Although we can increasingly measure transcription, chromatin, methylation, etc., at single cell resolution, most assays only survey one or two at a time. This paper reports a new method, “sci-CAR” – a combinatorial indexing-based co-assay that jointly profiles chromatin accessibility and mRNA in each of thousands of single cells. As proof-of-concept, sci-CAR was applied to 4,825 cells representing a time-series of dexamethasone treatment, and to 11,296 cells from adult mouse kidney. The pseudotemporal dynamics of chromatin accessibility and gene expression were compared, chromatin accessibility profiles reconstructed for cell types defined by RNA profiles, and cis-regulatory sites linked to target genes using the covariance of chromatin accessibility and transcription. The general relevance of such high-resolution studies will be discussed.