Figure S1

Figure S1: Analysis of genomic TP53 BSs. (**A**) Relative affinities compared to the consensus TP53 BS (BS100) of genomic TP53 BSs as computed by the TP53 *No Read Left Behind* model (25). Displayed are 250 BSs with the highest predicted affinities. Affinities of BS014 and BS006 are indicated by red lines. (**B**) Number of genomic TP53 response elements with one, two, or three TP53 BSs. Only BSs with a relative affinity of > 0.0001 as defined by the TP53 *No Read Left Behind* model were taken into consideration. (**C**) BS-BS spacer length distribution of all genomic response elements with two TP53 BSs.

Supplementary Table S1: Sequences of the primers used in the study.

Name	Used for	Sequence (5'-3')
MT024	Oligo library amplification and addition EcoRI overhang	ACCTTGGAATTCCGGAGCGAACCGAGTTAG
MT025	Oligo library amplification and addition NheI overhang	CGCTTAGCTAGCCTCTTGGATGCGACGATG
MT165	Gene-specific primer for cDNA synthesis	CCTCTCCGCCGCCCACCAGCTCGAACTCCAC
MT164	cDNA amplification indexed primer including Illumina S1 and p7	CAAGCAGAAGACGGCATACGAGATNNNNNNNGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGTGATGCGGCACTCGATCTTCATGGC
MT397	cDNA amplification indexed primer including Illumina S2 and p5	AATGATACGGCGACCACCGAGATCTACACNNNNNNNNNACACTCTTTCCCTACACGACGCTCTTCCGATCT