Figure S1. Prognostic values of seven potential miRNAs in breast cancer analyzed using Kaplan-Meier plotter. (A) miR-369, (B) miR-318, (C) miR-410, (D) miR-432 and (E) miR-494, (F) miR-543 and (G) miR-655. miRNA/miR, microRNA; HR, hazard ratio.

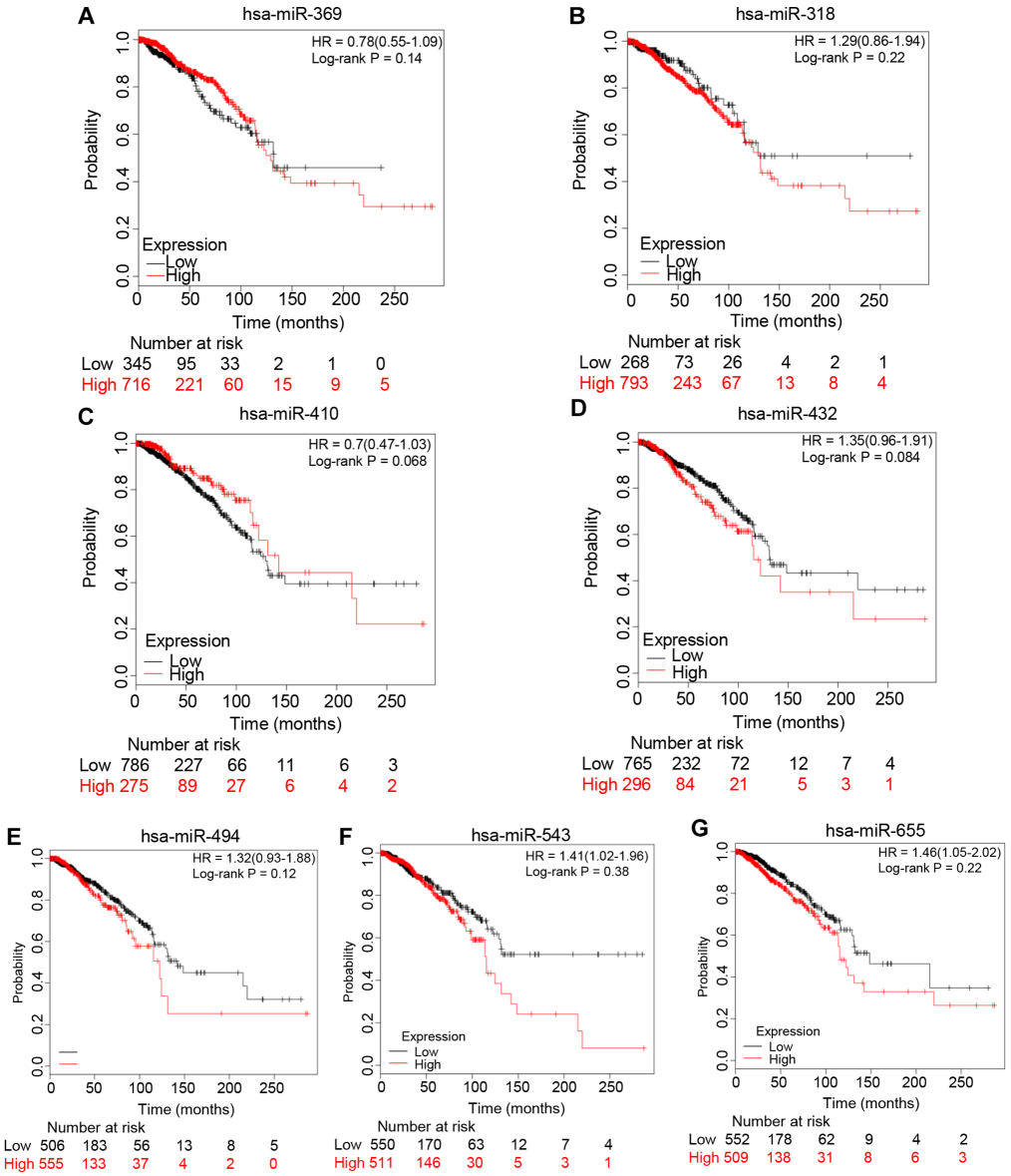

Figure S2. Correlation of NCAPG and CDC25C expression in breast cancer analyzed by (A) GEPIA (Pearson's correlation), (B) cBioPortal, (C) bc-GenExMiner and (D) UALCAN. GEPIA, Gene Expression Profiling Interactive Analysis; cBioPortal, cBio Cancer Genomics Portal; NCAPG, non-SMC condensin I complex subunit G; CDC25C, cell division cyclin 25 homolog C; Seq, sequencing; TPM, transcripts per million; BC, breast cancer; RSEM, align and estimate abundance.

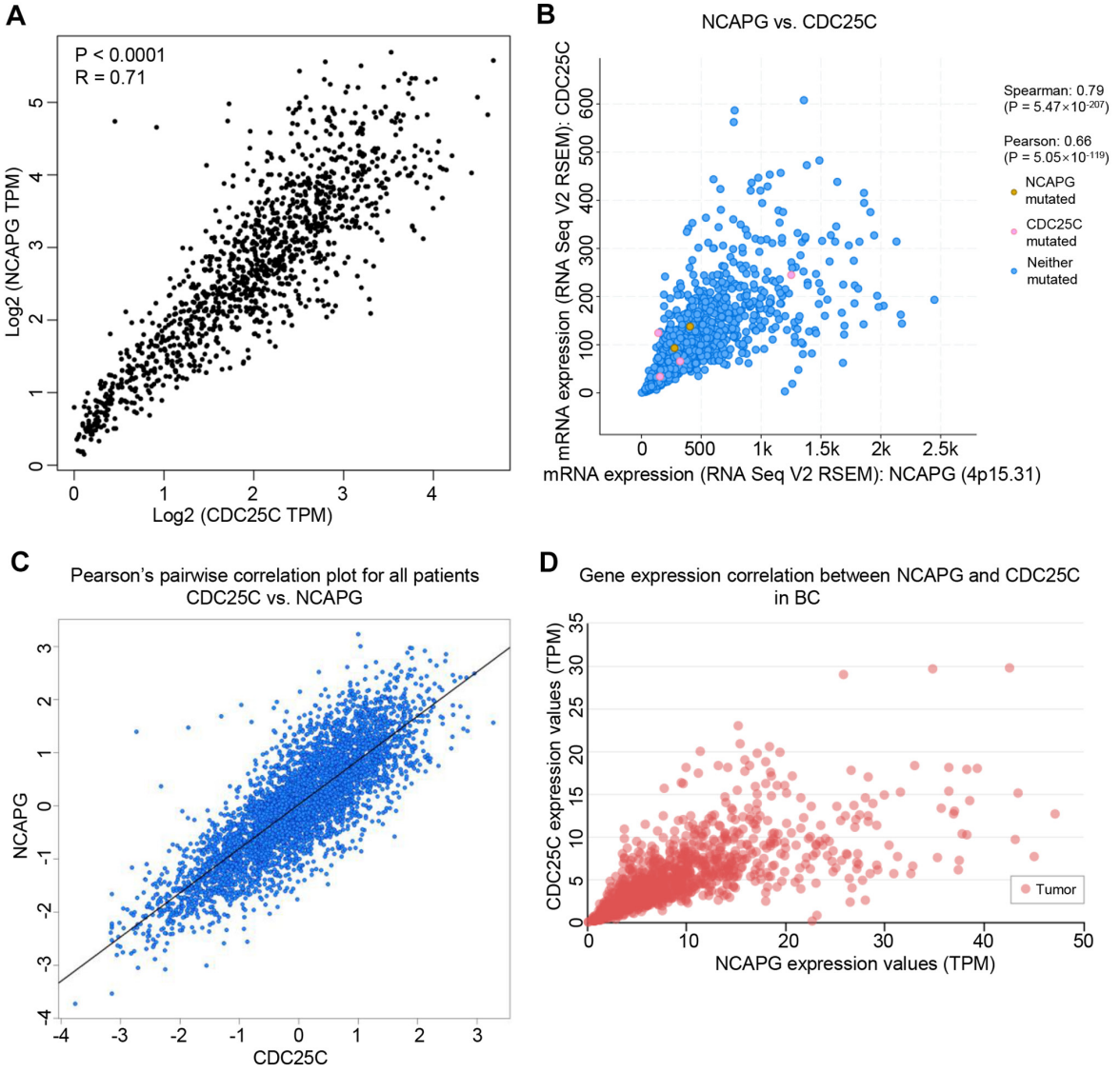

Table SI. Sequences of primers and siRNAs used in the present study.

Primers/siRNAs	Sequences
NCAPG forward	5'-GCCCCTGCATCTTCTCCTTT-3'
NCAPG reverse	5'-CAGCAGTCTGACACCTCCTG-3'
CDC25C forward	5'-GAACCCCAAAACGTTGCCTC-3'
CDC25C reverse	5'-CTGAGCTTTCCTTGGCCAGA-3'
GAPDH forward	5'-AATGGACAACTGGTCGTGGAC-3'
GAPDH reverse	5'-CCCTCCAGGGGATCTGTTTG-3'
siRNA-NC	5'-TTCTCCGAACGTGTCACGTdTdT-3'
siRNA-NCAPG1 sense	5'-GGAGUUCAUUCAUUACCUUTT-3'
siRNA-NCAPG1 antisense	5'-AAGGUAAUGAAUGAACUCCTT-3'
siRNA-NCAPG2 sense	5'-GCUGAAACAUUGCAGAAAUTT-3'
siRNA-NCAPG2 antisense	5'-AUUUCUGCAAUGUUUCAGCTT-3'

siRNA, small interfering RNA; NC, negative control; NCAPG, non-SMC condensin I complex subunit G; CDC25C, cell division cyclin 25 homolog C.

Table SII. Cell signaling pathways from NCI-Nature, KEGG and Panther databases.

A, KEGG

Term	P-value
Cell cycle	9.58×10^{-30}
DNA replication	4.17×10^{-16}
Mismatch repair	3.13×10^{-10}
Oocyte meiosis	9.90×10^{-10}
Cellular senescence	3.01×10^{-09}
Fanconi anemia pathway	3.05×10^{-08}
Human T-cell leukemia virus 1 infection	3.22×10^{-08}
Homologous recombination	4.97×10^{-08}
Progesterone-mediated oocyte maturation	6.93×10^{-08}
p53 signaling pathway	3.97×10^{-07}
One carbon pool by folate	1.16×10^{-04}
Small cell lung cancer	2.17×10^{-04}
Nucleotide excision repair	3.57×10^{-04}
Base excision repair	8.61×10^{-04}

B, NCI-Nature

Term	P-value
PLK1 signaling events	2.28×10^{-24}
ATR signaling pathway	2.02×10^{-22}
Aurora B signaling	2.02×10^{-22}
FOXM1 transcription factor network	1.99×10^{-20}
E2F transcription factor network	3.66×10^{-17}
Fanconi anemia pathway	6.46×10^{-16}
Aurora A signaling	1.45×10^{-10}
p73 transcription factor network	5.23×10^{-09}
BARD1 signaling events	7.08×10^{-08}
FoxO family signaling	3.54×10^{-05}
ATM pathway	7.30×10^{-05}
Regulation of retinoblastoma protein	1.82×10^{-04}
p53 pathway	8.62×10^{-04}
PLK3 signaling events	0.001640528

C, Panther

Term	P-value
DNA replication	2.55×10^{-09}
De novo purine biosynthesis	1.88×10^{-05}
Formyltetrahydroformate biosynthesis	2.13×10^{-05}
De novo pyrimidine deoxyribonucleotide biosynthesis	2.44×10^{-04}
Ubiquitin proteasome pathway	0.002312862
p53 pathway	0.002313549
FAS signaling pathway	0.007461145
Cell cycle	0.017916515
p53 pathway feedback loops 2	0.020628413

KEGG, Kyoto Encyclopedia of Genes and Genomes; NCI, National Cancer Institute.