

## *Supplementary Material*

# **A Mitochondrial Quality Regulation Gene Signature for Prognosis and Tumor Microenvironment Characterization in Breast Cancer: An Integrative Analysis with Experimental Validation**

**Huaiwen Pu<sup>1,#</sup>, Renji Liang<sup>2,#</sup>, Zhongxiang Fan<sup>1</sup>, Bowen Tang<sup>1</sup>, Yongmei Luo<sup>1</sup>, Xinyu Yi<sup>1</sup>, Liming Xie<sup>1</sup>, Yuehua Li<sup>1,\*</sup>**

<sup>1</sup>Department of Oncology, The First Affiliated Hospital, Hengyang Medical School, University of South China, Hengyang 421001, China.

<sup>2</sup>Department of Thoracic Surgery, The First Affiliated Hospital, Hengyang Medical School, University of South China, Hengyang 421001, China.

<sup>#</sup>These authors have contributed equally to this work.

\*Correspondence:

Yuehua Li, Email: [liyuehua2020@stu.usc.edu.cn](mailto:liyuehua2020@stu.usc.edu.cn)

## **1 Supplementary Figures and Tables**

### **1.1 Supplementary Figures**

## Supplementary Figure S1.

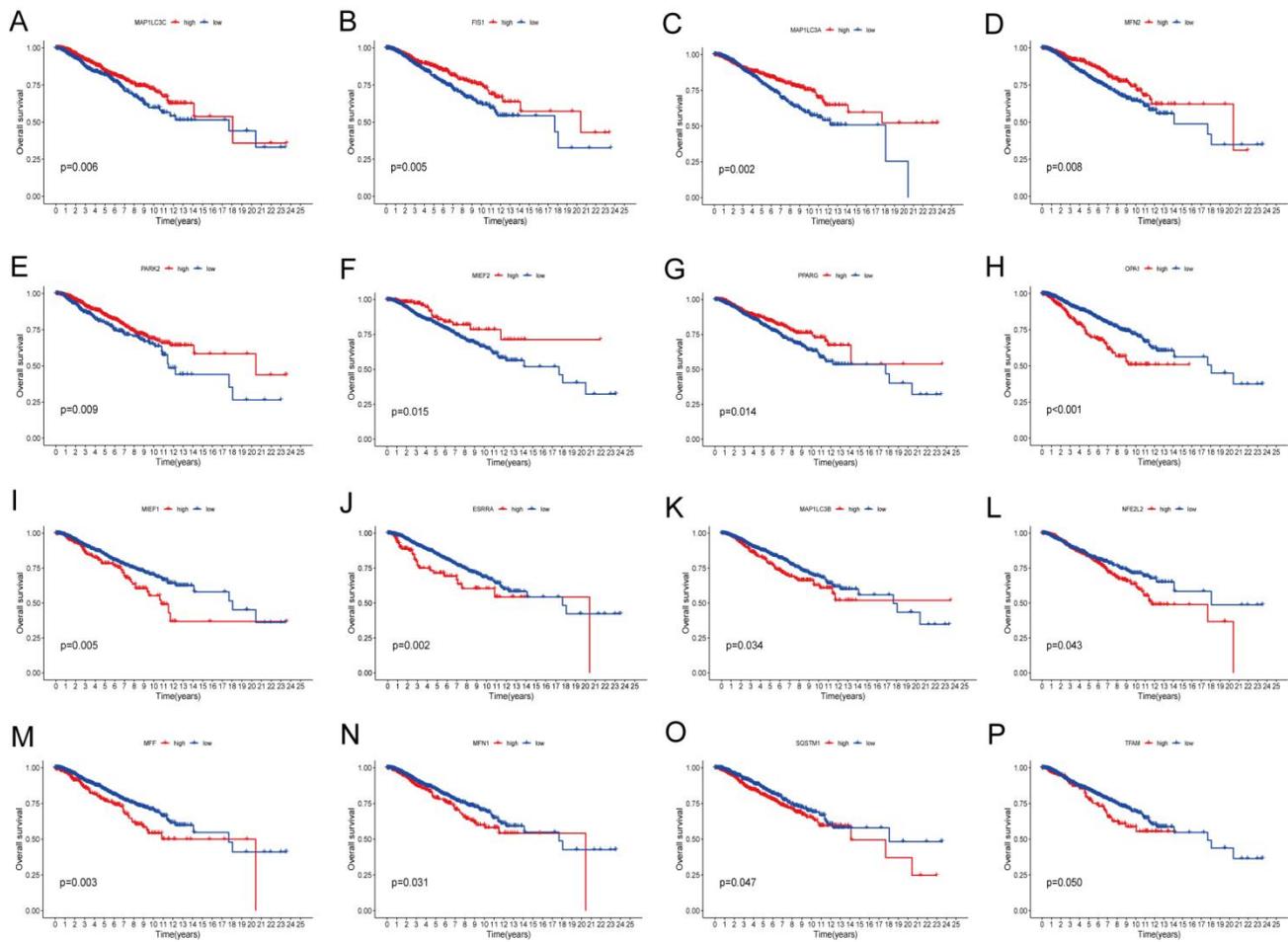
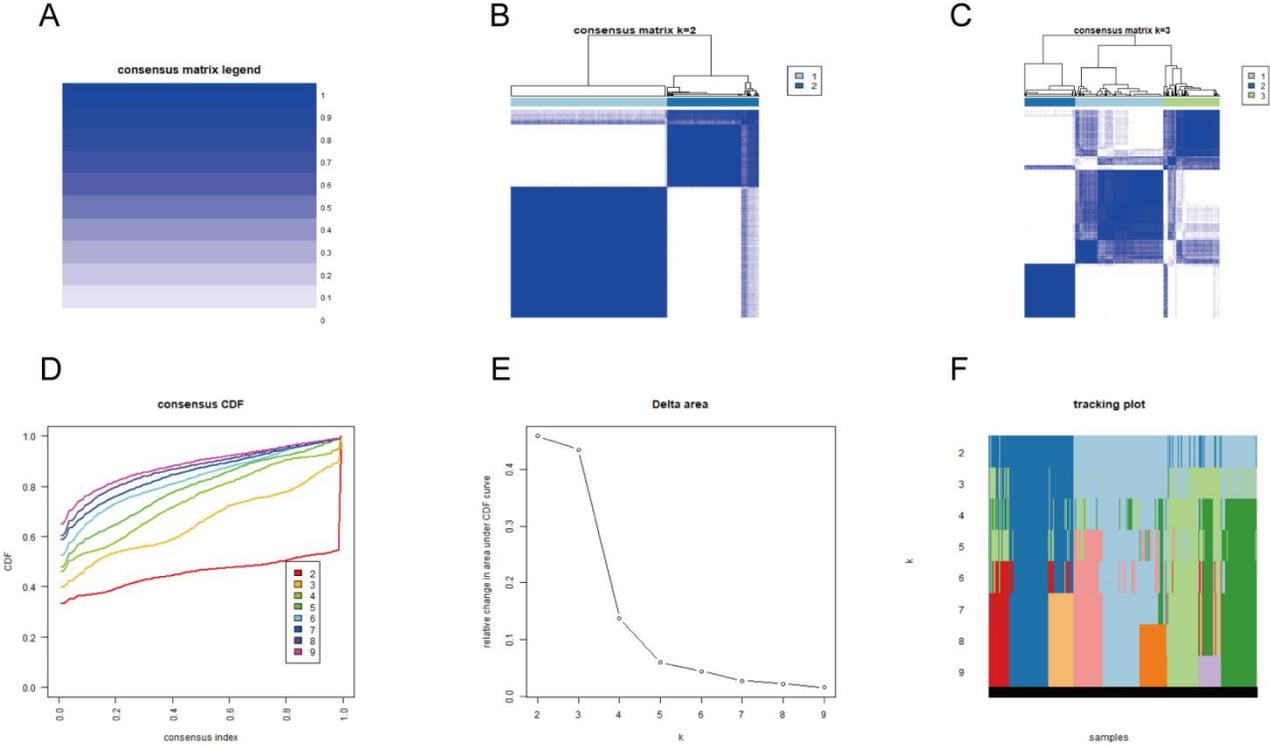


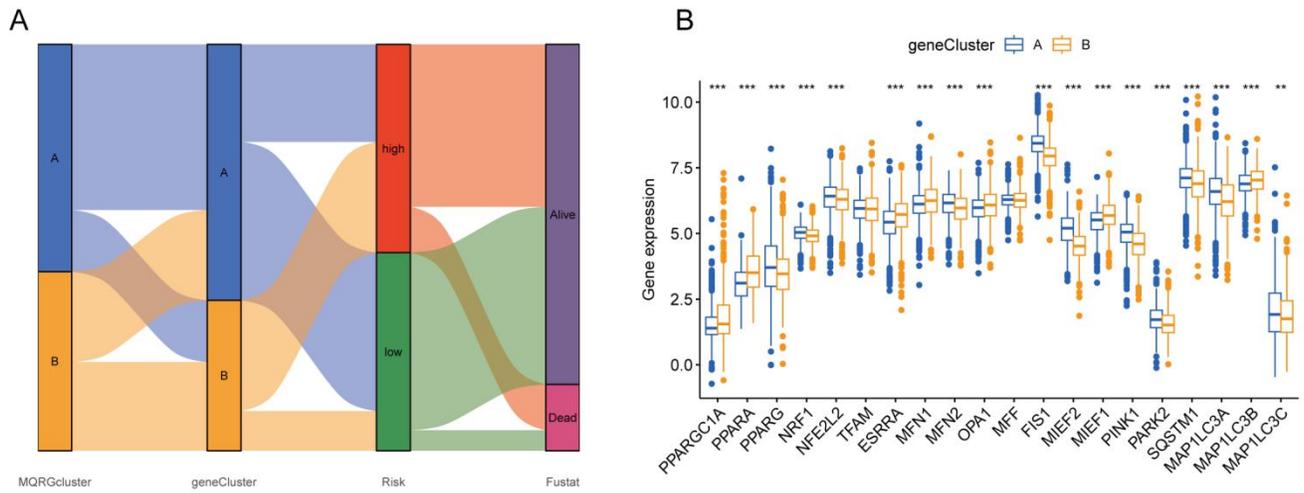
Figure S1 KM curve results of LUAD patients with different MQRGs expression.

Supplementary Figure S2.



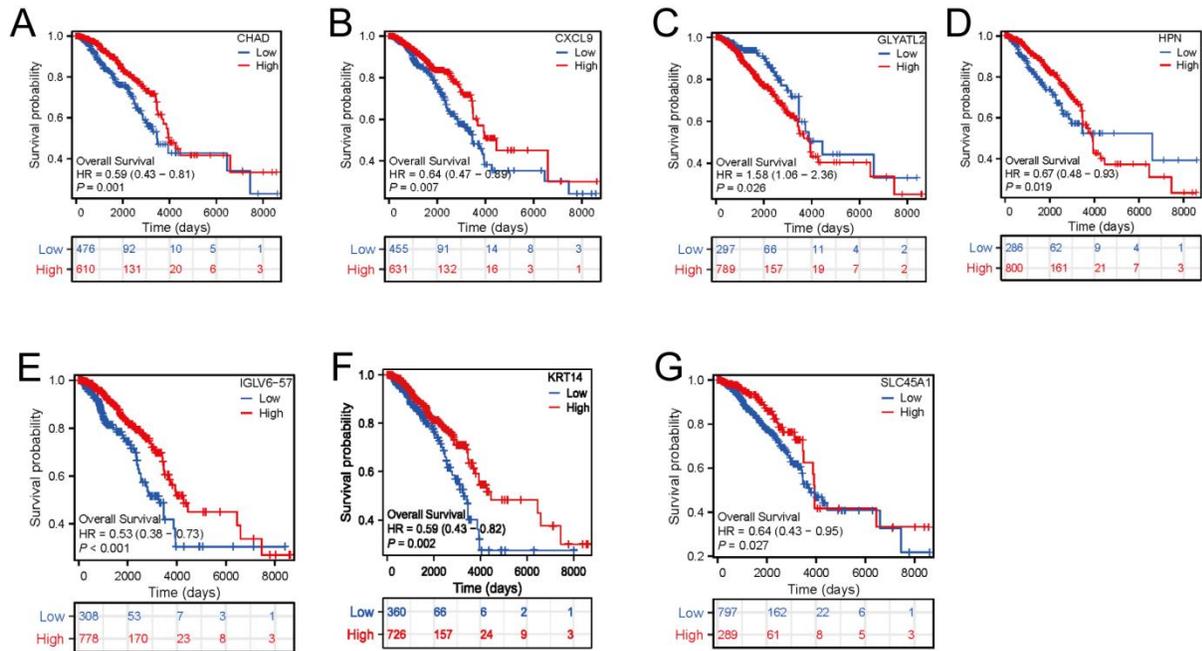
**Figure S2** (A-C) Consensus Matrix Heatmaps and Unsupervised Clustering for MQRG genecluster.(D) CDF displays Cumulative Co-clustering Fraction of Samples at Specified Consensus Index for each tested k.(E) Delta Area Curve of Consensus Clustering showing CDF Area changes relative to k-1 by Category Number k.(F) Tracking plot.

## Supplementary Figure S3.



**Figure S3** (A) Alluvial diagram Showing correspondence among Subtypes, Risk Scores and Overall Survival. (B) Expression variations of the 20 MQRGs Between the two Gene Subtypes.

Supplementary Figure S4.



**Figure S4 Kaplan-Meier (KM) survival analysis of Prognostic Genes in breast cancer.**

KM curves show overall survival (OS) stratified by (A) CHAD, (B) CXCL9, (C) GLYATL2, (D) HPN, (E) GIMAP7, (F) KRT14, and (G) SLC45A1 expression. Red and blue lines represent high- and low-expression groups, respectively. HR (95% CI) and log-rank P-values are indicated.

## Supplementary Figure S5.

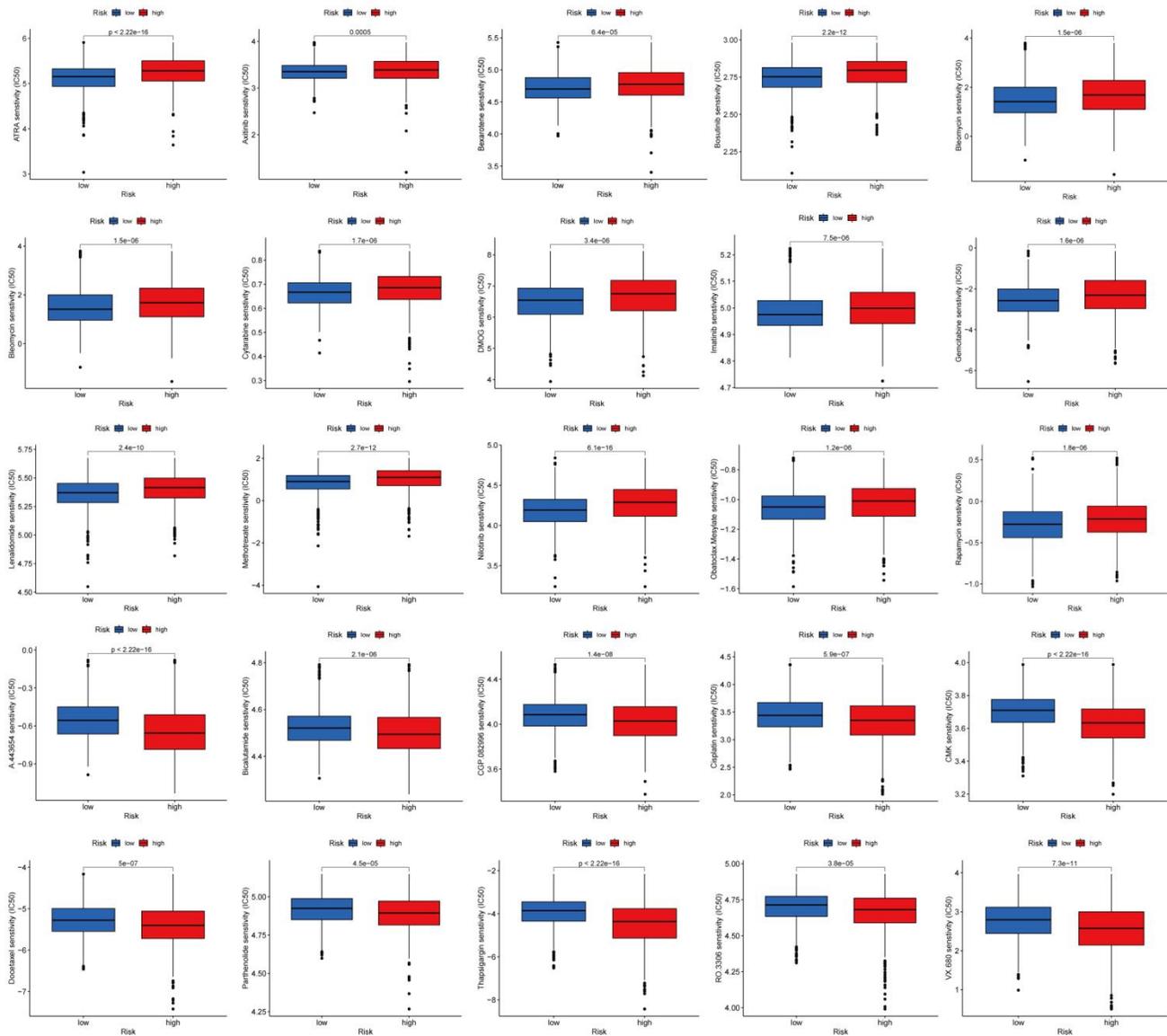


Figure S5 Connections between drug sensitivity and different MQRG score groups.

## 1.2 Supplementary Tables

**Supplementary Table S1.** 20 Mitochondrial quality-related genes

<b>Type</b>	<b>MQRGs</b>
<b>Gene</b>	PPARGC1A, PPARA, PPARG, NRF1, NFE2L2, TFAM, ESRRA, MFN1, MFN2, OPA1, MFF, FIS1, MIEF2, MIEF1, PINK1, PARK2, SQSTM1, MAP1LC3A, MAP1LC3B, MAP1LC3C

**Supplementary Table S2.** Primer sequences of hub genes for real-time polymerase chain reaction.

Target	Sequence of primers
GAPDH-Forward	AGGTCGGAGTCAACGGATTT
GAPDH-Reward	TGACAAGCTTCCCGTTCTCA
IGLV6-57-Forward	ACTTCTCACCTCCTCGCTC
IGLV6-57-Reward	TGGGGAGAGATGAAGACTGGT
CHAD-Forward	AGCTGCTCAACCTACAGCG
CHAD-Reward	CAGGTGCAATGACACGAGG
CXCL9-Forward	CCAGTAGTGAGAAAGGGTCGC
CXCL9-Reward	AGGGCTTGGGGCAAATTGTT
GLYATL2-Forward	AGGGCTTGGATGAAGCAATAAG
GLYATL2-Reward	CCTGCATGTGAAGCATCTAAGA
KRT14-Forward	TCGCAGTCATCCAGAGATGTGAC
KRT14-Reward	ACCACCTTGCCATCGTGC
HPN-Forward	ACGCAGTACTATGGCCAACA
HPN-Reward	TCCGAGAGATGCTGTCCTCA
SLC45A1-Forward	CTTGAGCTGGTGGACTTCGG
SLC45A1-Reward	GGCTGCAGTAGGAATCCGAG

**Supplementary Table S3** The clinical parameters of BC in TMA.

Variables	Number of samples
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TMA (120)

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Gender

Female 120

Age

≤40/>40 30/90

T

T1/T2/T3/T4/Tx 20/79/20/1/0

N

N0/N1/N2/N3/Nx 35/32/34/19/0

M

M0/M1/Mx 109/11/0

TNM Stage

I/II/III/IV/NA 13/45/52/10/0

Grade

G1/G2/G3/G4/Gx 0/30/90/0/0

Tumor Size

≤3cm/>3cm 46/74

Her2 expression level

0/1+/3+ 33/44/43

ER

Positive/Negative/unknown 68/52/0

Treatment

Supplementary Material

Surgery / Chemotherapy / Adjuvant Chemotherapy / Adjuvant Radiotherapy / Neoadjuvant Chemotherapy / Endocrine therapy/Traditional Chinese Medicine 95/23/33/3/3/2/2

Status As of November 2022

Dead/Alive/Unknow 19/101/0

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TMA :tumor tissue microarrays;ER: (Estrogen Receptor)