

## Supplementary Material

### Genome-wide DNA methylation profile of prepubertal porcine testis

*Xi Chen<sup>A</sup>, Liu-Hong Shen<sup>A</sup>, Li-Xuan Gui<sup>B</sup>, Fang Yang<sup>A</sup>, Jie Li<sup>A</sup>, Sui-Zhong Cao<sup>A</sup>, Zhi-Cai Zuo<sup>A</sup>, Xiao-Ping Ma<sup>A</sup>, Jun-Liang Deng<sup>A</sup>, Zhi-Hua Ren<sup>A</sup>, Zhong-Xu Chen<sup>B,C</sup> and Shu-Min Yu<sup>A,C</sup>*

<sup>A</sup>College of Veterinary Medicine, Sichuan Agricultural University, No. 211 Huimin Road, Wenjiang District, Chengdu, 611130, China.

<sup>B</sup>OnMath Science and Technology Limited Company, No. 500 Tianfu Road, Chengdu, Sichuan, 611130, China.

<sup>C</sup>Corresponding authors. Emails: [czhongxu@gmail.com](mailto:czhongxu@gmail.com); [yayushumin@163.com](mailto:yayushumin@163.com)

**Table S1. Basic information about sequencing and alignments**

Sample	Reads passed filtering	Aligned reads	Aligned rate
T1-Rep1	16,522,028	12,815,016	77.56%
T1-Rep2	16,986,507	13,778,774	81.12%
T1-Rep3	21,621,317	18,258,253	84.45%
T2-Rep1	21,727,202	18,233,367	83.92%
T2-Rep2	22,238,013	17,802,977	80.06%
T2-Rep3	21,554,963	17,926,686	83.17%
T3-Rep1	24,908,577	21,288,301	85.47%
T3-Rep2	20,709,922	17,923,793	86.55%
T3-Rep3	24,106,082	20,294,622	84.19%
<b>Total</b>	190,374,611	158,321,789	82.94%

**Table S2. MeDIP-seq Signal Profiles of Mapped CGIs**

	<b>Total</b>	<b>Intergenic region</b>	<b>Promoter region</b>	<b>Intragenic region</b>
Number of mapped CGIs	43,642	39,870	2,299	1,473
Average length of mapped CGIs (bp)	643	631	876	611
Average CpG number	57	56	85	50

**Table S3. Distribution of CGIs on porcine chromosome**

Chr	Chr length (Mb)	CGI <sup>a</sup>		Promoter CGI <sup>b</sup>		Gene body CGI <sup>c</sup>	
		Number	Density	Number	Density	Number	Density
1	314	3722	11.85	435	1.39	313	1.00
2	162	3175	19.60	381	2.35	291	1.80
3	144	3709	25.76	224	1.56	171	1.19
4	143	1985	13.88	264	1.85	216	1.51
5	111	1761	15.86	250	2.25	200	1.80
6	157	4253	27.09	374	2.38	283	1.80
7	137	2620	19.12	390	2.85	302	2.20
8	148	1586	10.72	160	1.08	133	0.90
9	153	1952	12.76	234	1.53	194	1.27
10	78	1450	18.59	103	1.32	88	1.13
11	87	1786	20.53	60	0.69	53	0.61
12	63	2630	41.75	216	3.43	157	2.49
13	218	1732	7.94	289	1.33	221	1.01
14	153	2277	14.88	273	1.78	211	1.38
15	157	1618	10.31	163	1.04	137	0.87
16	86	894	10.40	73	0.85	59	0.69
17	69	1295	18.77	204	2.96	161	2.33
18	61	1351	22.15	89	1.46	68	1.11
X	144	1498	10.40	152	1.06	113	0.78

Density=CGI number/Chromosome length (Mb).

<sup>a</sup> All of the detected CGIs.

<sup>b</sup> The CGIs located in promoter regions.

<sup>c</sup> The CGIs located in gene body regions.

**Table S4. Quality Assessment of MeDIP<sup>a</sup>**

Sample	Control	Input DNA (Ct)	MeDIP DNA (Ct)	%(MeDIP/Input)	Negative control (IgG)(Ct)	%(Negative control/Input)	Fold Enrichment
T1-Rep1	Positive <sup>c</sup>	21.656	24.342	3.108	NA	1.92E-03	1.62E+03
	Negative <sup>d</sup>	21.695	28.664	0.16	NA	1.98E-03	80.784
T1-Rep2	Positive	21.732	25.195	1.814	NA	2.03E-03	8.95E+02
	Negative	21.891	29.888	7.83E-02	NA	2.26E-03	34.583
T1-Rep3	Positive	21.792	24.653	2.753	NA	2.11E-03	1.30E+03
	Negative	21.848	27.163	0.502	NA	2.20E-03	2.29E+02
T2-Rep1	Positive	21.66	24.852	2.188	NA	1.93E-03	1.13E+03
	Negative	21.837	28.663	0.176	NA	2.18E-03	80.840
T2-Rep2	Positive	21.98	24.78	2.872	NA	2.41E-03	1.19E+03
	Negative	21.779	28.321	0.215	NA	2.09E-03	1.02E+02
T2-Rep3	Positive	21.729	24.666	2.612	NA	2.02E-03	1.29E+03
	Negative	21.801	28.986	0.137	NA	2.13E-03	64.624
T3-Rep1	Positive	21.673	24.835	2.234	NA	1.95E-03	1.15E+03
	Negative	21.826	29.1	0.129	NA	2.16E-03	59.714
T3-Rep2	Positive	21.606	24.744	2.272	NA	1.86E-03	1.22E+03
	Negative	21.752	28.667	0.166	NA	2.06E-03	80.616
T3-Rep3	Positive	21.483	25.968	0.893	NA	1.71E-03	5.23E+02
	Negative	21.47	28.771	0.127	NA	1.69E-03	75.009

<sup>a</sup> MeDIP-qPCR data were analysed according to  $\Delta\Delta$ Ct method.

<sup>b</sup> Positive and Negative Control Primer set: Primers design according to specific methylated site (Positive) or non-methylated site (Negative).

<sup>c</sup> Positive Control Primer: H19 (79bp) F:5' TGAATGCTGCGATAGGAGG3'  
R:5' CCGTAATCCACGGTAAACACT3'

<sup>d</sup> Negative Control Primer: GAPDH (71bp) F:5' CTCTGCTCCCTCCCGTT 3'  
R:5' TCCACTCCGCCAGGCTTTA 3'

**Table S5. The significantly enriched Pathway terms for differentially methylated genes**

<b>KEGG ID</b>	<b>Pathway terms</b>	<b>Gene numbers</b>	<b>Q-value</b>
3320	PPAR signaling pathway	42	2.21e-09
5416	Viral myocarditis	33	1.39e-06
4145	Phagosome	60	3.16e-06
4610	Complement and coagulation cascades	36	3.16e-06
4920	Adipocytokine signaling pathway	35	3.16e-06
5150	Staphylococcus aureus infection	26	8.39e-06
5145	Toxoplasmosis	50	8.39e-06
5330	Allograft rejection	23	8.39e-06
1100	Metabolic pathways	291	8.39e-06
5140	Leishmaniasis	34	1.08e-05
4612	Antigen processing and presentation	32	2.46e-05
4940	Type I diabetes mellitus	24	2.53e-05
5332	Graft-versus-host disease	20	3.59e-05
5142	Chagas disease (American trypanosomiasis)	44	5.39e-05
5320	Autoimmune thyroid disease	26	5.39e-05
4640	Hematopoietic cell lineage	35	0.000100583
4514	Cell adhesion molecules (CAMs)	50	0.000181629
250	Alanine, aspartate and glutamate metabolism	16	0.000181629
4672	Intestinal immune network for IgA production	23	0.000230517
5310	Asthma	14	0.000435507
140	Steroid hormone biosynthesis	18	0.000507326
5160	Hepatitis C	49	0.000744212
5410	Hypertrophic cardiomyopathy (HCM)	32	0.00092832
4964	Proximal tubule bicarbonate reclamation	11	0.001022355
4975	Fat digestion and absorption	18	0.001359641
10	Glycolysis / Gluconeogenesis	22	0.001500157
591	Linoleic acid metabolism	13	0.001636355
71	Fatty acid degradation	19	0.001636355

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4621	NOD-like receptor signaling pathway	21	0.001636355
4380	Osteoclast differentiation	41	0.001636355
4976	Bile secretio	23	0.002319769
4350	TGF-beta signaling pathway	27	0.002765674
5212	Pancreatic cancer	25	0.00294283
4060	Cytokine-cytokine receptor interaction	65	0.003330236
4972	Pancreatic secretion	30	0.003407761
20	Citrate cycle (TCA cycle)	14	0.00357447
5340	Primary immunodeficiency	16	0.00369844
620	Pyruvate metabolism	16	0.00369844
590	Arachidonic acid metabolism	23	0.003852045
982	Drug metabolism - cytochrome P450	21	0.004071486
4146	Peroxisome	26	0.005049804
4620	Toll-like receptor signaling pathway	34	0.006164232
5215	Prostate cancer	31	0.006598628
5221	Acute myeloid leukemia	20	0.006598628
980	Metabolism of xenobiotics by cytochrome P450	18	0.007028608
100	Steroid biosynthesis	9	0.007199715
830	Retinol metabolism	19	0.00770614
5323	Rheumatoid arthritis	32	0.008012145
900	Terpenoid backbone biosynthesis	7	0.009061643
4622	RIG-I-like receptor signaling pathway	25	0.009065876
30	Pentose phosphate pathway	10	0.009734593
561	Glycerolipid metabolism	19	0.009734593

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