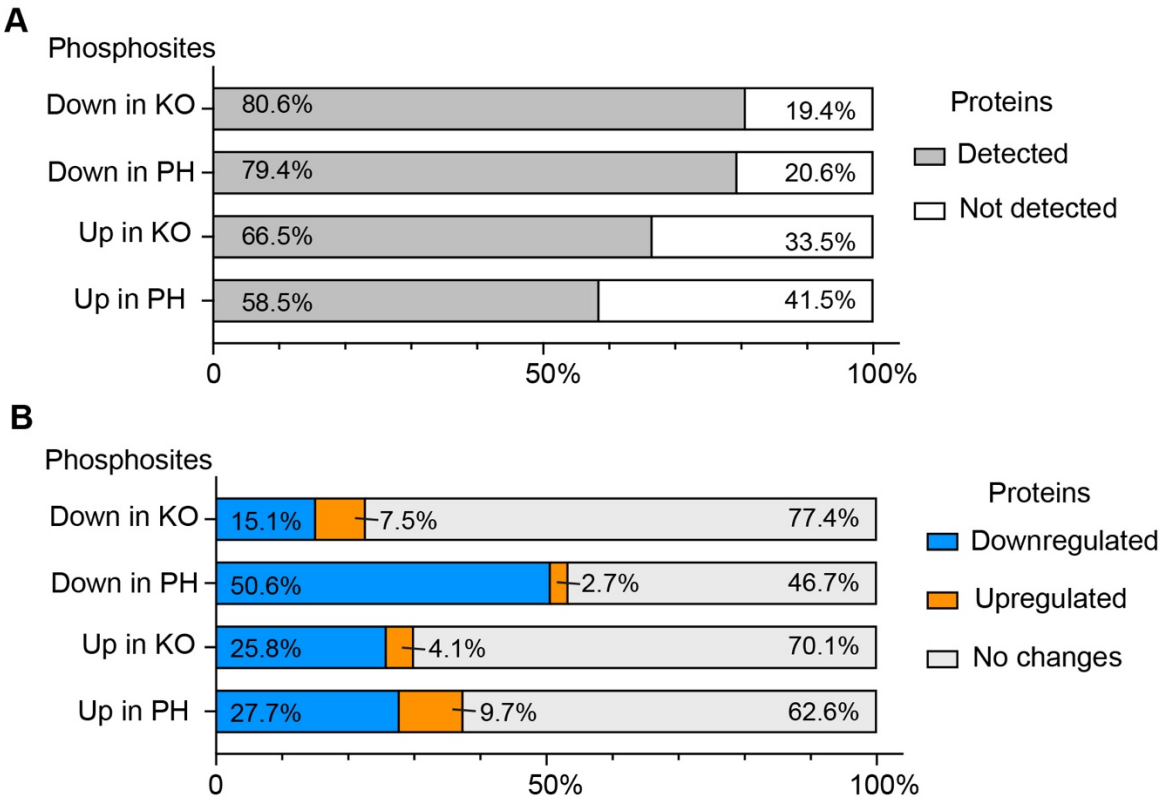
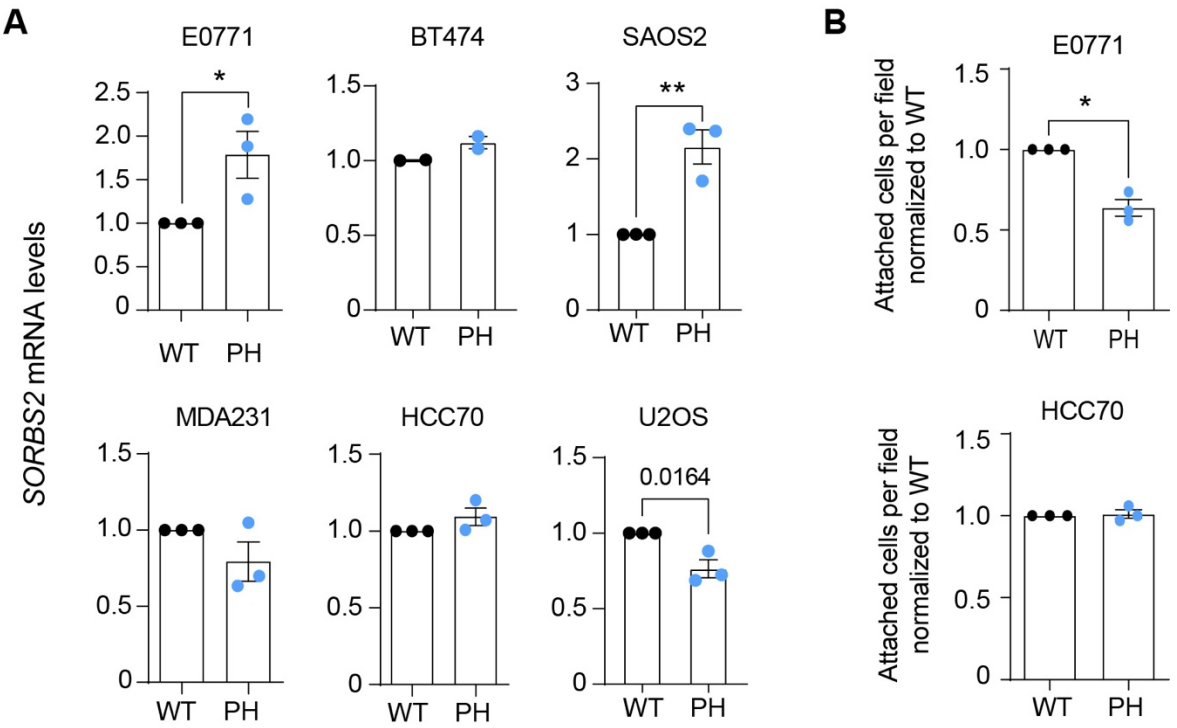
SUPPLEMENTAL DATA



Supplemental Fig. S1. Overlap between the proteome and phosphoproteome datasets. *A*, percentage of phosphosites either upregulated (Up) or downregulated (Down) in p38α KO or PH-797804 treated cells, and that are located in proteins detected or not detected in the proteome analysis. *B*, percentage of phosphosites that change in p38α KO or PH-797804 treated cell as indicated (Up or Down) and are located in proteins whose expression was either downregulated, upregulated or no changed. A cutoff of FC >1.2 in KO/WT or PH/WT was used to consider that the protein was downregulated or upregulated.



Supplemental Fig. S2. Regulation of *SORBS2* expression by p38α in different human cancer cell lines. *A, SORBS2* mRNA levels were determined by qRT-PCR in the indicated cancer cell lines treated with the p38α inhibitor PH797804 (PH) for 48 h. $*p < 0.05$, $**p < 0.01$. When no p-value is indicated the differences are not significant. Each dot indicates one biological replicate. *B,* the indicated cell lines were pre-incubated with either DMSO or PH, and 24 h later 30,000 cells (E0771) or 50,000 cells (HCC70) were plated and incubated for 1 or 2 h, respectively. Attached cells were counted and normalized to DMSO.

Supplemental Table S1. Quantification of the total protein raw data *(Excel Table)*

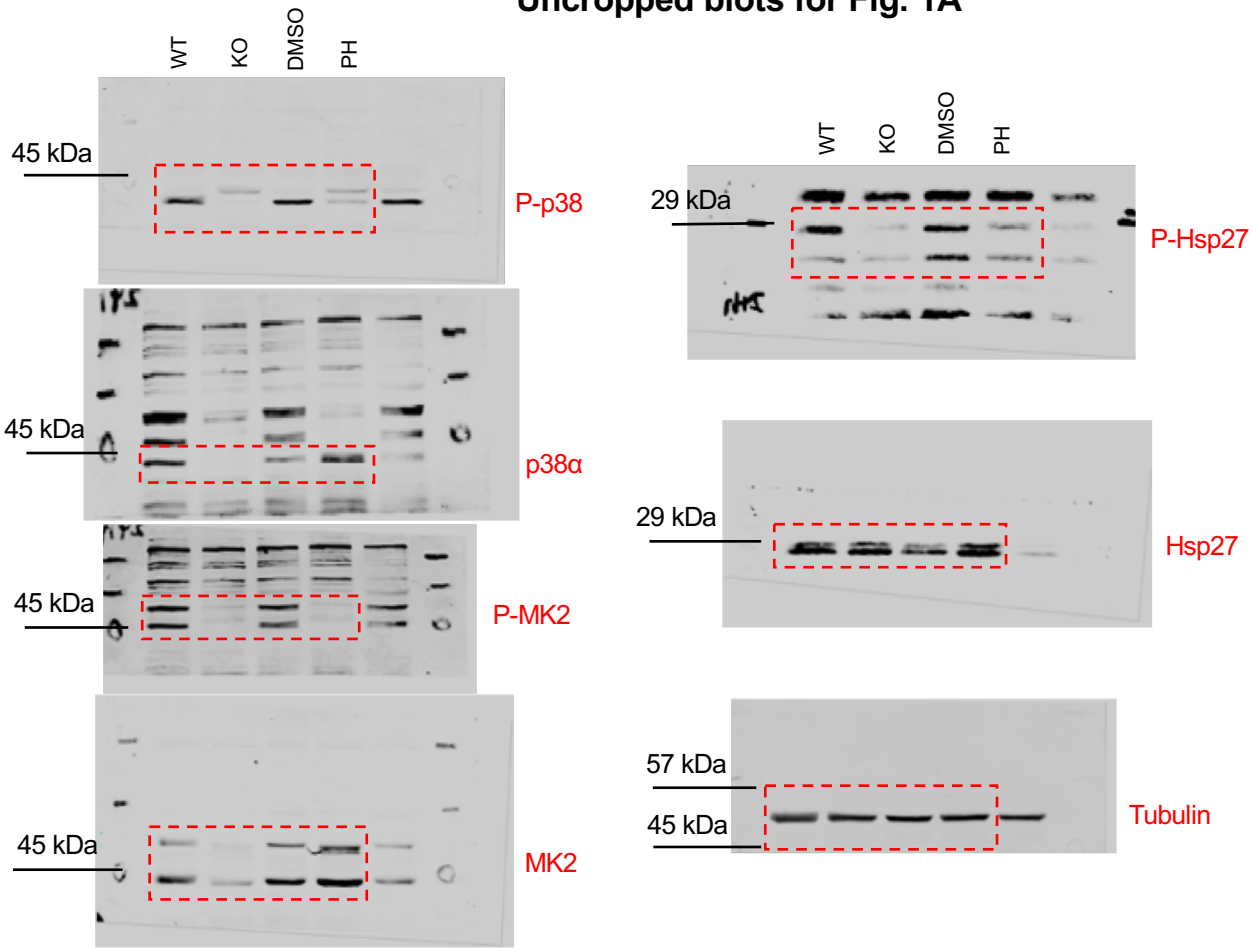
Supplemental Table S2. Phosphopeptides *(Excel Table)*

Supplemental Table S3. Quantification of the total phosphosite raw data *(Excel Table)*

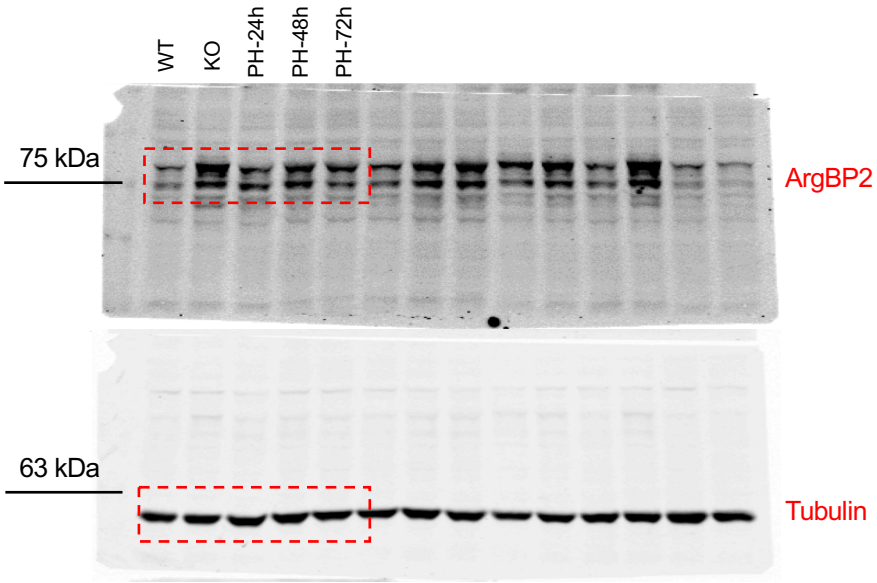
Supplemental Table S4. Proteins that change in both KO and PH-treated cells compared with WT cells *(Excel Table)*

Supplemental Table S5. Phosphosites that change in both KO and PH-treated cells compared with WT cells *(Excel Table)*

Uncropped blots for Fig. 1A



Uncropped blots for Fig. 7B



Uncropped blots for Fig. 7E