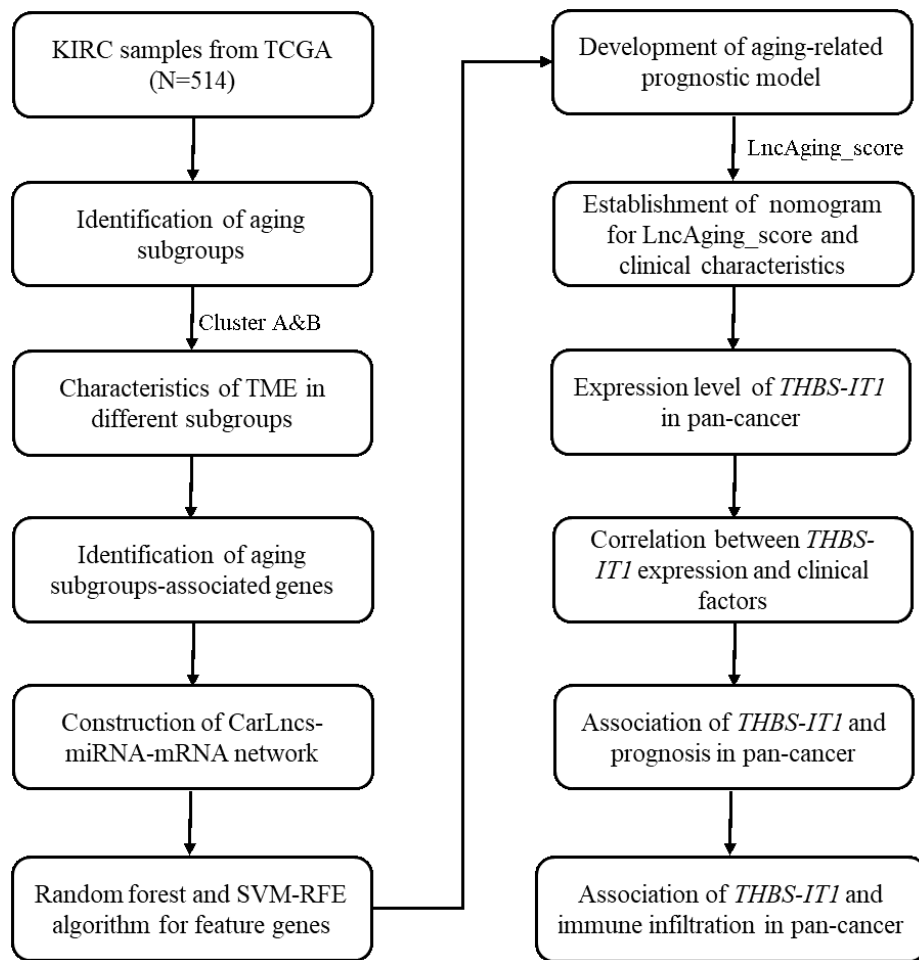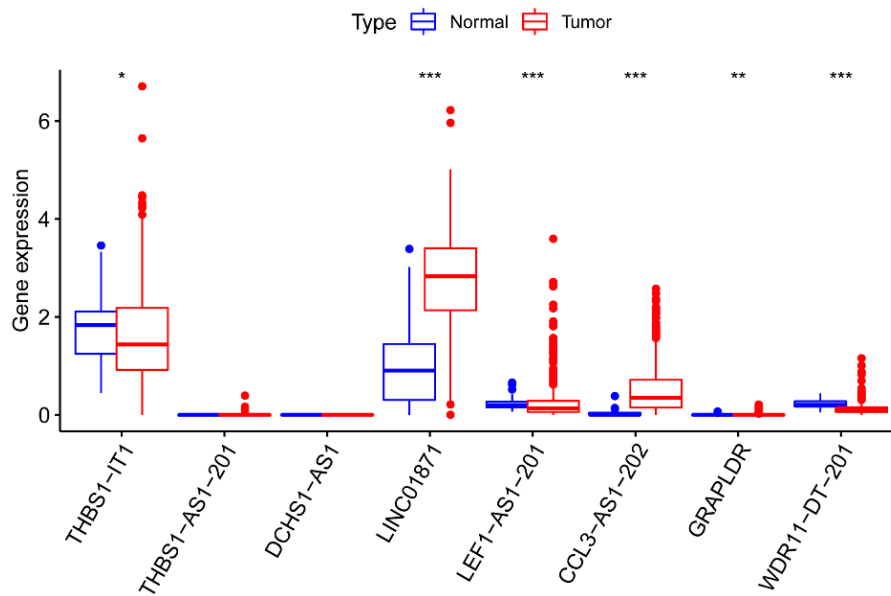Supplementary Figure 1. Dynamic expression patterns of five Car-Lncs include DCHS1-AS1 (**A**, **B**), LEF1-AS1-201 (**C**–**E**), LINC01871 (**F**–**H**), THBS1-IT1 (**I**–**K**) and WDR11-DT-201 (**M**–**O**).

Supplementary Figure 2. The entire analytical process of the study.

Supplementary Figure 3. Comparison of expression levels of 8 CarLncs between tumor and adjacent tissues of KIRC patients.
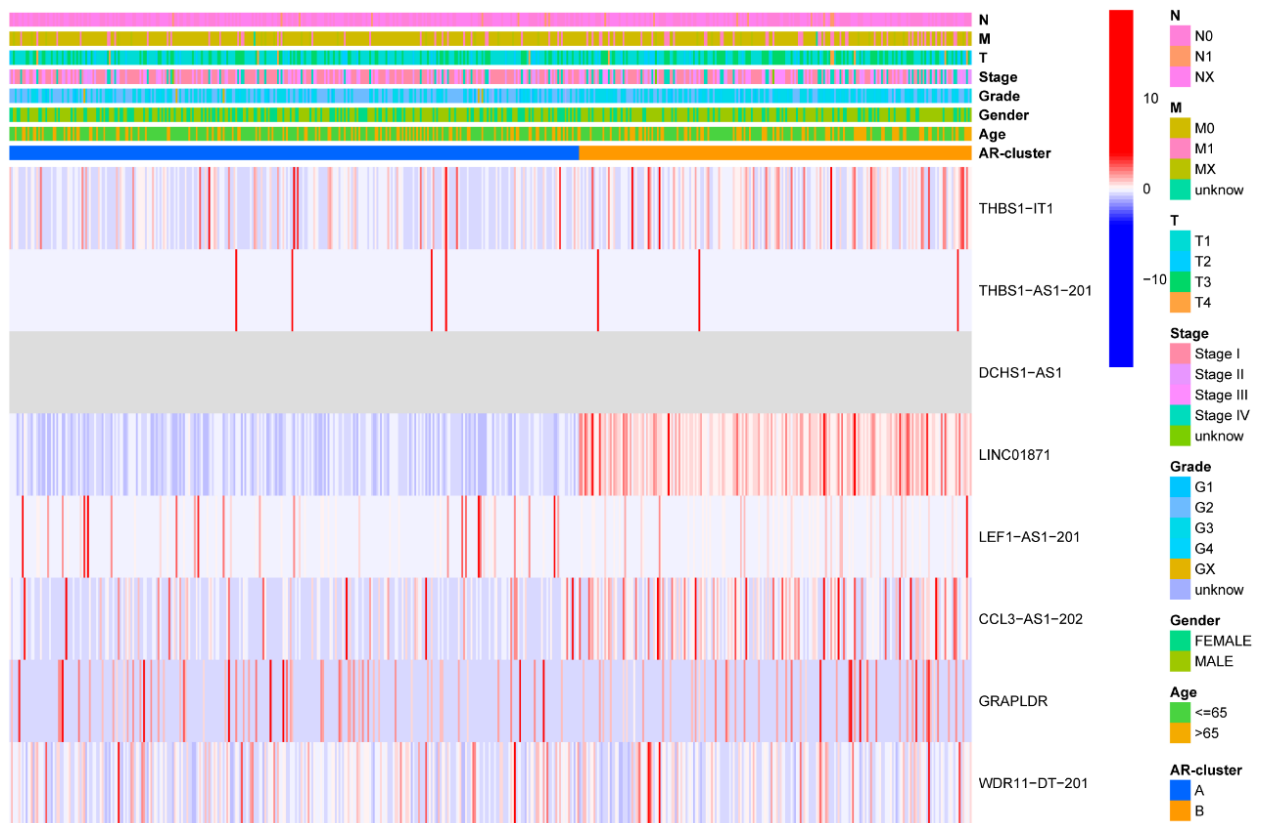
Supplementary Figure 4. Comparisons of the expression level of 8 CarLncs and clinicopathological variables.

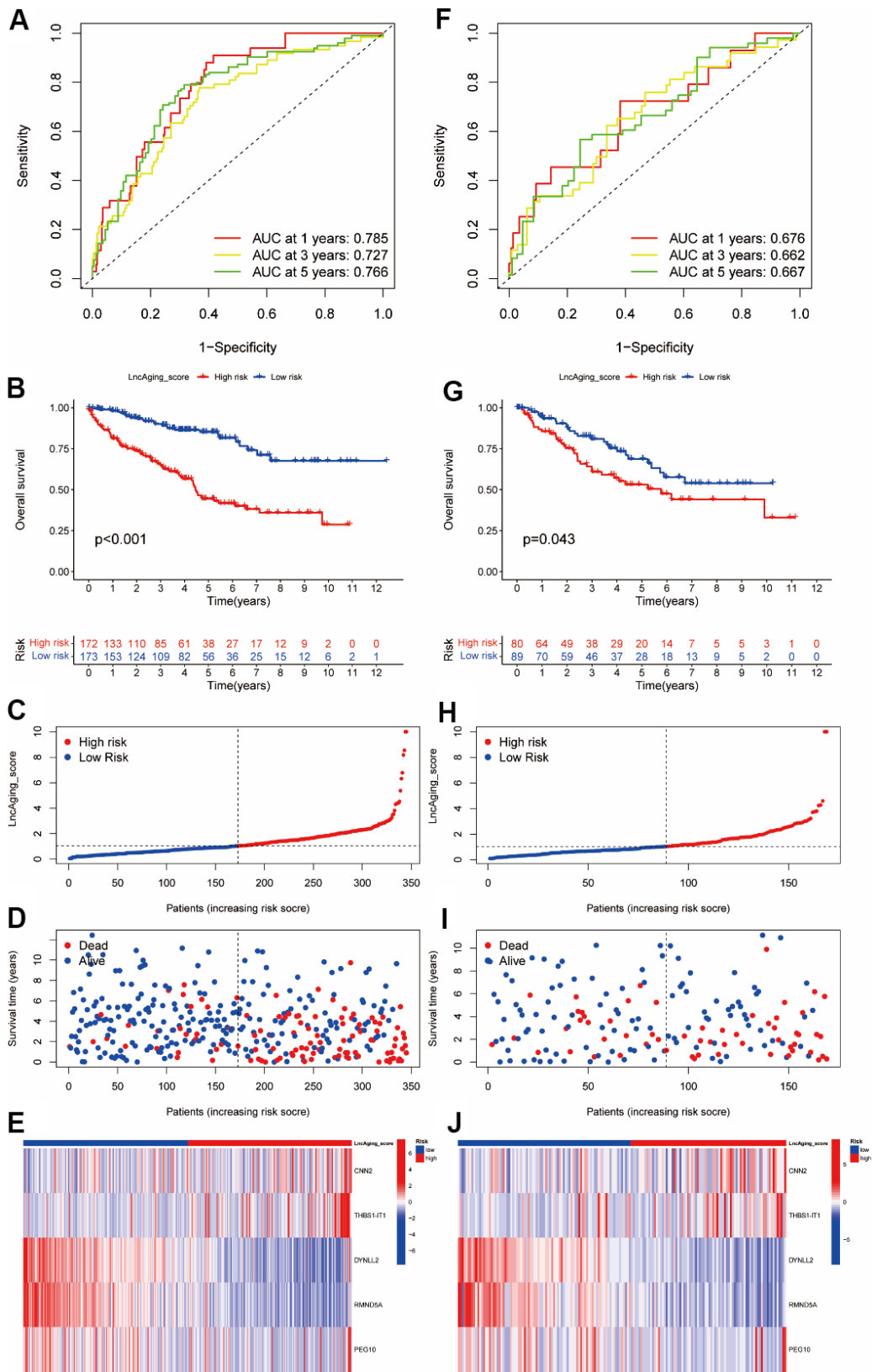**Supplementary Figure 5.** Validation of LncAging_score in training (**A**–**E**) and validation (**F**–**J**) cohort. (**A**, **F**) ROC curves to predict the sensitivity and specificity of 1-, 3-, and 5-year survival according to the LncAging_score. (**B**, **G**) KM analysis of the OS between the two groups. (**C**, **D**, **H**, **I**) The ranked dot plot indicates the LncAging_score distribution and scatter plot presenting the patients' survival status. (**E**, **J**) Expression patterns of 5 selected prognostic genes in high- and low-risk groups.
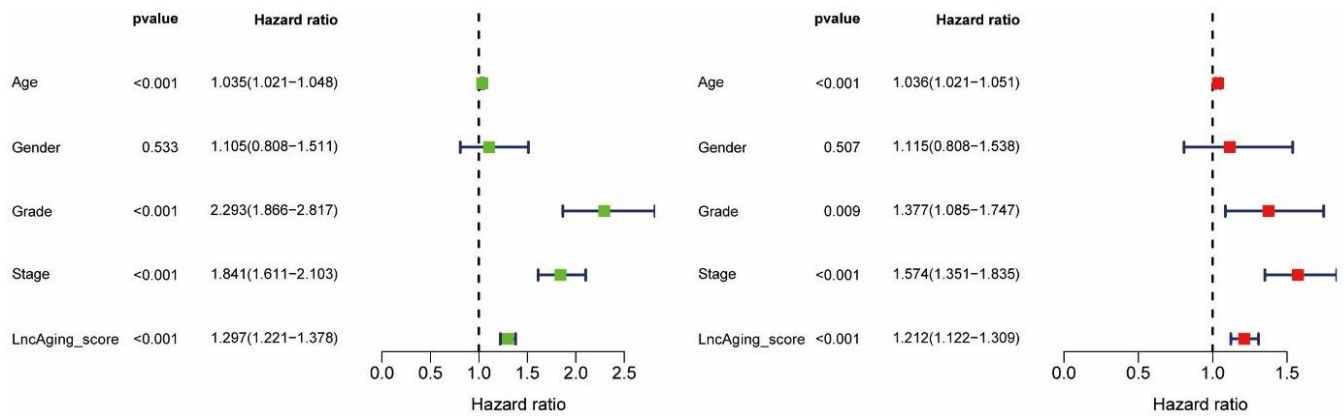
Supplementary Figure 6. The independent prognosis analysis of LncAging_score and clinicopathological variables in KIRC. Univariate (left panel) and multivariate (right panel) analyses showed the prognostic value of the LncAging_score in the entire cohort.
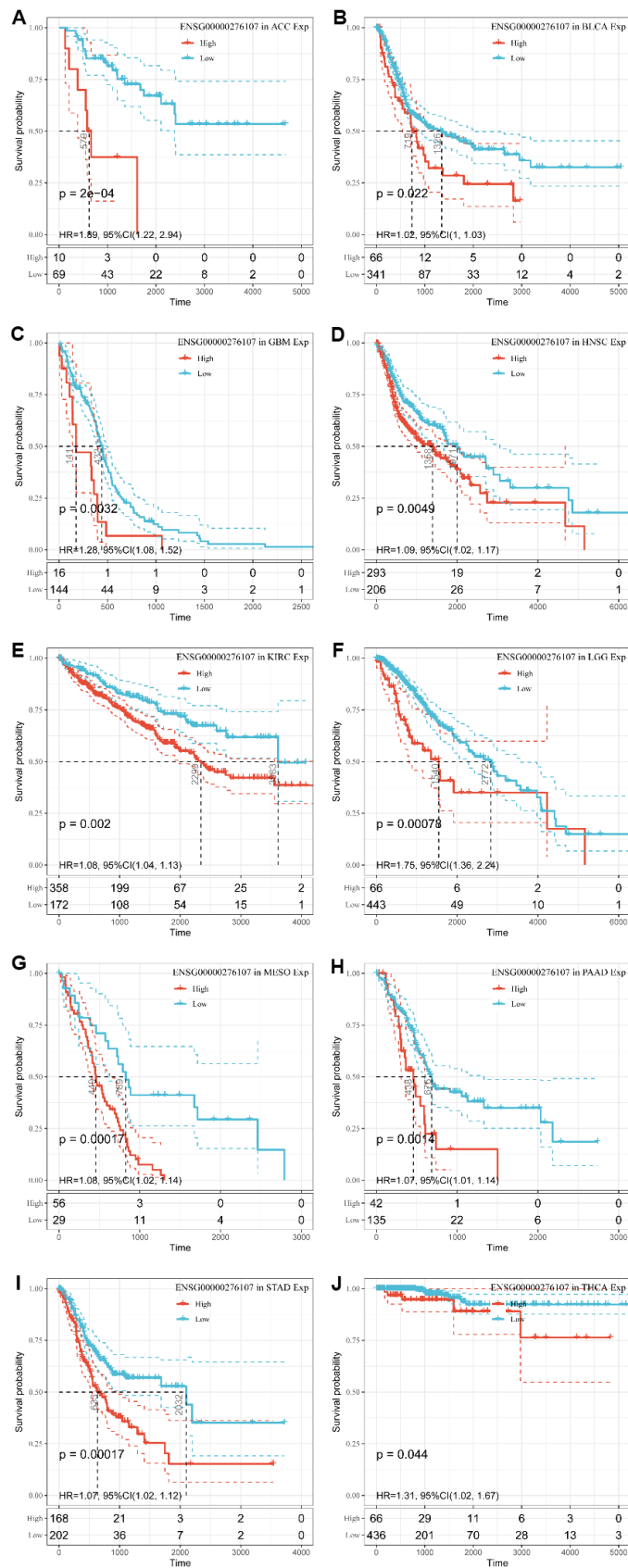
Supplementary Figure 7. Kaplan-Meier analysis of the association between *THBS1-IT1* (ensemble ID: ENSG00000276107) expression and OS. (**A**) ACC; (**B**) BLCA; (**C**) GBM; (**D**) HNSC; (**E**) KIRC; (**F**) LGG; (**G**) MESO; (**H**) PAAD; (**I**) STAD; (**J**) THCA.

	HR	P Value
ACC	1.92(1.23 ~ 3)	3.9e-03
BLCA	1.02(1.01 ~ 1.04)	5.5e-03
BRCA	1(0.98 ~ 1.01)	9.6e-01
CESC	0.97(0.85 ~ 1.1)	6.6e-01
CHOL	0.95(0.78 ~ 1.14)	5.7e-01
COAD	0.98(0.91 ~ 1.05)	5.7e-01
DLBC	1.44(0.35 ~ 5.87)	6.1e-01
ESCA	1.05(0.96 ~ 1.15)	3.0e-01
GBM	1.3(1.09 ~ 1.54)	3.0e-03
HNSC	1.12(1.04 ~ 1.22)	3.5e-03
KICH	0.5(0.01 ~ 21.72)	7.2e-01
KIRC	1.09(1.04 ~ 1.15)	4.5e-04
KIRP	1.09(0.88 ~ 1.37)	4.3e-01
LAML	NA(NA ~ NA)	
LGG	1.75(1.37 ~ 2.25)	1.1e-05
LIHC	1.05(0.96 ~ 1.14)	2.7e-01
LUAD	1(0.99 ~ 1)	6.1e-01
LUSC	1.03(0.99 ~ 1.07)	1.5e-01
MESO	1.07(0.98 ~ 1.16)	1.4e-01
OV	1.05(1 ~ 1.12)	7.2e-02
PAAD	1.09(1.02 ~ 1.16)	1.2e-02
PCPG	0.45(0.04 ~ 4.8)	5.1e-01
PRAD	0.99(0.74 ~ 1.34)	9.7e-01
READ	0.67(0.4 ~ 1.14)	1.4e-01
SARC	1.02(0.98 ~ 1.06)	3.9e-01
SKCM	1.01(0.94 ~ 1.09)	8.0e-01
STAD	1.06(1 ~ 1.13)	5.8e-02
TGCT	0.04(0 ~ 14.9)	2.8e-01
THCA	1.26(0.89 ~ 1.79)	1.9e-01
THYM	1.01(0.3 ~ 3.42)	9.9e-01
UCEC	1(0.97 ~ 1.03)	8.0e-01
UCS	1(0.98 ~ 1.03)	6.7e-01
UVM	22.85(0.47 ~ 1108.54)	1.1e-01

Supplementary Figure 8. Forest plot of association of *THBS1-IT1* with disease-specific survival (DSS) for 33 types of tumors.
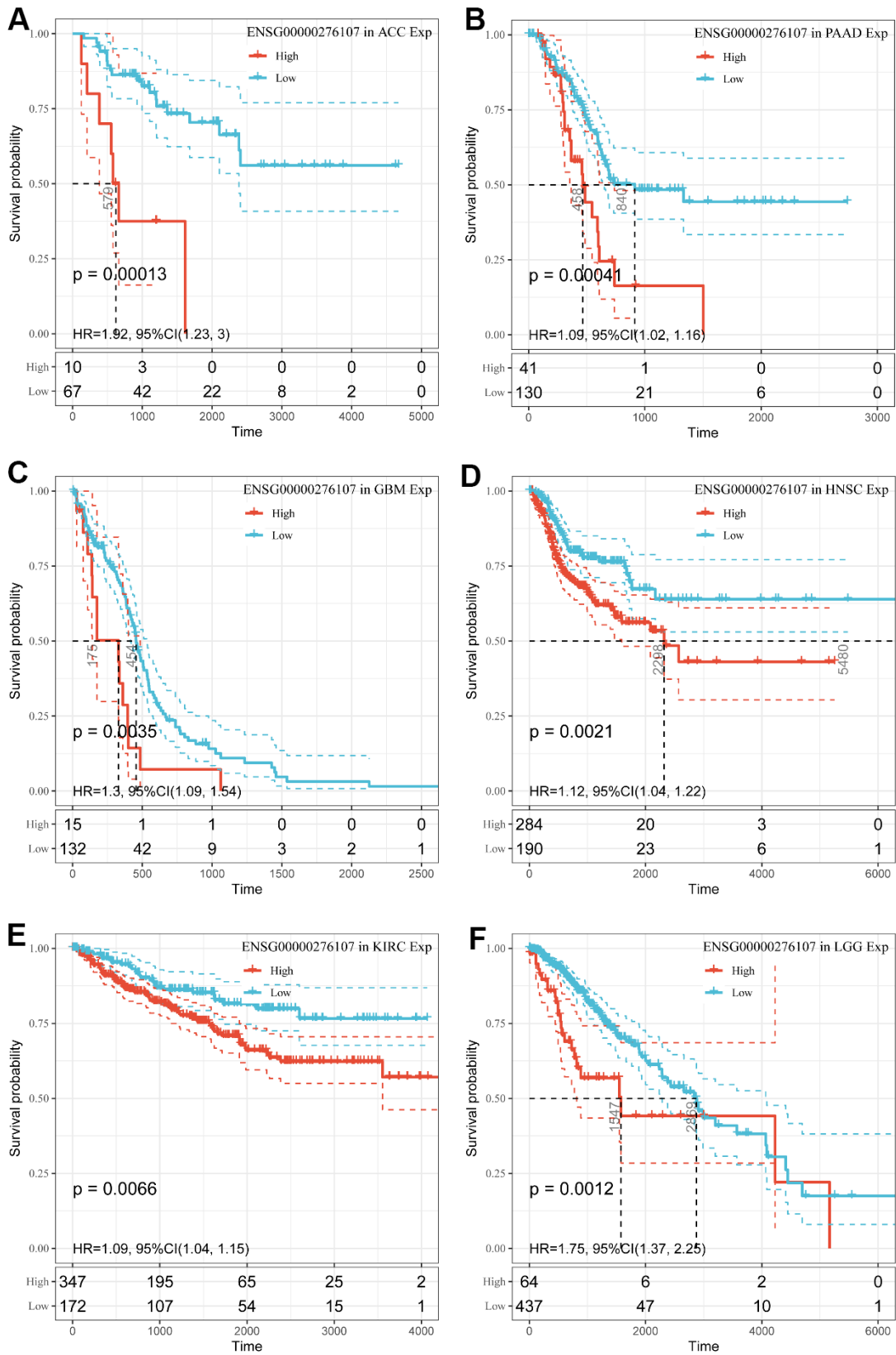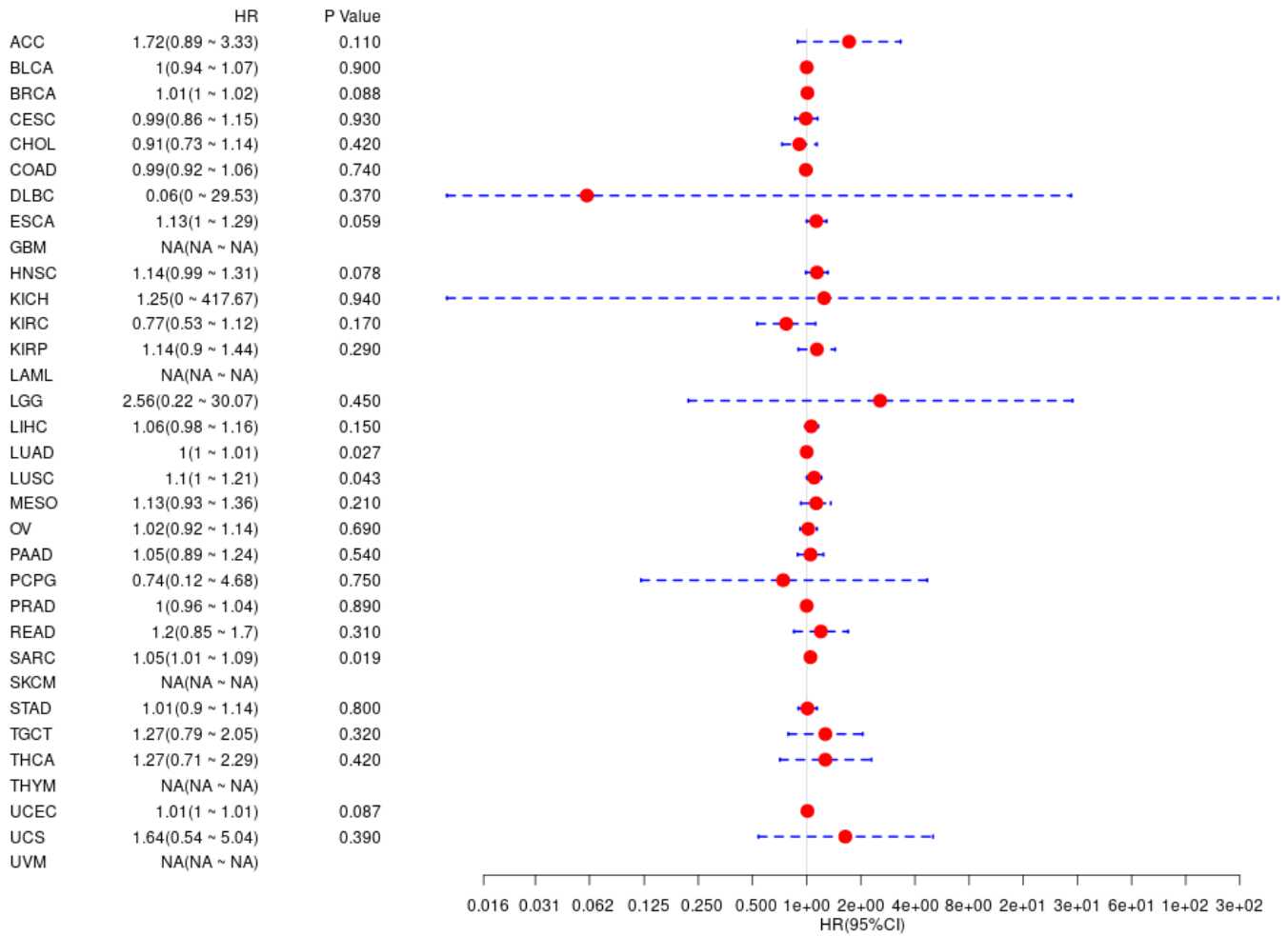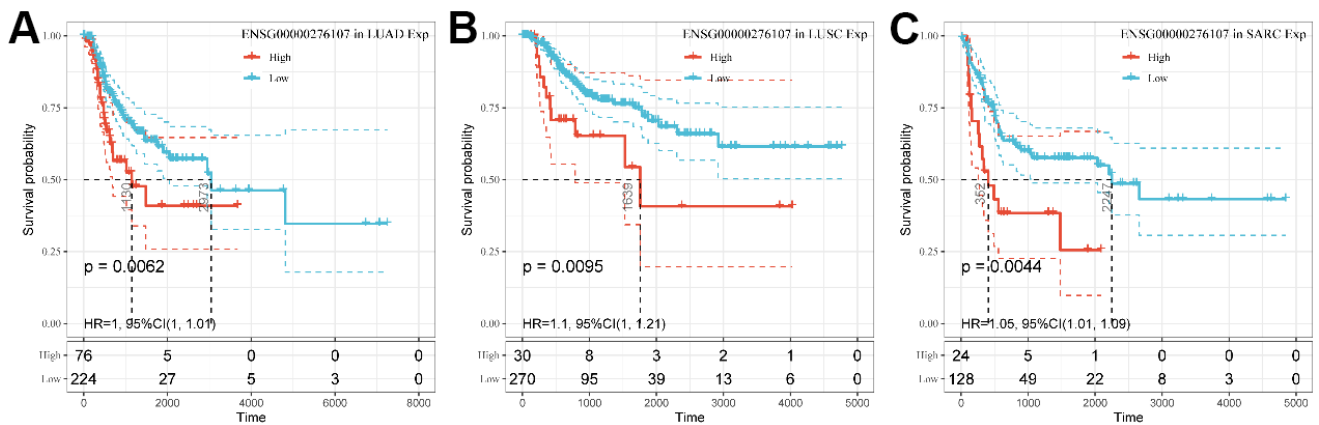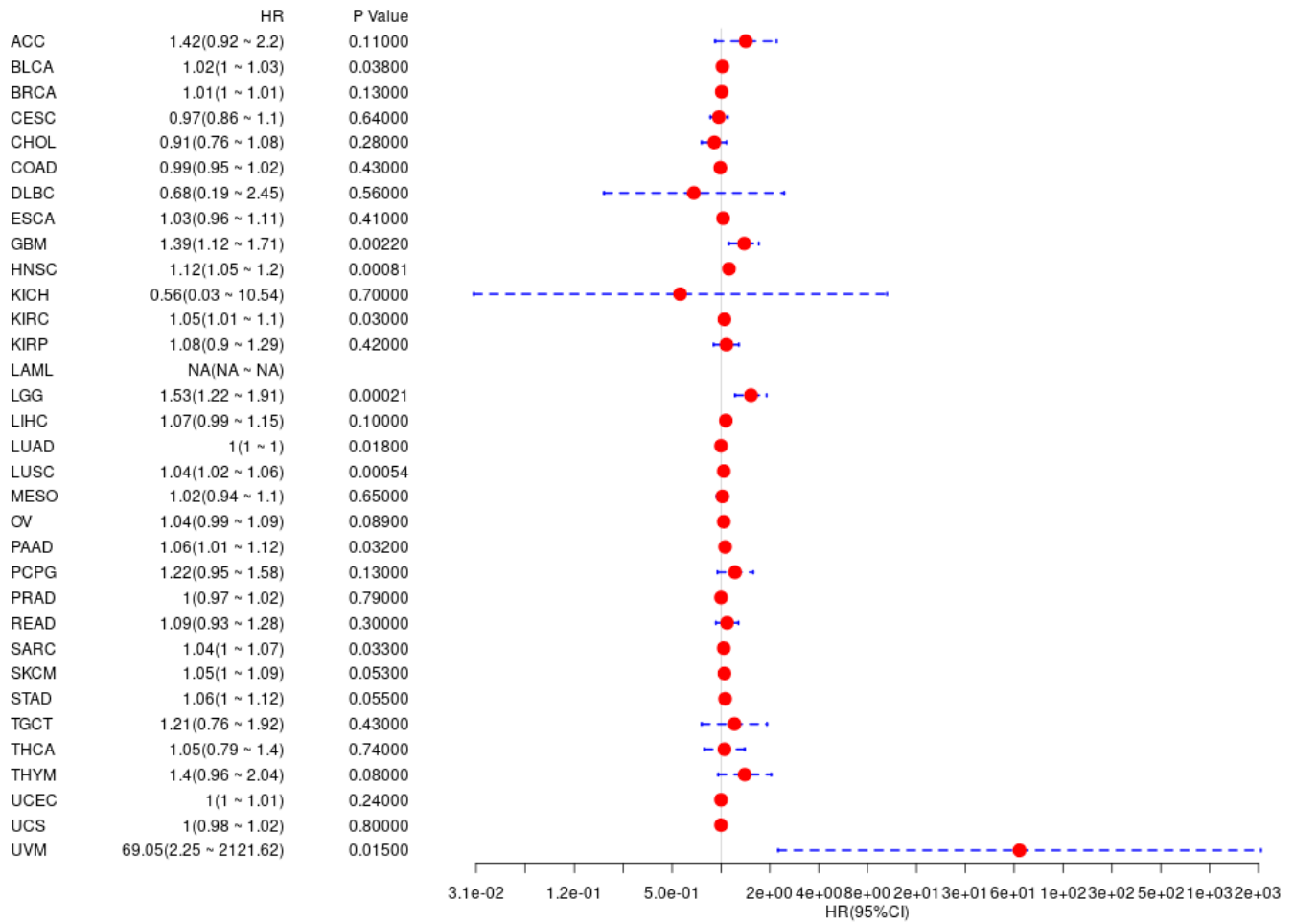
Supplementary Figure 9. Kaplan-Meier analysis of the association between *THBS1-IT1* (ensemble ID: ENSG00000276107) expression and DSS. (**A**) ACC; (**B**) PAAD; (**C**) GBM; (**D**) HNSC; (**E**) KIRC; (**F**) LGG.

|	HR	P Value
ACC	1.72(0.89 ~ 3.33)	0.110
BLCA	1(0.94 ~ 1.07)	0.900
BRCA	1.01(1 ~ 1.02)	0.088
CESC	0.99(0.86 ~ 1.15)	0.930
CHOL	0.91(0.73 ~ 1.14)	0.420
COAD	0.99(0.92 ~ 1.06)	0.740
DLBC	0.06(0 ~ 29.53)	0.370
ESCA	1.13(1 ~ 1.29)	0.059
GBM	NA(NA ~ NA)	
HNSC	1.14(0.99 ~ 1.31)	0.078
KICH	1.25(0 ~ 417.67)	0.940
KIRC	0.77(0.53 ~ 1.12)	0.170
KIRP	1.14(0.9 ~ 1.44)	0.290
LAML	NA(NA ~ NA)	
LGG	2.56(0.22 ~ 30.07)	0.450
LIHC	1.06(0.98 ~ 1.16)	0.150
LUAD	1(1 ~ 1.01)	0.027
LUSC	1.1(1 ~ 1.21)	0.043
MESO	1.13(0.93 ~ 1.36)	0.210
OV	1.02(0.92 ~ 1.14)	0.690
PAAD	1.05(0.89 ~ 1.24)	0.540
PCPG	0.74(0.12 ~ 4.68)	0.750
PRAD	1(0.96 ~ 1.04)	0.890
READ	1.2(0.85 ~ 1.7)	0.310
SARC	1.05(1.01 ~ 1.09)	0.019
SKCM	NA(NA ~ NA)	
STAD	1.01(0.9 ~ 1.14)	0.800
TGCT	1.27(0.79 ~ 2.05)	0.320
THCA	1.27(0.71 ~ 2.29)	0.420
THYM	NA(NA ~ NA)	
UCEC	1.01(1 ~ 1.01)	0.087
UCS	1.64(0.54 ~ 5.04)	0.390
UVM	NA(NA ~ NA)	

Supplementary Figure 10. Forest plot of association of *THBS1-IT1* with disease-free interval (DFI) for 33 types of tumors.


Supplementary Figure 11. Kaplan-Meier analysis of the association between *THBS1-IT1* (ensemble ID: ENSG00000276107) expression and DFI in LUAD (**A**), LUSC (**B**) and SARC (**C**).

|	HR	P Value
ACC	1.42(0.92 ~ 2.2)	0.11000
BLCA	1.02(1 ~ 1.03)	0.03800
BRCA	1.01(1 ~ 1.01)	0.13000
CESC	0.97(0.86 ~ 1.1)	0.64000
CHOL	0.91(0.76 ~ 1.08)	0.28000
COAD	0.99(0.95 ~ 1.02)	0.43000
DLBC	0.68(0.19 ~ 2.45)	0.56000
ESCA	1.03(0.96 ~ 1.11)	0.41000
GBM	1.39(1.12 ~ 1.71)	0.00220
HNSC	1.12(1.05 ~ 1.2)	0.00081
KICH	0.56(0.03 ~ 10.54)	0.70000
KIRC	1.05(1.01 ~ 1.1)	0.03000
KIRP	1.08(0.9 ~ 1.29)	0.42000
LAML	NA(NA ~ NA)	
LGG	1.53(1.22 ~ 1.91)	0.00021
LIHC	1.07(0.99 ~ 1.15)	0.10000
LUAD	1(1 ~ 1)	0.01800
LUSC	1.04(1.02 ~ 1.06)	0.00054
MESO	1.02(0.94 ~ 1.1)	0.65000
OV	1.04(0.99 ~ 1.09)	0.08900
PAAD	1.06(1.01 ~ 1.12)	0.03200
PCPG	1.22(0.95 ~ 1.58)	0.13000
PRAD	1(0.97 ~ 1.02)	0.79000
READ	1.09(0.93 ~ 1.28)	0.30000
SARC	1.04(1 ~ 1.07)	0.03300
SKCM	1.05(1 ~ 1.09)	0.05300
STAD	1.06(1 ~ 1.12)	0.05500
TGCT	1.21(0.76 ~ 1.92)	0.43000
THCA	1.05(0.79 ~ 1.4)	0.74000
THYM	1.4(0.96 ~ 2.04)	0.08000
UCEC	1(1 ~ 1.01)	0.24000
UCS	1(0.98 ~ 1.02)	0.80000
UVM	69.05(2.25 ~ 2121.62)	0.01500

Supplementary Figure 12. Forest plot of association of *THBS1-IT1* with progression-free interval (PFI) for 33 types of tumors.
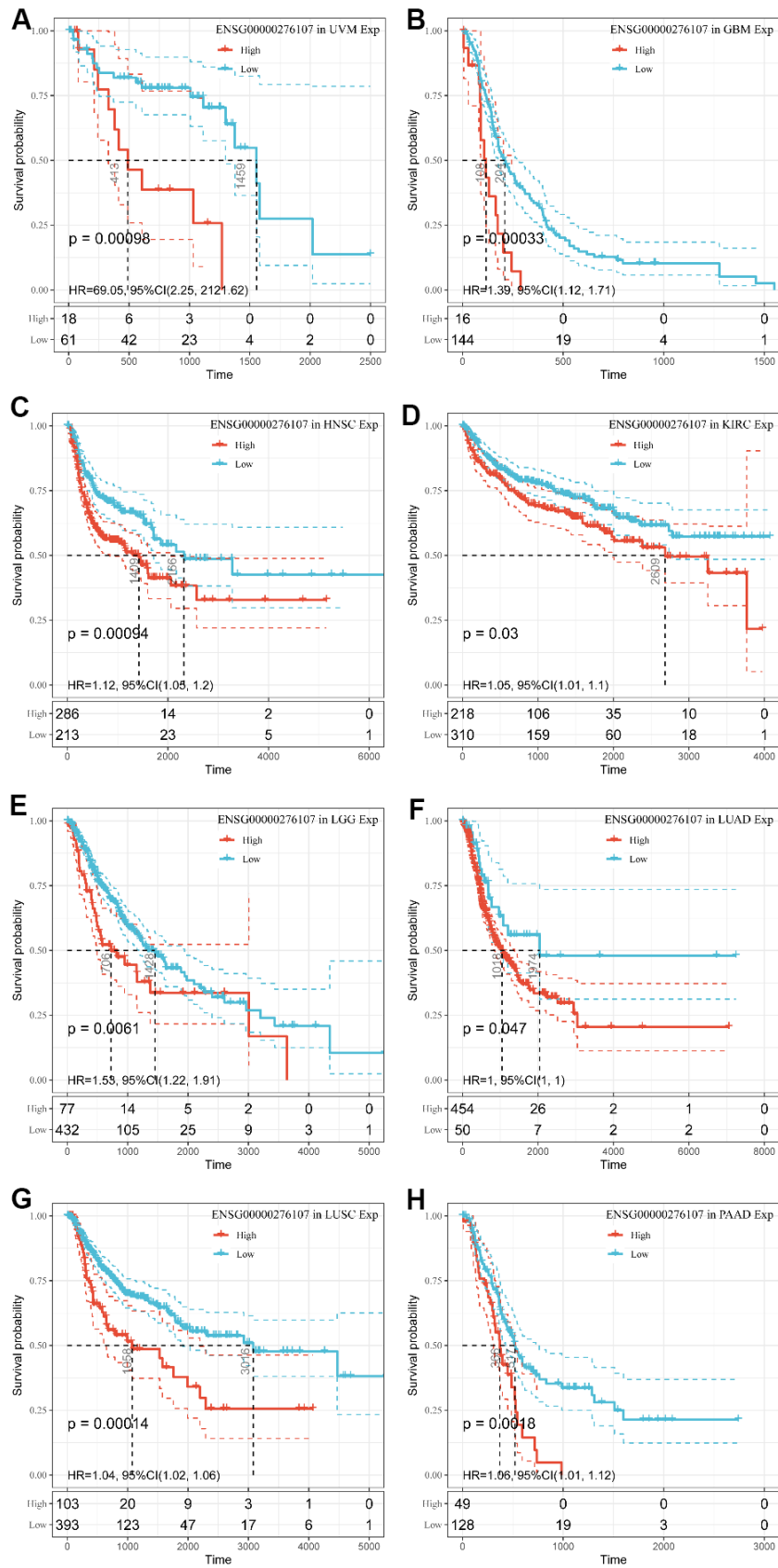
Supplementary Figure 13. Kaplan-Meier analysis of the association between *THBS1-IT1* (ensemble ID: ENSG00000276107) expression and PFI. (**A**) UVM; (**B**) GBM; (**C**) HNSC; (**D**) KIRC; (**E**) LGG; (**F**) LUAD; (**G**) LUSC; (**H**) PAAD.
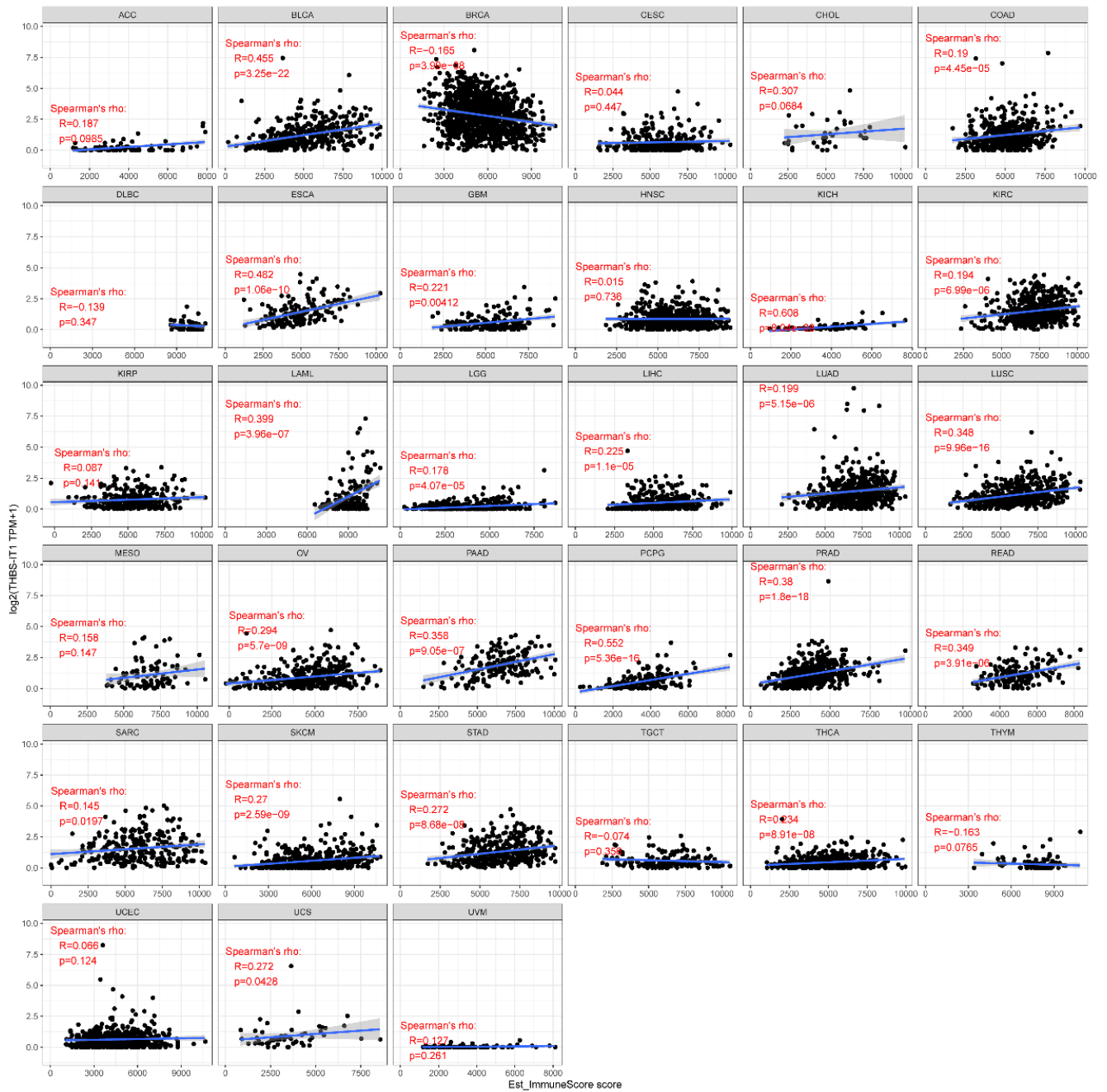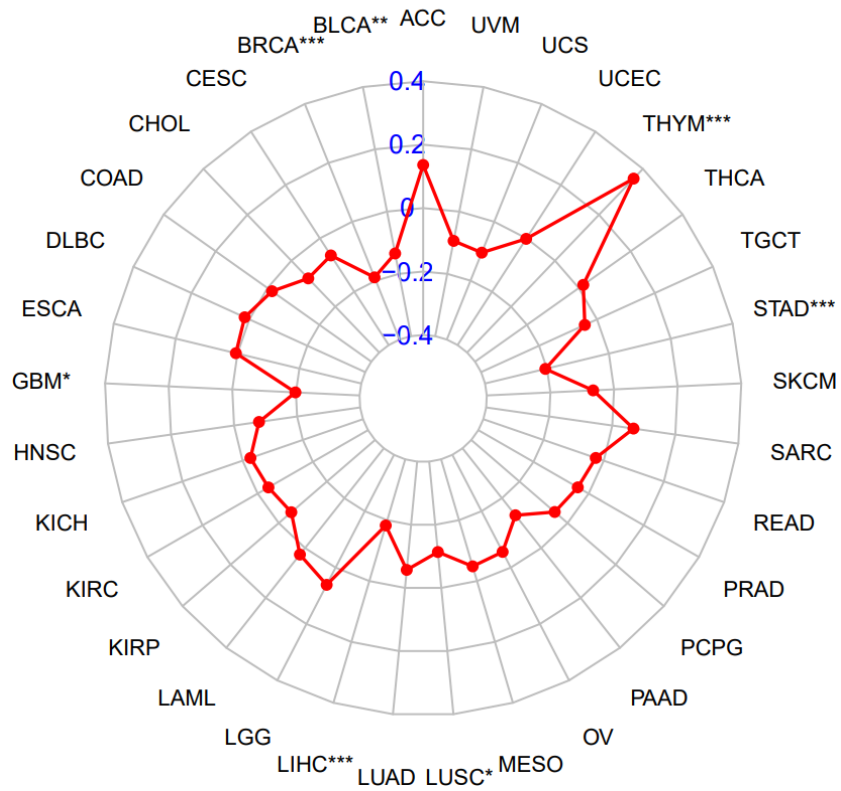
Supplementary Figure 14. Correlation between *THBS1-IT1* expression and immune scores in 33 types of tumors.
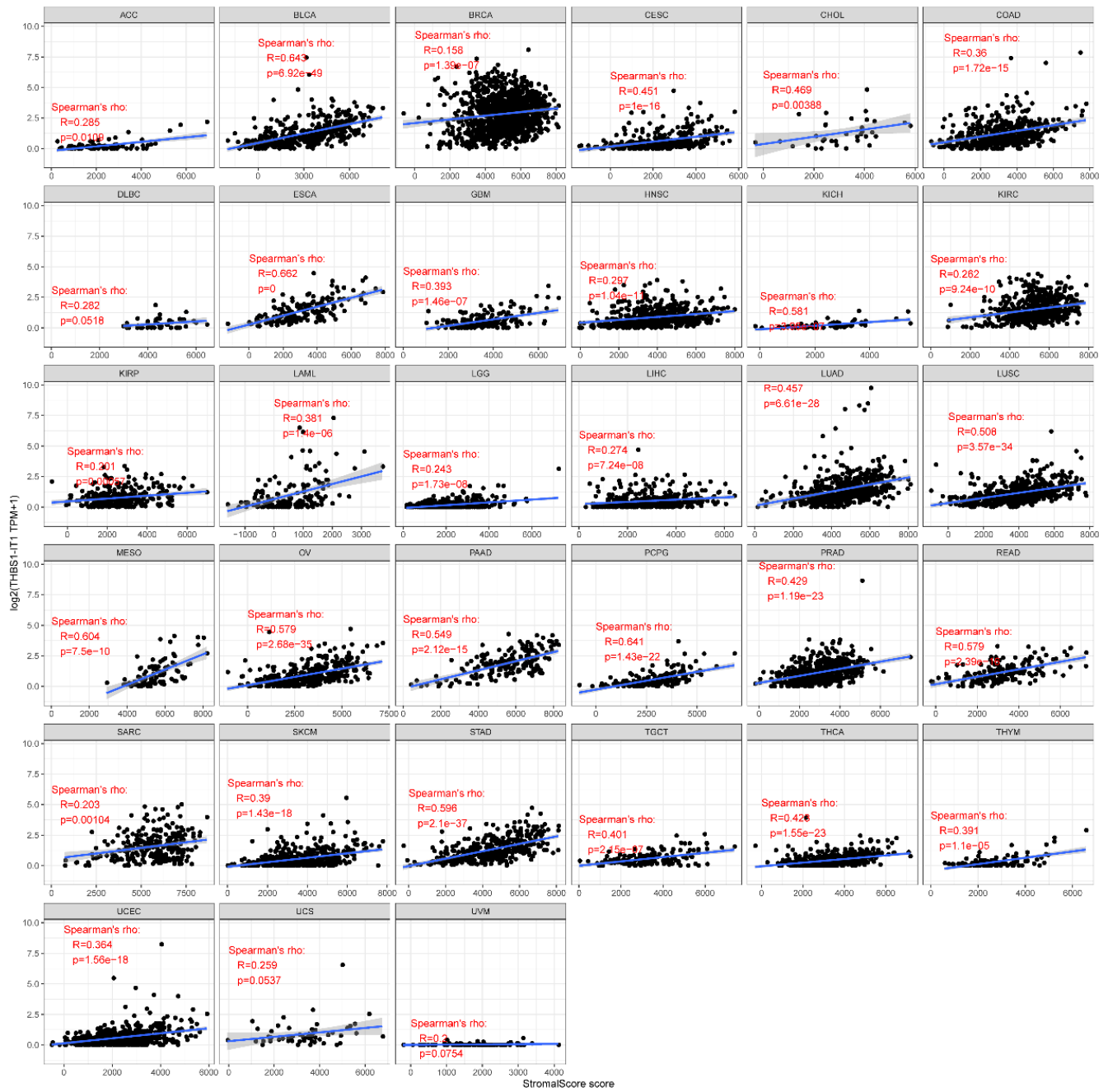
Supplementary Figure 15. Correlation between *THBS1-IT1* expression and stromal scores in 33 types of tumors.
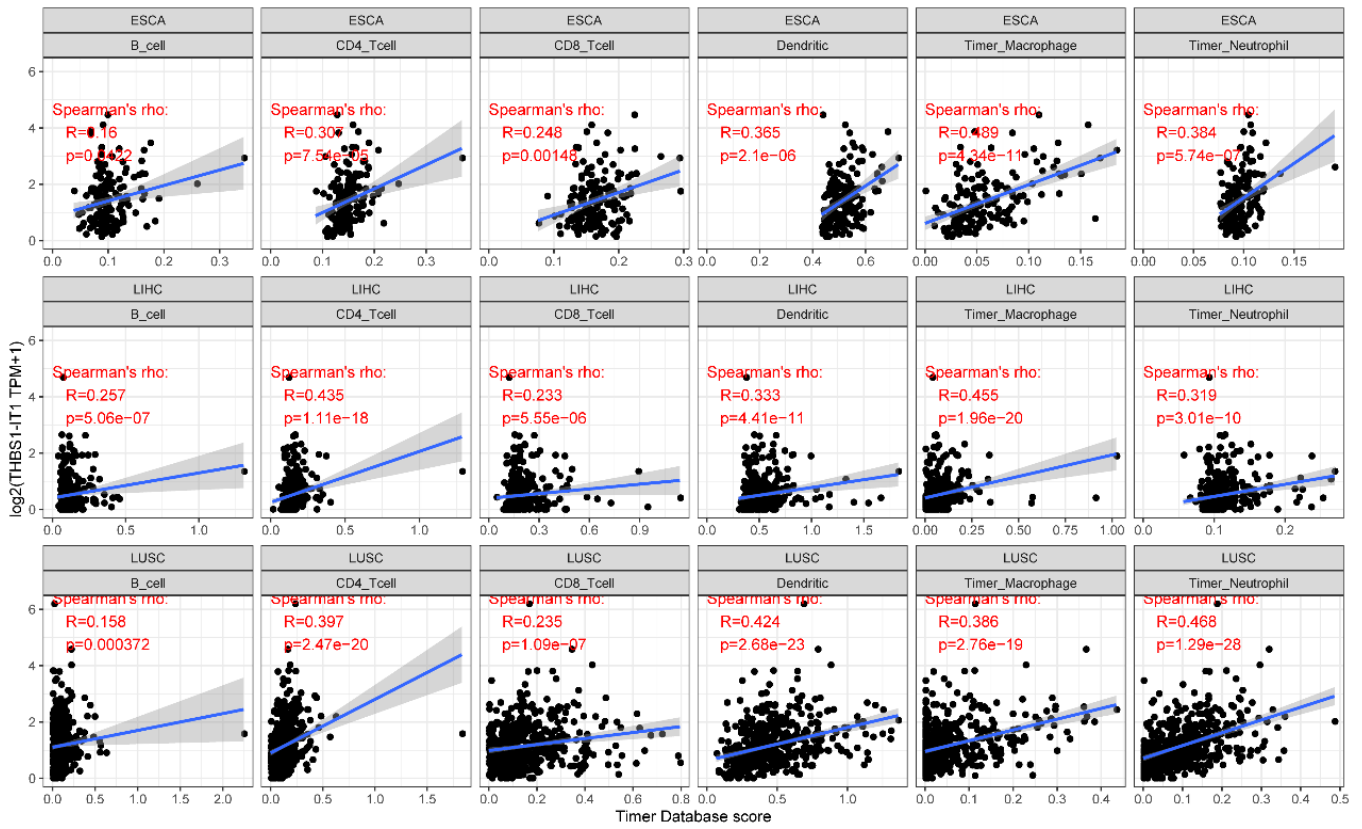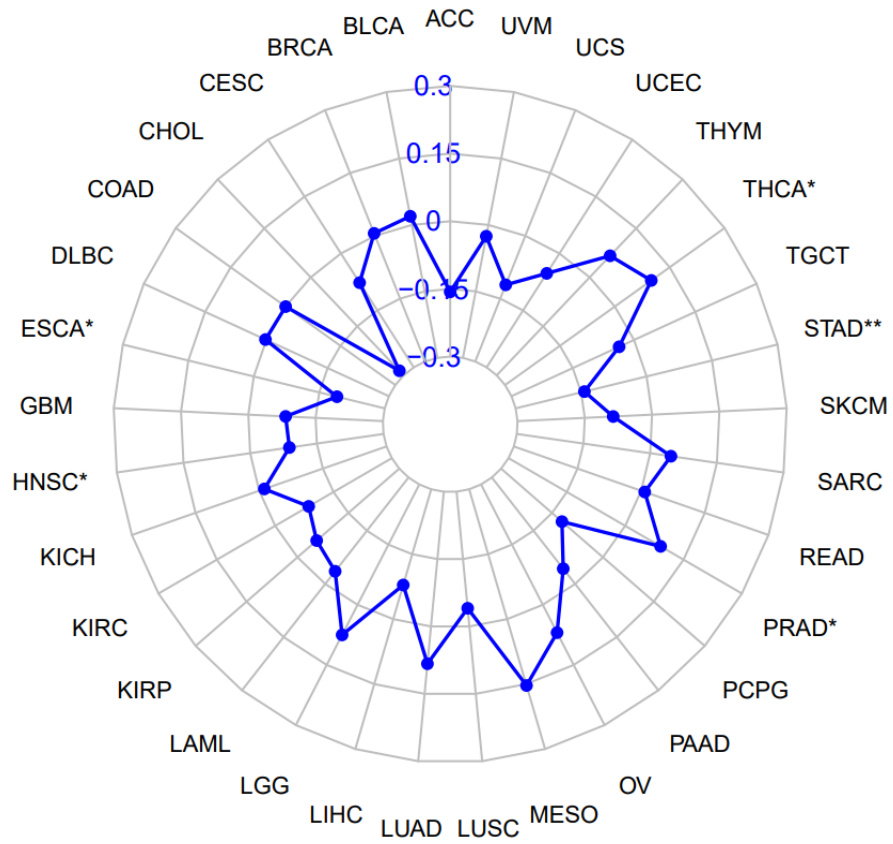
Supplementary Figure 16. Correlation between TREM2 expression and immune cell infiltration in ESCA, LIHC and LUSC.

Tumor mutation burden

Supplementary Figure 17. Associations between *THBS1-IT1* expression and tumor mutational burden (TMB). The correlation coefficient *p < 0.05, **p < 0.01, and ***p < 0.001.

Microsatellite instability

Supplementary Figure 18. Associations between *THBS1-IT1* expression and microsatellite instability (MSI). The correlation coefficient *p < 0.05, **p < 0.01, and ***p < 0.001.