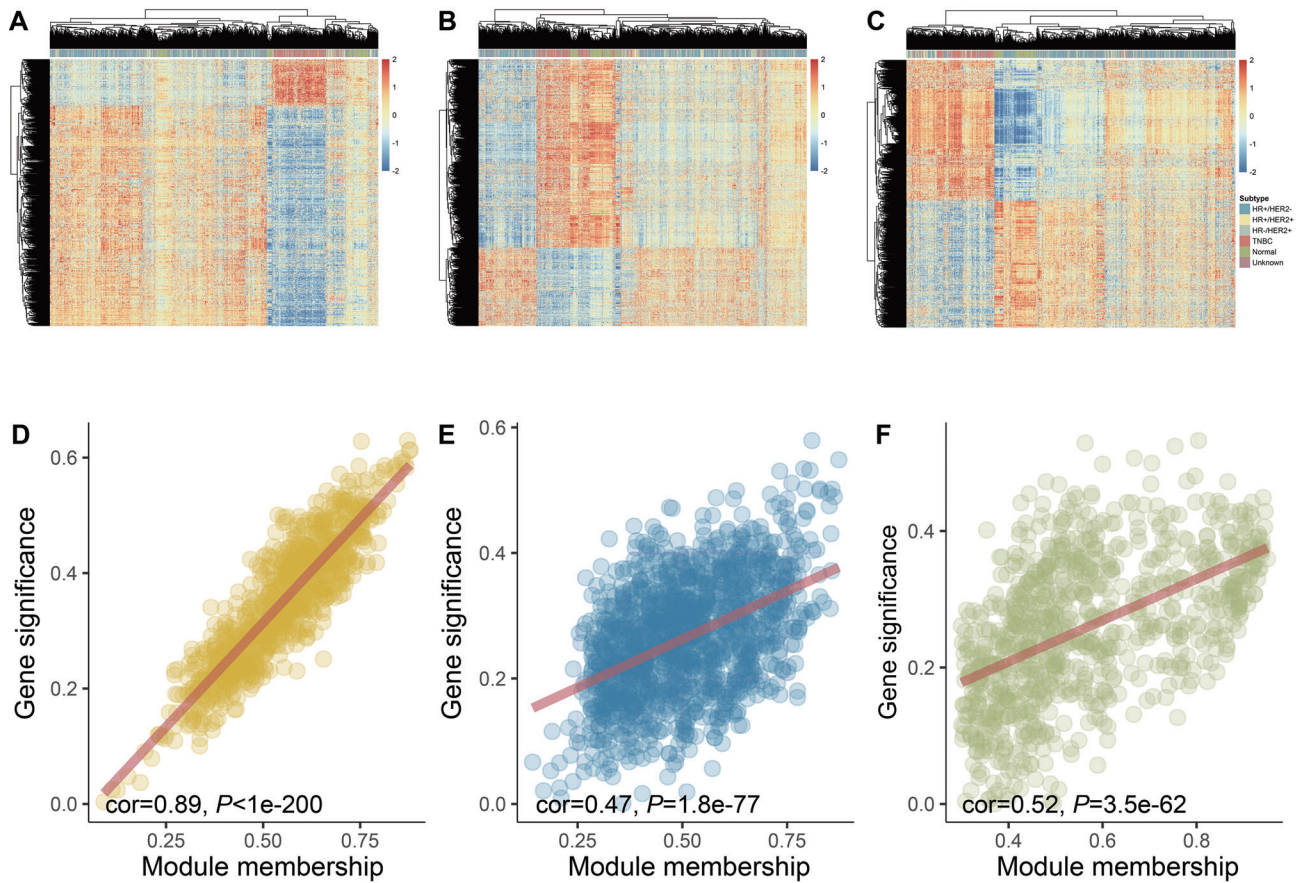
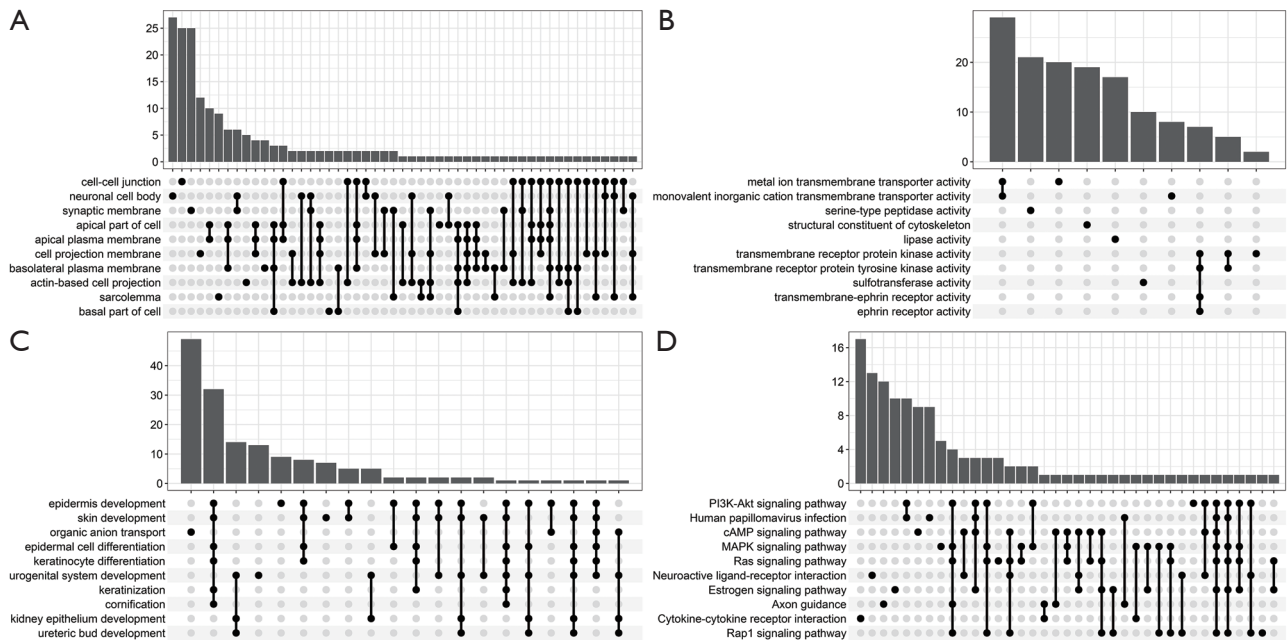


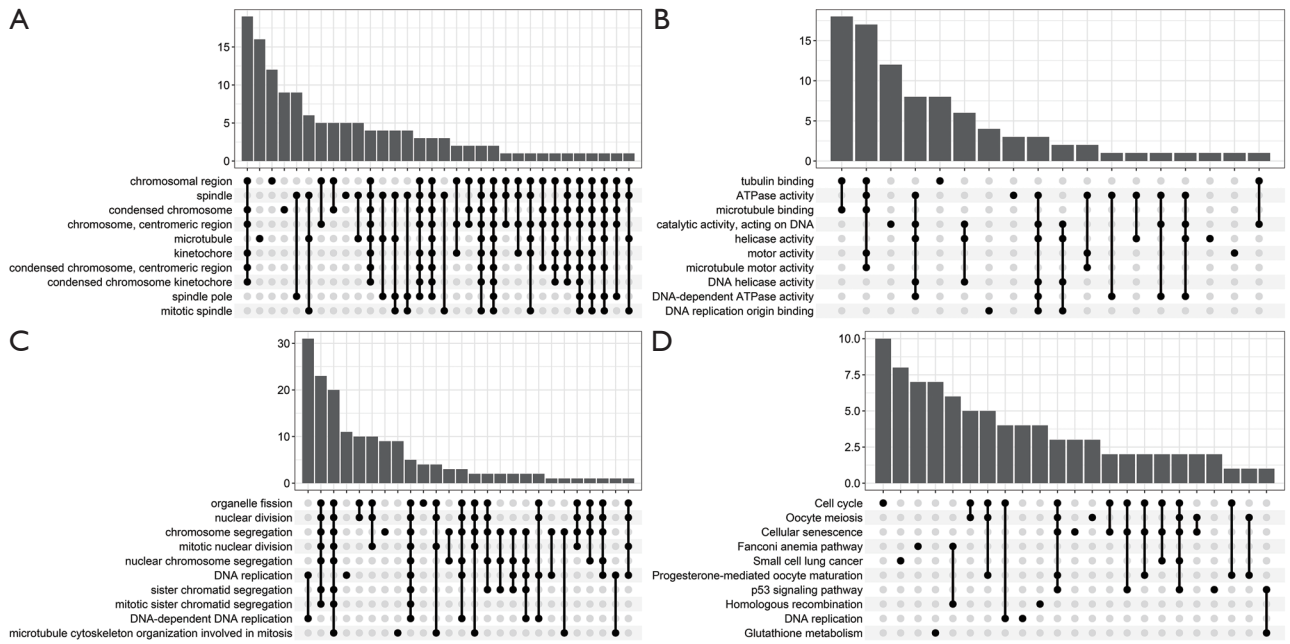
**Figure S1** Gene set enrichment analysis plot of the DEGs between TNBC and non-TNBC. DEG, differentially expressed gene; TNBC, triple-negative breast cancer.



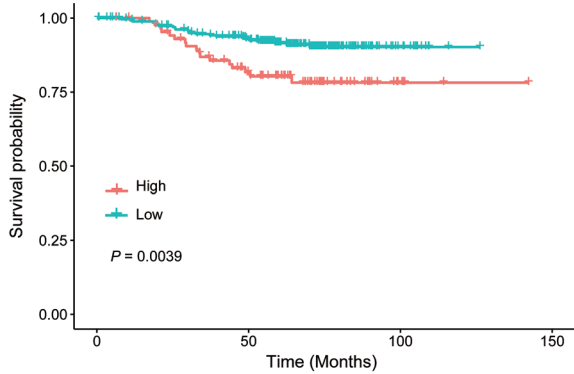
**Figure S2** Heatmap of gene expression profile (A-C) and scatter plot of gene significance for TNBC vs. module membership (D-F) in the yellow (A, D), blue (B, E), and green (C, F) module. TNBC, triple-negative breast cancer.



**Figure S3** GO and KEGG pathway enrichment analysis for the blue module. (A) Cellular component. (B) Molecular function. (C) Biological process. (D) KEGG pathway enrichment analysis. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.



**Figure S4** GO and KEGG pathway enrichment analysis for the green module. (A) Cellular component. (B) Molecular function. (C) Biological process. (D) KEGG pathway enrichment analysis. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.



**Figure S5** Kaplan-Meier plots of the high- and low-risk scores grouped by the top quartile.

**Table S1** Baseline characteristic for patients with TNBC in TCGA-BRCA

Characteristics	Number of patients (%)
<b>Age, year</b>	
<55	79 (50.0)
≥55	79 (50.0)
<b>Menopausal status</b>	
Postmenopausal	98 (63.2)
Premenopausal	44 (28.4)
Indeterminate or unknown	13 (8.4)
<b>Race</b>	
White	90 (57.0)
Black or African American	53 (33.5)
Asian	8 (5.1)
Unknown	7 (4.4)
<b>Histology</b>	
Infiltrating ductal carcinoma	134 (84.8)
Infiltrating lobular carcinoma	6 (3.8)
Other	18 (11.4)
<b>pT stage</b>	
pT1	41 (25.9)
pT2	97 (61.4)
pT3	15 (9.5)
pT4	5 (3.2)
<b>pN stage</b>	
pN0	105 (66.5)
pN1	32 (20.3)
pN2	13 (8.2)
pN3	8 (5.1)
<b>Pathological stage</b>	
Stage I	29 (18.4)
Stage II	101 (63.9)
Stage III	26 (16.4)
Stage IV	2 (1.3)
<b>Breast surgery type</b>	
Lumpectomy	56 (35.4)
Mastectomy	95 (60.2)
Unknown	7 (4.4)
<b>Axillary surgery type</b>	
Sentinel lymph node biopsy	66 (41.8)
Axillary lymph node dissection	87 (55.1)
Unknown	5 (3.2)

TNBC, triple-negative breast cancer; TCGA, The Cancer Genome Atlas; BRCA, breast cancer.

**Table S2** Univariable and multivariable analysis for OS

Variables	Univariable analysis		Multivariable analysis	
	HR (95% CI)	P value	HR (95% CI)	P value
Risk score	4.34 (2.35–8.03)	<0.001	7.49 (3.57–15.70)	<0.001
Age, years				
<55	Reference	–	Reference	–
≥55	1.11 (0.46–2.69)	0.815	2.19 (0.86–5.58)	0.100
Menopausal status				
Postmenopausal	Reference	–	Reference	–
Premenopausal	0.98 (0.36–2.71)	0.976	3.27 (1.2–8.89)	0.020
Unknown	1.81 (0.56–5.84)	0.319	1.92 (0.57–6.39)	0.290
Race				
White	Reference	–	Reference	–
Black or African American	0.99 (0.37–2.67)	0.984	0.59 (0.15–2.28)	0.446
Asian	6.25 (0.78–50.28)	0.085	33.92 (0.97–1180.63)	0.052
Unknown	3.22 (0.38–26.93)	0.281	0 (0–Inf)	1.000
Histology				
Infiltrating ductal carcinoma	Reference	–	Reference	–
Infiltrating lobular carcinoma	2.32 (0.49–10.96)	0.289	0.32 (0.07–1.52)	0.151
Other	1.12 (0.31–4.04)	0.858	0.97 (0.28–3.36)	0.960
Pathological stage				
Stage I	Reference	–	Reference	–
Stage II	2.43 (0.30–19.47)	0.404	1.91 (0.69–5.3)	0.216
Stage III	18.84 (2.37–149.60)	0.005	12.32 (4.55–33.39)	<0.001
Stage IV	19.10 (1.17–312.45)	0.039	14.29 (1.59–128.34)	0.018
Breast surgery				
Lumpectomy	Reference	–	Reference	–
Mastectomy	1.36 (0.51–3.63)	0.545	1.37 (0.52–3.6)	0.522
Unknown	2.46 (0.29–20.88)	0.409	0 (0–0)	<0.001
Axillary surgery				
Sentinel lymph node biopsy	Reference	–	Reference	–
Axillary lymph node dissection	5.26 (1.53–18.14)	0.009	2.54 (0.81–7.95)	0.109
Unknown	17.24 (1.67–178.53)	0.017	Inf (Inf–Inf)	<0.002

OS, overall survival; HR, hazard ratio; CI, confidence interval.