

Figure S1 Differential expression analysis of *C4BPA* in high/low expression groups. (A) Volcano map of differentially expressed genes, blue for down-regulated genes, red for up-regulated genes, logFC >1.5 and adj.P <0.05. (B) Heat map of co-expression differential genes of *C4BPA* presented after it was divided into high expression group and low expression group. TPM, transcripts per million.

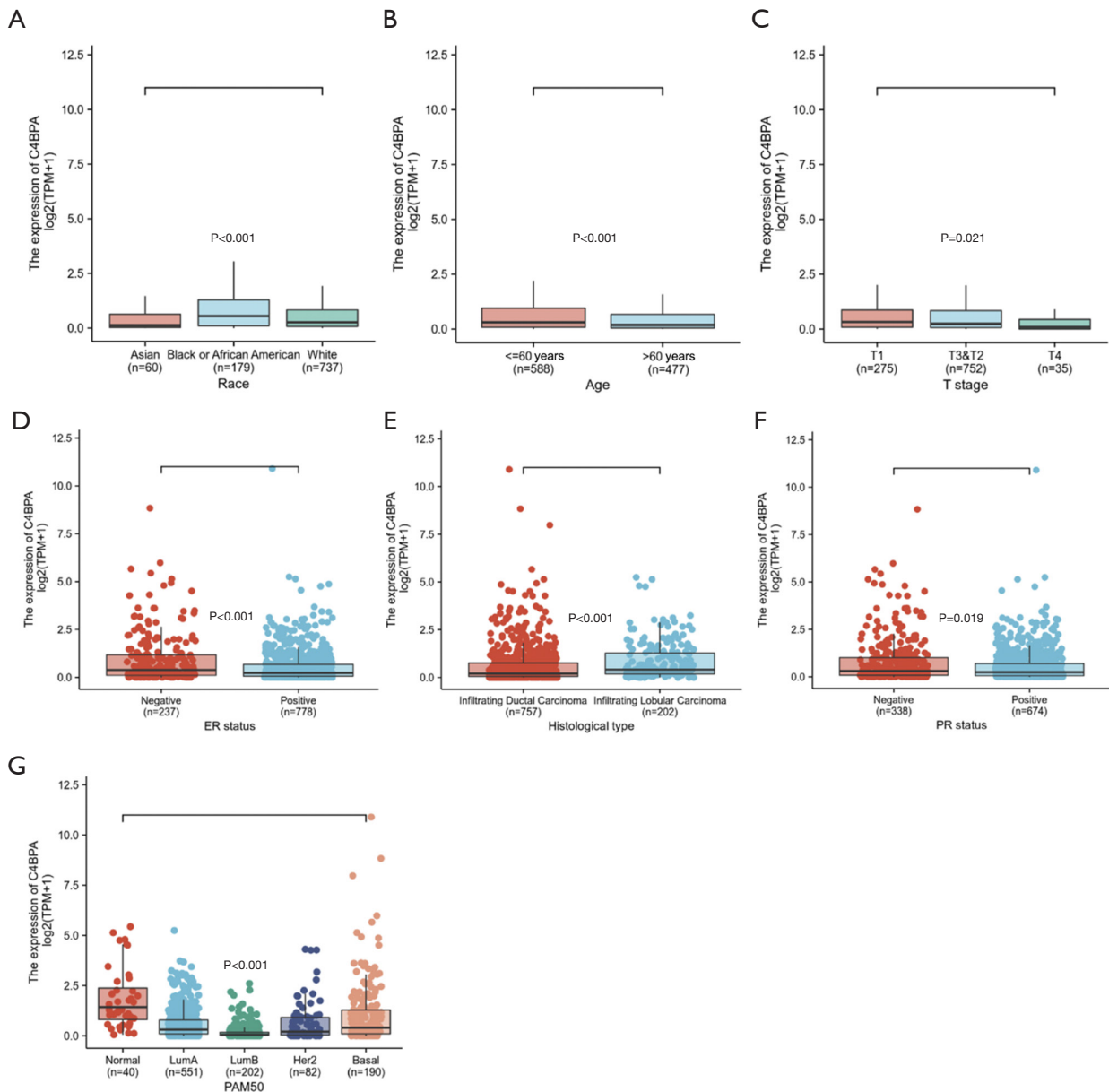


Figure S2 Association between *C4BPA* expression and clinicopathologic characteristics in BC. (A-G) Wilcoxon rank-sum test was used to compare the relationship between the expression of *C4BPA* and race, age, T stage, ER status, histological type, PR status, PAM50 of BC patients in the TCGA database. TPM, transcripts per million; ER, estrogen receptor; PR, progesterone receptor; BC, breast cancer; TCGA, The Cancer Genome Atlas.

Table S1 GO enrichment analysis of DEGs in the high/low expression group of C4BPA

Ontology	ID	Description	p.adjust	Count
BP	GO:0023061	Signal release	0.006031397	15
BP	GO:1903532	Positive regulation of secretion by cell	0.011635207	13
BP	GO:0051047	Positive regulation of secretion	0.019492866	13
CC	GO:0005771	Multivesicular body	0.017945116	5
CC	GO:0001533	Cornified envelope	0.028645845	5
CC	GO:0042599	Lamellar body	0.03093414	3
MF	GO:0048018	Receptor ligand activity	0.004458927	15
MF	GO:0017075	Syntaxin-1 binding	0.007947667	4
MF	GO:0005179	Hormone activity	0.007947667	7

GO, Gene Ontology; DEGs, differentially expressed genes; BP, biological process; CC, cellular component; MF, molecular function.

Table S2 KEGG function enrichment analysis of DEGs in the high/low expression group of C4BPA

ID	Description	p.adjust	Count
hsa00982	Drug metabolism—cytochrome P450	0.000765976	6
hsa00980	Metabolism of xenobiotics by cytochrome P450	0.000765976	6
hsa05204	Chemical carcinogenesis	0.000786773	6
hsa00830	Retinol metabolism	0.002539669	5
hsa04610	Complement and coagulation cascades	0.006262823	5
hsa04080	Neuroactive ligand-receptor interaction	0.009503852	9
hsa00053	Ascorbate and aldarate metabolism	0.012275253	3
hsa00040	Pentose and glucuronate interconversions	0.021214964	3
hsa00983	Drug metabolism—other enzymes	0.02506077	4
hsa00860	Porphyrin and chlorophyll metabolism	0.031280522	3
hsa04970	Salivary secretion	0.034252134	4
hsa00140	Steroid hormone biosynthesis	0.074324908	3
hsa04614	Renin-angiotensin system	0.085668442	2

KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes.

Table S3 GSEA enrichment analysis of DEGs in the high/low expression group of C4BPA

ID	NES	Adj.P	FDR
REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	-2.268	0.099	0.079
FARMER_BREAST_CANCER_CLUSTER_6	-2.265	0.099	0.079
FINETTI_BREAST_CANCER_KINOME_RED	-2.19	0.099	0.079
SMID_BREAST_CANCER_RELAPSE_IN_LIVER_DN	-2.178	0.09	0.072

GSEA, gene set enrichment analysis; DEGs, differentially expressed genes; NES, normalized enrichment score; adj.P, adjusted P value; FDR, false discovery rate.