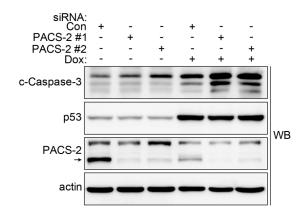
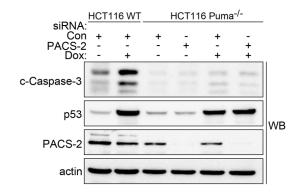
Α



В



С

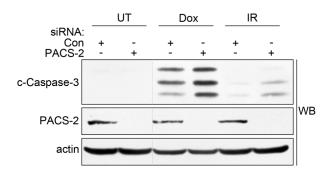


Figure S1, Related to Figure 1. **(A)** HCT116 cells were transfected with Control (Con) or PACS-2 siRNAs from Dharmacon (#1) or Qiagen (#2) for 48hr, treated for an additional 48hr with 0.5 μM Dox, harvested and analyzed by western blot. Quantitation (AlphaView, Protein Simple) showed PACS-2 knockdown led to a 2.3-fold increase in cleaved caspase-3 compared to Dox-treated control cells. Arrow, PACS-2. **(B)** HCT116 WT or HCT116 Puma-cells were transfected with Con or PACS-2 siRNAs for 48hr, treated for an additional 48hr with 0.5 μM Dox, harvested and analyzed by western blot. **(C)** HCT116 WT cells were transfected with Con or PACS-2 siRNAs for 48hr, treated for an additional 48hr with 0.5 μM Dox or 20 Gy IR, harvested and analyzed by western blot.



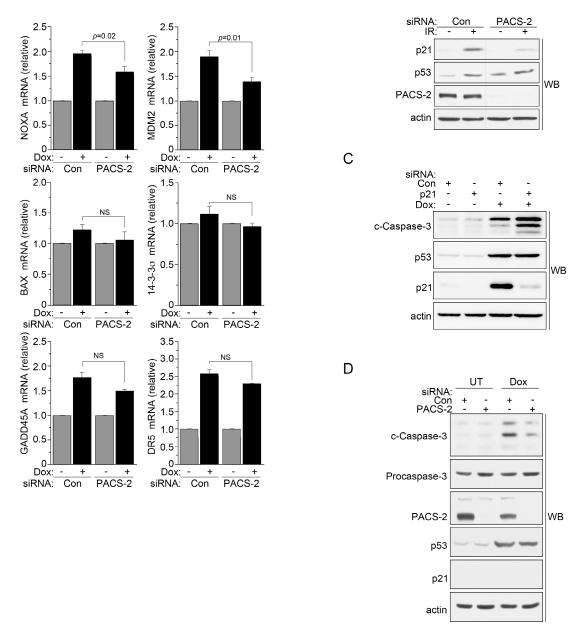


Figure S2, Related to Figure 1. (A) HCT116 WT cells from Figure 1, panel C were analyzed for the indicated transcripts by qRT-PCR (normalized to GAPDH). NS ≥ 0.05. (B) U2OS cells were transfected with Con or PACS-2 siRNAs for 72hr, treated with 20 Gy IR 24hr prior to harvest and analyzed by western blot. (C) HCT116 WT cells were transfected with Con or p21 siRNAs for 48hr, treated for an additional 48hr with 0.5 μM Dox and analyzed by western blot. Quantitation (AlphaView, Protein Simple) showed p21 knockdown led to a 2.2-fold increase in cleaved caspase-3 compared to p21 replete cells. (D) HCT116 p21- $^{1/2}$ cells were transfected with control or PACS-2 siRNAs for 48 hr and then treated for an additional 48 hr with 0.5 μM Dox, harvested and analyzed by western blot.

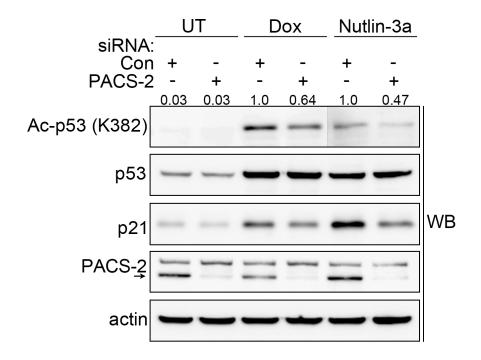
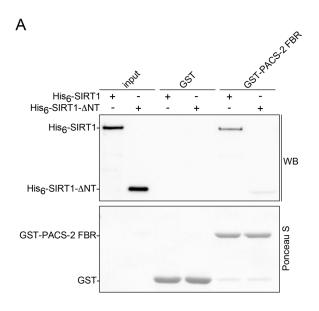
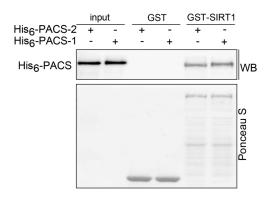


Figure S3, Related to Figure 2. HCT116 WT cells were transfected with Con or PACS-2 siRNAs for 48hr, treated for an additional 24hr with 0.5 μM Dox or 4 μM Nutlin-3a and analyzed by western blot. Ac-p53 (K_{382}) was quantified and normalized to total p53 (AlphaView, Protein Simple). A longer exposure of the Ac-p53 (K_{382}) blot for the Nutlin-3a treated samples is shown. Arrow, PACS-2.



В



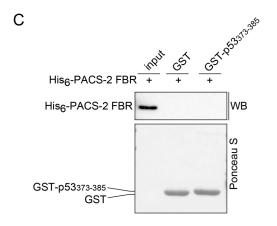


Figure S4, Related to Figure 7. (A) His₆-tagged full-length SIRT1 or SIRT1-ΔNT were incubated with GST-PACS-2_{FBR} or GST, captured with glutathione sepharose and bound SIRT1 or SIRT1-ΔNT were detected by western blot. Input GST and GST-PACS-2_{FBR} were detected with Ponceau S. **(B)** Full length His₆-tagged PACS-1 or PACS-2 were incubated with GST-SIRT1 or GST, captured with glutathione agarose and bound PACS-1 or PACS-2 were detected by western blot. Input GST and GST-SIRT1 were detected with Ponceau S. **(C)** His₆-tagged PACS-2_{FBR} was incubated with GST-p53₃₇₃₋₃₈₅ or GST, captured with glutathione sepharose and bound PACS-2_{FBR} was detected by western blot. Input GST and GST-p53₃₇₃₋₃₈₅ were detected with Ponceau S.

TABLE S1

Mean percentage of cells in each cell cycle phase \pm SD from 4 independent experiments. Statistical significance determined using an unpaired Student's t-test. Related to Figure 1.

	untreated		Doxorubicin (24 hr)		
siRNA:	Con	PACS-2	Con	PACS-2	p value
G ₀ /G ₁	7.4 ± 0.4	6.8 ± 1.4	24.7 ± 3.1	15.3 ± 1.7	0.004
S	87.7 ± 0.5	88.6 ± 3.4	63 ± 3.1	70.5 ± 1.6	0.012
G ₂ /M	3.8 ± 0.5	3.6 ± 2.1	10.1 ± 0.3	11.6 ± 0.7	0.013

TABLE S2

Mean percentage of cells in each cell cycle phase \pm SD from 3 independent experiments. Statistical significance determined using an unpaired Student's t-test to compare Dox vs. Dox + EX-527 for each siRNA condition. Related to Figure 5.

siRNA	Control						
	UT	Dox	Dox + EX-527	p value			
G₀/G₁	6.2 ± 0.5	28.4 ± 1.2	29.9 ±1.0	0.17			
S	91.1 ± 0.6	59.6 ± 2.1	55.8 ± 1.6	0.07			
G ₂ /M	2.8 ± 0.5	12 ± 1.1	14.2 ± 0.6	0.05			
siRNA	PACS-2						
G ₀ /G ₁	4.9 ± 0.6	18.0 ± 0.9	25.7 ± 0.9	<0.001			
S	92.8 ± 0.5	67.0 ± 2.5	58.8 ± 3.2	0.03			
G ₂ /M	2.3 ± 0.4	15 ± 1.8	15.5 ± 3.6	0.9			
siRNA	p21						
G ₀ /G ₁	5.2 ± 0.2	10.1 ± 1.5	11.3 ± 0.6	0.6			
S	92.3 ± 0.5	79.0 ± 1.2	75.5 ± 1.4	0.1			
G ₂ /M	2.5 ± 0.6	10.3 ± 2.7	13.2 ± 1.4	0.2			