

Supplementary file 1

Table S1 Characteristics of gene-specific primers

Gene	Forward primer (from 5' to 3') Reverse primer (from 5' to 3')	PCR product size (bp)	NCBI GenBank Accession no.	Annealing temperature
<i>Reference genes</i>				
<i>ACTB</i>	GACATCCGCAAGGACCTCTA ACATCTGCTGGAAGGTGGAC	205	XM_003124280	60
<i>ATP5G1</i>	CAGTCACCTTGAGCCGGGCGA TAGCGCCCCGGTGGTTTGC	94	NM_001025218	64
<i>GAPDH</i>	GTCGGAGTGAACGGATTTGG CCACTCCGGACACGCTTGCA	218	NM_001206359	59
<i>RPS9</i>	GTCGCAAGACTTATGTGACC AGCTTAAAGACCTGGGTCTG	325	XM_003356050	60
<i>HAS2</i>	GAAAAGGCTAACCTACCCTG TGTTGGACAAGACCAGTTGG	218	NM_214053	60
<i>Target genes</i>				
<i>AKR1C1</i>	TACAAGCCCGTCTGCAACCA GCGAAGGGCAATTACGGCTG	225	NM_001044569	60
<i>AKR1C2</i>	ACCTTGCTCCTCCTACACAATG TCAGGTGCATACGTGCCAAA	207	NM_001044570	60
<i>ARL2BP</i>	GCTGTCTTCTCTTCCGCCT GCCGCCATGTTAAACCCAGG	146	XM_003126968	60
<i>ATP6V0D2</i>	GACCCTTACCCAACCTGTGG ATGTCTTTCCCCCACTGCCAT	180	XM_003125581	60
<i>BCO2</i>	AATGCCTTTGAGGACCAGGG TCAGCCTGTTTCACAGCACT	248	XM_003129854	60
<i>C3</i>	GCCACATCCTACGCCCTCTT GGTACATGGTCACCACCGACA	352	NM_214009	60

<i>CCL2</i>	CTGCACCCAGGTCCTTGC GACCCACTTCTGCTTGGGTTC	199	NM_214214	60
<i>CP</i>	GGTGGGAGACACCATCCGAG GTGAGGCAGAAGGAGGCACA	155	NM_001267694	60
<i>CRP</i>	GAAGCTGTCACTGTGTCTCCTGG AGTAAAGGCCGTGAGTGGTTTGG	154	NM_213844	60
<i>CYCS</i>	ACAAGGTCAGGCTGTTAGAATGC GCTGATGGTACAGCTCCCCTA	144	NM_001129970	60
<i>CYP2E1</i>	TCTCCATCTGGAAGCACATC TAGTGGAGCAAGACCTCCTT	220	NM_214421	60
<i>DNAJC9</i>	TGCTGGAGAGGTCCCATCCTAT CCACTCCTTCATCAAGCCCCA	137	XM_003483498	60
<i>ENPP4</i>	TCGACCCGGCAGACTACACT CCGTGGTCACCTAGTTTGAGGG	247	XM_001924940	60
<i>EPB42</i>	GGCATTTCCTGTGGTCAAGTGG TGCTCGGCATTGTTTCTCGC	103	XM_013993102	60
<i>ESM1</i>	CCTTCGGGATGGAATGCAAGC CACCCAGGATCAGCGTGGA	245	XM_013984770	60
<i>FGF14</i>	AACAGGAATCTGGTAGAGCCTGG GTTCTCGGTACATGGCAACTTCC	135	XM_001924895	60
<i>FGF21</i>	CGATACCTCTACACGGATGA CGTTGTAGCCATCCTCAAGA	262	NM_001163410	60
<i>FMO5</i>	TGATCCAGCCCTTAGGTGCC GTATGGCGTTGGCTGTCCAC	169	XM_001928594	60
<i>GINS1</i>	AGGCTTGGACATCACACAGGAT GCAATGGGCGAGTGAGGTTATG	213	XM_003483911	60
<i>HP</i>	GTTTCGCTATCACTGCCAAAC CAGTTTCTCTCCAGTGACCT	108	NM_214000	60
<i>HEMGN</i>	GCCTGAGGACTGTGCATCTG CTCTGGTTCTTCTGCTTTGGGT	250	XM_021066411	60
<i>ICAM1</i>	CGGTGGCAGCCGTGGCTATC TTGATGCAGCCCCGCTCGTC	208	NM_213816	60

<i>IL6</i>	AAGGTGATGCCACCTCAGAC TCTGCCAGTACCTCCTTGCT	151	NM_001252429	60
<i>IL8</i>	ACTTCCAAACTGGCTGTTGC GGAATGCGTATTTATGCACTGG	120	NM_213867	60
<i>LRRC59</i>	AGCCTCAGCGACCTGAATGA CCACAGAACTCCGACGGTAGA	113	NM_001244951	60
<i>MPO</i>	ACTTTACCCCTGAGCCTGCC CGTTGGTTCTTGATGCGGGG	130	XM_003131655	58
<i>MUC13</i>	TGTGTGTTGCTTTGGGTCCAG CACAGCCAACTCCACTGTAGC	171	NM_001105293	60
<i>MVK</i>	CTGTGGCCTTGAACCTTGAGA CTGCTGGATGCCAATGTTTG	92	XM_001929184	60
<i>NDUFAF4</i>	AGTTGAAACCTTCCCCTGCTCC CCTTTGGCTTCTGATGTGCTCC	204	XM_001925477	60
<i>PCLAF</i>	GGAAGGTGTTGGGTTCTCCA TGTGTCTTCAGGTGGCAAAGGA	60	NM_001244997	248
<i>RANBP1</i>	TCCACCGAGAATGCTGACGA CCTTCCACTCTGGGAGGTCG	60	NM_001185070	166
<i>SKA1</i>	GCAGAGCTTCACTTTACCTCGC TTGGCTGGTTCTTCAGGGTCA	386	XM_001926548	58
<i>SLC51B</i>	TTCAAGAGGTGACAGCCGTGT TGCTCTGTTCCTGGTTGGG	230	XM_003121716	58
<i>SOD1</i>	TCCATGTCCATCAGTTTGGA CTGCCCCAAGTCATCTGGTTT	250	NM_001190422	60
<i>STEAP2</i>	ATGTTGCCTACAGCCTCTGCT GGATGGAGGTGACTGCCAGG	192	XM_003357423	60
<i>TNF</i>	CCAAGGACTCAGATCATCGT GCTGGTTGTCTTTCAGCTTC	146	NM_214022	60
<i>XDH</i>	AGACCACAAGCAGGTCACCC CGCTCCCCTTCAAAACGCAG	147	NM_001285974	60

Table S2 Fold change (FC) and *P*-value of all differentially expressed transcripts*

Gene Symbol	Gene Description	SINS high vs. SINS low		
		FC	P-value	FDR
Upregulated				
FMO5	flavin containing monooxygenase 5	3.84	0.0494	0.482
CD207	CD207 molecule, langerin	3.75	0.0250	0.441
AKR1C1	aldo-keto reductase family 1, member C1	3.32	0.0197	0.429
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2	2.78	0.0291	0.453
ESM1	endothelial cell-specific molecule 1	2.70	0.0152	0.431
FGF14	fibroblast growth factor 14	2.47	0.0043	0.441
GYPA	glycophorin A (MNS blood group)	2.43	0.0383	0.466
LOC733635	aldo-keto reductase family 1 member C2-like	2.30	0.0080	0.419
EPB42	erythrocyte membrane protein band 4.2	2.25	0.0043	0.444
PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	2.13	0.0067	0.422
LOC100736962	liver carboxylesterase	2.11	0.0247	0.440
HEMGN	hemogen	2.03	0.0123	0.429
SFTPA1	surfactant protein A1	2.03	0.0193	0.428
LOC100627616	calcium-activated potassium channel subunit alpha-1-like	2.02	0.0156	0.432
AKAP5	A kinase (PRKA) anchor protein 5	2.02	0.0003	0.555
ADGRG6	adhesion G protein-coupled receptor G6	1.97	0.0074	0.416
CRP	C-reactive protein, pentraxin-related	1.96	0.0253	0.444
LOC100738010	deoxyribonuclease gamma	1.93	0.0053	0.430
BCO2	beta-carotene oxygenase 2	1.91	0.0087	0.423
NRN1L	neuritin 1-like	1.90	0.0014	0.449
LOC100517145	complement C3	1.88	0.0299	0.456
TDO2	tryptophan 2,3-dioxygenase	1.88	0.0304	0.456
MPO	myeloperoxidase	1.86	0.0262	0.446
XDH	xanthine dehydrogenase	1.84	0.0226	0.436
CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	1.83	0.0388	0.467
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.78	0.0051	0.430
AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.78	0.0051	0.432
LOC100512160	serine protease inhibitor Kazal-type 5	1.78	0.0237	0.438
LOC100513690	putative sodium-coupled neutral amino acid transporter 11	1.77	0.0007	0.630
DPYS	dihydropyrimidinase	1.76	0.0114	0.429
FNDC1	fibronectin type III domain containing 1	1.76	0.0307	0.457
MVK	mevalonate kinase	1.70	0.0006	0.650
CP	ceruloplasmin (ferroxidase)	1.68	0.0404	0.470
C4BPB	complement component 4 binding protein, beta	1.68	0.0149	0.429
CLEC2D	C-type lectin domain family 2, member D	1.68	0.0068	0.422
MAN1C1	mannosidase, alpha, class 1C, member 1	1.68	0.0073	0.419
RHAG	Rh-associated glycoprotein	1.67	0.0300	0.456
GRB7	growth factor receptor-bound protein 7	1.67	0.0198	0.429
CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	1.67	0.0223	0.436
WIP1	WD repeat domain, phosphoinositide interacting 1	1.66	0.0054	0.431
ADHFE1	alcohol dehydrogenase, iron containing, 1	1.66	0.0219	0.436
VNN3	vanin 3	1.66	0.0173	0.429
KCNN2	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 2	1.65	0.0299	0.455
ALAS2	5-aminolevulinate synthase 2	1.65	0.0073	0.419
KIF28P	kinesin family member 28, pseudogene	1.64	0.0103	0.422
INSIG1	insulin induced gene 1	1.64	0.0330	0.460
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	1.63	0.0053	0.429
ACSM3	acyl-CoA synthetase medium-chain family member 3	1.63	0.0337	0.460
LOC100739121	uncharacterized LOC100739121	1.63	0.0115	0.427
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	1.62	0.0414	0.473
MAT1A	methionine adenosyltransferase I, alpha	1.62	0.0252	0.443

ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	1.61	0.0284	0.452
01. Mrz	mitochondrial amidoxime reducing component 1	1.61	0.0469	0.478
MIR107	microRNA mir-107	1.59	0.0069	0.419
GCLC	glutamate-cysteine ligase, catalytic subunit	1.58	0.0364	0.465
APOF	apolipoprotein F	1.58	0.0219	0.436
HSD17B11	hydroxysteroid (17-beta) dehydrogenase 11	1.58	0.0137	0.433
GPR156	G protein-coupled receptor 156	1.57	0.0267	0.447
ZCCHC16	zinc finger, CCHC domain containing 16	1.57	0.0468	0.479
NNMT	nicotinamide N-methyltransferase	1.56	0.0479	0.480
TCN2	transcobalamin II	1.54	0.0002	0.682
PAIP2B	poly(A) binding protein interacting protein 2B	1.54	0.0070	0.416
SPIC	Spi-C transcription factor (Spi-1/PU.1 related)	1.54	0.0131	0.434
PPAT	phosphoribosyl pyrophosphate amidotransferase	1.53	0.0213	0.434
ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	1.51	0.0056	0.425
LOC100513372	probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial	1.51	0.0153	0.431
MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	1.51	0.0168	0.436
HBB	hemoglobin, beta	1.50	0.0128	0.434
ETNK2	ethanolamine kinase 2	1.50	0.0425	0.476
LOC106507301	uncharacterized LOC106507301	1.50	0.0135	0.435
GPC4	glypican 4	1.49	0.0015	0.452
TLR4	toll-like receptor 4	1.49	0.0184	0.428
LOC100156705	melanoma-associated antigen 8-like	1.49	0.0100	0.421
AKR1C4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydrodiol dehydrogenase 4)	1.49	0.0347	0.464
PIK3C2G	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	1.49	0.0352	0.463
PRDM1	PR domain containing 1, with ZNF domain	1.48	0.0009	0.547
SLA-DMA	SLA-DM alpha chain	1.48	0.0459	0.479
SOAT2	sterol O-acyltransferase 2	1.48	0.0008	0.621
TEK	TEK tyrosine kinase, endothelial	1.48	0.0348	0.464
HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3	1.47	0.0023	0.456
GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	1.47	0.0034	0.442
RNLS	renalase, FAD-dependent amine oxidase	1.47	0.0427	0.476
ATP2B2	ATPase, Ca ⁺⁺ transporting, plasma membrane 2	1.47	0.0373	0.466
SPTA1	spectrin, alpha, erythrocytic 1	1.46	0.0083	0.419
LOC100154752	olfactory receptor 6C3-like	1.46	0.0186	0.430
LOC100525819	FGGY carbohydrate kinase domain-containing protein	1.45	0.0168	0.435
SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	1.45	0.0176	0.429
KCNT2	potassium channel, sodium activated subfamily T, member 2	1.45	0.0055	0.427
HIP1R	huntingtin interacting protein 1 related	1.45	0.0049	0.437
MMP19	matrix metalloproteinase 19	1.45	0.0038	0.440
DLG2	discs, large homolog 2 (Drosophila)	1.45	0.0168	0.435
MCTP1	multiple C2 domains, transmembrane 1	1.45	0.0045	0.438
LOC396634	receptor-type tyrosine-protein phosphatase C-like	1.45	0.0490	0.481
SCIMP	SLP adaptor and CSK interacting membrane protein	1.45	0.0013	0.476
MAB21L3	mab-21-like 3 (C. elegans)	1.44	0.0029	0.428
C4A	complement component 4A (Rodgers blood group)	1.44	0.0103	0.423
TRPC5	transient receptor potential cation channel, subfamily C, member 5	1.44	0.0166	0.436
LOC102160410	uncharacterized LOC102160410	1.44	0.0163	0.437
LOC100520032	myeloid-associated differentiation marker-like	1.44	0.0316	0.459
TAT	tyrosine aminotransferase	1.44	0.0490	0.481
ATP6V1G2	ATPase, H ⁺ transporting, lysosomal 13kDa, V1 subunit G2	1.44	0.0019	0.452
LOC100518644	glycine N-acyltransferase-like	1.44	0.0447	0.478

FMO1	flavin containing monooxygenase 1	1.44	0.0298	0.456
EFNA1	ephrin-A1	1.44	0.0352	0.462
LOC100511504	maestro heat-like repeat-containing protein family member 1	1.43	0.0034	0.441
LOC100736871	myeloid-associated differentiation marker-like	1.43	0.0034	0.439
CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	1.43	0.0432	0.476
LOC100523985	cytoplasmic dynein 1 intermediate chain 1	1.43	0.0468	0.479
LOC100737684	estrogen receptor-like	1.43	0.0493	0.482
MATN2	matrilin 2	1.43	0.0079	0.420
CPLX4	complexin 4	1.43	0.0177	0.428
DEPTOR	DEP domain containing MTOR-interacting protein	1.42	0.0116	0.426
LOC100156240	CDK5 regulatory subunit-associated protein 2	1.42	0.0367	0.465
RSC1A1	regulatory solute carrier protein, family 1, member 1	1.42	0.0356	0.463
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.42	0.0066	0.427
LOC100621650	protein furry homolog	1.42	0.0373	0.466
YPEL5	yippee-like 5	1.42	0.0080	0.419
LOC100739748	glutaryl-CoA dehydrogenase, mitochondrial-like	1.42	0.0405	0.470
C5	complement component 5	1.42	0.0144	0.430
ALDH6A1	aldehyde dehydrogenase 6 family, member A1	1.42	0.0278	0.448
ZNF366	zinc finger protein 366	1.42	0.0340	0.462
LOC100737965	runt-related transcription factor 2	1.42	0.0405	0.470
ADCK3	aarF domain containing kinase 3	1.41	0.0289	0.454
VSIG4	V-set and immunoglobulin domain containing 4	1.41	0.0227	0.436
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	1.41	0.0093	0.425
LOC100739233	nidogen-1-like	1.41	0.0131	0.433
LRG1	leucine-rich alpha-2-glycoprotein 1	1.41	0.0110	0.428
HAO2	hydroxyacid oxidase 2 (long chain)	1.41	0.0151	0.429
FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	1.41	0.0242	0.440
RIBC1	RIB43A domain with coiled-coils 1	1.40	0.0022	0.450
UROC1	urocanate hydratase 1	1.40	0.0460	0.479
DCAF11	DDB1 and CUL4 associated factor 11	1.40	0.0137	0.435
TIAM1	T-cell lymphoma invasion and metastasis 1	1.40	0.0067	0.423
BHLHB9	basic helix-loop-helix domain containing, class B, 9	1.40	0.0188	0.430
RBP7	retinol binding protein 7, cellular	1.40	0.0149	0.429
FAM198B	family with sequence similarity 198, member B	1.40	0.0367	0.466
CTNS	cystinosis, lysosomal cystine transporter	1.40	0.0312	0.457
TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	1.39	0.0009	0.598
IVD	isovaleryl-CoA dehydrogenase	1.39	0.0136	0.436
C1H6orf211	uncharacterized protein C6orf211 homolog	1.39	0.0434	0.476
LOC100737517	solute carrier family 40 member 1	1.39	0.0454	0.478
AQP11	aquaporin 11	1.39	0.0066	0.424
LOC100738724	24-hydroxycholesterol 7-alpha-hydroxylase-like	1.39	0.0252	0.443
TMEM120B	transmembrane protein 120B	1.39	0.0469	0.478
LOC100512076	solute carrier family 40 member 1	1.39	0.0467	0.480
LOC100737638	nesprin-1	1.39	0.0174	0.429
WBP1L	WW domain binding protein 1-like	1.39	0.0372	0.466
PINK1	PTEN induced putative kinase 1	1.39	0.0307	0.457
KEL	Kell blood group, metallo-endorpeptidase	1.39	0.0353	0.463
CTSS	cathepsin S	1.39	0.0307	0.457
LOC100737308	D-beta-hydroxybutyrate dehydrogenase, mitochondrial-like	1.39	0.0445	0.478
CHDH	choline dehydrogenase	1.39	0.0471	0.479
ALDH5A1	aldehyde dehydrogenase 5 family, member A1	1.39	0.0011	0.509
LOC100513779	solute carrier family 22 member 9-like	1.38	0.0386	0.467
CCDC69	coiled-coil domain containing 69	1.38	0.0396	0.469
CNTN4	contactin 4	1.38	0.0246	0.440
CSF1R	colony stimulating factor 1 receptor	1.38	0.0165	0.433
SUSD6	sushi domain containing 6	1.38	0.0173	0.429
LOC100517129	nuclear body protein SP140-like protein	1.38	0.0217	0.436

PLA1A	phospholipase A1 member A	1.38	0.0444	0.477
LOC100515273	putative 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	1.38	0.0081	0.419
PRC1	protein regulator of cytokinesis 1	1.38	0.0164	0.435
PTPRC	receptor-type tyrosine-protein phosphatase C	1.37	0.0442	0.478
SATB1	SATB homeobox 1	1.37	0.0259	0.448
LOC100520861	ATP-binding cassette sub-family A member 6	1.37	0.0084	0.420
AUH	AU RNA binding protein/enoyl-CoA hydratase	1.37	0.0424	0.476
NAGA	N-acetylgalactosaminidase, alpha-	1.37	0.0027	0.426
MAP2K6	mitogen-activated protein kinase kinase 6	1.37	0.0484	0.481
LOC100519209	BDNF/NT-3 growth factors receptor	1.36	0.0116	0.424
LOC100155953	serpin A11	1.36	0.0092	0.426
LOC102160066	uncharacterized LOC102160066	1.36	0.0419	0.475
FAM213A	family with sequence similarity 213, member A	1.36	0.0148	0.429
CD200R1	CD200 receptor 1	1.36	0.0380	0.466
CXCL11	chemokine (C-X-C motif) ligand 11	1.36	0.0487	0.481
GCDH	glutaryl-CoA dehydrogenase	1.36	0.0227	0.435
KAT6B	K(lysine) acetyltransferase 6B	1.36	0.0043	0.442
CUX2	cut-like homeobox 2	1.36	0.0422	0.476
LRRC8C	leucine rich repeat containing 8 family, member C	1.35	0.0246	0.441
CLCN6	chloride channel, voltage-sensitive 6	1.35	0.0073	0.419
RENBP	renin binding protein	1.35	0.0036	0.443
CCDC122	coiled-coil domain containing 122	1.35	0.0304	0.456
LOC100156587	olfactory receptor 4M1	1.35	0.0141	0.432
SDC2	syndecan 2	1.35	0.0028	0.431
CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.34	0.0046	0.434
DGAT2	diacylglycerol O-acyltransferase 2	1.34	0.0423	0.476
DBT	dihydrolipoamide branched chain transacylase E2	1.34	0.0056	0.426
AGMO	alkylglycerol monooxygenase	1.34	0.0122	0.431
HSF5	heat shock transcription factor family member 5	1.34	0.0372	0.466
PPP1R18	protein phosphatase 1, regulatory subunit 18	1.34	0.0172	0.431
LOC100737768	hemoglobin subunit alpha	1.34	0.0341	0.462
APBB3	amyloid beta (A4) precursor protein-binding, family B, member 3	1.34	0.0463	0.480
LOC100520083	molybdenum cofactor sulfurase-like	1.34	0.0359	0.464
IL7	interleukin 7	1.33	0.0211	0.435
LOC100521751	nephrocystin-3-like	1.33	0.0200	0.430
HPS3	Hermansky-Pudlak syndrome 3	1.33	0.0314	0.458
FGD2	FYVE, RhoGEF and PH domain containing 2	1.33	0.0397	0.469
CXCR4	chemokine (C-X-C motif) receptor 4	1.33	0.0383	0.466
FOXN3	forkhead box N3	1.33	0.0153	0.432
ZNF655	zinc finger protein 655	1.33	0.0025	0.435
LOC100519394	methyl-CpG-binding domain protein 5	1.33	0.0154	0.431
TSPAN3	tetraspanin 3	1.32	0.0172	0.431
TMEM204	transmembrane protein 204	1.32	0.0154	0.432
LOC100520241	olfactory receptor 10J1-like	1.32	0.0385	0.466
LOC100520241	olfactory receptor 10J1-like	1.32	0.0385	0.467
LOC100518411	anoctamin-1	1.32	0.0047	0.434
CTSK	cathepsin K	1.32	0.0308	0.457
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	1.32	0.0418	0.475
MIR144	microRNA mir-144	1.32	0.0315	0.459
LOC100621998	stannin	1.32	0.0109	0.430
LOC100739280	pro-neuregulin-1, membrane-bound isoform-like	1.32	0.0267	0.448
MAP10	microtubule-associated protein 10	1.32	0.0170	0.433
GLRX5	glutaredoxin 5	1.32	0.0012	0.473
ADGRL2	adhesion G protein-coupled receptor L2	1.32	0.0322	0.458
ARHGAP30	Rho GTPase activating protein 30	1.32	0.0177	0.428
ACAA1	acetyl-CoA acyltransferase 1	1.31	0.0039	0.440
TRERF1	transcriptional regulating factor 1	1.31	0.0444	0.477
LOC100738248	endonuclease/exonuclease/phosphatase family domain-containing protein 1-like	1.31	0.0031	0.433

LOC100524975	olfactory receptor 10H1	1.31	0.0337	0.460
IFN-ALPHA-16	interferon-alpha-16	1.31	0.0062	0.424
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	1.31	0.0219	0.436
SCARA5	scavenger receptor class A, member 5	1.31	0.0243	0.441
LPIN3	lipin 3	1.31	0.0136	0.436
CLK1	CDC-like kinase 1	1.31	0.0310	0.456
Downregulated				
CSPG4	chondroitin sulfate proteoglycan 4	-1.31	0.0278	0.448
RPL12	ribosomal protein L12	-1.31	0.0101	0.423
ICMT	isoprenylcysteine carboxyl methyltransferase	-1.31	0.0051	0.430
RCC2	regulator of chromosome condensation 2	-1.31	0.0164	0.435
SFXN4	sideroflexin 4	-1.31	0.0146	0.430
LOC100737729	polyribonucleotide nucleotidyltransferase 1, mitochondrial-like	-1.31	0.0459	0.479
PERP	PERP, TP53 apoptosis effector	-1.31	0.0262	0.447
FAM20B	family with sequence similarity 20, member B	-1.31	0.0151	0.430
ORMDL1	ORMDL sphingolipid biosynthesis regulator 1	-1.31	0.0391	0.469
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	-1.31	0.0014	0.470
MRPL10	mitochondrial ribosomal protein L10	-1.31	0.0070	0.420
LOC100623012	cofilin-1 pseudogene	-1.31	0.0396	0.469
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	-1.31	0.0338	0.461
LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	-1.31	0.0170	0.432
RPS6KL1	ribosomal protein S6 kinase-like 1	-1.31	0.0329	0.459
PGAM1	phosphoglycerate mutase 1 (brain)	-1.31	0.0466	0.480
VMP1	vacuole membrane protein 1	-1.31	0.0205	0.434
MCU	mitochondrial calcium uniporter	-1.31	0.0226	0.437
USP10	ubiquitin specific peptidase 10	-1.31	0.0227	0.435
URM1	// ubiquitin related modifier 1 // ubiquitin related modifier 1	-1.31	0.0272	0.448
URM1				
ANAPC5	anaphase promoting complex subunit 5	-1.31	0.0489	0.481
GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	-1.31	0.0115	0.430
MRPS14	mitochondrial ribosomal protein S14	-1.31	0.0137	0.433
RAD51C	RAD51 paralog C	-1.31	0.0384	0.466
DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	-1.31	0.0075	0.418
SSB	Sjogren syndrome antigen B (autoantigen La)	-1.31	0.0096	0.421
COPS7A	COP9 signalosome subunit 7A	-1.31	0.0318	0.459
RPL31	ribosomal protein L31	-1.31	0.0019	0.456
PRNP	prion protein	-1.32	0.0393	0.470
UBA2	ubiquitin-like modifier activating enzyme 2	-1.32	0.0201	0.431
MRPL21	mitochondrial ribosomal protein L21	-1.32	0.0042	0.440
PTBP1	polypyrimidine tract binding protein 1	-1.32	0.0115	0.430
MRPL11	mitochondrial ribosomal protein L11	-1.32	0.0353	0.462
CRYM	crystallin, mu	-1.32	0.0261	0.447
RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	-1.32	0.0494	0.482
MLST8	MTOR associated protein, LST8 homolog	-1.32	0.0391	0.469
HSPA9	heat shock 70kDa protein 9 (mortalin)	-1.32	0.0041	0.444
G3BP1	GTPase activating protein (SH3 domain) binding protein 1	-1.32	0.0032	0.435
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	-1.32	0.0016	0.457
METAP1	methionyl aminopeptidase 1	-1.32	0.0091	0.425
TAGLN2	transgelin 2	-1.32	0.0442	0.478
HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-1.32	0.0039	0.437
EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	-1.32	0.0168	0.436
CCNC	cyclin C	-1.32	0.0067	0.422

ZBTB10	zinc finger and BTB domain containing 10	-1.32	0.0327	0.459
ZNF280B	zinc finger protein 280B	-1.32	0.0196	0.429
LOC100525232	cytochrome c oxidase assembly protein COX16 homolog, mitochondrial	-1.32	0.0094	0.422
LOC100520848	prickle-like protein 4	-1.33	0.0036	0.443
LOC100738600	prickle-like protein 4	-1.33	0.0036	0.445
ADSL	adenylosuccinate lyase	-1.33	0.0259	0.447
MYBBP1A	MYB binding protein (P160) 1a	-1.33	0.0475	0.480
LOC100739335	ruvB-like 1	-1.33	0.0051	0.437
THOP1	thimet oligopeptidase 1	-1.33	0.0031	0.429
E2F4	E2F transcription factor 4, p107/p130-binding	-1.33	0.0316	0.459
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	-1.33	0.0115	0.430
CDK20	cyclin-dependent kinase 20	-1.33	0.0139	0.432
GSTA4	glutathione S-transferase alpha 4	-1.33	0.0411	0.472
BPNT1	3(2), 5-bisphosphate nucleotidase 1	-1.33	0.0012	0.462
RRP12	ribosomal RNA processing 12 homolog	-1.33	0.0323	0.458
CPLX3	complexin 3	-1.33	0.0107	0.428
SLC9B1	solute carrier family 9, subfamily B (NHA1, cation proton antiporter 1), member 1	-1.33	0.0378	0.467
MRS2	MRS2 magnesium transporter	-1.33	0.0472	0.479
PN01	partner of NOB1 homolog	-1.33	0.0082	0.418
ETF1	eukaryotic translation termination factor 1	-1.33	0.0068	0.423
QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	-1.33	0.0043	0.446
POLE3	polymerase (DNA directed), epsilon 3, accessory subunit	-1.33	0.0154	0.431
LARS	leucyl-tRNA synthetase	-1.33	0.0422	0.476
CEP78	centrosomal protein 78kDa	-1.34	0.0223	0.437
MRPS35	mitochondrial ribosomal protein S35	-1.34	0.0019	0.454
C4H8orf59	chromosome 4 open reading frame, human C8orf59	-1.34	0.0103	0.422
PRRC2A	proline-rich coiled-coil 2A	-1.34	0.0063	0.425
TMEM33	transmembrane protein 33	-1.34	0.0116	0.425
SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	-1.34	0.0179	0.429
HSF2	heat shock transcription factor 2	-1.34	0.0116	0.424
TXNDC9	thioredoxin domain containing 9	-1.34	0.0053	0.429
MMGT1	membrane magnesium transporter 1	-1.34	0.0107	0.428
YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	-1.34	0.0333	0.459
EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	-1.34	0.0152	0.431
EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	-1.34	0.0152	0.431
CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	-1.34	0.0024	0.447
DDX21	DEAD (Asp-Glu-Ala-Asp) box helicase 21	-1.34	0.0217	0.436
RPUSD3	RNA pseudouridylate synthase domain containing 3	-1.34	0.0289	0.454
EXOSC2	exosome component 2	-1.34	0.0002	0.737
TRMT5	tRNA methyltransferase 5	-1.34	0.0092	0.425
LOC100738939	nuclear envelope integral membrane protein 1	-1.34	0.0466	0.479
LOC100738939	nuclear envelope integral membrane protein 1	-1.34	0.0466	0.480
MITD1	MIT, microtubule interacting and transport, domain containing 1	-1.34	0.0059	0.423
PTCD3	pentatricopeptide repeat domain 3	-1.34	0.0013	0.469
IL27RA	interleukin 27 receptor, alpha	-1.34	0.0311	0.457
ERH	enhancer of rudimentary homolog (Drosophila)	-1.34	0.0282	0.449
LOC102161054	olfactory receptor 7G3-like	-1.34	0.0080	0.419
COPS3	COP9 signalosome subunit 3	-1.34	0.0127	0.431
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	-1.34	0.0428	0.476
LOC100525076	solute carrier family 35 member B1	-1.34	0.0476	0.480
PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	-1.34	0.0077	0.421
MRI1	methylthioribose-1-phosphate isomerase 1	-1.35	0.0138	0.430
YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	-1.35	0.0433	0.476

KCNH6	potassium channel, voltage gated eag related subfamily H, member 6	-1.35	0.0012	0.455
METTL16	methyltransferase like 16	-1.35	0.0075	0.419
SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	-1.35	0.0011	0.490
ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.35	0.0239	0.439
DTD2	D-tyrosyl-tRNA deacylase 2 (putative)	-1.35	0.0205	0.433
CCNJ	cyclin J	-1.35	0.0013	0.473
BID	BH3 interacting domain death agonist	-1.35	0.0040	0.439
HSPA14	heat shock 70kDa protein 14	-1.35	0.0075	0.418
MAGED1	melanoma antigen family D, 1	-1.35	0.0350	0.462
FAM167B	family with sequence similarity 167, member B	-1.35	0.0454	0.478
MAMLD1	mastermind-like domain containing 1	-1.35	0.0486	0.481
CCNYL1	cyclin Y-like 1	-1.36	0.0089	0.428
IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-1.36	0.0382	0.466
TRMT2A	tRNA methyltransferase 2 homolog A (S. cerevisiae)	-1.36	0.0169	0.434
MMP7	matrix metalloproteinase 7	-1.36	0.0270	0.449
ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.36	0.0139	0.431
NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	-1.36	0.0294	0.455
EXOSC4	exosome component 4	-1.36	0.0124	0.429
TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	-1.36	0.0055	0.429
YBX3	Y box binding protein 3	-1.36	0.0399	0.469
LOC102161719	uncharacterized LOC102161719	-1.36	0.0057	0.421
SMIM11A	small integral membrane protein 11A	-1.36	0.0096	0.421
DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	-1.37	0.0056	0.424
TKFC	triokinase/FMN cyclase	-1.37	0.0331	0.459
GEMIN6	gem (nuclear organelle) associated protein 6	-1.37	0.0093	0.424
HAUS6	HAUS augmin-like complex, subunit 6	-1.37	0.0193	0.428
NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	-1.37	0.0215	0.436
LOC100738751	F-box only protein 6-like	-1.37	0.0066	0.426
PRPS1	phosphoribosyl pyrophosphate synthetase 1	-1.37	0.0235	0.437
MRPL53	mitochondrial ribosomal protein L53	-1.37	0.0170	0.433
UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	-1.37	0.0095	0.422
GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	-1.37	0.0109	0.429
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1	-1.37	0.0078	0.417
PSME3	proteasome activator subunit 3	-1.37	0.0019	0.453
LOC100739849	28S ribosomal protein S16, mitochondrial	-1.37	0.0047	0.434
NAA20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	-1.37	0.0070	0.416
EIF4A1	eukaryotic translation initiation factor 4A1	-1.38	0.0104	0.422
LOC100737594	exportin-5-like	-1.38	0.0186	0.430
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	-1.38	0.0157	0.432
GALT	galactose-1-phosphate uridylyltransferase	-1.38	0.0437	0.477
SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	-1.38	0.0476	0.480
LOC100152843	forkhead box protein Q1	-1.38	0.0006	0.594
SUZ12	SUZ12 polycomb repressive complex 2 subunit	-1.38	0.0101	0.423
DAP	death-associated protein	-1.38	0.0176	0.429
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-1.38	0.0004	0.579
CCT2	chaperonin containing TCP1, subunit 2 (beta)	-1.38	0.0025	0.451
PDCD11	programmed cell death 11	-1.38	0.0119	0.429
LOC100524598	cytochrome c-type heme lyase	-1.38	0.0409	0.472
LOC100155823	olfactory receptor 4F3/4F16/4F29-like	-1.38	0.0403	0.470
NUTF2	nuclear transport factor 2	-1.38	0.0121	0.429
PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	-1.38	0.0208	0.433
CDK2	cyclin-dependent kinase 2	-1.38	0.0076	0.419

SCAMP5	secretory carrier membrane protein 5	-1.39	0.0078	0.417
SRSF7	serine/arginine-rich splicing factor 7	-1.39	0.0154	0.431
LOC100157467	DNA polymerase alpha catalytic subunit	-1.39	0.0415	0.474
CFL2	cofilin 2 (muscle)	-1.39	0.0035	0.440
MAGOH	mago homolog, exon junction complex core component	-1.39	0.0055	0.430
MRPL13	mitochondrial ribosomal protein L13	-1.39	0.0041	0.444
NUP160	nucleoporin 160kDa	-1.39	0.0051	0.428
FHL3	four and a half LIM domains 3	-1.39	0.0005	0.582
CCT7	chaperonin containing TCP1, subunit 7 (eta)	-1.39	0.0195	0.429
CCDC91	coiled-coil domain containing 91	-1.39	0.0307	0.456
FAM98A	family with sequence similarity 98, member A	-1.39	0.0354	0.462
TMEM167A	transmembrane protein 167A	-1.39	0.0194	0.427
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	-1.39	0.0237	0.438
DOCK5	dedicator of cytokinesis 5	-1.39	0.0378	0.467
IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	-1.39	0.0081	0.418
INTS7	integrator complex subunit 7	-1.39	0.0169	0.435
LOC100737174	nucleolin-like	-1.39	0.0046	0.433
LOC100155138	tubulin alpha-3 chain	-1.40	0.0101	0.422
LOC100739768	beta-parvin	-1.40	0.0275	0.448
PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	-1.40	0.0320	0.459
PPID	peptidylprolyl isomerase D	-1.40	0.0459	0.479
NANP	N-acetylneuraminic acid phosphatase	-1.40	0.0250	0.441
LOC100737210	nucleolin	-1.40	0.0096	0.421
LOC102167832	uncharacterized LOC102167832	-1.40	0.0060	0.423
KPNB1	karyopherin (importin) beta 1	-1.40	0.0212	0.435
RAB23	RAB23, member RAS oncogene family	-1.40	0.0220	0.437
PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	-1.40	0.0297	0.456
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-1.40	0.0218	0.436
PRELID3B	PRELI domain containing 3B	-1.40	0.0051	0.434
NOP56	NOP56 ribonucleoprotein	-1.40	0.0069	0.422
LOC102163346	malate dehydrogenase, cytoplasmic	-1.40	0.0224	0.436
DCLRE1B	DNA cross-link repair 1B	-1.40	0.0189	0.431
AAAS	achalasia, adrenocortical insufficiency, alacrimia	-1.40	0.0162	0.437
SRPK1	SRSF protein kinase 1	-1.40	0.0002	0.757
APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	-1.40	0.0265	0.446
POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	-1.41	0.0176	0.429
LSM3	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated	-1.41	0.0105	0.422
MRPS30	mitochondrial ribosomal protein S30	-1.41	0.0183	0.428
LOC100523894	DNA-directed RNA polymerase III subunit RPC5	-1.41	0.0068	0.422
TWF1	twinfilin actin binding protein 1	-1.41	0.0182	0.429
CWC15	CWC15 spliceosome-associated protein	-1.41	0.0060	0.423
PHF6	PHD finger protein 6	-1.41	0.0090	0.424
TIMM8A	translocase of inner mitochondrial membrane 8 homolog A (yeast)	-1.41	0.0285	0.451
SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-1.41	0.0312	0.457
ILF2	interleukin enhancer binding factor 2	-1.42	0.0074	0.418
NOLC1	nucleolar and coiled-body phosphoprotein 1	-1.42	0.0053	0.430
ARF6	ADP-ribosylation factor 6	-1.42	0.0070	0.417
LOC100519524	origin recognition complex subunit 3	-1.42	0.0422	0.476
TRIM37	tripartite motif containing 37	-1.42	0.0014	0.462
CEP57L1	centrosomal protein 57kDa-like 1	-1.42	0.0004	0.586
PGC	progastricsin (pepsinogen C)	-1.42	0.0403	0.470
LOC100519729	tax1-binding protein 3-like	-1.43	0.0070	0.419
ZDHHC21	zinc finger, DHHC-type containing 21	-1.43	0.0327	0.459
AATF	apoptosis antagonizing transcription factor	-1.43	0.0305	0.456
UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	-1.43	0.0257	0.447

AVEN	apoptosis, caspase activation inhibitor	-1.43	0.0383	0.466
HSPD1	heat shock 60kDa protein 1 (chaperonin)	-1.43	0.0055	0.431
FRRS1	ferric-chelate reductase 1	-1.43	0.0441	0.478
PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	-1.43	0.0434	0.475
CASP2	caspase 2, apoptosis-related cysteine peptidase	-1.43	0.0131	0.433
ABHD6	abhydrolase domain containing 6	-1.43	0.0446	0.478
LOC100517015	cAMP-dependent protein kinase inhibitor beta-like	-1.43	0.0187	0.430
TUBA8	tubulin, alpha 8	-1.43	0.0224	0.436
PAK1IP1	PAK1 interacting protein 1	-1.43	0.0239	0.440
SMIM8	small integral membrane protein 8	-1.44	0.0038	0.437
WDR77	WD repeat domain 77	-1.44	0.0202	0.432
HSPA8	heat shock 70kDa protein 8	-1.44	0.0389	0.468
BIVM // BIVM	basic, immunoglobulin-like variable motif containing // basic, immunoglobulin-like variable motif containing	-1.44	0.0200	0.430
FASTKD2	FAST kinase domains 2	-1.44	0.0142	0.431
POLD3	polymerase (DNA-directed), delta 3, accessory subunit	-1.44	0.0141	0.430
RBPMS2	RNA binding protein with multiple splicing 2	-1.44	0.0299	0.456
MRE11A	MRE11 homolog A, double strand break repair nuclease	-1.44	0.0176	0.429
FARSA	phenylalanyl-tRNA synthetase, alpha subunit	-1.44	0.0359	0.464
CCT4	chaperonin containing TCP1, subunit 4 (delta)	-1.44	0.0224	0.436
NAP1L4	nucleosome assembly protein 1-like 4	-1.44	0.0057	0.421
FKBP3	FK506 binding protein 3, 25kDa	-1.44	0.0295	0.455
SGMS2	sphingomyelin synthase 2	-1.44	0.0215	0.435
DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	-1.44	0.0340	0.463
DYNLL1	dynein, light chain, LC8-type 1	-1.45	0.0166	0.436
KRT8	keratin 8, type II	-1.45	0.0429	0.476
MIF	macrophage migration inhibitory factor (glycosylation- inhibiting factor)	-1.45	0.0118	0.426
RAD54L	RAD54-like (S. cerevisiae)	-1.45	0.0377	0.466
PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y	-1.45	0.0160	0.434
HVCN1	hydrogen voltage gated channel 1	-1.45	0.0299	0.456
ATP5G1	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)	-1.45	0.0331	0.459
CCDC34	coiled-coil domain containing 34	-1.45	0.0305	0.456
TIMELESS	timeless circadian clock	-1.45	0.0397	0.469
ERI2	ERI1 exoribonuclease family member 2	-1.45	0.0247	0.441
EIF4A3	eukaryotic translation initiation factor 4A3	-1.46	0.0026	0.434
UMPS	uridine monophosphate synthetase	-1.46	0.0063	0.427
SMN1	survival of motor neuron 1, telomeric	-1.46	0.0099	0.421
LOC100153768	acidic leucine-rich nuclear phosphoprotein 32 family member E	-1.46	0.0396	0.469
LOC100515066	U6 snRNA-associated Sm-like protein LSm8	-1.46	0.0038	0.441
LOC100515066	U6 snRNA-associated Sm-like protein LSm8	-1.46	0.0038	0.443
LRRC40	leucine rich repeat containing 40	-1.47	0.0120	0.429
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-1.47	0.0102	0.423
CACYBP	calcyclin binding protein	-1.47	0.0063	0.426
RAN	RAN, member RAS oncogene family	-1.47	0.0165	0.434
DPCD	deleted in primary ciliary dyskinesia homolog (mouse)	-1.47	0.0004	0.597
DENR	density-regulated protein	-1.47	0.0127	0.432
DKC1	dyskeratosis congenita 1, dyskerin	-1.47	0.0065	0.430
ATF3	activating transcription factor 3	-1.48	0.0129	0.435
TIMM9	translocase of inner mitochondrial membrane 9 homolog (yeast)	-1.48	0.0060	0.424
LTA4H	leukotriene A4 hydrolase	-1.49	0.0002	0.865
TTC27	tetratricopeptide repeat domain 27	-1.49	0.0086	0.421
PDCD5	programmed cell death 5	-1.49	0.0145	0.430
CCT3	chaperonin containing TCP1, subunit 3 (gamma)	-1.49	0.0026	0.428
NUP155	nucleoporin 155kDa	-1.50	0.0082	0.416
CHORDC1	cysteine and histidine-rich domain (CHORD) containing 1	-1.50	0.0078	0.417
TAMM41	TAM41, mitochondrial translocator assembly and maintenance protein, homolog (S. cerevisiae)	-1.50	0.0347	0.465

RPF2	ribosome production factor 2 homolog	-1.50	0.0099	0.421
POLA2	polymerase (DNA directed), alpha 2, accessory subunit	-1.50	0.0365	0.466
PSMA5	proteasome subunit alpha 5	-1.50	0.0046	0.433
VDAC2	voltage-dependent anion channel 2	-1.50	0.0092	0.425
LOC100157391	mitochondrial import inner membrane translocase subunit Tim23	-1.50	0.0058	0.422
FAM136A	family with sequence similarity 136, member A	-1.50	0.0071	0.416
HSPA4	heat shock 70kDa protein 4	-1.51	0.0032	0.436
CENPV	centromere protein V	-1.51	0.0000	1.203
ACOT4	acyl-CoA thioesterase 4	-1.51	0.0374	0.466
NUP43	nucleoporin 43kDa	-1.51	0.0044	0.438
LOC100519773	proliferation-associated protein 2G4	-1.51	0.0052	0.428
TUBG1	tubulin, gamma 1	-1.51	0.0037	0.442
PLN	phospholamban	-1.52	0.0086	0.421
HIGD1A	HIG1 hypoxia inducible domain family, member 1A	-1.52	0.0159	0.434
SRSF3	serine/arginine-rich splicing factor 3	-1.52	0.0073	0.419
LOC102158249	uncharacterized protein KIAA1841	-1.52	0.0018	0.455
PRMT1	protein arginine methyltransferase 1	-1.52	0.0140	0.432
CDK2AP1	cyclin-dependent kinase 2 associated protein 1	-1.52	0.0051	0.436
NAT10	N-acetyltransferase 10 (GCN5-related)	-1.53	0.0100	0.420
POLD1	polymerase (DNA directed), delta 1, catalytic subunit	-1.53	0.0366	0.465
LOC100626307	DNA primase large subunit-like	-1.53	0.0347	0.465
EIF4E	eukaryotic translation initiation factor 4E	-1.53	0.0080	0.419
MRT04	MRT4 homolog, ribosome maturation factor	-1.53	0.0202	0.431
NPM3	nucleophosmin/nucleoplasmin 3	-1.53	0.0060	0.426
SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	-1.54	0.0099	0.423
NIP7	NIP7, nucleolar pre-rRNA processing protein	-1.54	0.0051	0.439
OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	-1.54	0.0046	0.433
IMPDH2	IMP (inosine 5-monophosphate) dehydrogenase 2	-1.54	0.0043	0.444
NACC1	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	-1.55	0.0168	0.435
PUS7	pseudouridylate synthase 7 (putative)	-1.55	0.0171	0.431
LOC100516390	ankyrin repeat domain-containing protein 26	-1.55	0.0150	0.429
HN1L	hematological and neurological expressed 1-like	-1.55	0.0216	0.436
LOC100739488	exportin-1-like	-1.55	0.0186	0.430
LOC100514269	phosphatidylinositol 4-phosphate 5-kinase type-1 alpha-like	-1.56	0.0284	0.452
PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	-1.56	0.0328	0.459
SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	-1.56	0.0184	0.429
FKBP4	FK506 binding protein 4, 59kDa	-1.56	0.0050	0.440
CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	-1.56	0.0205	0.433
LOC100523881	focadhesin-like	-1.56	0.0347	0.464
SLC35B4	solute carrier family 35 (UDP-xylose/UDP-N-acetylglucosamine transporter), member B4	-1.56	0.0031	0.431
PSRC1	proline/serine-rich coiled-coil 1	-1.57	0.0159	0.434
PREP	prolyl endopeptidase	-1.57	0.0016	0.463
TEX12	testis expressed 12	-1.57	0.0367	0.465
LOC100523980	zinc finger protein 827	-1.57	0.0051	0.438
SNRPG	small nuclear ribonucleoprotein polypeptide G	-1.57	0.0137	0.436
TCP1	t-complex 1	-1.57	0.0030	0.432
LOC100626654	dipeptidyl peptidase 3	-1.58	0.0172	0.429
ARPC5L	actin related protein 2/3 complex, subunit 5-like	-1.58	0.0137	0.434
APOO	apolipoprotein O	-1.58	0.0116	0.426
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	-1.58	0.0090	0.425
JUN	jun proto-oncogene	-1.58	0.0248	0.441
FANCM	Fanconi anemia, complementation group M	-1.59	0.0111	0.429
HAUS1	HAUS augmin-like complex, subunit 1	-1.59	0.0457	0.479
HINT3	histidine triad nucleotide binding protein 3	-1.59	0.0025	0.437
TUBA4A	tubulin, alpha 4a	-1.59	0.0009	0.564
MRPS28	mitochondrial ribosomal protein S28	-1.59	0.0109	0.431

XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	-1.59	0.0443	0.478
LOC102161664	uncharacterized LOC102161664	-1.60	0.0038	0.439
DPH3	diphthamide biosynthesis 3	-1.60	0.0056	0.424
LOC100517579	olfactory receptor 4C46-like	-1.60	0.0111	0.429
CTPS1	CTP synthase 1	-1.60	0.0086	0.421
NAA40	N(alpha)-acetyltransferase 40, NatD catalytic subunit	-1.61	0.0080	0.420
GAR1	GAR1 homolog, ribonucleoprotein	-1.61	0.0155	0.430
PTPMT1	protein tyrosine phosphatase, mitochondrial 1	-1.61	0.0444	0.478
LOC106508523	breast cancer type 2 susceptibility protein-like	-1.62	0.0301	0.455
RFK	riboflavin kinase	-1.62	0.0012	0.471
LOC100738016	MKI67 FHA domain-interacting nucleolar phosphoprotein-like	-1.62	0.0068	0.422
CENPK	centromere protein K	-1.63	0.0441	0.478
RTN4IP1	reticulon 4 interacting protein 1	-1.63	0.0004	0.600
TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.63	0.0065	0.435
PSMC3IP	PSMC3 interacting protein	-1.64	0.0174	0.429
ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	-1.64	0.0120	0.430
NOP14	NOP14 nucleolar protein	-1.65	0.0045	0.436
NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	-1.65	0.0450	0.478
DSCC1	DNA replication and sister chromatid cohesion 1	-1.67	0.0295	0.455
TUBA1B	tubulin, alpha 1b	-1.68	0.0228	0.435
SNRPA1	small nuclear ribonucleoprotein polypeptide A	-1.68	0.0011	0.497
SNRPA	small nuclear ribonucleoprotein polypeptide A	-1.68	0.0086	0.421
UBE2N	ubiquitin-conjugating enzyme E2N	-1.68	0.0070	0.421
TUBB	tubulin, beta class I	-1.69	0.0167	0.437
KRT18	keratin 18, type I	-1.69	0.0195	0.429
GFM2	G elongation factor, mitochondrial 2	-1.70	0.0014	0.447
HELLS	helicase, lymphoid-specific	-1.72	0.0170	0.432
HSPH1	heat shock 105kDa/110kDa protein 1	-1.72	0.0449	0.478
RAB34	RAB34, member RAS oncogene family	-1.72	0.0125	0.429
LOC100622080	decaprenyl-diphosphate synthase subunit 1-like	-1.73	0.0050	0.440
CCNE1	cyclin E1	-1.73	0.0267	0.448
AMD1	adenosylmethionine decarboxylase 1	-1.74	0.0164	0.435
C14H1orf131	chromosome 14 open reading frame, human C1orf131	-1.75	0.0037	0.439
RFC4	replication factor C (activator 1) 4, 37kDa	-1.75	0.0222	0.436
HSPA4L	heat shock 70kDa protein 4-like	-1.76	0.0234	0.438
LOC100526069	testis-expressed sequence 30 protein	-1.76	0.0052	0.427
RAD51	RAD51 recombinase	-1.77	0.0412	0.473
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	-1.77	0.0025	0.441
CDO1	cysteine dioxygenase type 1	-1.77	0.0441	0.478
SNRPF	small nuclear ribonucleoprotein polypeptide F	-1.79	0.0130	0.432
MCM4	minichromosome maintenance complex component 4	-1.79	0.0412	0.472
FAM169A	family with sequence similarity 169, member A	-1.80	0.0086	0.422
LOC100624445	gamma-glutamylcyclotransferase-like	-1.80	0.0222	0.437
LOC100737936	dynammin-1-like protein	-1.80	0.0017	0.459
LRRCS9	leucine rich repeat containing 59	-1.81	0.0461	0.479
CHAF1B	chromatin assembly factor 1, subunit B (p60)	-1.81	0.0226	0.437
DDIAS	DNA damage-induced apoptosis suppressor	-1.81	0.0298	0.456
TIPIN	TIMELESS interacting protein	-1.82	0.0155	0.430
SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	-1.82	0.0320	0.459
LOC100621671	ectonucleotide pyrophosphatase/phosphodiesterase family member 3	-1.85	0.0180	0.429
LOC100153906	DNA replication ATP-dependent helicase/nuclease DNA2	-1.86	0.0312	0.457
LOC100738210	bis(5-adenosyl)-triphosphatase ENPP4	-1.86	0.0140	0.432
CCL2	chemokine (C-C motif) ligand 2	-1.91	0.0277	0.448
SLC16A6	solute carrier family 16, member 6	-1.91	0.0006	0.630
CYCS	cytochrome c, somatic	-1.92	0.0005	0.577

LOC100154105	kelch repeat and BTB domain-containing protein 6	-1.94	0.0103	0.423
BFSP1	beaded filament structural protein 1, filensin	-1.95	0.0467	0.479
LYAR	Ly1 antibody reactive	-1.95	0.0245	0.441
LOC102163415	T-complex protein 1 subunit zeta	-1.96	0.0082	0.418
SLC51A	solute carrier family 51, alpha subunit	-1.96	0.0476	0.480
RANBP1	RAN binding protein 1	-1.97	0.0054	0.431
ATP6V0D2	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d2	-2.00	0.0198	0.429
NDUFAF4	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4	-2.00	0.0026	0.429
SKA1	spindle and kinetochore associated complex subunit 1	-2.00	0.0331	0.459
MUC13	mucin 13, cell surface associated	-2.02	0.0180	0.429
DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	-2.06	0.0200	0.429
TUBA1C	tubulin, alpha 1c	-2.06	0.0065	0.432
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	-2.08	0.0061	0.424
OSGIN2	oxidative stress induced growth inhibitor family member 2	-2.09	0.0171	0.431
ARL2BP	ADP-ribosylation factor-like 2 binding protein	-2.14	0.0010	0.555
STEAP2	STEAP family member 2, metalloreductase	-2.16	0.0461	0.479
LOC100623233	PCNA-associated factor	-2.24	0.0447	0.478
SLC51B	solute carrier family 51, beta subunit	-2.28	0.0123	0.430
GINS1	GINS complex subunit 1 (Psf1 homolog)	-2.38	0.0260	0.447
WBP5	WW domain binding protein 5	-2.44	0.0376	0.466
UQCR10	ubiquinol-cytochrome c reductase complex 7.2 kDa protein	-3.02	0.0216	0.436
LOC100511841	UDP-glucuronosyltransferase 1-10	-3.38	0.0093	0.424

*Filter criteria: FC > 1.3 and < -1.3 and $P < 0.05$ between SINS high vs. SINS low. FCs were calculated from the signal log ratios, which were calculated from n = 6 microarrays per group.

Table S3 Plasma concentrations of amino acids in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
Alanine	466.2 $\pm$ 157.3	494.7 $\pm$ 108.5
Arginine	152.7 $\pm$ 22.84	144.1 $\pm$ 53.56
Asparagine	44.1 $\pm$ 30.2	58.4 $\pm$ 24.0
Aspartate	13.0 $\pm$ 3.59	11.6 $\pm$ 1.42
Citrulline	59.5 $\pm$ 12.3	69.8 $\pm$ 28.8
Glutamine	520.8 $\pm$ 139.7	428.8 $\pm$ 76.27
Glutamate	106.8 $\pm$ 27.57	86.0 $\pm$ 43.2
Glycine	875.5 $\pm$ 268.6	1037.3 $\pm$ 233.5
Histidine	98.2 $\pm$ 19.6	106.1 $\pm$ 40.74
Isoleucine	130.3 $\pm$ 18.16	120.9 $\pm$ 48.97
Leucine	233.5 $\pm$ 90.52	202.2 $\pm$ 61.42
Lysine	166.0 $\pm$ 30.96	154.7 $\pm$ 33.72
Methionine	37.2 $\pm$ 5.62	39.3 $\pm$ 17.4
Ornithine	63.1 $\pm$ 16.0	78.6 $\pm$ 11.7 [#]
Phenylalanine	81.4 $\pm$ 23.4	100.4 $\pm$ 33.2
Proline	461.5 $\pm$ 141.9	490.7 $\pm$ 130.2
Serine	160.8 $\pm$ 68.6	230.1 $\pm$ 118.5
Threonine	168.5 $\pm$ 49.0	165.8 $\pm$ 66.8
Tryptophan	66.5 $\pm$ 13.9	48.6 $\pm$ 20.6
Tyrosine	109.1 $\pm$ 53.4	140.5 $\pm$ 78.6
Valine	356.2 $\pm$ 103.1	324.3 $\pm$ 74.9

Data are means $\pm$ SD for n = 6 piglets/group. * P < 0.05; [#] P < 0.1

Table S4 Plasma concentrations of biogenic amines and other amino acid metabolites in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
Asymmetric dimethylarginine	1.07 ± 0.33	1.12 ± 0.21
Alpha-aminoadipic acid	12.8 ± 6.81	11.9 ± 9.78
Carnosine	12.7 ± 3.11	$16.7 \pm 3.96^{\#}$
Creatinine	114.1 ± 46.5	93.6 ± 59.3
Histamine	0.34 ± 0.30	0.50 ± 0.46
Kynurenine	1.28 ± 1.56	1.21 ± 1.25
Methionine-sulfoxide	2.49 ± 0.66	$3.60 \pm 0.96^*$
Putrescine	0.46 ± 0.17	1.01 ± 0.81
Sarcosine	2.16 ± 0.53	3.04 ± 1.40
Symmetric dimethylarginine	0.50 ± 0.28	0.96 ± 0.62
Serotonin	0.10 ± 0.05	0.14 ± 0.10
Spermidine	0.21 ± 0.01	0.24 ± 0.05
Spermine	0.16 ± 0.01	0.17 ± 0.03
trans-4-hydroxyproline	39.4 ± 16.5	63.8 ± 32.7
Taurine	62.4 ± 18.2	$91.8 \pm 31.4^{\#}$

Data are means $\pm$ SD for n = 6 piglets/group. $^*P < 0.05$; $^{\#}P < 0.1$

Table S5 Plasma concentrations of carnitine and acylcarnitines in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
Carnitine (free), C0	17.12 ± 3.55	15.40 ± 5.35
Acetylcarnitine, C1	1.79 ± 0.79	2.77 ± 2.13
Propionylcarnitine, C3	0.21 ± 0.15	0.18 ± 0.05
Hydroxybutyrylcarnitine, C4-OH	0.10 ± 0.02	0.09 ± 0.01
Butyrylcarnitine, C4	0.091 ± 0.057	0.093 ± 0.046
Tetradecenoylcarnitine, 14:1	0.034 ± 0.018	0.050 ± 0.034

Data are means $\pm$ SD for n = 6 piglets/group.

Table S6 Plasma concentrations of lysophosphatidylcholine (LPC) species in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
lysoPC a C16:0	33.93 ± 11.09	29.88 ± 6.54
lysoPC a C16:1	1.41 ± 0.25	1.87 ± 0.67
lysoPC a C17:0	1.11 ± 0.60	0.91 ± 0.45
lysoPC a C18:0	22.33 ± 8.22	20.25 ± 3.70
lysoPC a C18:1	17.27 ± 3.65	21.57 ± 9.29
lysoPC a C18:2	18.42 ± 4.85	19.42 ± 9.53
lysoPC a C20:3	1.33 ± 0.39	1.63 ± 0.53
lysoPC a C20:4	4.61 ± 1.05	5.59 ± 1.59
lysoPC a C26:0	0.082 ± 0.028	0.081 ± 0.031
lysoPC a C26:1	0.058 ± 0.027	0.061 ± 0.017
lysoPC a C28:1	0.149 ± 0.057	0.145 ± 0.057

Data are means $\pm$ SD for n = 6 piglets/group.

Table S7 Plasma concentrations of sphingomyelin (SM) and hydroxy sphingomyelin (SM (OH)) species in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
SM C16:0	39.95 ± 6.17	40.73 ± 1.25
SM C16:1	7.03 ± 2.24	6.64 ± 0.54
SM C18:0	13.08 ± 3.04	14.20 ± 1.93
SM C18:1	3.79 ± 0.96	4.16 ± 0.83
SM C20:2	0.52 ± 0.11	0.65 ± 0.19
SM C22:3	2.95 ± 0.83	3.85 ± 0.91
SM C24:0	11.04 ± 3.79	9.38 ± 1.26
SM C24:1	12.29 ± 3.70	10.96 ± 1.70
SM C26:0	0.12 ± 0.05	0.10 ± 0.03
SM C26:1	0.34 ± 0.15	0.29 ± 0.03
SM (OH) C14:1	2.86 ± 0.52	3.63 ± 1.20
SM (OH) C16:1	3.02 ± 0.96	3.19 ± 0.67
SM (OH) C22:1	4.53 ± 2.08	2.92 ± 1.49
SM (OH) C22:2	2.11 ± 0.65	1.89 ± 0.43
SM (OH) C24:1	0.79 ± 0.21	0.87 ± 0.15

Data are means $\pm$ SD for n = 6 piglets/group. * $P < 0.05$; # $P < 0.1$

Table S8 Plasma concentrations of diacyl (aa) and acyl-alkyl (ae) phosphatidylcholine (PC) species in suckling piglets of the SINS high group and the SINS low group

	SINS low	SINS high
	$\mu\text{mol/L}$	
PC aa C28:1	0.87 ± 0.16	1.14 ± 0.38
PC aa C30:0	2.24 ± 0.50	3.06 ± 1.40
PC aa C30:2	0.44 ± 0.18	0.42 ± 0.09
PC aa C32:0	14.12 ± 11.01	27.46 ± 18.66
PC aa C32:1	7.01 ± 4.25	13.12 ± 7.57
PC aa C32:2	1.36 ± 0.33	2.09 ± 0.88
PC aa C32:3	0.25 ± 0.04	0.26 ± 0.06
PC aa C34:1	64.37 ± 10.08	80.98 ± 18.50
PC aa C34:2	71.90 ± 12.15	79.85 ± 13.43
PC aa C34:3	11.10 ± 2.92	13.94 ± 4.02
PC aa C34:4	0.63 ± 0.19	1.00 ± 0.39
PC aa C36:0	7.17 ± 2.92	11.09 ± 5.46
PC aa C36:1	46.53 ± 7.13	57.15 ± 12.90
PC aa C36:2	69.32 ± 12.33	89.10 ± 28.01
PC aa C36:3	38.57 ± 8.50	51.23 ± 15.46
PC aa C36:4	43.5 ± 7.01	$50.9 \pm 6.48^{\#}$
PC aa C36:5	16.81 ± 4.38	19.68 ± 4.44
PC aa C36:6	0.66 ± 0.19	$1.05 \pm 0.31^*$
PC aa C38:0	0.89 ± 0.32	1.38 ± 0.66
PC aa C38:1	1.28 ± 0.50	1.29 ± 0.19
PC aa C38:3	29.33 ± 7.87	32.85 ± 2.89
PC aa C38:4	51.45 ± 8.15	55.93 ± 3.00
PC aa C38:5	40.58 ± 7.75	43.90 ± 2.30
PC aa C38:6	29.3 ± 4.49	$36.3 \pm 6.57^{\#}$
PC aa C40:2	0.30 ± 0.11	0.37 ± 0.07
PC aa C40:3	0.37 ± 0.10	$0.66 \pm 0.24^*$
PC aa C40:4	7.36 ± 3.55	7.08 ± 3.78
PC aa C40:5	29.77 ± 11.80	26.08 ± 9.81
PC aa C40:6	31.82 ± 7.07	33.67 ± 2.91

PC aa C42:0	0.12 ± 0.04	0.14 ± 0.03
PC aa C42:1	0.14 ± 0.04	0.17 ± 0.05
PC aa C42:4	0.23 ± 0.09	0.30 ± 0.13
PC aa C42:5	0.42 ± 0.32	0.74 ± 0.50
PC aa C42:6	0.91 ± 0.22	1.26 ± 0.65
PC ae C30:0	0.32 ± 0.15	$0.62 \pm 0.37^{\#}$
PC ae C30:1	0.23 ± 0.07	$0.36 \pm 0.15^{\#}$
PC ae C32:1	1.71 ± 0.57	$2.90 \pm 1.46^{\#}$
PC ae C32:2	0.61 ± 0.42	1.06 ± 0.56
PC ae C34:0	1.28 ± 0.61	2.48 ± 1.63
PC ae C34:1	8.20 ± 2.27	$13.21 \pm 4.91^*$
PC ae C34:2	7.26 ± 1.54	8.38 ± 1.35
PC ae C34:3	3.28 ± 0.69	3.19 ± 0.54
PC ae C36:0	0.52 ± 0.13	$0.87 \pm 0.36^{\#}$
PC ae C36:1	8.66 ± 3.15	11.24 ± 3.26
PC ae C36:2	10.71 ± 3.25	13.92 ± 4.06
PC ae C36:3	4.17 ± 0.84	$5.80 \pm 1.67^{\#}$
PC ae C36:4	3.95 ± 0.59	$5.20 \pm 1.42^{\#}$
PC ae C36:5	2.87 ± 1.25	3.71 ± 1.67
PC ae C38:0	1.48 ± 0.38	$2.23 \pm 0.67^*$
PC ae C38:1	0.96 ± 0.41	1.23 ± 0.29
PC ae C38:2	2.08 ± 0.82	2.59 ± 0.79
PC ae C38:3	2.99 ± 1.21	3.80 ± 1.06
PC ae C38:4	6.78 ± 2.24	8.12 ± 2.54
PC ae C38:5	5.23 ± 1.09	$6.94 \pm 1.62^{\#}$
PC ae C38:6	2.14 ± 1.39	3.28 ± 1.97
PC ae C40:1	0.87 ± 0.31	$1.53 \pm 0.78^{\#}$
PC ae C40:2	0.77 ± 0.31	0.75 ± 0.14
PC ae C40:3	1.14 ± 0.74	1.11 ± 0.62
PC ae C40:4	1.81 ± 0.92	1.89 ± 0.85
PC ae C40:5	3.70 ± 1.63	3.61 ± 1.35
PC ae C40:6	3.03 ± 0.77	3.66 ± 0.69
PC ae C42:1	0.50 ± 0.15	0.62 ± 0.15
PC ae C42:2	0.49 ± 0.21	0.63 ± 0.11

PC ae C42:3	0.37 ± 0.10	0.66 ± 0.30*
PC ae C44:3	0.12 ± 0.04	0.13 ± 0.03
PC ae C44:5	0.25 ± 0.03	0.30 ± 0.08
PC ae C44:6	0.17 ± 0.04	0.15 ± 0.03
Sum PC aa	621.1 ± 98.6	745.7 ± 123.9 [#]
Sum PC ae	88.6 ± 20.2	116.1 ± 26.3 [#]
Sum PC aa+ae	709.7 ± 118.7	861.8 ± 147.0 [#]

Data are means ± SD for n = 6 piglets/group. * $P < 0.05$; [#] $P < 0.1$