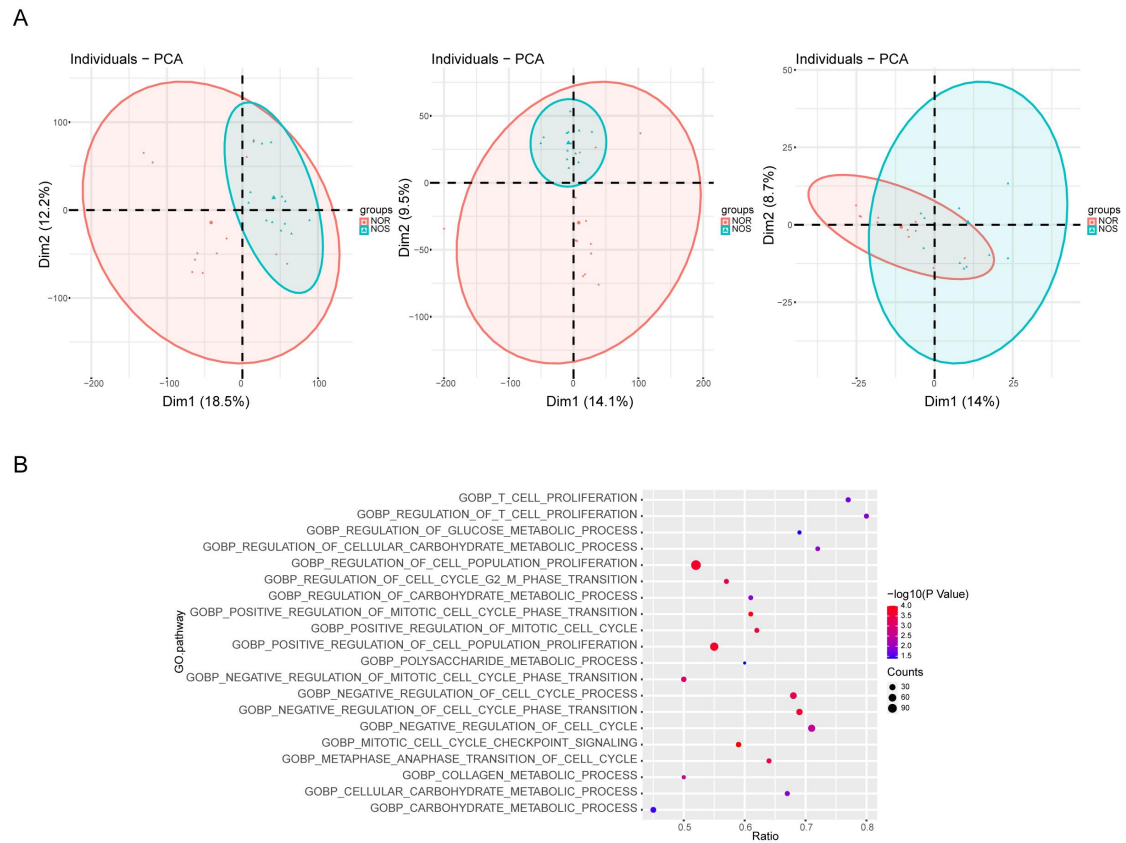
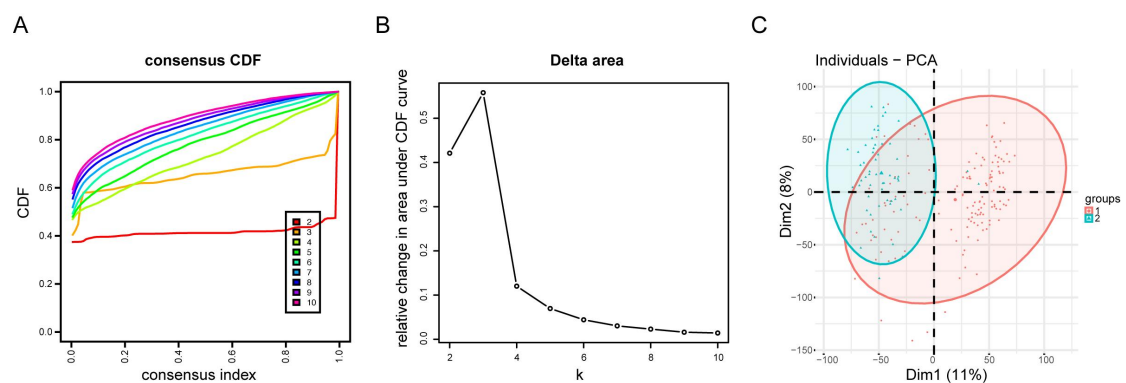




Supplementary Figure 1

(A) PCA depicted the distribution for clusters of ELOVL5, AL139023.1 and miR-139-5p.

(B) C5-GO enrichment analysis of differential expression analysis in mRNAs



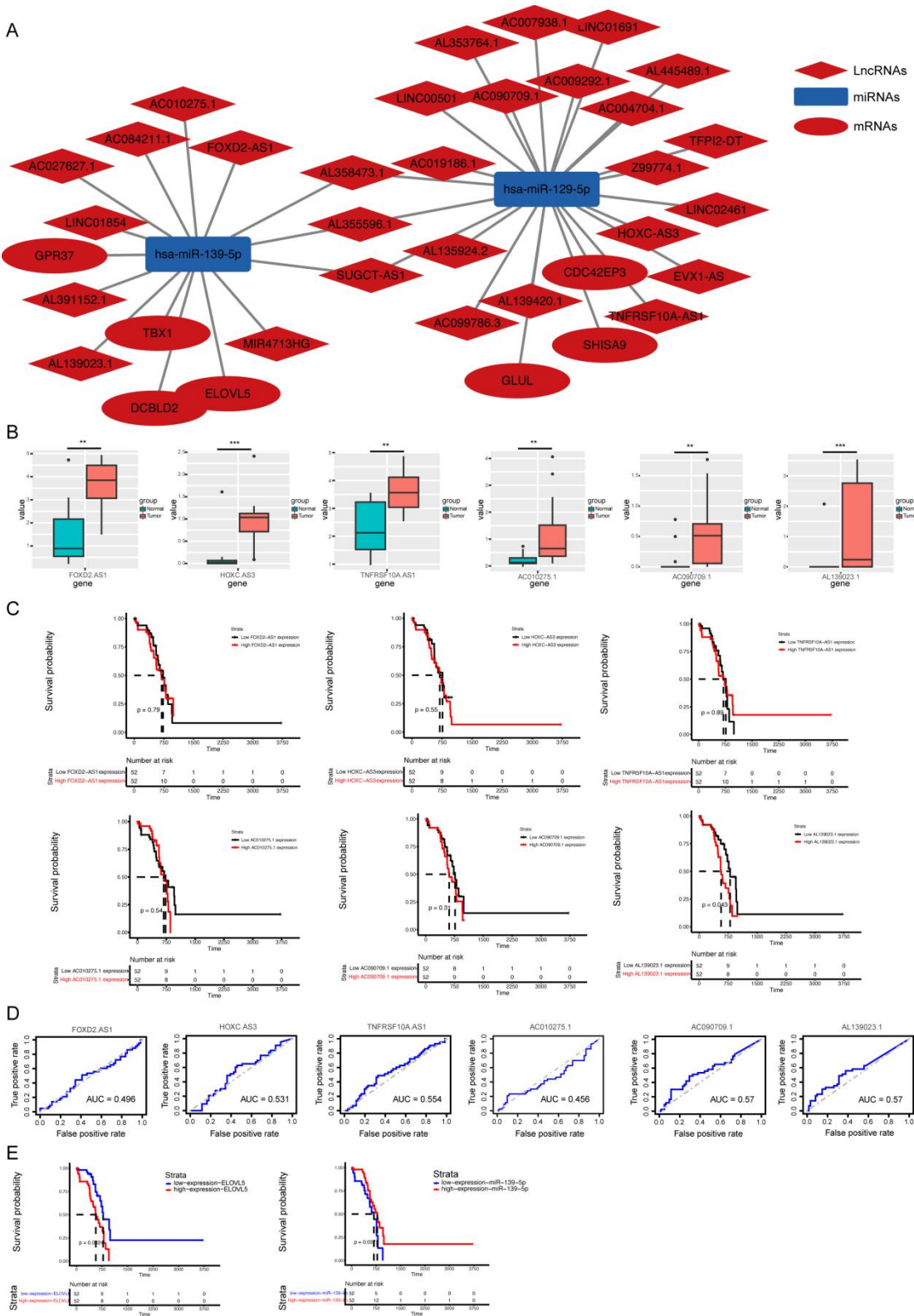
Supplementary Figure 2

(A) Cumulative distribution function (CDF) curves for $K = 2$ to $K = 10$. The x-axis represents the consensus index (ranging from 0 to 1), and the y-axis represents the cumulative distribution function value. The curves show the stability of cluster assignments.

(B) Delta area plot. The relative change in the area under the CDF curve for $K = 2$ to $K = 10$.

(C) PCA depicted the distribution for clusters of cuproptosis related genes. 1 represents group 1,

and 2 represents group 2.



(B) The expression of potential lncRNAs between tumor and normal tissues in ESCC patients.

The red box indicates the tumor tissue and the green box indicates the normal tissue.

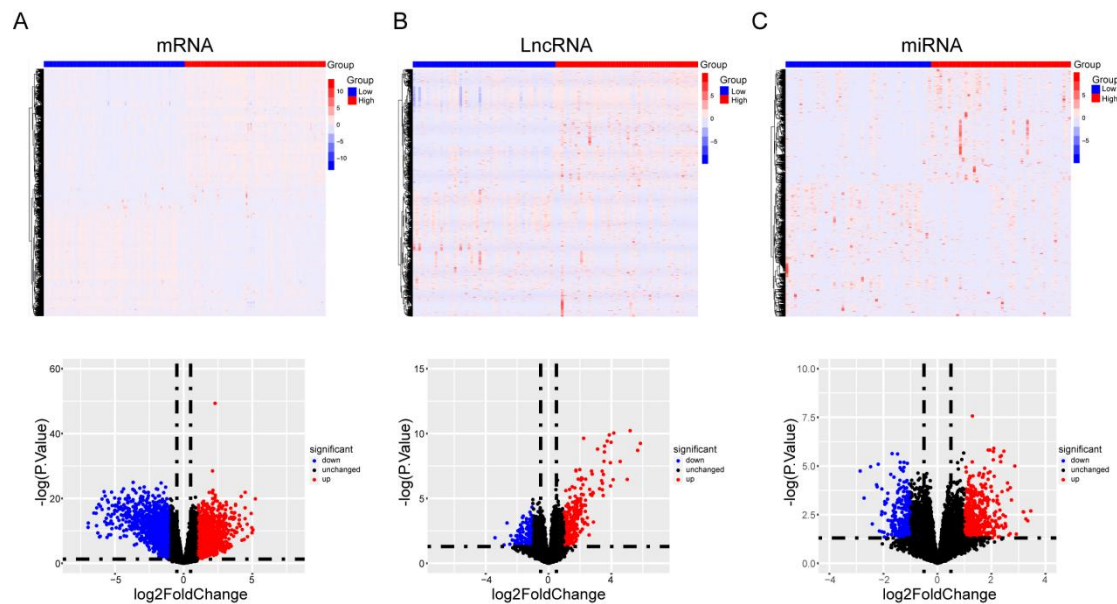
(C) Survival analysis of potential lncRNAs.

(D) The ROC curves of potential lncRNAs.

(E) Association of the expression levels of ELOVL5 and miR-139-5p with patient survival

The statistical method is T-test. Values were expressed as the mean $\pm$ SD from three experiments,

and the asterisk indicates the statistical significance compared to the controls. (**, $p < 0.01$, ***, $p < 0.001$).



Supplementary Figure 4

(A) The heatmap and the volcano plots of differential expression analysis of ELOVL5 in low expression group and high expression group.

(B) The heatmap and the volcano plots of differential expression analysis of AL139023.1 in low expression group and high expression group.

(C) The heatmap and the volcano plots of differential expression analysis of miR-139-5p in low expression group and high expression group.

Box S1 The sequence of siRNA	
gene	Sequence (5'→3')
siELOVL5	GGAACATTTTGATGCATCA

Box S2 The sequence of primer	
gene	Primer sequence (5'→3')
ELOVL5	F:CAAGAACAACCACCAGATCACG R:CCAGTTCATCACAAACCACCAG
miR-139-5P	ACTTCCTCTCTACAGTGCACGTG
AL139023.1	F:TGCTACAGCAAGTTGCCCT R:CCACTGAGTCAAAAGAAA

Box S3 Correlation of ELOVL5, AL139023.1, and miR-139-5p expression levels with clinicopathological parameters

Characteristics	ELOVL5 expression		P-value
	Low	High	
	(%)	(%)	
Over all	99(50.0%)	99(50.0%)	<0.0001
WHO grades			
G1	5(7.6%)	12(21.1%)	
G2	19(28.8%)	38(66.7%)	
G3	19(28.8%)	2(3.5%)	
GX	23(34.8%)	5(8.8%)	0.366
lymphatic metastasis			
N0	2(14.3%)	13(39.4%)	
N1	8(57.1%)	13(39.4%)	
N2	2(14.3%)	2(6.1%)	
NX	2(14.3%)	5(15.2%)	

Characteristics	AL139023.1 expression		P-value
	Low	High	
	(%)	(%)	
Over all	52(50.0%)	52(50.0%)	0.909
WHO grades			
G1	6(12.5%)	8(17.8%)	

G2	18(37.5%)	17(37.8%)	0.799
G3	13(27.1%)	11(24.4%)	
GX	11(22.9%)	9(20.0%)	
lymphatic metastasis			
N0	5(45.5%)	8(36.4%)	
N1	5(45.5%)	10(45.5%)	0.886
N2	-	1(4.5%)	
NX	1(9.1%)	3(13.6%)	
Characteristics	miR-139-5p expression		P-value
	Low	High	
	(%)	(%)	
Over all	52(51.0%)	50(49.0%)	0.716
WHO grades			
G1	9(19.6%)	5(11.1%)	
G2	18(39.1%)	17(37.8%)	
G3	10(21.7%)	12(26.7%)	
GX	9(19.6%)	11(24.4%)	0.886
lymphatic metastasis			
N0	8(40.0%)	4(33.3%)	
N1	9(45.0%)	6(50.0%)	
N2	1(5.0%)	-	
NX	2(10.0%)	2(16.7%)	