Supplementary

Table S1 The description of CPRGs

Cuprotosis
FDX1
LIAS
LIPT1
DLD
DLAT
PDHA1
PDHB
MTF1
GLS
CDKN2A

CPRGs, cuproptosis-related genes.

Table S2 Lasso_coef for calculating risk_score

Genes	lasso_coef
GOLT1A	–0.00577
STXBP2	–0.02566
DCXR	0.135932
ILVBL	0.091837
ZNF524	–0.19804
COX7B	–0.00812
MED19	0.070801
FKBP9	0.042239
ALDH1L2	0.095136
RILP	–0.03035
EXT1	–0.01006
TPST1	0.064143
EMP1	0.143527
LIPT1	–0.176

https://dx.doi.org/10.21037/tau-24-456

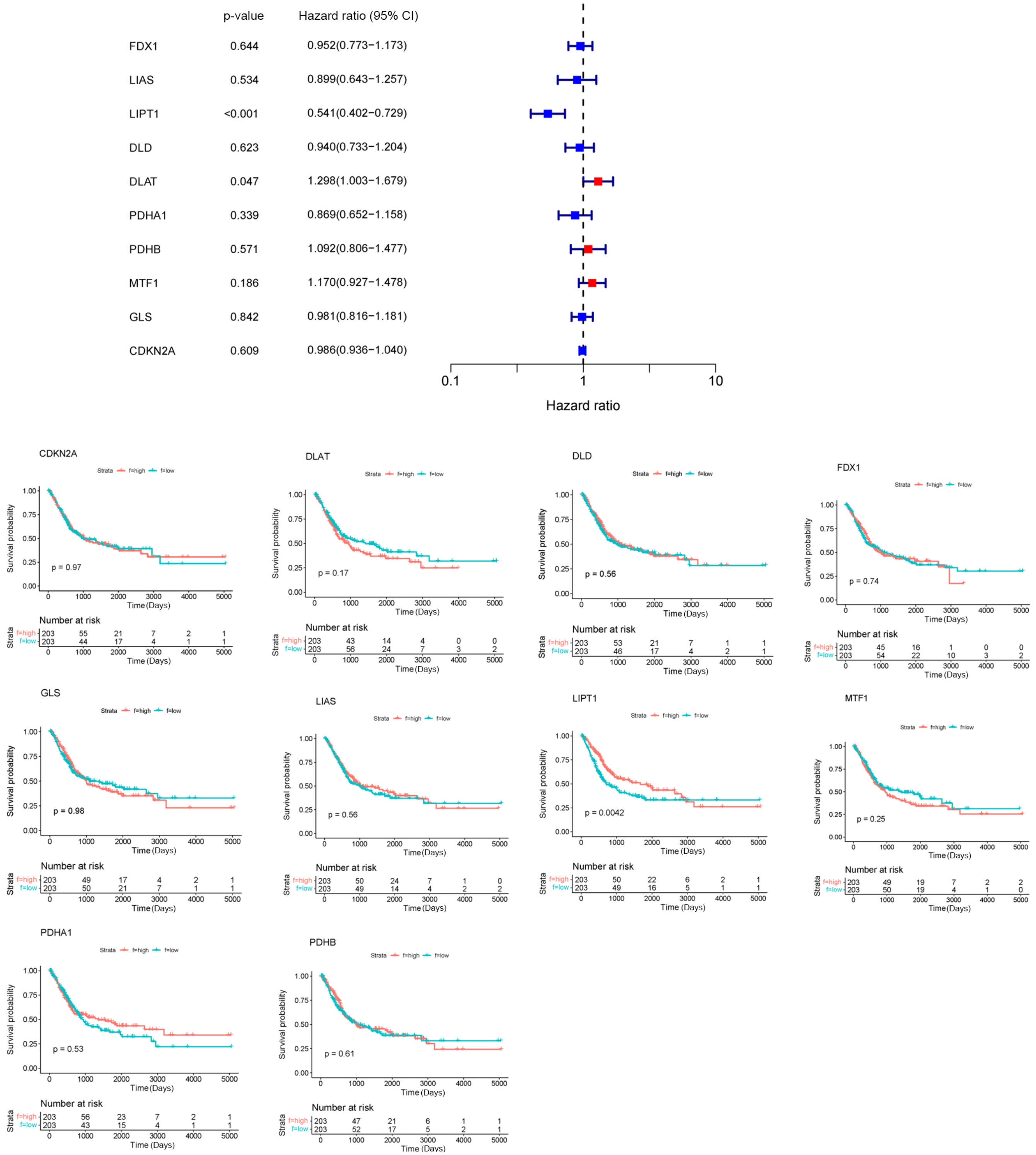

Figure S1. Prognostic analysis of cuproptosis-related genes in BLCA. BLCA, bladder cancer.

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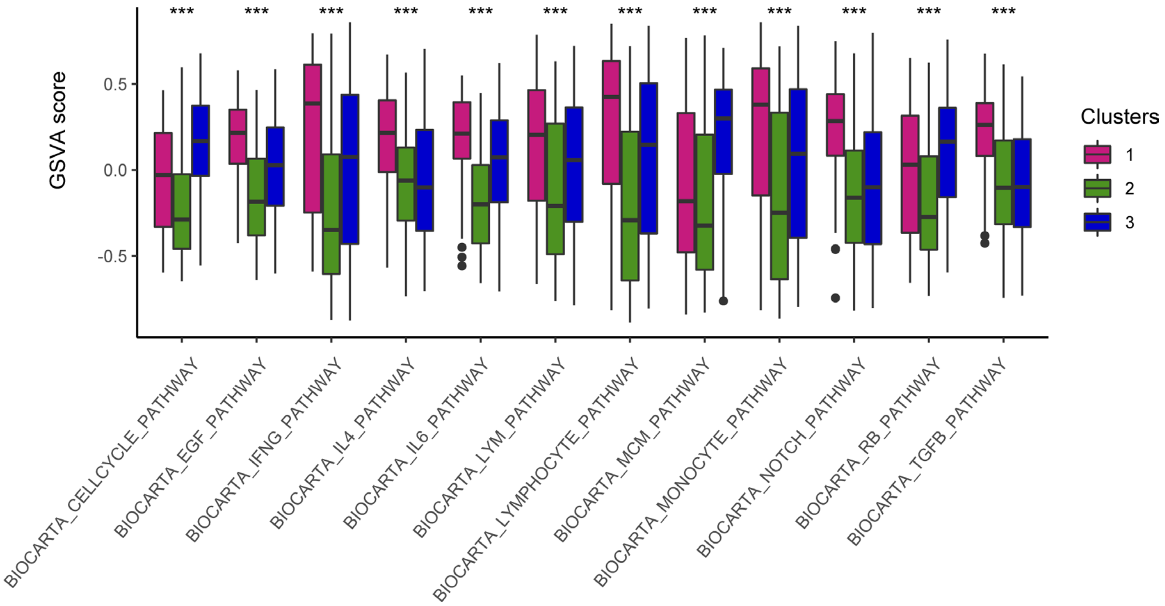

Figure S2 Pathway analysis of NMF clusters in BLCA. ***, P<0.001. BLCA, bladder cancer; NMF, non-negative matrix factorization; GSVA, gene set variation analysis.

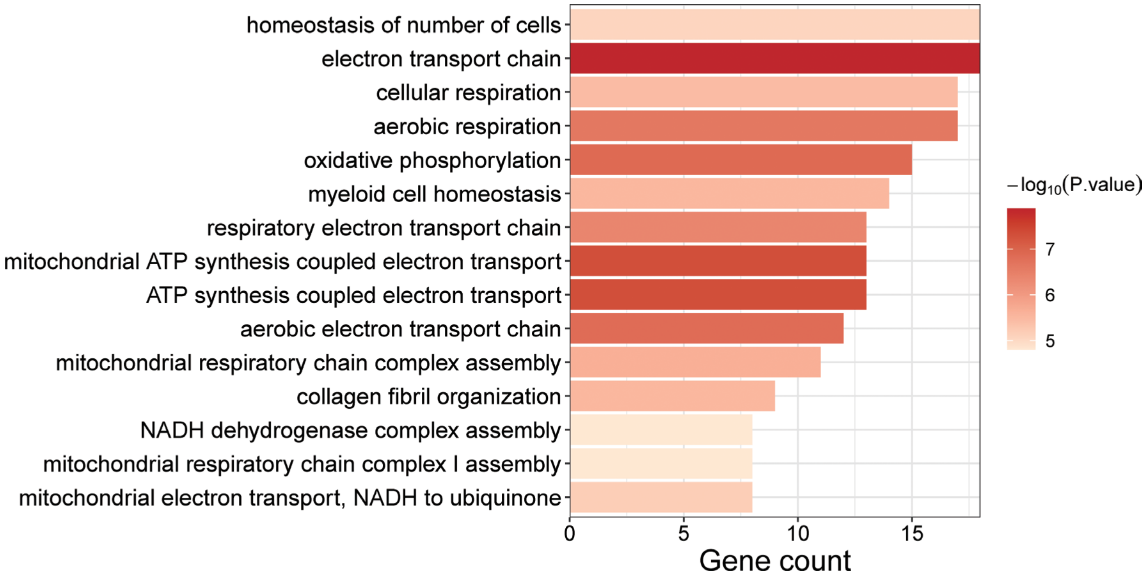

Figure S3 Gene ontology analysis of DEGs. DEGs, differentially expressed genes; ATP, adenosine triphosphate; NADH, nicotinamide adenine dinucleotide.

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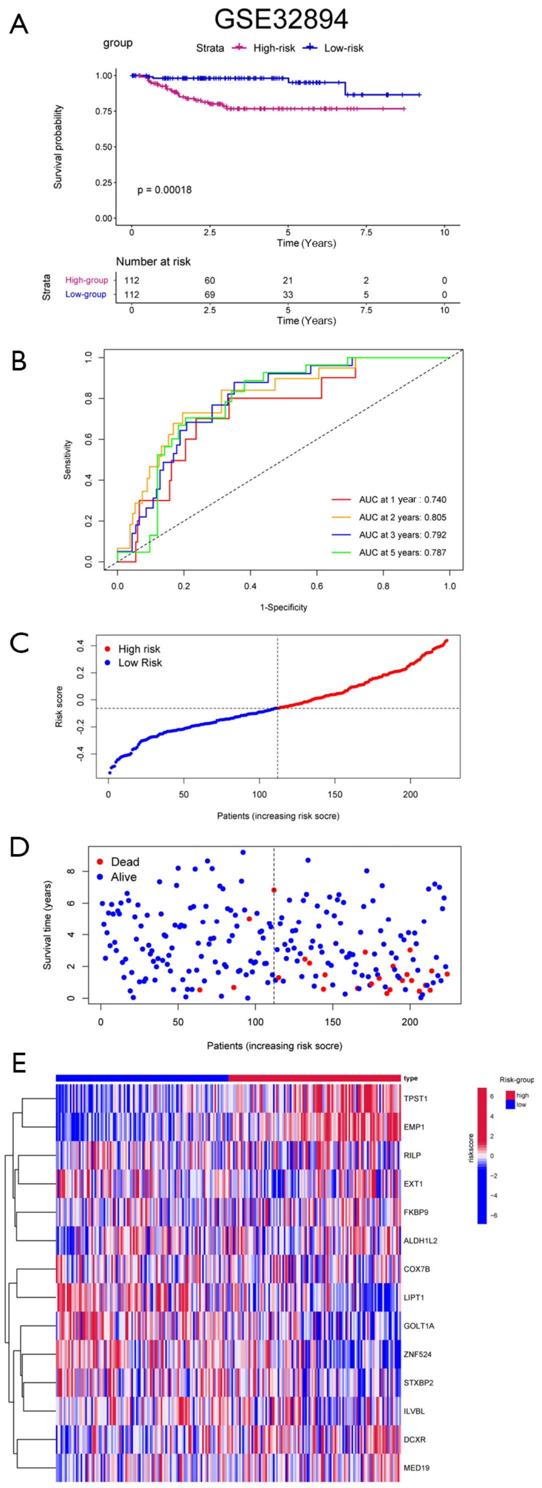

Figure S4 Predictive capacity of CPRG_score in prognosis of patients from an external control. CPRGs, cuproptosis-related genes; AUC, area under the curve.

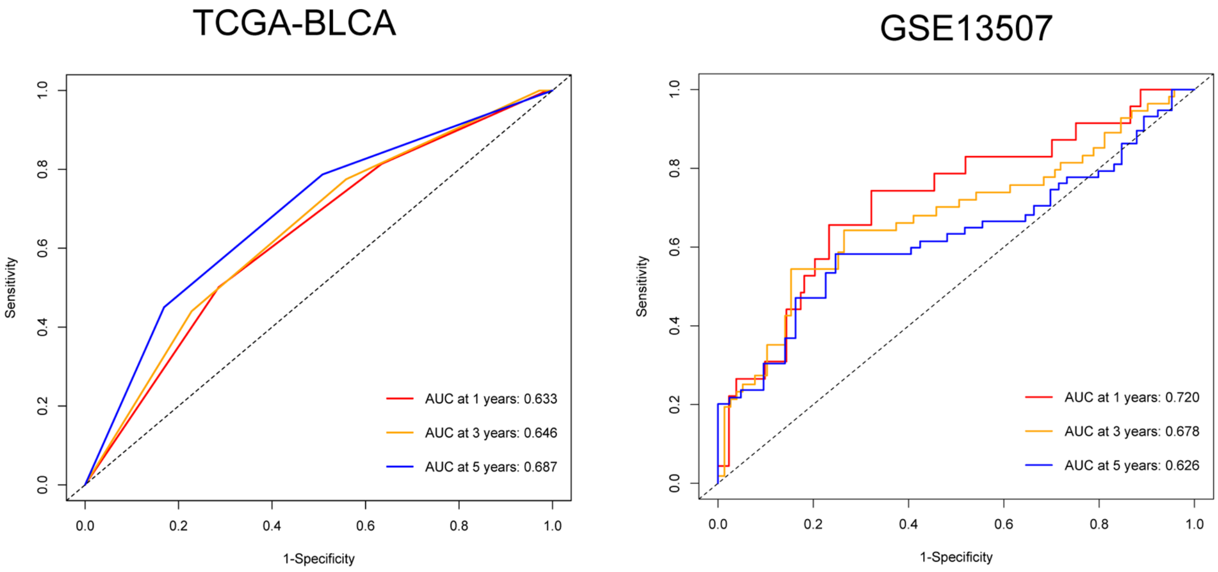

Figure S5 Predictive capacity of CPRG_score in patients' prognosis. CPRGs, cuproptosis-related genes; AUC, area under the curve.

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