

Figure S1. (A) Western blot analysis of MDA-MB-231 cells with USP1 knockdown and analysis for indicated antibodies. GAPDH was used as a loading control and blots were normalized to GAPDH. (B) Cytotoxicity experiments using 4 different cell lines and varying concentrations of ML323 (USP1/UAF1i).

TAZ Amino Acid Conservation



The conservation scale:



Variable Average Conserved

- o - An exposed residue according to the neural-network algorithm.
- b - A buried residue according to the neural-network algorithm.
- f - A predicted functional residue (highly conserved and exposed).
- s - A predicted structural residue (highly conserved and buried).
- Y - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

Figure S2. TAZ conservation across species.

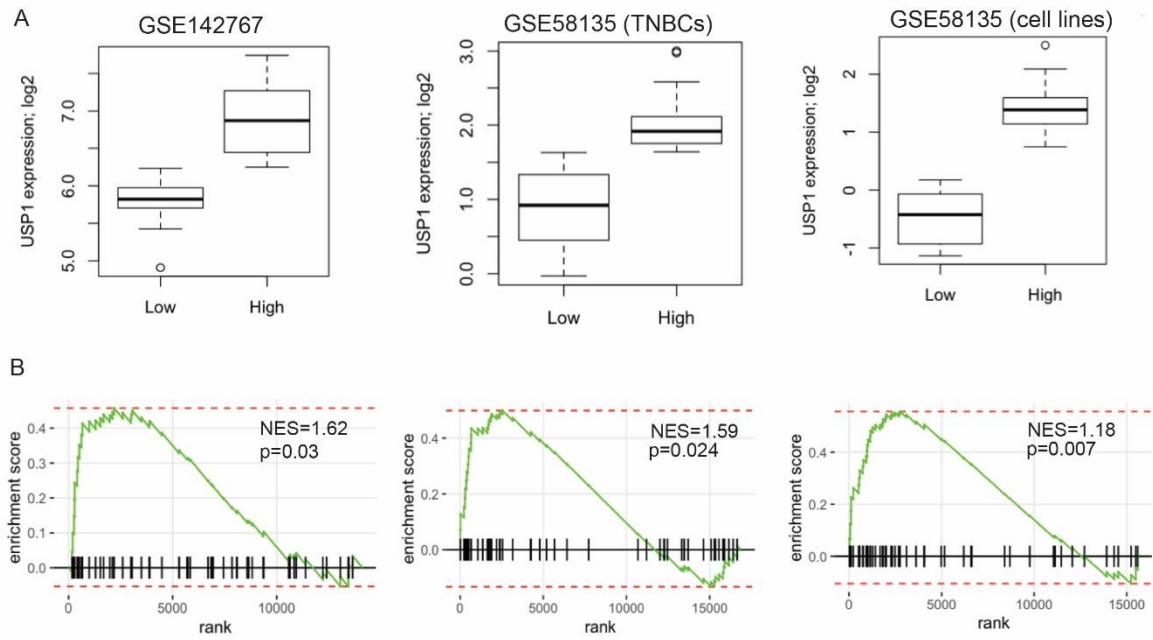


Figure S3. Stratification of GSE58135 (TNBCs), GSE58135 (Cell lines), and GSE142767 into USP1 low and USP1 high subsets. Cordenosi YAP/TAZ gene signature is shown.

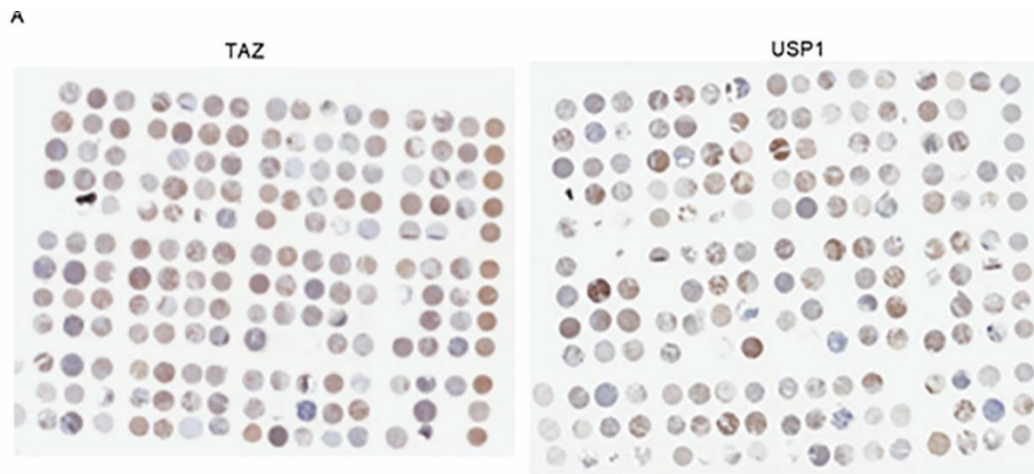


Figure S4. Representative images of TMAs stained with USP1 or TAZ antibody.

Details of Western Blot

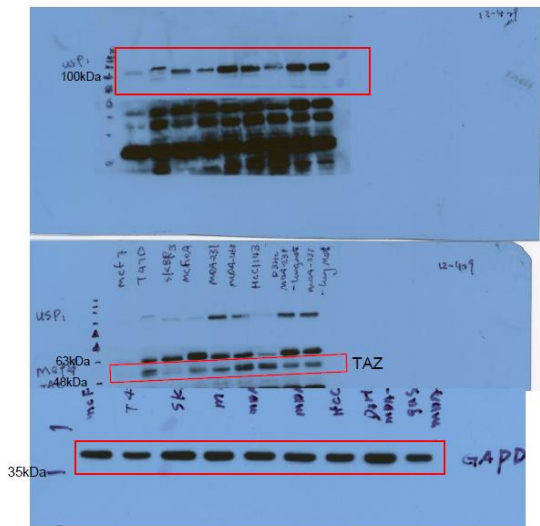


Figure 1D: Breast Cell panel

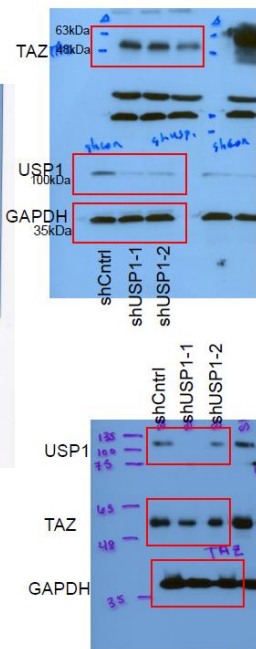


Figure 2A: shUSP1 in MCF10A

Figure 2A: shUSP1 in MDA-MB-231

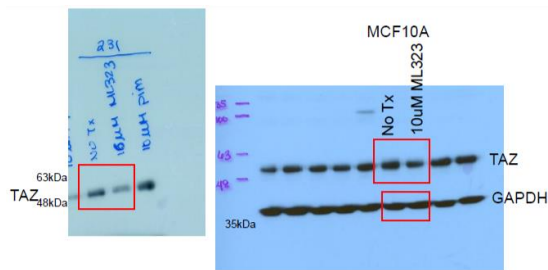


Figure 2C: ML323 treatment

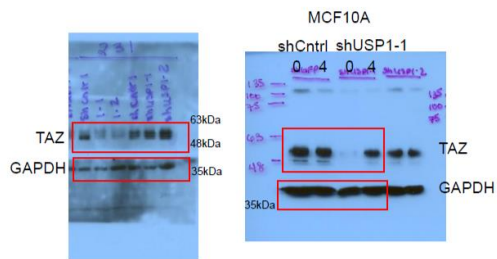


Figure 2D: MG132 TX

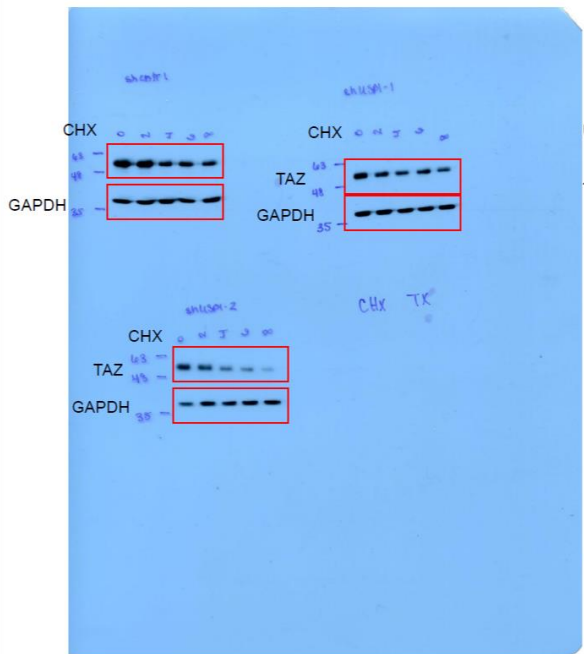


Figure 2E: CHX TX in shUSP1 MDA-MB-231

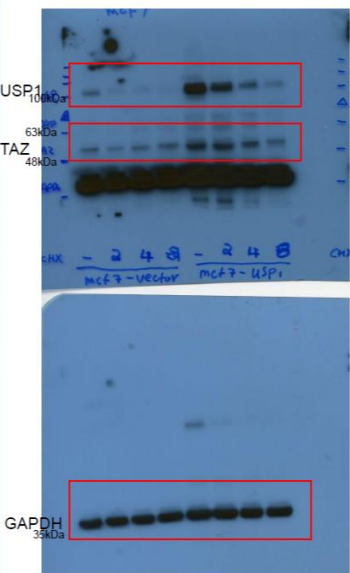


Figure 2F: CHX TX in OEUSP1 MCF7

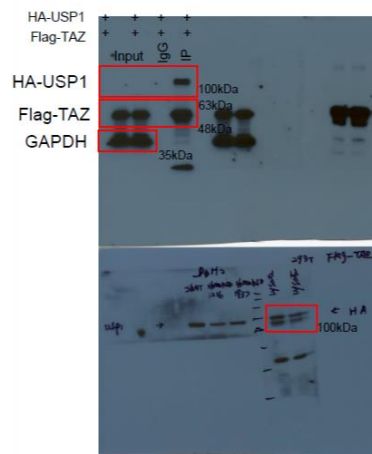


Figure 3A: Flag-TAZ_Flag-IP

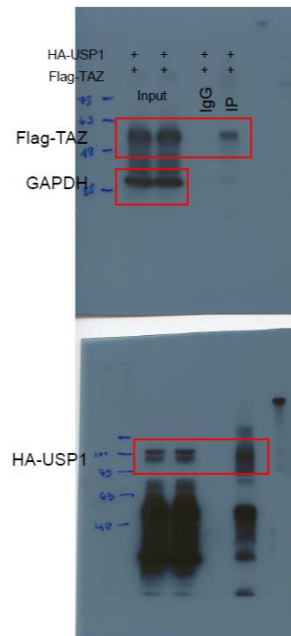


Figure 3A: HA-USP1_HA-IP

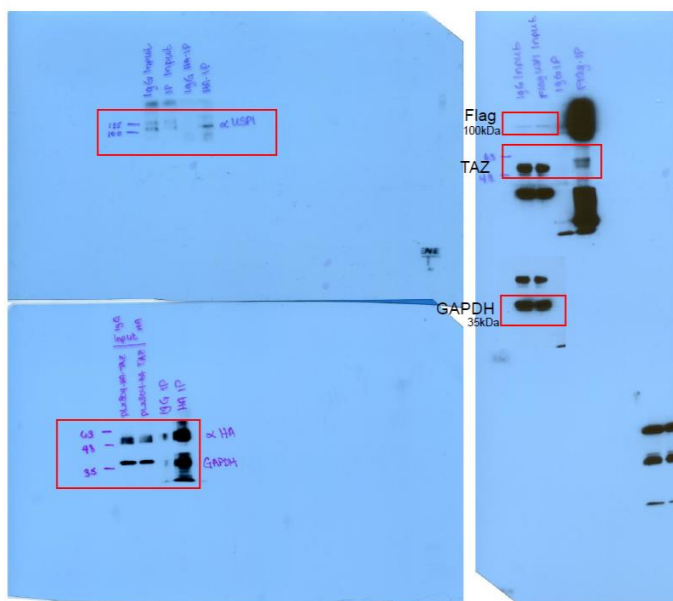


Figure 3B: Original_Exogenous with endogenous interaction

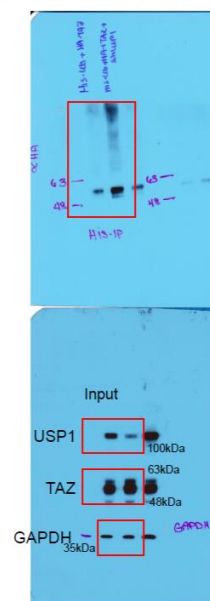
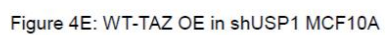
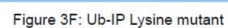
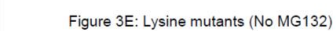


Figure 3C: Original (His-IP of TAZ-Ub with and without USP1)



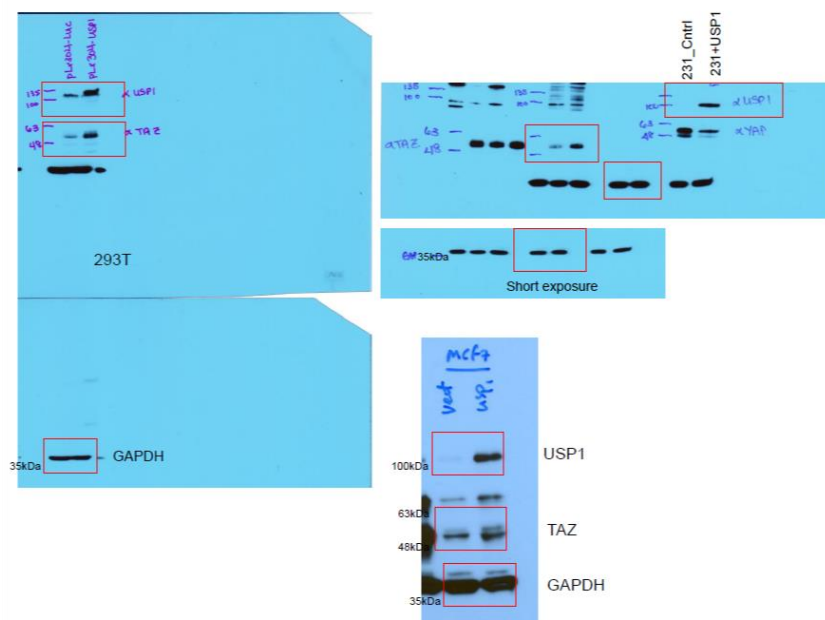


Figure 5A: USP1 OE in 293T, MDA-MB-231, and MCF7

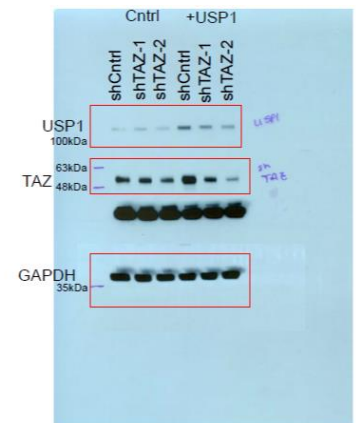
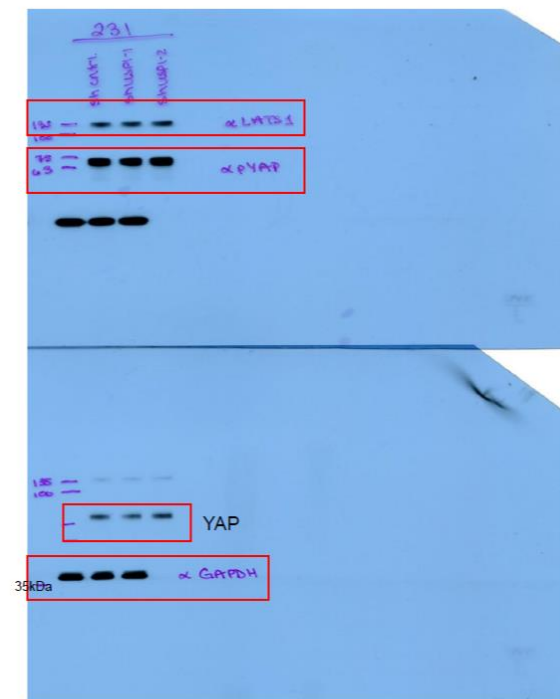


Figure 5E: shTAZ in USP1-OE MDA-MB-231



S1A: shUSP1 in MDA-MB-231 Hippo genes