Oxidative Medicine and Cellular Longevity –

Special Issue: Cardiolipin and Mitochondria-Targeted Antioxidants in Oxidative Stress, Disease, and Aging

Prediabetes induced by fructose-enriched diet influences cardiac lipidome and proteome and leads to deterioration of cardiac function prior to the development of excessive oxidative stress and cell damage

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Working Title: Cardiolipin in prediabetic cardiac dysfunction.

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Supplementary Methods

Lipidomics

Lipidomic analyses were performed on an LTQ-Orbitrap Elite instrument (Thermo Fisher Scientific) equipped with a robotic nanoflow ion source TriVersa NanoMate (Advion BioSciences) using chips with the diameter of 5.5-µm spraying nozzles. The ion source was controlled by Chipsoft 8.3.1 software. The ionization voltages were +1.3 kV and −1.9 kV in positive and negative mode, respectively, and the back-pressure was set at 1 psi in both modes. The temperature of the ion transfer capillary was 330 °C. Acquisitions were performed at the mass resolution $R_{m/z\ 400}$ = 240,000.

Phosphatidylcholine (PC, diacyl and PC-P, alkenyl-acyl), lysophosphatidylcholine (LPC), sphingomyelin (SM), giacylglycerol (DG) and triacylglycerol (TG) were detected and quantified using the positive ion mode, while phosphatidylethanolamine (PE, diacyl and PE-Pl, alkenyl-acyl), phosphatidylinositol (PI), phosphatidylserine (PS), phosphatidic acid (PA), phosphatidylglycerol (PG), cardiolipin (CL), the corresponding lyso derivatives LPE, LPI, LPS, LPG and monolysocardiolipin (MLCL) as well as ceramide (Cer) and ganglioside GM3 were detected and quantified using the negative ion mode.

For quantification, tenfold dilution was prepared from the lipid extracts, from which 8 µl was further diluted with 142 µl infusion solvent mixture (chloroform:methanol:iso-propanol 1:2:1, by vol.; extract concentration upon injection ca. 100 ng ww/µl) containing an internal standard mix (71 pmol PC d31-16:0/18:1, 5 pmol SM d18:1/17:0, 5 pmol DG 15:0-d7-15:0, 19 pmol TG 15:0-18:1-d7-15:0, and 25 pmol PE d31-16:0/18:1, 11 pmol PI d31-16:0/18:1, 19 pmol PS d31-16:0/18:1, 2.5 pmol PG d31-16:0/18:1, 1 pmol PA d31-16:0/18:1, 1.5 pmol CL 56:0, 2 pmol Cer d18:1/17:0, and 5 pmol GM3 d3-d18:1/18:0. Next, the mixture was halved, and 5% dimethylformamide (additive for the negative ion mode) or 3 mM ammonium chloride (additive for the positive ion mode) were added to the split sample halves. The mass tolerance was 3 ppm.

For fragmentation analyses, HCD collision energy values were determined for each lipid class. Data-dependent MS/MS fragmentation experiments were performed based on mass lists from survey scans. Data files generated by LipidXplorer queries were further processed by in-house Excel macros.

Lipid classes and species were annotated according to the lipid classification systems [38], [39]. For glycerolipids, in sum formulas, e.g., PC(34:2), the total numbers of carbons followed by double bonds for all chains are indicated. The Lipid class(FA1_FA2) format specifies the structures of the fatty acyl (FA) side chains, e.g., PC(16:0_18:2), whereas the Lipid class(sn1/sn2) format specifies the side chain regiochemistry, too, e.g., PC(16:0/18:2). For sphingolipids, the sum formula, e.g., Cer(42:2:2), specifies first the total number of carbons in the long chain base and FA moiety then the sum of double bonds in the long chain base and the FA moiety followed by the sum of hydroxyl groups in the long chain base and the FA moiety. In the detailed formula, first the number of hydroxyl groups in the long chain base

(e.g., “d” for the two hydroxyls of sphingosine), the number of carbon atoms and then the number of double bonds are indicated followed by the N-acyl chain composition, such as Cer(d18:1/24:1).
The double bond index (DBI) was calculated for the major membrane phospholipids and TG as Σ(mol % of unsaturated fatty acids in the given lipid class x number of double bonds of each unsaturated fatty acid)/100.

Proteomics

Protein extraction

Approximately 30 mg of powered left ventricular tissue samples were homogenized in lysate buffer (contained 2 % SDS and 0.1 M DTT in 0.1 Tris solution). The homogenized samples were incubated at 98 °C for 5 min. Proteins were precipitated by addition of methanol/chloroform mixture (4:1) and were resuspended in 8 M urea. The total protein contents were determined using BCA (Thermo) protocol.

SDS-PAGE

SDS-PAGE was performed to pre-fractionate proteins for building a more comprehensive protein library of the heart proteome. For gel separation 20 μg protein from a pooled sample of all individual powered left ventricular tissue samples subjected to SDS-PAGE analysis on a 12 % SDS polyacrylamide gel (8*8 cm) using one-dimensional separation. Electrophoresis was performed on 80 V for 30 minutes to introduce the sample into the 5 % stacking gel. After that, the electrophoresis was carried out on 100 V for 2 hours. The protein bands were stained using Coomassie BrilliantBlue G-250 solution. After fixation (with 30 % ethanol, 10 % acetic acid) the gel was cut to 19 pieces, and the proteins were ’in-gel’ digested by trypsin.

’In gel’ digestion

The excised gel bands were cut into small pieces and destained in 0.1 M NH_4HCO_3 (pH = 8.0), dehydrated with acetonitrile and dried using Speed-Vac. Alkylation and reduction of proteins were performed using 10 mM DTT and 55 mM IAA solutions. After dehydration, the gel pieces were rehydrated with 12.5 ng/µl trypsin (Promega, Madison, WI, US) solution (in 25 mM NH_4HCO_3 pH = 8.0) and incubated overnight at 37 °C. Peptides were extracted with 5 % aqueous formic acid, and twice with 60 % acetonitrile in 1 % formic acid (20 min each). Samples were dried with vacuum centrifugation before LC/MS analysis.

’In solution’ digestion

Proteins were digested using the following protocol: all individual powdered left ventricular tissue samples containing 20 μg protein were diluted to 10 μl with 0.1 M NH_4HCO_3 (pH = 8.0) buffer; 12 μl 0.1 % RapiGest SF (Waters) and 2 μl 55 mM DTT solution was added and kept at 60 °C for 30 minutes to unfold and reduce proteins. A volume of 2 μl 200 mM IAA solution was added to alkylate the proteins which were kept for an additional 30 min in the dark at room temperature. The samples were digested with trypsin (Promega, the enzyme/protein ratio: 0.4/1) for 3h at 37 ^{o}C. The digestion was stopped by addition of 1 μl of concentrated hydrochloric acid.

A pooled sample was created by mixing equal amounts of all digested samples to extend the protein library built from the gel separated pooled sample.

LC-MS analysis

The separation of the digested samples was carried out on a nanoAcquity UPLC, (Waters, Milford, MA, US) using Waters ACQUITY UPLC M-Class Peptide C18 (130 Å, 1,78 μm, 75 μm*250mm) column with 90 min gradient. Eluents were water (A), and acetonitrile (B) containing 0.1 V/V % formic acid and the separation of the peptide mixture was performed at 45 °C with 0.35 μl/min flow rate using an optimized nonlinear LC gradient (3 %-40 % B). The LC was coupled to a high-resolution Q Exactive Plus quadrupole-orbitrap hybrid mass spectrometer (Thermo Scientific, Waltham, Massachusetts, US). In measurements to build the protein library, the mass spectrometer was operated in DDA (Data Dependent Acquisition) mode.

The ,,fast” method from Kelstrup[1] was used for DDA acquisition. The mass spectrometer was operated in the data-dependent mode to automatically switch between full scan MS and MS/MS acquisition. The full scan was performed between 300 – 1750 m/z with 70000 resolution at 200 m/z. The MS/MS scans were carried out with 17500 resolution after the accumulation of ions to a 1×10^{6} target value based on predictive AGC from the previous full scan. The 12 most intense multiply charged ions were fragmented in the octopole collision cell by normalized HCD collision energy (25 %). The spray voltage was set to 1.8 kV, and the capillary was heated to 275 °C. The MS/MS ion selection threshold was set to 1×10^{5} counts.

The quantitative measurements of digested individual samples were performed in DIA (Data Independent Acquisition) mode. The survey scan for DIA method operated with 35000 resolution. The full scan was performed between 380 to 1020 m/z. The AGC target was set to $5*10^{6}$ or 120 ms maximum injection time. In the 400-1000 m/z region 22 m/z wide overlapping windows were acquired at 17500 resolution (AGC target: $3*10^{6}$ or 100 ms injection time, normalized collision energy: 30 for charge 2).

Data analysis

The DDA spectra were processed with SearchGUI Version 1.6.1.6. analysis software[2] using four of the built-in search engines (Andromeda, Comet, OMSSA, X!Tandem). The minimal peptide length was set to 6. Search criteria included carbamidomethylation of cysteine as a fixed modification and oxidation of methionine and acetyl (protein N-terminus) as variable modifications. The mass tolerance for the precursor was 10 ppm and for the fragment ions was 0.15 Da. The DDA files were searched against rat reference proteome from the UniProt database. Trypsin was defined as enzyme with a maximum of 2 missed cleavages allowed. Protein identifications were validated in Peptideshaker[3] 3.65 using 1 % FDR limits both on peptide and protein level. The quantitative analysis was performed in Encyclopedia[4] 0.81. The statistical evaluations were carried out using Perseus software on text reports exported from Encyclopedia software. MSstats 3.73[5] was used to determine the minimal acceptable fold change for our sample size (n=8) at a statistical power of 80%. This minimal fold change was found to be 1.5, and this limit, together with a maximum of p=0.05 of Welch's t-test were used as a criterion for significant changes.

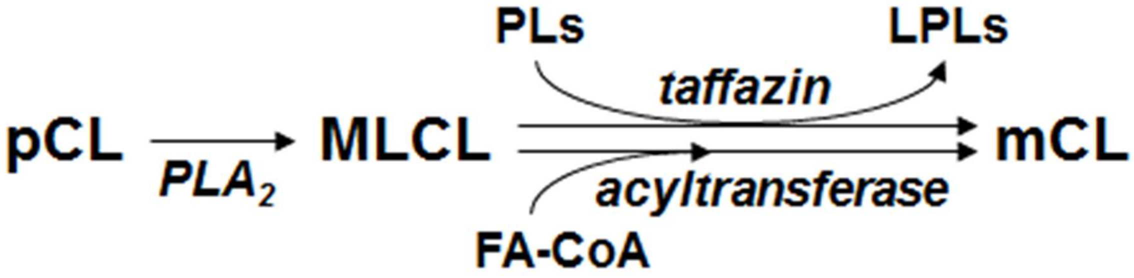
Subcellular localization of signifiacantly changing proteins was assigned based on Gene Onthology (www.ebi.ac.uk/QuickGO/).

Supplementary proteomics tables contain measured peptide intensities and assignments, quantification data of proteins with $p \leq 0.05$ in t-test, and pathway assignment of significantly changing proteins from Reactome (www.reactome.org) after assignment to human genes, for higher annotation coverage.

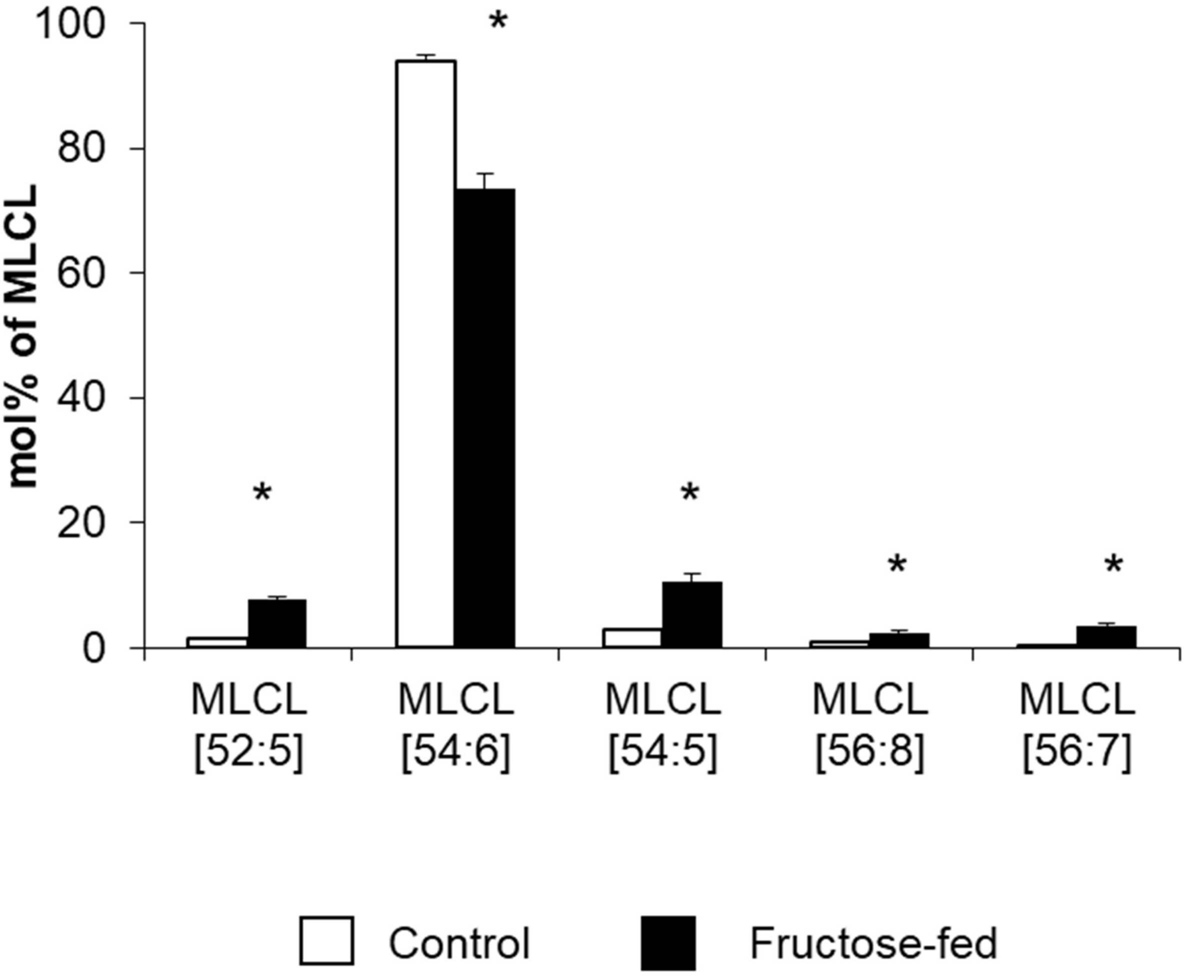
Supplementary references

1. Kelstrup CD, Young C, Lavallee R, et al. Optimized fast and sensitive acquisition methods for shotgun proteomics on a quadrupole orbitrap mass spectrometer. J Proteome Res. 2012;11:3487-3497.
2. Barsnes H, Vaudel M. SearchGUI: A Highly Adaptable Common Interface for Proteomics Search and de Novo Engines. J Proteome Res. 2018;17:2552-2555. doi:10.1021/acs.jproteome.8b00175.
3. Vaudel M, Burkhart JM, Zahedi RP, et al. PeptideShaker enables reanalysis of MS-derived proteomics data sets. Nat Biotechnol. 2015;33:22-24. doi:10.1038/nbt.3109.
4. Searle BC, Pino LK, Egertson JD, et al. Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. Nat Commun. 2018;9:5128. doi:10.1038/s41467-018-07454-w.
5. Choi M, Chang CY, Clough T, et al. MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Bioinformatics. 2014;30:2524-2526.

Supplementary Figures



Supplementary Figure 1: Cardiolipin (CL) maturation. After its initial biosynthesis, premature CL (pCL) undergoes intensive remodeling processes to produce matured CL (mCL). First, the removal of a single acyl chain is executed by a calcium-independent phospholipase A_2 (PLA_2) to produce monolysocardiolipin (MLCL). Reacylation is catalyzed either by CoA-dependent acyltransferases or the CoA-independent, reversible phospholipid (PL)-lysophospholipid (LPL) transacylase taffazin.



Supplementary Figure 2: Alterations in monolysocardiolipin (MLCL) species composition due to fructose-rich diet. ESI-MS data are expressed as mol% of MLCL or calculated from the corresponding values and presented as means ± SEM (n=8), *$p<0.05$.

Supplementary Tables

Lipid compositional data (mol% of membrane lipids)

Lipid compositional data

Data are expressed as mol% of membrane lipids and given as mean ± SEM, n = 8

****p<0.05 corresponding to false discovery rate <0.05; FC, fold change***

	Control		*Fructose*				
Species name	avg	*SEM*	avg	*SEM*	*p*		FC
PC(32:1)	0.132	*0.012*	0.202	*0.014*	1.7E-03	*	*1.53*
PC(32:0)	0.947	*0.037*	0.921	*0.042*	6.5E-01		*0.97*
PC(34:3)	0.064	*0.007*	0.062	*0.008*	8.2E-01		*0.96*
PC(34:2)	2.731	*0.208*	1.960	*0.231*	2.6E-02	*	*0.72*
PC(34:1)	3.556	*0.082*	4.803	*0.121*	6.4E-07	*	*1.35*
PC(34:0)	0.100	*0.006*	0.082	*0.005*	2.8E-02	*	*0.82*
PC(36:5)	0.164	*0.015*	0.194	*0.005*	7.3E-02		*1.18*
PC(36:4)	8.764	*0.173*	8.739	*0.256*	9.4E-01		*1.00*
PC(36:3)	1.111	*0.068*	1.354	*0.201*	2.7E-01		*1.22*
PC(36:2)	3.412	*0.246*	3.045	*0.398*	4.5E-01		*0.89*
PC(36:1)	1.233	*0.061*	1.859	*0.077*	1.8E-05	*	*1.51*
PC(38:6)	1.786	*0.146*	1.342	*0.051*	1.2E-02	*	*0.75*
PC(38:5)	1.977	*0.077*	2.618	*0.067*	2.0E-05	*	*1.32*
PC(38:4)	15.081	*0.464*	14.759	*0.547*	6.6E-01		*0.98*
PC(40:8)	0.127	*0.013*	0.091	*0.004*	2.2E-02	*	*0.72*
PC(40:7)	0.156	*0.005*	0.170	*0.006*	8.7E-02		*1.09*
PC(40:6)	0.560	*0.030*	0.548	*0.043*	8.3E-01		*0.98*
PC(40:5)	0.479	*0.028*	0.571	*0.054*	1.5E-01		*1.19*
PC(40:4)	0.190	*0.009*	0.181	*0.012*	6.0E-01		*0.96*
PC	**42.569**	***0.382***	**43.501**	***0.414***	1.2E-01		*1.02*
PC-P(34:1)	0.006	*0.002*	0.007	*0.002*	6.6E-01		*1.17*
PC-P(34:0)	0.010	*0.001*	0.016	*0.001*	7.8E-03	*	*1.59*
PC-P(36:4)	0.379	*0.100*	0.378	*0.066*	9.9E-01		*1.00*
PC-P(38:5)	0.071	*0.019*	0.079	*0.015*	7.4E-01		*1.11*
PC-P(38:4)	0.033	*0.007*	0.030	*0.005*	7.0E-01		*0.90*
PC-P	**0.500**	***0.127***	**0.510**	***0.087***	9.5E-01		*1.02*
LPC(16:0)	0.058	*0.003*	0.065	*0.004*	2.1E-01		*1.12*
LPC(18:2)	0.001	*0.000*	0.001	*0.000*	4.3E-01		*0.69*
LPC(18:1)	0.005	*0.001*	0.011	*0.001*	1.5E-03	*	*2.12*
LPC(18:0)	0.096	*0.005*	0.097	*0.008*	8.9E-01		*1.01*
LPC(20:4)	0.013	*0.003*	0.011	*0.002*	5.8E-01		*0.82*
LPC	**0.173**	***0.009***	**0.184**	***0.013***	4.7E-01		*1.07*
LPE(16:0)	0.004	*0.000*	0.007	*0.002*	9.4E-02		*1.88*
LPE(18:1)	0.032	*0.001*	0.035	*0.002*	1.7E-01		*1.10*
LPE(18:0)	0.027	*0.001*	0.033	*0.001*	2.0E-02	*	*1.19*
LPE	**0.063**	***0.002***	**0.075**	***0.004***	1.4E-02	*	*1.19*
PE(34:2)	0.598	*0.046*	0.331	*0.027*	2.1E-04	*	*0.55*
PE(34:1)	0.379	*0.021*	0.518	*0.014*	1.1E-04	*	*1.36*
PE(36:4)	1.430	*0.074*	1.735	*0.076*	1.2E-02	*	*1.21*
PE(36:3)	0.621	*0.055*	0.424	*0.060*	2.9E-02	*	*0.68*

PE(36:2)	1.816	*0.165*	1.076	*0.111*	2.3E-03	*	*0.59*
PE(36:1)	0.207	*0.012*	0.250	*0.012*	2.2E-02	*	*1.21*
PE(38:6)	1.831	*0.074*	1.425	*0.139*	2.2E-02	*	*0.78*
PE(38:5)	1.550	*0.065*	2.602	*0.049*	3.7E-09	*	*1.68*
PE(38:4)	8.254	*0.364*	8.801	*0.198*	2.1E-01		*1.07*
PE(38:3)	0.020	*0.004*	0.080	*0.013*	7.1E-04	*	*4.04*
PE(40:7)	0.489	*0.016*	0.592	*0.022*	2.2E-03	*	*1.21*
PE(40:6)	4.225	*0.234*	4.115	*0.330*	7.9E-01		*0.97*
PE(40:5)	2.407	*0.231*	3.138	*0.296*	7.2E-02		*1.30*
PE(40:4)	0.429	*0.014*	0.347	*0.012*	4.4E-04	*	*0.81*
PE	**24.256**	***0.350***	**25.435**	***0.616***	1.2E-01		*1.05*
PE-P(34:2)	0.146	*0.006*	0.095	*0.005*	8.8E-06	*	*0.65*
PE-P(34:1)	0.076	*0.004*	0.113	*0.008*	8.1E-04	*	*1.48*
PE-P(36:4)	3.144	*0.146*	3.365	*0.129*	2.8E-01		*1.07*
PE-P(36:2)	0.066	*0.003*	0.053	*0.003*	7.6E-03	*	*0.80*
PE-P(38:6)	1.141	*0.068*	0.727	*0.034*	9.2E-05	*	*0.64*
PE-P(38:5)	2.257	*0.170*	2.464	*0.163*	3.9E-01		*1.09*
PE-P(38:4)	1.928	*0.112*	1.456	*0.068*	2.8E-03	*	*0.76*
PE-P(40:7)	0.371	*0.017*	0.322	*0.015*	4.4E-02	*	*0.87*
PE-P(40:6)	0.398	*0.023*	0.293	*0.011*	9.2E-04	*	*0.74*
PE-P(40:5)	0.194	*0.010*	0.170	*0.005*	4.9E-02	*	*0.87*
PE-P(40:4)	0.116	*0.003*	0.096	*0.002*	2.4E-05	*	*0.82*
PE-P	**9.839**	***0.417***	**9.153**	***0.370***	2.4E-01		*0.93*
LPI(18:1)	0.017	*0.001*	0.018	*0.001*	3.5E-01		*1.09*
LPI(18:0)	0.004	*0.000*	0.004	*0.000*	9.5E-01		*0.99*
LPI(20:4)	0.004	*0.000*	0.004	*0.001*	7.2E-01		*0.93*
LPI	**0.025**	***0.001***	**0.026**	***0.002***	5.4E-01		*1.04*
PI(34:2)	0.042	*0.004*	0.026	*0.002*	1.8E-03	*	*0.62*
PI(34:1)	0.004	*0.003*	0.030	*0.007*	5.4E-03	*	*7.70*
PI(36:4)	0.117	*0.004*	0.128	*0.004*	8.0E-02		*1.10*
PI(36:3)	0.079	*0.005*	0.067	*0.008*	2.8E-01		*0.86*
PI(36:2)	0.452	*0.022*	0.218	*0.016*	5.5E-07	*	*0.48*
PI(36:1)	0.032	*0.002*	0.045	*0.004*	1.0E-02	*	*1.40*
PI(38:6)	0.019	*0.001*	0.011	*0.001*	1.0E-05	*	*0.58*
PI(38:5)	0.177	*0.005*	0.263	*0.013*	2.5E-05	*	*1.49*
PI(38:4)	3.452	*0.036*	3.411	*0.079*	6.4E-01		*0.99*
PI(40:6)	0.035	*0.002*	0.024	*0.002*	5.9E-04	*	*0.69*
PI(40:5)	0.039	*0.004*	0.032	*0.002*	1.3E-01		*0.83*
PI(40:4)	0.021	*0.002*	0.017	*0.001*	2.4E-02	*	*0.78*
PI	**4.469**	***0.038***	**4.274**	***0.063***	1.9E-02	*	*0.96*
LPS(18:1)	0.012	*0.001*	0.013	*0.001*	3.3E-01		*1.10*
LPS	**0.012**	***0.001***	**0.013**	***0.001***	3.3E-01		*1.10*
PS(34:1)	0.005	*0.001*	0.011	*0.001*	9.9E-05	*	*2.15*
PS(36:2)	0.125	*0.009*	0.096	*0.007*	1.9E-02	*	*0.77*
PS(36:1)	0.168	*0.004*	0.194	*0.008*	1.1E-02	*	*1.16*
PS(38:6)	0.006	*0.001*	0.004	*0.001*	7.8E-02		*0.64*
PS(38:5)	0.008	*0.001*	0.013	*0.001*	5.6E-04	*	*1.67*
PS(38:4)	0.377	*0.010*	0.345	*0.007*	1.7E-02	*	*0.92*
PS(38:3)	0.042	*0.001*	0.059	*0.004*	1.2E-03	*	*1.41*

PS(38:2)	0.003	*0.000*	0.005	*0.000*	2.2E-03	*	*1.63*
PS(40:7)	0.004	*0.001*	0.009	*0.001*	1.7E-03	*	*2.16*
PS(40:6)	1.007	*0.055*	0.955	*0.041*	4.6E-01		*0.95*
PS(40:5)	0.677	*0.054*	0.896	*0.045*	7.5E-03	*	*1.32*
PS(40:4)	0.296	*0.006*	0.245	*0.006*	5.1E-05	*	*0.83*
PS(40:3)	0.022	*0.007*	0.031	*0.004*	2.9E-01		*1.42*
PS	**2.739**	***0.036***	**2.863**	***0.049***	6.0E-02		*1.05*
LPG(18:2)	0.001	*0.000*	0.000	*0.000*	1.5E-01		*0.42*
LPG(18:1)	0.001	*0.000*	0.002	*0.000*	3.5E-03	*	*1.92*
LPG	**0.002**	***0.000***	**0.002**	***0.000***	4.3E-01		*1.20*
PG(32:1)	0.003	*0.001*	0.006	*0.001*	1.0E-03	*	*2.22*
PG(34:2)	0.172	*0.011*	0.105	*0.004*	7.2E-05	*	*0.61*
PG(34:1)	1.018	*0.036*	1.174	*0.058*	3.8E-02	*	*1.15*
PG(36:4)	0.040	*0.002*	0.029	*0.002*	4.6E-04	*	*0.73*
PG(36:3)	0.052	*0.003*	0.052	*0.002*	1.0E+00		*1.00*
PG(36:2)	0.142	*0.008*	0.109	*0.006*	7.8E-03	*	*0.77*
PG(36:1)	0.047	*0.004*	0.047	*0.002*	9.5E-01		*1.01*
PG(38:6)	0.013	*0.001*	0.005	*0.001*	8.4E-04	*	*0.37*
PG(38:5)	0.010	*0.001*	0.015	*0.002*	9.8E-03	*	*1.52*
PG(38:4)	0.023	*0.001*	0.023	*0.001*	9.9E-01		*1.00*
PG(40:8)	0.007	*0.001*	0.001	*0.000*	4.0E-04	*	*0.10*
PG(40:7)	0.011	*0.001*	0.009	*0.001*	1.6E-01		*0.79*
PG(40:6)	0.011	*0.001*	0.017	*0.002*	4.8E-03	*	*1.57*
PG	**1.548**	***0.047***	**1.591**	***0.059***	5.8E-01		*1.03*
PA(34:2)	0.011	*0.001*	0.010	*0.001*	5.7E-01		*0.93*
PA(34:1)	0.037	*0.002*	0.046	*0.003*	3.0E-02	*	*1.26*
PA(36:4)	0.006	*0.001*	0.004	*0.001*	3.3E-01		*0.78*
PA(36:3)	0.003	*0.001*	0.005	*0.001*	2.6E-01		*1.35*
PA(36:2)	0.013	*0.002*	0.015	*0.002*	5.1E-01		*1.15*
PA(36:1)	0.001	*0.000*	0.001	*0.000*	5.6E-01		*1.27*
PA(38:5)	0.003	*0.001*	0.003	*0.001*	7.0E-01		*1.20*
PA	**0.073**	***0.007***	**0.085**	***0.006***	2.4E-01		*1.16*
CL(68:6)	0.024	*0.002*	0.064	*0.003*	3.4E-08	*	*2.62*
CL(68:5)	0.005	*0.001*	0.017	*0.002*	1.9E-04	*	*3.63*
CL(70:7)	0.358	*0.046*	0.908	*0.040*	3.4E-07	*	*2.54*
CL(70:6)	0.026	*0.002*	0.118	*0.026*	3.1E-03	*	*4.60*
CL(70:5)	0.013	*0.002*	0.027	*0.004*	8.8E-03	*	*2.13*
CL(70:4)	0.008	*0.001*	0.015	*0.002*	1.1E-02	*	*1.84*
CL(72:9)	0.067	*0.003*	0.062	*0.003*	2.8E-01		*0.93*
CL(72:8)	8.615	*0.306*	5.481	*0.268*	2.1E-06	*	*0.64*
CL(72:7)	1.751	*0.021*	1.961	*0.084*	3.0E-02	*	*1.12*
CL(72:5)	0.001	*0.000*	0.003	*0.000*	5.3E-03	*	*2.58*
CL(74:11)	0.003	*0.001*	0.018	*0.003*	5.8E-04	*	*5.17*
CL(74:10)	0.193	*0.013*	0.289	*0.032*	1.4E-02	*	*1.50*
CL(74:9)	0.149	*0.013*	0.474	*0.027*	3.5E-08	*	*3.19*
CL(74:8)	0.037	*0.003*	0.043	*0.010*	5.7E-01		*1.17*
CL(76:12)	0.080	*0.010*	0.118	*0.019*	9.3E-02		*1.47*
CL(76:11)	0.082	*0.009*	0.160	*0.025*	1.1E-02	*	*1.96*
CL(76:10)	0.025	*0.002*	0.049	*0.005*	1.3E-03	*	*1.95*
CL(78:13)	0.001	*0.000*	0.012	*0.003*	2.2E-03	*	*10.73*
CL(78:12)	0.001	*0.000*	0.008	*0.002*	6.6E-04	*	*10.57*

CL	**11.437**	***0.244***	**9.827**	***0.164***	8.3E-05	*	*0.86*
MLCL(52:5)	0.002	*0.000*	0.013	*0.002*	1.2E-05	*	*7.66*
MLCL(52:4)	0.000	*0.000*	0.001	*0.000*	2.0E-02	*	*11.21*
MLCL(54:6)	0.112	*0.009*	0.120	*0.009*	5.3E-01		*1.07*
MLCL(54:5)	0.004	*0.000*	0.019	*0.004*	8.2E-04	*	*5.30*
MLCL(54:4)	0.000	*0.000*	0.001	*0.000*	5.4E-02		*6.64*
MLCL(56:8)	0.001	*0.000*	0.004	*0.001*	2.8E-02	*	*4.27*
MLCL(56:7)	0.000	*0.000*	0.006	*0.001*	1.3E-04	*	*12.89*
MLCL(58:10)	0.000	*0.000*	0.002	*0.001*	5.6E-02		*5.16*
MLCL(58:9)	0.000	*0.000*	0.002	*0.001*	6.1E-02		*8.02*
MLCL	**0.119**	***0.010***	**0.167**	***0.018***	3.4E-02	*	*1.40*
SM(34:2:2)	0.004	*0.001*	0.003	*0.001*	5.7E-01		*0.83*
SM(34:1:2)	0.313	*0.013*	0.385	*0.011*	9.3E-04	*	*1.23*
SM(36:2:2)	0.031	*0.003*	0.030	*0.003*	7.8E-01		*0.96*
SM(36:1:2)	0.297	*0.013*	0.354	*0.014*	9.6E-03	*	*1.19*
SM(38:2:2)	0.057	*0.004*	0.045	*0.004*	5.5E-02		*0.80*
SM(38:1:2)	0.220	*0.009*	0.212	*0.007*	4.7E-01		*0.96*
SM(39:2:2)	0.003	*0.000*	0.001	*0.000*	3.1E-03	*	*0.29*
SM(39:1:2)	0.035	*0.002*	0.020	*0.002*	9.6E-05	*	*0.59*
SM(40:2:2)	0.088	*0.003*	0.071	*0.003*	2.7E-03	*	*0.80*
SM(40:1:2)	0.267	*0.008*	0.205	*0.007*	3.3E-05	*	*0.77*
SM(41:2:2)	0.038	*0.004*	0.032	*0.003*	2.3E-01		*0.85*
SM(41:1:2)	0.107	*0.006*	0.097	*0.004*	2.0E-01		*0.91*
SM(42:2:2)	0.181	*0.006*	0.283	*0.016*	2.6E-05	*	*1.57*
SM(41:2:3)	0.012	*0.004*	0.011	*0.003*	9.1E-01		*0.95*
SM(42:1:2)	0.232	*0.008*	0.225	*0.007*	5.1E-01		*0.97*
SM	**1.886**	***0.030***	**1.976**	***0.031***	5.8E-02		*1.05*
Cer(34:1:2)	0.002	*0.000*	0.003	*0.000*	2.0E-01		*1.27*
Cer(36:1:2)	0.003	*0.000*	0.004	*0.001*	1.8E-01		*1.40*
Cer(38:1:2)	0.002	*0.000*	0.003	*0.000*	9.6E-02		*1.50*
Cer(40:2:2)	0.001	*0.000*	0.001	*0.000*	8.6E-01		*1.06*
Cer(40:1:2)	0.008	*0.001*	0.009	*0.001*	4.5E-01		*1.12*
Cer(41:2:2)	0.001	*0.000*	0.001	*0.000*	1.7E-01		*1.58*
Cer(41:1:2)	0.007	*0.001*	0.007	*0.001*	5.0E-01		*1.13*
Cer(42:3:2)	0.001	*0.000*	0.003	*0.000*	4.6E-05	*	*4.21*
Cer(42:2:2)	0.012	*0.001*	0.022	*0.001*	6.0E-05	*	*1.74*
Cer(42:1:2)	0.021	*0.001*	0.024	*0.001*	8.9E-02		*1.15*
Cer	**0.057**	***0.003***	**0.077**	***0.005***	3.5E-03	*	*1.34*
GM3(34:1:2)	0.010	*0.001*	0.013	*0.002*	2.3E-01		*1.30*
GM3(36:1:2)	0.031	*0.004*	0.046	*0.001*	5.1E-03	*	*1.49*
GM3(38:1:2)	0.073	*0.003*	0.065	*0.002*	4.9E-02	*	*0.90*
GM3(40:1:2)	0.055	*0.002*	0.042	*0.003*	4.5E-03	*	*0.78*
GM3(42:2:2)	0.036	*0.006*	0.043	*0.005*	4.2E-01		*1.19*
GM3(42:1:2)	0.029	*0.005*	0.032	*0.002*	5.1E-01		*1.12*
GM3	**0.233**	***0.005***	**0.242**	***0.010***	4.2E-01		*1.04*
DG(34:2)	0.029	*0.009*	0.041	*0.014*	5.0E-01		*1.40*
DG(34:1)	0.114	*0.016*	0.154	*0.030*	2.6E-01		*1.35*
DG(36:4)	0.030	*0.004*	0.018	*0.004*	4.2E-02	*	*0.59*
DG(36:3)	0.031	*0.005*	0.032	*0.015*	9.4E-01		*1.04*

DG(36:2)	0.098	*0.032*	0.111	*0.032*	7.7E-01		*1.14*
DG(38:5)	0.010	*0.003*	0.013	*0.003*	5.4E-01		*1.26*
DG(38:4)	0.176	*0.018*	0.174	*0.015*	9.4E-01		*0.99*
DG	**0.488**	***0.062***	**0.543**	***0.108***	6.6E-01		*1.11*
TG(50:5)	0.003	*0.001*	0.000	*0.000*	1.7E-01		*0.13*
TG(50:4)	0.057	*0.015*	0.033	*0.008*	1.8E-01		*0.59*
TG(50:3)	0.166	*0.057*	0.096	*0.051*	3.8E-01		*0.58*
TG(50:2)	0.438	*0.120*	0.377	*0.128*	7.3E-01		*0.86*
TG(50:1)	0.251	*0.065*	0.334	*0.103*	5.1E-01		*1.33*
TG(50:0)	0.021	*0.001*	0.023	*0.001*	4.2E-01		*1.06*
TG(52:5)	0.066	*0.022*	0.019	*0.007*	6.2E-02		*0.28*
TG(52:4)	0.378	*0.117*	0.137	*0.042*	7.4E-02		*0.36*
TG(52:3)	0.755	*0.203*	0.551	*0.182*	4.7E-01		*0.73*
TG(52:2)	0.463	*0.139*	0.669	*0.229*	4.5E-01		*1.44*
TG(52:1)	0.059	*0.006*	0.058	*0.011*	9.3E-01		*0.98*
TG(52:0)	0.007	*0.001*	0.008	*0.001*	2.8E-01		*1.18*
TG(54:7)	0.012	*0.005*	0.001	*0.000*	5.0E-02	*	*0.08*
TG(54:6)	0.129	*0.041*	0.032	*0.009*	3.9E-02	*	*0.25*
TG(54:5)	0.391	*0.100*	0.233	*0.048*	1.8E-01		*0.60*
TG(54:4)	0.363	*0.096*	0.272	*0.092*	5.0E-01		*0.75*
TG(54:3)	0.246	*0.071*	0.349	*0.120*	4.7E-01		*1.42*
TG(54:2)	0.056	*0.006*	0.060	*0.015*	7.8E-01		*1.08*
TG(56:8)	0.026	*0.005*	0.001	*0.001*	9.0E-05	*	*0.05*
TG(56:7)	0.055	*0.007*	0.028	*0.006*	1.3E-02	*	*0.50*
TG(56:6)	0.075	*0.009*	0.058	*0.013*	2.6E-01		*0.77*
TG(56:5)	0.058	*0.006*	0.070	*0.012*	3.8E-01		*1.20*
TG(56:4)	0.014	*0.003*	0.013	*0.005*	8.4E-01		*0.92*
TG(56:3)	0.010	*0.003*	0.011	*0.004*	8.1E-01		*1.13*
TG(58:9)	0.011	*0.002*	0.001	*0.000*	7.6E-04	*	*0.11*
TG(58:8)	0.022	*0.004*	0.006	*0.002*	2.8E-03	*	*0.28*
TG(58:7)	0.016	*0.004*	0.013	*0.004*	6.2E-01		*0.83*
TG(58:6)	0.011	*0.003*	0.011	*0.004*	9.8E-01		*0.99*
TG(58:5)	0.002	*0.001*	0.002	*0.001*	7.9E-01		*1.20*
TG(58:4)	0.000	*0.000*	0.000	*0.000*	1.7E-01		*0.29*
TG	**4.160**	***0.982***	**3.469**	***1.053***	6.4E-01		*0.83*
Class composition							
PC	42.569	*0.382*	43.501	*0.414*	1.2E-01		*1.02*
PC-P	0.500	*0.127*	0.510	*0.087*	9.5E-01		*1.02*
LPC	0.173	*0.009*	0.184	*0.013*	4.7E-01		*1.07*
LPE	0.063	*0.002*	0.075	*0.004*	1.4E-02	*	*1.19*
PE	24.256	*0.350*	25.435	*0.616*	1.2E-01		*1.05*
PE-P	9.839	*0.417*	9.153	*0.370*	2.4E-01		*0.93*
LPI	0.025	*0.001*	0.026	*0.002*	5.4E-01		*1.04*
PI	4.469	*0.038*	4.274	*0.063*	1.9E-02	*	*0.96*
LPS	0.012	*0.001*	0.013	*0.001*	3.3E-01		*1.10*
PS	2.739	*0.036*	2.863	*0.049*	6.0E-02		*1.05*
LPG	0.002	*0.000*	0.002	*0.000*	4.3E-01		*1.20*
PG	1.548	*0.047*	1.591	*0.059*	5.8E-01		*1.03*
PA	0.073	*0.007*	0.085	*0.006*	2.4E-01		*1.16*
CL	11.437	*0.244*	9.827	*0.164*	8.3E-05	*	*0.86*
MLCL	0.119	*0.010*	0.167	*0.018*	3.4E-02	*	*1.40*
SM	1.886	*0.030*	1.976	*0.031*	5.8E-02		*1.05*
Cer	0.057	*0.003*	0.077	*0.005*	3.5E-03	*	*1.34*
GM3	0.233	*0.005*	0.242	*0.010*	4.2E-01		*1.04*
DG	0.488	*0.062*	0.543	*0.108*	6.6E-01		*1.11*
TG	4.160	*0.982*	3.469	*1.053*	6.4E-01		*0.83*

Species composition of individual lipid classes (mol% of individulal classes)

Species composition of individual lipid classes

Data are expressed as mol% of the given lipid class and presented as mean ± SEM, n = 8, *p<0.05

	Control		*Fructose*			
Species name	avg	*SEM*	avg	*SEM*	*p*	
PC(32:1)	0.310	*0.025*	0.465	*0.031*	1.6E-03	*
PC(32:0)	2.223	*0.074*	2.120	*0.102*	4.3E-01	
PC(34:3)	0.150	*0.015*	0.141	*0.019*	7.1E-01	
PC(34:2)	6.423	*0.500*	4.487	*0.506*	1.7E-02	*
PC(34:1)	8.357	*0.198*	11.049	*0.303*	3.2E-06	*
PC(34:0)	0.235	*0.012*	0.188	*0.011*	1.3E-02	*
PC(36:5)	0.385	*0.031*	0.447	*0.010*	8.1E-02	
PC(36:4)	20.580	*0.280*	20.114	*0.682*	5.4E-01	
PC(36:3)	2.611	*0.160*	3.097	*0.447*	3.2E-01	
PC(36:2)	8.032	*0.609*	6.966	*0.876*	3.3E-01	
PC(36:1)	2.898	*0.148*	4.273	*0.171*	2.9E-05	*
PC(38:6)	4.182	*0.310*	3.086	*0.116*	5.2E-03	*
PC(38:5)	4.644	*0.179*	6.019	*0.154*	4.3E-05	*
PC(38:4)	35.418	*0.986*	33.944	*1.270*	3.7E-01	
PC(40:8)	0.298	*0.029*	0.210	*0.009*	1.2E-02	*
PC(40:7)	0.367	*0.011*	0.391	*0.014*	2.0E-01	
PC(40:6)	1.314	*0.069*	1.264	*0.107*	7.0E-01	
PC(40:5)	1.127	*0.069*	1.319	*0.133*	2.2E-01	
PC(40:4)	0.446	*0.024*	0.419	*0.031*	4.9E-01	
PC	100.000	*0.000*	100.000	*0.000*		
PC-P(34:1)	1.295	*0.143*	1.301	*0.203*	9.8E-01	
PC-P(34:0)	4.249	*1.861*	3.980	*0.870*	9.0E-01	
PC-P(36:4)	74.512	*0.882*	73.649	*0.836*	4.9E-01	
PC-P(38:5)	12.698	*1.682*	15.036	*0.593*	2.1E-01	
PC-P(38:4)	7.246	*0.352*	6.035	*0.394*	3.8E-02	*
PC-P	100.000	*0.000*	100.000	*0.000*		
LPC(16:0)	33.535	*0.913*	35.132	*0.641*	1.7E-01	
LPC(18:2)	0.479	*0.083*	0.324	*0.157*	4.0E-01	
LPC(18:1)	3.180	*0.443*	6.384	*0.836*	4.4E-03	*
LPC(18:0)	55.206	*1.110*	52.418	*1.322*	1.3E-01	
LPC(20:4)	7.600	*1.783*	5.742	*1.064*	3.9E-01	
LPC	100.000	*0.000*	100.000	*0.000*		
LPE(16:0)	6.223	*0.762*	9.233	*1.859*	1.6E-01	
LPE(18:1)	50.502	*1.984*	47.111	*1.948*	2.4E-01	
LPE(18:0)	43.274	*1.611*	43.656	*1.602*	8.7E-01	
LPE	100.000	*0.000*	100.000	*0.000*		
PE(34:2)	2.454	*0.168*	1.316	*0.125*	8.8E-05	*
PE(34:1)	1.568	*0.095*	2.047	*0.087*	2.3E-03	*
PE(36:4)	5.882	*0.257*	6.824	*0.265*	2.3E-02	*
PE(36:3)	2.557	*0.220*	1.703	*0.265*	2.6E-02	*
PE(36:2)	7.454	*0.624*	4.297	*0.511*	1.6E-03	*

PE(36:1)	0.854	*0.051*	0.988	*0.061*	1.1E-01	
PE(38:6)	7.557	*0.303*	5.544	*0.427*	1.8E-03	*
PE(38:5)	6.418	*0.331*	10.267	*0.285*	4.3E-07	*
PE(38:4)	33.982	*1.230*	34.699	*0.902*	6.5E-01	
PE(38:3)	0.082	*0.019*	0.321	*0.057*	1.4E-03	*
PE(40:7)	2.019	*0.077*	2.327	*0.063*	7.8E-03	*
PE(40:6)	17.411	*0.915*	16.049	*0.943*	3.2E-01	
PE(40:5)	9.990	*1.016*	12.252	*0.952*	1.3E-01	
PE(40:4)	1.772	*0.065*	1.365	*0.027*	4.4E-05	*
PE	100.000	*0.000*	100.000	*0.000*		
PE-P(34:2)	1.512	*0.100*	1.041	*0.048*	8.3E-04	*
PE-P(34:1)	0.779	*0.039*	1.232	*0.073*	8.4E-05	*
PE-P(36:4)	31.923	*0.560*	36.788	*0.385*	4.9E-06	*
PE-P(36:2)	0.683	*0.055*	0.575	*0.024*	9.4E-02	
PE-P(38:6)	11.646	*0.607*	8.010	*0.429*	2.4E-04	*
PE-P(38:5)	22.807	*1.085*	26.748	*0.760*	1.0E-02	*
PE-P(38:4)	19.616	*0.829*	15.898	*0.268*	7.8E-04	*
PE-P(40:7)	3.807	*0.190*	3.545	*0.197*	3.6E-01	
PE-P(40:6)	4.056	*0.170*	3.234	*0.179*	5.0E-03	*
PE-P(40:5)	1.972	*0.045*	1.871	*0.083*	3.0E-01	
PE-P(40:4)	1.198	*0.053*	1.058	*0.050*	7.8E-02	
PE-P	100.000	*0.000*	100.000	*0.000*		
LPI(18:1)	67.413	*2.155*	70.379	*2.902*	4.3E-01	
LPI(18:0)	14.574	*1.420*	14.012	*1.083*	7.6E-01	
LPI(20:4)	18.013	*1.489*	15.609	*2.509*	4.2E-01	
LPI	100.000	*0.000*	100.000	*0.000*		
PI(34:2)	0.950	*0.084*	0.620	*0.045*	3.8E-03	*
PI(34:1)	0.087	*0.064*	0.703	*0.176*	5.4E-03	*
PI(36:4)	2.622	*0.103*	3.004	*0.088*	1.4E-02	*
PI(36:3)	1.760	*0.116*	1.585	*0.209*	4.8E-01	
PI(36:2)	10.099	*0.453*	5.119	*0.379*	7.3E-07	*
PI(36:1)	0.720	*0.045*	1.053	*0.088*	4.7E-03	*
PI(38:6)	0.419	*0.023*	0.253	*0.015*	3.0E-05	*
PI(38:5)	3.958	*0.118*	6.169	*0.348*	3.1E-05	*
PI(38:4)	77.254	*0.579*	79.781	*1.092*	6.0E-02	
PI(40:6)	0.787	*0.045*	0.568	*0.031*	1.2E-03	*
PI(40:5)	0.866	*0.078*	0.755	*0.038*	2.2E-01	
PI(40:4)	0.476	*0.037*	0.391	*0.011*	4.3E-02	*
PI	100.000	*0.000*	100.000	*0.000*		
LPS(18:1)	100.000	*0.000*	100.000	*0.000*		
LPS	100.000	*0.000*	100.000	*0.000*		
PS(34:1)	0.191	*0.019*	0.395	*0.034*	1.3E-04	*
PS(36:2)	4.594	*0.352*	3.370	*0.256*	1.4E-02	*
PS(36:1)	6.122	*0.156*	6.795	*0.328*	8.6E-02	
PS(38:6)	0.205	*0.027*	0.123	*0.024*	4.0E-02	*
PS(38:5)	0.279	*0.024*	0.446	*0.027*	4.4E-04	*
PS(38:4)	13.763	*0.336*	12.064	*0.265*	1.4E-03	*
PS(38:3)	1.519	*0.056*	2.051	*0.143*	3.8E-03	*
PS(38:2)	0.117	*0.017*	0.180	*0.009*	5.9E-03	*

PS(40:7)	0.158	*0.024*	0.328	*0.039*	2.3E-03	*
PS(40:6)	36.750	*1.931*	33.379	*1.372*	1.8E-01	
PS(40:5)	24.687	*1.911*	31.253	*1.325*	1.4E-02	*
PS(40:4)	10.809	*0.262*	8.547	*0.182*	5.5E-06	*
PS(40:3)	0.804	*0.268*	1.069	*0.134*	3.9E-01	
PS	100.000	*0.000*	100.000	*0.000*		
LPG(18:2)	41.679	*7.007*	16.420	*3.268*	5.6E-03	*
LPG(18:1)	58.321	*7.007*	83.580	*3.268*	5.6E-03	*
LPG	100.000	*0.000*	100.000	*0.000*		
PG(32:1)	0.178	*0.045*	0.380	*0.034*	3.0E-03	*
PG(34:2)	11.194	*0.822*	6.669	*0.407*	2.2E-04	*
PG(34:1)	65.727	*0.997*	73.609	*1.023*	7.6E-05	*
PG(36:4)	2.570	*0.111*	1.799	*0.056*	2.3E-05	*
PG(36:3)	3.346	*0.153*	3.300	*0.220*	8.7E-01	
PG(36:2)	9.135	*0.386*	6.971	*0.596*	8.7E-03	*
PG(36:1)	2.977	*0.200*	2.960	*0.129*	9.4E-01	
PG(38:6)	0.820	*0.105*	0.282	*0.060*	5.6E-04	*
PG(38:5)	0.638	*0.048*	0.917	*0.072*	6.2E-03	*
PG(38:4)	1.474	*0.060*	1.433	*0.060*	6.4E-01	
PG(40:8)	0.493	*0.108*	0.046	*0.013*	1.1E-03	*
PG(40:7)	0.739	*0.063*	0.558	*0.073*	8.2E-02	
PG(40:6)	0.708	*0.059*	1.075	*0.073*	1.6E-03	*
PG	100.000	*0.000*	100.000	*0.000*		
PA(34:2)	15.658	*1.662*	12.193	*1.121*	1.1E-01	
PA(34:1)	51.381	*2.474*	54.854	*2.071*	3.0E-01	
PA(36:4)	7.403	*1.053*	5.130	*0.716*	9.6E-02	
PA(36:3)	4.460	*0.484*	5.318	*0.502*	2.4E-01	
PA(36:2)	16.790	*1.680*	17.241	*0.900*	8.2E-01	
PA(36:1)	1.047	*0.287*	1.259	*0.291*	6.1E-01	
PA(38:5)	3.260	*1.026*	4.007	*1.130*	6.3E-01	
PA	100.000	*0.000*	100.000	*0.000*		
CL(68:6)	0.215	*0.024*	0.650	*0.033*	4.4E-08	*
CL(68:5)	0.040	*0.007*	0.171	*0.027*	3.2E-04	*
CL(70:7)	3.179	*0.445*	9.236	*0.353*	4.2E-08	*
CL(70:6)	0.226	*0.021*	1.232	*0.287*	3.6E-03	*
CL(70:5)	0.113	*0.019*	0.283	*0.049*	6.3E-03	*
CL(70:4)	0.072	*0.008*	0.153	*0.025*	8.2E-03	*
CL(72:9)	0.584	*0.024*	0.634	*0.044*	3.4E-01	
CL(72:8)	75.177	*1.086*	55.593	*1.928*	4.1E-07	*
CL(72:7)	15.359	*0.392*	19.986	*0.895*	3.2E-04	*
CL(72:5)	0.009	*0.002*	0.027	*0.004*	2.0E-03	*
CL(74:11)	0.031	*0.007*	0.184	*0.035*	7.5E-04	*
CL(74:10)	1.698	*0.132*	2.981	*0.367*	5.4E-03	*
CL(74:9)	1.311	*0.129*	4.833	*0.276*	1.5E-08	*
CL(74:8)	0.323	*0.023*	0.452	*0.115*	2.9E-01	
CL(76:12)	0.704	*0.088*	1.217	*0.207*	3.9E-02	*
CL(76:11)	0.720	*0.087*	1.651	*0.274*	6.0E-03	*
CL(76:10)	0.221	*0.023*	0.504	*0.062*	7.3E-04	*
CL(78:13)	0.010	*0.003*	0.124	*0.031*	2.6E-03	*
CL(78:12)	0.007	*0.002*	0.088	*0.019*	8.9E-04	*
CL	100.000	*0.000*	100.000	*0.000*		

MLCL(52:5)	1.333	*0.295*	7.694	*0.464*	1.5E-08	*
MLCL(52:4)	0.067	*0.029*	0.486	*0.147*	1.5E-02	*
MLCL(54:6)	94.082	*0.804*	73.409	*2.600*	2.5E-06	*
MLCL(54:5)	2.883	*0.225*	10.543	*1.301*	4.6E-05	*
MLCL(54:4)	0.092	*0.061*	0.302	*0.106*	1.1E-01	
MLCL(56:8)	0.779	*0.208*	2.298	*0.493*	1.3E-02	*
MLCL(56:7)	0.371	*0.097*	3.545	*0.350*	4.8E-07	*
MLCL(58:10)	0.225	*0.090*	0.804	*0.271*	6.2E-02	
MLCL(58:9)	0.167	*0.058*	0.919	*0.318*	3.5E-02	*
MLCL	100.000	*0.000*	100.000	*0.000*		
SM(34:2:2)	0.215	*0.054*	0.171	*0.030*	4.8E-01	
SM(34:1:2)	16.576	*0.472*	19.498	*0.599*	1.8E-03	*
SM(36:2:2)	1.641	*0.139*	1.497	*0.169*	5.2E-01	
SM(36:1:2)	15.764	*0.647*	17.895	*0.505*	2.1E-02	*
SM(38:2:2)	3.001	*0.193*	2.288	*0.176*	1.6E-02	*
SM(38:1:2)	11.695	*0.430*	10.725	*0.254*	7.2E-02	
SM(39:2:2)	0.136	*0.025*	0.039	*0.007*	2.4E-03	*
SM(39:1:2)	1.830	*0.093*	1.030	*0.089*	2.3E-05	*
SM(40:2:2)	4.685	*0.177*	3.586	*0.128*	1.8E-04	*
SM(40:1:2)	14.191	*0.429*	10.393	*0.392*	1.3E-05	*
SM(41:2:2)	2.034	*0.197*	1.649	*0.140*	1.3E-01	
SM(41:1:2)	5.672	*0.313*	4.929	*0.287*	1.0E-01	
SM(42:2:2)	9.595	*0.326*	14.317	*0.672*	1.9E-05	*
SM(41:2:3)	0.635	*0.193*	0.570	*0.162*	8.0E-01	
SM(42:1:2)	12.330	*0.423*	11.413	*0.471*	1.7E-01	
SM	100.000	*0.000*	100.000	*0.000*		
Cer(34:1:2)	4.307	*0.602*	4.121	*0.374*	8.0E-01	
Cer(36:1:2)	4.304	*0.484*	4.461	*0.697*	8.6E-01	
Cer(38:1:2)	2.941	*0.428*	3.303	*0.454*	5.7E-01	
Cer(40:2:2)	2.294	*0.321*	1.654	*0.481*	2.9E-01	
Cer(40:1:2)	14.259	*0.593*	11.783	*0.990*	5.0E-02	*
Cer(41:2:2)	1.543	*0.305*	1.759	*0.331*	6.4E-01	
Cer(41:1:2)	11.124	*0.832*	9.500	*0.971*	2.2E-01	
Cer(42:3:2)	1.137	*0.227*	3.518	*0.278*	1.1E-05	*
Cer(42:2:2)	21.803	*1.523*	28.367	*1.574*	9.6E-03	*
Cer(42:1:2)	36.287	*1.101*	31.534	*2.228*	7.6E-02	
Cer	100.000	*0.000*	100.000	*0.000*		
GM3(34:1:2)	4.409	*0.472*	5.439	*0.796*	2.8E-01	
GM3(36:1:2)	13.168	*1.989*	18.998	*0.607*	1.4E-02	*
GM3(38:1:2)	31.316	*1.250*	27.261	*1.110*	2.9E-02	*
GM3(40:1:2)	23.514	*1.241*	17.519	*0.789*	1.1E-03	*
GM3(42:2:2)	15.315	*2.445*	17.552	*1.777*	4.7E-01	
GM3(42:1:2)	12.278	*1.970*	13.232	*0.728*	6.6E-01	
GM3	100.000	*0.000*	100.000	*0.000*		
DG(34:2)	6.552	*1.860*	6.137	*1.222*	8.5E-01	
DG(34:1)	23.094	*0.818*	28.814	*1.121*	1.0E-03	*
DG(36:4)	7.098	*1.535*	3.312	*0.387*	3.1E-02	*
DG(36:3)	6.401	*0.750*	4.177	*1.338*	1.7E-01	
DG(36:2)	18.032	*2.765*	18.549	*1.495*	8.7E-01	

DG(38:5)	2.082	*0.520*	2.561	*0.464*	5.0E-01	
DG(38:4)	36.741	*1.672*	36.449	*3.341*	9.4E-01	
DG	100.000	*0.000*	100.000	*0.000*		
TG(50:5)	0.047	*0.022*	0.005	*0.004*	8.3E-02	
TG(50:4)	1.376	*0.140*	1.308	*0.462*	8.9E-01	
TG(50:3)	3.171	*0.942*	1.426	*0.707*	1.6E-01	
TG(50:2)	9.790	*0.889*	9.765	*1.019*	9.9E-01	
TG(50:1)	6.076	*0.465*	9.513	*0.432*	9.1E-05	*
TG(50:0)	0.724	*0.155*	1.091	*0.231*	2.1E-01	
TG(52:5)	1.459	*0.264*	0.431	*0.110*	2.9E-03	*
TG(52:4)	8.576	*0.821*	3.838	*0.290*	8.7E-05	*
TG(52:3)	17.029	*0.893*	14.696	*1.040*	1.1E-01	
TG(52:2)	10.565	*1.080*	17.699	*1.133*	4.5E-04	*
TG(52:1)	1.792	*0.301*	2.091	*0.219*	4.3E-01	
TG(52:0)	0.220	*0.047*	0.401	*0.104*	1.3E-01	
TG(54:7)	0.257	*0.070*	0.032	*0.008*	6.2E-03	*
TG(54:6)	3.219	*0.384*	1.020	*0.193*	1.6E-04	*
TG(54:5)	10.546	*1.572*	10.520	*3.840*	1.0E+00	
TG(54:4)	8.455	*0.379*	7.366	*0.446*	8.4E-02	
TG(54:3)	5.694	*0.472*	9.290	*0.602*	3.4E-04	*
TG(54:2)	1.702	*0.332*	1.945	*0.150*	5.2E-01	
TG(56:8)	0.795	*0.150*	0.026	*0.012*	1.5E-04	*
TG(56:7)	1.642	*0.253*	0.959	*0.164*	4.0E-02	*
TG(56:6)	2.270	*0.365*	2.067	*0.294*	6.7E-01	
TG(56:5)	1.879	*0.397*	2.839	*0.590*	2.0E-01	
TG(56:4)	0.402	*0.084*	0.323	*0.077*	5.0E-01	
TG(56:3)	0.398	*0.214*	0.274	*0.046*	5.8E-01	
TG(58:9)	0.348	*0.099*	0.055	*0.023*	1.2E-02	*
TG(58:8)	0.680	*0.145*	0.173	*0.040*	4.5E-03	*
TG(58:7)	0.473	*0.122*	0.429	*0.096*	7.8E-01	
TG(58:6)	0.341	*0.097*	0.350	*0.087*	9.5E-01	
TG(58:5)	0.048	*0.033*	0.063	*0.019*	7.0E-01	
TG(58:4)	0.023	*0.014*	0.004	*0.002*	2.0E-01	
TG	100.000	*0.000*	100.000	*0.000*		

Lipid/protein values (nmol/mg)

Lipid/prot values

Data are expressed as lipid/prot (nmol/mg) and given as mean ± SEM, n = 8

****p<0.05 corresponding to false discovery rate <0.05; FC, fold change***

	Control		*Fructose*			
Species name	avg	*SEM*	avg	*SEM*	*p*	
PC(32:1)	0.438	*0.047*	0.573	*0.053*	7.6E-02	
PC(32:0)	3.137	*0.210*	2.579	*0.151*	4.9E-02	*
PC(34:3)	0.209	*0.022*	0.176	*0.026*	3.5E-01	
PC(34:2)	8.960	*0.679*	5.622	*0.749*	5.3E-03	*
PC(34:1)	11.820	*0.817*	13.588	*0.885*	1.6E-01	
PC(34:0)	0.332	*0.025*	0.231	*0.022*	8.8E-03	*
PC(36:5)	0.544	*0.056*	0.553	*0.042*	8.9E-01	
PC(36:4)	29.240	*2.209*	24.736	*1.717*	1.3E-01	
PC(36:3)	3.672	*0.290*	3.894	*0.626*	7.5E-01	
PC(36:2)	11.191	*0.802*	8.764	*1.301*	1.3E-01	
PC(36:1)	4.121	*0.384*	5.292	*0.427*	6.1E-02	
PC(38:6)	5.956	*0.626*	3.837	*0.311*	9.0E-03	*
PC(38:5)	6.617	*0.605*	7.512	*0.652*	3.3E-01	
PC(38:4)	50.217	*3.821*	42.010	*3.426*	1.3E-01	
PC(40:8)	0.423	*0.051*	0.262	*0.022*	1.1E-02	*
PC(40:7)	0.523	*0.046*	0.485	*0.040*	5.3E-01	
PC(40:6)	1.881	*0.198*	1.560	*0.178*	2.5E-01	
PC(40:5)	1.599	*0.166*	1.629	*0.210*	9.1E-01	
PC(40:4)	0.631	*0.059*	0.515	*0.053*	1.6E-01	
PC	**141.512**	***9.217***	**123.818**	***8.694***	1.8E-01	
PC-P(34:1)	0.022	*0.008*	0.020	*0.005*	8.1E-01	
PC-P(34:0)	0.033	*0.005*	0.044	*0.005*	1.3E-01	
PC-P(36:4)	1.368	*0.461*	1.066	*0.197*	5.6E-01	
PC-P(38:5)	0.255	*0.084*	0.223	*0.044*	7.5E-01	
PC-P(38:4)	0.117	*0.032*	0.084	*0.015*	3.6E-01	
PC-P	**1.795**	***0.584***	**1.438**	***0.259***	5.8E-01	
LPC(16:0)	0.192	*0.015*	0.179	*0.011*	5.0E-01	
LPC(18:2)	0.003	*0.001*	0.002	*0.001*	2.9E-01	
LPC(18:1)	0.018	*0.003*	0.033	*0.005*	2.2E-02	*
LPC(18:0)	0.319	*0.028*	0.265	*0.008*	8.8E-02	
LPC(20:4)	0.042	*0.010*	0.031	*0.007*	3.8E-01	
LPC	**0.574**	***0.042***	**0.510**	***0.027***	2.2E-01	
LPE(16:0)	0.013	*0.002*	0.020	*0.004*	1.4E-01	
LPE(18:1)	0.105	*0.006*	0.098	*0.006*	4.4E-01	
LPE(18:0)	0.093	*0.011*	0.092	*0.007*	9.5E-01	
LPE	**0.211**	***0.017***	**0.210**	***0.012***	9.6E-01	
PE(34:2)	1.972	*0.170*	0.940	*0.093*	1.1E-04	*
PE(34:1)	1.257	*0.103*	1.461	*0.092*	1.6E-01	
PE(36:4)	4.731	*0.338*	4.862	*0.281*	7.7E-01	
PE(36:3)	2.038	*0.185*	1.218	*0.196*	8.9E-03	*
PE(36:2)	5.978	*0.558*	3.078	*0.394*	8.2E-04	*

PE(36:1)	0.685	*0.054*	0.709	*0.061*	7.7E-01	
PE(38:6)	6.164	*0.617*	4.020	*0.487*	1.6E-02	*
PE(38:5)	5.173	*0.456*	7.405	*0.544*	7.2E-03	*
PE(38:4)	27.399	*1.991*	24.857	*1.528*	3.3E-01	
PE(38:3)	0.066	*0.016*	0.232	*0.043*	2.7E-03	*
PE(40:7)	1.635	*0.143*	1.676	*0.129*	8.3E-01	
PE(40:6)	14.102	*1.342*	11.596	*1.206*	1.9E-01	
PE(40:5)	8.069	*1.100*	8.964	*1.166*	5.9E-01	
PE(40:4)	1.430	*0.119*	0.985	*0.076*	7.0E-03	*
PE	**80.697**	***5.481***	**72.002**	***4.897***	2.6E-01	
PE-P(34:2)	0.481	*0.022*	0.270	*0.024*	1.5E-05	*
PE-P(34:1)	0.252	*0.019*	0.322	*0.034*	9.4E-02	
PE-P(36:4)	10.427	*0.809*	9.549	*0.777*	4.5E-01	
PE-P(36:2)	0.218	*0.014*	0.151	*0.015*	5.3E-03	*
PE-P(38:6)	3.774	*0.302*	2.052	*0.161*	1.8E-04	*
PE-P(38:5)	7.493	*0.757*	7.046	*0.764*	6.8E-01	
PE-P(38:4)	6.402	*0.543*	4.168	*0.400*	5.1E-03	*
PE-P(40:7)	1.237	*0.109*	0.908	*0.072*	2.5E-02	*
PE-P(40:6)	1.322	*0.115*	0.833	*0.071*	2.8E-03	*
PE-P(40:5)	0.643	*0.050*	0.484	*0.040*	2.7E-02	*
PE-P(40:4)	0.388	*0.028*	0.272	*0.020*	4.5E-03	*
PE-P	**32.636**	***2.503***	**26.057**	***2.275***	7.2E-02	
LPI(18:1)	0.055	*0.002*	0.051	*0.004*	3.6E-01	
LPI(18:0)	0.012	*0.001*	0.010	*0.001*	3.3E-01	
LPI(20:4)	0.015	*0.002*	0.011	*0.002*	2.0E-01	
LPI	**0.082**	***0.005***	**0.073**	***0.005***	1.8E-01	
PI(34:2)	0.138	*0.010*	0.075	*0.007*	1.3E-04	*
PI(34:1)	0.011	*0.009*	0.086	*0.023*	9.6E-03	*
PI(36:4)	0.388	*0.026*	0.362	*0.024*	4.8E-01	
PI(36:3)	0.256	*0.011*	0.193	*0.028*	5.7E-02	
PI(36:2)	1.483	*0.075*	0.620	*0.064*	5.1E-07	*
PI(36:1)	0.106	*0.009*	0.126	*0.013*	2.2E-01	
PI(38:6)	0.062	*0.005*	0.030	*0.003*	1.2E-04	*
PI(38:5)	0.585	*0.036*	0.747	*0.064*	4.5E-02	*
PI(38:4)	11.499	*0.825*	9.650	*0.645*	9.9E-02	
PI(40:6)	0.119	*0.014*	0.069	*0.006*	4.8E-03	*
PI(40:5)	0.130	*0.017*	0.091	*0.008*	5.8E-02	
PI(40:4)	0.071	*0.008*	0.047	*0.003*	1.8E-02	*
PI	**14.848**	***0.974***	**12.097**	***0.791***	4.6E-02	*
LPS(18:1)	0.038	*0.001*	0.036	*0.003*	5.4E-01	
LPS	**0.038**	***0.001***	**0.036**	***0.003***	5.4E-01	
PS(34:1)	0.018	*0.003*	0.032	*0.003*	6.0E-03	*
PS(36:2)	0.410	*0.027*	0.272	*0.026*	2.5E-03	*
PS(36:1)	0.559	*0.043*	0.554	*0.050*	9.4E-01	
PS(38:6)	0.019	*0.003*	0.010	*0.002*	2.3E-02	*
PS(38:5)	0.026	*0.004*	0.036	*0.004*	6.8E-02	
PS(38:4)	1.260	*0.103*	0.975	*0.062*	3.3E-02	*
PS(38:3)	0.138	*0.010*	0.167	*0.018*	1.7E-01	
PS(38:2)	0.010	*0.001*	0.015	*0.001*	3.8E-02	*

PS(40:7)	0.015	*0.003*	0.027	*0.004*	3.0E-02	*
PS(40:6)	3.368	*0.310*	2.687	*0.177*	7.8E-02	
PS(40:5)	2.270	*0.275*	2.556	*0.228*	4.4E-01	
PS(40:4)	0.985	*0.074*	0.690	*0.042*	3.8E-03	*
PS(40:3)	0.070	*0.021*	0.087	*0.013*	5.0E-01	
PS	**9.148**	***0.716***	**8.108**	***0.537***	2.6E-01	
LPG(18:2)	0.002	*0.001*	0.001	*0.000*	1.1E-01	
LPG(18:1)	0.003	*0.000*	0.004	*0.000*	2.0E-02	*
LPG	**0.005**	***0.001***	**0.005**	***0.001***	9.2E-01	
PG(32:1)	0.009	*0.002*	0.017	*0.002*	1.1E-02	*
PG(34:2)	0.564	*0.035*	0.298	*0.022*	1.7E-05	*
PG(34:1)	3.376	*0.244*	3.294	*0.222*	8.1E-01	
PG(36:4)	0.131	*0.008*	0.081	*0.006*	1.4E-04	*
PG(36:3)	0.169	*0.009*	0.147	*0.011*	1.3E-01	
PG(36:2)	0.472	*0.041*	0.311	*0.030*	7.3E-03	*
PG(36:1)	0.155	*0.017*	0.132	*0.009*	2.5E-01	
PG(38:6)	0.042	*0.006*	0.013	*0.003*	2.8E-04	*
PG(38:5)	0.033	*0.004*	0.041	*0.004*	1.8E-01	
PG(38:4)	0.076	*0.007*	0.065	*0.005*	1.9E-01	
PG(40:8)	0.025	*0.005*	0.002	*0.001*	4.9E-04	*
PG(40:7)	0.039	*0.006*	0.025	*0.004*	7.2E-02	
PG(40:6)	0.037	*0.005*	0.048	*0.005*	1.4E-01	
PG	**5.129**	***0.339***	**4.472**	***0.280***	1.6E-01	
PA(34:2)	0.036	*0.003*	0.030	*0.004*	2.0E-01	
PA(34:1)	0.122	*0.011*	0.131	*0.012*	6.1E-01	
PA(36:4)	0.019	*0.004*	0.012	*0.002*	1.6E-01	
PA(36:3)	0.011	*0.002*	0.013	*0.002*	4.8E-01	
PA(36:2)	0.042	*0.006*	0.042	*0.005*	9.7E-01	
PA(36:1)	0.003	*0.001*	0.003	*0.001*	7.8E-01	
PA(38:5)	0.009	*0.003*	0.009	*0.002*	9.2E-01	
PA	**0.241**	***0.025***	**0.239**	***0.023***	9.5E-01	
CL(68:6)	0.080	*0.008*	0.180	*0.015*	3.7E-05	*
CL(68:5)	0.015	*0.002*	0.045	*0.005*	5.7E-05	*
CL(70:7)	1.189	*0.166*	2.590	*0.230*	2.1E-04	*
CL(70:6)	0.084	*0.006*	0.312	*0.062*	2.6E-03	*
CL(70:5)	0.043	*0.007*	0.075	*0.010*	1.8E-02	*
CL(70:4)	0.028	*0.004*	0.040	*0.005*	6.3E-02	
CL(72:9)	0.219	*0.011*	0.173	*0.011*	9.7E-03	*
CL(72:8)	28.462	*1.662*	15.713	*1.417*	4.3E-05	*
CL(72:7)	5.829	*0.409*	5.639	*0.525*	7.8E-01	
CL(72:5)	0.004	*0.001*	0.008	*0.001*	3.5E-02	*
CL(74:11)	0.011	*0.002*	0.048	*0.008*	6.3E-04	*
CL(74:10)	0.637	*0.052*	0.806	*0.093*	1.3E-01	
CL(74:9)	0.489	*0.045*	1.365	*0.148*	5.8E-05	*
CL(74:8)	0.122	*0.010*	0.114	*0.025*	7.8E-01	
CL(76:12)	0.264	*0.034*	0.325	*0.053*	3.4E-01	
CL(76:11)	0.271	*0.035*	0.449	*0.080*	6.1E-02	
CL(76:10)	0.084	*0.011*	0.138	*0.018*	2.4E-02	*
CL(78:13)	0.004	*0.001*	0.033	*0.008*	2.6E-03	*
CL(78:12)	0.003	*0.001*	0.023	*0.005*	1.1E-03	*
CL	**37.837**	***2.117***	**28.078**	***2.144***	5.9E-03	*

MLCL(52:5)	0.006	*0.001*	0.037	*0.005*	2.8E-05	*
MLCL(52:4)	0.000	*0.000*	0.002	*0.001*	1.2E-02	*
MLCL(54:6)	0.378	*0.049*	0.342	*0.037*	5.6E-01	
MLCL(54:5)	0.012	*0.002*	0.051	*0.009*	1.2E-03	*
MLCL(54:4)	0.000	*0.000*	0.002	*0.001*	5.7E-02	
MLCL(56:8)	0.004	*0.001*	0.012	*0.004*	5.9E-02	
MLCL(56:7)	0.002	*0.001*	0.017	*0.003*	5.0E-04	*
MLCL(58:10)	0.001	*0.001*	0.005	*0.002*	9.9E-02	
MLCL(58:9)	0.001	*0.000*	0.005	*0.002*	9.1E-02	
MLCL	**0.404**	***0.055***	**0.473**	***0.059***	4.1E-01	
SM(34:2:2)	0.014	*0.004*	0.010	*0.002*	3.3E-01	
SM(34:1:2)	1.052	*0.095*	1.093	*0.080*	7.5E-01	
SM(36:2:2)	0.104	*0.011*	0.089	*0.012*	3.9E-01	
SM(36:1:2)	0.991	*0.082*	1.016	*0.091*	8.4E-01	
SM(38:2:2)	0.187	*0.016*	0.132	*0.014*	2.1E-02	*
SM(38:1:2)	0.732	*0.054*	0.605	*0.046*	9.2E-02	
SM(39:2:2)	0.009	*0.002*	0.002	*0.000*	3.7E-03	*
SM(39:1:2)	0.115	*0.010*	0.058	*0.006*	2.5E-04	*
SM(40:2:2)	0.294	*0.023*	0.204	*0.017*	7.1E-03	*
SM(40:1:2)	0.890	*0.066*	0.577	*0.034*	8.8E-04	*
SM(41:2:2)	0.128	*0.017*	0.094	*0.011*	9.8E-02	
SM(41:1:2)	0.356	*0.033*	0.270	*0.012*	2.7E-02	*
SM(42:2:2)	0.606	*0.055*	0.817	*0.083*	5.3E-02	
SM(41:2:3)	0.044	*0.016*	0.034	*0.010*	6.2E-01	
SM(42:1:2)	0.777	*0.068*	0.631	*0.034*	7.7E-02	
SM	**6.301**	***0.481***	**5.632**	***0.407***	3.1E-01	
Cer(34:1:2)	0.008	*0.001*	0.009	*0.001*	7.4E-01	
Cer(36:1:2)	0.008	*0.001*	0.010	*0.002*	4.5E-01	
Cer(38:1:2)	0.005	*0.001*	0.007	*0.001*	2.2E-01	
Cer(40:2:2)	0.004	*0.001*	0.004	*0.001*	6.3E-01	
Cer(40:1:2)	0.027	*0.002*	0.026	*0.003*	8.2E-01	
Cer(41:2:2)	0.003	*0.001*	0.004	*0.001*	4.4E-01	
Cer(41:1:2)	0.022	*0.003*	0.020	*0.002*	7.2E-01	
Cer(42:3:2)	0.002	*0.000*	0.008	*0.001*	5.4E-04	*
Cer(42:2:2)	0.041	*0.004*	0.061	*0.005*	7.1E-03	*
Cer(42:1:2)	0.069	*0.005*	0.067	*0.005*	8.0E-01	
Cer	**0.190**	***0.014***	**0.216**	***0.017***	2.6E-01	
GM3(34:1:2)	0.033	*0.003*	0.035	*0.004*	6.7E-01	
GM3(36:1:2)	0.102	*0.016*	0.129	*0.009*	1.5E-01	
GM3(38:1:2)	0.242	*0.017*	0.186	*0.014*	2.4E-02	*
GM3(40:1:2)	0.182	*0.015*	0.119	*0.009*	2.8E-03	*
GM3(42:2:2)	0.115	*0.015*	0.122	*0.018*	7.5E-01	
GM3(42:1:2)	0.099	*0.021*	0.089	*0.005*	6.4E-01	
GM3	**0.772**	***0.048***	**0.681**	***0.042***	1.7E-01	
DG(34:2)	0.090	*0.024*	0.124	*0.045*	5.2E-01	
DG(34:1)	0.368	*0.049*	0.453	*0.106*	4.7E-01	
DG(36:4)	0.103	*0.018*	0.050	*0.011*	2.8E-02	*
DG(36:3)	0.098	*0.011*	0.097	*0.044*	9.9E-01	
DG(36:2)	0.315	*0.102*	0.332	*0.103*	9.1E-01	

DG(38:5)	0.033	*0.008*	0.037	*0.009*	7.5E-01	
DG(38:4)	0.575	*0.058*	0.502	*0.063*	4.0E-01	
DG	**1.581**	***0.186***	**1.596**	***0.365***	9.7E-01	
TG(50:5)	0.008	*0.004*	0.001	*0.001*	1.3E-01	
TG(50:4)	0.182	*0.041*	0.090	*0.020*	6.3E-02	
TG(50:3)	0.534	*0.166*	0.287	*0.148*	2.8E-01	
TG(50:2)	1.393	*0.324*	1.116	*0.382*	5.9E-01	
TG(50:1)	0.799	*0.169*	0.990	*0.319*	6.1E-01	
TG(50:0)	0.071	*0.005*	0.065	*0.007*	4.6E-01	
TG(52:5)	0.213	*0.064*	0.056	*0.021*	3.5E-02	*
TG(52:4)	1.208	*0.330*	0.406	*0.128*	4.0E-02	*
TG(52:3)	2.394	*0.550*	1.635	*0.553*	3.5E-01	
TG(52:2)	1.460	*0.363*	1.993	*0.705*	5.1E-01	
TG(52:1)	0.193	*0.017*	0.169	*0.038*	5.9E-01	
TG(52:0)	0.021	*0.001*	0.022	*0.003*	9.3E-01	
TG(54:7)	0.039	*0.015*	0.003	*0.001*	3.2E-02	*
TG(54:6)	0.411	*0.115*	0.098	*0.027*	1.9E-02	*
TG(54:5)	1.229	*0.265*	0.625	*0.117*	5.6E-02	
TG(54:4)	1.151	*0.260*	0.811	*0.285*	3.9E-01	
TG(54:3)	0.774	*0.184*	1.043	*0.375*	5.3E-01	
TG(54:2)	0.183	*0.019*	0.180	*0.050*	9.6E-01	
TG(56:8)	0.084	*0.013*	0.004	*0.002*	1.8E-05	*
TG(56:7)	0.178	*0.019*	0.083	*0.020*	3.9E-03	*
TG(56:6)	0.243	*0.021*	0.171	*0.041*	1.4E-01	
TG(56:5)	0.186	*0.011*	0.198	*0.039*	7.8E-01	
TG(56:4)	0.044	*0.008*	0.038	*0.014*	7.1E-01	
TG(56:3)	0.030	*0.009*	0.033	*0.014*	8.6E-01	
TG(58:9)	0.033	*0.006*	0.004	*0.001*	1.8E-04	*
TG(58:8)	0.070	*0.009*	0.019	*0.006*	5.5E-04	*
TG(58:7)	0.051	*0.010*	0.041	*0.012*	5.4E-01	
TG(58:6)	0.035	*0.008*	0.034	*0.011*	9.2E-01	
TG(58:5)	0.005	*0.003*	0.006	*0.002*	7.9E-01	
TG(58:4)	0.002	*0.001*	0.000	*0.000*	1.4E-01	
TG	**13.226**	***2.609***	**10.219**	***3.276***	4.8E-01	
Class						
PC	141.512	*9.217*	123.818	*8.694*	1.8E-01	
PC-P	1.795	*0.584*	1.438	*0.259*	5.8E-01	
LPC	0.574	*0.042*	0.510	*0.027*	2.2E-01	
LPE	0.211	*0.017*	0.210	*0.012*	9.6E-01	
PE	80.697	*5.481*	72.002	*4.897*	2.6E-01	
PE-P	32.636	*2.503*	26.057	*2.275*	7.2E-02	
LPI	0.082	*0.005*	0.073	*0.005*	1.8E-01	
PI	14.848	*0.974*	12.097	*0.791*	4.6E-02	*
LPS	0.038	*0.001*	0.036	*0.003*	5.4E-01	
PS	9.148	*0.716*	8.108	*0.537*	2.6E-01	
LPG	0.005	*0.001*	0.005	*0.001*	9.2E-01	
PG	5.129	*0.339*	4.472	*0.280*	1.6E-01	
PA	0.241	*0.025*	0.239	*0.023*	9.5E-01	
CL	37.837	*2.117*	28.078	*2.144*	5.9E-03	*
MLCL	0.404	*0.055*	0.473	*0.059*	4.1E-01	
SM	6.301	*0.481*	5.632	*0.407*	3.1E-01	
Cer	0.190	*0.014*	0.216	*0.017*	2.6E-01	
GM3	0.772	*0.048*	0.681	*0.042*	1.7E-01	
DG	1.581	*0.186*	1.596	*0.365*	9.7E-01	
TG	13.226	*2.609*	10.219	*3.276*	4.8E-01	

sumML/prot (nmol/mg)mg	332.421	*21.731*	284.143	*19.348*	1.2E-01	

Double bonds (db) and double bond index (DBI)

db data are expressed as mol% of membrane lipids and given as mean ± SEM, n = 8, *p<0.05

The double bond index (DBI) was calculated for the major membrane phospholipids and TG as Σ(mol % of unsaturated fatty acids in the given lipid class x number of double bonds of each unsaturated fatty acid)/100.

	Control		*Fructose*			
Species name	avg	*SEM*	avg	*SEM*	*p*	
PC [db 0]	2.459	*0.083*	2.308	*0.111*	2.9E-01	
PC [db 1]	11.565	*0.309*	15.788	*0.460*	2.4E-06	*
PC [db 2]	14.455	*1.086*	11.453	*1.377*	1.1E-01	
PC [db 3]	2.761	*0.169*	3.238	*0.465*	3.5E-01	
PC [db 4]	56.444	*1.094*	54.477	*1.854*	3.8E-01	
PC [db 5]	6.155	*0.220*	7.785	*0.245*	2.2E-04	*
PC [db 6]	5.496	*0.321*	4.350	*0.191*	8.4E-03	*
PC [db 7]	0.367	*0.011*	0.391	*0.014*	2.0E-01	
PC [db 8]	0.298	*0.029*	0.210	*0.009*	1.2E-02	*
PE [db 1]	2.423	*0.143*	3.036	*0.143*	9.0E-03	*
PE [db 2]	9.908	*0.787*	5.614	*0.627*	7.8E-04	*
PE [db 3]	2.639	*0.230*	2.024	*0.317*	1.4E-01	
PE [db 4]	41.636	*1.376*	42.888	*0.981*	4.7E-01	
PE [db 5]	16.408	*1.274*	22.519	*0.858*	1.4E-03	*
PE [db 6]	24.968	*1.070*	21.593	*1.344*	7.0E-02	
PE [db 7]	2.019	*0.077*	2.327	*0.063*	7.8E-03	*
PE-Pl [db 1]	0.779	*0.039*	1.232	*0.073*	8.4E-05	*
PE-Pl [db 2]	2.195	*0.143*	1.616	*0.065*	2.4E-03	*
PE-Pl [db 4]	52.737	*1.152*	53.744	*0.495*	4.4E-01	
PE-Pl [db 5]	24.780	*1.092*	28.619	*0.710*	1.1E-02	*
PE-Pl [db 6]	15.702	*0.678*	11.244	*0.591*	2.1E-04	*
PE-Pl [db 7]	3.807	*0.190*	3.545	*0.197*	3.6E-01	
PI [db 1]	0.807	*0.101*	1.756	*0.255*	3.9E-03	*
PI [db 2]	11.049	*0.522*	5.739	*0.410*	1.4E-06	*
PI [db 3]	1.760	*0.116*	1.585	*0.209*	4.8E-01	
PI [db 4]	80.353	*0.560*	83.176	*1.112*	4.0E-02	*
PI [db 5]	4.824	*0.144*	6.924	*0.318*	3.2E-05	*
PI [db 6]	1.206	*0.052*	0.821	*0.042*	4.7E-05	*
PS [db 1]	6.314	*0.159*	7.190	*0.350*	3.9E-02	*
PS [db 2]	4.711	*0.357*	3.550	*0.257*	2.0E-02	*
PS [db 3]	2.324	*0.307*	3.120	*0.180*	4.2E-02	*
PS [db 4]	24.573	*0.454*	20.610	*0.340*	6.4E-06	*
PS [db 5]	24.966	*1.929*	31.700	*1.337*	1.2E-02	*
PS [db 6]	36.955	*1.936*	33.503	*1.381*	1.7E-01	
PS [db 7]	0.158	*0.024*	0.328	*0.039*	2.3E-03	*
PG [db 1]	68.881	*1.112*	76.949	*0.919*	6.6E-05	*
PG [db 2]	20.330	*0.832*	13.640	*0.974*	1.3E-04	*
PG [db 3]	3.346	*0.153*	3.300	*0.220*	8.7E-01	

PG [db 4]	4.045	*0.132*	3.233	*0.097*	2.2E-04	*
PG [db 5]	0.638	*0.048*	0.917	*0.072*	6.2E-03	*
PG [db 6]	1.529	*0.110*	1.357	*0.109*	2.9E-01	
PG [db 7]	0.739	*0.063*	0.558	*0.073*	8.2E-02	
PG [db 8]	0.493	*0.108*	0.046	*0.013*	1.1E-03	*
PA [db 1]	52.428	*2.353*	56.112	*1.957*	2.5E-01	
PA [db 2]	32.448	*1.419*	29.434	*1.471*	1.6E-01	
PA [db 3]	4.460	*0.484*	5.318	*0.502*	2.4E-01	
PA [db 4]	7.403	*1.053*	5.130	*0.716*	9.6E-02	
PA [db 5]	3.260	*1.026*	4.007	*1.130*	6.3E-01	
CL [db 4]	0.072	*0.008*	0.153	*0.025*	8.2E-03	*
CL [db 5]	0.163	*0.020*	0.481	*0.076*	1.2E-03	*
CL [db 6]	0.441	*0.042*	1.883	*0.297*	2.8E-04	*
CL [db 7]	18.538	*0.698*	29.222	*0.655*	2.3E-08	*
CL [db 8]	75.500	*1.086*	56.044	*1.834*	2.8E-07	*
CL [db 9]	1.895	*0.135*	5.467	*0.281*	1.7E-08	*
CL [db 10]	1.919	*0.143*	3.486	*0.423*	3.5E-03	*
CL [db 11]	0.751	*0.091*	1.835	*0.305*	4.3E-03	*
CL [db 12]	0.711	*0.089*	1.304	*0.224*	2.8E-02	*
CL [db 13]	0.010	*0.003*	0.124	*0.031*	2.6E-03	*
TG [db 0]	0.945	*0.200*	1.492	*0.332*	1.8E-01	
TG [db 1]	7.868	*0.552*	11.604	*0.509*	2.0E-04	*
TG [db 2]	22.057	*1.743*	29.409	*1.999*	1.5E-02	*
TG [db 3]	26.292	*1.738*	25.686	*1.996*	8.2E-01	
TG [db 4]	18.833	*1.107*	12.840	*0.228*	1.1E-04	*
TG [db 5]	13.979	*1.847*	13.858	*4.315*	9.8E-01	
TG [db 6]	5.830	*0.673*	3.437	*0.526*	1.4E-02	*
TG [db 7]	2.373	*0.338*	1.420	*0.261*	4.3E-02	*
TG [db 8]	1.475	*0.289*	0.199	*0.048*	6.5E-04	*
TG [db 9]	0.348	*0.099*	0.055	*0.023*	1.2E-02	*
Class DBI						
PC [DBI]	3.432	*0.026*	3.358	*0.046*	1.8E-01	
PE [DBI]	4.427	*0.043*	4.503	*0.051*	2.7E-01	
PE-Pl [DBI]	4.609	*0.020*	4.548	*0.016*	3.2E-02	*
PI [DBI]	3.810	*0.015*	3.902	*0.015*	6.7E-04	*
PS [DBI]	4.687	*0.028*	4.679	*0.032*	8.6E-01	
PG [DBI]	1.572	*0.023*	1.441	*0.008*	7.7E-05	*
PA [DBI]	1.766	*0.067*	1.715	*0.056*	5.6E-01	
CL [DBI]	7.907	*0.008*	7.887	*0.017*	3.2E-01	
TG [DBI]	3.426	*0.103*	3.008	*0.093*	9.2E-03	*
sum DBI						
sum DBI with CL	4.217	*0.019*	4.124	*0.036*	3.7E-02	*
sum DBI wo CL	3.313	*0.028*	3.349	*0.042*	4.9E-01	
db sum for PLs (wo CL)						
db1	6.897	*0.168*	9.299	*0.224*	6.0E-07	*
db2	9.728	*0.683*	7.145	*0.791*	2.7E-02	*
db3	7.201	*0.224*	7.049	*0.414*	7.5E-01	

db4	40.930	*0.555*	41.398	*0.824*	6.5E-01	
db5	9.029	*0.439*	11.366	*0.417*	1.7E-03	*
db6	9.996	*0.398*	8.914	*0.551*	1.3E-01	

Protein quantification

Protein names	Gene names	Entry name	*mean control (intensity)*	*CV control (%)*	*mean fructose-fed (intensity)*	*CV fructose-fed (%)*	P-value	fold change
Alpha-1-inhibitor III	Mug1 LOC297568	D4A6E3_RAT	*76039*	*26*	*475882*	*89*	0.018	8.82
Sarcolemmal membrane-associated protein (Slmap protein)	Slmap	B5DF63_RAT	*19779*	*6*	*278041*	*149*	0.029	6.55
LIM domain-binding 3	Ldb3	A0A0G2JXR0_RAT	*194927*	*7*	*1134344*	*50*	≤0.001	5.90
Alpha-crystallin B chain (Alpha(B)-crystallin)	Cryab	CRYAB_RAT	*221980*	*11*	*1415791*	*146*	0.047	5.56
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (EC 3.1.2.4) (3-hydroxyisobutyryl-coenzyme A hydrolase) (HIB-CoA hydrolase) (HIBYL-CoA-H)	Hibch	HIBCH_RAT	*127444*	*110*	*220589*	*73*	0.042	5.44
Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	Prelp	PRELP_RAT	*95044*	*15*	*480320*	*96*	0.001	5.23
Calsequestrin	Casq2 rCG_51991	F1M944_RAT	*652101*	*8*	*3989458*	*98*	0.001	4.95
Myosin light chain 3 (Myosin alkali light chain 1, ventricular) (MLClV) (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1SB) (Ventricular myosin light chain 1) (rVMLC1)	Myl3 Mlc1v	MYL3_RAT	*420037*	*12*	*2432804*	*117*	0.002	4.90
WD repeat-containing protein 1	Wdr1	WDR1_RAT	*25059*	*25*	*96155*	*63*	0.039	4.85
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Myl2	D3Z9K3_RAT	*418863*	*20*	*1865458*	*69*	0.007	4.58
3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Mitochondrial 3-oxoacyl-CoA thiolase)	Acaa2	THIM_RAT	*642848*	*5*	*5647964*	*178*	0.005	4.56
Core histone macro-H2A.1 (Histone macroH2A1) (mH2A1) (H2A.y) (H2A/y)	H2afy	H2AY_RAT	*115423*	*15*	*478494*	*48*	0.009	4.44
Histone H1.5	Hist1h1b	H15_RAT	*22825740*	*51*	*83180995*	*82*	0.032	4.41
Alpha-aminoadipic semialdehyde dehydrogenase (Alpha-AASA dehydrogenase) (EC 1.2.1.31) (Aldehyde dehydrogenase family 7 member A1) (EC 1.2.1.3) (Antiquitin-1) (Betaine aldehyde dehydrogenase) (EC 1.2.1.8) (Delta1-piperideine-6-carboxylate dehydrogenase) (P6c dehydrogenase)	Aldh7a1 Ald7a1	AL7A1_RAT	*106034*	*7*	*442182*	*5*	≤0.001	4.34
Malic enzyme	Me3	A0A0G2K4C6_RAT	*224396*	*47*	*647274*	*75*	0.022	4.27
Serine protease inhibitor	LOC299282 LOC500712 Serpina3n	A0A0G2KB85_RAT	*278769*	*30*	*818927*	*39*	0.001	3.42
60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (HSP-65) (Heat shock protein 60) (HSP-60) (Hsp60) (Mitochondrial matrix protein P1)	Hspd1 Hsp60	CH60_RAT	*85878*	*28*	*244447*	*54*	0.010	3.37
Citrate synthase	Cs rCG_42519	G3V936_RAT	*7464774*	*9*	*25193057*	*54*	≤0.001	3.14

Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (ETF-QO) (ETF-ubiquinone oxidoreductase) (EC 1.5.5.1) (Electron-transferring-flavoprotein dehydrogenase) (ETF dehydrogenase)	Etfdh	ETFD_RAT	*1389566*	*5*	*6399194*	*108*	0.004	3.13
Platelet glycoprotein 4 (Adipocyte membrane protein) (Fatty acid translocase) (Fatty acid transport protein) (Glycoprotein IIIb) (GPIIIB) (PAS IV) (PAS-4) (Platelet glycoprotein IV) (GPIV) (CD antigen CD36)	Cd36 Fat	CD36_RAT	*172468*	*25*	*462608*	*50*	0.008	3.12
Myosin-6 (Myosin heavy chain 6) (Myosin heavy chain, cardiac muscle alpha isoform) (MyHC-alpha)	Myh6	MYH6_RAT	*61986755*	*20*	*184578704*	*55*	0.003	3.06
Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.4) (Antioxidant protein 2) (Non-selenium glutathione peroxidase) (NSGPx) (Thiol-specific antioxidant protein)	Prdx6 Aipla2 Aop2 Tsa	PRDX6_RAT	*536119*	*15*	*1628926*	*58*	0.001	2.87
Myoglobin	Mb	MYG_RAT	*2656386*	*18*	*6507411*	*35*	0.013	2.80
Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphohexomutase) (Phosphomannose isomerase) (PMI)	Mpi	MPI_RAT	*549146*	*8*	*2154904*	*76*	0.029	2.74
Platelet-activating factor acetylhydrolase IB subunit beta (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH subunit beta) (PAFAH subunit beta) (Platelet-activating factor acetylhydrolase alpha 2 subunit) (PAF-AH alpha 2)	Pafah1b2 Pafahb	PA1B2_RAT	*2907760*	*12*	*7667887*	*24*	≤0.001	2.72
ADP/ATP translocase 1 (ADP,ATP carrier protein 1) (Adenine nucleotide translocator 1) (ANT 1) (Solute carrier family 25 member 4)	Slc25a4 Ant1	ADT1_RAT	*5408721*	*5*	*16358449*	*69*	0.005	2.47
Laminin subunit gamma 1	Lamc1	F1MAA7_RAT	*2630586*	*13*	*6156540*	*11*	≤0.001	2.44
Filamin-C (FLN-C) (ABP-280-like protein) (ABP-L) (Actin-binding-like protein) (Filamin-2) (Gamma-filamin)	Flnc Abpl Fln2	FLNC_RAT	*691495*	*43*	*1278490*	*40*	0.034	2.31
Voltage-dependent anion-selective channel protein 3	Vdac3	A0A0G2JSR0_RAT	*706855*	*12*	*1867734*	*84*	0.018	2.17
Radixin	Rdx	A0A0G2K095_RAT	*26410*	*13*	*58358*	*52*	0.014	2.08
Fermitin family member 2	Fermt2	A0A0G2JWC7_RAT	*342282*	*26*	*709270*	*49*	0.014	2.08
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	Ndufa2 Ndufa2_predicted rCG_49583	D3ZS58_RAT	*26710711*	*28*	*46827617*	*35*	0.047	2.06
Cofilin 2 (Cofilin 2, muscle (Predicted), isoform CRA_b)	Cfl2 Cfl2_predicted rCG_62072	M0RC65_RAT	*241814*	*34*	*438288*	*24*	0.006	2.00
Hemopexin	Hpx	HEMO_RAT	*131796*	*22*	*238157*	*14*	0.003	1.95

Tropomyosin alpha-1 chain (Alpha-tropomyosin) (Tropomyosin-1)	Tpm1 Alpha-tm Tpma	TPM1_RAT	*24888098*	*22*	*46057208*	*27*	0.002	1.92
Biglycan (Bone/cartilage proteoglycan I) (PG-S1)	Bgn	PGS1_RAT	*1063640*	*23*	*1894712*	*31*	0.018	1.91
Transgelin-2	Tagln2	TAGL2_RAT	*2533078*	*14*	*4537500*	*20*	≤0.001	1.82
Tropomodulin-1 (Erythrocyte tropomodulin) (E-Tmod)	Tmod1 Tmod	TMOD1_RAT	*1183693*	*11*	*2243877*	*51*	0.002	1.78
Laminin subunit alpha 5 (Laminin, alpha 5, isoform CRA_a)	Lama5 rCG_38528	F1MAN8_RAT	*480972*	*30*	*800729*	*42*	0.048	1.77
Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic (GPD-C) (GPDH-C) (EC 1.1.1.8)	Gpd1	GPDA_RAT	*20523*	*25*	*34783*	*30*	0.033	1.73
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	Ndufa1 LOC108348144	A0A0U1RRQ1_RAT	*545074*	*19*	*977429*	*46*	0.029	1.71
Aspartate aminotransferase, cytoplasmic (cAspAT) (EC 2.6.1.1) (EC 2.6.1.3) (Cysteine aminotransferase, cytoplasmic) (Cysteine transaminase, cytoplasmic) (cCAT) (Glutamate oxaloacetate transaminase 1) (Transaminase A)	Got1	AATC_RAT	*2822165*	*14*	*5240623*	*64*	0.021	1.70
Troponin I, cardiac muscle (Cardiac troponin I)	Tnni3 Ctni Tni	TNNI3_RAT	*162841838*	*11*	*271569764*	*31*	0.007	1.61
NADH-ubiquinone oxidoreductase chain 4 (EC 7.1.1.2) (NADH dehydrogenase subunit 4)	Mtnd4 mt-Nd4 Nd4	NU4M_RAT	*976935*	*16*	*1580926*	*34*	0.007	1.59
MICOS complex subunit Mic60 (Mitochondrial inner membrane protein) (Mitofilin) (Fragment)	Immt Mic60	MIC60_RAT	*12232588*	*20*	*18907890*	*18*	0.003	1.58
Cytochrome c, testis-specific	Cyct	CYC2_RAT	*71695305*	*22*	*108712209*	*24*	0.011	1.56
Phosphoglycerate kinase 1 (EC 2.7.2.3)	Pgk1 Pgk-1	PGK1_RAT	*20860377*	*7*	*34148076*	*36*	0.011	1.54
Hypoxanthine-guanine phosphoribosyltransferase (HGPRT) (HGPRTase) (EC 2.4.2.8)	Hprt1 Hprt	HPRT_RAT	*2264099*	*15*	*3742948*	*56*	0.048	1.53
Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D 12 kDa light chain; Cathepsin D 9 kDa light chain; Cathepsin D 34 kDa heavy chain; Cathepsin D 30 kDa heavy chain]	Ctsd	CATD_RAT	*10125331*	*13*	*15354134*	*23*	0.002	1.52
Enoyl CoA hydratase domain-containing 2 (Enoyl Coenzyme A hydratase domain containing 2 (Predicted), isoform CRA_a)	Echdc2 Echdc2_predicted rCG_50417	D3ZIL6_RAT	*3807294*	*10*	*6091062*	*44*	0.018	1.50
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)	Aldoa	ALDOA_RAT	*45535968*	*17*	*69169730*	*32*	0.038	1.48
Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	Hnrnpa3 Hnrpa3	ROA3_RAT	*2155257*	*19*	*3070443*	*11*	0.005	1.46
Electron transfer flavoprotein subunit beta (Beta-ETF)	Etfb	ETFB_RAT	*8263784*	*15*	*12139394*	*30*	0.029	1.46
Growth hormone-inducible transmembrane protein (Mitochondrial morphology and cristae structure 1) (MICS1)	Ghitm Mics1	GHITM_RAT	*3579322*	*17*	*5154891*	*27*	0.028	1.45

Prelamin-A/C [Cleaved into: Lamin-A/C]	Lmna Lmn1	LMNA_RAT	7302903	8	10221275	11	≤0.001	1.40
Carnitine O-acetyltransferase (Carnitine acetylase) (EC 2.3.1.7) (Carnitine acetyltransferase) (CAT) (CrAT)	Crat	CACP_RAT	11413004	13	15796019	23	0.009	1.37
Nicotinamide nucleotide transhydrogenase	Nnt	Q5BJZ3_RAT	23966346	10	33184444	23	0.007	1.36
Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC) (Solute carrier family 25 member 20)	Slc25a20 Cact	MCAT_RAT	27697292	22	36433037	15	0.034	1.36
Histone H1.1 (Histone H1a)	Hist1h1a	H11_RAT	13803990	14	18807812	26	0.024	1.35
Acyl-CoA synthetase family member 2, mitochondrial (EC 6.2.1.-)	Acsf2	ACSF2_RAT	5847132	12	7921102	21	0.011	1.34
Desmoplakin	Dsp	F1LMV6_RAT	12733679	8	17267733	20	0.002	1.34
Glutathione S-transferase kappa 1 (EC 2.5.1.18) (GST 13-13) (GST class-kappa) (GSTK1-1) (rGSTK1) (Glutathione S-transferase subunit 13)	Gstk1	GSTK1_RAT	3288213	13	4357727	16	0.007	1.33
Bcl2-associated athanogene 3 (RCG40209, isoform CRA_b)	Bag3 rCG_40209	Q5U2U8_RAT	2532563	14	3355204	18	0.013	1.33
Hexokinase-1 (EC 2.7.1.1) (Brain form hexokinase) (Hexokinase type I) (HK I)	Hk1	HXK1_RAT	8794800	15	11579240	17	0.013	1.32
Myosin-6 (Myosin heavy chain 6) (Myosin heavy chain, cardiac muscle alpha isoform) (MyHC-alpha)	Myh6	MYH6_RAT	103912915	22	132925633	11	0.037	1.32
Mitochondrial ribosomal protein S36 (RCG44686, isoform CRA_a)	Mrps36 rCG_44686	M0R776_RAT	28116950	15	36414128	9	0.007	1.31
Heterogeneous nuclear ribonucleoprotein M (hnRNP M) (M4 protein)	Hnrnpm Hnrpm	HNRPM_RAT	5120910	10	6792210	25	0.018	1.31
Acyl carrier protein	Ndufab1 Ndufab1_predicted rCG_40178	D3ZF13_RAT	22329527	16	29071100	21	0.032	1.30
Caveolae-associated protein 1 (Polymerase I and transcript release factor (Predicted))	Cavin1 Ptrf Ptrf_predicted rCG_32735	G3V8L9_RAT	9389237	11	12215483	18	0.009	1.29
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial (Complex I-39kD) (CI-39kD) (NADH-ubiquinone oxidoreductase 39 kDa subunit) (Sperm flagella protein 3)	Ndufa9	NDUA9_RAT	30526703	14	39103911	11	0.007	1.29
Caveolae-associated protein 2 (Cavin-2) (Phosphatidylserine-binding protein) (Serum deprivation-response protein)	Cavin2 Sdpr	CAVN2_RAT	5850134	14	7496480	17	0.024	1.29
Trifunctional enzyme subunit beta, mitochondrial (TP-beta) [Includes: 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase)]	Hadhb	ECHB_RAT	244590289	10	315231267	16	0.004	1.29
Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase)	Ak2 AK2 rCG_31186	A0A0G2JSG6_RAT	10137754	15	12939680	15	0.019	1.28

(Adenylate monophosphate kinase)								
Acyl-coenzyme A thioesterase 2, mitochondrial (Acyl-CoA thioesterase 2) (EC 3.1.2.2) (ARTISt/p43) (Acyl coenzyme A thioester hydrolase) (MTE-I) (Very-long-chain acyl-CoA thioesterase)	Acot2 Mte1	ACOT2_RAT	*136213380*	*13*	*176769180*	*23*	0.030	1.28
60S ribosomal protein L7	Rpl7	RL7_RAT	*15573548*	*17*	*19640371*	*13*	0.027	1.28
Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase)	Mdh1 Mdh	MDHC_RAT	*228804074*	*10*	*292827896*	*14*	0.004	1.28
14-3-3 protein zeta/delta (Mitochondrial import stimulation factor S1 subunit) (Protein kinase C inhibitor protein 1) (KCIP-1)	Ywhaz Msfs1	1433Z_RAT	*16977000*	*7*	*21775844*	*15*	0.002	1.28
Elongation factor Tu, mitochondrial	Tufm	EFTU_RAT	*59257027*	*13*	*75190628*	*14*	0.013	1.27
Histone H4 [Cleaved into: Osteogenic growth peptide (OGP)]	Hist1h4b Hist4; Hist1h4m; Hist4h4 H4ft	H4_RAT	*173772828*	*3*	*222989162*	*15*	0.001	1.27
NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4)	Por	NCPR_RAT	*5943847*	*7*	*7647255*	*20*	0.007	1.27
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (EC 5.3.3.-)	Ech1	ECH1_RAT	*111356860*	*6*	*142067004*	*12*	0.001	1.27
Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 5) (LACS 5)	Acsl5 Acs5 Facl5	ACSL5_RAT	*74670106*	*5*	*95496211*	*14*	0.001	1.27
Plasminogen activator inhibitor 1 RNA-binding protein (PAI1 RNA-binding protein 1) (PAI-RBP1) (RDA288) (SERPINE1 mRNA-binding protein 1)	Serbp1 Pairbp1 Rda288	PAIRB_RAT	*2286908*	*16*	*2886708*	*18*	0.031	1.27
Sorbin and SH3 domain-containing protein 2 (Arg-binding protein 2) (ArgBP2) (Arg/Abl-interacting protein 2) (Neural ArgBP2) (nArgBP2) (Sorbin)	Sorbs2 Argbp2	SRBS2_RAT	*35875812*	*6*	*45791962*	*16*	0.002	1.27
Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP) [Cleaved into: Triakontatetraneuropeptide (TTN); Octadecaneuropeptide (ODN)]	Dbi	ACBP_RAT	*20762087*	*12*	*26368047*	*18*	0.012	1.26
Long-chain specific acyl-CoA dehydrogenase, mitochondrial (LCAD) (EC 1.3.8.8)	Acadl	ACADL_RAT	*107900036*	*8*	*134483394*	*4*	≤0.001	1.25
Neurofilament medium polypeptide (NF-M) (160 kDa neurofilament protein) (Neurofilament 3) (Neurofilament triplet M protein)	Nefm Nef3 Nfm	NFM_RAT	*305495779*	*12*	*379612936*	*11*	0.011	1.25
Sodium/potassium-transporting ATPase subunit alpha-1 (Na(+)/K(+) ATPase alpha-1 subunit) (EC 7.2.2.13) (Sodium pump subunit alpha-1)	Atp1a1	AT1A1_RAT	*57351481*	*6*	*72349439*	*19*	0.006	1.25

Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	Acadvl Vlcad	ACADV_RAT	*82019269*	*9*	*102295670*	*11*	0.002	1.25
NADH:ubiquinone oxidoreductase subunit A7 (Ndufa7 protein) (RCG37550, isoform CRA_a)	Ndufa7 Ndufa7l rCG_37550	A9UMV9_RAT	*39569667*	*16*	*48774386*	*13*	0.029	1.25
Long-chain fatty acid transport protein 1 (Solute carrier family 27 (Fatty acid transporter), member 1) (Solute carrier family 27 (Fatty acid transporter), member 1, isoform CRA_a)	Slc27a1 rCG_38707	Q6GMM8_RAT	*7027963*	*11*	*8724499*	*11*	0.005	1.24
Enoyl-CoA delta isomerase 1, mitochondrial (EC 5.3.3.8) (3,2-trans-enoyl-CoA isomerase) (Delta(3),Delta(2)-enoyl-CoA isomerase) (D3,D2-enoyl-CoA isomerase) (Dodecenoyl-CoA isomerase)	Eci1 Dci	ECI1_RAT	*173934445*	*9*	*217360265*	*15*	0.008	1.24
Fibrillin 1 (Fibrillin 1, isoform CRA_a)	Fbn1 rCG_27283	G3V9M6_RAT	*32474420*	*14*	*39844980*	*8*	0.011	1.24
Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	Vcp	TERA_RAT	*10563372*	*13*	*13075350*	*18*	0.034	1.23
Moesin (Moesin, isoform CRA_a)	Msn rCG_36474	A0A096MK30_RAT	*38065027*	*4*	*48344967*	*28*	0.041	1.23
Trifunctional enzyme subunit alpha, mitochondrial (TP-alpha) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]	Hadha	ECHA_RAT	*108964806*	*10*	*134342233*	*13*	0.005	1.23
Heat shock protein HSP 90-beta (Heat shock 84 kDa) (HSP 84) (HSP84)	Hsp90ab1 Hsp84 Hspcb	HS90B_RAT	*47916531*	*7*	*59331315*	*16*	0.006	1.23
Citramalyl-CoA lyase, mitochondrial (EC 4.1.3.25) (Beta-methylmalate synthase) (EC 2.3.3.-) (Citrate lyase subunit beta-like protein, mitochondrial) (Citrate lyase beta-like) (Malate synthase) (EC 2.3.3.9)	Clybl	CLYBL_RAT	*5818855*	*8*	*7202042*	*18*	0.011	1.23
Basic leucine zipper and W2 domain-containing protein 2 (Brain development-related molecule 2)	Bzw2 Bdm2 Hfb2	BZW2_RAT	*27367163*	*9*	*33877630*	*19*	0.014	1.23
Leucine-rich PPR motif-containing protein, mitochondrial (130 kDa leucine-rich protein) (LRP 130) (Leucine rich protein 157) (rLRP157)	Lrpprc Lrp157	LPPRC_RAT	*8218170*	*7*	*10140289*	*14*	0.004	1.23
Creatine kinase S-type, mitochondrial (EC 2.7.3.2) (Basic-type mitochondrial creatine kinase) (Mib-CK) (Sarcomeric mitochondrial creatine kinase) (S-MtCK)	Ckmt2	KCRS_RAT	*93055532*	*16*	*112466628*	*10*	0.030	1.22
NADH-ubiquinone oxidoreductase 75 kDa	Ndufs1	NDUS1_RAT	*48333875*	*8*	*59196389*	*12*	0.006	1.22

subunit, mitochondrial (EC 1.6.99.3) (EC 7.1.1.2)								
AHNAK nucleoprotein	Ahnak	A0A0G2JUA5_RAT	5538224	14	6690333	11	0.025	1.22
Phospholemman (FXYD domain-containing ion transport regulator 1) (Sodium/potassium-transporting ATPase subunit FXYD1)	Fxyd1 Plm	PLM_RAT	56096971	7	68014386	6	≤0.001	1.21
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial (Complex I-ASHI) (NADH-ubiquinone oxidoreductase ASHI subunit)	Ndufb8 Ndufb8_predicted rCG_57427	B2RYS8_RAT	116488876	12	141249810	14	0.021	1.21
EH domain-containing protein 3	Ehd3 Ehd2	EHD3_RAT	18543496	5	22774632	21	0.018	1.21
NADH:ubiquinone oxidoreductase subunit B3 (RCG22355)	Ndufb3 rCG_22355	D4A4P3_RAT	126171571	12	151684214	12	0.021	1.21
Heterogeneous nuclear ribonucleoprotein D-like	Hnrnpdl	A0A0G2KAZ7_RAT	8854228	15	10582278	10	0.028	1.21
Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	Lum Lcn Ldc	LUM_RAT	58608507	13	70318072	11	0.022	1.21
Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase)	Aco2	ACON_RAT	579367896	7	697040074	7	≤0.001	1.20
NADH:ubiquinone oxidoreductase subunit B10 (RCG32945)	Ndufb10 rCG_32945	D4A0T0_RAT	119647546	10	143490387	9	0.008	1.20
Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86)	Hsp90aa1 Hsp86 Hspca	HS90A_RAT	33041406	7	40242845	20	0.034	1.20
Sarcoglycan, alpha (Sarcoglycan, alpha (Dystrophin-associated glycoprotein) (Predicted), isoform CRA_a)	Sgca Sgca_predicted rCG_34071	D3ZDQ9_RAT	20796676	5	25086379	11	0.001	1.20
Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	Hspa8 Hsc70 Hsc73	HSP7C_RAT	51329080	6	61736955	10	0.001	1.20
Spectrin beta chain	Sptbn1	A0A0G2JZY6_RAT	11766524	7	14182537	13	0.007	1.20
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (Flavoprotein subunit of complex II) (Fp)	Sdha	SDHA_RAT	119633020	4	143631747	8	≤0.001	1.20
NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 9 (NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 9 (Predicted)) (NADH:ubiquinone oxidoreductase subunit B9) (Ndufb9 protein)	Ndufb9 Ndufb9_predicted rCG_60288	B2RYW3_RAT	148687496	8	178052768	10	0.003	1.20
Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (eIF-4D)	Eif5a	IF5A1_RAT	3909444	14	4628547	8	0.027	1.20
Cytochrome b (Complex III subunit 3) (Complex III subunit III) (Cytochrome b-c1 complex subunit 3) (Ubiquinol-cytochrome-c reductase complex cytochrome b subunit)	Mt-Cyb Cob Cytb mt-Cytb Mtcyb	CYB_RAT	108423775	8	129441386	9	0.002	1.20
60S ribosomal protein L19	Rpl19	RL19_RAT	9871351	3	11860718	14	0.003	1.19

40S ribosomal protein S3a	Cyld LOC100362727 RPS3A	Q6TXJ6_RAT	*12180369*	*8*	*14572029*	*15*	0.017	1.19
Apoptosis-inducing factor 1, mitochondrial (Programmed cell death 8, isoform CRA_a)	Aifm1 Pdcd8 rCG_53222	A0A0G2K7K2_RAT	*10230420*	*7*	*12229880*	*14*	0.014	1.19
Uncharacterized protein		F1LTJ5_RAT	*22358172*	*8*	*26671204*	*17*	0.024	1.19
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (MCAD) (EC 1.3.8.7)	Acadm	ACADM_RAT	*159857755*	*8*	*189287044*	*8*	0.002	1.18
Palmdelphin	Palmd	PALMD_RAT	*13977611*	*10*	*16498440*	*10*	0.013	1.18
Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	Uqcrc2	QCR2_RAT	*158614412*	*12*	*185813688*	*5*	0.014	1.18
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase subunit alpha) (NAD(+)-specific ICDH subunit alpha)	Idh3a	IDH3A_RAT	*116744312*	*5*	*138935589*	*17*	0.017	1.18
Laminin subunit beta-2 (Laminin chain B3) (Laminin-11 subunit beta) (Laminin-14 subunit beta) (Laminin-15 subunit beta) (Laminin-3 subunit beta) (Laminin-4 subunit beta) (Laminin-7 subunit beta) (Laminin-9 subunit beta) (S-laminin subunit beta) (S-LAM beta)	Lamb2	LAMB2_RAT	*15453559*	*9*	*18095855*	*7*	0.004	1.17
Uncharacterized protein		D4A6W6_RAT	*11066533*	*6*	*12935397*	*8*	0.002	1.17
Pyruvate kinase PKM (EC 2.7.1.40) (Pyruvate kinase muscle isozyme)	Pkm Pkm2 Pykm	KPYM_RAT	*331632330*	*6*	*387978412*	*11*	0.006	1.17
Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (Isocitric dehydrogenase subunit beta) (NAD(+)-specific ICDH subunit beta)	Idh3B	IDH3B_RAT	*41704638*	*8*	*48630221*	*9*	0.007	1.17
Peroxiredoxin 3 (Thioredoxin-dependent peroxide reductase, mitochondrial)	Prdx3 rCG_57612	G3V7I0_RAT	*262272674*	*8*	*304330623*	*7*	0.005	1.16
Mitochondrial import receptor subunit TOM22 homolog (rTOM22) (Translocase of outer membrane 22 kDa subunit homolog)	Tomm22 Tom22	TOM22_RAT	*140791982*	*7*	*163990206*	*11*	0.010	1.16
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 (Complex I-B14.7) (CI-B14.7) (NADH-ubiquinone oxidoreductase subunit B14.7)	Ndufa11	NDUAB_RAT	*117713138*	*6*	*134508318*	*7*	0.003	1.14
Glutamate dehydrogenase 1, mitochondrial (GDH 1) (EC 1.4.1.3) (Memory-related gene 2 protein) (MRG-2)	Glud1 Glud	DHE3_RAT	*27262527*	*4*	*23314448*	*11*	0.002	-1.18
Myosin-binding protein C, cardiac-type (Cardiac MyBP-C) (C-protein, cardiac muscle isoform)	Mybpc3	MYPC_RAT	*122240540*	*11*	*104428084*	*15*	0.021	-1.18
3-oxo-5-beta-steroid 4-dehydrogenase (EC 1.3.1.3)	Akr1d1	AK1D1_RAT	*74456095*	*17*	*62121341*	*12*	0.020	-1.19

(Aldo-keto reductase family 1 member D1) (Delta(4)-3-ketosteroid 5-beta-reductase) (Delta(4)-3-oxosteroid 5-beta-reductase)								
Aldose reductase-related protein 1 (EC 1.1.1.21) (Aldehyde reductase) (Aldo-keto reductase family 1 member B7) (Aldose reductase-like protein AKR1B14)	Akr1b7 Akr1b14	ALD1_RAT	*74456095*	*17*	*62121341*	*12*	0.020	-1.19
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (B36-VDAC) (Outer mitochondrial membrane protein porin 2)	Vdac2	VDAC2_RAT	*359743034*	*14*	*302419463*	*17*	0.031	-1.20
Glypican-1 (HSPG M12) [Cleaved into: Secreted glypican-1]	Gpc1	GPC1_RAT	*16480007*	*17*	*13546811*	*11*	0.011	-1.21
Phosphoglycerate mutase 2 (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 2) (Muscle-specific phosphoglycerate mutase) (Phosphoglycerate mutase isozyme M) (PGAM-M)	Pgam2	PGAM2_RAT	*181191048*	*16*	*148579334*	*17*	0.019	-1.22
ES1 protein homolog, mitochondrial		ES1_RAT	*73924744*	*17*	*59412836*	*7*	0.003	-1.24
Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	Echs1	ECHM_RAT	*91350440*	*16*	*74761837*	*22*	0.046	-1.24
Myomesin 2	Myom2 rCG_43076	G3V7K1_RAT	*38061733*	*14*	*30824497*	*15*	0.014	-1.24
Cytochrome c oxidase subunit 5B, mitochondrial (Cytochrome c oxidase polypeptide Vb) (Cytochrome c oxidase subunit VIA*)	Cox5b	COX5B_RAT	*192194389*	*12*	*157063543*	*24*	0.041	-1.25
Propionyl coenzyme A carboxylase, beta polypeptide (Propionyl coenzyme A carboxylase, beta polypeptide, isoform CRA_b) (Propionyl-CoA carboxylase beta chain, mitochondrial)	Pccb rCG_25130	Q68FZ8_RAT	*12626766*	*18*	*10075119*	*14*	0.012	-1.25
2-oxoisovalerate dehydrogenase subunit beta, mitochondrial (EC 1.2.4.4) (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain) (BCKDE1B) (BCKDH E1-beta)	Bckdhb	ODBB_RAT	*36314045*	*9*	*29690203*	*26*	0.031	-1.25
Atypical kinase COQ8A, mitochondrial (EC 2.7.-.-) (Chaperone activity of bc1 complex-like) (Chaperone-ABC1-like) (Coenzyme Q protein 8A) (aarF domain-containing protein kinase 3)	Coq8a Adck3 Cabc1	COQ8A_RAT	*56826673*	*17*	*45920797*	*21*	0.039	-1.26
D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome tautomerase)	Ddt	DOPD_RAT	*55850295*	*25*	*43643389*	*18*	0.025	-1.28
Solute carrier family 25 member 13	Slc25a13	F1LZW6_RAT	*39142675*	*10*	*30756744*	*14*	0.001	-1.28
Uncharacterized protein		D4A647_RAT	*2115265*	*19*	*1651398*	*20*	0.014	-1.29
Creatine kinase M-type (Creatine kinase, muscle)	Ckm rCG_54105	A0A0G2JSP8_RAT	*550454545*	*15*	*430406122*	*16*	0.005	-1.29

Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	Pcca	PCCA_RAT	*11077243*	*18*	*8602750*	*18*	0.008	-1.29
Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	Actb	ACTB_RAT	*413643032*	*13*	*324093236*	*23*	0.014	-1.30
Glutathione S-transferase, mu 6-like	Gstm6l	A0A0G2JZ09_RAT	*12321808*	*24*	*9313511*	*15*	0.010	-1.31
4-trimethylaminobutyraldehyde dehydrogenase (TMABADH) (EC 1.2.1.47) (Aldehyde dehydrogenase family 9 member A1) (EC 1.2.1.3)	Aldh9a1	AL9A1_RAT	*22203216*	*21*	*16941450*	*21*	0.008	-1.32
NADH dehydrogenase (Ubiquinone) Fe-S protein 8 (Predicted), isoform CRA_a (NADH:ubiquinone oxidoreductase core subunit S8) (Ndufs8 protein)	Ndufs8 Ndufs8_predicted rCG_47133	B0BNE6_RAT	*43775792*	*37*	*32333873*	*16*	0.029	-1.33
Actin, aortic smooth muscle	Acta2	A0A0G2K4M6_RAT	*507545976*	*13*	*394499398*	*29*	0.028	-1.33
Prostaglandin reductase 1 (PRG-1) (EC 1.3.1.-) (15-oxoprostaglandin 13-reductase) (EC 1.3.1.48) (Dithiolethione-inducible gene 1 protein) (D3T-inducible gene 1 protein) (DIG-1) (NADP-dependent leukotriene B4 12-hydroxydehydrogenase) (EC 1.3.1.74)	Ptgr1 Dig1 Ltb4dh	PTGR1_RAT	*8128407*	*27*	*6064182*	*20*	0.020	-1.33
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.-)	Pdhx	A0A0G2JZH8_RAT	*23681246*	*15*	*18250713*	*26*	0.025	-1.34
Transcription initiation factor TFIID subunit 6 (Transcription initiation factor TFIID 70 kDa subunit) (TAF(II)70) (TAFII70) (Transcription initiation factor TFIID 80 kDa subunit) (TAF(II)80) (TAFII-80) (TAFII80) (p80)	Taf6 Taf2e	TAF6_RAT	*8288069*	*17*	*6248834*	*19*	0.005	-1.34
Myozenin 2 (Myozenin 2 (Predicted), isoform CRA_b)	Myoz2 Myoz2_predicted rCG_28510	D3ZX18_RAT	*74894703*	*24*	*56640375*	*29*	0.021	-1.34
Heat shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27)	Hspb1 Hsp27	HSPB1_RAT	*52367625*	*8*	*39662474*	*22*	0.005	-1.35
Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2) (ALDH-E2) (ALDH1)	Aldh2	ALDH2_RAT	*45588834*	*15*	*33620414*	*10*	≤0.001	-1.35
Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	Anxa5 Anx5	ANXA5_RAT	*52708583*	*25*	*38890303*	*20*	0.013	-1.36
40S ribosomal protein S3 (EC 4.2.99.18)	Rps3	RS3_RAT	*18972696*	*9*	*14540543*	*32*	0.028	-1.37

Branched-chain-amino-acid aminotransferase, mitochondrial (BCAT(m)) (EC 2.6.1.42)	Bcat2 Bcatm Eca40	BCAT2_RAT	*21303576*	*21*	*15600033*	*20*	0.004	-1.38
Short-chain specific acyl-CoA dehydrogenase, mitochondrial (SCAD) (EC 1.3.8.1) (Butyryl-CoA dehydrogenase)	Acads	ACADS_RAT	*102637147*	*19*	*76078963*	*26*	0.015	-1.38
2-oxoglutarate dehydrogenase, mitochondrial (EC 1.2.4.2) (2-oxoglutarate dehydrogenase complex component E1) (OGDC-E1) (Alpha-ketoglutarate dehydrogenase)	Ogdh Ogdhl	ODO1_RAT	*39616976*	*13*	*28812119*	*15*	≤0.001	-1.38
Histidine triad nucleotide binding protein 2 (Predicted), isoform CRA_a (Histidine triad nucleotide-binding protein 2)	Hint2 Hint2_predicted rCG_54875	D4AB01_RAT	*10739362*	*21*	*8064611*	*42*	0.046	-1.42
Glucagon-like peptide 2 receptor (GLP-2 receptor) (GLP-2-R) (GLP-2R)	Glp2r	GLP2R_RAT	*25590216*	*30*	*17839643*	*22*	0.008	-1.43
Tripartite motif-containing protein 72 (Mitsugumin-53) (Mg53)	Trim72 Mg53	TRI72_RAT	*6183900*	*21*	*4310379*	*19*	0.001	-1.44
Isocitrate dehydrogenase [NADP], mitochondrial (IDH) (EC 1.1.1.42) (ICD-M) (IDP) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	Idh2	IDHP_RAT	*260632596*	*13*	*187914432*	*36*	0.011	-1.46
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Pfkm	A0A0G2KBC7_RAT	*5373693*	*28*	*3797132*	*34*	0.025	-1.47
LIM domain-binding 3	Ldb3	A0A096MJ01_RAT	*84387670*	*15*	*58727923*	*30*	0.006	-1.49
Myosin-4	Myh4 Myh2	F1LMU0_RAT	*1399408891*	*36*	*941403190*	*24*	0.007	-1.50
Myosin-7 (Myosin heavy chain 7) (Myosin heavy chain slow isoform) (MyHC-slow) (Myosin heavy chain, cardiac muscle beta isoform) (MyHC-beta)	Myh7	MYH7_RAT	*212881703*	*34*	*136971592*	*21*	0.002	-1.54
Enoyl-[acyl-carrier-protein] reductase, mitochondrial (EC 1.3.1.104) (2-enoyl thioester reductase) (Nuclear receptor-binding factor 1) (NRBF-1)	Mecr Nrbf1	MECR_RAT	*822847*	*41*	*547069*	*50*	0.029	-1.61
Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	LOC100911252	A0A0G2K2E4_RAT	*3140460*	*35*	*2076420*	*44*	0.040	-1.64
Prohibitin-2 (B-cell receptor-associated protein BAP37) (BAP-37)	Phb2 Bcap37	PHB2_RAT	*26250521*	*13*	*16637134*	*34*	0.001	-1.65
40S ribosomal protein S9	Rps9	RS9_RAT	*3780381*	*59*	*2263795*	*50*	0.032	-1.75
Erlin-2 (Endoplasmic reticulum lipid raft-associated protein 2) (Stomatin-prohibitin-flotillin-HflC/K domain-containing protein 2) (SPFH domain-containing protein 2)	Erlin2 Spfh2	ERLN2_RAT	*2363741*	*19*	*1535462*	*40*	0.045	-1.78
Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1)	Sod2	SODM_RAT	*31144681*	*35*	*19768666*	*56*	0.033	-1.82

Cytoplasmic dynein 1 heavy chain 1 (RCG27764, isoform CRA_a)	Dync1h1 rCG_27764	M0R9X8_RAT	*347572*	*57*	*186920*	*36*	0.003	-1.89
Glycogenin-1 (GN-1) (GN1) (EC 2.4.1.186)	Gyg1 Gyg	GLYG_RAT	*6994496*	*41*	*4440418*	*70*	0.040	-1.89
Isovaleryl-CoA dehydrogenase, mitochondrial (IVD) (EC 1.3.8.4)	Ivd	IVD_RAT	*56599875*	*22*	*32614222*	*42*	0.004	-1.90
Electron transfer flavoprotein subunit alpha, mitochondrial (Alpha-ETF)	Etfa	ETFA_RAT	*21862626*	*77*	*10758456*	*16*	0.001	-1.94
Cytochrome b-c1 complex subunit Rieske, mitochondrial (EC 7.1.1.8) (Complex III subunit 5) (Cytochrome b-c1 complex subunit 5) (Liver regeneration-related protein LRRGT00195) (Rieske iron-sulfur protein) (RISP) (Rieske protein UQCRFS1) (Ubiquinol-cytochrome c reductase iron-sulfur subunit) [Cleaved into: Cytochrome b-c1 complex subunit 9 (Su9) (Subunit 9) (8 kDa subunit 9) (Complex III subunit IX) (Cytochrome b-c1 complex subunit 11) (Ubiquinol-cytochrome c reductase 8 kDa protein)]	Uqcrfs1	UCRI_RAT	*40492785*	*40*	*21733079*	*36*	0.001	-1.95
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial (MCCase subunit beta) (EC 6.4.1.4) (3-methylcrotonyl-CoA carboxylase 2) (3-methylcrotonyl-CoA carboxylase non-biotin-containing subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta)	Mccc2	MCCB_RAT	*2609545*	*58*	*1460929*	*73*	0.046	-2.18
Vinculin (Metavinculin)	Vcl	VINC_RAT	*2696005*	*68*	*1287417*	*56*	0.034	-2.32
Interferon-inducible double-stranded RNA-dependent protein kinase activator A (Protein activator of the interferon-induced protein kinase) (Protein kinase, interferon-inducible double-stranded RNA-dependent activator)	Prkra	PRKRA_RAT	*72141*	*171*	*26215*	*45*	0.026	-2.64
Adenylosuccinate synthetase isozyme 1 (AMPSase 1) (AdSS 1) (EC 6.3.4.4) (Adenylosuccinate synthetase, basic isozyme) (Adenylosuccinate synthetase, muscle isozyme) (M-type adenylosuccinate synthetase) (IMP--aspartate ligase 1)	Adssl1 ADSS1 ADSSL1 rCG_27771	M0R629_RAT	*45531*	*29*	*16636*	*27*	0.017	-2.80
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10) (Type I keratin Ka10)	Krt10 Ka10	K1C10_RAT	*939301*	*94*	*419557*	*101*	0.011	-2.90
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial (Complex I-42kD) (CI-42kD) (NADH-	Ndufa10	NDUAA_RAT	*791094*	*114*	*265487*	*49*	0.038	-3.15

ubiquinone oxidoreductase 42 kDa subunit)								
Galectin-1 (Gal-1) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (RL 14.5) (S-Lac lectin 1)	Lgals1	LEG1_RAT	*35144549*	*33*	*15042046*	*86*	0.005	-3.23
Complement C3	C3	M0RBJ7_RAT	*2061209*	*34*	*1003265*	*77*	0.031	-3.28
Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta)	P4hb Pdia1	PDIA1_RAT	*8136997*	*84*	*2874527*	*67*	0.001	-3.40
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial (EC 2.3.1.12) (70 kDa mitochondrial autoantigen of primary biliary cirrhosis) (PBC) (Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex) (Pyruvate dehydrogenase complex component E2) (PDC-E2) (PDCE2)	Dlat	ODP2_RAT	*222948*	*252*	*55631*	*22*	0.022	-3.47
Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 (EC 1.-.-.-)	Pyroxd2	PYRD2_RAT	*1405732*	*88*	*517493*	*98*	0.013	-5.32
Dynein light chain roadblock-type 1 (Bithoraxoid-like protein) (BLP) (robl/LC7-like protein) (Dynein light chain 2A, cytoplasmic) (Dynein-associated protein Km23)	Dynlrb1 Dncl2a Dnlc2a	DLRB1_RAT	*11777318*	*65*	*5063311*	*102*	0.024	-6.43
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.-)	Dbt rCG_28617	B2GV15_RAT	*598046*	*61*	*262677*	*109*	0.039	-9.53

Reactome pathways

Pathway identifier	**Pathway name**	**#Entities found**	***#Interactors found***	**Submitted entities found**
R-HSA-1430728	**Metabolism**	**29**	***9***	**Mecr;Ndufa1;Ndufa2;Aldh7a1;Adssl1;Cs;Ndufa10;Acaa2;Uqcrfs1;Dbt;Pgk1;Prelp;Gyg1;Hibch;Rps9;Got1;Mtnd4;Bgn;Etfa;Hprt1;Ivd;Gpd1;Mccc2;Etfdh;Me3;Dlat;Cd36**
R-HSA-168256	**Immune System**	**14**	***23***	**Lama5;C3;Ctsd;Pafah1b2;P4hb;Cd36;Prdx6;Sod2;Dync1h1;Vcl;Gyg1**
R-HSA-1643685	**Disease**	**12**	***11***	**Rps9;Mpi;Mccc2;Bgn;Erlin2;Prelp;Slc25a4;Cd36;Sod2;Vcl;Gyg1**
R-HSA-162582	**Signal Transduction**	**12**	***13***	**C3;Lama5;Ctsd;Rdx;Cyct;Dbt;Lamc1;Dlat;P4hb;Dync1h1;Vcl**
R-HSA-1428517	**The citric acid (TCA) cycle and respiratory electron transport**	**10**	***3***	**Cs;Ndufa10;Uqcrfs1;Mtnd4;Ndufa1;Etfdh;Ndufa2;Me3;Dlat;Etfa**
R-HSA-392499	**Metabolism of proteins**	**9**	***11***	**C3;Ctsd;Rps9;Mpi;Vdac3;Lamc1;P4hb;Lgals1;Dync1h1**
R-HSA-397014	**Muscle contraction**	**8**	***1***	**Tmod1;Myl2;Tpm1;Myl3;Casq2;Tnni3;Vcl;Myh6;Myh7**
R-HSA-6798695	**Neutrophil degranulation**	**8**	***0***	**C3;Ctsd;Pafah1b2;Cd36;Prdx6;Dync1h1;Vcl;Gyg1**

R-HSA-71291	**Metabolism of amino acids and derivatives**	**8**	***0***	**Hibch;Rps9;Got1;Ivd;Dbt;Mccc2;Aldh7a1;Dlat**
R-HSA-449147	**Signaling by Interleukins**	**8**	***7***	**Lama5;P4hb;Cd36;Sod2;Vcl**
R-HSA-168249	**Innate Immune System**	**8**	***11***	**C3;Ctsd;Pafah1b2;Cd36;Prdx6;Dync1h1;Vcl;Gyg1**
R-HSA-1280215	**Cytokine Signaling in Immune system**	**8**	***11***	**Lama5;P4hb;Cd36;Sod2;Vcl**
R-HSA-611105	**Respiratory electron transport**	**7**	***1***	**Ndufa10;Uqcrfs1;Mtnd4;Ndufa1;Etfdh;Ndufa2;Etfa**
R-HSA-163200	**Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.**	**7**	***1***	**Ndufa10;Uqcrfs1;Mtnd4;Ndufa1;Etfdh;Ndufa2;Etfa**
R-HSA-382551	**Transport of small molecules**	**7**	***0***	**Mb;Vdac3;Erlin2;Casq2;Slc25a4;P4hb;Phb2**
R-HSA-597592	**Post-translational protein modification**	**7**	***7***	**C3;Mpi;Vdac3;Lamc1;P4hb;Lgals1;Dync1h1**
R-HSA-390522	**Striated Muscle Contraction**	**6**	***0***	**Tmod1;Myl2;Tpm1;Myl3;Tnni3;Myh6;Myh7**
R-HSA-71387	**Metabolism of carbohydrates**	**6**	***1***	**Got1;Bgn;Pgk1;Prelp;Gyg1**
R-HSA-2262752	**Cellular responses to stress**	**6**	***2***	**Hist1h1b;P4hb;Prdx6;Sod2;Dync1h1;Cryab**
R-HSA-8953897	**Cellular responses to external stimuli**	**6**	***4***	**Hist1h1b;P4hb;Prdx6;Sod2;Dync1h1;Cryab**
R-HSA-1266738	**Developmental Biology**	**6**	***9***	**Rps9;Rdx;Lamc1;Krt10;Cd36**
R-HSA-1474244	**Extracellular matrix organization**	**5**	***9***	**Lama5;Ctsd;Bgn;Lamc1;P4hb**
R-HSA-1852241	**Organelle biogenesis and maintenance**	**5**	***4***	**Dbt;Immt;Sod2;Dynlrb1;Dync1h1**
R-HSA-109582	**Hemostasis**	**5**	***5***	**Wdr1;Cyct;Tagln2;Cd36;Vcl**
R-HSA-556833	**Metabolism of lipids**	**5**	***3***	**Acaa2;Mecr;Gpd1;Cd36**
R-HSA-74160	**Gene expression (Transcription)**	**5**	***12***	**Prkra;Sod2;Hspd1**
R-HSA-70895	**Branched-chain amino acid catabolism**	**4**	***0***	**Hibch;Ivd;Dbt;Mccc2**
R-HSA-8957275	**Post-translational protein phosphorylation**	**4**	***0***	**C3;Lamc1;P4hb;Lgals1**
R-HSA-6799198	**Complex I biogenesis**	**4**	***1***	**Ndufa10;Mtnd4;Ndufa1;Ndufa2**
R-HSA-114608	**Platelet degranulation**	**4**	***0***	**Wdr1;Tagln2;Cd36;Vcl**
R-HSA-76005	**Response to elevated platelet cytosolic Ca2+**	**4**	***0***	**Wdr1;Tagln2;Cd36;Vcl**
R-HSA-381426	**Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)**	**4**	***0***	**C3;Lamc1;P4hb;Lgals1**
R-HSA-6785807	**Interleukin-4 and Interleukin-13 signaling**	**4**	***0***	**Lama5;Cd36**
R-HSA-76002	**Platelet activation, signaling and aggregation**	**4**	***3***	**Wdr1;Tagln2;Cd36;Vcl**
R-HSA-5653656	**Vesicle-mediated transport**	**4**	***5***	**Hpx;Pafah1b2;Cd36;Dync1h1**
R-HSA-1280218	**Adaptive Immune System**	**4**	***12***	**C3;Ctsd;Cd36;Dync1h1**
R-HSA-212436	**Generic Transcription Pathway**	**4**	***10***	**Sod2;Hspd1**
R-HSA-73857	**RNA Polymerase II Transcription**	**4**	***10***	**Sod2;Hspd1**
R-HSA-1268020	**Mitochondrial protein import**	**3**	***0***	**Cs;Slc25a4;Hspd1**
R-HSA-3000178	**ECM proteoglycans**	**3**	***0***	**Lama5;Bgn;Lamc1**
R-HSA-70263	**Gluconeogenesis**	**3**	***1***	**Got1;Pgk1**
R-HSA-71406	**Pyruvate metabolism and Citric Acid (TCA) cycle**	**3**	***2***	**Cs;Me3;Dlat**
R-HSA-1474228	**Degradation of the extracellular matrix**	**3**	***0***	**Lama5;Ctsd;Lamc1**
R-HSA-70326	**Glucose metabolism**	**3**	***1***	**Got1;Pgk1**
R-HSA-3781865	**Diseases of glycosylation**	**3**	***0***	**Mpi;Bgn;Prelp**
R-HSA-9609507	**Protein localization**	**3**	***0***	**Cs;Slc25a4;Hspd1**
R-HSA-3299685	**Detoxification of Reactive Oxygen Species**	**3**	***0***	**P4hb;Prdx6;Sod2**
R-HSA-9020591	**Interleukin-12 signaling**	**3**	***3***	**P4hb;Sod2**
R-HSA-5617833	**Cilium Assembly**	**3**	***1***	**Dbt;Dynlrb1;Dync1h1**
R-HSA-447115	**Interleukin-12 family signaling**	**3**	***5***	**P4hb;Sod2**
R-HSA-9006931	**Signaling by Nuclear Receptors**	**3**	***2***	**Ctsd;Dlat**
R-HSA-422475	**Axon guidance**	**3**	***5***	**Rps9;Rdx;Lamc1**
R-HSA-8949215	**Mitochondrial calcium ion transport**	**2**	***0***	**Vdac3;Phb2**
R-HSA-3000157	**Laminin interactions**	**2**	***0***	**Lama5;Lamc1**
R-HSA-8869496	**TFAP2A acts as a transcriptional repressor during retinoic acid induced cell differentiation**	**2**	***0***	**Hspd1**

R-HSA-3560782	Diseases associated with glycosaminoglycan metabolism	2	0	Bgn;Prelp
R-HSA-380320	Recruitment of NuMA to mitotic centrosomes	2	0	Dbt;Dync1h1
R-HSA-8854518	AURKA Activation by TPX2	2	0	Dbt;Dync1h1
R-HSA-71403	Citric acid cycle (TCA cycle)	2	0	Cs;Me3
R-HSA-389661	Glyoxylate metabolism and glycine degradation	2	0	Dbt;Dlat
R-HSA-8874081	MET activates PTK2 signaling	2	0	Lama5;Lamc1
R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	2	0	Dbt;Dync1h1
R-HSA-9615017	FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	2	2	Sod2
R-HSA-5578775	Ion homeostasis	2	0	Casq2;Tnni3
R-HSA-6811436	COPI-independent Golgi-to-ER retrograde traffic	2	2	Pafah1b2;Dync1h1
R-HSA-70171	Glycolysis	2	0	Pgk1
R-HSA-445355	Smooth Muscle Contraction	2	1	Tpm1;Vcl
R-HSA-380259	Loss of Nlp from mitotic centrosomes	2	0	Dbt;Dync1h1
R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	2	0	Dbt;Dync1h1
R-HSA-8875878	MET promotes cell motility	2	0	Lama5;Lamc1
R-HSA-380287	Centrosome maturation	2	0	Dbt;Dync1h1
R-HSA-446353	Cell-extracellular matrix interactions	2	1	Flnc;Fermt2
R-HSA-5620912	Anchoring of the basal body to the plasma membrane	2	0	Dbt;Dync1h1
R-HSA-77289	Mitochondrial Fatty Acid Beta-Oxidation	2	0	Acaa2;Mecr
R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	2	0	Hpx;Cd36
R-HSA-2565942	Regulation of PLK1 Activity at G2/M Transition	2	1	Dbt;Dync1h1
R-HSA-1630316	Glycosaminoglycan metabolism	2	0	Bgn;Prelp
R-HSA-3000171	Non-integrin membrane-ECM interactions	2	2	Lama5;Lamc1
R-HSA-5576891	Cardiac conduction	2	0	Casq2;Tnni3
R-HSA-2132295	MHC class II antigen presentation	2	1	Ctsd;Dync1h1
R-HSA-68877	Mitotic Prometaphase	2	0	Dbt;Dync1h1
R-HSA-8856688	Golgi-to-ER retrograde transport	2	2	Pafah1b2;Dync1h1
R-HSA-5668914	Diseases of metabolism	2	0	Mccc2;Gyg1
R-HSA-15869	Metabolism of nucleotides	2	0	Adssl1;Hprt1
R-HSA-446728	Cell junction organization	2	2	Flnc;Fermt2
R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	2	3	Sod2
R-HSA-1592230	Mitochondrial biogenesis	2	3	Immt;Sod2
R-HSA-6806834	Signaling by MET	2	2	Lama5;Lamc1
R-HSA-381340	Transcriptional regulation of white adipocyte differentiation	2	3	Cd36
R-HSA-1989781	PPARA activates gene expression	2	0	Cd36
R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	2	2	Pafah1b2;Dync1h1
R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	2	0	Rps9;Dbt
R-HSA-400206	Regulation of lipid metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)	2	0	Cd36
R-HSA-5358351	Signaling by Hedgehog	2	0	Rdx;P4hb
R-HSA-1500931	Cell-Cell communication	2	2	Flnc;Fermt2
R-HSA-8868773	rRNA processing in the nucleus and cytosol	2	0	Rps9;Dbt
R-HSA-68886	M Phase	2	0	Dbt;Dync1h1
R-HSA-69275	G2/M Transition	2	1	Dbt;Dync1h1
R-HSA-453274	Mitotic G2-G2/M phases	2	1	Dbt;Dync1h1
R-HSA-9614085	FOXO-mediated transcription	2	2	Sod2
R-HSA-72312	rRNA processing	2	0	Rps9;Dbt
R-HSA-8978868	Fatty acid metabolism	2	1	Acaa2;Mecr
R-HSA-446203	Asparagine N-linked glycosylation	2	0	Mpi;Dync1h1

R-HSA-373760	L1CAM interactions	2	2	Rdx;Lamc1
R-HSA-8864260	Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	2	4	Hspd1
R-HSA-8863678	Neurodegenerative Diseases	2	5	Sod2
R-HSA-8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	2	5	Sod2
R-HSA-9018519	Estrogen-dependent gene expression	2	1	Ctsd
R-HSA-8939211	ESR-mediated signaling	2	2	Ctsd
R-HSA-5663202	Diseases of signal transduction	2	1	Erlin2;Vcl
R-HSA-69278	Cell Cycle, Mitotic	2	1	Dbt;Dync1h1
R-HSA-5663205	Infectious disease	2	5	Rps9;Slc25a4
R-HSA-199991	Membrane Trafficking	2	5	Pafah1b2;Dync1h1
R-HSA-1640170	Cell Cycle	2	7	Dbt;Dync1h1
R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	2	6	Lama5;Lamc1
R-HSA-388396	GPCR downstream signalling	2	1	C3;Cyct
R-HSA-8953854	Metabolism of RNA	2	1	Rps9;Dbt
R-HSA-372790	Signaling by GPCR	2	1	C3;Cyct
R-HSA-4043916	Defective MPI causes MPI-CDG (CDG-1b)	1	0	Mpi
R-HSA-3814836	Glycogen storage disease type XV (GYG1)	1	0	Gyg1
R-HSA-5357609	Glycogen storage disease type II (GAA)	1	0	Gyg1
R-HSA-3828062	Glycogen storage disease type 0 (muscle GYS1)	1	0	Gyg1
R-HSA-180897	Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	1	0	Slc25a4
R-HSA-8981607	Intracellular oxygen transport	1	0	Mb
R-HSA-3656244	Defective B4GALT1 causes B4GALT1-CDG (CDG-2d)	1	0	Prelp
R-HSA-3595174	Defective CHST14 causes EDS, musculocontractural type	1	0	Bgn
R-HSA-3656243	Defective ST3GAL3 causes MCT12 and EIEE15	1	0	Prelp
R-HSA-3656225	Defective CHST6 causes MCDC1	1	0	Prelp
R-HSA-3595172	Defective CHST3 causes SEDCJD	1	0	Bgn
R-HSA-426486	Small interfering RNA (siRNA) biogenesis	1	0	Prkra
R-HSA-3595177	Defective CHSY1 causes TPBS	1	0	Bgn
R-HSA-3785653	Myoclonic epilepsy of Lafora	1	0	Gyg1
R-HSA-2022923	Dermatan sulfate biosynthesis	1	0	Bgn
R-HSA-1236973	Cross-presentation of particulate exogenous antigens (phagosomes)	1	0	Cd36
R-HSA-173736	Alternative complement activation	1	0	C3
R-HSA-140342	Apoptosis induced DNA fragmentation	1	0	Hist1h1b
R-HSA-8949664	Processing of SMDT1	1	0	Phb2
R-HSA-4420332	Defective B3GALT6 causes EDSP2 and SEMDJL1	1	0	Bgn
R-HSA-3560783	Defective B4GALT7 causes EDS, progeroid type	1	0	Bgn
R-HSA-418457	cGMP effects	1	0	Cyct
R-HSA-3560801	Defective B3GAT3 causes JDSSDHD	1	0	Bgn
R-HSA-3229121	Glycogen storage diseases	1	0	Gyg1
R-HSA-2022857	Keratan sulfate degradation	1	0	Prelp
R-HSA-77346	Beta oxidation of decanoyl-CoA to octanoyl-CoA-CoA	1	0	Mecr
R-HSA-6798163	Choline catabolism	1	0	Aldh7a1
R-HSA-2022870	Chondroitin sulfate biosynthesis	1	0	Bgn
R-HSA-174577	Activation of C3 and C5	1	0	C3
R-HSA-1237112	Methionine salvage pathway	1	0	Got1
R-HSA-5603041	IRAK4 deficiency (TLR2/4)	1	0	Cd36
R-HSA-2024101	CS/DS degradation	1	0	Bgn
R-HSA-8853336	Signaling by plasma membrane FGFR1 fusions	1	0	Erlin2
R-HSA-3322077	Glycogen synthesis	1	0	Gyg1

R-HSA-3371599	**Defective HLCS causes multiple carboxylase deficiency**	**1**	***0***	**Mccc2**
R-HSA-203927	**MicroRNA (miRNA) biogenesis**	**1**	***0***	**Prkra**
R-HSA-3323169	**Defects in biotin (Btn) metabolism**	**1**	***0***	**Mccc2**
R-HSA-434313	**Intracellular metabolism of fatty acids regulates insulin secretion**	**1**	***0***	**Cd36**
R-HSA-446205	**Synthesis of GDP-mannose**	**1**	***0***	**Mpi**
R-HSA-1971475	**A tetrasaccharide linker sequence is required for GAG synthesis**	**1**	***0***	**Bgn**
R-HSA-5602498	**MyD88 deficiency (TLR2/4)**	**1**	***0***	**Cd36**
R-HSA-2022854	**Keratan sulfate biosynthesis**	**1**	***0***	**Prelp**
R-HSA-5686938	**Regulation of TLR by endogenous ligand**	**1**	***0***	**Cd36**
R-HSA-3000471	**Scavenging by Class B Receptors**	**1**	***0***	**Cd36**
R-HSA-8963888	**Chylomicron assembly**	**1**	***0***	**P4hb**
R-HSA-196780	**Biotin transport and metabolism**	**1**	***0***	**Mccc2**
R-HSA-8866423	**VLDL assembly**	**1**	***0***	**P4hb**
R-HSA-1638074	**Keratan sulfate/keratin metabolism**	**1**	***0***	**Prelp**
R-HSA-70221	**Glycogen breakdown (glycogenolysis)**	**1**	***0***	**Gyg1**
R-HSA-204174	**Regulation of pyruvate dehydrogenase (PDH) complex**	**1**	***0***	**Dlat**
R-HSA-176033	**Interactions of Vpr with host cellular proteins**	**1**	***0***	**Slc25a4**
R-HSA-5609975	**Diseases associated with glycosylation precursor biosynthesis**	**1**	***0***	**Mpi**
R-HSA-83936	**Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane**	**1**	***0***	**Slc25a4**
R-HSA-392154	**Nitric oxide stimulates guanylate cyclase**	**1**	***0***	**Cyct**
R-HSA-74217	**Purine salvage**	**1**	***0***	**Hprt1**
R-HSA-3296482	**Defects in vitamin and cofactor metabolism**	**1**	***0***	**Mccc2**
R-HSA-2022377	**Metabolism of Angiotensinogen to Angiotensins**	**1**	***0***	**Ctsd**
R-HSA-6802948	**Signaling by high-kinase activity BRAF mutants**	**1**	***0***	**Vcl**
R-HSA-5674135	**MAP2K and MAPK activation**	**1**	***0***	**Vcl**
R-HSA-1483166	**Synthesis of PA**	**1**	***0***	**Gpd1**
R-HSA-8963693	**Aspartate and asparagine metabolism**	**1**	***0***	**Got1**
R-HSA-71064	**Lysine catabolism**	**1**	***0***	**Aldh7a1**
R-HSA-1442490	**Collagen degradation**	**1**	***0***	**Ctsd**
R-HSA-8982491	**Glycogen metabolism**	**1**	***0***	**Gyg1**
R-HSA-72695	**Formation of the ternary complex, and subsequently, the 43S complex**	**1**	***0***	**Rps9**
R-HSA-77286	**mitochondrial fatty acid beta-oxidation of saturated fatty acids**	**1**	***0***	**Mecr**
R-HSA-1793185	**Chondroitin sulfate/dermatan sulfate metabolism**	**1**	***0***	**Bgn**
R-HSA-3371571	**HSF1-dependent transactivation**	**1**	***0***	**Cryab**
R-HSA-72649	**Translation initiation complex formation**	**1**	***0***	**Rps9**
R-HSA-6802946	**Signaling by moderate kinase activity BRAF mutants**	**1**	***0***	**Vcl**
R-HSA-6802955	**Paradoxical activation of RAF signaling by kinase inactive BRAF**	**1**	***0***	**Vcl**
R-HSA-72702	**Ribosomal scanning and start codon recognition**	**1**	***0***	**Rps9**
R-HSA-1638091	**Heparan sulfate/heparin (HS-GAG) metabolism**	**1**	***0***	**Bgn**
R-HSA-8956321	**Nucleotide salvage**	**1**	***0***	**Hprt1**
R-HSA-6802952	**Signaling by BRAF and RAF fusions**	**1**	***0***	**Vcl**
R-HSA-73817	**Purine ribonucleoside monophosphate biosynthesis**	**1**	***0***	**Adssl1**
R-HSA-6802949	**Signaling by RAS mutants**	**1**	***0***	**Vcl**
R-HSA-70268	**Pyruvate metabolism**	**1**	***2***	**Dlat**
R-HSA-1650814	**Collagen biosynthesis and modifying enzymes**	**1**	***0***	**P4hb**
R-HSA-6790901	**rRNA modification in the nucleus and cytosol**	**1**	***0***	**Rps9**
R-HSA-5362517	**Signaling by Retinoic Acid**	**1**	***0***	**Dlat**

R-HSA-72689	Formation of a pool of free 40S subunits	1	0	Rps9
R-HSA-5678895	Defective CFTR causes cystic fibrosis	1	0	Erlin2
R-HSA-72764	Eukaryotic Translation Termination	1	0	Rps9
R-HSA-2559584	Formation of Senescence-Associated Heterochromatin Foci (SAHF)	1	0	Hist1h1b
R-HSA-2168880	Scavenging of heme from plasma	1	0	Hpx
R-HSA-8956320	Nucleobase biosynthesis	1	0	Adssl1
R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	1	0	Rps9
R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	1	0	Rps9
R-HSA-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	1	0	Dync1h1
R-HSA-156902	Peptide chain elongation	1	0	Rps9
R-HSA-5663084	Diseases of carbohydrate metabolism	1	0	Gyg1
R-HSA-8963898	Plasma lipoprotein assembly	1	0	P4hb
R-HSA-201688	WNT mediated activation of DVL	1	1	Dbt
R-HSA-6802957	Oncogenic MAPK signaling	1	0	Vcl
R-HSA-192823	Viral mRNA Translation	1	1	Rps9
R-HSA-211000	Gene Silencing by RNA	1	0	Prkra
R-HSA-5620924	Intraflagellar transport	1	1	Dynlrb1
R-HSA-5358346	Hedgehog ligand biogenesis	1	0	P4hb
R-HSA-2408557	Selenocysteine synthesis	1	0	Rps9
R-HSA-166663	Initial triggering of complement	1	0	C3
R-HSA-1474290	Collagen formation	1	0	P4hb
R-HSA-400451	Free fatty acids regulate insulin secretion	1	1	Cd36
R-HSA-5619084	ABC transporter disorders	1	0	Erlin2
R-HSA-8949613	Cristae formation	1	2	Immt
R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	1	0	Rps9
R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	1	0	Rps9
R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	1	0	Rps9
R-HSA-156842	Eukaryotic Translation Elongation	1	0	Rps9
R-HSA-2672351	Stimuli-sensing channels	1	0	Casq2
R-HSA-9020933	Interleukin-23 signaling	1	1	P4hb
R-HSA-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	1	2	Dync1h1
R-HSA-141424	Amplification of signal from the kinetochores	1	2	Dync1h1
R-HSA-437239	Recycling pathway of L1	1	0	Rdx
R-HSA-382556	ABC-family proteins mediated transport	1	0	Erlin2
R-HSA-977606	Regulation of Complement cascade	1	2	C3
R-HSA-425397	Transport of vitamins, nucleosides, and related molecules	1	0	Slc25a4
R-HSA-69618	Mitotic Spindle Checkpoint	1	2	Dync1h1
R-HSA-5602358	Diseases associated with the TLR signaling cascade	1	0	Cd36
R-HSA-5260271	Diseases of Immune System	1	0	Cd36
R-HSA-2467813	Separation of Sister Chromatids	1	0	Dync1h1
R-HSA-1614635	Sulfur amino acid metabolism	1	0	Got1
R-HSA-927802	Nonsense-Mediated Decay (NMD)	1	0	Rps9
R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	1	0	Rps9
R-HSA-166658	Complement cascade	1	2	C3
R-HSA-5663220	RHO GTPases Activate Formins	1	0	Dync1h1
R-HSA-2500257	Resolution of Sister Chromatid Cohesion	1	0	Dync1h1
R-HSA-6809371	Formation of the cornified envelope	1	0	Krt10
R-HSA-2408522	Selenoamino acid metabolism	1	0	Rps9
R-HSA-68882	Mitotic Anaphase	1	0	Dync1h1

R-HSA-6807878	COPI-mediated anterograde transport	1	0	Dync1h1
R-HSA-1839124	FGFR1 mutant receptor activation	1	1	Erlin2
R-HSA-446219	Synthesis of substrates in N-glycan biosythesis	1	0	Mpi
R-HSA-72737	Cap-dependent Translation Initiation	1	0	Rps9
R-HSA-72613	Eukaryotic Translation Initiation	1	0	Rps9
R-HSA-168273	Influenza Viral RNA Transcription and Replication	1	1	Rps9
R-HSA-9010553	Regulation of expression of SLITs and ROBOs	1	0	Rps9
R-HSA-983712	Ion channel transport	1	0	Casq2
R-HSA-418346	Platelet homeostasis	1	0	Cyct
R-HSA-2151201	Transcriptional activation of mitochondrial biogenesis	1	1	Sod2
R-HSA-422356	Regulation of insulin secretion	1	1	Cd36
R-HSA-446193	Biosynthesis of the N-glycan precursor (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein	1	0	Mpi
R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	1	0	P4hb
R-HSA-5655302	Signaling by FGFR1 in disease	1	1	Erlin2
R-HSA-2559586	DNA Damage/Telomere Stress Induced Senescence	1	2	Hist1h1b
R-HSA-1236974	ER-Phagosome pathway	1	0	Cd36
R-HSA-6805567	Keratinization	1	0	Krt10
R-HSA-3371556	Cellular response to heat stress	1	0	Cryab
R-HSA-2555396	Mitotic Metaphase and Anaphase	1	0	Dync1h1
R-HSA-1236975	Antigen processing-Cross presentation	1	0	Cd36
R-HSA-1226099	Signaling by FGFR in disease	1	1	Erlin2
R-HSA-163685	Integration of energy metabolism	1	1	Cd36
R-HSA-5689880	Ub-specific processing proteases	1	1	Vdac3
R-HSA-5632684	Hedgehog 'on' state	1	0	Rdx
R-HSA-5619115	Disorders of transmembrane transporters	1	0	Erlin2
R-HSA-196849	Metabolism of water-soluble vitamins and cofactors	1	0	Mccc2
R-HSA-168255	Influenza Life Cycle	1	2	Rps9
R-HSA-5673001	RAF/MAP kinase cascade	1	0	Vcl
R-HSA-375276	Peptide ligand-binding receptors	1	0	C3
R-HSA-199977	ER to Golgi Anterograde Transport	1	0	Dync1h1
R-HSA-1483206	Glycerophospholipid biosynthesis	1	0	Gpd1
R-HSA-168254	Influenza Infection	1	3	Rps9
R-HSA-948021	Transport to the Golgi and subsequent modification	1	0	Dync1h1
R-HSA-5684996	MAPK1/MAPK3 signaling	1	0	Vcl
R-HSA-75153	Apoptotic execution phase	1	4	Hist1h1b
R-HSA-2980736	Peptide hormone metabolism	1	1	Ctsd
R-HSA-69620	Cell Cycle Checkpoints	1	2	Dync1h1
R-HSA-400253	Circadian Clock	1	2	Dbt
R-HSA-166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	1	1	Cd36
R-HSA-168188	Toll Like Receptor TLR6:TLR2 Cascade	1	1	Cd36
R-HSA-168179	Toll Like Receptor TLR1:TLR2 Cascade	1	1	Cd36
R-HSA-181438	Toll Like Receptor 2 (TLR2) Cascade	1	1	Cd36
R-HSA-376176	Signaling by ROBO receptors	1	0	Rps9
R-HSA-196854	Metabolism of vitamins and cofactors	1	0	Mccc2
R-HSA-198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	1	7	C3
R-HSA-9607240	FLT3 Signaling	1	1	Vcl
R-HSA-983169	Class I MHC mediated antigen processing & presentation	1	0	Cd36
R-HSA-166016	Toll Like Receptor 4 (TLR4) Cascade	1	2	Cd36
R-HSA-72766	Translation	1	0	Rps9
R-HSA-2559583	Cellular Senescence	1	2	Hist1h1b
R-HSA-162909	Host Interactions of HIV factors	1	0	Slc25a4

R-HSA-1483257	Phospholipid metabolism	1	2	Gpd1
R-HSA-418555	G alpha (s) signalling events	1	0	Cyct
R-HSA-168898	Toll-like Receptor Cascades	1	2	Cd36
R-HSA-5683057	MAPK family signaling cascades	1	1	Vcl
R-HSA-5688426	Deubiquitination	1	1	Vdac3
R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	1	0	C3
R-HSA-425407	SLC-mediated transmembrane transport	1	0	Slc25a4
R-HSA-109581	Apoptosis	1	5	Hist1h1b
R-HSA-5357801	Programmed Cell Death	1	5	Hist1h1b
R-HSA-449836	Other interleukin signaling	1	1	Vcl
R-HSA-162906	HIV Infection	1	2	Slc25a4
R-HSA-195258	RHO GTPase Effectors	1	3	Dync1h1
R-HSA-500792	GPCR ligand binding	1	0	C3
R-HSA-418594	G alpha (i) signalling events	1	1	C3
R-HSA-194315	Signaling by Rho GTPases	1	3	Dync1h1
R-HSA-201681	TCF dependent signaling in response to WNT	1	3	Dbt
R-HSA-195721	Signaling by WNT	1	3	Dbt
R-HSA-169131	Inhibition of PKR	0	2	
R-HSA-194306	Neurophilin interactions with VEGF and VEGFR	0	1	
R-HSA-195399	VEGF binds to VEGFR leading to receptor dimerization	0	1	
R-HSA-194313	VEGF ligand-receptor interactions	0	1	
R-HSA-193634	Axonal growth inhibition (RHOA activation)	0	1	
R-HSA-193697	p75NTR regulates axonogenesis	0	1	
R-HSA-111457	Release of apoptotic factors from the mitochondria	0	1	
R-HSA-416700	Other semaphorin interactions	0	1	
R-HSA-189451	Heme biosynthesis	0	1	
R-HSA-1368071	NR1D1 (REV-ERBA) represses gene expression	0	2	
R-HSA-1362409	Mitochondrial iron-sulfur cluster biogenesis	0	2	
R-HSA-1660502	PIPs transport between early and late endosome membranes	0	2	
R-HSA-1660537	PIPs transport between early endosome and Golgi membranes	0	2	
R-HSA-1660508	PIPs transport between late endosome and Golgi membranes	0	2	
R-HSA-189445	Metabolism of porphyrins	0	1	
R-HSA-171306	Packaging Of Telomere Ends	0	2	
R-HSA-75892	Platelet Adhesion to exposed collagen	0	2	
R-HSA-399954	Sema3A PAK dependent Axon repulsion	0	1	
R-HSA-446343	Localization of the PINCH-ILK-PARVIN complex to focal adhesions	0	1	
R-HSA-168276	NS1 Mediated Effects on Host Pathways	0	2	
R-HSA-390450	Folding of actin by CCT/TriC	0	2	
R-HSA-168316	Assembly of Viral Components at the Budding Site	0	1	
R-HSA-446388	Regulation of cytoskeletal remodeling and cell spreading by IPP complex components	0	1	
R-HSA-5627117	RHO GTPases Activate ROCKs	0	1	
R-HSA-418217	G beta:gamma signalling through PLC beta	0	1	
R-HSA-8983711	OAS antiviral response	0	1	
R-HSA-8866907	Activation of the TFAP2 (AP-2) family of transcription factors	0	1	
R-HSA-168253	Host Interactions with Influenza Factors	0	2	
R-HSA-168268	Virus Assembly and Release	0	1	
R-HSA-171286	Synthesis and processing of ENV and VPU	0	2	
R-HSA-918233	TRAF3-dependent IRF activation pathway	0	1	
R-HSA-9027277	Erythropoietin activates Phospholipase C gamma (PLCG)	0	1	
R-HSA-434316	Fatty Acids bound to GPR40 (FFAR1) regulate insulin secretion	0	1	

R-HSA-198745	**Signalling to STAT3**	**0**	*1*	
R-HSA-8875791	**MET activates STAT3**	**0**	*1*	
R-HSA-8847453	**Synthesis of PIPs in the nucleus**	**0**	*1*	
R-HSA-418990	**Adherens junctions interactions**	**0**	*1*	
R-HSA-5205685	**Pink/Parkin Mediated Mitophagy**	**0**	*2*	
R-HSA-264870	**Caspase-mediated cleavage of cytoskeletal proteins**	**0**	*1*	
R-HSA-933541	**TRAF6 mediated IRF7 activation**	**0**	*1*	
R-HSA-3134973	**LRR FLII-interacting protein 1 (LRRFIP1) activates type I IFN production**	**0**	*2*	
R-HSA-351906	**Apoptotic cleavage of cell adhesion proteins**	**0**	*2*	
R-HSA-9028335	**Activated NTRK2 signals through PI3K**	**0**	*1*	
R-HSA-389958	**Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding**	**0**	*2*	
R-HSA-372708	**p130Cas linkage to MAPK signaling for integrins**	**0**	*1*	
R-HSA-1660516	**Synthesis of PIPs at the early endosome membrane**	**0**	*2*	
R-HSA-1250342	**PI3K events in ERBB4 signaling**	**0**	*1*	
R-HSA-1483248	**Synthesis of PIPs at the ER membrane**	**0**	*2*	
R-HSA-1660517	**Synthesis of PIPs at the late endosome membrane**	**0**	*2*	
R-HSA-1855204	**Synthesis of IP3 and IP4 in the cytosol**	**0**	*1*	
R-HSA-390247	**Beta-oxidation of very long chain fatty acids**	**0**	*1*	
R-HSA-1963642	**PI3K events in ERBB2 signaling**	**0**	*1*	
R-HSA-8851907	**MET activates PI3K/AKT signaling**	**0**	*1*	
R-HSA-399997	**Acetylcholine regulates insulin secretion**	**0**	*1*	
R-HSA-9027276	**Erythropoietin activates Phosphoinositide-3-kinase (PI3K)**	**0**	*1*	
R-HSA-8849471	**PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases**	**0**	*2*	
R-HSA-2892247	**POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation**	**0**	*1*	
R-HSA-982772	**Growth hormone receptor signaling**	**0**	*2*	
R-HSA-8849474	**PTK6 Activates STAT3**	**0**	*1*	
R-HSA-5690714	**CD22 mediated BCR regulation**	**0**	*2*	
R-HSA-5621480	**Dectin-2 family**	**0**	*1*	
R-HSA-418890	**Role of second messengers in netrin-1 signaling**	**0**	*1*	
R-HSA-111471	**Apoptotic factor-mediated response**	**0**	*1*	
R-HSA-175474	**Assembly Of The HIV Virion**	**0**	*2*	
R-HSA-9022692	**Regulation of MECP2 expression and activity**	**0**	*1*	
R-HSA-198203	**PI3K/AKT activation**	**0**	*1*	
R-HSA-2586552	**Signaling by Leptin**	**0**	*1*	
R-HSA-8853334	**Signaling by FGFR3 fusions in cancer**	**0**	*1*	
R-HSA-8985947	**Interleukin-9 signaling**	**0**	*1*	
R-HSA-389357	**CD28 dependent PI3K/Akt signaling**	**0**	*1*	
R-HSA-8876725	**Protein methylation**	**0**	*2*	
R-HSA-5205647	**Mitophagy**	**0**	*2*	
R-HSA-1660514	**Synthesis of PIPs at the Golgi membrane**	**0**	*2*	
R-HSA-392451	**G beta:gamma signalling through PI3Kgamma**	**0**	*1*	
R-HSA-5218921	**VEGFR2 mediated cell proliferation**	**0**	*1*	
R-HSA-421270	**Cell-cell junction organization**	**0**	*1*	
R-HSA-9603381	**Activated NTRK3 signals through PI3K**	**0**	*1*	
R-HSA-450408	**AUF1 (hnRNP D0) binds and destabilizes mRNA**	**0**	*1*	
R-HSA-3000170	**Syndecan interactions**	**0**	*2*	
R-HSA-180292	**GAB1 signalosome**	**0**	*1*	
R-HSA-1266695	**Interleukin-7 signaling**	**0**	*1*	
R-HSA-390466	**Chaperonin-mediated protein folding**	**0**	*2*	
R-HSA-109704	**PI3K Cascade**	**0**	*1*	
R-HSA-6783783	**Interleukin-10 signaling**	**0**	*1*	

R-HSA-5655291	**Signaling by FGFR4 in disease**	**0**	***1***	
R-HSA-4641262	**Disassembly of the destruction complex and recruitment of AXIN to the membrane**	**0**	***2***	
R-HSA-5663213	**RHO GTPases Activate WASPs and WAVEs**	**0**	***1***	
R-HSA-157579	**Telomere Maintenance**	**0**	***2***	
R-HSA-1483249	**Inositol phosphate metabolism**	**0**	***1***	
R-HSA-8984722	**Interleukin-35 Signalling**	**0**	***2***	
R-HSA-9006335	**Signaling by Erythropoietin**	**0**	***1***	
R-HSA-5654710	**PI-3K cascade:FGFR3**	**0**	***1***	
R-HSA-5654720	**PI-3K cascade:FGFR4**	**0**	***1***	
R-HSA-391251	**Protein folding**	**0**	***2***	
R-HSA-1839117	**Signaling by cytosolic FGFR1 fusion mutants**	**0**	***1***	
R-HSA-5654689	**PI-3K cascade:FGFR1**	**0**	***1***	
R-HSA-390918	**Peroxisomal lipid metabolism**	**0**	***1***	
R-HSA-5654695	**PI-3K cascade:FGFR2**	**0**	***1***	
R-HSA-9020956	**Interleukin-27 signaling**	**0**	***2***	
R-HSA-373755	**Semaphorin interactions**	**0**	***2***	
R-HSA-2219530	**Constitutive Signaling by Aberrant PI3K in Cancer**	**0**	***1***	
R-HSA-8854691	**Interleukin-20 family signaling**	**0**	***1***	
R-HSA-418885	**DCC mediated attractive signaling**	**0**	***1***	
R-HSA-112399	**IRS-mediated signalling**	**0**	***1***	
R-HSA-5655332	**Signaling by FGFR3 in disease**	**0**	***1***	
R-HSA-8853338	**Signaling by FGFR3 point mutants in cancer**	**0**	***1***	
R-HSA-5625886	**Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3**	**0**	***1***	
R-HSA-2028269	**Signaling by Hippo**	**0**	***1***	
R-HSA-73886	**Chromosome Maintenance**	**0**	***2***	
R-HSA-9008059	**Interleukin-37 signaling**	**0**	***1***	
R-HSA-2428928	**IRS-related events triggered by IGF1R**	**0**	***1***	
R-HSA-2730905	**Role of LAT2/NTAL/LAB on calcium mobilization**	**0**	***1***	
R-HSA-5250924	**B-WICH complex positively regulates rRNA expression**	**0**	***2***	
R-HSA-2428924	**IGF1R signaling cascade**	**0**	***1***	
R-HSA-4086398	**Ca2+ pathway**	**0**	***1***	
R-HSA-2404192	**Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)**	**0**	***1***	
R-HSA-2871809	**FCERI mediated Ca+2 mobilization**	**0**	***1***	
R-HSA-5655253	**Signaling by FGFR2 in disease**	**0**	***1***	
R-HSA-1660499	**Synthesis of PIPs at the plasma membrane**	**0**	***2***	
R-HSA-3928662	**EPHB-mediated forward signaling**	**0**	***2***	
R-HSA-8940973	**RUNX2 regulates osteoblast differentiation**	**0**	***2***	
R-HSA-8874211	**CREB3 factors activate genes**	**0**	***1***	
R-HSA-264876	**Insulin processing**	**0**	***1***	
R-HSA-2424491	**DAP12 signaling**	**0**	***1***	
R-HSA-114604	**GPVI-mediated activation cascade**	**0**	***2***	
R-HSA-452723	**Transcriptional regulation of pluripotent stem cells**	**0**	***1***	
R-HSA-1632852	**Macroautophagy**	**0**	***2***	
R-HSA-1489509	**DAG and IP3 signaling**	**0**	***1***	
R-HSA-397795	**G-protein beta:gamma signalling**	**0**	***1***	
R-HSA-1236382	**Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants**	**0**	***1***	
R-HSA-5637815	**Signaling by Ligand-Responsive EGFR Variants in Cancer**	**0**	***1***	
R-HSA-74751	**Insulin receptor signalling cascade**	**0**	***1***	
R-HSA-432722	**Golgi Associated Vesicle Biogenesis**	**0**	***1***	
R-HSA-912446	**Meiotic recombination**	**0**	***1***	
R-HSA-2172127	**DAP12 interactions**	**0**	***1***	
R-HSA-5625740	**RHO GTPases activate PKNs**	**0**	***1***	

R-HSA-8856828	Clathrin-mediated endocytosis	0	1	
R-HSA-202433	Generation of second messenger molecules	0	1	
R-HSA-182971	EGFR downregulation	0	1	
R-HSA-9034015	Signaling by NTRK3 (TRKC)	0	1	
R-HSA-112043	PLC beta mediated events	0	1	
R-HSA-936440	Negative regulators of DDX58/IFIH1 signaling	0	1	
R-HSA-389356	CD28 co-stimulation	0	1	
R-HSA-109606	Intrinsic Pathway for Apoptosis	0	1	
R-HSA-112040	G-protein mediated events	0	1	
R-HSA-2029485	Role of phospholipids in phagocytosis	0	1	
R-HSA-8941326	RUNX2 regulates bone development	0	2	
R-HSA-983695	Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	0	2	
R-HSA-6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	0	1	
R-HSA-74752	Signaling by Insulin receptor	0	1	
R-HSA-1433557	Signaling by SCF-KIT	0	1	
R-HSA-8857538	PTK6 promotes HIF1A stabilization	0	1	
R-HSA-5250913	Positive epigenetic regulation of rRNA expression	0	2	
R-HSA-5674400	Constitutive Signaling by AKT1 E17K in Cancer	0	1	
R-HSA-8983432	Interleukin-15 signaling	0	2	
R-HSA-186763	Downstream signal transduction	0	2	
R-HSA-199418	Negative regulation of the PI3K/AKT network	0	1	
R-HSA-6811555	PI5P Regulates TP53 Acetylation	0	1	
R-HSA-354192	Integrin alphaIIb beta3 signaling	0	2	
R-HSA-9006921	Integrin signaling	0	2	
R-HSA-1483255	PI Metabolism	0	2	
R-HSA-202424	Downstream TCR signaling	0	1	
R-HSA-9006115	Signaling by NTRK2 (TRKB)	0	1	
R-HSA-76009	Platelet Aggregation (Plug Formation)	0	2	
R-HSA-216083	Integrin cell surface interactions	0	7	
R-HSA-8953750	Transcriptional Regulation by E2F6	0	1	
R-HSA-447043	Neurofascin interactions	0	1	
R-HSA-186797	Signaling by PDGF	0	2	
R-HSA-3108214	SUMOylation of DNA damage response and repair proteins	0	1	
R-HSA-1221632	Meiotic synapsis	0	4	
R-HSA-6804758	Regulation of TP53 Activity through Acetylation	0	1	
R-HSA-5637810	Constitutive Signaling by EGFRvIII	0	1	
R-HSA-5637812	Signaling by EGFRvIII in Cancer	0	1	
R-HSA-388841	Costimulation by the CD28 family	0	1	
R-HSA-2029482	Regulation of actin dynamics for phagocytic cup formation	0	2	
R-HSA-909733	Interferon alpha/beta signaling	0	1	
R-HSA-5654708	Downstream signaling of activated FGFR3	0	1	
R-HSA-1169410	Antiviral mechanism by IFN-stimulated genes	0	1	
R-HSA-5654716	Downstream signaling of activated FGFR4	0	1	
R-HSA-1834949	Cytosolic sensors of pathogen-associated DNA	0	2	
R-HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	0	1	
R-HSA-1643713	Signaling by EGFR in Cancer	0	1	
R-HSA-5654696	Downstream signaling of activated FGFR2	0	1	
R-HSA-5654687	Downstream signaling of activated FGFR1	0	1	
R-HSA-1227986	Signaling by ERBB2	0	1	
R-HSA-451927	Interleukin-2 family signaling	0	2	
R-HSA-5607764	CLEC7A (Dectin-1) signaling	0	2	
R-HSA-111465	Apoptotic cleavage of cellular proteins	0	4	
R-HSA-9009391	Extra-nuclear estrogen signaling	0	1	

R-HSA-8866910	**TFAP2 (AP-2) family regulates transcription of growth factors and their receptors**	**0**	***3***	
R-HSA-381038	**XBP1(S) activates chaperone genes**	**0**	***1***	
R-HSA-162599	**Late Phase of HIV Life Cycle**	**0**	***2***	
R-HSA-2219528	**PI3K/AKT Signaling in Cancer**	**0**	***1***	
R-HSA-3769402	**Deactivation of the beta-catenin transactivating complex**	**0**	***2***	
R-HSA-5687128	**MAPK6/MAPK4 signaling**	**0**	***1***	
R-HSA-5693606	**DNA Double Strand Break Response**	**0**	***1***	
R-HSA-8986944	**Transcriptional Regulation by MECP2**	**0**	***1***	
R-HSA-983705	**Signaling by the B Cell Receptor (BCR)**	**0**	***4***	
R-HSA-381070	**IRE1alpha activates chaperones**	**0**	***1***	
R-HSA-162587	**HIV Life Cycle**	**0**	***2***	
R-HSA-187037	**Signaling by NTRK1 (TRKA)**	**0**	***2***	
R-HSA-168928	**DDX58/IFIH1-mediated induction of interferon-alpha/beta**	**0**	***2***	
R-HSA-2029480	**Fcgamma receptor (FCGR) dependent phagocytosis**	**0**	***2***	
R-HSA-1236394	**Signaling by ERBB4**	**0**	***1***	
R-HSA-373752	**Netrin-1 signaling**	**0**	***2***	
R-HSA-195253	**Degradation of beta-catenin by the destruction complex**	**0**	***2***	
R-HSA-3858494	**Beta-catenin independent WNT signaling**	**0**	***1***	
R-HSA-111885	**Opioid Signalling**	**0**	***1***	
R-HSA-4090294	**SUMOylation of intracellular receptors**	**0**	***3***	
R-HSA-193704	**p75 NTR receptor-mediated signalling**	**0**	***1***	
R-HSA-5654743	**Signaling by FGFR4**	**0**	***1***	
R-HSA-202403	**TCR signaling**	**0**	***1***	
R-HSA-5654741	**Signaling by FGFR3**	**0**	***1***	
R-HSA-432720	**Lysosome Vesicle Biogenesis**	**0**	***2***	
R-HSA-5654736	**Signaling by FGFR1**	**0**	***1***	
R-HSA-4551638	**SUMOylation of chromatin organization proteins**	**0**	***2***	
R-HSA-450531	**Regulation of mRNA stability by proteins that bind AU-rich elements**	**0**	***1***	
R-HSA-9612973	**Autophagy**	**0**	***2***	
R-HSA-212165	**Epigenetic regulation of gene expression**	**0**	***2***	
R-HSA-3928664	**Ephrin signaling**	**0**	***1***	
R-HSA-1500620	**Meiosis**	**0**	***4***	
R-HSA-177929	**Signaling by EGFR**	**0**	***1***	
R-HSA-201722	**Formation of the beta-catenin:TCF transactivating complex**	**0**	***2***	
R-HSA-5654738	**Signaling by FGFR2**	**0**	***1***	
R-HSA-1474165	**Reproduction**	**0**	***4***	
R-HSA-446652	**Interleukin-1 family signaling**	**0**	***1***	
R-HSA-4420097	**VEGFA-VEGFR2 Pathway**	**0**	***4***	
R-HSA-5357905	**Regulation of TNFR1 signaling**	**0**	***1***	
R-HSA-190236	**Signaling by FGFR**	**0**	***1***	
R-HSA-8878166	**Transcriptional regulation by RUNX2**	**0**	***2***	
R-HSA-194138	**Signaling by VEGF**	**0**	***5***	
R-HSA-2454202	**Fc epsilon receptor (FCERI) signaling**	**0**	***3***	
R-HSA-5621481	**C-type lectin receptors (CLRs)**	**0**	***2***	
R-HSA-199992	**trans-Golgi Network Vesicle Budding**	**0**	***3***	
R-HSA-75893	**TNF signaling**	**0**	***1***	
R-HSA-166520	**Signaling by NTRKs**	**0**	***2***	
R-HSA-5693532	**DNA Double-Strand Break Repair**	**0**	***1***	
R-HSA-5619507	**Activation of HOX genes during differentiation**	**0**	***2***	
R-HSA-5617472	**Activation of anterior HOX genes in hindbrain development during early embryogenesis**	**0**	***2***	
R-HSA-8848021	**Signaling by PTK6**	**0**	***4***	
R-HSA-9006927	**Signaling by Non-Receptor Tyrosine Kinases**	**0**	***4***	

R-HSA-2682334	**EPH-Ephrin signaling**	**0**	***3***	
R-HSA-381119	**Unfolded Protein Response (UPR)**	**0**	***2***	
R-HSA-913531	**Interferon Signaling**	**0**	***2***	
R-HSA-1257604	**PIP3 activates AKT signaling**	**0**	***1***	
R-HSA-5633007	**Regulation of TP53 Activity**	**0**	***1***	
R-HSA-73887	**Death Receptor Signalling**	**0**	***2***	
R-HSA-73894	**DNA Repair**	**0**	***1***	
R-HSA-9006925	**Intracellular signaling by second messengers**	**0**	***1***	
R-HSA-3108232	**SUMO E3 ligases SUMOylate target proteins**	**0**	***5***	
R-HSA-2990846	**SUMOylation**	**0**	***5***	
R-HSA-3700989	**Transcriptional Regulation by TP53**	**0**	***1***	