Supporting information

Characterization and functional inferences of a genome-wide DNA methylation profile in the loin (*longissimus dorsi*) muscle of swine

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Table S1. Summary of methylated DNA immunoprecipitation sequence (MeDIP-seq) data.

Sample	Raw reads size	Trimmed reads size	Trimmed reads		Reads mapped to the genome*	
			Counts	% total	Counts	% trimmed
L1-1	969,183,648	857,594,240	25,791,831	88.5	22,173,816	86.0
L1-2	992,990,304	933,664,115	26,924,162	94.0	22,927,268	85.2
L2-1	899,934,876	850,525,266	24,482,128	94.5	20,827,471	85.1
L2-2	897,008,004	846,921,057	24,366,523	94.4	20,725,260	85.1
L3-1	1,226,667,816	1,132,364,480	32,789,017	92.3	27,980,732	85.3
L3-2	1,333,901,016	1,218,236,273	35,430,895	91.3	30,277,564	85.5
L4-1	1,269,581,976	1,169,449,736	33,894,765	92.1	28,901,385	85.3
L4-2	1,399,512,816	1,252,972,604	36,936,761	89.5	31,666,900	85.7
Average	1,123,597,557	1,032,715,971	30,077,010	92.1	25,685,050	85.4

*The reference pig genome build Sscrofa_10.2

Table S2. Statistics of DNA methylation peaks on each chromosome.

Chromosome	L1-1	L1-2	L2-1	L2-2	L3-1	L3-2	L4-1	L4-2	PMR[†]	CMR[‡]
1	10,286	12,303	9,538	7,964	11,505	12,034	15,780	9,601	3,850	78
2	6,248	6,802	5,602	4,752	6,528	6,743	8,815	5,173	2,825	93
3	4,785	5,606	4,665	3,832	5,304	5,544	7,586	4,230	2,060	74
4	4,989	5,755	4,701	3,872	5,537	5,769	7,505	4,416	1,824	82
5	3,543	4,413	3,411	2,853	3,941	4,165	5,672	3,341	1,401	23
6	5,380	6,152	5,132	4,164	5,739	5,960	8,320	4,512	2,025	117
7	4,670	5,339	4,522	3,484	4,964	5,076	7,037	3,975	1,704	27
8	4,901	5,816	4,486	3,792	5,600	5,791	7,499	4,542	1,675	45
9	5,126	6,107	4,761	3,938	5,793	6,111	7,903	4,673	1,927	62
10	2,995	3,517	2,904	2,442	3,310	3,285	4,452	2,661	1,498	91
11	2,662	3,240	2,508	2,111	3,096	3,317	4,379	2,542	974	39
12	1,927	2,314	1,916	1,552	2,150	2,273	3,250	1,499	780	19
13	7,627	9,003	7,178	5,844	8,412	8,906	11,211	6,997	2,671	29
14	5,475	6,326	5,147	4,263	5,947	6,023	8,078	4,525	1,945	39
15	5,059	6,063	4,801	3,914	5,779	6,024	7,792	4,724	1,836	71
16	2,898	3,434	2,677	2,238	3,237	3,351	4,362	2,706	962	33
17	2,311	2,677	2,224	1,735	2,509	2,567	3,638	1,894	893	52
18	1,948	2,331	1,797	1,524	2,211	2,255	3,091	1,710	666	21
X	4,997	5,814	4,558	3,911	5,462	5,834	7,293	4,523	1,990	34
Total	87,827	03,012	82,528	68,185	97,024	101,028	33,663	78,244	33,506	1,029

[†] Putative methylated regions in the loin muscle of Duroc pigs: the methylated regions overlapped in at least two individual samples

[‡] Conserved methylated regions: the methylated regions overlapped in all eight individual loin muscle samples

Table S3. Classification of methylation peaks among different genomic regions*

Type	L1-1	L1-2	L2-1	L2-2	L3-1	L3-2	L4-1	L4-2
Promoter	1,489	1,779	1,520	1,243	1,620	1,556	2,376	1,260
UTR	2,575	3,053	2,586	1,950	2,939	3,009	3,916	2,247
Exon	1,723	1,715	1,577	1,176	1,611	1,646	2,380	1,193
Intron	26,216	31,167	25,488	20,304	29,012	30,086	40,220	22,859
CGI	5,092	6,649	5,390	4,671	5,510	5,267	9,027	2,735
Repeats	49,661	60,601	48,711	41,062	57,475	59,624	77,505	45,505
Intergenic	24,895	27,700	21,720	17,955	26,502	27,522	36,497	22,052

*Classification was done non-exclusively

Table S4. Classification of methylation peaks among different repeat types*

Type	L1-1	L1-2	L2-1	L2-2	L3-1	L3-2	L4-1	L4-2
DNA	2,677	3,085	2,552	2,044	2,950	3,150	4,036	2,506
LINE	23,048	28,037	21,447	18,502	28,608	29,084	35,420	26,548
Low complexity	504	739	622	612	884	909	1,000	733
LTR	4,445	4,643	3,625	2,867	3,988	4,294	5,753	3,085
RC	15	20	14	10	10	16	30	12
RNA	10	3	5	1	2	4	7	4
rRNA	30	29	26	23	26	30	22	29
Satellite	145	151	167	157	149	166	167	170
scRNA	0	0	1	0	0	0	0	0
Simple repeat	1,547	1,858	1,600	1,509	2,243	1,983	2,495	1,574
SINE	17,039	21,792	18,448	15,196	18,404	19,753	28,221	10,716
snRNA	8	11	9	6	12	9	24	13
tRNA	142	171	150	102	147	159	251	82
Unknown	51	62	45	33	52	67	79	33

*Classification was done exclusively

Table S5. Classification of methylation peaks in CpG islands among different genomic regions*

Type	L1-1	L1-2	L2-1	L2-2	L3-1	L3-2	L4-1	L4-2
Promoter	194	269	204	193	235	189	342	98
UTR	185	279	196	181	198	175	332	77
Exon	204	223	188	154	164	135	313	67
Intron	1,743	2,487	1,962	1,625	1,995	1,935	3,270	920
Intergenic	3,055	3,805	3,164	2,778	3,220	3,088	5,297	1,693

*Classification was done non-exclusively

Table S6. Enriched functional annotations of genes containing putative methylated regions (PMR) in their gene body. Genes were analyzed for functional enrichment based on gene ontology terms and KEGG pathways (P-value < 0.05).

Category	Term	Count	*P*-value	Fold enrichment
GO_BP	GO:0019538~protein metabolic process	539	3.0.E-06	1.168
GO_BP	GO:0006793~phosphorus metabolic process	222	4.7.E-06	1.301
GO_BP	GO:0031589~cell-substrate adhesion	32	2.2.E-04	1.878
GO_BP	GO:0006810~transport	495	3.7.E-04	1.130
GO_BP	GO:0006811~ion transport	161	1.1.E-03	1.244
GO_BP	GO:0006974~response to DNA damage stimulus	85	1.3.E-03	1.362
GO_BP	GO:0033554~cellular response to stress	122	2.4.E-03	1.267
GO_BP	GO:0016192~vesicle-mediated transport	120	3.9.E-03	1.253
GO_BP	GO:0045184~establishment of protein localization	157	4.3.E-03	1.211
GO_BP	GO:0015031~protein transport	155	4.9.E-03	1.208
GO_BP	GO:0008104~protein localization	177	8.3.E-03	1.177
GO_BP	GO:0010829~negative regulation of glucose transport	5	1.1.E-02	4.342
GO_BP	GO:0000902~cell morphogenesis	75	1.2.E-02	1.287
GO_BP	GO:0046907~intracellular transport	132	1.4.E-02	1.194
GO_BP	GO:0005996~monosaccharide metabolic process	52	1.8.E-02	1.336

GO_BP	GO:0007131~reciprocal meiotic recombination	9	2.5.E-02	2.299
GO_BP	GO:0032989~cellular component morphogenesis	80	2.7.E-02	1.232
GO_BP	GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	27	2.8.E-02	1.484
GO_BP	GO:0048858~cell projection morphogenesis	53	3.2.E-02	1.293
GO_BP	GO:0051649~establishment of localization in cell	164	3.2.E-02	1.141
GO_BP	GO:0032990~cell part morphogenesis	55	3.2.E-02	1.284
GO_BP	GO:0016051~carbohydrate biosynthetic process	29	3.6.E-02	1.431
GO_BP	GO:0007018~microtubule-based movement	26	3.6.E-02	1.466
GO_BP	GO:0010646~regulation of cell communication	196	3.6.E-02	1.123
GO_BP	GO:0070727~cellular macromolecule localization	86	4.3.E-02	1.197
GO_BP	GO:0006403~RNA localization	22	4.7.E-02	1.493
GO_BP	GO:0050658~RNA transport	22	4.7.E-02	1.493
GO_BP	GO:0051236~establishment of RNA localization	22	4.7.E-02	1.493
GO_BP	GO:0031175~neuron projection development	55	4.7.E-02	1.257
GO_BP	GO:0048193~Golgi vesicle transport	30	4.9.E-02	1.386
GO_CC	GO:0005737~cytoplasm	1318	2.7.E-08	1.096

GO_CC	GO:0019898~extrinsic to membrane	111	1.2.E-04	1.384
GO_CC	GO:0044424~intracellular part	1744	3.4.E-04	1.038
GO_CC	GO:0012505~endomembrane system	164	3.6.E-04	1.271
GO_CC	GO:0042995~cell projection	145	4.6.E-04	1.286
GO_CC	GO:0043232~intracellular non-membrane-bounded organelle	460	7.1.E-04	1.131
GO_CC	GO:0044444~cytoplasmic part	874	7.8.E-04	1.080
GO_CC	GO:0005622~intracellular	1792	1.1.E-03	1.033
GO_CC	GO:0043005~neuron projection	76	2.7.E-03	1.360
GO_CC	GO:0046930~pore complex	27	3.5.E-03	1.722
GO_CC	GO:0044420~extracellular matrix part	30	4.1.E-03	1.650
GO_CC	GO:0005643~nuclear pore	22	4.2.E-03	1.827
GO_CC	GO:0016020~membrane	1151	5.8.E-03	1.050
GO_CC	GO:0044446~intracellular organelle part	727	8.7.E-03	1.070
GO_CC	GO:0044430~cytoskeletal part	163	1.1.E-02	1.178
GO_CC	GO:0005903~brush border	14	1.3.E-02	1.987
GO_CC	GO:0005635~nuclear envelope	46	1.4.E-02	1.386
GO_CC	GO:0044463~cell projection part	47	1.4.E-02	1.379
GO_CC	GO:0044431~Golgi apparatus part	65	1.9.E-02	1.288
GO_CC	GO:0005604~basement membrane	20	2.0.E-02	1.661
GO_CC	GO:0042734~presynaptic membrane	11	2.2.E-02	2.105
GO_CC	GO:0043204~perikaryon	11	2.2.E-02	2.105
GO_CC	GO:0031252~cell leading edge	34	2.4.E-02	1.425
GO_CC	GO:0000123~histone acetyltransferase complex	16	2.5.E-02	1.760
GO_CC	GO:0044433~cytoplasmic vesicle part	42	3.0.E-02	1.349

GO_CC	GO:0045211~postsynaptic membrane	31	3.3.E-02	1.421
GO_CC	GO:0031090~organelle membrane	204	3.9.E-02	1.118
GO_CC	GO:0030426~growth cone	15	4.3.E-02	1.693
GO_CC	GO:0030027~lamellipodium	20	4.3.E-02	1.544
GO_CC	GO:0031410~cytoplasmic vesicle	124	4.6.E-02	1.154
GO_CC	GO:0031984~organelle subcompartment	9	4.7.E-02	2.084
GO_MF	GO:0001883~purine nucleoside binding	351	6.3.E-08	1.269
GO_MF	GO:0017076~purine nucleotide binding	398	2.0.E-06	1.211
GO_MF	GO:0032553~ribonucleotide binding	379	3.1.E-06	1.213
GO_MF	GO:0043169~cation binding	733	7.7.E-05	1.108
GO_MF	GO:0008092~cytoskeletal protein binding	121	1.5.E-04	1.353
GO_MF	GO:0016772~transferase activity, transferring phosphorus-containing groups	212	1.7.E-04	1.243
GO_MF	GO:0030695~GTPase regulator activity	93	4.1.E-04	1.384
GO_MF	GO:0005516~calmodulin binding	40	1.3.E-03	1.610
GO_MF	GO:0016817~hydrolase activity, acting on acid anhydrides	155	3.7.E-03	1.215
GO_MF	GO:0005518~collagen binding	15	4.8.E-03	2.113
GO_MF	GO:0043168~anion binding	25	5.7.E-03	1.704
GO_MF	GO:0019904~protein domain specific binding	76	6.9.E-03	1.311

GO_MF	GO:0008233~peptidase activity	112	7.4.E-03	1.239
GO_MF	GO:0005543~phospholipid binding	41	2.0.E-02	1.386
GO_MF	GO:0022803~passive transmembrane transporter activity	86	3.8.E-02	1.203
KEGG	hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	29	3.2.E-05	2.120
KEGG	hsa04130:SNARE interactions in vesicular transport	13	1.6.E-02	2.002
KEGG	hsa04910:Insulin signaling pathway	34	2.0.E-02	1.438
KEGG	hsa04360:Axon guidance	34	2.3.E-02	1.424
KEGG	hsa05410:Hypertrophic cardiomyopathy (HCM)	22	2.4.E-02	1.581
KEGG	hsa00500:Starch and sucrose metabolism	11	2.4.E-02	2.063
KEGG	hsa04510:Focal adhesion	45	2.9.E-02	1.329
KEGG	hsa05211:Renal cell carcinoma	20	3.0.E-02	1.597
KEGG	hsa00310:Lysine degradation	15	3.1.E-02	1.749
KEGG	hsa04530:Tight junction	33	3.8.E-02	1.382
KEGG	hsa04730:Long-term depression	20	4.3.E-02	1.540
KEGG	hsa00640:Propanoate metabolism	11	4.4.E-02	1.898
KEGG	hsa05200:Pathways in cancer	70	4.8.E-02	1.212
KEGG	hsa04914:Progesterone-mediated oocyte maturation	22	4.9.E-02	1.483

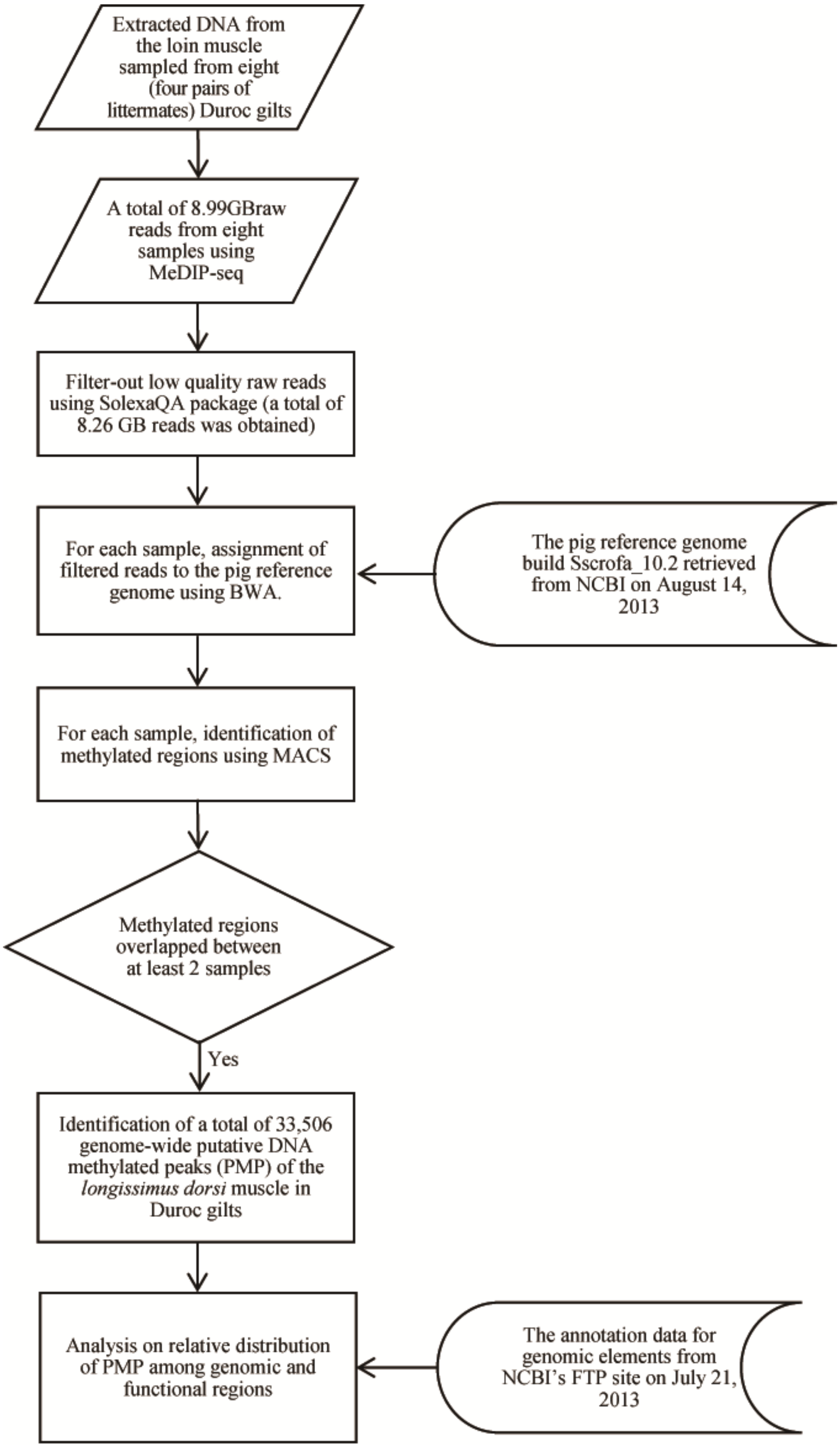

Figure S1. Experimental approach used to identify a genome-wide DNA methylation profile of the loin (*longissimus dorsi*) muscle in swine. Solid arrows represent flow of data