**Fig. S8**

**A**. Common genes between the CC7 signature and enriched genes in high- or low-SNAI2 groups from the TCGA and SU2C cohorts. **B**. Correlation between SNAI2 levels and CC7 signature scores in the TCGA, DKFN, and SU2C/PCF cohorts. **C**. Correlation between SNAI2 levels and Tyekucheva metastasis stromal signature score in the TCGA and SU2C cohorts. **D** and **E**, Profiling of immune cells by CIBERSORT in the TCGA (D) and SU2C/PCF (E) cohorts. Significance was determined using Wilcoxon’s rank sum test.

Figure S8. SNAI2 interacts with the tumor microenvironment in PC. A, Common genes between the CC7 signature and enriched genes in high- or low-SNAI2 groups from the TCGA and SU2C cohorts. B, Correlation between SNAI2 levels and CC7 signature scores in the TCGA, DKFN, and SU2C/PCF cohorts. C, Correlation between SNAI2 levels and Tyekucheva metastasis stromal signature score in the TCGA and SU2C cohorts. D and E, Profiling of immune cells by CIBERSORT in the TCGA (D) and SU2C/PCF (E) cohorts. Significance was determined using Wilcoxon’s rank sum test.