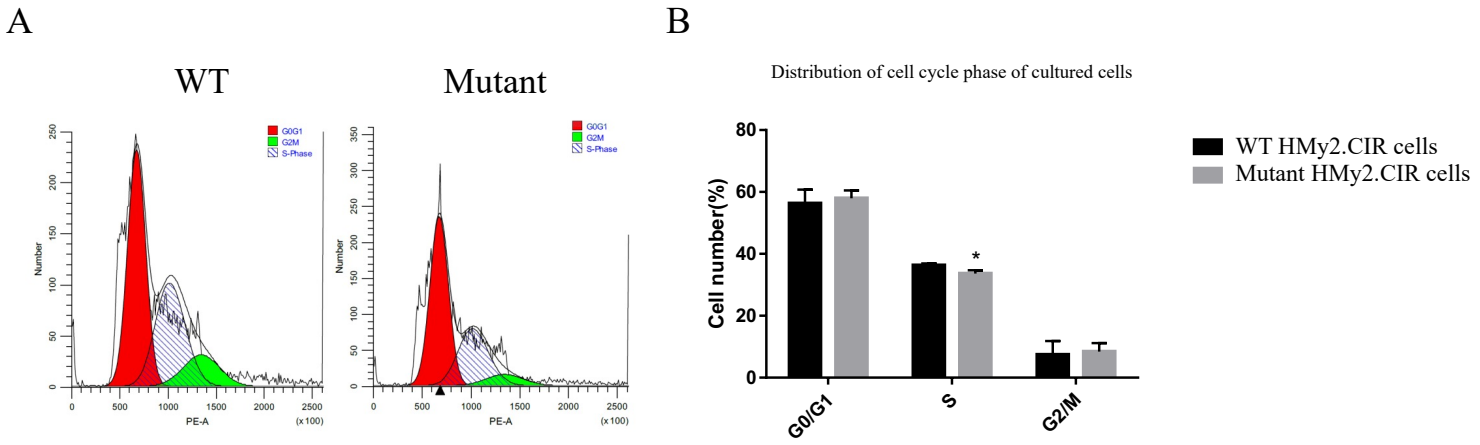


Figure S1. (A) Flow cytometry detectes the distribution of cell cycle phase in WT HMy2.CIR or mutant HMy2.CIR cells ($n = 3$). (B) Statistical results of (A). *$p < 0.05$; NS, no significance.

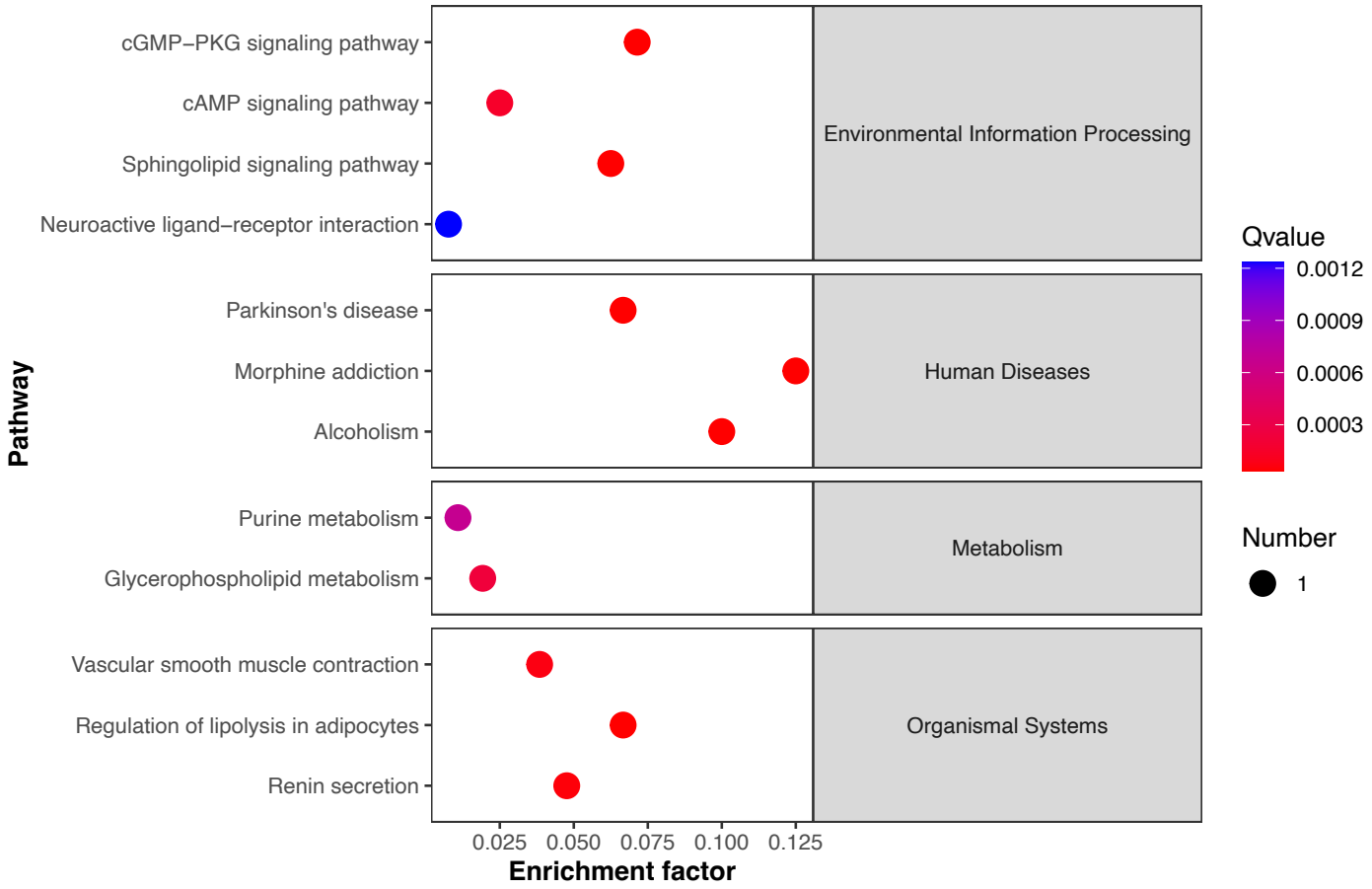
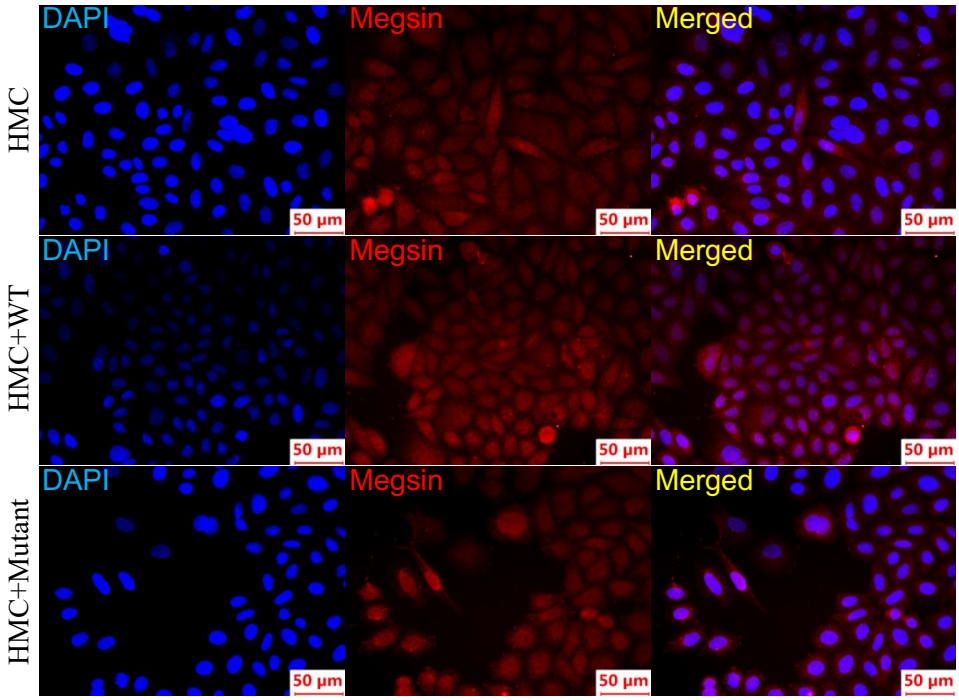


Figure S2. HMy2.CIR cells carrying c.26C>T mutation mutation in MDH2 exhibited metabolic changes. Kegg enrichment results were shown as bubble chart. Enrichment factor indicates the number of differential metabolites located in the KEGG/the total number of metabolites located in the KEGG. The smaller the p value, the higher the enrichment of KEGG.

A



B

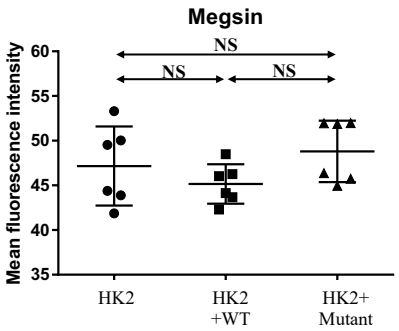


Figure S3. (A-B) Representative pictures and quantification of immunofluorescence staining of megsin (red) and DAPI (blue) in HMC after co-culturing with WT or mutant HMy2.CIR cells. Six random fields were taken from each coverslip (mean ± SD, n = 6). Scale bar = 50 μm. HMC, human mesangial cells; NS, no significance.

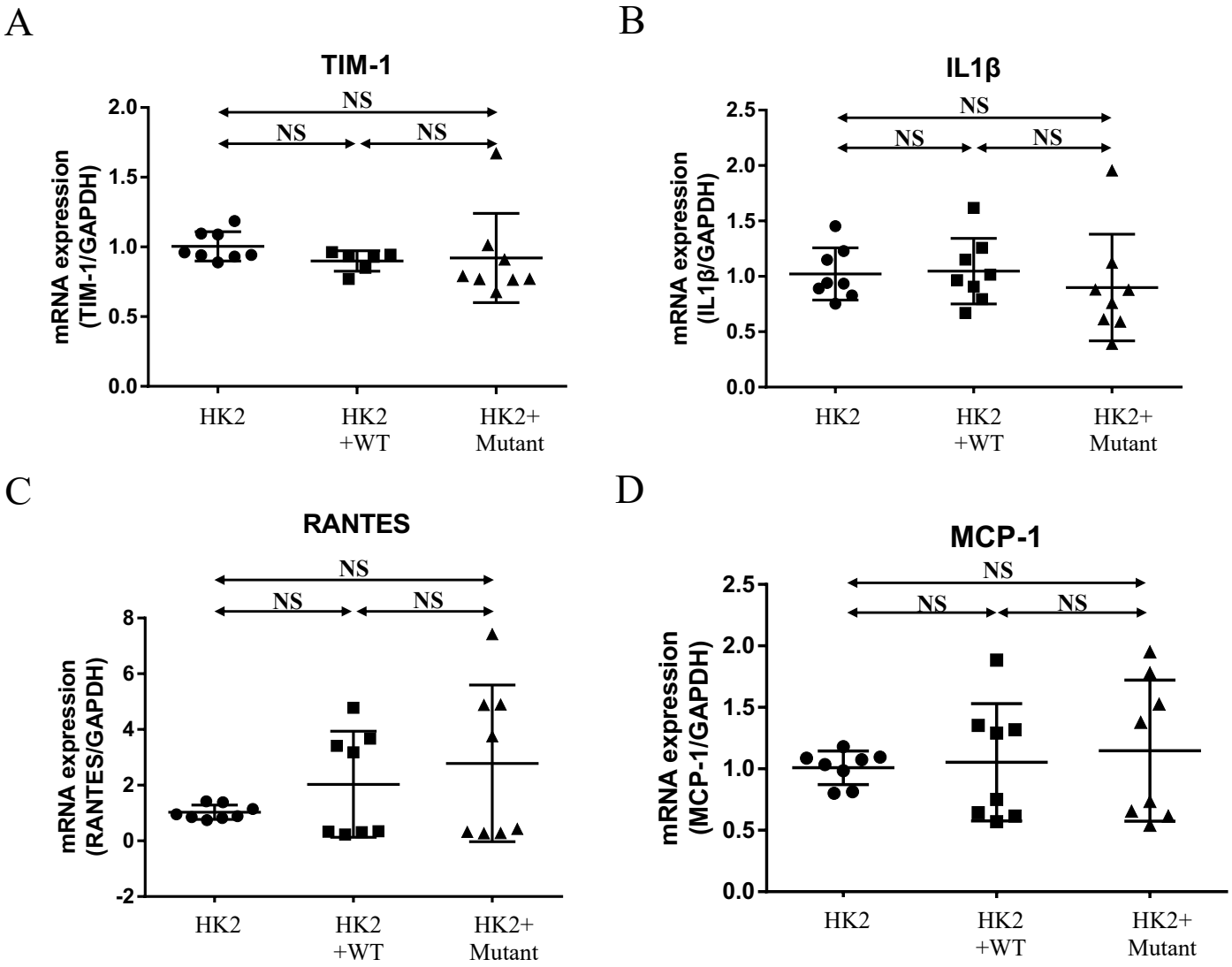


Figure S4. Relative mRNA expression level of (A) TIM-1, (B) IL1β, (C) TANTES and (D) MCP-1 in HK2 cells after co-culturing with WT or mutant HMy2.CIR cells. NS, no significance.