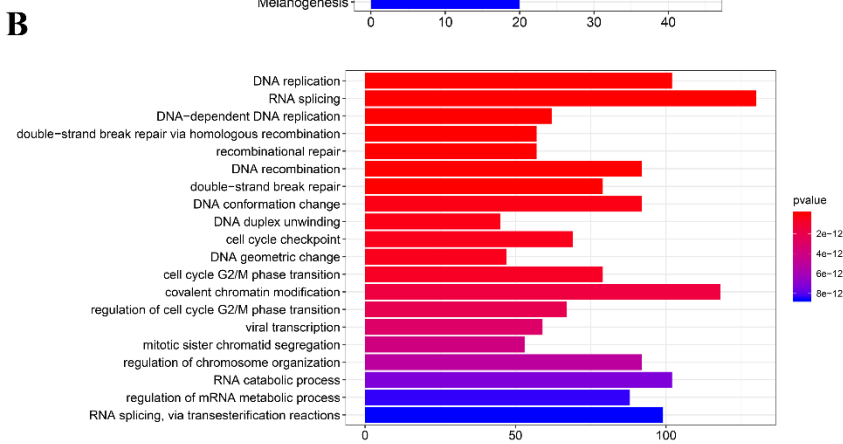
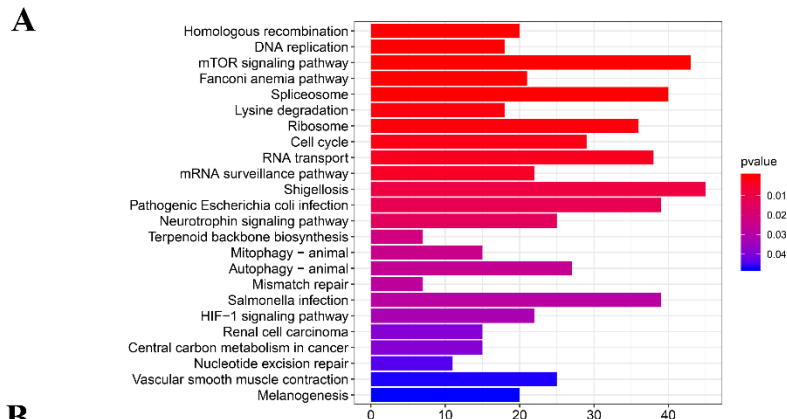
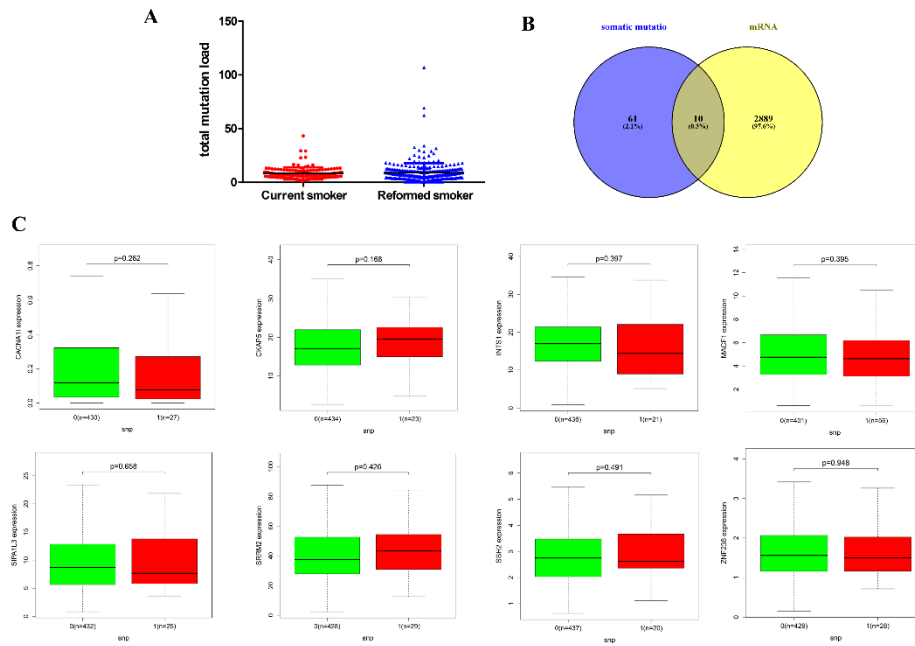


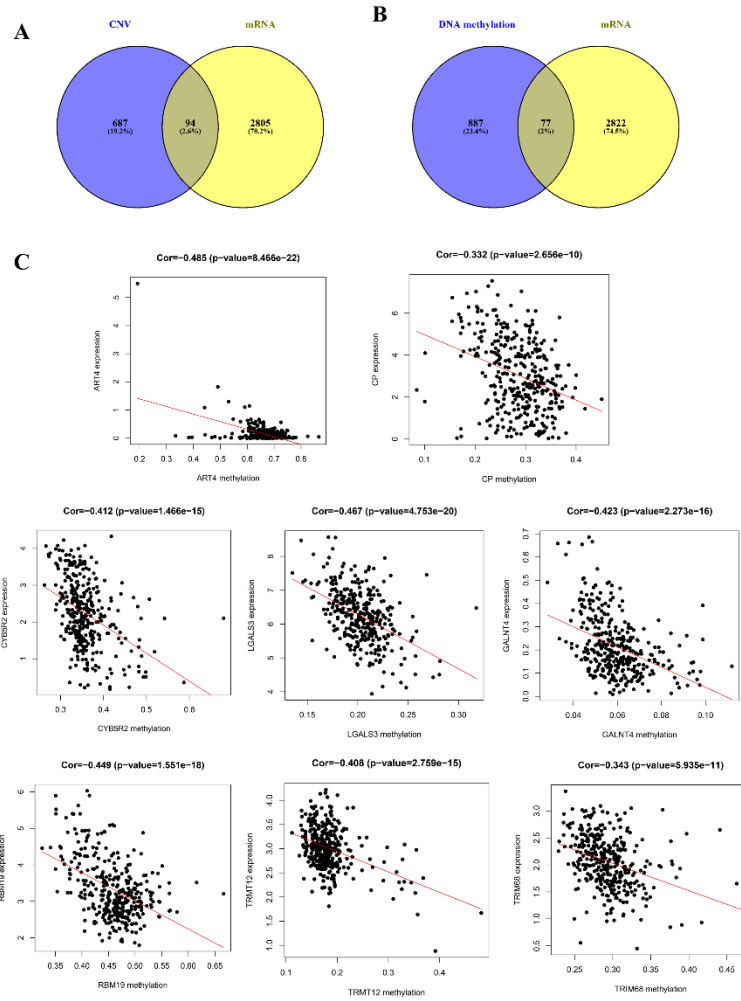
Supplementary Figure 1: the GO and KEGG analysis of DEGs. A: GO analysis. B: KEGG analysis



Supplementary Figure 2: Differences in somatic mutations related to smoking status. A: total mutation load between reformed smokers and current smokers. **B:** mutations frequency of ten DEGs was significantly different between reformed smokers and current smokers. **C:** the association between somatic mutations and expression of ten DEGs.

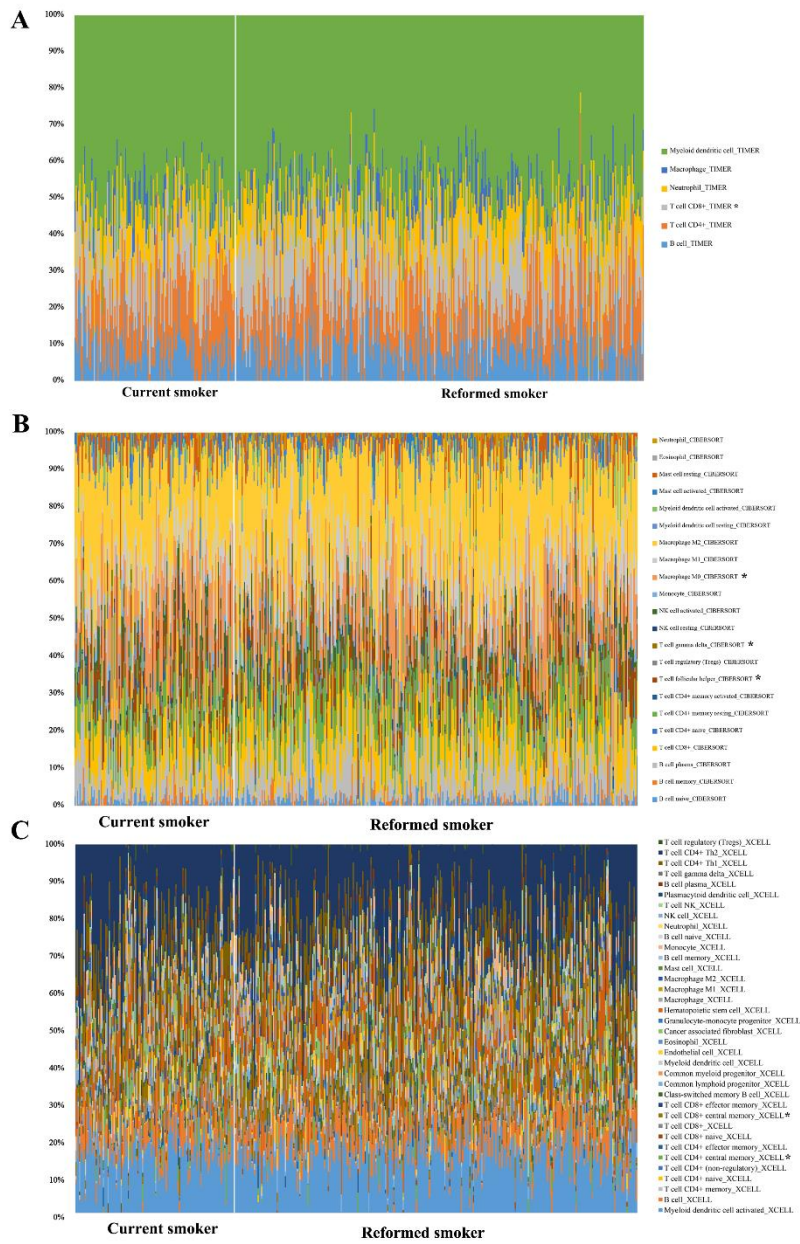


Supplementary Figure 3: Differences in DNA methylation related to smoking status. A: 94 DEGs with different CNV between reformed smokers and current smokers. B: 77 DEGs with different DNA methylation. C: expression of ten DEGs were significantly associated with methylation level.

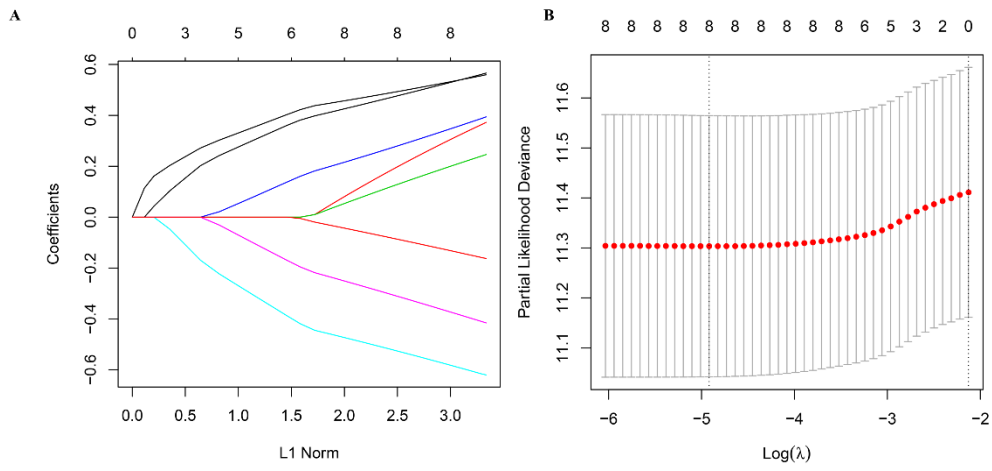


Supplementary Figure 4: Understanding the immune microenvironment using three algorithms.

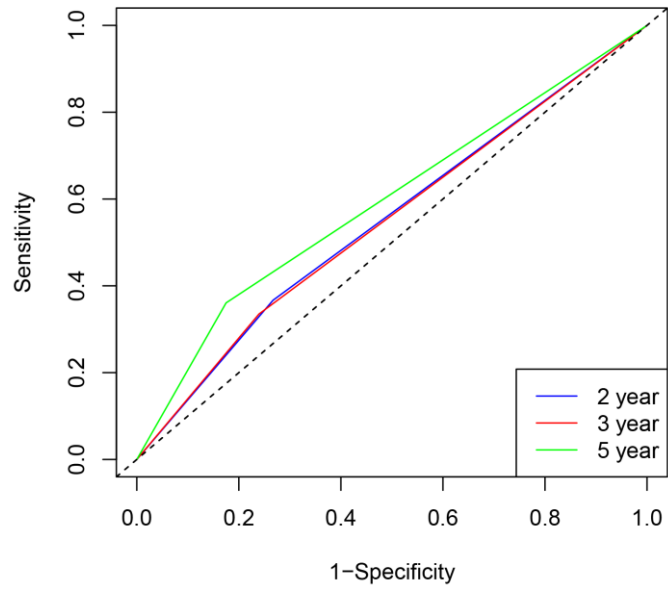
A: TIMER. B: CIBERSORT. C: XCELL.



Supplementary Figure 5: Smoking signature built using the LASSO model. A: LASSO coefficient profiles of different factors. B: Tenfold cross-validation for tuning parameter selection in the LASSO model.



Supplementary Figure 6: Survival receiver–operating characteristic (ROC) curves of smoking status for 2,3, 5-year prediction.



Supplementary Figure 7: Clinical application of nomograms with smoking signature in smoking-related cancers. A: BLAC. B: CESC. C: ESCA. D: HNSC. E: LUAD. F: PAAD.

