### Supplementary Material

#### Table S1  PCR primers and condition.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer</th>
<th>Primers for bisulfite pyrosequencing</th>
<th>Product length (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Resistin</td>
<td>Forward</td>
<td>TATGTTGTGTTAGGGGTTCCTTTTTT</td>
<td>163</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>AAAAAACAACTATACCTACCCCCCCTC</td>
<td></td>
</tr>
<tr>
<td>RBP4</td>
<td>Forward</td>
<td>TGTTAAATGGGATTTTCCAAGGTA</td>
<td>226</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>ACCCTAATCTACAACCTACACTC</td>
<td></td>
</tr>
<tr>
<td>GLUT3</td>
<td>Forward</td>
<td>TAAAGGAAATCTTCTTATTTTTCG</td>
<td>192</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>CATAAAACACCCACCACAAAC</td>
<td></td>
</tr>
<tr>
<td>PPARα</td>
<td>Forward</td>
<td>GGTTCAGATGGTTTTTGTGTGAT</td>
<td>165</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>TCAAACTCCTAATCTCAATAAATACC</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Reagents</th>
<th>Final conc.</th>
<th>Temperature</th>
<th>Cycles</th>
</tr>
</thead>
<tbody>
<tr>
<td>10X HotStarTaq Buffer</td>
<td>1X</td>
<td>Initial denaturation: 95°C</td>
<td>10 min</td>
</tr>
<tr>
<td>MgCl₂</td>
<td>1.25 mM</td>
<td>Denaturation: 95°C</td>
<td>40 s</td>
</tr>
<tr>
<td>dNTP</td>
<td>200 mM</td>
<td>Annealing: 50°C</td>
<td>40 s × 40 cycles</td>
</tr>
<tr>
<td>Forward primer</td>
<td>200 nM</td>
<td>Extension: 72°C</td>
<td>40 s</td>
</tr>
<tr>
<td>Reverse primer</td>
<td>200 nM</td>
<td>Final extension: 72°C</td>
<td>7 min</td>
</tr>
<tr>
<td>HotStarTaq</td>
<td>0.04 U</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total reaction volume</td>
<td>25 ul</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Fig. S1  Distribution of DNA methylation level on human placental genome.