Supplementary Methods

Pipeline for time series transcriptome data analysis

- Identify differentially expressed genes (DEGs) by EDGE.

- Extend the DEG set by including genes which have at least 1.5 fold change between their maxima and minima and genes which have minimum standard deviation of 0.25 (in log2 transformed scale).

- Determine co-expressed modules by using unsigned option of WGCNA.

- Re-allocate genes to the identified modules by using only positive correlations between genes and module eigengenes (*signedKME*) (Figure S1).
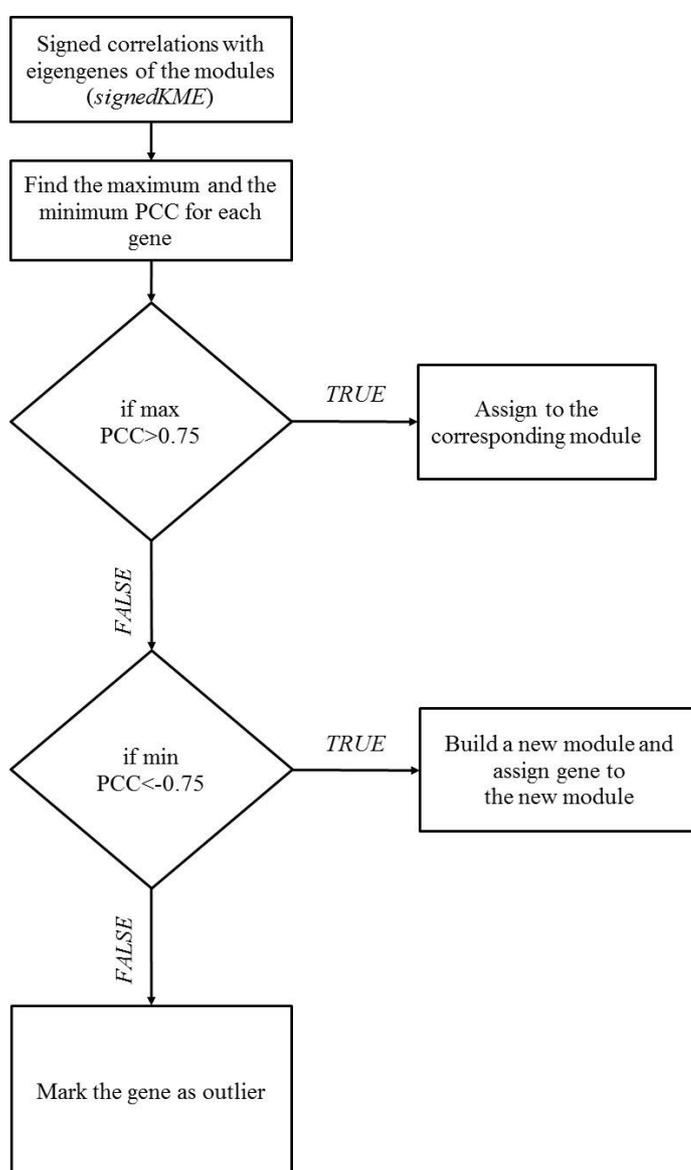

Fig. S1. Reallocation pipeline for genes to the WGCNA modules.