MCB 140 Midterm 1
Spring 2016

Name:……..
Student ID #:……..

PLEASE PRINT YOUR NAME AND STUDENT ID# ON EACH PAGE OF THE EXAM. WIRELESS DEVICES OF ANY SORT ARE NOT PERMITTED! You are welcome to use pen or pencils. Please look over the entire exam, so you don't spend too much time on hard questions, leaving easy questions unanswered. Please check your answers to make sure that they make sense. To help us give partial credit, show your work and briefly state any assumptions that you make.

Best of luck!

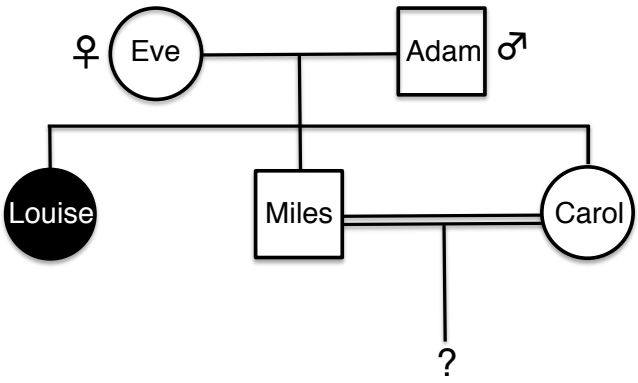
Question 1 (20) ……
Question 2 (25) ……
Question 3 (10) ……
Question 4 (25) ……
Question 5 (40) ……
Question 6 (30) ……

TOTAL …….. / 150

Name: **student ID #:**

Question 1:
Your pet hamsters Adam and Eve have 3 children: Louise, Carol and Miles. It turns out that Louise has an amazing talent: she can play the trumpet like a jazz prodigy! However, neither of her siblings nor her parents have this talent. One day, you realize that Carol and Miles are going to have a baby hamster. You are excited about this new baby, but also curious to know whether he/she could play the trumpet one day, just like her auntie Louise. The pedigree below summarizes the inheritance pattern of the trumpet-talent trait. Assume that the trait is contributed by one gene and is completely penetrant.

● exhibits trumpet-talent trait



a) (4 points) What are the genotypes for Adam and Eve? Use + for the wild type allele and a letter of your choice for the trumpet-talent trait.

b) (8 points) What is the probability that Miles is a heterozygote given that he cannot play the trumpet?

c) (8 points) What is the probability that the unborn baby hamster will exhibit the trumpet-talent trait?

Name: **student ID #:**

Question 2:

Wild type jewel beetles have brown eyes and brown bodies. You have isolated mutations in three new beetle genes. The mutation **SP** confers a dominant spotted-body phenotype. The mutation **gr** confers a recessive green-body phenotype. The mutation **bl** confers a recessive black-eye phenotype. The **+** sign indicates wild type allele. You start by crossing two true-breeding mutant strains to produce F1 females heterozygous for **SP**, **gr** and **bl**. You then cross these F1 females to true-breeding black-eyed, green-bodied males. The phenotypes of 3000 progeny are scored below:

phenotype	number
SP + +	73
+ bl gr	71
+ bl +	2
SP + gr	4
SP bl +	1350
+ + gr	1386
SP bl gr	55
+ + +	59

a) (5 points) What are the genotypes of the two true-breeding parental lines?

b) (10 points) Please draw a simple map, indicating the distances between **Sp**, **gr** and **bl**. Include the map distances in relevant units.

Name: **student ID #:**

c) (10 points) You identify a new dominant mutation, eyeless (**EY**). You want to map **EY** relative to **bl**, but your lab mate says: "No way! You obviously can't score the presence of black or brown eyes in an eyeless beetle!!!" You don't agree and you cross a true-breeding eyeless beetle to a true-breeding black-eyed beetle. You next cross the resulting F1 female to a true-breeding black-eyed male. You record the phenotypes of 200 progeny. What is the map distance between **EY** and **bl**?

phenotype	number
eyeless	102
black-eyed	78
brown-eyed	20

Question 3 (10 points): Please indicate whether each statement below is true (T) or false (F):

T **F** Homologous chromosomes are segregated from each other in mitosis.

T **F** In most organisms, mitotic and meiotic recombination occurs at similar rates.

T **F** In meiosis, recombination occurs after DNA replication.

T **F** In humans, homolog non-disjunction only occurs during female meiosis.

Name: **student ID #:**

Question 4: Loss of function mutations in the *cut wings* gene on the X chromosome give rise to cut-winged flies. You have isolated 2 different mutations in the *cut wings* gene: a dominant mutation named **CT-1** and a recessive mutation named **ct-2**. Both mutations give rise to cut winged flies and you establish true-breeding lines for each mutant.

a) (4 points) If you cross true-breeding lines of **CT-1** females with **ct-2** males, what fraction of the progeny is expected to have normal wings? Do you expect to observe a different outcome if you perform a reciprocal cross? Explain your logic briefly.

b) (7 points) A cut-winged male from the **CT-1** line is crossed to a true-breeding wild-type female. What type of wings will the female and male progeny have?

c) (7 points) One of the female progeny from the cross in part **(b)** is mated to a cut-winged male from the **ct-2** line. What fraction of the cut-winged progeny from this cross will be female?

Name: **student ID #**

d) (7 points) A cut-winged female from the cross in **(c)** is crossed to a wild type male. Among 500 male progeny produced by this cross, 5 of them have normal looking wings. What is the distance between **CT-1** and **ct-2**? Use proper units to indicate the genetic distance.

Question 5: You decide to study how yeast cells grow on melibiose, a type of disaccharide. You find that both melibiose and glucose regulate the expression of Mel1, the main enzyme used in melibiose utilization. In cells grown without melibiose, Mel1 is not expressed, but when melibiose is added to the growth medium, Mel1 is induced. Mel1 is not expressed in cells grown in medium that contains both melibiose and glucose. You have isolated loss of function mutations in three different genes that alter Mel1 regulation, called **A**$^{-}$, **B**$^{-}$ and **C**$^{-}$. All three mutations are recessive and none of the mutations are linked. Mel1 expression in wild type and in each of the three mutants are shown below:

strain	Mel1 expression		
	-glucose -melibiose	-glucose +melibiose	+glucose +melibiose
Wild type	–	+	–
A^{-}	–	+	+
B^{-}	+	+	–
C^{-}	–	–	–

a) (9 points) Fill out the chart below, stating (i) whether the given gene affects regulation by melibiose or glucose and (ii) whether the gene is a positive or a negative regulator of the *MEL1* gene.

Gene name	Affects regulation by melibiose or glucose?	Positive or negative regulator ?
A		
B		
C		

Name: **student ID #:**

Next you cross **B**$^{-}$ mutant to **C**$^{-}$ mutant. After tetrad dissection and evaluation of spore clones for Mel1 expression in the presence or absence of melibiose, you observe the following tetrad classes:

TYPE 1	TYPE 2	TYPE 3
constitutive	uninducible	constitutive
uninducible	uninducible	constitutive
regulated	regulated	uninducible
uninducible	regulated	uninducible

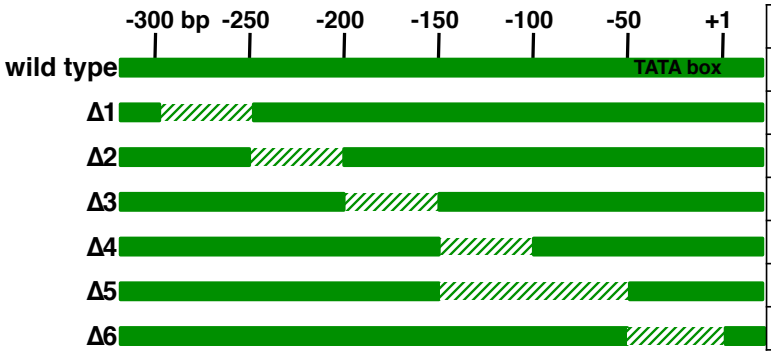
b) (6 points) Indicate which of the tetrad types are parental (**PD**), nonparental ditype (**NPD**) and tetratype (**T**)

c) (6 points) What is the phenotype of the **B**$^{-}$ **C**$^{-}$ double mutant? Briefly explain your logic (i.e. how you came up with your answer).

d) (6 points) Draw a model showing the interactions between the different regulatory factors encoded by **B** and **C**. **Please include the *MEL1* gene in your model and indicate where and how melibiose acts in the regulatory pathway.**

Name: **student ID #:**

Next you construct a series of 50 to 100 base-pair (bp) deletions within the *MEL1* gene promoter. The ability of each of these deletions to express Mel1 in cells grown on different sugars is shown below. Striped boxes indicate the deleted sequences from the promoter region. +1bp indicates the transcription start site for the maltase gene. TATA box sequence is located between -50 bp and +1 bp region. + indicates Mel1 expression, – indicates no Mel1 expression.



+melibiose	+melibiose & glucose
+	–
+	–
+	+
–	–
+	–
+	–
–	–

e) (4 points) Based on this analysis, which region of the promoter is likely to contain a melibiose response element?

f) (5 points) When you clone gene **A**, your sequence analysis reveals that this gene is likely to encode a DNA-binding protein. Assuming that the product of gene **A** binds to the promoter region of the *MEL1* gene, where is it most likely to bind? Explain your logic briefly.

g) (4 points) Which of the deletion mutants shown above demonstrate that the distance between the upstream activation sequence and the TATA box has little or no effect to the expression of the *MEL1* gene?

Name: **student ID #:**

Question 6: The proteins that normally transport arginine into yeast cells also transport a toxic amino acid analog called canavanine. You isolate 9 canavanine resistant mutants (Can^R) based on their ability to grow on minimal plates supplemented with canavanine. Mutants 1 through 4 are of Mat*alpha* mating type and mutants 5 through 9 are of Mat**a** mating type. The table below summarizes the pairwise crosses between different mutants as well as crosses to wild type. (+) indicates growth and (–) indicates no growth on canavanine plates.

(–): no growth on canavanine (+): growth on canavanine		Strains of mating type Mat*alpha*				
		1	**2**	**3**	**4**	**wild type**
Strains of mating type Mat**a**	**5**	–	–	–	–	–
	6	–	–	–	+	–
	7	+	+	+	+	+
	8	+	–	+	–	–
	9	–	–	–	–	–
	wild type	–	–	–	–	–

a) (6 points) Indicate which of the Can^R mutants are dominant and which ones are recessive.

b) (10 points) Sort the mutations into complementation groups and indicate which mutations are in the same complementation group. Indicate any ambiguity in the assignment of complementation groups, in addition to the fact that any complementation test with mutant 7 is inconclusive.

Name: **student ID #:**

c) (8 points) Propose a simple experiment to address whether strains 5 and 9 belong to the same complementation group.

d) (6 points) You decide to plate the diploid strains generated from crosses between wild type and mutant 7 as well as between wild type and mutant 8 on plates lacking arginine (-Arg). Do you expect to see growth on –Arg plates in either of these strains? Explain your logic briefly.

e) BONUS!!! Propose a genetic strategy other than whole genome sequencing to identify the nature of the mutation causing canavanine resistance in strain 7. Hint: you need to use some kind of a yeast genomic library.

THE END!