Electronic Supplementary Material (ESI) for RSC Advances.

Supporting Information

for

"Determination of DNA Adenine Methylation in Genomes of Mammals and Plants by Liquid Chromatography / Mass Spectrometry"

Wei Huang,[1] Jun Xiong,[1] Ying Yang,[2] Song-Mei Liu,[2] Bi-Feng Yuan[1,*] ,Yu-Qi Feng[1]

[1] Key Laboratory of Analytical Chemistry for Biology and Medicine (Ministry of Education), Department of Chemistry, Wuhan University, Wuhan 430072, P.R. China

[2] Center for Gene Diagnosis, Zhongnan Hospital of Wuhan University, Donghu Road 169#, Wuhan, 430071, P.R. China

*To whom correspondence should be addressed. Tel.:+86-27-68755595; fax: +86-27-68755595. E-mail address: bfyuan@whu.edu.cn

Table S1. The MRM transitions and optimal parameters for the analysis of nucleosides by mass spectrometry.

Nuclosides	Precursor ion	Product ion	DP/V	EP / V	CEP / V	CE / V	CXP / V
m^6dA	266.1	150.2	21.8	7.0	16.6	19.0	2.5
dA	252.4	136.2	15.0	5.0	15.0	23.0	2.0
dC	228.4	112.2	11.0	5.0	15.0	23.0	3.0
dG	268.4	152.4	15.0	5.0	20.0	23.0	5.0
dT	243.3	127.2	25.0	5.0	15.0	23.0	5.0
m^6A	282.2	150.1	32.0	8.0	10.0	27.0	2.6
rA	268.4	152.4	15.0	5.0	16.6	23.0	2.0
rC	244.1	112.1	20.0	8.0	10.0	21.3	2.4
rG	284.5	152.2	40.0	5.0	9.0	23.0	6.0
rU	245.4	113.1	24.7	6.0	13.0	13.7	3.8

Table S2. m^6dA and m^6A contents in 15 T2DM patients and 15 control subjects.

Sample Name	m^6A/A,%	m^6dA/dA,%
T2DM-1	0.11	0.00030
T2DM-2	0.09	0.00031
T2DM-3	0.10	0.00029
T2DM-4	0.10	0.00031
T2DM-5	0.10	0.00023
T2DM-6	0.10	0.00027
T2DM-7	0.12	0.00033
T2DM-8	0.13	0.00027
T2DM-9	0.12	0.00034
T2DM-10	0.13	0.00025
T2DM-11	0.13	0.00025
T2DM-12	0.14	0.00028
T2DM-13	0.12	0.00023
T2DM-14	0.11	0.00027
T2DM-15	0.12	0.00028
Control-1	0.12	0.00034
Control-2	0.18	0.00033
Control-3	0.17	0.00030
Control-4	0.16	0.00030
Control-5	0.16	0.00032
Control-6	0.16	0.00034
Control-7	0.17	0.00031
Control-8	0.17	0.00038
Control-9	0.19	0.00048
Control-10	0.20	0.00039
Control-11	0.16	0.00022
Control-12	0.21	0.00037
Control-13	0.23	0.00033
Control-14	0.26	0.00028
Control-15	0.19	0.00033

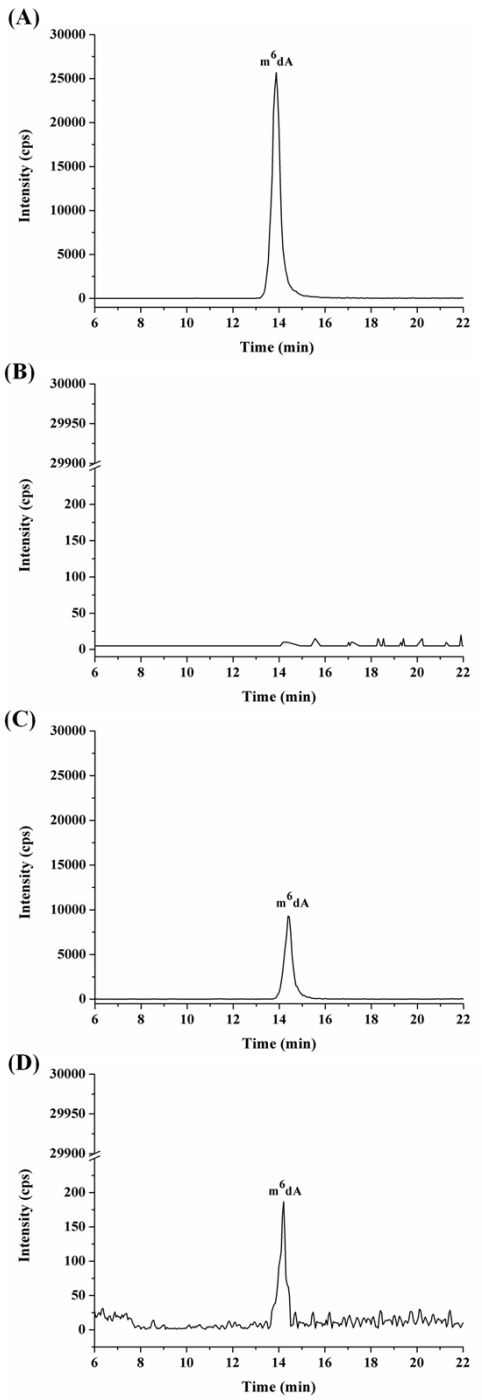

Figure S1. Elimination of possible bacterial DNA by Dpn I cleavage coupled with size-exclusion ultrafiltration. MRM chromatograms of m^6dA from (A) 100 ng bacterial DNA, (B) the retentate of 100 ng bacterial DNA treated by Dpn I cleavage coupled with size-exclusion ultrafiltration, (C) 5 μg 293T DNA, (D) the retentate of 5 μg 293T DNA treated by Dpn I cleavage coupled with size-exclusion ultrafiltration.

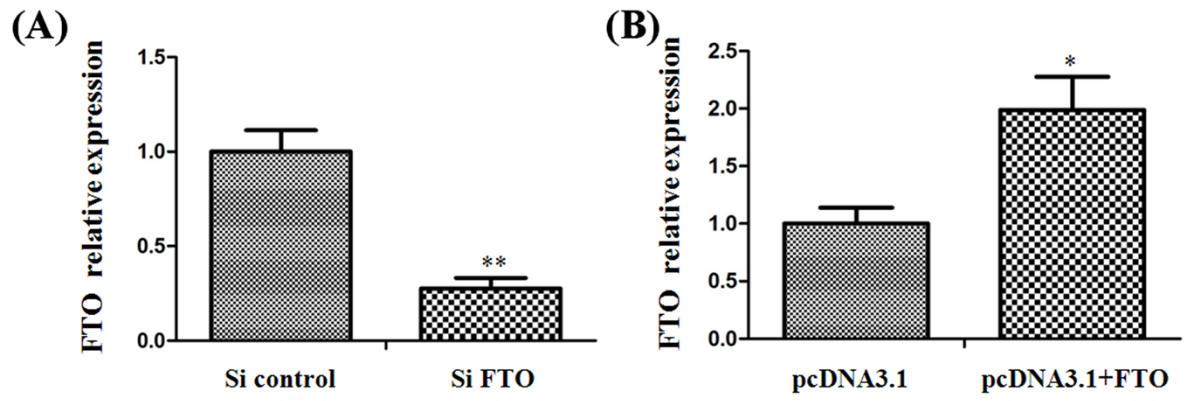

Figure S2. Expression levels of *FTO* gene in cells upon knockdown and overexpression.* p＜0.05，**p＜0.01.