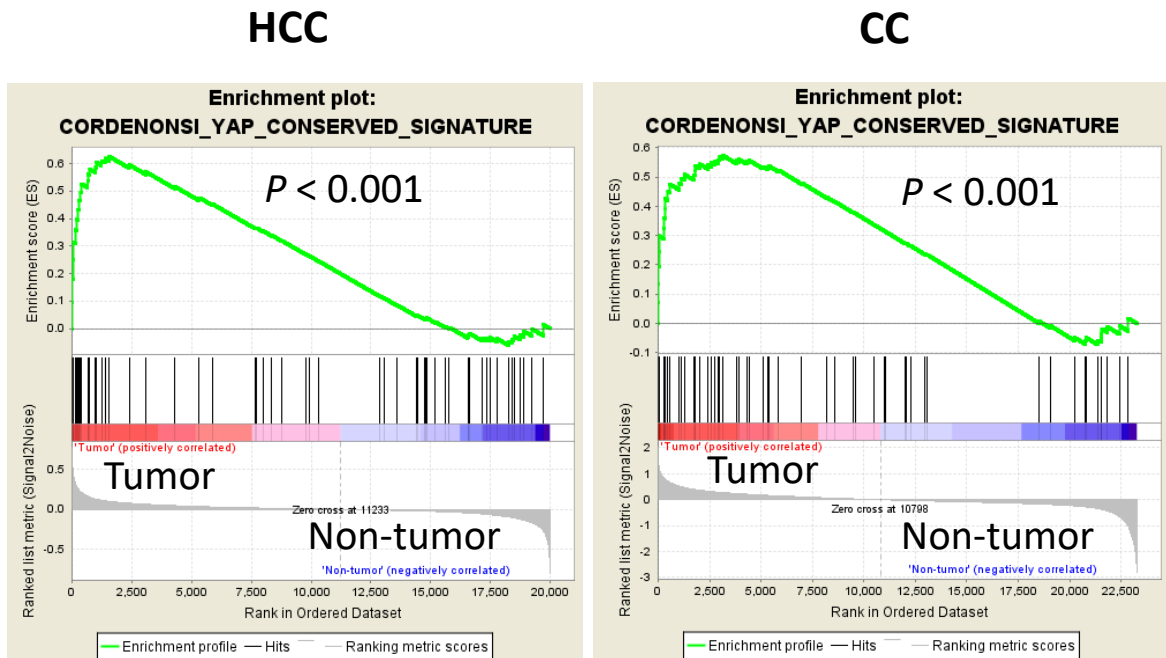


# Supplementary Figure 1



	<u>Tumor vs Non-tumor</u>	
<u>DataSet</u>	GSE64041 (HCC)	GSE32958 (CC)
<u>GENESET</u>	CORDENONSI_YAP_CONSERVED_SIGNATURE	
<u>SIZE</u>	57	57
<u>NES</u>	1.9171263	1.9856614
<u>NOM p-val</u>	0	0
<u>FDR q-val</u>	0	0

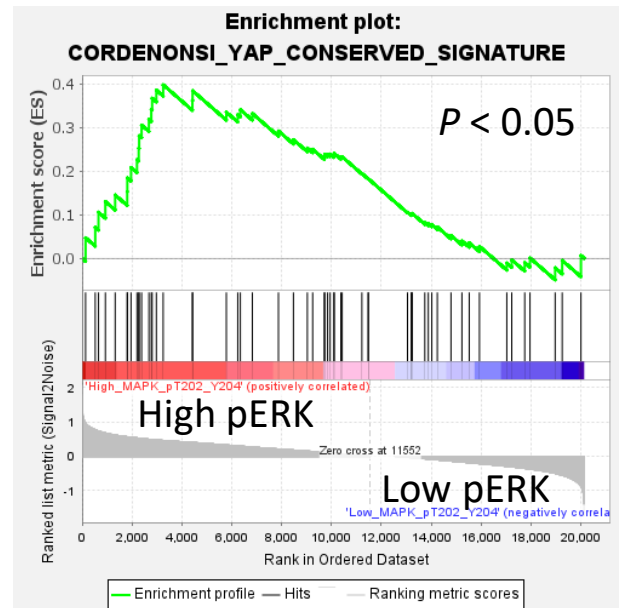
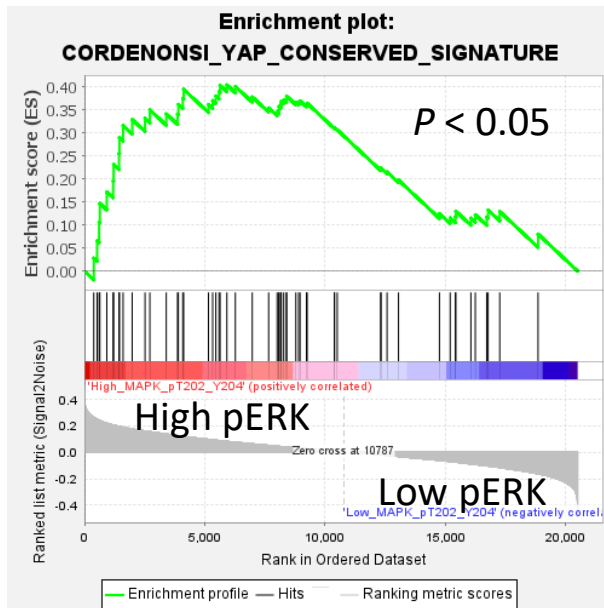
NES, normalized enrichment score; FDR, false discovery rate.

**Supplementary Figure 1.** Enrichment plots from gene set enrichment analysis (GSEA). YAP/TAZ signals are highly enriched both in HCC and CC ( $P < 0.001$ ). Barcode indicates gene positions and the y-axis indicates the extent of enrichment.

# Supplementary Figure 2

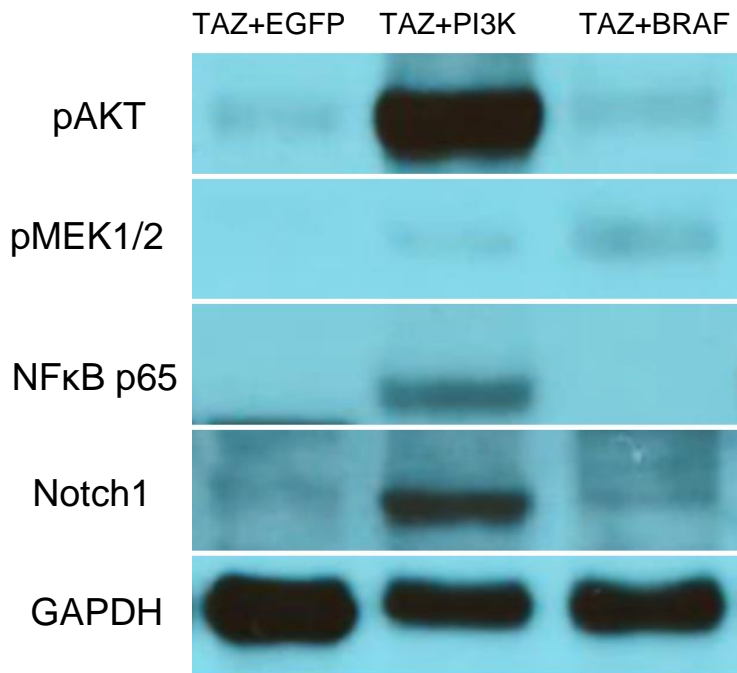
TCGA\_HCC (n = 181)

TCGA\_CC (n = 30)



**Supplementary Figure 2.** Correlation between the YAP/TAZ signals and levels of phosphorylated ERK (pERK). GSEA was performed with regard to high and low levels of pERK using the TCGA database. Barcode indicates gene positions and the y-axis indicates the extent of enrichment.

# Supplementary Figure 3



**Supplementary Figure 3.** Western blots showing expression levels of indicated genes in tumors from each group shown in Figure 5.