

Weighted correlation network analysis of triple-negative breast cancer progression: Identifying specific modules and hub genes based on the GEO and TCGA database

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Abstract. Triple-negative breast cancer (TNBC) represents an aggressive malignancy of frequent high histologic grade with no effective specific targeted therapies. The present study aimed to identify specific modules and hub genes that may influence the progression of TNBC. The key words 'breast cancer' were used to search microarray datasets in the Gene Expression Omnibus and The Cancer Genome Atlas databases that included 5 datasets. A total of 11 co-expression modules were constructed based on the expression levels of 5,782 genes obtained from 456 patients with TNBC using the weighted correlation network analysis (WGCNA). The results demonstrated that the red module was significantly associated with relapse-free survival (RFS) in patients with TNBC [hazard ratio (HR)=0.381, 95% confidence interval (CI), 0.183-0.793; P=0.010]. The functional enrichment analysis revealed that the biological processes corresponding to the red module were 'mRNA processing', 'histone lysine methylation' and 'regulation of TOR signaling'. In addition, Hedgehog signaling pathways were considered to serve a critical role in the development of this disease (P<0.001). A total of 12 hub genes were identified, of which α -thalassemia/mental retardation syndrome X-linked (ATR_X) was significantly associated with RFS in patients with TNBC (HR=0.601; 95%CI, 0.376-0.960;

P=0.033). The receiver operating characteristic curve indicated that ATR_X could distinguish relapse from non-relapse in patients with TNBC (area under the curve=0.570; P=0.023). In conclusion, the present study demonstrated that ATR_X was associated with TNBC progression, which suggested that ATR_X may be involved in a recombination-mediated telomere maintenance mechanism.

Introduction

Breast cancer is the most commonly diagnosed cancer in women and the leading cause of cancer-associated mortality worldwide. In 2018, ~41,400 patients succumbed to this malignancy in the United States. Estimations highlight that ~268,670 new cases may be diagnosed every year (1). Triple-negative breast cancer (TNBC) represents 10-20% of all breast cancer cases and is defined by a lack of estrogen receptor (ER) and progesterone receptors (PR) expression and the absence of amplification or overexpression of human epidermal growth factor receptor 2 (HER2) (2). In addition, TNBC is associated with a higher risk of distant and early recurrence and more aggressive metastases in the viscera and central nervous system, particularly in the lungs and brain (3). Due to the lack of specific targeted therapies in TNBC, endocrine or anti-HER2 therapies display no benefits, and chemotherapy is the only established therapeutic option available in clinical practice (3-6). It is therefore crucial to identify and develop specific molecular targets for the development of effective treatment of TNBC.

With the development of genomic technologies, a large volume of molecular information including Gene Expression Omnibus (GEO) and The Cancer Genome Atlas (TCGA), represent a remarkable opportunity to analyze the gene expression data for the discovery of novel targets (7). Furthermore, co-expression analysis has emerged as a powerful technique for multigene analysis in large-scale data. Gene co-expression analysis is used to associate genes of unknown function with biological processes, in order to prioritize candidate disease genes or to differentiate transcriptional regulatory programs (8). In comparison with the traditional

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one-dimensional molecular biology methods, the weighted correlation network analysis (WGCNA) is a method that can highlight the modules of highly correlated genes and describe the characteristics of the biological system more accurately and effectively (9,10). This method has been successfully used to identify targeted modules and hub genes in cancer research. For example, Chen *et al* (11) and Wan *et al* (12) identified novel biomarkers for human clear renal cell carcinoma and uveal melanoma, respectively, via WGCNA. In addition, Clarke *et al* (13) used WGCNA to analyze a breast cancer dataset and identified certain modules associated with different molecular subtypes. In the present study, WGCNA has highlighted numerous biologically significant results in cancer study, and to the best of our knowledge, it was applied for the first time to the study of TNBC. WGCNA represents an R package for weighted correlation network analysis, including network construction, module detection, gene selection, topological property calculation and visualization (14). In the present study, WGCNA was used to construct a TNBC gene co-expression network. Firstly, the initial phase of the WGCNA method allowed identification of co-expression modules. Secondly, a survival analysis for modules identified in the first step was performed. Thirdly, a functional enrichment analysis was achieved on the modules of interest. The identified hub genes may therefore be beneficial to assess the malignancy and prognosis of TNBC.

Materials and methods

Search strategy. In the present study, mRNA expression data and clinical trait information of patients with breast cancer were downloaded from the GEO database using the keywords ‘breast cancer’ in NCBI (<http://www.ncbi.nlm.nih.gov/geo/>) and TCGA database (<https://cancergenome.nih.gov/>, last updated July 2017). The search strategy of the study was designed as follows: The type of study was ‘expression profiling by array’, and the entry type was ‘datasets’. The sample size of the selected datasets was ≥ 100 . The organism was *homo sapiens*. The database searching was independently carried out by two researchers.

Data preprocessing. Four microarray datasets (GSE16446, GSE25055, GSE25065 and GSE58812) that contained survival outcomes and clinical information of ER, PR and HER2 were selected from the GEO database. Data of samples from patients with TNBC were obtained from the TCGA database (Fig. 1). Table I presents the clinical characteristics of the patients with TNBC included in these five datasets. In addition, four endpoints were integrated and defined as relapse-free survival (RFS), which represented survival outcomes. The mRNA expression value of each gene considered in the present study represented the mean of the gene expression values extracted from the five datasets. The mRNA gene expression from the five datasets were normalized and merged by gene name; however, each gene that was not present in all datasets was excluded from the study. In order to ensure the quality of the expression data, genes were excluded if $\geq 10\%$ of the samples were missing expression data. Subsequently, the variance of each mRNA gene expression value was calculated and the genes with variance ranked in the top 50% were selected. Eventually,

Table I. Clinical characteristics of patients with TNBC.

Dataset	Patients, n	Survival endpoints	Event (0/1)
TCGA	83	RFS	69/14
GSE58812	107	MFS	76/31
GSE25065	64	DRFS	37/27
GSE25055	114	DRFS	77/37
GSE16446	45	DMFS	32/13

Event 0, occurred; Event 1, did not occur. DMFS, distant meta-free survival; DRFS, distant relapse-free survival; MFS, meta-free survival; RFS, relapse-free survival; TCGA, The Cancer Genome Atlas.

Table II. Clinical characteristics of patients with TNBC.

Variables	Patients, n (%)
Age, years	
≤50	208 (45.3)
>50	251 (54.7)
Stage	
I	23 (7.8)
II	162 (55.1)
III	108 (36.7)
IV	1 (0.4)
Lymph Node	
N0	148 (42.0)
N1	135 (38.4)
N2	40 (11.4)
N3	29 (8.2)
T stage	
T1	44 (12.6)
T2	199 (56.9)
T3	67 (19.1)
T4	40 (11.4)
Metastasis	
Yes	116 (99.1)
No	1 (0.9)
OS ^a , months	41.97 (21.16,70.83)
RFS ^a , months	31.87 (17.80,57.36)

RFS represents all endpoints of survival information, including distant meta-free survival, distant relapse-free survival, meta-free survival and RFS. OS, overall survival; RFS, relapse-free survival; TNBC, triple-negative breast cancer. ^aOS and RFS describe the P_{50} (P_{25}, P_{75}) of survival time.

a final dataset containing 459 patients with TNBC and mRNA expression of 5,782 genes was compiled. Table II presents the baseline clinical characteristics of the final dataset.

Construction of the WGCNA. The WGCNA was carried out by using the R WGCNA package (15). The goodSamplesGenes

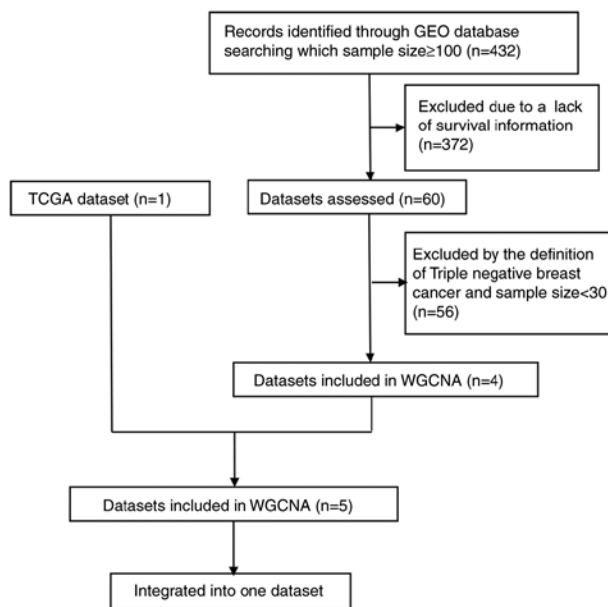


Figure 1. Flow diagram of dataset collection process. GEO, Gene Expression Omnibus; TCGA, The Cancer Genome Atlas; WGCNA, weighted correlation network analysis.

function in the R WGCNA package was used to check the gene expression data of all TNBC samples for excessive missing values and identification of outlier microarray samples. The samples were clustered with hierarchical clustering analysis by using the *hclust* function to check if there were any outliers. A correlation matrix was created by using a similarity measure to summarize the association between all genes. In addition, to identify specific modules, WGCNA uses a soft-thresholding procedure to avoid the selection of an arbitrary cut-off. The β value represented a soft-thresholding parameter that could emphasize strong correlations between genes and penalize weak correlations to ensure a scale-free network (14). The *cutreeDynamic* function was used for adaptive branch pruning of hierarchical clustering dendrograms and the *dynamicTreeCut* package was adopted to generate co-expression modules. Subsequently, to further analyze the module, the dissimilarity of the module eigengenes (ME) was calculated using the *moduleEigengenes* function in the R WGCNA package, which was defined as the first principal component of a given module and considered to be representative of the gene expression profiles in a module. A cut-off line for the module dendrogram was selected and the module was merged. Eventually, the adjacency was converted into a topological overlap matrix (TOM), and modules were subjected to hierarchical cluster analysis according to the TOM-based dissimilarity measure.

To assess the potential associations between modules and clinical variables, approaches based on WGCNA to identify modules associated with to the progression of TNBC were used. Firstly, the gene significance (GS) was defined as the \log_{10} transformation of the corresponding P-value ($GS = \lg P$) of the correlation between gene expression and pathological stage. Secondly, each ME considered as the major component in the principal component analysis was chosen and represented the mean measure for the overall co-expression

network. Ultimately, the correlation between MEs and the clinical characteristics was calculated to identify the relevant module (16-18).

Statistical analysis. For survival analysis, MEs and gene expression values were divided into low and high expression groups by using the Cutoff Finder (<http://molpath.charite.de/cutoff/index.jsp>) (19). The hazard ratio (HR) was determined via a Cox regression model, and survival curves were plotted from Kaplan-Meier estimations. $P < 0.05$ was considered to indicate a statistically significant difference.

Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways enrichment analyses for the identified modules were performed using Cytoscape software (version 3.5.1; <https://cytoscape.org/>) with the ClueGO plug-in (version 2.5.0; <http://apps.cytoscape.org/apps/cluego>) (20). The ClueGO plug-in generates grouped GO annotation and KEGG pathways, and integrates the terms to create a functionally organized GO/pathway term network by using κ statistics to determine the association strength between the terms (21). In the present study, the statistical test used by the ClueGO plug-in for the enrichment was based on two-sided hypergeometric tests with a Benjamini-Hochberg adjustment. GO terms and KEGG pathways with $P < 0.05$ were considered as significantly different, and a κ score threshold ≥ 0.4 was used to functionally divide these pathways into different groups.

Identification of hub genes in the co-expression module. WGCNA is used to find hub genes in the module of interest, which is highly interconnected with other genes that have higher biological relevance compared with the whole network. The absolute value of Pearson's correlation between gene expression and MEs was used to identify the importance of a gene in the module, which is known as the module membership (MM). In the present study, hub genes were selected for $MM > 0.55$ in the specific module. In addition, the modules of interest were constructed using Cytoscape and defined as hub genes for a connectivity degree ≥ 15 in the co-expression network. The common hub genes with the higher MM and connectivity degree were considered as 'real' hub genes in the module of interest.

Results

Construction of the WGCNA. A total of 459 TNBC samples were used as input for the hierarchical clustering analysis that was performed with the function *hclust* to cluster the samples to see if there were any clear outliers. Three samples (GSM149983, GSM1419985 and GSM411317) were removed as outliers. The co-expression network was constructed from the expression values of 5,782 genes in 456 TNBC samples with the WGCNA package. Prior to further studying the TNBC samples, an analysis of network topology was performed for various soft-thresholding powers to obtain the relatively balanced scale independence and mean connectivity. As presented in Fig. 2A, power 3, which is the lowest power for which the scale-free topology fit index reached 0.90, was selected to ensure a scale-free network and to produce a hierarchical clustering dendrogram. The dynamic tree cut function was used to prune the branches in hierarchical

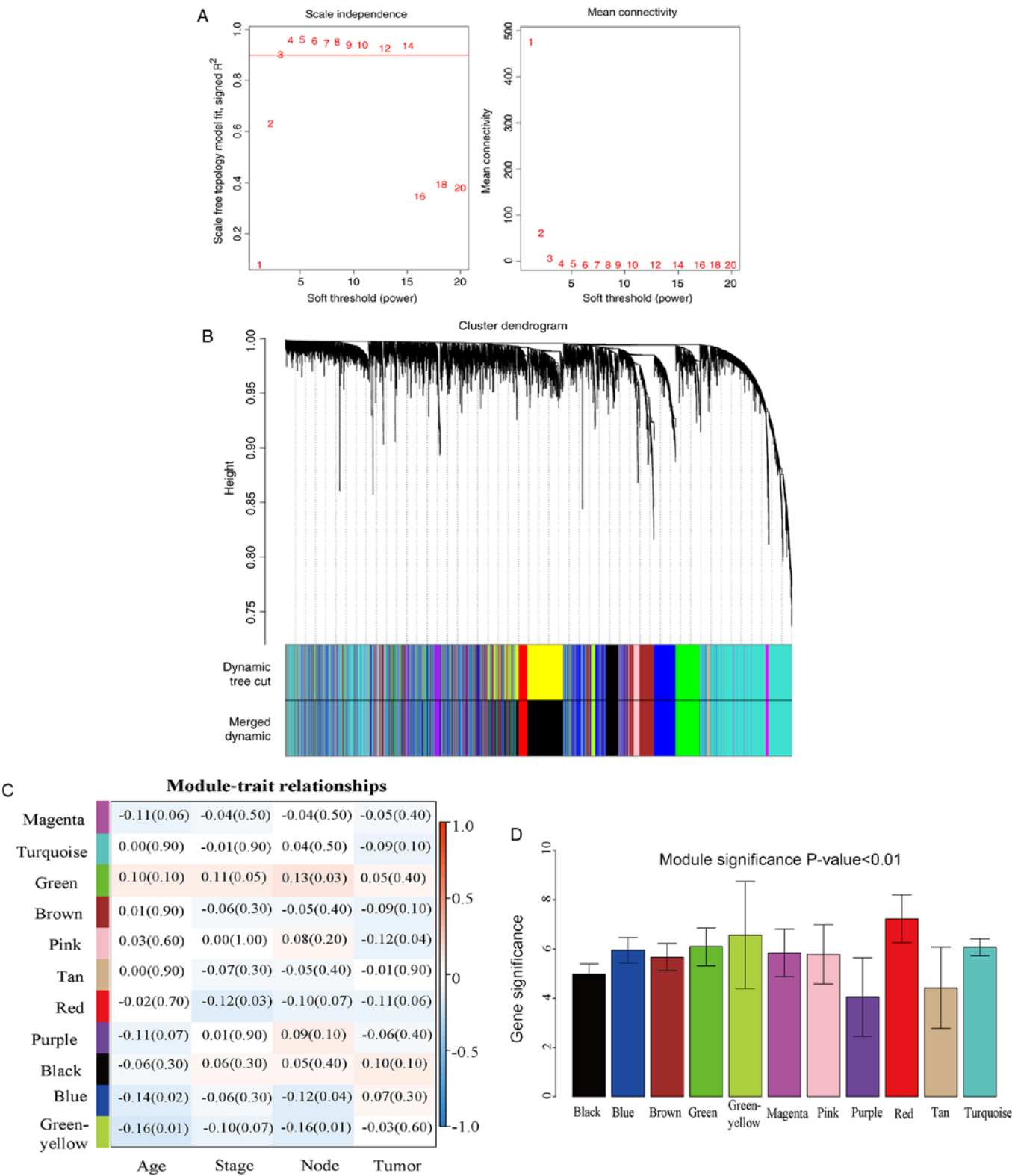


Figure 2. (A) Determination of soft-thresholding power in WGCNA. (B) Dendrogram of the genes modules based on a dissimilarity measure. (C) Heatmap of the correlation between module eigengenes and clinical characteristics of TNBC: Each row corresponds to a module eigengene and each column corresponds to a clinic characteristic. Each cell contains the corresponding correlation and P-value. The red key represents a positive correlation between modules and clinical variables, while the blue key represents opposite. (D) Distribution of mean gene significance and standard deviation in the modules associated with pathological stage of TNBC. TNBC, triple-negative breast cancer; WGCNA, weighted correlation network analysis.

clustering dendrograms that determined the generation of the co-expression modules. Then, the MEs were calculated by the moduleEigengenes function to quantify the co-expression similarity of the modules and the clustered modules were

merged based on the similarity. A total of 11 distinct co-expression modules (ranging in size from 38-2,251 genes), were identified. These co-expression modules are represented by different colors in Fig. 2B.

Table III. Comparison between non-relapse and relapse occurrence in patients with TNBC by Mann-Whitney U test.

Module	Ngene	Non-relapse	Relapse	Z score	P-value
ME black	848	-0.008 (-0.03,0.02)	-0.003 (-0.03,0.04)	-1.579	0.114
ME blue	869	0.006 (-0.03,0.03)	0.001 (-0.03,0.03)	-0.241	0.810
ME brown	654	-0.003 (-0.04,0.03)	-0.001 (-0.03,0.03)	-0.297	0.766
ME green	338	-0.018 (-0.03,0.01)	-0.018 (-0.03,0.03)	-0.434	0.665
ME green yellow	56	-0.008 (-0.03,0.03)	-0.011(-0.03,0.02)	-0.800	0.424
ME magenta	173	0.002 (-0.03,0.04)	-0.001 (-0.04,0.02)	-1.099	0.272
ME pink	204	-0.009 (-0.03,0.02)	-0.007 (-0.03,0.02)	-0.021	0.984
ME purple	75	-0.001 (-0.03,0.03)	-0.002 (-0.03,0.02)	-0.565	0.572
ME red	276	0.007 (-0.02,0.03)	0.000 (-0.03,0.02)	-2.393	0.017
ME tan	38	-0.005 (-0.03,0.03)	-0.002 (-0.03,0.03)	-1.049	0.294
ME turquoise	2251	-0.008 (-0.04,0.03)	-0.012 (-0.04,0.03)	-0.450	0.653

Non-relapse and relapse describe the P_{50} (P_{25}, P_{75}) of MEs in each module. ME, module eigengenes; TNBC, triple-negative breast cancer; Ngene, number of genes identified in each module by WGCNA.

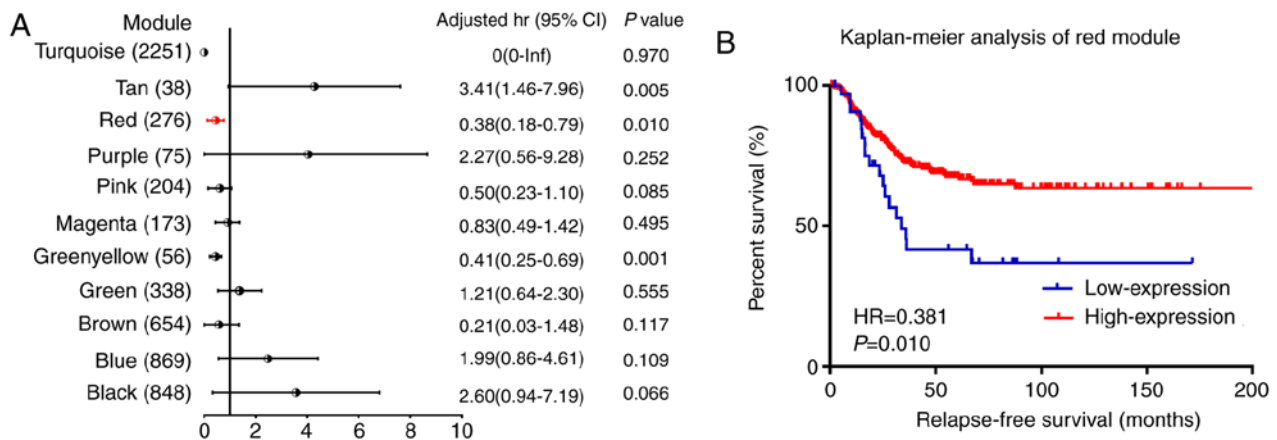


Figure 3. Survival analysis between module eigengenes and RFS in patients with TNBC. (A) Forest plot of hazard ratios in each module for RFS (B) Kaplan-Meier analysis of RFS for the red module. CI, confidence interval; HR, hazard ratio; RFS, relapse-free survival.

Identification of module associations with clinical characteristics of patients with TNBC. To determine the modules that were significantly associated with clinical characteristics, 294 TNBC samples with clinical variables were included to calculate the module-trait association (Fig. 2C). GS were also determined to evaluate the correlation between gene expression and pathological stage (Fig. 2D). Results of the module-trait association revealed a weak correlation between the red module and the pathological stage ($r=-0.12$, $P=0.03$) in which GS was the most significant. In addition, to identify associations between the co-expression modules and RFS endpoints, Cox regression was used to calculate the HRs and P-values for each ME. Following the survival analysis, 3 co-expression modules (green-yellow, red and tan colors) were significantly associated with the RFS in multivariate analysis (Fig. 3A). As presented in Fig. 3B, the increased mRNA expression of the red module was associated with good outcome for RFS, which was consistent with the correlation observed between pathological stage and ME. Furthermore, based on patients' status of relapse

and non-relapse, each module was divided into two groups, and MEs were compared within these two groups with the Mann-Whitney U test. The results in Table III demonstrated that MEs in the red module were significantly different between the two groups of relapse and non-relapse patients with TNBC. These results allowed the selection of the red module as the module of interest, which was further studied in subsequent analyses.

Enrichment analysis of the key modules. GO and KEGG enrichment were performed in the red module using ClueGO. Following GO analysis of the red module, 40 GO terms were significantly enriched and were divided into 16 groups (Table IV), which reflected the biological processes. The top 10 enriched GO terms were defined as follows: 'mRNA processing', 'regulation of mitotic nuclear division', 'cellular response to topologically incorrect protein', 'interaction with symbiont', 'golgi vesicle transport', 'mitotic cytokinesis', 'regulation of target of rapamycin (TOR) signaling', 'transcription elongation from RNA polymerase II promoter', 'organelle

Table IV. Biological processes for genes in the module red.

Term ID	P-value	Benjamini-Hochberg adjustment	Term name	Gene names
GO:0006397	<0.01	<0.01	mRNA processing	AICF, CCNT1, CDK13, CTR9, GEMIN7, GTF2H1, HNRNPA3, HNRNPH1, LUC7L3, NOVA2, PAPOLA, PPWD1, PRKACA, PTCD2, RBM15B, RBM25, RBM39, RBM7, RBMX2, SON, SPEN, WBP4, YTHDC1
GO:0000910	<0.01	0.01	Cytokinesis	ANK3, APC, CUL3, PDCD6IP, PKN2, RASA1, SETD2, SON
GO:0008360	<0.01	0.01	Regulation of cell shape	CSNK1G1, CSNK1G3, F2, FGD6, KIF3A, PHIP, RASA1, TTBK2
GO:0006888	<0.01	0.01	ER to Golgi vesicle-mediated transport	ACTR10, ANK3, ARFGAP1, COPB1, CUL3, F2, SEC23IP, SEC24B, USO1
GO:0007088	<0.01	0.01	Regulation of mitotic nuclear division	APC, ATRX, BTC, CDK13, CHMP2B, CUL3, PHIP, SLF2
GO:0051702	<0.01	0.01	Interaction with symbiont	CCNT1, CHD1, EP300, F2, REST
GO:0016482	<0.01	0.01	Cytosolic transport	DNAJC13, DOPEY1, EEA1, GCC2, MON2, PIKFYVE, RAB21
GO:0140056	<0.01	0.01	Organelle localization by membrane tethering	AKAP9, B9D1, EXOC5, HAUS3, PRKACA, TTBK2, USO1
GO:0035967	<0.01	0.01	Cellular response to topologically incorrect protein	ARFGAP1, ATF6, CUL3, DZIP3, EDEM3, EP300, GSK3A
GO:0006368	<0.01	0.02	Transcription elongation from RNA polymerase II promoter	CCNT1, CDK13, CTR9, GTF2A1, GTF2H1, SETD2
GO:0032006	0.01	0.02	Regulation of TOR signaling	ARNTL, CRYBA1, GSK3A, HTR6, MTM1
GO:0051651	0.01	0.02	Maintenance of location in cell	AKAP9, ANK3, MORC3, PDIA2, SYNE2
GO:0009791	0.02	0.02	Post-embryonic development	ACADM, ATRX, IREB2, MORC3, PLEKHA1
GO:0007030	0.03	0.03	Golgi organization	AKAP9, GCC2, SEC23IP, USO1, VAMP4
GO:0034968	0.03	0.03	Histone lysine methylation	ATRX, BCOR, CTR9, KDM6A, SETD2
GO:0003231	0.03	0.03	Cardiac ventricle development	C5orf42, GSK3A, MDM2, PTCD2, TNNT1
ER, endoplasmic reticulum; TOR, target of rapamycin.				

Table V. Survival analysis of hub genes for RFS in patients with TNBC.

Gene	Univariate analysis (413 ^a)			Multivariate analysis (294 ^b)			Cutoff value
	HR	P-value	95% CI	HR	P-value	95% CI	
APC	1.236	0.266	0.851-1.797	1.064	0.800	0.658-1.721	-0.289
ATRAX	0.603	0.007	0.417-0.870	0.601	0.033	0.376-0.960	0.180
CHD1	0.643	0.120	0.368-1.122	0.727	0.394	0.349-1.514	0.949
CHD9	0.547	0.057	0.294-1.017	0.373	0.033	0.151-0.925	1.077
COL4A3BP	0.609	0.015	0.406-0.911	0.803	0.432	0.464-1.389	-0.725
DCP2	0.451	0.030	0.220-0.924	0.471	0.060	0.215-1.032	1.209
DMXL1	0.570	0.019	0.356-0.912	0.608	0.094	0.339-1.089	0.728
KIAA1033	0.793	0.203	0.554-1.134	0.900	0.650	0.572-1.417	-0.930
RAPGEF6	0.687	0.063	0.462-1.021	0.653	0.093	0.397-1.073	0.328
TRIM23	0.361	0.015	0.159-0.821	0.294	0.038	0.092-0.934	1.187
TTC37	0.725	0.100	0.494-1.064	0.654	0.100	0.395-1.085	0.418
ZFYVE16	1.562	0.027	1.051-2.322	1.309	0.304	0.783-2.188	-0.290

^aIndicates that 413 TNBC samples were analyzed for RFS in univariate survival analysis; ^bindicates that 294 TNBC samples were analyzed for RFS in multivariate analysis with adjustment of pathological stage. CI, confidence interval; HR, hazard ratio; TNBC, triple-negative breast cancer; RFS, relapse-free survival.

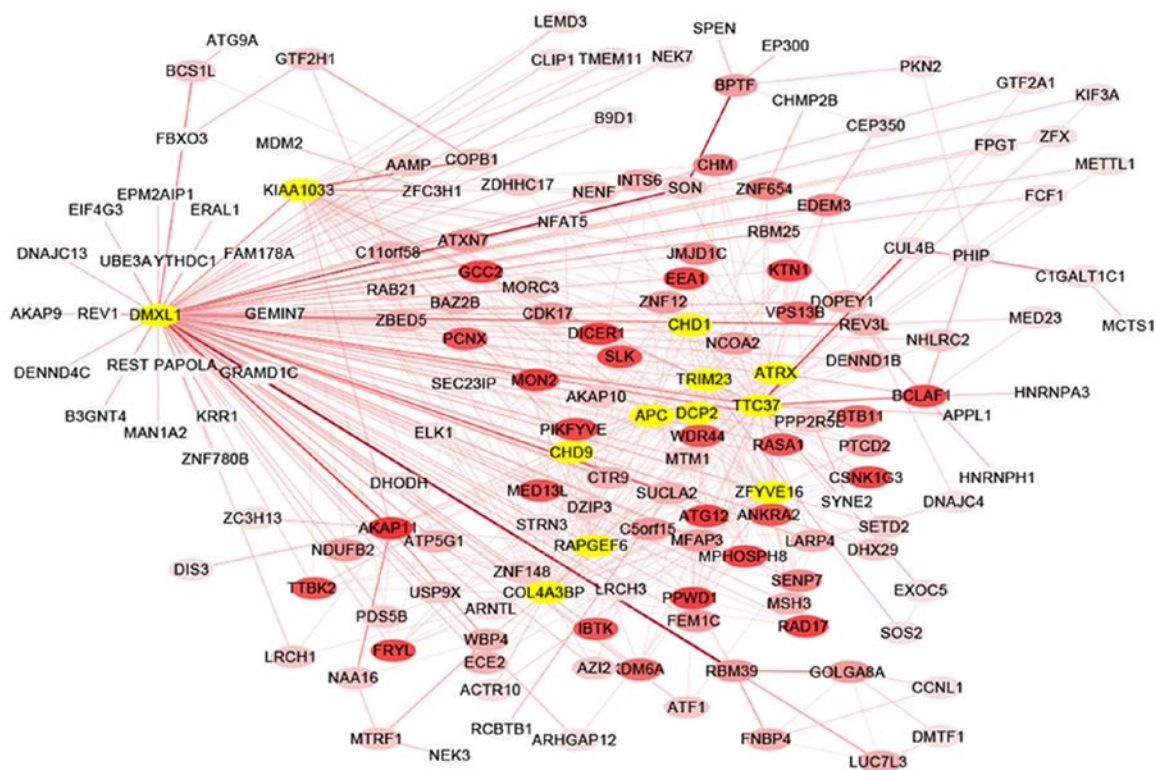


Figure 4. Visualization of the weighted gene correlation network in the red module: Cytoscape analysis identified 12 hub genes that are highlighted in bold and yellow.

localization by membrane tethering' and 'histone lysine methylation'. Following KEGG analysis, 3 KEGG pathways were significantly identified, including the Hedgehog (Hh) signaling pathway (KEGG: 04340), the gonadotropin-releasing hormone (GnRH) signaling pathway (KEGG: 04912) and the thyroid hormone signaling pathway (KEGG: 04919).

Hub gene identification in the interested module. The co-expression network of selected hub genes from all genes in the red module were constructed with Cytoscape (Fig. 4). Following the measure of the absolute value of Pearson's correlation ($MM > 0.55$), 26 genes with higher connectivity were identified. Amongst these genes, those that were connected

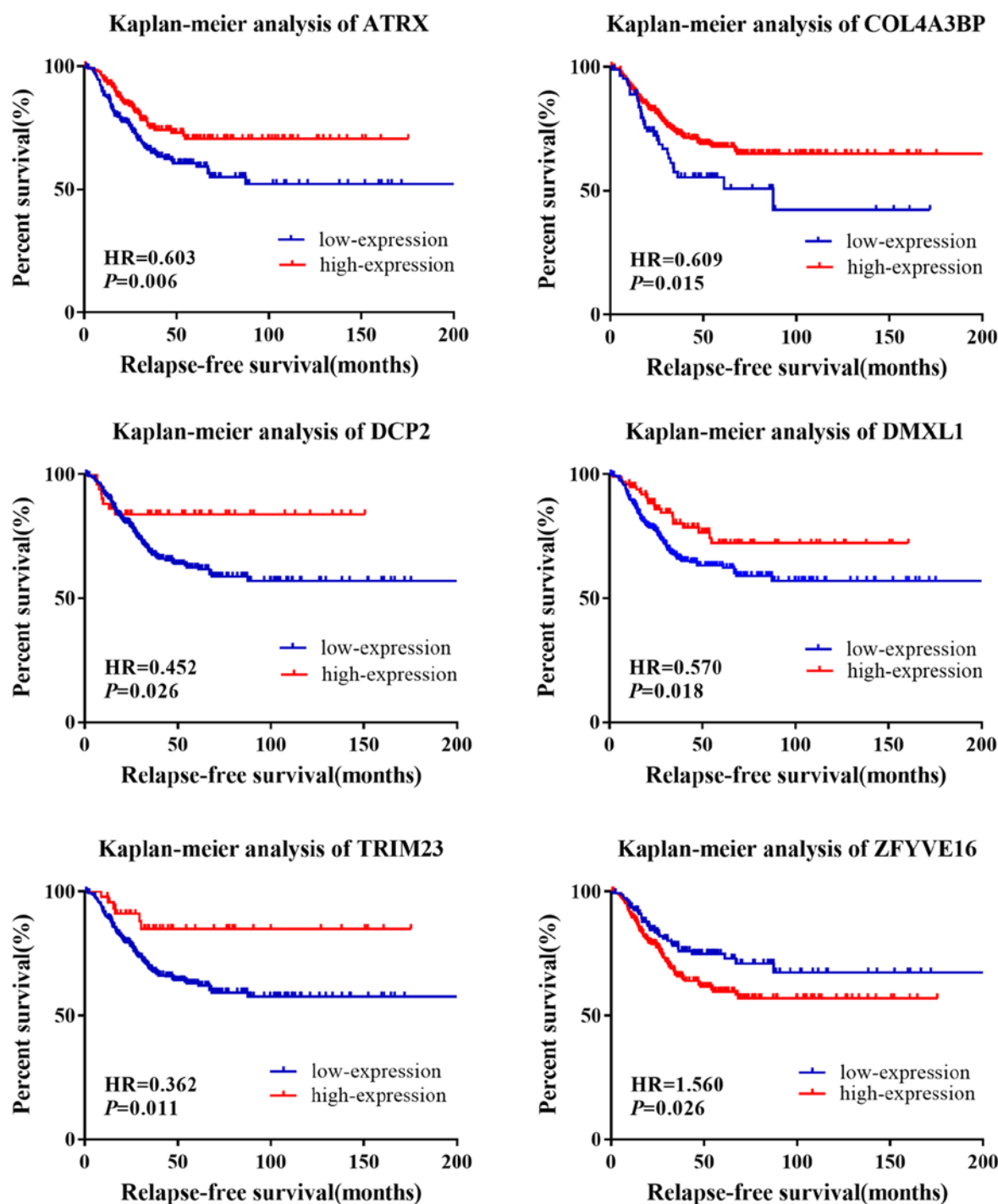


Figure 5. Association between mRNA expression of hub genes and relapse-free survival in patients with TNBC. HR, hazard ratio; TNBC, triple-negative breast cancer.

with >15 nodes were selected in the red module. A total of 12 common genes were eventually defined as hub genes and comprised WNT signaling pathway regulator (APC), α thalassemia/mental retardation syndrome X-linked (ATRX), chromodomain helicase DNA binding protein 1 (CHD1) and 9 (CHD9), collagen type IV α 3 binding protein (COL4A3BP), decapping mRNA 2 (DCP2), Dmx like 1 (DMXL1), WASH complex subunit 4 (KIAA1033), Rap guanine nucleotide exchange factor 6 (RAPGEF6), tripartite motif containing 23 (TRIM23), tetratricopeptide repeat domain 37 (TTC37) and zinc finger FYVE-type containing 16 (ZFYVE16).

The HRs and P-values were calculated for the 12 genes in the survival analysis (Table V). Following the univariate survival analysis, ATRX, COL4A3BP, DCP2, DMXL1, TRIM23 and ZFYVE16 were found to be significantly associated with RFS in patients with TNBC (Fig. 5). The pathological stage variable in the multivariate survival analysis was adjusted and the result showed that ATRX, CHD9 and TRIM23 were significantly associated with RFS in patients with TNBC. To validate these three genes, 413 TNBC samples were divided into two groups based on the occurrence history of tumor relapse in patients with TNBC.

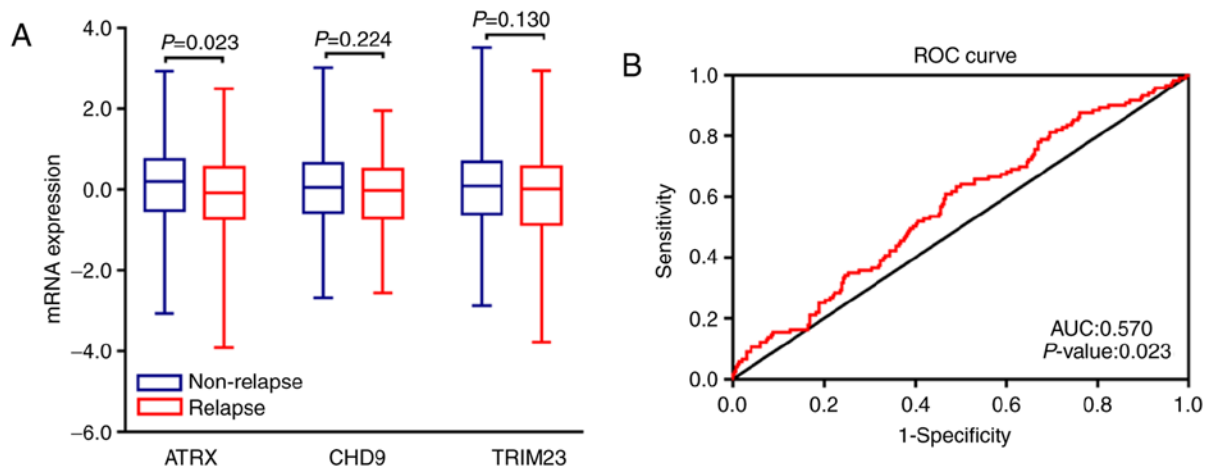


Figure 6. Comparison between non-relapse and relapse of hub genes in patients with TNBC. (A) Boxplots of mRNA expression in ATRX, CHD9 and TRIM23 between non-relapse and relapse groups of patients with TNBC: 413 TNBC samples were divided into two groups according to tumor relapse occurrence. (B) ROC curves: AUC was calculated to evaluate the diagnostic efficiency of ATRX to distinguish between relapse and non-relapse in patients with TNBC. CHD9, chromodomain helicase DNA binding protein 9; ATRX, α thalassemia/mental retardation syndrome X-linked; AUC, area under the curve; ROC, receiver operating characteristic; TNBC, triple-negative breast cancer; TRIM23, tripartite motif containing 23.

The independent sample Mann-Whitney U test was performed between two groups. The results suggested that the mRNA expression of ATRX could be used to distinguish the relapse from non-relapse in patients with TNBC (Fig. 6A). In addition, the ROC curve analysis further validated that ATRX may distinguish relapse from non-relapse in patients with TNBC ($P=0.023$; $AUC=0.570$; Fig. 6B). Patients with lower mRNA expression of ATRX presented significantly shorter overall survival time, suggesting that ATRX may be considered as a prognosis biomarker of TNBC.

Discussion

In the present study, 11 co-expression modules were constructed based on the expression levels of 5,782 genes obtained from 456 patients with TNBC using the WGCNA method. WGCNA is a powerful method used to investigate biological mechanisms and identify genes in large-scale cancer gene expression datasets. The WGCNA method uses a soft threshold to weight the correlation between genes to determine the degree of association between them, which makes the co-expression network more consistent with biological network characteristics, and it provides results with high reliability and biological significance (22,23). To the best of our knowledge, the analysis of TNBC mRNA expression using WGCNA has not yet been investigated. Results of survival analysis and WGCNA from the present study may therefore be considered as relevant for prognosis in TNBC.

With regards to the GO enrichment analysis, results demonstrated that the red module was associated with the biological processes involved in the regulation of intracellular signal activities, including the 'regulation of TOR signaling' and 'histone lysine methylation'. It has been reported that the phosphoinositide 3-kinase (PI3K)/protein kinase B/mechanistic (m)TOR pathway is essential in cell proliferation, metabolism, proliferation, differentiation, survival and angiogenesis, and in TNBC (24-27). As a key downstream component of the PI3K pathway, mTOR is a crucial regulator of tumor formation and progression. Crown *et al* (28) reported that targeting mTOR

pathway inhibits tumor growth. mTOR inhibitors are being evaluated in patients with TNBC in clinical characteristics. In addition, histone lysine methylation is associated with nucleosome remodeling and gene expression regulation and is therefore considered as the key epigenetic process (29-31). Increasing evidence suggests that aberrant regulation of gene expression via histone methylation has emerged as an important mechanism for cancer initiation and progression (30,32,33).

With regards to the KEGG pathway analysis, results demonstrated that the Hh signaling was the most significantly identified pathway. The Hh pathway serves a key role in embryonic development and regulates stem cell renewal and tissue homeostasis (34). It has been reported that dysregulated Hh signaling leads to increased aggressiveness of TNBC tumors, and that activation of Hh pathway enhances proliferation, invasion and migration of TNBC cells (35-37). Furthermore, the present study demonstrated that GnRH signaling was significantly identified in the red module. Effective therapies for patients with hormone-receptor-positive or HER2-positive breast cancer are available; however, treatments for TNBC are lacking (38). The present study demonstrated that the GnRH, also known as luteinizing hormone-releasing hormone (LHRH), and its receptor may be involved in the negative regulation of cell proliferation in malignant tumors. Previous studies have reported that LHRH receptors are expressed in a significant proportion of TNBC, and are successfully targeted by cytotoxic LHRH analogs *in vivo* (38-42). Subsequently, further clinical trials using LHRH agonists in patients with TNBC may be considered in the future.

Hub genes, defined as highly connected genes in co-expression modules (14) are considered to serve important roles in the underlying mechanisms of malignancy, for example, uveal melanoma, colon cancer and human osteosarcoma (17,43). In the present study, 12 hub genes were identified in the red module, including APC, ATRX, CHD1, CHD9, COL4A3BP, DCP2, DMXL1, KIAA1033, RAPGEF6, TRIM23, TTC37 and ZFYVE16. Notably, ATRX was significantly associated with RFS in TNBC samples, and Mann-Whitney U test

demonstrated that ATRX mRNA expression may distinguish relapse from non-relapse occurrence in patients with TNBC. It has been reported that ATRX can modulate numerous cellular processes including transcription, DNA repair and mitotic recombination (44). In addition, an alternative lengthening of telomeres (ALT), one role of which is to maintain telomere lengths, has been detected in breast cancer (45), which suggests that ATRX may be a suppressor of ALT (46,47). Furthermore, the loss of ATRX expression is associated with a poor prognosis and rapid tumor progression in melanoma, leiomyosarcomas and pancreatic neuroendocrine tumors (48-50). This may be of interest in the development of ALT-specific targets for TNBC treatment.

In conclusion, the present study attempted to explore potential molecular mechanisms in TNBC by using bioinformatics analyses. The red module identified has been associated with prognosis in TNBC, and functional analyses demonstrated that regulation of TOR signaling, histone lysine methylation and Hh signaling pathway may facilitate relapse and metastasis in patients with TNBC. In addition, the hub genes that were identified, including ATRX, may be considered as potential targets in TNBC. However, as the present study is mainly based on the analysis of five publicly available datasets, further detailed experimental research is required to confirm the results.

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Availability of data and materials

The datasets analyzed during the current study are available in The Cancer Genome Atlas (cancergenome.nih.gov/) and the Gene Expression Omnibus database (ncbi.nlm.nih.gov/gds/).

Authors' contributions

YS and JJ designed the study and presented the results for group discussions. QC and LL collected the public datasets and preprocessed the data. QC, BX and LL provided methods and finished the description of the results for the manuscript. BX and LL programmed R codes and organized the manuscript. YS and JJ were responsible for the supervision and direction of all of the work. All authors have read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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