

**Table S1. List of RT-PCR primers**

PCR Primer	Sequence (5'-3')	Product size(bp)
ZBTB28F	CTACGTCCGCGAGTTCACTC	170bp
ZBTB28R	CCCGGAAAATTGAATAGAAG	
VIMF	TGCCAACCTTACAGACCTA	390bp
VIMR	CTCATCTCCCTCCTCACTCA	
EcadF	CCTCCGTTCTGGAATCCAA	282bp
EcadR	GTTCTCTATCCAGAGGCTCT	
IFN $\alpha$ F	GCCTCGCCCTTGCTTTACT	89bp
IFN $\alpha$ R	CTGTGGGTCTCAGGGAGATCA	
IFN $\beta$ F	GCTTGGATT CCTACAAAGAAGCA	166bp
IFN $\beta$ R	ATAGATGGTCAATGCGGCGTC	
IFN $\gamma$ F	TCGGTAACTGACTTGAATGTCCA	93bp
IFN $\gamma$ R	TCGCTTCCCTGTTTAGCTGC	
IFNL1F	CACATTGGCAGGTTCAAATCTCT	386bp
IFNL1R	CCAGCGGACTCCTTTTGG	
IFNL3F	TAAGAGGGCCAAAGATGCCTT	205bp
IFNL3R	CTGGTCCAAGACATCCCCC	
SIRPaF	GCCCTCTACCTCGTCCGAAT	193bp
SIRPaR	CATACTCCGTGTGGTTGTTGG	
Siglec10F	AAGGGACTCATCTAACGGC	114bp
Siglec10R	CCGTCTCTCGGTAGAATCTTCA	
$\beta$ -actinF	TCCTGTGGCATCCACGAACT	315bp
$\beta$ -actinR	GAAGCATTGCGGTGGACGAT	

**Table S2. List of qRT-PCR Primers**

PCR Primer	Sequence (5'-3')	Product size (bp)	Annealing temperature (°C)	
qRT-PCR	iNOSF	CAGGATGACCTTCAGTATCACA	106bp	60
	iNOSR	CATCCAGCTTGACCAGAGAT		
	CD80F	AAACTCGCATCTACTGGCAA	87bp	60
	CD80R	GGTTCTTGTACTCGGCCATA		
	CD86F	CTGCTCATCTACACGGTTACC	133bp	60
	CD86R	GGAAACGTCGTACAGTTCTGT		
	CD40F	ACTGAAACGGAATGCCTTCCT	181bp	60
	CD40R	CCTCACTCGTACAGTGCCA		
	IL-1bF	ACAGTGGCAATGAGGATG	129bp	60
	IL-1bR	TGTAGTGGTGGTCGGAGA		
	ARG1F	GTGGAAACTTGCATGGACAAC	76bp	60
	ARG1R	AATCCTGGCACATCGGAAATC		
	MRC1F	TCCGGGTGCTGTTCTCCTA	211bp	60
	MRC1R	CCAGTCTGTTTGATGGCACT		
	IL-10F	GCCAAGCCTTGCTGAGATGA	80bp	60
	IL-10R	CTTGATGTCTGGTCTGGTTCT		
	IFNAR1F	ATTTACACCATTTCGCAAAGCTC	120bp	60
	IFNAR1R	TCCAAAGCCCACATAACACTATC		
	IFNAR2F	TCATGGTGTATATCAGCCTCGT	143bp	60
	IFNAR2R	AGTTGGTACAATGGAGTGGTTTT		
	IFNGR1F	AGCAGGAAGTCGATTATGATCCC	137bp	60
	IFNGR1R	CTGGCACTGAATCTCGTCACA		
	IFNGR2F	CTCCTCAGCACCCGAAGATT	136bp	60
	IFNGR2R	GCCGTGAACCATTACTGTGCG		
	IFIT1F	AGCCATTTCCTTGCTTCCC	205bp	60
	IFIT1R	ACAGAGCCTTCTTCGGTA		
	IFIT2F	AAGCACCTCAAAGGGCAAAAC	147bp	60
	IFIT2R	TCGGCCCCATGTGATAGTAGAC		
	IFIT3F	GGAAACTACGCCCTGGTC	180bp	60
	IFIT3R	CACCTCGCCCTTCATT		
	OAS1F	CTGACCTGGTTGTCTTCC	137bp	60
	OAS1R	GACCTCAAACCTCACCGA		
	OAS2F	TGAAGCCCTACGAAGAAT	176bp	60
	OAS2R	ACTGAAGAAGAGGGACAAGG		
	OAS3F	GAAGGAGTTCGTAGAGAAGGCG	114bp	60
	OAS3R	CCCTGACAGTTTCAGCACC		
	SAMD9LF	GCTAGAACGCTCTGAGAGCAGA	116bp	60
	SAMD9LR	TGCTGCAGTAGGAAGGCATA		
	XAF1F	GTTGGGTGTACGATGTGTCA	200bp	60

	XAF1R	ATGCGGTGCATGATGAAC TG		
	RARRES3F	ATGGCTACGTGATCCATCTG	151bp	60
	RARRES3R	AAGCTGTTGTTGACCCGATAG		
	ASCL1F	AACTTCAGCGGCTTGCGCTAC	302bp	60
	ASCL1R	ATGGAGTTCAAGTCGTTGGAG		
	CD24F	AAGTAACTCCTCCCAGAGTACT	120bp	60
qRT-PCR	CD24R	GAGAGAGTGAGACCACGAAG		
	CD47F	CCAGAGAAGG TGAAACGATC	122bp	60
	CD47R	AAACTGTCCCCAGAACAGGA		
	IFN $\beta$ F	ATGACCAACAAGTGTCTCCTCC	88bp	60
	IFN $\beta$ R	GGAATCCAAGCAAGTTTAGCTC		
	$\beta$ -actinF1	GTCTTCCCCTCCATCGTG	113bp	60
	$\beta$ -actinR1	AGGGTGAGGATGCCTCTCTT		

**Table S3. List of ChIP-PCR Primers**

Primer	Sequence (5'-3')	Product size (bp)	Annealing temperature (°C)
chip IFNAR1 F	AAAGTGGTGTCTGGTCCT	249bp	60
chip IFNAR1 R	AATCCTGGCCACACTTAGCT		
chip IFNAR2 F1	CAAAACTGCACTTGTACCCC	99bp	60
chip IFNAR2 R1	AAGTGATCTGAAGATGAAGGCA		
chip IFNAR2 F2	GCAGGAAGTCGCAAACTCAT	232bp	60
chip IFNAR2 R2	GAGGAAGAAAGCGTGTAGGAG		
chip IFNAR2 F3	CTCCTAACACGCTTCTTCCTC	131bp	60
chip IFNAR2 R3	GGAATGTCTCAGAGGCAATTG		
chip CD24 F1	GCCCGGTTCCCCCTTCCTCT	226bp	60
chip CD24 R1	TTTCCCGGGACCTGCCATCTTA		
chip CD24 F2	TAAGATGGCAGGTCCGGAAA	164bp	60
chip CD24 R2	TGCTGGTACCCGGCTGGTAT		
chip CD24 F3	ATACCAGCCGGTACCAAGCA	221bp	60
chip CD24 R3	AAAGCCACAATAGCCGTGACGT		
chip CD24 F4	ACGTCACGGCTATTGTGGCTT	161bp	60
chip CD24 R4	CACCATTGCTCTGCCATGT		
chip CD24 F5	ACATGGGCAGAGCAATGGTG	200bp	60
chip CD24 R5	AAGATTCTCTCCGGTCCCT		
chip CD47 F1	ATGCCTGTTGCGACAATGCTC	172bp	60
chip CD47 R1	TACTCGCTCTGCTCTCCCTAT		
chip CD47 F2	ATAGGGAAGAGCAGAGCGAGTA	185bp	60
chip CD47 R2	GACACCTAGGCTTCACCA		
chip CD47 F3	TGGTGAAGCCTAGGTGTC	150bp	60
chip CD47 R3	CCACTGTCTCTCTCTACTT		
chip CD47 F4	AAGTAGAGAGAGAGGACAGTGG	177bp	60
chip CD47 R4	TTCCAGGTACGTCTGT		
chip CD47 F5	ACAGGACGTGACCTGGAA	257bp	60
chip CD47 R5	TCACAGGCAGGACCCACT		
chip CD47 F6	AGTGGGTCTGCCTGTGA	178bp	60
chip CD47 R6	TTCTCTCCCTCTTCACCG		

**Table S4.** *ZBTB28* methylation and clinicopathological features of breast tumors

Clinicopathological features	Number (n=174)	Methylated status		<i>p</i> value
		methylated	unmethylated	
<b>Age</b>				
<45	57	36	21	<b>0.032</b>
≥45	116	91	25	
Unknown	1	1		
<b>Tumor size</b>				
≤5.0 cm	142	108	34	0.125
>5.0 cm	17	10	7	
Unknown	15	10	5	
<b>Stage (AJCC)</b>				
I-II	112	84	28	0.840
III-IV	51	39	12	
Unknown	11	5	6	
<b>Lymph node metastasis</b>				
Positive	84	58	26	0.205
Negative	81	63	18	
Unknown	9	7	2	
<b>Distant metastasis</b>				
Positive	4	3	1	0.670
Negative	125	90	35	
Unknown	45	35	10	
<b>ER</b>				
Positive	87	59	28	0.162
Negative	72	56	16	
Unknown	15	13	2	
<b>PR</b>				
Positive	70	47	23	0.263
Negative	85	64	21	
Unknown	19	17	2	
<b>HER2</b>				
Positive	115	83	32	0.956
Negative	46	33	13	
Unknown	13	12	1	
<b>P53</b>				
Positive	80	58	22	0.908
Negative	67	48	19	
Unknown	27	22	5	
<b>Ki-67</b>				
Positive	135	100	35	0.883
Negative	9	7	2	
Unknown	30	21	9	

**Figure S1.**

(A, B) Down-regulated *ZBTB28* mRNA expression and methylation of *ZBTB28* promoter were accessed via The Cancer Genome Atlas and MethHC databases. (C) Multiple targeted bisulfite enrichment sequencing (MethTarget) of 5 BrCa cases and 9 controls. (D) Cells were exposed to demethylating agent 5-Aza. *ZBTB28* expression was detected with qRT-PCR and demethylation was measured by qMSP. (E) The relationship between *ZBTB28* methylation and survival of breast cancer patients were illustrated through Survivalmeth database.

**Figure S2.**

(A) For colony formation assay, pictures were taken on the 14th day. (B) Representative pictures of AO/EB staining assay. (C) Flow cytometry analysis of cell cycle. (D) The localization of ZBTB28 and E-cad or Vimentin in the nucleus of MB231 was analyzed by immunofluorescence. (E) Phase contrast microscopy obtained the changes of morphological for gain-of-function breast cancer cell lines. (F) Pictures were taken at 24h after seeding during transwell assay. (G) Photographs were captured at 0 h and 24 h, then the ratio of wound healing was calculated.

\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .

**Figure S3.**

(A) 48 hours after transfection with siZBTB28 or control siRNA, the expression of ZBTB28 were evaluated by RT-PCR.  $\beta$ -actin was used as control. (B) BT549 cells were transfected with siZBTB28 and control siRNA. Cell viability was assessed by CCK8 assay. (C, D) Pictures were taken at 48 h after transfecting, the relative ratio of

migration and invasion cells per field was shown.

\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .

**Figure S4.**

(A) RT-PCR results of the regulation of IFNs by ZBTB28. (B) qRT-PCR confirmed that ZBTB28 upregulated IFN- $\gamma$ . (C) Ectopic expression of ZBTB28 in breast cancer cells influenced the expression of IFNGR1 and IFNGR2. (D) Cancer cells were pretreatment with/without anti-IFNGR2 mAb for 8 hours, then co-culture with THP-1 macrophages for another 24 hours. Protein levels of IFNGR2 and IFN- $\gamma$  were measured by western blotting;  $\beta$ -actin was used as a loading control.

**Figure S5.**

(A) Association of *ZBTB28* and *BCL6* expression in breast cancer which was obtained from TCGA cancer dataset ([www.cbioportal.org](http://www.cbioportal.org)). (B, C) qRT-PCR of CD24 or CD47 mRNA in MCF7 and MB231 underwent with pcDNA 3.1, pcDNA-ZBTB28, siRNA of BCL6, and pcDNA-ZBTB28 with or without siRNA of BCL6. (D) The expression of CD24 and CD47 was detected by qRT-PCR in BCL6-overexpression, ZBTB28-overexpression, BCL6+ZBTB28 overexpression and control group in K562 cells. (E) The expression of SIRP $\alpha$  and Siglec10 were detected by RT-PCR in THP-1 cells and PMA treated THP-1 macrophages.

**(B) Figure S6.**

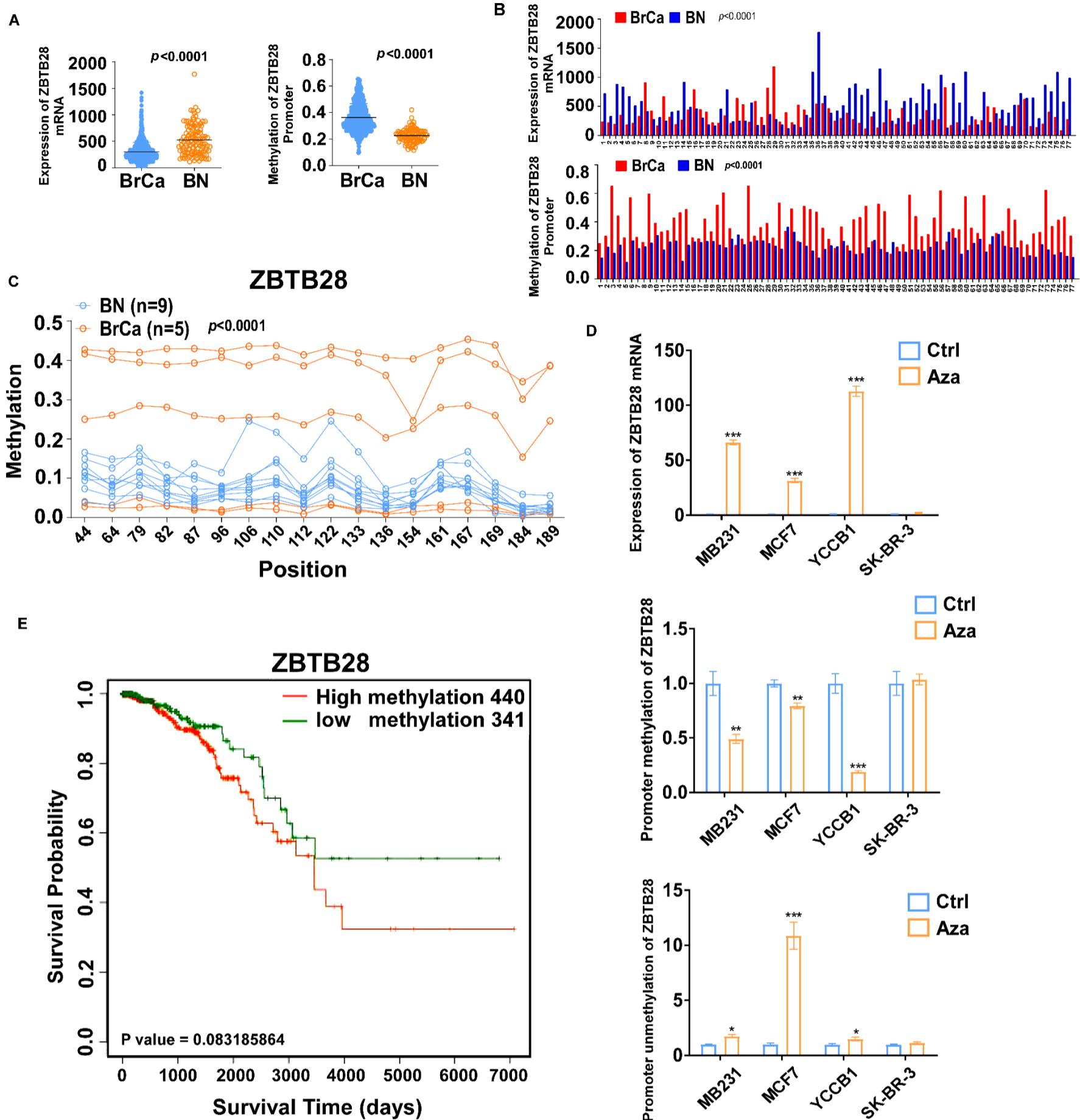
(A) Representative flow-cytometry plots of the phagocytosis of MCF7 cells treated with different treatment. (B) Phagocytosis efficiency was shown as a bar graph. (C) Phagocytosis images of THP-1 macrophages engulfing MCF7 cells. The white arrows

indicate macrophages that engulfed cancer cells.

**Figure S7.**

(A, B) Representative plots showed the percentage of THP-1 macrophages phagocytosing cancer cells in vitro. (C) Statistical analysis was shown as a bar graph.

**Figure S1.**



**Figure S2.**

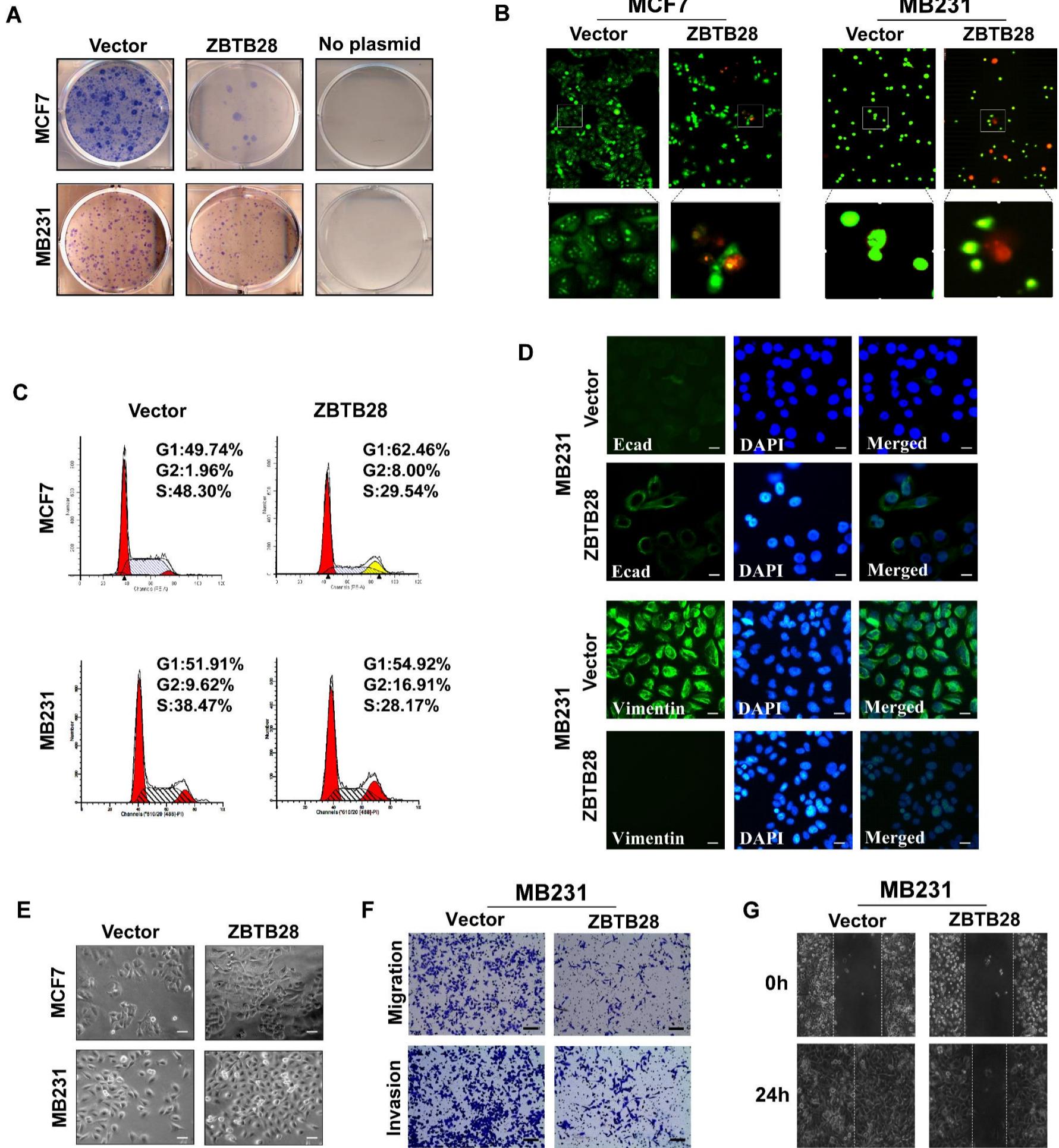


Figure S3.

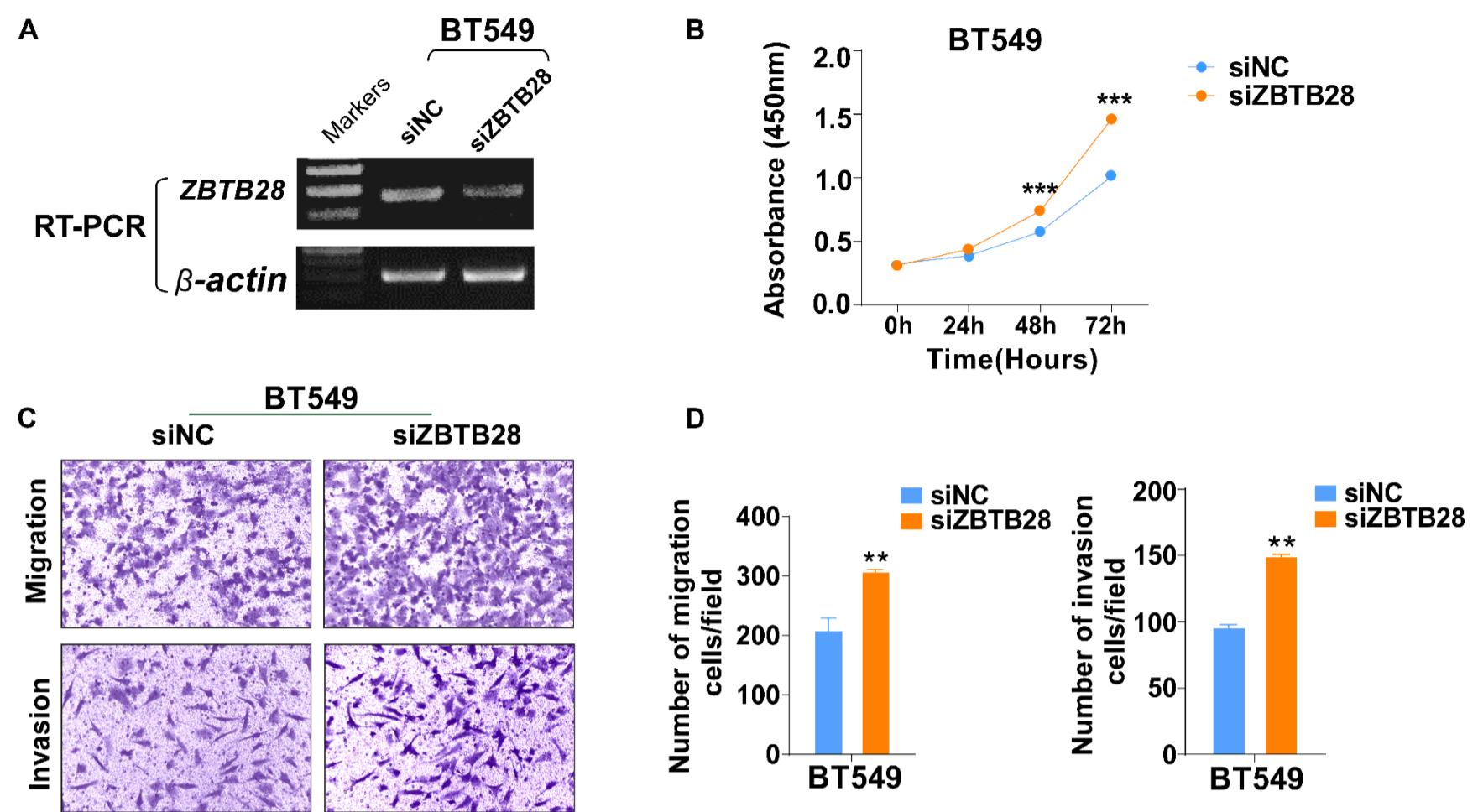
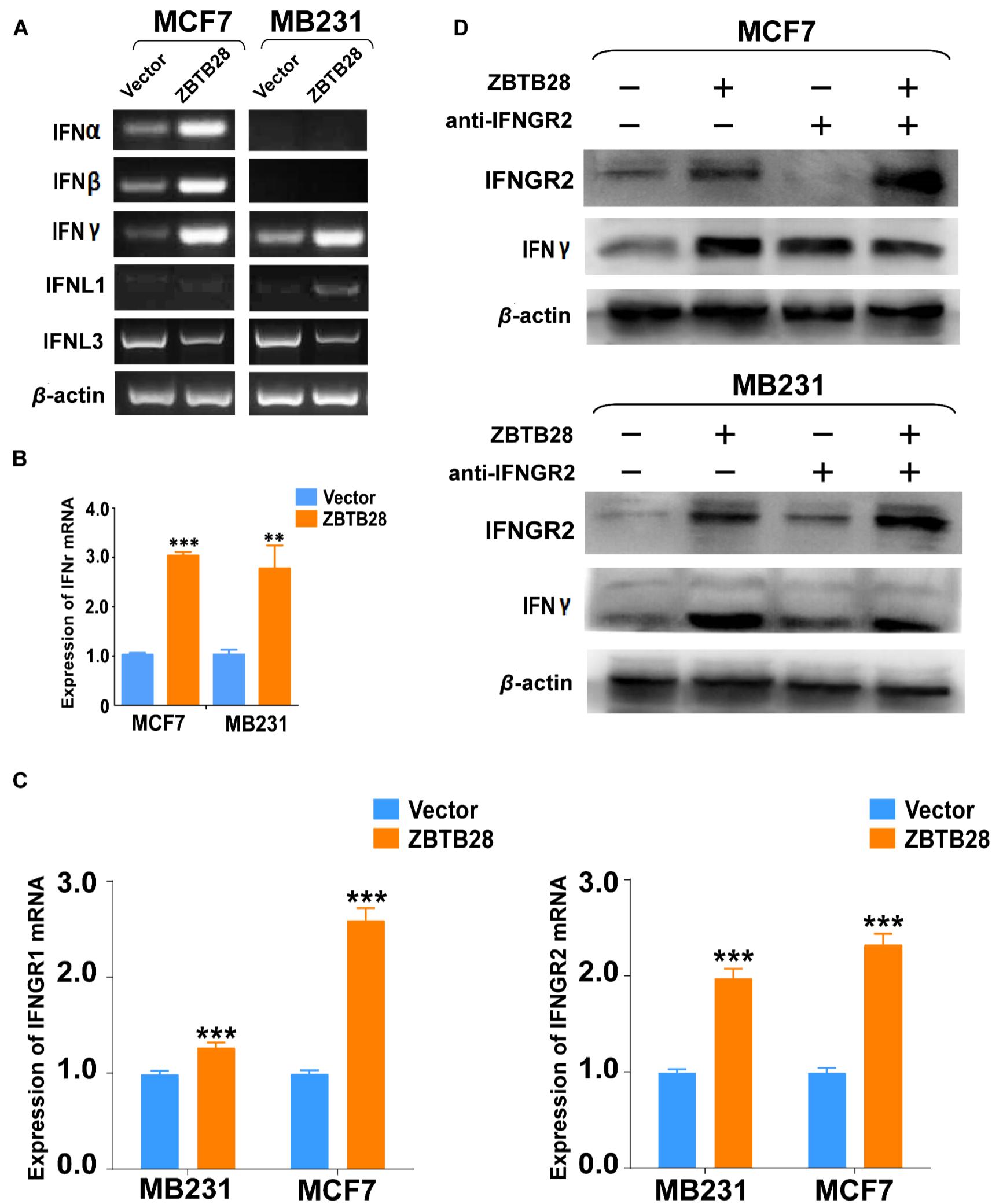
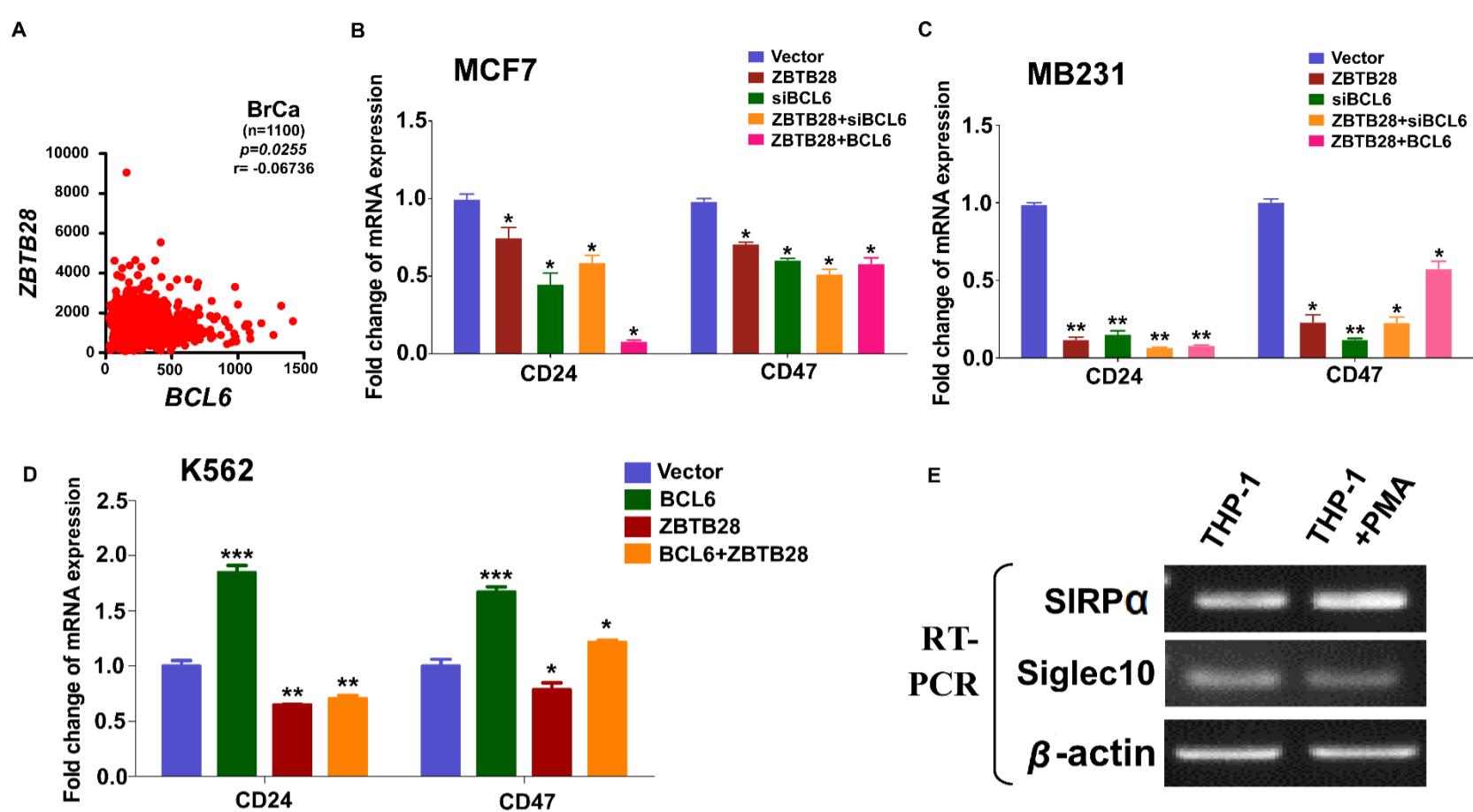


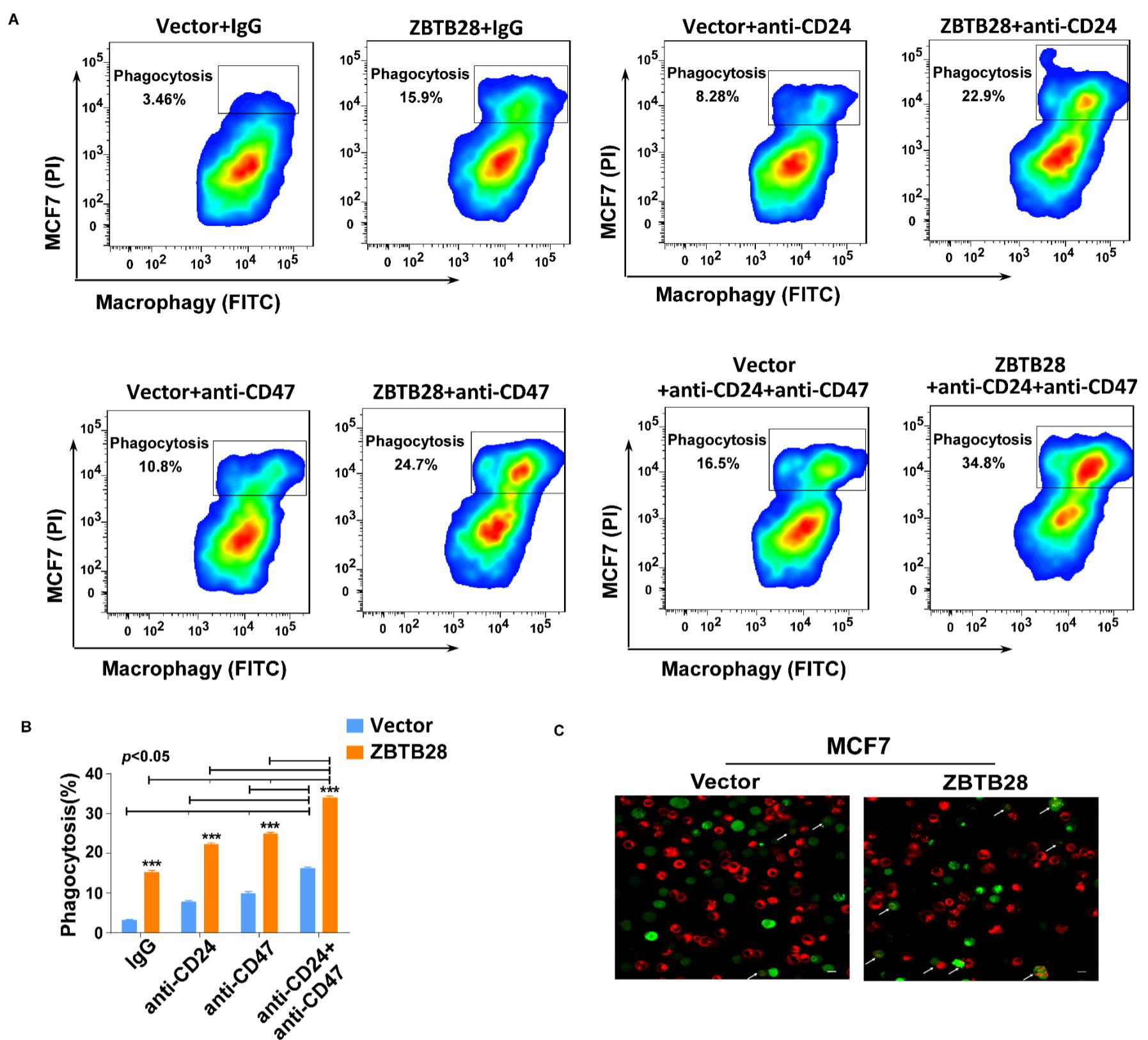
Figure S4.



**Figure S5.**

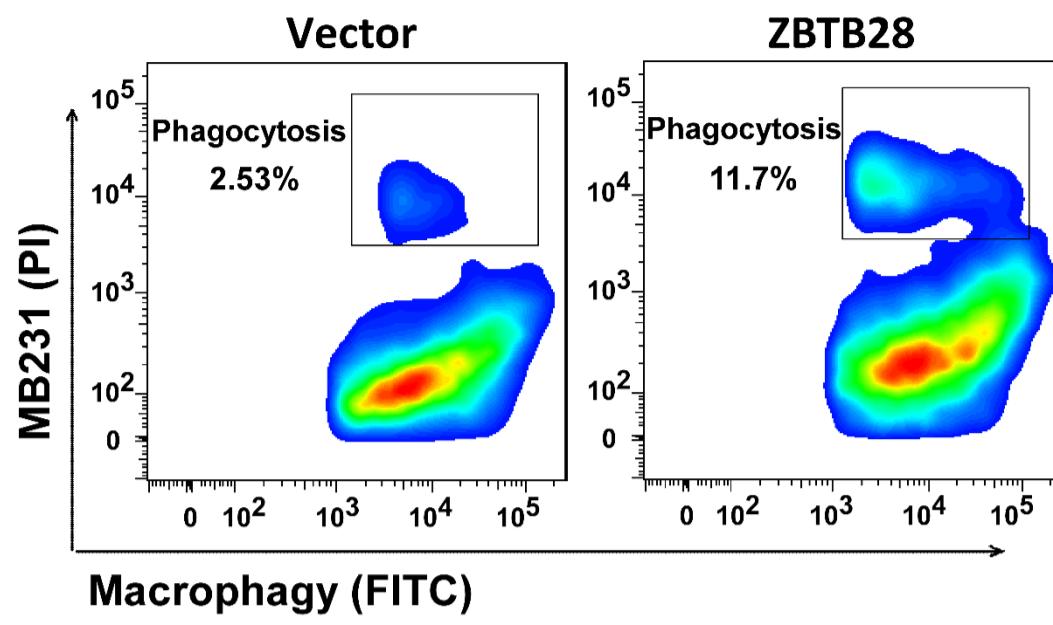


**Figure S6.**

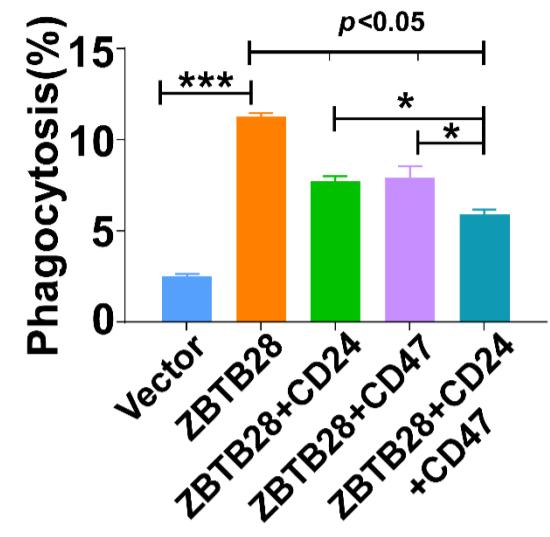


**Figure S7.**

**A**



**C**



**B**

