peptide	deacetylation by SIRT1
H2BK12Ac	+
H2BK15Ac	+
H2BK20Ac	+
H3K9Ac	+
H3K18Ac	+
H4K5Ac	+
H4K8Ac	+
H4K12Ac	+

Supplementary Table 1. SIRT1 deacetylates multiple histone peptides *in vitro*. Deacetylase reactions were performed in the absence or presence of recombinant SIRT1 protein and NAD+, and deacetylation was detected by mass spectrometry. Table summarizes positive substrates identified for SIRT1.

	Number of reads (factor)	Number of peaks (factor)	Number of top 40% peaks overlapping with other replicate (percentage)
ENCODE requirements	factor < 2	factor < 2	percentage > 80
SIRT7 rep1	6,232,566 (0.94)	496 (1.56)	102 (80.3)
SIRT7 rep2	6,599,572 (1.06)	317 (0.64)	113 (89.0)

Supplementary Table 4. Reproducibility analysis of the two SIRT7 ChIP-sequencing replicates. Table summarizing read and peak overlap between SIRT7 ChIP-sequencing replicates 1 and 2 (rep1 and rep2). According to the NIH guideline, the longer list (496 peaks) was trimmed to the length of the shorter list (317 peaks) in the overlap analysis. ChIP-sequencing peaks were identified using MACS with p-value cutoff 1e-6. Factors are with respect to the opposite replicate.

	SIRT7 ChIP-seq rep1	SIRT7 ChIP-seq rep2	Common peaks between rep1 and rep2	SIRT7 pooled
Number of peaks	496	317	209	276
Number of peaks containing ELK4 motif	251	224	109	159
Percent of peaks containing ELK4 motif	50.6	70.7	52.2	57.6

Supplementary Table 5. Overlap between SIRT7 ChIP-sequencing peaks and the ELK4-consensus motif. Analysis of ChIP-sequencing data pooled from two replicates, the individual replicates, or the peaks in common, yielded very similar numbers with significant enrichment for ELK4 motif containing peaks. Analysis of the pooled data was performed using the highly stringent p-value cutoff 1e-8. Separate analysis of the individual replicates, using a p-value cutoff of 1e-6, identified more peaks: 496 and 317 peaks for replicates 1 and 2, respectively, and 209 peaks were common to the two replicates.

ELK4 motif

position	1	2	3	4	5	6	7	8	9
A	0.80	0.00	0.00	0.00	0.00	1.00	0.80	0.20	0.05
C	0.05	1.00	1.00	0.00	0.00	0.00	0.00	0.05	0.30
G	0.10	0.00	0.00	1.00	1.00	0.00	0.00	0.75	0.00
T	0.05	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.65

SIRT7 motif

position	1	2	3	4	5	6	7	8
A	0.05	0.05	0.03	0.83	0.77	0.14	0.03	0.07
C	0.69	0.03	0.05	0.09	0.04	0.08	0.21	0.11
G	0.19	0.88	0.86	0.03	0.14	0.58	0.06	0.74
T	0.07	0.03	0.06	0.05	0.04	0.21	0.71	0.07

Supplementary Table 6. ELK4 and SIRT7 concensus motifs. Matrix of JASPAR motif MA0076.1 ELK4 as well as SIRT7 motif generated by STAMP. The numeric values indicate the relative weight of each nucleotide [ACGT] at each position of the motif on a scale of 0-1.

Antibodies	Source	Catalog #
beta-tubulin	Upstate	05-661
E1A	Abcam	ab33183
ELK1	Epitomics	1277-1
ELK4	Sigma	HPA028863
FLAG M2	Sigma	F3165
GABPα	Abcam	ab55052
H2A	Abcam	ab18255
H2AK5Ac	Abcam	ab45152
H3	Abcam	ab1791
H3K14Ac	Abcam	ab52946
H3K18Ac	Abcam	ab1191
H3K23Ac	Abcam	ab46982
H3K56Ac	Epitomics	2134-1
H3K9Ac	Abcam	ab4441
H4	Abcam	ab7311
H4K16Ac	Abcam	ab23352
H4K8Ac	Abcam	ab15823
HA-tag	Abcam	ab9110
NME1	Sigma	WH0004830M2
p53	Calbiochem	OP43
p53 K382Ac	Abcam	ab75754
RPS14	Abcam	ab50390
RPS20	Abcam	ab74700
SIRT1	Santa Cruz	sc-15404
SIRT7	ref. 8	-

Supplementary Table 7. Antibodies used in this study.

Gene	Primer	Sequence
COPS2	forward	gtgcgatgatgaggaggact
	reverse	cacatttggctcggagttacta
CCNT1	forward	cttacttcatggcaaccaacag
	reverse	cttgcaagccaggtgaatg
ELK4	forward	ctcgagtttccagcgtgag
	reverse	cagggtgatagcactgtccat
FAF1	forward	gaagtccagcgggagtacaa
	reverse	aaggtcatacacatttctctttacctc
GAPDH	forward	agccacatcgctcagacac
	reverse	gcccaatacgaccaaatcc
GPR108	forward	caggaaacaacccgtacctg
	reverse	ggaacccagagtccgtcat
MORG1	forward	cgggaaggtgttcttctgg
	reverse	actgcaccacaccggaac
NME1	forward	cagccggagttcaaacctaa
	reverse	gcaatgaaggtacgctcaca
RPS7	forward	tcgcgagatttgggtctct
	reverse	ggcgctcgaactgaacat
RPS14	forward	tcgttcctggtctcagaagg
	reverse	cctttcgaggtgccatttt
RPS20	forward	agggctgaggatttttggtc
	reverse	gggtgtttttccggtatcct
SIRT7 (ref. 8)		

Target	Primer	Sequence
COPS2 promoter	forward	cgaatcagctacaagtcgagataa
	reverse	cgccttccagtccctctt
GAPDH promoter	forward	gaccttccgtgcagaaacc
	reverse	ctggctcctggcatctct
NME1 promoter	forward	ccgtaatacttggctctcgaa
	reverse	gaatagacctgcatgaagtgagg
RPS7 promoter	forward	cggctgaaagtaactcttgcat
	reverse	gctgtggacagggaatttaatc
RPS14 promoter	forward	acaggaggacggattgagc
	reverse	acggggtctccctgtgtt
RPS20 promoter	forward	aagttctttcttttgaggaagacg
	reverse	gaacagcggtgagtcagga
TIMM9 promoter	forward	atgtccggagtttgtttcca
	reverse	aagctaagcgctctctggtg
TMEM71 promoter	forward	agccccatctaatgctcgat
	reverse	ctagcctgggttgtctgctt
UBE2N promoter	forward	cgtgccttccaggaacttag
	reverse	gcccttaacacattggattgtaa
γ*–tubulin* promoter	forward	acgggtttcatcatgtttgtt
	reverse	ggcagatcccctgaggtc

Supplementary Table 8. PCR primers used in this study. Sequences of PCR primers used for gene expression (top panel) or ChIP (bottom panel) analysis.