

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Source data of the relevant figures.

File Name: Supplementary Data 2

Description: Metadata of scRNA-seq data from 6 CRPC samples.

File Name: Supplementary Data 3

Description: DEGs of each cluster in epithelial cells of 6 CRPC samples (Log2 fold change > 0.25, FDR < 0.001; one-tailed Wilcoxon rank sum test, P values adjusted for multiple testing using the Bonferroni correction).

File Name: Supplementary Data 4

Description: Characteristics of TMA from 297 patients.

File Name: Supplementary Data 5

Description: ScVelo_Gene_likelihood calculated by RNA velocity.

File Name: Supplementary Data 6

Description: This table contains the 30 genes with the highest NMF score for each factor in each sample. Association to meta-programs is indicated below.

File Name: Supplementary Data 7

Description: Pearson Correlation Coefficients of genes in P1, P2 and P4.