

Select soft-thresholding power

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SELECT DIAGNOSIS HERE

```
dx <- "bipolar"
```

Read in count data

Gene expression data have been filtered, cleaned, explored, and regressed based on covariate exploration. Selecting soft-thresholding power (SFT) is the first step in WGCNA analysis.

Data should be in the format of a gene x sample matrix, saved as a csv called “gene_expression_data.csv” in the data/ directory.



