

Article title: Transcriptome analysis of adipose tissue from pigs divergent in feed efficiency reveals alteration in gene networks related to adipose growth, lipid metabolism, extracellular matrix and immune response

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**Table S1** Differentially expressed transcripts (n = 209) at a P < 0.01 in FE-divergent pigs.

Gene Symbol	Gene Name	Fold Change	p-value	q-value	Networks*
COL11A2	collagen type XI alpha 2 chain	25.7	0.009	0.638	2
PLEKHB1	pleckstrin homology domain containing B1	7.49	0.004	0.548	3
DIRAS3	DIRAS family GTPase 3	7.37	0.009	0.613	8
KCNMA1	potassium calcium-activated channel subfamily M alpha 1	6.16	0.001	0.399	4
COL28A1	collagen type XXVIII alpha 1 chain	5.27	0.002	0.455	7
GARNL3	GTPase activating Rap/RanGAP domain like 3	4.95	0.002	0.472	11
COL11A1	collagen type XI alpha 1 chain	4.80	0.008	0.607	7
NFASC	neurofascin	4.25	0.001	0.455	5
BMPR1B	bone morphogenetic protein receptor type 1B	4.16	0.000	0.209	3
CYP1A1	cytochrome P450 family 1 subfamily A member 1	3.87	0.005	0.548	8
MRAP2	melanocortin 2 receptor accessory protein 2	3.63	0.004	0.548	5
KRT18	keratin 18	3.60	0.003	0.499	1
COLGALT2	collagen beta(1-O)galactosyltransferase 2	3.32	0.003	0.527	12
ADIRF	adipogenesis regulatory factor	3.21	0.006	0.559	12
SHISA2	shisa family member 2	2.99	0.005	0.548	8
CNKS2	connector enhancer of kinase suppressor of Ras 2	2.88	0.005	0.548	11
KRT19	keratin 19	2.70	0.007	0.600	1
ZBTB7C	zinc finger and BTB domain containing 7C	2.67	0.000	0.091	1
PLP1	proteolipid protein 1	2.66	0.003	0.515	7
EPHA7	EPH receptor A7	2.50	0.008	0.607	4
WISP1	WNT1 inducible signaling pathway protein 1	2.49	0.008	0.607	2
KLF5	Kruppel like factor 5	2.47	0.000	0.261	8
KERA	keratocan	2.35	0.010	0.643	2
KCNT2	potassium sodium-activated channel subfamily T member 2	2.33	0.003	0.548	7
MYBL1	MYB proto-oncogene like 1	2.28	0.010	0.644	6
GRIP2	glutamate receptor interacting protein 2	2.18	0.005	0.548	7
EGFL6	EGF like domain multiple 6	2.12	0.009	0.638	4
PODNL1	podocan like 1	2.12	0.010	0.643	9
PON3	paraoxonase 3	2.08	0.007	0.586	4
CA11	carbonic anhydrase 11	2.06	0.008	0.607	6
RPL15	ribosomal protein L15	2.03	0.005	0.548	11
MMP16	matrix metallopeptidase 16	2.03	0.003	0.499	2
SYNC	syncoilin, intermediate filament protein	1.99	0.001	0.455	4
CHN1	chimerin 1	1.98	0.007	0.580	3
KANK4	KN motif and ankyrin repeat domains 4	1.90	0.002	0.499	-
NOV	nephroblastoma overexpressed	1.89	0.002	0.499	2
CADM3	cell adhesion molecule 3	1.84	0.000	0.186	4
ADGRG2	adhesion G protein-coupled receptor G2	1.81	0.004	0.548	7,12
CEP126	centrosomal protein 126	1.80	0.007	0.607	12
PIWIL4	piwi like RNA-mediated gene silencing 4	1.80	0.008	0.607	5

RARB	retinoic acid receptor beta	1.77	0.000	0.217	2
ROBO2	roundabout guidance receptor 2	1.74	0.009	0.615	1
AMPH	amphiphysin	1.73	0.009	0.613	3
MAP6	microtubule associated protein 6	1.73	0.009	0.638	2
CFI	complement factor I	1.71	0.006	0.563	9
EXPH5	exophilin 5	1.69	0.005	0.548	10
SEMA3D	semaphorin 3D	1.67	0.002	0.472	1
SYNM	synemin	1.65	0.001	0.399	1
PRKG1	protein kinase, cGMP-dependent, type I	1.65	0.001	0.449	3
PLCE1	phospholipase C epsilon 1	1.63	0.000	0.091	2
GALNT5	polypeptide N-acetylgalactosaminyltransferase 5	1.62	0.002	0.499	12
SGSM1	small G protein signaling modulator 1	1.62	0.000	0.091	10
CFHR3	complement factor H related 3	1.60	0.000	0.267	14
EPB41L2	erythrocyte membrane protein band 4.1 like 2	1.58	0.001	0.455	1
MET	MET proto-oncogene, receptor tyrosine kinase	1.57	0.001	0.397	3
SLC7A10	solute carrier family 7 member 10	1.57	0.002	0.499	11
SEMA3C	semaphorin 3C	1.57	0.002	0.499	1
NECAB3	N-terminal EF-hand calcium binding protein 3	1.56	0.005	0.548	5
DPYSL3	dihydropyrimidinase like 3	1.53	0.007	0.607	11
CDC42BPG	CDC42 binding protein kinase gamma	1.52	0.009	0.634	14
RFTN2	raftlin family member 2	1.52	0.000	0.000	9
CFB	complement factor B	1.52	0.008	0.607	6
SPARCL1	SPARC like 1	1.49	0.005	0.548	10
C14orf93	chromosome 14 open reading frame 93	1.48	0.009	0.617	5
ZNF180	zinc finger protein 180	1.47	0.006	0.570	11
NUDT22	nudix hydrolase 22	1.47	0.000	0.166	11
PLEKHA4	pleckstrin homology domain containing A4	1.47	0.002	0.472	12
ABCB1	ATP binding cassette subfamily B member 1	1.47	0.001	0.399	6
DCLRE1A	DNA cross-link repair 1A	1.46	0.008	0.612	11
CLU	clusterin	1.46	0.005	0.548	4
ITGB8	integrin subunit beta 8	1.45	0.005	0.548	1
MYO1D	myosin ID	1.44	0.005	0.548	6
C15orf41	chromosome 15 open reading frame 41	1.44	0.008	0.607	9
CCNE2	cyclin E2	1.44	0.004	0.548	3
ADAMTSL3	ADAMTS like 3	1.44	0.003	0.499	11
CD109	CD109 molecule	1.41	0.002	0.464	10
SNORA62	small nucleolar RNA, H/ACA box 62	1.41	0.008	0.607	15
NCKAP5	NCK associated protein 5	1.39	0.006	0.578	5
PCDH11X	protocadherin 11 X-linked	1.38	0.005	0.548	14
NAALADL2	N-acetylated alpha-linked acidic dipeptidase like 2	1.38	0.001	0.441	5
GPC6	glypican 6	1.37	0.007	0.592	9
CEP162	centrosomal protein 162	1.37	0.010	0.644	10
RGS5	regulator of G protein signaling 5	1.37	0.002	0.472	2
AFF3	AF4/FMR2 family member 3	1.37	0.006	0.573	12
ANGPTL1	angiopoietin like 1	1.36	0.005	0.548	1
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6	1.36	0.002	0.472	7
GLIS2	GLIS family zinc finger 2	1.36	0.005	0.548	3
ZFPM2	zinc finger protein, FOG family member 2	1.36	0.004	0.548	1
SEMA3B	semaphorin 3B	1.35	0.005	0.548	1
COL14A1	collagen type XIV alpha 1 chain	1.35	0.001	0.455	5
PRTFDC1	phosphoribosyl transferase domain containing 1	1.34	0.008	0.607	14
PLA2G4A	phospholipase A2 group IVA	1.33	0.005	0.548	4
FAM129A	family with sequence similarity 129 member A	1.32	0.003	0.499	14
PLOD2	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	1.31	0.005	0.548	2
ADD3	adducin 3	1.31	0.000	0.091	4
MAP1A	microtubule associated protein 1A	1.30	0.006	0.556	2,5,12
C18orf21	chromosome 18 open reading frame 21	1.30	0.006	0.574	5
NREP	neuronal regeneration related protein	1.29	0.008	0.607	3

SSPN	sarcospan	1.29	0.000	0.221	2
NTN4	netrin 4	1.28	0.002	0.455	2
RFC3	replication factor C subunit 3	1.28	0.006	0.561	13
CHL1	cell adhesion molecule L1 like	1.28	0.005	0.548	9
ABCA8	ATP binding cassette subfamily A member 8	1.27	0.008	0.607	9
CARF	calcium responsive transcription factor	1.26	0.005	0.548	5
TGFB2	transforming growth factor beta 2	1.25	0.010	0.643	1
ZBTB37	zinc finger and BTB domain containing 37	1.24	0.005	0.548	9
ERCC6L2	ERCC excision repair 6 like 2	1.23	0.005	0.548	11
KDELR3	KDEL endoplasmic reticulum protein retention receptor 3	1.21	0.006	0.580	8
NBAS	neuroblastoma amplified sequence	1.21	0.003	0.545	9
ADNP2	ADNP homeobox 2	1.21	0.008	0.607	10
SYDE2	synapse defective Rho GTPase homolog 2	1.20	0.002	0.455	10
NAPA	NSF attachment protein alpha	-1.15	0.009	0.615	8
ELMO2	engulfment and cell motility 2	-1.15	0.002	0.499	5
NCLN	nicalin	-1.15	0.009	0.617	10
ETV6	ETS variant 6	-1.18	0.010	0.643	1
STK35	serine/threonine kinase 35	-1.18	0.004	0.548	3
AHCYL1	adenosylhomocysteinase like 1	-1.19	0.007	0.607	3
HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	-1.19	0.005	0.548	-
TNFRSF1B	TNF receptor superfamily member 1B	-1.19	0.005	0.548	6
ZDHHC5	zinc finger DHHC-type containing 5	-1.19	0.003	0.499	12
IRAK1	interleukin 1 receptor associated kinase 1	-1.20	0.006	0.565	13
CIC	capicua transcriptional repressor	-1.20	0.004	0.548	12
RIPK3	receptor interacting serine/threonine kinase 3	-1.20	0.009	0.617	6
SLC6A8	solute carrier family 6 member 8	-1.20	0.008	0.607	4
TGFB1	transforming growth factor beta 1	-1.21	0.010	0.640	3
UBE2J2	ubiquitin conjugating enzyme E2 J2	-1.21	0.002	0.464	1
FZD4	frizzled class receptor 4	-1.21	0.001	0.399	7
EDNRB	endothelin receptor type B	-1.22	0.003	0.515	7
RAB32	RAB32, member RAS oncogene family	-1.22	0.002	0.472	8
POGK	pogo transposable element derived with KRAB domain	-1.22	0.005	0.548	13
HEXIM1	hexamethylene bisacetamide inducible 1	-1.23	0.003	0.545	8
UBN1	ubinuclein 1	-1.23	0.004	0.548	8
PPP1R10	protein phosphatase 1 regulatory subunit 10	-1.23	0.003	0.499	13
MAN1C1	mannosidase alpha class 1C member 1	-1.23	0.003	0.548	10
S1PR1	sphingosine-1-phosphate receptor 1	-1.24	0.005	0.548	7
LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	-1.25	0.008	0.607	5
ARHGEF15	Rho guanine nucleotide exchange factor 15	-1.25	0.009	0.638	11
C11orf84	chromosome 11 open reading frame 84	-1.25	0.005	0.548	5
AP1B1	adaptor related protein complex 1 beta 1 subunit	-1.25	0.003	0.499	2
VWF	von Willebrand factor	-1.25	0.005	0.548	2
MED26	mediator complex subunit 26	-1.26	0.003	0.499	8
ORAI3	ORAI calcium release-activated calcium modulator 3	-1.26	0.006	0.569	13
MAFB	MAF bZIP transcription factor B	-1.27	0.002	0.472	4
ITGAM	integrin subunit alpha M	-1.28	0.006	0.567	13
SSH2	slingshot protein phosphatase 2	-1.29	0.010	0.643	10,13
JMJD6	arginine demethylase and lysine hydroxylase	-1.29	0.008	0.607	6
FOSL2	FOS like 2, AP-1 transcription factor subunit	-1.29	0.001	0.399	4
PACS1	phosphofuran acidic cluster sorting protein 1	-1.30	0.008	0.607	2
NLRP3	NLR family pyrin domain containing 3	-1.30	0.002	0.499	13
LMNB2	lamin B2	-1.30	0.003	0.515	8
CDC42EP4	CDC42 effector protein 4	-1.31	0.000	0.223	3
GTF2IRD1	GTF2I repeat domain containing 1	-1.31	0.010	0.640	13
AHCY	adenosylhomocysteinase	-1.31	0.000	0.136	3
GPER1	G protein-coupled estrogen receptor 1	-1.32	0.004	0.548	7
STAB1	stabilin 1	-1.33	0.006	0.556	4
BAG3	BCL2 associated athanogene 3	-1.33	0.000	0.166	10

ETS2	ETS proto-oncogene 2, transcription factor	-1.33	0.003	0.499	1
PIM2	Pim-2 proto-oncogene, serine/threonine kinase	-1.34	0.006	0.573	4
BTG2	BTG anti-proliferation factor 2	-1.34	0.008	0.607	3
CLCN4	chloride voltage-gated channel 4	-1.35	0.007	0.600	9
VEGFA	vascular endothelial growth factor A	-1.35	0.000	0.221	3
ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	-1.36	0.000	0.166	9
USP31	ubiquitin specific peptidase 31	-1.37	0.004	0.548	9
DAGLB	diacylglycerol lipase beta	-1.38	0.005	0.548	14
HSD17B14	hydroxysteroid 17-beta dehydrogenase 14	-1.38	0.005	0.548	11
CTPS1	CTP synthase 1	-1.38	0.009	0.616	8
PLXNA4	plexin A4	-1.38	0.007	0.599	12
LPAR2	lysophosphatidic acid receptor 2	-1.39	0.007	0.603	7
IFNAR2	interferon alpha and beta receptor subunit 2	-1.39	0.005	0.548	6
PLIN2	perilipin 2	-1.40	0.000	0.262	1
ITPKC	inositol-trisphosphate 3-kinase C	-1.42	0.004	0.548	14
NFIL3	nuclear factor, interleukin 3 regulated	-1.42	0.003	0.499	6
AMY1C	amylase, alpha 1C (salivary)	-1.42	0.007	0.585	6
NKG7	natural killer cell granule protein 7	-1.42	0.001	0.350	13
CLIC5	chloride intracellular channel 5	-1.43	0.004	0.548	6
SLC25A25	solute carrier family 25 member 25	-1.44	0.006	0.556	14
MRC1	mannose receptor C-type 1	-1.45	0.007	0.585	3
DYSF	dysferlin	-1.45	0.003	0.515	8
SLC6A6	solute carrier family 6 member 6	-1.45	0.002	0.472	4
HYAL2	hyaluronoglucosaminidase 2	-1.45	0.005	0.548	6
LNX1	ligand of numb-protein X 1	-1.45	0.004	0.548	5
SELL	selectin L	-1.46	0.004	0.548	6
PKHD1	PKHD1, fibrocystin/polyductin	-1.48	0.009	0.617	1
ANPEP	alanyl aminopeptidase, membrane	-1.49	0.002	0.499	1
LRRC8D	leucine rich repeat containing 8 VRAC subunit D	-1.52	0.000	0.261	10
C5AR1	complement C5a receptor 1	-1.52	0.004	0.548	7
TNFSF9	TNF superfamily member 9	-1.59	0.007	0.586	6
DUSP2	dual specificity phosphatase 2	-1.60	0.001	0.336	4
STS	steroid sulfatase	-1.60	0.008	0.607	8
MS4A7	membrane spanning 4-domains A7	-1.62	0.004	0.548	16
SLC6A2	solute carrier family 6 member 2	-1.64	0.004	0.548	1
UNC5A	unc-5 netrin receptor A	-1.65	0.006	0.561	7
P2RY1	purinergic receptor P2Y1	-1.66	0.000	0.267	7
SULT2A1	sulfotransferase family 2A member 1	-1.68	0.002	0.472	1
AHSA2	activator of HSP90 ATPase homolog 2	-1.68	0.005	0.548	5
RPH3A	rabphilin 3A	-1.70	0.001	0.379	12
CBFA2T3	CBFA2/RUNX1 translocation partner 3	-1.71	0.002	0.499	1
ADORA3	adenosine A3 receptor	-1.73	0.000	0.091	7
CSF3R	colony stimulating factor 3 receptor	-1.87	0.001	0.420	1
OSM	oncostatin M	-1.88	0.005	0.548	3
NLRP12	NLR family pyrin domain containing 12	-2.24	0.000	0.221	13
TXK	TXK tyrosine kinase	-2.26	0.008	0.607	2
TREH	trehalase	-2.28	0.007	0.607	9
TEX33	testis expressed 33	-2.72	0.001	0.399	5
LTF	lactotransferrin	-2.85	0.002	0.455	1
FAT2	FAT atypical cadherin 2	-2.93	0.009	0.628	10
MMP8	matrix metallopeptidase 8	-3.23	0.000	0.133	2
AKR1C4	aldo-keto reductase family 1 member C4	-3.59	0.002	0.455	4,9
SRXN1	sulfiredoxin 1	-3.85	0.000	0.091	6

\*Network ID's are presented in Table S4