Figure S1. (A) SALL4 expression in different cancer types and healthy tissues. The top, middle and bottom lines of the boxes indicate the third quartiles, median and first quartiles, respectively. The whiskers indicate the SD, and the circles indicate the values beyond the SD. The different cancer types are displayed on the x-axis. (B) Top 19 pathways enriched in SALL4-associated genes identified by WebMeV in ccRCC. The size of the circle is proportional to the ratio.

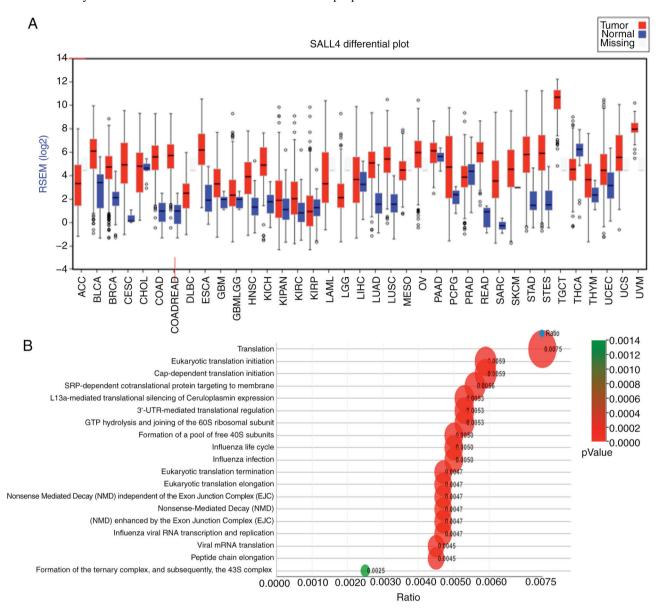


Figure S2. (A) Efficiency of the knockdown of SALL4 in OSRC-2 and SW839 cells. (B) SALL4 mRNA expression level in HK2 cells and the three RCC cell lines was detected by reverse transcription-quantitative PCR.\*\*P<0.01, \*\*\*P<0.001. SALL4, spalt like transcription factor 4; RCC, renal cell carcinoma; sh, short hairpin RNA.

