

Figure S1. GO analysis in the treated versus HBV(+) groups. (A) BPs, (B) CCs and (C) MFs were classified by GO annotation in treated mice compared with that of HBV(+) mice. GO, Gene Ontology; HBV, hepatitis B virus; BPs, biological processes; CCs, cell components; MFs, molecular functions.

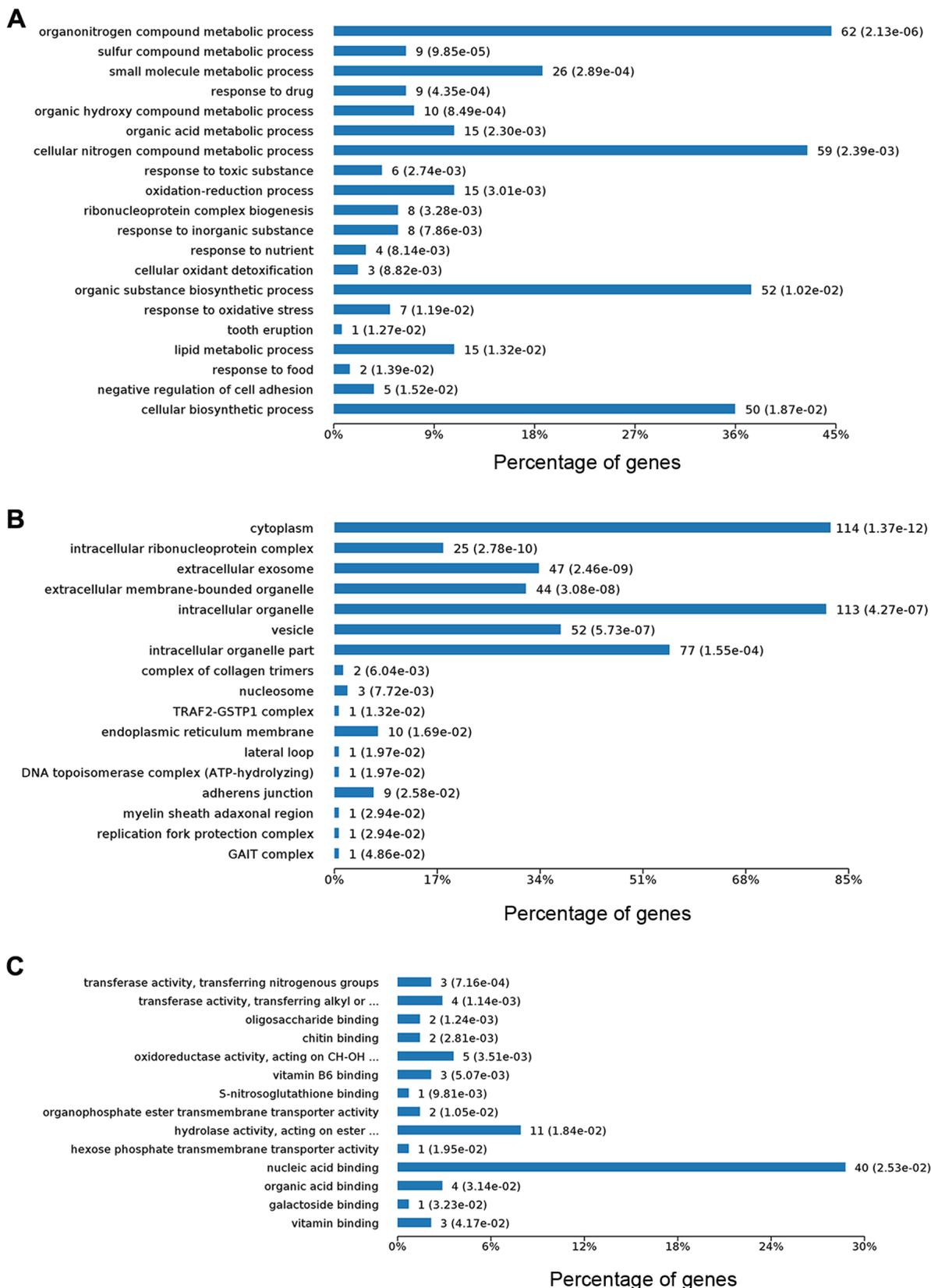


Figure S2. KEGG analysis in the treated vs. HBV(+) groups. (A) The PPAR signaling pathway was significantly enriched. (B) FABP1 and ME1 were regulated in PPAR signaling pathway after treatment. KEGG, Kyoto Encyclopedia of Genes and Genomes; HBV, hepatitis B virus; PPAR, peroxisome proliferator-activated receptor; FABP1, fatty acid binding protein 1; ME1, malic enzyme 1.

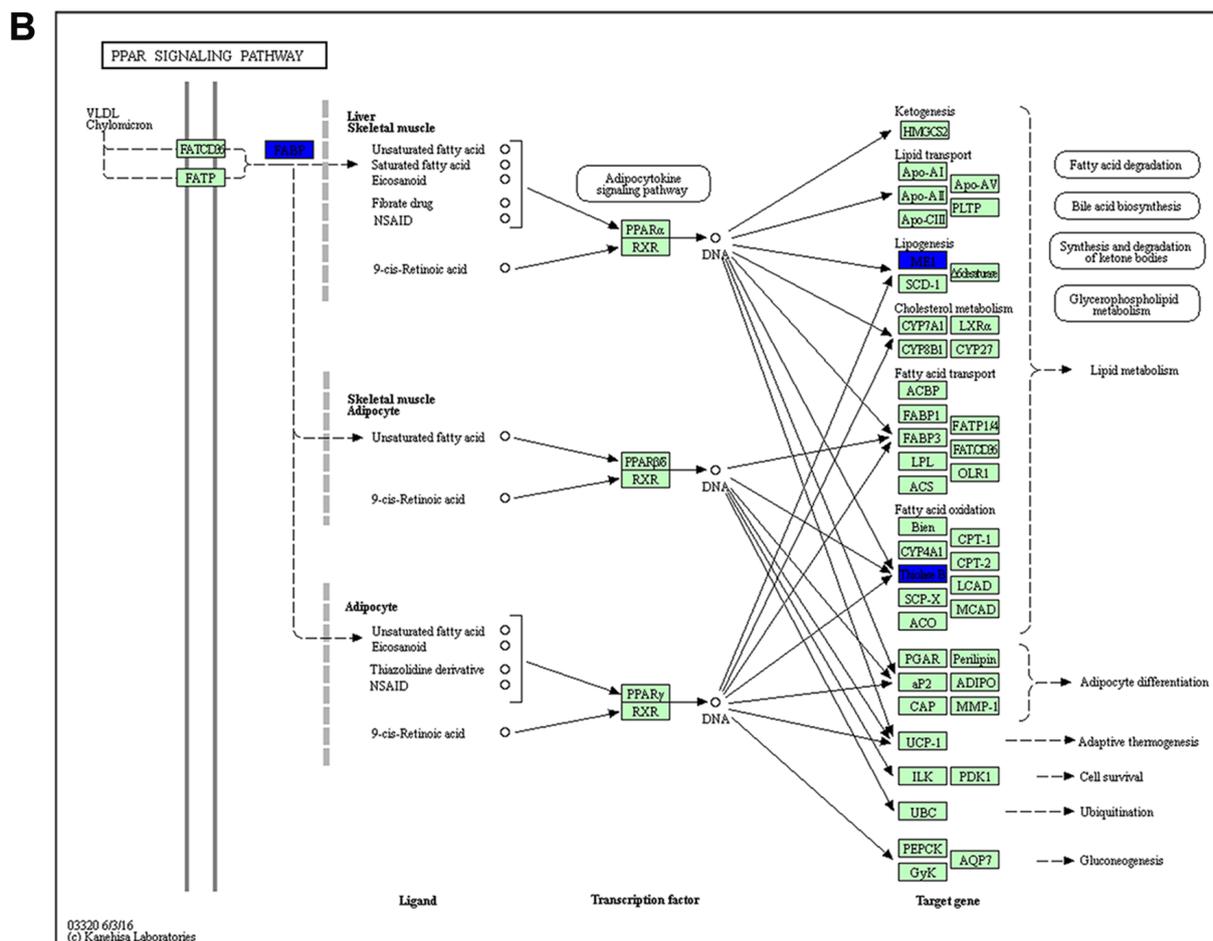
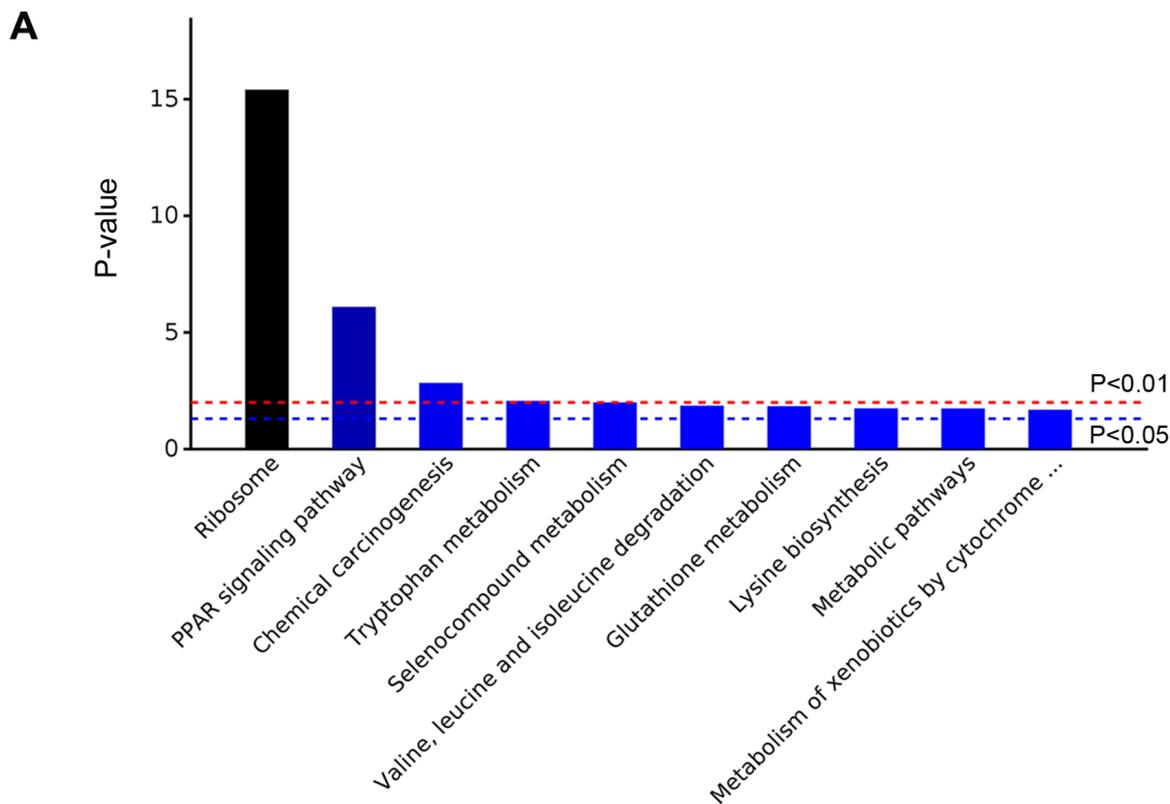


Figure S3. Verification of transfection. LX-2 cells were transfected with pSSV9-HBV with or without pAAV-shRNA. (A) HBsAg and (B) HBeAg in the supernatant were detected by ELISA. Positive and negative were the controls in the ELISA kit. HBV, hepatitis B virus; HBsAg, HBV surface antigen; HBeAg, HBV e antigen; ELISA, enzyme-linked immunosorbent assay.

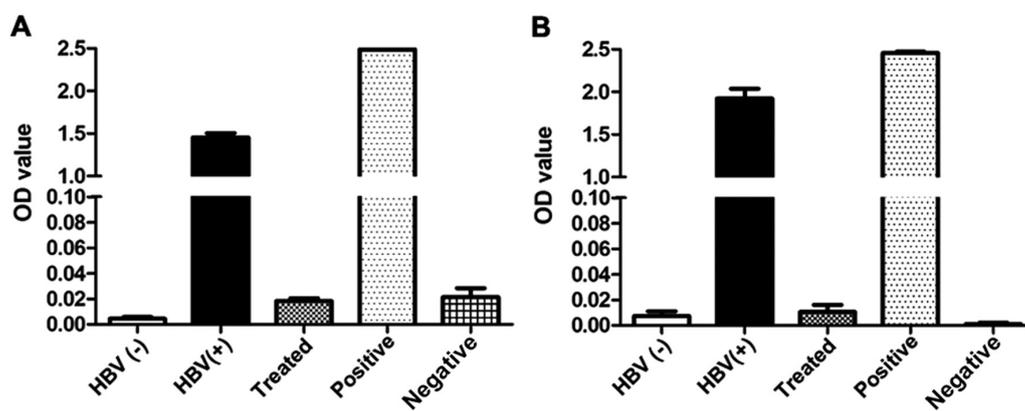


Table SI. The sequence of shRNAs for HBV and TGF- $\beta$ .

Oligos	Sequence (5'→3')
shRNA-1	TTCCAGGATCCTCAACAAC
shRNA-3	TGTC AACGACCGACCTTGA
shRNA-TGF- $\beta$	CTATTGCTTCAGCTCCACAGA
shRNA-Scrambler	GCACCTATAACAACGGTAG

shRNAs, short hairpin RNAs; HBV, hepatitis B virus; TGF, transforming growth factor.

Table SII. Basic information for iTRAQ-labeling reagents.

Group	iTRAQ-labeling		
Treated	127N	129C	130N
HBV(+) mice	128N	130C	129N
HBV(-) mice	128C	131	127C
Mix	126		

iTRAQ, isobaric tags for relative and absolute quantitation;  
HBV, hepatitis B virus.

Table SIII. Total proteins in the treated vs. HBV(+) groups.

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Fold change	<0.77	0.77-1.0	1.0-1.3	>1.3
Number of proteins	76	1262	1283	122
Total proteins	2743			

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HBV, hepatitis B virus.

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Table SIV. Total proteins in the HBV(+) vs. HBV(-) groups.

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Fold change	<0.77	0.77-1.0	1.0-1.3	>1.3
Number of proteins	134	1236	1312	61
Total proteins	2743			

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HBV, hepatitis B virus.

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Table SV. Venn-Euler diagrams of differentially expressed proteins.

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A-up and B-up	A-up and B-down	A-down and B-up	A-down and B-down
2	41	15	2

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A, represents the treated vs. the HBV(+) group; and B, represents the HBV(+) vs. the HBV(-) group. HBV, hepatitis B virus; up, upregulated; down, downregulated.

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Table SVI. All differentially expressed proteins in the treated vs. HBV(+) groups and HBV(+) vs. HBV(-) groups.

Uniprot (ID)	Gene name	A, Fold change in treated vs. HBV(+)	B, Fold change in HBV(+) vs. HBV(-)
P02798	Mt2	3.995913	0.092066
P07361	Orm2	2.257602	0.388889
P47911	Rpl6	2.179884	0.757093
Q6ZWV7	Rpl35	2.161765	0.597896
Q9R022	Dnajc12	2.130309	0.63393
Q9D1R9	Rpl34	2.025305	0.696021
P83882	Rpl36a	1.936119	0.681394
Q9CXI3	Moxd1	1.911517	0.76518
Q5SZA3	Hist1h1c	1.900669	0.669223
Q60842	Chromosome 24p3 (not gen name)	1.846715	0.376411
Q5I0T8	Rpl19	1.784706	0.708595
Q9D823	Rpl37	1.717697	0.616717
Q9DCS1	Tmem176a	1.635518	0.70068
Q4JFI8	Apcs	1.608	0.531582
P05366	Saa1	1.583124	0.405788
Q3UP42	S100a9	1.580916	0.755238
P62301	Rps13	1.572274	0.763842
Q6ZWN5	Rps9	1.565274	0.728843
P47963	Rpl13	1.543248	0.644208
Q9D0B6	Pbdc1	1.54087	0.766402
P14115	Rpl27a	1.536258	0.70685
O88952	Lin7c	1.489902	0.628274
Q9CY73	Mrpl44	1.488852	0.727983
Q99KI3	Emc3	1.487815	0.722794
P59999	Arpc4	1.48156	0.735235
Q5BLK1	Rps6	1.47944	0.616778
P62918	Rpl8	1.477906	0.723801
Q9D958	Spes1	1.471158	0.694444
Q60590	Orm1	1.413357	0.511719
Q3TDD9	Ppp1r21	1.403767	0.481371
Q5BLJ9	Rpl27	1.390682	0.696258
P61255	Rpl26	1.384379	0.627564
Q00898	Serpina1e	1.336757	0.674751
Q8BFZ3	Actbl2	1.336664	0.745452
Q3UBS3	Hp	1.329032	0.5
Q923B6	Steap4	1.325286	0.576755
P01027	C3	1.323758	0.704981
Q3TGR2	Fgb	1.322275	0.502707
E9Q035	Gm20425	1.309105	0.713509
A0A140T8K6	Rpl36-ps3	1.30471	0.670018
Q60FD1	Tmem258	1.304535	0.715024
P97457	Mylpf	0.276411	3.60362
Q4KL41	Tom20	0.318241	2.202279
P05977	Myl1	0.363473	2.661874
P07310	Ckm	0.459601	2.174762
P11087	Colla1	0.551724	1.356554
Q14DH7	Acss3	0.561717	1.568651
C6EQJ5	ASL1/3110003A17Rik fusion protein (not gene name)	0.584546	1.809277
Q61344	Tpm2	0.589612	1.631265
B1ATI0	Aldh3a2	0.655485	1.351542
Q8C4C9	Dnajb12	0.671179	1.508049
Q64176	Ces1e	0.688548	1.365719
B2RQY8	Spg7	0.719531	1.584646

Table SVI. Continued.

Uniprot (ID)	Gene name	A, Fold change in treated vs. HBV(+)	B, Fold change in HBV(+) vs. HBV(-)
Q62150	Rnps1	0.742181	1.318841
P08122	Col4a2	0.753799	1.347858
Q3TG75	Oat	0.756885	1.43599
Q61102	Abcb7	1.53617	1.378299
O35744	Chil3	1.519316	1.418709
Q8BK99	Opa1	0.606939	0.744911
E9QK48	Eml2	0.72063	0.301089

A, indicates the treated vs. the HBV(+) group; and B, indicates HBV(+) vs. HBV(-) group. HBV, hepatitis B virus.

Table SVII. All differentially expressed proteins in HBV(+) vs. HBV(-) groups.

	Description	Fold change
P02798	Metallothionein-2 OS=Mus musculus GN=Mt2	0.092066479
E9QK48	Echinoderm microtubule-associated protein-like 2 OS=Mus musculus GN=Eml2	0.301089184
Q60842	Chromosome 24p3 (Fragment) OS=Mus musculus	0.376410558
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a OS=Mus musculus GN=Serpina3n	0.377971609
P07361	Alpha-1-acid glycoprotein 2 OS=Mus musculus GN=Orm2	0.388888889
P05366	Serum amyloid A-1 protein OS=Mus musculus GN=Saa1	0.40578824
A0A0A6YXJ7	Protein Larpl1b (Fragment) OS=Mus musculus GN=Larpl1b	0.479370915
Q3TDD9	Protein phosphatase 1 regulatory subunit 21 OS=Mus musculus GN=Ppp1r21	0.481370923
Q91XT4	Protein transport protein Sec16B OS=Mus musculus GN=Sec16b	0.482274034
Q91XL1	Leucine-rich HEV glycoprotein OS=Mus musculus GN=Lrg1	0.493495415
A0A075DCF9	NADH-ubiquinone oxidoreductase chain 2 OS=Mus musculus GN=ND2	0.499900616
Q3UBS3	Haptoglobin OS=Mus musculus GN=Hp	0.5
Q3TGR2	Fibrinogen, B beta polypeptide, isoform CRA_a OS=Mus musculus GN=Fgb	0.502707386
Q921J3	Dnajc5 protein OS=Mus musculus GN=Dnajc5	0.510492108
Q60590	Alpha-1-acid glycoprotein 1 OS=Mus musculus GN=Orm1	0.511719201
A8DUK4	Beta-globin OS=Mus musculus GN=Hbbt1	0.526553672
Q4JF18	Pentaxin OS=Mus musculus GN=Apcs	0.531582239
E9PV24	Fibrinogen alpha chain OS=Mus musculus GN=Fga	0.541205412
A0A0R4IZW9	Stromal cell-derived factor 2 OS=Mus musculus GN=Sdf2	0.549628629
Q91VR8	Protein BRICK1 OS=Mus musculus GN=Brk1	0.569789675
Q923B6	Metalloreductase STEAP4 OS=Mus musculus GN=Steap4	0.576755162
P81117	Nucleobindin-2 OS=Mus musculus GN=Nucb2	0.584385902
Q9D727	Uncharacterized protein C6orf226 homolog OS=Mus musculus	0.587249782
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4 OS=Mus musculus GN=Itih4	0.587637204
P00920	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2	0.589340323
P06728	Apolipoprotein A-IV OS=Mus musculus GN=Apoa4	0.590027701
Q64523	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac	0.590345727
Q6ZWW7	60S ribosomal protein L35 OS=Mus musculus GN=Rpl35	0.597896059
P56379	6.8 kDa mitochondrial proteolipid OS=Mus musculus GN=Mp68	0.600716315
Q9DAV9	Trimeric intracellular cation channel type B OS=Mus musculus GN=Tmem38b	0.611675788
Q9D823	60S ribosomal protein L37 OS=Mus musculus GN=Rpl37	0.616717194
Q5BLK1	40S ribosomal protein S6 OS=Mus musculus GN=Rps6	0.616778149
A0A0R4J0J8	Cytospin-A OS=Mus musculus GN=Specc11	0.618977745
Q3U2W2	MYB binding protein (P160) 1a, isoform CRA_b OS=Mus musculus GN=Mybbp1a	0.627356874
P61255	60S ribosomal protein L26 OS=Mus musculus GN=Rpl26	0.627564367
O88952	Protein lin-7 homolog C OS=Mus musculus GN=Lin7c	0.628273955
Q5M9K7	MCG21688 OS=Mus musculus GN=Rps10	0.632273263
Q9R022	DnaJ homolog subfamily C member 12 OS=Mus musculus GN=Dnajc12	0.633929937
Q8VD31	Tapasin-related protein OS=Mus musculus GN=Tapbp1	0.640988605
Q3UER8	Fibrinogen gamma chain OS=Mus musculus GN=Fgg	0.641609719
Q91X72	Hemopexin OS=Mus musculus GN=Hpx	0.642086782
P47963	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13	0.644207534
Q9JIG7	Coiled-coil domain-containing protein 22 OS=Mus musculus GN=Ccdc22	0.661542403
Q8K232	Adducin 1 (Alpha) OS=Mus musculus GN=Add1	0.664189503
A0A0R4J104	Disabled homolog 2 OS=Mus musculus GN=Dab2	0.667714473
Q04207	Transcription factor p65 OS=Mus musculus GN=Rela	0.669104205
Q5SZA3	Histone cluster 1, H1c OS=Mus musculus GN=Hist1h1c	0.669223394
A0A140T8K6	60S ribosomal protein L36 OS=Mus musculus GN=Rpl36-ps3	0.670018154
Q00898	Alpha-1-antitrypsin 1-5 OS=Mus musculus GN=Serpina1e	0.674750974
A0A0R4J0I1	MCG1051009 OS=Mus musculus GN=Serpina3k	0.677147239
Q9CYA0	Cysteine-rich with EGF-like domain protein 2 OS=Mus musculus GN=Creltd2	0.67844342
P27641	X-ray repair cross-complementing protein 5 OS=Mus musculus GN=Xrcc5	0.680461838
P83882	60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a	0.681394207
P53702	Cytochrome c-type heme lyase OS=Mus musculus GN=Hccs	0.682671082
E9PZ91	Bis(5'-adenosyl)-triphosphatase OS=Mus musculus GN=Fhit	0.683034554

Table SVII. Continued.

	Description	Fold change
B2RUH3	Selenoprotein X 1 OS=Mus musculus GN=Msrbl	0.684246112
Q8R4R6	Nucleoporin NUP53 OS=Mus musculus GN=Nup35	0.684430512
Q69ZX3	MKIAA0866 protein (Fragment) OS=Mus musculus GN=Myh11	0.685644571
Q571F3	MFLJ00061 protein (Fragment) OS=Mus musculus GN=Necap1	0.687150075
P29341	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1	0.689484127
Q3U2P8	Putative uncharacterized protein OS=Mus musculus GN=Mapkap2	0.694264069
Q9D958	Signal peptidase complex subunit 1 OS=Mus musculus GN=Spes1	0.694444444
Q921I1	Serotransferrin OS=Mus musculus GN=Tf	0.69476906
Q9D1R9	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34	0.696020874
Q5BLJ9	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27	0.696258358
Q80V08	Rpl17 protein (Fragment) OS=Mus musculus GN=Rpl17	0.697021277
P47915	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29	0.700468541
Q9DCS1	Transmembrane protein 176A OS=Mus musculus GN=Tmem176a	0.700680272
P01027	Complement C3 OS=Mus musculus GN=C3	0.704980843
P14115	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a	0.706850182
A0A0R4J1R1	E3 ubiquitin-protein ligase synoviolin OS=Mus musculus GN=Syvn1	0.707614077
Q5I0T8	Ribosomal protein L19 OS=Mus musculus GN=Rpl19	0.708595388
Q9D1N9	39S ribosomal protein L21, mitochondrial OS=Mus musculus GN=Mrpl21	0.708803612
P29788	Vitronectin OS=Mus musculus GN=Vtn	0.710795902
B2RTP7	Krt2 protein OS=Mus musculus GN=Krt2	0.71087017
B7ZWC4	Insulin-like growth factor 2 receptor OS=Mus musculus GN=Igf2r	0.711488733
Q8BM72	Heat shock 70 kDa protein 13 OS=Mus musculus GN=Hspa13	0.711904762
E9Q035	Protein Gm20425 OS=Mus musculus GN=Gm20425	0.713508992
P18608	Non-histone chromosomal protein HMG-14 OS=Mus musculus GN=Hmgn1	0.714750389
Q60FD1	MCG1963, isoform CRA_b OS=Mus musculus GN=Tmem258	0.715024458
Q9CWE0	Mitochondrial fission regulator 1-like OS=Mus musculus GN=Mtfr11	0.716600266
E9Q8I0	Complement factor H OS=Mus musculus GN=Cfh	0.716940767
O35143	ATPase inhibitor, mitochondrial OS=Mus musculus GN=Atpif1	0.721555647
F6TVX7	Protein Gm20671 (Fragment) OS=Mus musculus GN=Gm20671	0.722356739
Q99KI3	ER membrane protein complex subunit 3 OS=Mus musculus GN=Emc3	0.722794447
Q3TIQ3	Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Pitpna	0.723556318
P62918	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8	0.723800652
Q9CY73	39S ribosomal protein L44, mitochondrial OS=Mus musculus GN=Mrpl44	0.727983168
Q6ZWN5	40S ribosomal protein S9 OS=Mus musculus GN=Rps9	0.728842832
Q61838	Pregnancy zone protein OS=Mus musculus GN=Pzp	0.729438139
A2AVJ7	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1	0.729874776
P18572	Basigin OS=Mus musculus GN=Bsg	0.73027184
Q8QZR5	Alanine aminotransferase 1 OS=Mus musculus GN=Gpt	0.731449219
P29699	Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahs	0.732466829
Q8BJF9	Charged multivesicular body protein 2b OS=Mus musculus GN=Chmp2b	0.733572282
P59999	Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4	0.735234533
Q564G0	Guanylate kinase OS=Mus musculus GN=Guk1	0.73746791
A0A0R4J1V1	Solute carrier family 39 (Zinc transporter), member 14, isoform CRA_a OS=Mus musculus GN=Slc39a14	0.738303485
P62862	40S ribosomal protein S30 OS=Mus musculus GN=Fau	0.738995109
Q546G4	Albumin 1 OS=Mus musculus GN=Alb	0.739011739
Q9D8W7	OCIA domain-containing protein 2 OS=Mus musculus GN=Ociad2	0.73948028
P41241	Tyrosine-protein kinase CSK OS=Mus musculus GN=Csk	0.74046331
B8JJN0	Protein Gm20547 OS=Mus musculus GN=Gm20547	0.740740741
Q571A2	MKIAA4106 protein (Fragment) OS=Mus musculus GN=Cul2	0.742118454
Q8BK99	Putative uncharacterized protein OS=Mus musculus GN=Opa1	0.744910604
B2RQZ6	GPRIN family member 3 OS=Mus musculus GN=Gprn3	0.745030745
Q8BFZ3	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2	0.745451941
Q5M9P3	Rps19 protein (Fragment) OS=Mus musculus GN=Rps19	0.746424642
G5E8V9	MCG18094 OS=Mus musculus GN=Arfp1	0.747883484
P70697	Uroporphyrinogen decarboxylase OS=Mus musculus GN=Urod	0.748376623

Table SVII. Continued.

	Description	Fold change
O35405	Phospholipase D3 OS=Mus musculus GN=Pld3	0.750479321
P35585	AP-1 complex subunit mu-1 OS=Mus musculus GN=Ap1m1	0.750638298
Q9CQI7	U2 small nuclear ribonucleoprotein B'' OS=Mus musculus GN=Snrpb2	0.751065292
P34884	Macrophage migration inhibitory factor OS=Mus musculus GN=Mif	0.751252579
Q9D1B9	39S ribosomal protein L28, mitochondrial OS=Mus musculus GN=Mrpl28	0.751559533
E9PV48	Protein Ifit3b OS=Mus musculus GN=Ifit3b	0.752527609
Q8CFX3	Protein Pcdh1 OS=Mus musculus GN=Pcdh1	0.752955083
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Mus musculus GN=Coq6	0.753026634
Q059U9	A kinase (PRKA) anchor protein 8 OS=Mus musculus GN=Akap8	0.753882353
Q3UP42	Putative uncharacterized protein OS=Mus musculus GN=S100a9	0.755238095
A2AS03	Helicase with zinc finger domain 2 OS=Mus musculus GN=Helz2	0.755883963
Q8R035	Peptidyl-tRNA hydrolase ICT1, mitochondrial OS=Mus musculus GN=Mrpl58	0.756695157
P47911	60S ribosomal protein L6 OS=Mus musculus GN=Rpl6	0.757093172
P12382	ATP-dependent 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkl	0.757852077
Q8VCQ3	Nuclear receptor-binding factor 2 OS=Mus musculus GN=Nrbf2	0.758136925
A0A140T8M7	Protein Rpl23a-ps3 OS=Mus musculus GN=Rpl23a-ps3	0.758877947
Q9CQM8	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21	0.760292772
Q8BHC0	Lymphatic vessel endothelial hyaluronic acid receptor 1 OS=Mus musculus GN=Lyve1	0.762184874
P62301	40S ribosomal protein S13 OS=Mus musculus GN=Rps13	0.763841808
Q9CXI3	DBH-like monooxygenase protein 1 OS=Mus musculus GN=Moxd1	0.765180011
Q64191	N(4)-(beta-N-acetylglucosaminy)-L-asparaginase OS=Mus musculus GN=Aga	0.765581021
Q9D0B6	Protein PBDC1 OS=Mus musculus GN=Pbdc1	0.766401745
P50543	Protein S100-A11 OS=Mus musculus GN=S100a11	0.767962309
A0A0R4J038	Kininogen-1 OS=Mus musculus GN=Kng1	0.769803753
Q7TNL5	Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_a OS=Mus musculus GN=Ppp2r5d	1.302700524
Q8R1G2	Carboxymethylenebutenolidase homolog OS=Mus musculus GN=Cmb1	1.30617867
O35386	Phytanoyl-CoA dioxygenase, peroxisomal OS=Mus musculus GN=Phyh	1.308146399
Q9DCM2	Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1	1.311996779
P28474	Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5	1.313218391
Q62150	RNA/DNA-binding protein OS=Mus musculus GN=Rnps1	1.31884058
B5X0G2	Major urinary protein 17 OS=Mus musculus GN=Mup17	1.322107081
Q9WV85	Nucleoside diphosphate kinase 3 OS=Mus musculus GN=Nme3	1.333333333
P10833	Ras-related protein R-Ras OS=Mus musculus GN=Rras	1.333751044
Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial OS=Mus musculus GN=Sdhd	1.335814723
Q5DTH1	MKIAA4216 protein (Fragment) OS=Mus musculus GN=Ube3a	1.337582324
G3X9M0	28S ribosomal protein S29, mitochondrial OS=Mus musculus GN=Dap3	1.338839475
P97872	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Mus musculus GN=Fmo5	1.34051542
P13516	Acyl-CoA desaturase 1 OS=Mus musculus GN=Scd1	1.346128392
Q91XG5	Protein S100 OS=Mus musculus GN=S100g	1.347759563
P08122	Collagen alpha-2(IV) chain OS=Mus musculus GN=Col4a2	1.347858473
Q91YT2	E3 ubiquitin-protein ligase RNF185 OS=Mus musculus GN=Rnf185	1.350534928
B1ATI0	Aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2	1.351542178
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1	1.356335515
P11087	Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1	1.356553929
O09158	Cytochrome P450 3A25 OS=Mus musculus GN=Cyp3a25	1.36504114
Q64176	Carboxylesterase 1E OS=Mus musculus GN=Ces1e	1.365718799
P24549	Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1	1.368194281
Q3TR93	Putative uncharacterized protein OS=Mus musculus GN=Decr2	1.374294671
Q8R0J2	Mannose-P-dolichol utilization defect 1 OS=Mus musculus GN=Mpdu1	1.376531672
Q61102	ATP-binding cassette sub-family B member 7, mitochondrial OS=Mus musculus GN=Abcb7	1.37829912
Q8K154	UDP-glucuronosyltransferase OS=Mus musculus GN=Ugt2b34	1.378640777

Table SVII. Continued.

	Description	Fold change
B2RT14	UDP-glucuronosyltransferase OS=Mus musculus GN=Ugt1a5	1.382552801
Q8CHK3	Lysophospholipid acyltransferase 7 OS=Mus musculus GN=Mboat7	1.38270015
Q8VCC1	15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Mus musculus GN=Hpgd	1.389158576
Q3UEM0	MCG9091, isoform CRA_d OS=Mus musculus GN=Akr1c6	1.389879123
Q8K2Q0	COMM domain-containing protein 9 OS=Mus musculus GN=Commd9	1.398805847
Q9CR67	Transmembrane protein 33 OS=Mus musculus GN=Tmem33	1.401459854
P16331	Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah	1.406329114
Q9CXR1	Dehydrogenase/reductase SDR family member 7 OS=Mus musculus GN=Dhrs7	1.407916667
Q64471	Glutathione S-transferase theta-1 OS=Mus musculus GN=Gstt1	1.418475947
O35744	Chitinase-like protein 3 OS=Mus musculus GN=Chil3	1.418708827
Q3TG75	Ornithine aminotransferase, isoform CRA_b OS=Mus musculus GN=Oat	1.435989615
L7MUC7	Protein Mup7 (Fragment) OS=Mus musculus GN=Mup7	1.449275362
P46737	Lys-63-specific deubiquitinase BRCC36 OS=Mus musculus GN=Brcc3	1.458992806
P63300	Selenoprotein W OS=Mus musculus GN=Selenow	1.461002179
P55096	ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3	1.475149957
E9PUL7	Protein Nat8f1 OS=Mus musculus GN=Nat8f1	1.476835353
Q4FZF3	Probable ATP-dependent RNA helicase DDX49 OS=Mus musculus GN=Ddx49	1.489889106
Q91W52	Transmembrane protein 19 OS=Mus musculus GN=Tmem19	1.493278651
Q8C4C9	DnaJ (Hsp40) homolog, subfamily B, member 12, isoform CRA_d OS=Mus musculus GN=Dnajb12	1.508048685
Q5XK33	Succinate dehydrogenase complex, subunit C, integral membrane protein OS=Mus musculus GN=Sdhc	1.511111111
Q64458	Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29	1.537494582
Q9JI78	Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase OS=Mus musculus GN=Ngly1	1.544929545
Q14DH7	Acyl-CoA synthetase short-chain family member 3, mitochondrial OS=Mus musculus GN=Acss3	1.568651032
B2RQY8	Spastic paraplegia 7 homolog (Human) OS=Mus musculus GN=Spg7	1.584646465
Q61344	Beta-tropomyosin OS=Mus musculus GN=Tpm2	1.631264916
P00186	Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2	1.641937146
Q3TV62	Putative uncharacterized protein OS=Mus musculus GN=Tor1a	1.69937821
Q8BVW3	Tripartite motif-containing protein 14 OS=Mus musculus GN=Trim14	1.733739837
Q3UEN8	MCG15287 OS=Mus musculus GN=Cyp3a11	1.759142791
C6EQJ5	ASL1/3110003A17Rik fusion protein OS=Mus musculus	1.809277238
P07310	Creatine kinase M-type OS=Mus musculus GN=Ckm	2.174761905
Q4KL41	MCG10089 OS=Mus musculus GN=Tomm20	2.202279202
P05977	Myosin light chain 1/3, skeletal muscle isoform OS=Mus musculus GN=My11	2.661874334
P97457	Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=My1pf	3.60361991