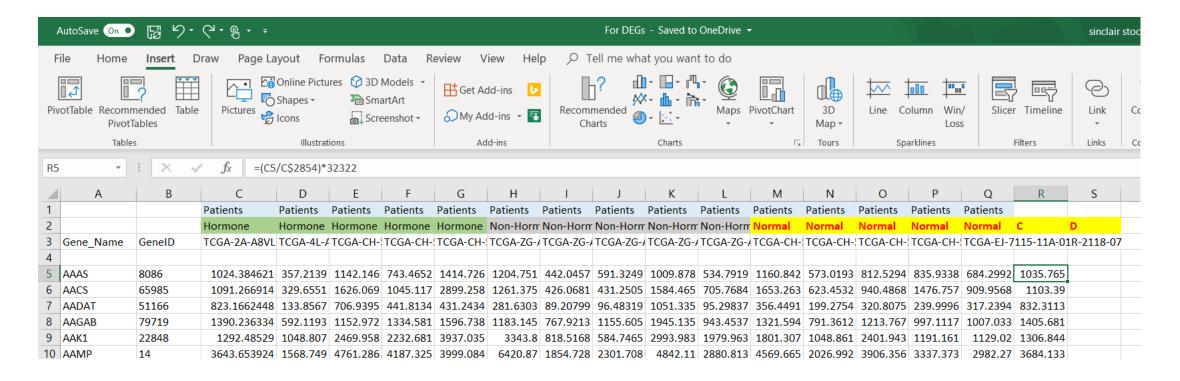


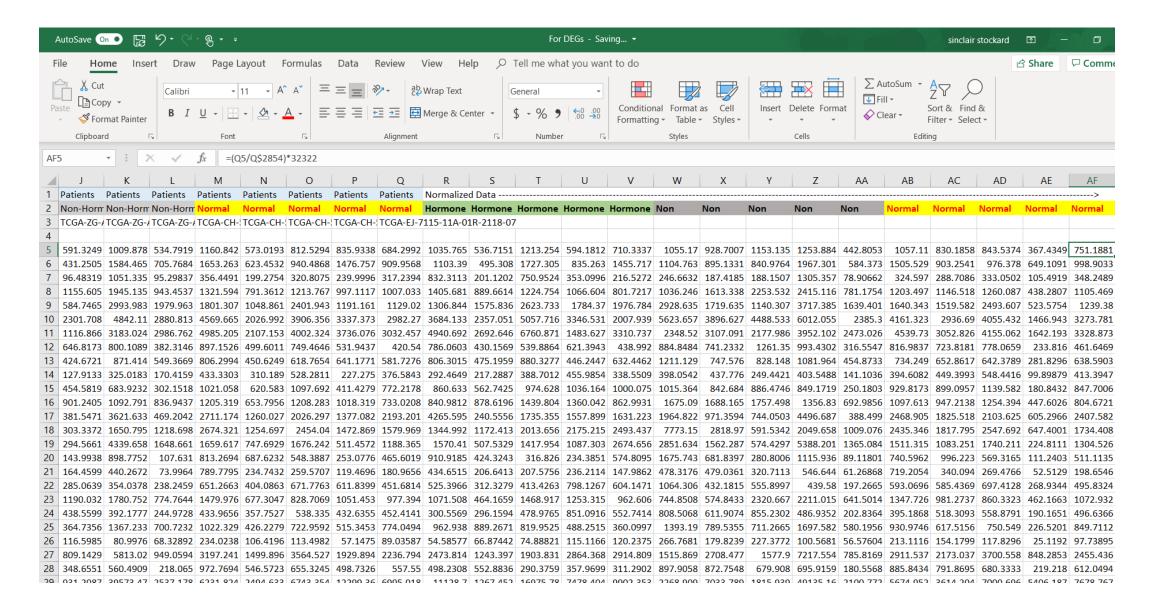
I used Ctrl + F to find GAPDH in the data. It is row 2854.

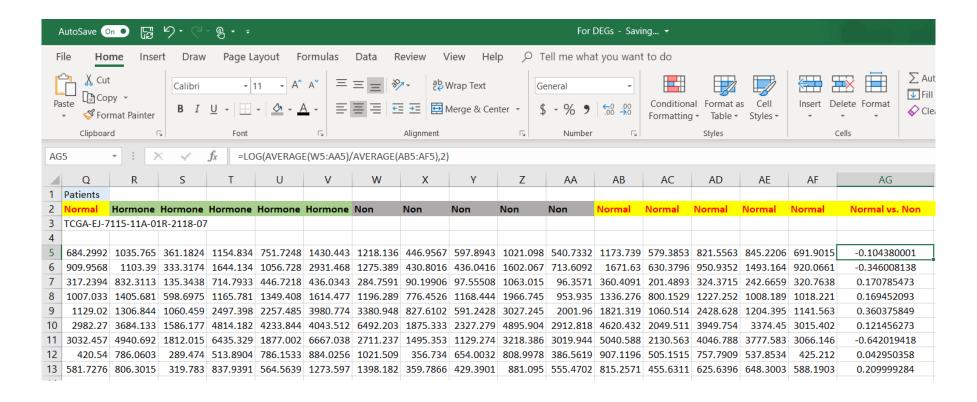


In order to normalize the data, I had to make a new column for each subject (ex: see columns C and D above). I then used the formula shown above to normalize the data to GAPDH.

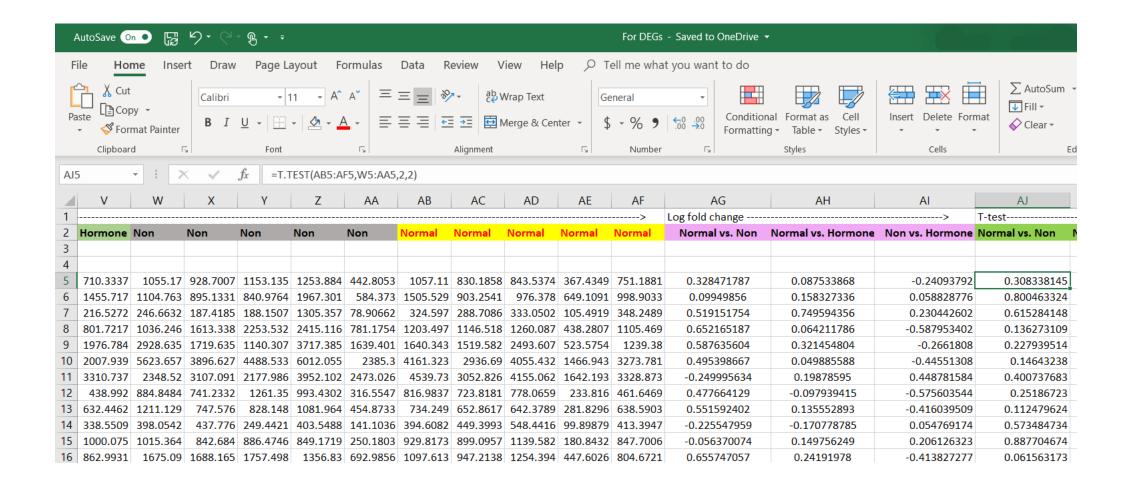
For example, I first normalized row C, which is the first Hormone column. I made a new C column and filled it using the formula above. C5 is the first value in the original Hormone column. C\$2854 corresponds to the GAPDH expression in column C. 32322 is the mean expression of GAPDH. I double clicked in the right corner of the cell to fill the cells below. For each remaining column, I used the same formula but changed the columns.

Finished normalized data

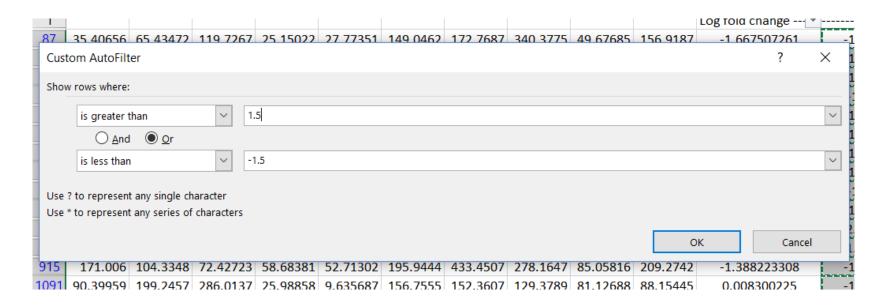




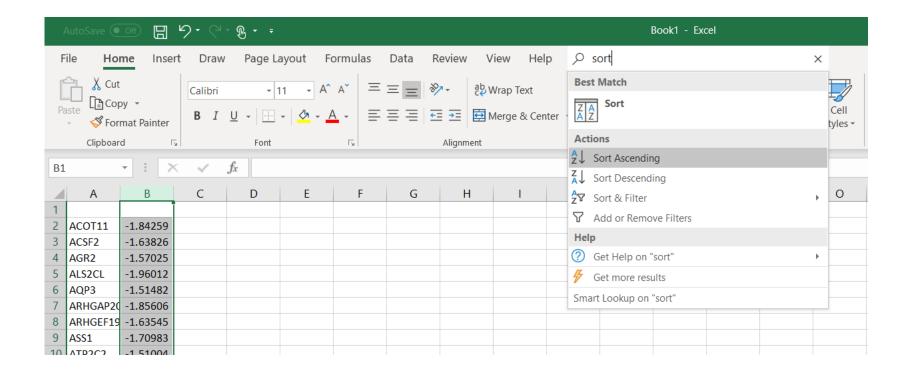
I created a new column for each comparison, and used the above formula to calculate log fold change. For each analysis, I had to change which columns were used depending on the groups that were being compared.



For T-test, I used the formula above and created columns as described previously.



To find differentially expressed genes, I used the filter tool. For each comparison group, I filtered for genes with a log fold change over >1.5 and -1.5. I added a second filter on top of this for genes with <.05 p-value.



I pasted the genes and corresponding log fold changes of the remaining rows into a new file and sorted them. The negative values are downregulated genes for that analysis and the positives are upregulated. I uploaded the file with the final results. For #3, there were 74 upregulated genes. For #4, there were 124 downregulated genes.

To find overlapping genes, I used the formula below in a new column called "Match?" This formula prints a 0 if a gene in the upregulated column for Normal vs. Hormone also appears in the downregulated column for Normal vs. Non. 1 is printed if there is a match. There were no overlapping genes.

