

Figure S1 Prognostic value evaluation of the risk model in the validation set. (A) The Kaplan-Meier curve shows that the overall survival rate is lower in the high-risk group than in the low-risk group. (B) Determine the AUC of the prognostic risk model based on the ROC curve. (C-E) Distribution of patient risk scores (based on prognostic features, survival status, and RMLncRNAs expression). RMLncRNAs, lncRNAs related to RNA methylation regulators; ROC, receiver operating characteristic; TPR, true positive rate; FPR, false positive rate; AUC, area under the curve.

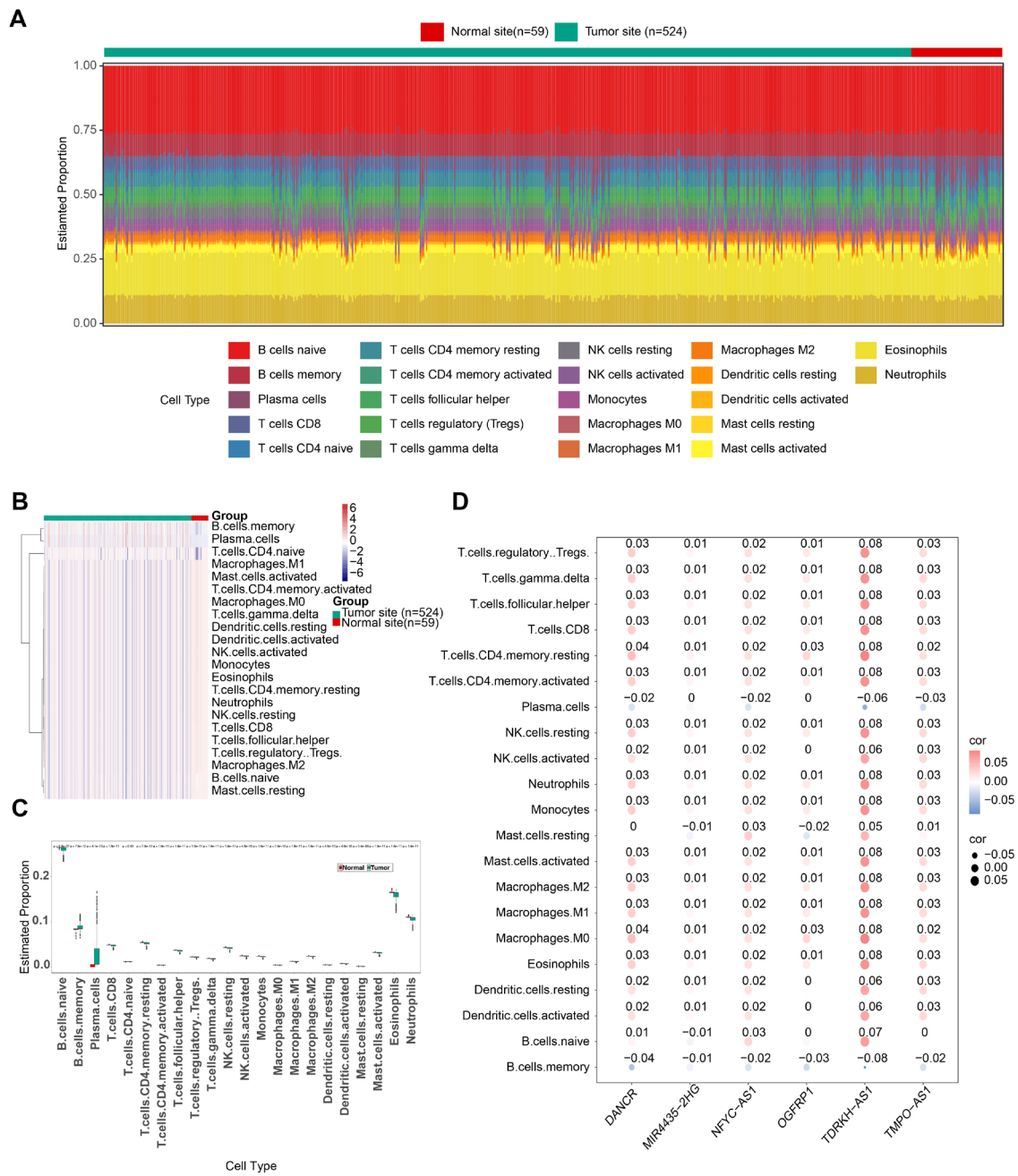


Figure S2 Results of immunoinfiltration analysis. (A) Distribution of 22 types of immune cells in the tumor group and the control group. (B) Heatmap of the expression levels of 22 types of immune cells in the tumor group and the control group. (C) Differential expression of 22 types of immune cells between the tumor group and the control group. (D) Correlation analysis between immune cells and RMLncRNAs. RMLncRNAs, lncRNAs related to RNA methylation regulators.

Table S1 76 RNA methylation-related genes and RNA methylation types

| Gene | Methylation |
|------------------|-------------|
| <i>METTL3</i> | m6A |
| <i>METTL14</i> | m6A |
| <i>METTL16</i> | m6A |
| <i>WTAP</i> | m6A |
| <i>KIAA1429</i> | m6A |
| <i>VIRMA</i> | m6A |
| <i>RBM1</i> | m6A |
| <i>RBM15</i> | m6A |
| <i>RBM15B</i> | m6A |
| <i>ZC3H13</i> | m6A |
| <i>FTO</i> | m6A |
| <i>ALKBH5</i> | m6A |
| <i>YTHDC1</i> | m6A |
| <i>YTHDC2</i> | m6A |
| <i>YTHDF1</i> | m6A |
| <i>YTHDF2</i> | m6A |
| <i>YTHDF3</i> | m6A |
| <i>IGF2BP2</i> | m6A |
| <i>IGF2BP3</i> | m6A |
| <i>HNRNPA2B1</i> | m6A |
| <i>HNRNPC</i> | m6A |
| <i>HNRNPG</i> | m6A |
| <i>RBMX</i> | m6A |
| <i>LRPPRC</i> | m6A |
| <i>FMR1</i> | m6A |
| <i>IGF2BP1</i> | m6A |
| <i>TRMT6</i> | m1A |
| <i>TRMT61A</i> | m1A |
| <i>TRMT61B</i> | m1A |
| <i>TRMT61C</i> | m1A |
| <i>TRMT10C</i> | m1A |
| <i>BMT2</i> | m1A |
| <i>RRP8</i> | m1A |
| <i>ALKBH1</i> | m1A |
| <i>ALKBH3</i> | m1A |
| <i>NOP2</i> | m5C |
| <i>NSUN1</i> | m5C |

Table S1 (continued)

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| Gene | Methylation |
|-----------------|-------------|
| <i>NSUN2</i> | m5C |
| <i>NSUN3</i> | m5C |
| <i>NSUN4</i> | m5C |
| <i>NSUN5</i> | m5C |
| <i>NSUN7</i> | m5C |
| <i>DNMT1</i> | m5C |
| <i>TRDMT1</i> | m5C |
| <i>DNMT3A</i> | m5C |
| <i>DNMT3B</i> | m5C |
| <i>TET2</i> | m5C |
| <i>YBX1</i> | m5C |
| <i>ALYREF</i> | m5C |
| <i>METTL1</i> | m7G |
| <i>WDR4</i> | m7G |
| <i>DCP2</i> | m7G |
| <i>DCPS</i> | m7G |
| <i>NUDT10</i> | m7G |
| <i>NUDT11</i> | m7G |
| <i>NUDT16</i> | m7G |
| <i>NUDT3</i> | m7G |
| <i>NUDT4</i> | m7G |
| <i>AGO2</i> | m7G |
| <i>CYFIP1</i> | m7G |
| <i>EIF4E</i> | m7G |
| <i>EIF4E1B</i> | m7G |
| <i>EIF4E2</i> | m7G |
| <i>EIF4E3</i> | m7G |
| <i>GEMIN5</i> | m7G |
| <i>LARP1</i> | m7G |
| <i>NCBP1</i> | m7G |
| <i>NCBP2</i> | m7G |
| <i>C17orf85</i> | m7G |
| <i>EIF3D</i> | m7G |
| <i>EIF4A1</i> | m7G |
| <i>EIF4G3</i> | m7G |
| <i>IFIT5</i> | m7G |
| <i>LSM1</i> | m7G |
| <i>NCBP2L</i> | m7G |
| <i>SNUPN</i> | m7G |

Table S2 The correlation of clinical features between high- and low-risk groups

| Characteristic | Low-risk group (n=82) | High-risk group (n=95) | P |
|------------------|-----------------------|------------------------|------|
| Age (years) | 64.89±10.09 | 66.44±10.10 | 0.74 |
| Gender | | | 0.76 |
| Female | 44 (24.86) | 48 (27.12) | |
| Male | 38 (21.47) | 47 (26.55) | |
| Pathologic stage | | | 0.16 |
| Stage I | 50 (28.25) | 43 (24.29) | |
| Stage II | 14 (7.91) | 26 (14.69) | |
| Stage III | 15 (8.47) | 19 (10.73) | |
| Stage IV | 3 (1.69) | 7 (3.95) | |
| T stage | | | 0.22 |
| T1 | 27 (15.25) | 22 (12.43) | |
| T2 | 45 (25.42) | 56 (31.64) | |
| T3 | 5 (2.82) | 13 (7.34) | |
| T4 | 5 (2.82) | 4 (2.26) | |
| N stage | | | 0.16 |
| N0 | 59 (33.33) | 56 (31.64) | |
| N1 | 11 (6.21) | 22 (12.43) | |
| N2 | 12 (6.78) | 17 (9.60) | |
| M stage | | | 0.34 |
| M0 | 79 (44.63) | 88 (49.72) | |
| M1 | 3 (1.69) | 7 (3.95) | |

Measurement data with normal distribution were obtained as mean ± standard deviation and compared using a two independent-sample *t*-test. Numerical data were presented by frequency (percentage) and compared using the Chi-square test.