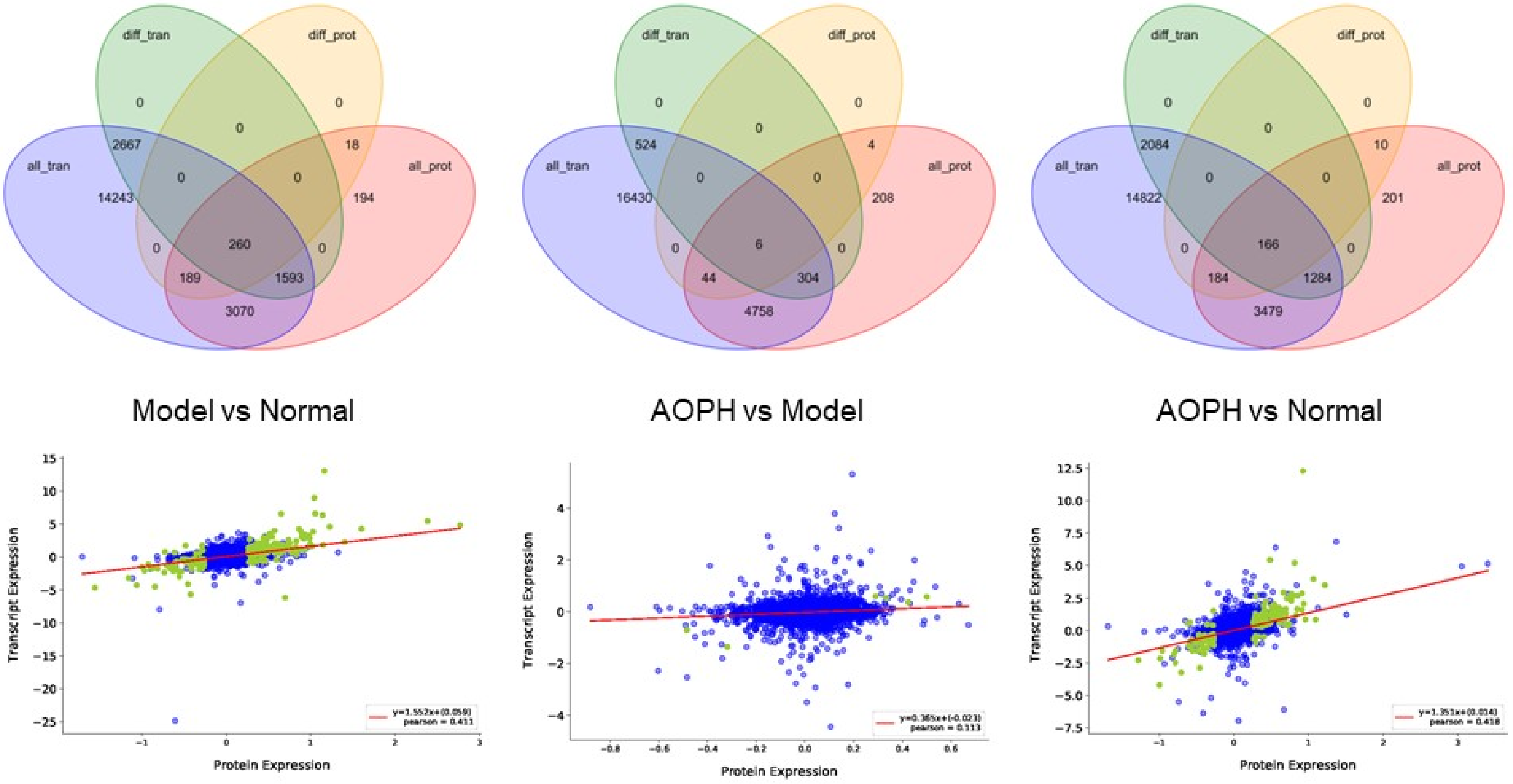
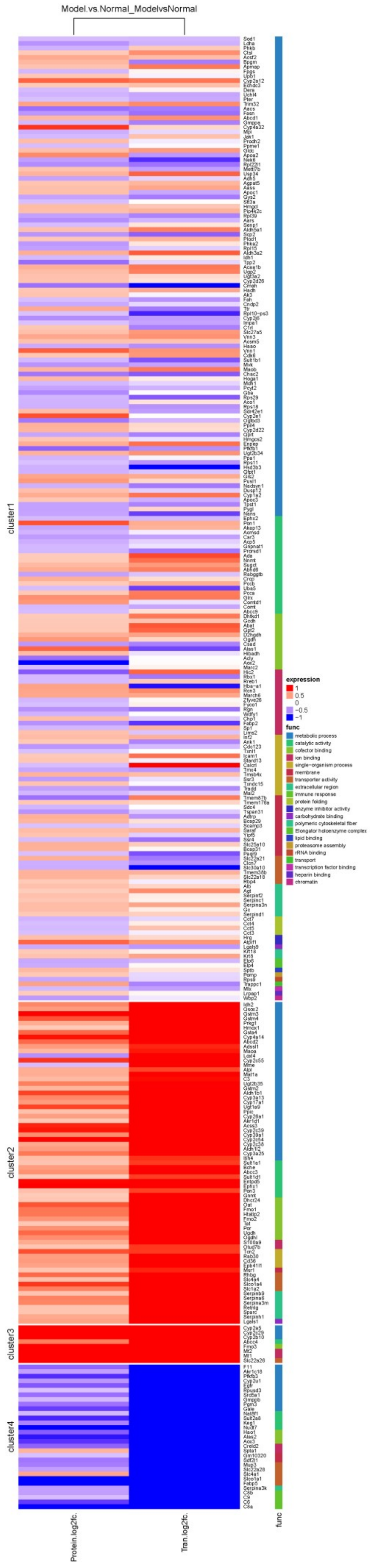


Figure S1 Venn diagram and expression correlation analysis of transcriptomic and proteomic expression regulation.

Note: a) all_tran represents all genes obtained from the transcriptome, diff_tran represents differentially expressed genes identified by the transcriptome; b) all_prot represents all proteins identified by the proteome, and diff_prot represents differential proteins identified by the proteome. c) Each point in the graph represents a protein, green points represent proteins with significant differences in expression, blue points represent proteins with no significant differences in expression, d) the horizontal coordinate is the fold of difference (log2 value) of the corresponding protein in the proteomic data, the vertical coordinate is the fold of difference (log2 value) of the corresponding gene in the transcriptomic data.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cluster2
cluster3
cluster4
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Tran.log2fc.
func
expression
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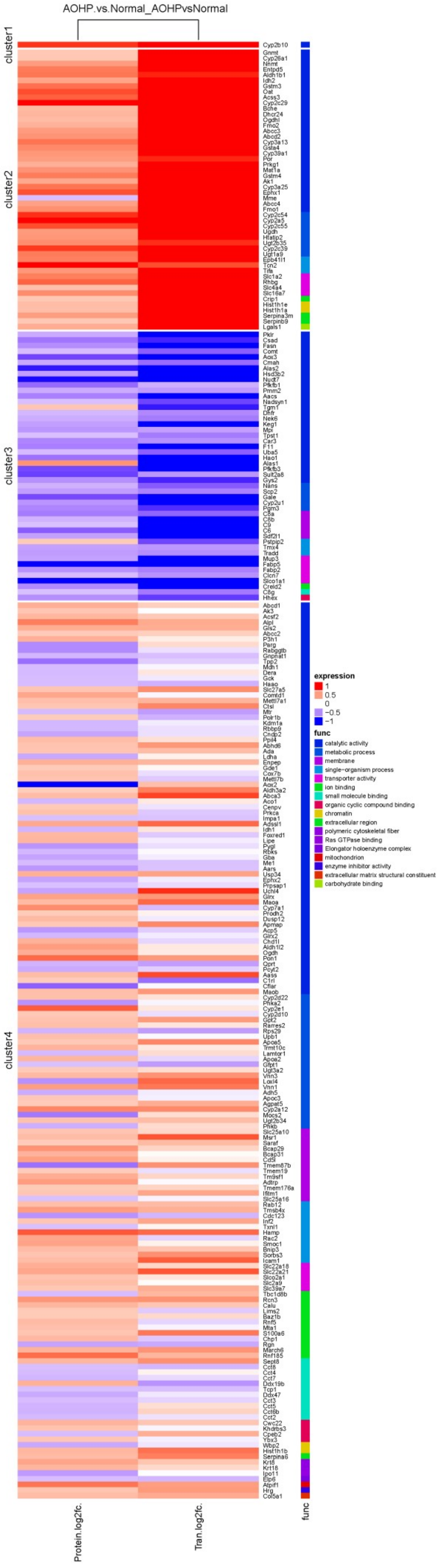
0
−0.5
−1
func
metabolic process
catalytic activity
cofactor binding
ion binding
single−organism process
membrane
transporter activity
extracellular region
immune response
protein folding
enzyme inhibitor activity
carbohydrate binding
polymeric cytoskeletal fiber
Elongator holoenzyme complex
lipid binding
proteasome assembly
rRNA binding
transport
transcription factor binding
heparin binding
chromatin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cluster1
cluster2
cluster3
cluster4
Protein.log2fc.
Tran.log2fc.
func
expression
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0.5
0
−0.5
−1
func
catalytic activity
metabolic process
membrane
single−organism process
transporter activity
ion binding
small molecule binding
organic cyclic compound binding
chromatin
extracellular region
polymeric cytoskeletal fiber
Ras GTPase binding
Elongator holoenzyme complex
mitochondrion
enzyme inhibitor activity
extracellular matrix structural constituent
carbohydrate binding

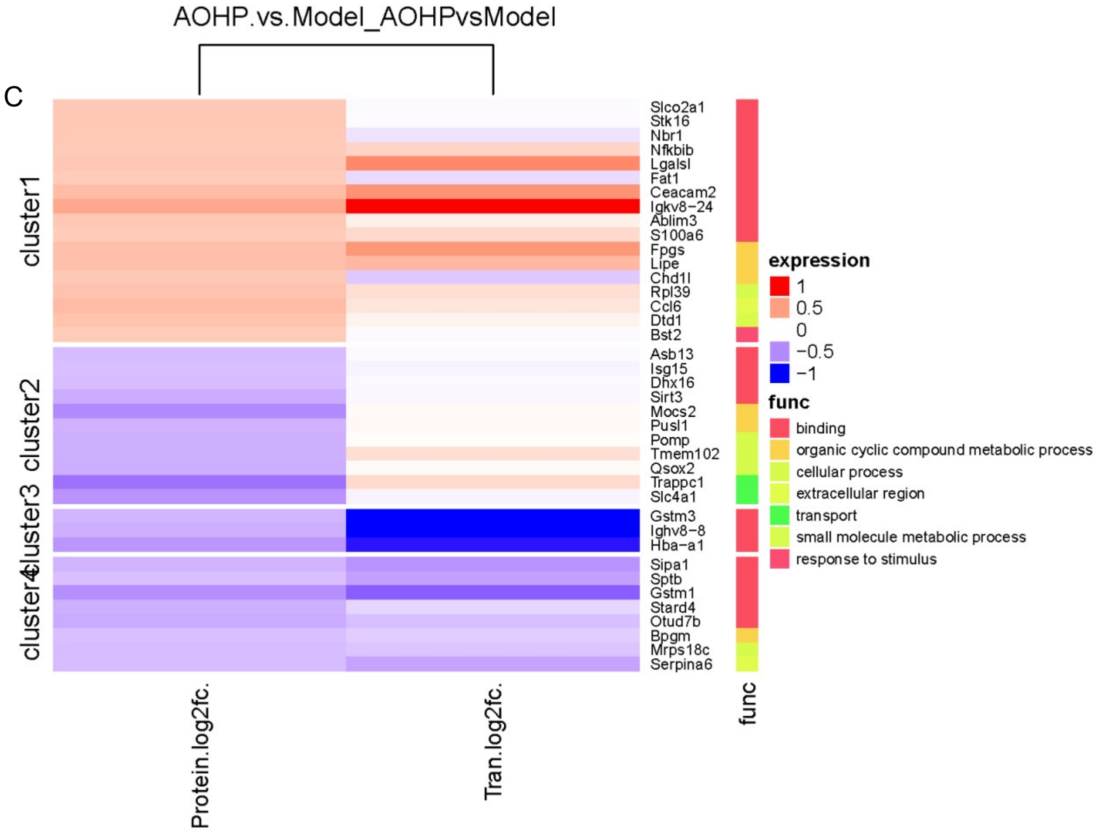
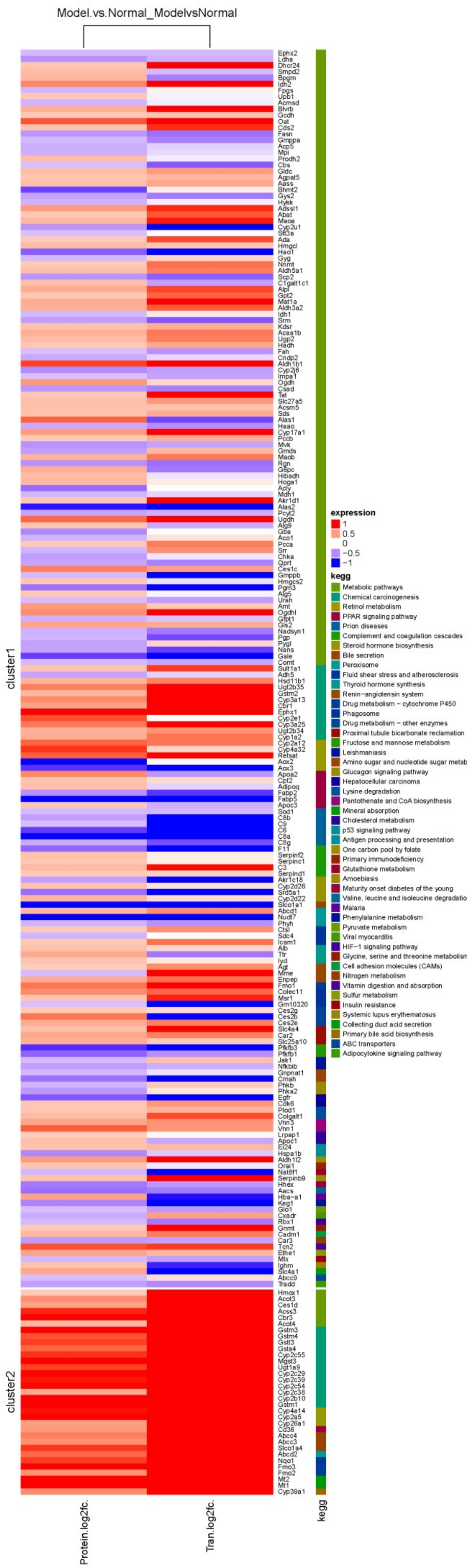


Figure S2 Heat map of GO functional enrichment clustering

Note: Red in the graph represents up-regulation, blue represents down-regulation, horizontal clustering is the clustering of protein expression at the transcriptome and proteome levels. A: Model vs Normal, B: AOPH vs Normal, C: AOPH vs Model.


Model.vs.Normal_ModelvsNormal
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cluster2
Ephx2
Ldha
Dhcr24
Smpd2
Bpgm
Idh2
Fpgs
Upb1
Acmsd
Blvrb
Gcdh
Oat
Cds2
Fasn
Gmppa
Acp5
Mpi
Prodh2
Cbs
Gldc
Agpat5
Aass
Bhmt2
Gys2
Hykk
Adssl1
Abat
Maoa
Cyp2u1
St3a
Ada
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Hao1
Gyg
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C1galt1c1
Alpl
Gpt2
Mat1a
Aldh3a2
Idh1
Srm
Kdsr
Acaa1b
Ugp2
Hadh
Fah
Cndp2
Aldh1b1
Cyp2j6
Impa1
Ogdh
Csad
Tat
Slc27a5
Acsm5
Sds
Alas1
Haao
Cyp17a1
Pccb
Mvk
Gmds
Maob
Rgn
G6pc
Hibadh
Hoga1
Acly
Mdh1
Akr1d1
Alas2
Pcyt2
Ugdh
Alg9
Gba
Aco1
Pcca
Srr
Chka
Qprt
Ces1c
Gmppb
Hmgcs2
Pgm3
Alg5
Urah
Amt
Ogdhl
Gfpt1
Gls2
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Pgp
Pygl
Nans
Gale
Comt
Sult1a1
Adh5
Hsd11b1
Ugt2b35
Gstm2
Cyp3a13
Cbr1
Ephx1
Cyp2e1
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Ugt2b34
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Cyp2a12
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Retsat
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Aox3
Apoa2
Cpt2
Adipoq
Fabp2
Fabp5
Apoc3
Sod1
C8b
C9
C6
C8a
C8g
F11
Serpinf2
Serpinc1
C3
Serpind1
Akr1c18
Cyp2d26
Srd5a1
Cyp2d22
Slco1a1
Abcd1
Nudt7
Phyh
Ctsl
Sdc4
Icam1
Alb
Ttr
Lyd
Agt
Mme
Enpep
Fmo1
Colec11
Msr1
Gm10320
Ces2g
Ces2b
Ces2e
Slc4a4
Car2
Slc25a10
Pfkfb3
Pfkfb1
Jak1
Nfkbib
Gnpnat1
Cmah
Phkb
Phka2
Egfr
Cdk6
Plod1
Colgalt1
Vnn3
Vnn1
Lrpap1
Apoc1
Ei24
Hspa1b
Aldh1l2
Orai1
Nat8f1
Serpinb9
Hhex
Aacs
Hba-a1
Keg1
Glo1
Cxadr
Rbx1
Gnmt
Cadm1
Car3
Tcn2
Ethe1
Ighm
Mlx
Slc4a1
Abcc9
Tradd
Hmox1
Acot3
Ces1d
Acss3
Cbr3
Acot4
Gstm3
Gstm4
Gstt3
Gsta4
Cyp2c55
Mgst3
Ugt1a9
Cyp2c29
Cyp2c39
Cyp2c54
Cyp2c38
Cyp2b10
Gstm1
Cyp4a14
Cyp2a5
Cyp26a1
Cd36
Abcc4
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Slco1a4
Abcd2
Nqo1
Fmo3
Fmo2
Mt2
Mt1
Cyp39a1
expression
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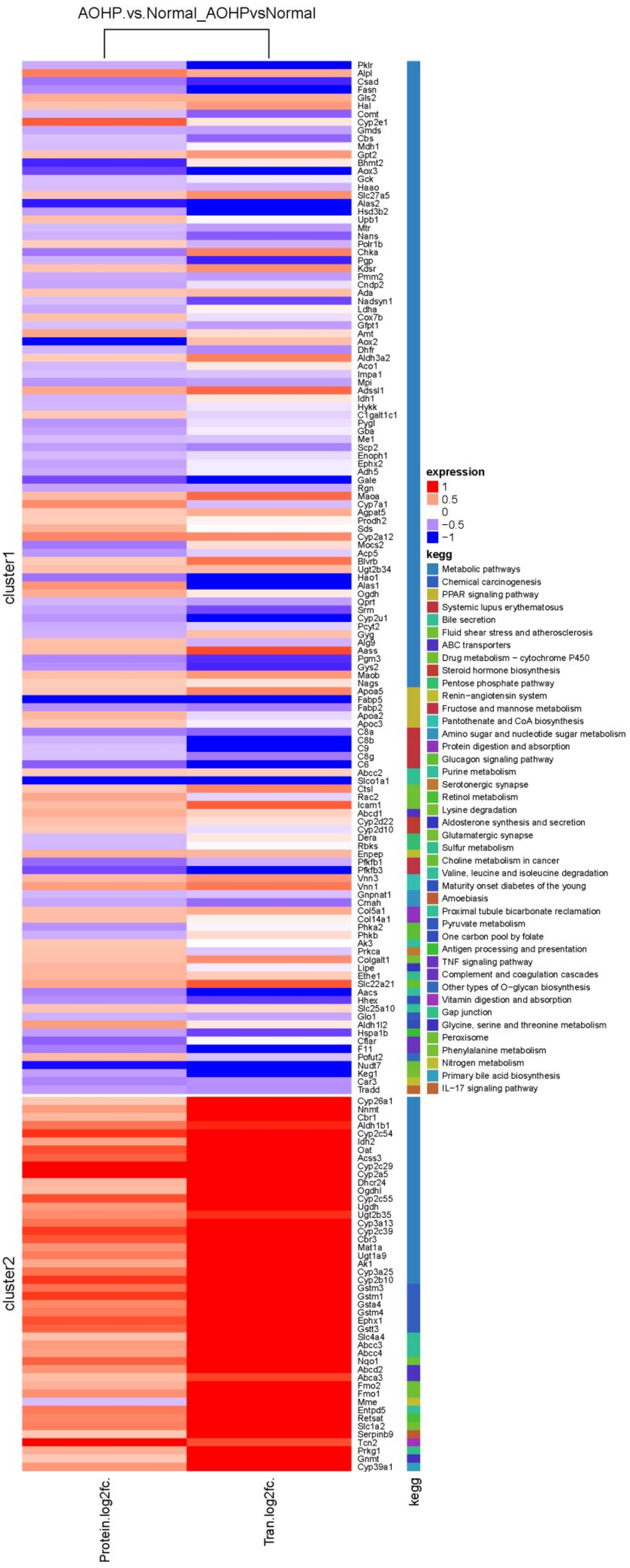
−0.5
−1
kegg
Metabolic pathways
Chemical carcinogenesis
Retinol metabolism
PPAR signaling pathway
Prion diseases
Complement and coagulation cascades
Steroid hormone biosynthesis
Bile secretion
Peroxisome
Fluid shear stress and atherosclerosis
Thyroid hormone synthesis
Renin−angiotensin system
Drug metabolism − cytochrome P450
Phagosome
Drug metabolism − other enzymes
Proximal tubule bicarbonate reclamation
Fructose and mannose metabolism
Leishmaniasis
Amino sugar and nucleotide sugar metab
Glucagon signaling pathway
Hepatocellular carcinoma
Lysine degradation
Pantothenate and CoA biosynthesis
Mineral absorption
Cholesterol metabolism
p53 signaling pathway
Antigen processing and presentation
One carbon pool by folate
Primary immunodeficiency
Glutathione metabolism
Amoebiasis
Maturity onset diabetes of the young
Valine, leucine and isoleucine degradatio
Malaria
Phenylalanine metabolism
Pyruvate metabolism
Viral myocarditis
HIF−1 signaling pathway
Glycine, serine and threonine metabolism
Cell adhesion molecules (CAMs)
Nitrogen metabolism
Vitamin digestion and absorption
Sulfur metabolism
Insulin resistance
Systemic lupus erythematosus
Collecting duct acid secretion
Primary bile acid biosynthesis
ABC transporters
Adipocytokine signaling pathway
Protein.log2fc.
Tran.log2fc.
kegg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cluster2
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Alpl
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Hal
Comt
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Cbs
Mdh1
Gpt2
Bhmt2
Aox3
Gck
Haao
Slc27a5
Alas2
Hsd3b2
Upb1
Mtr
Nans
Polr1b
Chka
Pgp
Kdsr
Pmm2
Cndp2
Ada
Nadsyn1
Ldha
Cox7b
Gfpt1
Amt
Aox2
Dhfr
Aldh3a2
Aco1
Impa1
Mpi
Adssl1
Idh1
Hykk
C1galt1c1
Pygl
Gba
Me1
Scp2
Enoph1
Ephx2
Adh5
Gale
Rgn
Maoa
Cyp7a1
Agpat5
Prodh2
Sds
Cyp2a12
Mocs2
Acp5
Blvrb
Ugt2b34
Hao1
Alas1
Ogdh
Qprt
Srm
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C8b
C9
C8g
C6
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Rac2
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Colgalt1
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Hhex
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Car3
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Cyp2c55
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Ugt2b35
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Cyp2c39
Cbr3
Mat1a
Ugt1a9
Ak1
Cyp3a25
Cyp2b10
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Gstm1
Gsta4
Gstm4
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Gstt3
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Abca3
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Retsat
Slc1a2
Serpinb9
Tcn2
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Gnmt
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kegg
Metabolic pathways
Chemical carcinogenesis
PPAR signaling pathway
Systemic lupus erythematosus
Bile secretion
Fluid shear stress and atherosclerosis
ABC transporters
Drug metabolism − cytochrome P450
Steroid hormone biosynthesis
Pentose phosphate pathway
Renin−angiotensin system
Fructose and mannose metabolism
Pantothenate and CoA biosynthesis
Amino sugar and nucleotide sugar metabolism
Protein digestion and absorption
Glucagon signaling pathway
Purine metabolism
Serotonergic synapse
Retinol metabolism
Lysine degradation
Aldosterone synthesis and secretion
Glutamatergic synapse
Sulfur metabolism
Choline metabolism in cancer
Valine, leucine and isoleucine degradation
Maturity onset diabetes of the young
Amoebiasis
Proximal tubule bicarbonate reclamation
Pyruvate metabolism
One carbon pool by folate
Antigen processing and presentation
TNF signaling pathway
Complement and coagulation cascades
Other types of O−glycan biosynthesis
Vitamin digestion and absorption
Gap junction
Glycine, serine and threonine metabolism
Peroxisome
Phenylalanine metabolism
Nitrogen metabolism
Primary bile acid biosynthesis
IL−17 signaling pathway
Protein.log2fc.
Tran.log2fc.
kegg

C

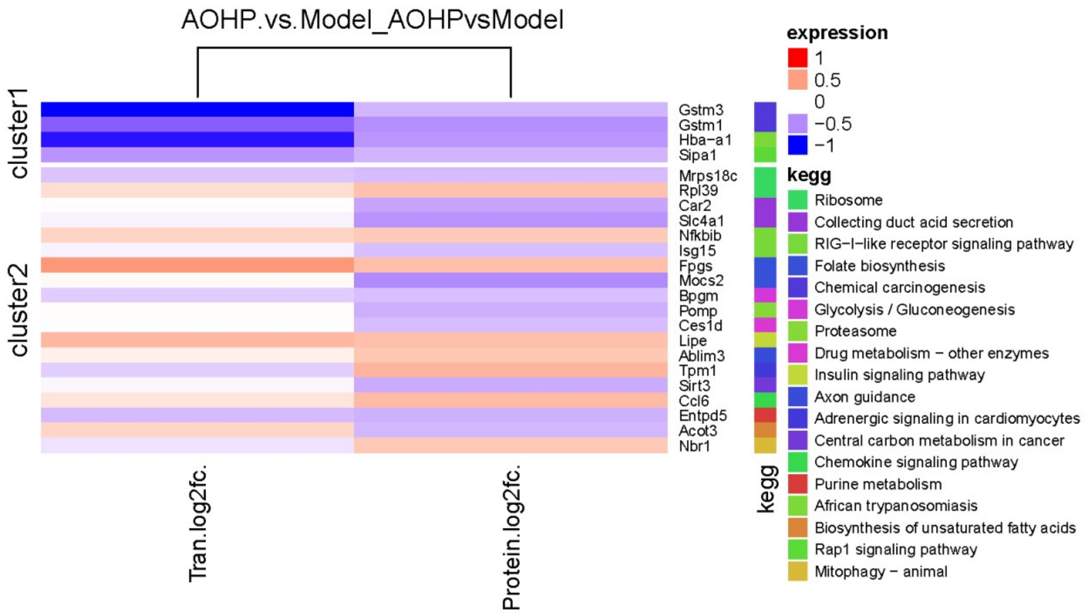

Figure S3 Heat map of KEGG pathway enrichment clustering

Note: Red in the graph represents upregulation, blue represents downregulation, and horizontal clustering is the clustering of protein expression at the transcriptome and proteome levels. A: Model vs Normal, B: AOPH vs Normal, C: AOPH vs Model.

Table S1 Significant DEGs in comparison of Model and Normal, AOPH and Model, AOPH and Normal ($p < 0.05$ and FC >2.0)

	gene_name	**log2FoldChange**	**p-value**	**gene_description**
Model vs Normal	Cyp4a12b	-6.02	6.87E-90	cytochrome P450, family 4, subfamily a, polypeptide 12B [Source:MGI Symbol;Acc:MGI:3611747]
	Abcc4	6.54	1.58E-63	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:MGI Symbol;Acc:MGI:2443111]
	Cyp2c29	4.58	5.48E-55	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI Symbol;Acc:MGI:103238]
	Cyp2b13	11.23	1.77E-50	cytochrome P450, family 2, subfamily b, polypeptide 13 [Source:MGI Symbol;Acc:MGI:88599]
	Gstm1	2.29	8.73E-50	glutathione S-transferase, mu 1 [Source:MGI Symbol;Acc:MGI:95860]
	Gsta2	3.88	6.41E-46	glutathione S-transferase, alpha 2 (Yc2) [Source:MGI Symbol;Acc:MGI:95863]
	Cbr3	6.56	1.17E-43	carbonyl reductase 3 [Source:MGI Symbol;Acc:MGI:1309992]
	Ugt1a9	3.86	2.47E-43	UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI Symbol;Acc:MGI:3576092]
	Cyp2a5	4.29	2.95E-41	cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI Symbol;Acc:MGI:88597]
	Adh6-ps1	-3.20	4.13E-40	alcohol dehydrogenase 6 (class V), pseudogene 1 [Source:MGI Symbol;Acc:MGI:1918999]
	Cyp7b1	-3.23	1.65E-39	cytochrome P450, family 7, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:104978]
	Gsta1	5.57	6.90E-39	glutathione S-transferase, alpha 1 (Ya) [Source:MGI Symbol;Acc:MGI:1095417]
	Gstm2-ps1	2.60	4.10E-36	glutathione S-transferase mu 2 (muscle), pseudogene 1 [Source:MGI Symbol;Acc:MGI:3648223]
	Cyp2a22	7.57	9.17E-36	cytochrome P450, family 2, subfamily a, polypeptide 22 [Source:MGI Symbol;Acc:MGI:3648316]
	Gstm3	3.84	2.63E-35	glutathione S-transferase, mu 3 [Source:MGI Symbol;Acc:MGI:106026]
	Acnat2	3.41	4.73E-32	acyl-coenzyme A amino acid N-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444345]
	Nqo1	3.39	3.18E-31	NAD(P)H dehydrogenase, quinone 1 [Source:MGI Symbol;Acc:MGI:103187]
	Fmo3	8.99	3.65E-30	flavin containing monooxygenase 3 [Source:MGI Symbol;Acc:MGI:1100496]
	Cyp2u1	-4.09	1.43E-29	cytochrome P450, family 2, subfamily u, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1918769]
	Cyp3a11	2.37	2.12E-27	cytochrome P450, family 3, subfamily a, polypeptide 11 [Source:MGI Symbol;Acc:MGI:88609]
	Fabp5	-4.26	2.82E-26	fatty acid binding protein 5, epidermal [Source:MGI Symbol;Acc:MGI:101790]
	Cyp2c38	2.98	5.53E-26	cytochrome P450, family 2, subfamily c, polypeptide 38 [Source:MGI Symbol;Acc:MGI:1306819]
	Cyp3a59	4.02	9.20E-26	cytochrome P450, family 3, subfamily a, polypeptide 59 [Source:MGI Symbol;Acc:MGI:3769707]
	Gstt3	3.07	1.14E-25	glutathione S-transferase, theta 3 [Source:MGI Symbol;Acc:MGI:2143526]

	Cyp39a1	2.12	1.30E-25	cytochrome P450, family 39, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1927096]
	Gsta4	2.12	2.64E-25	glutathione S-transferase, alpha 4 [Source:MGI Symbol;Acc:MGI:1309515]
	Cyp2b10	13.05	1.91E-23	cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88598]
	Cyp4a14	2.86	6.37E-23	cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI Symbol;Acc:MGI:1096550]
	Cyp4a10	2.36	6.40E-22	cytochrome P450, family 4, subfamily a, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88611]
	Cyp26a1	3.05	1.99E-20	cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1096359]
	Gm8834	2.80	6.07E-20	predicted gene 8834 [Source:MGI Symbol;Acc:MGI:3646859]
	Gstm4	2.42	2.00E-19	glutathione S-transferase, mu 4 [Source:MGI Symbol;Acc:MGI:95862]
	Cyp2c37	2.36	2.08E-19	cytochrome P450, family 2. subfamily c, polypeptide 37 [Source:MGI Symbol;Acc:MGI:1306806]
	Acss3	3.04	2.10E-18	acyl-CoA synthetase short-chain family member 3 [Source:MGI Symbol;Acc:MGI:2685720]
	Gpat3	2.45	1.44E-17	glycerol-3-phosphate acyltransferase 3 [Source:MGI Symbol;Acc:MGI:3603816]
	Abcb1a	2.71	1.77E-17	ATP-binding cassette, sub-family B (MDR/TAP), member 1A [Source:MGI Symbol;Acc:MGI:97570]
	Egfr	-2.34	2.81E-17	epidermal growth factor receptor [Source:MGI Symbol;Acc:MGI:95294]
	Cyp2c39	3.20	4.44E-15	cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI Symbol;Acc:MGI:1306818]
	Cyp26b1	3.10	3.48E-14	cytochrome P450, family 26, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:2176159]
	Srd5a1	-2.14	9.80E-13	steroid 5 alpha-reductase 1 [Source:MGI Symbol;Acc:MGI:98400]
	Cyp2a21-ps	4.61	1.16E-12	cytochrome P450, family 2, subfamily a, polypeptide 21, pseudogene [Source:MGI Symbol;Acc:MGI:3647278]
	Cyp2c55	3.42	9.92E-12	cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI Symbol;Acc:MGI:1919332]
	Hao2	4.63	1.28E-10	hydroxyacid oxidase 2 [Source:MGI Symbol;Acc:MGI:96012]
	Cyp2a4	8.59	1.87E-10	cytochrome P450, family 2, subfamily a, polypeptide 4 [Source:MGI Symbol;Acc:MGI:88596]
	Pde4d	2.37	6.03E-10	phosphodiesterase 4D, cAMP specific [Source:MGI Symbol;Acc:MGI:99555]
	Tcf24	2.64	7.63E-10	transcription factor 24 [Source:MGI Symbol;Acc:MGI:3780500]
	Acot4	2.18	3.10E-09	acyl-CoA thioesterase 4 [Source:MGI Symbol;Acc:MGI:2159621]
	Cyp2b9	9.18	3.84E-09	cytochrome P450, family 2, subfamily b, polypeptide 9 [Source:MGI Symbol;Acc:MGI:88600]
	Capn3	-2.39	4.58E-07	calpain 3 [Source:MGI Symbol;Acc:MGI:107437]

	Moxd1	-7.34	5.77E-07	monooxygenase, DBH-like 1 [Source:MGI Symbol;Acc:MGI:1921582]
	Cyp3a16	6.80	5.90E-07	cytochrome P450, family 3, subfamily a, polypeptide 16 [Source:MGI Symbol;Acc:MGI:106099]
	Acot3	3.97	5.73E-06	acyl-CoA thioesterase 3 [Source:MGI Symbol;Acc:MGI:2159619]
	Eci3	6.18	1.05E-05	enoyl-Coenzyme A delta isomerase 3 [Source:MGI Symbol;Acc:MGI:1916373]
	Capn8	-2.57	2.63E-05	calpain 8 [Source:MGI Symbol;Acc:MGI:2181366]
	Cyp4a12a	-3.87	3.57E-05	cytochrome P450, family 4, subfamily a, polypeptide 12a [Source:MGI Symbol;Acc:MGI:88612]
	Cyp2g1	2.29	6.53E-05	cytochrome P450, family 2, subfamily g, polypeptide 1 [Source:MGI Symbol;Acc:MGI:109612]
	Cyp4f39	4.40	0.000313681	cytochrome P450, family 4, subfamily f, polypeptide 39 [Source:MGI Symbol;Acc:MGI:2445210]
	Acot1	2.50	0.000532366	acyl-CoA thioesterase 1 [Source:MGI Symbol;Acc:MGI:1349396]
	Cyp3a44	5.06	0.001140132	cytochrome P450, family 3, subfamily a, polypeptide 44 [Source:MGI Symbol;Acc:MGI:2449818]
	Cyp21a1	-5.16	0.001858316	cytochrome P450, family 21, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:88591]
	Hmox1	2.74	0.002210191	heme oxygenase 1 [Source:MGI Symbol;Acc:MGI:96163]
	Aldh3b3	4.84	0.003734354	aldehyde dehydrogenase 3 family, member B3 [Source:MGI Symbol;Acc:MGI:1920708]
	Ppp1r3g	3.21	0.011020479	protein phosphatase 1, regulatory subunit 3G [Source:MGI Symbol;Acc:MGI:1923737]
	Acsl6	-4.24	0.01228847	acyl-CoA synthetase long-chain family member 6 [Source:MGI Symbol;Acc:MGI:894291]
	Scn4b	4.00	0.016415868	sodium channel, type IV, beta [Source:MGI Symbol;Acc:MGI:2687406]
	Cyp2d12	-2.10	0.020090135	cytochrome P450, family 2, subfamily d, polypeptide 12 [Source:MGI Symbol;Acc:MGI:88604]
	Gfpt2	2.04	0.02615212	glutamine fructose-6-phosphate transaminase 2 [Source:MGI Symbol;Acc:MGI:1338883]
AOPH vs Model	Gsta1	-2.12	1.73E-10	glutathione S-transferase, alpha 1 (Ya) [Source:MGI Symbol;Acc:MGI:1095417]
	Cyp4a12b	3.39	0.001742922	cytochrome P450, family 4, subfamily a, polypeptide 12B [Source:MGI Symbol;Acc:MGI:3611747]
AOPH vs Normal	Cyp2c29	3.97	8.10E-59	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI Symbol;Acc:MGI:103238]
	Gstt3	2.82	2.35E-54	glutathione S-transferase, theta 3 [Source:MGI Symbol;Acc:MGI:2143526]
	Cyp4a10	2.67	1.47E-51	cytochrome P450, family 4, subfamily a, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88611]
	Gsta2	3.28	1.45E-39	glutathione S-transferase, alpha 2 (Yc2) [Source:MGI Symbol;Acc:MGI:95863]
	Cyp4a14	2.83	1.19E-37	cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI Symbol;Acc:MGI:1096550]
	Acot2	2.71	1.15E-36	acyl-CoA thioesterase 2 [Source:MGI Symbol;Acc:MGI:2159605]

Abcc4	5.45	1.84E-32	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:MGI Symbol;Acc:MGI:2443111]
Cyp2b10	12.29	2.35E-32	cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI Symbol;Acc:MGI:88598]
Acnat2	3.66	2.55E-28	acyl-coenzyme A amino acid N-acyltransferase 2 [Source:MGI Symbol;Acc:MGI:2444345]
Cyp2a22	6.41	1.38E-27	cytochrome P450, family 2, subfamily a, polypeptide 22 [Source:MGI Symbol;Acc:MGI:3648316]
Acot1	2.64	1.83E-23	acyl-CoA thioesterase 1 [Source:MGI Symbol;Acc:MGI:1349396]
Cyp26a1	2.61	2.49E-23	cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1096359]
Cyp2c54	2.07	2.55E-23	cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI Symbol;Acc:MGI:3642960]
Cyp3a11	2.16	9.74E-23	cytochrome P450, family 3, subfamily a, polypeptide 11 [Source:MGI Symbol;Acc:MGI:88609]
Ugt1a9	2.94	1.59E-22	UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI Symbol;Acc:MGI:3576092]
Cyp7b1	-2.56	2.23E-21	cytochrome P450, family 7, subfamily b, polypeptide 1 [Source:MGI Symbol;Acc:MGI:104978]
Cyp2c38	2.72	5.70E-21	cytochrome P450, family 2, subfamily c, polypeptide 38 [Source:MGI Symbol;Acc:MGI:1306819]
Cyp2b13	10.06	2.02E-20	cytochrome P450, family 2, subfamily b, polypeptide 13 [Source:MGI Symbol;Acc:MGI:88599]
Acot4	2.12	2.26E-18	acyl-CoA thioesterase 4 [Source:MGI Symbol;Acc:MGI:2159621]
Cyp2c37	2.05	2.31E-17	cytochrome P450, family 2. subfamily c, polypeptide 37 [Source:MGI Symbol;Acc:MGI:1306806]
Nqo1	2.51	2.32E-17	NAD(P)H dehydrogenase, quinone 1 [Source:MGI Symbol;Acc:MGI:103187]
Abcd2	2.03	1.27E-16	ATP-binding cassette, sub-family D (ALD), member 2 [Source:MGI Symbol;Acc:MGI:1349467]
Acss3	2.57	7.71E-16	acyl-CoA synthetase short-chain family member 3 [Source:MGI Symbol;Acc:MGI:2685720]
Adh6-ps1	-2.29	1.66E-15	alcohol dehydrogenase 6 (class V), pseudogene 1 [Source:MGI Symbol;Acc:MGI:1918999]
Gstm3	2.49	1.75E-14	glutathione S-transferase, mu 3 [Source:MGI Symbol;Acc:MGI:106026]
Cyp2c55	2.69	6.27E-13	cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI Symbol;Acc:MGI:1919332]
Acot3	4.18	1.16E-12	acyl-CoA thioesterase 3 [Source:MGI Symbol;Acc:MGI:2159619]
Cyp2a5	3.51	1.28E-12	cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI Symbol;Acc:MGI:88597]
Cyp2c39	2.87	7.56E-12	cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI Symbol;Acc:MGI:1306818]
Gsta1	3.47	4.29E-11	glutathione S-transferase, alpha 1 (Ya) [Source:MGI Symbol;Acc:MGI:1095417]
Fabp5	-4.20	3.11E-10	fatty acid binding protein 5, epidermal [Source:MGI Symbol;Acc:MGI:101790]
Cyp2a21-ps	4.12	5.78E-10	cytochrome P450, family 2, subfamily a, polypeptide 21, pseudogene [Source:MGI

			Symbol;Acc:MGI:3647278]
Atp6v0d2	2.73	1.54E-09	ATPase, H+ transporting, lysosomal V0 subunit D2 [Source:MGI Symbol;Acc:MGI:1924415]
Cyp3a16	7.19	5.03E-08	cytochrome P450, family 3, subfamily a, polypeptide 16 [Source:MGI Symbol;Acc:MGI:106099]
Cyp2b9	8.50	5.14E-08	cytochrome P450, family 2, subfamily b, polypeptide 9 [Source:MGI Symbol;Acc:MGI:88600]
Cyp3a59	3.45	1.39E-07	cytochrome P450, family 3, subfamily a, polypeptide 59 [Source:MGI Symbol;Acc:MGI:3769707]
Cyp2a4	7.01	4.33E-06	cytochrome P450, family 2, subfamily a, polypeptide 4 [Source:MGI Symbol;Acc:MGI:88596]
Cyp2u1	-2.87	5.28E-06	cytochrome P450, family 2, subfamily u, polypeptide 1 [Source:MGI Symbol;Acc:MGI:1918769]
Cyp4a12a	-2.55	9.38E-06	cytochrome P450, family 4, subfamily a, polypeptide 12a [Source:MGI Symbol;Acc:MGI:88612]
Moxd1	-4.88	3.23E-05	monooxygenase, DBH-like 1 [Source:MGI Symbol;Acc:MGI:1921582]
Eci3	6.02	7.05E-05	enoyl-Coenzyme A delta isomerase 3 [Source:MGI Symbol;Acc:MGI:1916373]
Cyp3a44	5.59	0.000204	cytochrome P450, family 3, subfamily a, polypeptide 44 [Source:MGI Symbol;Acc:MGI:2449818]
Cyp4f39	4.05	0.001485	cytochrome P450, family 4, subfamily f, polypeptide 39 [Source:MGI Symbol;Acc:MGI:2445210]
Cyp4a12b	-2.66	0.006171	cytochrome P450, family 4, subfamily a, polypeptide 12B [Source:MGI Symbol;Acc:MGI:3611747]
Hao2	2.84	0.006412	hydroxyacid oxidase 2 [Source:MGI Symbol;Acc:MGI:96012]
Acsl6	-3.36	0.036752	acyl-CoA synthetase long-chain family member 6 [Source:MGI Symbol;Acc:MGI:894291]
Aldh3b3	4.04	0.045571	aldehyde dehydrogenase 3 family, member B3 [Source:MGI Symbol;Acc:MGI:1920708]
Mrps36-ps2	-2.71	0.046408	mitochondrial ribosomal protein S36, pseudogene 2 [Source:MGI Symbol;Acc:MGI:3704298]

Table S2 The results of DEPs KEGG-enrichment in comparison of Model and Normal, AOPH and Model, AOPH and Normal (*p* < 0.05 and FC >2.0)

Description	Gene name	Up	Down

Model vs Normal	Drug metabolism-cytochrome P450	Gstm1/Gsta2/Ugt1a9/Gsta1/Gstm3/Fmo3/Gstt3/Gsta4/Gstm4/Ugt1a1/Mgst3/Aox3/Aox1/Gsta3/Fmo1/Ugt2b35/Fmo5/Maoa/Adh4/Gstp1/Gstm2/Aldh3b1/Cyp2e1/Ugt2b37/Gstm6/Adh1/Ugt2b38/Maob/Cyp1a2/Ugt2b34/Adh7/Ugt2b1/Gsto1/Ugt1a6b/Aldh3b3/Gstm5/Hpgds/Mgst1/Fmo4/Ugt1a5	30	10
	Steroid hormone biosynthesis	Hsd3b5/Cyp2c29/Cyp2b13/Ugt1a9/Cyp7b1/Cyp3a11/Cyp2c38/Cyp2b10/Cyp2c37/Ugt1a1/Hsd3b2/Cyp2c50/Cyp3a13/Cyp2c39/Srd5a1/Cyp2c54/Cyp2c55/Hsd17b2/Cyp2b9/Cyp3a16/Cyp3a25/Cyp2c23/Ugt2b35/Cyp17a1/Akr1d1/Ugt2b37/Ugt2b38/Cyp2d9/Cyp2d40/Cyp1a2/Ugt2b34/Cyp3a44/Ugt2b1/Cyp21a1/Ugt1a6b/Hsd11b1/Hsd17b6/Cyp2c68/Cyp2d12/Cyp2c70/Ugt1a5/Srd5a2	26	16
	Drug metabolism-other enzymes	Gstm1/Gsta2/Ugt1a9/Gsta1/Gstm3/Gstt3/Gsta4/Gstm4/Ces1d/Ugt1a1/Mgst3/Gsta3/Ces2b/Ugt2b35/Dpys/Dpyd/Gstp1/Gstm2/Ugt2b37/Gstm6/Gusb/Ugt2b38/Ces1f/Ces2c/Ugt2b34/Nme6/Ces1c/Ugt2b1/Ces2e/Ces2h/Gsto1/Ugt1a6b/Nme1/Umps/Gstm5/Impdh2/Ces2a/Xdh/Dut/Mgst1/Ces1e/Ugt1a5/Uck2/Rrm2b	29	15
	PPAR signaling pathway	Cyp4a12b/Cd36/Fabp5/Cyp4a14/Cyp4a10/Fabp1/Pparg/Fabp4/Dbi/Acaa1b/Ppara/Scp2/Sorbs1/Scd2/Ehhadh/Fabp2/Slc27a1/Apoa1/Ubc/Cyp4a12a/Plin4/Plin5/Acox3/Lpl/Slc27a5/Pdpk1/Apoa5/Acadm/Acsl4/Acox1/Acsl6/Scd1/Hmgcs1/Nr1h3/Acox2/Pck2/Apoa2	21	16
	Peroxisome	Nudt7/Idh2/Abcd2/Hao1/Hao2/Acaa1b/Scp2/Ehhadh/Eci3/Pex10/Pex11b/Acox3/Pex11a/Prdx5/Amacr/Pex12/Mlycd/Pex26/Crat/Abcd1/Pex6/Pex1/Abcd3/Pex7/Acsl4/Agxt/Acox1/Acsl6/Xdh/Far1/Far2/Pex11g/Phyh/Baat/Paox/Acox2/Decr2	17	20
	Glutathione metabolism	Gstm1/Gsta2/Gsta1/Gstm3/Gstt3/Gsta4/Idh2/Gstm4/Mgst3/Gsta3/Nat8f1/Gclc/Nat8/Gstp1/Gstm2/Gsr/Gstm6/Ggt6/Chac2/Gsto1/Pgd/Gstm5/Hpgds/Ggt5/Srm/Gpx4/Mgst1/Gclm/Rrm2b	21	8
	Linoleic acid metabolism	Cyp2c29/Cyp3a11/Cyp2c38/Cyp2c37/Cyp2c50/Cyp3a13/Cyp2c39/Cyp2c54/Cyp2c55/Cyp3a16/Cyp3a25/Cyp2c23/Cyp1a2/Cyp3a44/Cyp2c68/Cyp2c70/Cyp2j6/Pla2g12a	15	3
	Oxidative phosphorylation	Atp6v0d2/Atp4a/mt-Nd5/Atp6v1b2/Ndufb3/Ndufs7/Ndufa8/Ndufa12/Atp6v1a/Uqcr11/Lhpp/mt-Nd6/Cox5b/mt-Cytb/Atp5e/Atp5b/Ndufv3/Ndufb2/Ndufb7/Sdha/Ndufs8/Cox7a2/Cox6b1/Cox8a/mt-Nd4/Ndufb10/Atp5a1/Atp6v1g1/Ndufa11/Atp5k/Uqcrq/Cox6a1/Uqcrb/Atp5o/Ndufa5/Atp6v0e/Ndufa13/Ndufs5/Ndufa6/Ndufa1/Atp5j/Cox7c/Atp6v1f/Atp5j2/Ndufa3/Ndufs1/mt-Atp6/Uqcr10/Ndufb4/Ndufs4	9	41
AOPH vs	Drug metabolism - cytochrome P450	Gsta1/Fmo2/Gstm2/Ugt1a9/Gsta2/Gstm4/Fmo3/Aox1/Ugt1a1/Ugt2b38/Gstp1/Gstm1/Gstm3/Cyp1a2	1	13

Model	Glutathione metabolism	Gsta1/Gstm2/Gsta2/Gstm4/Nat8/Pgd/Nat8f2/Gstp1/Gstm1/Gstm3/Odc1/Nat8f1	4	8
	Drug metabolism - other enzymes	Gsta1/Gstm2/Upp2/Ugt1a9/Gsta2/Gstm4/Tymp/Ugt1a1/Xdh/Cda/Ugt2b38/Gstp1/Gstm1/Gstm3	3	11
	Steroid hormone biosynthesis	Cyp2b9/Hsd17b6/Ugt1a9/Hsd17b2/Ugt1a1/Cyp17a1/Cyp7b1/Ugt2b38/Cyp2c29/Cyp1a2/Cyp2b13	2	9
	PPAR signaling pathway	Me1/Cyp4a12b/Plin2/Sorbs1/Cyp4a31/Cyp4a32/Plin4/Ppara/Acsl3/Rxrg	6	4
AOPH vs Normal	Drug metabolism - cytochrome P450	Gstt3/Gsta2/Ugt1a9/Gsta4/Gsta3/Gstm3/Aox3/Ugt2b38/Ugt1a1/Gsta1/Gstm6/Gstm4/Gstm1/Mgst3/Fmo1/Fmo3/Ugt2b35/Adh1/Gstm5/Ugt2b37/Maoa/Fmo5/Gsto1/Aox1/Adh4/Maob/Adh7/Gstm7/Fmo2/Ugt2b1/Gstp1/Gstt1/Fmo4/Ugt2b34/Gstk1/Aldh3b3	27	9
	PPAR signaling pathway	Cyp4a10/Cyp4a14/Cd36/Ehhadh/Fabp5/Ubc/Fabp4/Fabp1/Slc27a1/Ppara/Pparg/Acaa1b/Plin5/Plin2/Cyp4a12a/Acox1/Rxrg/Slc27a5/Scp2/Apoa1/Acox3/Apoa5/Lpl/Gk/Plin4/Scd2/Cyp4a32/Dbi/Sorbs1/Acadm/Cyp4a12b/Cpt2/Acsl4/Fabp2/Fads2/Cyp4a31/Acsl3/Hmgcs1/Acox2/Acsl6	26	14
	Drug metabolism - other enzymes	Gstt3/Gsta2/Ugt1a9/Gsta4/Ces1d/Gsta3/Gstm3/Ugt2b38/Ugt1a1/Gsta1/Gstm6/Ces2b/Gstm4/Gstm1/Mgst3/Dpyd/Ugt2b35/Gstm5/Ugt2b37/Dpys/Umps/Ces2a/Gsto1/Gstm7/Ces1f/Impdh2/Ces2e/Ces2c/Ugt2b1/Gstp1/Cda/Nme6/Gstt1/Nme1/Dut/Ugt2b34/Upp2/Ces1e/Ces1c/Ces2h	25	15
	Steroid hormone biosynthesis	Cyp2c29/Cyp2b10/Cyp2c50/Cyp2c54/Cyp3a11/Ugt1a9/Cyp7b1/Cyp3a13/Cyp2c38/Cyp2b13/Cyp2c37/Ugt2b38/Cyp2c55/Cyp2c39/Ugt1a1/Hsd17b6/Srd5a1/Cyp3a16/Cyp2b9/Hsd3b2/Cyp3a25/Hsd3b5/Akr1d1/Cyp2c23/Ugt2b35/Ugt2b37/Cyp3a44/Hsd17b2/Cyp2d40/Hsd11b1/Ugt2b1/Comt/Cyp2d9/Cyp2d12/Ugt2b34/Cyp17a1	22	14
	Fatty acid degradation	Cyp4a10/Cyp4a14/Ehhadh/Aldh1b1/Acaa1b/Cyp4a12a/Acox1/Adh1/Eci3/Aldh3a2/Acox3/Cyp4a32/Adh4/Hadh/Acadvl/Adh7/Acadm/Cyp4a12b/Cpt2/Acsl4/Cyp4a31/Acsl3/Gcdh/Acsl6	17	7
	Glutathione metabolism	Gstt3/Gsta2/Gsta4/Gsta3/Gstm3/Idh2/Gsta1/Nat8f1/Gstm6/Gstm4/Gstm1/Mgst3/Ggt6/Gstm5/Chac2/Gclc/Gsto1/Gstm7/Srm/Gstp1/Ggt5/Gstt1/Gpx4/Lap3/Gsr/Oplah/Gstk1	20	7
	Peroxisome	Ehhadh/Abcd2/Nudt7/Idh2/Crat/Hao1/Pex11a/Acaa1b/Pex10/Acox1/Pex1/Eci3/Agxt/Scp2/Acox3/Abcd3/Hacl1/Pex12/Mvk/Pex26/Hao2/Prdx5/Far2/Acsl4/Acsl3/Pex6/Pex11b/Pex7/Paox/Pex13/Pex11g/Acox2/Acsl6/Gstk1	18	16

	Oxidative phosphorylation	Atp6v0d2/mt-Nd4l/Ndufa8/mt-Nd5/Lhpp/mt-Nd6/Atp6v1b2/mt-Co3/Ndufs7/Ndufb3/Ndufb2/Atp4a/Uqcr11/Ndufs8/Ndufv3/Cox5b/mt-Nd4/mt-Co2/mt-Cytb/Cox6a1/Cox7a2/Atp5o/Ndufs5/Tcirg1/Ndufb10/Ndufa11/Ndufa13/Ndufb7/Cox8a/Atp6v0e/Ndufa6/Atp5b/Atp5e/Atp6v1a/Uqcrq/Ndufa1/Atp6v1f/Atp5a1/Atp5j/mt-Nd2/Atp6v1g1/Ndufb6/mt-Co1/Cox6b1/Atp5g1	7	38

Table S3 The results of DAPs GO-enrichment in comparison of Model and Normal, AOPH and Model, AOPH and Normal ($p < 0.05$ and FC > 2.0)

GO_Term	GO_Class	Model vs Normal		AOPH vs Model		AOPH vs Normal	
		Up	Down	Up	Down	Up	Down
Oxidation-reduction process	BP	54	22	/	/	35	20
Single-organism metabolic process	BP	66	37	/	/	43	36
Metabolic process	BP	110	76	/	/	83	60
Tricarboxylic acid cycle	BP	3	0	/	/	/	/
Single-organism process	BP	83	49	/	/	62	46
Steroid biosynthetic process	BP	2	2	/	/	2	2
Isocitrate metabolic process	BP	1	1	/	/	/	/
Oxygen transport	BP	2	0	0	2	/	/
Small molecule catabolic process	BP	6	1	/	/	/	/
Organic acid catabolic process	BP	6	0	/	/	/	/
NAD biosynthetic process	BP	0	2	/	/	0	2
Small molecule metabolic process	BP	17	13	/	/	12	18

Coenzyme metabolic process	BP	/	/	1	2	/	/
Mo-molybdopterin cofactor biosynthetic process	BP	/	/	0	1	/	/
Coenzyme biosynthetic process	BP	/	/	1	1	/	/
Single-organism catabolic process	BP	/	/	2	1	7	3
Cholesterol metabolic process	BP	/	/	1	0	2	0
Folic acid-containing compound biosynthetic process	BP	/	/	1	0	/	/
Lipid catabolic process	BP	/	/	1	0	5	0
Steroid metabolic process	BP	/	/	/	/	3	2
Organic acid metabolic process	BP	/	/	/	/	10	9
Cholesterol homeostasis	BP	/	/	/	/	1	1
Alcohol catabolic process	BP	/	/	/	/	1	1
Iron ion binding	MF	25	4	0	3	17	2
Tetrapyrrole binding	MF	25	2	/	/	17	2
Heme binding	MF	24	2	0	3	16	1
Oxidoreductase activity	MF	38	13	/	/	27	15
Cofactor binding	MF	19	7	/	/	11	7
Monooxygenase activity	MF	11	1	0	1	10	1
Catalytic activity	MF	96	71	/	/	74	61
Transition metal ion binding	MF	31	11	2	4	25	5
Anion binding	MF	7	5	/	/	4	3
Glutathione transferase activity	MF	5	1	0	1	4	1
Transferase activity, transferring alkyl or aryl (other than methyl) groups	MF	6	1	/	/	5	1

Coenzyme binding	MF	13	2	/	/	7	4
Ion binding	MF	43	26	/	/	/	/
Oxidoreductase activity, acting on CH-OH group of donors	MF	4	4	/	/	1	5
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MF	4	1	/	/	3	1
Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	MF	4	3	/	/	1	4
Isocitrate dehydrogenase (NADP+) activity	MF	1	1	/	/	/	/
Metal ion binding	MF	38	23	4	5	/	/
FMN binding	MF	1	1	/	/	1	1
Oxygen binding	MF	2	0	0	2	/	/
Intramolecular transferase activity	MF	/	/	0	2	/	/
Thiol oxidase activity	MF	/	/	0	1	/	/
Lipid binding	MF	/	/	0	2	/	/
Oxidoreductase activity, acting on the CH-NH group of donors	MF	/	/	/	/	2	1
Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	MF	/	/	/	/	3	0

Hemoglobin complex	CC	2	0	0	2	/	/

Note: a) GO_Term: description of GO identification number function; b) GO_Class: GO category (BP (Biological Process), MF(Molecular Function), CC (Cell Component)); c) Up: the number of up-regulated proteins, Down: the number of down-regulated proteins. d) All results were selected based on *p* value < 0.05 and correlation with oxidative metabolism.

Table S4 The results of DAPs KEGG-enrichment in comparison of Model and Normal, AOPH and Model, AOPH and Normal ($p < 0.05$ and log2 fold change >2.0)

Group	MapTitle	*p*-value	counts	Description
Model vs Normal	Retinol metabolism	3.31E-20	23	aldehyde oxidase 3 [Source:MGI SymbolAcc:MGI:1918974]
				cytochrome P450, family 2, subfamily a, polypeptide 12 [Source:MGI SymbolAcc:MGI:105055]
				cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI SymbolAcc:MGI:103238]
				cytochrome P450, family 1, subfamily a, polypeptide 2 [Source:MGI SymbolAcc:MGI:88589]
				cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI SymbolAcc:MGI:3642960]
				alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929]
				retinol saturase (all trans retinol 13,14 reductase) [Source:MGI SymbolAcc:MGI:1914692]
				cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI SymbolAcc:MGI:88597]
				cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI SymbolAcc:MGI:88610]
				cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI SymbolAcc:MGI:1096550]
				cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI SymbolAcc:MGI:88598]
				UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962]
				UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092]
				UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]
				cytochrome P450, family 2, subfamily b, polypeptide 23 [Source:MGI SymbolAcc:MGI:3646735]
				cytochrome P450, family 4, subfamily a, polypeptide 32 [Source:MGI SymbolAcc:MGI:3717148]

			cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI SymbolAcc:MGI:1306818] cytochrome P450, family 2, subfamily c, polypeptide 38 [Source:MGI SymbolAcc:MGI:1306819] cytochrome P450, family 3, subfamily a, polypeptide 25 [Source:MGI SymbolAcc:MGI:1930638] cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI SymbolAcc:MGI:1919332] cytochrome P450, family 2, subfamily c, polypeptide 65 [Source:MGI SymbolAcc:MGI:1919553] cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:1096359] aldehyde oxidase 2 [Source:MGI SymbolAcc:MGI:3529596]
Metabolic pathways	3.31E-16	133	fatty acid synthase [Source:MGI SymbolAcc:MGI:95485] liver glycogen phosphorylase [Source:MGI SymbolAcc:MGI:97829] aldehyde oxidase 3 [Source:MGI SymbolAcc:MGI:1918974] epoxide hydrolase 2, cytoplasmic [Source:MGI SymbolAcc:MGI:99500] aminoadipate-semialdehyde synthase [Source:MGI SymbolAcc:MGI:1353573] 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Source:MGI SymbolAcc:MGI:101939] oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI SymbolAcc:MGI:1098267] sterol carrier protein 2, liver [Source:MGI SymbolAcc:MGI:98254] propionyl-Coenzyme A carboxylase, alpha polypeptide [Source:MGI SymbolAcc:MGI:97499] ATP citrate lyase [Source:MGI SymbolAcc:MGI:103251] aconitase 1 [Source:MGI SymbolAcc:MGI:87879] acetyl-Coenzyme A acyltransferase 1B [Source:MGI SymbolAcc:MGI:3605455] carboxylesterase 1D [Source:MGI SymbolAcc:MGI:2148202] UDP-glucose pyrophosphorylase 2 [Source:MGI SymbolAcc:MGI:2183447] isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI SymbolAcc:MGI:96413] cytochrome P450, family 2, subfamily a, polypeptide 12 [Source:MGI SymbolAcc:MGI:105055] cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI SymbolAcc:MGI:103238] UDP-glucose dehydrogenase [Source:MGI SymbolAcc:MGI:1306785]

	cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607]
	fumarylacetoacetate hydrolase [Source:MGI SymbolAcc:MGI:95482]
	glycine decarboxylase [Source:MGI SymbolAcc:MGI:1341155]
	cytochrome P450, family 1, subfamily a, polypeptide 2 [Source:MGI SymbolAcc:MGI:88589]
	propionyl Coenzyme A carboxylase, beta polypeptide [Source:MGI SymbolAcc:MGI:1914154]
	lactate dehydrogenase A [Source:MGI SymbolAcc:MGI:96759]
	4-aminobutyrate aminotransferase [Source:MGI SymbolAcc:MGI:2443582]
	regucalcin [Source:MGI SymbolAcc:MGI:108024]
	methionine adenosyltransferase I, alpha [Source:MGI SymbolAcc:MGI:88017]
	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:MGI SymbolAcc:MGI:96414]
	cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI SymbolAcc:MGI:3642960]
	ornithine aminotransferase [Source:MGI SymbolAcc:MGI:97394]
	acyl-CoA synthetase medium-chain family member 5 [Source:MGI SymbolAcc:MGI:2444086]
	alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929]
	aldehyde dehydrogenase 1 family, member B1 [Source:MGI SymbolAcc:MGI:1919785]
	proline dehydrogenase [Source:MGI SymbolAcc:MGI:97770]
	aldehyde dehydrogenase family 3, subfamily A2 [Source:MGI SymbolAcc:MGI:1353452]
	aldo-keto reductase family 1, member D1 [Source:MGI SymbolAcc:MGI:2384785]
	solute carrier family 27 (fatty acid transporter), member 5 [Source:MGI SymbolAcc:MGI:1347100]
	hydroxyacyl-Coenzyme A dehydrogenase [Source:MGI SymbolAcc:MGI:96009]
	monoamine oxidase B [Source:MGI SymbolAcc:MGI:96916]
	aldhehyde dehydrogenase family 5, subfamily A1 [Source:MGI SymbolAcc:MGI:2441982]
	glutaminase 2 (liver, mitochondrial) [Source:MGI SymbolAcc:MGI:2143539]
	cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI SymbolAcc:MGI:88597]
	glutaryl-Coenzyme A dehydrogenase [Source:MGI SymbolAcc:MGI:104541]
	glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:MGI SymbolAcc:MGI:1915391]

	glycogen synthase 2 [Source:MGI SymbolAcc:MGI:2385254]
	cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI SymbolAcc:MGI:88610]
	serine dehydratase [Source:MGI SymbolAcc:MGI:98270]
	biliverdin reductase B (flavin reductase (NADPH)) [Source:MGI SymbolAcc:MGI:2385271]
	3-hydroxyanthranilate 3,4-dioxygenase [Source:MGI SymbolAcc:MGI:1349444]
	cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI SymbolAcc:MGI:1096550]
	cystathionine beta-synthase [Source:MGI SymbolAcc:MGI:88285]
	3-hydroxy-3-methylglutaryl-Coenzyme A lyase [Source:MGI SymbolAcc:MGI:96158]
	carboxylesterase 1C [Source:MGI SymbolAcc:MGI:95420]
	cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI SymbolAcc:MGI:88598]
	3-hydroxyisobutyrate dehydrogenase [Source:MGI SymbolAcc:MGI:1889802]
	catechol-O-methyltransferase [Source:MGI SymbolAcc:MGI:88470]
	predicted gene 20390 [Source:MGI SymbolAcc:MGI:5141855]
	UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962]
	carbonyl reductase 1 [Source:MGI SymbolAcc:MGI:88284]
	cysteine sulfinic acid decarboxylase [Source:MGI SymbolAcc:MGI:2180098]
	proline dehydrogenase (oxidase) 2 [Source:MGI SymbolAcc:MGI:1929093]
	hydroxysteroid 11-beta dehydrogenase 1 [Source:MGI SymbolAcc:MGI:103562]
	malate dehydrogenase 1, NAD (soluble) [Source:MGI SymbolAcc:MGI:97051]
	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:MGI SymbolAcc:MGI:1913304]
	UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092]
	acyl-CoA thioesterase 3 [Source:MGI SymbolAcc:MGI:2159619]
	phosphate cytidylyltransferase 2, ethanolamine [Source:MGI SymbolAcc:MGI:1915921]
	acyl-CoA thioesterase 4 [Source:MGI SymbolAcc:MGI:2159621]
	quinolinate phosphoribosyltransferase [Source:MGI SymbolAcc:MGI:1914625]
	phosphoglucomutase 3 [Source:MGI SymbolAcc:MGI:97566]

	hydroxyacid oxidase 1, liver [Source:MGI SymbolAcc:MGI:96011]
	acyl-CoA synthetase short-chain family member 3 [Source:MGI SymbolAcc:MGI:2685720]
	4-hydroxy-2-oxoglutarate aldolase 1 [Source:MGI SymbolAcc:MGI:1914682]
	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) [Source:MGI SymbolAcc:MGI:105124]
	spermidine synthase [Source:MGI SymbolAcc:MGI:102690]
	adenylosuccinate synthetase like 1 [Source:MGI SymbolAcc:MGI:87947]
	carbonyl reductase 3 [Source:MGI SymbolAcc:MGI:1309992]
	hydroxylysine kinase 1 [Source:MGI SymbolAcc:MGI:2443139]
	aminomethyltransferase [Source:MGI SymbolAcc:MGI:3646700]
	ureidopropionase, beta [Source:MGI SymbolAcc:MGI:2143535]
	glutamine fructose-6-phosphate transaminase 1 [Source:MGI SymbolAcc:MGI:95698]
	UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]
	galactose-4-epimerase, UDP [Source:MGI SymbolAcc:MGI:1921496]
	cytochrome P450, family 2, subfamily b, polypeptide 23 [Source:MGI SymbolAcc:MGI:3646735]
	cytochrome P450, family 4, subfamily a, polypeptide 32 [Source:MGI SymbolAcc:MGI:3717148]
	inositol (myo)-1(or 4)-monophosphatase 1 [Source:MGI SymbolAcc:MGI:1933158]
	2,3-bisphosphoglycerate mutase [Source:MGI SymbolAcc:MGI:1098242]
	GDP-mannose pyrophosphorylase B [Source:MGI SymbolAcc:MGI:2660880]
	cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI SymbolAcc:MGI:1306818]
	heme oxygenase 1 [Source:MGI SymbolAcc:MGI:96163]
	glucose-6-phosphatase, catalytic [Source:MGI SymbolAcc:MGI:95607]
	asparagine-linked glycosylation 5 (dolichyl-phosphate beta-glucosyltransferase) [Source:MGI SymbolAcc:MGI:1913498]
	monoamine oxidase A [Source:MGI SymbolAcc:MGI:96915]
	mevalonate kinase [Source:MGI SymbolAcc:MGI:107624]

	24-dehydrocholesterol reductase [Source:MGI SymbolAcc:MGI:1922004]
	N-acetylneuraminic acid synthase (sialic acid synthase) [Source:MGI SymbolAcc:MGI:2149820]
	phosphoglycolate phosphatase [Source:MGI SymbolAcc:MGI:1914328]
	cytochrome P450, family 2, subfamily c, polypeptide 38 [Source:MGI SymbolAcc:MGI:1306819]
	serine racemase [Source:MGI SymbolAcc:MGI:1351636]
	aminolevulinic acid synthase 1 [Source:MGI SymbolAcc:MGI:87989]
	GDP-mannose pyrophosphorylase A [Source:MGI SymbolAcc:MGI:1916330]
	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 [Source:MGI SymbolAcc:MGI:1332236]
	oxoglutarate dehydrogenase-like [Source:MGI SymbolAcc:MGI:3616088]
	betaine-homocysteine methyltransferase 2 [Source:MGI SymbolAcc:MGI:1891379]
	adenosine deaminase [Source:MGI SymbolAcc:MGI:87916]
	urate (5-hydroxyiso-) hydrolase [Source:MGI SymbolAcc:MGI:1916142]
	nicotinamide N-methyltransferase [Source:MGI SymbolAcc:MGI:1099443]
	tyrosine aminotransferase [Source:MGI SymbolAcc:MGI:98487]
	predicted gene 15294 [Source:MGI SymbolAcc:MGI:3708114]
	cytochrome P450, family 3, subfamily a, polypeptide 25 [Source:MGI SymbolAcc:MGI:1930638]
	NAD synthetase 1 [Source:MGI SymbolAcc:MGI:1926164]
	glucosidase, beta, acid [Source:MGI SymbolAcc:MGI:95665]
	mannose phosphate isomerase [Source:MGI SymbolAcc:MGI:97075]
	amino carboxymuconate semialdehyde decarboxylase [Source:MGI SymbolAcc:MGI:2386323]
	3-ketodihydrosphingosine reductase [Source:MGI SymbolAcc:MGI:1918000]
	sphingomyelin phosphodiesterase 2, neutral [Source:MGI SymbolAcc:MGI:1278330]
	cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI SymbolAcc:MGI:1919332]
	cytochrome P450, family 2, subfamily j, polypeptide 6 [Source:MGI SymbolAcc:MGI:1270148]
	acid phosphatase 5, tartrate resistant [Source:MGI SymbolAcc:MGI:87883]

				glycogenin [Source:MGI SymbolAcc:MGI:1351614] cytochrome P450, family 17, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:88586] GDP-mannose 4, 6-dehydratase [Source:MGI SymbolAcc:MGI:1891112] cytochrome P450, family 2, subfamily c, polypeptide 65 [Source:MGI SymbolAcc:MGI:1919553] folylpolyglutamyl synthetase [Source:MGI SymbolAcc:MGI:95576] alkaline phosphatase, liver/bone/kidney [Source:MGI SymbolAcc:MGI:87983] 1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:MGI SymbolAcc:MGI:3603816] asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase) [Source:MGI SymbolAcc:MGI:1924753] cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:1096359] choline kinase alpha [Source:MGI SymbolAcc:MGI:107760]aldehyde oxidase 2 [Source:MGI SymbolAcc:MGI:3529596] cytochrome P450, family 2, subfamily u, polypeptide 1 [Source:MGI SymbolAcc:MGI:1918769] aminolevulinic acid synthase 2, erythroid [Source:MGI SymbolAcc:MGI:87990] C1GALT1-specific chaperone 1 [Source:MGI SymbolAcc:MGI:1913493] 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) [Source:MGI SymbolAcc:MGI:1196345]
	Drug metabolism - cytochrome P450	4.88E-11	21	aldehyde oxidase 3 [Source:MGI SymbolAcc:MGI:1918974] cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] cytochrome P450, family 1, subfamily a, polypeptide 2 [Source:MGI SymbolAcc:MGI:88589] alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929] flavin containing monooxygenase 1 [Source:MGI SymbolAcc:MGI:1310002] monoamine oxidase B [Source:MGI SymbolAcc:MGI:96916] glutathione S-transferase, mu 2 [Source:MGI SymbolAcc:MGI:95861] glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862]

			glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026] UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962] UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526] UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100] glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515] monoamine oxidase A [Source:MGI SymbolAcc:MGI:96915] flavin containing monooxygenase 2 [Source:MGI SymbolAcc:MGI:1916776] flavin containing monooxygenase 3 [Source:MGI SymbolAcc:MGI:1100496] microsomal glutathione S-transferase 3 [Source:MGI SymbolAcc:MGI:1913697] aldehyde oxidase 2 [Source:MGI SymbolAcc:MGI:3529596]
	Metabolism of xenobiotics by cytochrome P450	3.56E-09	18	cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] cytochrome P450, family 1, subfamily a, polypeptide 2 [Source:MGI SymbolAcc:MGI:88589] epoxide hydrolase 1, microsomal [Source:MGI SymbolAcc:MGI:95405] alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929] glutathione S-transferase, mu 2 [Source:MGI SymbolAcc:MGI:95861] glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862] glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026] UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962] carbonyl reductase 1 [Source:MGI SymbolAcc:MGI:88284] hydroxysteroid 11-beta dehydrogenase 1 [Source:MGI SymbolAcc:MGI:103562] UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526]

				carbonyl reductase 3 [Source:MGI SymbolAcc:MGI:1309992] UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100] glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515] microsomal glutathione S-transferase 3 [Source:MGI SymbolAcc:MGI:1913697]
	Glutathione metabolism	6.28E-05	12	isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI SymbolAcc:MGI:96413] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:MGI SymbolAcc:MGI:96414] glutathione S-transferase, mu 2 [Source:MGI SymbolAcc:MGI:95861] glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862] glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860] glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526] spermidine synthase [Source:MGI SymbolAcc:MGI:102690] glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515] N-acetyltransferase 8 (GCN5-related) family member 1 [Source:MGI SymbolAcc:MGI:1913366] microsomal glutathione S-transferase 3 [Source:MGI SymbolAcc:MGI:1913697]
	PPAR signaling pathway	0.002262266	12	sterol carrier protein 2, liver [Source:MGI SymbolAcc:MGI:98254] acetyl-Coenzyme A acyltransferase 1B [Source:MGI SymbolAcc:MGI:3605455] carnitine palmitoyltransferase 2 [Source:MGI SymbolAcc:MGI:109176] solute carrier family 27 (fatty acid transporter), member 5 [Source:MGI SymbolAcc:MGI:1347100] cytochrome P450, family 4, subfamily a, polypeptide 14 [Source:MGI SymbolAcc:MGI:1096550] fatty acid binding protein 5, epidermal [Source:MGI SymbolAcc:MGI:101790] cytochrome P450, family 4, subfamily a, polypeptide 32 [Source:MGI SymbolAcc:MGI:3717148] fatty acid binding protein 2, intestinal [Source:MGI SymbolAcc:MGI:95478] apolipoprotein A-II [Source:MGI SymbolAcc:MGI:88050] CD36 antigen [Source:MGI SymbolAcc:MGI:107899]

				apolipoprotein C-III [Source:MGI SymbolAcc:MGI:88055] adiponectin, C1Q and collagen domain containing [Source:MGI SymbolAcc:MGI:106675]
AOPH vs Model	Glutathione metabolism	0.008966	2	glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026] glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
	Metabolism of xenobiotics by cytochrome P450	0.014253457		
	Drug metabolism - cytochrome P450	0.015678866		
	Fatty acid elongation	0.029847386	1	acyl-CoA thioesterase 3 [Source:MGI SymbolAcc:MGI:2159619]
	Biosynthesis of unsaturated fatty acids	0.044784504		
AOPH vs Normal	Metabolic pathways	4.80E-15	104	fatty acid synthase [Source:MGI SymbolAcc:MGI:95485] liver glycogen phosphorylase [Source:MGI SymbolAcc:MGI:97829] aldehyde oxidase 3 [Source:MGI SymbolAcc:MGI:1918974] epoxide hydrolase 2, cytoplasmic [Source:MGI SymbolAcc:MGI:99500] aminoadipate-semialdehyde synthase [Source:MGI SymbolAcc:MGI:1353573] oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) [Source:MGI SymbolAcc:MGI:1098267] sterol carrier protein 2, liver [Source:MGI SymbolAcc:MGI:98254] aconitase 1 [Source:MGI SymbolAcc:MGI:87879] isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI SymbolAcc:MGI:96413] cytochrome P450, family 2, subfamily a, polypeptide 12 [Source:MGI SymbolAcc:MGI:105055] cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI SymbolAcc:MGI:103238] UDP-glucose dehydrogenase [Source:MGI SymbolAcc:MGI:1306785] cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607] malic enzyme 1, NADP(+)-dependent, cytosolic [Source:MGI SymbolAcc:MGI:97043]

		pyruvate kinase liver and red blood cell [Source:MGI SymbolAcc:MGI:97604]
		lactate dehydrogenase A [Source:MGI SymbolAcc:MGI:96759]
		regucalcin [Source:MGI SymbolAcc:MGI:108024]
		methionine adenosyltransferase I, alpha [Source:MGI SymbolAcc:MGI:88017]
		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:MGI SymbolAcc:MGI:96414]
		cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI SymbolAcc:MGI:3642960]
		ornithine aminotransferase [Source:MGI SymbolAcc:MGI:97394]
		alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929]
		aldehyde dehydrogenase 1 family, member B1 [Source:MGI SymbolAcc:MGI:1919785]
		histidine ammonia lyase [Source:MGI SymbolAcc:MGI:96010]
		proline dehydrogenase [Source:MGI SymbolAcc:MGI:97770]
		aldehyde dehydrogenase family 3, subfamily A2 [Source:MGI SymbolAcc:MGI:1353452]
		solute carrier family 27 (fatty acid transporter), member 5 [Source:MGI SymbolAcc:MGI:1347100]
		monoamine oxidase B [Source:MGI SymbolAcc:MGI:96916]
		glutaminase 2 (liver, mitochondrial) [Source:MGI SymbolAcc:MGI:2143539]
		cytochrome P450, family 2, subfamily a, polypeptide 5 [Source:MGI SymbolAcc:MGI:88597]
		glutamic pyruvate transaminase (alanine aminotransferase) 2 [Source:MGI SymbolAcc:MGI:1915391]
		glycogen synthase 2 [Source:MGI SymbolAcc:MGI:2385254]
		cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI SymbolAcc:MGI:88610]
		serine dehydratase [Source:MGI SymbolAcc:MGI:98270]
		biliverdin reductase B (flavin reductase (NADPH)) [Source:MGI SymbolAcc:MGI:2385271]
		3-hydroxyanthranilate 3,4-dioxygenase [Source:MGI SymbolAcc:MGI:1349444]
		cystathionine beta-synthase [Source:MGI SymbolAcc:MGI:88285]
		cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI SymbolAcc:MGI:88598]
		catechol-O-methyltransferase [Source:MGI SymbolAcc:MGI:88470]
		predicted gene 20390 [Source:MGI SymbolAcc:MGI:5141855]

	UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962]
	carbonyl reductase 1 [Source:MGI SymbolAcc:MGI:88284]
	cysteine sulfinic acid decarboxylase [Source:MGI SymbolAcc:MGI:2180098]
	proline dehydrogenase (oxidase) 2 [Source:MGI SymbolAcc:MGI:1929093]
	malate dehydrogenase 1, NAD (soluble) [Source:MGI SymbolAcc:MGI:97051]
	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:MGI SymbolAcc:MGI:1913304]
	UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092]
	phosphate cytidylyltransferase 2, ethanolamine [Source:MGI SymbolAcc:MGI:1915921]
	quinolinate phosphoribosyltransferase [Source:MGI SymbolAcc:MGI:1914625]
	phosphoglucomutase 3 [Source:MGI SymbolAcc:MGI:97566]
	glucokinase [Source:MGI SymbolAcc:MGI:1270854]
	hydroxyacid oxidase 1, liver [Source:MGI SymbolAcc:MGI:96011]
	acyl-CoA synthetase short-chain family member 3 [Source:MGI SymbolAcc:MGI:2685720]
	spermidine synthase [Source:MGI SymbolAcc:MGI:102690]
	adenylosuccinate synthetase like 1 [Source:MGI SymbolAcc:MGI:87947]
	carbonyl reductase 3 [Source:MGI SymbolAcc:MGI:1309992]
	hydroxylysine kinase 1 [Source:MGI SymbolAcc:MGI:2443139]
	aminomethyltransferase [Source:MGI SymbolAcc:MGI:3646700]
	ureidopropionase, beta [Source:MGI SymbolAcc:MGI:2143535]
	glutamine fructose-6-phosphate transaminase 1 [Source:MGI SymbolAcc:MGI:95698]
	UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]
	galactose-4-epimerase, UDP [Source:MGI SymbolAcc:MGI:1921496]
	cytochrome P450, family 2, subfamily b, polypeptide 23 [Source:MGI SymbolAcc:MGI:3646735]
	phosphomannomutase 2 [Source:MGI SymbolAcc:MGI:1859214]
	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 [Source:MGI SymbolAcc:MGI:96234]

	inositol (myo)-1(or 4)-monophosphatase 1 [Source:MGI SymbolAcc:MGI:1933158]
	N-acetylglutamate synthase [Source:MGI SymbolAcc:MGI:2387600]
	cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI SymbolAcc:MGI:1306818]
	dihydrofolate reductase [Source:MGI SymbolAcc:MGI:94890]
	monoamine oxidase A [Source:MGI SymbolAcc:MGI:96915]
	24-dehydrocholesterol reductase [Source:MGI SymbolAcc:MGI:1922004]
	N-acetylneuraminic acid synthase (sialic acid synthase) [Source:MGI SymbolAcc:MGI:2149820]
	phosphoglycolate phosphatase [Source:MGI SymbolAcc:MGI:1914328]
	aminolevulinic acid synthase 1 [Source:MGI SymbolAcc:MGI:87989]
	oxoglutarate dehydrogenase-like [Source:MGI SymbolAcc:MGI:3616088]
	betaine-homocysteine methyltransferase 2 [Source:MGI SymbolAcc:MGI:1891379]
	adenosine deaminase [Source:MGI SymbolAcc:MGI:87916]
	nicotinamide N-methyltransferase [Source:MGI SymbolAcc:MGI:1099443]
	cytochrome P450, family 3, subfamily a, polypeptide 25 [Source:MGI SymbolAcc:MGI:1930638]
	NAD synthetase 1 [Source:MGI SymbolAcc:MGI:1926164]
	glucosidase, beta, acid [Source:MGI SymbolAcc:MGI:95665]
	mannose phosphate isomerase [Source:MGI SymbolAcc:MGI:97075]
	3-ketodihydrosphingosine reductase [Source:MGI SymbolAcc:MGI:1918000]
	cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI SymbolAcc:MGI:1919332]
	acid phosphatase 5, tartrate resistant [Source:MGI SymbolAcc:MGI:87883]
	glycogenin [Source:MGI SymbolAcc:MGI:1351614]
	GDP-mannose 4, 6-dehydratase [Source:MGI SymbolAcc:MGI:1891112]
	enolase-phosphatase 1 [Source:MGI SymbolAcc:MGI:1915120]
	alkaline phosphatase, liver/bone/kidney [Source:MGI SymbolAcc:MGI:87983]
	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:MGI SymbolAcc:MGI:3603816]
	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase) [Source:MGI

			SymbolAcc:MGI:1924753] 5-methyltetrahydrofolate-homocysteine methyltransferase [Source:MGI SymbolAcc:MGI:894292] cytochrome P450, family 26, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:1096359] cytochrome P450, family 7, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:106091] molybdenum cofactor synthesis 2 [Source:MGI SymbolAcc:MGI:1336894] choline kinase alpha [Source:MGI SymbolAcc:MGI:107760] aldehyde oxidase 2 [Source:MGI SymbolAcc:MGI:3529596] cytochrome P450, family 2, subfamily u, polypeptide 1 [Source:MGI SymbolAcc:MGI:1918769] aminolevulinic acid synthase 2, erythroid [Source:MGI SymbolAcc:MGI:87990] C1GALT1-specific chaperone 1 [Source:MGI SymbolAcc:MGI:1913493] 1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) [Source:MGI SymbolAcc:MGI:1196345] adenylate kinase 1 [Source:MGI SymbolAcc:MGI:87977] polymerase (RNA) I polypeptide B [Source:MGI SymbolAcc:MGI:108014] cytochrome c oxidase subunit VIIb [Source:MGI SymbolAcc:MGI:1913392]
	Steroid hormone biosynthesis	4.66E-10	17	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI SymbolAcc:MGI:103238] cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607] cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI SymbolAcc:MGI:3642960] cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI SymbolAcc:MGI:88610] cytochrome P450, family 2, subfamily d, polypeptide 22 [Source:MGI SymbolAcc:MGI:1929474] cytochrome P450, family 2, subfamily b, polypeptide 10 [Source:MGI SymbolAcc:MGI:88598] catechol-O-methyltransferase [Source:MGI SymbolAcc:MGI:88470] UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962] cytochrome P450, family 2, subfamily d, polypeptide 10 [Source:MGI SymbolAcc:MGI:88602] UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092] UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]

			cytochrome P450, family 2, subfamily b, polypeptide 23 [Source:MGI SymbolAcc:MGI:3646735]
			hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 [Source:MGI SymbolAcc:MGI:96234]
			cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI SymbolAcc:MGI:1306818]
			cytochrome P450, family 3, subfamily a, polypeptide 25 [Source:MGI SymbolAcc:MGI:1930638]
			cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI SymbolAcc:MGI:1919332]
			cytochrome P450, family 7, subfamily a, polypeptide 1 [Source:MGI SymbolAcc:MGI:106091]
Drug metabolism - cytochrome P450	7.17E-10	17	aldehyde oxidase 3 [Source:MGI SymbolAcc:MGI:1918974]
			cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
			alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929]
			flavin containing monooxygenase 1 [Source:MGI SymbolAcc:MGI:1310002]
			monoamine oxidase B [Source:MGI SymbolAcc:MGI:96916]
			glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862]
			glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026]
			UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962]
			UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
			glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526]
			UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]
			glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515]
			monoamine oxidase A [Source:MGI SymbolAcc:MGI:96915]
			flavin containing monooxygenase 2 [Source:MGI SymbolAcc:MGI:1916776]
			aldehyde oxidase 2 [Source:MGI SymbolAcc:MGI:3529596]
Metabolism of xenobiotics by cytochrome P450	8.67E-08	14	cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]

			epoxide hydrolase 1, microsomal [Source:MGI SymbolAcc:MGI:95405]
			alcohol dehydrogenase 5 (class III), chi polypeptide [Source:MGI SymbolAcc:MGI:87929]
			glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862]
			glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026]
			UDP glucuronosyltransferase 2 family, polypeptide B34 [Source:MGI SymbolAcc:MGI:2140962]
			carbonyl reductase 1 [Source:MGI SymbolAcc:MGI:88284]
			UDP glucuronosyltransferase 1 family, polypeptide A9 [Source:MGI SymbolAcc:MGI:3576092]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
			glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526]
			carbonyl reductase 3 [Source:MGI SymbolAcc:MGI:1309992]
			UDP glucuronosyltransferase 2 family, polypeptide B35 [Source:MGI SymbolAcc:MGI:3576100]
			glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515]
Linoleic acid metabolism	0.000100769	7	cytochrome P450, family 2, subfamily c, polypeptide 29 [Source:MGI SymbolAcc:MGI:103238]
			cytochrome P450, family 2, subfamily e, polypeptide 1 [Source:MGI SymbolAcc:MGI:88607]
			cytochrome P450, family 2, subfamily c, polypeptide 54 [Source:MGI SymbolAcc:MGI:3642960]
			cytochrome P450, family 3, subfamily a, polypeptide 13 [Source:MGI SymbolAcc:MGI:88610]
			cytochrome P450, family 2, subfamily c, polypeptide 39 [Source:MGI SymbolAcc:MGI:1306818]
			cytochrome P450, family 3, subfamily a, polypeptide 25 [Source:MGI SymbolAcc:MGI:1930638]
			cytochrome P450, family 2, subfamily c, polypeptide 55 [Source:MGI SymbolAcc:MGI:1919332]
Glutathione metabolism	0.000325354	9	isocitrate dehydrogenase 1 (NADP+), soluble [Source:MGI SymbolAcc:MGI:96413]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
			isocitrate dehydrogenase 2 (NADP+), mitochondrial [Source:MGI SymbolAcc:MGI:96414]
			glutathione S-transferase, mu 4 [Source:MGI SymbolAcc:MGI:95862]
			glutathione S-transferase, mu 3 [Source:MGI SymbolAcc:MGI:106026]
			glutathione S-transferase, mu 1 [Source:MGI SymbolAcc:MGI:95860]
			glutathione S-transferase, theta 3 [Source:MGI SymbolAcc:MGI:2143526]

	spermidine synthase [Source:MGI SymbolAcc:MGI:102690]
	glutathione S-transferase, alpha 4 [Source:MGI SymbolAcc:MGI:1309515]

Table S5 Basic nutritional composition of oyster samples and AOPH (g/100g, dry basis)

Composition	**Content**	
	Oyster	**AOPH**
Protein	49.16 ± 1.31	80.77 ± 6.33
Total sugar	33.52 ± 9.55	6.12 ± 0.89
Fat	3.91 ± 0.41	1.65 ± 0.15
Taurine	3.67 ± 0.31	10.58 ± 0.27
Ash	7.83 ± 0.22	2.54 ± 0.22
Total free amino acid	1.33 ± 0.16	/

Original protein	Protein Accession	Peptide	-10lgP	Mass	Length	PTM
Filamin-C OS=Crassostrea gigas OX=29159 GN=CGI_10003521 PE=3 SV=1	tr|K1PW06|K1PW06_CRAGI	M.A(+42.01)DSE.S	36.08	499.3348	4	Acetylation
		D.TRDAGYG.G	36	695.4672	7	
		H.AGAPGA.G	35.93	459.3915	6	
		P.VEEGNI.D	34.54	688.4349	6	
		P.GSPF.T	34.03	422.3235	4	
		Y.IPLKQ.G	32.99	645.5283	5	
		M.EQDI.N	32.44	544.3926	4	
		D.IRIP.V	31.93	450.4752	4	
		E.TFSAGKG.S	31.24	695.4923	7	
		P.VAEGV.V	31.19	458.381	5	
		D.WNDGRA.I	30.85	658.462	6	
		P.NSPF.K	30.16	461.4072	4	
		P.DQPI.K	29.8	560.4392	4	
		Y.LPSKP.G	29.65	589.4545	5	
		Y.VPTM(+15.99)P.G	28.5	594.4157	5	Oxidation (M)
		D.SDLSD.G	28.24	561.4192	5	
		D.SDLSDG.L	27.81	674.5032	6	
		D.TRDAGY.G	26.82	608.4352	6	
		H.AGAPG.A	26.77	312.3231	5	

Table S6 Sequence of peptides identified from AOPH

		M.GVKTGAP.A	26.72	647.5076	7	
		D.AGYGG.L	26.36	436.3755	5	
		D.IKGAGQGG.L	25.33	669.5607	8	
		L.DSDLSD.G	24.85	676.4461	6	
Myosin regulatory light chain A smooth adductor muscle OS=Crassostrea gigas OX=29159 GN=CGI_10001587 PE=4 SV=1	tr|K1Q801|K1Q801_CRAGI	F.VGIIKGS.S	49.74	675.5236	7	
		E.APIEGG.K	40.93	598.476	6	
		F.IDAND.L	40.59	616.4501	5	
		N.DLKEM(+15.99).F	35.78	650.4015	5	Oxidation (M)
		P.DDKT.L	34.89	547.4287	4	
		F.DKDGKG.K	33.9	656.5291	6	
		M.IDQNR.D	33.76	663.441	5	
		K.EAPIEG.G	33.18	612.4916	6	
		E.APIEG.G	32.59	483.449	5	
		F.IDAN.D	32.49	487.4075	4	
		E.GGKLD.Y	31.21	608.4603	5	
		P.IEGGK.L	28.48	593.4494	5	
		L.GSTPD.D	28.08	519.361	5	
		K.DEM(+15.99)R.Q	27.05	641.3913	4	Oxidation (M)
		F.TKDE.M	25.65	606.4229	4	
		I.IKGSS.S	20.92	606.4294	6	
		L.GGTDP.E	20.22	476.2824	5	
		L.DFVG.K	42.3	476.4432	4	
		A.VSYSN.V	34.02	636.5029	5	
		G.IASGP.E	32.21	458.381	5	
		F.DISPTK.T	32.19	687.5237	6	
		L.LGIA.S	31.74	313.3435	4	

		G.IASGPES.V	31.23	699.56	7	
		P.NFDT.Q	30.96	559.3824	4	
		D.SSSS.I	28.13	462.3548	4	
		S.PTKTQ.V	27.11	514.4548	5	
		F.DVDSL.E	24.67	546.397	5	
		E.SVIK.V	22.46	460.433	4	
		R.ENELQ.D	22.12	687.4872	5	
		L.GIASGP.E	21.34	515.4025	6	
Actin 2 OS=Crassostrea gigas OX=29159 GN=actin 2 PE=2 SV=1	tr|Q8TA69|Q8TA69_CRAGI	H.GIVTN.W	45.01	618.4083	5	
		M.VGM(+15.99)GQK.D	39.45	699.4331	6	Oxidation (M)
		E.KIWH.H	39.17	667.5028	4	
		Y.DESGPS.I	39.05	639.4297	6	
		I.ADRM(+15.99)Q.K	38.94	602.428	5	Oxidation (M)
		F.YNELR.V	38.84	660.5029	5	
		L.DLAGRD.L	38.35	674.4669	6	
		L.TERG.Y	35.39	558.3871	4	
		Y.PIEH(+14.02)G.I	34.1	669.5283	5	Methylation(others)
		Y.NELR.V	32.89	497.4395	4	
		M.WISK.Q	31.64	652.4654	4	
		D.DAPR.A	31.36	474.4024	4	
		F.PSIV.G	30.78	424.4232	4	
		N.TVLSG.G	30.65	434.381	5	
		L.RVAPE.E	30.02	633.4668	5	
		Y.PIEHG(+14.02).I	29.05	669.5283	5	Methylation(C-term)

		I.IAPPE.R	27.5	672.5392	5	
		L.DLAG.R	26.73	458.3922	4	
		D.VDIR.K	26.46	557.497	4	
		L.RVAP.E	25.52	536.4141	4	
		G.FAGD.D	24.27	391.2812	4	
		L.DLAGR.D	24.01	559.4399	5	
		E.LRVAP.E	22.63	649.4981	5	
		Y.PIE(+14.02)HGI.V	21.48	692.5291	6	Methylation(others)
		L.GM(+15.99)ESAG.I	21.26	645.3862	6	Oxidation (M)
		F.YNEL.R	20.33	563.4501	4	
		L.YASGR.T	20.24	511.3824	5	
		E.KIW(+15.99)H.H	20.18	683.4977	4	Oxidation (HW)
Collagen alpha-6(VI) chain OS=Crassostrea gigas OX=29159 GN=CGI_10003289 PE=4 SV=1	tr|K1QEB9|K1QEB9_CRAGI	A.VSYSN.V	34.02	636.5029	5	
		G.IASGP.E	32.21	458.381	5	
		F.DISPTK.T	32.19	687.5237	6	
		L.LGIA.S	31.74	313.3435	4	
		G.IASGPES.V	31.23	699.56	7	
		P.NFDT.Q	30.96	559.3824	4	
		L.NTISDA.V	28.32	632.4814	6	
		D.SSSS.I	28.13	462.3548	4	
		S.PTKTQ.V	27.11	514.4548	5	
		R.ENELQ.D	22.12	687.4872	5	
		L.GIASGP.E	21.34	515.4025	6	
		H.GIVTN.W	45.01	618.4083	5	

OX=29159 GN=CGI_10003490 PE=3 SV=1	M.VGM(+15.99)GQK.D	39.45	699.4331	6	Oxidation (M)
	E.KIWH.H	39.17	667.5028	4	
	Y.DESGPS.I	39.05	639.4297	6	
	I.ADRM(+15.99)Q.K	38.94	602.428	5	Oxidation (M)
	F.YNELR.V	38.84	660.5029	5	
	L.DLAGRD.L	38.35	674.4669	6	
	L.TERG.Y	35.39	558.3871	4	
	Y.PIEH(+14.02)G.I	34.1	669.5283	5	Methylation(others)
	Y.NELR.V	32.89	497.4395	4	
	M.WISK.Q	31.64	652.4654	4	
	D.DAPR.A	31.36	474.4024	4	
	F.PSIV.G	30.78	424.4232	4	
	L.RVAPE.E	30.02	633.4668	5	
	Y.PIEHG(+14.02).I	29.05	669.5283	5	Methylation(C-term)
	I.IAPPE.R	27.5	672.5392	5	
	L.DLAG.R	26.73	458.3922	4	
	D.VDIR.K	26.46	557.497	4	
	L.RVAP.E	25.52	536.4141	4	
	G.FAGD.D	24.27	391.2812	4	
	L.DLAGR.D	24.01	559.4399	5	
	E.LRVAP.E	22.63	649.4981	5	
	Y.PIE(+14.02)HGI.V	21.48	692.5291	6	Methylation(others)
	F.YNEL.R	20.33	563.4501	4	

		L.YASGR.T	20.24	511.3824	5	
		E.KIW(+15.99)H.H	20.18	683.4977	4	Oxidation (HW)
Actin OS=Crassostrea gigas OX=29159 GN=act PE=2 SV=1	tr|C4NY59|C4NY59_CRAGI	H.GIVTN.W	45.01	618.4083	5	
		M.VGM(+15.99)GQK.D	39.45	699.4331	6	Oxidation (M)
		E.KIWH.H	39.17	667.5028	4	
		Y.DESGPS.I	39.05	639.4297	6	
		I.ADRM(+15.99)Q.K	38.94	602.428	5	Oxidation (M)
		F.YNELR.V	38.84	660.5029	5	
		L.DLAGRD.L	38.35	674.4669	6	
		L.TERG.Y	35.39	558.3871	4	
		Y.PIEH(+14.02)G.I	34.1	669.5283	5	Methylation(others)
		Y.NELR.V	32.89	497.4395	4	
		M.WISK.Q	31.64	652.4654	4	
		D.DAPR.A	31.36	474.4024	4	
		F.PSIV.G	30.78	424.4232	4	
		L.RVAPE.E	30.02	633.4668	5	
		Y.PIEHG(+14.02).I	29.05	669.5283	5	Methylation(C-term)
		V.IAPPE.R	27.5	672.5392	5	
		L.DLAG.R	26.73	458.3922	4	
		D.VDIR.K	26.46	557.497	4	
		L.RVAP.E	25.52	536.4141	4	
		G.FAGD.D	24.27	391.2812	4	
		L.DLAGR.D	24.01	559.4399	5	

		I.V(+42.01)LSGG.T	23.6	488.428	5	Acetylation (N-term)
		E.LRVAP.E	22.63	649.4981	5	
		Y.PIE(+14.02)HGI.V	21.48	692.5291	6	Methylation(others)
		F.YNEL.R	20.33	563.4501	4	
		L.YASGR.T	20.24	511.3824	5	
		E.KIW(+15.99)H.H	20.18	683.4977	4	Oxidation (HW)
Myosin heavy chain striated muscle OS=Crassostrea gigas OX=29159 GN=CGI_10022093 PE=3 SV=1	tr|K1RSS3|K1RSS3_CRAGI	L.GHYAGS.V	43.61	609.3981	6	
		F.SLGHYAG.S	40.49	646.4508	7	
		L.NEASVL.H	40.06	695.5036	6	
		L.LSASKE.H	39.6	682.5447	6	
		A.VNPYK.R	37.71	685.5709	5	
		Y.LAVDR.K	35.54	584.5443	5	
		G.SVGYN.I	31.65	552.3977	5	
		A.SKEHL.V	31.13	668.5291	5	
		M.A(+42.01)AFDP.N	29.45	587.3661	5	Acetylation (Protein N-term)
		E.ASVL.H	26.94	452.4181	4	
		A.VADNA.Y	24.2	626.4134	5	
		M.EQ(+.98)KN.R	23.41	650.4821	4	Deamidation (NQ)
		A.PIKVKM(+15.99).M	48.58	687.5423	6	Oxidation (M)
		P.IKVKM(+15.99).M	36.37	572.5153	5	Oxidation (M)

PE=2 SV=1		G.ITVA.G	35.86	345.3333	4	
		I.TVAG.D	34.33	379.3177	4	
		Q.ANDL.S	27	446.3446	4	
		P.DAAP.I	23.67	412.4119	4	
		Q.DEKT.I	22.62	516.4592	4	
		E.IQANDL.S	20.56	687.4872	6	
Titin OS=Crassostrea gigas OX=29159 GN=CGI_10026641 PE=3 SV=1	tr|K1RVK9|K1RVK9_CRAGI	F.TVM(+15.99)GL.Q	43.69	549.3902	5	Oxidation (M)
		V.VVLGPP.T	41.71	606.5538	6	
		V.WM(+15.99)NG.I	40.43	493.3429	4	Oxidation (M)
		D.APDTP.G	39.98	466.3861	5	
		A.AINNAG.L	39.87	557.4243	6	
		F.RVIA.E	34.67	547.4552	4	
		M.GLQEGT.V	21.24	630.4658	6	
Troponin T skeletal muscle OS=Crassostrea gigas OX=29159 GN=CGI_10017461 PE=3 SV=1	tr|K1QPC9|K1QPC9_CRAGI	F.AGAPPK.I	36.72	593.5334	6	
		L.SGLDE.E	36.37	589.4392	5	
		F.DRLA.D	30.18	563.4501	4	
		E.ELSKP.I	23.32	611.4963	5	
		E.LSKP.I	20.27	482.4537	4	
LIM domain and actin-binding protein 1 OS=Crassostrea gigas OX=29159 GN=CGI_10012729 PE=4 SV=1	tr|K1QT91|K1QT91_CRAGI	Y.ENEPV.R	34.15	668.4563	5	
		P.ISEEGV.V	29.68	646.4971	6	
		M.SVEG.G	29.23	409.3282	4	
		P.ISEEG.V	20.79	559.4651	5	
		E.LSTHP.I	41.55	596.4603	5	
		E.LSTHP.L	39.11	554.4498	5	
		E.INELS.T	38.83	609.4556	5	
		D.EVSTHP.L	37.97	669.4767	6	

		E.GLSID.D	36.44	575.4236	5	
		D.DKEYR.V	30.31	678.5134	5	
		L.PEVGS.A	29.28	504.4017	5	
		A.ERDQ.I	29.22	586.4508	4	
		P.EVGS.A	28.57	407.349	4	
		F.VYSVV.E	27.64	635.5328	5	
		G.INLN(+.98)D.T	25.07	647.4083	5	Deamidation (NQ)
		E.STSN.I	24.94	390.3548	4	
		L.GLVSYS.T	23.9	678.5134	6	
Actin OS=Crassostrea gigas OX=29159 GN=CGI_10022731 PE=3 SV=1	tr|K1RA57|K1RA57_CRAGI	R.GIVTN.W	45.01	618.4083	5	
		E.KIWH.H	39.17	667.5028	4	
		Y.DESGPS.I	39.05	639.4297	6	
		I.ADRM(+15.99)Q.K	38.94	602.428	5	Oxidation (M)
		M.WISK.Q	31.64	652.4654	4	
		I.IAPPE.R	27.5	672.5392	5	
		G.FAGD.D	24.27	391.2812	4	
		L.TERG.Y	22.25	524.4028	4	
		L.YASGR.T	20.24	511.3824	5	
		E.KIW(+15.99)H.H	20.18	683.4977	4	Oxidation (HW)
Collagen alpha-1(XII) chain OS=Crassostrea gigas OX=29159 GN=CGI_10022003 PE=4 SV=1	tr|K1RHA0|K1RHA0_CRAGI	G.IASGP.E	32.21	458.381	5	
		L.LGIA.S	31.74	313.3435	4	
		G.IASGPES.V	31.23	699.56	7	
		L.NTISD.A	28.32	632.4814	6	
		R.ENELQ.D	22.12	687.4872	5	

		L.GIASGP.E	21.34	515.4025	6	
Actin OS=Crassostrea gigas OX=29159 GN=CGI_10017753 PE=3 SV=1	tr|K1RHJ4|K1RHJ4_CRAGI	F.YNELR.V	38.84	660.5029	5	
		Y.NELR.V	32.89	497.4395	4	
		M.WISK.Q	31.64	652.4654	4	
		L.RVAPE.E	30.02	633.4668	5	
		L.RVAP.E	25.52	536.4141	4	
		E.LRVAP.E	22.63	649.4981	5	
		F.YNEL.R	20.33	563.4501	4	
		L.YASGR.T	20.24	511.3824	5	
Actin-1/3 OS=Crassostrea gigas OX=29159 GN=CGI_10017112 PE=3 SV=1	tr|K1RBG6|K1RBG6_CRAGI	F.YNELR.V	38.84	660.5029	5	
		R.GYSF.T	35.39	558.3871	4	
		Y.PIEH(+14.02)G.I	34.1	669.5283	5	Methylation(others)
		Y.NELR.V	32.89	497.4395	4	
		A.PEEHP.V	30.02	633.4668	5	
		Y.PIEHG(+14.02).I	29.05	669.5283	5	Methylation(C-term)
		V.DLAG.R	26.73	458.3922	4	
		D.VDIR.K	26.46	557.497	4	
		L.RVAP.E	25.52	536.4141	4	
		V.DLAGR.D	24.01	559.4399	5	
		E.LRVAP.E	22.63	649.4981	5	
		P.TRIK(+42.01).E	21.4	612.5392	4	Acetylation (K)
		L.GM(+15.99)ESAG.I	21.26	645.3862	6	Oxidation (M)
		F.YNEL.R	20.33	563.4501	4	
		P.AVLEGI.A	37.44	645.5032	6	

muscle OS=Crassostrea gigas OX=29159 GN=CGI_10025110 PE=4 SV=1		M.A(+42.01)DQKM(+15.99).T	34.05	687.4695	5	Acetylation (Protein N-term); Oxidation (M)
		I.LGDLT.R	21.87	650.4821	5	
Myosin essential light chain OS=Crassostrea gigas OX=29159 PE=2 SV=1	tr|A0A286SBX9|A0A286SBX9_CRAGI	I.HETIM(+15.99).N	35.51	668.5001	5	Oxidation (M)
		E.DLEGN.V	32.69	636.4552	5	
		A.EVDASK.I	31.65	632.4451	6	
		D.LEGN.V	28.75	521.4283	4	
		F.LPIH.E	26.22	521.4647	4	
		M.S(+42.01)KLS.K	25.05	561.4443	4	Acetylation
Myosin essential light chain (Fragment) OS=Crassostrea gigas OX=29159 GN=mlc PE=2 SV=1	tr|Q70MN9|Q70MN9_CRAGI	I.HETIM(+15.99).N	35.51	668.5001	5	Oxidation (M)
		E.DLEGN.V	32.69	636.4552	5	
		A.EVDASK.I	31.65	632.4451	6	
		D.LEGN.V	28.75	521.4283	4	
		F.LPIH.E	26.22	521.4647	4	
		M.S(+42.01)KLS.K	25.05	561.4443	4	Acetylation (Protein N-term)
Myosin heavy chain striated muscle OS=Crassostrea gigas OX=29159 GN=CGI_10025109 PE=3 SV=1	tr|K1QRU8|K1QRU8_CRAGI	L.NEASVL.H	40.06	695.5036	6	
		E.ASVL.H	26.94	452.4181	4	
Actin OS=Crassostrea gigas OX=29159 GN=CGI_10020413	tr|K1RVF3|K1RVF3_CRAGI	L.TERG.Y	35.39	558.3871	4	
		L.DLAG.R	26.73	458.3922	4	
		L.DLAGR.D	24.01	559.4399	5	

		Y.PIE(+14.02)HGI.V	21.48	692.5291	6	Methylation(others)
		L.YASGR.T	20.24	511.3824	5	
Actin cytoplasmic OS=Crassostrea gigas OX=29159 GN=CGI_10017757 PE=3 SV=1	tr|K1QXE8|K1QXE8_CRAGI	F.YNELR.V	38.84	660.5029	5	
		L.DLAGRD.L	38.35	674.4669	6	
		Y.NELR.V	32.89	497.4395	4	
		M.WISK.Q	31.64	652.4654	4	
		F.PSIV.G	30.78	424.4232	4	
		L.RVAPE.E	30.02	633.4668	5	
		I.TIGN.E	29.66	492.4017	4	
		L.DLAG.R	26.73	458.3922	4	
		L.RVAP.E	25.52	536.4141	4	
		L.DLAGR.D	24.01	559.4399	5	
		E.LRVAP.E	22.63	649.4981	5	
		F.YNEL.R	20.33	563.4501	4	
		L.YASGR.T	20.24	511.3824	5	
Actin-1 OS=Crassostrea gigas OX=29159 GN=CGI_10028603 PE=3 SV=1	tr|K1QVI5|K1QVI5_CRAGI	E.KIWH.H	39.17	667.5028	4	
		F.YNELR.V	38.84	660.5029	5	
		Y.NELR.V	32.89	497.4395	4	
		D.DAPR.A	31.36	474.4024	4	
		V.DLAG.R	26.73	458.3922	4	
		G.FAGD.D	24.27	391.2812	4	
		V.DLAGR.D	24.01	559.4399	5	
		F.YNEL.R	20.33	563.4501	4	
		E.KIWH.H	39.17	667.5028	4	
		F.YNELR.V	38.84	660.5029	5	

PE=3 SV=1		Y.NELR.V	32.89	497.4395	4
		D.DAPR.A	31.36	474.4024	4
		V.DLAG.R	26.73	458.3922	4
		G.FAGD.D	24.27	391.2812	4
		V.DLAGR.D	24.01	559.4399	5
		F.YNEL.R	20.33	563.4501	4
Actin-1 OS=Crassostrea gigas OX=29159 GN=CGI_10028601 PE=3 SV=1	tr|K1RHB1|K1RHB1_CRAGI	E.KIWH.H	39.17	667.5028	4
		F.YNELR.V	38.84	660.5029	5
		Y.NELR.V	32.89	497.4395	4
		D.DAPR.A	31.36	474.4024	4
		V.DLAG.R	26.73	458.3922	4
		G.FAGD.D	24.27	391.2812	4
		V.DLAGR.D	24.01	559.4399	5
		F.YNEL.R	20.33	563.4501	4
Actin-1 OS=Crassostrea gigas OX=29159 GN=CGI_10028599 PE=3 SV=1	tr|K1R557|K1R557_CRAGI	E.KIWH.H	39.17	667.5028	4
		F.YNELR.V	38.84	660.5029	5
		Y.NELR.V	32.89	497.4395	4
		D.DAPR.A	31.36	474.4024	4
		V.DLAG.R	26.73	458.3922	4
		G.FAGD.D	24.27	391.2812	4
		V.DLAGR.D	24.01	559.4399	5
		F.YNEL.R	20.33	563.4501	4
Collagen alpha-4(VI) chain OS=Crassostrea gigas OX=29159 GN=CGI_10023716 PE=4 SV=1	tr|K1QTV9|K1QTV9_CRAGI	S.ISGQ.D	28.39	432.3654	4
		F.IGS.G	24.61	341.3748	4

Table S7 Effects of AOPH on the liver index (%, w/w) and liver-specific biochemical indicators of serum in alcoholic liver injury mice

	Groups					
	Normal	**Model**	**AOPH-L**	**AOPH-M**	**AOPH-H**	**Positive**
Liver index (%)	4.13 ± 0.14	4.62 ± 0.22 #	4.54 ± 0.10	4.27 ± 0.31	4.19 ± 0.11 *	4.36 ± 0.19
TC (mmol/L)	3.53 ± 0.22	4.32 ± 0.12 #	3.67 ± 0.16	3.24 ± 0.24 **	3.26 ± 0.26 **	3.60 ± 0.39
ALT (U/L)	42.31 ± 7.54	86.12 ± 9.58 ##	73.50 ± 12.72	65.40 ± 15.11	58.80 ± 5.22 *	73.90 ± 6.30
AST (U/L)	129.44 ± 14.82	201.5 ± 26.43 ##	189.21 ± 32.5	151.32 ± 20.6 **	139.23 ± 17.97 **	176.85 ± 19.21
TP (g/L)	49.02 ± 3.23	49.46 ± 3.92	54.38 ± 5.73	56.63 ± 7.32	50.98 ± 4.13	50.69 ± 2.94

ALB (g/L)	36.80 ± 7.65	31.98 ± 4.03	32.12 ± 3.14	30.91 ± 2.31	33.11 ± 3.07	31.26 ± 2.58
LDH (U/L)	357.68 ± 83.26	652.90 ± 153.32 ##	756.77 ± 73.88	395.43 ± 96.32 **	346.62 ± 62.31 **	386.12 ± 46.75 **

Note: Data were expressed as mean ± SD, TC: Serum total cholesterol; ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; TP: Total protein; ALB: albumin; LDH: Lactate dehydrogenase. $^{\#}$ or * indicates a significant difference ($p < 0.05$) compared with the Normal or Model group, $^{\#\#}$ or ** indicates a highly significant difference ($p < 0.01$) compared with the Normal or Model group.