

Figure S1 Study scheme. TNBC, triple-negative breast cancer; PBC, primary breast cancer; MBC, metastasis breast cancer; TCGA, The Cancer Genome Atlas.

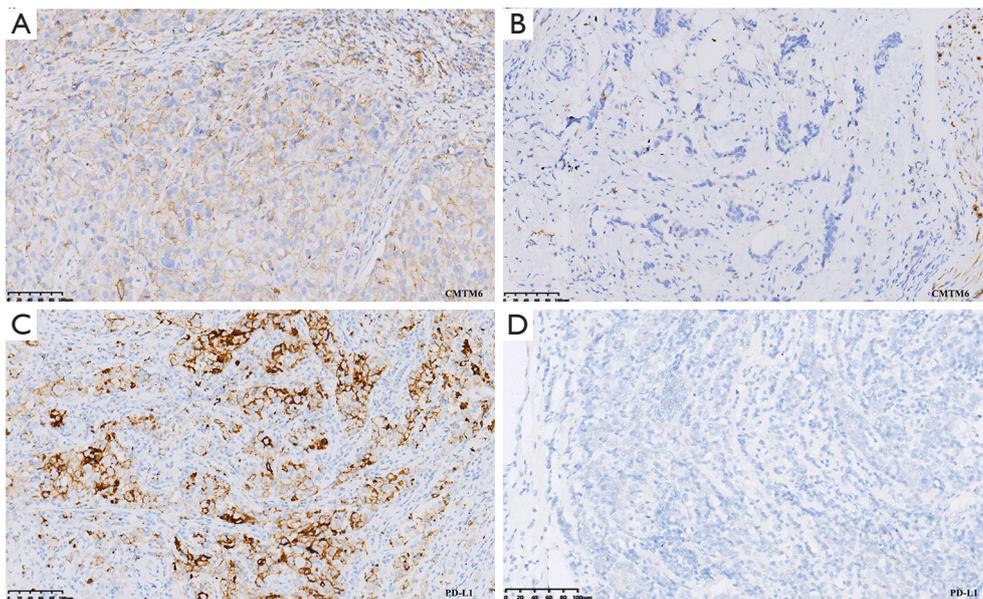


Figure S2 CMTM6 and PD-L1 protein expression in breast cancer using IHC staining. (A) and (C) are positive staining for CMTM6 and PD-L1, respectively. (B) and (D) are negative staining for CMTM6 and PD-L1, respectively.

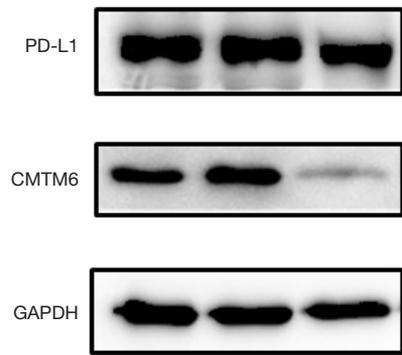


Figure S3 Western blot was used to confirm the detection of IHC.

Table S1 The mRNA expression level of CMTM6 and PD-L1 in HER2-driven PBC and triple-negative PBC

Variable	N	Median (P25–P75)	P
CMTM6			
Her2-driven	30	0.026 (0.0062–0.042)	0.036
Triple negative	30	0.037 (0.021–0.059)	
PD-L1			
Her2-driven	30	0.00012 (0.00005–0.0026)	0.040
Triple negative	30	0.00026 (0.00015–0.00043)	

P values are determined based on Mann-Whitney.

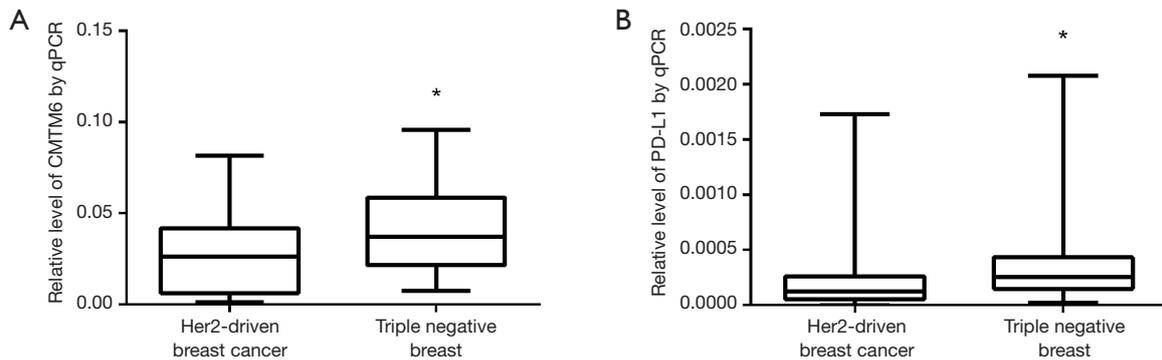


Figure S4 CMTM6 (A) and PD-L1 (B) mRNA expression levels of HER2-driven breast cancer and triple-negative breast cancer. P values are determined based on the Mann-Whitney test. *, $P < 0.05$.

Table S2 CMTM6 and PD-L1 mRNA expression in HER2-driven breast cancer and triple-negative breast cancer expression using TCGA dataset

Variable	N	Mean \pm SD	P
CMTM6			
Her2-driven	30	11.23 \pm 0.626	0.039
Triple negative	123	11.51 \pm 0.728	
PD-L1			
Her2-driven	30	4.7 \pm 1.803	0.283
Triple negative	123	5.05 \pm 1.536	

CMTM6 and PD-L1 mRNA expression levels of HER2-driven PBC and triple-negative PBC in The Cancer Genome Atlas (TCGA) dataset (see URLs <http://cancergenome.nih.gov/>). P values are determined based on Student's *t* test.