Original Article

Identification of Fanconi anemia pathway genes as novel prognostic biomarkers and therapeutic targets for breast cancer

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Background: Globally, breast cancer is one of the most common cancers with poor prognosis. The Fanconi anemia (FA) pathway genes maintain genome stability and play important roles in human diseases, including cancer. However, the prognostic values and biological roles of FA pathway genes in breast cancer have not been clarified. This study aims to investigate the potential of FA pathway genes as prognostic biomarkers and therapeutic targets in breast cancer.

Methods: In this study, the Oncomine Cancer Microarray (ONCOMINE), University of ALabama at Birmingham Cancer (UALCAN), Kaplan-Meier plotter, cBio Cancer Genomics Portal (cBioPortal), Gene Expression Profiling Interactive Analysis (GEPIA), Gene Multi-Association Network Integration Algorithm (GeneMANIA), the Database for Annotation, Visualization and Integrated Discovery (DAVID) and Tumor Immune Estimation Resource (TIMER) databases were used to investigate the transcriptional and survival data of FA pathway genes in patients with breast cancer.

Results: Most of the FA pathway genes were found to be significantly upregulated in breast cancer tissues when compared to normal tissues. Additionally, the elevated expression levels of FA pathway genes were significantly associated with poor survival outcomes in breast cancer patients. Through functional enrichment analysis, the FA pathway genes were positively associated with cell cycle and nucleoplasm and negatively correlated with signal recognition particle-dependent co-translational protein targeting to membrane and ribosome. Furthermore, the expression levels of FA pathway genes exhibited a significant positive association with immune infiltration.

Conclusions: The FA pathway genes are potential prognostic biomarkers for breast cancer and may offer effective as well as new strategies for cancer management.

Keywords: Breast cancer; biomarker; Fanconi anemia pathway (FA pathway); prognosis; DNA repair

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Introduction

Breast cancer is the most common type of cancer among women. It accounts for 30% of all new cancer diagnoses, and is the second leading cause of cancer associated mortalities among women (1). It is comprised of a heterogeneous group of diseases with different histopathological characteristics and high genetic variability, and is therefore, characterized by different prognostic outcomes. Specific breast cancer subtypes are defined by their histopathological appearance and expression of hormone receptors, including oestrogen receptor (ER), progesterone receptor (PR) and human epidermal growth factor receptor 2 (HER2) (2). Among the genetic risk factors, pathogenic mutations in high- and moderate-risk cancer predisposition genes such as *BRCA1* and *BRCA2*, have an important impact on breast cancer development (3). Due to tumor heterogeneity, the current breast cancer biomarkers for predicting prognosis have some limitations, therefore, there is a need to establish new biomarkers as prognostic indicators to effectively enhance prognosis and individualize breast cancer treatment.

Fanconi anemia (FA) is a rare, cancer prone disease with mutations in at least 22 genes (4). In addition, protein products of these 22 FA genes along with the FA-associated proteins, interact in a common cellular pathway, known as the FA pathway, to repair DNA interstrand cross-links (ICLs). The FA pathway plays a major role in responses to replication stress by facilitating the resolution of DNA lesions arising from DNA replication (5). Moreover, amplification and gain-of-function mutations in FA genes are advantageous in cancer cells by alleviating replication stress and mitigating chemotherapeutics induced DNA damage (6). Studies have documented the key functions of FA genes in different kinds of cancers, including prostate cancer (7), colorectal cancer (8), hepatocellular carcinoma (9), bladder cancer (10), and breast cancer (11). Breast cancer susceptibility genes, *BRCA1* and *BRCA2*, also known as *FANCS* and *FANCD1*, respectively, are involved in the FA pathway. Furthermore, some of the FA pathway genes are associated with clinicopathological features in breast cancer and could serve as cancer diagnostic or prognostic biomarkers (12). However, studies regarding the expression patterns and prognostic values of all the FA pathway genes are few. Therefore, on the basis of the analysis of thousands of gene expressions or variations in copy numbers published online, this study explored expressions and mutations in FA pathway genes in patients with breast cancer to determine their expression patterns, distinct prognostic values, and potential functions of these genes in breast cancer. We present this article in accordance with the REMARK reporting checklist (available at https://tcr.amegroups.com/article/view/10.21037/tcr-24-772/rc).

Highlight box

Key findings

- This study suggests that Fanconi anemia (FA) pathway genes have potential as prognostic biomarkers and therapeutic targets in breast cancer treatment.

What is known and what is new?

- FA pathway genes play a role in DNA repair, and mutations in these genes are linked to certain cancers, including breast cancer.
- This manuscript provides evidence that the expression and mutations of FA pathway genes could serve as indicators for breast cancer prognosis. Additionally, the study identifies these genes as possible targets for therapeutic intervention, suggesting that their modulation could have clinical benefits.

What is the implication, and what should change now?

- The findings imply that FA pathway genes could be utilized to improve prognostic accuracy in breast cancer patients, aiding in personalized treatment strategies. They may also offer a new avenue for targeted therapy.

Methods

The Oncomine Cancer Microarray (ONCOMINE) database

ONCOMINE (www.oncomine.org) is a cancer microarray database that allows genome-wide expression analysis (13). In this study, the FA pathway gene transcriptional levels in different cancers were analyzed using ONCOMINE in this study. Datasets were screened with thresholds of P value (1E−4), fold change (2) and gene rank (top 10%). The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013).

University of ALabama at Birmingham Cancer (UALCAN) database

UALCAN (http://ualcan.path.uab.edu) is a web-portal used for performing in-depth analyses on The Cancer Genome Atlas (TCGA) transcriptomic data (14). It was used to assess the messenger RNA (mRNA) expression levels of FA pathway genes in breast cancer tissues and in the corresponding normal tissues.

Kaplan-Meier plotter

The prognostic values of FA pathway genes in breast cancer were evaluated using the Kaplan-Meier Plotter (www.kmplot.com). This online platform can be used to assess the significance of the expression levels of various genes on clinical outcomes in cancer patients (15). Furthermore, the platform was used to analyze the associations between the expression levels of FA pathway genes and clinicopathological features in breast cancer.

cBio Cancer Genomics Portal (cBioPortal) database

The cBioPortal for Cancer Genomics (http://cbioportal.org) is a comprehensive web resource that can visualize and analyze multidimensional cancer genomic data (16). Therefore, data from this platform was used to analyze changes in the frequency of FA pathway genes in breast cancer.

Gene Expression Profiling Interactive Analysis (GEPIA) database

GEPIA (http://gepia.cancer-pku.cn/) is an interactive web application for gene expression analysis. It is based on 9,736 tumor and 8,587 normal tissue samples from TCGA and the Genotype-Tissue Expression (GTEx) databases (17). Thus, it was used to assess the correlations between the expression levels of FA pathway genes in breast cancer.

Gene Multi-Association Network Integration Algorithm (GeneMANIA) database

GeneMANIA (http://www.genemania.org) is a web interface for the identification of related genes from many large, publicly available biological datasets (18). In this study, the relationship between FA pathway genes and their interactive genes was analyzed using this database.

The Database for Annotation, Visualization and Integrated Discovery (DAVID)

DAVID (http://david.abcc.ncifcrf.gov) is an annotation, visualization and integrated discovery database that is able to extract biological features associated with specific genes (19). Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of FA pathway genes and their closely associated genes in breast cancer were performed by DAVID and visualized using R language.

Tumor Immune Estimation Resource (TIMER) database

TIMER (cistrome.shinyapps.io/timer) is a web interface for comprehensive molecular characterization of tumor-immune interactions (20). The expression level of FA pathway genes in breast cancer and their correlation with tumor purity and infiltrating immune cells such as B cells, $CD8^+$ T cells, $CD4^+$ T cells, macrophages, neutrophils and dendritic cells were assessed using TIMER.

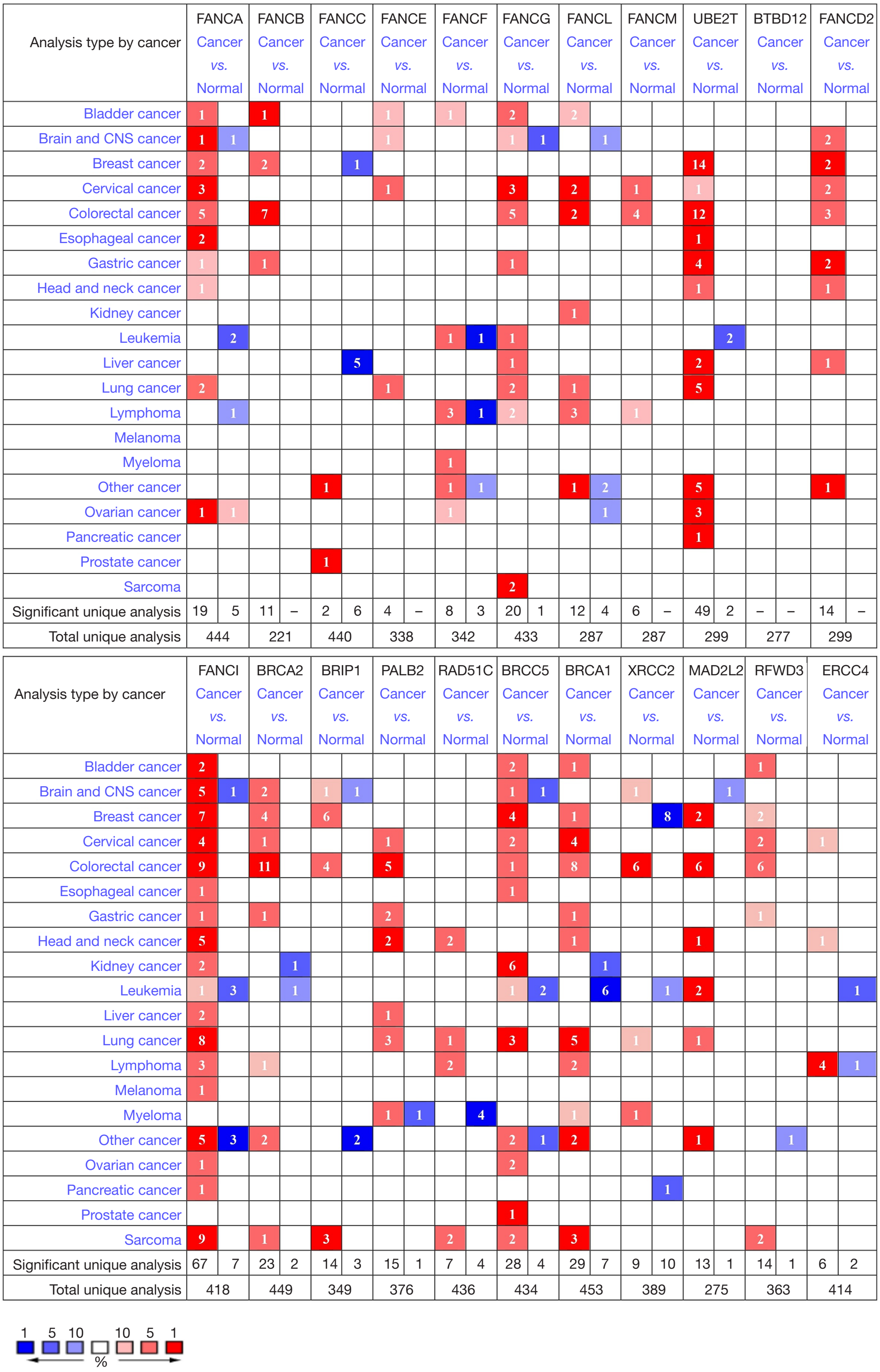
Statistical analysis

The statistical analysis was performed using R (version 4.2.3) and SPSS (version 25.0). Descriptive statistics for continuous data were presented as mean ± standard deviation (SD). For comparing two groups or multiple groups, independent *t*-tests or one-way analysis of variance (ANOVA) were applied for normally distributed data. For data that did not meet the assumption of normality, the Mann-Whitney *U* test or Kruskal-Wallis test was used. Survival analysis was performed using the Kaplan-Meier method, and differences between survival curves were evaluated using the log-rank test. Correlation analysis was conducted to assess the strength and direction of relationships between variables using Pearson correlation coefficients, depending on the data distribution. Hazard ratios and their 95% confidence intervals were calculated through Cox proportional hazards regression analysis to identify independent risk factors. All statistical tests were two-tailed, with a significance level set at $P<0.05$.

Results

mRNA expression levels of FA pathway genes in breast cancer

Based on the ONCOMINE data, the transcriptional levels of various FA pathway genes were found to be elevated in various types of cancers, such as colorectal cancer, cervical cancer and breast cancer (*Figure 1*). We further compared the mRNA expression levels of FA pathway genes in breast cancer and their corresponding normal tissues. Results from the UALCAN database revealed that the genes were significantly upregulated in breast cancer compared to their corresponding normal tissues, except for *FANCE* and *FANCM* which were downregulated in tumors (*Figure 2*).

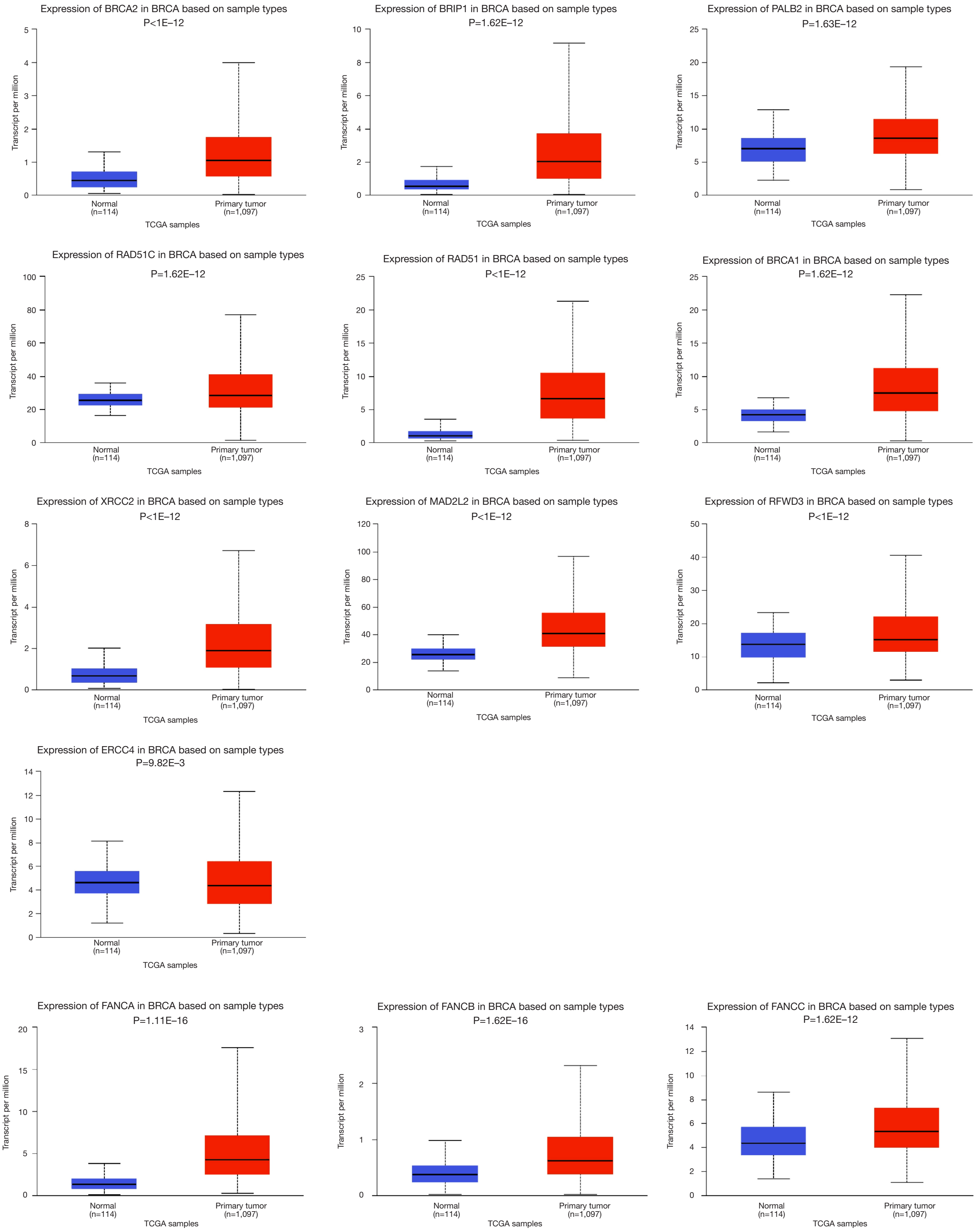


Analysis type by cancer	FANCA Cancer vs. Normal		FANCB Cancer vs. Normal		FANCC Cancer vs. Normal		FANCE Cancer vs. Normal		FANCF Cancer vs. Normal		FANCG Cancer vs. Normal		FANCL Cancer vs. Normal		FANCM Cancer vs. Normal		UBE2T Cancer vs. Normal		BTBD12 Cancer vs. Normal		FANCD2 Cancer vs. Normal	
Bladder cancer	1		1				1		1		2		2									
Brain and CNS cancer	1	1					1				1	1		1							2	
Breast cancer	2		2			1											14				2	
Cervical cancer	3						1				3		2		1		1				2	
Colorectal cancer	5		7								5		2		4		12				3	
Esophageal cancer	2																1					
Gastric cancer	1		1								1						4				2	
Head and neck cancer	1																1				1	
Kidney cancer													1									
Leukemia		2							1	1	1							2				
Liver cancer						5					1						2				1	
Lung cancer	2						1				2		1				5					
Lymphoma		1							3	1	2		3		1							
Melanoma																						
Myeloma									1													
Other cancer					1				1	1			1	2			5				1	
Ovarian cancer	1	1							1					1			3					
Pancreatic cancer																	1					
Prostate cancer					1																	
Sarcoma											2											
Significant unique analysis	19	5	11	–	2	6	4	–	8	3	20	1	12	4	6	–	49	2	–	–	14	–
Total unique analysis	444		221		440		338		342		433		287		287		299		277		299	

Analysis type by cancer	FANCI Cancer vs. Normal		BRCA2 Cancer vs. Normal		BRIP1 Cancer vs. Normal		PALB2 Cancer vs. Normal		RAD51C Cancer vs. Normal		BRCC5 Cancer vs. Normal		BRCA1 Cancer vs. Normal		XRCC2 Cancer vs. Normal		MAD2L2 Cancer vs. Normal		RFWD3 Cancer vs. Normal		ERCC4 Cancer vs. Normal	
Bladder cancer	2										2		1						1			
Brain and CNS cancer	5	1	2		1	1					1	1			1			1				
Breast cancer	7		4		6						4		1			8	2		2			
Cervical cancer	4		1				1				2		4						2		1	
Colorectal cancer	9		11		4		5				1		8		6		6		6			
Esophageal cancer	1										1											
Gastric cancer	1		1				2						1						1			
Head and neck cancer	5						2		2				1				1				1	
Kidney cancer	2			1							6			1								
Leukemia	1	3		1							1	2		6		1	2					1
Liver cancer	2						1															
Lung cancer	8						3		1		3		5		1		1					
Lymphoma	3		1						2				2								4	1
Melanoma	1																					
Myeloma							1	1		4			1		1							
Other cancer	5	3	2			2					2	1	2				1			1		
Ovarian cancer	1										2											
Pancreatic cancer	1															1						
Prostate cancer											1											
Sarcoma	9		1		3				2		2		3						2			
Significant unique analysis	67	7	23	2	14	3	15	1	7	4	28	4	29	7	9	10	13	1	14	1	6	2
Total unique analysis	418		449		349		376		436		434		453		389		275		363		414	

Cell color is determined by the best gene rank percentile for the analyses within the cell.

Figure 1 The transcription levels of FA pathway genes in different types of cancers using ONCOMINE database. FA, Fanconi anemia; ONCOMINE, The Oncomine Cancer Microarray; CNS, central nervous system.


Expression of BRCA2 in BRCA based on sample types
P<1E−12
Expression of BRIP1 in BRCA based on sample types
P=1.62E−12
Expression of PALB2 in BRCA based on sample types
P=1.63E−12
Expression of RAD51C in BRCA based on sample types
P=1.62E−12
Expression of RAD51 in BRCA based on sample types
P<1E−12
Expression of BRCA1 in BRCA based on sample types
P=1.62E−12
Expression of XRCC2 in BRCA based on sample types
P<1E−12
Expression of MAD2L2 in BRCA based on sample types
P<1E−12
Expression of RFWD3 in BRCA based on sample types
P<1E−12
Expression of ERCC4 in BRCA based on sample types
P=9.82E−3
Expression of FANCA in BRCA based on sample types
P=1.11E−16
Expression of FANCB in BRCA based on sample types
P=1.62E−16
Expression of FANCC in BRCA based on sample types
P=1.62E−12
Transcript per million
Normal
(n=114)
Primary tumor
(n=1,097)
TCGA samples

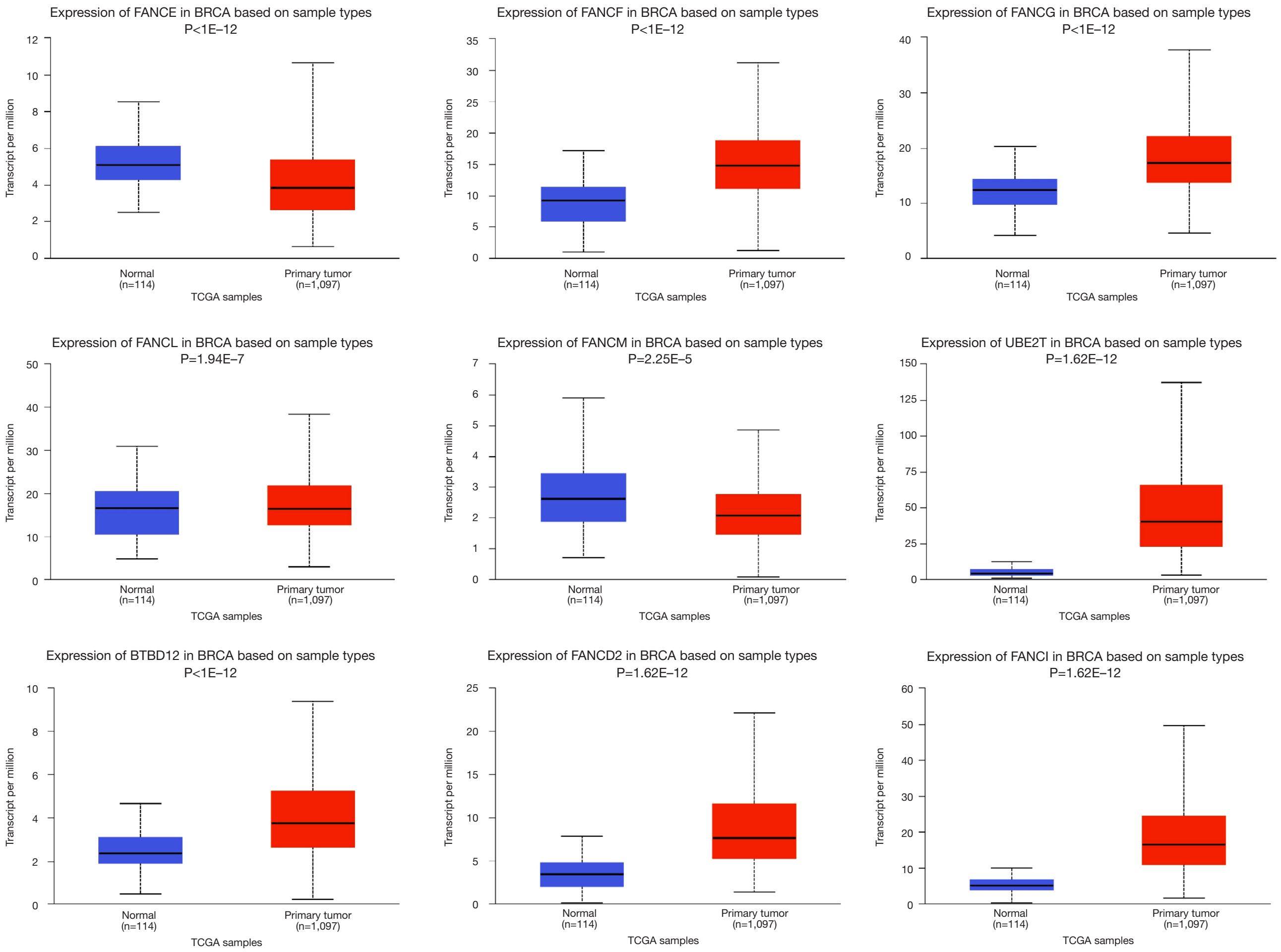


Figure 2 The mRNA expression of FA pathway genes varied in primary tumor and in corresponding normal tissues in patients with breast cancer using UALCAN database. FA, Fanconi anemia; UALCAN, University of ALabama at Birmingham Cancer; TCGA, The Cancer Genome Atlas.

The prognostic value of FA pathway genes in breast cancer

The Kaplan-Meier plotter was used to determine the potential prognostic value of FA pathway genes in breast cancer (*Figure 3*). About half of the genes that were highly expressed were shown to exhibit a significant positive correlation with worse recurrence-free survival (RFS) of breast cancer patients. These genes include: *FANCB*, *FANCG*, *FANCL*, *UBE2T* (*FANCT*), *FANCI*, *BRIP1* (*FANCJ*), *BRCC5* (*FANCR*), *BRCA1* (*FANCS*), *MAD2L2* (*FANCV*) and *RFWD3* (*FANCW*). In contrast, elevated mRNA expression levels of *FANCC*, *SLX4* (*FANCP*), *PALB2* (*FANCN*), *XRCC2* (*FANCU*) and *ERCC4* (*FANCQ*) were associated with favorable RFS. The other genes did not exhibit a significant correlation with the RFS of breast cancer patients.

We further used the Cox proportional hazards regression analysis to investigate the correlations between the expression levels of FA pathway genes and patients' overall survival (OS), distant metastasis-free survival (DMFS) and post progression survival (PPS). The result forest plots are presented in *Figure 4*.

Association between the prognostic value of FA pathway genes in breast cancer with different clinicopathological features

The relationship between FA pathway genes and different clinicopathological features was investigated to elucidate on the roles of these genes in breast cancer prognosis.

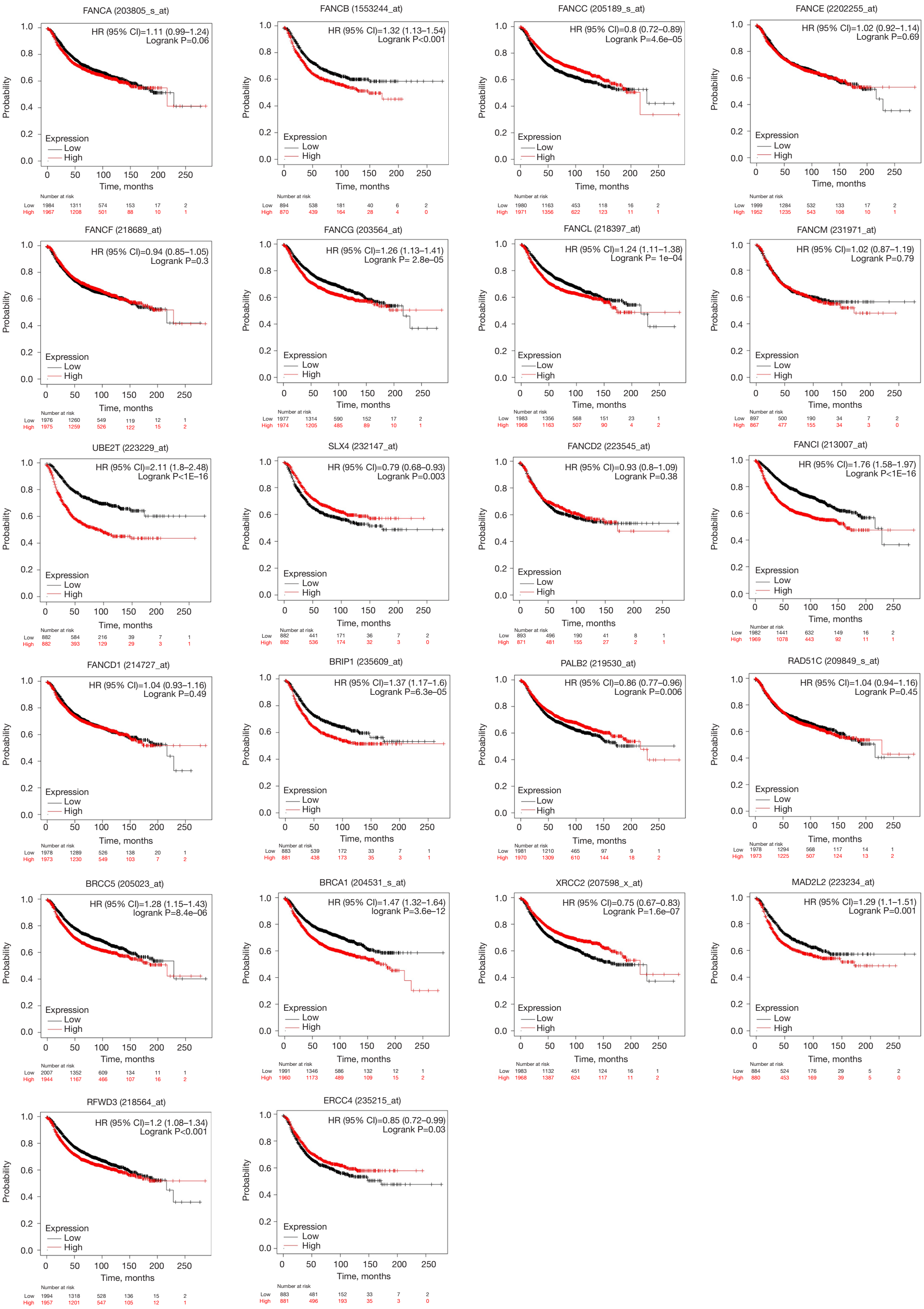

FANCA (203805_s_at)
FANCB (1553244_at)
FANCC (205189_s_at)
FANCE (2202255_at)
FANCF (218689_at)
FANCG (203564_at)
FANCL (218397_at)
FANCM (231971_at)
UBE2T (223229_at)
SLX4 (232147_at)
FANCD2 (223545_at)
FANCI (213007_at)
FANCD1 (214727_at)
BRIP1 (235609_at)
PALB2 (219530_at)
RAD51C (209849_s_at)
BRCC5 (205023_at)
BRCA1 (204531_s_at)
XRCC2 (207598_x_at)
MAD2L2 (223234_at)
RFWD3 (218564_at)
ERCC4 (235215_at)

Figure 3 Survival analysis of FA pathway genes in patients with breast cancer using Kaplan-Meier plotter. FA, Fanconi anemia; HR, hazard ratio; CI, confidence interval.

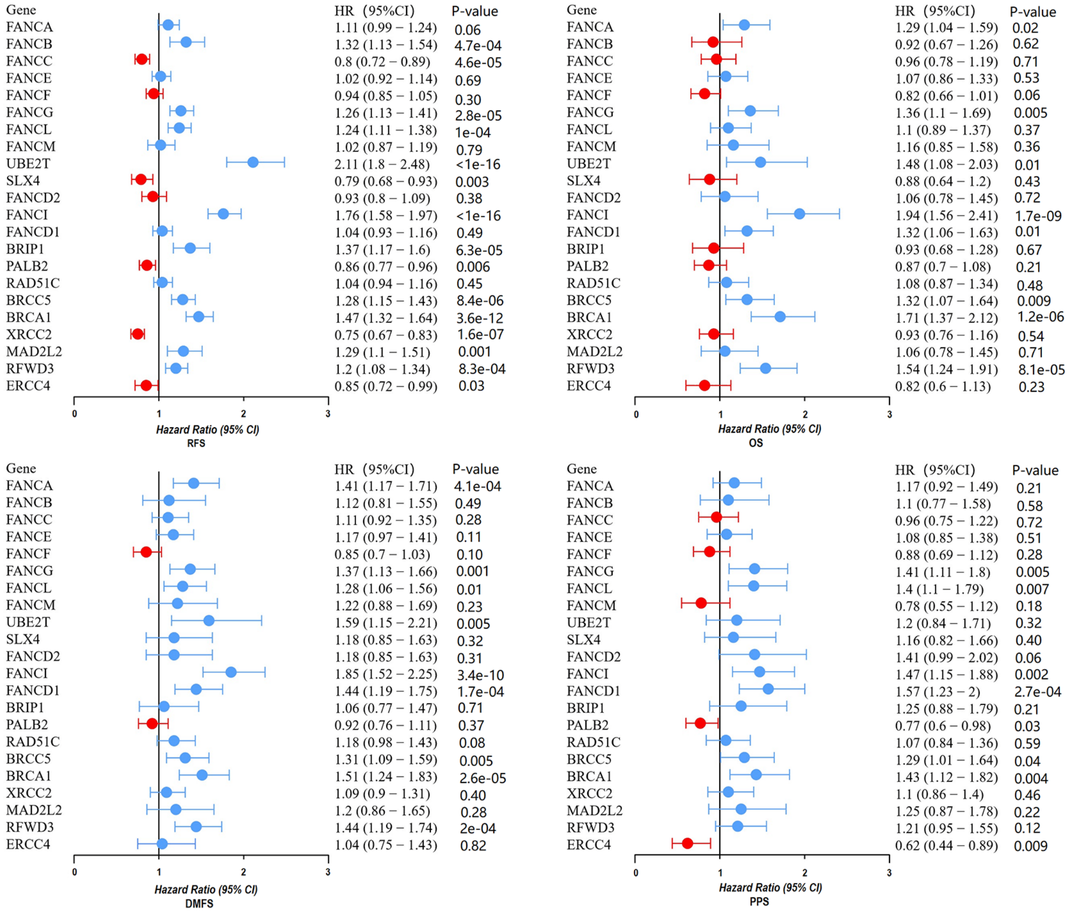


Figure 4 The correlation between expression of FA pathway genes and RFS, OS, DMFS, and PPS of patients with breast cancer. FA, Fanconi anemia; RFS, recurrence-free survival; OS, overall survival; DMFS, distant metastasis free survival; PPS, post progression survival; HR, hazard ratio; CI, confidence interval.

The clinicopathological features included cancer grade, ER status, PR status, and HER2 status (Table S1). It was revealed that elevated mRNA expression levels of *FANCI* were associated with poor RFS in grade 1 breast cancer. Additionally, elevated mRNA expression levels of *FANCA*, *FANCE*, *FANCL*, *FANCI*, *BRCC5* and *RFWD3* were correlated to worse RFS in grade 2 breast cancer. However, *FANCF* and *PALB2* were associated with better RFS in grade 2 breast cancer. Moreover, low mRNA expression levels of *FANCI* and *BRCA1* were associated with better RFS in grade 3 breast cancer, while *BRIP1* and *RAD51C* were identified as good prognostic factors for grade 3 breast cancer. These results are presented in *Table 1*.

Moreover, *BRCA1* was found to be a promising marker for unfavorable prognosis in both ER positive and negative patients, while *FANCA*, *FANCB*, *FANCE*, *FANCG*, *FANCL*, *UBE2T*, *FANCI*, *BRIP1*, *RAD51C*, *BRCC5* and *RFWD3* were significantly associated with unfavorable RFS in ER positive patients. However, *FANCC* and *FANCD1* were associated with favorable RFS in ER negative patients (*Table 2*, Table S2).

Furthermore, elevated mRNA expression levels of *FANCA*, *FANCG*, *UBE2T*, *FANCI*, *BRIP1*, *RAD51C*, *BRCC5* and *BRCA1* were shown to contribute to unfavorable RFS in PR positive patients while elevated expression levels of *SLX4* and *ERCC4* were associated with shorter RFS in PR negative patients (*Table 3*, Table S2).

PALB2 exhibited a significant association with unfavorable RFS in HER2 positive patients. However,

Table 1 The association between FA pathway genes expression and breast cancer grade of patients

Gene	Grade	Cases	HR (95% CI)	P value
FANCA	1	345	1.62 (0.95–2.77)	0.07
	2	901	1.41 (1.11–1.79)	0.005**
	3	903	1.04 (0.84–1.29)	0.72
FANCB	1	108	1.13 (0.39–3.22)	0.82
	2	227	1.17 (0.71–1.95)	0.54
	3	444	0.9 (0.66–1.22)	0.49
FANCC	1	345	1.16 (0.69–1.95)	0.58
	2	901	0.93 (0.73–1.19)	0.56
	3	903	0.94 (0.75–1.17)	0.57
FANCE	1	345	1.32 (0.78–2.23)	0.30
	2	901	1.3 (1.02–1.65)	0.03*
	3	903	0.98 (0.79–1.22)	0.84
FANCF	1	345	0.73 (0.43–1.22)	0.23
	2	901	0.75 (0.59–0.96)	0.02*
	3	903	0.93 (0.75–1.16)	0.52
FANCG	1	345	1.66 (0.97–2.82)	0.059
	2	901	1.19 (0.93–1.51)	0.16
	3	903	1.19 (0.96–1.48)	0.11
FANCL	1	345	1.2 (0.71–2.03)	0.49
	2	901	1.35 (1.06–1.72)	0.01*
	3	903	1.16 (0.93–1.44)	0.19
FANCM	1	108	1.34 (0.46–3.87)	0.59
	2	227	1.49 (0.9–2.49)	0.12
	3	444	1.1 (0.81–1.5)	0.54
UBE2T (FANCT)	1	108	1.33 (0.46–3.85)	0.59
	2	227	1.23 (0.74–2.04)	0.43
	3	444	0.83 (0.61–1.14)	0.24
SLX4 (FANCP)	1	108	1.29 (0.45–3.71)	0.64
	2	227	1.19 (0.71–1.99)	0.51
	3	444	1.01 (0.74–1.37)	0.97
FANCD2	1	108	1.09 (0.38–3.11)	0.87
	2	227	0.72 (0.43–1.2)	0.21
	3	444	0.89 (0.65–1.22)	0.47
FANCI	1	345	1.81 (1.06–3.1)	0.02*
	2	901	1.72 (1.35–2.2)	1e–05***
	3	903	1.31 (1.05–1.62)	0.01*

Table 1 *(continued)*

Table 1 *(continued)*

Gene	Grade	Cases	HR (95% CI)	P value
FANCD1	1	345	1.15 (0.68–1.93)	0.61
	2	901	1.22 (0.96–1.55)	0.11
	3	903	0.96 (0.77–1.2)	0.74
BRIP1 (FANCJ)	1	345	0.94 (0.33–2.69)	0.91
	2	901	1.16 (0.7–1.92)	0.57
	3	903	0.72 (0.53–0.99)	0.041*
PALB2 (FANCN)	1	345	1.21 (0.72–2.03)	0.47
	2	901	0.78 (0.61–0.99)	0.041*
	3	903	1.13 (0.91–1.4)	0.28
RAD51C (FANCO)	1	345	0.95 (0.57–1.59)	0.84
	2	901	1.04 (0.82–1.32)	0.74
	3	903	0.8 (0.64–0.99)	0.042*
BRCC5 (FANCR)	1	345	1.1 (0.65–1.84)	0.72
	2	901	1.36 (1.07–1.73)	0.01*
	3	903	1.1 (0.89–1.37)	0.37
BRCA1 (FANCS)	1	345	1.46 (0.86–2.47)	0.16
	2	901	1.21 (0.95–1.54)	0.11
	3	903	1.5 (1.2–1.87)	3e–04***
XRCC2 (FANCU)	1	345	1.5 (0.88–2.56)	0.13
	2	901	1.1 (0.87–1.4)	0.41
	3	903	1.1 (0.89–1.37)	0.38
MAD2L2 (FANCV)	1	108	0.78 (0.27–2.26)	0.65
	2	227	1.47 (0.88–2.45)	0.14
	3	444	0.85 (0.62–1.16)	0.30
RFWD3 (FANCW)	1	345	1.67 (0.97–2.85)	0.06
	2	901	1.5 (1.18–1.91)	1e–04***
	3	903	1.23 (0.99–1.53)	0.06
ERCC4 (FANCQ)	1	345	0.66 (0.23–1.9)	0.44
	2	901	0.85 (0.51–1.42)	0.54
	3	903	1.05 (0.77–1.43)	0.77

*, P<0.05; **, P<0.01; ***, P<0.001. FA, Fanconi anemia; HR, hazard ratio; CI, confidence interval.

FANCA, *FANCB*, *FANCC*, *FANCF*, *FANCG*, *UBE2T*, *SLX4*, *FANCI*, *BRIP1*, *RAD51C*, *BRCA1* and *ERCC4* were associated with poor RFS while *FANCF* was associated with better RFS in HER2 negative patients. Nevertheless, *FANCD2* was a good prognostic factor in both HER2 positive and negative patients (*Table 4*, Table S2).

Based on the TP53 status, elevated expression levels of *UBE2T* were strongly associated with worse RFS while *FANCL*, *FAND2* and *RAD51C* were correlated with better RFS in TP53-mutated patients. In patients with wild type TP53, *FANCA*, *FANCI*, *BRCA1* and *RFWD3* were associated with unfavorable RFS (*Table 5*, Table S2).

Table 2 The association between FA pathway genes expression and ER status of patients with breast cancer

Gene	ER status	Cases	HR (95% CI)	P value
FANCA	Positive	2,061	1.41 (1.19–1.66)	4.3e–05***
	Negative	801	0.95 (0.76–1.19)	0.67
FANCB	Positive	762	1.61 (1.2–2.15)	0.001**
	Negative	347	0.82 (0.59–1.14)	0.23
FANCC	Positive	2,061	1.08 (0.92–1.28)	0.33
	Negative	801	0.75 (0.6–0.94)	0.01*
FANCE	Positive	2,061	1.19 (1.01–1.4)	0.04*
	Negative	801	1.02 (0.81–1.27)	0.88
FANCG	Positive	2,061	1.39 (1.18–1.64)	8.5e–05***
	Negative	801	1.02 (0.81–1.28)	0.86
FANCL	Positive	2,061	1.18 (1–1.39)	0.049*
	Negative	801	1.16 (0.93–1.46)	0.19
UBE2T (FANCT)	Positive	762	1.89 (1.4–2.55)	2.4e–05***
	Negative	347	0.89 (0.64–1.24)	0.50
FANCI	Positive	2061	1.86 (1.57–2.2)	1.5e–13***
	Negative	801	1.12 (0.89–1.4)	0.32
FANCD1	Positive	2,061	1.16 (0.98–1.36)	0.08
	Negative	801	0.75 (0.6–0.95)	0.01*
BRIP1 (FANCJ)	Positive	2,061	1.67 (1.24–2.24)	6.3e–04***
	Negative	801	0.91 (0.65–1.26)	0.56
RAD51C(FANCO)	Positive	2,061	1.32 (1.12–1.56)	8.3e–04***
	Negative	801	0.85 (0.68–1.07)	0.17
BRCC5 (FANCR)	Positive	2,061	1.33 (1.13–1.57)	6.6e–04***
	Negative	801	1.06 (0.85–1.33)	0.62
BRCA1 (FANCS)	Positive	2,061	1.6 (1.36–1.89)	1.9e–08***
	Negative	801	1.53 (1.22–1.92)	2.4e–04***
RFWD3 (FANCW)	Positive	2,061	1.32 (1.12–1.56)	8.2e–04***
	Negative	801	1.18 (0.94–1.47)	0.16

*, $P<0.05$; **, $P<0.01$; ***, $P<0.001$. FA, Fanconi anemia; ER, estrogen receptor; HR, hazard ratio; CI, confidence interval.

Genetic alterations and interaction analysis of FA pathway genes in breast cancer

We further performed a comprehensive analysis of the molecular characteristics of genes in the FA pathway. The frequency of genetic alterations in these genes among breast cancer patients was determined using the cBioPortal database. It was found that mRNA deregulation was one of the most important single factors for genetic alterations in different kinds of breast cancers (*Figure 5A*). Mutation and amplification were the most common alterations in these samples. In addition, OncoPrint was used to show a visual summary of alterations in the FA pathway genes across a set of breast cancer samples (*Figure 5B*). Moreover, expression correlations were determined using GEPIA to

Table 3 The association between FA pathway genes expression and PR status of patients with breast cancer

Gene	PR status	Cases	HR (95% CI)	P value
FANCA	Positive	589	1.5 (1.06–2.13)	0.02*
	Negative	549	1.08 (0.81–1.45)	0.59
FANCG	Positive	589	1.78 (1.24–2.54)	0.001**
	Negative	549	1.19 (0.89–1.59)	0.24
UBE2T (FANCT)	Positive	489	1.71 (1.16–2.52)	0.006**
	Negative	372	1.05 (0.74–1.51)	0.77
SLX4 (FANCP)	Positive	489	1.13 (0.77–1.65)	0.52
	Negative	372	1.77 (1.23–2.55)	0.002**
FANCI	Positive	589	1.83 (1.28–2.61)	7.4e–04***
	Negative	549	1.13 (0.85–1.51)	0.41
BRIP1 (FANCJ)	Positive	589	1.97 (1.33–2.93)	5.5e–04***
	Negative	549	0.94 (0.66–1.35)	0.75
RAD51C (FANCO)	Positive	589	1.49 (1.05–2.11)	0.02*
	Negative	549	1.02 (0.76–1.37)	0.88
BRCC5 (FANCR)	Positive	589	1.44 (1.01–2.04)	0.041*
	Negative	549	1.32 (0.98–1.76)	0.06
BRCA1 (FANCS)	Positive	589	1.7 (1.19–2.43)	0.003**
	Negative	549	1.27 (0.95–1.7)	0.11
ERCC4 (FANCQ)	Positive	589	1.02 (0.7–1.49)	0.90
	Negative	549	1.58 (1.1–2.27)	0.01*

*, P<0.05; **, P<0.01; ***, P<0.001. FA, Fanconi anemia; PR, progesterone receptor; HR, hazard ratio; CI, confidence interval.

further define the relationships among the FA pathway genes. There was a low to high positive correlation among most FA pathway genes (Figure S1A). Additionally, a network of FA pathway genes and their functionally related genes was constructed using GeneMANIA (Figure S1B). Twenty genes were found to be closely associated with the regulatory functions of differentially expressed FA pathway genes. These genes were *FAAP24*, *FAAP100*, *RAD51B*, *XRCC3*, *RAD52*, *BARD1*, *BLM*, *RMI1*, *TOP3A*, *ATR*, *FAN1*, *APITD1*, *TOPBP1*, *USP1*, *G2E3*, *RAD51D*, *RPA1*, *RPA2*, *ERCC1* and *ATRIP*.

Functional enrichment analysis of FA-related genes in breast cancer

We used UALCAN to isolate the top 50 genes that were positively and negatively correlated with individual genes of the FA pathway in breast cancer. This was done to explore the underlying mechanisms of FA pathway genes in cancer. In addition, DAVID was used to perform GO and KEGG pathway enrichment analysis of the FA-associated genes in breast cancer. Figure S2 shows the most highly enriched GO items that were positively and negatively correlated with FA pathway genes in breast cancer. Among the positively correlated GO items, the most enriched biological process (BP) term was cell division, the most enriched cellular component (CC) term was nucleoplasm, and the most enriched molecular function (MF) term was protein binding (Figure S2A). In the negatively correlated GO items, the FA-associated genes were shown to participate in various functions, especially signal recognition particle (SRP)-dependent co-translational protein targeting to membrane as well as ribosome and structural constituent of ribosome (Figure S2B). Moreover, KEGG pathway

Table 4 The association between FA pathway genes expression and HER2 status of patients with breast cancer

Gene	HER2 status	Cases	HR (95% CI)	P value
FANCA	Positive	252	1.02 (0.66–1.57)	0.95
	Negative	800	1.35 (1.04–1.75)	0.02*
FANCB	Positive	150	1.01 (0.59–1.73)	0.97
	Negative	635	1.41 (1.05–1.9)	0.02*
FANCC	Positive	252	0.83 (0.54–1.29)	0.41
	Negative	800	1.37 (1.05–1.78)	0.02*
FANCF	Positive	252	0.89 (0.58–1.38)	0.60
	Negative	800	0.76 (0.58–0.99)	0.04*
FANCG	Positive	252	1.42 (0.91–2.19)	0.12
	Negative	800	1.32 (1.01–1.71)	0.04*
UBE2T (FANCT)	Positive	150	0.61 (0.35–1.06)	0.08
	Negative	635	2.28 (1.67–3.12)	9.7e–08***
SLX4 (FANCP)	Positive	150	1.45 (0.84–2.51)	0.18
	Negative	635	1.45 (1.07–1.96)	0.02*
FANCD2	Positive	150	0.51 (0.29–0.9)	0.02*
	Negative	635	1.39 (1.03–1.87)	0.03*
FANCI	Positive	252	1.11 (0.72–1.71)	0.64
	Negative	800	1.79 (1.37–2.34)	1.5e–05***
BRIP1 (FANCJ)	Positive	252	0.61 (0.35–1.05)	0.07
	Negative	800	1.98 (1.46–2.69)	8.4e–06***
PALB2 (FANCN)	Positive	252	1.63 (1.05–2.53)	0.03*
	Negative	800	1.2 (0.92–1.56)	0.17
RAD51C (FANCO)	Positive	252	0.74 (0.48–1.14)	0.17
	Negative	800	1.44 (1.1–1.87)	0.007**
BRCA1 (FANCS)	Positive	252	1.13 (0.73–1.75)	0.58
	Negative	800	1.73 (1.32–2.26)	5.9e–05***
ERCC4 (FANCQ)	Positive	252	0.81 (0.47–1.4)	0.46
	Negative	800	1.36 (1.01–1.83)	0.044*

*, P<0.05; **, P<0.01; ***, P<0.001. FA, Fanconi anemia; HER2, human epidermal growth receptor 2; HR, hazard ratio; CI, confidence interval.

enrichment analysis revealed that the positively correlated pathways were mainly involved in cell cycle, oocyte meiosis and viral carcinogenesis (Figure S2C). Besides, ribosomes, along with their metabolic pathways, were the most enriched pathways that were found to be negatively correlated with FA pathway genes in breast cancer (Figure S2D).

Correlation between immune infiltration and FA pathway genes in patients with breast cancer

Given that inflammatory responses and infiltrating immune cells can affect breast cancer prognosis, we evaluated the association between differentially expressed FA pathway

Table 5 The association between FA pathway genes expression and TP53 status of patients with breast cancer

Gene	TP53 status	Cases	HR (95% CI)	P value
FANCA	Mutated	188	0.87 (0.54–1.41)	0.58
	Wild type	273	1.84 (1.19–2.83)	0.005**
FANCL	Mutated	188	0.62 (0.38–1)	0.049*
	Wild type	273	1.09 (0.72–1.66)	0.68
UBE2T (FANCT)	Mutated	132	2.04 (1.12–3.73)	0.02*
	Wild type	82	1.45 (0.62–3.4)	0.39
FANCD2	Mutated	132	0.54 (0.3–0.99)	0.043*
	Wild type	82	1.58 (0.67–3.7)	0.29
FANCI	Mutated	188	0.88 (0.55–1.41)	0.60
	Wild type	273	1.75 (1.14–2.69)	0.01*
RAD51C (FANCO)	Mutated	188	0.58 (0.36–0.95)	0.03*
	Wild type	273	1.1 (0.72–1.68)	0.64
BRCA1 (FANCS)	Mutated	188	1.09 (0.68–1.75)	0.71
	Wild type	273	1.69 (1.1–2.59)	0.02*
RFWD3 (FANCW)	Mutated	188	0.98 (0.61–1.57)	0.94
	Wild type	273	1.72 (1.12–2.65)	0.01*

*, P<0.05; **, P<0.01. FA, Fanconi anemia; HR, hazard ratio; CI, confidence interval.

genes and immune cell infiltration using the TIMER database. It was found that the mRNA expression levels of FA pathway genes were positively associated with tumor purity, while *FANCE*, *FANCM*, *BRCA2* (*FANCD1*) and *MAD2L2* (*FANCV*) had no significant correlation with the tumor purity of patients with breast cancer (*Figure 6*). Furthermore, most FA pathway genes were positively associated with immune infiltration levels of B cells, CD8$^+$ T cells, CD4$^+$ T cells, macrophages, neutrophils and dendritic cells, except for *FANCE* of macrophages, *FANCF* of dendritic cells, *FANCG* of macrophages, *FANCL* of macrophages, *UBE2T* of macrophages, *RAD51C* of CD4$^+$ T cells, *MAD2L2* of CD8$^+$ T cells and macrophages, which showed significant negative associations.

Discussion

Chemotherapy is one of the most important treatments for breast cancer after surgery. Approximately one-third of patients with breast cancer present metastases, which are the main cause of death in these patients (21). It has been documented that tumor responses to chemotherapeutic drugs are closely associated with the regulation of the DNA repair system (22). Some tumor cells can resist DNA damage drugs by activating self-DNA repair mechanisms (23). Moreover, deficiency in the proteins involved in DNA damage repair is considered a major determinant of the responses to chemotherapy in cancer cells (24). Previous study reported that the FA pathway, also referred to as the FA-BRCA pathway, can modulate tumor progression and immunotherapeutic effects (6). However, the prognostic values and biological functions of FA pathway genes in breast cancer have not been well elucidated.

DNA repair involves multiple enzymes and genes. Inactivating mutations in DNA repair components are common and often lead to certain DNA repair deficiencies. Therefore, cancer cells become hyperdependent on the remaining repair pathways for survival and proliferation (25). The FA pathway is a stepwise multiprotein complex pathway that confers cellular hypersensitivity to DNA intercalating substances, such as cisplatin, that trigger DNA ICLs (26). FA pathway activation status may serve as a clinical biomarker for cancer patients at different treatment stages. Herein, the expression levels of FA pathway genes in breast cancer were

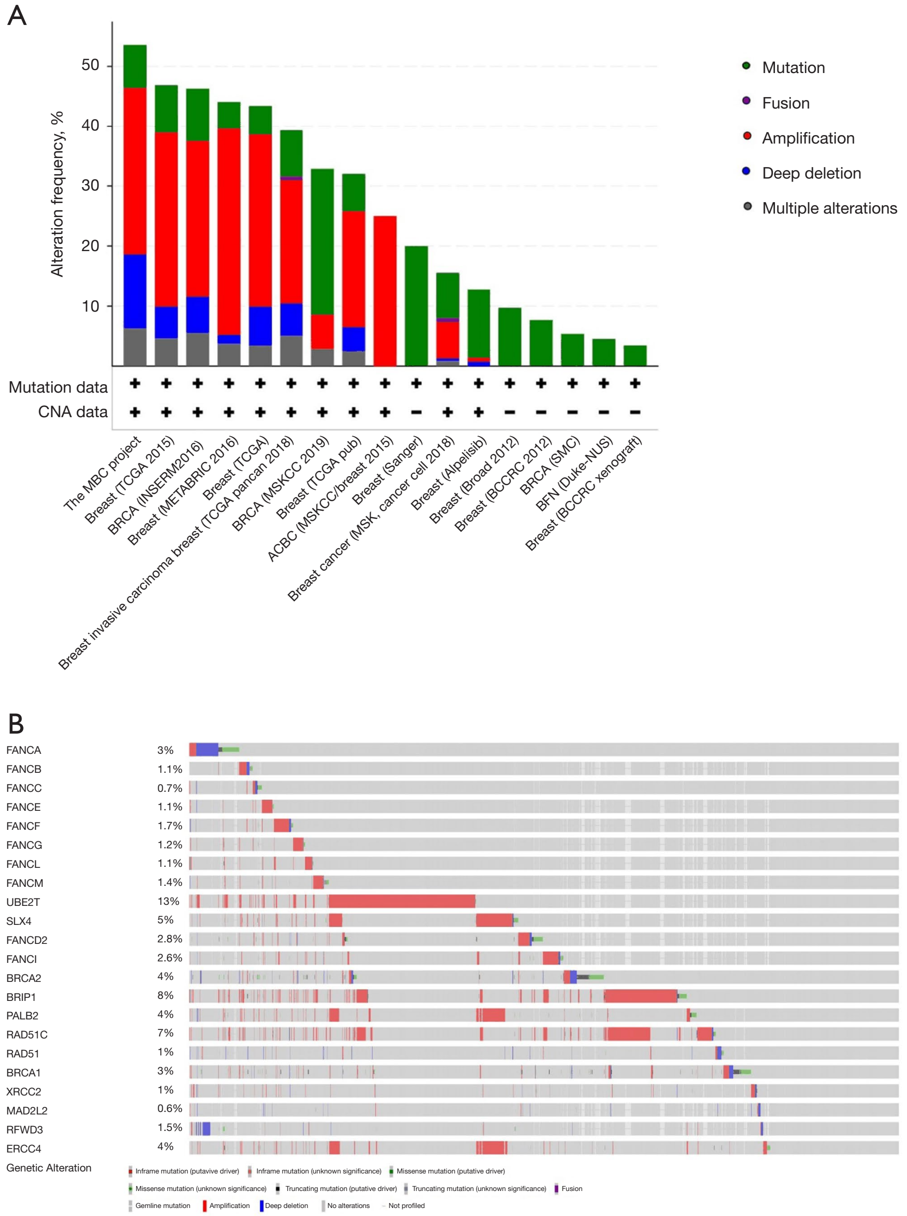
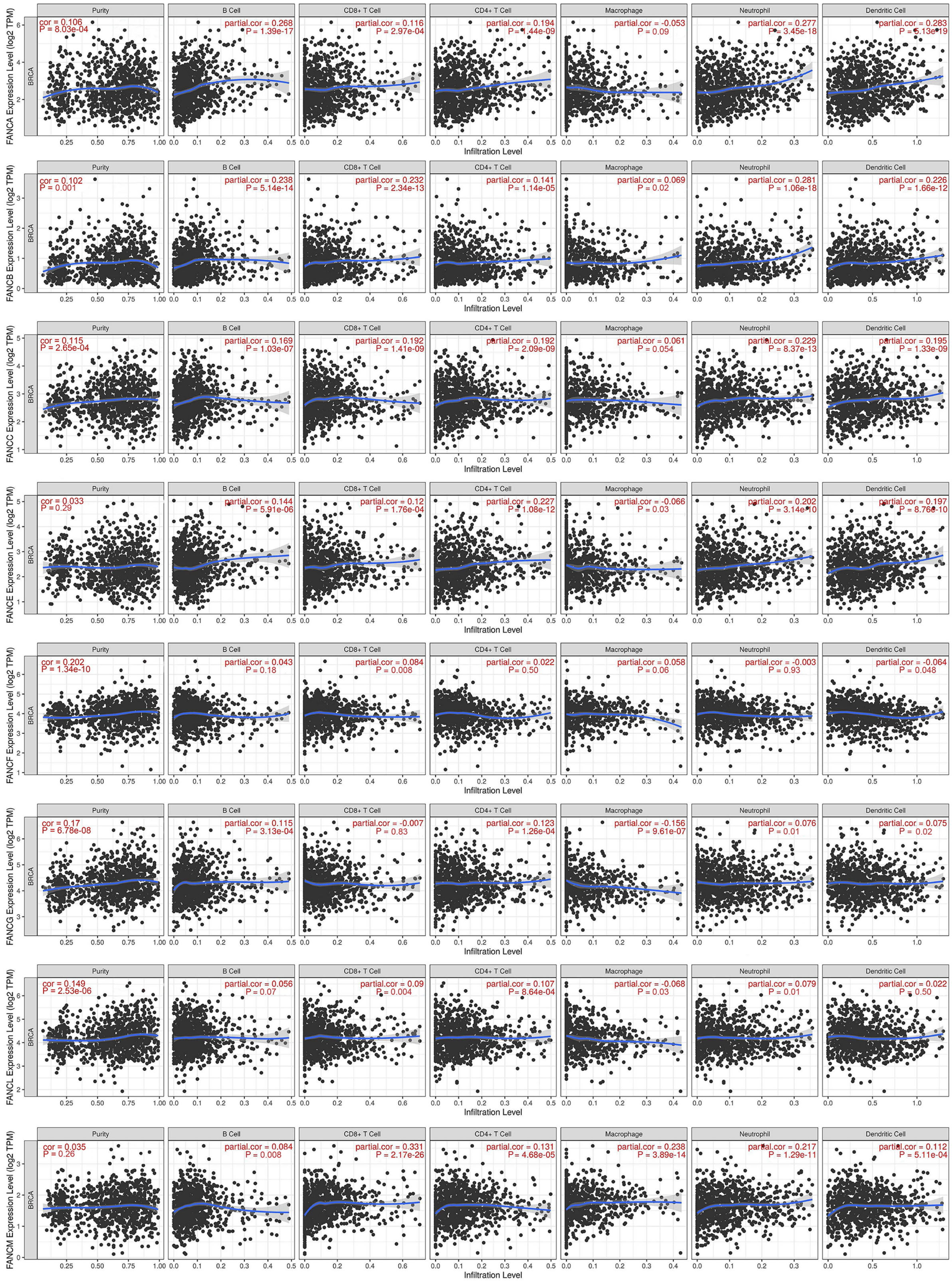
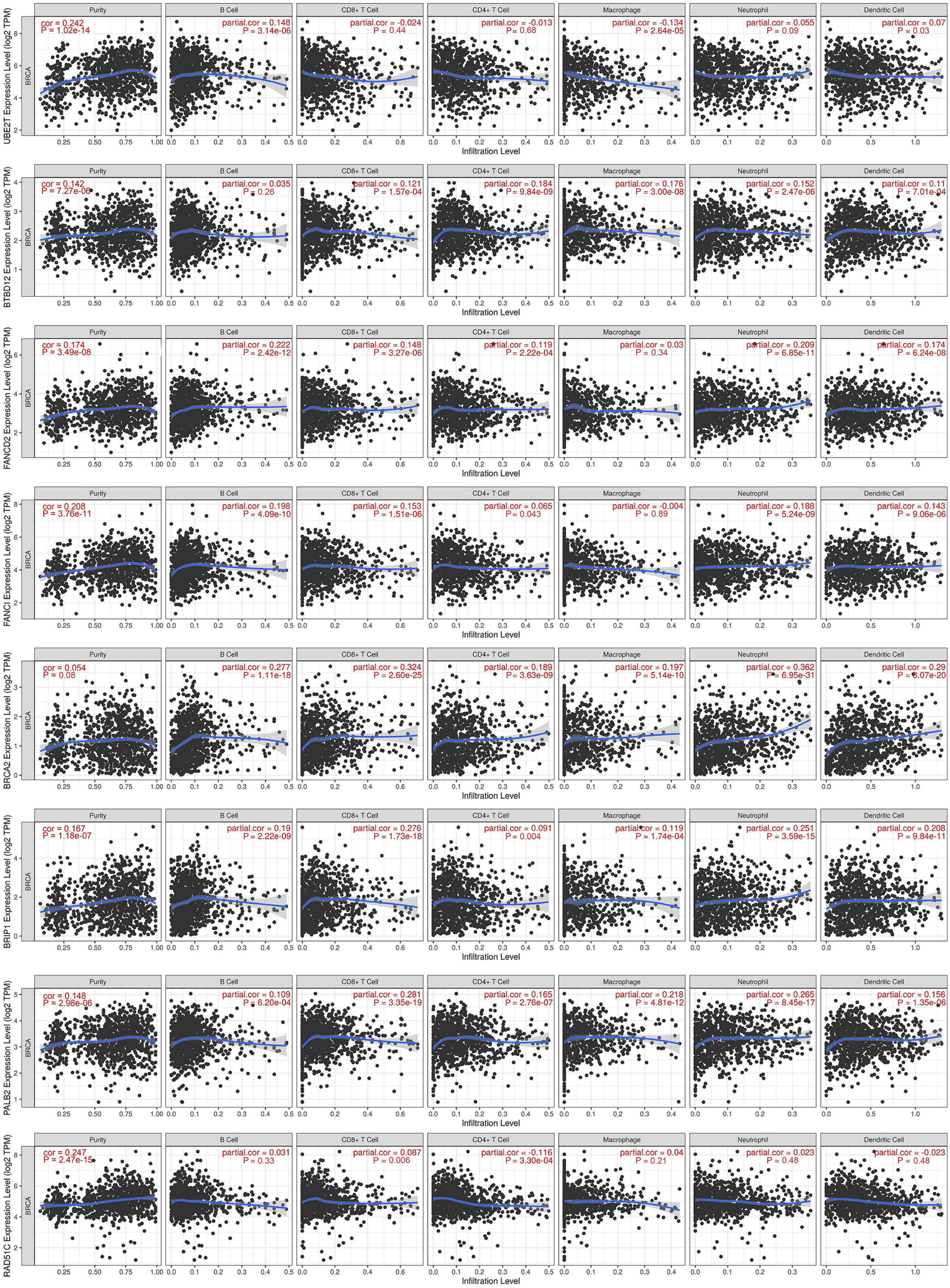


Figure 5 Alteration analysis was performed using cBioPortal database. (A) Alteration frequency of FA pathway genes in breast cancer. (B) OncoPrint visual summary of FA pathway genes alterations in breast cancer. FA, Fanconi anemia; cBioPortal, cBio cancer genomics portal; CNA, copy number alteration.

determined before evaluating their association with survival outcomes in breast cancer patients. Expression levels of 20 genes were shown to be significantly higher in breast cancer tissues than in the corresponding normal tissues, except for *FANCE* and *FANCM*, which were downregulated in tumors. Moreover, elevated expression levels of *FANCB*, *FANCG*, *FANCL*, *UBE2T*, *FANCI*, *BRIP1*, *BRCC5*, *BRCA1*, *MAD2L2* and *RFWD3* in breast cancer were associated with worse RFS. However, elevated mRNA levels of *FANCC*, *SLX4*, *PALB2*, *XRCC2* and *ERCC4* were correlated with a favorable RFS. Furthermore, elevated expression levels of *FANCA*, *FANCG*, *UBE2T*, *FANCI*, *FANCD1*, *BRCC5*, *BRCA1* and *RFWD3* were associated with worse OS. These findings imply that FANCG, UBE2T, FANCI,


Purity
B Cell
CD8+ T Cell
CD4+ T Cell
Macrophage
Neutrophil
Dendritic Cell
BRCA
Infiltration Level
FANCA Expression Level (log2 TPM)
cor = 0.106 P = 8.03e-04
partial.cor = 0.268 P = 1.39e-17
partial.cor = 0.116 P = 2.97e-04
partial.cor = 0.194 P = 1.44e-09
partial.cor = -0.053 P = 0.09
partial.cor = 0.277 P = 3.45e-18
partial.cor = 0.283 P = 5.13e-19
FANCB Expression Level (log2 TPM)
cor = 0.102 P = 0.001
partial.cor = 0.238 P = 5.14e-14
partial.cor = 0.232 P = 2.34e-13
partial.cor = 0.141 P = 1.14e-05
partial.cor = 0.069 P = 0.02
partial.cor = 0.281 P = 1.06e-18
partial.cor = 0.226 P = 1.66e-12
FANCC Expression Level (log2 TPM)
cor = 0.115 P = 2.65e-04
partial.cor = 0.169 P = 1.03e-07
partial.cor = 0.192 P = 1.41e-09
partial.cor = 0.192 P = 2.09e-09
partial.cor = 0.061 P = 0.054
partial.cor = 0.229 P = 8.37e-13
partial.cor = 0.195 P = 1.33e-09
FANCE Expression Level (log2 TPM)
cor = 0.033 P = 0.29
partial.cor = 0.144 P = 5.91e-06
partial.cor = 0.12 P = 1.76e-04
partial.cor = 0.227 P = 1.08e-12
partial.cor = -0.066 P = 0.03
partial.cor = 0.202 P = 3.14e-10
partial.cor = 0.197 P = 8.76e-10
FANCF Expression Level (log2 TPM)
cor = 0.202 P = 1.34e-10
partial.cor = 0.043 P = 0.18
partial.cor = 0.084 P = 0.008
partial.cor = 0.022 P = 0.50
partial.cor = 0.058 P = 0.06
partial.cor = -0.003 P = 0.93
partial.cor = -0.064 P = 0.048
FANCG Expression Level (log2 TPM)
cor = 0.17 P = 6.78e-08
partial.cor = 0.115 P = 3.13e-04
partial.cor = -0.007 P = 0.83
partial.cor = 0.123 P = 1.26e-04
partial.cor = -0.156 P = 9.61e-07
partial.cor = 0.076 P = 0.01
partial.cor = 0.075 P = 0.02
FANCL Expression Level (log2 TPM)
cor = 0.149 P = 2.53e-06
partial.cor = 0.056 P = 0.07
partial.cor = 0.09 P = 0.004
partial.cor = 0.107 P = 8.64e-04
partial.cor = -0.068 P = 0.03
partial.cor = 0.079 P = 0.01
partial.cor = 0.022 P = 0.50
FANCM Expression Level (log2 TPM)
cor = 0.035 P = 0.26
partial.cor = 0.084 P = 0.008
partial.cor = 0.331 P = 2.17e-26
partial.cor = 0.131 P = 4.68e-05
partial.cor = 0.238 P = 3.89e-14
partial.cor = 0.217 P = 1.29e-11
partial.cor = 0.112 P = 5.11e-04
0.25 0.50 0.75 1.00
0.0 0.1 0.2 0.3 0.4 0.5
0.0 0.2 0.4 0.6
0.0 0.1 0.2 0.3 0.4 0.5
0.0 0.1 0.2 0.3 0.4
0.0 0.1 0.2 0.3
0.0 0.5 1.0


Purity
B Cell
CD8+ T Cell
CD4+ T Cell
Macrophage
Neutrophil
Dendritic Cell
BRCA
Infiltration Level
UBE2T Expression Level (log2 TPM)
cor = 0.242 P = 1.02e-14
partial.cor = 0.148 P = 3.14e-06
partial.cor = -0.024 P = 0.44
partial.cor = -0.013 P = 0.68
partial.cor = -0.134 P = 2.64e-05
partial.cor = 0.055 P = 0.09
partial.cor = 0.07 P = 0.03
BTBD12 Expression Level (log2 TPM)
cor = 0.142 P = 7.27e-06
partial.cor = 0.035 P = 0.26
partial.cor = 0.121 P = 1.57e-04
partial.cor = 0.184 P = 9.84e-09
partial.cor = 0.176 P = 3.00e-08
partial.cor = 0.152 P = 2.47e-06
partial.cor = 0.11 P = 7.01e-04
FANCD2 Expression Level (log2 TPM)
cor = 0.174 P = 3.49e-08
partial.cor = 0.222 P = 2.42e-12
partial.cor = 0.148 P = 3.27e-06
partial.cor = 0.119 P = 2.22e-04
partial.cor = 0.03 P = 0.34
partial.cor = 0.209 P = 6.85e-11
partial.cor = 0.174 P = 6.24e-08
FANCI Expression Level (log2 TPM)
cor = 0.208 P = 3.76e-11
partial.cor = 0.198 P = 4.09e-10
partial.cor = 0.153 P = 1.51e-06
partial.cor = 0.065 P = 0.043
partial.cor = -0.004 P = 0.89
partial.cor = 0.188 P = 5.24e-09
partial.cor = 0.143 P = 9.06e-06
BRCA2 Expression Level (log2 TPM)
cor = 0.054 P = 0.08
partial.cor = 0.277 P = 1.11e-18
partial.cor = 0.324 P = 2.60e-25
partial.cor = 0.189 P = 3.63e-09
partial.cor = 0.197 P = 5.14e-10
partial.cor = 0.362 P = 6.95e-31
partial.cor = 0.29 P = 8.07e-20
BRIP1 Expression Level (log2 TPM)
cor = 0.167 P = 1.18e-07
partial.cor = 0.19 P = 2.22e-09
partial.cor = 0.276 P = 1.73e-18
partial.cor = 0.091 P = 0.004
partial.cor = 0.119 P = 1.74e-04
partial.cor = 0.251 P = 3.59e-15
partial.cor = 0.208 P = 9.84e-11
PALB2 Expression Level (log2 TPM)
cor = 0.148 P = 2.98e-06
partial.cor = 0.109 P = 6.20e-04
partial.cor = 0.281 P = 3.35e-19
partial.cor = 0.165 P = 2.76e-07
partial.cor = 0.218 P = 4.81e-12
partial.cor = 0.265 P = 8.45e-17
partial.cor = 0.156 P = 1.35e-06
RAD51C Expression Level (log2 TPM)
cor = 0.247 P = 2.47e-15
partial.cor = 0.031 P = 0.33
partial.cor = 0.087 P = 0.006
partial.cor = -0.116 P = 3.30e-04
partial.cor = 0.04 P = 0.21
partial.cor = 0.023 P = 0.48
partial.cor = -0.023 P = 0.48

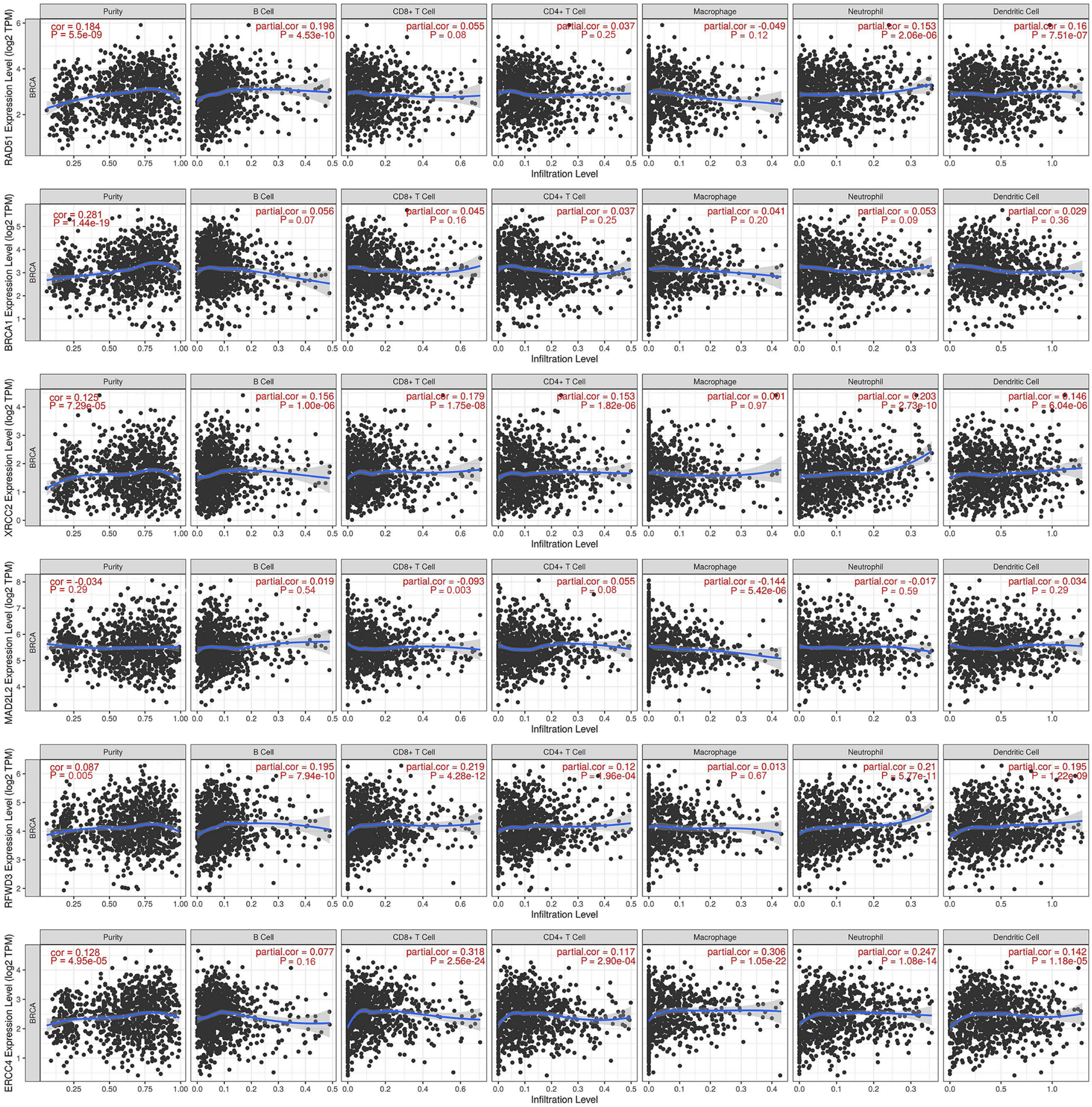


Figure 6 The correlation between differently expressed FA pathway genes and immune cell infiltration in breast cancer using TIMER database. FA, Fanconi anemia; TIMER, tumor immune estimation resource; TPM, transcripts per million.

BRCC5, BRCA1 and RFWD3 exhibited better prospects for utilization as prognostic biomarkers in breast cancer patients. It has been documented that the prognosis of breast cancer patients is associated with tumor pathological tissue type, such as ER, PR and HER2 status, which have played a role in the identification of which patients are likely to benefit from endocrine therapy or targeted therapy (27). TP53 is the most frequent mutational target in human cancers. Mutations in TP53 are associated with different types of malignancies and adverse prognoses, including during breast cancer (28). In this study, most FA pathway genes showed a close relationship with worse RFS of breast cancer patients with different clinicopathological features including cancer grade, ER status, PR status, HER2 status and TP53 status. Collectively, the FA pathway genes are potential therapeutic targets and prognostic biomarkers for breast cancer.

Next-generation sequencing has uncovered the frequency of mutations and copy number alterations across different cancer types and demonstrated that alterations in DNA repair mechanisms are common events in carcinogenesis. Mutations with high variant allele frequencies (VAFs) indicate early appearance of tumorigenesis or tremendous contribution to the later expansion of tumor cells (29). Moreover, compensatory mutations in BRCA1 and BRCA2 that restore homologous recombination (HR) functionality in initially cisplatin sensitive tumors are able to develop cisplatin resistance (30). Comprehensively revealing mutation characteristics in breast cancer elucidates on the mutational diversity among different molecular subtypes, enables the identification of potential treatment biomarkers, and provides a basis for genomic targeting strategies and clinical trials (31). Given the significant differential expression of genes in the FA pathway, we further explored their molecular characteristics. It was found that mutation, fusion, amplification, deep deletion and multiple alterations were the main mutational signatures of FA pathway genes in breast cancer. Notably, amplification was the main characteristic of gene mutations in the FA pathway genes, which meant that the FA pathway could be a significant compensatory DNA repair pathway for cancer cells. More importantly, these mutational signatures may be new therapeutic targets for precision medicine, providing opportunities for personalized treatment strategies based on the imperfection of patient's DNA repair networks.

Cell response to DNA damage is a complex mechanism involving multiple protein networks with interconnected functions that are responsible for damage detection, cell cycle regulation and DNA repair. Establishing the underlying mechanisms involved in the association between FA pathway and breast cancer, besides DNA damage repair, will have significant implications in clinical practice (32). In this study, a low to high expression correlation among FA pathway genes in breast cancer was obtained, suggesting that they played a synergistic role in tumorigenesis and cancer progression. Then, we determined the core genes that were potentially associated with FA pathway gene functions. Some of them were identified as important gene regulators. For instance, it has been shown that *FANCM* and its binding partner, *FAAP24*, suppress the formation of DNA double-stranded breaks and mitotic recombination in a manner that is dependent on FANCM translocase activity (33). Moreover, BRCA1-BARD1 are required for fork protection and are associated with cancer development (34). Functional enrichment analysis was then performed to elucidate on the biological functions of FA pathway genes in breast cancer. The FA-related genes were found to be primarily positively associated with the cell cycle and nucleoplasm. However, the FA pathway genes were also negatively correlated with genes involved in SRP-dependent cotranslational protein targeting to membrane and ribosome. The ribosome plays a critical role in normal cellular physiology, in cellular responses to internal and external environmental stimuli, and in the pathogenesis of human diseases (35). Under stress situations, a decreased ribosomal activity and reduced protein synthesis are shown, subsequently leading to nuclear mobilization and DNA repair activation to minimize the negative impact to cell growth (36). This may be the mechanism through which ribosome-related genes are down-regulated. Recent finding has begun to elucidate the interplay between ribosomal biogenesis, which means ribosomal synthesis and DNA repair (37). FANCI is required for ribosomal biogenesis, and may function by coordinating rDNA replication and transcription (38). Nonetheless, the exact functions of FA pathway genes in breast cancer should be investigated further.

The cancer immune microenvironment plays an important role in tumor progression (39). In recent years, immunotherapy has been found to be a promising therapy for cancer, and the development of immunological biomarkers has been of increasing importance (40). In this study, there was a significant positive correlation between the mRNA expressions of FA pathway genes and tumor purity in breast cancer. Tumor purity is highly associated with genomic patterns and immune phenotypes, which is substantially inversely correlated with tumor heterogeneity (41). Targeting DNA repair processes may influence the adaptive immune system by leading to an increased number of mutations, and subsequently increased burden of neoantigens, which in turn increases tumor heterogeneity, resulting in a higher probability of recognition by the immune system, and this has the potential to be exploited in therapeutic approaches (42). Pan-cancer analysis suggested that increasing mutation load is linearly correlated with increasing immune activity in the tumor microenvironment of a tumor and is likely to influence immune recognition (43). Therefore, FA pathway genes were found to be potential therapeutic targets for breast cancer and could be combined with immunotherapy. In addition, the mRNA expression levels of FA pathway genes were also highly correlated with various immune cell infiltrations. These findings imply that FA pathway genes are not only prognostic indicators but also reflect the “immune-hot” status in breast cancer. DNA repair can also influence how the innate immune system initially responds to a tumor and recruits the adaptive immune system to the malignancy site (44). Alterations in DNA repair can influence how the adaptive, innate, or both parts of the immune system respond to the underlying malignancy. However, further studies are required to verify the potential role of FA pathway genes in breast cancer as predictive biomarkers of immunotherapeutic responses.

There are some limitations in this study. Analysis on the transcriptional level can reflect some immune status aspects, but not wholesome changes. Independent cohort and *in vitro* or *in vivo* studies should be performed to validate our results.

In summary, there is a significant correlation between the mRNA expression levels of FA pathway genes and tumor prognosis as well as the cancer immune infiltration. This implies that the genes may mediate tumor progression and exert immunotherapeutic effects in breast cancer. Therefore, elucidation of how these genes is regulated during tumor progression may highlight their potential prognostic and therapeutic role in breast cancer.

Conclusions

This study elucidates on the expression, mutations and prognostic values of FA pathway genes in breast cancer. Analysis of the relationship between FA pathway gene expression and clinicopathological characteristics in breast cancer indicated that FA pathway genes could be promising prognostic biomarkers in patients with breast cancer, and may be novel targets for breast cancer therapy. More studies are needed to explore the exact mechanisms and therapeutic roles of FA pathway genes in breast cancer. It is possible that the FA pathway genes will be effective prognostic markers of breast cancer in future.

Acknowledgments

None.

Footnote

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