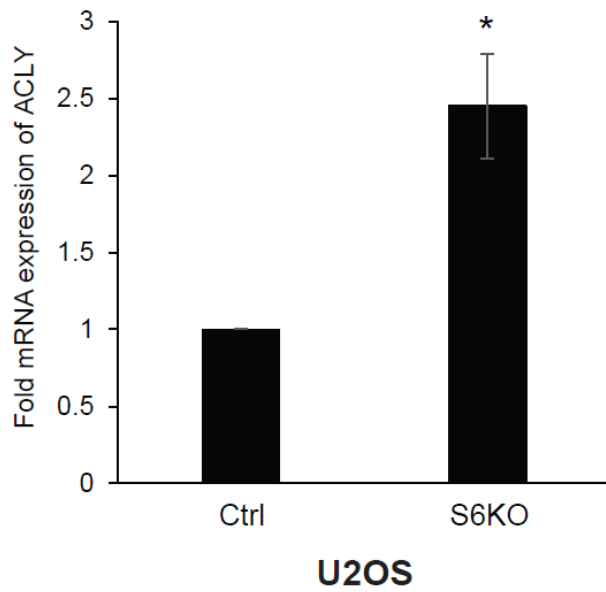


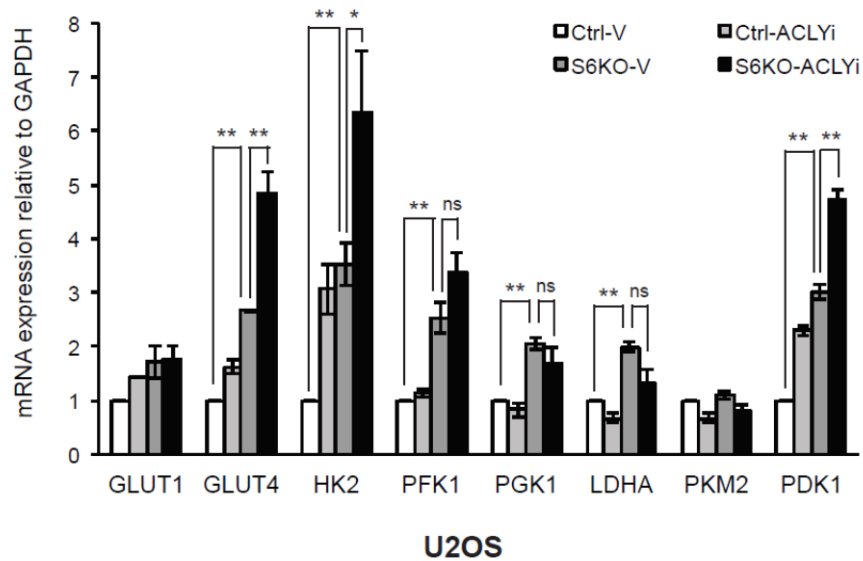
Supplementary Figure S1



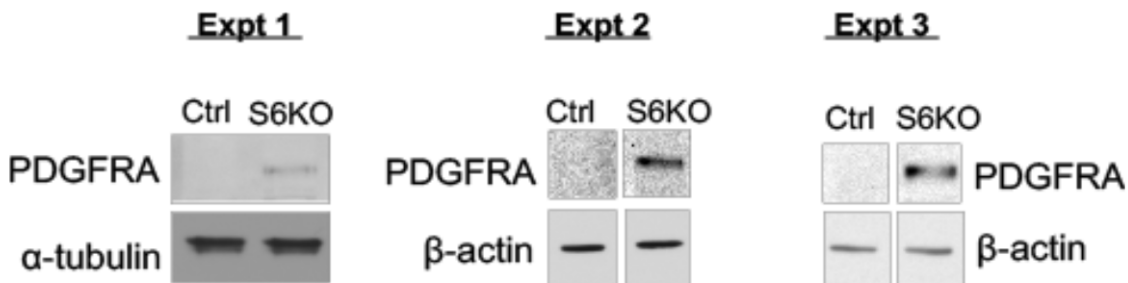
Supplementary Figure S1. ACLY mRNA levels in SIRT6-deficient U2OS cells. Increased expression of ACLY mRNA in S6KO compared to control U2OS cells, normalized to GAPDH (Mean \pm SEM of 3 independent experiments, * $p < 0.05$, two-tailed Student's t-test).

Supplementary Figure S2

A



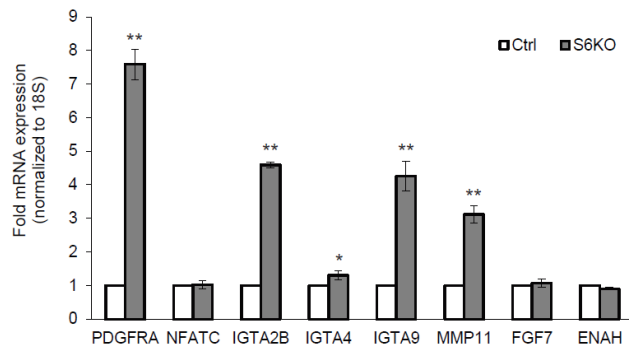
B



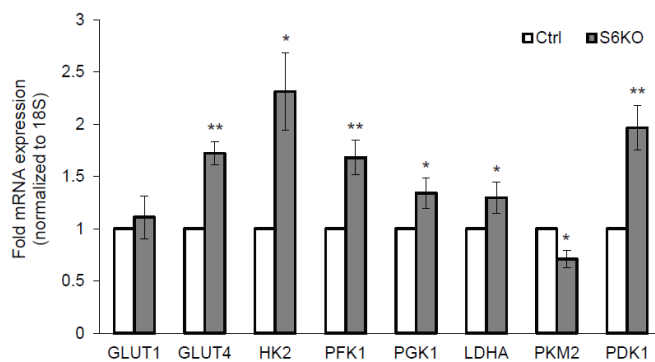
Supplementary Figure S2. Impact of SIRT6-deficiency and ACLY inhibition on expression of major glycolytic genes and PDGFRA in U2OS cells. **A.** mRNA levels of major glycolytic genes in control and SIRT6 KO U2OS cells treated with 50 μ M ACLY inhibitor for 24 hours (Mean \pm SEM of 3 independent experiments, * $p < 0.05$, ** $p < 0.01$, ns: not significant, two-tailed Student's t-test). **B.** Western blots showing increased PDGFRA protein in SIRT6 knockout (S6KO) U2OS cells. Three independent experiments are shown. Tubulin or beta-actin are shown as loading controls. In experiments 2 and 3, the lanes are cropped to remove irrelevant lanes between them, and the control and S6KO lanes show identical exposures.

Supplementary Figure S3

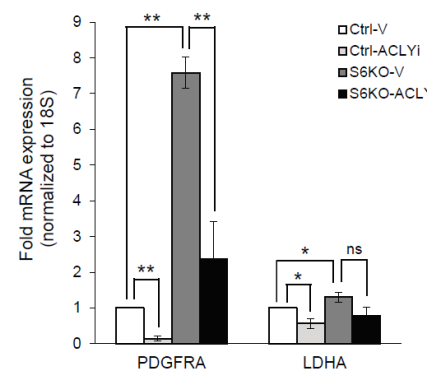
A



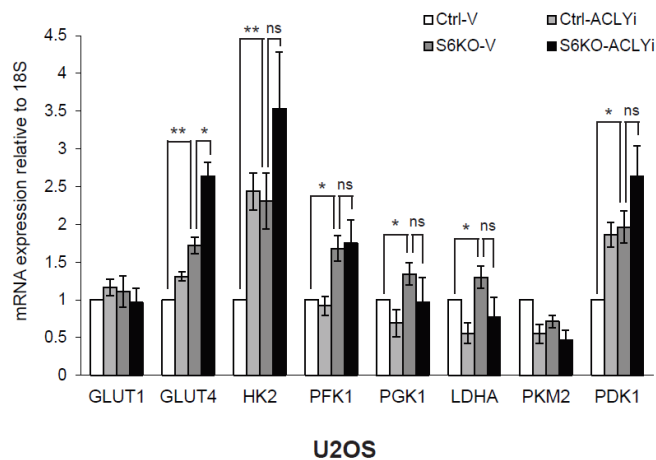
B



C



D



Supplementary Figure S3. qPCR data analysis of mRNA levels normalized to 18S rRNA in U2OS cells. **A.** Expression of acetyl-CoA responsive genes in control and SIRT6 KO U2OS cells normalized to 18S rRNA (Mean \pm SEM of 3 independent experiments, * $p < 0.05$, ** $p < 0.01$, two-tailed Student's t-test). **B.** Expression of glycolytic genes in control and SIRT6 KO cells normalized to 18S rRNA (Mean \pm SEM of 3 independent experiments, * $p < 0.05$, ** $p < 0.01$, two-tailed Student's t-test).

0.01, one-tailed Student's t-test). **C.** Increased expression of PDGFRA but not LDHA in SIRT6 KO cells is attenuated by ACLY inhibitor (ACLYi, 50 uM; 24 hours). Data are normalized to 18S rRNA and show Mean \pm SEM of 3 independent experiments, * $p < 0.05$, ** $p < 0.01$, ns: not significant, one-tailed Student's t-test). **D.** Expression of glycolytic genes in control and SIRT6 KO cells treated with 50 uM ACLY inhibitor for 24 hours, normalized to 18S rRNA (Mean \pm SEM of 3 independent experiments, * $p < 0.05$, ** $p < 0.01$, ns: not significant, one-tailed Student's t-test).

Supplementary Table S1

Table S1 Primers used in QPCR analysis	
mRNA Expression	Primer sequence
GLUT1	Forward: 5'- TATCGTCAACACGGCCTTCACTGT-3' Reverse: 5'- CACAAAGCCAAAGATGGCCACGAT-3'
GLUT4	Forward: 5'- CAACAGATAGGCTCCGAAGATG-3' Reverse: 5'- CCAAGCCACTGAGAGATGATAC-3'
LDHA	Forward: 5'- TGGTCCAGCGTAACGTGAACATCT-3' Reverse: 5'- TTGCAACCGCTTCCAATAACACGG-3'
HK2	Forward: 5'- CTGCAGCGCATCAAGGAGAACAAA-3' Reverse: 5'- ACGGTCTTATGTAGACGCTTGGCA-3'
PGK1	Forward: 5'- TCACTCGGGCTAAGCAGATTGTGT-3' Reverse: 5'- CGTGTTCATTGTCACAGCAAGT-3'
PDK1	Forward: 5'- TCATGTCACGCTGGGTAATGAGGA-3' Reverse: 5'- AACACGAGGTCTTGGTGCAGTTGA-3'
PFK1	Forward: 5'- GTGGCTCTAACTTGGGACTAAA-3' Reverse: 5'- GTTGGAGACTGTAGCAGGAATG-3'
PKM2	Forward: 5'- ATTATTTGAGGAACTCCGCCGCCT-3' Reverse: 5'- CATTTCATGGCAAAGTTCACCCGGA-3'