

**Supplementary Table 9:** Global DNA methylation in human pancreatic islets. Average DNA methylation (%) in gene- and CpG-regions in human pancreatic islets treated for 48 h with control media or palmitate containing media.

<b>Relation to gene region</b>					
<b>Region</b>	<b>Control mean <math>\pm</math> sd (%)</b>	<b>Palmitate mean <math>\pm</math> sd (%)</b>	<b>Diff. palmitate - control</b>	<b>P-value</b>	<b>q-value</b>
TSS1500	27.2 $\pm$ 1.3	27.9 $\pm$ 1.2	0.8	0.0032	0.0056
TSS200	12.2 $\pm$ 0.7	12.4 $\pm$ 0.7	0.2	0.0767	0.0895
5'UTR	22.7 $\pm$ 1.1	23.3 $\pm$ 1.0	0.6	0.0151	0.0211
1stExon	13.9 $\pm$ 0.9	14.1 $\pm$ 0.8	0.3	0.0948	0.0948
Body	59.7 $\pm$ 1.3	60.7 $\pm$ 0.5	1.0	0.0011	0.0025
3'UTR	70.7 $\pm$ 1.3	71.8 $\pm$ 0.5	1.0	0.0003	0.0018
Intergenic	56.9 $\pm$ 1.4	58.0 $\pm$ 0.8	1.1	0.0011	0.0025
<b>Relation to CpG island region</b>					
<b>Region</b>	<b>Control mean <math>\pm</math> sd (%)</b>	<b>Palmitate mean <math>\pm</math> sd (%)</b>	<b>Diff. palmitate - control</b>	<b>P-value</b>	<b>q-value</b>
N Shelf	72.5 $\pm$ 1.3	73.5 $\pm$ 0.6	1.0	0.0022	0.0026
N Shore	41.9 $\pm$ 1.5	43.0 $\pm$ 1.1	1.1	0.0009	0.0026
Island	14.7 $\pm$ 0.8	15.0 $\pm$ 0.7	0.2	0.1189	0.1189
S Shore	40.6 $\pm$ 1.5	41.7 $\pm$ 1.1	1.1	0.0010	0.0026
S Shelf	73.1 $\pm$ 1.3	74.1 $\pm$ 0.6	1.0	0.0022	0.0026
Open Sea	68.7 $\pm$ 1.3	69.7 $\pm$ 0.6	1.1	0.0013	0.0026