

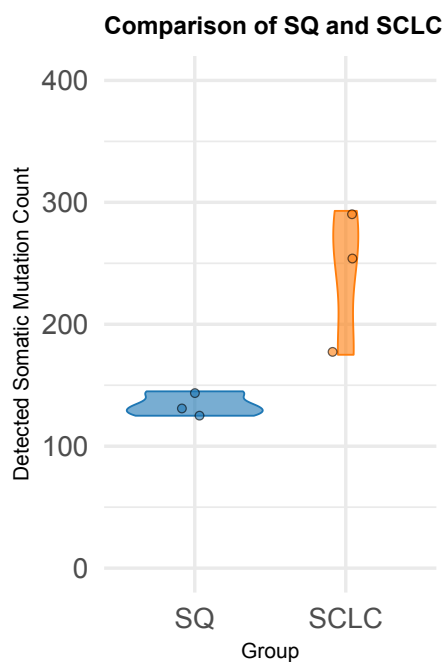


Figure S1 Numbers of somatic mutations detected in primary SQ and SCLC. The numbers of somatic mutations detected in the primary SQ and SCLC samples are presented in the form of a dot plot combined with a violin plot.

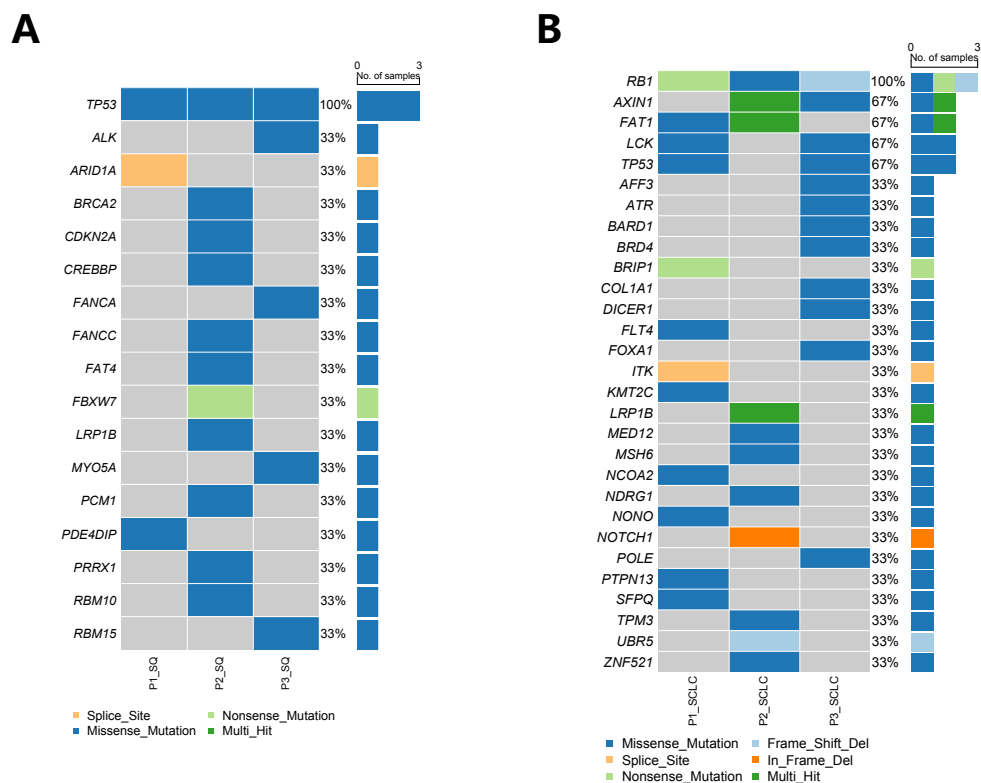


Figure S2 Comparison of tumor-associated mutations in primary lung cancer SQ and SCLC in each patient. The mutation information of the tumor-associated genes detected in the SQ in each patient (Figure A) and the SCLC in each patient (Figure B) is presented in the form of CoMut plots. Each row represents a gene, and each column represents a sample. Different colors indicate different mutation types, and the bar plot on the right shows the number of samples with mutations.

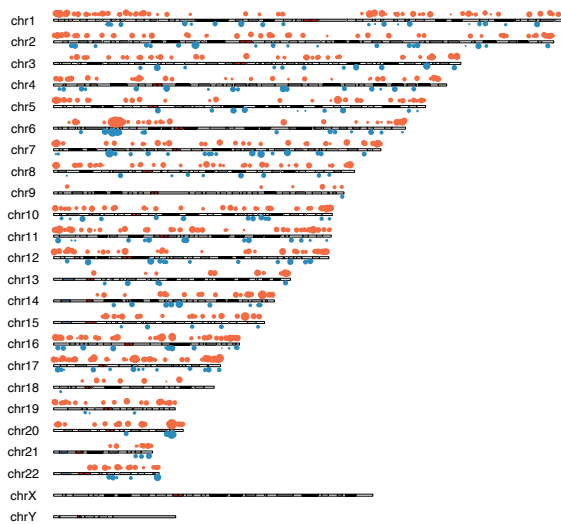
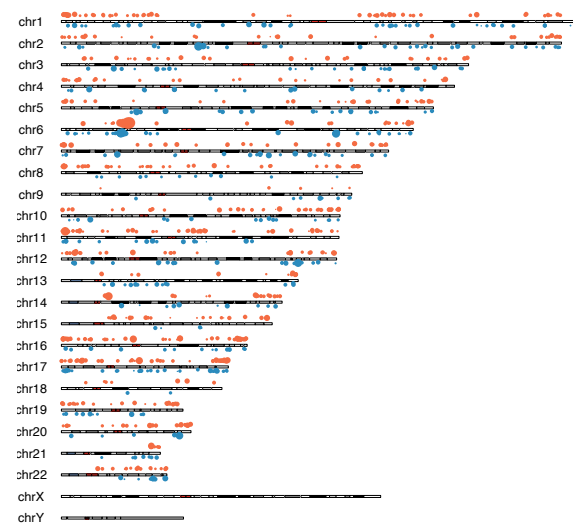
A**SQ****B****SCLC**

Figure S3 DMR results in primary lung cancer SQs and SCLCs in all three patients. DMRs detected in SQs (A) and SCLCs (B) compared with normal tissues. These DMRs are displayed on chromosomes based on their specific locations.

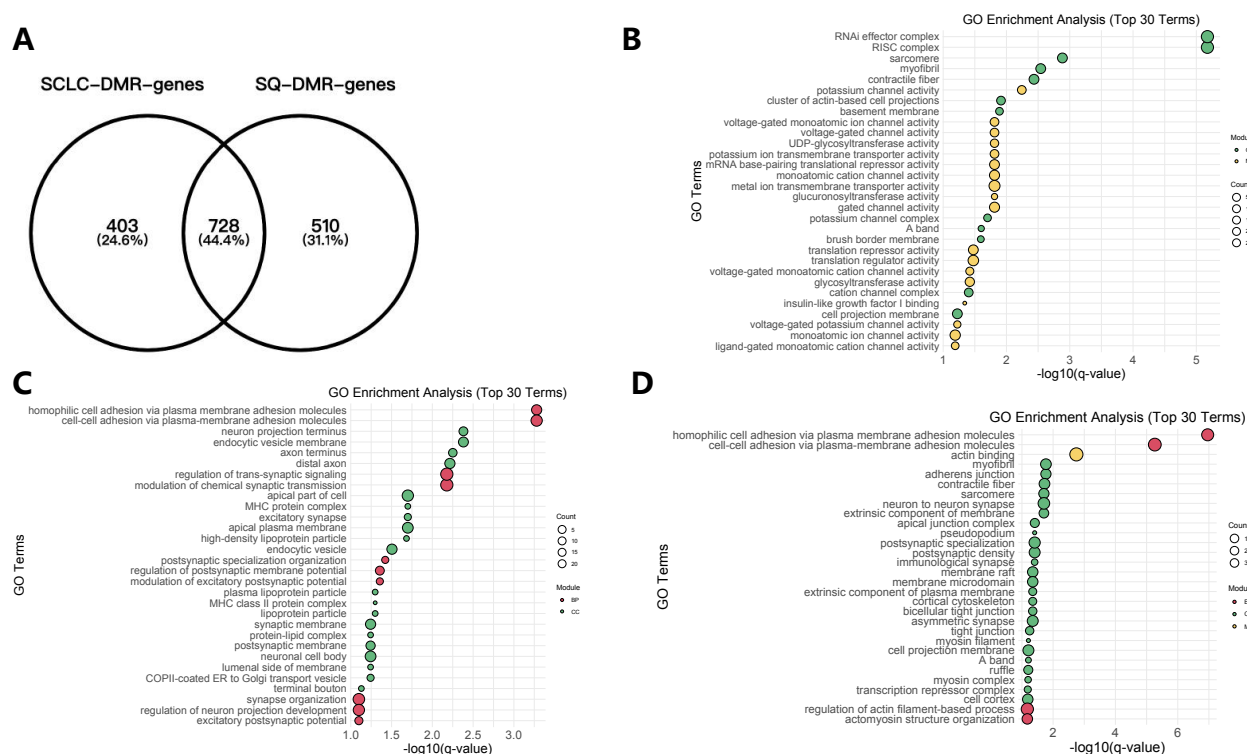


Figure S4 Characteristics of DMR-related genes in primary lung cancer SQs and SCLCs in all three patients. (A) Overlap of DMR-related genes in the SQs and SCLCs of all three patients shown in the Venn diagram. (B) GO enrichment results (Top 30 GO terms) of DMR-related genes, specifically in primary lung SQs. (C) GO enrichment results (Top 30 GO terms) of DMR-related genes specific to primary lung SCLC. (D) GO enrichment results (Top 30 GO terms) of DMR-related genes discovered in both primary lung SQs and SCLCs.

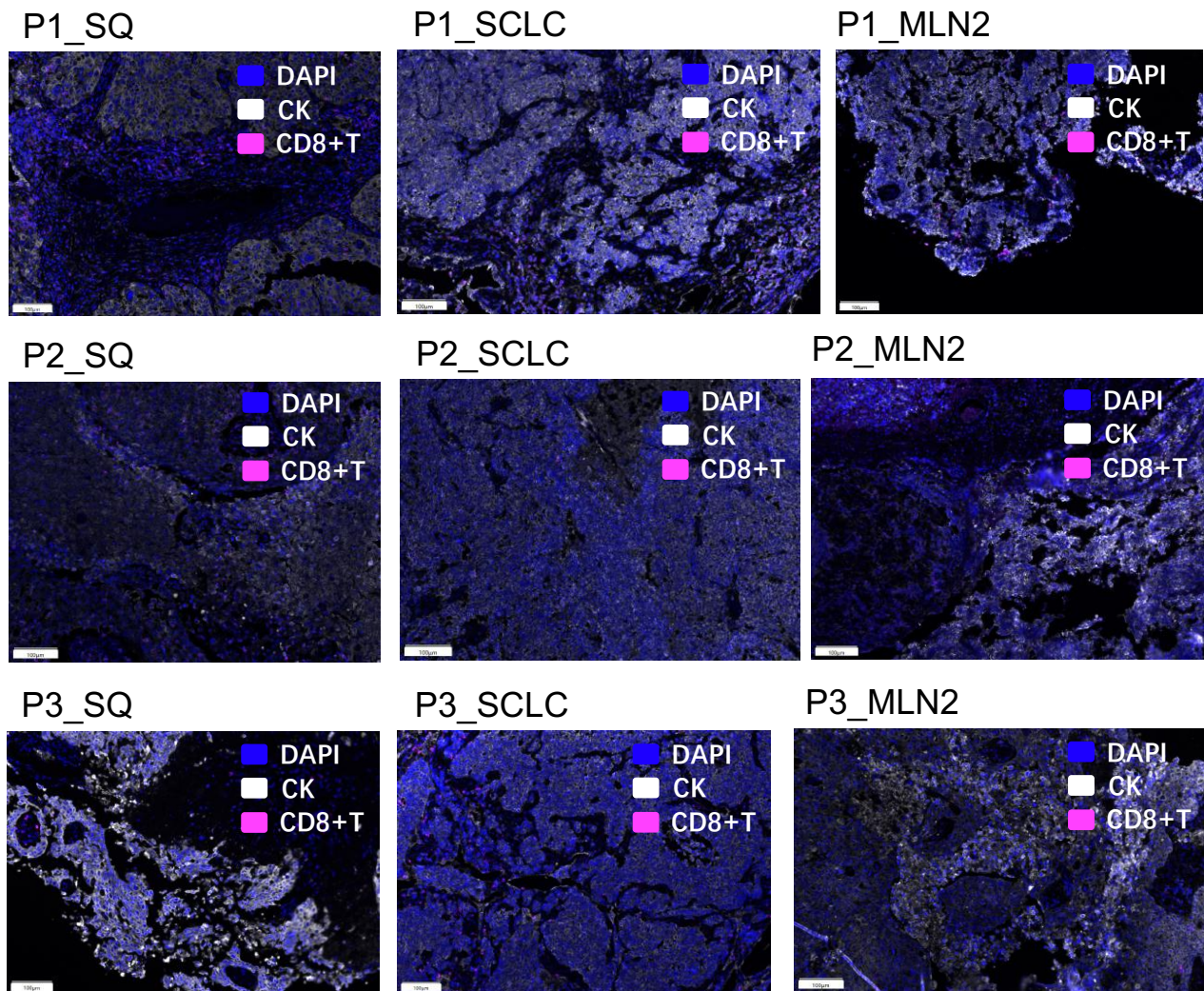


Figure S5 Representative regions of CD8+ T cells in the tumor microenvironment based on immunofluorescence (mIF) detection. DAPI was used to stain all the cells, and the CK marker was specifically expressed in the tumor cells. The white bar in the bottom left corner represents 100 μm .