Table S1 The baseline characteristics of patients in the TCGA-HNSCC cohort

Characteristic	Levels	Overall (N=502)
T stage, n (%)	T1	33 (6.8)
	T2	144 (29.6)
	T3	131 (26.9)
	T4	179 (36.8)
N stage, n (%)	N0	239 (49.8)
	N1	80 (16.7)
	N2	154 (32.1)
	N3	7 (1.5)
Clinical stage, n (%)	Stage I	19 (3.9)
	Stage II	95 (19.5)
	Stage III	102 (20.9)
	Stage IV	272 (55.7)
Gender, n (%)	Female	134 (26.7)
	Male	368 (73.3)
Age, n (%)	≤60 years	245 (48.9)
	>60 years	256 (51.1)
Histologic grade, n (%)	G1	62 (12.8)
	G2	300 (62.1)
	G3	119 (24.6)
	G4	2 (0.4)
Race, n (%)	Asian	10 (2.1)
	Black or African American	47 (9.7)
	White	428 (88.2)
Smoker, n (%)	No	111 (22.6)
	Yes	381 (77.4)
Alcohol history, n (%)	No	158 (32.2)
	Yes	333 (67.8)
Lymphovascular invasion, n (%)	No	219 (64.2)
	Yes	122 (35.8)
Age, median (IQR)		61 (53, 69)

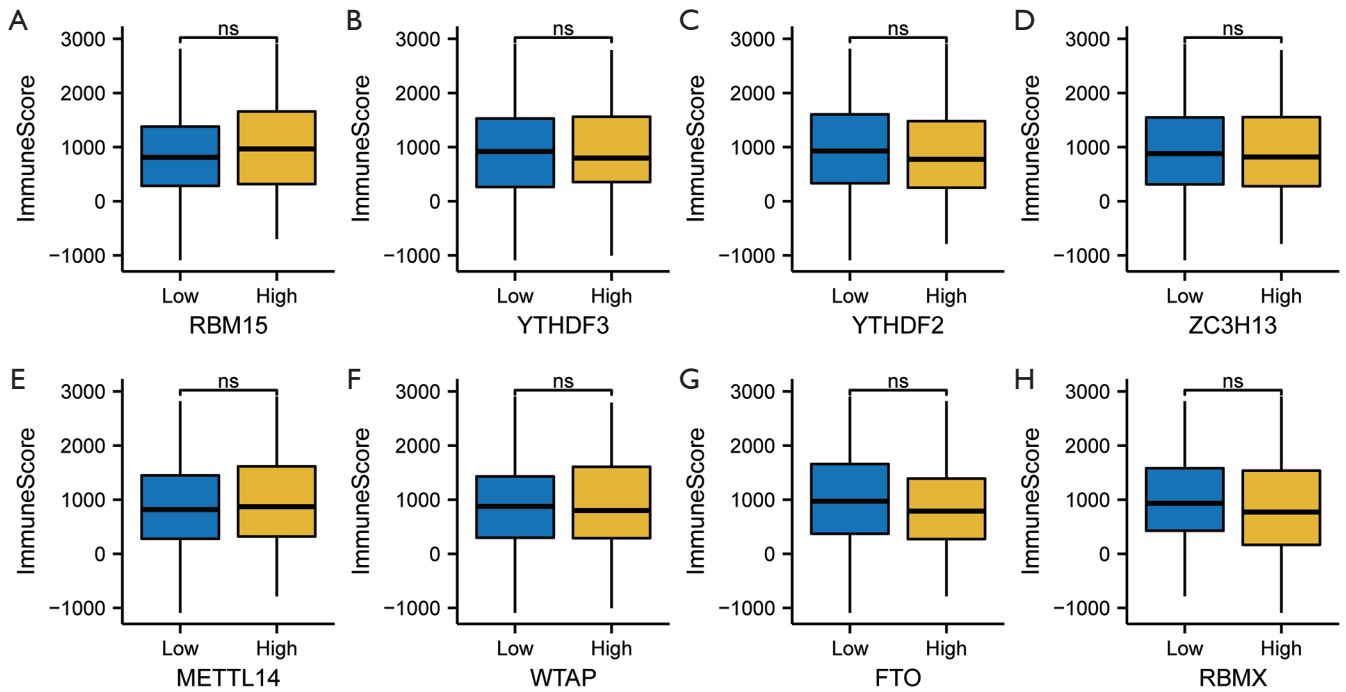TCGA, The Cancer Genome Atlas; HNSCC, head and neck squamous cell carcinoma; IQR, interquartile range.

Figure S1 The ImmuneScore in differentially expressed m6A methylation-related genes group. ns, P>0.05. (A) The immune score of high and low expression of RBM15. (B) The immune score of high and low expression of YTHDF3. (C) The immune score of high and low expression of YTHDF2. (D) The immune score of high and low expression of ZC3H13. (E) The immune score of high and low expression of METTL14. (F) The immune score of high and low expression of WTAP. (G) The immune score of high and low expression of FTO. (H) The immune score of high and low expression of RBMX.