
Supplementary Material

Table S1 Statistical analysis for genome-wide DNA methylation sequencing data

Samples	Raw Reads No. (10 ⁶)	Clean Reads No. (10 ⁶)	N (%) (10 ⁻⁴)	Q20 (%)	Q30 (%)	Mapping rate (%)
1-1-h	207.57	194.95	3.62	95.26	89.42	87.42
1-1-o	198.94	185.00	2.81	94.93	89.12	89.66
1-2-h	252.75	240.04	3.60	95.43	89.22	87.17
1-2-o	257.64	229.35	2.78	93.32	87.22	87.13
1-3-h	198.41	187.64	3.63	95.35	89.28	88.90
1-3-o	219.17	200.25	2.86	94.24	88.07	89.99
2-1-h	215.91	205.48	3.60	95.44	89.23	89.42
2-1-o	207.98	190.66	2.79	93.73	87.33	89.40
2-2-h	255.97	242.89	3.60	95.27	89.03	88.44
2-2-o	201.76	190.63	2.81	95.53	89.55	87.90
2-3-h	285.94	270.01	3.64	95.51	89.58	84.55
2-3-o	205.54	192.99	2.80	94.98	88.90	87.26
3-1-h	266.11	189.92	4.20	95.36	89.29	90.81
3-1-o	211.14	178.33	4.24	94.84	88.60	90.65
3-2-h	225.12	204.88	4.19	95.57	89.66	88.86
3-2-o	236.00	192.22	4.20	95.20	89.38	90.92
3-3-h	256.75	193.91	4.20	95.65	89.84	88.39
3-3-o	259.27	199.33	4.22	95.49	89.58	91.07
4-1-h	199.21	170.42	6.62	94.82	88.21	86.60
4-1-o	186.41	204.49	5.06	94.48	87.56	90.07
4-2-h	214.32	198.53	4.98	94.65	87.93	90.89
4-2-o	202.12	192.68	6.34	94.35	87.65	92.16
4-3-h	212.69	208.73	7.62	95.19	88.59	88.26
4-3-o	209.87	176.54	6.85	94.84	88.45	91.29
5-1-h	222.63	212.72	13.12	95.38	89.53	90.64
5-1-o	214.89	199.83	7.61	94.88	88.35	89.87

5-2-h	213.99	207.46	6.38	95.49	89.22	90.62
5-2-o	223.05	203.17	6.13	94.46	87.75	88.72
5-3-h	244.23	218.40	7.48	95.02	88.36	87.30
5-3-o	246.91	185.97	6.19	94.75	88.28	88.98

Note: Sample: The sample names;

Reads No.: The total reads;

N(%): the percentage of fuzzy bases;

Q20(%): The percentage of bases with a base recognition accuracy of more than 99%;

Q30(%): The percentage of bases with a base recognition accuracy of more than 99.9%;

Mapping rate (%): the rate of reads mapped to chicken reference genomes;

i-j-o (i=1,2,3,4,5; j=1,2,3) stand for three biological replicates from five periods in ovarian samples;

i-j-h (i=1,2,3,4,5; j=1,2,3) stand for three biological replicates from five periods in hypothalamic samples;

Table S2 The proportion of methylated C sites in CG, CHG and CHH contexts of 30 samples from forced molting

Samples	mC (%)	mCG (%)	mCHG (%)	mCHH (%)
1-1-h	4.39	88.36	1.70	9.94
1-1-o	3.72	93.23	1.07	5.70
1-2-h	4.53	90.92	1.36	7.72
1-2-o	3.44	93.86	1.03	5.10
1-3-h	4.30	89.60	1.58	8.82
1-3-o	3.93	93.38	1.07	5.54
2-1-h	4.59	78.23	3.36	18.41
2-1-o	4.03	93.47	1.08	5.45
2-2-h	4.67	90.92	1.37	7.71
2-2-o	4.17	93.84	1.02	5.14
2-3-h	4.65	90.69	1.40	7.91
2-3-o	4.24	93.87	1.02	5.10
3-1-h	4.32	92.94	1.11	5.96
3-1-o	3.04	94.45	0.94	4.61
3-2-h	3.27	91.43	1.29	7.28
3-2-o	4.22	94.15	1.00	4.85
3-3-h	4.38	92.16	1.20	6.64
3-3-o	3.87	94.49	0.94	4.57
4-1-h	3.56	91.78	1.26	6.96
4-1-o	4.38	94.14	0.99	4.87
4-2-h	4.16	91.50	1.30	7.20
4-2-o	4.36	94.12	0.99	4.89
4-3-h	1.42	91.98	1.24	6.78
4-3-o	1.60	94.07	1.00	4.93
5-1-h	4.81	76.45	3.68	19.86

5-1-o	4.06	93.85	1.00	5.15
5-2-h	4.42	91.97	1.22	6.81
5-2-o	4.35	94.04	1.01	4.95
5-3-h	4.57	91.36	1.29	7.35
5-3-o	4.48	93.88	1.01	5.11

Note: mC (%) represents the percentage of methylated C sites out of the total number of C sites in the whole genome. The mCG (%), mCHG (%) and mCHH (%) represent the proportion of methylated C sites in all methylated C sites from different sequence environments, where H stands for A, C and T.

Table S9 The DMGs associated with cellular aging in three different periods

1-vs-2	hypothalamus	hyper_DMGs	SYNJ1 [1], UBE3A [2,3], ARHGEF7 [4]
	hypothalamus	hypo_DMGs	ATAD2B [5], RARS2 [6], WNT9A [7]
	ovary	hyper_DMGs	DIP2C [8], DOCK7 [9], HSF1 [10]
	ovary	hypo_DMGs	BRSK1 [11], KCNK2 [12], UBE2D3 [13]
2-vs-3	hypothalamus	hyper_DMGs	ABCA1 [14-16], CCPG1 [17], COL4A2 [18]
	hypothalamus	hypo_DMGs	GADD45A [19], HOXA3 [20], MEIS1 [21]
	ovary	hyper_DMGs	DNAJC1 [22], FBXL7 [23,24], KIF5C [25], PANK3 [26]
	ovary	hypo_DMGs	DCLK1 [27-29]
3-vs-5	hypothalamus	hyper_DMGs	ATOH8 [30], NUMB [31], POT1[32]
	hypothalamus	hypo_DMGs	SEPT5 [33], ZEB2 [34-36], YAP1 [37,38], RXRA [39]
	ovary	hyper_DMGs	CEP128 [40], EXOC4 [41], ZDHHC13 [42-44]
	ovary	hypo_DMGs	BIN3 [45], CPXM1 [46], RARB [47,48], RPS15 [49]

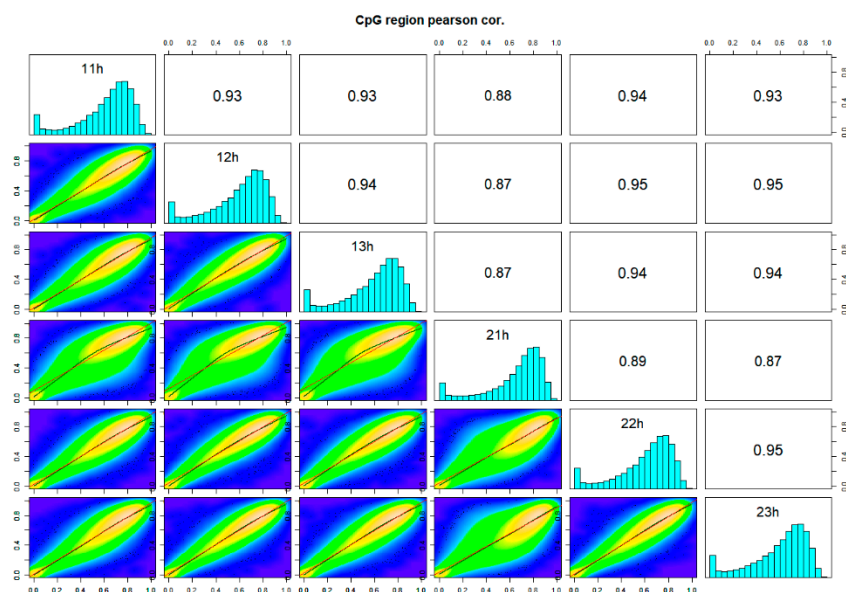


Figure S1. The CpG region correlation of samples for 1-vs-2 group in hypothalamus

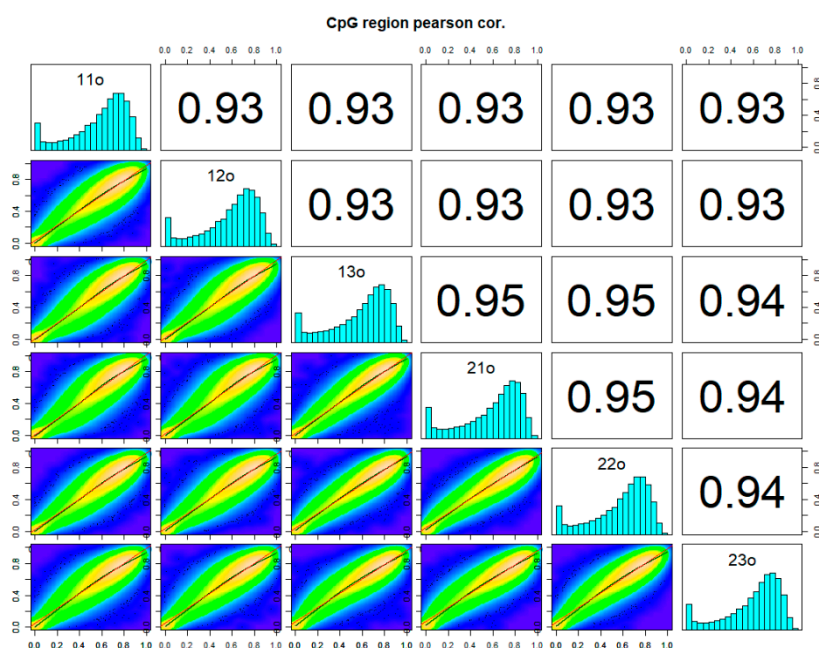


Figure S2. The CpG region correlation of samples for 1-vs-2 group in ovary

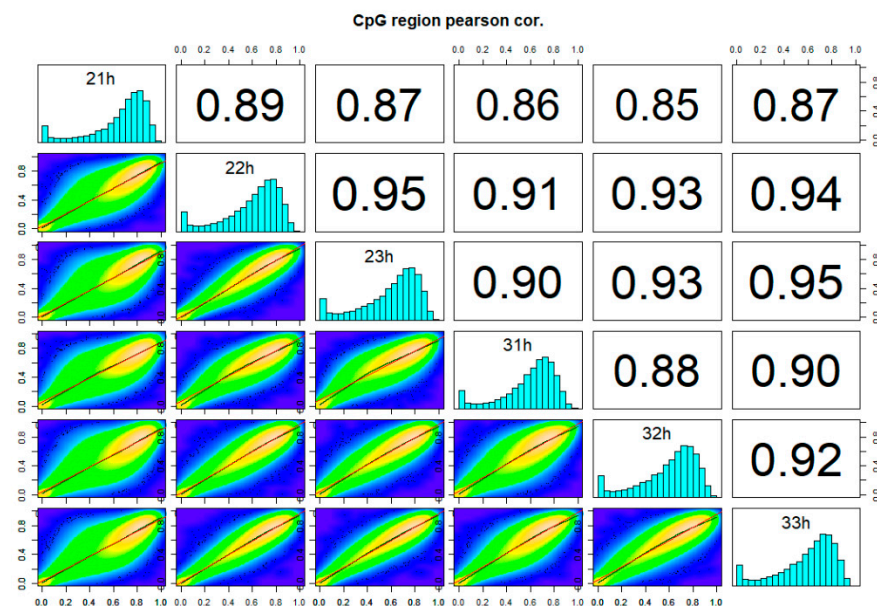


Figure S3. The CpG region correlation of samples for 2-vs-3 group in hypothalamus

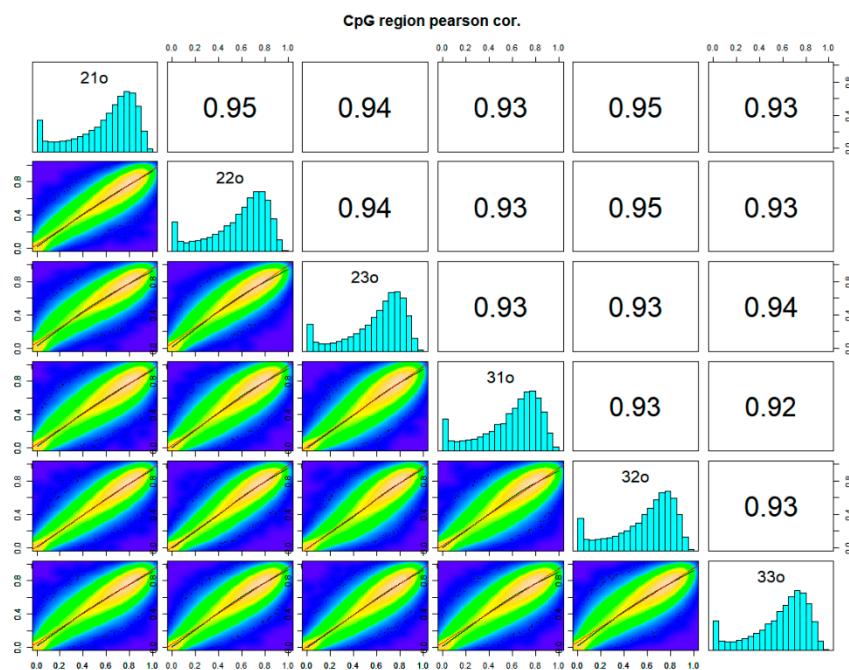


Figure S4. The CpG region correlation of samples for 2-vs-3 group in ovary

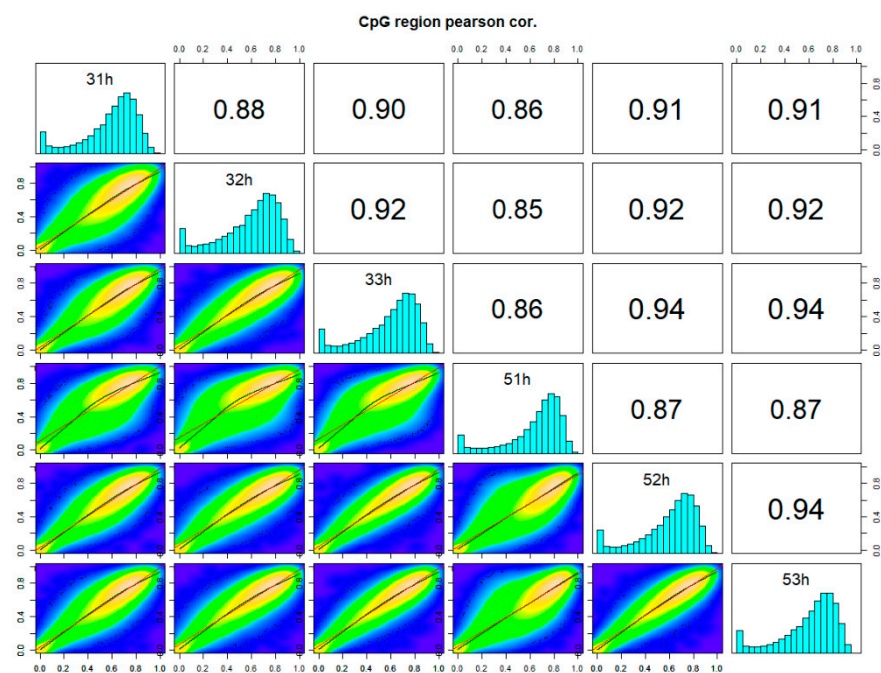


Figure S5. The CpG region correlation of samples for 3-vs-5 group in hypothalamus

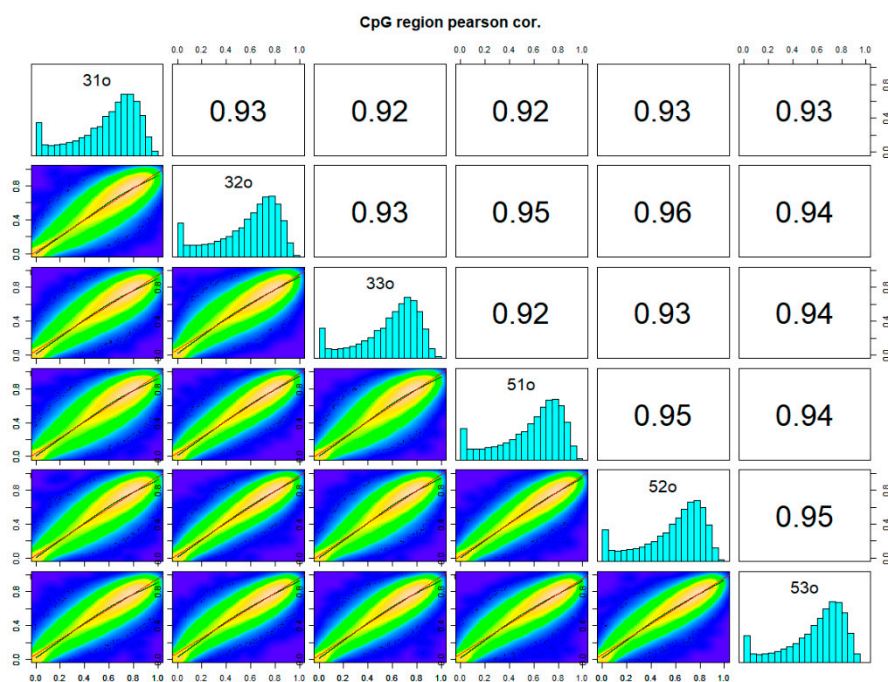


Figure S6. The CpG region correlation of samples for 3-vs-5 group in ovary

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