Table S1. Characteristics of Zlotnicka White pigs representing high and low-fat deposition traits, means ±SD

Traits	HFD (n=8)		LFD (n=8)		P-value	Group diff*	All pigs (n=72)	
	mean	SD	mean	SD			mean	SD
Daily gain (g)	641 a	34.5	718 b	84.2	0.03	11%	700	106
Backfat thickness (cm)	2.09 A	0.31	1.53 B	0.36	0.004	27%	1.90	0.39
Peritoneal fat (kg)	0.72 A	0.11	0.46 B	0.06	0.0001	36%	0.61	0.16
Backfat thickness in the K1 point (cm)	2.23 A	0.37	1.44 B	0.20	0.0002	35%	2.00	0.52
Ham fat mass with skin (kg)	2.49 A	0.21	1.80 B	0.23	1.86E-05	28%	2.15	0.37
Loin fat mass with skin (kg)	2.37 A	0.17	1.58 B	0.28	2.06E-05	33%	2.03	0.48
Fat over shoulder thickness (cm)	2.85 A	0.27	2.11 B	0.31	0.0002	26%	2.75	0.61
Lumbar fat I thickness (cm)	2.43 A	0.26	1.44 B	0.32	1.096E-05	41%	2.16	0.55
Lumbar fat II thickness (cm)	2.20 A	0.47	1.26 B	0.21	0.0004	43%	1.95	0.54
Lumbar fat III thickness (cm)	2.74 A	0.63	1.80 B	0.29	0.003	34%	2.40	0.59
Average backfat thickness (cm)	2.46 A	0.27	1.60 B	0.17	8.63E-06	35%	2.27	0.45

Abbreviations: SD – standard deviation, HDF – high-fat deposition, LFD – low-fat deposition. *Group diff – differences between groups in percentage. Values with different letters belong to various statistical group (A, B = $P< 0.01$; a, b = $P<0.05$).

Table S2. Primers and probes used in qPCR analysis

Gene		Primers and probe or Taqman Gene Expression Assay ID	AL [bp]	Label	Reference sequences accession numbers	Exon Boundary
RPL27	60S ribosomal protein L27 housekeeping gene	5`NED – CGGTCATCGTAAAGAA CGCTACTCCGGACGCAAA GGTCTGAGGTGCCATCATCA	55	NED	ENSSSCG00000025507	1–2
OAZ1	ornithine decarboxylase antizyme 1 housekeeping gene	Ss03387505_u1	177	FAM	NM_001122994.1	5–5
RPS29	ribosomal protein S29 housekeeping gene	Ss03391548_g1	71	VIC	NM_001001633.2	2–3
AHSG	alpha 2-HS glycoprotein (fetuin)	Ss03374810_m1	60	FAM	XM_005652369.3	6–7
ACACA	acetyl-CoA carboxylase alpha	Ss03389963_m1	61	FAM	NM_001114269.1	54–55
CYP1A1	cytochrome P450 family 1 subfamily A member 1	Ss03394918_g1	78	FAM	NM_214412.1	3–4
GYS2	glycogen synthase 2	Ss04248111_m1	62	FAM	NM_001195511.1	8–9
PON3	paraoxonase 3	Ss03388478_m1	105	FAM	NM_001044604.1	9–10
ACAA2	acetyl-CoA acyltransferase 2	Ss04245775_m1	71	FAM	NM_001167638.1	7–8
PCK1	phosphoenolpyruvate carboxykinase 1, mitochondrial	Ss03390599_g1	65	FAM	NM_001123158.1	3–4
PCK2	phosphoenolpyruvate carboxykinase 2, mitochondrial	Ss03373733_m1	68	FAM	NM_001161753.1	4–5
C4	complement C4A	Ss03390274_m1	63	FAM	NM_001123089.2	35–36
LDHD	lactate dehydrogenase D	AGCCCTGTGCTATGACCAAG GTTCCACCAACACGGAAAAG	160	EvaGreen	ENSSSCG00000002712	3–4
PIK3R1	phosphoinositide-3-kinase regulatory subunit 1	ACATGAATATAACACTCAATTTCAAGA TTCTTTGCTGTACCGCTCCT	175	EvaGreen	ENSSSCG00000047442	10–11
HP	haptoglobin	CTCTGCGGGCAGCTTTTT CGTGCGCAGTTTGTAGTAGG	147	EvaGreen	ENSSSCG00000002749	3–4
LPIN3	lipin 3	CTTCCGATGCTCACCCTTC CACATGTTCCTCATCGCTGT	171	EvaGreen	ENSSSCG00000007359	4–5
FADS1	fatty acid desaturase 1	TGAGCTCTCTCCTGATTGGA GTGCAGCAGGTGCATTAAGA	161	EvaGreen	ENSSSCG00000024015	2–3
CPT1A	carnitine palmitoyltransferase 1A	AATGGGATCCACGCCATC GGTGCTGGATGGTGTCTGTTT	160	EvaGreen	ENSSSCG00000012880	9–10
FASN	fatty acid synthase	Ss03386194_u1	95	FAM	NM_001099930.1	40
FGB	fibrinogen beta chain	Ss04328981_g1	127	FAM	NM_001244113.1	1

AL – amplicon length.

Table S3. Validation of RNA-seq result using qPCR method

Gene	Pearson correlation coefficient (r)	P-value
AHSG	0.66	0.0051
ACACA	0.87	<0.0001
CYP1A1	0.96	<0.0001
GYS2	0.81	<0.0001
PON3	0.97	<0.0001
ACAA2	0.78	0.0004
PCK1	0.94	<0.0001
LDHD	0.72	0.0018
PIK3R1	0.92	<0.0001
HP	0.81	0.0002
FADS1	0.96	<0.0001
CPT1A	0.95	<0.0001
FASN	0.59	0.016
FGB	0.96	<0.0001

Pearson correlation coefficient (r) and p-value generated using the SAS Enterprise 7.1.