



Supplementary Figure 2 Transcriptome and methylome profiling of the upstream region of the *GNAS* complex locus. The *STX16* and *NPEPL1* genes are depicted in the upstream of the *GNAS* complex locus. Biallelic enrichments of RNA-seq reads are displayed with a comparable expression level between CN (dark cyan) and PA (grey). Mean methylation ratios are shown in the bottom tracks representing PA (blue histogram lines) and CN (pink histogram lines). PA-CN track indicates the difference in mean methylation ratios between PA and AI. A significant DMR (FDR < 0.05) is marked by a red horizontal bar. *I*, CpG islands; GC %, GC content.