Figure S1 Heatmap of TME-related radiomics features. Heatmap showing the 100 TME-related radiomics features selected by non-parametric Spearman correlation analysis with ImmuneScore and StromalScore (P<0.05). TME, tumor microenvironment.
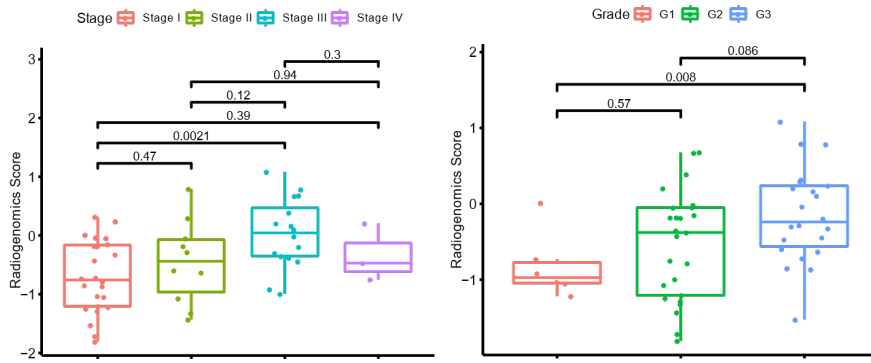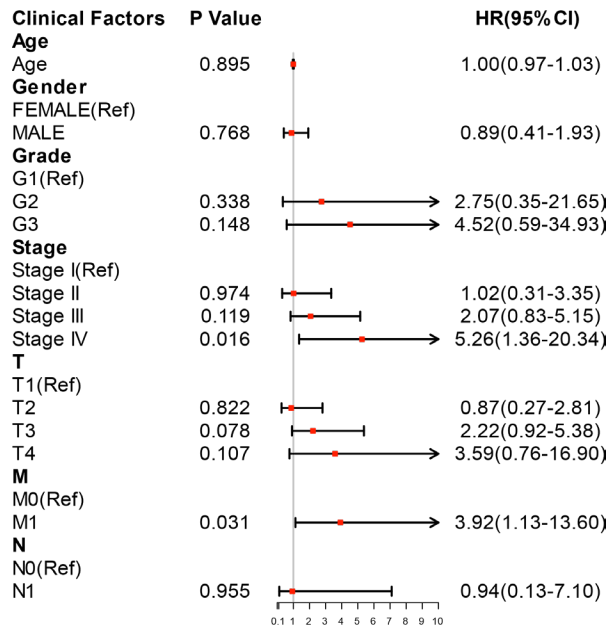

Figure S2 Analysis of correlation between radiogenomics score and clinical characteristics. Box-plots showing significant difference in the radiogenomics score between stage I and stage III (left), and between grade 1 and grade 3 (right). The differences were compared through the Wilcoxon test.
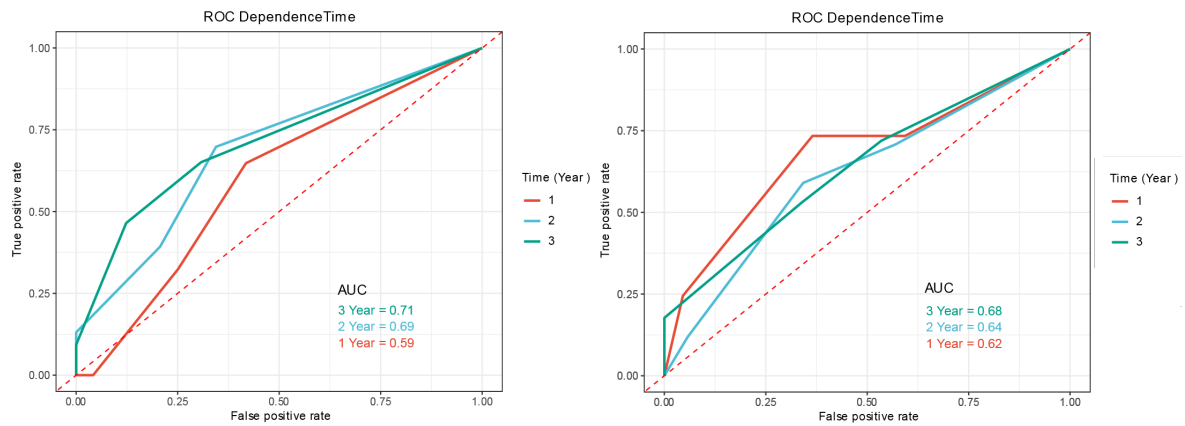

Clinical Factors	P Value		HR(95%CI)
Age			
Age	0.895		1.00(0.97-1.03)
Gender			
FEMALE(Ref)			
MALE	0.768		0.89(0.41-1.93)
Grade			
G1(Ref)			
G2	0.338		2.75(0.35-21.65)
G3	0.148		4.52(0.59-34.93)
Stage			
Stage I(Ref)			
Stage II	0.974		1.02(0.31-3.35)
Stage III	0.119		2.07(0.83-5.15)
Stage IV	0.016		5.26(1.36-20.34)
T			
T1(Ref)			
T2	0.822		0.87(0.27-2.81)
T3	0.078		2.22(0.92-5.38)
T4	0.107		3.59(0.76-16.90)
M			
M0(Ref)			
M1	0.031		3.92(1.13-13.60)
N			
N0(Ref)			
N1	0.955		0.94(0.13-7.10)

Figure S3 Multivariate Cox regression analysis for clinical factors. To evaluate the independent prediction performance of the clinical factors, multivariate Cox regression analyses were conducted on the TCGA-HCC cohort (n=365) and demonstrated that TNM staging was independent risk factor. ROC curves were plotted based on TNM staging in the training cohort (left) the test cohort (right). TCGA, The Cancer Genome Atlas; HCC, hepatocellular carcinoma; ROC, receiver operating characteristic; AUC, area under the curve.
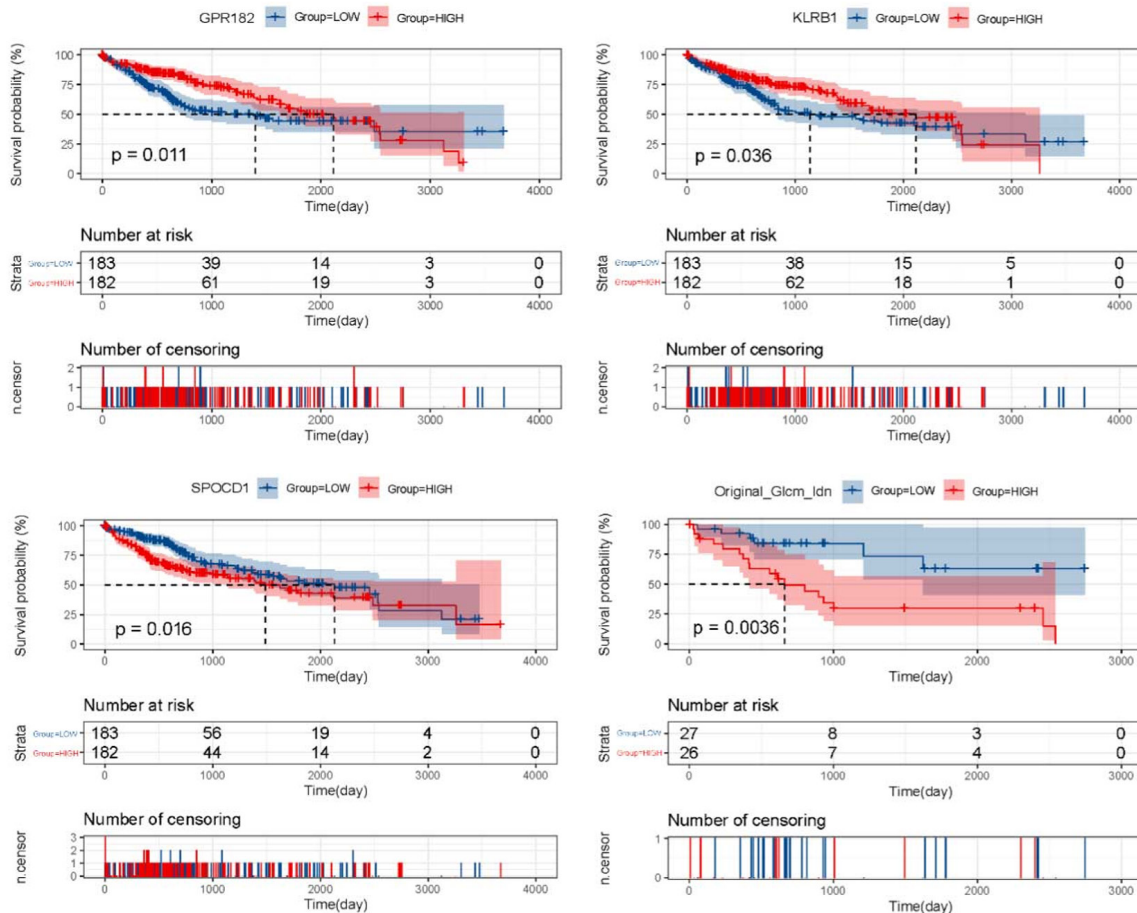

Figure S4 Survival analysis of four radiogenomics predictors. Survival analysis using the Kaplan-Meier method according to high (above the median) and low (below the median) expression of 3 genes (*GPR182*, *KLRB1*, and *SPOCD1*) in TCGA-HCC cohort and value of a radiomics feature (Original_Glcm_Idn) in TCIA-HCC cohort. TCGA, The Cancer Genome Atlas; HCC, hepatocellular carcinoma; TCIA, The Cancer Imaging Archive.
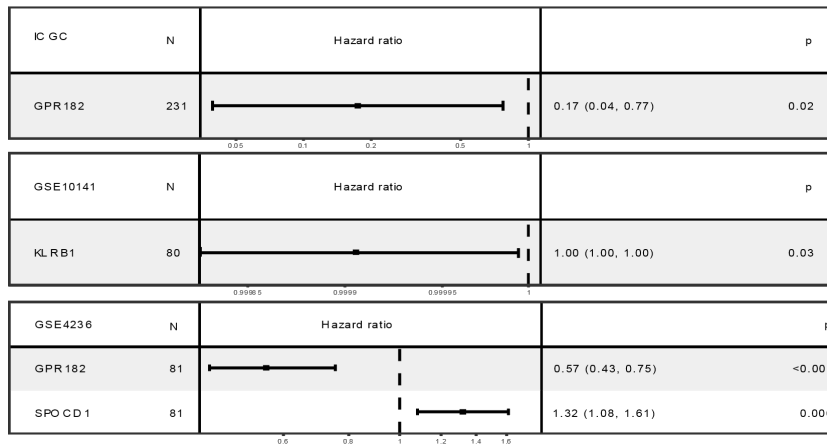
ICGC	N	Hazard ratio		p
GPR182	231			0.17 (0.04, 0.77) 0.02

GSE10141	N	Hazard ratio		p
KLRB1	80			1.00 (1.00, 1.00) 0.03

GSE4236	N	Hazard ratio		p
GPR182	81			0.57 (0.43, 0.75) <0.001
SPOCD1	81			1.32 (1.08, 1.61) 0.006

Figure S5 Verification of prognostic genes of the model in other three test sets. Three prognostic genes of the model were further validated by other three sets of validation datasets (ICGC, GSE10141 and GSE4236).
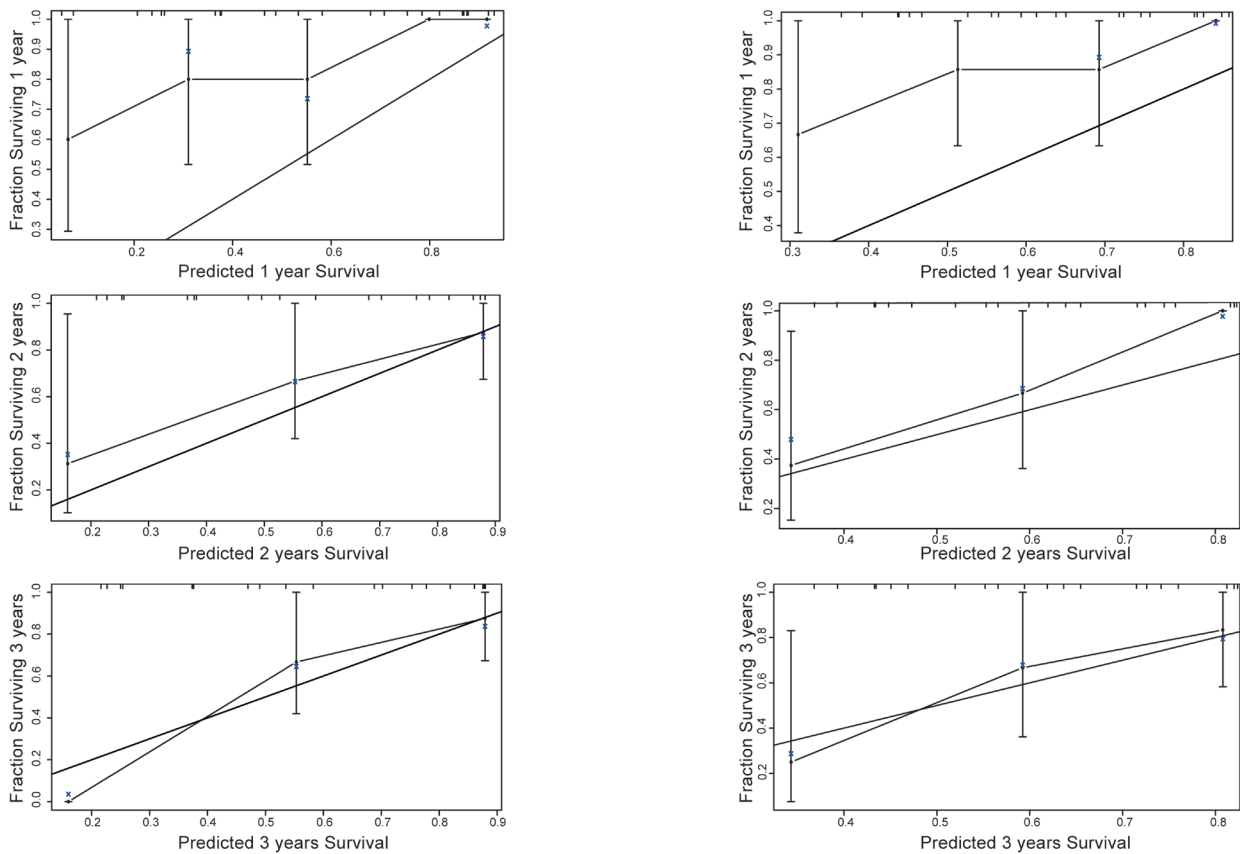

Figure S6 Calibration curve of prediction model in training set and test set. The 1-, 2- and 3-year calibration plots of prediction model in the training cohort (left) the test cohort (right). (Cmethod="KM", Method="boot", B=100, Hosmer-Lemeshow test: P>0.05).
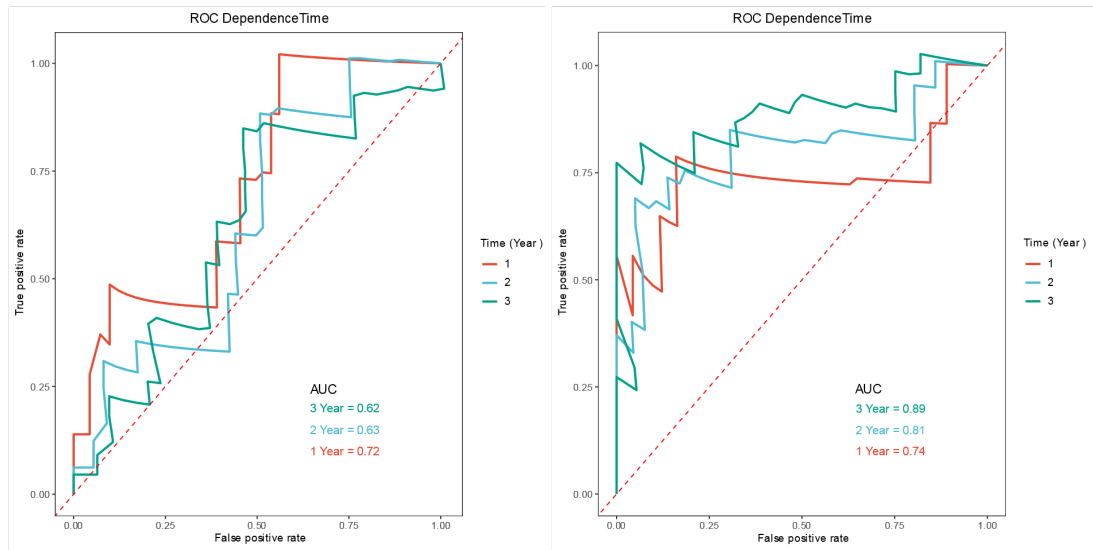
Figure S7 Based on the entire dataset (TCIA-HCC, n=53), ROC curves of 3-gene classifier (left) and 1 radiomics feature (original_glcm_Idn) (right) in the radiogenomics model for prognosis prediction. TCIA, The Cancer Imaging Archive; HCC, hepatocellular carcinoma; ROC, receiver operating characteristic; AUC, area under the curve.
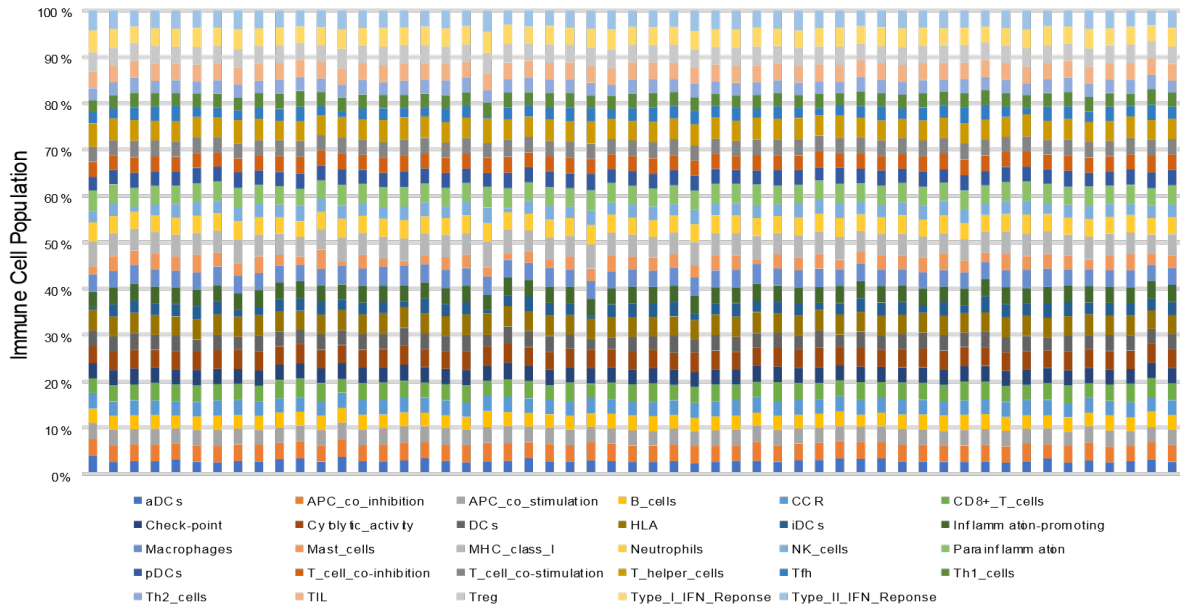

Figure S8 Proportion of tumor-infiltrating immune cells in TCIA-HCC cohort. Barplot showing the proportion of 29 kinds of tumor-infiltrating immune cells in TCIA-HCC cohort. TCIA, The Cancer Imaging Archive; HCC, hepatocellular carcinoma
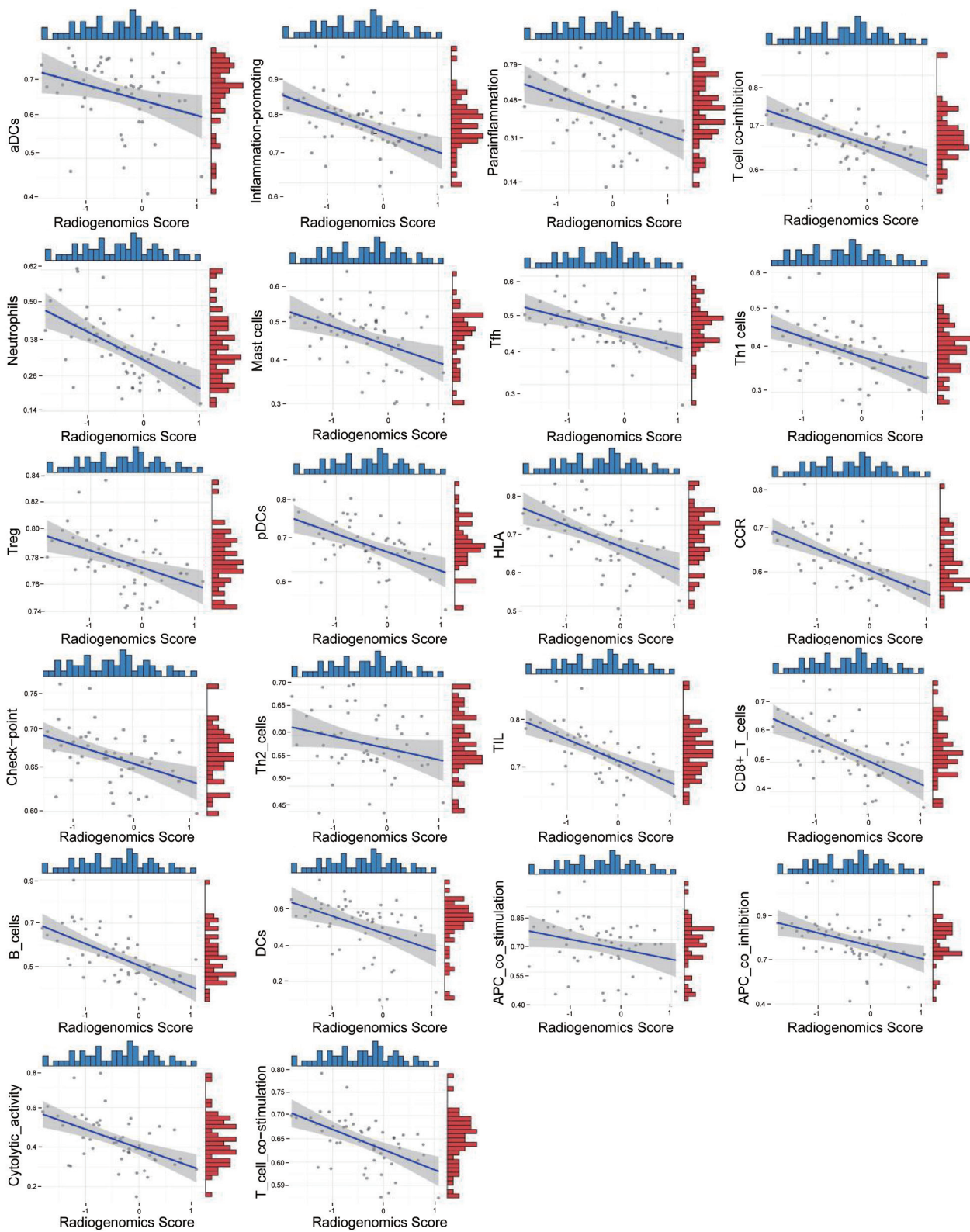
Figure S9 Analysis of correlation between radiogenomics score and tumor-infiltrating immune cells. Scatter plot showed the correlation of 22 kinds of tumor-infiltrating immune cells with the radiogenomics score and Spearman coefficient was used for the correlation test.