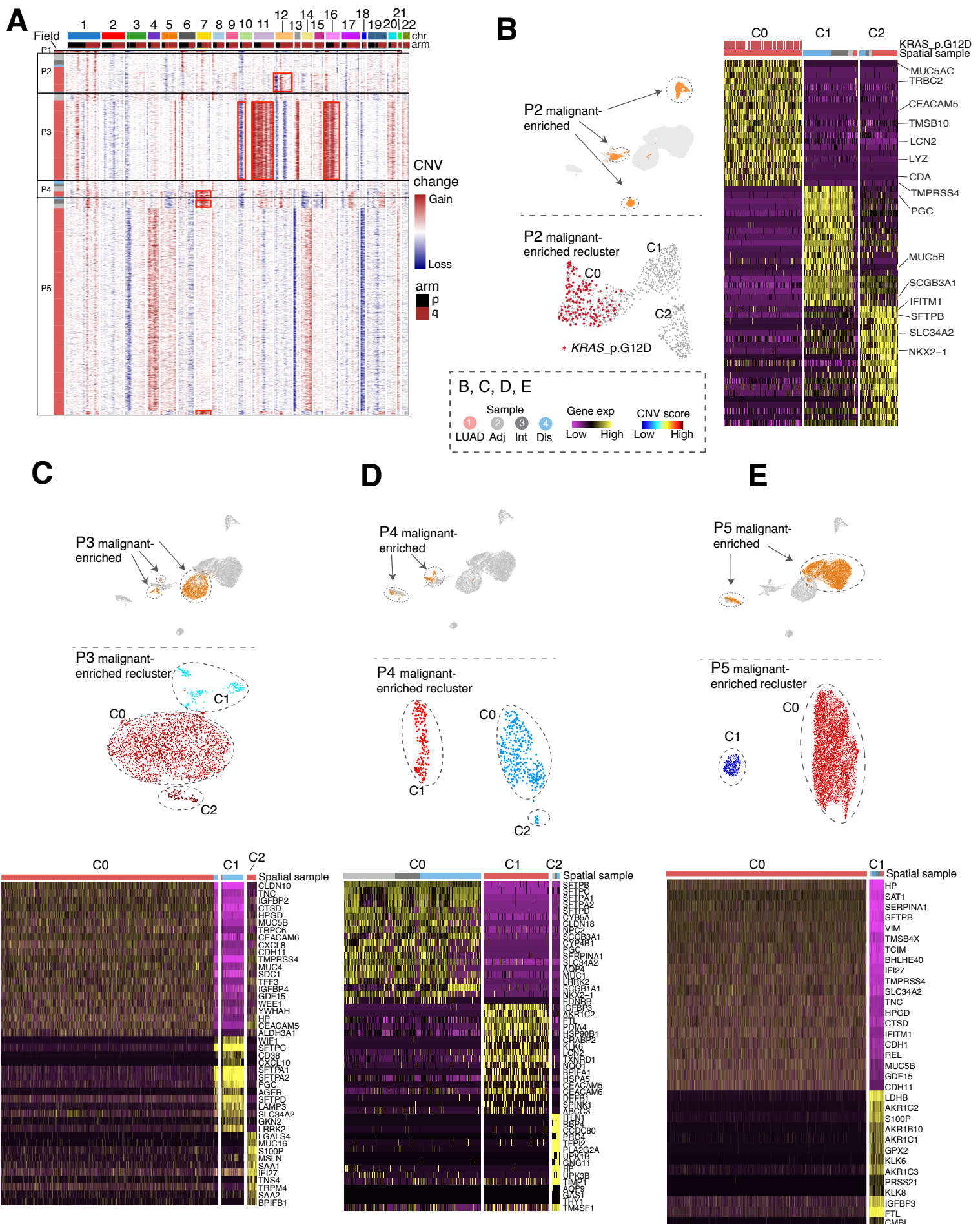


**Resolving the spatial and cellular architecture of lung adenocarcinoma by multi-region single-cell sequencing**

**SUPPLEMENTARY DATA FILE 3**

**Supplementary Figure S8**

# Supplementary Fig. S8





**Supplementary Fig. S8. Inference of copy number variation (CNV) and by-patient subclustering of cells from the malignant-enriched cluster.** **A**, Heatmap showing CNV scores of cells in the malignant-enriched cluster. **B**, UMAP highlighting P2 cells among all patient cells in the malignant-enriched cluster (top left). Subclustering of P2 cells from malignant-enriched cluster showing (with red asterisk) cells harboring *KRAS*-G12D mutation (bottom left). Heatmap of top differentially expressed genes (DEGs) between cells of P2 malignant-enriched subclusters (right). UMAPs highlighting P3 (**C**), P4 (**D**) and P5 (**E**) cells among all patient subsets in the malignant-enriched cluster (top). UMAPs of by-patient subclustering of the malignant-enriched cluster (middle). Heatmaps of top DEGs between cells of by-patient malignant-enriched subclusters (bottom).