

Figure S1. Expression of RAC2 is upregulated in ccRCC patients. (A-D) Reverse transcription-quantitative PCR assays of RAC1, RAC2, RAC3 and RhoG the tissues of mRNA expression in 50 paired tissue samples of ccRCC patients. (E) Immunohistochemistry data in RCC tissues from The Human Protein Atlas (<http://www.proteinatlas.org>) show the relative high expression of RAC2. RAC, Rac family small GTPase; RhoG, Rho family member G; ccRCC, clear cell renal cell carcinoma.

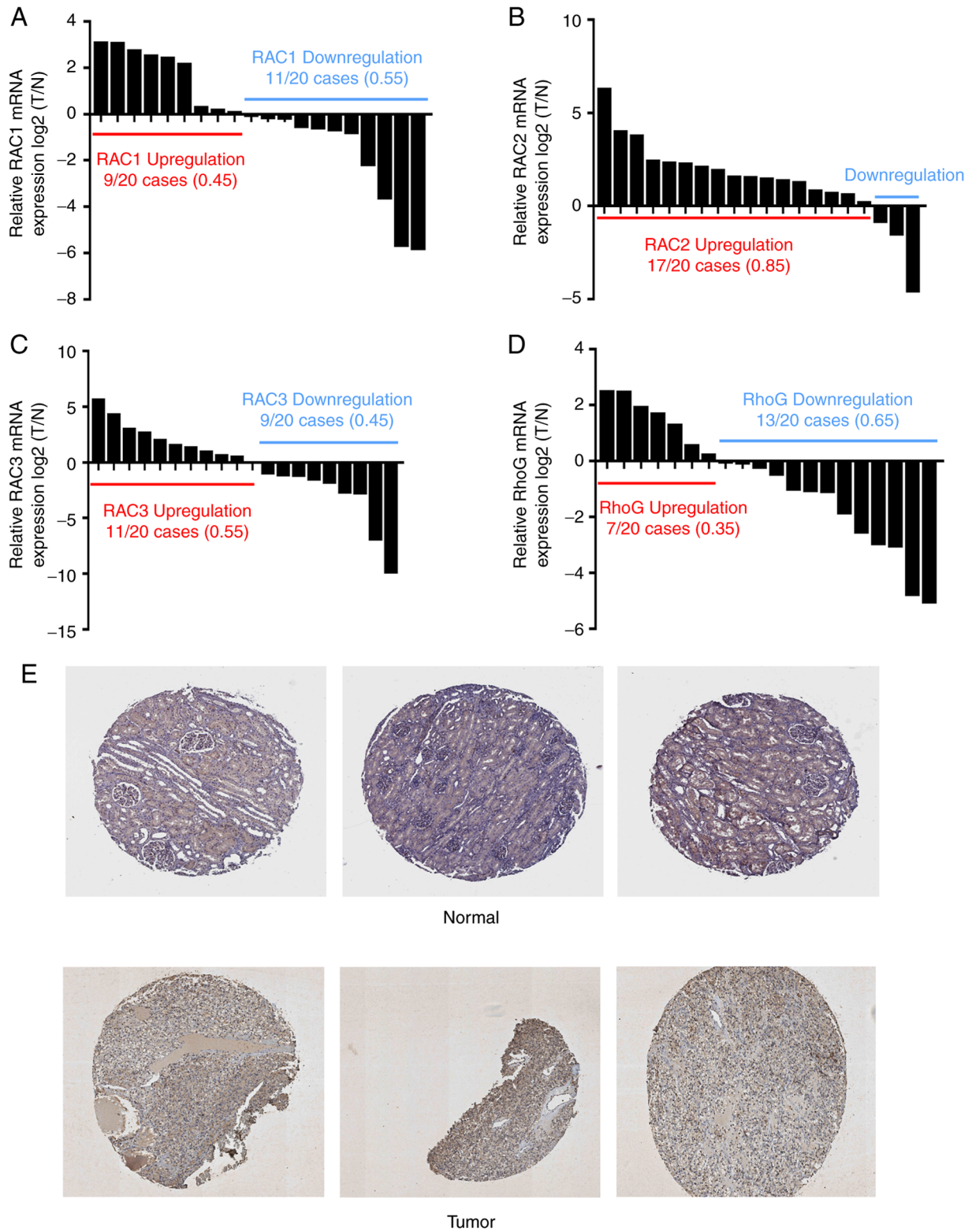


Figure S2. No significant cytotoxicity of siRNA delivery method. (A) Reverse transcription-quantitative polymerase chain reaction assays of RAC2 mRNA expression in untreated or negative control transfected 786-O cells. (B) Cell Counting Kit-8 assays detected the proliferative ability of untreated or negative control transfected 786-O cells. (C and D) Representative images of migration and invasion assays performed using untreated or negative control transfected 786-O cells (magnification, x100). Data are presented as the mean \pm standard deviation from three independent experiments. Ns, not significant; RAC2, Rac family small GTPase 2; NC, negative control; si-RNA, small interfering RNA; OD value, optical density value.

