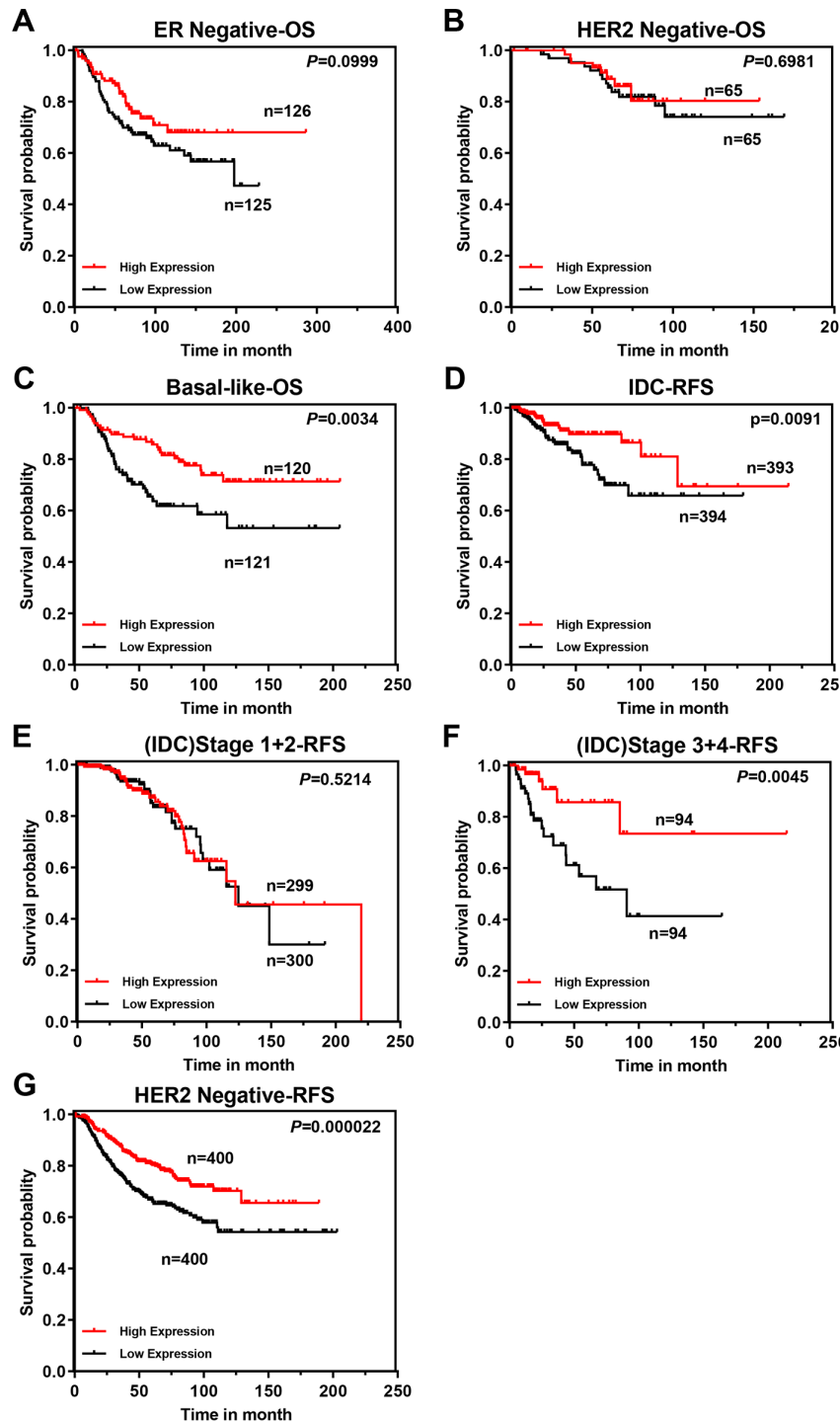**Figure S1** The expression of ZNF589 correlated with hormone receptor status and age. The expression of ZNF589 in BRCA tissue grouped by (A) ER status, (B) PR status, (C) HER2 status and (D) age. **, P<0.01; ****, P<0.0001. BRCA, breast cancer; ER, oestrogen receptor; PR, progesterone receptor; HER2, human epidermal growth factor receptor 2.

Figure S2 The expression of ZNF589 was important in OS for PR negative BRCA, but not in (A) ER and (B) HER2 negative status. ZNF589 expression may be a relapse-free prognostic factor for basal-like BRCA and IDC. (C) Low ZNF589 expression means poor OS in basal-like BC patients and the data was reached from KM plotter database. (D) Low ZNF589 expression means poor RFS in invasive ductal cancer patients. (E,F) They show that ZNF589 is not important in RFS of early-stage IDC but significant in terminal period. (G) The expression of ZNF589 was important in RFS for HER2 negative BC and the data was reached from K-M plotter database. IDC, invasive ductal carcinoma. OS, overall survival; PR, progesterone receptor; BRCA, breast cancer; ER, oestrogen receptor; HER2, human epidermal growth factor receptor 2; IDC, invasive ductal carcinoma; RFS, relapse-free survival; K-M, Kaplan-Meier.

Table S1 GSEA core enrichment genes in cell cycle

Gene name	Rank metric score	Running enrichment score
CCNE1	−0.288668424	0.002449723
PLK1	−0.286605865	−0.0186176
CCNB2	−0.273230791	−0.03811296
YWHAQ	−0.25690937	−0.056137748
YWHAG	−0.255838722	−0.07482749
CCNA2	−0.247039527	−0.091675065
MAD2L1	−0.246948376	−0.10978812
CDC20	−0.241275787	−0.12681669
CDC45	−0.240181714	−0.14436017
BUB1	−0.237607449	−0.16118655
HDAC2	−0.229461938	−0.17581557
PTTG1	−0.225459203	−0.19156203
TTK	−0.223908648	−0.20765188
YWHAH	−0.215837166	−0.22073759
PKMYT1	−0.213666379	−0.23563205
MCM6	−0.202016711	−0.24639909
CDK1	−0.199004576	−0.25949636
E2F4	−0.198980197	−0.2740875
CHEK1	−0.194735169	−0.2864722
CDK4	−0.192257181	−0.29888865
CCNB1	−0.183446452	−0.30754703
BUB1B	−0.181066513	−0.31918478
CDC25B	−0.175188035	−0.32800248
E2F1	−0.171499342	−0.33785892
CDC25C	−0.170346707	−0.34974745
DBF4	−0.166094989	−0.35748526
PCNA	−0.158068687	−0.3622168
ANAPC11	−0.154473722	−0.3695443
MCM5	−0.153699517	−0.37993956
YWHAZ	−0.150444567	−0.3877305
MCM2	−0.150441617	−0.39876118
CDKN2A	−0.149845734	−0.40920374
CDC6	−0.149303034	−0.4197006
RBX1	−0.146690831	−0.4277571
E2F3	−0.137344509	−0.42631385

Table S1 (*continued*)

Table S1 (*continued*)

Gene name	Rank metric score	Running enrichment score
TFDP1	–0.13522853	–0.43349355
ESPL1	–0.135166824	–0.44340858
CCND3	–0.133078381	–0.45028162
CHEK2	–0.13015227	–0.4557768
E2F2	–0.12944518	–0.46443778
CDC25A	–0.125626907	–0.46824583
CDK6	–0.123509049	–0.47363558
MCM3	–0.119423702	–0.47666547
CUL1	–0.117711961	–0.48169836
CDC7	–0.114194013	–0.4836173
SMC1B	–0.112961881	–0.49003044
MCM4	–0.11028304	–0.49243397
CCNE2	–0.109432951	–0.4991972
SFN	–0.107769698	–0.5039875
MCM7	–0.104619861	–0.50650024

GSEA, Gene Set Enrichment Analysis.