MCB 140 Exam 1
Spring 2015

Name:……..
Student ID #:……..

Please print your name and student ID# on each page of the exam. A portion of the exams will be photocopied after being graded. You are welcome to use a one-page front and back hand-written notes. WIRELESS DEVICES OF ANY SORT ARE NOT PERMITTED! 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 (30) ……
Question 2 (35) ……
Question 3 (30) ……
Question 4 (35) ……
Question 5 (20) ……

TOTAL …….. / 150

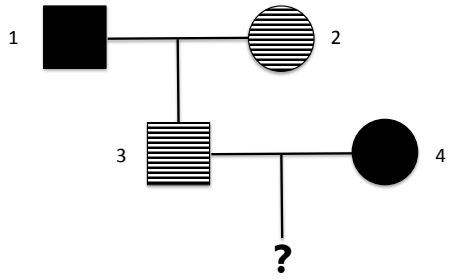
Name: **student ID #:**

Question 1) Huntington's disease is an autosomal dominant disorder. The pedigree below shows inheritance of Huntington's disease in a family. Also present in this family is a particular blood antigen, which is a recessive trait. The **Huntington's disease locus** and the **locus for the blood antigen** are located on the same chromosome, chromosome 4, and are **5 cM apart**. Circles represent females and squares represent males. Assume complete penetrance and that no new mutations occur in the families shown.


affected with Huntington's disease


exhibits recessive blood antigen

None of the individuals shown below are both affected with Huntington's disease and exhibit the blood antigen.



a) **(5 points)** Indicate the genotype of each individual shown in the pedigree, 1 through 4. If there is more than one possibility, write down all the possible genotypes for a given individual. Use **+** for wild-type allele for a given gene. Please write down the genotype next to each numbered individual shown in the pedigree. **H**: allele for Huntington's disease, **a**: allele for the blood antigen.

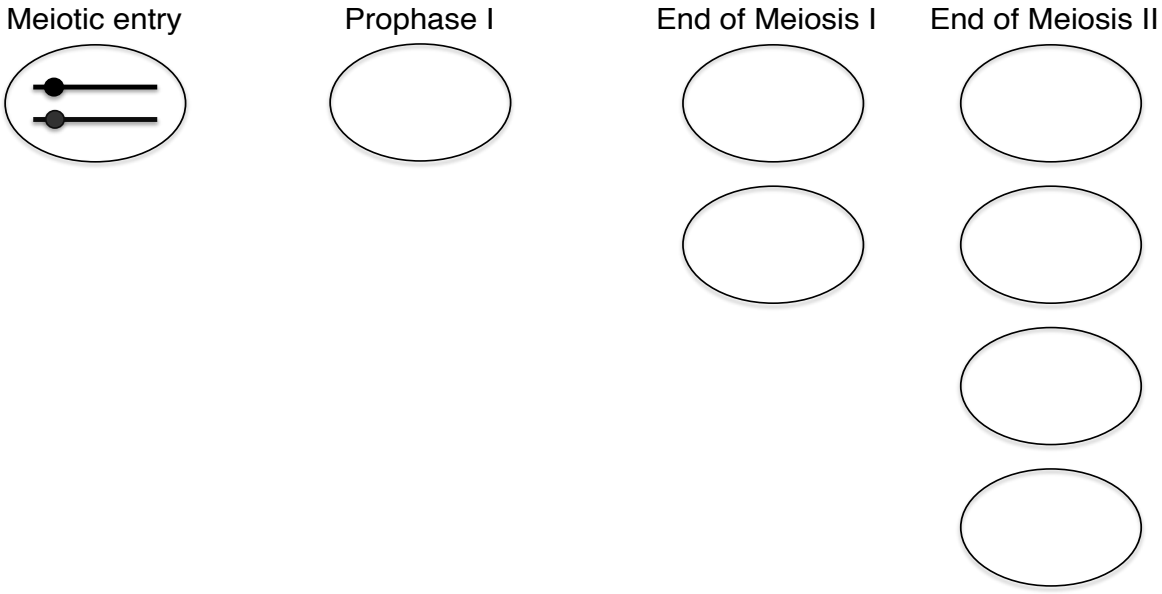
b) **(5 points)** What is the probability that the indicated grandchild (shown as "?") will develop Huntington's disease?

c) **(5 points)** What is the probability that the indicated grandchild (shown as "?") will both exhibit the recessive blood antigen and develop Huntington's disease? Show your work.

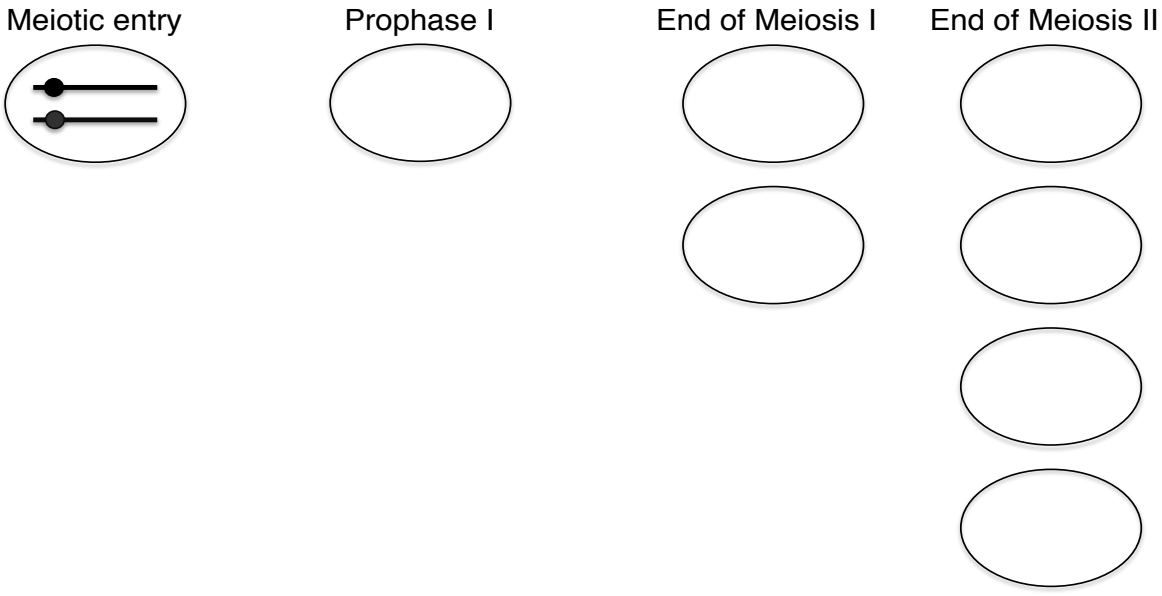
Name: **student ID #:**

d) (15 points) The schematic below is intended to represent the behavior of the chromosome 4 homologs (shown in black bars) during meiosis for the individual # 3. Fill out the empty circles by drawing chromosome 4 homologs in each stage of meiosis, paying attention to the number of chromatids in each stage. Use X to indicate the site of crossover, only during the stage of meiosis that it actually occurs. Write down the allele information for each locus, for each homolog pair. Use **+** for wild-type allele for a given gene. **H**: allele for Huntington's disease, **a**: allele for the blood antigen.

Meiosis without a crossover between H and a loci:



Meiosis with a single crossover between H and a loci:

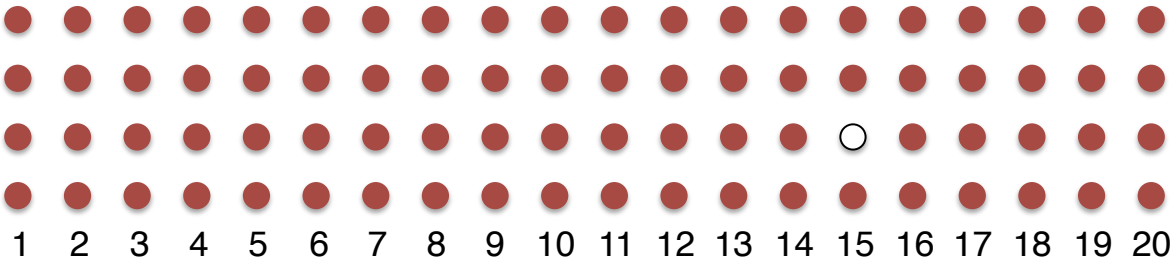


Name: **student ID #:**

Question 2) In budding yeast, mutations in some of the enzymes involved in adenine biosynthesis results in the formation red colonies due to accumulation of an intermediate in the pathway, which is a red pigment.

a) (5 points) You have isolated two different red colored mutants in haploid strains of different mating types, which you call *ade1*$^-$ and *ade2*$^-$. When either *ade1*$^-$ or *ade2*$^-$ mutant is mated to wild type, the resulting diploid forms white colonies, like those of wild type yeast. When the *ade1*$^-$ mutant is mated to the *ade2*$^-$ mutant, the resulting diploid makes red colonies. From these observations, what conclusions can you make about the *ade1*$^-$ and *ade2*$^-$ mutations and the relationship between them.

b) (5 points) Next you sporulate the diploid that was formed by mating *ade1*$^-$ and *ade2*$^-$ haploid strains. From the 20 tetrads shown below, only one spore clone is white, the rest are red.

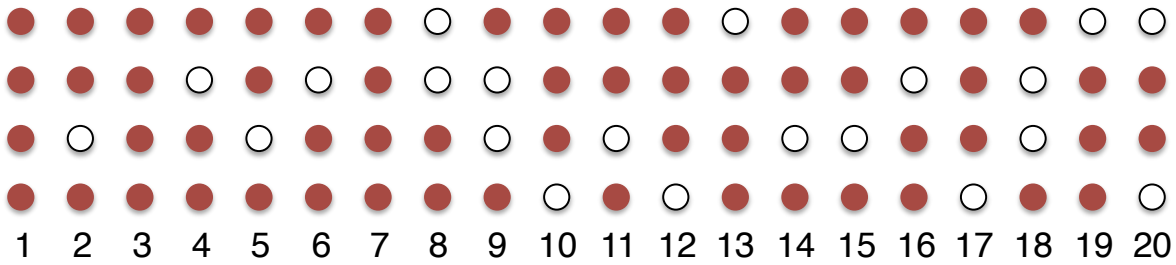


What does this result tell you about the linkage and distance between *ade1*$^-$ and *ade2*$^-$ mutations?

c) (5 points) Next you isolate a new red colored mutant, which you call *ade3*$^-$. When the *ade3*$^-$ mutant is mated to wild type, the resulting diploid is red. You mate *ade3*$^-$ mutant to *ade1*$^-$ mutant, and the resulting diploid is also red. What do these results tell you about the *ade3*$^-$ mutant and the relationship between *ade3*$^-$ and *ade1*$^-$ mutations?

Name: **student ID #:**

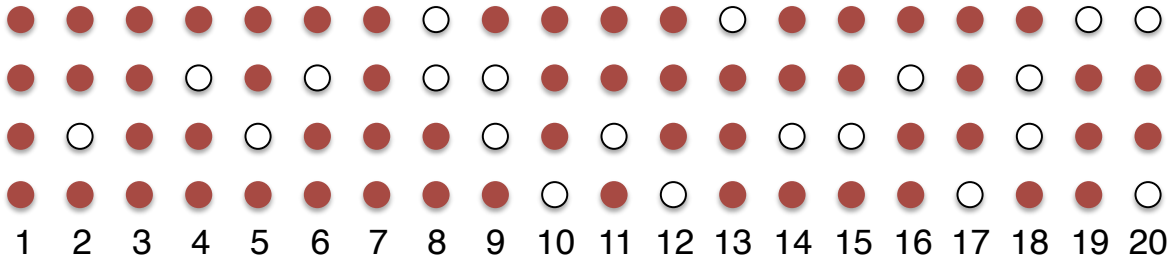
d) (5 points) When you sporulate the diploid that was formed by mating *ade3*$^{-}$ and *ade1*$^{-}$ haploid strains, you obtain the results shown below:



From the 20 dissected tetrads shown above, how many tetrads of each class parental ditype (PD), nonparental ditype (NPD) and tetratype (T) are there? Indicate the class for each tetrad by writing down the class type (PD, NPD or T), above each tetrad.

e) (5 points) What do the results from this tetrad analysis tell you about the relationship between the *ade3*$^{-}$ and *ade1*$^{-}$ mutations? Can these mutations be in the same gene?

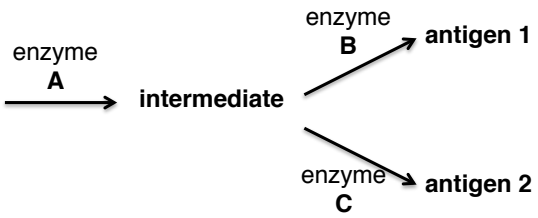
f) (5 points) Suppose that you wanted to do some experiments with an ade3^{-} ade1^{-} double mutant. On the image of the tetrads from the cross between the ade3^{-} and ade1^{-} mutants, circle each spore clone that you can be sure is ade3^{-} ade1^{-} double mutant, without any further testing.



g) (5 points) If you crossed an *ade3*$^{-}$ mutant to an *ade2*$^{-}$ mutant and dissected 18 tetrads, how many tetratype (T) tetrads would you expect to see? Explain your reasoning briefly.

Name: **student ID #:**

Question 3) Consider two different antigens produced on the blood cells of wild type mice according to the biosynthetic pathway shown below:



Mice that are homozygous for recessive mutations that block the production of enzyme A (genotype **aa**) do not make either antigen 1 or antigen 2. Mice homozygous for recessive mutations in enzyme B (genotype **bb**) do not make antigen 1. Mice homozygous for recessive mutations in enzyme C (genotype **cc**) do not make antigen 2. Genes encoding enzymes A, B and C are located on different chromosomes.

a) (5 points) Two different true breeding strains of mice have been isolated that **do not make either antigen 1 or antigen 2**. When an individual from one strain is crossed with an individual from the other strain, **all of the F1 mice produce both antigens**. Write down the genotypes for the parental strains and the resulting F1 progeny. Use A, B, C to designate the wild type and a, b, c to designate the mutant alleles of the three enzymes.

b) (18 points) Mice of the AaBbCc genotype are crossed to one another. The possible phenotypes for the F2 progeny are shown below. Please write down the possible genotypes for each phenotypic class and the fraction of F2 with a given phenotype. **For dominant traits, denote the genotype such that it includes both the homozygous and heterozygous individual (e.g use A– instead of AA or Aa)**

Phenotype	Genotype	Fraction of F2
antigen 1+, antigen 2+		
antigen 1+, antigen 2-		
antigen 1-, antigen 2+		
antigen 1-, antigen 2-		

Name: **student ID #:**

d) (7 points) Suppose you wanted to test whether a given F2 mouse that does not express either antigen is defective in the production of **Enzyme A**. What genotype would you choose for a mouse used for such a test cross of the F2 mouse? Describe the possible outcomes of this cross and how you would interpret them.

Question 4) In *C.elegans,* vulva is formed from a group of precursor cells called the vulval precursor cells (VPCs). Normally, 3 VPCs participate in forming the vulva. If additional VPCs take on the vulval fate, extra vulvae will form (multivulva or **Muv** phenotype). If no VPCs take on the vulva fate, no vulva will form (Vulvaless or **Vul** phenotype). In a genetic screen for additional mutations affecting the signaling pathway that determines vulval development in *C. elegans*, you have isolated a new mutant named ***m***.

a) (5 points) In order to characterize ***m*** in more detail, you generate homozygous and heterozygous worms and compare them to genotypically wild-type worms (+/+) and obtain the following results:

+/+ and **+/*m*** worms have a normal vulva.
m*/*m worms display a Vulvaless (Vul) phenotype.

Is ***m*** inherited in a recessive or dominant manner? Is ***m*** likely a gain-of-function (gof) or a loss-of-function (lof) mutation?

b) (9 points) After confirming that the mutation mentioned above defines a new gene, you name it *egl-65*. Now you want to determine where *egl-65* acts in the vulval development pathway. The known components of the vulval development pathway are shown below (pointed arrow indicates activation and blunt arrow indicates inhibition.)

lin-3 → ***let-60*** ⊣ ***lin-1*** ⊣ **Vulval cell fate**

In the chart below, fill out the expected phenotypes for the gain-of-function (gof) or loss-of-function (lof) mutations in these genes (i.e indicate whether they will display a Muv or a Vul phenotype.)

	lof	**gof**
lin-3		
let-60		
lin-1		

Name: **student ID #:**

c) (12 points) Next you decide to construct double mutants, each homozygous for a loss-of-function allele of *egl-65* and a mutation in one of the known vulval determination genes. Assuming you have all the mutants below in your collection, indicate all the double mutant combinations that you'd choose for further analysis. Pick only the combinations that will allow you to interpret something meaningful about the relationship between *egl-65 and* the other genes in the vulval development pathway. Explain your reasoning briefly.

i) *let-60 (gof)* and *egl-65 (lof)*

ii) *let-60 (lof*) and *egl-65 (lof)*

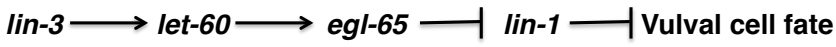
iii) *lin-3 (gof)* and *egl-65 (lof)*

iv) *lin-3 (lof)* and *egl-65 (lof)*

v) *lin-1 (gof)* and *egl-65 (lof)*

vi) *lin-1 (lof)* and *egl-65 (lof)*

d) (9 points) From your epistasis test(s) above, you conclude that *egl-65* acts between *let-60* and *lin- 1* and draw the following pathway:



What phenotypes that you see in the double mutant worms will allow you to make this conclusion?

Answers below this line for question 4 won't be graded, use this space as a worksheet if you need to.

Name: **student ID #:**

Question 5) You decided to establish a new insect species as a genetic model system and have identified three different recessive traits. For simplicity, let's designate the phenotypes of the three distinct recessive traits **a**, **b**, and **c** and the corresponding wild-type phenotypes with "**+**". Two different true breeding lines are crossed and the F1 progeny all appear as wild type. These F1 progeny are then crossed to individuals from a true breeding line that has all three recessive traits (**a b c**) and 100 progeny from this cross are analyzed. The phenotypes and numbers are as follows:

Phenotype	Number
+ + +	6
a b c	4
a + c	36
+ b +	34
+ b c	9
a + +	11
+ + c	0
a b +	0

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

b) (5 points) Why are the **+ + c** and **a b +** phenotypic classes missing? Please provide a brief explanation.

c) (10 points) Please draw a simple map, indicating the chromosomal position of a, b and c. Include the relevant map distances in cM as part of your answer.

d) (BONUS!!!) Given the map distances in (c), if F1 insects are crossed to one another, what frequency of the resulting F2 progeny would have all three recessive traits (phenotype a b c)? Hint: Assume that both single and double crossovers can occur.