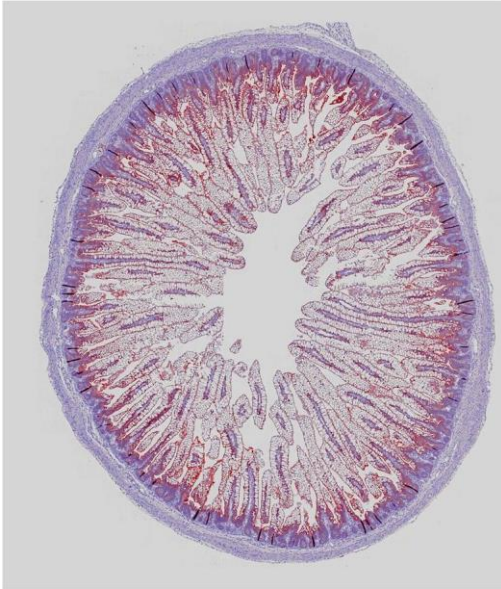


Figure S1: Immunohistochemistry (IHC) analysis of epithelial marker between CON and AB groups.

(A) Representative image of IHC result. (B) No significant difference of the area stained by cytokeratin between CON and AB groups was revealed according to Mann–Whitney U test. Values were presented as the mean \pm SEM.

A



B

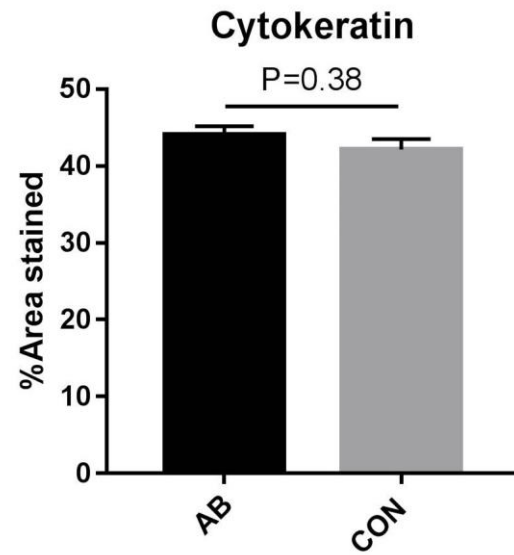


Figure S2: Methylation level in 5 allele-specific methylation (ASM) genes between CON and AB groups.

No significant differences of allele-specific methylation levels between CON and AB groups revealed for 5 ASM genes according to Mann–Whitney U test.

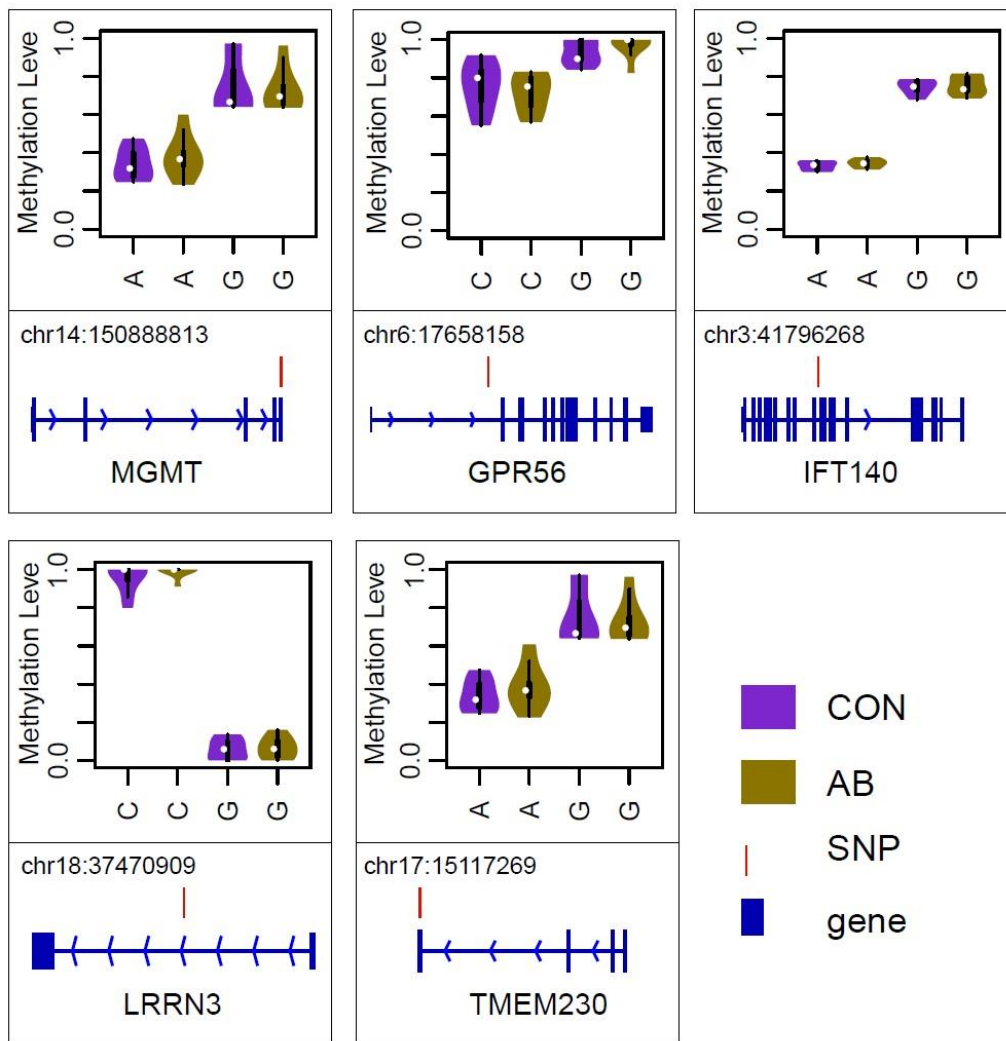


Figure S3: Pvclust hierarchical clustering on DNA methylation of 14 samples.

Hierarchical clustering was performed based on methylation levels of all CpG sites. In the cluster dendrogram, sample IDs were listed along X-axis (green for CON group, and red for AB group) and inter-cluster distance was indicated on Y-axis; Values at branches are approximately unbiased (AU) p-values (left), bootstrap probability (BP) values (right), and cluster labels (bottom).

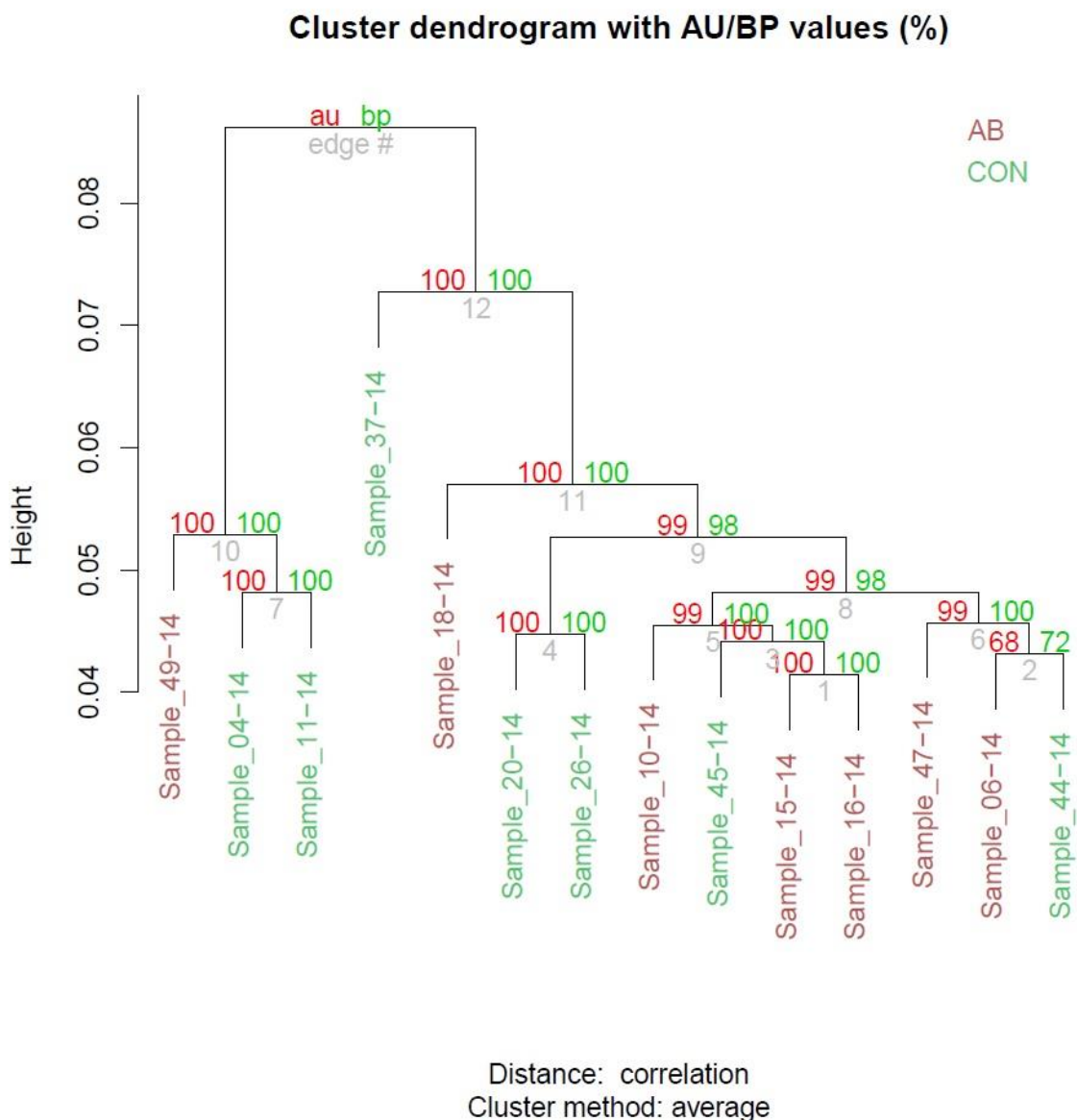


Figure S4: Overview of methylation level in the genic regions.

Plot of DNA methylation level in intra-group samples averaged across all genebody regions and $\pm 5\text{kb}$ from transcriptional start sites (TSS). Smoothing was done using cubic splines.

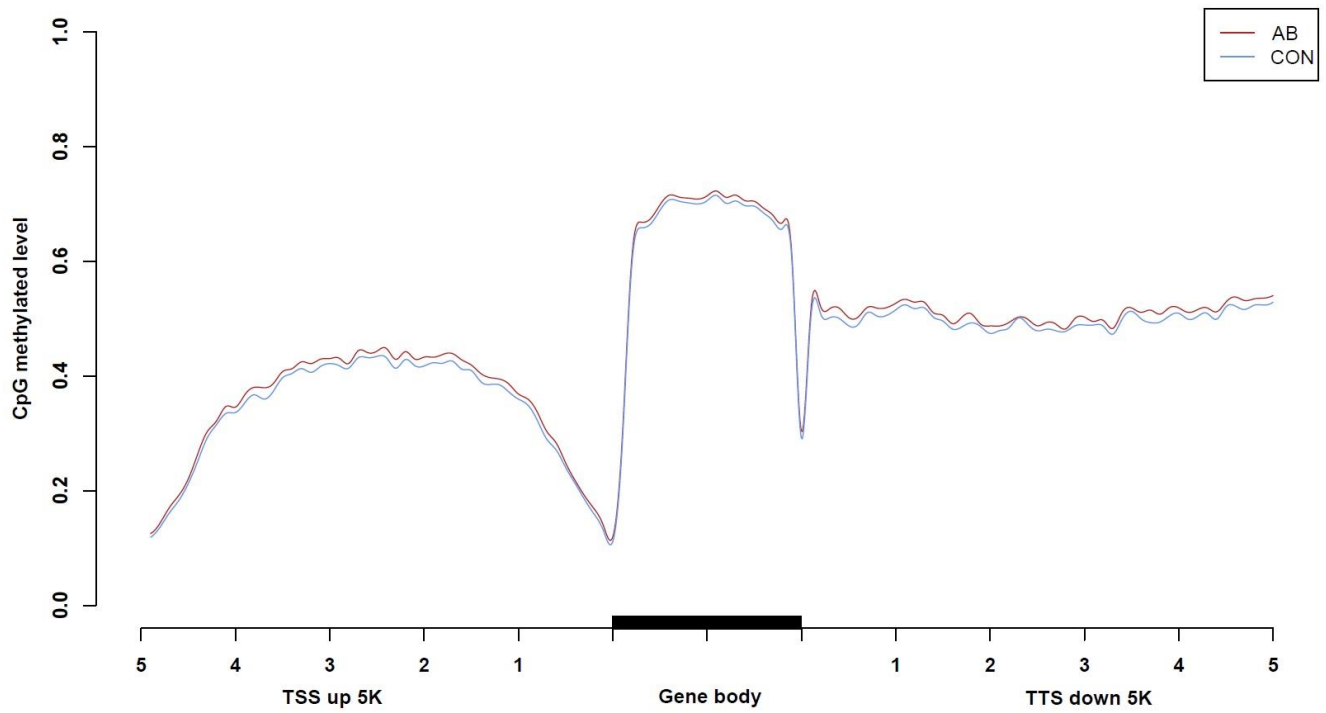


Figure S5: Validation of DNA methylation by bisulfite sequencing PCR (BSP).

According to the examination on DMRs in five genes, significant correlation between RRBS data and BSP data was revealed ($P < 0.0001$, $R^2 = 0.78$). As an example, the methylation level of the DMR in GNAS calculated from different approaches was shown.

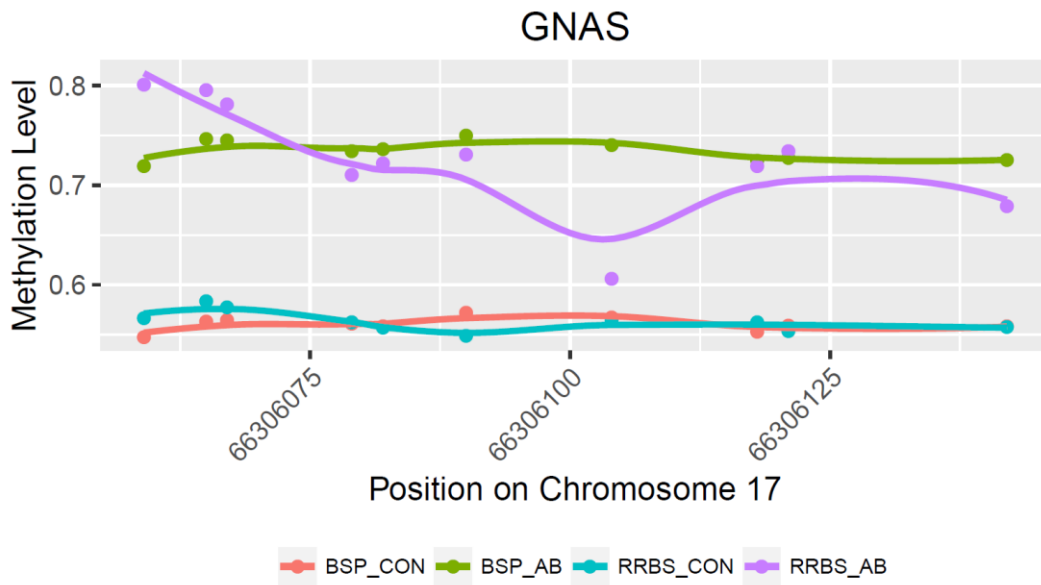


Figure S6: Relative mRNA expression of DMR-genes.

Relative quantification of target genes was normalized to housekeeping gene HPRT1, and was presented as the mean values \pm SEM.

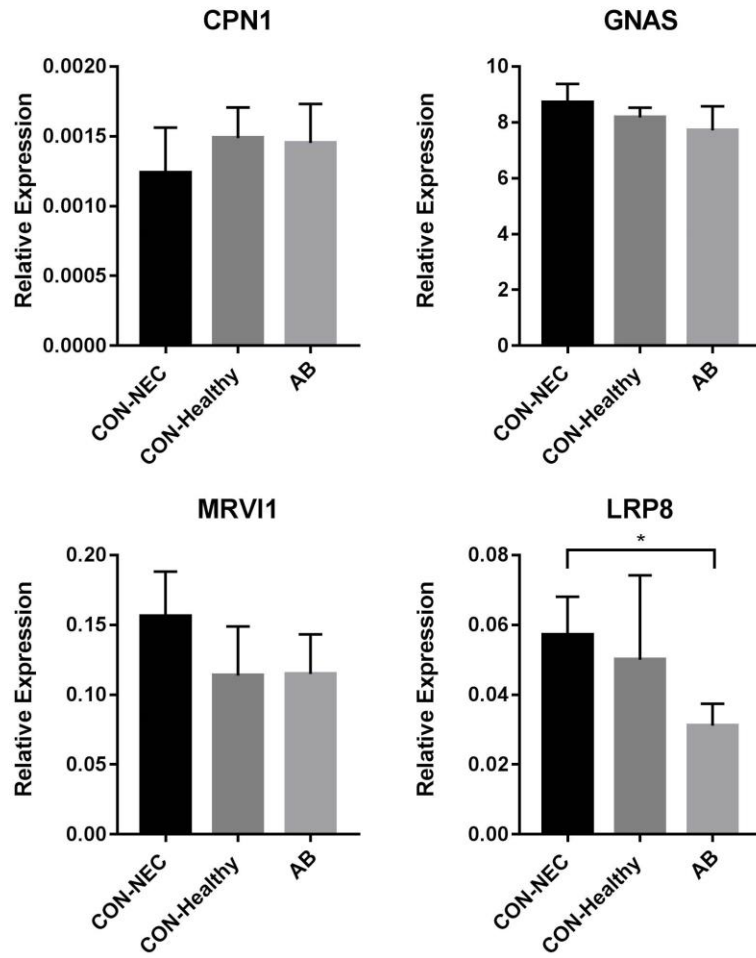
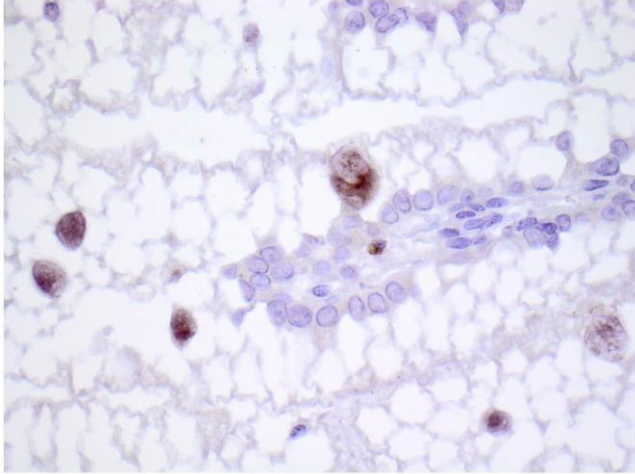


Figure S7: Immunohistochemistry (IHC) analysis of neutrophils marker (myeloperoxidase, MPO) between CON and AB groups.

(A) Representative image of IHC result. (B) The average number of MPO-positive cells in each pig was calculated from 10 well-oriented villi. A tendency of reduced number of MPO-positive cells in the AB versus CON group was revealed according to Mann–Whitney U test. Values were presented as the mean \pm SEM.

A



B

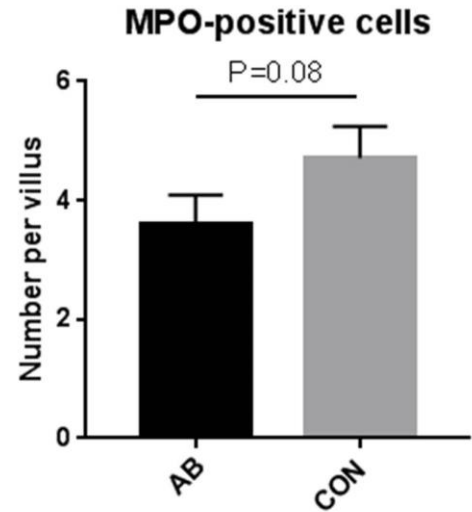


Figure S8: Differentially expressed proteins related to glycolysis and gluconeogenesis.

Compared with CON pigs, ALDOA (in glycolysis) was less expressed while FBP1 and PCK2 (in gluconeogenesis) were more expressed in the AB pigs. Expression quantity expressed in $(\text{mean} \pm \text{SEM}) \times 10^5$ (n=6) defined as the sum of optical density of the each pixel of spot area, using Gel-based proteomics.

