

Table S1 The clinical characteristics of patients

Characteristics	Cases
<i>Age</i>	
<60 years	1,820
≥60 years	1,764
<i>Grade</i>	
G1	408
G2	1,011
G3	1,162
<i>ER status</i>	
Positive	2,314
Negative	842
<i>PR status</i>	
Positive	895
Negative	688
<i>HER2 status</i>	
Positive	248
Negative	1,264

ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth receptor 2.

Table S2 The association between FA pathway genes expression and status of patients with breast cancer

Gene	Status	Cases	HR (95% CI)	P value
<i>ER status</i>				
FANCF	Positive	2061	0.94 (0.8–1.11)	0.45
	Negative	801	0.98 (0.78–1.23)	0.86
FANCM	Positive	762	1.11 (0.83–1.49)	0.47
	Negative	347	0.89 (0.64–1.24)	0.50
SLX4 (FANCP)	Positive	762	1.24 (0.93–1.66)	0.14
	Negative	347	1.18 (0.85–1.65)	0.32
FANCD2	Positive	762	1.07 (0.8–1.43)	0.66
	Negative	347	0.91 (0.66–1.27)	0.60
PALB2 (FANCN)	Positive	2061	1.07 (0.91–1.26)	0.40
	Negative	801	1.04 (0.83–1.3)	0.73
XRCC2 (FANCU)	Positive	2061	0.92 (0.78–1.08)	0.30
	Negative	801	0.93 (0.74–1.16)	0.51
MAD2L2 (FANCV)	Positive	762	1.02 (0.77–1.37)	0.88
	Negative	347	0.9 (0.64–1.25)	0.52
ERCC4 (FANCO)	Positive	2061	1.21 (0.91–1.62)	0.20
	Negative	801	1.27 (0.91–1.77)	0.16
<i>PR status</i>				
FANCB	Positive	489	1.42 (0.97–2.08)	0.07
	Negative	372	0.93 (0.65–1.33)	0.68
FANCC	Positive	589	1.41 (0.99–2)	0.054
	Negative	549	1.01 (0.75–1.35)	0.97
FANCE	Positive	589	1.12 (0.79–1.58)	0.53
	Negative	549	0.96 (0.71–1.28)	0.76
FANCF	Positive	589	0.85 (0.6–1.21)	0.36
	Negative	549	0.81 (0.6–1.08)	0.15
FANCL	Positive	589	1.15 (0.81–1.62)	0.44
	Negative	549	0.95 (0.71–1.28)	0.76
FANCM	Positive	489	0.97 (0.66–1.42)	0.87
	Negative	372	1.03 (0.72–1.47)	0.86
FANCD2	Positive	489	1.23 (0.84–1.8)	0.28
	Negative	372	1.28 (0.89–1.82)	0.18
FANCD1	Positive	589	1.41 (1–2.01)	0.051
	Negative	549	0.86 (0.64–1.15)	0.32
PALB2 (FANCN)	Positive	589	1.09 (0.77–1.54)	0.62
	Negative	549	1.3 (0.97–1.74)	0.08
XRCC2 (FANCU)	Positive	589	0.98 (0.69–1.39)	0.89
	Negative	549	1.04 (0.78–1.39)	0.80
MAD2L2(FANCV)	Positive	489	1.18 (0.81–1.73)	0.38
	Negative	372	1.14 (0.8–1.63)	0.47
RFWD3 (FANCW)	Positive	589	1.24 (0.88–1.76)	0.22
	Negative	549	1.32 (0.99–1.77)	0.06
<i>HER2 status</i>				
FANCE	Positive	252	0.89 (0.58–1.38)	0.60
	Negative	800	1.12 (0.86–1.45)	0.41
FANCL	Positive	252	1.1 (0.71–1.7)	0.67
	Negative	800	1.06 (0.81–1.37)	0.67
FANCM	Positive	150	0.75 (0.44–1.3)	0.31
	Negative	635	1.09 (0.81–1.46)	0.58
FANCD1	Positive	252	0.87 (0.56–1.35)	0.53
	Negative	800	1.22 (0.94–1.59)	0.13
BRCC5 (FANCR)	Positive	252	1.41 (0.91–2.19)	0.12
	Negative	800	1.18 (0.9–1.53)	0.22
XRCC2 (FANCU)	Positive	252	1.02 (0.66–1.57)	0.95
	Negative	800	0.83 (0.64–1.08)	0.16
MAD2L2(FANCV)	Positive	150	0.81 (0.47–1.39)	0.44
	Negative	635	1.16 (0.86–1.56)	0.34
RFWD3 (FANCW)	Positive	252	1.53 (0.98–2.37)	0.06
	Negative	800	1.21 (0.93–1.57)	0.16
<i>TP53 status</i>				
FANCB	Mutated	132	0.69 (0.38–1.26)	0.23
	Wild type	82	0.57 (0.24–1.36)	0.20
FANCC	Mutated	188	1.1 (0.68–1.77)	0.70
	Wild type	273	1.44 (0.94–2.2)	0.09
FANCE	Mutated	188	0.72 (0.45–1.17)	0.19
	Wild type	273	0.82 (0.54–1.25)	0.35
FANCF	Mutated	188	1.13 (0.7–1.81)	0.62
	Wild type	273	0.86 (0.56–1.3)	0.47
FANCG	Mutated	188	0.9 (0.56–1.45)	0.67
	Wild type	273	1.38 (0.9–2.11)	0.13
FANCM	Mutated	132	0.8 (0.45–1.45)	0.47
	Wild type	82	0.93 (0.4–2.15)	0.86
SLX4 (FANCP)	Mutated	132	0.86 (0.48–1.55)	0.61
	Wild type	82	1.4 (0.6–3.27)	0.44
FANCD1	Mutated	188	0.94 (0.59–1.51)	0.80
	Wild type	273	1.47 (0.96–2.24)	0.08
BRIP1 (FANCI)	Mutated	188	0.92 (0.51–1.65)	0.78
	Wild type	273	1.74 (0.74–4.08)	0.20
PALB2 (FANCN)	Mutated	188	1.18 (0.74–1.9)	0.49
	Wild type	273	0.87 (0.57–1.32)	0.50
BRCC5 (FANCR)	Mutated	188	0.65 (0.4–1.04)	0.07
	Wild type	273	1.14 (0.75–1.73)	0.55
XRCC2 (FANCU)	Mutated	188	1.32 (0.82–2.12)	0.26
	Wild type	273	1.12 (0.73–1.7)	0.60
MAD2L2(FANCV)	Mutated	132	1.77 (0.97–3.22)	0.06
	Wild type	82	0.5 (0.21–1.19)	0.11
ERCC4 (FANCO)	Mutated	188	1.17 (0.65–2.1)	0.61
	Wild type	273	1.2 (0.52–2.78)	0.67

FA, Fanconi anemia; ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth receptor 2; HR, hazard ratio; CI, confidence interval.

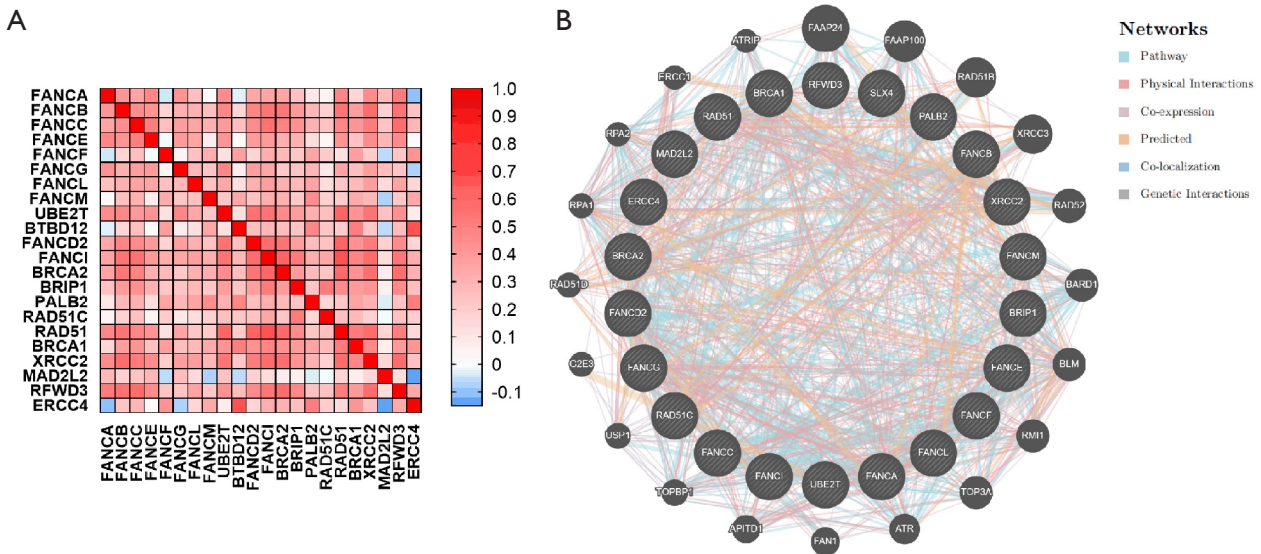


Figure S1 Interaction analysis of FA pathway genes. (A) Expression correlation heatmap of differently expressed FA pathway genes in breast cancer using GEPIA database. (B) Gene-gene interaction network of FA pathway genes using GeneMANIA database. FA, Fanconi anemia; GEPIA, gene expression profiling interactive analysis; GeneMANIA, Gene Multi-Association Network Integration Algorithm.

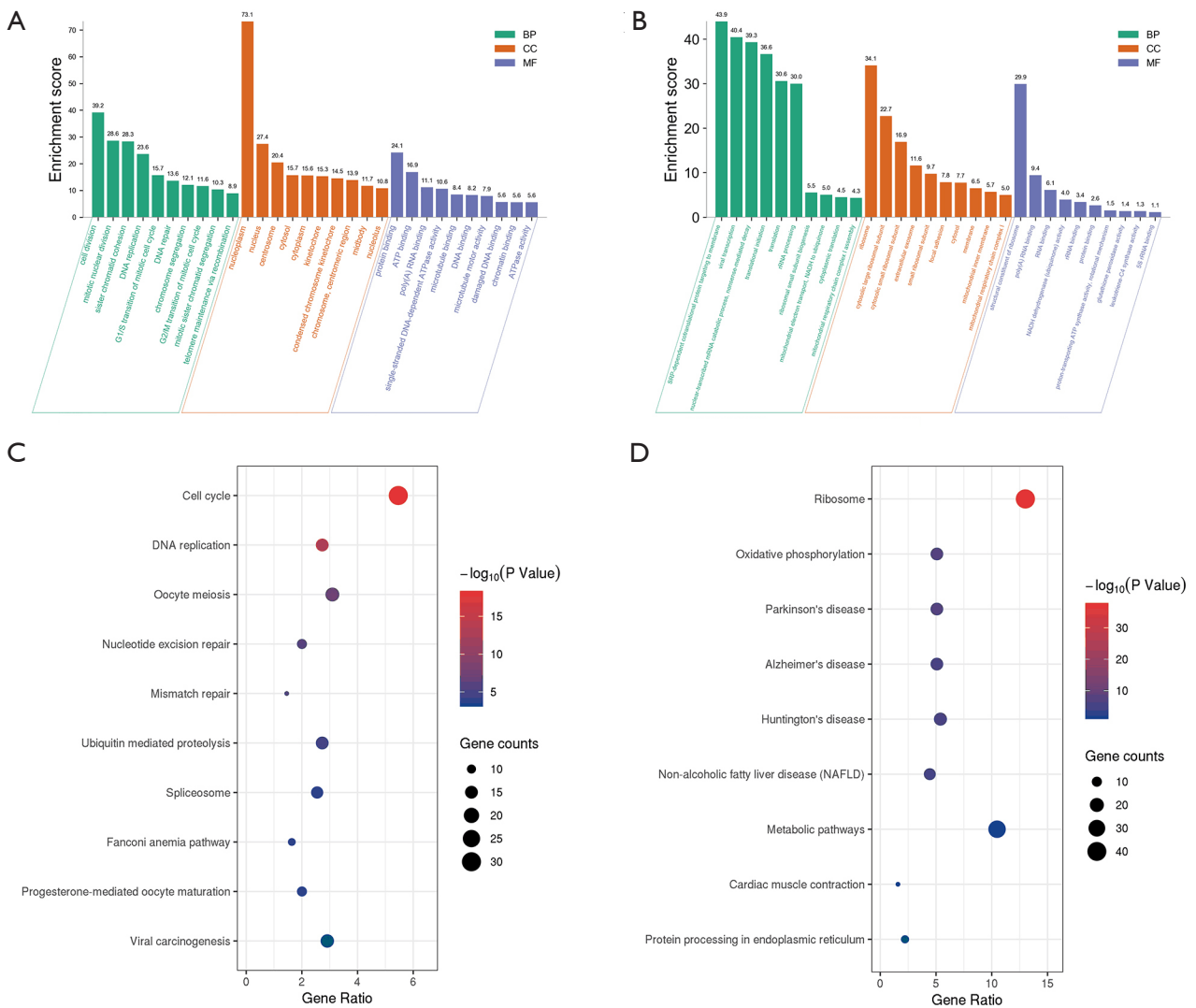


Figure S2 GO and KEGG pathway enrichment analysis of FA-related genes in breast cancer. (A) The most highly enriched GO items positively correlated with FA pathway genes. (B) The most highly enriched GO items negatively correlated with FA pathway genes. (C) The most highly enriched pathways positively correlated with FA pathway genes. (D) The most highly enriched pathways negatively correlated with FA pathway genes. FA, Fanconi anemia; level; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; CC, cellular component; MF, molecular function.