Lab 3 Rubric:

Section	Excellent	Good	Acceptable	Needs Improvement	Not Done
1: Understanding the data	Correctly identifies the following: Sequenced on Illumina HiSeq 2500 by Seoul National University Plant Developmental Genetics Laboratory, Department of Plant Science. Identifies that these are paired reads. The conditions are: Normal conditions, ABA (plant hormone) present, high saline conditions, and dehydration conditions. Describes the full conditions for these. Identifies the genes as ROS1 and DML2&DML3.	Correctly identifies the following: Sequenced on Illumina HiSeq 2500 by Seoul National University Plant Developmental Genetics Laboratory, Department of Plant Science. Identifies that these are paired reads. The conditions are: Normal conditions, ABA (plant hormone) present, high saline conditions, and dehydration conditions. Does not fully describe these conditions. The genes are *ros1-3* and *dml2;3*. Identifies that these are DNA	Correctly identifies the following: Sequenced on Illumina HiSeq 2500 by Seoul National University Plant Developmental Genetics Laboratory, Department of Plant Science. Does not identify that these are paired reads. The conditions are: Control, aba, saline, and dry. Does not fully describe these conditions. The genes are *ros1-3* and *dml2;3*. Identifies that these are DNA demethylases.	Incorrectly identifies the following: Sequenced on Illumina HiSeq 2500 by Seoul National University Plant Developmental Genetics Laboratory, Department of Plant Science The conditions are: Control, aba, saline, and dry. Does not fully describe these conditions. The genes are *ros1-3* and *dml2;3*. Doesn't identify the function of the genes.	Has no answer for at least 3 of these questions.

	These are all DNA demethylases. And involved in the gene silencing.	demethylases.			
2: Mapping the Reads	Explains that we used the ENSEMBL transcriptome as it is well annotated, and meant we didn't have to build it ourselves, which takes a long time. Identifies benefits for using an annotated transcriptome and for using a *de novo* transcriptome. Gives supported explanations of when you want to build your own transcriptome and when you don't. Examples include that you want to build your own when one doesn't exist, or when you are trying to identify new splicing events or	Explains that we used the ENSEMBL transcriptome as it is well annotated, and meant we didn't have to build it ourselves, which takes a long time. Identifies benefits for using an annotated transcriptome and for using a *de novo* transcriptome. Gives not well-supported explanations of when you want to build your own transcriptome and when you don't. Examples include that you want to build your own when one doesn't exist, or when you are trying to identify new	Explains that we used the ENSEMBL transcriptome as it is well annotated, and meant we didn't have to build it ourselves, which takes a long time. Identifies benefits for using an annotated transcriptome and for using a *de novo* transcriptome. Gives incorrect explanations of when you want to build your own transcriptome and when you don't. Does not identify that there are reads with no transcript, and that these are likely errors or contamination. Can not identify	Does not explain that we used the ENSEMBL transcriptome as it is well annotated, and meant we didn't have to build it ourselves, which takes a long time. Identifies benefits for using an annotated transcriptome and for using a *de novo* transcriptome. Gives incorrect explanations of when you want to build your own transcriptome and when you don't. Does not identify that there are reads with no transcript, and that these are likely errors or contamination.	Does not answer 3 or more of the questions.

	new genes. Identifies that there are reads with no transcript, and that these are likely errors or contamination. Should identify that it would take a few hours, but could be sped up by running these on a cluster where they can be run on more cores.	splicing events or new genes. Identifies that there are reads with no transcript, and that these are likely errors or contamination. Should identify that it would take a few hours. Does not identify that running these on a cluster where they can be run on more cores could speed it up.	that it would take a few hours. Does not identify that running these on a cluster where they can be run on more cores could speed it up.	Can not identify that it would take a few hours. Does not identify that running these on a cluster where they can be run on more cores could speed it up.	
3: Analyzing the data	They identify 2 groups in PCA1/2 and 4 in PCA 2/3. Identify that in 1/2 it is the presence or absence of osmotic stress and that in 2/3 it is the 4 different growth conditions. Indicate that the largest difference in gene expression is the conditions they are grown in, not the genetic	They identify 2 groups in PCA1/2 and 4 in PCA 2/3. Identify that in 1/2 it is the presence or absence of osmotic stress and that in 2/3 it is the 4 different growth conditions. Describe that osmotic stress conditions have similar changes as compared to unstressed or	They identify 2 groups in PCA1/2 and 4 in PCA 2/3. Identify that in 1/2 it is the presence or absence of osmotic stress and that in 2/3 it is the 4 different growth conditions. Does not discuss why these separations arise. Identifies 5 genes. Describes the size	They identify 2 groups in PCA1/2 and 4 in PCA 2/3. Identify that in 1/2 it is the presence or absence of osmotic stress and that in 2/3 it is the 4 different growth conditions. Does not discuss why these separations arise. Identifies 5 genes. Does not describe	They identify 2 groups in PCA1/2 and 4 in PCA 2/3. Does not discuss why these separations arise. Identifies fewer than 5 genes. Does not describe the size of the change and the level of significance of the change. Does not describe how these genes are related

	background. Also, osmotic stress conditions have similar changes as compared to unstressed or stressed by hormones. Identifies 5 genes and explains why they chose these. Describes the size of the change and the level of significance of the change. Describes how these genes are related to each other (same or different direction of change). Graphs are present and annotated clearly with a clear caption.	stressed by hormones. Identifies 5 genes. Describes the size of the change and the level of significance of the change. Describes how these genes are related to each other (same direction of change). Graphs are present and annotated thought not clearly with an unclear caption.	of the change and the level of significance of the change. Describes how these genes are related to each other (same direction of change). Graphs are present though not annotated or with a caption.	the size of the change and the level of significance of the change. Does not describe how these genes are related to each other (same direction of change). Graphs are present though not annotated or with a caption.	to each other (same direction of change). Graphs are present though not annotated or with a caption.
4: Interpreting the results	Identifies their top 5 genes correctly. Discusses the biological role of these genes. Reasons from the functions why they	Identifies their top 5 genes correctly. Discusses the biological role of these genes. Does not reason from the functions why	Identifies their top 5 genes correctly. Discusses the biological role of these genes superficially or incorrectly. Does	Identifies their top 5 genes incorrectly. Discusses the biological role of these genes superficially or	Identifies their top 5 genes incorrectly or not at all. Does not discuss the biological role of these genes. Does not reason

	might be influenced by osmotic stress. Discusses how the data supports their reasoning. Describes an effective a way to test their hypothesis experimentally or computationally. Appropriate figures are provided with annotations and clear captions.	they might be influenced by osmotic stress. Discusses how the data supports their reasoning. Describes a way to test their hypothesis experimentally or computationally that is not appropriate. Appropriate figures are provided with annotations and clear captions.	not reason from the functions why they might be influenced by osmotic stress. Does not discuss how the data supports their reasoning. Describes a way to test their hypothesis experimentally or computationally that is not appropriate. Appropriate figures are provided without annotations and clear captions.	incorrectly. Does not reason from the functions why they might be influenced by osmotic stress. Does not discuss how the data supports their reasoning. Describes a way to test their hypothesis experimentally or computationally that is not appropriate. Appropriate figures are not provided.	from the functions why they might be influenced by osmotic stress. Does not discuss how the data supports their reasoning. Does not propose a way to test their hypothesis experimentally or computationally. Appropriate figures are not provided.
Overall	Written clearly in paragraph form. Writing has a flow. Scientific vocabulary is correctly used.		Written in paragraph form. Writing is stilted. Scientific vocabulary is used incorrectly.		Written in bullet form. Writing is stilted. Scientific vocabulary is used incorrectly.
Citations	All tools and sources used are properly cited.		All sources and some tools used are cited.		No citations