Pan-cancer single epithelial cell analysis identified specific and common regulatory features of various cancers.

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Deciphering gene regulatory networks (GRN) is a key to understand the development and progression of various types of cancer. With the hypothesis of the existence of hallmark of cancer, we investigated GRN structures obtained from single cell RNAseq in a Pan-cancer scale. Single cell expression of epithelial cells was collected, encompassing 1.5M cells from 24 organs of cancer. To elucidate the transcriptomic dynamics in the progression of each cancer type, we inferred trajectory for each cancer type starting from each differentiated organ-specific region to the common cancer region. Comprehensive GRN analysis using TENET, a GRN inference tool based on Transfer Entropy (TE), identified top Transcription Factors (TFs) regulating the trajectories for 14 major cancer types: bile duct, bladder, breast, colon, head and neck, kidney, liver, lung, ovary, pancreas, prostate, skin, stomach, and thyroid, finally yielding an integrated regulatory network. To identify specific and common TFs for various cancer types, we formulated specificity and commonality based on TF-target TE scores. This Pan-cancer analysis equipped by GRN inference offers crucial insights of general cancer regulators and specific regulators.