Supplementary

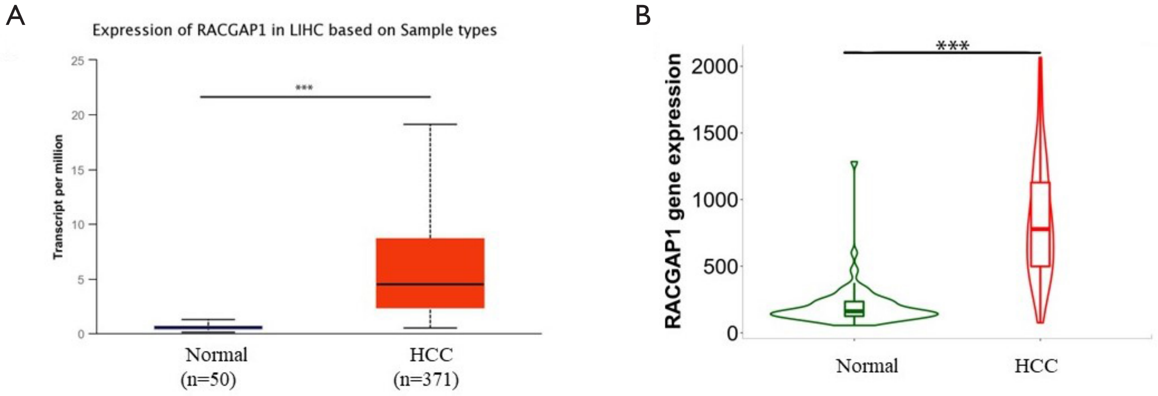

Figure S1 RACGAP1 expression in HCC. (A,B) RACGAP1 mRNA expression in HCC was examined through the UALCAN and TNM plot datasets. ***, P<0.001.

https://dx.doi.org/10.21037/tcr-23-1474

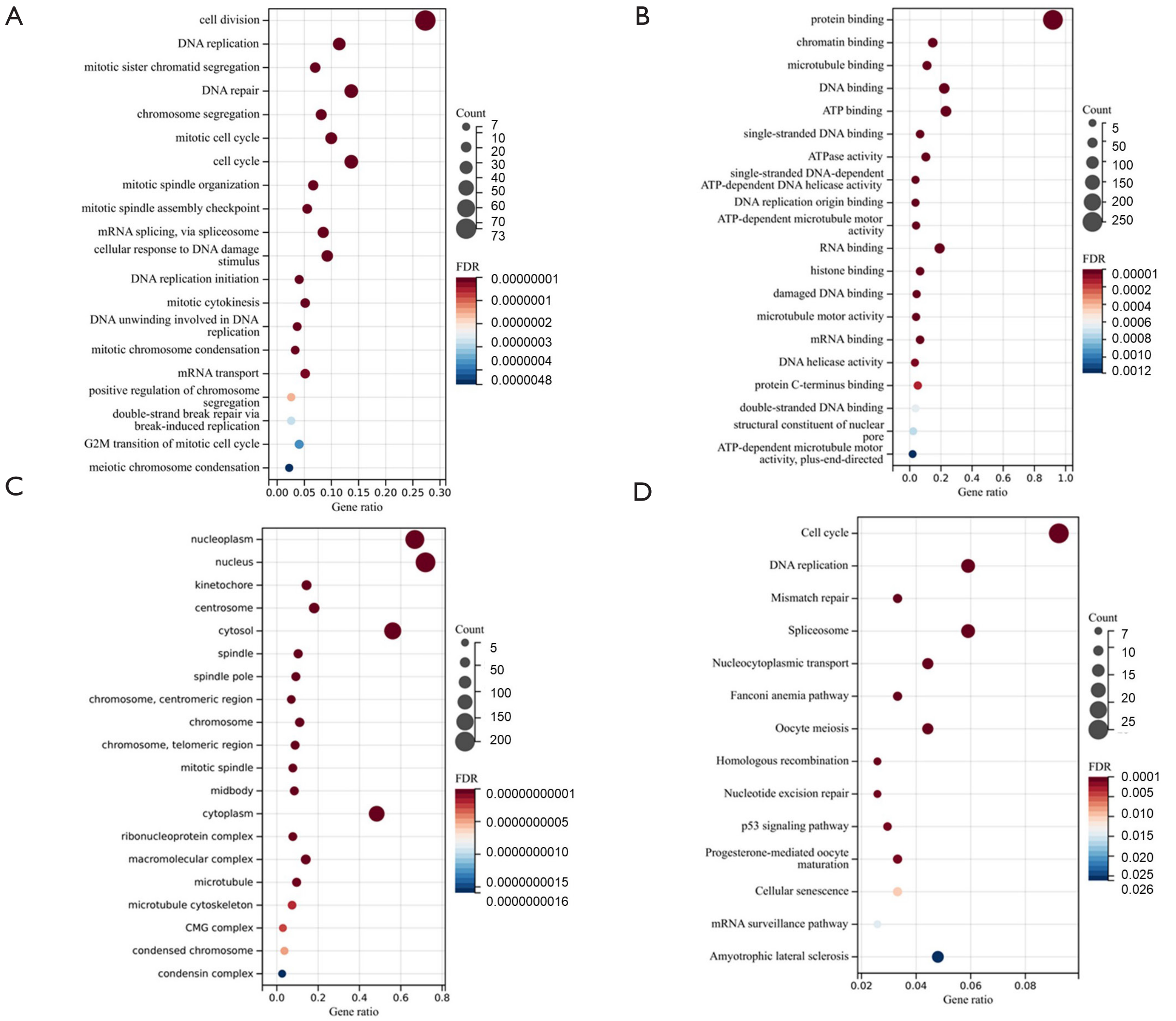

Figure S2 Functional enrichment analysis of RACGAP1-interacting genes and proteins. (A) Biological process (BP), (B) molecular function (MF), (C) cellular component (CC) and (D) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways of the genes related to RACGAP1.

https://dx.doi.org/10.21037/tcr-23-1474

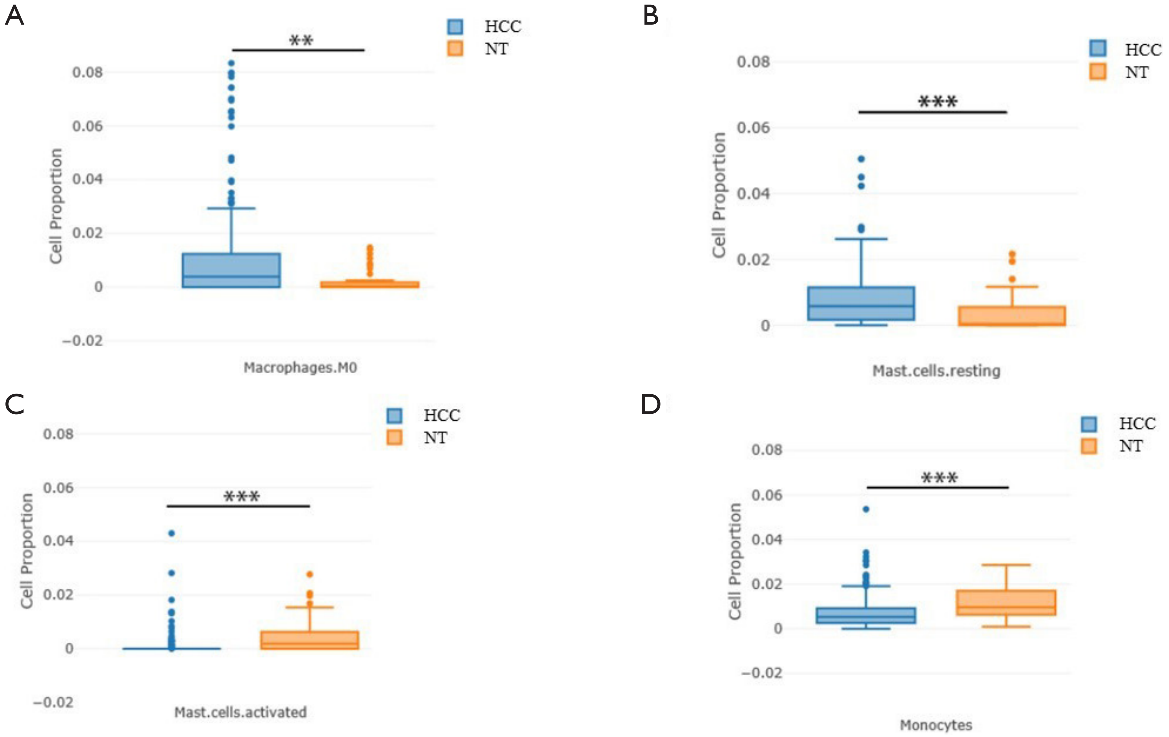

Figure S3 The proportion of tumor-infiltrating lymphocytes in hepatocellular carcinoma and normal tissues. (A-D) the proportion of macrophages M0, resting mast cell, activated mast cell and monocyte in HCC and NT. **, P<0.01; ***, P<0.001.

Table S1 Correlation analysis between RACGAP1 and cytokines using TIMER

Cytokines	Liver hepatocellular carcinoma			
	None		Purity	
	Cor	P	Cor	P
CCR4	0.219	2.10–05*	0.329	3.75e–10*
CCR5	0.199	1.14e–04*	0.371	1.03e–12*
CCR8	0.403	6.91e–16*	0.516	6.63e–25*
CCR10	0.438	7.56e–19*	0.474	9.43e–21*
CCL22	0.052	3.20e–01	0.169	1.67e–03*
CCL5	0.065	2.14e–01	0.185	5.42e–04*
CCL1	0.147	4.61e–03*	0.173	1.26e–03*
CCL28	0.334	3.98e–11*	0.311	3.46e–09*

*, $P<0.05$.

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