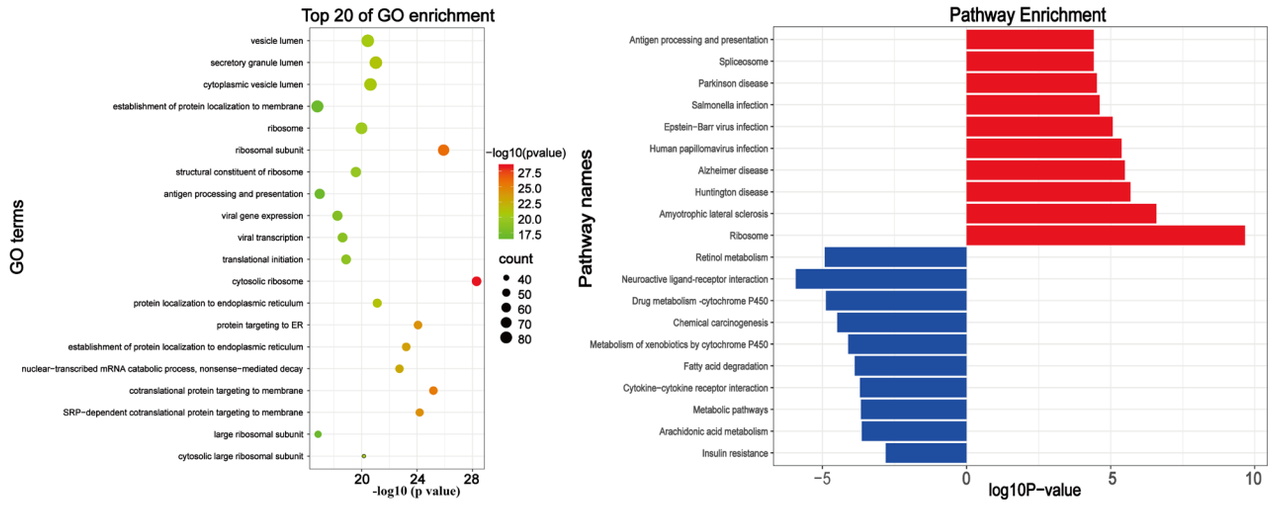

Figure S1 GO and KEGG analyses of the screened 2,207 up- and down-regulation molecules in HCC. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; HCC, hepatocellular carcinoma.

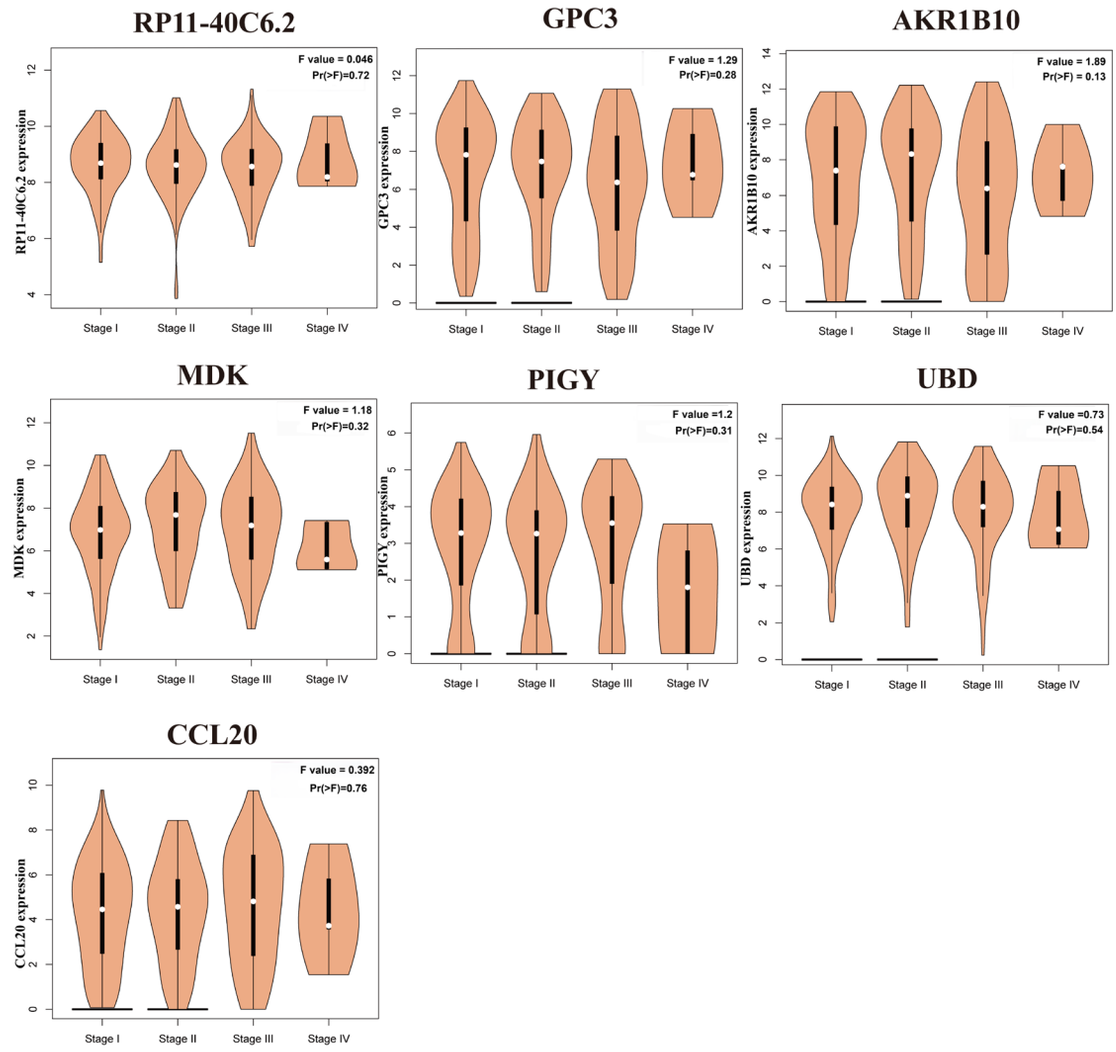

Figure S2 The correlation of the expression of candidate molecules with clinical stage of HCC patients. Analyses were performed using the F test, and differences between the two groups were considered significant when Pr (>F) was less than 0.05. *GPC3*, *glypican 3*; *AKR1B10*, *aldo-keto reductase family 1 member B10*; *MDK*, *midkine*; *PIGY*, *phosphatidylinositol glycan anchor biosynthesis class Y*; *UBD*, *ubiquitin D*; *CCL20*, *C-C motif chemokine ligand 20*; HCC, hepatocellular carcinoma.

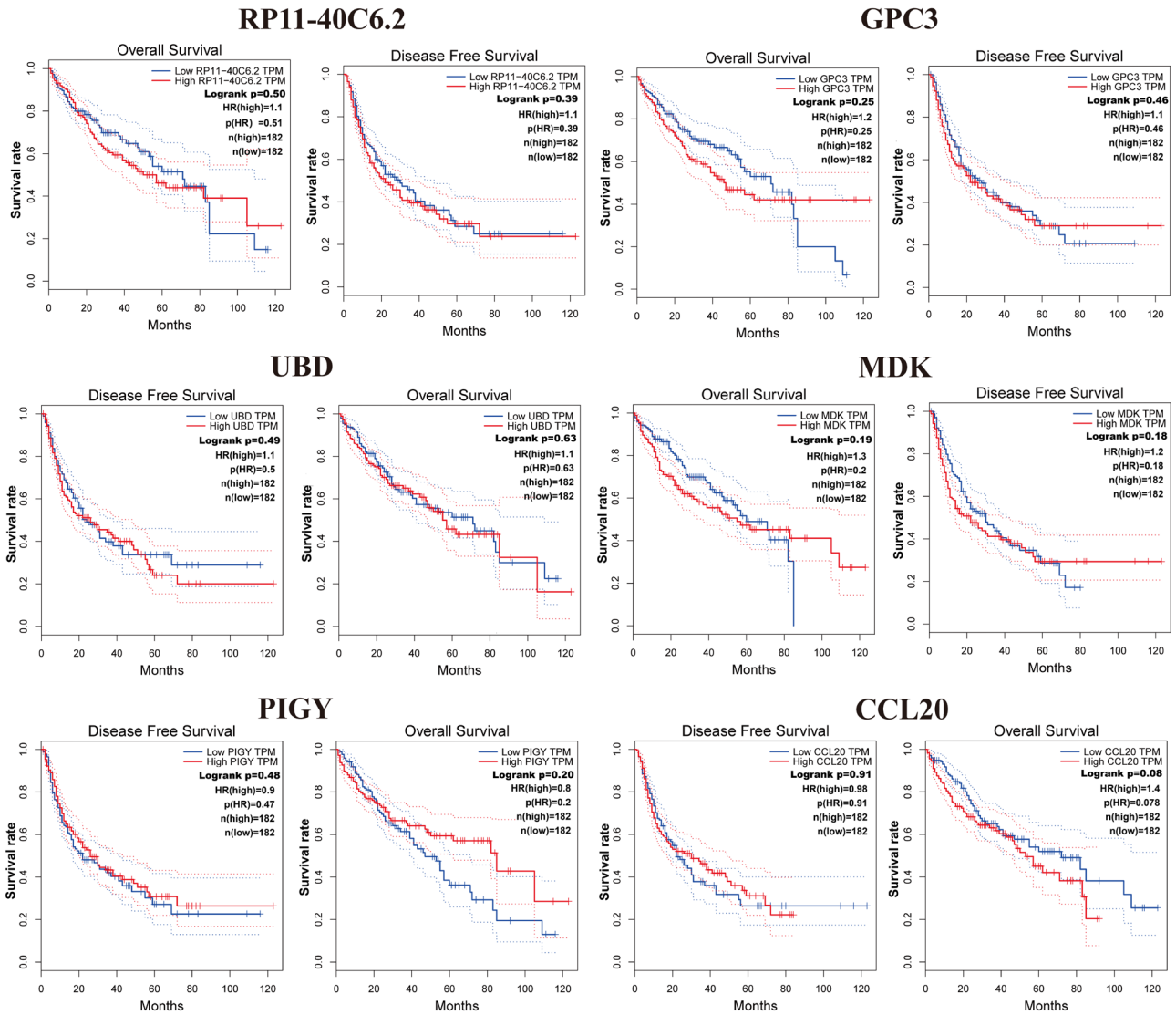

Figure S3 The relationship between candidate molecule expression and prognosis of HCC patients. The median expression values were used for group cutoff. The survival was analyzed using the log-rank test. The P value less than 0.05 indicates significant difference. The "n" represents number of samples. TPM, transcripts per kilobase million; HR, hazard ratio; *GPC3*, *glypican 3*; *AKR1B10*, *aldo-keto reductase family 1 member B10*; *MDK*, *midkine*; *PIGY*, *phosphatidylinositol glycan anchor biosynthesis class Y*; *UBD*, *ubiquitin D*; *CCL20*, *C-C motif chemokine ligand 20*; HCC, hepatocellular carcinoma.

https://dx.doi.org/10.21037/tcr-24-1845

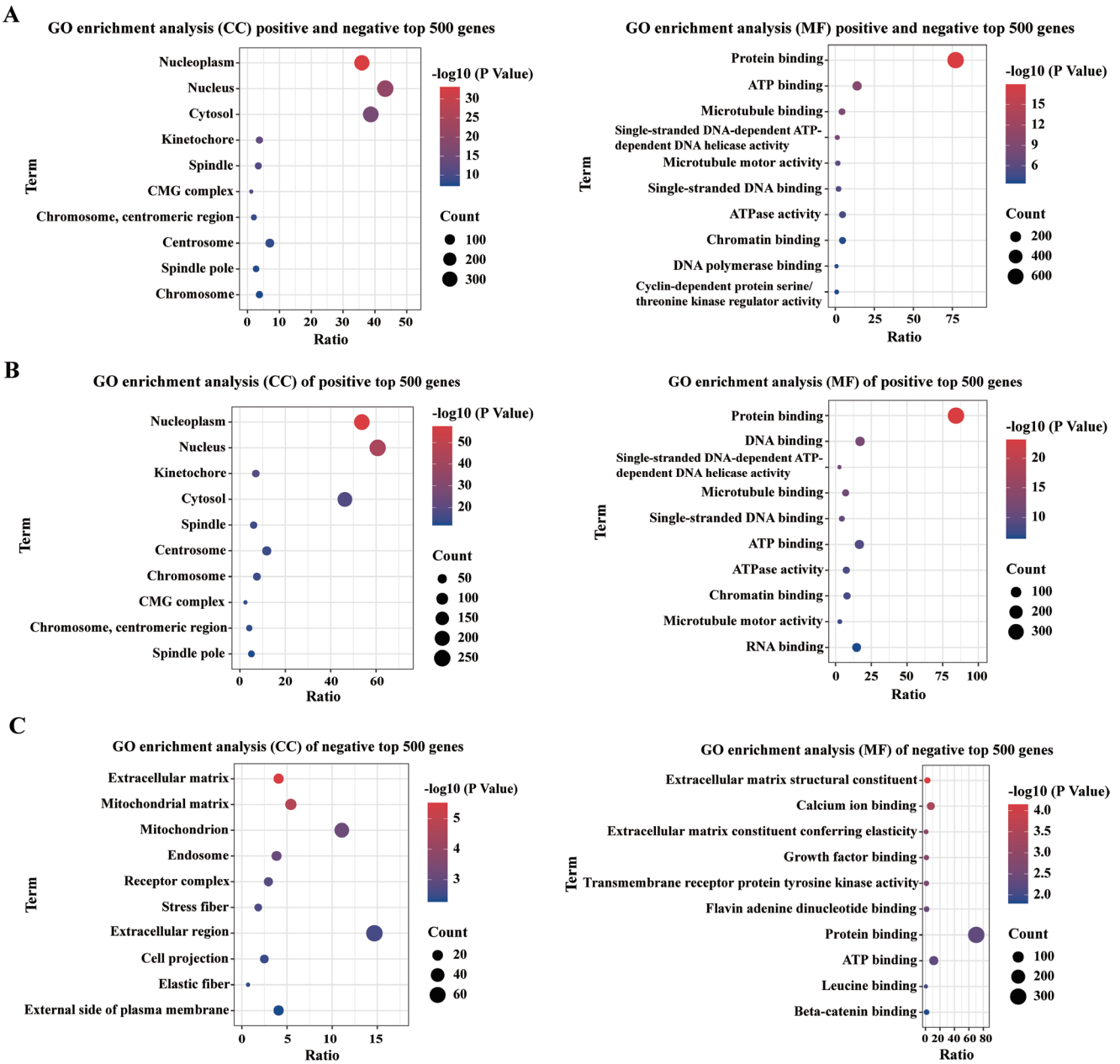

Figure S4 The GO annotation and KEGG pathway enrichments of *CDKN2A*-related top 500 positively and negatively associated genes in HCC cohorts. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; *CDKN2A*, *cyclin-dependent kinase inhibitor 2A*; HCC, hepatocellular carcinoma.

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