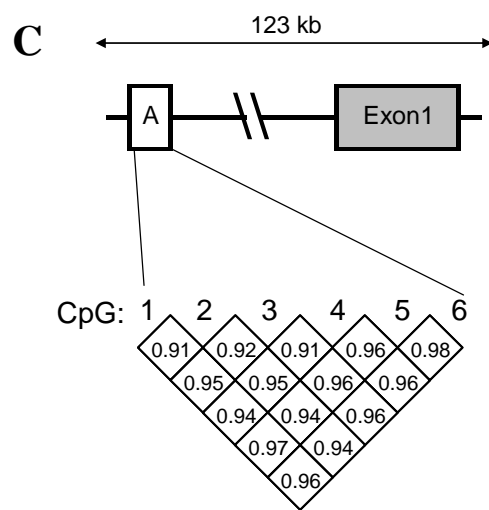
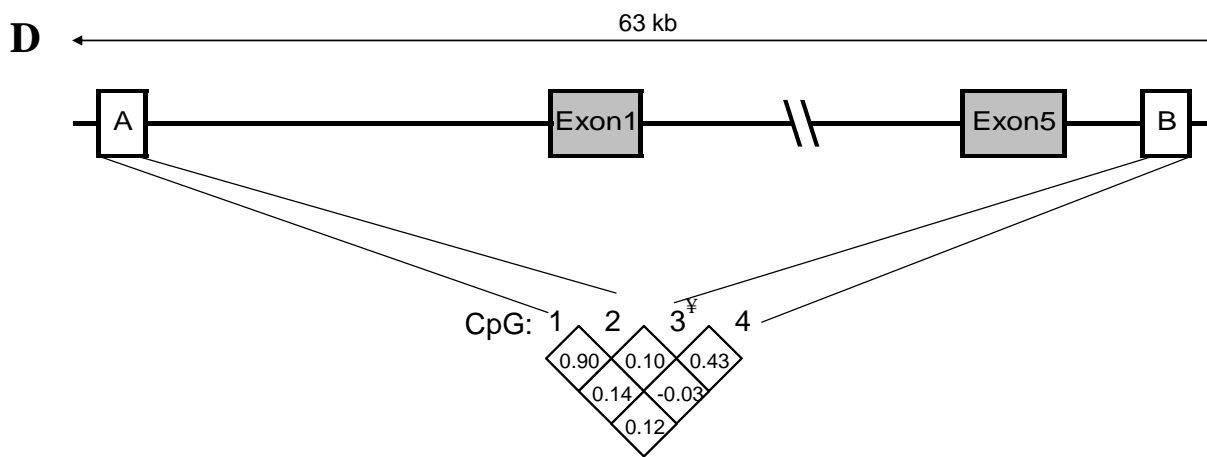


Mean DNA methylation: $29.3 \pm 6.5\%$



Mean DNA methylation: $49.8 \pm 13.7\%$



Mean DNA methylation CpG1 and CpG2 : $11.7 \pm 7.6\%$

Figure 1S. Loci analysed in E-21. *PRDM16* (A), *BMP7* (B), *CTBP2* (C) and *PPARGC1 α* (D) genes CpGs epigenotyped are shown. The CpGs within *BMP7*-A, *CTBP2*-A and *PPARGC1 α* -A locus were significantly well correlated with each other. For Gen3G, when the CpGs identified in E-21 was covered by 450k array probesets, the exact same CpGs were selected (*cg01046951; [#]cg04873098; [¥]cg08550435). Since some CpGs were not covered by the 450k array, probesets covering variable CpGs in close vicinity to those identified in E-21 were selected. *PRDM16*: cg06814194 (1st intron) and cg23738647 (exon 6); *BMP7*: cg18759209 (proximal promoter); and *PPARGC1 α* : cg11270806 and cg27514608 (both intron 5).