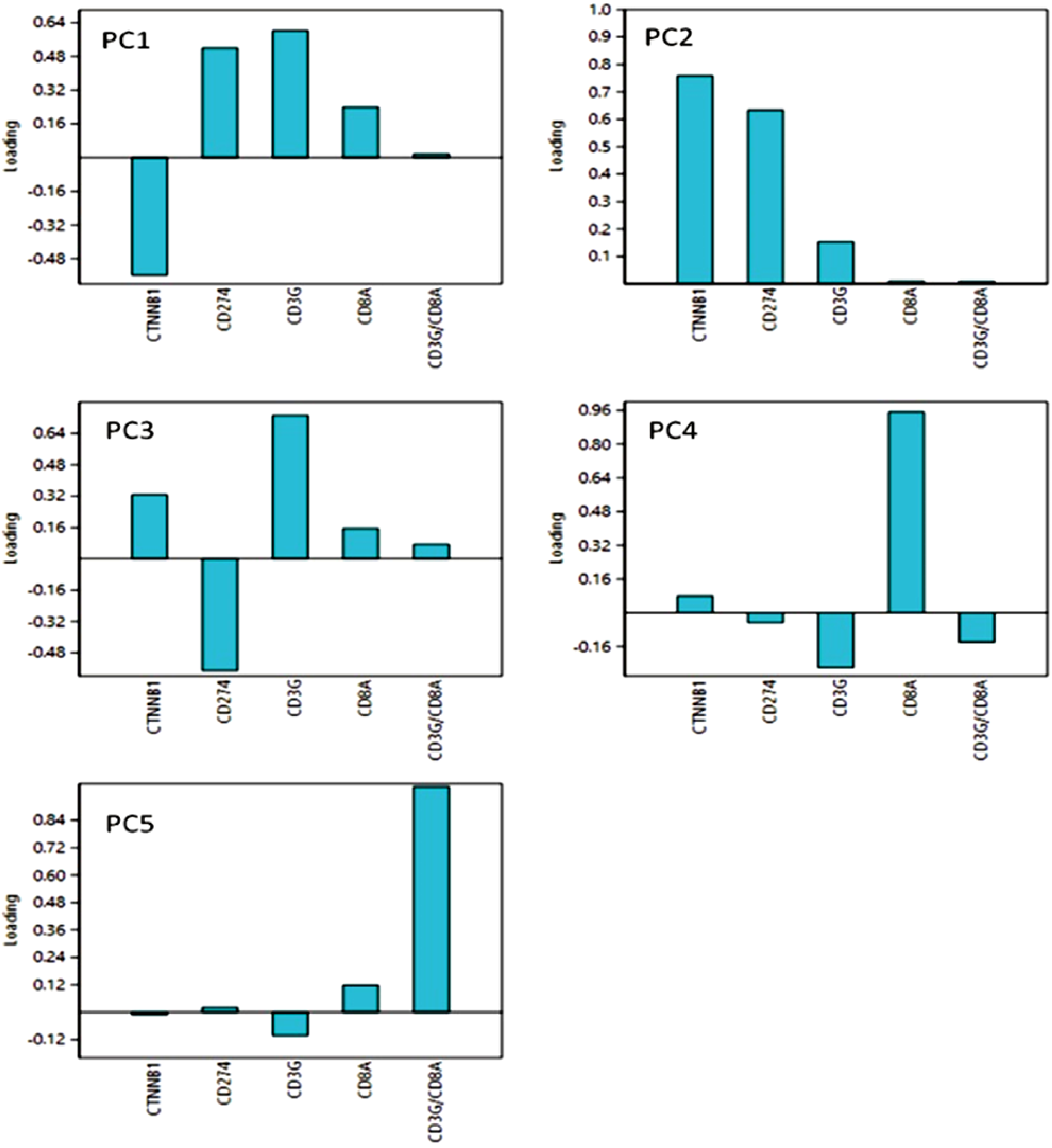
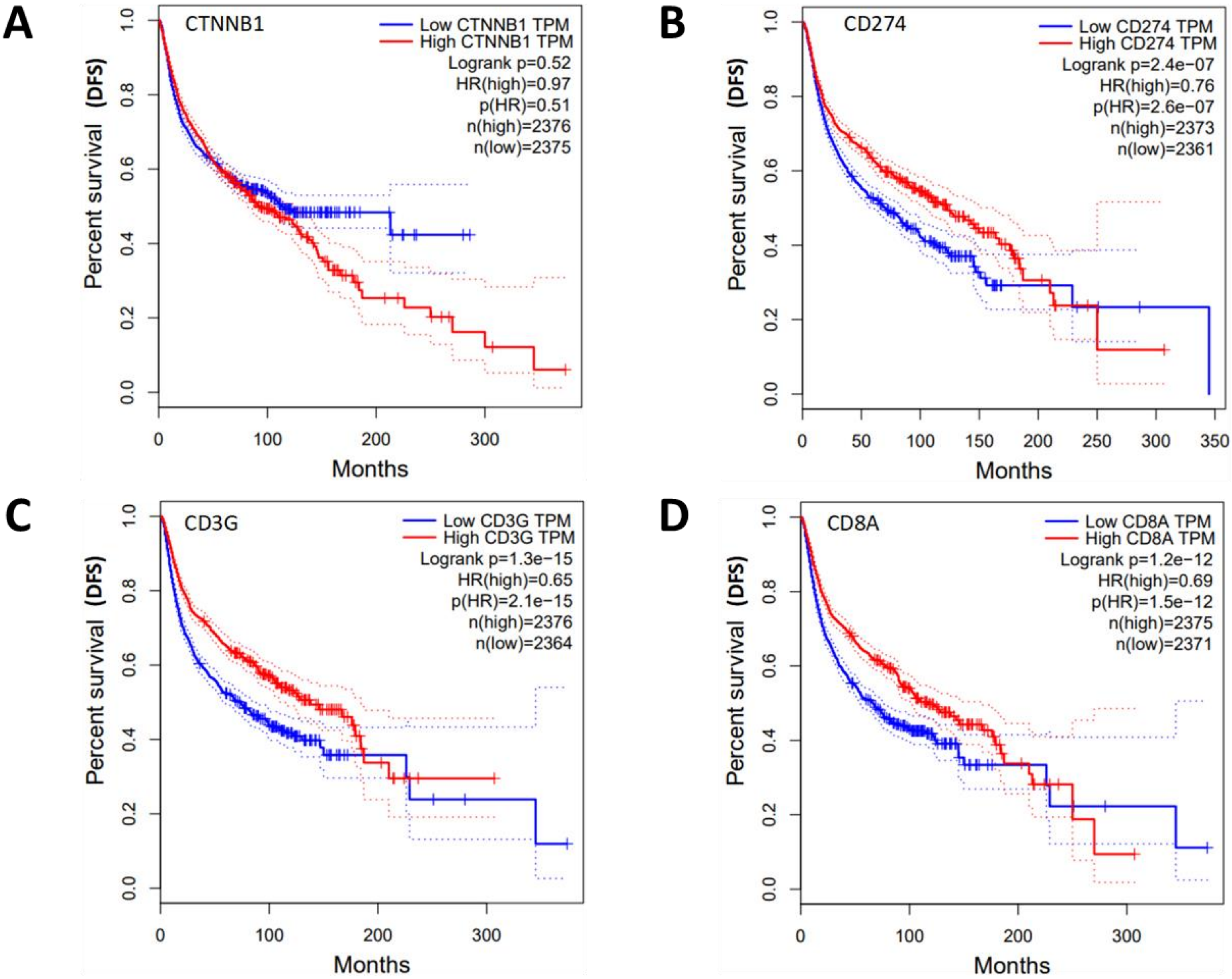
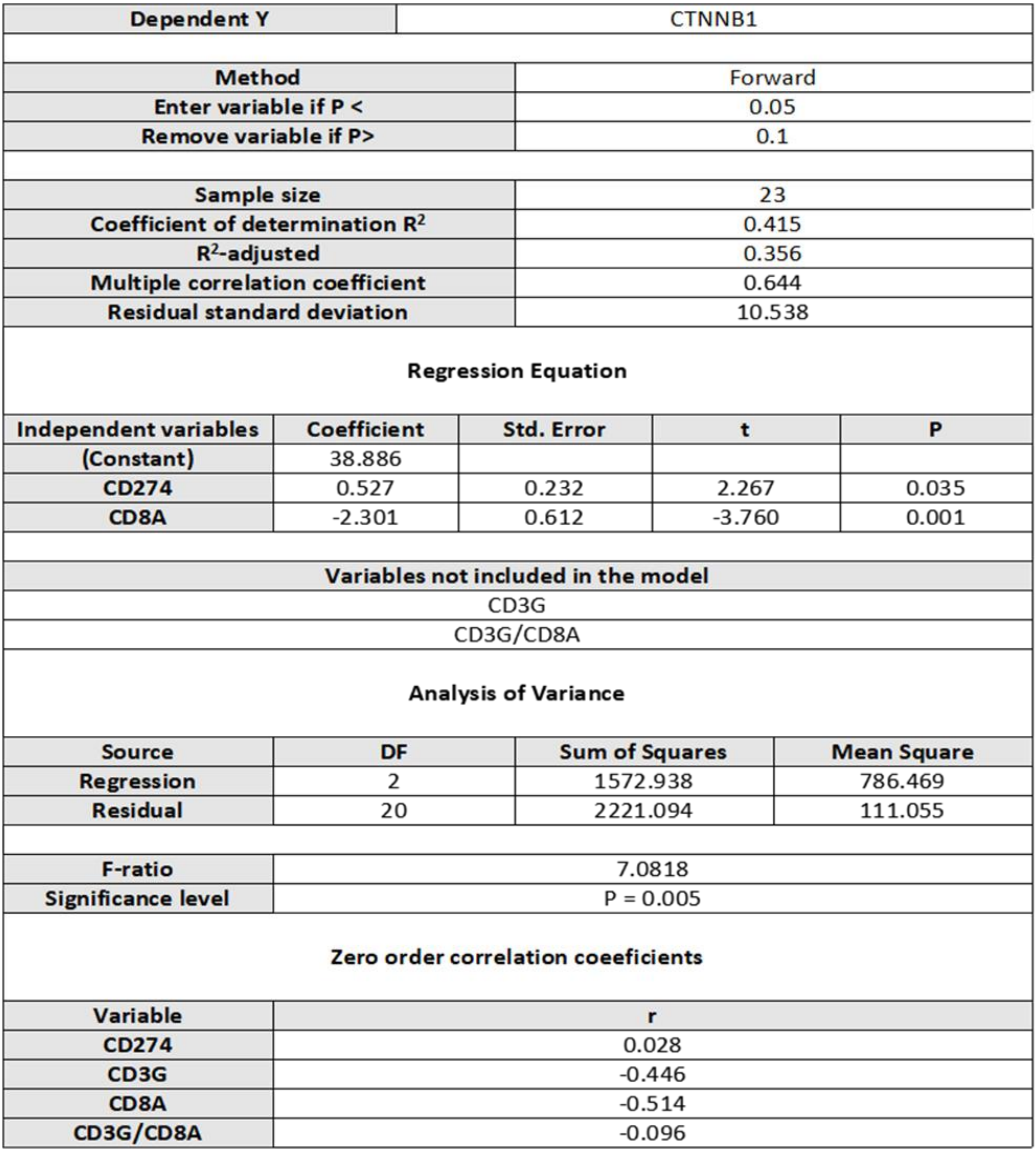


Supplementary Figure S1



Supplementary Figure S2

Supplementary Table S1. Multiple regression analysis of cohort proteome profile show protein factors relevant for the prediction model and their statistical significance



Dependent Y	CTNNB1

Method	Forward
Enter variable if P <	0.05
Remove variable if P>	0.1

Sample size	23
Coefficient of determination R^2	0.415
R^2-adjusted	0.356
Multiple correlation coefficient	0.644
Residual standard deviation	10.538

Regression Equation

Independent variables	**Coefficient**	**Std. Error**	**t**	**P**
(Constant)	38.886			
CD274	0.527	0.232	2.267	0.035
CD8A	-2.301	0.612	-3.760	0.001

Variables not included in the model
CD3G
CD3G/CD8A

Analysis of Variance

Source	**DF**	**Sum of Squares**	**Mean Square**
Regression	2	1572.938	786.469
Residual	20	2221.094	111.055

F-ratio	7.0818
Significance level	P = 0.005

Zero order correlation coeeficients

Variable	**r**
CD274	0.028
CD3G	-0.446
CD8A	-0.514
CD3G/CD8A	-0.096

Supplementary Table S2. Analyses of the quality of our novel patient specific mathematical ICBT response prediction algorithm

Model : **'Fit' Analysis**	**Predict Response** = 0.111 + 0.438*__CD8A__ + -5.7284/__CTNNB1__ + 0.005*__CD274__^2 + -0.757/__CD274__^2 - 0.017*__CD274__*__CD8A__ - 6.003e-5*__CD8A__^4 - 0.0006*__CTNNB1__^2
R^2 Goodness of Fit	0.99998393
Correlation Coefficient	0.99999219
Maximum Error (ME)	0.011190485
Mean Squared Error (MSE)	1.3388473e-5
Mean Absolute Error (MAE)	0.001940829
Coefficients	8
Complexicity	45
Primary Objective	0.001940829
Fit (Normalized Primary Objective)	0.0023406983