

PYCR1 reshapes the TME in ccRCC

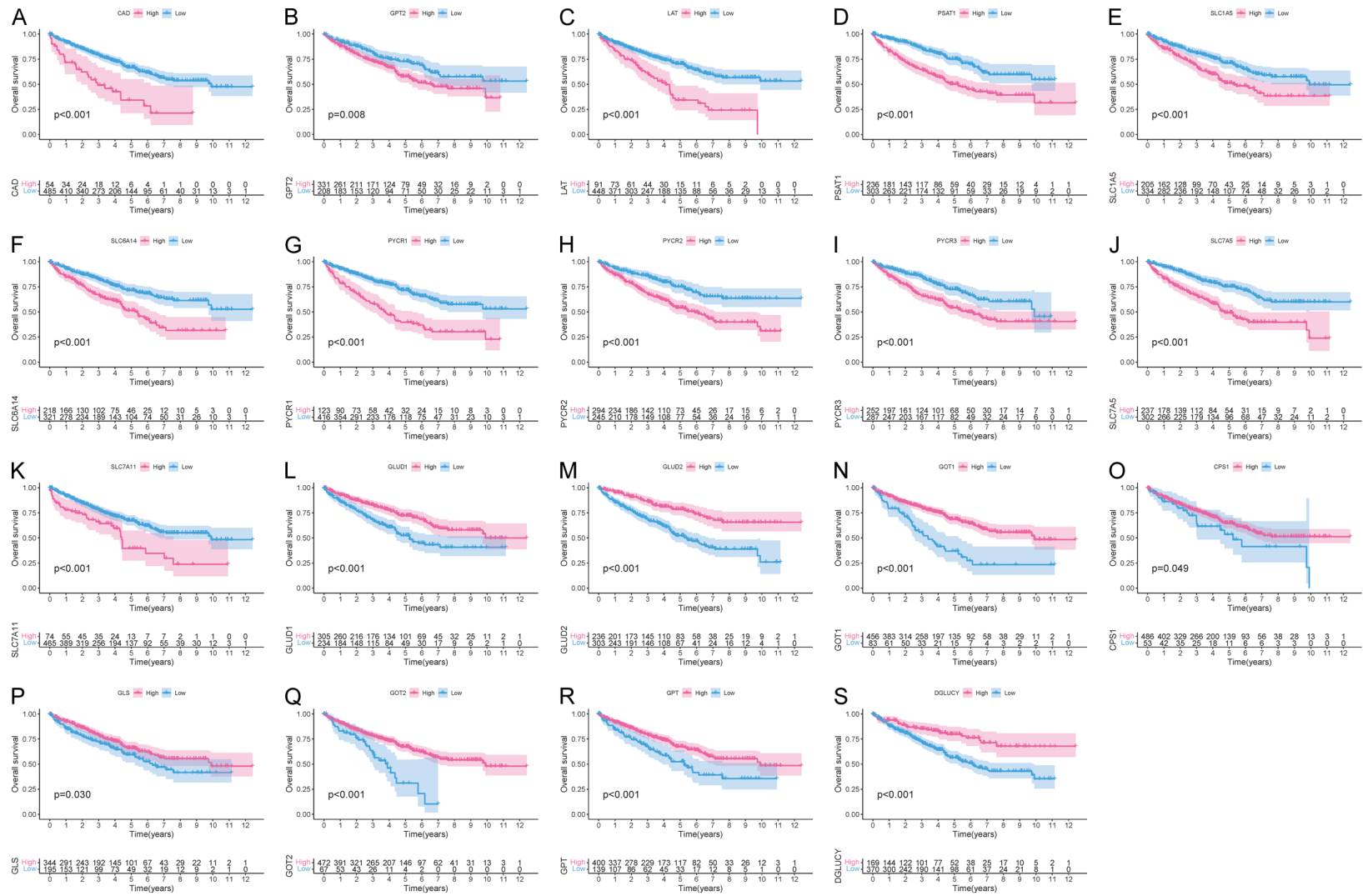


Figure S1. Survival analysis for each GMG based on 539 patients with ccRCC from the TCGA. Kaplan-Meier curves with Log-rank $P < 0.05$ showed a significant difference in survival between high expression group and low expression group.

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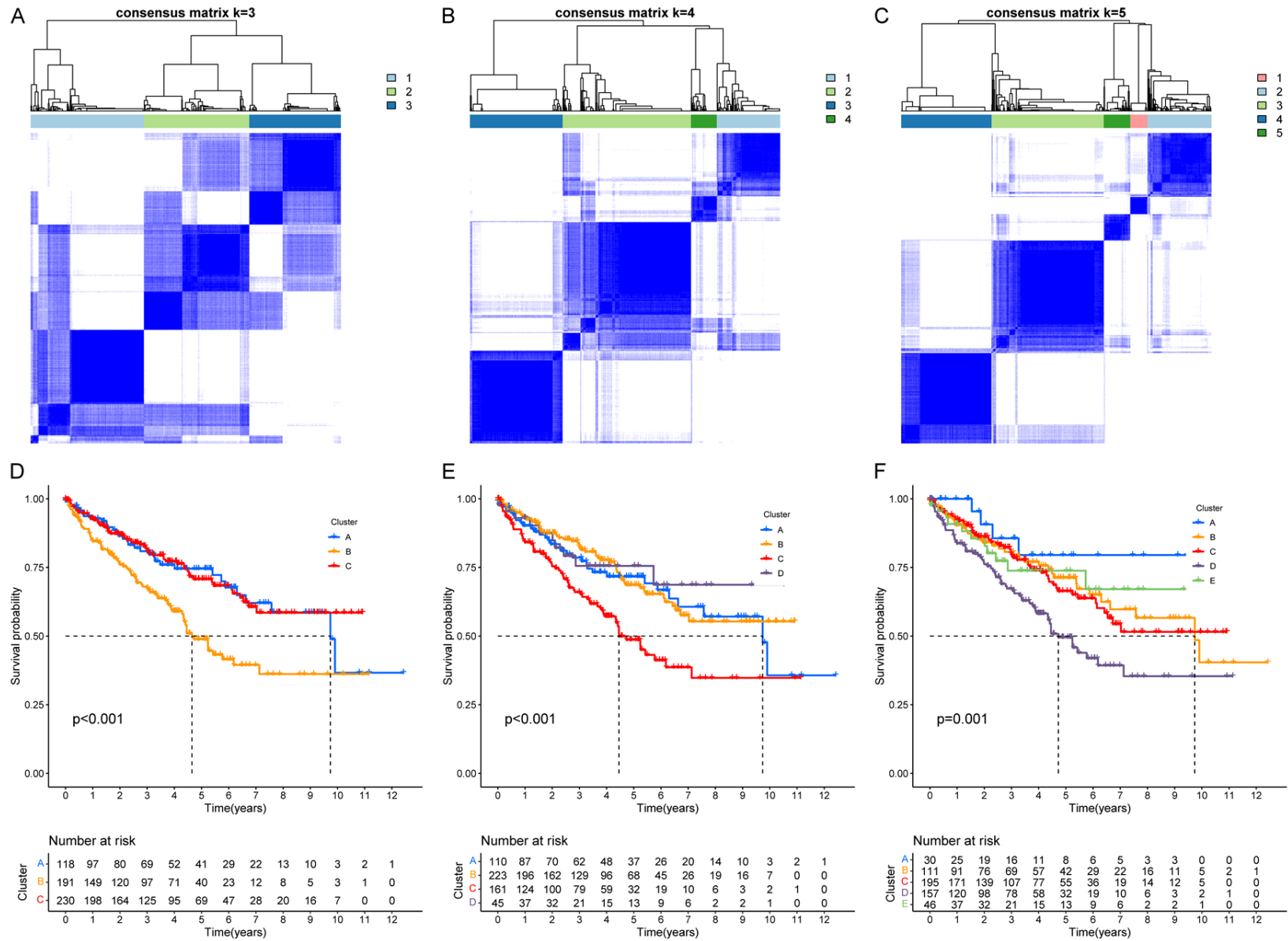


Figure S2. Consensus clustering matrixes for K = 3-5 (A-C) and Kaplan-Meier overall survival (OS) curves for 539 ccRCC patients in 3 (D), 4 (E), or 5 (F) subgroups.

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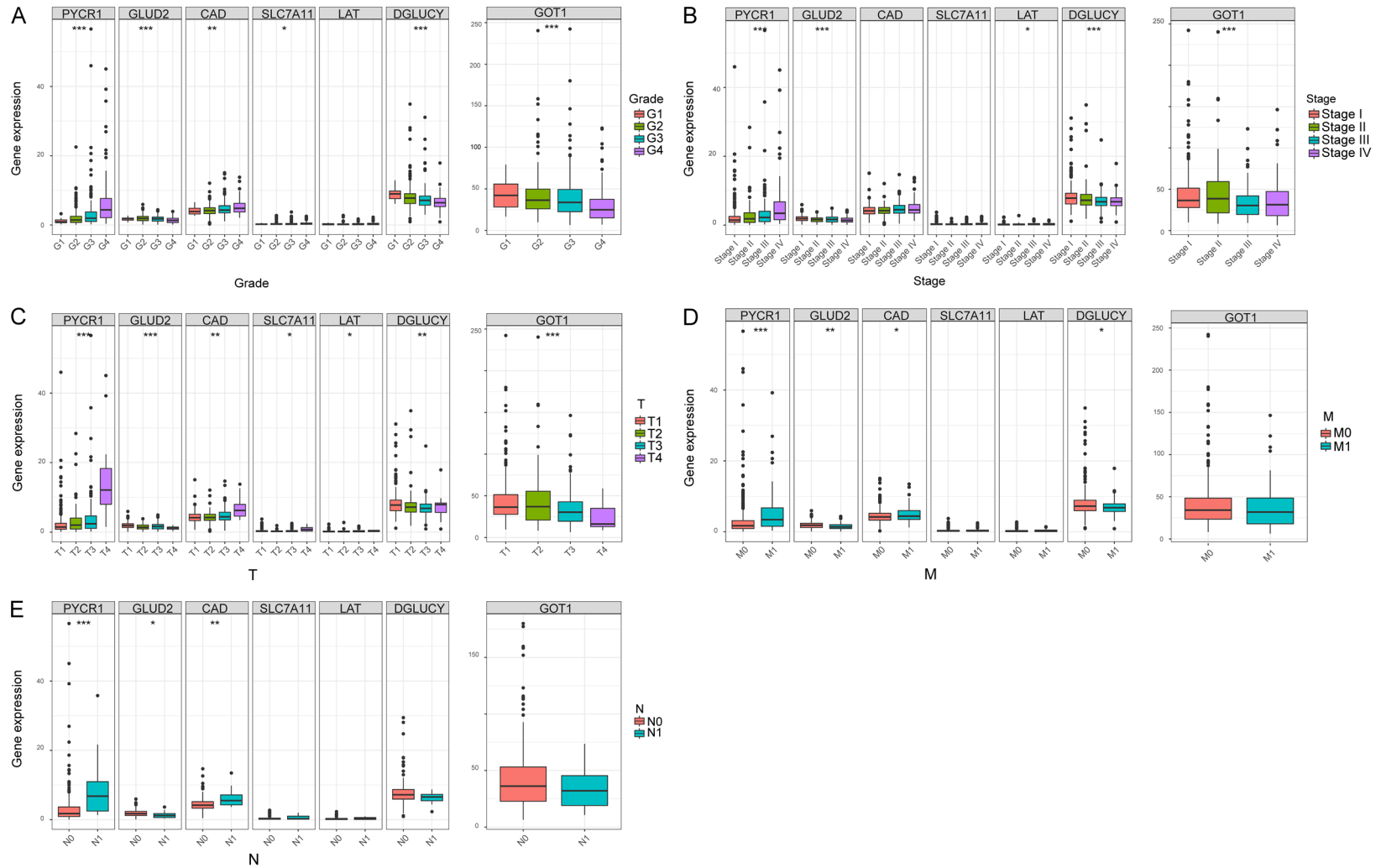


Figure S3. Correlation analyses of the expression of representative genes with clinicopathological factors. A. Expression levels of PYCR1, GLUD2, CAD, SLC7A11, LAT, DGLUCY, and GOT1 were associated with histological grade, stage, T stage, N stage, and M stage in ccRCC. B. Expression levels of PYCR1, GLUD2, LAT, DGLUCY, and GOT1 were associated with pathological stage in ccRCC. C. Expression levels of PYCR1, GLUD2, CAD, SLC7A11, LAT, DGLUCY, and GOT1 were associated with T stage in ccRCC. D. Expression levels of PYCR1, GLUD2, CAD, and DGLUCY were associated with M stage in ccRCC. E. Expression levels of PYCR1, GLUD2, and CAD were associated with N stage in ccRCC. Wilcox test was used, and the asterisks represent the statistical P value (* P <0.05, ** P <0.01, *** P <0.001).