Lab 1 Rubric:

Section	Excellent 4 points	Good 3 points	Needs Improvement 2 points	Not Acceptable 1 points	Not present 0 points
1: Results Multiplier 1x	Contains a graph that clearly shows the results of the class Graph has a descriptive caption	Contains a graph that clearly shows the results of the class Graph does not have a descriptive caption	Contains a table of the results of the class Table has a descriptive caption	Contains a table of the results of the class Table does not have a descriptive caption	No results from class presented
1: Analysis Multiplier 2x	Identified strip 1 as a negative control. Indicates the presence or lack of correlation between PTC, thiourea, and sodium benzoate tasting Expresses a hypothesis about the binding of thiourea or sodium benzoate the protein that recognizes PTC. Provides evidence to support this hypothesis/conclusion.	Indicates the presence or lack of correlation between PTC, thiourea, and sodium benzoate tasting Expresses a hypothesis about the binding of thiourea or sodium benzoate the protein that recognizes PTC. Does not provide evidence to support this hypothesis/conclusion. **OR** Did not identify strip 1 as a negative control.	Indicates the presence or lack of correlation between PTC, thiourea, and sodium benzoate tasting Expresses a hypothesis about the binding of thiourea or sodium benzoate the protein that recognizes PTC. Does not provide evidence to support this hypothesis/conclusion. **AND** Did not identify strip 1 as a negative control.	Did not identify strip 1 as a negative control. Does not indicate the presence or lack of correlation between PTC, thiourea, and sodium benzoate tasting Expresses a hypothesis about the binding of thiourea or sodium benzoate the protein that recognizes PTC. Does not provide evidence to support this hypothesis/conclusion.	No analysis included
1: Genetics Multiplier 4x	Accurately describes the position of the gene on the chromosome as toward the centromere and with no other genes nearby. Correctly identifies the number of exons as 1 and introns as 0. Indicates 4 common SNPs, three of which have phenotypes associated with them. rs10246939 chimp C, C minor allele at 47-48%, associated with phenotype rs1726866 chimp C, C minor allele at 49-50%, associated with phenotype rs145970530 Chimp T, C minor allele at 1%, not associated with phenotype rs713598 Chimp C, C minor allele at 44-45%, associated with phenotype. Contains population variance for 1 of the phenotype associated SNPs.	Accurately describes the position of the gene on the chromosome as toward the centromere and with no other genes nearby. Correctly identifies the number of exons as 1 and introns as 0. Indicates 4 common SNPs, three of which have phenotypes associated with them. Does not contain full information about the 4 common SNPs. Contains population variance for 1 of the phenotype associated SNPs. Contains a hypothesis about what their haplotype is.	Does not contain full information about the 4 common SNPs. Is missing ANY of the following: Accurately describes the position of the gene on the chromosome as toward the centromere and with no other genes nearby. Correctly identifies the number of exons as 1 and introns as 0. Indicates 4 common SNPs, three of which have phenotypes associated with them. Contains population variance for 1 of the phenotype associated SNPs. Contains a hypothesis about what their haplotype is.	Does not contain full information about the 4 common SNPs. Is missing ANY TWO of the following: Accurately describes the position of the gene on the chromosome as toward the centromere and with no other genes nearby. Correctly identifies the number of exons as 1 and introns as 0. Indicates 4 common SNPs, three of which have phenotypes associated with them. Contains population variance for 1 of the phenotype associated SNPs. Contains a hypothesis about what their haplotype is.	Does not contain full information about the 4 common SNPs. Is missing ANY THREE of the following: Accurately describes the position of the gene on the chromosome as toward the centromere and with no other genes nearby. Correctly identifies the number of exons as 1 and introns as 0. Indicates 4 common SNPs, three of which have phenotypes associated with them. Contains population variance for 1 of the phenotype associated SNPs. Contains a hypothesis about what their haplotype is.

	Contains a hypothesis about what their haplotype is.				
2: LCT Multiplier 2X	Identifies that it is on chromosome 2, going toward centromere. Start position: 135, 837,180 end position: 135,787,849 It has 17 exons and 16 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	ONE of the following is missing or incomplete Identifies that it is on chromosome 2, going toward centromere. Start position: 135, 837,180 end position: 135,787,849 It has 17 exons and 16 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	TWO of the following are missing or incomplete Identifies that it is on chromosome 2, going toward centromere. Start position: 135, 837,180 end position: 135,787,849 It has 17 exons and 16 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	THREE of the following are missing or incomplete Identifies that it is on chromosome 2, going toward centromere. Start position: 135, 837,180 end position: 135,787,849 It has 17 exons and 16 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	FOUR of the following are missing or incomplete Identifies that it is on chromosome 2, going toward centromere. Start position: 135, 837,180 end position: 135,787,849 It has 17 exons and 16 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.
2: BRCA1 Multiplier 2X	Identifies that it is on chromosome 17, going toward centromere. Start position: 43,125,483 end position: 43,045,629 It has 22 exons and 21 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	ONE of the following is missing or incomplete Identifies that it is on chromosome 17, going toward centromere. Start position: 43,125,483 end position: 43,045,629 It has 22 exons and 21 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated..	TWO of the following are missing or incomplete. Identifies that it is on chromosome 17, going toward centromere. Start position: 43,125,483 end position: 43,045,629 It has 22 exons and 21 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	THREE of the following are missing or incomplete Identifies that it is on chromosome 17, going toward centromere. Start position: 43,125,483 end position: 43,045,629 It has 22 exons and 21 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	FOUR of the following are missing or incomplete Identifies that it is on chromosome 17, going toward centromere. Start position: 43,125,483 end position: 43,045,629 It has 22 exons and 21 introns At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.
2: IL4R Multiplier 2X	Identifies that it is on chromosome 16, going toward telomere. Start position: 27,313,913 end position: 27,364,778 Highly alternatively spliced. 9-11 exons possible. At least 1 SNP associated with a phenotype is identified with minor allele frequency given. Population differences are indicated.	ONE of the following is missing or incomplete Identifies that it is on chromosome 16, going toward telomere. Start position: 27,313,913 end position: 27,364,778 Highly alternatively spliced. 9-11 exons possible. At least 1 SNP associated with a phenotype is identified with minor allele frequency given.	TWO of the following are missing or incomplete. Identifies that it is on chromosome 16, going toward telomere. Start position: 27,313,913 end position: 27,364,778 Highly alternatively spliced. 9-11 exons possible. At least 1 SNP associated with a phenotype is identified with minor allele frequency given.	THREE of the following are missing or incomplete Identifies that it is on chromosome 16, going toward telomere. Start position: 27,313,913 end position: 27,364,778 Highly alternatively spliced. 9-11 exons possible. At least 1 SNP associated with a phenotype is identified with minor allele frequency given.	FOUR of the following are missing or incomplete Identifies that it is on chromosome 16, going toward telomere. Start position: 27,313,913 end position: 27,364,778 Highly alternatively spliced. 9-11 exons possible. At least 1 SNP associated with a phenotype is identified with minor allele frequency given.

		Population differences are indicated..	Population differences are indicated.	Population differences are indicated.	Population differences are indicated.
3: Gene of choice Multiplier 3X	Explains why gene is of interest. Identifies where in genome gene is found including chromosome and which direction on chromosome. At least 1 SNP associated with a phenotype is identified with allele frequencies given. Population differences are indicated.	ONE of the following is missing or incomplete Explains why gene is of interest. Identifies where in genome gene is found including chromosome and which direction on chromosome. At least 1 SNP associated with a phenotype is identified with allele frequencies given. Population differences are indicated.	TWO of the following is missing or incomplete Explains why gene is of interest. Identifies where in genome gene is found including chromosome and which direction on chromosome. At least 1 SNP associated with a phenotype is identified with allele frequencies given. Population differences are indicated.	THREE of the following is missing or incomplete Explains why gene is of interest. Identifies where in genome gene is found including chromosome and which direction on chromosome. At least 1 SNP associated with a phenotype is identified with allele frequencies given. Population differences are indicated.	ALL of the following is missing or incomplete Explains why gene is of interest. Identifies where in genome gene is found including chromosome and which direction on chromosome. At least 1 SNP associated with a phenotype is identified with allele frequencies given. Population differences are indicated
Structure Multiplier 1X	Report is given in complete sentences and full paragraphs without bullet points		Report is given in complete sentences, though many bullet points		Report is mainly bullet points
Language usage Multiplier 1X	Report is clearly written with few grammatical errors and no spelling errors		Report contains few grammatical errors and some spelling errors, though is mostly understandable		Report contains many grammatical and spelling errors. Report is confusing to read and not easy to understand.