

## SUPPLEMENTARY INFORMATION

### **DNA Methylation Profiles of Blood Cells Are Distinct between Early-Onset Obese and Control Individuals**

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	TSS1500	TSS200	5UTR	1stExon	Body	3UTR	p-value
<i>MIR1185-2</i>	1	1			1		3.17E-06
<i>C21orf56</i>			4		1		7.97E-07
<i>ZNF154</i>	1	1	1				1.41E-05
<i>SDK1</i>					13		2.91E-05
<i>KIAA0146</i>	3				3		3.34E-05
<i>SKIV2L</i>			1		5		3.84E-05
<i>GPR125</i>					4		5.58E-05
<i>SORBS2</i>			3		4		7.17E-05
<i>C14orf70</i>	1	1			1		1.06E-04
<i>POLR3E</i>	1		1		2		2.28E-04
<i>CTBP2</i>			4		3		2.67E-04
<i>DLGAP2</i>			2		7		3.05E-04
<i>CAPS2</i>	1				4		4.60E-04
<i>FLJ39609</i>	3						4.79E-04
<i>GIMAP1</i>					3		4.79E-04
<i>RNF213</i>			1		5		5.46E-04
<i>MND1</i>	1				2		6.32E-04
<i>SRM</i>				1	1	1	6.32E-04
<i>CELA2A</i>		1	1				6.41E-04
<i>TGM6</i>					4		8.12E-04
<i>WDR27</i>					6		9.77E-04

**Supplementary Fig. 3.** Genes significantly enriched with CpGs differentially methylated between obese and control individuals. The number in each cell is the number of the differentially methylated CpGs in the corresponding genomic region. Red and blue represent obese-hypermethylated and obese-hypomethylated CpGs, respectively. TSS1500, 1,500 bp regions upstream of the transcription start site; TSS200, 200 bp regions upstream of the transcription start site; UTR, untranslated region.