HOW TO USE A GENOME BROWSER - WORKSHEET

1. Using the ORF information website, record the chromosome number, start and stop coordinates, and strand for your proto-gene.

2. Using the genome browser, what is the length of your proto-gene in base pairs? How many amino acids is this?

3. Is your proto-gene on the + or - strand?

4. What is the nucleotide sequence of the second codon for your proto-gene?

5. What is the name of the annotated gene closest to the 3' end of your proto-gene? What is its function? Is this gene on the same strand as your proto-gene? (If your proto-gene is on the + strand, 3' is the region to the right of your proto-gene, otherwise if your proto-gene is on the - strand, 3' is the region to the left of your proto-gene.)

6. What is the name of the annotated gene closest to the 5' end of your proto-gene? What is its function? Is this gene on the same strand as your proto-gene? (If your proto-gene is on the + strand, 5' is the region to the left of your proto-gene,

otherwise if your proto-gene is on the - strand, 5' is the region to the right of your proto-gene.)

7. Does it appear that ribo-seq reads are spread evenly across your proto-gene or are there spatial patterns and trends you observe? For example, do there tend to be more reads early in the proto-gene sequence or towards the end?

8. In general, do annotated genes tend to be translated more or less than proto-genes?

9. What is the translation confidence score for your proto-gene?

10. Do you find transcripts covering your proto-gene in either YPD or galactose? Do you notice any difference between the two conditions?

11. Are there certain regions of your proto-gene that are more conserved than others?

12. How does the nucleotide conservation of your proto-gene compare relative to those of the closest 3' and 5' annotated genes?