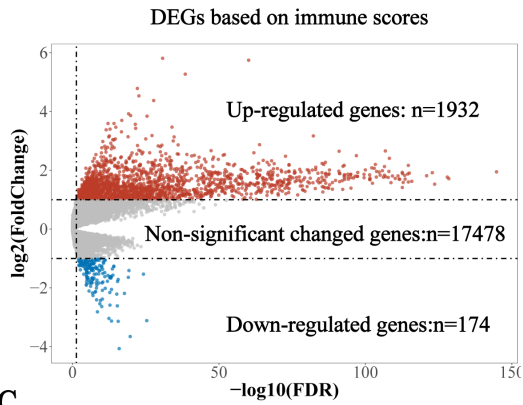
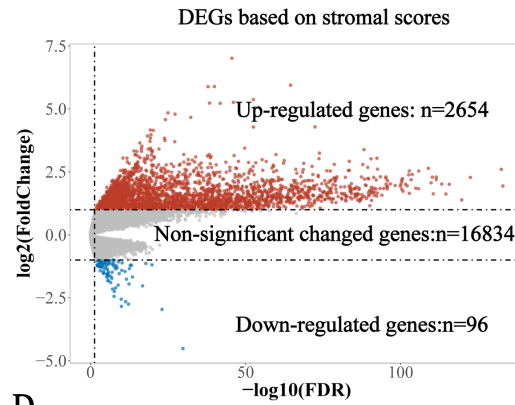


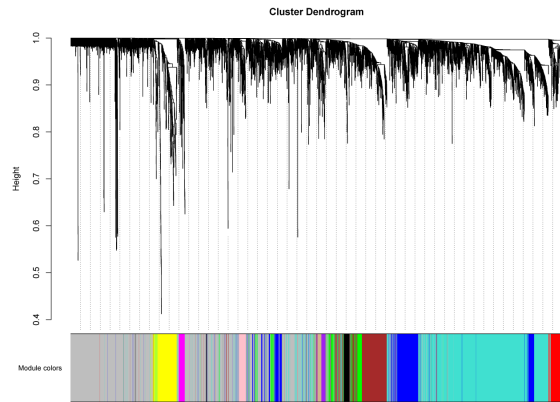
A



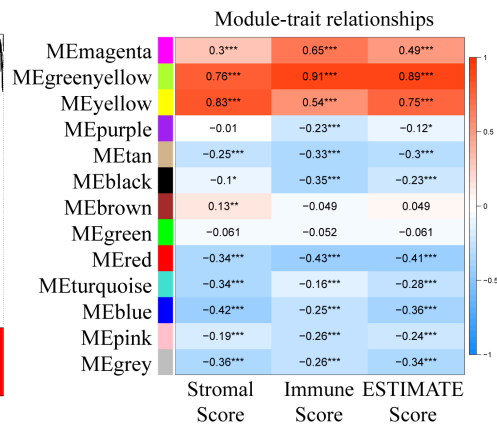
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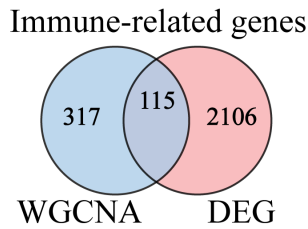
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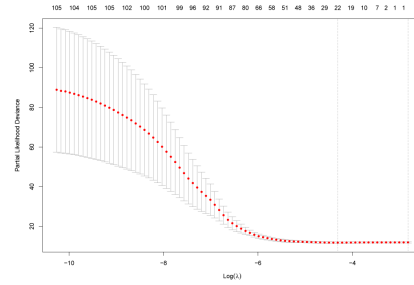
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E



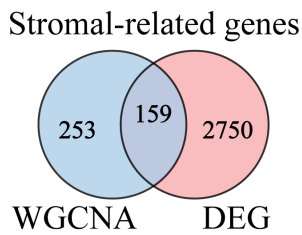
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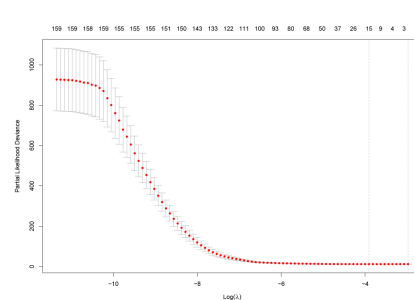
Output:

ACP5 BGN **BST2** C1QA C1QB
 CHI3L1 COL6A1 CTSK CYBB
 DCN FBLN2 IFI16 MMP1 MXRA5
 OAS2 SERPINE1 SPP1 STAB1
 TNC TNFAIP2 UBE2L6 WARS1

F



H



Output:

ACTG2 BGN C1QA
 CAV1 CHI3L1 COL12A1
 CYBB DKK3 MMP1
 NOTCH3 PDGFRA SERPINE1
 SPP1 STAB1 TUBA1A

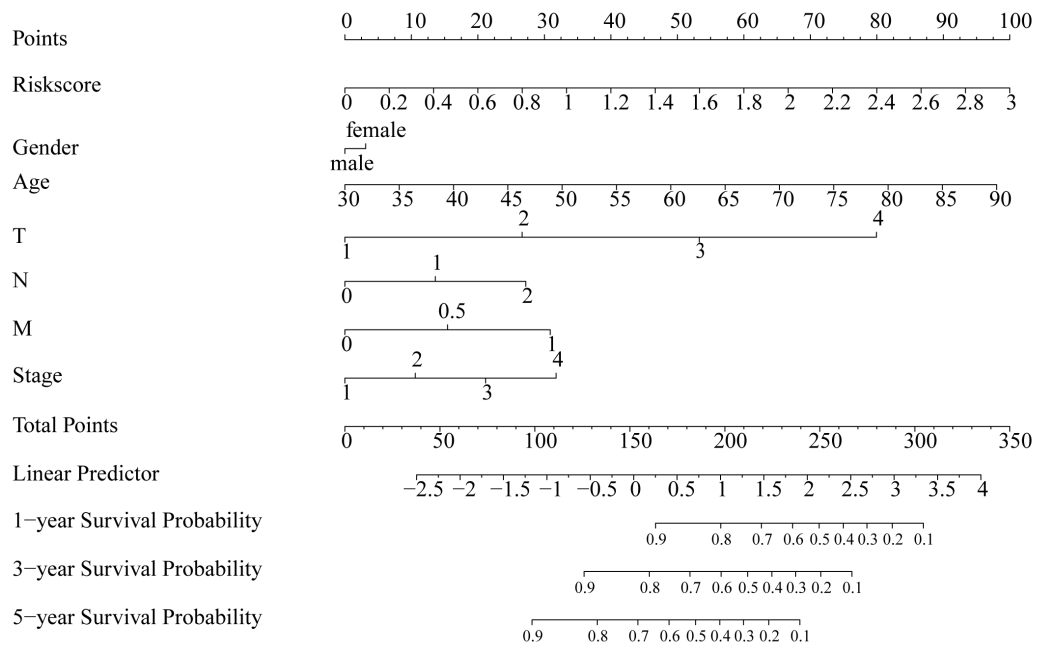
Figure S1 **Screening for targeted genes.** **A** DEG analysis between low and high immune scores. **B** DEG analysis between low and high stromal scores. **C** WGCNA analysis for identifying gene modules. **D** Correlation between immune, stromal and ESTIMATE scores and gene modules. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. **E** Venn plot displays the number of immune-related genes between DEG analysis and WGCNA. **F** Venn plot displays the number of stromal-related genes between DEG analysis and WGCNA. **G** The immune-related genes were further inputted into LASSO analysis. **H** The intersection stromal-related genes were further inputted into LASSO analysis. The Y-axis shows LASSO coefficients and the X-axis is $-\log(\lambda)$. And the output genes were in the right rectangle boxes.

Abbreviations: DEG, differentially expressed gene); WGCNA, weighted correlation network analysis ; LASSO, Least absolute shrinkage and selection operator

A

Factor	Univariate Cox analysis		Multivariate Cox analysis	
	HR(95% CI)	p value	HR(95% CI)	p value
riskscore	2.545 (1.584-4.090)	<0.001	2.080 (1.313-3.295)	0.002
M	4.052 (2.593-6.333)	<0.002	1.946 (0.881-4.299)	0.1
N	1.961 (1.560-2.464)	<0.003	1.340 (0.899-2.000)	0.151
T	2.411 (1.648-3.527)	<0.004	1.789 (1.120-2.859)	0.015
Stage	2.046 (1.628-2.571)	<0.005	1.266 (0.711-2.252)	0.422
Age	1.028 (1.010-1.046)	0.002	1.036 (1.018-1.054)	<0.001

B



C

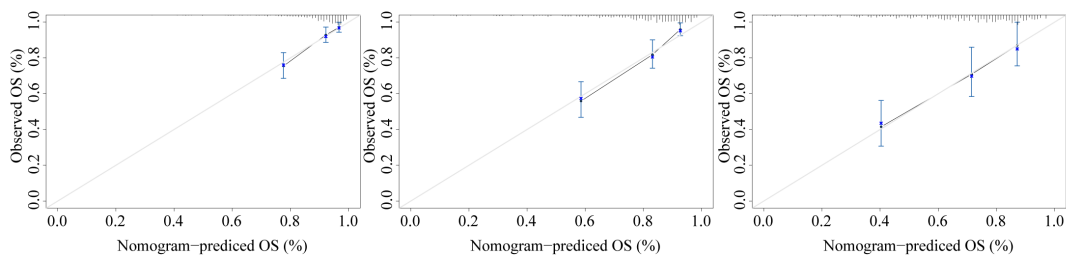


Figure S2 **Prognostic analysis of BST2 in CRC.** **A** Univariate and multivariate Cox regression analysis of riskscore, TNM stage, age and gender. **B** Prognostic nomograms based on risk score, TNM stage, age and gender. **C** Calibration analysis of the nomogram for predicting 1-year, 3-year and 5-year overall survival, respectively.

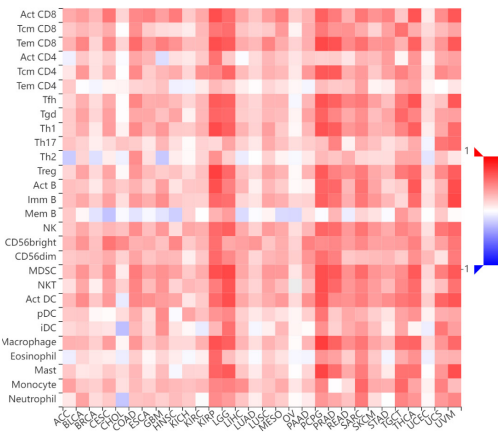
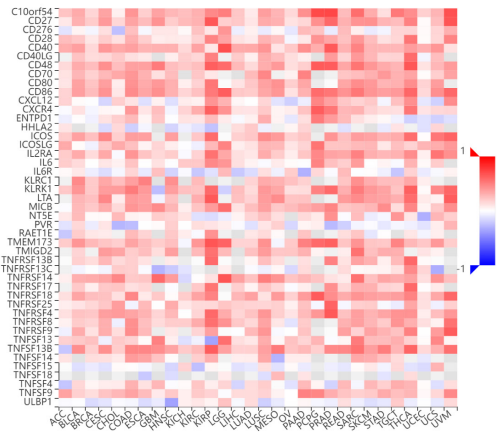
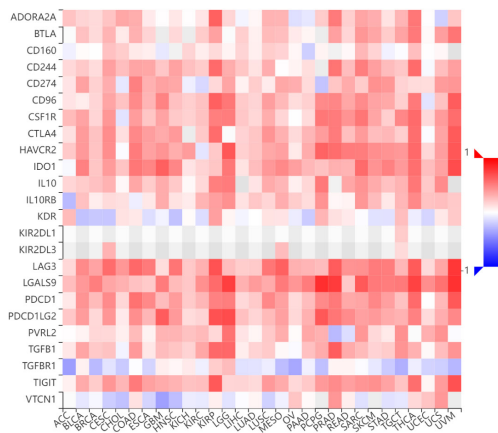
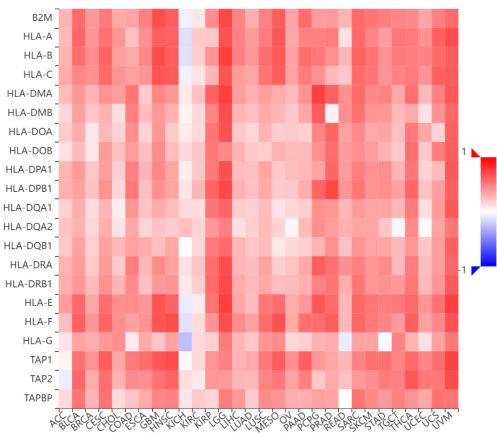
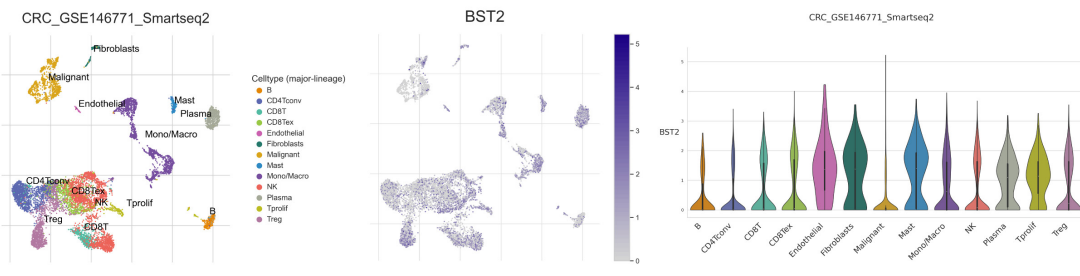
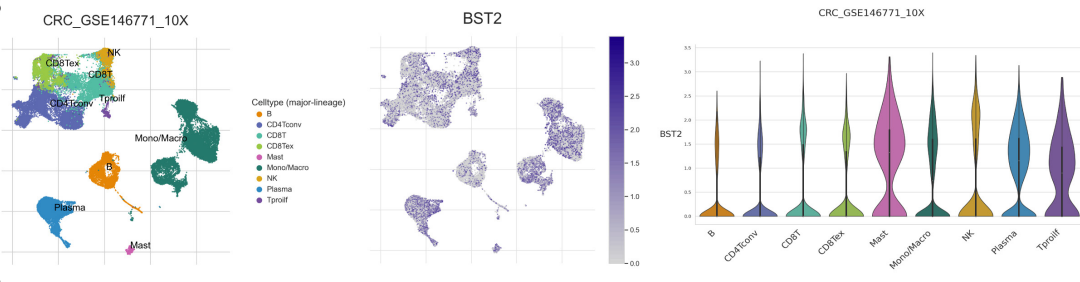
A**B****C****D**

Figure S3 **The correlation analysis between BST2 and various immune factors.** **A** The heatmap showed the correlation between BST2 and immune cells in various cancers. **B** The heatmap showed the correlation between BST2 and immune stimulators in various cancers. **C** The heatmap showed the correlation between BST2 and immune inhibitors in various cancers. **D** The heatmap showed the correlation between BST2 and MHC molecules in various cancers. The plot above were downloaded from <http://cis.hku.hk/TISIDB/>

A



B



C

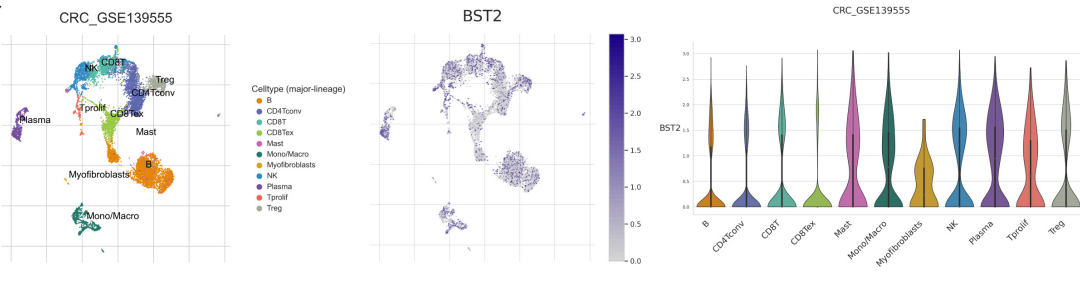


Figure S4 **Distribution of BST2 in different types of immune cells analyzed in three single cell RNA-seq datasets. A** GSE146771; **B** GSE146771; **C** GSE139555; Different colors represent different kinds of immune cells.

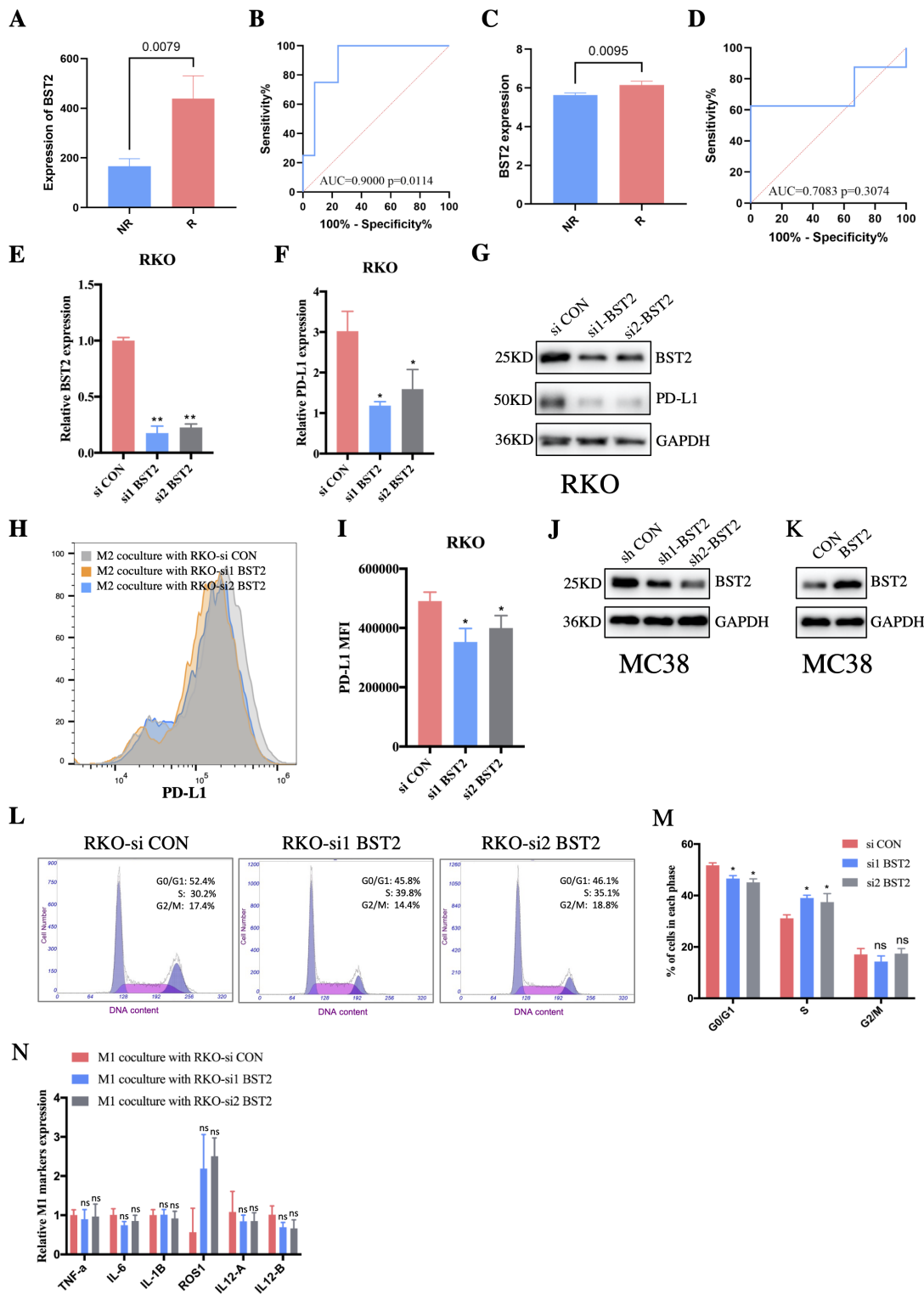


Figure S5 **A** Difference analysis of the distribution of BST2 expression between non-responder and responder prior therapy. **B** ROC analysis of BST2 expression prior therapy in predicting the ICB response. **C** Difference analysis of the distribution of BST2 expression between non-responder and responder post therapy. **D** ROC analysis of BST2 expression post therapy in predicting the ICB response. **E-I** qRT-PCR (E-F), Western blot analysis (G) were used to certificate the knockdown of BST2 in RKO, and the downregulation of PD-L1 in RKO. Flow cytometry analysis to further certificate the downregulation of PD-L1 in RKO (H-I). **J** Western blot analysis was used to certificate knockdown of shRNA-BST2 in RKO. **K** Western blot analysis was used to certificate the overexpression of BST2 in RKO. **L** BST2-knockdown RKO cells were applied to cell cycle analysis assays. **M** The percentage of RKO cells in G0/G1, S and G2/M phases. *P < 0.05; **P < 0.01; ns, not significant. **N** qRT-PCR analysis was applied to demonstrate the M1 polarization when TAMs cocultured with BST2-knockdown RKO cells.