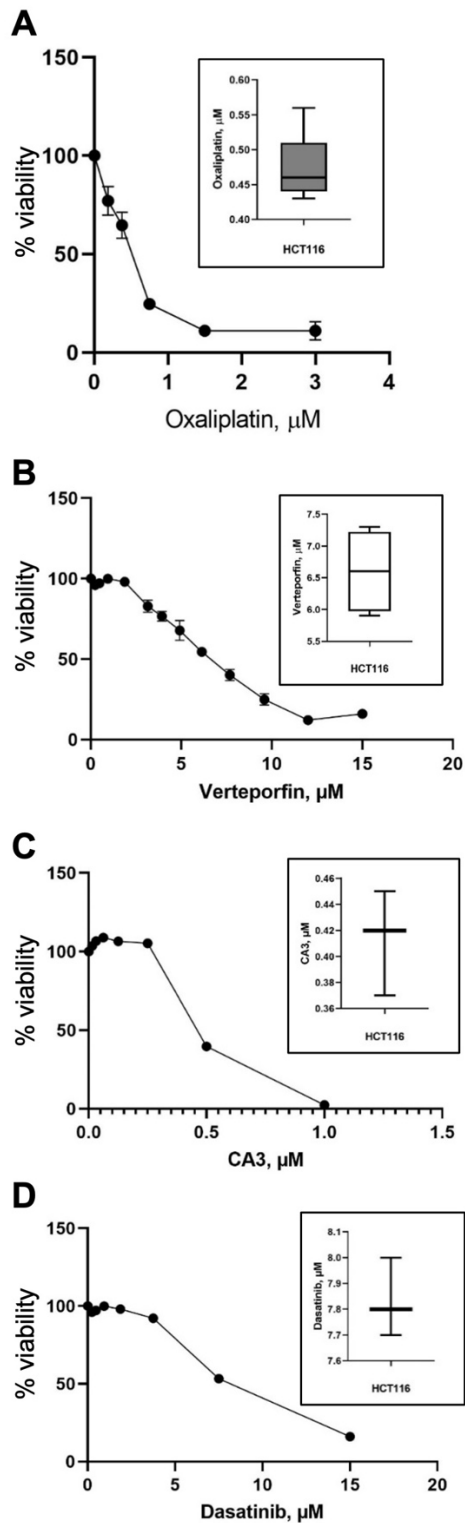


SUPPLEMENTARY MATERIAL

The Hippo pathway terminal effector TAZ/WWTR1 mediates oxaliplatin sensitivity in p53 proficient colon cancer cells

Věra Slaninová, Lisa Heron-Milhavet, Mathilde Robin, Laura Jeanson, Adam Aissanou, Diala Kantar, Diego Tosi, Laurent Bréhélin, Céline Gongora, and Alexandre Djiane

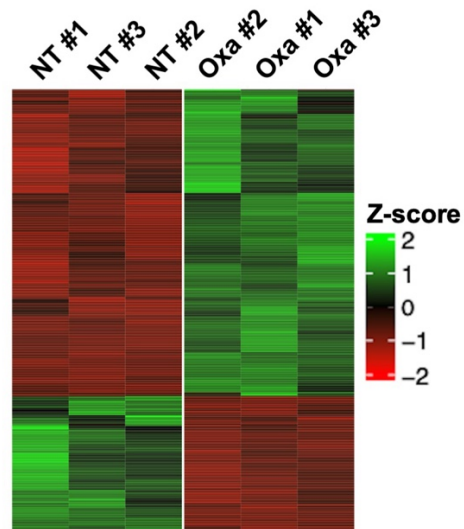
Slaninova et al. Figure S1



Supplemental Figure S1. Cell viability in response to drugs

Cells were treated with increasing doses of oxaliplatin (A), Verteporfin (B), CA3 (C) and Dasatinib (D) for 96h. Cell viability analysis was then assessed using SRB assay and the IC50 of each drug could be calculated as the concentration that reduced cell numbers by 50% (shown in the insets).

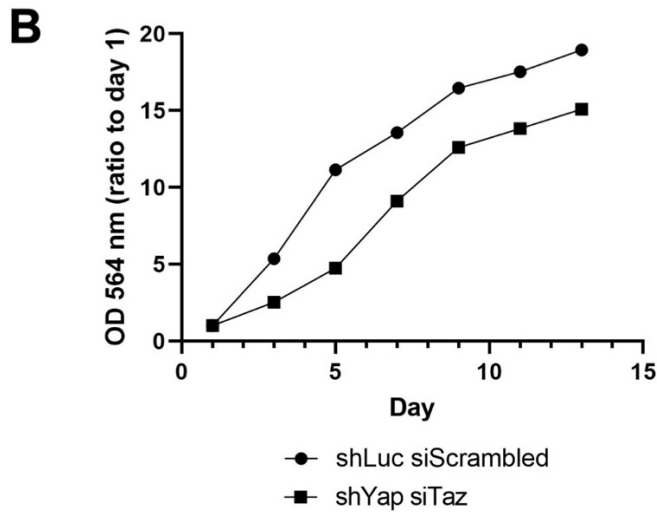
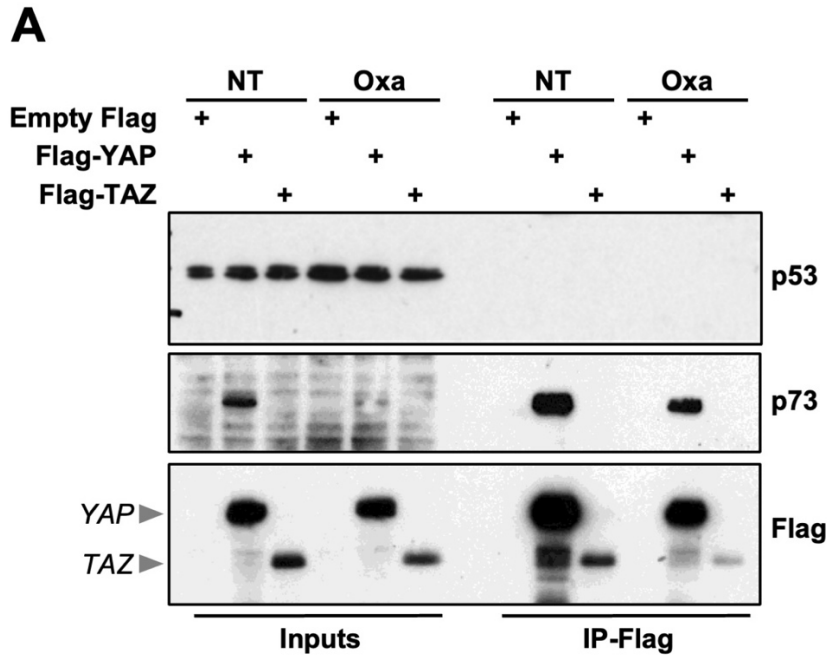
Slaninova et al. Figure S2



Supplemental Figure S2. Genes regulated by oxaliplatin treatment

Heat map corresponding to the genes differentially expressed in HCT116 cells after 24h of oxaliplatin treatment at IC50 (see Supplemental Table 1). The three replicates for the non-treated (NT) and treated (Oxa) are shown.

Slaninova et al. Figure S3



Supplemental Figure S3.

A. Interaction between YAP/TAZ and p53 protein family members in HCT116 cells

Western blot analysis of Flag (YAP or TAZ) immunoprecipitates on protein extracts from HCT116 treated (Oxa), or not (NT) showing an interaction between YAP and p73 (n=3).

B. Effect of shYAP/siTaz on the growth of HCT116 cells

Proliferation curve measured by colorimetric SRB assay

Figure 1C

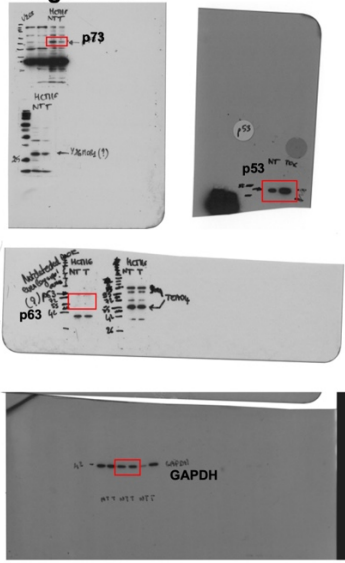


Figure 2B



Figure 2C

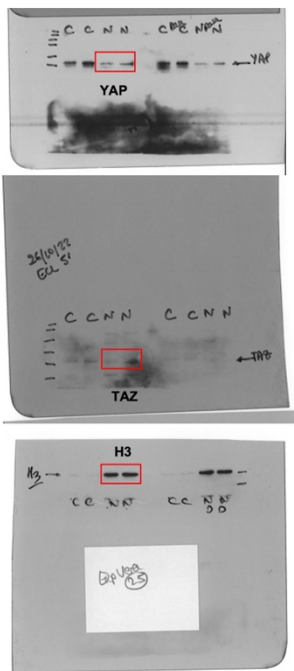
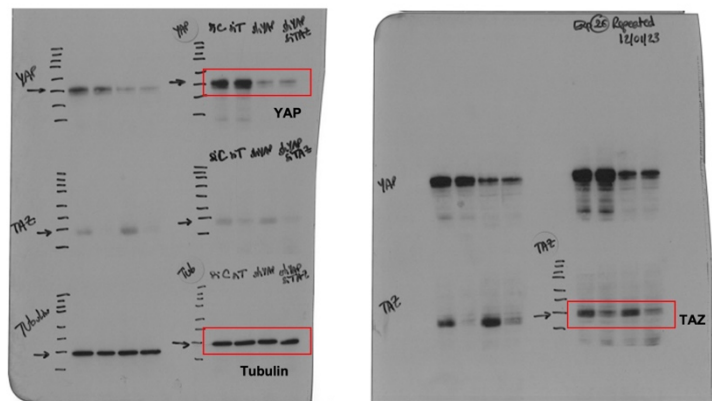


Figure 3C



Supplemental Figure S4. Uncropped western-blot - part 1

Figure 3E

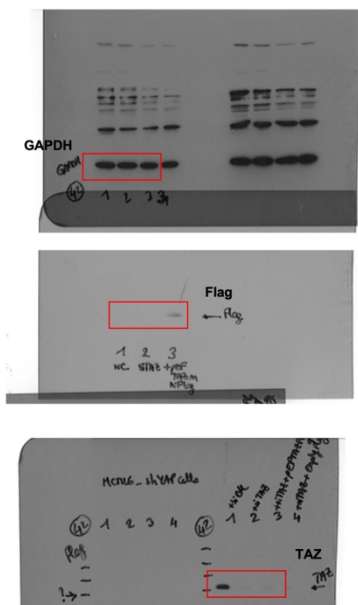


Figure 6A

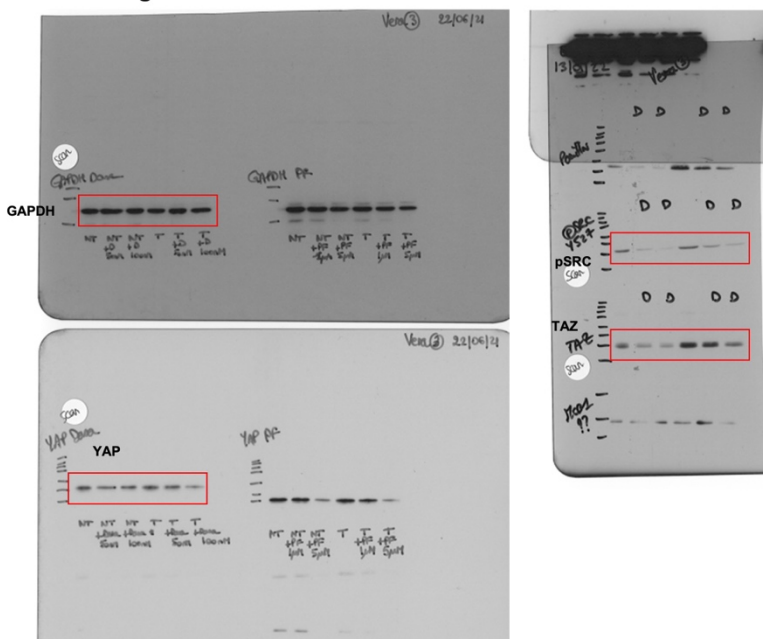
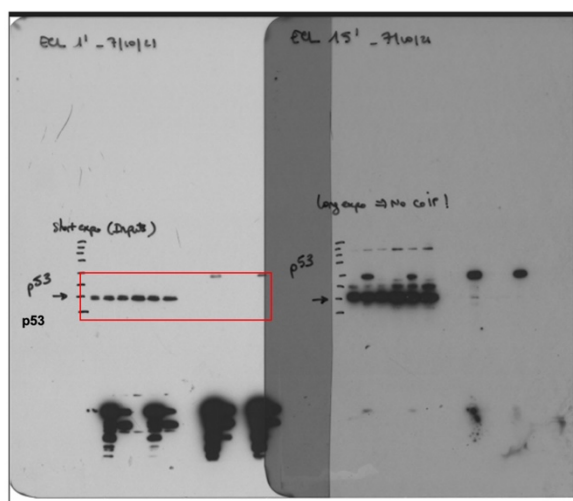
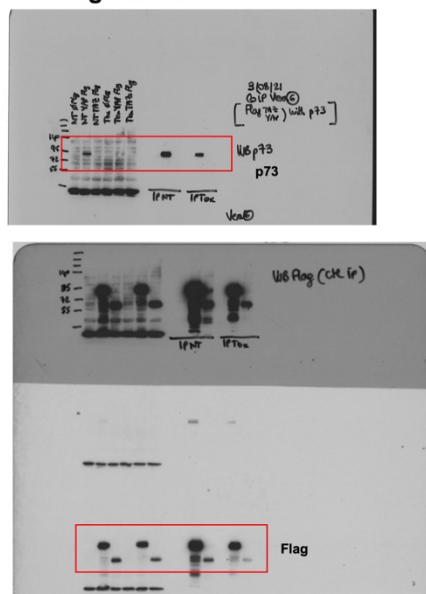


Figure S3A



Supplemental Figure S5. Uncropped western-blots - part 2

Supplemental Table 1. Differentially expressed genes in HCT116 cells after oxaliplatin treatment for 24h at IC50

Only differentially expressed genes with an adjusted p-value < 0.05 are shown. Columns are:

test_id: position and description of the feature tested

ENSG_ID: Ensemble gene ID

symbol: gene symbol

sample_1: first group in the comparison; untreated cells

sample_2: second group in the comparison; cells treated with oxaliplatin

mean_1: mean of normalized count for the first group in the comparison

mean_2: mean of normalized count for the second group in the comparison

log2FoldChange: log2 fold change estimates

pvalue: pvalue

padj: pvalue adjusted for multiple testing with the Benjamini-Hochberg procedure, which controls false discovery rate (FDR)

Supplemental Table 2. g:profiler functional enrichment analyses

Columns are :

GO_ID: Gene Ontology

KEGG_ID: KEGG pathways

REAC_ID: Reactome pathways

WP_ID: WikiPathways

TF_ID: regulatory motif matches from TRANSFAC

MIRNA_ID: miRNA targets from miRTarBase

CORUM_ID: protein complexes from CORUM

HPA_ID: tissue specificity from Human Protein Atlas

HP_ID: human disease phenotypes from Human Phenotype Ontology

Description: description of the functional group

p.Val: p-value

FDR: false discovery rate

Genes: genes found in the intersection