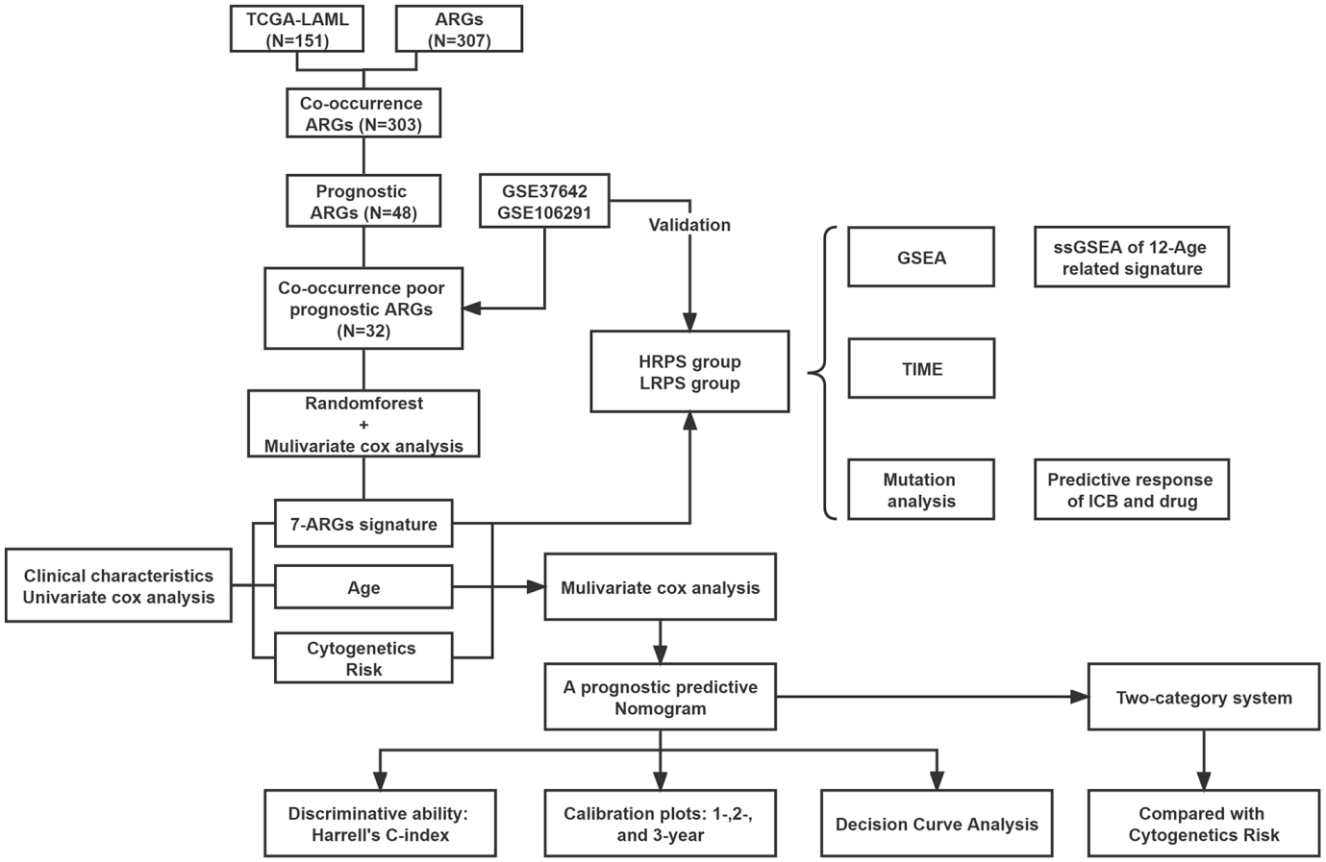
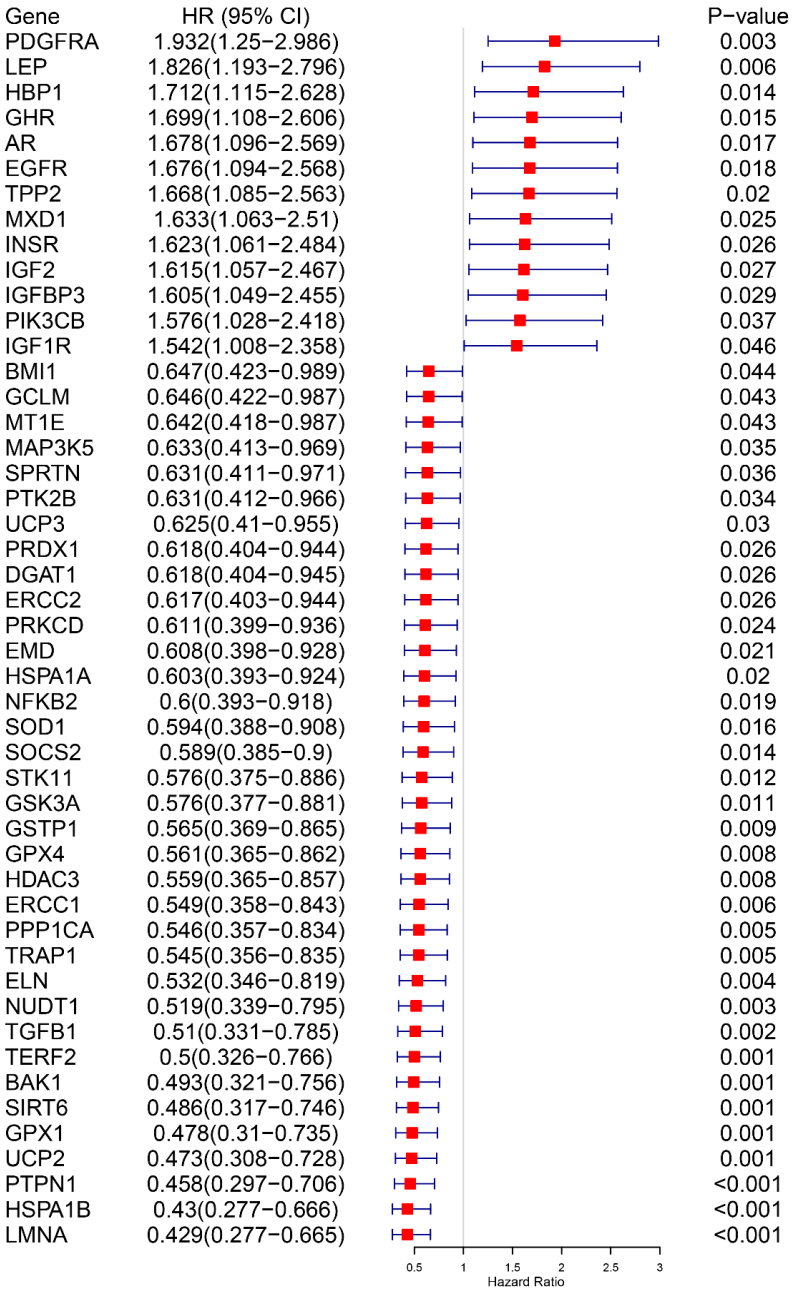
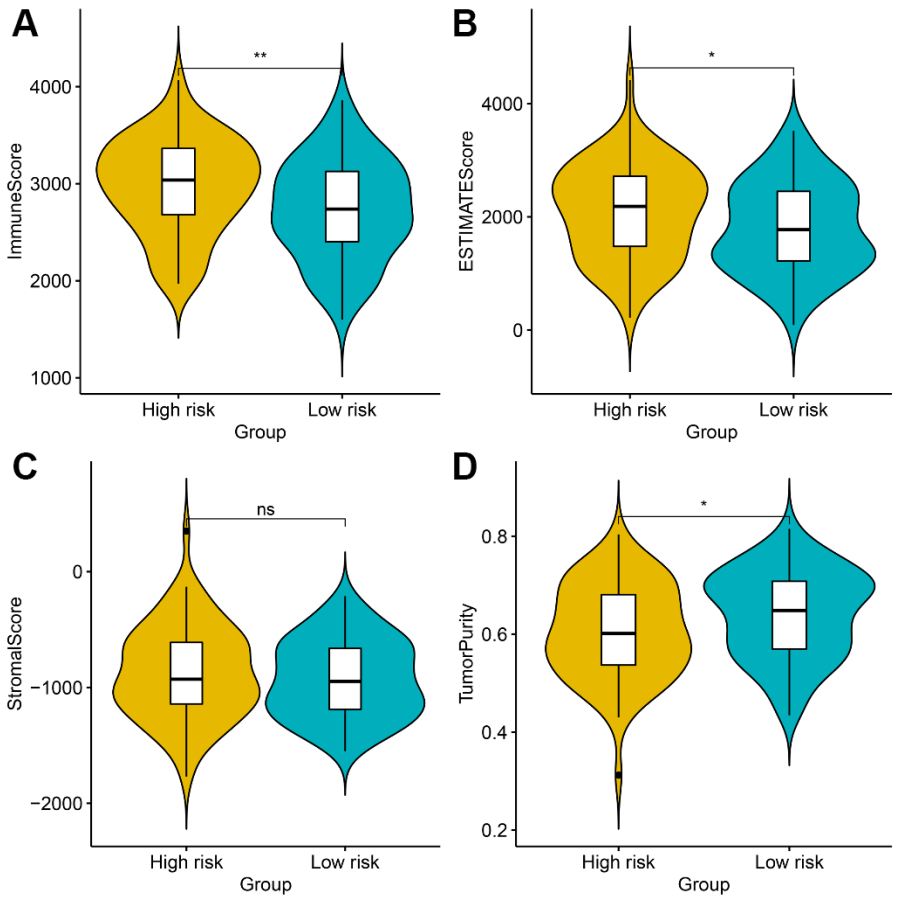
SUPPLEMENTARY FIGURES



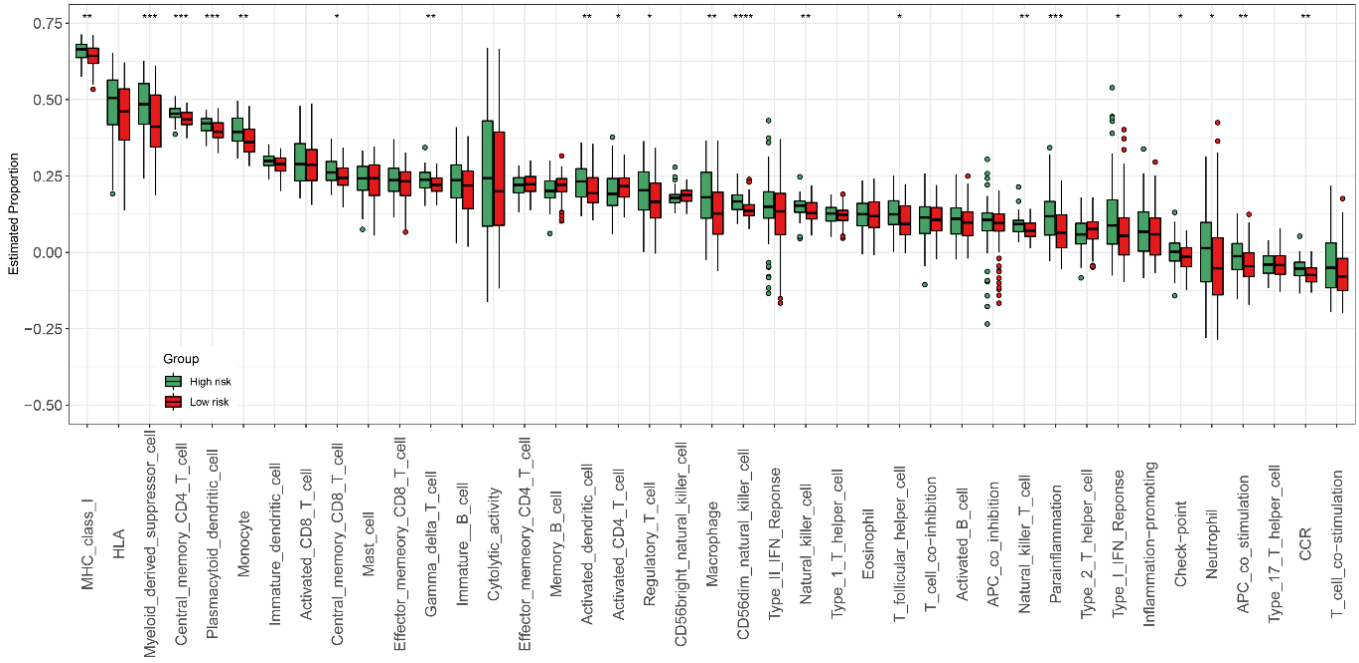
Supplementary Figure 1. Work flow of the current study. ARGs indicated aging-related genes. TIME indicated immune microenvironment of tumor.



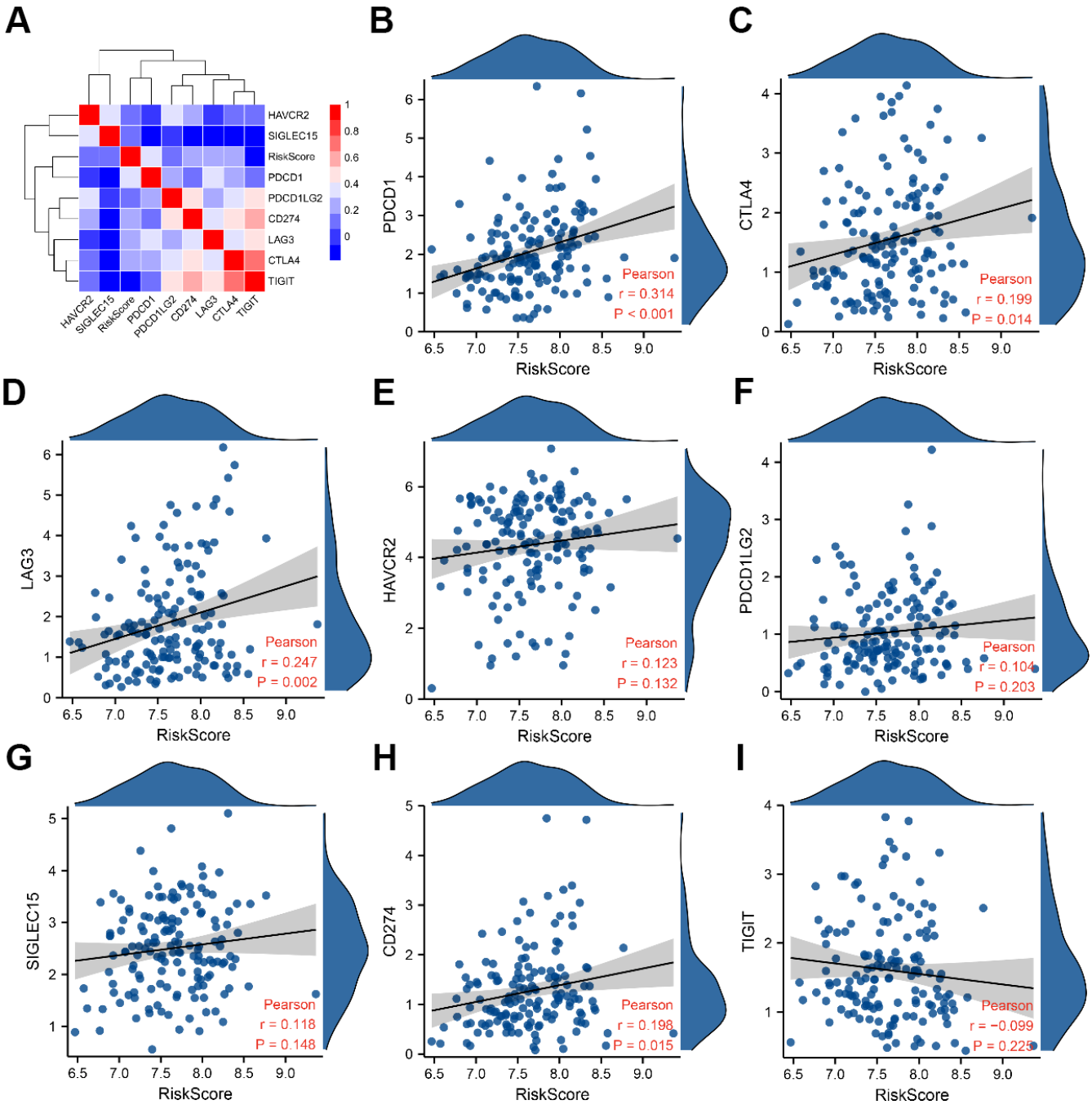
Supplementary Figure 2. Prognostic analyses of 84 ARGs in training cohort. Median expression values of genes were used as the threshold values, and patients with high value than which were set as a reference group.



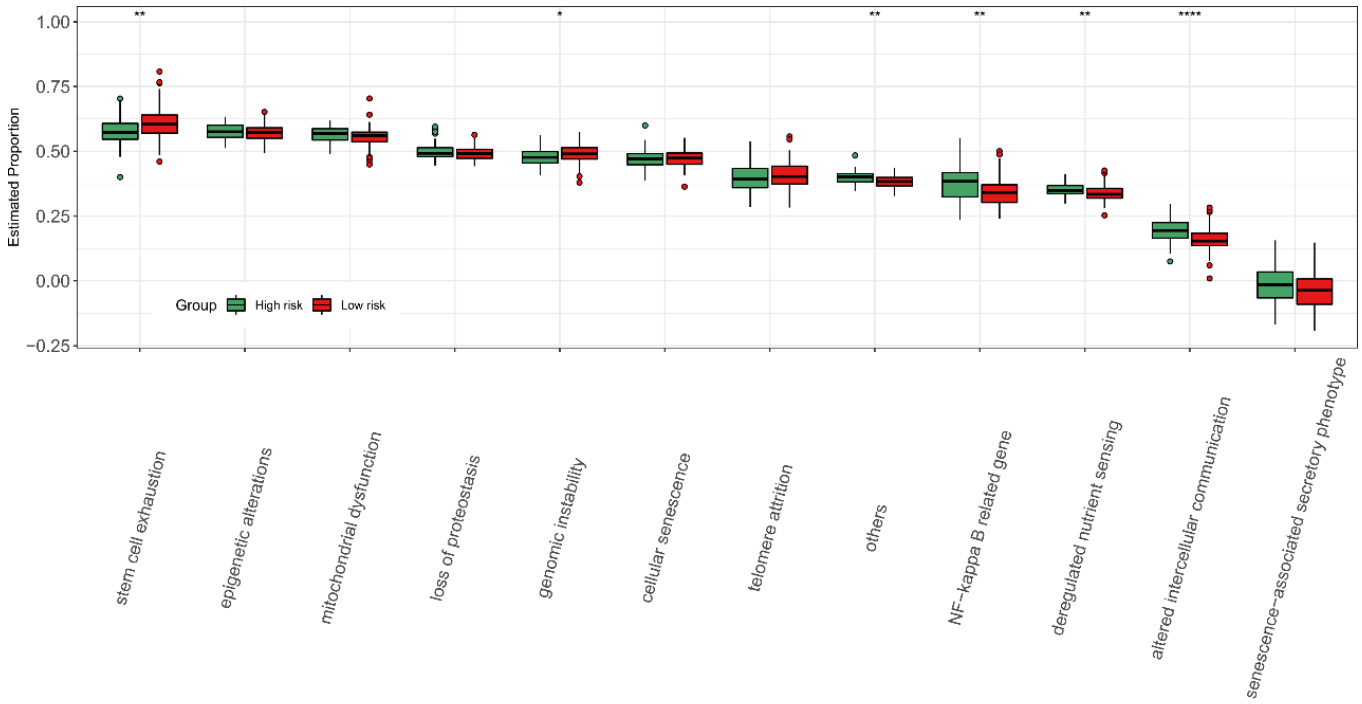
Supplementary Figure 3. Characteristics of immune-related microenvironment in HRPS-group/high-risk group and LRPS-group/low-risk group. (**A**) Immune Scores. (**B**) ESTIMATE Scores. (**C**) Stromal scores. (**D**) Tumor Purity. (*P < 0.05, **P <0.01, ***P < 0.001).



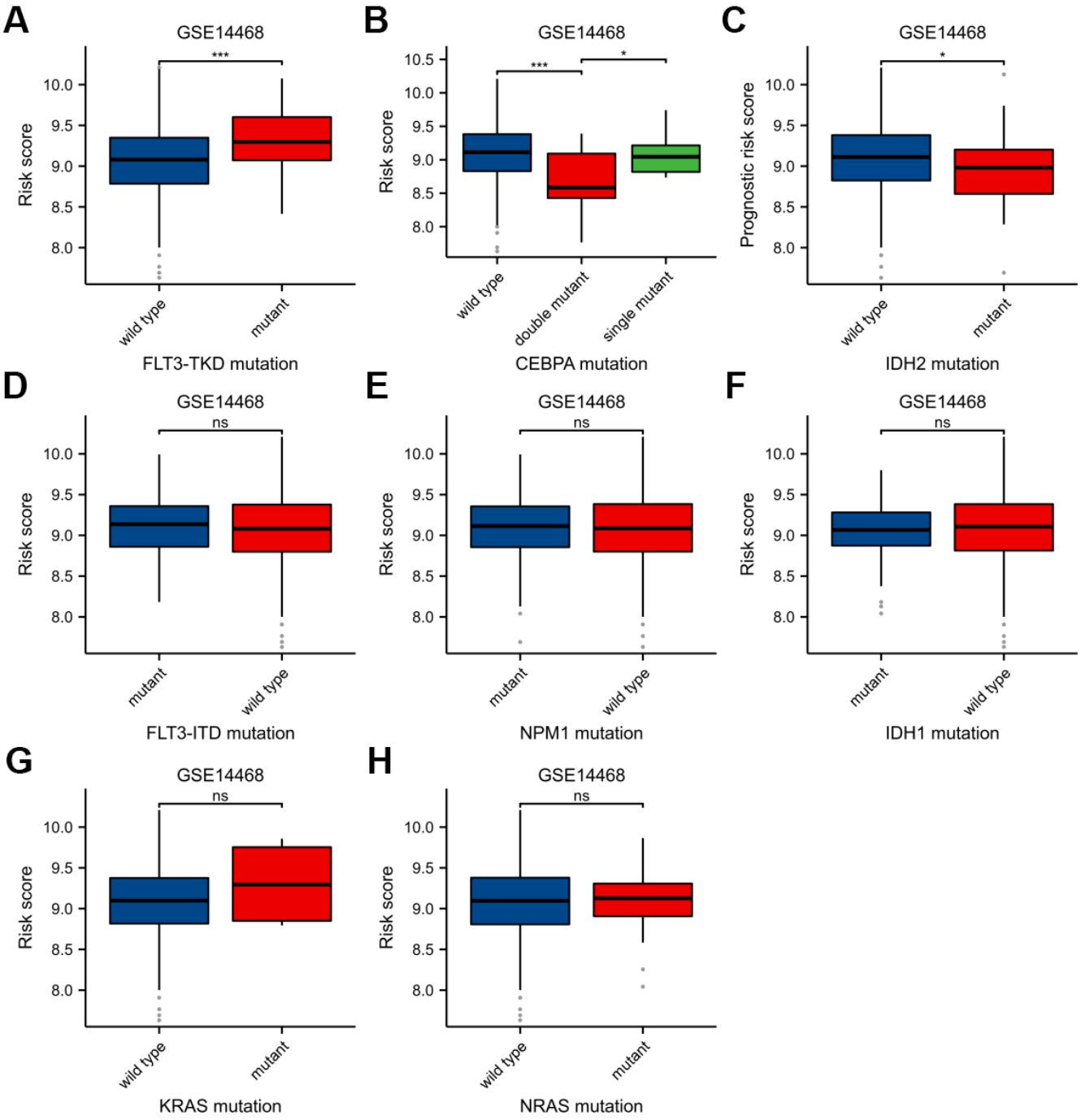
Supplementary Figure 4. Different cell abundance of forty-one immune categories between HRPS-group/high-risk group and LRPS-group/low-risk group. (*P < 0.05, **P <0.01, ***P < 0.001).



Supplementary Figure 5. Relationship between PRS and 8 checkpoints' expression. (**A**) The heatmap of correlation between PRS score and 8 immune checkpoint expression levels. (**B**–**I**) Scatter plot of correlation between PRS score and expression level of each immune checkpoint.



Supplementary Figure 6. Difference of ssGSEA scores about 12 aging-related gene signals between two different PRS groups according to ARGs prognostic signature. (*P < 0.05, **P <0.01, ***P < 0.001).



Supplementary Figure 7. Differences of PRS between wild-type and mutation of several common genes. (**A**) *FLT3-TKD,* (**B**) *CEBPA*, (**C**) *IDH2*, (**D**) *FLT3-ITD*, (**E**) *NPM*1, (**F**) *IDH1*, (**G**) *KRAS*, (**H**) *NRAS*. (*P < 0.05, **P <0.01, ***P < 0.001).