Supplemental Information

Comprehensive Analysis of the PD-L1 and Immune Infiltrates of m^{6}A RNA Methylation Regulators in Head and Neck Squamous Cell Carcinoma

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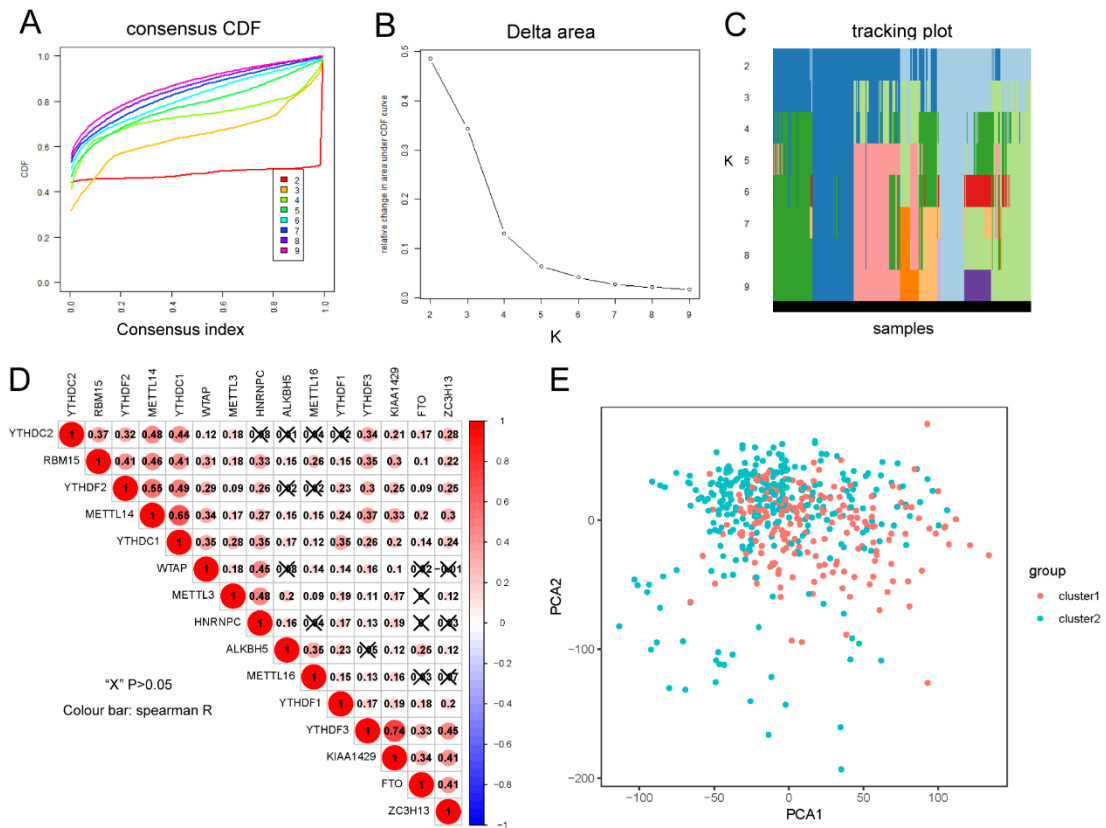
Supplemental information

Figure S1. Consensus clusters by m^{6}A regulators in TCGA cohort. (A) Consensus clustering cumulative distribution function (CDF) for k=2 to 9. (B) Relative change in area under the CDF curve for k=2 to 9. (C) Tracking plot for k=2 to 9. (D) Spearman correlation analysis of the 15 m^{6}A methylation regulators. (E) Principal component analysis of the total mRNA expression profile in 499 patients with HNSCC.
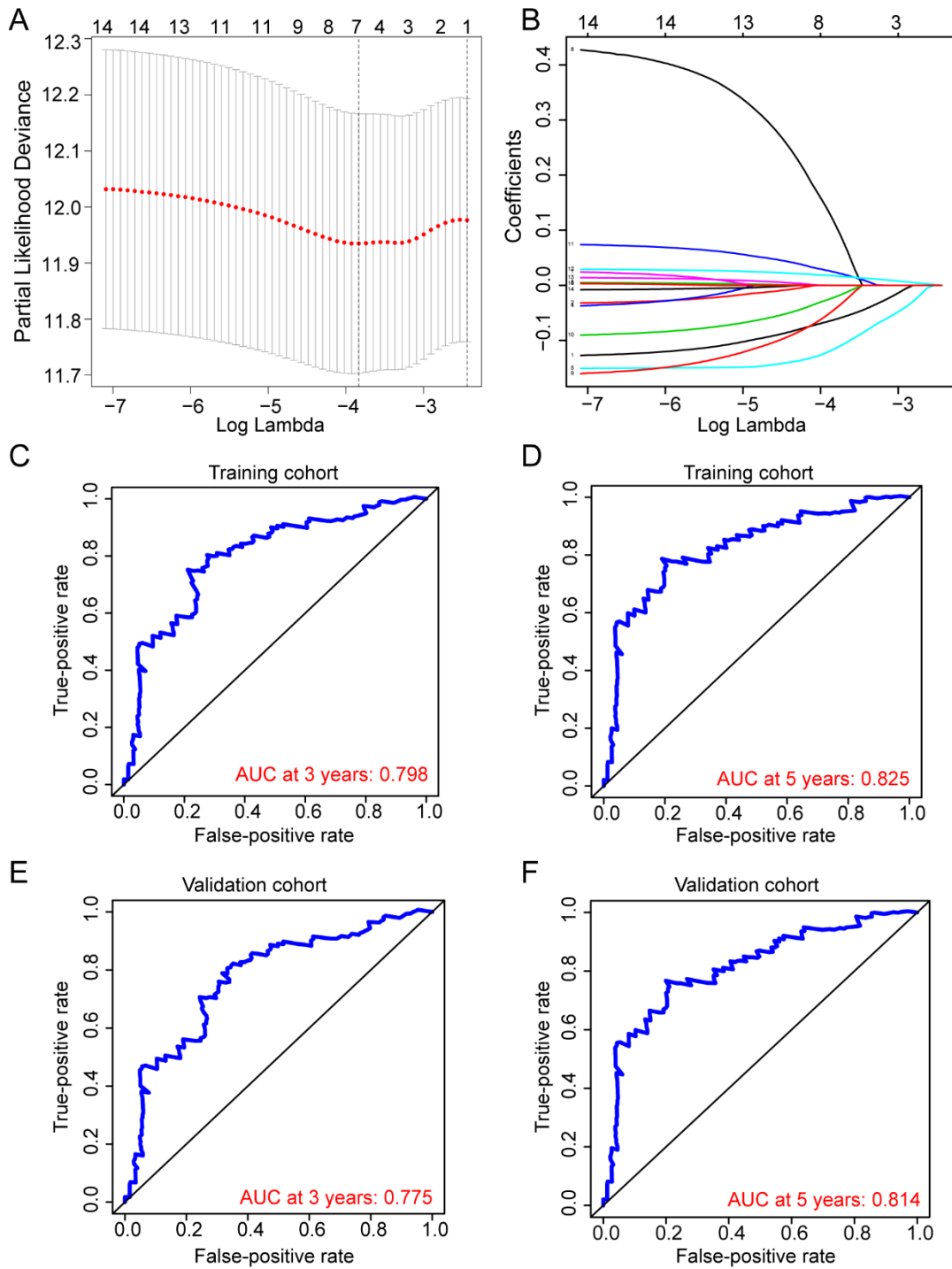
Figure S2. (A) Partial likelihood deviance for tuning the parameter selection in the LASSO regression model in TCGA cohort. (B) LASSO coefficient profiles of the 15 m⁶A RNA methylation regulators in TCGA cohort. (C–F) Receiver operating characteristic curves of 3 and 5 years based on the seven m⁶A regulator signatures in

the TCGA training cohort (C, D) and TCGA validation cohort (E, F).

A — Univariate analysis

	p-value	Hazard ratio
Gender	0.352	1.177 (0.835−1.658)
Age	0.002	1.024 (1.009−1.039)
Grade	0.599	0.905 (0.623−1.314)
T stage	0.112	1.165 (0.965−1.407)
N stage	0.027	1.414 (1.040−1.922)
M stage	0.017	2.732 (1.197−6.235)
TNM stage	0.001	1.805 (1.269−2.566)
Risk score	<0.001	2.064 (1.526−2.791)

B — Multivariate analysis

	p-value	Hazard ratio
Gender	0.536	1.121 (0.780−1.610)
Age	<0.001	1.030 (1.013−1.047)
Grade	0.512	0.880 (0.601−1.289)
T stage	0.581	0.935 (0.738−1.186)
N stage	0.260	1.226 (0.860−1.746)
M stage	0.093	2.062 (0.885−4.804)
TNM stage	0.009	1.887 (1.170−3.044)
Risk score	<0.001	1.933 (1.441−2.593)

C — Univariate analysis

	p-value	Hazard ratio
Gender	0.087	1.294 (0.964−1.736)
Age	<0.001	1.023 (1.010−1.037)
Grade	0.838	0.968 (0.708−1.323)
T stage	0.291	1.091 (0.928−1.282)
N stage	0.015	1.385 (1.064−1.802)
M stage	0.074	1.999 (0.936−4.271)
TNM stage	<0.001	1.715 (1.270−2.315)
Risk score	<0.001	3.809 (2.199−6.597)

D — Multivariate analysis

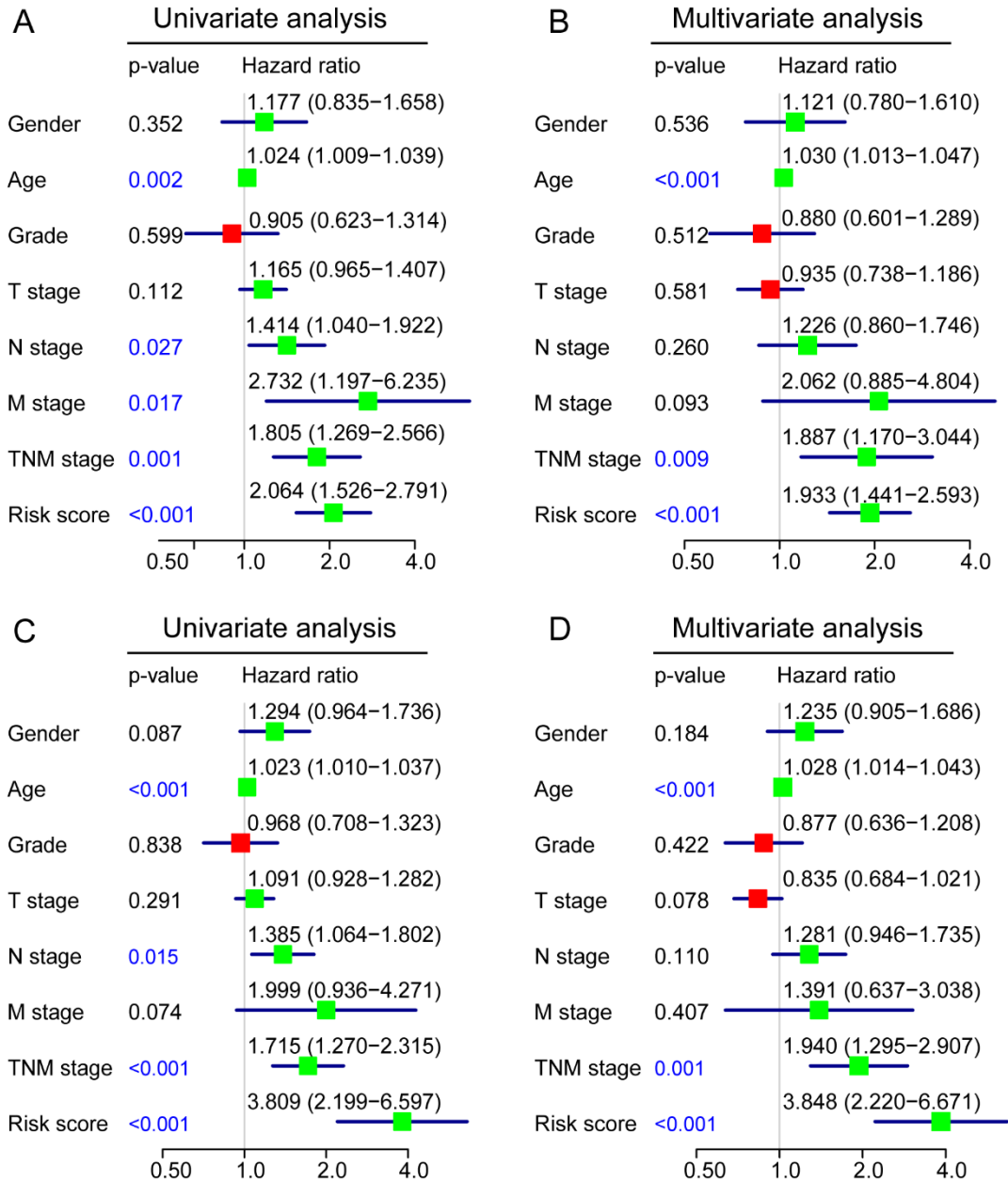|	p-value	Hazard ratio
Gender	0.184	1.235 (0.905−1.686)
Age	<0.001	1.028 (1.014−1.043)
Grade	0.422	0.877 (0.636−1.208)
T stage	0.078	0.835 (0.684−1.021)
N stage	0.110	1.281 (0.946−1.735)
M stage	0.407	1.391 (0.637−3.038)
TNM stage	0.001	1.940 (1.295−2.907)
Risk score	<0.001	3.848 (2.220−6.671)

Figure S3. (A–B) Univariate (A) and multivariate (B) Cox regression analyses in the TCGA training cohort. (C–D) Univariate (C) and multivariate (D) Cox regression analyses in the TCGA validation cohort.

Table S1. Clinicopathological features of patients in TCGA training and validation cohorts.

Variables		Training cohort No. (%)	Validation cohort No. (%)	P-value
No. of patients		351	148	
Age		61(49,73)	61(50,72)	0.92
Gender	Female	98(27.9)	35(23.6)	0.324
	Male	253(72.1)	113(76.4)	
T stage	T1	26(7.4)	11(7.4)	0.344
	T2	107(30.5)	38(25.7)	
	T3	98(27.9)	36(24.3)	
	T4	120(34.2)	63(42.6)	
N stage	N0	173(49.3)	71(48.0)	0.806
	N1	62(17.7)	26(17.6)	
	N2	111(31.6)	47(31.8)	
	N3	5(1.4)	4(2.7)	
M stage	M0	432(97.4)	145(98)	0.721
	M1	9(2.6)	3(2)	
TNM stage	I	17(4.8)	8(5.4)	0.172
	II	60(17.1)	20(13.5)	
	III	55(15.7)	35(23.6)	
	IV	219(62.4)	85(57.4)	
Grade	G1	43(12.3)	21(14.2)	0.826
	G2	216(61.5)	88(59.5)	
	G3	87(24.8)	38(25.7)	
	G4	5(1.4)	1(0.7)	