Supporting Information

for

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

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

<table>
<thead>
<tr>
<th>Nucleosides</th>
<th>Precursor ion</th>
<th>Product ion</th>
<th>DP/V</th>
<th>EP / V</th>
<th>CEP / V</th>
<th>CE / V</th>
<th>CXP / V</th>
</tr>
</thead>
<tbody>
<tr>
<td>m6dA</td>
<td>266.1</td>
<td>150.2</td>
<td>21.8</td>
<td>7.0</td>
<td>16.6</td>
<td>19.0</td>
<td>2.5</td>
</tr>
<tr>
<td>dA</td>
<td>252.4</td>
<td>136.2</td>
<td>15.0</td>
<td>5.0</td>
<td>15.0</td>
<td>23.0</td>
<td>2.0</td>
</tr>
<tr>
<td>dC</td>
<td>228.4</td>
<td>112.2</td>
<td>11.0</td>
<td>5.0</td>
<td>15.0</td>
<td>23.0</td>
<td>3.0</td>
</tr>
<tr>
<td>dG</td>
<td>268.4</td>
<td>152.4</td>
<td>15.0</td>
<td>5.0</td>
<td>20.0</td>
<td>23.0</td>
<td>5.0</td>
</tr>
<tr>
<td>dT</td>
<td>243.3</td>
<td>127.2</td>
<td>25.0</td>
<td>5.0</td>
<td>15.0</td>
<td>23.0</td>
<td>5.0</td>
</tr>
<tr>
<td>m6A</td>
<td>282.2</td>
<td>150.1</td>
<td>32.0</td>
<td>8.0</td>
<td>10.0</td>
<td>27.0</td>
<td>2.6</td>
</tr>
<tr>
<td>rA</td>
<td>268.4</td>
<td>152.4</td>
<td>15.0</td>
<td>5.0</td>
<td>16.6</td>
<td>23.0</td>
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<td>244.1</td>
<td>112.1</td>
<td>20.0</td>
<td>8.0</td>
<td>10.0</td>
<td>21.3</td>
<td>2.4</td>
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<tr>
<td>rG</td>
<td>284.5</td>
<td>152.2</td>
<td>40.0</td>
<td>5.0</td>
<td>9.0</td>
<td>23.0</td>
<td>6.0</td>
</tr>
<tr>
<td>rU</td>
<td>245.4</td>
<td>113.1</td>
<td>24.7</td>
<td>6.0</td>
<td>13.0</td>
<td>13.7</td>
<td>3.8</td>
</tr>
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</table>
Table S2. \( \text{m}^6\text{dA} \) and \( \text{m}^6\text{A} \) contents in 15 T2DM patients and 15 control subjects.

<table>
<thead>
<tr>
<th>Sample Name</th>
<th>( \text{m}^6\text{A}/\text{A},% )</th>
<th>( \text{m}^6\text{dA}/\text{dA},% )</th>
</tr>
</thead>
<tbody>
<tr>
<td>T2DM-1</td>
<td>0.11</td>
<td>0.00030</td>
</tr>
<tr>
<td>T2DM-2</td>
<td>0.09</td>
<td>0.00031</td>
</tr>
<tr>
<td>T2DM-3</td>
<td>0.10</td>
<td>0.00029</td>
</tr>
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<td>T2DM-4</td>
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<td>0.00031</td>
</tr>
<tr>
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<tr>
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<td>0.00027</td>
</tr>
<tr>
<td>T2DM-7</td>
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<td>0.00033</td>
</tr>
<tr>
<td>T2DM-8</td>
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<td>0.00027</td>
</tr>
<tr>
<td>T2DM-9</td>
<td>0.12</td>
<td>0.00034</td>
</tr>
<tr>
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<td>0.00025</td>
</tr>
<tr>
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<td>0.13</td>
<td>0.00025</td>
</tr>
<tr>
<td>T2DM-12</td>
<td>0.14</td>
<td>0.00028</td>
</tr>
<tr>
<td>T2DM-13</td>
<td>0.12</td>
<td>0.00023</td>
</tr>
<tr>
<td>T2DM-14</td>
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<td>0.00027</td>
</tr>
<tr>
<td>T2DM-15</td>
<td>0.12</td>
<td>0.00028</td>
</tr>
<tr>
<td>Control-1</td>
<td>0.12</td>
<td>0.00034</td>
</tr>
<tr>
<td>Control-2</td>
<td>0.18</td>
<td>0.00033</td>
</tr>
<tr>
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<tr>
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<td>0.16</td>
<td>0.00030</td>
</tr>
<tr>
<td>Control-5</td>
<td>0.16</td>
<td>0.00032</td>
</tr>
<tr>
<td>Control-6</td>
<td>0.16</td>
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<td>0.26</td>
<td>0.00028</td>
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<tr>
<td>Control-15</td>
<td>0.19</td>
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</tbody>
</table>
Figure S1. Elimination of possible bacterial DNA by Dpn I cleavage coupled with size-exclusion ultrafiltration. MRM chromatograms of m6dA 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.