Figure S1. Intratumoral NE heterogeneity in SCLC patient tumors and intra-cell line NE heterogeneity in SCLC and NBL cell lines

A. Distribution of NE scores for lung cancer patient tumors from HTAN datasets. Sample names are labeled on the y-axis. Each dot represents a cell within the sample and is colored by the cell type annotated by the original study, violin plot is overlaid to visualize the overall distribution. Note that two SCLC-N tumors (RU1231 and RU1215) have broad NE score distributions. **B**-**C**. High- and low- NE score tumor cells are found to coexist within the same SCLC tumor. Single cells are in columns. Due to the high dropout rate of scRNA-seq data, only the top abundantly expressed genes are visualized. **D**, NE score (x-axis) correlation with EMT score, interferon response program score, and epithelial senescence program score (y-axis) in single cells of SCLC cell line NCIH1048 and NBL cell line SKNAS from Kinker et al.'s study.