

Supplementary Material

1 Supplementary Tables

Supplementary Table S1. Sequence of primers used for qRT-PCR analysis of mRNA levels

Gene Name	Sequence	T _m (°C)	Product Size (bp)
GAPDH	F:5' GCTCTCTGCTCCTCCCTGTTCTA3'	60	124
	R:5' TGGTAACCAGGCGTCCGATA3'		
METTL3	F:5' TTGACTACAGTGGCTACCTTT3'	60	220
	R:5' CCTTGGCTGTTGTGGTATT3'		
METTL14	F:5' GAGTATGTTTGCGAAAGTGGG3'	60	84
	R:5' TTGTCTTTCCAGGATTGTTCTT 3'		
WTAP	F:5' GAAAACTAAAGCAGCAACAG3'	60	267
	R:5' CGTAAACTTCCAGGCACTC3'		
YTHDF1	F:5' GCCAGGAGGAAGAGGAGGTA 3'	60	131
	R:5' AGACAGCACCAAGCATAACAGC 3'		
YTHDF3	F:5' GCCATGCGAAGGGAGAGAA3'	60	278
	R:5' AGCTTCAGGACACAAAGTGCT3'		
FTO	F:5' GAGCGGGAAGCTAAGAAA 3'	60	100
	R:5' GCTGCCACTGCTGATAGAA 3'		

METTL3, methyltransferase-like 3; METTL14, methyltransferase-like 14; WTAP, Wilms tumor 1-associated protein; YTHDF1, YTH domain family 1; YTHDF3, YTH domain family 3; FTO, fat mass and obesity associated protein.

Supplementary Table S2. Sequence of primers used for m⁶A single base site qPCR analysis of relative mRNA methylation levels

Gene Name	Sequence	T _m (°C)	Product Size (bp)
XR_595034	F:5' ATCTCATCCTGCCGCTCCTT3' R:5' TCTCCGCCTCCAGCACTTA3'	60	276
XR_346771	F:5' GAATTTGCTGAGTAAACACCCTAT3' R:5' CACTGGTGGTCGCCTATTGT3'	60	147
XR_338486	F:5' TGTGGAGGGATCTGGTTCTTG3' R:5' CTGCGGGACTGTATGGAGTG3'	60	191
XR_596592	F:5' ATCTGACGGCAGGATTTGGAG 3' R:5' TTGCACTTTGAGCGTGGACAT3'	60	85
Clec1b	F:5' GATTGGATTATCACGCCAGAA3' R:5' ACTCTTGTCAGGGCAGCATT3'	60	201
Tnfrsf21	F:5' TGCCTTGACTGACCGAGAAT3' R:5' CACTGCTTACACCGCACATC3'	60	141
Ptk2b	F:5' CCTGCCTTGCCTTTGGTTAT3' R:5' GTGTCTGTGCCAGAGTCCTT3'	60	147
Tnfrsf26	F:5' GCTGTCCTGAGGGCAGAGTC3' R:5' TGACGGGAGTAGCGAATGAA3'	60	184
Ankrd54	F:5' TGGAGACCAAGAGCGAGCAG 3' R:5' GAGCCGGATTTCCCAATTTC3'	60	226
Stk38l	F:5' ATTTGCCCTGTTGGTTTGA3' R:5' ATGTTGCGGTGGAGGTGAGA3'	60	182

2 Supplementary Figure

Supplementary Figure S1. Expressions of m⁶A-related enzymes were detected by western blot analysis. n = 3-4; **P* < 0.05. Ctrl, control; LPS, lipopolysaccharide.

