

Figure S1 Samples clustering of GSE18520 and GSE27651 to detect outliers.

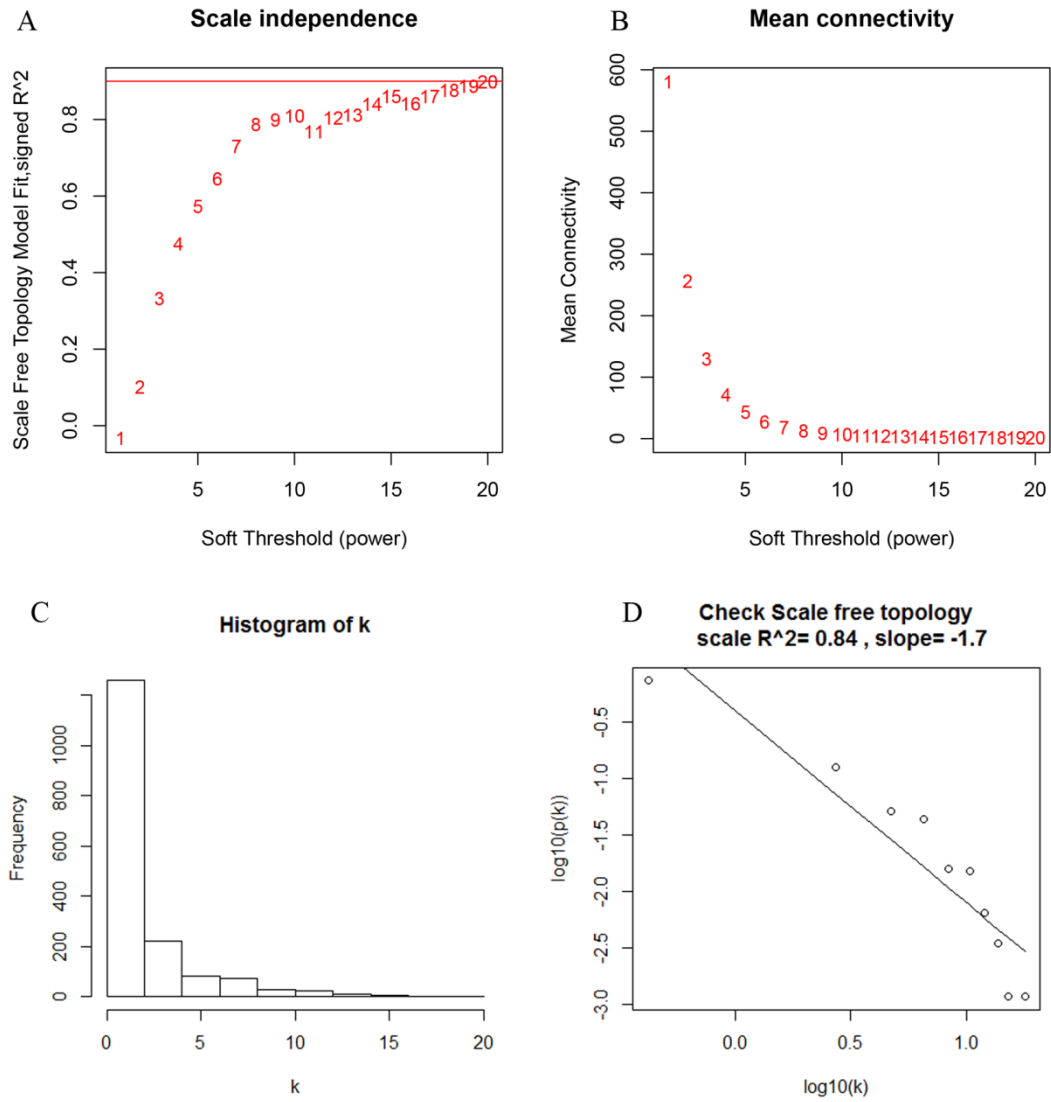


Figure S2 Determination of soft-thresholding power in WGCNA.

Note: (A) Analysis of the scale-free fit index for various soft-thresholding powers (β). (B) Analysis of the mean connectivity for various soft-thresholding powers. (C) Histogram of connectivity distribution when $\beta=15$. (D) Checking the scale free topology when $\beta=15$.

Abbreviations: WGCNA, weighted gene co-expression network analysis.

dynamicColors									
black	blue	brown	green	grey	magenta	pink	red	turquoise	yellow
78	297	168	86	472	29	44	83	325	118

moduleColors						
black	blue	brown	grey	magenta	turquoise	yellow
161	341	254	472	29	325	118

Figure S3 Genes number of Clusters

Note: (A) All the clusters. (B) Clusters after merged.

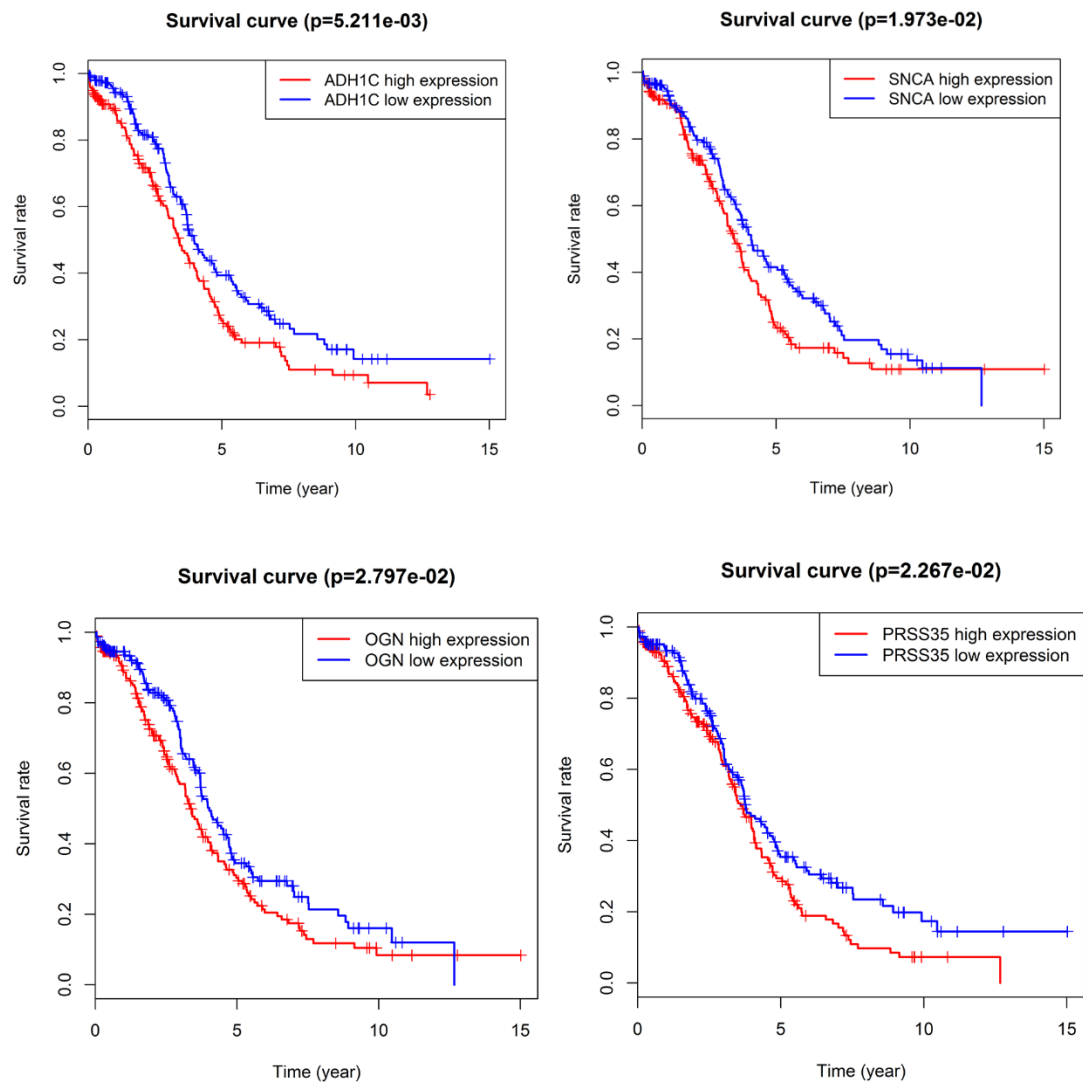


Figure S4 Survival analysis of the other four top genes.

Note: (A) ADH1C, (B) SNCA, (C) OGN, (D) PRSS35