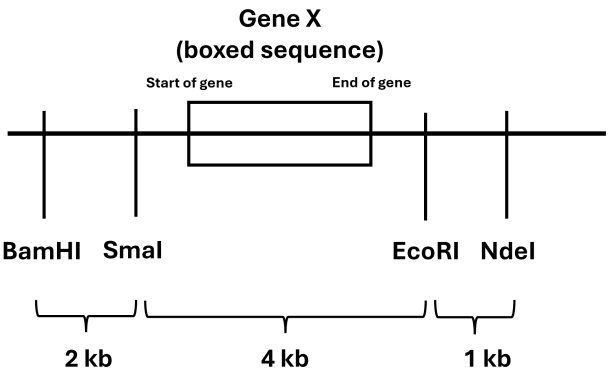
Most transposons in the human genome utilize an RNA intermediate.

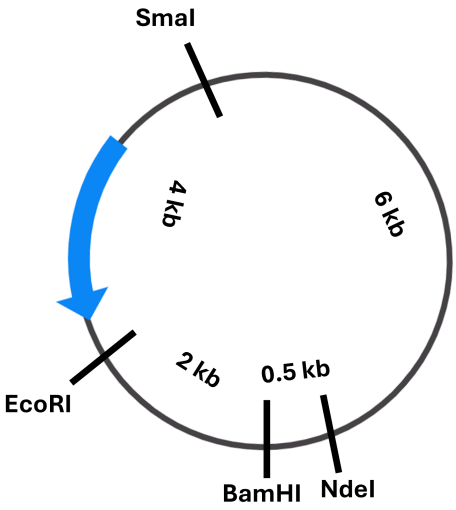
mRNA will be produced by the majority of DNA in the genome.

Question 21 4 pts

You are trying to insert Gene X (boxed sequence) into the plasmid shown below for a protein expression experiment. The blue arrow indicates the promoter that will be *required to remain in the plasmid* in order to express Gene X. The directionality of the start and the end of the gene is indicated as shown.

Which combination of restriction enzymes would lead to the correct insertion of Gene X into the plasmid which could then allow for normal gene expression?





BamHI & NdeI

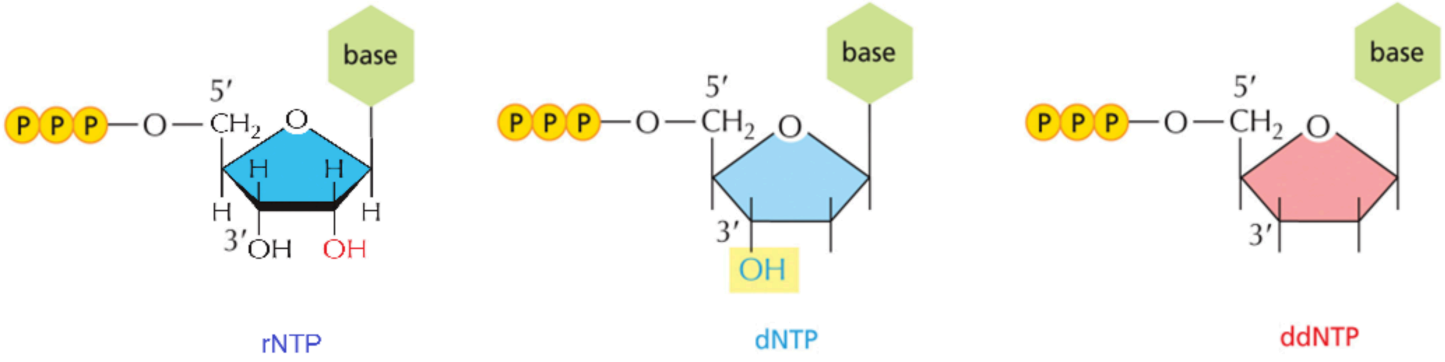
EcoRI & NdeI

SmaI & EcoRI

BamHI & EcoRI

Question 22 4 pts

Which of the following would be the correct ingredients to conduct Sanger sequencing (dideoxy sequencing)?



Only a small amount of labeled ddNTPs and an excess of dNTPs, primers are not required.

Only a small amount of labeled ddNTPs and an excess of rNTPs, primers are not required.

A forward and reverse primer for the target sequence of interest, a small amount of labeled dNTPs, and an excess of rNTPs.

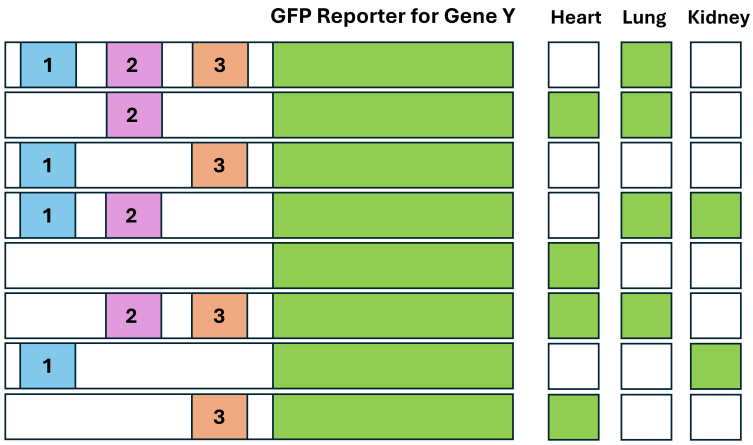
○
A forward and reverse primer for the target sequence of interest, a small amount of labeled ddNTPs, and an excess of dNTPs.

Question 23 4 pts

You are interested in studying the expression pattern of the protein produced from Gene Y. To do this, you create a reporter gene that will express GFP in tissues when Gene Y is active.

You are aware of 3 regulatory DNA sequences known to control transcription upstream of Gene Y. You perform a series of experiments in which you mutate the nucleotide sequence of combinations of these 3 regulatory sequences, and observe expression of your protein in the heart, lung, and kidney. If the box labeled 1, 2, or 3 is present consider this regulatory sequence to be unaltered, if a box is missing consider this regulatory sequence mutated and inactive.

Given the experimental results below, which of the following is FALSE concerning transcriptional regulation of Gene Y?



○
In the kidney, regulatory sequence 1 acts as a repressor and regulatory sequence 3 acts as an activator.

○
There is some other regulatory sequence not studied here that acts as an activator in the heart.

○
Regulatory sequence 2 acts as an activator in the lung.

○
Regulatory sequence 1 acts as a repressor in the heart.

Question 24 4 pts

You are interested in knocking down expression of a protein in the cell using RNA interference. Given the following section of processed mRNA that produces the protein of interest, which synthetic siRNA would accomplish this task?

5' AACCGGUUGGAAAUUUGGCAUGGCCAAAUCAG **3'**

5' AACCUUUAAACCGUACCGGU **3'**

3' CCAACCUUUAAACCGUACCG **5'**

5' AACCGGUUGGAAAUUUGGCAUG **3'**

3' AAAUUUGGCAUGGCCAAAUCA **5'**

Question 25 4 pts

In creating a transgenic mouse model, the first round of breeding will produce *chimeric mice*, with some of the cells containing the transgene and some of the cells not containing the transgene.

Which of the following is TRUE?

Breeding two chimeric mice that each have the transgene present in somatic cells only could produce offspring containing the transgene.

Breeding these chimeric mice with normal mice could produce a pup that has the transgene present in all of its cells if the parent had the transgene present in the germ line.

It is possible that some of the mice already produced in this first found of breeding will already have the transgene in all of their cells.

Breeding a chimeric mouse which has the transgene present in the germ line with a normal mouse will produce chimeric mice, where some cells contain the transgene and other cells do not contain the transgene.

Quiz saved at 8:20pm Submit Quiz