

Jacob Risch

Prof. Wylie

BIO321G

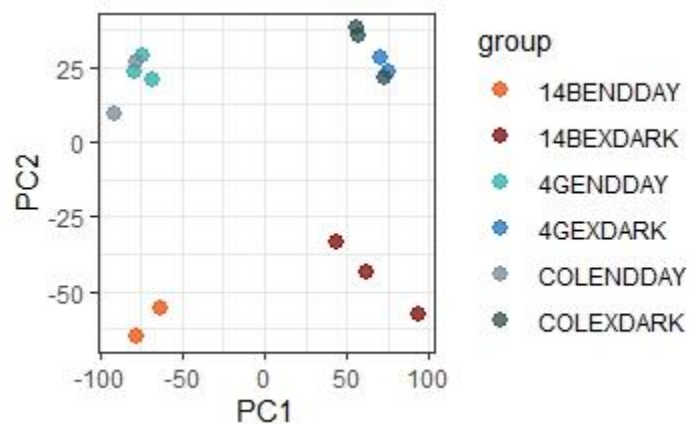
11/24/20

RNA Sequencing Project Report

Gene ID- GO:0071495

- 1.) There are 1429 sequences with an FDR less than or equal to 10%, so we would expect approximately 143 sequences to have been false positives.
- 2.) The data was normalized with DESeq and log base 2 transformed with an offset of 1.
- 3.) It appears that samples 4GENDDAY, COLENDDAY, and 14BENDDAY

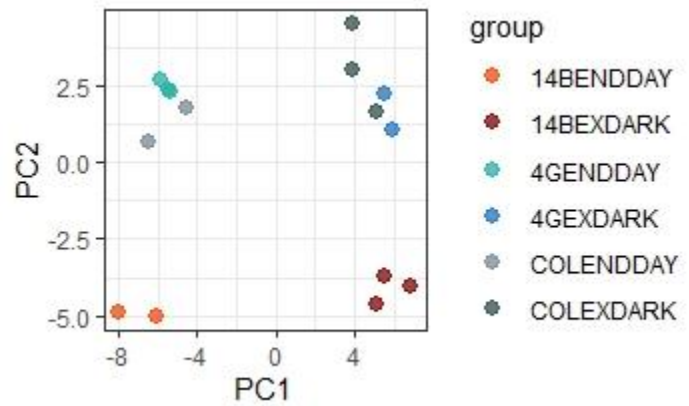
are most separated across PC1 from COLEXDARK, 4GEXDARK, and 14BEXDARK,



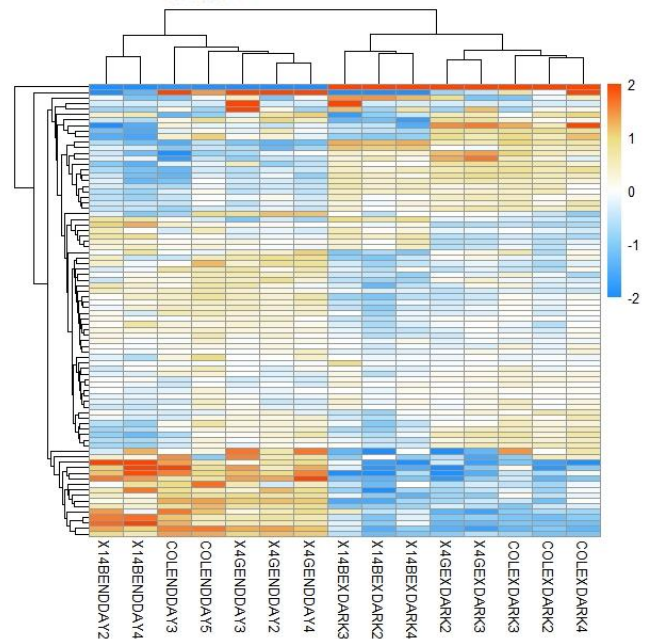
and that 4GENDDAY, COLENDDAY, COLEXDARK, and 4GEXDARK are most separated across PC2 from 14BENDDAY and 14BEXDARK.

- 4.) The tab-delimited file has been provided with the name "Risch_go.tsv".
- 5.) lgGo is simply lgNorm by with genes that correspond to my gene set.

6.) In general, it appears that the groups from my smaller gene set vary much less than those from the entire set across PC2 and PC1 by a factor of around 10.



7.) It appears that the two largest sample clusters appear to be those with differing times of expression (“Day” and “Dark”).



8.) It appears that the expression levels of 14B are in general heightened during the daytime, while 4G and Col are heightened during nighttime.

