Supplementary Table 2. The genes regulated by AICAR treatment in the rat liver

Gene Name*	Gene Symbol	Mean	Median	p-Value
unknown gene	NA	-3.423260827	-3.423260827	1.37E-05
aspartyl aminopeptidase	Dnpep	-2.767715661	-2.767715661	3.59E-05
RT1 class Ib gene, H2-TL-like, grc region (N1)	RT1-N1	-2.636064538	-2.636064538	3.11E-05
unknown gene	NA	-2.299878374	-2.299878374	0.000113324
hypothetical protein LOC680687	LOC680687	-2.209012228	-2.209012228	0.000531042
hepcidin antimicrobial peptide	Hamp	-2.166576105	-2.166576105	3.11E-05
development and differentiation enhancing (predicted)	Ddef1_predicted	-2.123611743	-2.123611743	1.64E-05
RT1 class I, CE12	RT1-CE12	-1.962518249	-1.962518249	0.000224923
alpha-2-macroglobulin	A2m	-1.885711115	-1.885711115	0.000143511
one cut domain, family member 1	Onecut1	-1.839204674	-1.839204674	4.74E-06
serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 7	Serpina7	-1.821761207	-1.821761207	5.69E-05
unknown gene	NA	-1.793545436	-1.793545436	4.11E-06
lysyl oxidase	Lox	-1.78884158	-1.78884158	6.49E-07
lysyl oxidase	Lox	-1.743733328	-1.743733328	8.28E-06
similar to F-box only protein 3 isoform 1	LOC690634	-1.672687692	-1.672687692	1.18E-06
unknown gene	NA	-1.66062916	-1.66062916	4.43E-05
unknown gene	NA	-1.637328556	-1.637328556	0.000138394
unknown gene	NA	-1.619044407	-1.619044407	0.000107615
phospholipase C, beta 1	Plcb1	-1.597244861	-1.597244861	3.66E-05
cytochrome P450, family 26, subfamily b, polypeptide 1	Cyp26b1	-1.594838205	-1.594838205	5.76E-06
unknown gene	NA	-1.587168937	-1.587168937	0.00107012
syncollin	Sycn	-1.538924155	-1.538924155	4.89E-05
similar to hypothetical protein MGC42105 (predicted)	RGD1308116_predicted	-1.464232165	-1.464232165	0.002742295
peroxisomal membrane protein 4	Pxmp4	-1.438923704	-1.438923704	0.001861313
RT1 class II, locus Bb	RT1-Bb	-1.427358385	-1.427358385	5.73E-05
Murinoglobulin 1 homolog (mouse)	Mug1	-1.395316999	-1.395316999	0.000421804
similar to liver-specific bHLH-Zip transcription factor	LOC685277	-1.38949769	-1.38949769	1.89E-06
epoxide hydrolase 2, cytoplasmic	Ephx2	-1.384129879	-1.384129879	8.38E-08
unknown gene	NA	-1.320458391	-1.320458391	7.36E-05
unknown gene	NA	-1.317246028	-1.317246028	0.001035939
N-acetyltransferase 8 (camello like)	Nat8	-1.313945283	-1.313945283	7.62E-05
similar to 20-alpha-hydroxysteroid dehydrogenase (predicted)	RGD1564865_predicted	-1.31122327	-1.31122327	2.99E-06
adenosine A2B receptor	Adora2b	-1.305311082	-1.305311082	1.55E-05
dual specificity phosphatase 6	Dusp6	-1.297883934	-1.297883934	4.68E-06
sulfotransferase family, cytosolic, 1C, member 2	Sult1c2	-1.282552237	-1.282552237	0.000147917
similar to immunoglobulin heavy chain 6 (Igh-6)	RGD1359202	-1.273304536	-1.273304536	0.000715208
carbonic anhydrase 1 (predicted)	Car1_predicted	-1.269758922	-1.269758922	3.39E-06
serine dehydratase	Sds	-1.255907209	-1.255907209	1.51E-05
unknown gene	NA	-1.249196843	-1.249196843	0.000881702
neuronal regeneration related protein	Nrep	-1.242300215	-1.242300215	1.56E-06
unknown gene	NA	-1.228149712	-1.228149712	2.49E-05
similar to indolethylamine N-methyltransferase	LOC368066	-1.224895977	-1.224895977	0.000132652
unknown gene	NA	-1.216284954	-1.216284954	0.000217658
cytochrome P450, family 17, subfamily a, polypeptide 1	Cyp17a1	-1.215700929	-1.215700929	2.89E-07
similar to Small inducible cytokine B13 precursor (CXCL13) (B lymphocyte chemoattractant) (CXC chemokine BLC)	LOC498335	-1.193902963	-1.193902963	2.40E-05
aldehyde dehydrogenase family 1, member A1	Aldh1a1	-1.168395499	-1.168395499	0.000103328
alpha-methylacyl-CoA racemase	Amacr	-1.163597025	-1.163597025	7.20E-05
synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	-1.158987684	-1.158987684	0.000142626
unknown gene	NA	-1.152359441	-1.152359441	0.000158827
carbonic anhydrase 3	Ca3	-1.150770608	-1.150770608	5.46E-05

ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) (predicted)	Elavl1_predicted	-1.149846678	-1.149846678	6.56E-06
unknown gene	NA	-1.148841454	-1.148841454	0.003269327
unknown gene	NA	-1.145133085	-1.145133085	0.000677855
unknown gene	NA	-1.139363074	-1.139363074	0.001224547
dermatopontin (predicted)	Dpt_predicted	-1.13350913	-1.13350913	1.32E-05
unknown gene	NA	-1.130925289	-1.130925289	8.61E-05
unknown gene	NA	-1.125975022	-1.125975022	0.001981349
apolipoprotein B editing complex 1	Apobec1	-1.125127285	-1.125127285	0.000105634
PDZ domain containing RING finger 3 (predicted)	Pdzrn3_predicted	-1.112054187	-1.112054187	0.000631358
Unknown gene	NA	-1.108779755	-1.108779755	0.002302176
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	-1.10868786	-1.10868786	4.98E-05
cyclin D1	Ccnd1	-1.090306487	-1.090306487	1.30E-06
similar to SR rich protein	RGD1307395	-1.087084873	-1.087084873	0.000133883
transmembrane protein 2 (predicted)	Tmem2_predicted	-1.082083932	-1.082083932	0.002238583
acyl-Coenzyme A oxidase 2, branched chain	Acox2	-1.077081169	-1.077081169	1.34E-05
chemokine (C-X-C motif) ligand 1	Cxcl1	-1.076813511	-1.076813511	0.000698495
candidate mediator of the p53-dependent G2 arrest	Rprm	-1.07668894	-1.07668894	4.43E-05
solute carrier family 10, member 2	Slc10a2	-1.075934112	-1.075934112	6.27E-06
carnitine O-octanoyltransferase	Crot	-1.072817839	-1.072817839	0.000250085
Unknown gene	NA	-1.06795631	-1.06795631	0.000281557
cyclin D1	Ccnd1	-1.067211451	-1.067211451	0.000228796
Unknown gene	NA	-1.065799832	-1.065799832	6.65E-06
serum/glucocorticoid regulated kinase	Sgk	-1.065741894	-1.065741894	2.49E-06
Unknown gene	NA	-1.061919169	-1.061919169	0.00017231
Unknown gene	NA	-1.055511223	-1.055511223	0.003962804
Unknown gene	NA	-1.05277525	-1.05277525	0.004469053
filamin, beta (predicted)	Flnb_predicted	-1.052567696	-1.052567696	0.00449697
aldehyde dehydrogenase 1 family, member B1	Aldh1b1	-1.041328095	-1.041328095	0.00048473
hypothetical LOC312654 (predicted)	RGD1311909_predicted	-1.039119168	-1.039119168	0.000680477
rat senescence marker protein 2A gene, exons 1 and 2	Smp2a	-1.037943451	-1.037943451	0.001339963
claudin 10 (predicted)	Cldn10_predicted	-1.030872961	-1.030872961	0.000598064
cysteine rich protein 61	Cyr61	-1.028681432	-1.028681432	0.003179718
similar to netrin G1 (predicted)	RGD1563465_predicted	-1.025397798	-1.025397798	0.004509068
similar to liver-specific bHLH-Zip transcription factor	LOC685277	-1.018665952	-1.018665952	0.000814979
myeloid/lymphoid or mixed-lineage leukemia,translocated to, 3 (trithorax homolog, Drosophila)	Mllt3	-1.013107418	-1.013107418	6.44E-05
nuclear receptor subfamily 3, group C, member 1	Nr3c1	-1.009696734	-1.009696734	0.000266919
similar to TSC22 domain family protein 2 (TSC22-related-inducible leucine zipper protein 4)	LOC499624	-1.006035304	-1.006035304	0.004055708
retinol binding protein 1, cellular	Rbp1	-1.002709918	-1.002709918	3.12E-05
unknown gene	NA	1.003052512	1.003052512	0.007462544
regulated endocrine-specific protein 18	Resp18	1.003336777	1.003336777	0.00129165
capping protein (actin filament), gelsolin-like	Capg	1.010005058	1.010005058	0.00031621
pyruvate kinase, muscle	Pkm2	1.010029718	1.010029718	0.000527834
keratin 10	Krt10	1.012331377	1.012331377	7.36E-05
integrin alpha 1	Itga1	1.018949855	1.018949855	0.000108094
ADP-ribosyltransferase 2b	Art2b	1.021722534	1.021722534	0.002416605
nicotinate phosphoribosyltransferase domain containing 1	Naprt1	1.023896999	1.023896999	0.000265444
lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp	1.030252991	1.030252991	6.64E-05
insulin-like growth factor binding protein 1	Igfbp1	1.032837002	1.032837002	0.000111394
integral membrane transport protein UST4r	UST4r	1.042059057	1.042059057	4.19E-05
solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9	1.046282258	1.046282258	0.000535308
lipoprotein lipase	Lpl	1.068481674	1.068481674	0.000199801
orosomucoid 1	Orm1	1.070962035	1.070962035	4.96E-06
similar to Reticulocalbin-1 precursor	LOC502737	1.076642611	1.076642611	8.77E-05
procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	Plod2	1.079632361	1.079632361	0.000911095
microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.087590816	1.087590816	0.002889721

similar to Diphosphoinositol polyphosphate phosphohydrolase 3 alpha (DIPP-3 alpha) (DIPP3 alpha)	LOC680248	1.089426694	1.089426694	3.35E-05
unknown gene	NA	1.091099465	1.091099465	0.003480045
chemokine (C-X-C motif) ligand 9	Cxcl9	1.103651108	1.103651108	4.95E-05
similar to nucleolar protein with MIF4G domain 1	LOC682058	1.105444584	1.105444584	3.39E-05
cytochrome P450, family 8, subfamily b, polypeptide 1	Cyp8b1	1.106401612	1.106401612	1.54E-05
similar to killer activatory receptor-like protein p91D (predicted)	RGD1562625_predicted	1.114607828	1.114607828	5.69E-05
S100 calcium binding protein A6 (calcyclin)	S100a6	1.150322169	1.150322169	0.000403115
aldo-keto reductase family 1, member C6	Akr1c6	1.164459731	1.164459731	5.76E-06
unknown gene	NA	1.171038101	1.171038101	0.000698897
chemokine (C-X-C motif) ligand 9	Cxcl9	1.174764811	1.174764811	1.51E-08
microfibrillar-associated protein 4	Mfap4	1.183189551	1.183189551	0.001138222
similar to ecotropic viral integration site 2A	LOC685433	1.188875945	1.188875945	0.005807165
solute carrier family 30 (zinc transporter), member 2	Slc30a2	1.191961721	1.191961721	0.002069689
aryl hydrocarbon receptor	Ahr	1.204095162	1.204095162	7.74E-06
RT1 class II, locus Da	RT1-Da	1.206663509	1.206663509	5.69E-06
prolylcarboxypeptidase (angiotensinase C) (predicted)	Prcp_predicted	1.219124305	1.219124305	0.005727018
lectin, galactose binding, soluble 1	Lgals1	1.235449253	1.235449253	1.14E-05
lectin, galactose binding, soluble 3	Lgals3	1.240445296	1.240445296	6.42E-06
reticulocalbin 1 (predicted)	Rcn1_predicted	1.263112942	1.263112942	0.00115911
interleukin enhancer binding factor 3	Ilf3	1.27097377	1.27097377	0.000281707
unknown gene	NA	1.286653638	1.286653638	0.000841458
unknown gene	NA	1.301952325	1.301952325	1.19E-05
RT1 class II, locus Bb	RT1-Bb	1.308940409	1.308940409	0.00010959
unknown gene	NA	1.338818412	1.338818412	0.000325035
thyroid hormone responsive protein	Thrsp	1.351519543	1.351519543	1.22E-06
procollagen, type 1, alpha 1	Col1a1	1.365722314	1.365722314	0.000108671
similar to RIKEN cDNA 4632417N05 (predicted)	RGD1308481_predicted	1.367960613	1.367960613	1.25E-05
hydroxysteroid (17-beta) dehydrogenase 9	Hsd17b9	1.3783708	1.3783708	4.03E-05
RT1 class Ib, locus Aw2	RT1-Aw2	1.390933728	1.390933728	0.005156243
metallothionein 1a	Mt1a	1.39745468	1.39745468	1.64E-05
unknown gene	NA	1.402153766	1.402153766	3.67E-06
thyroid hormone responsive protein	Thrsp	1.41699897	1.41699897	4.20E-06
RT1 class Ib, locus Aw2	RT1-Aw2	1.421629909	1.421629909	1.72E-05
nuclear receptor subfamily 1, group D, member 1	Nr1d1	1.433451835	1.433451835	0.001673906
unknown gene	NA	1.448741365	1.448741365	9.07E-06
dual specificity phosphatase 1	Dusp1	1.46300805	1.46300805	7.52E-05
unknown gene	NA	1.464516737	1.464516737	0.000906557
unknown gene	NA	1.478596075	1.478596075	7.33E-07
unknown gene	NA	1.487350981	1.487350981	0.00057783
hepatic protein EIIH	Eiih	1.492572417	1.492572417	5.12E-06
ubiquitin D	Ubd	1.509036814	1.509036814	1.58E-05
similar to paired immunoglobin-like type 2 receptor alpha	LOC685020	1.516286059	1.516286059	8.36E-05
thyroid hormone responsive protein	Thrsp	1.517992233	1.517992233	1.70E-06
glycoprotein (transmembrane) nmb	Gpnmb	1.53452046	1.53452046	4.59E-05
similar to myo-inositol 1-phosphate synthase A1	LOC290651	1.5804253	1.5804253	0.000163209
lumican	Lum	1.610766523	1.610766523	5.57E-05
similar to chromosome 17 open reading frame 27	LOC688296	1.705693101	1.705693101	0.000471035
protocadherin alpha 4	Pcdha4	1.84361225	1.84361225	0.000218366
similar to Metallothionein-2 (MT-2) (Metallothionein-II) (MT-II)	LOC689415	1.858190924	1.858190924	2.26E-07
myxovirus (influenza virus) resistance 2	Mx2	1.858276846	1.858276846	4.60E-05
abhydrolase domain containing 3 (predicted)	Abhd3_predicted	1.915300322	1.915300322	0.000660823
phospholipase A2, group IIA (platelets, synovial fluid)	Pla2g2a	1.962449102	1.962449102	4.22E-05
tissue inhibitor of metallopeptidase 1	Timp1	2.053312245	2.053312245	1.10E-05
NAD(P)H dehydrogenase, quinone 1	Nqo1	2.063984417	2.063984417	1.21E-07
cytochrome P450, family 7, subfamily a, polypeptide 1	Cyp7a1	2.108664652	2.108664652	2.58E-06

RT1 class II, locus Ba	RT1-Ba	2.326897698	2.326897698	7.93E-06
protocadherin alpha 4	Pcdha4	2.37689204	2.37689204	1.44E-08
similar to Sulfide:quinone oxidoreductase, mitochondrial precursor	LOC691966	2.64720803	2.64720803	0.000365799
RT1 class Ib, locus Aw2	RT1-Aw2	2.702473306	2.702473306	2.93E-07
lipopolysaccharide binding protein	Lbp	2.882621416	2.882621416	1.13E-06
serine protease inhibitor, Kazal type 1	Spink1	3.121455981	3.121455981	2.40E-05
WDNM1 homolog	LOC360228	3.470666205	3.470666205	1.14E-07
serine protease inhibitor, Kazal type 1	Spink1	3.859106329	3.859106329	2.80E-05
lipocalin 2	Lcn2	5.878918798	5.878918798	2.74E-08

* Genes up- or down-regulated by over 2-fold are shown.