

**Identification and Validation of a Mitochondria Calcium Uptake-Related Gene Signature for
Predicting Prognosis in COAD**

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Supplementary figure legend

Figure S1 The mRNA expressions of MCU complex members in colon cancer (GSE39582). * $P < 0.05$; ** $P < 0.01$.

Figure S2 The relationships between the mRNA expression of MCU complex members and clinicopathological characteristics

Figure S3 The prognostic value of individual MCU complex members in COAD patients (GEPIA). **A**, OS. **B**, RFS

Figure S4 Genetic variations of the mutation of MCU complex members (cBioPortal), and Gene-gene interaction network, protein-protein interaction network and correlation analysis of the MCU complex members in colon cancer. **A**, Overview the genetic variations analyses of MCU complex members. **B**, Correlation analysis between the mRNA expression of MCU complex members and tumor mutational burden (TMB) of COAD patients. **C**, Co-mutation analysis between the MCU complex members and high-frequency genes in COAD. **D**, Protein-protein interaction network analysis through String database. **E**, Correlation analysis of the MCU complex members. **F**, Gene-gene interaction network analysis of MCU complex members through GeneMANIA.

Figure S5 The relationships between the mRNA expression of MCU complex members and immune cell infiltration.

Figure S6 The relationships between the mRNA expression of MCU complex members and immune checkpoint and immunotherapy. **a**, The expression of PD1, PDL-L1 and CTLA4 in the low-expression and high-expression groups based on the median expressions of each MCU complex members in COAD, respectively. **b**, The distribution of responder and non-responder to anti CTLA-4/PD-1 immunotherapy in the low-expression and high-expression groups based on the median expressions of each MCU complex members in COAD, respectively.

Figure S7 Correlation analysis between the expression of MCU complex members and immune checkpoint molecules.

Figure S8 The relationships between risk scores and clinicopathological characteristics of COAD patients from training set.

Figure S9 Validation of the risk signature in the validation datasets (GSE29623 and GSE39582). **A**, Heatmap of mRNA expression of MCU complex members in low-risk and high-risk group. **B**, The mRNA expression of cMCU complex members in low-risk and high-risk group. **C**, K-M survival between low-risk and high-risk group. **D**, ROC curve and AUC at 1, 3, and 5 years for the risk score. ** $P < 0.01$; *** $P < 0.001$.

Figure S10 Functional enrichment analysis of MCU and its co-expression genes. Gene Ontology (GO) analysis.

Figure S11 The associations between risk scores and immune cell infiltration. **A**, The abundance of 22 immune infiltrates between the low-risk and high-risk group. **B**, The relationship between risk score and the estimate score. **C**, The relationship between risk score and the expression of macrophages marker genes.

Figure S12 The associations between risk scores and immune cell infiltration.

Supplementary Table

Supplementary Table 1 Detail information of MCU complex members.

Gene symbol	Full name	Function of the encoded protein	Also known as
MCU	mitochondrial calcium uniporter	This gene encodes a calcium transporter that localizes to the mitochondrial inner membrane. The encoded protein interacts with mitochondrial calcium uptake 1.	HsMCU; C10orf42; CCDC109A
MCUb	mitochondrial calcium uniporter dominant negative subunit beta	Predicted to enable calcium channel inhibitor activity. Predicted to be involved in calcium import into the mitochondrion and mitochondrial calcium ion homeostasis. Located in mitochondrion and nucleoplasm. Is integral component of mitochondrial inner membrane. Part of uniplex complex	CCDC109B
MCUR1	mitochondrial calcium uniporter regulator 1	Involved in calcium import into the mitochondrion and positive regulation of mitochondrial calcium ion concentration. Is integral component of mitochondrial inner membrane	FMP32; C6orf79; CCDC90A
SMDT1	single-pass membrane protein with aspartate rich tail 1	This gene encodes a core regulatory component of a calcium channel in the mitochondrial inner membrane	DDDD; EMRE; C22orf32
MICU1	mitochondrial calcium uptake 1	This gene encodes an essential regulator of mitochondrial Ca ²⁺ uptake under basal conditions. The encoded protein interacts with the mitochondrial calcium uniporter, a mitochondrial inner membrane Ca ²⁺ channel, and is essential in preventing mitochondrial Ca ²⁺ overload, which can cause excessive production of reactive oxygen species and cell stress.	CALC; EFHA3; MPXPS; CBARA1; ara CALC
MICU2	mitochondrial calcium uptake 2	Enables protein heterodimerization activity. Involved in calcium import into the mitochondrion and negative regulation of mitochondrial calcium ion concentration. Located in mitochondrial inner membrane and mitochondrial intermembrane space. Part of uniplex complex	EFHA1; 1110008L20Rik
MICU3	mitochondrial calcium uptake family member 3	Predicted to enable calcium ion binding activity. Predicted to be involved in calcium import into the mitochondrion and mitochondrial calcium ion homeostasis. Predicted to be located in mitochondrial inner membrane. Predicted to be part of uniplex complex	EFHA2

Figure S1

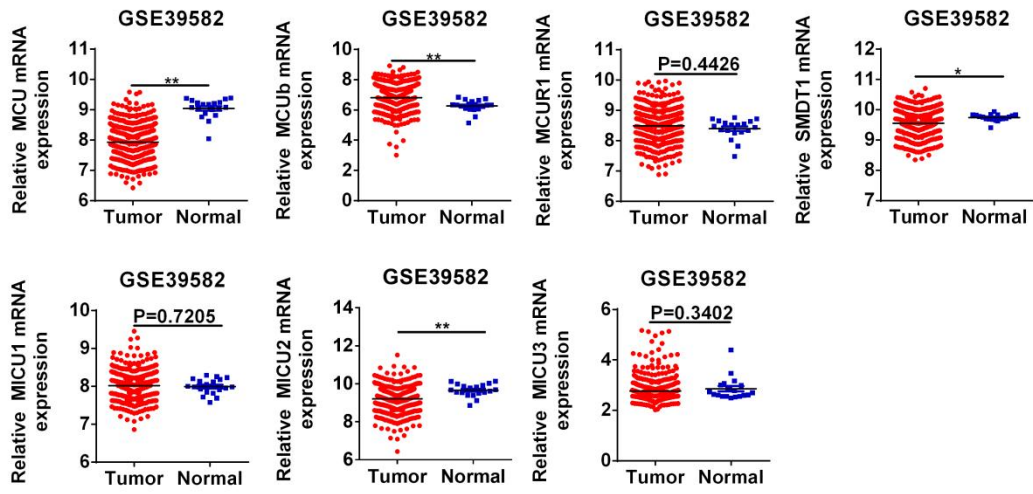


Figure S2

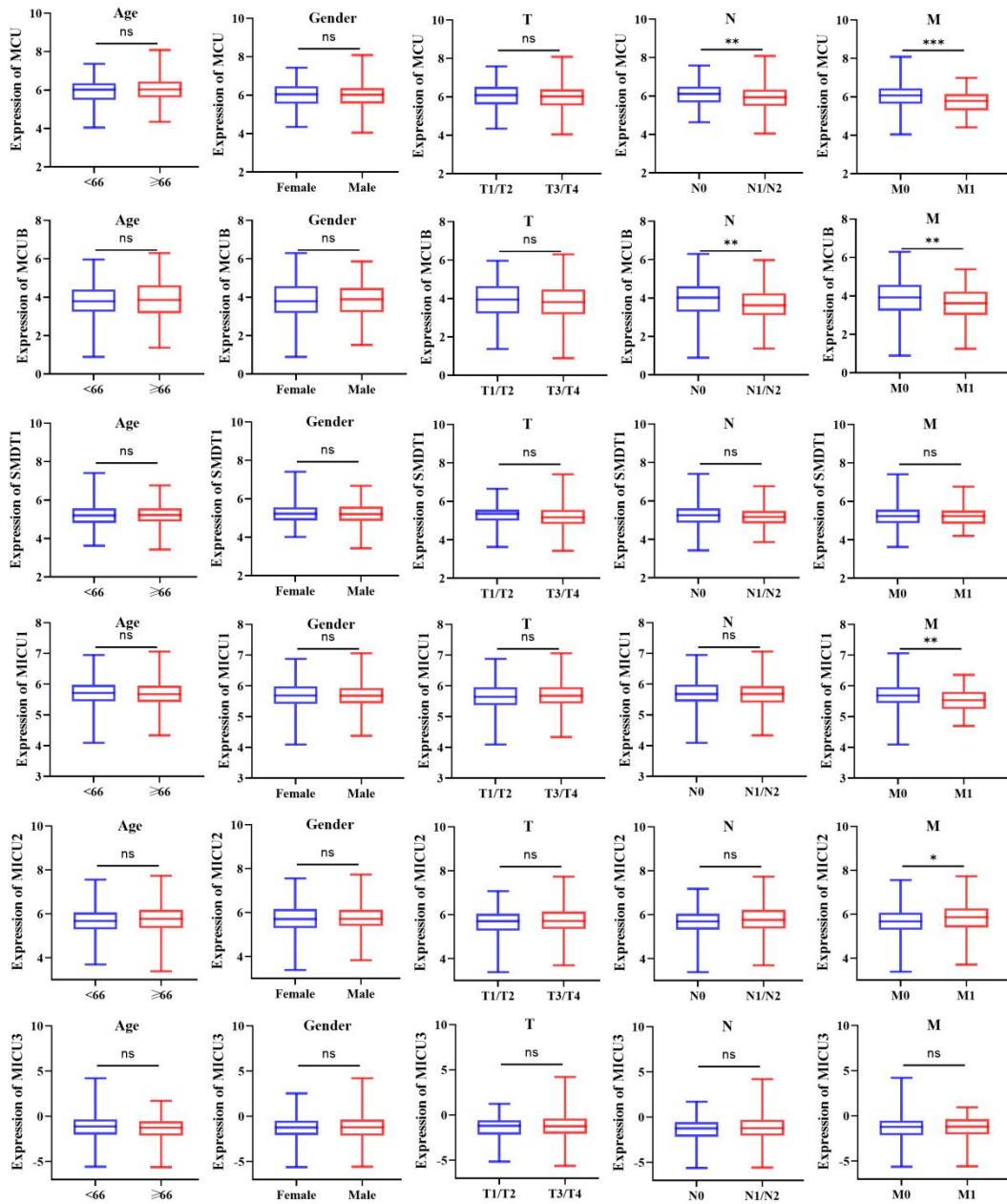
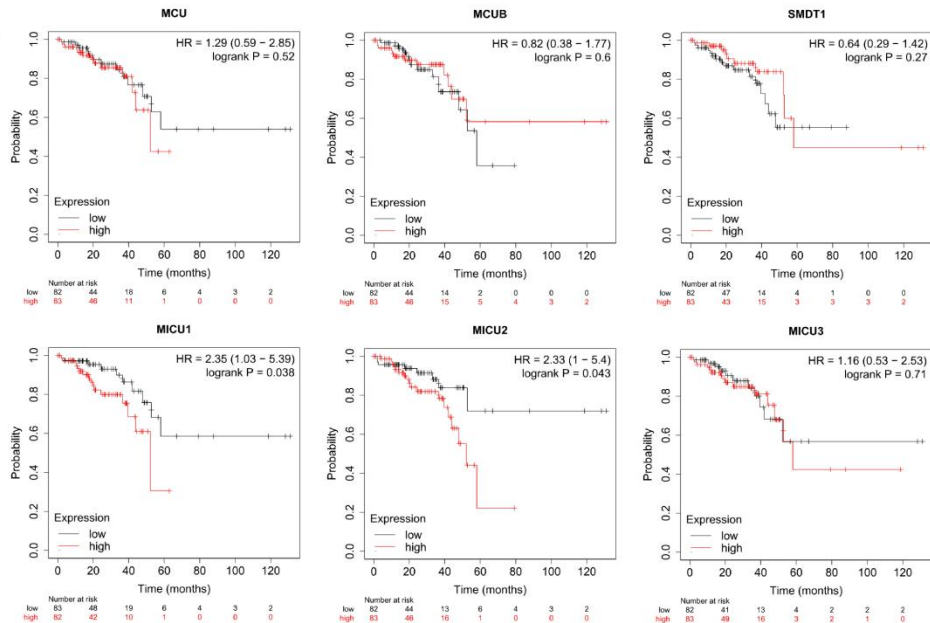


Figure S3

A



B

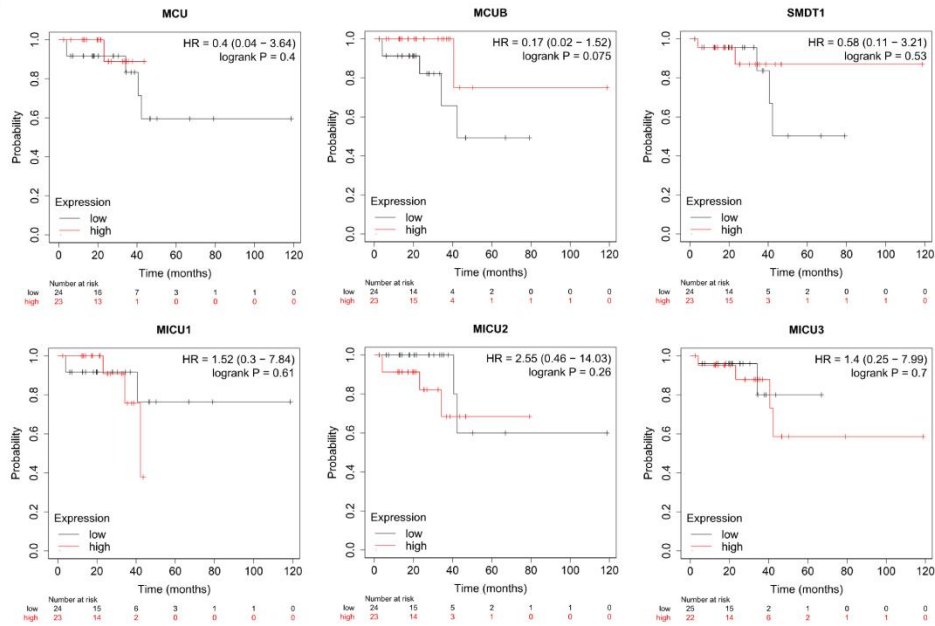


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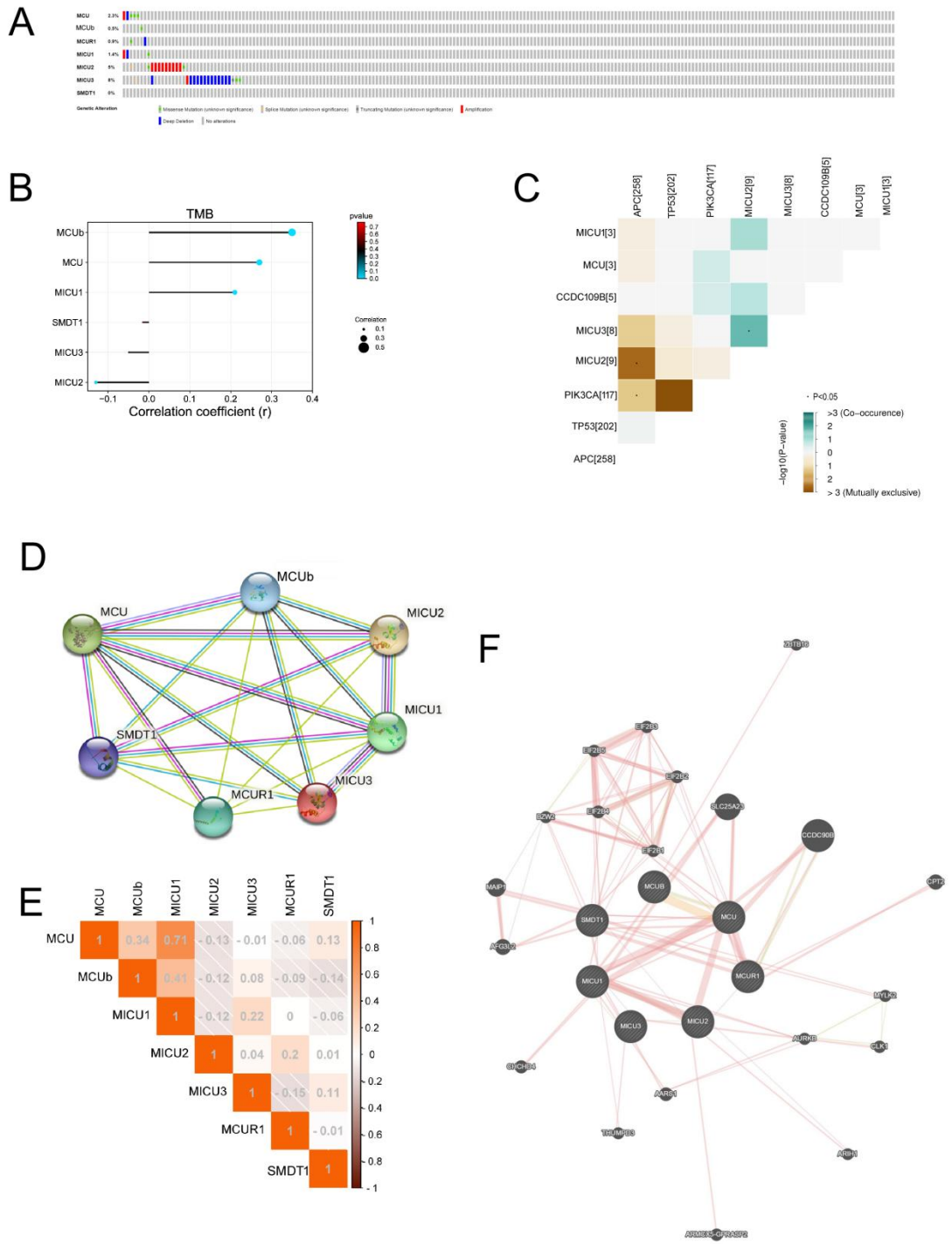


Figure S5

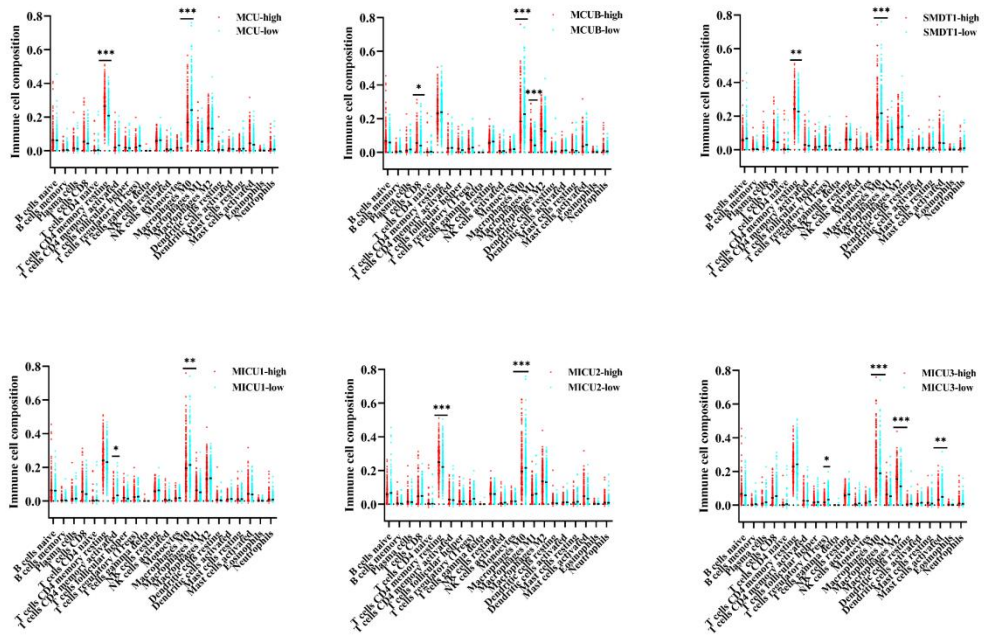


Figure S6

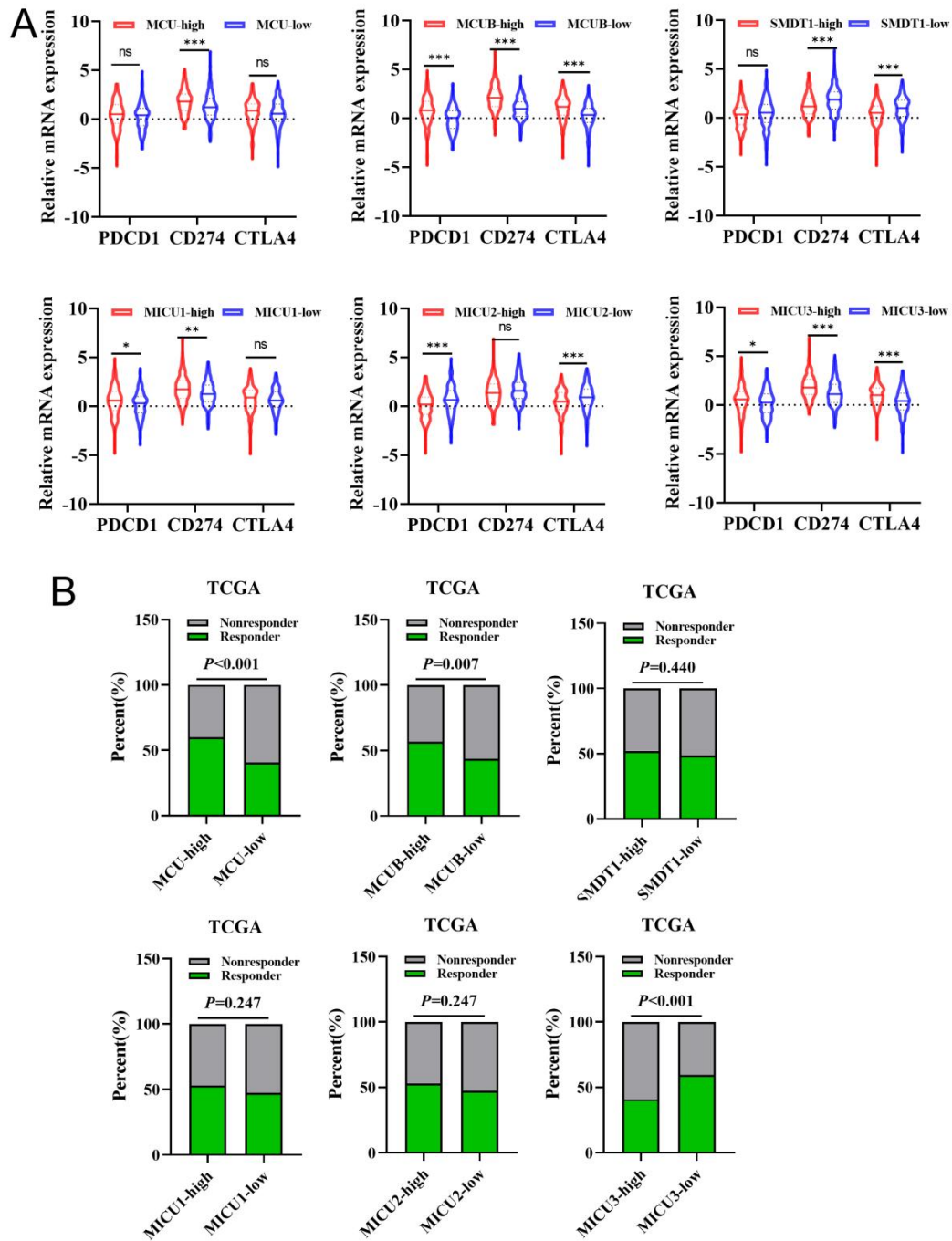


Figure S7

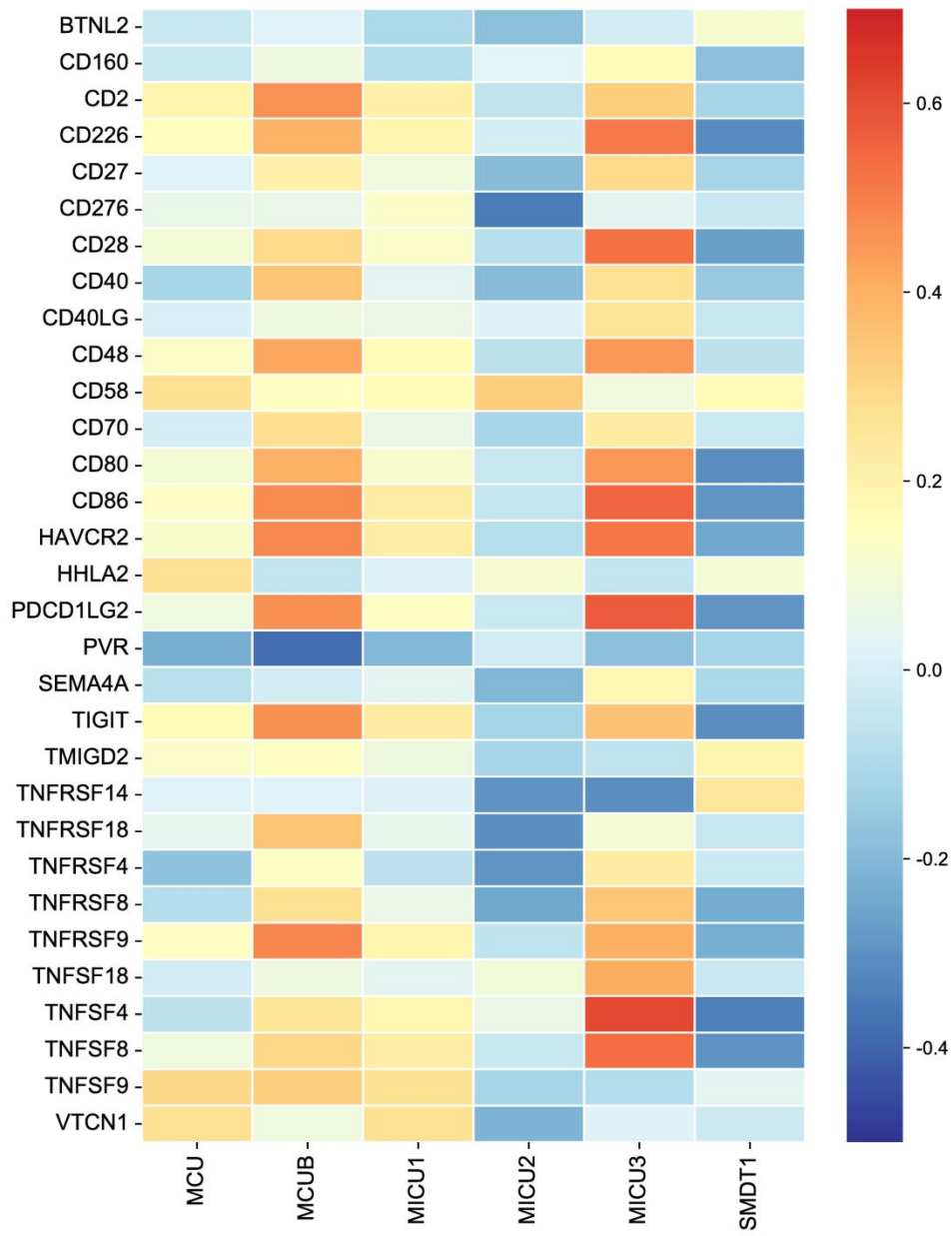


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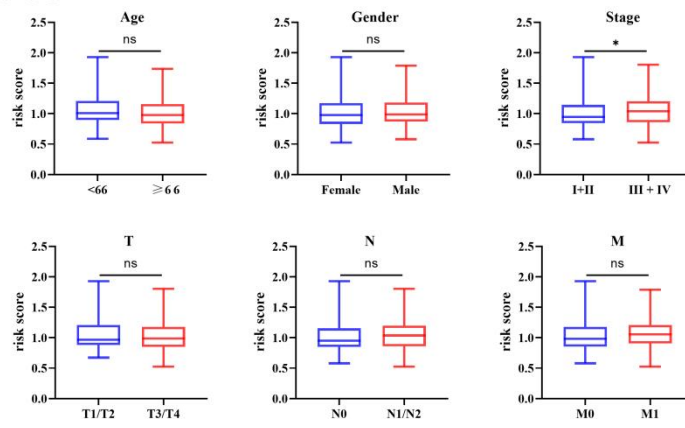


Figure S9

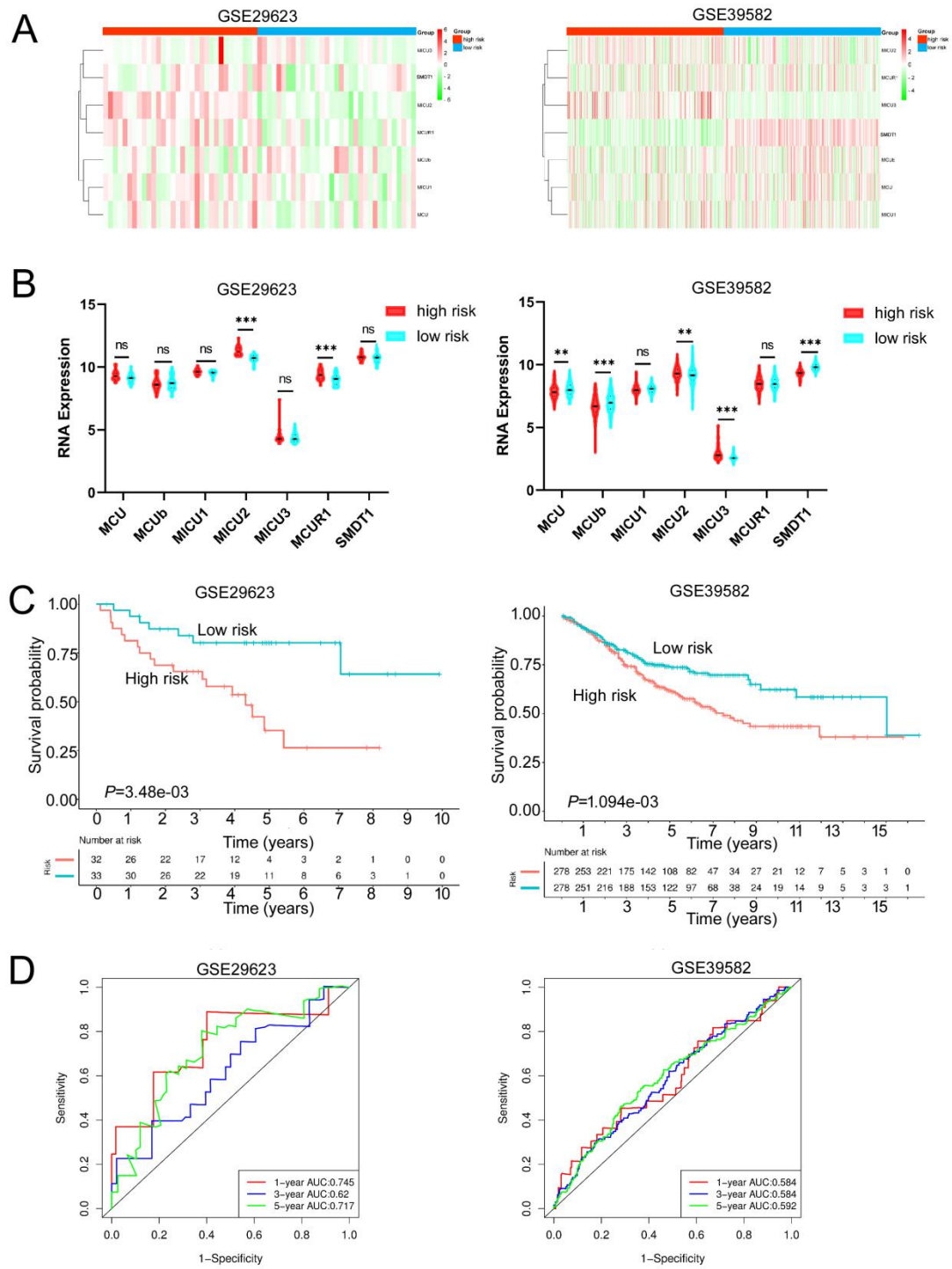


Figure S10

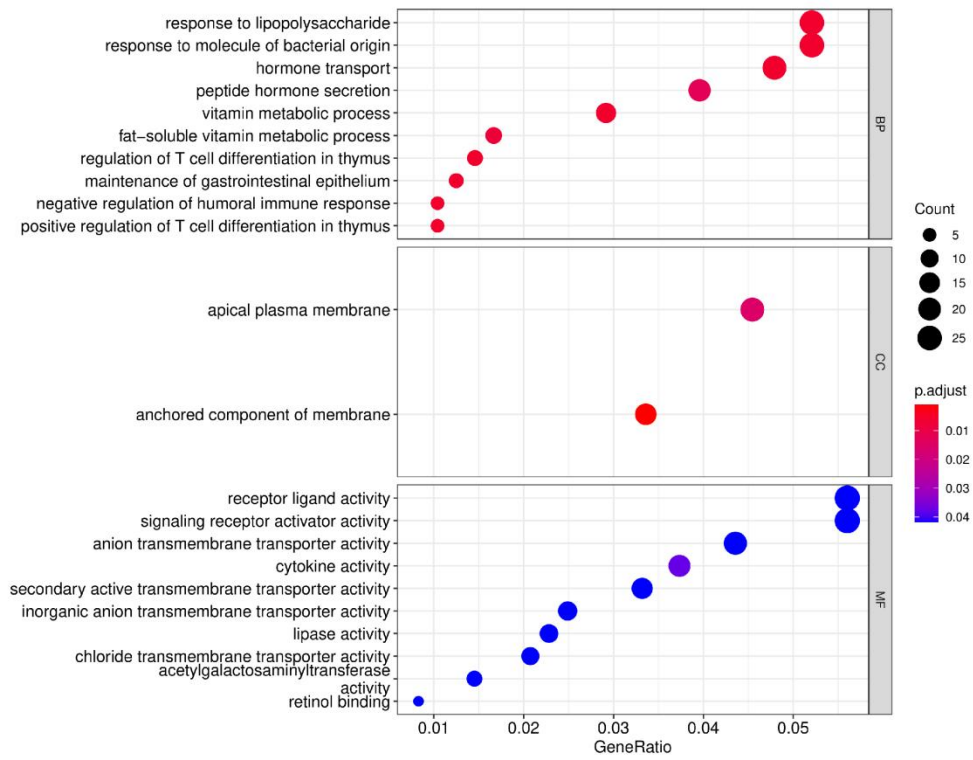


Figure S11

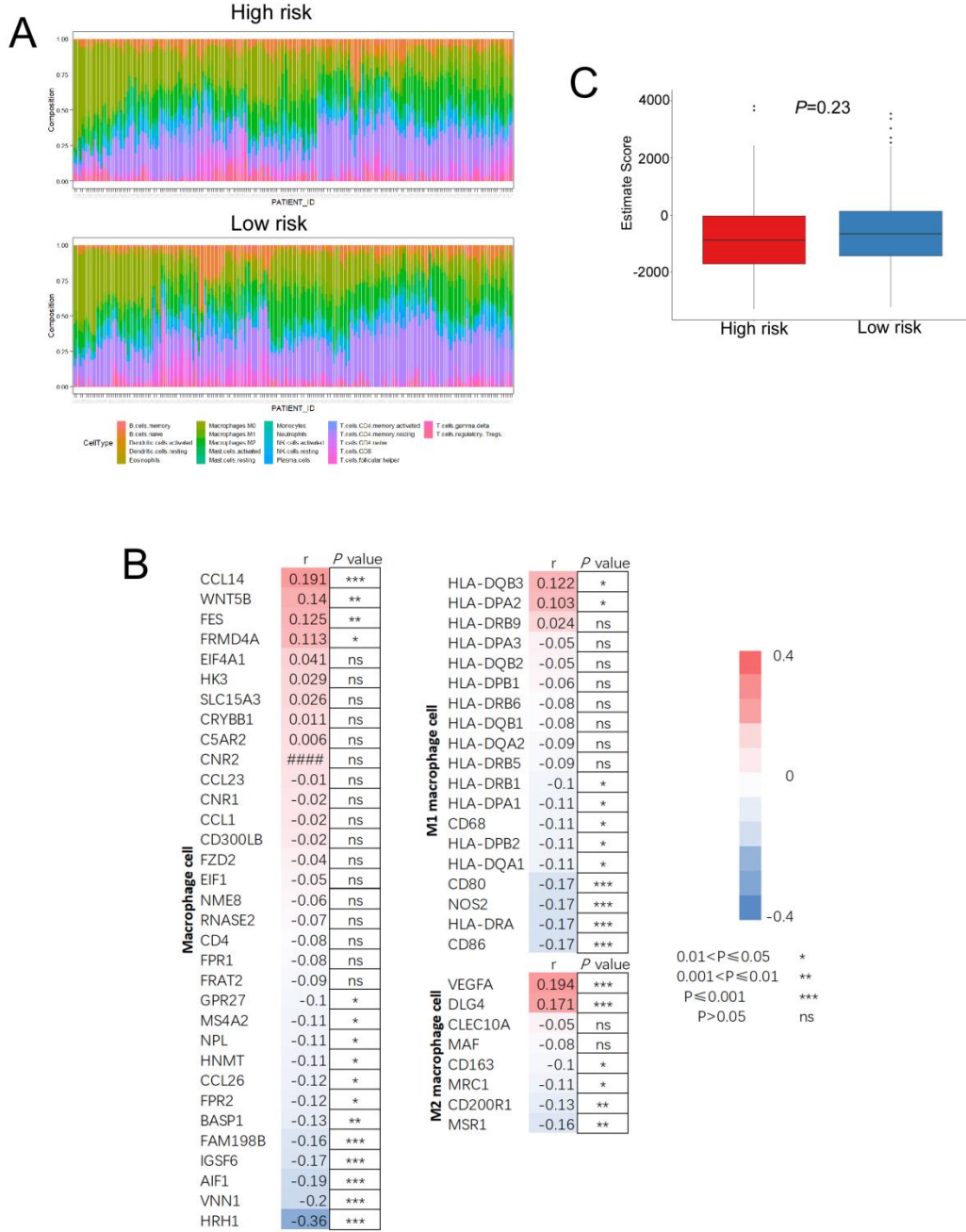


Figure S12

