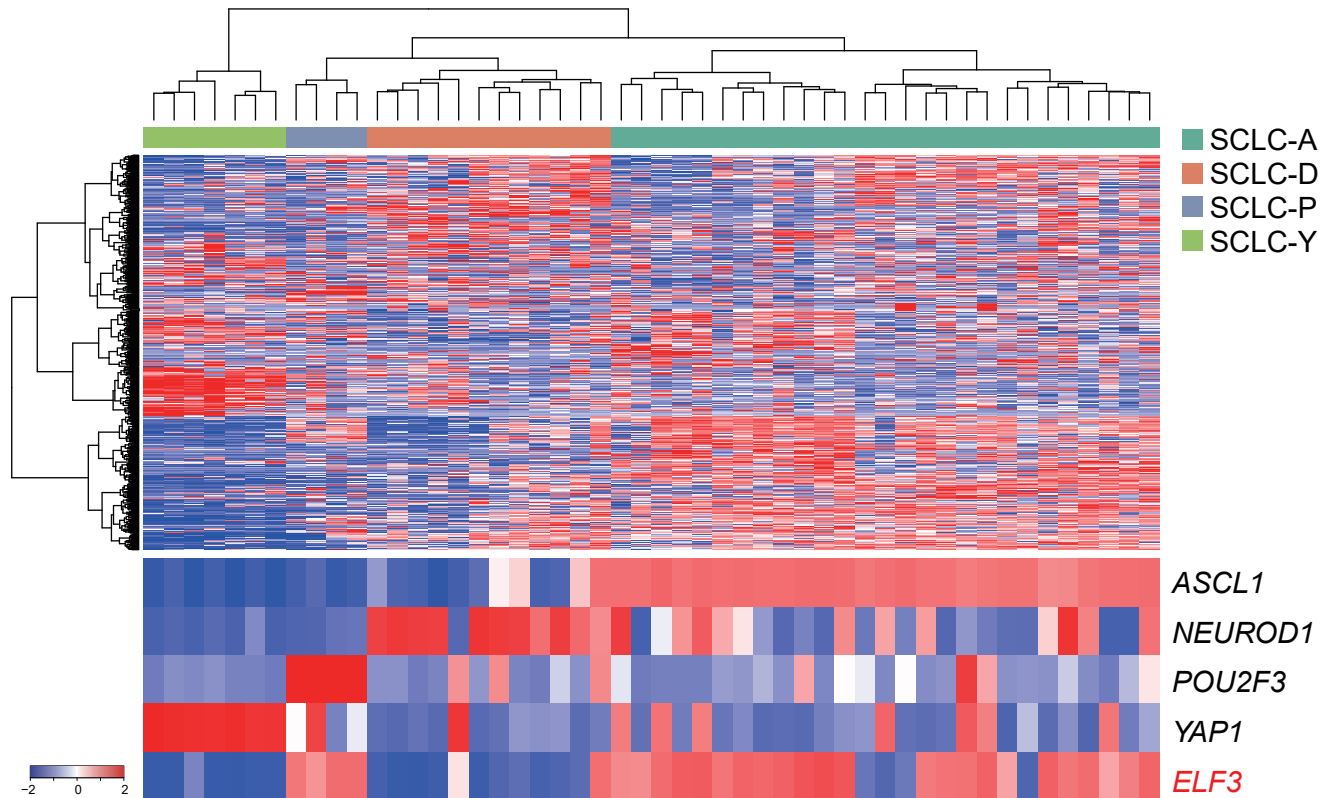# Supplementary Figure S5

Figure S5. *ELF3* expression in four molecular subtypes of 50 SCLC cell lines based on the Cancer Cell Line Encyclopedia (CCLE) dataset.

A heatmap showing the gene expression pattern generated based on the RNA-seq data of 50 SCLC cell lines. Based on unsupervised clustering with 1,200 highly variant genes, SCLC cell lines were divided into four clusters, specifically SCLC-A, SCLC-D, SCLC-P, and SCLC-Y. The lower panel shows the expression of genes encoding the representative transcription factors in each subgroup and *ELF3*.