



Supplementary Figure 4. Hierarchical clustering analysis of YAP1 signature in 5 GC cell lines.

Gene expression data from 5 GC cell lines were merged with YAP1-specific gene expression data from MKN45 and MCF10A cells and clustered together. ACS, KatoIII, and SNU1 were co-clustered with cell lines overexpressing YAP1 and their expression patterns were highly similar to YAP1-overexpressing cell lines. 74 genes were shared by both data sets.