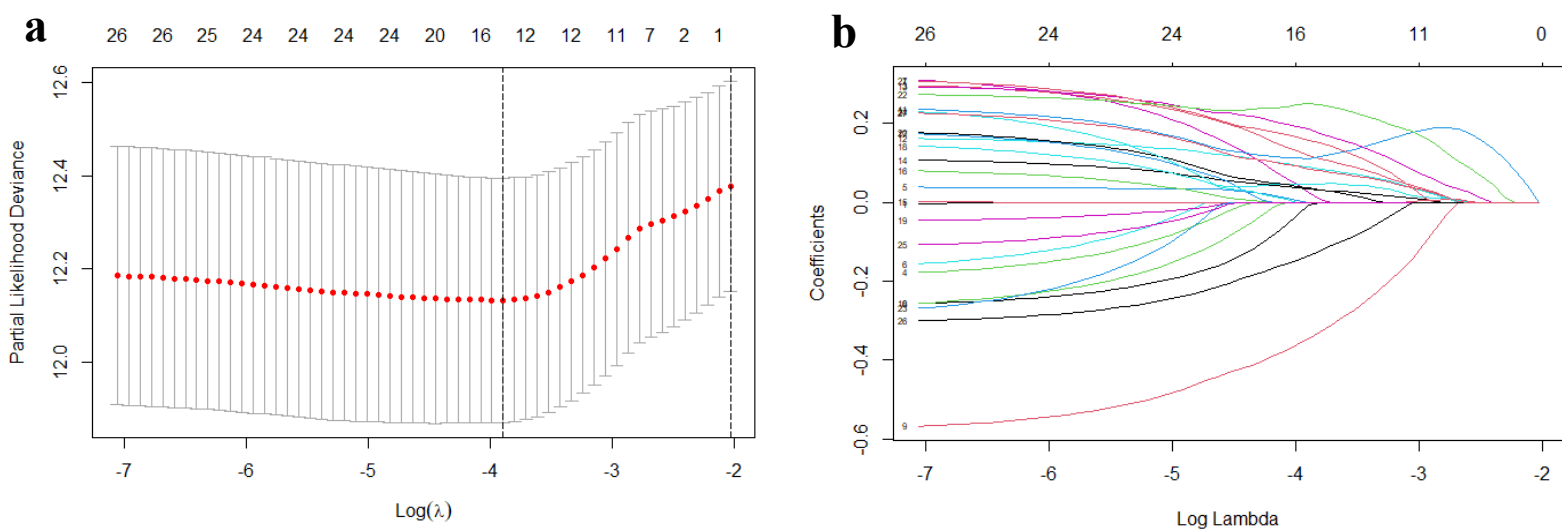
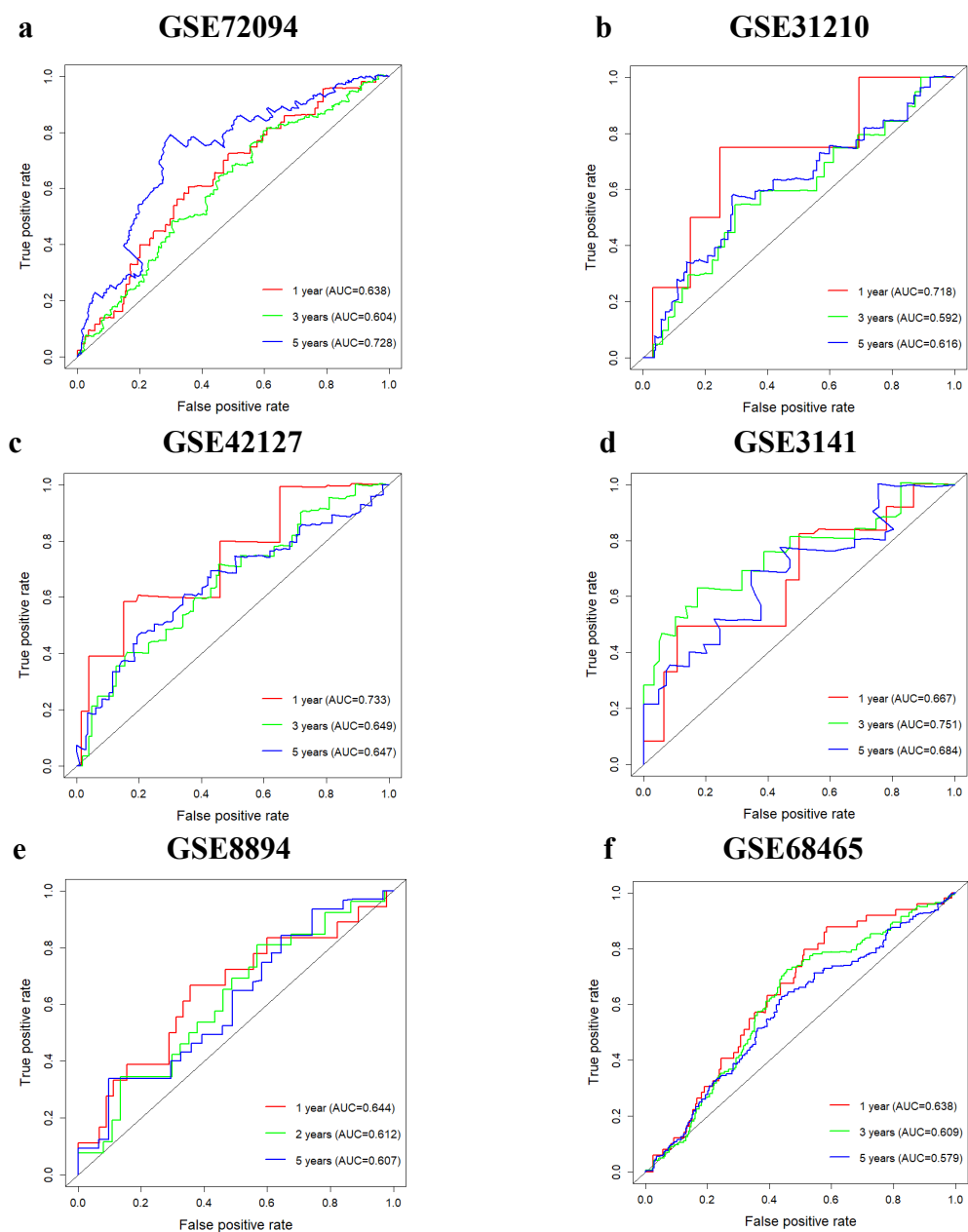
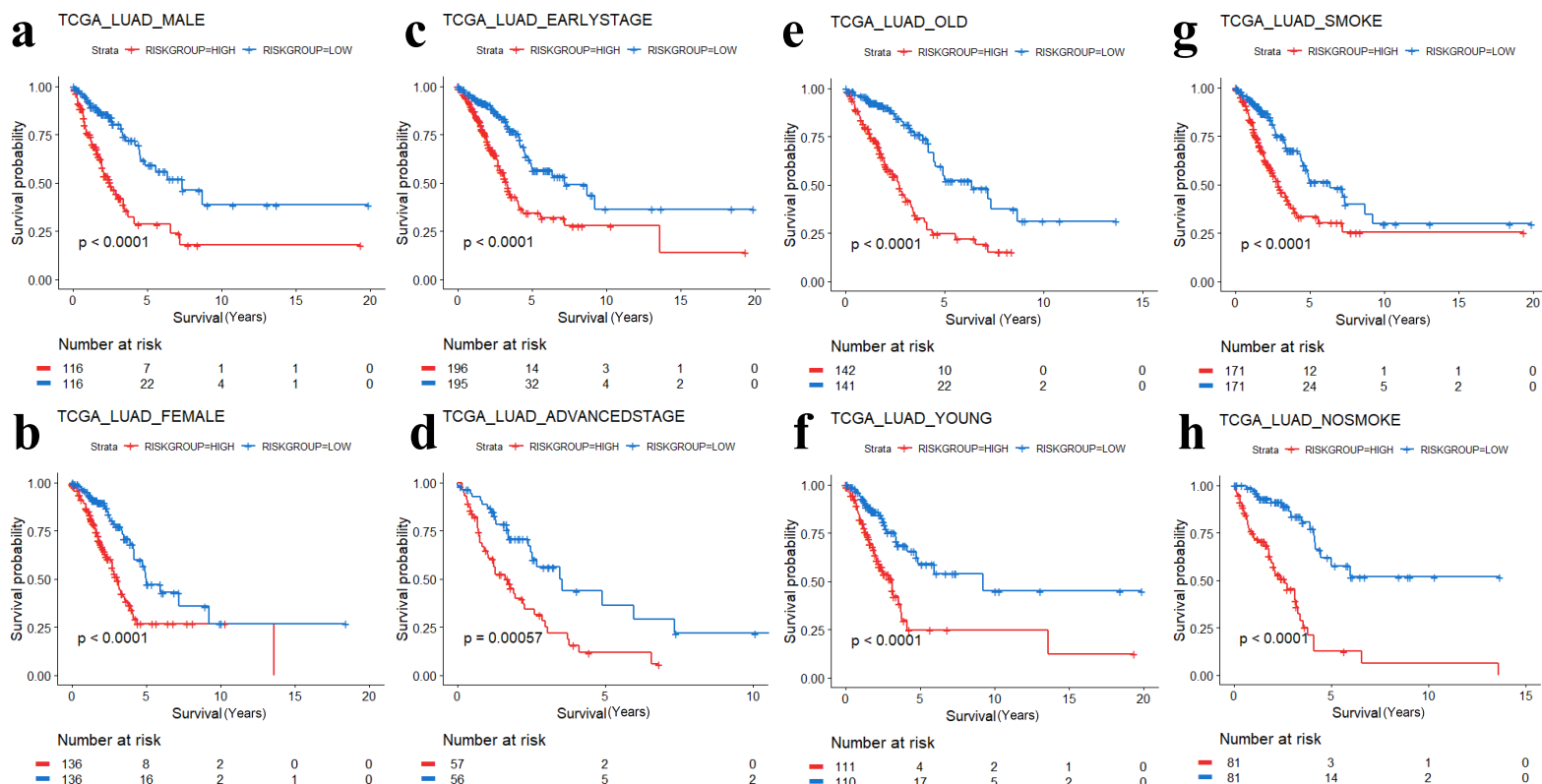




**Supplementary Figure 1.** Construction of classical monocyte marker genes signature in TCGA LUAD cohorts. (a) LASSO coefficient profiles of the 28 prognostic genes. (b) 10-fold cross-validation for tuning parameter selection in the LASSO model.



**Supplementary Figure 2.** Time-dependent ROC curves of risk score for predicting overall survival in GSE72094 cohort (a), GSE31210 cohort (b), GSE42127 cohort (c), GSE3141 cohort (d), GSE8894 cohort (e) and GSE68465 cohort (f).

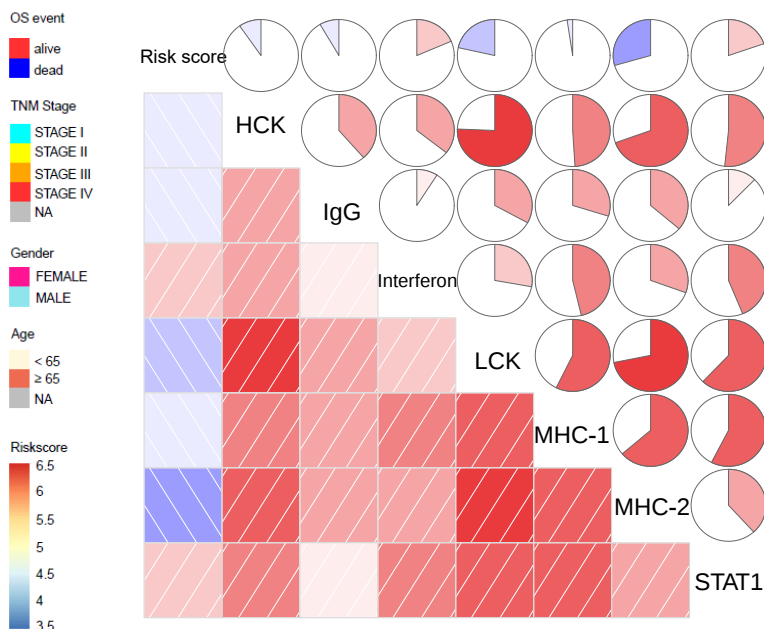


**Supplementary Figure 3.** Validation of the prognostic predictive ability of classical monocyte marker genes signature in different clinical subgroups. Kaplan–Meier curves of overall survival in male (a), female (b), early stage (c), advanced stage (d), old (e), young (f), smokers (g) and non-smokers (h) patients based on risk score in TCGA LUAD cohort

Heatmap visualization showing gene expression data across various melanoma samples. The y-axis lists genes, and the x-axis represents individual samples. A color scale at the top indicates OS event (red), TNM Stage (yellow), Gender (green), Age (blue), and Risk score (orange).

Genes listed on the y-axis (from top to bottom):

- C1QB
- HCP
- C1QA
- AIPI
- LST1
- DOCK2
- LAPTM5
- TYROBP
- M54AAA
- M54AA
- CD163
- TGEC
- SLC7A7
- VAR1
- TPEC
- IFI30
- MND4
- FCER1G
- RNASEB
- SLC10B1
- CCR1
- IGSF3
- ISLR2
- IGSF21
- IGSF1
- IGSF22
- IGSF33
- IGHD
- IGSF11
- IGSF5
- IGSF6
- IFI1
- IFI3
- IFI4L
- OAS3
- MX1
- RSAD2
- IFI44
- OAS2
- OAS1
- CD2
- LC
- G2MK
- G2MA
- CD3D
- CD53
- ARHGAP15
- CCL5
- GMFG
- SELL
- STAT1
- SAMSN1
- RAC2
- KCLF1
- CCR7
- PK3CD
- CD3D1A
- CD48
- IL2RG
- SH2D1A
- SLAMF1
- ILTR
- INPP5D
- ILKAP1
- FSL2
- IFIT1
- SELPLG
- IL10RA
- SIA
- CCR2
- CSF2RB
- TAP1
- STAT1
- CXCL10
- CXCL11
- GBP1
- CXCL9
- CD74
- PTPRC
- HLA-DQB1
- HLA-DQB1
- HLA-DQA1
- HLA-DPB5
- HLA-DQA1
- HLA-DMA
- HLA-DRA
- HLA-DPB1
- HLA-DPB2
- HLA-DPA1
- HLA-DQB2
- HLA-DQA2
- HLA-DQB
- HLA-DMB
- HLA-B
- HLA-C
- HLA-E
- HLA-J
- HLA-G
- HLA-F
- HLA-H
- HLA-A
- HLA-L



**Supplementary Figure 4.** Relationship between the CMMGS and inflammatory metagenes in TCGA LUAD cohort. (a) Heatmap showed the expression characteristics of 7 clusters of metagenes. (b) The plot of Correlogram was produced by using Pearson R-value between metagenes and risk scores