SUPPLEMENTARY INFORMATION

Supplementary Figure S1: Linear regression analysis of the three SILAC biological replicate experiments. Normalized protein ratios were compared across each of the three replicate experiments. Each scatter-plot only included protein ratios common to both experiments with at least three ratio counts per experiment. Biological Replicate One versus Two: r^2 = 0.7385; Biological Replicate One versus Three: r^2 = 0.8142; Biological Replicate Two versus Three: r^2 = 0.8589.

Supplementary Figure S2: Western blot validation of differentially expressed SILAC proteins. A selection of proteins found to be differentially expressed within the SILAC analysis were confirmed by Western blotting. Shown are SILAC fold changes and corresponding immunoblots for the following proteins: Mcm2, Mcm7, PCNA, ribosomal protein S6, ferritin heavy chain (FTH1), NDRG1, p16 (CDKN2A), GPX1, and beta-actin.

Supplementary Figures S3 – S12: Individual IPA canonical pathways which were found to be over-represented in the Cdc7 depletion dataset (corresponding to Table 2). Molecules coloured in green were down-regulated in abundance following Cdc7 depletion, molecules coloured red were up-regulated and molecules coloured grey were unchanged in abundance. Uncoloured molecules were not quantified in this SILAC analysis. A key is given to explain the shapes of molecules.

Supplementary Figure S3: NRF2-mediated Oxidative Stress Response
Supplementary Figure S4: Synthesis and Degradation of Ketone Bodies
Supplementary Figure S5: Butanoate Metabolism

Supplementary Figure S6: Bile Acid Biosynthesis

Supplementary Figure S7: Valine, Leucine and Isoleucine Degradation

Supplementary Figure S8: Biosynthesis of Steroids

Supplementary Figure S9: Granzyme A Signalling

Supplementary Figure S10: Oxidative Phosphorylation

Supplementary Figure S11: Glutathione Metabolism

Supplementary Figure S12: Propanoate Metabolism

Supplementary Table S1: Protein information for each of the 315 differentially expressed proteins including various identifiers, functional annotations, number of sequenced peptides, sequence coverage, predicted molecular weight, sequence length, posterior error probability (PEP) score, normalized protein abundance ratio, Significance B score, ratio count, ratio variability and summed peptide intensity. Additionally, this table provides further information for all sequenced peptides within each Protein Group, including peptide sequence, whether the peptide was unique, how many ratio counts were obtained for each sequenced peptide as well as individual peptide scores and ratios.

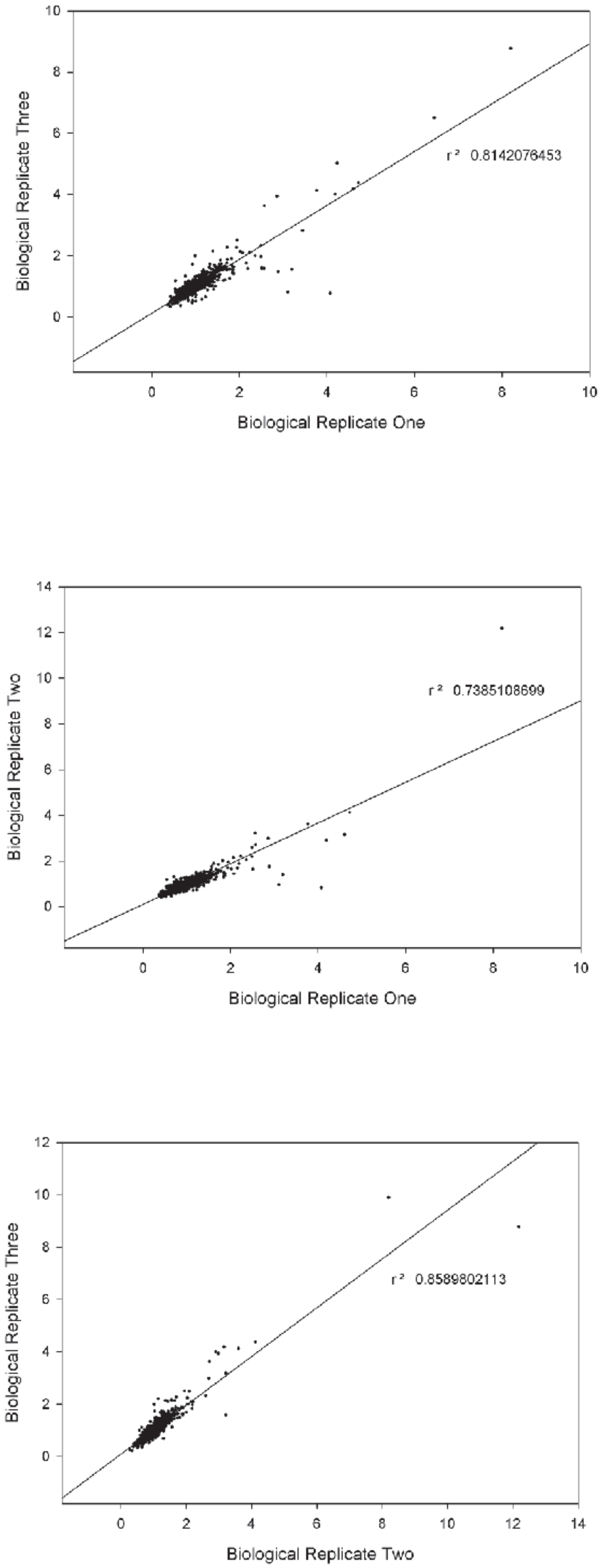
Supplementary Table S2: Protein information for all 1730 proteins which were quantified but found to be unchanged in abundance following Cdc7 depletion (Significance B > 0.05).

Supplementary Table S3: Protein names, HUGO gene symbols, fold changes and p-values for all molecules mapped to each of the ten top-scoring IPA pathways (corresponding to Table 2 and

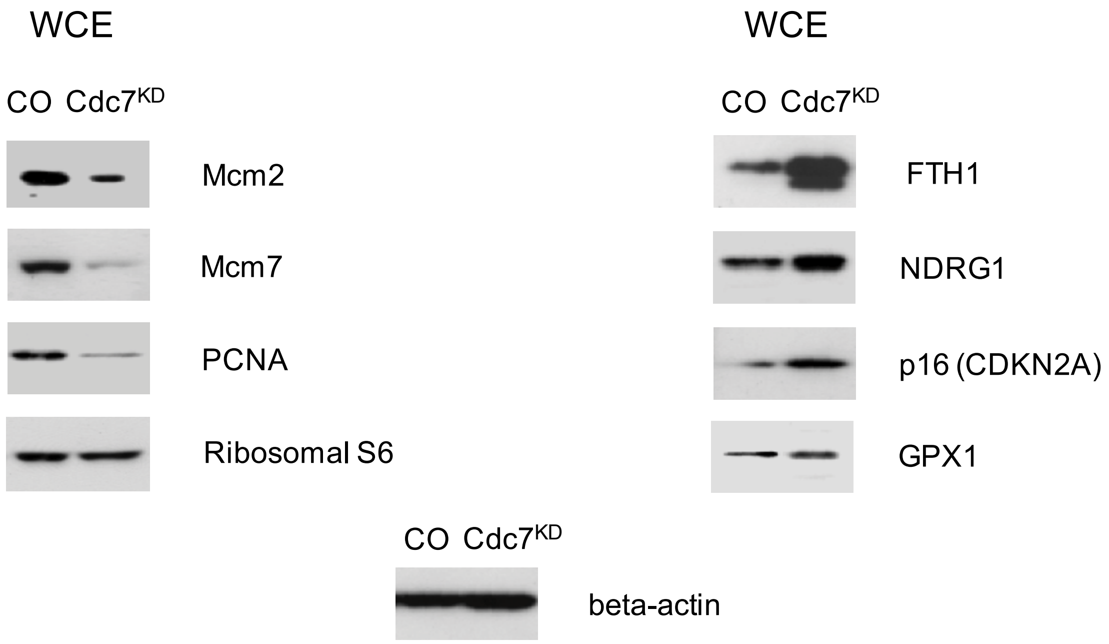
Supplementary Figures S3 - S12). Significantly changed proteins are shown in bold red and unchanged identified proteins are in black.

Supplementary Table S4: GO enrichment annotation data for up and down regulated protein groups (corresponding to information in Table 3). Each GO category (GOBP, GOCC and GOMF) was processed separately. Shown are the top scoring 10 annotations for each category, with corresponding GO-ID reference number, number of proteins found to be associated with each term (x), p-value, corrected p-value, cluster size of dataset, number of available molecules per term and a list of all proteins identified within each term.

Supplementary Table S5: Generic GOSlim enrichment annotation data for up and down regulated protein groups (represented graphically in Figure 4). Shown are the top scoring 10 annotations for each category, with corresponding GO-ID reference number, number of proteins found to be associated with each term (x), p-value, corrected p-value, cluster size of dataset, number of available molecules per term and a list of all proteins identified within each term.

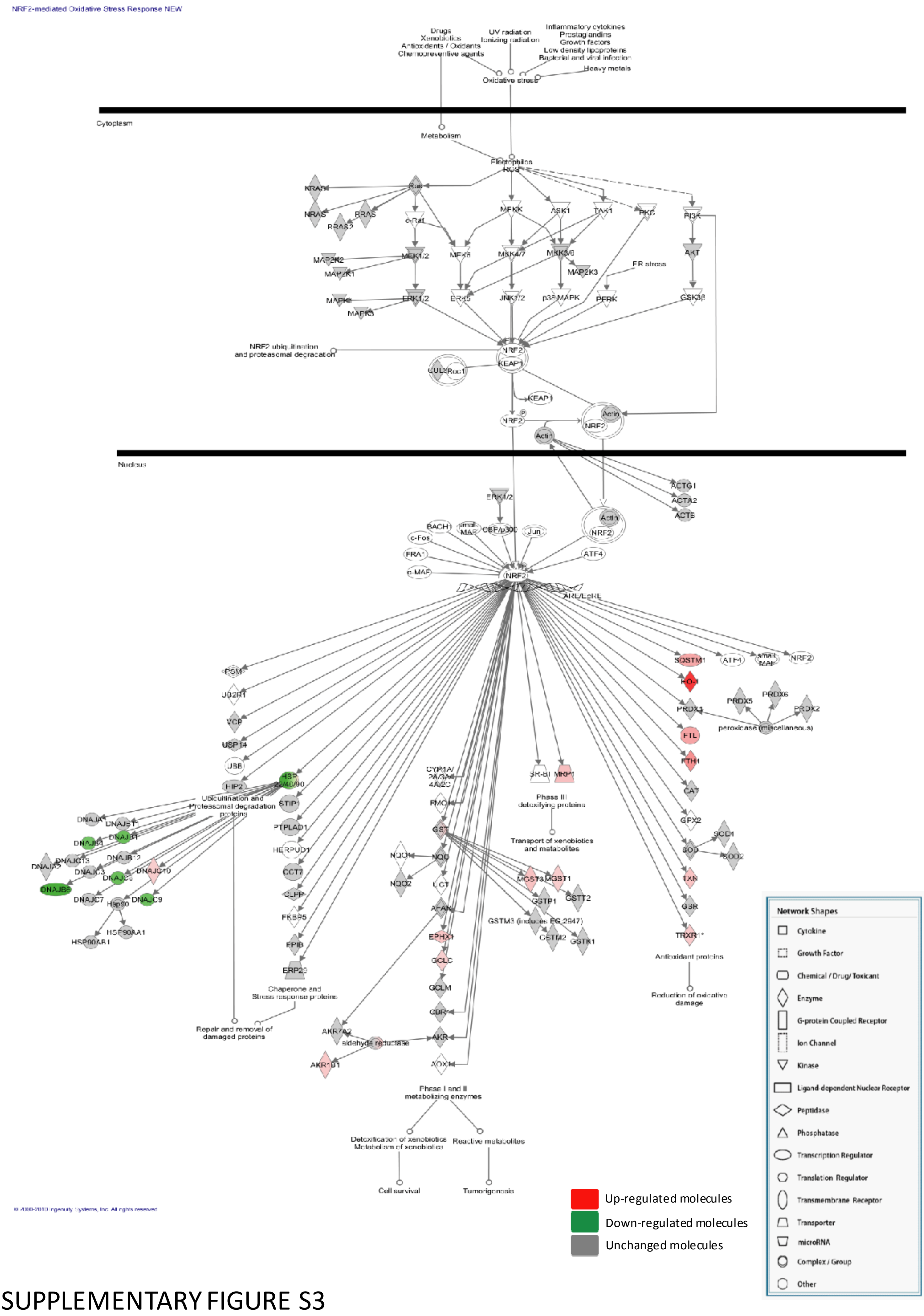


SUPPLEMENTARY FIGURE S1



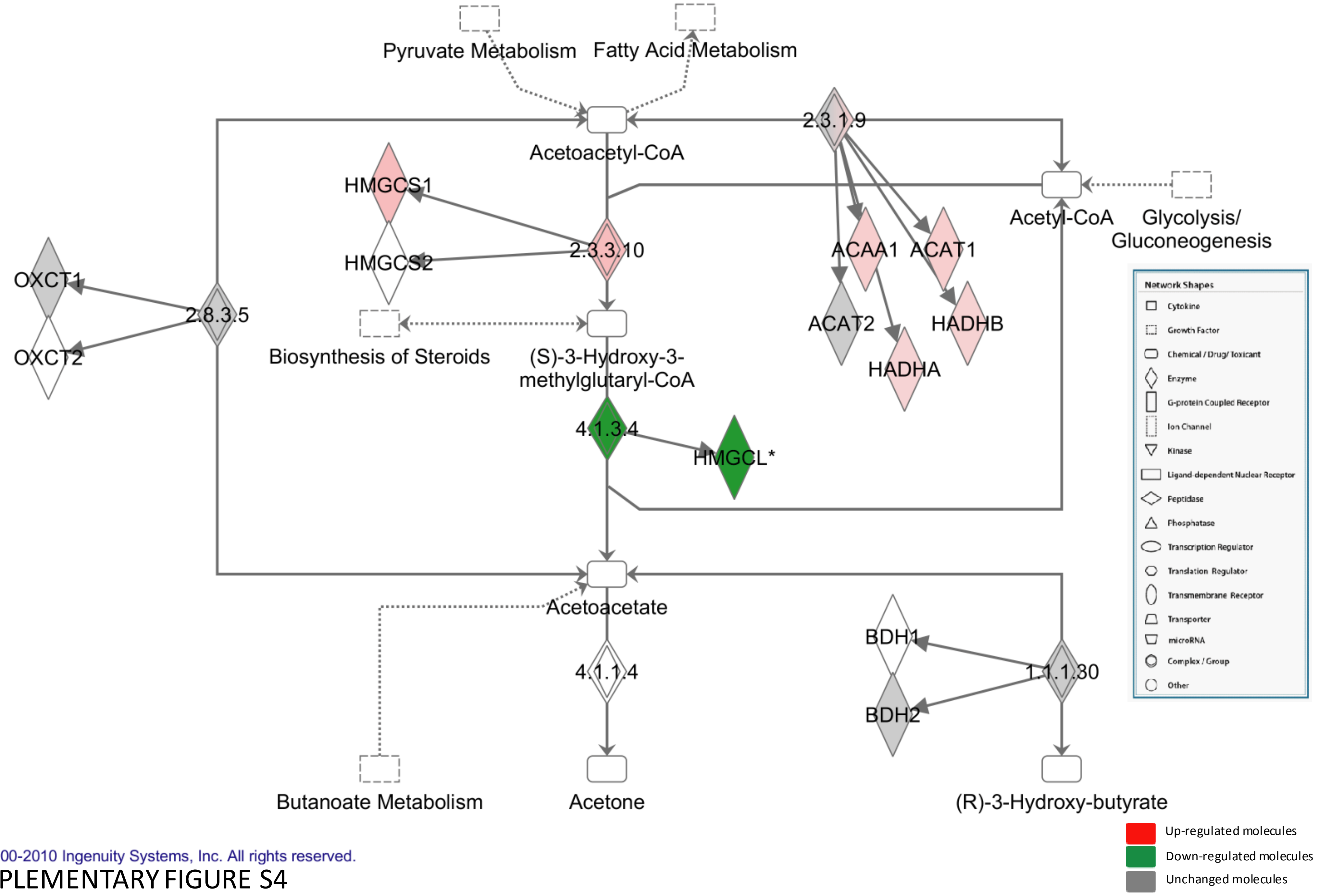
Protein Name	Gene Name	Normalized SILAC Ratio (CDC7^{KD} / CO)	Fold Change	Ratio Significance (B)
DNA replication licensing factor MCM2;Minichromosome maintenance protein 2 homolog;Nuclear protein BM28	**MCM2**	0.66578	**-1.50**	0.048311
DNA replication licensing factor MCM7;CDC47 homolog;P1.1-MCM3;cDNA FLJ30817 fis, clone FEBRA2001581, highly similar to DNA REPLICATION LICENSING FACTOR MCM7;MCM7 minichromosome maintenance deficient 7 (S. cerevisiae);MCM7 minichromosome maintenance deficient 7 (S. cerevisiae), isoform CRA_a	**MCM7**	0.56455	**-1.77**	0.0092728
Proliferating cell nuclear antigen;Cyclin	**PCNA**	0.52672	**-1.90**	2.98E-05
40S ribosomal protein S6;Phosphoprotein NP33;Ribosomal protein S6;Ribosomal protein S6, isoform CRA_a	**RPS6**	0.68759	**-1.45**	0.010506
Ferritin heavy chain;Cell proliferation-inducing gene 15 protein;Ferritin	**FTH1**	3.6533	**+3.65**	8.09E-08
Protein NDRG1;N-myc downstream-regulated gene 1 protein;Differentiation-related gene 1 protein;Reducing agents and tunicamycin-responsive protein;Nickel-specific induction protein Cap43;Rit42;cDNA FLJ39243 fis, clone OCBBF2008283, highly similar to Protein NDRG1	**NDRG1**	1.8103	**+1.81**	0.0073095
Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3;Cyclin-dependent kinase 4 inhibitor A;p16-INK4a;Multiple tumor suppressor 1	**CDKN2A**	6.2537	**+6.25**	1.68E-09
Glutathione peroxidase 1;GSHPx-1;Cellular glutathione peroxidase	**GPX1**	2.1258	**+2.12**	0.00087102
Beta-actin;Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed;cDNA FLJ58286, highly similar to Actin, cytoplasmic 2	**ACTB**	0.89391	**-1.12**	NS

SUPPLEMENTARY FIGURE S2

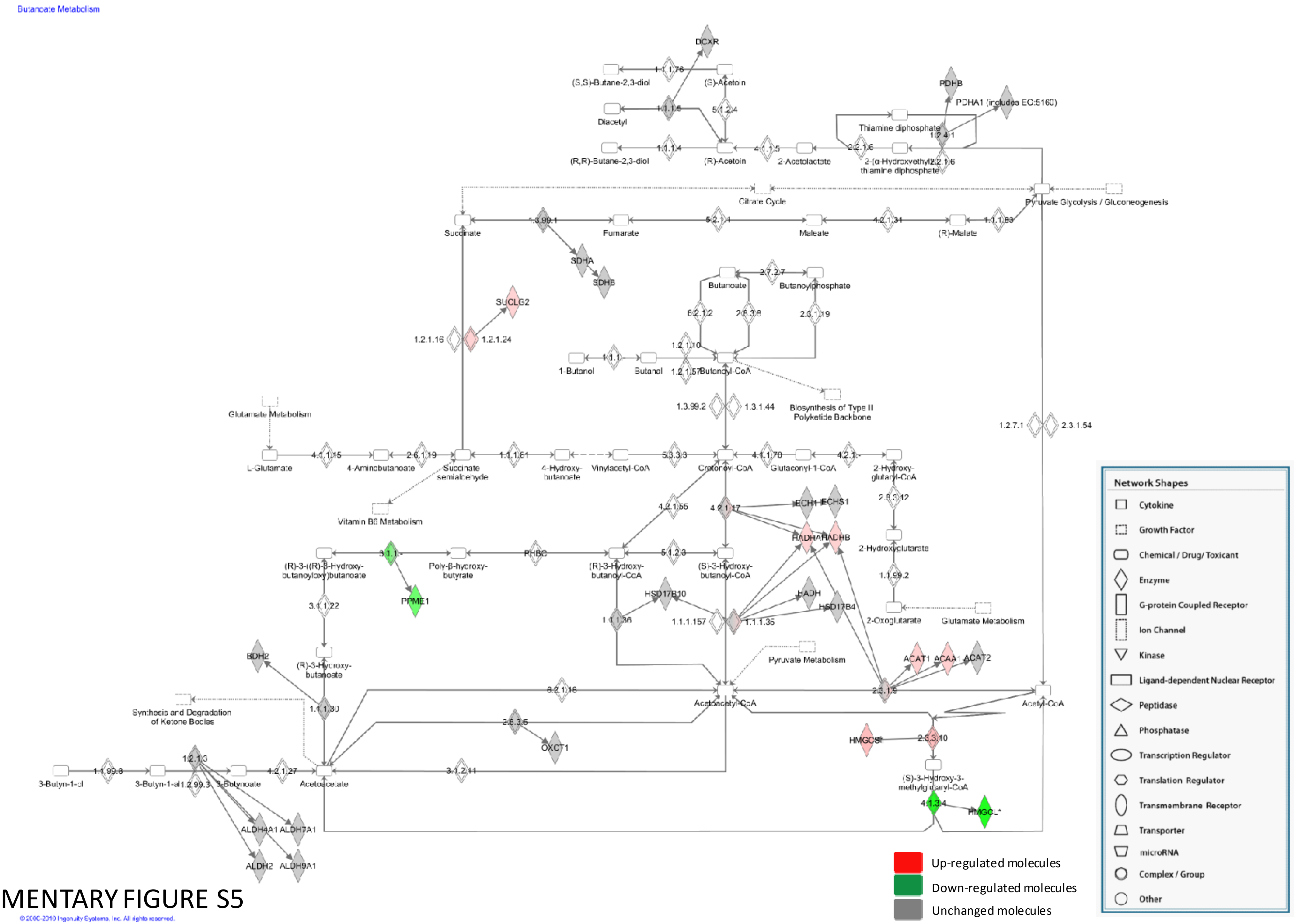


SUPPLEMENTARY FIGURE S3

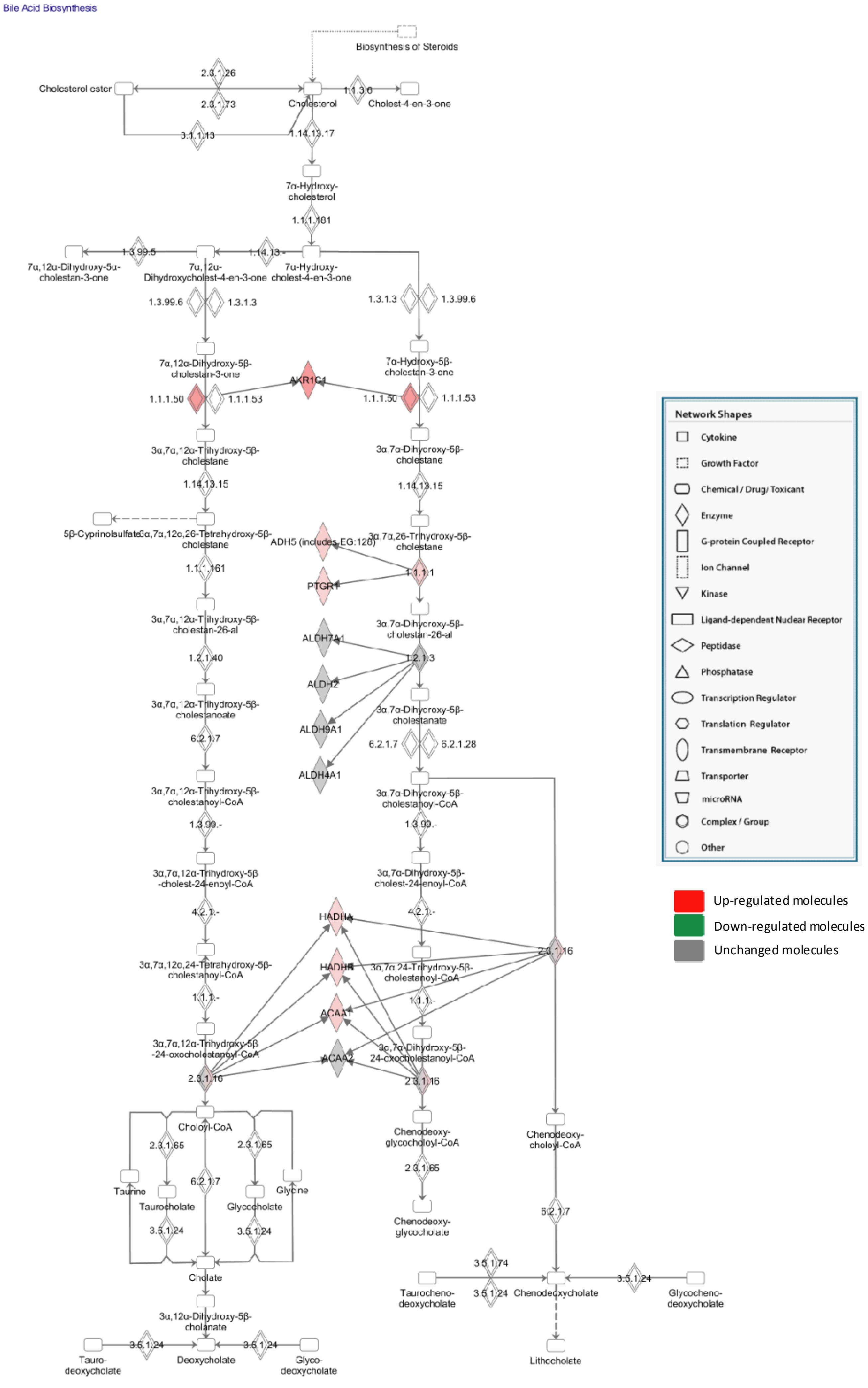
Synthesis and Degradation of Ketone Bodies



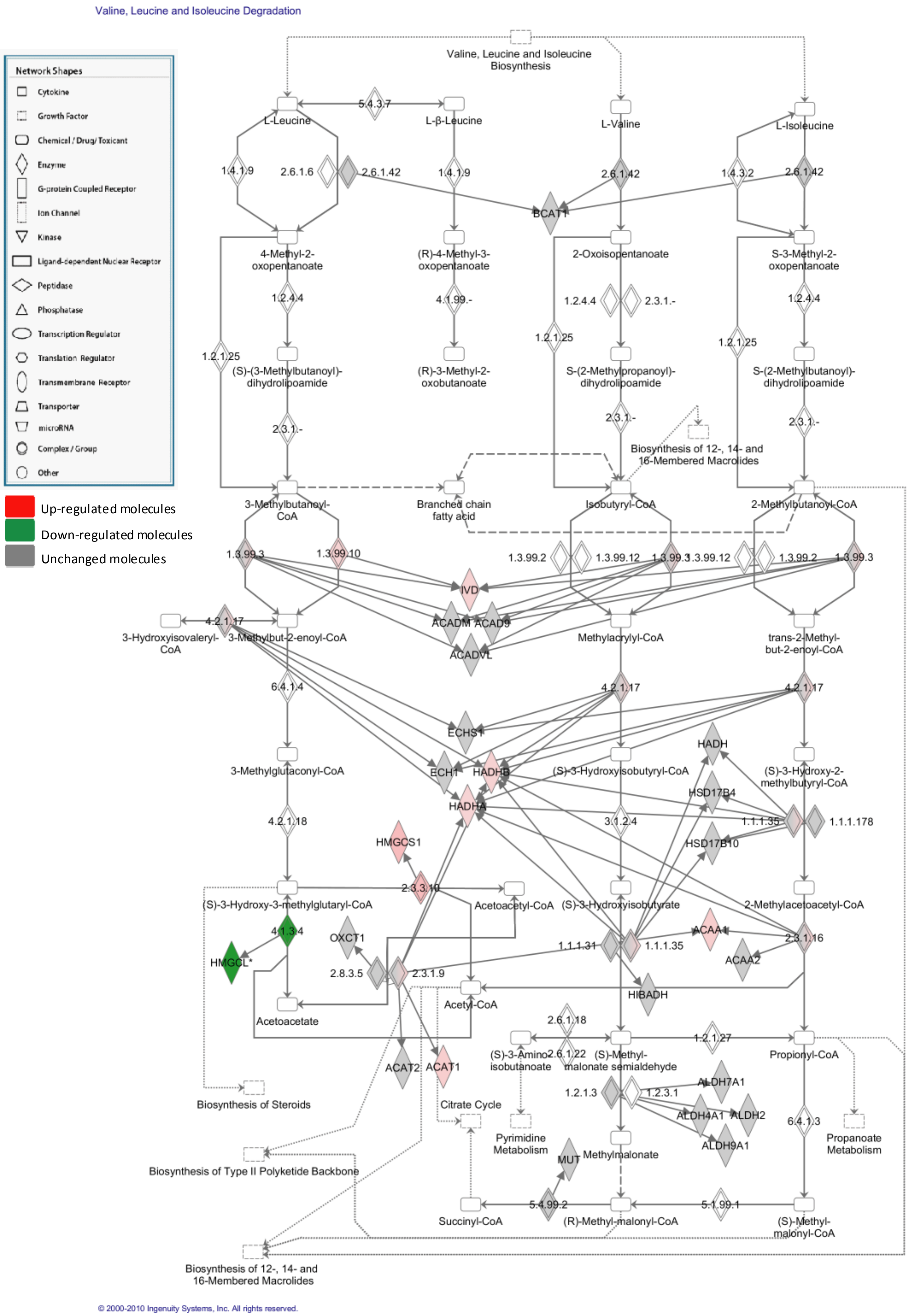
SUPPLEMENTARY FIGURE S4



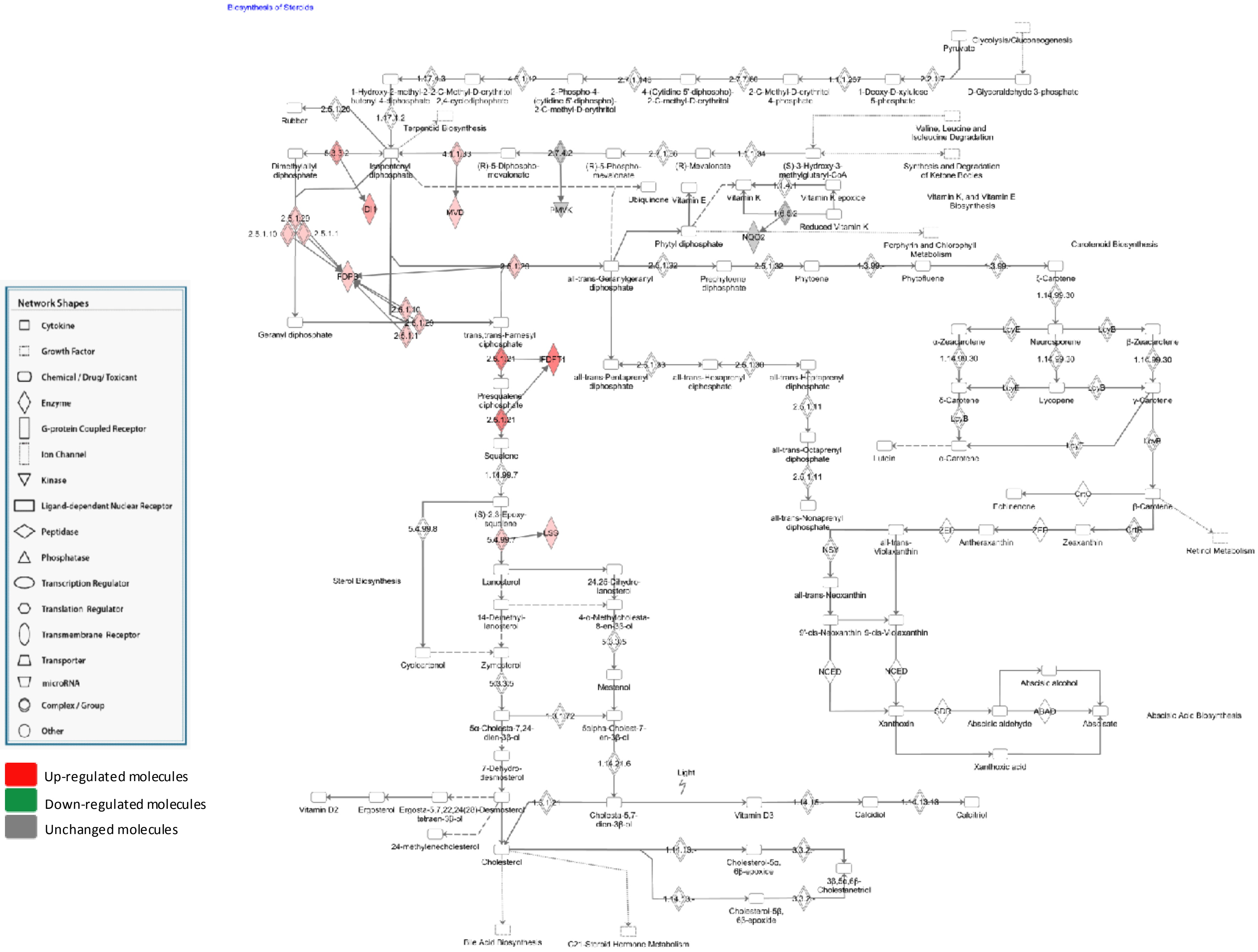
SUPPLEMENTARY FIGURE S5



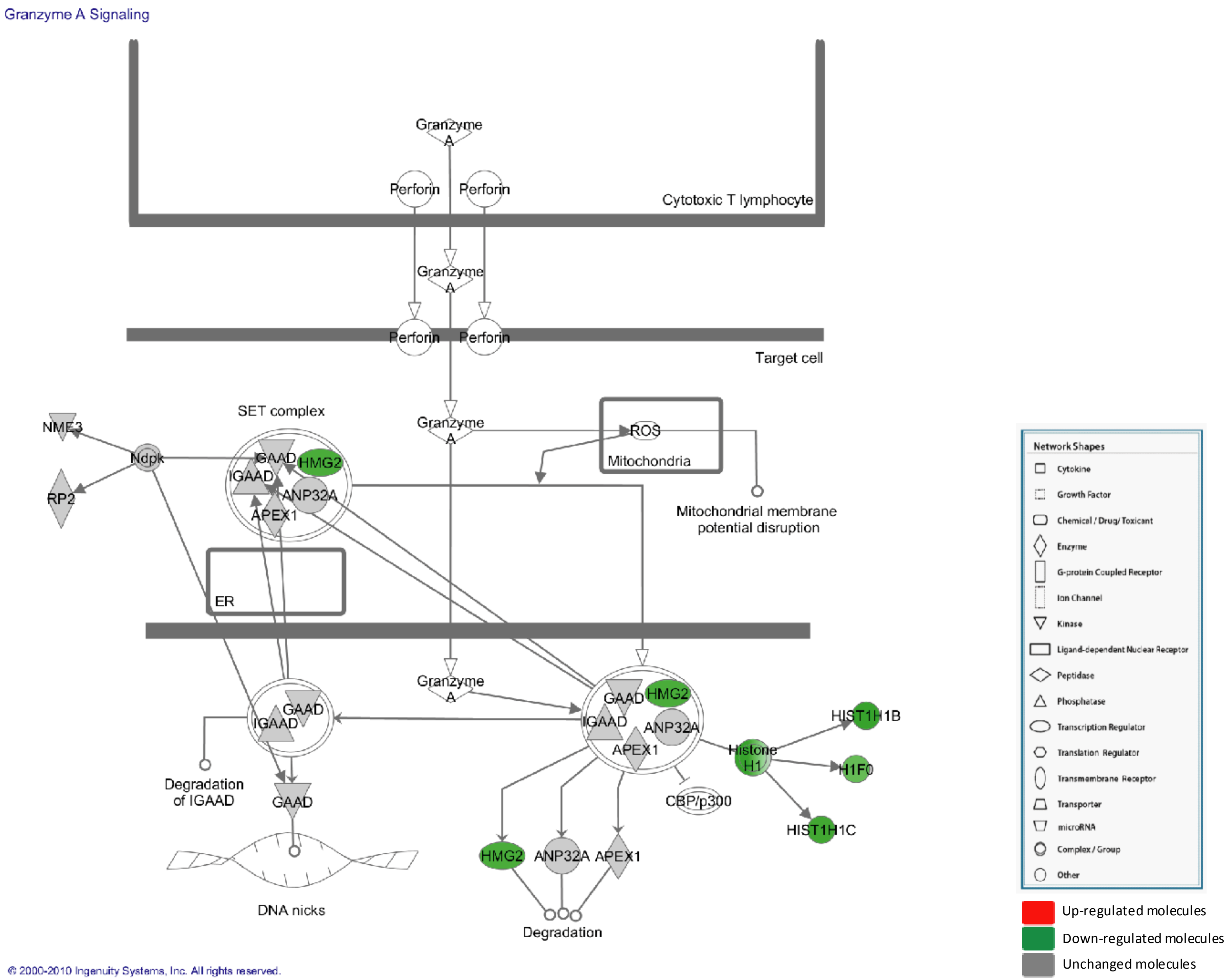
SUPPLEMENTARY FIGURE S6



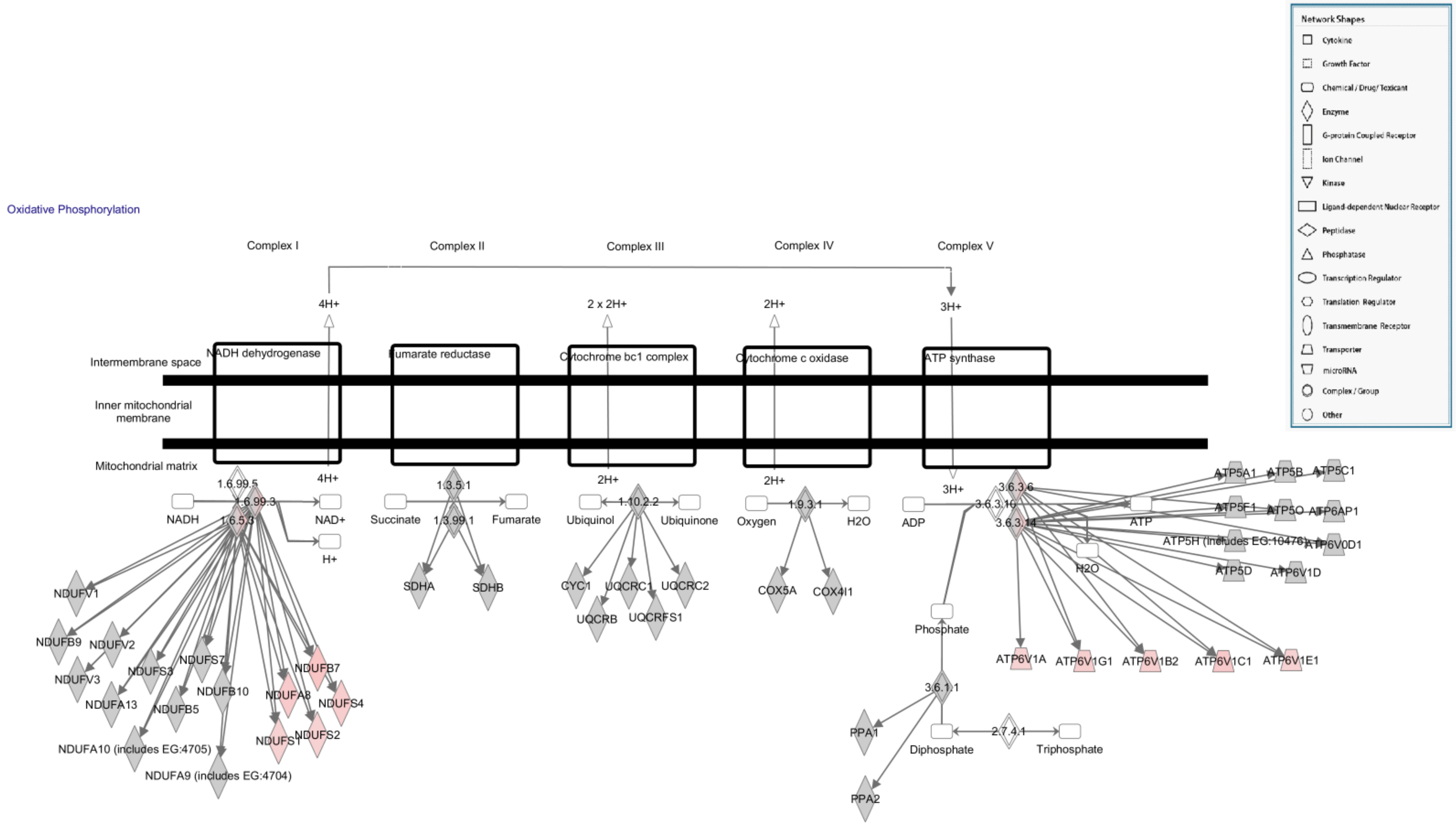
SUPPLEMENTARY FIGURE S7



SUPPLEMENTARY FIGURE S8

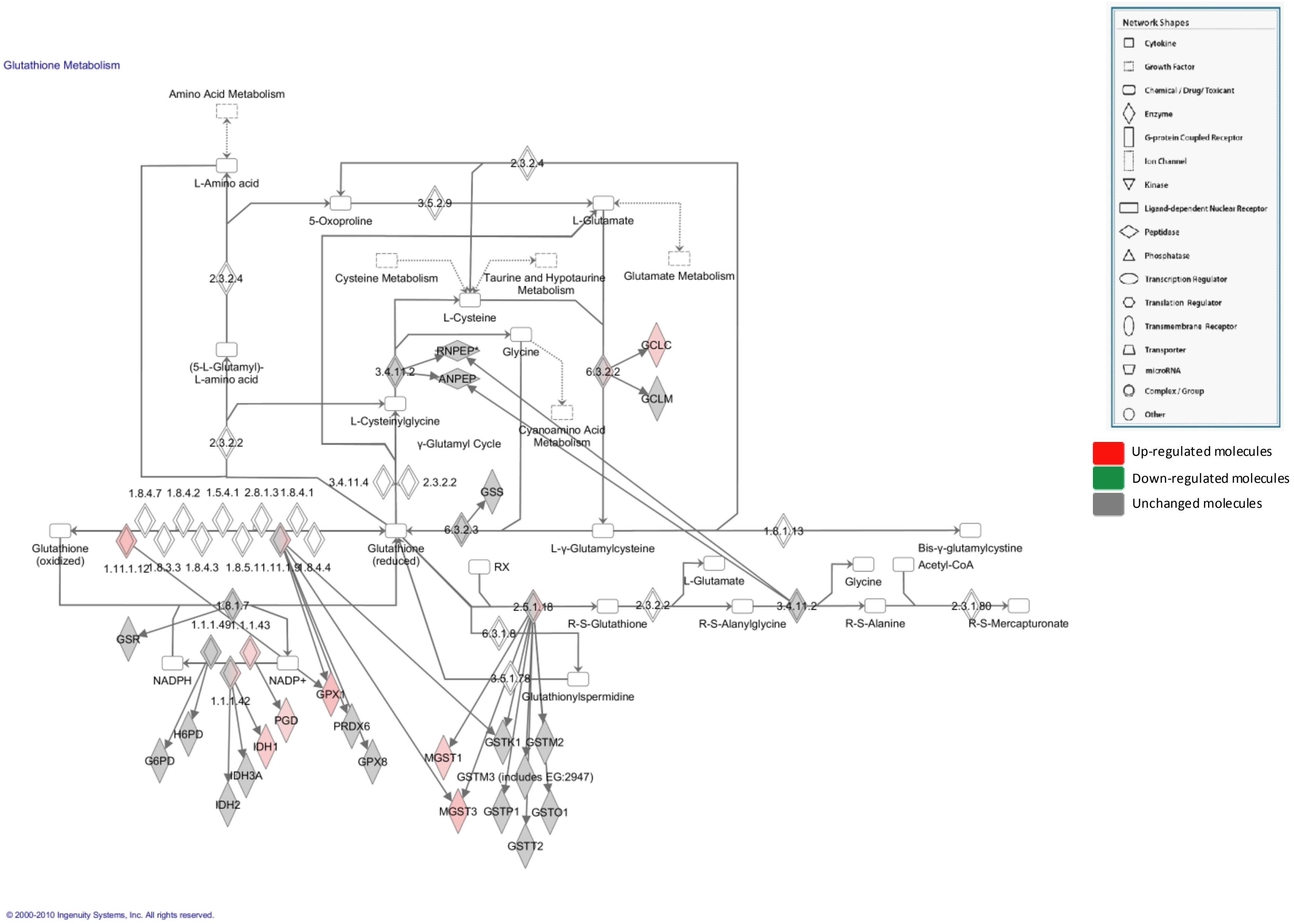


SUPPLEMENTARY FIGURE S9

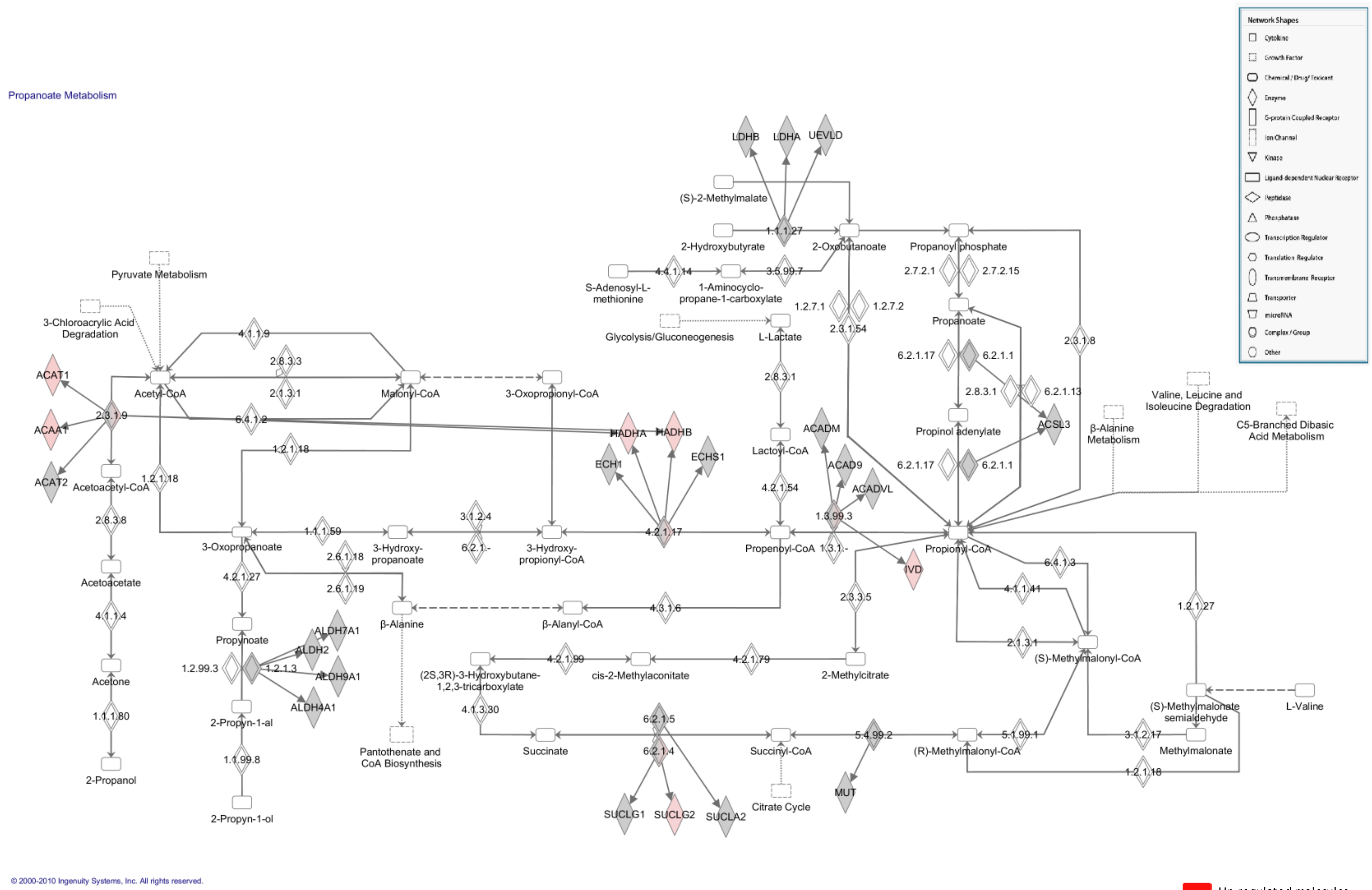


🟥 Up-regulated molecules
🟩 Down-regulated molecules
⬛ Unchanged molecules

SUPPLEMENTARY FIGURE S10



SUPPLEMENTARY FIGURE S11



🟥 Up-regulated molecules
🟩 Down-regulated molecules
⬛ Unchanged molecules

SUPPLEMENTARY FIGURE S12

SUPPLEMENTARY TABLE S3

PATHWAY: NRF2-mediated oxidative stress response

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ACTA2	0610041G09RIK, a-SMA, AAT6, ACTSA, Actvs, ALPHA ACTIN VSM, ALPHA SMA, ALPHA SMOOTH MUSCLE ACTIN, ALPHA-ACTIN 2, FLJ45296, MGC127800, RGD: 621676, Similar to vascular alpha actin, Sm alpha actin, SMalphaA, SMOOTH MUSCLE ALPHA ACTIN	actin, alpha 2, smooth muscle, aorta	ACTA2	**-1.14**	**0.23465**	Cytoplasm	other	59
ACTB	A-X actin, Actin beta, Actx, BETA ACTIN, BETA CA, E430023M04Rik, Melanoma x actin, MGC128179, PS1TP5BP1	actin, beta	NP_001092	**-1.12**	**0.26517**	Cytoplasm	other	60
ACTG1	ACT, ACTG, Actin gamma, ACTL, AL023024, beta-actin, Chi-actin, DFNA20, DFNA26, E51, GAMMA ACTIN, MGC28612, MGC117491	actin, gamma 1	NP_001605	**-1.08**	**0.35337**	Cytoplasm	other	71
AKR	2610201A18Rik, Akr1a4, Akra, ALDEHYDE REDUCTASE, ALDR1, ALR, ARM, DD3, MGC1380, MGC12529	aldo-keto reductase family 1, member A1 (aldehyde reductase)	NP_006057	**1.27**	**0.15481**	Cytoplasm	enzyme	10327
AKR1B1	ADR, Ahr-1, Akr1b3, Akr1b4, Aldolase Reductase, Aldor1, aldose reductase, ALDR1, ALDRED, Alr, ALR2, ALR-P-I, Androgen-induced aldose reductase, AR, MGC1804, RATALDRED	aldo-keto reductase family 1, member B1 (aldose reductase)	NP_001619	**1.82**	**0.0010301**	Cytoplasm	enzyme	231
AKR7A2	2-Cba Reductase, 0610025K21Rik, AFAR, AFAR1, AFB1-AR1, Aiar, AKR7, Akr7a5	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	NP_003680	**1.25**	**0.17548**	Cytoplasm	enzyme	8574
AKT	AKT, MGC99656, PKB, PKB-ALPHA, PKB/AKT, PRKBA, Protein kinase B, RAC, RAC-ALPHA, Thymoma viral proto-oncogene 1	v-akt murine thymoma viral oncogene homolog 1	NP_001014431	**-1.18**	**0.25703**	Cytoplasm	kinase	207
CAT	2210418N07, ACATALASIA, Cas-1, CATALASE, Catalase1, Cs-1, MGC128112, MGC138422, MGC138424, RATCAT01, RATCATL	catalase	NP_001743	**1.12**	**0.31249**	Cytoplasm	enzyme	847
CBR1	AW261796, Carbonyl Reductase, CBR, CR, CRN, hCBR1, MGC124927, Ocr, SDR21C1	carbonyl reductase 1	NP_001748	**1.24**	**0.12776**	Cytoplasm	enzyme	873
CCT7	AA408524, AL022769, CCT-ETA, CCTH, Cctz, Chaperonin 7, Chaperonin subunit 7, MGC110985, NIP7-1, TCP1ETA	chaperonin containing TCP1, subunit 7 (eta)	NP_006420	**-1.04**	**0.44457**	Cytoplasm	other	10574
CLPP	AU019820, D17Wsu160e	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	NP_006003	**1.28**	**0.17218**	Cytoplasm	peptidase	8192
CUL3	AI467304, AW146203, MGC189292, mKIAA0617	cullin 3	NP_003581	**-1.12**	**0.33617**	Nucleus	enzyme	8452
DNAJA1	DJ-2, DjA1, DNAJL2, HDJ, HDJ2, Heat shock 40-kDa protein 4, HSDJ, HSJ2, HSPF4, Nedd7	DnaJ (Hsp40) homolog, subfamily A, member 1	NP_001530	**-1.11**	**0.31384**	Nucleus	other	3301
DNAJA2	1500017M13RIK, 2010206B19RIK, CPR3, DJ3, DJA2, DNAJ, Dnaj3, DNJ3, DNJA2, HIRIP4, mDj3, MGC93325, PRO3015, RDJ2, Similar to hsp40	DnaJ (Hsp40) homolog, subfamily A, member 2	NP_005871	**-1.07**	**0.38747**	Nucleus	enzyme	10294
DNAJB1	0610007I11Rik, HDJ1, HSP40, HSPF1, RSPH16B, Sis1	DnaJ (Hsp40) homolog, subfamily B. member 1	NP_006136	**-1.51**	**0.015504**	Nucleus	other	3337
DNAJB11	1810031F23Rik, ABBP-2, AL024055, DJ9, EDJ, ERdj3, ERj3, hDj9, HEDJ, LRRGT00084, MGC112680, PRO1080, UNQ537	DnaJ (Hsp40) homolog, subfamily B, member 11	NP_057390	**-1.10**	**0.3223**	Cytoplasm	other	51726
DNAJB12	DJ10, DKFZp586B2023, mDj10, MGC94679	DnaJ (Hsp40) homolog, subfamily B, member 12	NP_001002762	**-1.05**	**0.43731**	Cytoplasm	other	54788
DNAJB4	1700029A20Rik, 2010306G19RIK, 5730460G06Rik, DjB4, DNAJW, HLJ1	DnaJ (Hsp40) homolog, subfamily B. member 4	NP_008965	**-1.40**	**0.041249**	Nucleus	other	11080
DNAJB6	DJ4, DKFZp566D0824, DnaJ, FLJ42837, HHDJ1, HSJ-2, mDj4, MGC1152, MGC102124, MGC117297, MGC139792, MRJ. MSJ-1	DnaJ (Hsp40) homolog, subfamily B. member 6	NP_490647	**-1.80**	**0.007898**	Nucleus	ıscription regula	10049
DNAJC10	1200006L06Rik, D2Ertd706e, DKFZp434J1813, ERDJ5, JPDI, MGC104194	DnaJ (Hsp40) homolog, subfamily C. member 10	NP_061854	**1.67**	**0.046982**	Cytoplasm	enzyme	54431
DNAJC13	D030002L11Rik, FLJ25863, Gm1124, KIAA0678, mKIAA0678, RME-8	DnaJ (Hsp40) homolog, subfamily C, member 13	NP_056083	**1.43**	**0.1182**	unknown	other	23317
DNAJC3	58kda Inhibitor Of RNA Activated Protein Kinase, AA408985, AU067833, Dnajc3a, Dnajc3b, FLJ21288, HP58, LOC144871, LOC63880, MGC6474, mp58, P58, P58IPK, p58K, Pkip58, PRKRI	DnaJ (Hsp40) homolog, subfamily C, member 3	NP_006251	**1.05**	**0.463**	Cytoplasm	other	5611
DNAJC7	2010003F24Rik, 2010004G07Rik, Ccrp, DJ11, DJC7, mDj11, MGC105609, mTpr2, TPR2, TTC2	DnaJ (Hsp40) homolog, subfamily C, member 7	NP_003306	**-1.20**	**0.1942**	Cytoplasm	other	7266
DNAJC8	1110021D09Rik, 2010009J04RIK, AL024084, AU019262, AU044514, HSPC331, SPF31	DnaJ (Hsp40) homolog, subfamily C. member 8	NP_055095	**-1.52**	**0.035792**	Nucleus	other	22826

DNAJC9	5330419I01Rik, AU020082, HDJC9, JDD1, KIAA0974, SB73	DnaJ (Hsp40) homolog, subfamily C, member 9	NP_056005	-1.48	0.054613	unknown	other	23234
EPHX1	AI195553, Ehm, Eph-1, EPHX, EPOX, Epoxide Hydrolase, EPXH1, MEH, MEH8, MICROSOMAL EPOXIDE HYDROLASE	epoxide hydrolase 1, microsomal (xenobiotic)	NP_000111	1.95	0.0033081	Cytoplasm	peptidase	2052
ERP29	1200015M03Rik, 2810446M09Rik, AW209030, C12ORF8, ERp28, ERp31, PDI-DB, PDIA9	endoplasmic reticulum protein 29	NP_006808	1.27	0.10543	Cytoplasm	transporter	10961
FTH1	AL022624, AL033366, APOFERRITIN H CHAIN, FERRITIN H, FERRITIN H CHAIN, Ferritin heavy chain, Ferritin subunit H, FHC, Frih, FTH, FTHL6, H FERRITIN, Hcf, MFH, MGC104426, PIG15, PLIF	ferritin, heavy polypeptide 1	NP_002023	3.65	8.09E-08	Cytoplasm	enzyme	2495
FTL	EG665937, ENSMUSG00000062382, FERRITIN LIGHT CHAIN, FRIL, Fril1, FTL1, Ftl2, L-FERRITIN, MGC71996, MGC102130, MGC102131, MGC118079, MGC118080, NBIA3, RGD1560687, RGD1561055, RGD1566189, YB24D08	ferritin, light polypeptide	NP_000137	3.04	3.36E-06	Cytoplasm	other	2512
GCLC	D9Wsu168e, GAMMA GCS HEAVY CHAIN, Gamma Glutamyl Cysteine Synthetase Light Subunit, Gamma Glutamylcysteine Synthetase, Gamma glutamylcysteine synthetase heavy subunit, GAMMA-GCS, GAMMA-GCSH, GCL, GCS, GCS, Catalytic, GCS-HS, GCSH, Ggcs-hs, GLCL, GLCL-H, GLCLC, Glutamate-Cysteine Ligase, Catalytic Subunit, MGC93096	glutamate-cysteine ligase, catalytic subunit	NP_001489	1.65	0.020921	Cytoplasm	enzyme	2729
GCLM	AI649393, Gamma gclm, GAMMA GCS LIGHT CHAIN, Gamma glutamylcysteine synthase (regulatory), GAMMA GLUTAMYLCYSTEINE SYNTHETASE, GCS1, Gcs Ls, Gcs, Regulatory, GCS-L, Gcslc, GLCLR, glutamat-cystein ligase, regulatory subunit, Glutamate-Cysteine Ligase, Modifier Subunit	glutamate-cysteine ligase, modifier subunit	NP_002052	1.18	0.27621	Cytoplasm	enzyme	2730
GSR	AI325518, D8Ertd238e, GLUTATHIONE REDUCTASE, Gr, Gr-1, Gred, GRX, MGC78522	glutathione reductase	NP_000628	1.40	0.082832	Cytoplasm	enzyme	2936
GSTK1	0610025I19Rik, AW260476, DsbA-L, GST, GST13, GST class-kappa, GST13-13, GSTK1-1, GSTkappa, hGSTK1, LOC51064	glutathione S-transferase kappa 1	NP_001137151	1.40	0.080445	Cytoplasm	enzyme	373156
GSTM2	0610005A07Rik, AI894236, Cd203c, GST4, Gst Yb3, GSTA4, Gstb-2, GSTM, Gstm3, Gstm7, GSTM2-2, GTHMUS, MGC117303	glutathione S-transferase mu 2 (muscle)	NP_000839	1.14	0.28327	Cytoplasm	enzyme	2946
GSTM3 (includes EG:2947)	FSC2, GST5, Gst mu 5, GSTB, GSTM3, Gstm5, GSTM3-3, GTM3, MGC3310, MGC3704	glutathione S-transferase mu 3 (brain)	NP_000840	1.25	0.11884	Cytoplasm	enzyme	2947
GSTP1	DFN7, FAEES3, GLUTATHIONE S TRANSFERASE PHI, GLUTATHIONE S-TRANSFERASE PI, Glutathione s-transferase, chain b, Gm3934, GST3, GST P1-1, GST PI, Gst pi-class subunit 7, Gst Yf, GST-P, Gst7-7, Gst7pi, Gstp2, GSTpiA, GstpiB, Lysyl Oxidase 2, MGC72668, MGC72669, PI	glutathione S-transferase pi 1	NP_000843	1.04	0.3933	Cytoplasm	enzyme	2950
GSTT2	AI266894, Glutathione-s-transferase theta2, GSTT, MGC182032, mGSTT2, Yrs	glutathione S-transferase theta 2	NP_000845	1.24	0.23331	Cytoplasm	enzyme	2953
HIP2	AW492011, D5Ertd601e, DKFZp564C1216, DKFZp686J24237, E2-25K, HIP2, HYPG, LIG, UBIQUITIN CARRIER, UBIQUITIN CARRIER PROTEIN	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	NP_005330	-1.17	0.21223	Cytoplasm	scription regul	3093
HO-1	bK286B10, D8Wsu38e, HEME OXYGENASE, HEME OXYGENASE (DECYCLIZING) 1, HEME OXYGENASE-1, Hemox, Heox, HEOXG, Hmox, HO-1, HSP32	heme oxygenase (decycling) 1	NP_002124	6.65	1.07E-14	Cytoplasm	enzyme	3162
HSP90AA1	86kDa, 89kDa, AL024080, AL024147, FLJ31884, Heat shock protein 1, alpha, hsp4, HSP86, HSP89, Hsp90, Hsp86-1, Hsp89-alpha-delta-N, HSP89A, HSP90 ALPHA, HSP90A, HSP90N, HSPC1, HSPCA, HSPCAL1, HSPCAL4, HSPN, LAP2, MGC105293	heat shock protein 90kDa alpha (cytosolic), class A member 1	NP_001017963	-1.05	0.41083	Cytoplasm	other	3320
HSP90AB1	90kDa, AL022974, C81438, D6S182, FLJ26984, HSP84, HSP90, Hsp1beta, Hsp84-1, Hsp90 alpha, HSP90-BETA, HSP90B, HSPC2, HSPCB, MGC94263, MGC115780	heat shock protein 90kDa alpha (cytosolic), class B member 1	NP_031381	-1.08	0.33909	Cytoplasm	other	3326
KRAS	AI929937, C-K-RAS, c-Ki-ras, c-Ki-ras p21, Ha-ras, K-RAS B, K-RAS2A, K-RAS2B, K-RAS4A, KI-RAS, KI-RAS4B, KRAS1, KRAS2, MGC7141, NS, NS3, p21, p21B, p21ras, RAS, RAS1, RASH, RASK2	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	NP_004976	-1.23	0.20399	Cytoplasm	enzyme	3845
MAP2K1	Map Kinase Kinase, MAPKK1, Mek, MEK1, MEKK1, MKK1, Mkp1, PRKMK1	mitogen-activated protein kinase kinase 1	NP_002746	-1.03	0.41162	Cytoplasm	kinase	5604
MAP2K2	AA589381, ERK ACTIVATOR KINASE 2, FLJ26075, MAPKK2, MEK2, Mitogen activated protein kinase kinase 2, MK2, MKK2, p45 MAPK KINASE, PRKMK2	mitogen-activated protein kinase kinase 2	NP_109587	1.06	0.43694	Cytoplasm	kinase	5605
MAP2K3	AW212142, MAP KINASE KINASE 3B, MAPKK3, MEK3, MKK3, MKK3B, mMKK3b, PRKMK3	mitogen-activated protein kinase kinase 3	NP_659731	-1.20	0.23519	Cytoplasm	kinase	5606
MAPK1	9030612K14Rik, AA407128, AU018647, C78273, ERK, ERK2, ERK42, ERT1, MAPK2, Mapk p42, Mapk1,2, MITOGEN ACTIVATED PROTEIN KINASE 2, Mpk2, p38, p40, p41, P42, p40 HERAK, p41mapk, p42 Erk, P42MAPK, PRKM1, PRKM2	mitogen-activated protein kinase 1	NP_002736	1.07	0.3449	Cytoplasm	kinase	5594
MAPK3	ERK-1, Esrk1, HS44KDAP, HUMKER1A, Mapk p44, Mapkapk3, MGC20180, Mtap2k, P44, p44-erk, P44ERK1, P44MAPK, PRKM3	mitogen-activated protein kinase 3	NP_002737	1.43	0.068843	Cytoplasm	kinase	5595
MGST1	1500002K10Rik, Glutathione s-transferase 1, Gst, GST12, MGC14525, MGC72699, MGST, MGST-I, MICROSOMAL GT	microsomal glutathione S-transferase 1	NP_064696	1.68	0.016618	Cytoplasm	enzyme	4257
MGST3	2010012L10RIK, 2010306B17Rik, 2700004G04RIK, AA516734, GST-III, Loc289197	microsomal glutathione S-transferase 3	NP_004519	2.02	0.010773	Cytoplasm	enzyme	4259
MRP1	ABC29, ABCC, Abcc1a, Abcc1b, Avcc1a, DKFZp686N04233, DKFZp781G125, GS-X, Mdrap, MRP, MRP1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	NP_004987	2.13	8.66E-04	lasma Membrar	transporter	4363

NQO2	DHQV, DIA6, MGC94180, NMO2, NMOR2, Ox-2, QR2	NAD(P)H dehydrogenase, quinone 2	NP_000895	**1.05**	**0.42868**	Cytoplasm	enzyme	4835
NRAS	ALPS4, AV095280, c-N-ras p21, DNA Segment, Chr 3, Mjeffers 1, NRAS1, NRASR, NS6, RAS, v-Ras	neuroblastoma RAS viral (v-ras) oncogene homolog	NP_002515	**-1.05**	**0.37592**	asma Membrar	enzyme	4893
PPIB	AA408962, AA553318, AI844835, CPHN2, Cy-Lp, CYCLOPHILIN-B, CyP-20b, CYP-S1, CYPB, MGC2224, MGC14109, OI9, SCYLP	peptidylprolyl isomerase B (cyclophilin B)	NP_000933	**1.12**	**0.25918**	Cytoplasm	enzyme	5479
PRDX1	ENHANCER, Enhancer protein, Hbp23, MGC108617, MSP23, NKEFA, OSF-3, PAG, PAGA, PAGB, PEROXIREDOXIN 1, PEROXYREDOXIN 1, PrdxI, PRX1, PRX I, TDPX2, TDX2, TPX2, TPxA	peroxiredoxin 1	NP_002565	**1.15**	**0.21492**	Cytoplasm	enzyme	5052
PRDX2	AL022839, Band-8, MGC4104, NATURAL KILLER CELL ENHANCING FACTOR B, NKEFB, Peroxide reductase, Peroxiredoxin 2, PRDX-2 ISOFORM A, PRP, PRX2, PRX II, TDPX1, TDX1, Thioredoxin dependent peroxide reductase, Torin, TPx, TPx1, TPx-B, TR, TSA	peroxiredoxin 2	NP_005800	**1.10**	**0.28559**	Cytoplasm	enzyme	7001
PRDX5	ACR1, AOEB166, AOPP, B166, MGC117264, MGC142283, MGC142285, Peroxiredoxin 5, PLP, PMP20, PRDX6, PRXV, SBBI10, THIOREDOXIN PEROXIDASE 5	peroxiredoxin 5	NP_036226	**1.26**	**0.10597**	Cytoplasm	enzyme	25824
PRDX6	1 CYS PEROXIREDOXIN, 1-Cys, 1-Cys PRX, 9430088D19RIK, AA690119, AIPLA2, ANTI-OXIDANT PROTEIN2, Antioxidant Enzyme B166, AOP2, Aop2-rs3, Brp-12, CP-3, GPx, KIAA0106, KIAA106, LPLA2, Ltw-4, Lvtw-4, MGC46173, mKIAA0106, NSGP, NSGPx, ORF06, p29, PEROXIREDOXIN 6, Prdx5, PRDX6-RS3, PRX, PRX6, PrxV	peroxiredoxin 6	NP_004896	**-1.15**	**0.21527**	Cytoplasm	enzyme	9588
PTPLAD1	4930523M17RIK, AW742319, B-IND1, FLJ90376, HSPC121, MGC25483	protein tyrosine phosphatase-like A domain containing 1	NP_057479	**1.54**	**0.078113**	Cytoplasm	other	51495
RRAS	AI573426, MGC129444, MGC129445	related RAS viral (r-ras) oncogene homolog	NP_006261	**-1.16**	**0.22769**	Cytoplasm	enzyme	6237
RRAS2	2610016H24Rik, C86394, MGC109327, TC21	related RAS viral (r-ras) oncogene homolog 2	NP_036382	**-1.05**	**0.44202**	asma Membrar	enzyme	22800
SOD1	ALS, ALS1, B430204E11Rik, CU/ZN-SOD, CUZNSOD, czSOD, EG667310, homodimer, Ipo-1, IPOA, MGC107553, SOD, SOD1L1, SODC	superoxide dismutase 1, soluble	NP_000445	**1.22**	**0.13941**	Cytoplasm	enzyme	6647
SOD2	IPOB, MANGANESE DEPENDENT SOD, Manganese Superoxide Dismutase 2, MGC5618, MGC6144, MGC128371, MITOCHONDRIAL SOD, Mn superoxide dismutase, MNSOD, MVCD6	superoxide dismutase 2, mitochondrial	NP_000627	**1.09**	**0.34609**	Cytoplasm	enzyme	6648
SQSTM1	A170, OSF-6, Osi, OSIL, Oxidative Stress, p60, P62, p62B, PDB3, Pkc zeta interacting, STAP, Ubiquitin-binding protein a, ZIP, ZIP3	sequestosome 1	NP_003891	**2.93**	**6.62E-06**	Cytoplasm	ıscription regula	8878
STIP1	HOP, IEF-SSP-3521, mSTI1, P60, SIP1, STI1, STI1L, Stress-induced phosphoprotein 1	stress-induced-phosphoprotein 1	NP_006810	**-1.03**	**0.46429**	Cytoplasm	other	10963
TRXR1	GRIM-12, KM 102 DERIVED REDUCTASE LIKE FACTOR, MGC9145, MGC93353, Tgr, Thioredoxin reductase, TR, TR1, TRXR1, TXNR	thioredoxin reductase 1	NP_001087240	**1.76**	**0.0017543**	Cytoplasm	enzyme	7296
TXN	ADF, AW550880, DKFZp686B1993, EOSINOPHIL CYTOTOXICITY FACTOR, MGC61975, MGC151960, THIOREDOXIN, TRX, TRX1, Txn1	thioredoxin	NP_003320	**2.01**	**0.0022687**	Cytoplasm	enzyme	7295
USP14	2610005K12Rik, 2610037B11RIK, AW107924, ax, C78769, MGC95160, TGT, Ubiquitin specific protease 14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	NP_005142	**-1.03**	**0.45801**	Cytoplasm	peptidase	9097
VCP	3110001E05, CDC48, IBMPFD, MGC8560, MGC131997, MGC148092, P97, P97 kinase, p97/VCP, Ter atpase, TERA, TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE, XSG7	valosin-containing protein	NP_009057	**1.07**	**0.34417**	Cytoplasm	enzyme	7415

PATHWAY: **Synthesis and degradation of ketone bodies**

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ACAA1	3-oxoacyl-coa Thiolase, ACAA, Acaa1a, Acaa1b, D9Ertd25e, MGC108766, MGC7090, Peroxisomal 3-Ketoacyl CoA Thiolase, peroxisomal 3-oxoacyl-Coenzyme A thiolase, Peroxisomal thiolase, Pktaa, Pt, PTHIO, pThiol, PTL, RGD1562373, THIO, THIOLASE	acetyl-Coenzyme A acyltransferase 1	NP_001598	**1.62**	**0.023554**	Cytoplasm	enzyme	30
ACAT1	3-Ketothiolase, 6330585C21Rik, AA CoA Thiolase, ACAT, Acetyl-CoA acetlytransferase 1, Acyl-coa acetyltransferase, Acyl-coa acetyltransferase 1, MAT, RATACAL, T2, THIL	acetyl-Coenzyme A acetyltransferase 1	NP_000010	**1.65**	**0.0050079**	Cytoplasm	enzyme	38
ACAT2	Ab2-076, Acat3, Acetoacetyl Coa Thiolase, ACETOCOENZYME A ACETYLTRANSFERASE 2, ACTL, AW742799, MGC95138, Similar to tcp1x, T2, Tcp-1x, Tcp-x1, Tcp1-rs1	acetyl-Coenzyme A acetyltransferase 2	NP_005882	**1.23**	**0.19111**	Cytoplasm	enzyme	39
BDH2	1810026B04Rik, DHRS6, EFA6R, FLJ13261, PRO20933, SDR15C1, UCPA-OR, UNQ6308	3-hydroxybutyrate dehydrogenase, type 2	NP_064524	**1.28**	**0.17058**	Cytoplasm	enzyme	56898
HADHA	C77020, ECHA, Enoyl-CoA Hydratase, GBP, HADH, LCHAD, MGC1728, MGC105338, Mitochondrial long chain enoyl CoA hydratase, Mitochondrial trifunctional protein alpha, MTPA, RGD1560655, TP-ALPHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	NP_000173	**1.46**	**0.025326**	Cytoplasm	enzyme	3030

HADHB	3-ketoacyl-CoA thiolase, 4930479F15Rik, A hydratase (trifunctional protein), beta subunit, ECHB, Gm13910, LOC100048492, MGC87480, Mitochondrial long chain 3-ketoacyl-CoA thiolase, MSTP029, Mtpb, OTTMUSG00000015054, TP-BETA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	NP_000174	**1.50**	**0.017067**	Cytoplasm	enzyme	3032
HMGCL	3-Hydroxy-3-methylglutaryl coa lyase, AW476067, HL, HMG CoA lyase	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	HMGCL	**-7.76**	**1.04E-17**	Cytoplasm	enzyme	3155
HMGCS1	B130032C06Rik, HMGCS, Hydroxymethylglutaryl-CoA synthase, cytoplasmic, LOC100040592, MGC36662, MGC90332, MGC98430	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NP_001091742	**2.20**	**5.31E-04**	Cytoplasm	enzyme	3157
OXCT1	2610008O03Rik, 3-Oxoacid coa transferase, LOC678860, LOC690109, LOC690163, MGC187935, OXCT, Oxct1 (predicted), Oxct2a, SCOT, Scot-s, Succinyl coa:3-ketoacid coa transferase, Succinyl COA:3-OXOACID COA TRANSFERASE	3-oxoacid CoA transferase 1	NP_000427	**-1.00**	**0.4867**	Cytoplasm	enzyme	5019

PATHWAY: **Butanoate Metabolism**

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ACAA1	3-oxoacyl-coa Thiolase, ACAA, Acaa1a, Acaa1b, D9Ertd25e, MGC7090, MGC108766, Peroxisomal 3-Ketoacyl CoA Thiolase, peroxisomal 3-oxoacyl-Coenzyme A thiolase, Peroxisomal thiolase, Pktaa, Pt, PTHIO, pThiol, PTL, RGD1562373, THIO, THIOLASE	acetyl-Coenzyme A acyltransferase 1	NP_001598	**1.62**	**0.023554**	Cytoplasm	enzyme	30
ACAT1	3-Ketothiolase, 6330585C21Rik, AA CoA Thiolase, ACAT, Acetyl-CoA acetlytransferase 1, Acyl-coa acetyltransferase, Acyl-coa acetyltransferase 1, MAT, RATACAL, T2, THIL	acetyl-Coenzyme A acetyltransferase 1	NP_000010	**1.65**	**0.0050079**	Cytoplasm	enzyme	38
ACAT2	Ab2-076, Acat3, Acetoacetyl Coa Thiolase, ACETOCOENZYME A ACETYLTRANSFERASE 2, ACTL, AW742799, MGC95138, Similar to tcp1x, T2, Tcp-1x, Tcp-x1, Tcp1-rs1	acetyl-Coenzyme A acetyltransferase 2	NP_005882	**1.23**	**0.19111**	Cytoplasm	enzyme	39
ALDH2	Ahd-5, Aldehyde dehydr 2,A2, ALDH-E2, ALDHI, ALDM, Hepatic aldehyde dehydrogenase 2, MGC1806	aldehyde dehydrogenase 2 family (mitochondrial)	NP_000681	**1.22**	**0.20106**	Cytoplasm	enzyme	217
ALDH4A1	A930035F14Rik, Ahd-1, ALDH4, Aldh5a1, DKFZp779M035, E330022C09, P5CD, P5CDh, P5cdhl, P5cdhs, Ssdh1	aldehyde dehydrogenase 4 family, member A1	NP_003739	**1.53**	**0.080166**	Cytoplasm	enzyme	8659
ALDH7A1	Aldehyde dehydrogenase family 7 member a1, antiquitin, ATQ1, D18Wsu181e, EPD, FLJ11738, FLJ92814, PDE	aldehyde dehydrogenase 7 family, member A1	NP_001173	**1.21**	**0.21109**	Cytoplasm	enzyme	501
ALDH9A1	4-Trimethylaminobutyraldehyde Dehydrogenase 9a, AA139417, Abaldh, ALDH4, ALDH7, ALDH9, E3, ESTM40, TMABA-DH	aldehyde dehydrogenase 9 family, member A1	NP_000687	**1.18**	**0.23452**	Cytoplasm	enzyme	223
BDH2	1810026B04Rik, DHRS6, EFA6R, FLJ13261, PRO20933, SDR15C1, UCPA-OR, UNQ6308	3-hydroxybutyrate dehydrogenase, type 2	NP_064524	**1.28**	**0.17058**	Cytoplasm	enzyme	56898
DCXR	0610038K04Rik, 1810027P18Rik, DCR, glb, HCR2, HCRII, KIDCR, P34H, SDR20C1	dicarbonyl/L-xylulose reductase	NP_057370	**1.14**	**0.32316**	Cytoplasm	enzyme	51181
ECH1	AA617331, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, peroxisomal, HIP11, HPXEL, MGC107274, Mitochondrial dienoyl-coa isomerase, Perox enolhydratase, Peroxisomal enoyl hydratase-like, Pxel	enoyl Coenzyme A hydratase 1, peroxisomal	NP_001389	**-1.04**	**0.4027**	Cytoplasm	enzyme	1891
ECHS1	C80529, Enoyl-CoA hydratase, short-chain, 1, mitochondrial, SCEH	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NP_004083	**1.34**	**0.11116**	Cytoplasm	enzyme	1892
HADH	3 Hydroxyacyl Coenzyme A Dehydrogenase, 3-hydroxyacyl-coa dehydrogenase, AA409008, AU019341, AW742602, Beta-3 Hydroxyacyl Coenzyme A Dehydrogenase, HAD, HADH1, HADHSC, HHF4, M/SCHAD, MGC8392, SCHAD	hydroxyacyl-Coenzyme A dehydrogenase	NP_005318	**1.09**	**0.37321**	Cytoplasm	enzyme	3033
HADHA	C77020, ECHA, Enoyl-CoA Hydratase, GBP, HADH, LCHAD, MGC1728, MGC105338, Mitochondrial long chain enoyl CoA hydratase, Mitochondrial trifunctional protein alpha, MTPA, RGD1560655, TP-ALPHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	NP_000173	**1.46**	**0.025326**	Cytoplasm	enzyme	3030
HADHB	3-ketoacyl-CoA thiolase, 4930479F15Rik, A hydratase (trifunctional protein), beta subunit, ECHB, Gm13910, LOC100048492, MGC87480, Mitochondrial long chain 3-ketoacyl-CoA thiolase, MSTP029, Mtpb, OTTMUSG00000015054, TP-BETA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	NP_000174	**1.50**	**0.017067**	Cytoplasm	enzyme	3032

HMGCL	3-Hydroxy-3-methylglutaryl coa lyase, AW476067, HL, HMG CoA lyase	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	HMGCL	-7.76	1.04E-17	Cytoplasm	enzyme	3155
HMGCS1	B130032C06Rik, HMGCS, Hydroxymethylglutaryl-CoA synthase, cytoplasmic, LOC100040592, MGC36662, MGC90332, MGC98430	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NP_001091742	2.20	5.31E-04	Cytoplasm	enzyme	3157
HSD17B10	17b-HSD10, ABAD, Ads9, CAMR, DUPXp11.22, ERAB, HADH2, HCD2, Hydroxysteroid dehydrogenase 10, MHBD, MRPP2, MRX17, MRX31, MRXS10, SCHAD, SDR5C1, XH98G2	hydroxysteroid (17-beta) dehydrogenase 10	NP_004484	1.26	0.16529	Cytoplasm	enzyme	3028
HSD17B4	17 beta Hydroxy Steroid Dehydrogenase Isoform 4, 17-BETA HSD4, 17[b]-HSD, AW208803, D-bifunctional, D-pbe, Dbf, DBP, HD, MFE-2, Mfp-2, NS1-I, perMFE-2, Ph, Pmeii, SDR8C1	hydroxysteroid (17-beta) dehydrogenase 4	NP_000405	1.42	0.075066	Cytoplasm	enzyme	3295
OXCT1	3-Oxoacid coa transferase, 2610008O03Rik, LOC678860, LOC690109, LOC690163, MGC187935, OXCT, Oxct1 (predicted), Oxct2a, SCOT, Scot-s, Succinyl coa:3-ketoacid coa transferase, Succinyl COA:3-OXOACID COA TRANSFERASE	3-oxoacid CoA transferase 1	NP_000427	-1.00	0.4867	Cytoplasm	enzyme	5019
PDHA1 (includes EG:5160)	E1 ALPHA PDH, MGC94854, MGC114215, Pdh e1alpha, PDHA, Pdha1, PDHCE1A, PHE1A, Pyruvate dehydrogenase e1 alpha1	pyruvate dehydrogenase (lipoamide) alpha 1	NP_000275	1.31	0.12954	Cytoplasm	enzyme	5160
PDHB	2610103L06Rik, AL024199, C81408, DKFZp564K0164, MGC94149, Odpb, PDHE1-B, PHE1B, Pyruvate dehydrogenase, Pyruvate dehydrogenase (lipoamide)	pyruvate dehydrogenase (lipoamide) beta	NP_000916	1.19	0.23003	Cytoplasm	enzyme	5162
PPME1	1110069N17Rik, 2700017M01Rik, FLJ22226, PME-1, RGD1309683	protein phosphatase methylesterase 1	NP_057231	-1.47	0.047468	unknown	enzyme	51400
SDHA	1500032O14RIK, 2310034D06Rik, 4921513A11, C81073, FP, SDH1, SDH2, SDHF, Succinate dehydrogenase complex, subunit A flavoprotein (Fp), Succinate-ubiquinone oxidoreductase 70-kda subunit	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	NP_004159	1.06	0.40684	Cytoplasm	enzyme	6389
SDHB	0710008N11Rik, FLJ92337, IP, PCHC, PGL4, SDH, SDH1, SDH2, SDHIP, Succinate Dehydrogenase Cytochrome B Subunit, Succinate Dehydrogenase Ip Cytochrome B Subunit, Succinate dehydrogenase putative iron sulfur subunit	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	NP_002991	1.09	0.39702	Cytoplasm	enzyme	6390
SUCLG2	AF171077, AW556404, D6Wsu120e, G-BETA, G-SCS, Loc362404, MGC91183, SCS-betaG	succinate-CoA ligase, GDP-forming, beta subunit	NP_003839	1.47	0.057346	Cytoplasm	enzyme	8801

PATHWAY: Bile acid synthesis

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ACAA1	3-oxoacyl-coa Thiolase, ACAA, Acaa1a, Acaa1b, D9Ertd25e, MGC7090, MGC108766, Peroxisomal 3-Ketoacyl CoA Thiolase, peroxisomal 3-oxoacyl-Coenzyme A thiolase, Peroxisomal thiolase, Pktaa, Pt, PTHIO, pThiol, PTL, RGD1562373, THIO, THIOLASE	acetyl-Coenzyme A acyltransferase 1	NP_001598	1.62	0.023554	Cytoplasm	enzyme	30
ACAA2	3-ketoacyl coa thiolase, 3-OXOACYL-COA THIOLASE, 0610011L04Rik, AI255831, AI265397, D18Ertd240e, DSAEC, FLJ35992, FLJ95265, T1	acetyl-Coenzyme A acyltransferase 2	NP_006102	1.34	0.10984	Cytoplasm	enzyme	10449
ADH5 (includes EG:128)	Adh5, ADH-3, ADHX, CLASS III ADH, FDH, Gs fdh, GSNOR	alcohol dehydrogenase 5 (class III), chi polypeptide	NP_000662	1.59	0.029378	Cytoplasm	enzyme	128
AKR1C1	2-ALPHA-HSD, 20-ALPHA-HSD, 9430025F20Rik, AI315367, Akr1c2, Akr1c21, C9, DD1, DDH, DDH1, DIHYDRODIOL DEHYDROGENASE, H-37, HAKRC, Hepatic Bile Acid Binding, MBAB, MGC8954, MGC102401	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	NP_001344	3.35	4.93E-07	Cytoplasm	enzyme	1645
ALDH2	Ahd-5, Aldehyde dehydr 2,A2, ALDH-E2, ALDHI, ALDM, Hepatic aldehyde dehydrogenase 2, MGC1806	aldehyde dehydrogenase 2 family (mitochondrial)	NP_000681	1.22	0.20106	Cytoplasm	enzyme	217
ALDH4A1	A930035F14Rik, Ahd-1, ALDH4, Aldh5a1, DKFZp779M035, E330022C09, P5CD, P5CDh, P5cdhl, P5cdhs, Ssdh1	aldehyde dehydrogenase 4 family, member A1	NP_003739	1.53	0.080166	Cytoplasm	enzyme	8659
ALDH7A1	Aldehyde dehydrogenase family 7 member a1, antiquitin, ATQ1, D18Wsu181e, EPD, FLJ11738, FLJ92814, PDE	aldehyde dehydrogenase 7 family, member A1	NP_001173	1.21	0.21109	Cytoplasm	enzyme	501
ALDH9A1	4-Trimethylaminobutyraldehyde Dehydrogenase 9a, AA139417, Abaldh, ALDH4, ALDH7, ALDH9, E3, ESTM40, TMABA-DH	aldehyde dehydrogenase 9 family, member A1	NP_000687	1.18	0.23452	Cytoplasm	enzyme	223
HADHA	C77020, ECHA, Enoyl-CoA Hydratase, GBP, HADH, LCHAD, MGC1728, MGC105338, Mitochondrial long chain enoyl CoA hydratase, Mitochondrial trifunctional protein alpha, MTPA, RGD1560655, TP-ALPHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	NP_000173	1.46	0.025326	Cytoplasm	enzyme	3030

HADHB	3-ketoacyl-CoA thiolase, 4930479F15Rik, A hydratase (trifunctional protein), beta subunit, ECHB, Gm13910, LOC100048492, MGC87480, Mitochondrial long chain 3-ketoacyl-CoA thiolase, MSTP029, Mtpb, OTTMUSG00000015054, TP-BETA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta	NP_000174	**1.50**	**0.017067**	Cytoplasm	enzyme	3032
PTGR1	2510002C21Rik, Ao, Dig1, FLJ99229, LTB4DH, MGC34943, PGR1, ZADH3	prostaglandin reductase 1	NP_036344	**1.50**	**0.01743**	Cytoplasm	enzyme	22949

PATHWAY: Valine, leucine, isoleucine degradation

Symbol	**Synonym(s)**	**Entrez Gene Name**	**HUGO Gene Symbol/RefSeq**	**Fold Change**	**p-value**	**Location**	**Family**	**Entrez Gene ID for Human**
ACAA1	3-oxoacyl-coa Thiolase, ACAA, Acaa1a, Acaa1b, D9Ertd25e, MGC7090, MGC108766, Peroxisomal 3-Ketoacyl CoA Thiolase, peroxisomal 3-oxoacyl-Coenzyme A thiolase, Peroxisomal thiolase, Pktaa, Pt, PTHIO, pThiol, PTL, RGD1562373, THIO, THIOLASE	acetyl-Coenzyme A acyltransferase 1	NP_001598	**1.62**	**0.023554**	Cytoplasm	enzyme	30
ACAA2	3-ketoacyl coa thiolase, 3-OXOACYL-COA THIOLASE, 0610011L04Rik, AI255831, AI265397, D18Ertd240e, DSAEC, FLJ35992, FLJ95265, T1	acetyl-Coenzyme A acyltransferase 2	NP_006102	**1.34**	**0.10984**	Cytoplasm	enzyme	10449
ACAD9	2600017P15RIK, 4732402K02, C630012L17RIK, FLJ23533, MGC14452, NPD002, NYGGF2	acyl-Coenzyme A dehydrogenase family, member 9	NP_054768	**1.23**	**0.21954**	Cytoplasm	enzyme	28976
ACADM	ACAD1, Acetyl coenzyme a dehydrogenase, medium chain, Acetyl-Coenzyme A Dehydrogenase, Acyl-CoA dehydrogenase, medium chain, AU018656, FLJ18227, FLJ93013, FLJ99884, MCAD, MCADH, MEDIUM-CHAIN FATTY ACYL-COA DEHYDROGENASE	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	NP_001120800	**1.33**	**0.16878**	Cytoplasm	enzyme	34
ACADVL	ACAD6, LCACD, MGC93660, VERY LONG-CHAIN FATTY ACYL-COA DEHYDROGENASE, VLACD, VLCAD	acyl-Coenzyme A dehydrogenase, very long chain	NP_000009	**-1.04**	**0.43264**	Cytoplasm	enzyme	37
ACAT1	3-Ketothiolase, 6330585C21Rik, AA CoA Thiolase, ACAT, Acetyl-CoA acetyltransferase 1, Acyl-coa acetyltransferase, Acyl-coa acetyltransferase 1, MAT, RATACAL, T2, THIL	acetyl-Coenzyme A acetyltransferase 1	NP_000010	**1.65**	**0.0050079**	Cytoplasm	enzyme	38
ACAT2	Ab2-076, Acat3, Acetoacetyl Coa Thiolase, ACETOCOENZYME A ACETYLTRANSFERASE 2, ACTL, AW742799, MGC95138, Similar to tcp1x, T2, Tcp-1x, Tcp-x1, Tcp1-rs1	acetyl-Coenzyme A acetyltransferase 2	NP_005882	**1.23**	**0.19111**	Cytoplasm	enzyme	39
ALDH2	Ahd-5, Aldehyde dehydr 2,A2, ALDH-E2, ALDHI, ALDM, Hepatic aldehyde dehydrogenase 2, MGC1806	aldehyde dehydrogenase 2 family (mitochondrial)	NP_000681	**1.22**	**0.20106**	Cytoplasm	enzyme	217
ALDH4A1	A930035F14Rik, Ahd-1, ALDH4, Aldh5a1, DKFZp779M035, E330022C09, P5CD, P5CDh, P5cdhl, P5cdhs, Ssdh1	aldehyde dehydrogenase 4 family, member A1	NP_003739	**1.53**	**0.080166**	Cytoplasm	enzyme	8659
ALDH7A1	Aldehyde dehydrogenase family 7 member a1, antiquitin, ATQ1, D18Wsu181e, EPD, FLJ11738, FLJ92814, PDE	aldehyde dehydrogenase 7 family, member A1	NP_001173	**1.21**	**0.21109**	Cytoplasm	enzyme	501
ALDH9A1	4-Trimethylaminobutyraldehyde Dehydrogenase 9a, AA139417, Abaldh, ALDH4, ALDH7, ALDH9, E3, ESTM40, TMABA-DH	aldehyde dehydrogenase 9 family, member A1	NP_000687	**1.18**	**0.23452**	Cytoplasm	enzyme	223
BCAT1	BCATc, BCT1, DKFZp686E12175, ECA39, MECA39, MGC105472, PNAS-121, PP18	branched chain aminotransferase 1, cytosolic	NP_005495	**-1.01**	**0.49371**	Cytoplasm	enzyme	586
ECH1	AA617331, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, peroxisomal, HIP11, HPXEL, MGC107274, Mitochondrial dienoyl-coa isomerase, Perox enolhydratase, Peroxisomal enoyl hydratase-like, Pxel	enoyl Coenzyme A hydratase 1, peroxisomal	NP_001389	**-1.04**	**0.4027**	Cytoplasm	enzyme	1891
ECHS1	C80529, Enoyl-CoA hydratase, short-chain, 1, mitochondrial, SCEH	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NP_004083	**1.34**	**0.11116**	Cytoplasm	enzyme	1892
HADH	3 Hydroxyacyl Coenzyme A Dehydrogenase, 3-hydroxyacyl-coa dehydrogenase, AA409008, AU019341, AW742602, Beta-3 Hydroxyacyl Coenzyme A Dehydrogenase, HAD, HADH1, HADHSC, HHF4, M/SCHAD, MGC8392, SCHAD	hydroxyacyl-Coenzyme A dehydrogenase	NP_005318	**1.09**	**0.37321**	Cytoplasm	enzyme	3033
HADHA	C77020, ECHA, Enoyl-CoA Hydratase, GBP, HADH, LCHAD, MGC1728, MGC105338, Mitochondrial long chain enoyl CoA hydratase, Mitochondrial trifunctional protein alpha, MTPA, RGD1560655, TP-ALPHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha	NP_000173	**1.46**	**0.025326**	Cytoplasm	enzyme	3030
HADHB	3-ketoacyl-CoA thiolase, 4930479F15Rik, A hydratase (trifunctional protein), beta subunit, ECHB, Gm13910, LOC100048492, MGC87480, Mitochondrial long chain 3-ketoacyl-CoA thiolase, MSTP029, Mtpb, OTTMUSG00000015054, TP-BETA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta	NP_000174	**1.50**	**0.017067**	Cytoplasm	enzyme	3032

HIBADH	6430402H10RIK, AI265272, MGC40361, NS5ATP1	3-hydroxyisobutyrate dehydrogenase	NP_689953	**1.39**	**0.097442**	Cytoplasm	enzyme	11112
HMGCL	3-Hydroxy-3-methylglutaryl coa lyase, AW476067, HL, HMG CoA lyase	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	HMGCL	**-7.76**	**1.04E-17**	Cytoplasm	enzyme	3155
HMGCS1	B130032C06Rik, HMGCS, Hydroxymethylglutaryl-CoA synthase, cytoplasmic, LOC100040592, MGC36662, MGC90332, MGC98430	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NP_001091742	**2.20**	**5.31E-04**	Cytoplasm	enzyme	3157
HSD17B10	17b-HSD10, ABAD, Ads9, CAMR, DUPXp11.22, ERAB, HADH2, HCD2, Hydroxysteroid dehydrogenase 10, MHBD, MRPP2, MRX17, MRX31, MRXS10, SCHAD, SDR5C1, XH98G2	hydroxysteroid (17-beta) dehydrogenase 10	NP_004484	**1.26**	**0.16529**	Cytoplasm	enzyme	3028
HSD17B4	17 beta Hydroxy Steroid Dehydrogenase Isoform 4, 17-BETA HSD4, 17[b]-HSD, AW208803, D-bifunctional, D-pbe, Dbf, DBP, HD, MFE-2, Mfp-2, NS1-I, perMFE-2, Ph, Pmeii, SDR8C1	hydroxysteroid (17-beta) dehydrogenase 4	NP_000405	**1.42**	**0.075066**	Cytoplasm	enzyme	3295
IVD	1300016K07Rik, 6720455E18Rik, ACAD2, AI463340, FLJ12715, FLJ34849, Isovaleryl-Coa Dehydrogenase	isovaleryl Coenzyme A dehydrogenase	NP_002216	**1.48**	**0.055705**	Cytoplasm	enzyme	3712
MUT	D230010K02RIK, MCM, MMCOAMUT, RGD1564912	methylmalonyl Coenzyme A mutase	NP_000246	**1.21**	**0.25761**	Cytoplasm	enzyme	4594
OXCT1	3-Oxoacid coa transferase, 2610008O03Rik, LOC678860, LOC690109, LOC690163, MGC187935, OXCT, Oxct1 (predicted), Oxct2a, SCOT, Scot-s, Succinyl coa:3-ketoacid coa transferase, Succinyl COA:3-OXOACID COA TRANSFERASE	3-oxoacid CoA transferase 1	NP_000427	**-1.00**	**0.4867**	Cytoplasm	enzyme	5019

PATHWAY: **Biosynthesis of steroids**

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
FDFT1	DGPT, ERG9, FARNESYL DIPHOSPHATE FARNESYL TRANSFERASE, Farnesyl diphosphate farnesyl transferase 1, Fpp farnesyl transferase 1, MGC93486, SQS, SQUALENE SYNTHASE, Squalene Synthetase, SS	farnesyl-diphosphate farnesyltransferase 1	NP_004453	**4.23**	**6.01E-10**	Cytoplasm	enzyme	2222
FDPS	6030492I17Rik, Ac2-125, AI256750, FARNESYL DIPHOSPHATE SYNTHASE, FARNESYL PYROPHOSPHATE SYNTHASE, Fdpsl1, FPP SYNTHASE, FPP synthetase, FPPS, FPS, KIAA1293, MGC107162, mKIAA1293	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltranstransferase)	NP_001129293	**1.70**	**0.014711**	Cytoplasm	enzyme	2224
IDI1	4832416K17Rik, IDP ISOMERASE, IPP1, Ipp delta isomerase, IPP ISOMERASE, IPP isomerase 1, IPPI1, Isopentenyl diphosphate:dimethylallyl diphosphate isomerase, ISOPENTENYL PYROPHOSPHATE ISOMERASE, MGC8139, MGC108635, MGC118013, Similar to isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase 1	NP_004499	**2.92**	**3.62E-06**	Cytoplasm	enzyme	3422
LSS	2,3-OXIDOSQUALENE-LANOSTEROL CYCLASE, 2810025N20Rik, BC029082, D10Ertd116e, FLJ25486, FLJ35015, FLJ39450, FLJ46393, LANOSTEROL CYCLASE, LANOSTEROL SYNTHASE, MGC27893, OSC	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	NP_001001438	**1.63**	**0.022782**	Cytoplasm	enzyme	4047
MVD	C78718, diphosphomevalonate decarboxylase, Erg19, FP17780, MEVALONATE PYROPHOSPHATE DECARBOXYLASE, MPD, Mvpd	mevalonate (diphospho) decarboxylase	NP_002452	**1.68**	**0.016721**	Cytoplasm	enzyme	4597
NQO2	DHQV, DIA6, MGC94180, NMO2, NMOR2, Ox-2, QR2	NAD(P)H dehydrogenase, quinone 2	NP_000895	**1.05**	**0.42868**	Cytoplasm	enzyme	4835
PMVK	1110011E12RIK, 2900002L22Rik, AV001327, HUMPMKI, MGC105660, PHOSPHOMEVALONATE KINASE, PMK, PMKA, PMKASE, PMKI	phosphomevalonate kinase	NP_006547	**-1.03**	**0.41846**	Cytoplasm	kinase	10654

PATHWAY: **Granzyme A signalling**

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ANP32A	Anp32, C15orf1, I1PP2A, LANP, LNAP, MAPM, MGC105504, MGC119787, MGC150373, PHAP1, PHAPI, PP32, PUTATIVE HLA CLASS II ASSOIATED PROTEIN I, PUTATIVEHLA CLASS II ASSOCIATED PROTEIN I, W91701	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	NP_006296	**1.27**	**0.17621**	Nucleus	other	8125
APEX1	APE, APE-1, APEN, APEX, APEX NUCLEASE, APX, HAP1, REF-1	APEX nuclease (multifunctional DNA repair enzyme) 1	NP_001632	**1.12**	**0.31404**	Nucleus	enzyme	328
GAAD	AL024257, AWD, GAAD, NB, NBS, NDKA, NDPK-A, NM23, NM23-H1, NM23-M1, NM23A, Nucleotide diphosphate kinase beta	non-metastatic cells 1, protein (NM23A) expressed in	NP_937818	**1.02**	**0.4395**	Nucleus	kinase	4830
H1F0	D130017D06Rik, H10, H1(0), H1FV, Histone h1, HISTONE H1-0, MGC5241, MGC19309, MGC98218, MGC117919	H1 histone family, member 0	NP_005309	**-1.54**	**0.03801**	Nucleus	other	3005
HIST1H1B	H1, H1.5, H1B, H1F5, H1s-3, LOC682425, MGC126630, MGC126632	histone cluster 1, H1b	NP_005313	**-2.03**	**9.01E-05**	Nucleus	other	3009
HIST1H1C	0610008C09Rik, H1.2, H1c, H1F2, H1var1, His1a, Histone h1, member 2, Histone h1.2, MGC3992, MGC107646	histone cluster 1, H1c	NP_005310	**-1.89**	**3.48E-05**	Nucleus	other	3006
HMG2	C80539, High mobility group 2, HMG-2, MGC103184, MGC108899, MGC125103, RGD1564519	high-mobility group box 2	NP_001124160	**-1.79**	**0.0083483**	Nucleus	transcription regulator	3148

IGAAD	2PP2A, 2610030F17Rik, 5730420M11Rik, AA407739, Ab1-115, ENSMUSG00000079225, Gm9531, I2PP2A, IGAAD, IPP2A2, MGC118419, PHAPII, StF-IT-1, TAF-I, TAF-IBETA, Template activating factor-1	SET nuclear oncogene	NP_003002	**1.03**	**0.42211**	Nucleus	phosphatase	6418
NME3	1810009F08Rik, AI413736, c371H6.2, DR-NM23, KIAA0516, Ndk3, NDPK-C, Nm23-DR, NM23-H3, Nm23-M3	non-metastatic cells 3, protein expressed in	NP_002504	**1.14**	**0.32251**	Cytoplasm	kinase	4832
RP2	AI662636, DELXp11.3, KIAA0215, NME10, RGD1565124, Rp2h, TBCCD2, XRP2	retinitis pigmentosa 2 (X-linked recessive)	NP_008846	**-1.03**	**0.47459**	Cytoplasm	enzyme	6102

PATHWAY: **Oxidative Phosphorylation**

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ATP5A1	AI035633, AL022851, AL023067, ALPHA SUBUNIT OF THE F1F0 ATP SYNTHASE (COMPLEX V), Atp synthase (f0f1), subunit alpha, Atp synthase alpha chain, ATP SYNTHASE ALPHA SUBUNIT, ATP Synthase F1 alpha, ATP synthase mitochondrial f1complex, ATP5A, ATP5AL2, ATPM, D18Ertd206e, F1 atpase, hATP1, MGC139059, MOM2, OMR, ORM, Q3u452	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	NP_001001937	**1.27**	**0.10129**	Cytoplasm	transporter	498
ATP5B	ATP Synthase Beta, ATP Synthase F1 Beta, Atpd, ATPMB, ATPSB, Beta atp synthase, BETA SUBUNIT ATP SYNTHASE, F1 Atp Synthase beta, F1 ATPASE BETA, F1 BETA ATPASE, H+ ATP Synthase Beta, MGC5231, OXPHOS COMPLEX V, SUBUNIT B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	NP_001677	**1.28**	**0.098157**	Cytoplasm	transporter	506
ATP5C1	1700094F02Rik, ATP5C, ATP5CL1, F1 gamma, GAMMA SUBUNIT F1F0 ATPASE	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	NP_005165	**1.17**	**0.19897**	Cytoplasm	transporter	509
ATP5D	0610008F14RIK, 1500000I11Rik, AA960090, AI876556, ATP Synthase F1 Delta, Atpase D, AU020773, C85518, F1F0 ATPase delta	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	NP_001001975	**1.39**	**0.096273**	Cytoplasm	transporter	513
ATP5F1	C76477, MGC24431, PIG47	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	NP_001679	**1.19**	**0.17187**	Cytoplasm	transporter	515
ATP5H (includes EG:10476)	0610009D10RIK, Atp synthase d subunit, ATP Synthase Subunit D, ATP5H, ATP5JD, ATPQ, RGD1559626	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	NP_006347	**1.20**	**0.21424**	Cytoplasm	transporter	10476
ATP5O	Atp Synthase, H+ Transporting, Mitochondrial F1 Complex, O Subunit, Atp synthase-mitochondrial f1, ATPO, D12Wsu28e, EG432676, MGC72688, OSCP	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	NP_001688	**1.19**	**0.17799**	Cytoplasm	transporter	539
ATP6AP1	16A, AC45, AI316502, ATP6IP1, ATP6S1, AW108110, C7-1, CF2, FLJ00383, mFLJ00383, MGC129781, ORF, V-ATPase S1 subunit, Vacuolar ATP synthase subunit s1, VATPS1, XAP-3	ATPase, H+ transporting, lysosomal accessory protein 1	NP_001174	**1.14**	**0.32827**	Cytoplasm	transporter	537
ATP6V0D1	Ac39, AI267038, ATP6D, ATP6DV, FLJ43534, LOC100132855, P39, Physophilin, VATX, VMA6, VPATPD	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	NP_004682	**1.33**	**0.1144**	Cytoplasm	transporter	9114
ATP6V1A	AI647066, ATP6A1, Atp6a2, ATP6V1A1, ATPase Vacuolar Subunit A, HO68, VA68, Vaa1, Vatpase 70 kd a subunit, Vma1, VPP2	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	NP_001681	**1.49**	**0.019803**	Cytoplasm	transporter	523
ATP6V1B2	AI194269, AI790362, ATP6B2, ATP6B1B2, Atpase H+ Transporting Lysosomal Isoform 2, HO57, R74844, V-ATPASE B2, VATB, Vma2, VPP3	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2	NP_001684	**1.61**	**0.0251**	Cytoplasm	transporter	526
ATP6V1C1	1700025B18Rik, ATP6C, ATP6D, FLJ20057, MGC109315, MGC140015, U13839, V-Atpase c, VATC, Vma5	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	NP_001686	**1.76**	**0.010395**	Cytoplasm	transporter	528
ATP6V1D	1110004P10Rik, ATP6M, Vacuolar ATPase Subunit D, VACUOLAR H ATPASE SUBUNIT D, VATD, VMA8	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	NP_057078	**1.06**	**0.44172**	Cytoplasm	transporter	51382
ATP6V1E1	2410029D23Rik, ATP6E, ATP6E2, ATP6V1E, D6Ertd385e, E2, H+ Atpase E, MGC72933, P31, V-ATPASE E, Vacuolar H+ATPase 31kDa, Vma4	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	NP_001687	**1.49**	**0.048933**	Cytoplasm	transporter	529
ATP6V1G1	1810024D14Rik, AA960677, Atp synthase g1, ATP6G, ATP6G1, ATP6GL, ATP6J, DKFZp547P234, VAG1, Vma10	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1	NP_004879	**1.62**	**0.02471**	Cytoplasm	transporter	9550
COX4I1	AL024441, COX4, COX4A, COXIV, CYTOCHROME OXIDASE SUBUNIT IV, MGC72016, MGC105470	cytochrome c oxidase subunit IV isoform 1	NP_001852	**1.35**	**0.10692**	Cytoplasm	enzyme	1327
COX5A	AA959768, CcOX, COX, COX-VA, Cytochrome c oxidase subunit va, Mitochondrial Cytochrome C Oxidase Va, VA	cytochrome c oxidase subunit Va	NP_004246	**1.16**	**0.30688**	Cytoplasm	enzyme	9377
CYC1	2610002H19Rik, AA408921, Cytochrome c1, MGC134266, UQCR4	cytochrome c-1	NP_001907	**1.32**	**0.1793**	Cytoplasm	enzyme	1537

NDUFA10 (includes EG:4705)	2900053E13Rik, CI-42KD, Complex I-42KD, FLJ21923, MGC5103, Nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, NDUFA10, Ndufa10l1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	NP_004535	**1.20**	**0.25345**	Cytoplasm	enzyme	4705
NDUFA13	2700054G14Rik, AU022060, B16.6, CDA016, CGI-39, FLJ58045, FLJ59191, GRIM-19, RGD1565358	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NP_057049	**1.41**	**0.12832**	Cytoplasm	enzyme	51079
NDUFA8	0610033L03Rik, Aa2-258, AW261656, CI-19KD, CI-PGIV, Complex I-19KD, Complex I-PGIV, MGC793, PGIV	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	NP_055037	**1.72**	**0.013275**	Cytoplasm	enzyme	4702
NDUFA9 (includes EG:4704)	39 Kda, ci, 1010001N11Rik, Complex I-39KD, MGC111043, NADH UBIQUINONE OXYDOREDUCTASE, ND39, NDUFA9, NDUFS2L, SDR22E1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NP_004993	**1.42**	**0.082609**	Cytoplasm	enzyme	4704
NDUFB10	22kDa, 0610011B04Rik, Complex I-PDSW, LOC681867, PDSW	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NP_004539	**1.14**	**0.32751**	Cytoplasm	enzyme	4716
NDUFB5	0610007D05Rik, AU015782, CISGDH, Complex I-SGDH, DKFZp686N02262, FLJ30597, MGC12314, MGC111204, Nadh, SGDH	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	NP_002483	**1.38**	**0.1424**	Cytoplasm	enzyme	4711
NDUFB7	1110002H15Rik, B18, CI-B18, MGC2480, NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 7, 18KDA, SQM1, UBIQUINONE OXIDOREDUCTASE	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NP_004137	**1.93**	**0.015804**	Cytoplasm	enzyme	4713
NDUFB9	1190008J14Rik, B22, Complex I-B22, DKFZp566O173, FLJ22885, LYRM3, NADH Dehydrogenase (Ubiquinone) 1 Beta B22 Subunit, Nadh Ubiquinone Oxidoreductase B22 Subunit, Nadh-Q Oxidoreductase B22, UQOR22	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	NP_004996	**1.40**	**0.13454**	Cytoplasm	enzyme	4715
NDUFS1	5830412M15RIK, 9930026A05Rik, CI-75Kd, MGC7850, MGC19199, MGC26839, MGC93795, MITOCHONDRIAL COMPLEX I 75-KDA SUBUNIT, NADH dehydrogenase precursor, 75kDa subunit, Nadh Ubiquinone Oxidoreductase 75 Kda Subunit, NADH-coenzyme Q reductase, PRO1304	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NP_004997	**1.48**	**0.051719**	Cytoplasm	enzyme	4719
NDUFS2	AL033311, Complex I-49KD, MGC27667, Nadh Ubiquinone Oxidoreductase 49 Kda Subunit, Nadh-coenzyme q reductase	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NP_004541	**1.49**	**0.049889**	Cytoplasm	enzyme	4720
NDUFS3	30 Kda, ci, 0610010M09Rik, Gm12251, NADH Dehydrogenase 30kDa, NADH-UBIQUINONE REDUCTASE, OTTMUSG00000005734	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NP_004542	**1.39**	**0.084917**	Cytoplasm	enzyme	4722
NDUFS4	18 kda subunit of complex i, 6720411N02RIK, AQDQ, C1-18k, CI-18 kDa, Complex I-18 kDa	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	NP_002486	**1.67**	**0.017814**	Cytoplasm	enzyme	4724
NDUFS7	1010001M04Rik, CI-20KD, FLJ45860, FLJ46880, MGC105684, MGC120002, MY017, NADH-coenzyme Q reductase, PSST	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	NP_077718	**1.22**	**0.24648**	Cytoplasm	enzyme	374291
NDUFV1	CI51KD, FLJ59059, MGC94599, MITOCHONDRIAL COMPLEX 1-51KDA SUBUNIT, NADH DEHYDROGENASE 51KD, ND51, UQOR1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NP_009034	**1.37**	**0.1062**	Cytoplasm	enzyme	4723
NDUFV2	24KDA SUBUNIT-MITOCHONDRIAL COMPLEX 1, 2900010C23Rik	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NP_066552	**1.30**	**0.15677**	Cytoplasm	enzyme	4729
NDUFV3	1500032D16RIK, CI-9KD, MGC72817, Mipp65, MITOCHONDRIAL COMPLEX 1-10KDA SUBUNIT, Ndufv3l	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	NP_066553	**-1.04**	**0.39126**	Cytoplasm	enzyme	4731
PPA1	2010317E03RIK, IOPPP, MGC111556, PP, PP1, Pyp, pyp rattus protein, Pyrophosphatase Inorganic, Pyrophosphatase inorganic 1, Pyrophosphate Phosphohydrolase, SID6-8061	pyrophosphatase (inorganic) 1	NP_066952	**1.08**	**0.36341**	Cytoplasm	enzyme	5464
PPA2	1110013G13Rik, FLJ20459, HSPC124, MGC6539, MGC49850, RGD1307965, SID6-306	pyrophosphatase (inorganic) 2	NP_001029363	**1.45**	**0.06787**	Cytoplasm	enzyme	27068
SDHA	1500032O14RIK, 2310034D06Rik, 4921513A11, C81073, FP, SDH1, SDH2, SDHF, Succinate dehydrogenase complex, subunit A flavoprotein (Fp), Succinate-ubiquinone oxidoreductase 70-kda subunit	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	NP_004159	**1.06**	**0.40684**	Cytoplasm	enzyme	6389

SDHB	0710008N11Rik, FLJ92337, IP, PCHC, PGL4, SDH, SDH1, SDH2, SDHIP, Succinate Dehydrogenase Cytochrome B Subunit, Succinate Dehydrogenase lp Cytochrome B Subunit, Succinate dehydrogenase putative iron sulfur subunit	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	NP_002991	**1.09**	**0.39702**	Cytoplasm	enzyme	6390
UQCRB	2210415M14Rik, FLJ92016, FLJ97033, LOC685596, LOC687741, LOC690049, MGC35665, MGC107639, QCR7, QP-C, UQBC, UQBP, UQCR6, Uqcrbl, UQPC	ubiquinol-cytochrome c reductase binding protein	NP_006285	**-1.21**	**0.22263**	Cytoplasm	enzyme	7381
UQCRC1	1110032G10Rik, COR1, D3S3191, MGC93712, MGC97899, QCR1, Ubiquinol cytochrome c reductase 1, Ubiquinol Cytochrome C Reductase Core 1, UQCR1	ubiquinol-cytochrome c reductase core protein I	NP_003356	**1.26**	**0.11012**	Cytoplasm	enzyme	7384
UQCRC2	1500004O06Rik, AURA11, CORE PROTEIN 2 OF COMPLEX III, MGC94368, Mitochondrial Core Protein2, QCR2, Ubiquinol Cytochrome C Reductase Core Protein 2, Ubiquinol Cytochrome C Reductase Core Protein 2 Precursor, UQCR2	ubiquinol-cytochrome c reductase core protein II	NP_003357	**1.33**	**0.067677**	Cytoplasm	enzyme	7385
UQCRFS1	4430402G14Rik, AI875505, FE-S COX3 SUBUNIT, Fes subunit of complex iii, LRRGT00195, MGC105530, RIP1, RIS1, RISP, UBIQUINOL CYTOCHROME C REDUCTASE, UQCR5	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	NP_005994	**1.14**	**0.285**	Cytoplasm	enzyme	7386

PATHWAY: **Glutathione metabolism**

Symbol	**Synonym(s)**	**Entrez Gene Name**	**HUGO Gene Symbol/RefSeq**	**Fold Change**	**p-value**	**Location**	**Family**	**Entrez Gene ID for Human**
ANPEP	AAP, AMINOPEPTIDASE M, AMINOPEPTIDASE N, APM, APN, CD13, GP150, Kidney Aminopeptidase M, LAP1, P150, PEPN	alanyl (membrane) aminopeptidase	NP_001141	**1.32**	**0.17802**	Plasma Membrane	peptidase	290
G6PD	G28A, G6PD1, G6PDX, Glucose-6-P Dehydrogenase, Gpdx	glucose-6-phosphate dehydrogenase	NP_000393	**1.11**	**0.28079**	Cytoplasm	enzyme	2539
GCLC	D9Wsu168e, GAMMA GCS HEAVY CHAIN, Gamma Glutamyl Cysteine Synthetase Light Subunit, Gamma Glutamylcysteine Synthetase, Gamma glutamylcysteine synthetase heavy subunit, GAMMA-GCS, GAMMA-GCSH, GCL, GCS, GCS, Catalytic, GCS-HS, GCSH, Ggcs-hs, GLCL, GLCL-H, GLCLC, Glutamate-Cysteine Ligase, Catalytic Subunit, MGC93096	glutamate-cysteine ligase, catalytic subunit	NP_001489	**1.65**	**0.020921**	Cytoplasm	enzyme	2729
GCLM	AI649393, Gamma gclm, GAMMA GCS LIGHT CHAIN, Gamma glutamylcysteine synthase (regulatory), GAMMA GLUTAMYLCYSTEINE SYNTHETASE, GCS1, Gcs Ls, Gcs, Regulatory, GCS-L, Gcslc, GLCLR, glutamat-cystein ligase, regulatory subunit, Glutamate-Cysteine Ligase, Modifier Subunit	glutamate-cysteine ligase, modifier subunit	NP_002052	**1.18**	**0.27621**	Cytoplasm	enzyme	2730
GPX1	AI195024, AL033363, CGPx, GLUTATHIONE PEROXIDASE LIKE, GPX, GSHPx, GSHPX1, MGC14399, MGC88245, Se gpx1	glutathione peroxidase 1	NP_000572	**2.13**	**8.71E-04**	Cytoplasm	enzyme	2876
GPX8	2310016C16RIK, AU017063, RGD1307506, UNQ847	glutathione peroxidase 8 (putative)	NP_001008398	**-1.23**	**0.14268**	unknown	enzyme	493869
GSR	AI325518, D8Ertd238e, GLUTATHIONE REDUCTASE, Gr, Gr-1, Gred, GRX, MGC78522	glutathione reductase	NP_000628	**1.40**	**0.082832**	Cytoplasm	enzyme	2936
GSS	AI314904, Glutathione synthetase, GS-A/GS-B, Gsh synthetase, GSHS, MGC14098	glutathione synthetase	NP_000169	**1.09**	**0.34442**	Cytoplasm	enzyme	2937
GSTK1	0610025I19Rik, AW260476, DsbA-L, GST, GST13, GST class-kappa, GST13-13, GSTK1-1, GSTkappa, hGSTK1, LOC51064	glutathione S-transferase kappa 1	NP_001137151	**1.40**	**0.080445**	Cytoplasm	enzyme	373156
GSTM2	0610005A07Rik, AI894236, Cd203c, GST4, Gst Yb3, GSTA4, Gstb-2, GSTM, Gstm3, Gstm7, GSTM2-2, GTHMUS, MGC117303	glutathione S-transferase mu 2 (muscle)	NP_000839	**1.14**	**0.28327**	Cytoplasm	enzyme	2946
GSTM3 (includes EG:2947)	FSC2, GST5, Gst mu 5, GSTB, GSTM3, Gstm5, GSTM3-3, GTM3, MGC3310, MGC3704	glutathione S-transferase mu 3 (brain)	NP_000840	**1.25**	**0.11884**	Cytoplasm	enzyme	2947
GSTO1	AA407097, AI194287, AU018802, DKFZp686H13163, GSH-dependent DHA Reductase, GST HOMOLOG, GSTTLp28, GSTX, MGC94845, P28	glutathione S-transferase omega 1	NP_004823	**1.19**	**0.17462**	Cytoplasm	enzyme	9446
GSTP1	DFN7, FAEES3, GLUTATHIONE S TRANSFERASE PHI, GLUTATHIONE S-TRANSFERASE PI, Glutathione s-transferase, chain b, Gm3934, GST3, GST P1-1, GST PI, Gst pi-class subunit 7, Gst Yf, GST-P, Gst7-7, Gst7pi, Gstp2, GSTpiA, GstpiB, Lysyl Oxidase 2, MGC72668, MGC72669, PI	glutathione S-transferase pi 1	NP_000843	**1.04**	**0.3933**	Cytoplasm	enzyme	2950
GSTT2	AI266894, Glutathione-s-transferase theta2, GSTT, MGC182032, mGSTT2, Yrs	glutathione S-transferase theta 2	NP_000845	**1.24**	**0.23331**	Cytoplasm	enzyme	2953
H6PD	AI785303, DKFZp686A01246, G6PD1, G6PDH, GDH, Gpd-1, H6pdh, MGC87643	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	NP_004276	**1.10**	**0.38314**	Cytoplasm	enzyme	9563
IDH1	AI314845, AI788952, E030024J03Rik, Id-1, IDCD, IDH, IDP, IDPC, ISOCITRATE DEHYDROGENASE, MGC115782, PICD	isocitrate dehydrogenase 1 (NADP+), soluble	NP_005887	**1.70**	**0.0031842**	Cytoplasm	enzyme	3417
IDH2	E430004F23, ICD-M, IDH, IDHM, IDP, IDPM, Isocitrate dehydrogenase, ISOCITRATE DEHYDROGENASE 2, mNADP-IDH	isocitrate dehydrogenase 2 (NADP+), mitochondrial	NP_002159	**1.45**	**0.061914**	Cytoplasm	enzyme	3418
IDH3A	1110003P10Rik, 1500012E04Rik, AA407078, AI316514, Isocitrate/isopropylmalate Dehydrogenase	isocitrate dehydrogenase 3 (NAD+) alpha	NP_005521	**1.09**	**0.34122**	Cytoplasm	enzyme	3419

MGST1	1500002K10Rik, Glutathione s-transferase 1, Gst, GST12, MGC14525, MGC72699, MGST, MGST-I, MICROSOMAL GT	microsomal glutathione S-transferase 1	NP_064696	**1.68**	**0.016618**	Cytoplasm	enzyme	4257
MGST3	2010012L10RIK, 2010306B17Rik, 2700004G04RIK, AA516734, GST-III, Loc289197	microsomal glutathione S-transferase 3	NP_004519	**2.02**	**0.010773**	Cytoplasm	enzyme	4259
PGD	6PGD, 0610042A05Rik, AU019875, C78335, Cc2-27	phosphogluconate dehydrogenase	NP_002622	**1.42**	**0.034805**	Cytoplasm	enzyme	5226
PRDX6	1 CYS PEROXIREDOXIN, 1-Cys, 1-Cys PRX, 9430088D19RIK, AA690119, AIPLA2, ANTI-OXIDANT PROTEIN2, Antioxidant Enzyme B166, AOP2, Aop2-rs3, Brp-12, CP-3, GPx, KIAA0106, KIAA106, LPLA2, Ltw-4, Lvtw-4, MGC46173, mKIAA0106, NSGP, NSGPx, ORF06, p29, PEROXIREDOXIN 6, Prdx5, PRDX6-RS3, PRX, PRX6, PrxV	peroxiredoxin 6	NP_004896	**-1.15**	**0.21527**	Cytoplasm	enzyme	9588
RNPEP	Aminopeptidase B, Ap-B, DKFZp547H084, MGC29229	arginyl aminopeptidase (aminopeptidase B)	RNPEP	**1.10**	**0.36398**	Cytoplasm	peptidase	6051

PATHWAY: Propanoate metabolism

Symbol	Synonym(s)	Entrez Gene Name	HUGO Gene Symbol/RefSeq	Fold Change	p-value	Location	Family	Entrez Gene ID for Human
ACAA1	3-oxoacyl-coa Thiolase, ACAA, Acaa1a, Acaa1b, D9Ertd25e, MGC7090, MGC108766, Peroxisomal 3-Ketoacyl CoA Thiolase, peroxisomal 3-oxoacyl-Coenzyme A thiolase, Peroxisomal thiolase, Pktaa, Pt, PTHIO, pThiol, PTL, RGD1562373, THIO, THIOLASE	acetyl-Coenzyme A acyltransferase 1	NP_001598	**1.62**	**0.023554**	Cytoplasm	enzyme	30
ACAD9	2600017P15RIK, 4732402K02, C630012L17RIK, FLJ23533, MGC14452, NPD002, NYGGF2	acyl-Coenzyme A dehydrogenase family, member 9	NP_054768	**1.23**	**0.21954**	Cytoplasm	enzyme	28976
ACADM	ACAD1, Acetyl coenzyme a dehydrogenase, medium chain, Acetyl-Coenzyme A Dehydrogenase, Acyl-CoA dehydrogenase, medium chain, AU018656, FLJ18227, FLJ93013, FLJ99884, MCAD, MCADH, MEDIUM-CHAIN FATTY ACYL-COA DEHYDROGENASE	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	NP_001120800	**1.33**	**0.16878**	Cytoplasm	enzyme	34
ACADVL	ACAD6, LCACD, MGC93660, VERY LONG-CHAIN FATTY ACYL-COA DEHYDROGENASE, VLACD, VLCAD	acyl-Coenzyme A dehydrogenase, very long chain	NP_000009	**-1.04**	**0.43264**	Cytoplasm	enzyme	37
ACAT1	3-Ketothiolase, 6330585C21Rik, AA CoA Thiolase, ACAT, Acetyl-CoA acetyltransferase 1, Acyl-coa acetyltransferase, Acyl-coa acetyltransferase 1, MAT, RATACAL, T2, THIL	acetyl-Coenzyme A acetyltransferase 1	NP_000010	**1.65**	**0.0050079**	Cytoplasm	enzyme	38
ACAT2	Ab2-076, Acat3, Acetoacetyl Coa Thiolase, ACETOCOENZYME A ACETYLTRANSFERASE 2, ACTL, AW742799, MGC95138, Similar to tcp1x, T2, Tcp-1x, Tcp-x1, Tcp1-rs1	acetyl-Coenzyme A acetyltransferase 2	NP_005882	**1.23**	**0.19111**	Cytoplasm	enzyme	39
ACSL3	2610510B12Rik, ACS3, ACYL-COA SYNTHETASE 3, C85929, FACL3, LACS3, PRO2194	acyl-CoA synthetase long-chain family member 3	NP_004448	**1.07**	**0.42486**	Cytoplasm	enzyme	2181
ALDH2	Ahd-5, Aldehyde dehydr 2,A2, ALDH-E2, ALDHI, ALDM, Hepatic aldehyde dehydrogenase 2, MGC1806	aldehyde dehydrogenase 2 family (mitochondrial)	NP_000681	**1.22**	**0.20106**	Cytoplasm	enzyme	217
ALDH4A1	A930035F14Rik, Ahd-1, ALDH4, Aldh5a1, DKFZp779M035, E330022C09, P5CD, P5CDh, P5cdhl, P5cdhs, Ssdh1	aldehyde dehydrogenase 4 family, member A1	NP_003739	**1.53**	**0.080166**	Cytoplasm	enzyme	8659
ALDH7A1	Aldehyde dehydrogenase family 7 member a1, antiquitin, ATQ1, D18Wsu181e, EPD, FLJ11738, FLJ92814, PDE	aldehyde dehydrogenase 7 family, member A1	NP_001173	**1.21**	**0.21109**	Cytoplasm	enzyme	501
ALDH9A1	4-Trimethylaminobutyraldehyde Dehydrogenase 9a, AA139417, Abaldh, ALDH4, ALDH7, ALDH9, E3, ESTM40, TMABA-DH	aldehyde dehydrogenase 9 family, member A1	NP_000687	**1.18**	**0.23452**	Cytoplasm	enzyme	223
ECH1	AA617331, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial, Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, peroxisomal, HIP11, HPXEL, MGC107274, Mitochondrial dienoyl-coa isomerase, Perox enolhydratase, Peroxisomal enoyl hydratase-like, Pxel	enoyl Coenzyme A hydratase 1, peroxisomal	NP_001389	**-1.04**	**0.4027**	Cytoplasm	enzyme	1891
ECHS1	C80529, Enoyl-CoA hydratase, short-chain, 1, mitochondrial, SCEH	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	NP_004083	**1.34**	**0.11116**	Cytoplasm	enzyme	1892
HADHA	C77020, ECHA, Enoyl-CoA Hydratase, GBP, HADH, LCHAD, MGC1728, MGC105338, Mitochondrial long chain enoyl CoA hydratase, Mitochondrial trifunctional protein alpha, MTPA, RGD1560655, TP-ALPHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	NP_000173	**1.46**	**0.025326**	Cytoplasm	enzyme	3030

HADHB	3-ketoacyl-CoA thiolase, 4930479F15Rik, A hydratase (trifunctional protein), beta subunit, ECHB, Gm13910, LOC100048492, MGC87480, Mitochondrial long chain 3-ketoacyl-CoA thiolase, MSTP029, Mtpb, OTTMUSG00000015054, TP-BETA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	NP_000174	**1.50**	**0.017067**	Cytoplasm	enzyme	3032
IVD	1300016K07Rik, 6720455E18Rik, ACAD2, AI463340, FLJ12715, FLJ34849, Isovaleryl-Coa Dehydrogenase	isovaleryl Coenzyme A dehydrogenase	NP_002216	**1.48**	**0.055705**	Cytoplasm	enzyme	3712
LDHA	GSD11, I lactate dehydrogenase (m chain), I7R2, Lactate dehydrogenase 5, lactate dehydrogenase 1 A chain, Lactate dehydrogenase a, LACTATE DEHYDROGENASE M4, LDH1, LDH5, LDH muscle subunit, LDH-M, M-Ldh, PIG19, RGD1562690	lactate dehydrogenase A	NP_005557	**-1.04**	**0.44731**	Cytoplasm	enzyme	3939
LDHB	-lactate dehydrogenase h-chain, AI790582, H-Ldh, L-lactate dehydrogenase B chain, LDH2, LDH heart subunit, LDH-H, TRG-5	lactate dehydrogenase B	NP_002291	**1.04**	**0.38945**	Cytoplasm	enzyme	3945
MUT	D230010K02RIK, MCM, MMCOAMUT, RGD1564912	methylmalonyl Coenzyme A mutase	NP_000246	**1.21**	**0.25761**	Cytoplasm	enzyme	4594
SUCLA2	4930547K18RIK, A-BETA, A-SCS, Loc361071, SCS-betaA, Succinyl CoA Synthetase beta, Succinyl-CoA ligase (ADP-forming), -chain, Succinyl-CoA ligase [ADP-forming]	succinate-CoA ligase, ADP-forming, beta subunit	NP_003841	**1.40**	**0.081598**	Cytoplasm	enzyme	8803
SUCLG1	1500000I01Rik, FLJ21114, FLJ43513, GALPHA, SCS-ALPHA, Succinate-CoA ligase, Succinyl-CoA Synthetase Alpha, SUCLA1	succinate-CoA ligase, alpha subunit	NP_003840	**1.42**	**0.082704**	Cytoplasm	enzyme	8802
SUCLG2	AF171077, AW556404, D6Wsu120e, G-BETA, G-SCS, Loc362404, MGC91183, SCS-betaG	succinate-CoA ligase, GDP-forming, beta subunit	NP_003839	**1.47**	**0.057346**	Cytoplasm	enzyme	8801
UEVLD	8430408E05RIK, ATTP, FLJ11068, UEV3	UEV and lactate/malate dehyrogenase domains	NP_001035787	**1.04**	**0.43062**	Cytoplasm	enzyme	55293

SUPPLEMENTARY TABLE S4

Group	Ontology	GO-ID	GO term	p-value	corr p-value	identified molecules	identified cluster size	available molecules	identified molecules
Upregulated	**GOBP**	55114	oxidation reduction	2.39E-13	2.46E-10	28	134	568	NDUFB7|PGD|ADH5|HADHA|FTH1|FDFT1|GPX1|NDUFS4|IVD|HMOX1|IDH1|SPR|NDUFS2|AKR1C1|NDUFS1|NSDHL|SQRDL|PTGR1|NDUFA8|AIFM1|QDPR|POR|VAT1|NNT|AKR1B1|TXNRD1|PCYOX1|RETSAT
		44255	cellular lipid metabolic process	2.78E-09	1.43E-06	23	134	577	PTGR1|MVD|PSAP|HEXA|HEXB|ADH5|HMGCS1|FDPS|PIP5K2C|LSS|ACAT1|HADHA|MIF|FDFT1|HADHB|APOL2|NPC1|PCYT2|IDI1|AKR1C1|RETSAT|NSDHL|ACAA1
		16096	isoprenoid metabolic process	6.44E-09	2.21E-06	7	134	29	MVD|ADH5|FDPS|HMGCS1|IDI1|RETSAT|FDFT1
		42221	response to chemical stimulus	9.88E-09	2.54E-06	23	134	617	DCD|TF|GCLC|S100A7|S100A9|EPHX1|MMP14|VAT1|HADHA|MIF|GPX1|NPC1|NDUFS4|HSPA2|HMOX1|IDH1|ABCC1|HSPA4|TXNRD1|HSPE1|NDRG1|NDUFS2|AKR1C1
		44248	cellular catabolic process	1.84E-08	3.79E-06	23	134	638	GNPDA1|AIFM1|SUCLG2|HEXA|HEXB|PGD|HK2|QDPR|HK1|EPHX1|HADHA|HADHB|GNS|GPX1|CDKN2A|NNT|ISG15|SQSTM1|HMOX1|ENO2|IDH1|TXNRD1|PCYOX1
		6695	cholesterol biosynthetic process	2.68E-08	4.60E-06	6	134	21	MVD|FDPS|HMGCS1|IDI1|NSDHL|FDFT1
		6629	lipid metabolic process	3.58E-08	5.26E-06	24	134	717	PTGR1|MVD|PSAP|HEXA|HEXB|ADH5|HMGCS1|FDPS|PIP5K2C|LSS|ACAT1|HADHA|MIF|FDFT1|HADHB|MGST3|APOL2|NPC1|PCYT2|IDI1|AKR1C1|RETSAT|NSDHL|ACAA1
		6091	generation of precursor metabolites and energy	5.39E-08	6.93E-06	14	134	243	GNPDA1|NDUFA8|NDUFB7|SUCLG2|HK2|HK1|LAMP2|NNT|NDUFS4|ENO2|IDH1|NDUFS2|NDUFS1|ACAA1
		9056	catabolic process	1.18E-07	1.35E-05	24	134	764	PEPD|GNPDA1|AIFM1|SUCLG2|HEXA|HEXB|PGD|HK2|QDPR|HK1|EPHX1|HADHA|HADHB|GNS|GPX1|CDKN2A|NNT|ISG15|SQSTM1|HMOX1|ENO2|IDH1|TXNRD1|PCYOX1
		16126	sterol biosynthetic process	2.21E-07	2.27E-05	6	134	29	MVD|FDPS|HMGCS1|IDI1|NSDHL|FDFT1
Upregulated	**GOMF**	16491	oxidoreductase activity	5.42E-15	2.27E-12	32	133	729	NDUFB7|PGD|ADH5|HADHA|FTH1|HADHB|FDFT1|GPX1|NDUFS4|IVD|HMOX1|IDH1|SPR|NDUFS2|AKR1C1|NDUFS1|NSDHL|FTL|SQRDL|PTGR1|NDUFA8|AIFM1|QDPR|POR|VAT1|MGST3|NNT|AKR1B1|SDCBP|TXNRD1|PCYOX1|RETSAT
		3824	catalytic activity	1.14E-11	2.39E-09	81	133	5151	SGSH|GNPDA1|QPCTL|HEXA|PGD|HEXB|LSS|FDFT1|FAHD1|GPX1|NDUFS4|HMOX1|SPR|PCYT2|NDUFS2|AKR1C1|NDUFS1|FTL|SQRDL|PEPD|AIFM1|SUCLG2|QDPR|PPGB|PIP5K2C|NPEPPS|CDK4|MMP14|VAT1|POR|ATP6V1C1|GNS|ATP6V1A|NNT|ASCC3|IGF2R|PDE5A|PRCP|SDCBP|TXNRD1|PCYOX1|CTSB|PRPS1|ACAA1|RAB7A|GCLC|NDUFB7|MVD|HK2|ADH5|NFS1|HMGCS1|HK1|ATP6V1G1|ATP6V1B2|ACAT1|FTH1|HADHA|MIF|HADHB|RRAGC|IVD|TGM2|ENO2|CAMK2D|IDH1|NSDHL|PTGR1|NDUFA8|PSAP|FDPS|EPHX1|TKT|MGST3|PPIF|ATP6V1E1|AKR1B1|ABCC1|IDI1|MGST1|RETSAT
		16616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	1.19E-08	1.66E-06	10	133	101	PTGR1|AKR1B1|PGD|ADH5|IDH1|SPR|AKR1C1|HADHA|NSDHL|HADHB
		9055	electron carrier activity	2.26E-08	2.36E-06	14	133	250	AIFM1|PGD|QDPR|ADH5|POR|NNT|IVD|AKR1B1|TXNRD1|NDUFS2|NDUFS1|ETFB|RETSAT|ETFA
		16614	oxidoreductase activity, acting on CH-OH group of donors	3.25E-08	2.72E-06	10	133	112	PTGR1|AKR1B1|PGD|ADH5|IDH1|SPR|AKR1C1|HADHA|NSDHL|HADHB
		50662	coenzyme binding	5.84E-08	4.07E-06	11	133	152	GCLC|NNT|AIFM1|IVD|PGD|TXNRD1|SPR|NDUFS2|HADHA|POR|ETFA
		16651	oxidoreductase activity, acting on NADH or NADPH	1.18E-07	7.03E-06	8	133	70	NDUFS4|NNT|NDUFA8|NDUFB7|TXNRD1|NDUFS2|NDUFS1|POR
		48037	cofactor binding	3.04E-07	1.59E-05	12	133	219	GCLC|NNT|AIFM1|IVD|PGD|NFS1|TXNRD1|SPR|NDUFS2|HADHA|POR|ETFA
		16408	C-acyltransferase activity	2.19E-06	9.49E-05	4	133	12	ACAT1|HADHA|HADHB|ACAA1
		3988	acetyl-CoA C-acyltransferase activity	2.27E-06	9.49E-05	3	133	4	HADHA|HADHB|ACAA1
Upregulated	**GOCC**	44444	cytoplasmic part	1.73E-23	3.32E-21	87	132	4031	SGSH|S100A7|HEXA|HEXB|DNAJC10|PDCD4|FDFT1|FAHD1|GPX1|NDUFS4|HMOX1|NDUFS2|NDUFS1|AKR1C1|SQRDL|AIFM1|SUCLG2|PPGB|MYH4|TMEM126A|NPEPPS|CDK4|MMP14|RIC8B|BCL2L13|VAT1|POR|GNS|ATP6V1A|NPC1|BGN|NNT|NPC2|IGF2R|TXN|PRCP|SDCBP|TXNRD1|PCYOX1|CTSB|PRPS1|ACAA1|TF|RAB7A|GCLC|NDUFB7|MVD|HK2|NFS1|HMGCS1|HK1|ATP6V1G1|ATP6V1B2|ACAT1|HADHA|HADHB|CD9|HSPA2|SQSTM1|IVD|KRT8|TGM2|ENO2|IDH1|VPS35|HSPE1|SCARB2|LAMB1|ARL6IP5|ETFB|NSDHL|ETFA|NDUFA8|PSAP|EPHX1|TKT|CD63|MGST3|NCSTN|PPIF|APOL2|LAMP1|LAMP2|AKR1B1|IDI1|MGST1|RETSAT
		5737	cytoplasm	5.76E-22	5.53E-20	107	132	6541	GNPDA1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|SUCLG2|QDPR|TMEM126A|MYH4|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|ACAA1|PRPS1|RAB7A|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|FDPS|EPHX1|TKT|CD63|APOL2|PPIF|LAMP1|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|MMP14|CDK4|VAT1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|COL6A2|ENO2|TGM2|COL6A1|HSPA4|VPS35|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|AKR1B1|MGST1|RETSAT
		323	lytic vacuole	3.22E-14	1.55E-12	18	132	198	SGSH|RAB7A|PSAP|HEXA|HEXB|PPGB|ATP6V1G1|CD63|GNS|LAMP1|NPC1|LAMP2|NPC2|IGF2R|PRCP|PCYOX1|CTSB|SCARB2
		5764	lysosome	3.22E-14	1.55E-12	18	132	198	SGSH|RAB7A|PSAP|HEXA|HEXB|PPGB|ATP6V1G1|CD63|GNS|LAMP1|NPC1|LAMP2|NPC2|IGF2R|PRCP|PCYOX1|CTSB|SCARB2
		5773	vacuole	2.17E-13	8.35E-12	18	132	221	SGSH|RAB7A|PSAP|HEXA|HEXB|PPGB|ATP6V1G1|CD63|GNS|LAMP1|NPC1|LAMP2|NPC2|IGF2R|PRCP|PCYOX1|CTSB|SCARB2

		44429	mitochondrial part	1.01E-11	3.22E-10	24	132	542	SQRDL|NDUFA8|NDUFB7|PSAP|AIFM1|SUCLG2|HK2|NFS1|HK1|BCL2L13|ACAT1|HADHA|HADHB|FAHD1|PPIF|NNT|NDUFS4|IVD|HSPE1|NDUFS2|MGST1|ETFB|NDUFS1|ETFA
		5739	mitochondrion	3.17E-11	8.71E-10	30	132	911	NDUFB7|NFS1|HK2|HK1|ACAT1|HADHA|HADHB|FAHD1|GPX1|NDUFS4|HSPA2|IVD|TGM2|HSPE1|NDUFS2|ETFB|NDUFS1|ETFA|SQRDL|NDUFA8|PSAP|SUCLG2|AIFM1|TMEM126A|BCL2L13|PPIF|ATP6V1A|NNT|CTSB|MGST1
		44424	intracellular part	5.78E-10	1.39E-08	114	132	10110	GNPDA1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|FTL|SUCLG2|QDPR|TMEM126A|MYH4|BASP1|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|PRPS1|ACAA1|RAB7A|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|FDPS|EPHX1|TKT|CD63|PPIF|APOL2|LAMP1|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|KRT6A|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|TGM2|COL6A2|CAMK2D|ENO2|COL6A1|VPS35|HSPA4|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|AKR1B1|H2AFY2|MGST1|RETSAT
		31090	organelle membrane	3.01E-08	6.42E-07	34	132	1517	NDUFB7|HK2|HK1|ATP6V1G1|ACAT1|HADHA|HADHB|FDFT1|FAHD1|CD9|NDUFS4|SCARB2|ARL6IP5|NDUFS2|NDUFS1|NSDHL|SQRDL|NDUFA8|PSAP|EPHX1|BCL2L13|CD63|POR|VAT1|MGST3|APOL2|LAMP1|NPC1|LAMP2|NNT|IGF2R|SDCBP|MGST1|RETSAT
		5622	intracellular	3.86E-08	7.40E-07	114	132	10629	GNPDA1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|FTL|SUCLG2|QDPR|TMEM126A|MYH4|BASP1|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|PRPS1|ACAA1|RAB7A|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|FDPS|EPHX1|TKT|CD63|PPIF|APOL2|LAMP1|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|KRT6A|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|TGM2|COL6A2|CAMK2D|ENO2|COL6A1|VPS35|HSPA4|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|AKR1B1|H2AFY2|MGST1|RETSAT
Downregulated	**GOBP**	6374	nuclear mRNA splicing, via spliceosome	2.62E-08	6.68E-06	12	144	148	FUSIP1|PABPN1|HNRNPH3|HNRNPA2B1|DNAJC8|SF1|THOC4|HNRNPH1|HNRNPA1|RBMX|YBX1|HNRNPA0
		375	RNA splicing, via transesterification reactions	2.62E-08	6.68E-06	12	144	148	FUSIP1|PABPN1|HNRNPH3|HNRNPA2B1|DNAJC8|SF1|THOC4|HNRNPH1|HNRNPA1|RBMX|YBX1|HNRNPA0
		377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	2.62E-08	6.68E-06	12	144	148	FUSIP1|PABPN1|HNRNPH3|HNRNPA2B1|DNAJC8|SF1|THOC4|HNRNPH1|HNRNPA1|RBMX|YBX1|HNRNPA0
		16071	mRNA metabolic process	2.41E-07	3.76E-05	16	144	338	FUSIP1|RALY|PABPN1|KHDRBS1|HNRNPA2B1|SF1|ELAVL1|DDX5|RBMX|HNRNPA1|HNRNPA0|YBX1|HNRNPH3|DNAJC8|THOC4|HNRNPH1
		6397	mRNA processing	2.46E-07	3.76E-05	15	144	296	FUSIP1|RALY|PABPN1|KHDRBS1|HNRNPA2B1|SF1|DDX5|RBMX|HNRNPA1|HNRNPA0|YBX1|HNRNPH3|DNAJC8|THOC4|HNRNPH1
		6394	RNA processing	3.19E-07	4.07E-05	19	144	485	FUSIP1|KHDRBS1|RALY|PABPN1|RBM3|AARS|HNRNPA2B1|SF1|DDX5|RBMX|HNRNPA1|YBX1|HNRNPA0|HNRPDL|HNRNPH3|DNAJC8|RBMS2|THOC4|HNRNPH1
		6395	RNA splicing	4.79E-07	5.24E-05	14	144	270	FUSIP1|RALY|PABPN1|HNRNPA2B1|SF1|DDX5|RBMX|HNRNPA1|HNRNPA0|YBX1|HNRNPH3|DNAJC8|THOC4|HNRNPH1
		22607	cellular component assembly	6.56E-07	6.27E-05	11	144	163	H1F0|TJP1|HMGB2|HIST1H2BN|HIST1H1C|ITGA6|HIST1H1B|H2AFZ|MCM2|HIST3H2BB|HIST2H3PS2
		6334	nucleosome assembly	8.90E-07	7.56E-05	9	144	104	H1F0|HMGB2|HIST1H2BN|HIST1H1C|HIST1H1B|H2AFZ|MCM2|HIST3H2BB|HIST2H3PS2
		31497	chromatin assembly	2.08E-06	1.59E-04	9	144	115	H1F0|HMGB2|HIST1H2BN|HIST1H1C|HIST1H1B|H2AFZ|MCM2|HIST3H2BB|HIST2H3PS2
Downregulated	**GOMF**	3723	RNA binding	1.24E-13	4.08E-11	32	155	692	FUSIP1|RALY|RPL19|RBM3|RPL27A|YBX1|DDX3X|RBMS2|RPL10|RPL5|PABPN1|KHDRBS1|HNRNPA2B1|AARS|SF1|ELAVL1|RPL23A|DDX5|RPS6|RBMX|HNRNPA1|HNRNPA0|EIF4G1|HNRPDL|HNRNPH3|EIF4H|CIRBP|THOC4|RPS10|SRP72|RBM14|HNRNPH1
		5515	protein binding	6.02E-09	9.93E-07	104	155	7030	PDLIM7|CTPS|PDLIM5|CHMP4A|LMO7|RANGAP1|EDIL3|TFG/ALK|CBX5|DNAJC9|DNAJC8|SERPINE1|PABPN1|HNRNPA2B1|MFGE8|CSDA|UNC84B|RIC8A|KRT18|TAGLN|COL1A2|RPS10|STMN1|TGFB1I1|ERC1|CAV2|PPME1|TAGLN2|PEF1|EIF3A|RPL5|EMD|CDC42EP3|LGALS1|PPFIBP1|RPL23A|CSRP1|RPS6|DDX5|HNRNPA1|RBMX|HNRNPH3|ITGA6|PCNA|CIRBP|DNAJB1|TMPO|DNAJB4|HNRNPH1|DNAJB6|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|YBX1|MCM7|P4HA2|SDPR|CHST14|RHOC|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|HNRPDL|EIF4G1|EPB41L2|CCDC50|PDCL3|PFDN1|SMTN|RRM2|THOC4|KPNA2|FUSIP1|SNX18|RAB3A|CNN3|CALD1|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|CNN1|PAPSS2|FEN1|MLTK|NASP|ELAVL1|TJP1|RBM14
		8092	cytoskeletal protein binding	2.59E-07	2.45E-05	18	155	437	KIAA1949|LIMA1|CNN3|CALD1|PDLIM5|LMO7|NEXN|PALLD|TPM1|TPM4|UNC84B|EPB41L2|SMTN|TAGLN|CNN2|CNN1|STMN1|CDC42EP3
		3779	actin binding	2.97E-07	2.45E-05	15	155	305	KIAA1949|LIMA1|CNN3|PDLIM5|CALD1|LMO7|NEXN|PALLD|TPM1|TPM4|EPB41L2|SMTN|TAGLN|CNN2|CNN1

<table>
<tr><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></tr>
<tr><td></td><td></td><td>5488</td><td>binding</td><td>6.66E-06</td><td>4.40E-04</td><td>141</td><td>155</td><td>12313</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|RBM3|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|FSTL1|EDIL3|TFG/ALK|CBX5|HIST1H2BN|DNAJC9|SERPINE1|DNAJC8|RBMS2|H2AFZ|RPL10|RAB21|PABPN1|H1F0|HNRNPA2B1|AARS|MFGE8|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|GBP1|CAV2|HMGB2|PPME1|TAGLN2|PEF1|EIF3A|DDX3X|RPL5|HIST2H3PS2|CDC42EP3|EMD|CRIP2|LGALS1|MRC2|PPFIBP1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|ITGA6|EIF4H|PCNA|CIRBP|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB4|DNAJB6|DUT|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|NT5E|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|HIST1H1B|CDC2|ANP32E|SF1|SLC3A2|MCM2|PALLD|NEXN|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|SNX18|CNN3|FAM98A|CALD1|RPL27A|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|CNN1|PAPSS2|FEN1|MLTK|NASP|ELAVL1|ANXA3|TJP1|PHGDH|SUMF2|PSAT1|RBM14</td></tr>
<tr><td></td><td></td><td>31072</td><td>heat shock protein binding</td><td>2.75E-05</td><td>1.52E-03</td><td>6</td><td>155</td><td>61</td><td>NASP|DNAJC9|DNAJC8|DNAJB1|DNAJB4|DNAJB6</td></tr>
<tr><td></td><td></td><td>43566</td><td>structure-specific DNA binding</td><td>3.64E-05</td><td>1.72E-03</td><td>7</td><td>155</td><td>94</td><td>HNRPDL|HMGB2|HNRNPA2B1|CSDA|HNRNPA1|FEN1|YBX1</td></tr>
<tr><td></td><td></td><td>3697</td><td>Mol Funct single-stranded DNA binding</td><td>4.62E-05</td><td>1.91E-03</td><td>5</td><td>155</td><td>41</td><td>HNRPDL|HMGB2|HNRNPA2B1|HNRNPA1|YBX1</td></tr>
<tr><td></td><td></td><td>3690</td><td>double-stranded DNA binding</td><td>2.28E-04</td><td>8.36E-03</td><td>5</td><td>155</td><td>57</td><td>HNRPDL|HMGB2|CSDA|FEN1|YBX1</td></tr>
<tr><td></td><td></td><td>42805</td><td>actinin binding</td><td>5.58E-04</td><td>1.84E-02</td><td>2</td><td>155</td><td>4</td><td>PDLIM5|PALLD</td></tr>
<tr><td>Downregulated</td><td>GOCC</td><td>30530</td><td>heterogeneous nuclear ribonucleoprotein complex</td><td>8.29E-13</td><td>1.73E-10</td><td>8</td><td>147</td><td>17</td><td>HNRPDL|RALY|HNRNPH3|HNRNPA2B1|HNRNPH1|HNRNPA1|RBMX|HNRNPA0</td></tr>
<tr><td></td><td></td><td>44424</td><td>intracellular part</td><td>2.11E-10</td><td>1.39E-08</td><td>126</td><td>147</td><td>10114</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|LUZP1|CBX5|HIST1H2BN|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|RPL36AL|PABPN1|PLD3|INA|H1F0|AARS|HNRNPA2B1|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|CAV2|CDV3|HMGB2|PEF1|EIF3A|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|CDC42EP3|UAP1|LGALS1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|EIF4H|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB6|DUT|LIMA1|AP3S1|DEK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|HIST3H2BB|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|CCDC50|EPB41L2|HNRPDL|EIF4G1|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|CALD1|RPL27A|ASNS|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|GOLPH3|SUMF2|RBM14</td></tr>
<tr><td></td><td></td><td>43228</td><td>non-membrane-bounded organelle</td><td>2.66E-10</td><td>1.39E-08</td><td>46</td><td>147</td><td>1929</td><td>LIMA1|HMGB2|RPL19|PDLIM7|CALD1|PDLIM5|RPL27A|TPM1|TPM4|CBX5|EIF3A|MCM7|HIST1H2BN|H2AFZ|RPL10|CNN2|RPL5|HIST3H2BB|HIST2H3PS2|CDC42EP3|RPL36AL|H1F0|INA|KIAA1949|NES|HIST1H1C|HIST1H1B|CDC2|SF1|RPL23A|MCM2|PALLD|NEXN|SUGT1|RPS6|UNC84B|EPB41L2|SMTN|KRT18|PCNA|RPS10|TMPO|SRP72|STMN1|TGFB1I1|FILIP1L</td></tr>
<tr><td></td><td></td><td>43232</td><td>intracellular non-membrane-bounded organelle</td><td>2.66E-10</td><td>1.39E-08</td><td>46</td><td>147</td><td>1929</td><td>LIMA1|HMGB2|RPL19|PDLIM7|CALD1|PDLIM5|RPL27A|TPM1|TPM4|CBX5|EIF3A|MCM7|HIST1H2BN|H2AFZ|RPL10|CNN2|RPL5|HIST3H2BB|HIST2H3PS2|CDC42EP3|RPL36AL|H1F0|INA|KIAA1949|NES|HIST1H1C|HIST1H1B|CDC2|SF1|RPL23A|MCM2|PALLD|NEXN|SUGT1|RPS6|UNC84B|EPB41L2|SMTN|KRT18|PCNA|RPS10|TMPO|SRP72|STMN1|TGFB1I1|FILIP1L</td></tr>
<tr><td></td><td></td><td>5622</td><td>intracellular</td><td>1.71E-09</td><td>7.16E-08</td><td>128</td><td>147</td><td>10633</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|LUZP1|CBX5|HIST1H2BN|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|RPL36AL|PABPN1|PLD3|INA|H1F0|AARS|HNRNPA2B1|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|CAV2|CDV3|HMGB2|PEF1|EIF3A|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|CDC42EP3|UAP1|LGALS1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|EIF4H|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB6|DUT|LIMA1|AP3S1|DEK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|CALD1|RPL27A|ASNS|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|GOLPH3|SUMF2|RBM14</td></tr>
<tr><td></td><td></td><td>30529</td><td>ribonucleoprotein complex</td><td>1.51E-08</td><td>5.27E-07</td><td>22</td><td>147</td><td>588</td><td>RALY|RPL19|HNRNPA2B1|RPL27A|SF1|RPL23A|DDX5|RPS6|HNRNPA1|RBMX|HNRNPA0|HNRPDL|HNRNPH3|EIF3A|RPL10|THOC4|RPS10|RPL5|SRP72|RBM14|HNRNPH1|RPL36AL</td></tr>
<tr><td></td><td></td><td>44446</td><td>intracellular organelle part</td><td>2.06E-08</td><td>6.01E-07</td><td>64</td><td>147</td><td>3725</td><td>RALY|LIMA1|RPL19|CHMP4A|AP3S1|RANGAP1|CBX5|HIST1H2BN|MCM7|P4HA2|H2AFZ|CHST14|HIST3H2BB|RAB21|HMGCL|PABPN1|PLD3|INA|H1F0|HIST1H1C|HIST1H1B|CDC2|HNRNPA2B1|SF1|MCM2|PALLD|UNC84B|EPB41L2|HNRPDL|KRT18|THOC4|RPS10|TGFB1I1|STMN1|SRP72|ERC1|KPNA2|FILIP1L|FUSIP1|CAV2|HMGB2|RPL27A|TPM1|TPM4|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|NES|RPL23A|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|PCNA|SUMF2|GOSR2|TMPO|RBM14|HNRNPH1</td></tr>
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<table>
<tr><td>44422</td><td>organelle part</td><td>2.30E-08</td><td>6.01E-07</td><td>64</td><td>147</td><td>3735</td><td>RALY|LIMA1|RPL19|CHMP4A|AP3S1|RANGAP1|CBX5|HIST1H2BN|MCM7|P4HA2|H2AFZ|CHST14|HIST3H2BB|RAB21|HMGCL|PABPN1|PLD3|INA|H1F0|HIST1H1C|HIST1H1B|CDC2|HNRNPA2B1|SF1|MCM2|PALLD|UNC84B|EPB41L2|HNRPDL|KRT18|THOC4|RPS10|TGFB1I1|STMN1|SRP72|ERC1|KPNA2|FILIP1L|FUSIP1|CAV2|HMGB2|RPL27A|TPM1|TPM4|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|NES|RPL23A|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|PCNA|SUMF2|GOSR2|TMPO|RBM14|HNRNPH1</td></tr>
<tr><td>32991</td><td>macromolecular complex</td><td>6.83E-08</td><td>1.59E-06</td><td>47</td><td>147</td><td>2375</td><td>RALY|RPL19|RPL27A|AP3S1|LMO7|RANGAP1|TPM4|CBX5|EIF3A|MCM7|HIST1H2BN|AP3M1|H2AFZ|RPL10|RPL5|HIST3H2BB|HIST2H3PS2|AP3B1|RPL36AL|H1F0|HIST1H1C|HIST1H1B|HNRNPA2B1|SF1|RPL23A|MCM2|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|EIF4G1|HNRPDL|PFDN1|HNRNPH3|ITGA6|EIF4H|PCNA|THOC4|RPS10|SRP72|RBM14|HNRNPH1|ERC1|KPNA2|FILIP1L</td></tr>
<tr><td>5737</td><td>cytoplasm</td><td>8.13E-08</td><td>1.70E-06</td><td>91</td><td>147</td><td>6546</td><td>LIMA1|RPL19|PDLIM7|CTPS|CHMP4A|PDLIM5|DTYMK|PITPNB|AP3S1|LMO7|RANGAP1|YBX1|ASAH1|MTHFD2|P4HA2|SDPR|CHST14|RPL10|RAB21|HMGCL|AP3B1|GOLGA2|RPL36AL|PLD3|PABPN1|KIAA1949|CDC2|ANP32E|AARS|SF1|SLC3A2|PALLD|NEXN|CSDA|DAPK3|UNC84B|RIC8A|CCDC50|EPB41L2|EIF4G1|HNRPDL|PYCR1|PFDN1|PDCL3|SMTN|KRT18|TAGLN|RRM2|COL1A2|CTSD|THOC4|RPS10|LEPREL1|SRP72|STMN1|TGFB1I1|ERC1|KPNA2|FUSIP1|RAB3A|CAV2|HMGB2|CDV3|RPL27A|ASNS|TPM1|TPM4|PEF1|EIF3A|KDELC2|DDX3X|AP3M1|PPP1R12A|RPL5|CDC42EP3|UAP1|MLTK|NASP|LGALS1|RPL23A|RPS6|HNRNPA1|ANXA3|GOLPH3|EIF4H|SUMF2|GOSR2|HSPA13|DNAJB1|DNAJB6|DUT</td></tr>
</table>

SUPPLEMENTARY TABLE S5

Group	Ontology	GO-ID	GO term	p-value	corr p-value	identified molecules	identified cluster size	cluster frequency (%)	available molecules	identified molecules
Upregulated	**GOSlim**	5737	cytoplasm	1.07E-22	1.10E-20	107	141	75.9	6541	GNPDA1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|SUCLG2|QDPR|TMEM126A|MYH4|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|ACAA1|PRPS1|RAB7A|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|FDPS|EPHX1|TKT|CD63|APOL2|PPIF|LAMP1|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|MMP14|CDK4|VAT1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|COL6A2|ENO2|TGM2|COL6A1|HSPA4|VPS35|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|AKR1B1|MGST1|RETSAT
		5764	lysosome	1.29E-14	6.62E-13	18	141	12.8	198	SGSH|RAB7A|PSAP|HEXA|HEXB|PPGB|ATP6V1G1|CD63|GNS|LAMP1|NPC1|LAMP2|NPC2|IGF2R|PRCP|PCYOX1|CTSB|SCARB2
		5773	vacuole	8.74E-14	3.00E-12	18	141	12.8	221	SGSH|RAB7A|PSAP|HEXA|HEXB|PPGB|ATP6V1G1|CD63|GNS|LAMP1|NPC1|LAMP2|NPC2|IGF2R|PRCP|PCYOX1|CTSB|SCARB2
		3824	catalytic activity	1.80E-13	4.63E-12	81	141	57.4	5151	SGSH|GNPDA1|QPCTL|HEXA|PGD|HEXB|LSS|FDFT1|FAHD1|GPX1|NDUFS4|HMOX1|SPR|PCYT2|NDUFS2|AKR1C1|NDUFS1|FTL|SQRDL|PEPD|AIFM1|SUCLG2|QDPR|PPGB|PIP5K2C|NPEPPS|CDK4|MMP14|VAT1|POR|ATP6V1C1|GNS|ATP6V1A|NNT|ASCC3|IGF2R|PDE5A|PRCP|SDCBP|TXNRD1|PCYOX1|CTSB|PRPS1|ACAA1|RAB7A|GCLC|NDUFB7|MVD|HK2|ADH5|NFS1|HMGCS1|HK1|ATP6V1G1|ATP6V1B2|ACAT1|FTH1|HADHA|MIF|HADHB|RRAGC|IVD|TGM2|ENO2|CAMK2D|IDH1|NSDHL|PTGR1|NDUFA8|PSAP|FDPS|EPHX1|TKT|MGST3|PPIF|ATP6V1E1|AKR1B1|ABCC1|IDI1|MGST1|RETSAT
		5739	mitochondrion	8.79E-12	1.81E-10	30	141	21.3	911	NDUFB7|NFS1|HK2|HK1|ACAT1|HADHA|HADHB|FAHD1|GPX1|NDUFS4|HSPA2|IVD|TGM2|HSPE1|NDUFS2|ETFB|NDUFS1|ETFA|SQRDL|NDUFA8|PSAP|SUCLG2|AIFM1|TMEM126A|BCL2L13|PPIF|ATP6V1A|NNT|CTSB|MGST1
		6629	lipid metabolic process	1.04E-09	1.78E-08	24	141	17.0	717	PTGR1|MVD|PSAP|HEXA|HEXB|ADH5|HMGCS1|FDPS|PIP5K2C|LSS|ACAT1|HADHA|MIF|FDFT1|HADHB|MGST3|APOL2|NPC1|PCYT2|IDI1|AKR1C1|RETSAT|NSDHL|ACAA1
		9056	catabolic process	3.63E-09	5.35E-08	24	141	17.0	764	PEPD|GNPDA1|AIFM1|SUCLG2|HEXA|HEXB|PGD|HK2|QDPR|HK1|EPHX1|HADHA|HADHB|GNS|GPX1|CDKN2A|NNT|ISG15|SQSTM1|HMOX1|ENO2|IDH1|TXNRD1|PCYOX1
		5622	intracellular	4.19E-09	5.39E-08	114	141	80.9	10629	GNPDA1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|FTL|SUCLG2|QDPR|TMEM126A|MYH4|BASP1|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|PRPS1|ACAA1|RAB7A|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|FDPS|EPHX1|TKT|CD63|PPIF|APOL2|LAMP1|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|KRT6A|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|TGM2|COL6A2|CAMK2D|ENO2|COL6A1|VPS35|HSPA4|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|AKR1B1|H2AFY2|MGST1|RETSAT
		6091	generation of precursor metabolites and energy	5.42E-09	6.20E-08	14	141	9.9	243	GNPDA1|NDUFA8|NDUFB7|SUCLG2|HK2|HK1|LAMP2|NNT|NDUFS4|ENO2|IDH1|NDUFS2|NDUFS1|ACAA1
		9055	electron carrier activity	7.79E-09	8.02E-08	14	141	9.9	250	AIFM1|PGD|QDPR|ADH5|POR|NNT|IVD|AKR1B1|TXNRD1|NDUFS2|NDUFS1|ETFB|RETSAT|ETFA
		6810	transport	2.34E-08	2.19E-07	45	141	31.9	2534	TF|SNX9|RAB7A|SLC38A2|NDUFB7|SNX5|PGD|HK2|HK1|ATP6V1G1|ATP6V1B2|FTH1|NDUFS4|SQSTM1|COL6A3|COL6A2|COL6A1|VPS35|FYCO1|ARL6IP5|NDUFS2|ETFB|AKR1C1|NDUFS1|ETFA|FTL|COL4A2|NDUFA8|PSAP|STXBP1|MYH4|PPGB|VAT1|APOL2|ATP6V1C1|ATP6V1A|NPC1|NNT|NPC2|ATP6V1E1|IGF2R|TXN|SDCBP|ABCC1|TXNRD1
		5829	cytosol	4.40E-08	3.77E-07	24	141	17.0	870	GCLC|MVD|S100A7|HK2|NFS1|HMGCS1|HK1|TKT|NPEPPS|CDK4|RIC8B|PDCD4|GPX1|SQSTM1|HMOX1|AKR1B1|TXN|ENO2|IDH1|VPS35|TXNRD1|IDI1|AKR1C1|PRPS1

<table>
<tr><td>8150</td><td>biological_process</td><td>5.21E-08</td><td>4.13E-07</td><td>134</td><td>141</td><td>95.0</td><td>14511</td><td>GNPDA1|QPCTL|CADM1|S100A8|S100A7|PGD|S100A9|FDFT1|FAHD1|CDKN2A|ISG15|TGFBI|SPR|FTL|SUCLG2|QDPR|MYH4|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|HSPB6|ASCC3|PDE5A|PRCP|SDCBP|PRPS1|ACAA1|SNX9|RAB7A|SLC38A2|GCLC|MVD|SNX5|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|CD276|FDPS|EPHX1|TKT|CD63|PPIF|APOL2|LAMP2|IDI1|SGSH|HEXA|HEXB|DNAJC10|LSS|PDCD4|GPX1|NDUFS4|HMOX1|PCYT2|NDUFS2|AKR1C1|NDUFS1|SQRDL|PEPD|AIFM1|STXBP1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1C1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|DCD|KRT6A|NDUFB7|HK2|ADH5|NFS1|HK1|ATP6V1G1|DCN|MIF|CD9|HSPA2|SQSTM1|COL6A3|KRT8|TGM2|ENO2|CAMK2D|COL6A2|COL6A1|VPS35|HSPA4|CALML5|FYCO1|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|HSPG2|ANXA4|MGST3|NCSTN|ATP6V1E1|AKR1B1|H2AFY2|ABCC1|MGST1|RETSAT</td></tr>
<tr><td>8152</td><td>metabolic process</td><td>1.39E-07</td><td>1.03E-06</td><td>85</td><td>141</td><td>60.3</td><td>7111</td><td>SGSH|GNPDA1|QPCTL|HEXA|PGD|HEXB|DNAJC10|LSS|FDFT1|FAHD1|GPX1|CDKN2A|NDUFS4|ISG15|HMOX1|SPR|PCYT2|NDUFS2|NDUFS1|AKR1C1|SQRDL|PEPD|AIFM1|SUCLG2|QDPR|PPGB|PIP5K2C|NPEPPS|CDK4|MMP14|HMGA2|VAT1|POR|GNS|ATP6V1A|NPC1|NNT|ASCC3|PDE5A|PRCP|SDCBP|TXNRD1|PCYOX1|CTSB|PRPS1|ACAA1|DCD|GCLC|NDUFB7|MVD|HK2|ADH5|NFS1|HMGCS1|HK1|ATP6V1B2|ACAT1|FTH1|HADHA|MIF|HADHB|RRAGC|SQSTM1|IVD|TGM2|ENO2|CAMK2D|IDH1|HSPE1|NSDHL|PTGR1|NDUFA8|PSAP|FDPS|EPHX1|TKT|MGST3|NCSTN|PPIF|APOL2|LAMP2|AKR1B1|IDI1|MGST1|RETSAT</td></tr>
<tr><td>19725</td><td>cellular homeostasis</td><td>5.35E-07</td><td>3.67E-06</td><td>13</td><td>141</td><td>9.2</td><td>300</td><td>TF|AIFM1|HEXA|HEXB|DNAJC10|HK2|FTH1|CD9|TXN|TGM2|TXNRD1|NDUFS1|FTL</td></tr>
<tr><td>5578</td><td>proteinaceous extracellular matrix</td><td>2.16E-06</td><td>1.39E-05</td><td>12</td><td>141</td><td>8.5</td><td>287</td><td>COL4A2|BGN|PSAP|COL6A3|TGFBI|HSPG2|COL6A2|COL6A1|DCN|MMP14|LAMB1|GPC1</td></tr>
<tr><td>5515</td><td>protein binding</td><td>1.18E-05</td><td>7.14E-05</td><td>79</td><td>141</td><td>56.0</td><td>7030</td><td>SGSH|S100A8|CADM1|QPCTL|S100A7|MARCKSL1|HEXA|S100A9|PGD|HEXB|DNAJC10|PDCD4|FDFT1|FAHD1|GPX1|CDKN2A|ISG15|HMOX1|TGFBI|SPR|NDUFS1|FTL|AIFM1|MYH4|PPGB|PIP5K2C|NPEPPS|CDK4|RIC8B|HMGA2|MMP14|ATP6V1C1|NPC1|BGN|NPC2|HSPB6|IGF2R|TXN|SDCBP|CTSB|DCD|SNX9|RAB7A|KRT6A|GCLC|SNX5|HK2|NFS1|HK1|ATP6V1G1|DCN|ACAT1|FTH1|MIF|RRAGC|CD9|HSPA2|SQSTM1|COL6A3|KRT8|TGM2|CAMK2D|COL6A2|COL6A1|VPS35|HSPE1|NDRG1|CALML5|SCARB2|LAMB1|ARL6IP5|PSAP|HSPG2|CD276|TKT|NCSTN|APOL2|ATP6V1E1|AKR1B1</td></tr>
<tr><td>16023</td><td>cytoplasmic membrane-bounded vesicle</td><td>2.08E-05</td><td>1.19E-04</td><td>12</td><td>141</td><td>8.5</td><td>359</td><td>NCSTN|CD9|TF|RAB7A|LAMP2|BGN|IGF2R|SDCBP|CTSB|ATP6V1B2|MMP14|VAT1</td></tr>
<tr><td>6950</td><td>response to stress</td><td>2.82E-05</td><td>1.53E-04</td><td>24</td><td>141</td><td>17.0</td><td>1257</td><td>DCD|TF|GCLC|S100A8|S100A7|AIFM1|S100A9|MMP14|MIF|APOL2|CD9|GPX1|HSPA2|HSPB6|SQSTM1|HMOX1|AKR1B1|IDH1|HSPA4|TXNRD1|SPR|HSPE1|CTSB|NDUFS2</td></tr>
<tr><td>22904</td><td>respiratory electron transport chain</td><td>6.25E-05</td><td>3.09E-04</td><td>5</td><td>141</td><td>3.5</td><td>55</td><td>NDUFS4|NDUFA8|NDUFB7|NDUFS2|NDUFS1</td></tr>
<tr><td>5488</td><td>binding</td><td>6.58E-05</td><td>3.09E-04</td><td>115</td><td>141</td><td>81.6</td><td>12304</td><td>QPCTL|CADM1|S100A8|S100A7|PGD|S100A9|FDFT1|FAHD1|CDKN2A|ISG15|TGFBI|SPR|FTL|SUCLG2|QDPR|MYH4|NPEPPS|RIC8B|POR|GNS|NPC1|NPC2|NNT|HSPB6|ASCC3|PDE5A|SDCBP|PRPS1|SNX9|RAB7A|SLC38A2|GCLC|MVD|SNX5|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|HPCAL1|CD276|TKT|PPIF|APOL2|IDI1|SGSH|MARCKSL1|HEXA|HEXB|DNAJC10|PDCD4|GPX1|HMOX1|NDUFS2|AKR1C1|NDUFS1|PEPD|AIFM1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1C1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|DCD|KRT6A|NFS1|ADH5|HK2|HK1|DCN|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|KRT8|COL6A3|TGM2|ENO2|COL6A2|CAMK2D|COL6A1|VPS35|HSPA4|CALML5|FYCO1|NSDHL|ETFA|COL4A2|PSAP|HSPG2|ANXA4|NCSTN|ATP6V1E1|AKR1B1|H2AFY2|ABCC1</td></tr>
<tr><td>5768</td><td>endosome</td><td>6.60E-05</td><td>3.09E-04</td><td>9</td><td>141</td><td>6.4</td><td>228</td><td>TF|LAMP1|RAB7A|LAMP2|NPC1|SQSTM1|IGF2R|VPS35|CD63</td></tr>
<tr><td>6811</td><td>ion transport</td><td>1.16E-04</td><td>5.21E-04</td><td>17</td><td>141</td><td>12.1</td><td>791</td><td>TF|COL4A2|SLC38A2|PSAP|HK2|HK1|ATP6V1B2|ATP6V1G1|FTH1|ATP6V1C1|ATP6V1A|NNT|ATP6V1E1|COL6A3|COL6A2|COL6A1|FTL</td></tr>
<tr><td>5975</td><td>carbohydrate metabolic process</td><td>1.63E-04</td><td>6.98E-04</td><td>12</td><td>141</td><td>8.5</td><td>445</td><td>SGSH|GNS|LAMP2|GNPDA1|HEXA|AKR1B1|HEXB|PGD|ENO2|HK2|HK1|IDH1</td></tr>
<tr><td>5783</td><td>endoplasmic reticulum</td><td>2.12E-04</td><td>8.74E-04</td><td>17</td><td>141</td><td>12.1</td><td>832</td><td>S100A7|DNAJC10|EPHX1|PPGB|ACAT1|POR|FDFT1|MGST3|NCSTN|APOL2|NPC1|HMOX1|SDCBP|ARL6IP5|MGST1|RETSAT|NSDHL</td></tr>
<tr><td>16265</td><td>death</td><td>3.50E-04</td><td>1.34E-03</td><td>12</td><td>141</td><td>8.5</td><td>484</td><td>GPX1|CDKN2A|CADM1|PSAP|SQSTM1|AIFM1|HMOX1|HSPE1|BCL2L13|PDCD4|NDUFS1|RRAGC</td></tr>
<tr><td>8219</td><td>cell death</td><td>3.50E-04</td><td>1.34E-03</td><td>12</td><td>141</td><td>8.5</td><td>484</td><td>GPX1|CDKN2A|CADM1|PSAP|SQSTM1|AIFM1|HMOX1|HSPE1|BCL2L13|PDCD4|NDUFS1|RRAGC</td></tr>
<tr><td>19748</td><td>secondary metabolic process</td><td>4.92E-04</td><td>1.81E-03</td><td>4</td><td>141</td><td>2.8</td><td>48</td><td>HMOX1|ADH5|IDI1|RETSAT</td></tr>
</table>

43226	organelle	9.44E-04	3.35E-03	83	141	58.9	8385	SGSH|S100A7|HEXA|HEXB|DNAJC10|PDCD4|FDFT1|FAHD1|GPX1|CDKN2A|NDUFS4|HMOX1|NDUFS2|NDUFS1|SQRDL|SUCLG2|AIFM1|PPGB|MYH4|TMEM126A|BASP1|NPEPPS|CDK4|MMP14|HMGA2|BCL2L13|VAT1|POR|GNS|ATP6V1A|NPC1|BGN|NNT|NPC2|IGF2R|PRCP|SDCBP|TXNRD1|PCYOX1|CTSB|ACAA1|TF|RAB7A|KRT6A|NDUFB7|HK2|NFS1|HK1|ATP6V1G1|ATP6V1B2|ACAT1|HADHA|RRAGC|HADHB|CD9|HSPA2|SQSTM1|IVD|KRT8|TGM2|IDH1|VPS35|HSPE1|NDRG1|SCARB2|ARL6IP5|ETFB|NSDHL|ETFA|NDUFA8|PSAP|EPHX1|CD63|MGST3|NCSTN|PPIF|APOL2|LAMP1|LAMP2|H2AFY2|IDI1|MGST1|RETSAT
44238	primary metabolic process	1.53E-03	5.27E-03	66	141	46.8	6344	SGSH|GNPDA1|QPCTL|HEXA|PGD|HEXB|DNAJC10|LSS|FDFT1|CDKN2A|NDUFS4|ISG15|PCYT2|AKR1C1|NDUFS1|PEPD|AIFM1|QDPR|PPGB|PIP5K2C|NPEPPS|HMGA2|MMP14|CDK4|GNS|ATP6V1A|NPC1|ASCC3|PDE5A|PRCP|PCYOX1|CTSB|PRPS1|ACAA1|GCLC|MVD|HK2|ADH5|NFS1|HMGCS1|HK1|ATP6V1B2|ACAT1|HADHA|MIF|RRAGC|HADHB|SQSTM1|TGM2|ENO2|CAMK2D|IDH1|HSPE1|NSDHL|PTGR1|PSAP|FDPS|TKT|MGST3|NCSTN|PPIF|APOL2|LAMP2|AKR1B1|IDI1|RETSAT
50876	reproduction	1.79E-03	5.93E-03	11	141	7.8	506	APOL2|CD9|GNPDA1|HSPA2|CADM1|HEXA|HEXB|HK2|HK1|MMP14|MIF
3674	molecular_function	1.91E-03	6.15E-03	133	141	94.3	15912	GNPDA1|QPCTL|CADM1|S100A8|S100A7|PGD|S100A9|FDFT1|FAHD1|CDKN2A|ISG15|TGFBI|SPR|FTL|SUCLG2|QDPR|MYH4|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|HSPB6|ASCC3|PDE5A|PRCP|SDCBP|PRPS1|ACAA1|SNX9|RAB7A|SLC38A2|GCLC|MVD|SNX5|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|SCARB2|LAMB1|ARL6IP5|PTGR1|HPCAL1|CD276|FDPS|EPHX1|TKT|PPIF|APOL2|IDI1|SGSH|MARCKSL1|HEXA|HEXB|DNAJC10|LSS|PDCD4|GPX1|NDUFS4|HMOX1|PCYT2|NDUFS2|AKR1C1|NDUFS1|SQRDL|PEPD|AIFM1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1C1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|DCD|KRT6A|NDUFB7|HK2|ADH5|NFS1|HK1|ATP6V1G1|DCN|MIF|CD9|HSPA2|SQSTM1|COL6A3|KRT8|TGM2|ENO2|CAMK2D|COL6A2|COL6A1|VPS35|HSPA4|CALML5|FYCO1|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|HSPG2|ANXA4|MGST3|NCSTN|ATP6V1E1|AKR1B1|H2AFY2|ABCC1|MGST1|RETSAT
16787	hydrolase activity	1.99E-03	6.21E-03	29	141	20.6	2180	SGSH|RAB7A|GNPDA1|QPCTL|HEXA|HEXB|HK2|HK1|ATP6V1G1|ATP6V1B2|RRAGC|FAHD1|HMOX1|PEPD|PSAP|EPHX1|PPGB|NPEPPS|MMP14|GNS|ATP6V1C1|ATP6V1A|ASCC3|ATP6V1E1|PDE5A|PRCP|ABCC1|CTSB|IDI1
16043	cellular component organization and biogenesis	4.56E-03	1.38E-02	23	141	16.3	1687	RAB7A|COL4A2|PSAP|AIFM1|HEXA|S100A9|HEXB|HK2|HK1|MYH4|HMGA2|MIF|CD9|GPX1|NPC1|CDKN2A|NDUFS4|IGF2R|H2AFY2|KRT8|COL6A2|SDCBP|LAMB1
16740	transferase activity	4.70E-03	1.38E-02	23	141	16.3	1691	QPCTL|MVD|HK2|NFS1|HMGCS1|FDPS|HK1|PIP5K2C|TKT|CDK4|ACAT1|POR|HADHA|FDFT1|HADHB|MGST3|IGF2R|TGM2|CAMK2D|PCYT2|MGST1|ACAA1|PRPS1
9607	response to biotic stimulus	5.40E-03	1.55E-02	7	141	5.0	276	DCD|HSPA2|ISG15|S100A7|KRT8|HSPA4|HSPE1
5623	cell	6.49E-03	1.81E-02	125	141	88.7	14823	GNPDA1|QPCTL|CADM1|S100A7|FDFT1|FAHD1|CDKN2A|ISG15|SPR|FTL|SUCLG2|QDPR|MYH4|TMEM126A|BASP1|NPEPPS|RIC8B|BCL2L13|POR|GNS|NPC1|NPC2|NNT|ASCC3|PRCP|SDCBP|PRPS1|ACAA1|RAB7A|SLC38A2|GCLC|MVD|HMGCS1|ATP6V1B2|ACAT1|HADHA|FTH1|RRAGC|HADHB|IVD|IDH1|NDRG1|HSPE1|FAM162A|SCARB2|LAMB1|ARL6IP5|PTGR1|CD276|FDPS|EPHX1|TKT|CD63|PPIF|APOL2|LAMP1|LAMP2|IDI1|SGSH|MARCKSL1|HEXA|HEXB|DNAJC10|PDCD4|GPX1|NDUFS4|HMOX1|GPC1|NDUFS2|AKR1C1|NDUFS1|SQRDL|AIFM1|STXBP1|PPGB|PIP5K2C|HMGA2|MMP14|CDK4|VAT1|ATP6V1C1|ATP6V1A|BGN|IGF2R|TXN|TXNRD1|CTSB|PCYOX1|TF|KRT6A|NDUFB7|NFS1|ADH5|HK2|HK1|ATP6V1G1|MIF|CD9|HSPA2|SQSTM1|COL6A3|KRT8|TGM2|ENO2|CAMK2D|COL6A2|COL6A1|VPS35|HSPA4|FYCO1|ETFB|NSDHL|ETFA|COL4A2|NDUFA8|PSAP|ANXA4|MGST3|NCSTN|ATP6V1E1|AKR1B1|H2AFY2|ABCC1|MGST1|RETSAT
16209	antioxidant activity	6.98E-03	1.89E-02	3	141	2.1	51	MGST3|GPX1|TXNRD1
8283	cell proliferation	7.15E-03	1.89E-02	7	141	5.0	291	HMOX1|TXN|TGFBI|CD276|TXNRD1|MMP14|MIF
31386	protein tag	7.65E-03	1.97E-02	1	141	0.7	1	ISG15
8289	Mol Funct lipid binding	8.96E-03	2.25E-02	8	141	5.7	380	APOL2|SNX9|NPC2|PSAP|SNX5|ADH5|ANXA4|HADHA
5576	extracellular region	1.03E-02	2.52E-02	24	141	17.0	1912	DCD|TF|COL4A2|PSAP|S100A7|PGD|HSPG2|DNAJC10|DCN|MMP14|MIF|APOL2|NPC2|BGN|ISG15|HMOX1|AKR1B1|COL6A3|TGFBI|COL6A2|COL6A1|CTSB|LAMB1|GPC1
43234	protein complex	1.08E-02	2.58E-02	22	141	15.6	1711	GCLC|NDUFA8|NDUFB7|HK2|HK1|MYH4|ATP6V1G1|ATP6V1B2|CDK4|FTH1|HADHA|ATP6V1C1|ATP6V1A|NDUFS4|ATP6V1E1|ENO2|CAMK2D|SDCBP|LAMB1|NDUFS2|NDUFS1|FTL
166	nucleotide binding	1.17E-02	2.73E-02	26	141	18.4	2146	RAB7A|GCLC|MVD|HK2|HK1|RRAGC|HSPA2|IVD|CAMK2D|TGM2|HSPE1|HSPA4|ETFA|AIFM1|SUCLG2|MYH4|TKT|PIP5K2C|CDK4|POR|ATP6V1C1|ATP6V1A|ASCC3|PDE5A|ABCC1|TXNRD1
5509	calcium ion binding	1.23E-02	2.81E-02	14	141	9.9	933	SGSH|HPCAL1|S100A8|S100A7|PSAP|S100A9|TKT|MMP14|ANXA4|MIF|FAHD1|GNS|TGM2|CALML5

<table>
<tr><td></td><td></td><td>6996</td><td>organelle organization and biogenesis</td><td>1.54E-02</td><td>3.45E-02</td><td>16</td><td>141</td><td>11.3</td><td>1155</td><td>PSAP|AIFM1|HEXA|S100A9|HEXB|HK2|MYH4|HK1|HMGA2|MIF|GPX1|CDKN2A|NDUFS4|H2AFY2|KRT8|SDCBP</td></tr>
<tr><td></td><td></td><td>9605</td><td>response to external stimulus</td><td>1.97E-02</td><td>4.32E-02</td><td>10</td><td>141</td><td>7.1</td><td>614</td><td>APOL2|CD9|TF|S100A8|HMOX1|S100A9|SPR|CTSB|MMP14|MIF</td></tr>
</table>

<table>
<tr><th>Group</th><th>Ontology</th><th>GO-ID</th><th>GO term</th><th>p-value</th><th>corr p-value</th><th>identified molecules</th><th>identified cluster size</th><th>cluster frequency (%)</th><th>available molecules</th><th>identified molecules</th></tr>
<tr><td>Downregulated</td><td>GOSlim</td><td>3723</td><td>RNA binding</td><td>5.92E-15</td><td>6.10E-13</td><td>32</td><td>160</td><td>20.0</td><td>692</td><td>FUSIP1|RALY|RPL19|RBM3|RPL27A|YBX1|DDX3X|RBMS2|RPL10|RPL5|PABPN1|KHDRBS1|HNRNPA2B1|AARS|SF1|ELAVL1|RPL23A|DDX5|RPS6|RBMX|HNRNPA1|HNRNPA0|EIF4G1|HNRPDL|HNRNPH3|EIF4H|CIRBP|THOC4|RPS10|SRP72|RBM14|HNRNPH1</td></tr>
<tr><td></td><td></td><td>5515</td><td>protein binding</td><td>4.53E-12</td><td>2.33E-10</td><td>104</td><td>160</td><td>65.0</td><td>7030</td><td>PDLIM7|CTPS|PDLIM5|CHMP4A|LMO7|RANGAP1|EDIL3|TFG/ALK|CBX5|DNAJC9|DNAJC8|SERPINE1|PABPN1|HNRNPA2B1|MFGE8|CSDA|UNC84B|RIC8A|KRT18|TAGLN|COL1A2|RPS10|STMN1|TGFB1I1|ERC1|CAV2|PPME1|TAGLN2|PEF1|EIF3A|RPL5|EMD|CDC42EP3|LGALS1|PPFIBP1|RPL23A|CSRP1|RPS6|DDX5|HNRNPA1|RBMX|HNRNPH3|ITGA6|PCNA|CIRBP|DNAJB1|TMPO|DNAJB4|HNRNPH1|DNAJB6|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|YBX1|MCM7|P4HA2|SDPR|CHST14|RHOC|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|HNRPDL|EIF4G1|EPB41L2|CCDC50|PDCL3|PFDN1|SMTN|RRM2|THOC4|KPNA2|FUSIP1|SNX18|RAB3A|CNN3|CALD1|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|CNN1|PAPSS2|FEN1|MLTK|NASP|ELAVL1|TJP1|RBM14</td></tr>
<tr><td></td><td></td><td>5488</td><td>binding</td><td>3.61E-10</td><td>1.24E-08</td><td>141</td><td>160</td><td>88.1</td><td>12313</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|RBM3|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|FSTL1|EDIL3|TFG/ALK|CBX5|HIST1H2BN|DNAJC9|SERPINE1|DNAJC8|RBMS2|H2AFZ|RPL10|RAB21|PABPN1|H1F0|HNRNPA2B1|AARS|MFGE8|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|GBP1|CAV2|HMGB2|PPME1|TAGLN2|PEF1|EIF3A|DDX3X|RPL5|HIST2H3PS2|CDC42EP3|EMD|CRIP2|LGALS1|MRC2|PPFIBP1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|ITGA6|EIF4H|PCNA|CIRBP|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB4|DNAJB6|DUT|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|NT5E|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|HIST1H1B|CDC2|ANP32E|SF1|SLC3A2|MCM2|PALLD|NEXN|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|SNX18|CNN3|FAM98A|CALD1|RPL27A|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|CNN1|PAPSS2|FEN1|MLTK|NASP|ELAVL1|ANXA3|TJP1|PHGDH|SUMF2|PSAT1|RBM14</td></tr>
<tr><td></td><td></td><td>5622</td><td>intracellular</td><td>1.70E-09</td><td>4.37E-08</td><td>128</td><td>160</td><td>80.0</td><td>10633</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|LUZP1|CBX5|HIST1H2BN|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|RPL36AL|PABPN1|PLD3|INA|H1F0|AARS|HNRNPA2B1|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|CAV2|CDV3|HMGB2|PEF1|EIF3A|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|CDC42EP3|UAP1|LGALS1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|EIF4H|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB6|DUT|LIMA1|AP3S1|DEK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|CALD1|RPL27A|ASNS|TPM1|TPM4|AP3M1|PPP1R12A|CNN2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|GOLPH3|SUMF2|RBM14</td></tr>
<tr><td></td><td></td><td>5737</td><td>cytoplasm</td><td>2.54E-08</td><td>5.23E-07</td><td>91</td><td>160</td><td>56.9</td><td>6546</td><td>LIMA1|RPL19|PDLIM7|CTPS|CHMP4A|PDLIM5|DTYMK|PITPNB|AP3S1|LMO7|RANGAP1|YBX1|ASAH1|MTHFD2|P4HA2|SDPR|CHST14|RPL10|RAB21|HMGCL|AP3B1|GOLGA2|RPL36AL|PLD3|PABPN1|KIAA1949|CDC2|ANP32E|AARS|SF1|SLC3A2|PALLD|NEXN|CSDA|DAPK3|UNC84B|RIC8A|CCDC50|EPB41L2|EIF4G1|HNRPDL|PYCR1|PFDN1|PDCL3|SMTN|KRT18|TAGLN|RRM2|COL1A2|CTSD|THOC4|RPS10|LEPREL1|SRP72|STMN1|TGFB1I1|ERC1|KPNA2|FUSIP1|RAB3A|CAV2|HMGB2|CDV3|RPL27A|ASNS|TPM1|TPM4|PEF1|EIF3A|KDELC2|DDX3X|AP3M1|PPP1R12A|RPL5|CDC42EP3|UAP1|MLTK|NASP|LGALS1|RPL23A|RPS6|HNRNPA1|ANXA3|GOLPH3|EIF4H|SUMF2|GOSR2|HSPA13|DNAJB1|DNAJB6|DUT</td></tr>
<tr><td></td><td></td><td>8092</td><td>cytoskeletal protein binding</td><td>4.89E-08</td><td>8.39E-07</td><td>18</td><td>160</td><td>11.3</td><td>437</td><td>KIAA1949|LIMA1|CNN3|CALD1|PDLIM5|LMO7|NEXN|PALLD|TPM1|TPM4|UNC84B|EPB41L2|SMTN|TAGLN|CNN2|CNN1|STMN1|CDC42EP3</td></tr>
<tr><td></td><td></td><td>3779</td><td>actin binding</td><td>6.99E-08</td><td>1.03E-06</td><td>15</td><td>160</td><td>9.4</td><td>305</td><td>KIAA1949|LIMA1|CNN3|PDLIM5|CALD1|LMO7|NEXN|PALLD|TPM1|TPM4|EPB41L2|SMTN|TAGLN|CNN2|CNN1</td></tr>
</table>

43226	organelle	8.72E-08	1.12E-06	106	160	66.3	8389	RALY|RPL19|PDLIM7|PDLIM5|CHMP4A|PITPNB|LMO7|RANGAP1|LUZP1|CBX5|HIST1H2BN|H2AFZ|RBMS2|RPL10|RAB21|HMGCL|RPL36AL|PABPN1|PLD3|INA|H1F0|HNRNPA2B1|CSDA|UNC84B|PYCR1|KRT18|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|CAV2|HMGB2|EIF3A|KDELC2|DDX3X|RPL5|HIST2H3PS2|EMD|CDC42EP3|RPL23A|CSRP1|RPS6|SUGT1|DDX5|HNRNPA1|RBMX|HNRNPA0|HNRNPH3|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB6|DUT|LIMA1|AP3S1|DEK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|CHST14|HIST3H2BB|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|CDC2|HIST1H1B|ANP32E|SLC3A2|SF1|MCM2|NEXN|PALLD|DAPK3|HNRPDL|EPB41L2|SMTN|CTSD|THOC4|LEPREL1|KPNA2|FUSIP1|RAB3A|CALD1|RPL27A|TPM1|TPM4|AP3M1|CNN2|FEN1|NES|MLTK|NASP|ELAVL1|GOLPH3|SUMF2|RBM14
16043	cellular component organization and biogenesis	8.99E-07	1.03E-05	35	160	21.9	1688	FUSIP1|CAV2|HMGB2|LIMA1|CNN3|PDLIM7|LMO7|CBX5|EIF3A|HIST1H2BN|H2AFZ|CNN2|CNN1|HIST2H3PS2|HIST3H2BB|AP3B1|H1F0|INA|HIST1H1C|HIST1H1B|NASP|MRC2|SF1|MCM2|PALLD|DAPK3|UNC84B|EPB41L2|TJP1|ITGA6|GOSR2|STMN1|RBM14|KPNA2|DNAJB6
5694	chromosome	1.24E-06	1.28E-05	15	160	9.4	382	H1F0|HMGB2|HIST1H1C|HIST1H1B|MCM2|SUGT1|UNC84B|CBX5|HIST1H2BN|MCM7|H2AFZ|PCNA|TMPO|HIST2H3PS2|HIST3H2BB
6996	organelle organization and biogenesis	2.23E-06	2.08E-05	27	160	16.9	1155	CAV2|HMGB2|LIMA1|CNN3|LMO7|CBX5|EIF3A|HIST1H2BN|H2AFZ|CNN2|CNN1|HIST2H3PS2|HIST3H2BB|H1F0|INA|HIST1H1C|HIST1H1B|NASP|MCM2|PALLD|DAPK3|UNC84B|EPB41L2|STMN1|RBM14|KPNA2|DNAJB6
3674	molecular_function	6.05E-06	5.20E-05	155	160	96.9	15925	RALY|RPL19|PDLIM7|CTPS|PDLIM5|RBM3|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|FSTL1|EDIL3|TFG/ALK|CBX5|HIST1H2BN|DNAJC9|SERPINE1|DNAJC8|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|RPL36AL|H1F0|INA|PLD3|PABPN1|HNRNPA2B1|AARS|MFGE8|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|GBP1|CAV2|CDV3|HMGB2|PPME1|TAGLN2|PEF1|EIF3A|DDX3X|RPL5|HIST2H3PS2|CDC42EP3|EMD|UAP1|CRIP2|LGALS1|MRC2|PPFIBP1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|ITGA6|EIF4H|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB4|DNAJB6|DUT|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|NT5E|AP3B1|GOLGA2|KHDRBS1|KIAA1949|HIST1H1C|HIST1H1B|CDC2|ANP32E|SF1|SLC3A2|MCM2|PALLD|NEXN|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|FKBP11|KPNA2|FUSIP1|RAB3A|SNX18|CNN3|FAM98A|CALD1|RPL27A|ASNS|TPM1|TPM4|ATXN2L|AP3M1|PPP1R12A|CNN2|CNN1|PAPSS2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|TJP1|PHGDH|SUMF2|PSAT1|RBM14
5829	cytosol	2.08E-05	1.65E-04	21	160	13.1	869	CAV2|RPL19|CDC2|CTPS|PDLIM5|DTYMK|RPL27A|ASNS|RPL23A|RPS6|EIF4G1|PFDN1|EIF3A|RRM2|SDPR|EIF4H|RPL10|RPS10|RPL5|ERC1|DUT
3676	nucleic acid binding	3.96E-05	2.91E-04	50	160	31.3	3345	RALY|RPL19|RBM3|DEK|YBX1|HIST1H2BN|RBMS2|H2AFZ|RPL10|HIST3H2BB|PABPN1|H1F0|KHDRBS1|HIST1H1C|CDC2|HIST1H1B|AARS|HNRNPA2B1|SF1|MCM2|CSDA|HNRPDL|EIF4G1|PFDN1|RPS10|THOC4|SRP72|FUSIP1|HMGB2|RPL27A|EIF3A|DDX3X|RPL5|HIST2H3PS2|FEN1|ELAVL1|RPL23A|RPS6|DDX5|HNRNPA1|RBMX|HNRNPA0|HNRNPH3|EIF4H|PCNA|CIRBP|TMPO|RBM14|HNRNPH1|DNAJB6
166	nucleotide binding	6.98E-05	4.79E-04	36	160	22.5	2146	FUSIP1|RALY|RAB3A|RBM3|DTYMK|TFG/ALK|MCM7|DDX3X|RBMS2|RHOC|PAPSS2|NT5E|RAB21|PABPN1|MLTK|CDC2|HNRNPA2B1|AARS|ELAVL1|RPL23A|MCM2|DDX5|DAPK3|RBMX|HNRNPA1|HNRNPA0|ARL3|HNRPDL|HNRNPH3|EIF4H|CIRBP|THOC4|HSPA13|RBM14|HNRNPH1|GBP1
8150	biological_process	1.28E-04	8.21E-04	144	160	90.0	14524	RALY|RPL19|PDLIM7|CTPS|RBM3|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|FSTL1|EDIL3|TFG/ALK|CBX5|HIST1H2BN|NUDCD1|SERPINE1|DNAJC8|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|RPL36AL|H1F0|INA|PLD3|PABPN1|HNRNPA2B1|AARS|MFGE8|CSDA|UNC84B|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|GBP1|CAV2|CDV3|HMGB2|PPME1|TAGLN2|PEF1|EIF3A|DDX3X|RPL5|HIST2H3PS2|CDC42EP3|EMD|UAP1|CRIP2|LGALS1|MRC2|PPFIBP1|RPL23A|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|ITGA6|EIF4H|PCNA|CIRBP|GOSR2|TMPO|DNAJB1|HNRNPH1|DNAJB4|DNAJB6|DUT|LIMA1|FAM3C|IGFBP7|AP3S1|DEK|PSPH|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|CHST14|RHOC|HIST3H2BB|NT5E|AP3B1|KHDRBS1|HIST1H1C|HIST1H1B|CDC2|SF1|SLC3A2|MCM2|PALLD|NEXN|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|FKBP11|KPNA2|FUSIP1|RAB3A|SNX18|CNN3|CALD1|RPL27A|ASNS|TPM1|TPM4|ATXN2L|AP3M1|CNN2|CNN1|PAPSS2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|TJP1|PHGDH|PSAT1|RBM14
6259	DNA metabolic process	6.31E-04	3.82E-03	12	160	7.5	455	HMGB2|MCM7|CDC2|NASP|RRM2|PCNA|MCM2|RBM14|KPNA2|NT5E|FEN1|DUT

<table>
<tr><td>44238</td><td>primary metabolic process</td><td>7.13E-04</td><td>4.08E-03</td><td>75</td><td>160</td><td>46.9</td><td>6344</td><td>RALY|RPL19|CTPS|RBM3|DTYMK|PITPNB|LMO7|PSPH|TFG/ALK|ASAH1|YBX1|MCM7|P4HA2|DNAJC8|RBMS2|CHST14|RPL10|NT5E|RPL36AL|KHDRBS1|PLD3|PABPN1|CDC2|HNRNPA2B1|AARS|SF1|SLC3A2|MCM2|CSDA|DAPK3|EIF4G1|HNRPDL|PYCR1|PFDN1|RRM2|CTSD|THOC4|RPS10|LEPREL1|TGFB1I1|STMN1|SRP72|ERC1|FKBP11|KPNA2|FUSIP1|CAV2|HMGB2|PPME1|RPL27A|ASNS|EIF3A|RPL5|FEN1|UAP1|MLTK|NASP|ELAVL1|RPL23A|DDX5|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|EIF4H|PHGDH|PCNA|DNAJB1|PSAT1|RBM14|HNRNPH1|DNAJB4|DNAJB6|DUT</td></tr>
<tr><td>7010</td><td>cytoskeleton organization and biogenesis</td><td>8.52E-04</td><td>4.62E-03</td><td>12</td><td>160</td><td>7.5</td><td>471</td><td>EPB41L2|INA|LIMA1|CNN3|LMO7|CNN2|CNN1|STMN1|PALLD|KPNA2|DNAJB6|UNC84B</td></tr>
<tr><td>5840</td><td>ribosome</td><td>9.20E-04</td><td>4.74E-03</td><td>10</td><td>160</td><td>6.3</td><td>347</td><td>EIF3A|RPL19|RPL27A|SF1|RPL10|RPL23A|RPL5|RPS10|RPS6|RPL36AL</td></tr>
<tr><td>5635</td><td>nuclear envelope</td><td>1.03E-03</td><td>4.98E-03</td><td>7</td><td>160</td><td>4.4</td><td>181</td><td>PCNA|RANGAP1|TMPO|KPNA2|EMD|UNC84B|CBX5</td></tr>
<tr><td>5198</td><td>structural molecule activity</td><td>1.06E-03</td><td>4.98E-03</td><td>17</td><td>160</td><td>10.6</td><td>843</td><td>INA|NES|RPL19|RPL27A|RPL23A|RPS6|TPM1|TPM4|EPB41L2|EIF3A|KRT18|SMTN|COL1A2|RPL10|RPS10|RPL5|RPL36AL</td></tr>
<tr><td>228</td><td>nuclear chromosome</td><td>1.30E-03</td><td>5.82E-03</td><td>5</td><td>160</td><td>3.1</td><td>93</td><td>HMGB2|MCM7|MCM2|UNC84B|CBX5</td></tr>
<tr><td>5856</td><td>cytoskeleton</td><td>1.46E-03</td><td>6.28E-03</td><td>20</td><td>160</td><td>12.5</td><td>1106</td><td>INA|KIAA1949|NES|LIMA1|PDLIM7|CDC2|CALD1|PDLIM5|NEXN|PALLD|TPM1|TPM4|EPB41L2|SMTN|KRT18|CNN2|STMN1|TGFB1I1|FILIP1L|CDC42EP3</td></tr>
<tr><td>15031</td><td>protein transport</td><td>2.28E-03</td><td>9.41E-03</td><td>14</td><td>160</td><td>8.8</td><td>675</td><td>SNX18|RAB3A|NASP|CHMP4A|AP3S1|KRT18|AP3M1|PCNA|GOSR2|SRP72|ERC1|KPNA2|RAB21|AP3B1</td></tr>
<tr><td>6416</td><td>translation</td><td>2.41E-03</td><td>9.48E-03</td><td>11</td><td>160</td><td>6.9</td><td>463</td><td>EIF3A|RPL19|EIF4H|AARS|RPL27A|RPL10|RPL23A|RPL5|RPS10|RPS6|RPL36AL</td></tr>
<tr><td>6139</td><td>nucleobase, nucleoside, nucleotide and nucleic acid metabolic process</td><td>2.55E-03</td><td>9.48E-03</td><td>38</td><td>160</td><td>23.8</td><td>2785</td><td>FUSIP1|RALY|HMGB2|CTPS|RBM3|DTYMK|YBX1|MCM7|DNAJC8|RBMS2|NT5E|FEN1|PABPN1|KHDRBS1|UAP1|CDC2|NASP|HNRNPA2B1|AARS|SF1|ELAVL1|MCM2|CSDA|DDX5|RBMX|HNRNPA1|HNRNPA0|EIF4G1|HNRPDL|HNRNPH3|RRM2|PCNA|THOC4|TGFB1I1|RBM14|HNRNPH1|KPNA2|DUT</td></tr>
<tr><td>5634</td><td>nucleus</td><td>2.58E-03</td><td>9.48E-03</td><td>57</td><td>160</td><td>35.6</td><td>4688</td><td>RALY|LMO7|LUZP1|RANGAP1|DEK|YBX1|CBX5|HIST1H2BN|MCM7|RBMS2|H2AFZ|HIST3H2BB|PABPN1|H1F0|KHDRBS1|HIST1H1C|CDC2|HIST1H1B|HNRNPA2B1|ANP32E|SF1|MCM2|CSDA|PALLD|DAPK3|UNC84B|HNRPDL|THOC4|TGFB1I1|SRP72|KPNA2|FUSIP1|HMGB2|EIF3A|DDX3X|RPL5|HIST2H3PS2|EMD|FEN1|MLTK|NASP|ELAVL1|CSRP1|RPS6|DDX5|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|PCNA|CIRBP|TMPO|DNAJB1|RBM14|HNRNPH1|DNAJB6|DUT</td></tr>
<tr><td>7049</td><td>cell cycle</td><td>3.02E-03</td><td>1.07E-02</td><td>13</td><td>160</td><td>8.1</td><td>621</td><td>KHDRBS1|MLTK|CDC2|NASP|DTYMK|MCM2|SUGT1|UNC84B|PFDN1|KRT18|MCM7|STMN1|KPNA2</td></tr>
<tr><td>9628</td><td>response to abiotic stimulus</td><td>4.04E-03</td><td>1.39E-02</td><td>6</td><td>160</td><td>3.8</td><td>173</td><td>MLTK|CDC2|CIRBP|DNAJB4|CSDA|FEN1</td></tr>
<tr><td>8152</td><td>metabolic process</td><td>5.41E-03</td><td>1.80E-02</td><td>78</td><td>160</td><td>48.8</td><td>7113</td><td>RALY|RPL19|CTPS|RBM3|DTYMK|PITPNB|LMO7|PSPH|TFG/ALK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|DNAJC8|CHST14|RBMS2|RPL10|NT5E|HMGCL|RPL36AL|KHDRBS1|PLD3|PABPN1|CDC2|HNRNPA2B1|AARS|SF1|SLC3A2|MCM2|CSDA|DAPK3|EIF4G1|HNRPDL|PYCR1|PFDN1|RRM2|CTSD|THOC4|RPS10|LEPREL1|TGFB1I1|STMN1|SRP72|ERC1|FKBP11|KPNA2|FUSIP1|CAV2|HMGB2|PPME1|RPL27A|ASNS|EIF3A|RPL5|PAPSS2|FEN1|UAP1|MLTK|NASP|ELAVL1|RPL23A|DDX5|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|EIF4H|PHGDH|PCNA|DNAJB1|PSAT1|RBM14|HNRNPH1|DNAJB4|DNAJB6|DUT</td></tr>
<tr><td>5623</td><td>cell</td><td>6.59E-03</td><td>2.12E-02</td><td>141</td><td>160</td><td>88.1</td><td>14831</td><td>RALY|RPL19|PDLIM7|CTPS|PDLIM5|CHMP4A|PITPNB|DTYMK|LMO7|RANGAP1|LUZP1|TFG/ALK|CBX5|HIST1H2BN|SERPINE1|RBMS2|H2AFZ|RPL10|RAB21|HMGCL|FNDC3B|RPL36AL|H1F0|PABPN1|PLD3|INA|HNRNPA2B1|AARS|MFGE8|CSDA|UNC84B|RIC8A|PYCR1|KRT18|TAGLN|COL1A2|RPS10|TGFB1I1|STMN1|SRP72|ERC1|FILIP1L|GBP1|CAV2|CDV3|HMGB2|PEF1|EIF3A|KDELC2|DDX3X|RPL5|HIST2H3PS2|CDC42EP3|EMD|UAP1|LGALS1|MRC2|PPFIBP1|RPL23A|CSRP1|DDX5|SUGT1|RPS6|RBMX|HNRNPA1|HNRNPA0|HNRNPH3|ITGA6|EIF4H|PCNA|CIRBP|GOSR2|TMPO|HSPA13|DNAJB1|HNRNPH1|DNAJB6|DUT|LIMA1|AP3S1|DEK|ASAH1|YBX1|MTHFD2|MCM7|P4HA2|SDPR|CHST14|RHOC|HIST3H2BB|NT5E|GOLGA2|AP3B1|KHDRBS1|KIAA1949|HIST1H1C|HIST1H1B|CDC2|ANP32E|SF1|SLC3A2|MCM2|PALLD|NEXN|DAPK3|ARL3|CCDC50|EPB41L2|EIF4G1|HNRPDL|PFDN1|PDCL3|SMTN|RRM2|CTSD|THOC4|LEPREL1|FKBP11|KPNA2|FUSIP1|RAB3A|SNX18|CALD1|RPL27A|ASNS|TPM1|TPM4|ATXN2L|AP3M1|PPP1R12A|CNN2|FEN1|NES|MLTK|NASP|ELAVL1|ANXA3|TJP1|GOLPH3|SUMF2|RBM14</td></tr>
<tr><td>6519</td><td>amino acid and derivative metabolic process</td><td>1.47E-02</td><td>4.57E-02</td><td>7</td><td>160</td><td>4.4</td><td>295</td><td>PYCR1|CTPS|AARS|PHGDH|ASNS|PSAT1|PSPH</td></tr>
<tr><td>5794</td><td>Golgi apparatus</td><td>1.56E-02</td><td>4.72E-02</td><td>12</td><td>160</td><td>7.5</td><td>680</td><td>CAV2|AP3M1|GOLPH3|PITPNB|CHST14|AP3S1|GOSR2|LEPREL1|ERC1|RAB21|AP3B1|GOLGA2</td></tr>
</table>