

Table S1 Details of Modification Sites of ferroptosis-related Proteins

Protein	Ubiquitination site	Matched peptides	Cancer/normal ratio	Regulated type
CYBB	K521	HLNDDVVKIDFEDVIAEPEGTHSFDGIWK	0.456	Down
SCP2	K491	GSVLPNSDKK	0.205	Down
SCP2	K492	KADCTITMADSDFLALMTGK	0.185	Down
SLC1A5	K537	GPAGDATVASEKESVM	0.35	Down
DUOX1	K734	GALKESGLSIQEWELR	0.221	Down
DUOX1	K1005	KVTSFQPLLFTAHR	0.256	Down
KRAS	K5	TEYKLVVVGAGGVGK	1.568	Up
CAV1	K26	EQGNIIKPNK	0.396	Down
CAV1	K65	HLNDDVVKIDFEDVIAEPEGTHSFDGIWK	4.142	Up

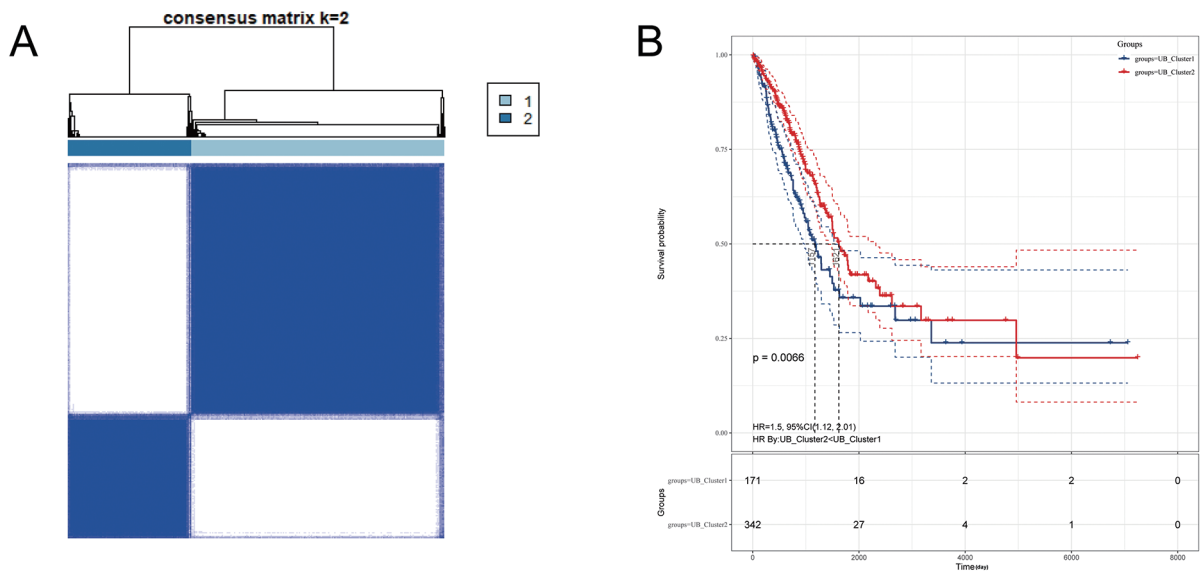


Figure S1 Identification of prognostically related ubiquitinated protein-encoding gene expression patterns in The Cancer Genome Atlas (TCGA)-lung carcinoma (LUAD) dataset. (A) Consensus clustering of prognostically relevant genes for all TCGA samples. (B) Survival analysis between two expression patterns.

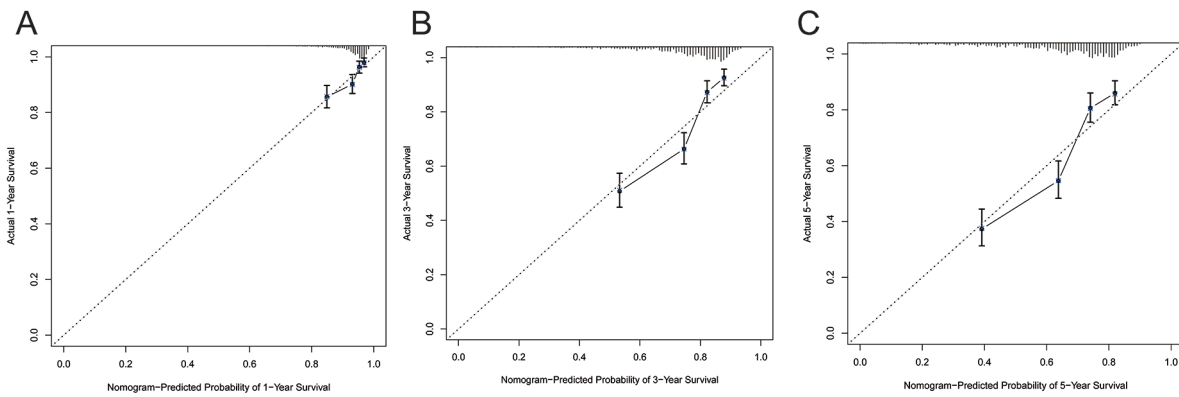


Figure S2 Predictive effect evaluation of nomogram. (A) Nomogram-Predicted Probability of 1-Year Survival. (B) Nomogram-Predicted Probability of 3-Year Survival. (C) Nomogram-Predicted Probability of 5-Year Survival.