Figure S1. Differential expression analysis of ELF1 and 2 between ccRCC and normal tissues in multiple databases. mRNA expression levels of (A) ELF1 and (B) ELF2 in ccRCC and normal tissues in the Gene Expression Profiling Interactive Analysis database. mRNA expression levels of (C) ELF1 and (D) 2 in ccRCC and normal tissues in the Gene Expression Omnibus database. mRNA expression levels of (E) ELF1 and (F) ELF2 in ccRCC and normal tissues in the UALCAN database. ELF, E47-like factor; ccRCC, clear cell renal cell carcinoma.



Figure S2. ELF1-5 expression levels in common types of cancer, as determined using the Oncomine database. (A) ELF1, (B) ELF2, (C) ELF3, (D) ELF4 and (E) ELF5 expression levels in various malignant tumor types. \*P<0.05, \*\*P<0.01 and \*\*\*P<0.001. ELF, E47-like factor.



Figure S3. Genetic alteration analyses of ELF3-5 using cBioPortal. Genetic alteration frequencies of (A) ELF3, (B) ELF4 and (C) ELF5 in clear cell renal cell carcinoma. ELF, E47-like factor; CNA, copy number alterations.



Figure S4. Association between ELF3-5 expression and OS and DFS of clear cell renal cell carcinoma determined using Gene Expression Profiling Interactive Analysis. OS analysis patients split according to (A) ELF3, (B) ELF4 and (C) ELF5 expression; DFS analysis patients split according to (D) ELF3, (E) ELF4 and (F) ELF5 expression. ELF, E47-like factor; OS, overall survival; DFS, disease-free survival.

