Supplemental Material

CBE—Life Sciences Education

Sieke *et al.*

Supplemental Materials

Supplemental Table 1. Changes in student ideas from pre- to post-activity. The number of students relative to their pre-activity ideas (rows) and post-activity ideas (columns)is shown, as well as the percent of pre-activity ideas in each post-activity category. Of note, 67% of students who initially responded with mixed ideas, and 64% of all students who initially responded with only incorrect ideas before the activity,responded with fully correct ideas post-activity (highlighted in blue).

		Post-activity		
		Correct (n = 208)	Mixed (n = 21)	Incorrect (n = 29)
Pre-activity	Correct (n = 182)	158 (87%)	14 (8%)	10 (5%)
	Mixed (n = 39)	26 (67%)	5 (13%)	8 (20%)
	Incorrect (n = 36)	23 (64%)	2 (6%)	11 (30%)

Supplemental Table 2. Changes in student ideas from post-activity to final exam multiple-choice question. The number of students relative to their post-activity ideas (rows) and exam question correctness (columns) is shown, as well as the percent of post-activity ideas in each exam category. 90% of all students who initially responded with mixed, and 62% of students who initially responded with only incorrect ideas before the activity, responded with fully correct ideas post-instruction (highlighted in blue).

		Exam Question	
		Correct (n = 225)	Incorrect (n = 31)
Post-activity	Correct (n = 206)	188 (91%)	18 (9%)
	Mixed (n = 21)	19 (90%)	2 (10%)
	Incorrect (n = 29)	18 (62%)	11 (38%)

Supplemental Figure 1. Non-coding mutation classroom activity. Students completed this activity in class. They worked in groups to answer how mutations in different regions of a DNA strand, indicated by letters A through G, would affect transcription initiation, amount or sequence of mRNA, translation initiation, and the amount or sequence of protein. This figure shows the entire table (excerpted in Figure 2), with example responses shown in red.

Using the sequence diagrammed below: (1) Explain how a single base deletion mutation at each of the regions indicated could affect the process of transcription and the amount of mRNA made. (2) Explain how this single base deletion could affect the process of translation and/or the amount or sequence of the protein product by filling out the table below.
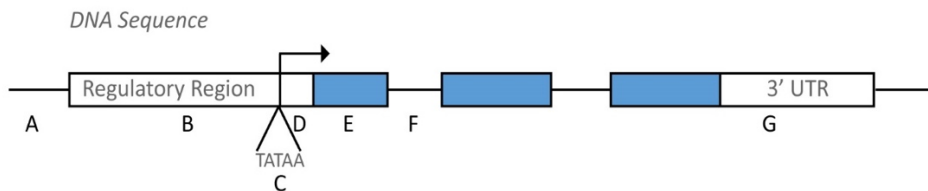
	Transcription begins?	Amount or sequence of mRNA different? (explain)	Translation begins?	Amount or sequence of protein different? (explain)
A	Yes	No	Yes	No
B	Yes	Yes: could be increased or decreased	Yes	No: unless you get more/less protein because had more/less mRNA
C	No (promoter will not be recognized)	Yes: unlikely that mRNA can be transcribed, so no product	No	No: mRNA not produced, so no protein produced
D	Yes	No	Maybe	Since this is the 5' UTR, this could affect the export of mRNA out of the nucleus, so there may be no translation or less of the product
E	Yes	The mRNA will be one nucleotide shorter, but otherwise not different	Yes	Since the mRNA is shorter due to a frameshift in an exon, the amino acid sequence will be different, and protein function could be different
F	Yes, unless this is a regulatory sequence	mRNA sequence will not be different, but it's possible that product levels will be different if mutation is in a regulatory sequence	Yes	No effect unless the level of mRNA is different to start with, or unless a splice site has been altered (which would then affect the sequence of amino acids)
G	Yes	No	Yes	mRNA will be less stable, so it will degrade, and thus, there will likely be less protein made (but no change to the sequence)

Supplemental Figure 2. Non-coding mutation in-class clicker questions.
After working on the activity (Supplemental Figure 1) for 5 to 10 minutes, students responded to clicker questions asking how (A) region A, (B) region B, and (C) region E influence transcription and translation (excerpt shown in Figure 2). The correct answer is indicated by the red arrow. In the case of the translation question in (B), although A is the most common correct answer, B is also correct under circumstances where significant changes in mRNA transcription may affect translated protein levels; this is a good conversation-generator in group discussion.

A You discover a single base deletion in region A of this DNA sequence.
Regarding transcription, this mutation will likely:

- A) Prevent transcription initiation at the TATAA box.
- B) Result in an alteration to the mRNA sequence.
- C) Result in an increase or decrease in the amount of mRNA transcribed.
➡ D) Have no effect on transcription or the mRNA sequence.

You discover a single base deletion in region A of this DNA sequence.
Regarding translation, this mutation will likely:

➡ A) Have no effect on translation or the sequence of amino acids produced.
- B) Increase or Decrease the amount of protein translated.
- C) Result in shorter protein due to shorter mRNA sequence.
- D) Result in an alteration of the amino acid sequence due to the frameshift mutation.

B You discover a single base deletion in region B of this DNA sequence.
Regarding transcription, this mutation will likely:

- A) Prevent transcription initiation at the TATAA box.
- B) Result in an alteration to the mRNA sequence.
➡ C) Result in an increase or decrease in the amount of mRNA transcribed.
- D) Have no effect on transcription or the mRNA sequence.

You discover a single base deletion in region B of this DNA sequence.
Regarding translation, this mutation will likely:

➡ A) Have no effect on translation or the sequence of amino acids produced.
- B) Increase or Decrease the amount of protein translated.
- C) Result in shorter protein due to shorter mRNA sequence.
- D) Result in an alteration of the amino acid sequence due to the frameshift mutation.

C You discover a single base deletion in region E of this DNA sequence.
Regarding transcription, this mutation will likely:

- A) Prevent transcription initiation at the TATAA box.
➡ B) Result in an alteration to the mRNA sequence.
- C) Result in an increase or decrease in the amount of mRNA transcribed.
- D) Have no effect on transcription or the mRNA sequence.

You discover a single base deletion in region E of this DNA sequence.
Regarding translation, this mutation will likely:

- A) Have no effect on translation or the sequence of amino acids produced.
- B) Increase or Decrease the amount of protein translated.
- C) Result in shorter protein due to shorter mRNA sequence.
➡ D) Result in an alteration of the amino acid sequence due to the frameshift mutation.

Supplemental Figure 3: Co-occurrence of student ideas calculated as the fraction of the total number of student ideas.

These diagrams plot the frequency of the idea category within the dataset, illustrated by the size of the node (percent shown below category titles), and the frequency of co-occurring ideas as a fraction of the total number of student ideas recorded. This frequency of co-occurrence is illustrated by lines of varying thickness and saturation. (A) The co-occurrence network diagrams of the entire computer-training dataset (left) and all mixed ideas (right). (B) The co-occurrence network diagrams of the pre- (left) and post-instruction (right) student ideas. The data output on the AACR website shows co-occurrence network diagrams of ideas calculated in this way, but you can access the co-occurrences normalized by the presence of each code by viewing the co-occurrence bar graphs by coded category.
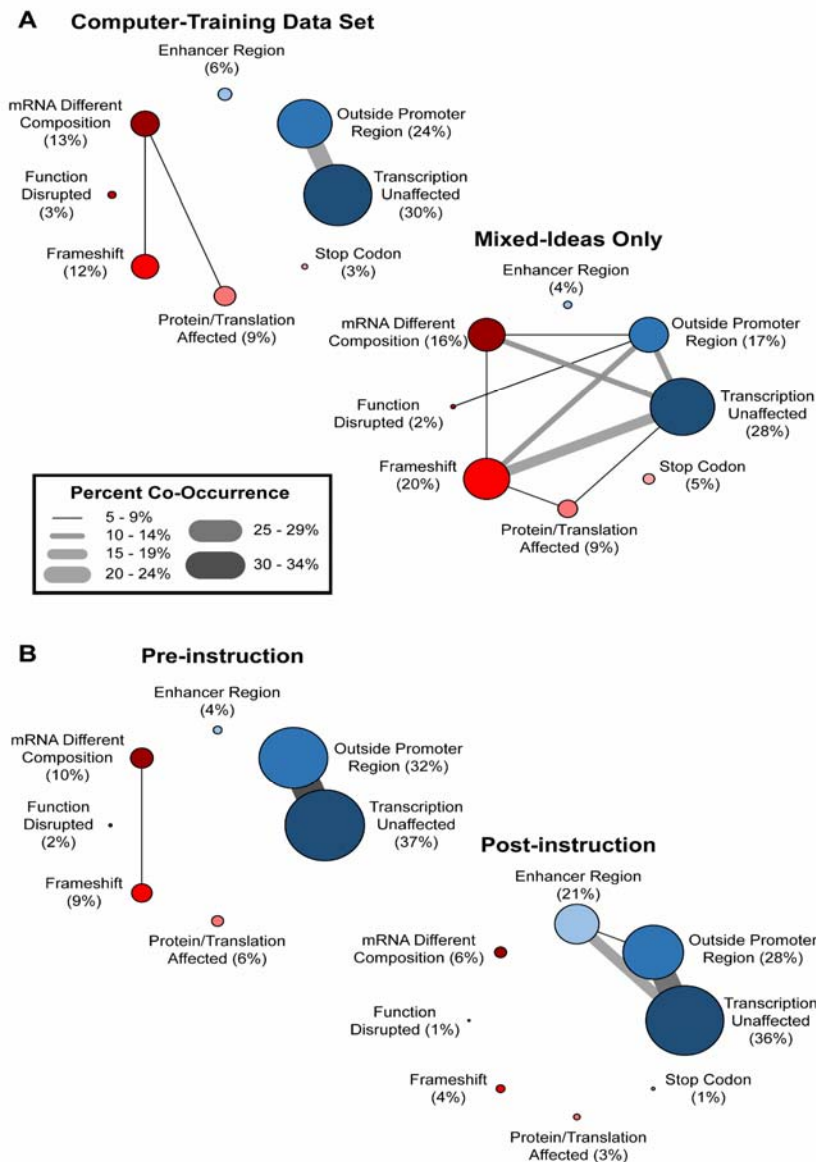
Supplemental Figure 4. Exam question

Below is a diagram of a gene. The shaded boxes represent exons. Region B is the only known regulatory region. A 7-base insertion mutation in region A would most likely lead to what consequence for the mRNA and amino acid sequences?
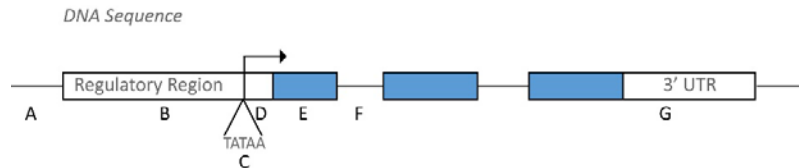
A) a change in the amino acid sequence due to a frameshift
B) a longer mRNA sequence
C) a longer mRNA sequence and a change in the amino acid sequence due to a frameshift
D) a change in the rate of transcription
E) a change in the rate of translation
F) a change in the rate of both transcription and translation
G) no change (Correct answer)