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Corrigendum: Comprehensive landscape of junctional genes and their association with overall survival of patients with lung adenocarcinoma

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In the published article, there is an error in Figure 4D as published. Kaplan-Meier survival curves based on the JGRS in GSE72094 is incorrectly inserted. After checking the original data, we realized that the error was due to repeated insertion of Kaplan-Meier survival curves of GSE37745 during the figure assembly. In addition, for GSE31210, the red (high JGRS) and blue (low JGRS) lines are labeled oppositely. The corrected Figure 4 appears below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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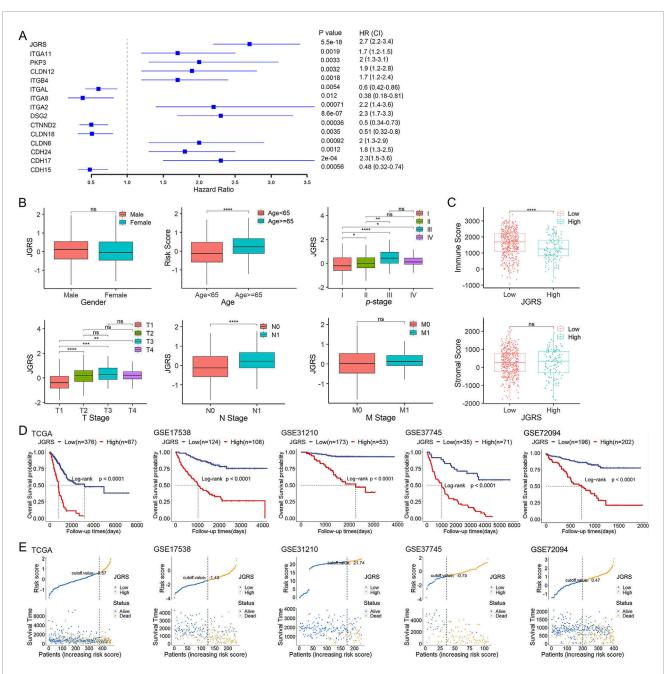


FIGURE 4

The JGRS can distinguish different clinicopathological features of LUAD. (A) A forest plot of the univariate Cox regression analysis of JGRS and 14 genes that were chosen for establishing a prognosis signature. (B) Different analyses of JGRS distribution based on sex, age, p-stage, as well as T, N, and M stages in TCGA cohort. (C) Distribution of immune and stromal scores between low- and high-JGRS groups in TCGA cohort. (D) Kaplan-Meier survival curves based on the JGRS in TCGA and four GEO cohorts. (E) JGRS distribution in TCGA and four GEO cohorts.