

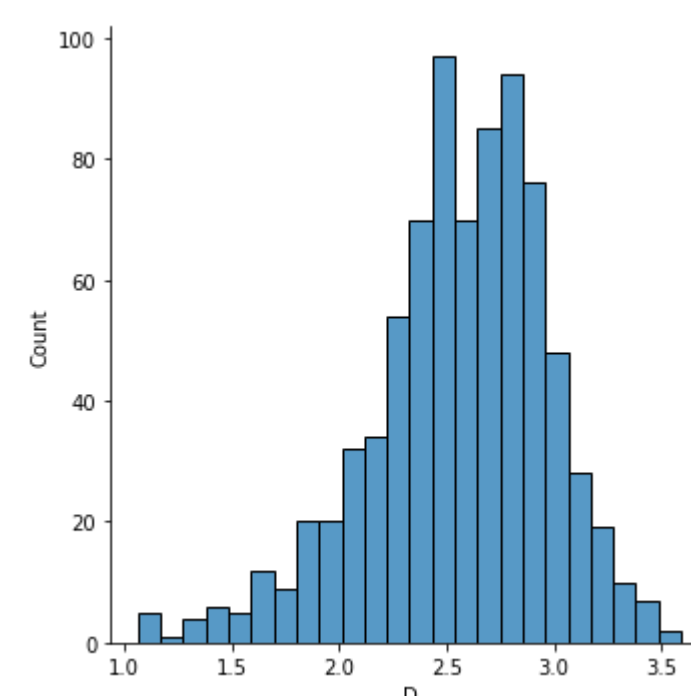
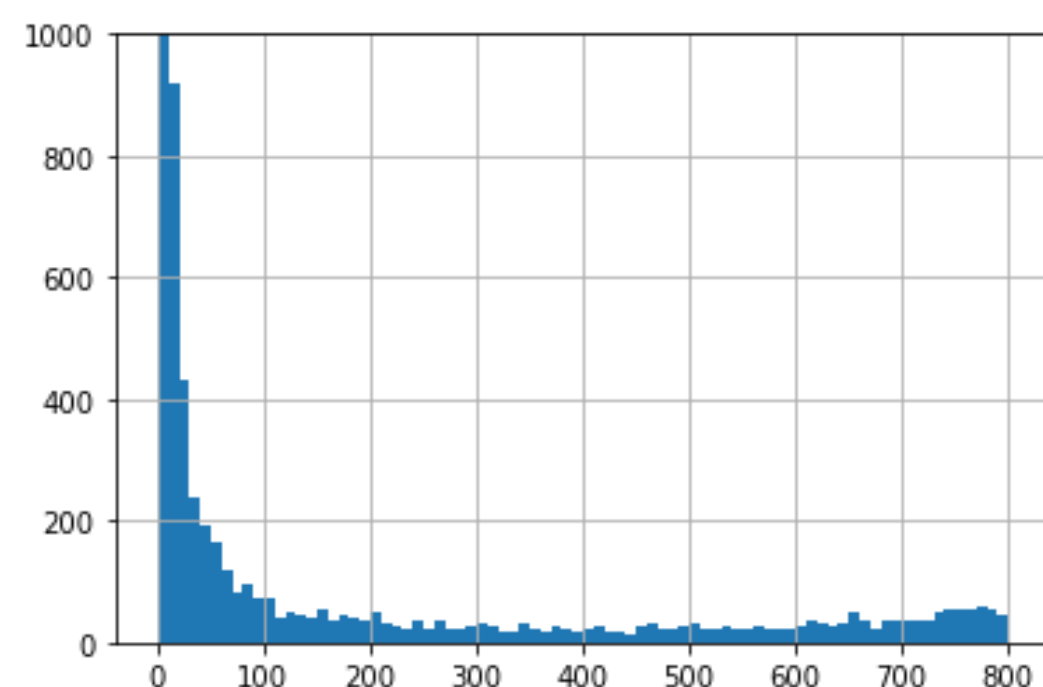
Background

- Essential genes are a necessity that cells need in order to thrive and reproduce.
- Removal of essential genes results in a cell's loss of function or fitness.
- Identifying genes that are essential in cancerous cells but not in somatic cells will enable us to target those essential cancerous genes without harming the healthy somatic cells of a patient.
- Comparing the correlating functions of these essential genes leads to a better understanding of the human genome.

Methods

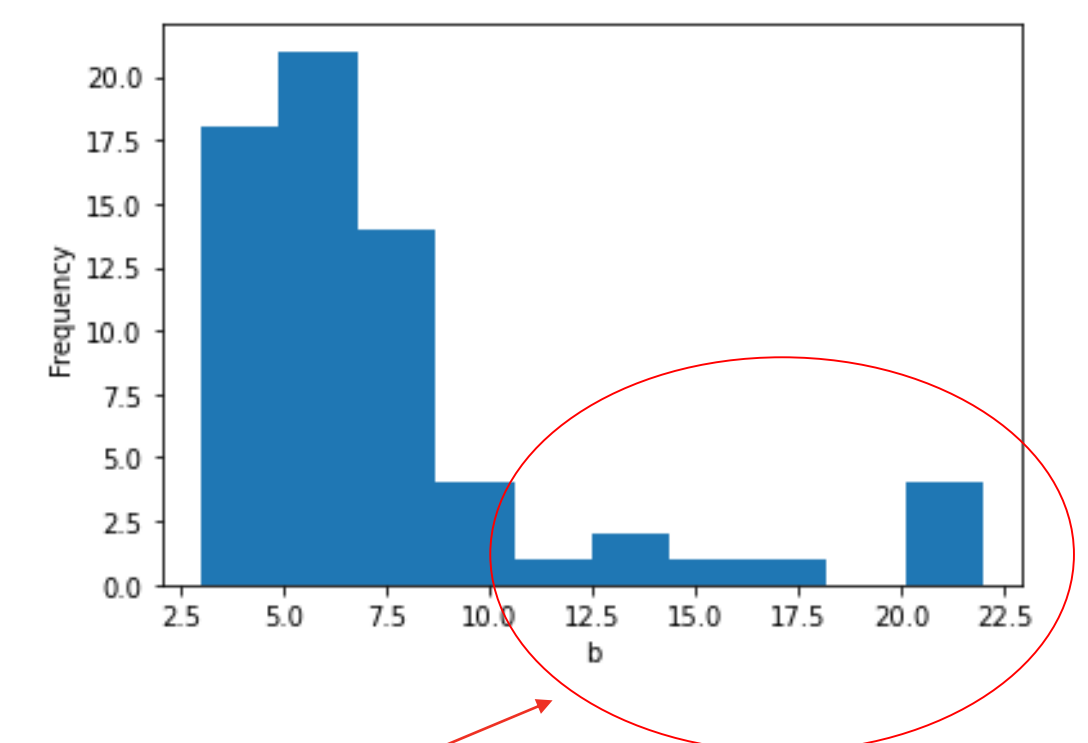
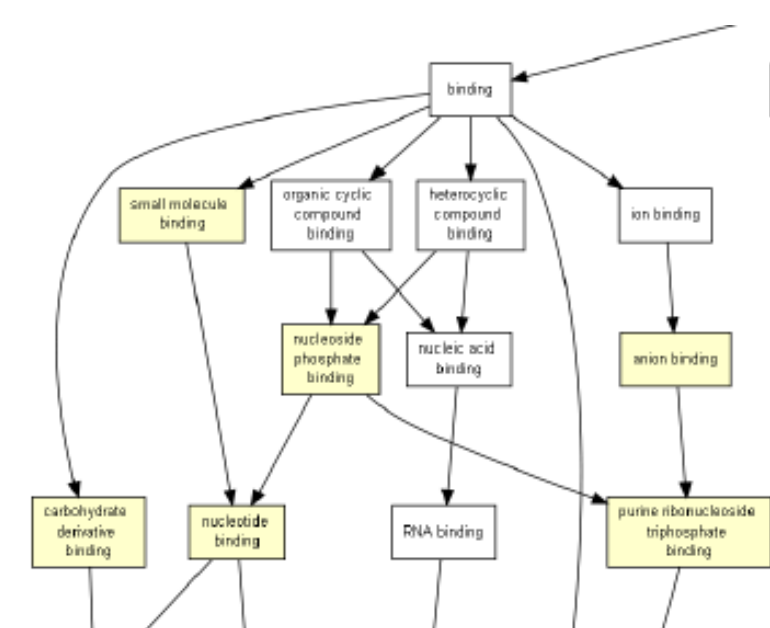
Defining Essentiality

- Data set analyzed consisted of n= 17,000? genes across 808 cell lines
- an essentiality score was given for each gene in each cell line
- **Finding "Good Data" with Cohen's D Statistic**



GORilla and Always Essential Major Functions

- Gene Ontology Enrichment Analysis and Visualization Tool
- Used two unranked list of genes
 - Target vs background list
 - Target list was found earlier when defining essentiality
 - Ontology: Functions



Results

"Good Data"- Always Essential Genes

- Starting Data Set of n = 17,000?
- 11,413 genes determined "never essential"
- 717 genes determined "always essential"
 - These genes were essential 600+ cell lines
- Used Cohen's D score of greater than or equal to 2

Always Essential Major Functions

- 5'-3' RNA Polymerase Activity
- RNA Polymerase Activity
- DNA-directed 5'-3' RNA Polymerase activity
- snRNA Binding
- Translation Initiation Factor Activity
- snoRNA Binding
- General Transcription Initiation Factor Activity
- U6 snRNA Binding
- Ribosome Binding
- RNA Polymerase II General Transcription Initiation Factor Activity

Conclusion

- Major Functions that are always essential have more essential genes involved
- Expected Functions
- Binding
- Transporter Activity

References

- Chen, L., Zhang, Y. H., Wang, S., Zhang, Y., Huang, T., & Cai, Y. D. (2017). Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. *PloS one*, 12(9), e0184129. <https://doi.org/10.1371/journal.pone.0184129>
- Hart, T., Tong, A., Chan, K., Van Leeuwen, J., Seetharaman, A., Aregger, M., Chandrashekhar, M., Hustedt, N., Seth, S., Noonan, A., Habsid, A., Sizova, O., Nedyalkova, L., Climie, R., Tworzyanski, L., Lawson, K., Sartori, M. A., Alibeh, S., Tieu, D., Masud, S., ... Moffat, J. (2017). Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. *G3 (Bethesda, Md.)*, 7(8), 2719-2727. <https://doi.org/10.1534/g3.117.041277>