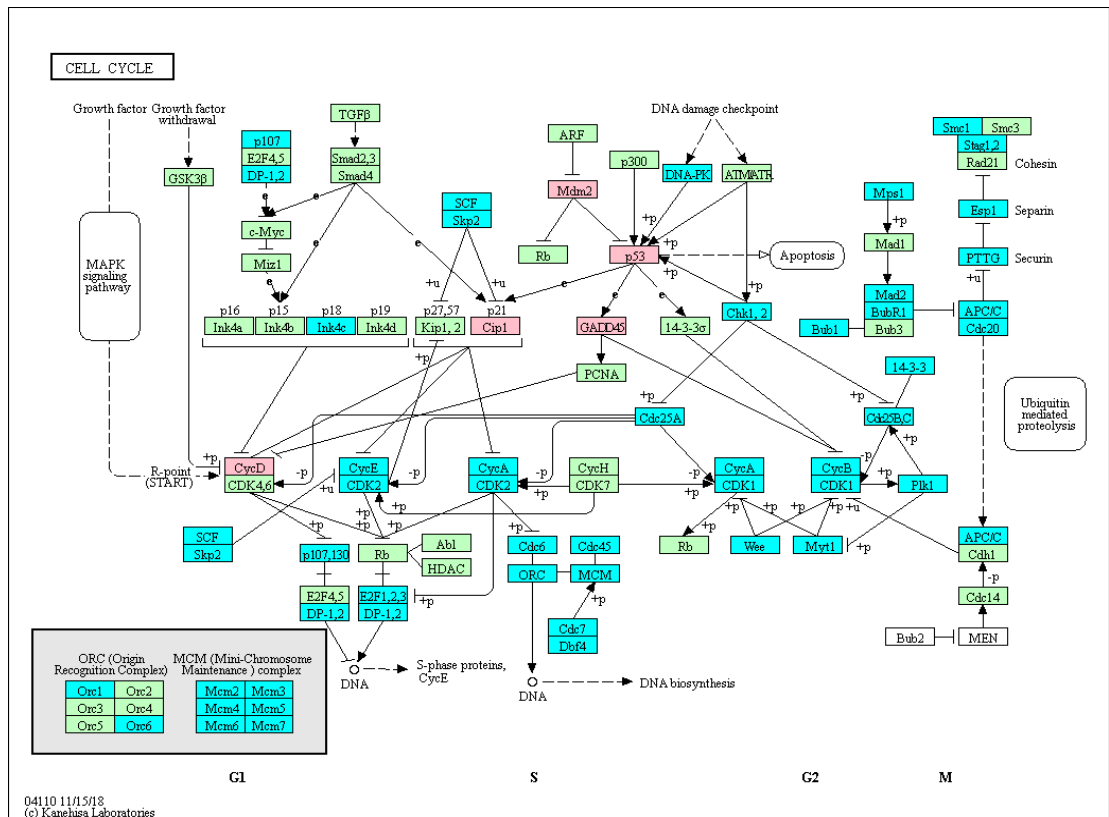
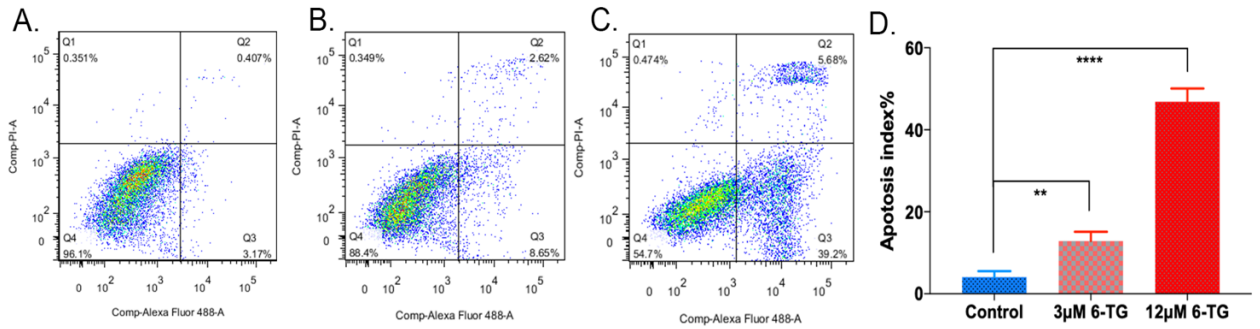


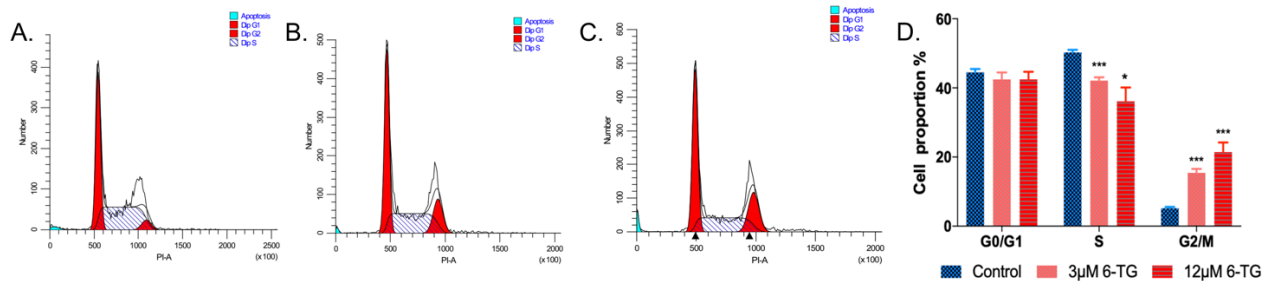
Supplementary Figure S1 KEGG pathway enrichment analysis on pathways in cancer. Red represented high expression. Green represented low expression.



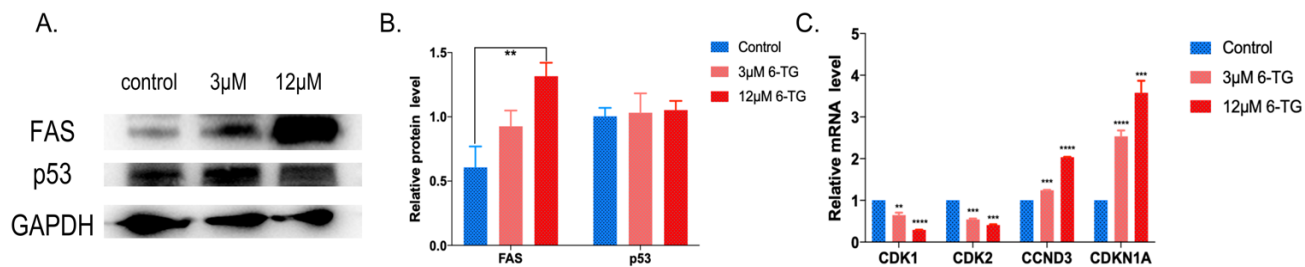
Supplementary Figure S2 KEGG pathway enrichment analysis between the p53 and cell cycle pathway. Pink represented high expression. Blue represented low expression.



Supplementary Figure S3 6-TG induced cell apoptosis in MCF-7 breast cancer cells. (A) control. (B) 3µM 6-TG. (C) 12µM 6-TG. (D) Quantitation of the percentage of MCF-7 cells in three groups. The data are presented as the mean ± SD of three replicates. **p value < 0.01 and ****p value < 0.0001 compared with the control column.



Supplementary Figure S4 6-TG induced cell cycle arrest in MCF-7 breast cancer cells. (A) control. (B) 3µM 6-TG. (C) 12µM 6-TG. (D) Quantitation of the percentage of MCF-7 cells in different cell cycle stages. The data are presented as the mean ± SD of three replicates. MCF-7 cells caused G2/M cell cycle arrest after 6-TG treatment. *p value < 0.05, ***p value < 0.001 compared with the control column.



Supplementary Figure S5 Western blotting and qPCR results. (A) The protein level of FAS and p53 relative to that of GAPDH. (B) The data of western blotting are presented as the mean ± SD of three replicates. **p value < 0.01 compared with the control column. (C) The mRNA expression levels of hub genes. Each data point represents the mean ± SD of three replicates. **p value < 0.01, ***p value < 0.001 and ****p value < 0.0001 compared with the control column.

Supplementary Table S1 The primers of hub genes.

Symbol	Sense Primer	Anti-sense Primer
CDK1	GAAGCTAGGGTAGTCTGGTCTTTC	ACACCTACAACCACCACTCTG
CDK2	CCCTTGTTTGTCCCTTCT	TCTCTCACCTGCCTCATA
CDKN1A	GATTAGCAGCGGAACAAG	GCCAGGAAAGACAACACTAC
CCND3	CTGATGGGACAGAATTGG	GGGACAACACCTTTAGAAG
DNMT1	GTGAGAGTGAGAGCAGTC	GAAGGGAATCTGGGTCAG
FAS	ACTCACCAGCAACACCAA	CTTCCTTTCTCTTCACCCAAAC
TP53	TCAGCATCTTATCCGAGTG	TACAGTCAGAGCCAACCT