Bio393: Genetic Analysis **Name:**_____
Midterm (10 pages, 120 points)

Question 1 (12 points):
Alfred Sturtevant kept careful track of horse coat colors on his farm when he was growing up. He observed that a black mare crossed to a chestnut stallion produced all bay offspring. Mating these bay offspring gave rise to offspring of four different coat colors: black, bay, chestnut, and liver. Crossing liver offspring back to the black mare gave all black offspring. Crossing liver offspring back to the chestnut stallion gave all chestnut offspring. Explain how coat color is being inherited in horses and what the genotypes of each color are.

Question 2 (6 points):
Using linkage mapping, you determined the genetic distance between A and B is 150 cM. What is the minimum number of intermediate markers between A and B that you would need to make this estimate possible? Please explain your reasoning.

Question 3 (6 points each):
Over the past summer, you mentored a high school student in the lab. He worked hard but did not take any notes or keep a lab notebook. You had him look for suppressors of a mutant phenotype caused by a point mutation resulting in a null phenotype (not necessarily a stop codon mutation).

(a) Propose a cross to differentiate revertants (or back suppressors) from extragenic suppressors and how the outcomes of the cross would show either option.

(b) Is it possible that he isolated an intragenic suppressor? Explain why or why not.

Question 4 (6 points):
Please give two reasons why it is difficult to identify the mutation causing the mutant phenotype of interest just from sequencing the whole genome of a wild-type and a mutant organism.

Question 5 (18 points):

On a recent hike in the woods, you start digging through some rotting logs (highly recommended). You see some terrestrial isopods of the species *Porcellio scaber*, including an entire log populated by isopods that are bright purple. You begin to dream of Norwestern-marketed isopod pets for every new Wildcat. Oh the profits! You collect a bunch of individuals along with some wild-type looking (grayish) individuals from another log.

Back in the lab, you cross purple by purple isopods. You only get purple isopods. You also cross gray by gray isopods, and you only get gray isopods. Feeling confident that you have pure-breeding strains, you cross a purple isopod with a gray isopod. All of the F1 individuals are gray. You then mate these gray F1 individuals back with the purple parent (a test cross). After a lot of work, you are excited to count 1000 offspring. The color phenotype data are below.

Phenotype	Number
Gray	513
Purple	482
Red	3
Blue	2

(a, 12 points) Describe a genetic model for how the four color phenotypes are controlled and the relationships between the gene(s).

You identify a rare white isopod in a culture of your gray true-breeding strain. You generate a true-breeding white strain of isopods. When you cross white and purple isopods, you get gray isopods again. You allow these F1 isopods to interbreed. In the next generation, you see gray, purple, and white isopods again (along with rare red and blue isopods) at a 9:3:4 ratio. When you cross these purple isopods, you get white isopods about two-thirds of the time.

(b, 6 points) Assuming that white mutants have an absence of red and blue pigments, what can you say about the relationship of the white gene and the previous color gene(s)?

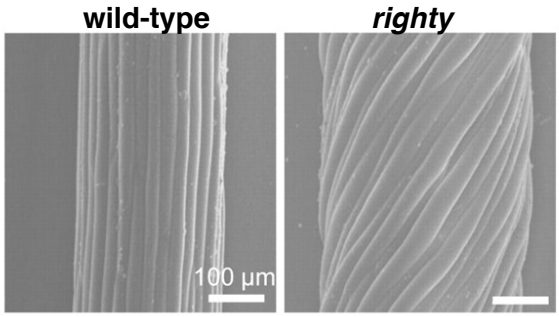
Question 6 (18 points):
Your poli sci roommate does not believe all this mumbo jumbo about genetics. He says that there is no way for you to predict the phenotypes of offspring from the following cross.

$$\frac{x^- \; y^- \; z^-}{+ \; + \; +} \times \frac{x^- \; y^- \; z^-}{x^- \; y^- \; z^-}$$

You look up on wikipedia that the x, y, and z genes are all linked. Also, x is 20 map units from y, and y is 10 map units from z. The gene order is x, y, z. Fill out the table below for numbers of offspring with each phenotype (Total offspring = 1000).

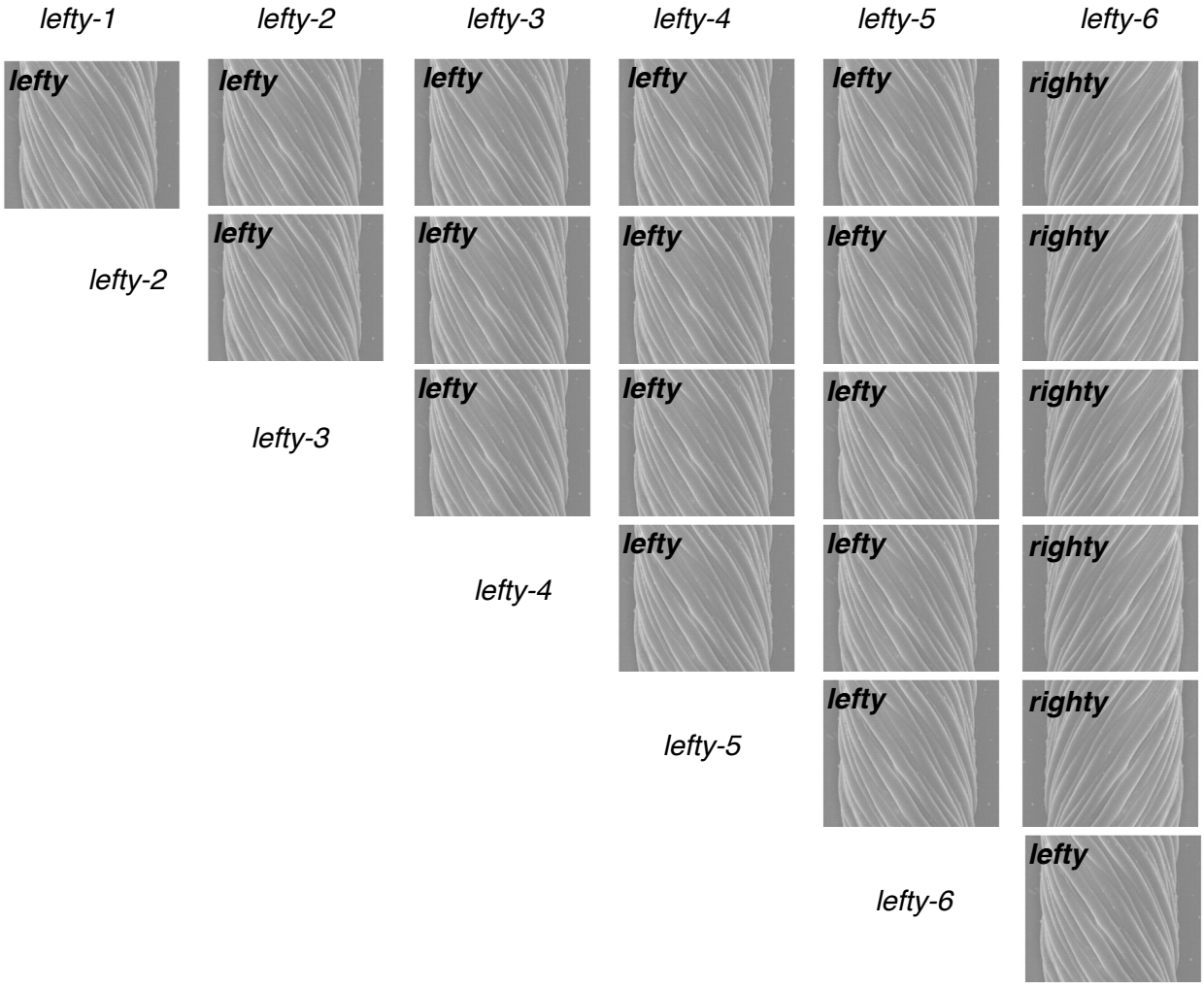
Phenotype	Number of offspring
x y z	
+ + +	
x y +	
+ + z	
x + +	
+ y z	
x + z	
+ y +	

Question 7 (36 points):
The mustard weed *Arabidopsis thaliana* is a powerful model to understand many plant traits. You are interested in the development of the axial organ or stem because you want to genetically engineer taller plants. In wild-type plants, the axial organ grows with little twisting and the flowers are radially symmetric. The post-doc you work with gave you a mutant strain that has a right-handed helical twist (*righty*).



(a, 12 points) Write out a genetic screen to identify suppressor mutants (*sup*) of *righty*.

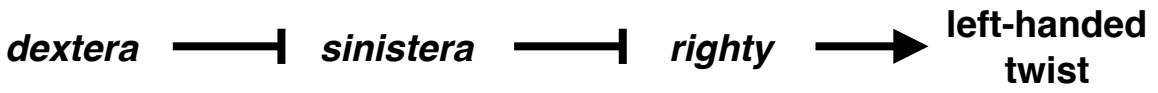
(b, 6 points) You are incredibly successful in your screen and identify six independent suppressor mutants. Interestingly, all of them have a recessive left axial twist phenotype (*lefty* mutants). Describe the number of genes and which mutants share a common perturbation of function.



(c, 4 points): Please describe what a mutant with a dominant left axial twist look like in the crosses in part (b).

(d, 4 points): You PI tells you to keep screening because you have not found many of the genes for control of axial organ outgrowth orientation. Given the data you have so far, why would she say that statement?

(e, 10 points) A collaborator sends two other mutants to you so that you can build a genetic pathway for control of axial organ twist. Using your original *righty* mutant and the two new mutants, right-handed twist (*dextera*) and left-handed twist (*sinistera*), along with the genetic relationships shown below, fill out the single and double mutant phenotypes that would give you this pathway. Describe the reasoning behind your double mutant phenotypes after the table.



Genotype	Phenotype
righty	
dextera	
sinistera	
dextera; sinistera	
dextera; righty	
sinistera; righty	

Question 8 (4 points each):
With respect to a typical genetic screen, please answer the following questions:

(a) What types of mutations are **most** common and why?

(b) What type of phenotype is **least** common and why?

(c) What phenotype is **most** often observed and why?

Please fill out the post-midterm survey at bio393.andersenlab.org