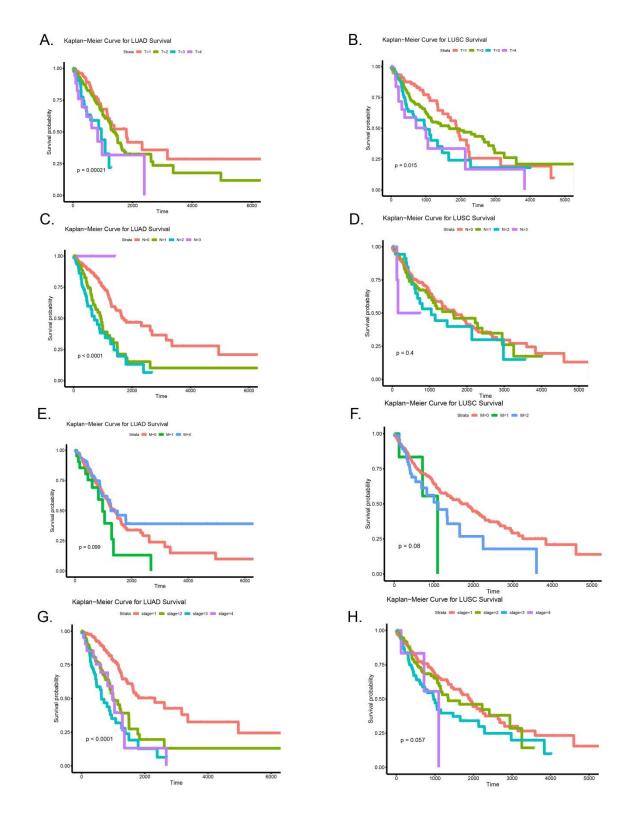
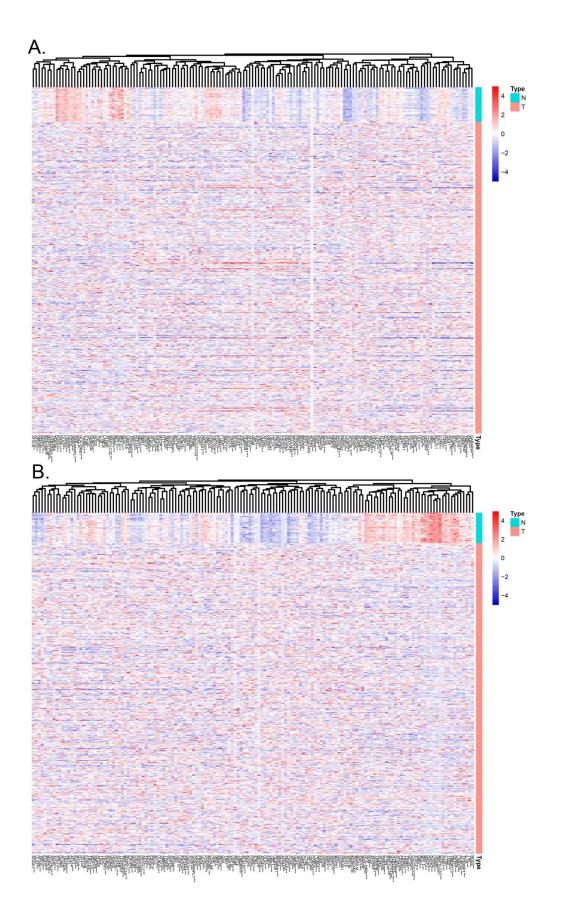
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Kaplan-Meier survival curves regarding the clinical features in TCGA lung cancer cohorts. Survival curves for LUAD (A, C, E, and G) and LUSC (B, D, F, and H) were exhibited on the left and right panels, respectively.



Supplementary Figure 2. mRNA expression profiles of 148 autophagy-associated genes in TCGA lung cancer cohorts. Gene expression profiles for LUAD (A) and LUSC (B) were exhibited in the up and low panels, respectively.



| MCL1 | 16% |
|--|--|
| EGFR | 17% |
| ATG12 | 0.9% |
| EPG5 | |
| TFEB | 5% |
| ATG16L2 | |
| HLA-DRB1 PIK3CA | 0% |
| TMEM173 | 9% • • • • • • • • • • • • • • • • • • • |
| TECPR1 | 4% |
| DAPK2 | 2.2% |
| BCL2L1 | 3% |
| DRAM1 | 1.7% |
| ULK3 | 1.3% |
| DMD | |
| RPTOR | 7% |
| ATG4A | 1.7% |
| UBC | 4% * * * |
| PRKAG2 | 4% |
| TP53INP2 RUBCNL | 2.2% |
| CTSD | 2.6% 0.4% |
| Genetic Alte | |
| Ochelie All | Amplification Deep Deletion No alterations |
| | |
| В. | |
| TRIM5 | |
| | 0.6% |
| DRAM2 | |
| DRAM2 | 1.3% |
| CTSD | 1.3% 1.5% |
| CTSD MAP1LC3C | 1.3% 1.5% 1.5% 1.5% 1.5% 1.5% 1.5% 1.5% 1.5 |
| CTSD MAP1LC3C ATG5 | 1.3% 1.5% 4% 1.7% |
| CTSD MAP1LC3C ATG5 VMA21 | 1.3% 1.5% 4% 1.7% 2.3% |
| CTSD MAP1LC3C ATG5 | 1.3% 1.5% 4% 1.7% 2.3% 7% |
| CTSD MAP1LC3C ATG5 VMA21 | 1.3% 1.5% 4% 1.7% 2.3% |
| CTSD MAP1LC3C ATG5 VMA21 EPG5 | 1.3% 1.5% 4% 1.7% 2.3% 7% |
| CTSD MAP1LC3C ATG5 VMA21 EPG5 LAMP2 | 1.3% 1.5% 4% 1.7% 2.3% 7% 1 1 0.9% |
| CTSD MAP1LC3C ATG5 VMA21 EPG5 LAMP2 DRAM1 | 1.3% 1.5% 4% 1.7% 2.3% 7% 1 0.9% |
| CTSD MAP1LC3C ATG5 VMA21 EPG5 LAMP2 DRAM1 PINK1 | 1.3% 1.5% 4% 1.7% 2.3% 7% 0.9% 0.9% 1.1% 1.1% 1.1% |

Supplementary Figure 3. Genetic alteration of genes included in the gene signatures (TCGA, PanCancer Atlas). (A) Genetic alteration of the 22 genes in the TCGA-LUAD cohort. (B) Genetic alteration of the 11 genes in the TCGA-LUSC cohort.