Table S1 The primer sequences of RT-qPCR

| Gene	Primer
LINC00957-F	TCAAGGGCGGAGCAAACATC
LINC00957-R	AGTTTGCAAAGCCTTCCTGTG
miR-17-5p	CAAAGTGCTTACAGTGCAGGTAG
NPNT-F	TGGGGACAGTGCCAACCTTTCT
NPNT-R	TGTGCTTACAGGGCCGAGGCT
ACTB-F	ATGTGGCCGAGGACTTTGATT
ACTB-R	AGTGGGGTGGCTTTTAGGATG

RT-qPCR, reverse transcription-quantitative polymerase chain reaction; F, forward; R, reverse.
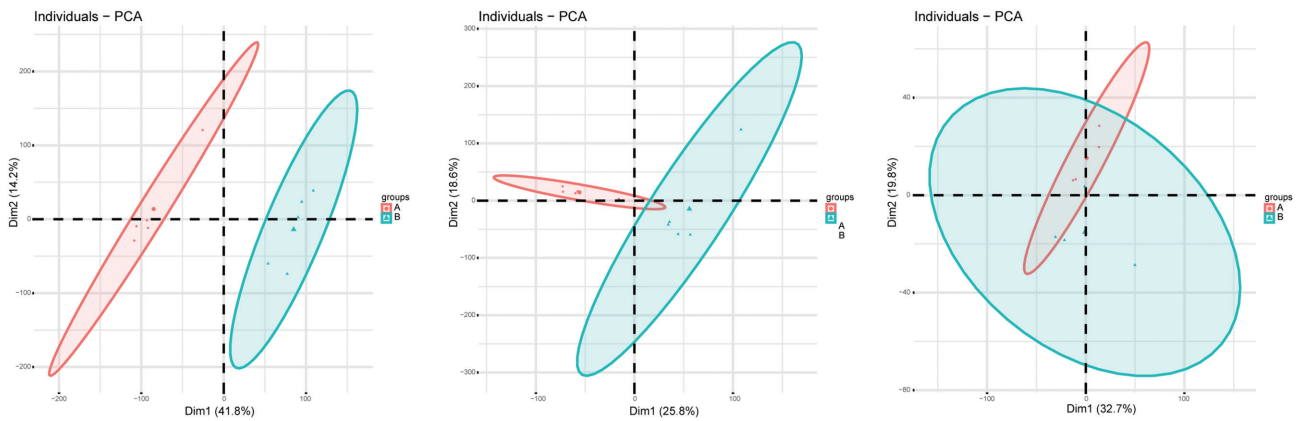
Figure S1 PCA of patients in normal and tumor glioma patients. PCA, principal component analysis.
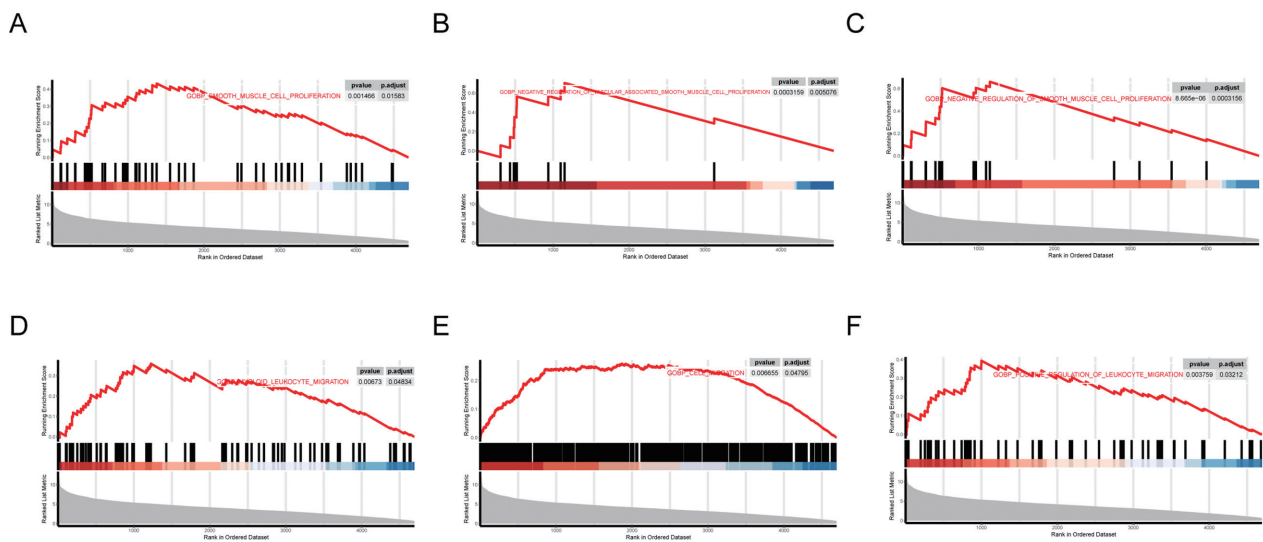
Figure S2 The detailed GSEA results (A-F). GSEA, gene set enrichment analysis.
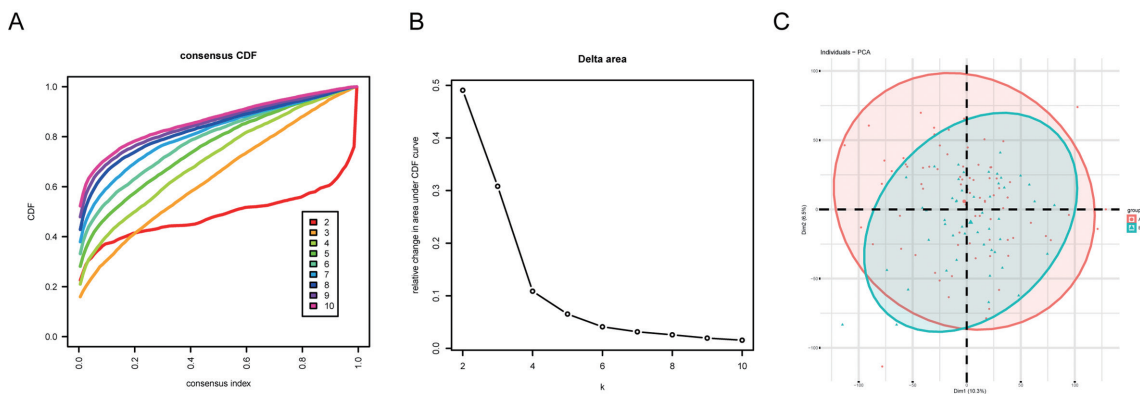

Figure S3 Consensus clustering analysis of CRGs. (A) Consensus clustering CDF for k=2 to 10 in TCGA dataset. (B) Relative change in area under the CDF curve for k=2 to 10 in TCGA dataset. (C) PCA of patients in two cuproptosis-associated clusters. CDF, cumulative distribution function; PCA, principal component analysis; CRG, cuproptosis-related gene; TCGA, The Cancer Genome Atlas.
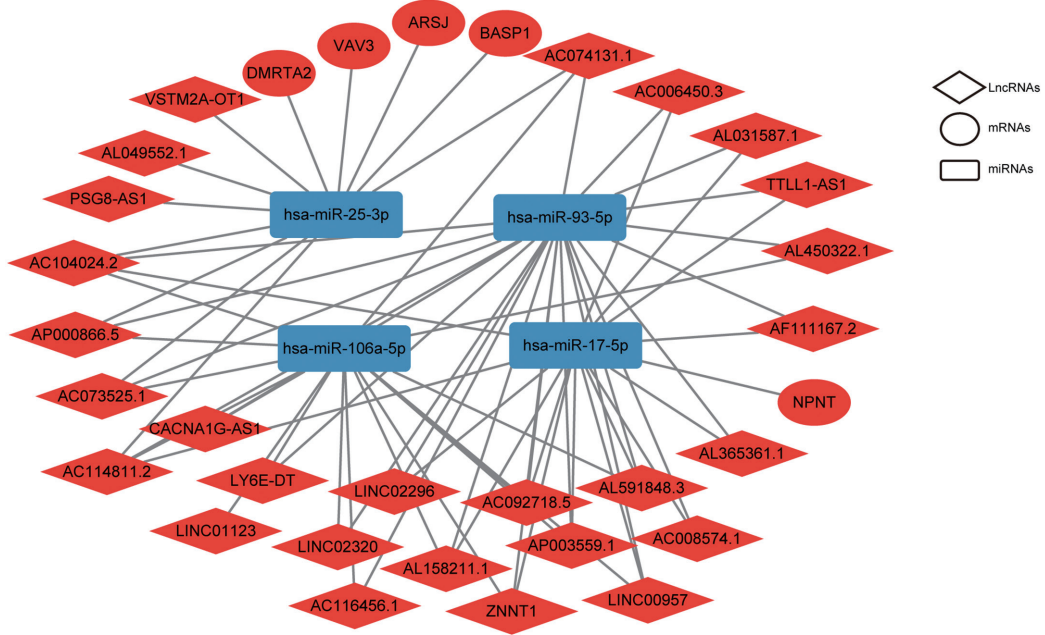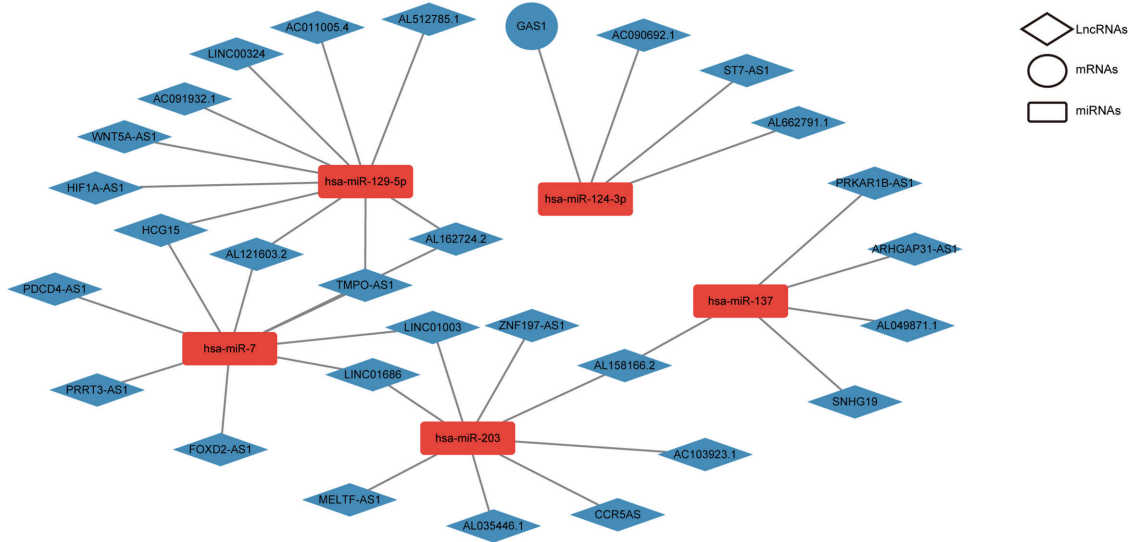
Figure S4 The cuproptosis-related ceRNA network. (A,B) Overview of cuproptosis-related ceRNA network. Red nodes were defined as oncogenes, and blue nodes were defined as anti-oncogenes. Round rectangle, diamond and circle represent miRNAs, lncRNAs and mRNAs, respectively. LncRNA, long non-coding RNA; mRNA, messenger RNA; miRNA, microRNA; NPNT, nephronectin; ceRNA, competing endogenous RNA.
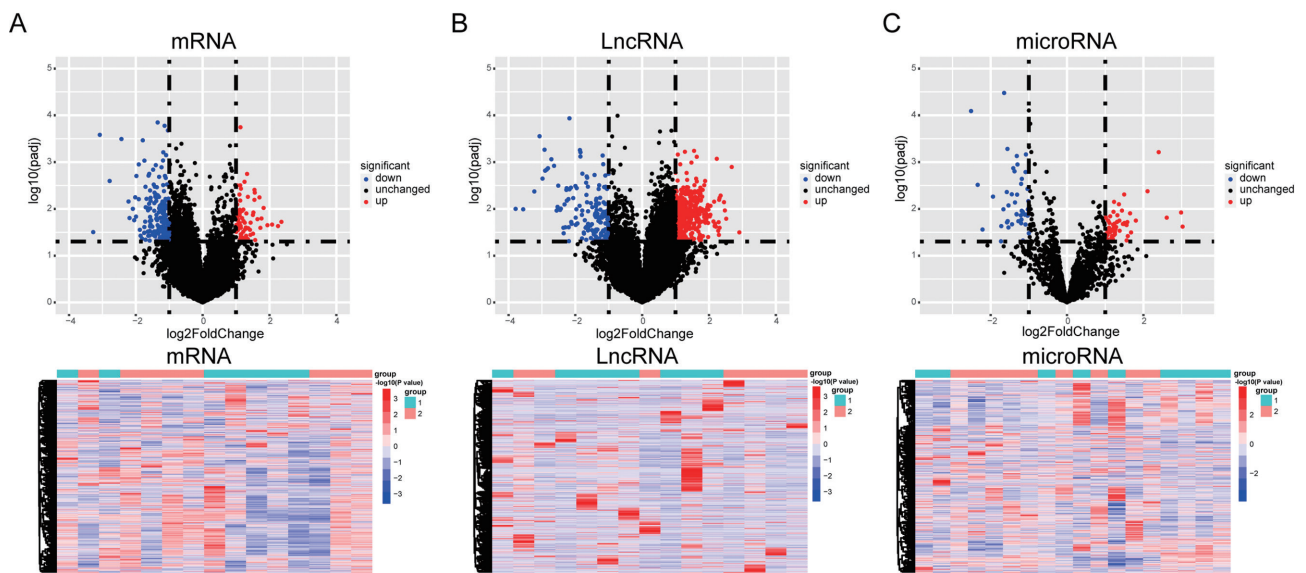
Figure S5 The volcano maps and heat maps results. (A) The volcano plots and heatmap of the DEGs in low expression group 1 and high expression group 2 among NPNT. (B) The volcano plots and heatmap of the DEGs in low expression group 1 and high expression group 2 among LINC00957. (C) The volcano plots and heatmap of the DEGs in low expression group 1 and high expression group 2 among miR-17-5p. The groups between low and high expression of the three genes were stratified according to the median expression level of them. Red dots, significantly upregulated genes. Blue dots, significantly downregulated genes. Black dots, non-DEGs. LncRNA, long non-coding RNA; mRNA, messenger RNA; miRNA, microRNA; DEG, differentially expressed gene; NPNT, nephronectin.
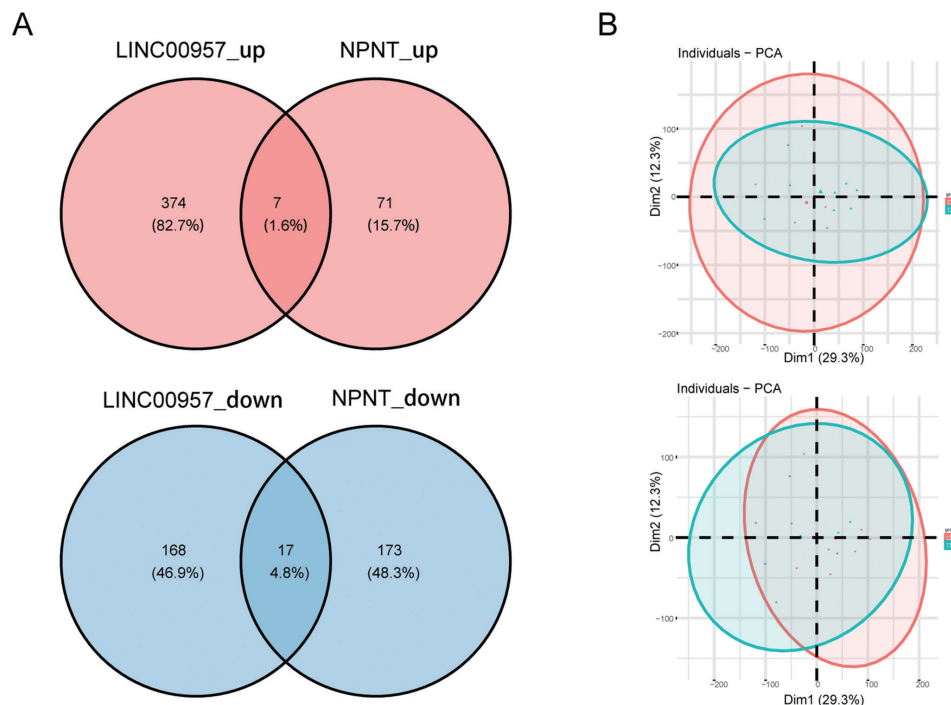
Figure S6 The venn diagram and PCA results. (A) The overlapped genes between low expression group and high expression group between LINC00957 and NPNT. (B) The PCA results of TCGA-GBM. NPNT, nephronectin; PCA, principal component analysis; TCGA, The Cancer Genome Atlas; GBM, glioblastoma.