

SUPPLEMENTARY METHODS

Human hepatocytes

Primary human hepatocytes were isolated using a three-step collagenase digestion technique as previously described (1). Briefly, cell isolation was initiated by perfusion with pre-warmed to 37°C calcium-free HBSS supplemented with 0.5 mM EGTA and collagenase solution (VitaCyte, Indianapolis, IN) until the tissue was fully digested. The digested liver was cooled with ice-cold Leibovitz's L-15 medium and strained through a series of progressively smaller stainless-steel sieves with a final filtration through a 100 µm mesh. The final crude cell suspension was centrifuged twice, and the post-digest medium was aspirated. Cell viability was assessed after isolation using trypan blue exclusion, and only cell preparations with viability greater than 80% were cryopreserved. Single vials of cryopreserved hepatocytes were obtained from In Vitro ADMET Laboratories (Malden, MA), Novabiosis (Durham, NC), and Anabios (San Diego, CA). Specific information on age, gender, and cell viability of human liver tissue and hepatocytes used in this study is described in Supplementary Table S1.

Genotyping

DNA was extracted with the DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany), and samples were genotyped using TaqMan SNP genotyping assays for *PNPLA3* (rs738409) (Thermo Fisher Scientific, San Jose, CA)(2) and listed in the Supplementary Table S2. Amplification and genotype clustering were performed using a StepOnePlus system (Applied Biosystems, Foster City, CA).

Immunostaining

Human liver tissue was fixed in 4% paraformaldehyde for 12 hours and 70% ethanol overnight at 4°C and then embedded in paraffin. Cut sections (5-7 microns) were mounted on glass slides for immunofluorescence and immunohistochemistry. Each sample was first stained with hematoxylin and eosin for histological examination. Slides were deparaffinized with xylenes and dehydrated with ethanol. Antigen unmasking was performed by boiling in 10 mM citrate buffer, pH 6.0. For immunofluorescence, the slides were then blocked for 1 hour with 10% goat serum, left incubating overnight at 4°C with primary antibodies listed in the Supplementary Table S2, and then incubated with secondary antibody for 1 hour at room temperature. Sections were covered with DAPI-containing mounting media. For immunohistochemistry staining after the antigen unmasking, the slides were exposed to 3% hydrogen peroxide and incubated overnight at 4°C with primary antibodies listed in the Supplementary Table S2. Tissue sections were then incubated with the

secondary biotinylated antibody corresponding to the animal species of the primary antibody (BA-1000; Vector Laboratories, Burlingame, CA) and exposed to 3,3'-diaminobenzidine (SK-4105; Vector Laboratories) to visualize the peroxidase activity. Counterstaining was performed with Richard-Allan Scientific Signature Series Hematoxylin (Thermo Scientific, Waltham, MA). All procedures followed the kit instructions. Images were captured with a Nikon Eclipse Ti microscope. Following that, images were analyzed using ImageJ software. RGB stacks were generated, pre-processed to equalize the illumination within the stack, thresholded, and measured.

ATF6 and E-Cadherin immunohistochemistry images were acquired using the PE Opera Phenix using the Harmony 5.1 software. Images were acquired with a 40X/1.1 NA Water Immersion objective. Fluorescence images were acquired with the following channels: Hoechst Ex. 405/Em. 435-480, ATF6 640 Ex./Em. 650-760, and E-Cadherin Ex. 488/Em. 500-550. To gather maximum intensity projections, a z-stack was acquired in confocal mode with 14 planes and a distance between each plane of 1.2 μm . To determine the number of ATF6-positive nuclei, we used Harmony 5.1 to create an analysis protocol that identifies nuclei based on Hoechst signal. Then, to determine ATF6 signal, we sampled a ring region of 1.5X the outer border of the nuclear region. ATF6-positive cells were then quantified by thresholding signal above the ATF6 negative control well average signal. The overall percent of ATF6-positive cells was determined by taking the total count of ATF6-positive cells and expressing it as a percent of the total number of nuclei (Hoechst-positive cells) in 49 fields per condition.

Intracellular Lipid Staining

Samples were fixed with 4% PFA for 15 minutes and washed three times with phosphate-buffered saline (PBS). After that, the samples were incubated with a 0.3 mM Nile Red (Sigma Aldrich, ON, Canada) or 1x HCS LipidTOXTM Red neutral lipid stain (Thermo Scientific, Waltham, MA) solution for 30 minutes at room temperature. Then, they were washed twice with PBS and counterstained with 1 $\mu\text{g}/\text{mL}$ of DAPI (Sigma Aldrich, ON, Canada) for 1 minute. Samples were imaged using an Eclipse Ti inverted microscope (Nikon) and the NIS-Elements software platform (Nikon, NY, USA). Following that, images were analyzed using ImageJ software.

XBP1 splicing quantification

Total cellular RNA was isolated using the RNeasy Mini kit (QIAGEN, Hilden, Germany) and reverse transcribed using SuperScript III (Invitrogen, Carlsbad, CA) following the manufacturers'

instructions. Complementary DNA was amplified using two sets of primers: total XBP1 (tXBP1) and a sequence that distinguished between the unspliced (uXBP1) and spliced XBP1 (sXBP1) (3). The primer sequences are listed in Supplementary Table S2. The amplification products were resolved in a 2% agarose gel, and the quantification was performed using ImageJ software.

Transmission electron microscopy

Human hepatocytes in suspension were briefly centrifuged and washed with PBS solution. Samples were then fixed with 2.5% glutaraldehyde overnight at 4°C. Fixed samples were processed by the Center for Biologic Imaging at the University of Pittsburgh and treated with 1% osmium tetroxide and 1% potassium ferricyanide for 1 hour at room temperature. Samples were washed with PBS and dehydrated in a graded series of ethanol solutions (30%, 50%, 70%, and 90% - 10 minutes each) and three 15-minute changes in fresh 100% ethanol. Infiltration was done with four 1-hour changes of EPON embedding plastic. The last change of EPON was allowed to polymerize overnight at 37°C and then for 48 hours at 60°C. Resin blocks were removed from the Eppendorf tubes, and 70 nm sections were taken and placed onto copper TEM grids. Image acquisition was made using either the JEM-1011 or the JEM-1400Plus transmission electron microscopes (Jeol, Peabody, MA) at 80 kV fitted with a side mount AMT 2k digital camera (Advanced Microscopy Techniques, Danvers, MA). The mitochondrial shape was evaluated as published previously using ImageJ (4). Briefly, individual mitochondria were analyzed for circularity ($4\pi \text{ area/perimeter}^2$) and its reciprocal value used as the form factor. The form factor has a minimum value of 1 where mitochondria are a perfect circle, increasing in mitochondria with a rod shape.

Mitochondrial DNA (mtDNA)

Genomic DNA was extracted with the DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) following the manufacturers' instructions. mtDNA content was analyzed by SYBER green qPCR using primers amplifying mitochondrial cytochrome C oxidase subunit 1 (*MT-CO1*), mitochondrial cytochrome B (*MT-CYB*), and mitochondrial NADH-Ubiquinone Oxidoreductase Chain 1 (*MT-ND1*). Relative gene expression was normalized to β -actin (*ACTB*) mRNA and was calculated using the $\Delta\Delta CT$ method. Primers are listed in the Supplementary Table S2.

Mitochondria stress

MitoSOX Red mitochondrial superoxide indicator (Thermo Fisher Scientific) was used to detect mitochondrial superoxide in hepatocytes. A 5 mM stock solution was prepared in DMSO and

diluted in PBS to a working concentration of 5 μ M immediately before use. Hepatocytes were washed twice with warm PBS before staining. MitoSOX Red working solution was added to the cells and incubated at 37°C for 30 minutes, protected from light. After incubation, cells were washed twice with PBS to remove unbound dye. Tetramethylrhodamine ethyl ester (TMRE, Thermo Fisher Scientific) was used to assess mitochondrial membrane potential in the iHeps. A 2 mM stock solution was prepared in DMSO and diluted in cell culture medium to a working concentration of 100 nM immediately before use. TMRE working solution was added to the cells, and they were incubated at 37°C for 60 minutes, protected from light. After incubation, cells were washed twice with warm PBS to remove unbound dye. Fluorescence was analyzed using a fluorescence microscope, and images were analyzed using ImageJ software.

ATP measurement

The intracellular ATP content was measured in hepatocytes by using the ATP Determination Kit (Thermo Fisher Scientific, Waltham, MA) following the manufacturer's instructions. The cells were incubated at 37°C for 1 hour in the absence or presence of 10 μ g/ml oligomycin A (Cayman Chemical, Ann Arbor, MI) or 10 mM 2-deoxyglucose (Cayman Chemical, Ann Arbor, MI). The ATP content was measured by luminescence with an integration time of 1 second per well.

Mitochondria Respiration

Oxygen consumption rate (OCR) was measured with an XF96 Extracellular Flux Analyzer (Seahorse Bioscience). Hepatocytes were seeded in Seahorse 96-well collagen-coated microplates, and the respiration was assayed the following day. The culture media was replaced with 100 μ L of assay medium (DMEM 10 mM glucose, 1 mM pyruvate, 2 mM glutamine, and 1% penicillin-streptomycin without serum and bicarbonate) and incubated at 37°C without CO₂ for 1 hour. The cells were then exposed to 1.5 μ M of oligomycin A, 1 μ M of carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP), and 0.5 μ M of rotenone/antimycin A (ROT/AA). Basal, ATP-linked, and maximal OCR were measured and compared between Hep-PNPLA3-WT and Hep-PNPLA3-I148M.

Lipidomics

Hepatocytes originally stored at -80°C were retrieved and transferred into a 15 mL centrifuge glass tube. 1 mL of water was added to lyse the cells, and the mixture was allowed to rest on ice for 10 minutes. Next, 2 mL of methanol and 0.9 mL of methylene chloride were added to the mixture. The mixture was vortexed to ensure a monophasic solution; otherwise, we stepwise

added 50 μ L of methanol and vortexed until a monophasic solution was achieved. Next, we added 5 μ L of the SPLASH™ LIPIDOMIX® internal standard mixture to each sample. Next, we added 1 mL of water and 0.9 mL of methylene chloride and vortexed. Next, we centrifuged at 1200 rpm for 10 minutes at 4°C. The lower lipid layer was collected and transferred to a fresh glass tube. Next, we added 2 mL of methylene chloride to the remains in the extraction tube and mixed, centrifuged, and collected the lower lipid layer and added it to the first extract. The extract was evaporated under nitrogen and resuspended in 500 μ L of mobile phase A. Mobile phase A (MPA) was 2 mM ammonium acetate in 7/93 methylene chloride/acetonitrile. Mobile phase B (MPB) was 2 mM ammonium acetate in 50/50 water/acetonitrile. Samples were run on our SCIEX Triple Quad™ LC-MS/MS system coupled with ExionLC™. 5 μ L of each sample was injected per run and eluted based on the following gradient: 0min: 0% MPB, 2min: 0% MPB, and at flowrate of 0.2 ml/min.; 2.01min: 0% MPB, at flowrate of 0.7 ml/min; 11min: 50% MPB; 11.5min: 70% MPB; 12.5min: 100% MPB; 15min: 100% MPB, 15.1min: 0% MPB at flowrate of 0.2 ml/min; 17min: 0% MPB. Lipids were detected based on an optimized scheduled multiple reaction monitoring (MRM) MS method that ran concurrently in both positive and negative modes based on our in-house MRM list of over 1100 lipids. The MS method was set up using the following parameters: GS1 = 45 psi, GS2 = 70 psi, spray voltage = 1600 V, temperature = 450°C, settling time = 15 ms, and pause time = 3 ms. Analytes were separated using Phenomenex's Luna® 3 μ m NH2, 2 x 100 mm column (00D-4377-B0) fitted with NH2 Standard Security Guard column (AJ0-4301) kept at 35°C. Peaks were extracted using SCIEX OS (version 3.1.6.44), and our in-house algorithm, implemented in R (CRAN 4.1.1), was utilized to filter out analytes with poor quality. Only unique metabolites with good quality across all samples were considered in the downstream analysis. Peaks were further normalized to the internal standards, and, finally, metabolite abundance was normalized to the cell number. Further downstream analyses were performed in Metaboanalyst® (V. 6.0), GraphPad Prism (Version 10.4.0), Python (ver. 3.11.4), and BioRender.com. Lipid classes legend; TAG: Triacylglycerols, PS: Phosphatidylserine, PI: Phosphatidylinositol, PG: Phosphatidylglycerol, PE: Phosphatidylethanolamine, PC: Phosphatidylcholine, MAG: Monoacylglycerol, LPS: Lipopolysaccharide, LPI: Lysophosphatidylinositol, LPG: Lysophosphatidylglycerol, LPC: Lysophosphatidylcholine, DAG: Diacylglycerol, CL: Cardiolipin, CE: Cholesteryl Ester, PG: Phosphatidylglycerol, PS: Phosphatidylserine. PUFAs legend: Arachidonic acid (20:4), Docosahexaenoic acid (DHA, 22:6), Eicosapentaenoic acid (EPA, 20:5), Linoleic acid (18:2), Alpha-Linolenic Acid (18:3).

Western Blot

Cells were trypsinized, pelleted, and washed with PBS. Lysis was performed with RIPA buffer (Sigma-Aldrich, Saint Louis, Missouri) and 1x Halt™ Protease and Phosphatase Inhibitor Cocktail (Thermo Fisher Scientific, Waltham, MA) for 30 minutes at 4°C, followed by centrifuging at 13,000 x g for 10 min at 4°C. Protein concentrations of the supernatant were determined by comparison with a known concentration of bovine serum albumin using a Pierce BCA Protein Assay Kit (ThermoFisher Scientific, Waltham, MA). 30 µg of lysate were loaded per well into 10% Mini-PROTEAN TGX™ gel (BioRad, Hercules, CA). Proteins were transferred onto a PVDF Transfer Membrane (Thermo Fisher Scientific, Waltham, MA). Membranes were incubated with a primary antibody solution overnight and then washed before incubation in a secondary antibody solution for 1 hour. Target antigens were finally detected using SuperSignal™ West Pico PLUS Chemiluminescent Substrate (Thermo Fisher Scientific, Waltham, MA). Images were scanned and analyzed using ImageJ software. The antibodies used are listed in the Supplementary Table S2.

Stable Isotopic Tracing Experiment

Primary human hepatocytes were cultured in Hepatocyte Culture Medium (Lonza, Walkersville, MD) on type I rat tail collagen-coated plates (Corning, Corning, NY) and kept at 37°C in 5% CO₂ overnight for attachment. The following day, cells were cultured with docosanoic-1,2,3,4-¹³C₄ acid (#57527, Sigma-Aldrich, Saint Louis, MO) and ¹³C₁-labelled palmitic acid (#28749, Cayman Chemical, Ann Arbor, MI) conjugated in 5% BSA free-fatty acid. After 48 hours, the cell pellets were stored at -80°C until we were ready for Acetyl-CoA measurement based on a protocol adopted from well-established methods from the literature (5-7). Briefly, on the day of analysis, the cell pellets were transferred to the pre-chilled 2 mL Precellys homogenizer tubes preloaded with 300-350 mg of the small ceramic beads (1.4 mm OD). Next, 200 µL of pre-chilled extraction solvent (10% (wt/vol) trichloroacetic acid (TCA) in optimal grade water) was added to each sample. Subsequently, samples were homogenized to disintegrate the cellular organelles using the Precellys + Cyrollys Evolution Homogenizer with the following settings: speed = 6000 rpm; cycle = 4 x 20 seconds; pause = 120 seconds; Cyolys = On; temperature = 4°C; and Mode Auto. After complete homogenization, 300 µL of the extraction solvent was added to achieve a final volume of 500 µL, and the sample tubes were incubated on ice for 10 minutes, followed by centrifugation for 10 minutes at 1700 x g at 4°C. The supernatant was collected for solid phase extraction (SPE). SPE was performed using the Oasis PRiME HLB 96-well µElution Plate with 3 mg Sorbent per well. Briefly, the vacuum pressure was set at 5 in Hg and the columns were conditioned with 200 µL of methanol, followed by equilibration with 200 µL of water. Next, 500 µL

of the metabolite extract was loaded, and the column was desalted with 200 μ L of water. Finally, the samples were eluted three times with 50 μ L of 25 mM ammonium acetate, resuspended in 5% salicylic acid, and analyzed using Sciex 7500 LC-MS/MS system. Samples were run on the Kinetex 2.6 μ m F5 100 A, LC Column 150 x 2.1 mm C18 column (Phenomenex). The flow rate was set to 0.1 mL/min with 5 mM ammonium acetate and 2.5 mM DMBA (N,N-Dimethylbutylamine) as mobile phase A and 100% methanol as mobile phase B. The gradient for the 22 min method was set as follows- 0 min: 2% B; 5 min: 25% B; 5.5 min: 100% B; 16 min: 2% B. The MRMs for isotopologue measurements are in Table S4. The data was corrected for natural abundance using IsoCorrectorR (v3.18) (8).

Analysis of reactive oxygen species

Total ROS in live cells was measured using the Cellular ROS Assay Kit (Abcam, Cambridge, UK). Following the manufacturer's instructions, the fluorescence (Ex/Em = 520/605 nm) was quantitatively measured on a Synergy HTX microplate reader (Biotek, Winooski, VT). [ROS unit is arbitrary unity, and the values were normalized to the mean of the PNPLA3 WT non-treated group.](#) To detect hydrogen peroxide (H₂O₂), a HyPerRed vector (Addgene 48249, Watertown, MA) was transfected, and live cells were imaged with a Nikon Inverted Research Fluorescence Microscope ECLIPSE Ti(9). Images were scanned and analyzed using ImageJ software.

Analysis of Lipid peroxidation

Malondialdehyde (MDA) is a natural byproduct of lipid peroxidation, and its quantification is generally used as a marker for lipid peroxidation. The MDA content in primary human hepatocytes was quantified using *Lipid Peroxidation (MDA) Assay Kit*, a commercially available kit from Sigma-Aldrich (Sigma-Aldrich, Saint Louis, MO). Cryopreserved primary human hepatocytes were pelleted and analyzed directly or cultured for 3 hours in suspension before the analysis. Cell lysates were deproteinized, and thiobarbituric acid (TBA) was added to generate an MDA-TBA adduct. The MDA-TBA adduct was quantified by fluorometric detection (Ex/Em = 430 nm/590 nm). The oxidation-sensitive probe C11-BODIPY 581/591 (Invitrogen, Carlsbad, CA) was used to evaluate lipid peroxidation under a fluorescence microscope. Untreated hepatocytes were prepared with a cytocentrifuge, incubated for 30 minutes with 10 μ M C11-BODIPY, and washed with PBS. Cultured cells were incubated with 10 μ M C11-BODIPY dissolved in culture media for 30 minutes at 37°C and washed with PBS.

Pex2 knockdown

The following siRNAs were ordered from GE Dharmacon: Accell Human Pex2 siRNA SMARTpool (E-006548-00-0050) and Accell Non-targeting Pool (D-001910-10-50). siRNAs were reconstituted in siRNA Buffer (B-002000-UB-100, Dharmacon, CO) at 100 μ M. Hepatocytes were plated into collagen-coated plates. The following day, cells were washed once with PBS and siRNAs in media were added at a final concentration of 1 μ M. After 24 hours, fresh media was added. Hepatocytes were cultured for an additional 24 hours after which samples were collected for analysis.

PNPLA3 gene edition

The single-guide RNA (sgRNA) sequence was designed to cut the human *PNPLA3* gene at the position chr22:43,928,854 to replace the minor allele (G) with the major allele (C). The sgRNA sequence can be found in Supplementary Figure 3 and Figure 12A. The sgRNA was cloned into a plasmid vector and nucleofected into a hepatocellular cell line or human iPSC line together with the donor DNA (ACTTCTCTCTCCTTTGCTTTCACAGGCCTTGGTATGTTCTGCTTCATCCCCTTTTACAGTG GCCTTATCCCTCCTTCCTTCAGAGGCGTGGTAAGT). Antibiotic selection was performed, and DNA from selected clonal cells was extracted, amplified, and purified before sequencing as previously described (Synthego, Redwood City, CA). Major homozygous clones were identified, expanded, and cryopreserved, and one was used to perform the experiments.

Sanger sequencing

DNA extraction was performed with the KAPA Express Extract DNA Extraction Kit (Kapa Biosystems, London, UK). Polymerase chain reaction (PCR) amplification was conducted with the KOD ONE PCR Master Mix (Toyobo, Osaka, Japan) using the forward primer: 5'-CCA ACA ACC CTT GGT CCT GT-3' and reverse primer: 5'-GGG TAG CCT GGA AAT AGG GC-3' for *PNPLA3*. PCR products were then purified using the ExoSAP-IT Express PCR cleanup kit (Applied Biosystems, Foster City, CA) and sequenced at the Genomics Research Core at the University of Pittsburgh (Pittsburgh, PA). Sequencing buffer and a 1:4 dilution of BigDye 3.1 (ThermoFisher Scientific, Waltham, MA) were added, and thermocycling was performed according to ABI recommendations. According to manufacturer instructions, removing unincorporated sequencing reagents was performed using CleanSeq magnetic beads (Agencourt, Beckman Coulter, Brea, CA). Two control samples were included with every sequencing to ensure the proper performance of reagents and equipment.

RNA sequencing

RNA extraction, library preparation, and sequencing were performed at the University of Pittsburgh HSCRF Genomics Research Core. Briefly, total RNA was extracted from isolated primary human hepatocytes using the RNeasy Plus Micro Kit (Qiagen). RNA integrity was assessed using the High Sensitivity RNA ScreenTape system on an Agilent 2200 TapeStation (Agilent). The SMART-Seq HT Kit (Takara Bio) was used to generate cDNA from 10 ng of total RNA, and the cDNA product was checked by an Agilent Fragment Analyzer system (Agilent) for quality control. The sequencing library was constructed by following the Illumina Nextera XT Sample Preparation Guide. One nanogram of input cDNA was tagmented and amplified using the Illumina Nextera XT kit. Equimolar amounts of each sample were finally pooled and sequenced on an Illumina Nextseq 500 system using a paired-end 75-bp strategy.

RNA-seq data analysis

All memory-intensive computations were performed on clusters from the University of Michigan Great Lakes Advanced Research Computing resources. The quality of the raw fastq files was checked using FASTQC (version 0.11.9). In summary, the FastQC reports show that the guanine-cytosine content of the samples ranged from 47% to 54%. As a reference, a guanine-cytosine content between 30-40% is considered too low, as the DNA will be unstable, while a guanine-cytosine content between 70-80% is considered too high because it makes PCR amplification more difficult. So, a guanine-cytosine content of about 50 to 60% is desirable (10). Another important metric is the mean quality scores. All the samples have a score that falls within the acceptable threshold of 30. The QC-passed raw reads were then aligned to the genome with STAR (version 2.7.5a) (11). The quality of the aligned reads was assessed using QoRTs (version 1.3.6) (12). The quality of the aligned reads was assessed based on the percentage of novel splice events. For all of the samples, the percentage of novel splice events is about 1%, within acceptable limits. All samples passed the strandedness test. For all the samples, about 97% of the reads are mapped to the first strand. This attests to the quality of the sequenced RNA fragments. Downstream analyses were performed using DESeq2 in R (CRAN 4.04), BEAVR (a Browser-based tool for the Exploration And Visualization of RNAseq data) (13), GSEA (14, 15), and GraphPad Prism version 8. The p-value was computed based on Wald test statistics. Genes with a fold change greater than 1.5 and p-value less than 0.05 are considered significant.

Flux propensity analysis

The flux propensity of hepatocytes was computed by integrating RNA-Seq data with the reconstructed genome-scale model of human metabolism (also known as Recon 2.2) (16) based

on the COMPASS algorithm detailed in Wagner, Wang (17). First, the vector of maximum flux, x_r^{opt} , through each and every metabolic reaction in Recon 2.2 was computed. This was achieved by solving the following optimization problem:

$$\text{Maximize: } \|x\|, x \in \mathbb{R}^m$$

$$\begin{aligned} \text{Subjected to: } & A \cdot x = 0 \\ & \omega \leq x \leq \lambda \\ & x_{rev} = 0 \end{aligned}$$

Where x is a vector of metabolic flux through each metabolic pathway in Recon 2.2, m is the number of metabolic reactions in Recon 2.2, A is the stoichiometry matrix of all metabolites with respect to their metabolic reactions, and ω and λ are the lower and upper bounds of the flux, x . The bounds are set to a default value of ± 1000 . x_{rev} denotes the reverse fluxes of reversible reactions, which was set to zero to ensure only forward reactions were used in computing the maximum fluxes.

Next, gene expression data from samples was utilized to design a penalty variable for each metabolic reaction such that the numerical value of the penalty variable is inversely proportional to the level of expression of genes that participate in each reaction. The implication is that genes with low expression will impose stricter penalties on their corresponding reaction. Subsequently, a linear optimization problem was designed to determine the set of penalty variables that minimize the penalty imposed on the metabolic pathways. This was achieved by solving the following optimization problem:

$$\text{Minimize: } \|P \cdot x\|, x \in \mathbb{R}^m$$

$$\begin{aligned} \text{Subjected to: } & A \cdot x = 0 \\ & \omega \leq x \leq \lambda \\ & x_{rev} = 0 \\ & x_r \geq 0.95x_r^{opt} \end{aligned}$$

The resulting penalty values were aggregated to generate a reaction propensity score that is inversely proportional to the aggregated penalty value for each reaction in Recon 2.2.

Downstream analyses were performed in Python on the Google Colab platform, R (CRAN 4.04), and GraphPad Prism version 8. To compare the relative activity of each metabolic reaction between *PNPLA3* rs738409:G and wild-type hepatocytes, Cohen's D statistics were used to compute the fold change difference between the means of two groups:

$$\text{Cohen's } D = \frac{M_1 - M_2}{SD_{\text{pooled}}}$$

where,

$$SD_{\text{pooled}} = \sqrt{(\sum(s_1^2 + s_2^2))/2}$$

Where M_1 and M_2 are the means of propensity score for group 1 (*PNPLA3* rs738409:G hepatocytes) and group 2 (wild-type hepatocytes), respectively. s_1 and s_2 are the standard deviations of group 1 and group 2, respectively.

A positive Cohen's D value indicates a reaction that is relatively more active in *PNPLA3* rs738409:G hepatocytes, while a negative value indicates relatively higher activity in wild-type hepatocytes. The higher the magnitude of Cohen's D, the higher the relative difference in activity between the two groups. We also computed the statistical significance of these Cohen's D using Wilcoxon's p-value adjusted based on the Benjamini-Hochberg (BH) method. Because of the small sample size (n=3), an absolute Cohen's D value greater than 1.5 and a Wilcoxon's p-value less than 0.1 are considered significant. Table S3 contains detailed information of the results from our flux propensity analysis. Below, we defined some of the metabolic reactions mentioned in the manuscript.

metadata_r_id	reaction_name	subsystem
PYRt2p	pyruvate peroxisomal transport via proton symport	D-alanine metabolism
r0173	(S)-Lactate:NAD ⁺ oxidoreductase Glycolysis / Gluconeogenesis / Pyruvate metabolism EC:1.1.1.27	Glycolysis/gluconeogenesis
LDH_L	L-lactate dehydrogenase	Glycolysis/gluconeogenesis
CYSGLTH	Glutathione:cystine oxidoreductase	Methionine and cysteine metabolism
GAPD	glyceraldehyde-3-phosphate dehydrogenase	Glycolysis/gluconeogenesis

Untargeted metabolomics

Global metabolomics was carried out based on our previously reported protocol (18, 19). Briefly, hepatocytes stored at -80°C were retrieved and transferred into a 15 mL centrifuge tube. After adding 4 mL of 80% (v/v) MEOH/water to each sample, they were briefly vortexed and deprotenated by incubating at -80°C for 20 minutes. Samples were then vortexed at 4°C for 5 minutes, followed by centrifugation at 4°C, 4696 x g (maximum speed) for 10 minutes. Supernatants were transferred to a fresh tube. 500 µL of 80% (v/v) MEOH/water was added to the remaining pellets, vortexed for 5 minutes at 4°C, and then centrifuged at 4°C, 4696 x g

(maximum speed) for 10 minutes. Supernatant was added to the previously collected supernatant. Next, the supernatant was completely dried in a vacuum concentrator. Dried pellets were stored at -80°C until they were processed the day of analysis. On the day of the analysis, the dried extracts were reconstituted in 200 µL of methanol/water (50/50 v/v), sonicated for 10 minutes, vortexed for a few seconds, and then filtered. 100 µL of reconstituted samples were transferred to the LC vials, and 10 µL of each sample was pooled to the QC samples. The samples were analyzed on both HILIC and C18 columns with both positive and negative ion modes.

For the C18 column in positive mode, 10 µL (8 µL for negative mode) of the samples were injected for analysis on an Agilent 6520 QTOF LC/MS machine using an ACQUITY UPLC BEH C18 Column (130 Å, 1.7 µm, 2.1 mm X 150 mm) coupled with 5 mm Van-Guard Pre-Columns. The column compartment was set at 40°C, and the analysis was performed in both positive and negative modes. Mobile phase A was water with 0.1% formic acid, while mobile phase B contained acetonitrile with 0.1% formic acid. The gradient method is as follows: 0 min: 1% B; 1 min: 1% B; 8 min: 99% B; 13 min: 85% B; 13.1 min: 1% B; 16 min: 1% B.

For the HILIC column in positive mode, 5 µL (2 µL for negative mode) of the samples were injected for analysis on an Agilent 6520 QTOF LC/MS machine using an XBridgeBEH Amide XP Column (130 Å, 2.5 µm, 4.6 mm X 150 mm) coupled with a 5 mm VanGuard Cartridge. The column compartment was set at 40°C, and the analysis was performed in both positive and negative modes. Mobile phase A was 10 mM ammonium formate in water with 0.1% formic acid, while mobile phase B contained 10 mM ammonium formate in acetonitrile with 0.1% formic acid. The gradient method is as follows: 0 min: 1% B; 1 min: 1% B; 11.8 min: 80% B; 12.5 min: 1% B; 14.7 min: 1% B; 16 min: 1% B.

The metabolite peaks were extracted using Agilent Masshunter Profinder based on our in-house library. Any metabolites whose RSD is greater than 30% in the QC measurements were removed from further analysis. The peak areas were normalized with cell numbers. Other downstream analysis was performed with Metaboanalyst® (ver. 6.0) and GraphPad Prism version 8. Figures were created with Biorender.com. Metabolites with more than a 1.5-fold change and with a p-value less than 0.05 were considered to be significantly different between the two groups.

Quantitative Real-Time PCR

Total cellular RNA was isolated using the RNeasy Mini kit (QIAGEN, Hilden, Germany) and reverse transcribed using SuperScript III (Invitrogen, Carlsbad, CA) following the manufacturers' instructions. We performed qPCR with a StepOnePlus system (Applied Biosystems, Foster City, CA) using TaqMan Fast Advanced Master Mix (Life Technologies, Waltham, MA). Relative gene

expression was normalized to β -actin (*ACTB*) mRNA. TaqMan probes are listed in Supplementary Table S2. Relative expression was calculated using the $\Delta\Delta CT$ method.

Cell Viability Measurements

Cell viability was assessed in a 96-well format by Alamar Blue (Invitrogen, Carlsbad, CA) absorbance (570 nm/600 nm) measured on a Synergy HTX microplate reader (Biotek, Winooski, VT). Post-isolation and post-thaw viability of primary human hepatocytes was evaluated by trypan blue dye exclusion counting using a Countess 3 automated cell counter (Invitrogen, Carlsbad, CA).

Production of High Titer Lentivirus

Vector cloning, vector sequencing, and production of high-titer lentivirus were performed by Vectorbuilder (Chicago, IL). Briefly, lentiviruses were produced by co-transfecting 293T cells with the expression vectors pLV[Exp]-CMV>EGFP or pLV[Exp]-CMV>hGPX4 (transcript variant NM_001039848.4 containing a selenocysteine insertion sequence (SECIS) element to ensure proper incorporation of selenocysteine), envelope plasmid (pMD2. G), and packaging plasmids (pMDLg/pRRE and pRSV-Rev) using FuGENE 6 transfection reagent (Promega Corporation, Madison, WI, USA). After cell debris and macromolecular contaminants were filtered by a 0.45 μ m filter, the filtrate was collected and concentrated with PEG6000 (Sigma-Aldrich, Saint-Louis, MO) to increase the virus titer to yield $> 1 \times 10^9$ viral particles/mL before being stored at -80°C .

Generation and Culture of Human iPSC

Human fibroblasts were derived from fetal hepatocytes as previously described. Briefly, human fetal hepatocytes were cultured in DMEM medium (GIBCO, Life Technologies, Carlsbad, CA, USA) containing 1X Penicillin/Streptomycin (ThermoFisher Scientific, Waltham, MA), 10^{-7} M of insulin (Sigma-Aldrich, Saint-Louis, MO), and 5% bovine serum albumin (GIBCO, Life Technologies, Carlsbad, CA, USA) for 2-3 weeks.

hiPSC-PNPLA3^{GG} were generated from fibroblasts. Reprogramming of fibroblasts was performed using episomal plasmid vectors adapted from a previously described method (20). Briefly, for each nucleofection, 1 million cells were resuspended in 100 mL of the AmaxaTM NHDF Nucleofector kit (Lonza, Walkersville, MD) containing 1 mg of each of the four episomal plasmid vectors encoding OCT3/4 and p53 shRNA, SOX2 and KLF4, L-MYC and LIN28, and enhanced green fluorescent protein (eGFP) (Addgene, Boston, MA, USA). Cells were nucleofected using

the Amaxa 4D-Nucleofector (Lonza, Walkersville, MD) and plated in mTeSR on human embryonic stem cell-qualified Matrigel (Corning, New York, NY)-coated plates. Colonies were isolated around 60 days after induction based on morphology. The cell line underwent karyotyping, and its pluripotency was validated by the expression of NANOG, OCT4, and membrane markers SSEA and TRA-1-60 at different passages. Additionally, the cell line was routinely tested and found to be negative for mycoplasma contamination. After 10 passages, a stable hiPSC-PNPLA3^{GG} colony was selected to be gene edited as previously mentioned.

Differentiation of human iPSC into induced hepatocytes (iHeps)

Our hepatocyte differentiation protocol was based on previously published methods(21-25). Briefly, hiPSC-PNPLA3^{CC} and hiPSC-PNPLA3^{GG} were passaged with Accutase (Stem Cell Technologies, Vancouver, Canada) and re-plated at a density of 1 to 2x10⁵ per cm² in growth factor reduced Matrigel (Corning Incorporated, Corning, NY)-coated plates in mTeSR. The day after the hiPSC passage, cells were exposed to a defined differentiation medium containing RPMI (Invitrogen, Carlsbad, CA), 1x B-27 without insulin supplement (Invitrogen, Carlsbad, CA), 0.5% penicillin/streptomycin (Millipore, Billerica, MA), 0.5% of Non-Essential Amino Acids (Millipore, Billerica, MA), 100 ng/mL Activin A (R&D Systems, Minneapolis, MN), 10 ng/mL BMP4 (R&D Systems, Minneapolis, MN), and 20 ng/mL FGF2 (BD, Franklin Lakes, NJ) for two days and placed in a normal O₂ incubator (endoderm induction). Cells were subsequently maintained in a similar medium without FGF2 and BMP4 for two days in ambient O₂ (definitive endoderm). Cells were then grown for 10 days in a defined medium containing 45% DMEM low glucose (ThermoFisher Scientific, Waltham, MA), 45% F-12 (ThermoFisher Scientific, Waltham, MA), 10% CTS KnockOut SR XenoFree Medium (ThermoFisher Scientific, Waltham, MA), 0.5% Non-Essential Amino Acids (ThermoFisher Scientific, Waltham, MA), 0.5% L-glutamine (ThermoFisher Scientific, Waltham, MA), 50 ng/mL HGF (R&D Systems, Minneapolis, MN), and 1% DMSO (Sigma-Aldrich, Saint Louis, MO). Medium was changed every other day (hepatic specification). At the end of Stage 3, cells were detached and re-plated at 30%–40% confluence in thin type 1 collagen layer (Corning Incorporated, Corning, NY) for further maturation. Cells were grown for 4 days in a defined medium containing 45% DMEM low glucose (ThermoFisher Scientific, Waltham, MA), 45% F-12 (ThermoFisher Scientific, Waltham, MA), 10% CTS KnockOut SR XenoFree Medium, 0.5% Non-Essential Amino Acids (ThermoFisher Scientific, Waltham, MA), 0.5% L-glutamine (ThermoFisher Scientific, Waltham, MA), 0.1% of Gentamicin/Amphotericin-B (ThermoFisher Scientific, Waltham, MA), 1% of penicillin/streptomycin (ThermoFisher Scientific, Waltham, MA), 50 ng/mL HGF (R&D Systems, Minneapolis, MN), 1% DMSO, 0.5uM

Dexamethasone (Sigma-Aldrich, Saint Louis, MO), 0.1% of Ascorbic Acid (Sigma-Aldrich, Saint Louis, MO), 0.1% of Bovine Serum Albumin Free of Fatty Acids, 0.1% of Hydrocortisone, 0.1% of Transferrin, 0.1% of Insulin (HCM Bullet Kit, ThermoFisher Scientific, Waltham, MA), 100 μ M of Ursodeoxycolic acid (Sigma-Aldrich, Saint Louis, MO), 20 μ M of palmitic acid (Sigma-Aldrich, Saint Louis, MO), 30 μ M of oleic acid (Sigma-Aldrich, Saint Louis, MO), 400 μ M of linoleic acid (Sigma-Aldrich, Saint Louis, Missouri), 400 μ M of α -linoleic acid (Cayman Chemical, Ann Arbor, MI), 20 μ M of rifampicin (Sigma-Aldrich, Saint Louis, Missouri), and 1x of cholesterol (ThermoFisher Scientific, Waltham, MA) (Stage 4, hepatic maturation).

Catalase Activity

Catalase activity in live cells was measured using the Catalase Colorimetric Activity Kit (Invitrogen, Carlsbad, CA) after exposing the cells to docosanoic for 48 hours. Following the manufacturer's instructions, the absorbance (560 nm) was quantitatively measured on a Synergy HTX microplate reader (Biotek, Winooski, VT).

Differentiation of human iPSCs into induced hepatic stellate cells (iHSC)

The iHSC differentiation protocol was based on a previously published method(26). Briefly, hiPSC-PNPLA3^{CC} and hiPSC-PNPLA3^{GG} were passaged with Accutase (Stem Cell Technologies, Vancouver, Canada) and re-plated at a density of 1 to 2x10⁵ per cm² in growth factor reduced Matrigel (Corning Incorporated, Corning, NY)-coated plates in mTeSR. One day after passage, the cells were exposed to a defined differentiation medium containing 10 μ g/mL BMP4 to induce mesoderm formation. After 4 days, the medium was replaced with fresh medium containing 10 μ g/mL BMP4 along with 100 μ g/mL FGF1 and FGF3 for 48 hours. This was followed by a medium change to a defined medium supplemented with 100 μ g/mL FGF1 and FGF3, 30 mM retinol, and 200 μ M palmitic acid for another 48 hours. In the final step of the differentiation protocol, the cells were cultured in a defined medium containing 30 mM retinol and 200 μ M palmitic acid.

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Supplementary Table 1a. Normal human hepatocyte and tissue used in this study.

Hepatocyte ID	AGE	SEX	VIABILITY	PNPLA3 rs738409
HH035	77	female	85%	GG
HH104*	11	male	96%	CG
HH98*	15	male	95%	CG
001	46	male	80%	GG
DEC	53	male	86%	GG
JDL	54	male	80%	GG
EXW	50	male	97%	GG
BRX	45	male	92%	CC
JYN	49	female	86%	CC
HU8339	31	female	91%	CG
HH1072	40	female	89%	GG
HH112	74	male	86%	CG
HH48	33	female	84%	CG
HH46	74	female	90%	CC
HH68	32	male	84%	CC
HH1110	47	male	83%	GG
HH1050	9	male	80%	CC
HH1083	45	female	86%	CG
HH1043	37	male	87%	GG
HH1098	43	female	80%	GG
HH1121	23	female	90%	CG
962	68	female	85%	GG
1081	36	male	80%	GG
HH012	83	male	N/A (tissue)	GG
HH080	16	male	N/A (tissue)	CC
HH133	12	male	N/A (tissue)	GG
HH160	24	male	N/A (tissue)	GG
HH162	60	male	N/A (tissue)	CC

* Cases which we have used isolated primary human hepatocyte and liver tissue.

Supplementary Table 1b.

Parameter (mean $\pm$ SD)	PNPLA3 WT (CC/CG)	PNPLA3 I148M (GG)	p-value
BMI	28.7 $\pm$ 7.74	31.79 $\pm$ 7.51	0.4516
Age (years)	38.5 $\pm$ 21.9	45.2 $\pm$ 20.3	0.4204
Albumin secretion <i>in vitro</i> (ng/mL)	300.4 $\pm$ 54.5	285.3 $\pm$ 45.4	0.6155
Urea secretion <i>in vitro</i> (mg/dL)	18.7 $\pm$ 9.3	19.5 $\pm$ 4.5	0.8438

Supplementary table 2a. Taqman® SNP Genotyping Assay IDs used in this study

Target gene	SNP ID	Assay ID	Company
PNPLA3	rs738409	C_____7241_10	Life Technologies

Supplementary table 2b. Taqman® Primers used in this study

Target gene	Assay ID	Company
ACTB	Hs01060665_g1	Life Technologies
FADS2	Hs00927433_m1	Life Technologies
GPX4	Hs00989766_g1	Life Technologies
SCD	Hs01682761_m1	Life Technologies
HNF4a	Hs00604431_m1	Life Technologies
FOXA1	Hs04187555_m1	Life Technologies
FOXA2	Hs00232764_m1	Life Technologies
PPARa	Hs00947536_m1	Life Technologies
CEBPa	Hs00269972_s1	Life Technologies
PNPLA3	Hs00228747_m1	Life Technologies
ATF4	Hs00909569_g1	Life Technologies
ERN1	Hs00980095_m1	Life Technologies

Supplementary table 2c. Antibodies and dilutions used for Western blots and Immunohistochemistry.

Target protein	Catalog number	Clone	Company	Dilution	Host
ACOX1	ab184032	EPR19038	Abcam	1:1000	Rabbit
ACSL4	ab124805	EPR2761(2)	Abcam	1:5000	Rabbit
GAPDH	600041IG150UL	1E6D9	Proteintech	1:10000	Mouse
HSPA5	ab21685		Abcam	1:1000	Rabbit
ACAA1	NBP1-55156	N/A	Novus Biologicals	1:200	Rabbit
CHOP	NB600-1335	9C8	Novus Biologicals	1:100	Mouse
ATF6	ab37149	N/A	Abcam	1:100	Rabbit
E-cadherin	NBP2-19051	7H12	Novus Biologicals	1:500	Mouse
FSP1	68049-1-Ig	1A2B2	Proteintech	1:200	Rabbit
TRF1	13-6800	H68.4	Thermo Fisher	1:250	Mouse
Adipophilin 2	610102	AP125	Progen	1:200	Mouse
GPX4	ab125066	EPNCIR144	Abcam	1:1000	Rabbit
PMP70	ab85550	N/A	Abcam	1:1000	Rabbit
Vinculin	700062	42H89L44	Thermo Fisher	1:1000	Rabbit
TFRC	MABC1765	3F3-FMA	Millipore	1:50	Mouse
Nanog	4893	1E6C4	Cell Signalling	1:2000	Mouse
OTC4	sc-9081	N/A	Santa Cruz	1:250	Rabbit
TRA-1-60	560173	N/A	BD PharMingen	1:10	Mouse
SSE4A	560218	N/A	BD PharMingen	1:10	Mouse
SOX17	NL1924R	N/A	R&D Systems	1:50	Goat
HNF4a	ab41898	K9218	Abcam	1:500	Mouse

ALB	A80-229A	N/A	Bethyl	1:100	Goat
AFP	180003	N/A	Invitrogen	1:300	Mouse

Supplementary table 2d. Recombinant DNA

Construction ID	Company	Catalog number
HyPerRed	Addgene	Cat#48249
pLV[Exp]-CMV>EGFP	Vectorbuilder	This paper
pLV[Exp]-CMV>hGPX4	Vectorbuilder	This paper

Supplementary table 2e. SYBER green primers used in this study

Target	Sequence	Company
u/s XBP1 foward	GGTCTGCTGAGTCCGCAGCA	Life Technologies
u/s XBP1 reverse	AAGGGAGGCTGGTAAGGAAC	Life Technologies
t XBP1 foward	TGAAAAACAGAGTAGCAGCTCAGA	Life Technologies
t XBP1 reverse	CCCAAGCGCTGTCTTAACTC	Life Technologies
MT-CO1 foward	CCTACTCCTGCTCGCATCTG	Life Technologies
MT-CO1 reverse	AGAATGGGGTCTCCTCCTCC	Life Technologies
MT-CYB foward	AACTTCGGCTCACTCCTTGG	Life Technologies
MT-CYB reverse	GGAGGTGATTCCTAGGGGGT	Life Technologies
MT-ND1 foward	CACCCAAGAACAGGGTTTGT	Life Technologies
MT-ND1 reverse	TGGCCATGGGATAGTTGTTAA	Life Technologies
ACTB foward	GGCATCCTCACCTGAAGTA	Life Technologies
ACTB reverse	GAAGGTGTGGTGCCAGATTT	Life Technologies

RX nmæ	wilcox_sta	wilcox_pos	wilcox_neg	10(wilcox_pos)	cohens_d	Abs(cohens_d)	High/low	adjusted_p	metadata	reaction_name	formula	associated	subsystem	Subsystem	EC_number	confidence
G5SAdrm_pos	7	0.382733	0.4171041	1.164738	1.164738	1	0.518179	0.518179	G5SAdrm	L-glutamate 5-semialdehyde dehydrogenase, reversible, mitochondrial	1.00 * L-Glutamate 5-semialdehyde [m] -> 1.00 * proton	1.00 * L-Gl	Arginine and Proline Metabolism		1	4
PSCR_pos	2	0.382733	0.4171041	-0.73416	0.734162	2	0.518179	0.518179	PSCR	pyrroline-5-carboxylate reductase	2.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	4
r0615_pos	6	0.662521	0.1788004	0.382054	0.382054	1	0.758498	0.758498	r0615	trans-4-Hydroxy-L-proline:NAD+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * tra	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
r0617_neg	6	0.662521	0.1788004	0.382054	0.382054	1	0.758498	0.758498	r0617	trans-4-Hydroxy-L-proline:NADP+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
r0615_neg	4	1	0	0.001664	0.001664	1	1	0.616	r0615	trans-4-Hydroxy-L-proline:NAD+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * tra	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
r0616_neg	5	1	0	0.002186	0.002186	1	1	0.616	r0616	trans-4-Hydroxy-L-proline:NAD+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * tra	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
r0617_pos	4	1	0	0.001664	0.001664	1	1	0.617	r0617	trans-4-Hydroxy-L-proline:NAD+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
r0618_pos	5	1	0	0.002186	0.002186	1	1	0.618	r0618	trans-4-Hydroxy-L-proline:NADP+ 5-oxido reductase Arginine and pro	1.00 * Nicotinamide adenine dinucleotide phosphate [m]	1.00 * PYC	Arginine and Proline Metabolism		1.5.1.2	0
RE1807C_pos	0	0.080856	1.0922877	-3.14927	3.149265	2	0.240222	0.240222	RE1807C	RE1807	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * Wat	Bile acid synthesis		2	0
RE2626C_pos	0	0.080856	1.0922877	-0.02292	0.022918	2	0.240222	0.240222	RE2626C	RE2626	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * Wat	Bile acid synthesis		2	0
RE2626M_pos	0	0.080856	1.0922877	-1.86992	1.86992	2	0.240222	0.240222	RE2626M	RE2626	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	CYP27A1	Bile acid synthesis		2	0
RE3346C_pos	0	0.080856	1.0922877	-0.02292	0.022918	2	0.240222	0.240222	RE3346C	RE3346	2.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH3A1;	Bile acid synthesis		2.1.2.1.3	0
RE3346M_pos	0	0.080856	1.0922877	-1.86992	1.86992	2	0.240222	0.240222	RE3346M	RE3346	2.00 * proton [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1B1;	Bile acid synthesis		2.1.2.1.3	0
r0688_neg	0	0.080856	1.0922877	-3.14927	3.149265	2	0.240222	0.240222	r0688	3alpha,7alpha-Dihydroxy-5-beta-cholestan-26-ol:NAD+ oxidoreduct	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1B1;	Bile acid synthesis		2.1.2.1.3	0
P45027A12m_pos	1	0.19043	0.7202646	-1.61331	1.613311	2	0.347218	0.347218	P45027A1	5-beta-cholestan-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase	1.00 * Nicotinamide adenine dinucleotide phosphate [m]	CYP27A1	Bile acid synthesis		2.114.13.15	4
RE2625M_neg	1	0.19043	0.7202646	-1.61331	1.613311	2	0.347218	0.347218	RE2625M	RE2625	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * S	CYP27A1	Bile acid synthesis		2	0
BAAT1x_pos	2	0.382733	0.4171041	-1.30963	1.309628	2	0.518179	0.518179	BAAT1x	bile acid Coenzyme A: amino acid N-acyltransferase	1.00 * Glycine [x] + 1.00 * choloyl-CoA(4-) [x] -> 1.00 * Co	BAAT	Bile acid synthesis		2.3.1.65	4
HSD3B7P_pos	7	0.382733	0.4171041	1.185273	1.185273	2	0.518179	0.518179	HSD3B7P	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-5	1.00 * Nicotinamide adenine dinucleotide phosphate [r]	HSDB37	Bile acid synthesis		2	4
RE1796R_neg	7	0.382733	0.4171041	1.185273	1.185273	2	0.518179	0.518179	RE1796R	RE1796	1.00 * Nicotinamide adenine dinucleotide [r] + 1.00 * 20	HSDB32	Bile acid synthesis		2.5.3.1.1	0
RE1845C_neg	7	0.382733	0.4171041	0.998664	0.998664	1	0.518179	0.518179	RE1845C	RE1845	1.00 * Taurine [c] + 1.00 * chenodeoxychocolyl coenzyme	BAAT	Bile acid synthesis		2.3.1.65	0
RE1845C_pos	2	0.382733	0.4171041	-1.30963	1.309646	2	0.518179	0.518179	RE1845C	RE1845	1.00 * Taurine [c] + 1.00 * chenodeoxychocolyl coenzyme	BAAT	Bile acid synthesis		2.3.1.65	0
r0629_neg	2	0.382733	0.4171041	-1.30963	1.309628	2	0.518179	0.518179	r0629	Choloyl-CoA:glycine N-choloyltransferase Bile acid biosynthesis / Ta	1.00 * Glycine [c] + 1.00 * choloyl-CoA(4-) [c] -> 1.00 * Co	BAAT	Bile acid synthesis		2.3.1.65	0
r0797_neg	2	0.382733	0.4171041	-1.30963	1.309628	2	0.518179	0.518179	r0797	glycine N-choloyltransferase EC:2.3.1.65	1.00 * Glycine [c] + 1.00 * chenodeoxychocolyl coenzyme	BAAT	Bile acid synthesis		2	0
BAAT2x_pos	6	0.662521	0.1788004	0.939309	0.939309	1	0.758498	0.758498	BAAT2x	bile acid Coenzyme A: amino acid N-acyltransferase	1.00 * choloyl-CoA(4-) [x] + 1.00 * Taurine [c] -> 1.00 * Co	BAAT	Bile acid synthesis		2.3.1.65	4
RE1807C_neg	3	0.662521	0.1788004	-0.9529	0.952905	2	0.758498	0.758498	RE1807C	RE1807	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * Wat	Bile acid synthesis		2	0
RE2626C_neg	3	0.662521	0.1788004	-0.82231	0.822307	2	0.758498	0.758498	RE2626C	RE2626	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * Wat	Bile acid synthesis		2	0
RE3346C_neg	3	0.662521	0.1788004	-0.82231	0.822307	2	0.758498	0.758498	RE3346C	RE3346	2.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH3A1;	Bile acid synthesis		2.1.2.1.3	0
r0630_pos	6	0.662521	0.1788004	0.939309	0.939309	1	0.758498	0.758498	r0630	Choloyl-CoA:glycine N-choloyltransferase Bile acid biosynthesis / Ta	1.00 * Taurine [c] + 1.00 * choloyl-CoA(4-) [c] -> 1.00 * Co	BAAT	Bile acid synthesis		2.3.1.65	0
r0688_pos	3	0.662521	0.1788004	-0.9529	0.952905	2	0.758498	0.758498	r0688	3alpha,7alpha-Dihydroxy-5-beta-cholestan-26-ol:NAD+ oxidoreduct	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1B1;	Bile acid synthesis		2.1.2.1.3	0
AKR1C41_pos	4	1	0	-0.35507	0.355066	2	1	0.681	AKR1C41	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	AKR1C6	Bile acid synthesis		2.1.1.50	4
AKR1C42_pos	4	1	0	-0.35507	0.355066	2	1	0.681	AKR1C42	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	AKR1C6	Bile acid synthesis		2.1.1.50	4
r0743_pos	5	1	0	0.038147	0.038147	1	1	0.743	r0743	hydroxysteroid (17-beta) dehydrogenase 4 Bile acid biosynthesis EC:	1.00 * Nicotinamide adenine dinucleotide [x] + 1.00 * 3a	HSDB1784	Bile acid synthesis		2.1.1.35	0
r0744_pos	5	1	0	0.038147	0.038147	1	1	0.744	r0744	[24R,25R]-3alpha,7alpha,12alpha,24-tetrahydroxy-5beta-cholestan	1.00 * Water [x] + 1.00 * 3alpha,7alpha,12alpha-Trihydroxy	HSDB1784	Bile acid synthesis		4.2.2.1.107	0
r0747_pos	4	1	0	-0.35507	0.355066	2	1	0.747	r0747	3alpha,7alpha-Dihydroxy-5beta-cholestan:NADP+ oxidoreductase	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	AKR1C6	Bile acid synthesis		2.1.1.50	0
r0750_pos	4	1	0	-0.35507	0.355066	2	1	0.750	r0750	3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan:NADP+ oxidore	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	AKR1C6	Bile acid synthesis		2.1.1.50	0
DHCR241r_pos	1	0.19043	0.7202646	-1.58511	1.585111	2	0.347218	0.347218	DHCR241r	24-dehydrocholesterol reductase [Precursor]	1.00 * zymosterol [r] + 1.00 * Flavin adenine dinucleotide	DHCR24	Cholesterol metabolism		3	4
DHCR242r_pos	1	0.19043	0.7202646	-1.58512	1.585115	2	0.347218	0.347218	DHCR242r	24-dehydrocholesterol reductase [Precursor]	1.00 * Flavin adenine dinucleotide reduced [r] + 1.00 * S	CYP7A1; D	Cholesterol metabolism		3	4
r0783_pos	1	0.19043	0.7202646	-1.58512	1.585115	2	0.347218	0.347218	r0783	lanosterol D24-reductase Biosynthesis of steroids EC:1.3.1.72	1.00 * Nicotinamide adenine dinucleotide phosphate [r]	DHCR24	Cholesterol metabolism		3.1.3.1.72	0
r1380_neg	1	0.19043	0.7202646	-1.58511	1.585111	2	0.347218	0.347218	r1380	delta24-sterol reductase Biosynthesis of steroids EC:1.3.1.72	1.00 * proton [r] + 1.00 * Nicotinamide adenine dinucleotide	DHCR24	Cholesterol metabolism		3.1.3.1.72	0
SQLSr_pos	2	0.382733	0.4171041	-0.93048	0.930477	2	0.518179	0.518179	SQLSr	Squalene synthase	1.00 * proton [r] + 1.00 * Nicotinamide adenine dinucleotide	FDDT1	Cholesterol metabolism		3.5.1.2.1	0
r0170_neg	2	0.382733	0.4171041	-0.93048	0.930477	2	0.518179	0.518179	r0170	Farnesyl-diphosphate:farnesyl-diphosphate farnesyltransferase Bios	2.00 * Farnesyl diphosphate [r] -> 1.00 * Diphosphate [r]	FDDT1	Cholesterol metabolism		3.5.2.1.21	0
r0575_neg	2	0.382733	0.4171041	-0.93048	0.930477	2	0.518179	0.518179	r0575	Presqualene diphosphate:farnesyl-diphosphate farnesyltransferase B	1.00 * proton [r] + 1.00 * Nicotinamide adenine dinucleotide	FDDT1	Cholesterol metabolism		3.5.2.1.21	0
ICDH4rnm_neg	9	0.080856	1.0922877	2.461852	2.461852	1	0.240222	0.240222	ICDH4rnm	Isocitrate dehydrogenase (NADP+)	1.00 * Nicotinamide adenine dinucleotide phosphate [m]	IDH2	Citric acid cycle		4.1.1.14.2	4
SUCOA51m_neg	1	0.19043	0.7202646	-1.85174	1.851739	2	0.347218	0.347218	SUCOA51m	Succinate-CoA ligase (GDP-forming)	1.00 * Coenzyme A [m] + 1.00 * GTP [m] + 1.00 * Succinat	SUCLG1; S	Citric acid cycle		4.6.2.1.4	0
SUCOA51m_pos	1	0.19043	0.7202646	-1.85174	1.851739	2	0.347218	0.347218	SUCOA51m	Succinate-CoA ligase (GDP-forming)	1.00 * Coenzyme A [m] + 1.00 * GTP [m] + 1.00 * Succinat	SUCLG1; S	Citric acid cycle		4.6.2.1.4	0
SUCOA5m_neg	1	0.19043	0.7202646	-1.85174	1.851739	2	0.347218	0.347218	SUCOA5m	Succinate-CoA ligase (ADP-forming)	1.00 * Coenzyme A [m] + 1.00 * ATP [m] + 1.00 * Succinat	SUCLA2; S	Citric acid cycle		4.6.2.1.5	0
SUCOA5m_pos	1	0.19043	0.7202646	-1.85174	1.851739	2	0.347218	0.347218	SUCOA5m	Succinate-CoA ligase (ADP-forming)	1.00 * Coenzyme A [m] + 1.00 * ATP [m] + 1.00 * Succinat	SUCLA2; S	Citric acid cycle		4.6.2.1.5	0
FUM_neg	3	0.662521	0.1788004	0.706368	0.706368	1	0.758498	0.758498	FUM	fumarase	1.00 * Water [c] + 1.00 * Fumarate [c] -> 1.00 * (S)-malat	FH1	Citric acid cycle		4.2.1.2	0
FUM_pos	3	0.662521	0.1788004	0.706368	0.706368	1	0.758498	0.758498	FUM	fumarase	1.00 * Water [c] + 1.00 * Fumarate [c] -> 1.00 * (S)-malat	FH1	Citric acid cycle		4.2.1.2	0
FUMm_neg	3	0.662521	0.1788004	0.706368	0.706368	1	0.758498	0.758498	FUMm	fumarase, mitochondrial	1.00 * Water [m] + 1.00 * Fumarate [m] -> 1.00 * (S)-malat	FH1	Citric acid cycle		4.2.1.2	0
FUMm_pos	3	0.662521	0.1788004	0.706368	0.706368	1	0.758498	0.758498	FUMm	fumarase, mitochondrial	1.00 * Water [m] + 1.00 * Fumarate [m] -> 1.00 * (S)-malat	FH1	Citric acid cycle		4.2.1.2	0
r0081_neg	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	0.758498	r0081	L-Alanine-2-oxoglutarate aminotransferase Glutamate metabolism	1.00 * 2-Oxoglutarate [m] + 1.00 * L-alanine [m] -> 1.00 * GPT; GPT2		Citric acid cycle		4.2.6.1.2	0
r0081_pos	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	0.758498	r0081	L-Alanine-2-oxoglutarate aminotransferase Glutamate metabolism	1.00 * 2-Oxoglutarate [m] + 1.00 * L-alanine [m] -> 1.00 * GPT; GPT2		Citric acid cycle		4.2.6.1.2	0
ACONT_neg	4	1	0	-0.91613	0.916131	2	1	0.601	ACONT	aconitase	1.00 * Citrate [c] -> 1.00 * Isocitrate [c] AC01; IREB2	AC01; IREB	Citric acid cycle		4.2.1.3	0
ACONT_pos	4	1	0	-0.91613	0.916131	2	1	0.601	ACONT	aconitase	1.00 * Citrate [c] -> 1.00 * Isocitrate [c] AC01; IREB2	AC01; IREB	Citric acid cycle		4.2.1.3	0
ACONTm_neg	5	1	0	0.111631	0.111631	1	1	0.601	ACONTm	Aconitate hydratase	1.00 * Citrate [m] -> 1.00 * Isocitrate [m] AC01; AC02	AC01; AC0	Citric acid cycle		4.2.1.3	0
ACONTm_pos	5	1	0	0.111631	0.111631	1	1	0.601	ACONTm	Aconitate hydratase	1.00 * Citrate [m] -> 1.00 * Isocitrate [m] AC01; AC02	AC01; AC0	Citric acid cycle		4.2.1.3	0
ICDH4m_pos	5	1	0	0.576024	0.576024	1	1	0.601	ICDH4m	Isocitrate dehydrogenase (NAD+)	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * S	IDH3A; IDI	Citric acid cycle		4.1.1.14.1	0
r0679_pos	3	0.662521	0.1788004	-0.27302	0.273018	2	0.758498	0.758498	r0679	ATP-pantothenate 4-phosphotransferase Pantothenate and CoA bios	1.00 * ATP [c] + 1.00 * N-[(R)-pantothenoyl]-L-cysteinate	PANK1; PA	CoA catabolism		5.2.7.1.33	0
r0680_neg	3	0.662521	0.1788004	-0.27302	0.273018	2	0.758498	0.758498	r0680	ATP-pantothenate 4-phosphotransferase Pantothenate and CoA bios	1.00 * ATP [m] + 1.00 * N-[(R)-pantothenoyl]-L-cysteinate	PANK1; PA	CoA catabolism		5.2.7.1.33	0
PPCDC_pos	3	0.662521	0.1788004	-0.27302	0.273018	2	0.758498	0.758498								

VACCCPT1_pos	8	0.19043	0.7202646	1.381802	1.381802	1	0.347218	VACCCPT1	carnitine O-palmitoyltransferase	1.00 * L-Carnitine [c] + 1.00 * vaccenyl coenzyme A [c] ->	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	4
VACCCPT2_pos	8	0.19043	0.7202646	1.381802	1.381802	1	0.347218	VACCCPT2	carnitine transferase	1.00 * Coenzyme A [m] + 1.00 * Vaccenyl carnitine [m] ->	CP1T2	Fatty acid oxidation	9		
VACCCRNt_pos	8	0.19043	0.7202646	1.381802	1.381802	1	0.347218	VACCCRNt	transport into the mitochondria (carnitine)	1.00 * Vaccenyl carnitine [c] -> 1.00 * Vaccenyl carnitine	SLC25A20	Fatty acid oxidation	9		
C160CPT1_pos	7	0.382733	0.4171041	1.115609	1.115609	1	0.518179	C160CPT1	production of Palmitoylcarnitine	1.00 * L-Carnitine [c] + 1.00 * Palmitoyl-CoA (n-C16:0CoA)	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	4
C40CPT1_pos	7	0.382733	0.4171041	0.839865	0.839865	1	0.518179	C40CPT1	production of butyrylcarnitine	1.00 * L-Carnitine [c] + 1.00 * Butanoyl-CoA [c] -> 1.00 *	CP1T1A; CP	Fatty acid oxidation	9		
C4CRNCP12_pos	7	0.382733	0.4171041	0.839865	0.839865	1	0.518179	C4CRNCP12	transport of butyryl carnitine in the mitochondrial matrix for final	1.00 * Coenzyme A [m] + 1.00 * butyryl carnitine [m] ->	CP1T2	Fatty acid oxidation	9		
FAC0AL1831_neg	7	0.382733	0.4171041	0.957852	0.957852	1	0.518179	FAC0AL1831	fatty acid-CoA ligase	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * gamma-lin	ACSBG2; A	Fatty acid oxidation	9	6.2.1.3	4
RE3076X_neg	7	0.382733	0.4171041	0.858628	0.858628	1	0.518179	RE3076X	RE3076	1.00 * Nicotinamide adenine dinucleotide [x] + 1.00 * W	1.00 * Nic	Fatty acid oxidation	9	1.2.1.48	0
r0434_pos	7	0.382733	0.4171041	1.115609	1.115609	1	0.518179	r0434	Palmitoyl-CoA-L-carnitine O-palmitoyltransferase Fatty acid metabo	1.00 * L-Carnitine [r] + 1.00 * Palmitoyl-CoA (n-C16:0CoA)	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	0
r1257_pos	7	0.382733	0.4171041	0.938989	0.938989	1	0.518179	r1257	EC:6.2.1.3	1.00 * ATP [r] + 1.00 * Coenzyme A [r] + 1.00 * linoleate [r]	ACSBG2; A	Fatty acid oxidation	9	6.2.1.3	0
r1260_pos	7	0.382733	0.4171041	0.957852	0.957852	1	0.518179	r1260	EC:6.2.1.3	1.00 * ATP [r] + 1.00 * Coenzyme A [r] + 1.00 * gamma-lin	ACSBG2; A	Fatty acid oxidation	9	6.2.1.3	0
r1401_pos	7	0.382733	0.4171041	0.839865	0.839865	1	0.518179	r1401	Facilitated diffusion	1.00 * Butanoyl-CoA [m] + 1.00 * L-Carnitine [c] -> 1.00 *	1.00 * But	Fatty acid oxidation	9		
C161CPT1_pos	6	0.662521	0.1788004	0.852074	0.852074	1	0.758498	C161CPT1	production of palmitoleylcarnitine	1.00 * L-Carnitine [c] + 1.00 * Hexadecenyl-CoA (n-C16:3	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	4
C30CPT1_pos	6	0.662521	0.1788004	0.74055	0.74055	1	0.758498	C30CPT1	production of propionylcarnitine	1.00 * Propanoyl-CoA [c] + 1.00 * L-Carnitine [c] -> 1.00 *	CP1T1A; CP	Fatty acid oxidation	9		
C60CPT1_pos	6	0.662521	0.1788004	0.518912	0.518912	1	0.758498	C60CPT1	production of hexanoylcarnitine	1.00 * L-Carnitine [c] + 1.00 * Hexanoyl-CoA (n-C6:0CoA)	CP1T1A; CP	Fatty acid oxidation	9		
C80CPT1_neg	6	0.662521	0.1788004	0.224924	0.224924	1	0.758498	C80CPT1	production of octanoylcarnitine	1.00 * L-Carnitine [c] + 1.00 * Octanoyl-CoA (n-C8:0CoA)	CP1T1A; CP	Fatty acid oxidation	9		
CSNAT2m_pos	6	0.662521	0.1788004	0.74055	0.74055	1	0.758498	CSNAT2m	carnitine O-acyltransferase, mitochondrial	1.00 * Coenzyme A [m] + 1.00 * propionyl-carnitine [m]	CRAT	Fatty acid oxidation	9	2.3.1.7	4
CSNAT2x_neg	3	0.662521	0.1788004	-0.29731	0.29731	1	0.758498	CSNAT2x	carnitine dimethyl nonanoyl transferase, reversible, peroxisomal	1.00 * L-Carnitine [x] + 1.00 * 4,8 dimethylnonanoyl-CoA	CRAT; CRO	Fatty acid oxidation	9	2.3.1.7	4
FAC0AL161_pos	6	0.662521	0.1788004	0.852074	0.852074	1	0.758498	FAC0AL161	fatty acid-CoA ligase (hexadecenoate)	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * Hexadecen	ACSBG2; A	Fatty acid oxidation	9		
PCRNtm_pos	6	0.662521	0.1788004	0.637578	0.637578	1	0.758498	PCRNtm	transport into the mitochondria from cytosol (carnitine)	1.00 * propionyl-carnitine [c] -> 1.00 * propionyl-carnit	SLC25A20	Fatty acid oxidation	9		
RE2759X_neg	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE2759X	RE2759	1.00 * (2S)-pristanoyl-CoA [x] -> 1.00 * (2R)-pristanoyl-CoA	AMACR	Fatty acid oxidation	9	5.1.99.4	4
RE2759X_pos	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE2759X	RE2759	1.00 * (2S)-pristanoyl-CoA [x] -> 1.00 * (2R)-pristanoyl-CoA	AMACR	Fatty acid oxidation	9	5.1.99.4	4
RE3074X_neg	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE3074X	RE3074	1.00 * Coenzyme A [x] + 1.00 * ATP [x] + 1.00 * (2R,6S,10S)	ACSL1; ACS	Fatty acid oxidation	9	6.2.1.3	0
RE3074X_pos	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE3074X	RE3074	1.00 * Coenzyme A [x] + 1.00 * ATP [x] + 1.00 * (2R,6S,10S)	ACSL1; ACS	Fatty acid oxidation	9	6.2.1.3	0
RE3079X_neg	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE3079X	RE3079	1.00 * Coenzyme A [x] + 1.00 * ATP [x] + 1.00 * (2R,6S,10S)	SLC27A2	Fatty acid oxidation	9		
RE3079X_pos	6	0.662521	0.1788004	0.160261	0.160261	1	0.758498	RE3079X	RE3079	1.00 * Coenzyme A [x] + 1.00 * ATP [x] + 1.00 * (2R,6S,10S)	SLC27A2	Fatty acid oxidation	9		
r0444_neg	6	0.662521	0.1788004	0.899335	0.899335	1	0.758498	r0444	Palmitoyl-CoA-L-carnitine O-palmitoyltransferase Fatty acid metabo	1.00 * L-Carnitine [r] + 1.00 * palmitoleyl-CoA (n-C16:1)	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	0
r0445_neg	6	0.662521	0.1788004	0.852074	0.852074	1	0.758498	r0445	Palmitoyl-CoA-L-carnitine O-palmitoyltransferase Fatty acid metabo	1.00 * L-Carnitine [c] + 1.00 * palmitoleyl-CoA (n-C16:1)	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	0
r0445_pos	6	0.662521	0.1788004	0.742638	0.742638	1	0.758498	r0445	Palmitoyl-CoA-L-carnitine O-palmitoyltransferase Fatty acid metabo	1.00 * L-Carnitine [c] + 1.00 * palmitoleyl-CoA (n-C16:1)	CP1T1A; CP	Fatty acid oxidation	9	2.3.1.21	0
r0637_pos	6	0.662521	0.1788004	0.224924	0.224924	1	0.758498	r0637	Octanoyl-CoA-L-carnitine O-octanoyltransferase EC:2.3.1.137	1.00 * Octanoyl-CoA (n-C8:0CoA) [x] + 1.00 * L-Carnitine	CROT	Fatty acid oxidation	9	2.3.1.137	0
r1400_pos	6	0.662521	0.1788004	0.564266	0.564266	1	0.758498	r1400	Active transport	1.00 * Propanoyl-CoA [c] + 1.00 * L-Carnitine [m] -> 1.00	1.00 * Pro	Fatty acid oxidation	9		
r1487_neg	6	0.662521	0.1788004	0.899335	0.899335	1	0.758498	r1487	EC:6.2.1.3	1.00 * ATP [r] + 1.00 * Coenzyme A [r] + 1.00 * Hexadecen	ACSBG2; A	Fatty acid oxidation	9	6.2.1.3	0
r1488_neg	6	0.662521	0.1788004	0.852074	0.852074	1	0.758498	r1488	EC:6.2.1.3	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * Hexadecen	1.00 * ATP	Fatty acid oxidation	9	6.2.1.3	0
r1488_pos	6	0.662521	0.1788004	0.742638	0.742638	1	0.758498	r1488	EC:6.2.1.3	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * Hexadecen	1.00 * ATP	Fatty acid oxidation	9	6.2.1.3	0
C161CRNt_pos	5	1	0	0.333815	0.333815	1	1	C161CRNt	C161 transport into the mitochondria	1.00 * Hexadecenyl carnitine [c] -> 1.00 * Hexadecenyl	SLC25A20	Fatty acid oxidation	9		
CSNAT2x_pos	4	1	0	-0.07871	0.078708	2	1	CSNAT2x	carnitine dimethyl nonanoyl transferase, reversible, peroxisomal	1.00 * L-Carnitine [x] + 1.00 * 4,8 dimethylnonanoyl-CoA	CRAT; CRO	Fatty acid oxidation	9	2.3.1.7	4
CSNAT3x_pos	4	1	0	-0.11711	0.117112	2	1	CSNAT3x	carnitine O-acyltransferase, peroxisomal	1.00 * L-Carnitine [x] + 1.00 * Propanoyl-CoA [x] -> 1.00	CRAT	Fatty acid oxidation	9	2.3.1.7	4
FAC0AL1812_neg	4	1	0	0.355967	0.355967	1	1	FAC0AL1812	fatty acid-CoA ligase	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * trans-vacc	ACSL1	Fatty acid oxidation	9	6.2.1.3	4
FAOX1C1018m_pos	4	1	0	-0.48616	0.486157	2	1	FAOX1C1018	fatty acid beta oxidation (C10:1->C8)m	1.00 * Water [m] + 1.00 * Coenzyme A [m] + 1.00 * Nicotin	ACAA2; EC	Fatty acid oxidation	9		
PCRNtc_pos	4	1	0	0.04023	0.04023	1	1	PCRNtc	transport into the cytosol from peroxisome (carnitine)	1.00 * propionyl-carnitine [x] -> 1.00 * propionyl-carnit	1.00 * pro	Fatty acid oxidation	9		
RE3248X_neg	5	1	0	0.038147	0.038147	1	1	RE3248X	RE3248	1.00 * Water [x] + 1.00 * 3alpha,7alpha,12alpha-Trihydro	EHHADH	Fatty acid oxidation	9	4.2.1.17	0
RE3250X_neg	5	1	0	0.038147	0.038147	1	1	RE3250X	RE3250	1.00 * Nicotinamide adenine dinucleotide [x] + 1.00 * 24	EHHADH; H	Fatty acid oxidation	9	1.1.1.35	0
r0634_pos	4	1	0	-0.48616	0.486157	2	1	r0634	Octanoyl-CoA-acyl-CoA C-acyltransferase Fatty acid elongation in r	1.00 * Acetyl-CoA [m] + 1.00 * Octanoyl-CoA (n-C8:0CoA)	ACAA18; A	Fatty acid oxidation	9	2.3.1.16	0
r0641_neg	4	1	0	-0.00857	0.008568	2	1	r0641	(5-Glutamyl)-peptide:amino-acid 5-glutamyltransferase Arachidoni	1.00 * Water [c] + 1.00 * leukotriene C4(2-) [c] -> 1.00 * L	GGT1; GGT	Fatty acid oxidation	9	2.3.2.2	0
r0641_pos	4	1	0	-0.00857	0.008568	2	1	r0641	(5-Glutamyl)-peptide:amino-acid 5-glutamyltransferase Arachidoni	1.00 * Water [c] + 1.00 * leukotriene C4(2-) [c] -> 1.00 * L	GGT1; GGT	Fatty acid oxidation	9	2.3.2.2	0
r0726_neg	4	1	0	-0.48616	0.486157	2	1	r0726	(S)-Hydroxydecanoyl-CoA:NAD+ oxidoreductase Fatty acid elongatid	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * (S)	EHHADH; H	Fatty acid oxidation	9	1.1.1.35	0
r0728_pos	4	1	0	-0.48616	0.486157	2	1	r0728	(S)-Hydroxydecanoyl-CoA:hydro-lyase Fatty acid elongation in mitot	1.00 * (S)-Hydroxydecanoyl-CoA [m] -> 1.00 * Water [m]	EC51; EH	Fatty acid oxidation	9	4.2.1.17	0
r0224_pos	1	0.19043	0.7202646	-1.44404	1.444038	2	0.347218	r0224	5,6,7,8-Tetrahydrofolate:NAD+ oxidoreductase One carbon pool by	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleo	DHFR	Folate metabolism	10	1.5.1.3	0
r0512_pos	1	0.19043	0.7202646	-0.99725	0.997247	2	0.347218	r0512	Dihydrofolate:NAD+ oxidoreductase Folate biosynthesis EC:1.5.1.3	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 7,8	DHFR	Folate metabolism	10	1.5.1.3	0
MTHFDm_neg	7	0.382733	0.4171041	1.18664	1.18664	1	0.518179	MTHFDm	methylentetrahydrofolate dehydrogenase (NADP), mitochondrial	1.00 * Nicotinamide adenine dinucleotide phosphate [m]	MTHFD1; I	Folate metabolism	10	1.5.1.5	4
MTHFDm_pos	7	0.382733	0.4171041	1.18664	1.18664	1	0.518179	MTHFDm	methylentetrahydrofolate dehydrogenase (NADP), mitochondrial	1.00 * Nicotinamide adenine dinucleotide phosphate [m]	MTHFD1; I	Folate metabolism	10	1.5.1.5	4
MTHFD_neg	6	0.662521	0.1788004	-0.28968	0.289683	2	0.758498	MTHFD	methylentetrahydrofolate dehydrogenase (NADP)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	MTHFD1; I	Folate metabolism	10	1.5.1.5	4
MTHFD_pos	3	0.662521	0.1788004	-0.75694	0.756944	2	0.758498	MTHFD	methylentetrahydrofolate dehydrogenase (NADP)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	MTHFD1; I	Folate metabolism	10	1.5.1.5	4
r0792_pos	3	0.662521	0.1788004	-0.79078	0.790781	2	0.758498	r0792	5-methyltetrahydrofolate:NAD+ oxidoreductase One carbon pool by	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 5-m	MTHFR	Folate metabolism	10	1.5.1.20	0
r0191_pos	1	0.19043	0.7202646	-1.28899	1.288988	2	0.347218	r0191	UTP-D-fructose-6-phosphate 1-phosphotransferase EC:2.7.1.11	1.00 * UTP [c] + 1.00 * D-Fructose 6-phosphate [c] -> 1.00	PFKL	Fructose and mannose metabolism	11	2.7.1.11	0
GALT_neg	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	GALT	galactose-1-phosphate uridylyltransferase	1.00 * proton [c] + 1.00 * UTP [c] + 1.00 * (2R,3R,4S,5R,6R)	GALT	Galactose metabolism	12	2.7.7.12	0
GALT_pos	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	GALT	galactose-1-phosphate uridylyltransferase	1.00 * proton [c] + 1.00 * UTP [c] + 1.00 * (2R,3R,4S,5R,6R)	GALT	Galactose metabolism	12	2.7.7.12	0
GALU_neg	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	GALU	UTP-glucose-1-phosphate uridylyltransferase	1.00 * proton [c] + 1.00 * D-Glucose 1-phosphate [c] + 1.0	UGP2	Galactose metabolism	12	2.7.7.9	0
GALU_pos	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	GALU	UTP-glucose-1-phosphate uridylyltransferase	1.00 * proton [c] + 1.00 * D-Glucose 1-phosphate [c] + 1.0	UGP2	Galactose metabolism	12	2.7.7.9	0
UGLT_neg	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	UGLT	UDP-glucose-hexose-1-phosphate uridylyltransferase	1.00 * (2R,3R,4S,5R,6R)-3,4,5-trihydroxy-6-(hydroxymet	GALT	Galactose metabolism	12	2.7.7.12	0
UGLT_pos	1	0.19043	0.7202646	-1.98565	1.985646	2	0.347218	UGLT	UDP-glucose-hexose-1-phosphate uridylyltransferase	1.00 * (2R,3R,4S,5R,6R)-3,4,5-trihydroxy-6-(hydroxymet	GALT	Galactose metabolism	12	2.7.7.12	0
GLUDxm_neg	0	0.080856	1.0922877	-1.79286	1.792864	2	0.240222	GLUDxm	glutamate dehydrogenase (NAD) (mitochondrial)	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleo	GLUD1	Glutamate metabolism	13	1.4.1.3	4
GLUDxm_pos	0	0.080856	1.0922877	-1.79286	1.792864	2	0.240222	GLUDxm	glutamate dehydrogenase (NAD) (mitochondrial)	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleo	GLUD1	Glutamate metabolism	13	1.4.1.3	4
GLUDym_neg	0	0.080856	1.0922877	-1.79286	1.792864	2	0.240222	GLUDym	glutamate dehydrogenase (NADP), mitochondrial	1.00 * Water [m] +					

PCOLPr_hs_pos	3	0.662521	0.1788004	-1.04961	1.049612	2	0.758498	PCOLPr_hs	choline phosphatase	1.00 * Water [r] + 1.00 * Phosphatidylcholine [r] -> 1.00	PLD1	Glycerophospholipid metabolism	15	3.1.4.4	4	
PSSA1_hs_neg	3	0.662521	0.1788004	-0.96585	0.965851	2	0.758498	PSSA1_hs	Phosphatidylserine synthase homo sapiens	1.00 * L-serine [c] + 1.00 * Phosphatidylcholine [c] -> 1.00	PTDSS1	Glycerophospholipid metabolism	15	2.7.8.8	4	
RE3301C_neg	3	0.662521	0.1788004	-0.96585	0.965851	2	0.758498	RE3301C	RE3301	1.00 * Water [c] + 1.00 * phosphatidylserine [c] -> 1.00	PLD2	Glycerophospholipid metabolism	15	3.1.4.4	0	
r0552_neg	0	0.080856	1.0922877	-2.51343	2.51343	2	0.240222	r0552	p-cumic alcohol:NAD+ oxidoreductase Glycine, serine and threonine	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	ALDH7A1	Glycine, serine, alanine and threonine metabolism	16	1.2.1.8	0	
r0552_pos	0	0.080856	1.0922877	-1.56317	1.563172	2	0.240222	r0552	p-cumic alcohol:NAD+ oxidoreductase Glycine, serine and threonine	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	ALDH7A1	Glycine, serine, alanine and threonine metabolism	16	1.2.1.8	0	
r0553_neg	0	0.080856	1.0922877	-1.56317	1.563172	2	0.240222	r0553	p-Cumic alcohol:NADP+ oxidoreductase Glycine, serine and threonine	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	ALDH7A1	Glycine, serine, alanine and threonine metabolism	16	1.2.1.8	0	
r0553_pos	0	0.080856	1.0922877	-2.51343	2.51343	2	0.240222	r0553	p-Cumic alcohol:NADP+ oxidoreductase Glycine, serine and threonine	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	ALDH7A1	Glycine, serine, alanine and threonine metabolism	16	1.2.1.8	0	
GC22am_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GC22am	glycine-cleavage complex (lipamide), mitochondrial	1.00 * proton [m] + 1.00 * Glycine [m] + 1.00 * lipamide [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	2.1.2.10	4	
GC22bm_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GC22bm	glycine-cleavage system (lipamide) irreversible, mitochondrial	1.00 * 5,6,7,8-Tetrahydrofolate [m] + 1.00 * 5-Aminomethyl [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	1.8.1.4	4	
GC22cm_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GC22cm	glycine-cleavage complex (lipamide), mitochondrial	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * dATP [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	2.1.2.10	4	
GCCam_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial	1.00 * proton [m] + 1.00 * Glycine [m] + 1.00 * Lipoylpro [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	2.1.2.10	4	
GCCbm_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GCCbm	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial	1.00 * 5,6,7,8-Tetrahydrofolate [m] + 1.00 * 5-Aminomethyl [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	1.8.1.4	4	
GCCcm_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * dATP [m] -> 1.00	AMT; DLD;	Glycine, serine, alanine and threonine metabolism	16	2.1.2.10	4	
r0295_pos	1	1.19043	0.7202646	-1.73098	1.730978	2	0.347218	r0295	glycine synthase Nitrogen metabolism EC:2.1.2.10	1.00 * carbon dioxide [m] + 1.00 * Nicotinamide adenine [m] -> 1.00	AMT	Glycine, serine, alanine and threonine metabolism	16	2.1.2.10	0	
PGCD_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	PGCD	phosphoglycerate dehydrogenase	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 3-PHGDH [c] -> 1.00	PHGDH	Glycine, serine, alanine and threonine metabolism	16	1.1.1.95	4	
PSEPT_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	PSEPT	phosphoserine transaminase	1.00 * L-glutamate [c] + 1.00 * 3-phosphonotaxopyrr [c] -> 1.00	PSAT1	Glycine, serine, alanine and threonine metabolism	16	2.6.1.52	4	
PSP_L_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	PSP_L	phosphoserine phosphatase (L-serine)	1.00 * Water [c] + 1.00 * proton [c] + 1.00 * O-Phospho-L [c] -> 1.00	PSPH	Glycine, serine, alanine and threonine metabolism	16	3.1.3.3	4	
r0160_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	r0160	L-Serine:pyruvate aminotransferase Glycine, serine and threonine m	1.00 * pyruvate [c] + 1.00 * L-serine [c] -> 1.00	L-alanine	AGXT	Glycine, serine, alanine and threonine metabolism	16	2.6.1.51	0
r0173_neg	9	0.080856	1.0922877	5.692481	5.692481	1	0.240222	r0173	(S)-Lactate:NAD+ oxidoreductase Glycolysis / Gluconeogenesis / Pyr	1.00 * Nicotinamide adenine dinucleotide [x] + 1.00 * (S)- [x] -> 1.00	LDHA; LDH	Glycolysis/gluconeogenesis	17	1.1.1.27	0	
FBA_pos	1	1.19043	0.7202646	-1.46042	1.460419	2	0.347218	FBA	fructose-bisphosphate aldolase	1.00 * D-Fructose 1,6-bisphosphate [c] -> 1.00	Dihydroxy	ALDOA2T2	Glycolysis/gluconeogenesis	17	4.1.2.13	0
GAPD_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	GAPD	glyceraldehyde 3-phosphate dehydrogenase	1.00 * hydrogenphosphate [c] + 1.00 * Nicotinamide ade [c] -> 1.00	GAPDH5;	Glycolysis/gluconeogenesis	17	1.2.1.12	0	
LDH_L_neg	7	0.382733	0.4171041	0.858628	0.858628	1	0.518179	LDH_L	L-lactate dehydrogenase	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * (S)- [c] -> 1.00	LDHA; LDH	Glycolysis/gluconeogenesis	17	1.1.1.27	0	
PGK_neg	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	PGK	phosphoglycerate kinase	1.00 * ATP [c] + 1.00 * 3-Phospho-D-glycerate [c] -> 1.00	MIA3; PGK	Glycolysis/gluconeogenesis	17		0	
TPI_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	TPI	triose-phosphate isomerase	1.00 * Dihydroxyacetone phosphate [c] -> 1.00	Glycerate	TPP1	Glycolysis/gluconeogenesis	17	5.3.1.1	0
r0173_pos	7	0.382733	0.4171041	0.858628	0.858628	1	0.518179	r0173	(S)-Lactate:NAD+ oxidoreductase Glycolysis / Gluconeogenesis / Pyr	1.00 * Nicotinamide adenine dinucleotide [x] + 1.00 * (S)- [x] -> 1.00	LDHA; LDH	Glycolysis/gluconeogenesis	17	1.1.1.27	0	
LDH_L_pos	3	0.662521	0.1788004	-0.61458	0.61458	2	0.758498	LDH_L	L-lactate dehydrogenase	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * (S)- [c] -> 1.00	LDHA; LDH	Glycolysis/gluconeogenesis	17	1.1.1.27	0	
PKV_pos	4	1	0	0.406305	0.406305	1	1	PKV	pyruvate kinase	1.00 * ADP [c] + 1.00 * proton [c] + 1.00 * Phosphoenolpy [c] -> 1.00	PKLR; PKM	Glycolysis/gluconeogenesis	17		0	
r0122_pos	4	1	0	0.331588	0.331588	1	1	r0122	GTP:pyruvate O2-phosphotransferase Purine metabolism EC:2.7.1.4	1.00 * proton [c] + 1.00 * Phosphoenolpyruvate [c] + 1.00	PKLR	Glycolysis/gluconeogenesis	17	2.7.1.40	0	
r0153_pos	4	1	0	0.331588	0.331588	1	1	r0153	CTP:pyruvate O2-phosphotransferase EC:2.7.1.40	1.00 * proton [c] + 1.00 * Phosphoenolpyruvate [c] + 1.00	PKLR	Glycolysis/gluconeogenesis	17	2.7.1.40	0	
r0165_pos	4	1	0	0.331588	0.331588	1	1	r0165	UTP:pyruvate O2-phosphotransferase EC:2.7.1.40	1.00 * proton [c] + 1.00 * UDP [c] + 1.00 * Phosphoenolpy [c] -> 1.00	PKLR	Glycolysis/gluconeogenesis	17	2.7.1.40	0	
r0280_pos	4	1	0	0.331588	0.331588	1	1	r0280	dATP:pyruvate O2-phosphotransferase Purine metabolism EC:2.7.1	1.00 * proton [c] + 1.00 * Phosphoenolpyruvate [c] + 1.00	PKLR	Glycolysis/gluconeogenesis	17	2.7.1.40	0	
r0413_pos	4	1	0	0.331588	0.331588	1	1	r0413	dATP:pyruvate O2-phosphotransferase Purine metabolism EC:2.7.1	1.00 * proton [c] + 1.00 * Phosphoenolpyruvate [c] + 1.00	PKLR	Glycolysis/gluconeogenesis	17	2.7.1.40	0	
HPYRr_pos	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	HPYRr	Hydroxypyruvate reductase (NADPH)	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	GRHPR	Glyoxylate and dicarboxylate metabolism	18	1.1.1.79	4	
SACCD4m_pos	1	1.19043	0.7202646	-1.40385	1.403852	2	0.347218	SACCD4m	saccharopine dehydrogenase (NAD, L-glutamate forming), mitocho	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	AASS	Lysine metabolism	19	1.5.1.10	4	
r0525_neg	1	1.19043	0.7202646	-1.40385	1.403852	2	0.347218	r0525	N6-(L-1,3-Dicarboxypropyl)-L-lysine:NAD+ oxidoreductase; N6-(L-1,3	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide [c] -> 1.00	AASS	Lysine metabolism	19	1.5.1.9	0	
ZAMADPTm_pos	3	0.662521	0.1788004	-0.85086	0.850863	2	0.758498	ZAMADPTm	L-2-aminoadipate shuttle (cytosol/mitochondria)	1.00 * L-2-aminoadipate (1-) [c] + 1.00 * 2-Oxoglutarate [c] -> 1.00	SLC25A21	Lysine metabolism	19		4	
AATA1_pos	3	0.662521	0.1788004	-0.85086	0.850863	2	0.758498	AATA1	L-2-aminoadipate transaminase, irreversible	1.00 * L-2-aminoadipate (1-) [c] + 1.00 * 2-Oxoglutarate [c] -> 1.00	AADAT	Lysine metabolism	19	2.6.1.39	4	
r0450_pos	3	0.662521	0.1788004	-0.85086	0.850863	2	0.758498	r0450	L-2-Aminoadipate 2-oxoglutarate aminotransferase Lysine biosynth	1.00 * 2-Oxoglutarate [m] + 1.00 * L-2-aminoadipate (1-) [c] -> 1.00	AADAT	Lysine metabolism	19	2.6.1.39	0	
CYSGLTH_pos	8	1.19043	0.7202646	1.095385	1.095385	1	0.347218	CYSGLTH	Glutathione:cystine oxidoreductase	1.00 * L-cystine [c] + 2.00 * Reduced glutathione [c] -> 2.00	1.00 * L-cy	Methionine and cysteine metabolism	20	1.8.4.4	4	
r0027_pos	8	1.19043	0.7202646	1.095385	1.095385	1	0.347218	r0027	NADPH:CoA-glutathione oxidoreductase EC:1.8.1.9	1.00 * Nicotinamide adenine dinucleotide phosphate [c] -> 1.00	TXNRD1; T	Methionine and cysteine metabolism	20	1.8.1.9	0	
CYSGLTH_neg	7	0.382733	0.4171041	1.076682	1.076682	1	0.518179	CYSGLTH	Glutathione:cystine oxidoreductase	1.00 * L-cystine [c] + 2.00 * Reduced glutathione [c] -> 2.00	1.00 * L-cy	Methionine and cysteine metabolism	20	1.8.4.4	4	
r0027_neg	7	0.382733	0.4171041	1.076682	1.076682	1	0.518179	r0027	NADPH:CoA-glutathione oxidoreductase EC:1.8.1.9	1.00 * Nicotinamide adenine dinucleotide phosphate [c] -> 1.00	TXNRD1; T	Methionine and cysteine metabolism	20	1.8.1.9	0	
H2C030Dm_neg	0	0.080856	1.0922877	-2.31899	2.318987	2	0.240222	H2C030Dm	carboxylic acid dissociation	1.00 * Water [m] + 1.00 * carbon dioxide [m] -> 1.00	pro CARSA; CA	Miscellaneous	4	2.2.1.1	4	
H2C030Dm_pos	0	0.080856	1.0922877	-2.94107	2.941075	2	0.240222	H2C030Dm	carboxylic acid dissociation	1.00 * Water [m] + 1.00 * carbon dioxide [m] -> 1.00	pro CARSA; CA	Miscellaneous	4	2.2.1.1	4	
H2C030_pos	0	0.080856	1.0922877	-1.79567	1.795669	2	0.240222	H2C030D	carboxylic acid dissociation	1.00 * Water [c] + 1.00 * carbon dioxide [c] -> 1.00	pro CAR1; CAR	Miscellaneous	4	2.2.1.1	0	
H2C030_neg	1	1.19043	0.7202646	-1.43187	1.431873	2	0.347218	H2C030	carboxylic acid dissociation	1.00 * Water [c] + 1.00 * carbon dioxide [c] -> 1.00	pro CAR1; CAR	Miscellaneous	4	2.2.1.1	0	
RE0383C_pos	3	0.662521	0.1788004	-0.79031	0.790314	2	0.758498	RE0383C		1.00 * Nicotinamide adenine dinucleotide phosphate [c] -> 1.00	AKR1A1	Miscellaneous	21	1.1.1.2	0	
THD1m_pos	0	0.080856	1.0922877	-2.43874	2.43874	2	0.240222	THD1m	NAD(P) transhydrogenase	1.00 * Nicotinamide adenine dinucleotide phosphate [m] -> 1.00	NNT	NAD metabolism	21	1.6.1.2	4	
CYTK10_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK10	cytidylate kinase (CMP, dGTP)	1.00 * CMP [c] + 1.00 * dGTP [c] -> 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4	
CYTK10_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK10	cytidylate kinase (CMP, dGTP)	1.00 * CMP [c] + 1.00 * dGTP [c] -> 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4	
CYTK11_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK11	cytidylate kinase (dCMP, dGTP)	1.00 * dGTP [c] + 1.00 * dCMP [c] -> 1.00	* dGDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK11_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK11	cytidylate kinase (dCMP, dGTP)	1.00 * dGTP [c] + 1.00 * dCMP [c] -> 1.00	* dGDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK12_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK12	cytidylate kinase (dCMP, dCTP)	1.00 * dCMP [c] + 1.00 * dCTP [c] -> 2.00	* dGDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK12_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK12	cytidylate kinase (dCMP, dCTP)	1.00 * dCMP [c] + 1.00 * dCTP [c] -> 2.00	* dGDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK13_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK13	cytidylate kinase (dCMP, dATP)	1.00 * dATP [c] + 1.00 * dCMP [c] -> 1.00	* dADP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK13_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK13	cytidylate kinase (dCMP, dATP)	1.00 * dATP [c] + 1.00 * dCMP [c] -> 1.00	* dADP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK14_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK14	cytidylate kinase (dCMP, dATP)	1.00 * UTP [c] + 1.00 * dCMP [c] -> 1.00	* UDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK14_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	CYTK14	cytidylate kinase (dCMP, UTP)	1.00 * UTP [c] + 1.00 * dCMP [c] -> 1.00	* UDP [c] + 1.00	* CMPK1	Nucleotide interconversion	22	2.7.4.14	4
CYTK1_neg	9	0.080856	1.0922877	2.295253	2.295253	1	0.240222	CYTK1	cytidylate kinase (CMP)	1.00 * ATP [c] + 1.00 * CMP [c] -> 1.00	* ADP [c] + 1.00	* CMPK1	Nucleotide interconversion	22		4
CYTK1_pos	9	0.080856	1.0922877	2.295253	2.295253	1	0.240222	CYTK1	cytidylate							

NDP2_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP2	nucleoside-diphosphate kinase (ATP:UDP)	1.00 * ATP [c] + 1.00 * UDP [c] --> 1.00 * ADP [c] + 1.00 * U	GM20390	Nucleotide interconversion	23		4
NDP3_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP3	nucleoside-diphosphate kinase (ATP:CDP)	1.00 * ATP [c] + 1.00 * CDP [c] --> 1.00 * ADP [c] + 1.00 * C	GM20390	Nucleotide interconversion	23		4
NDP3_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP3	nucleoside-diphosphate kinase (ATP:CDP)	1.00 * ATP [c] + 1.00 * CDP [c] --> 1.00 * ADP [c] + 1.00 * C	GM20390	Nucleotide interconversion	23		4
NDP5_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP5	nucleoside-diphosphate kinase (ATP:dGDP)	1.00 * ATP [c] + 1.00 * dGDP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP5_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP5	nucleoside-diphosphate kinase (ATP:dGDP)	1.00 * ATP [c] + 1.00 * dGDP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP6_pos	9	0.080856	1.0922877	0.013967	0.013967	1	0.240222	NDP6	Nucleoside-diphosphate kinase (ATP:dUDP)	1.00 * ATP [c] + 1.00 * dUDP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP7_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP7	nucleoside-diphosphate kinase (ATP:dCDP)	1.00 * ATP [c] + 1.00 * dCDP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP7_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP7	nucleoside-diphosphate kinase (ATP:dCDP)	1.00 * ATP [c] + 1.00 * dCDP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP8_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP8	Nucleoside-diphosphate kinase (ATP:dADP)	1.00 * ATP [c] + 1.00 * dADP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
NDP8_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	NDP8	Nucleoside-diphosphate kinase (ATP:dADP)	1.00 * ATP [c] + 1.00 * dADP [c] --> 1.00 * ADP [c] + 1.00 *	GM20390	Nucleotide interconversion	23		4
PUNP7_neg	0	0.080856	1.0922877	5.40841	5.408411	2	0.240222	PUNP7	purine-nucleoside phosphorylase (Xanthosine)	1.00 * hydrogensphosphate [c] + 1.00 * xanthosine [c] -->	PNP2	Nucleotide interconversion	23	3,4,2,1	0
RNDR3_pos	9	0.080856	1.0922877	1.801074	1.801074	1	0.240222	RNDR3	ribonucleoside-diphosphate reductase (CDP)	1.00 * CDP [c] + 1.00 * Reduced thioredoxin [c] --> 1.00 *	RRM1; RRM	Nucleotide interconversion	22	1,7,14,1	4
UMP2_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP2	UMP kinase (CTP)	1.00 * CTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP2_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP2	UMP kinase (CTP)	1.00 * CTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP3_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP3	UMP kinase (UTP)	1.00 * UTP [c] + 1.00 * UMP [c] --> 2.00 * UDP [c] [CMPK1]	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP3_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP3	UMP kinase (UTP)	1.00 * UTP [c] + 1.00 * UMP [c] --> 2.00 * UDP [c] [CMPK1]	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP4_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP4	UMP kinase (GTP)	1.00 * GTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP4_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP4	UMP kinase (GTP)	1.00 * GTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP5_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP5	UMP kinase (dATP)	1.00 * dATP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP5_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP5	UMP kinase (dATP)	1.00 * dATP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP6_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP6	UMP kinase (dCTP)	1.00 * dCTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP6_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP6	UMP kinase (dCTP)	1.00 * dCTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP7_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP7	UMP kinase (dGTP)	1.00 * dGTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP7_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP7	UMP kinase (dGTP)	1.00 * dGTP [c] + 1.00 * UMP [c] --> 1.00 * UDP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
UMP8_neg	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP8	UMP kinase	1.00 * ATP [c] + 1.00 * UMP [c] --> 1.00 * ADP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22		4
UMP8_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP8	UMP kinase	1.00 * ATP [c] + 1.00 * UMP [c] --> 1.00 * ADP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22		4
UMP9_pos	9	0.080856	1.0922877	2.263577	2.263577	1	0.240222	UMP9	UMP kinase	1.00 * ATP [c] + 1.00 * UMP [c] --> 1.00 * ADP [c] + 1.00 *	CMPK1	Nucleotide interconversion	22		4
o472_pos	9	0.080856	1.0922877	1.835454	1.835454	1	0.240222	o472	2-Deoxyadenosine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase	1.00 * Water [c] + 1.00 * dGTP [c] + 1.00 * Oxidized thior	RRM1; RRM	Nucleotide interconversion	22	1,17,4,1	0
o474_pos	9	0.080856	1.0922877	1.801074	1.801074	1	0.240222	o474	2-Deoxyadenosine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase	1.00 * Water [c] + 1.00 * dCTP [c] + 1.00 * Oxidized thior	RRM1; RRM	Nucleotide interconversion	22	1,17,4,1	0
o475_pos	9	0.080856	1.0922877	0.013967	0.013967	1	0.240222	o475	2-Deoxyadenosine 5-phosphate:oxidized-thioredoxin 2-oxidoreductase	1.00 * Water [c] + 1.00 * dUTP [c] + 1.00 * Oxidized thior	RRM1; RRM	Nucleotide interconversion	22	1,17,4,1	0
o531_neg	9	0.080856	1.0922877	1.563427	1.563427	1	0.240222	o531	dUTP:cytidine 5-phosphotransferase Pyrimidine metabolism EC:2.7.4.1	1.00 * Cytidine [c] + 1.00 * dUTP [c] --> 1.00 * proton [c]	UCCK1; UCK	Nucleotide interconversion	22	2,7,14,8	0
r1384_neg	0	0.080856	1.0922877	5.40841	5.408411	2	0.240222	r1384	Guanosine aminohydrolase EC:3.5.4.15	1.00 * Water [c] + 1.00 * proton [c] + 1.00 * Guanosine [c]	1.00 * Wat		22	3,5,4,15	0
ADK1m_neg	1	0.19043	0.702646	-1.45529	1.455287	2	0.347218	ADK1m	adenylate kinase, mitochondrial	1.00 * ATP [m] + 1.00 * AMP [m] --> 2.00 * ADP [m] [AK2; AK	AK2; AK4	Nucleotide interconversion	22	2,7,4,3	4
ADK1m_pos	1	0.19043	0.702646	-1.45529	1.455287	2	0.347218	ADK1m	adenylate kinase, mitochondrial	1.00 * ATP [m] + 1.00 * AMP [m] --> 2.00 * ADP [m] [AK2; AK	AK2; AK4	Nucleotide interconversion	22	2,7,4,3	4
ADK3m_neg	1	0.19043	0.702646	-1.45529	1.455287	2	0.347218	ADK3m	adenylate kinase (GTP)	1.00 * AMP [m] + 1.00 * GTP [m] --> 1.00 * ADP [m] + 1.00 *	AK3	Nucleotide interconversion	22		4
ADK3m_pos	1	0.19043	0.702646	-1.45529	1.455287	2	0.347218	ADK3m	adenylate kinase (GTP)	1.00 * AMP [m] + 1.00 * GTP [m] --> 1.00 * ADP [m] + 1.00 *	AK3	Nucleotide interconversion	22		4
o470_pos	8	0.19043	0.702646	1.709019	1.709019	1	0.347218	o470	2-Deoxyadenosine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase	1.00 * Water [c] + 1.00 * dATP [c] + 1.00 * Oxidized thior	RRM1; RRM	Nucleotide interconversion	22	1,17,4,1	0
CYTK10n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK10n	cytidylate kinase (CMP, dGTP), nuclear	1.00 * CMP [n] + 1.00 * dGTP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK10n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK10n	cytidylate kinase (CMP, dGTP), nuclear	1.00 * CMP [n] + 1.00 * dGTP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK11n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK11n	cytidylate kinase (dCMP, dGTP), nuclear	1.00 * dGTP [n] + 1.00 * dCMP [n] --> 1.00 * dGDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK11n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK11n	cytidylate kinase (dCMP, dGTP), nuclear	1.00 * dGTP [n] + 1.00 * dCMP [n] --> 1.00 * dGDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK12n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK12n	cytidylate kinase (dCMP, dCTP), nuclear	1.00 * dCMP [n] + 1.00 * dCTP [n] --> 2.00 * dCDP [n] [CMP	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK12n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK12n	cytidylate kinase (dCMP, dCTP), nuclear	1.00 * dCMP [n] + 1.00 * dCTP [n] --> 2.00 * dCDP [n] [CMP	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK13n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK13n	cytidylate kinase (dCMP, dATP), nuclear	1.00 * dCMP [n] + 1.00 * dATP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK13n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK13n	cytidylate kinase (dCMP, dATP), nuclear	1.00 * dCMP [n] + 1.00 * dATP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK14n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK14n	cytidylate kinase (dCMP, CTP), nuclear	1.00 * dCMP [n] + 1.00 * UTP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK14n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK14n	cytidylate kinase (dCMP, CTP), nuclear	1.00 * dCMP [n] + 1.00 * UTP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK1n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK1n	cytidylate kinase (CMP), nuclear	1.00 * ATP [n] + 1.00 * CMP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK1n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK1n	cytidylate kinase (CMP), nuclear	1.00 * ATP [n] + 1.00 * CMP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK2n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK2n	cytidylate kinase (dCMP), nuclear	1.00 * ATP [n] + 1.00 * dCMP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK2n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK2n	cytidylate kinase (dCMP), nuclear	1.00 * ATP [n] + 1.00 * dCMP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK3n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK3n	cytidylate kinase (dCMP, CTP), nuclear	1.00 * CTP [n] + 1.00 * dCMP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK3n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK3n	cytidylate kinase (dCMP, CTP), nuclear	1.00 * CTP [n] + 1.00 * dCMP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK4n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK4n	cytidylate kinase (dCMP, dGTP), nuclear	1.00 * dCMP [n] + 1.00 * GTP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK4n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK4n	cytidylate kinase (dCMP, dGTP), nuclear	1.00 * dCMP [n] + 1.00 * GTP [n] --> 1.00 * dCDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK5n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK5n	cytidylate kinase (CMP), nuclear	1.00 * CMP [n] + 1.00 * GTP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK5n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK5n	cytidylate kinase (CMP), nuclear	1.00 * CMP [n] + 1.00 * GTP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK6n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK6n	cytidylate kinase (CMP, CTP), nuclear	1.00 * CTP [n] + 1.00 * CMP [n] --> 2.00 * CDP [n] [CMPK1]	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK6n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK6n	cytidylate kinase (CMP, CTP), nuclear	1.00 * CTP [n] + 1.00 * CMP [n] --> 2.00 * CDP [n] [CMPK1]	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK7n_neg	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK7n	cytidylate kinase (CMP, UTP), nuclear	1.00 * CMP [n] + 1.00 * UTP [n] --> 1.00 * CDP [n] + 1.00 *	CMPK1	Nucleotide interconversion	22	2,7,14,4	4
CYTK7n_pos	9	0.382733	0.4171041	1.077892	1.077892	1	0.518179	CYTK7n	cytidylate kinase						

ADKd_neg	6	0.662521	0.1788004	1.628283	1.628283	1	0.758498	ADKd	adenylate kinase (d form)	1.00 * dAMP(2-) [c] + 1.00 * dATP [c] -> 2.00 * dADP [c]	AK5	Nucleotide interconversion	22	2.7.4.3	4
ADKd_pos	6	0.662521	0.1788004	1.628283	1.628283	1	0.758498	ADKd	adenylate kinase (d form)	1.00 * dAMP(2-) [c] + 1.00 * dATP [c] -> 2.00 * dADP [c]	AK5	Nucleotide interconversion	22	2.7.4.3	4
NDPK10_neg	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK10	nucleoside-diphosphate kinase (ATP:diDP)	1.00 * ATP [c] + 1.00 * diDP [c] -> 1.00 * ADP [c] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK10_pos	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK10	nucleoside-diphosphate kinase (ATP:diDP)	1.00 * ATP [c] + 1.00 * diDP [c] -> 1.00 * ADP [c] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK10n_neg	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK10n	nucleoside-diphosphate kinase (ATP:diDP), nuclear	1.00 * ATP [n] + 1.00 * diDP [n] -> 1.00 * ADP [n] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK10n_pos	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK10n	nucleoside-diphosphate kinase (ATP:diDP), nuclear	1.00 * ATP [n] + 1.00 * diDP [n] -> 1.00 * ADP [n] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK9n_neg	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK9n	nucleoside-diphosphate kinase (ATP:IDP), nuclear	1.00 * ATP [n] + 1.00 * IDP(3-) [n] -> 1.00 * ADP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK9n_pos	3	0.662521	0.1788004	0.123933	0.123933	1	0.758498	NDPK9n	nucleoside-diphosphate kinase (ATP:IDP), nuclear	1.00 * ATP [n] + 1.00 * IDP(3-) [n] -> 1.00 * ADP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
r0345_neg	6	0.662521	0.1788004	1.628283	1.628283	1	0.758498	r0345	ATP-AMP phosphotransferase Purine metabolism EC:2.7.4.11	1.00 * ATP [c] + 1.00 * dAMP(2-) [c] -> 1.00 * ADP [c] + 1.0A	AK1; AK2;	Nucleotide interconversion	22	2.7.4.11	0
r0345_pos	6	0.662521	0.1788004	1.628283	1.628283	1	0.758498	r0345	ATP-AMP phosphotransferase Purine metabolism EC:2.7.4.11	1.00 * ATP [c] + 1.00 * dAMP(2-) [c] -> 1.00 * ADP [c] + 1.0A	AK1; AK2;	Nucleotide interconversion	22	2.7.4.11	0
NDPK1n_neg	4	1	0	0.341896	0.341896	1	1	NDPK1n	nucleoside-diphosphate kinase (ATP:GDP), nuclear	1.00 * ATP [n] + 1.00 * GDP [n] -> 1.00 * ADP [n] + 1.00 * G	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK1n_pos	4	1	0	0.341896	0.341896	1	1	NDPK1n	nucleoside-diphosphate kinase (ATP:GDP), nuclear	1.00 * ATP [n] + 1.00 * GDP [n] -> 1.00 * ADP [n] + 1.00 * G	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK2n_neg	4	1	0	0.341896	0.341896	1	1	NDPK2n	nucleoside-diphosphate kinase (ATP:UDP), nuclear	1.00 * ATP [n] + 1.00 * UDP [n] -> 1.00 * UTP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK2n_pos	4	1	0	0.341896	0.341896	1	1	NDPK2n	nucleoside-diphosphate kinase (ATP:UDP), nuclear	1.00 * ATP [n] + 1.00 * UDP [n] -> 1.00 * UTP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK3n_neg	4	1	0	0.341896	0.341896	1	1	NDPK3n	nucleoside-diphosphate kinase (ATP:CDP), nuclear	1.00 * ATP [n] + 1.00 * CDP [n] -> 1.00 * CTP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK3n_pos	4	1	0	0.341896	0.341896	1	1	NDPK3n	nucleoside-diphosphate kinase (ATP:CDP), nuclear	1.00 * ATP [n] + 1.00 * CDP [n] -> 1.00 * CTP [n] + 1.00 * A	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK4_pos	4	1	0	0.406305	0.406305	1	1	NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	1.00 * ATP [c] + 1.00 * dTDP [c] -> 1.00 * ADP [c] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK4n_neg	4	1	0	0.312921	0.312921	1	1	NDPK4n	nucleoside-diphosphate kinase (ATP:dTDP), nuclear	1.00 * ATP [n] + 1.00 * dTDP [n] -> 1.00 * ADP [n] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK4n_pos	4	1	0	0.312921	0.312921	1	1	NDPK4n	nucleoside-diphosphate kinase (ATP:dTDP), nuclear	1.00 * ATP [n] + 1.00 * dTDP [n] -> 1.00 * ADP [n] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK5n_neg	4	1	0	0.341896	0.341896	1	1	NDPK5n	nucleoside-diphosphate kinase (ATP:dGDP), nuclear	1.00 * ATP [n] + 1.00 * dGDP [n] -> 1.00 * dGTP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK5n_pos	4	1	0	0.341896	0.341896	1	1	NDPK5n	nucleoside-diphosphate kinase (ATP:dGDP), nuclear	1.00 * ATP [n] + 1.00 * dGDP [n] -> 1.00 * dGTP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK6_neg	4	1	0	0.306167	0.306167	1	1	NDPK6	Nucleoside-diphosphate kinase (ATP:dUDP)	1.00 * ATP [c] + 1.00 * dUDP [c] -> 1.00 * ADP [c] + 1.00 * d	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK7n_neg	4	1	0	0.341896	0.341896	1	1	NDPK7n	nucleoside-diphosphate kinase (ATP:dCDP), nuclear	1.00 * ATP [n] + 1.00 * dCDP [n] -> 1.00 * dCTP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK7n_pos	4	1	0	0.341896	0.341896	1	1	NDPK7n	nucleoside-diphosphate kinase (ATP:dCDP), nuclear	1.00 * ATP [n] + 1.00 * dCDP [n] -> 1.00 * dCTP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK8n_neg	4	1	0	0.341896	0.341896	1	1	NDPK8n	nucleoside-diphosphate kinase (ATP:dADP), nuclear	1.00 * ATP [n] + 1.00 * dADP [n] -> 1.00 * dATP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK8n_pos	4	1	0	0.341896	0.341896	1	1	NDPK8n	nucleoside-diphosphate kinase (ATP:dADP), nuclear	1.00 * ATP [n] + 1.00 * dADP [n] -> 1.00 * dATP [n] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK9n_neg	4	1	0	0.480189	0.480189	1	1	NDPK9n	nucleoside-diphosphate kinase (ATP:IDP)	1.00 * ATP [c] + 1.00 * IDP(3-) [c] -> 1.00 * ADP [c] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
NDPK9n_pos	4	1	0	0.480189	0.480189	1	1	NDPK9n	nucleoside-diphosphate kinase (ATP:IDP)	1.00 * ATP [c] + 1.00 * IDP(3-) [c] -> 1.00 * ADP [c] + 1.00	GM20390	Nucleotide interconversion	22	2.7.4.6	4
r1156_neg	4	1	0	0.306167	0.306167	1	1	r1156	dUTP:uridine 5-phosphotransferase Pyrimidine metabolism EC:2.7.4.11	1.00 * Uridine [c] + 1.00 * dUTP [c] -> 1.00 * proton [c] + 1.00	UCK1; UCK	Nucleotide interconversion	22	2.7.4.18	0
XYLUR_neg	0	0.080856	1.0922877	-6.95104	6.951038	2	0.240222	XYLUR	xylulose reductase	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	DCXR	Pentose phosphate pathway	23	1.1.1.10	0
XYLUR_pos	0	0.080856	1.0922877	-1.98662	1.986624	2	0.240222	XYLUR	xylulose reductase	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	DCXR	Pentose phosphate pathway	23	1.1.1.10	4
r0784_neg	0	0.080856	1.0922877	-6.95104	6.951038	2	0.240222	r0784	xylitol:NAD oxidoreductase Pentose and glucuronate interconversio	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * xyl	1.00 * Nic	Pentose phosphate pathway	23	1.1.1.15	0
r0784_pos	0	0.080856	1.0922877	-1.98662	1.986624	2	0.240222	r0784	xylitol:NAD oxidoreductase Pentose and glucuronate interconversio	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * xyl	1.00 * Nic	Pentose phosphate pathway	23	1.1.1.15	4
RPI_neg	8	0.19043	0.7202646	-1.414492	1.414492	1	0.347218	RPI	ribose 5-phosphate isomerase	1.00 * alpha-D-Ribose 5-phosphate [c] -> 1.00 * D-ribulose	RPIA	Pentose phosphate pathway	23	5.3.1.6	0
RPI_pos	8	0.19043	0.7202646	-1.414492	1.414492	1	0.347218	RPI	ribose 5-phosphate isomerase	1.00 * alpha-D-Ribose 5-phosphate [c] -> 1.00 * D-ribulose	RPIA	Pentose phosphate pathway	23	5.3.1.6	4
TALA_neg	1	0.19043	0.7202646	-1.46042	1.460419	2	0.347218	TALA	transaldolase	1.00 * Glyceraldehyde 3-phosphate [c] + 1.00 * Sedohept	TALDO1	Pentose phosphate pathway	23	2.2.1.2	0
r0249_neg	8	0.19043	0.7202646	-1.414492	1.414492	1	0.347218	r0249	D-Ribose 5-phosphate ketol-isomerase Pentose phosphate pathway	1.00 * alpha-D-Ribose 5-phosphate [r] -> 1.00 * D-ribulose	RPIA	Pentose phosphate pathway	23	5.3.1.6	0
r0249_pos	8	0.19043	0.7202646	-1.414492	1.414492	1	0.347218	r0249	D-Ribose 5-phosphate ketol-isomerase Pentose phosphate pathway	1.00 * alpha-D-Ribose 5-phosphate [r] -> 1.00 * D-ribulose	RPIA	Pentose phosphate pathway	23	5.3.1.6	4
GGPDH1r_neg	6	0.662521	0.1788004	0.722007	0.722007	1	0.758498	GGPDH1r	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	1.00 * Nicotinamide adenine dinucleotide [r] + 1.00 * D-	H6PD	Pentose phosphate pathway	23	1.1.1.47	4
GGPDH1r_pos	6	0.662521	0.1788004	0.722007	0.722007	1	0.758498	GGPDH1r	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	1.00 * Nicotinamide adenine dinucleotide [r] + 1.00 * D-	H6PD	Pentose phosphate pathway	23	1.1.1.47	4
GGPDH2r_neg	6	0.662521	0.1788004	0.722007	0.722007	1	0.758498	GGPDH2r	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	1.00 * Nicotinamide adenine dinucleotide [r] + 1.00 * D-	GGPD2; H6	Pentose phosphate pathway	23	1.1.1.47	4
GGPDH2r_pos	6	0.662521	0.1788004	0.722007	0.722007	1	0.758498	GGPDH2r	glucose-6-phosphate dehydrogenase, endoplasmic reticulum	1.00 * Nicotinamide adenine dinucleotide [r] + 1.00 * D-	GGPD2; H6	Pentose phosphate pathway	23	1.1.1.47	4
PHETHPTOX2_pos	2	0.382733	0.4171041	-0.86474	0.864735	2	0.518179	PHETHPTOX2	L-Phenylalanine,tetrahydrobiopterin:oxygen oxidoreductase (4-hyd	1.00 * O2 [c] + 1.00 * 5,6,7,8-tetrahydrobiopterin [c] + 1.00	PAH	Phenylalanine metabolism	24	1.14.161	4
r0545_pos	6	0.662521	0.1788004	1.000342	1.000342	1	0.758498	r0545	Phenylacetaldehyde:NAD+ oxidoreductase Phenylalanine metabolism	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1A3;	Phenylalanine metabolism	24	1.2.1.5	0
r0547_neg	6	0.662521	0.1788004	1.000342	1.000342	1	0.758498	r0547	Aldehyde:NADP+ oxidoreductase Phenylalanine metabolism EC:1.2	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1A3;	Phenylalanine metabolism	24	1.2.1.5	0
GUAD_pos	0	0.080856	1.0922877	-5.40841	5.408411	2	0.240222	GUAD	guanine deaminase	1.00 * Water [c] + 1.00 * proton [c] + 1.00 * Guanine [c] -> 1	GDA	Purine catabolism	25	3.5.4.3	4
PUNP3_pos	0	0.080856	1.0922877	-5.40841	5.408411	2	0.240222	PUNP3	purine-nucleoside phosphorylase (Guanosine)	1.00 * hydrogenphosphate [c] + 1.00 * Guanosine [c] -> 1.00	PNP2	Purine catabolism	25	3.4.2.1	4
r0809_neg	2	0.382733	0.4171041	-1.29337	1.293368	2	0.518179	r0809	Facilitated diffusion	1.00 * Adenosine [c] + 1.00 * Inosine [e] -> 1.00 * Inosine	1.00 * Ade	Purine catabolism	25	0	0
r0809_pos	2	0.382733	0.4171041	-1.29337	1.293368	2	0.518179	r0809	Facilitated diffusion	1.00 * Adenosine [c] + 1.00 * Inosine [e] -> 1.00 * Inosine	1.00 * Ade	Purine catabolism	25	0	0
DURAD2_pos	0	0.080856	1.0922877	-4.19166	4.191658	2	0.240222	DURAD2	dihydrorhymine dehydrogenase (NADP)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	DPYD	Pyrimidine catabolism	26	1.3.1.2	4
r0330_pos	0	0.080856	1.0922877	-4.19166	4.191658	2	0.240222	r0330	5,6-Dihydrothymine:NAD+ oxidoreductase Pyrimidine metabolism	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * prot	Pyrimidine catabolism	26	1.3.1.1	0
DURAD_neg	1	0.19043	0.7202646	-1.15486	1.154858	2	0.347218	DURAD	dihydrouracil dehydrogenase (NADP)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	DPYD	Pyrimidine catabolism	26	1.3.1.2	4
r0236_pos	1	0.19043	0.7202646	-1.15486	1.154858	2	0.347218	r0236	5,6-Dihydrouracil:NAD+ oxidoreductase Pyrimidine metabolism EC	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 5,6,1	1.00 * Nic	Pyrimidine catabolism	26	1.3.1.1	0
D3AIBTm_neg	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	D3AIBTm	D-3-Amino-isobutanoate:pyruvate aminotransferase, mitochondrial	1.00 * pyruvate [m] + 1.00 * D-3-Amino-isobutanoate [m]	AGXT2	Pyrimidine catabolism	26	2.6.1.40	4
D3AIBTm_pos	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	D3AIBTm	D-3-Amino-isobutanoate:pyruvate aminotransferase, mitochondrial	1.00 * pyruvate [m] + 1.00 * D-3-Amino-isobutanoate [m]	AGXT2	Pyrimidine catabolism	26	2.6.1.40	4
r0483_neg	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	r0483	(R)-3-Amino-2-methylpropanoate:2-oxoglutarate aminotransferase	1.00 * 2-Oxoglutarate [m] + 1.00 * D-3-Amino-isobutano	ABAT	Pyrimidine catabolism	26	2.6.1.22	0
r0483_pos	6	0.662521	0.1788004	-0.32478	0.324776	2	0.758498	r0483	(R)-3-Amino-2-methylpropanoate:2-oxoglutarate aminotransferase	1.00 * 2-Oxoglutarate [m] + 1.00 * D-3-Amino-isobutano	ABAT	Pyrimidine catabolism	26	2.6.1.22	0
RE1530C_neg	9	0.080856	1.0922877	4.748812	4.748812	1	0.240222	RE1530C	RE1530C	1.00 * dGTP [c] + 1.00 * Deoxyuridine [c] -> 1.00 * proton [c] + 1.00 * dGDP [c] + 1.00 * dUMP [c]	1.00 * dGT	Pyrimidine synthesis	27	2.7.1.21	0
RE0453C_neg	7	0.382733	0.4171041	1.039213	1.039213	1	0.518179	RE0453C	RE0453C	1.00 * dATP [c] + 1.00 * dTDP [c] -> 1.00 * dADP [c] + 1.00	1.00 * dAT	Pyrimidine synthesis	27	2.7.4.6	0
RE0453C_pos	7	0.382733	0.4171041	1.039213	1.039213	1	0.518179	RE0453C	RE0453C	1.00 * dATP [c] + 1.00 * dTDP [c] -> 1.00 * dADP [c] + 1.00	1.00 * dAT	Pyrimidine synthesis	27	2.7.4.6	4
URIK1_pos	4	1	0	0.306167	0.306167	1	1	URIK1	uridine kinase (ATP:Uridine)	1.00 * ATP [c] + 1.00 * Uridine [c] -> 1.00 * ADP [c] + 1.00	UCK1; UCK	Pyrimidine synthesis	27	2.7.1.48	4
RE0453N_neg	4	1	0	0.312921	0.312921	1	1	RE0453N	RE						

HSD11B2r_neg	4	1	0	-0.0199	0.019897	2	1	HSD11B2r	11-beta-hydroxysteroid dehydrogenase type 2	1.00 * proton [r] + 1.00 * Nicotinamide adenine dinucleotide	HSD11B2	Steroid metabolism	29	4	
HSD11B2r_pos	4	1	0	-0.0199	0.019897	2	1	HSD11B2r	11-beta-hydroxysteroid dehydrogenase type 2	1.00 * proton [r] + 1.00 * Nicotinamide adenine dinucleotide	HSD11B2	Steroid metabolism	29	4	
THBP4ACAMDASE	2	0.382733	0.4171041	-0.86474	0.864735	2	0.518179	THBP4AC	Tetrahydrobiopterin-4a-carbinolamine dehydrogenase	1.00 * 4a-hydroxytetrahydrobiopterin [c] -> 1.00 * Water	PCBD1	Tetrahydrobiopterin metabolism	30	4.2.1.96	4
g0399_neg	2	0.382733	0.4171041	-0.86474	0.864735	2	0.518179	g0399	L-Phenylalanine,tetrahydrobiopterin:oxygen oxidoreductase (4-hydroxy)	1.00 * O2 [c] + 1.00 * 5,6,7,8-tetrahydrobiopterin [c] + 1.00	PAH	Tetrahydrobiopterin metabolism	30	1.14.16.1	0
GTPC1_pos	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	GTPC1	GTP cyclohydrolase I	1.00 * Water [c] + 1.00 * GTP [c] -> 1.00 * proton [c] + 1.00	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	4
GTPC1n_pos	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	GTPC1n	GTP cyclohydrolase I, nuclear	1.00 * Water [n] + 1.00 * GTP [n] -> 1.00 * proton [n] + 1.00	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	4
RE0830N_neg	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE0830N	RE0830	1.00 * 4a-hydroxytetrahydrobiopterin [n] -> 1.00 * Water	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
RE0830N_pos	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE0830N	RE0830	1.00 * 4a-hydroxytetrahydrobiopterin [n] -> 1.00 * Water	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
RE1709N_neg	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE1709N	RE1709	1.00 * 4a-hydroxytetrahydrobiopterin [n] -> 1.00 * Water	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
RE1709N_pos	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE1709N	RE1709	1.00 * 4a-hydroxytetrahydrobiopterin [n] -> 1.00 * Water	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
RE2660N_neg	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE2660N	RE2660	1.00 * O2'-4a-cyclic-tetrahydrobiopterin [n] -> 1.00 * qu	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
RE2660N_pos	3	0.662521	0.1788004	-0.69243	0.692431	2	0.758498	RE2660N	RE2660	1.00 * O2'-4a-cyclic-tetrahydrobiopterin [n] -> 1.00 * qu	PCBD1; PC	Tetrahydrobiopterin metabolism	30	4.2.1.96	0
r0120_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0120	GTP 7,8-9-dihydrolase Folate biosynthesis EC:3.5.4.16	1.00 * Water [c] + 4.00 * proton [c] + 1.00 * GTP [c] -> 1.00	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0121_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0121	r0121	1.00 * Water [n] + 4.00 * proton [n] + 1.00 * GTP [n] -> 1.00	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0403_neg	6	0.662521	0.1788004	0.007222	0.007222	1	0.758498	r0403	L-Tryptophan,tetrahydrobiopterin:oxygen oxidoreductase (5-hydroxy)	1.00 * O2 [c] + 1.00 * 5,6,7,8-tetrahydrobiopterin [c] + 1.00	TPH1; TPH	Tetrahydrobiopterin metabolism	30	1.14.16.4	0
r0708_pos	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0708	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl) dihydropterin	1.00 * Water [c] + 4.00 * proton [c] + 1.00 * 7,8-dihydro	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0709_pos	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0709	r0709	1.00 * Water [n] + 4.00 * proton [n] + 1.00 * 7,8-dihydro	ECHS1; EHH	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0776_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0776	r0776	1.00 * Water [n] + 1.00 * Formamidopyrimidine nucleoside	ECHS1; EHH	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0777_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0777	GTP 7,8-8,9-dihydrolase Folate biosynthesis EC:3.5.4.16	4.00 * proton [c] + 1.00 * 2,5-Diaminopyrimidine nucleoside	GCH1	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
r0778_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0778	r0778	4.00 * proton [n] + 1.00 * 2,5-Diaminopyrimidine nucleoside	EHADH; H	Tetrahydrobiopterin metabolism	30	3.5.4.16	0
ACCOAtr_neg	9	0.080856	1.0922877	1.613406	1.613406	1	0.240222	ACCOAtr	acetyl-coa transport	1.00 * Acetyl-CoA [c] -> 1.00 * Acetyl-CoA [r]SLC33A1	SLC33A1	Transport, endoplasmic reticular		0	
ACCOAtr_pos	9	0.080856	1.0922877	1.613406	1.613406	1	0.240222	ACCOAtr	acetyl-coa transport	1.00 * Acetyl-CoA [c] -> 1.00 * Acetyl-CoA [r]SLC33A1	SLC33A1	Transport, endoplasmic reticular		0	
r0995_neg	9	0.080856	1.0922877	1.613406	1.613406	1	0.240222	r0995	Mitochondrial Carrier (MC) TCDB:2.A.29.8.3	1.00 * L-Carnitine [c] + 1.00 * O-acetylcarnitine [r] -> 1.00	SLC25A20	Transport, endoplasmic reticular		0	
r0995_pos	9	0.080856	1.0922877	1.613406	1.613406	1	0.240222	r0995	Mitochondrial Carrier (MC) TCDB:2.A.29.8.3	1.00 * L-Carnitine [c] + 1.00 * O-acetylcarnitine [r] -> 1.00	SLC25A20	Transport, endoplasmic reticular		0	
r0840_neg	8	0.19043	0.7202646	1.414492	1.414492	1	0.347218	r0840	Free diffusion	1.00 * alpha-D-Ribose 5-phosphate [c] -> 1.00 * alpha-D-ribose	1.00 * alph	Transport, endoplasmic reticular		0	
r0840_pos	8	0.19043	0.7202646	1.414492	1.414492	1	0.347218	r0840	Free diffusion	1.00 * alpha-D-Ribose 5-phosphate [c] -> 1.00 * alpha-D-ribose	1.00 * alph	Transport, endoplasmic reticular		0	
r0841_neg	8	0.19043	0.7202646	1.414492	1.414492	1	0.347218	r0841	Free diffusion	1.00 * D-ribulose 5-phosphate(2-) [c] -> 1.00 * D-ribulose	1.00 * D-ri	Transport, endoplasmic reticular		0	
r0841_pos	8	0.19043	0.7202646	1.414492	1.414492	1	0.347218	r0841	Free diffusion	1.00 * D-ribulose 5-phosphate(2-) [c] -> 1.00 * D-ribulose	1.00 * D-ri	Transport, endoplasmic reticular		0	
G6Pter_neg	2	0.382733	0.4171041	-1.13714	1.137136	2	0.518179	G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion	1.00 * D-Glucose 6-phosphate [c] -> 1.00 * D-Glucose 6-phosphate	SLC37A4	Transport, endoplasmic reticular		4	
HPETFABP1tc_pos	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	HPETFABP1	transport of 5-HPETE into the enterocytes	2.00 * 5(S)-HPETE(1-) [c] -> 2.00 * 5(S)-HPETE(1-) [r]FABP1	FABP1	Transport, endoplasmic reticular		4	
OCDEAFABP1tc_neg	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	OCDEAFABP1	Transport of octadecenoyle coA into the enterocytes	2.00 * octadecenoate (n-C18:1) [c] -> 2.00 * octadecenoate	FABP1	Transport, endoplasmic reticular		4	
OCDEAFABP1tc_pos	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	OCDEAFABP1	Transport of octadecenoyle coA into the enterocytes	2.00 * octadecenoate (n-C18:1) [c] -> 2.00 * octadecenoate	FABP1	Transport, endoplasmic reticular		4	
PMTCOAFABP1tc_pos	7	0.382733	0.4171041	1.115609	1.115609	1	0.518179	PMTCOAFABP1	transport of palmitoyl coA into the enterocytes	2.00 * Palmitoyl-CoA (n-C16:0CoA) [c] -> 2.00 * Palmitoyl	FABP1	Transport, endoplasmic reticular		4	
r0002_neg	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	r0002	Active transport	1.00 * L-Carnitine [c] -> 1.00 * L-Carnitine [r]No genes	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r0002_pos	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	r0002	Active transport	1.00 * L-Carnitine [c] -> 1.00 * L-Carnitine [r]No genes	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r0998_neg	7	0.382733	0.4171041	1.115609	1.115609	1	0.518179	r0998	Facilitated diffusion	1.00 * L-Carnitine [c] + 1.00 * L-palmitoylcarnitine [r] -> 1.00	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r1051_neg	7	0.382733	0.4171041	1.272298	1.272298	1	0.518179	r1051	Vesicular transport	1.00 * cholesterol [l] -> 1.00 * cholesterol [r]No genes	1.00 * chol	Transport, endoplasmic reticular		0	
r1051_pos	7	0.382733	0.4171041	1.272298	1.272298	1	0.518179	r1051	Vesicular transport	1.00 * cholesterol [l] -> 1.00 * cholesterol [r]No genes	1.00 * chol	Transport, endoplasmic reticular		0	
r1318_neg	7	0.382733	0.4171041	0.938989	0.938989	1	0.518179	r1318	Transport reaction	1.00 * linoleic coenzyme A [c] -> 1.00 * linoleic coenzyme	1.00 * lino	Transport, endoplasmic reticular		0	
r2473_pos	2	0.382733	0.4171041	-1.13714	1.137136	2	0.518179	r2473	Major Facilitator (MFS) TCDB:2.A.1.4.5	1.00 * hydrogenphosphate [r] + 1.00 * D-Glucose 6-phosphate	SLC37A4	Transport, endoplasmic reticular		0	
r2509_neg	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	r2509	Utilized transport	1.00 * L-Carnitine [r] + 1.00 * octadecenoate (n-C18:1) [c]	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r2509_pos	2	0.382733	0.4171041	-1.29111	1.291104	2	0.518179	r2509	Utilized transport	1.00 * L-Carnitine [r] + 1.00 * octadecenoate (n-C18:1) [c]	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r2511_neg	7	0.382733	0.4171041	0.938989	0.938989	1	0.518179	r2511	Utilized transport	1.00 * L-Carnitine [r] + 1.00 * linoleate [c] -> 1.00 * L-Carr	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r2521_neg	2	0.382733	0.4171041	-1.14825	1.148251	2	0.518179	r2521	Utilized transport	1.00 * Diphosphate [c] + 1.00 * hydrogenphosphate [r] -> 1.00	1.00 * Dip	Transport, endoplasmic reticular		0	
r2521_pos	2	0.382733	0.4171041	-1.14825	1.148251	2	0.518179	r2521	Utilized transport	1.00 * Diphosphate [c] + 1.00 * hydrogenphosphate [r] -> 1.00	1.00 * Dip	Transport, endoplasmic reticular		0	
r2537_neg	7	0.382733	0.4171041	0.957852	0.957852	1	0.518179	r2537	Utilized transport	1.00 * gamma-linolenoyl-CoA(4-) [c] -> 1.00 * gamma-lin	1.00 * gam	Transport, endoplasmic reticular		0	
r0960_neg	3	0.662521	0.1788004	-0.39029	0.390288	2	0.758498	r0960	Resistance-Modulation-Cell Division (RND) TCDB:2.A.65.1.1	1.00 * Sodium [c] + 1.00 * bilirubin(2-) [c] -> 1.00 * bilirubin	CP	Transport, endoplasmic reticular		0	
r0960_pos	3	0.662521	0.1788004	-0.39029	0.390288	2	0.758498	r0960	Resistance-Modulation-Cell Division (RND) TCDB:2.A.65.1.1	1.00 * Sodium [c] + 1.00 * bilirubin(2-) [c] -> 1.00 * bilirubin	CP	Transport, endoplasmic reticular		0	
r1000_neg	6	0.662521	0.1788004	0.899335	0.899335	1	0.758498	r1000	Facilitated diffusion	1.00 * L-Carnitine [c] + 1.00 * palmitoleoyl-Carnitine [r] -> 1.00	1.00 * L-Ca	Transport, endoplasmic reticular		0	
r1010_neg	3	0.662521	0.1788004	-0.27302	0.273018	2	0.758498	r1010	Postulated transport reaction	1.00 * N-[R]-pantothenoyl-L-cysteine [c] -> 1.00 * N-[R]-pantothenoyl-L-cysteine	1.00 * N-[R]	Transport, endoplasmic reticular		0	
r2506_neg	3	0.662521	0.1788004	-0.39029	0.390288	2	0.758498	r2506	Utilized transport	1.00 * hydrogenphosphate [c] + 1.00 * Sodium [c] -> 1.00	1.00 * hyd	Transport, endoplasmic reticular		0	
r2506_pos	3	0.662521	0.1788004	-0.39029	0.390288	2	0.758498	r2506	Utilized transport	1.00 * hydrogenphosphate [c] + 1.00 * Sodium [c] -> 1.00	1.00 * hyd	Transport, endoplasmic reticular		0	
UDPGLCAtcr_neg	5	1	0	0.130644	0.130644	1	1	UDPGLCAtcr	UDPGlcA endoplasmic reticulum transport via UMP antiport	1.00 * UMP [c] + 1.00 * UDP-D-glucuronate [r] -> 1.00 * U	SLC35D1	Transport, endoplasmic reticular		4	
UDPGLCAtcr_pos	5	1	0	0.130644	0.130644	1	1	UDPGLCAtcr	UDPGlcA endoplasmic reticulum transport via UMP antiport	1.00 * UMP [c] + 1.00 * UDP-D-glucuronate [r] -> 1.00 * U	SLC35D1	Transport, endoplasmic reticular		4	
r2519_neg	5	1	0	0.130644	0.130644	1	1	r2519	Utilized transport	1.00 * UDP-D-glucuronate [c] -> 1.00 * UDP-D-glucurona	1.00 * UDP	Transport, endoplasmic reticular		4	
r2519_pos	5	1	0	0.130644	0.130644	1	1	r2519	Utilized transport	1.00 * UDP-D-glucuronate [c] -> 1.00 * UDP-D-glucurona	1.00 * UDP	Transport, endoplasmic reticular		4	
SMTHF2_pos	0	0.080856	1.0922877	-1.93455	1.934552	2	0.240222	SMTHF2	5-methyltetrahydrofolate transport via anion exchange	1.00 * Water [c] + 1.00 * 5-Methyltetrahydrofolate [e] ->	SLC19A1	Transport, extracellular		4	
ABUT4_2_r_neg	0	0.080856	1.0922877	-1.62626	1.626257	2	0.240222	ABUT4_2	4-aminobutyrate reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * 4-Aminobutanoate [e] -> 2.00	SLC6A1; SL	Transport, extracellular		4	
ALACYSNaFex_pos	9	0.080856	1.0922877	3.071466	3.071466	1	0.240222	ALACYSNaFex	L-alanine/L-cysteine Na-dependent exchange (Ala-Lin)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-cysteine	SLC14A4; SL	Transport, extracellular		4	
BTN2_neg	0	0.080856	1.0922877	-2.15646	2.156456	2	0.240222	BTN2	Biotin reversible transport via proton symport	1.00 * proton [e] + 1.00 * Biotin [e] -> 1.00 * proton [c] +	SLC16A1	Transport, extracellular		4	
BTN2_pos	0	0.080856	1.0922877	-2.07298	2.072982	2	0.240222	BTN2	Biotin reversible transport via proton symport	1.00 * proton [e] + 1.00 * Biotin [e] -> 1.00 * proton [c] +	SLC16A1	Transport, extracellular		4	
BTN41_pos	0	0.080856	1.0922877	-2.15646	2.156456	2	0.240222	BTN41	Biotin uptake (antiport)	1.00 * proton [c] + 1.00 * Biotin [e] -> 1.00 * proton [e] +	SLC19A3	Transport, extracellular		4	
CYSSErNaFex_pos	9	0.080856	1.0922877	2.266923	2.266923	1	0.240222	CYSSErNaFex	L-serine/L-cysteine Na-dependent exchange (Cys-Lin)	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-serine	SLC14A4; SL	Transport, extracellular		4	
CYSTRNaFex_pos	9	0.080856	1.0922877	2.266923	2.266923	1	0.240222	CYSTRNaFex	L-cysteine/L-threonine Na-dependent exchange (Cys-Lin)	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-threonine	SLC14A4; SL	Transport, extracellular		4	
ESTRONES12_pos	0	0.080856	1.0922877	-1.52674	1.526737	2	0.240222								

INST4_2_neg	0	0.080856	1.0922877	-1.86623	1.866225	2	0.240222	INST4_2	Inositol transport via sodium symport	2.00 * Sodium [e] + 1.00 * myo-inositol [e] → 2.00 * Sod	SLC5A11	Transport, extracellular			4
INST4_2_pos	0	0.080856	1.0922877	-1.77669	1.776693	2	0.240222	INST4_2	Inositol transport via sodium symport	2.00 * Sodium [e] + 1.00 * myo-inositol [e] → 2.00 * Sod	SLC5A11	Transport, extracellular			4
LEUtec_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	LEUtec	L-leucine transport via diffusion (extracellular to cytosol)	1.00 * L-leucine [e] → 1.00 * L-leucine [c]SLC43A1; SLC43	SLC43A1; S	Transport, extracellular			4
LYSAtB0tc_pos	9	0.080856	1.0922877	2.025314	2.025314	1	0.240222	LYSAtB0tc	transport of L-lysine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-lysine [1+] [e] + 1.00 * Chlo	SLC6A14	Transport, extracellular			4
LYStiDF_pos	9	0.080856	1.0922877	3.880678	3.880678	1	0.240222	LYStiDF	L-lysine transport via diffusion (extracellular to cytosol)	1.00 * L-lysine [1+] [e] → 1.00 * L-lysine [1+] [c]SLC3	SLC38A4; S	Transport, extracellular			4
METLEuex_pos	9	0.080856	1.0922877	2.497908	2.497908	1	0.240222	METLEuex	Methionine/L-leucine exchange (Met in)	1.00 * L-methionine [e] + 1.00 * L-leucine [c] → 1.00 * L-	SLC3A2; SL	Transport, extracellular			4
ORNALArBAAtc_pos	9	0.080856	1.0922877	2.660891	2.660891	1	0.240222	ORNALArBA	transport of L-Ornithine into the cell in exchange for L-Alanine by b0	1.00 * L-alanine [c] + 1.00 * Ornithine [e] → 1.00 * Ornith	SLC3A1; S	Transport, extracellular			4
ORNLEuArBAAtc_pos	9	0.080856	1.0922877	2.581164	2.581164	1	0.240222	ORNLEuArBA	transport of L-Ornithine into the cell in exchange for L-Leucine by b0	1.00 * Ornithine [e] + 1.00 * L-leucine [c] → 1.00 * Ornith	SLC3A1; S	Transport, extracellular			4
ORNIrDF_pos	9	0.080856	1.0922877	2.854084	2.854084	1	0.240222	ORNIrDF	ornithine transport via diffusion (extracellular to cytosol)	1.00 * Ornithine [e] → 1.00 * Ornithine [c]SLC7A1; SLC7A	SLC7A1; S	Transport, extracellular			4
Pit7_neg	0	0.080856	1.0922877	-2.77478	2.774783	2	0.240222	Pit7	phosphate transport in/out via three Na+ symporter	3.00 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC17A1; S	Transport, extracellular			4
Pit7_pos	0	0.080856	1.0922877	-2.44786	2.447855	2	0.240222	Pit7	phosphate transport in/out via three Na+ symporter	3.00 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC17A1; S	Transport, extracellular			4
Pit8_neg	0	0.080856	1.0922877	-2.86625	2.866254	2	0.240222	Pit8	phosphate transport in/out via Na+ symporter	1.50 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC20A1; S	Transport, extracellular			4
Pit8_pos	0	0.080856	1.0922877	-2.77478	2.774783	2	0.240222	Pit8	phosphate transport in/out via Na+ symporter	1.50 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC20A1; S	Transport, extracellular			4
Pit9_neg	0	0.080856	1.0922877	-6.81309	6.813093	2	0.240222	Pit9	phosphate transport in/out via two Na+ symporter	2.00 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC34A3	Transport, extracellular			4
Pit9_pos	0	0.080856	1.0922877	-6.81309	6.813093	2	0.240222	Pit9	phosphate transport in/out via two Na+ symporter	2.00 * Sodium [e] + 1.00 * hydrogenphosphate [e] → 1.00	SLC34A3	Transport, extracellular			4
PROSTGF2t_neg	0	0.080856	1.0922877	-2.17032	2.170324	2	0.240222	PROSTGF2t	prostaglandin uniport	1.00 * prostaglandin F2alpha(1-) [e] → 1.00 * prostagland	SLC22A1; S	Transport, extracellular			4
PROSTGF2t_pos	0	0.080856	1.0922877	-2.17032	2.170324	2	0.240222	PROSTGF2t	prostaglandin uniport	1.00 * prostaglandin F2alpha(1-) [e] → 1.00 * prostagland	SLC22A1; S	Transport, extracellular			4
SERALANaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	SERALANaEx	L-alanine/L-serine Na-dependent exchange (Ser-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-serine [e]	SLC1A4; SL	Transport, extracellular			4
SERASNNaEx_pos	9	0.080856	1.0922877	2.402062	2.402062	1	0.240222	SERASNNaEx	L-serine/L-asparagine Na-dependent exchange (Ser-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-serin	SLC1A5	Transport, extracellular			4
SERCYSNaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	SERCYSNaEx	L-serine/L-cysteine Na-dependent exchange (Ser-L in)	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-serine [e]	SLC1A4; SL	Transport, extracellular			4
SERTHRNaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	SERTHRNaEx	L-serine/L-threonine Na-dependent exchange (Ser-L in)	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-threonine [e]	SLC1A4; SL	Transport, extracellular			4
SERT4_pos	9	0.080856	1.0922877	1.969429	1.969429	1	0.240222	SERT4	L-serine via sodium symport	1.00 * Sodium [e] + 1.00 * L-serine [e] → 1.00 * Sodium [c]	ACE2; SLC3	Transport, extracellular			4
TCHOLAT2_pos	0	0.080856	1.0922877	-1.71208	1.712078	2	0.240222	TCHOLAT2	taurocholate transport via sodium cotransport	2.00 * Sodium [e] + 1.00 * taurocholate [e] → 2.00 * Sod	SLC10A1; S	Transport, extracellular			4
THRALANaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	THRALANaEx	L-alanine/L-threonine Na-dependent exchange (Thr-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-threonin	SLC1A4; SL	Transport, extracellular			4
THRASNNaEx_pos	9	0.080856	1.0922877	2.402062	2.402062	1	0.240222	THRASNNaEx	L-threonine/L-asparagine Na-dependent exchange (Thr-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-threo	SLC1A5	Transport, extracellular			4
THRCYSNaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	THRCYSNaEx	L-cysteine/L-threonine Na-dependent exchange (Thr-L in)	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-threon	SLC1A4; SL	Transport, extracellular			4
THRSERNaEx_pos	9	0.080856	1.0922877	3.151917	3.151917	1	0.240222	THRSERNaEx	L-serine/L-threonine Na-dependent exchange (Thr-L in)	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-threonine [e]	SLC1A4; SL	Transport, extracellular			4
ThRt4_pos	9	0.080856	1.0922877	2.195997	2.195997	1	0.240222	ThRt4	L-threonine via sodium symport	1.00 * Sodium [e] + 1.00 * L-threonine [e] → 1.00 * Sodium [c]	ACE2; SLC3	Transport, extracellular			4
THYOX12_neg	0	0.080856	1.0922877	-1.89558	1.895578	2	0.240222	THYOX12	T4 transport via facilitated diffusion	1.00 * L-thyroxine [e] → 1.00 * L-thyroxine [c]SLC16A2	SLC16A2	Transport, extracellular			4
THYOX12_pos	0	0.080856	1.0922877	-1.95293	1.952935	2	0.240222	THYOX12	T4 transport via facilitated diffusion	1.00 * L-thyroxine [e] → 1.00 * L-thyroxine [c]SLC16A2	SLC16A2	Transport, extracellular			4
THYOX1_neg	0	0.080856	1.0922877	-1.95293	1.952935	2	0.240222	THYOX1	T4 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * L-thyroxine [e] → 1.00 * B	SLC10A1; S	Transport, extracellular			4
THYOX1_pos	0	0.080856	1.0922877	-1.89558	1.895578	2	0.240222	THYOX1	T4 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * L-thyroxine [e] → 1.00 * B	SLC10A1; S	Transport, extracellular			4
TRIODTHY2_neg	0	0.080856	1.0922877	-1.94365	1.943647	2	0.240222	TRIODTHY2	T3 transport via facilitated diffusion	1.00 * 3,3',5'-triiodo-L-thyronine [e] → 1.00 * 3,3',5'-tri	SLC16A2	Transport, extracellular			4
TRIODTHY2_pos	0	0.080856	1.0922877	-2.00456	2.004563	2	0.240222	TRIODTHY2	T3 transport via facilitated diffusion	1.00 * 3,3',5'-triiodo-L-thyronine [e] → 1.00 * 3,3',5'-tri	SLC16A2	Transport, extracellular			4
TRIODTHY_neg	0	0.080856	1.0922877	-2.00456	2.004563	2	0.240222	TRIODTHY	T3 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * 3,3',5'-triiodo-L-thyronine [e]	SLC10A1; S	Transport, extracellular			4
TRIODTHY_pos	0	0.080856	1.0922877	-1.94365	1.943647	2	0.240222	TRIODTHY	T3 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * 3,3',5'-triiodo-L-thyronine [e]	SLC10A1; S	Transport, extracellular			4
TRP1_neg	9	0.080856	1.0922877	2.352854	2.352854	1	0.240222	TRP1	L-tryptophan transport	1.00 * L-tryptophan [e] → 1.00 * L-tryptophan [c]SLC16A	SLC16A10; S	Transport, extracellular			4
TRP1_pos	9	0.080856	1.0922877	2.352854	2.352854	1	0.240222	TRP1	L-tryptophan transport	1.00 * L-tryptophan [e] → 1.00 * L-tryptophan [c]SLC16A	SLC16A10; S	Transport, extracellular			4
VALtec_neg	9	0.080856	1.0922877	2.477097	2.477097	1	0.240222	VALtec	L-valine transport via diffusion (extracellular to cytosol)	1.00 * L-valine [e] → 1.00 * L-valine [c]SLC43A1; SLC43A2	SLC43A1; S	Transport, extracellular			4
VALtec_pos	9	0.080856	1.0922877	2.477097	2.477097	1	0.240222	VALtec	L-valine transport via diffusion (extracellular to cytosol)	1.00 * L-valine [e] → 1.00 * L-valine [c]SLC43A1; SLC43A2	SLC43A1; S	Transport, extracellular			4
r0817_neg	9	0.080856	1.0922877	2.739064	2.739064	1	0.240222	r0817	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.2	1.00 * L-citrulline [c] → 1.00 * L-citrulline [e]SLC7A2	SLC7A2	Transport, extracellular			0
r0817_pos	9	0.080856	1.0922877	2.12943	2.129425	2	0.240222	r0817	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.2	1.00 * L-citrulline [c] → 1.00 * L-citrulline [e]SLC7A2	SLC7A2	Transport, extracellular			0
r0946_neg	9	0.080856	1.0922877	2.610324	2.610324	1	0.240222	r0946	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.15	1.00 * L-citrulline [c] + 1.00 * Ornithine [e] → 1.00 * Orn	SLC7A9	Transport, extracellular			0
r0946_pos	9	0.080856	1.0922877	2.937499	2.937499	1	0.240222	r0946	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.15	1.00 * L-citrulline [c] + 1.00 * Ornithine [e] → 1.00 * Orn	SLC7A9	Transport, extracellular			0
r0992_neg	0	0.080856	1.0922877	-1.29975	1.299745	2	0.240222	r0992	Na(+)/bile acid cotransporter Active transport	1.00 * glycocholate [e] + 1.00 * Lepididoide [e] → 1.00 *	SLC10A1	Transport, extracellular			0
r0992_pos	0	0.080856	1.0922877	-1.43197	1.431969	2	0.240222	r0992	Na(+)/bile acid cotransporter Active transport	1.00 * glycocholate [e] + 1.00 * Lepididoide [e] → 1.00 *	SLC10A1	Transport, extracellular			0
r1027_neg	0	0.080856	1.0922877	-1.43197	1.431969	2	0.240222	r1027	Active transport	1.00 * glycochenodeoxycholate [e] + 1.00 * Lepididoide	1.00 * glyc	Transport, extracellular			0
r1027_pos	0	0.080856	1.0922877	-1.29975	1.299745	2	0.240222	r1027	Active transport	1.00 * glycochenodeoxycholate [e] + 1.00 * Lepididoide	1.00 * glyc	Transport, extracellular			0
r1043_pos	0	0.080856	1.0922877	-2.81968	2.819676	2	0.240222	r1043	Concentrative Nucleoside Transporter (CNT) TCDB:2.A.41.2.3	1.00 * Sodium [e] + 1.00 * 2-deoxyadenosine [e] → 1.00 *	SLC28A1; S	Transport, extracellular			0
r1044_pos	0	0.080856	1.0922877	-2.81968	2.819676	2	0.240222	r1044	Concentrative Nucleoside Transporter (CNT) TCDB:2.A.41.2.3	1.00 * Sodium [e] + 1.00 * Deoxycytidine [e] → 1.00 * Sod	SLC28A1; S	Transport, extracellular			0
r1498_pos	0	0.080856	1.0922877	-2.63559	2.635594	2	0.240222	r1498	Glycoside-Pentose-Hexuronide (GPH) Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * glycochenodeoxycholate [e] →	SLC10A1	Transport, extracellular			0
r1544_neg	9	0.080856	1.0922877	2.191991	2.191991	1	0.240222	r1544	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [c] + 1.00 * Glycine [e] → 1.00 * L-glut	SLC7A5	Transport, extracellular			0
r1546_pos	9	0.080856	1.0922877	2.605207	2.605207	1	0.240222	r1546	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-methionine [c] → 1.00 * Glyc	SLC7A5	Transport, extracellular			0
r1547_neg	9	0.080856	1.0922877	2.067733	2.067733	1	0.240222	r1547	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-tryptophan [c] → 1.00 * Glyc	SLC7A5	Transport, extracellular			0
r1547_pos	9	0.080856	1.0922877	2.27118	2.27118	1	0.240222	r1547	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-tryptophan [c] → 1.00 * Glyc	SLC7A5	Transport, extracellular			0
r1548_neg	9	0.080856	1.0922877	2.08185	2.08185	1	0.240222	r1548	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-phenylalanine [c] → 1.00 * G	SLC7A5	Transport, extracellular			0
r1548_pos	9	0.080856	1.0922877	3.055923	3.055923	1	0.240222	r1548	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-phenylalanine [c] → 1.00 * G	SLC7A5	Transport, extracellular			0
r1549_neg	9	0.080856	1.0922877	2.067733	2.067733	1	0.240222	r1549	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-tyrosine [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1549_pos	9	0.080856	1.0922877	2.090819	2.090819	1	0.240222	r1549	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-tyrosine [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1551_neg	9	0.080856	1.0922877	2.022618	2.022618	1	0.240222	r1551	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-leucine [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1551_pos	9	0.080856	1.0922877	2.605207	2.605207	1	0.240222	r1551	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-leucine [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1552_neg	9	0.080856	1.0922877	2.156029	2.156029	1	0.240222	r1552	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-proline [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1552_pos	9	0.080856	1.0922877	2.133601	2.133601	1	0.240222	r1552	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-proline [c] → 1.00 * Glycine	SLC7A5	Transport, extracellular			0
r1553_neg	9	0.080856	1.0922877	2.072464	2.072464	1	0.240222	r1553	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * Glycine [e] → 1.00 * L-as	SLC7A5	Transport, extracellular			0
r1553_pos															

1566	neg	9	0.080856	1.0922877	2.666195	2.666195	1	0.240222	1566	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-proline [c] -> 1.00 * L-alanin	SLC7A5	Transport, extracellular						0
1566	pos	9	0.080856	1.0922877	2.958855	2.958855	1	0.240222	1566	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-proline [c] -> 1.00 * L-alanin	SLC7A5	Transport, extracellular						0
1568	neg	9	0.080856	1.0922877	2.30644	2.30644	1	0.240222	1568	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-valine [c] -> 1.00 * L-alanine	SLC7A5	Transport, extracellular						0
1568	pos	9	0.080856	1.0922877	3.821305	3.821305	1	0.240222	1568	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-valine [c] -> 1.00 * L-alanine	SLC7A5	Transport, extracellular						0
1569	neg	9	0.080856	1.0922877	2.691027	2.691027	1	0.240222	1569	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-threonine [c] -> 1.00 * L-alan	SLC7A5	Transport, extracellular						0
1569	pos	9	0.080856	1.0922877	2.763417	2.763417	1	0.240222	1569	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-threonine [c] -> 1.00 * L-alan	SLC7A5	Transport, extracellular						0
1570	neg	9	0.080856	1.0922877	2.306891	2.306891	1	0.240222	1570	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-al	SLC7A5	Transport, extracellular						0
1570	pos	9	0.080856	1.0922877	2.695255	2.695255	1	0.240222	1570	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-al	SLC7A5	Transport, extracellular						0
1571	neg	9	0.080856	1.0922877	2.30644	2.30644	1	0.240222	1571	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-alan	SLC7A5	Transport, extracellular						0
1571	pos	9	0.080856	1.0922877	3.821305	3.821305	1	0.240222	1571	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-alan	SLC7A5	Transport, extracellular						0
1573	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1573	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-methionine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1575	neg	9	0.080856	1.0922877	1.968055	1.968055	1	0.240222	1575	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-phenylalanine [c] -> 1.00	SLC7A5	Transport, extracellular						0
1575	pos	9	0.080856	1.0922877	1.968055	1.968055	1	0.240222	1575	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-phenylalanine [c] -> 1.00	SLC7A5	Transport, extracellular						0
1578	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1578	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-leucine [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1578	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1578	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-leucine [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1579	neg	9	0.080856	1.0922877	2.40533	2.40533	1	0.240222	1579	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-proline [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1579	pos	9	0.080856	1.0922877	2.404344	2.404344	1	0.240222	1579	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-proline [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1581	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1581	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-valine [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1581	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1581	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-valine [c] -> 1.00 * L-gl	SLC7A5	Transport, extracellular						0
1583	neg	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1583	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-homoserine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1583	pos	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1583	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-homoserine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1584	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1584	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1584	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1584	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1585	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1585	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-methionine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1587	neg	9	0.080856	1.0922877	1.968055	1.968055	1	0.240222	1587	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-phenylalanine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1587	pos	9	0.080856	1.0922877	1.968055	1.968055	1	0.240222	1587	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-phenylalanine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1589	neg	9	0.080856	1.0922877	0.047343	0.047343	1	0.240222	1589	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-serine [e] -> 1.00 * L-cyste	SLC7A5	Transport, extracellular						0
1589	pos	9	0.080856	1.0922877	0.993375	0.993375	1	0.240222	1589	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-serine [e] -> 1.00 * L-cyste	SLC7A5	Transport, extracellular						0
1590	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1590	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-leucine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1590	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1590	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-leucine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1591	neg	9	0.080856	1.0922877	2.40533	2.40533	1	0.240222	1591	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-proline [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1591	pos	9	0.080856	1.0922877	2.306891	2.306891	1	0.240222	1591	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-proline [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1592	neg	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1592	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-serine [e] -> 1.00 * L-as	SLC7A5	Transport, extracellular						0
1592	pos	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1592	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-serine [e] -> 1.00 * L-as	SLC7A5	Transport, extracellular						0
1593	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1593	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-valine [c] -> 1.00 * L-serine	SLC7A5	Transport, extracellular						0
1593	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1593	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-valine [c] -> 1.00 * L-serine	SLC7A5	Transport, extracellular						0
1594	neg	9	0.080856	1.0922877	2.123095	2.123095	1	0.240222	1594	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-threonine [c] -> 1.00 * L-seri	SLC7A5	Transport, extracellular						0
1594	pos	9	0.080856	1.0922877	2.123095	2.123095	1	0.240222	1594	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-threonine [c] -> 1.00 * L-seri	SLC7A5	Transport, extracellular						0
1595	neg	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1595	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-se	SLC7A5	Transport, extracellular						0
1595	pos	9	0.080856	1.0922877	0.004175	0.004175	1	0.240222	1595	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-se	SLC7A5	Transport, extracellular						0
1596	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1596	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1596	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1596	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1596	pos	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1596	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-ser	SLC7A5	Transport, extracellular						0
1597	pos	9	0.080856	1.0922877	3.132677	3.132677	1	0.240222	1597	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-tryptophan [c] -> 1.00	SLC7A5	Transport, extracellular						0
1598	neg	9	0.080856	1.0922877	1.988084	1.988084	1	0.240222	1598	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-phenylalanine [c] -> 1.0	SLC7A5	Transport, extracellular						0
1599	pos	9	0.080856	1.0922877	2.961327	2.961327	1	0.240222	1599	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1602	neg	9	0.080856	1.0922877	2.411045	2.411045	1	0.240222	1602	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-proline [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1602	pos	9	0.080856	1.0922877	0.402755	0.402755	1	0.240222	1602	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-proline [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1603	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1603	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-methionine [e] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1604	neg	9	0.080856	1.0922877	2.046774	2.046774	1	0.240222	1604	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-valine [c] -> 1.00 * L-m	SLC7A5	Transport, extracellular						0
1604	pos	9	0.080856	1.0922877	3.104513	3.104513	1	0.240222	1604	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-valine [c] -> 1.00 * L-m	SLC7A5	Transport, extracellular						0
1605	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1605	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-methionine [e] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1606	neg	9	0.080856	1.0922877	0.25473	0.25473	1	0.240222	1606	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5	Transport, extracellular						0
1607	neg	9	0.080856	1.0922877	2.046774	2.046774	1	0.240222	1607	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1607	pos	9	0.080856	1.0922877	3.104513	3.104513	1	0.240222	1607	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1610	neg	9	0.080856	1.0922877	4.381375	4.381375	1	0.240222	1610	Amino Acid-Polyamine-Organization (APC) TCDB.2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-tryptophan [e] -> 1.00 * L	SLC7A5	Transport, extracellular						0
1610	pos	9	0.080856	1.0922877	1.886905	1													

1650_pos	9	0.080856	1.0922877	2.306891	2.306891	1	0.240222	1650	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-proline [e] -> 1.00 * L-thr	SLC7A5	Transport, extracellular				0
1650_pos	9	0.080856	1.0922877	2.40533	2.40533	1	0.240222	1650	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-proline [e] -> 1.00 * L-thr	SLC7A5	Transport, extracellular				0
1651_neg	9	0.080856	1.0922877	2.306891	2.306891	1	0.240222	1651	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-proline [e] + 1.00 * L-homoserine [c] -> 1.00 * L-h	SLC7A5	Transport, extracellular				0
1651_pos	9	0.080856	1.0922877	2.40533	2.40533	1	0.240222	1651	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-proline [e] + 1.00 * L-homoserine [c] -> 1.00 * L-h	SLC7A5	Transport, extracellular				0
1652_neg	9	0.080856	1.0922877	2.30644	2.30644	1	0.240222	1652	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-proline [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5	Transport, extracellular				0
1652_pos	9	0.080856	1.0922877	2.411045	2.411045	1	0.240222	1652	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-proline [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5	Transport, extracellular				0
1653_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1653	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-valine [c] -> 1.00 * L-as	SLC7A5	Transport, extracellular				0
1653_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1653	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-valine [c] -> 1.00 * L-as	SLC7A5	Transport, extracellular				0
1654_neg	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1654	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-threonine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1654_pos	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1654	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-threonine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1655_neg	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1655	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1655_pos	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1655	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1656_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1656	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1656_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1656	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-asparagine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1657_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1657	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-valine [e] -> 1.00 * L-thr	SLC7A5	Transport, extracellular				0
1657_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1657	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-valine [e] -> 1.00 * L-thr	SLC7A5	Transport, extracellular				0
1658_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1658	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-valine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-h	SLC7A5	Transport, extracellular				0
1658_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1658	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-valine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-h	SLC7A5	Transport, extracellular				0
1659_neg	9	0.080856	1.0922877	2.046774	2.046774	1	0.240222	1659	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-valine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5	Transport, extracellular				0
1659_pos	9	0.080856	1.0922877	2.046774	2.046774	1	0.240222	1659	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-valine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5	Transport, extracellular				0
1660_neg	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1660	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1660_pos	9	0.080856	1.0922877	2.004175	2.004175	1	0.240222	1660	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1661_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1661	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1661_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1661	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-threonine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L	SLC7A5	Transport, extracellular				0
1662_neg	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1662	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-homoserine [e] + 1.00 * L-isoleucine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1662_pos	9	0.080856	1.0922877	2.025473	2.025473	1	0.240222	1662	Amino Acid-Polyamine-Organocation (APC) TCDB.2.A.3.8.1	1.00 * L-homoserine [e] + 1.00 * L-isoleucine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1664_neg	9	0.080856	1.0922877	2.814368	2.814368	1	0.240222	1664	Y-LAT2 Utilized transport	1.00 * L-homoserine [e] + 1.00 * L-isoleucine [c] -> 1.00	SLC7A5	Transport, extracellular				0
1664_pos	9	0.080856	1.0922877	3.031531	3.031531	1	0.240222	1664	Y-LAT2 Utilized transport	1.00 * Ornithine [c] + 1.00 * L-lysine [1+] [e] -> 1.00 * L	SLC7A6	Transport, extracellular				0
1665_neg	9	0.080856	1.0922877	2.465985	2.465985	1	0.240222	1665	Y-LAT2 Utilized transport	1.00 * Ornithine [c] + 1.00 * L-lysine [1+] [e] -> 1.00 * L	SLC7A6	Transport, extracellular				0
1665_pos	9	0.080856	1.0922877	2.577006	2.577006	1	0.240222	1665	Y-LAT2 Utilized transport	1.00 * L-lysine [1+] [e] + 1.00 * L-histidine [c] -> 1.00	SLC7A6	Transport, extracellular				0
1666_neg	9	0.080856	1.0922877	2.814368	2.814368	1	0.240222	1666	Y-LAT2 Utilized transport	1.00 * L-lysine [1+] [e] + 1.00 * L-histidine [c] -> 1.00	SLC7A6	Transport, extracellular				0
1666_pos	9	0.080856	1.0922877	3.024584	3.024584	1	0.240222	1666	Y-LAT2 Utilized transport	1.00 * L-lysine [1+] [e] + 1.00 * L-citrulline [c] -> 1.00	SLC7A6	Transport, extracellular				0
1667_neg	9	0.080856	1.0922877	2.773087	2.773087	1	0.240222	1667	Y-LAT2 Utilized transport	1.00 * L-lysine [1+] [e] + 1.00 * L-citrulline [c] -> 1.00	SLC7A6	Transport, extracellular				0
1667_pos	9	0.080856	1.0922877	2.604285	2.604285	1	0.240222	1667	Y-LAT2 Utilized transport	1.00 * Ornithine [c] + 1.00 * L-arginine [1+] [e] -> 1.00	SLC7A6	Transport, extracellular				0
1668_neg	9	0.080856	1.0922877	2.465985	2.465985	1	0.240222	1668	Y-LAT2 Utilized transport	1.00 * Ornithine [c] + 1.00 * L-arginine [1+] [e] -> 1.00	SLC7A6	Transport, extracellular				0
1668_pos	9	0.080856	1.0922877	2.508715	2.508715	1	0.240222	1668	Y-LAT2 Utilized transport	1.00 * L-arginine [1+] [e] + 1.00 * L-histidine [c] -> 1.00	SLC7A6	Transport, extracellular				0
1669_neg	9	0.080856	1.0922877	2.773087	2.773087	1	0.240222	1669	Y-LAT2 Utilized transport	1.00 * L-arginine [1+] [e] + 1.00 * L-histidine [c] -> 1.00	SLC7A6	Transport, extracellular				0
1669_pos	9	0.080856	1.0922877	2.880757	2.880757	1	0.240222	1669	Y-LAT2 Utilized transport	1.00 * L-arginine [1+] [e] + 1.00 * L-citrulline [c] -> 1.00	SLC7A6	Transport, extracellular				0
1670_neg	9	0.080856	1.0922877	2.39885	2.39885	1	0.240222	1670	Y-LAT2 Utilized transport	1.00 * Ornithine [e] + 1.00 * L-histidine [c] -> 1.00 * Orn	SLC7A6	Transport, extracellular				0
1670_pos	9	0.080856	1.0922877	2.812316	2.812316	1	0.240222	1670	Y-LAT2 Utilized transport	1.00 * Ornithine [e] + 1.00 * L-histidine [c] -> 1.00 * Orn	SLC7A6	Transport, extracellular				0
1671_neg	9	0.080856	1.0922877	2.812316	2.812316	1	0.240222	1671	Y-LAT2 Utilized transport	1.00 * L-citrulline [c] + 1.00 * L-histidine [e] -> 1.00 * L-h	SLC7A6	Transport, extracellular				0
1671_pos	9	0.080856	1.0922877	2.272751	2.272751	1	0.240222	1671	Y-LAT2 Utilized transport	1.00 * L-citrulline [c] + 1.00 * L-histidine [e] -> 1.00 * L-h	SLC7A6	Transport, extracellular				0
1672_pos	9	0.080856	1.0922877	2.3904	2.3904	1	0.240222	1672	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * Glycine [e]	SLC7A6	Transport, extracellular				0
1673_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1673	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * Glycine [e]	SLC7A6	Transport, extracellular				0
1674_pos	9	0.080856	1.0922877	2.3904	2.3904	1	0.240222	1674	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-serine [c]	SLC7A6	Transport, extracellular				0
1675_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1675	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular				0
1676_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1676	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular				0
1677_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1677	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular				0
1678_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1678	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular				0
1679_pos	9	0.080856	1.0922877	2.459877	2.459877	1	0.240222	1679	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * Glycine [c]	SLC7A6	Transport, extracellular				0
1680_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1680	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular				0
1681_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1681	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular				0
1682_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1682	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * Glycine [c]	SLC7A6	Transport, extracellular				0
1683_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1683	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular				0
1684_pos	9	0.080856	1.0922877	2.3904	2.3904	1	0.240222	1684	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-threonine [c]	SLC7A6	Transport, extracellular				0
1685_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1685	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular				0
1686_pos	9	0.080856	1.0922877	2.44266	2.44266	1	0.240222	1686	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular				0
1687_pos	9	0.080856	1.0922877	2.3904	2.3904	1	0.240222	1687	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * Glycine [c]	SLC7A6	Transport, extracellular				0
1690_pos	9	0.080856	1.0922877	2.834972	2.834972	1	0.240222	1690	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular				0
1691_pos	9	0.080856	1.0922877	3.009969	3.009969	1	0.240222	1691	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular				0
1692_pos	9	0.080856	1.0922877	2.822181	2.822181	1	0.240222	1692	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular				0
1693_pos	9	0.080856	1.0922877	3.131513	3.131513	1	0.240222	1693	Y-LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular				0
1695_pos	9	0.080856	1.0922877	2.834972	2.834972	1	0.240222	1695	Y-LAT2 Utilized transport							

r1726_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1726	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular	0
r1728_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1728	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular	0
r1730_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1730	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular	0
r1731_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1731	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1732_pos	9	0.080856	1.0922877	3.37221	3.37221	1	0.240222	r1732	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1733_pos	9	0.080856	1.0922877	2.743461	2.743461	1	0.240222	r1733	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1734_pos	9	0.080856	1.0922877	2.912398	2.912398	1	0.240222	r1734	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1735_pos	9	0.080856	1.0922877	2.912398	2.912398	1	0.240222	r1735	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1736_pos	9	0.080856	1.0922877	2.99593	2.99593	1	0.240222	r1736	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1737_pos	9	0.080856	1.0922877	2.949743	2.949743	1	0.240222	r1737	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1738_pos	9	0.080856	1.0922877	2.97248	2.97248	1	0.240222	r1738	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1739_pos	9	0.080856	1.0922877	3.442199	3.442199	1	0.240222	r1739	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1740_pos	9	0.080856	1.0922877	2.907355	2.907355	1	0.240222	r1740	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular	0
r1741_pos	9	0.080856	1.0922877	2.743461	2.743461	1	0.240222	r1741	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular	0
r1742_pos	9	0.080856	1.0922877	2.912398	2.912398	1	0.240222	r1742	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1743_pos	9	0.080856	1.0922877	2.907355	2.907355	1	0.240222	r1743	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular	0
r1744_pos	9	0.080856	1.0922877	2.912398	2.912398	1	0.240222	r1744	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1745_pos	9	0.080856	1.0922877	2.912398	2.912398	1	0.240222	r1745	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular	0
r1746_pos	9	0.080856	1.0922877	2.907355	2.907355	1	0.240222	r1746	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1747_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1747	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1748_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1748	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1749_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1749	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1750_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1750	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1751_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1751	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1752_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1752	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1753_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1753	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1754_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1754	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1755_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1755	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular	0
r1756_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1756	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular	0
r1757_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1757	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1758_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1758	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular	0
r1759_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1759	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1760_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1760	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular	0
r1761_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1761	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1762_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1762	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1763_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1763	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1764_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1764	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1765_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1765	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1766_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1766	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1767_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1767	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular	0
r1768_pos	9	0.080856	1.0922877	3.054027	3.054027	1	0.240222	r1768	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-threonine [c]	SLC7A6	Transport, extracellular	0
r1769_pos	9	0.080856	1.0922877	3.515568	3.515568	1	0.240222	r1769	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1770_pos	9	0.080856	1.0922877	2.97239	2.97239	1	0.240222	r1770	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1771_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1771	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular	0
r1772_pos	9	0.080856	1.0922877	2.3704	2.3704	1	0.240222	r1772	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1773_pos	9	0.080856	1.0922877	2.97239	2.97239	1	0.240222	r1773	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular	0
r1774_pos	9	0.080856	1.0922877	2.978131	2.978131	1	0.240222	r1774	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1775_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1775	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular	0
r1776_pos	9	0.080856	1.0922877	2.97239	2.97239	1	0.240222	r1776	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1777_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1777	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1778_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1778	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1779_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1779	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1780_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1780	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1781_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1781	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1782_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1782	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1783_pos	9	0.080856	1.0922877	3.546102	3.546102	1	0.240222	r1783	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1784_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1784	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1785_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1785	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular	0
r1786_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1786	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular	0
r1787_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1787	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1788_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1788	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular	0
r1789_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1789	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-tyrosine [c]	SLC7A6	Transport, extracellular	0
r1790_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1790	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-homoserine [c]	SLC7A6	Transport, extracellular	0
r1791_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1791	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-isoleucine [c]	SLC7A6	Transport, extracellular	0
r1792_pos	9	0.080856	1.0922877	2.459877	2.459877	1	0.240222	r1792	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * Glycine [c]	SLC7A6	Transport, extracellular	0
r1796_pos	9	0.080856	1.0922877	2.907355	2.907355	1	0.240222	r1796	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-methionine [c]	SLC7A6	Transport, extracellular	0
r1797_pos	9	0.080856	1.0922877	2.99593	2.99593	1	0.240222	r1797	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-tryptophan [c]	SLC7A6	Transport, extracellular	0
r1798_pos	9	0.080856	1.0922877	2.949743	2.949743	1	0.240222	r1798	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-phenylalanine [c]	SLC7A6	Transport, extracellular	0
r1799_pos	9	0.080856	1.0922877	2.97248	2.97248	1	0.240222	r1799	Y+LAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] +			

r1816_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1816	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-leucine [e] + 1.00 * L-proline	SLC7A6	Transport, extracellular				0
r1817_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1817	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-leuci	SLC7A6	Transport, extracellular				0
r1818_pos	9	0.080856	1.0922877	3.032817	3.032817	1	0.240222	r1818	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-leucine [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular				0
r1819_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1819	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-leucin	SLC7A6	Transport, extracellular				0
r1820_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1820	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-leucine [e] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1821_pos	9	0.080856	1.0922877	3.032817	3.032817	1	0.240222	r1821	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-leucine [e] + 1.00 * L-isoleucin	SLC7A6	Transport, extracellular				0
r1822_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1822	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-proline [e]	SLC7A6	Transport, extracellular				0
r1823_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1823	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-proline	SLC7A6	Transport, extracellular				0
r1824_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1824	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-proli	SLC7A6	Transport, extracellular				0
r1825_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1825	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-proline [e]	SLC7A6	Transport, extracellular				0
r1826_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1826	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-pro	SLC7A6	Transport, extracellular				0
r1827_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1827	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-tryptoph	SLC7A6	Transport, extracellular				0
r1828_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1828	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-phenyla	SLC7A6	Transport, extracellular				0
r1829_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1829	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-tyrosine	SLC7A6	Transport, extracellular				0
r1830_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1830	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-proline	SLC7A6	Transport, extracellular				0
r1831_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1831	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-leucine	SLC7A6	Transport, extracellular				0
r1832_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1832	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-proli	SLC7A6	Transport, extracellular				0
r1833_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1833	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-valine [c]	SLC7A6	Transport, extracellular				0
r1834_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1834	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-proli	SLC7A6	Transport, extracellular				0
r1835_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1835	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1836_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1836	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-isoleuci	SLC7A6	Transport, extracellular				0
r1837_pos	9	0.080856	1.0922877	3.61083	3.61083	1	0.240222	r1837	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * Glycin	SLC7A6	Transport, extracellular				0
r1841_pos	9	0.080856	1.0922877	3.272606	3.272606	1	0.240222	r1841	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-meth	SLC7A6	Transport, extracellular				0
r1842_pos	9	0.080856	1.0922877	2.724286	2.724286	1	0.240222	r1842	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-trypt	SLC7A6	Transport, extracellular				0
r1843_pos	9	0.080856	1.0922877	2.704224	2.704224	1	0.240222	r1843	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-phen	SLC7A6	Transport, extracellular				0
r1844_pos	9	0.080856	1.0922877	3.74619	3.74619	1	0.240222	r1844	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-tyros	SLC7A6	Transport, extracellular				0
r1846_pos	9	0.080856	1.0922877	3.272606	3.272606	1	0.240222	r1846	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-leuci	SLC7A6	Transport, extracellular				0
r1847_pos	9	0.080856	1.0922877	3.361208	3.361208	1	0.240222	r1847	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-proli	SLC7A6	Transport, extracellular				0
r1848_pos	9	0.080856	1.0922877	3.272606	3.272606	1	0.240222	r1848	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-valin	SLC7A6	Transport, extracellular				0
r1850_pos	9	0.080856	1.0922877	3.276495	3.276495	1	0.240222	r1850	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-hom	SLC7A6	Transport, extracellular				0
r1851_pos	9	0.080856	1.0922877	3.272606	3.272606	1	0.240222	r1851	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-isole	SLC7A6	Transport, extracellular				0
r1852_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1852	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular				0
r1853_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1853	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular				0
r1854_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1854	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-valine	SLC7A6	Transport, extracellular				0
r1855_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1855	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular				0
r1856_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1856	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-vali	SLC7A6	Transport, extracellular				0
r1857_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1857	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-tryptoph	SLC7A6	Transport, extracellular				0
r1858_pos	9	0.080856	1.0922877	3.080632	3.080632	1	0.240222	r1858	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-phenylala	SLC7A6	Transport, extracellular				0
r1859_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1859	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-tyrosine	SLC7A6	Transport, extracellular				0
r1860_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1860	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular				0
r1861_pos	9	0.080856	1.0922877	3.037857	3.037857	1	0.240222	r1861	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-leucine [c]	SLC7A6	Transport, extracellular				0
r1862_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1862	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-proline [c]	SLC7A6	Transport, extracellular				0
r1863_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1863	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-valin	SLC7A6	Transport, extracellular				0
r1864_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1864	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-valine	SLC7A6	Transport, extracellular				0
r1865_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1865	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1866_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1866	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-valine [e] + 1.00 * L-isoleucin	SLC7A6	Transport, extracellular				0
r1867_pos	9	0.080856	1.0922877	2.3904	2.3904	1	0.240222	r1867	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-threonine	SLC7A6	Transport, extracellular				0
r1871_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1871	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-meth	SLC7A6	Transport, extracellular				0
r1872_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1872	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-trypt	SLC7A6	Transport, extracellular				0
r1873_pos	9	0.080856	1.0922877	3.094535	3.094535	1	0.240222	r1873	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-phen	SLC7A6	Transport, extracellular				0
r1874_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1874	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-tyros	SLC7A6	Transport, extracellular				0
r1876_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1876	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-leucin	SLC7A6	Transport, extracellular				0
r1877_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1877	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-proli	SLC7A6	Transport, extracellular				0
r1879_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1879	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-valine	SLC7A6	Transport, extracellular				0
r1880_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1880	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-hom	SLC7A6	Transport, extracellular				0
r1881_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1881	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [e] + 1.00 * L-isole	SLC7A6	Transport, extracellular				0
r1882_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1882	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [c] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1883_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1883	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1884_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1884	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-hom	SLC7A6	Transport, extracellular				0
r1885_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1885	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [c] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1886_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1886	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [c] + 1.00 * L-hom	SLC7A6	Transport, extracellular				0
r1887_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1887	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-homoserine [e] + 1.00 * L-try	SLC7A6	Transport, extracellular				0
r1888_pos	9	0.080856	1.0922877	2.854938	2.854938	1	0.240222	r1888	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-homoserine [e] + 1.00 * L-ph	SLC7A6	Transport, extracellular				0
r1889_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1889	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-homoserine [e] + 1.00 * L-tyr	SLC7A6	Transport, extracellular				0
r1890_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1890	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-homoser	SLC7A6	Transport, extracellular				0
r1891_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	r1891	YsLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-homoserine [e] + 1.0						

1909_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	1909	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-isoleucine [e] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular					0
1910_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	1910	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-threonine [c] + 1.00 * L-isoleucine [e]	SLC7A6	Transport, extracellular					0
1911_pos	9	0.080856	1.0922877	1.444266	1.444266	1	0.240222	1911	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-isoleucine [e] + 1.00 * L-homoserine [e]	SLC7A6	Transport, extracellular					0
1912_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1912	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1913_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1913	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1914_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1914	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * Glycine [e]	SLC7A6	Transport, extracellular					0
1915_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1915	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1916_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1916	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * L-citrulline [e]	SLC7A6	Transport, extracellular					0
1917_pos	9	0.080856	1.0922877	2.679384	2.679384	1	0.240222	1917	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1918_pos	9	0.080856	1.0922877	2.679384	2.679384	1	0.240222	1918	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1919_pos	9	0.080856	1.0922877	2.65646	2.65646	1	0.240222	1919	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-alanine [e]	SLC7A6	Transport, extracellular					0
1920_pos	9	0.080856	1.0922877	2.695763	2.695763	1	0.240222	1920	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1921_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1921	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-citrulline [e]	SLC7A6	Transport, extracellular					0
1922_pos	9	0.080856	1.0922877	2.538532	2.538532	1	0.240222	1922	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1923_pos	9	0.080856	1.0922877	2.538532	2.538532	1	0.240222	1923	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1924_pos	9	0.080856	1.0922877	2.525797	2.525797	1	0.240222	1924	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-glutamine [e]	SLC7A6	Transport, extracellular					0
1925_pos	9	0.080856	1.0922877	2.545382	2.545382	1	0.240222	1925	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1926_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1926	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-citrulline [e]	SLC7A6	Transport, extracellular					0
1928_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1928	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1929_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1929	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-serine [e]	SLC7A6	Transport, extracellular					0
1930_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1930	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1931_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1931	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * L-citrulline [e]	SLC7A6	Transport, extracellular					0
1932_pos	9	0.080856	1.0922877	2.885731	2.885731	1	0.240222	1932	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-methionine [e]	SLC7A6	Transport, extracellular					0
1933_pos	9	0.080856	1.0922877	2.885731	2.885731	1	0.240222	1933	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1934_pos	9	0.080856	1.0922877	2.854084	2.854084	1	0.240222	1934	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-methionine [e]	SLC7A6	Transport, extracellular					0
1935_pos	9	0.080856	1.0922877	2.90081	2.90081	1	0.240222	1935	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-methionine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1936_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1936	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-methionine [e]	SLC7A6	Transport, extracellular					0
1937_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1937	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-tryptophan [e]	SLC7A6	Transport, extracellular					0
1938_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1938	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1939_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1939	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-tryptophan [e]	SLC7A6	Transport, extracellular					0
1940_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1940	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tryptophan [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1941_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1941	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-tryptophan [e]	SLC7A6	Transport, extracellular					0
1942_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1942	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-phenylalanine [e]	SLC7A6	Transport, extracellular					0
1943_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1943	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1944_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1944	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-phenylalanine [e]	SLC7A6	Transport, extracellular					0
1945_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1945	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1946_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1946	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-phenylalanine [e]	SLC7A6	Transport, extracellular					0
1947_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1947	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-tryptophan [e]	SLC7A6	Transport, extracellular					0
1948_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1948	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1949_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1949	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-tyrosine [e]	SLC7A6	Transport, extracellular					0
1950_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1950	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-tyrosine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1951_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1951	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-tyrosine [e]	SLC7A6	Transport, extracellular					0
1952_pos	9	0.080856	1.0922877	2.885731	2.885731	1	0.240222	1952	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1953_pos	9	0.080856	1.0922877	2.885731	2.885731	1	0.240222	1953	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1954_pos	9	0.080856	1.0922877	2.854084	2.854084	1	0.240222	1954	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-cysteine [e]	SLC7A6	Transport, extracellular					0
1955_pos	9	0.080856	1.0922877	2.90081	2.90081	1	0.240222	1955	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1956_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1956	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * L-citrulline [c]	SLC7A6	Transport, extracellular					0
1957_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1957	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-leucine [e]	SLC7A6	Transport, extracellular					0
1958_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1958	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1959_pos	9	0.080856	1.0922877	2.660891	2.660891	1	0.240222	1959	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-leucine [e]	SLC7A6	Transport, extracellular					0
1960_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1960	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-leucine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1961_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1961	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-leucine [e]	SLC7A6	Transport, extracellular					0
1962_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1962	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-proline [e]	SLC7A6	Transport, extracellular					0
1963_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1963	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1964_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1964	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-proline [e]	SLC7A6	Transport, extracellular					0
1965_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1965	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-proline [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1966_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1966	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-citrulline [c] + 1.00 * L-proline [e]	SLC7A6	Transport, extracellular					0
1967_pos	9	0.080856	1.0922877	2.538532	2.538532	1	0.240222	1967	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					0
1968_pos	9	0.080856	1.0922877	2.538532	2.538532	1	0.240222	1968	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-arginine [e]	SLC7A6	Transport, extracellular					0
1969_pos	9	0.080856	1.0922877	2.525797	2.525797	1	0.240222	1969	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * Ornithine [c] + 1.00 * L-asparagine [e]	SLC7A6	Transport, extracellular					0
1970_pos	9	0.080856	1.0922877	2.545382	2.545382	1	0.240222	1970	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-histidine [e]	SLC7A6	Transport, extracellular					0
1971_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1971	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-citrulline [c]	SLC7A6	Transport, extracellular					0
1972_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1972	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-lysine [e] + 1.00 * L-valine [e]	SLC7A6	Transport, extracellular					0
1973_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	1973	YvLAT2 Utilized transport	1.00 * Sodium [e] + 1.00 * L-arginine [e] + 1.00 * L-lysine [e]	SLC7A6	Transport, extracellular					

1993_pos	9	0.080856	1.0922877	3.224989	3.224989	1	0.240222	1993	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-alanine [c] + 1.00 * L-lysiumium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
1994_pos	9	0.080856	1.0922877	3.039758	3.039758	1	0.240222	1994	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-glutamine [c] + 1.00 * L-lysiumium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
1996_pos	9	0.080856	1.0922877	3.039849	3.039849	1	0.240222	1996	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-methionine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
1997_pos	9	0.080856	1.0922877	2.957988	2.957988	1	0.240222	1997	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-tryptophan [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
1998_pos	9	0.080856	1.0922877	3.091586	3.091586	1	0.240222	1998	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-phenylalanine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
1999_pos	9	0.080856	1.0922877	2.969658	2.969658	1	0.240222	1999	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-tyrosine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2000_pos	9	0.080856	1.0922877	2.969658	2.969658	1	0.240222	2000	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-cysteine [c] + 1.00 * L-lysiumium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2001_pos	9	0.080856	1.0922877	3.039849	3.039849	1	0.240222	2001	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-leucine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2002_pos	9	0.080856	1.0922877	2.969658	2.969658	1	0.240222	2002	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-proline [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2003_pos	9	0.080856	1.0922877	2.834945	2.834945	1	0.240222	2003	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-asparagine [c] + 1.00 * L-lysiumium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2004_pos	9	0.080856	1.0922877	2.832987	2.832987	1	0.240222	2004	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-valine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2005_pos	9	0.080856	1.0922877	2.834945	2.834945	1	0.240222	2005	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-threonine [c] + 1.00 * L-lysiumium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2006_pos	9	0.080856	1.0922877	2.834945	2.834945	1	0.240222	2006	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2007_pos	9	0.080856	1.0922877	2.832987	2.832987	1	0.240222	2007	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-lysiumium[1+][e] + 1.00 * L-isoleucine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2008_pos	9	0.080856	1.0922877	3.203779	3.203779	1	0.240222	2008	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Glycine [c] + 1.00 * L-argininium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2011_pos	9	0.080856	1.0922877	2.332727	2.332727	1	0.240222	2011	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-serine [c] + 1.00 * L-argininium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2013_pos	9	0.080856	1.0922877	2.417374	2.417374	1	0.240222	2013	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-tryptophan [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2015_pos	9	0.080856	1.0922877	2.508021	2.508021	1	0.240222	2015	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-tyrosine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2016_pos	9	0.080856	1.0922877	2.902113	2.902113	1	0.240222	2016	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-cysteine [c] + 1.00 * L-argininium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2018_pos	9	0.080856	1.0922877	2.949726	2.949726	1	0.240222	2018	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-proline [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2019_pos	9	0.080856	1.0922877	2.22485	2.22485	1	0.240222	2019	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-asparagine [c] + 1.00 * L-argininium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2020_pos	9	0.080856	1.0922877	2.262072	2.262072	1	0.240222	2020	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-valine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2021_pos	9	0.080856	1.0922877	2.33227	2.33227	1	0.240222	2021	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-threonine [c] + 1.00 * L-argininium[1+][e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2022_pos	9	0.080856	1.0922877	2.321032	2.321032	1	0.240222	2022	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2023_pos	9	0.080856	1.0922877	2.262072	2.262072	1	0.240222	2023	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-argininium[1+][e] + 1.00 * L-isoleucine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2024_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	2024	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Glycine [c] + 1.00 * Ornithine [e] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2026_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2026	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-glutamine [c] + 1.00 * Ornithine [e] -> 1.00 * Orn	SLC7A9	Transport, extracellular				0
2027_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2027	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-serine [c] + 1.00 * Ornithine [e] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2028_pos	9	0.080856	1.0922877	2.517151	2.517151	1	0.240222	2028	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-methionine [c] + 1.00 * Ornithine [e] -> 1.00 * Or	SLC7A9	Transport, extracellular				0
2029_pos	9	0.080856	1.0922877	2.588227	2.588227	1	0.240222	2029	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-tryptophan [c] -> 1.00 * Or	SLC7A9	Transport, extracellular				0
2030_pos	9	0.080856	1.0922877	2.526388	2.526388	1	0.240222	2030	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-phenylalanine [c] -> 1.00 * Or	SLC7A9	Transport, extracellular				0
2031_pos	9	0.080856	1.0922877	2.594964	2.594964	1	0.240222	2031	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-tyrosine [c] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2032_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	2032	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-cysteine [c] + 1.00 * Ornithine [e] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2034_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	2034	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-proline [c] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2035_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2035	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-asparagine [c] + 1.00 * Ornithine [e] -> 1.00 * Orn	SLC7A9	Transport, extracellular				0
2036_pos	9	0.080856	1.0922877	2.517151	2.517151	1	0.240222	2036	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-valine [c] -> 1.00 * Ornith	SLC7A9	Transport, extracellular				0
2037_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2037	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-threonine [c] + 1.00 * Ornithine [e] -> 1.00 * Orn	SLC7A9	Transport, extracellular				0
2038_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2038	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-homoserine [c] -> 1.00 * Or	SLC7A9	Transport, extracellular				0
2039_pos	9	0.080856	1.0922877	2.517151	2.517151	1	0.240222	2039	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Ornithine [e] + 1.00 * L-isoleucine [c] -> 1.00 * Orn	SLC7A9	Transport, extracellular				0
2040_pos	9	0.080856	1.0922877	2.176635	2.176635	1	0.240222	2040	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Glycine [c] + 1.00 * L-histidine [e] -> 1.00 * Glycine	SLC7A9	Transport, extracellular				0
2041_pos	9	0.080856	1.0922877	3.225423	3.225423	1	0.240222	2041	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-alanine [c] + 1.00 * L-histidine [e] -> 1.00 * L-alan	SLC7A9	Transport, extracellular				0
2042_pos	9	0.080856	1.0922877	3.22542	3.225423	1	0.240222	2042	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-glutamine [c] + 1.00 * L-histidine [e] -> 1.00 * L-g	SLC7A9	Transport, extracellular				0
2043_pos	9	0.080856	1.0922877	2.219019	2.219019	1	0.240222	2043	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-serine [c] + 1.00 * L-histidine [e] -> 1.00 * L-serin	SLC7A9	Transport, extracellular				0
2044_pos	9	0.080856	1.0922877	2.294707	2.294707	1	0.240222	2044	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-methionine [c] + 1.00 * L-histidine [e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2045_pos	9	0.080856	1.0922877	2.832089	2.832089	1	0.240222	2045	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-tryptophan [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2046_pos	9	0.080856	1.0922877	2.257394	2.257394	1	0.240222	2046	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-phenylalanine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2047_pos	9	0.080856	1.0922877	2.58432	2.58432	1	0.240222	2047	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-tyr	SLC7A9	Transport, extracellular				0
2048_pos	9	0.080856	1.0922877	2.198259	2.198259	1	0.240222	2048	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-cysteine [c] + 1.00 * L-histidine [e] -> 1.00 * L-cys	SLC7A9	Transport, extracellular				0
2049_pos	9	0.080856	1.0922877	2.444748	2.444748	1	0.240222	2049	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-leucine [c] -> 1.00 * L-leuc	SLC7A9	Transport, extracellular				0
2050_pos	9	0.080856	1.0922877	2.425681	2.425681	1	0.240222	2050	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-proline [c] -> 1.00 * L-pro	SLC7A9	Transport, extracellular				0
2051_pos	9	0.080856	1.0922877	3.22542	3.225423	1	0.240222	2051	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-asparagine [c] + 1.00 * L-histidine [e] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2052_pos	9	0.080856	1.0922877	2.444748	2.444748	1	0.240222	2052	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-valine [c] -> 1.00 * L-valin	SLC7A9	Transport, extracellular				0
2053_pos	9	0.080856	1.0922877	2.452797	2.452797	1	0.240222	2053	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-threonine [c] + 1.00 * L-histidine [e] -> 1.00 * L-t	SLC7A9	Transport, extracellular				0
2054_pos	9	0.080856	1.0922877	2.335223	2.335223	1	0.240222	2054	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2055_pos	9	0.080856	1.0922877	2.444748	2.444748	1	0.240222	2055	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-histidine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-	SLC7A9	Transport, extracellular				0
2056_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	2056	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * Glycine [c] + 1.00 * L-citrulline [e] -> 1.00 * Glycine	SLC7A9	Transport, extracellular				0
2057_pos	9	0.080856	1.0922877	2.59361	2.59361	1	0.240222	2057	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-alanine [c] + 1.00 * L-citrulline [e] -> 1.00 * L-alan	SLC7A9	Transport, extracellular				0
2058_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2058	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-glutamine [c] + 1.00 * L-citrulline [e] -> 1.00 * L-g	SLC7A9	Transport, extracellular				0
2059_pos	9	0.080856	1.0922877	2.518744	2.518744	1	0.240222	2059	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-serine [c] + 1.00 * L-citrulline [e] -> 1.00 * L-serin	SLC7A9	Transport, extracellular				0
2060																

r2295_pos	0	0.080856	1.0922877	-2.21417	2.21417	2	0.240222	r2295	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5	1.00 * Bicarbonate [c] + 1.00 * prostaglandin F2alpha[1]	SLCO1B2	Transport, extracellular	0
r2447_pos	0	0.080856	1.0922877	-2.81968	2.819676	2	0.240222	r2447	Concentrative Nucleoside Transporter (CNT) TCDB:2.A.41.2.3	1.00 * Sodium [e] + 1.00 * Deoxyuridine [e] -> 1.00 * Sod	SLC28A1;S	Transport, extracellular	0
r2525_pos	9	0.080856	1.0922877	2.131356	2.131356	1	0.240222	r2525	Major Facilitator (MFS) TCDB:2.A.1.4.4.1	1.00 * L-glutamine [e] -> 1.00 * L-glutamine [c]SLC43A1	SLC43A1	Transport, extracellular	0
r2526_pos	9	0.080856	1.0922877	2.266923	2.266923	1	0.240222	r2526	Major Facilitator (MFS) TCDB:2.A.1.4.4.1	1.00 * L-serine [e] -> 1.00 * L-serine [c]SLC43A1	SLC43A1	Transport, extracellular	0
r2532_pos	9	0.080856	1.0922877	0.092413	2.092413	1	0.240222	r2532	Major Facilitator (MFS) TCDB:2.A.1.4.4.1	1.00 * L-asparagine [e] -> 1.00 * L-asparagine [c]SLC43A1	SLC43A1	Transport, extracellular	0
r2534_pos	9	0.080856	1.0922877	2.266923	2.266923	1	0.240222	r2534	Major Facilitator (MFS) TCDB:2.A.1.4.4.1	1.00 * L-threonine [e] -> 1.00 * L-threonine [c]SLC43A1	SLC43A1	Transport, extracellular	0
3HC03_Nat_neg	1	0.19043	0.7202646	-1.45591	1.455908	2	0.347218	3HC03_NAT		3.00 * Bicarbonate [e] + 1.00 * Sodium [e] -> 3.00 * Bicar	SLC44A4;SL	Transport, extracellular	4
3HC03_Nat_pos	1	0.19043	0.7202646	-1.46297	1.46297	2	0.347218	3HC03_NAT		3.00 * Bicarbonate [e] + 1.00 * Sodium [e] -> 3.00 * Bicar	SLC44A4;SL	Transport, extracellular	4
ACETON1E2_pos	1	0.19043	0.7202646	-1.89059	1.890593	2	0.347218	ACETON1E2	acetone transport via proton symport	1.00 * proton [e] + 1.00 * acetone [e] -> 1.00 * proton [c]	SLC16A1;S	Transport, extracellular	4
ADN1A_pos	1	0.19043	0.7202646	-1.80803	1.808029	2	0.347218	ADN1A	adenosine transport (Na/Adn cotransport)	1.00 * Sodium [e] + 1.00 * Adenosine [e] -> 1.00 * Sodium	SLC28A1;S	Transport, extracellular	4
ADN1_neg	1	0.19043	0.7202646	-1.80803	1.808029	2	0.347218	ADN1	adenosine facilitated transport in cytosol	1.00 * Adenosine [e] -> 1.00 * Adenosine [c]SLC29A1;SLC	SLC29A1;S	Transport, extracellular	4
ADN1_pos	1	0.19043	0.7202646	-1.46943	1.469431	2	0.347218	ADN1	adenosine facilitated transport in cytosol	1.00 * Adenosine [e] -> 1.00 * Adenosine [c]SLC29A1;SLC	SLC29A1;S	Transport, extracellular	4
ALAASNNaEx_pos	8	0.19043	0.7202646	1.240088	1.240088	1	0.347218	ALAASNNaE	L-alanine/L-asparagine Na-dependent exchange (Ala-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-asparagi	SLC1A5	Transport, extracellular	4
ALASERNaEx_pos	8	0.19043	0.7202646	1.908201	1.908201	1	0.347218	ALASERNaE	L-alanine/L-serine Na-dependent exchange (Ala-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-serine [c]	SLC1A4;SL	Transport, extracellular	4
ALATHRNAEx_pos	8	0.19043	0.7202646	1.908201	1.908201	1	0.347218	ALATHRNAE	L-alanine/L-threonine Na-dependent exchange (Ala-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-threonin	SLC1A4;SL	Transport, extracellular	4
ARGTIDF_pos	8	0.19043	0.7202646	1.4084	1.4084	1	0.347218	ARGTIDF	L-arginine transport via diffusion (extracellular to cytosol)	1.00 * L-argininium[1+] [e] -> 1.00 * L-argininium[1+] [c]	SLC38A4;S	Transport, extracellular	4
ASNCYSNaEx_pos	8	0.19043	0.7202646	1.993983	1.993983	1	0.347218	ASNCYSNaE	L-cysteine/L-asparagine Na-dependent exchange (Asn-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-cyste	SLC1A5	Transport, extracellular	4
ASNSERNaEx_pos	8	0.19043	0.7202646	1.515545	1.515545	1	0.347218	ASNSERNaE	L-serine/L-asparagine Na-dependent exchange (Asn-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-serin	SLC1A5	Transport, extracellular	4
ASNTHNaEx_pos	8	0.19043	0.7202646	1.515545	1.515545	1	0.347218	ASNTHNaE	L-threonine/L-asparagine Na-dependent exchange (Asn-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * L-thre	SLC1A5	Transport, extracellular	4
ASN4_pos	1	0.19043	0.7202646	-1.66853	1.668526	2	0.347218	ASN4	L-asparagine transport in via sodium symport	1.00 * Sodium [e] + 1.00 * L-asparagine [e] -> 1.00 * Sodi	ACE2;SLC3	Transport, extracellular	4
BILDGLCURT_neg	1	0.19043	0.7202646	-1.78936	1.789358	2	0.347218	BILDGLCURT	bilirubin beta-digluconide transport via bicarbonate countertran	1.00 * Bicarbonate [c] + 1.00 * bis(beta-glucosyluronate)	SLCO1B2	Transport, extracellular	4
BILDGLCURT_pos	1	0.19043	0.7202646	-1.61251	1.612512	2	0.347218	BILDGLCURT	bilirubin beta-digluconide transport via bicarbonate countertran	1.00 * Bicarbonate [c] + 1.00 * bis(beta-glucosyluronate)	SLCO1B2	Transport, extracellular	4
BILGLCURT_neg	1	0.19043	0.7202646	-1.80401	1.804011	2	0.347218	BILGLCURT	bilirubin monoglucuronide transport via bicarbonate countertrans	1.00 * Bicarbonate [c] + 1.00 * mono(glucosyluronic acid)	SLCO1B2	Transport, extracellular	4
BILGLCURT_pos	1	0.19043	0.7202646	-1.6198	1.619795	2	0.347218	BILGLCURT	bilirubin monoglucuronide transport via bicarbonate countertrans	1.00 * Bicarbonate [c] + 1.00 * mono(glucosyluronic acid)	SLCO1B2	Transport, extracellular	4
CHOLAT1E2_pos	1	0.19043	0.7202646	-1.69187	1.691867	2	0.347218	CHOLAT1E2	cholate transport via sodium cotransport	2.00 * Sodium [e] + 1.00 * Cholate [e] -> 2.00 * Sodium [c]	SLC10A1;S	Transport, extracellular	4
CHOLAT1E2_neg	1	0.19043	0.7202646	-1.44763	1.447631	2	0.347218	CHOLAT1E2	cholate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * Cholate [e] -> 1.00 * Bicar	SLC10A1;S	Transport, extracellular	4
CIT14_2_neg	1	0.19043	0.7202646	-1.21355	1.213555	2	0.347218	CIT14_2	citrate transport via sodium symport	2.00 * Sodium [e] + 1.00 * Citrate [e] -> 2.00 * Sodium [c]	SLC13A2	Transport, extracellular	4
CIT14_2_pos	1	0.19043	0.7202646	-1.25788	1.257882	2	0.347218	CIT14_2	citrate transport via sodium symport	2.00 * Sodium [e] + 1.00 * Citrate [e] -> 2.00 * Sodium [c]	SLC13A2	Transport, extracellular	4
CIT14_4_neg	1	0.19043	0.7202646	-1.25788	1.257882	2	0.347218	CIT14_4	citrate transport via sodium symport	4.00 * Sodium [e] + 1.00 * Citrate [e] -> 4.00 * Sodium [c]	SLC13A5	Transport, extracellular	4
CIT14_4_pos	1	0.19043	0.7202646	-1.21355	1.213555	2	0.347218	CIT14_4	citrate transport via sodium symport	4.00 * Sodium [e] + 1.00 * Citrate [e] -> 4.00 * Sodium [c]	SLC13A5	Transport, extracellular	4
CYSALANaEx_pos	8	0.19043	0.7202646	1.626676	1.626676	1	0.347218	CYSALANaE	L-alanine/L-cysteine Na-dependent exchange (Cys-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-cysteine	SLC1A4;SL	Transport, extracellular	4
CYTD4_pos	1	0.19043	0.7202646	-1.81321	1.813214	2	0.347218	CYTD4	cytidine transport in via sodium symport	1.00 * Sodium [e] + 1.00 * Cytidine [e] -> 1.00 * Sodium	SLC28A1;S	Transport, extracellular	4
CYTD4_neg	1	0.19043	0.7202646	-1.81321	1.813214	2	0.347218	CYTD4	cytidine facilitated transport in cytosol	1.00 * Cytidine [e] -> 1.00 * Cytidine [c]SLC29A1;SLC29A	SLC29A1;S	Transport, extracellular	4
DHEAST_neg	1	0.19043	0.7202646	-1.79879	1.798793	2	0.347218	DHEAST	dehydroepiandrosterone sulfate transport via bicarbonate countertr	1.00 * Bicarbonate [c] + 1.00 * 3beta-hydroxyandrost-5-e	SLCO1A1;S	Transport, extracellular	4
DHEAST_pos	1	0.19043	0.7202646	-1.63257	1.632568	2	0.347218	DHEAST	dehydroepiandrosterone sulfate transport via bicarbonate countertr	1.00 * Bicarbonate [c] + 1.00 * 3beta-hydroxyandrost-5-e	SLCO1A1;S	Transport, extracellular	4
ESTRONE1E2_pos	1	0.19043	0.7202646	-1.79202	1.792024	2	0.347218	ESTRONE1E2	estrone 3-sulfate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * estrone 3-sulfate[1-] [e] ->	SLCO1A1;S	Transport, extracellular	4
ESTRONE1E2_neg	1	0.19043	0.7202646	-1.6324	1.632396	2	0.347218	ESTRONE1E2	estrone 3-sulfate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * estrone 3-sulfate[1-] [e] ->	SLCO1A1;S	Transport, extracellular	4
FATP5t_neg	1	0.19043	0.7202646	-1.43663	1.436632	2	0.347218	FATP5t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * arachidonate [c] -> 1.00 * Sod	SLC27A5	Transport, extracellular	4
FATP5t_pos	1	0.19043	0.7202646	-1.65516	1.655156	2	0.347218	FATP5t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * arachidonate [c] -> 1.00 * Sod	SLC27A5	Transport, extracellular	4
FATP8t_pos	1	0.19043	0.7202646	-1.24228	1.24228	2	0.347218	FATP8t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * lignocerate [c] -> 1.00 * Sodium	SLC27A2;S	Transport, extracellular	4
FRUT1r_neg	1	0.19043	0.7202646	-1.56102	1.561021	2	0.347218	FRUT1r	D-fructose transport in via uniport	1.00 * D-Fructose [e] -> 1.00 * D-Fructose [c]SLC2A2;SLC	SLC2A2;SL	Transport, extracellular	4
FRUT1r_pos	1	0.19043	0.7202646	-1.66491	1.664907	2	0.347218	FRUT1r	D-fructose transport in via uniport	1.00 * D-Fructose -> 1.00 * D-Fructose [c]SLC2A2;SLC	SLC2A2;SL	Transport, extracellular	4
FRUT4_neg	1	0.19043	0.7202646	-1.66491	1.664907	2	0.347218	FRUT4	D-fructose transport via sodium cotransport	1.00 * Sodium [e] + 1.00 * D-Fructose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
FRUT4_pos	1	0.19043	0.7202646	-1.56102	1.561021	2	0.347218	FRUT4	D-fructose transport via sodium cotransport	1.00 * Sodium [e] + 1.00 * D-Fructose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
GALT1r_neg	1	0.19043	0.7202646	-1.49646	1.496462	2	0.347218	GALT1r	galactose transport (uniport)	1.00 * D-Galactose [e] -> 1.00 * D-Galactose [c]SLC2A1;SLC	SLC2A1;SL	Transport, extracellular	4
GALT1r_pos	1	0.19043	0.7202646	-1.61356	1.613559	2	0.347218	GALT1r	galactose transport (uniport)	1.00 * D-Galactose [e] -> 1.00 * D-Galactose [c]SLC2A1;SLC	SLC2A1;SL	Transport, extracellular	4
GALT2_2_neg	1	0.19043	0.7202646	-1.87488	1.874881	2	0.347218	GALT2_2	D-galactose transport via proton symport	2.00 * proton [e] + 1.00 * D-Galactose [e] -> 2.00 * proton	SLC5A1	Transport, extracellular	4
GALT4_neg	1	0.19043	0.7202646	-1.61356	1.613559	2	0.347218	GALT4	galactose transport via sodium symport	1.00 * Sodium [e] + 1.00 * D-Galactose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
GALT4_pos	1	0.19043	0.7202646	-1.49646	1.496462	2	0.347218	GALT4	galactose transport via sodium symport	1.00 * Sodium [e] + 1.00 * D-Galactose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
GCHOLAT_neg	1	0.19043	0.7202646	-1.46197	1.461972	2	0.347218	GCHOLAT	glycocholate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * glycocholate [e] -> 1.00 * S	SLCO1A1;S	Transport, extracellular	4
GLCT2_2_neg	1	0.19043	0.7202646	-1.72302	1.723023	2	0.347218	GLCT2_2	D-glucose transport in via proton symport	2.00 * proton [e] + 1.00 * D-glucose [e] -> 2.00 * proton [c]	SLC5A1	Transport, extracellular	4
GLCT4_neg	1	0.19043	0.7202646	-1.70077	1.700774	2	0.347218	GLCT4	glucose transport via sodium symport	1.00 * Sodium [e] + 1.00 * D-glucose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
GLN4_pos	1	0.19043	0.7202646	-1.66853	1.668526	2	0.347218	GLN4	L-glutamine reversible transport via sodium symport	1.00 * Sodium [e] + 1.00 * L-glutamine [e] -> 1.00 * Sodium	ACE2;SLC3	Transport, extracellular	4
GLNLYAThtc_pos	1	0.19043	0.7202646	-1.45585	1.455852	2	0.347218	GLNLYAThtc	transport of Glutamine by y-LAT1 or y-LAT2 with co-transporter of h	1.00 * proton [e] + 1.00 * L-glutamine [e] + 1.00 * L-argini	SLC3A2;SL	Transport, extracellular	4
GLY7_311_r_pos	8	0.19043	0.7202646	1.318925	1.318925	1	0.347218	GLY7_311	glycine reversible transport via sodium and chloride symport (3:1:1	3.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * Chloride [e]	SLC6A5	Transport, extracellular	4
HCO3_NAT_pos	8	0.19043	0.7202646	0.87311	0.87311	1	0.347218	HCO3_NAT	bicarbonate transport (Na/HCO3 cotransport)	1.00 * Bicarbonate [e] + 1.00 * Sodium [e] -> 1.00 * Bicar	SLC4A7	Transport, extracellular	4
HISTN1_neg	1	0.19043	0.7202646	-1.2026	1.202596	2	0.347218	HISTN1	Histidine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-histidine [c]	SLC38A3	Transport, extracellular	4
HISyLATtc_pos	8	0.19043	0.7202646	1.95066	1.95066	1	0.347218	HISyLATtc	Transport of L-Histidine by y-LAT1 or y-LAT2 transporters in small in	1.00 * Sodium [e] + 1.00 * L-argininium[1+] [c] + 1.00 * L-	SLC3A2;SL	Transport, extracellular	4
LEUKTRC4t_neg	1	0.19043	0.7202646	-1.80401	1.804011	2	0.347218	LEUKTRC4t	leukotriene C4 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * leukotriene C4(2-)[e] -> 1.	SLCO1B2	Transport, extracellular	4
LEUKTRC4t_pos	1	0.19043	0.7202646	-1.6198	1.619795	2	0.347218	LEUKTRC4t	leukotriene C4 transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * leukotriene C4(2-)[e] -> 1.	SLCO1B2	Transport, extracellular	4
LEUtec_pos	8	0.19043	0.7202646	1.562783	1.562783	1	0.347218	LEUtec	L-leucine transport via diffusion (extracellular to cytosol)	1.00 * L-leucine [e] -> 1.00 * L-leucine [c]SLC43A1;SLC43	SLC43A1;S	Transport, extracellular	4
LEUyLAThtc_pos	1	0.19043	0.7202646	-1.45585	1.455852	2	0.347218	LEUyLAThtc	transport of Leucine by y-LAT1 or y-LAT2 with co-transporter of h	1.00 * proton [e] + 1.00 * L-argininium[1+] [c] + 1.00 * L-	SLC3A2;SL	Transport, extracellular	4
LINOATPtc_pos	1	0.19043	0.7202646	-1.46238	1.462381	2	0.347218	LINOATPtc	uptake of linoleic acid by the enterocytes	1.00 * ATP [c] + 1.00 * Coenzyme A [c] + 1.00 * linoleate [e]	SLC27A4	Transport, extracellular	4
MANT1r_neg	1	0.19043	0.7202646	-1.54813	1.548133	2	0.347218	MANT1r	mannose transport (uniport)	1.00 * D-Mannose [e] -> 1.00 * D-Mannose [c]SLC2A1;SLC	SLC2A1;SL	Transport, extracellular	4
MANT1r_pos	1	0.19043	0.7202646	-1.65385	1.653849	2	0.347218	MANT1r	mannose transport (uniport)	1.00 * D-Mannose [e] -> 1.00 * D-Mannose [c]SLC2A1;SLC	SLC2A1;SL	Transport, extracellular	4
MANT4_neg	1	0.19043	0.7202646	-1.65385	1.653849	2	0.347218	MANT4	D-mannose transport via sodium cotransport	1.00 * Sodium [e] + 1.00 * D-Mannose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
MANT4_pos	1	0.19043	0.7202646	-1.54813	1.548133	2	0.347218	MANT4	D-mannose transport via sodium cotransport	1.00 * Sodium [e] + 1.00 * D-Mannose [e] -> 1.00 * Sodium	SLC5A10;S	Transport, extracellular	4
METyLAThtc_pos	1	0.19043	0.7202646	-1.45585	1.455852	2	0.347218	METyLAThtc	transport of Methionine by y-LAT1 or y-LAT2 with co-transporter of	1.00 * proton [e] + 1.00 * L-argininium[1+] [c] + 1.00 * L-	SL		

UREAt_neg		1	0.19043	0.7202646	-1.59449	1.594489	2	0.347218	UREAt	Urea transport via facilitate diffusion	1.00 * Urea [e] -> 1.00 * Urea [c]	SLC14A1; SLC14A2; SLC5	SLC14A1; S	Transport, extracellular		4
UREAt_pos		1	0.19043	0.7202646	-1.59449	1.594489	2	0.347218	UREAt	Urea transport via facilitate diffusion	1.00 * Urea [e] -> 1.00 * Urea [c]	SLC14A1; SLC14A2; SLC5	SLC14A1; S	Transport, extracellular		4
UR14_pos		1	0.19043	0.7202646	-1.80803	1.808029	2	0.347218	UR14	uridine transport in via sodium symport	1.00 * Sodium [e] + 1.00 * Uridine [e] -> 1.00 * Sodium [c]	SLC28A1; S	Transport, extracellular		4	
UR1t_neg		1	0.19043	0.7202646	-1.80803	1.808029	2	0.347218	UR1t	uridine facilitated transport in cytosol	1.00 * Uridine [e] -> 1.00 * Uridine [c]	SLC29A1; SLC29A2	SLC29A1; S	Transport, extracellular		4
r1088_neg		1	0.19043	0.7202646	-1.23609	1.236089	2	0.347218	r1088	Active transport	1.00 * proton [e] + 1.00 * Citrate [e] -> 1.00 * proton [c] + 1.00 * prot			Transport, extracellular		0
r1088_pos		1	0.19043	0.7202646	-1.40635	1.406346	2	0.347218	r1088	Active transport	1.00 * proton [e] + 1.00 * Citrate [e] -> 1.00 * proton [c] + 1.00 * prot			Transport, extracellular		0
r1423_pos		1	0.19043	0.7202646	-1.42433	1.424332	2	0.347218	r1423	Facilitated diffusion	1.00 * hydrogenphosphate [c] -> 1.00 * hydrogenphosph	1.00 * hyd		Transport, extracellular	4.2.1.1	0
r1493_pos		1	0.19043	0.7202646	-1.87454	1.874543	2	0.347218	r1493	Utilized transport	1.00 * Reduced glutathione [c] -> 1.00 * Reduced glutath	1.00 * Red		Transport, extracellular		0
r1512_pos		1	0.19043	0.7202646	-1.44583	1.445826	2	0.347218	r1512	Utilized transport	1.00 * bilirubin(2-) [e] -> 1.00 * bilirubin(2-) [c]	No genes	1.00 * bili	Transport, extracellular		0
r1544_pos		8	0.19043	0.7202646	1.939551	1.939551	1	0.347218	r1544	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [c] + 1.00 * Glycine [e] -> 1.00 * L-glut	SLC7A5		Transport, extracellular		0
r1546_neg		8	0.19043	0.7202646	1.776681	1.776681	1	0.347218	r1546	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * Glycine [e] + 1.00 * L-methionine [c] -> 1.00 * Glyc	SLC7A5		Transport, extracellular		0
r1560_neg		8	0.19043	0.7202646	1.810288	1.810288	1	0.347218	r1560	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-methionine [c] -> 1.00 * L-a	SLC7A5		Transport, extracellular		0
r1564_neg		8	0.19043	0.7202646	1.810288	1.810288	1	0.347218	r1564	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-cysteine [c] -> 1.00 * L-alan	SLC7A5		Transport, extracellular		0
r1567_neg		8	0.19043	0.7202646	1.022377	1.022377	1	0.347218	r1567	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-asparagine [c] -> 1.00 * L-al	SLC7A5		Transport, extracellular		0
r1567_pos		8	0.19043	0.7202646	1.120517	1.120517	1	0.347218	r1567	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-alanine [e] + 1.00 * L-asparagine [c] -> 1.00 * L-al	SLC7A5		Transport, extracellular		0
r1573_neg		8	0.19043	0.7202646	1.776681	1.776681	1	0.347218	r1573	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-methionine [c] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1574_neg		8	0.19043	0.7202646	1.63147	1.63147	1	0.347218	r1574	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-tryptophan [c] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1574_pos		8	0.19043	0.7202646	1.63147	1.63147	1	0.347218	r1574	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-tryptophan [c] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1576_neg		8	0.19043	0.7202646	1.2716	1.2716	1	0.347218	r1576	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-gl	SLC7A5		Transport, extracellular		0
r1576_pos		8	0.19043	0.7202646	1.445123	1.445123	1	0.347218	r1576	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-glutamine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-gl	SLC7A5		Transport, extracellular		0
r1580_neg		8	0.19043	0.7202646	1.173168	1.173168	1	0.347218	r1580	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-glutamine [e] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1580_pos		8	0.19043	0.7202646	1.173168	1.173168	1	0.347218	r1580	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-glutamine [e] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1585_neg		8	0.19043	0.7202646	1.776681	1.776681	1	0.347218	r1585	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-methionine [c] -> 1.00 * L-ser	SLC7A5		Transport, extracellular		0
r1586_neg		8	0.19043	0.7202646	1.63147	1.63147	1	0.347218	r1586	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-tryptophan [c] -> 1.00 * L-ser	SLC7A5		Transport, extracellular		0
r1586_pos		8	0.19043	0.7202646	1.63147	1.63147	1	0.347218	r1586	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-tryptophan [c] -> 1.00 * L-ser	SLC7A5		Transport, extracellular		0
r1588_neg		8	0.19043	0.7202646	1.2716	1.2716	1	0.347218	r1588	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-serine	SLC7A5		Transport, extracellular		0
r1588_pos		8	0.19043	0.7202646	1.032076	1.032076	1	0.347218	r1588	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-serine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-serine	SLC7A5		Transport, extracellular		0
r1597_neg		8	0.19043	0.7202646	1.643382	1.643382	1	0.347218	r1597	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-tryptophan [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1598_pos		8	0.19043	0.7202646	1.810288	1.810288	1	0.347218	r1598	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-phenylalanine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1599_neg		8	0.19043	0.7202646	1.278018	1.278018	1	0.347218	r1599	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1600_neg		8	0.19043	0.7202646	1.774119	1.774119	1	0.347218	r1600	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-methionine [e] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1600_pos		8	0.19043	0.7202646	1.774119	1.774119	1	0.347218	r1600	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-methionine [e] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1603_pos		8	0.19043	0.7202646	1.776681	1.776681	1	0.347218	r1603	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-methionine [e] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1605_pos		8	0.19043	0.7202646	1.728661	1.728661	1	0.347218	r1605	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-methionine [e] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1606_pos		8	0.19043	0.7202646	1.867029	1.867029	1	0.347218	r1606	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-methionine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1608_neg		8	0.19043	0.7202646	1.49946	1.49946	1	0.347218	r1608	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-phenylalanine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1608_pos		8	0.19043	0.7202646	1.49946	1.49946	1	0.347218	r1608	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-phenylalanine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1609_neg		8	0.19043	0.7202646	1.276776	1.276776	1	0.347218	r1609	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1609_pos		8	0.19043	0.7202646	1.276776	1.276776	1	0.347218	r1609	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-tyrosine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1611_neg		8	0.19043	0.7202646	1.643382	1.643382	1	0.347218	r1611	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-leucine [c] -> 1.00 * L-le	SLC7A5		Transport, extracellular		0
r1611_pos		8	0.19043	0.7202646	1.643382	1.643382	1	0.347218	r1611	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-leucine [c] -> 1.00 * L-le	SLC7A5		Transport, extracellular		0
r1612_neg		8	0.19043	0.7202646	1.797795	1.797795	1	0.347218	r1612	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-proline [c] -> 1.00 * L-p	SLC7A5		Transport, extracellular		0
r1612_pos		8	0.19043	0.7202646	1.760981	1.760981	1	0.347218	r1612	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e] + 1.00 * L-proline [c] -> 1.00 * L-p	SLC7A5		Transport, extracellular		0
r1621_neg		8	0.19043	0.7202646	1.487099	1.487099	1	0.347218	r1621	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-phenylalanine [e] + 1.00 * L-proline [c] -> 1.00 *	SLC7A5		Transport, extracellular		0
r1625_neg		8	0.19043	0.7202646	1.170708	1.170708	1	0.347218	r1625	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-phenylalanine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1625_pos		8	0.19043	0.7202646	1.170708	1.170708	1	0.347218	r1625	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-phenylalanine [e] + 1.00 * L-homoserine [c] -> 1.00	SLC7A5		Transport, extracellular		0
r1628_neg		8	0.19043	0.7202646	1.037064	1.037064	1	0.347218	r1628	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-leucine [c] -> 1.00 * L-leuc	SLC7A5		Transport, extracellular		0
r1628_pos		8	0.19043	0.7202646	1.278018	1.278018	1	0.347218	r1628	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-leucine [c] -> 1.00 * L-leuc	SLC7A5		Transport, extracellular		0
r1630_neg		8	0.19043	0.7202646	1.445123	1.445123	1	0.347218	r1630	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-tyrosine [e] -> 1.00 * L-a	SLC7A5		Transport, extracellular		0
r1630_pos		8	0.19043	0.7202646	1.2716	1.2716	1	0.347218	r1630	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-tyrosine [e] -> 1.00 * L-a	SLC7A5		Transport, extracellular		0
r1631_neg		8	0.19043	0.7202646	1.037064	1.037064	1	0.347218	r1631	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-valine [c] -> 1.00 * L-valine	SLC7A5		Transport, extracellular		0
r1631_pos		8	0.19043	0.7202646	1.278018	1.278018	1	0.347218	r1631	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-valine [c] -> 1.00 * L-valine	SLC7A5		Transport, extracellular		0
r1633_neg		8	0.19043	0.7202646	1.032076	1.032076	1	0.347218	r1633	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1633_pos		8	0.19043	0.7202646	1.2716	1.2716	1	0.347218	r1633	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r1634_neg		8	0.19043	0.7202646	1.037064	1.037064	1	0.347218	r1634	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5		Transport, extracellular		0
r1634_pos		8	0.19043	0.7202646	1.278018	1.278018	1	0.347218	r1634	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-tyrosine [e] + 1.00 * L-isoleucine [c] -> 1.00 * L-is	SLC7A5		Transport, extracellular		0
r1637_neg		8	0.19043	0.7202646	1.787212	1.787212	1	0.347218	r1637	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-cysteine [e] -> 1.00 * L-a	SLC7A5		Transport, extracellular		0
r1637_pos		8	0.19043	0.7202646	1.776681	1.776681	1	0.347218	r1637	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-asparagine [c] + 1.00 * L-cysteine [e] -> 1.00 * L-a	SLC7A5		Transport, extracellular		0
r1640_pos		8	0.19043	0.7202646	1.867029	1.867029	1	0.347218	r1640	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.1	1.00 * L-cysteine [c] + 1.00 * L-homoserine [c] -> 1.00 * L-	SLC7A5		Transport, extracellular		0
r2009_pos		1	0.19043	0.7202646	-1.45585	1.455852	2	0.347218	r2009	Amino Acid-Polyamine-Organization (APC) TCDB:2.A.3.8.15	1.00 * L-alanine [c] + 1.00 * L-argininium(1+) [e] -> 1.00 *	SLC7A9		Transport, extracellular		0
r2010_pos		1	0.19043	0.7202646	-1.45585	1.45										

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r2366_neg		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2366	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin-f2beta [e] -> 1.00 * prostaglandin-f2	1.00 * pro	Transport, extracellular		0
r2366_pos		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2366	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin-f2beta [e] -> 1.00 * prostaglandin-f2	1.00 * pro	Transport, extracellular		0
r2367_neg		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2367	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin-g2 [e] -> 1.00 * prostaglandin-g2 [c]	1.00 * pro	Transport, extracellular		0
r2367_pos		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2367	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin-g2 [e] -> 1.00 * prostaglandin-g2 [c]	1.00 * pro	Transport, extracellular		0
r2368_neg		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2368	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin H2(1)-[e] -> 1.00 * prostaglandin H2(1)-[c]	1.00 * pro	Transport, extracellular		0
r2368_pos		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2368	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin H2(1)-[e] -> 1.00 * prostaglandin H2(1)-[c]	1.00 * pro	Transport, extracellular		0
r2369_neg		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2369	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin I2(1)-[e] -> 1.00 * prostaglandin I2(1)-[c]	1.00 * pro	Transport, extracellular		0
r2369_pos		1	0.19043	0.7202646	-1.97541	1.975412	2	0.347218	r2369	Organic anion transporter 5 Utilized transport	1.00 * prostaglandin I2(1)-[e] -> 1.00 * prostaglandin I2(1)-[c]	1.00 * pro	Transport, extracellular		0
r2465_pos		8	0.19043	0.7202646	1.686657	1.686657	1	0.347218	r2465	Cation Diffusion Facilitator (CDF) TCDB:2.A.4.2.3	1.00 * Zinc [c] -> 1.00 * Zinc [e]SLC30A1		Transport, extracellular		0
r2535_pos		8	0.19043	0.7202646	1.197693	1.197693	1	0.347218	r2535	Major Facilitator(MFS) TCDB:2.A.1.4.1	1.00 * L-homoserine [e] -> 1.00 * L-homoserine [c]SLC43A1		Transport, extracellular		0
2HBt2_neg		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2HBt2	2-hydroxybutyrate cotransport with proton	1.00 * 2-Hydroxybutyrate [e] + 1.00 * proton [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
2HBt2_pos		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2HBt2	2-hydroxybutyrate cotransport with proton	1.00 * 2-Hydroxybutyrate [e] + 1.00 * proton [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
2HCO3_NAT_pos		2	0.382733	0.4171041	-0.51537	0.515372	2	0.518179	2HCO3_NAT	bicarbonate transport (Na/HCO3 1:2 cotransport)	2.00 * Bicarbonate [e] + 1.00 * Sodium [e] -> 2.00 * Bicarbonate [c]	1.00 * pro	Transport, extracellular		4
ABUT14_2_r_pos		2	0.382733	0.4171041	-1.34621	1.346206	2	0.518179	ABUT14_2	4-aminobutyrate reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * 4-Aminobutanoate [e] -> 2.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
ACAC12_neg		2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	ACAC12	acetoacetate transport via proton symport	1.00 * proton [e] + 1.00 * acetoacetate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
ACAC12_pos		2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	ACAC12	acetoacetate transport via proton symport	1.00 * proton [e] + 1.00 * acetoacetate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
ACT2r_neg		2	0.382733	0.4171041	-1.10346	1.103457	2	0.518179	ACT2r	acetate reversible transport via proton symport	1.00 * proton [e] + 1.00 * acetate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
ACT2r_pos		2	0.382733	0.4171041	-1.10346	1.103457	2	0.518179	ACT2r	acetate reversible transport via proton symport	1.00 * proton [e] + 1.00 * acetate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
ASCB14_pos		2	0.382733	0.4171041	-0.86601	0.866007	2	0.518179	ASCB14	L-ascorbate transport via proton symport	1.00 * Sodium [e] + 1.00 * L-ascorbate [e] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
ASNALNaEx_pos		7	0.382733	0.4171041	1.479592	1.479592	1	0.518179	ASNALNaEx	L-alanine/L-asparagine Na-dependent exchange (Asn-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-asparagine [c]	1.00 * pro	Transport, extracellular		4
ASNGLNNaEx_pos		7	0.382733	0.4171041	1.356376	1.356376	1	0.518179	ASNGLNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Asn-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-glutamine [c]	1.00 * pro	Transport, extracellular		4
ASNN1_neg		2	0.382733	0.4171041	-1.05893	1.058928	2	0.518179	ASNN1	Asparagine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-asparagine [c]	1.00 * pro	Transport, extracellular		4
BUT12r_neg		2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	BUT12r	Butyrate transport via a proton symport, reversible	1.00 * proton [e] + 1.00 * butyrate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
BUT12r_pos		2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	BUT12r	Butyrate transport via a proton symport, reversible	1.00 * proton [e] + 1.00 * butyrate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
CREAT14_2_r_pos		7	0.382733	0.4171041	0.688468	0.688468	1	0.518179	CREAT14_2	Creatine transport (sodium symport) (2:1)	2.00 * Sodium [e] + 1.00 * creatine [e] -> 2.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
CYSASNNaEx_pos		7	0.382733	0.4171041	1.197484	1.197484	1	0.518179	CYSASNNaEx	L-cysteine/L-asparagine Na-dependent exchange (Cys-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-cysteine [c]	1.00 * pro	Transport, extracellular		4
CYSGLNNaEx_pos		7	0.382733	0.4171041	1.197484	1.197484	1	0.518179	CYSGLNNaEx	L-cysteine/L-glutamine Na-dependent exchange (Cys-L in)	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-glutamine [c]	1.00 * pro	Transport, extracellular		4
CYSTLEU/BAT1c_pos		2	0.382733	0.4171041	-1.07129	1.071291	2	0.518179	CYSTLEU/BAT1c	transport of L-Cystine into the cell in exchange for L-Leucine by bo, L-serine	1.00 * L-cystine [e] + 1.00 * L-leucine [c] -> 1.00 * L-cystine [c]	1.00 * pro	Transport, extracellular		4
CYSTSEREX_pos		2	0.382733	0.4171041	-1.04745	1.04745	2	0.518179	CYSTSEREX	L-cystine/glycine exchange (cystine in)	1.00 * L-serine [c] + 1.00 * L-cystine [e] -> 1.00 * L-serine [c]	1.00 * pro	Transport, extracellular		4
CyStec_neg		7	0.382733	0.4171041	0.389589	0.389589	1	0.518179	CyStec	L-cysteine transport via diffusion (extracellular to cytosol)	1.00 * L-cysteine [e] -> 1.00 * L-cysteine [c]SLC43A2		Transport, extracellular		4
CyStec_pos		7	0.382733	0.4171041	0.632644	0.632644	1	0.518179	CyStec	L-cysteine transport via diffusion (extracellular to cytosol)	1.00 * L-cysteine [e] -> 1.00 * L-cysteine [c]SLC43A2		Transport, extracellular		4
CYTDT_pos		2	0.382733	0.4171041	-1.43165	1.431651	2	0.518179	CYTDT	cytidine facilitated transport in cytosol	1.00 * Cytidine [e] -> 1.00 * Cytidine [c]SLC29A1; SLC29A1		Transport, extracellular		4
DOPAtu_neg		2	0.382733	0.4171041	-0.3751	0.375097	2	0.518179	DOPAtu	Dopamine uniport	1.00 * dopaminium(1+) [e] -> 1.00 * dopaminium(1+) [c]	1.00 * pro	Transport, extracellular		4
DOPAtu_pos		2	0.382733	0.4171041	-0.99699	0.996991	2	0.518179	DOPAtu	Dopamine uniport	1.00 * dopaminium(1+) [e] -> 1.00 * dopaminium(1+) [c]	1.00 * pro	Transport, extracellular		4
FATP11_pos		2	0.382733	0.4171041	-0.72451	0.724511	2	0.518179	FATP11	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * Hexadecanoate (n-C16:0) [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP21_neg		2	0.382733	0.4171041	-0.76468	0.764685	2	0.518179	FATP21	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * octadecanoate (n-C18:1) [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP21_pos		2	0.382733	0.4171041	-1.00027	1.000272	2	0.518179	FATP21	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * octadecanoate (n-C18:1) [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP31_pos		2	0.382733	0.4171041	-0.89073	0.89073	2	0.518179	FATP31	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * octadecanoate (n-C18:0) [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP41_pos		2	0.382733	0.4171041	-1.47086	1.470858	2	0.518179	FATP41	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * arachidate [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP61_pos		2	0.382733	0.4171041	-1.11579	1.115788	2	0.518179	FATP61	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * adrenic acid [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP71_pos		2	0.382733	0.4171041	-1.11579	1.115788	2	0.518179	FATP71	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * cervonic acid, C22:6 n-3 [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
FATP91_pos		2	0.382733	0.4171041	-1.11579	1.115788	2	0.518179	FATP91	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * nervonate [c] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
GLCT4_pos		2	0.382733	0.4171041	-1.01431	1.014308	2	0.518179	GLCT4	glucose transport via sodium symport	1.00 * Sodium [e] + 1.00 * D-glucose [e] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
GLNASNNaEx_pos		7	0.382733	0.4171041	1.356376	1.356376	1	0.518179	GLNASNNaEx	L-glutamine/L-asparagine Na-dependent exchange (Gln-L in)	1.00 * Sodium [e] + 1.00 * L-asparagine [c] + 1.00 * L-glutamine [c]	1.00 * pro	Transport, extracellular		4
GLNCYSNaEx_pos		7	0.382733	0.4171041	1.088228	1.088228	1	0.518179	GLNCYSNaEx	L-cysteine/L-glutamine Na-dependent exchange (Gln-L in)	1.00 * Sodium [e] + 1.00 * L-cysteine [c] + 1.00 * L-glutamine [c]	1.00 * pro	Transport, extracellular		4
GLNN1_neg		2	0.382733	0.4171041	-1.05893	1.058928	2	0.518179	GLNN1	Glutamine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-glutamine [c]	1.00 * pro	Transport, extracellular		4
GLYSNAT51c_pos		7	0.382733	0.4171041	0.974459	0.974459	1	0.518179	GLYSNAT51c	transport of Glycine into the cell coupled with co-transport with So	1.00 * proton [c] + 1.00 * Sodium [e] + 1.00 * Glycine [e]	1.00 * pro	Transport, extracellular		4
GSNI_neg		2	0.382733	0.4171041	-1.39802	1.398016	2	0.518179	GSNI	guanosine facilitated transport in cytosol	1.00 * Guanosine [e] -> 1.00 * Guanosine [c]SLC29A1; SLC29A1		Transport, extracellular		4
GSNI_pos		2	0.382733	0.4171041	-1.43165	1.431651	2	0.518179	GSNI	guanosine facilitated transport in cytosol	1.00 * Guanosine [e] -> 1.00 * Guanosine [c]SLC29A1; SLC29A1		Transport, extracellular		4
ILEATB0tc_pos		7	0.382733	0.4171041	1.004822	1.004822	1	0.518179	ILEATB0tc	Transport of L-Isoleucine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * Chloride [e] + 1.00 * L-Isoleucine [c]	1.00 * pro	Transport, extracellular		4
INST_neg		2	0.382733	0.4171041	-1.39802	1.398016	2	0.518179	INST	Inosine transport (diffusion)	1.00 * inosine [e] -> 1.00 * inosine [c]SLC29A1; SLC29A2		Transport, extracellular		4
INST_pos		2	0.382733	0.4171041	-1.39884	1.398841	2	0.518179	INST	Inosine transport (diffusion)	1.00 * inosine [e] -> 1.00 * inosine [c]SLC29A1; SLC29A2		Transport, extracellular		4
KCC2t_neg		7	0.382733	0.4171041	0.882528	0.882528	1	0.518179	KCC2t	K+-Cl- cotransporter (NH4+)	1.00 * Ammonium [e] + 1.00 * Chloride [e] -> 1.00 * Ammonium [c]	1.00 * pro	Transport, extracellular		4
KCC2t_pos		7	0.382733	0.4171041	0.882528	0.882528	1	0.518179	KCC2t	K+-Cl- cotransporter (NH4+)	1.00 * Ammonium [e] + 1.00 * Chloride [e] -> 1.00 * Ammonium [c]	1.00 * pro	Transport, extracellular		4
LEUATB0tc_pos		7	0.382733	0.4171041	0.973951	0.973951	1	0.518179	LEUATB0tc	Transport of L-Leucine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * Chloride [e] + 1.00 * L-Leucine [c]	1.00 * pro	Transport, extracellular		4
L_LACT2r_neg		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	L_LACT2r	L-lactate reversible transport via proton symport	1.00 * proton [e] + 1.00 * (S)-lactate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
L_LACT2r_pos		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	L_LACT2r	L-lactate reversible transport via proton symport	1.00 * proton [e] + 1.00 * (S)-lactate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
PHET4_pos		7	0.382733	0.4171041	0.866035	0.866035	1	0.518179	PHET4	L-phenylalanine transport in via sodium symport	1.00 * Sodium [e] + 1.00 * L-phenylalanine [e] -> 1.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
PRO14_2_r_pos		2	0.382733	0.4171041	-1.60504	1.60504	2	0.518179	PRO14_2_r	Proline transport (sodium symport) (2:1)	2.00 * Sodium [e] + 1.00 * L-proline [e] -> 2.00 * Sodium [c]	1.00 * pro	Transport, extracellular		4
PYR12r_neg		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	PYR12r	pyruvate reversible transport via proton symport	1.00 * proton [e] + 1.00 * pyruvate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
PYR12r_pos		2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	PYR12r	pyruvate reversible transport via proton symport	1.00 * proton [e] + 1.00 * pyruvate [e] -> 1.00 * proton [c]	1.00 * pro	Transport, extracellular		4
SERATB0tc_pos		7	0.382733	0.4171041	1.003441	1.003441	1	0.518179	SERATB0tc	transport of L-Serine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-serine [e] + 1.00 * Chloride [e]	1.00 * pro	Transport, extracellular		4
SRTNtu_neg		2	0.382733	0.4171041	-0.88333	0.883326	2	0.518179	SRTNtu	Serotonin uniport	1.00 * serotonin(1+) [e] -> 1.00 * serotonin(1+) [c]SLC22A1		Transport, extracellular		4
TAUBETAtc_pos		7	0.382733	0.4171041	0.962828	0.962828	1	0.518179	TAUBETAtc	transport of taurine into the intestinal cells by beta transport system	2.00 * Sodium [e] + 1.00 * Chloride [e] + 1.00 * Taurine [c]	1.00 * pro	Transport, extracellular		4
TAUR14_2_r_neg		7	0.382733	0.4171041	0.95223	0.95223	1	0.518179	TAUR14_2_r	taurine transport (sodium symport) (2:1)					

1617_neg	7	0.382733	0.4171041	1.185461	1.185461	1	0.518179	1617	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e]+1.00 * L-isoleucine [c] ->1.00 *	SLC7A5	Transport, extracellular		0
1617_pos	7	0.382733	0.4171041	1.185461	1.185461	1	0.518179	1617	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-tryptophan [e]+1.00 * L-isoleucine [c] ->1.00 *	SLC7A5	Transport, extracellular		0
1621_pos	7	0.382733	0.4171041	1.328521	1.328521	1	0.518179	1621	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-phenylalanine [e]+1.00 * L-proline [c] ->1.00 *	SLC7A5	Transport, extracellular		0
2079_neg	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2079	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * pyruvate [e] ->1.00 * pyr	SLC16A1	Transport, extracellular		0
2079_pos	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2079	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * pyruvate [e] ->1.00 * pyr	SLC16A1	Transport, extracellular		0
2080_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2080	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * acetate [e] ->1.00 * aceto	SLC16A1	Transport, extracellular		0
2080_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2080	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * acetate [e] ->1.00 * aceto	SLC16A1	Transport, extracellular		0
2081_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2081	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * Formate [e] ->1.00 * acet	SLC16A1	Transport, extracellular		0
2081_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2081	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * Formate [e] ->1.00 * acet	SLC16A1	Transport, extracellular		0
2082_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2082	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * propionate [e] ->1.00 * a	SLC16A1	Transport, extracellular		0
2082_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2082	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * propionate [e] ->1.00 * a	SLC16A1	Transport, extracellular		0
2083_neg	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2083	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * (S)-lactate [e] ->1.00 * ac	SLC16A1	Transport, extracellular		0
2083_pos	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2083	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * (S)-lactate [e] ->1.00 * ac	SLC16A1	Transport, extracellular		0
2084_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2084	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * all-trans-retinoate [e] ->1	SLC16A1	Transport, extracellular		0
2084_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2084	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c]+1.00 * all-trans-retinoate [e] ->1	SLC16A1	Transport, extracellular		0
2085_neg	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2085	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [e]+1.00 * acetoacetate [c] ->	SLC16A1	Transport, extracellular		0
2085_pos	2	0.382733	0.4171041	-0.83341	0.833415	2	0.518179	2085	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [e]+1.00 * acetoacetate [c] ->	SLC16A1	Transport, extracellular		0
2086_neg	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2086	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * pyruvate [e] ->1.00	SLC16A1	Transport, extracellular		0
2086_pos	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2086	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * pyruvate [e] ->1.00	SLC16A1	Transport, extracellular		0
2087_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2087	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * acetate [e] ->1.00	SLC16A1	Transport, extracellular		0
2087_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2087	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * acetate [e] ->1.00	SLC16A1	Transport, extracellular		0
2088_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2088	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * Formate [e] ->1.00	SLC16A1	Transport, extracellular		0
2088_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2088	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * Formate [e] ->1.00	SLC16A1	Transport, extracellular		0
2089_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2089	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * propionate [e] ->1	SLC16A1	Transport, extracellular		0
2089_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2089	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * propionate [e] ->1	SLC16A1	Transport, extracellular		0
2090_neg	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2090	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * (S)-lactate [e] ->1.0	SLC16A1	Transport, extracellular		0
2090_pos	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2090	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * (S)-lactate [e] ->1.0	SLC16A1	Transport, extracellular		0
2091_neg	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	2091	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * butyrate [e] ->1.00	SLC16A1	Transport, extracellular		0
2091_pos	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	2091	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * butyrate [e] ->1.00	SLC16A1	Transport, extracellular		0
2092_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2092	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * all-trans-retinoate [e]	SLC16A1	Transport, extracellular		0
2092_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2092	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c]+1.00 * all-trans-retinoate [e]	SLC16A1	Transport, extracellular		0
2094_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2094	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [c]+1.00 * pyruvate [e] ->1.00 * pyruvate	SLC16A1	Transport, extracellular		0
2094_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2094	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [c]+1.00 * pyruvate [e] ->1.00 * pyruvate	SLC16A1	Transport, extracellular		0
2095_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2095	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * Formate [c]+1.00 * pyruvate [e] ->1.00 * pyruvate	SLC16A1	Transport, extracellular		0
2095_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2095	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * Formate [c]+1.00 * pyruvate [e] ->1.00 * pyruvate	SLC16A1	Transport, extracellular		0
2096_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2096	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * pyruvate [e] ->1.00 * pyrux	SLC16A1	Transport, extracellular		0
2096_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2096	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * pyruvate [e] ->1.00 * pyrux	SLC16A1	Transport, extracellular		0
2097_neg	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2097	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * pyruvate [e]+1.00 * (S)-lactate [c] ->1.00 * pyrux	SLC16A1	Transport, extracellular		0
2097_pos	2	0.382733	0.4171041	-0.82228	0.82228	2	0.518179	2097	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * pyruvate [e]+1.00 * (S)-lactate [c] ->1.00 * pyrux	SLC16A1	Transport, extracellular		0
2098_neg	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	2098	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * butyrate [c]+1.00 * pyruvate [e] ->1.00 * pyruvat	SLC16A1	Transport, extracellular		0
2098_pos	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	2098	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * butyrate [c]+1.00 * pyruvate [e] ->1.00 * pyruvat	SLC16A1	Transport, extracellular		0
2099_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2099	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * pyruvate [e]+1.00 * all-trans-retinoate [c] ->1.00	SLC16A1	Transport, extracellular		0
2099_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2099	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * pyruvate [e]+1.00 * all-trans-retinoate [c] ->1.00	SLC16A1	Transport, extracellular		0
2100_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2100	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c]+1.00 * pyruvate [e] ->1	SLC16A1	Transport, extracellular		0
2100_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2100	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c]+1.00 * pyruvate [e] ->1	SLC16A1	Transport, extracellular		0
2101_neg	7	0.382733	0.4171041	0.449832	0.449832	1	0.518179	2101	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [c]+1.00 * 2-Oxoglutarate [e] ->1.00 * 2-O	SLC16A1	Transport, extracellular		0
2103_neg	7	0.382733	0.4171041	0.449832	0.449832	1	0.518179	2103	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * 2-Oxoglutarate [e] ->1.00	SLC16A1	Transport, extracellular		0
2106_neg	7	0.382733	0.4171041	0.504348	0.504348	1	0.518179	2106	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e]+1.00 * butyrate [c] ->1.00 * 2	SLC16A1	Transport, extracellular		0
2107_pos	2	0.382733	0.4171041	-0.60529	0.605294	2	0.518179	2107	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e]+1.00 * all-trans-retinoate [c] ->1	SLC16A1	Transport, extracellular		0
2108_neg	7	0.382733	0.4171041	0.449832	0.449832	1	0.518179	2108	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e]+1.00 * (R)-3-hydroxybutyrate [e]	SLC16A1	Transport, extracellular		0
2110_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2110	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * Formate [c] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2110_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2110	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * Formate [c] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2111_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2111	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * acetate [e] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2111_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2111	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * acetate [e] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2112_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2112	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * (S)-lactate [c] ->1.00 * acetate	SLC16A1	Transport, extracellular		0
2112_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2112	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * (S)-lactate [c] ->1.00 * acetate	SLC16A1	Transport, extracellular		0
2113_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2113	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * butyrate [c] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2113_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2113	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * butyrate [c] ->1.00 * acetate [c]	SLC16A1	Transport, extracellular		0
2114_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2114	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * all-trans-retinoate [c] ->1.00 *	SLC16A1	Transport, extracellular		0
2114_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	2114	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * all-trans-retinoate [c] ->1.00 *	SLC16A1	Transport, extracellular		0
2115_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2115	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * (R)-3-hydroxybutyrate [c] ->1.0	SLC16A1	Transport, extracellular		0
2115_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2115	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [e]+1.00 * (R)-3-hydroxybutyrate [c] ->1.0	SLC16A1	Transport, extracellular		0
2116_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2116	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * Formate [e] ->1.00 * Formate	SLC16A1	Transport, extracellular		0
2116_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	2116	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c]+1.00 * Formate [e] ->1.00 * Formate	SLC16A1	Transport, extracellular		0</

r2126_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2126	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [e] + 1.00 * (R)-3-hydroxybutyrate [c]	SLC16A1	Transport, extracellular				0
r2127_neg	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	r2127	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * butyrate [c] + 1.00 * (S)-lactate [e] → 1.00 * butyrate	SLC16A1	Transport, extracellular				0
r2128_pos	2	0.382733	0.4171041	-1.3338	1.333799	2	0.518179	r2128	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * butyrate [c] + 1.00 * (S)-lactate [e] → 1.00 * butyrate	SLC16A1	Transport, extracellular				0
r2128_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2128	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (S)-lactate [e] + 1.00 * all-trans-retinoate [c] → 1.00	SLC16A1	Transport, extracellular				0
r2129_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2129	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (S)-lactate [e] + 1.00 * all-trans-retinoate [c] → 1.00	SLC16A1	Transport, extracellular				0
r2129_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2129	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c] + 1.00 * (S)-lactate [e] →	SLC16A1	Transport, extracellular				0
r2130_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2130	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * butyrate [e] + 1.00 * all-trans-retinoate [c] → 1.00	SLC16A1	Transport, extracellular				0
r2130_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2130	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * butyrate [e] + 1.00 * all-trans-retinoate [c] → 1.00	SLC16A1	Transport, extracellular				0
r2131_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2131	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c] + 1.00 * butyrate [e] → 1	SLC16A1	Transport, extracellular				0
r2131_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2131	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c] + 1.00 * butyrate [e] → 1	SLC16A1	Transport, extracellular				0
r2132_pos	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2132	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c] + 1.00 * all-trans-retino	SLC16A1	Transport, extracellular				0
r2132_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2132	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * (R)-3-hydroxybutyrate [c] + 1.00 * all-trans-retino	SLC16A1	Transport, extracellular				0
r2133_pos	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2133	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c] + 1.00 * (R)-3-hydroxybutyr	SLC16A1	Transport, extracellular				0
r2133_neg	2	0.382733	0.4171041	-1.64322	1.643222	2	0.518179	r2133	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c] + 1.00 * (R)-3-hydroxybutyr	SLC16A1	Transport, extracellular				0
r2196_pos	2	0.382733	0.4171041	-0.68538	0.685377	2	0.518179	r2196	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLCO1A1	Transport, extracellular				0
r2196_neg	2	0.382733	0.4171041	-0.68538	0.685377	2	0.518179	r2196	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLCO1A1	Transport, extracellular				0
r2525_pos	7	0.382733	0.4171041	0.291953	0.291953	2	0.518179	r2525	Major Facilitator(MFS) TCDB:2.A.1.44.1	1.00 * L-glutamine [e] → 1.00 * L-glutamine [c]SLC43A1	SLC43A1	Transport, extracellular				0
r2526_pos	7	0.382733	0.4171041	0.291953	0.291953	2	0.518179	r2526	Major Facilitator(MFS) TCDB:2.A.1.44.1	1.00 * L-serine [e] → 1.00 * L-serine [c]SLC43A1	SLC43A1	Transport, extracellular				0
r2532_pos	7	0.382733	0.4171041	0.291953	0.291953	2	0.518179	r2532	Major Facilitator(MFS) TCDB:2.A.1.44.1	1.00 * L-asparagine [e] → 1.00 * L-asparagine [c]SLC43A1	SLC43A1	Transport, extracellular				0
r2535_pos	7	0.382733	0.4171041	0.487157	0.487157	2	0.518179	r2535	Major Facilitator(MFS) TCDB:2.A.1.44.1	1.00 * L-homoserine [e] → 1.00 * L-homoserine [c]SLC43A1	SLC43A1	Transport, extracellular				0
2HCO3_Nat_neg	3	0.662521	0.1788004	-0.76786	0.767865	2	0.58498	2HCO3_NA12	bicarbonate transport (Na/HCO3 1:2 cotransport)	2.00 * Bicarbonate [e] + 1.00 * Sodium [e] → 2.00 * Bicar	SLC44A4;SL	Transport, extracellular				0
5MTHF2_neg	3	0.662521	0.1788004	-1.10744	1.10744	2	0.58498	5MTHF2	5-methyltetrahydrofolate transport via anion exchange	1.00 * Water [c] + 1.00 * 5-Methyltetrahydrofolate [e] →	SLC19A1	Transport, extracellular				0
ALAAAT80tc_pos	3	0.662521	0.1788004	-0.64698	0.646976	2	0.58498	ALAAAT80tc	transport of L-Alanine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * Chloride [e]	SLC6A14	Transport, extracellular				0
ALAGLrNaEx_pos	6	0.662521	0.1788004	0.986437	0.986437	1	0.58498	ALAGLrNaEx	L-alanine/L-glutamine Na-dependent exchange (Ala-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [e] + 1.00 * L-glutami	SLC1A5	Transport, extracellular				0
ALAT4_pos	6	0.662521	0.1788004	0.151522	0.151522	2	0.58498	ALAT4	Alanine-Sodium symporter	1.00 * Sodium [e] + 1.00 * L-alanine [e] → 1.00 * Sodium	ACE2;SLC3	Transport, extracellular				0
ALATN1_pos	3	0.662521	0.1788004	-0.86973	0.869725	2	0.58498	ALATN1	Alanine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-alanine [e]	SLC38A3;S	Transport, extracellular				0
ALayLAThtc_pos	6	0.662521	0.1788004	0.515453	0.515453	1	0.58498	ALayLAThtc	transport of Alanine by yLAT1 or yLAT2 with co-transporter of h	1.00 * proton [e] + 1.00 * L-alanine [e] + 1.00 * L-argininu	SLC3A2;SL	Transport, extracellular				0
ARGLYSex_pos	6	0.662521	0.1788004	0.822236	0.822236	1	0.58498	ARGLYSex	Arginine/Lysine exchanger (Arg in)	1.00 * L-lysine[1+] [c] + 1.00 * L-arginine[1+] [e] → 1	SLC3A2;SL	Transport, extracellular				0
ASNAAT80tc_pos	3	0.662521	0.1788004	-0.88955	0.889548	2	0.58498	ASNAAT80tc	transport of L-Asparagine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-asparagine [e] + 1.00 * Chlori	SLC6A14	Transport, extracellular				0
ASN1N1_pos	3	0.662521	0.1788004	-0.88552	0.88552	2	0.58498	ASN1N1	Asparagine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-asparagin	SLC38A3;S	Transport, extracellular				0
ASPD6_pos	3	0.662521	0.1788004	-0.37691	0.376908	2	0.58498	ASPD6	D-aspartate transport via Na, H symport and K antiport	1.00 * proton [e] + 3.00 * Sodium [e] + 1.00 * D-aspartate	SLC1A1;SL	Transport, extracellular				0
ASPI6_pos	3	0.662521	0.1788004	-0.37691	0.376908	2	0.58498	ASPI6	L-aspartate transport via Na, H symport and K antiport	1.00 * proton [e] + 3.00 * Sodium [e] + 1.00 * potassium [e]	SLC1A1;SL	Transport, extracellular				0
BALABETAtc_pos	6	0.662521	0.1788004	0.964896	0.964896	1	0.58498	BALABETAtc	transport of beta alanine into the intestinal cells by beta transport s	2.00 * Sodium [e] + 1.00 * beta-alanine [e] + 1.00 * Chlori	SLC6A6	Transport, extracellular				0
BILIRUB12_neg	3	0.662521	0.1788004	-0.46888	0.468877	2	0.58498	BILIRUB12	bilirubin transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * bilirubin[2-] [e] → 1.00 * B	SLCO182	Transport, extracellular				0
CaT7r_neg	6	0.662521	0.1788004	0.579153	0.579153	1	0.58498	CaT7r	calcium / sodium antiporter (1:3), reversible	3.00 * Sodium [e] + 1.00 * calcium[2+] [c] → 3.00 * Sodi	SLC8A1;SL	Transport, extracellular				0
CaT7r_pos	6	0.662521	0.1788004	0.504285	0.504285	1	0.58498	CaT7r	calcium / sodium antiporter (1:3), reversible	3.00 * Sodium [e] + 1.00 * calcium[2+] [c] → 3.00 * Sodi	SLC8A1;SL	Transport, extracellular				0
CHOLT4_neg	3	0.662521	0.1788004	-0.44559	0.445591	2	0.58498	CHOLT4	choline, sodium cotransport	1.00 * Sodium [e] + 1.00 * Choline [e] → 1.00 * Sodium [c]	SLC5A7	Transport, extracellular				0
CHOLTu_pos	3	0.662521	0.1788004	-0.44559	0.445591	2	0.58498	CHOLTu	Choline uniport	1.00 * Choline [e] → 1.00 * Choline [c]SLC22A2;SLC22A5	SLC22A2;S	Transport, extracellular				0
CREAT14_2_r_neg	6	0.662521	0.1788004	0.475077	0.475077	1	0.58498	CREAT14_2	Creatine transport (sodium symport) (2:1)	2.00 * Sodium [e] + 1.00 * creatine [e] → 2.00 * Sodium [c]	SLC6A8	Transport, extracellular				0
CRNH8_pos	6	0.662521	0.1788004	0.266364	0.266364	1	0.58498	CRNH8	L-carnitine outward transport (H+ antiport)	1.00 * proton [e] + 1.00 * L-Carnitine [c] → 1.00 * proton	SLC22A4	Transport, extracellular				0
CRNH_neg	6	0.662521	0.1788004	0.10815	0.10815	1	0.58498	CRNH	L-carnitine reversible transport	1.00 * L-Carnitine [e] → 1.00 * L-Carnitine [c]SLC22A5	SLC22A5	Transport, extracellular				0
CRNH_pos	6	0.662521	0.1788004	0.266364	0.266364	1	0.58498	CRNH	L-carnitine reversible transport	1.00 * L-Carnitine [e] → 1.00 * L-Carnitine [c]SLC22A5	SLC22A5	Transport, extracellular				0
CRNHuNa_pos	6	0.662521	0.1788004	0.10815	0.10815	1	0.58498	CRNHuNa	L-carnitine inward transport by Na+ symport	1.00 * Sodium [e] + 1.00 * L-Carnitine [e] → 1.00 * Sodi	SLC22A5	Transport, extracellular				0
CYSATB0tc_pos	6	0.662521	0.1788004	0.670927	0.670927	1	0.58498	CYSATB0tc	transport of L-Cysteine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-cysteine [e] + 1.00 * Chloride	SLC6A14	Transport, extracellular				0
CYSSNAT5tc_neg	6	0.662521	0.1788004	0.896923	0.896923	1	0.58498	CYSSNAT5tc	transport of L-Cysteine into the cell coupled with co-transport with	1.00 * proton [c] + 1.00 * Sodium [e] + 1.00 * L-cysteine [e]	SLC38A5	Transport, extracellular				0
CYSSNAT5tc_pos	6	0.662521	0.1788004	0.877626	0.877626	1	0.58498	CYSSNAT5tc	transport of L-Cysteine into the cell coupled with co-transport with	1.00 * proton [c] + 1.00 * Sodium [e] + 1.00 * L-cysteine [e]	SLC38A5	Transport, extracellular				0
CYSTALArBATtc_pos	3	0.662521	0.1788004	-0.86028	0.86028	2	0.58498	CYSTALArBATtc	transport of L-Cysteine into the cell in exchange for L-Alanine by b0,4	1.00 * L-alanine [c] + 1.00 * L-cystine [e] → 1.00 * L-alani	SLC3A1;SL	Transport, extracellular				0
CYSTGLUex_pos	6	0.662521	0.1788004	0.772541	0.772541	1	0.58498	CYSTGLUex	L-cystine/L-glutamate exchanger	1.00 * L-glutamate[1-] [c] + 1.00 * L-cystine [e] → 1.00 * L	SLC3A2;SL	Transport, extracellular				0
FATP6t_neg	3	0.662521	0.1788004	-0.63376	0.633759	2	0.58498	FATP6t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * adreic acid [c] → 1.00 * Sodi	SLC27A2;S	Transport, extracellular				0
FATP7t_neg	3	0.662521	0.1788004	-0.63376	0.633759	2	0.58498	FATP7t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * ceronic acid, C22:6 n-3 [c] →	SLC27A2;S	Transport, extracellular				0
FATP9t_neg	3	0.662521	0.1788004	-0.63376	0.633759	2	0.58498	FATP9t	fatty acid electroneutral transport	1.00 * Sodium [c] + 1.00 * nervonate [c] → 1.00 * Sodium	SLC27A2;S	Transport, extracellular				0
GLNALANaEx_pos	6	0.662521	0.1788004	0.859427	0.859427	1	0.58498	GLNALANaEx	L-alanine/L-glutamine Na-dependent exchange (Gln-L in)	1.00 * Sodium [e] + 1.00 * L-alanine [c] + 1.00 * L-glutami	SLC1A5	Transport, extracellular				0
GLNAT80tc_pos	3	0.662521	0.1788004	-0.88955	0.889548	2	0.58498	GLNAT80tc	Transport of L-Glutamine into the intestinal cells by ATB0 transporter	2.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * Chlori	SLC6A14	Transport, extracellular				0
GLNSERNaEx_pos	6	0.662521	0.1788004	0.832336	0.832336	1	0.58498	GLNSERNaEx	L-serine/L-glutamine Na-dependent exchange (Gln-L in)	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-serin	SLC1A5	Transport, extracellular				0
GLNTHRNaEx_pos	6	0.662521	0.1788004	0.832336	0.832336	1	0.58498	GLNTHRNaEx	L-threonine/L-glutamine Na-dependent exchange (Gln-L in)	1.00 * Sodium [e] + 1.00 * L-glutamine [e] + 1.00 * L-threo	SLC1A5	Transport, extracellular				0
GLN1N1_pos	3	0.662521	0.1788004	-0.86973	0.869725	2	0.58498	GLN1N1	Glutamine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-glutamine	SLC38A3;S	Transport, extracellular				0
GLYSNAT5tc_neg	6	0.662521	0.1788004	0.895213	0.895213	1	0.58498	GLYSNAT5tc	transport of Glycine into the cell coupled with co-transport with So	1.00 * proton [c] + 1.00 * Sodium [e] + 1.00 * Glycine [e]	SLC38A5	Transport, extracellular				0
GLY14_pos	6	0.662521	0.1788004	1.244595	1.244595	1	0.58498	GLY14	glycine transport via sodium symport	1.00 * Sodium [e] + 1.00 * Glycine [e] → 1.00 * Sodium [c]	ACE2;SLC3	Transport, extracellular				0
HCO3_NAT_neg	6	0.662521	0.1788004	0.292216	0.292216	1	0.58498	HCO3_NAT	bicarbonate transport (Na/HCO3 cotransport)	1.00 * Bicarbonate [e] + 1.00 * Sodium [e] → 1.00 * Bicar	SLC4A7	Transport, extracellular				0
HIS14_pos	3	0.662521	0.1788004	-0.53967	0.539673	2	0.58498	HIS14	L-histidine transport in via sodium symport	1.00 * Sodium [e] + 1.00 * L-histidine [e] → 1.00 * Sodium	SLC38A2;S	Transport, extracellular				0
ILELAT1tc_pos	6	0.662521	0.1788004	0.889707	0.889707	1	0.58498	ILELAT1tc	transport of L-Isoleucine by LAT1 in association with 4F2hc, across t	1.00 * L-Isoleucine [e] + 1.00 * L-leucine [c] → 1.00 * L-leu	SLC3A2;SL	Transport, extracellular				0
ILEPHELAT2tc_pos	6	0.662521	0.1788004	0.832843	0.832843	1	0.58498	ILEPHELAT2tc	transport of L-Isoleucine into the cell and efflux of L-Phenylalanine	1.00 * L-Isoleucine [e] + 1.00 * L-phenylalanine [c] → 1.00	SLC3A2;SL	Transport, extracellular				0
KCC1_neg	6	0.662521	0.1788004	0.794038	0.794038	1	0.58498	KCC1	K+-Cl- cotransport	1.00 * potassium [e] + 1.00 * Chloride [e] → 1.00 * potas	SLC12A4;S	Transport, extracellular				0
KCC1_pos	6															

PROSTGE2t2_pos	3	0.662521	0.1788004	-0.67693	0.676932	2	0.758498	PROSTGE2t2	prostaglandin uniport	1.00 * prostaglandin E2(1-)[e] → 1.00 * prostaglandin E2	SLC22A1;S	Transport, extracellular				4
PROSTGE2t_neg	3	0.662521	0.1788004	-0.67693	0.676932	2	0.758498	PROSTGE2t2	prostaglandin transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * prostaglandin E2(1-)[e] →	SLC01A1;S	Transport, extracellular				4
PROSTGE2t_pos	3	0.662521	0.1788004	-0.61964	0.619645	2	0.758498	PROSTGE2t2	prostaglandin transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * prostaglandin E2(1-)[e] →	SLC01A1;S	Transport, extracellular				4
PRO4_2_r_neg	3	0.662521	0.1788004	-1.4783	1.478299	2	0.758498	PRO4_2_r	Proline transport (sodium symport) (2:1)	2.00 * Sodium [e] + 1.00 * L-proline [e] → 2.00 * Sodium	SLC6A7	Transport, extracellular				4
SERGLNNaEx_pos	6	0.662521	0.1788004	0.853722	0.853722	1	0.758498	SERGLNNaEx	L-serine/L-glutamine Na-dependent exchange (Ser-Lin)	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-serine	SLC1A5	Transport, extracellular				4
SERT1_neg	6	0.662521	0.1788004	0.921057	0.921057	1	0.758498	SERT1	Serine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-serine [e]	SLC38A5	Transport, extracellular				4
SERT1_pos	6	0.662521	0.1788004	0.928035	0.928035	1	0.758498	SERT1	Serine transport (Na, H coupled)	1.00 * proton [c] + 2.00 * Sodium [e] + 1.00 * L-serine [e]	SLC38A5	Transport, extracellular				4
S04t4_2_pos	3	0.662521	0.1788004	-0.03739	0.037393	2	0.758498	S04t4_2	sulfate transport via sodium symport	2.00 * Sodium [e] + 1.00 * sulfate [e] → 2.00 * Sodium [c]	SLC13A4	Transport, extracellular				4
SRTN6_2_r_pos	6	0.662521	0.1788004	0.003858	0.003858	1	0.758498	SRTN6_2	Serotonin reversible transport in via sodium symport/potassium ant	2.00 * Sodium [e] + 2.00 * potassium [c] + 1.00 * serotonin	SLC6A4	Transport, extracellular				4
TAUPAT1c_pos	6	0.662521	0.1788004	1.013934	1.013934	1	0.758498	TAUPAT1c	transport of taurine into the intestinal cells by PAT1	1.00 * proton [e] + 1.00 * Taurine [e] → 1.00 * proton [c]	SLC36A1	Transport, extracellular				4
TAURt4_2_r_pos	6	0.662521	0.1788004	0.798705	0.798705	1	0.758498	TAURt4_2	taurine transport (sodium symport) (2:1)	2.00 * Sodium [e] + 1.00 * Taurine [e] → 2.00 * Sodium [c]	SLC6A6	Transport, extracellular				4
THRGLNNaEx_pos	6	0.662521	0.1788004	0.853722	0.853722	1	0.758498	THRGLNNaEx	L-threonine/L-glutamine Na-dependent exchange (Thr-Lin)	1.00 * Sodium [e] + 1.00 * L-glutamine [c] + 1.00 * L-threo	SLC1A5	Transport, extracellular				4
THRPHELAT2t_pos	6	0.662521	0.1788004	0.791739	0.791739	1	0.758498	THRPHELAT2t	transport of L-Threonine into the cell and efflux of L-Phenylalanine ou	1.00 * L-threonine [e] + 1.00 * L-phenylalanine [c] → 1.00	SLC3A2;SL	Transport, extracellular				4
TYPHRELAT2t_pos	3	0.662521	0.1788004	-0.68569	0.68569	2	0.758498	TYPHRELAT2t	transport of L-Tyrosine into the cell and efflux of L-Phenylalanine ou	1.00 * L-tyrosine [e] + 1.00 * L-phenylalanine [c] → 1.00	SLC3A2;SL	Transport, extracellular				4
VALLAT1t_pos	6	0.662521	0.1788004	0.889707	0.889707	1	0.758498	VALLAT1t	transport of L-Valine by LAT1 in association with 4F2hc, across the a	1.00 * L-valine [e] + 1.00 * L-leucine [c] → 1.00 * L-leucine	SLC3A2;SL	Transport, extracellular				4
VALPHELAT2t_pos	6	0.662521	0.1788004	0.832843	0.832843	1	0.758498	VALPHELAT2t	transport of L-Valine into the cell and efflux of L-Phenylalanine out	1.00 * L-valine [e] + 1.00 * L-phenylalanine [c] → 1.00 * L	SLC3A2;SL	Transport, extracellular				4
r0942_neg	6	0.662521	0.1788004	0.475077	0.475077	1	0.758498	r0942	Neurotransmitter-Sodium Symporter (NSS) TCDB:2.A.22.3.4	1.00 * creatine [c] → 1.00 * creatine [e]SLC6A8	SLC6A8	Transport, extracellular				0
r0961_pos	3	0.662521	0.1788004	-0.46888	0.468877	2	0.758498	r0961	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.65.1.1	1.00 * Sodium [e] + 1.00 * bilirubin(2-)[e] → 1.00 * Sodi	CP	Transport, extracellular				0
r0974_pos	3	0.662521	0.1788004	-0.57167	0.571673	2	0.758498	r0974	Active transport	1.00 * Sodium [e] + 1.00 * (R)-Pantothenate [e] → 1.00 * Sod	CP	Transport, extracellular				0
r1045_pos	3	0.662521	0.1788004	-0.38014	0.380138	2	0.758498	r1045	Concentrative Nucleoside Transporter (CNT) TCDB:2.A.41.2.4	1.00 * Sodium [e] + 1.00 * Deoxyguanosine [e] → 1.00 * Sod	SLC28A2;S	Transport, extracellular				0
r1143_pos	3	0.662521	0.1788004	-0.57167	0.571673	2	0.758498	r1143	Major Facilitator(MFS) TCDB:2.A.18.6.3	1.00 * Sodium [e] + 1.00 * L-aspartate(1-)[e] → 1.00 * Sod	SLC38A3	Transport, extracellular				0
r1495_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1495	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * chenodeoxycholate [e] → 2.00	SLC10A1	Transport, extracellular				0
r1497_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1497	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * taurochenodeoxycholate [e] →	SLC10A1	Transport, extracellular				0
r1499_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1499	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * tauroolithocholate [e] → 2.00	SLC10A1	Transport, extracellular				0
r1500_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1500	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * glycolithocholate [e] → 2.00	SLC10A1	Transport, extracellular				0
r1501_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1501	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * taurosodeoxycholate [e] → 2	SLC10A1	Transport, extracellular				0
r1502_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1502	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * glyoursodeoxycholate [e] → 2	SLC10A1	Transport, extracellular				0
r1503_pos	3	0.662521	0.1788004	-0.33919	0.339191	2	0.758498	r1503	Glycoside-Pentose-Hexuronide (GPH):Cation Symporter TCDB:2.A	2.00 * Sodium [e] + 1.00 * sulfochenodeoxycholate [e] →	SLC10A1	Transport, extracellular				0
r1538_pos	3	0.662521	0.1788004	-0.39301	0.393012	2	0.758498	r1538	Anion Exchanger (AE) TCDB:2.A.31.2.8	1.00 * Bicarbonate [e] + 2.00 * Sodium [e] → 1.00 * Bicar	SLC4A5	Transport, extracellular				0
r1632_pos	6	0.662521	0.1788004	0.509084	0.509084	1	0.758498	r1632	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-tyrosine [e] → 1.00 * L-th	SLC7A5	Transport, extracellular				0
r1995_pos	3	0.662521	0.1788004	-0.83331	0.833313	2	0.758498	r1995	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.15	1.00 * L-serine [c] + 1.00 * L-lysine(1+)[e] → 1.00 * L-se	SLC7A9	Transport, extracellular				0
r2102_neg	6	0.662521	0.1788004	0.636543	0.636543	1	0.758498	r2102	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e] + 1.00 * Formate [c] → 1.00 * 2	SLC16A1	Transport, extracellular				0
r2157_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2157	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * chenodeoxycholate [e] + 1	SLC01A1	Transport, extracellular				0
r2158_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2158	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * chenodeoxycholate [e] + 1	SLC01A1	Transport, extracellular				0
r2159_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2159	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * chenodeoxycholate [e] + 1	SLC01A1	Transport, extracellular				0
r2163_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2163	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taurochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2164_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2164	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taurochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2165_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2165	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taurochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2169_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2169	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * tauroolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2170_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2170	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * tauroolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2171_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2171	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * tauroolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2172_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2172	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glycolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2173_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2173	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glycolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2174_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2174	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glycolithocholate [e] + 1	SLC01A1	Transport, extracellular				0
r2178_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2178	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2179_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2179	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2180_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2180	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * taoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2181_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2181	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glyoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2182_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2182	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glyoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2183_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2183	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glyoursodeoxycholate [e]	SLC01A1	Transport, extracellular				0
r2190_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2190	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * sulfochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2191_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2191	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * sulfochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2192_neg	3	0.662521	0.1788004	-0.30634	0.306337	2	0.758498	r2192	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * sulfochenodeoxycholate	SLC01A1	Transport, extracellular				0
r2197_neg	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2197	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLC01A1	Transport, extracellular				0
r2197_pos	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2197	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLC01A1	Transport, extracellular				0
r2212_neg	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2212	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glutathionyl-Hec4 [c] + 1	SLC01A1	Transport, extracellular				0
r2212_pos	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2212	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * glutathionyl-Hec4 [c] + 1	SLC01A1	Transport, extracellular				0
r2213_neg	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2213	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * S-glutathionyl-2,4-dinitro	SLC01A1	Transport, extracellular				0
r2213_pos	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2213	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * S-glutathionyl-2,4-dinitro	SLC01A1	Transport, extracellular				0
r2214_neg	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2214	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * S-glutathionyl-ethacrynic	SLC01A1	Transport, extracellular				0
r2214_pos	3	0.662521	0.1788004	-0.49385	0.493845	2	0.758498	r2214	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * S-glutathionyl-ethacrynic	SLC01A1	Transport, extracellular				0
r2309_neg	3	0.662521	0.1788004	-0.48327	0.483274	2	0.758498	r2309	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLC01A1	Transport, extracellular				0

CHOL4_pos	5	1	0	0.32394	0.32394	1	1	CHOL4	choline, sodium cotransport	1.00 * Sodium [e] + 1.00 * Choline [e] → 1.00 * Sodium [c]	SLC5A7	Transport, extracellular					4
CHOLtu_neg	5	1	0	0.32394	0.32394	1	1	CHOLtu	Choline uniport	1.00 * Choline [e] → 1.00 * Choline [c]	SLC22A2; SLC22A5	Transport, extracellular					4
CYPHELAT2tc_pos	5	1	0	-0.20179	0.201789	2	1	CYPHELAT2	transport of L-Cysteine into the cell and efflux of L-Phenylalanine out	1.00 * L-cysteine [e] + 1.00 * L-phenylalanine [c] → 2.00 * L-cysteine [c]	SLC3A2; SLC6A2	Transport, extracellular					4
DOPA4_2_r_neg	4	1	0	0.192035	0.192035	1	1	DOPA4_2	Dopamine reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * dopaminium[1+] [e] → 2.00 * dopaminium[1+] [c]	SLC6A2; SLC6A2	Transport, extracellular					4
DOPA4_2_r_pos	4	1	0	0.233182	0.233182	1	1	DOPA4_2	Dopamine reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * dopaminium[1+] [e] → 2.00 * dopaminium[1+] [c]	SLC6A2; SLC6A2	Transport, extracellular					4
GCHOLAT_pos	4	1	0	-0.19193	0.191931	2	1	GCHOLAT	glycocholate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * glycocholate [e] → 1.00 * Bicarbonate [e] + 1.00 * glycocholate [c]	SLC10A1; SLC10A1	Transport, extracellular					4
GLU6_pos	5	1	0	-0.01603	0.016032	2	1	GLU6	Glutamate transport via Na, H symport and K antiport	1.00 * proton [e] + 3.00 * Sodium [e] + 1.00 * potassium [e] → 1.00 * proton [c] + 3.00 * Sodium [c] + 1.00 * potassium [c]	SLC1A1; SLC1A1	Transport, extracellular					4
GLY7_311_r_neg	5	1	0	0.541023	0.541023	1	1	GLY7_311	glycine reversible transport via sodium and chloride symport (3:1:1)	3.00 * Sodium [e] + 1.00 * Glycine [e] + 1.00 * Chloride [e] → 3.00 * Sodium [c] + 1.00 * Glycine [c] + 1.00 * Chloride [c]	SLC6A5	Transport, extracellular					4
HCO3_CLT_neg	4	1	0	-0.03983	0.039827	2	1	HCO3_CLT	bicarbonate transport (Cl-/HCO3- exchange)	1.00 * Bicarbonate [e] + 1.00 * Chloride [c] → 1.00 * Bicarbonate [c] + 1.00 * Chloride [e]	SLC4A1; SLC4A1	Transport, extracellular					4
HISTatu_neg	4	1	0	-0.10307	0.103066	2	1	HISTatu	Histamine uniport	1.00 * histaminium [e] → 1.00 * histaminium [c]	SLC22A2; SLC22A2	Transport, extracellular					4
HISTatu_pos	4	1	0	-0.10307	0.103066	2	1	HISTatu	Histamine uniport	1.00 * histaminium [e] → 1.00 * histaminium [c]	SLC22A2; SLC22A2	Transport, extracellular					4
INST2r_neg	5	1	0	0.33103	0.33103	1	1	INST2r	inositol transport in via proton symport	1.00 * proton [e] + 1.00 * myo-inositol [e] → 1.00 * proton [c] + 1.00 * myo-inositol [c]	SLC2A13	Transport, extracellular					4
INST2r_pos	5	1	0	0.33103	0.33103	1	1	INST2r	inositol transport in via proton symport	1.00 * proton [e] + 1.00 * myo-inositol [e] → 1.00 * proton [c] + 1.00 * myo-inositol [c]	SLC2A13	Transport, extracellular					4
INST4_neg	5	1	0	-0.39897	0.398975	2	1	INST4	inositol transport via sodium symport	1.00 * Sodium [e] + 1.00 * myo-inositol [e] → 1.00 * Sodium [c] + 1.00 * myo-inositol [c]	SLC5A3	Transport, extracellular					4
INST4_pos	5	1	0	0.33103	0.33103	1	1	INST4	inositol transport via sodium symport	1.00 * Sodium [e] + 1.00 * myo-inositol [e] → 1.00 * Sodium [c] + 1.00 * myo-inositol [c]	SLC5A3	Transport, extracellular					4
It_neg	4	1	0	0.787431	0.787431	1	1	It	Iodide uniport	1.00 * iodide [e] → 1.00 * iodide [c]	SLC5A8	Transport, extracellular					4
It_pos	5	1	0	-0.50353	0.50353	2	1	It	Iodide uniport	1.00 * iodide [e] → 1.00 * iodide [c]	SLC5A8	Transport, extracellular					4
METtec_pos	5	1	0	0.426401	0.426401	1	1	METtec	L-methionine transport via diffusion (extracellular to cytosol)	1.00 * L-methionine [e] → 1.00 * L-methionine [c]	SLC43A1; SLC43A1	Transport, extracellular					4
NAit_neg	4	1	0	0.72995	0.72995	1	1	NAit	Na+ / iodide cotransport	2.00 * Sodium [e] + 1.00 * iodide [e] → 2.00 * Sodium [c] + 1.00 * iodide [c]	SLC5A5	Transport, extracellular					4
NA5_pos	4	1	0	-0.24311	0.243107	2	1	NA5	sodium/ammonium proton antiporter	1.00 * Sodium [c] + 1.00 * Ammonium [e] → 1.00 * Sodium [e] + 1.00 * Ammonium [c]	SLC9A1; SLC9A1	Transport, extracellular					4
NCKt_neg	4	1	0	-0.20667	0.206673	2	1	NCKt	Na+/Ca2+-K+ exchange	4.00 * Sodium [c] + 1.00 * potassium [e] + 1.00 * calcium [e] → 4.00 * Sodium [e] + 1.00 * potassium [c] + 1.00 * calcium [c]	SLC24A1; SLC24A1	Transport, extracellular					4
NCKt_pos	4	1	0	-0.20667	0.206673	2	1	NCKt	Na+/Ca2+-K+ exchange	4.00 * Sodium [c] + 1.00 * potassium [e] + 1.00 * calcium [e] → 4.00 * Sodium [e] + 1.00 * potassium [c] + 1.00 * calcium [c]	SLC24A1; SLC24A1	Transport, extracellular					4
NCNt_neg	4	1	0	-0.25173	0.251729	2	1	NCNt	Na+/Ca2+-NH4+ exchange	4.00 * Sodium [c] + 1.00 * Ammonium [e] + 1.00 * calcium [e] → 4.00 * Sodium [e] + 1.00 * Ammonium [c] + 1.00 * calcium [c]	SLC24A1; SLC24A1	Transport, extracellular					4
NCNt_pos	4	1	0	-0.25173	0.251729	2	1	NCNt	Na+/Ca2+-NH4+ exchange	4.00 * Sodium [c] + 1.00 * Ammonium [e] + 1.00 * calcium [e] → 4.00 * Sodium [e] + 1.00 * Ammonium [c] + 1.00 * calcium [c]	SLC24A1; SLC24A1	Transport, extracellular					4
NRPPHRT4_2_r_neg	4	1	0	0.168047	0.168047	1	1	NRPPHRT4	Norepinephrine reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * Norepinephrine [e] → 2.00 * Sodium [c] + 1.00 * Norepinephrine [c]	SLC6A2; SLC6A2	Transport, extracellular					4
NRPPHRT4_2_r_pos	4	1	0	0.210376	0.210376	1	1	NRPPHRT4	Norepinephrine reversible transport in via sodium symport (1:2)	2.00 * Sodium [e] + 1.00 * Norepinephrine [e] → 2.00 * Sodium [c] + 1.00 * Norepinephrine [c]	SLC6A2; SLC6A2	Transport, extracellular					4
NRPPHRTu_neg	4	1	0	-0.21047	0.210468	2	1	NRPPHRTu	Norepinephrine uniport	1.00 * Norepinephrine [e] → 1.00 * Norepinephrine [c]	SLC22A1; SLC22A1	Transport, extracellular					4
NRPPHRTu_pos	4	1	0	-0.21047	0.210468	2	1	NRPPHRTu	Norepinephrine uniport	1.00 * Norepinephrine [e] → 1.00 * Norepinephrine [c]	SLC22A1; SLC22A1	Transport, extracellular					4
PHetec_neg	4	1	0	-0.14896	0.148963	2	1	PHetec	L-phenylalanine transport via diffusion (extracellular to cytosol)	1.00 * L-phenylalanine [e] → 1.00 * L-phenylalanine [c]	SLC16A10	Transport, extracellular					4
SO44_2_r_neg	4	1	0	-0.00519	0.005193	2	1	SO44_2	sulfate transport via sodium symport	2.00 * Sodium [e] + 1.00 * sulfate [e] → 2.00 * Sodium [c] + 1.00 * sulfate [c]	SLC13A4	Transport, extracellular					4
SRTM6_2_r_neg	4	1	0	-0.05534	0.055341	2	1	SRTM6_2	Serotonin reversible transport in via sodium symport/potassium antiport	2.00 * Sodium [e] + 2.00 * potassium [c] + 1.00 * serotonin [e] → 2.00 * Sodium [c] + 2.00 * potassium [e] + 1.00 * serotonin [c]	SLC6A4	Transport, extracellular					4
TCHOLAT_pos	4	1	0	-0.1917	0.191698	2	1	TCHOLAT	taurocholate transport via bicarbonate countertransport	1.00 * Bicarbonate [c] + 1.00 * taurocholate [e] → 1.00 * Bicarbonate [e] + 1.00 * taurocholate [c]	SLC10A1; SLC10A1	Transport, extracellular					4
TYRT_neg	5	1	0	0.370945	0.370945	1	1	TYRT	L-tyrosine transport	1.00 * L-tyrosine [e] → 1.00 * L-tyrosine [c]	SLC16A10	Transport, extracellular					4
TYRT_pos	5	1	0	0.370945	0.370945	1	1	TYRT	L-tyrosine transport	1.00 * L-tyrosine [e] → 1.00 * L-tyrosine [c]	SLC16A10	Transport, extracellular					4
r0879_pos	5	1	0	0.142464	0.142464	1	1	r0879	TCDB:2.A.29.2.4 TCDB:2.A.29.16.1	1.00 * Sodium [e] + 1.00 * 2-Oxoglutarate [e] → 1.00 * Sodium [c] + 1.00 * 2-Oxoglutarate [c]	SLC25A19	Transport, extracellular					0
r0899_pos	5	1	0	0.288107	0.288107	1	1	r0899	Amino acid transporter ATB0+ Facilitated diffusion	1.00 * beta-alanine [c] → 1.00 * beta-alanine [e]	1.00 * beta-alanine [c]	Transport, extracellular					0
r0963_pos	5	1	0	0.0576	0.0576	1	1	r0963	Facilitated diffusion	1.00 * Folate [e] → 1.00 * Folate [c]	FOLR1; FOLR2	Transport, extracellular					0
r1492_pos	5	1	0	0.06379	0.06379	1	1	r1492	Utilized transport	1.00 * potassium [c] → 1.00 * potassium [e]	ABCC8; ABCB8; ABCB8; ABCB8	Transport, extracellular					0
r1632_neg	4	1	0	0.046539	0.046539	1	1	r1632	Amino Acid-Polyamine-Organocation (APC) TCDB:2.A.3.8.1	1.00 * L-threonine [c] + 1.00 * L-tyrosine [e] → 1.00 * L-threonine [e] + 1.00 * L-tyrosine [c]	SLC7A5	Transport, extracellular					0
r2093_neg	5	1	0	0.238242	0.238242	1	1	r2093	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [c] + 1.00 * pyruvate [e] → 1.00 * 2-Oxoglutarate [e] + 1.00 * pyruvate [c]	SLC16A1	Transport, extracellular					0
r2101_pos	4	1	0	-0.07152	0.071519	2	1	r2101	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetate [c] + 1.00 * 2-Oxoglutarate [e] → 1.00 * acetate [e] + 1.00 * 2-Oxoglutarate [c]	SLC16A1	Transport, extracellular					0
r2102_pos	4	1	0	-0.07152	0.071519	2	1	r2102	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e] + 1.00 * Formate [c] → 1.00 * 2-Oxoglutarate [c] + 1.00 * Formate [e]	SLC16A1	Transport, extracellular					0
r2103_pos	4	1	0	-0.07152	0.071519	2	1	r2103	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * propionate [c] + 1.00 * 2-Oxoglutarate [e] → 1.00 * propionate [e] + 1.00 * 2-Oxoglutarate [c]	SLC16A1	Transport, extracellular					0
r2104_pos	5	1	0	0.233676	0.233676	1	1	r2104	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * acetoacetate [c] + 1.00 * 2-Oxoglutarate [e] → 1.00 * acetoacetate [e] + 1.00 * 2-Oxoglutarate [c]	SLC16A1	Transport, extracellular					0
r2105_pos	5	1	0	0.238242	0.238242	1	1	r2105	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e] + 1.00 * (S)-lactate [c] → 1.00 * 2-Oxoglutarate [c] + 1.00 * (S)-lactate [e]	SLC16A1	Transport, extracellular					0
r2106_pos	4	1	0	-0.08049	0.080493	2	1	r2106	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e] + 1.00 * butyrate [c] → 1.00 * 2-Oxoglutarate [c] + 1.00 * butyrate [e]	SLC16A1	Transport, extracellular					0
r2108_pos	4	1	0	-0.07152	0.071519	2	1	r2108	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Oxoglutarate [e] + 1.00 * (R)-3-hydroxybutyrate [c] → 1.00 * 2-Oxoglutarate [c] + 1.00 * (R)-3-hydroxybutyrate [e]	SLC16A1	Transport, extracellular					0
r2109_pos	5	1	0	0.238242	0.238242	1	1	r2109	Major Facilitator (MFS) TCDB:2.A.1.13.1	1.00 * 2-Hydroxybutyrate [c] + 1.00 * 2-Oxoglutarate [e] → 1.00 * 2-Hydroxybutyrate [e] + 1.00 * 2-Oxoglutarate [c]	SLC16A1	Transport, extracellular					0
r2139_neg	4	1	0	-0.21608	0.216076	2	1	r2139	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Cholate [e] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Cholate [c] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2139_pos	4	1	0	-0.21608	0.216076	2	1	r2139	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Cholate [e] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Cholate [c] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2140_neg	4	1	0	-0.21328	0.213278	2	1	r2140	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2140_pos	4	1	0	-0.21328	0.213278	2	1	r2140	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2141_neg	4	1	0	-0.21304	0.213043	2	1	r2141	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2141_pos	4	1	0	-0.21304	0.213043	2	1	r2141	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2142_neg	4	1	0	-0.10035	0.100347	2	1	r2142	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2142_pos	4	1	0	-0.10035	0.100347	2	1	r2142	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2143_neg	4	1	0	-0.10035	0.100347	2	1	r2143	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2143_pos	4	1	0	-0.10035	0.100347	2	1	r2143	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2144_neg	4	1	0	-0.10035	0.100347	2	1	r2144	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2144_pos	4	1	0	-0.10035	0.100347	2	1	r2144	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2145_neg	4	1	0	-0.10035	0.100347	2	1	r2145	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2145_pos	4	1	0	-0.10035	0.100347	2	1	r2145	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2146_neg	4	1	0	-0.10035	0.100347	2	1	r2146	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.00 * Reduced glutathione [c]	SLC01A1	Transport, extracellular					0
r2146_pos	4	1	0	-0.10035	0.100347	2	1	r2146	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [e] → 1.00 * Bicarbonate [e] + 1.							

r2156_pos	4	1	0	-0.19193	0.191931	2	1	r2156	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycocholate[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2157_pos	4	1	0	-0.10035	0.100347	2	1	r2157	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * chenodeoxycholate[e] +1	SLCO1A1	Transport, extracellular				0
r2158_pos	4	1	0	-0.10035	0.100347	2	1	r2158	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * chenodeoxycholate[e] +1	SLCO1A1	Transport, extracellular				0
r2159_pos	4	1	0	-0.10035	0.100347	2	1	r2159	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * chenodeoxycholate[e] +1	SLCO1A1	Transport, extracellular				0
r2160_neg	4	1	0	-0.1917	0.191698	2	1	r2160	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * g	SLCO1A1	Transport, extracellular				0
r2160_pos	4	1	0	-0.1917	0.191698	2	1	r2160	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * g	SLCO1A1	Transport, extracellular				0
r2161_neg	4	1	0	-0.1917	0.191698	2	1	r2161	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2161_pos	4	1	0	-0.1917	0.191698	2	1	r2161	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2162_neg	4	1	0	-0.1917	0.191698	2	1	r2162	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2162_pos	4	1	0	-0.1917	0.191698	2	1	r2162	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurocholate[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2163_pos	4	1	0	-0.10035	0.100347	2	1	r2163	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurochenodeoxycholate	SLCO1A1	Transport, extracellular				0
r2164_pos	4	1	0	-0.10035	0.100347	2	1	r2164	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurochenodeoxycholate	SLCO1A1	Transport, extracellular				0
r2165_pos	4	1	0	-0.10035	0.100347	2	1	r2165	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurochenodeoxycholate	SLCO1A1	Transport, extracellular				0
r2166_neg	4	1	0	-0.10035	0.100347	2	1	r2166	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2166_pos	4	1	0	-0.10035	0.100347	2	1	r2166	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2167_neg	4	1	0	-0.10035	0.100347	2	1	r2167	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2167_pos	4	1	0	-0.10035	0.100347	2	1	r2167	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2168_neg	4	1	0	-0.10035	0.100347	2	1	r2168	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2168_pos	4	1	0	-0.10035	0.100347	2	1	r2168	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2169_pos	4	1	0	-0.10035	0.100347	2	1	r2169	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * tauroolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2170_pos	4	1	0	-0.10035	0.100347	2	1	r2170	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * tauroolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2171_pos	4	1	0	-0.10035	0.100347	2	1	r2171	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * tauroolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2172_pos	4	1	0	-0.10035	0.100347	2	1	r2172	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2173_pos	4	1	0	-0.10035	0.100347	2	1	r2173	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2174_pos	4	1	0	-0.10035	0.100347	2	1	r2174	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycolithocholate[e] +1.0	SLCO1A1	Transport, extracellular				0
r2175_neg	4	1	0	-0.10035	0.100347	2	1	r2175	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2175_pos	4	1	0	-0.10035	0.100347	2	1	r2175	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2176_neg	4	1	0	-0.10035	0.100347	2	1	r2176	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2176_pos	4	1	0	-0.10035	0.100347	2	1	r2176	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2177_neg	4	1	0	-0.10035	0.100347	2	1	r2177	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2177_pos	4	1	0	-0.10035	0.100347	2	1	r2177	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2178_pos	4	1	0	-0.10035	0.100347	2	1	r2178	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurosodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2179_pos	4	1	0	-0.10035	0.100347	2	1	r2179	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurosodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2180_pos	4	1	0	-0.10035	0.100347	2	1	r2180	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * taurosodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2181_pos	4	1	0	-0.10035	0.100347	2	1	r2181	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycoursoeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2182_pos	4	1	0	-0.10035	0.100347	2	1	r2182	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycoursoeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2183_pos	4	1	0	-0.10035	0.100347	2	1	r2183	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glycoursoeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2184_neg	4	1	0	-0.10035	0.100347	2	1	r2184	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2184_pos	4	1	0	-0.10035	0.100347	2	1	r2184	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2185_neg	4	1	0	-0.10035	0.100347	2	1	r2185	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2185_pos	4	1	0	-0.10035	0.100347	2	1	r2185	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2186_neg	4	1	0	-0.10035	0.100347	2	1	r2186	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2186_pos	4	1	0	-0.10035	0.100347	2	1	r2186	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2187_neg	4	1	0	-0.10035	0.100347	2	1	r2187	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2187_pos	4	1	0	-0.10035	0.100347	2	1	r2187	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * glutathionyl-leuc4[c] +1	SLCO1A1	Transport, extracellular				0
r2188_neg	4	1	0	-0.10035	0.100347	2	1	r2188	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2188_pos	4	1	0	-0.10035	0.100347	2	1	r2188	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-2-4-dinitro	SLCO1A1	Transport, extracellular				0
r2189_neg	4	1	0	-0.10035	0.100347	2	1	r2189	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2189_pos	4	1	0	-0.10035	0.100347	2	1	r2189	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * S-glutathionyl-ethacrynic	SLCO1A1	Transport, extracellular				0
r2190_pos	4	1	0	-0.10035	0.100347	2	1	r2190	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * sulfochenodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2191_pos	4	1	0	-0.10035	0.100347	2	1	r2191	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * sulfochenodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2192_pos	4	1	0	-0.10035	0.100347	2	1	r2192	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * sulfochenodeoxycholate[e]	SLCO1A1	Transport, extracellular				0
r2193_neg	4	1	0	-0.21713	0.217134	2	1	r2193	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * Re	SLCO1A1	Transport, extracellular				0
r2193_pos	4	1	0	-0.21713	0.217134	2	1	r2193	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * Re	SLCO1A1	Transport, extracellular				0
r2194_neg	4	1	0	-0.21579	0.215791	2	1	r2194	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * Reduced glutathione[c] +	SLCO1A1	Transport, extracellular				0
r2194_pos	4	1	0	-0.21579	0.215791	2	1	r2194	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * Reduced glutathione[c] +	SLCO1A1	Transport, extracellular				0
r2195_neg	4	1	0	-0.21304	0.213043	2	1	r2195	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * Reduced glutathione[c] +	SLCO1A1	Transport, extracellular				0
r2195_pos	4	1	0	-0.21304	0.213043	2	1	r2195	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * Reduced glutathione[c] +	SLCO1A1	Transport, extracellular				0
r2203_neg	4	1	0	-0.10734	0.107335	2	1	r2203	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * gl	SLCO1A1	Transport, extracellular				0
r2203_pos	4	1	0	-0.19569	0.195687	2	1	r2203	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * gl	SLCO1A1	Transport, extracellular				0
r2204_neg	4	1	0	-0.10734	0.107335	2	1	r2204	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2204_pos	4	1	0	-0.19569	0.195687	2	1	r2204	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2205_neg	4	1	0	-0.10734	0.107335	2	1	r2205	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2205_pos	4	1	0	-0.19569	0.195687	2	1	r2205	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * bilirubin(2-)[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2206_neg	4	1	0	-0.19439	0.194385	2	1	r2206	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * glu	SLCO1A1	Transport, extracellular				0
r2206_pos	4	1	0	-0.19439	0.194385	2	1	r2206	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * glu	SLCO1A1	Transport, extracellular				0
r2207_neg	4	1	0	-0.19439	0.194385	2	1	r2207	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2207_pos	4	1	0	-0.19439	0.194385	2	1	r2207	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2208_neg	4	1	0	-0.19439	0.194385	2	1	r2208	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2208_pos	4	1	0	-0.19439	0.194385	2	1	r2208	Resistance-Nodulation-Cell Division (RND) TDCB:2.A.60.1.14	1.00 * Bicarbonate[c] +1.00 * L-thyroxine[e] +1.00 * S	SLCO1A1	Transport, extracellular				0
r2209_neg	4	1	0	-0.1917	0.191698</											

r2308_pos	4	1	0	-0.38204	0.382035	2	1	r2308	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLCO1A1	Transport, extracellular				0
r2312_neg	4	1	0	-0.38204	0.382035	2	1	r2312	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLCO1A1	Transport, extracellular				0
r2312_pos	4	1	0	-0.38204	0.382035	2	1	r2312	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [c] + 1.00 * Reduced glutathione [c] +	SLCO1A1	Transport, extracellular				0
r2338_neg	4	1	0	-0.22233	0.222328	2	1	r2338	Major Facilitator (MFS) TCDB:2.A.1.19.1	1.00 * acetylcholine [e] -> 1.00 * acetylcholine [c]SLC22A	SLC22A1	Transport, extracellular				0
r2338_pos	4	1	0	-0.22233	0.222328	2	1	r2338	Major Facilitator (MFS) TCDB:2.A.1.19.1	1.00 * acetylcholine [e] -> 1.00 * acetylcholine [c]SLC22A	SLC22A1	Transport, extracellular				0
r2370_pos	4	1	0	-0.52556	0.525562	2	1	r2370	Nucleobase:Cation Symporter-2 (NC52) TCDB:2.A.40.6.1	2.00 * Sodium [e] + 1.00 * L-ascorbate [e] -> 2.00 * Sodium	SLC23A1	Transport, extracellular				0
r2482_neg	4	1	0	-0.10307	0.103066	2	1	r2482	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * glut	SLCO1A1	Transport, extracellular				0
r2482_pos	4	1	0	-0.10307	0.103066	2	1	r2482	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * glut	SLCO1A1	Transport, extracellular				0
r2483_neg	4	1	0	-0.10307	0.103066	2	1	r2483	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * S-gl	SLCO1A1	Transport, extracellular				0
r2483_pos	4	1	0	-0.10307	0.103066	2	1	r2483	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * S-gl	SLCO1A1	Transport, extracellular				0
r2484_neg	4	1	0	-0.10307	0.103066	2	1	r2484	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * S-gl	SLCO1A1	Transport, extracellular				0
r2484_pos	4	1	0	-0.10307	0.103066	2	1	r2484	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * histamine [c] + 1.00 * S-gl	SLCO1A1	Transport, extracellular				0
r2485_neg	4	1	0	-0.21047	0.210468	2	1	r2485	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2485_pos	4	1	0	-0.21047	0.210468	2	1	r2485	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2486_neg	4	1	0	-0.21047	0.210468	2	1	r2486	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2486_pos	4	1	0	-0.21047	0.210468	2	1	r2486	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2487_neg	4	1	0	-0.21047	0.210468	2	1	r2487	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2487_pos	4	1	0	-0.21047	0.210468	2	1	r2487	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * Norepinephrine [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2488_neg	4	1	0	-0.22233	0.222333	2	1	r2488	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * g	SLCO1A1	Transport, extracellular				0
r2488_pos	4	1	0	-0.22233	0.222333	2	1	r2488	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * g	SLCO1A1	Transport, extracellular				0
r2489_neg	4	1	0	-0.22233	0.222333	2	1	r2489	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2489_pos	4	1	0	-0.22233	0.222333	2	1	r2489	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2490_neg	4	1	0	-0.22233	0.222333	2	1	r2490	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2490_pos	4	1	0	-0.22233	0.222333	2	1	r2490	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * serotonin(1+) [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2491_neg	4	1	0	-0.22233	0.222328	2	1	r2491	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * g	SLCO1A1	Transport, extracellular				0
r2491_pos	4	1	0	-0.22233	0.222328	2	1	r2491	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * g	SLCO1A1	Transport, extracellular				0
r2492_neg	4	1	0	-0.22233	0.222328	2	1	r2492	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2492_pos	4	1	0	-0.22233	0.222328	2	1	r2492	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2493_neg	4	1	0	-0.22233	0.222328	2	1	r2493	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2493_pos	4	1	0	-0.22233	0.222328	2	1	r2493	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * acetylcholine [c] + 1.00 * S	SLCO1A1	Transport, extracellular				0
r2494_neg	4	1	0	-0.10307	0.103066	2	1	r2494	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2494_pos	4	1	0	-0.10307	0.103066	2	1	r2494	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2495_neg	4	1	0	-0.10307	0.103066	2	1	r2495	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2495_pos	4	1	0	-0.10307	0.103066	2	1	r2495	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2496_neg	4	1	0	-0.10307	0.103066	2	1	r2496	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2496_pos	4	1	0	-0.10307	0.103066	2	1	r2496	Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14	1.00 * Bicarbonate [e] + 1.00 * dopaminium(1+) [c] + 1.00	SLCO1A1	Transport, extracellular				0
r2534_neg	5	1	0	0.128895	0.128895	1	1	r2534	Major Facilitator (MFS) TCDB:2.A.1.44.1	1.00 * L-threonine [e] -> 1.00 * L-threonine [c]SLC43A1	SLC43A1	Transport, extracellular				0
r1052_pos	7	0.382733	0.4171041	1.272298	1.272298	1	0.518179	r1052	Vesicular transport	1.00 * cholesterol [l] -> 1.00 * cholesterol [c]No genes	1.00 * cho	Transport, lysosomal				0
r1301_pos	2	0.382733	0.4171041	-1.2911	1.291104	2	0.518179	r1301	Vesicular transport	1.00 * octadecenoate (n-C18:1) [l] -> 1.00 * octadecenoa	1.00 * octa	Transport, lysosomal				0
r1302_neg	2	0.382733	0.4171041	-1.2911	1.291104	2	0.518179	r1302	Vesicular transport	1.00 * octadecenoate (n-C18:1) [l] -> 1.00 * octadecenoa	1.00 * octa	Transport, lysosomal				0
AHCYSTd_neg	0	0.080856	1.0922877	-2.62935	2.629346	2	0.240222	AHCYSTd	diffusion of S-Adenosyl-L-homocysteine	1.00 * S-Adenosyl-L-homocysteine [m] -> 1.00 * S-Adeno	1.00 * S-Ad	Transport, mitochondrial				4
AHCYSTd_pos	0	0.080856	1.0922877	-2.62935	2.629346	2	0.240222	AHCYSTd	diffusion of S-Adenosyl-L-homocysteine	1.00 * S-Adenosyl-L-homocysteine [m] -> 1.00 * S-Adeno	1.00 * S-Ad	Transport, mitochondrial				4
AKGMALtm_neg	0	0.080856	1.0922877	-2.29702	2.297021	2	0.240222	AKGMALtm	alpha-ketoglutarate/malate transporter	1.00 * 2-Oxoglutarate [m] + 1.00 * (S)-malate(2-) [c] -> 1.00	SLC25A10	Transport, mitochondrial				4
AKGMALtm_pos	0	0.080856	1.0922877	-2.29702	2.297021	2	0.240222	AKGMALtm	alpha-ketoglutarate/malate transporter	1.00 * 2-Oxoglutarate [m] + 1.00 * (S)-malate(2-) [c] -> 1.00	SLC25A10	Transport, mitochondrial				4
AMET2m_neg	0	0.080856	1.0922877	-2.62935	2.629346	2	0.240222	AMET2m	S-Adenosyl-L-methionine reversible transport, mitochondrial	1.00 * S-Adenosyl-L-methionine [c] + 1.00 * S-Adenosyl-L-	SLC25A26	Transport, mitochondrial				4
AMET2m_pos	0	0.080856	1.0922877	-2.62935	2.629346	2	0.240222	AMET2m	S-Adenosyl-L-methionine reversible transport, mitochondrial	1.00 * S-Adenosyl-L-methionine [c] + 1.00 * S-Adenosyl-L-	SLC25A26	Transport, mitochondrial				4
ARGtm_neg	0	0.080856	1.0922877	-2.57949	2.579493	2	0.240222	ARGtm	arginine mitochondrial transport via ornithine carrier	1.00 * proton [m] + 1.00 * L-argininium(1+) [c] -> 1.00 * p	SLC25A2	Transport, mitochondrial				4
ARGtm_pos	0	0.080856	1.0922877	-2.57949	2.579493	2	0.240222	ARGtm	arginine mitochondrial transport via ornithine carrier	1.00 * proton [m] + 1.00 * L-argininium(1+) [c] -> 1.00 * p	SLC25A2	Transport, mitochondrial				4
CITRtm_neg	0	0.080856	1.0922877	-2.57949	2.579493	2	0.240222	CITRtm	citulline mitochondrial transport via proton antiport	1.00 * L-citrulline [m] -> 1.00 * L-citrulline [c]SLC25A2	SLC25A2	Transport, mitochondrial				4
CITRtm_pos	0	0.080856	1.0922877	-2.57949	2.579493	2	0.240222	CITRtm	citulline mitochondrial transport via proton antiport	1.00 * L-citrulline [m] -> 1.00 * L-citrulline [c]SLC25A2	SLC25A2	Transport, mitochondrial				4
CITtm_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	CITtm	citrate transport, mitochondrial	1.00 * Citrate [c] + 1.00 * (S)-malate(2-) [m] -> 1.00 * Citr	SLC25A1	Transport, mitochondrial				4
CITtm_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	CITtm	citrate transport, mitochondrial	1.00 * Citrate [c] + 1.00 * (S)-malate(2-) [m] -> 1.00 * Citr	SLC25A1	Transport, mitochondrial				4
CITbm_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	CITbm	citrate transport, mitochondrial	1.00 * Citrate [c] + 1.00 * Phosphoenolpyruvate [m] -> 1.	SLC25A1	Transport, mitochondrial				4
CO2tm_neg	0	0.080856	1.0922877	-2.31899	2.318987	2	0.240222	CO2tm	CO2 transport (diffusion), mitochondrial	1.00 * carbon dioxide [c] -> 1.00 * carbon dioxide [m]No	1.00 * carb	Transport, mitochondrial				4
CO2tm_pos	0	0.080856	1.0922877	-2.31899	2.318987	2	0.240222	CO2tm	CO2 transport (diffusion), mitochondrial	1.00 * carbon dioxide [c] -> 1.00 * carbon dioxide [m]No	1.00 * carb	Transport, mitochondrial				4
DNDP129m_pos	9	0.080856	1.0922877	1.685929	1.685929	1	0.240222	DNDP129m	dCDP transport via dADP antiport	1.00 * dCDP [c] + 1.00 * dADP [m] -> 1.00 * dADP [c] + 1.0	SLC25A19	Transport, mitochondrial				4
DNDP135m_pos	9	0.080856	1.0922877	1.685929	1.685929	1	0.240222	DNDP135m	dGDP transport via dADP antiport	1.00 * dGDP [c] + 1.00 * dADP [m] -> 1.00 * dADP [c] + 1.0	SLC25A19	Transport, mitochondrial				4
DNDP140m_pos	9	0.080856	1.0922877	1.678948	1.678948	1	0.240222	DNDP140m	dUTP transport via dADP antiport	1.00 * dADP [m] + 1.00 * dUTP [c] -> 1.00 * dADP [c] + 1.0	SLC25A19	Transport, mitochondrial				4
DNDP18m_pos	9	0.080856	1.0922877	1.678948	1.678948	1	0.240222	DNDP18m	dADP transport via dUDP antiport	1.00 * dADP [c] + 1.00 * dUDP [m] -> 1.00 * dADP [m] + 1.	SLC25A19	Transport, mitochondrial				4
DNDP19m_pos	9	0.080856	1.0922877	1.685929	1.685929	1	0.240222	DNDP19m	dADP transport via dTDP antiport	1.00 * dADP [c] + 1.00 * dTDP [m] -> 1.00 * dADP [m] + 1.	SLC25A19	Transport, mitochondrial				4
FUMS03tm_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMS03tm	Fumarate:sulfite antiport, mitochondrial	1.00 * Sulfite [m] + 1.00 * Fumarate [c] -> 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				4
FUMS03tm_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMS03tm	Fumarate:sulfite antiport, mitochondrial	1.00 * Sulfite [m] + 1.00 * Fumarate [c] -> 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				4
FUMS04tm_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMS04tm	Fumarate:sulfate antiport, mitochondrial	1.00 * Fumarate [c] + 1.00 * sulfate [m] -> 1.00 * Fumarat	SLC25A10	Transport, mitochondrial				4
FUMS04tm_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMS04tm	Fumarate:sulfate antiport, mitochondrial	1.00 * Fumarate [c] + 1.00 * sulfate [m] -> 1.00 * Fumarat	SLC25A10	Transport, mitochondrial				4
FUMSULTm_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMSULTm	Fumarate:thiosulfate antiport, mitochondrial	1.00 * Fumarate [c] + 1.00 * thiosulfate(2-) [m] -> 1.00 * F	SLC25A10	Transport, mitochondrial				4
FUMSULTm_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	FUMSULTm	Fumarate:thiosulfate antiport, mitochondrial	1.00 * Fumarate [c] + 1.00 * thiosulfate(2-) [m] -> 1.00 * F	SLC25A10	Transport, mitochondrial				4
FUMtm_neg	0	0.08														

r0819_pos	0	0.080856	1.0922877	-1.95861	1.958608	2	0.240222	r0819	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * 2-Oxoglutarate[c] + 1.00 * Succinate[m] → 1.00 *	SLC25A10	Transport, mitochondrial				0
r0821_neg	0	0.080856	1.0922877	-1.73617	1.736166	2	0.240222	r0821	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Fumarate[c] + 1.00 * Succinate[m] → 1.00 * Succ	SLC25A10	Transport, mitochondrial				0
r0821_pos	0	0.080856	1.0922877	-1.73617	1.736166	2	0.240222	r0821	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Fumarate[c] + 1.00 * Succinate[m] → 1.00 * Succ	SLC25A10	Transport, mitochondrial				0
r0822_neg	0	0.080856	1.0922877	-1.73617	1.736166	2	0.240222	r0822	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Fumarate[c] + 1.00 * (S)-malate[2-] [m] → 1.00 * (S	SLC25A10	Transport, mitochondrial				0
r0822_pos	0	0.080856	1.0922877	-1.73617	1.736166	2	0.240222	r0822	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Fumarate[c] + 1.00 * (S)-malate[2-] [m] → 1.00 * (S	SLC25A10	Transport, mitochondrial				0
r0829_neg	0	0.080856	1.0922877	-2.27787	2.277875	2	0.240222	r0829	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Succinate[c] + 1.00 * sulfate [m] → 1.00 * sulfate [c]	SLC25A10	Transport, mitochondrial				0
r0829_pos	0	0.080856	1.0922877	-2.27787	2.277875	2	0.240222	r0829	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Succinate[c] + 1.00 * sulfate [m] → 1.00 * sulfate [c]	SLC25A10	Transport, mitochondrial				0
r0830_neg	0	0.080856	1.0922877	-2.27787	2.277875	2	0.240222	r0830	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Sulfite [m] + 1.00 * Succinate[c] → 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				0
r0830_pos	0	0.080856	1.0922877	-2.27787	2.277875	2	0.240222	r0830	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Sulfite [m] + 1.00 * Succinate[c] → 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				0
r0834_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0834	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * hydrogenphosphate [m] + 1.00 * Malonate [c] → 1	SLC25A10	Transport, mitochondrial				0
r0834_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0834	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * hydrogenphosphate [m] + 1.00 * Malonate [c] → 1	SLC25A10	Transport, mitochondrial				0
r0835_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0835	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * sulfate [m] + 1.00 * Malonate [c] → 1.00 * sulfate [c]	SLC25A10	Transport, mitochondrial				0
r0835_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0835	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * sulfate [m] + 1.00 * Malonate [c] → 1.00 * sulfate [c]	SLC25A10	Transport, mitochondrial				0
r0836_neg	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0836	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Sulfite [m] + 1.00 * Malonate [c] → 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				0
r0836_pos	0	0.080856	1.0922877	-1.74841	1.748415	2	0.240222	r0836	Mitochondrial Carrier (MC) TCDB:2.A.29.2.2	1.00 * Sulfite [m] + 1.00 * Malonate [c] → 1.00 * Sulfite [c]	SLC25A10	Transport, mitochondrial				0
r0911_neg	9	0.080856	1.0922877	2.494541	2.494541	1	0.240222	r0911	Facilitated diffusion	1.00 * L-glutamate[1-] [m] + 1.00 * L-proline [c] → 1.00 *	1.00 * L-gl	Transport, mitochondrial				0
r0911_pos	0	0.080856	1.0922877	-2.391	2.391	2	0.240222	r0911	Facilitated diffusion	1.00 * L-glutamate[1-] [m] + 1.00 * L-proline [c] → 1.00 *	1.00 * L-gl	Transport, mitochondrial				0
r0913_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r0913	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * (S)-malate[2-] [c] → 1.00 * Is	SLC25A1	Transport, mitochondrial				0
r0913_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r0913	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * (S)-malate[2-] [c] → 1.00 * Is	SLC25A1	Transport, mitochondrial				0
r0915_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r0915	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [c] + 1.00 * Succinate [m] → 1.00 * Citrate	SLC25A1	Transport, mitochondrial				0
r0915_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r0915	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [c] + 1.00 * Succinate [m] → 1.00 * Citrate	SLC25A1	Transport, mitochondrial				0
r0941_neg	0	0.080856	1.0922877	-2.94107	2.941075	2	0.240222	r0941	Free diffusion	1.00 * Bicarbonate [c] → 1.00 * Bicarbonate [m] No genes	1.00 * Bica	Transport, mitochondrial				0
r0941_pos	0	0.080856	1.0922877	-2.31899	2.318987	2	0.240222	r0941	Free diffusion	1.00 * Bicarbonate [c] → 1.00 * Bicarbonate [m] No genes	1.00 * Bica	Transport, mitochondrial				0
r0947_neg	0	0.080856	1.0922877	-2.63549	2.635493	2	0.240222	r0947	Mitochondrial Carrier (MC) TCDB:2.A.29.19.1	1.00 * Ornithine [m] + 1.00 * L-citrulline [c] → 1.00 * Orn	SLC25A2	Transport, mitochondrial				0
r0947_pos	0	0.080856	1.0922877	-2.66231	2.662308	2	0.240222	r0947	Mitochondrial Carrier (MC) TCDB:2.A.29.19.1	1.00 * Ornithine [m] + 1.00 * L-citrulline [c] → 1.00 * Orn	SLC25A2	Transport, mitochondrial				0
r1155_pos	0	0.080856	1.0922877	-3.09389	3.093893	2	0.240222	r1155	TCDB:2.A.1.13.5 TCDB:2.A.1.13.1	1.00 * proton [c] + 1.00 * 2-Oxobutanoate [c] → 1.00 * pr	SLC16A1;S	Transport, mitochondrial				0
r1427_pos	0	0.080856	1.0922877	-2.42231	2.422306	2	0.240222	r1427	TCDB:2.A.1.13.5 TCDB:2.A.1.13.1	1.00 * proton [c] + 1.00 * L-histidine [c] → 1.00 * proton	SLC25A2	Transport, mitochondrial		4.2.1.1		0
r1454_pos	0	0.080856	1.0922877	-3.09389	3.093893	2	0.240222	r1454	TCDB:2.A.1.13.5 TCDB:2.A.1.13.1	1.00 * proton [c] + 1.00 * 2-Oxobutanoate [m] → 1.00 * p	SLC16A1;S	Transport, mitochondrial				0
r1455_pos	0	0.080856	1.0922877	-2.99797	2.997971	2	0.240222	r1455	Transport reaction	1.00 * proton [c] + 1.00 * L-phenylalanine [c] → 1.00 * pr	1.00 * pro	Transport, mitochondrial				0
r1456_pos	0	0.080856	1.0922877	-2.99797	2.997971	2	0.240222	r1456	Transport reaction	1.00 * proton [c] + 1.00 * L-phenylalanine [m] → 1.00 * p	1.00 * pro	Transport, mitochondrial				0
r2371_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2371	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [m] + 1.00 * cis-aconitate[3-] [c] → 1.00 * C	SLC25A1	Transport, mitochondrial				0
r2371_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2371	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [m] + 1.00 * cis-aconitate[3-] [c] → 1.00 * C	SLC25A1	Transport, mitochondrial				0
r2372_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2372	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * cis-aconitate[3-] [c] → 1.00	SLC25A1	Transport, mitochondrial				0
r2372_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2372	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * cis-aconitate[3-] [c] → 1.00	SLC25A1	Transport, mitochondrial				0
r2373_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2373	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * Citrate [m] → 1.00 * 2	SLC25A1	Transport, mitochondrial				0
r2373_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2373	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * Citrate [m] → 1.00 * 2	SLC25A1	Transport, mitochondrial				0
r2374_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2374	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [m] + 1.00 * oxalate[2-] [c] → 1.00 * Citrate	SLC25A1	Transport, mitochondrial				0
r2374_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2374	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [m] + 1.00 * oxalate[2-] [c] → 1.00 * Citrate	SLC25A1	Transport, mitochondrial				0
r2375_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2375	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * Succinate [c] → 1.00 * Isoc	SLC25A1	Transport, mitochondrial				0
r2375_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2375	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * Succinate [c] → 1.00 * Isoc	SLC25A1	Transport, mitochondrial				0
r2376_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2376	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * oxalate[2-] [c] → 1.00 * Isoc	SLC25A1	Transport, mitochondrial				0
r2376_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2376	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Isocitrate [m] + 1.00 * oxalate[2-] [c] → 1.00 * Isoc	SLC25A1	Transport, mitochondrial				0
r2377_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2377	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * cis-aconitate[3-] [m] →	SLC25A1	Transport, mitochondrial				0
r2377_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2377	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * cis-aconitate[3-] [m] →	SLC25A1	Transport, mitochondrial				0
r2378_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2378	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Succinate [c] + 1.00 * cis-aconitate[3-] [m] → 1.00	SLC25A1	Transport, mitochondrial				0
r2378_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2378	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Succinate [c] + 1.00 * cis-aconitate[3-] [m] → 1.00	SLC25A1	Transport, mitochondrial				0
r2379_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2379	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * (S)-malate[2-] [c] + 1.00 * cis-aconitate[3-] [m] → 1	SLC25A1	Transport, mitochondrial				0
r2379_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2379	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * (S)-malate[2-] [c] + 1.00 * cis-aconitate[3-] [m] → 1	SLC25A1	Transport, mitochondrial				0
r2380_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2380	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * oxalate[2-] [c] + 1.00 * cis-aconitate[3-] [m] → 1.00	SLC25A1	Transport, mitochondrial				0
r2380_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2380	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * oxalate[2-] [c] + 1.00 * cis-aconitate[3-] [m] → 1.00	SLC25A1	Transport, mitochondrial				0
r2381_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2381	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * 2-Oxoglutarate [m] + 1.00 * Citr	SLC25A1	Transport, mitochondrial				0
r2382_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2382	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Citrate [c] + 1.00 * Succinate [m]	SLC25A1	Transport, mitochondrial				0
r2384_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2384	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Citrate [c] + 1.00 * oxalate[2-] [m]	SLC25A1	Transport, mitochondrial				0
r2385_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2385	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * 2-Oxoglutarate [m] + 1.00 * Isoc	SLC25A1	Transport, mitochondrial				0
r2386_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2386	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Isocitrate [c] + 1.00 * Succinate	SLC25A1	Transport, mitochondrial				0
r2387_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2387	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Isocitrate [c] + 1.00 * (S)-malate	SLC25A1	Transport, mitochondrial				0
r2388_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2388	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Isocitrate [c] + 1.00 * oxalate[2-	SLC25A1	Transport, mitochondrial				0
r2389_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2389	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * 2-Oxoglutarate [m] + 1.00 * cis	SLC25A1	Transport, mitochondrial				0
r2390_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2390	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * Succinate [m] + 1.00 * cis-aconi	SLC25A1	Transport, mitochondrial				0
r2391_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2391	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * (S)-malate[2-] [m] + 1.00 * cis-ac	SLC25A1	Transport, mitochondrial				0
r2392_pos	0	0.080856	1.0922877	-4.53377	4.533774	2	0.240222	r2392	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * proton [c] + 1.00 * cis-aconitate[3-] [c] + 1.00 * oxa	SLC25A1	Transport, mitochondrial				0
r2393_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r2393	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Phosphoenolpyruvate [c] + 1.00 * Isocitrate [m] →	SLC25A1	Transport, mitochondrial				0
r2394_pos	0	0.080856	1.0922877	-1.94736	1.94											

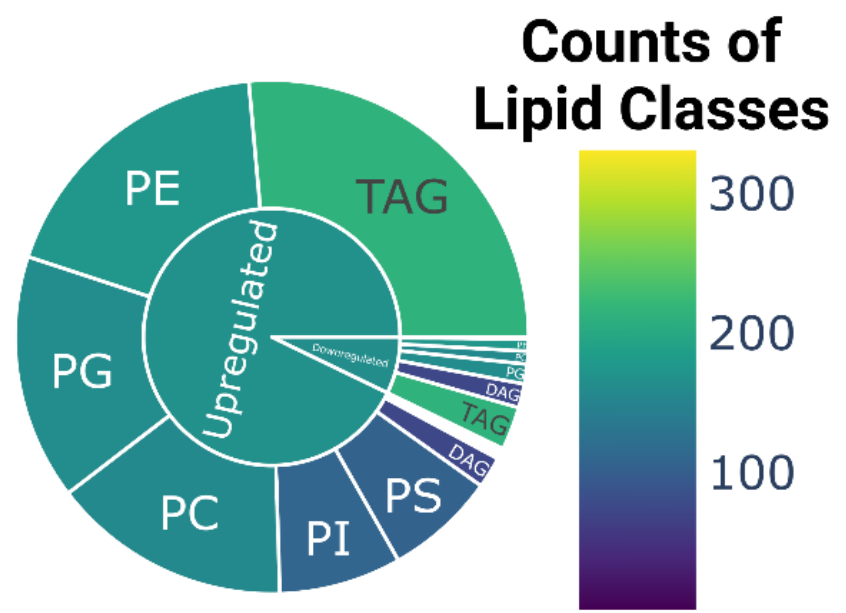
r2420_pos	0	0.080856	1.0922877	2.27787	2.277875	2	0.240222	r2420	Mitochondrial Carrier (MC) TCDB:2.A.29.2.7	1.00 * hydrogenphosphate [m] + 1.00 * oxalate[2-] [c] ->	SLC25A10	Transport, mitochondrial				0
MALtm_neg	1	0.19043	0.7202646	-1.51471	1.51471	2	0.347218	MALtm	malate transport, mitochondrial	1.00 * hydrogenphosphate [m] + 1.00 * (S)-malate[2-] [c]	SLC25A10	Transport, mitochondrial				4
ACETONET2m_pos	1	0.19043	0.7202646	-1.89059	1.890593	2	0.347218	ACETONET2	acetone mitochondrial transport via proton symport	1.00 * proton [c] + 1.00 * acetone [c] -> 1.00 * proton [m]	SLC16A1	Transport, mitochondrial				0
L_LACtm_neg	1	0.19043	0.7202646	-1.91888	1.918884	2	0.347218	L_LACtm	L-lactate transport, mitochondrial	1.00 * proton [c] + 1.00 * (S)-lactate [c] -> 1.00 * proton [m]	SLC16A1	Transport, mitochondrial				0
r0801_neg	8	0.19043	0.7202646	-1.20162	1.201062	1	0.347218	r0801	mitochondrial Carrier (MC) TCDB:2.A.29.21.1	1.00 * GTP [c] + 1.00 * GDP [m] -> 1.00 * GDP [c] + 1.00 * GTP [m]	1.00 * GTP	Transport, mitochondrial				0
r0885_neg	1	0.19043	0.7202646	-1.39467	1.394674	2	0.347218	r0885	Mitochondrial Carrier (MC) TCDB:2.A.29.2.7	1.00 * hydrogenphosphate [m] + 1.00 * Reduced glutathione [c]	SLC25A10	Transport, mitochondrial				0
r0885_pos	1	0.19043	0.7202646	-1.23647	1.236474	2	0.347218	r0885	Mitochondrial Carrier (MC) TCDB:2.A.29.2.7	1.00 * hydrogenphosphate [m] + 1.00 * Reduced glutathione [c]	SLC25A10	Transport, mitochondrial				0
r0927_pos	1	0.19043	0.7202646	-1.89059	1.890593	2	0.347218	r0927	Free diffusion	1.00 * acetone [m] -> 1.00 * acetone [e]No genes	1.00 * acet	Transport, mitochondrial				0
r2419_pos	1	0.19043	0.7202646	-1.51471	1.51471	2	0.347218	r2419	Mitochondrial Carrier (MC) TCDB:2.A.29.2.7	1.00 * 2-Oxoglutarate [c] + 1.00 * hydrogenphosphate [m]	SLC25A10	Transport, mitochondrial				0
r2520_neg	1	0.19043	0.7202646	-1.23647	1.236474	2	0.347218	r2520	Mitochondrial Carrier (MC) TCDB:2.A.29.2.1	1.00 * 2-Oxoglutarate [m] + 1.00 * Reduced glutathione [c]	SLC25A11	Transport, mitochondrial				0
r2520_pos	1	0.19043	0.7202646	-1.39467	1.394674	2	0.347218	r2520	Mitochondrial Carrier (MC) TCDB:2.A.29.2.1	1.00 * 2-Oxoglutarate [m] + 1.00 * Reduced glutathione [c]	SLC25A11	Transport, mitochondrial				0
3MOBT21m_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	3MOBT21m	3-methyl-2-oxobutanoate mitochondrial transport via proton sym	1.00 * proton [c] + 1.00 * 3-methyl-2-oxobutanoate [c] ->	1.00 * prot	Transport, mitochondrial				4
3MOP21m_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	3MOP21m	3-Methyl-2-oxopentanoate mitochondrial transport via proton sym	1.00 * proton [c] + 1.00 * 3-methyl-2-oxopentanoate [c] ->	1.00 * prot	Transport, mitochondrial				4
4MOP21m_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	4MOP21m	4-methyl-2-oxopentanoate mitochondrial transport via proton sym	1.00 * proton [c] + 1.00 * 4-methyl-2-oxopentanoate [c] ->	1.00 * prot	Transport, mitochondrial				4
ATPtm_pos	7	0.382733	0.4171041	1.240929	1.240929	1	0.518179	ATPtm	ADP/ATP transporter, mitochondrial	1.00 * ADP [c] + 1.00 * ATP [m] -> 1.00 * ATP [c] + 1.00 * A	SLC25A4;S	Transport, mitochondrial				4
C4tmc_pos	7	0.382733	0.4171041	0.83477	0.83477	1	0.518179	C4tmc	transport of butyrylcarnitine into mitochondrial matrix	1.00 * butyryl carnitine [c] -> 1.00 * butyryl carnitine [m]	SLC25A20	Transport, mitochondrial				4
DNDP22m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP22m	dTDP transport via dUDP antiport	1.00 * dTDP [c] + 1.00 * dUDP [m] -> 1.00 * dTDP [m] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP26m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP26m	dCDP transport via dUDP antiport	1.00 * dCDP [c] + 1.00 * dUDP [m] -> 1.00 * dCDP [m] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP27m_pos	7	0.382733	0.4171041	1.243483	1.243483	1	0.518179	DNDP27m	dCDP transport via dTDP antiport	1.00 * dCDP [c] + 1.00 * dTDP [m] -> 1.00 * dCDP [m] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP33m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP33m	dGDP transport via dUDP antiport	1.00 * dGDP [c] + 1.00 * dUDP [m] -> 1.00 * dGDP [m] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP34m_pos	7	0.382733	0.4171041	1.243483	1.243483	1	0.518179	DNDP34m	dGDP transport via dTDP antiport	1.00 * dGDP [c] + 1.00 * dTDP [m] -> 1.00 * dGDP [m] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP36m_pos	7	0.382733	0.4171041	1.243483	1.243483	1	0.518179	DNDP36m	dGDP transport via dCDP antiport	1.00 * dGDP [c] + 1.00 * dCDP [m] -> 1.00 * dCDP [c] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP37m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP37m	dUTP transport via dTDP antiport	1.00 * dTDP [m] + 1.00 * dUTP [c] -> 1.00 * dTDP [c] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP38m_pos	7	0.382733	0.4171041	1.240929	1.240929	1	0.518179	DNDP38m	dUTP transport via dUDP antiport	1.00 * dUDP [m] + 1.00 * dUTP [c] -> 1.00 * dUDP [c] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP39m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP39m	dUTP transport via dGDP antiport	1.00 * dGDP [m] + 1.00 * dUTP [c] -> 1.00 * dGDP [c] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
DNDP41m_pos	7	0.382733	0.4171041	1.243093	1.243093	1	0.518179	DNDP41m	dUTP transport via dCDP antiport	1.00 * dCDP [m] + 1.00 * dUTP [c] -> 1.00 * dCDP [c] + 1.00 * d	SLC25A19	Transport, mitochondrial				4
ILEt5m_neg	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	ILEt5m	Isoleucine mitochondrial transport	1.00 * L-isoleucine [c] -> 1.00 * L-isoleucine [m]No genes	1.00 * L-isd	Transport, mitochondrial				4
LEUt5m_neg	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	LEUt5m	leucine mitochondrial transport	1.00 * L-leucine [c] -> 1.00 * L-leucine [m]No genes	1.00 * L-lel	Transport, mitochondrial				4
VALt5m_neg	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	VALt5m	Valine reversible mitochondrial transport	1.00 * L-valine [c] -> 1.00 * L-valine [m]No genes	1.00 * L-val	Transport, mitochondrial				4
r0801_pos	2	0.382733	0.4171041	-0.86031	0.860315	2	0.518179	r0801	Mitochondrial Carrier (MC) TCDB:2.A.29.21.1	1.00 * GTP [c] + 1.00 * GDP [m] -> 1.00 * GDP [c] + 1.00 * GTP [m]	1.00 * GTP	Transport, mitochondrial				0
r2436_pos	7	0.382733	0.4171041	0.918523	0.918523	1	0.518179	r2436	Mitochondrial Carrier (MC) TCDB:2.A.29.8.3	1.00 * L-Carnitine [m] + 1.00 * L-Oleoylcarnitine [c] -> 1.00 * L	SLC25A20	Transport, mitochondrial				0
C4tmc_neg	6	0.662521	0.7888004	0.487932	0.487932	1	0.758498	C4tmc	transport of butyrylcarnitine into mitochondrial matrix	1.00 * butyryl carnitine [c] -> 1.00 * butyryl carnitine [m]	SLC25A20	Transport, mitochondrial				4
COAatm_pos	6	0.662521	0.7888004	0.518912	0.518912	1	0.758498	COAatm	CoA transporter	1.00 * Coenzyme A [c] -> 1.00 * Coenzyme A [m]SLC25A1	SLC25A16	Transport, mitochondrial				4
CRNtm_pos	6	0.662521	0.7888004	0.518912	0.518912	1	0.758498	CRNtm	L-carnitine transport out of mitochondria via diffusion	1.00 * L-Carnitine [m] -> 1.00 * L-Carnitine [c]SLC25A20	SLC25A20	Transport, mitochondrial				4
H2Otm_neg	3	0.662521	0.7888004	0.706368	0.706368	1	0.758498	H2Otm	H2O transport, mitochondrial	1.00 * Water [c] -> 1.00 * Water [m]AQP8	AQP8	Transport, mitochondrial				4
H2Otm_pos	3	0.662521	0.7888004	0.706368	0.706368	1	0.758498	H2Otm	H2O transport, mitochondrial	1.00 * Water [c] -> 1.00 * Water [m]AQP8	AQP8	Transport, mitochondrial				4
PIt2m_pos	6	0.662521	0.7888004	0.677144	0.677144	1	0.758498	PIt2m	phosphate transporter, mitochondrial	1.00 * proton [c] + 1.00 * hydrogenphosphate [c] -> 1.00 * d	SLC25A3	Transport, mitochondrial				4
GLYctm_pos	6	0.662521	0.7888004	0.739151	0.739151	1	0.758498	GLYctm	glycerol transport	1.00 * Glycerol [c] -> 1.00 * Glycerol [m]No genes	1.00 * Glyc	Transport, mitochondrial				4
r0973_pos	3	0.662521	0.7888004	-0.27302	0.273018	2	0.758498	r0973	Facilitated diffusion	1.00 * pantheine [m] -> 1.00 * pantheine [c]No genes	1.00 * pan	Transport, mitochondrial				0
r1291_neg	6	0.662521	0.7888004	0.74055	0.74055	1	0.758498	r1291	Postulated transport reaction	1.00 * Propanoyl-CoA [c] -> 1.00 * Propanoyl-CoA [m]No	1.00 * Pro	Transport, mitochondrial			6.2.1.3	0
r2437_pos	6	0.662521	0.7888004	0.74055	0.74055	1	0.758498	r2437	Mitochondrial Carrier (MC) TCDB:2.A.29.8.3	1.00 * L-Carnitine [m] + 1.00 * O-Propanoylcarnitine [c] ->	SLC25A20	Transport, mitochondrial				0
r2438_pos	6	0.662521	0.7888004	0.487932	0.487932	1	0.758498	r2438	Mitochondrial Carrier (MC) TCDB:2.A.29.8.3	1.00 * L-Carnitine [m] + 1.00 * O-Butanoylcarnitine [c] ->	SLC25A20	Transport, mitochondrial				0
r2472_pos	6	0.662521	0.7888004	0.677144	0.677144	1	0.758498	r2472	Major Facilitator(MFS) TCDB:2.A.1.4.7	1.00 * hydrogenphosphate [m] + 1.00 * Glycerol 3-phosph	SLC37A1	Transport, mitochondrial				0
r0917_neg	4	1	0	-0.91613	0.916131	2	1	r0917	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [c] + 1.00 * Isocitrate [m] -> 1.00 * Isocitrat	SLC25A1	Transport, mitochondrial				0
r0917_pos	4	1	0	-0.91613	0.916131	2	1	r0917	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * Citrate [c] + 1.00 * Isocitrate [m] -> 1.00 * Isocitrat	SLC25A1	Transport, mitochondrial				0
r1001_pos	5	1	0	0.333815	0.333815	1	1	r1001	Facilitated diffusion	1.00 * L-Carnitine [c] + 1.00 * palmitoleoyl-Carnitine [m]	1.00 * L-Ca	Transport, mitochondrial				0
NADHtpu_pos	9	0.080856	1.0922877	5.692481	5.692481	1	0.240222	NADHtpu	NADH transporter, peroxisome	1.00 * Nicotinamide adenine dinucleotide - reduced [c]	1.00 * Nic	Transport, peroxisomal				0
r1147_neg	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r1147	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * Isocitrate [m] -> 1.00 * S	SLC25A1	Transport, peroxisomal				0
r1147_pos	0	0.080856	1.0922877	-1.94736	1.94736	2	0.240222	r1147	Mitochondrial Carrier (MC) TCDB:2.A.29.7.2	1.00 * 2-Oxoglutarate [c] + 1.00 * Isocitrate [m] -> 1.00 * S	SLC25A1	Transport, peroxisomal				0
Htx_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	Htx	H transporter, peroxisome	1.00 * proton [c] -> 1.00 * proton [x]No genes	1.00 * prot	Transport, peroxisomal				0
Htx_pos	7	0.382733	0.4171041	1.051667	1.051667	1	0.518179	Htx	H transporter, peroxisome	1.00 * proton [c] -> 1.00 * proton [x]No genes	1.00 * prot	Transport, peroxisomal				0
PRISTtx_neg	7	0.382733	0.4171041	0.858628	0.858628	1	0.518179	PRISTtx	prist peroxisomal transport	1.00 * pristanic acid [x] -> 1.00 * pristanic acid [c]No gen	1.00 * pris	Transport, peroxisomal				0
r0934_pos	7	0.382733	0.4171041	1.035927	1.035927	1	0.518179	r0934	Neurotransmitter-Sodium Symporter (NSS) TCDB:2.A.22.3.3	1.00 * Taurine [c] -> 1.00 * Taurine [x]SLC6A6	SLC6A6	Transport, peroxisomal				0
r1019_neg	2	0.382733	0.4171041	-1.30963	1.309628	2	0.518179	r1019	Postulated transport reaction	1.00 * chenodeoxycholoyl coenzyme A [x] -> 1.00 * chen	1.00 * che	Transport, peroxisomal				0
r1019_pos	2	0.382733	0.4171041	-1.30963	1.309646	2	0.518179	r1019	Postulated transport reaction	1.00 * chenodeoxycholoyl coenzyme A [x] -> 1.00 * chen	1.00 * che	Transport, peroxisomal				0
r2516_neg	2	0.382733	0.4171041	-1.6311	1.631095	2	0.518179	r2516	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * proton [x] + 1.00 * (S)-lactate [x] -> 1.00 * proton	SLC16A1	Transport, peroxisomal				0
r2516_pos	7	0.382733	0.4171041	1.051667	1.051667	1	0.518179	r2516	Major Facilitator(MFS) TCDB:2.A.1.13.1	1.00 * proton [x] + 1.00 * (S)-lactate [x] -> 1.00 * proton	SLC16A1	Transport, peroxisomal				0
C2tcx_neg	6	0.662521	0.7888004	0.310264	0.310264	1	0.758498	C2tcx	transport of acetyl carnitine from peroxisomes to cytosol	1.00 * O-acetylcarnitine [x] -> 1.00 * O-acetylcarnitine [c]	SLC25A20	Transport, peroxisomal				4
SCP22x_neg	3	0.662521	0.7888004	-0.29731	0.29731	2	0.758498	SCP22x	Sterol carrier protein 2	1.00 * 4,8 dimethylnonanoyl-CoA [c] -> 1.00 * 4,8 dimet	SCP2	Transport, peroxisomal				4
CRNCARTp_pos	6	0.662521	0.7888004	0.310264	0.310264	1	0.758498	CRNCARTp	carnitine-acetyl carnitine carrier, peroxisomal	1.00 * L-Carnitine [c] + 1.00 * O-acetylcarnitine [x] -> 1.00	CRAT	Transport, peroxisomal				0
r0990_neg	6	0.662521	0.7888004	0.939309	0.939309	1	0.758498	r0990	Postulated transport reaction	1.00 * choloyl-CoA[4-] [x] -> 1.00 * choloyl-CoA[4-] [c]No	1.00 * cho	Transport, peroxisomal				0
r0997_pos	6	0.662521	0.7888004	0.224924	0.224924	1	0.758498	r0997	COT facilitated diffusion	1.00 * L-Carnitine [c] + 1.00 * L-Octanoylcarnitine [x] ->	CROT	Transport, peroxisomal				0
C9BRxtc_neg	5	1	0	0.335028	0.335028	1	1	C9BRxtc	transport of dimethylnonanoyl carnitine from peroxisomes to cytosol	1.00 * 4,8 dimethylnonanoyl carnitine [x] -> 1.00 * 4,8-	SLC25A20	Transport, peroxisomal				0
C9BRxtc_pos	5	1	0	0.335028	0.335028	1	1	C9BRxtc	transport of dimethylnonanoyl carnitine from peroxisomes to cytosol							

r0755_pos	0	0.080856	1.0922877	-1.96346	1.963461	2	0.240222	r0755	3-Methoxy-4-hydroxyphenylacetaldehyde:NADP+ oxidoreductase T	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1A3; Unassigned		1.2.1.5	0	
r0756_neg	0	0.080856	1.0922877	-1.96346	1.963461	2	0.240222	r0756	3-Methoxy-4-hydroxyphenylglycolaldehyde:NADP+ oxidoreductase T	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1A3; Unassigned		1.2.1.5	0	
r0757_pos	0	0.080856	1.0922877	-1.96346	1.963461	2	0.240222	r0757	3-Methoxy-4-hydroxyphenylglycolaldehyde:NADP+ oxidoreductase	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1A3; Unassigned		1.2.1.5	0	
r1418_pos	0	0.080856	1.0922877	-1.79567	1.795669	2	0.240222	r1418	Carbonic acid hydro-lyase Nitrogen metabolism EC:4.2.1.1	1.00 * proton [e] + 1.00 * Bicarbonate [e] -> 1.00 * Water	CAR1; CAR	Unassigned	4.2.1.1	0	
r0407_neg	1	0.19043	0.7202646	-1.46042	1.460419	2	0.347218	r0407	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase	1.00 * sedoheptulose 1,7-bisphosphate(4-) [c] -> 1.00 * S	ALDOART2	Unassigned	4.1.2.13	0	
r0408_neg	1	0.19043	0.7202646	-1.46042	1.460419	2	0.347218	r0408	ATP-Sedoheptulose 7-phosphate 1-phosphotransferase EC:2.7.1.11	1.00 * ATP [c] + 1.00 * Sedoheptulose 7-phosphate [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0425_pos	8	0.19043	0.7202646	1.387465	1.387465	1	0.347218	r0425	EC:1.1.1.42	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * S	IDH1; IDH2	Unassigned	1.1.1.42	0	
r1377_neg	1	0.19043	0.7202646	-1.28682	1.286817	2	0.347218	r1377	S-(hydroxymethyl)glutathione synthase Methane metabolism EC:4.4.	1.00 * formaldehyde [c] + 1.00 * Reduced glutathione [c] ->	1.00 * form	Unassigned	4.4.1.22	0	
r1377_pos	1	0.19043	0.7202646	-1.28682	1.286817	2	0.347218	r1377	S-(hydroxymethyl)glutathione synthase Methane metabolism EC:4.4.	1.00 * formaldehyde [c] + 1.00 * Reduced glutathione [c] ->	1.00 * form	Unassigned	4.4.1.22	0	
r1378_neg	1	0.19043	0.7202646	-1.28682	1.286817	2	0.347218	r1378	S-(hydroxymethyl)glutathione dehydrogenase Methane metabolism	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * S	ADH5	Unassigned	1.1.1.284	0	
r1378_pos	1	0.19043	0.7202646	-1.28682	1.286817	2	0.347218	r1378	S-(hydroxymethyl)glutathione dehydrogenase Methane metabolism	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * S	ADH5	Unassigned	1.1.1.284	0	
r1418_neg	1	0.19043	0.7202646	-1.43187	1.431873	2	0.347218	r1418	Carbonic acid hydro-lyase Nitrogen metabolism EC:4.2.1.1	1.00 * proton [e] + 1.00 * Bicarbonate [e] -> 1.00 * Water	CAR1; CAR	Unassigned	4.2.1.1	0	
r0392_neg	7	0.382733	0.4171041	0.954814	0.954814	1	0.518179	r0392	D-Glyceraldehyde:NAD+ oxidoreductase Glycerolipid metabolism EC:1.1.1.41	1.00 * Water [c] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1B1; Unassigned		1.2.1.3	0	
r0196_neg	3	0.662521	0.1788004	-0.91402	0.914024	2	0.758498	r0196	Succinyl-CoA:glycine C-succinyl-transferase(decarboxylating) EC:2.3.1.37	1.00 * Glycine [m] + 1.00 * Succinyl-CoA [m] -> 1.00 * CoA	ALAS1; ALA	Unassigned	2.3.1.37	0	
r0267_neg	3	0.662521	0.1788004	-0.60479	0.604793	2	0.758498	r0267	CMP-N-acetylneuraminase, ferrocyclochrome-b5: oxygen oxidoreductase	1.00 * O2 [c] + 1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * O2	Unassigned	1.14.18.2	0	
r0268_pos	3	0.662521	0.1788004	-0.60479	0.604793	2	0.758498	r0268	cytidine monophospho-N-acetylneuraminic acid hydroxylase EC:1.1.1.42	1.00 * O2 [c] + 1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * O2	Unassigned	1.14.18.2	0	
r0408_pos	3	0.662521	0.1788004	-0.28597	0.285972	2	0.758498	r0408	ATP-Sedoheptulose 7-phosphate 1-phosphotransferase EC:2.7.1.11	1.00 * ATP [c] + 1.00 * Sedoheptulose 7-phosphate [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0409_neg	3	0.662521	0.1788004	-0.28597	0.285972	2	0.758498	r0409	UTP-Sedoheptulose 7-phosphate 1-phosphotransferase EC:2.7.1.11	1.00 * UTP [c] + 1.00 * Sedoheptulose 7-phosphate [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0409_pos	3	0.662521	0.1788004	-0.28597	0.285972	2	0.758498	r0409	UTP-Sedoheptulose 7-phosphate 1-phosphotransferase EC:2.7.1.11	1.00 * UTP [c] + 1.00 * Sedoheptulose 7-phosphate [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0517_neg	3	0.662521	0.1788004	-0.91402	0.914024	2	0.758498	r0517	Succinyl-CoA:glycine C-succinyl-transferase(decarboxylating) EC:2.3.1.37	1.00 * proton [m] + 1.00 * 2-Amino-3-oxoadipate [m] ->	1.00 * ALAS1; ALA	Unassigned	2.3.1.37	0	
r0775_neg	6	0.662521	0.1788004	0.206319	0.206319	1	0.758498	r0775	Formamidopyrimidine nucleoside triphosphate 7,8,9-dihydrolase	1.00 * Water [c] + 1.00 * Formamidopyrimidine nucleoside	GCH1	Unassigned	3.5.4.16	0	
r0317_neg	5	1	0	0.111631	0.111631	1	1	r0317	citrate hydro-lyase Citrate cycle (TCA cycle) / Glyoxylate and dicarboxylate	1.00 * Citrate [m] -> 1.00 * Water [m] + 1.00 * cis-aconitate	ACO1; ACO	Unassigned	4.2.1.4	0	
r0317_pos	5	1	0	0.111631	0.111631	1	1	r0317	citrate hydro-lyase Citrate cycle (TCA cycle) / Glyoxylate and dicarboxylate	1.00 * Citrate [m] -> 1.00 * Water [m] + 1.00 * cis-aconitate	ACO1; ACO	Unassigned	4.2.1.4	0	
r0425_neg	5	1	0	0.576024	0.576024	1	1	r0425	EC:1.1.1.42	1.00 * Nicotinamide adenine dinucleotide [m] + 1.00 * S	IDH1; IDH2	Unassigned	1.1.1.42	0	
r0426_neg	5	1	0	0.111631	0.111631	1	1	r0426	isocitrate hydro-lyase Citrate cycle (TCA cycle) / Glyoxylate and dicarboxylate	1.00 * Isocitrate [m] -> 1.00 * Water [m] + 1.00 * cis-aconitate	ACO1; ACO	Unassigned	4.2.1.3	0	
r0426_pos	5	1	0	0.111631	0.111631	1	1	r0426	isocitrate hydro-lyase Citrate cycle (TCA cycle) / Glyoxylate and dicarboxylate	1.00 * Isocitrate [m] -> 1.00 * Water [m] + 1.00 * cis-aconitate	ACO1; ACO	Unassigned	4.2.1.3	0	
r0610_neg	4	1	0	0.480189	0.480189	1	1	r0610	CTP-D-Tagatose 6-phosphate 1-phosphotransferase Galactose metabolism	1.00 * CTP [c] + 1.00 * D-tagatofuranose 6-phosphate(2-) [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0610_pos	4	1	0	0.480189	0.480189	1	1	r0610	CTP-D-Tagatose 6-phosphate 1-phosphotransferase Galactose metabolism	1.00 * CTP [c] + 1.00 * D-tagatofuranose 6-phosphate(2-) [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0611_neg	4	1	0	0.480189	0.480189	1	1	r0611	ITP-D-Tagatose 6-phosphate 1-phosphotransferase Galactose metabolism	1.00 * ITP(3-) [c] + 1.00 * D-tagatofuranose 6-phosphate(2-) [c] ->	PFKL	Unassigned	2.7.1.11	0	
r0611_pos	4	1	0	0.480189	0.480189	1	1	r0611	ITP-D-Tagatose 6-phosphate 1-phosphotransferase Galactose metabolism	1.00 * ITP(3-) [c] + 1.00 * D-tagatofuranose 6-phosphate(2-) [c] ->	PFKL	Unassigned	2.7.1.11	0	
CK_pos	1	0.19043	0.7202646	-0.96781	0.967811	2	0.347218	CK	ATP Creatine kinase	1.00 * ATP [m] + 1.00 * creatine [m] -> 1.00 * ADP [m] + 1.00 * Pi	CKMT1; CKM	Urea cycle	33	2.7.3.2	4
Ckc_neg	1	0.19043	0.7202646	-0.96781	0.967811	2	0.347218	Ckc	ATP Creatine kinase (c)	1.00 * ATP [c] + 1.00 * creatine [c] -> 1.00 * ADP [c] + 1.00 * Pi	CKB; CKM	Urea cycle	33	2.7.3.2	4
r0074_neg	7	0.382733	0.4171041	1.164738	1.164738	1	0.518179	r0074	L-Glutamate 5-semialdehyde:NAD+ oxidoreductase Arginine and proline metabolism	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH4A1	Urea cycle	33	1.5.1.12	0
ILETA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	ILETA	isoleucine transaminase	1.00 * 2-Oxoglutarate [c] + 1.00 * L-isoleucine [c] -> 1.00 * L-glutamate	BCAT1	Valine, leucine, and isoleucine metabolism	34	2.6.1.42	4
ILETA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	ILETA	isoleucine transaminase, mitochondrial	1.00 * 2-Oxoglutarate [m] + 1.00 * L-isoleucine [m] -> 1.00 * L-glutamate	BCAT2	Valine, leucine, and isoleucine metabolism	34	2.6.1.42	4
LEUTA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	LEUTA	leucine transaminase	1.00 * 2-Oxoglutarate [c] + 1.00 * L-leucine [c] -> 1.00 * L-glutamate	BCAT1	Valine, leucine, and isoleucine metabolism	34	2.6.1.6	4
LEUTA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	LEUTA	leucine transaminase, mitochondrial	1.00 * 2-Oxoglutarate [m] + 1.00 * L-leucine [m] -> 1.00 * L-glutamate	BCAT2	Valine, leucine, and isoleucine metabolism	34	2.6.1.6	4
MMEm_pos	2	0.382733	0.4171041	-0.68412	0.684123	2	0.518179	MMEm	methylmalonyl-CoA epimerase/racemase	1.00 * (R)-methylmalonyl-CoA(5-) [m] -> 1.00 * (S)-methylmalonyl-CoA(5-) [m]	MCEE	Valine, leucine, and isoleucine metabolism	34	5.1.99.1	4
VALTA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	VALTA	valine transaminase	1.00 * 2-Oxoglutarate [c] + 1.00 * L-valine [c] -> 1.00 * L-glutamate	BCAT1	Valine, leucine, and isoleucine metabolism	34	2.6.1.42	4
VALTA_pos	7	0.382733	0.4171041	0.681567	0.681567	1	0.518179	VALTA	valine transaminase, mitochondrial	1.00 * 2-Oxoglutarate [m] + 1.00 * L-valine [m] -> 1.00 * L-glutamate	BCAT2	Valine, leucine, and isoleucine metabolism	34	2.6.1.42	4
r0571_pos	2	0.382733	0.4171041	-0.68412	0.684123	2	0.518179	r0571	(S)-Methylmalonyl-CoA hydrolase Propanoate metabolism EC:3.1.2.1	1.00 * Water [m] + 1.00 * (S)-methylmalonyl-CoA(5-) [m] ->	1.00 * Water	Valine, leucine, and isoleucine metabolism	34	3.1.2.17	0
r0643_neg	2	0.382733	0.4171041	-0.68412	0.684123	2	0.518179	r0643	(S)-Methylmalonate semialdehyde:NAD+ oxidoreductase Valine, leucine, and isoleucine metabolism	1.00 * Water [m] + 1.00 * Nicotinamide adenine dinucleotide	ALDH1B1; Unassigned		34	1.2.1.3	0
RDH1_neg	0	0.080856	1.0922877	-1.45296	1.452961	2	0.240222	RDH1	retinol dehydrogenase (all-trans)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * retinol	RDH16F1; Vitamin A metabolism		1.1.1.105	4	
RDH1a_pos	0	0.080856	1.0922877	-1.45296	1.452961	2	0.240222	RDH1a	retinol dehydrogenase (all-trans, NADPH)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	RDH10; RDH11	Vitamin A metabolism	1.1.1.105	4	
RDH2_neg	1	0.19043	0.7202646	-1.45601	1.456005	2	0.347218	RDH2	retinol dehydrogenase (9-cis, NADH)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 9-oxo-L-tryptophan	RDH5	Vitamin A metabolism	1.1.1.105	4	
RDH2a_pos	1	0.19043	0.7202646	-1.45601	1.456005	2	0.347218	RDH2a	retinol dehydrogenase (9-cis, NADPH)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	RDH11; RDH12	Vitamin A metabolism	1.1.1.105	4	
RDH3_neg	1	0.19043	0.7202646	-1.45601	1.456005	2	0.347218	RDH3	retinol dehydrogenase (11-cis, NADH)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 11-oxo-L-tryptophan	RDH5	Vitamin A metabolism	1.1.1.105	4	
RDH3a_pos	1	0.19043	0.7202646	-1.45601	1.456005	2	0.347218	RDH3a	retinol dehydrogenase (11-cis, NADPH)	1.00 * Nicotinamide adenine dinucleotide phosphate [c]	RDH11; RDH12	Vitamin A metabolism	1.1.1.105	4	
RDH1_pos	2	0.382733	0.4171041	-0.60313	0.603125	2	0.518179	RDH1	retinol dehydrogenase (all-trans)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * retinol	RDH16F1; Vitamin A metabolism		1.1.1.105	4	
RDH2_pos	2	0.382733	0.4171041	-0.60313	0.603125	2	0.518179	RDH2	retinol dehydrogenase (9-cis, NADH)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 9-oxo-L-tryptophan	RDH5	Vitamin A metabolism	1.1.1.105	4	
RDH3_pos	2	0.382733	0.4171041	-0.60313	0.603125	2	0.518179	RDH3	retinol dehydrogenase (11-cis, NADH)	1.00 * Nicotinamide adenine dinucleotide [c] + 1.00 * 11-oxo-L-tryptophan	RDH5	Vitamin A metabolism	1.1.1.105	4	
RE3347C_pos	0	0.080856	1.0922877	-2.27244	2.272442	2	0.240222	RE3347C	RE3347	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * proton	Vitamin B2 metabolism	1.5.1.29	0	
RE3347C_neg	2	0.382733	0.4171041	-0.73078	0.730783	2	0.518179	RE3347C	RE3347	1.00 * proton [c] + 1.00 * Nicotinamide adenine dinucleotide	1.00 * proton	Vitamin B2 metabolism	1.5.1.29	0	

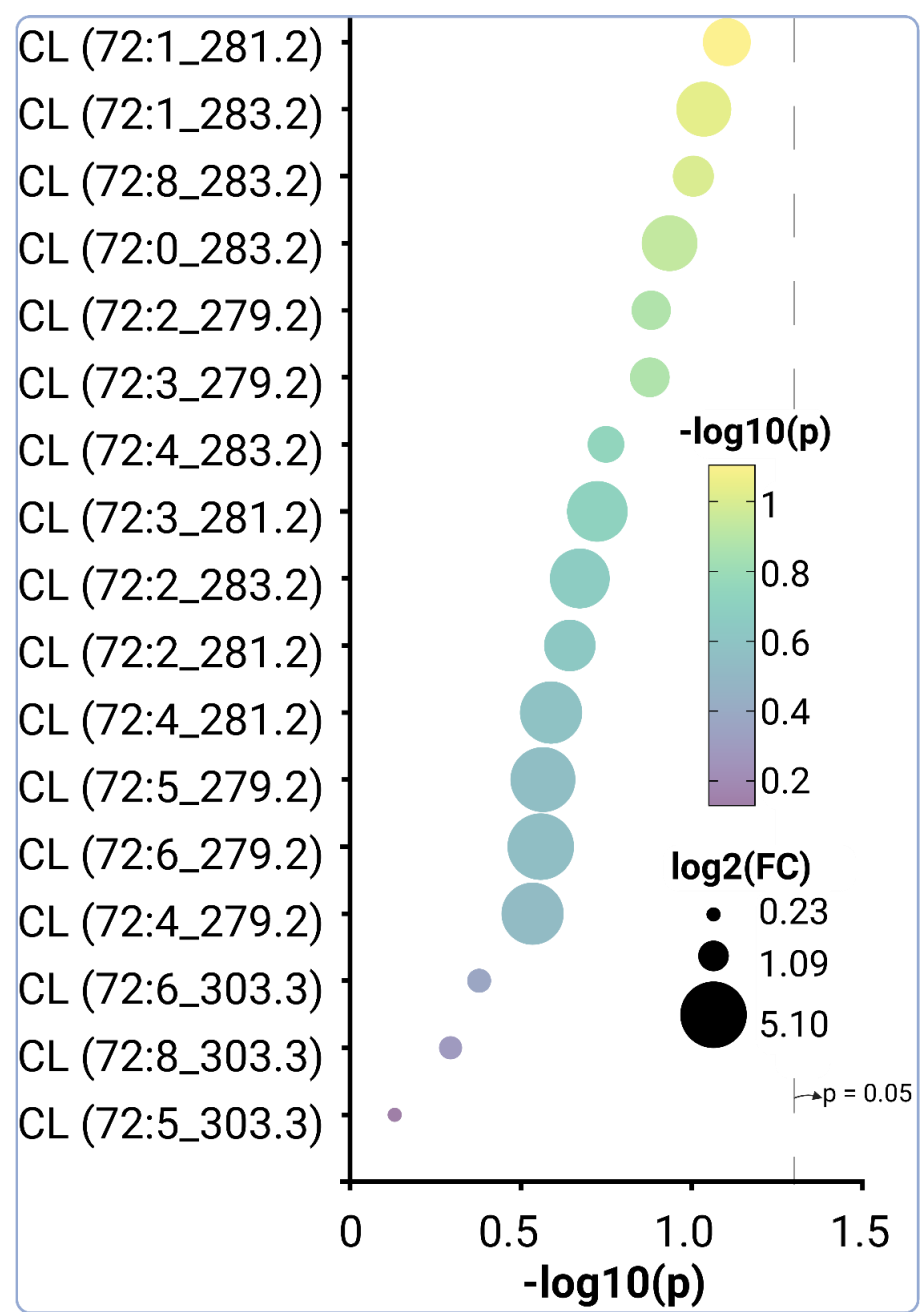
Supplementary Table 4.

Metabolite	Isotopologue	Q1	Q3
Acetyl CoA	Acetyl CoA.1 M0	810.1	303.1
Acetyl CoA	Acetyl CoA.1 M1	811.1	304.1
Acetyl CoA	Acetyl CoA.1 M2	812.1	305.1
Acetyl CoA	Acetyl CoA.1 M3	813.1	306.1
Acetyl CoA	Acetyl CoA.1 M4	814.1	307.1
Acetyl CoA	Acetyl CoA.1 M5	815.1	308.1
Propionyl CoA	Propionyl CoA.1 M0	824.1	317.1
Propionyl CoA	Propionyl CoA.1 M1	825.1	318.1
Propionyl CoA	Propionyl CoA.1 M2	826.1	319.1
Propionyl CoA	Propionyl CoA.1 M3	827.1	320.1
Propionyl CoA	Propionyl CoA.1 M4	828.1	321.1
Propionyl CoA	Propionyl CoA.1 M5	829.1	322.1

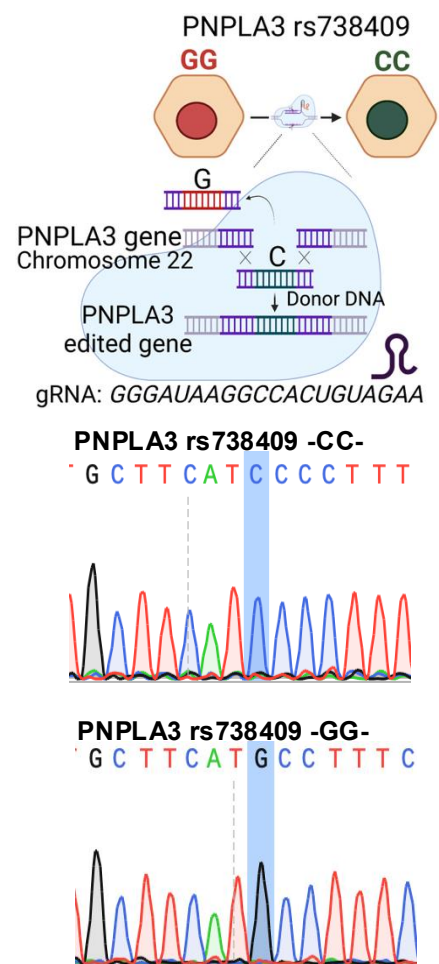
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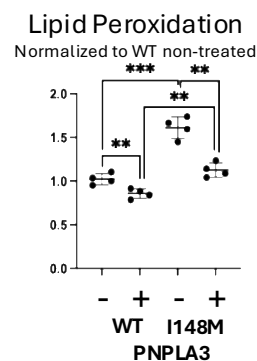
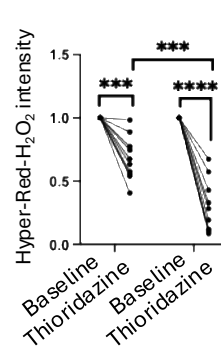
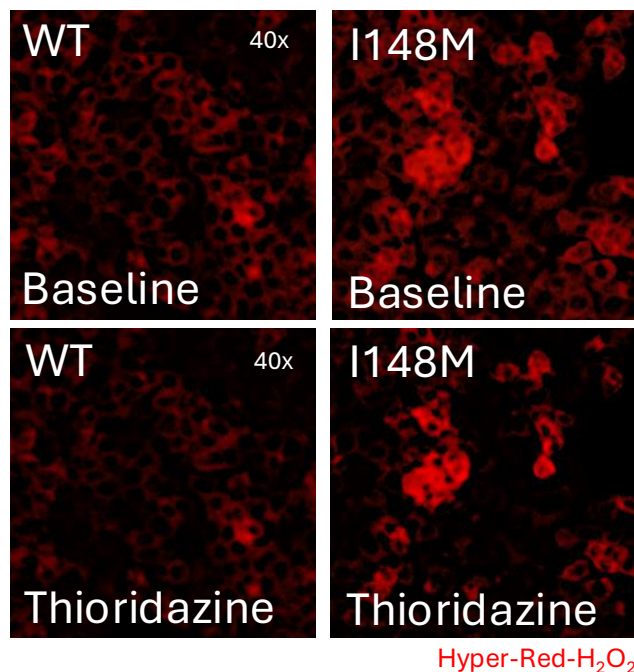
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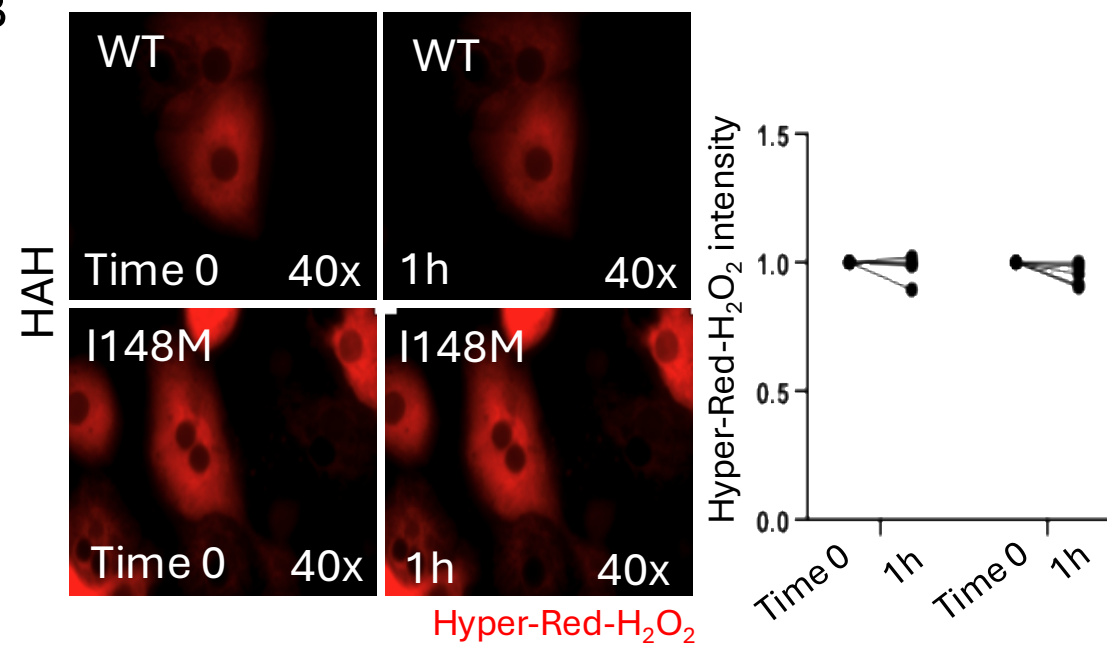
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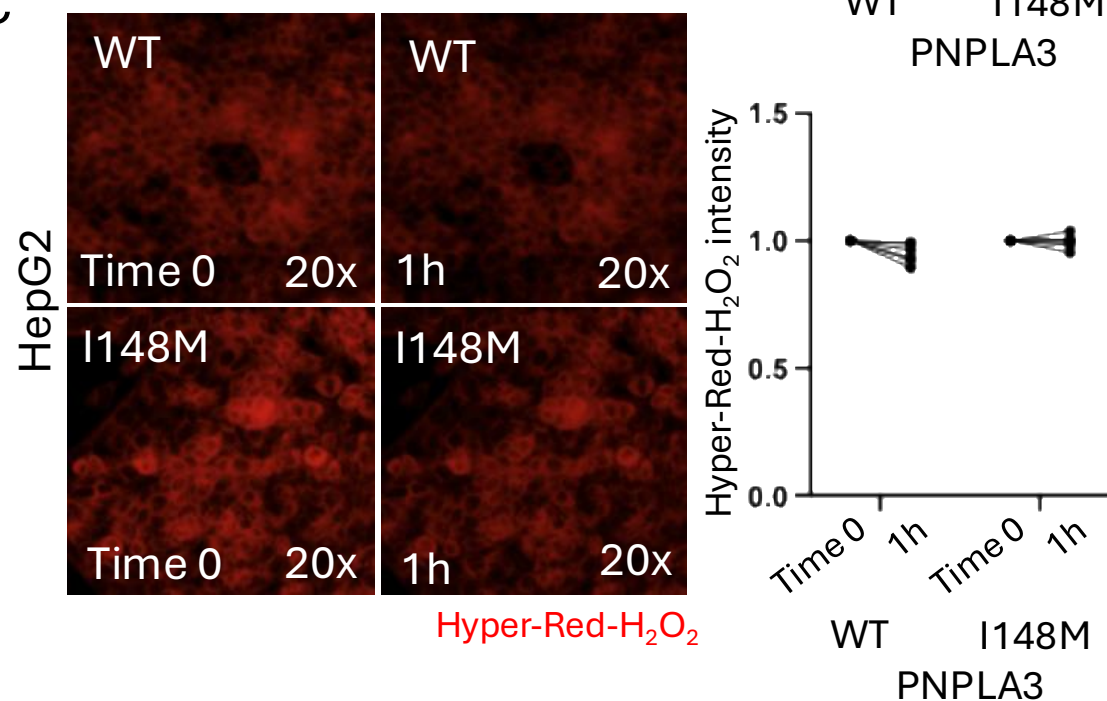
PNPLA3



B

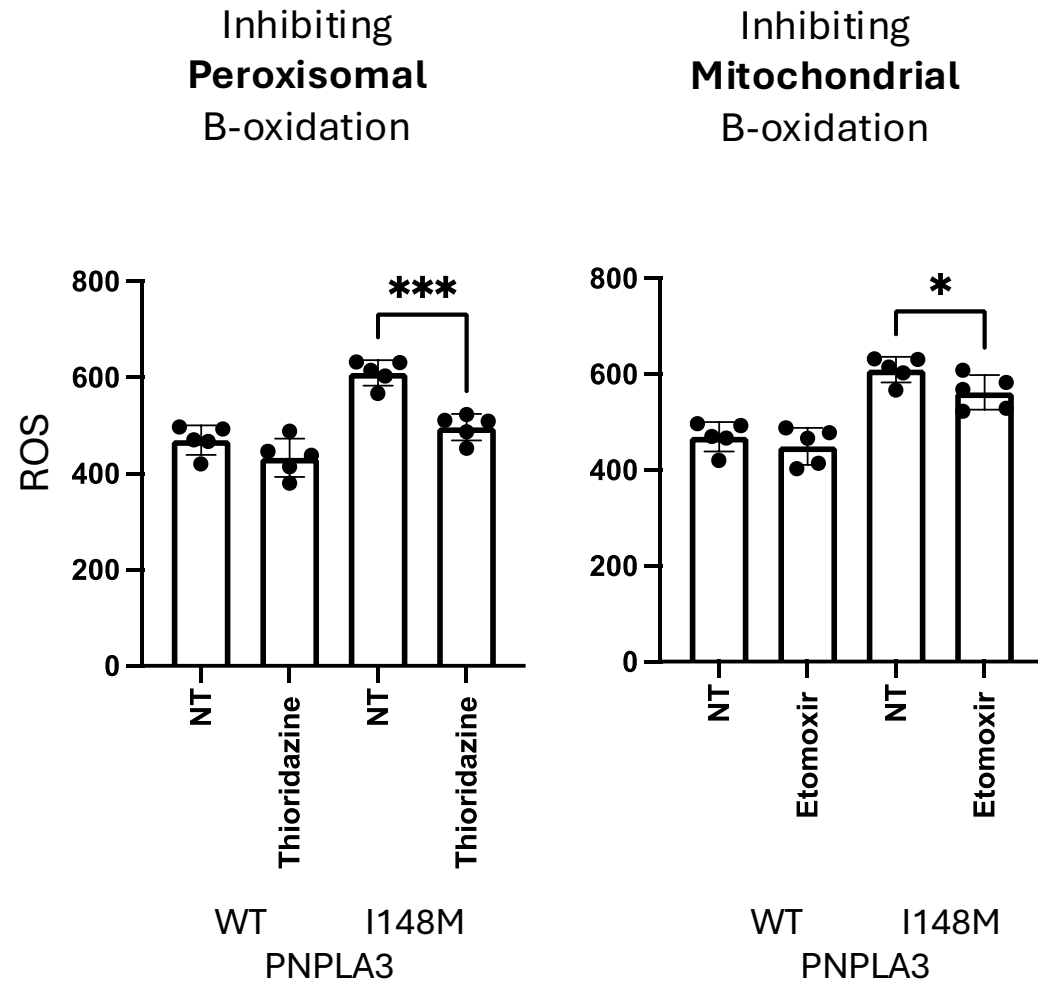


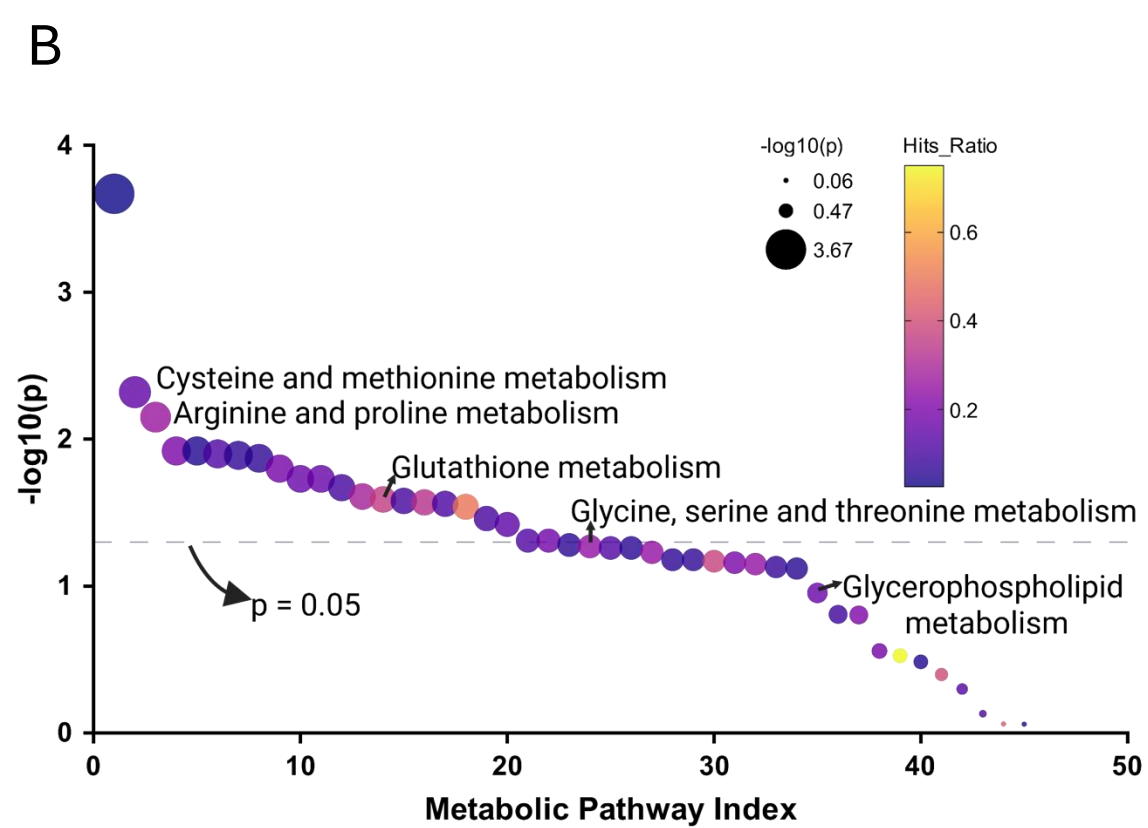
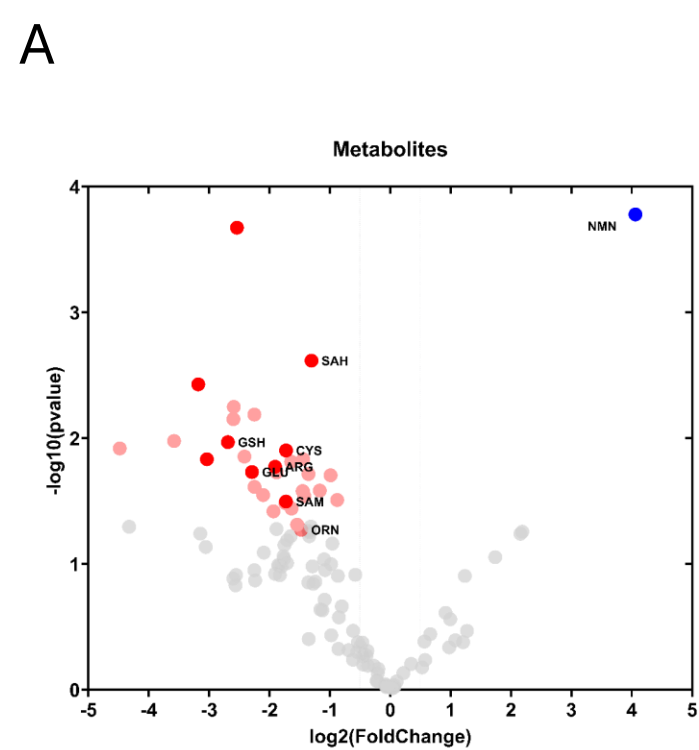
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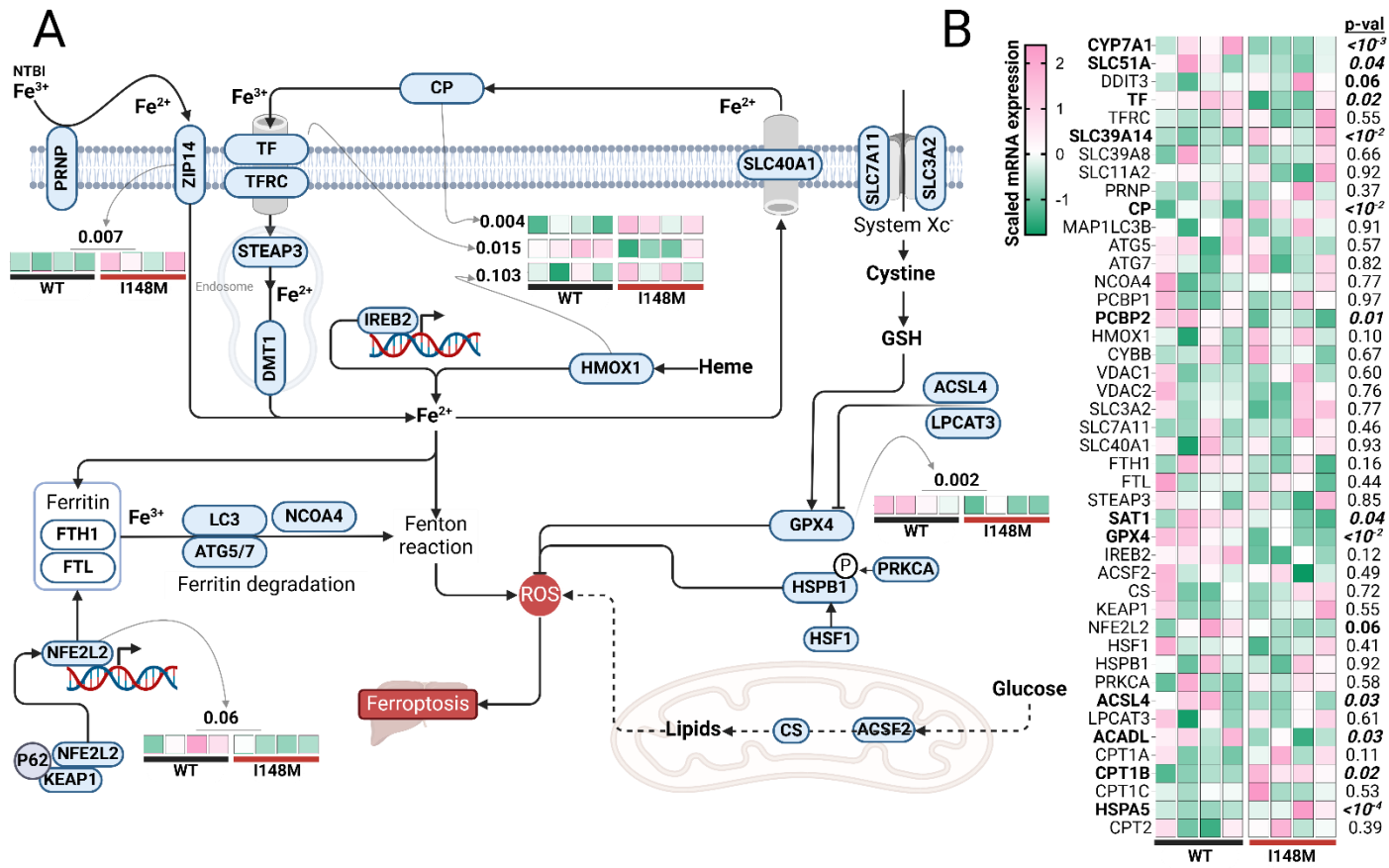


Supplementary Figure 2

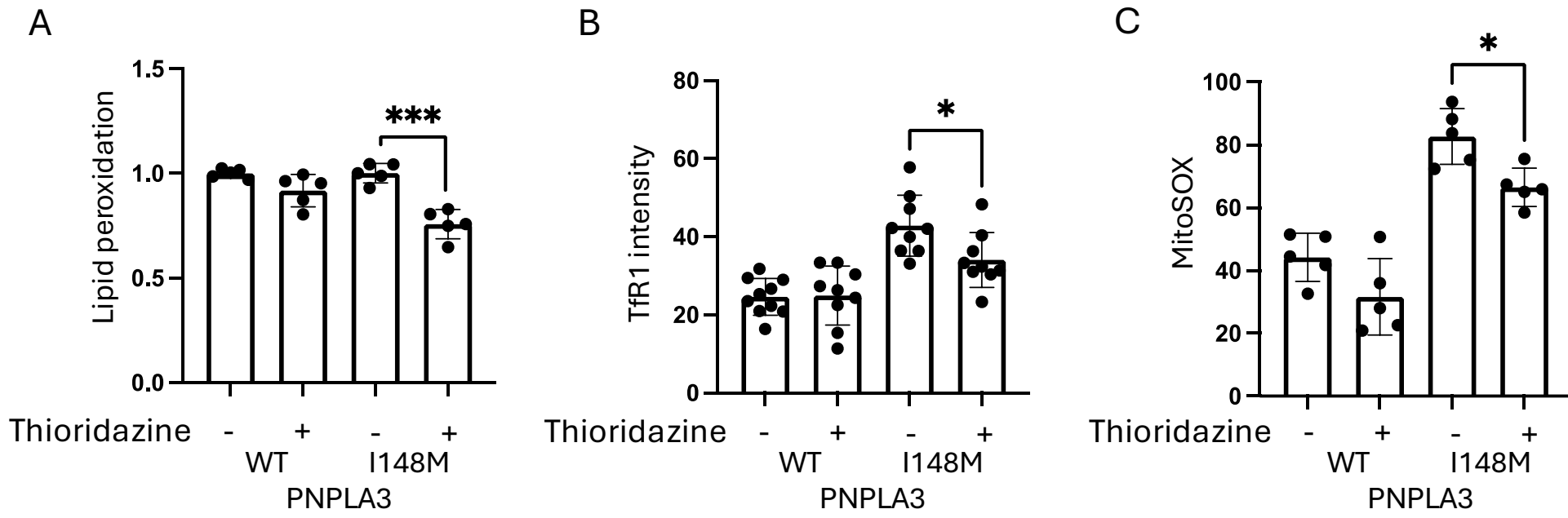
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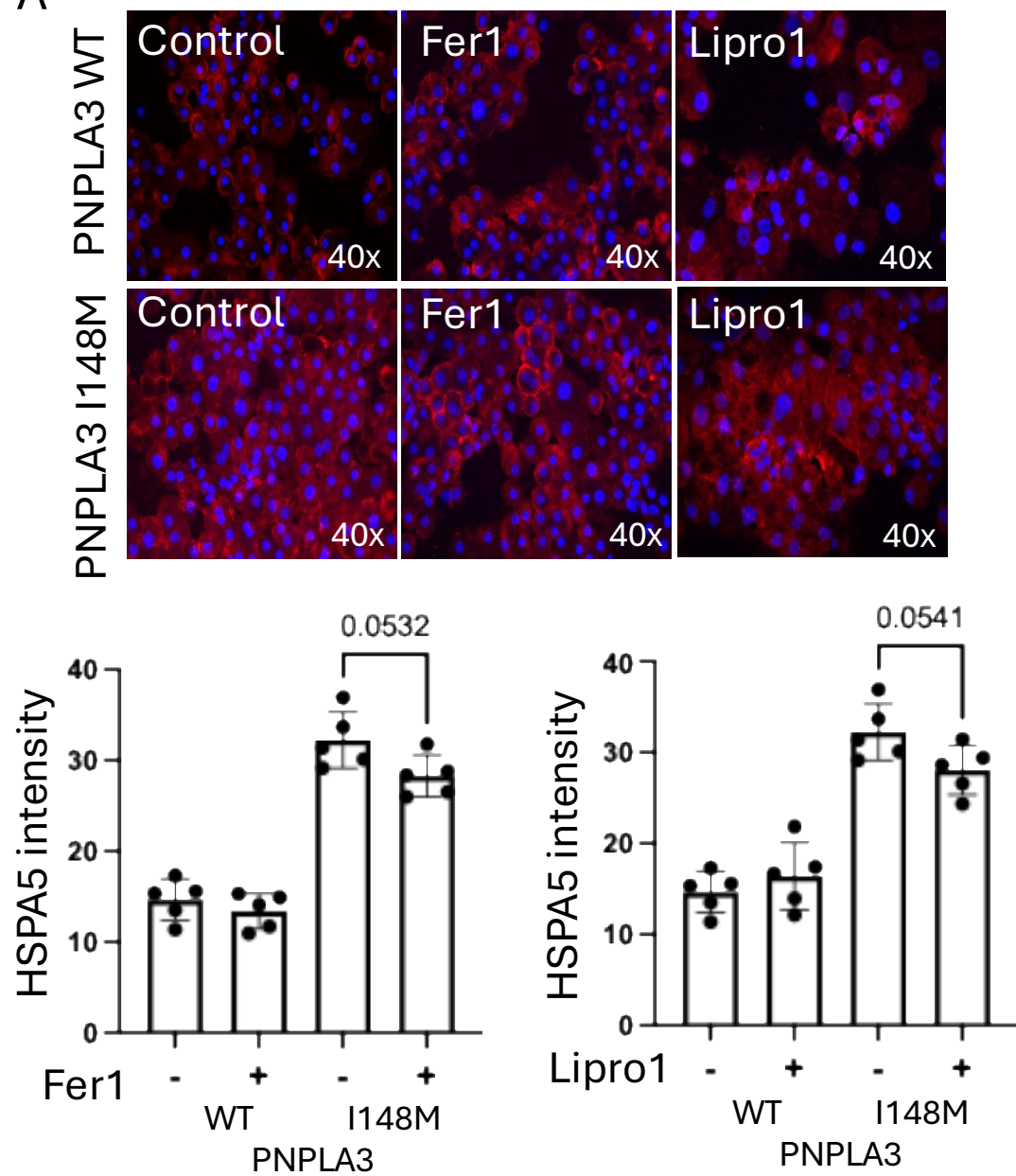


Supplementary Figure 5

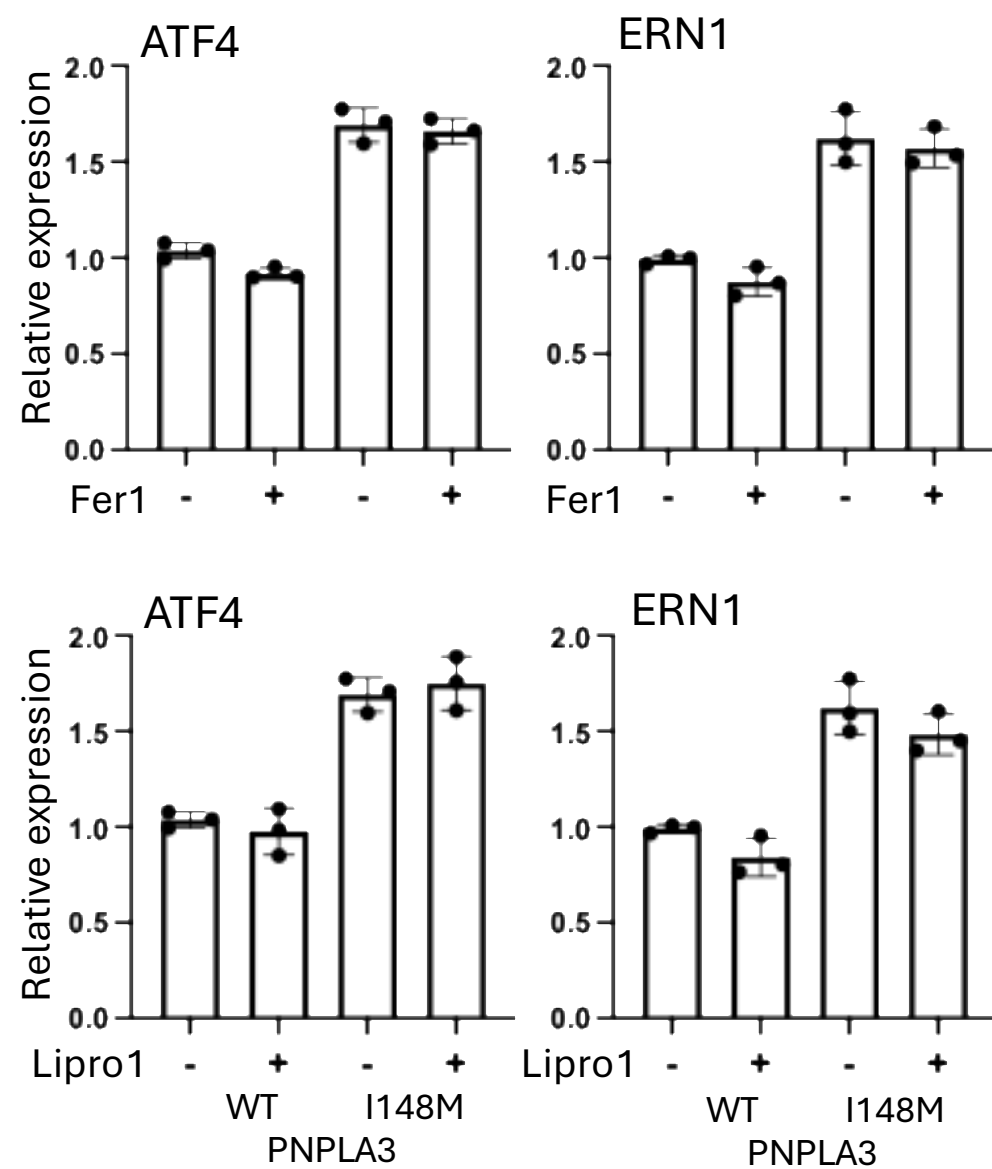


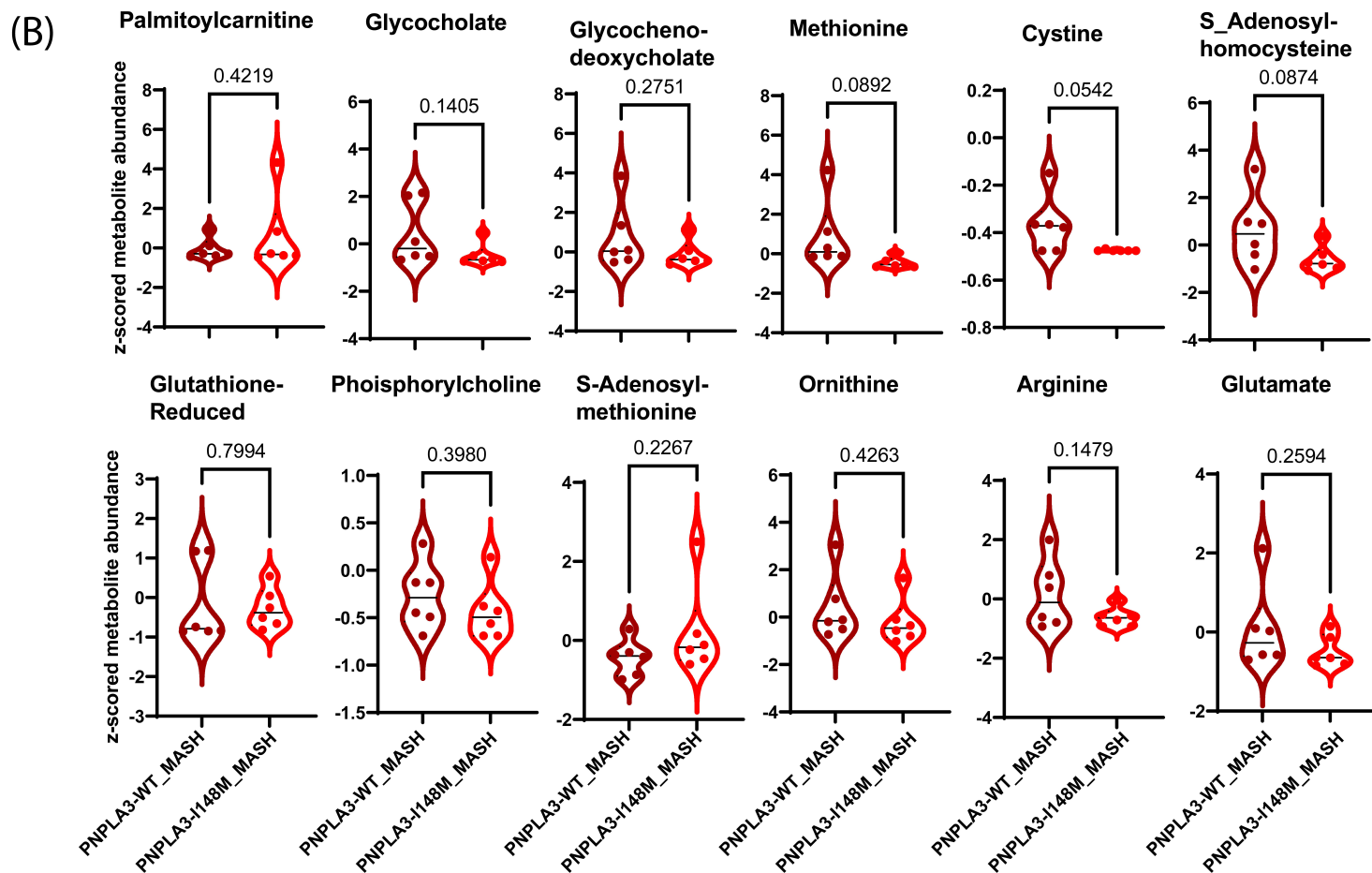
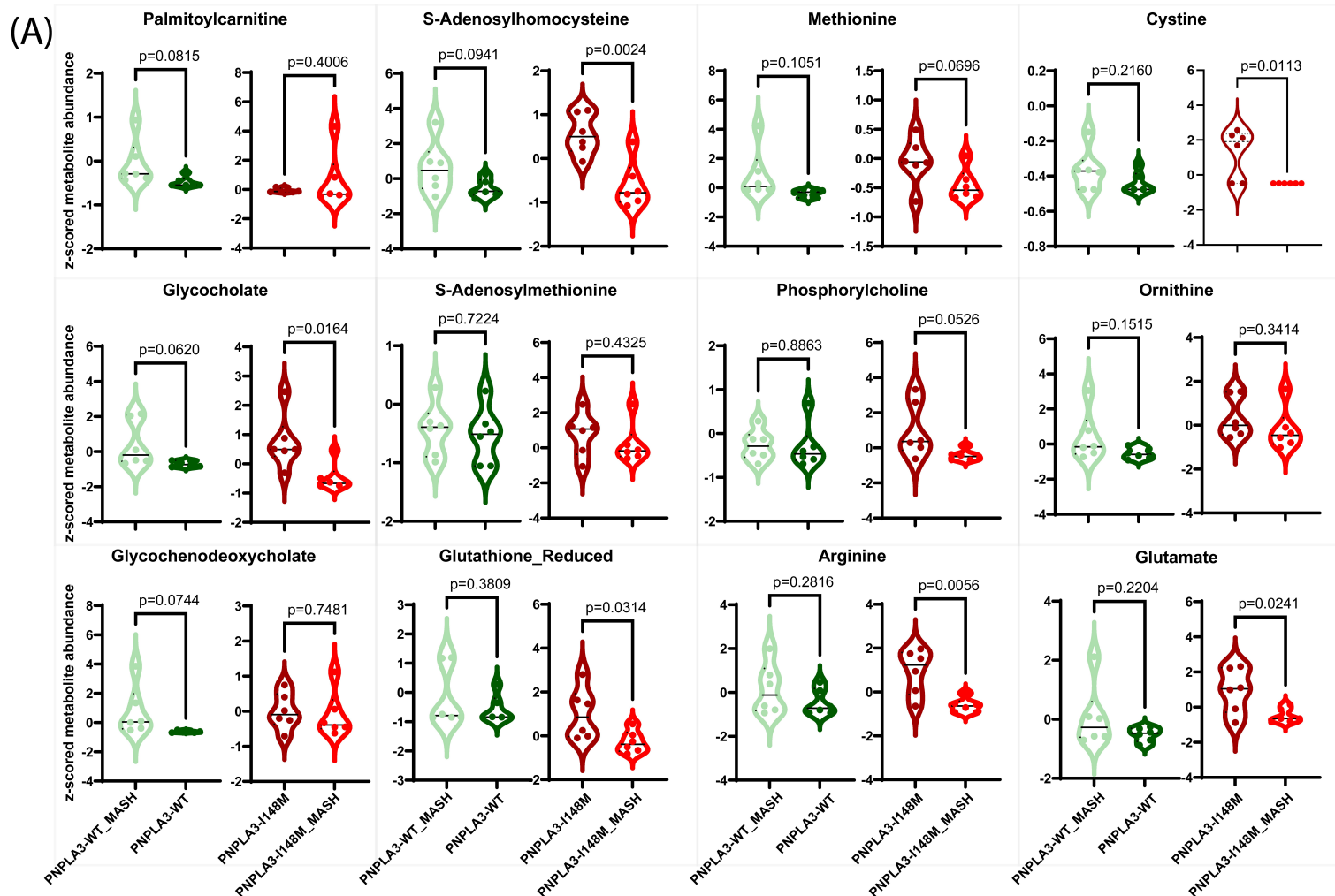
Supplementary Figure 6

A

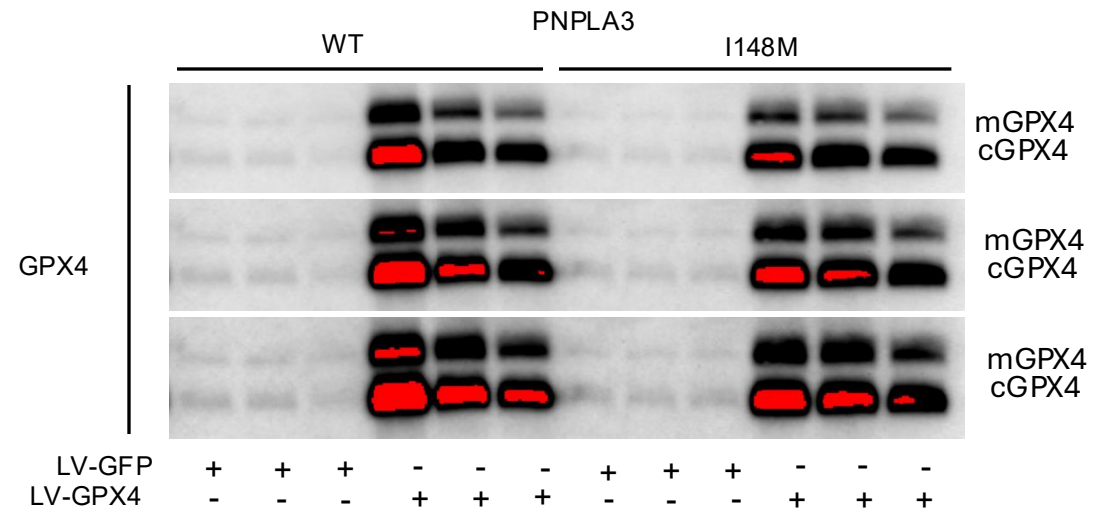


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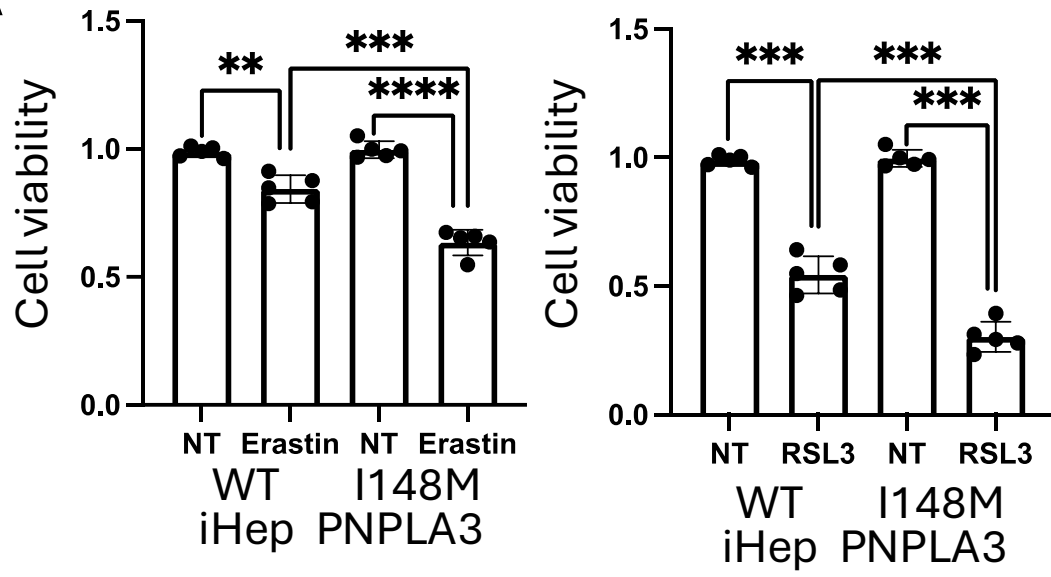




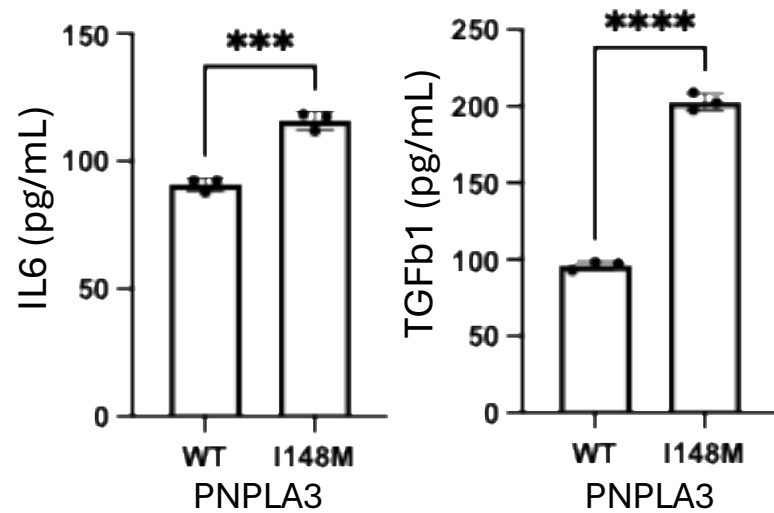
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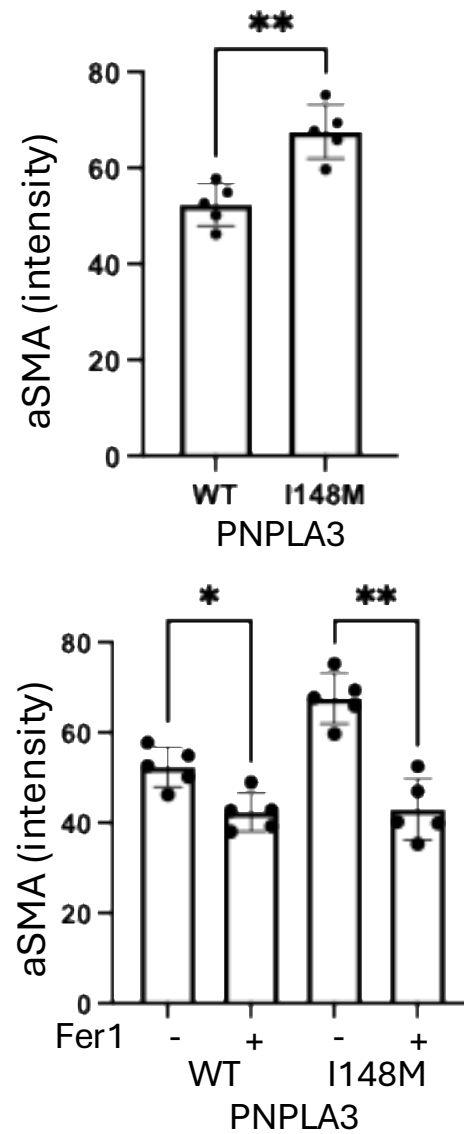
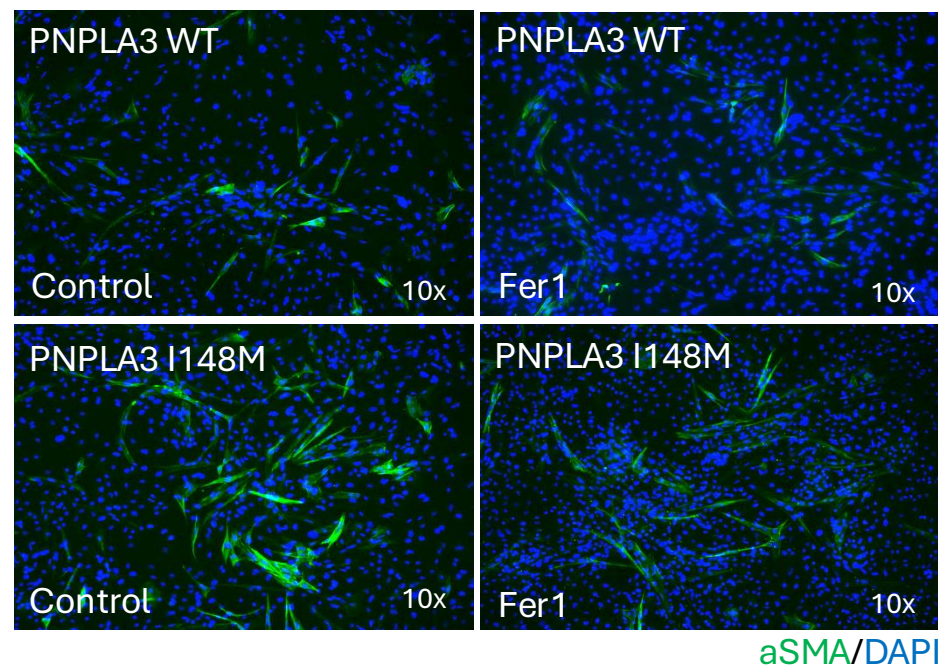
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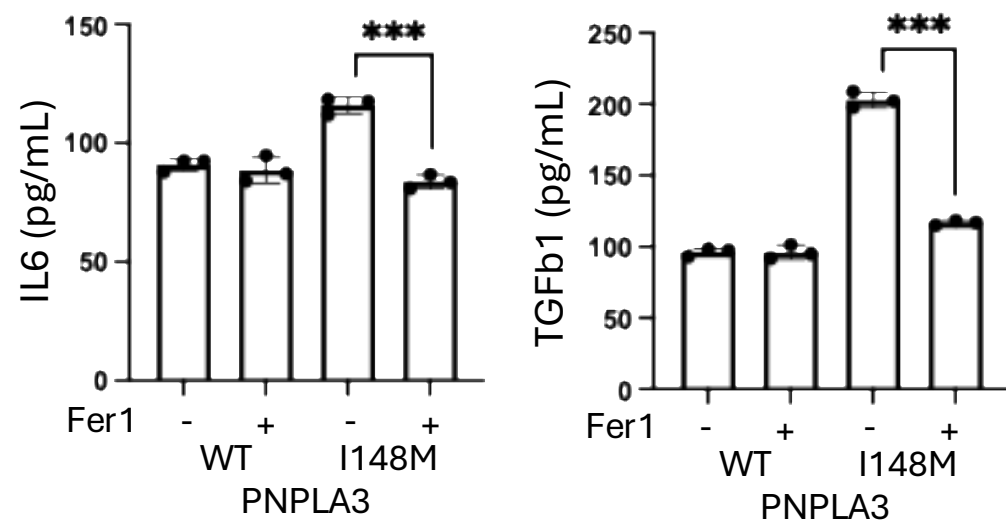
A



C



B



Supplementary Figures Footnotes:

Supplementary figure 1: (A) Sunburst plot shows the distribution of upregulated and downregulated lipid classes in Figure 1I. Lipid classes legend; TAG: Triacylglycerols, PS: Phosphatidylserine, PI: Phosphatidylinositol, PG: Phosphatidylglycerol, PE: Phosphatidylethanolamine, PC: Phosphatidylcholine, MAG: Monoacylglycerol, LPS: Lipopolysaccharide, LPI: Lysophosphatidylinositol, LPG: Lysophosphatidylglycerol, LPC: Lysophosphatidylcholine, DAG: Diacylglycerol, CL: Cardiolipin, CE: Cholesteryl Ester. **(B)** Bubble plot showing the level of mitochondria-associated cardiolipins (CL) in Hep-PNPLA3-I148M compared to Hep-PNPLA3-WT. The size of the bubbles indicates the log₂ fold change of the lipid cardiolipins upregulated in Hep-PNPLA3-I148M versus WT. The color of the bubbles corresponds to the $-\log_{10}(\text{p-value})$. Test statistics were computed with Metaboanalyst® (ver. 6.0). Example of cardiolipin naming convention: CL (72:4_281.2) implies a cardiolipin with 72 carbons (four C18 acyl chains); 4 total double bonds in all the four constituting fatty acids. A daughter ion with molecular weight of 281.2 results from its fragmentation which corresponds to oleic acid (C18:1) in this case.

Supplementary Figure 2: (A) The single-guide RNA (sgRNA) sequence was designed to cut at chr22:43,928,854 to replace the minor allele -G- with the major allele -C- using a donor template. Sanger sequences of the PNPLA3 genotypes. Fluorescent micrographs of HyPer-Red in transfected HepG2-PNPLA3-I148M and HepG2-PNPLA3-WT controls exposed to thioridazine for 1h between micrographs. Quantification of H₂O₂ by HyPer-Red intensity (***p<0.001, ****p<0.0001, Welch's t-test, WT: n=10, I148M: n=10). Lipid peroxidation suppression on HepG2-PNPLA3-I148M and HepG2-PNPLA3-WT controls exposed to thioridazine (**p=0.001, ****p<0.0001, Welch's t-test, WT: n=3 I148M: n=4). Hyper-Red-H₂O₂ intensity at time 0 and after 1 hour without exposing **(B)** primary human hepatocytes and **(C)** HepG2 cells to thioridazine. No significant decrease in the fluorescence signal was observed over time.

Supplementary Figure 3: The major ROS source in Hep-PNPLA3-I148M is peroxisomal β -oxidation. Primary human Hep-PNPLA3-WT or Hep-PNPLA3-I148M were exposed to thioridazine or etomoxir, inhibitors of peroxisomal and mitochondrial β -oxidation respectively. About 20% of ROS was decreased in the mutated cells when treated with thioridazine (***p<0.001, Welch's t-test, WT: n=6, I148M: n=6) and about 9% was reduced when the cells were exposed to etomoxir (*p<0.05, Welch's t-test, WT: n=6, I148M: n=6).

Supplementary Figure 4: (A) Volcano plot indicating various metabolites that are differentially expressed between Hep-PNPLA3-I148M (n=6) and Hep-PNPLA3-WT (n=6). Red circles indicate metabolites significantly upregulated (p value < 0.05, fold change > 1.5) while blue indicates metabolites that are significantly downregulated (p value < 0.05, fold change < 1/1.5) in Hep-PNPLA3-I148M compared to Hep-PNPLA3-WT. Test statistics were computed with Metaboanalyst® (ver. 4.0). Metabolites legend; SAH: s-adenosylhomocysteine, GSH: Glutathione, GLU: Glutamate, ARG: arginine, CYS: cystine, SAM: s-adenosylmethionine, ORN: ornithine, NMN: nicotinamide mononucleotide. (B) Bubble plot showing various metabolic pathways that are significantly different between Hep-PNPLA3-I148M (n=6) and Hep-PNPLA3-WT (n=6). The plot was generated from data obtained from metabolic set enrichment analysis performed in Metaboanalyst® (ver. 4.0).

Supplementary Figure 5: (A) Simplified Kyoto Encyclopedia of Genes and Genomes (KEGG) ferroptosis pathway overlayed with transcriptomic data of genes involved in hepatocellular ferroptosis and iron metabolism comparing Hep-PNPLA3-I148M (n=4) and Hep-PNPLA3-WT (n=4). (B) Heatmap showing differential expression based on z-score of genes related to oxidative stress, ferroptosis, and iron metabolism in Hep-PNPLA3-I148M (n=4) and Hep-PNPLA3-WT (n=4). The genes with bold names are the ones with statistically significant differences between the two groups (p value < 0.05). The p value was computed based on Wald test statistics.

Supplementary Figure 6: Ferroptosis characterization after inhibiting peroxisomal β -oxidation with thioridazine in Hep-PNPLA3-WT and Hep-PNPLA3-I148M. Lipid peroxidation (**p<0.001, Welch's t-test, WT: n=5, I148M: n=5); TfR1 intensity (*p<0.05, Welch's t-test, WT: n=10, I148M: n=10), and MitoSOX (*p<0.05, Welch's t-test, WT: n=5, I148M: n=5).

Supplementary Figure 7: Inhibition of ferroptosis did not reduce ER stress in primary human hepatocytes carrying the PNPLA3-I148M variant. (A) HSPA5 immunostaining was performed after exposing primary human hepatocytes to Fer1 and Lipro1. While high signal was observed in non-treated Hep-PNPLA3-I148M in comparison to Hep-PNPLA3-WT, no statistical difference was observed after ferroptosis inhibition (Welch's t-test, WT: n=5, I148M: n=5). (B) The same phenomenon was observed at the mRNA levels of ATF and ERN1, components of the unfolded protein response (Welch's t-test, WT: n=3, I148M: n=3).

Supplementary Figure 8: Comparing levels of metabolites **(A)** between samples from healthy and MASH patients and **(B)** between PNPLA3-WT MASH patients and PNPLA3-I148M MASH patients

Supplementary Figure 9: Overexposure of the primary human hepatocytes transduced with the LV-GPX to show the basal level of GPX4 expression in the cells transduced with the LV-GFP.

Supplementary Figure 10: iHep-PNPLA3-I148M are more susceptible to cell death after exposure to ferroptosis inducers, such as erastin (** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, Welch's t-test, WT: $n=5$, I148M: $n=5$) and RSL3 (*** $p < 0.001$, Welch's t-test, WT: $n=5$, I148M: $n=5$).

Supplementary Figure 11: PNPLA3-I148M and ferroptosis play a role in the inflammation and fibrosis process. A co-culture of hepatocytes (iHep) and hepatic stellate cells (iHSC) derived from iPSC-PNPLA3-WT and iPSC-PNPLA3-I148M was used to measure the secretion of key cytokines and activation of iHSC through α SMA immunostaining. **(A)** The system carrying the PNPLA3-I148M variant had increased production of IL6 (*** $p < 0.001$, Welch's t-test, WT: $n=3$, I148M: $n=3$) and TGF β 1 (**** $p < 0.0001$, Welch's t-test, WT: $n=3$, I148M: $n=3$). **(B)** Ferroptosis inhibition with Ferrostatin 1 (Fer1) reduced the production both proinflammatory cytokines: IL6 (*** $p < 0.001$, Welch's t-test, WT: $n=3$, I148M: $n=3$) and TGF β 1 (*** $p < 0.001$, Welch's t-test, WT: $n=3$, I148M: $n=3$). **(C)** The impact of PNPLA3 mutation in the fibrosis was assessed by α SMA intensity. The system carrying the mutation started with a high basal level of activated iHSC (** $p < 0.01$, Welch's t-test, WT: $n=5$, I148M: $n=5$), which was reduced upon Fer1 treatment (* $p < 0.05$, ** $p < 0.01$, Welch's t-test, WT: $n=5$, I148M: $n=5$).