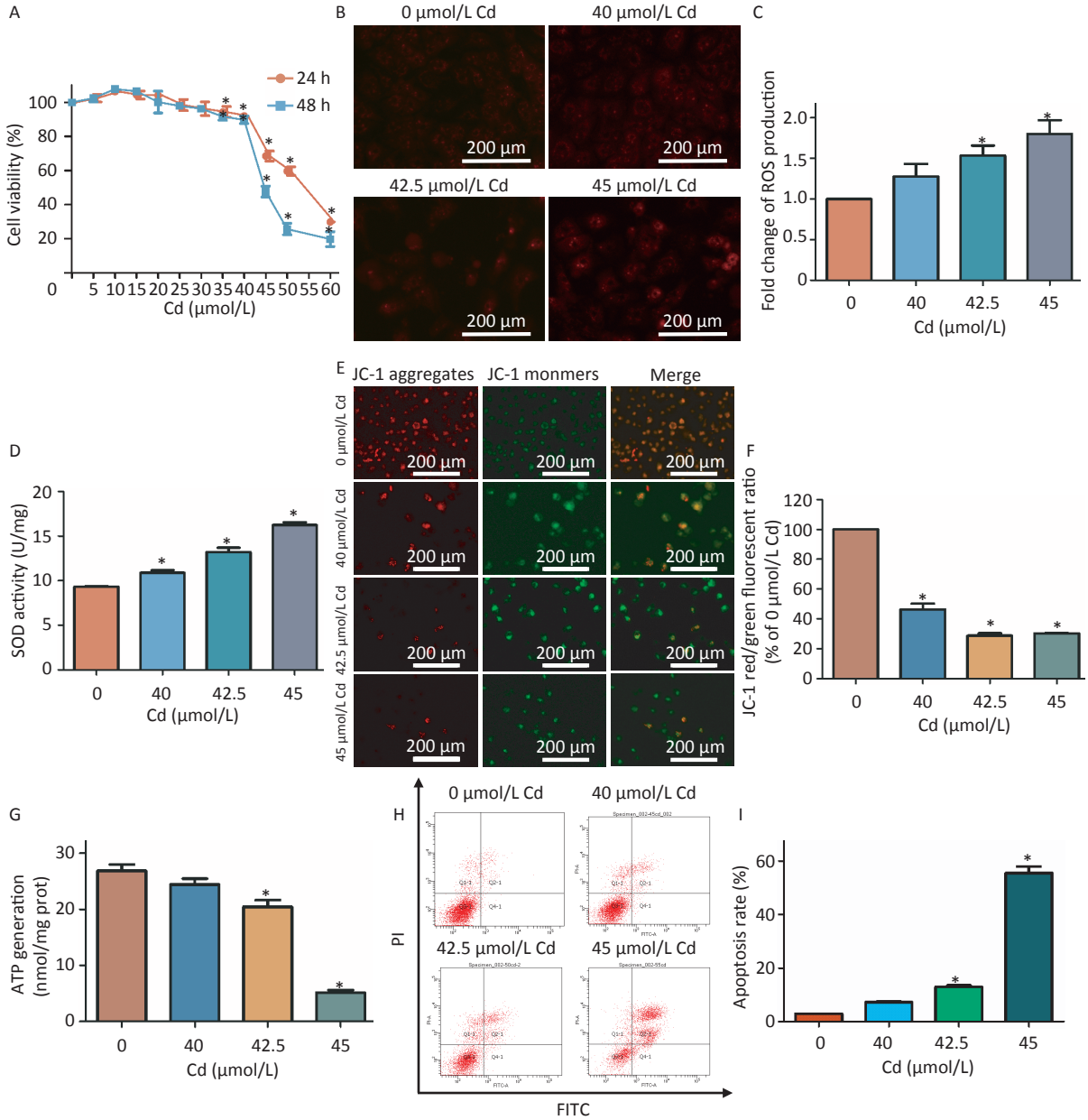
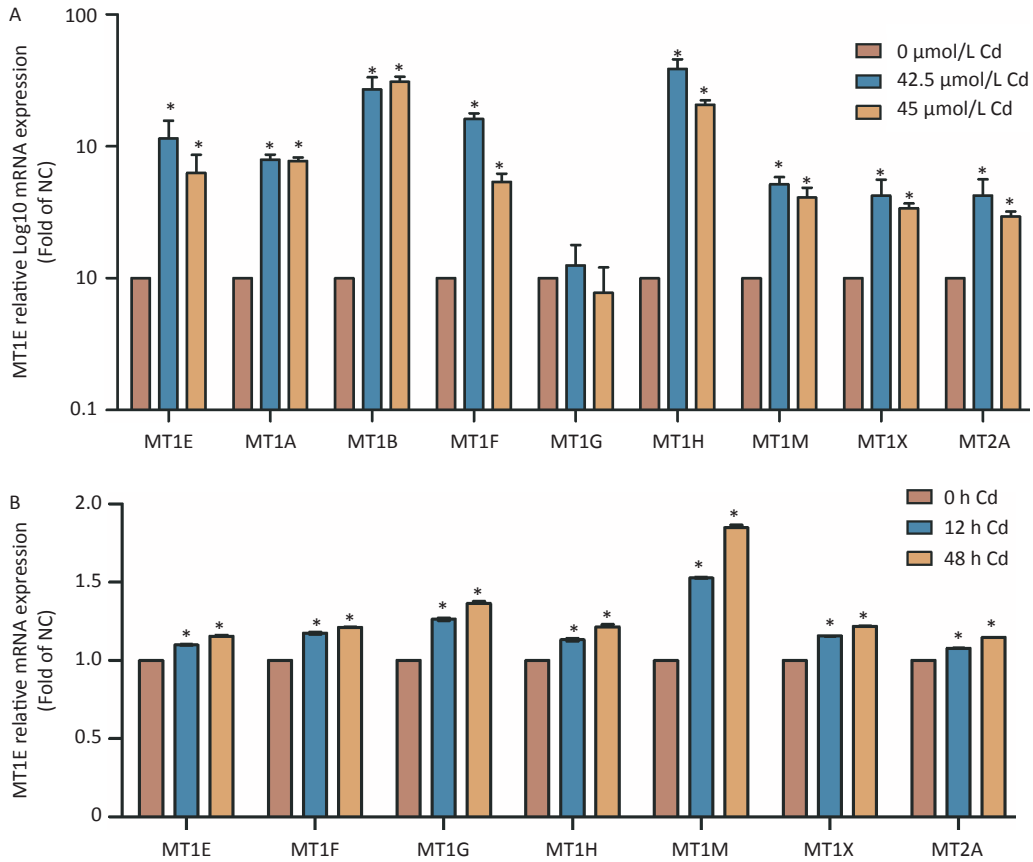
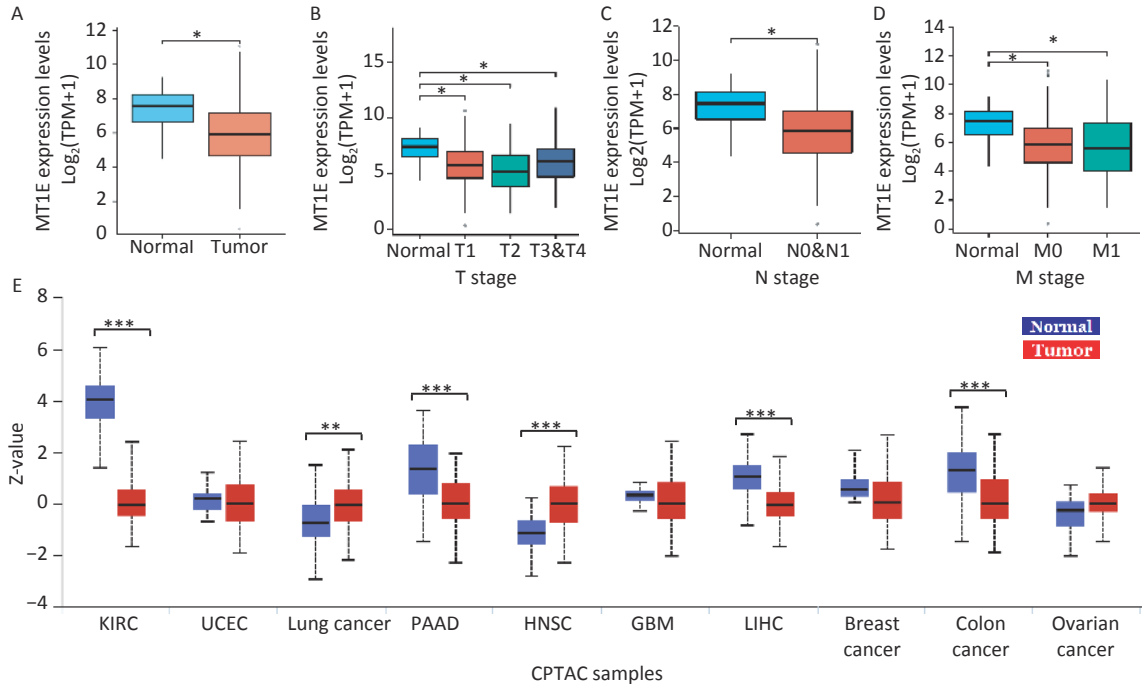


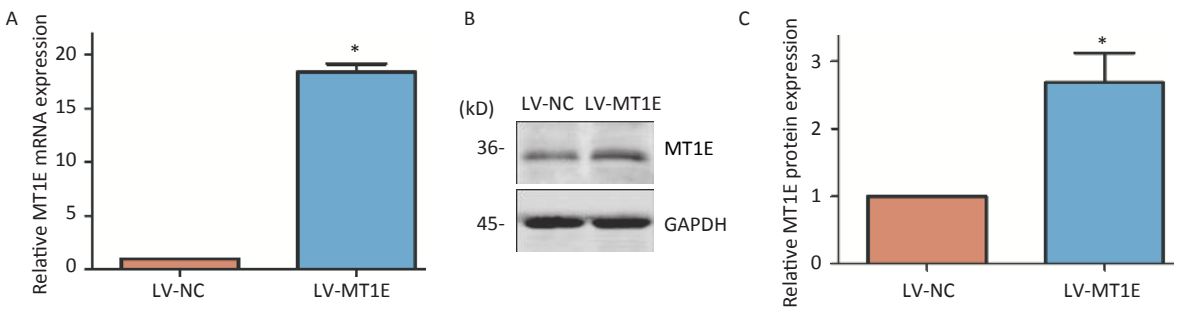
Supplementary Figure S1. Evaluating oxidative stress and mitochondrial impairment in HK-2 cells exposed to Cd. (A) Survival rate of HK-2 cells treated with 0−60 μmol/L Cd for either 24 h or 48 h, measured using CCK-8, compared to controls. (B–C) Fluorescent images showing ROS in HK-2 cells exposed to 0, 40, 42.5, and 45 μmol/L Cd for 48 h (ROS emits red fluorescence). Quantitative analysis for ROS production was conducted. Scale bar represents 200 μm. (D) SOD activity was quantitatively assessed. (E–F) Mitochondrial membrane potential represented by the JC-1 red/green fluorescence ratio with corresponding quantification. Scale bar equals 200 μm. (G) Quantitative analysis for ATP levels. (H–I) Rates of apoptosis were ascertained using Annexin V-FITC flow cytometry (*vs.* control group, $^{*}P < 0.05$).



Supplementary Figure S2. Analysis of MTs isoform mRNA expression post Cd treatment. (A) mRNA expression levels of MTs isoforms, following exposure to 42.5 and 45 μmol/L Cd for 48 h, were evaluated using RT-PCR. (B) Bioinformatic investigation pertaining to the mRNA expression of MTs isoforms based on the GSE27211 database, featuring HK-2 cells subjected to Cd treatment (concentration unspecified) at intervals of 12 h and 48 h (*vs*. control group, $^{*}P < 0.05$).



Supplementary Figure S3. Examination of MT1E expression trends in KIRC *via* TCGA and CPTAC datasets. (A) mRNA expression levels of MT1E in both normal and tumor tissues were assessed, derived from 613 kidney renal clear cell carcinoma (KIRC) specimens as recorded in the TCGA database. (B–D) MT1E expression patterns across different KIRC-TNM stages, according to the TCGA dataset. (E) Protein expression metrics for MT1E across various cancers were ascertained using the CPTAC database (*vs.* normal group, $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$).



Supplementary Figure S4. Confirmation of the MT1E overexpression cellular model. (A) Quantitative RT-PCR was employed to analyze the expression in cells transfected with lentiviral plasmids stably expressing MT1E. (B–C) Western blot methodology was utilized to validate MT1E overexpression, with subsequent quantitative analysis executed *via* Image J (*vs.* control group, $^{*}P < 0.05$).