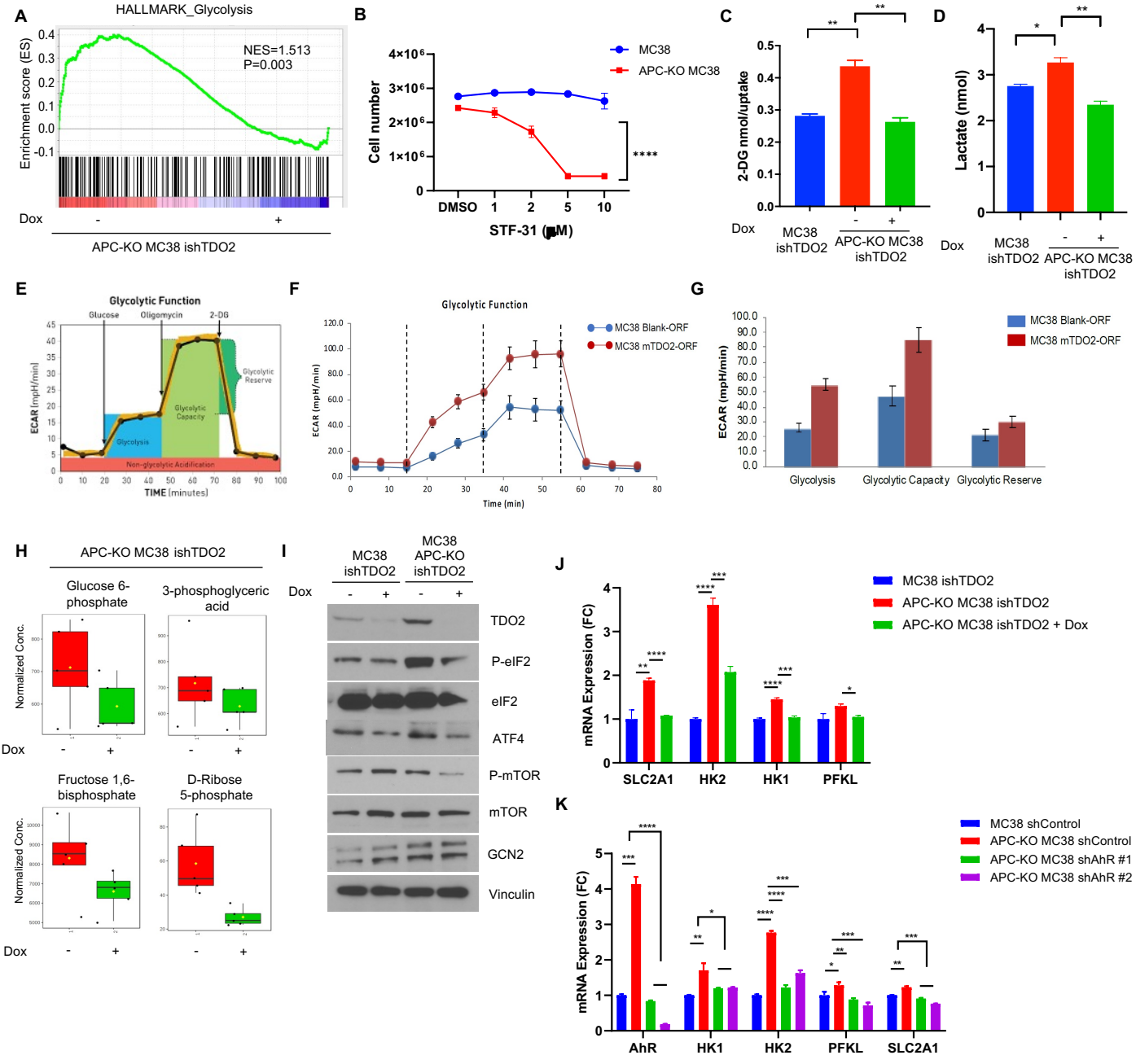
Supplementary Fig. S6.



Supplementary Fig. S6.

(A) GSEA correlation of glycolysis with altered gene expression in TDO2 depleted APC-KO MC38 cells. Normalized enrichment score (NES) and nominal P value are shown. **(B)** Cell viability assay of APC-WT and APC-KO MC38 cells treated with STF-31 for 24 hr in a dose-dependent manner. Six replicates per group. ***P<0.001, Two-way ANOVA. Two independent experiments were performed. **(C)** 2-DG uptake assay with ishTDO2 APC-WT and APC-KO MC38 cell lines with and without dox treatment. **P<0.01, ***P<0.001 **(D)** Measurement of secreted lactate with conditioned media from ishTDO2 APC-WT and APC-KO MC38 cell lines with and without dox treatment. *P<0.05, **P<0.01 **(E)** Representation of key parameters of glycolytic flux measured by Seahorse experiment. **(F and G)** Measured extracellular acidification rate (ECAR) in MC38 Blank-ORF and mouse TDO2-ORF expressing cell lines. **(H)** Changes in concentration of key glycolysis metabolites in ishTDO2 APC-KO MC38 cell line lysates. The red bars indicate cells without dox treatment and the green bars indicate dox-treated cells. n=5 per biological replicates. **(I)** Western blot of GCN2 and mTOR pathway components in ishTDO2 APC-WT and APC-KO MC38 cells. **(J)** RT-qPCR analysis of glycolysis pathway genes in ishTDO2 APC-WT and APC-KO MC38 cell lines. **P<0.01, ***P<0.001, ****P<0.0001 **(K)** RT-qPCR analysis of glycolysis pathway genes in APC-WT and APC-KO MC38 cell lines expressing shControl or two shAhR constructs. *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001