Supplementary

Table S1 Cuproptosis-related genes

ID
FDX1
LIPT1
LIAS
DLD
DBT
GCSH
DLST
DLAT
PDHA1
PDHB
SLC31A1
ATP7A
ATP7B

Table S2 Primers used in this study

Gene	Forward/reverse primer	Sequence
ATP7A	F	CTGTACAGGGCAAAACATCAG
	R	ACTGTGCTGCCAGGTTTCTT
LIPT1	F	GGGGTCGTATGACGCACTTT
	R	TGGGACCTGGCAGTTACAAA
DLAT	F	CTCCCACAGGTCCTGGAATG
	R	TGCTTCTCCCTTCTAATATCTGG
GAPDH	F	GCACCGTCAAGGCTGAGAAC
	R	TGGTGAAGACGCCAGTGGA
DLAT-shRNA		CCACTCTGTATCATTGTAGAA

Table S3 Immune_checkpoint_genes

Immune_checkpoint_genes
ADORA2A
BTLA
BTNL2
C10orf54
CD160
CD200
CD200R1
CD244

Table S3 *(continued)*

Immune_checkpoint_genes
CD27
CD274
CD276
CD28
CD40
CD40LG
CD44
CD48
CD70
CD80
CD86
CTLA4
HAVCR2
HHLA2
ICOS
ICOSLG
IDO1
IDO2
KIR3DL1
LAG3
LAIR1
LGALS9
NRP1
PDCD1
PDCD1LG2
TIGIT
TMIGD2
TNFRSF14
TNFRSF18
TNFRSF25
TNFRSF4
TNFRSF8
TNFRSF9
TNFSF14
TNFSF15
TNFSF18
TNFSF4
TNFSF9
VTCN1

https://dx.doi.org/10.21037/jgo-24-609

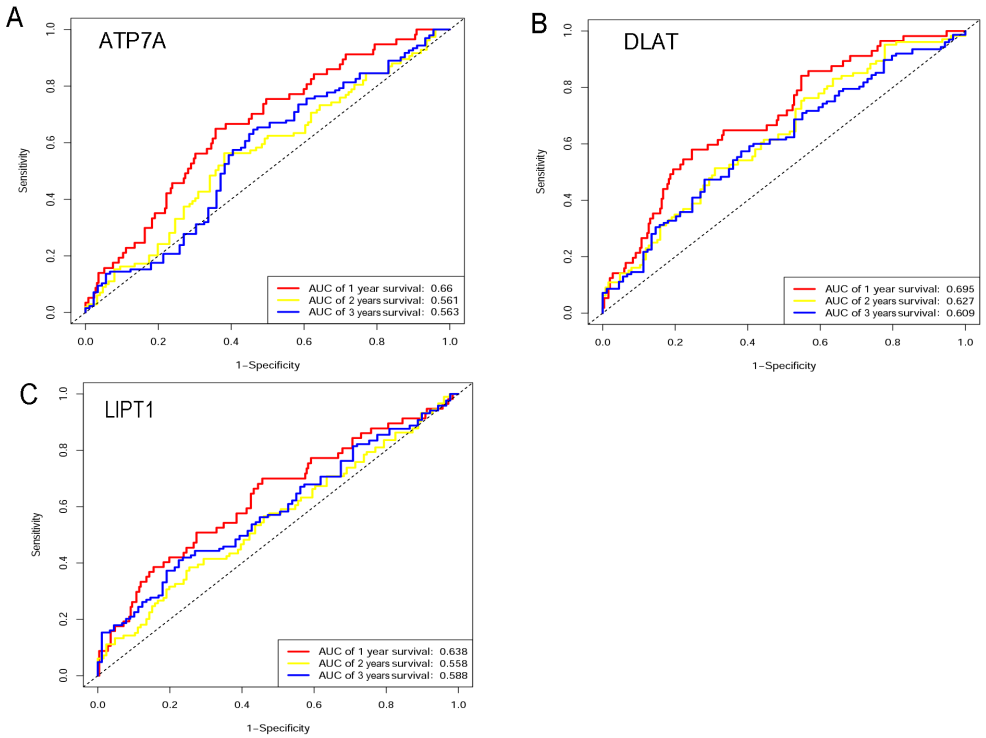

Figure S1 AUC curve of *ATP7A*, *DLAT*, and *LIPT1*. AUC, area under the curve.

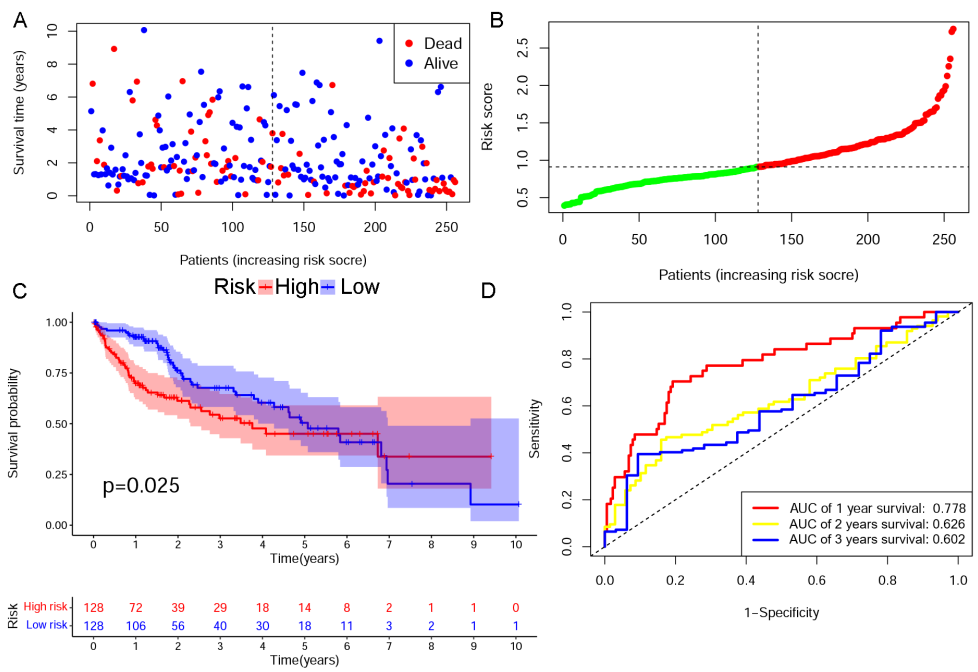

Figure S2 Validation of the risk model with GEO dataset. Green dots: these are located on the left side of the graph and represent patients with lower risk scores; Red dots: these are on the right side of the graph and represent patients with higher risk scores. GEO, Gene Expression Omnibus; AUC, area under the curve.

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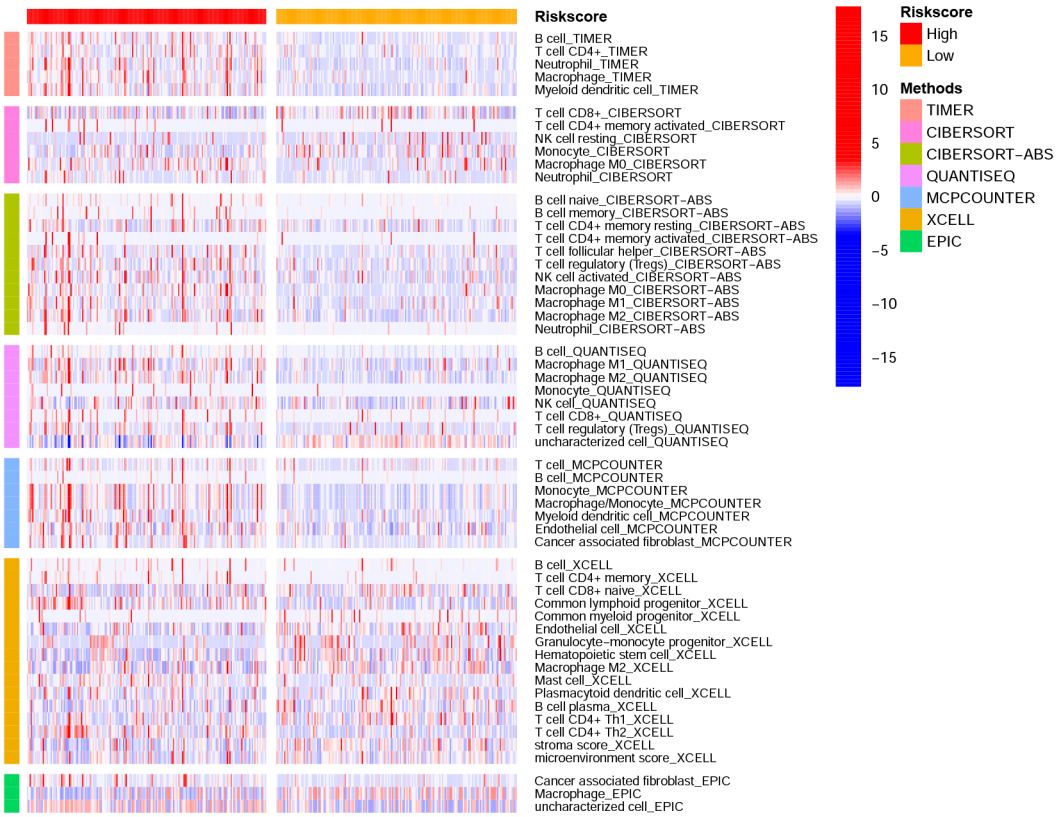

Figure S3 Immune cells infiltration between high-risk groups and low-risk groups.

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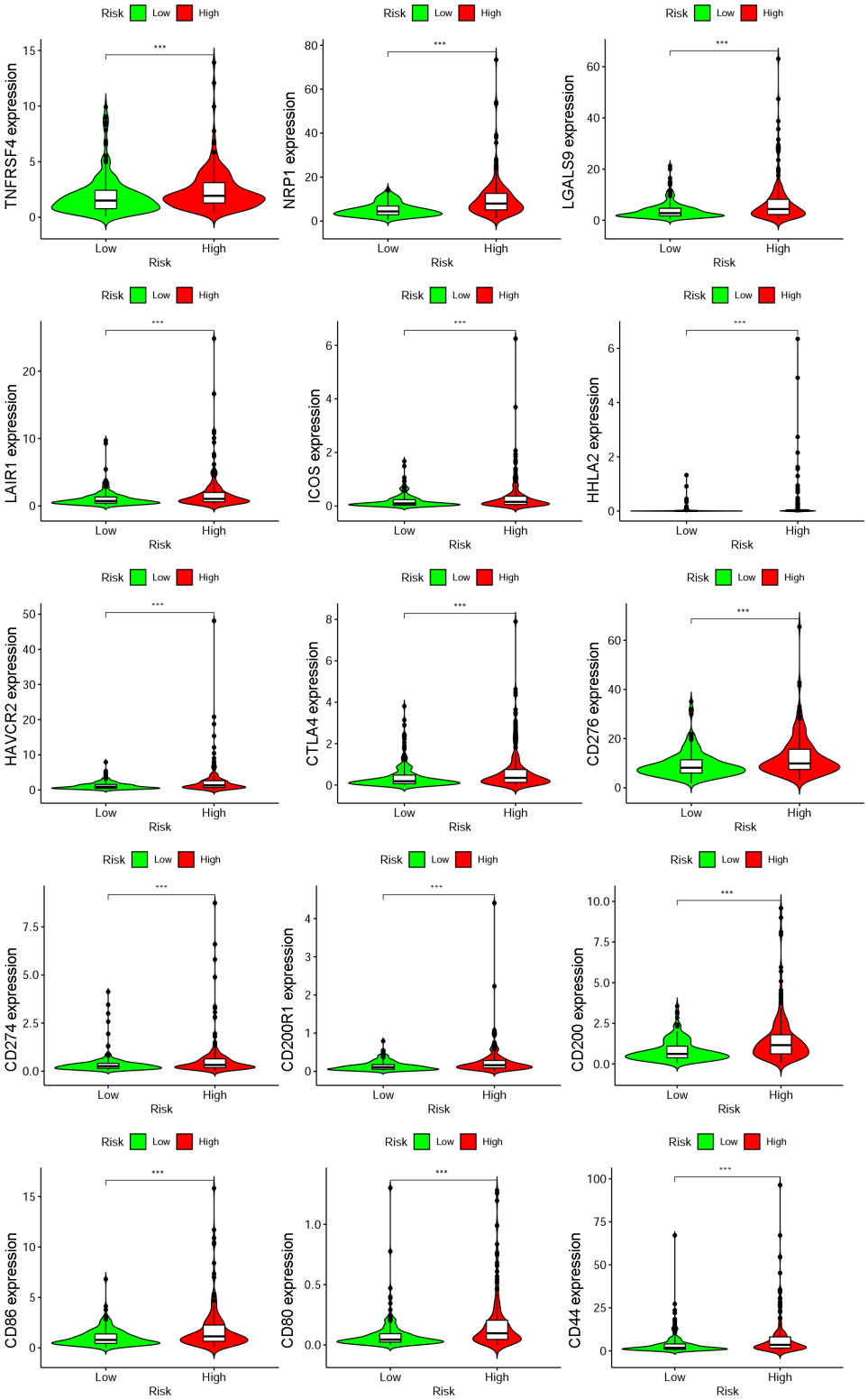

Figure S4 The relationship between prognostic signature and immune checkpoints. ***, P<0.001. NRP1, Neuropilin 1; LGALS9, Galectin 9; LAIR1, Leukocyte Associated Immunoglobulin Like Receptor 1; ICOS, Inducible T Cell Costimulator; HHLA2, HERV-H LTR-Associating 2; HAVCR2, Hepatitis A Virus Cellular Receptor 2; CTLA4, Cytotoxic T Lymphocyte Associated Protein 4.

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