Figure S1. (A) Semi-quantification of western blot analysis of α-SMA and COL1A1 in LX-2 cells transfected with miR-29b-3p mimic or inhibitor. (B) Kyoto Encyclopedia of Genes and Genomes enrichment analysis of the target genes of miR-29b-3p. Different colors (C1-C5 and other) represent different clusters. (C) Semi-quantification of western blot analysis of LPL and HMGCR in LX-2 cells transfected with miR-29b-3p mimic or inhibitor. *P<0.05, **P<0.01, ***P<0.001. miR, microRNA; NC, negative control; LPL, lipoprotein lipase.

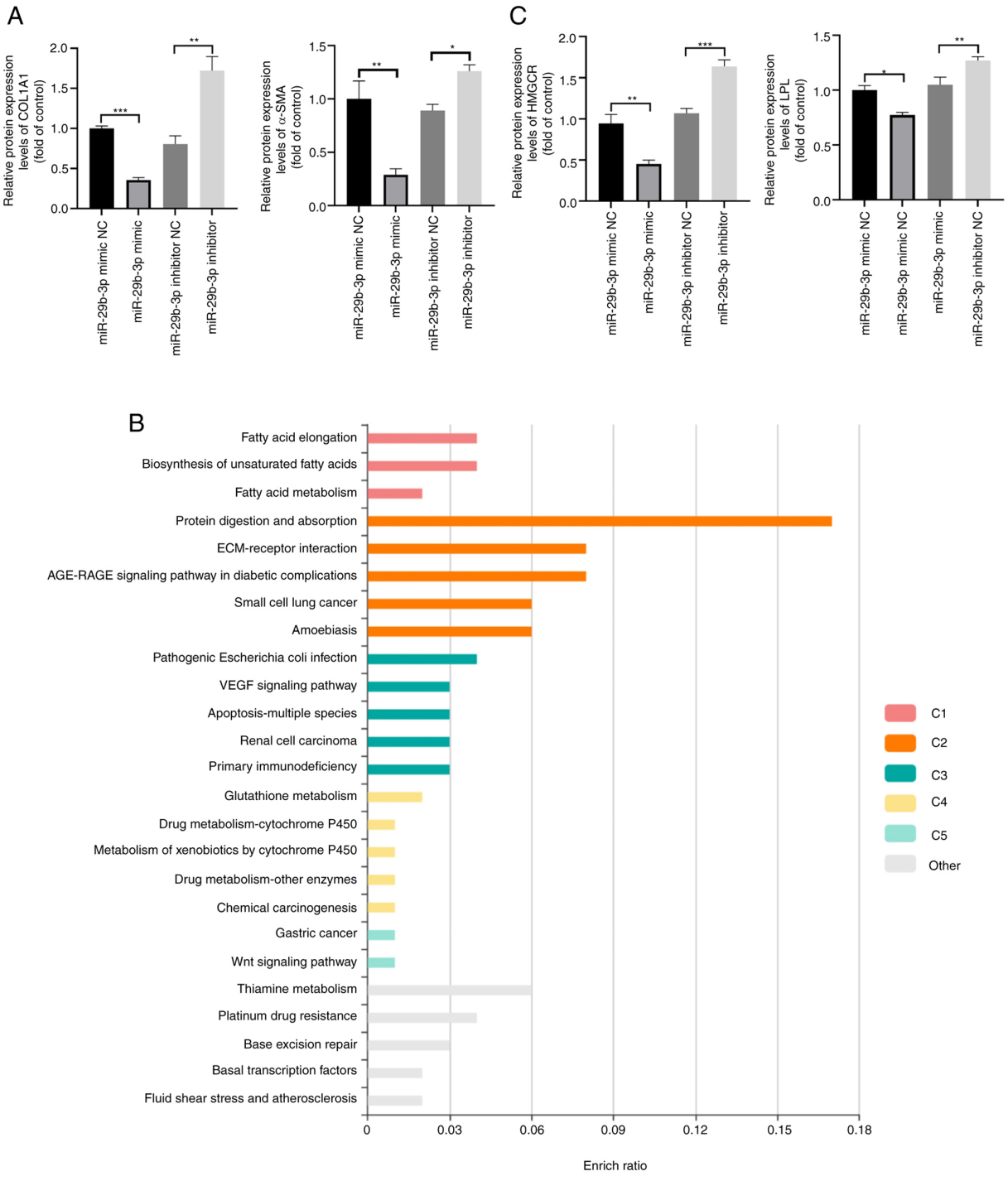

Figure S2. (A) Prediction of target relationship between VEGFA and miR-29b-3p through TargetScanHuman, miRWalk and miRDB analyses. (B) Semi-quantification of western blot analysis of VEGFA in LX-2 cells transfected with miR-29b-3p mimic or inhibitor. (C) Reverse transcription-quantitative PCR analysis of VEGFA in LX-2 cells transfected with VEGFA siRNA NC and VEGFA siRNA. (D) Semi-quantification of western blot analysis of α-SMA, COL1A1, VEGFA, Bax/Bcl-2, p62 and LC3-II/LC3-I in LX-2 cells transfected with miR-29b-3p inhibitor and VEGFA siRNA. *P<0.05, **P<0.01, ***P<0.001. miR, microRNA; si/siRNA, small interfering RNA.

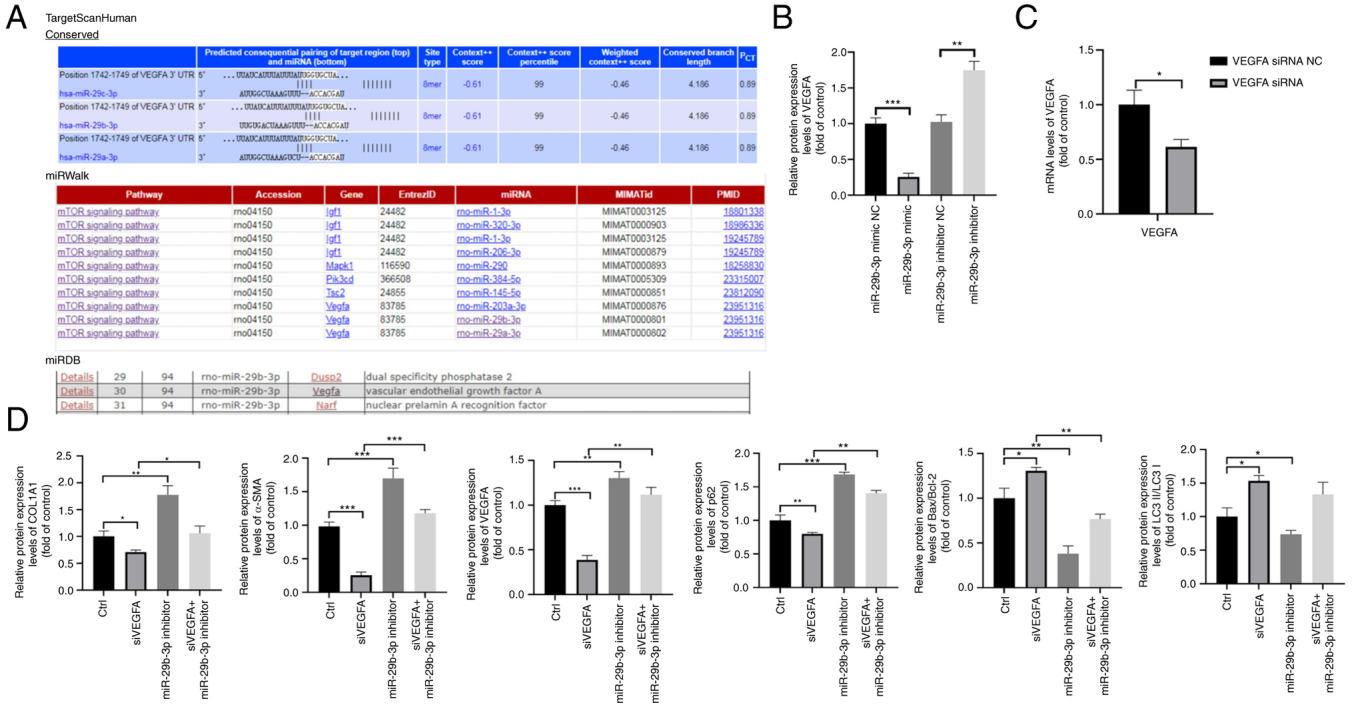

Figure S3. (A) RT-qPCR analysis of VEGFR1 in LX-2 cells transfected with VEGFR1 siRNA NC and VEGFR1 siRNA. (B) RT-qPCR analysis of VEGFR2 in LX-2 cells transfected with VEGFR2 siRNA NC and VEGFR2 siRNA. (C) Western blot analysis of VEGFR1 in LX-2 cells treated with 2 μM GNQWFI and transfected with VEGFR1 siRNA, and western blot analysis of VEGFR2 in LX-2 cells treated with 0.2 μM SU5416 and transfected with VEGFR2 siRNA. (D) Semi-quantification of western blot analysis of Bax/Bcl-2, p62 and LC3-II/LC3-I in LX-2 cells transfected with VEGFR1 siRNA and VEGFR2 siRNA. (E) RT-qPCR analysis of VEGFR1 and VEGFR2 in LX-2 cells treated with GNQWFI and SU5416 at different concentrations. (F) Semi-quantification of western blot analysis of Bax/Bcl-2, p62 and LC3-II/LC3-I in LX-2 cells transfected with GNQWFI and SU5416. Data are expressed as the mean ± SD (n=3). *P<0.05, **P<0.01, ***P<0.001. NC, negative control; siRNA, small interfering RNA; RT-qPCR, reverse transcription-quantitative PCR.

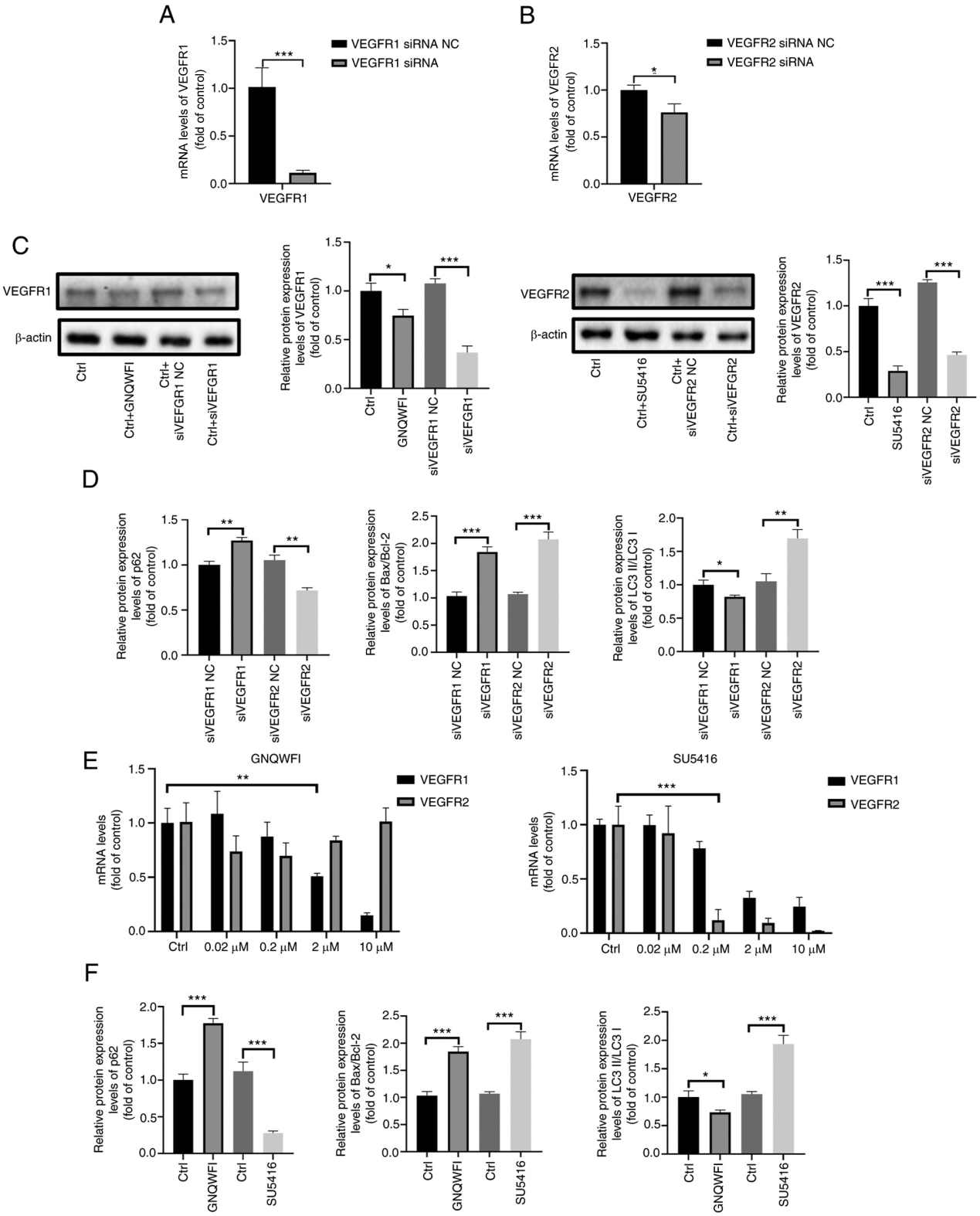

Figure S4. (A) Semi-quantification of western blot analysis of PI3K, p-PI3K, AKT, p-AKT, mTOR, p-mTOR, ULK1, p-ULK1, p62 and LC3-II/ LC3-I in LX-2 cells transfected with VEGFR2 siRNA and treated with 740Y-P. (B) VEGFR2 has a potential interaction with HSP60, as determined through GeneMania analysis. (C) Reverse transcription-quantitative PCR analysis of HSP60 in LX-2 cells transfected with CMV-14-HSP60. (D) Semi-quantification of western blot analysis of α-SMA, COL1A1, AIF, HSP60, cleaved caspase-9/pro-caspase-9, Bax/Bcl-2 and cytochrome *c* in LX-2 cells transfected with VEGFR2 siRNA and HSP60 plasmid. (E) Semi-quantification of immunoprecipitation analysis of ubiquitination and HSP60 in LX-2 cells. *P<0.05, **P<0.01, ***P<0.001. siRNA/si, small interfering RNA; p-, phosphorylated; miR, microRNA; NC, negative control; si/siRNA, small interfering RNA; HSP60, heat shock protein 60; RT-qPCR, reverse transcription-quantitative PCR.

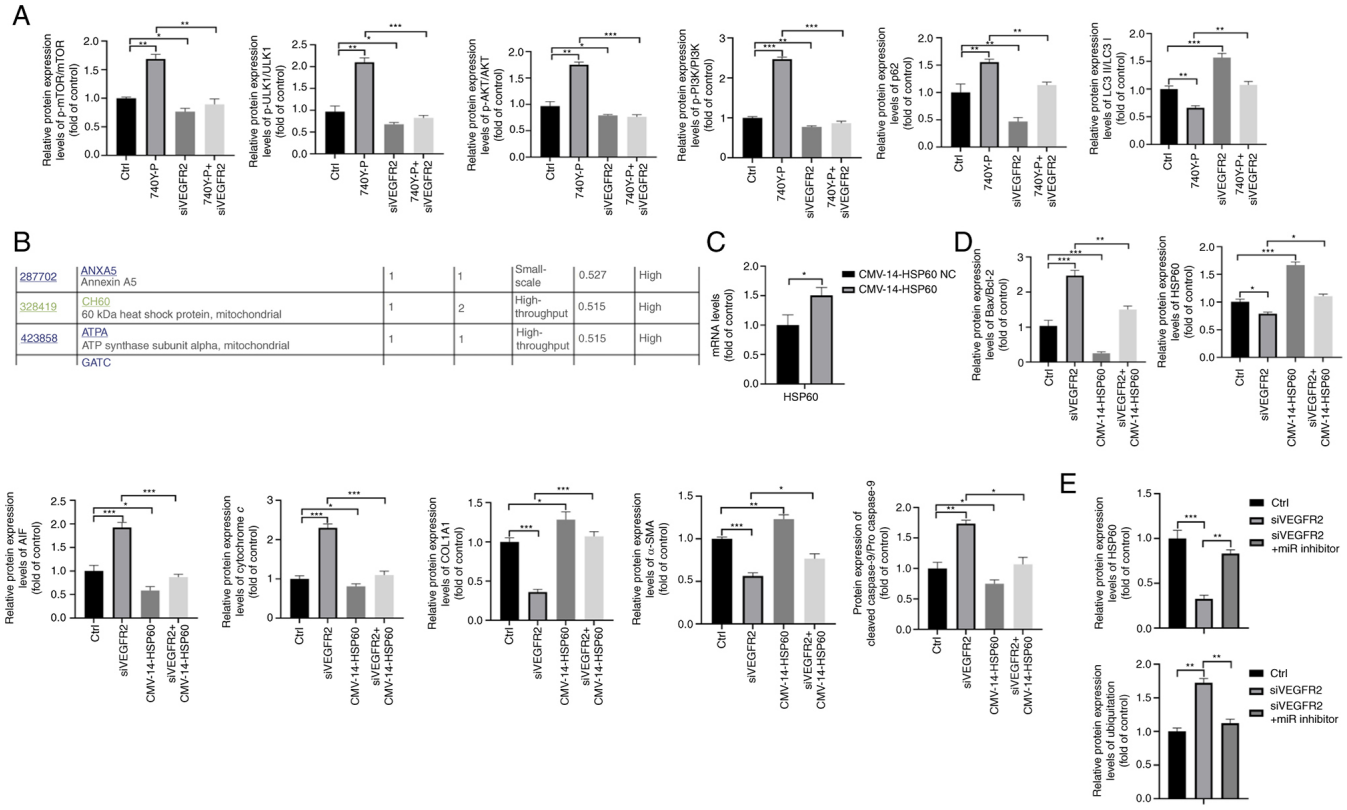

Figure S5. (A) Semi-quantification of western blot analysis of LPL, VEGFA and HSP60 in LX-2 cells treated with DHA at different concentrations. (B) Semi-quantification of western blot analysis of Bax/Bcl-2, p62, LC3-II/LC3-I, Cleaved caspase-9/Pro-caspase-9, VEGFA, α-SMA, HSP60 and COL1A1 in LX-2 cells treated with DHA and transfected with miR-29b-3p inhibitor. (C) Reverse transcription-quantitative PCR analysis of miR-29b-3p in liver tissues of rats injected with AAV8 miR-29b-3p mimic via the caudal vein. (D) Semi-quantification of western blot analysis of α-SMA and COL1A1 in liver tissue. *P<0.05, **P<0.01, ***P<0.001. miR, microRNA; NC, negative control; LPL, lipoprotein lipase; si/siRNA, small interfering RNA; DHA, dihydroartemisinin; HSP60, heat shock protein 60; miR, microRNA; NC, negative control; RT-qPCR, reverse transcription-quantitative PCR.

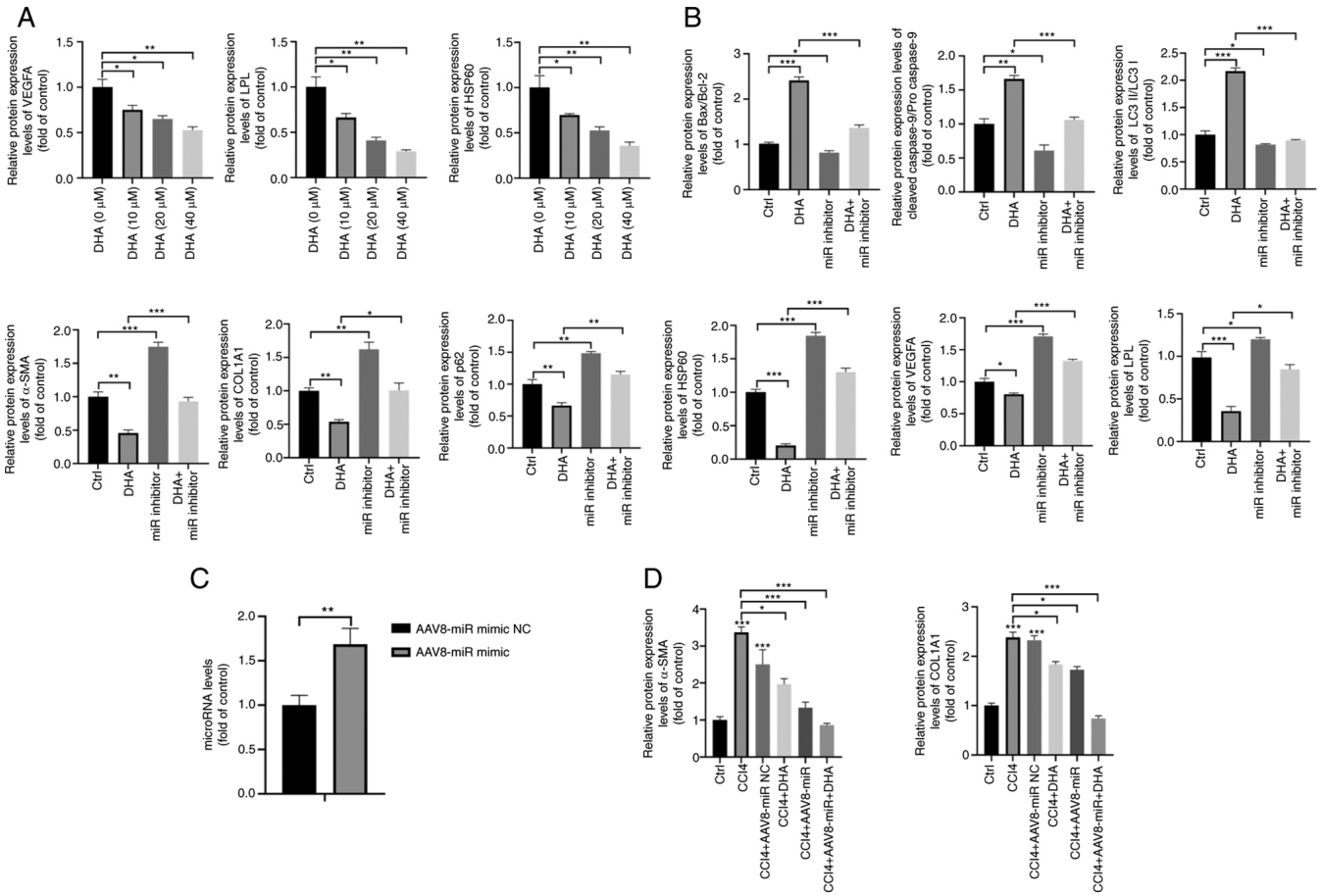

Figure S6. DHA restored resting HSCs and induced programmed cell death of HSCs via miR-29b-3p. VEGFR2 regulated autophagy via the PI3K/AKT/mTOR/ULK1 pathway and inhibited apoptosis by binding with HSP60 to prevent its ubiquitination and degradation. HSCs, hepatic stellate cells; HSP60, heat shock protein 60; miR, microRNA.