

Figure S1 The survival analysis of different IDH1 mutation status groups. (A) TCGA; (B) CGGA. TCGA, The Cancer Genome Atlas; CGGA, Chinese Glioma Genome Atlas.

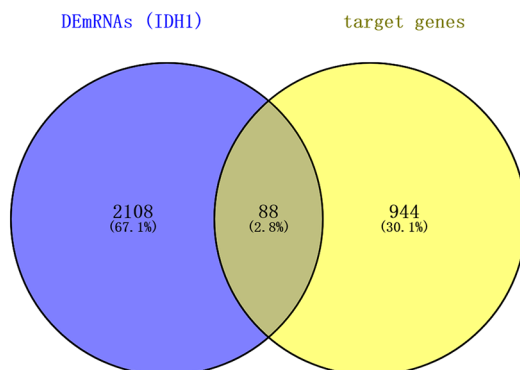


Figure S2 The Venn chart of DEmRNAs of the ceRNA network.

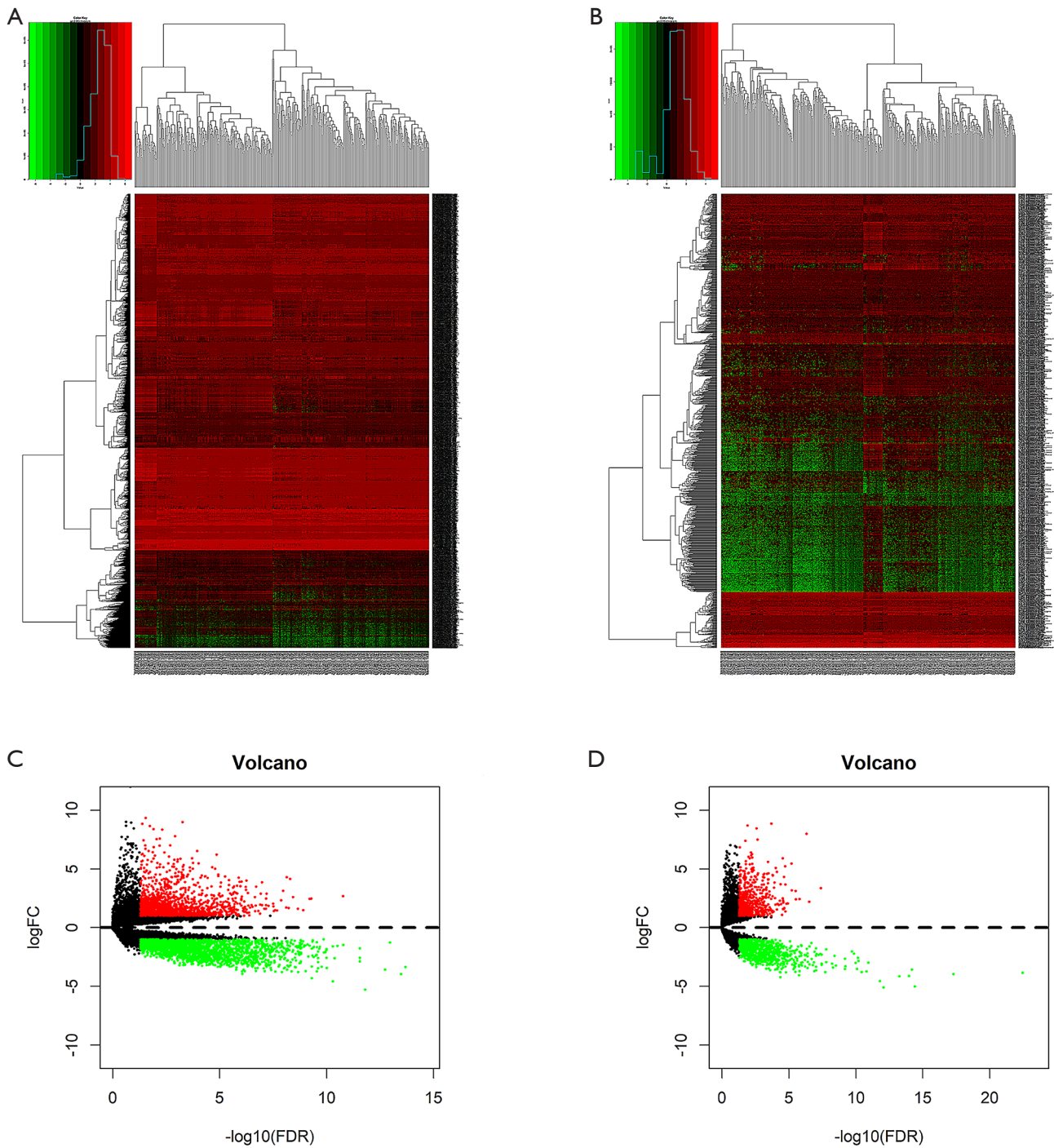


Figure S3 Identification of the DE^{LGG} lncRNAs and DE^{LGG} mRNAs in LGG and normal tissue samples: (A) Volcano plot of differentially expressed mRNAs, (B) lncRNAs. The red and green ones represent upregulated and downregulated RNAs, respectively. (C) Heatmap of DEmRNAs and (D) DElncRNAs. LGG, low-grade glioma.

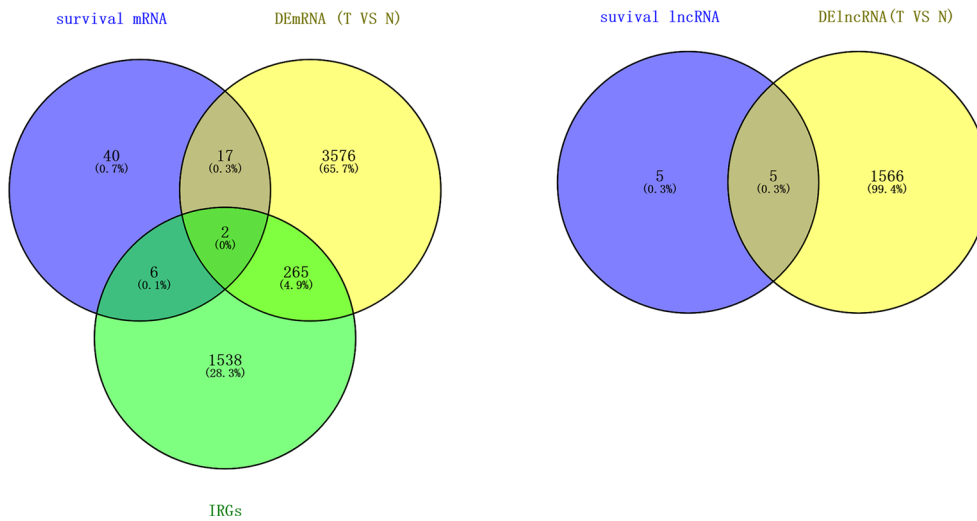


Figure S4 Venn diagram of DE mRNAs and DE lncRNAs in new ceRNA network. (A) mRNA; (B) lncRNA.

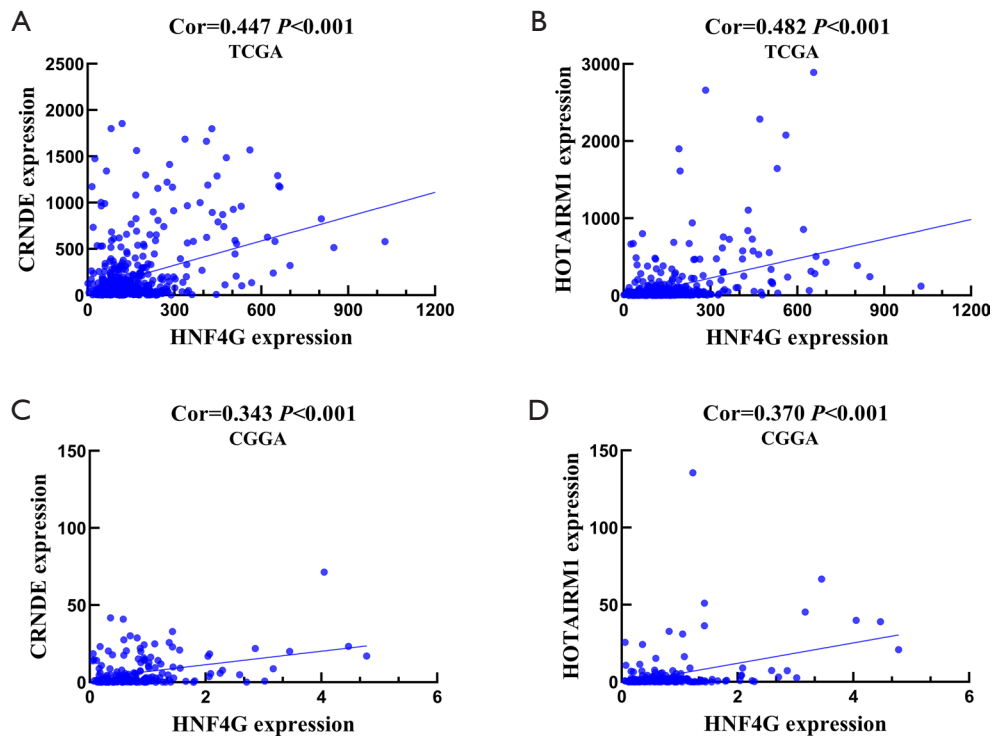


Figure S5 The relationship between the gene expression of *HNF4G* with *CRNDE* or *HOTAIRM1*. (A) The relationship between *HNF4G* with *CRNDE* in TCGA; (B) the relationship between *HNF4G* with *HOTAIRM1* in TCGA; (C) the relationship between *HNF4G* with *CRNDE* in the CGGA; (D) the relationship between *HNF4G* with *HOTAIRM1* in the CGGA. TCGA, The Cancer Genome Atlas; CGGA, Chinese Glioma Genome Atlas.

Table S1 Primer sequences for qRT-PCR

Primer	Sequence 5'-3'
HNF4G forward	TGCCATGCGGCTCTCTGATG
HNF4G reverse	CTTGACGGAGGCCGTTGGGTT
ANGPTL2 forward	TGTACCCCCAGGAGAGCCCCG
ANGPTL2reverse	CGCCGGTACCACTGCTCCTC
CRNDE forward	CCTTTCCACCTC GTCGGTCT
CRNDE reverse	GCCTTAAACT CCCAGTGTGC
HOTAIRM1 forward	CCAATGCGGATGATAGTG
HOTAIRM1 reverse	AACATCTGTGCGGGAAct
GLYCTK-AS1 forward	TCTACAGCCTTAACGAGGGCTAC
GLYCTK-AS1 reverse	AGCCTTCTCCATGACGTAGGCCA
GAPDH forward	CAACGAATTTGGCTACAGCA
GAPDH reverse	AGGGGTCTACATGGCAACTG

QT-PCR, quantitative real-time PCR.

Table S2 GO analysis

GO ID	Description	Genes	Count	P value
GO:0006351	transcription, DNA-templated	<i>HMX1, IRX5, E2F7, DMRT2, FASLG, RORB, VAX2, DEPDC1, HNF4G, SOX6, TOX3, VSX1, ARX, HOXA1, VDR, HOXC8, EBF2, SP6, NHLH2, ARNTL2, NR2F2, CHAF1B, DEDD2</i>	23	<0.001
GO:0003700	transcription factor activity, sequence-specific DNA binding	<i>IKZF3, E2F7, DMRT2, HOXD13, SOX4, RORB, VAX2, HNF4G, SOX6, VSX1, VDR, DLX2, HOXC8, ARNTL2, NR2F2</i>	15	<0.001
GO:0043565	sequence-specific DNA binding	<i>VDR, HOXA1, HOXC8, IKZF3, IRX5, DMRT2, RORB, SOX6, HNF4G, NR2F2, VSX1</i>	11	<0.001
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	<i>ARX, VDR, DLX2, HOXC8, HMX1, E2F7, FASLG, VAX2, SOX6, HMGA2, NR2F2, EPO</i>	12	<0.001
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	<i>IKZF3, E2F7, HOXD13, SOX4, DMRT2, SOX6, HGF, HMGA2, VDR, DLX2, HOXC11, EBF2, NHLH2, ARNTL2</i>	14	<0.001

DNA, deoxyribonucleic acid; GO, Gene Ontology; RNA, ribonucleic acid.

Table S3 KEGG analysis

Pathway ID	Description	Gene	Count	P value
hsa04151	PI3K-Akt signaling pathway	<i>ANGPT1, HGF, FASLG, G6PC, EPO, LAMC1, EPHA2, ITGB3</i>	8	0.000168
hsa04360	Axon guidance	<i>EPHA7, EPHA5, EPHB2, SEMA3A, EPHA2</i>	5	0.001351
hsa04512	ECM-receptor interaction	<i>FREM2, LAMC1, ITGB3</i>	3	0.007601
hsa04974	Protein digestion and absorption	<i>COL5A3, COL21A1, KCNJ13</i>	3	0.009378
hsa04015	Rap1 signaling pathway	<i>ANGPT1, HGF, EPHA2, ITGB3</i>	4	0.015407
hsa04014	Ras signaling pathway	<i>ANGPT1, HGF, FASLG, EPHA2</i>	4	0.021417
hsa04060	Cytokine-cytokine receptor interaction	<i>FASLG, EPO, IL1RN, CXCL14</i>	4	0.045387
hsa04010	MAPK signaling pathway	<i>ANGPT1, HGF, FASLG, EPHA2</i>	4	0.045862
hsa05206	MicroRNAs in cancer	<i>SOX4, HMGA2, SPRY2, ITGB3</i>	4	0.048322
hsa04510	Focal adhesion	<i>HGF, LAMC1, TGB3</i>	3	0.048544

ECM, extracellular matrix; KEGG, Kyoto Encyclopedia of Genes and Genomes; MAPK, mitogen-activated protein kinase; PI3K, phosphatidylinositol 3'-kinase.