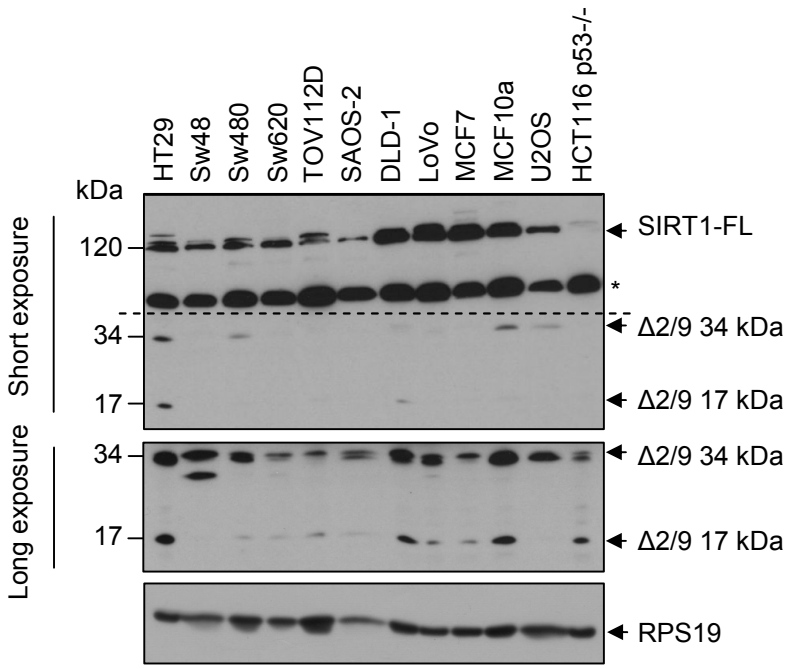
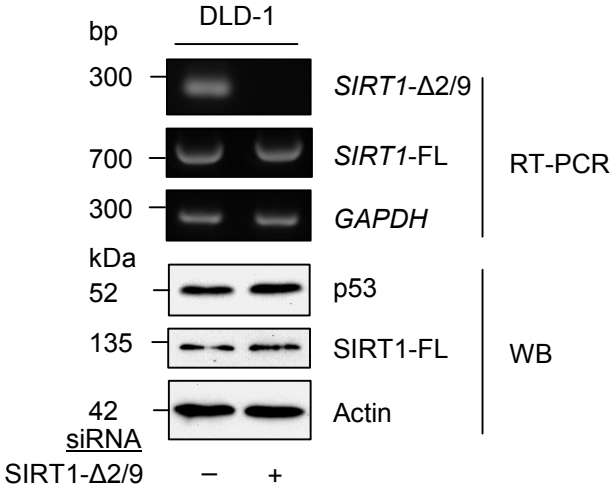
Shah *et al.*, Suppl Figure 1

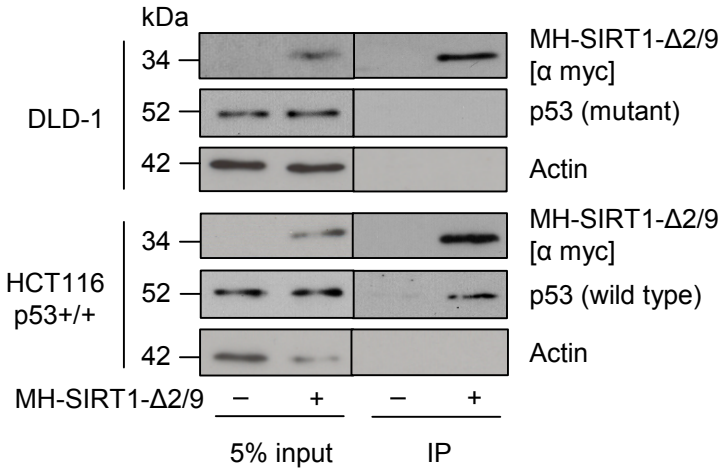
**Supplemental Figure 1. Alignment of *SIRT1*-Δ2/9 wild type and codon-optimised sequences in pcDNA3.1 expression construct.** *SIRT1*-Δ2/9 sequence including part of its 3'-UTR (full 3'-UTR of *SIRT1*-Δ2/9 is not known) together with sequences for c-Myc and His epitope tags (underlined) was codon-optimised, 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.



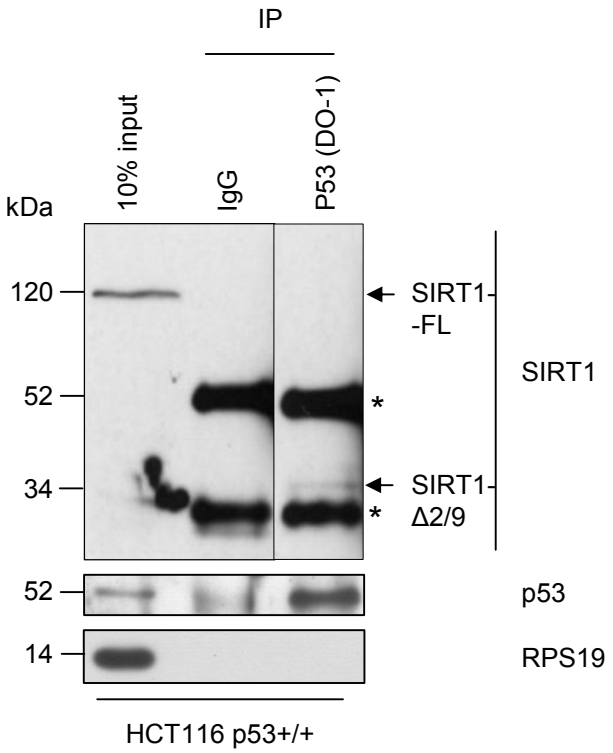

**Supplemental Figure 2. Expression of SIRT1-FL and SIRT1-Δ2/9 in a range of human cell lines**. Total cell lysates from indicated cell lines were immunoblotted for SIRT1 protein using anti-SIRT1 antibodies (N-terminus; Epitomics); similar but weaker results were obtained with an independent SIRT1 N-terminal 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+/+ 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'-ataaccttctgttcgttct-3' |
| 2-9F | 5'-ataaccttctgttcgttct-3' |
| 8Rvs | 5'-aagaggtgtgggtggcaactctg-3' |
| 10R | 5'-ctatgatttgtttgatggatagttc-3' |
| *APAF-1*-F | 5'-tgcgctgctctgccttct-3' |
| *APAF-1*-R | 5'-ccatgggtagcagctccttct-3' |
| BGH-Rvs | 5'-tagaaggcacagtcgagg-3' |
| *CUGBP1*-F | 5'-gataggagccaaaacccgcc-3' |
| *CUGBP1*-R | 5'-tcacaaatgcacaacctcgg-3' |
| *CUGBP2*-F | 5'-gtgaaaagtccaacgctgtg-3' |
| *CUGBP2*-R | 5'-ccaggtggcagtgttgagc-3' |
| *GAPDH*-F | 5'-cggagtcaacggatttggtcg-3' |
| *GAPDH*-R | 5'-agccttctccatggtggtgaa-3' |
| *HO-1*-F | 5'-ccagtgccaccaagttcaag-3' |
| *HO-1*-R | 5'-cagctcctgcaactcctcaa -3' |
| *HO-1*pF | 5'-gtcaacgcctgcctcctctc-3' |
| *HO-1*pR | 5'-tcgggttgcggacgctccat-3' |
| *IGFBP3*-iF | 5'-agagatgtaacggggacctaga-3' |
| *IGFBP3*-iR | 5'-accagtaccgtcctcaatgct-3' |
| *IGFBP3*-F | 5'-gacagaatatggtccctgccg-3' |
| *IGFBP3*-R | 5'-ttggaagggcgacactgct-3' |
| *IGFBP3*-pF | 5'-cgggcacaccttggttcttg-3' |
| *IGFBP3*-pR | 5'-cttcgccctgagcagccg-3' |
| *MMP-1*-F | 5'-tttgatgtaccctagctacaccttca-3' |
| *MMP-1*-R | 5'-aaaggttagcttactgtcacatgcttt-3' |
| *TP53*E5F | 5'-cccctgccctcaacaagatgt-3' |
| *TP53*E8R | 5'-ctgaagggtgaaatattctcc-3' |
| *TP53*-up1 | 5'-atggaggagccgcagtcagat-3' |
| *TP53*-dn1 | 5'-tcagtctgagtcaggcccttc-3' |
| SEx1 | 5'-ccagagcgtgaggtgcc-3' |
| SEx4 | 5'-gggatggtatttatgctcgc-3' |
| *TBP*-F | 5'-caggagccaagagtgaagaaca-3' |
| *TBP*-R | 5'-agctggaaaacccaacttctgt-3' |
| *PLAT*-F | 5'-atgcccgattcagaagagg-3' |
| *PLAT* -R | 5'-gacaggcactgagtggcact-3' |

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

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