Supplementary

Table S1 Cuproptosis-related genes according to the study of Tsvetkov *et al.*

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

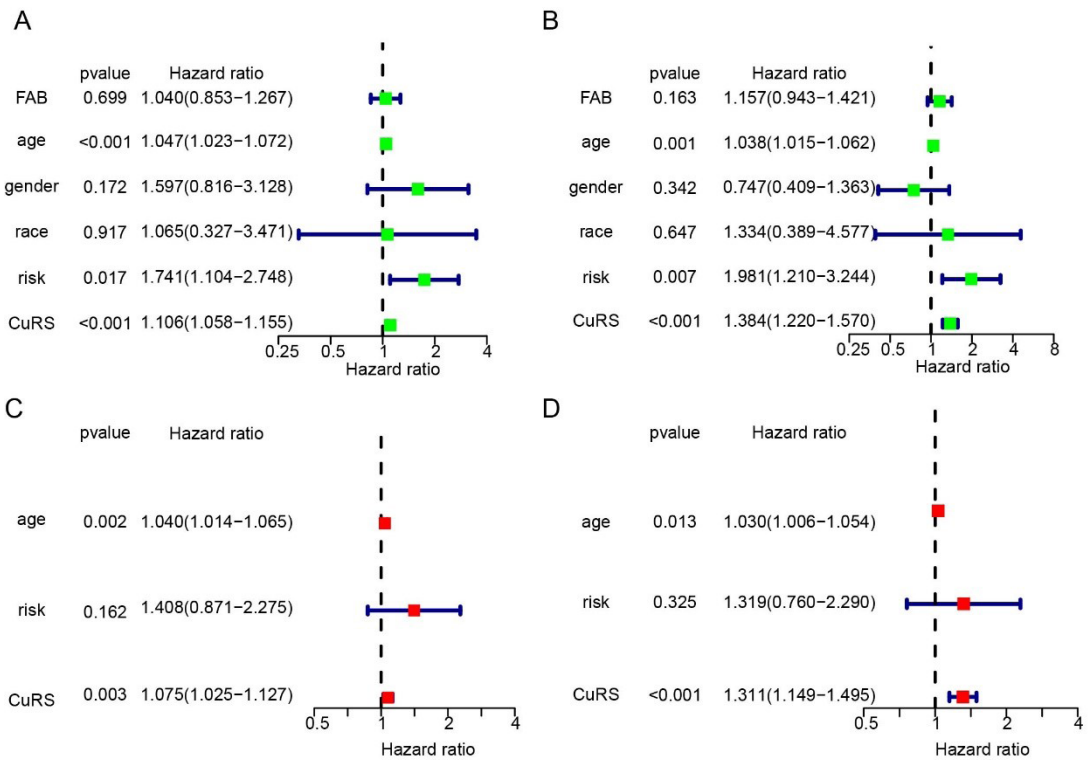

Figure S1 Univariate and multivariate Cox analysis of CuRS and other clinical characteristics. The impact on survival due to continuous variables can be analyzed using Cox proportional risk regression models, as well as multivariate analysis of the impact on survival. The univariate Cox analysis showed that age, risk, and CuRS were associated with patient prognosis in both the training and testing sets (P<0.05) (A,B). The subsequent multivariate Cox analysis proved that age and CuRS could predict prognosis independently of other factors (C,D).

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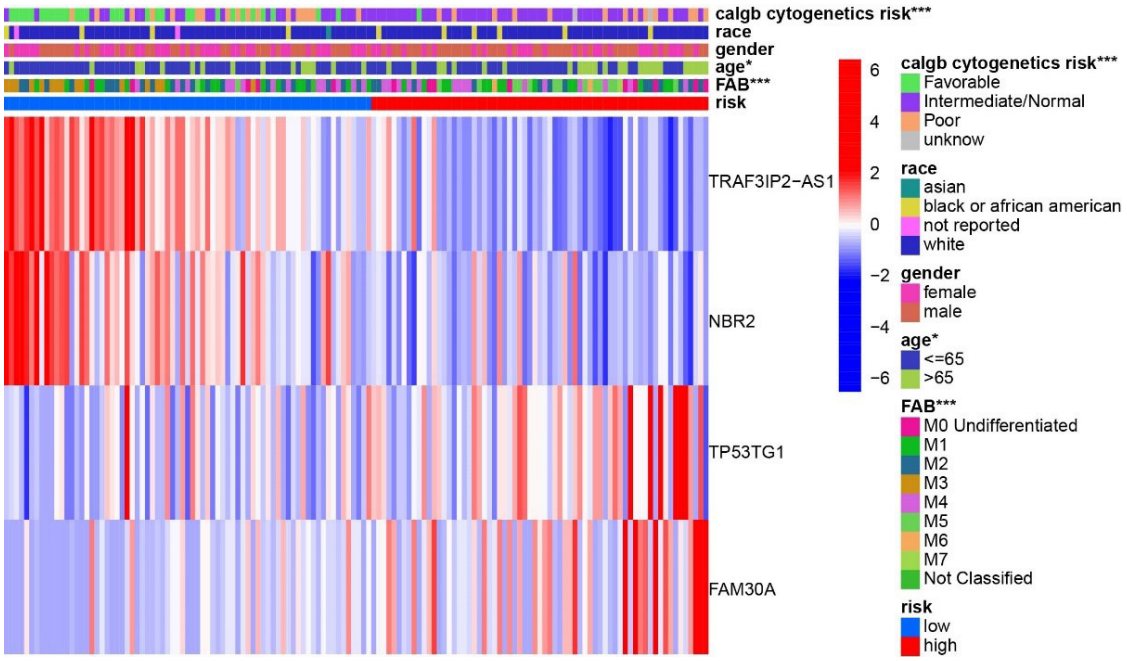

Figure S2 A heatmap displaying the expression of CuRS lncRNA in each individual with different clinical traits. The horizontal coordinates from left to right represent a progressive increase in the patient's risk. Blue indicates low expression and red indicates high expression of CuRS lncRNAs. There was a variance in the calgb cytogenetics risk, age, and FAB type of patients between the high and low-risk groups.

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Table S2 Results of GSEA enrichment analysis of between-group differential genes

GS DETAILS	Size	ES	NES	NOM P value	FDR q value
KEGG_SPHINGOLIPID_METABOLISM	39	0.57	1.99	0	0.051
KEGG_GLYCEROLIPID_METABOLISM	49	0.49	1.74	0	0.164
KEGG_ABC_TRANSPORTERS	44	0.53	1.79	0	0.17
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	0.63	1.76	0	0.199
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	54	0.47	1.72	0.002	0.183
KEGG_ENDOCYTOSIS	181	0.41	1.67	0.006	0.22
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	16	0.68	1.83	0.008	0.162
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	76	0.44	1.64	0.008	0.165
KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	32	0.53	1.65	0.008	0.18
KEGG_PEROXISOME	78	0.5	1.75	0.008	0.183
KEGG_MELANOGENESIS	101	0.42	1.62	0.01	0.152
KEGG_PRION_DISEASES	35	0.56	1.65	0.012	0.193
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	61	0.49	1.69	0.015	0.196
KEGG_CHEMOKINE_SIGNALING_PATHWAY	188	0.46	1.65	0.018	0.2
KEGG_PROTEASOME	46	0.65	1.84	0.02	0.22
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	52	0.4	1.47	0.022	0.208
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	66	0.45	1.57	0.025	0.143
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	263	0.39	1.51	0.026	0.176
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	56	0.47	1.62	0.03	0.146
KEGG_LONG_TERM_DEPRESSION	70	0.37	1.46	0.033	0.206
KEGG_PPAR_SIGNALING_PATHWAY	69	0.43	1.58	0.034	0.144
KEGG_AXON_GUIDANCE	129	0.38	1.44	0.034	0.217
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	102	0.48	1.63	0.035	0.174
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	0.62	1.66	0.035	0.209
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	96	0.46	1.6	0.04	0.142
KEGG_TYPE_I_DIABETES_MELLITUS	41	0.58	1.62	0.04	0.171
KEGG_PHENYLALANINE_METABOLISM	18	0.59	1.58	0.041	0.145
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	68	0.46	1.6	0.041	0.146
KEGG_NOTCH_SIGNALING_PATHWAY	47	0.46	1.53	0.041	0.168
KEGG_VIBRIO_CHOLERAE_INFECTION	54	0.43	1.54	0.042	0.169
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	132	0.46	1.62	0.043	0.16
KEGG_VEGF_SIGNALING_PATHWAY	76	0.37	1.43	0.044	0.219
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	79	0.38	1.46	0.046	0.209
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	81	0.49	1.62	0.048	0.142
KEGG_GRAFT_VERSUS_HOST_DISEASE	37	0.65	1.62	0.048	0.167

The filter condition is |normalized enrichment score (NES)| >1.5, P<0.05 and false discovery rate (FDR) <0.20.

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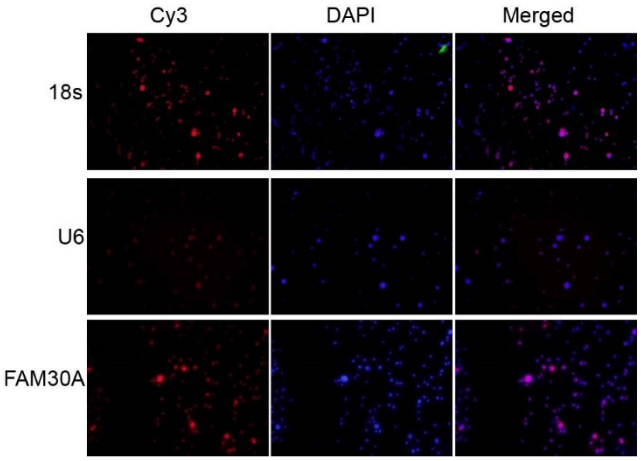

Figure S3 The intracellular localization of *FAM30A* by RNA FISH. 18S is a reference in the cytoplasm, while U6 is an intranuclear reference. The figure shows that most FAM30A is distributed in the cytoplasm.

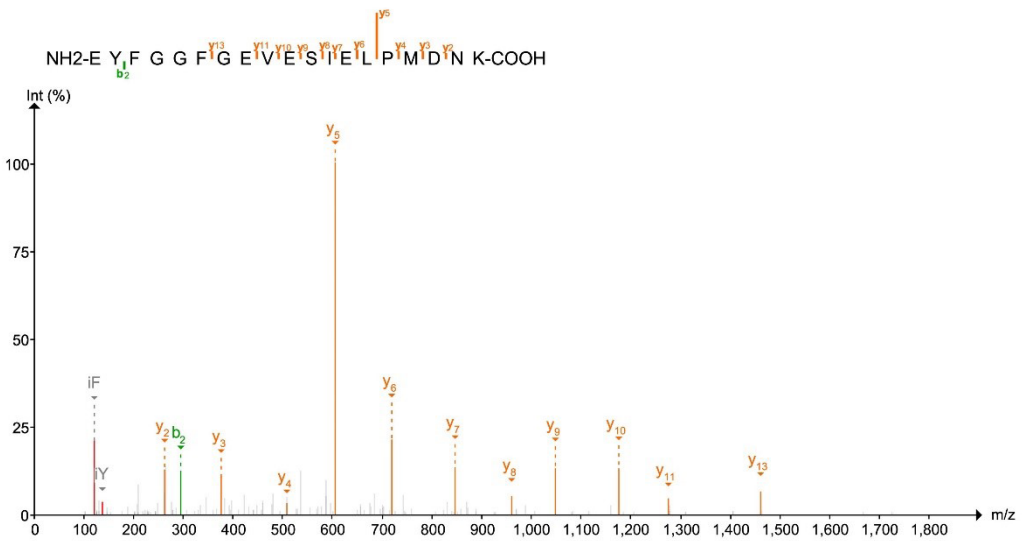

Figure S5 The presence of *AUF1* in protein-bound magnetic beads detected by mass spectrometry. The specific detection sequence is EYFGGFGEVESIELPMDNK.

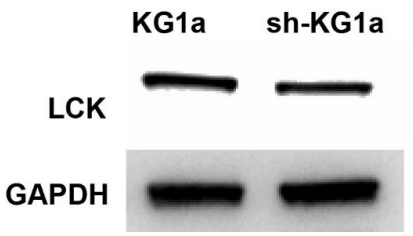

Figure S5 Expression of *LCK* protein in knockdown cells and control cells. Proteins were extracted in the KG1a cell line and FAM30A knockdown KG1a cell line and detected using a western blot. GAPDH was selected as a quantitative reference. It can be seen that in the knock-down group, the LCK is expressed at a lower level.

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