Genome-wide DNA methylation analysis of the porcine hypothalamus-pituitary-ovary axis

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Table S1 | Average methylation levels of different genomic features in HPO methylomes

	CpG methylation level			CpH methylation level		
	Hypothalamus	Pituitary	Ovary	Hypothalamus	Pituitary	Ovary
Genome	57.62%	55.60%	55.44%	0.79%	0.61%	0.55%
Upstream	30.45%	29.83%	28.74%	0.59%	0.58%	0.49%
Exon	50.06%	48.81%	48.74%	0.60%	0.68%	0.49%
Intron	68.22%	65.75%	66.16%	0.82%	0.60%	0.57%
Downstream	61.12%	58.96%	58.12%	0.71%	0.57%	0.53%
Intergenic	61.79%	59.33%	59.17%	0.87%	0.62%	0.56%
CGI	36.88%	36.35%	35.81%	0.56%	0.57%	0.49%
CGI shores	64.96%	62.43%	61.63%	0.78%	0.63%	0.55%
CGI shelves	75.68%	72.42%	72.11%	0.85%	0.63%	0.56%

Table S2 | Correlation coefficients between DNA methylation and gene density

Correlation Coefficients	CpG methylation			CpH methylation		
	Hypothalamus	Pituitary	Ovary	Hypothalamus	Pituitary	Ovary
Gene density	-0.079 ($P = 9.14\times10^{-5}$)	-0.073 ($P = 2.91\times10^{-4}$)	-0.079 ($P = 1.41\times10^{-7}$)	-0.19 ($P = 2.20\times10^{-16}$)	-0.03 ($P = 1.30\times10^{-1}$)	-0.11 ($P = 1.55\times10^{-8}$)

Correlation coefficients were calculated by Pearson's correlation. The DNA methylation and density of genes were quantified per 1 Mb window.

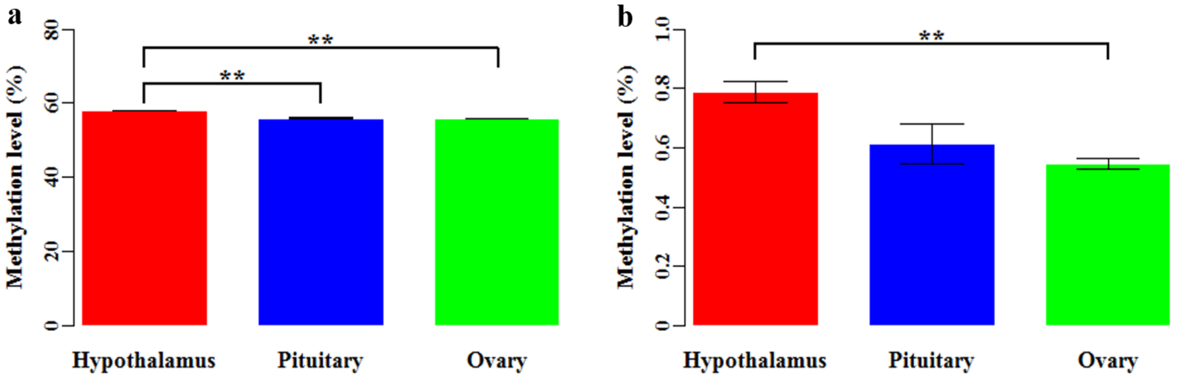

Figure S1 | Average methylation levels of hypothalamus-pituitary-ovary tissues in the CpG (a) and CpH (b) context. ** denotes p-value < 0.01

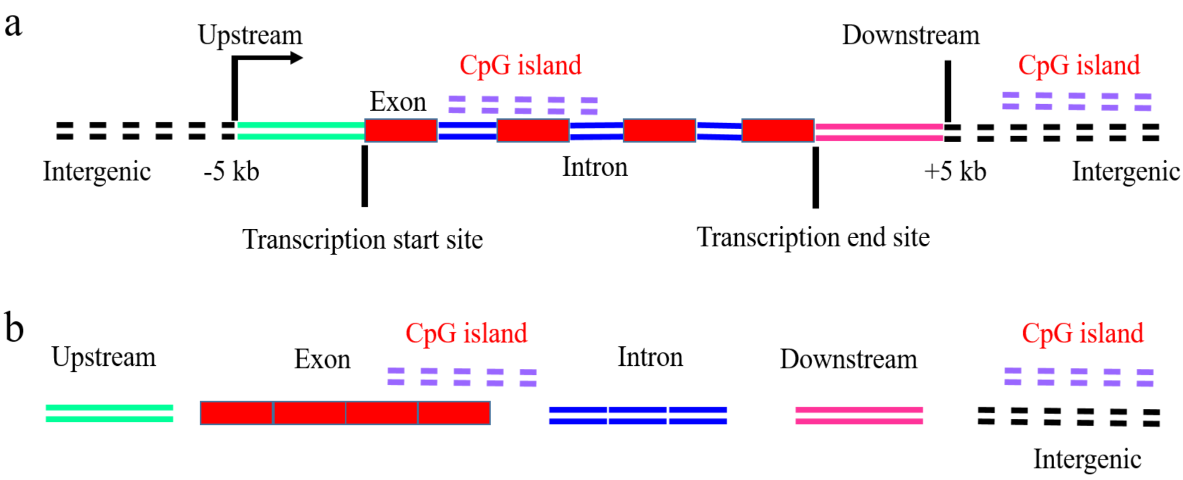

Figure S2 | Localizations of CGIs based on genic features. a) Gene locations were integrated and classified into upstream, exon, intron, downstream and intergenic regions. **b**) When more than 50% of a CGI overlapped with a specific genic feature, that CGI was classified with the specific genic feature. For example, when the overlap ratio between a CGI and the upstream genome sequences was greater than 50%, that CGI was defined as an upstream CGI, and the related genes were referred to as the CGI-Upstream genes. When the overlap ratio between a CGI and exons was greater than 50%, that CGI was defined as an exonic CGI, and the related genes were referred to as the CGI-Exon genes

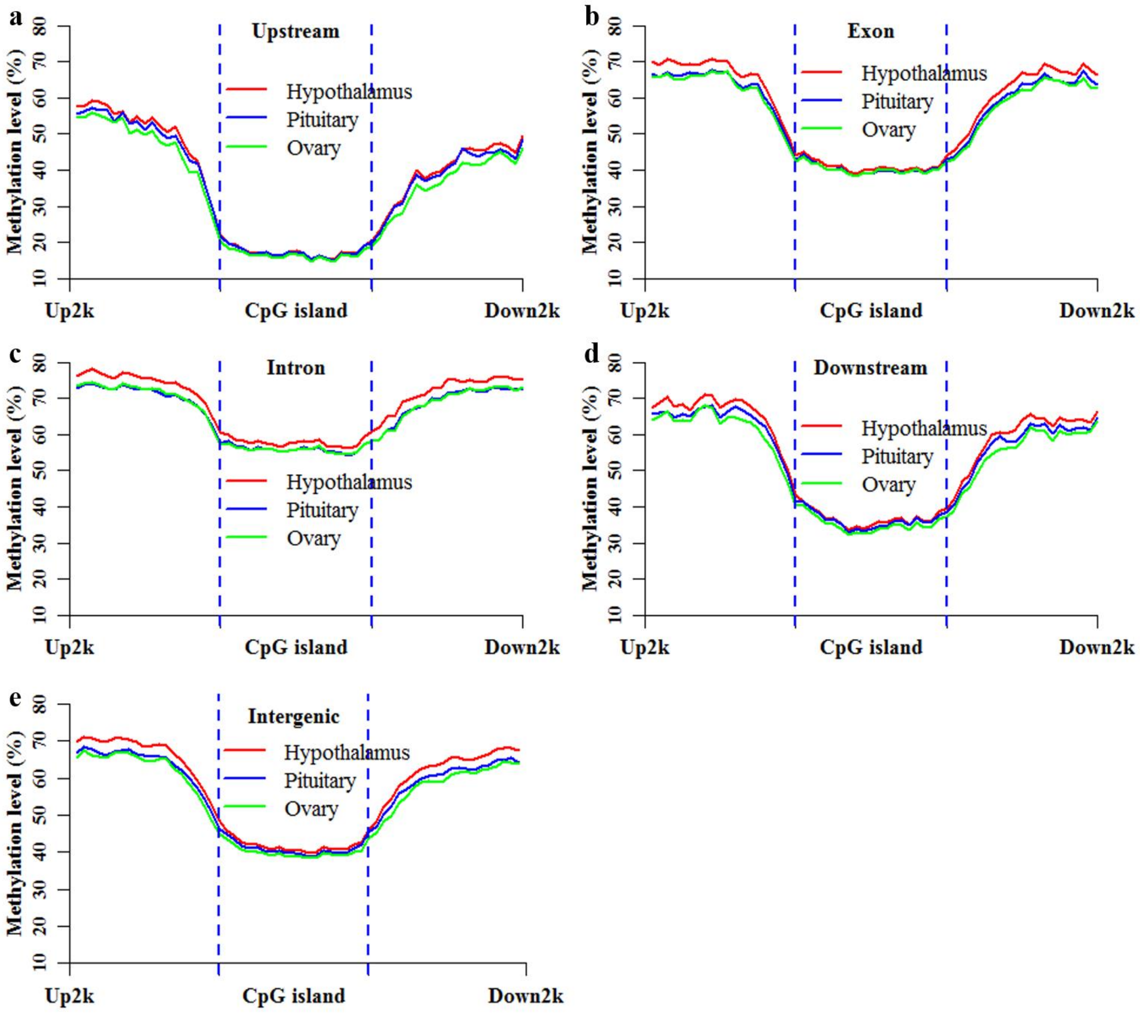

Figure S3 | Methylation patterns of CGIs located in different genic features in the CpG context. The methylation patterns of CGIs which located in upstream regions (**a**), exons (**b**), introns (**c**), downstream regions (**d**) and intergenic regions (**e**).

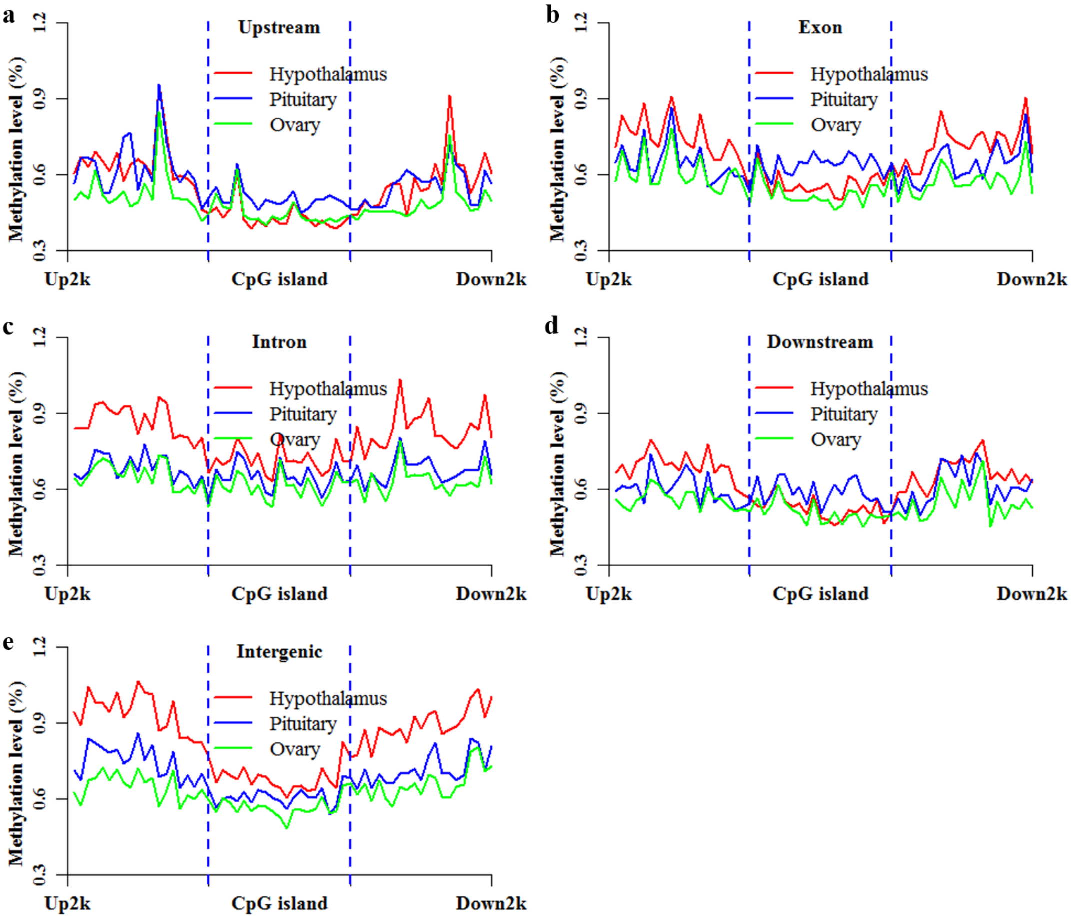

Figure S4 | **Methylation patterns of CGIs located in different genic features in the CpH context.** The methylation patterns of CGIs locating at upstream regions (**a**), exons (**b**), introns (**c**), downstream regions (**d**) and intergenic regions (**e**).

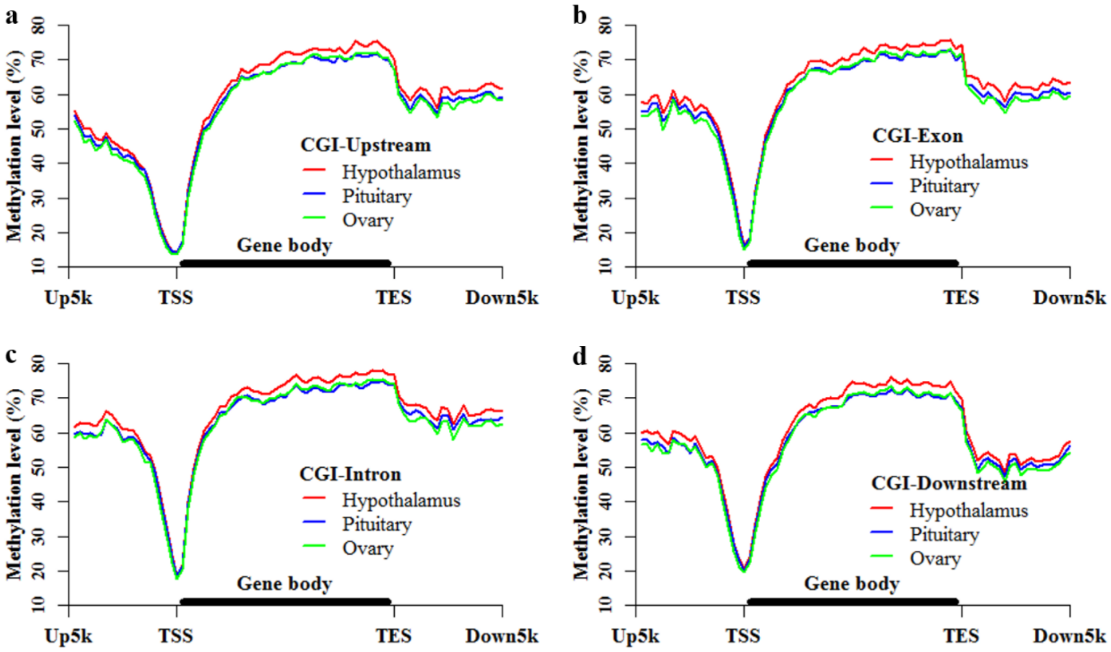

Figure S5 | Methylation patterns of genes based on different CGI locations in the CpG context. The methylation patterns of CGI-Upstream (**a**), CGI-Exon (**b**), CGI-Intron (**c**) and CGI-Downstream (**d**) genes.

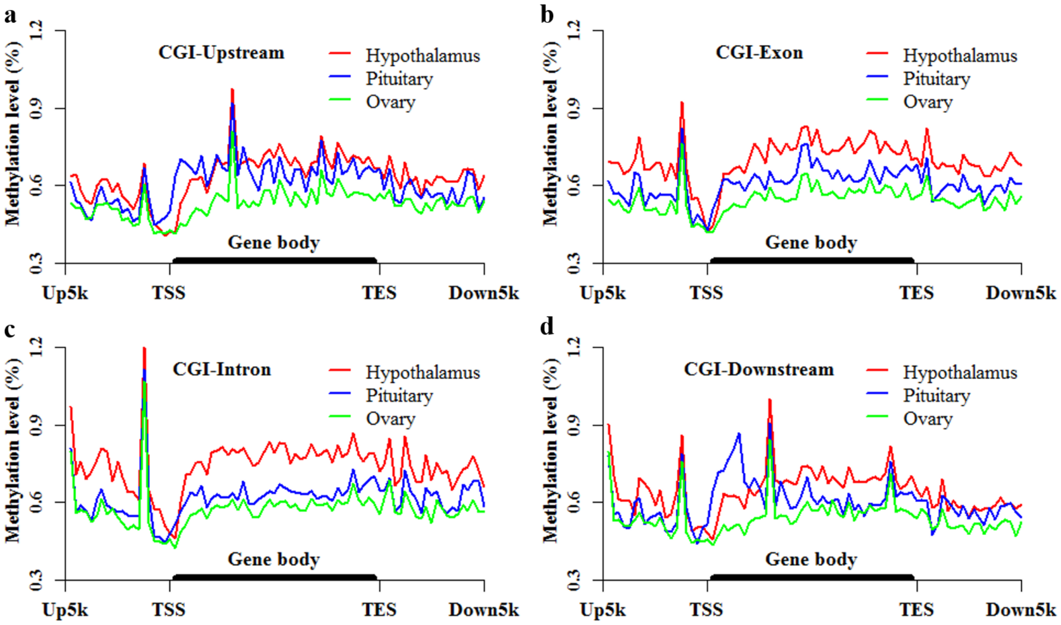

Figure S6 | Methylation patterns of genes based on different CGI locations in the CpH context. The methylation patterns of CGI-Upstream (**a**), CGI-Exon (**b**), CGI-Intron (**c**) and CGI-Downstream (**d**) genes.

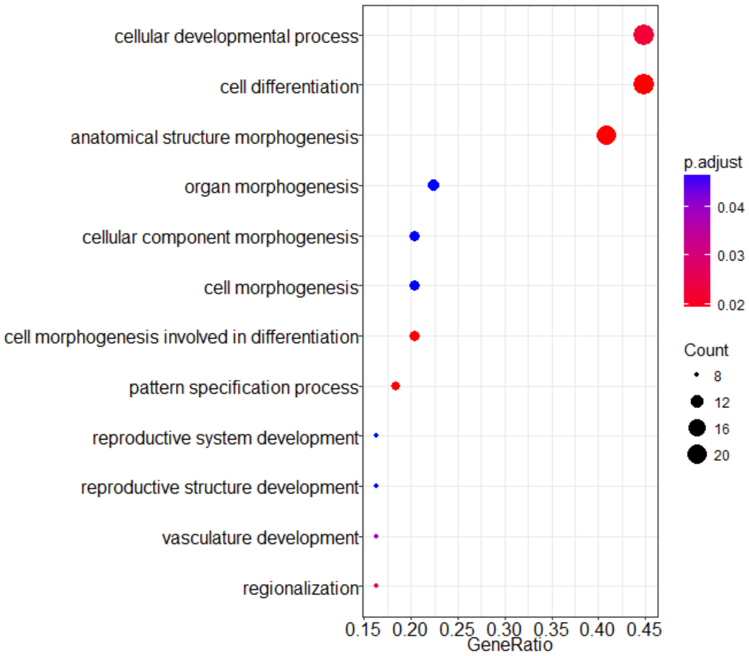

Figure S7 | Gene ontology enrichment analysis of biological processes