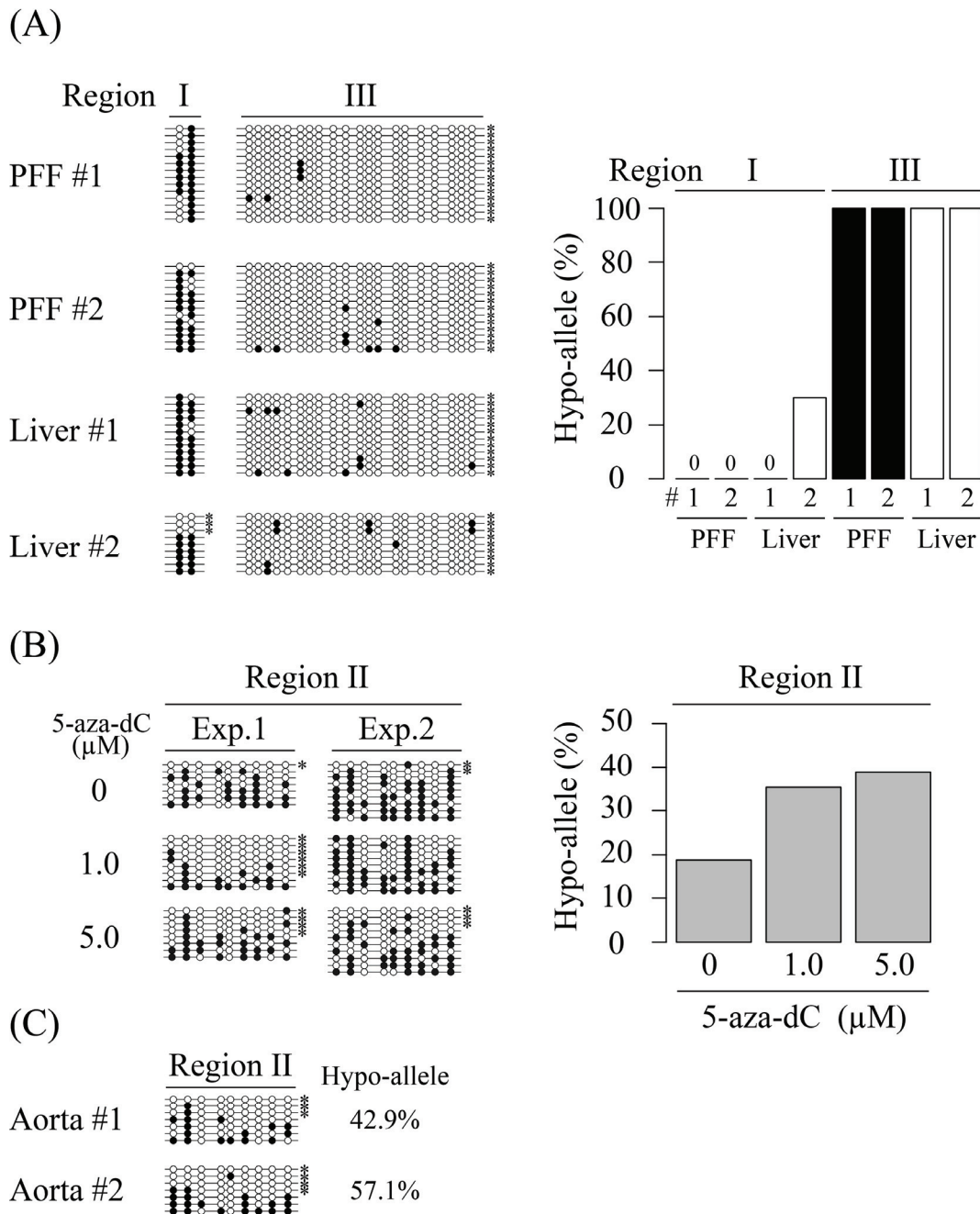


Supplementary Fig. 1.



Supplementary Fig. 1.

Hypo-allele ratio of Regions I and III within the *FBNI* CpG island shore.

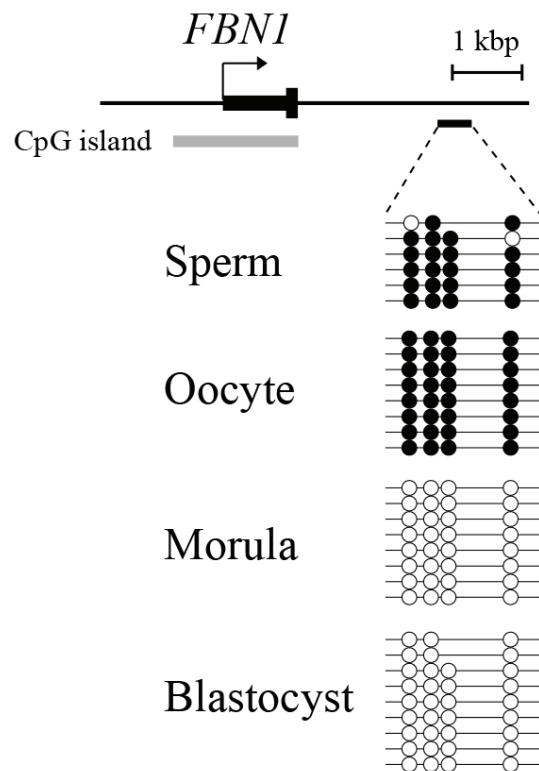
(A) Hypo-allele ratios of the Regions I and III within the *FBNI* CpG island shore in porcine fetal fibroblast (PFF) and the liver were calculated based on the sodium bisulfite sequencing data of Fig. 1A (left panel). The sequenced fragments that contain $\geq 75\%$ unmethylated CpG sites (the two CpGs in Region I and ≥ 15 of the 20 CpG sites in Region III are considered as $\geq 75\%$) were defined as Hypo-alleles, and their Hypo-allele percentages are represented as a bar graph (right panel).

(B) Changes of Hypo-allele ratios in the Region II of the *FBNI* CpG island shore by 5-aza-dC treatment. PFF was cultured with 5-aza-dC (0, 1.0, 5.0 μM) for four days, and the DNA methylation status of the *FBNI* CpG

island shore was analyzed using sodium bisulfite sequencing. Sequenced fragments that contain $\geq 75\%$ unmethylated CpG sites (7–9 unmethylated CpGs out of the 9 CpG sites in the Region II) were defined as Hypo-allele. DNA methylation analysis was performed twice independently (Exps 1 and 2) (left panel), and Hypo-allele ratios were calculated from the sum of the two experiments (right panel). Open and closed circles indicate unmethylated and methylated CpGs, respectively. *, Hypo-allele.

(C) Hypo-allele percentages in the Region II of the *FBNI* CpG island shore in two aorta samples. In this experiment, Hypo-allele was defined in the same manner as in (B) (7–9 unmethylated CpGs out of the 9 CpG sites in the Region II). Open and closed circles mean unmethylated and methylated CpGs, respectively. *, Hypo-allele.

Supplementary Fig. 2.



Supplementary Fig. 2. DNA methylation patterns of the *FBNI* intronic CpG island shore about 2.5 kb downstream of the *FBNI* exon 1.

DNA methylation status was analyzed in the sperm, oocyte, IVF-derived morula, and blastocyst by sodium bisulfite sequencing using specific PCR primers for the intronic CpG island shore (*FBNI*_Bis_F2: 5'-AATAAGAAAATGGTTTTTGAGAGGTAAG-3', *FBNI*_Bis_R2: 5'-AAAAATCACCTCTCTATATTCCTCATAAC-3'). Open and closed circles indicate unmethylated and methylated CpGs, respectively.