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Supplemental Information

Multi-omics Data Analyses Construct TME and Identify the Immune-Related Prognosis Signatures in Human LUAD

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Supplemental Figures

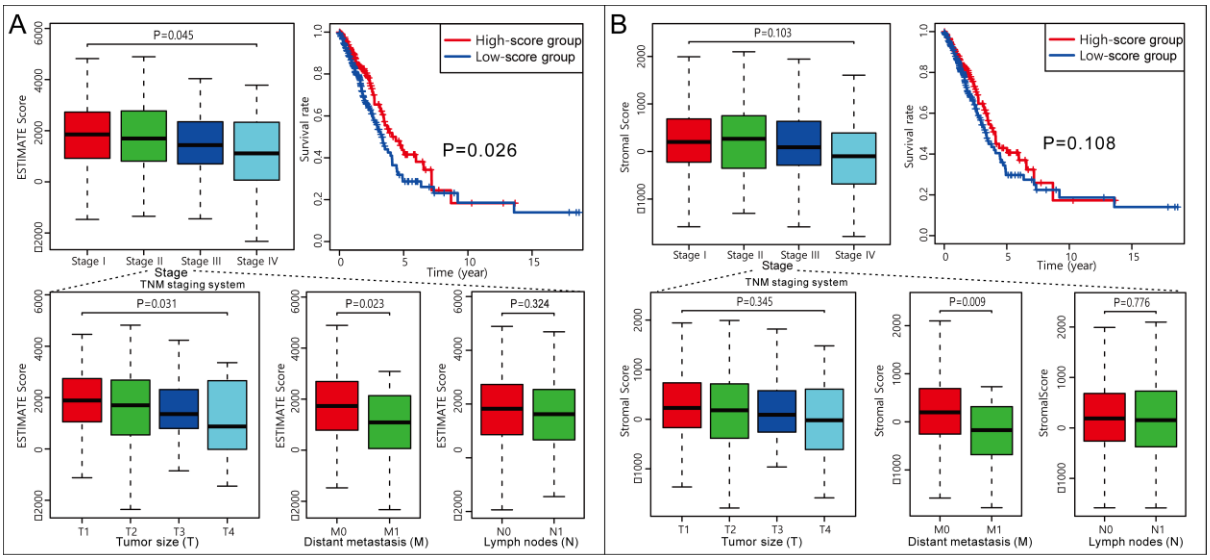

Figure S1 The comparisons of the distributions of **(A)** estimate scores and **(B)** stromal scores on TNM stage, tumor size, distant metastasis, lymph nodes and overall survival time.

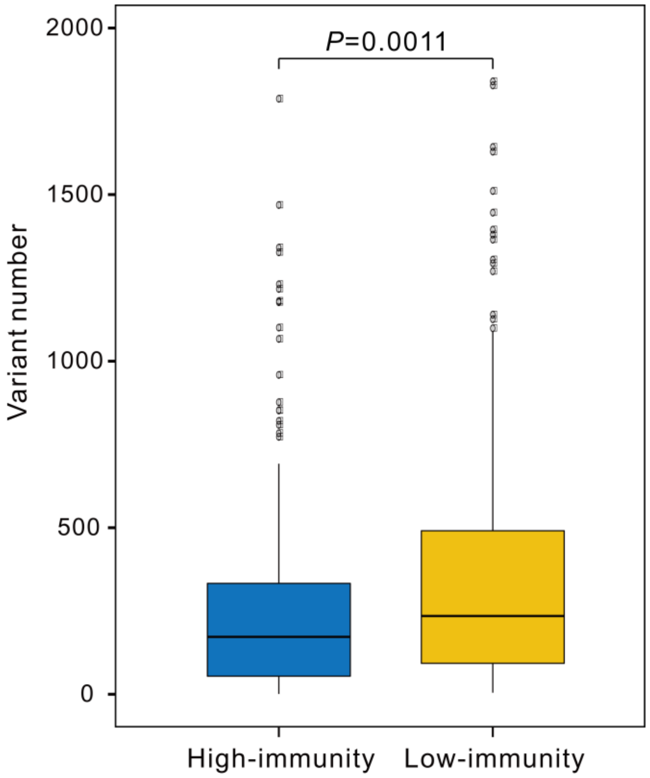

Figure S2 The comparison of the variant number between high-immunity and low-immunity cohorts.

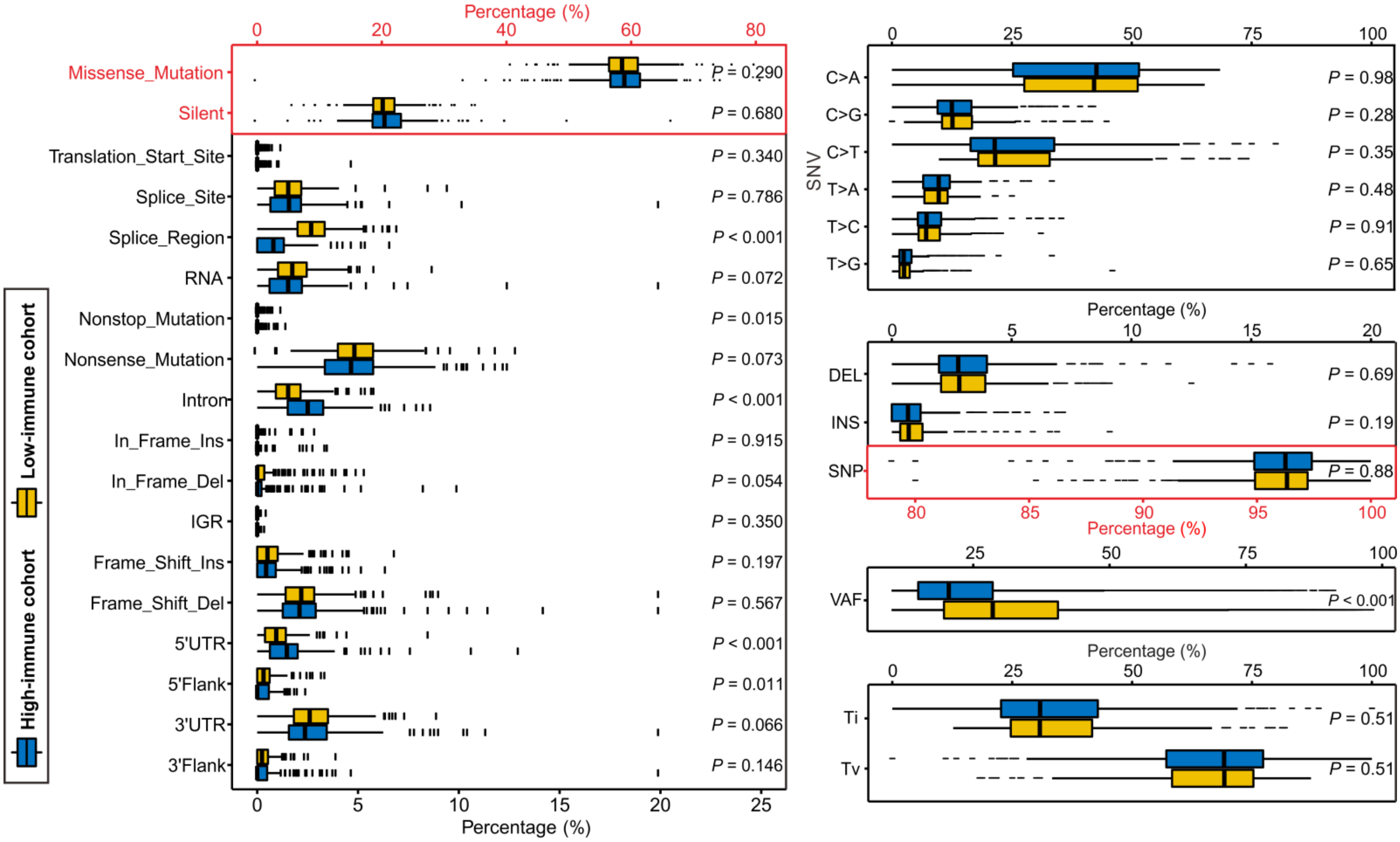

Figure S3 The percentages of various mutation types in high-immunity and low-immunity cohorts. Boxplots respectively display the comparisons of the percentages of **(A)** every mutation type classified by effects, **(B)** SNV, **(C)** INDEL and SNP, and **(D)** DNA substitution types including transition (Ti) and transversion (Tv).

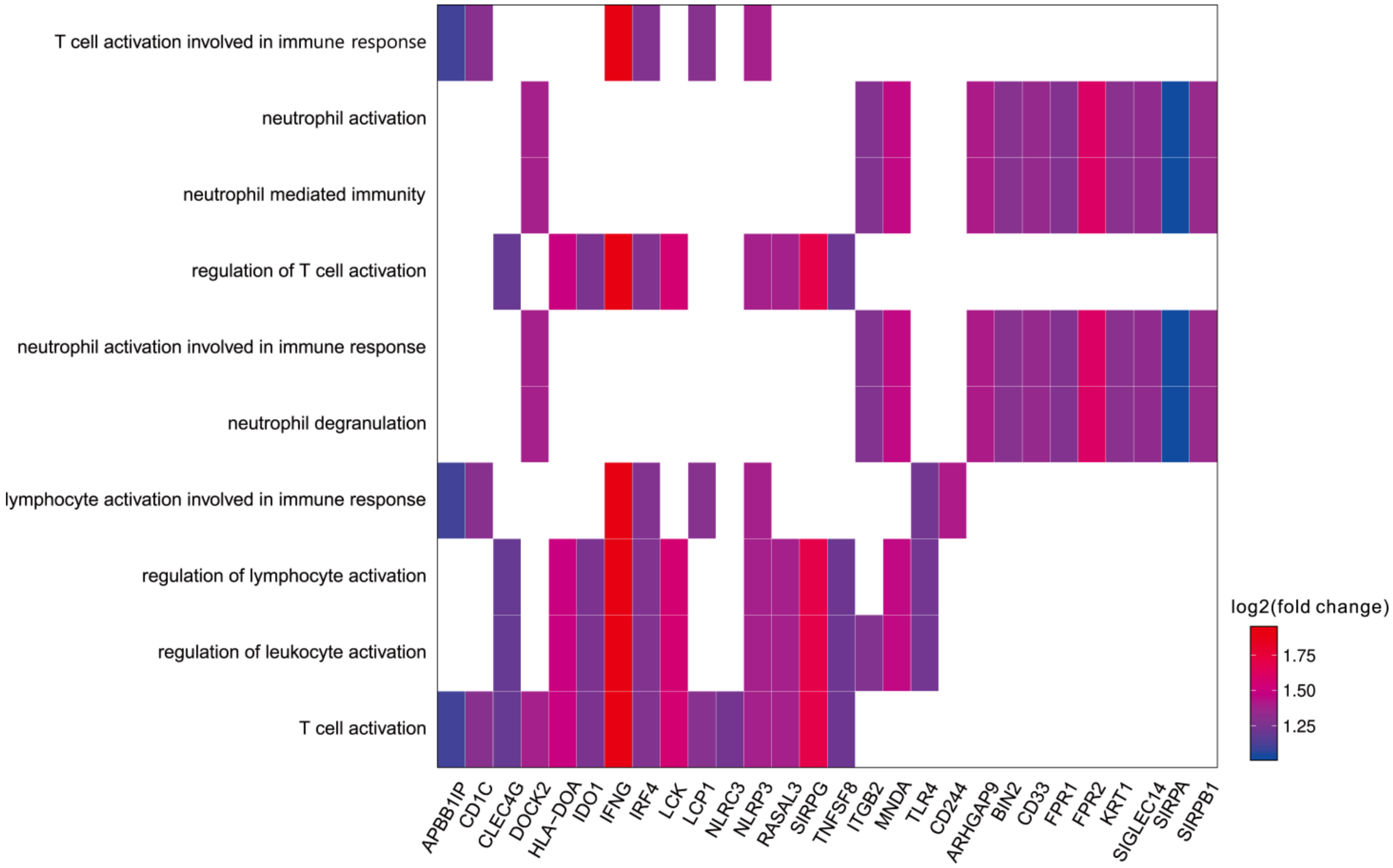

Figure S4 Functional enrichment analysis of the hypermethylation-associated up-regulated DEGs in high –immunity cohort. The y-axis and x-axis respectively represent the significant GOBP terms and the genes in terms. The color of the cells represents the gradient of expression fold change.

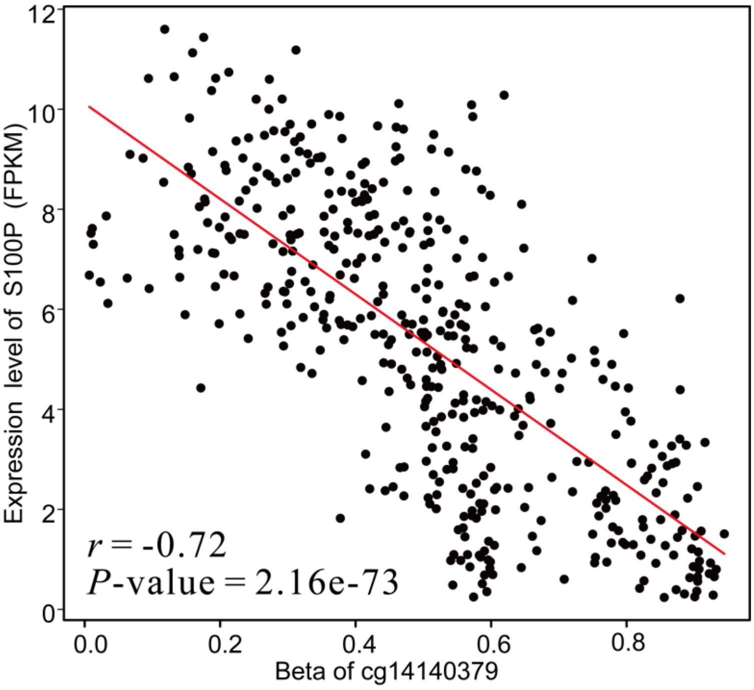

Figure S5 The correlation between the expression level and the beta value of *S100P*.

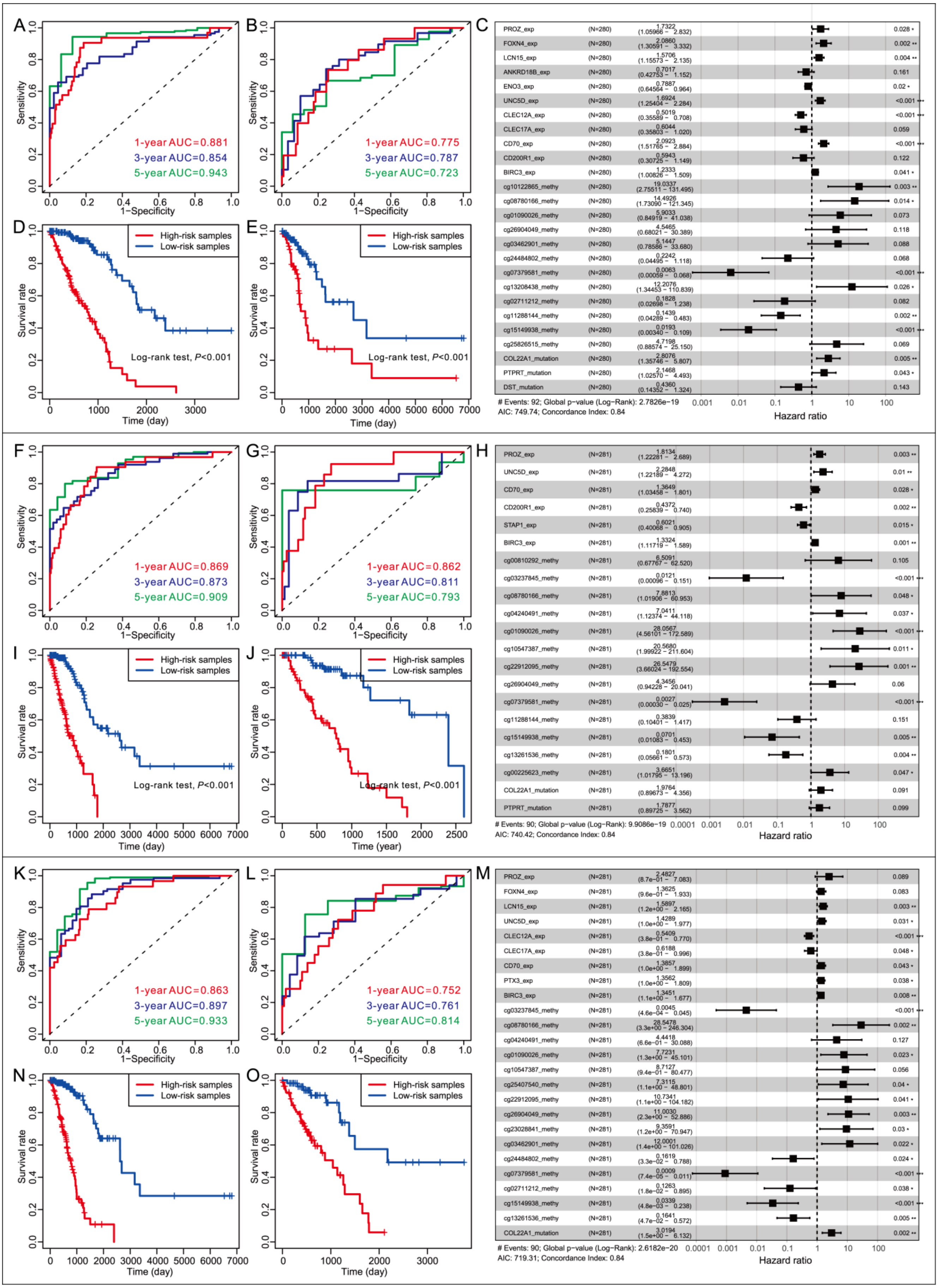

Figure S6 The performance of the trained model 1 (A-E), model 2 (F-J) and model 3 (K-O). Subplot (A/F/K) and (B/G/L) show the roc curves of the risk score for 1-year, 3-year and 5-year survival prediction on the training set and test set, respectively. Subplot (D/I/N) and (E/J/O) are the Kaplan-Meier curves showing the independent relevance between overall survival time and risk scores when training sets and test sets were respectively used. Subplot C, H, and M are the forest plots showing the prognostic impact of variables.

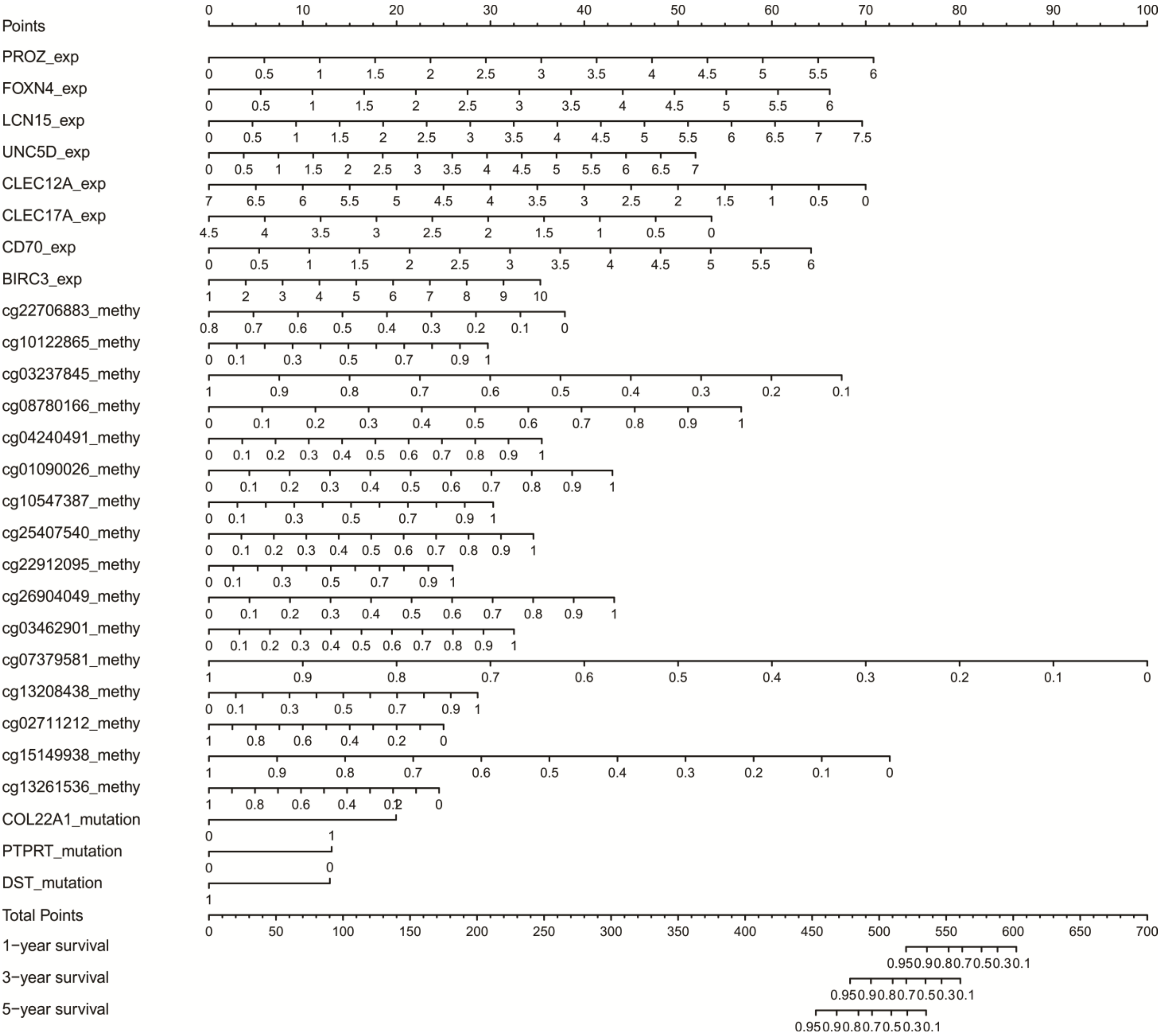

Figure S7 Nomogram for prediction of overall survival time based on multi-Omics characteristics in LUAD. Each variable is assigned a point value. The total points in the bottom panel can be used to estimate the probability of 1-year, 3-year and 5-year survival.

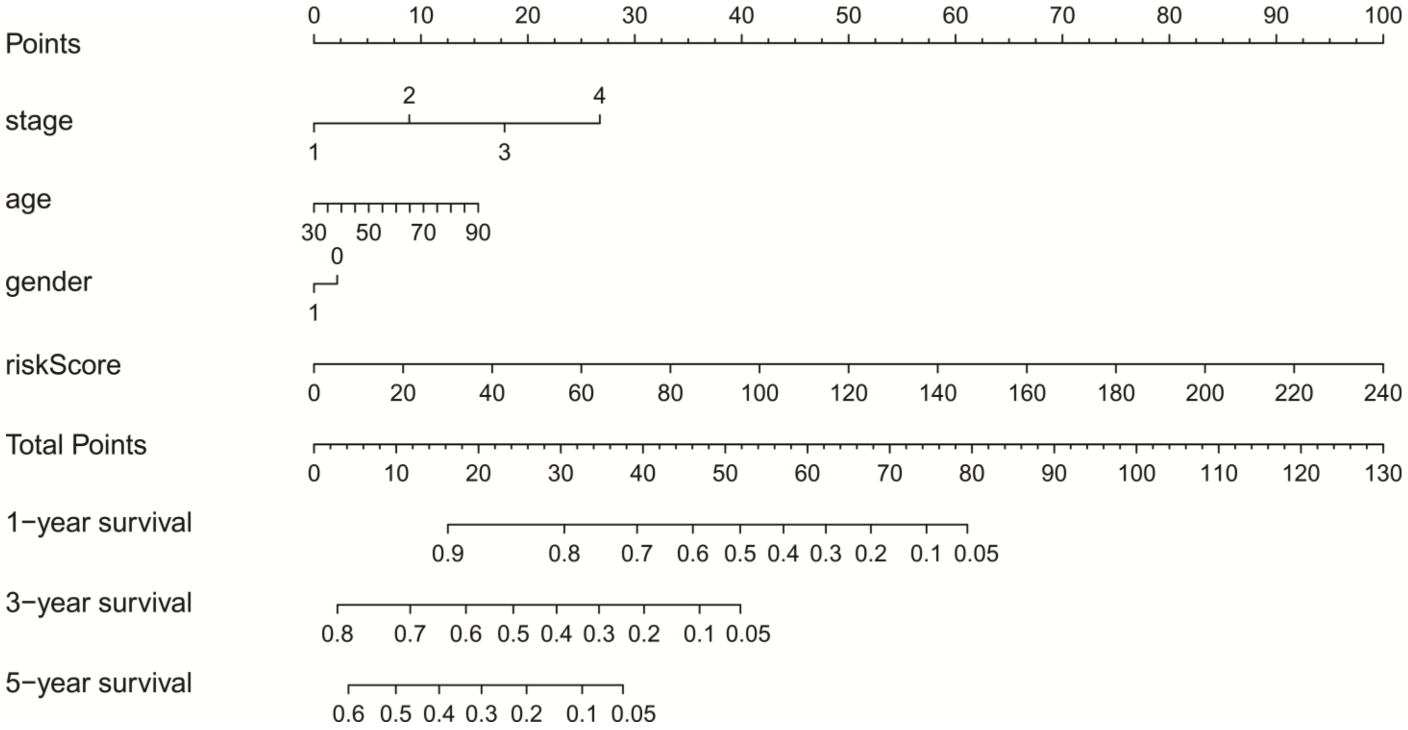

Figure S8 Nomogram for prediction of overall survival time based on the combination of multi-Omics characteristics and clinical factors in LUAD. Each variable is assigned a point value. The total points in the bottom panel can be used to estimate the probability of 1-year, 3-year and 5-year survival.

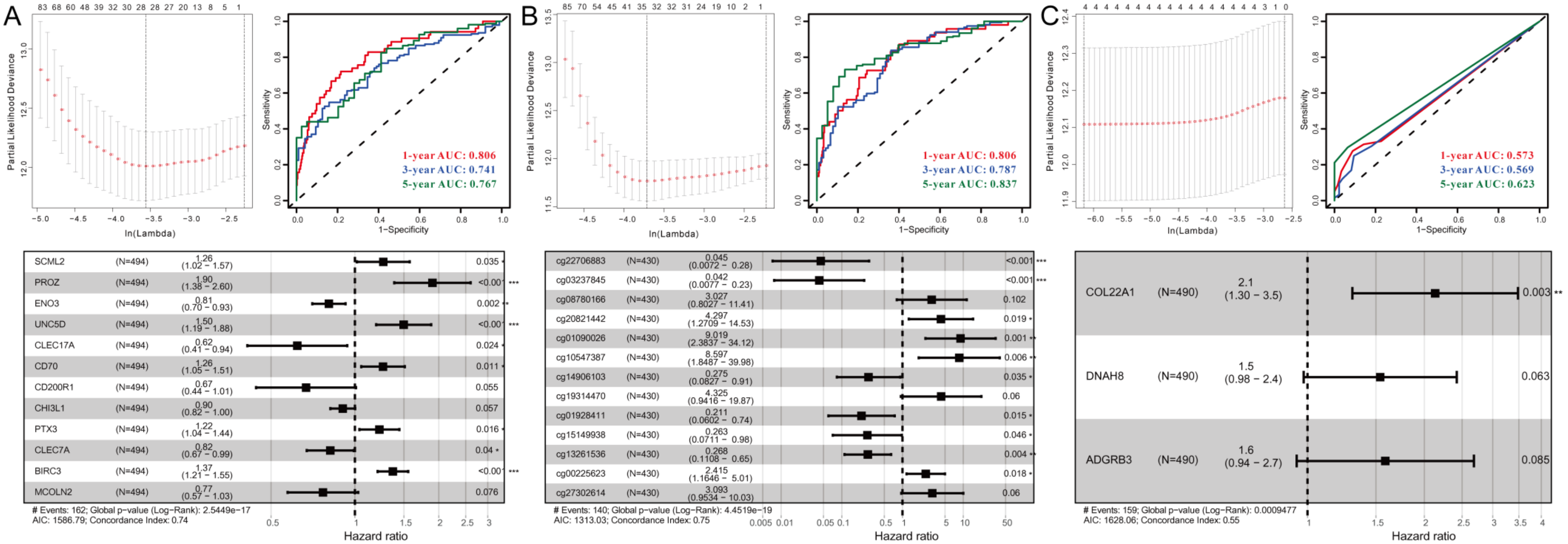

Figure S9 The prognosis prediction models based on **(A)** gene expression change, **(B)** DNA methylation and **(C)** somatic mutation**.**

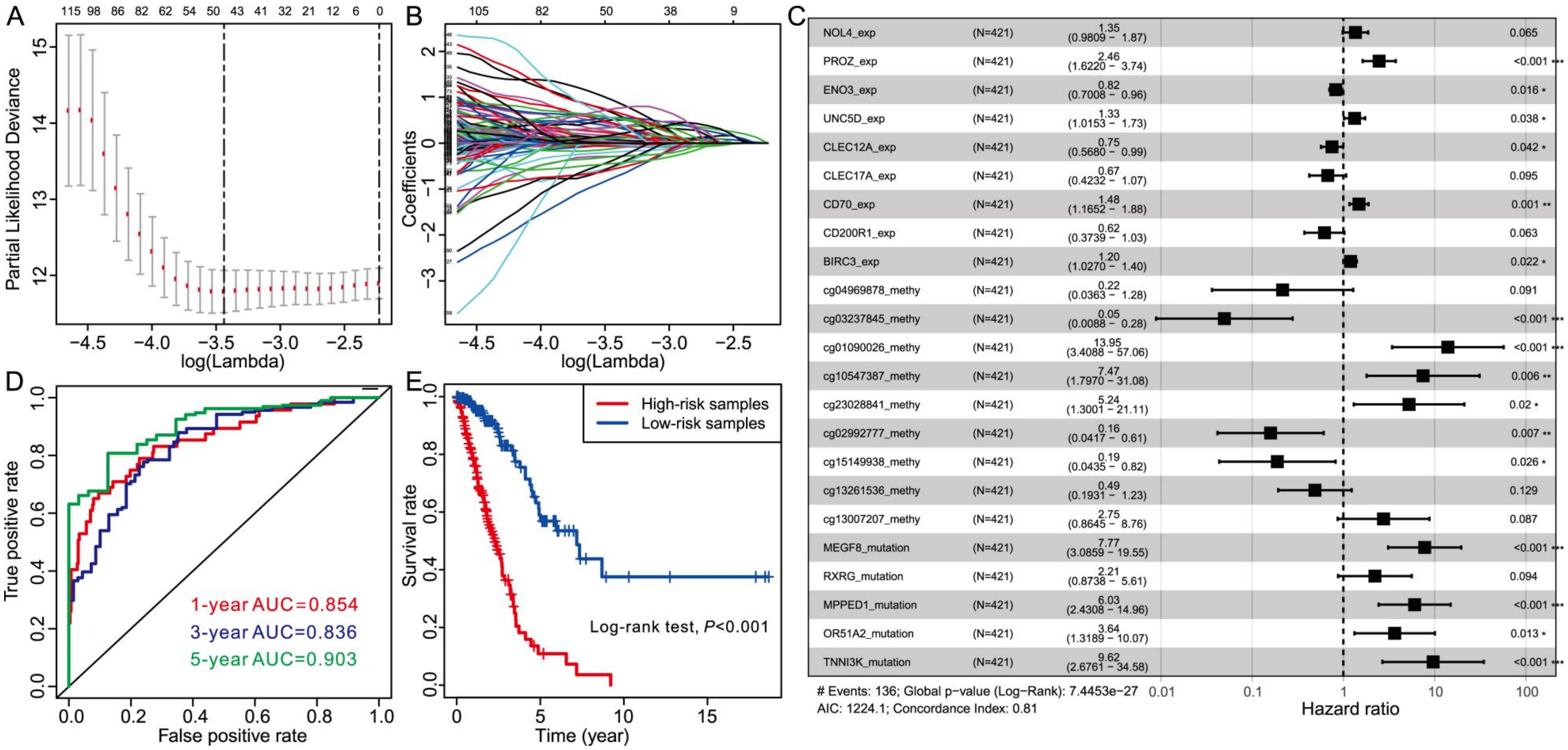

Figure S10 The prognosis prediction model based on differential mutations, gene expression change and DNA methylation. (A-B) Identification of the optimal penalization coefficient lambda in Lasso regression model. **(C)** Forest plot of the prognostic impact of 23 variables. **(D)** ROC curves of the risk score for predicting 1-year, 3-year and 5-year survival. **(E)** Kaplan-Meier curves show the independent relevance between overall survival time and risk scores.

Supplemental Tables

Table S1 The results of pairwise comparisons of estimate score and immune score on tumor size and stage.
(see Excel file)

Table S2 The list of the differentially mutated genes between high-immunity and low-immunity cohorts.
(see Excel file)

Table S3 The list of the differentially methylated probes.
(see Excel file)

Table S4 The list of the hypermethylation-associated DEGs in high-immunity cohort

Gene_symbol	Expression_status	Methylation_probes
PYHIN1	up-regulated	cg02490589,cg21576886,cg25464787,
PIK3R5	up-regulated	cg02505918,
SIRPA	up-regulated	cg25458147,
IL16	up-regulated	cg05042034,
NLRP3	up-regulated	cg25602756,cg18126557,cg07164722,
BIN2	up-regulated	cg02023138,
CD1E	up-regulated	cg09478478,cg10976626,
KLHL6	up-regulated	cg02939781,
DNAJC5B	up-regulated	cg21649629,
LSP1	up-regulated	cg23670188,
IDO1	up-regulated	cg24188163,
RGS1	up-regulated	cg22360028,
XIRP1	up-regulated	cg07165610,
AGAP2	up-regulated	cg23377551,cg11511175,cg00769161,cg15539944,cg14845962,cg12116027,
CD244	up-regulated	cg13240206,
SIGLEC14	up-regulated	cg03240663,
HLA-DQA2	up-regulated	cg17471365,
CLEC4G	up-regulated	cg05626117,
RASGRP2	up-regulated	cg22749107,
ACSM5	up-regulated	cg02147009,
IRF4	up-regulated	cg17336615,
CD1B	up-regulated	cg04574507,cg15952487,
KRT1	up-regulated	cg10538533,cg10926148,
S100B	up-regulated	cg11064537,
IFNG	up-regulated	cg01281450,
LCP2	up-regulated	cg21748244,
IKZF1	up-regulated	cg26746878,
ARHGAP15	up-regulated	cg17600630,cg27492839,
LCP1	up-regulated	cg11274337,
FCER1A	up-regulated	cg14696870,
CIITA	up-regulated	cg07371747,
MAP4K1	up-regulated	cg05258935,cg08230957,
APOE	up-regulated	cg14123992,cg01032398,
CD1C	up-regulated	cg09149672,
HLA-DOA	up-regulated	cg18030265,cg09132634,cg26175846,cg18043773,cg17777731,cg07699648,
MNDA	up-regulated	cg14216734,
BLK	up-regulated	cg24861686,
DOCK2	up-regulated	cg26794227,cg27591502,cg09175734,cg02732152,cg04730794,cg01057132,cg25076039,
APBB1IP	up-regulated	cg17954226,
TLR4	up-regulated	cg14629571,
ARHGAP9	up-regulated	cg03886558,
CMKLR1	up-regulated	cg13248299,cg07919167,
ZNF831	up-regulated	cg04068564,cg18826352,cg19787906,cg21296613,
TNFRSF8	up-regulated	cg13689066,
WIPF1	up-regulated	cg11778734,cg24401656,
TNFSF8	up-regulated	cg14187242,
KCNE1	up-regulated	cg03123557,

PRKCB	up-regulated	cg00795205,cg04086239,cg07959068,cg06401532,
ACAP1	up-regulated	cg08324090,cg25900902,cg19175364,
FPR1	up-regulated	cg17724366,
FPR2	up-regulated	cg02309029,
NLRC3	up-regulated	cg02819734,
ITGB2	up-regulated	cg27103348,
CADM3	up-regulated	cg11388664,cg24580655,cg01803258,
LCK	up-regulated	cg03243362,
RASAL3	up-regulated	cg01062942,cg22808633,
CD33	up-regulated	cg24809544,
ASB2	up-regulated	cg18485877,
SIRPG	up-regulated	cg23295754,
SIRPB1	up-regulated	cg26616780,cg04103198,cg27365103,
GIMAP4	up-regulated	cg00832923,
LILRB5	up-regulated	cg13535489,
MYO1F	up-regulated	cg22568423,cg08283130,
S100P	down-regulated	cg22266967,cg14140379,cg14323984,cg27027375,cg14900031,
EYS	down-regulated	cg23028841,
CABYR	down-regulated	cg05060976,cg21978251,
SLC38A8	down-regulated	cg02671204,
CGA	down-regulated	cg12078738,
DDC	down-regulated	cg19107055,
GPT2	down-regulated	cg04839706,
FSTL4	down-regulated	cg09024962,
VWA5B2	down-regulated	cg24363374,
MSMB	down-regulated	cg17030820,
F7	down-regulated	cg01089602,cg24269657,cg20329620,cg08266168,
CRABP1	down-regulated	cg07199257,
ATP4B	down-regulated	cg15154339,cg05201344,cg01020475,
LRFN2	down-regulated	cg18454510,
TMED6	down-regulated	cg18368125,cg27009392,cg16148454,
DEPDC7	down-regulated	cg00035630,
RNF186	down-regulated	cg23214395,cg04994456,
KCNQ2	down-regulated	cg04605816,cg01378999,cg13782274,
PROZ	down-regulated	cg16019436,
ATOH7	down-regulated	cg00001874,
HGD	down-regulated	cg04546097,
GREB1	down-regulated	cg25744579,cg14653284,
GNRH2	down-regulated	cg01583485,cg23848712,
OPRD1	down-regulated	cg09970593,
PROC	down-regulated	cg10021288,cg22856114,
PPARGC1A	down-regulated	cg27514608,
PLA2G10	down-regulated	cg27058221,
GAS2	down-regulated	cg25982561,cg17679980,cg23840044,
TFF3	down-regulated	cg21970261,
AKR7A3	down-regulated	cg07447773,
ADPRHL1	down-regulated	cg10624914,cg00767058,
GPX2	down-regulated	cg09643186,cg13844922,cg10880599,

Table S5 The list of the hypomethylation-associated DEGs in high-immunity cohort

Gene_symbol	**Expression_status**	**Methylation_probes**
HLA-B	up-regulated	cg25954539,
CASP1	up-regulated	cg05671385,
FAM78A	up-regulated	cg17936488,
SLAMF8	up-regulated	cg07625783,
PSMB9	up-regulated	cg07156249,
CARD16	up-regulated	cg13775050,
SLA2	up-regulated	cg07598052,cg03841065,

Table S6 The list of the genes with expression-methylation correlations in high-immunity cohort (see Excel file)

Table S7 The list of the genes with expression-methylation correlations in low-immunity cohort (see Excel file)

Table S8 The list of 52 reserved variables in the lasso regression model.

No.	Variables
1	PROZ_exp
2	FOXN4_exp
3	LCN15_exp
4	INSL4_exp
5	GAS2_exp
6	ANKRD18B_exp
7	ENO3_exp
8	UNC5D_exp
9	CLEC12A_exp
10	CLEC17A_exp
11	CD70_exp
12	CD200R1_exp
13	PTX3_exp
14	ACSM5_exp
15	STAP1_exp
16	BIRC3_exp
17	LILRA4_exp
18	MCOLN2_exp
19	CCR2_exp
20	cg00810292_methy
21	cg22706883_methy
22	cg26605164_methy
23	cg04969878_methy
24	cg10122865_methy
25	cg03237845_methy
26	cg08780166_methy
27	cg04240491_methy
28	cg01090026_methy
29	cg04275847_methy
30	cg10547387_methy
31	cg25407540_methy
32	cg22912095_methy
33	cg26904049_methy
34	cg23028841_methy
35	cg03462901_methy
36	cg00874480_methy
37	cg24484802_methy
38	cg07379581_methy
39	cg17665652_methy
40	cg13208438_methy
41	cg02711212_methy
42	cg02992777_methy
43	cg11288144_methy
44	cg15149938_methy
45	cg13261536_methy
46	cg13007207_methy
47	cg25826515_methy

48	cg00225623_methy
49	COL22A1_mutation
50	PTPRT_mutation
51	DNAH8_mutation
52	DST_mutation

Table S9 The table shows the contribution of 27 variables and risk score for each sample (see Excel file)