

**Supplementary table 1.** Percentages of CpG methylation in the three groups (normal-weight, overweight/obese and morbidly obese) measured by Sequenom's MassARRAY®. Two regions of *CLOCK* gene were quantified (with the pairs of primers R1 and R2), whereas only one region of *BMAL1* and *PER2* was analyzed. The data are the average percentage of cytosine methylation  $\pm$  SEM.

**A.** Percentages (%) of methylation in *CLOCK* gene as measured with the pair of primers R1.

	CLOCK1_QpG_1	CLOCK1_QpG_2	CLOCK1_QpG_4	CLOCK1_QpG_5.6	CLOCK1_QpG_8	CLOCK1_QpG_9	CLOCK1_QpG_10
<b>Control</b>	1.1 $\pm$ 0.2	4.3 $\pm$ 0.4	5.5 $\pm$ 0.7	12.4 $\pm$ 0.7	8.7 $\pm$ 0.8	0.6 $\pm$ 0.1	0.6 $\pm$ 0.2
<b>Obese</b>	1.8 $\pm$ 0.5	4.3 $\pm$ 0.5	5.8 $\pm$ 0.7	16.2 $\pm$ 0.8	11.8 $\pm$ 0.9	0.8 $\pm$ 0.1	0.7 $\pm$ 0.2
<b>Morbid</b>	2.4 $\pm$ 0.6	5.7 $\pm$ 0.8	6.8 $\pm$ 1.6	17.4 $\pm$ 0.9	10.7 $\pm$ 0.8	0.5 $\pm$ 0.1	0.9 $\pm$ 0.4

**B.** Percentages (%) of methylation in *CLOCK* gene as measured with the pair of primers R2.

	CLOCK3_QpG_1.2	CLOCK3_QpG_4.5.6	CLOCK3_QpG_7	CLOCK3_QpG_8	CLOCK3_QpG_9	CLOCK3_QpG_10	CLOCK3_QpG_11.12.13.14	CLOCK3_QpG_15.16	CLOCK3_QpG_23	CLOCK3_QpG_24.25.26	CLOCK3_QpG_27.28	CLOCK3_QpG_29
<b>Control</b>	82.9 $\pm$ 2.2	72.0 $\pm$ 2.6	1.7 $\pm$ 0.3	1.4 $\pm$ 0.3	5.5 $\pm$ 0.5	0.9 $\pm$ 0.1	59.5 $\pm$ 4.0	94.9 $\pm$ 1.0	2.0 $\pm$ 0.3	5.7 $\pm$ 0.5	6.3 $\pm$ 0.3	2.4 $\pm$ 1.4
<b>Obese</b>	81.4 $\pm$ 2.7	74.3 $\pm$ 1.9	2.4 $\pm$ 0.3	1.3 $\pm$ 0.2	5.0 $\pm$ 0.5	1.1 $\pm$ 0.1	52.3 $\pm$ 3.4	93.4 $\pm$ 1.1	2.2 $\pm$ 0.6	5.6 $\pm$ 0.4	6.4 $\pm$ 0.4	1.0 $\pm$ 0.4
<b>Morbid</b>	77.2 $\pm$ 2.4	72.3 $\pm$ 2.3	2.2 $\pm$ 0.3	1.4 $\pm$ 0.1	6.3 $\pm$ 0.7	1.2 $\pm$ 0.1	49.5 $\pm$ 2.7	94.4 $\pm$ 0.8	1.6 $\pm$ 0.4	5.4 $\pm$ 0.5	6.3 $\pm$ 0.3	2.2 $\pm$ 1.1

**C. Percentages (%) of methylation in the different CpGs analyzed in *PER2* gene.**

	PER2_3_CpG_1	PER2_3_CpG_2,3,4	PER2_3_CpG_5,6	PER2_3_CpG_7	PER2_3_CpG_9	PER2_3_CpG_10,11	PER2_3_CpG_12	PER2_3_CpG_13	PER2_3_CpG_22	PER2_3_CpG_23	PER2_3_CpG_24	PER2_3_CpG_25	PER2_3_CpG_26	PER2_3_CpG_27
<b>Control</b>	1.5±0.1	2.8±0.3	21.8±1.3	5.7±0.4	5.1±0.3	4.6±0.3	1.0±0.1	5.1±0.4	31.9±1.2	20.1±1.5	20.0±1.3	2.8±0.3	1.0±0.1	0.4±0.1
<b>Obese</b>	1.5±0.1	3.3±0.3	21.1±1.5	5.4±0.4	5.5±0.5	3.7±0.4	0.9±0.1	5.4±0.4	30.7±0.9	23.0±1.2	18.7±1.2	3.3±0.3	0.9±0.1	0.6±0.1
<b>Morbid</b>	1.3±0.1	3.6±0.2	23.0±1.3	5.3±0.4	5.1±0.6	4.3±0.4	1.1±0.1	5.3±0.4	31.2±1.2	21.4±1.6	19.0±0.9	3.6±0.2	1.0±0.2	0.5±0.1

**D. Percentages (%) of methylation in the different CpGs analyzed in *BMAL1* gene.**

	BMAL1_CpG_1	BMAL1_CpG_2	BMAL1_CpG_3,4	BMAL1_CpG_5	BMAL1_CpG_6,7	BMAL1_CpG_8	BMAL1_CpG_9	BMAL1_CpG_10,11	BMAL1_CpG_12	BMAL1_CpG_13,14	BMAL1_CpG_15	BMAL1_CpG_16,17	BMAL1_CpG_18	BMAL1_CpG_19
<b>Control</b>	2.5±0.1	0.1±0.0	4.2±0.2	1.4±0.2	5.4±0.3	1.2±0.2	1.8±0.3	1.8±0.2	14.5±0.7	2.3±0.2	1.2±0.2	5.5±0.3	3.8±1.3	4.8±0.4
<b>Obese</b>	2.7±0.1	0.7±0.4	4.3±0.4	1.6±0.2	7.0±0.7	2.0±0.4	1.3±0.2	2.1±0.5	14.1±0.6	2.1±0.1	2.0±0.4	7.4±0.7	2.8±0.9	6.1±0.8
<b>Morbid</b>	2.6±0.1	0.3±0.1	4.4±0.3	1.6±0.1	5.7±0.4	1.5±0.3	1.7±0.2	1.8±0.2	14.9±1.6	2.5±0.2	1.5±0.3	6.8±0.4	2.8±0.9	5.2±0.8