The text discusses the challenge of evaluating heterogeneity and its impact on outcomes and drug responses in cancer cells within a tumor, given their diverse phenotypes and dynamic plasticity. To address this, the authors perform transcriptional profiling on 35,276 individual cells from 32 breast cancer cell lines, resulting in a comprehensive single-cell atlas. The findings reveal a high degree of heterogeneity in the expression of biomarkers among the individual cells. Subsequently, the authors employ a deconvolution algorithm trained on the atlas to identify the cell line composition from bulk gene expression profiles of tumor biopsies. This approach enables patient stratification based on the cell line composition. Furthermore, the study links results from large-scale in vitro drug screening in cell lines to the single-cell data, allowing for the computational prediction of drug responses starting from single-cell profiles. A key observation is that transcriptional heterogeneity allows cells with varying drug sensitivity to coexist within the same population. In summary, the work establishes a framework for determining tumor heterogeneity by assessing cell line composition and drug response. This approach offers valuable insights into the coexistence of cells with differential drug sensitivity within a population, contributing to our understanding of cancer cell dynamics.