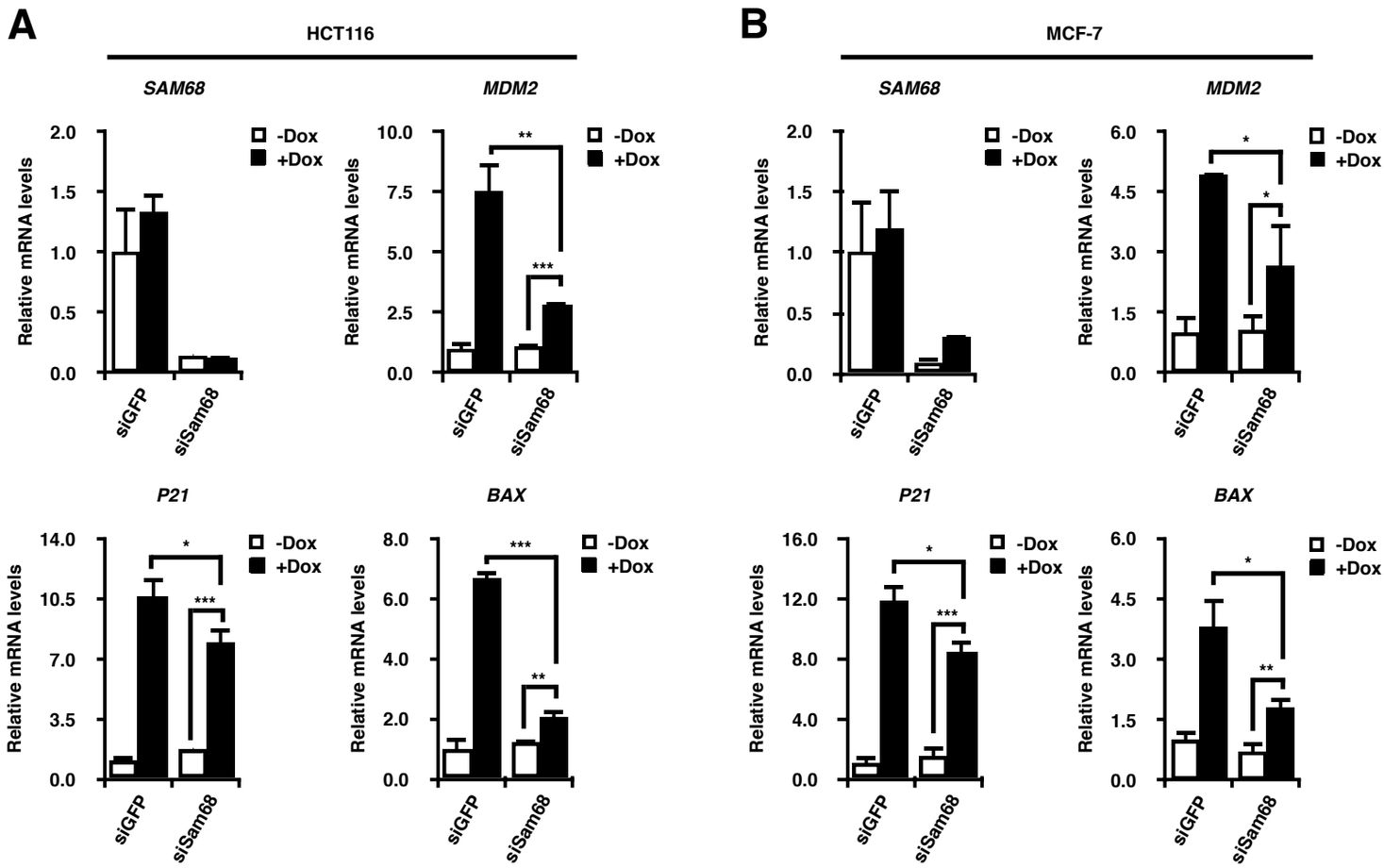
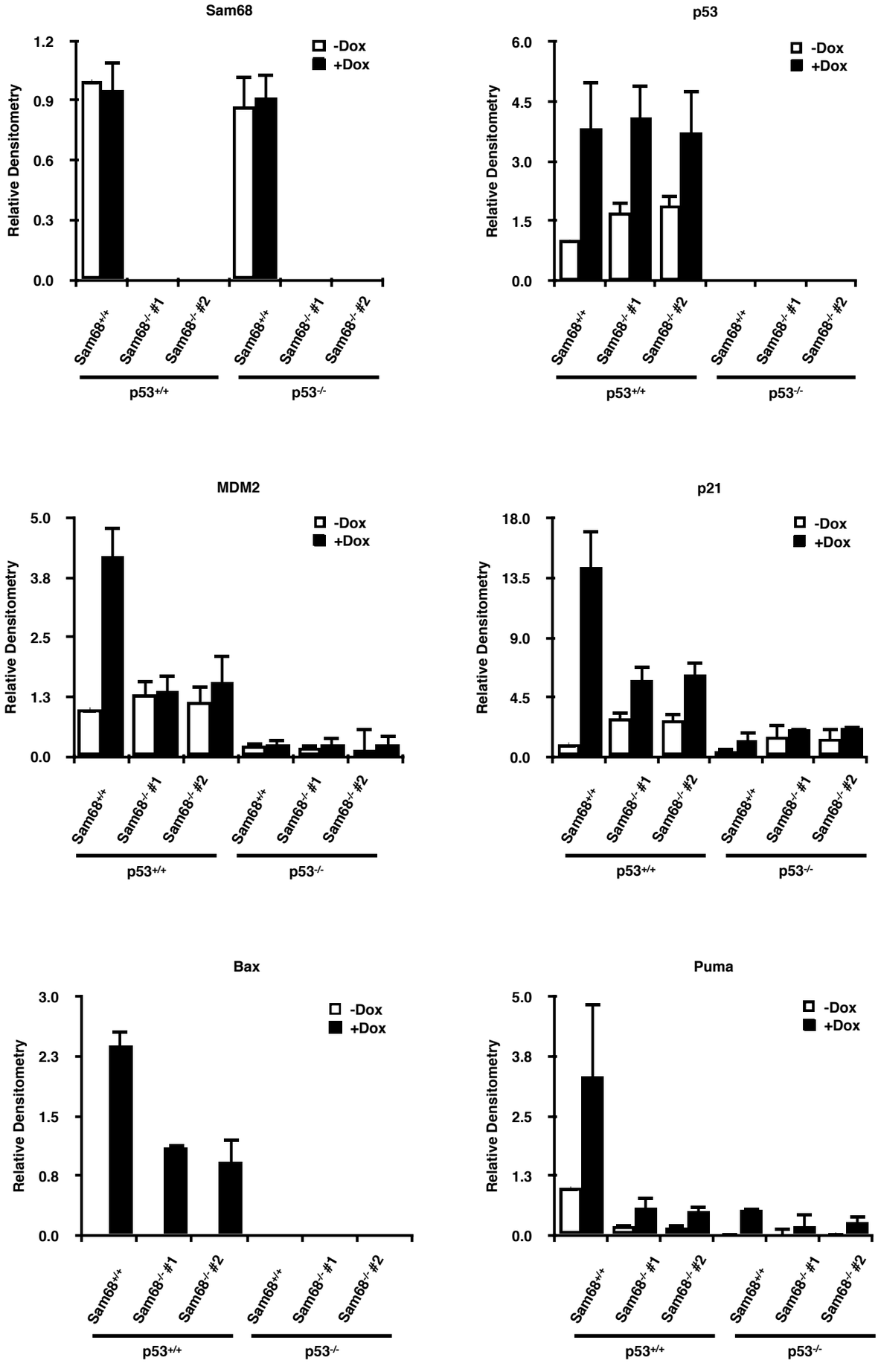
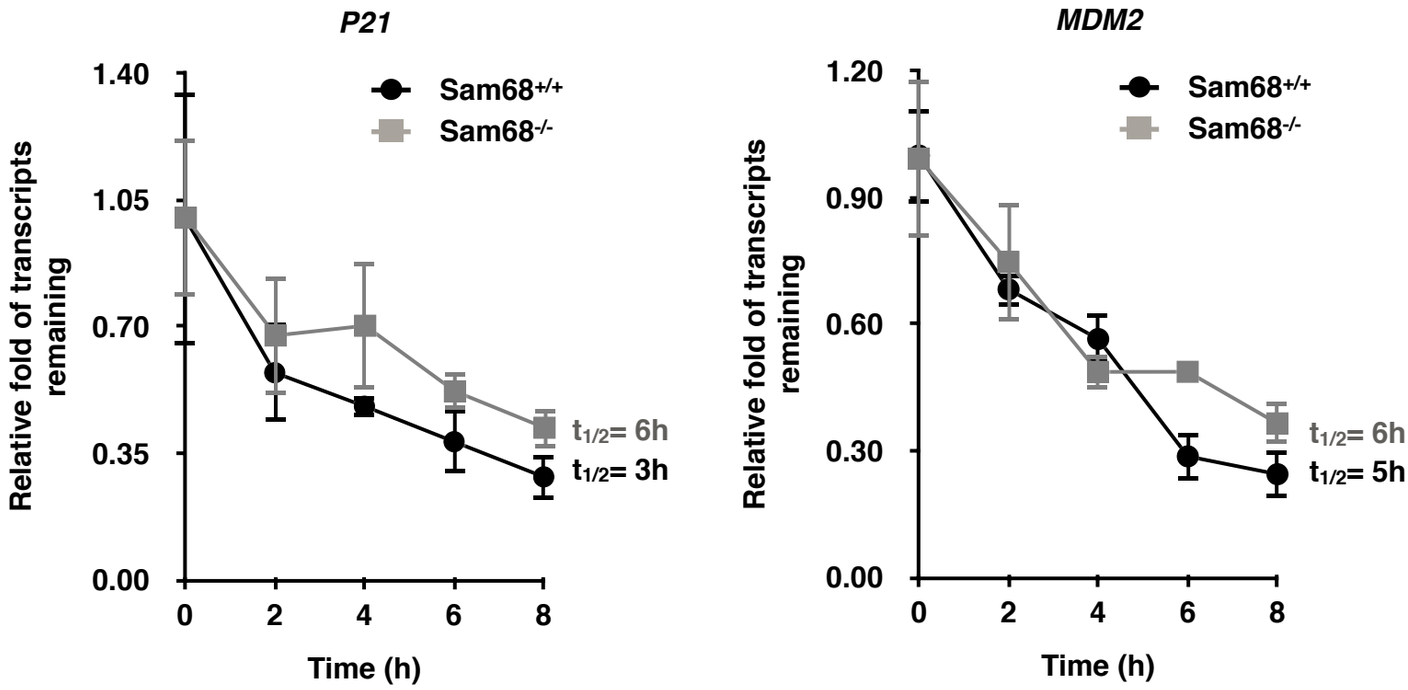
Li and Richard, Figure S1



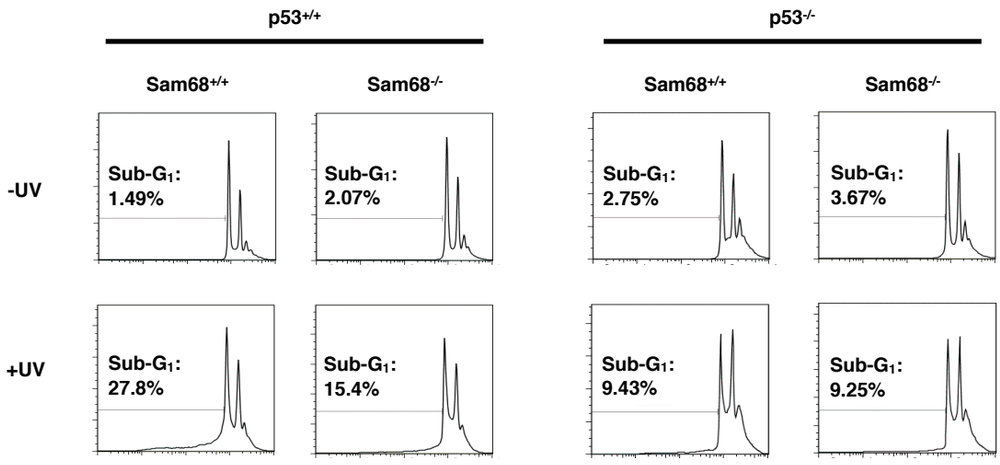
Li and Richard, Figure S2



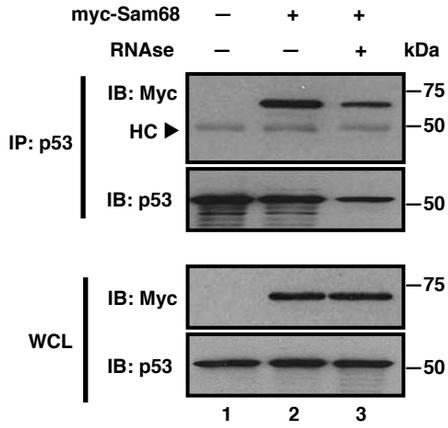
Li and Richard, Figure S3

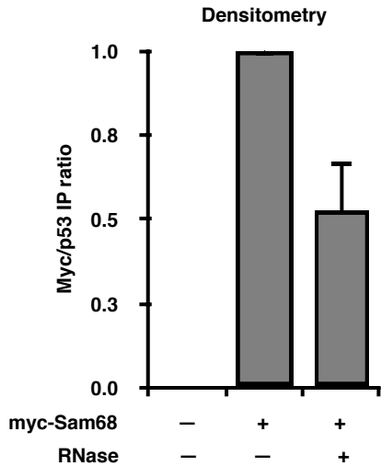


Li and Richard, Figure S4

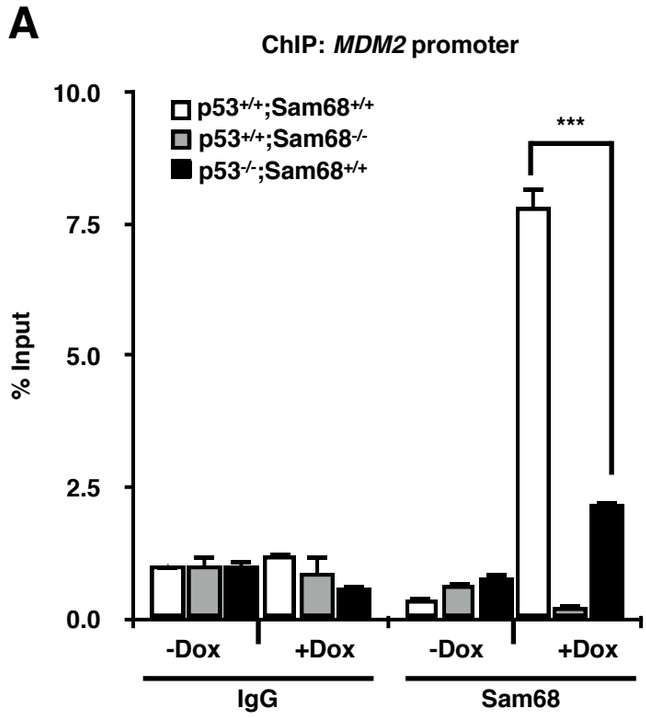


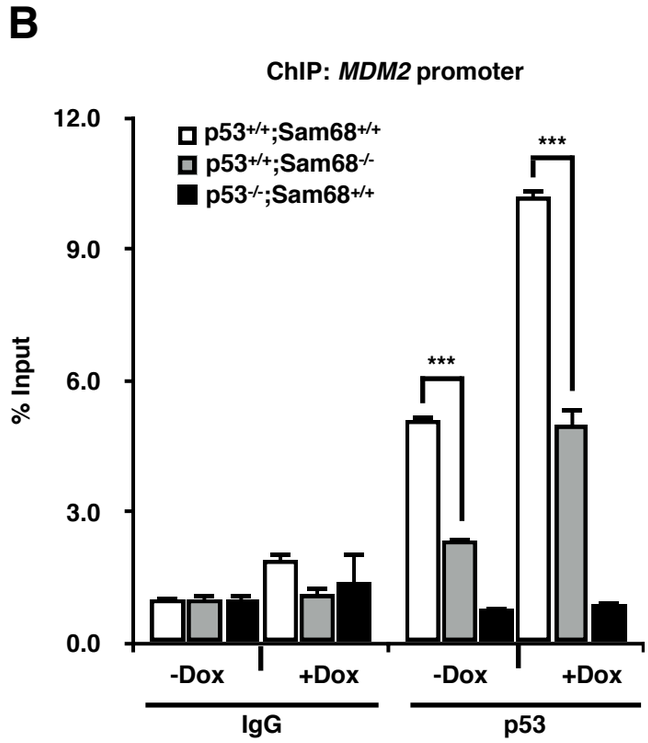
Li and Richard, Figure S5





Li and Richard, Figure S6





Li and Richard, Table S1

Primers			
Gene	**Application**	**Forward (5'-3')**	**Reverse (5'-3')**
P21	qPCR	TGCCGAAGTCAGTTCCTTGT	GTTCTGACATGGCGCCTCC
	ChIP-qPCR	AGCAGGCTGTGGCTCTGATT	CAAAATAGCCACCAGCCTCTTCT
PUMA	qPCR	GACCTCAACGCACAGTACGA	GAGATTGTACAGGACCCTCCA
	ChIP-qPCR	GGTTGACTCAGCTTTTCCTCTTG	GGAAAATGCATGGTTTAAATAGCC
BAX	qPCR	GGGTTGTCGCCCTTTTCTAC	GGAGGAAGTCCAATGTCCAG
MDM2	qPCR	AGGAGATTTGTTTGGCGTGC	TGAGTCCGATGATTCCTGCTG
	ChIP-qPCR	GGTTGACTCAGCTTTTCCTCTTG	GGAAAATGCATGGTTTAAATAGCC
SAM68	qPCR	CTCCTGCTAGGCCAGTGAA	TTGTGGGTAAAGCAACAGGA
	PCR	TGTTCAGTCTGGCTTGTGAGT	CACTGCAAGAGAAGAGGGCA
PR-lncRNA-1	qPCR	AAGTCACTTGCCTGAGTTTGG	CTGCTGGGGCTCAACTGT
lincRNA-p21	qPCR	GGGTGGCTCACTCTTCTGGC	TGGCCTTGCCCGGGCTTGTC
GAPDH	qPCR	GACAGTCAGCCGCATCTTCT	GCGCCCAATACGACCAAAT
18S	qPCR	GCAGGCGCGGGTAACC	AAGCTTATGACCCGCACTTACTG
ACTB	qPCR	ACCACACCTTCTACAATGAGC	GATAGCACAGCCTGGATAGC

Li and Richard, Table S2

	Sam68	Deletion (bp)
HCT116 p53	clone #1	899
	clone #2	757
HCT116 p53	clone #1	515
	clone #2	877

SUPPLEMENTARY DATA
SUPPLEMENTAL TABLE AND FIGURE LEGENDS

Figure S1. RNAi-depletion of Sam68 attenuates upregulation of p53 targets in response to DNA damage.
(**A**) RT-qPCR analysis of *SAM68* and direct p53 targets (*MDM2, P21, BAX*) in p53 wild type HCT116 or
(**B**) MCF-7 cells. Cells were either untreated or treated with 1 μM of doxorubicin for 24 h before RNA extraction. Expression levels were normalized to *GAPDH*. Data are represented as mean ± S.D. from 3 independent experiments done in biological triplicates. Statistical significance was calculated with student's *t*-test (*$p \leq 0.05$, **$p \leq 0.005$, ***$p \leq 0.0005$).

Figure S2. Densitometry quantification.
Quantification of p53, Sam68, and p53 targets (MDM2, p21, Bax, Puma) in HCT116 cells untreated (-Dox) or treated with doxorubicin (+Dox). Densitometry analysis was performed using ImageJ. Expression levels were normalized to loading control. Data are represented as mean ± S.D. from 3 independent experiments.

Figure S3. Sam68 selectively regulates *P21* mRNA stability.
Transcript stability was assessed in $Sam68^{+/+}$ or $Sam68^{-/-}$ HCT116 cells treated with actinomycin D (5μg/ mL). mRNA was extracted at the indicated time points and transcripts were quantified by qPCR using primers specific for *P21* and *MDM2* which were normalized to *GAPDH* expression levels. Transcript half-life ($t_{1/2}$) was calculated based on the relative fold of mRNA remaining compared to initial levels (0 h). Data, replicated in 3 independent experiments, are represented as mean ± S.D. of technical triplicates. Statistical significance was calculated with student's *t*-test (*$p \leq 0.05$, **$p \leq 0.005$, ***$p \leq 0.0005$).

Figure S4. Sam68-deficiency reduces p53-mediated apoptosis.
Cell death was analyzed by flow cytometry in untreated (-UV) and treated (+UV, 60 J/m^2) isogenic HCT116 cells. Total apoptosis was assessed by measuring sub-G_1 cells after PI staining, and quantification was done using FlowJo software.

Figure S5. RNA enhances the interaction between Sam68 and p53.
p53 immunoprecipitation in doxorubicin-treated HCT116 cells transiently transfected with either empty vector (-) or myc-Sam68 (+). Lysates were untreated (-) or treated (+) with RNase A (1mg/ mL) at 37°C prior to immunoprecipitation. Densitometry analysis (bottom) was performed using ImageJ. Levels were calculated as the ratio of total immunoprecipitated myc-Sam68 over total immunoprecipitated p53, and then normalized to the positive control (myc-Sam68 -RNase). Data are represented as mean ± S.D. from 3 independent experiments. IP, immunoprecipitation; IB, immunoblot; WCL, whole cell lysate; HC, heavy chain.

Figure S6. Sam68 and p53 are recruited to the *MDM2* promoter in an interdependent manner.
(**A** and **B**) ChIP-qPCR analysis of HCT116 cells. Cell lysates from untreated and doxorubicin-treated cells were immunoprecipitated with either nonspecific IgG, p53- or Sam68-specific antibodies. Precipitated DNA was quantified by qPCR with primers specific for p53-response elements of the *MDM2* promoter. Data, replicated in 3 independent experiments, are represented as mean ± S.D. of technical triplicates. Statistical significance was calculated with student's *t*-test (*$p \leq 0.05$, **$p \leq 0.005$, ***$p \leq 0.0005$).

Table S1. List of primers.

Table S2. HCT116 Sam68$^{-/-}$ clones.