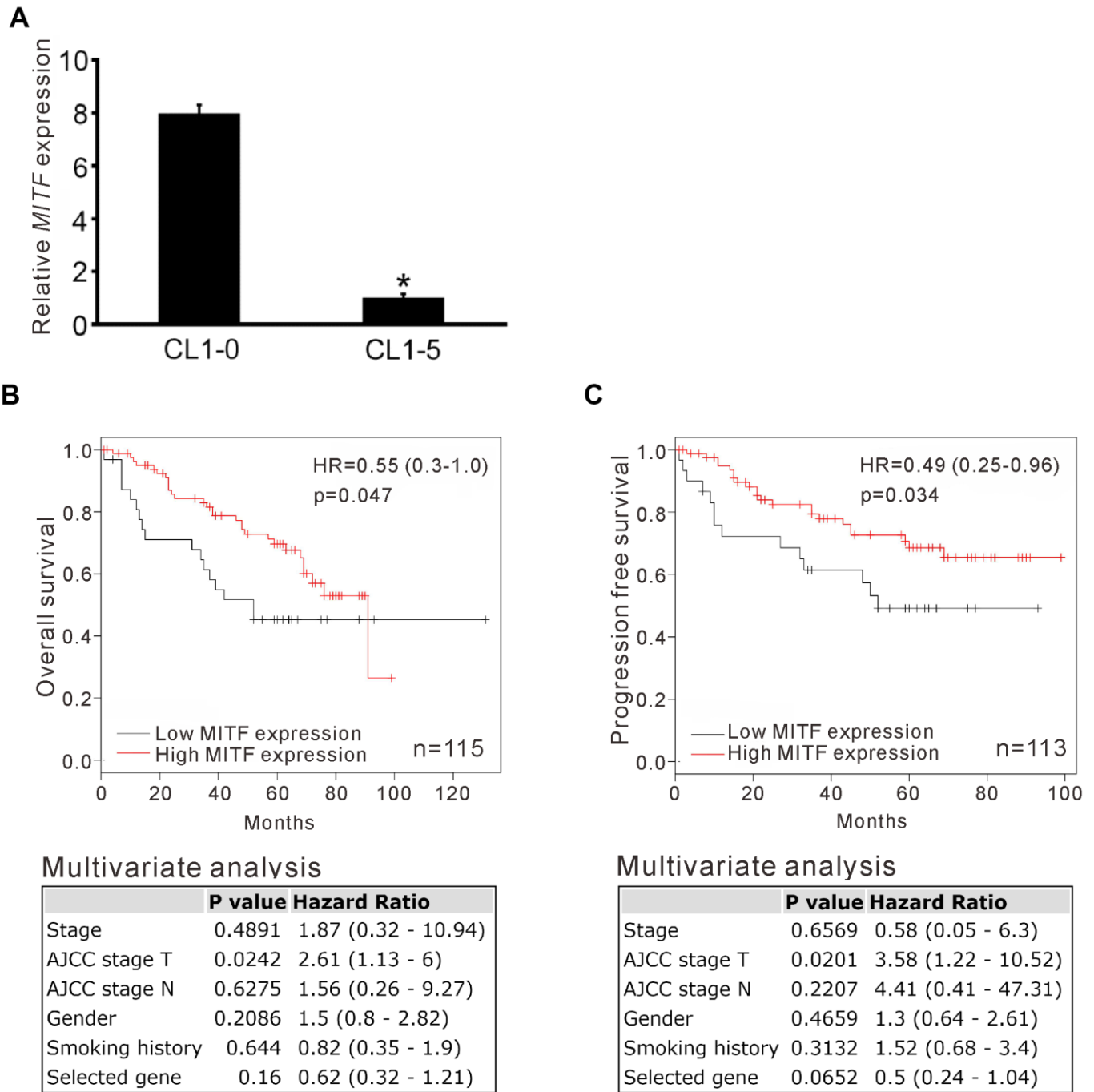
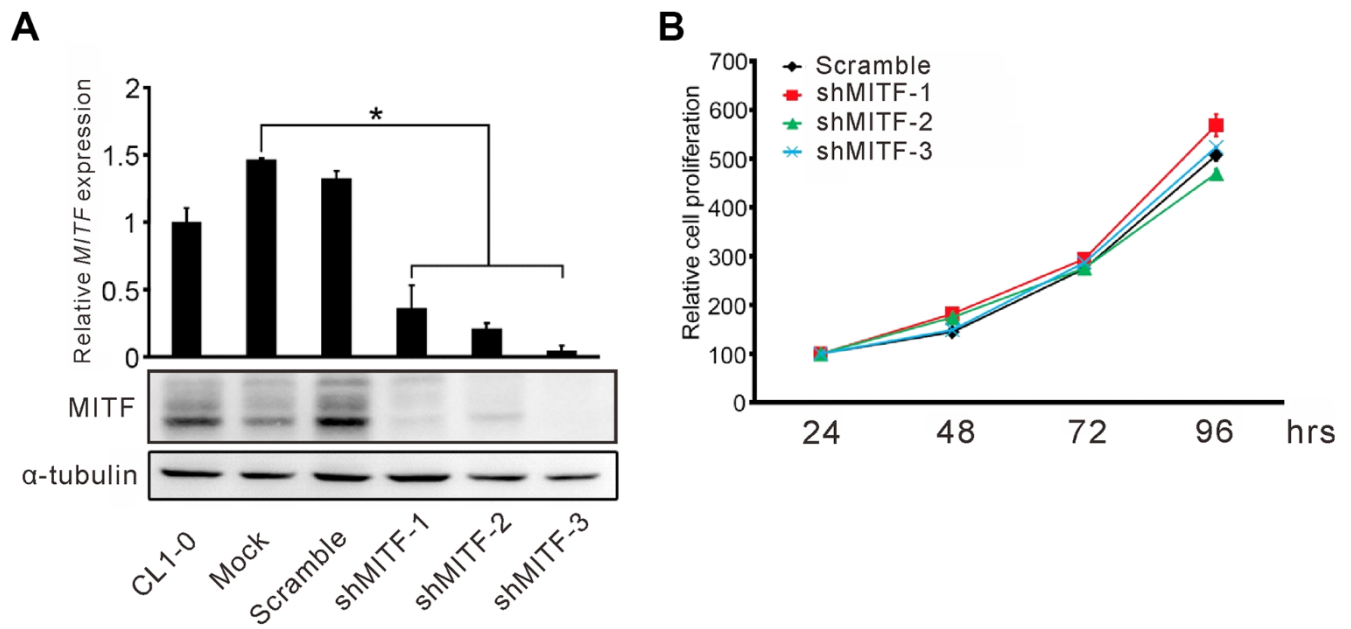


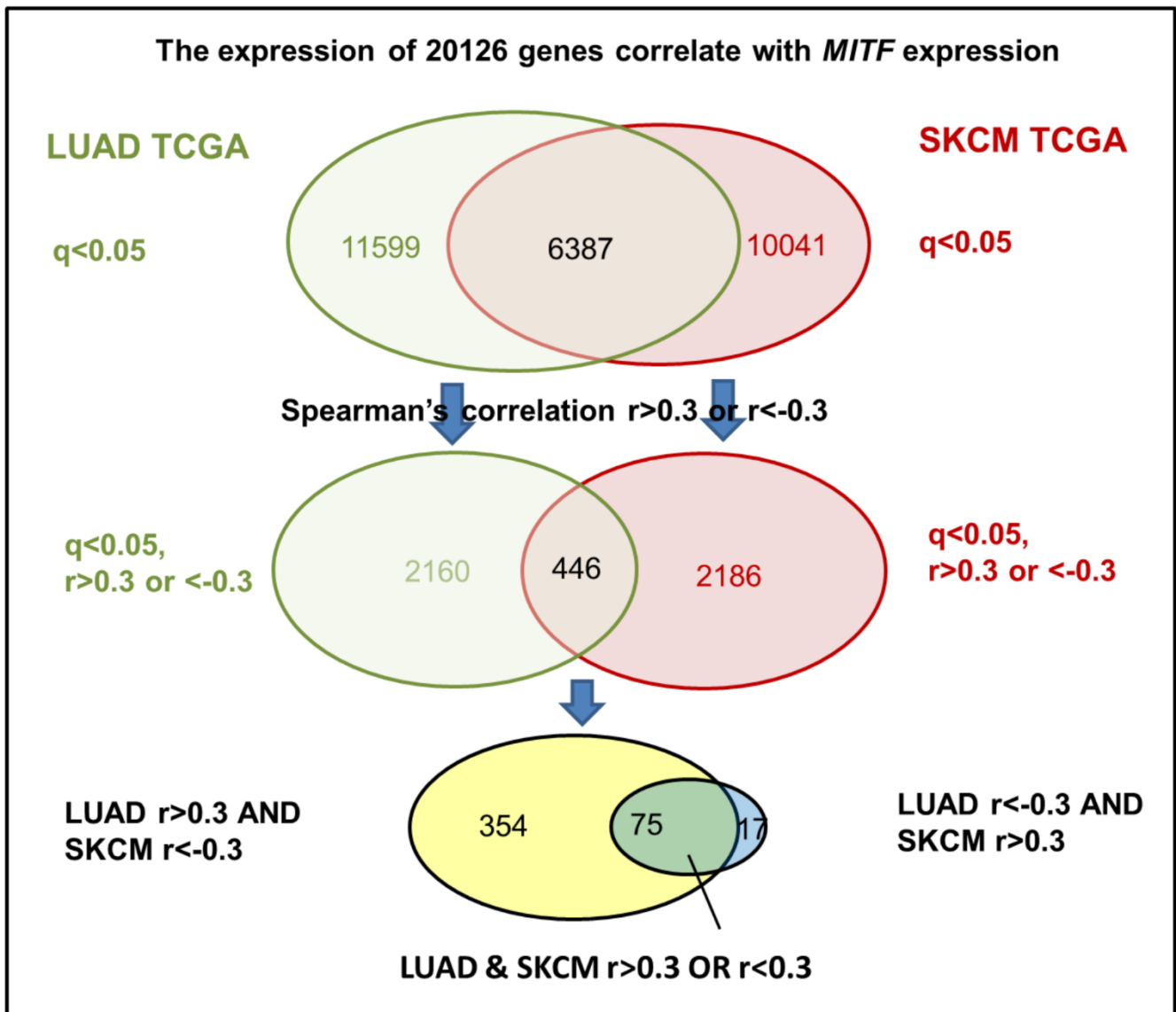
**SUPPLEMENTARY FIGURES**



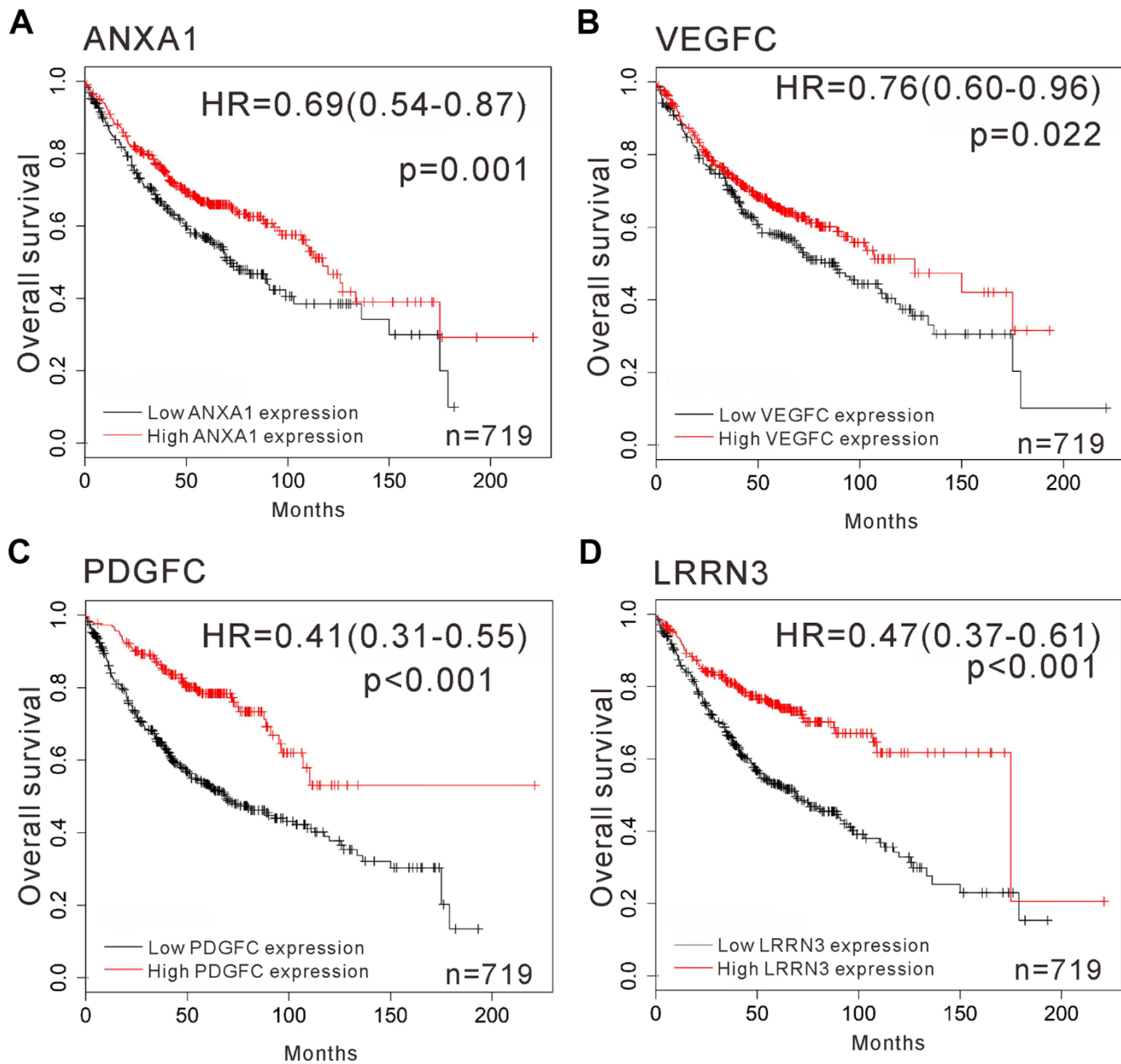
**Supplementary Figure 1. MITF expression in an invasive cell line model and associated with survival in lung adenocarcinoma.** (A) The relative MITF expression in low-invasive CL1-0 and high-invasive CL1-5 cells evaluated by expression microarray. (B, C) The survival curve of NSCLC was estimated with array probe of MITF (226066\_at) by Kaplan-Meier plotter (<https://kmplot.com/>). The Hazard Ratio (HR) and p-value in the upper plots were estimated by univariate analysis and log-rank test, respectively. Lower panel listed the HR and p-value estimated by multivariate Cox's regression analysis.



**Supplementary Figure 2. The stable MITF-knockdown clones were assayed the cell proliferation. (A)** Stable-expressed shMITF in CL1-0 cells were established in culture with puromycin. **(B)** The cell proliferation was analyzed by MTT assay at indicated time points.



**Supplementary Figure 3. The step-wise selection of Table 3.** The spearman's correlations of *MITF* expression with 20,126 genes were sorted by cBioportal from the LUAD and SKCM TCGA datasets. The correlations with  $q < 0.05$  and  $r > 0.3$  or  $r < -0.3$  were filtered and intersected by the two datasets. Only 75 genes had the same expression directions along with *MITF* expression in LUAD and SKCM datasets. In contrast, 371 genes showed inverse correlations. The final data was presented in Table 3.



**Supplementary Figure 4. The correlation of overall survival and *ANXA1*, *VEGFC*, *PDGFC* and *LRRN3* expressions in lung adenocarcinoma by Kaplan-Meier analysis.** The available microarray databases of lung adenocarcinoma analyzed by Kaplan-Meier plotter (<https://kmplot.com/>). The probe (A) *ANXA1* (201012\_at), (B) *VEGFC* (209946\_at), (C) *PDGFC* (218718\_at) and (D) *LRRN3* (209840\_s\_at). The p-value was estimated by log-rank test. Univariate Cox's regression generated the hazard ratio.