Figure S1 The left graph shows the relationship coefficients of log(k) and log(p(k)) for different soft thresholds. The higher the coefficient, the more the network conforms to the scale-free network distribution. The graph on the right shows the mean of the gene contiguous coefficients in the gene network corresponding to different soft thresholds, which reflects the average connection level of the network.
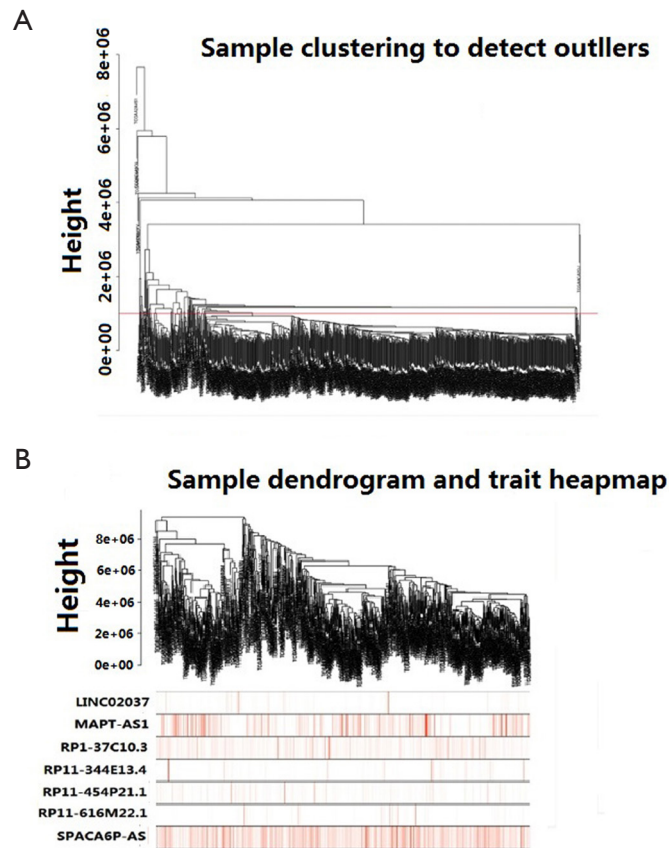
Figure S2 The distance matrix is constructed by 1-IAC, and the class average method is used to hierarchically cluster the samples. (A) Clustering tree of 913 tumor samples in combined cohort. (B) The cluster clustering map of the combined cohort after excluding the outlier samples and the LncRNA expression profile data of the corresponding samples showed that the height of the clustering tree was significantly lower than that of the left graph (from 8,000,000 to 1,000,000). The larger the value of LncRNA expression, the darker the color.
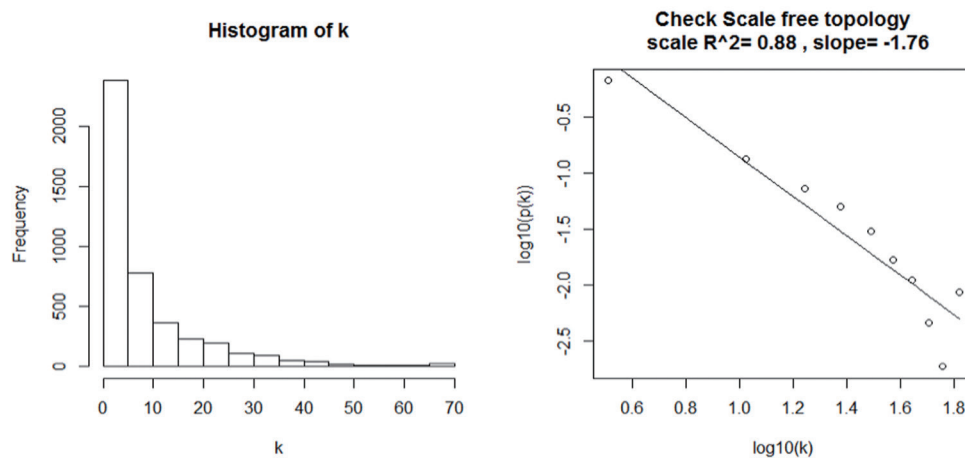

Figure S3 Verify that the network meets the scale-free network distribution for selected soft threshold β=4. The left picture shows the distribution of the connectivity of each node in the network. The right picture shows the scatter plot of log (k) and log (p (k)). The linear regression results show that the correlation coefficient is 0.88, which is consistent with the characteristics of the scale-free network.
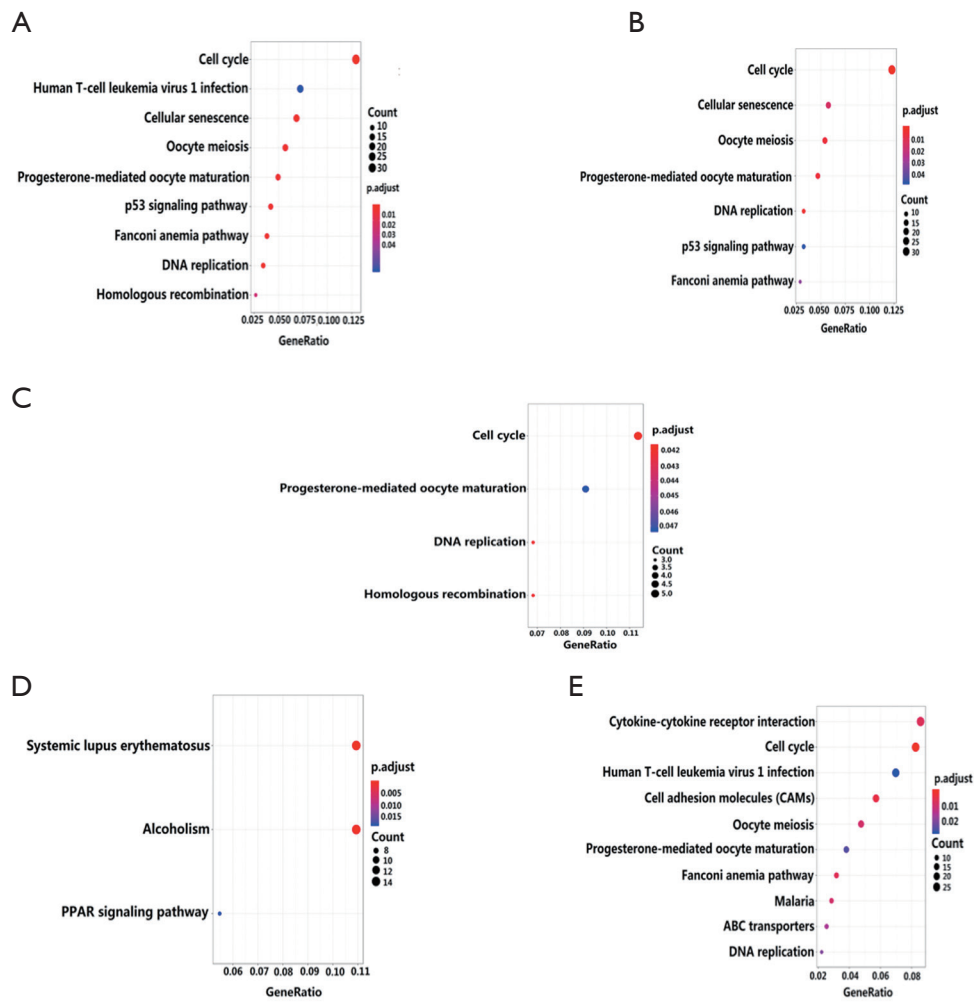
Figure S4 KEGG functional enrichment analysis of 5 lncRNAs. (A) Analysis of KEGG pathway in which lncRNA MAPT-AS1 is enriched in differentially co-expressed protein-encoding RNA. (B) Analysis of the KEGG pathway of lncRNA RP1-37C10.3 enriched in different co-expression protein-encoding RNA. (C) LncRNA RP11-344E13.4 is enriched in KEGG pathway analysis of differentially co-expressed protein-encoding RNA. (D) LncRNA RP11-454P21.1 was enriched in the KEGG pathway analysis of different co-expression protein-encoding RNA. (E) LncRNA SPACA6P-AS is enriched in KEGG pathway analysis of distinguishingly co-expressed protein-encoding RNA.
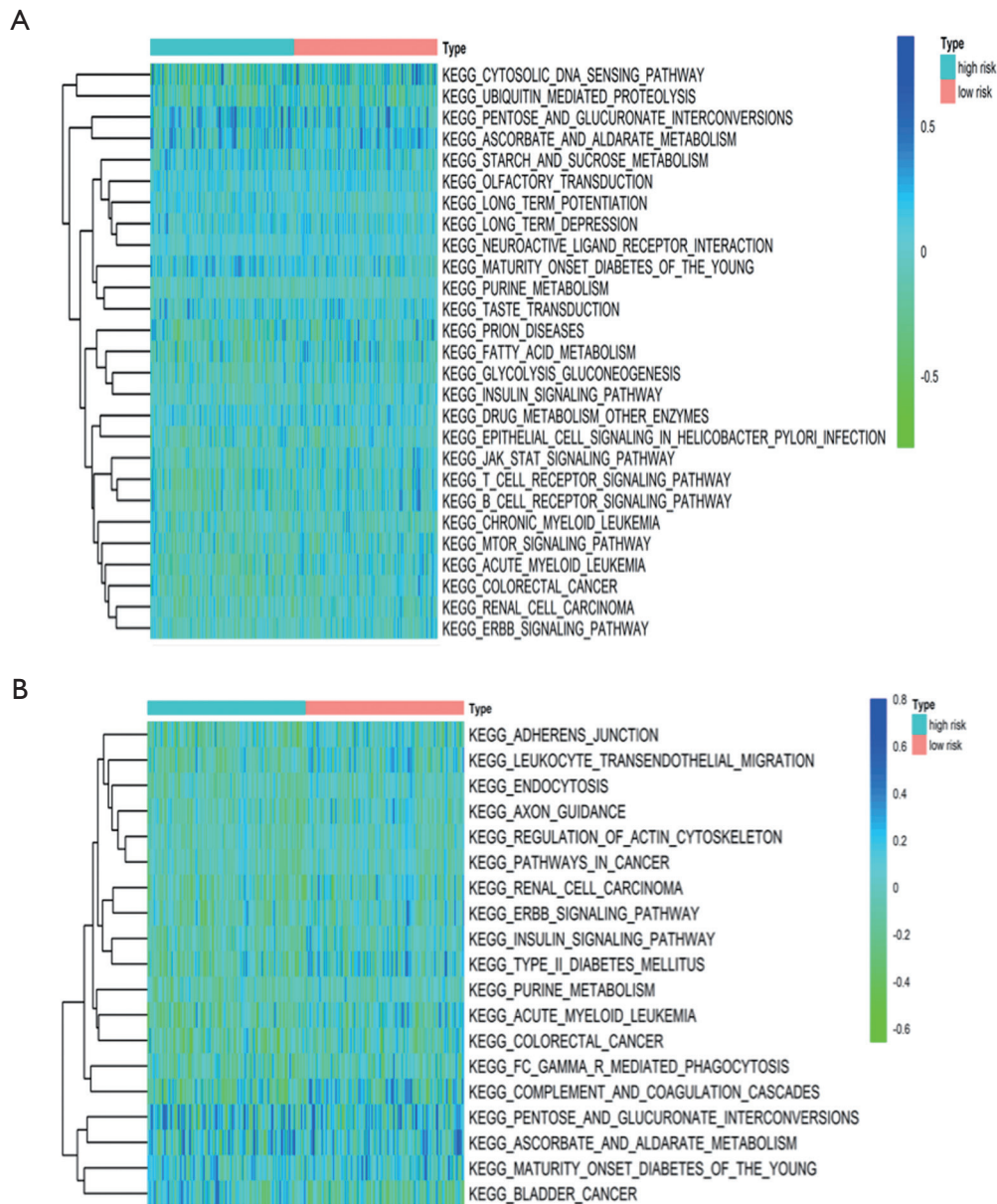
Figure S5 GSVA enrichment analysis between high and low risk score groups. (A) GSEA unsupervised hierarchical clustering heat map between the high- and low-risk score groups of training set. (B) GSEA unsupervised hierarchical clustering heat map between the high- and low-risk score groups in test dataset.

Table S1 LncRNA significantly associated with overall survival in breast cancer patients

Groups	Training dataset			Training dataset			Combined cohort		
LncRNAs	HR	z	P value	HR	z	P value	HR	z	P value
AC025016.1	1.155	2.672	0.008	1.182	2.682	0.007	1.172	3.925	<0.001
LINC02037	1.327	3.537	<0.001	1.287	2.049	0.040	1.307	3.972	<0.001
MAPT-AS1	0.888	−2.584	0.010	0.856	−2.721	0.007	0.875	−3.734	<0.001
RP1-37C10.3	1.277	2.189	0.029	1.663	3.258	0.001	1.379	3.606	<0.001
RP11-120K18.2	1.242	2.598	0.009	1.266	2.089	0.037	1.259	3.484	<0.001
RP11-344E13.4	1.286	3.770	<0.001	0.598	-2.054	0.040	1.159	2.186	0.0289
RP11-454P21.1	1.353	3.236	0.001	1.430	2.698	0.007	1.361	4.110	<0.001
RP11-616M22.1	1.274	2.771	0.006	1.297	2.192	0.028	1.278	3.560	<0.001
SPACA6P-AS	1.251	2.376	0.018	1.591	3.007	0.003	1.327	3.547	<0.001
Xxyac-YM21GA2.7	1.248	2.862	0.004	1.423	2.237	0.025	1.282	3.735	<0.001

Table S2 1–5 years survival rate for high- and low-risk groups

Time (year)	Number of risks	Survival rate	Standard deviation	95% confidence interval	
				Lower limit	Upper limit
High-risk					
1.0000	152	0.93	0.01744	0.896	0.965
2.0137	95	0.871	0.0271	0.819	0.926
3.1014	63	0.765	0.03948	0.692	0.847
3.6685	45	0.733	0.04393	0.652	0.824
5.0658	23	0.65	0.05968	0.543	0.778
Low-risk					
1.0548	180	0.973	0.01119	0.9508	0.995
2.0658	129	0.959	0.01471	0.9303	0.988
2.7973	103	0.933	0.02052	0.8936	0.974
4.9123	52	0.915	0.02685	0.8639	0.969

Table S3 Univariate and multivariate Cox regression analyses in the training, testing and entire TCGA datasets

Characteristics		Univariate analysis			Multivariate analysis		
		HR	CI95%	P value	HR	CI95%	P value
Training dataset (n=608)							
Age	Continuous variable	1.03	1.01–1.05	0.002	1.03	1.01–1.06	0.014
Gender	Negative *vs.* positive	0.71	0.1–5.17	0.737			
Race	Asian and Black *vs.* White	1.37	0.79–2.37	0.264			
Stage	III–IV *vs.* I–II	4.51	2.71–7.51	<0.001	3.9	1.87–8.15	<0.001
Cancer status	With tumor *vs.* tumor free	6.18	3.59–10.62	<0.001	5.17	2.68–9.97	<0.001
Number of lymph nodes positive	Continuous variable	1.10	1.06–1.14	<0.001	1.00	0.94–1.05	0.872
Progesterone receptor status	Negative *vs.* positive	1.65	0.96–2.82	0.068			
Estrogen receptor status	Negative *vs.* positive	1.75	0.98–3.13	0.057			
Her2 receptor status	Negative *vs.* positive	1.01	0.45–2.28	0.973			
Triple-negative breast cancer	Yes *vs.* no	1.70	0.89–3.26	0.108			
Risk	high risk *vs.* low risk	4.15	2.38–7.25	<0.001	2.44	1.2–4.99	0.014
Cancer subtype	Triple negative *vs.* Luminal A	1.85	0.91–3.78	0.089			
	Triple negative *vs.* Luminal B	1.57	0.50–4.9	0.437			
	Triple negative *vs.* HER2A enriched	1.39	0.31–6.22	0.667			
Testing dataset (n=305)							
Age	Continuous variable	1.03	1.01–1.05	0.012	1.05	1.02–1.08	0.001
Gender	Negative *vs.* Positive	1217467.94	0–Inf	0.997			
Race	Asian and Black *vs.* White	1.60	0.79–3.26	0.194			
Stage	III–IV *vs.* I–II	1.43	0.73–2.77	0.295			
Cancer status	With tumor *vs.* Tumor free	5.34	2.67–10.69	<0.001	5.56	2.69–11.47	<0.001
Number of lymph nodes positive	Continuous variable	1.03	0.98–1.09	0.213			
Progesterone receptor status	Negative *vs.* Positive	1.29	0.67–2.47	0.447			
Estrogen receptor status	Negative *vs.* Positive	0.93	0.45–1.91	0.835			
Her2 receptor status	Negative *vs.* Positive	1.22	0.36–4.13	0.751			
Triple-negative breast cancer	Yes *vs.* No	1.86	0.80–4.35	0.152			
Risk	high risk *vs.* low risk	3.83	1.92–7.65	<0.001	3.72	1.69–8.18	0.001
Cancer subtype	Triple negative *vs.* Luminal A	2.39	0.84–6.82	0.103			
	Triple negative *vs.* Luminal B	2.26	0.47–10.93	0.312			
	Triple negative *vs.* HER2A enriched	227497607.3	0–Inf	0.999			

Table S3 (*continued*)

Characteristics		Univariate analysis			Multivariate analysis		
		HR	CI95%	P value	HR	CI95%	P value
Entire TCGA dataset (n=913)							
Age	Continuous variable	1.03	1.02-1.05	<0.001	1.04	1.02-1.06	<0.001
Gender	Negative *vs.* Positive	0.82	0.11-5.88	0.84			
Race	Asian and Black *vs.* White	1.43	0.93-2.2	0.106			
Stage	III–IV *vs.* I–II	2.76	1.86-4.08	<0.001	1.76	0.97-3.21	0.064
Cancer status	With tumor *vs.* Tumor free	5.77	3.78-8.81	<0.001	4.62	2.69-7.93	<0.001
Number of lymph nodes positive	Continuous variable	1.07	1.04-1.1	<0.001	1.02	0.97-1.07	0.499
Progesterone receptor status	Negative *vs.* Positive	1.45	0.97-2.17	0.069			
Estrogen receptor status	Negative *vs.* Positive	1.31	0.84-2.03	0.235			
Her2 receptor status	Negative *vs.* Positive	1.06	0.54-2.08	0.862			
Triple-negative breast cancer	Yes *vs.* No	1.78	1.06-2.97	0.029	2.31	1.23-4.34	0.01
Risk	high risk *vs.* low risk	3.75	2.46-5.71	<0.001	2.05	1.13-3.72	0.019
Cancer subtype	Triple negative *vs.* Luminal A	1.13-3.61	0.017	1.59	0.88-2.86	0.125	1.13-3.61
	Triple negative *vs.* Luminal B	0.71-4.49	0.214				0.71-4.49
	Triple negative *vs.* HER2A enriched	0.44-8.25	0.386				0.44-8.25