

**Table S1** The list of culture mediums for different breast cancer cell lines

Names of cell lines	Culture medium
MCF-7	DMED medium supplemented with 10% FBS and insulin (0.023U/ml)
ZR-75-1	RPMI-1640 medium supplemented with 10% FBS
BT-474	RPMI-1640 medium supplemented with 10% FBS
SK-BR-3	DMEM medium supplemented with 10% FBS
MDA-MB-453	L-15 medium supplemented with 10% FBS
MDA-MB-231	L-15 medium supplemented with 10% FBS
BT-549	RPMI-1640 medium supplemented with 10% FBS and insulin (0.023U/ml)
Hs-578T	DMEM medium supplemented with 10% FBS
HCC-1806	RPMI-1640 medium supplemented with 10% FBS
HCC-1937	RPMI-1640 medium supplemented with 10% FBS

**Table S2** Functional Category of the common co-expressed immune-related genes of TMED2/3/4/9

Gene Symbol	Category
<i>RFX5</i>	Antigen_Processing_and_Presentation
<i>SEMA4D</i>	Chemokines
<i>CCR9</i>	Chemokine_Receptors
<i>PTGFR</i>	Cytokine_Receptors
<i>TNFAIP3</i>	Antimicrobials
<i>CCR6</i>	Antimicrobials
<i>TXK</i>	Antimicrobials
<i>TSLP</i>	Cytokines
<i>TCF7L2</i>	Antimicrobials
<i>TSHR</i>	Cytokine_Receptors
<i>BACH2</i>	Antimicrobials

**Table 3** Expression of the common TMED2/3/4/9 co-expressed immune-related genes analyzed by Oncomine and UALCAN database

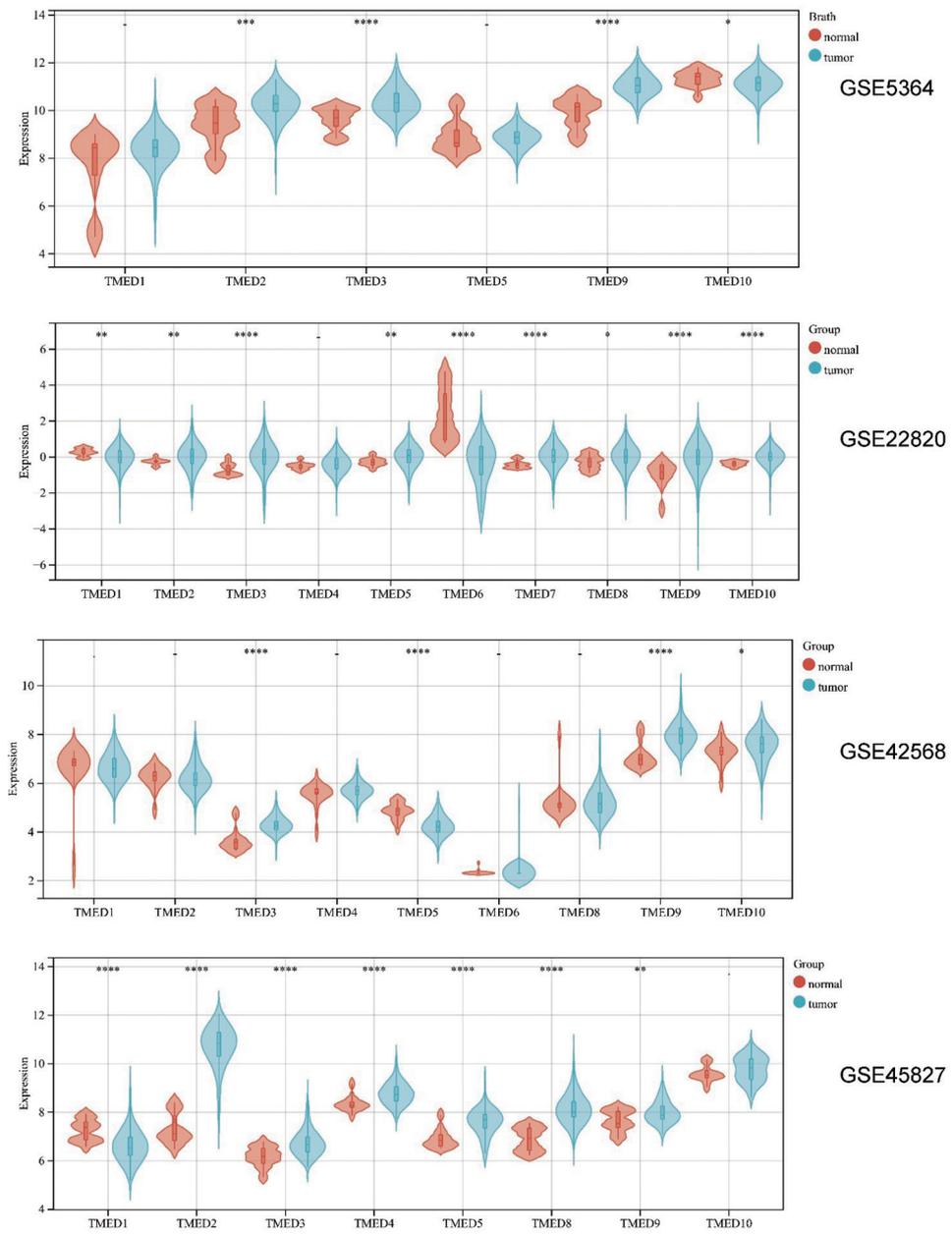
	Gene Symbol										
	RFX5	SEMA4D	CCR9	PTGFR	TNFAIP3	CCR6	TXK	TSLP	TCF7L2	TSHR	BACH2
Oncomine	High	High	NS	Low	High	Low	Low	Low	Low	High	Low
Ualcan	High	High	Low	Low	Low	Low	NS	Low	Low	Low	Low

The highly expressed genes in breast cancer were excluded for their negative correlations with TMED2/3/4/9.

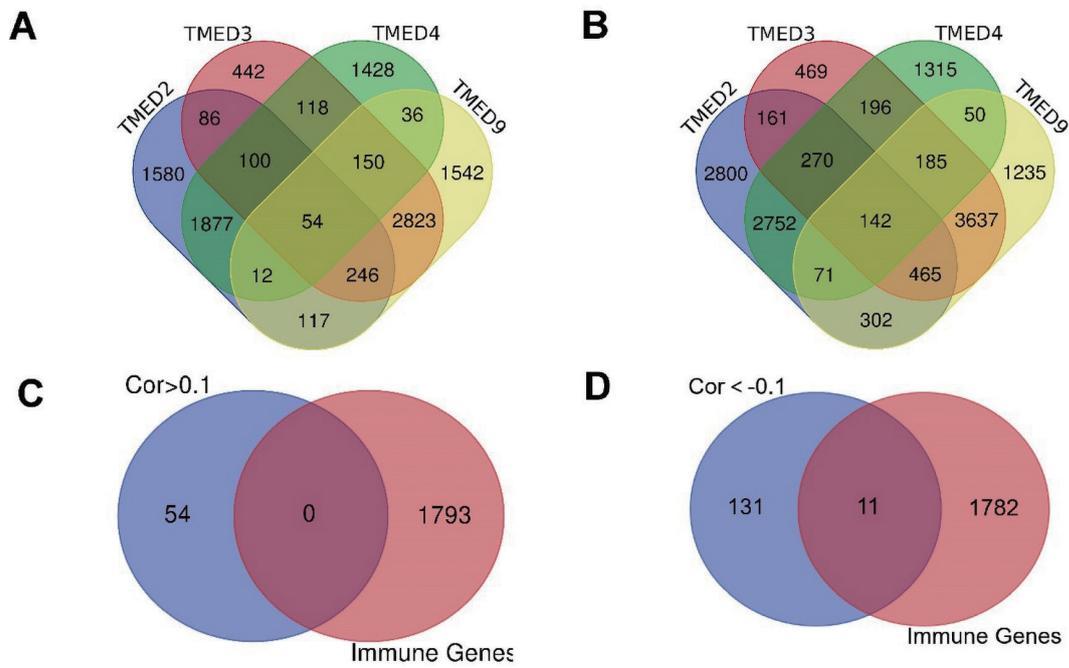
**Table 4** Further screening of the common TMED2/3/4/9 co-expressed immune-related genes based on their survival data in breast cancer analyzed by the KM-plotter database

	Gene Symbol						
	CCR9	PTGFR	CCR6	TXK	TSLP	TCF7L2	BACH2
RFS	NS	NS	Favorable	Favorable	Favorable	NS	Favorable
OS	NS	Favorable	Favorable	NS	NS	NS	Favorable
DMFS	NS	NS	Favorable	NS	NS	NS	NS

NS: statistically insignificant. CCR9 and TCF7L2 were excluded for their insignificant value for predicting the patient outcomes in breast cancer.

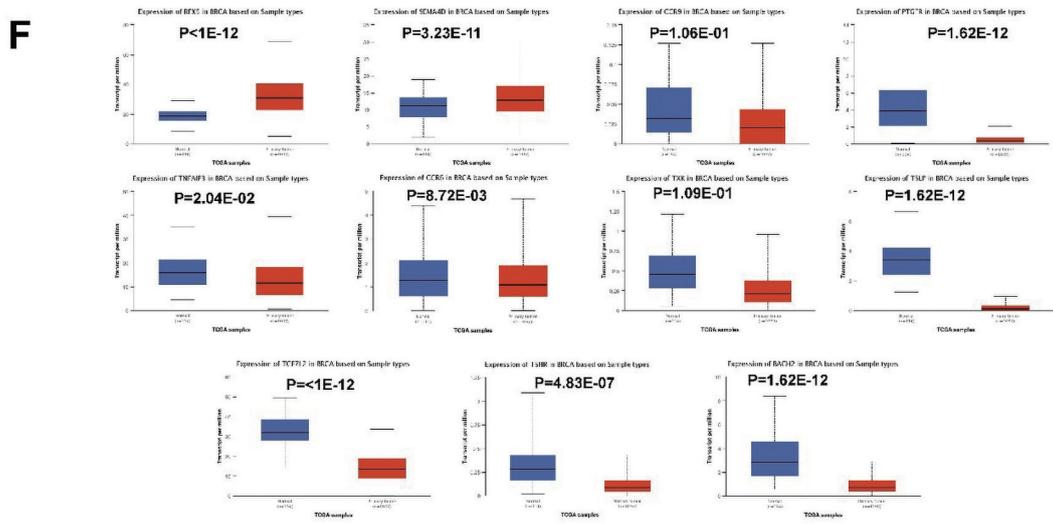


**Figure S1** Expressions of TMED family in GEO microarray datasets GSE5364, GSE22820, GSE42568, GSE45827. \*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001, \*\*\*\*, P<0.0001.



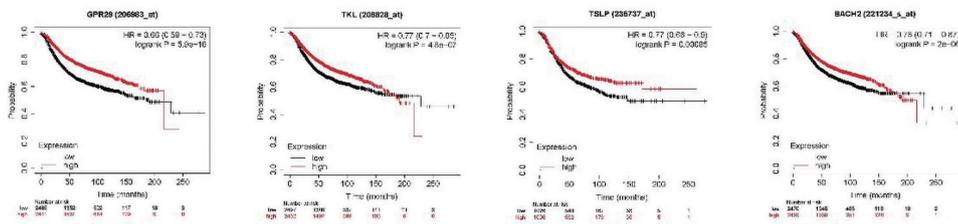
**E**

	RFX5	SEMA4D	CCR9	PTGFR	TNFAIP3	CCR6	TXK	TSLP	TCF7L2	TSHR	BACH2
Analysis Type by Cancer	Cancer vs. Normal										
Bladder Cancer	2	1	1	2	2	2			2		
Brain and CNS Cancer	2	1	10	2	3		5	1	8	2	3
Breast Cancer	20	11	1	2	3	1	2	11	4	24	1
Cervical Cancer	5		1	1	1	1			2		
Colorectal Cancer	2	2		1	1	1	1				3
Esophageal Cancer	1	1			4				6	10	
Gastric Cancer	1	1	4		1		2				1
Head and Neck Cancer	3	5			9	1	1		2	3	1
Kidney Cancer		1	3	3	1	6	1		2	1	2
Leukemia	9	1	3	2	1	3	4	3	1	6	7
Liver Cancer	6	2			1	1	1		1	6	7
Lung Cancer	1	3			2	3			1	11	
Lymphoma	6	1			2	5	8	5	4	5	1
Melanoma	1				1	1	1		1	4	
Myeloma	2		1								1
Other Cancer		4			1		1		1	8	2
Ovarian Cancer					1	1	1		1	1	2
Pancreatic Cancer	1	1	1	1	1	2	2		5	3	1
Prostate Cancer	3	2	1			1	1		3	3	1
Sarcoma	8				4				2	3	4
Significant Unique Analyses	69	5	31	37	4	9	8	31	51	25	10
Total Unique Analyses	320		370		295		307		396		342
									356		4
									11		1
									23		1
									45	77	8
									19		17
									45	77	17
									23		45
									176		356
									356		337
									176		289

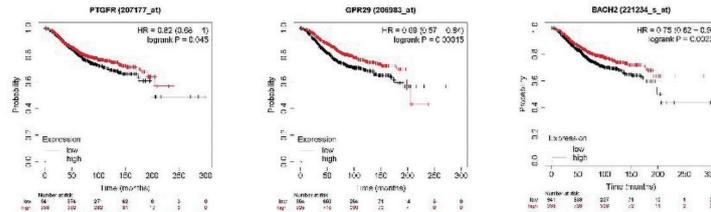


**Figure S2** The identification process of TMED2/3/4/9 immune related co-expressed genes (A,B) The intersections of TMED2/3/4/9 co-expressed genes generated by the “Co-Expression” module of “cBioPortal”. The common co-expressed genes of TMED2/3/4/9 (54 positively correlated and 142 negatively correlated) were obtained by Venn diagram (q value < 0.05). (C,D) The intersection between the common co-expressed genes of TMED2/3/4/9 and immune related genes from ImmPort generated by Venn diagram. RFX5, SEMA4D, CCR9, PTGFR, TNFAIP3, CCR6, TXK, TSLP, TCF7L2, TSHR and BACH2 were identified as the eleven common co-expressed immune-related genes of TMED2/3/4/9 (Negatively correlated, Rho < -0.1), and further screened according to their expressions in breast cancer and impacts on patient survival. (E) The expressions of RFX5, SEMA4D, CCR9, PTGFR, TNFAIP3, CCR6, TXK, TSLP, TCF7L2, TSHR and BACH2 in breast cancer and normal tissues analyzed by OncoPrint database. (F) The transcriptional data of RFX5, SEMA4D, CCR9, PTGFR, TNFAIP3, CCR6, TXK, TSLP, TCF7L2, TSHR and BACH2 in breast cancer and normal tissues analyzed by UALCAN database.

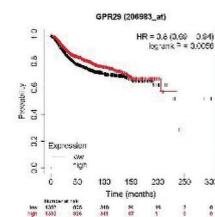
**A RFS**



**OS**

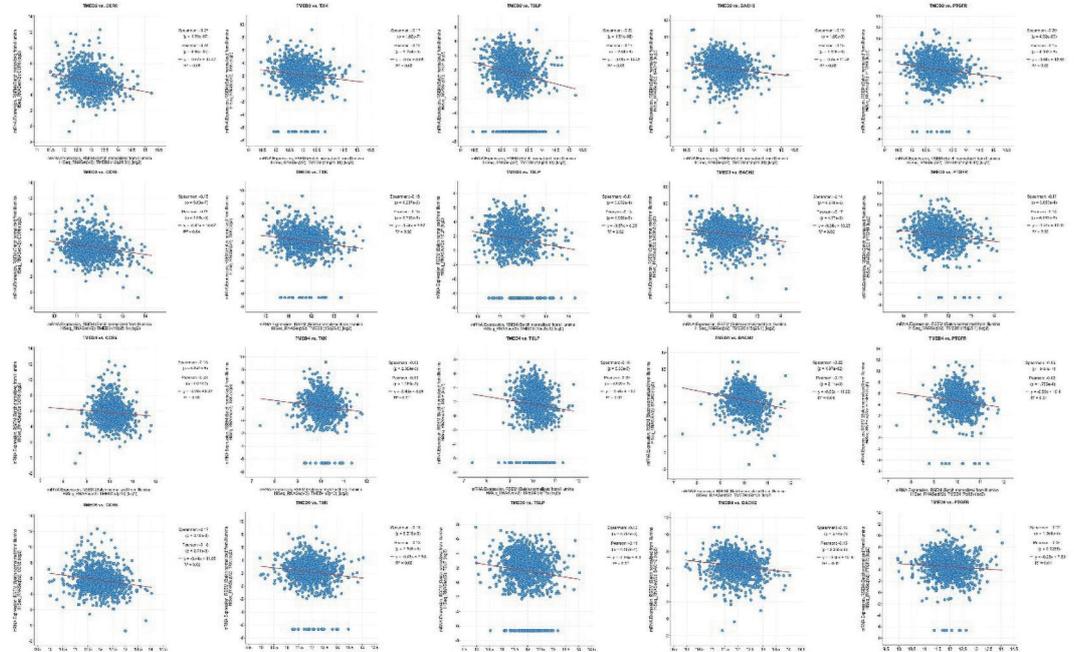


**DMFS**

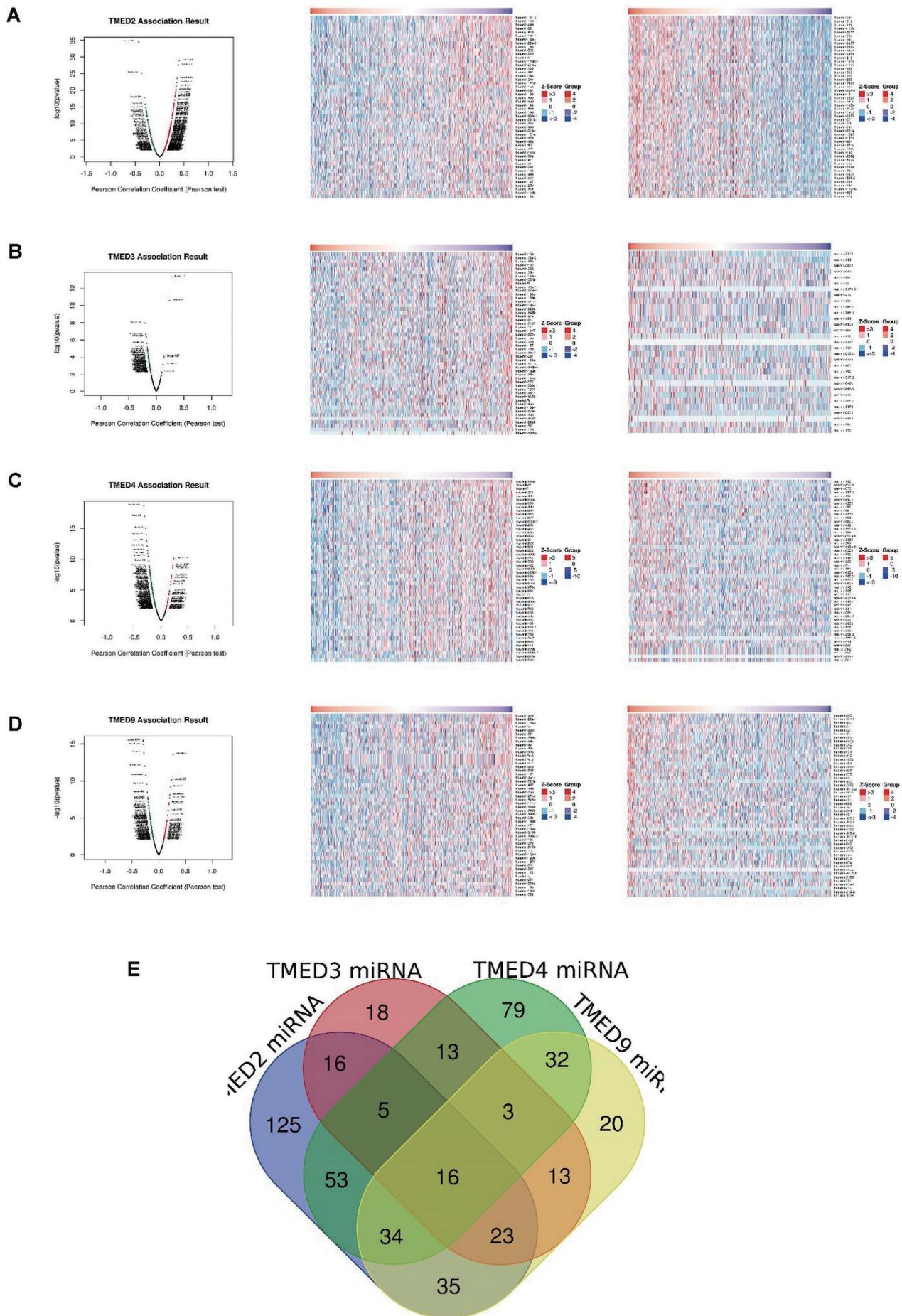


**B TMED2**

**CCR6 TXK TSLP BACH2 PTGFR**



**Figure S3** The prognostic value of filtered TMED2/3/4/9 immune related co-expressed genes and their correlations with TMED2/3/4/9 (A) The significant survival data of CCR6(GPR29), TXK, TSLP, BACH2, and PTGFR in breast cancer analyzed by the KM-plotter database. (B) The correlations between TMED2/3/4/9 and their common co-expressed immune-related genes. TMED2/3/4/9 was inversely correlated to the screened common immune related genes which had been screen by the combined analysis of Omcomine, Ualcan and KM-plotter.



**Figure S4** The correlated microRNAs of TMED2/3/4/9 in breast cancer from LinkedOmics database and their common associated microRNAs generated by Venn diagram. (A) Volcano plot of TMED2 associated microRNAs and the heatmaps for the negatively correlated significant microRNAs and positively correlated significant microRNAs. (B) Volcano plot of TMED3 associated microRNAs and the heatmaps for the negatively correlated significant microRNAs and positively correlated significant microRNAs. (C) Volcano plot of TMED4 associated microRNAs and the heatmaps for the negatively correlated significant microRNAs and positively correlated significant microRNAs. (D) Volcano plot of TMED9 associated microRNAs and the heatmaps for the negatively correlated significant microRNAs and positively correlated significant microRNAs. (E) The overlap of TMED2/3/4/9 associated microRNAs from LinkedOmics database.