Recitation 7

1. Use readr to load the files 20170926_tidy_table1.csv and 20170926_tidy_table2.csv.

2. Figure out how to combine up the data into a tidy table.

3. Figure out how to how to put the ref and alt nucleotides in separate columns.

4. Figure out how to standardize the chromosome names.

5. What are the most significant snps?

6. Write out the tibble with the top three most significant snps to a new csv file.

7. Use readr to load the files 20170926_diffGene_Run1.csv, 20170926_diffGene_Run2.csv, 20170926_diffGene_Run3.csv, 20170926_diffGene_genes.csv.

8. Figure out how to put all the runs into a single tibble.

9. What genes are present in all three runs?

10. What pathways are the highest and lowest value genes in?

11. Write out the tibble with the highest and lowest value genes with their pathways to a new csv file.