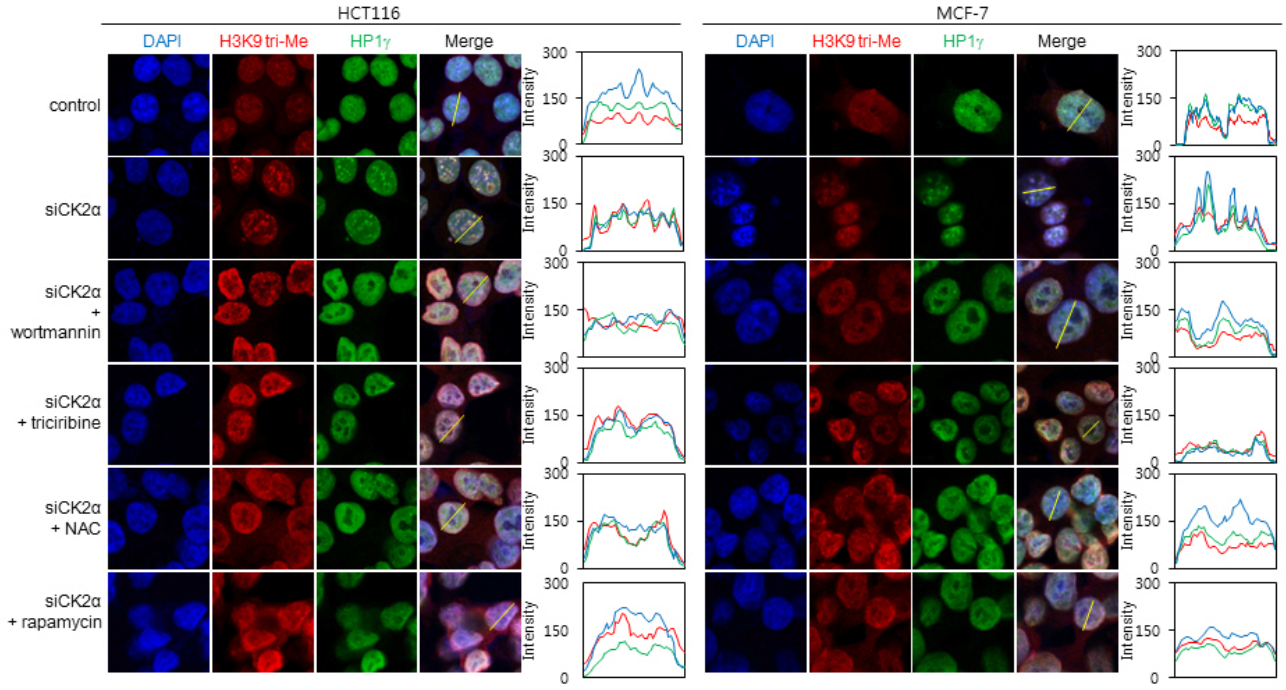
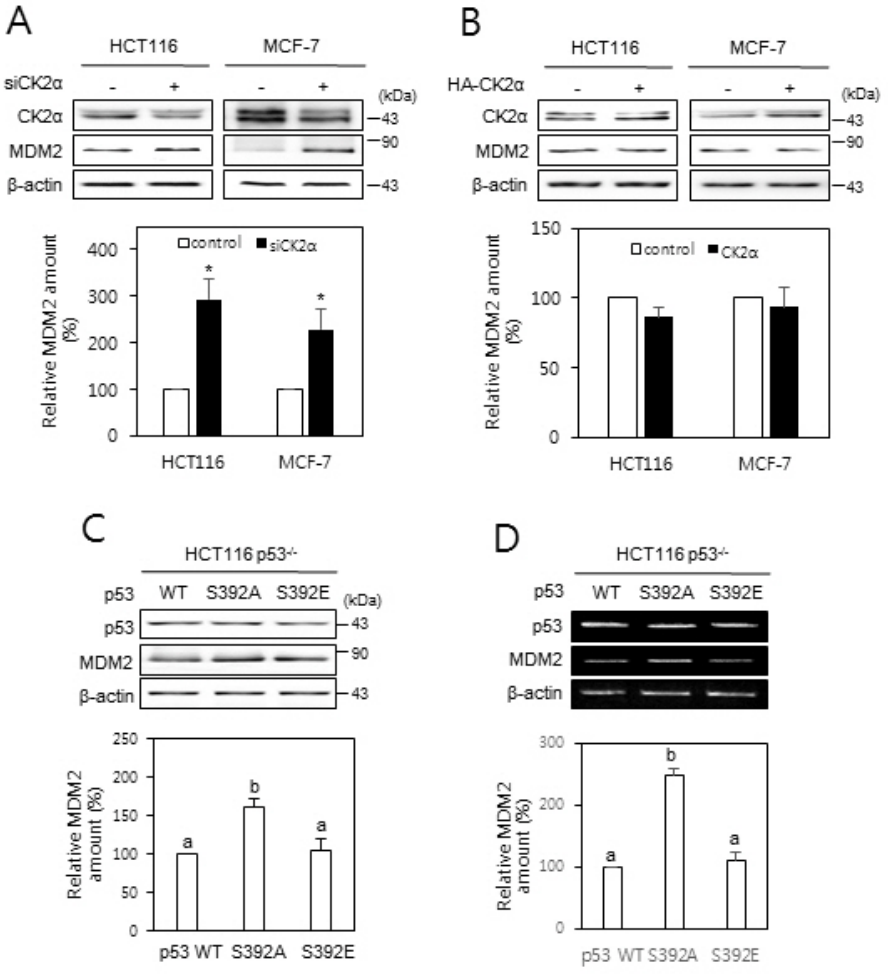
Supplementary Table S1. Primers used for RT-PCR analyses

Gene		Primer sequence
p53	Forward	5′-CCTCACCATCATCACACTGG-3′
	Reverse	5′-CCTCATTCAGCTCTCGGAAC-3′
p21	Forward	5′-ATGGAACTTCGACTTTGTCA-3′
	Reverse	5′-GCTTCCTCTTGGAGAAGATC-3′
MDM2	Forward	5′-ATCAGGCAGGGGAGAGTGAT-3′
	Reverse	5′-TCTACATACTGGGCAGGGCT-3′
β-actin	Forward	5′-TCCCTGGAGAAGAGCTAC-3′
	Reverse	5′-AGCACTGTGTTGGCGTACAG-3′



Supplementary Fig. S1. PI3K-AKT-mTOR-ROS pathway is required for SAHFs formation after CK2 downregulation. Confocal immunofluorescent images of co-localization of chromatin foci with H3K9me3 (red) and HP1γ (green) in cells after treatment with CK2α siRNA in the presence of 100 nM wortmannin, 10 μM triciribine, 5 mM NAC, or 100 nM rapamycin. DAPI staining (blue) was used to visualize DNA foci. Fluorescence intensity was quantified using ImageJ software (right panels). Arbitrary intensity values for H3K9me3 (red), HP1γ (green), or DAPI (blue) are shown relative to the reference line (white) used for analysis.



Supplementary Fig. S2. Enhanced MDM2 expression by CK2 downregulation and dephosphorylation of S392 on p53. (A and B) Cells were treated with CK2α siRNA (A) or pcDNA3.1-HA-CK2α (B). Cell lysates were visualized by immunoblotting (upper panels). Graph represents quantification of each protein relative to β-actin (bottom panels). Values indicate mean ± SEM. $*P < 0.05$. (C and D) Cells were treated with pcDNA3.1-p53 wild type (WT) or -p53 mutants (S392A and S392E). (C) Cell lysates were visualized by immunoblotting (upper panels). Graph represents quantification of each protein relative to β-actin (bottom panels). (D) RT-PCR analysis using specific primers for *p53* and *MDM2*. Graph represents quantification of the mRNA levels of each gene relative to those of *β-actin*. Bars that do not share a common letter (a, b) were significantly different among groups at $P < 0.05$.