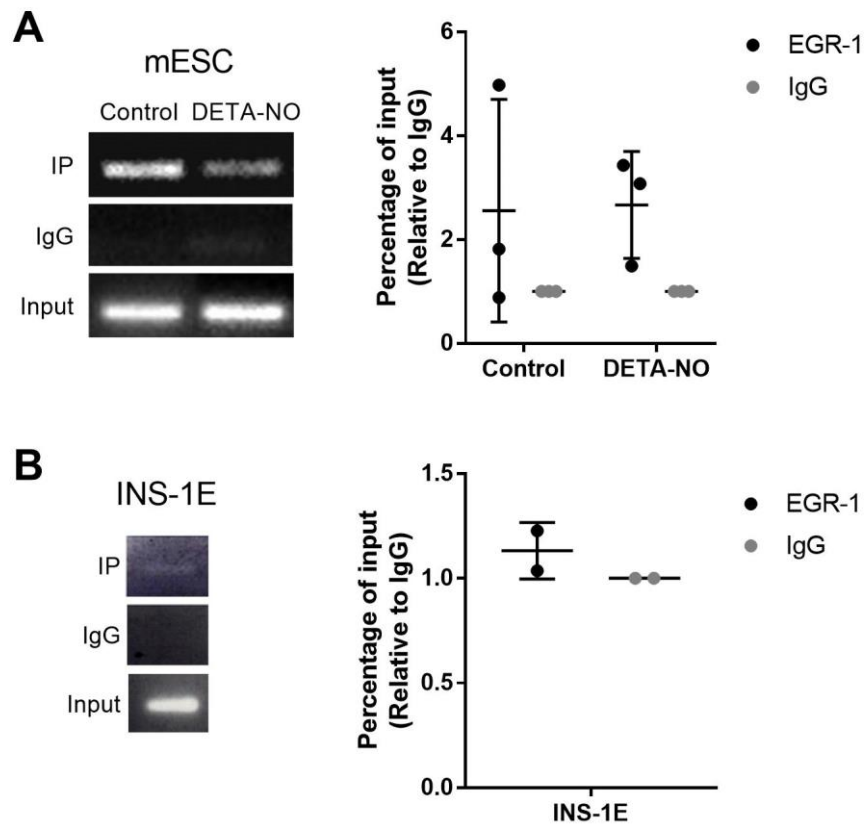


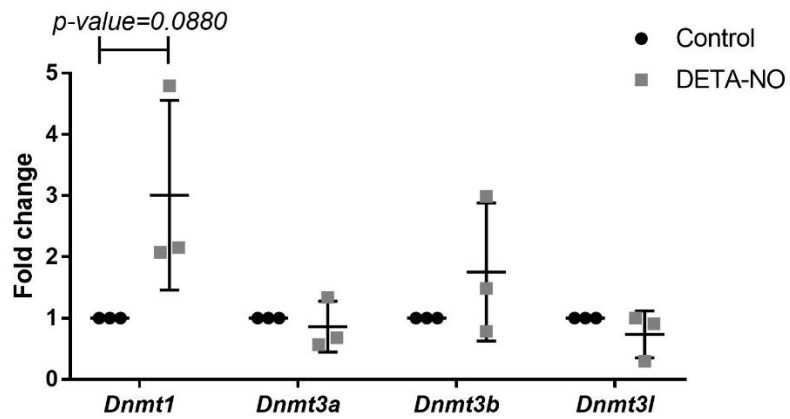
Supplementary Figures

Figure S1



Supplementary Figure 1. Chromatin immunoprecipitation (ChIP) assays of EGR-1 on *Pdx1* promoter at regulatory area III in (a) mESCs and (b) INS-1E cell line. The figure shows (left panels) two representative ChIP results by qualitative PCR and (right panels) the means \pm SD of two (a) and three (b) independent experiments. The Y axis corresponds to the percent input relativized to IgG binding.

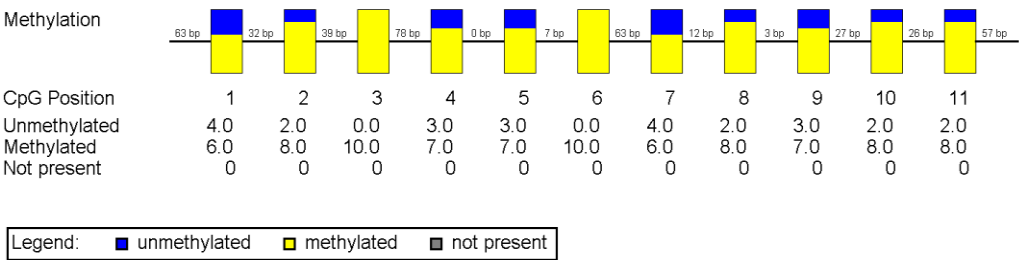
Figure S2



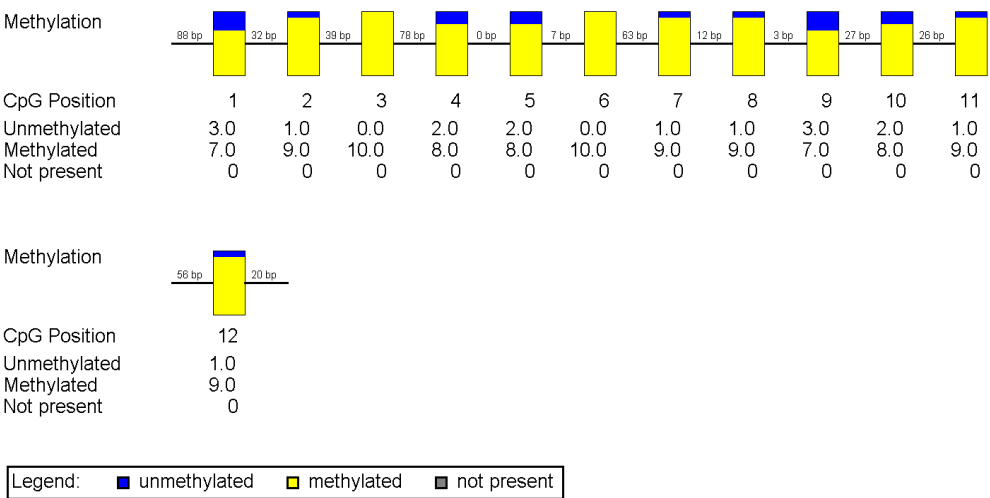
Supplementary Figure 2. DNA methyltransferase expression in mESCs. Analysis of DNA methyltransferases (Dnmt) expression after DETA-NO treatment by real time-PCR. These values were normalized to the expression values of the *β -Actin*, used as loading control. The data is analyzed using $\Delta\Delta C_t$ algorithm and relativized to control condition. They represent the average of three independent experiments. Data are means \pm Standard deviation (SD).

Figure S3

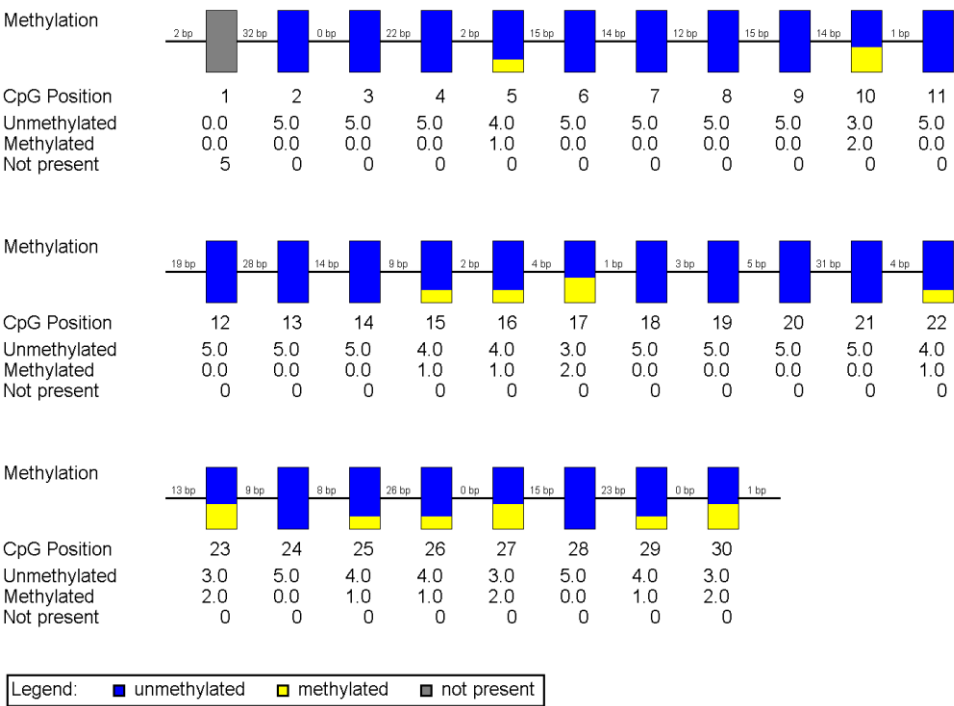
A) Control condition



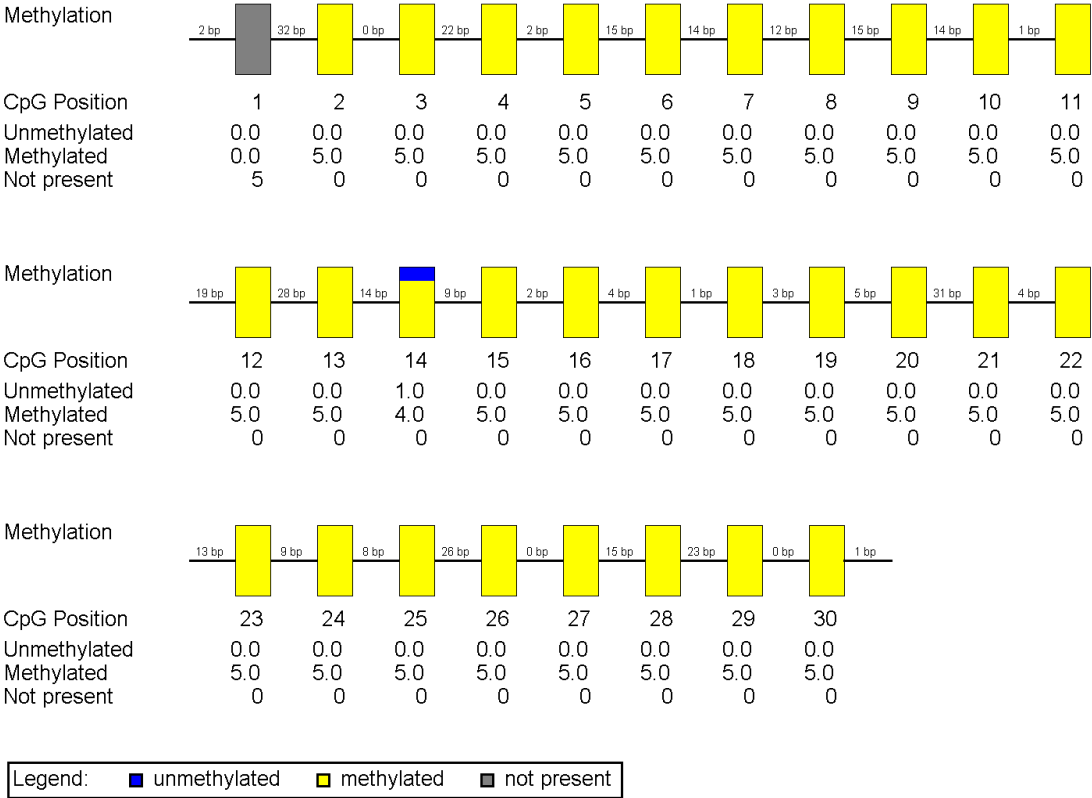
B) DETA-NO condition



C) Technical control: Untreated DNA and analysis of *Pdx1* proximal CpG Island



D) Technical control: DNA treated with the CpG Methyltransferase, M.SssI and analysis of Pdx1 proximal CpG Island



Supplementary Figure 3. Methylation analysis of *Pdx1* promoter by bisulfite sequencing PCR (BSP). The graphs show the CpG sites studied, which are represented by vertical rectangles. The methylation status is represented by the color of the rectangles: yellow-methylated and blue-unmethylated. The number of methylated or unmethylated CpG sites found in each condition is detailed under each rectangle. Graphs show the methylation results of four *Pdx1* promoter regions or cell culture conditions: EGR-1 binding site in mESCs cultured in control (A) and (B) DETA-NO conditions; and *Pdx1* proximal CpG Island in mESCs cultured in control condition, untreated (C) and treated with CpG Methyltransferase, M.SssI (D).