

Supplementary Materials

Cancer Essential Genes Stratified Lung Adenocarcinoma Patients with Distinct Survival Outcomes and Identified a Subgroup from the Terminal Respiratory Unit Type with Different Proliferative Signatures in Multiple Cohorts

Kuo-Hao Ho ^{1,2}, Tzu-Wen Huang ^{1,3}, Ann-Jeng Liu ⁴, Chwen-Ming Shih ^{1,2,*} and Ku-Chung Chen ^{1,2,*}

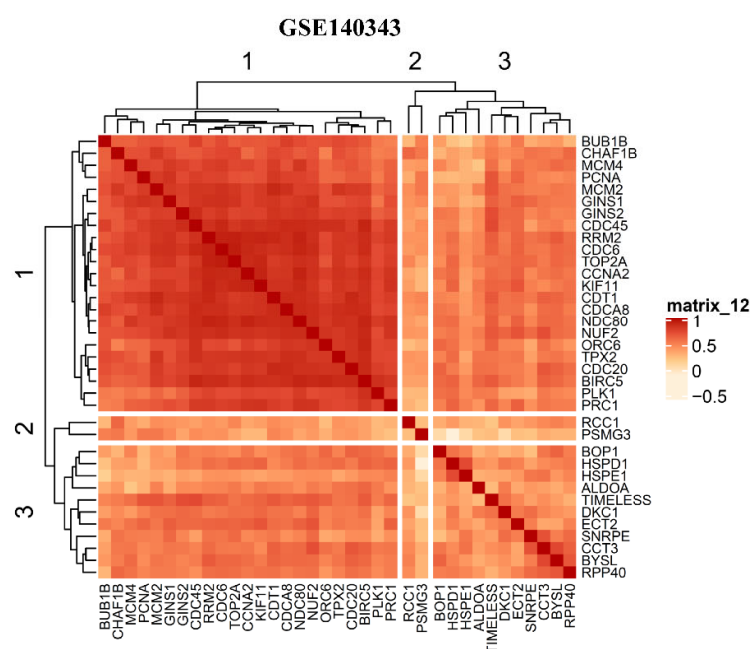


Figure S1. Associations of cancer essential genes from GSE140343 data shown as a correlation heatmap.

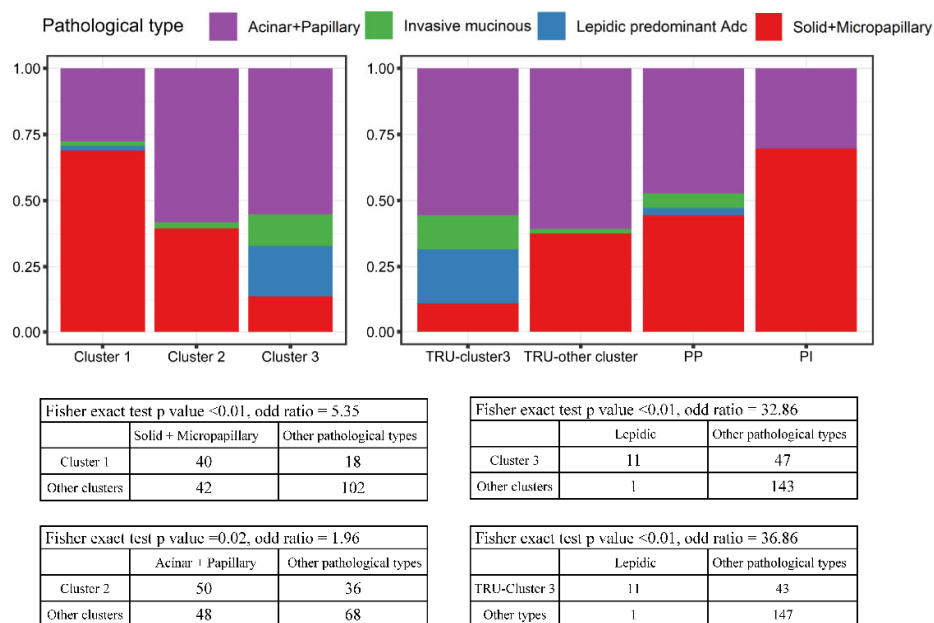


Figure S2. Association between pathological type and essential gene-stratified cluster in LUAD patients. The ratios of LUAD patients with different pathological types were presented in stacked bar plot. The 2x2 contingency tables which indicated the number of patients in a given cluster and pathological type were shown. A Fisher exact test was conducted to investigate their association.

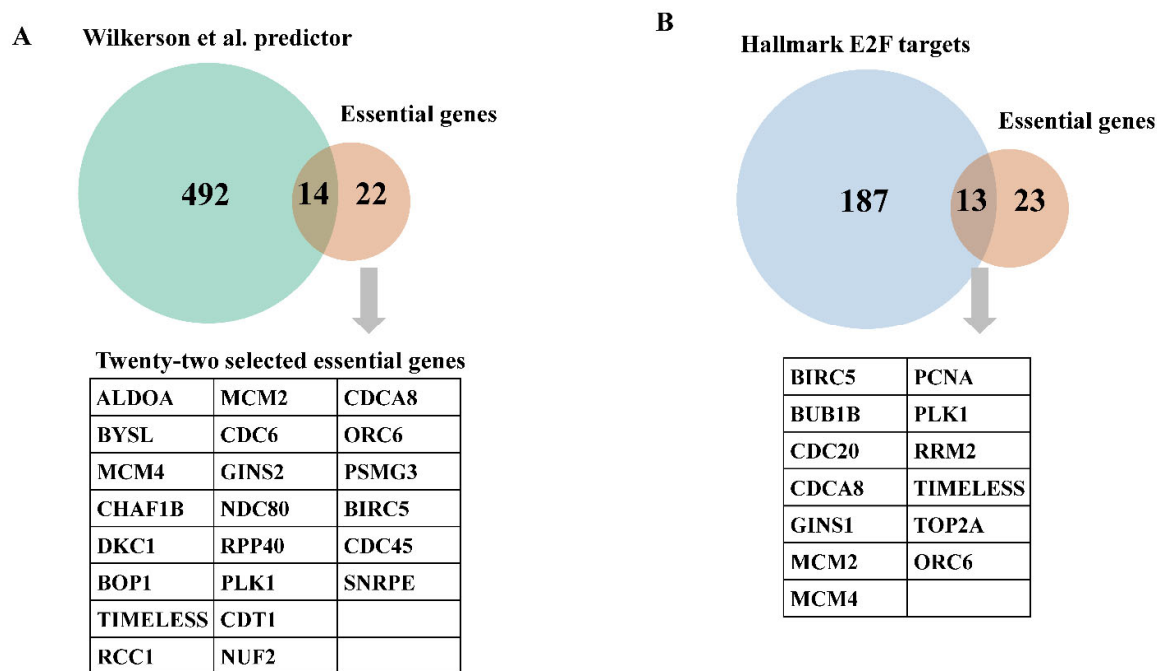
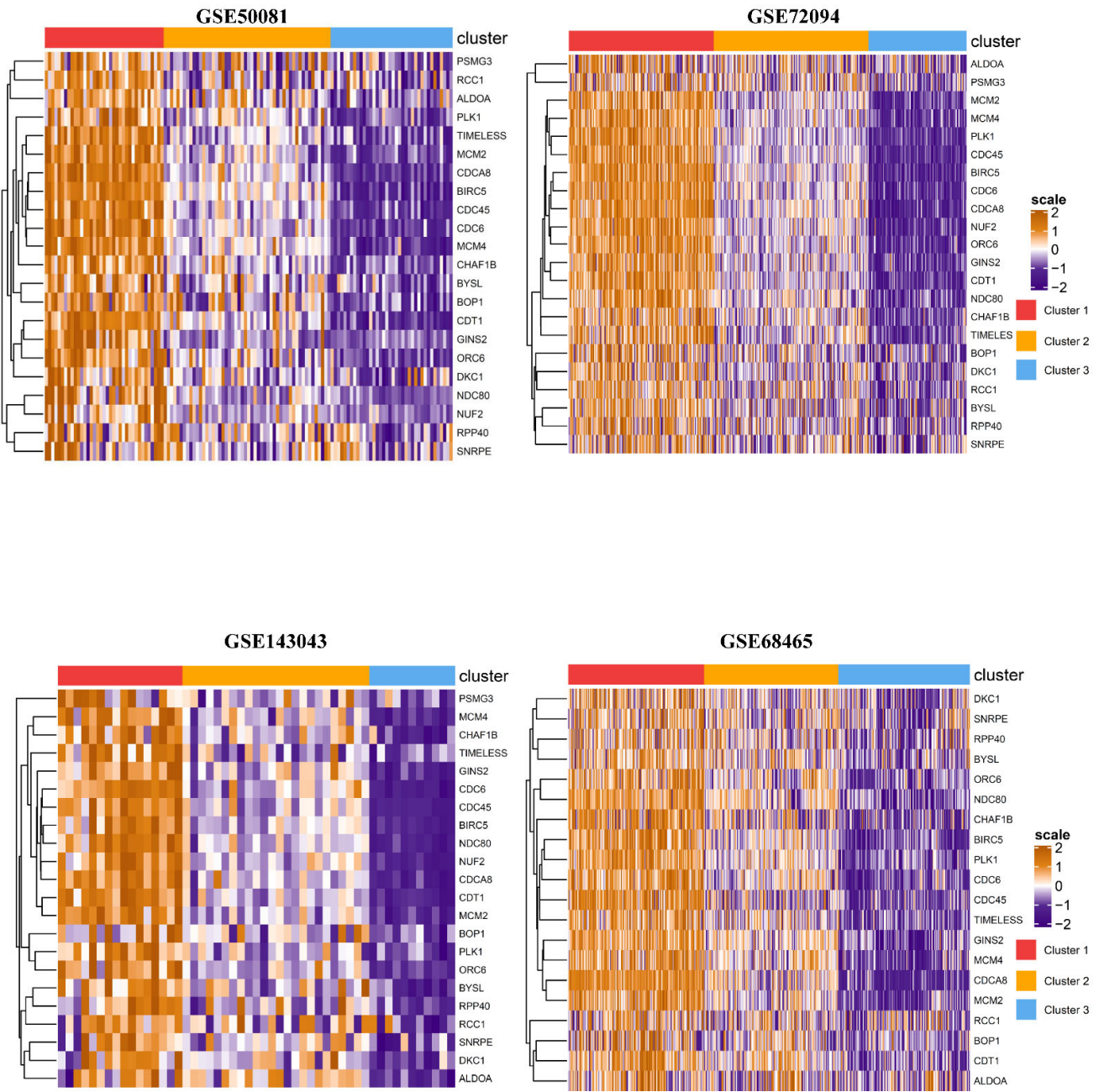


Figure S3. List of 22 selected essential genes and 13 E2F target genes. (A) selected essential genes (B) E2F target genes.



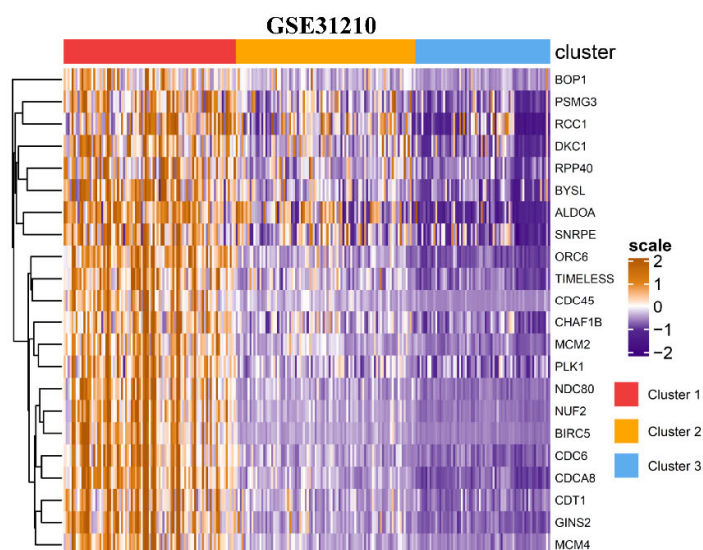
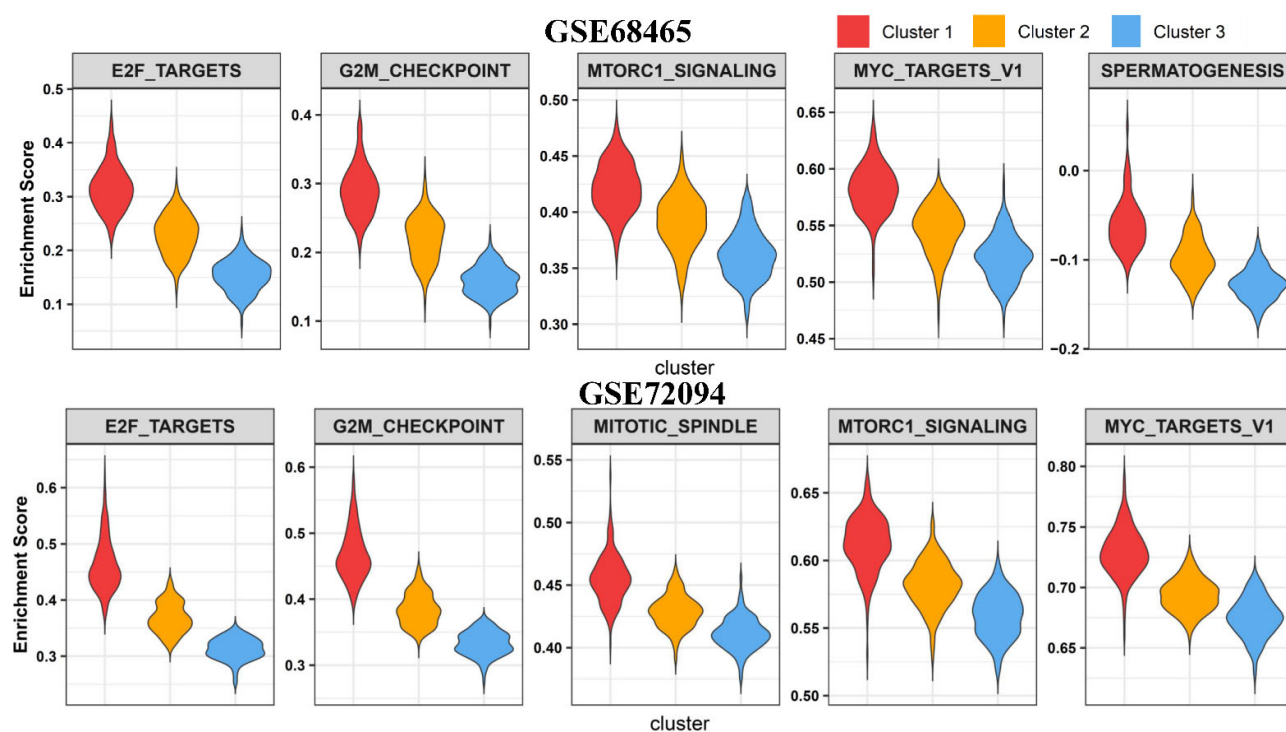


Figure S4. Validation of expression patterns in essential gene-classified clusters from GEO datasets. A heatmap demonstrates patterns of essential gene expressions in three clusters from the GSE140343, GSE68465, GSE72094, GSE50081, and GSE31210 datasets.



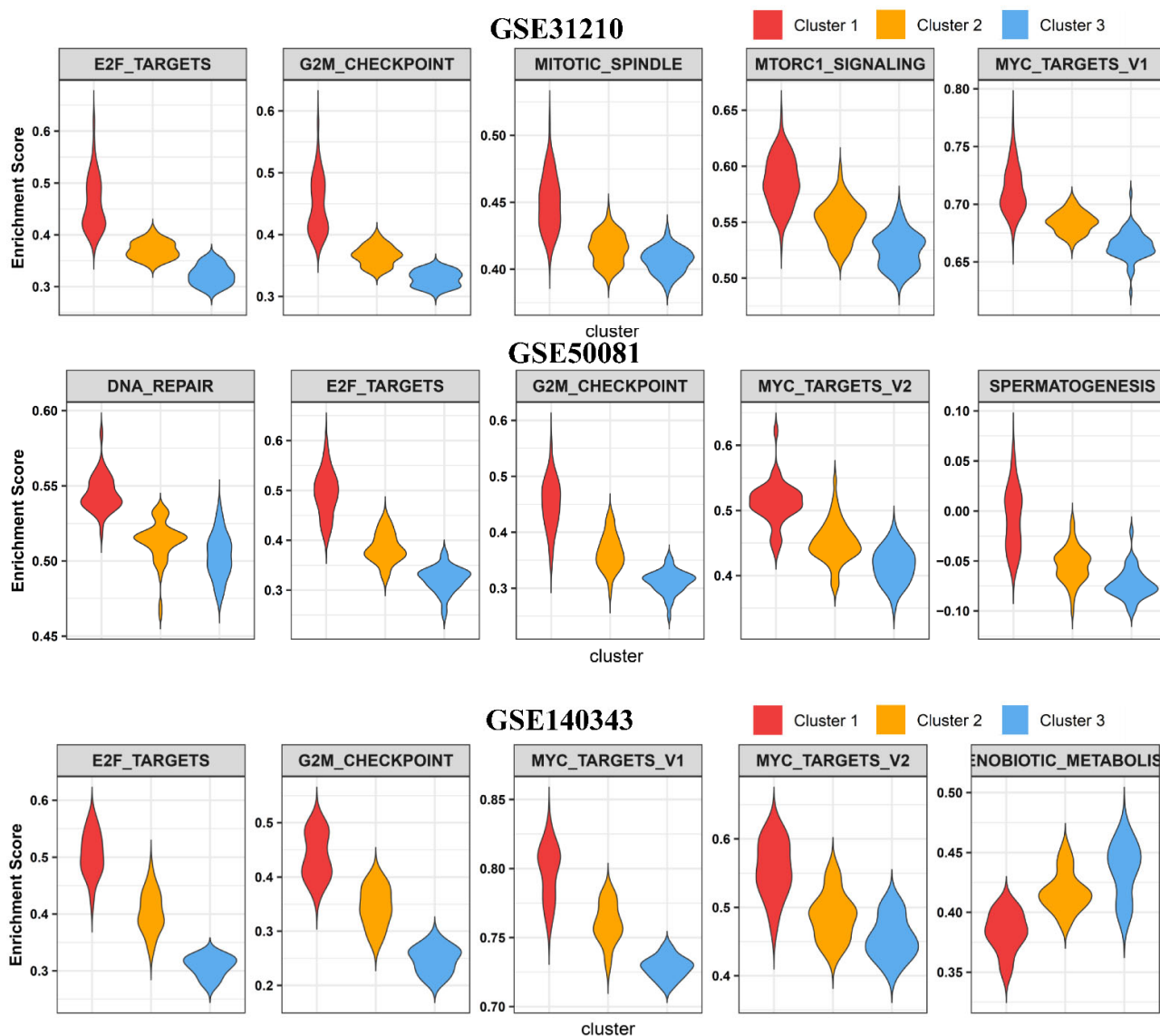
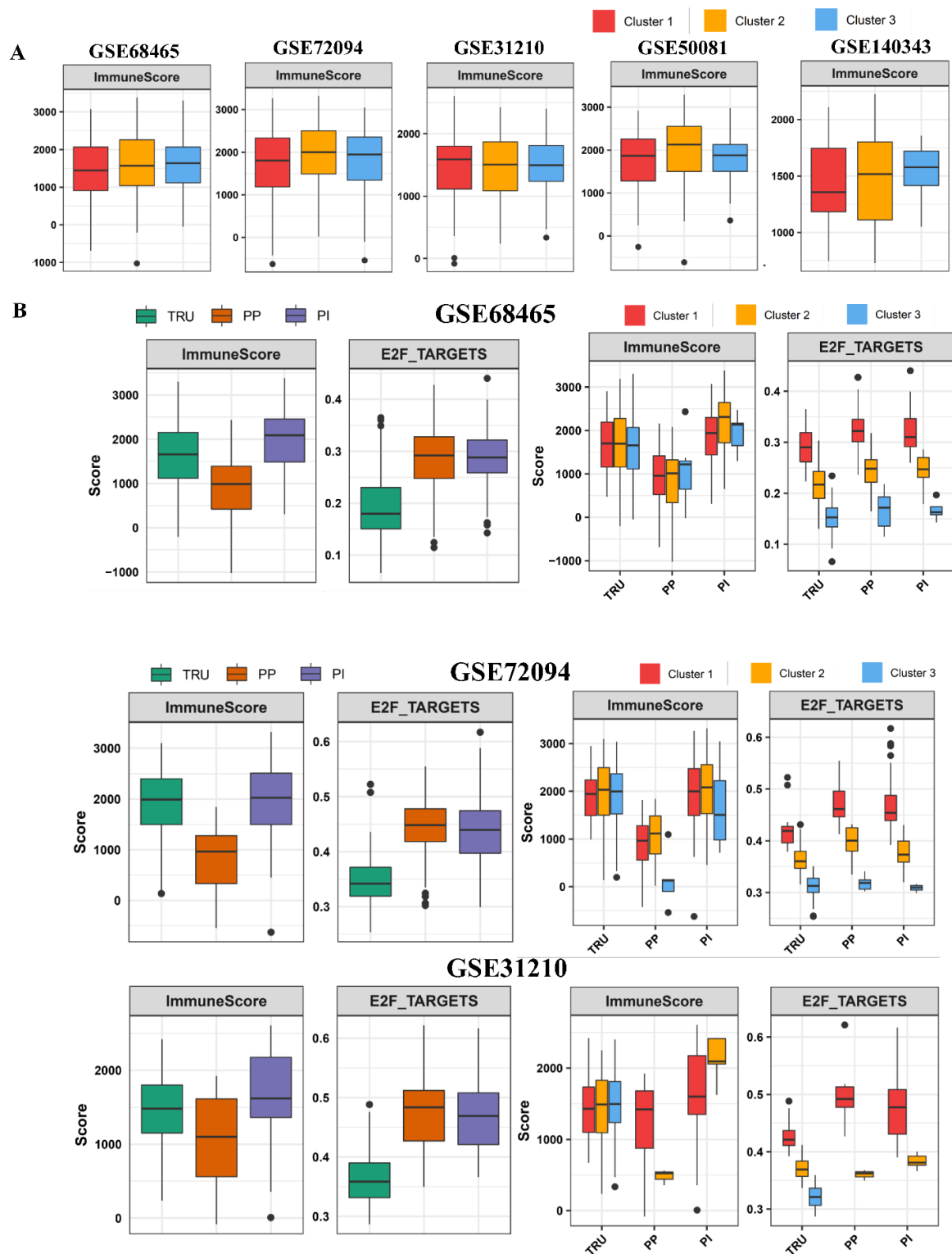


Figure S5. Validation of associated signaling in essential gene-classified clusters from GEO datasets. ssGSEA scores of top signaling pathways from the GSE140343, GSE68465, GSE72094, GSE50081, and GSE31210 datasets are shown as violin plots.



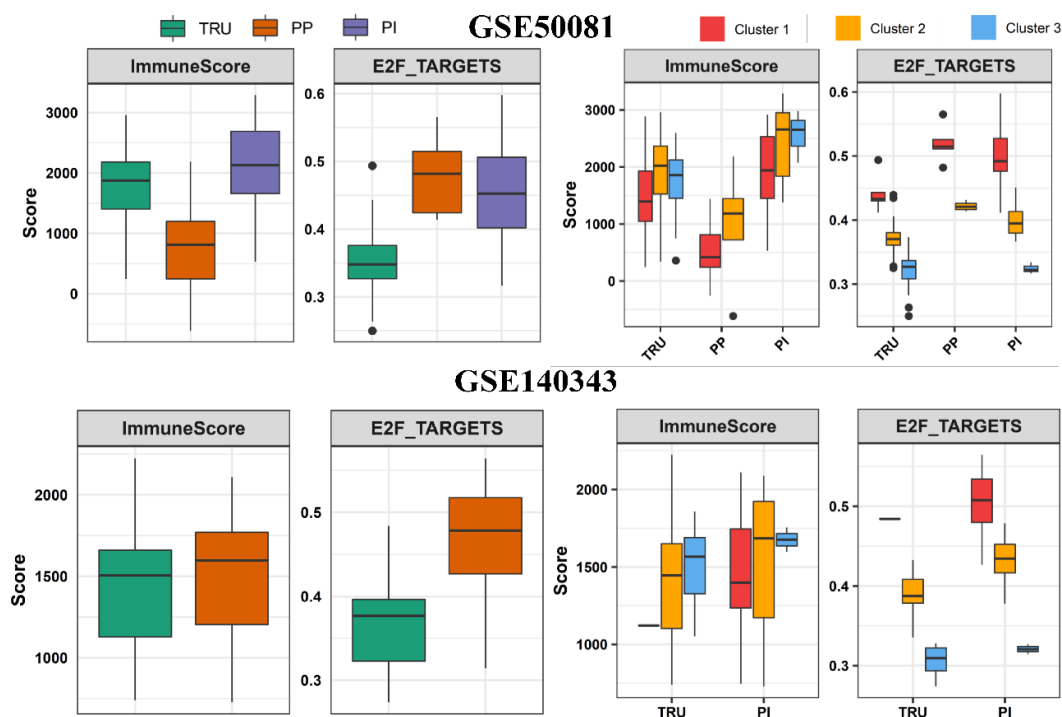


Figure S6. Immune infiltration and E2F signaling profiles of lung adenocarcinoma (LUAD) patients in GEO datasets. (A) ESTIMATE-derived immune infiltration levels from the GSE140343, GSE68465, GSE72094, GSE50081, and GSE31210 datasets were compared among essential gene-stratified clusters and are shown as boxplots. (B) ESTIMATE-derived immune infiltration levels and ssGSEA-inferred E2F target signaling from the GSE140343, GSE68465, GSE72094, GSE50081, and GSE31210 datasets were compared among previously reported expression subtypes with or without subdivision into essential gene-classified clusters.