

## Supplementary Figure Legends

### **Supplementary Figure 1. Gene expression patterns of the co-expressed gene set of *FOXMI* in the Pan-cancer cohort.**

A total of 722 genes with expression patterns that highly correlated with *FOXMI* were selected for cluster analysis. Patients were divided into the following two subgroups: *FOXMI*-high (FH) and *FOXMI*-low (FL).

### **Supplementary Figure 2. Gene set enrichment analysis of the co-expressed gene set of *FOXMI* that was associated with the prognosis of HCC patients.**

Classification enrichment was determined using the Ingenuity Pathway Analysis tool ([www.ingenuity.com](http://www.ingenuity.com)). The threshold of significance was  $-\log(P = 0.05)$ .

### **Supplementary Figure 3. Comparison of expression levels between *FOXMI*-high (FH) and *FOXMI*-low (FL) subgroups in the TCGA cohort.**

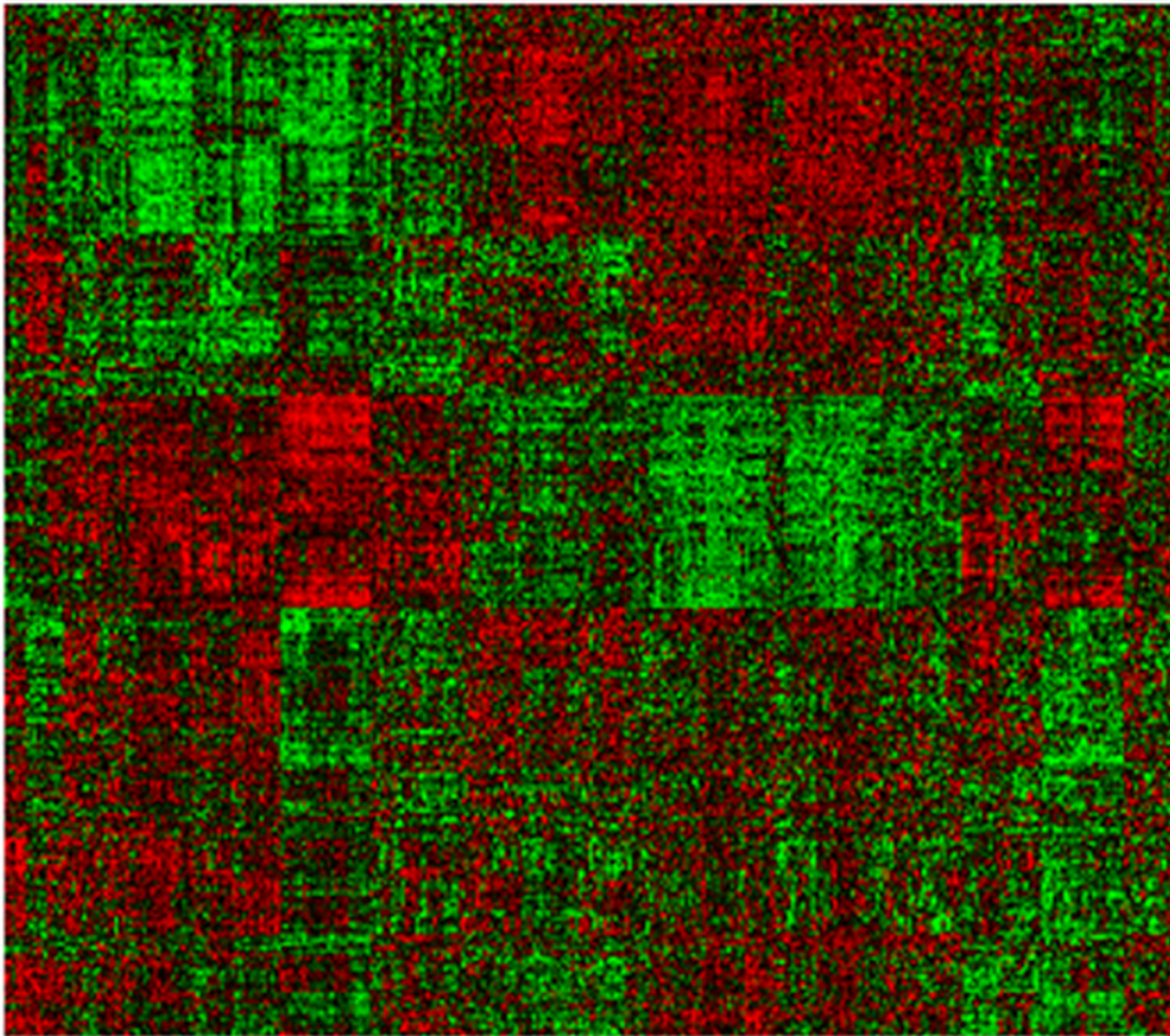
Two group box plots comparing the expression levels of (a) *FOXMI* and (b) miR-34a in the FH and FL subgroups. The *P*-value was obtained by two-sample *t*-test between FH and FL. The value of *r* indicates the correlation coefficient of the gene compared to *FOXMI*. The expression level of miR-34a was inversely correlated with the gene expression level of *FOXMI*.

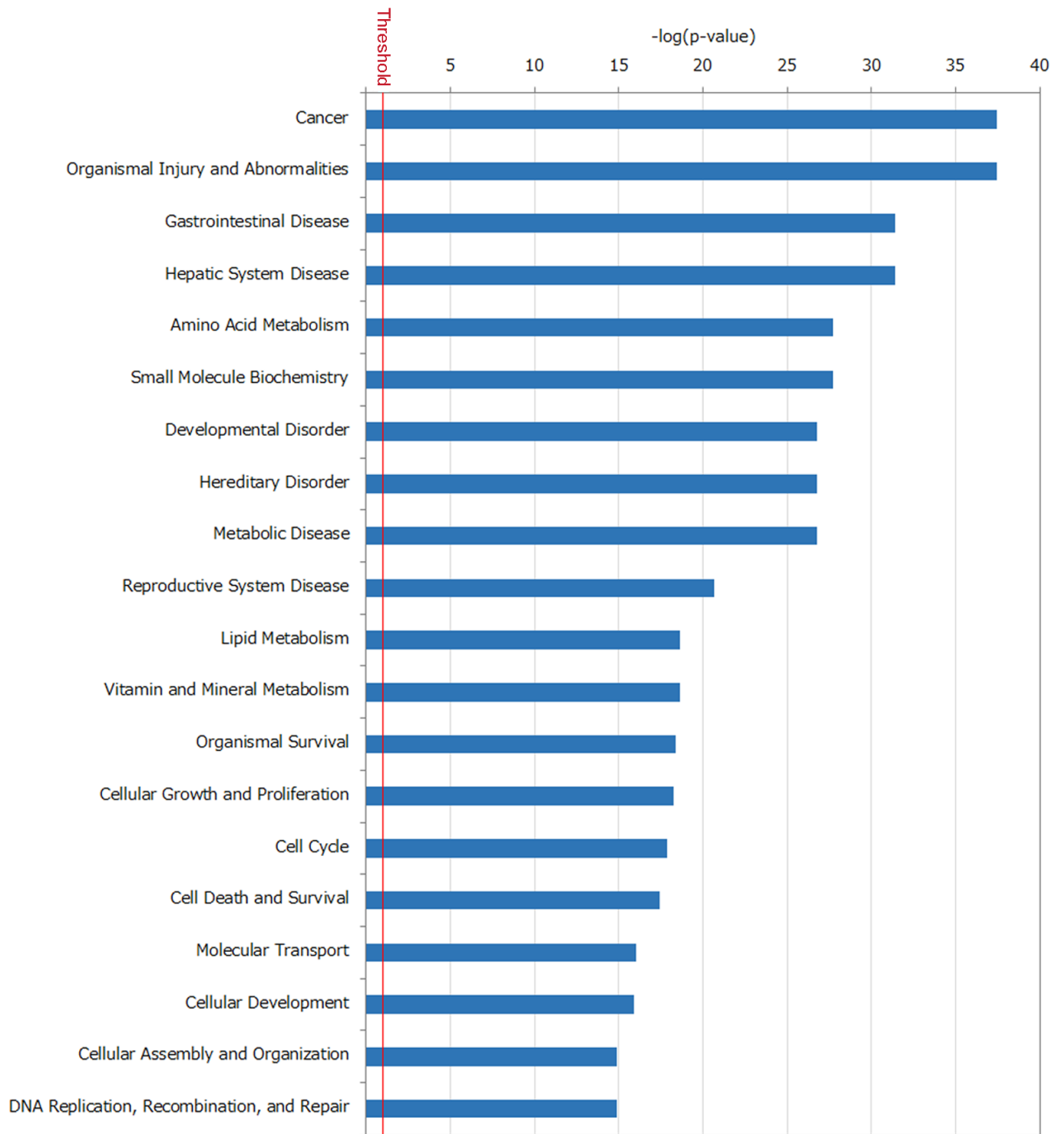
FL

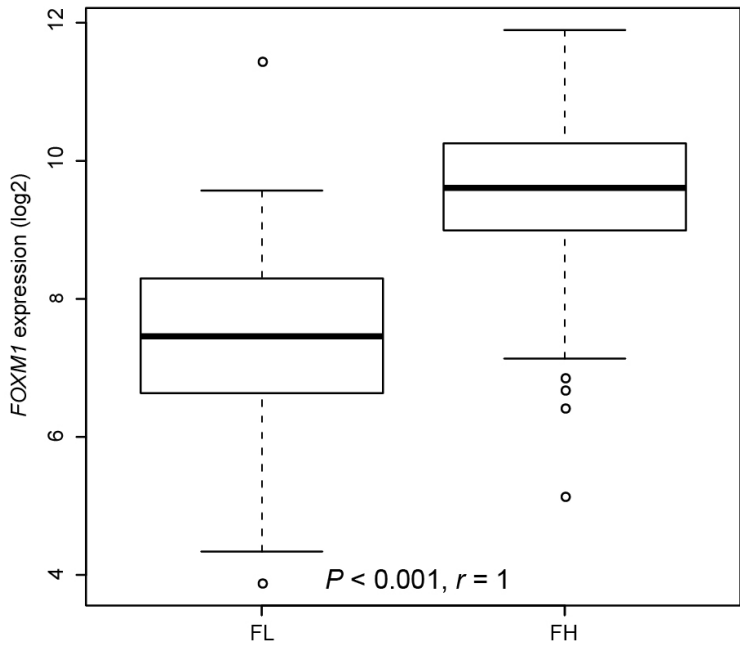
FH

Subgroups  
Cancer types

← *FOXM1*





**a****b**