



Additional file 1. Organization of the *HSD17B1* gene (A), the positions of CpG-rich regions and promoter.

The *HSD17B1* gene (chr17: 37 957 510 - 37 960 757, NC_000017) (A) is composed of six exons separated by introns (lines). The white and black boxes correspond to the untranslated or translated region of exons, respectively. The promoter II, including the TATA sequence, occupies 100 nucleotides that can be found within the short *HSD17B1* transcript (C) (chr17: 37 958 368 - 37 958 468)[10-13]. The 90 CpG-rich regions (D) were localized on chromosome 17:37 953 426 – 37 954 646. Arrows correspond to the position of primers used for the ChIP assays for promoter (1), for RQ-PCR analysis *HSD17B1* transcript (2), and primer localization for bisulfite sequencing within the CpG-rich regions (3). The numbers from 4 to 6 in the CpG-rich regions (D) represent the position of the primers used to assess DNA methylation levels by HRM analysis (Additional file 2).