Supplementary

Table S1 Primers for quantitative real-time PCR

Genes	Forward primers (5'-3')	Reverse primers (5'-3')
SFTPA2	ACTTGGAGGCAGAGACCCAA	GGGCTTCCAACACAAACGTC
SPP1	CTCCATTGACTCGAACGACTC	CAGGTCTGCGAAACTTCTTAGAT
SFTPB	TGGAGCAAGCATTGCAGTG	ACTCTTGGCATAGGTCATCGG
KRT19	AACGGCGAGCTAGAGGTGA	GGATGGTCGTGTAGTAGTGGC
EMP2	GTGCTTCTTGCTTTCATCATCG	TGCAATTCGTGTTGTTGGTACA
CCL20	CCAAGAGTTTGCTCCTGGCT	GGATTTGCGCACACAGACAA

PCR, polymerase chain reaction.

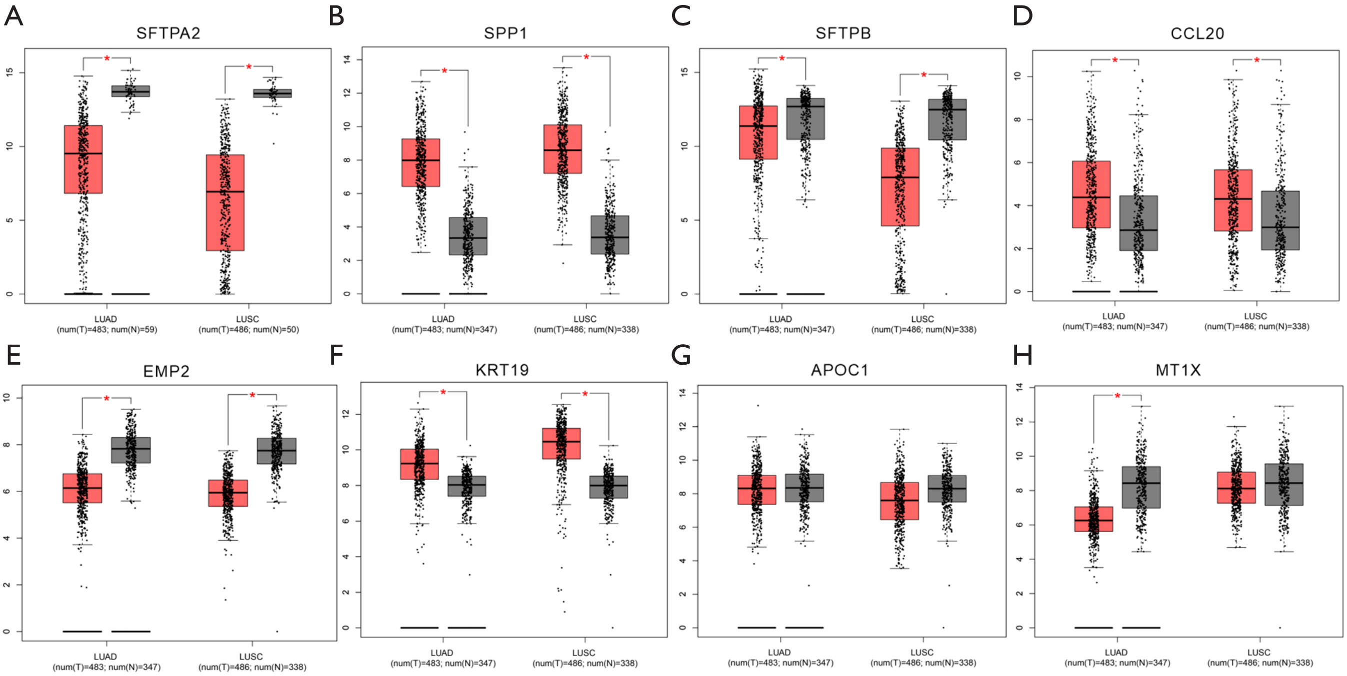

Figure S1 Analysis of GEPIA database data. (A-H) The GEPIA website was used to verify these 8 genes. The Y-axis represents gene expression. *, P<0.05. LUSC, lung squamous cell carcinoma; LUAD, lung squamous cell carcinoma; GEPIA, gene expression profiling interactive analysis.

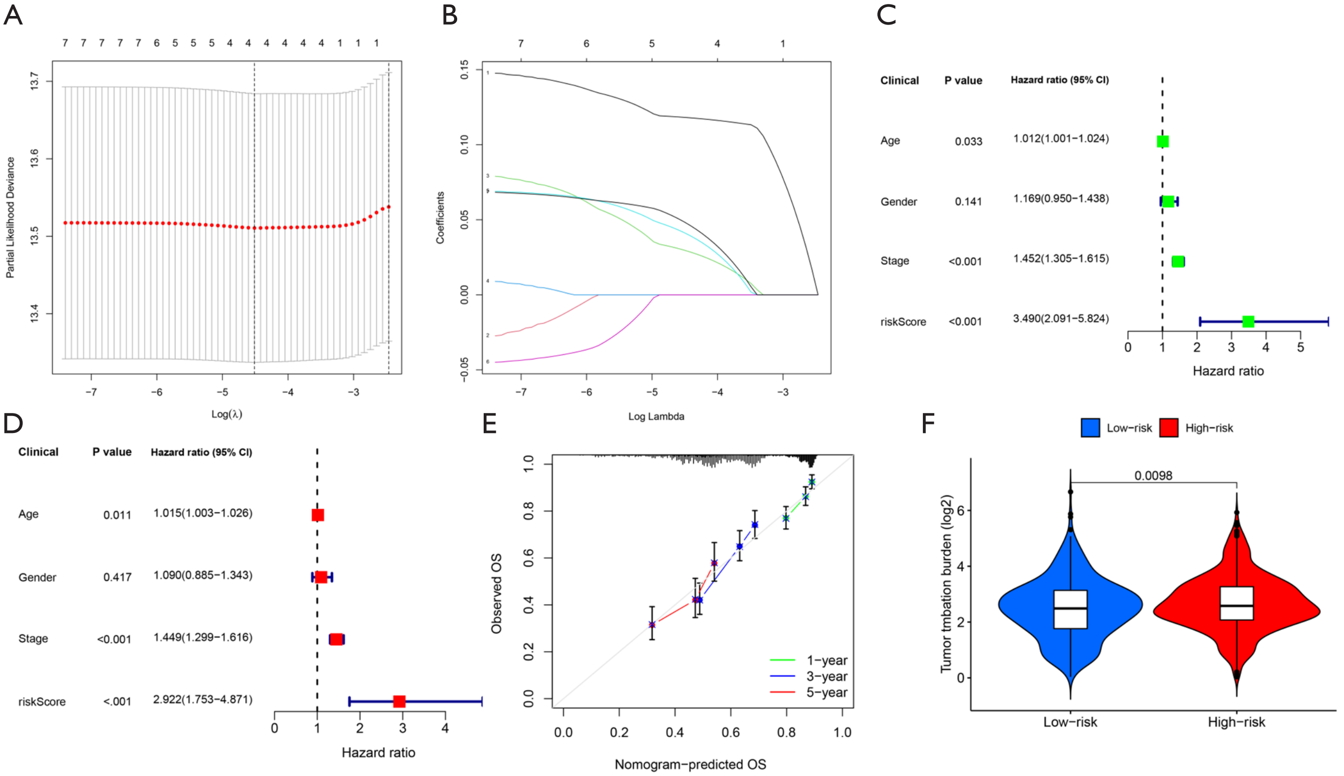

Figure S2 Additional information. (A) Cross-validation for tuning parameter (lambda, screening in the LASSO regression model. (B) LASSO coefficient profiles of 7 prognostic MRGs. (C,D) Univariate and multivariate Cox regression analyses. (E) The calibration curve of the 1, 3, and 5-year survival. (F) TMB of NSCLC patients with high/low risk. CI, confidence interval; LASSO, least absolute shrinkage and selection operator; NSCLC, non-small cell lung cancer; MRGs, metabolism-related genes; TMB, tumor mutation burden; OS, overall survival.

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