

Supplementary Material

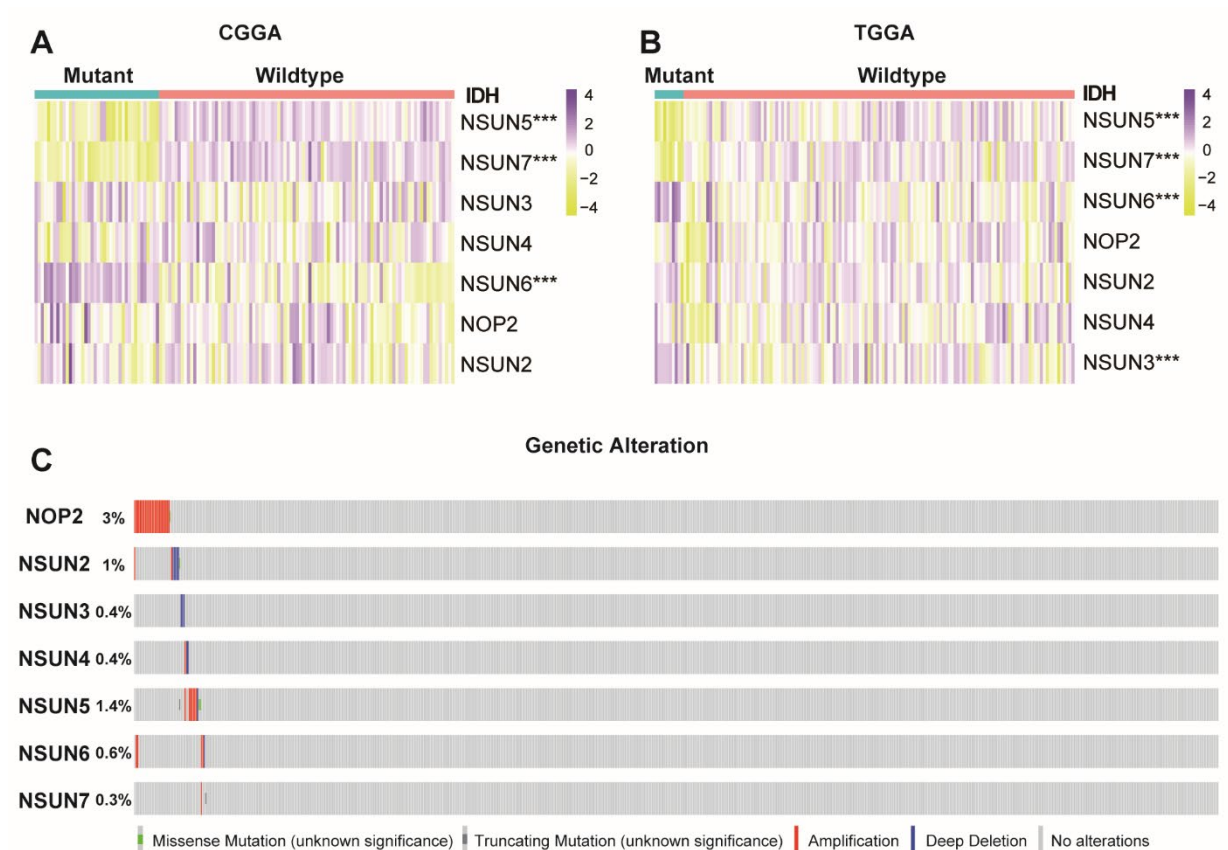
1 Supplementary Data

None

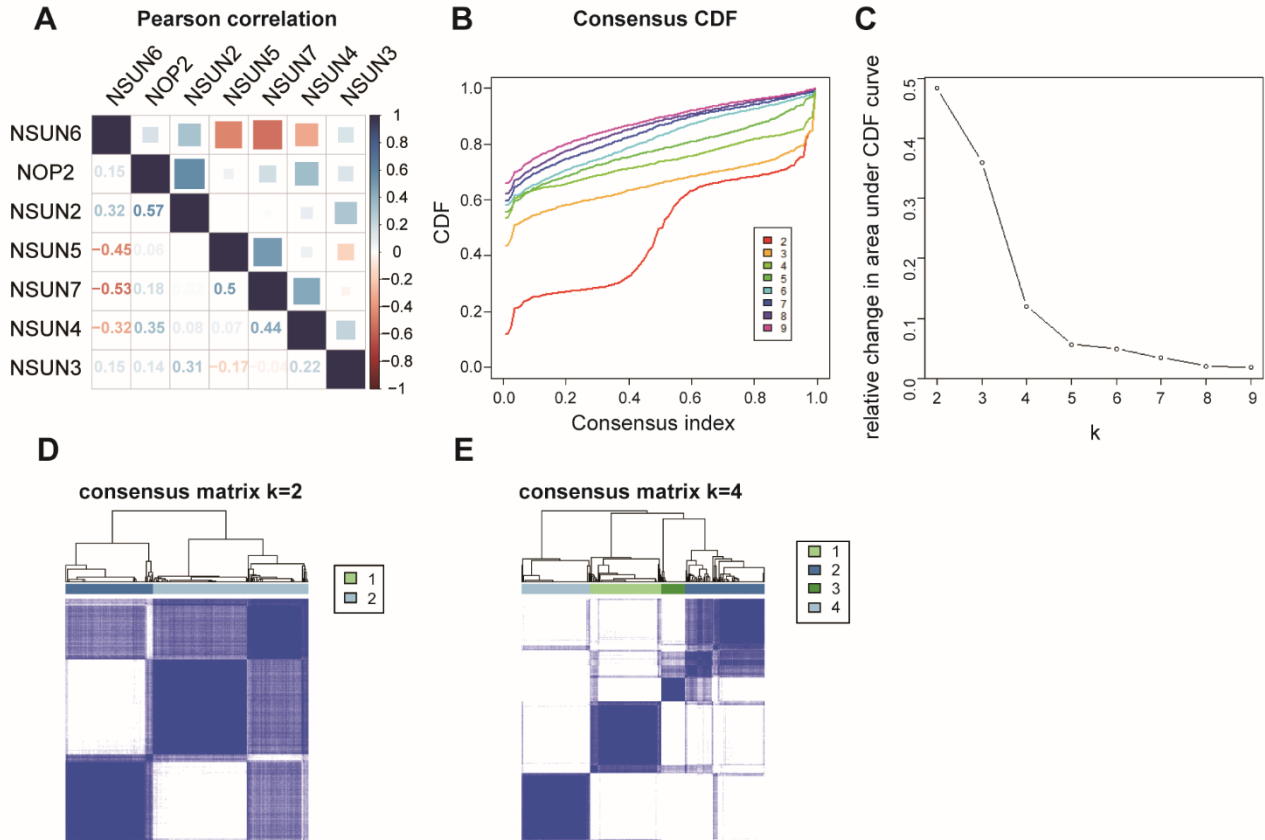
2 Supplementary Figures and Tables

2.1 Supplementary Figures

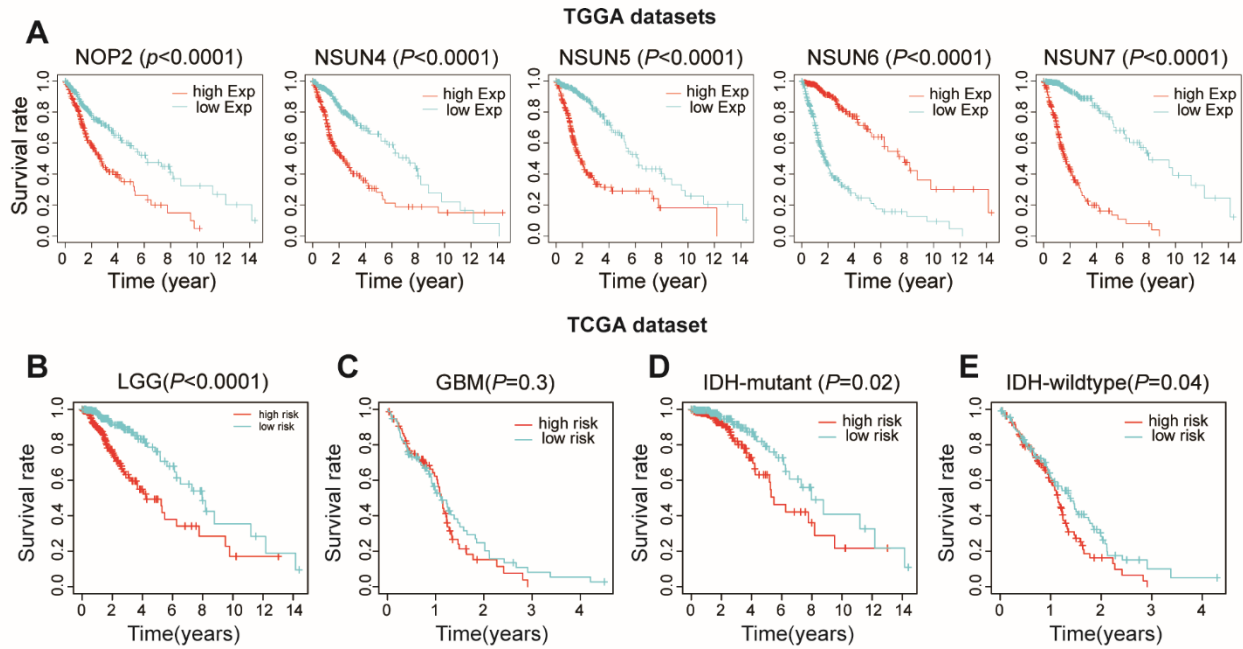
Supplementary Figure S1. The genetic alteration and differential expression of RNA:m⁵C methyltransferases. **(A-B)** The differential expression of seven RNA:m⁵C methyltransferases with different IDH-mutant status in glioblastoma. **(C)** The gene mutation frequencies of seven RNA:m⁵C methyltransferases.



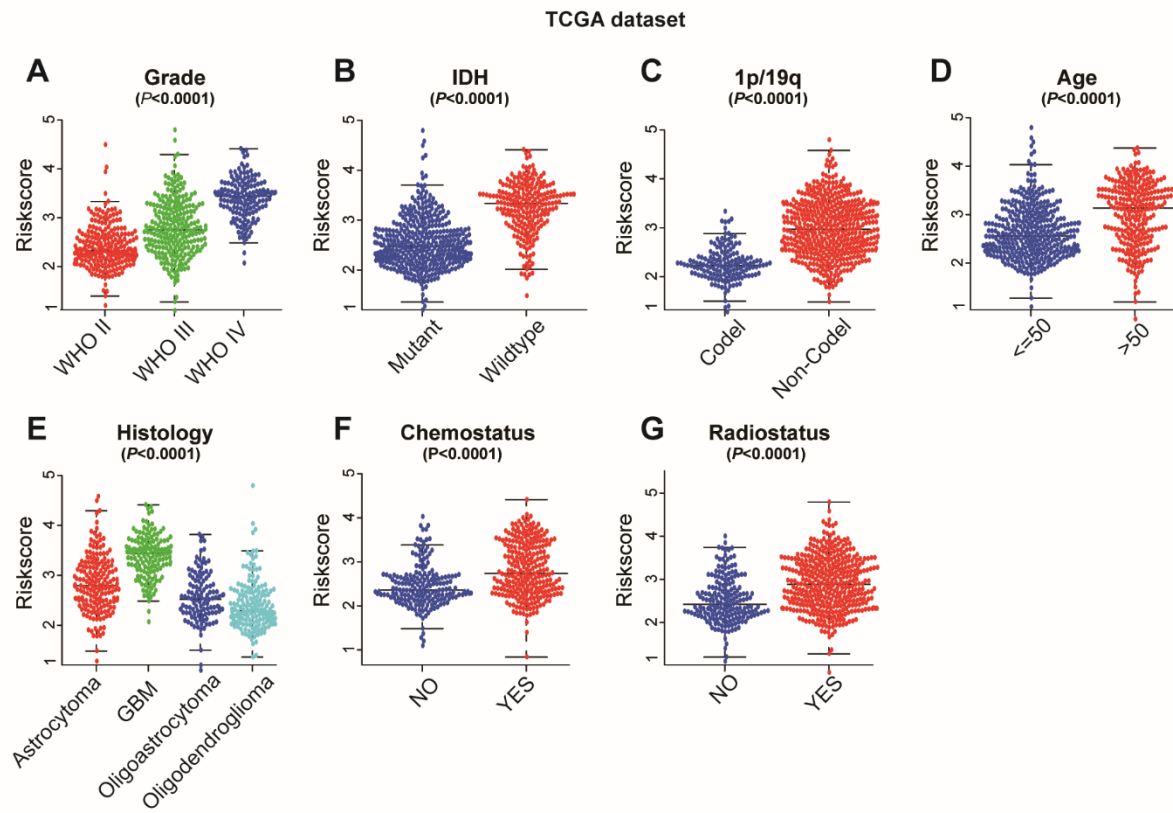
Supplementary Figure S2. Pearson correlation and unsupervised consensus analysis of selected RNA:m⁵C methyltransferases. **(A)** Pearson correlation analysis of seven RNA:m⁵C methyltransferase expression profiles in the TCGA dataset. **(B-C)** Consensus clustering cumulative distribution function for k=2 to 9. Relative change in area under CDF for k=2 to 9. **(D-E)** Consensus clustering matrix for k=2 and k=4.



Supplementary Figure S3. Kaplan-Meier overall survival curves for patients in the TCGA dataset. (A) Kaplan-Meier overall survival curves for each prognostic gene in the TCGA dataset. (B-C), Kaplan-Meier overall survival curves for patients in the TCGA dataset stratified by WHO grade. (D-E) Kaplan-Meier overall survival curves for patients in the TCGA dataset stratified by IDH-mutant status.



Supplementary Figure S4. A-G, The relationship between the risk scores and each clinicopathological characteristic in TCGA dataset.



2.2 Supplementary Tables

Supplementary Table S1. The clinicopathological information of glioma patients in the CGGA and the TCGA datasets.

Characteristics		CGGA dataset	TCGA dataset
Total patients		306	616
Gender	Female	117	261
	Male	189	355
Age	>50	85	260
	<=50	221	356
Grade	II	97	221
	III	74	244
	IV	135	151
Histology	Oligodendroglioma	36	169
	Oligoastrocytoma	73	119
	Astrocytoma	62	177
	GBM	135	151
IDH	Mutant	167	387
	Wildtype	139	221
	NA	0	8
1p/19q	Codel	63	155
	Non-codel	239	457
	NA	4	4
Chemostatus	Yes	173	256
	No	118	185
	NA	15	175
Radiostatus	Yes	251	382
	No	44	184
	NA	11	50

Supplementary Table S2. The clinicopathological characteristics of glioma patients in three subtypes identified by selected RNA:m⁵C methyltransferases with the CGGA dataset.

Characteristics		MC1	MC2	MC3	P-value
Total patients		104	120	82	
Gender	Female	41	38	38	0.104
	Male	63	82	44	
Age		42(17-70)	47(8-79)	38(19-61)	<0.0001
Grade	II	61	7	29	<0.0001
	III	25	26	23	
	IV	18	87	30	
Histology	Oligodendroglioma	26	1	9	<0.0001
	Oligoastrocytoma	33	18	22	
	Astrocytoma	27	14	21	
IDH	GBM	18	87	30	<0.0001
	Mutant	70	20	77	
	Wildtype	34	100	5	
1p19q	Codel	42	5	16	<0.0001
	Non-codel	60	115	64	
	NA	2	0	2	
Chemostatus	Yes	47	80	46	0.006
	No	51	35	32	
	NA	6	5		
Radiostatus	Yes	88	96	67	0.602
	No	12	19	13	
	NA	4	5	2	

Significance: $P^* < 0.05$, $P^{**} < 0.01$, $P^{***} < 0.001$.

Supplementary Table S3. The clinicopathological characteristics of glioma patients with low-risk and high-risk groups in CGGA dataset

Characteristics		CGGA dataset			TCGA dataset		
		low-risk	high-risk	<i>P</i> -value	low-risk	high-risk	<i>P</i> -value
Total patients		153	153		308	308	
Gender	Female	62	55	0.41	136	125	0.37
	Male	91	98		172	183	
Age	>50	26	59	<0.0001	92	168	<0.0001
	<=50	127	94		216	140	
Grade	II	82	15	<0.0001	178	43	<0.0001
	III	38	36		119	125	
	IV	33	102		11	140	
Histology	Oligodendroglioma	2	34	<0.0001	137	32	<0.0001
	Oligoastrocytoma	20	53		81	38	
	Astrocytoma	29	33		79	140	
	GBM	102	33		11	98	
IDH	Mutant	112	55	<0.0001	268	119	<0.0001
	Wildtype	41	98		36	185	
	NA	0	0		4	4	
1p/19q	Codel	63	0	<0.0001	141	14	<0.0001
	Non-codel	88	151		166	291	
	NA	2	2		1	3	
Chemostatus	Yes	76	97	0.01	128	128	<0.0001
	No	70	48		151	34	
	NA	7	8		29	146	
Radiostatus	Yes	129	122	0.3	163	219	<0.0001
	No	19	25		130	54	
	NA	5	6		15	35	

Note: Significance: $P^* < 0.05$, $P^{**} < 0.01$, $P^{***} < 0.001$.

Supplementary Table S4. The somatic mutation data of seven RNA:m⁵C methyltransferases from the TCGA dataset.

Symbol	Gene Id	Chromosome	Variant Classification	Variant Type	Tumor Sample	Mutation Status
NOP2	4839	chr12	Missense_Mutation	SNP	TCGA-02-2485-01	Somatic
NSUN2	54888	chr5	Missense_Mutation	SNP	TCGA-76-4926-01	Somatic
NSUN5	55695	chr7	Missense_Mutation	SNP	TCGA-DU-A5TR-01	Somatic
NSUN5	55695	chr7	Translation_Start_Site	SNP	TCGA-76-4926-01	Somatic
NSUN5	55695	chr7	Missense_Mutation	SNP	TCGA-06-0744-01	Somatic
NSUN7	79730	chr4	Nonsense_Mutation	SNP	TCGA-02-2486-01	Somatic