MODULE 1: INTRODUCTION TO THE GENOME BROWSER: WHAT IS A GENE?

ANSWER SHEET

Questions

Q1. How many genes are there in contig1?

Q2. What are the names of these genes?

Q3. Which gene has the largest span (i.e. the largest distance between the start and end of the gene)?

Q4. What is the relationship between the bases displayed when the arrow is pointed to the left versus when it is pointed to the right?

Q5. Why do you think the bases are displayed in this way in the Genome Browser?

Q6. How many exons does tra-RA contain?

Q7. How many introns does tra-RA contain?

Q8. Why do you think it takes three lines to display the amino acid information? Hint: remember that a codon is specified by three bases, e.g. CCG = Proline (circled in Figure 12).

Q9. Based on the screenshot shown in **Figure 22**, which reading frame contains the amino acid sequence for the second coding exon of tra-RA?

Q10. Does frame +2 have an ORF in the coding region of this exon? What about frame +1 and frame +3?

Q11. Given that 3 of the 64 possible codons are stop codons, what is the chance of having a stop codon at any given position, assuming that the sequence is random?

Summary Question 1. How many exons and introns are present in this gene?

Summary Question 2. What is the orientation of this gene relative to contig1? How do you know? Where are the start codon and the stop codon - give the base position numbers (coordinates) of the start and the stop codon)?

Bonus: Take a little time to explore some of the other evidence tracks on the browser.

Bonus Question 1. While looking at contig1 (size 11,000 bp), put the "GC Percent" track on **full.** What sort of pattern do you see, relative to the map of the genes? What can you conclude about gene structure?