Dear Editor,

We would like to submit a manuscript titled “*Development of a novel prognostic score combining clinicopathologic variables, gene expression and mutation profiles for lung adenocarcinoma*”. The study was motivated by the clinical need of improving prognostic prediction for lung adenocarcinoma. We found that the model integrating conventional clinicopathologic variables, gene expression and mutation profiles achieved the most reliable predictions of event-free survival (EFS). The resultant risk score outperformed clinicopathologic ones by providing a higher-resolution risk stratification within pathologically-defined subgroups, and accounting for extra EFS-related variations. When being validated for recurrence-free survival (RFS) prediction under a bias-correcting competing risks modeling framework, the score showed a significantly higher time-dependent AUC as compared to that of the conventional clinicopathologic variables-based model (0.772 vs. 0.646, p-value< 0.001). We also found that the higher-risk patients identified by the score were characterized with transcriptional aberrations of multiple immune-related genes, and a significant depletion of innate immune cells.

This study developed a new risk score with improved prediction accuracy, which was an significant predictor of both EFS and RFS. We think the results from this study will be helpful to researchers as they consider how to improve prognosis and precision therapies for lung adenocarcinoma patients.

We all authors declare that the study is an original research, which has not been published elsewhere. We would greatly appreciate your kind consideration on reviewing this manuscript.

Sincerely,

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