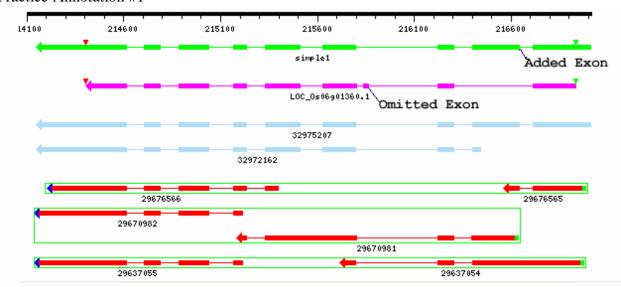
Name _	Class Period Date
	Gene Annotation Activity Six: Gene Annotation Practice Session
Briefly describe what is wrong with each of the practice annotations in this section and describe how the annotations should be modified	
1.	
2.	
3.	
4.	
4.	

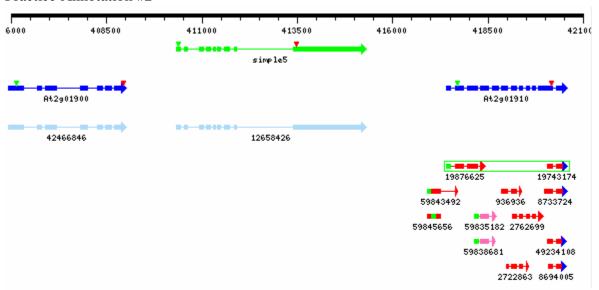


## Practice Annotation #1



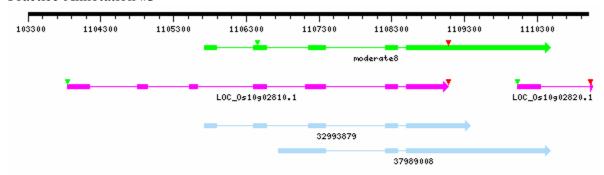
In this example you can see the UCA (green) differs from the pink TIGR TU annotation is several locations. First, both the 5' and 3' ends have been extended, as supported by the cDNA. Second a small exon has been ommitted, while a larger exon has been added.

## Practice Annotation #2



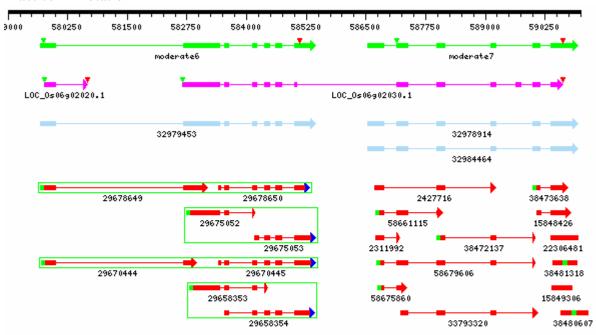
In this example the two GenBank annotations are supported by evidence However, there is also cDNA evidence that suggest another gene is present, but has not been annotated. The green UCA structure in this image is based on that cDNA sequence.

## Practice Annotation #3



In this example the UCA structure is supported by exons from two different cDNA structures. The first four exons in the UCA model are from cDNA 32993879 and the last exon is from cDNA 37989008. The UCA structure spans the gap between the two TIGR TU annotations and results in the fusion of these gene structures.

## Practice Annotation #4



This annotation would actually require two separtat annotations and submissions. First, the two TIGR TU annotations need to be fused as shown by the green UCA structure on the left, moderate6. Also, the larger TIGR TU annotation needs to be split as shown by the green UCA structure moderate7.



The Evidence Plot and the Evidence Table

- 1. The Evidence Plot
- 2. The entire structure (all of the exons) are added to the (green) gene model
- 3. First click and it is selected (not the other exons on the same structure) on the second click it is deselected.
- 4. The coordinates of the exon correspond to nucleotide bases in the genome, basically defining where the exon starts and stops in the sequence a chromosome
- 5. The Max Sim Score and the number of cDNA and EST structures that contain the exons in question
- 6. A color block represents a groups of variants for the same exon, so only one should be selected for each gene model
- 7. Exons