Supplementary Materials: ERK Dephosphorylation through MKP1 Deacetylation by SIRT1 Attenuates RAS-Driven Tumorigenesis



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Figure S1. Protective role of *SIRT1* in cancer with *K*-*RAS* mutation. **(A)** Distribution of *SIRT1* gene expression levels of human cancers in TCGA Pan-cancer cohort. The RNA-seq data (log₂TPM) of 9,345 tumor samples comprising 33 cancer types are shown. SIRT1-high and -low groups were defined using the median expression as a cut-off. **(B)** The Kaplan-Meier curves showing the overall survival (OS) of cancer patients in the TCGA cohorts: pancreatic cancer (PAAD), colorectal cancer (COADREAD), and lung adenocarcinoma (LUAD). **(C)** The OS stratified by SIRT1-high and -low groups. **(D)** The OS stratified by *K*-*RAS* mutation status (wild-type or G12; the missense mutant that occurred at glycine 12). Hazard ratio (HR) and p-value (P) were calculated using Cox regression and log-rank test, respectively.



Figure S2. Establishment of Ctrl-iRas and Sirt1-iRas cell lines **(A)** Cell enrichment of the inducible H-Ras in control (Ctrl-iRas) or Sirt1 overexpression (Sirt1-iRas) NIH3T3 cells by flow cytometric cell sorting with humanized Kusabira-Orange fluorescence. **(B)** Immunoblotting (IB) analysis of H-Ras and Sirt1 expression in both Ctrl-iRas and Sirt1-iRas NIH3T3 cells after treatment with Dox. **(C)** The mRNA expression of endogenous (left) and exogenous (right) SIRT1 in Ctrl-iRas and Sirt1-iRas cells. **(D)** Relative mRNA levels of Ras were analyzed by qRT-PCR in Ctrl-iRas and Sirt1-iRas NIH3T3 cells at indicated time points following Dox treatment. **(E)** IB analysis for SIRT1 and H-RAS after Dox treatment (3 h) in a dose-dependent manner. α -tubulin, an equal loading control.



Figure S3. Regulation of phosphorylated ERK by the SIRT1 activity. (A) IB analysis of phospho-ERK, H-RAS, and SIRT1 in the E1a-Ras MEF cells after treatment with resveratrol (RSV) or nicotinamide (NAM). (B) IB analysis of phopho-ERK, ERK2 and α -tubulin in human breast cancer MDA-MB-231 cells after treatment with NAM for 24 h. (C) IB analysis of phopho-ERK, SIRT1, and phospho-MEK in Ctrl-iRas and Sirt1-iRas cells exposed to Dox (24 h) with or without U0126.



Figure S4. Sirt1 directly binds to MKP1. (**A**) The 293T cells were transiently transfected with Flagtagged Sirt1 and Myc-tagged MKP1 CS and then IP was performed with an anti-Myc antibody, followed by IB with anti-Flag or anti-MKP1 antibodies. IgG, a negative control for IP. (**B**) The 293T cells were transiently transfected with the Myc-Sirt1 vector and then IP was performed with an anti-Myc antibody, followed by IB with an anti-MKP1 antibody.



Figure S5. Acetylation of MKP1 mediated by p300. The 293T cells were transiently transfected with p300 and Myc-tagged MKP1 CS vectors and then IP was performed with an anti-Myc antibody, followed by IB with anti-Myc or anti-pan-acetyl lysine (panAcK) antibodies.



Figure S6. MKP1 expression levels in various human cancer types. Gene expression levels of *MKP1* in the TCGA pan-cancer cohort grouped by cancer type. The RNA-seq data (log₂TPM) of 9,345 tumor samples comprising 33 cancer types are shown. Cancer types were ordered by the median expression levels of MKP1.

HR and p-values calculated from each group comparison in Figure 6 are listed as follows: SIRT1 high (MKP1 high vs low) = HR: 0.63, P: 0.09 SIRT1 low (MKP1 high vs low) = HR: 0.83, P: 0.37 MKP1 high (SIRT1 high vs low) = HR: 0.47, P: 0.0024 MKP1 low (SIRT1 high vs low) = HR: 0.61, P: 0.034 SIRT1 high, MKP high vs SIRT1 low, MKP low = HR: 0.39, P: 0.000019.



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Figure 3E











Figure 4C



Figure 3F

Figure 4B

Figure 5A



anti-pERK



anti-Myc



anti-Myc



anti-ERK2

Figure 5B





Figure 5C





Figure S2B



Figure S3A

anti-pERK	
anti-H-Ras	
anti-Sirt1	



Figure S7. The whole western blot images of Figure 3A–F, Figure 4A–C, Figure 5A–C, Figure S2B, Figure S3A,B and Figure S4.



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