

Figure S1 Comparison of the new biomarker using the average/weighted expression of the custom gene set with existing biomarkers. The biomarker correlation of the 9 DEGs and the predictive efficacy area under the curve in different immunotherapy cohort studies, assessed by comparing the 9 DEGs with standardized biomarkers.



**Figure S2** Patient risk scores and patient survival time in the two risk groups (top) and heat maps of 9 genes expression levels in the risk models of the two risk groups (bottom) in the all (A), test (B), and train (C) sets.



Figure S3 Nomogram to predict 1-, 3-, and 5-year survival probability by integrating the risk score model and clinicopathologic risk factors.



Figure S4 LUAD patient radiomics heatmap of 12 radiomics features (Y axis) across 103 samples (Y axis). It shows the contribution of 12 radiomics features in 103 samples, respectively.



**Figure S5** A heatmap depicting the correlation among 12 selected radiomics features, 9 selected DEGs, and clinical features, which supports the immunotherapy prediction efficacy of the radiomics features.