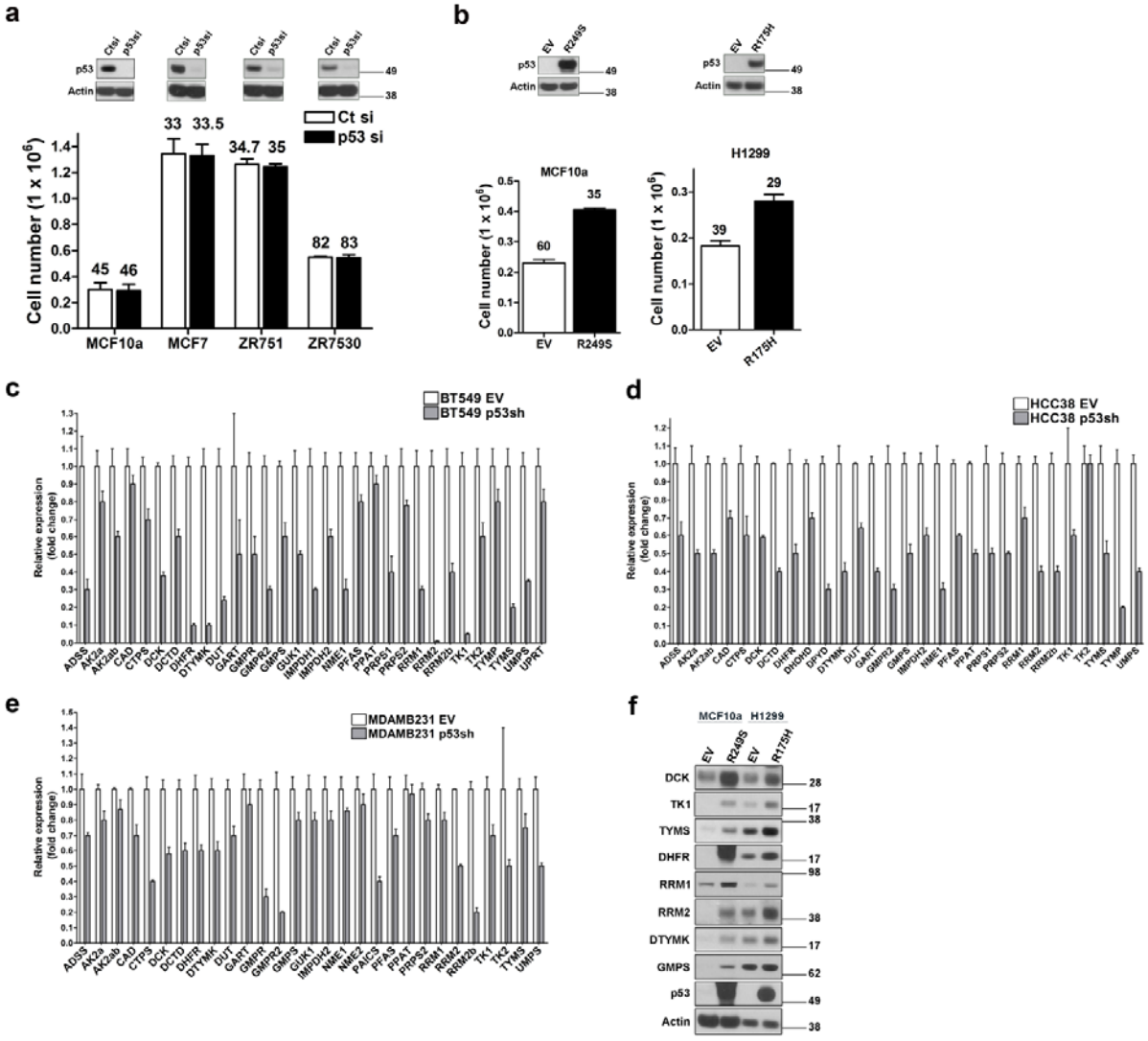
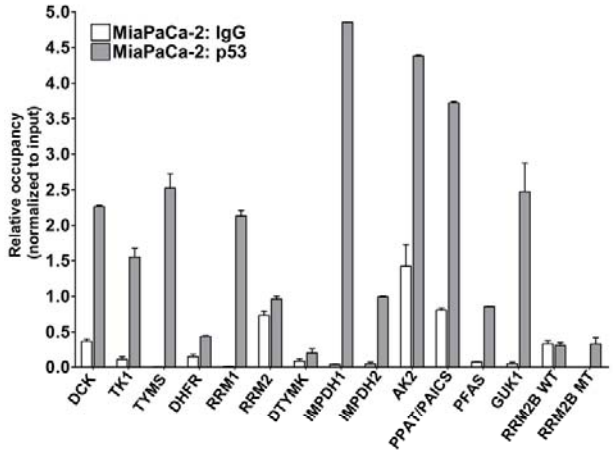
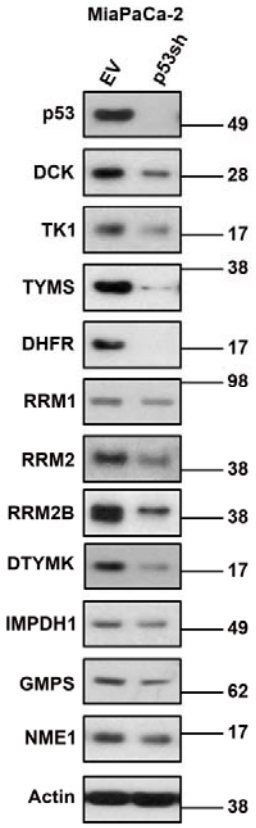

a
Ctsi
p53si
p53
Actin
49
38
Ct si
p53 si
Cell number (1 x 10^6)
33
33.5
34.7
35
82
83
45
46
MCF10a
MCF7
ZR751
ZR7530
b
EV
R249S
R175H
MCF10a
H1299
60
35
39
29
c
BT549 EV
BT549 p53sh
Relative expression (fold change)
ADSS AK2a AK2ab CAD CTPS DCK DCTD DHFR DTYMK DUT GART GMPR GMPR2 GMPS GUK1 IMPDH1 IMPDH2 NME1 PFAS PPAT PRPS1 PRPS2 RRM1 RRM2 RRM2b TK1 TK2 TYMP TYMS UMPS UPRT
d
HCC38 EV
HCC38 p53sh
ADSS AK2a AK2ab CAD CTPS DCK DCTD DHFR DHOHD DPYD DTYMK DUT GART GMPR2 GMPS IMPDH2 NME1 PFAS PPAT PRPS1 PRPS2 RRM1 RRM2 RRM2b TK1 TK2 TYMS TYMP UMPS
e
MDAMB231 EV
MDAMB231 p53sh
ADSS AK2a AK2ab CAD CTPS DCK DCTD DHFR DTYMK DUT GART GMPR GMPR2 GMPS GUK1 IMPDH2 NME1 NME2 PAICS PFAS PPAT PRPS2 RRM1 RRM2 RRM2b TK1 TK2 TYMS UMPS
f
MCF10a
H1299
EV
R249S
EV
R175H
DCK
TK1
TYMS
DHFR
RRM1
RRM2
DTYMK
GMPS
p53
Actin
28
17
38
17
98
38
17
62
49
38

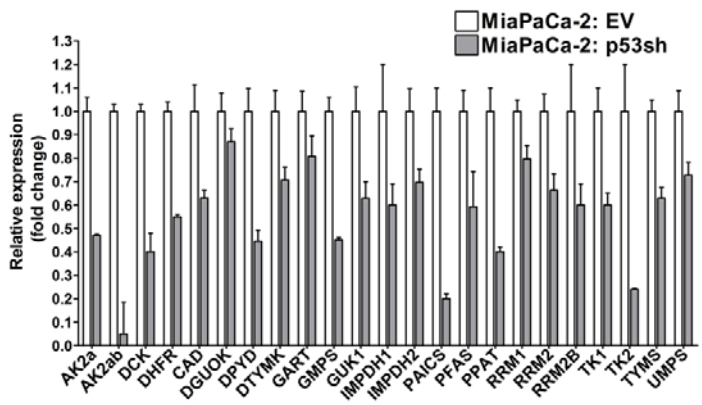
g

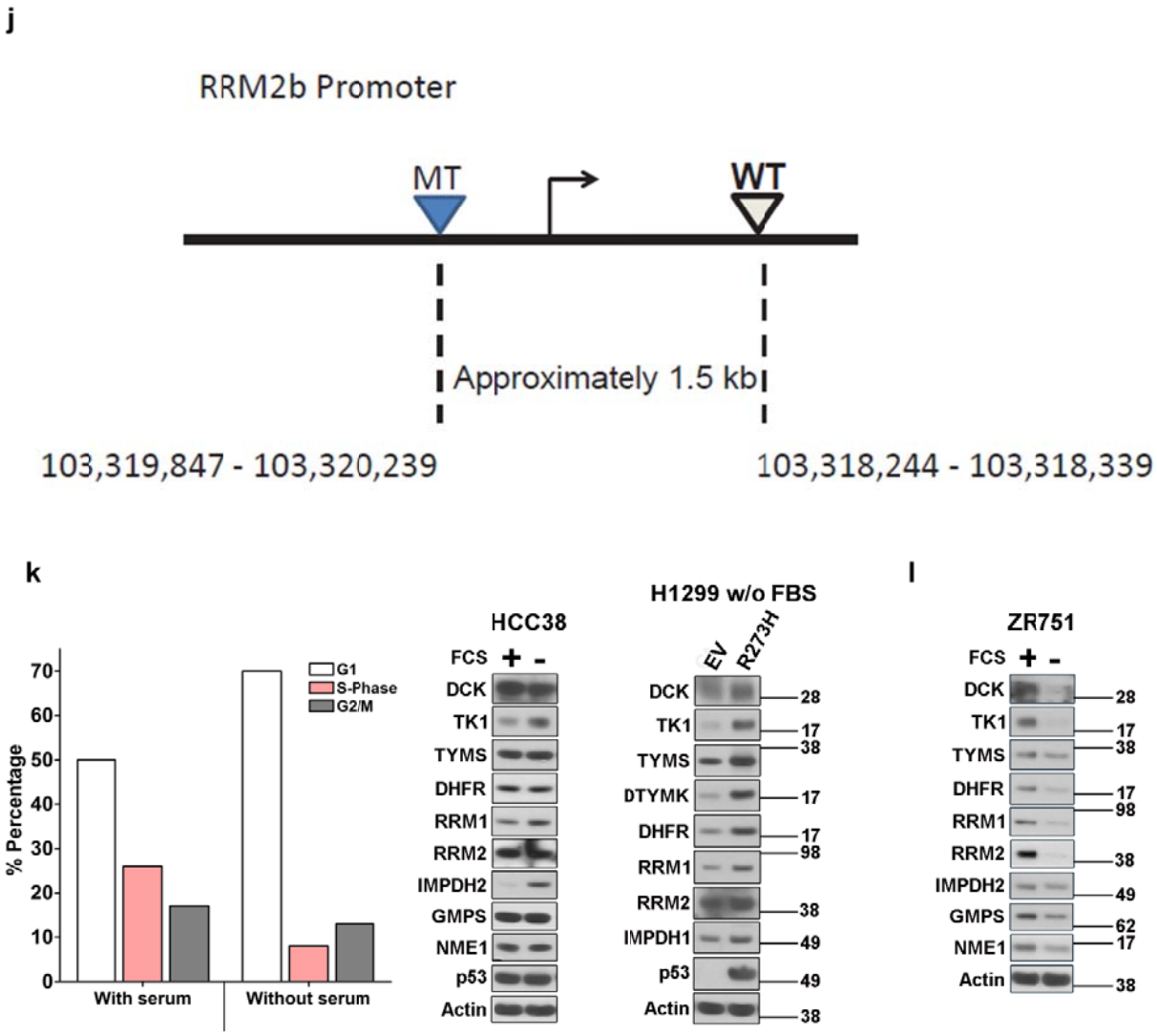

MiaPaCa-2: IgG
MiaPaCa-2: p53
Relative occupancy (normalized to input)
5.0
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
DCK
TK1
TYMS
DHFR
RRM1
RRM2
DTYMK
IMPDH1
IMPDH2
AK2
PPAT/PAICS
PFAS
GUK1
RRM2B WT
RRM2B MT

h


MiaPaCa-2
EV
p53sh
p53
49
DCK
28
TK1
17
TYMS
38
DHFR
17
RRM1
98
RRM2
38
RRM2B
38
DTYMK
17
IMPDH1
49
GMPS
62
NME1
17
Actin
38

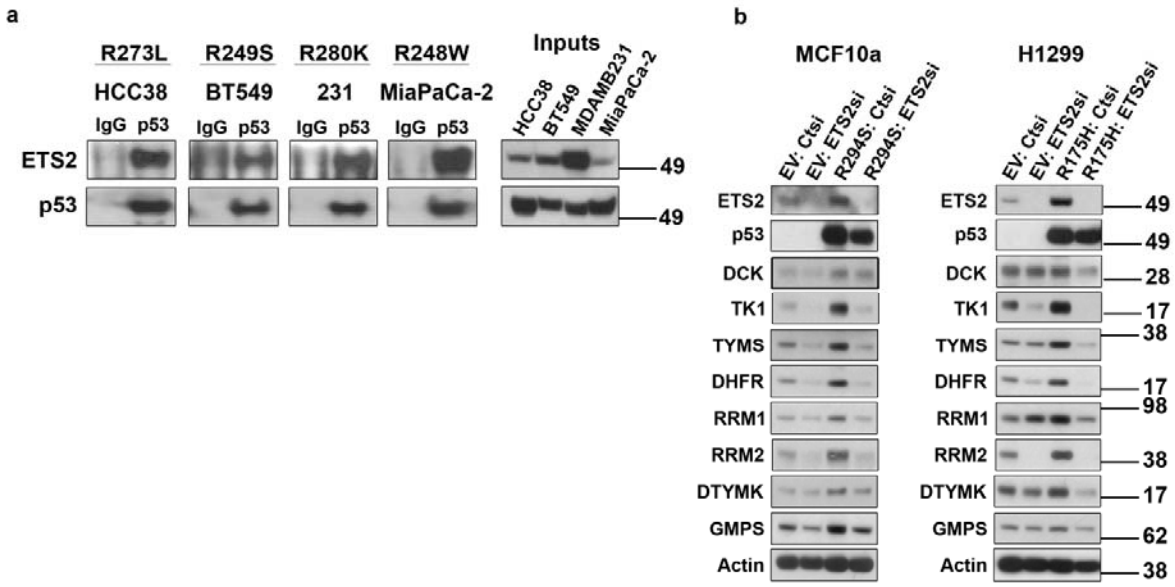
i


MiaPaCa-2: EV
MiaPaCa-2: p53sh
Relative expression (fold change)
1.3
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
AK2a
AK2ab
DCK
DHFR
CAD
DGUOK
DPYD
DTYMK
GART
GMPS
GUK1
IMPDH1
IMPDH2
PAICS
PFAS
PPAT
RRM1
RRM2
RRM2B
TK1
TK2
TYMS
UMPS

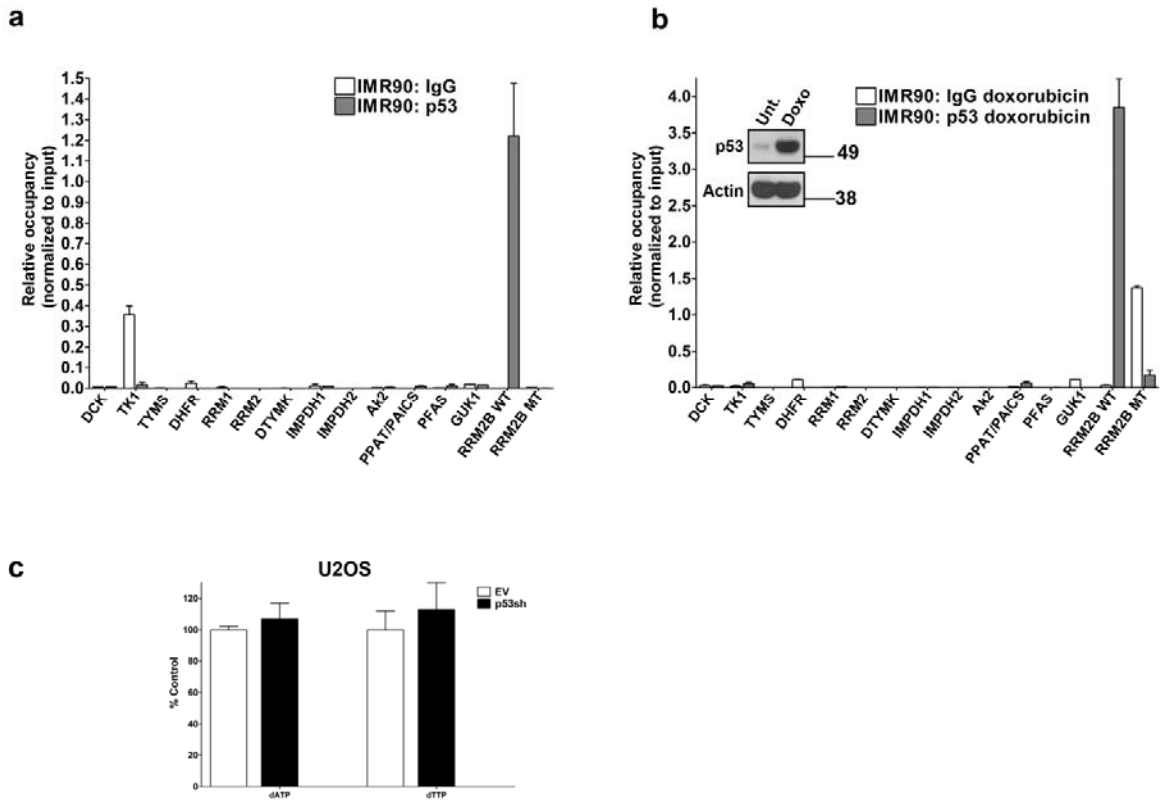


Supplementary Figure 1 (Related to Figure 1). Mtp53 promotes cell proliferation by directly activating NMG. (**a**) MCF10a, MCF7, ZR751 and ZR7530 cells were transfected with either a control (Ct) or p53 siRNA (p53si) and cell counts and doubling times were estimated after 72 hours. Error bars indicate mean ±SD of three independent replicates. Inset is the western blot showing p53 knockdown. (**b**) MCF10a cells were infected with R249S p53 mutant, selected for 7 days. After selection cells were seeded and doubling times were estimated after 72 hours.

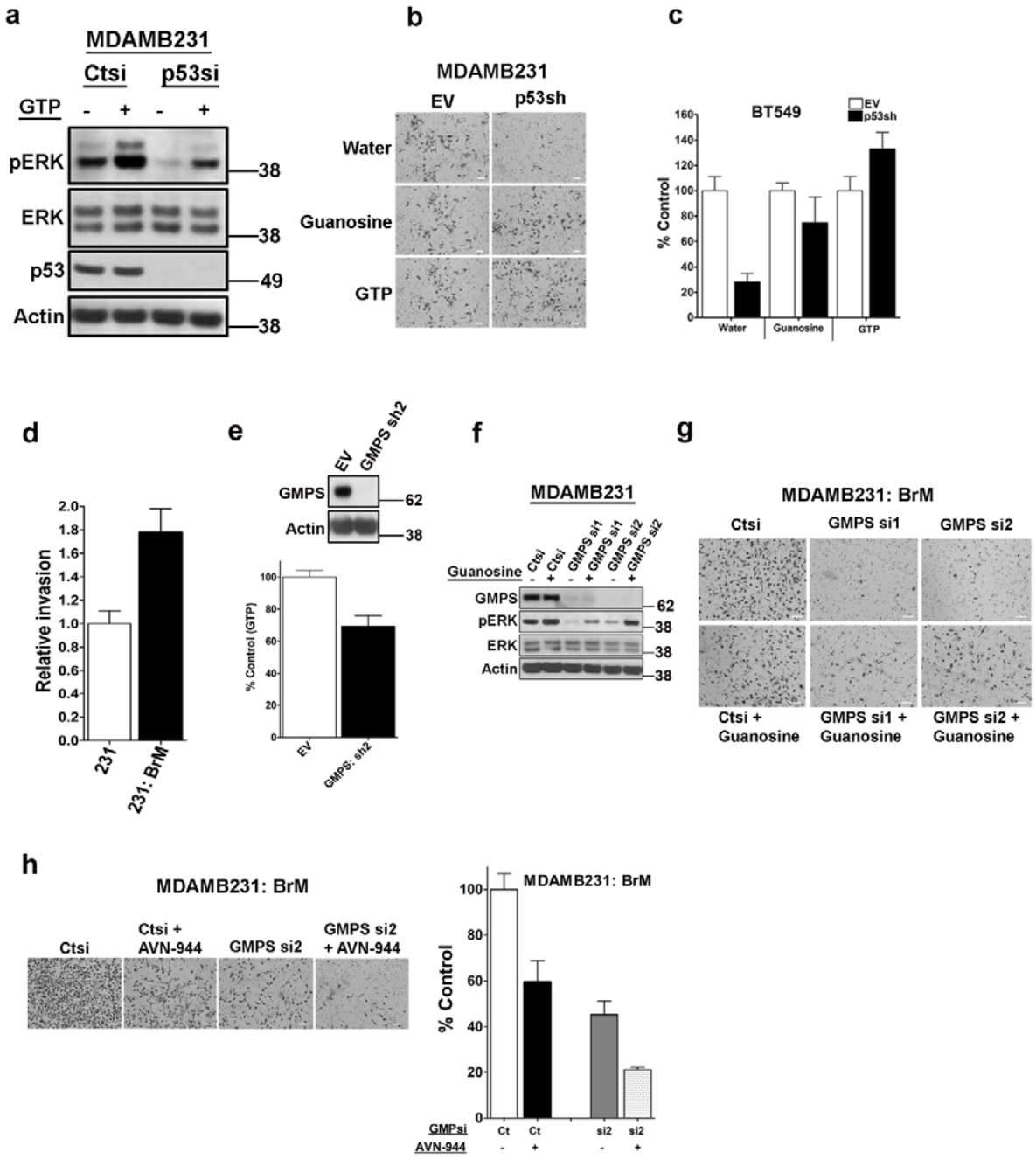
H1299 empty vector or R175H stable expressing cells were plated and cell counts and doubling times were determined after 72 hours. Error bars indicate mean ±SD of three independent replicates. Insets are the western blots showing R249S and R175H p53 mutant stable expression. (**c**) Cells were infected with an empty vector (EV) or p53 shRNA vector (p53sh) and harvested for real-time RT-PCR analysis. Shown is the data for BT549 (**c**), HCC38 (**d**), and MDAMB231 (**e**). Error bars indicate mean ±SD of two independent replicates. (**f**) MCF10a cells were infected with either an empty vector (EV) or R249S p53 mutant (R249S), selected for 7 days and then processed for western blot analysis of the indicated proteins. H1299 cells either empty vector (EV) and R175H were plated and then processed for western blot analysis of the indicated proteins. (**g**) Chromatin immunoprecipitation was performed on the MiaPaCa-2 cells with either a control or p53 antibody. Show is real-time PCR analysis normalized to input DNA. Error bars indicate mean ±SD of two independent replicates. (**h**) Western blot analysis of MiaPaCa-2 cells infected with either empty vector (EV) or p53 shRNA (p53sh). (**i**) Real-time RTPCR analysis of NMG expression was performed on MiaPaCa-2 cells infected with either an empty vector (PLKO) or p53 shRNA (p53sh). Error bars indicate mean ±SD of two independent replicates. (**j**) Schematic representation of the RRM2b promoter showing the binding sites for mutant p53 (MT) and wildtype p53 (WT). The numbers below the schematic are the genomic coordinates of the binding sites on human chromosome 8 (HG18 build). (**k**) Cell cycle analysis of HCC38 in the presence or absence of serum for 24 hours. Western blot analysis of indicated genes prepared from cell cultures incubated with and without serum for 24 hours. H1299 empty vector and H1299: R175H cells were serum starved for 24 hours and then processed for western blot for indicated proteins. (**l**) ZR751 western blot analysis of indicated genes prepared from cell cultures incubated with and without serum for 24 hours.



Supplemental Figure 2 (Related to Figure 2). mtp53 associates with ETS2 to regulate NMG. (**a**) HCC38, BT549, MDAMB231 were plated and lysates were prepared to immunoprecipitate p53 subsequently to determine if ETS2 interacts with various p53 mutants. (**b**) Stable mutant p53 expressing cells including MCF10a: R249S and H1299: R175H cells were transfected with either a control (Ct) or ETS2 siRNA (ETS2si) to determine the contribution of ETS2 in regulating nucleotide metabolism genes.

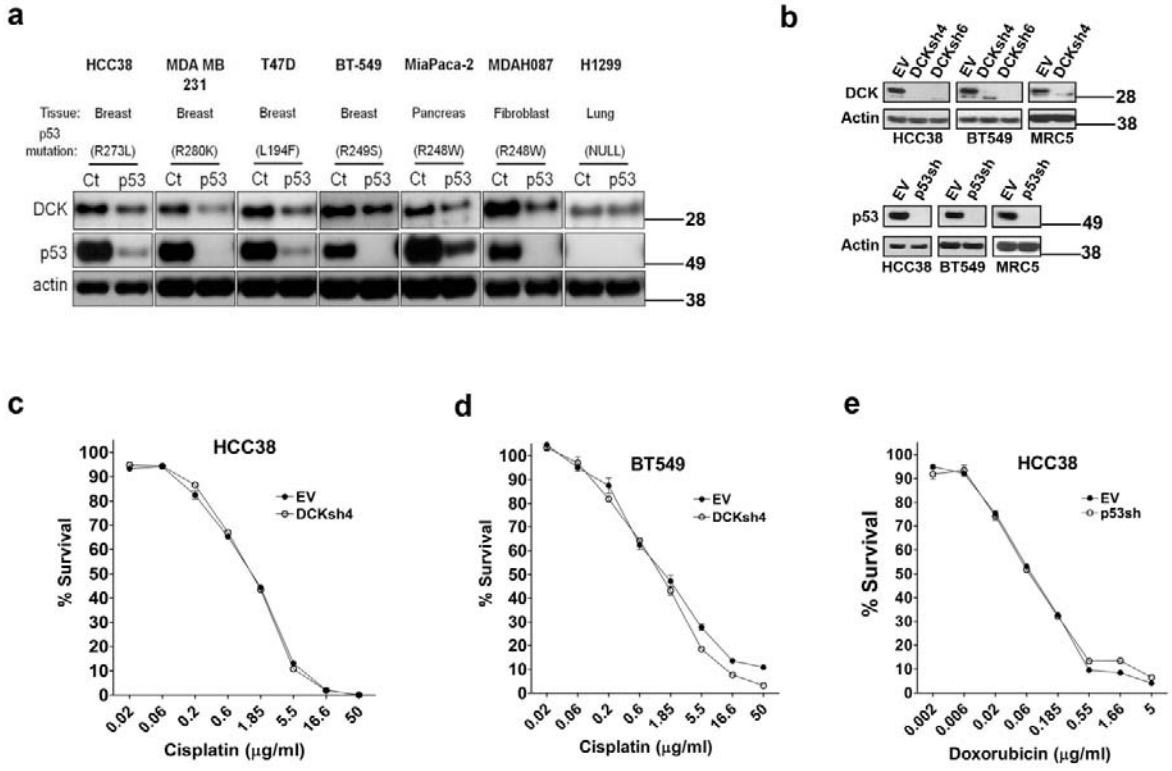


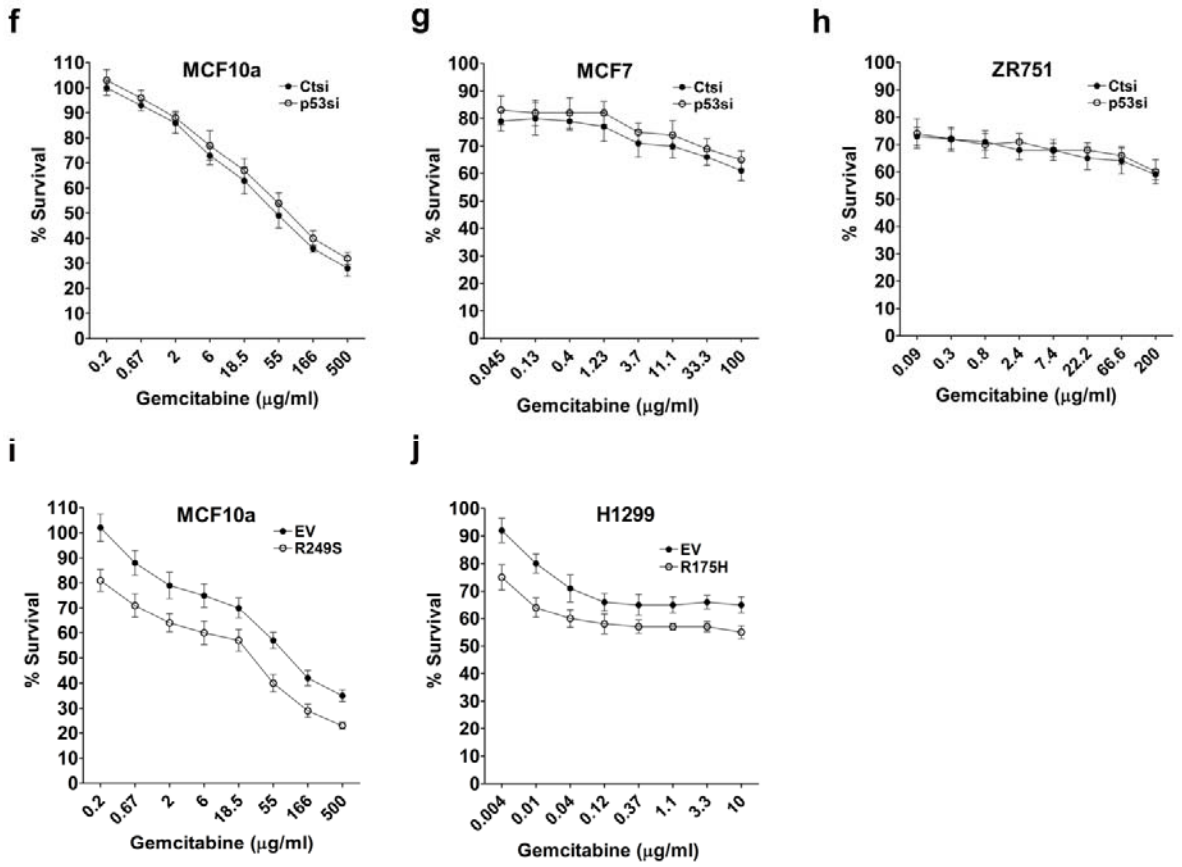
Supplemental Figure 3 (Related to Figure 3). WTp53 does not associate with mtp53 binding sites in promoters of NMG and does not control dATP or dTTP levels. Chromatin immunoprecipitation was performed on IMR90 cells that were not treated (**a**) or treated with doxorubicin (**b**). Inset is a western blot to show p53 induction by doxorubicin. Real-time PCR was performed to detect the association of WTp53 with the mtp53 binding regions and also its association with the WTp53 binding site in the RRM2b promoter. Error bars indicate mean ±SD of two independent replicates. (**c**) U2OS cells infected with either empty vector (EV) or p53 shRNA (p53sh) were processed to detect dATP and dTTP levels. Error bars indicate mean ±SD of three replicates. Western blot analysis confirming the knockdown is shown in Figure 3A.



Supplemental Figure 4 (Related to Figure 4). Control of cell invasion by guanosine and mutant p53. (**a**) MDAMB231 cells were transfected with either control (Ct) or p53 siRNA (p53si) and then harvested for western blot analysis to detect phospho-ERK (related to Fig. 4b). (**b**) Invasion images of the Matrigel invasion assay (related Fig. 4d) which was performed on

MDAMB231 cells infected with either empty vector (EV) or p53 shRNA (p53sh); 100 μM of exogenous guanosine or 1 mM of GTP was supplemented in the medium as indicated. Scale bars, 100 μm. (**c**) BT549 cells infected with either an empty vector (EV) or p53 shRNA (p53sh) were analyzed for their invasive activity in a Matrigel invasion assay. 100 μM of guanosine or 1 mM of GTP was added to the medium where indicated. Error bars indicate mean ±SD of two independent replicates. (**d**) Comparison of invasive activity of parental 231 and 231-BrM. Error bars indicate mean ±SD of two independent replicates. (**e**) Western blot analysis confirming the stable knockdown GMPS in 231: BrM which was used for in vivo studies. Western blot analysis of cells infected with either empty vector (EV) or GMPS shRNA (GMPS sh). Quantitation of GTP levels in cells infected with either empty vector (EV) or GMPS shRNA (GMPS sh). Error bars indicate mean ±SD of two independent replicates. (**f**) MDAMB231 cells were transfected with either control (Ct) or GMPS siRNAs (GMPS si) and then harvested for western blot analysis to detect phospho-ERK. (**g**) Invasion images: Analysis of GMPS knockdown in 231-BrM invasive activity and rescue by supplementation of guanosine in the medium (related to Fig. 4f). Scale bars, 100 μm. (**h**) Invasion images: 231: BrM cells were transfected with either a control (Ct) or GMPS siRNA2, treated with either DMSO or AVN-944 (1 μM) for 12 hours prior to seeding for invasion assay as indicated. Scale bars, 100 μm. Quantification of percentage inhibition of invasion after inhibiting IMPDH2 and GMPS together or alone. Error bars indicate mean ±SD of two independent replicates.

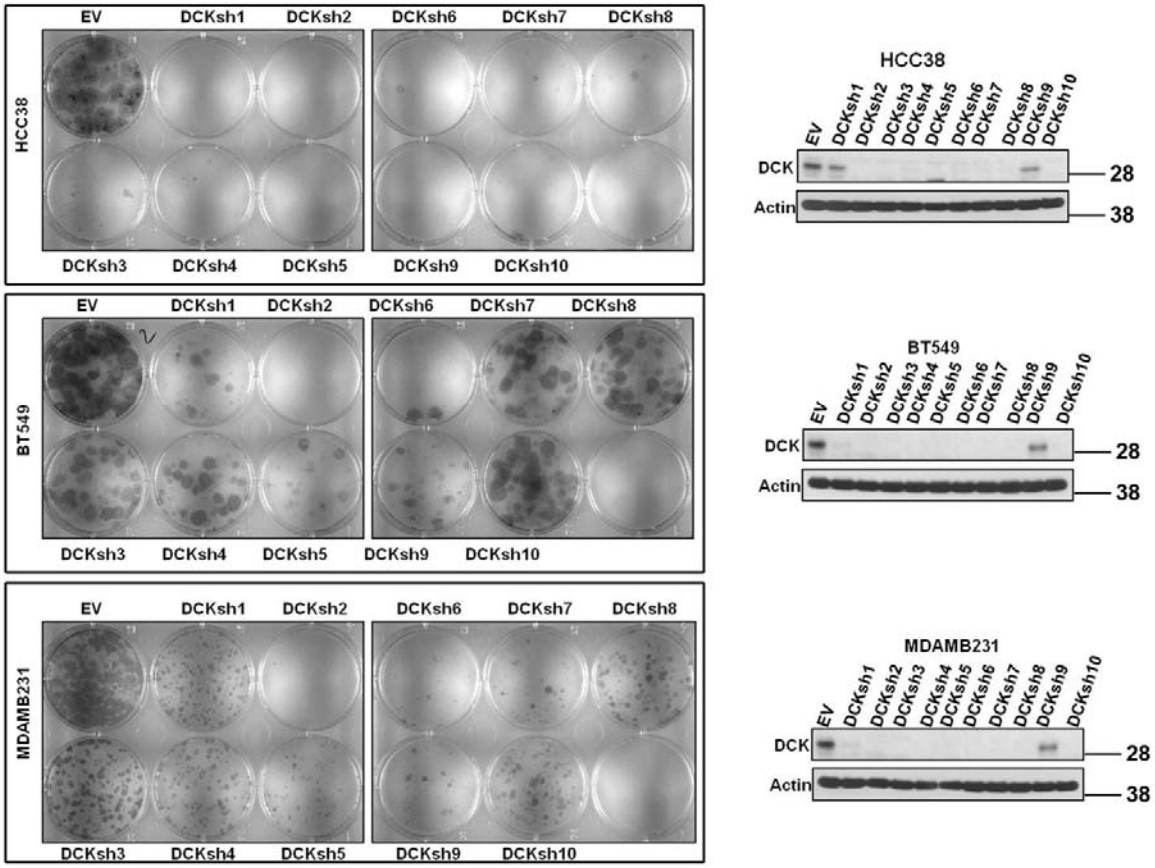

a
HCC38
MDA MB 231
T47D
BT-549
MiaPaca-2
MDAH087
H1299
Tissue: Breast Breast Breast Breast Pancreas Fibroblast Lung
p53 mutation: (R273L) (R280K) (L194F) (R249S) (R248W) (R248W) (NULL)
Ct p53
DCK
p53
actin
28
49
38
b
EV DCKsh4 DCKsh6
DCK
Actin
HCC38 BT549 MRC5
28
38
EV p53sh
p53
Actin
HCC38 BT549 MRC5
49
38
c
HCC38
EV
DCKsh4
% Survival
Cisplatin (μg/ml)
d
BT549
EV
DCKsh4
% Survival
Cisplatin (μg/ml)
e
HCC38
EV
p53sh
% Survival
Doxorubicin (μg/ml)



Supplementary Figure 5 (Related to Figure 5). Role of dCK in response to cytotoxic agents. (**a**) A panel of mtp53 harboring cell lines (HCC38, MDAMB231, T47D, BT549, MiaPaCa-2, MDAH087) or p53 null (H1299) were transiently transfected with either a control (Ct) or p53 siRNA (p53si), and then harvested two days later for western blot analysis as indicated. (**b**) Western blot analysis of dCK knockdown (top) in HCC38, BT549, MRC5, and p53 (bottom) in HCC38, BT549, MRC5. MTT assay showing the response of HCC38 (**c**) or BT549 (**d**) cells infected with an empty vector (EV) or dCK shRNA (dCKsh) to treatment with cisplatin. (**e**) HCC38 cells infected with an empty vector (EV) or p53 shRNA (p53sh) were treated with doxorubicin for 72 hours and then processed for analysis by MTT assay. (**f-h**) MCF10a, MCF7 and ZR751 cells transfected with either a control (Ct) or p53 siRNA (p53si) were treated with

different doses of Gemcitabine and after 72 hours, analyzed by MTT assay. (**i-j**) MCF10a: R249S and H1299: R175H stable mtp53 expressing cells were treated with different doses of Gemcitabine and after 72 hours, analyzed by MTT assay. In all dose-response curves, error bars indicate mean ±SD of three independent replicates.

a


EV
DCKsh1
DCKsh2
DCKsh6
DCKsh7
DCKsh8
HCC38
DCKsh3
DCKsh4
DCKsh5
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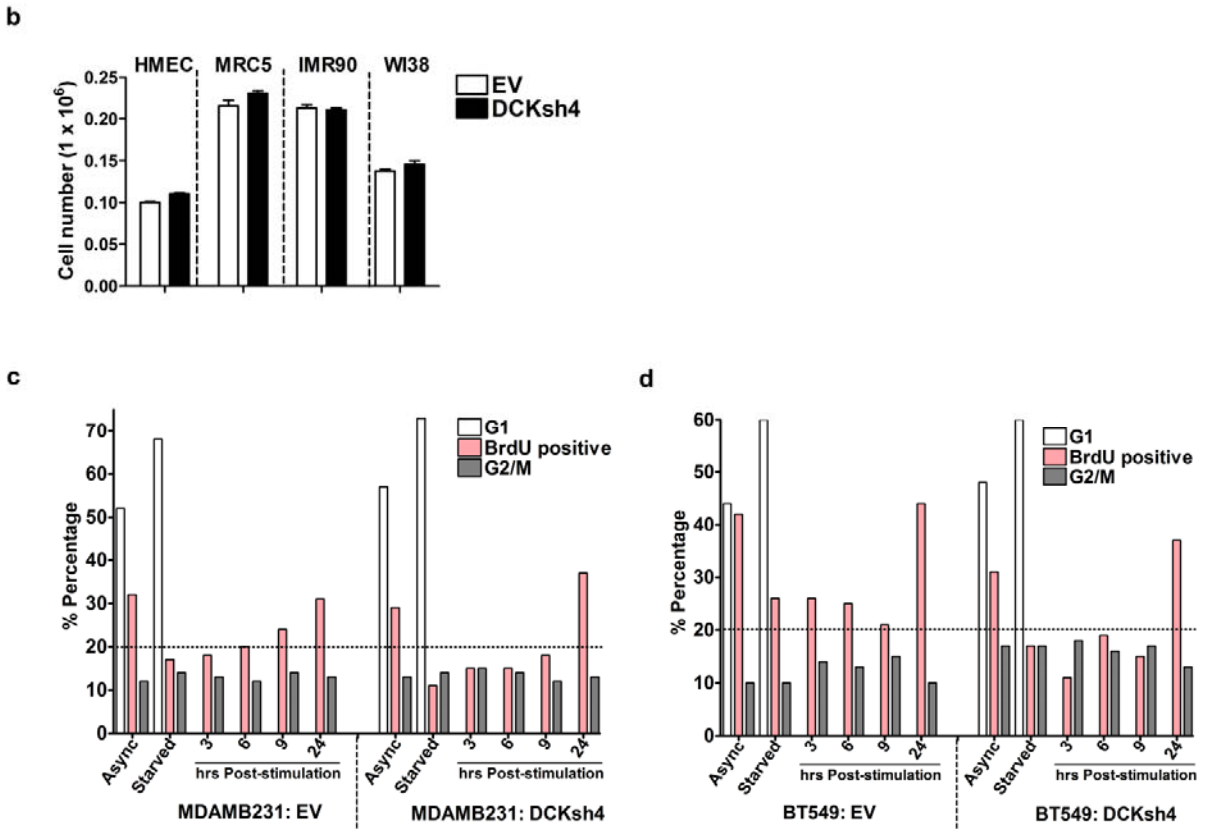
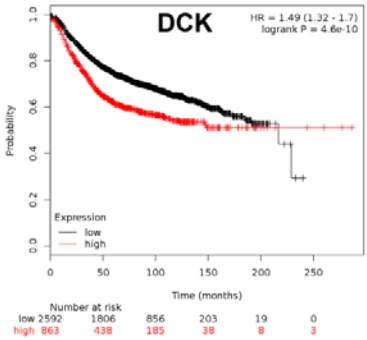
DCK
Actin
28
38
BT549
MDAMB231

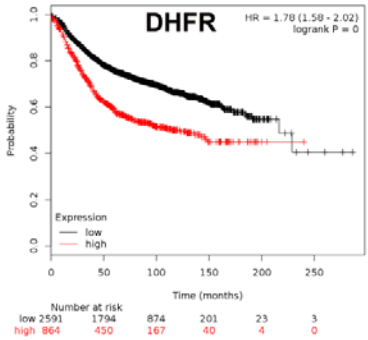


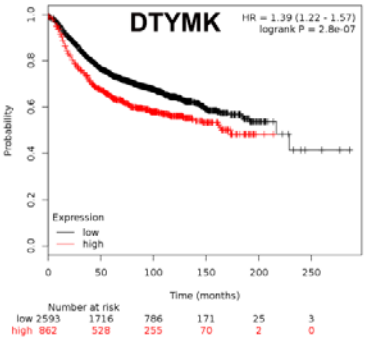
Supplemental Figure 6 (Related to Figure 6). dCK knockdown reduces colony formation in mtp53 expressing cells. (**a**) Three breast cancer cell lines that harbor mtp53 (HCC38, BT549, and MDAMB231) were infected with either an empty vector (EV) or 10 distinct shRNAs targeting dCK. After selection with puromycin for two days, 1000 cells/well were seeded and allowed to grow until for approximately two weeks. The dishes were then fixed and stained to visualize colonies. The right panel is a western blot analysis of dCK knockdown with the shRNAs used for the colony formation assay. (**b**) The normal cell strains HMEC, MRC5, IMR90 and WI38 were infected with either an empty vector (EV) or dCK shRNA (dCKsh4), selected with puromycin and then analyzed to determine cell doubling times. Error bars indicate mean ±SD of three independent replicates. (**c-d**) MDAMB231 and BT549 cells were infected with an empty vector (EV) or dCK shRNA (dCKsh4) and selected for 3 days. The cells were then left in

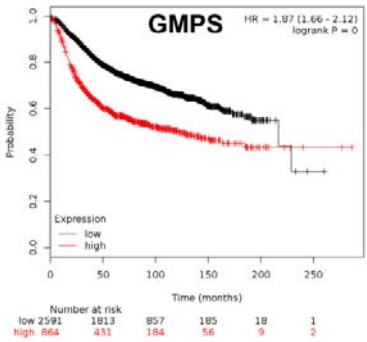
serum containing medium (asynch), or serum starved overnight (starved). The cells were then stimulated to grow by the addition of medium supplemented with serum (hours post-stimulation). The cells were pulse labeled with BrdU for 1 hour prior to harvest at the indicated time points, and then processed to determine BrdU incorporation and cell cycle distribution by FACS analysis.

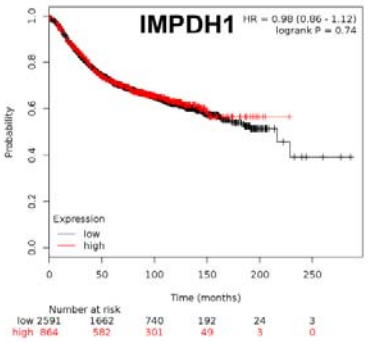
Relapse Free Survival (RFS)

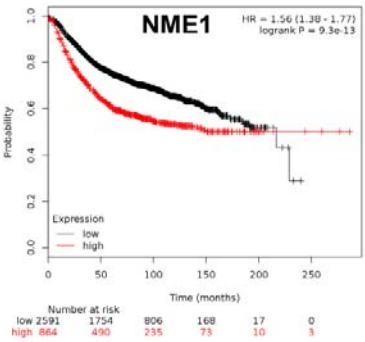




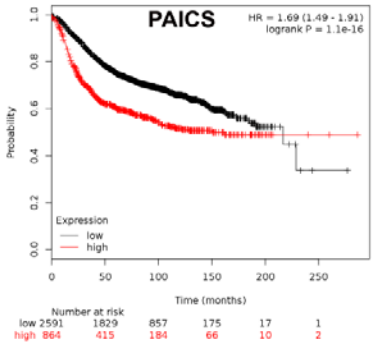


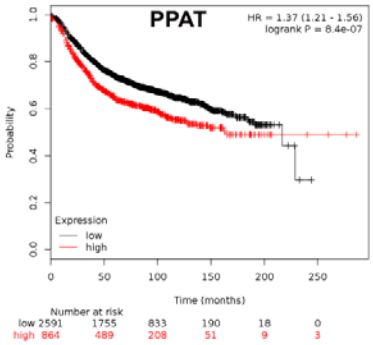


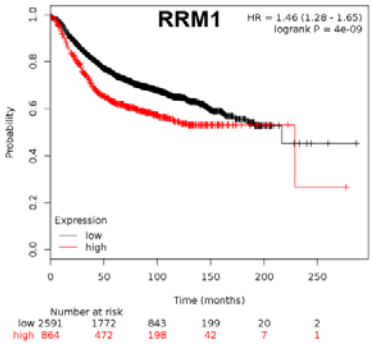


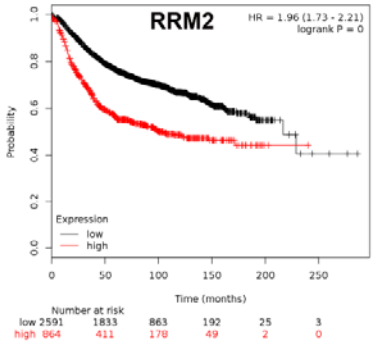


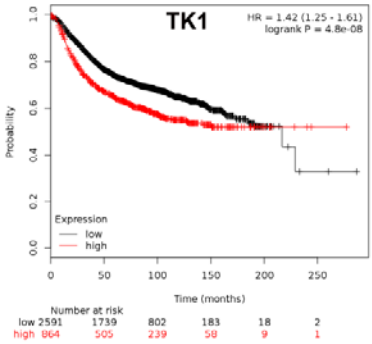
Relapse Free Survival (RFS)

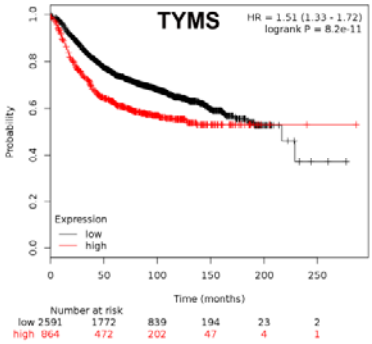


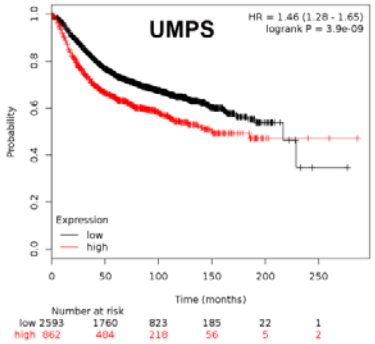




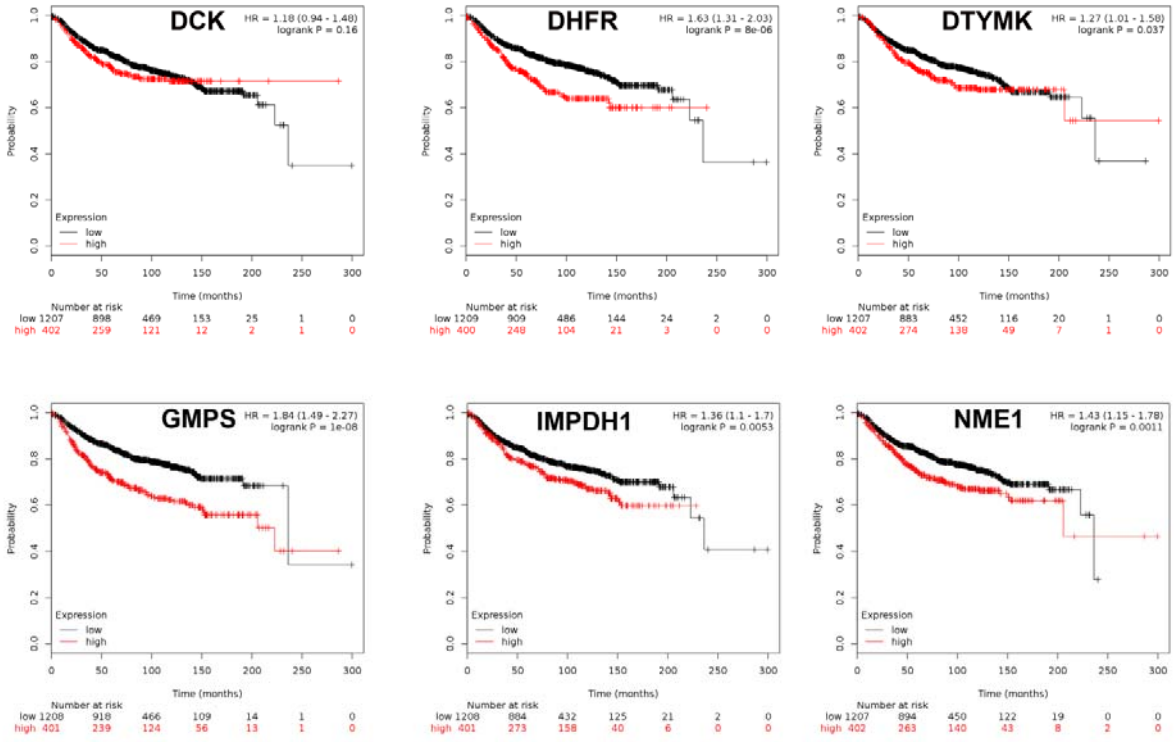


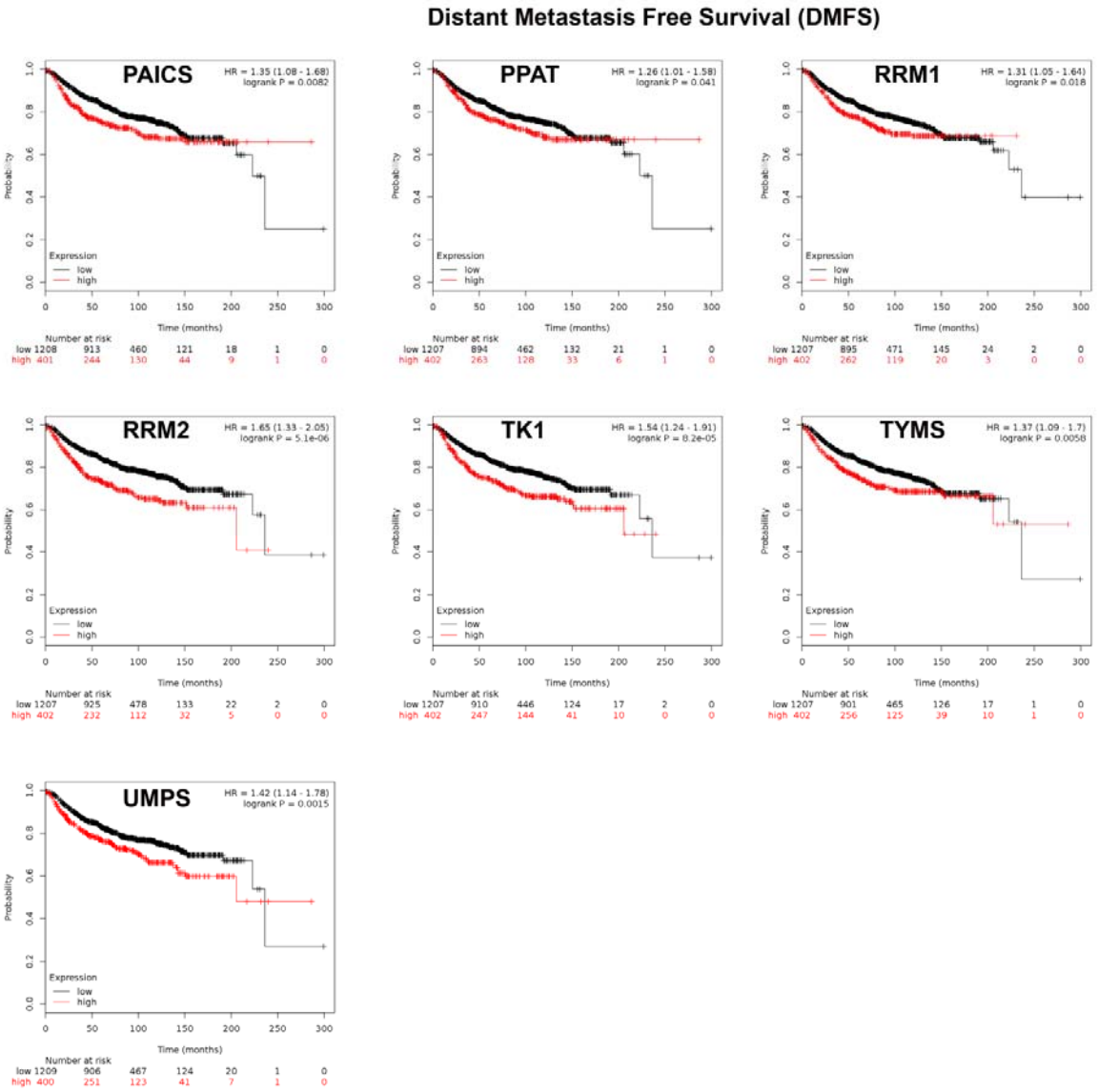






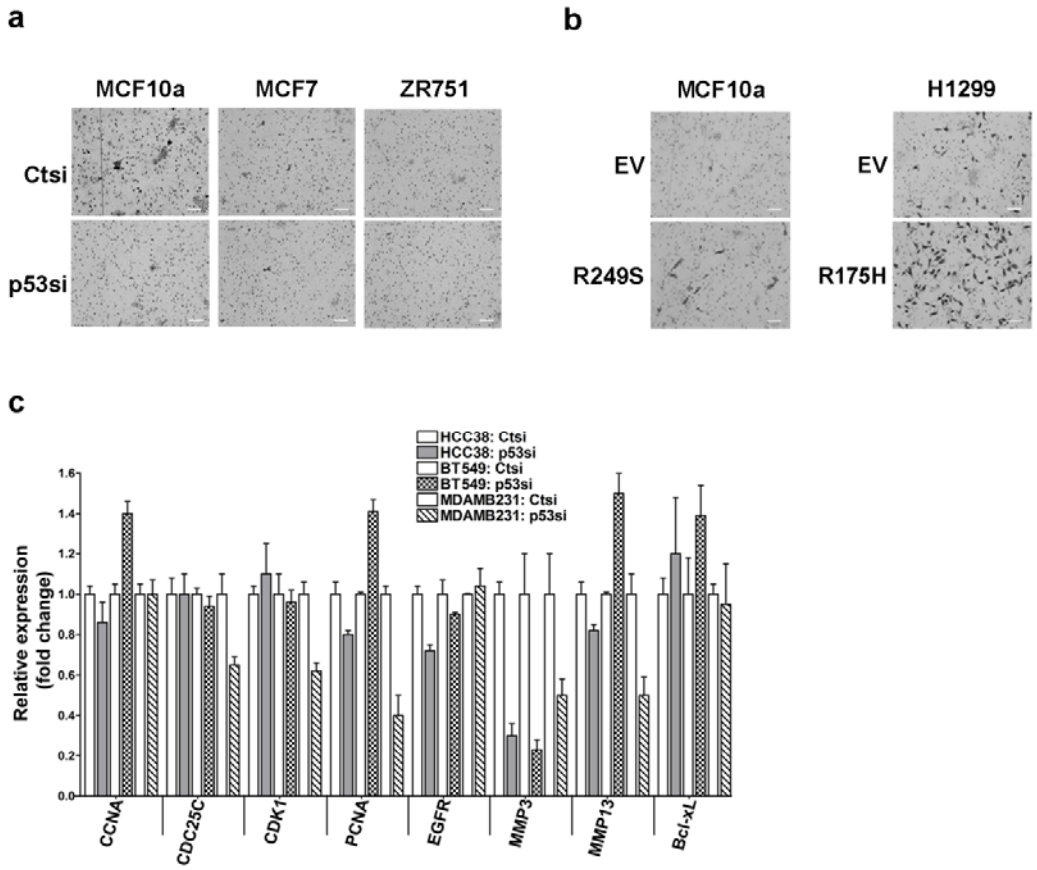
Distant Metastasis Free Survival (DMFS)





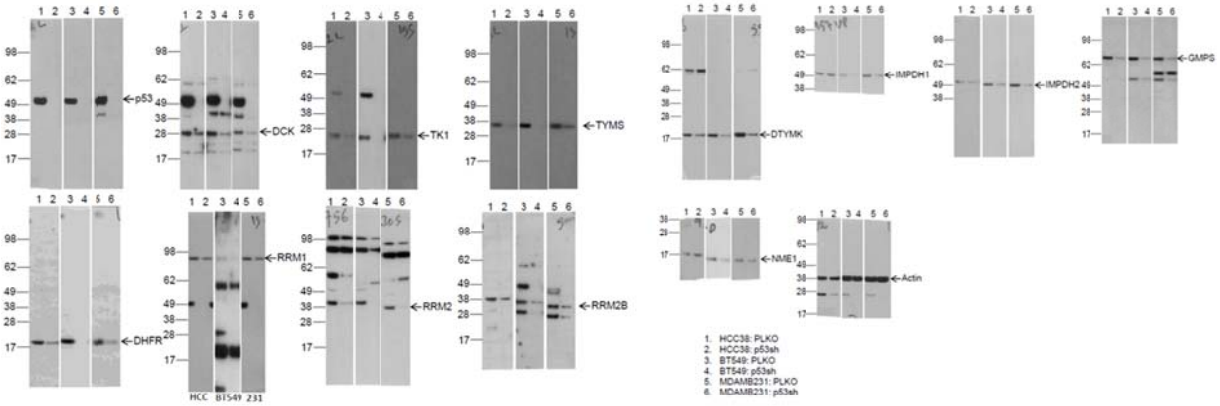
Supplemental Figure 7 (Related to Figure 7). Kaplan-Meier curves of mtp53 target genes showing clinical outcome in terms of RFS and DMFS. To study the relationship between the indicated mtp53 target genes and relapse free survival (RFS) (**a-b**) and distant metastasis free survival (DMFS) (**c-d**), we performed Kaplan-Meier analysis using a dataset of 4142 breast cancer transcriptomes with clinical outcome data [76]. Kaplan-Meier curves were constructed by dividing the patient cohort between samples in the upper quartile of expression for each

particular gene and the rest of the samples. Analysis was performed using the Kaplan-Meier Plotter software (kmplot.com) using the default parameters. Results are expressed as a hazard ratio with 95% confidence intervals and log rank test *P* value. *P* values of <0.05 were considered statistically significant.



Supplemental Figure 8. **mtp53 promotes invasion.** (**a**) Invasion images: MCF10a, MCF7 and ZR751 cells were transfected with either Control (Ct) or p53 siRNA (p53si) and then performed Matrigel invasion assay. Scale bars, 100 μm. (**b**) Invasion images of MCF10a cells infected with either an empty vector (EV) or R249S p53 mutant (R249S). Invasion images of H1299 cells infected with either an empty vector (EV) or R175H p53 mutant (R175H). Scale bars, 100 μm. (**c**) HCC38, BT549 and MDAMB231 cells were transfected with either a control (Ct) or p53 siRNA (p53si), harvested RNA and cDNA was prepared to quantify indicated genes by Real-time PCR. Error bars indicate mean ±SD of three independent replicates.

Fig.1c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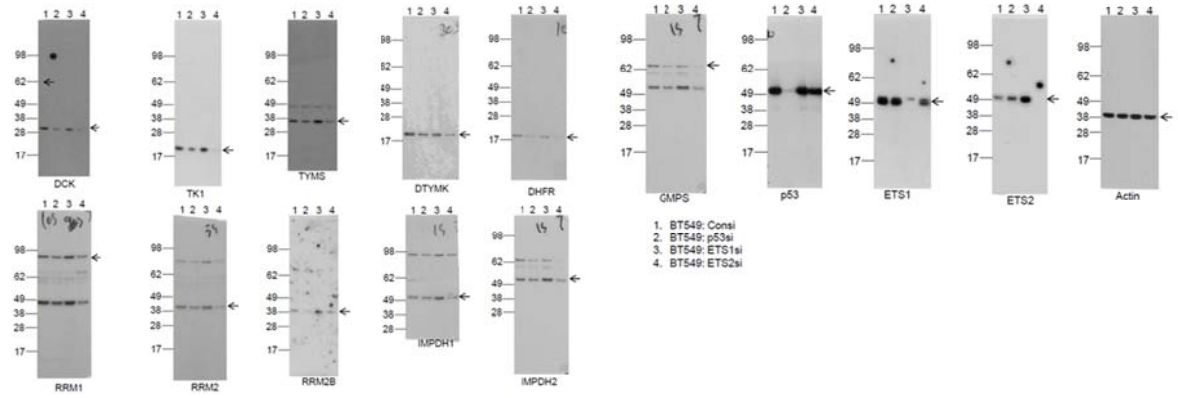
TK1
TYMS
DHFR
RRM1
RRM2
RRM2B
DTYMK
IMPDH1
IMPDH2
GMPS
NME1
Actin
1. HCC38: PLKO
2. HCC38: p53sh
3. BT549: PLKO
4. BT549: p53sh
5. MDAMB231: PLKO
6. MDAMB231: p53sh

Fig.2a


DCK
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DTYMK
DHFR
GMPS
p53
ETS1
ETS2
Actin
RRM1
RRM2
RRM2B
IMPDH1
IMPDH2
1. BT549: Consi
2. BT549: p53si
3. BT549: ETS1si
4. BT549: ETS2si

Fig.3a

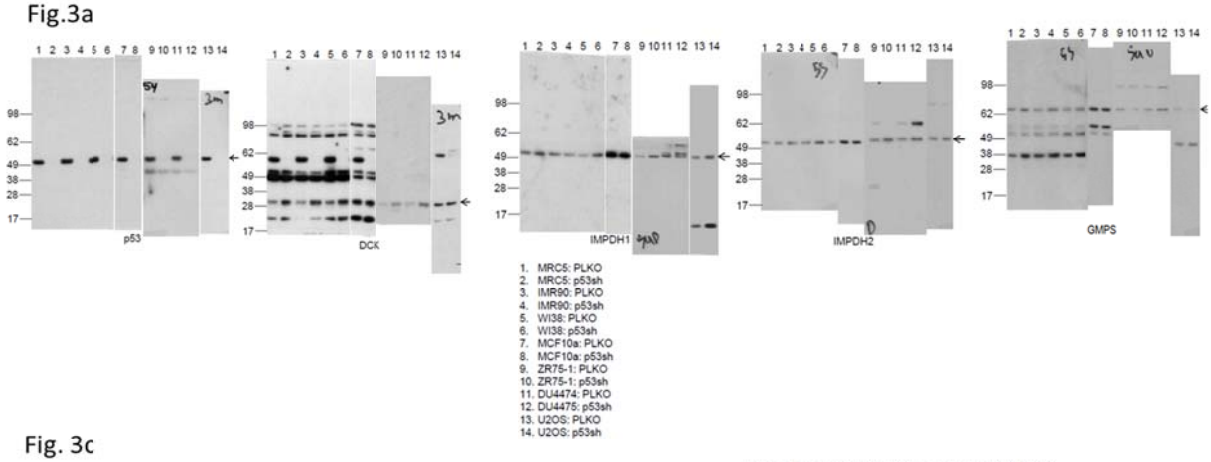
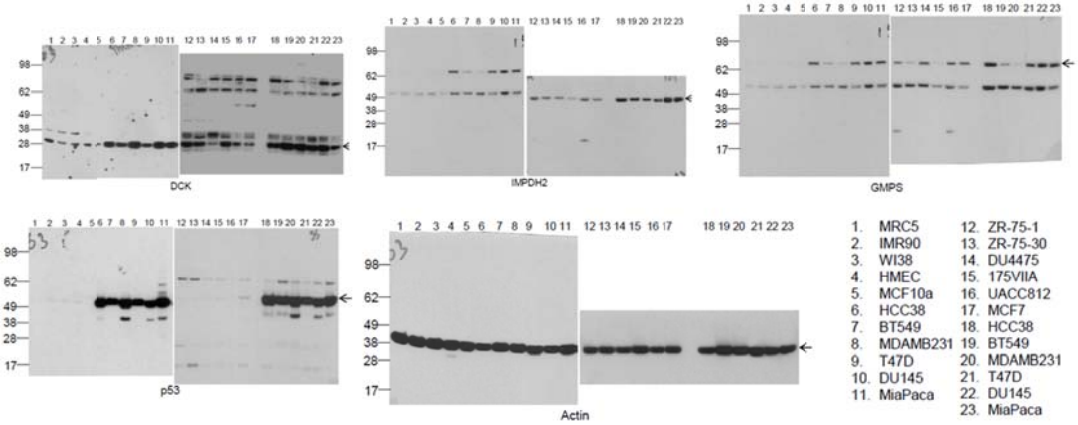
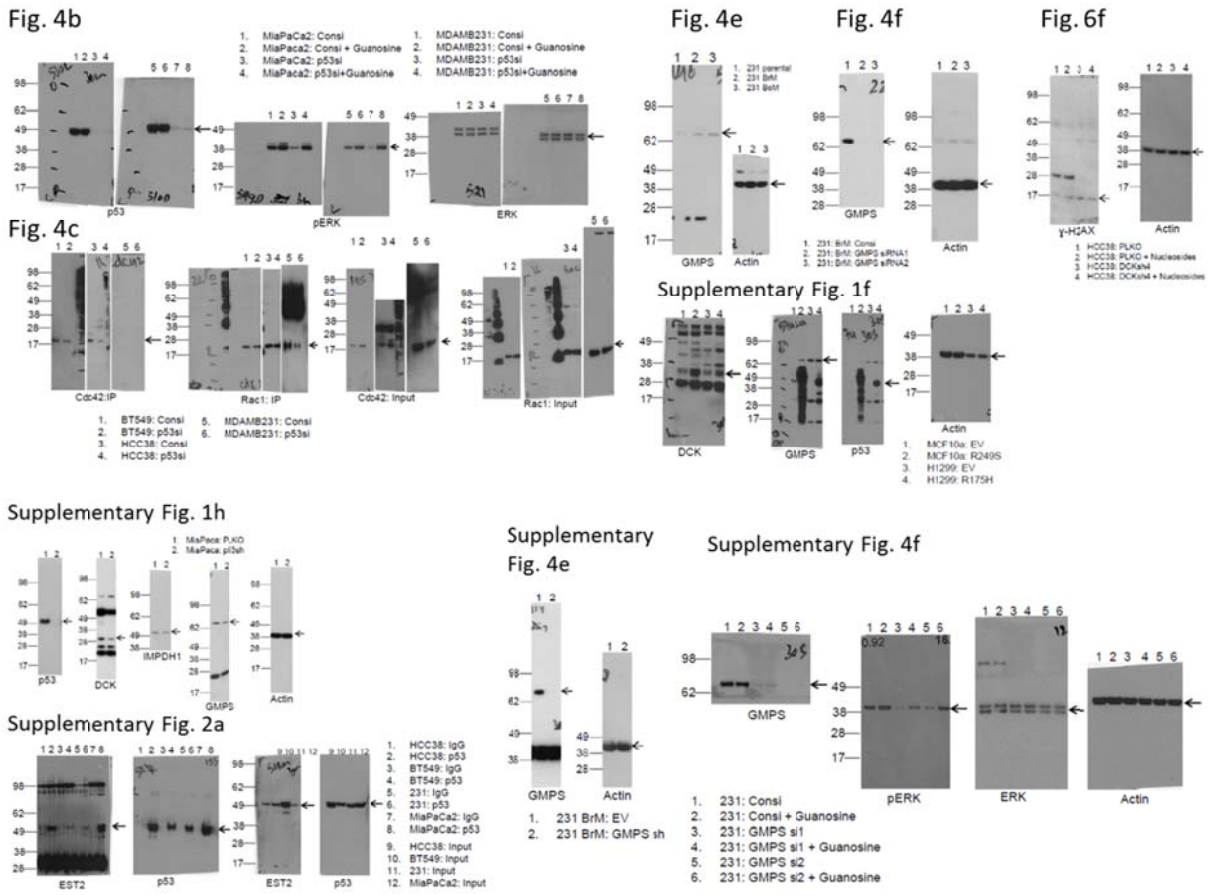

p53
DCK
IMPDH1
IMPDH2
GMPS
1. MRC5: PLKO
2. MRC5: p53sh
3. IMR90: PLKO
4. IMR90: p53sh
5. WI38: PLKO
6. WI38: p53sh
7. MCF10a: PLKO
8. MCF10a: p53sh
9. ZR75-1: PLKO
10. ZR75-1: p53sh
11. DU4474: PLKO
12. DU4475: p53sh
13. U2OS: PLKO
14. U2OS: p53sh

Fig. 3c


DCK
IMPDH2
GMPS
p53
Actin
1. MRC5
2. IMR90
3. WI38
4. HMEC
5. MCF10a
6. HCC38
7. BT549
8. MDAMB231
9. T47D
10. DU145
11. MiaPaca
12. ZR-75-1
13. ZR-75-30
14. DU4475
15. 175VIIA
16. UACC812
17. MCF7
18. HCC38
19. BT549
20. MDAMB231
21. T47D
22. DU145
23. MiaPaca



Supplemental Figure 9. The most important uncropped scanned full western blots.

Supplementary Table 1: IC50 values for gemcitabine on mtp53 and wildtype p53

Mtp53 cancer cell line	Gemcitabine: IC50 (µg/ml)	WTp53 cancer cell line	Gemcitabine: IC50 (µg/ml)
HCC38	0.003 (±0.0002)	ZR751 (breast)	>20 (NA)
BT549	0.01(±0.001)	ZR7530 (breast)	>20 (NA)
MiaPaCa-2	0.1 (±0.031)	MBAMD175V11A (breast)	>20 (NA)
		UACC893 (breast)	3 (±0.6)
		A549 (lung)	3 (±1)
		U2OS (osteosarcoma)	>200

*IC50 was derived from three independent experiments.
*Values in parentheses represent standard deviation calculated from three independent experiments.

Supplementary Table 2: Resistant factor values

Cell line	Gemcitabine (IC50: µg/ml)	Resistant factor
HCC38: EV	0.003 (±0.0002)	
HCC38: DKCsh4	0.07 (±0.015)	23
HCC38: DCKsh6	0.007 (±0.0001)	2.3
BT549: EV	0.01 (±0.001)	
BT549: DKCsh4	6 (±1.8)	600
BT549: DCKsh6	6.4 (±2)	640
MRC5: EV	700 (±21.3)	
MRC5: DKCsh4	>1000 (NA)	>1.4
HCC38: EV	0.007 (±0.002)	
HCC38: p53sh	>2 (NA)	>286
BT549: EV	0.08 (±0.02)	
BT549: p53sh	25 (±3.6)	31
MRC5: EV	>1000 (NA)	
MRC5: p53sh	>1000 (NA)	NA

*IC50 was deduced from three independent experiments.
*Values in parentheses represent standard deviation calculated from three independent experiments.

Supplementary Table 3: NMG definitions

Gene symbol	Definition
ADSS	Adenylosuccinate synthase
AK2	Adenylate kinase 2
AK2ab	Adenylate kinase isoenzyme 2 ab
CAD	Carbomyl-phosphate synthetase 2, Aspartate transcarbomylase and dihydroorotase
CTPS	Cytidine triphosphate synthetase
DCK	Deoxycytidine kinase
DCTD	Deoxycytidylate deaminase
DGUOK	Deoxyguanosine kinase
DHFR	Dihydrofolate reductase
DHODH	Dihydroorotate dehydrogenase
DPYD	Dihydropyrimidine dehydrogenase
DTYMK	Deoxythymidylate kinase
DUT	Dexoyuridine triphosphatase
GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
GMPR	Guanosine monophosphate reductase
GMPR2	Guanosine monophosphate reductase 2
GMPS	Guanosine monophosphate synthase
GUK1	Guanylate kinase 1
IMPDH1	Inosine monophosphate dehydrogenase 1
IMPDH2	Inosine monophosphate dehydrogenase 2
NME1	NME/NM23 nucleoside diphosphate kinase 1
NME2	NME/NM23 nucleoside diphosphate kinase 2
PAICS	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
PFAS	Phosphoribosylformylglycinamide synthase
PPAT	Phosphoribosyl pyrophosphate amidotransferase
PRPS1	Phosphoribosyl pyrophosphate synthetase 1
PRPS1	Phosphoribosyl pyrophosphate synthetase 2
RRM1	Ribonucleotide reductase M1
RRM2	Ribonucleotide reductase M2
RRM2b	Ribonucleotide reductase M2 B
TK1	Thymidine kinase 1
TK2	Thymidine kinase 1
TYMP	Thymidine phosphorylase
TYMS	Thymidylate synthetase
UMPS	Uridine monophosphate synthetase
UPRT	Uracil phosphoribosyl transferase

Supplementary Methods

Western blotting

Western blot analysis was performed using DCK (Genetex: GTX107636; 1:2000), RRM2 (Genetex: GTX103193; 1:2000), RRM2B (Genetex: GTX109620; 1:2000), TK1 (Genetex: GTX62133; 1:2000), RRM1 (Cell signaling: 8637S; 1:3000), TYMS (Cell signaling: 9045P; 1:3000), NME1 (Cell Signaling: 3345S; 1:3000), PARP (Cell Signaling: 9542I; 1:3000), DTYMK (Protein Tech: 15360-1-AP; 1:3000), DHFR (Protein Tech:15194-1-AP; 1:3000), IMPDH1 (Protein Tech: 22092-1-AP; 1:3000), IMPDH2 (Abcam: Ab131158; 1:3000), GMPS (Santa Cruz: sc-376163; 1:3000), p53 (Santa Cruz: sc-126; 1:3000), ETS1 (Santa Cruz: sc-5558;1:500), ETS2 (Santa Cruz: sc-365666; 1:200), gamma H2A.X (Bethyl: A300-081A; 1:2000), c-Myc (Santa Cruz: 9E10; 1:1000) and actin HRP (Sigma: A3854; 1:40000) antibodies.

siRNA

GMPS#1: HSC.RNAI.N003875.12.1 (Integrated DNA Technologies)
GMPS#2: HSC.RNAI.N003875.12.2 (Integrated DNA Technologies)
ETS1 #5: CAGCTTCGACTCAGAGGACTA (Qiagen)
ETS1 #6: CACGACCTAAGTTGAAGAGTT (Qiagen)
ETS2 #1: CCCGGTCAAGTTGGTTTCAAA (Qiagen)
ETS2 #3: AGGGATTTATGTAGCAGCTAT (Qiagen)
ETS2 #6: CTGTGATGAGTCAAGCCTTAA (Qiagen)
p53 #7 CAGCATCTTATCCGAGTGGAA (Qiagen)

shRNA

DCK:	TRCN0000009932 (Dharmacon/GE Healthcare)
	TRCN0000009933 (Dharmacon/GE Healthcare)
	TRCN0000009934 (Dharmacon/GE Healthcare)
	TRCN0000009940 (Dharmacon/GE Healthcare)
	TRCN0000009941 (Dharmacon/GE Healthcare)
	TRCN0000194818 (Sigma-Aldrich)
	TRCN0000195182 (Sigma-Aldrich)
	TRCN0000196362 (Sigma-Aldrich)
	TRCN0000196616 (Sigma-Aldrich)
	TRCN0000196649 (Sigma-Aldrich)
p53:	shp53 pLKO.1 puro (Addgene #19119)
GMPS:	RHS4740-EG8833 (Thermo Scientific)
Empty Vector	pLKO.1 puro (Addgene #8453)

shRNA resistant p53 expression vector

Silent mutations were introduced into the p53 coding sequence for the R280K or R249S, and then the cDNAs were cloned into the lentiviral vector pLVX-Hygromycin (Clontech) and lentiviruses were used to infect cell lines in which endogenous mutant p53 had been knocked down using shp53 pLKO.1. The cells were selected with hygromycin for one week.

Real-Time RT-PCR primers

ADSS rt f	TAC TGT TGG AGG TGT TTG TA
ADSS rt r	CCC CTT GTT TGT AAT AAT TC
AK2a rt f	AAGCCTACCACACTCAAAC
AK2a rt r	CTTGGACCCAACATTAGATA
AK2ab rt f	AATCACAGGAAGGCTGATT
AK2ab rt r	TACTCTATGAGTGGGGTGGT
CAD rt f	CGAAAGATGGGATATAAGAC
CAD rt r	TCAAAGTAGAGTCGATCACA
CTPS rt f	CCA CAG TGA AAG ACC ATC
CTPS rt r	CAA GCT TAC TCT CTT GAA GG
DCK rt F	GCCAGATGGTGCAATGTTC
DCK rt R	GCATCTTTGAGCTTGCCATT
DCTD rt f	AAC ATG AGT GAA GTT TCC TG
DCTD rt r	TTC TCT GTG CTG ATA AGA AG
DGUOK rt f	ATTACATGGCTTCATCTACC
DGUOK rt r	CTTCGTTGTCTTGTGAATAA
DHFR rt f	TCC CAG ACA GAA CCT ACT AT
DHFR rt r	CGA TTC TTC CAG TCT ACG
DHODH rt f	TATTATTGCTGAGTCATTGG
DHODH rt r	AGTAAAGAATGCAGGTCAAT
DTYMK rt f	CTA CTT GCA AAA GAA AAG TG
DTYMK rt r	GCT GTT TAC ACC AAT CTA GG
DPYD rt f	GTATGTCCAACCTCTGATCT
DPYD rt r	ATTGCTTTGAATACCTCAGT
DUT rt f	CTC TAT TGA CTG GGT AGA GG
DUT rt r	TAC TTC ACT GAG GGA AAA CT
GART rt f	CCTTTGGAATTTCTGCTTTA
GART rt r	CAGTGTGGTCACTGATTGAG
GMPR rt f	GCAATTCATAAGCATTACTC
GMPR rt r	GGCAAATAAACTTAACCTGT
GMPR2 rt f	GGTAGAAGAAGGAAGTGTAGC
GMPR2 rt r	CCTCTCTTCGCTTAAGTTG
GMPS rt f	GGTGGAGTAGACTCAACAGT
GMPS rt r	CATTGTAGAAAGAATGAGCA
GUK1 rt f	GGTCATCATTAACGACAGC
GUK1 rt r	TTTGAGCTTTCTTGATTTCC
IMPDH1 rt f	CTAGATTGGACCTCGCTACA
IMPDH1 rt r	GATCCATCTGGACACCAAC
IMPDH2 rt f	CTCACCTACAATGACTTTCTC
IMPDH2 rt r	GGGTCTTAAGAGTGATTTTC
NME1 rt f	TGGACTACAGTGCTAAGATGCTG
NME1 rt r	CATCTGGTTTGATCGCAATG
NME2 rt f	CTGGGTCTATGAATAAGAGG
NME2 rt r	GGCAAATATGCTCTATAAAAG
PFAS rt f	CCAGTCCTTCACTTCTATGT

PFAS rt r	TTGTAGCACAGTTCAGTCTC
PPAT rt f	TCATGGTATTGGTCTGTCTA
PPAT rt r	TTCCATAAGGATCTCGTACT
PRPS1 rt f	CCGCTTTGGGTAATTTAGA
PRPS1 rt r	AGATTTTGATATTCGGCATC
PRPS2 rt f	CAAGGTAGGAGAGAGTCGT
PRPS2 rt r	CAAATTATCCACAGGAATATC
RRM1 rt f	AGA AGA TTG CAA AGT ATG GT
RRM1 rt r	GTA AGG TTC AAT GGA CTC AT
RRM2 rt f	TAG AGG TGG TTC CTA CAA GT
RRM2 rt r	GGG TGA CTG AAG TAT GAA CT
RRM2B rt f	CTGGGTGCTGTCGTAGTT
RRM2B rt r	TGGCTCTTCATTTGACTTTA
TK1 rt2 f	CAATGAGCTGCATTAACCT
TK1 rt2 r	GTGTCTTTGGCATACTTGAT
TK2 rt2 f	ATTAATTAACCCTTCAGTCG
TK2 rt2 r	CAAGAGGAGAAATACTCGAA
TYMP rt f	TGG ATA AGC TGG AGT CTA TT
TYMP rt r	CAT CTC TGG CTG CAT ATA G
TYMS rt f	CTA CAG CCT GAG AGA TGA AT
TYMS rt r	GAA GAC AGC TCT TTA GCA TT
UMPS rt f1	TTAGGAGGTCTAAGATTCCA
UMPS rt r1	TACCTCCCCTCTACTAATGA
UPRT rt f	GTCCTTCTGATGTATCCAAT
UPRT rt r	GGTTGAACTCCATGTTCTAT
CCNA rt f	GGTCTGTGTTCTGTGAATAA
CCNA rt r	GAAAACTAAGAAATGCCTCT
CDC25C rt f	AAGAAGGTTTTGTTTTTCTC
CDC25C rt r	CATTTTCCTTTGATTAGACC
CDK1 rt f	AATAATAAGCCGGGATCTA
CDK1 rt r	GAATTGCAGTACTAGGAACC
PCNA rt f	TCGTTGTCTTTCTAGGTCTC
PCNA rt r	GAGGAAAGTCTAGCTGGTT
EGFR rt f	GTCTTGAAGGCTGTCCAA
EGFR rt r	CTTCTCCACTGGGTGTAAG
MMP3 rt f	AAAGTGACACACACTTTGAA
MMP3 rt r	ATACAGATTCACGCTCAAGT
MMP13 rt f	ATTTTACCAGACTTCACGAT
MMP13 rt r	GTTGTAGCCTTTGGAACTAC
BCLXL rt f	CCCTTCAGAATCTTATCTTG
BCLXL rt r	TGTAGGAGAGAAAGTCAACC

Luciferase assays

The promoters were cloned into the PGL4 Luciferase reporter construct using the primers below. Genomic DNA from PC3 cells was initially amplified with the primers indicated as "out" and 1 microliter of this PCR was used as a template for PCR with the primers carrying restriction sites (in bold). Typically, 4-5 random bases were added on the 5' end of the primer to permit optimal restriction enzyme binding and cleavage.

TK1 pro out f	GCACTAGGCGCTCTGCAT
TK1 pro out r	ATGCCTGGACACAGGCTATC
TK1 pro f KPN1	**ggtacc**ATGCCCACAGGAGTGCTCTA
TK1 pro r NHE1	**gctagc**CAGCACAGTGGGCAGGTTA
RRM1 pro out f	GCGGACGGCAGTGTTAGTAT
RRM1 pro out r	CCCTGTGCCTAAGACAGCTC
RRM1 pro f xho	**ctcgag**GAGACGCGCAGGTGAGAG
RRM1 pro r HindIII	**aagctt**GCGTACGCAGTCACTACTCG
RRM2 pro out f	AGCCTGGGTAGGGGCAAG
RRM2 pro out r	GATGTGAAAACGTGGCTGTC
RRM2 pro f HindII	**aagctt** TAAAGGCTGCTGGAGTGAGG
RRM2 pro r Xho1	**ctcgag**GCCTAGGCGGGAAAGGAG
TYMS out f	CCAGCTTCAGTGCTCTCCTC
TYMS out r	CTCCTGACCTCAGGTGATCC
TYMS pro f xho	**ctcgag**AGCTCTCCCTAACCCTCCAG
TYMS pro r HindIII	**aagctt**ATACCACTTGCTTCGGTTGC
DTYMK out f	ACACACACACGGACTTTCCA
DTYMK out r	CCATACCCCGCACTTAAAGA
DTYMK pro f xho	**ctcgag**TCAAACACAGCGTTTCCAGA
DTYMK pro r HindIII	**aagctt**GCCTATGTTCCCGGCTACC
DHFR out f	AGGCCTGCCATTAAAAACCT
DHFR out r	AAGTCTGGCCCCATCCTCT
DHFR pro f HindIII	**aagctt**CTTCCTCCTCCAGCCCTATC
DHFR pro r XhoI	**ctcgag**AAGTCTGGCCCCATCCTCT

Cell based luciferase assays were performed using the Promega dual luciferase assay kit according to the manufacturer's protocol. Cells were plated the day before transfection and then transfected with a mix of siRNA, luciferase promoter construct and a Renilla luciferase construct. Two days later, the cells were harvested and processed to detect luciferase activity.

CHIP primers:

In most cases, primers were designed to amplify a PCR product ranging from 70-200 base pairs surrounding the predicted binding site for mutant p53 as determined after analysis of our previously reported CHIP-Seq data. If suitable primers could not be obtained, primers were designed to amplify a PCR product within 100-200 base pairs of the predicted binding site.

DCK ch f	GCGTCTGTTCATCTCCAACA
DCK ch r	AAGAGGTTCCGGAGTCGG
TYMS ch f	GCTGTTTGAGATCTGTTTCC
TYMS ch r	TGCATTATACCACTTGCTTC
DHFR ch f	AACGGAAGTACTAAAACCTCA
DHFR ch r	ATGATAGGGCTGGAGGAG
RRM2 ch f	TTCCCATAATCAGCGTCTAA
RRM2 ch r	ATTACGTGGCCAGGAACTAA
DTYMK ch f	TAATCCAGGGCTACACAGAT
DTYMK ch r	ATGTGCCATATTGTCAGTTG
PFAS ch f	ACGGGGAACTGAATGTATTT
PFAS ch r	TTGGTGGGGAGAGGTTTAT
TK1 ch f	AATGAGCTGCATTAACCTG
TK1 ch r	ACAGGCTATCACCACGAC
RRM1 ch f	GGTAGGCTTCACAGACTGAC
RRM1 ch r	AAAACATGGTAGCAGGAGAG
IMPDH1 ch f	CCTAGACTCGGTTCGTCTCT
IMPDH1 ch r	TTCCTCTTCTGGTTTTCCTC
IMPDH2 ch f	CCCCCACTAATCAGGTAGTC
IMPDH2 ch r	AATCGGCTGGTTTATATTGG
AK2 ch f	CTTGACCTTGGAGTTCAGC
AK2 ch r	CCGAGTATCCTAAAGGCATC
PPAT/PAICS ch f	AGGCTAAAGTTCATGGAAGC
PPAT/PAICS ch r	CTCTCCGACCTAAGCCAGTA
GUK1 ch f	GGGAAGAACGAGTGAGACAT
GUK1 ch r	CACTGAACCTACGTGACAGC
RRM2b WT ch f	GAATGCCTACTGCTAAACTT
RRM2b WT ch r	CACTGGTCTAATGAAGGATT
RRM2b mt ch f	TGAGGTAAATGTTGCTGTT
RRM2b mt ch r	GGCGAATAACATTTCCTA