**Figure Legends**

**Figure S1. Average C-statistics of the top *N* pathways (*N* = 1, 2, …, 28).**

**Figure S2. Hierarchical cluster analysis on the GSE3494 pathway profiles of the top 20 pathways inferred by the SPCA method.**

**Figure S3. Hierarchical cluster analysis on the GSE3494 pathway profiles of the top 20 pathways inferred by the PAC method.**

**Figure S4. Hierarchical cluster analysis on the GSE3494 pathway profiles of the top 20 pathways inferred by the Mean method.**

**Figure S5. Hierarchical cluster analysis on the GSE3494 pathway profiles of the top 20 pathways inferred by the Median method.**

**Figure S6. Hierarchical cluster analysis on the GSE3494 pathway profiles of the 771 significant genes.**

**Figure S7. Kaplan–Meier curves for patients in GSE3494, GSE1456 and GSE45255** **stratified by the SPCA, Mean, Median, and Genes method, respectively.** (A) The samples in GSE3494 are stratified by subtypes identified by cluster analysis on the pathway profiles inferred by SPCA. The samples in GSE1456 and GSE45255 are stratified by predicted subtypes using the multiclass classifier against subtypes trained from the GSE3494 pathway profiles. (B), (C) and (D) followed the same procedure as (A) using the Mean, Median and Genes method, respectively.

**Figure S8. Predictive performance of the DRWPSurv method with three different networks.** (A) Box plots of C-statistics by DRWPSurv with the KEGG, HPRD and co-expression network using within-dataset experiments and cross-dataset experiments, respectively. (B) Box plots of C-indexes by DRWPSurv with the KEGG, HPRD and co-expression network using within-dataset experiments and cross-dataset experiments, respectively.