Biol 322 F12 Final Study Problems – some answers

1. a. Since the F1 animals are wildtype, these two mutant strains complement each other; therefore, the mutation in roller #1 is in a different gene than the mutation in roller #2.
b. First consider what you would expect in the F2 if the two genes were assorting independently: 9/16 wildtype and 7/16 roller (assumes a roller double mutant is roller as well). Now consider that the two genes are closely linked and recombination rarely occurs:

A= wt allele of roller #1 gene
a = roller mutation

B= wt allele of roller #2 gene
b = roller mutation

Using the conventions for linked genes:
Roller #1 aB/aB X Roller #2 Ab/Ab → WT F1 aB/Ab → self

→ assume no recombinants: ¼ aB/aB ¼ Ab/Ab ½ aB/Ab = 50% roller & 50% WT

NOTE about genotype conventions:

- AaBb indicates that the worm is het for both genes but does not indicate whether the genes are known to be linked or assorting independently
- Aa;Bb indicates that the worm is het for two genes that are on different chromosomes
- AB/ab or Ab/aB indicates that the genes are on the same chromosome: on the left and right sides of the slash are the genotypes of each homolog. The genotypes of the parents tell us the allele configurations of the homologs. ONLY use this type of genotype designation if you know or suspect the genes are linked

2. Answer is d. **<u>Be sure that you understand why each of the other options are incorrect.</u>**

6. (i) answer is c. (ii) True: one X-linked gene + (at least*) four autosomal. *Don't know about the dominant mutation. It could be defining a 6th gene or it could be allelic with one of the other genes. (iii) b. This mutation does not show an X-linked inheritance pattern so it cannot be allelic with #3.

7. Review RNAi lecture.

8. Review models lecture

9. Part 1
a. & b The key to the initial analysis in this problem is to remember that males are haploid and their genotypes will directly reflect the meiotic output of mom.
c. hypothesis: single gene trait following mendel's principle of segregation
chi square = 5 df=1 p= 0.0253 = significant Take the straight statisticians line here and in explain in words what the p value says and how it helps you assess your observations
d. In this part of the question, consider alternative explanations for the deviation from expected assuming that your hypothesis is correct

Part 2   RNAi OK here as well as targeted knockouts in known genes. Might want to start with genes that are known to affect eye development in other organisms (distantly related OK here). Does knocking out a single gene produce a squinty phenotype?