**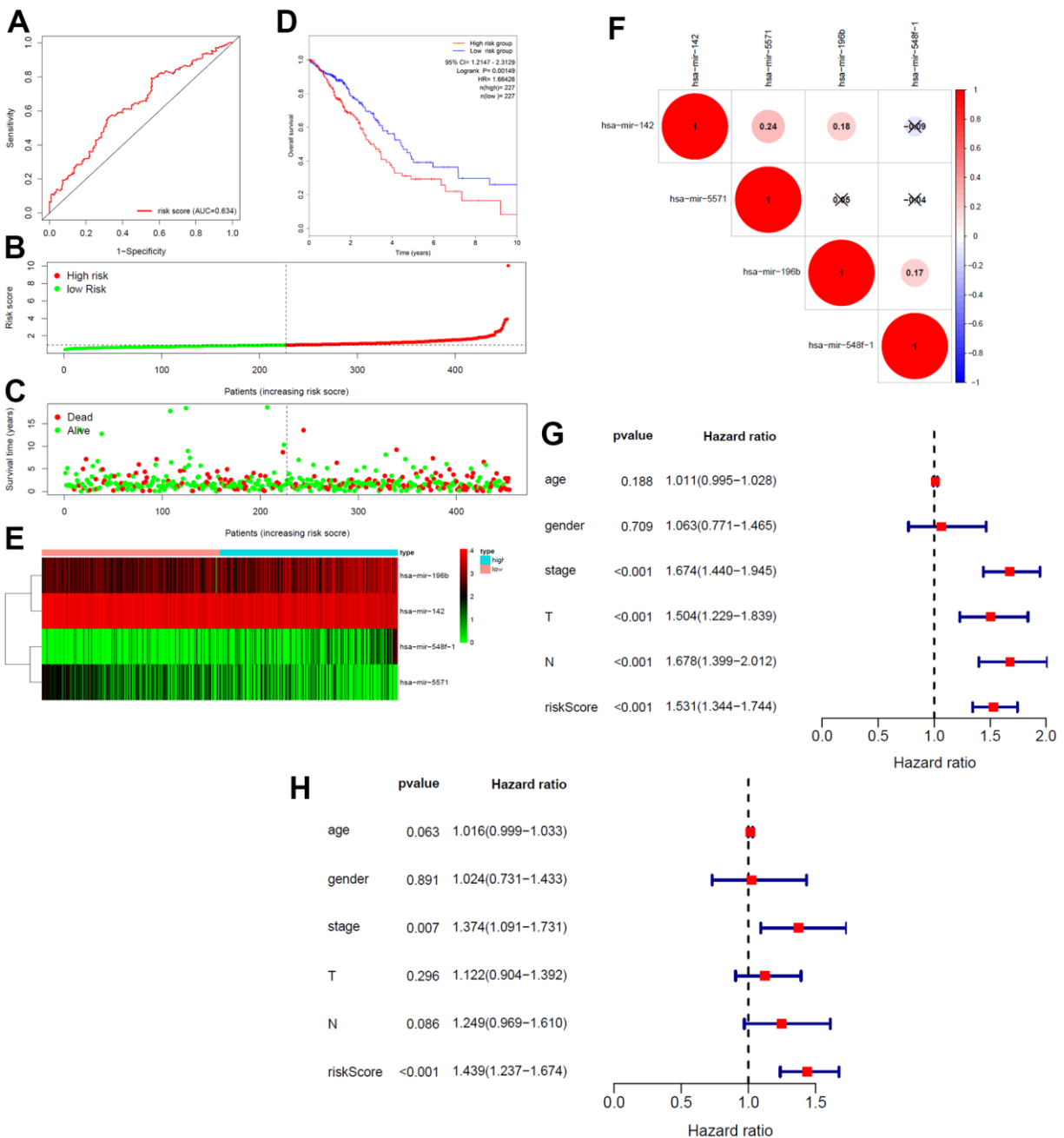Supplementary Figure 1. Prognostic signature analysis of key DEmiRNAs.** (**A**) ROC curve. The 3-year AUC of the 4-miRNA signature (mir-196b, mir-142, mir-548f-1, mir-5571) was 0.634 in the ROC curve. (**B**) Risk score distribution. According to the median risk score, the patients were divided into the high- and low-risk groups. (**C**) Survival overview. The distribution of survival times of LUAD patients in the high- and low-risk subgroups. (**D**) Survival curve. LUAD patients had a higher HR and a lower OS in the high-risk group (*p*=0.00149, HR=1.6643, 95%CI=1.2147-2.3129). (**E**) The expression heatmap of four miRNAs. Two miRNAs (mir-196b and mir-548f-1) were highly expressed and 2 miRNAs (mir-142 and mir-5571) were lowly expressed in the high-risk group. (**F**) The expression correlations among 4 miRNAs. The correlations among 4 miRNAs were low in expression. (**G**, **H**) Independently prognostic analysis. The 4-miRNA risk signature was significantly correlated with the survival of LUAD patients by a univariate (*p*<0.001, HR=1.531, 95%CI=1.344-1.744) and a multivariate (*p*<0.001, HR=1.439, 95%CI=1.237-1.674) Cox regression analyses. ROC, receiver operating characteristic; AUC, area under the curve; LUAD, lung adenocarcinoma; HR, hazard ratio; OS, overall survival; CI, confidence interval.
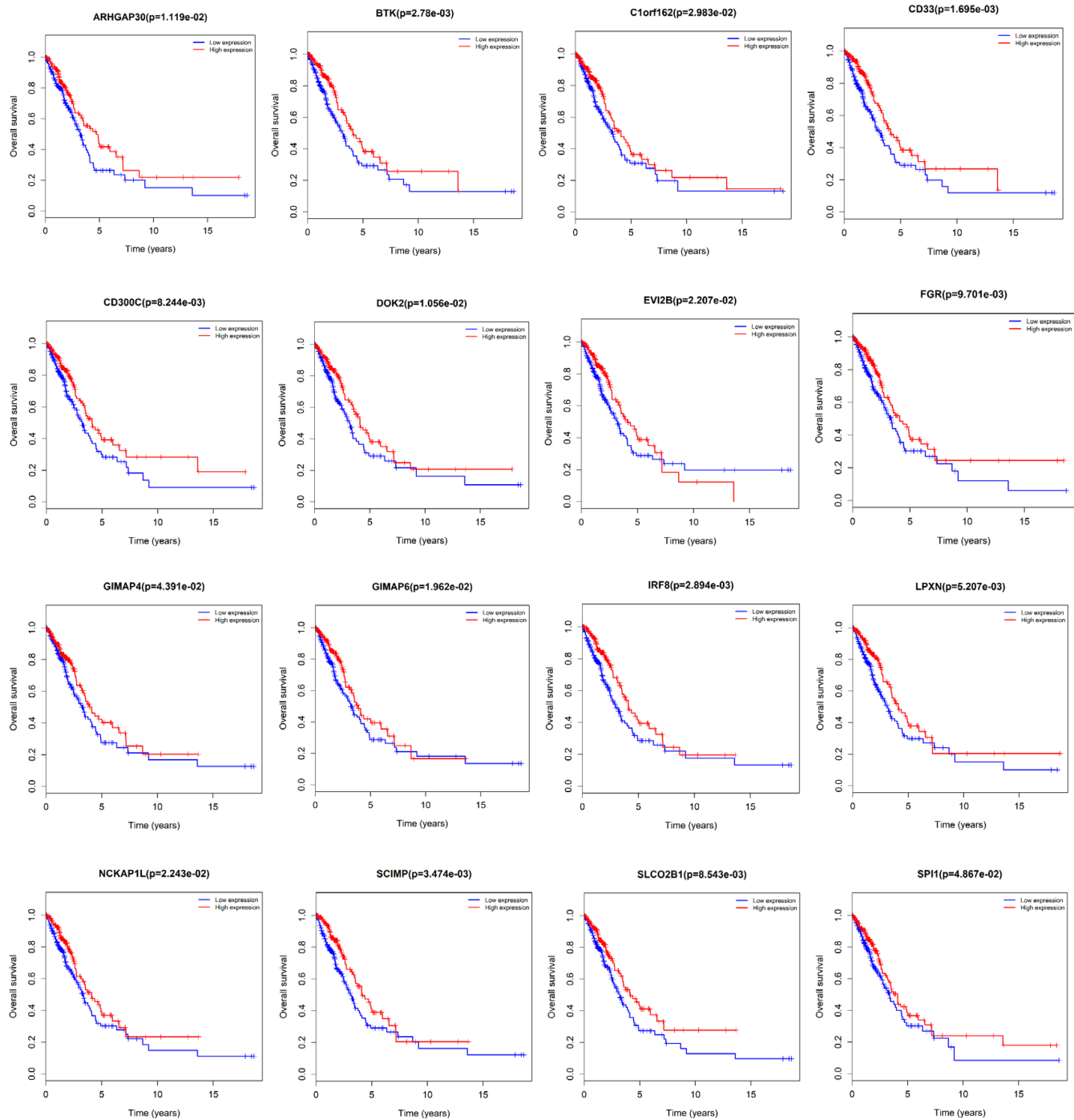
# DElncRNAs associated with the OS of LUAD patients
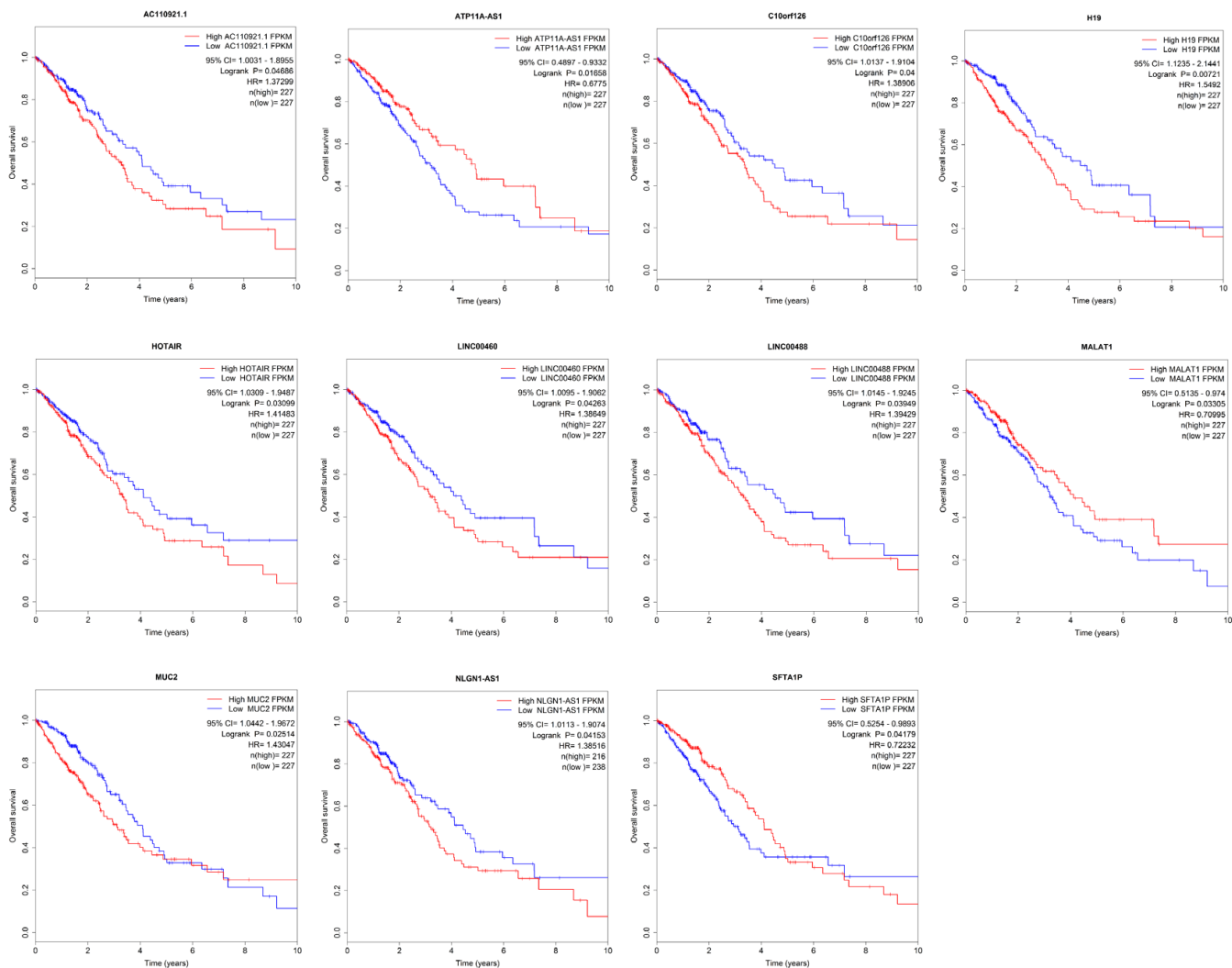


# DEmRNAs associated with the OS of LUAD patients
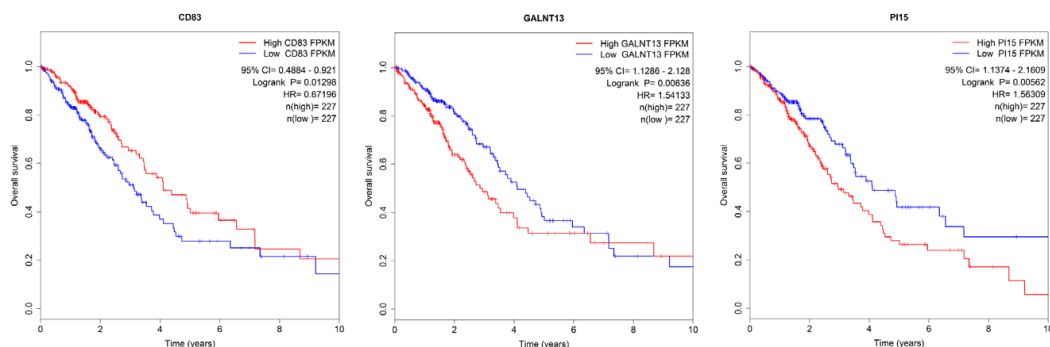


**Supplementary Figure 2. Survival curves of DERNAs in the ceRNA network.**

**Supplementary Figure 3. Survival curves of 16 genes.**