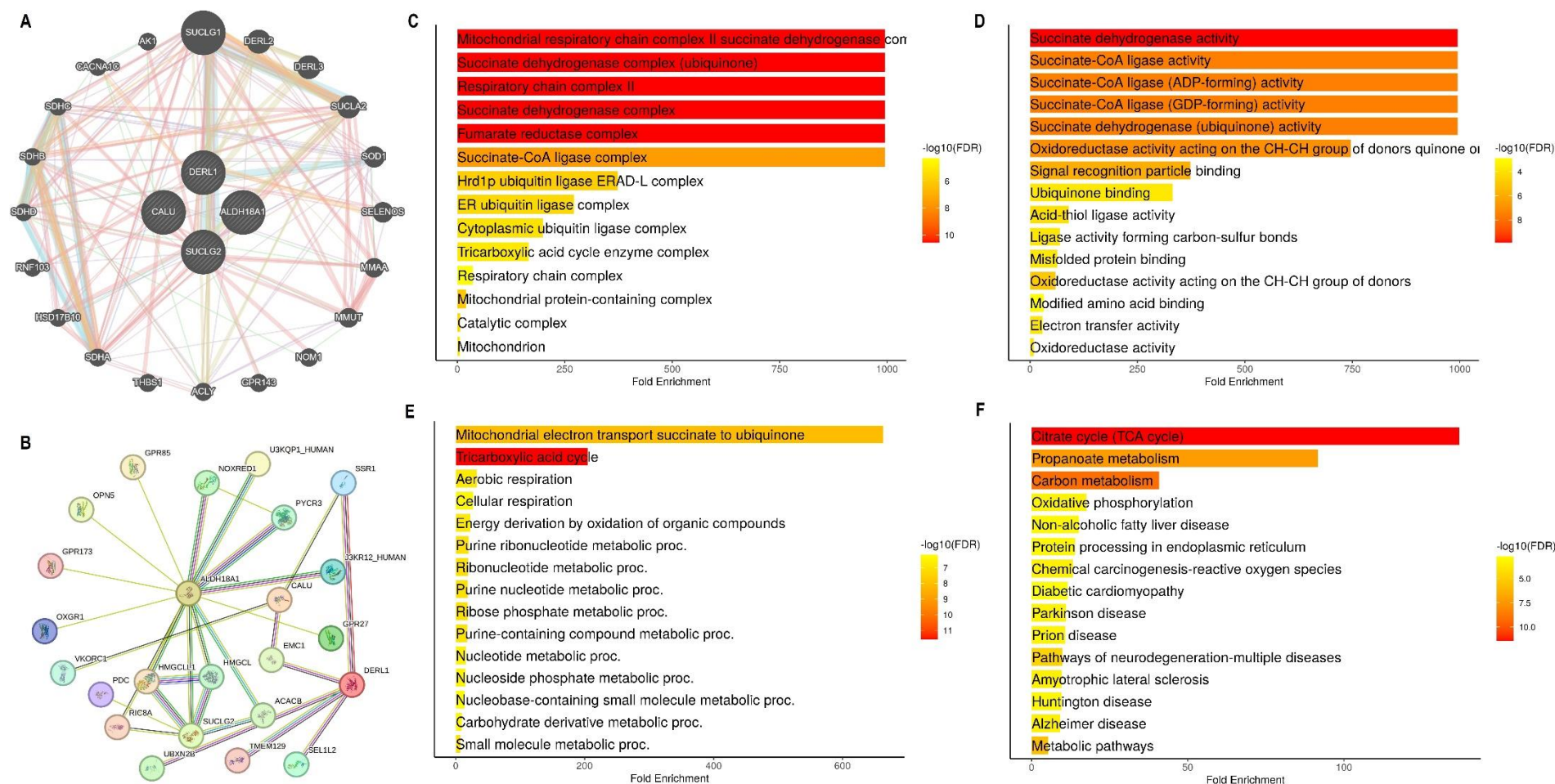
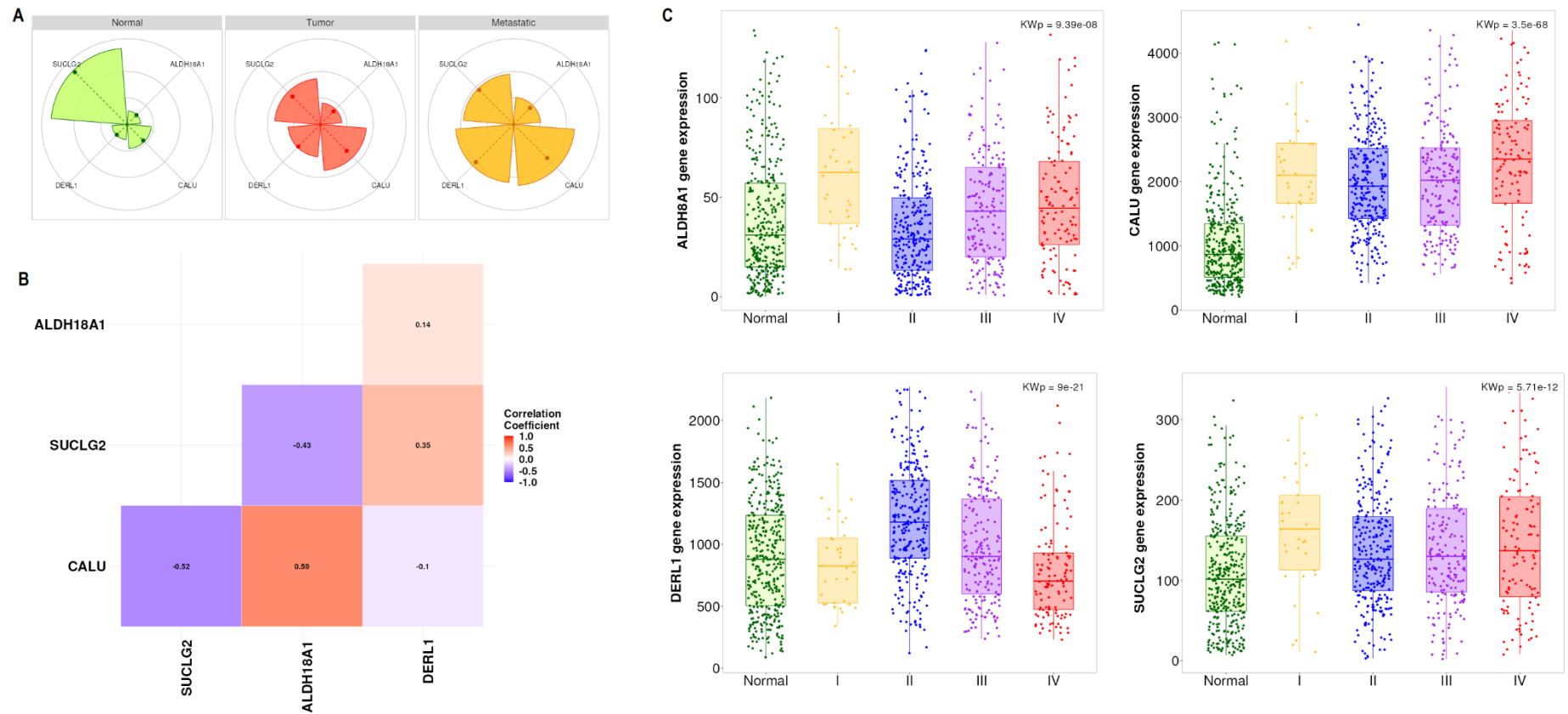




Supplementary data Figure 1: PPI network construction and functional enrichment analysis of hub genes. (A) Protein-protein interaction (PPI) network constructed using the GeneMANIA database. (B) PPI network constructed using the STRING database. (C) Cellular component enrichment analysis of the hub genes. (D) Molecular function enrichment analysis of the hub genes. (E) Biological process enrichment analysis of the hub genes. (F) KEGG pathway enrichment analysis revealing several relevant metabolic pathways, including the TCA cycle (citrate cycle), propanoate metabolism, carbon metabolism, and non-alcoholic fatty liver disease. p-value < 0.05.



Supplementary data Figure 2: Expression and correlation analysis of hub genes across KIRC stages and samples. (A) Expression analysis of ALDH18A1, SUCLG2, CALU, and DERL1 in normal, primary KIRC, and metastatic KIRC samples using the TNMPlot database. (B) Correlation analysis between the hub genes in KIRC using the TNMPlot database. (C) Expression of the hub genes across different stages of KIRC, as analyzed through the TNMPlot database. p-value < 0.05.

Figure 9B

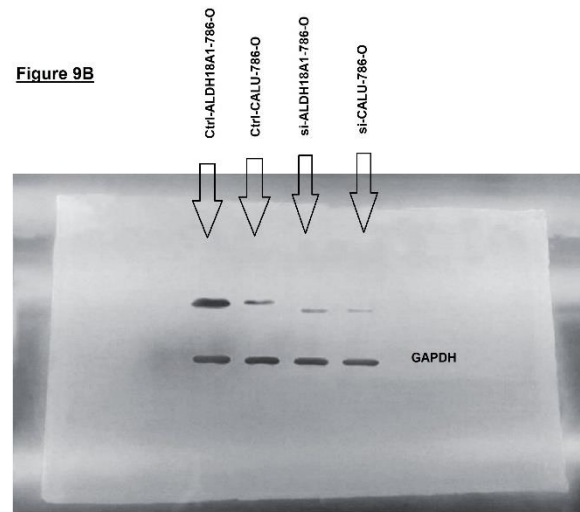


Figure 12C

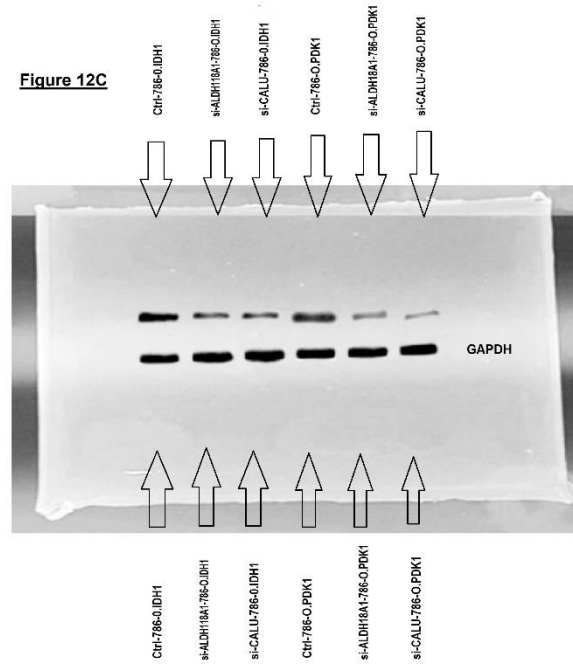
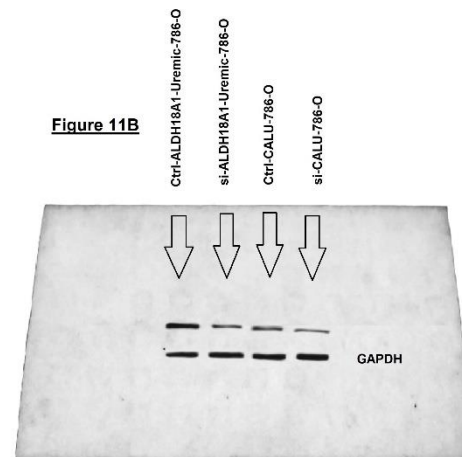
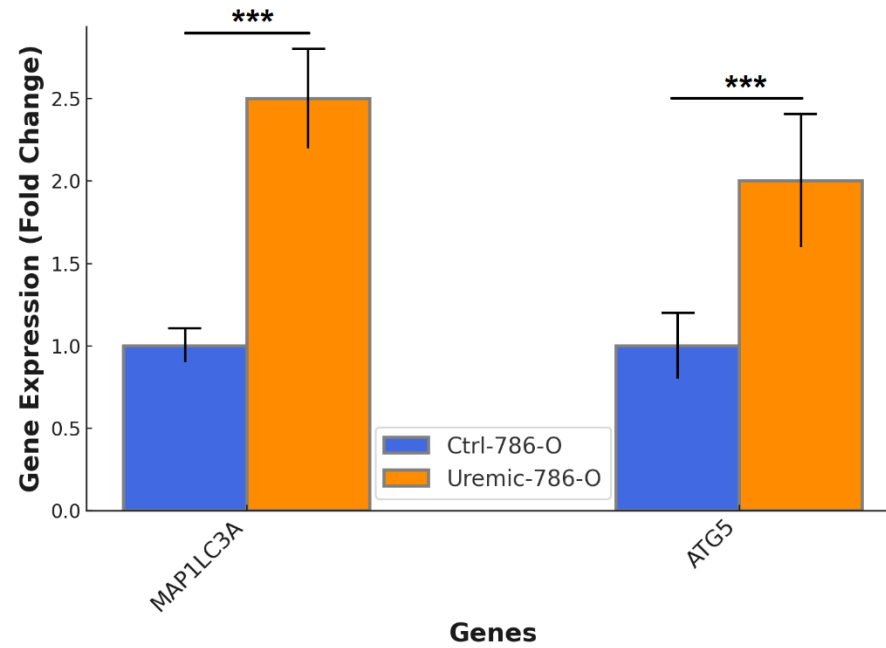


Figure 11B



Supplementary data Figure 3: Uncut Western blot bands of GAPDH, ALDH18A1, CALU, PDK1, and IDH1.

Gene Expression of MAP1LC3A and ATG5 in Ctrl-786-O and Uremic-786-O Cells



Supplementary data Figure 4. Gene expression of autophagy markers in Uremic-786-O and control cells. Gene expression of MAP1LC3A and ATG5 was analyzed in Uremic-786-O and Ctrl-786-O cells following 24-hour exposure to uremic toxins (urea and creatinine). ***p-value < 0.001