



Additional file 9: Figure S9. Construction of weighted co-expression network. **A** Clustering dendrogram of 412 patients in the GSE10846 dataset and heatmap of clinical trait (i.e. risk group). According to the median risk score, 412 patients were divided into high- and low- risk groups. In terms of the color in heatmap, white means low-risk group and red means high-risk group. The cluster was based on the genes with variance within the first 5000 in the GSE10846 dataset. **B** Analysis of the scale-free fit index (left) and the mean connectivity (right) for various soft-thresholding power value. **C** Correlation between the modules and clinical trait (i.e. risk group). Blue represents the negative correlation and red represents the positive correlation.