



Supplementary Figure 2. YAP1 signature and selection of candidate genes

(A) YAP1-specific gene expression signature shared by two cell lines. The two-sample t-test was independently applied to gene expression data from two groups of samples (YAP1 and control) in two cell lines, MKN45 and MCF10A. The association between a gene and YAP1 activation was considered statistically significant if the P value was less than 0.005. Expression of 88 genes was significantly altered in both cell lines when YAP1 was overexpressed. The data are presented in a matrix format in which each row represents a gene and each column represents a tissue sample. Each cell in the matrix represents the expression level of a gene feature in an individual tissue sample. The red and green coloring in the cells reflects relatively high and low expression levels, respectively, as indicated by the scale bar at the bottom (log₂-transformed scale).

(B) Cross-comparison of candidate gene lists obtained using three independent approaches. A Venn diagram of genes whose expression was significantly associated with overall survival (OS), recurrence-free survival (RFS), and YAP1 activation in gastric cancer is shown. Genes whose expression was significantly associated with recurrence-free survival or overall survival were identified using Cox univariate proportional hazards models. Genes whose expression is significantly associated with YAP1 activation were identified by the t-test. Association was considered statistically significant if the P value was less than 0.001.