

Figure S1 The process of m^5C RNA methylation mediated by regulators.

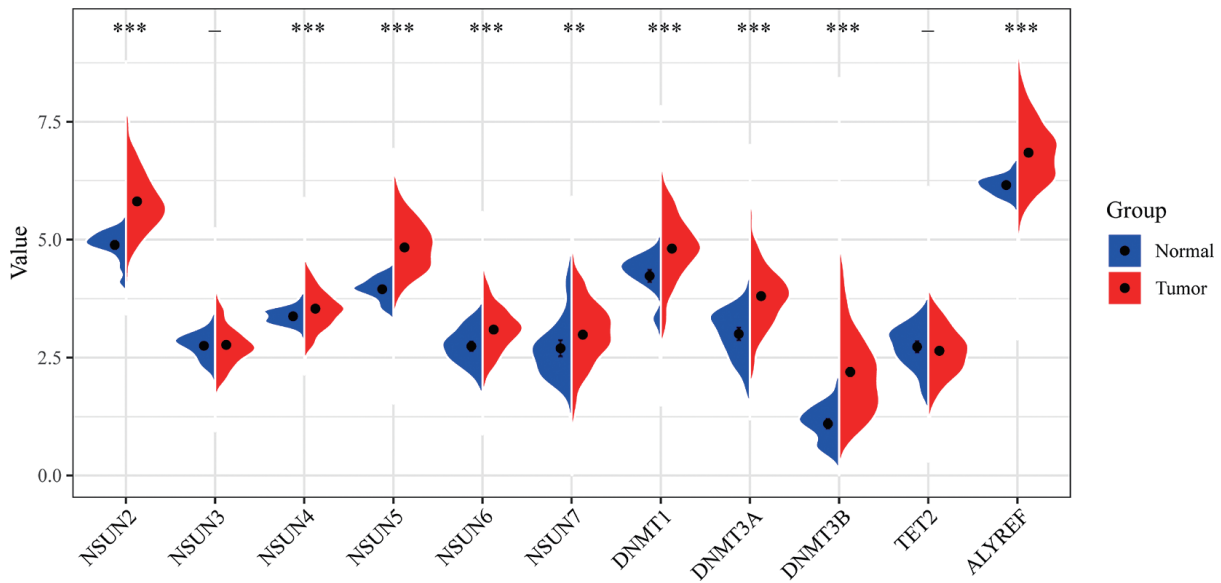


Figure S2 The expression of 11 m^5C regulators between normal tissues and LAUD tissues. Tumor, red; Normal, blue. **, $P < 0.01$; ***, $P < 0.001$. LAUD, lung adenocarcinoma.

Table S1 The interaction between m⁵C regulators in LUAD

from	to	pvalue	cor	weight	color
NSUN3	NSUN2	9.28E-05	0.17195286	4.0324767	#C6DBEF
NSUN4	NSUN2	1.28E-09	0.2648461	8.89121472	#C6DBEF
NSUN5	NSUN2	0	0.41406303	Inf	#C6DBEF
NSUN6	NSUN2	5.62E-11	0.28530344	10.2503662	#C6DBEF
NSUN7	NSUN2	2.44E-07	0.22613398	6.61262551	#C6DBEF
NSUN6	NSUN3	2.49E-12	0.30416041	11.6043272	#C6DBEF
NSUN7	NSUN3	2.83E-07	0.22494816	6.54869035	#C6DBEF
DNMT1	NSUN3	1.45E-08	0.24775946	7.83919998	#C6DBEF
DNMT3A	NSUN3	3.74E-10	0.273108	9.42682302	#C6DBEF
NSUN6	NSUN4	8.42E-09	0.25169354	8.07484959	#C6DBEF
NSUN7	NSUN4	9.51E-14	0.32246131	13.021756	#C6DBEF
DNMT1	NSUN4	5.23E-07	0.2199184	6.28129578	#C6DBEF
DNMT3A	NSUN4	7.47E-08	0.23544234	7.12643018	#C6DBEF
NSUN7	NSUN5	9.69E-05	0.17149368	4.0135231	#C6DBEF
DNMT3A	NSUN5	8.91E-10	0.26732271	9.04990545	#C6DBEF
DNMT3B	NSUN5	2.59E-12	0.3039158	11.586107	#C6DBEF
NSUN7	NSUN6	1.88E-13	0.31876927	12.7266334	#C6DBEF
DNMT1	NSUN6	1.09E-13	0.32172987	12.9628856	#C6DBEF
DNMT3B	NSUN6	2.44E-15	0.3411941	14.6128325	#C6DBEF
TET2	NSUN6	3.09E-13	0.31602253	12.5102525	#C6DBEF
DNMT1	NSUN7	7.32E-10	0.26865004	9.13560993	#C6DBEF
DNMT3B	NSUN7	6.84E-06	0.19753793	5.16496991	#C6DBEF
TET2	NSUN7	8.11E-14	0.32331914	13.0910608	#C6DBEF
TET2	DNMT1	2.34E-13	0.31756247	12.6312402	#C6DBEF
ALYREF	DNMT3A	3.90E-15	0.33892201	14.4094214	#C6DBEF

Table S4 Enrichment results of the high and low m⁵C score groups were analysed

KEGG	subtype
KEGG_HOMOLOGOUS_RECOMBINATION	C1
KEGG_BASE_EXCISION_REPAIR	C1
KEGG_SPLICEOSOME	C1
KEGG_DNA_REPLICATION	C1
KEGG_CELL_CYCLE	C1
KEGG_MISMATCH_REPAIR	C1
KEGG_PROTEASOME	C1
KEGG_NUCLEOTIDE_EXCISION_REPAIR	C1
KEGG_RNA_DEGRADATION	C1
KEGG_PYRIMIDINE_METABOLISM	C1
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	C1
KEGG_BASAL_TRANSCRIPTION_FACTORS	C1
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	C1
KEGG_ONE_CARBON_POOL_BY_FOLATE	C1
KEGG_GLYCOPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	C2
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	C2
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	C2
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	C2
KEGG_PPAR_SIGNALING_PATHWAY	C2
KEGG_RENIN_ANGIOTENSIN_SYSTEM	C2
KEGG_HEDGEHOG_SIGNALING_PATHWAY	C2
KEGG_LONG_TERM_DEPRESSION	C2
KEGG_ARACHIDONIC_ACID_METABOLISM	C2
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	C2
KEGG_APOPTOSIS	C2
KEGG_ASTHMA	C2
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	C2
KEGG_LYSOSOME	C2
KEGG_O_GLYCAN_BIOSYNTHESIS	C2
KEGG_NITROGEN_METABOLISM	C2
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	C2
KEGG_FATTY_ACID_METABOLISM	C2
KEGG_ETHER_LIPID_METABOLISM	C2
KEGG_CELL_ADHESION_MOLECULES_CAMS	C2
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	C2
KEGG_MAPK_SIGNALING_PATHWAY	C2
KEGG_HEMATOPOIETIC_CELL_LINEAGE	C2
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	C2
KEGG_CALCIIUM_SIGNALING_PATHWAY	C2