Select soft-thresholding power

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SELECT DIAGNOSIS HERE

```
dx <- "schizo"
```

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.

```
## pickSoftThreshold: will use block size 3160.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 3160 of 14155
##     ..working on genes 3161 through 6320 of 14155
##     ..working on genes 6321 through 9480 of 14155
##     ..working on genes 9481 through 12640 of 14155
##     ..working on genes 12641 through 14155 of 14155
##    Power SFT.R.sq  slope truncated.R.sq mean.k. median.k. max.k.
## 1      1    0.105 -0.859          0.913 2630.00  2.53e+03 4430.0
## 2      2    0.647 -1.570          0.955  775.00  6.82e+02 2070.0
## 3      3    0.832 -1.790          0.970  292.00  2.27e+02 1180.0
## 4      4    0.896 -1.870          0.972  130.00  8.70e+01  754.0
## 5      5    0.926 -1.850          0.975   65.30  3.66e+01  524.0
## 6      6    0.937 -1.810          0.971   36.00  1.67e+01  385.0
## 7      7    0.954 -1.740          0.976   21.40  8.03e+00  296.0
## 8      8    0.966 -1.670          0.978   13.50  4.05e+00  235.0
## 9      9    0.975 -1.610          0.981    8.99  2.13e+00  192.0
## 10    10    0.968 -1.570          0.972    6.24  1.17e+00  162.0
## 11    11    0.971 -1.530          0.972    4.50  6.60e-01  139.0
## 12    12    0.971 -1.490          0.972    3.34  3.80e-01  121.0
## 13    13    0.975 -1.450          0.975    2.55  2.25e-01  106.0
## 14    14    0.976 -1.420          0.975    1.99  1.36e-01   93.9
## 15    15    0.977 -1.390          0.976    1.58  8.33e-02   83.6
## 16    16    0.981 -1.370          0.981    1.28  5.16e-02   74.9
```

schizo

schizo