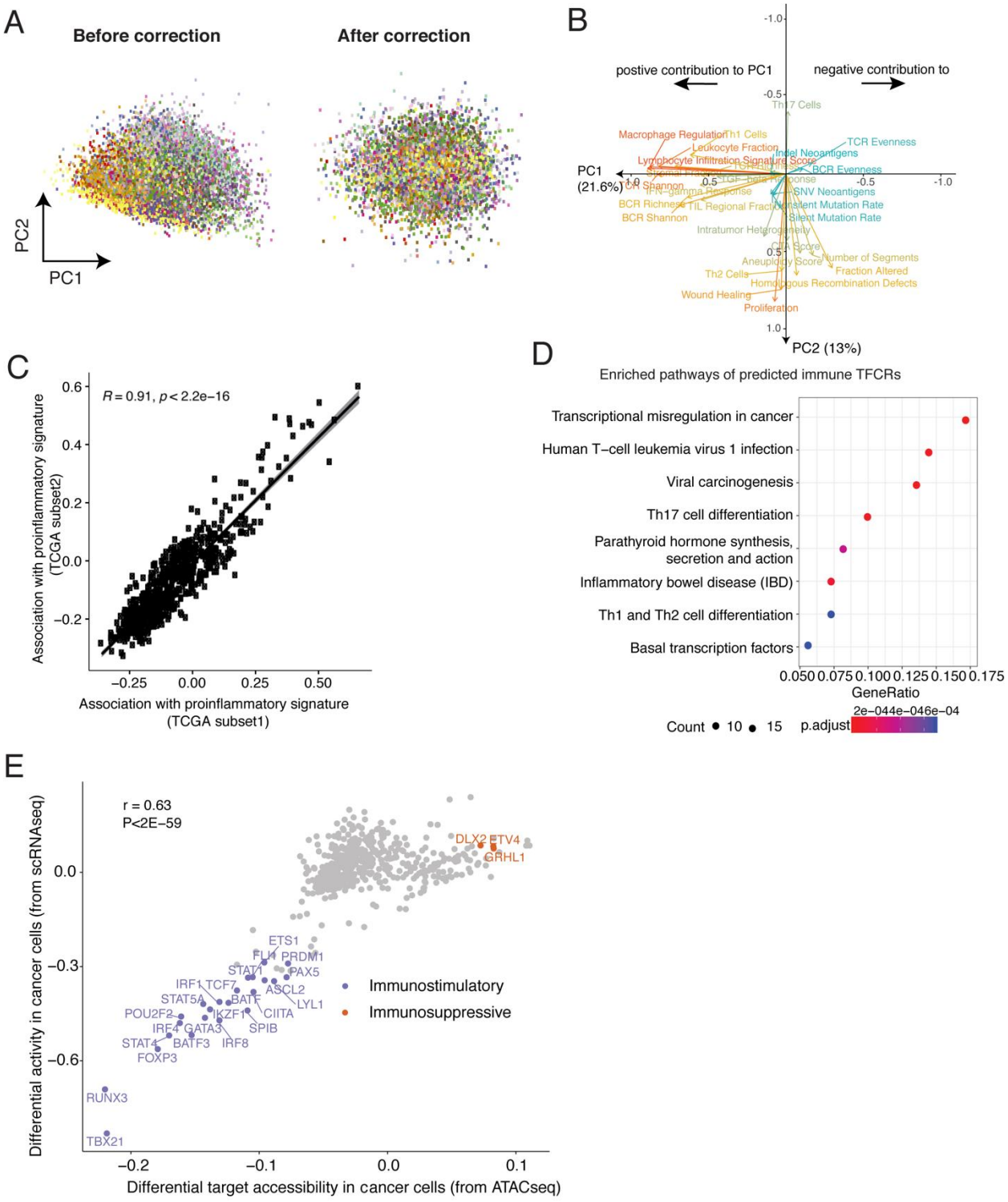

Fig. S1. The description and validation of the BipotentR immune module.

(A) Cancer-type (color) specific effects of TCGA samples based on their principal components (PC1 and PC2) of 32 immune signatures. Samples before (left) and after (right) correction of cancer-type specific effects are shown. Cancer types populations are seen to be mixed after the correction. (B) The contribution of 32 immune signatures to principal component 1 (PC1). The contribution of a signature is proportional to the X-axis component of its arrow. The

direction of the arrow shows the positive (towards left) or negative (towards right) contribution to PC1. (**C**) The proinflammatory association of TFCRs (Methods) calculated from randomly selected two subsets of TCGA cancer types. (**D**) KEGG pathways enriched in predicted immune TFCRs. Significance (color) and the ratio (size) of enriched genes in pathways are displayed in the enrichment plot. (**E**) The TFCR differential activity (Y-axis) and differential target accessibility (X-axis) in cancer cells were calculated respectively from scRNA-seq and scATAC-seq. Pearson correlation (and p-value) between differential scRNA-seq and scATAC-seq signals is displayed. Top TFCRs are labeled.