Supplementary Table 1. Functional-annotation statistics for m5C-regulating genes in HNSCC samples

Hugo Symbol	Frame Shift Del	Frame Shift Ins	In Frame Del	Missense Mutation	Nonsense Mutation	Splice Site	Total	Mutated Samples	Altered Samples
DNMT3B	0	0	0	8	1	0	9	9	9
DNMT3A	0	0	0	9	0	0	9	8	8
TET2	0	0	1	2	4	0	7	7	7
DNMT1	0	0	0	6	0	0	6	6	6
NSUN2	0	0	0	6	0	0	6	6	6
NSUN6	0	0	0	3	1	0	4	4	4
NSUN7	0	1	0	3	0	0	4	3	3
NSUN5	0	0	0	3	0	0	3	3	3
NSUN3	0	0	0	3	0	0	3	2	2
ALYREF	0	0	0	1	0	1	2	2	2
NSUN4	1	0	0	1	0	0	2	2	2

Supplementary Table 2. Copy-number variation statistics for m5C-regulating genes in HNSCC samples

Function	Genes	Diploid	Deletion	Amplification	CNV sum	Amplification %	Deletion %	Percentage
writer	NSUN1	-	-	-	-	-	-	-
	NSUN2	326	12	186	524	35.50%	2.29%	61.65%
	NSUN3	335	23	168	526	31.94%	4.37%	61.09%
	NSUN4	456	33	34	523	6.50%	6.31%	53.42%
	NSUN5	424	28	66	518	12.74%	5.41%	54.99%
	NSUN6	383	110	33	526	6.27%	20.91%	57.87%
	NSUN7	363	136	27	526	5.13%	25.86%	59.17%
	DNMT1	434	59	32	91	35.16%	64.84%	17.33%
	DNMT2		-	-	-	-	-	-
	DNMT3A	465	14	44	58	75.86%	24.14%	11.09%
	DNMT3B	369	9	154	163	94.48%	5.52%	30.64%
eraser	TET2	418	94	14	108	12.96%	87.04%	20.53%
reader	ALYREF	423	41	58	99	58.59%	41.41%	18.97%

Supplementary Table 3. The relationship between different expression levels in m5C-regulatory genes and patient prognoses

Genes	beta	HR (95% CI for HR)	wald.test	p.value
DNMT1	-0.031	0.97 (0.95-0.99)	7.9	0.005
TET2	-0.13	0.87 (0.77-0.99)	4.3	0.038
NSUN6	-0.15	0.86 (0.75-0.99)	4.2	0.04
DNMT3A	-0.081	0.92 (0.85-1)	3.3	0.071
NSUN7	-0.21	0.81 (0.62-1)	2.6	0.11
NSUN5	0.014	1 (0.99-1)	0.93	0.34
NSUN2	0.0075	1 (0.99-1)	0.85	0.36
DNMT3B	-0.02	0.98 (0.92-1)	0.32	0.57
ALYREF	-0.0016	1 (0.99-1)	0.28	0.6