



Supplementary Figure 1: Position and relative methylation level of analyzed CpGs near the DM1 CTG repeat

*DMPK* exons are represented by blue rectangles, the tall bits represent the coding regions. *SIX5* exons are represented by orange rectangles, the tall bits represent the coding region.

Hypomethylated CpGs are represented by white rectangles, whereas CpG with variability is shown by green rectangles. CTG repeats are represented by a red line. CTCF binding sites are represented by yellow rectangles. The CpG island is represented by a burgundy red line. Yellow diamonds represent correlation  $>0.7$ . Tables present DNA methylation mean  $\pm$  standard deviation for each CpG in the region. One star stands for  $p < 0.05$ , two stars for  $p < 0.001$ .