



Supplementary Figure 1. Transcriptome and methylome profiling of the centromere-proximal region of the pig *SGCE/PEG10* locus. Five protein-coding genes (*CALCR*, *GNGT1*, *TFPI2*, *GNG11* and *BET1*) are depicted. Biallelic enrichments of RNA-seq reads are displayed with a comparable expression level between parthenote (PA, pink) and control (CN, blue). Mean methylation ratios are shown in the bottom tracks representing PA (pink histogram lines) and CN (blue histogram lines). PA-CN track indicates the difference in mean methylation ratios between PA and CN. *I*, CpG islands; GC %, GC content.