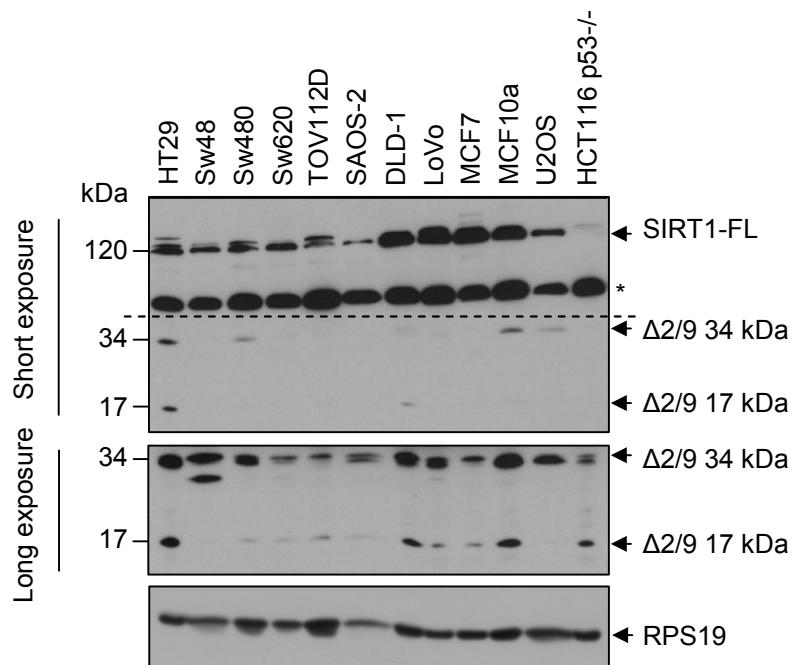


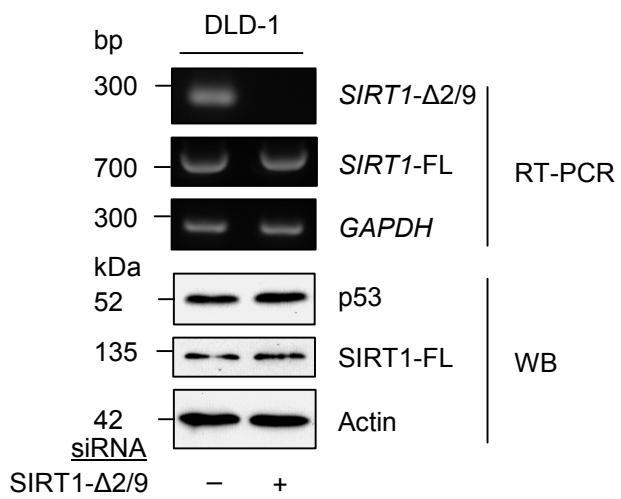
Shah et al., Suppl Figure 1

<i>SIRT1</i> -Δ2/9	GGATCCAGATCTGCTAGCATGGAACAAAA
<i>SIRT1</i> -Δ2/9 optimised	-----M E Q K
Protein sequence	
 <i>SIRT1</i> -Δ2/9	
 <i>SIRT1</i> -Δ2/9 optimised	ACTCATCTCAGAAGAGGATCTGAATCATACCGTCATCATCACCATCACCATGAGCTCGCCGATGAGGCCG
Protein sequence	L I S E E D L N H T G H H H H H E L A D E A c-Myc epitope His epitope
 <i>SIRT1</i> -Δ2/9	CCCTCGCCCTCAGCCGGCGGCCTCCCCCTCGGCCGCGGGGGGCCGACAGGGAGGCCGCGTCGTCCCCGCC 87
 <i>SIRT1</i> -Δ2/9 optimised	CATTGGCCCTACAGCTGGCGATCTCCAGTGAGCAGCCGGAGCAGATCGCGAGGCCGTTCCACCCGCA
Protein sequence	A L A L Q P G G S P S A A G A D R E A A S S P A
 <i>SIRT1</i> -Δ2/9	GGGGAGCCGCTCCGCAAGAGGCCGCGGAGAGATGGTCCCGGCCCTCGAGCGGAGGCCGGCGAGCCC GTGG 158
 <i>SIRT1</i> -Δ2/9 optimised	GGGGAACCCCTTCGGAAGAGACCGCGCAGAGATGGCCTGGTCTCGAACGGAGGCCAGGAGAACCTGGCGG
Protein sequence	G E P L R K R P R R D G P G L E R S P G E P G G
 <i>SIRT1</i> -Δ2/9	GGCGGGCCCCAGAGCGTGAGGTGCGCGCGGCCAGGGCTGCCGGGGCTGCCGGCGGCCGCGCTGTGGC 229
 <i>SIRT1</i> -Δ2/9 optimised	TGCAGCTCCAGAGCGTGAAAGTACCCGCTGCCGCAAGAGGGTGCCCTGGTCCGCGACTGCCGCGCTCTGGC
Protein sequence	A A P E R E V → P A A A R G C P G A A A A A L W SEx1
 <i>SIRT1</i> -Δ2/9	GGGAGGCGGGAGCAGAGGGCGGGCGGAGCGGGGGAGCAAGAGGCCAGGGCAGTCCGGCGGGCTGGGAA 300
 <i>SIRT1</i> -Δ2/9 optimised	GAGAGGCCAGAGCCGAGGCCGCTGCAGCCGGAGGCGAACAGGAGGCTCAAGGCCACAGCTGCAGCCGGGAA
Protein sequence	R E A E A E A A A A G G E Q E A Q A T A A A G E
 <i>SIRT1</i> -Δ2/9	GGAGACAATGGCCGGCCCTGCAGGGCCATCTCGGAGGCCACCGCTGGCCGACAACCTGTACGACGAAGA 371
 <i>SIRT1</i> -Δ2/9 optimised	GCGCAGACATGGACCCGGTTACAGGGCCAAGCAGGGAAACCACCGCTTCCGACAACTGTATGACGAGGA
Protein sequence	G D N G P G L Q G P S R E P P L A D N L Y D E D
 <i>SIRT1</i> -Δ2/9	CGACGACGAGGGCGAGGGAGGAAGAGCGGGCGGGCGATTGGGTACCGAGATAACCTCTGT 442
 <i>SIRT1</i> -Δ2/9 optimised	CGATGACGATGAGGGCGAGGAAGAGGAGGAGGCTGCTGCCGCGCATTGGCTACAGGGACAACTGTCTGT
Protein sequence	D D D E G E E E A A A A I G Y R D N L L
 <i>SIRT1</i> -Δ2/9	TCGTTCTGTGGCAGTAACAGTGATAGTGGACATGCCAGAGTCAAGTTTAGAAGAACCCATGGAGGATG 513
 <i>SIRT1</i> -Δ2/9 optimised	TCTGTTCTGTGGCTGTGACCGTGATCGTCGGTCAACGCCAGGGTTCAAGGTCTGAAAGAACCCATGGAGGATG
Protein sequence	F V L V A V T V I V G H A R V Q V *
 <i>SIRT1</i> -Δ2/9	AAAGTGAATTGAAAGATTCTACAATGGCTTAGAAGATGAGCCTGATGTTCCAGAGAGAGCTGGAGGAGCT 584
 <i>SIRT1</i> -Δ2/9 optimised	AAAGTGAATTGAAAGATTCTACAATGGCTTAGAAGATGAGCCTGATGTTCCAGAGAGAGCTGGAGGAGCT
 <i>SIRT1</i> -Δ2/9	GGATTGGACTGATGGAGATGATCAAGAGGAATTATGAAGCTATATCTGTGAAACAGGAAGTAACAGA 655
 <i>SIRT1</i> -Δ2/9 optimised	GGATTGGACTGATGGAGATGATCAAGAGGAATTATGAAGCTATATCTGTGAAACAGGAAGTAACAGA
 <i>SIRT1</i> -Δ2/9	CATGAACTATCCATCAAACAAATCATAG 683
 <i>SIRT1</i> -Δ2/9 optimised	CATGAACTATCCATCAAACAAATCATAGAAGCTTCGTCGACGATATC cagcacagtggcgccgtcgag
	← 10R primer
	tctagaggcccgcgttcgaacaaaactcatctcagaagaggatctgaatatgcataccggcatcatc
	accatcaccattgagttaaacctcgatcagcctcgactgtgccttcta
	← BGH-Rvs

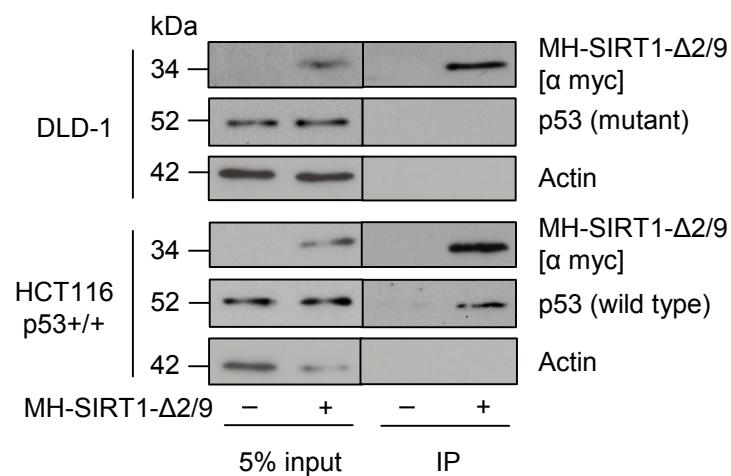
**Supplemental Figure 1. Alignment of *SIRT1*-Δ2/9 wild type and codon-optimised sequences in pcDNA3.1 expression construct.** *SIRT1*-Δ2/9 sequence including part of its 3'-UTR (full 3'-UTR of *SIRT1*-Δ2/9 is not known) together with sequences for c-Myc and His epitope tags (underlined) was codon-optimised, chemically synthesized and cloned in pcDNA3.1 vector. The codon-optimised sequence is compared with the original wild type nucleotide sequence of *SIRT1*-Δ2/9, vertical bars and dots indicate identity and silent changes introduced for codon-optimisation respectively. ATG start and TAG stop codons are shown bold. Boxed, yellow and red labeled sequences indicate exon 2, 2-9F primer and novel C-terminal amino acids respectively. Arrows represent location of other primers as indicated. Primer pairs Sex1/BGH-Rvs and 2-9F/10R amplify exogenous- and endogenous-specific *SIRT1*-Δ2/9 transcripts respectively. Small lettered nucleotides are pcDNA3.1 vector sequence.



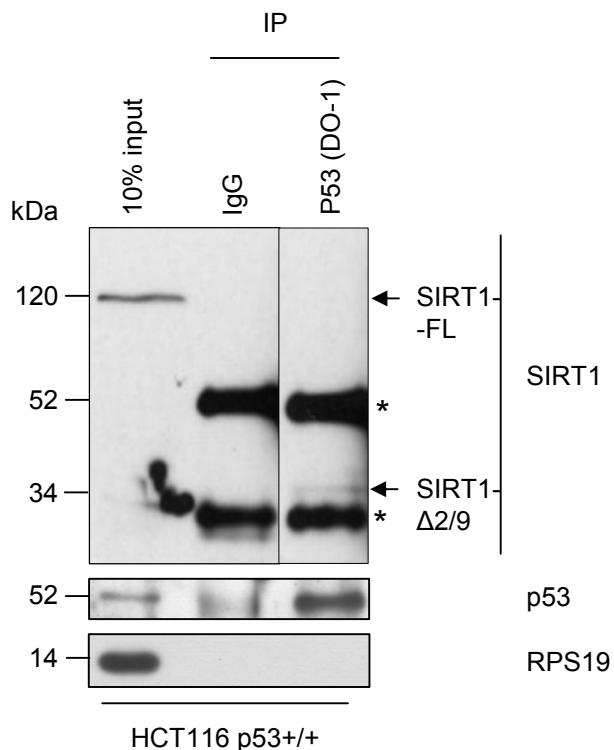
**Supplemental Figure 2. Expression of SIRT1-FL and SIRT1-Δ2/9 in a range of human cell lines.** Total cell lysates from indicated cell lines were immunoblotted for SIRT1 protein using anti-SIRT1 antibodies (N-terminus; Epitomics); similar but weaker results were obtained with an independent SIRT1 N-terminal antibody (Millipore). Loading control was the ribosomal protein RPS19. SIRT-FL was readily detectable in short exposures (upper panel) whilst longer exposure was required to detect SIRT1-Δ2/9 in most of the cell lines (lower panel). Dotted line in short exposure panel delineates area shown in the panel below (long exposure). Both 17kDa and 34kDa forms of SIRT1-Δ2/9 are evident (see Results section). \* = a strong, non-specific band cross reactive with the Epitomics antibody.



**Supplemental Figure 2. Mutant p53 protein levels are not affected by SIRT1-Δ2/9 depletion.** Protein levels of mutant p53 (S241F), SIRT1-FL and actin in DLD-1 cell line following depletion of *SIRT1-Δ2/9* by siRNA (lower panel) and mRNA levels of *SIRT1-Δ2/9*, *SIRT1-FL* and *GAPDH* (upper panel).



**Supplemental Figure 3. SIRT1-Δ2/9 does not interact with mutant p53.** MH-SIRT1-Δ2/9 was expressed in HCT116 p53<sup>+/+</sup> and DLD-1 cells, immunoprecipitated with anti-His antibody and probed for SIRT1-Δ2/9 and p53.



**Supplemental Figure 5. Complexing between endogenous SIRT1-Δ2/9 and p53 proteins.** Lysates of HCT116 cells cultured under normal conditions (i.e. in the absence of applied stress) were immunoprecipitated using anti-p53 monoclonal antibody DO-1, followed by immunoblotting for SIRT1 (N-terminus, Epitomics), p53 (FL-393) or RPS19 as indicated. SIRT1-FL and SIRT1-Δ2/9 proteins are indicated by arrows; \* = heavy and light IgG chains of DO-1 antibody. On long exposures the IgG light chain signal masks the co-immunoprecipitated SIRT1-Δ2/9 protein band (not shown). Note that SIRT1-FL was undetectable in p53 pull-downs even in long exposures of the immunoblot (see text, Results section for further discussion of this observation).

**Supplemental Table 1. Primers used in this study.**

Primers	Sequence
1F	5'-ataacccctgttgcgttc-3'
2-9F	5'-ataacccctgttgcgttc-3'
8Rvs	5'-aagagggtgtgggtggcaactctg-3'
10R	5'-ctatgattttatggatggatgttc-3'
<i>APAF-1</i> -F	5'-tgcgtgcgtgccttc-3'
<i>APAF-1</i> -R	5'-ccatggtagcagtccttc-3'
BGH-Rvs	5'-tagaaggcacagtcgagg-3'
<i>CUGBP1</i> -F	5'-gataggagccaaaacccgcc-3'
<i>CUGBP1</i> -R	5'-tcacaaatgcacaacctcg-3'
<i>CUGBP2</i> -F	5'-gtgaaaagtccaacgcgttg-3'
<i>CUGBP2</i> -R	5'-ccaggtggcagtgttgagc-3'
<i>GAPDH</i> -F	5'-cggagtcaacggatttgtcg-3'
<i>GAPDH</i> -R	5'-agcctctccatggtgaa-3'
<i>HO-1</i> -F	5'-ccagtgcaccaagttcaag-3'
<i>HO-1</i> -R	5'-cagctctgcaactcctcaa -3'
<i>HO-1</i> pF	5'-gtcaacgcctgcctccttc-3'
<i>HO-1</i> pR	5'-tcgggttgcggacgcctccat-3'
<i>IGFBP3</i> -iF	5'-agagatgttaacggggacctaga-3'
<i>IGFBP3</i> -iR	5'-accagtaccgtctcaatgtc-3'
<i>IGFBP3</i> -F	5'-gacagaatatggccctgccg-3'
<i>IGFBP3</i> -R	5'-ttgaaggcgacactgtc-3'
<i>IGFBP3</i> -pF	5'-cggcacacccctggttctg-3'
<i>IGFBP3</i> -pR	5'-cttcgccttgagcagccg-3'
<i>MMP-1</i> -F	5'-tttgcgttaccctagctacacccatca-3'
<i>MMP-1</i> -R	5'-aaaggtagcttactgtcacatgttt-3'
<i>TP53E5F</i>	5'-cccctgcctcaacaagatgt-3'
<i>TP53E8R</i>	5'-ctgaagggtgaaatattctcc-3'
<i>TP53-up1</i>	5'-atggaggagccgcagtcagat-3'
<i>TP53-dn1</i>	5'-tcagtctgagtcaggcccttc-3'
SEx1	5'-ccagagcgtgaggtgcc-3'
SEx4	5'-gggatggtatttatgctcgc-3'
<i>TBP</i> -F	5'-caggagccaagagtgaagaaca-3'
<i>TBP</i> -R	5'-agctggaaaacccaactctgt-3'
<i>PLAT</i> -F	5'-atgcccgttgcagaagagg-3'
<i>PLAT</i> -R	5'-gacaggactgagtgccact-3'

**Supplemental Table 2. RT-PCR annealing and cycling conditions.**

Primer sets for gene	Annealing temperature/ no. of cycles
<b>Standard RT-PCR</b>	
<i>CUGBP1</i>	58°C/35
<i>GAPDH</i>	58°C/30
<i>TP53</i>	58°C/35
<i>SIRT1</i> -Δ2/9	53°C/44
<i>SIRT1</i> -FL	58°C/34
<b>qRT-PCR</b>	
<i>APAF-1</i>	60°C/40
<i>CUGBP2</i>	58°C/35
<i>HO-1</i>	60°C/40
<i>HO-1</i> promoter	60°C/45
<i>IGFBP3</i>	60°C/40
<i>IGFBP3</i> intron	60°C/45
<i>IGFBP3</i> promoter	60°C/45
<i>MMP-1</i>	60°C/40
<i>TP53</i>	58°C/33
<i>TBP</i>	58°C/35
<i>PLAT</i>	60°C/35