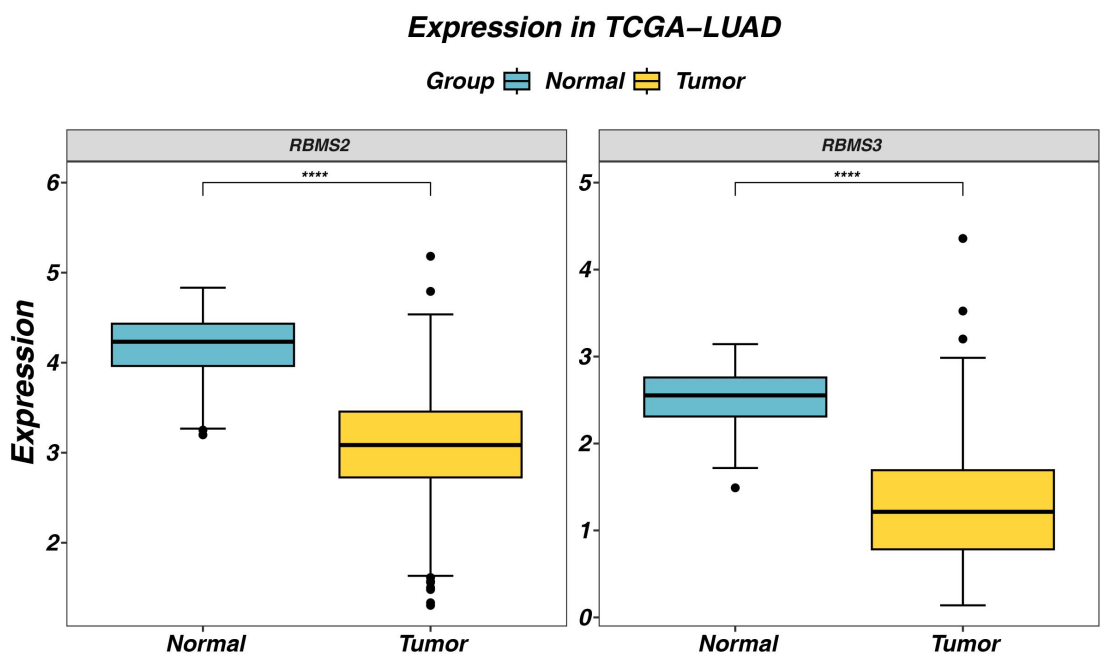
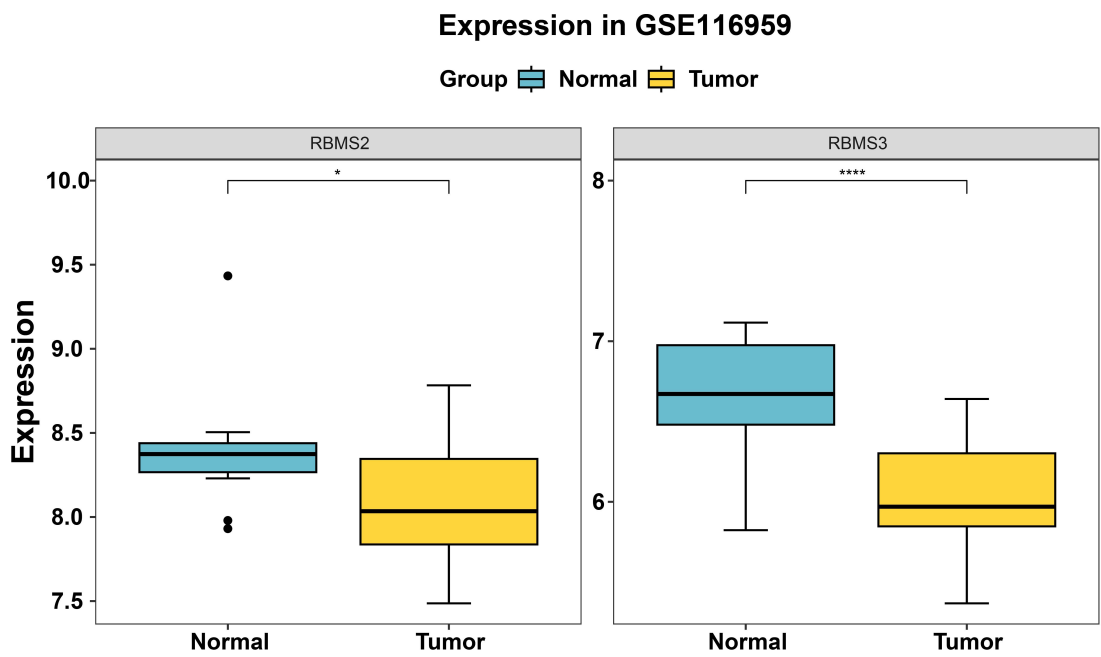


Supplementary Information

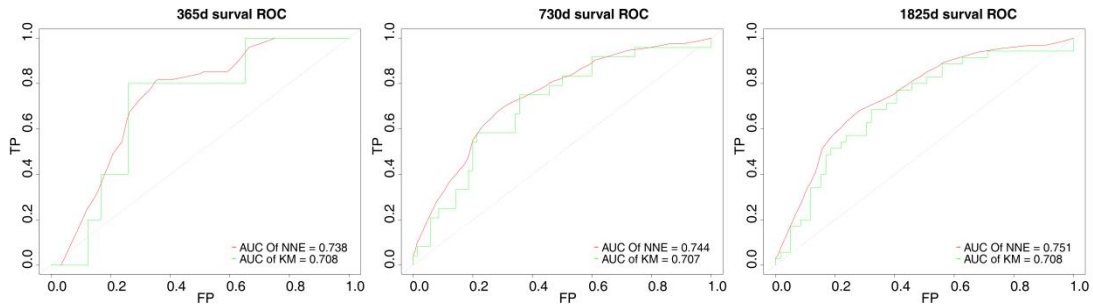


Supplementary Figure 1: Differential Expression Analysis of RBMS2 and RBMS3 in Tumor and Control Samples from TCGA-LUAD Dataset.

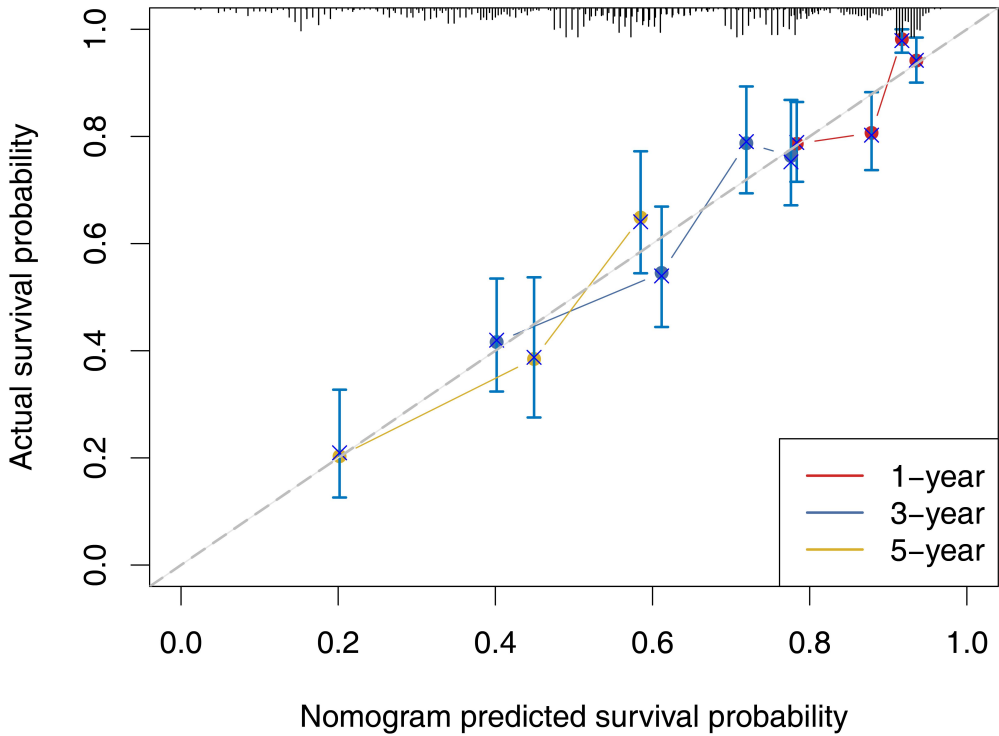


Supplementary Figure 2: Expression Profiling of RBMS2 and RBMS3 in Tumor

and Control Samples from GSE116959 Dataset.



Supplementary Figure 3: Validation of RBMS2 and RBMS3 Expression Using ROC Curve Analysis in GSE11969 Dataset.



Supplementary Figure 4: Calibration Curve for the Nomogram Predictive Model.

Supplementary Table 1: Target Sequences of RBMS3 Transfection Plasmids. The table presents the target sequences used for the transfection plasmids designed for the human RBMS3 gene (RNA Binding Motif Single-Stranded Interacting Protein 3), specifically transcript variant 6. The species analyzed is Homo sapiens, and the

nucleotide sequence is referenced from NCBI Reference Sequence NM_001330696.1, spanning positions 371 to 1681. The table includes partial nucleotide sequences that were targeted in the plasmid construction, which are essential for understanding the genetic manipulation and subsequent experiments involving RBMS3 gene expression analysis.

Category	Details
Gene Name	RBMS3 (RNA Binding Motif Single-Stranded Interacting Protein 3)
Species	Homo sapiens
Transcript Variant	6
Reference Sequence	NM_001330696.1
Nucleotide Range	371-1681
Nucleotide Sequence (Partial)	ATGGGCAAACGCCTGGATCAGCCACAAATGTACCCCCAGTACACTTACTACTA TCCTCATTATCTCCAAACCAAGTCCTATGCACCAGCTCCCCACCCCATGGCTC CTCCCAGCCCCAGCACAAACAGCAGCAGCAACAACAGCAGCAACAACAGCA GCGGGGAACAGTTGAGTAAAACCAACCTGTACATTCGAGGCCTCCCACCAGG CACCCTGACCAGGACCTAATCAAGCTGTGCCAACCGTATGGAAAAATTGTA TCTACAAAGGCAATTCTTGACAAAAACACAAATCAGTGCAAAGGTTATGGTTT TGTAGATTTTGACAGTCCTGCAGCCGCACAGAAAGCGGTAGCATCTCTCAAGG CAAATGGCGTGCAGGCACAGATGGCTAAGCAACAAGAGCAAGACCCAACAA ACCTATACATCTCAAATCTCCCCATTTCTATGGATGAGCAGGAGCTTGAGAAT ATGCTGAAACCCTTTGGACATGTCATTTCCACAAGAATACTAAGAGACGCTAA TGGAGTCAGCAGAGGTGTTGGCTTTGCCAGAATGGAGTCTACTGAAAAATGT GAAGTGGAATTCAACATTTTAATGGAAAATATCTGAAAAACACCACCAGGCA TCCCAGCCCCCAGTGAGCCTTTGCTGTGCAAATTCGCTGATGGAGGACAAAAG AAGCGACAGAATCAAAGCAAATATACCCAGAATGGGAGGCCTTGGCCCAGGG AAGGAGAGGCTGGCATGGCTTTGACCTATGACCCACAGCTGCCATACAGAA TGGATTTTATTCTTCACCGTACAGTATTGCAACCAACCGCATGATTCCACAGA CATCTATCACGCCATTCAATTGCTGCTTCCCCTGTCTCCACATACCAGGTCCAGA GTACTTCATGGATGCCTCATCCGCCATACGTTATGCAACCAACAGGTGCTGTG ATTACACCAACCATGGACCATCCCATGTCAATGCAGCCAGCCAACATGATGG GCCCCACTGACACAGCAGATGAATCACCTTTCGTTGGGCACAACAGGAACGAT TCAATCCCAAGACAGGATTATGATACTCCACCAGCTGTTGTGTCAGTATATGA CTGCTGCTGCTCCTATGCAAGGGACCTACATTCCTCAGTACACGCCTGTGCCT CCGACAGCTGTTTCTATTGAAGGTGTTGTTGCTGATACCTCTCCCCAGACAGT GGCACCTTCATCCCAGGACACCAGTGGTCAGCAGCAACAGATAGCAGTGGAC ACATCCAACGAACATGCACCTGCATATTCTTACCAACAGTCTAAACCATAA

Supplementary Table 2: Comprehensive List of Differentially Expressed Genes in TCGA Lung Adenocarcinoma Dataset. The table provides detailed insights into the

genes with altered expression in lung adenocarcinoma, highlighting key candidates for further functional studies and potential therapeutic targets. Gene: The official gene symbol representing the differentially expressed gene. Log2FC (Log2 Fold Change): The logarithm (base 2) of the fold change in expression levels between lung adenocarcinoma samples and normal controls. A negative value indicates downregulation, while a positive value indicates upregulation in lung adenocarcinoma tissues. AveExpr (Average Expression): The average expression level of the gene across all samples analyzed in the TCGA dataset. t (t-statistic): The t-statistic value from the differential expression analysis, representing the magnitude and direction of the difference in gene expression.

P.Value: The unadjusted p-value obtained from the statistical test, indicating the probability that the observed difference in expression occurred by chance. Adj.P.Val (Adjusted P-Value): The p-value adjusted for multiple testing using the Benjamini-Hochberg method, which controls for false discovery rate (FDR). Genes with a lower adjusted p-value are considered statistically significant. B (B-statistic): The log-odds of differential expression, representing the probability that a given gene is differentially expressed.

Supplementary Table 3: Differential Expression Analysis of RBMS Gene Family in LUAD Compared to Normal Tissues. The table shows the differential expression analysis of RBMS gene family members, comparing LUAD tissues to normal tissues. The analysis was performed using the "limma" package. Both RBMS2 and RBMS3 show significant downregulation in LUAD tissues compared to normal tissues, with logFC values of -1.10457088 and -1.208346696, respectively. This downregulation is statistically significant, with adjusted p-values of 8.61E-40 for RBMS2 and 1.25E-39 for RBMS3. The data highlights the potential importance of RBMS2 and RBMS3 in LUAD, as their downregulation might contribute to tumor progression, making them potential targets for further functional studies. LogFC: Log2 fold change representing the expression difference between LUAD and normal tissues. A negative value indicates lower expression in LUAD, while a positive value indicates higher expression in LUAD. AveExpr: Average expression level across all samples. t: t-statistic value from the linear model. P. Value: Unadjusted p-value for the

differential expression. adj. P. Val: Adjusted p-value using the Benjamini-Hochberg method to control for false discovery rate. B: Log-odds that the gene is differentially expressed.

Gene	Log ₂ FC	AveExpr	t	P.Value	Adj.P.Val	B
RBMS2	-1.10457088	10.0245287	-14.49686655	8.61E-41	8.61E-40	80.64994974
RBMS3	-1.208346696	3.009348921	-14.39697644	2.49E-40	1.25E-39	79.59080834
RBMX	0.390810205	28.9666349	8.879837577	8.61E-18	2.87E-17	28.00039471
RBMS1	-0.441355398	8.748839365	-7.138733675	2.87E-12	7.17E-12	15.45381697
RBMXL1	-0.359993534	5.306385409	-6.123793533	1.70E-09	3.40E-09	9.196093667
RBMX1J	-0.00388992	1.001023643	-4.596726517	5.28E-06	8.81E-06	1.396554146
RBMXL2	-0.015218654	1.014341653	-3.660042276	0.0002755	0.000393572	-2.363258857
RBMX1A1	0.000508789	1.000323298	0.698650391	0.485054289	0.606317861	-8.750253497
RBMXL3	6.40E-05	1.001107451	0.046442786	0.962973533	1	-8.99351479
RBMX2DP	0	1	0	1	1	-8.994594975