22,412 mRNAs from 375 tumor samples and 32 normal samples in TCGA cohort

6047 mRNAs identified by differentially expressed analyses in TCGA cohort

2352 immune genes identified by differentially expressed analyses in TCGA cohort

160 prognostic immune genes identified by univariate Cox analyses

Construction of transcription factor regulatory network with 19 transcription factor and 70 immune genes

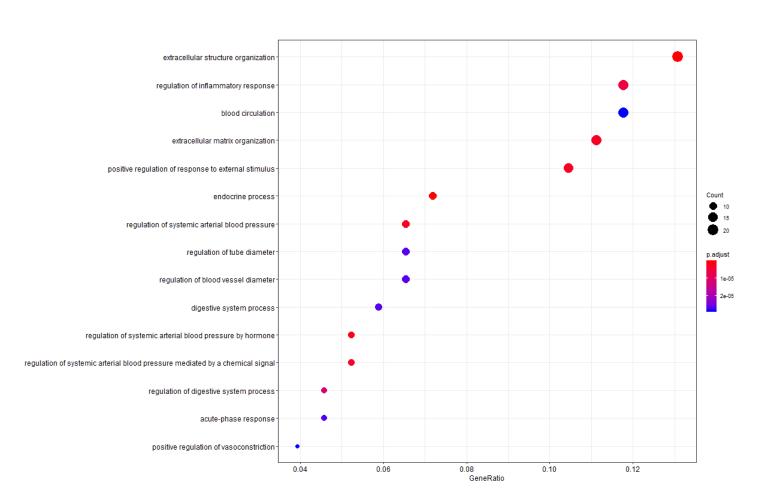
Multivariate Cox regression identified 14 immune genes based on previous immune gene biomarkers

Development of prognostic signature based on 14 immune genes in model cohort (n=265)

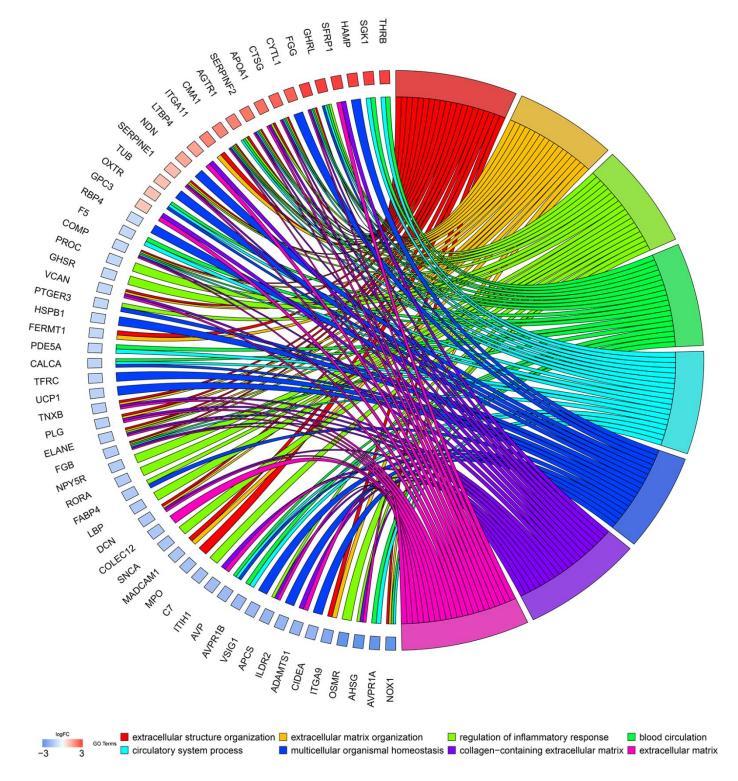
Clinical performance of prognostic signature in model cohort

External validation of prognostic signature in validation cohort (n=279)

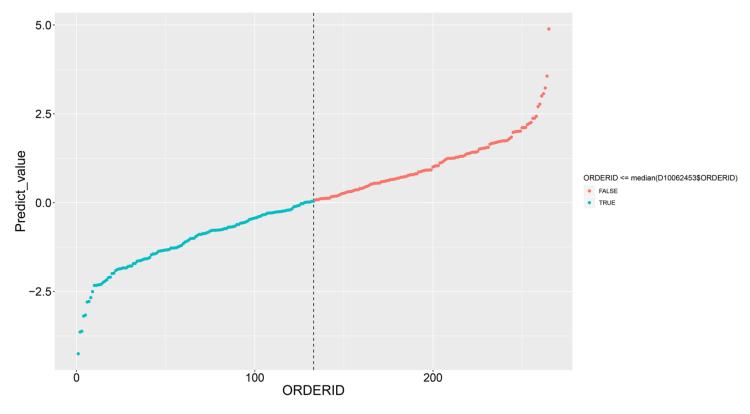
Supplementary Figure 1. Flow chart in current study



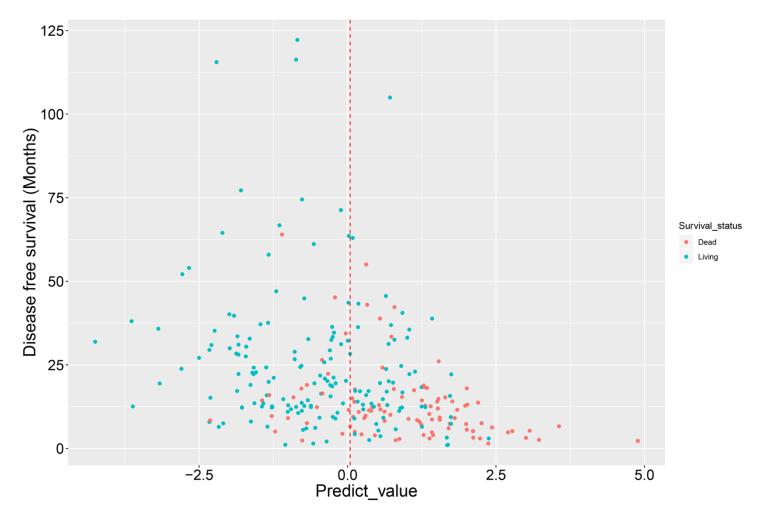
Supplementary Figure 2. Bubble chart of prognostic genes



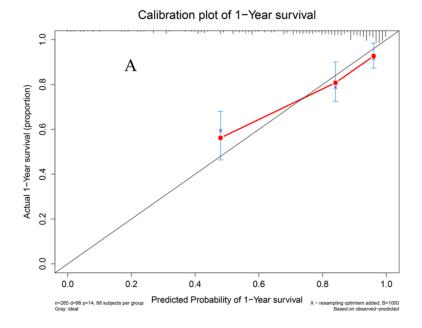
Supplementary Figure 3. Chord chart of prognostic genes

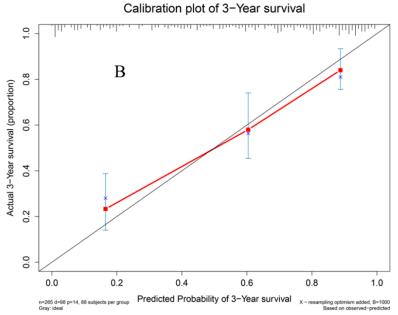


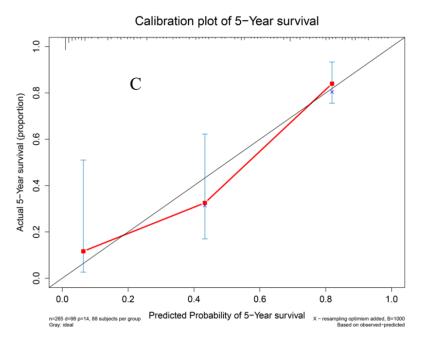
Supplementary Figure 4. Predictive value distribution chart



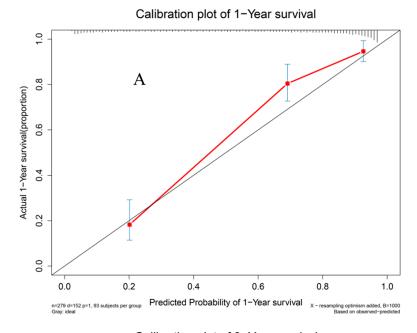
Supplementary Figure 5. Survival status scatter plot

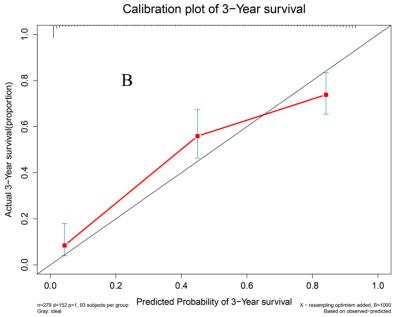


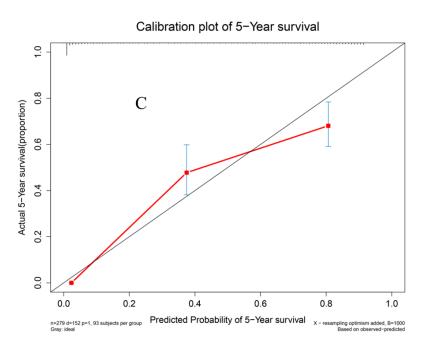




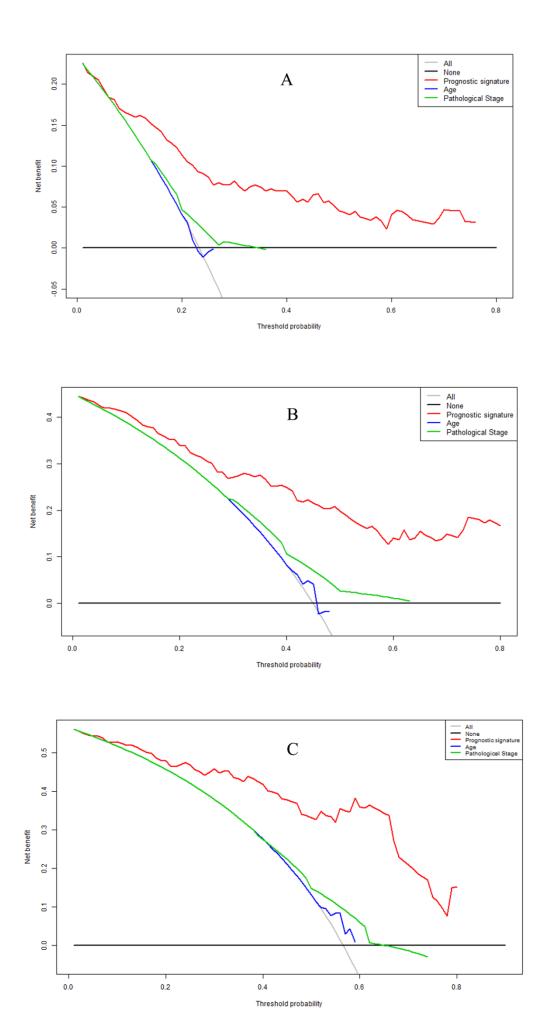
Supplementary Figure 6. Calibration curves for model cohort: (A) Calibration curve for 1-year survival; (B) Calibration curve for 3-year survival; (C) Calibration curve for 5-year survival







Supplementary Figure 7. Calibration curves for validation cohort: (A) Calibration curve for 1-year survival; (B) Calibration curve for 3-year survival; (C) Calibration curve for 5-year survival



Supplementary Figure 8. Decision curve chart: (A) Decision curve chart for 1-year survival; (B) Decision curve chart for 3-year survival; (C) Decision curve chart for 5-year survival

Correlation significance heatmap

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СМТМ1	0.44	0.48	0.67	0.07	0.82	0.10	0.06	0.96
LRP8	0.44	0.04	0.67	0.96	0.03	0.67		0.96
GJB6	0.18	0.21	0.15	0.62	0.64	0.76	0.43	0.63
GPC3	0.44	0.84	0.36	0.04	0.44	0.67	0.00	0.64
CDSN	0.94	0.01	0.26	0.85	0.24	0.03	0.04	0.77
CIDEA	0.39		0.18	0.82	0.85	0.30	0.01	0.95
VSIG1	0.44	0.19	0.18	0.02	0.76	0.06		0.03
RETN	0.50	0.01	0.93	0.61	0.73	0.67	0.49	0.06
NOX1	0.84		0.35	0.92	0.22	0.67	0.07	0.90
FERMT1	0.79		0.98	0.29	0.19	0.67	0.36	0.57
IFI44L	0.81		0.64	0.04	0.00	0.02	0.08	0.41
NLRC5	0.44	0.65	0.98	0.42	0.19	0.24	0.50	0.76
B3GNTL1	0.21	0.42	0.67	0.12	0.76	0.85	0.10	0.13
FGB	0.48	0.73	0.96	0.16	0.34	0.00	0.76	0.25
Predict_value	0.79	0.02	0.46		0.99	0.14	0.01	0.48
-	turnor	Grade	SW	847	é,	Stage	POE	Gender
	<i>\$</i> 0`′	0.02 Grade Residu						-

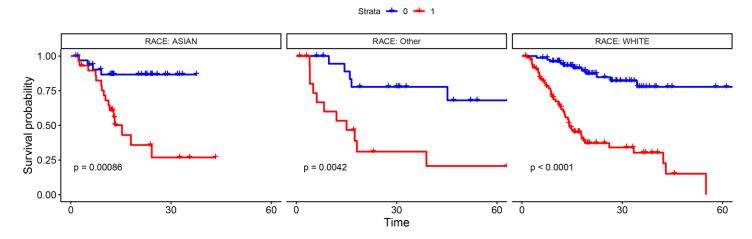
Supplementary Figure 9. Clinical variable correlation significance heatmap

0.8 0.6 0.4 0.2 0 **Correlation significance heatmap**

			illoulloc i		•••••	
CMTM1	0.45	0.10	0.99	0.37	0.98	0.25
LRP8	0.02	0.00	0.37	0.02	0.00	0.28
GJB6	0.01	0.28	0.05	0.01	0.68	0.76
GPC3	0.31	0.00	0.30	0.26	0.00	0.74
CDSN	0.01	0.26	0.13	0.00	0.52	0.35
CIDEA	0.28	0.00	0.77	0.80	0.00	0.35
VSIG1	0.99	0.90	0.86	0.67	0.27	0.03
RETN			0.00	0.32	0.59	0.01
NOX1	0.31	0.17	0.86	0.76	0.21	0.09
FERMT1			0.06	0.01	0.02	0.00
IFI44L					0.00	0.82
NLRC5	0.00	0.21			0.00	0.04
B3GNTL1	0.09	0.01	0.02	0.00	0.84	0.71
FGB	0.43	0.20	0.24	0.55	0.05	0.11
Predict_value	0.11	0.00	0.61	0.54	0.09	0.97
	Dendritic	crophage	Aeutrophil Me	Do Tool	JA Tool	Ø/
	00	idio,	76, NS	b , 4	Sp., c	C

Supplementary Figure 10.Immune gene correlation significance heatmap

0.8 0.6 0.4 0.2



Supplementary Figure 11. Subgroup analyses among different races