Identification of TAZ-dependent breast cancer vulnerabilities using a chemical genomics screening approach

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Supplemental Material

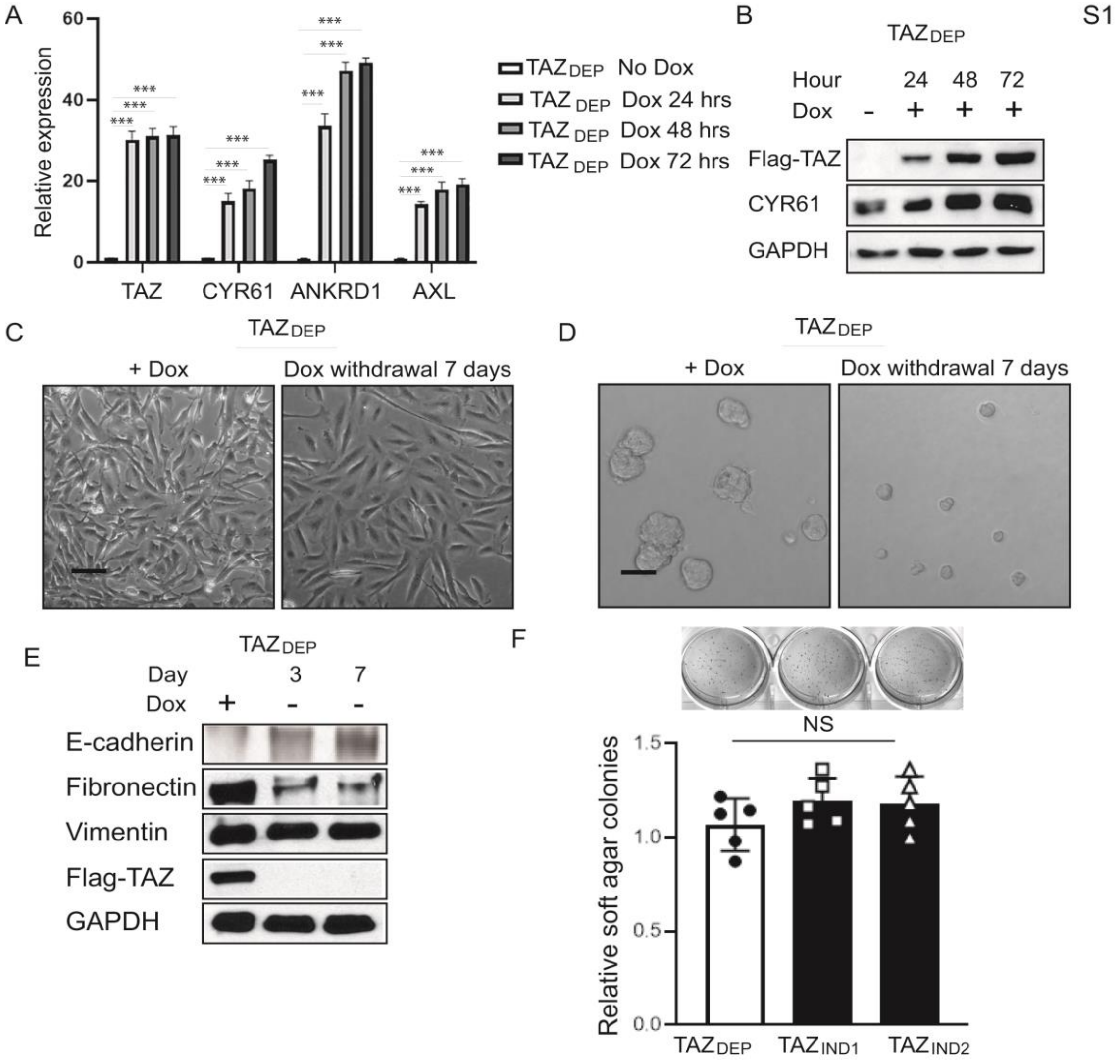

Figure S1 Dox withdrawal inhibits TAZ$_{DEP}$ cell proliferation

- **A.** qRT-PCR experiment detection of TAZ, CYR61, ANKRD1 and AXL expression in TAZ$_{DEP}$ cells in response to dox treatment. Relative expression was normalized by GAPDH expression. Unpaired two-tailed student t-test: *** $p<0.001$
- B. Immunoblotting detection of CYR61 in response to dox treatment in TAZ$_{DEP}$ cells. GAPDH was used as a loading control.

C. Representative images of TAZ_{DEP} cell morphology in a 2D culture under the condition of Dox treatment or Dox withdrawal. TAZ_{DEP} cells grown in the presence of 2 µg/ml dox. Scale bar=50 µm.
D. Representative images of TAZ_{DEP} cell morphology in a 3D culture under the condition of Dox treatment or Dox withdrawal. TAZ_{DEP} cells grown in the presence of 2 µg/ml dox. Scale bar=50 µm.
E. Representative images and quantification of colony formation in soft agar of TAZ_{DEP} and TAZ_{IND} cells. Data are shown as the mean ± SD. Unpaired two-tailed student t-test: NS=not significant.

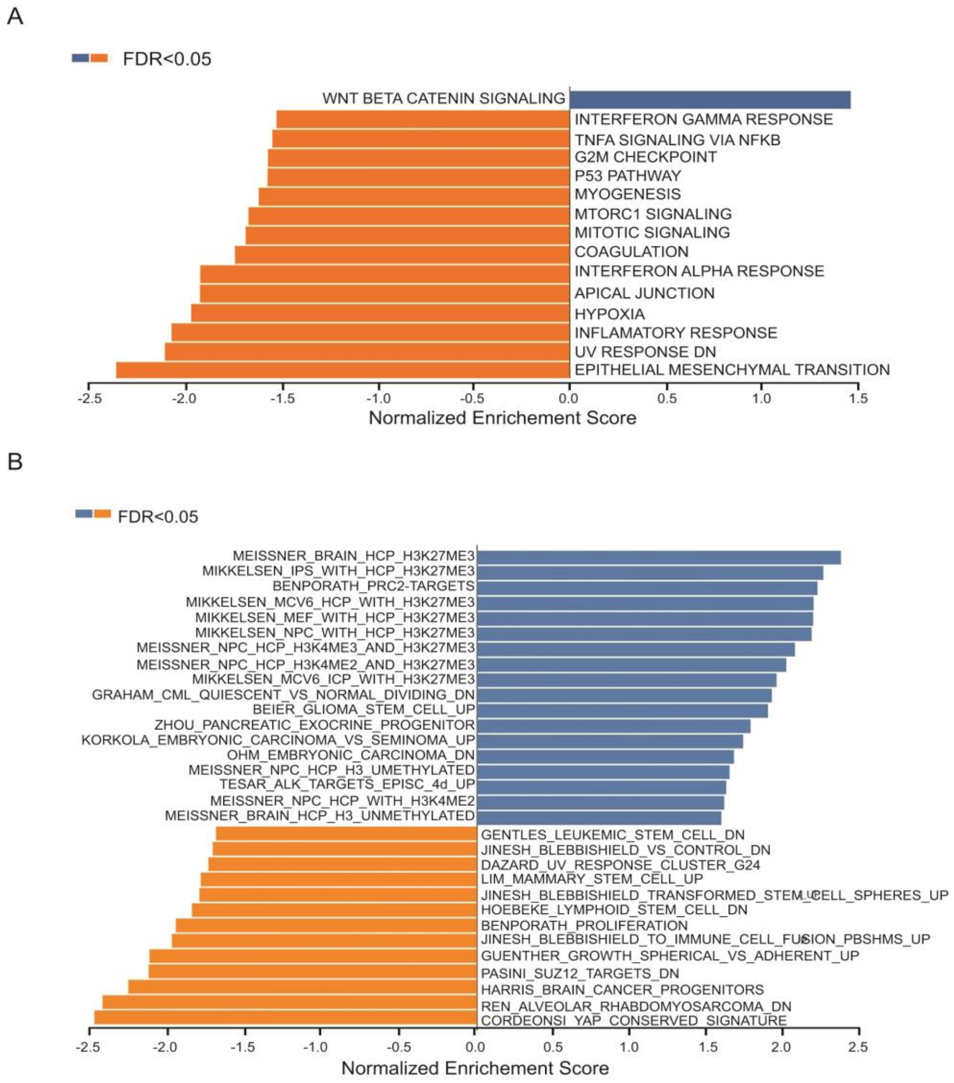

Figure S2 KEGG and GO term analysis of TAZ_{DEP} and TAZ_{IND} enriched pathways.
A. KEGG analysis for pathway alterations in TAZ_{DEP} and TAZ_{IND} cells.
B. GO term analysis identified enrichment biological processes in TAZ_{DEP} and TAZ_{IND} cells.

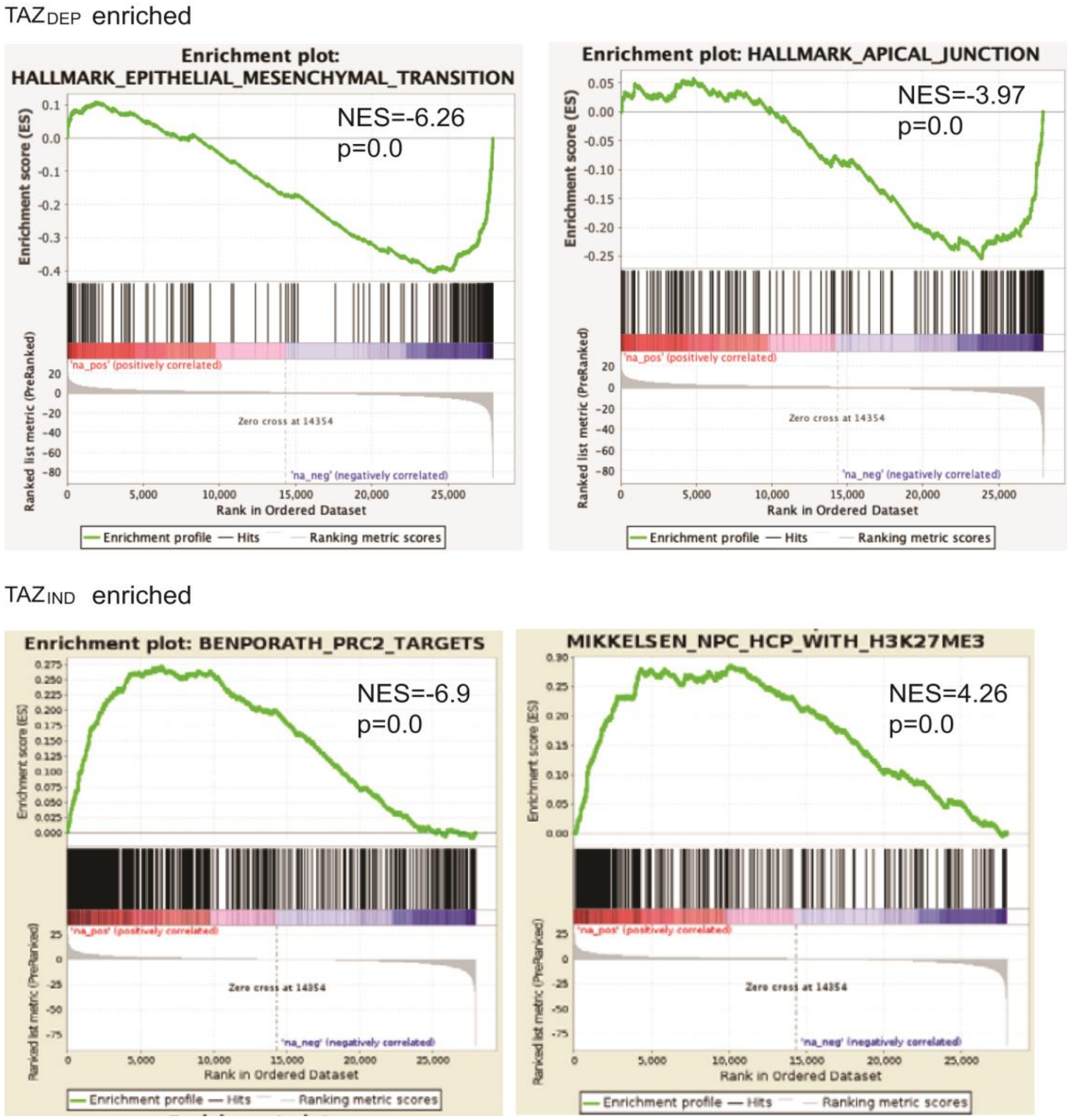

Figure S3 GSEA analysis of $\mathrm{TAZ}_{\mathrm{DEP}}$ and $\mathrm{TAZ}_{\mathrm{IND}}$ enriched pathways.

Supplemental Tables

Table-S1 Genetically characterization of $\mathrm{TAZ}_{\mathrm{DEP}}$ and $\mathrm{TAZ}_{\mathrm{IND}}$ cells.

Table-S2 Differential expression gene changes of $\mathrm{TAZ}_{\mathrm{IND}}$ versus $\mathrm{TAZ}_{\mathrm{DEP}}$ cells.

Table-S3 List of ~600 compounds library.

Table-S4 List of TAZ_{DEP} cells sensitive compounds.