Supplementary Figure Legends

Supplementary Figure 1. Gene expression patterns of the co-expressed gene set of FOXM1 in the Pan-cancer cohort.
A total of 722 genes with expression patterns that highly correlated with FOXM1 were selected for cluster analysis. Patients were divided into the following two subgroups: FOXM1-high (FH) and FOXM1-low (FL).

Supplementary Figure 2. Gene set enrichment analysis of the co-expressed gene set of FOXM1 that was associated with the prognosis of HCC patients.
Classification enrichment was determined using the Ingenuity Pathway Analysis tool (www.ingenuity.com). The threshold of significance was –log$(P = 0.05)$.

Supplementary Figure 3. Comparison of expression levels between FOXM1-high (FH) and FOXM1-low (FL) subgroups in the TCGA cohort.
Two group box plots comparing the expression levels of (a) FOXM1 and (b) miR-34a in the FH and FL subgroups. The $P$-value was obtained by two-sample $t$-test between FH and FL. The value of $r$ indicates the correlation coefficient of the gene compared to FOXM1. The expression level of miR-34a was inversely correlated with the gene expression level of FOXM1.
Subgroups Cancer types

← FOXM1

HCC  PAAD  LUAD  BRCA  BLCA

-4  -2  0  2  4