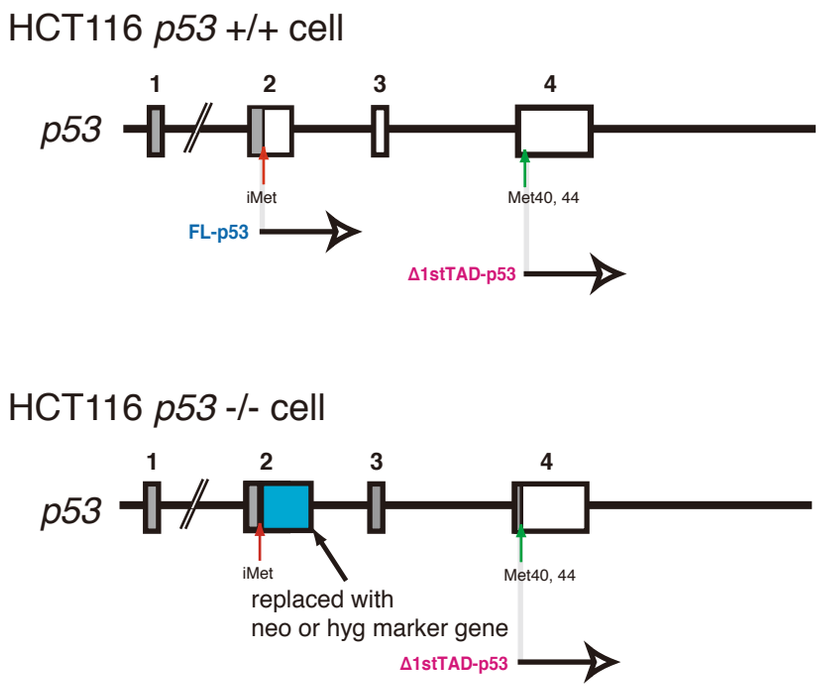

Fig. S1 Genomic structure of the *p53* gene and expression of FL- and Δ1stTAD-p53 in HCT116 *p53*+/+ and -/- cells.
HCT116 *p53*-/- cells have been artificially created from HCT116 *p53*+/+ cells (human colorectal carcinoma), and are deficient in FL-p53.

A

Ingenuity Canonical Pathways	-log(p-value)	Molecules
Pyrimidine Deoxyribonucleotides De Novo Biosynthesis I	4.47E+00	TYMS,RRM2B,AK4
VEGF Signaling	3.55E+00	PTK2,ACTB,EIF2B3,ACTN1
Regulation of Cellular Mechanics by Calpain Protease	3.09E+00	PTK2,CAPN2,ACTN1
Death Receptor Signaling	2.69E+00	ACTB,TNFRSF10B,MAP4K4
FAK Signaling	2.46E+00	PTK2,ACTB,CAPN2
AMPK Signaling	2.45E+00	CPT1A,ACTB,STK11,AK4
Integrin Signaling	2.43E+00	PTK2,ACTB,CAPN2,ACTN1
EIF2 Signaling	2.41E+00	EIF3D,ACTB,RPS27L,EIF2B3
Actin Cytoskeleton Signaling	2.40E+00	PTK2,F2R,ACTB,ACTN1
Paxillin Signaling	2.31E+00	PTK2,ACTB,ACTN1
Molybdenum Cofactor Biosynthesis	1.96E+00	GPHN
Regulation of eIF4 and p70S6K Signaling	1.95E+00	EIF3D,RPS27L,EIF2B3
Tec Kinase Signaling	1.87E+00	PTK2,ACTB,TNFRSF10B
Creatine-phosphate Biosynthesis	1.86E+00	MAP4K4
dTMP De Novo Biosynthesis	1.86E+00	TYMS
Mitotic Roles of Polo-Like Kinase	1.84E+00	PLK2,CDC27
Germ Cell-Sertoli Cell Junction Signaling	1.82E+00	PTK2,ACTB,ACTN1
Remodeling of Epithelial Adherens Junctions	1.81E+00	ACTB,ACTN1
ILK Signaling	1.72E+00	PTK2,ACTB,ACTN1
Agrin Interactions at Neuromuscular Junction	1.71E+00	PTK2,ACTB
Leukocyte Extravasation Signaling	1.68E+00	PTK2,ACTB,ACTN1
HIPPO signaling	1.64E+00	SCRIB,MOB1A
mTOR Signaling	1.63E+00	EIF3D,STK11,RPS27L
Thrombin Signaling	1.62E+00	PTK2,F2R,ARHGEF3
Protein Kinase A Signaling	1.61E+00	PTK2,PTPRA,PTP4A1,CDC27
Glioma Invasiveness Signaling	1.59E+00	PTK2,F2R
Calcium Transport I	1.56E+00	ATP2B4
Apoptosis Signaling	1.51E+00	CAPN2,MAP4K4

B

Ingenuity Canonical Pathways	-log(p-value)	Molecules
Cell Cycle Regulation by BTG Family Proteins	3.34E+00	BTG2,PPP2R5C,PRMT1
HIPPO signaling	2.29E+00	NF2,PPP2R5C,FRMD6
Spermine Biosynthesis	2.09E+00	SMS
Formaldehyde Oxidation II (Glutathione-dependent)	2.09E+00	ADH5
CTLA4 Signaling in Cytotoxic T Lymphocytes	2.09E+00	PTPN6,CLTB,PPP2R5C
Inosine-5'-phosphate Biosynthesis II	1.91E+00	ATIC
1D-myo-inositol Hexakisphosphate Biosynthesis V (from Ins(1,3,4)P3)	1.91E+00	IPPK
Tetrapyrrole Biosynthesis II	1.69E+00	HMBS
Phagosome Maturation	1.65E+00	VPS39,PRDX5,VAMP3
Selenocysteine Biosynthesis II (Archaea and Eukaryotes)	1.62E+00	SEPHS1
Glycogen Biosynthesis II (from UDP-D-Glucose)	1.62E+00	GBE1
Autophagy	1.59E+00	VPS39,NBR1
Mitotic Roles of Polo-Like Kinase	1.53E+00	FBXO5,PPP2R5C
Regulation of eIF4 and p70S6K Signaling	1.50E+00	RPS19,RPS16,PPP2R5C

Fig. S2 The ingenuity canonical pathways of the potential target genes of Δ1stTAD-p53.
A. Pathway for genes with binding sites common for FL- and Δ1stTAD-p53. *PLK2*, *PTP4A1* and *RPS27L* genes are shown in red.
B. Pathway for genes specifically bound by Δ1stTAD-p53.

Fig. S3

A

Gene Symbol	Probe Set ID	FL-p53 without treatment			Δ1stTAD-p53 without treatment			Δ1stTAD-p53 serum deprived		
PLK2	201939_at	174.6	261.6	261.6	497.2	643.9	660.5	438.5	471.9	384.3
PTP4A1	200731_s_at	474.8	569.7	569.7	1192.9	910.1	1215.7	1046.6	1245.3	1216.5
RPS27L	218007_s_at	2398	2136.5	2136.5	1926.6	1889.5	1960.4	2653.3	2696.2	2193.5

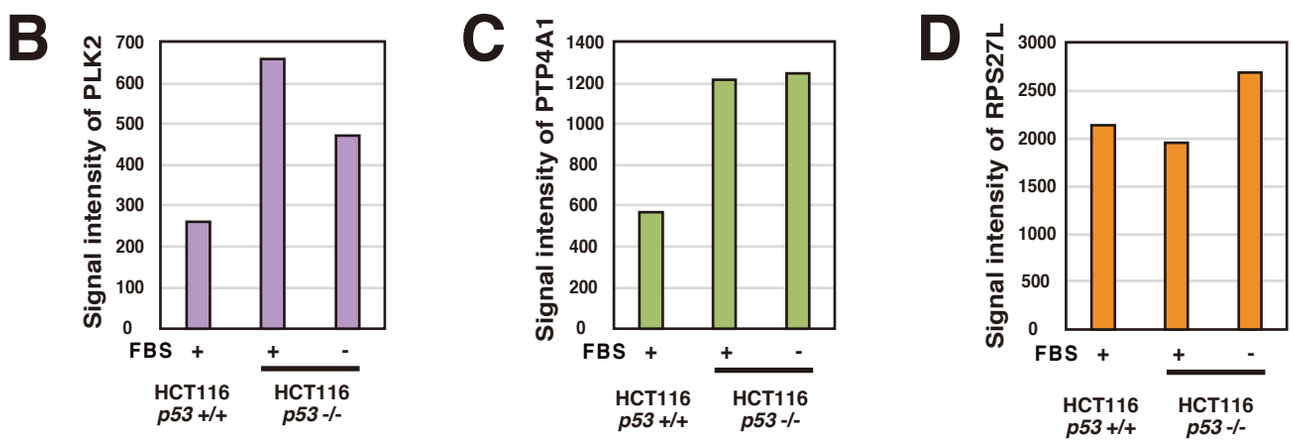

Fig. S3 Endogenous Δ1stTAD-p53 induces *PLK2*, *PTP4A1* and *RPS27L*.

A. Expression of *PLK2* (201939_at), *PTP4A1* (200731_s_at), and *RPS27L* (218007_s_at) were analyzed by microarray expression analysis using HCT 116 *p53* +/+ and -/- cells. HCT116 *p53* -/- cells were cultured in normal FBS or subjected to FBS deprivation.

For each condition, 3 independent samples were analyzed.

B-D. Representative microarray expression analysis results of *PLK2* (B), *PTP4A1* (C), and *RPS27L* (D) expression are shown.

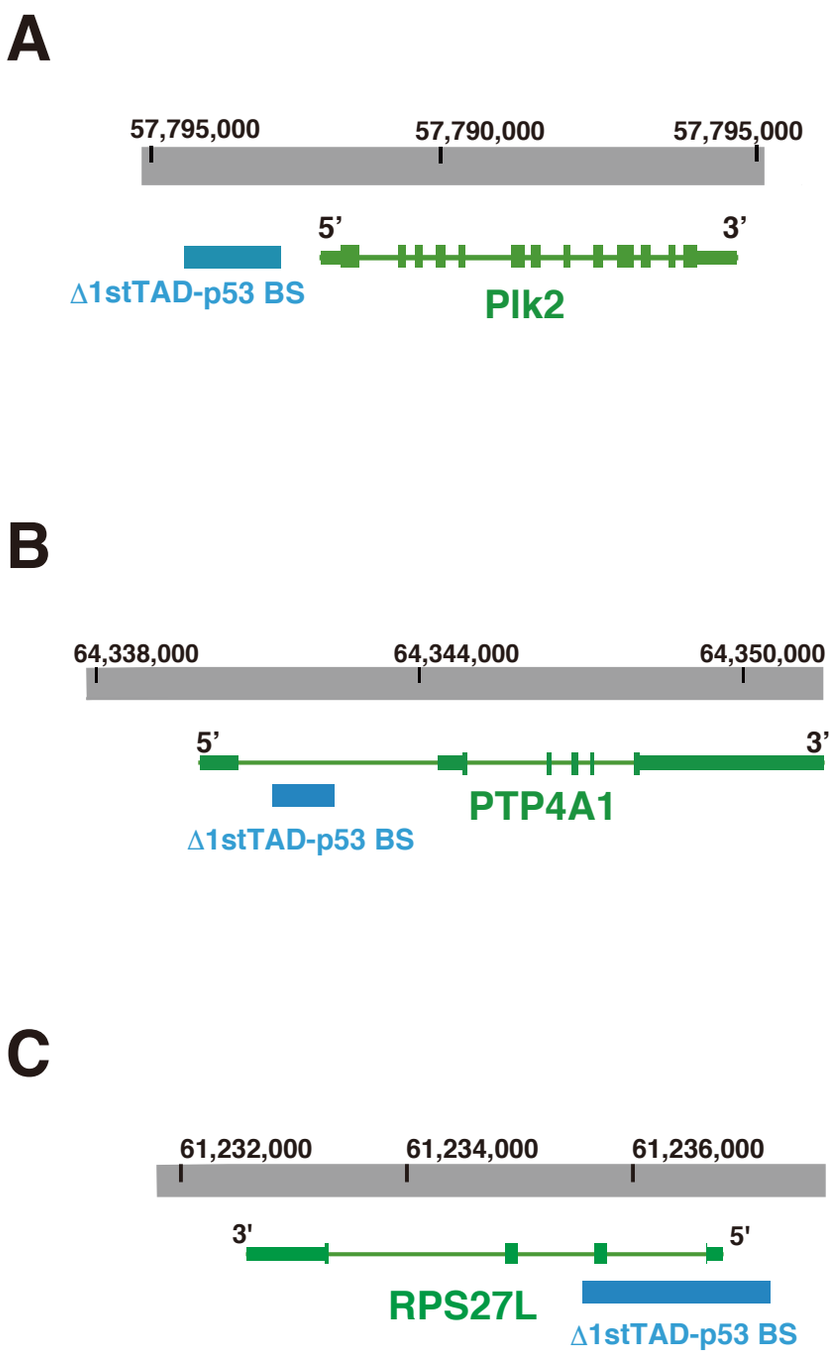

Fig. S4 Δ1stTAD-p53 binds to the genomic region of the *PLK2*, *PTP4A1* and *RPS27L* genes.

Serum-deprived HCT116 *p53* -/- cells were harvested, and p53 ChIP-chip analysis using anti-p53 antibody (FL393) was performed. Genomic loci of *PLK2* (A), *PTP4A1* (B) and *RPS27L* (C) are shown together with the results obtained. Blue areas indicate the p53-binding region. The resulting sequences were mapped to the build #36 reference human genome (hg18).

Fig.S5

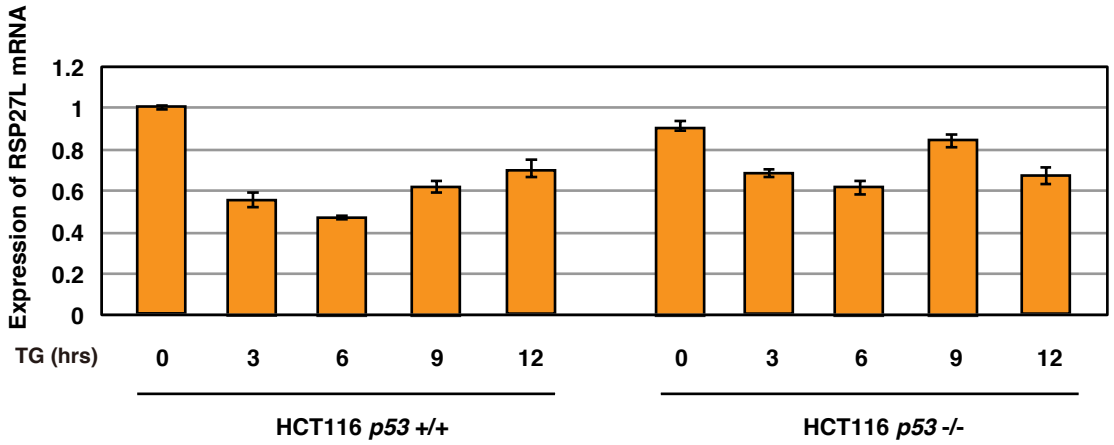

Fig. S5 *RPS27L* is not induced upon ER stress.
HCT 116 *p53*+/+ and -/- cells were treated with TG and analyzed as in Fig. 6. *RPS27L* mRNA levels were analyzed by quantitative RT-PCR.