8

14

16

18

24

- 1 The effect of micronutrient supplementation on growth and hepatic
- 2 metabolism in diploid and triploid Atlantic salmon (Salmo salar) parr
- 3 fed a low marine ingredient diet
- John F. Taylor a\*, Luisa M. Vera a, Christian De Santis a, Erik-Jan Lock b, Marit Espe b,
- 6 Kaja H. Skjærven b, Daniel Leeming c, Jorge del Pozo d, Jose Mota-Velasco e, Herve
- 7 Migaud a, Kristin Hamre b, Douglas R. Tocher a
- 9 a Institute of Aquaculture, University of Stirling, Stirling, FK9 4LA, UK
- 10 b Institute of Marine Research, PO box 1870 Nordnes, 5817 Bergen, Norway
- <sup>c</sup> BioMar Ltd., Grangemouth, FK3 8UL, UK
- <sup>d</sup> The Royal (Dick) School of Veterinary Studies, Edinburgh, EH25 9RG, UK
- <sup>e</sup> Hendrix Genetics, Landcatch Natural Selection Ltd., Lochgilphead, PA31 8PE, UK
- 15 **Running Title:** Dietary micronutrient supplementation in Atlantic salmon
- ms. has 31 pg.s, 4 figures, 9 tables, 4 suppl. files
- 19 Corresponding Author:
- 20 Dr John F. Taylor
- 21 Institute of Aquaculture, University of Stirling, Stirling, FK9 4LA, UK
- 22 Tel: +44-01786 467929 ; Fax: +44-01768 472133
- 23 j.f.taylor@stir.ac.uk

Accepted refereed manuscript of:

Taylor JF, Vera LM, De Santis C, Lock E, Espe M, Skjaerven KH, Leeming D, Del Pozo J, Mota-Velasco J, Migaud H, Hamre K & Tocher DR (2019) The effect of micronutrient supplementation on growth and hepatic metabolism in diploid and triploid Atlantic salmon (Salmo salar) parr fed a low marine ingredient diet. *Comparative Biochemistry and Physiology. Part B, Biochemistry and Molecular Biology*, 227, pp. 106-121.

DOI: https://doi.org/10.1016/j.cbpb.2018.10.004

© 2018, Elsevier. Licensed under the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International <a href="http://creativecommons.org/licenses/by-nc-nd/4.0/">http://creativecommons.org/licenses/by-nc-nd/4.0/</a>

#### **Abstract**

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

The effects of low marine ingredient diets supplemented with graded levels (L1, L2, L3) of a micronutrient package (NP) on growth and metabolic responses were studied in diploid and triploid salmon parr. Diploids fed L2 showed significantly improved growth and reduced liver, hepatic steatosis, and viscerosomatic indices, while fish fed L3 showed suppressed growth rate 14 weeks post feeding. In contrast, dietary NP level had no effect on triploid performance. Whole body mineral composition, with exception of copper, did not differ between diet or ploidy. Whole fish total AAs and N-metabolites showed no variation by diet or ploidy. Free circulating AAs and white muscle N-metabolites were higher in triploids than diploids, while branch-chained amino acids were higher in diploids than triploids. Diploids had higher whole body  $\alpha$ -tocopherol and hepatic vitamins  $K_1$  and  $K_2$  than triploids. Increased tissue B-vitamins for niacin and whole-body folate with dietary NP supplementation were observed in diploids but not triploids, while whole body riboflavin was higher in diploids than triploids. Hepatic transcriptome profiles showed that diploids fed diet L2 was more similar to that observed in triploids fed diet L3. In particular, sterol biosynthesis pathways were down-regulated, whereas cytochrome P450 metabolism was up-regulated. One-carbon metabolism was also affected by increasing levels of supplementation in both ploidies. Collectively, results suggested that, for optimised growth and liver function, micronutrient levels be supplemented above current National Research Council (2011) recommendations for Atlantic salmon when fed low marine ingredient diets. The study also suggested differences in nutritional requirements between ploidy.

46 47

**Keywords**: Atlantic salmon; micronutrient; vegetable; ingredients; nutrition

#### 1. Introduction

All animals, including fish, have specific macro- and micronutrient requirements for optimal growth, development and health (Halver and Hardy, 2002). Whereas macro-nutrient requirements (e.g. protein and lipid) have been extensively studied in Atlantic salmon (*Salmo salar* L.) (e.g. Hillestad and Johnsen, 1994; Einen and Roem, 1997; Grisdale-Helland et al., 2013), micronutrients (e.g. vitamins and minerals) have been less well researched and only a few have been the subject of empirical studies (see Waagbø, 2010; NRC, 2011; Hansen et al., 2015; Hamre, et al., 2016; Hemre, et al., 2016). This lack of empirically derived data in salmon for many micronutrients has not prevented the development of a large and highly successful salmon farming industry worldwide (Kontali, 2015). Traditionally, many of the micronutrients were provided by raw materials, such as fishmeal (FM) and fish oil (FO) (NRC, 2011). However, FM and FO are finite, on an annual basis, and limited resources (Shepherd and Jackson, 2013; IFFO, 2014) and, with steadily increasing price, their use in fish feed has become commercially less viable (Tacon and Metian, 2008; Jackson and Shepherd, 2012).

Plant products have increasingly replaced FM and FO in salmon feeds (Gatlin et al., 2007; Hardy et al., 2010; Turchini et al., 2011). For example, in Norwegian salmon feeds from 1990 to 2013, the proportions of marine ingredients decreased from almost 90 % to under 30 %, with plant ingredients increasing from very low levels to around 67 % of feeds (Ytrestøyl et al., 2015). This has been a progressive change as shown by the levels in 2000 (65 % marine and 33 % plant) and 2010 (42 % marine and 56 % plant). Therefore today, commercially available feeds for salmon are predominantly formulated with plant ingredients, with consequent changes to the nutritional profile (Sissener et al., 2013). While it seems that salmon can tolerate and grow well on diets with very low levels of marine ingredients, such that they can be considered as net producers of marine protein and oil (Bendiksen et al., 2011; Crampton et al., 2010; Sanden et al., 2011), in some cases high dietary levels of plant proteins and vegetable oils (VO) can result in lower weight gain, increased adiposity and lower feed efficiency in salmon, even when requirements for all essential nutrients are met (Torstensen et al., 2008, 2011; Collins et al., 2013). Furthermore, replacement of FM and FO with plant-based alternatives has been shown to have a wide range of metabolic effects that can also impact on fish development and health, as well as nutritional quality of the final product (Montero and Izquierdo, 2011; Rosenlund et al., 2011; Oliva-Teles, 2012; Pohlenz and Gatlin, 2014). There are now concerns that, with these major changes in raw materials, low marine / high plant feeds will affect not only the composition and contents of nutrients, but also the bioavailability and, combined with the limited knowledge of micronutrient requirements for Atlantic salmon, this might impact growth performance and health of the fish (Bell and Waagbø, 2008; Hemre et al., 2009; Torstensen and Tocher, 2011; Tocher and Glencross, 2015; Shepherd et al., 2017). Therefore, knowledge of practical nutrient requirements of Atlantic salmon when fed plant-based diets is pivotal (Hansen et al., 2015).

82

83

84

85

86

87

88

89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

105

106

107

108

109

110

111

112

113

114

115

In this respect, there is growing interest within the Scottish and Norwegian farming sector to consider commercial implementation of triploid Atlantic salmon within certain farming localities. Triploid salmons are fish carrying a chromosomal abnormality (i.e. an extra set of chromosomes) that can be artificially induced by hydrostatic pressure, thermal or chemical shock (Benfey, 2016). As a result of their chromosomal state, triploids are sterile, hence offering potential advantages for farming such as reproductive containment of escapees and potential for faster growth with subsequent reduction of production cycle length (Benfey, 2016). However, specific dietary requirement trials in triploids are limited to date, although it was previously suggested that differences between ploidy might exist (Fjelldal & Hansen, 2010). Apparent digestibility coefficients for dry matter, protein, or lipid do not appear to differ between ploidy (Burke et al., 2010; Tibbetts et al., 2013), whereas energy and nitrogen retention efficiencies may be higher in triploids than diploids (Burke et al., 2010). Evidence exists to hypothesise that triploids may have higher dietary requirement for certain macro-minerals such as phosphorous, which must be met to prevent the onset of skeletal deformities (Fjelldal et al., 2015). In addition, a higher requirement for the essential amino acid histidine was also reported to prevent cataract formation in post-smolts and, possibly, to improve feed conversion efficiency (Taylor et al., 2015). It stands to reason that, similar to phosphorus and histidine, other dietary requirements may vary between ploidy, especially in respect to nutrient profile alterations in low marine ingredients diets. However, few studies have examined triploid performance in response to a diet with low levels of FM or FO (Ganga et al., 2015), or how dietary micronutrient supplementation would affect growth and metabolism. It is therefore essential to establish the dietary requirements of triploid Atlantic salmon, and ensure their performance is at least equal or better than their diploid counterparts under a dietary regime with low marine ingredients in order to establish their viability for integration in commercial operations.

The present study investigated the effects of feeding graded levels of a nutrient package (NP) containing 24 nutrients in total (NRC, 2011 minimum nutrient recommendations for Atlantic salmon modified based on the studies by Hamre et al., 2016; Hemre et al. 2016) supplemented to feeds formulated with low levels of marine ingredients in diploid and triploid Atlantic salmon from parr until smolt. Specifically, fish were fed a diet supplemented with one

of three inclusion levels of the NP (L1, 100 %; L2, 200 % and L3, 400% NP) and the effects on growth performance, biochemical composition, liver histology, hepatic gene expression (transcriptome) and smoltification efficiency determined.

118119

120121

122

123

124

125

126

127

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

116

117

### 2. Methods and Materials

2.1 Fish Stock

All experimental procedures and husbandry practices were conducted in compliance with the Animals Scientific Procedures Act 1986 (Home Office Code of Practice) in accordance with EU regulation (EC Directive 2010/63/EU) and approved by the Animal Ethics and Welfare Committee of the University of Stirling. All fish were monitored daily by the Named Animal Care and Welfare Officer (NACWO).

The feeding trial was carried out at the Niall Bromage Freshwater Research Facility, University of Stirling (Buckieburn, Scotland) for just over a year from March one year to April the following year using a mixed population of fish obtained from a commercial Atlantic salmon stock (Landcatch Natural Selection, Ormsary, UK). Briefly, ova and milt were collected from a total of 20 unrelated dams and 5 sires. Per dam, ova were fertilised as one batch and a 1 L sub-sample was removed to induce triploidy using hydrostatic pressure shock (9500 PSI applied 300 degree minutes post-fertilisation at 8 °C for a duration of 6.25 min). This procedure was repeated for each dam x sire cross creating 20 diploid incubators and 20 triploid incubators, reared in constant darkness at  $8.0 \pm 0.5$  °C. Eyed ova (380 °days post fertilisation) were shipped to University of Stirling facilities and ova were pooled per ploidy and reared in 6 x 250 L tanks in complete darkness until first feeding (~ 850 °dpf). At first feeding, diploids were fed a standard commercial salmon fry feed (Inicio Plus, BioMar, UK; 13.0g kg<sup>-1</sup> total phosphorus) whereas triploids were fed the same standard commercial formulation but with a boosted phosphorous level (16.7g kg<sup>-1</sup> total phosphorus) based on data obtained in previous studies on triploid salmon (Smedley et al., 2018). All other dietary components were comparable between starter feeds. Fry were reared under constant light, and feed was supplied throughout the 24 h by belt feeders according to manufacturer's tables (specific feeding rate [SFR], 2-3 % body weight day<sup>-1</sup>).

To verify ploidy status, smears were prepared according to Woznicki & Kuzminski, (2002) from blood collected following the caudal peduncle from euthanised fish at 5 g (100 / ploidy). After air drying, slides were fixed in 100 % methanol and then placed into Giemsa stain for 10 min. Erythrocyte length and diameter were measured at 100× magnification using image capture software (Image-Pro Premier, MediaCybernetics, Rockville, USA). A total of 20

randomly chosen nuclei per slide were measured to the nearest 0.01  $\mu m$ . Diploid control groups had significantly smaller erythrocyte nuclear lengths with no overlaps with the pressure shock triploid groups (2N 6.8–7.7  $\mu m$ ; 3N 9.0–10.2  $\mu m$ ) confirming that the majority of fish subjected to hydrostatic pressure shock were likely to be triploids. Cumulative mortality from first-feeding to start of the feeding trial was  $2.8 \pm 0.02$  % for diploids and  $3.5 \pm 0.01$  % for triploids.

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

150

151

152

153

154

# 2.2 Feeding Trial

Two groups of Atlantic salmon parr of mean weight 37.5  $\pm$  2.2 g (diploid) and 27.4  $\pm$ 0.7 g (triploid) were stocked into 12 x 1.8 m<sup>3</sup> circular fibreglass tanks (6 tanks / ploidy, n = 1000 / tank). Fish were acclimated to the experimental conditions for 2 weeks before being fed the experimental diets. Duplicate groups were fed low FM / FO diets (= 15% FM / 8% FO) formulated to have identical protein / oil content (480 / 215 g kg<sup>-1</sup> respectively of which 72 / 17 g kg<sup>-1</sup> were of marine origin) and supplemented with a nutrient package (NP) at graded inclusion levels. The NP contained 24 nutrients in total these being; vitamins (A, D<sub>3</sub>, E, K<sub>3</sub>, C, thiamin, riboflavin, B6, B12, niacin, pantothenic acid, folic acid and biotin), minerals (Ca, Co, I, Se, Fe, Mn, Cu and Zn), crystalline amino acids (L-histidine and taurine) and cholesterol. Specifically, the NP was added at three inclusion levels to produce 3 dietary treatments: L1, 100 % NP; L2, 200 % NP; L3, 400 % NP, the assumption being that the 100% NP package should contain 100 % of assumed requirement based on the given requirement levels reported for Atlantic salmon at the time (NRC, 2011) and modified according to an earlier trial as part of the EU-funded ARRAINA project (Hamre et al., 2016). Total and available phosphorus were fixed in all diets at 13.0 and 9.0 g kg<sup>-1</sup> respectively, and magnesium at 1.5 g kg<sup>-1</sup>, and were not part of the NP. Pellet size was adjusted according to fish weight, with a 2 mm pellet fed for 23 weeks and a 3 mm pellet fed for the final 8 weeks. All non-oil ingredients were mixed and pellets produced by extrusion to produce three base pellets that had oil added by vacuum coating. All feeds were produced at the BioMar Tech-Centre (Brande, Denmark). Feed formulations, added micronutrient concentrations within the nutrient package and analysed micronutrient concentration are provided in Tables 1, 2 and 3 respectively, while fatty acid profiles are provided in Supplementary file 1. With the exception of histidine, there were generally positive relationships between added and analysed nutrients in the 2 mm pellet (Table 3). In the 3 mm pellet, vitamin A, vitamin K3, pantothenic and folic acid, vitamin C, iron and manganese deviated from the positive relationship.

Fish were fed continuously during the light period of the light-dark cycle by automatic feeders (Arvotec T2000, Arvotec, Finland) controlled by a PC system. Although feed collection

was not possible due to system constraints, presence of waste feed was ensured each day prior to tank flushing. Specific feeding rates (SFR; % tank biomass per day) were adjusted automatically according to predicted growth and daily temperature. A simulated natural photoperiod (SNP) was applied to produce S1+ smolts, with lighting provided by two 28 W fluorescent daylight bulbs (4000 °K, RS Components, UK) mounted centrally within the tank lid. Water was supplied by an upstream reservoir under flow through conditions (10 L min<sup>-1</sup>), with ambient temperatures decreasing from 15.5 °C (September) to 2.0 °C (February), and increasing to 9 °C by April. Oxygen levels were consistently >8 mg L<sup>-1</sup>.

# 2.3 Sampling Procedures

Fish were sampled for growth at 3, 7, 14 and 31 weeks post application of the experimental feeds. At each time point, 50 fish / tank were anaesthetised (MS222, PHARMAQ, UK), individual weights ( $\pm$  0.1 g) and fork lengths ( $\pm$  1.0 mm) measured, and fish allowed to recover in aerated water before returning to experimental tanks. Sex was not assessed. Fulton's condition factor (K) was calculated using:  $K = (WL^{-3})100$ ; where W is body weight (g) and L is fork length (cm). Weight data were used to calculate specific growth rate (SGR<sub>wt</sub>), and feed conversion rate (FCR) for each sampling period where SGR<sub>wt</sub> was calculated as:  $(e^{g-1})\times100$ , where  $g = (ln(W_f) - ln(W_i)) \times (t_2-t_1)^{-1}$ . Relative Weight gain (RWG) was calculated as (*Wf-Wi*)/W*i* x 100. FCR was calculated as:  $F / (B_f - B_i + B_m)^{-1}$  where F is the feed fed (kg),  $B_f$  is the final biomass (kg),  $B_i$  is the initial biomass (kg), and  $B_m$  is the mortality biomass for the period (kg). Uneaten feed recovery was not feasible for this study and, therefore, FCR provided only a crude estimate of feed conversion.

At the end of the feeding trial (31 weeks), a total of 7 fish / tank were euthanised by an overdose of MS222 and 3 carcasses frozen at -20 °C for whole fish proximate composition analyses. Livers were dissected from the remaining 4 fish / tank (n=8 / diet) and a small sample (~ 100 mg) collected into RNALater® (Sigma, Poole, UK) for transcriptomic analyses, before the liver was divided into two portions. One portion was stored in 10 % neutral buffered formalin prior to histological analyses with the remaining portion snap frozen in liquid nitrogen, then stored at -20 °C prior to fatty acid composition analysis. Finally, further 10 fish / tank were euthanised and viscera (intestines and associated fat deposits without liver or gonad) and livers dissected, individually weighed to calculate viscerosomatic (VSI, %) and hepatosomatic (HSI, %) indices: where VSI was calculated as viscera weight / (body weight – viscera weight) x 100; and HSI as liver weight / (body weight – liver weight) x 100.

Liver and white muscle were dissected after fish were anaesthetised from five fish per tank, divided into two, and used for analysis of vitamins, S-adenosylmethionine (SAM), S-adenosylhomocysteine (SAH) and free amino acids at week 31. Samples were frozen at -30 °C until analysed. In addition, samples of whole fish were collected, minced and analysed for total amino acids and vitamins. Whole fish were pooled into 3 samples of 2 fish (1 per tank/replicate) and homogenised in a blender (Waring Laboratory Science, Winsted, CT, USA) to produce pates, and feeds were ground prior to analyses.

### 2.4 Histological analysis

Formalin-fixed livers from 4 fish per tank (n = 8 / diet) were assessed for micro- and macro-vesicular steatosis by light microscopy of haematoxylin and eosin-stained sections (Gu et al., 2013). Sections were viewed at  $20 \times$  original magnification and scored for presence of vesicles in individual hepatocytes. The term steatosis was applied when clear vacuoles with a diameter greater than 5  $\mu$ m were observed in the hepatocytes, and measurement was achieved using a four-point scoring system (Fig.1; 0 - no vacuolation; 1 - mild vacuolation, < 25 % of hepatocyte area (one small vacuole not displacing the nucleus); 2 - moderate vacuolation, 25-75 % of hepatocyte area (one or more small vacuoles mildly displacing the nucleus); and 3 - severe vacuolation, > 75 % of hepatocyte area (one large vacuole filling the cytoplasm, and displacing the nucleus).

### 2.5 Biochemical analysis of diets, whole fish and liver

Proximate compositions of feeds and whole fish were determined according to standard procedures (AOAC, 2000). Moisture contents were obtained after drying in an oven at 110 °C for 24 h and ash content determined after incineration at 600 °C for 16 h. Crude protein content was measured by determining nitrogen content (N × 6.25) using automated Kjeldahl analysis (Tecator Kjeltec Auto 1030 analyser, Foss, Warrington, U.K), and crude lipid content determined after acid hydrolysis followed by Soxhlet lipid extraction (Tecator Soxtec system 2050 Auto Extraction apparatus, Foss, Warrington, U.K). Total lipid was extracted from liver by homogenisation in chloroform/methanol (2:1, v/v) and content determined gravimetrically (Folch et al., 1957). Fatty acid methyl esters (FAME) were prepared from total lipid by acid-catalysed transesterification at 50 °C for 16 h (Christie, 2003), and FAME extracted and purified as described previously (Tocher and Harvie, 1988). FAME were separated and quantified by gas-liquid chromatography using a Fisons GC-8160 (Thermo Scientific, Milan, Italy) equipped with a 30 m × 0.32 mm i.d. × 0.25 μm ZB-wax column (Phenomenex, Cheshire, UK), on-

column injector and a flame ionisation detector. Data were collected and processed using Chromcard for Windows (version 2.01; Thermoquest Italia S.p.A., Milan, Italy). Individual FAME were identified by comparison to known standards and published data (Tocher and Harvie, 1988). Whole fish samples were hydrolysed in 6M HCL for 22 h before being analysed for total amino acid content and composition by UPLC as described (Espe et al., 2014), while free amino acids and N-metabolites in muscle and liver were analysed after deproteinisation using sulfosalicylic acid, and separated on Biochrome and detected by post-column derivatisation with ninhydrin, as described elsewhere (Espe et al., 2006). Liver, plasma and muscle samples were analysed for SAM and SAH after extraction using 4 % per chloric acid and separated on HPLC as described in detail previously (Espe et al., 2008). The B-vitamins, biotin, niacin, folate, pantothenic acid and cobalamin were all determined by microbiological methods (Feldsine et al., 2002; Mæland et al., 2000). Other B-vitamins were determined by HPLC; thiamine (CEN, 2003), vitamin B6 (CEN, 2006) and riboflavin (Brønstad et al., 2002). Ascorbic acid was determined by HPLC (Mæland and Waagbø, 1998), as were tocopherols and vitamin K (CEN, 1999). Total TBARS was determined according to Hamre et al. (2001). Multielement determination of macro- and microminerals in the feed and tissue samples was performed by ICP-MS (inductively coupled plasma mass spectrometry) (Julshamn et al., 1999).

### 2.6 Smoltification assessment

Smoltification was confirmed through a combination of smolt index scoring (Sigholt et al, 1995), gill Na<sup>+</sup>K<sup>+</sup>-ATPase activity, and 24 h saltwater challenge and plasma chloride analysis were conducted during the feeding trial on 28-Jan, 27-Feb, 21-Mar, and at final smolt, 21-Apr 2014 (equivalent to 122, 199, 324 and 430 °days post-winter solstice rise in daylength respectively). Thirty individuals per tank were scored for smolt index. Na<sup>+</sup>K<sup>+</sup>-ATPase activity was determined from 5 individual gill biopsy / tank (3-6 gill filaments in 100 μl SEI buffer, snap frozen in liquid nitrogen), with a kinetic assay run in 96-well microplates at 26 °C and read at a wavelength of 340 nm for 10 min according to the method of McCormick (1993). Protein concentrations were determined thereafter using a BCA (Bicinchoninic acid) protein assay kit (SIGMA, Aldrich, UK). Saltwater challenge was conducted for 24 h in 100 L tanks of 10 °C aerated seawater (35 ppt) (Instant Ocean; Animal House, Batley, UK). Ten individual fish per diet (5 / tank) were placed into separate 100 L saltwater challenge tanks at respective time points, and following challenge, all fish were removed, numbers of surviving fish counted to determine seawater survival, and were then culled and blood removed from the caudal vein before centrifugation at 500 g for 15 min at 4 °C. Plasma was collected and stored at −20 °C

until analysis using a chloride analyser (Sherwood Instruments Inc., UK). Plasma samples were analysed in triplicate per individual and the average taken of the three technical replicates.

287 288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

285

286

# 2.7 Hepatic transcriptome analysis

Transcriptomic analysis was conducted using a custom-made 4 x 44K Atlantic salmon oligo microarray (Agilent Technologies, Wokingham, UK; ArrayExpress accession no. A-MEXP-2065) as described in detail previously (Tacchi et al., 2011). Furthermore, this salmon custom array and the laboratory protocols used in the present study have been used widely and validated by previous studies (Morais et al., 2012; Betancor et al., 2016; Vera et al., 2017). Briefly, RNA was extracted from 50 mg of liver tissue, originating from six individual fish from each feed group, using TRI Reagent (Sigma-Aldrich, Dorset, UK). The resulting RNA samples were amplified using TargetAmp<sup>TM</sup> 1-Round Aminoallyl-aRNA Amplification Kit, (Epicentre Technologies Corporation, Madison, Wisconsin, USA) following recommended procedures. Aminoallyl-amplified RNA (aRNA) samples were labelled with Cy3 dye (GE HealthCare Life Sciences, Buckinghamshire, UK) while a pool of all aRNA samples was labelled with Cy5 dye (GE HealthCare Life Sciences) and used as a common reference in a dual-label common reference design, and finally hybridised to one array. Scanning was performed using a GenePix 4200 AL Scanner (Molecular Devices (UK) Ltd., Wokingham, UK), and the resulting images analysed with Agilent Feature Extraction Software v.9.5 (Agilent Technologies) to extract intensity values and identify the features. Features considered outliers (i.e., defined as those probes whose background intensity was between the 0.05th and 99.95th percentile of the distribution) in two or more replicates within at least one treatment were excluded from further analyses. Additionally, features consistently expressed just above background noise (defined as those features whose intensity was lower than 5<sup>th</sup> percentile of the distribution in 75 % or more of the analysed samples) were also removed. The full protocol for microarray laboratory and data analysis has been reported previously (De Santis et al., 2015). The output of the microarray experiment was submitted to ArrayExpress under accession number E-MTAB-6302. In order to avoid confounding effects associated with differential expression associated with the increased genetic material possessed by triploid fish, the two ploidy were analysed separately and independently and are herein presented relative to diet L1.

314315

316

317

318

### 2.8 Statistical and data analysis

Differences between weight, condition factor (K), plasma chloride and gill Na<sup>+</sup>K<sup>+</sup>-ATPase activity were assessed using a general linear model (GLM) and two-way ANOVA (diet

x ploidy) with replicate tank nested within treatment. Percentage data (Mortality, SGRwt, HSI and VSI) were subjected to arcsine square-root transformation prior to statistical analyses. Data were tested for normality and homogeneity of variances with Levene's test prior to two-way ANOVA (diet x ploidy) followed by a Tukey–Kramer HSD multiple comparisons of means. Contingency Chi-square tests were used to compare significant differences between survival under saltwater challenge. Vitamins, minerals, amino acids, SAM and SAH were analysed by two-way ANOVA (ploidy x diet) using the tank means as the statistical unit. ANOVA was used to test the hypothesis that diet was more influential than ploidy. Tank means were accepted as statistical different at p < 0.05. Results are reported as mean  $\pm$  standard deviation (SD).

Transcriptomic data analysis was performed using Bioconductor v.2.13 (Gentleman et al., 2004). Quality control, data pre-processing and analysis of differential expression were conducted using the software package limma (Smyth, 2004). To avoid redundancy, features representing the same target gene as implied from KEGG annotation were reduced into a unique value obtained by selecting the feature with the highest F-value calculated on all contrasts. For analysis of gene expression, gene-set testing was adopted using the function *roast* of the limma package (Wu et al., 2010). Gene set testing is a differential expression analysis in which a set of *a priori* defined (putatively co-regulated) genes is treated as a unit. All *p*-values reported in this work were corrected for false discovery rate (FDR) unless otherwise specified (Benjamini and Hochberg, 1995).

## 3. Results

3.1 Mortality, Maturation, Growth and Deformity

There were no significant differences in cumulative mortality between dietary treatments or between ploidy (Table 4). However, in diploids, for diet L1 there was a tank effect, in which one tank showed higher mortality due to fungus in the final 3 weeks of the trial (7.5 % out of 9.1 % total mortality).

Precocious parr-maturation (n = 50 /tank) was not observed in any of the populations assessed any time point.

Diploids had a significantly higher initial weight than triploids that was maintained for the 31 weeks of experimental feeding until smolt (Table 4). However, diet significantly affected weight in diploids, with fish fed diet L2 having a significantly higher final smolt weight than fish fed diets L1 and L3. In contrast, diet did not affect final smolt weight in triploids (Table 4). Although weight differed between ploidy, overall growth rate (SGRwt) and subsequent weight gain did not differ between ploidy and diet, with the exception of diploids fed diet L2, which

showed a significantly higher SGRwt than all other treatments. However, examining growth profiles over time showed that diploids fed diets L2 and L3 exhibited the fastest weight gain, with significant differences evident as early as 3 weeks of feeding on the experimental diets. By 14 weeks post-feeding, diet L3 weight gain slowed, such that weight of fish fed diets L3 and L1 were no longer significantly different (Fig. 2). As such, ploidy did not affect relative % weight gain (RWG, p = 0.215), while a significant effect of diet and an interaction with ploidy was evident (Table 4). RWG was not statistically different between ploidy in fish fed diet L1, significantly higher in triploids fed diet L3 relative to diploids, but significantly lower in triploids fed diet L2 relative to diploids. Within triploids, RWG did not differ between diets, while in diploids RWG was significantly higher in fish fed diet L2 than diets L1 and L3. The crude FCR data suggested an interaction between diet and ploidy, whereby diploids fed diet L2 had lower FCR than triploids fed L2, while there were no other significant effects on FCR between ploidy or diet (Table 4).

Both VSI and HSI were affected by diet, ploidy and their interaction (Table 4). Within diploids, fish fed diet L2 had a significantly lower VSI and HSI than fish fed diets L1 and L3, while in triploids VSI and HSI were not affected by diet. Within diets, VSI and HSI differed only in diet L1 between ploidy.

Externally visible deformity was < 1 % in fish fed all diets and ploidy at the end of the freshwater phase.

# 3.2 Proximate composition of fish and fatty acid composition of liver

Whole fish % oil and ash composition did not differ significantly between dietary micronutrient inclusion level or ploidy (Table 5). Triploids had significantly lower whole body % protein and a higher % moisture at smolt than diploids, but was not affected by diet. Although not always statistically different, the fatty acid compositions of liver showed some trends that might be informative. Specifically, in diploids the proportion of total saturated fatty acids, particularly 16:0, significantly increased, and total monoenes, especially 18:1n-9 and 20:1n-9, significantly decreased with increasing micronutrient supplementation (Table 5). Furthermore, there was an increasing trend, albeit non-significant, in the proportions of total polyunsaturated fatty acids (PUFA) and total n-3 PUFA, due mainly to increasing trends in eicosapentaenoic (EPA, 20:5n-3) and docosahexaenoic (DHA, 22:6n-3) acids, whereas the proportions of n-6 PUFA showed a decreasing trend with increasing dietary micronutrient concentrations.

The effect of dietary micronutrient supplementation on liver fatty acid composition in triploid salmon was less pronounced than in diploids and the trends appeared to be in the opposite direction compared with diploid fish (Table 5). Thus, in triploids lower proportions of saturated fatty acids and n-3 PUFA, and higher proportions of monoenes and n-6 PUFA were found in fish fed diet L3 compared to those fed diet L1.

3.3 Total amino acid concentration in whole body and free amino acids and N-metabolites in white muscle tissue

Whole fish total amino acids and N-metabolites, at the end of the experiment, showed no variation by treatment (Table 6). There was a tendency that whole fish taurine was slightly higher in triploids than in diploids (p = 0.048). Muscle free amino acids and N-metabolites including taurine, asparagine, hydroxyproline, glutamine, glutamate, and  $\beta$ -alanine were all higher in triploids than in diploids, while branched chain amino acids, lysine and anserine were higher in diploids than in triploids (Table 7). All the other metabolites analysed in muscle were not affected by treatments (data not shown). The varying dietary nutrient package had little influence on muscle free amino acids or N-metabolites as only a significant increase in threonine and a decrease in cystathionine was observed.

### 3.4 Vitamin concentrations in whole fish and tissues

For the B-vitamins, increasing dietary levels led to increasing tissue levels for niacin (p = 0.006), while whole body pantothene showed a trend of dietary effect (p = 0.051) (Table 8). Whole body folate increased in diploids, but not in triploids, giving a significant interaction between diet and ploidy (p = 0.035). Riboflavin was higher in whole body of diploids compared to triploids (p = 0.016). The tissue concentrations of the lipid soluble vitamins and vitamin C increased with increasing concentration in the diet (p < 0.015), except for muscle  $\alpha$ -TOH where the apparent increase was non-significant. Alpha-tocopherol (TOH) and vitamin K showed higher retention in diploids compared to triploids (p < 0.001). Gamma-TOH, which was present in the feed ingredients but not supplemented in the diets, decreased in response to increasing nutrient supplementation in both muscle and whole body (p < 0.001).

### 3.5 Mineral concentrations in whole fish

Whole body mineral concentrations were not affected by diet (Table 9). Diploid fish had a slightly higher whole body concentration of Cu than triploid fish (p = 0.01) but the other minerals were not affected by ploidy.

# 3.6 Liver histology and steatosis

A significant interaction between diet and ploidy was evident (p = 0.003). In diploids, steatosis was significantly greater in fish fed diet L2 than fish fed diet L1, but not diet L3, while fish fed diets L1 and L3 were comparable (Table 4). Steatosis did not differ significantly between diets in triploids. However, steatosis was affected by ploidy (p = 0.004), and was generally higher in triploids than diploids. Surprisingly, steatosis scores appeared to be inversely related to HSI (Table 4).

## 3.7 Smoltification efficiency

Diploid salmon fed dietary treatment L2 showed 100 % survival during seawater challenge from 28-Jan final smolt (21-Apr) (Fig. 3). Diploids fed diet L1 had 100 % mortality on 28-Jan 2014. A slight dip in survival was observed in diploids fed diets L1 and L3 at 300 °days post-winter solstice (21-Mar), but survival at smolt (21-Apr) was 100 % irrespective of diet. In triploid salmon, seawater challenge mortalities were only observed on 28-Jan, thereafter and irrespective of diet, survival was 100 % during seawater challenge until smolt (21-Apr).

In both ploidy, plasma chloride levels decreased with time post-winter solstice (Fig. 3). Significant differences were apparent between diploids fed diets L2 and L3 on 28-Jan, and between fish fed diet L1 and diets L2 and L3 on 21-Mar (~300 °days), however, no differences were apparent between dietary treatments at final smolt (21-Apr 2014). In triploids, fish fed diet L1 had significantly higher plasma chloride levels on 28-Jan 2014 (~100 °days) than fish fed diet L2, with fish fed diet L3 intermediary to both. Thereafter, plasma chloride level steadily declined to smolt, at which point triploids fed diet L3 had a significantly higher plasma chloride level than fish fed either diets L1 or L2.

In both ploidy, gill Na<sup>+</sup>,K<sup>+</sup>-ATPase activity increased post-winter solstice until final smolt 21-Apr 2014 (Fig. 3). In diploids, fish fed diet L1 showed lower activity than fish fed diets L2 and L3 on 21-Mar (~300 °days), which correlated with differences evident in seawater challenge survival at this time point. At no other time point were significant differences observed between diets in diploids. In triploids, no significant differences were observed between fish fed the different diets at any time point.

### 3.8 Liver gene expression

At individual gene level and using cut-off measures generally applied to microarray studies (i.e. FDR p < 0.1, Fold Change, FC > 1.3) no significant differences were found in any of the contrasts except for diet L3 versus L1 in triploids, where 7 differentially expressed genes (DEGs) were identified. However, to identify interesting trends similarly affected in both

ploidies a less stringent cut-off was used (p < 0.05, FC > 1.3). Under these conditions a larger number of affected genes were identified ( $L2_{dip}$  vs.  $L1_{dip} = 300$ ,  $L3_{dip}$  vs.  $L1_{dip} = 192$ ,  $L2_{trip}$  vs. L1<sub>trip</sub> =134, L2<sub>trip</sub> vs. L3<sub>trip</sub> =398). To restrict the range of potentially interesting pools of candidate markers affected by micronutrient supplementation, genes affected in diploids (either diets L2 or L3 versus L1) were intersected with those affected in triploids (either L2 or L3 versus L1) (Fig. 4). A total of 63 DEGs were obtained explaining common mechanisms affected in diploids and triploids. Noteworthy, this pool of markers suggested that diet L2 in diploids triggered a hepatic profile that highly resembled that triggered by diet L3 in triploids, sharing approximately 80 % of the similarities. This list of genes contained several genes regulating the terpenoid backbone biosynthesis and sterol biosynthetic processes, such as sterol 14demethylase, 7-dehydrocholesterol reductase, squalene monooxygenase genes, and farnesyl diphosphate synthase. KEGG pathway analysis suggested that the DEGs were enriched for biological processes involved in cholesterol and lipid biosynthetic process, whereas for the cellular components indicated that endoplasmic reticulum and membranes structures were differentially regulated between diet groups. In addition, microarray analysis revealed that lipid digestion and absorption, steroid biosynthesis and PPAR signalling pathways were significantly altered due to diet nutrient package.

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

Gene-set testing enables focus on biologically meaningful processes and provides a more powerful and robust approach than traditional gene-wise tests as evidence is accumulated from many genes. Using this approach, a significantly higher number of processes potentially affected by dietary micronutrient supplementation was identified (Supplementary file 2). In diploids, diets L2 and L3 differed from L1 for only one gene-set, respectively circadian rhythm (increased expression in fish fed diet L2 vs. L1) and insulin signalling pathway (lower expression in fish fed diet L3 vs. L1). In contrast, triploid livers appeared to be more affected by dietary treatments compared with diploids. In fact, diet L2 resulted in at least six gene-sets significantly affected whereas diet L3 triggered the response of 43 gene-sets. Within these 43 sets, up-regulation of key pathways involved in carbohydrate metabolism, digestion and absorption of carbohydrate, protein and lipid as well as bile acid biosynthesis was observed. Immune functions were also up-regulated in triploid salmon fed diet L3 (complement and coagulation cascades, leukocyte transendothelial migration and intestinal immune network for IgA production), as well as metabolism of xenobiotics by cytochrome P450. However, diet L3 in triploids resulted in down-regulation of steroid biosynthesis, terpenoid backbone biosynthesis and energy metabolism (oxidative phosphorylation). In

addition, several functional categories within genetic information processing were also down-regulated (RNA degradation, proteasome, RNA polymerase, spliceosome and ribosome).

Different supplementation levels of micronutrients affected the expression of key enzymes involved in one-carbon metabolism in both ploidies. In particular, increasing levels of supplementation resulted in up-regulation of genes involved in cysteine biosynthesis and catabolism (cysteine beta-synthase, cysteine dioxygenase), methionine synthesis (betaine-homocysteine S-methyltransferase), folate homeostasis (folylpolyglutamate synthase), histidine catabolism and glutamate synthesis (glutamate formiminotransferase) and serine conversion to glycine and tetrahydrofolate (glycine hydroxymethyltransferase). In diploids, several genes involved in carbohydrate and lipid metabolism, and using B-vitamins as cofactors and coenzymes, were also affected. Thus, acetyl-CoA carboxylase (fatty acid biosynthesis), 6-phosphogluconate dehydrogenase and transketolase (pentose phosphate pathway) were upregulated in diploid fish fed diet L2 (compared to fish fed diet L1). In addition, the expression of specific cytochrome P450 genes were also up-regulated in fish fed diets L2 and L3 in both diploids and triploids (Supplementary file 3).

**4. Discussion** 

In the present study, diploids were significantly larger at the start of the trial, and maintained a significantly greater weight than their triploid siblings irrespective of dietary micronutrient supplementation. However, growth rates (SGRwt) were comparable between ploidy and relative weight gain did not differ between ploidy, with the exception of diet L2. Recent studies have shown triploids to have greater growth potential than diploids in freshwater phases of development (Fjelldal & Hansen, 2010; Taylor et al., 2012; Fraser et al., 2013; Taylor et al., 2013; Fjelldal et al., 2016), so the apparent lack of better growth was unexpected. This may in part be due to higher water temperatures (15-16 °C) experienced for 7 weeks prior to, and the initial first two weeks of feeding at start of the trial, under which conditions triploids have been reported to show sub-optimal growth (Sambraus et al., 2017). However, specific dietary requirement trials in triploids are also limited to date, although it has been suggested that differences between ploidy might exist (Fjelldal & Hansen, 2010) particularly with regards to energy and nitrogen retention efficiencies (Burke et al., 2010), dietary phosphorous (Fjelldal et al., 2015; Smedley et al., 2018) and histidine requirements (Taylor et al., 2015; Sambraus et al., 2017). To date, no study has examined the interaction of ploidy and micronutrients when fed low marine ingredient diets. However, the results of the current study may indicate that specific dietary micronutrients could be different between diploid and triploid siblings when they are fed low marine feeds. More specifically, the present data may suggest that dietary micronutrient levels could be rate-limiting for triploid growth potential when fed low marine ingredient diets. However, the specific nutrients that may be rate-limiting could not be determined within the present study. As such, it was evident that diploids supplemented with double the nutrient package levels significantly outperformed their diploid siblings and all triploid groups when fed a low marine ingredient diet. They also had lower HSI and VSI than the diploids fed the L1 diet, which was consistent with results from Hemre et al., (2016). Given the approximate halving of the FM/FO content compared to a traditional marine ingredient based salmon diet, it appeared that a doubling of the specific nutrients is required to satisfy all dietary requirements for growth in diploid Atlantic salmon at least. However, care must be taken with respect to regulation for feed additive inclusion that they do not exceed current EU limits (Supplementary File 4). Should recommendations for any nutrient exceed current limits, then successful implementation within industrial aquafeeds may require revision of current legislation. Of further interest was the apparent loss in growth performance of diploids fed diet L3 (400 % premix) after 14 weeks of feeding. Collectively, the results suggest that, for minerals at least, dietary levels provided by diet L1 were probably sufficient, as there was no significant effect on whole body mineral composition of diet or ploidy with the exception of copper. It is plausible that the addition of extra minerals and vitamins, especially with respect to diet L3 in the case of diploids, may require that the fish expend additional energy in detoxification and excretion, which may subsequently be the cause of reduced growth in these fish towards the latter part of the experiment. In fact, high levels of some minerals in fish diets has been previously associated with reduced growth and feed efficiency (Al-Ghanem, 2011; Berntssen et al., 2017), indicating that mineral levels in fish diets need to be optimised and that their inclusion in excess might be counterproductive.

522

523

524

525

526

527

528

529

530

531

532

533

534

535

536

537

538

539

540

541

542

543

544

545

546

547

548

549

550

551

552

553

554

555

Regarding amino acid and N-metabolite concentrations, higher levels of free amino acids and N-metabolites including taurine, asparagine, hydroxyproline, glutamine, glutamate and β-alanine were observed in muscle of triploids. Methionine was not included in the nutrient package thus the higher taurine present in muscle in triploids might indicate that more methionine has been trans-sulfurated to taurine in triploids as compared to diploids (Espe et al 2008). Free amino acids are precursors for protein synthesis and so these data are consistent with other studies that have provided evidence of higher nitrogen retention and growth potential in triploid salmon as compared to diploids (Burke et al., 2010; Smedley et al., 2016). In particular, elevated levels of free hydroxyproline have been associated to high connective tissue degradation and protein turnover for remodelling of protein in white muscle during growth

(Rungruangsak-Torrissen and Fosseidengen, 2007). In addition, glutamine has been shown to inhibit muscle proteolysis and correlates with muscle protein synthesis (Millward, 1989), whereas high levels of free alanine and taurine may be related to higher intracellular buffering capacity in white muscle (Rungruangsak Torrissen and Male, 2000).

Although some variation in plasma chloride and gill Na<sup>+</sup>,K<sup>+</sup>-ATPase activity was observed during the spring increase in daylength, diet or ploidy appeared to have little effect on achieving successful parr-smolt transformation and osmotic competence. However, in diploids, it was apparent that the rate of increase in gill Na<sup>+</sup>,K<sup>+</sup>-ATPase activity was slower in fish fed diet L1 than in fish fed diets L2 and L3. This may reflect a stimulatory effect on increased gill ion excretion following increased dietary mineral supplementation as in diets L2 and L3, which has been previously reported to stimulate osmoregulatory adaptation in salmonids (Zaugg, 1992). Conversely, it may also represent a deficiency in certain minerals such as magnesium, which have been reported to impair osmoregulation when in deficit (El-Mowafi et al., 1997). This effect was, however, not evident in triploids, but may reflect differential patterns of smoltification between ploidy (Taylor et al., 2012) or differences in gill architecture between ploidy (Leclercq et al., 2011) and cellular physiology and function (Maxime, 2008).

Microarray analysis revealed that the hepatic transcriptome profile of diploid fish fed diet L2 was more similar to that observed in triploids fed diet L3 than to those fed L2, suggesting that micronutrient requirements of triploid salmon may differ from levels accepted in diploid salmon, as reported previously (Taylor et al., 2015; Fjelldall et al., 2016; Smedley et al., 2016). Different levels of micronutrient supplementation affected the expression of key genes involved in lipid metabolism. In particular sterol biosynthesis pathways (steroid and terpenoid backbone synthesis) were down-regulated in both L2-fed diploids and L3-fed triploids, when compared with diet L1-fed diploids and triploids, respectively. This effect on gene expression may be in response to the increased supplementation of cholesterol in the L2 and L3 diets, as part of the micronutrient premix, and therefore probably reflects increased requirement and synthesis of this lipid in fish fed diet L1. However, bile acid biosynthesis was up-regulated in these groups. These results are consistent with a previous study by Kortner et al. (2014) showing that supplementation of plant-based diets with cholesterol suppressed cholesterol synthesis and induced bile acid production in Atlantic salmon. In fact, the conversion of cholesterol into bile acids represents the main route for cholesterol elimination in fish and, consequently, the transcriptomic response observed in the present study would be a mechanism of cholesterol homeostasis in fish being fed diets containing higher levels of cholesterol.

Gene sets analysis showed an up-regulation of genes involved in immune processes in triploid salmon fed diet L3. This fact might be related to higher levels of vitamin C in whole body and liver as well as higher vitamin E levels in whole body of fish from this experimental group, when compared to triploid salmon fed diet L1. In particular, there was an up-regulation of complement and coagulation cascades, which agreed with previous research showing an effect of vitamin C supplementation on complement activity in Atlantic salmon (Hardie et al., 1991). Vitamin E content in salmon diets has also been correlated to variations in the response of fish to infectious diseases and immune response (Hardie et al., 1990). Both vitamin C and E can improve the immune status of fish due to their antioxidant activity and previous studies have indicated interaction between these vitamins (Hamre et al., 1997, 2011). In diploid salmon, there was also a positive correlation between increasing levels of micronutrient supplementation and body content of vitamins C and E, however no sets of genes involved in immune functions were differentially expressed. This fact further supports the hypothesis that triploid salmon may have different micronutrient requirements and responses to feed supplementation with vitamins. The expression of cytochrome P450 enzymes was also upregulated in response to higher levels of micronutrient supplementation in both ploidies. These enzymes are involved in the activation of vitamin D to its hormonal form, which then regulates the expression of a broad range of genes, including osteocalcin, osteopontin, calbindin and calcium channels that play key roles in the control of calcium homeostasis and skeletal integrity (Suzuki et al., 2008). In addition, different P450 enzymes control vitamin D metabolism and inactivation, which can also be induced by vitamin D itself via CYP24A1 activation (Schuster, 2011). In the present study, up-regulation of cyp24a1 (vitamin D3 24-hydroxylase) was observed in diploid salmon fed diet L3. However, in triploid fish the expression of this gene was not affected by diet. In the present study, vitamin D was included in the micronutrient mix and therefore vitamin D concentration in diet L3 was four times higher than in diet L1, which might have induced the expression of its metabolising enzyme, suggesting that levels in diet L3 may be excessive for diploid Atlantic salmon. However, the microarray results also suggested that this may not be the case for triploids. In fact, triploid salmon have a higher predisposition to develop skeletal deformities, when compared to diploid fish, which seems to be reduced when feeds are supplemented with phosphorus (Fjelldal et al., 2016; Smedley et al., 2016, 2018). It is also known that vitamin D is an important regulator of phosphorus metabolism (DeLuca, 1980) and, consequently, results suggest that vitamin D requirements in triploid salmon may also be different, although further research is required to define its optimal concentration in feeds for triploids.

589

590

591

592

593

594

595

596

597

598

599

600

601

602

603

604

605

606

607

608

609

610

611

612

613

614

615

616

617

618

619

620

621

Another biological category affected by diet in triploid salmon was genetic information processing. In fish fed diet L3, down-regulation of RNA degradation, proteasome, RNA polymerase, spliceosome and ribosome was observed, suggesting a decrease in protein turnover in this group, which may indicate a decrease in energy expenditure (Houlihan et al., 1995) that was consistent with down-regulation of oxidative phosphorylation in this group. However, this was in contrast to the growth and feed conversion rates observed in triploid fish, since no differences were found in these parameters between dietary treatments. In contrast, growth was affected by micronutrient supplementation in diploid salmon that showed better performance when fed diet L2. In addition, microarray data also revealed higher expression of igf1 in this group. Regarding carbohydrate metabolism, there was up-regulation of key pathways in triploids fed diet L3, which could be related to higher availability of B-vitamins, when compared to L1-fed fish. Vitamins B1 (thiamine), B7 (biotine) and B12 (cobalamine) are involved in several reactions of carbohydrate metabolism, acting as coenzymes, and vitamin B12 deficiency has been linked to gluconeogenesis impairment in mammals (Mahmood, 2014). In diploids, microarray analysis also found a number of vitamin B-dependent genes that were up-regulated in the fish fed diet L2. In particular, these genes were involved in lipid and carbohydrate metabolism, in accordance with the functions previously reported for these vitamins (Waagbø, 2010).

623

624

625

626

627

628

629

630

631

632

633

634

635

636

637

638

639

640

641

642

643

644

645

646

647

648

649

650

651

652

653

654

655

656

One-carbon metabolism comprises a number of biochemical reactions that provide methyl groups for biological methylation of proteins, phospholipids and nucleic acids (Friso et al., 2017). B-vitamins act as coenzymes and methyl acceptors and donors in one-carbon metabolism and, consequently, deficiency of some of these vitamins can have an impact on these biochemical processes. In the present study, one-carbon metabolism was affected by diet in diploid and triploid salmon. In diploids, homocysteine re-methylation to form methionine by betaine-homocysteine S-methyltransferase (bhmt) was up-regulated in fish fed L2 compared to L1. Previous studies have shown an inverse correlation between B-vitamins status and homocysteine concentrations (Wallace et al., 2008) and therefore higher dietary levels of these vitamins may increase methionine synthesis from homocysteine. In addition, homocysteine can also enter the transulfuration pathway and be degraded to cystathionine by cysteine betasynthase (cbs) and then to cysteine, which can be metabolised ultimately into glutathione and taurine (Friso et al., 2017). In diploids fed diet L2, there was up-regulation of cbs and cysteine catabolism by cysteine dioxygenase that, in turn, could be related to up-regulation of glutathione metabolism in this group, since cysteine is one of the major determinants of glutathione synthesis (Stipanuk et al., 2006). Regarding triploid salmon, microarray data revealed upregulation of *glycine hydroxymethyltransferase*, a vitamin B6-containing enzyme that converts glycine to serine, and tetrahydrofolate (THF) to 5,10-methylenetetrahydrofolate (5,10-MTHF) in the folate cycle (Friso et al., 2017), suggesting than higher dietary levels of B-vitamins may have induced up-regulation of this key pathway within one-carbon metabolism. In addition, *glutamate formiminotrasferase* was also up-regulated in this group. This enzyme is involved in glutamate synthesis and depends on histidine and folate (Mahmood, 2014).

### **Conclusions**

As the industry moves towards achieving increased sustainability and greater utilisation of plant-based ingredients there is a clear need adjust micronutrient supplementation accordingly to ensure optimal growth and metabolic function. Results, certainly in the case of diploids, suggest that under low marine ingredient diets, while micromineral requirements appear to be met within the refined NP levels as suggested by the short-term studies of Hamre et al., (2016) and Hemre et al., (2016), that for other micronutrients (specific amino acids, water- and fat-soluble vitamins) it is recommended that levels be supplemented above current NRC (2011) recommendations for optimised growth and liver function of Atlantic salmon in long-term freshwater grow out. The differential effect between ploidy for certain micronutrients also supports the hypothesis that there are yet further differences in nutritional requirements beyond the previously established increased histidine and phosphorous requirements of triploid salmon.

#### 5. Acknowledgements

- This study, JFT, LV and CdS were partly funded by the European Commission FP7 Integrated
- Project No. 288925, Advanced Research Initiatives for Nutrition & Aquaculture (ARRAINA).

# 6. References

- 685 Al-Ghanem, K.A., 2011. Effect of cobalt-supplemented diets on bioaccumulation, digestive
- enzyme activities and growth of *Cyprinus carpio*. Toxicol. Environ. Chem. 93, 985-995.
- 687 AOAC, 2000. Official methods of analysis. Association of Official Analytical Chemists, 17th
- 688 ed. Washington DC: AOAC International.

- Bell, J.G., Waagbø, R., 2008. Safe and nutritious aquaculture produce: benefits and risks of
- alternative sustainable aquafeeds, in: Holmer, M., Black, K., Duarte, C.M., Marba, N.,
- Karakassis, I. (Eds.), Aquaculture in the Ecosystem. Springer Verlag BV, London, pp.185-225.
- Bendiksen, E.Å., Johnsen, C.A., Olsen, H.J., Jobling, M., 2011. Sustainable aquafeeds:
- 693 Progress towards reduced reliance upon marine ingredients in diets for farmed Atlantic salmon
- 694 (*Salmo salar* L.). Aquaculture 314, 132-139.
- Benfey, T.J., 2016. Effectiveness of triploidy as a management tool for reproductive
- 696 containment of farmed fish: Atlantic salmon (Salmo salar) as a case study. Rev. Aquacult. 8,
- 697 264-282.
- Benjamini, Y., Hochberg, Y., 1995. Controlling the False Discovery Rate: A Practical and
- Powerful Approach to Multiple Testing. J. Royal Statistical Soc., Series B (Methodological)
- 700 57, 289-300.
- 701 Berntssen, M.H.G., Sundal, T.K., Olsvik, P.A., Amlund, H., Rasinger, J.D., Sele, V., Hamre,
- K., Hillestad, M., Buttle, L., Ørnsrud, R., 2017. Sensitivity and toxic mode of action of
- 703 dietary organic and inorganic selenium in Atlantic salmon (*Salmo salar*). Aquatic Toxicol.
- 704 192, 116-126.
- 705 Betancor, M.B., Olsen, R.E., Solstorm, D., Skulstad, O.F., Tocher, D.R., 2016. Assessment of
- a land-locked Atlantic salmon (Salmo salar L.) population as a potential genetic resource with
- a focus on long-chain polyunsaturated fatty acid biosynthesis. Biochim. Biophys. Acta. 1861,
- 708 227-238.
- Brønstad, I., Bjerkas, I., Waagbø, R., 2002. The need for riboflavin supplementation in high
- and low energy diets for Atlantic salmon *Salmo salar* L. parr. Aquacult. Nutr. 8, 209-220.
- Burke, H.A., Sacobie, C.F.D., Lall, S., Benfey, T., 2010. The effect of triploidy on juvenile
- 712 Atlantic salmon (*Salmo salar*) response to varying levels of dietary phosphorus. Aquaculture
- 713 306, 295-301.
- 714 CEN, 1999. Foodstuffs Determination of vitamin E by high performance liquid
- 715 chromatography Measurement of alpha-, beta-, gamma- and delta-tocopherols. Comitè
- 716 Europèen de Normalisation prEN 12822.

- 717 Christie, W.W., 2003. Preparation of derivatives of fatty acids. In: Lipid Analysis: Isolation,
- Separation and Structural Analysis of Lipids, 3rd ed., pp. 205–225 (Christie, W.W., Ed.).
- 719 Somerset: Oily Press.
- 720 Collins, S.A., Øverland, M., Skrede, A., Drew, M.D., 2013. Effect of plant protein sources on
- 721 growth rate in salmonids: Meta-analysis of dietary inclusion of soybean, pea and
- canola/rapeseed meals and protein concentrates. Aquaculture 400-401, 85-100.
- 723 Crampton, V.O., Nanton, D.A., Ruohonen, K., Skjervold, P.-O., El-Mowafi, A., 2010.
- Demonstration of salmon farming as a net producer of fish protein and oil. Aquacult. Nutr. 16,
- 725 437-446.
- DeLuca, H.F., 1980. The control of calcium and phosphorus metabolism by the vitamin D
- endocrine system. Ann. N. Y. Acad. Sci. 355, 1-17.
- De Santis, C., Olsen, R.E., Bartie, K., Taggart, J.B., Tocher, D.R., 2015. Nutrigenomic profiling
- of transcriptional processes affected in liver and distal intestine in response to a soybean meal-
- 730 induced nutritional stress in Atlantic salmon (Salmo salar). Comp. Biochem. Physiol. D. 15, 1-
- 731 11.
- Einen, O., Roem, A.J., 1997. Dietary protein/energy ratios for Atlantic salmon in relation to
- fish size: growth, feed utilisation and slaughter quality. Aquacult. Nutr. 3, 115-126.
- 734 El-Mowafi, A.R.A., Waagbø, R., Maage, A., 1997. Effect of low dietary magnesium on
- 735 immune response and osmoregulation of Atlantic salmon. J. Aquat. Anim. Health 9, 8-17.
- Espe, M., Lemme, A., Petri, A., El-Mowafi, A., 2006. Can Atlantic salmon (Salmo salar) grow
- on diets devoid of fish meal? Aquaculture 255, 255-262.
- Espe, M., Hevrøy, E.M., Liaset, B., Lemme, A., El-Mowafi, A., 2008 Methionine intake affect
- hepatic sulphur metabolism in Atlantic salmon, *Salmo salar*. Aquaculture 274, 132-141.
- Espe, M., Andersen, S.M., Holen, E., Rønnestad, I., Veiseth-Kent, E., Zerrahn, J.-E., Aksnes,
- A., 2014 Methionine deficiency does not increase polyamine turnover through depletion of liver
- S-adenosylmethionine (SAM) in juvenile Atlantic salmon. Br. J. Nutr. 112, 1274-1283.
- Feldsine, P., Abeyta, C., Andrews, W.H., 2002. AOAC International methods committee guidelines
- for validation of qualitative and quantitative food microbiological official methods of analysis. J. AOAC
- 745 Int. 85,1187-200.

- Fjelldal, P.G., Hansen, T., 2010. Vertebral deformities in triploid Atlantic salmon (Salmo salar
- 747 L.) underyearling smolts. Aquaculture 309, 131–136.
- 748 Fjelldal, P.G., Hansen, T.J., Lock, E.-J., Wargelius, A., Fraser, T.W.K., Sambraus, F., El-
- Mowafi, A., Albrektsen, S., Waagbø, R., Ørnsrud, R., 2016. Increased dietary phosphorus
- 750 prevents vertebral deformities in triploid Atlantic salmon (Salmo salar L.). Aquacult. Nutr. 22,
- 751 72-90.
- 752 Folch, J., Lees, M., Sloane-Stanley, G.H., 1957. A simple method for the isolation and
- purification of total lipids from animal tissues. J. Biol. Chem. 226, 497-509.
- Fraser, T.W.K., Hansen, T., Skjæraasen, J.E., Mayer, I., Sambraus, F., Fjelldal, P.G., 2013. The
- effect of triploidy on the culture performance, deformity prevalence, and heart morphology in
- 756 Atlantic salmon. Aquaculture 416–417, 255–264.
- Friso, S., Udali, S., De Santis, D., Choi, S.-W., 2017. One-carbon metabolism and epigenetics.
- 758 Mol. Aspects Med. 54, 28-36.
- Ganga, R., Tibbetts, S.M., Wall, C.L., Plouffe, D.A., Bryenton, M.D., Peters, A.R., Runighan,
- 760 C.D., Buchanan, J.T., Lall, S.P., 2015. Influence of feeding a high plant protein diet on growth
- and nutrient utilization to combined 'all-fish' growth-hormone transgenic diploid and triploid
- Atlantic salmon (*Salmo salar* L.). Aquaculture 446, 272-282.
- Gatlin, D.M., Barrows, F.T., Brown, P., Dabrowski, K., Gibson, G.T., Hardy, R.W., Elliot, H.,
- Hu, G., Krogdahl, A., Nelson, R., Overturf, K., Rust, M., Sealey, W., Skonberg, D., Souza, E.J.,
- Stone, D., Wilson, R., Wurtele, E., 2007. Expanding the utilization of sustainable plant products
- in aquafeeds: a review. Aquacult. Res. 38, 551-579.
- Gentleman, R., Carey, V., Bates, D., Bolstad, B., Dettling, M., Dudoit, S., Ellis, B., Gautier,
- L., Ge, Y., Gentry, J., Hornik, K., Hothorn, T., Huber, W., Iacus, S., Irizarry, R., Leisch, F.,
- Li, C., Maechler, M., Rossini, A., Sawitzki, G., Smith, C., Smyth, G., Tierney, L., Yang, J.,
- Zhang, J., 2004. Bioconductor: open software development for computational biology and
- bioinformatics. Genome Biol. 5, R80.
- 772 Grisdale-Helland, B., Gatlin III, D.M., Helland, S.J., 2013. Optimization of dietary
- macronutrients for Atlantic salmon post-smolts using increasing ration levels. Aquaculture 408-
- 774 409, 88-94

- Gu, M., Kortner, T.M., Penn, M., Hansen, A.K., Krogdahl, Å. 2013. Effects of dietary plant
- meal and soya-saponin supplementation on intestinal and hepatic lipid droplet accumulation
- and lipoprotein and sterol metabolism in Atlantic salmon (Salmo salar L.). Brit. J. Nutr. 111,
- 778 432–444.
- Halver, J.E., Hardy, R.W. (Eds.), 2002. Fish Nutrition, 3rd Edition, Academic Press, San Diego,
- 780 824 pp.
- Hamre, K., 2011. Metabolism, interactions and requirements of vitamin E in fish. Aquacult.
- 782 Nutr. 17, 98-115.
- Hamre, K., Næss, T., Espe, M., Holm, J.C., Lie, Ø., 2001. A formulated diet for Atlantic halibut
- 784 (*Hippoglossus hippoglossus*, L.) larvae. Aquacult. Nutr. 7, 123–132.
- Hamre, K., Sissener, N.H., Lock, E., Olsvik, P.A., Espe, M., Torstensen, B.E., Silva, J.,
- Johansen, J., Waagbø, R., Hemre, G., 2016. Antioxidant nutrition in Atlantic salmon (Salmo
- 787 salar) parr and post-smolt, fed diets with high inclusion of plant ingredients and graded levels
- of micronutrients and selected amino acids. PeerJ 11, e2688.
- Hamre K., Waagbø R., Berge R.K., Lie Ø., 1997. Vitamins C and E interact in juvenile Atlantic
- 790 salmon (Salmo salar, L.). Free Radic. Biol. Med. 22, 137-149.
- Hansen, A.-C., Waagbø, R, Hemre, G.-I., 2015. New B vitamin recommendations in fish when
- fed plant-based diets. Aquacult. Nutr. 21, 507-527.
- Hardie, L.J., Fletcher, T.C., Secombes, C.J., 1990. The effect of vitamin-E on the immune
- response of the Atlantic salmon (*Salmo salar* L). Aquaculture 87, 1-13.
- Hardie, L.J., Fletcher, T.C., Secombes, C.J., 1991. The effect of dietary vitamin C on the
- immune response of the Atlantic salmon (*Salmo salar* L.). Aquaculture 95, 201-214.
- 797 Hardy, R.W., 2010. Utilization of plant proteins in fish diets: effects of global demand and
- results supplies of fishmeal. Aquacult. Res. 41, 770–776.
- 799 Huang da, W., Sherman, B.T., Lempicki, R.A., 2009. Systematic and integrative analysis of
- large gene lists using DAVID bioinformatics resources. Nat. Protoc. 4, 44-57.

- Hemre, G.-I., Amlund, H., Aursand, A., Bakke, A.M., Olsen, R.E., Ringo, E., Svihus, B., 2009.
- 802 Criteria for safe use of plant ingredients in diets for aquacultured fish, Opinion of the Panel on
- Animal Feed of the Norwegian Scientific Committee for Food Safety. Oslo, Norway: VKM.
- Hemre, G., Lock, E., Olsvik, P.A., Hamre, K., Espe, M., Torstensen, B.E., Silva, J., Hansen,
- A., Waagbø, R., Johansen, J.S., Sanden, M., Sissener, N.H., 2016. Atlantic salmon (Salmo
- salar) require increased dietary levels of B-vitamins when fed diets with high inclusion of plant
- based ingredients. PeerJ 9, e2493.
- Hillestad, M., Johnsen, F., 1994. High-energy/low-protein diets for Atlantic salmon: effects on
- growth, nutrient retention and slaughter quality. Aquaculture 124, 109-116.
- Houlihan, D.F., Carter, C.G., McCarthy, I.D., 1995. Protein turnover in animals. In: Wright, P.,
- Walsh, P. (Eds.). Nitrogen metabolism and excretion. CRC Press, Boca Raton, pp. 1-29.
- 812 IFFO, 2014. The Marine Ingredients Organisation: Fishmeal and Fish Oil Statistical Yearbook
- 813 2014. In IFFO [online]. www.iffo.net
- Jackson, A.J., Shepherd, C.J., 2012. The future of fishmeal and fish oil, in: Ryder, J., Ababouch,
- L., Balaban, M. (Eds), Second International Congress on Seafood Technology on Sustainable,
- 816 Innovative and Healthy Seafood FAO Fisheries and Aquaculture Proceedings. No. 22. Food
- and Agriculture Organisation, Rome, 238 pp.
- Julshamn, K., Brenna, J., Holland, R., Tanner, S., 1999. Plasma source mass spectrometry- New
- developments and applications. Roy. Soc. Chem. 241, 167-172.
- 820 Kontali, 2015. Salmon World 2015. Nystøl, R., Ed. Kontali Analyse AS, Kristiansund, Norway,
- 821 30 pp. http://www.kontali.com/?div\_id=156&pag\_id=244&art\_id=1109
- 822 Kortner, T.M., Björkhem, I., Krasnov, A., Timmerhaus, G., Krogdahl, A., 2014. Dietary
- 823 cholesterol supplementation to a plant-based diet suppresses the complete pathway of
- cholesterol synthesis and induces bile acid production in Atlantic salmon (Salmo salar L). Br.
- 825 J. Nutr. 111, 2089-2103.
- Leclercq, E., Taylor, J.F., Fison, D., Fjelldal, P.G., Diez-Padrisa, M., Hansen, T., Migaud, H.,
- 827 (2011) Comparative seawater performance and deformity prevalence in out-of-season diploid
- and triploid Atlantic salmon (Salmo salar) post-smolts. Comp. Biochem. Physiol. A. Mol.
- 829 Integr. Physiol, 158, 116–125.

- Mahmood, L., 2014. The metabolic processes of folic acid and Vitamin B12 deficiency. J.
- 831 Health Res. Rev. 1, 5-9.
- Maxime, V., (2008) The physiology of triploid fish: current knowledge and comparisons with
- 833 diploid fish. Fish Fisheries, 9, 67–78.
- McCormick, S.D., 1993. Methods for nonlethal gill biopsy and measurement of Na+,K+-
- ATPase activity. Can. J. Fish. Aquatic Sci. 50, 656–658.
- Mæland, A., Waagbø, R., 1998. Examination of the qualitative ability of some cold water
- marine teleosts to synthesise ascorbic acid. Comp. Biochem. Physiol. 121A, 249-255.
- Mæland, A., Rønnestad, I., Fyhn, H.J., Berg, L., Waagbø, R., 2000. Water-soluble vitamins in
- natural plankton (copepods) during two consecutive spring blooms compared to vitamins in
- 840 Artemia franciscana nauplii and metanauplii. Mar. Biol. 136, 765-772.
- Millward, D.J., 1989. The nutritional regulation of muscle growth and protein turnover.
- 842 Aquaculture 79, 1-28.
- Montero, D., Izquierdo, M., 2011. Welfare and health of fish fed vegetable oils as alternative
- lipid sources to fish oil, in: Turchini, G.M., Ng, W.-K., Tocher, D.R. (Eds.), Fish Oil
- Replacement and Alternative Lipid Sources in Aquaculture Feeds. Taylor & Francis, CRC
- 846 Press, Boca Raton, pp. 439-485.
- Morais, S., Taggart, J.B., Guy, D.R., Bell, G., Tocher, D.R., 2012. Hepatic transcriptome
- analysis of inter-family variability in flesh n-3 long-chain polyunsaturated fatty acid content in
- 849 Atlantic salmon. BMC Genomics 13, 410.
- National Research Council (NRC), 2011. Nutrient Requirements of Fish and Shrimp. The
- National Academies Press, Washington DC.
- Oliva-Teles, A., 2012. Nutrition and health of aquaculture fish. J. Fish Dis. 35, 83–108.
- Pohlenz, C., Gatlin III, D.M., 2014. Interrelationships between fish nutrition and health.
- 854 Aquaculture 431, 111-117.
- 855 Rosenlund, G., Corraze, G., Izquierdo, M., Torstensen, B.E., 2011. The effects of fish oil
- replacement on nutritional and organoleptic qualities of farmed fish, in: Turchini, G.M., Ng,

- W.-K., Tocher, D.R. (Eds.), Fish Oil Replacement and Alternative Lipid Sources in Aquaculture
- Feeds. Taylor & Francis, CRC Press, Boca Raton, pp. 487-522.
- Rungruangsak-Torrissen, K., Fosseidengen, J.E., 2007. Effect of artificial feeding on digestive
- efficiency, growth and qualities of muscle and oocyte of maturing Atlantic mackerel (*Scomber*
- 861 *scombrus* L.). J. Fd. Biochem. 31, 726–747.
- Rungruangsak Torrissen, K., Male, R., 2000. Trypsin isozymes: development, digestion and
- structure. In: Haard, N.F., Simpson, B.K. (eds.) Seafood enzymes, utilization and influence on
- postharvest seafood quality. Marcel Dekker, New York, USA, pp. 215–269.
- Sambraus, F., Fjelldal, P.G., Remø, S.C., Hevrøy, E.M., Nilsen, T.O., Thorsen, A., Hansen,
- 866 T.J., Waagbø, R., 2017. Water temperature and dietary histidine affect cataract formation in
- Atlantic salmon (Salmo salar L.) diploid and triploid yearling smolt. J. Fish Dis., 40, 1195-
- 868 1212.
- 869 Sanden, M., Stubhaug, I., Berntssen, M.H.G., Lie, Ø., Torstensen, B.E., 2011. Atlantic Salmon
- 870 (Salmo salar L.) as a net producer of long-chain marine ω-3 fatty acids. J. Agric. Fd. Chem. 59,
- 871 12697–12706.
- Schuster, I., 2011. Cytochromes P450 are essential players in the vitamin D signaling system.
- Biochim. Biophys. Acta, Proteins Proteomics 1814, 186-199.
- 874 Shepherd, C.J., Jackson, A.J., 2013. Global fishmeal and fish-oil supply: inputs, outputs and
- 875 markets. J. Fish Biol. 83, 1046-66.
- Shepherd, C.J., Monroig, Ó., Tocher, D.R., 2017. Future availability of Scottish salmon feeds
- and supply chain implications. Aquaculture 467, 49-62.
- 878 Sigholt, T., Staurnes, M., Jakobsen, H.J., Asgard, T., 1995. Effects of continuous light and
- short-day photoperiod on smolting seawater survival and growth in Atlantic salmon (Salmo
- 880 *salar*). Aquaculture 130, 373-388.
- Sissener, N.H., Julshamn, K., Espe, M., Lunestad, B.T., Hemre, G.I., Waagbø, R., Måge, A.,
- 882 2013. Surveillance of selected nutrients, additives and undesirables in commercial Norwegian
- fish feeds in the years 2000-2010. Aquacult. Nutr. 19, 555-572.
- 884 Smedley, M.A., Clokie, B.G.J., Migaud, H., Campbell, P., Walton, J., Hunter, D., Corrigan, D.,
- Taylor, J.F., 2016. Dietary phosphorus and protein supplementation enhances seawater growth

- and reduces severity of vertebral malformation in triploid Atlantic salmon (Salmo salar L.).
- 887 Aquaculture 451, 357-368.
- 888 Smedley, M.A., Migaud, H., McStay, E.L., Clarkson, M., Bozzolla, P., Campbell P., Taylor
- J.F., 2018. Dietary freshwater phosphorous requirements of triploid Atlantic salmon (Salmo
- salar L.) are different to diploid with reference to early skeletal development. Aquaculture 490,
- 891 329-343.
- 892 Smyth, G.K., 2004. Linear models and empirical bayes methods for assessing differential
- expression in microarray experiments. Stat. Appl. Genet. Mol. Biol. 3, Article 3.
- 894 Stipanuk, M.H., Dominy, J.E. Jr., Lee, J.I., Coloso, R.M., 2006. Mammalian cysteine
- metabolism: new insights into regulation of cysteine metabolism. J. Nutr. 136, 1652S-1659S.
- 896 Suzuki, Y., Landowski, C.P., Hediger, M.A., 2008. Mechanism and regulation of epithelial
- 897 Ca<sup>2+</sup> absorption in health and disease. Ann. Rev. Physiol. 70, 257-271.
- Tacchi, L., Bron, J.E., Taggart, J.B., Secombes, C.J., Bickerdike, R., Adler, M.A., Takle, H.,
- Martin, S.A.M., 2011. Multiple tissue transcriptomic responses to *Piscirickettsia salmonis* in
- 900 Atlantic salmon (*Salmo salar*). Physiological Genomics 43, 1241-1254.
- Tacon, A.G.J., Metian, M., 2008. Global overview on the use of fish meal and fish oil in
- industrially compounded aquafeeds: Trends and future prospects. Aquaculture 285, 146-158.
- Taylor, J.F., Leclercq, E., Preston, A.C., Guy, D., Migaud, H., 2012. Parr-smolt transformation
- 904 in out-of-season triploid Atlantic salmon. Special Issue, Smoltification workshop, Oregon
- 905 2009. Aquaculture 362–363, 255–263.
- Taylor J.F., Sambraus, F., Velasco, J.C., Guy, D., Migaud, H., 2013. Ploidy and family effects
- 907 on Atlantic salmon (Salmo salar) growth, deformity and harvest quality during a full
- 908 commercial. Aquaculture 410-411, 41-50.
- Taylor, J.F., Waagbø, R., Diez-Padrisa, M., Campbell, P., Walton, J., Hunter, D., Matthew, C.,
- 910 Migaud, H., 2015. Adult triploid Atlantic salmon (Salmo salar) have higher dietary histidine
- 911 requirements to prevent cataract development in seawater. Aquacult. Nutr. 21, 18-32.
- 912 Tibbetts, S.M., Wall, C.L., Barbosa-Solomieu, V., M.D. Bryenton, M.D., Plouffe, D.A.,
- Buchanan, J.T., Lall, S.P., 2013. Effects of combined "all-fish' growth hormone transgenics

- and triploidy on growth and nutrient utilization of Atlantic salmon (Salmo salar L.) fed a
- 915 practical grower diet of known composition. Aquaculture 406-407, 141-152.
- Tocher, D.R., Glencross, B.D., 2015. Lipids and fatty acids. In: Dietary Nutrients, Additives,
- and Fish Health. (Lee, C.-S., Lim, C., Webster, C. and Gatlin III, D.M., Eds.), Ch.3. pp. 47-94,
- 918 Wiley-Blackwell.
- Tocher, D.R., Harvie D.G., 1988. Fatty acid compositions of the major phosphoglycerides from
- 920 fish neural tissues; (n-3) and (n-6) polyunsaturated fatty acids in rainbow trout (Salmo
- 921 *gairdneri*) and cod (*Gadus morhua*) brains and retinas. Fish Physiol. Biochem. 5, 229–239.
- Torstensen, B.E., Espe, M., Sanden, M., Stubhaug, I., Waagbø, R., Hemre, G.-I., Fontanillas,
- 923 R., Nordgarden, U., Hevrøy, E.M., Olsvik, P., Berntssen, M.H.G., 2008. Novel production of
- Atlantic salmon (Salmo salar) protein based on combined replacement of fishmeal and fish oil
- with plant meal and vegetable oil blends. Aquaculture 285, 193–200.
- Torstensen, B.E., Espe, M., Stubhaug, I., Lie, Ø., 2011. Dietary plant proteins and vegetable oil
- blends increase adiposity and plasma lipids in Atlantic salmon (Salmo salar L.). Br. J. Nutr.
- 928 106, 633–647.
- 929 Torstensen, B.E., Tocher, D.R., 2011. The Effects of fish oil replacement on lipid metabolism
- 930 of fish. In: Turchini, G.M., Ng, W.-K., Tocher, D.R. (Eds.), Fish Oil Replacement and
- 931 Alternative Lipid Sources in Aquaculture Feeds. Taylor & Francis, CRC Press, Boca Raton,
- 932 pp.405-437.
- Turchini, G.M., Ng, W.-K., Tocher, D.R. (Eds), 2011. Fish Oil Replacement and Alternative
- Lipid Sources in Aquaculture Feeds. Taylor & Francis, CRC Press, Boca Raton, p.533.
- Vera, L.M., Metochis, C., Skjærven, K.H., Clarkson M., Taylor, J.F., Migaud, H., Tocher, D.R.,
- 936 2017. Early nutritional programming affects liver transcriptome in diploid and triploid Atlantic
- 937 salmon, Salmo salar. BMC Genomics 18, 886.
- Waagbø, R., 2010. Water-soluble vitamins in fish ontogeny. Aquacult. Res. 41, 433–744.
- Wallace, J.M.W., Bonham, M.P., Strain, J.J., Duffy, E.M., Robson, P.J., Ward, M., McNulty,
- 940 H., Davidson, P.W., Myers, G.J., Shamlaye, C.F., Clarkson, T.W., Molloy, A.M., Scott, J.M.,
- 941 Ueland, P.M., 2008. Homocysteine concentration, related B vitamins, and betaine in pregnant
- women recruited to the Seychelles Child Development Study. Am. J. Clin. Nutr. 87, 391-397.

- 943 Warnes, G.R., Bolker, B., Bonebakker, L., Gentleman, R., Liaw, W.H.A., Lumley, T.,
- Maechler, M., Magnusson, A., Moeller, S., Schwartz, M., Venables, B., 2013. gplots: Various
- R programming tools for plotting data. R package version 2.12. 1. 2013
- Woznicki, P., Kuzminski, H. 2002. Chromosome number and erythrocyte nuclei length in
- 947 triploid brook trout (Salvelinus fontinalis). Caryologia. 55, 295-298.
- Wu, D., Lim, E., Vaillant, F., Asselin-Labat, M., Visvader, J.E., Smyth, G.K., 2010. ROAST:
- rotation gene set tests for complex microarray experiments. Bioinformatics 26, 2176-2182.
- Ytrestøyl, T., Aas, T.S., Åsgård, T., 2015. Utilisation of feed resources in production of Atlantic
- 951 salmon (*Salmo salar*) in Norway. Aquaculture 448, 365-374.

- 252 Zar, J.H., 2010. Biostatistical analyses, 5<sup>th</sup> Edn. Prentice Hall, 944 pp.
- 253 Zaugg, W.S., 1992. Some changes in smoltification and seawater adaptability of salmonids
- resulting from environmental and other factors. Aquaculture 28, 143-151.

# Figure Legends

- 957 Figure 1. Scoring system for hepatocyte steatosis. Representative examples of the
- 958 histopathological scoring of steatosis in hepatic sections. Bars represent 100 μm.

959

956

- Figure 2. Weight gain profiles (mean  $\pm$  SD) of diploid and triploid Atlantic salmon parr fed a
- low FM/FO formulation (15/8 %) supplemented with a micronutrient premix (modified NRC
- 2011 recommendation) at three inclusion levels: Diet L1 100 % premix, Diet L2 200 % premix,
- and Diet L3 400 % premix. Superscripts denote significant differences (Two-Way ANOVA, p
- 964 < 0.05) between dietary treatments.

965

- 966 Figure 3. Changes in survival, plasma chloride concentration of seawater (SWC) challenged
- 967 (24h, 35ppt at 10°C) and gill Na<sup>+</sup>,K<sup>+</sup>-ATPase of diploid and triploid Atlantic salmon parr fed a
- low FM/FO formulation (15/8 %) supplemented with a micronutrient premix (modified NRC
- 2011 recommendation) at three inclusion levels: Diet L1 100 % premix, Diet L2 200 % premix,
- and Diet L3 400 % premix. Superscripts denote significant differences (Two-Way ANOVA, p
- 971 < 0.05) between diets. SWC or gill Na<sup>+</sup>,K<sup>+</sup>-ATPase were conducted were conducted on 28-Jan,
- 972 27-Feb, 21-Mar, and 21-Apr 2014 (equivalent to 122, 199, 324 and 430 °days post-winter
- 973 solstice rise in daylength respectively).

974

- Figure 4. Heatmap of differentially expressed genes (p < 0.05, FC > 1.3) in both diploids (either
- 976 diets L2 or L3 compared with diet L1) and triploids (either diets L2 or L3 compared with diet
- 977 L1). Red denotes upregulation whereas green denotes downregulation. Expression data is log2
- 978 transformed. P-values were corrected for false discovery rate. The heatmap was generated using
- 979 the package gplots (Warnes et al., 2013).

- **Supplementary File Captions**
- 982 Supplementary File 1. Fatty acid compositions (percentage of total fatty acids) of the
- 983 experimental base feed.
- 984 Supplementary File 2. Gene sets significantly affected by different micronutrient
- 985 supplementation in diploid and triploid salmon. Red denotes upregulation and green
- 986 downregulation.

Supplementary File 3. - List of genes differentially expressed and affected by different 987 micronutrient levels in diploid and triploid salmon. Red denotes upregulation and green 988 downregulation. 989 990

Supplementary File 4. Current EU limits for additive inclusion within fish feeds

**Table 1.** Formulation (g.100g diet<sup>-1</sup>) and proximate composition (analysed) of experimental diets

	Diet		
Ingredients	L1	L2	L3
Fish Meal <sup>1</sup>	13.00	13.00	13.00
Krill Meal <sup>2</sup>	2.00	2.00	2.00
Soy Protein Concentrate <sup>3</sup>	17.94	18.00	17.65
Corn Gluten <sup>4</sup>	4.49	3.00	3.00
Pea Protein Concentrate <sup>5</sup>	17.94	18.49	18.15
Wheat Gluten <sup>4</sup>	14.36	14.79	14.52
Wheat <sup>6</sup>	8.63	8.26	7.46
Fish Oil <sup>7</sup>	8.00	8.00	8.00
Rapeseed oil <sup>4</sup>	5.25	5.32	5.47
Linseed oil	1.27	1.28	1.32
Palm kernel oil	3.17	3.21	3.30
ARRAINA Nutrient Package <sup>8</sup> †‡	0.75	1.50	3.00
Monosodium phosphate	2.52	2.53	2.54
Amino acid Premix <sup>9</sup> ,*	0.68	0.62	0.59
Proximate Composition (Analysed)			
Moisture (%)	6.3	6.8	6.1
Crude lipid (%)	20.8	21.1	22.7
Crude protein (%)	48.9	47.0	48.1
Ash (%)	6.5	6.8	7.4
Energy (MJ / kg)	23.4	23.4	23.4

<sup>1</sup>Feed Services, Bremen, Germany; <sup>2</sup>Aker Biomarine, Norway; <sup>3</sup>Caramuru, Brazil; <sup>4</sup>Cargill, Germany; <sup>5</sup>Agrident, Germany; <sup>6</sup>WN Lindsey, UK; <sup>7</sup>ED & F Man, Germany; <sup>8</sup>DSM, Netherlands; <sup>9</sup>Evonik, Germany; <sup>†</sup>Added as components of the nutrient package (NP), and times requirement based on NRC (2011) minimum requirement for Atlantic salmon and modified according to Hamre et al., (2016), diet L1 achieving assumed 100 % minimum requirement; \*Balanced for lysine, methionine, threonine and valine. Contains antioxidant.

**Table 2.** Added micronutrient concentrations (mg.kg<sup>-1</sup>) within the nutrient package (NP): selected amino acids (histidine and taurine), minerals, vitamins and cholesterol.

	Diet				
Premix Formulations	L1	L2	L3		
Vitamin A	3.79	7.58	15.16		
Vitamin D3	0.05	0.10	0.20		
Vitamin E	102.44	204.88	409.76		
Vitamin K3	9.82	19.64	39.28		
Thiamin	2.67	5.34	10.68		
Riboflavin	8.30	16.60	33.20		
B6	4.77	9.54	19.08		
B12	0.25	0.50	1.00		
Niacin	24.80	49.60	99.20		
Pantothenic Acid	17.15	34.30	68.60		
Folic Acid	2.82	5.64	11.28		
Biotin	0.14	0.28	0.56		
Vitamin C	80	160	320		
Calcium	0.4	0.8	1.6		
Cobalt	0.94	1.88	3.76		
Iodine	0.67	1.34	2.68		
Selenium	0.23	0.46	0.92		
Iron	32.64	65.28	130.56		
Manganese	12.03	24.06	48.12		
Copper	3.24	6.48	12.96		
Zinc	66.92	133.84	267.68		
Taurine	2450	4900	9800		
Histidine	1400	2800	5600		
Cholesterol	1100	2200	4400		

**Table 3.** Analysed concentrations of selected amino acids (taurine, histidine and methionine g.kg<sup>-1</sup>) macro-minerals (calcium, magnesium and phosphorous, g.kg<sup>-1</sup>) micro-minerals and vitamins (mg.kg<sup>-1</sup>) of the experimental diets for the 2 mm and 3 mm pellets. Nutrients added at graded levels to the feeds are shown with an asterisk. "-" denotes not analysed.

Pellet Size		2mm			3mm		
	L1	L2	L3	L1	L2	L3	NRC 2011 <sup>‡</sup>
Vitamin A*	5.2	7.2	14.2	6.2	5.1	7.2	0.75 <sup>a</sup>
Vitamin D3*	0.17	0.19	0.29	0.17	0.18	0.26	$0.04^{a}$
Vitamin E*	85	146	203	75	151	273	$60^{\rm b}$
Vitamin K3*	0.43	0.78	1.60	0.70	1.12	1.12	$< 10^{b}$
Thiamin*	3.3	5.8	9.3	3.7	20.2	29.9	1 <sup>a</sup> ,
Riboflavin*	12.1	20.6	35.8	11.7	34.4	57.6	4 <sup>a</sup> ,
Vitamin B6*	11.5	14.3	22.2	11.0	18.1	30.5	5 <sup>b</sup>
Vitamin B12*	0.17	0.30	0.49	0.14	0.34	0.66	NT
Niacin*	75	107	163	80	221	434	$10^{a}$ ,
Pantothenic acid*	18.6	33.2	50.2	20.2	74.3	66.0	$20^{a}$
Folic acid*	2.82	-	7.53	2.82	19.95	12.54	1 <sup>a</sup>
Biotin*	0.44	0.71	1.03	0.47	1.10	1.91	$0.15^{a}$
Vitamin C*	83	180	312	77	238	244	20 <sup>b</sup>
Cobalt*	1.0	1.6	3.5	0.95	2.3	3.4	NT
Iodine*	-	-	-	1.1	3.4	6.1	1.1 <sup>a</sup>
Selenium*	1.2	1.5	2.2	1.3	1.6	2.5	$0.15^{a}$
Iron*	300	330	510	330	310	410	$30-60^{b}$
Manganese*	43	57	110	47	49	75	$10^{b}$
Copper*	10	12	19	10	13	19	5 <sup>b</sup>
Zinc*	160	190	300	100	200	350	37 <sup>b</sup>
Taurine*	2.8	4.6	8.1	2.7	5.0	9.5	$NR^b$
Methionine	8.7	8.8	8.6	9.0	8.8	9.1	$7.0^{b}$
Histidine*	11.6	11.7	14.0	11.9	13.1	14.5	$8.0^{b}$
Calcium*	6.6	6.9	8.6	6.3	6.7	7.5	$NR^{b*}$
Magnesium	1.5	1.5	1.5	1.3	1.3	1.3	$0.4^{b}$
Phosphorus	12.0	12.0	12.0	11.0	11.0	11.0	$8.0^{b}$
Cholesterol*	n.a.	n.a.	n.a	n.a	n.a.	n.a.	NR

‡Current NRC, 2011 minimum requirement recommendations determined in <sup>a</sup> rainbow trout, <sup>b</sup> Atlantic salmon are shown for comparison. n.a. not analysed; NR\* no requirement freshwater; NT, not tested.

**Table 4.** Mortality, initial and final weight and somatic indices recorded at the end (week 31) of freshwater rearing of juvenile diploid and triploid Atlantic salmon fed low marine diets (FM 15 % / FO 8 %) diets with differing micronutrient supplementation level (diets L1, L2 and L3). Superscripts denote significant differences between diets and ploidy.

		Diploid			Triploid			P values	
Diet	L1	L2	L3	L1	L2	L3	P	D	P * D
Mortality (%)† (n=2)	$4.8 \pm 4.3$	$1.4 \pm 0.6$	$0.6 \pm 0.1$	$1.6 \pm 0.5$	$1.1 \pm 0.2$	$1.1 \pm 0.3$	n/a	n/a	n/a
Initial Parr Wt (g) (n=50)	$37.2\pm1.8~^{\rm a}$	$37.2\pm1.8~^{\rm a}$	$37.2\pm1.8~^{a}$	$27.6 \pm 0.8$ $^{b}$	$27.6 \pm 0.8$ $^{\rm b}$	$27.6\pm0.8$ b	0.005	0.378	0.299
Final Smolt Wt (g) (n=50)	$94.4 \pm 14.2^{\ b}$	$113.8 \pm 9.4~^{\rm a}$	$94.1 \pm 15.7$ b	$75.4 \pm 6.8~^{c}$	$75.2 \pm 2.6$ °	$77.5 \pm 0.9$ °	0.001	0.065	0.036
SGRwt (n=2)	$0.62 \pm 0.02^{\ b}$	$0.70\pm0.04^{\rm \ a}$	$0.61 \pm 0.04^{\ b}$	$0.63 \pm 0.02^{\ b}$	$0.61 \pm 0.03^{b}$	$0.63\pm0.02^{\;b}$	0.056	0.063	0.001
RWG (%) (n=2)	$150.8 \pm 12.2^{bc}$	$206.5\pm4.8^a$	$138.9 \pm 17.2^{\circ}$	$175.3\pm13.0^{ab}$	$163.3 \pm 13.6$ bc	$180.2\pm8.8^{ab}$	0.215	0.008	0.001
FCR (n=2)	$0.90\pm0.24^{~ab}$	$0.71 \pm 0.10^{b}$	$0.87\pm0.03^{~ab}$	$0.93\pm0.12^{ab}$	$1.02\pm0.18^{\rm \ a}$	$0.92\pm0.00^{ab}$	0.015	0.716	0.050
VSI (%) (n=10)	$8.61\pm0.55~^{\rm a}$	$7.24 \pm 0.23^{\ b}$	$8.48\pm0.65^a$	$6.99\pm0.32^b$	$7.11 \pm 0.09$ b	$7.42\pm0.21^{ab}$	0.001	0.009	0.031
HSI (%) (n=10)	$1.36\pm0.19~^{\rm a}$	$1.19 \pm 0.03$ b	$1.35\pm0.25~^{\mathrm{a}}$	$1.05\pm0.06~^{\rm b}$	$1.12\pm0.07~^{ab}$	$1.15\pm0.01~^{ab}$	0.057	0.018	0.006
Hepatic Steatosis (%) (n=4)	$1.6 \pm 0.8$ c	$2.5 \pm 0.5~^{ab}$	$1.7 \pm 0.2$ bc	$2.3 \pm 0.5$ abc	$2.2\pm0.2^{~abc}$	$2.8\pm0.1^a$	0.004	0.183	0.003

Data are presented as means ± SD. † Mortality data analysed by Contingency Chi-square tests

FCR, feed conversion ratio; HSI, hepatosomatic index; RWG, relative weight gain (%); SGRwt, specific growth rate weight (% day-1); VSI, viscerosomatic index

**Table 5.** Whole fish proximate composition (%) and fatty acid compositions (% of total fatty acids) of liver of diploid and triploid salmon fed low marine diets with differing micronutrient supplementation level. Significant effect is highlighted in bold and superscripts denote significant differences between diets and ploidy (two-way ANOVA).

Ploidy (P)		Diploid			Triploid			p values	
Diet (D)	L1	L2	L3	L1	L2	L3	P	D	P * D
Moisture (%)	$68.9 \pm 0.1$	$68.2 \pm 0.1$	$69.0 \pm 0.2$	$69.7 \pm 0.3$	$69.2 \pm 0.1$	$69.2 \pm 0.7$	0.011	0.087	0.316
Oil (%)	$10.4 \pm 1.0$	$10.5 \pm 0.4$	$10.4 \pm 0.1$	$9.9 \pm 0.0$	$10.6 \pm 0.0$	$10.5 \pm 0.3$	0.719	0.429	0.493
Protein (%)	$17.5 \pm 0.6$	$18.1 \pm 0.6$	$17.7 \pm 0.6$	$17.2 \pm 0.4$	$16.8 \pm 0.1$	$16.9 \pm 0.6$	0.035	0.885	0.443
Ash (%)	$2.3 \pm 0.1$	$2.3 \pm 0.1$	$2.2 \pm 0.1$	$2.3 \pm 0.0$	$2.3 \pm 0.0$	$2.3 \pm 0.0$	0.191	0.546	0.955
14:0	$2.3 \pm 0.3^{ab}$	$2.3\pm0.3^{a}$	$1.9 \pm 0.1^{ab}$	$1.7 \pm 0.1^{b}$	$1.7\pm0.3^{b}$	$2.1 \pm 0.3^{ab}$	0.006	0.888	0.015
16:0	$16.1 \pm 0.6^{b}$	$17.5 \pm 0.5^{ab}$	$18.7 \pm 0.8^{a}$	$18.4 \pm 1.8^{a}$	$18.8 \pm 0.5^{\rm a}$	$16.9 \pm 0.9^{b}$	0.250	0.354	0.015
18:0	$4.7 \pm 0.2^{a}$	$4.3 \pm 0.5^{ab}$	$4.2\pm0.4^{ab}$	$4.6\pm0.3^{\rm a}$	$4.2\pm0.5^{ab}$	$3.6\pm0.2^{b}$	0.126	0.009	0.508
Total Saturated <sup>1</sup>	$23.4 \pm 0.3^{\mathrm{b}}$	$24.4 \pm 0.5^{ab}$	$25.1 \pm 0.5^{\mathrm{a}}$	$25.0 \pm 1.7^{\mathrm{a}}$	$25.0 \pm 0.7^{\rm a}$	$22.9 \pm 0.9^{\mathrm{b}}$	0.968	0.457	0.017
16:1n-7	$2.4 \pm 0.3^{a}$	$2.2 \pm 0.3^{ab}$	$1.9 \pm 0.1^{ab}$	$1.8 \pm 0.0^{b}$	$1.8\pm0.1^{\rm b}$	$2.1 \pm 0.2^{ab}$	0.009	0.777	0.009
18:1n-9	$21.6 \pm 2.9^{a}$	$17.3 \pm 1.9^{ab}$	$16.5 \pm 0.8^{b}$	$15.3 \pm 1.6^{b}$	$14.7 \pm 1.1^{b}$	$18.0 \pm 2.5^{ab}$	0.019	0.130	0.015
18:1n-7	$2.8\pm0.3^a$	$2.4 \pm 0.2^{ab}$	$2.3 \pm 0.1^{ab}$	$2.2 \pm 0.2^{b}$	$2.0 \pm 0.0^{b}$	$2.1 \pm 0.$ b	0.001	0.056	0.177
20:1n-9	$2.5 \pm 0.4^{a}$	$2.4 \pm 0.2^{ab}$	$1.8 \pm 0.0^{b}$	$1.7 \pm 0.3^{b}$	$1.7 \pm 0.6^{b}$	$2.6 \pm 0.4^a$	0.213	0.756	0.002
22:1n-11	$0.6 \pm 0.1$	$0.6 \pm 0.1$	$0.4 \pm 0.1$	$0.5 \pm 0.1$	$0.5 \pm 0.2$	$0.7 \pm 0.1$	0.307	0.865	0.150
Total Monoenes <sup>2</sup>	$31.3 \pm 3.7^{\mathrm{a}}$	$26.3 \pm 2.6^{ab}$	$24.2 \pm 0.7^{\mathrm{b}}$	$23.3 \pm 1.6^{\rm b}$	$22.4 \pm 2.2^{\mathrm{b}}$	$27.4 \pm 3.2^{ab}$	0.031	0.168	0.007
18:2n-6	$6.8 \pm 0.7^{ab}$	$6.6 \pm 0.2^{ab}$	$5.9 \pm 0.1$ ab	$5.5 \pm 0.7^{b}$	$6.1 \pm 1.1^{ab}$	$7.4 \pm 0.1^{a}$	0.710	0.412	0.004
20:4n-6	$2.3 \pm 0.1^{a}$	$1.6 \pm 0.1^{bc}$	$2.1 \pm 0.3^{ab}$	$1.9 \pm 0.2$ abc	$1.8 \pm 0.3^{\rm \ abc}$	$1.4 \pm 0.2^{c}$	0.017	0.008	0.10
Total n-6 PUFA <sup>3</sup>	$12.0 \pm 0.6$	$10.8 \pm 0.3$	$10.5 \pm 1.0$	$9.7 \pm 1.3$	$9.9 \pm 1.0$	$11.6 \pm 0.6$	0.103	0.447	0.022
18:3n-3	$1.7 \pm 0.3$	$1.9 \pm 0.1$	$1.6 \pm 0.1$	$1.5 \pm 0.1$	$1.8 \pm 0.3$	$2.0 \pm 0.3$	0.460	0.226	0.066
18:4n-3	$0.4 \pm 0.2$	$0.3 \pm 0.0$	$0.3 \pm 0.0$	$0.3 \pm 0.0$	$0.3 \pm 0.1$	$0.4 \pm 0.0$	0.824	0.329	0.156
20:4n-3	$0.7 \pm 0.2^{\rm \ b}$	$0.9 \pm 0.1^{ab}$	$0.7 \pm 0.1^{\rm \ b}$	$0.8 \pm 0.1$ ab	$0.9 \pm 0.2^{ab}$	$1.1 \pm 0.1^{a}$	0.023	0.80	0.058
20:5n-3	$4.4 \pm 0.5$	$5.0 \pm 0.3$	$5.3 \pm 0.4$	$4.7 \pm 0.3$	$4.9 \pm 0.2$	$5.2 \pm 0.2$	0.744	0.017	0.600
22:5n-3	$0.9 \pm 0.2$	$1.1 \pm 0.1$	$1.2 \pm 0.2$	$1.1 \pm 0.0$	$1.1 \pm 0.1$	$1.2 \pm 0.1$	0.288	0.049	0.833
22:6n-3	$25.0 \pm 3.5^{b}$	$29.0 \pm 2.5$ ab	$30.9 \pm 1.5$ ab	$33.3 \pm 0.7^a$	$33.3 \pm 3.4^{a}$	$27.8 \pm 2.9^{~ab}$	0.020	0.337	0.006
Total n-3 PUFA <sup>4</sup>	$33.2 \pm 4.1$ b	$38.3 \pm 2.7^{\rm ab}$	$40.1 \pm 1.0^{\rm ab}$	$41.9 \pm 0.6^{\mathrm{a}}$	$42.6\pm2.5~^{\rm a}$	$38.0 \pm 3.0^{\rm ab}$	0.011	0.186	0.010
Total PUFA <sup>5</sup>	$45.3 \pm 3.5^{\text{ b}}$	49.2 ±3.0 ab	$50.7\pm0.3^{\rm \ ab}$	$51.6 \pm 1.2^{\text{ a}}$	$52.6 \pm 1.5^{a}$	$49.6 \pm 2.6^{\text{ ab}}$	0.019	0.201	0.45

Data are mean ± SD (n = 2). <sup>1</sup>Totals include 15:0, 20:0, 22:0 and 24:0 at up to 0.3%; <sup>2</sup>Totals include 16:1n-9, 20:1n-11, 20:1n-7, 22:1n-9 and 24:1n-9 at up to 1.9%; <sup>3</sup>Totals include 18:3n-6, 20:2n-6, 20:3n-6 and 22:5n-6 at up to 2.9%; <sup>4</sup>Totals include 20:3n-3 at up to 0.2%; <sup>5</sup>Includes C16 PUFA at up to 0.1%

**Table 6.** Whole fish total amino acids (g.kg wet wt<sup>-1</sup>) in diploid and triploid salmon fed low marine diets with differing micronutrient supplementation level. The supplemented amino acids (histidine, taurine and methionine) are marked with an asterisk (\*). Superscripts denote significant differences between diets within ploidy (two-way ANOVA).

Ploidy (P)		Diploids			Triploids			<i>p</i> -values	
Diet (D)	L1	L2	L3	L1	L2	L3	Ploidy	Diet	P * D
OH-pro	0.7±0.0	0.7±0.0	0.7±0.2	$0.6\pm0.0$	$0.8\pm0.0$	0.6±0.0	0.59	0.32	0.35
His*	$3.9\pm0.0$	$4.1 \pm 0.1$	4.1±0.2	$4.0\pm0.1$	4.1±0.0	$3.9\pm0.1$	0.64	0.42	0.61
Taurine*	$1.2\pm0.0$	$1.1\pm0.0$	$1.2\pm0.1$	$1.4\pm0.1$	$1.3\pm0.0$	$1.2\pm0.0$	0.048	0.29	0.65
Ser	$6.7 \pm 0.0$	$7.0\pm0.2$	$6.9\pm0.1$	$6.9\pm0.0$	$7.0\pm0.0$	$6.6\pm0.0$	0.72	0.07	0.06
Arg	$9.0\pm0.0$	$9.2 \pm 0.1$	$9.0\pm0.2$	$9.0\pm0.3$	$9.2\pm0.0$	$8.7 \pm 0.1$	0.59	0.16	0.73
Gly	9.1±0.1	$9.2 \pm 0.1$	$8.9\pm0.3$	$9.5\pm0.9$	$9.2\pm0.0$	$8.8\pm0.2$	0.74	0.52	0.77
Asp	17.0±1	18±1	17±1	17.3±0.6	17.9±0.2	17.6±0.3	0.67	0.31	0.93
Glu	23±0	24±0	22±1	$22.7 \pm 0.6$	23.1±0.1	$22.4\pm0.1$	0.64	0.19	0.91
Thr	$7.6 \pm 0.1$	$7.9 \pm 0.1$	$7.9 \pm 0.1$	$7.7 \pm 0.1$	$7.9\pm0.0$	$7.6 \pm 0.1$	0.76	0.09	0.24
Ala	9.9±0.1	10±0.2	$9.9\pm0.3$	$9.8 \pm 0.0$	10.1±0.1	$9.9\pm0.0$	0.67	0.22	0.82
Pro	$5.9\pm0.0$	$6.2\pm0.1$	$6.0\pm0.2$	6.1±0.2	$6.1 \pm 0.0$	$5.9\pm0.1$	0.79	0.30	0.58
Lys	15±1	16±0	16±1	$15.3\pm0.8$	16.1±0.3	16.0±0.3	0.95	0.35	0.84
Tyr	5.3±0.0	5.4±0.0	5.5±0.1	5.3±0.2	$5.5\pm0.0$	$5.2\pm0.1$	0.60	0.23	0.17
Met*	5.0±0.0	5.2±0.1	5.1±0.1	5.1±0.0	$5.2\pm0.0$	$4.9\pm0.1$	0.67	0.08	0.09
Val	$8.8 \pm 0.1$	$9.2 \pm 0.1$	$8.7\pm0.5$	$8.4\pm0.0$	$8.6 \pm 0.2$	$8.7 \pm 0.2$	0.16	0.44	0.63
Ile	$7.0\pm0.1$	5.5±1.9	$7.0\pm0.4$	$6.7 \pm 0.0$	$7.0\pm0.2$	$7.0\pm0.2$	0.61	0.63	0.55
Leu	13±0.0	13±0.2	13±0.4	12.6±0.2	13.0±0.1	12.6±0.3	0.63	0.11	0.69
Phe	$6.8 \pm 0.0$	$6.9\pm0.1$	$7.0\pm0.1$	$6.9\pm0.2$	$7.1\pm0.0$	$6.6\pm0.1$	0.87	0.39	0.21

Data are presented as mean  $\pm$  SD (n=2).

**Table 7**. Free amino acids and N-metabolites within white muscle tissues ( $\mu$ mol / 100g wet wt) of diploid and triploid salmon fed low marine diets with differing micronutrient supplementation level. Only the N-metabolites being significantly affected are shown (two-way ANOVA, Tukey p < 0.05, Kruskall Wallis when not fulfilling ANOVA assumptions). Histidine and taurine were supplemented in graded levels. Significant effect is highlighted in bold and superscripts denote significant differences between diets within ploidy (two-way ANOVA).

Ploidy (P)		Diploids			Triploids			<i>p</i> -values	
Diet (D)	L1	L2	L3	L1	L2	L3	Ploidy	Diet	P * D
Taurine*	195±21	124±7	195±46	266±19	222±47	260±22	0.020	0.192	0.85
Asp	9±0.3	10±2.	9±0.4	12±1	13±0.6	15±0.7	0.008	0.41	0.40
OH-pro	19±11	40±12	25±15	53±5	45±7	48±7	0.021	0.81	0.44
Thr	$55{\pm}2^b$	65±1 <sup>a</sup>	$68\pm5^a$	$45\pm1^b$	$55\pm4^a$	$53\pm4^a$	0.24	0.019	0.69
Glu	60±5	55±4	57±3	66±3	67±5	71±1	0.021	0.78	0.58
Gln	22±3	26±8	23±5	35±0.5	$30\pm2$	34±1	0.035	0.99	0.62
Val	39±4	27±3	37±5	23±1	27±0.1	28±0.1	0.024	0.26	0.11
Cystath	4±0.3a	1±0.3 <sup>b</sup>	$3\pm1^b$	$5\pm0.4^a$	$2\pm0.1^{b}$	$1\pm 0.1^{b}$	0.85	0.004	0.13
Ile	23±1	13±2	20±4	11±0.1	$14\pm0.6$	$14\pm0.1$	0.025	0.32	0.12
Leu	36±2	25±1	34±6	22±2	26±1	26±1	0.025	0.26	0.06
β-Ala	69±14	63±12	41±5	104±3	$105\pm25$	93±11	0.006	0.315	0.80
Lys	23±3	15±2	24±2	10±1	14±3	15±1	0.007	0.17	0.09
Anserine	1810±71	1972±184	21441	1560±7	1756±15	1710±9	0.014	0.057	0.41

Data are presented as mean ± SD (n=2). Muscle N-metabolites (µmol/100g wet wt, n=2), Cystath, cystathionine.

**Table 8.** Concentrations of vitamins (mg kg<sup>-1</sup> wet wt) in whole body, muscle, liver and gill in diploid and triploid salmon fed low marine diets with differing micronutrient supplementation level (Diets L1, L2 and L3). The supplemented vitamins are marked with an asterisk. Significant effect is highlighted in bold and superscripts denote significant differences between diets within ploidy (two-way ANOVA).

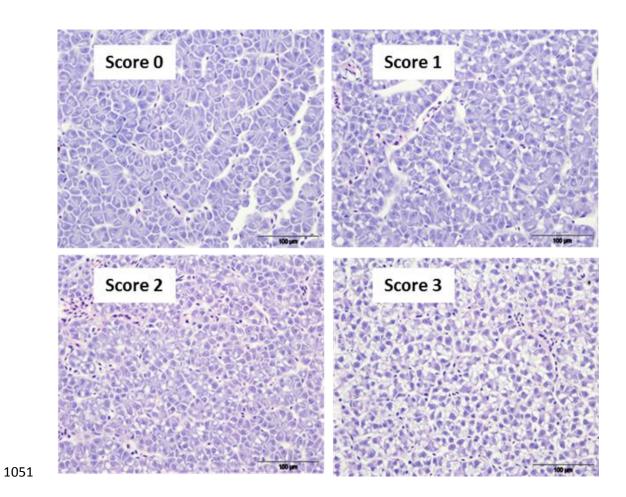
Ploidy (P)		Diploid			Triploid			<i>p</i> -values	
Diet (D)	L1	L2	L3	L1	L2	L3	Ploidy	Diet	P * D
Whole body									
Biotin*	63±4	67±10	60±4	80±4	74±9	74±4	0.129	0.925	0.546
Folate*	$0.21\pm0.04$	$0.27 \pm 0.05$	$0.30\pm0.01$	$0.27\pm0.01$	$0.26\pm0.01$	$0.27 \pm 0.01$	0.084	0.149	0.035
Niacin*	43±3ª	$48\pm4^{ab}$	54±4 <sup>b</sup>	41±1 a	$45{\pm}1^{ab}$	$49\pm2^{b}$	0.273	0.006	0.083
Pantothene*	$5.3\pm2.1$	$7.3\pm0.4$	8.0±1.9	5.5±0.6	$7.4 \pm 0.8$	$6.9 \pm 0.3$	0.372	0.051	0.184
Riboflavine*	1.60±0.14 b	1.75±0.07 b	$1.90\pm0.14^{b}$	1.50±0.00 a	1.55±0.21 a	1.50±0.00 a	0.016	0.286	0.286
Thiamin*	$0.70\pm0.14$	$0.80\pm0.14$	$0.90\pm0.14$	$0.75 \pm 0.07$	$0.80\pm0.00$	$0.80 \pm 0.00$	0.791	0.304	0.609
Vit-C*	11.1±1.3 a	18.5±0.1 ab	$26{\pm}10^{b}$	12.6±0.5 a	19.7±1.5 ab	$23.1 \pm 0.6^{b}$	0.994	0.015	0.746
α-ТОН*	28±0°a	41±0°	$48\pm2^{c}$	28±1 a	$30\pm3$ bc	$40\pm4^{\rm c}$	< 0.001	<0.001	0.037
ү-ТОН	$2.8\pm0.4$ b	2.6±0.1 b	1.7±0.0 a	$3.1\pm0.4^{b}$	$2.6\pm0.3$ b	1.6±0.1 <sup>a</sup>	0.922	<0.001	0.559
Muscle									
Vit-B6*	$5.6\pm0.1$	6.3±1.1	$5.0\pm2.4$	$4.8\pm0.4$	$5.3\pm0.4$	$5.8\pm0.4$	0.331	0.416	0.593
Riboflavin*	$1.10\pm0.00$	$0.95\pm0.07$	1.15±0.21	$1.10\pm0.00$	$1.05\pm0.07$	$1.05\pm0.07$	0.631	0.475	0.475
Thiamin*	$0.55\pm0.21$	$0.80\pm0.28$	$0.55\pm0.21$	$0.85 \pm 0.07$	$0.70\pm0.14$	$0.90\pm0.42$	0.128	0.962	0.594
α-ТОН*	12.0±0.0	$14.5 \pm 0.7$	$17.0\pm5.7$	$12.0\pm4.2$	13.0±0.0	$16.0\pm2.8$	0.521	0.063	0.981
ү-ТОН	1.60±0.14 b	1.25±0.07 a	0.90±0.28 a	1.85±0.35 b	1.25±0.07 a	0.80±0.14 a	0.527	<0.001	0.594
Liver									
Folate*	7.4±1.6	8.5±0.8	$7.9\pm0.9$	7.3±0.8	$8.9\pm0.7$	$9.4 \pm 0.7$	0.689	0.132	0.281
A1*	9.5±2.1a	12.0±2.8 a	21.5±6.4 b	7.5±2.1 a	14.0±5.7 a	19.0±2.8 b	0.446	0.012	0.746
A2	70±12 a	83±21 a	135±21 b	51±5 a	79±30 a	115±7 <sup>b</sup>	0.089	0.004	0.849
C*	82±5 a	$108\pm18^{\mathrm{b}}$	114±2°	$78{\pm}7^{a}$	102±5 b	140±10 °	0.914	<0.001	0.052
$K1^1$	40±9	37±12	31±4	20±8	12±3	17±0	0.001	0.004	0.238
$MK4^1$	31±4	34±10	40±5	14±0	14±3	17±1	< 0.001	0.051	0.292
Gill									
Pantothene*	5.3±1.8	8.9±1.1	9.1±0.1	7.2	7.3±0.0	6.1±3.0	0.423	0.416	0.248

Data are presented as mean  $\pm$  SD (n=2). <sup>1</sup>Menadione sodium bisulfate (vitamin K<sub>3</sub>) was added.

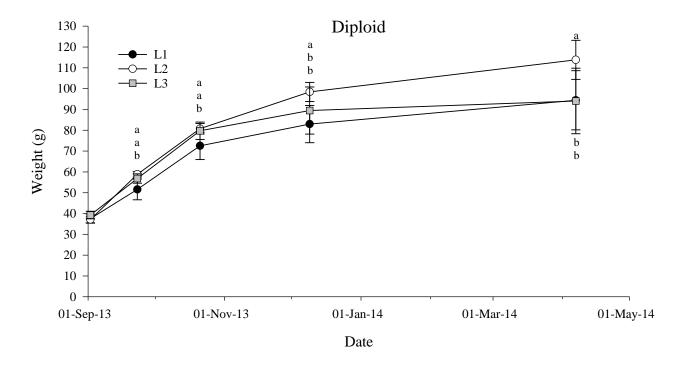
Table 9. Concentrations of minerals (mg kg<sup>-1</sup> wet wt) in whole body of diploid and triploid salmon fed low marine diets with differing micronutrient supplementation level. The supplemented elements are marked with an asterisk. Significant effect is highlighted in bold (two-way ANOVA)

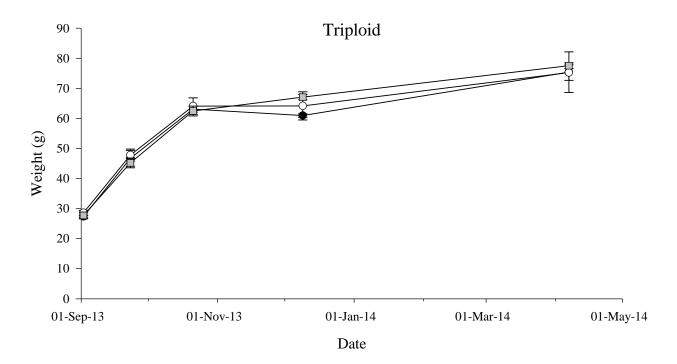
Ploidy (P)		Dip			Trip			p-values	
Diet (D)	L1	L2	L3	L1 L2 L3		L3	Ploidy	Diet	P *D
Ca*	3782±1018	4788±1182	4634±565	4094±684	3536±378	3850±981	0.28	0.87	0.45
Cu*	$0.98\pm0$	$0.96\pm0$	1±0	$0.9\pm0$	$0.9\pm0$	$0.85\pm0$	0.01	0.96	0.36
Fe*	$9.03\pm0.7$	8.8±0	10±1	10±0.8	$10\pm0.7$	10±0.3	0.24	0.27	0.7
I*	$0.08\pm0$	n.d.	$0.12\pm0$	$0.30\pm0.3$	$0.14\pm0$	$0.25\pm0.1$	0.11	0.66	0.61
K	3528±40	3663±18	3469±118	$3523\pm2$	3570±56	3609±262	0.84	0.54	0.43
Mn*	$1.6\pm0.4$	$1.8\pm0.2$	2±0	$1.7\pm0.2$	1.3±0	1±0.3	0.19	0.83	0.43
Mg	274±3	292±7	283±16	291±6	277±7	287±33	0.85	0.96	0.39
Na	551±24	605±88	588±9	669±56	600±5	589±63	0.24	0.83	0.23
P	3925±369	4616±748	4423±352	4135±324	3918±220	4064±560	0.33	0.73	0.42
Se*	$0.22\pm0$	$0.25\pm0$	$0.26\pm0$	$0.25\pm0$	$0.2\pm0$	0.3±0	0.46	0.09	0.60
Zn*	32±1.8	42±11	34±6	39±6	28±0.8	32±1	0.19	0.83	0.43

Data are presented as mean  $\pm$  SD (n=2).

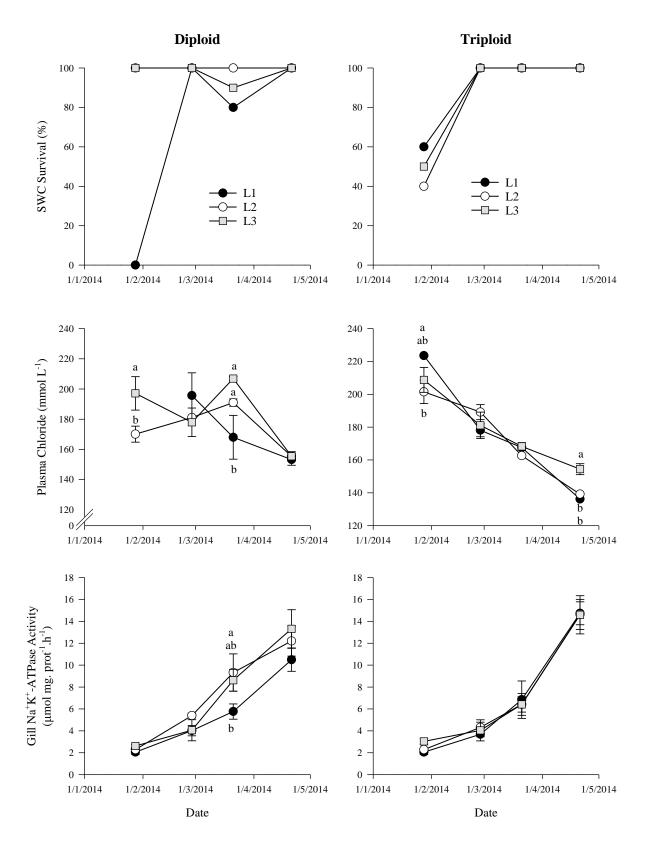


**Figure 1.** 

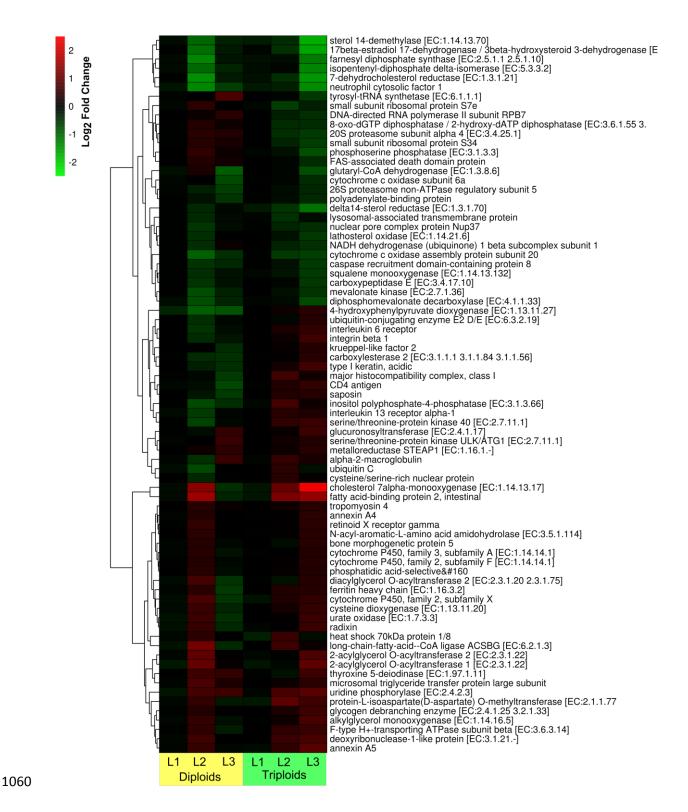




**Figure 2.** 



**Figure 3.** 



#### Figure 4

## 1063 Supplementary File 1.

	L1-L3
14:0	$5.3 \pm 0.2$
16:0	$11.8 \pm 0.3$
18:0	$2.5 \pm 0.0$
Total Saturates <sup>1</sup>	$25.7 \pm 0.3$
16:1n-7	$3.6 \pm 0.1$
18:1n-9	$26.3 \pm 0.2$
18:1n-7	$2.7 \pm 0.1$
20:1n-9	$3.9 \pm 0.2$
22:1n-11	$4.7 \pm 0.2$
Total Monoenes <sup>2</sup>	$42.8 \pm 0.6$
18:2n-6	$12.9 \pm 0.1$
20:4n-6	$0.3 \pm 0.0$
Total n-6 PUFA <sup>3</sup>	$13.5 \pm 0.1$
18:3n-3	$6.9 \pm 1.1$
18:4n-3	$1.1~\pm~0.0$
20:4n-3	$0.3 \pm 0.0$
20:5n-3	$4.5 \pm 0.1$
22:5n-3	$0.5 \pm 0.0$
22:6n-3	$3.6 \pm 0.1$
Total n-3 PUFA <sup>4</sup>	$16.8 \pm 0.9$
Total PUFA <sup>5</sup>	$31.5 \pm 0.8$

- Values are the averaged data for the L1, L2, and L3 in both 2 and 3 mm feeds (± SD provided
- to illustrate variance between feeds).
- 1066 PUFA, polyunsaturated fatty acids.
- 1067 <sup>1</sup>Totals include 14:0, 15:0, 20:0 and 22:0;
- <sup>2</sup>Totals include 16:1n-9, 20:1n-11, 20:1n-722:1n-9 and 24:1n-9;
- 1069 <sup>3</sup>Totals include 18:3n-6, 20:2n-6, and 22:5n-6;
- <sup>4</sup>Totals include 20:3n-3; <sup>5</sup>Totals include C16 PUFA.

1071

# 1073 Supplementary File 2.

Diet	Ploidy	Pathway	NGenes	Prop Down	Prop Up	FDR	Class
L2	DIPLOIDS	ko04710 Circadian rhythm	19	5.3%	52.6%	0.0124	Environmental adaptation
L3	DIPLOIDS	ko04910 Insulin signaling pathway	67	28.4%	13.4%	0.0185	Endocrine system
L2	TRIPLOIDS	ko00562 Inositol phosphate metabolism	34	8.8%	17.6%	0.0648	Carbohydrate metabolism
L2	TRIPLOIDS	ko04973 Carbohydrate digestion and absorption	16	6.3%	31.3%	0.0648	Digestive system
L2		ko03018 RNA degradation	53	34.0%			Folding, sorting and degradation
L2		ko04740 Olfactory transduction	11				Sensory system
L2		ko04512 ECM-receptor interaction	45	_			Signaling molecules and interaction
L2		ko04514 Cell adhesion molecules (CAMs)	71	9.9%	_		Signaling molecules and interaction
L3	TRIPLOIDS	ko00360 Phenylalanine metabolism	12	8.3%	33.3%	0.0854	Amino acid metabolism
L3		ko00010 Glycolysis / Gluconeogenesis		15.6%	_		Carbohydrate metabolism
L3		ko00040 Pentose and glucuronate interconversions	13	_			Carbohydrate metabolism
L3		ko00052 Galactose metabolism	17	-			Carbohydrate metabolism
L3		ko00500 Starch and sucrose metabolism	21	_			Carbohydrate metabolism
L3		ko04510 Focal adhesion	120	_			Cell communication
L3		ko04520 Adherens junction	56	=	_	_	Cell communication
L3		ko04810 Regulation of actin cytoskeleton	116	=			Cell motility
L3		ko04973 Carbohydrate digestion and absorption	16	_			Digestive system
L3			41	_			-
L3		koO4974 Protein digestion and absorption koO4975 Fat digestion and absorption		15.8%			Digestive system Digestive system
L3		koO4976 Bile secretion	43	=			Digestive system
L3			43	=			-
		ko03320 PPAR signaling pathway		=			Endocrine system
L3		ko04910 Insulin signaling pathway	68	=			Endocrine system
L3		ko04916 Melanogenesis	46		_		Endocrine system
L3		ko00190 Oxidative phosphorylation	107				Energy metabolism
L3		ko03018 RNA degradation	53				Folding, sorting and degradation
L3		ko03050 Proteasome	40				Folding, sorting and degradation
L3		ko04610 Complement and coagulation cascades	57				Immune system
L3		ko04623 Cytosolic DNA-sensing pathway	36			_	Immune system
L3		ko04662 B cell receptor signaling pathway	43	_			Immune system
L3		ko04670 Leukocyte transendothelial migration	64				Immune system
L3		ko04672 Intestinal immune network for IgA production	26				Immune system
L3		ko00100 Steroid biosynthesis	14		_		Lipid metabolism
L3		ko00140 Steroid hormone biosynthesis	23				Lipid metabolism
L3		ko00564 Glycerophospholipid metabolism	48	_			Lipid metabolism
L3	TRIPLOIDS	ko00830 Retinol metabolism	22	9.1%	45.5%	0.0340	Metabolism of cofactors and vitamins
L3		ko00900 Terpenoid backbone biosynthesis	16				Metabolism of terpenoids and polyketides
L3	TRIPLOIDS	ko00230 Purine metabolism	111			0.0755	Nucleotide metabolism
L3	TRIPLOIDS	ko00240 Pyrimidine metabolism	73	35.6%	8.2%	0.0270	Nucleotide metabolism
L3	TRIPLOIDS	ko03420 Nucleotide excision repair	36	44.4%	11.1%	0.0325	Replication and repair
L3	TRIPLOIDS	ko04740 Olfactory transduction	11	0.0%	27.3%	0.0293	Sensory system
L3	TRIPLOIDS	ko04742 Taste transduction	12	0.0%	16.7%	0.0484	Sensory system
L3	TRIPLOIDS	ko04012 ErbB signaling pathway	50	14.0%	34.0%	0.0807	Signal transduction
L3	TRIPLOIDS	ko04020 Calcium signaling pathway	89	13.5%	20.2%	0.0445	Signal transduction
L3	TRIPLOIDS	ko04310 Wnt signaling pathway	73	15.1%	26.0%	0.0379	Signal transduction
L3	TRIPLOIDS	ko04340 Hedgehog signaling pathway	23	13.0%	26.1%	0.0325	Signal transduction
L3	TRIPLOIDS	ko04512 ECM-receptor interaction	45	20.0%	24.4%	0.0484	Signaling molecules and interaction
L3	TRIPLOIDS	ko04514 Cell adhesion molecules (CAMs)	71	11.3%	25.4%	0.0025	Signaling molecules and interaction
L3	TRIPLOIDS	ko03020 RNA polymerase	27	44.4%	0.0%	0.0053	Transcription
L3	TRIPLOIDS	ko03040 Spliceosome	111	43.2%	11.7%	0.0235	Transcription
L3	TRIPLOIDS	ko03010 Ribosome	120	61.7%	5.8%	0.0270	Translation
L3	TRIPLOIDS	ko00980 Metabolism of xenobiotics by cytochrome P450	15	0.0%	46.7%	0.0278	Xenobiotics biodegradation and metabolism

# **Supplementary File 3.**

## 1076 Diploid L2 vs L1

KOID K00061	Gene Abbreviation RDH5	KEGG Annotation 11-cis-retinol dehydrogenase [EC:1.1.1.315]	Class ko00830 Retinol metabolism	Log Fold Cha	nge -1.05		adj P Val 0.285374
K00061 K00069	HPGD	15-hydroxyprostaglandin dehydrogenase (NAD) [EC:1.1.1.141]	ko05202 Transcriptional misregulation in cancer		-0.38	0.0006	
K13373	HSD17B7	17beta-estradiol 17-dehydrogenase / 3beta-hydroxysteroid 3-dehydrogenase	[ko00100 Steroid biosynthesis; ko00140 Steroid hormone biosynthesis; ko04913 Ovarian steroid		-1.07	0.0001	0.285374
K02731	PSMA7	20S proteasome subunit alpha 4 [EC:3.4.25.1]	ko03050 Proteasome		0.46		0.334596
K02729 K07439	PSMA5 CYP39A1	20S proteasome subunit alpha 5 [EC:3.4.25.1]	ko03050 Proteasome		0.43		0.361087 0.356921
K14458	MOGAT1, MGAT1	24-hydroxycholesterol 7alpha-hydroxylase [EC:1.14.13.99] 2-acylglycerol O-acyltransferase 1 [EC:2.3.1.22]	ko00120 Primary bile acid biosynthesis NA		.23		0.322942
K14457	MOGAT2, MGAT2	2-acylglycerol O-acyltransferase 2 [EC:2.3.1.22]	ko04975 Fat digestion and absorption		1.05		0.320209
K08683	HSD17B10		gko00280 Valine, leucine and isoleucine degradation; ko05010 Alzheimer's disease		0.43		0.356414
K01724	PCBD, phhB	4a-hydroxytetrahydrobiopterin dehydratase [EC:4.2.1.96]	NA		0.47		0.355469
K13524 K00457	ABAT HPD, hppD	4-aminobutyrate aminotransferase / (s)-3-amino-2-metnyipropionate transan 4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	ko00250 Alanine, aspartate and glutamate metabolism; ko00280 Valine, leucine and isoleucine ko00130 Ubiquinone and other terpenoid-quinone biosynthesis; ko00350 Tyrosine metabolism		0.89 -0.56	0.0067	0.322942 0.361087
K07127	uraH, pucM, hiuH	5-hydroxyisourate hydrolase [EC:3.5.2.17]	ko00230 Purine metabolism		-0.76		0.322942
K19029	PFKFB2	6-phosphofructo-2-kinase / fructose-2,6-biphosphatase 2 [EC:2.7.1.105 3.1.3.	NA		-0.69	0.0115	0.327913
K00033	PGD, gnd, gntZ	6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]	ko00030 Pentose phosphate pathway; ko00480 Glutathione metabolism		0.55		0.356414
K00213 K17816	DHCR7	7-dehydrocholesterol reductase [EC:1.3.1.21] 8-oxo-dGTP diphosphatase / 2-hydroxy-dATP diphosphatase [EC:3.6.1.55 3.	ko00100 Steroid biosynthesis NA		-1.37 0.40		0.285374 0.361087
K11259	NUDT1, MTH1 ILVBL	acetolactate synthase-like protein [EC:2.2.1]	NA NA		0.40		0.339247
K11262	ACAC	acetyl-CoA carboxylase / biotin carboxylase [EC:6.4.1.2 6.3.4.14]	ko00061 Fatty acid biosynthesis; ko00620 Pyruvate metabolism; ko00640 Propanoate metabolis		1.87		0.322942
K05756	ARPC3	actin related protein 2/3 complex, subunit 3	ko04666 Fc gamma R-mediated phagocytosis; ko04810 Regulation of actin cytoskeleton; ko0510		-0.52		0.334596
K05755	ARPC4	actin related protein 2/3 complex, subunit 4	ko04666 Fc gamma R-mediated phagocytosis; ko04810 Regulation of actin cytoskeleton; ko0510		0.41		0.361087
K18532 K01756	AK6, FAP7 purB, ADSL	adenylate kinase [EC:2.7.4.3] adenylosuccinate lyase [EC:4.3.2.2]	NA ko00230 Purine metabolism; ko00250 Alanine, aspartate and glutamate metabolism		-0.59 0.53		0.322942
K07296	ACDC	adiponectin	ko03320 PPAR signaling pathway; ko04920 Adipocytokine signaling pathway; ko04930 Type II di	_ =	0.77		0.359115
K12333	ADM	adrenomedullin	ko04270 Vascular smooth muscle contraction	<b>_</b>	0.49	0.0208	0.348275
K00827	AGXT2		tko00250 Alanine, aspartate and glutamate metabolism; ko00260 Glycine, serine and threonine		0.63		0.348275
K00002	AKR1A1, adh	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	ko00010 Glycolysis / Gluconeogenesis; ko00561 Glycerolipid metabolism; ko00930 Caprolactam		-0.41		0.322942
K00011 K15537	E1.1.1.21, AKR1 AGMO	aldehyde reductase [EC:1.1.1.21] alkylglycerol monooxygenase [EC:1.14.16.5]	ko00040 Pentose and glucuronate interconversions; ko00051 Fructose and mannose metabolisi NA	- =	0.58	0.0436	0.361087
K03910	A2M	alpha-2-macroglobulin	ko04610 Complement and coagulation cascades		-0.43		0.34213
K01231	MAN2	alpha-mannosidase II [EC:3.2.1.114]	ko00510 N-Glycan biosynthesis; ko00513 Various types of N-glycan biosynthesis		0.38		0.320209
K00764	purF, PPAT	amidophosphoribosyltransferase [EC:2.4.2.14]	ko00230 Purine metabolism; ko00250 Alanine, aspartate and glutamate metabolism		-0.68		0.322942
K09821	AGT	angiotensinogen	ko04270 Vascular smooth muscle contraction; ko04614 Renin-angiotensin system; ko05410 Hyp		-0.59		0.351561
K17093 K16646	ANXA4 ANXA5	annexin A4 annexin A5	NA NA	=======================================	0.46		0.356921
K08760	APOA4	apolipoprotein A-IV	ko04975 Fat digestion and absorption; ko04977 Vitamin digestion and absorption		0.03	0.0231	
K05641	ABCA1	ATP-binding cassette, subfamily A (ABC1), member 1	ko02010 ABC transporters; ko04975 Fat digestion and absorption	<b></b>	0.52	0.0425	0.361087
K05654	ABCB3, TAP2	ATP-binding cassette, subfamily B (MDR/TAP), member 3	ko02010 ABC transporters; ko04145 Phagosome; ko04612 Antigen processing and presentation;		-0.74		0.327913
K05668	ABCC5	ATP-binding cassette, subfamily C (CFTR/MRP), member 5	ko02010 ABC transporters		0.78		0.322942
K17675 K07970	SUPV3L1, SUV3 B3GNT3	ATP-dependent RNA helicase SUPV3L1/SUV3 [EC:3.6.4.13] beta-1,3-N-acetylglucosaminyltransferase 3 [EC:2.4.1]	NA ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series		-0.57 -0.65		0.356414
K00544	BHMT	betaine-homocysteine S-methyltransferase [EC:2.1.1.5]	ko00260 Glycine, serine and threonine metabolism; ko00270 Cysteine and methionine metabo		140		0.320209
K04663	BMP5	bone morphogenetic protein 5	ko04350 TGF-beta signaling pathway; ko04390 Hippo signaling pathway	<b>=</b>	0.46	0.0378	0.359115
K12873	BUD31, G10	bud site selection protein 31	ko03040 Spliceosome		-0.55		0.328871
K04001	SERPING1, C1INH	C1 inhibitor	ko04610 Complement and coagulation cascades; ko05133 Pertussis		-0.44		0.322942
K17610 K10364	CHP, CHP1 CAPZA	calcineurin B homologous protein 1 capping protein (actin filament) muscle Z-line, alpha	NA NA		-0.48 0.55		0.351668
K01948	CPS1	carbamoyl-phosphate synthase (ammonia) [EC:6.3.4.16]	ko00250 Alanine, aspartate and glutamate metabolism; ko00330 Arginine and proline metaboli		-0.58	0.000	0.285374
K11540	CAD		tko00240 Pyrimidine metabolism; ko00250 Alanine, aspartate and glutamate metabolism		0.45	0.0134	0.328871
K03927	CES2	carboxylesterase 2 [EC:3.1.1.1 3.1.1.84 3.1.1.56]	ko00983 Drug metabolism - other enzymes		-0.42	0.0498	
K01294	CPE	carboxypeptidase E [EC:3.4.17.10]	ko04940 Type I diabetes mellitus		-0.45		0.361087
K02187 K04396	CASP3 CASP6	caspase 3 [EC:3.4.22.56] caspase 6 [EC:3.4.22.59]	ko04010 MAPK signaling pathway; ko04115 p53 signaling pathway; ko04210 Apoptosis; ko04650 ko04210 Apoptosis	==	0.53		0.322942
K04397	CASP7	caspase 7 [EC:3.4.22.60]	ko04210 Apoptosis; ko04668 TNF signaling pathway; ko04932 Non-alcoholic fatty liver disease (	= =	0.52		0.322942
K12801	CARD8, CARDINAL	caspase recruitment domain-containing protein 8	ko04621 NOD-like receptor signaling pathway		-0.48	0.0296	0.356921
K09055	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	ko04932 Non-alcoholic fatty liver disease (NAFLD); ko05200 Pathways in cancer; ko05202 Transc		0.41		0.346585
K00720	UGCG	ceramide glucosyltransferase [EC:2.4.1.80]	ko00600 Sphingolipid metabolism		-0.58		0.351668
K18283 K05011	PDE2A CLCN2	cGMP-dependent 3',5'-cyclic phosphodiesterase [EC:3.1.4.17] chloride channel 2	NA ko04978 Mineral absorption		-0.40 -0.45		0.336403 0.322942
K12408	HSD3B7	cholest-5-ene-3beta,7alpha-diol 3beta-dehydrogenase [EC:1.1.1.181]	ko00120 Primary bile acid biosynthesis		0.66		0.361087
K00489	CYP7A1	cholesterol 7alpha-monooxygenase [EC:1.14.13.17]	ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko03320 PPAR	_	1.49		0.322942
K11367	CHD1	chromodomain-helicase-DNA-binding protein 1 [EC:3.6.4.12]	NA		-0.47		0.327913
K05752	C3ORF10, HSPC300	chromosome 3 open reading frame 10	ko04810 Regulation of actin cytoskeleton		0.47		0.361087
K03902 K01320	F5 F7	coagulation factor V (labile factor) coagulation factor VII [EC:3.4.21.21]	ko04610 Complement and coagulation cascades ko04610 Complement and coagulation cascades		-0.49 0.50		0.356234 0.361087
K17513	CLEC17A	C-type lectin superfamily 17 member A	NA		-0.43		0.356921
K09048	CREB3	cyclic AMP-responsive element-binding protein 3	ko04151 PI3K-Akt signaling pathway; ko04668 TNF signaling pathway; ko04725 Cholinergic syna		0.42	0.0021	0.320209
K01697	E4.2.1.22, CBS	cystathionine beta-synthase [EC:4.2.1.22]	ko00260 Glycine, serine and threonine metabolism; ko00270 Cysteine and methionine metabo		0.42		0.356921
K04487 K00456	iscS, NFS1 CDO1	cysteine desulfurase [EC:2.8.1.7]	ko00730 Thiamine metabolism; ko04122 Sulfur relay system		0.40		0.355469
K00456 K08342	ATG4	cysteine dioxygenase [EC:1.13.11.20] cysteine protease ATG4 [EC:3.4.22]	ko00270 Cysteine and methionine metabolism; ko00430 Taurine and hypotaurine metabolism ko04140 Regulation of autophagy		0.69		0.322942 0.356921
K17494	CSRNP	cysteine/serine-rich nuclear protein	NA		-0.39		0.356921
K18184	COX20	cytochrome c oxidase assembly protein subunit 20	NA		-0.93	0.0053	0.322942
K02263	COX4	cytochrome c oxidase subunit 4	ko00190 Oxidative phosphorylation; ko04260 Cardiac muscle contraction; ko04932 Non-alcohol		0.77		0.36668
K07416	CYP2F	cytochrome P450, family 2, subfamily F [EC:1.14.14.1]	ko00980 Metabolism of xenobiotics by cytochrome P450		0.42		0.366052
K17858 K07424	CYP2X CYP3A	cytochrome P450, family 2, subfamily X  cytochrome P450, family 3, subfamily A [EC:1.14.14.1]	NA ko00140 Steroid hormone biosynthesis; ko00591 Linoleic acid metabolism; ko00627 Aminobeni		0.86		0.356921 0.361087
K07424 K00326	E1.6.2.2	cytochrome-b5 reductase [EC:1.6.2.2]	ko00520 Amino sugar and nucleotide sugar metabolism	- 5	0.45		0.351087
K16342	PLA2G4, CPLA2	cytosolic phospholipase A2 [EC:3.1.1.4]	ko00564 Glycerophospholipid metabolism; ko00565 Ether lipid metabolism; ko00590 Arachidor		-0.42	0.0048	0.322942
K01493	comEB	dCMP deaminase [EC:3.5.4.12]	ko00240 Pyrimidine metabolism		-0.53		0.361087
K06051	DLL TM7552 EDG24	delta	ko04330 Notch signaling pathway		-0.50		0.322942
K00222 K11995	TM7SF2, ERG24 DNASE1L	delta14-sterol reductase [EC:1.3.1.70] deoxyribonuclease-1-like protein [EC:3.1.21]	ko00100 Steroid biosynthesis NA		-0.39 0.74		0.364258 0.356921
K11160	DGAT2	diacylglycerol O-acyltransferase 2 [EC:2.3.1.20 2.3.1.75]	ko00561 Glycerolipid metabolism; ko04975 Fat digestion and absorption		0.80		0.34213
K01278	DPP4	dipeptidyl-peptidase 4 [EC:3.4.14.5]	ko04974 Protein digestion and absorption		-0.55	0.0331	0.356921
K01597	MVD, mvaD	diphosphomevalonate decarboxylase [EC:4.1.1.33]	ko00900 Terpenoid backbone biosynthesis		-0.63		0.361087
K03509 K03027	POLH RPC40, POLR1C	DNA polymerase eta [EC:2.7.7.7] DNA-directed RNA polymerases I and III subunit RPAC1	ko03460 Fanconi anemia pathway ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polymerase; ko046		-0.57 0.44		0.361087 0.361087
K03027 K03009	RPC40, POLRIC RPB12, POLR2K	DNA-directed RNA polymerases I and III subunit RPAC1  DNA-directed RNA polymerases I, II, and III subunit RPABC4	ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polymerase; ko04 ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polymerase; ko046		-0.38		0.361087
K10428	DCTN6	dynactin 6	ko04962 Vasopressin-regulated water reabsorption		-0.56		0.351561
K10408	DNAH	dynein heavy chain, axonemal	ko05016 Huntington's disease		-0.51	0.0172	0.34213
K12172	RANBP2, NUP358	E3 SUMO-protein ligase RanBP2	ko03013 RNA transport		0.40		0.320209
K10249	ELOVL4	elongation of very long chain fatty acids protein 4 [EC:2.3.1.199] elongation of very long chain fatty acids protein 5 [EC:2.3.1.199]	ko00062 Fatty acid elongation: ko01000 Biosynthesis of unsaturated fatty acids		0.40		0.33425
K10244 K10203	ELOVL5 ELOVL6	elongation of very long chain fatty acids protein 5 [EC:2.3.1.199] elongation of very long chain fatty acids protein 6 [EC:2.3.1.199]	ko00062 Fatty acid elongation; ko01040 Biosynthesis of unsaturated fatty acids ko00062 Fatty acid elongation; ko01040 Biosynthesis of unsaturated fatty acids		0.53		0.366052 0.322942
K01415	ECE	endothelin-converting enzyme [EC:3.4.24.71]	NA		0.43		0.356921
K07511	ECHS1	enoyl-CoA hydratase [EC:4.2.1.17]	ko00062 Fatty acid elongation; ko00071 Fatty acid degradation; ko00280 Valine, leucine and iso	_ <b>, [</b>	0.48	0.0193	0.343412
K17277	EPS8	epidermal growth factor receptor kinase substrate 8	NA		-0.52		0.322942
K10084	EDEM1	ER degradation enhancer, mannosidase alpha-like 1	ko04141 Protein processing in endoplasmic reticulum		-0.84	0.0049	0.322942

K00894	ETNK, EKI	ethanolamine kinase [EC:2.7.1.82]	ko00564 Glycerophospholipid metabolism		0.85	0.0125	0.327913
K15593		etnanolamine kinase [EC:2.7.1.82] ets translocation variant 5	ko05202 Transcriptional misregulation in cancer				0.327913
K18645	EIF4EBP3	eukaryotic translation initiation factor 4E binding protein 3	NA		0.81	0.0263	0.356414
K00787		farnesyl diphosphate synthase [EC:2.5.1.12.5.1.10]	ko00900 Terpenoid backbone biosynthesis; ko05164 Influenza A; ko05166 HTLV-I infection		-1.23		0.322942
K02373		FAS-associated death domain protein	ko04210 Apoptosis; ko04620 Toll-like receptor signaling pathway; ko04622 RIG-I-like receptor s		0.41		0.343412
K10226 K00665		fatty acid desaturase 2 (delta-6 desaturase) [EC:1.14.19] fatty acid synthase, animal type [EC:2.3.1.85]	ko00592 alpha-Linolenic acid metabolism; ko01040 Biosynthesis of unsaturated fatty acids; ko0 ko00061 Fatty acid biosynthesis; ko04910 Insulin signaling pathway		-0.44 1.15		0.361087
K08751		fatty acid-binding protein 2, intestinal	ko03320 PPAR signaling pathway; ko04975 Fat digestion and absorption		1.68		0.330936
K05717		fibronectin 1	ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-receptor interactio		-0.42		
K01930		folylpolyglutamate synthase [EC:6.3.2.17]	ko00790 Folate biosynthesis		0.59		0.327913
K03096	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	ko04310 Wnt signaling pathway	_	0.68	0.0272	0.356732
K02133		F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]	ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkinson's disease		0.50		0.356921
K02135		F-type H+-transporting ATPase subunit epsilon	ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkinson's disease		0.47		0.324819
K02140		F-type H+-transporting ATPase subunit g	ko00190 Oxidative phosphorylation		0.39		0.366052
K02136 K01555		F-type H+-transporting ATPase subunit gamma	ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkinson's disease ko00350 Tyrosine metabolism; ko00643 Styrene degradation		0.42		0.34213
K08892		fumarylacetoacetase [EC:3.7.1.2] fyn-related kinase [EC:2.7.10.2]	NA		0.54		0.301087
K13134		gem associated protein 6	ko03013 RNA transport		-0.39		0.354448
K01084		glucose-6-phosphatase [EC:3.1.3.9]	ko00010 Glycolysis / Gluconeogenesis; ko00052 Galactose metabolism; ko00500 Starch and sucr		-0.40		0.328024
K02366		glucuronyl/N-acetylglucosaminyl transferase EXT1 [EC:2.4.1.224 2.4.1.225]	ko00534 Glycosaminoglycan biosynthesis - heparan sulfate / heparin		-1.15		0.322942
K11205	GCLM	glutamatecysteine ligase regulatory subunit	ko00480 Glutathione metabolism		0.60		0.322942
K01196		glycogen debranching enzyme [EC:2.4.1.25 3.2.1.33]	ko00500 Starch and sucrose metabolism		0.42		0.356921
K18443		golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	NA		-0.60		0.356414
K01495		GTP cyclohydrolase I [EC:3.5.4.16]	ko00790 Folate biosynthesis		0.70 0.79		0.322942
K01487 K03283		guanine deaminase [EC:3.5.4.3] heat shock 70kDa protein 1/8	ko00230 Purine metabolism ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein processing in endopl		0.79		0.322942 0.34213
K00510		heme oxygenase [EC:1.14.99.3]	ko00860 Porphyrin and chlorophyll metabolism; ko04978 Mineral absorption		1.28		0.322942
K02503		histidine triad (HIT) family protein	NA		0.52		0.361087
K11253		histone H3	ko05034 Alcoholism; ko05202 Transcriptional misregulation in cancer; ko05322 Systemic lupus €	<b>- </b>	0.41		0.356921
K11424	WHSC1, MMSET, NSD2	histone-lysine N-methyltransferase NSD2 [EC:2.1.1.43]	ko00310 Lysine degradation; ko05202 Transcriptional misregulation in cancer		-0.51		0.363386
K00451	HGD, hmgA	homogentisate 1,2-dioxygenase [EC:1.13.11.5]	ko00350 Tyrosine metabolism; ko00643 Styrene degradation		0.76	0.0280	0.356921
K16817	PLA2G16	HRAS-like suppressor 3 [EC:3.1.1.32 3.1.1.4]	ko00564 Glycerophospholipid metabolism; ko00565 Ether lipid metabolism; ko00590 Arachidor		-0.53		0.322942
K06092		InaD-like protein	ko04390 Hippo signaling pathway; ko04530 Tight junction		-0.60		0.361087
K00463		indoleamine 2,3-dioxygenase [EC:1.13.11.52]	ko00380 Tryptophan metabolism; ko05143 African trypanosomiasis		0.56		0.359115
K15046 K01107		influenza virus NS1A-binding protein inositol polyphosphate 1-phosphatase [EC:3.1.3.57]	ko05164 Influenza A ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signaling system		-0.51		0.322942
K01107 K01109		inositol polyphosphate 1-phosphatase [EC:3.1.3.5/] inositol polyphosphate-4-phosphatase [EC:3.1.3.66]	ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signaling system ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signaling system		-0.41		0.356921
K05459		insulin-like growth factor 1	ko04066 HIF-1 signaling pathway; ko04114 Oocyte meiosis; ko04115 p53 signaling pathway; ko0		0.64		0.322942
K05719		integrin beta 1	ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance; ko04510 Fo		-0.42		0.333403
K05132		interferon gamma receptor 1	ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway; ko04380 Ost		-0.72		0.322942
K05076	IL13RA1	interleukin 13 receptor alpha-1	koO4060 Cytokine-cytokine receptor interaction; koO4630 Jak-STAT signaling pathway		-0.47	0.0403	0.361087
K05055	IL6R	interleukin 6 receptor	ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway; ko04151 PI3		-0.50		0.322942
K05050		interleukin 8 receptor beta	ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pathway; ko041				0.333013
K01823		isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]	ko00900 Terpenoid backbone biosynthesis	_ <b></b>			0.353307
K00253		isovaleryl-CoA dehydrogenase [EC:1.3.8.4]	ko00280 Valine, leucine and isoleucine degradation				0.34213
K03898 K09228		kininogen KRAB domain-containing zinc finger protein	ko04610 Complement and coagulation cascades  NA		-0.41 -0.72		0.337954 0.322942
K09208		krueppel-like factor 9/13/14/16	NA NA		0.99		0.322942
K01852		lanosterol synthase [EC:5.4.99.7]	ko00100 Steroid biosynthesis		-0.42		0.361087
K00227		lathosterol oxidase [EC:1.14.21.6]	ko00100 Steroid biosynthesis		-0.42		0.356921
K02431	fucU, FUOM	L-fucose mutarotase [EC:5.1.3.29]	NA .		-0.39	0.0372	0.359115
K15013	ACSBG	long-chain-fatty-acidCoA ligase ACSBG [EC:6.2.1.3]	ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipocytokine signa		<b>1</b> 34	0.0022	0.320209
K03159		lymphotoxin beta receptor TNFR superfamily member 3	koO4060 Cytokine-cytokine receptor interaction; koO4064 NF-kappa B signaling pathway; koO40		-0.49		0.363326
K04294		lysophosphatidic acid receptor 3	koO4080 Neuroactive ligand-receptor interaction; koO4151 PI3K-Akt signaling pathway		-0.99		
K12387		lysosomal-associated transmembrane protein	ko04142 Lysosome		-0.38		0.356921
K13646 K04679		lysyl hydroxylase/galactosyltransferase/glucosyltransferase [EC:1.14.11.4 2.4 MAD, mothers against decapentaplegic interacting protein	ko00310 Lysine degradation; ko00514 Other types of O-glycan biosynthesis ko04144 Endocytosis; ko04350 TGF-beta signaling pathway		-1.29 -0.45		0.322942 0.351668
K09262		MADS-box transcription enhancer factor 2D	NA		-0.43		0.322942
K00029		malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.	ko00620 Pyruvate metabolism; ko00710 Carbon fixation in photosynthetic organisms		0.94		0.337954
K00140		malonate-semialdehyde dehydrogenase (acetylating) / methylmalon	ko00280 Valine, leucine and isoleucine degradation; ko00410 beta-Alanine metabolism; ko0050		0.76		0.320209
K06560		mannose receptor, C type	ko04145 Phagosome; ko05152 Tuberculosis		-0.52	0.0233	0.353307
K07994	MMP13	matrix metalloproteinase-13 (collagenase 3) [EC:3.4.24]	NA		-1.35	0.0263	0.356414
K08001	MMP23	matrix metalloproteinase-23 (CA-MMP) [EC:3.4.24]	NA		0.50	0.0313	0.356921
K01394		matrix metalloproteinase-3 (stromelysin 1, progelatinase) [EC:3.4.24.17]	koO4668 TNF signaling pathway; koO5202 Transcriptional misregulation in cancer; koO5323 Rheu		-1.32		0.353307
K01403		matrix metalloproteinase-9 (gelatinase B) [EC:3.4.24.35]	ko04668 TNF signaling pathway; ko04670 Leukocyte transendothelial migration; ko04915 Estrog		-1.31		0.339247
K05607		methylglutaconyl-CoA hydratase [EC:4.2.1.18]	ko00280 Valine, leucine and isoleucine degradation				0.359621
K00869 K14463		mevalonate kinase [EC:2.7.1.36] microsomal triglyceride transfer protein large subunit	ko00900 Terpenoid backbone biosynthesis; ko04146 Peroxisome ko04975 Fat digestion and absorption		-0.71		0.322942
K17885		mitochondrial carrier	NA				0.327913
K17781		mitochondrial import inner membrane translocase subunit TIM13	NA NA				0.356921
K17804		mitochondrial import inner membrane translocase subunit TIM44	NA		0.64	0.0193	0.343412
K17732		mitochondrial-processing peptidase subunit beta [EC:3.4.24.64]	NA	<b>_</b>	0.59		0.327913
K02539		myeloid leukemia cell differntiation protein MCL-1	ko04151 PI3K-Akt signaling pathway; ko05206 MicroRNAs in cancer		0.68		0.285374
K12751		myosin light chain 6	ko04270 Vascular smooth muscle contraction		-0.53		0.322942
K12757		myosin regulatory light chain 12	ko04510 Focal adhesion; ko04530 Tight junction; ko04670 Leukocyte transendothelial migration		0.56		0.328024
K03375 K00781	SIAT7E, ST6GalNAc V SIAT6	N-acetylgalactosaminide alpha-2,6-sialyltransferase (sialyltran N-acetyllactosaminide alpha-2,3-sialyltransferase (sialyltransferase 6) [EC:2	ko00604 Glycosphingolipid biosynthesis - ganglio series ko00513 Various types of N-glycan biosynthesis; ko00514 Other types of O-glycan biosynthesis;		-0.44 -0.59		0.327913 0.322942
K18458		N-acetyllactosaminide aipna-2,3-sialytransferase (sialytransferase 6) [EC:2 N-acyl-aromatic-L-amino acid amidohydrolase [EC:3.5.1.114]	NA		0.47		0.322942
K00775		NAD(P)-arginine ADP-ribosyltransferase [EC:2.4.2.31]	NA NA		-0.56		0.348275
K00858		NAD+kinase [EC:2.7.1.23]	ko00760 Nicotinate and nicotinamide metabolism		-0.60		0.322942
K03957		NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 1	ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic fatty liver disease (NAFLD); ko0501		-0.43		0.356921
K03963		NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 7	ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic fatty liver disease (NAFLD); ko0501	<b>=</b>	0.38		0.356921
K03968		NADH dehydrogenase (ubiquinone) 1 subunit C2	ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic fatty liver disease (NAFLD); ko0501		-0.47		0.361087
K03936		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [EC:1.6.5.3 1.6.99.3]	ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic fatty liver disease (NAFLD); ko0501		0.47		0.356921
K08008		NADPH oxidase	ko04066 HIF-1 signaling pathway; ko04145 Phagosome; ko04380 Osteoclast differentiation; ko0		-0.44		0.337954
K05750		NCK-associated protein 1 neurofascin	ko04810 Regulation of actin cytoskeleton ko04514 Cell adhesion molecules (CAMs)		-0.43 -0.44		0.322942
K06757 K08011		neurorascin neutrophil cytosolic factor 1	ko04062 Chemokine signaling pathway; ko04145 Phagosome; ko04380 Osteoclast differentiatio		-0.44		0.343412
K00767		nicotinate-nucleotide pyrophosphorylase (carboxylating) [EC:2.4.2.19]	k000760 Nicotinate and nicotinamide metabolism		-0.56		0.322942
K14461		Niemann-Pick C1-like protein 1	ko04975 Fat digestion and absorption		-0.48		0.356921
K18764		nocturnin [EC:3.1.13.4]	NA NA		-0.50		0.355469
K17108		non-lysosomal glucosylceramidase [EC:3.2.1.45]	ko00511 Other glycan degradation; ko00600 Sphingolipid metabolism		-0.57		0.35692
K14537		nuclear GTP-binding protein	ko03008 Ribosome biogenesis in eukaryotes		-0.39		0.35692
K14302		nuclear pore complex protein Nup37	ko03013 RNA transport		-0.50		0.359115
K08064		nuclear transcription factor Y, alpha	koO4612 Antigen processing and presentation; koO5152 Tuberculosis		-0.50		0.322942
K03768	PPIB, ppiB	peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]	NA .		-0.44		0.363326
144.00==					0.45	0.0093	0.322942
K13279		peroxiredoxin 1 [EC:1.11.1.15]	ko04146 Peroxisome				
K17594	PHACTR3	phosphatase and actin regulator 3	NA		-1.66	0.0073	0.322942
	PHACTR3 LIPH_I				-1.66 0.42	0.0073 0.0304	

VO10C2	DAFAII	alletelet estimation from a set allered and the set of	Lacoper Fabracia de manda di ser	<b>=</b>	0.004	0.2550-
K01062 K12862	PAFAH PLRG1, PRL1, PRP46	platelet-activating factor acetylhydrolase [EC:3.1.1.47] pleiotropic regulator 1	ko00565 Ether lipid metabolism ko03040 Spliceosome			0.356921
K12862 K04917	KCNK6	potassium channel subfamily K member 6	NA Kousu4u spiiceosome	0.43		0.356921
K04917 K00318	PRODH	proline dehydrogenase [EC:1.5]	ko00330 Arginine and proline metabolism			0.356921
K14443	TOB	protein Tob/BTG	ko03018 RNA degradation	0.46		0.327913
K18041	PTP4A	protein tyrosine phosphatase type IVA [EC:3.1.3.48]	NA	-0.44		0.322942
K00573	E2.1.1.77, pcm	protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77	NA	0.60		0.322342
K01021	TPST	protein-tyrosine sulfotransferase [EC:2.8.2.20]	NA .	0.60		0.322942
K05762	RDX	radixin	ko04810 Regulation of actin cytoskeleton; ko05205 Proteoglycans in cancer; ko05206 MicroRNA			0.348275
K07855	RERG	Ras-related and estrogen-regulated growth inhibitor	NA			0.354448
K06109	RAB13	Ras-related protein Rab-13	ko04530 Tight junction	-0.39		0.366052
K08847	RIPK3	receptor-interacting serine/threonine-protein kinase 3 [EC:2.7.11.1]	ko04623 Cytosolic DNA-sensing pathway; ko04668 TNF signaling pathway	-0.45		0.322942
K06778	PTPRS	receptor-type tyrosine-protein phosphatase S [EC:3.1.3.48]	NA	-0.43		0.322942
K10754	REC1	replication factor C subunit 1	ko03030 DNA replication; ko03420 Nucleotide excision repair; ko03430 Mismatch repair	-0.45		
K08526	NR2B3, RXRG	retinoid X receptor gamma	ko03320 PPAR signaling pathway; ko04920 Adipocytokine signaling pathway; ko05200 Pathway;	0.54		0.339247
K03539	RPP1, RPP30	ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5]	ko03008 Ribosome biogenesis in eukaryotes; ko03013 RNA transport	0.63		0.327913
K14000	RRBP1	ribosome-binding protein 1	ko04141 Protein processing in endoplasmic reticulum	-0.63		0.348275
K15216	RRN3, TIFIA	RNA polymerase I-specific transcription initiation factor RRN3	NA .	-0.60		0.348275
K14411	MSI	RNA-binding protein Musashi	ko03015 mRNA surveillance pathway	-0.46		0.322942
K00789	metK	S-adenosylmethionine synthetase [EC:2.5.1.6]	ko00270 Cysteine and methionine metabolism	-0.59		
K00314	SARDH	sarcosine dehydrogenase [EC:1.5.8.3]	ko00260 Glycine, serine and threonine metabolism	0.65		0.322942
K14381	SQSTM1	sequestosome 1	ko04380 Osteoclast differentiation	0.58		0.343412
K00654	SPT	serine palmitoyltransferase [EC:2.3.1.50]	ko00600 Sphingolipid metabolism	-0.45	0.0134	0.328871
K16312	STK40, SHIK	serine/threonine-protein kinase 40 [EC:2.7.11.1]	NA NA			0.322942
K02977	RP-S27Ae, RPS27A	small subunit ribosomal protein S27Ae	ko03010 Ribosome			0.322942
K02978	RP-S27e, RPS27	small subunit ribosomal protein S27e	ko03010 Ribosome			0.328024
K17409	MRPS30	small subunit ribosomal protein S30	NA			0.337954
K17412	MRPS34	small subunit ribosomal protein S34	NA			0.355469
K02993	RP-S7e, RPS7	small subunit ribosomal protein S7e	ko03010 Ribosome	0.54		0.356921
K05855	SYK	spleen tyrosine kinase [EC:2.7.10.2]	ko04064 NF-kappa B signaling pathway; ko04151 PI3K-Akt signaling pathway; ko04380 Osteoclas	-0.40		0.322942
K13219	SFPQ, PSF	splicing factor, proline- and glutamine-rich	NA	-0.70		0.322942
K00511	SQLE, ERG1	squalene monooxygenase [EC:1.14.13.132]	ko00909 Sesquiterpenoid and triterpenoid biosynthesis	-0.44	0.0068	0.322942
K00507	SCD, desC	stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]	koO1040 Biosynthesis of unsaturated fatty acids; koO3320 PPAR signaling pathway	1.04	0.0013	0.320209
K05917	CYP51	sterol 14-demethylase [EC:1.14.13.70]	ko00100 Steroid biosynthesis	-0.89	0.0105	0.322942
K06669	SMC3, CSPG6	structural maintenance of chromosome 3 (chondroitin sulfate proteoglyca	ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 Meiosis - yeast; ko04114 Oocyte meiosis	-0.65		0.322942
K00237	SDHD, SDH4	succinate dehydrogenase (ubiquinone) membrane anchor subunit	ko00020 Citrate cycle (TCA cycle); ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic f	0.48	0.0222	0.351668
K17254	SDCBP	syntenin-1	NA	-0.67	0.0111	0.327913
K00384	trxB	thioredoxin reductase (NADPH) [EC:1.8.1.9]	ko00240 Pyrimidine metabolism; ko00450 Selenocompound metabolism	0.68	0.0001	0.285374
K07754	DIO3	thyroxine 5-deiodinase [EC:1.97.1.11]	NA	0.65		0.356921
K12567	TTN	titin [EC:2.7.11.1]	ko05410 Hypertrophic cardiomyopathy (HCM); ko05414 Dilated cardiomyopathy	-0.92	0.0364	0.356921
K00616	E2.2.1.2, talA, talB	transaldolase [EC:2.2.1.2]	ko00030 Pentose phosphate pathway	0.56	0.0492	0.36668
K09275	TFCP2	transcription factor CP2 and related proteins	NA	0.42	0.0356	0.356921
K16796	SOX2	transcription factor SOX2 (SOX group B)	ko04390 Hippo signaling pathway	-0.40	0.0260	0.356414
K00615	E2.2.1.1, tktA, tktB	transketolase [EC:2.2.1.1]	ko00030 Pentose phosphate pathway; ko00710 Carbon fixation in photosynthetic organisms; ko	0.61	0.0016	0.320209
K03113	EIF1, SUI1	translation initiation factor 1	ko03013 RNA transport	-0.48	0.0263	0.356414
K03254	EIF3A	translation initiation factor 3 subunit A	ko03013 RNA transport	-0.49	0.0347	0.356921
K03247	EIF3H	translation initiation factor 3 subunit H	ko03013 RNA transport; ko05162 Measles	0.87	0.0264	0.356414
K03262	EIF5	translation initiation factor 5	ko03013 RNA transport	0.52	0.0098	0.322942
K01046	E3.1.1.3	triacylglycerol lipase [EC:3.1.1.3]	ko00561 Glycerolipid metabolism	-0.99	0.0049	0.322942
K12015	TRIM39	tripartite motif-containing protein 39 [EC:6.3.2.19]	NA	-0.50	0.0427	0.361087
K12034	TRIM69	tripartite motif-containing protein 69 [EC:6.3.2.19]	NA	-0.72	0.0097	0.322942
K10375	TPM4	tropomyosin 4	ko04260 Cardiac muscle contraction; ko05410 Hypertrophic cardiomyopathy (HCM); ko05414 Dil	0.44	0.0207	0.348275
K05865	TNNC1	troponin C, slow skeletal and cardiac muscles	ko04020 Calcium signaling pathway; ko04260 Cardiac muscle contraction; ko05410 Hypertrophic	-0.39	0.0004	0.285374
K17262	TBCB, CKAP1, ALF1	tubulin-folding cofactor B	NA	0.47	0.0091	0.322942
K05147	CD265, TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, activator	ko04060 Cytokine-cytokine receptor interaction; ko04064 NF-kappa B signaling pathway; ko043	-0.87	0.0019	0.320209
K06737	TACSTD1	tumor-associated calcium signal transducer 1	NA	0.38	0.0251	0.355469
K12842	SR140	U2-associated protein SR140	ko03040 Spliceosome	-0.45	0.0267	0.356414
K12626	LSM7	U6 snRNA-associated Sm-like protein LSm7	ko03018 RNA degradation; ko03040 Spliceosome	-0.54	0.0198	0.346585
K08770	UBC	ubiquitin C	ko03320 PPAR signaling pathway	-0.57	0.0180	0.34213
K10596	UBE4A	ubiquitin conjugation factor E4 A [EC:6.3.2.19]	ko04120 Ubiquitin mediated proteolysis	-0.50	0.0158	0.337954
K14016	UFD1	ubiquitin fusion degradation protein 1	koO4141 Protein processing in endoplasmic reticulum	0.38	0.0372	0.359115
K06689	UBE2D E, UBC4, UBC5	ubiquitin-conjugating enzyme E2 D/E [EC:6.3.2.19]	ko04120 Ubiquitin mediated proteolysis; ko04141 Protein processing in endoplasmic reticulum	-0.44	0.0075	0.322942
KOUUOJ			ko04141 Protein processing in endoplasmic reticulum	0.40	0.0364	0.356921
K14012		UBX domain-containing protein 1	KOO4141 Flotein processing in endoprasmic reticulum			
		urate oxidase [EC:1.7.3.3]	ko00230 Purine metabolism; ko00232 Caffeine metabolism	0.77	0.0326	0.356921
K14012	SHP1, UBX1, NSFL1C			0.77		0.356921
K14012 K00365	SHP1, UBX1, NSFL1C uaZ	urate oxidase [EC:1.7.3.3]	ko00230 Purine metabolism; ko00232 Caffeine metabolism		0.0451	
K14012 K00365 K00757	SHP1, UBX1, NSFL1C uaZ udp, UPP	urate oxidase [EC:1.7.3.3] uridine phosphorylase [EC:2.4.2.3]	ko00230 Purine metabolism; ko00232 Caffeine metabolism ko00240 Pyrimidine metabolism; ko00983 Drug metabolism - other enzymes	0.88	0.0451	0.363326
K14012 K00365 K00757 K01348	SHP1, UBX1, NSFL1C uaZ udp, UPP PLAU	urate oxidase [EC:1.7.3.3] uridine phosphorylase [EC:2.4.2.3] urokinase plasminogen activator [EC:3.4.21.73]	ko00239 Purine metabolism; ko00232 Caffeine metabolism ko00240 Pyrimidine metabolism; ko00983 Drug metabolism - other enzymes ko04064 NF-kappa B signaling pathway; ko04610 Complement and coagulation cascades; ko052	0.88	0.0451 0.0090 0.0488	0.363326

## 1082 Diploid L3 vs L1

KOID	Gene Abbreviation	KEGG Annotation	Class			adj P Val
K00725	B4GALNT1, GALGT	(N-Acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosami	ko00604 Glycosphingolipid biosynthesis - ganglio series			0.401932
K11517	HAO	(S)-2-hydroxy-acid oxidase [EC:1.1.3.15]	ko00630 Glyoxylate and dicarboxylate metabolism; ko04146 Peroxisome	-0.48		0.398783
K02731	PSMA7	20S proteasome subunit alpha 4 [EC:3.4.25.1] 20S proteasome subunit beta 9 [EC:3.4.25.1]	ko03050 Proteasome	0.39		0.437297
K02741 K06692	PSMB9, LMP2 PSMD5	26S proteasome non-ATPase regulatory subunit 5	ko03050 Proteasome NA	-2.05		0.398783
K03030	+	26S proteasome regulatory subunit N11	ko03050 Proteasome; ko05169 Epstein-Barr virus infection	0.49		0.398783
K05692	ACTB_G1	actin beta/gamma 1	ko04145 Phagosome; ko04390 Hippo signaling pathway; ko04391 Hippo signaling pat	0.53		0.422862
K05756	ARPC3	actin related protein 2/3 complex, subunit 3	ko04666 Fc gamma R-mediated phagocytosis; ko04810 Regulation of actin cytoskele	0.67		0.382122
K05699	ACTN	actinin alpha	ko04510 Focal adhesion; ko04520 Adherens junction; ko04530 Tight junction; ko0467	0.70	0.0033	
K12417	ACOT11	acyl-CoA thioesteraes 11 [EC:3.1.2]	NA	-0.52	0.0275	
K01512 K08047	acyP ADCY7	acylphosphatase [EC:3.6.1.7]	ko00620 Pyruvate metabolism; ko00627 Aminobenzoate degradation	-0.46 0.38	0.0057	0.398783 0.411219
K18532	AK6, FAP7	adenylate cyclase 7 [EC:4.6.1.1] adenylate kinase [EC:2.7.4.3]	ko00230 Purine metabolism; ko04020 Calcium signaling pathway; ko04062 Chemokii NA	-0.65		0.411219
K07296	ACDC	adiponectin	ko03320 PPAR signaling pathway; ko04920 Adipocytokine signaling pathway; ko0493	-0.88		0.401932
K01242	CD38	ADP-ribosyl cyclase 1 [EC:3.2.2.6 2.4.99.20]	ko00760 Nicotinate and nicotinamide metabolism; ko04020 Calcium signaling pathw	-0.41	0.0001	
K01872	AARS, alaS	alanyl-tRNA synthetase [EC:6.1.1.7]	ko00970 Aminoacyl-tRNA biosynthesis	0.55	0.0483	0.457001
K03910	A2M	alpha-2-macroglobulin	ko04610 Complement and coagulation cascades	0.64	0.0032	0.382122
K10331	ASB9	ankyrin repeat and SOCS box protein 9	NA	0.43	0.0275	0.436634
K17092	ANXA2	annexin A2	NA	-0.70		
K19502	ANO8, TMEM16H	anoctamin-8	NA	0.62	0.0118	
K01887 K01893	RARS, argS NARS, asnS	arginyl-tRNA synthetase [EC:6.1.1.19]	ko00970 Aminoacyl-tRNA biosynthesis	0.43	0.0189	0.401932
K05655	ABCB8	asparaginyl-tRNA synthetase [EC:6.1.1.22] ATP-binding cassette, subfamily B (MDR/TAP), member 8	ko00970 Aminoacyl-tRNA biosynthesis ko02010 ABC transporters	0.58	0.0382	
K12823	DDX5, DBP2	ATP-dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	ko03040 Spliceosome; ko05202 Transcriptional misregulation in cancer; ko05205 Pro	1.05	0.0142	
K11481	AURKA	aurora kinase A [EC:2.7.11.1]	ko04114 Oocyte meiosis	0.59	0.0399	
K08331	ATG13	autophagy-related protein 13	ko04140 Regulation of autophagy	-0.40	0.0398	
K03766	B3GNT5	beta-1,3-N-acetylglucosaminyltransferase 5 [EC:2.4.1.206]	ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series	0.87	0.0193	0.401932
K06712	BTN	butyrophilin	NA	-0.99	0.0238	
K01948	CPS1	carbamoyl-phosphate synthase (ammonia) [EC:6.3.4.16]	ko00250 Alanine, aspartate and glutamate metabolism; ko00330 Arginine and prolin	0.49	0.0027	
K03927	CES2	carboxylesterase 2 [EC:3.1.1.1.3.1.1.84 3.1.1.56]	ko00983 Drug metabolism - other enzymes	-0.45	0.0335	
K13049	PM20D1	carboxypeptidase PM20D1 [EC:3.4.17]	NA ko00071 Eathy acid doggadations ko03230 DDAR signaling nathway	-0.42	0.0251	
K08766 K04396	CPT2 CASP6	carnitine O-palmitoyltransferase 2 [EC:2.3.1.21] caspase 6 [EC:3.4.22.59]	ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway ko04210 Apoptosis	0.40		0.401932
K06454	CD4	CD4 antigen	ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presenta	-0.62	0.0149	0.000.00
K15360		centromere protein X	ko03460 Fanconi anemia pathway	0.39	0.0204	
K03998	C8B	complement component 8 subunit beta	ko04610 Complement and coagulation cascades; ko05020 Prion diseases; ko05146 Al	0.55	0.0261	
K06626	CCNE	cyclin E	ko04110 Cell cycle; ko04114 Oocyte meiosis; ko04115 p53 signaling pathway; ko0415	0.40	0.0080	
K01697	E4.2.1.22, CBS	cystathionine beta-synthase [EC:4.2.1.22]	ko00260 Glycine, serine and threonine metabolism; ko00270 Cysteine and methioni	-0.53	0.0076	0.398783
K02266	COX6A	cytochrome c oxidase subunit 6a	ko00190 Oxidative phosphorylation; ko04260 Cardiac muscle contraction; ko04932 N	-0.65	0.0057	
K07408	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1 [EC:1.14.14.1]	ko00140 Steroid hormone biosynthesis; ko00380 Tryptophan metabolism; ko00830 F	-1.03	0.0149	
K17854	CYP2K	cytochrome P450, family 2, subfamily K	NA NA	-0.52	0.0219	
K17951 K00058	CYP27C serA, PHGDH	cytochrome P450, family 27, subfamily C D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	NA ko00260 Glycine, serine and threonine metabolism; ko00680 Methane metabolism	0.41	0.0119	
K13989	DERL2_3	Derlin-2/3	ko04141 Protein processing in endoplasmic reticulum	0.55	0.0035	
K01277	DPP3	dipeptidyl-peptidase III [EC:3.4.14.4]	NA	0.51	0.0214	
K05125	DDR2, TKT	discoidin domain receptor family member 2 [EC:2.7.10.1]	NA NA	0.43		0.398783
K03509	POLH	DNA polymerase eta [EC:2.7.7.7]	ko03460 Fanconi anemia pathway	0.69	0.0168	
K02333	POLG2	DNA polymerase gamma 2	NA	-0.43	0.0297	0.436634
K02331	POL5, MYBBP1A	DNA polymerase phi [EC:2.7.7.7]	NA	0.51	0.0108	0.398783
K03015	RPB7, POLR2G	DNA-directed RNA polymerase II subunit RPB7	ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyme	0.42	0.0115	
K09504	DNAJA3	DnaJ homolog subfamily A member 3	ko05203 Viral carcinogenesis	-0.40		
K12232	HECTD2	E3 ubiquitin-protein ligase HECTD2 [EC:6.3.2.19]	NA	-0.50		0.457001
K17277 K15592	EPS8 ETV4	epidermal growth factor receptor kinase substrate 8	NA	0.43	0.0280	0.436634
K06110	EXOC3, SEC6L1	ets translocation variant 4 exocyst complex component 3	ko05202 Transcriptional misregulation in cancer ko04530 Tight junction	-0.46		
K10292	FBXO5, EMI1	F-box protein 5	ko04114 Oocyte meiosis	0.53		0.400203
K00522	FTH1	ferritin heavy chain [EC:1.16.3.2]	ko00860 Porphyrin and chlorophyll metabolism; ko04978 Mineral absorption	-0.53	0.0122	
K03904	FGB	fibrinogen beta chain	ko04610 Complement and coagulation cascades	0.92	0.0368	
K09571	FKBP4_5	FK506-binding protein 4/5 [EC:5.2.1.8]	ko04915 Estrogen signaling pathway	0.52		0.398783
K03841	FBP, fbp	fructose-1,6-bisphosphatase   [EC:3.1.3.11]	ko00010 Glycolysis / Gluconeogenesis; ko00030 Pentose phosphate pathway; ko000	-0.96	0.0383	0.440055
K02132	ATPeF1A, ATP5A1, ATP1	F-type H+-transporting ATPase subunit alpha	ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkinso	-0.44	0.0110	0.398783
K00849	galK	galactokinase [EC:2.7.1.6]	ko00052 Galactose metabolism; ko00520 Amino sugar and nucleotide sugar metabol	0.51	0.0046	
K00699	UGT	glucuronosyltransferase [EC:2.4.1.17]	ko00040 Pentose and glucuronate interconversions; ko00053 Ascorbate and aldarate	0.59	0.0305	
K00261	GLUD1_2, gdhA	glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]	ko00250 Alanine, aspartate and glutamate metabolism; ko00330 Arginine and prolin	-0.45	0.0140	
K11204 K01915	GCLC	glutamatecysteine ligase catalytic subunit [EC:6.3.2.2]	ko00480 Glutathione metabolism	-0.46 0.73	0.0028	
K01915 K00252	gInA, GLUL GCDH, gcdH	glutamine synthetase [EC:6.3.1.2] glutaryl-CoA dehydrogenase [EC:1.3.8.6]	ko00250 Alanine, aspartate and glutamate metabolism; ko00330 Arginine and prolin ko00071 Fatty acid degradation; ko00310 Lysine degradation; ko00380 Tryptophan m	-0.73		0.436634
K15839	GPSM1, AGS3	G-protein signaling modulator 1	ko05030 Cocaine addiction	-0.39		0.430034
K04534	GNAO, G-ALPHA-O	guanine nucleotide-binding protein G(o) subunit alpha	ko04713 Circadian entrainment; ko04723 Retrograde endocannabinoid signaling; ko			0.382122
K04538	GNB4	guanine nucleotide-binding protein subunit beta-4	ko04062 Chemokine signaling pathway; ko04151 PI3K-Akt signaling pathway; ko047:	-0.50	0.0183	0.401388
K16142	HP	haptoglobin	NA	0.90	0.0403	0.443212
K09489	HSPA4	heat shock 70kDa protein 4	ko04612 Antigen processing and presentation	0.49		0.437297
K13159	HNRNPL	heterogeneous nuclear ribonucleoprotein L	NA	0.61		0.382122
K00844 K11303	HK HAT1, KAT1	hexokinase [EC:2.7.1.1] histone acetyltransferase 1 [EC:2.3.1.48]	ko00010 Glycolysis / Gluconeogenesis; ko00051 Fructose and mannose metabolism; ko05034 Alcoholism	-0.38 0.68		0.357271 0.382122
K11303 K11424		histone acetyltransferase 1 [EC:2.3.1.48] histone-lysine N-methyltransferase NSD2 [EC:2.1.1.43]	koUSU34 Alcoholism koUSU310 Lysine degradation; koUS202 Transcriptional misregulation in cancer	0.68		0.382122
K11424 K14966	HCFC	host cell factor	ko05168 Herpes simplex infection	-0.47		0.398783
K09562	HSPBP1	hsp70-interacting protein	ko04141 Protein processing in endoplasmic reticulum	0.48	0.0028	
K06092	INADL, PATJ	InaD-like protein	ko04390 Hippo signaling pathway; ko04530 Tight junction	0.71	0.0028	
K05459	IGF1	insulin-like growth factor 1	koO4066 HIF-1 signaling pathway; koO4114 Oocyte meiosis; koO4115 p53 signaling pa	-0.64		0.423939
K18264	ITM2B	integral membrane protein 2B	NA	-0.44	0.0080	0.398783
K05414	IFNA	interferon alpha	ko04060 Cytokine-cytokine receptor interaction; ko04140 Regulation of autophagy;	0.57	0.0145	
K09228	KRAB	KRAB domain-containing zinc finger protein	NA	0.72		
K17845	KLF2	krueppel-like factor 2	NA	-0.43	0.0018	
K02920	RP-L36e, RPL36	large subunit ribosomal protein L36e	ko03010 Ribosome	-0.46		0.440055
K17989	SDS, SDH, CHA1 MEF2D	L-serine/L-threonine ammonia-lyase [EC:4.3.1.17 4.3.1.19]	NA NA	-0.44		0.382122 0.398783
K09262 K06751	MEF2D MHC1	MADS-box transcription enhancer factor 2D major histocompatibility complex, class I	NA ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules (CAMs	0.56		0.398783
K06/51 K09660	MPDU1	manor nistocompatibility complex, class i mannose-P-dolichol utilization defect 1	NA			0.436634
K17291	MARVELD2	MARVEL domain-containing protein 2	NA NA			0.436634
K17231	STEAP1	metalloreductase STEAP1 [EC:1.16.1]	ko04978 Mineral absorption	0.47		0.382122
K08199	SLC22A2, OCT2	MFS transporter, OCT family, solute carrier family 22 (organic cation	NA NA	-0.61		0.398783
K17656	MSS51	mitochondrial splicing suppressor protein 51	NA	0.39		0.398783
K04431	MAP2K7, MKK7	mitogen-activated protein kinase kinase 7 [EC:2.7.12.2]	ko04010 MAPK signaling pathway; ko04012 ErbB signaling pathway; ko04141 Protein	0.76		
K04676	SMAD1	mothers against decapentaplegic homolog 1	ko04350 TGF-beta signaling pathway; ko04390 Hippo signaling pathway; ko04391 Hip	-0.57	0.0093	0.398783
K04729	MYD88	myeloid differentiation primary response protein MyD88	ko04064 NF-kappa B signaling pathway; ko04210 Apoptosis; ko04620 Toll-like recept	0.44		0.398783
K10352	MYH	myosin heavy chain	ko04530 Tight junction; ko05416 Viral myocarditis	0.71		0.382122
K10356 K12800	MYO1 NLRP3, PYPAF1	myosin I NACHT, LRR and PYD domains-containing protein 3	NA ko04621 NOD-like receptor signaling pathway; ko05133 Pertussis; ko05164 Influenza	-0.49 0.93		0.398783 0.382122

				_			
K01097	NANP	N-acylneuraminate-9-phosphatase [EC:3.1.3.29]	ko00520 Amino sugar and nucleotide sugar metabolism		0.39		0.382122
K00323	NNT	NAD(P) transhydrogenase [EC:1.6.1.2]	ko00760 Nicotinate and nicotinamide metabolism		0.40		0.401932
K12347 K05750	SLC11A, NRAMP NCKAP1, NAP125	natural resistance-associated macrophage protein	ko04142 Lysosome; ko04978 Mineral absorption		-0.46 -0.41		0.457001 0.398783
K04573	NEF3, NF-M	NCK-associated protein 1 neurofilament medium polypeptide (neurofilament 3)	ko04810 Regulation of actin cytoskeleton ko05014 Amyotrophic lateral sclerosis (ALS)		0.75		0.398783
K04469	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2	ko04010 MAPK signaling pathway; ko04064 NF-kappa B signaling pathway; ko04380 (		0.45		0.398783
K08126	OGN	osteoglycin (osteoinductive factor, mimecan)	NA		-0.54		0.398783
K04441	P38	p38 MAP kinase [EC:2.7.11.24]	ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko04370	7	-0.39		0.398783
K13239	PECI	peroxisomal 3,2-trans-enoyl-CoA isomerase [EC:5.3.3.8]	ko00071 Fatty acid degradation; ko04146 Peroxisome		-0.48		0.411219
K08530	NR1C3, PPARG	peroxisome proliferator-activated receptor gamma	ko03320 PPAR signaling pathway; ko04380 Osteoclast differentiation; ko05016 Hunti		-0.55		0.437297
K01890	FARSB, pheT	phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	ko00970 Aminoacyl-tRNA biosynthesis	7	0.50	0.0098	0.398783
K07253	MIF	phenylpyruvate tautomerase [EC:5.3.2.1]	ko00350 Tyrosine metabolism; ko00360 Phenylalanine metabolism		-0.49	0.0088	0.398783
K17594	PHACTR3	phosphatase and actin regulator 3	NA		-1.28	0.0340	0.437297
K02649	PIK3R	phosphoinositide-3-kinase, regulatory subunit	ko04012 ErbB signaling pathway; ko04062 Chemokine signaling pathway; ko04066 HI		-0.39	0.0383	0.440055
K01922	PPCS, coaB	phosphopantothenate-cysteine ligase [EC:6.3.2.5]	ko00770 Pantothenate and CoA biosynthesis	<b></b>	0.39	0.0171	0.398783
K01952	purL, PFAS	phosphoribosylformylglycinamidine synthase [EC:6.3.5.3]	ko00230 Purine metabolism		0.41		0.398783
K13114	PNN	pinin	ko03013 RNA transport; ko03015 mRNA surveillance pathway		-0.59		0.398783
K03982	SERPINE1, PAI1	plasminogen activator inhibitor-1	koO4066 HIF-1 signaling pathway; koO4115 p53 signaling pathway; koO4390 Hippo sig		0.41		0.398783
K13126	PABPC	polyadenylate-binding protein	ko03013 RNA transport; ko03015 mRNA surveillance pathway; ko03018 RNA degrada		-0.49	0.0239	
K14399	CLP1, HERB	polyribonucleotide 5'-hydroxyl-kinase [EC:2.7.1.78]	ko03015 mRNA surveillance pathway		-0.42		0.457001
K05003	KCNJ10	potassium inwardly-rectifying channel subfamily J member 10	ko04971 Gastric acid secretion		0.54		0.436634
K12850	PRPF38B	pre-mRNA-splicing factor 38B	ko03040 Spliceosome		0.42		0.444617
K04727	PDCD8, AIF	programmed cell death 8 (apoptosis-inducing factor) [EC:1]	ko04210 Apoptosis		0.63		0.398783
K01322	PREP	prolyl oligopeptidase [EC:3.4.21.26]	NA NA		0.39		0.425293
K15719 K12328	NCOAT, MGEA5 PPP1R14A, CPI17	protein O-GlcNAcase / histone acetyltransferase [EC:3.2.1.169 2.3.1.48 protein phosphatase 1 regulatory subunit 14A	ko04270 Vascular smooth muscle contraction		-0.39 0.66		0.457001 0.436634
K04461	PPM1B. PP2CB	protein phosphatase 11 egulatory subuliit 14A	ko04010 MAPK signaling pathway	- 5	0.43		0.422862
K14004	SEC13	protein transport protein SEC13	ko03013 RNA transport; ko04141 Protein processing in endoplasmic reticulum		0.43		0.436634
K14005	SEC31	protein transport protein SEC31	koO4141 Protein processing in endoplasmic reticulum	<u> </u>	0.41		0.398783
K07342	SEC61G, SSS1, secE	protein transport protein SEC61 subunit gamma and related protei	ko03060 Protein export; ko04141 Protein processing in endoplasmic reticulum; ko04	<u> </u>	0.41	0.0444	0.452402
K08773	RALBP1	RalA-binding protein 1	ko05200 Pathways in cancer; ko05212 Pancreatic cancer	<u> </u>	0.42	0.0081	0.398783
K07874	RAB1A	Ras-related protein Rab-1A	ko05134 Legionellosis	<u> </u>	0.40	0.0022	0.382122
K10740	RPA3	replication factor A3	ko03030 DNA replication; ko03420 Nucleotide excision repair; ko03430 Mismatch re	_	0.74		0.437297
K06618	RB1	retinoblastoma-associated protein	ko04110 Cell cycle; ko05161 Hepatitis B; ko05166 HTLV-I infection; ko05169 Epstein-E		0.41	0.0068	0.398783
K10808	RRM2	ribonucleoside-diphosphate reductase subunit M2 [EC:1.17.4.1]	ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko00480 Glutathione	<b></b>	0.57	0.0138	0.398783
K12822	RBM25, S164	RNA-binding protein 25	ko03040 Spliceosome		0.77	0.0109	0.398783
K12822 K04499	.,	RNA-binding protein 25 RuvB-like protein 1 (pontin 52)	ko03040 Spliceosome ko04310 Wnt signaling pathway		-0.49	0.0245	0.422862
K04499 K12382	RUVBL1, RVB1, INO80H PSAP, SGP1	RuvB-like protein 1 (pontin 52) saposin	ko04310 Wnt signaling pathway ko04142 Lysosome		-0.49 -0.58	0.0245 0.0016	0.422862 0.382122
K04499 K12382 K06841	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5	RuvB-like protein 1 (pontin 52) saposin semaphorin 5	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance		-0.49 -0.58 -0.69	0.0245 0.0016 0.0033	0.422862 0.382122 0.382122
K04499 K12382 K06841 K09646	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA		-0.49 -0.58 -0.69 -0.43	0.0245 0.0016 0.0033 0.0110	0.422862 0.382122 0.382122 0.398783
K04499 K12382 K06841 K09646 K16311	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA NA		-0.49 -0.58 -0.69 -0.43 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496	0.422862 0.382122 0.382122 0.398783 0.457001
K04499 K12382 K06841 K09646 K16311 K08269	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase UUK/ATG1 [EC:2.7.11.1]	ko04310 Wnt signaling pathway ko04142 tysosome ko04360 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway		-0.49 -0.58 -0.69 -0.43 -0.39 0.63	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03015 mRNA surveillance pathway; ko04110 Cell cycle - yeast; ko04113 Meiosis - y		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, serS	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase UUK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11]	ko04310 Wnt signaling pathway ko04142 lysosome ko04360 Axon guidance NA NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03015 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko00970 Aminoacyl-tRNA biosynthesis		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141	RUVBLI, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1 2 3, ATG1 PPP2C SARS, SerS SESN	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03105 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko00970 Aminoacyl-tRNA biosynthesis ko04115 pS3 signaling pathway		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 UIK1 2 3, ATG1 PPP2C SARS, SerS SESN frmB, ESD, fghA	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protei kinase SIK2 [EC:2.7.11.1] serine/threonine-protei kinase SIK2 [EC:2.7.11.1] serine/threonine-protei phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestrin S-formy/glutathione hydrolase [EC:3.1.2.12]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03015 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko04190 Aminoacyl-tRNA biosynthesis ko04115 p53 signaling pathway ko00580 Methane metabolism		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, serS SESN FrmB, ESD, fghA RP-S27Ae, RPS27A	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestini S-formy/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein SZ7Ae	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9570 Aminoaqy-IRNA biosynthesis koO4115 pS3 signaling pathway koO6080 Methane metabolism koO3010 Ribosome		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151	RUVBL1, RVB1, INO80H PSAP, SGP1 SCMA5 SCPEP1 SIK2 UIK1 2_3, ATG1 PPP2C SARS, serS SESN frmB, ESD, fghA FN-527Ae, RPS27A SNUPM, RNUT1	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase UK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.2.12] small subunit ribosomal protein S27Ae synurportin-1	ko04310 Wnt signaling pathway ko04142 Lysosome ko04140 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03105 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko00970 Aminoacyl-tRNA biosynthesis ko04115 p53 signaling pathway ko00680 Methane metabolism ko03010 RNbosome ko03013 RNbosome		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43 -0.38	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783 0.398783 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, serS SESN FrmB, ESD, fghA RP-S27Ae, RPS27A	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestini S-formy/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein SZ7Ae	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9570 Aminoaqy-IRNA biosynthesis koO4115 pS3 signaling pathway koO6080 Methane metabolism koO3010 Ribosome		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 UKL1 2_3, ATG1 PPP2C SARS, SerS SESN frmB, ESD, fghA RP-S27Ae, RPS27Ae SNUPN, RNUT1 SMS	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/htreonine-protein kinase SIKZ [EC:2.7.11.1] serine/threonine-protein kinase SIKZ [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestrin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22]	ko04310 Wnt signaling pathway ko04142 Lysosome ko04360 Axon guidance NA NA ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03015 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko041970 Aminoacyl-tRNA biosynthesis ko04115 p53 signaling pathway ko00580 Methane metabolism ko03013 RNA transport ko00270 Cysteine and methionine metabolism; ko00330 Arginine and proline metat		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43 -0.38	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.398783 0.398783
K04499 K12382 K06841 K09846 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K06451	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527A SNUPN, RNUT1 SM5 MAP3K7IP2, TAB2 TEKEP1 CD3E	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestrin Serform/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKI-binding kinase 1-binding protein TANK-binding kinase 1-binding protein	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9570 Aminoaqy-IRNA biosynthesis koO4115 pS3 signaling pathway koO680 Methane metabolism koO3010 Ribosome		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43 -0.38 -0.56 0.38 0.43 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.382122 0.398783 0.398783 0.398783 0.409019 0.398783 0.401388
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K04659	RUVBL1, RVB1, INO80H PSAP, SGP1 SCMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527AS SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THISS2S	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seyl-tRNA synthetase [EC:6.1.1.11] sestrin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKL-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO0970 Aminoacyl-tRNA biosynthesis koO4115 p33 signaling pathway koO0600 Methane metabolism koO3010 Ribosome koO3013 RNA transport koO4020 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPS signaling pathway; koO4064 NF-kappa B signaling pathway; koO4060 Licel Licel pathway; koO4600 Licel Licel pathway; koO4600 Licel L		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43 -0.38 -0.56 0.38 0.43 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0318	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.409019 0.398783 0.409019 0.436634 0.436634 0.436634
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10161 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K04659 K04657	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 UIK1 2, 3, ATG1 PPP2C SARS, Ser5 SESN frmB, ESD, fghA RP-S27Ae, RPS27A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS2S tdk, TK	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestrin Serform/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKL-binding finase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 13/4/5	ko04310 Wnt signaling pathway ko04142 Lysosome ko04162 Nacon guidance NA NA Ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway ko03015 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko03015 mRNA surveillance pathway; ko04111 Cell cycle - yeast; ko04113 Meiosis - y ko040115 p53 ignaling pathway ko00580 Methane metabolism ko03010 Ribosome ko03013 RNA transport ko00307 Cysteine and methionine metabolism; ko00330 Arginine and proline metal ko04010 MAPK signaling pathway; ko04064 NF-kapa B signaling pathway; ko0482 RIG-l-like receptor signaling pathway ko0462 RIG-l-like receptor signaling pathway; ko04660 T cell receptor signaling pathway; ko040642 RIG-l-like receptor signaling pathway; ko04660 T cell receptor signaling pathway; ko040610 Focal adhesion; ko04145 Phagosome; ko04151 PI3K-kignaling pathway; ko04510 Focal adhesion; ko00240 Pyrimidine metabolism; ko00983 Drug metabolism - other enzymes		-0.49 -0.58 -0.69 -0.43 -0.39 0.63 -0.41 0.51 -0.72 -0.65 -0.43 -0.38 -0.56 0.38 0.43 -0.39 0.86	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0318 0.0318	0.422862 0.382122 0.382123 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.490019 0.490719 0.401388 0.43634 0.436634 0.436634 0.398783 0.436634
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10171 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K046557 K10170	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-SZ7Ae, RP5Z7A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TIBKBP1 TIBKB	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA 3ynthetase [EC:6.1.1.1] sestini S-formylgutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein SZPAe snurportin-1 spermine synthase [EC:2.5.1.22] TANK-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/34/5 thymidline kinase [EC:2.7.1.21] toll-like receptor 8	koO4310 Wnt signaling pathway koO442 Lysosome koO442 Lysosome NA NA koO440 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaq-l-RNA biosynthesis koO4115 pS3 signaling pathway koO680 Methane metabolism koO3010 Ribosome koO4010 PRIPA Signaling pathway; koO4064 NF-kappa B signaling pathway; koO4604 NF-kappa B signaling pathway; k		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.51 -0.72 -0.65 -0.43 -0.38 -0.56 -0.38 -0.39 -0.86 -0.00 -0.51	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0011 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0133 0.0251	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.40919 0.398783 0.401388 0.437297 0.401388 0.436634 0.398783 0.422862 0.382122
K04499 K12382 K06841 K09646 K16311 K08269 K04385 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K04659 K00857 K10170 K10161	RUVBL1, RVB1, INO80H PSAP, SGP1 SIM25 SCPEP1 SIK2 ULK1 2, 3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-S27Ae, RPS27Ae, RPS27Ae SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CO3E THES2S tdk, TK TLR8 TLR8	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding kinase 1-binding protein T-cell surface glycorportein CO3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 9	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO0970 Aminoacyl-tRNA biosynthesis koO4115 p53 signaling pathway koO0800 Methane metabolism koO3010 Ribosome koO3013 RNA transport koO0207 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4064 NF-kappa B signaling pathway; koO4064 RoO4104 MaPK signaling pathway; koO4660 T cell receptor signaling pathway; koO46040 Primidine metabolism; koO0304 Primidine metabolism; koO04064 Primidine metabolism; koO0406 VPrimidine metabolism; koO0460 T cell receptor signaling pathway; koO4506 Pocal adhesion; koO0420 Primidine metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO1420 Chagas disease (American try		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.43 -0.36 -0.38 -0.39 -0.86 -0.38 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.00116 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0318 0.0133 0.0251 0.0025	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.398783 0.407297 0.401388 0.403634 0.403634 0.403634 0.403634 0.403634 0.403634 0.403634 0.398783 0.403634 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K0404 K12652 K04404 K12652 K06451 K04659 K00857 K10170 K10170 K10170	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN FIRB, ESD, fghA RP-S27Ae, RPS27A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBSSS tdk, TK TLR8 TLR8 TLR9 SOX2	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestini Serformy[alutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKL-binding protein C3 epsilon chain thrombospondin 2/3/4/5 thyrvidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B)	koO4310 Wnt signaling pathway koO442 Lysosome koO442 Lysosome koO4360 xon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-IRNA biosynthesis koO4115 p53 signaling pathway koO680 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 MAPK signaling pathway; koO466 NF-kappa B signaling pathway; koO4606 NF-kappa B signaling pathway; koO4607 Cell receptor signaling pathway; koO4620 Tell receptor signaling pathway; koO4620 Tell-like receptor signaling pathway; koO4510 Focal adhesion; koO0460 Toll-like receptor signaling pathway koO4620 Toll-like receptor signaling pathway koO4620 Toll-like receptor signaling pathway koO4620 Toll-like receptor signaling pathway		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.43 -0.38 -0.36 -0.38 -0.39 -0.36 -0.38 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0133 0.0251 0.0255 0.0025 0.0025	0.422862 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.398783 0.437297 0.401388 0.436634 0.398783 0.422862 0.382122 0.382122 0.382122
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01077 K13151 K00802 K04404 K12652 K06451 K04659 K10170 K10161 K1079 K10161	RUVBL1, RVB1, INO80H PSAP, SGP1 SCMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-S27Ae, RPS27A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS25 tdk, TK TLR8 TLR9 SOX2 VCP, CDC48	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestine S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAXI-binding protein 2 TAXI-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase	koO4310 Wnt signaling pathway koO442 Lysosome koO442 Lysosome NA NA NA NA NO400400 Regulation of autophagy; koO4150 mTOR signaling pathway koO34015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-IRNA biosynthesis koO4115 p53 signaling pathway koO0500 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO0270 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4664 NF-kappa B signaling pathway; koO46040 Henatopoietic cell lineage; koO4660 Tcell receptor signaling pathway koO4640 Henatopoietic cell lineage; koO4660 Tcell receptor signaling house, koO4640 Pyrimidine metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO4510 Focal adhesion; koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO43010 Hippo signaling pathway;		-0.49 -0.58 -0.69 -0.43 -0.39 -0.41 -0.51 -0.72 -0.65 -0.43 -0.38 -0.38 -0.38 -0.39 -0.86 -0.05	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0212 0.0110 0.0367 0.0184 0.0318 0.0133 0.0251 0.0025 0.0025 0.0025	0.422862 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.409019 0.409019 0.40363 0.436634 0.398783 0.436634 0.398783 0.422662 0.382122 0.382122 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K06451 K04659 K00857 K10170 K10161 K16796 K13525	RUVBL1, RVB1, INO80H PSAP, SGP1 SIM25 SCPEP1 SIK2 UIK1 2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-SZ7Ae, RPSZ7A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBSZS tdk, TK TLR8 TLR9 SOX2 VCP, CDC48 EIF3A	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase UK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit if bosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKL-binding kinase 1-binding protein T-cell surface glycoprotein CO3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 transtitional endoplasmic reticulum ATPase transition initiation factor 53 subunit A	koO4310 Wnt signaling pathway koO4421 tysosome NA		-0.49 -0.58 -0.69 -0.43 -0.39 -0.65 -0.41 -0.72 -0.65 -0.43 -0.56 -0.38 -0.56 -0.38 -0.56 -0.51 -0.39 -0.51 -0.00 -0.51 -0.49 -0.49 -0.49 -0.51 -0.65	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0514 0.0116 0.0318 0.	0.422862 0.382122 0.398783 0.457001 0.398783 0.457001 0.398783 0.398783 0.398783 0.409019 0.398783 0.40919 0.437297 0.401388 0.43624 0.398783 0.42262 0.398783 0.42262 0.382122 0.382122
K04499 K12382 K06841 K09646 K16311 K09646 K16311 K08269 K04382 K01875 K10141 K101070 K02977 K13151 K00802 K04404 K12652 K06451 K04659 K0451 K04659 K04525	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-SZ7Ae, RP527A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 C103E THBS25 LTRR TLRB TLRB TLRB TLRB TLRB TLRB TLRB	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestrin seyl-tRNA synthetase [EC:6.1.1.1] sestrin sestrin S-formy/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAK1-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thyndine kinase [EC:2.7.1.21] toll-like receptor 9 transsription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 5AA	koO4310 Wnt signaling pathway koO4421 ysosome koO4462 tysosome NA NA koO4400 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-IRAN biosynthesis koO4115 pS3 signaling pathway koO6800 Methane metabolism koO3010 Ribosome koO4010 MAPK signaling pathway; koO4064 NF-kappa B signaling pathway; koO4060 Hemborgoeitic cell lineage; koO4660 T cell receptor signaling pathway; koO4660 Primidine metabolism; koO0640 Primidine metabolism; koO0640 Primidine metabolism; koO0630 Primidine metabolism; koO0301 Ribosome; koO4510 Focal adhesion; koO0240 Primidine metabolism; koO0303 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4300 Hippos signaling pathway koO4141 Protein processing in endoplasmic reticulum; koO5134 Legionellosis koO3013 RNA transport		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.38 -0.38 -0.39 -0.86 -0.39 -0.86 -0.39 -0	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0111 0.0054 0.0116 0.0112 0.0367 0.0184 0.0318 0.025 0.025 0.0054 0.0025 0.0054 0.0018 0.0018 0.0025 0.0054 0.0025 0.0054 0.0025	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.409019 0.401388 0.43262 0.402262 0.382122 0.382122 0.398783 0.4422862 0.382122 0.398783
K04499 K12382 K06841 K09646 K16311 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K01659 K0852 K04404 K12652 K04404 K12652 K06451 K04659 K00857 K10170 K10161 K16796 K13525 K03254 K03254	RUVBL1, RVB1, INO80H PSAP, SGP1 SCMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527AS SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS2S tdk, TK TLRB TLRB TLRB SOX2 VCP, CDC48 EIF3A EIF4A	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestrin S-form/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAXL-binding protein 2 TAXL-binding protein 2 TAXL-binding protein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 4A translaction protein SEC63	koO4310 Wnt signaling pathway koO4142 Lysosome NA NA NA NO400400 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9700 Aminoagyl-RNA biosynthesis koO4115 p53 signaling pathway koO0500 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO30270 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4064 NF-kappa B signaling pathway; koO4060 Neo404510 Ficel and proline metabolism; koO4000 MPK signaling pathway; koO4060 Proline metal koO4010 MAPK signaling pathway; koO4060 Tcell receptor signaling pathway; koO44151 Picel adhesion; koO4060 Primidine metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO43010 Till-like receptor signaling pathway; koO5142 Chagas disease (American try koO43010 Till-like receptor signaling pathway; koO5134 Legionellosis koO3013 RNA transport		-0.49 -0.58 -0.69 -0.43 -0.63 -0.41 -0.51 -0.72 -0.65 -0.38 -0.38 -0.38 -0.90 -0.51 -0.38 -0.90 -0.51 -0.90 -0.51 -0.90 -0.51 -0.90 -0.51 -0.90 -0.51 -0.90 -0.51 -0.90 -0.51 -0.90 -0	0.0245 0.0016 0.0033 0.0110 0.0096 0.0113 0.0022 0.0011 0.0054 0.0116 0.0212 0.0110 0.0367 0.0367 0.0025 0.0025 0.0025 0.0025 0.0040 0.0018 0.0025 0.0025 0.0025 0.0036 0.0018	0.422862 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.409019 0.401286 0.436634 0.398783 0.42262 0.382122 0.382122 0.398783 0.444822 0.398783
K04499 K12382 K06841 K09646 K16311 K09646 K16311 K08269 K04382 K01875 K10141 K101070 K02977 K13151 K00802 K04404 K12652 K06451 K04659 K0451 K04659 K04525	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THES25 TLRB TLRB TLRB TLRB TLRB TLRB TLRB TLRB	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestrin Serine/synthase [EC:3.1.11] sestrin Serine synthase [EC:3.1.212] small subunit ribosomal protein S27Ae suruportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKL-binding protein 2 TAKL-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thyrnidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum APasee translation initiation factor 3 subunit A translation initiation factor 4 subunit 4 translation initiation factor 3 subunit A translation initiation factor 4 subunit 4 translation initiation factor 4 subunit 4 translation initiation factor 3 subunit 4 translation initiation factor 4 subunit 4 translation initiation factor 3 subunit 4 translation initiation factor 4 translation initiation factor 3 subunit 4	koO4310 Wnt signaling pathway koO4421 ysosome koO4422 tysosome koO4420 xon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-IRNA biosynthesis koO4115 p53 signaling pathway koO680 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 MAPK signaling pathway; koO466 MF-kappa B signaling pathway; koO4600 MAPK signaling pathway; koO4660 Tell receptor signaling pathway; koO4600 Toll-like receptor signaling pathway koO4620 Ribosome; koO4151 P18K-Akt signaling pathway; koO4510 Focal adnesion; koO4620 Toll-like receptor signaling pathway; koO4600 Toll-like receptor signaling pathway koO4620 Toll-like rasport koO3013 RNA transport koO3013 RNA transport		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.38 -0.38 -0.39 -0.86 -0.39 -0.86 -0.39 -0	0.0245 0.0016 0.0033 0.0110 0.0496 0.0111 0.0021 0.0054 0.0116 0.0110 0.0367 0.0110 0.0367 0.0120 0.0033 0.0025 0.	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.409019 0.409019 0.401388 0.436634 0.398783 0.422862 0.382122 0.382122 0.382122 0.398783
K04499 K12382 K05841 K09646 K16311 K09646 K16311 K03826 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K04451 K04659 K00857 K10110 K10161 K16796 K13525 K03254 K03257 K09540	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMAS SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C UKK1_2_3, ATG1 PPP2C SARS, serS SESN RP-S27Ae, RPS27A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBSSS tdk, TK TLR8 TLR9 SOX2 VCP, CDC48 EIF3A EIF3A EIF4A EIF6A, DNAIC23 TRIMS9	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestrin S-form/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAXL-binding protein 2 TAXL-binding protein 2 TAXL-binding protein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 4A translaction protein SEC63	koO4310 Wnt signaling pathway koO4142 Lysosome NA NA NA NO400400 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9700 Aminoagyl-RNA biosynthesis koO4115 p53 signaling pathway koO0500 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO30270 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4064 NF-kappa B signaling pathway; koO4060 Neo404510 Ficel and proline metabolism; koO4000 MPK signaling pathway; koO4060 Proline metal koO4010 MAPK signaling pathway; koO4060 Tcell receptor signaling pathway; koO44151 Picel adhesion; koO4060 Primidine metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO43010 Till-like receptor signaling pathway; koO5142 Chagas disease (American try koO43010 Till-like receptor signaling pathway; koO5134 Legionellosis koO3013 RNA transport		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.43 -0.38 -0.39 -0.86 -0.05 -0.38 -0.39	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0011 0.0016 0.0116 0.0116 0.0116 0.0184 0.0133 0.025 0.0025 0.0025 0.0025 0.0025 0.0025 0.0025 0.0021 0.01078 0.0178	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.499019 0.398783 0.437297 0.401388 0.437297 0.401388 0.432624 0.382122 0.398783 0.422862 0.382122 0.398783 0.444822 0.398783 0.444822 0.398783
K04499 K12382 K05841 K09646 K16311 K09269 K04382 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K04645 K04659 K00857 K10170 K10161 K16796 K10170 K1	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-S27Ae, RPS27A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS2S tdk, TK TLRB TLRB TLRB TLRB TLRB TLRB TLRB TLRB	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestrin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein SZPAe sourportin-1 spermine synthase [EC:2.5.1.22] TAKI-binding protein 2 TANK-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 3 A4 translocation protein SEC63 tripartite motif-containing protein 39 [EC:6.3.2.19] tryptophanyl-tRNA synthetase [EC:6.1.1.2]	koO4310 Wnt signaling pathway koO442 Lysosome koO442 Lysosome NA		-0.49 -0.58 -0.69 -0.43 -0.39 -0.63 -0.41 -0.72 -0.65 -0.43 -0.38 -0.38 -0.38 -0.49 -0.56 -0.56 -0.56 -0.56 -0.56	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0054 0.0116 0.0054 0.0116 0.0318 0.0318 0.0318 0.0318 0.0055 0.0025 0.0081 0.0015 0.0017 0.0144 0.0167 0.0147 0.0137 0.0137	0.422862 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.398783 0.437297 0.401388 0.437297 0.401388 0.43282 0.398783 0.42282 0.398783 0.42482 0.398783 0.42488 0.398783 0.42488 0.398783 0.401388 0.401388
K04499 K12382 K05841 K09646 K16311 K09646 K16311 K01070 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K06451 K04659 K04055 K010170 K10161 K16796 K13525 K03254 K03254 K03257 K03254 K03257 K03256 K01215	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1 2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-S27Ae, RPS27Ae, RPS27Ae SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THISS2S tdk, TK TLRB TLRB TLRB TLRB SOX2 VCP, CDC48 EIF3A EIF4A SFC63, DNAIC23 TRIMB9 WARS, trpS TUBA	RuvB-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seyl-tRNA synthetase [EC:6.1.1.11] sestin S-formylglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKL-binding protein 2 TAKI-binding protein 2 TAKI-binding sinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic retriculum ATPase translation initiation factor 4A translation inprotein SEC63 tripartite motif-containing protein 3 [EC:6.3.2.19] tryptophanyl-tRNA synthetase [EC:6.1.1.2] tubulin alpha	koO4310 Wnt signaling pathway koO4142 Lysosome koO4360 Xxon guidance NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqvl-RNA biosynthesis koO4115 p53 signaling pathway koO0600 Methane metabolism koO3010 Ribosome koO3013 RNA transport koO0207 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO0101 MRN6 signaling pathway; koO4066 NF-kappa B signaling pathway; koO4060 NE-kappa B signaling pathway; koO4600 NE-kappa B signaling pathway; koO4600 NE-kappa B signaling pathway; koO4600 NE-kappa B signaling pathway; koO46060 To-li-like receptor signaling pathway; koO510 NE-kappa B signaling pathway; koO4600 To-li-like receptor signaling pathway; koO510 NE-kappa B signaling pathway; koO4600 To-li-like receptor signaling pathway; koO510 NE-kappa B signaling pathway; koO4600 To-li-like receptor signaling pathway; koO510 NE-kappa B signaling pathway; koO4600 To-li-like receptor signaling pathway; koO510 NE-kappa B signaling pathway; koO6000 NE-kappa B signaling pathway; koO510 NE-kappa B signaling pathway;		-0.49 -0.58 -0.69 -0.43 -0.39 -0.72 -0.65 -0.43 -0.38 -0.38 -0.39 -0.86 -0.38 -0.39 -0.51 -0.38 -0.50 -0.51 -0.38 -0.51 -0.51 -0.52 -0.52 -0.53 -0.54 -0.54 -0.55 -0.56 -0.51 -0.51 -0.52 -0.52 -0.55	0.0245 0.0016 0.0033 0.0110 0.0496 0.0113 0.0022 0.0116 0.0212 0.0116 0.0367 0.0367 0.0368 0.0358 0.0025	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.409019 0.398783 0.409019 0.398783 0.437297 0.401388 0.436282 0.398783 0.422862 0.398783 0.401388 0.409019 0.398783 0.401388 0.409019 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K08202 K04404 K12652 K04404 K12652 K04405 K10170 K10161 K16796 K13525 K03257 K09540 K10170 K10161 K10707	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN FmB, ESD, fghA RP-527Ae, RP527A SNUPN, RNUT1 SM5 MAPAX7IP2, TAB2 TRKBP1 CD3E THBS25 tidk, TK TLR8 TLR9 TLR9 TLR9 TLR9 WARS, TCP5 TRIM39 WARS, trp5 TRIM39 WARS, trp5 TRIM40 KRT1	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestind seryl-tRNA synthetase [EC:6.1.1.1] sestind seryl-tRNA synthetase [EC:3.1.2.12] small subunit ribosomal protein S27Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAK1-binding protein 2 TANK-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thynridine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 toll-like riboxy (SC) (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 4A translation initiation factor 4A translation initiation factor 91 tryptophanyl-tRNA synthetase [EC:6.1.1.2] tubulin alpha type I keratin, acidic	koO4310 Wnt signaling pathway koO442 Lysosome koO4360 Xxon guidance NA NA koO440 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-lrRNA biosynthesis koO4115 pS3 signaling pathway koO680 Methane metabolism koO3010 Ribosome koO3010 Ribosome; koO4060 NF-kappa B signaling pathway; koO4064 NF-kappa B signaling pathway; koO4064 NF-kappa B signaling pathway; koO4060 Hemotopoietic cell lineage; koO4660 T cell receptor signaling pathway; koO4660 Hemotopoietic cell lineage; koO4660 T cell receptor signaling pathway; koO46010 Fola adhesion; koO4640 PIII Ribosome; koO4151 PI3K-Akt signaling pathway; koO4510 Focal adhesion; koO4260 PToll-like receptor signaling pathway; koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4300 Hiposo signaling pathway koO44020 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4300 Hiposo signaling pathway koO44020 Toll-like receptor signaling pathway koO4600 Protein processing in endoplasmic reticulum; koO5131 RNA transport koO3013 RNA transport		-0.49 -0.58 -0.69 -0.43 -0.39 -0.61 -0.51 -0.72 -0.65 -0.38 -0.56 -0.38 -0.39 -0.86 -0.39 -0.39 -0.65 -0.38 -0.39	0.0245 0.0016 0.0093 0.0110 0.0496 0.0113 0.0092 0.0011 0.0089 0.0054 0.0116 0.0012 0.016 0.0101 0.0367 0.0184 0.0133 0.0251 0.0025 0.0081 0.0015 0.0017 0.0053 0.0178 0.0137 0.0137 0.0137 0.0338	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.409019 0.437297 0.401388 0.437297 0.401388 0.398783 0.43628 0.398783 0.436634 0.398783 0.422862 0.382122 0.382122 0.382122 0.382122 0.398783 0.409019 0.401388 0.398783
K04499 K12382 K05841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K04404 K12652 K0459 K00857 K10170 K10161 K10165 K103257 K09540 K103257 K09540 K12015 K01867 K07374 K01866 K17492	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-SZ7Ae, RPSZ7A SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THESZS tdk, TK TLRB TLR9 SOX2 VCP, CDC48 EIF3A SEC63, DN3LC23 TUBA SEC63, DN3LC23 TUBA KRT1 YARS, tyr5 UBN USN USN USN USN USN USN SCMAD SCMA	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.1] sestrin seyl-tRNA synthetase [EC:6.1.1.1] sestrin sestrin S-formy/glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein SZ7Ae snurportin-1 spermine synthase [EC:2.5.1.22] TAKI-binding protein 2 TANK-binding kinase 1-binding protein T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 9 transcription factor SOX2 (SOX group B) transitional endoplasmic reticulum ATPase translation initiation factor 4A	koO4310 Wnt signaling pathway koO442 Lysosome koO4360 Xxon guidance NA NA koO440 Regulation of autophagy; koO4150 mTOR signaling pathway koO3015 mRNA surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqy-lrRNA biosynthesis koO4115 pS3 signaling pathway koO680 Methane metabolism koO3010 Ribosome koO3010 Pilike receptor signaling pathway koO4010 MAPK signaling pathway; koO4604 Primatopoietic cell lineage; koO4660 Tell receptor signaling pathway; koO4604 Primatopoietic cell lineage; koO4660 Tell receptor signaling pathway; koO6500 Footal adhesion; koO4620 Toll-like receptor signaling pathway; koO5130 Footal adhesion; koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4300 Hippos signaling pathway koO4414 Protein processing in endoplasmic reticulum; koO5134 Legionellosis koO3013 RNA transport		-0.49 -0.58 -0.69 -0.63 -0.39 -0.61 -0.72 -0.65 -0.43 -0.38 -0.38 -0.38 -0.39 -0.65 -0.38 -0.39 -0.65 -0.38 -0.49 -0.39 -0.51 -0.72 -0.72 -0.72 -0.73 -0.72 -0.73 -0.74 -0.75 -0	0.0245 0.0016 0.0093 0.0110 0.0496 0.0113 0.0022 0.0111 0.0089 0.0054 0.0116 0.0012 0.0367 0.0104 0.0318 0.0025 0.0025 0.0025 0.0081 0.0017 0.0014 0.0017 0.0014 0.0017	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.499019 0.398783 0.437297 0.401388 0.437297 0.401388 0.436634 0.382122 0.382122 0.382122 0.382783 0.444822 0.398783 0.401388 0.409019 0.398783 0.4036634 0.398783 0.409019 0.382122 0.398783
K04499 K12382 K05841 K09646 K16311 K09646 K16311 K09675 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K04659 K00857 K10161 K16796 K10170 K10161 K16796 K103254 K03257 K03254 K03257 K03254 K03257 K03254 K03257 K03254 K	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527Ae, RP527Ae SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS2S tdk, TK TLR8 TLR9 SOX2 VCP, CDC48 EIF3A SECG3, DNAJC23 TRIM39 WARS, trp5 TUBA KRT1 VARS, tyr5 UBB USPS_2_8, UBP2	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16-] serine carboxypeptidase 1 [EC:34.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2k2 catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] serine/threonine-protein phosphatase 2k2 catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestine S-formy[glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae surportin-1 spermine synthase [EC:2.5.122] TAK1-binding protein 2 TAK1-binding protein 2 TAK1-binding protein 2 TAK1-binding protein 3 Servine Synthetase (EC:2.5.122) TAK1-binding kinase 1-binding protein 5 T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 transitional endoplasmic reticulum ATPase transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 4A translation protein SECG3 tripartite motif-containing protein 39 [EC:6.3.2.19] tryptophanyl-tRNA synthetase [EC:6.1.1.2] tubulin alpha type i keratin, acidi tyroysl-tRNA synthetase [EC:6.1.1.1] ubinuclein ubiquinol-cytochrome c reductase cytochrome b subunit ubiquinol-cytochrome c reductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit	koO4310 Wnt signaling pathway koO4142 Lysosome KoO4360 Xxon guidance NA NA KoO4400 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNAs surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9707 Aminoacyl-tRNA biosynthesis koO4115 p53 signaling pathway koO0800 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO30270 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4066 NF-kappa B signaling pathway; koO4060 KoO4010 Primiting pathway; koO4060 Tcell receptor signaling pathway; koO4060 Primiting pathway; koO44151 Primiting pathway; koO4600 Tcell receptor signaling pathway; koO44151 Primiting pathway; koO44510 Focal adhesion; koO0240 Primiting metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO46210 Toll-like receptor signaling pathway; koO5134 Legionellosis koO0313 RNA transport koO0313 RNA transport koO03013 RNA transport koO03013 RNA transport koO03014 Protein processing in endoplasmic reticulum NA koO0970 Aminoacyl-tRNA biosynthesis koO04145 Protein export; koO4450 Gap junction; koO5130 Pathogenic Escherichia coli info NA koO0970 Aminoacyl-tRNA biosynthesis		-0.49 -0.58 -0.69 -0.43 -0.39 -0.61 -0.72 -0.65 -0.43 -0.38 -0.56 -0.43 -0.39 -0.86 -0.51 -0.38 -0.51 -0.51 -0.52 -0.55 -0.53 -0.43 -0.43 -0.43 -0.49 -0.51 -0.51 -0.52 -0.53 -0.54 -0.55 -0.55 -0.43 -0.43 -0.51 -0.51 -0.51 -0.52 -0.53 -0.55 -0.55 -0.55 -0.55 -0.43 -0.55 -0.55 -0.43 -0.55	0.0245 0.0016 0.0093 0.0110 0.0996 0.0013 0.0013 0.0022 0.0111 0.0054 0.0016 0.0017 0.0054 0.0016 0.0054 0.0016 0.0057 0.0058 0.0058 0.0059 0.	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.409019 0.398783 0.409019 0.398783 0.409019 0.437297 0.401388 0.436634 0.398783 0.402862 0.382122 0.398783 0.401888 0.401888 0.401888 0.40634 0.398783 0.401888 0.40634 0.398783 0.40634 0.398783 0.406634 0.398783 0.406634 0.398783 0.406634 0.398783 0.406634 0.398783 0.406634 0.398783
K04499 K12382 K06841 K09646 K16311 K08269 K04382 K01875 K10141 K01070 K13151 K01070 K13151 K04404 K12655 K04404 K12655 K10170 K10161 K16796 K13525 K101867 K10170 K101867 K101867 K101866	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN FmB, ESD, fghA RP-527Ae, RP527A SNUPN, RNUT1 SMS MAP3X/IP2, TAB2 TBKBP1 CO3E THBS2S tdk, TK TLR8 TLR8 TLR9 TSOX2 VCP, CDC48 EIF3A EIF4A SECG3, DINAIC23 TRIM39 WARS, trp5 TUBA KRT1 YARS, tyr5 UBN CYTB, petB USP5_28, UBP2 SHP1, USK1, NSFLIC	Ruv8-like protein 1 (pontin 52) saposin saposin semaphorin 5 serine carboxypeptidase 1 [EC:3.4.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1] serine/threonine-protein phosphatase 2A catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.1.11] sestini Serformyglutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae soruportin-1 spermine synthase [EC:2.5.1.22] TAK1-binding protein 2 TAK4-binding protein 2 TAK4-binding kinase 1-binding protein T-cell surface glycoprotein CO3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-lice receptor 9 transitional endoplasmic reticulum APPase translation initiation factor 3 subunit A translation initiation factor 4 translation initiation factor 5 subunit A translation init	koO4310 Wnt signaling pathway koO4142 Lysosome NA NA koO4140 Regulation of autophagy; koO4150 mTOR signaling pathway koO3305 mRNA surveillance pathway; koO4110 cell cycle - yeast; koO4113 Meiosis - y koO970 Aminoaqvi-tRNA biosynthesis koO4115 pS3 signaling pathway koO3030 Ribosome koO3030 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 MAPK signaling pathway; koO4064 NF-kappa B signaling pathway; koO4662 RiG-lilke receptor signaling pathway koO4620 RiG-lilke receptor signaling pathway koO4620 Toll-like receptor signaling pathway; koO45050 Focal adhesion; koO4620 Toll-like receptor signaling pathway; koO45010 Focal adhesion; koO4620 Toll-like receptor signaling pathway; koO45010 Focal adhesion; koO4620 Toll-like receptor signaling pathway; koO45010 Focal adhesion; koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4309 Hippo signaling pathway koO44610 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4309 Hippo signaling pathway koO4141 Protein processing in endoplasmic reticulum; koO5134 Legionellosis koO40145 Phagosome; koO4540 Gap junction; koO5130 Pathogenic Escherichia coli info NA koO0790 Aminoacyl-tRNA biosynthesis NA koO0190 Oxidative phosphorylation; koO2020 Two-component system; koO4250 Carc NA koO0141 Protein processing in endoplasmic reticulum		-0.49 -0.58 -0.69 -0.43 -0.39 -0.41 -0.72 -0.65 -0.43 -0.56 -0.38 -0.56 -0.38 -0.56 -0.38 -0.56 -0.38 -0.56 -0.38 -0.56 -0.38 -0.51 -0.72 -0.57 -0.72 -0.43 -0.49 -0.51 -0.51 -0.49 -0.51 -0.49 -0.51 -0.51 -0.49 -0.51 -0.51 -0.51 -0.86	0.0245 0.0016 0.0033 0.0110 0.0966 0.0013 0.0022 0.0111 0.0054 0.0116 0.0054 0.0116 0.0054 0.0116 0.0054 0.0154 0.0156 0.0057 0.0058 0.0058 0.0059 0.0059 0.0051 0.0051 0.0051 0.0053 0.0051 0.0053 0.0051 0.0053 0.0054 0.0053 0.0054 0.0054 0.0054 0.0054 0.0055 0.0056 0.0057 0.0057 0.0016 0.0057 0.0017 0.0017 0.0017	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.409019 0.398783 0.409019 0.40188
K04499 K12382 K05841 K09646 K16311 K09646 K16311 K09675 K10141 K01070 K02977 K13151 K00802 K04404 K12652 K04659 K00857 K10161 K16796 K10170 K10161 K16796 K103254 K03257 K03254 K03257 K03254 K03257 K03254 K03257 K03254 K	RUVBL1, RVB1, INO80H PSAP, SGP1 SEMA5 SCPEP1 SIK2 ULK1_2_3, ATG1 PPP2C SARS, ser5 SESN frmB, ESD, fghA RP-527Ae, RP527Ae, RP527Ae SNUPN, RNUT1 SMS MAP3K7IP2, TAB2 TBKBP1 CD3E THBS2S tdk, TK TLR8 TLR9 SOX2 VCP, CDC48 EIF3A SECG3, DNAJC23 TRIM39 WARS, trp5 TUBA KRT1 VARS, tyr5 UBB USPS_2_8, UBP2	Ruv8-like protein 1 (pontin 52) saposin semaphorin 5 serine carboxypeptidase 1 [EC:34.16-] serine carboxypeptidase 1 [EC:34.16-] serine/threonine-protein kinase SIK2 [EC:2.7.11.1] serine/threonine-protein phosphatase 2k2 catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] serine/threonine-protein phosphatase 2k2 catalytic subunit [EC:3.1.3.16] seryl-tRNA synthetase [EC:6.1.11] sestine S-formy[glutathione hydrolase [EC:3.1.2.12] small subunit ribosomal protein S27Ae surportin-1 spermine synthase [EC:2.5.122] TAK1-binding protein 2 TAK1-binding protein 2 TAK1-binding protein 2 TAK1-binding protein 3 Servine Synthetase (EC:2.5.122) TAK1-binding kinase 1-binding protein 5 T-cell surface glycoprotein CD3 epsilon chain thrombospondin 2/3/4/5 thymidine kinase [EC:2.7.1.21] toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 toll-like receptor 8 transitional endoplasmic reticulum ATPase transitional endoplasmic reticulum ATPase translation initiation factor 3 subunit A translation initiation factor 4A translation protein SECG3 tripartite motif-containing protein 39 [EC:6.3.2.19] tryptophanyl-tRNA synthetase [EC:6.1.1.2] tubulin alpha type i keratin, acidi tyroysl-tRNA synthetase [EC:6.1.1.1] ubinuclein ubiquinol-cytochrome c reductase cytochrome b subunit ubiquinol-cytochrome c reductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit ubiquinol-cytochrome creductase cytochrome b subunit	koO4310 Wnt signaling pathway koO4142 Lysosome KoO4360 Xxon guidance NA NA KoO4400 Regulation of autophagy; koO4150 mTOR signaling pathway koO3105 mRNAs surveillance pathway; koO4111 Cell cycle - yeast; koO4113 Meiosis - y koO9707 Aminoacyl-tRNA biosynthesis koO4115 p53 signaling pathway koO0800 Methane metabolism koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO3010 Ribosome koO30270 Cysteine and methionine metabolism; koO0330 Arginine and proline metal koO4010 MAPK signaling pathway; koO4066 NF-kappa B signaling pathway; koO4060 KoO4010 Primiting pathway; koO4060 Tcell receptor signaling pathway; koO4060 Primiting pathway; koO44151 Primiting pathway; koO4600 Tcell receptor signaling pathway; koO44151 Primiting pathway; koO44510 Focal adhesion; koO0240 Primiting metabolism; koO0383 Drug metabolism - other enzymes koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO4620 Toll-like receptor signaling pathway; koO5142 Chagas disease (American try koO46210 Toll-like receptor signaling pathway; koO5134 Legionellosis koO0313 RNA transport koO0313 RNA transport koO03013 RNA transport koO03013 RNA transport koO03014 Protein processing in endoplasmic reticulum NA koO0970 Aminoacyl-tRNA biosynthesis koO04145 Protein export; koO4450 Gap junction; koO5130 Pathogenic Escherichia coli info NA koO0970 Aminoacyl-tRNA biosynthesis		-0.49 -0.58 -0.69 -0.43 -0.39 -0.61 -0.72 -0.65 -0.43 -0.38 -0.56 -0.43 -0.39 -0.86 -0.51 -0.38 -0.51 -0.51 -0.52 -0.55 -0.53 -0.43 -0.43 -0.43 -0.49 -0.51 -0.51 -0.52 -0.53 -0.54 -0.55 -0.55 -0.43 -0.43 -0.51 -0.51 -0.51 -0.52 -0.53 -0.55 -0.55 -0.55 -0.55 -0.43 -0.55 -0.55 -0.43 -0.55	0.0245 0.0016 0.0093 0.0110 0.0496 0.0013 0.0012 0.0015 0.0015 0.0015 0.0016 0.0016 0.0017 0.0021 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017 0.0036 0.0017	0.422862 0.382122 0.382122 0.398783 0.457001 0.398783 0.398783 0.398783 0.398783 0.409019 0.398783 0.409019 0.398783 0.437297 0.401388 0.436262 0.382122 0.382122 0.382122 0.398783 0.401888 0.401888 0.40634 0.398783 0.40634 0.398783 0.436634 0.398783 0.436634 0.398783 0.436634 0.398783 0.436634 0.398783 0.436634 0.398783

## 1086 Triploids L2 vs L1

KOID	Gene Abbreviation	KEGG Annotation	Class	Log Fold Change	P Value	adi P Val
K02731			ko03050 Proteasome	-0.4		0.366431979
K00643	E2.3.1.37, ALAS		ko00260 Glycine, serine and threonine metabolism; ko00860 Porphyrin and ch			0.406108274
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko00760 Nicotii			0.406108274
K19028		6-phosphofructo-2-kinase / fructose-2,6-biphosphatase 1 [EC:2.7.1.105 actin related protein 2/3 complex, subunit 1A/1B	NA ko04666 Fc gamma R-mediated phagocytosis; ko04810 Regulation of actin cyto	0.4		0.4226574
K03737			ko04610 Complement and coagulation cascades	0.6		0.406108274
			ko00500 Starch and sucrose metabolism; ko04973 Carbohydrate digestion and			0.406108274
K11140			ko00480 Glutathione metabolism; ko04614 Renin-angiotensin system; ko0464		7 0.0039	0.406108274
			ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 Meiosis - yeast; ko0411			
K10380			ko05205 Proteoglycans in cancer	0.7		0.406108274
K09864	ANXA7_11 ΔΩΡ1		NA ko04964 Proximal tubule bicarbonate reclamation; ko04976 Bile secretion	0.4		0.406108274
K09866			ko04962 Vasopressin-regulated water reabsorption; ko04976 Bile secretion	0.4		0.424389339
K09034			NA	-0.6		0.406108274
			ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series	0.3		0.406108274
K04726			ko04115 p53 signaling pathway; ko04210 Apoptosis; ko04650 Natural killer cell			0.406108274
K05901 K01435			ko00740 Riboflavin metabolism; ko00860 Porphyrin and chlorophyll metabolis ko00780 Biotin metabolism; ko04977 Vitamin digestion and absorption	s 0.7		0.406108274 0.426599288
K04739			ko04210 Apoptosis; ko04910 Insulin signaling pathway	0.4		0.426399288
K18245			NA	1.0		0.406108274
K01379			ko04142 Lysosome; ko05152 Tuberculosis	0.5		0.426599288
K01365			ko04142 Lysosome; ko04145 Phagosome; ko04612 Antigen processing and pre-			0.406108274
K06454			ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and pre			0.426599288
K05022 K03899			NA ko04610 Complement and coagulation cascades	0.3		0.406108274
	COL1AS		ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re			0.406108274
K01331			ko04610 Complement and coagulation cascades; ko05133 Pertussis; ko05150 S			0.406108274
K03997			ko04610 Complement and coagulation cascades; ko05020 Prion diseases; ko05			0.406108274
K01335	CFB	component factor B [EC:3.4.21.47]	ko04610 Complement and coagulation cascades; ko05150 Staphylococcus aure	0.6		0.426599288
K01334			ko04610 Complement and coagulation cascades; ko05150 Staphylococcus aure			0.406108274
K10059			ko05152 Tuberculosis	0.6		0.406108274
K05416			ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signalin ko04110 Cell cycle; ko04350 TGF-beta signaling pathway; ko05166 HTLV-I infec			0.4226574 0.406108274
K17494			NA	0.9		0.406108274
			ko00970 Aminoacyl-tRNA biosynthesis	-0.7		0.406108274
			ko00240 Pyrimidine metabolism; ko00983 Drug metabolism - other enzymes	0.7		0.410911565
K18184	COX20	cytochrome c oxidase assembly protein subunit 20	NA	-0.5		0.366431979
K02265			ko00190 Oxidative phosphorylation; ko04260 Cardiac muscle contraction; ko04			0.406108274
K02270			ko00190 Oxidative phosphorylation; ko04260 Cardiac muscle contraction; ko04			0.406108274
			NA ko04145 Phagosome; ko04962 Vasopressin-regulated water reabsorption; ko0	0.5		0.411688642 0.406108274
K10413			ko04120 Ubiquitin mediated proteolysis	0.5		0.406108274
K10615			ko04120 Ubiquitin mediated proteolysis	0.7		0.406108274
			NA	-0.5		0.406108274
K10205	ELOVL2	elongation of very long chain fatty acids protein 2 [EC:2.3.1.199]	ko00062 Fatty acid elongation; ko01040 Biosynthesis of unsaturated fatty acid	s -0.4	0.0180	0.406108274
K17286			NA	0.4		0.406108274
K05079			ko04060 Cytokine-cytokine receptor interaction; ko04151 PI3K-Akt signaling p	1.0		0.406108274
K08751			ko03320 PPAR signaling pathway; ko04975 Fat digestion and absorption ko04060 Cytokine-cytokine receptor interaction; ko04151 PI3K-Akt signaling p	0.4		0.411688642 0.406108274
K09409			NA	0.5		0.410911565
			ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Pa			0.406108274
K12900	FUSIP1		ko03040 Spliceosome	-0.5		0.406108274
K17894	FUSIP1 GATA2	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2	NA	-0.5	3 0.0266 4 0.0249	0.406108274
K17894 K02377	FUSIP1 GATA2 TSTA3, fcl	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo	-0.5 0.9 1 1	3 0.0266 4 0.0249 6 0.0143	0.406108274 0.406108274
K17894 K02377 K00799	FUSIP1 GATA2 TSTA3, fcl GST, gst	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOPIfucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto	-0.5 0.9 0.1 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092	0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDPL-fucose synthase [EC:1.1.271] glutathione 5-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo	-0.5 0.9 0.6 0.6 0.5	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412	0.406108274 0.406108274 0.406108274 0.424612243
K17894 K02377 K00799 K00049 K09223	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo	-0.5 0.9 0.1 0.6 0.5 0.5	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo	-0.5 0.9 0.1 0.6 0.5 0.5 0.5	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407	0.406108274 0.406108274 0.406108274 0.424612243
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOPL-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandifionacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol ko00620 Pyruvate metabol ko00620 Glycine, serine and threonine metabolism; ko00330 Arginine and pro	-0.5 0.9 0.1 0.6 0.5 0.5 0.5	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79.1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein B2	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00360 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein prot ko05134 Legionellosis	-0.5 0.9 1 1 1 0.0 0.0 0.5 0.5 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0485 2 0.0109	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GDPL-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko003040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05332 Systemic lupus erythematosus	-0.5 0.5 0.6 0.6 0.5 0.5 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0485 2 0.0109	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274 0.366431979
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMIT HSPA1_8 HSF1 HHSF1 HAGB2 HZA INPP4	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock ToKDa protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko003040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko003044 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali	-0.5 0.9 0.0 0.5 0.5 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0485 2 0.0109 1 0.0014	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INIP4	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79.1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone HZA inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko003040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05332 Systemic lupus erythematosus	-0.9 0.9 0.0 0.0 0.5 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0109 1 0.0014 5 0.0054 2 0.0054	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274 0.366431979
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HL2A INPP4 IFITM IL13RA1 IL13RA1	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-L-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypruvate reductase [EC:1.1.79.1.1.1.81]  growth factor independent 1  guanditionacetate N-methyltransferase [EC:2.1.1.2]  heat shock 70kDa protein 1/8  heat shock transcription factor 1  high mobility group protein 82  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 receptor alpha-1  interleukin 15	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein prot ko05134 Legionellosis  NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA	-0.9 0.9 0.0 0.5 0.5 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0109 1 0.0014 5 0.0054 2 0.0054 3 0.0266	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.42612243 0.406108274 0.426599288 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A IINPP4 IFITM ILI3RA1 ILI5 IFT27, RAYL, RABL4	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79.1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone HZA inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interflaeklia transport protein 27 homolog	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko0340 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p	-0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.0407 8 0.0258 2 0.0485 2 0.0485 2 0.0013 3 0.0054 2 0.0013 3 0.0266 2 0.0038 2 0.0038	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K07934	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 IFITM ILLISRA1 ILLISRA1 ILLISRA1 ILLISRA1 LAMB1	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAG protein 1/8 heat shock bkoa protein 1/8 heat shock bkoa protein 1/8 heigh mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 receptor alpha-1 interleukin 15 interlaelukin 15 interlaelukin 15	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko003040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p Ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re	-0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0407 0 0.0407 0 0.0407 1 0.0014 5 0.0054 5 0.0054 2 0.0033 3 0.0268 2 0.0033 3 0.0268 2 0.0033 3 0.0268	0.406108274 0.406108274 0.42612243 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K07934 K05636 K02873	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM ILITAM ILITAM ILITAM ILITAM ILITAM ILITAM ILITAM ILITAM ILITAM IRITAM ILITAM IRITAM ILITAM IRITAM IRITAM ILITAM IRITAM IR	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypruvate reductase [EC:1.1.79 1.1.1.81]  growth factor independent 1  guandidinoacetate N-methyltransferase [EC:2.1.1.2]  heat shock transcription factor 1  high mobility group protein 82  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 receptor alpha-1  interleukin 15  intraflagellar transport protein 27 homolog  laminin, beta 1  large subunit ribosomal protein I13e	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome	-0.9 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.0417 0 0.0407 8 0.0258 2 0.0485 2 0.0485 2 0.0054 5 0.0054 2 0.0013 3 0.0266 2 0.0038 2 0.0038 2 0.0037 1 0.0182	0.406108274 0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.426612243 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K09944 K05636 K05934 K07934 K05636	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 IFITM IL13RA1 IL15 IFT27, RAYL, RABL4 LAMB1 RP-127, MRPL27, rpmA	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79.1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interleukin 13 receptor alpha-1 interleukin 15 intraflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L13e large subunit ribosomal protein L27	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03240 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome	-0.9	3 0.0266 4 0.0249 6 0.0143 7 0.0092 0 0.0417 0 0.017 0 0.0407 8 0.0258 2 0.0485 2 0.0485 2 0.0054 3 0.0054 2 0.0038 3 0.0266 2 0.0038 3 0.0167 3 0.0167	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.4265108274 0.426599288 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K09944 K05636 K05934 K07934 K05636 K02873	FUSIP1 GATA2 TSTA3, fd GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 HITM HILISRA1 ILIS FITZP, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-L-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81]  growth factor independent 1  guandidinoacetate N-methyltransferase [EC:2.1.1.2]  heat shock Dkoa protein 1/8  heat shock bkoa protein 1/8  heat shock transcription factor 1  high mobility group protein B2  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interdeukin 13 receptor alpha-1  interleukin 15  interlaukin 13 receptor alpha-1  interlaukin 13 use 1  large subunit ribosomal protein L12  large subunit ribosomal protein L12  lectin, mannose-binding 1	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome	-0.9 0.5 0.5 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6	3 0.0266 4 0.0249 5 0.0143 7 0.0092 0 0.0412 0 0.0417 0 0.0407 0 0.0407 1 0.0014 5 0.0054 2 0.0403 3 0.0266 2 0.0483 2 0.0433 3 0.0266 1 0.0077 3 0.0167 1 0.0182 9 0.0218 8 0.0175	0.406108274 0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.426599288 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K09944 K05636 K05934 K07934 K05636	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM ILI3RA1 ILI3RA1 ILI4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LUTAF	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypruvate reductase [EC:1.1.79.1.1.1.81] growth factor independent 1 guanditionacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interleukin 13 receptor alpha-1 interleukin 15 intraflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein I13e large subunit ribosomal protein I27 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko003040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko04141 Protein processing in endoplasmic reticulum	-0.9	3 0.0266 4 0.0249 5 0.0143 7 0.0092 0 0.0412 0 0.0177 0 0.092 2 0.0485 2 0.0109 1 0.0014 5 0.0054 2 0.0013 3 0.0266 2 0.033 3 0.0167 1 0.0182 9 0.0216 8 0.0175 5 0.0136	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.4265108274 0.426599288 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K009223 K00542 K03283 K09414 K11251 K01109 K06566 K05076 K05076 K05433 K09344 K05636 K02873 K02899 K10080 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 IFITM ILI3RA1 ILI5 IFT27, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPACSBG	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock 70kD protein 1/8 heat shock NoDa protein 1/8 heat shock box portein 1/8 heat shock box protein 1/8 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 15 intraflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L13e large subunit ribosomal protein L12 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-aide-CoA ligase ACSBG [EC:6.2.1.3]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03141 legionellosis NA ko050314 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko04161 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko0490 Adi ko00501 Fotat ad degradation; ko03320 PPAR signaling pathway; ko0490 Adi	-0.9	3 0.0266 4 0.02494 6 0.0143 7 0.0092 0 0.0412 0 0.0472 0 0.0472 0 0.0407 8 0.0258 2 0.0485 2 0.0485 2 0.0054 2 0.0013 3 0.0266 2 0.003 3 0.0266 2 0.003 3 0.0266 8 0.015 9 0.0216 8 0.015 9 0.0216 9 0.0216	0.406108274 0.406108274 0.426108274 0.426112243 0.426112243 0.406108274 0.4266108274 0.366431979 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K09414 K11295 K11251 K01109 K06566 K05076 K05433 K07934 K05636 K02873 K02873 K02899 K10080 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363 K19363	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM ILI3RA1 ILI3RA1 ILI4 IFITZ, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF IPL ACSBG LAPTM	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypruvate reductase [EC:1.1.79 1.1.1.81]  growth factor independent 1  guandinoacetate N-methyltransferase [EC:2.1.1.2]  heat shock 70kDa protein 1/8  heat shock transcription factor 1  high mobility group protein 82  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 receptor alpha-1  interleukin 15  intraflagellar transport protein 27 homolog  laminin, beta 1  large subunit ribosomal protein I13e  large subunit ribosomal protein I27  letctin, mannose-binding 1  lipopolysaccharide-induced tumor necrosis factor-alpha factor  lipoprotein lipase [EC:3.1.1.34]  long-chain-fatty-acid—CoA ligase ACSBG [EC:6.2.1.3]  lysosomal-associated transmembrane protein	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko0340 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04050 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010/ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome	-0.9	3 0.0266 4 0.0249 4 0.0249 4 0.0249 5 0.00143 7 0.0092 0 0.0412 0 0.0177 8 0.052 2 0.0485 2 0.0485 2 0.0193 1 0.0014 5 0.0054 2 0.0013 3 0.0266 2 0.0077 3 0.0167 1 0.0182 9 0.0218 8 0.0175 5 0.0134 3 0.0054	0.406108274 0.406108274 0.42661242 0.426612243 0.406108274 0.424612243 0.406108274 0.426612828 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K00542 K11251 K01109 K06566 K05076 K05076 K05076 K05037 K02893 K10080 K19363 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K10080 K108	FUSIP1 GATA2 GATA2 GATA2 GATA2 GST, gst GGRIPR GFI1 GAMT HMF9A1_8 HSF1 HMGB2 HA2 INIPP4 IFITM ILISRA1 ILIS ILISRA1 ILIS ILISRA1 ILIS RP-L13R, RPL13 RP-L13R, RPL13 RR-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF IPL ACSBG LAPTM	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179.1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAG protein 1/8 heat shock Koba protein 1/8 heat shock bods protein 1/8 heat shock bods protein 1/8 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L12 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoportein [lipase [EC:3.1.34] long-chain-fatty-acid-coA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Gultathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03240 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko0340 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Rytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Rytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Rytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04514 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04900 Adi ko04142 Lysosome ko04142 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules (	-0.9	3 0.0266 4 0.0249 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.049 8 0.0258 2 0.0485 2 0.0054 5 0.0054 5 0.0054 1 0.0054 2 0.0038 3 0.0266 2 0.0077 3 0.0167 5 0.013 3 0.0266 6 0.0114 3 0.0054 5 0.013 6 0.0054	0.406108274 0.406108274 0.406108274 0.424612243 0.4246108274 0.4246108274 0.4266108274 0.4266108274 0.406108274 0.366431979 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K00542 K11295 K11251 K05566 K05076 K05433 K005636 K02873 K02899 K10080 K10508 K19363 K10509 K15013 K12887 K19363 K1059 K15013 K12887	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 IFITM ILI3RA1 ILI5 IFTZ7, RAYL, RABL4 LAMB1 RP-L12e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL ACSBG LAPTM MHC1 MATK	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock ToKDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 arceptor alpha-1 interleukin 15 large subunit ribosomal protein L12 large subunit ribosomal protein L27 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2]	NA ko00051 Pructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03514 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04051 Pl3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0311 Protein processing in endoplasmic reticulum NA ko00651 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko045010 Ak00071 Ertty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome	-0.9	3 0.0266 4 0.0249 4 0.0249 6 0.0143 7 0.0092 0 0.0412 0 0.047 0 0.0054 2 0.0485 2 0.0169 1 0.0014 2 0.0038 3 0.0266 5 0.0038 2 0.0038 2 0.0038 2 0.0038 2 0.0038 2 0.0038 3 0.0266 0 0.014 3 0.0054 5 0.0038 6 0.0054 6 0.0014 9 0.0214	0.406108274 0.406108274 0.42612243 0.42612243 0.406108274 0.424612243 0.406108274 0.42661283 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K09223 K00542 K03283 K01255 K11251 K01109 K05656 K05636 K05636 K05636 K05636 K05636 K05636 K0655 K0656 K0656 K0656 K0656 K0656 K0656 K0656 K0656 K065	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM ILI3RA1 ILI3RA1 ILI4 IFITZ, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL ACSBG LAPTM MHC1 MHC1 MATK TOM6	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypruvate reductase [EC:1.1.79 1.1.1.81]  growth factor independent 1  guandinoacetate N-methyltransferase [EC:2.1.1.2]  heat shock 70kDa protein 1/8  heat shock transcription factor 1  high mobility group protein 82  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 receptor alpha-1  interleukin 13 receptor alpha-1  interleukin 15  intraflagellar transport protein 27 homolog  laminin, beta 1  large subunit ribosomal protein I13e  large subunit ribosomal protein I27  letetin, mannose-binding 1  lipopolysaccharide-induced tumor necrosis factor-alpha factor  lipoprotein lipase [EC:3.1.1.34]  long-chain-fatty-acid—CoA ligase ACSBG [EC:6.2.1.3]  lysosomal-associated transmembrane protein  major histocompatibility complex, class I  megakaryocyte-associated tyrosine kinase [EC:2.7.10.2]  mitochondrial import receptor subunit 70M6	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko0340 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04061 Pl3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04144 Lysosome	-0.9	3 0.2666 0.01434 0.02491 0.0092 0.0092 0.0092 0.0092 0.0092 0.0093 0.0092 0.0093	0.406108274 0.406108274 0.406108274 0.4246112243 0.406108274 0.4246112243 0.406108274 0.424612243 0.406108274 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K00923 K00542 K03283 K09414 K11295 K11251 K11251 K11295 K101109 K06566 K05076 K05636 K02873 K07934 K102890 K10380 K10380 K10380 K10381	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HIMGB2 HZA INPPA HILISRA1 ILIS IFITM ILISRA1 ILIS IFITA, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L3e, RPL13 ITAF IPLA ACSBG LAPTIM MHC1 MATK TOM6 TOM7	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.S.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAG protein 1/8 heat shock XDAG protein 1/8 heat shock bods protein 1/8 heat shock bods protein 1/8 heat shock protein protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 large subunit ribosomal protein L13e large subunit ribosomal protein L13e large subunit ribosomal protein L17 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM6	NA ko00051 Pructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03514 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04051 Pl3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0311 Protein processing in endoplasmic reticulum NA ko00651 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko045010 Ak00071 Ertty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome	-0.9	3 0.2666 6 0.01434 6 0.0494 6 0.01434 6 0.01434 6 0.01434 6 0.01434 6 0.01434 6 0.0412	0.406108274 0.406108274 0.42612243 0.42612243 0.406108274 0.424612243 0.406108274 0.42661283 0.406108274 0.366431979 0.406108274
K17894 K02377 K00049 K00049 K09223 K03283 K09414 K11295 K01566 K05076 K05076 K05076 K05076 K05873 K10289 K10080 K10080 K10193 K1081	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM IL13RA1 IL15 IFT27, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL ACSBG LAPTIM MHC1 MATK TOMIG	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.5.1.18]  glyoxylate/hydroxypyruvate reductase [EC:1.1.79 1.1.1.81]  growth factor independent 1  guandidinoacetate N-methyltransferase [EC:2.1.12]  heat shock ToKDa protein 1/8  heat shock transcription factor 1  high mobility group protein 82  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 raceptor alpha-1  interleukin 13 raceptor alpha-1  interleukin 15 arceptor alpha-1  large subunit ribosomal protein 127 homolog  laminin, beta 1  large subunit ribosomal protein L12  lectin, mannose-binding 1  lipopolysaccharide-induced tumor necrosis factor-alpha factor  lipoprotein lipase [EC:3.1.34]  long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3]  lysosomal-associated transmembrane protein  major histocompatibility complex, class 1  megakaryocyte-associated tyrosine kinase [EC:2.7.10.2]  mitochondrial import receptor subunit TOM6  mitochondrial import receptor subunit TOM7  molecular chaperone HtpG	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03240 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko040610 Pika-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome	-0.9	3 0.0266 0.0413 0.0419 0.0419 0.0419 0.0419 0.0419 0.0419 0.0417 0.0419	0.406108274 0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.4266108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 K02377 K00049 K00029 K00049 K00524 K03283 K09414 K11295 K01526 K05076 K07777 K07777 K07777 K04079 K17771 K04079	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPPA HILISRA1 ILIS IFTZP, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 LTAF LMAN1, ERGICS3 LTAF LPL ACSBG LAPTM MHC1 MATK TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WOR11	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.S.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81] growth factor independent 1 guanidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAG protein 1/8 heat shock XDAG protein 1/8 heat shock bods protein 1/8 heat shock bods protein 1/8 heat shock yoko protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 13 raceptor alpha-1 large subunit ribosomal protein L13e large subunit ribosomal protein L3e large subunit ribosomal protein L13e large subunit ribosomal protein L1	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03141 legionellosis NA ko050314 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko04161 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko0490 Adi ko04142 Pysosome ko04144 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko05202 Transcriptional misregulation in cancer	-0.9	3 0.0264 6 0.0143 7 0.0029 7 0.0021 7 0.0021 8 0.027 9 0.001 8 0.027 9 0.001 8 0.0021 9 0.0021	0.406108274 0.406108274 0.426412243 0.406108274 0.424612243 0.406108274 0.4266108274 0.366431979 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K00542 K00542 K00542 K00542 K00542 K011251 K01109 K05436 K05436 K05436 K02879 K10080 K19363 K102879 K10080 K19363 K1080 K19363 K1080 K19363 K1080 K19363 K1080 K19363 K1080 K108	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM IL13RA1 IL15 IFTZ7, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF IPI MHC1 MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WDR11 EAG.31	FUS-interacting serine-arginine-rich protein 1  GATA-binding protein 2  GATA-binding protein 2  GOP-1-fucose synthase [EC:1.1.1.271]  glutathione S-transferase [EC:2.S.1.18]  glyoxylate/hydroxypyruvate reductase [EC:1.1.79 1.1.1.81]  growth factor independent 1  guandidinoacetate N-methyltransferase [EC:2.1.12]  heat shock transcription factor 1  high mobility group protein 1/8  heat shock transcription factor 1  high mobility group protein B2  histone H2A  inositol polyphosphate-4-phosphatase [EC:3.1.3.66]  interferon induced transmembrane protein  interleukin 13 raceptor alpha-1  interleukin 15 raceptor alpha-1  interleukin 15 arceptor alpha-1  large subunit ribosomal protein 27 homolog  laminin, beta 1  large subunit ribosomal protein L12  lectin, mannose-binding 1  lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.1.34]  long-chain-faty-acid-CoA ligase ACSBG [EC:6.2.1.3]  lysosomal-associated transmembrane protein  major histocompatibility complex, class 1  megakaryocyte-associated tyrosine kinase [EC:2.7.10.2]  mitochondrial import receptor subunit TOM6  mitochondrial import receptor subunit TOM7  molecular chaperone HtpG  nuclear protein, 1  PH-interacting protein  phospholipid-translocating ATPase [EC:3.6.3.1]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko05910 / ko00712 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Lysosome ko04142 Protein processing in endoplasmic reticulum; ko04514 Cell adhesion molecules ( ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko05202 Transcriptional misregulation in cancer	-0.9	3 0.0266 0.0412	0.406108274 0.406108274 0.4261243 0.406108274 0.424612243 0.406108274 0.4266108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 K02377 K00799 K00049 K00249 K00254 K03283 K09414 K11295 K11251 K01109 K05666 K05676 K05433 K05434 K05636 K05676 K05433 K05676 K05433 K05676 K05676 K05433 K05676 K05767 K05676 K05767 K0577 K057 K05	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GGRIPR GFI1 GAMT HMF9A1_8 HSF1 HMGB2 HA2 INIPP4 IFITM IL13RA1 IL15 IFITA, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF IPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WOR11 E36, 3.1 GFP	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruste reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAB protein 1/8 heat shock XDAB protein 1/8 heat shock bkoa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfleukin 13 receptor alpha-1 interfleukin 15 intraflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein I13e large subunit ribosomal protein I127 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acidCoA ligase ACSBG [EC:6.2.1.3] lyssomal-associated transmembrane protein major histocompatibility complex, dass I megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM6 mitochondrial protein J PH-interacting protein IX	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko0340 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04141 Protein processing in endoplasmic reticulum NA ko04061 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko04162 ECM-receptor interaction; ko04640 Hematopoietic cell lineage	-0.9	3 0.02666 0.01434 0.02499 0.01434 0.02499 0.01434 0.02499 0.0147 0.00292 0.0107 0.0407	0.406108274 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.42661283 0.406108274
K17894 (NO2377 NO2378 N	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 HITM HZA INPP4 HITM HZA INPP4 HITM HZA INPP4 HITM HZA INPP4 HAPA LAMB1 RP-123, RPL13 RP-123, RPL13 RP-127, RMRPL27, rpmA LMAN1, ERGICS3 UTAF LPL ACSBG LAPTM MHC1 MATK TOM/6 TOM/7 htp6, HSP90A NUPRI, COM1 PHIP, WDR11 E3.6.3.1 E3.6.9 PCSK6	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.S.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock Oxbo protein 1/8 heat shock Oxbo protein 1/8 heat shock box protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 13 large subunit ribosomal protein L13e large subunit ribosomal protein L12e lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acidCoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM/7 molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03140 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko005034 Alcoholism; ko05322 Systemic lupus erythematosus ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04051 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03101 Ribosome ko03101 Ribosome ko03101 Riposome ko03101 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Frotein processing in endoplasmic reticulum; ko04141 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04172 Neurotrophin signaling pathway NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko040451 ECM-receptor interaction; ko04640 Hematopoietic cell lineage	-0.9	3 0.2266 0.0143 0.0249 0.0049 0.0049 0.0050 0.0070	0.406108274 0.406108274 0.426412243 0.406108274 0.424612243 0.406108274 0.4264612243 0.406108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 (NO2377 K100594 (NO2378 K100594 K10159 K11251 K1125	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 H2A INPP4 IFITM IL13RA1 IL15 IFTZ7, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF IPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 htp6, HSP90A NUPRI, COM1 PHIP, WDR11 E3-6.3.1 GP9 PPCSK6 PPCSK6	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GATA-binding protein 2 GOP-1-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.S.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock transcription factor 1 high mobility group protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukn 13 raceptor alpha-1 interleukn 15 intraflagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L12 large subunit ribosomal protein L27 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.3.4] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM7 molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21] protease, serine, 16 (thymus) [EC:3.4]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko005134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lyososme ko04142 Lyososme ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signal ko05202 Transcriptional misregulation in cancer NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA	-0.9	3 0.2266 0.0412	0.406108274 0.406108274 0.4261243 0.406108274 0.424612243 0.406108274 0.4266108274 0.3666431979 0.406108274 0.3666431979 0.406108274
K17894 (NO2377 K10049) K10049 (NO2237 K100549 K100549 K10159 K10159 K10159 K10159 K10159 K100549 K100554 K100554 K100554 K100554 K100554 K100554 K100554 K100554 K100555 K10055 K10055 K10055 K10055 K	FUSIP1  GATA2  GATA2  GATA2  GATA2  STA3, fd  GST, gst  GRHPR  GFI1  GAMT  HSPA1_8  HSF1  HMGB2  HA2  INPP4  IFITM  IL13RA1  IL15  IL15  IL15  RP-L12, RAYL, RABL4  LAMB1  RR-L12, RPL13  RR-L27, MRPL27, rpm4  LMAN1, ERGICS3  LITAF  LACSBG  LAPTM  MHC1  MATK  TOM/6  TOM/7  htp6, HSP90A  NUPR1, COM1  PHIP, WDR11  E3.6.3.1  GP9  PCSSK6  PRSS16  OGT	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock XDAG protein 1/8 heat shock XDAG protein 1/8 heat shock Aboba protein 1/8 heat shock bods protein 1/8 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L12 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoportein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, dass 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM/S mitochondrial receptor in N PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proproteia convertase subtilisin/kexin type 6 [EC:3.4.21-] protein O-GloNAc transferase [EC:2.4.1.255]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03140 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko005034 Alcoholism; ko05322 Systemic lupus erythematosus ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04051 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03101 Ribosome ko03101 Ribosome ko03101 Riposome ko03101 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Frotein processing in endoplasmic reticulum; ko04141 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04172 Neurotrophin signaling pathway NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko040451 ECM-receptor interaction; ko04640 Hematopoietic cell lineage	-0.9	3 0.0266 0.0143 0.0249 0.0149	0.406108274 0.406108274 0.426412243 0.406108274 0.424612243 0.406108274 0.4264612243 0.406108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 K00237 K00799 K00049 K00049 K00049 K00049 K00049 K00049 K000542 K00254 K	FUSIP1 GATA2 GATA2 GATA2 GATA2 GATA2 GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 IFITM ILI3RA1 ILI5 IFT27, RAYL, RABL4 LAMB1 RP-13e, RPL13 RP-127, MRPL27, rpmA LMAN1, ERGICS3 UTAF UPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WDR11 E3.6.3.1 GP9 PCSK6 PRSS16 OOT	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GOP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock Oxbo protein 1/8 heat shock Oxbo protein 1/8 heat shock box protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interleukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 raceptor alpha-1 large subunit ribosomal protein L13e large subunit ribosomal protein L12e lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acidCoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM/ molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21] protease, serine, 15 ([Hymus) [EC:3.4] protein O-GicNAc transferase [EC:2.4.1.255] protein of ColicNac transferase [EC:2.4.1.255]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko00360 Slycine, serine and threonine metabolism; ko00330 Arginine and pro ko0036134 Legionellosis NA ko0056134 Legionellosis NA ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P18K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko0310 Ribosome ko0310 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 J ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04122 Neurotrophin signaling pathway NA NA ko040141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko005514 Other types of O-glycan biosynthesis	-0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9	3 0.2266 0.0143 0.0249 0.0149 0.0249 0.0059 0.0070	0.406108274 0.406108274 0.42661283 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.42661283 0.406108274
K17894 K00237 K00799 K00049 K00049 K00049 K00049 K00049 K00049 K000542 K00254 K	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HIMGB2 HZA INPP4 HITTM HILISRA1 HLIS HITZ, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 RP-L17, MRPL27, rpmA HANDA1, ERGICS3 HANDA1 HA	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glowylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock VAXDa protein 1/8 heat shock two protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 15 receptor alpha-1 interfeukin 16 receptor alpha-1 interfeukin 16 receptor alpha-1 interfeukin 17 receptor alpha-1 interfeukin 16 receptor alpha-1 interfeukin 17 receptor alpha-1 interfeukin 17 receptor alpha-1 interfeukin 18 receptor alpha-1 interfeukin 19 receptor alpha-1 in	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko040151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Riposome ko0310 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04722 Neurotrophin signaling pathway NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko00514 Other types of O-glycan biosynthesis	-0.9	3 0.0266 0.0143 0.0249 0.0143 0.0249 0.0143 0.0249 0.0147 0.0029 0.0177 0.0027 0.0077	0.406108274 0.406108274 0.426612243 0.406108274 0.426612243 0.406108274 0.426612243 0.406108274 0.3666431979 0.406108274 0.3666431979 0.406108274
K17894 K00237 K00799 K00049 K00049 K00049 K000542 K03283 K00542 K03283 K00542 K01109 K00566 K05076 K05077 K0507 K05	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 HITIM HLI3RA1 ILI5 IFT27, RAYL, RABL4 LAMB1 RP-113e, RPL13 RP-127, MRPL27, TPMA LAMB1, RFGICS3 LITAF LPC LAMB1 LAMB1 RP-13e, RPL13 RP-127, MRPL27, TPMA LMAN1, ERGICS3 LITAF LPC LAPTIM MHC1 MATK TOMG TOMG TOMG TOMG TOMG TOMG TOMG TOMG	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GOP-1-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock DXOB protein 1/8 heat shock DXOB protein 1/8 heat shock bx DxD protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interleukin 13 receptor alpha-1 interleukin 15 large subunit ribosomal protein L13e large subunit ribosomal protein L12e lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM/ molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proportein convertase subtilisin/kexin type 6 [EC:3.4.21] protein O-GlcNAc transferase [EC:2.4.1.25] protein phosphatase 1 regulatory subunit 27 protein-licosapartate[O-aspartate] O-methyltransferase [EC:2.1.1.71 queuine tRNAr-ribosyltransferase [EC:2.4.1.2]	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko040151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko000671 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04144 Endocytosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04722 Neurotrophin signaling pathway NA ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko00514 Other types of O-glycan biosynthesis NA NA ko000510 Purine metabolism; ko00240 Pyrimidine metabolism; ko00760 Nicotin NA	-0.9	3 0.2266 0.0143 0.0249 0.0149	0.406.108274 0.406108274 0.426612243 0.406108274 0.426612243 0.406108274 0.426612243 0.406108274 0.3666431979 0.406108274 0.4066108274
K17894 (K02377 K00598 (K00579 K000579 K00059 K00059 K00059 K00059 K00150 K00506 K005076 K005077 K005076 K005077 K005076 K005077 K005076 K005077 K005076 K005077 K00507	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HA2 INIPP4 IFITM ILI3RA1 ILI5 IFIZ7, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 RP-L17, MRPL27, rpm4 IMAN1, ERGICS3 LITAF IPL ACSBG LAPTM MHC1 MATK TOM/6 TOM/7 TOM/6 TOM/7 TOM/6 TOM/7 TOM/6 TOM/7 PPPRS516 OGT PPPPRS516 OGT PPPRS516 OGT PPPPRS516 OGT PPPRS516 OGT RSA02	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruste reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock toxoba protein 1/8 heat shock transferase [EC:2.1.1.2] histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeuchin 13 receptor alpha-1 interfeuchin 13 receptor alpha-1 interfeuchin 13 receptor alpha-1 interfeuchin 15 arge subunit ribosomal protein 113e large subunit ribosomal protein 127 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class I megakaryocyte-associated tryosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM7 molecular chaperone HtpG nuclear protein, 1 PH-interacting protein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21] protein O-GicNAc transferase [EC:2.4.1.25] protein phosphatase 1 regulatory subunit 27 protein-C-isospartate[O-aspartate] O-methyltransferase [EC:2.1.1.77 purine-nucleoside phosphorylase [EC:2.4.2.19] radical S-adenosyl methionine domain-containing protein 2	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Flososme ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Lysosome ko04142 Iysosome ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko040412 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04162 PCM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko04512 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko05202 Transcriptional misregulation in cancer NA NA ko052030 PURING RECEPTION REC	-0.9	3 0.0266 0.01434 0.02499 0.00493 0.00491 0.004	0.406108274 0.406108274 0.42611243 0.406108274 0.426411243 0.406108274 0.426611243 0.406108274 0.366431979 0.406108274
K17894 K00237 K00799 K00049 K00049 K00049 K00049 K00040 K00920 K00240 K00920 K00240 K00920 K10250 K11251 K00260 K11251 K00260 K10260 K1	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HZA INPPA HILISRA1 ILIS IFITM ILISRA1 ILIS IFITA, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 RP-L3C, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WDR11 E3.6.3.1 GF9 PCSK6 PRSS16 GF9 PCSK6 PRSS16 OGT PPP1R27 E2.1.177, pcm punA tgt, OTR11 RSAD2 PTPRC, CD45	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock Oxbo protein 1/8 heat shock Oxbo protein 1/8 heat shock box protein 1/8 heat shock box protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 raceptor alpha-1 interleukin 14 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabo NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03040 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein prot ko03140 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko005040 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko03131 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03101 Ribosome ko03101 Ribosome ko03010 Ribosome ko03010 Ribosome ko03014 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko00516 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Froderip processing in endoplasmic reticulum; ko04142 Lysosome ko04144 Endoctyosis; ko04145 Phagosome; ko04514 Cell adhesion molecules ( ko04122 Neurotrophin signaling pathway NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko04164 Loftodicytosis; ko04040 Hematopoietic cell lineage NA NA ko040514 Other types of O-glycan biosynthesis NA NA Ko05164 Influenza A ko04514 Cell adhesion molecules (CAMS); ko04660 T cell receptor signaling pa	-0.9	3 0.0266 0.0143 0.0249 0.0249 0.0041	0.406108274 0.406108274 0.426612243 0.406108274 0.424612243 0.406108274 0.426613243 0.406108274 0.3666431979 0.406108274
K17894 (1237) K00237 K00237 K00293 K000293 K000293 K000293 K000243 K00542 K03283 K009414 K11295 K11251 K112	FUSIP1 GATA2 GATA2 GATA2 GATA2 GATA2 GATA3 GGRHPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HA2 INPP4 IFITM ILI3RA1 ILI5 IFT27, RAYL, RABL4 LAMB1 RP-13E, RPL13 RP-127, MRPL27, rpm2 LMAN1, ERGICS3 ITAF IPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WOR11 E3.6.3.1 GF9 PCSK6 PRSS16 OGT PPPIRZ E21, 177, pcm punA FILT, 77, pcm punA INSAD2 PTPRC, CD45 STAT1	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GATA-binding protein 2 GATA-binding protein 2 GOP-1-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.2] heat shock ToKDa protein 1/8 heat shock ToKDa protein 1/8 heat shock ToKDa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 31 arceptor alpha-1 interleukin 15 interlageliar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein L13e large subunit ribosomal protein L12e lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.3.4] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial import receptor subunit TOM7 molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21-] protease, serine, 16 (thymus) [EC:3.4] protein-o-GicNAc transferase [EC:2.4.1.255] protein phosphatase 1 regulatory subunit 27 protein-i-isoaspartate [O-aspartate] O-methyltransferase [EC:2.1.1.77 purine-nucleoside phosphorylase [EC:2.4.2.1] queuine tRNA-ribosyltransferase [EC:2.4.2.29] radical S-adenosyl methionine domain-containing protein 2 receptor-type tyrosine-protein phosphatase C [EC:3.1.3.48] signal transducer and activator of transcription 1	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko095010/ ko00712 Fatty acid degradation; ko03320 PPAR signaling pathway; ko0920 Adi ko04142 Lysosome ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic ret	-0.9	3 0.0266 0.0412 0.0412 0.0412 0.0412 0.0412 0.0412 0.0417 0.0402 0.0412	0.406108274 0.406108274 0.42612243 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 K02377 K00549 K00549 K00549 K00549 K00549 K00549 K00540 K00573 K0	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GGRIPR GFI1 GAMT HSPA1_8 HSF1 HMGB2 HA2 INIPP4 HITIM HILISA1 HLIS HITZ, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 RP-L13e, RPL13 RP-L17, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL ACSBG LAPTM MHC1 MATK TOM6 TOM7 TOM6 TOM7 HIP, WDR11 E3.6.3.1 GF9 PCSK6 PPSS16 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS7 PPPRS516 OGT PPPIRS7 PPPRS516 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS516 OGT PPPIRS517 PPRS517 PPRS517 PRS517 PRS517 PRS517 PPRS517 PPRS517 PRS517 PPRS517 PRS517	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandidinoacetate N-methyltransferase [EC:2.1.1.2] heat shock NGAD protein 1/8 heat shock NGAD protein 1/8 heat shock bkoa protein 1/8 heat shock bkoa protein 1/8 heat shock transcription factor 1 high mobility group protein 82 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 15 interfagellar transport protein 27 homolog laminin, beta 1 large subunit ribosomal protein 113e large subunit ribosomal protein 112r lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoprotein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lyosomal-associated transmembrane protein major histocompatibility complex, class 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM6 mitochondrial protein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.21] protein O-GINAC transferase [EC:2.4.1.255] protein phosphatase 1 regulatory subunit 27 protein-C-isoaspartate[O-aspartate] O-methyltransferase [EC:2.1.1.77 purine-nucleoside phosphorylase [EC:2.4.2.29] radical S-adenosyl methionine domain-containing protein 2 receptor-type tyrosine-protein phosphatase C [EC:3.1.3.48] signal transducer and activator of transcription 3	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko05134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko040412 Plas-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Flosomic metabolism; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko05010 / ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lyosoome ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 PI3K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151	-0.9	3 0.0266 0.0143 0.0249 0.0149	0.406108274 0.406108274 0.4261243 0.406108274 0.424612243 0.406108274 0.42461243 0.406108274 0.42659288 0.406108274 0.366431979 0.406108274
K17894 (1923)  K00349 (1923)  K00542 (1923)  K00542 (1923)  K00542 (1923)  K00543 (1923)  K01109 (1923)  K01543 (1923)  K05433 (1923)  K05473 (1923)  K05474 (1923)  K05474 (1923)  K05474 (1923)  K05474 (1923)  K05474 (1923)  K05474 (1923)	FUSIP1 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT HSPA1_8 HSF1 HMG62 H2A INPP4 HITH HL13RA1 IL15 IFT27, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L13e, RPL13 LTAF LAMB1 RP-L13e, RPL13 LTAF LAMB1 RP-L13e, RPL13 LTAF LAMB1 RP-L13e, RPL13 LTAF LAMB1 RP-L13e, RPL13 LTAF LONG LAPTM MHC1 MATK TOM6 TOM7 htpG, HSP90A NUPR1, COM1 PHIP, WDR11 E3.6.3.1 GGP PCSK6 PRSS16 GGP PCSK6 PRSS16 GGP PCSK6 PRSS16 CGT PPP1R27 E2.1.1.77, pcm punA tgt, QTR11 RSAD2 STAT1 SNRPG, CD45 STAT1 SNRPG, SMG	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.179 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock Oxboa protein 1/8 heat shock Oxboa protein 1/8 heat shock Oxboa protein 1/8 heat shock box protein 1/8 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interdeukin 13 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 15 raceptor alpha-1 interleukin 13 raceptor alpha-1 interleukin 14 raceptor alpha-1 interleukin 15 raceptor a	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03134 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko0310 Ribosome ko04141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko095010/ ko00712 Fatty acid degradation; ko03320 PPAR signaling pathway; ko0920 Adi ko04142 Lysosome ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko04142 Protein processing in endoplasmic ret	-0.9	3 0.0266 0.0143 0.0249 0.0143 0.0249 0.00412 0	0.406.108274 0.406108274 0.42612243 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.366431979 0.406108274 0.366431979 0.406108274
K17894 (1237)  K00237  K00237  K00237  K00238  K00243  K00243  K00243  K00243  K00243  K00243  K00243  K00243  K00243  K00241  K01109  K06566  K05076  K05076  K05076  K06433  K02899  K1080  K	FUSIP1 GATA2 GATA2 TSTA3, fcl GST, gst GRHPR GFI1 GAMT GAMT HSPA1_8 HSF1 HMGB2 HZA INPP4 HITTM IL13RA1 IL15 IL15 IL15 IR7, RAYL, RABL4 LAMB1 RP-L13e, RPL13 RP-L27, MRPL27, rpmA LMAN1, ERGICS3 LITAF LPL MANTA TOM6 TOM7 TOM7 TOM7 TOM7 TOM7 TOM7 TOM7 TOM7	FUS-interacting serine-arginine-rich protein 1 GATA-binding protein 2 GDP-L-fucose synthase [EC:1.1.1.271] glutathione S-transferase [EC:2.5.1.18] glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81] growth factor independent 1 guandinoacetate N-methyltransferase [EC:2.1.1.2] heat shock Xtoba protein 1/8 heat shock Xtoba protein 1/8 heat shock Atoba protein 1/8 heat shock Atoba protein 1/8 heat shock transcription factor 1 high mobility group protein B2 histone H2A inositol polyphosphate-4-phosphatase [EC:3.1.3.66] interferon induced transmembrane protein interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 13 receptor alpha-1 interfeukin 15 intraflagellar transport protein 27 homolog laminin, bet 1 large subunit ribosomal protein L12 lectin, mannose-binding 1 lipopolysaccharide-induced tumor necrosis factor-alpha factor lipoportein lipase [EC:3.1.34] long-chain-fatty-acid-CoA ligase ACSBG [EC:6.2.1.3] lysosomal-associated transmembrane protein major histocompatibility complex, class 1 megakaryocyte-associated tyrosine kinase [EC:2.7.10.2] mitochondrial import receptor subunit TOM7 molecular chaperone HtpG nuclear protein, 1 PH-interacting protein phospholipid-translocating ATPase [EC:3.6.3.1] platelet glycoprotein IX proprotein convertase subtilisin/kexin type 6 [EC:3.4.2.1-] protease, serine, 16 (thymus) [EC:3.4] protein-GicNAc transferase [EC:2.4.1.255] protein phosphatase 1 regulatory subunit 27 protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77 purine-nucleoside phosphorylase [EC:2.4.2.29] rotein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77 purine-nucleoside phosphorylase [EC:2.4.2.29] signal transducer and activator of transcription 3 small nuclear ribonucleoprotein G small subunit ribosomal protein SSe small subunit ribosomal protein SSe	NA ko00051 Fructose and mannose metabolism; ko00520 Amino sugar and nucleo ko00480 Glutathione metabolism; ko00980 Metabolism of xenobiotics by cyto ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabol NA ko00260 Glycine, serine and threonine metabolism; ko00330 Arginine and pro ko03400 Spliceosome; ko04010 MAPK signaling pathway; ko04141 Protein pro ko03104 Legionellosis NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko00562 Inositol phosphate metabolism; ko04070 Phosphatidylinositol signali NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko04060 Cytokine-cytokine receptor interaction; ko04630 Jak-STAT signaling p NA ko040151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-re ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko030141 Protein processing in endoplasmic reticulum NA ko00561 Glycerolipid metabolism; ko03320 PPAR signaling pathway; ko04920 Adi ko04142 Lysosome ko04142 Exposome ko04142 Exposome ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signal ko04142 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signal ko04141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signal ko04162 ECM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko040141 Protein processing in endoplasmic reticulum; ko04151 P13K-Akt signa ko05202 Transcriptional misregulation in cancer NA NA ko00516 CEM-receptor interaction; ko04640 Hematopoietic cell lineage NA NA ko00516 CEM-receptor interaction; ko04660 T cell receptor signaling pathway; ko040510 Cell adhesion molecules (CAMs); ko04660 T cell receptor signaling pathway; ko04066 CHemokine signaling pathway; ko04066 HIF-1 signaling pathway; ko040066 Chemokine signaling pathway; ko04066 HIF-1 signaling pathway; ko04066 Chemokine signaling pathway; ko04066 HIF-1 signaling pathway; ko04066 Chemokine signaling pathway; ko04066 HIF-1 signaling pathway; ko04066 Chemokine signaling pathway; ko04066 HIF-1	-0.9. 0.9. 0.9. 0.9. 0.9. 0.9. 0.9. 0.9.	3 0.0266 0.0412 0.0412 0.0412 0.0412 0.0412 0.0412 0.0412 0.0413 0.0412 0.0413 0.0412 0.0413 0.0412 0.0413 0.0413 0.0414	0.406.108274 0.406108274 0.426412243 0.406108274 0.424612243 0.406108274 0.424612243 0.406108274 0.366431979 0.406108274

K06573	SLC4A1, AE1	solute carrier family 4 (anion exchanger), member 1	ko04966 Collecting duct acid secretion	1.15	0.0178	0.406108274
K12827	SF3A3, SAP61, PRP9	splicing factor 3A subunit 3	ko03040 Spliceosome	0.42	0.0136	0.406108274
K12892	SFRS3	splicing factor, arginine/serine-rich 3	ko03040 Spliceosome; ko05168 Herpes simplex infection	-0.50	0.0090	0.406108274
K10345	SPSB3, SSB3	SPRY domain-containing SOCS box protein 3	NA	-0.55	0.0201	0.406108274
K09497	CCT5	T-complex protein 1 subunit epsilon	NA	-0.38	0.0399	0.424389339
K09585	TXNDC10	thioredoxin domain-containing protein 10 [EC:5.3.4.1]	NA	0.65	0.0064	0.406108274
K10168	TLR5	toll-like receptor 5	ko04620 Toll-like receptor signaling pathway; ko05130 Pathogenic Escherichia	1 18	0.0445	0.426599288
K14736	TF	transferrin	ko04066 HIF-1 signaling pathway; ko04978 Mineral absorption	1.04	0.0088	0.406108274
K01312	PRSS	trypsin [EC:3.4.21.4]	ko04080 Neuroactive ligand-receptor interaction; ko04972 Pancreatic secretion	0.67	0.0132	0.406108274
K07375	TUBB	tubulin beta	ko04145 Phagosome; ko04540 Gap junction; ko05130 Pathogenic Escherichia co	1.01	0.0225	0.406108274
K00815	TAT	tyrosine aminotransferase [EC:2.6.1.5]	ko00130 Ubiquinone and other terpenoid-quinone biosynthesis; ko00270 Cyst	0.98	0.0004	0.366431979
K12621	LSM2	U6 snRNA-associated Sm-like protein LSm2	ko03018 RNA degradation; ko03040 Spliceosome	-0.41	0.0280	0.407707745
K08770	UBC	ubiquitin C	ko03320 PPAR signaling pathway	0.47	0.0052	0.406108274
K12161	URM1	ubiquitin related modifier 1	ko04122 Sulfur relay system	-0.39	0.0046	0.406108274
K02207	UBE2R, UBC3, CDC34	ubiquitin-conjugating enzyme E2 R [EC:6.3.2.19]	ko04120 Ubiquitin mediated proteolysis; ko05168 Herpes simplex infection	0.47	0.0057	0.406108274
K00757	udp, UPP	uridine phosphorylase [EC:2.4.2.3]	ko00240 Pyrimidine metabolism; ko00983 Drug metabolism - other enzymes	0.79	0.0230	0.406108274
K01719	hemD, UROS	uroporphyrinogen-III synthase [EC:4.2.1.75]	ko00860 Porphyrin and chlorophyll metabolism	0.63	0.0162	0.406108274
K02149	ATPeV1D, ATP6M	V-type H+-transporting ATPase subunit D	ko00190 Oxidative phosphorylation; ko04145 Phagosome; ko04721 Synaptic ve	-0.50	0.0327	0.410911565

# 1090 Triploids L3 vs L1

KOID	Gene Abbreviation	KEGG Annotation		Log Fold C			
			ko00100 Steroid biosynthesis; ko00140 Steroid hormone biosynthesis; ko04913 Ov	_			0.097393314
K02730		20S proteasome subunit alpha 1 [EC:3.4.25.1]	ko03050 Proteasome				0.15204453
K02731 K02732			ko03050 Proteasome ko03050 Proteasome				0.092606071 0.200624952
K06692		20S proteasome subunit beta 6 [EC:3.4.25.1] 26S proteasome non-ATPase regulatory subunit 5	NA NA	- 1			0.172884702
	PSMD4, RPN10		ko03050 Proteasome; ko05169 Epstein-Barr virus infection				0.172822126
	PSMD3, RPN3		ko03050 Proteasome; ko05169 Epstein-Barr virus infection				0.203851854
K03035	PSMD12, RPN5	26S proteasome regulatory subunit N5	ko03050 Proteasome; ko05169 Epstein-Barr virus infection		-0.46	0.0279	0.224952262
	PSMC1, RPT2	26S proteasome regulatory subunit T2	ko03050 Proteasome; ko05169 Epstein-Barr virus infection; ko05203 Viral carcinog				0.212426584
	PSMC4, RPT3	26S proteasome regulatory subunit T3	ko03050 Proteasome; ko05169 Epstein-Barr virus infection				0.14321829
	PSMC6, RPT4 PSMC5, RPT6		ko03050 Proteasome; ko05169 Epstein-Barr virus infection ko03050 Proteasome; ko05169 Epstein-Barr virus infection	-			0.165190087
			NA		_		0.18032030
			ko04975 Fat digestion and absorption				0.152539243
		4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	ko00130 Ubiquinone and other terpenoid-quinone biosynthesis; ko00350 Tyrosine		0.43	0.0195	0.203851854
K00213			ko00100 Steroid biosynthesis		-1.33		0.165190087
		8-oxo-dGTP diphosphatase / 2-hydroxy-dATP diphosphatase [EC:3.6.1.55 3.	NA .		-0.43		0.266543434
	ACSS, acs	acetyl-CoA synthetase [EC:6.2.1.1]	ko00010 Glycolysis / Gluconeogenesis; ko00620 Pyruvate metabolism; ko00640 Pro		0.69		0.143042222
K12348			ko00600 Sphingolipid metabolism; ko04142 Lysosome				0.237164916
K12314		actin related protein 2/3 complex, subunit 1A/1B actin, alpha cardiac muscle	ko04666 Fc gamma R-mediated phagocytosis; ko04810 Regulation of actin cytoskel ko04260 Cardiac muscle contraction; ko05410 Hypertrophic cardiomyopathy (HCM				0.165190087 0.186859932
	ACTL6A, INO80K	actin-like protein 6A	NA				0.232265167
	ACVR1, ALK2		ko04060 Cytokine-cytokine receptor interaction; ko04350 TGF-beta signaling paths	1			0.15204453
K17362	ACOT13	acyl-coenzyme A thioesterase 13 [EC:3.1.2]	NA		-0.50	0.0062	0.165190087
			ko00250 Alanine, aspartate and glutamate metabolism; ko00710 Carbon fixation ir				0.165190087
K15537		707	NA				0.187508268
K09516			ko00830 Retinol metabolism		0.38		0.196890943
			ko00830 Retinol metabolism ko00500 Starch and sucrose metabolism; ko04973 Carbohydrate digestion and abs		0.43		0.165133463
K11140			ko00480 Glutathione metabolism; ko04614 Renin-angiotensin system; ko04640 He				0.186740724
K03349			ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 Meiosis - yeast; ko04114 Oc	1			0.143042222
K08767	ANGPTL4, PGAR	angiopoietin-like 4	ko03320 PPAR signaling pathway		0.79	0.0047	0.165133463
K10327		, , , , , , , , , , , , , , , , , , , ,	NA .				0.18100852
K17091			NA NA				0.193046798
K17093			NA NA				0.212626738
K16646 K17095			NA NA	- 5		0.0057	
K17053			ko04975 Fat digestion and absorption; ko04977 Vitamin digestion and absorption	- 1			0.13204433
			ko00970 Aminoacyl-tRNA biosynthesis	ľ	-0.41	0.0134	0.187355725
K13184			NA .		-0.45	0.0033	0.152539243
			NA .		0.48		0.216901595
K13182			NA		-0.53		0.157088272
			NA NA	- 8 -	-0.46		0.187355725 0.226747861
K14810		ATP-dependent RNA helicase DDX56/DBP9 [EC:3.6.4.13] bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 [EC:1.1	NA NA		-0.45 -0.45		0.249525502
K12409		bifunctional UDP-N-acetylglucosamine 2-epimerase / N-acetylmannosamine kina		7	0.40	0.0370	
K01435		biotinidase [EC:3.5.1.12]	ko00780 Biotin metabolism; ko04977 Vitamin digestion and absorption				0.186087782
K04663	BMP5	bone morphogenetic protein 5	ko04350 TGF-beta signaling pathway; ko04390 Hippo signaling pathway	-	0.45	0.0180	0.198691113
K12332	CALCA		ko04270 Vascular smooth muscle contraction			0.0416	0.254344055
		calcitonin		_			
K17274	S100A10	calpactin-1 light chain	NA		0.58	0.0393	0.251981833
K17274 K03927	S100A10 CES2	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1.1 3.1.1.84 3.1.1.56]	NA ko00983 Drug metabolism - other enzymes	Į	0.58 0.45	0.0393 0.0085	0.251981833 0.172822126
K17274 K03927 K01294	S100A10 CES2 CPE	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1.1.3.1.1.84 3.1.1.56] carboxypeptidase E [EC:3.4.17.10]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus		0.58 0.45 -0.54	0.0393 0.0085 0.0014	0.251981833 0.172822126 0.143042222
K17274 K03927	S100A10 CES2 CPE CPZ	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1.1.3.1.1.84.3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA		0.58 0.45 -0.54 0.53	0.0393 0.0085 0.0014 0.0033	0.251981833 0.172822126
K17274 K03927 K01294 K13022 K08765	S100A10 CES2 CPE CPZ CPT1A	calpactin-1 light chain carboxyleptidase 2 [EC:3.1.1.3.1.1.84.3.1.1.56] carboxyleptidase 2 [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17] carnitine O-palmitoyltransferase 1, liver isoform [EC:2.3.1.21]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus		0.58 0.45 -0.54 0.53 0.62	0.0393 0.0085 0.0014 0.0033 0.0028	0.251981833 0.172822126 0.143042222 0.152539243
K17274 K03927 K01294 K13022 K08765 K12801 K03781	S100A10 CES2 CPE CPZ CPTIA CARDB, CARDINAL katE, CAT, catB, srpA	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1.1.3.1.1.84.3.1.1.56] carboxypeptidase [EC:3.4.17.10] carboxypeptidase Z [EC:3.4.17] carnitine O-palmitoyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NoD-like receptor signaling pathway ko0380 Trybtophan metabolism; ko0630 Glyoxylate and dicarboxylate metabolis		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545	S100A10 CES2 CPE CPZ CPTIA CARDB, CARDINAL katt, CAT, catB, srpA COMT	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17.1] carbixyleptidase 2 [EC:3.4.17.1] carpixyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00658 B		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371	S100A10 CES2 CPE CPZ CPTIA CARDB, CARDINAL katE, CAT, catB, srpA COMT CTSK	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase [ E(:2.3.4.17.10] carboxypeptidase 2 [EC:3.4.17] carmitine O-palmitoyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [ EC:1.11.1.6] catechol O-methyltransferase [ EC:2.1.1.6] cathepsin K [ EC:3.4.2.2.38]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko0623 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko0140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 Be ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512	S100A10 CES2 CPE CPZ CPTIA CARDB, CARDINAL kate, CAT, catB, srpA COMT CTSK CCL19, ELC	calpactin-1 light chain carboxylesterase 2 [EC.3.1.1.3.1.1.84.3.1.1.56] carboxypeptidase [ [EC.3.4.17.10] carboxypeptidase 2 [EC.3.4.17] carboxypeptidase 2 [EC.3.4.17] carpoxypeptidase 2 [EC.3.4.17] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase [EC.2.1.1.6] cathepian K [EC.3.4.22.38] C-C motif Chemokine 19	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko0380 Tryptophan metabolism; ko0030 Glyoxylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00956 Be ko01412 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko0460 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222 0.25121965
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371	S100A10 CES2 CPE CPE CPZ CPTIA CARDB, CARDINAL KatE, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carptine 0-palmitoyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] cathepsin K [EC:3.4.2.2.8] C-C motif Chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metaboli ko00140 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko009650 ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko0400 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.0387 0.0427	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050	S100A10 CES2 CPE CPE CPZ CPTIA CARRB, CARDINAL katE, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD CD4	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1.1 3.1.1.84 3.1.1.56] carboxypeptidase [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carnitine 0-paintivylitransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol 0-methyltransferase [EC:2.1.1.6] cathepsin K [EC:3.4.2.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko0380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 Be ko01412 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko0460 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.0387 0.0427 0.0076	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222 0.25121965 0.254716933
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454	S100A10 CES2 CPE CPE CPZ CPTIA CARDB, CARDINAL kate, CAT, catts, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17.1] carpase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] cathespin K [EC:3.4.2.38] C-C motif chemokine 19 CCAAT/enhance binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko0621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00360 Glyoxylate and dicarboxylate metabolisk ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 Bi ko00142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMS); ko04612 Antigen processing and presen		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44	0.0393 0.0085 0.0014 0.0033 0.0028 0.0107 0.0156 0.0015 0.0387 0.0427 0.0076 0.0019	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222 0.25121965 0.254716933 0.168745194 0.143042222 0.165133463
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624	S100A10 CES2 CPE CPZ CPTIA CAROB, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CERS CP	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] carboxypeptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase E [EC:2.1.1.6] cathepian K [EC:3.4.22.38] C-C motif Chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.16.3.1]	NA ko00983 Drug metabolism - other enzymes ko00940 Type i diabetes mellitus NA ko000971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko0480 Typtophan metabolism; ko06030 Glyovylate and dicarboxylate metabolis ko00340 Streorid hormone biosynthesis; ko00350 Tyrosine metabolism; ko0965 Bi ko04142 Lysosome; ko04380 Osteodast differentiation; ko0462 Toll-like receptor ko0460 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.0387 0.0427 0.0076 0.0019 0.0048	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.1820453 0.191823694 0.143042222 0.25121965 0.254716933 0.168745194 0.143042222 0.1651333463 0.254344055
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077	S100A10 CES2 CPE CPE CPZ CPTIA CARDB, CARDINAL katt, CAT, cattl, sypA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CPP groEL, HSPD1	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carptoxypeptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catepasin K [EC:3.4.22.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.16.3.1] chaperonin GroEL	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glycoyviate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658 ko014042 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko00800 Porphyrin and chlorophyll metabolism ko030318 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.68	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.0387 0.0427 0.0076 0.0019 0.0048 0.0417	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222 0.25121965 0.254716933 0.168745194 0.143042222 0.165133463 0.2547344055 0.14321829
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077	S100A10 CES2 CPE CPE CPE CPZ CPTIA CARDB, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP CPG CPC CPC CPC CRS CP CDC4 CCRS CP CDC4 CCRS CP CDC4 CCRS CP CDC6 CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [EC:2.1.1.6] cathepsin K [EC:3.4.22.38] C-C motif chemokine 19 C-CAT/enhance prinding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceruloplasmin [EC:1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00961 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko003050 Tyrosine metabolism; ko004658 ko04142 Lysosome; ko04800 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolijid metabolism ko00860 Porphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.68 0.44	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0015 0.0045 0.0042 0.0019 0.0048 0.0417 0.0022	0.251981833 0.172822126 0.152039243 0.15203453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.184946192 0.254121965 0.254716933 0.168745194 0.143042222 0.165133463 0.254344052 0.143241829 0.143042222
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077 K05022 K07440	S100A10 CES2 CPE CPE CPZ CPTIA CARD8, CARDINAL katé, CAT, caté, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CCC42 CER CP groEL, HSPD1 CLIC2 CVP46A1	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catebosis (EC:3.1.2.16) catebosis (EC:3.4.2.2.38) C-C motif chemokine 19 CCAA1/cenhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] cerculoplasmin [EC:1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesteroi 24(5)-hydroxylase [EC:1.4.13.98]	NA ko00983 Drug metabolism - other enzymes ko00490 Type I diabetes mellitus NA ko00901 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko003930 Tyrosine metabolism; ko00965 B ko01412 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04600 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04101 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00680 Orphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko000120 Primary bile acid biosynthesis		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.68	0.0393 0.0085 0.0014 0.0033 0.0028 0.00107 0.0156 0.0015 0.00427 0.0076 0.0019 0.0048 0.0417 0.0022 0.0012	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.15204453 0.184946192 0.191823694 0.143042222 0.25121965 0.25121965 0.254716933 0.168745194 0.143042222 0.165133463 0.254344055 0.14321829 0.143042222 0.143042222
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077 K05022 K07440 K00489	S100A10 CES2 CPE CPE CPE CPTA CARDB, CARDINAL kate, CAT, cate, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CCCCC CERS CP CPGUEL, HSPD1 CULC2 CCYP46A1 CVP7A1	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.84 3.1.56] carboxypeptidase E [EC:3.4.7.10] carboxypeptidase 2 [EC:3.4.7.7] carptoxylesterase 2 [EC:3.4.7.7] carptoxylesterase 2 [EC:3.4.7.7] caspase recruitment domain-containing protein 8 catalase [EC:1.11.16] cathepsin K [EC:3.4.2.2.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.6.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(S)-hydroxylase [EC:1.14.13.98] cholesterol 74pha-monooxygenase [EC:1.14.13.17]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00961 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko003050 Tyrosine metabolism; ko004658 ko04142 Lysosome; ko04800 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolijid metabolism ko00860 Porphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.68 0.44	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0156 0.0015 0.0387 0.0427 0.0076 0.0019 0.0048 0.0417 0.0022 0.0012	0.251981833 0.172822126 0.152039243 0.15203453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.184946192 0.254121965 0.254716933 0.168745194 0.143042222 0.165133463 0.254344052 0.143241829 0.143042222
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077 K05022 K07440 K04077 K05022 K07440 K04077	\$100A10 CES2 CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, cat8, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP CP CPC CUC2 CERS CP CP CUC2 CERS CP CP CUC4 CUC2 CUC4 CUC5 CUC4 CUC5 CUC4 CUC5 CUC4 CUC6 CUC7 CUC6 CUC7 CUC6 CUC7 CUC7 CUC7	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carpase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catcheol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catcheol 0-methyltransferase [EC:2.1.1.6] catcheol o-methyltransferase [EC:1.1.1.1.6] choral o-methyltransferase [EC:1.1.1.1.1] chaperonin Grott chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloride intracellular channel protein 3 chloridestroid 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin	NA ko00983 Drug metabolism - other enzymes ko00490 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxytate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658 ko001402 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04100 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko000500 Porphyrin and chiorophyll metabolism ko003018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.68 0.44 0.48 0.44 0.48 0.44 0.49 0.44 0.44 0.46 0.58 0.40 0.44 0.44 0.46 0.58 0.40 0	0.0393 0.0085 0.0014 0.0033 0.0030 0.0107 0.0156 0.0015 0.00427 0.0076 0.0019 0.0048 0.0417 0.0022 0.0012 0.0370 0.00055 0.0064	0.251981833 0.17282126 0.143042222 0.155239243 0.15204453 0.18204451 0.191823694 0.191823694 0.191823694 0.168745194 0.168745194 0.168745194 0.168745194 0.143042222 0.247118814 0.143042222 0.247118814 0.112669745 0.165190087 0.165190087
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077 K05022 K07440 K0489 K11586 K11586 K11586 K11586 K11586 K11586 K11586 K11586 K11586 K11586 K11586 K11586	S100A10 CES2 CPE CPE CPE CPE CPZ CAT, cat8, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CD4 CD4 CCC42 CERS CP CP CPCPAA1 CUC2 CVP46A1 CVP7A1 CBX3, HP1G CLU U CRES CP CES CP CRES CP CPPAA1 CRESA3, HP1G CLU CRES CPE CRES CRES CRES CRES CRES CRES CRES CRE	calpactin-1 light chain carboxylesterase 2 [EC.3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase [ EC.3.4.17.10] carboxypeptidase 2 [EC.3.4.17.1] carboxypeptidase 2 [EC.3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase [ Liver isoform [EC.2.3.1.21] cathepsin K [EC.3.4.22.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CDA artigen cell division control protein 42 cerramide synthetase [EC.2.3.1.24] ceruloplasmin [EC.1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC.1.14.13.98] cholesterol 24(5)-hydroxylase [EC.1.14.13.71] chromobox protein 3 clusterin	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko004040 Steroid hormone biosynthesis; ko003050 Tyrosine metabolism; ko004658 ko04142 Lysosome; ko04880 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway- yeast; ko040 ko00600 Sphingolipid metabolism ko00800 Porphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00120 Primary bile acid biosynthesis		0.58 0.45 -0.54 0.53 0.62 0.52 0.56 0.40 0.57 -0.54 0.44 0.46 0.58 0.44 0.48 2.61 0.44	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.00427 0.0042 0.0049 0.0041 0.0022	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.15204453 0.182946192 0.25121965 0.254716933 0.168745194 0.143042222 0.165133463 0.254344055 0.143042222 0.247118814 0.143042222 0.247118814 0.143042222 0.247118814 0.112669734 0.165190087 0.165190087 0.165190087
K17274 K03927 K01294 K13022 K08765 K12801 K03781 K00545 K01371 K05512 K10050 K06454 K04393 K04710 K13624 K04077 K07440 K00489 K11586 K1725 K11586 K1725 K13899 K13195	S100A10 CES2 CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CCL20 CERS CP groEL, HSPD1 CLIC2 CRR CYPFA6A1 C	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catepain (EC:3.4.22.38] C-C motif chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] cerarulogasmin [EC:1.6.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.4.13.198] cholesterol 24(5)-hydroxylase [EC:1.4.13.17] chromobox protein 3 clusterin coagulation factor VIII codid-inducible RNA-binding protein	NA koo0393 Drug metabolism - other enzymes koo0490 Type I diabetes mellitus NA koo0490 Type I diabetes mellitus NA koo00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko004040 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658 ko040412 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04620 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00680 Orphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko04510 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA NA ko04610 Complement and coagulation cascades		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 0.44 0.57 -0.44 0.46 0.48 0.48 0.44 0.48 0.44 0.57	0.0393 0.0085 0.0014 0.0033 0.0028 0.0028 0.0030 0.0107 0.0156 0.0015 0.0047 0.0048 0.0012 0.0022 0.0002 0.0002 0.0002 0.0002 0.0005 0.0002 0.00002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.00002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.00002 0.0002	0.251981833 0.172822126 0.143042222 0.155239243 0.15204453 0.15204453 0.1824946192 0.25121965 0.254716933 0.168745194 0.143042222 0.25121965 0.143121829 0.143121829 0.143121829 0.143042222 0.247118814 0.112669745 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087
K17274 K03927 K01294 K13022 K08765 K12801 K00545 K01371 K05512 K10050 K04710 K13624 K04077 K05022 K07440 K04077 K05022 K07440 K04077 K05022 K07440 K04077 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K05022 K07440 K0740 K07440 K07	\$100A10 CES2 CPE CPE CPE CPE CPTA CARD8, CARDINAL kate, CAT, cate, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP CPC CPC CPC CPC CPC CPC CPC CPC CPC	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.84 3.1.56] carboxypeptidase E [EC:3.4.7.10] carboxypeptidase E [EC:3.4.7.7] carnitine O-palmitoyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catchepism [EC:1.1.1.6] catchepism ( EC:3.4.2.2.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(S)-hydroxylase [EC:1.14.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type [II/IIII/Y/XI/XXIV/XXXII, alpha	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00360 Glyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko00958 E ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingollpid metabolism ko003018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko0120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA ko04610 Complement and coagulation cascades NA ko04515 IPJK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.56 0.40 -1.23 0.44 0.57 -0.44 0.58 -0.68 0.48 2.69 0.40 0.40 0.40 0.53 0.40 0.53 0.40 0.53 0.40 0.53 0.40 0.53 0.62 0.63 0.63 0.63 0.63 0.63 0.63 0.63 0.63	0.0393 0.0085 0.0014 0.0028 0.0028 0.0030 0.0107 0.0155 0.0035 0.0042 0.0048 0.0048 0.0048 0.0049 0.0022 0.0030 0.0002 0.0055 0.0064 0.0064 0.0018 0.0018	0.251981833 0.178822126 0.143042222 0.15239243 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.25121065 0.254716933 0.168745194 0.143042222 0.165133463 0.254344055 0.143042222 0.247118814 0.112669734 0.165190087 0.14321829 0.165190087 0.14321829 0.16599932 0.18368599932 0.1430422229
K17274 K03927 K01294 K03927 K01294 K03765 K12801 K03781 K05512 K10500 K05454 K04393 K04710 K13624 K04077 K05022 K07440 K04088 K11158 K17252 K03899 K13195 K166236 K06236	S100A10 CES2 CPE CPE CPE CPTIA CARD8, CARDINAL kate, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD CDC4 CEBPD CDC4 CEBP CDC4 CERS CPC GPGEL HSPD1 CULC2 CYP46A1 CYP7A1 CUP7A1 CUVP7A1 CULC1 CUCSX3, HP1G CLU F8 CIRBP COLIAS CORIAS	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase [ [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol 0-methyltransferase [EC:2.1.1.6] cathepsin K [EC:3.4.22.38] C-C motif chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmi [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloriderol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin cosqulation factor VIII cold-inducible RNA-binding protein collagen, type I/I/I/II/V/XXV/XXVII, alpha collagen, type I/I/I/II/V/XXVIXII, alpha	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00980 Type I diabetes mellitus NA ko000071 Fatty adid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko0140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 R ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04660 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pal NA ko04616 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04510 MPAP signaling pathway; ko04011 MAPR signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03600 Porphyrin and chlorophyll metabolism ko036080 Porphyrin and chlorophyll metabolism ko03618 NA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA NA ko04610 Complement and coagulation cascades NA ko04515 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.40 0.40 0.57 -0.44 0.58 -0.68 0.44 0.49 0.58 0.40 0.58 0.68 0.40 0.53 0.40 0.57 0.40 0.58 0.59 0.	0.0393 0.0085 0.0014 0.0028 0.0028 0.0028 0.0030 0.0107 0.0155 0.0387 0.0042 0.0012 0.0012 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0003 0.0003 0.0004	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.15204453 0.184946192 0.184946192 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.143042222 0.247118814 0.112669745 0.165190087 0.165190087 0.163128781 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.163128781
K17274 K03927 K01294 K03927 K01294 K03765 K12801 K03781 K05512 K10500 K05454 K04393 K04710 K13624 K04077 K05022 K07440 K04088 K11158 K17252 K03899 K13195 K166236 K06236	\$100A10 CES2 CPE CPE CPE CPTA CARD8, CARDINAL kate, CAT, cat8, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CPP groEL, HSPD1 CUC2 CYP4SA1 CYP7A1 CBW3, H1G CUL ERS COLIAS C	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catcheol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catcheol 0-methyltransferase [EC:2.1.1.6] catcheol 0-methyltransferase [EC:2.1.1.6] catcheol o-methyltransferase [EC:2.1.1.6] catcheol o-methyltransferase [EC:2.1.1.6] catcheol o-methyltransferase [EC:2.1.1.6] catcheoline (EC:3.4.22.38) CCA motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.16.3.1] chaperonin GroEt chloride intracellular channel protein 2 chlosetsrol 24(3-by-hydroxylase [EC:1.4.13.98] cholesterol 7alpha-monooxygenase [EC:1.4.13.17] chromobox protein 3 clusterin coagulation factor VIII codd-inducible RNA-binding protein collagen, type   ViI/III/V/XI/XXIV/XXVII, alpha collagen, type   ViI/IIII/V/XI/XXIV/XXVII, alpha collagen, type   ViI/IIII/V/XI/XXIV/XXVII, alpha collagen, type   ViI/IIII/V/XI/XXIV/XXVII, alpha collagen, type   ViI/IIII/V/XI/XXIV/XXVII, alpha collagen component (3b/4b) receptor 1	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00360 Glyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko00958 E ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingollpid metabolism ko003018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko0120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA ko04610 Complement and coagulation cascades NA ko04515 IPJK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.40 0.57 -0.44 0.46 0.58 -0.68 2.69 0.44 0.48 1.00 0.57 0.44 0.44 0.48	0.0393 0.0085 0.0014 0.0033 0.0030 0.0107 0.0156 0.0015 0.0076 0.0019 0.0019 0.0012 0.0012 0.0012 0.0002 0.0002 0.0054 0.0002 0.0056 0.0056 0.0057 0.0064 0.0057	0.251981833 0.178822126 0.143042222 0.15239243 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.25121065 0.254716933 0.168745194 0.143042222 0.165133463 0.254344055 0.143042222 0.247118814 0.112669734 0.165190087 0.14321829 0.165190087 0.14321829 0.16599932 0.18368599932 0.1430422229
K17274 K03927 K03927 K01294 K13022 K08765 K12801 K00545 K01371 K00545 K101371 K10512 K100510 K06454 K04393 K04077 K05022 K007440 K00489 K11596	S100A10 CES2 CPE CPE CPE CPTIA CAROR, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CERS CP groEL, HSPD1 CLU2 CYP4SA1 CVYPAA1 CWYPA1 CBR CLU2 CWPA1 CRB CIBBP COLIA CRB COLIAS C	calpactin-1 light chain carboxylesterase 2 [EC.3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC.3.4.17.10] carboxypeptidase E [EC.3.4.17.1] carboxypeptidase E [EC.3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase L, liver isoform [EC.2.3.1.21] cathepsin K [EC.3.4.22.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC.2.3.1.24] ceruloplasmin [EC.1.16.3.1] chapersonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC.1.14.13.98] cholesterol 7alpha-monooxygenase [EC.1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII codi-inducible RNA-binding protein collagen, type (IV)IIII/V/AI/XXIV/XXVII, alpha collagen, type (IV, alpha complement component [5.5.4.2.14.2]	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00981 Type I diabetes mellitus NA ko00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00363 Giyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko00363 Tyrosine metabolism; ko00965 B ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03610 Porphyrin and chlorophyll metabolism ko03610 Porphyrin and chlorophyll metabolism ko030120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA NA ko04151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04510 Complement and coagulation cascades NA ko04151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04510 Complement and coagulation cascades; ko04640 Hematopoietic cell lines		0.58 0.45 -0.54 0.53 0.62 -0.54 0.52 0.40 -1.23 0.44 0.57 -0.44 0.46 0.58 -0.48 -0.43 0.44 0.48 -0.44 0.48 -0.54 0.54 0.54 0.54 0.58	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0107 0.0156 0.0015 0.0087 0.0042 0.0012 0.0012 0.0012 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0003 0.	0.251981833 0.178822126 0.143042222 0.1525939243 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.25121965 0.25121965 0.25121965 0.25121965 0.25421065 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222
K17274 K03927 K13022 K08765 K08765 K08765 K08765 K00545 K00545 K00545 K00545 K00545 K00459 K00459 K11586 K004710 K05512 K004710 K055022 K07440 K11586 K17252 K00489 K11586	\$100A10 CES2 CPE CPE CPE CPE CPTIA CARD8, CARDINAL kate, CAT, cat8, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP CP CPC CPC CRS CPC CRS CPC CRS CPC CRS CPC CRS CRIA CRIA CRIA CRIA CRIA CRIA CRIA CRIA	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carpoxypeptidase E [EC:3.4.17.10] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catche Income Incom	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00981 Type I diabetes mellitus NA ko000071 Fatty add degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00360 Glyoxytate and dicarboxylate metaboli ko00140 Sterold hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 B ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04626 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko0600 Sphingollipid metabolism ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko0600 Sphingollipid metabolism ko003018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA ko040150 Complement and coagulation cascades NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04150 Complement and coagulation cascades; ko05130 Pertussis; ko05150 Staph ko04610 Complement and coagulation cascades; ko05130 Pertussis; ko05150 Staph ko04610 Complement and coagulation cascades; ko05130 Pertussis; ko05150 Staph		0.58 0.45 -0.54 0.62 -0.56 0.40 -1.23 0.57 -0.44 0.57 -0.48 0.48 -0.43 0.40 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 1.00 -0.54 -0.54 -0.54 -0.54 -0.54 -0.55 -0.56 -0.57 -0.48 -0.48 -0.48 -0.48 -0.48 -0.48 -0.49 -0.49 -0.40 -0.54 -0.54 -0.54 -0.55 -0	0.0393 0.0085 0.0014 0.0033 0.0028 0.0030 0.0016 0.0015 0.0015 0.0042 0.0027 0.0042 0.0042 0.0044 0.0012 0.005 0.0012 0.005 0.	0.251981833 0.178822126 0.143042222 0.1525939243 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.1520455 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.143042222 0.16133463 0.163904222 0.16190067 0.14321829 0.16190067 0.14321829 0.16190067 0.143042222 0.161928781 0.1623988260 0.2519881833 0.001870843 0.001870843
K17274 K03927 K01294 K13022 K08765 K08765 K01371 K00545 K10371 K00545 K04710 K0477 K	S100A10 CES2 CPE CPE CPE CPE CPTIA CARD8, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CDC4 CEBPD CDC4 CEBPD CDC4 CERS CPC GPGEL RSPD1 CUC2 CYP46A1 CYP7A1 CYP7A1 CUC2 CYP46A1 CYP7A1 CR3, P1G CUU R8 CIRBP COLIAS CO	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] carpoxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] cathepsin K [EC:3.4.22.38] C-C motif chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmi [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(S)-hydroxylase [EC:1.41.3.19] cholesterol 7alpha-monooxygenase [EC:1.41.3.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (1/I/III)/Y/I/X/XV/Y/XVII, alpha complement component 1, s subcomponent [EC:3.4.21.42] complement component 1, s subcomponent [EC:3.4.21.42] complement component 1, s subcomponent factor D [EC:3.4.21.42] complement component of EC:3.4.21.42] complement component 1, s subcomponent factor D [EC:3.4.21.42] complement component 1, s subcomponent factor Of EC:3.4.21.42] complement component 1, s condension complement complement component of EC:3.4.21.42] complement component 1, s condension complement complement component of EC:3.4.21.42] complement component 1, s condension complement complement complement complement component of EC:3.4.21.43	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00980 Type I diabetes mellitus NA ko000071 Fatty adid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko0140 Steroid hormone biosynthesis; ko00330 Tyrosine metabolism; ko00965 R ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor ko04606 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pa NA ko04616 Call adhesion molecules (CAMe); ko04612 Antigen processing and presen ko04101 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03608 Porphyrin and chlorophyll metabolism ko03608 Porphyrin and chlorophyll metabolism ko03608 Porphyrin and chlorophyll metabolism ko03609 Primary bile acid biosynthesis; ko0120 Primary bile acid biosynthesis; ko0120 Primary bile acid biosynthesis; ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04610 Complement and coagulation cascades NA ko04515 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04510 Complement and coagulation cascades; ko04540 Hematopoietic cell linee ko04610 Complement and coagulation cascades; ko05133 Pertussis ko04510 Complement and coagulation cascades; ko05133 Pertussis		0.58 0.45 -0.54 0.53 0.62 0.52 0.56 0.40 -1.23 0.57 -0.44 0.57 -0.44 0.58 -0.68 0.44 0.58 -0.68 1.01 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59	0.0393 0.0855 0.0014 0.0024 0.0033 0.0028 0.0010 0.0156 0.0015 0.0012 0.0012 0.0022 0.0012 0.0025 0.0048 0.0012 0.0025 0.0055 0.0064 0.0025 0.0055 0.0064 0.0025 0.0055 0.0064 0.0025 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0055 0.0064 0.0065 0.	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.152133463 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165128781 0.161328781 0.161328781 0.161328781 0.161328781 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981830 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.251981833 0.25198183 0.251981833 0.251981833 0.251981833 0.251981833 0.25198183 0.251981833 0.251981833 0.251981833 0.251981833 0.25198183 0.251981833 0.251981833 0.251981833 0.251981833 0.25198183 0.25198183 0.25198183 0.2519
K17274 K03927 K13022 K08765 K08765 K08765 K00545 K10037 K00545 K00454 K04373 K04710 K13627 K05022 K04089 K11586 K04393 K11586 K04645 K0489 K11586 K06454 K0489 K11586 K06454 K0489 K11586 K06454 K0480 K11586 K06454 K0480 K11586 K06236 K06236 K06031 K04002	S100A10 CES2 CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK CCCL19, ELC CEBPD CD4 CD4 CDC42 CERS CPP GPGEL, HSPD1 CUIC2 CWP6A1 CWP6A1 CWP7A1 CBBX3, HP1G CUI KBR COLIAS CO	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carpital carboxylest carbox 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catcheol 0-metinyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catcheol 0-metinyltransferase [EC:2.1.1.6] catchepisin K [EC:3.4.22.38] CC-C motif Chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.16.3.1] chaperonin GroEt. chloride intracellular channel protein 2 chlosterol 24[b-yhdroxylase [EC:1.4.13.98] cholesterol 74[b-yhdroxylase [EC:1.4.13.98] cholesterol 74[b-yhdroxylase [EC:1.4.13.17] chromobox protein 3 clusterin coagulation factor VIII codi-inducible RNA-binding protein collagen, type [V,IIIII/V/XIXXIV/XXVIV], alpha collagen, type [V,IIIIII/V/XIXXIV/XXVII], alpha collagen, type [V, alpha complement component (3b/4b) receptor 1 complement component (3b/4b) receptor 1 complement component 4 subcomponent [EC:3.4.21.42] complement component 4 subcomponent (EC:3.4.21.42) complement component 4 subcomponent (EC:3.4.21.43)	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00940 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00363 Giyoxylate and dicarboxylate metabolis ko00140 Sterold hormone biosynthesis; ko003630 Tyrosine metabolism; ko00965 B ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04100 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03610 Porphyrin and chlorophyll metabolism ko03610 Porphyrin and chlorophyll metabolism ko030120 Primary bile acid biosynthesis; ko00140 Sterold hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Sterold hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Sterold hormone biosynthesis; ko ko01210 Primary bile acid diosynthesis ko0140 Sterold hormone biosynthesis; ko ko01131 Pil3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04151 Pil3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi ko04510 Complement and coagulation cascades; ko04640 Hematopoietic cell linee ko04610 Complement and coagulation cascades; ko05139 Pertussis; ko05150 Staphylococcus aureus it ko04111 Cell cycle - yeast ko040978 Mineral absorption		0.58 0.45 0.53 0.62 -0.54 0.52 0.52 0.56 0.40 0.57 -1.23 0.44 0.46 0.58 8.60 0.44 0.48 2.61 0.40 0.41 0.60 0.44 0.50 0.44 0.50 0.44 0.51 0.44 0.52 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.44 0.58 0.58 0.44 0.58 0.58 0.58 0.58 0.58 0.58 0.58 0.58	0.0393 0.0865 0.0014 0.0028 0.0030 0.0028 0.0030 0.00107 0.0156 0.0015 0.0037 0.0042 0.0012 0.0012 0.0012 0.0012 0.005 0	0.251981833 0.172822126 0.143042222 0.1525939243 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.15204453 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.151288781 0.223988206 0.1519885932 0.161328781 0.223988206 0.215988593 0.21598859
K17274 K03927 K01294 K13022 K08765 K08765 K00371 K05512 K00552 K00430 K00430 K04710 K04710 K04710 K0472 K07440 K0472 K07440 K0472 K07440 K0472 K05022 K07440 K0472 K05022 K07440 K04710 K05022 K07440 K05022 K05022 K05023 K06236 K06236 K06236 K06236 K06236 K06236 K06231 K04033 K04033 K04033 K04033 K04033 K04033 K04033 K0603 K06	S100A10 CES2 CPE CPE CPE CPE CPTIA CARD8, CARDINAL Astate, CAT, cat8, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CERS CD4 CDC42 CERS CPE GROEL, HSPD1 CLU2 CYP46A1 CYP7A1 CSK3, HP16 CLU ERS CULAS COLIAS COLI	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] carboxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase E, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [EC:2.1.1.6] cathepian K [EC:3.4.2.2.38] C-C motif Chemokine 19 CCAA17enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmi [EC:1.6.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.14.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type I/I,IIII/V/XI/XXIV/XXXIVI, alpha collagen, type IV, alpha complement component 1, s subcomponent [EC:3.4.21.42] complement component 3,5 vabcomponent [EC:3.4.21.42] complement component 1,5 subcomponent [EC:3.4.21.42] complement component 4,5 inding protein, alpha component factor 0 [EC:3.4.21.46] condensin complex subunit 1 copper-chaperone	NA ko00983 Drug metabolism - other enzymes ko00940 Type I diabetes mellitus NA ko00981 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko0380 Tryptophan metabolism; ko00630 Glyovylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis, ko00350 Tyrosine metabolism; ko0965 Bt ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04606 Otytokine-cytokine receptor interaction; ko04626 Chemolise signaling pa NA ko004606 Otytokine-cytokine receptor interaction; ko04626 Chemolise signaling pa NA ko005140 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko046 ko00600 Orphinyin and chilorophyll metabolism ko03030 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04610 Complement and coagulation cascades NA NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Ocmplement and coagulation cascades; ko05139 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pertussis ko0400300 Arginine and proline metabolism		0.58 0.45 0.53 0.62 0.54 0.53 0.62 0.56 0.52 0.44 0.46 0.46 0.48 0.44 0.48 0.40 0.40 0.58 0.41 1.00 0.54 1.00 0.55 0.38 0.39 0.50 0.56 0.45 0.45 0.46 0.47 0.47 0.47 0.47 0.47 0.47 0.47 0.47	0.0393 0.0855 0.0014 0.0014 0.0033 0.0028 0.00107 0.0156 0.0015 0.0019 0.0019 0.0019 0.0012 0.0012 0.0022 0.0012 0.0022 0.00118 0.0027 0.0022 0.0023	0.251981833 0.172822126 0.143042222 0.152533243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.25416933 0.158745194 0.143042222 0.165130462 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087
K17274 K03927 K13922 K13922 K08765 K12801 K05781 K05512 K05512 K05512 K06454 K04077 K05022 K07440 K04077 K05022 K07440 K04077 K04077 K0407	\$100A10 CES2 CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP groEL, HSPD1 CLIC2 CYP46A1 CYP7A1 CWP6A1 CWP7A1 CWB, SWB, SWB, SWB, SWB, SWB, SWB, SWB, S	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.10] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catepain K [EC:3.4.22.38] C-Comotif chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 artligen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.63.31] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.4.13.19] cholesterol 24(5)-hydroxylase [EC:1.4.13.19] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (N, Jipha complement component (3b/4b) receptor 1 complement component (3b/4b) receptor 1 complement component (5b/4b) receptor 1 complement component 41 occupied component (EC:3.4.21.42) complement component 41 occupied condension componet subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CBB and subil domain-containing protein	NA koo0393 Drug metabolism - other enzymes koo0490 Type I diabetes mellitus NA koo0490 Type I diabetes mellitus NA koo00071 Fatty adid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658 ko01412 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04600 Cytokine-cytokine receptor interaction; ko04620 Toll-like receptor ko04600 Cytokine-cytokine receptor interaction; ko04620 Toll-like receptor ko04600 Sholman Signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko001010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Orphyrin and chlorophyll metabolism ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Drimary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Drimary bile acid biosynthesis; ko0140 Steroid hormone biosynthesis; ko ko0100 Complement and coagulation cascades ko04510 Complement and coagulation cascades; ko056137 Pertussi; ko05150 Staph ko04510 Complement and coagulation cascades; ko056137 Pertussi; ko05150 Staph ko04111 Cell Cycle - yeast		0.58 0.45 0.53 0.62 0.52 0.56 0.40 0.57 0.44 0.46 0.58 0.44 0.48 0.48 1.00 0.60 0.60 0.60 0.60 0.60 0.60 0.60	0.0393 0.0885 0.0014 0.0014 0.0033 0.0028 0.00107 0.0155 0.0387 0.0427 0.0012 0.0050 0	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.1520453 0.1520453 0.184946192 0.245121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.25121965 0.143042222 0.247118814 0.112669745 0.143042222 0.143042222 0.143042222 0.143042222 0.01870843 0.15195983 0.15195983 0.15195982 0.25198833 0.15195982 0.143042222 0.01870843 0.143042222 0.143042222 0.143042222
K17274 K03927 K01294 K13022 K08765 K08765 K00371 K05512 K00552 K00430 K00430 K04710 K04710 K04710 K0472 K07440 K0472 K07440 K0472 K07440 K0472 K05022 K07440 K0472 K05022 K07440 K04710 K05022 K07440 K05022 K05022 K05023 K06236 K06236 K06236 K06236 K06236 K06236 K06231 K04033 K04033 K04033 K04033 K04033 K04033 K04033 K0603 K06	\$100A10 CES2 CPE CPE CPE CPE CPTIA CARD8, CARDINAL kate, CAT, cate, sypa COMT CTSK CCL19, ELC CEBPD CD4 CD4 CDC42 CERS CP CPC GREN CPC CHARD1 CUC2 CYPASA1 CVPASA1 CVP	calpactin-1 light chain carboxylesterase 2 [EC.3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC.3.4.17.10] carboxypeptidase E [EC.3.4.17.1] carboxypeptidase E [EC.3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase L liver isoform [EC.2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase [EC.2.1.1.6] cathepian K [EC.3.4.22.38] C-C mottif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC.2.3.1.24] ceruloplasmin [EC.1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC.1.14.13.98] choloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC.1.14.13.77] chromobox protein 3 clusterin congulation factor VIII cold-inducible RNA-binding protein collagen, type (IV, III)II/V/XI/XIXV/XXVII, alpha collagen, type (IV, III)II/V/XI/XIXV/XXVII, alpha complement component (3b/4b) receptor 1 complement component (1 shub) receptor 1 complement component (1 shub) receptor 1 complement component (1 shub) receptor 1 complement component (2b/4b) receptor 1	NA ko00983 Drug metabolism - other enzymes ko00940 Type I diabetes mellitus NA ko00981 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko0380 Tryptophan metabolism; ko00630 Glyovylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis, ko00350 Tyrosine metabolism; ko0965 Bt ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04606 Otytokine-cytokine receptor interaction; ko04626 Chemolise signaling pa NA ko004606 Otytokine-cytokine receptor interaction; ko04626 Chemolise signaling pa NA ko005140 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko046 ko00600 Orphinyin and chilorophyll metabolism ko03030 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04610 Complement and coagulation cascades NA NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Ocmplement and coagulation cascades; ko05139 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pertussis ko0400300 Arginine and proline metabolism		0.58 0.45 0.53 0.62 0.52 0.56 0.40 0.40 0.44 0.46 0.48 0.48 2.61 0.40 0.40 0.40 0.40 0.40 0.40 0.40 0.4	0.0393 0.0085 0.0014 0.0033 0.0028 0.00107 0.0156 0.0015 0.0015 0.0017 0.0016 0.0017 0.0017 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0	0.251981833 0.172822126 0.143042222 0.152533243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.25416933 0.158745194 0.143042222 0.165130462 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087
K17274 K03927 K19022 K19022 K19025 K01294 K19022 K03781 K05121 K05512 K00545 K01371 K05512 K04710 K13624 K04710 K05237 K04011 K01331 K0	\$100A10  CES2  CPE  CPE  CPE  CPZ  CPTIA  CARD8, CARDINAL  kate, CAT, CatB, srpA  COMT  CTSK  CCL19, ELC  CEBPD  CDC42  CEBPD  CDC42  CERS  CPC  GPS  GPS  CPC  GPS  CPC  GPS  CPC  CPC	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] carpoxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] cathepsin K [EC:3.4.22.38] C-C motif chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.44] ceruloplasmi [EC:1.63.1] chapersonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.41.3.19] cholesterol 7alpha-monooxygenase [EC:1.41.3.17] chromobox protein 3 dusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (I)/IIII/IV/XIXVI/XXVII, alpha complement component 1, subscomponent [EC:3.4.21.42] complement component 4 binding protein, alpha complement component 1 subscomponent [EC:3.4.21.42] complement component 4 binding protein, alpha complement component 4 binding protein, alpha complement component 4 binding protein, alpha complement component 1 subscomponent [EC:3.4.21.42] complement component 4 binding protein, alpha complement component 3 binding protein, alpha complement component 4 binding protein, alpha complement component 4 binding protein, alpha complement component 5 binding protein, alpha complement component 5 binding protein, alpha complement component 5 binding protein, alpha complement component 6 binding protein, alpha complemen	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00981 Type I diabetes mellitus NA ko00071 Fatty add degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00363 Glycoystae and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658 ko01412 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor ko04060 Cytokine-cytokine receptor interaction; ko04620 Chemokine signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko04 ko00600 Sphingolipid metabolism ko004060 Porphyrin and chlorophyll metabolism ko003018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko NA ko04610 Complement and coagulation cascades NA ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Ocmplement and coagulation cascades; ko05139 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pertussis ko04110 Complement and coagulation cascades; ko05139 Pertussis ko04110 Complement and coagulation cascades; ko05130 Staphylococcus aureus it ko04110 Complement and coagulation cascades; ko05130 Staphylococcus aureus it ko04111 Cell cycle - yeast ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas		0.58 0.45 0.53 0.62 0.50 0.50 0.50 0.50 0.50 0.50 0.50 0.5	0.0393 0.0885 0.0014 0.0033 0.0028 0.0017 0.0156 0.0015 0.0037 0.0042 0.0016 0.0019 0.0016 0.0019 0.0018 0.0017 0.0021 0.0030 0.0011 0.0011 0.0021 0.0011 0.0011 0.0011 0.0011	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.152053 0.152
K17274 K03927 K101294 K13022 K12801 K13022 K12801 K13022 K12801 K13028 K12801 K13624 K12801 K13624 K12801 K13624 K12801 K13624 K12801 K13624 K12801 K	S100A10 CES2 CPE CPE CPE CPE CPE CPTIA CARD8, CARDINAL Astate, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CEBP CD4 CDC42 CERS CPC CPC CPC CPC CPC CPC CPC CPC CPC CP	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase L, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [EC:2.1.1.6] cathepsin K [EC:3.4.22.38] C-C motif Chemokine 19 CCAA17(enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceramide synthetase [EC:2.3.1.24] ceramide synthetase [EC:2.3.1.24] chapersonin GroEL chloride intracellular channel protein 2 chloeisterol 24(S)-hydroxylase [EC:1.14.13.19] cholesterol 24(S)-hydroxylase [EC:1.14.13.79] chromobox protein 3 clusterin congulation factor VIII cold-inducible RNA-binding protein collagen, type I/I, ily/II/V/XI/XIV/XIVI, alpha complement component 1, s subcomponent [EC:3.4.21.42] complement component 3b/db) receptor 1 complement component 1, s subcomponent [EC:3.4.21.42] complement component 1, s subcomponent [EC:3.4.21.43] conditional complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sushi domain-containing protein cytick-IMP-deperone creatine kinase [EC:2.7.3.2] CUB and sushi domain-containing protein cytochrome c cytochrome c cytochrome c cytochrome c cytochrome c cytochrome c	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00980 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00340 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 Bt ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor ko04606 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko004600 Spaningolipid metabolism ko03514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Spaningolipid metabolism ko03600 Spaningolipid metabolism ko03600 Primary bile acid biosynthesis; ko0140 Steroid hormone biosynthesis; ko ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04610 Complement and coagulation cascades NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04610 Complement and coagulation cascades; ko05404 Hematopoietic cell lines ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04610 Complement and coagulation cascades; ko05133 Pertussis ko04610 Complement and coagulation cascades; ko05139 Pretussis ko04610 Complement and coagulation cascades; ko05130 Pathylococcus aureus it ko04111 Cell cycle - yeast ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas ko00230 Arginine and proline metabolism NA ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas ko00230 Victine and methionine metabolism; ko00430 Taurine and hypotaurine ko02020 Sulfu		0.58 0.45 0.53 0.62 0.54 0.53 0.62 0.56 0.40 0.57 0.44 0.57 0.44 0.48 0.68 0.44 0.48 0.69 0.60 0.60 0.40 0.70 0.41 0.70 0.41 0.48 0.49 0.49 0.49 0.50 0.50 0.50 0.50 0.50 0.50 0.50 0.5	0.0393 0.0885 0.0014 0.0033 0.0028 0.0030 0.0107 0.0015 0.00427 0.0042 0.0042 0.0042 0.0042 0.0042 0.0042 0.0055 0.0055 0.0054 0.0055 0.0054 0.0012 0.0055 0.0054 0.0055 0.0054 0.0055 0.0055 0.0056 0	0.251981833 0.173822126 0.173822126 0.173822126 0.1520433 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.252121693 0.15213263 0.252121693 0.158745194 0.143042222 0.247118814 0.112669745 0.165190087 0.165190087 0.165190087 0.165190083 0.143042222 0.143042222 0.143042222 0.193753298 0.163028753198 0.143042222 0.193753298 0.143042222 0.193753298 0.143042222 0.193753298 0.143042222 0.193753298
K17274 K03927 K01294 K13022 K13022 K13022 K13020 K1	S100A10 CES2 CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CCL19, ELC CEBPD CD4 CCL19, ELC CEBPD CD4 CCR CR CP groEL, HSPD1 CLIC CP GROEN, HSPD1 CLIC CPPAGA1 CVPFAA1 CVPFAA	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxylesterase 2 [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17.1] carpioxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catalase [EC:1.11.6] catepoin (EC:3.4.2.2.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] cerculoplasmin [EC:1.6.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.4.13.19] cholesterol 24(5)-hydroxylase [EC:1.4.13.19] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (N, alpha complement component (Bb/db) receptor 1 complement component (Bb/db) receptor 1 complement component (Bb/db) receptor 1 complement component 4 binding protein, alpha complement component 4 binding protein condensin complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sush id domain-containing protein cyclic AMP-dependent transcription factor ATF-6 alpha cysteine dioxygenase [EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 17	NA  koo0393 Drug metabolism - other enzymes  koo0490 Type I diabetes mellitus  NA  koo0390 Type I diabetes mellitus  NA  koo00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis  ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658  ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor  ko04600 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pa  NA  ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen  ko04100 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko00600 Osphingolipid metabolism  ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko010151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep  ko04510 Complement and coagulation cascades  NA  Ko04151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep  ko04510 Complement and coagulation cascades; ko05139 Pertussi; ko05150 Staph  ko04101 Complement and coagulation cascades; ko05133 Pertussi; ko05150 Staph  ko04110 Complement and coagulation cascades; ko05133 Pertussi;  ko04510 Complement and coagulation cas		0.58 0.45 0.53 0.52 0.52 0.56 0.40 0.44 0.46 0.48 0.44 0.48 0.40 0.40 0.40 0.40 0.40	0.0939 (0.001) 0.0014 0.0038 (0.0014) 0.0038 (0.0014) 0.0038 (0.0017) 0.0056 (0.0019) 0.0016 (0.0019) 0.0017 (0.0019) 0.0018 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.0019 (0.0019) 0.00019 (0.0019) 0.00019 (0.0019) 0.00019 (0.0019)	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1521950 0.25121965 0.2521716933 0.168745194 0.143042222 0.247118814 0.112669745 0.14504222 0.165190087
K17274 K03927 K01294 K13022 K13022 K13020 K1	S100A10 CES22 CPE CPE CPE CPE CPE CPTIA CARD8, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CERS CPP GPEL, HSPD1 CLUC ECRS CPP GPOEL, HSPD1 CLUC CVPPAA1 CVPAA1 CVPAA1 CRBP COLIAS COL	calpactin-1 light chain carboxylesterase 2 [EC.3.1.1 3.1.1.84 3.1.1.56] carboxypeptidase E [EC.3.4.17.10] carboxypeptidase E [EC.3.4.17.1] carboxypeptidase E [EC.3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase L liver isoform [EC.2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC.1.11.1.6] catechol O-methyltransferase [EC.2.1.1.6] cathepian K [EC.3.4.2.2.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC.2.3.1.24] ceruloplasmin [EC.1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC.1.14.13.98] cholesterol 24(5)-hydroxylase [EC.1.14.13.98] cholesterol 7alpha-monooxygenase [EC.1.14.13.77] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (IV, alpha collagen, type (IV, alpha collagen, type (IV, alpha) complement component (3b/4b) receptor 1 complement component (3b/4b) receptor 1 complement component 3-binding protein, alpha component factor D [EC.3.4.2.14.2] complement component 4-binding protein, alpha component factor D [EC.3.4.2.14.6] condensin complex subunit 1 copper chaperone creatine kinase [EC.2.7.3.2] CUB and sushi domain-containing protein cyclic AIM-dependent transcription factor ATF-6alpha cysteine dioxygenase [EC.1.13.11.20] cyctorhome c oxidase assembly protein subunit 17 cytorhornee c oxidase assembly protein subunit 12	NA ko000983 Drug metabolism - other enzymes ko004940 Type I diabetes mellitus NA ko000971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyovylate and dicarboxylate metabolis ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00965 Bi ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Tooli-like receptor ko04060 Cytokine-cytokine receptor interaction; ko0462 Chemolise signaling pa NA ko04060 Cytokine-cytokine receptor interaction; ko0462 Chemolise signaling pa NA ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03600 Porphyrin and chlorophyli metabolism ko03600 Porphyrin and chlorophyli metabolism ko03019 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko01120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko01120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04151 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04151 Pi3K-Mat signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04510 Complement and coagulation cascades; ko05139 Perussis ko04110 Complement and coagulation cascades; ko05139 Perussis ko04510 Complement and coagulation cascades; ko05139 Perussis ko04510 Complement and coagulation cascades; ko05139 Perussis ko04510 Complement and proline metabolism ko04978 Mineral absorption ko04978 Mineral absorption ko04978 Mineral absorption ko04978 Mineral absorption		0.58 0.45 0.53 0.52 0.54 0.52 0.56 0.40 0.57 0.46 0.58 0.64 0.40 0.41 0.57 0.41 0.58 0.44 0.41 0.57 0.45 0.40 0.58 0.44 0.58 0.44 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.40 0.59 0.59 0.59 0.59 0.59 0.59 0.59 0.5	0.0939 (0.0014) (0.0015) (0.0014) (0.0015) (0.0014) (0.0014) (0.0014) (0.0014) (0.0014) (0.0015) (0.0015) (0.0014) (0.0015) (0.0015) (0.0015) (0.0015) (0.0015) (0.0016) (0.0016) (0.0016) (0.0016) (0.0016) (0.0016) (0.0016) (0.0016) (0.00076) (	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.15204453 0.152053 0.152053 0
K17274 K03227 K01294 K13022 K13022 K13022 K13024 K13022 K13024 K13022 K13024 K1	S100A10 CES2 CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, CatB, srpA COMT CTSK CCL19, ELC CEBPD CD04 CDC42 CERS CD4 CDC42 CERS CP GPGEL, HSPD1 CLLC2 CYP46A1 CYP7A1 CYP7A1 CRS, APPIG CLU F8 CRBP COLIAS COILAS	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.1.84 3.1.1.56] carboxyleptidase E [EC:3.4.17.10] carboxyleptidase E [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] carpoxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol 0-methyltransferase [EC:2.1.1.6] catechol 0-methyltransferase [EC:2.1.1.6] cathepsin K [EC:3.4.2.2.38] CCMotff chemokine 19 CCAA1/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] cerculoplasmin [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloride intracellular channel protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (I)/IIII/V/X/XXVI/XXVII, alpha complement component 1, subcomponent [EC:3.4.21.42] complement component 1, subcomponent [EC:3.4.21.42] complement component 4 binding protein, alpha complement component 4 binding protein, alpha complement component 4 binding protein, alpha complement component 1, subcomponent [EC:3.4.21.42] complement component 3, subcomponent [EC:3.4.21.42] complement component 3, subcomponent [EC:3.4.21.42] complement component 3, subcomponent [	NA  koo03983 Drug metabolism - other enzymes  koo04940 Type I diabetes mellitus  NA  koo0391 Tatty adid degradation; koo3320 PPAR signaling pathway; ko04920 Adipoc koo4621 NOD-like receptor signaling pathway koo0380 Tryptophan metabolism, koo0630 Glyoxylate and dicarboxylate metabolis koo0140 Steroid hormone biosynthesis; koo03530 Tyrosine metabolism; koo0965 B koo01412 Lysosome; koo4380 Osteoclast differentiation; koo4620 Toll-like receptor koo4660 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pat  NA  koo4514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen koo4610 MAPK signaling pathway; koo4011 MAPK signaling pathway - yeast; koo4  koo0600 Sphingolipid metabolism koo3018 NRA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis;  ko001610 Complement and coagulation cascades  NA  NA  ko04510 Complement and coagulation cascades  NA  Ko04510 Complement and coagulation cascades,  ko04510 Complement and coagulation cascades; ko05139 Perussis; ko05150 Staphylococcus aureus it  ko04510 Complement and coagulation cascades, ko05139 Perussis; ko05150 Staphylococcus aureus it  ko04510 Complement and coagulation cascades, ko05139 Perussis; ko05150 Staphylococcus aureus it  ko04510 Complement and coagulation cascades, ko05139 Perussis; ko05150 Staphylococcus aureus it  ko04510 Complement and coagulation cascades, ko05139 Perussis; ko0510 Staphylococcus aureus it  ko04510 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseat  ko04510 Complement and prolline metabolism  NA  ko04114 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseat  ko040270 Cysteine and methionine metabolism; ko004070 Taurine and hypotaurine  ko002030 Sulfur metabolism; ko02020 Two-component system; ko04115 p53 signali  NA  ko00190 Oxidative phosphorylation; ko04260 Cardiac musde contraction; ko0		0.58 0.45 0.52 0.52 0.52 0.56 0.40 0.57 0.56 0.44 0.48 0.44 0.48 0.44 0.48 0.49 0.50 0.50 0.50 0.50 0.50 0.50 0.50 0.5	0.0939 (0.0014) (0.0015) (0.0014) (0.0015) (0.0016) (0.0016) (0.0017) (0.0005) (0.0007) (0.0005) (0.0007) (0.0005) (0.0007) (0.0005) (0.0007) (0.0007) (0.0005) (0.0007) (0.00	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.152151265 0.2521716933 0.168745194 0.143042222 0.247118814 0.112669745 0.143042222 0.165139087 0.165190087 0.1
K17274 K03927 K01294 K13022 K13022 K13022 K12801 K13022 K12801 K13028 K12801 K13028 K12801 K13028 K12801 K1	S100A10 CES2 CPE CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK. CCL19, ELC CCL19, ELC CCL19, ELC CCL19, ELC CCL19, ELC CCBPD CD4 CD4 CDC42 CERS CP groEL, HSPD1 CUC2 CYPEAA1 CYPEAA1 CYPEAA1 CYPAA1 CRBP COLLAS	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase 2 [EC:3.4.17.10] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catachenio —methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] cathepsin K [EC:3.4.22.38] C-C motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmin [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 cholosterol 24(5)-hydroxylase [EC:1.4.13.98] cholesterol 74[9-hydroxylase [EC:1.4.13.98] cholesterol 74[9-hydroxylase [EC:1.4.13.7] chromobox protein 3 clusterin coagulation factor VIII codi-inducible RNA-binding protein collagen, type [VI/IIII/VX/IXXVI/XXVII, alpha collagen, type [VI/IIII/VX/IXXVI/XXVII, alpha complement component (3b/4b) receptor 1 complement component 4 binding protein, alpha component factor 0 [EC:3.4.21.46] condensin complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sushi domain-containing protein cyclic AWP-dependent transcription factor ATF-6 alpha cysteine dioxygenase [EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 16 cytochrome c oxidase assembly protein subunit 20 cytochrome c oxidase susembly protein subunit 20 cytochrome c oxidase susembly protein subunit 20 cytochrome c oxidase assembly protein subunit 20	NA k000983 Drug metabolism - other enzymes k000940 Type I diabetes mellitus NA k000940 Type I diabetes mellitus NA k0000071 Fatty acid degradation; k003320 PPAR signaling pathway; k004920 Adipoc k004621 NOD-like receptor signaling pathway k000380 Tryptophan metabolism; k000360 Glycvytale and dicarboxylate metabolis k000140 Sterold hormone biosynthesis; k000350 Tyrosine metabolism; k000956 8 k004142 Lysosome; k004380 Osteodast differentiation; k004620 Toll-like receptor k004060 Cytokine-cytokine receptor interaction; k004062 Chemokine signaling pa NA k004514 Cell adhesion molecules (CAMs); k004612 Antigen processing and presen k004010 MAPK signaling pathway; k004011 MAPK signaling pathway - yeast; k0040 k000600 Sphingolipid metabolism k003610 Porphyrin and chlorophyll metabolism k003610 Porphyrin and chlorophyll metabolism k0030120 Primary bile acid biosynthesis; k000140 Sterold hormone biosynthesis; k0 k00120 Primary bile acid biosynthesis; k000140 Sterold hormone biosynthesis; k0 k00120 Primary bile acid biosynthesis; k00140 Sterold hormone biosynthesis; k0 k00110 Complement and coagulation cascades NA k004151 PI3K-Akt signaling pathway; k004510 Focal adhesion; k004512 ECM-recepi k004151 PI3K-Akt signaling pathway; k004510 Focal adhesion; k004512 ECM-recepi k004151 Ocmplement and coagulation cascades; k004640 Hematopoietic cell linee k004610 Complement and coagulation cascades; k005139 Pertussis; k005150 Staphylococcus aureus it k004101 Cell cycle - yeast k004017 Mineral absorption k004303 Arginine and proline metabolism NA k004141 Protein processing in endoplasmic reticulum; k005010 Alzheimer's diseas k000270 Cysteine and methionine metabolism, k000430 Taurine and hypotaurine k000290 Sulfar metabolism k000330 Arginine and proline metabolism NA k0014010 Cysteine and methionine metabolism k000490 Cysteine and methionine metabolism, k000491 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k00049		0.58 0.45 0.53 0.53 0.53 0.54 0.52 -0.54 0.52 0.56 0.40 0.57 0.44 0.57 0.44 0.57 0.48 0.48 0.49 1.00 0.40 1.00 0.50 0.50 0.50 0.50 0.40 0.40 0.50 0.5	0.0930 0.0085 0.0014 0.0033 0.0016 0.0016 0.0017 0.0016 0.0017 0.0019 0.0018 0.0019 0.0019 0.0019 0.0019 0.0011 0.0022 0.0012 0.0010	0.2519481833 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.15204853 0.25121965 0.252121965 0.252121965 0.252121965 0.252121965 0.2521240655 0.143042222 0.165190087 0.165190
K17274 K03927 K01294 K13022 K13024 K13022 K13024 K13022 K13024 K1	S100A10 CES2 CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CEBP CD4 CDC42 CERS CP CPC CPC CPC CPC CPC CPC CPC CPC CPC	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] carboxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase L, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [EC:2.1.1.6] cathepian K [EC:3.4.2.2.38] C-C motif Chemokine 19 CCAA17(enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceramide synthetase [EC:2.3.1.24] chapersonin GroEL chloride intracellular channel protein 2 chloeisterol 24(S)-hydroxylase [EC:1.14.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin congulation factor VIII cold-inducible RNA-binding protein collagen, type IV, alpha complement component (3b/db) receptor 1 complement component (15) complement component 1, s subcomponent [EC:3.4.2.1.42] complement component 4 binding protein, alpha component factor D [EC:3.4.2.4.6] complement component 1, s subcomponent [EC:3.4.2.1.42] complement component 1, s subcomponent (2C:3.4.2.1.42) complement component 1, s subcomponent (2C:3.4.2.1.43) condomina complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sushi domain-containing protein cyclic AIMP-dependent transcription factor ATF-6 alpha cysteine dioxygenase [EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 16 cytochrome c oxidase subunit 1 cytochrome c oxidase subunit 2 cytochrome c oxidase subunit 3	NA ko00983 Drug metabolism - other enzymes ko04940 Type I diabetes mellitus NA ko00980 Type I diabetes mellitus NA ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc ko04621 NOD-like receptor signaling pathway ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis ko00340 Steroid hormone biosynthesis; ko00330 Tyrosine metabolism; ko00965 Bt ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor ko04606 Cytokine-cytokine receptor interaction; ko04062 Chemokine signaling pa NA ko004610 Call adhesion molecules (CAMs); ko04612 Antigen processing and presen ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040 ko00600 Sphingolipid metabolism ko03600 Sphingolipid metabolism ko03600 Sphingolipid metabolism ko03600 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko ko04610 Complement and coagulation cascades NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04610 Complement and coagulation cascades; ko05404 Hematopoietic cell lines ko04101 Pi3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko04610 Complement and coagulation cascades; ko05133 Pertussis ko04510 Complement and coagulation cascades; ko05133 Pertussis ko04610 Complement and coagulation cascades; ko05133 Pertussis ko04610 Complement and coagulation cascades; ko05133 Pertussis ko04610 Complement and coagulation cascades; ko05139 Protosio Staphylococcus aureus it ko04111 Cell cycle - yeast ko04010 Complement and coagulation cascades; ko05130 Pathylococcus aureus it ko04111 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas ko00270 Cysteine and methionine metabolism NA ko00190 Oxidative phosphorylation; ko04260 Cardiac musde contraction; ko04932 ko00190 Oxidative phosphorylation; ko04260 Cardiac musde contra		0.58 (0.54 (0.55 (	0.0939 (0.0012) (0.00	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.152151265 0.2521716933 0.168745194 0.143042222 0.247118814 0.112669745 0.143042222 0.165139087 0.165190087 0.1
K17274 K03927 K01294 K13022 K13022 K13022 K12801 K13022 K12801 K13028 K12801 K13028 K12801 K1	S100A10 CES2 CPE CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK CCL19, ELC CEBPD CD4 CD4 CCL19, ELC CEBPD CD4 CCH2 CERS CP groEL, HSPD1 CLU2 CYP46A1 CYP7A1 CERS, HPIG CUU R R R COLIAS COL	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxylesterase 2 [EC:3.4.17.10] carboxyleptidase 2 [EC:3.4.17.1] carboxyleptidase 2 [EC:3.4.17.1] carpoxyleptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catepas in (EC:3.4.2.2.38] C-C-C motif chemokine 19 CCAA1/genhancer binding protein (C/EBP), delta CD4 artligen cell division control protein 42 ceramide synthetase [EC:2.3.1.4] cerculoplasmin [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.4.13.19] cholesterol 24(5)-hydroxylase [EC:1.4.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (N, Jipha complement component (B/Ab) receptor 1 complement component 1, s subcomponent [EC:3.4.21.42] complement component 4, binding protein, alpha complement component 1, s subcomponent (EC:3.4.21.42) complement component 4 binding protein, alpha component factor D [EC:3.4.21.46] condensin complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sush id omain-containing protein cyclic AMP-dependent transcription factor ATF-6alpha cycteine dioxygenase [EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 16 cytochrome c oxidase assembly protein subunit 17 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 5	NA k000983 Drug metabolism - other enzymes k000940 Type I diabetes mellitus NA k000940 Type I diabetes mellitus NA k0000071 Fatty acid degradation; k003320 PPAR signaling pathway; k004920 Adipoc k004621 NOD-like receptor signaling pathway k000380 Tryptophan metabolism; k000360 Glycvytale and dicarboxylate metabolis k000140 Sterold hormone biosynthesis; k000350 Tyrosine metabolism; k000956 8 k004142 Lysosome; k004380 Osteodast differentiation; k004620 Toll-like receptor k004060 Cytokine-cytokine receptor interaction; k004062 Chemokine signaling pa NA k004514 Cell adhesion molecules (CAMs); k004612 Antigen processing and presen k004010 MAPK signaling pathway; k004011 MAPK signaling pathway - yeast; k0040 k000600 Sphingolipid metabolism k003610 Porphyrin and chlorophyll metabolism k003610 Porphyrin and chlorophyll metabolism k0030120 Primary bile acid biosynthesis; k000140 Sterold hormone biosynthesis; k0 k00120 Primary bile acid biosynthesis; k000140 Sterold hormone biosynthesis; k0 k00120 Primary bile acid biosynthesis; k00140 Sterold hormone biosynthesis; k0 k00110 Complement and coagulation cascades NA k004151 PI3K-Akt signaling pathway; k004510 Focal adhesion; k004512 ECM-recepi k004151 PI3K-Akt signaling pathway; k004510 Focal adhesion; k004512 ECM-recepi k004151 Ocmplement and coagulation cascades; k004640 Hematopoietic cell linee k004610 Complement and coagulation cascades; k005139 Pertussis; k005150 Staphylococcus aureus it k004101 Cell cycle - yeast k004017 Mineral absorption k004303 Arginine and proline metabolism NA k004141 Protein processing in endoplasmic reticulum; k005010 Alzheimer's diseas k000270 Cysteine and methionine metabolism, k000430 Taurine and hypotaurine k000290 Sulfar metabolism k000330 Arginine and proline metabolism NA k0014010 Cysteine and methionine metabolism k000490 Cysteine and methionine metabolism, k000491 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k000490 Cysteine and methionine metabolism, k00049		0.58 0.45 0.50 0.62 0.54 0.53 0.40 0.52 0.56 0.40 0.57 0.44 0.57 0.68 0.48 0.41 1.00 0.45 0.38 0.41 1.00 0.45 0.40 0.46 0.40 0.45 0.40 0.41 0.40 0.54	0.0935 0.0085 0.0014 0.0033 0.0016 0.0017 0.0015 0.0015 0.0015 0.0015 0.0017 0.0019 0.0019 0.0019 0.0019 0.0019 0.0019 0.0019 0.0011 0.0019 0.	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.15519057 0.1521826 0.1520573 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.155190087 0.15519087
K17274 K03927 K01724 K03927 K01724 K03927 K08765 K01294 K03781 K03781 K01725 K0524 K01725 K01	S100A10 CES2 CPE CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, cat8, srpA COMT CTSK CCL19, BLC CEBPD CD4 CDC42 CEBPD CD4 CDC42 CERS CPP GROEL, HSPD1 CLU2 CYP4A61 CVYP4A61 CVYP4A61 CSWARA1 COMPA COL43 CBR COL44 CR1, CD35 CLU ERS COL45 CARPA COL45 CSMD CARPA COL47 CSC CARPA COL57 CARPA COL67 COCC COCX COCX COCX COCX COCX COCX COC	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] carboxypeptidase E [EC:3.4.17.1] carpoxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [Liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [EC:2.1.1.6] cathepian K [EC:3.4.22.38] C-C motif Chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:3.1.24] ceruloplasmi [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.14.13.98] cholesterol 24(5)-hydroxylase [EC:1.14.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type IV, alpha collagen, type IV, alpha collagen, type IV, alpha complement component (33/4b) receptor 1 complement component (33/4b) receptor 1 complement component 4 binding protein, alpha component factor D [EC:3.4.2.14.2] complement component 1, s subcomponent [EC:3.4.21.42] complement component 4 binding protein, alpha component factor D [EC:3.4.2.14.4] condensin complex subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sushi domain-containing protein cytic AIMP-dependent transcription factor ATF-6 alpha cysteine dioxygenase [EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 15 cytochrome c oxidase subunit 15 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 5 cytochrome c oxidase subunit 5 cytochrome c oxidase subunit 6	NA  koo0393 Drug metabolism - other enzymes  koo04940 Type I diabetes mellitus  NA  koo03940 Type I diabetes mellitus  NA  koo00071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis  ko00140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko009658  ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor  ko04600 Cytokine-cytokine receptor interaction; ko04662 Chemokine signaling pa  NA  ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen  ko04100 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko00600 Osphingolipid metabolism  ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko0110 Complement and coagulation cascades  NA  NA  ko04515 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep  ko04510 Complement and coagulation cascades; ko05130 Perussi; ko04510 Complement and coagulation cascades; ko05133 Pertussi; ko04510 Complement and coagulation; ko04260 Cardiac muscle contraction; ko0430 Cavdiative		0.58 0.45 0.50 0.62 0.54 0.53 0.40 0.52 0.56 0.40 0.57 0.44 0.57 0.68 0.48 0.41 1.00 0.45 0.38 0.41 1.00 0.45 0.40 0.46 0.40 0.45 0.40 0.41 0.40 0.54	0.0935 0.0014 0.0035 0.0016 0.0017 0.0018 0.0017 0.0015 0.0017 0.	0.251981833 0.172822126 0.143042222 0.152593243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1521950 0.252121950 0.252121950 0.252121950 0.168745194 0.11266745 0.143042222 0.247118814 0.11266745 0.161328781 0.161328781 0.161328781 0.25998206 0.151328781 0.25998206 0.151328781 0.25998206 0.151328781 0.25998206 0.151328781 0.
K17274 K03927 K03927 K03927 K03927 K03927 K03927 K03927 K03927 K03928 K03927 K03928 K0	S100A10 CES2 CPE CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL kate, CAT, catts, srpA COMT CTSK. CCL19, ELC CC	calpactin-1 light chain carboxypeptidase [ EC.3.4.17.10] caspase recruitment domain-containing protein 8 catalase [EC.11.11.6] catechol O-methyltransferase [ Liver isoform [ EC.2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC.1.11.6] catechol O-methyltransferase [ EC.2.1.1.6] cathepin K [ EC.3.4.22.38] C-C mottif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 cerunidas synthetase [ EC.2.3.1.24] cerunidas synthetase [ EC.2.3.1.24] cerunidas synthetase [ EC.2.3.1.24] cerunidas synthetase [ EC.2.3.1.24] cerunidas min [ EC.1.16.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [ EC.1.14.13.98] choloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [ EC.1.14.13.98] cholosterol 71.9hp-monooxygenase [ EC.1.14.13.17] chromobox protein 3 clusterin congulation factor VIII cold-inducible RNA-binding protein collagen, type ( IV, IIII)/V/XI/XIXV/XXVII, alpha collagen, type ( IV, IIII)/V/XI/XIXV/XXVII, alpha collagen, type ( IV, IIII)/V/XI/XIXV/XXVII, alpha complement component ( 15/4b) receptor 1 complement component ( 15/4b) receptor	NA  ko00983 Drug metabolism - other enzymes  ko04940 Type I diabetes mellitus  NA  ko04940 Type I diabetes mellitus  NA  ko000071 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  ko00380 Tryptophan metabolism; ko00363 Glycvytate and dicarboxylate metabolism; ko004621 NOT-like receptor ko04620 Toll-like receptor  ko04160 Stevich dormone biosynthesis; ko00350 Tyrosine metabolism; ko009565 ko04142 Lysosome; ko04380 Osteodast differentiation; ko04620 Toll-like receptor  ko04060 Cytokine-cytokine receptor interaction; ko04602 Chemokine signaling pa NA  ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen  ko04100 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko000300 Sphingolipid metabolism  ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi NA  ko001610 Drimary bile acid biosynthesis  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid diosynthesis; ko0140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid diosynthesis; ko0140 Steroid hormone biosynthesis; ko  ko01510 Complement and coagulation cascades  NA  ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recepi  ko04510 Complement and coagulation cascades; ko04604 Hematopoietic cell lines  ko04510 Complement and coagulation cascades; ko05139 Pertussis; ko05150 Staphylococcus aureus ir  ko04510 Complement and coagulation cascades; ko05150 Staphylococcus aureus ir  ko04510 Complement and coagulation cascades; ko05150 Staphylococcus aureus ir  ko04111 Cell cycle - yeast  ko04110 Complement and coagulation cascades; ko05150 Staphylococcus aureus ir  ko04111 Cell cycle - yeast  ko04111 Cell cycle - yeast  ko04111 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseat  ko04111 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's		0.58 (0.54 (0.55 (0.54 (0.55 (0.54 (0.54 (0.54 (0.55 (0.54 (0.54 (0.54 (0.55 (0.54 (0.55 (0.54 (0.54 (0.55 (0.54 (0.55 (0.54 (0.55 (0.54 (0.55 (0.54 (0.55 (	0.0935 0.0055 0.0012 0.0028 0.0030 0.0030 0.0015 0.	0.251981833 0.172822126 0.143042222 0.1525930243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.15513263 0.155133463 0.155133463 0.155133463 0.16513046222 0.247118814 0.143042222 0.15128781 0.18659932 0.18659932 0.18659932 0.18659932 0.18659932 0.18659932 0.18659932 0.18630263 0.186659932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1867859932 0.1967858752 0.1967857575 0.1967857575 0.1967857575 0.1967857575 0.196785775 0.196785775 0.196785775 0.196785775 0.196785775 0.196785775 0.196786775 0.19
K17274 K03927 K01294 K13022 K029276 K02270 K02270 K02270 K02270 K03927 K	S100A10 CES2 CPE CPE CPE CPE CPE CPTIA CARD8, CARDINAL katte, CAT, catlB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CEBRD CD4 CDC42 CERS CPP GPE GPE GPE GPE GPE GPE GPE GPE GPE G	calpactin-1 light chain carboxypeptidase [ [EC:3.4.17.10] carboxypeptidase 2 [EC:3.4.17.1] carboxypeptidase 2 [EC:3.4.17.1] carboxypeptidase 2 [EC:3.4.17.1] carpoxypeptidase 2 [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol 0-methyltransferase 1, liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol 0-methyltransferase [EC:2.1.16] cathepian ( [EC:3.4.22.38] C-C motif chemokine 19 CCAA17(enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceramide synthetase [EC:2.3.1.24] ceramide synthetase [EC:2.3.1.24] chaperonin GroEL chloride intracellular channel protein 2 chloride intracellular channel protein 2 chloride intracellular channel protein 3 clusterin coagulation factor VIII codi-inducible RNA-binding protein collagen, type I/I/I/I/I/V/XIVI/XIVI/XIVI, alpha complement component (3b/db) receptor 1 complement component (15/db) receptor 1 complement component 4 binding protein, alpha complement factor D [EC:3.4.21.46] complement component 1 s subcomponent [EC:3.4.21.42] complement component 1, s subcomponent [EC:3.4.21.42] complement component 1, s subcomponent [CC:3.4.21.43] complement component 1, s subcomponent [CC:3.4.21.42] complement component 1, s subcomponent [CC:3.4.21.43] complement component 4 binding protein subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sush domain-containing protein cytochrome c coidase assembly protein subunit 16 cytochrome c coidase subunit 2 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 5 cytochrome c oxidase subunit 7 cytochrome c oxidase subunit 7 cytochrome c oxidase subunit 7 cytochrome c ox	NA  ko00983 Drug metabolism - other enzymes  ko04940 Type I diabetes mellitus  NA  ko00971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis  ko0140 Steroid hormone biosynthesis; ko00330 Tyrosine metabolism; ko00656 R  ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor  ko04606 Otyokine-cytokine receptor interaction; ko04620 Chemokine signaling pat  NA  ko04514 Cell adhesion molecules (CAMe); ko04612 Antigen processing and presen  ko04610 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko00600 Sphingolipid metabolism  ko03618 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko04101 Complement and coagulation cascades  NA  ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep  ko04610 Complement and coagulation cascades; ko05130 Percusion; ko04512 ECM-recep  ko04610 Complement and coagulation cascades; ko05139 Percusion  ko04110 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko04110 Complement and coagulation cascades; ko05139 Pertussis  ko04101 Complement and coagulation cascades; ko05139 Pertussis  ko04101 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05130 Staphylococcus aureus it  ko04110 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko00130 Oxidative phosphorylation  NA  ko00190 Oxidative phosphorylation; ko04260 Cardiac musde contraction; ko04932  ko00190 Oxidative phosphorylation; ko0426		0.58 (0.50 d.40 d.41 d.46 d.46 d.48 d.41 d.46 d.46 d.46 d.47 d.46 d.46 d.47 d.47 d.47 d.48 d.48 d.49 d.49 d.49 d.49 d.49 d.49 d.49 d.49	0.0936 0.0014 0.0038 0.0030 0.0014 0.0038 0.0030 0.0015 0.0015 0.0015 0.0015 0.0015 0.0016 0.0017 0.0012 0.0018 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0016 0.0017 0.0016 0.0017 0.0016 0.	0.251981833 0.172822126 0.173822126 0.173822126 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.15215126 0.152151
K17274 K03927 K03927 K03927 K03927 K03927 K03927 K03927 K03928 K0	\$100A10  CES2  CPE  CPE  CPE  CPE  CPE  CPZ  CPTIA  CARD8, CARDINAL  kate, CAT, catts, srpA  COMT  CTSK  CCL19, ELC  CEBPD  CD4  CCL19, ELC  CEBPD  CD4  CCCL19, ELC  CEBPD  CUC42  CERS  CP  groEL, HSPD1  CLU2  CYP4AC1  CYP7A1  CR3, CM3P  CR3, HPIG  CLU  CR1, CD35  CLS  CSSA, HPIG  CULAS  COLIAA  CR1, CD35  CLS  CSSA, CARDI, CAPD2  ATOXI, ATX1, cop2  E2,7-3, 2  E2,7-3, 2  CSMD  ATF6A  CD01  CYC  COX16  COX16  COX17  COX20  COX17  COX20  COX3  COX5A  COX6A  COX6A  COX6A  COX7A  COX7C  COX7C  CYP2F  CYP2F  CYP2Y	calpactin-1 light chain carboxylesterase 2 [EC:3.1.1 3.1.184 3.1.1.56] carboxypeptidase E [EC:3.4.17.10] carboxypeptidase E [EC:3.4.17.1] carpoxypeptidase E [EC:3.4.17.1] carpoxypeptidase E [EC:3.4.17.1] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catalase [EC:1.11.6] catepoin K [EC:3.4.22.38] C-C-motif chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.4] cerculoplasmin [EC:1.63.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [EC:1.4.13.98] cholesterol 24(5)-hydroxylase [EC:1.4.13.98] cholesterol 7alpha-monooxygenase [EC:1.14.13.17] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type (I)/IIII/V/XIXV/XXVIX, alpha complement component (3b/4b) receptor 1 complement component (3b/4b) receptor 1 complement component 4 (3b/4b) receptor 1 complement component 4 (3b/4b) receptor 1 complement propose subunit 1 copper chaperone creatine kinase [EC:2.7.3.2] CUB and sush id domain-containing protein cyclic AMP-dependent transcription factor ATF-6 alpha cycthormore coxidase assembly protein subunit 16 cycthormore coxidase assembly protein subunit 17 cytochrome coxidase subunit 2 cytochrome coxidase subunit 3 cytochrome coxidase subunit 5a cytochrome of coxidase subunit 7a cytochrome P450, family 2, subfamily X	NA  koo0393 Drug metabolism - other enzymes  koo0490 Type I diabetes mellitus  NA  koo03071 Fatty acid degradation; koo0320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  koo0380 Tryptophan metabolism; ko00363 Glyoxylate and dicarboxylate metabolis  koo0140 Steroid hormone biosynthesis; ko00350 Tyrosine metabolism; ko00958 koo1402 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toll-like receptor  ko04602 Cytokine-cytokine receptor interaction; ko04662 Toll-like receptor  ko04603 Cytokine-cytokine receptor interaction; ko04662 Chemokine signaling pa  NA  ko04514 Cell adhesion molecules (CAMs); ko04612 Antigen processing and presen  ko04010 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko00050 Sphingolipid metabolism  ko03018 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko0110 Complement and coagulation cascades  NA  NA  ko04151 PISK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recept  ko04510 Complement and coagulation cascades; ko04604 Hematopoietic cell linei  ko04510 Complement and coagulation cascades; ko05133 Pertussi; ko05150 Staph  ko04110 Complement and coagulation cascades; ko05133 Pertussi; ko05150 Staph  ko04111 Cell Cycle - yeast  ko04978 Mineral absorption  ko0310 Arginine and proline metabolism  NA  ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko04190 Oxidative phosphorylation; ko04260 Cardiac musde contraction; ko04932  ko00190 Oxidati		0.58 0.45 0.50 0.50 0.50 0.50 0.50 0.50 0.50	0.0930 0.0085 0.0014 0.0033 0.0016 0.0017 0.0016 0.0015 0.0017 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.143042222 0.254340055 0.143212829 0.143042222 0.1265139087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.165190087 0.16128781 0.1268745 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198753228 0.143042222 0.198691113 0.168745194 0.143042222 0.198691113 0.168745194 0.143042222 0.198691113 0.168745194 0.143042222 0.198691113 0.168745194 0.193046798 0.193046798
K17274 K03927 K01294 K13022 K029276 K02270 K02270 K02270 K02270 K03927 K	S100A10 CES2 CPE CPE CPE CPE CPE CPE CPZ CPTIA CARD8, CARDINAL Astate, CAT, catB, srpA COMT CTSK CCL19, ELC CEBPD CD4 CDC42 CEBP CD4 CDC42 CEBP CD6 CDC42 CEBP CD6 CDC42 CEBP CD6 CDC42 CEBP CD7 CD6 CDC42 CEBP CD7	calpactin-1 light chain carboxypeptidase [ EC:3.4.17.10] carpoxypeptidase [ EC:3.4.17.10] caspase recruitment domain-containing protein 8 catalase [EC:1.11.1.6] catechol O-methyltransferase [ Liver isoform [EC:2.3.1.21] caspase recruitment domain-containing protein 8 catalase [EC:1.11.6] catechol O-methyltransferase [ EC:2.1.1.6] cathepian K [EC:3.4.22.38] C-C motif Chemokine 19 CCAAT/enhancer binding protein (C/EBP), delta CD4 antigen cell division control protein 42 ceramide synthetase [EC:2.3.1.24] ceruloplasmi [EC:1.6.3.1] chaperonin GroEL chloride intracellular channel protein 2 cholesterol 24(5)-hydroxylase [ EC:1.14.13.98] cholesterol 7alpha-monooxygenase [ EC:1.14.13.77] chromobox protein 3 clusterin coagulation factor VIII cold-inducible RNA-binding protein collagen, type IV, alpha collagen, type IV, alpha collagen, type IV, alpha complement component (33/4b) receptor 1 complement component (33/4b) receptor 1 complement component 4 binding protein, alpha component factor D [EC:3.4.2.14.2] complement component 4 binding protein, alpha component factor D [EC:3.4.2.14.4] complement component (15.46) condensin complex subunit 1 copper chaperone creatine kinase [ EC:2.7.3.2] CUB and sushi domain-containing protein cytic AIMP-dependent transcription factor ATF-6 alpha cysteine dioxygenase [ EC:1.13.11.20] cytochrome c oxidase assembly protein subunit 16 cytochrome c oxidase assembly protein subunit 17 cytochrome c oxidase subunit 3 cytochrome c oxidase subunit 3 cytochrome oxidase subunit 7 cytochrome P450, family 2, subfamily F [ EC:1.4.14.1, 1]	NA  ko00983 Drug metabolism - other enzymes  ko04940 Type I diabetes mellitus  NA  ko00971 Fatty acid degradation; ko03320 PPAR signaling pathway; ko04920 Adipoc  ko04621 NOD-like receptor signaling pathway  ko00380 Tryptophan metabolism; ko00630 Glyoxylate and dicarboxylate metabolis  ko0140 Steroid hormone biosynthesis; ko00330 Tyrosine metabolism; ko00656 R  ko04142 Lysosome; ko04380 Osteoclast differentiation; ko04620 Toil-like receptor  ko04606 Otyokine-cytokine receptor interaction; ko04620 Chemokine signaling pat  NA  ko04514 Cell adhesion molecules (CAMe); ko04612 Antigen processing and presen  ko04610 MAPK signaling pathway; ko04011 MAPK signaling pathway - yeast; ko040  ko00600 Sphingolipid metabolism  ko03618 RNA degradation; ko04940 Type I diabetes mellitus; ko05134 Legionellosi  NA  ko00120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko0120 Primary bile acid biosynthesis; ko00140 Steroid hormone biosynthesis; ko  ko04101 Complement and coagulation cascades  NA  ko04151 P13K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep  ko04610 Complement and coagulation cascades; ko05130 Percusion; ko04512 ECM-recep  ko04610 Complement and coagulation cascades; ko05139 Percusion  ko04110 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko04110 Complement and coagulation cascades; ko05139 Pertussis  ko04101 Complement and coagulation cascades; ko05139 Pertussis  ko04101 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05139 Pertussis  ko04510 Complement and coagulation cascades; ko05130 Staphylococcus aureus it  ko04110 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko04141 Protein processing in endoplasmic reticulum; ko05010 Alzheimer's diseas  ko00130 Oxidative phosphorylation  NA  ko00190 Oxidative phosphorylation; ko04260 Cardiac musde contraction; ko04932  ko00190 Oxidative phosphorylation; ko0426		0.58 (0.54 (0.55 (0.54 (0.54 (0.55 (	0.0935 0.0014 0.0035 0.0016 0.0016 0.0017 0.0018 0.0017 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0018 0.0019 0.0019 0.0019 0.0018 0.0019 0.	0.251981833 0.172822126 0.143042222 0.152539243 0.15204453 0.15204453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.1520453 0.152133463 0.1520453 0.152133463 0.152053 0.14321829 0.165190087

K15730			ko00590 Arachidonic acid metabolism				0.212506754
			ko00100 Steroid biosynthesis		-0.87		0.186503889
K11995 K11160			NA ko00561 Glycerolipid metabolism; ko04975 Fat digestion and absorption		0.73		0.185417043 0.221905228
			NA	-	-0.45		0.168745194
			ko00900 Terpenoid backbone biosynthesis		-0.69		0.15204453
K12475			koO4144 Endocytosis		0.47		0.249020182
K02540	MCM2	DNA replication licensing factor MCM2 [EC:3.6.4.12]	ko03030 DNA replication; ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 N		-0.40		0.258205427
			ko03030 DNA replication; ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 N		-0.64		0.191823694
K02542			ko03030 DNA replication; ko04110 Cell cycle; ko04111 Cell cycle - yeast; ko04113 N		-0.87		0.182571981
K17693			NA		0.58		0.251981833
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn		-0.44 -0.44		0.20698367
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn		-0.44		0.205722905
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn				0.143042222
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn	- 1			0.168745194
			ko00230 Purine metabolism; ko00240 Pyrimidine metabolism; ko03020 RNA polyn		-0.50	0.0018	0.143042222
K10880	XRCC3	DNA-repair protein XRCC3	ko03440 Homologous recombination		-0.46	0.0000	0.063123807
			ko04145 Phagosome; ko04962 Vasopressin-regulated water reabsorption; ko05132				0.161328781
K10660			NA .				0.152539243
			ko04120 Ubiquitin mediated proteolysis; ko04141 Protein processing in endoplasr				0.246238756
			NA NA	- 1	-0.50		0.143042222
			NA NA		-0.39 -0.95		0.172822126 0.143042222
K10205			ko00062 Fatty acid elongation; ko01040 Biosynthesis of unsaturated fatty acids	7	-0.45		0.203851854
K01173			ko04210 Apoptosis	i	-0.51		0.187355725
			NA	-	0.49		0.186859932
			ko03018 RNA degradation		-0.61		0.143042222
K00787			ko00900 Terpenoid backbone biosynthesis; ko05164 Influenza A; ko05166 HTLV-l ir		-1.03		0.15204453
K02373			ko04210 Apoptosis; ko04620 Toll-like receptor signaling pathway; ko04622 RIG-l-li		-0.43		0.195337521
K08751 K08752			ko03320 PPAR signaling pathway; ko04975 Fat digestion and absorption	_	1.70		0.187641673
			ko03320 PPAR signaling pathway		0.46		0.206767944
K08755 K10285			ko03320 PPAR signaling pathway NA	- 1	0.40		0.161328781
K00522			ko00860 Porphyrin and chlorophyll metabolism; ko04978 Mineral absorption	- 5	0.43		0.18029481
K09570			NA		-0.54		0.187355725
K09409			NA	7	0.53	0.0306	0.229821398
		F-type H+-transporting ATPase subunit beta [EC:3.6.3.14]	ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkin		0.60		0.143042222
			ko00190 Oxidative phosphorylation; ko05010 Alzheimer's disease; ko05012 Parkin		-1.05		0.143042222
K12900			ko03040 Splice osome		-0.49	0.00.0	0.249741275
K08266			koO4150 mTOR signaling pathway; koO4151 PI3K-Akt signaling pathway		-0.44		0.161328781
K08426		- Programme and the second sec	NA		0.96		0.143042222
K11257		V	NA NA		0.42		0.205299668
K00699		0	ko00040 Pentose and glucuronate interconversions; ko00053 Ascorbate and aldara	- =	0.64	0.000	0.143042222
K13990		glutamate formiminotransferase / formiminotetrahydrofolate cyclodeaminase [EG]		- 5	0.75		0.203435986
		glutaryl-CoA dehydrogenase [EC:1.3.8.6]	ko00071 Fatty acid degradation; ko00310 Lysine degradation; ko00380 Tryptophan		-0.78		0.097393314
			ko00480 Glutathione metabolism; ko00590 Arachidonic acid metabolism; ko04918		0.75		0.246725736
			ko00260 Glycine, serine and threonine metabolism; ko00460 Cyanoamino acid me	<b>—</b>	0.42		0.187355725
K01196	AGL	glycogen debranching enzyme [EC:2.4.1.25 3.2.1.33]	ko00500 Starch and sucrose metabolism	<b>=</b>	0.65	0.0004	0.143042222
K00049	CDHDD	glyoxylate/hydroxypyruvate reductase [EC:1.1.1.79 1.1.1.81]	ko00260 Glycine, serine and threonine metabolism; ko00620 Pyruvate metabolism	=	0.55	0.0259	0.221989249
	OKI II K	gryoxyrate/rrydroxypyrdvate reductase [LC.1.1.1.75 1.1.1.01]			0.55		
K06232	GAS1	growth arrest-specific 1	ko04340 Hedgehog signaling pathway	Ē	0.49		0.18100852
K06232 K04630	GAS1 GNAI	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha	ko04340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur	j	0.49 0.39	0.0044	0.18100852 0.165133463
K06232 K04630 K01139	GAS1 GNAI spoT, HDDC3	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]	ko04340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko00230 Purine metabolism	Ī	0.49 0.39 -0.52	0.0044 0.0094	0.18100852 0.165133463 0.178297363
K06232 K04630 K01139 K11128	GAS1 GNAI spoT, HDDC3 GAR1, NOLA1	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3/5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA ribonucleoprotein complex subunit 1	ko04340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko02030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes		0.49 0.39 -0.52 -0.61	0.0044 0.0094 0.0185	0.18100852 0.165133463 0.178297363 0.200420738
K06232 K04630 K01139 K11128 K11129	GAS1 GNAI spoT, HDDC3 GAR1, NOLA1 NHP2, NOLA2	growth arrest-specific 1 guanine nucleotide-binding protein G(I) subunit alpha guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2	ko04340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko00230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes		0.49 0.39 -0.52 -0.61 -0.54	0.0044 0.0094 0.0185 0.0469	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686
K06232 K04630 K01139 K11128 K11129 K11130	GAS1 GNAI spot, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3;5-bisidiphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3	koO4340 Hedgehog signaling pathway koO4062 Chemokine signaling pathway; koO4360 Axon guidance; koO4530 Tight jur koO2030 Purine metabolism koO3008 Ribosome biogenesis in eukaryotes koO3008 Ribosome biogenesis in eukaryotes koO3008 Ribosome biogenesis in eukaryotes		0.49 0.39 -0.52 -0.61 -0.54 -0.55	0.0044 0.0094 0.0185 0.0469 0.0064	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087
K06232 K04630 K01139 K11128 K11129 K11130 K09414	GAS1 GNAI spoT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1	growth arrest-specific 1 guanosine-3;5-bisdiphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1	ko04340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko00230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05134 Legionellosis		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044	GAS1 GNAI spot, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis(diphosphate) 3: pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D	koO4340 Hedgehog signaling pathway koO4062 Chemokine signaling pathway; koO4360 Axon guidance; koO4530 Tight jur koO2030 Purine metabolism koO3008 Ribosome biogenesis in eukaryotes koO3008 Ribosome biogenesis in eukaryotes koO3008 Ribosome biogenesis in eukaryotes		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894	GAS1 GNAI Spot, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSS1 HNRNPABD HNRNPA0	growth arrest-specific 1  guanine nucleotide-binding protein G(i) subunit alpha guanien aufoctide-binding protein G(i) subunit alpha guanisine-3;5-bisidiphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]  H/ACA ribonucleoprotein complex subunit 1  H/ACA ribonucleoprotein complex subunit 2  H/ACA ribonucleoprotein complex subunit 3  heat shock transcription factor 1  heterogeneous nuclear ribonucleoprotein A/B/D  heterogeneous nuclear ribonucleoprotein A/B	kood440 Hedgehog signaling pathway koo40402 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko000230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko05104 Legionellosis NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12885 K11296	GAS1 GNA1 SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPABD HHRNNPAO RBMX, HNRNPG HMGB3	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3	ko04440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko030008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05134 Legioneilosis NA NA Ko030040 Spliceosome NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.254344055 0.258205427 0.246238756
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12885 K11296	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPABO RBMX, HNRNPG HMGB3 MYST2, HBO1, KAT7	growth arrest-specific 1  guanosine-3;5-bisidiphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]  H/ACA ribonucleoprotein complex subunit 1  H/ACA ribonucleoprotein complex subunit 2  H/ACA ribonucleoprotein complex subunit 3  heat shock transcription factor 1  heterogeneous nuclear ribonucleoprotein A/B/D  heterogeneous nuclear ribonucleoprotein A/B  heterogeneous nuclear ribonucleoprotein G  high mobility group protein B3  histone acetyltransferase MYST2 [EC:2.3.1.48]	koo4340 Hedgehog signaling pathway koo4052 Chemokine signaling pathway; ko04350 Axon guidance; ko04530 Tight jur ko04052 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko03030 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05134 Legionellosis NA NA ko03040 Spliceosome NA NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63 -0.63	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.254344055 0.258205427 0.246238756 0.143042222
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12885 K11296 K11307	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPA0 BRMX, HNRNPG HMGB3 MYST2, HBO1, KAT7 HZA	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 listone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A	koo4440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko05141 Legionellosis NA NA Ko03040 Spliceosome NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.63 -0.63 -0.45	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.254344055 0.258205427 0.246238756 0.143042222 0.168745194
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12885 K11296 K11307 K11251	GAS1 GMAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNPABD HNRNPAD RBMX, HNRNPG HMGB3 MYST2, HBO1, KAT7 HZB	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3;5-bisidighosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko02030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05141 kegionellosis NA NA ko03008 Spliceosome NA NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.63 -0.63 -0.45 -0.41	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.2543244055 0.258205427 0.246238756 0.143042222 0.168745194 0.197085215
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12885 K11296 K11307 K11251 K11252	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPAB HMRNPAB HMSB3 MYST2, HB01, KAT7 HZA HZB	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2B histone H2B homeebox protein HEX	kood440 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko04008 Pinrine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03140 Legionellosis NA NA ko03040 Spliceosome NA NA ko050343 Alcoholism; ko05322 Systemic lupus erythematosus ko050344 Alcoholism; ko05322 Systemic lupus erythematosus		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63 -0.63 -0.45 -0.41 -0.54 0.44	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077 0.0172 0.0053	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.2543244055 0.258205427 0.246238756 0.143042222 0.168745194 0.197085215 0.165190087
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12894 K12895 K11296 K11297 K11251 K11251 K08024 K09339	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPABD HHRNNPAO RBMX, HNRNPG HMGB3 MYST2, HBO1, KAT7 HZA HZB HHEX, HEX, PRH HHX1	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2B histone H2B homeobox protein HEX homeobox protein HEX	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko02030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05141 kegionellosis NA NA ko03008 Spliceosome NA NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63 -0.45 -0.41 -0.54 0.44	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077 0.0172 0.0053	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.254344055 0.258205427 0.26228756 0.143042222 0.168745194 0.197085215 0.165190087 0.163190087
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K12894 K12895 K11296 K11251 K11251 K11252 K08024 K09339 K08648	GAS1 GMAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNPABD HNRNPABD HNRNPABD HNRNPAB MWST2, HBO1, KAT7 HZA HLB HHEX, HEX, PRH HLL1 HABP2	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanosine-3;5-bisidighosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A histone H2A histone H2A homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HLX hyaluronan binding protein 2 [EC:3.4.21]	koo4440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05141 Legionellosis NA NA Ko03040 Spliceosome NA NA NA Ko050340 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe Ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregular		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63 -0.63 -0.45 -0.41 -0.54 0.44	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077 0.0172 0.0053 0.0021	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.2543244055 0.258205427 0.246238756 0.143042222 0.168745194 0.197085215 0.165190087
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K12894 K12896 K11295 K11251 K11251 K08024 K09339 K08684 K11394 K01507	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPABD HHRNNPABD HHRNPAD RBMX, HNRNPG HMGB3 MYST2, HB01, KAT7 HA2A HA2B HHEX, HEX, PRH HLX1 HABP2 PRODH2 ppa	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone actyltransferase MYST2 [EC:2.3.1.48] histone H2B homeobox protein HEX	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03104 Legionellosis NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.56 -0.63 -0.63 -0.45 -0.41 -0.54 0.44 0.48 0.75	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077 0.0172 0.0053 0.0021 0.0471 0.0141	0.18100852 0.165133463 0.178297363 0.200420738 0.200420738 0.260922686 0.185190087 0.246238756 0.25824055 0.258205427 0.246238756 0.168745194 0.197085215 0.165190087 0.143042222 0.26133498 0.187641673 0.187641673
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K12894 K12895 K11207 K11251 K11252 K08024 K09339 K08648 K11307 K05719	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HMSB3 MYST2, HB01, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HABP2 PRODH2 Ppa	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A homeobox protein HEX hydroxyproline oxidase [EC:3.4.21.] hydroxyproline oxidase [EC:1.5] inorganic pyrophosphatase [EC:3.6.1.1] integrin bet a1	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040082 Nerine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome losienesis in eukaryotes NA NA ko03040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA NA ko00330 Arginine and proline metabolism ko00130 Oxidative phosphorylation		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.63 -0.40 -0.54 -0.41 -0.54 0.44 0.48 0.49 0.49 0.40 0.75 0.40 0.4	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0016 0.0077 0.0172 0.0053 0.0021 0.00471 0.0141	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.2462288756 0.198691113 0.258240405 0.258205427 0.258205427 0.463288756 0.143042222 0.168745194 0.1671085215 0.165190087 0.143042222 0.1687461673 0.239193287 0.097393314
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12885 K11296 K11307 K11251 K11252 K08024 K09339 K08648 K11394 K01507 K05719	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 NSF1 HNRNPABD HNRNPABD HNRNPAO RBMX, HNRNPG HMGB3 MYST2, HBO1, KAT7 H2A H2B HHEX, HEX, PRH HLX1 HABP2 PROODH2 ppa ITGB1 IFITM	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2B homeobox protein HEX homeobox protein HEX homeobox protein E(EC:3.4.21] hydroxyproline oxidase [EC:1.5] inorganic pyrophosphatase [EC:3.6.1.1] integrin beta 1 integrin beta 1 integrin beta 1 interferon induced transmembrane protein	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05141 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko050344 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko050450 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA NA Ko00330 Arginine and proline metabolism ko00130 Oxidative phosphonylation ko04150 Phagosome; ko04151 Pl3K-Akt signaling pathway; ko04360 Axon guidance NA		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.63 -0.43 -0.41 -0.54 0.44 0.48 0.44 -0.42 0.66 0.45	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0017 0.0077 0.0073 0.0021 0.0471 0.0431 0.0335 0.0031	0.18100852 0.165133463 0.178297363 0.200420738 0.260922686 0.165190087 0.246238756 0.198691113 0.254344055 0.258205427 0.246238756 0.19869113 0.143042222 0.168745194 0.197085215 0.165190087 0.143042222 0.261133498 0.29193287 0.29193287 0.29193287
K06232 K04630 K01139 K11128 K11129 K11130 K09414 K13044 K12885 K11296 K11307 K11251 K11252 K08024 K09339 K08648 K11394 K01507 K05719 K05719 K056566	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNPAD HHRNPAD HHRNPAD RBMX, HHRNPG HMGB3 MYST2, HBO1, KAT7 H2B HHEX, HEX, PRH HLX1 HABP2 PRODH2 Ppa ITGB1 IFITM ILITR2	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3;5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA fibonucleoprotein complex subunit 2 H/ACA fibonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein B histone house nuclear ribonucleoprotein B histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A histone H2B homeobox protein HLX homeobox protein HLX hyaluronan binding protein 2 [EC:3.4.21] hydroxyproline oxidase [EC:1.5] integrain bydroxyproline oxidase [EC:1.5] integrain bydroxyproline oxidase [EC:1.5] integrain bydroxyproline oxidase [EC:3.6.1.1] integrin beta 1 interleukin 1 receptor type II	kood430 Hedgehog signaling pathway kood030 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko00200 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03104 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00330 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04195 Phagosome; ko04151 P13K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior		0.49 0.39 -0.52 -0.61 -0.54 -0.55 -0.63 -0.63 -0.41 -0.54 0.44 0.48 0.75 0.44 0.44 0.45 0.45 0.40 0.40 0.40 0.40 0.50 0.40 0.40 0.50 0.40 0.40 0.40 0.40 0.40 0.50 0.40	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0017 0.0077 0.0172 0.0053 0.0021 0.0471 0.0335 0.0001	0.18100852 0.165133463 0.178297363 0.200420738 0.200420738 0.260922668 0.165190087 0.246238756 0.138691113 0.254344055 0.258205427 0.46238756 0.143042222 0.168745194 0.187641673 0.187641673 0.187641673 0.187641673 0.187641673 0.187933314 0.143042222 0.043042222
K06232 K04630 K01139 K11129 K11129 K11130 K09414 K12894 K12894 K12885 K11296 K11307 K11251 K08024 K09339 K08648 K11394 K01507 K05719 K06566 K04387 K05055	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPABD HHRNNPABD HHRNPABD HHRNPABD HHRNPABD HHRNPAB HHRSB3 HHSB3 HHSB4 HBB4 HBB4 HBB7 HBB7 HBB7 HBB7 HBB7 HB	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MrST2 [EC:2.3.1.48] histone H2A histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HIX lynduronan binding protein 2 [EC:3.4.21] hydroxyproline oxidase [EC:1.5] inorganic pyrophosphatase [EC:3.6.1.1] interferon induced transmembrane protein interleukin 1 receptor type II interleukin 1 receptor type II interleukin 6 receptor	koo4440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040023 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome biogenesis in eukaryotes ko05144 Legionellosis NA NA Ko03040 Spliceosome NA NA ko050340 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko000330 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior; ko04066 HiF-1 signaling pathway;		0.49 0.39 -0.52 -0.61 -0.54 -0.55 -0.63 -0.45 -0.45 -0.44 0.48 0.75 0.44 -0.42 0.66 -0.40 0.66 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0.54 -0.54 -0.54 -0.55 -0.54 -0.55 -0.54 -0.55 -0	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0411 0.0459 0.0016 0.0077 0.0172 0.0053 0.0021 0.0471 0.0471 0.0141 0.0335 0.0001 0.0008 0.0001 0.0008	0.181/0852 0.165133463 0.2004/20738 0.2004/20738 0.2004/20738 0.16519/0087 0.246238756 0.16519/0087 0.246238756 0.14304/222 0.246238756 0.14304/222 0.261133498 0.18774197 0.18774197 0.1876119 0.1876119 0.1876119 0.1876119 0.1876119 0.1876119 0.1876119 0
K06232 K04630 K01139 K11128 K11129 K11129 K11130 K09414 K12894 K12885 K11296 K11296 K11251 K11252 K08024 K08024 K09339 K08648 K11394 K05575 K05719 K05566 K04387 K05555 K13089	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPAD HHRNNPAD HHRNNPAD HHRNPAD HILT HABP2 PRODH2 PRODH2 PRODH2 PRODH1 HITM HILT HILT LIER HLRP HLRP HLRP HLRP HLRP HLRP HLRP HLR	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein 6 high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein E(EC:3.4.21] hyduronan binding protein 2 [EC:3.6.1.1] integrin beta 1 interferon induced transmembrane protein interleukin 1 receptor type II interleukin 6 receptor interleukin 6 receptor interleukin 6 reaceptor interleukin 6 receptor interleukin 6 reaceptor interleukin 6 reaceptor interleukin 6 reaceptor	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05134 Legionellosis NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00330 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interactior; ko04066 HiF-1 signaling pathway.		0.49 0.39 -0.52 -0.61 -0.54 -0.66 -0.40 -0.63 -0.45 -0.41 -0.54 0.44 0.48 0.49 0.49 0.40 0.4	0.0044 0.0185 0.0469 0.0363 0.0176 0.0411 0.0459 0.0016 0.0016 0.0017 0.0017 0.0017 0.0071 0.0471 0.0471 0.0401 0.0001 0.0001	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.165190087 0.246238756 0.15859131 0.254244055 0.168745194 0.197085215 0.165190087 0.16745190087 0.16745190087 0.16745190087 0.16745190087 0.1674519087
K06232 K04630 K01139 K11128 K11128 K11128 K11294 K12895 K11296 K11297 K11251 K11252 K08024 K09339 K08648 K11394 K05519 K05519 K056566 K04387 K05055 K0505 K05	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNKBB HMGB3 MYST2, HB01, KAT7 HZA HZB HHEK, HEX, PRH HLX1 HABP2 PRODH2 Ppa ITGB1 IFITM LILT2 LIGR LICP LIGR LICP LIGR LICP LIGR LICP LIGR LICP LIGR LICP LIGR LIDD LIDD LIDD LIDD LIDD LIDD LIDD LID	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone actyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A homeobox protein HEX homeofox protein HEX home	kood430 Hedgehog signaling pathway kool062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA ko003040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA ko00330 Arginine and prolline metabolism ko00130 Oxidative phosphorylation ko04145 Phagosome; ko04151 PlaS-Kt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HiF-1 signaling pathway.		0.49 0.39 -0.52 -0.61 -0.54 -0.63 -0.45 -0.41 -0.54 0.44 0.48 0.49 -0.42 0.66 0.44 -0.42 -0.66 -0.45 -0.41 -0.54 -0.45 -0.45 -0.41 -0.54 -0.45 -0.45 -0.41 -0.54 -0.40 -0.55 -0.41 -0.54 -0.45 -0.40 -0.55 -0.41 -0.54 -0.40 -0.55 -0.41 -0.55 -0.41 -0.54 -0.45 -0.45 -0.45 -0.40 -0	0.0044 0.0185 0.0469 0.0064 0.0363 0.0176 0.0419 0.0362 0.0016 0.0077 0.0172 0.0053 0.0021 0.0049 0.0036 0.0015 0.0001 0.0008	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.2092268 0.165190087 0.246238756 0.143042222 0.16874519 0.197085215 0.16819098 0.187641673 0.293194222 0.165190087 0.165190087 0.165190087 0.165190087 0.16319034 0.197085215 0.143042222 0.15204453 0.143042222 0.15204453
K06232 K04630 K01139 K11128 K11129 K11129 K11130 K09414 K12894 K12885 K11296 K11296 K11251 K11252 K08024 K08024 K09339 K08648 K11394 K05575 K05719 K05566 K04387 K05555 K13089	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 NSF1 HNRNPABD HNRNPABD HNRNPAB HNRN	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA fibonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein E(EC:3.4.21] hydroxyproline oxidase [EC:1.5] inorganic pyrophosphatase [EC:3.6.1.1] integrin beta 1 integrin beta 1 interleukin 1 receptor type II interleukin enhancer-binding factor 2 isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2] krueppel-like factor 2	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko05134 Legionellosis NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00330 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interactior; ko04066 HiF-1 signaling pathway.		0.49 0.39 -0.52 -0.61 -0.54 -0.66 -0.40 -0.63 -0.45 -0.41 -0.54 0.44 0.48 0.49 0.49 0.40 0.4	0.0044 0.0185 0.01869 0.0064 0.0363 0.0176 0.0459 0.0362 0.0017 0.0077 0.0172 0.0033 0.0021 0.00008 0.0017 0.00008 0.0017 0.00008 0.0017 0.00008 0.00008	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.165190087 0.246238756 0.15859131 0.254244055 0.168745194 0.197085215 0.165190087 0.16745190087 0.16745190087 0.16745190087 0.16745190087 0.1674519087
K06232 K04630 K01139 K11128 K11129 K11129 K039414 K12894 K12895 K11296 K11297 K11251 K08023 K080339 K08648 K11394 K05070	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NIP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNRSH HNRSH HNST2, HBO1, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPA TIGG1 IFITM LILT2 LIGR LIEF LIEF LIEF LIEF LIEF LIEF LIEF LIEF	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-37,5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein A histone heterogeneous nuclear ribonucleoprotein B histone	koo4490 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko050341 kegionellosis NA NA Ko03040 Spliceosome NA NA Ko050340 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05030 Viral carcinogenesis; ko05202 Transcriptional misregulat NA NA Ko00330 Arginine and proline metabolism ko00130 Oxidative phosphonylation ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04660 Cytokine-cytokine receptor interactior; ko04666 HIF-1 signaling pathway, NA ko00900 Terpenoid backbone biosynthesis		0.49 0.39 -0.52 -0.61 -0.54 -0.55 0.66 -0.40 -0.63 -0.63 -0.44 0.48 0.75 0.44 -0.44 0.48 0.75 0.44 -0.49 -0.40 -0.40 -0.40 -0.40 -0.50 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.55 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.63 -0.64 -0.55 -0.63 -0.63 -0.63 -0.63 -0.64 -0.55 -0.64 -0.64 -0.55 -0.64 -0.64 -0.65 -0.75 -0.7	0.0044 0.0185 0.0185 0.0064 0.0363 0.0176 0.0411 0.0459 0.0362 0.0016 0.0077 0.0033 0.0021 0.0041 0.0033 0.0017 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.1810/0852 0.165133463 0.178297363 0.200420738 0.200420738 0.260922686 0.165190087 0.246238756 0.143042222 0.168745194 0.197085215 0.16304272 0.26133498 0.16745193 0.197085215 0.16745193 0.1674
K06232 K04630 K01139 K11128 K11129 K11130 K113044 K12885 K11296 K11307 K11251 K11251 K11252 K08024 K09343 K01507 K06566 K04387 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K05070 K07070 K	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNRSH HNRNPB HNRSH HNRNPB HNRSH HNRNPB HNRSH HNRNPB HNRSH H	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HLX hydroxyproline oxidase [EC:3.4.21] hydroxyproline oxidase [EC:3.5] inorganic pyrophosphatase [EC:3.6.1.1] interferion induced transmembrane protein interleukin 1 receptor type il interleukin 6 receptor interleu	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040082 Neime metabolism ko03008 Ribosome biogenesis in eukaryotes ko03104 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko03043 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko04500 Maturity onset diabetes of the young; ko05322 Systemic lupus erythe ko04500 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA NA Ko003040 Arginine and proline metabolism ko00190 Oxidative phosphonylation ko04160 Phagsoome; ko04151 PJSK-Akt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04160 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway; NA ko00900 Terpenoid backbone biosynthesis NA ko04151 PJSK-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep		0.49 0.39 -0.52 -0.61 -0.55 0.66 -0.40 -0.56 -0.63 -0.41 -0.54 0.44 -0.42 0.66 -0.40 -0.50 0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.40 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.56 -0.41 -0.42 -0.42 -0.42 -0.42 -0.43 -0.43 -0.43 -0.44 -0.42 -0.45 -	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0016 0.0016 0.0017 0.0012 0.0021 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.26992268 0.165190087 0.246238756 0.158991113 0.2543440055 0.2542440055 0.458205427 0.168745194 0.197085215 0.165190087 0.143042222 0.166190087 0.143042222 0.160193082 0.187641673 0.239193287 0.143042222 0.1613404222 0.1613404222 0.16134454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454 0.1637454
K06232 K04630 K11128 K11129 K11128 K11130 K09414 K12894 K12894 K12895 K11296 K11307 K11251 K11252 K11307 K11307 K08024 K09339 K08024 K09339 K08026 K08026 K08055 K1399 K06566 K04387 K13089 K17824 K17	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNKBB HMGB3 MYST2, HB01, KAT7 HZA HZB HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPA ITIGB1 IFITM ILITZ ILER ILEP LICP LICP LICP LAMB1 RP-L12, RRPL13 RR-L21, RRPL21, rpIU RR-L22, RRPL21, IU RR-L22, RRPL21, IU RR-L22, RRPL21, IV RP-L22, MRPL22, rpIU	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone actyltransferase MYST2 [EC:2.3.148] histone H2A histone H2B homeobox protein HEX homeofic prophosphatase [EC:3.51] interferon induced transmembrane protein interfeukin 1 receptor type il interfeukin 1 receptor type il interleukin 6 receptor interleukin 6 receptor interleukin 6 receptor interleukin 6 receptor interleukin 1 receptor type il interleukin 1 receptor type il interleukin 1 relipsophate delta-isomerase [EC:5.3.3.2] krueppel-like factor 2 lange subunit ribosomal protein L12 large subunit ribosomal protein L22 large subunit ribosomal protein L22	kood430 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040020 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA ko03040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA ko00300 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04145 Phagoome; ko04151 PlaS-kAt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HiF-1 signaling pathway NA ko000000 Terpenoid backbone biosynthesis NA ko04151 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recept ko03010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.54 -0.55 -0.66 -0.40 -0.56 -0.43 -0.44 -0.44 0.48 0.75 -0.44 -0.49 0.52 -0.68 -1.17 0.54 -0.69 -0.59 -0.52 -0.68 -1.17 -0.54 -0.69 -0.41 -0.40 -0.69	0.0044 0.0195 0.0165 0.0469 0.0064 0.0363 0.0016 0.0016 0.0016 0.0007 0.0012 0.0053 0.0021 0.0035 0.0001 0.0035 0.0001 0.0003 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0002 0.0001 0.0003 0.0001 0.0003 0.0001 0.	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.26922566 0.165190087 0.254240055 0.254244055 0.258205427 0.258205427 0.26238756 0.143042222 0.165190087 0.29193287 0.29193287 0.29193287 0.29193287 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.183745194 0.185745194 0.185745194 0.185768527 0.165133468 0.165133468 0.165133468
K06232 K04630 K11128 K11129 K11120 K09414 K12894 K12894 K12895 K11296 K11307 K1151 K1152 K1152 K1152 K1152 K1153 K06024 K09339 K0643 K0544 K0543 K0544	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 NSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNR	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX integrin beta 1 integrin beta 1 integrin beta 1 interferon induced transmembrane protein interleukin 1 receptor type II interleukin 6 receptor interleukin enhancer-binding factor 2 isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2] krueppel-like factor 2 laminin, beta 1 large subunit ribosomal protein L12 large subunit ribosomal protein L22	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko02030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko054030 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05090 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko000300 Ariginine and proline metabolism ko01415 Phagosome; ko04151 P13K-Akt signaling pathway; ko0460 Cytokine-cytokine receptor interactior ko04606 Cytokine-cytokine receptor interaction; ko04666 HIF-1 signaling pathway, NA Ko04010 Pix-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-receptoo3010 Ribosome ko03010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.51 -0.56 -0.66 -0.40 -0.56 -0.41 -0.54 0.44 0.48 0.75 0.44 -0.45 -0.49 -0.66 0.45 -0.39 -0.68 -0.17 0.56 -0.40 -0.40 -0.40 -0.41 -0.44 -0.45 -0.45 -0.45 -0.45 -0.45 -0.40 -0.	0.0044 0.0185 0.0469 0.0066 0.0076 0.0176 0.0362 0.0016 0.0077 0.0122 0.0053 0.0021 0.0017 0.0035 0.0001 0.0017 0.0001 0.000001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.00001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001 0.0001	0.18100852 0.165133463 0.178297363 0.200420738 0.200420738 0.200420738 0.269022686 0.165190087 0.246238756 0.14304222 0.26133498 0.18764163
K06232 K04630 K11128 K11128 K11129 K05141 K12885 K12885 K12885 K11296 K11296 K11307 K11251 K108024 K09349 K0540 K0	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRSH HNST2, HB01, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPA TITGB1 IFITM LILT2 LIGR LIFE LIGR LIFE LIFE LIFE RP-L13, RRPL13 RP-L12, RRPL2, rpIV RP-L22, RRPL22, rpIV RR-L22, RPL22	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA ribonucleoprotein complex subunit 1 H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein B histone actyltransferase MYST2 [EC:2.3.1.48] histone HAA histone HAA histone HAA histone HAB histone HAX histone HBA	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040082 Nerine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko05043 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA NA Ko003040 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulat NA NA Ko003040 Arginine and prolline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 P18K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interaction ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway; NA Ko00900 Terpenoid backbone biosynthesis NA Ko00310 Ribosome ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.54 -0.55 -0.66 -0.40 -0.56 -0.43 -0.45 -0.44 -0.42 -0.66 -0.45 -0.45 -0.49 -0.56 -0.41 -0.69 -0.41 -0.47 -0.48	0.0044 0.0934 0.0185 0.0165 0.0363 0.0176 0.0419 0.00172 0.00172 0.0052 0.0016 0.0031 0.0031 0.0001 0.0001 0.0002 0.0016 0.0024 0.0016 0.0024 0.0016 0.0024 0.0024 0.0024 0.0034	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.269922686 0.165190087 0.246238756 0.155190087 0.246238756 0.16390087 0.143042222 0.168745194 0.197085215 0.143042222 0.165190087 0.143042222 0.165190087 0.143042222 0.1520453 0.143042222 0.1520453 0.143042222 0.1520453 0.143042222 0.1520453 0.168745194
K06232 K04630 K11128 K11128 K11128 K11130 K09414 K12885 K11307 K11251 K08024 K01307 K05719 K0	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPAB HHNRNPAB HHNRPAB HHNRNPAB HHNRNPAB HHNRNPAB HHSB HHSB HHSB HHSB HHSB HHSB HISB HIS	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2A histone H2B homeobox protein HEX homeobox protein	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA ko050340 Alcoholism; ko05322 Systemic lupus erythematosus ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko00330 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway, NA ko04051 PI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.54 -0.55 -0.66 -0.40 -0.56 -0.63 -0.45 -0.41 -0.44 -0.42 -0.66 -0.45 -0.49 -0.49 -0.49 -0.49 -0.69 -0	0.0044 0.0935 0.0185 0.0166 0.0064 0.0363 0.0176 0.0411 0.0452 0.0016 0.0077 0.0017 0.0008 0.0017 0.0001 0.0007 0.	0.181/0852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.206202268 0.165190087 0.246238756 0.14304222 0.246238756 0.143042222 0.261133498 0.156190087 0.143042222 0.14304222 0.143042222 0.14304222 0.14304222
K06232 K04630 K11128 K11128 K111120 K09141 K12885 K12885 K11296 K11296 K11296 K11307 K11251 K08024 K11307 K1155 K08024 K11394 K09339 K05055 K13089 K13089 K13080 K1	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HHRNNPABD HHRNNPABD HHRNNPAB HHRNPABO HRMSB3 MYST2, HBO1, KAT7 HZA HZB HEX, HEX, PRH HLX1 HLX1 HLX1 HLX1 HLX1 HLX1 HLX2 HLX3 HRBP2 PROODH2 PROODH2 PROODH2 HRMSB3 HRBP1 HRBP1 HRBP1 HRBP1 HRBP1 HRBP1 HRBP1 RP-L12, MRPL21, rpIU RR-L22, MRPL22, rpIV RR-L22, MRPL22, rpIV RR-L22, MRPL22, RPL24 RR-L24A, RPL24 RR-L24A, RPL24 RR-L24A, RPL24 RR-L24A, RPL24 RR-L24A, RPL24 RR-L24A, RPL24 RR-L27, MRRL27, rpmA	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 HACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein A histone heterogeneous nuclear ribonucleoprotein B histone heterogeneous heterogeneou	kood430 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko04008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03140 Legionellosis NA NA Ko05140 Legionellosis NA NA Ko05040 Spliceosome NA NA Ko05040 Alcoholism; ko05322 Systemic lupus erythematosus ko05040 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00303 Arginine and proline metabolism ko00190 Oxidative phosphonylation ko04195 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway, ko04060 Cytokine-cytokine receptor interaction interaction; ko04066 HIF-1 signaling pathway, ko040510 Focal adhesion; ko04512 ECM-recep ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.54 -0.55 -0.63 -0.63 -0.63 -0.41 -0.54 0.44 -0.42 -0.45 -0.49 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.41 -0.47 -0.48 -0.49	0.0044 0.0095 0.0064 0.0064 0.0064 0.0063 0.00176 0.00172 0.0052 0.0017	0.1810/0852 0.165133463 0.165133463 0.200420738 0.200420738 0.200420738 0.260922268 0.165190087 0.246228756 0.143042222 0.168745194 0.197085215 0.165190087 0.143042222 0.16133498 0.1743042222 0.16133498 0.1743042222 0.16133498 0.1743042222 0.1613451417591 0.15204453 0.168745194 0.157088272 0.168745194 0.157088272 0.168745194 0.157088272 0.168735191 0.156190087 0.168785191 0.156190087 0.168785191 0.168785191 0.168785191 0.168785191 0.168785191 0.168785191 0.16878593 0.165190087 0.16889393 0.191417951 0.191417951 0.191417951 0.191417951 0.191417951 0.191417951
K06232 K04630 K01139 K11128 K11128 K11130 K09141 K12884 K12885 K11394 K12885 K11394 K11285 K11286 K11307 K08124 K1185 K08024 K10507 K05195 K04387 K05055 K04387 K05055 K04387 K05055 K02873 K02880 K02890 K02890 K02890 K02890 K02890	GAS1 GNAI SpOT, HDDC3 GAR1, NOLA1 NIP2, NOLA2 NOP10, NOLA3 HSTS1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNKBB HMGB3 MYST2, HB01, KAT7 HZA HZB HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPB TITGB1 IFITM ILITE2 ILIGR ILIF2 ILIFR ILIF2 ILIFR I	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2B homeobox protein HEX integrin beta 1 interferon induced transmembrane protein interfeukin 1 receptor type II interfeukin Greceptor vipe II interfeukin Greceptor subunit flosopha guaninin, beta 1 large subunit ribosomal protein L12 large subunit ribosomal protein L22 large subunit ribosomal protein L22 large subunit ribosomal protein L24	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA Ko05134 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe Ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00300 Arginine and proline metabolism Ko00190 Oxidative phosphorylation Ko04145 Phagoome; ko04151 PJRK-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior Ko04060 Cytokine-cytokine receptor interaction; ko04066 HiF-1 signaling pathway NA Ko000000 Terpenoid backbone biosynthesis NA Ko00310 Ribosome Ko03101 Ribosome Ko03101 Ribosome Ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.54 0.63 -0.41 -0.54 0.48 0.75 0.40 0.66 0.45 0.63 0.63 0.64 0.75 0.41 0.54 0.69 0.75 0.41 0.54 0.69 0.41 0.40 0.40 0.41 0.44 0.49 0.41 0.41 0.44 0.49 0.41 0.41 0.41	0.0044 0.0095 0.0066 0.0064 0.0077 0.0016 0.0016 0.0017 0.0016 0.0021 0.0021 0.0037 0.0016 0.0017 0.0017 0.0017 0.0017 0.0017 0.0018 0.0037 0.0018 0.0037 0.0019 0.	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.200420738 0.165190087 0.246238756 0.143042222 0.168745194 0.197085215 0.143042222 0.156190087 0.143042222 0.1504087 0.143042222 0.1504087 0.1504087 0.1504087 0.1504087 0.1504087 0.1504087 0.1504087 0.168745194 0.200909052 0.165130463 0.185945194 0.200909052 0.165130463 0.1651900605 0.165130463 0.1651900605 0.165130463 0.1651900605 0.165130463 0.1651900605 0.165130463 0.1651900605 0.165130463 0.1651900605 0.165130463 0.1651900605
K06222 K04630 K0139 K11128 K11129 K11129 K11129 K11129 K11129 K11129 K1129 K11	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNP2, NOLA2 NOP10, NOLA3 NSF1 HHRNPABD HILTR HI	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX interior H2B homeobox protein H2C interior H2B homeobox protein H2C interior H2B homeobox protein H2C interior H2B interior H2B homeobox protein H2C interior H2B interior H	koo440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040023 O Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05034 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05030 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04090 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko04030 Arginine and proline metabolism ko00300 Oxidative phosphorylation ko04145 Phagosome; ko04151 P13K-Akt signaling pathway; ko04360 Axon guidance NA Ko04100 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway, NA Ko04050 Terpenoid backbone biosynthesis NA KO0410 Ribosome Ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.54 -0.55 -0.63 -0.63 -0.63 -0.41 -0.54 0.44 -0.42 -0.45 -0.49 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.41 -0.47 -0.48 -0.49	0.0044 0.0093 0.0185 0.0469 0.0064 0.0363 0.0176 0.0419 0.0362 0.0016 0.0017 0.0017 0.0017 0.0024 0.0036 0.0017 0.0024 0.0036 0.0017 0.0027 0.0037 0.0038 0.0018 0.0018 0.0018 0.0019	0.1810/0852 0.165133463 0.165133463 0.200420738 0.200420738 0.200420738 0.260922268 0.165190087 0.246228756 0.143042222 0.168745194 0.197085215 0.165190087 0.143042222 0.16133498 0.1743042222 0.16133498 0.1743042222 0.16133498 0.1743042222 0.1613451417591 0.15204453 0.168745194 0.157088272 0.168745194 0.157088272 0.168745194 0.157088272 0.168735191 0.156190087 0.168785191 0.156190087 0.168785191 0.168785191 0.168785191 0.168785191 0.168785191 0.168785191 0.16878593 0.165190087 0.16889393 0.191417951 0.191417951 0.191417951 0.191417951 0.191417951 0.191417951
K06232 K04630 K01139 K11128 K11130 K05114 K12894 K11285 K11307 K111281 K11281 K	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNIP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNRNPAB HNRNPAB HNRSH HNST2, HB01, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HLX1 HABP2 PRODH2 PPA TIGGI LIFT LIFT LIFT LIFT LIFT LIFT LIFT LIF	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA ribonucleoprotein complex subunit 2 H/ACA ribonucleoprotein complex subunit 3 heat-shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein B histone acetyltransferase MYST2 [EC:2.3.1.48] histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A histone H2A histone H2B homeobox protein HEX homeo	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA Ko05134 Legionellosis NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe Ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko00300 Arginine and proline metabolism Ko00190 Oxidative phosphorylation Ko04145 Phagoome; ko04151 PJRK-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior Ko04060 Cytokine-cytokine receptor interaction; ko04066 HiF-1 signaling pathway NA Ko000000 Terpenoid backbone biosynthesis NA Ko00310 Ribosome Ko03101 Ribosome Ko03101 Ribosome Ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.54 -0.55 -0.60 -0.63 -0.63 -0.41 -0.54 -0.42 -0.63 -0.41 -0.54 -0.69 -0.52 -0.68 -0.17 -0.54 -0.59 -0.69 -0.41 -0.54 -0.69 -0.69 -0.52 -0.68 -0.41 -0.54 -0.69 -0.41 -0.40 -0.4	0.0044 0.0098 0.0469 0.0363 0.0176 0.0451 0.0016 0.0016 0.0077 0.0172 0.0015 0.0001 0.	0.1810/0852 0.165133463 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.26902268 0.165190087 0.246238756 0.143042222 0.261133498 0.197085215 0.16319037 0.234193498 0.197085215 0.163042222 0.261133498 0.18764163 0.18764163 0.18764163 0.18764163 0.18764163 0.18764163 0.18764163 0.18764163 0.168745194 0.16
K06222 K04630 K01139 K11128 K11129 K11121 K1129 K11129 K11129 K11129 K1129 K11	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 HSF1 HHNRNPABD HHSB3 HHSB3 HHSB4 HBB4 HBB7 HBB7 HBB7 HBB7 HBB7 HBB7 HB	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2A histone H2B homeobox protein HEX homeobox protein LE2 large subunit ribosomal protein LE2 large subunit ribosomal protein LE3 large subunit ribosomal prote	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03134 Legionellosis NA NA ko003040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko00303 Arginine and prolline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 P18K-Akt signaling pathway; ko04360 Axon guidance NA ko004100 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interaction ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway, NA ko00300 Terpenoid backbone biosynthesis NA ko00310 Ribosome ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.54 0.66 -0.40 0.55 -0.63 -0.63 -0.41 -0.54 -0.44 -0.42 -0.66 -0.40 -0.50 -0.69 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.41 -0.40 -0.41 -0.43 -0.43 -0.43 -0.44	0.0044 0.0095 0.0469 0.0064 0.0054 0.0076 0.0016 0.0017 0.0016 0.0077 0.0017 0.0027 0.0016 0.003 0.0017 0.0027 0.0017 0.0027 0.0017 0.0028 0.0017 0.0028 0.0017 0.0028 0.0017 0.0028 0.0017 0.0018 0.0019 0.0	0.18100852 0.165133463 0.178297363 0.200420738 0.200420738 0.2092268 0.165190087 0.2446238756 0.1598991113 0.254344055 0.254344055 0.1598052 0.168745194 0.197085215 0.163190087 0.163190087 0.163190087 0.143042222 0.150133483 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.15204453 0.143042222 0.1520453 0.143042222 0.1520453 0.143042222 0.1520453 0.168751991 0.1685991113 0.1986991113 0.1986999113 0.196899943 0.196899943 0.172622126 0.1247118814
K06222 K04630 K0139 K11128 K11129 K11130 K11129 K11130 K11129 K11130 K11284 K11284 K11284 K11284 K11284 K11285 K11296 K11307 K11251 K11252 K11251 K11	GAS1 GNAI SpOT, HDDC3 GAR1, NOLA1 NNIP2, NOLA2 NOP10, NOLA3 HSTS HNRNPABD HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNKSB HMSBB HMSB HMS	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2B homeobox protein HEX integrin beta 1 interferon induced transmembrane protein interfeukin 1 receptor type II interfeukin 1 receptor type II interfeukin 6 receptor type II interfeukin 6 receptor type II interfeukin 1 reliator 1 large subunit ribosomal protein L12 large subunit ribosomal protein L22 large subunit ribosomal protein L22 large subunit ribosomal protein L24 large subunit ribosomal protein L24 large subunit ribosomal protein L24 large subunit ribosomal protein L34 large subunit ribosomal protein L35 large subunit ribosomal protein L36 large subunit ribosomal prot	koo440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040023 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe Ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregula NA NA Ko003030 Arginine and proline metabolism Ko00190 Oxidative phosphorylation Ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior Ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway NA Ko00900 Terpenoid backbone biosynthesis NA Ko04015 IPI3K-Akt signaling pathway; ko04510 Focal adhesion; ko04512 ECM-receptosion Ribosome Ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.54 -0.66 -0.40 -0.63 -0.63 -0.63 -0.63 -0.45 -0.41 -0.55 -0.41 -0.54 -0.69 -0.59 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.40 -0.41 -0.40 -0.49 -0.41 -0.40 -0.49 -0.41 -0.40 -0.47 -0.48 -0.39 -0.41 -0.48 -0.39 -0.41 -0.48 -0.39 -0.41 -0.55	0.0044 0.0093 0.0466 0.0064 0.0064 0.0064 0.0017 0.0016 0.0017 0.0017 0.0017 0.0031 0.0017 0.0031 0.0017 0.0031 0.0017 0.0031 0.0017 0.0031 0.0017 0.0031 0.0017 0.	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.200420738 0.165190087 0.246238756 0.143042222 0.1637363 0.158745194 0.197085215 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.143042222 0.168745194 0.1570882793
K06222 K04630 K01139 K11128 K111130 K111129 K11130 K11129 K11130 K11129 K11130 K1129 K11130 K1129 K112	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 NSF1 HHRNPABD HRNPABD HRNP	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MfST2 [EC:2.3.1.48] histone H2A histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HIX interior High and the subunit ribosomal protein 1 interferon induced transmembrane protein interleukin 1 receptor type II interferon induced transmembrane protein interleukin 1 receptor type II interleukin 1 receptor type II interleukin 1 receptor type II interleukin 1 receptor 1 large subunit ribosomal protein L12 large subunit ribosomal protein L12 large subunit ribosomal protein L2a large subunit ribosomal protein L3a	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko0400230 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA NA Ko03040 Spliceosome NA NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko05034 Alcoholism; ko05303 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA Ko040300 Arignine and proline metabolism ko00300 Oxidative phosphorylation ko01435 Phagosome; ko04151 P13K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko0460 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway. NA Ko04010 RIbosome ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.55 0.66 -0.63 -0.40 -0.56 -0.41 0.48 0.75 0.44 0.48 0.75 0.44 -0.40 -0.40 -0.41 -0.40 -0.41 -0.43 -0.43 -0.41 -0.40 -0.41 -0.43 -0.43 -0.41 -0.44 -0.49 -0.40 -0.40 -0.40 -0.41 -0.41 -0.45 -0.40 -0.40 -0.41 -0.41 -0.45 -0.55 -0.48 -0.50	0.0044 0.0094 0.0185 0.0469 0.0064 0.0064 0.0074 0.0015 0.0016 0.0077 0.0015 0.0016 0.0017 0.0018 0.	0.18100852 0.165133463 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.206202268 0.165190087 0.246238756 0.143042222 0.168745194 0.197085215 0.143042222 0.1615190087 0.143042222 0.1615190087 0.143042222 0.1615190087 0.143042222 0.1615190087 0.1508745194 0.15708252 0.1508745194 0.1508875193 0.1568959932 0.19117951 0.1568959932 0.19117951 0.1568959932 0.19147951 0.196890931
K05222 K04630 K11128 K11129 K11120 K11120 K11120 K11120 K11120 K11281 K1281 K12	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNRNPAB HNST2, HB01, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HLX1 HABP2 PRODH2 PPA ITGB1 IFITM LILT2 LIGR LIF2 LIGR LIF2 LIGR LIF2 LIGR LIF2 LIGR RP-L13, MRPL27, rpIU RP-L22, MRPL27, rpIU RP-L22, RRPL23 RR-L34e, RPL34 RP-L31e, RPL31 RR-L34e, RPL31 RR-L34e, RPL34 RR-L34e, RPL37 RR-L36e, RPL37 RR-L36e, RPL37 RR-L37, FRR-L37, FRR-R-L37 RR-L36e, RPL37 RR-L36e, RPL37 RR-L36e, RPL37 RR-L37, FRR-L37, FRR-R-L37 RR-L36e, RPL37 RR-L36e, RPL37 RR-L37, FRR-L37, FRR-R-L37 RR-L36e, RPL37 RR-L36e, RPL37 RR-L36e, RR-L36e, RPL37 RR-L36e, RR-L	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein B histone acetyltransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A histone H2B homeobox protein HEX homeofox protein HEX homeofox protein HIXI interferon induced transmembrane protein interferucle in Teceptor type il interferucle i	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03040 Splicesome NA NA ko03040 Splicesome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko00303 Arginine and proline metabolism ko00190 Oxidative phosphorylation NA ko00303 Arginine and proline metabolism ko00190 Oxidative phosphorylation NA ko00303 Arginine and proline metabolism ko00410 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interaction ko04060 Cytokine-cytokine receptor interaction; ko04066 HiF-1 signaling pathway; NA ko00300 Ribosome ko03010 Ribosome		0.49 0.39 0.52 0.61 0.52 0.66 0.63 0.40 0.56 0.63 0.41 0.54 0.42 0.66 0.43 0.45 0.49 0.49 0.49 0.49 0.49 0.49 0.49 0.49	0.0044 0.0094 0.0185 0.0469 0.0054 0.0054 0.0071 0.0052 0.0016 0.0077 0.0021 0.0035 0.0008 0.0078 0.0035 0.0008 0.0035 0.	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.2092268 0.165190087 0.2446238756 0.155190087 0.2446238756 0.156190087 0.143042222 0.1668745194 0.197085215 0.197085215 0.143042222 0.150143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165130484 0.190143042222 0.165145194 0.190143042222 0.165145194 0.190143042222 0.165145194 0.190145194
K06222 K04630 K01139 K11128 K11129 K111120 K11121 K11129 K11129 K11129 K11129 K11129 K1129	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 HSF1 HHNRNPABD HHRS, HBD1, KAT7 HZA HZB HHEX, HEX, PRH HLX1 ILIZ ILIZ ILIZ ILIZ ILIZ ILIZ ILIZ ILI	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A0 heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2A histone H2B homeobox protein HEX homeobox prot	koo440 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040023 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA NA Ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus Ko05034 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe Ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregula NA NA Ko003030 Arginine and proline metabolism Ko00190 Oxidative phosphorylation Ko04145 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA Ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior Ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway NA Ko04010 RPK signaling pathway; ko04510 Focal adhesion; ko04512 ECM-recep Ko03010 Ribosome		0.49 0.39 0.52 0.61 0.54 0.60 0.63 0.45 0.63 0.45 0.64 0.63 0.45 0.63 0.45 0.40 0.65 0.63 0.45 0.63 0.45 0.63 0.45 0.63 0.45 0.49 0.65 0.49 0.65 0.63 0.65 0.63 0.65 0.65 0.65 0.65 0.65 0.65 0.65 0.65	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0362 0.0016 0.0052 0.0016 0.0077 0.0015 0.0016 0.0027 0.0027 0.0018 0.0018 0.0018 0.0018 0.0019 0.	0.1810/0852 0.165133463 0.1052133463 0.200420738 0.200420738 0.200420738 0.200420738 0.269022868 0.165190087 0.246238756 0.143042222 0.168745194 0.197085215 0.18764167 0.239193287 0.143042222
K05222 K04630 K01139 K11128 K11130 K11128 K11304 K12889 K11307 K11251 K11307 K11251 K11307 K11251 K11307 K11251 K11307 K11251 K11252 K11307 K1251 K11307 K1251 K11307 K1251 K11307 K1251 K11307 K1251	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNRNPAB HNRSH HMS1, HB01, KAT7 H2A H2B HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPA TIGG1 IFITM LITG2 LIGR LIFE LIGR LIFE LIFE LIFE LIFE RP-L12, MRPL21, rpIU RP-L22, MRPL22, rpIV RR-L24, RPL23 RR-L34, RPL31 RR-L31, RPL31 RR-L31, RPL31 RR-L31, RPL31 RR-L32, RPL32 RR-L34, RRPL32, rpIF RP-L32, MRPL32, rpII RR-L36, MRPL36, rpII MRPL46 MRPL47, NCM1 MRPL46 MRPL47, NCM1 MRPL46 MRPL47, NCM1	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-37, S-bis(diphosphate) 3', pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein B histone actyltransferase MYST2 [EC:2.3.1.48] histone HAA histone HAA histone HAA histone HAA histone HAB histone HAB histone HEX homeobox protein HEX histone HAB histone	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002080 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA Ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko03043 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko04050 Alcoholism; ko05322 Systemic lupus erythematosus ko04050 Alcoholism; ko05322 Systemic lupus erythematosus ko04050 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04050 Alcoholism; ko05323 Viral carcinogenesis; ko05322 Transcriptional misregulat NA NA KO00300 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04160 Pulgasoome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA ko00000 Terpenoid backbone biosynthesis NA ko00000 Terpenoid backbone biosynthesis NA ko00310 Ribosome ko03101 Ribosome ko03101 Ribosome ko03010 Ribosome		0.49 0.39 0.52 -0.61 -0.52 0.66 -0.40 -0.56 -0.41 -0.54 -0.41 -0.42 -0.63 -0.45 -0.49 -0.41 -0.40 -0.40 -0.40 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.40 -0.41 -0.43 -0.41 -0.43 -0.41 -0.43 -0.41 -0.43 -0.41 -0.43 -0.41 -0.43 -0.40 -0.51 -0.41	0.0044 0.0094 0.0185 0.0469 0.0056 0.0017 0.0051 0.0017 0.0017 0.0017 0.0017 0.0021 0.0017 0.0021 0.0017 0.0021 0.0017 0.0021 0.0017 0.0021 0.0017 0.0021 0.0017 0.0021 0.0021 0.0021 0.003 0.00	0.1810/0852 0.165133463 0.178297363 0.200420738 0.200420738 0.200420738 0.269222686 0.165190087 0.246238756 0.165190087 0.246238756 0.1630087 0.143042222 0.168745194 0.197085215 0.1691087 0.143042222 0.168745194 0.197085215 0.143042222 0.1520453 0.1530453 0.1530453 0.1530453 0.1530453 0.1530453 0.168745194 0.16874519
K05222 K04630 K11128 K11129 K11121 K1129 K11129 K11129 K11129 K11129 K1129 K11	GAS1 GNAI SpOT, HDDC3 GAR1, NOLA1 NNIP2, NOLA2 NOP10, NOLA3 HSTS HNRNPABD HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPG HMGB3 MYST2, HB01, KAT7 HZA HZB HHEK, HEX, PRH HLX1 HABP2 PRODH2 PPB ITGB1 IFITM ILIT2 ILIGR ILIF2 ILIGR ILIF2 ILIGR ILIF2 ILIGR ILIF2 ILIGR ILIF2 ILIFA RP-L13e, RPL13 RP-L13e, RPL13 RP-L22, MRPL21, rpIU RR-L22, GRPL22 RR-L22, RRPL23 RR-L24e, RPL23 RR-L24e, RPL23 RR-L34e, RPL34 RR-L36, RPL31 RR-L36, RPL32 RR-L37, MRRL32, rpmF RR-L36, RRPL32 RR-L37, MRRL32, rpmF RR-L36, MRRL32, rpmI RR-L37, MRRL32 RR-L38, MRRL32 RR-L38, MRRL32 RR-L39, MRRL32 RR-L36, MRRL36 RRPL47, MRRL41 MRRL41 MRRL41 MRRL41 MRRL41 MRRL41 MRRL42 MRRL41 MRRL	growth arrest-specific 1 guannian encleotide-binding protein G(i) subunit alpha guannian encleotide-binding protein G(i) subunit alpha guannian-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA fhonucleoprotein complex subunit 2 H/ACA fhonucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone H2A histone H2B homeobox protein HEX integrin beta 1 interferon induced transmembrane protein interfeukin 1 receptor type II interfeukin 1 receptor type II interfeukin 6 receptor interleukin 6 receptor type II interleukin 6 receptor type II interleukin 6 receptor type II interleukin 1 relation 1 lata large subunit ribosomal protein L22 large subunit ribosomal protein L22 large subunit ribosomal protein L22 large subunit ribosomal protein L24 large subunit ribosomal protein L34 large subunit ribosomal protein L36 large subunit ribosomal protein L41 large subunit ribosomal protein L41 large subunit ribosomal protein L41 large subunit ribosomal protein L43 large subunit ribosomal protein L44 large subunit ribosomal protein L45 large subunit ribosomal protein L43 large subunit ribosomal protein L43 large subunit ribosomal protein L54 large subunit ribosomal protein L54 large subunit ribosomal protein L54 large subunit ribosomal pro	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko003030 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04150 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interactior; ko04066 HIF-1 signaling pathway NA ko003010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.55 0.66 -0.40 -0.40 -0.41 -0.44 0.48 0.44 0.44 0.48 0.45 -0.41 0.63 -0.45 -0.63 -0.45 -0.63 -0.45 -0.63 -0.45 -0.40 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.40 -0.73 -0.50 -0.50 -0.50 -0.50 -0.40 -0.73 -0.50 -0.50 -0.40 -0.73 -0.50 -0.5	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.00172 0.00172 0.00172 0.00172 0.00172 0.00172 0.00172 0.00172 0.00172 0.00174 0.001	0.18100852 0.165133463 0.200420738 0.200420738 0.200420738 0.200420738 0.200420738 0.165190087 0.246238756 0.143042222 0.16874519 0.197085215 0.168745194 0.197085215 0.143042222 0.161320463 0.15204453 0.15204453 0.168745194 0.1006905052 0.168745194 0.1006905052 0.168745194 0.1006905052 0.168745194 0.1006905052
K06222 K04630 K0139 K11128 K11129 K11130 K09414 K12894 K11304 K12895 K11996 K11307 K09624 K09339 K09638 K09	GAS1 GNAI SPOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 NSF1 HHRNPABD HHRS, HBDI, KAT7 HZA HZB HHEX, HEX, PRH HLX1 HABP2 PROOHIZ PROOHIZ HIGH HITT HITT	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein B histone acetyltransferase MYST2 [EC:2.3.148] histone HZA histone	koo4340 Hedgehog signaling pathway koo4062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko040082 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko04008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03008 Ribosome biogenesis in eukaryotes ko03140 Legionellosis NA		0.49 0.39 0.52 0.61 0.54 0.55 0.66 0.63 0.63 0.43 0.44 0.44 0.48 0.75 0.68 0.69 0.41 0.54 0.40 0.40 0.66 0.45 0.39 0.41 0.54 0.40 0.41 0.54 0.40 0.41 0.54 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.40 0.41 0.41	0.0041 0.0094 0.0185 0.0469 0.0064 0.0064 0.0071 0.0012 0.0016 0.0071 0.0017 0.0016 0.0017 0.	0.18100852 0.165133463 0.178297363 0.200420738 0.200420738 0.200420738 0.200420738 0.269022686 0.165190087 0.246238756 0.143042222 0.168741914 0.197085215 0.143042222 0.1615190087 0.143042222 0.1615190087 0.143042222 0.1615190087 0.157082215 0.15708222 0.143042222 0.16374114 0.15708227 0.158741519 0.1570827 0.158741519 0.1570827 0.158741519 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827 0.158745191 0.1570827
K05222 K04630 K11128 K11129 K11129 K11120 K11129 K11120 K11129 K11120 K11285 K11296 K11296 K11297 K11251 K11251 K11252 K11296 K11297 K11251 K11252 K11296 K11297 K11251 K11251 K11252 K11296 K11297 K11251 K12261 K1	GAS1 GNAI SpOT, HDDC3 GAR1, NOLA1 NHP2, NOLA2 NOP10, NOLA3 HSF1 HNRNPABD HNRNPABD HNRNPABD HNRNPABD HNRNPAB HNRNPAB HNKSBB MYST2, HB01, KAT7 HZA HZB HHEK, HEX, PRH HLX1 HABP2 PRODH2 PR	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guansine-3; 5-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.17.2] H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone explytransferase MYST2 [EC:2.3.1.48] histone H2A histone H2A histone H2B homeobox protein HEX integrino exidase [EC:1.5] inorganic pyrophosphatase [EC:3.6.1.1] interferon induced transmembrane protein interleukin receptor type ii interleukin erhancer-binding factor 2 isopentenyi-diphosphate delta-isomerase [EC:5.3.3.2] krueppel-like factor 2 lange subunit ribosomal protein L12e lange subunit ribosomal protein L2a lange subunit ribosomal protein L2a lange subunit ribosomal protein L3a lange subunit ribosomal protein L4a lange subunit ribosomal protein L5a lange subunit ribosomal protein L5a lange subunit ribosomal protein L5a lange subunit ribosomal protein L5	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Spliceosome NA NA Ko03040 Spliceosome NA NA ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregulal NA NA ko003030 Arginine and proline metabolism ko00190 Oxidative phosphorylation ko04150 Phagosome; ko04151 PI3K-Akt signaling pathway; ko04360 Axon guidance NA ko04010 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interactior; ko04066 HIF-1 signaling pathway NA ko003010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.55 0.66 -0.40 -0.40 -0.41 -0.44 0.48 0.44 0.44 0.48 0.45 -0.41 0.63 -0.45 -0.63 -0.45 -0.63 -0.45 -0.63 -0.45 -0.40 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.50 -0.40 -0.73 -0.50 -0.50 -0.50 -0.50 -0.40 -0.73 -0.50 -0.50 -0.40 -0.73 -0.50 -0.5	0.0044 0.0094 0.0185 0.0469 0.0064 0.0363 0.0176 0.0017 0.0021 0.0021 0.0032 0.0008 0.0007 0.0035 0.0008 0.	0.1810/0852 0.165133463 0.178297363 0.200420738 0.200420738 0.200420738 0.2064208756 0.165190087 0.246238756 0.143042222 0.168745194 0.197085215 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.143042222 0.168745194 0.197085215 0.168745194 0.108745194
K06222 K04630 K01139 K11128 K11129 K111120 K11121 K11121 K11251 K11251 K11251 K11251 K11252 K11251 K11251 K11252 K11251 K11251 K11251 K11251 K11252 K11251 K	GAS1 GNAI SpOT, HDDC3 GAR1, NOLA1 NNHP2, NOLA2 NOP10, NOLA3 HSF1 HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPABD HHNRNPABD HHRNPABD HHRNPABD HHRNPABD HHRS, HBD1, KAT7 H2A H2B HHEX, HEX, PRH HLX1 ILIA ILIA ILIA ILITA	growth arrest-specific 1 guanine nucleotide-binding protein G(i) subunit alpha guanine nucleotide-binding protein G(i) subunit alpha guanosine-3; 5-bis (diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2] H/ACA flobnucleoprotein complex subunit 1 H/ACA flobnucleoprotein complex subunit 2 H/ACA flobnucleoprotein complex subunit 3 heat shock transcription factor 1 heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein A/B/D heterogeneous nuclear ribonucleoprotein AO heterogeneous nuclear ribonucleoprotein G high mobility group protein B3 histone acetyltransferase MrST2 [EC:2.3.1.48] histone H2A histone H2A histone H2B homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HEX homeobox protein HIX ingulurona binding protein 2 [EC:3.4.21] hydroxyproline oxidase [EC:3.6.1.1] interferon induced transmembrane protein interleukin 1 receptor type II interferon induced transmembrane protein interleukin 6 receptor interleukin 6 receptor interleukin enhancer-binding factor 2 sospentenyl-diphosphate delta-isomerase [EC:5.3.3.2] krueppel-like factor 2 aminin, bet a 1 large subunit ribosomal protein L12a large subunit ribosomal protein L2a large subunit ribosomal protein L2a large subunit ribosomal protein L3a large subunit ribosomal protein L5a large subunit ribosomal protein L5a large subunit ribos	koo4340 Hedgehog signaling pathway ko04062 Chemokine signaling pathway; ko04360 Axon guidance; ko04530 Tight jur ko002030 Purine metabolism ko03008 Ribosome biogenesis in eukaryotes ko03040 Ribosome biogenesis in eukaryotes ko03040 Splicesome NA NA ko050340 Alcoholism; ko05322 Systemic lupus erythematosus ko03040 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05322 Systemic lupus erythematosus ko05034 Alcoholism; ko05203 Viral carcinogenesis; ko05322 Systemic lupus erythe ko04950 Maturity onset diabetes of the young; ko05202 Transcriptional misregula NA ko00300 Arginine and prolline metabolism ko00190 Oxidative phosphorylation ko04145 Phagosome; ko04151 PlaS-kAt signaling pathway; ko04360 Axon guidance NA ko004100 MAPK signaling pathway; ko04060 Cytokine-cytokine receptor interactior ko04060 Cytokine-cytokine receptor interaction; ko04066 HIF-1 signaling pathway, NA ko003010 Ribosome ko03010 Ribosome		0.49 0.39 -0.52 -0.61 -0.54 -0.56 -0.40 -0.63 -0.43 -0.41 -0.44 -0.42 -0.69 -0.41 -0.44 -0.49 -0.40 -0.41 -0.40 -0.40 -0.41 -0.41 -0.43 -0.45 -0.40 -0.45 -0.55 -0.5	0.0041 0.0094 0.0185 0.0469 0.0064 0.0064 0.0072 0.0016 0.0072 0.0016 0.0072 0.0018 0.0021 0.0018 0.0019 0.	0.1810/0852 0.165133463 0.178297363 0.200420738 0.200420738 0.200420738 0.200420738 0.269022686 0.165190087 0.246238756 0.143042222 0.165190087 0.143042222 0.15204430 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.18519081 0.196891113 0.15519081 0.19689912 0.196899113 0.176822126 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.19689113 0.196890943 0.19689113 0.19689932 0.19689932 0.19689932 0.19689932 0.19689934

1982   1982	K00650 LCAT	lecithin-cholesterol acyltransferase [EC:2.3.1.43]	ko00564 Glycerophospholipid metabolism	0.46 0.0274 0.223998206
March   Marc	K01059 LPL	lipoprotein lipase [EC:3.1.1.34]		0.51 0.0017 0.143042222
10.000   10.0000   10.0000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.0000000   10.0000000   10.0000000   10.0000000000				
STAILS   Control of the August and Security Contr				
CHEFF  1997-1997   Comment of the PECE SEAT	K15135 MED18	mediator of RNA polymerase II transcription subunit 18		-0.42 0.0096 0.17983084
1,000   1,00		·		
1000   1737   1745				
MEMORY   Memory in the property of the prope	K00869 E2.7.1.36, MVK, mvaK1			-0.50 0.0048 0.165133463
1779   TOTAL   Inches				
1,1799 (1926)				-0.44 0.0254 0.220819904
MILESTONS   Imboundaria import recognize shared TOMAS   MILESTONS   MILESTON				
\$1777 0966				
\$1,777   ONG				-0.47 0.0021 0.14321829
SLASS PRINTED	K17772 TOM6			-0.49 0.0218 0.210559277
SEASO ACT   No. 14 per Season Seaso				
\$1,000 AVAIROR				
MODIS   MODIAL   Mode (eight eight person betanger)   1999 a subcomplex south 11   MODIS   M			ko04723 Retrograde endocannabinoid signaling	0.38 0.0017 0.143042222
MODES   DODAZA   Mode templemental deviaments   1 pages accomplex accomplex   1 pages   1 page				
MODIFICATION   Modified in physical poliuminosis   124 pill parts automorphis   1				
MOST   MAINT ethylogenesic (bigspening 1 bits abbetragins abbort)   MAINT ethylogenesic (bigspening 1 bits butter)   MAINT ethylogenesic (bitspening 1 bits butter)   MAINT ethylogenesic (bits butter)   MAINT ethylogenes				
MOST		NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 1	ko00190 Oxidative phosphorylation; ko04932 Non-alcoholic fatty liver disease (NA	-0.47 0.0044 0.165133463
MODIS   MODI				
MOSIDE CAPANAS   Neterminal particularies resigned exceptive shown   [C.2.1.18]   N. H. H. H. M. M. M. STAN, M. M. M. M. STAN, M.				
1.2889 (1972)   Concept on protect helps protect helps   1.2009/18/14/14/14/14/14/14/14/14/14/14/14/14/14/	K04807 CHRNA5	nicotinic acetylcholine receptor alpha-5	ko04080 Neuroactive ligand-receptor interaction	-0.40 0.0136 0.187355725
1.4.080 MOP3 GTC2   modeled proteorins 3				
1,4560   1,7552   1,7552   1,7552   1,5552   1				
12.1236 OPTALPH, GPTA, MICHAEL SIGN CONTRACTORS   10.0000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.00000   10.000000   10.00000   10.00000   10.00000   10.00000   10.00000   10.000000   10.00000   10.000000   10.00000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.000000   10.0000000   10.000000   10.000000   10.000000   10.000000   10.00000000   10.000000   10.0000000   10.000000   10.0000000   10.00000000   10.000000   10.0000000   10.0000000   10.0000000   10.000000000   10.00000000   10.0000000000				
MOZES   PRICE	K13288 orn, REX2, REXO2	oligoribonuclease [EC:3.1]	ko03008 Ribosome biogenesis in eukaryotes	
\$1,7259   PPILL				
MATTAPP   PRIL				
10.0794 FPTC				
KLASSE PMPS_UTFT				
1.0389   Priest, plants   phenylatury 48NA privateurs alpha chain (EC.1.1.2)   100076   Option (1900   Priest, priest)   100076   Option (1900   Priest, pri				
KISAMU LIP1				
MOSPAPE   EL1.130, NMT   phosphotethanolamies N methyltransferase [EC.2.1.1.03]   MOSPAPE   Action   Mospatibidide phosphatises [EC.3.1.3]   MOSPAPE   MOS				
Modified   Part				
MISSBB PLAIA   Phosphelipses A I member A [CC.3.1.1-]   NA   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism, isot0080 Methane metabolism   MO0250 Glycine, serine and threonine metabolism   MO0250 Gl				
MOSISS PRICE   plasmingen (EC.3.4.2.T)				
\$2,949.00				
NOZIO GANT				
MERISON DIVISIS, PRPAS   pre-mRNA-aplining factor API-dependent RNA helicase DH115/PRPAS   EC.3.   Mc00000 Splicescome and threonine metabolism, k000000 Tyrosine metabolism   0.43   0.0316   0.21790000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.000000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.00000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.000000   0.0000000   0.0000000   0.0000000   0.0000000   0.0000000   0.0000000   0.00000000				
MORBURD PLAN   Profiferating cell nuclear antigen   MoDBB	K12820 DHX15, PRP43			
MCRISTON DEST-1997 COPY   Depretagmental-T2D-isomerase [EC.2.1.125]   MCRISTON Proteins arginine N-methyltransferase [EC.2.1.125]   MCRISTON Protein NORGI   D. 103003 RNA transport; MCRISTON Protein Department of EC.2.1.125]   MCRISTON Protein NORGI   D. 103003 RNA transport; MCRISTON RNA   D.				
K1559 POMP_UMP1				
MAC     0.58   0.0360   0.24628795   MAC   0.58   0.0360   0.24628795   MAC   0.58   0.0360   0.24628795   MAC   0.0360   MAC   0.0				
NA   NA   NA   NA   NA   NA   NA   NA		protein arginine N-methyltransferase 5 [EC:2.1.1.125]		-0.49 0.0091 0.175063798
NA   0.033 0.133252686				
Mod   March   March				
K03738   DNA   purine-nucleoside phosphorylase [EC.24.2.1]				
K15306   RANBP1   Ran-binding protein 1	K03783 punA	purine-nucleoside phosphorylase [EC:2.4.2.1]		0.82 0.0015 0.143042222
K87906 RAB25   Ras-related protein Rab 25   Cal3804872   Cal3804872				
K09326 NR283, RXRG				
K00784 mr	K08526 NR2B3, RXRG	retinoid X receptor gamma	ko03320 PPAR signaling pathway; ko04920 Adipocytokine signaling pathway; ko05	0.46 0.0097 0.18029481
KL15433   CGI99, CLF7, RLLM1   RLL motif containing protein 1   NA   C03008 Ribosome biogenesis in eukaryotes; ko03013 RNA transport   -0.40   0.036   0.172822126   NA   0.0304   RNA-binding protein 5/10   NA   0.0304   0.0304   0.02821376   NA   0.0304   NRA-binding protein 5/10   NA   0.0304   0.02821376   NA   0.0304   0.0304   0.02821376   NA   0.0304   NA   0.0304   0.0304   0.0304   0.0304   NA				
K15432   CGIP9, CLE7, RILLM1   RLL motif containing protein 5   NA   0.030   0.229821398				
K13094   RBM5_10			, , ,	-0.42 0.0303 0.229821398
K12312   SAPI, SGP1   saposin   K04142 Lysosome   1,039   0,007   0,15513462   K16312   STR40, SHIK   serine/threonine-protein kinase QLEC.27.11.1]   NA   0,001   0,003   0,003   0,167353572   NA   NA   0,001   0,003   0,003   0,16735752   NA   NA   0,001   0,003	K13094 RBM5_10	RNA-binding protein 5/10		
K16925   STK40, SHIK   Serine/threonine-protein kinase 40 [CC-27.11.1]   NA     0.63   0.137357725   NOR5269   UK1_2_3_A TG1   Serine/threonine-protein kinase ULX/ATG1 [EC:27.11.1]   K004140 Regulation of autophagy; k004150 mTOR signaling pathway   0.38   0.0130   0.187357725   NOR5269   NA   NA   0.021   0.148042222   NA   0.022   0.0224   NA   0.02				
K08269   ULK1_2_3, ATG1				
K15141   ALB   serum albumin   NA   NANS, SAS   sialic acid synthase [EC.25.1.56 2.5.1.57]   k000520 Amino sugar and nucleotide sugar metabolism   0.40   0.052   0.165190087	K08269 ULK1_2_3, ATG1	serine/threonine-protein kinase ULK/ATG1 [EC:2.7.11.1]	ko04140 Regulation of autophagy; ko04150 mTOR signaling pathway	0.38 0.0103 0.182571981
K0520A   NANS, SAS   sialic acid synthase [EC-2.5.1.56 2.5.1.57]   k000520 Amino sugar and nucleotide sugar metabolism   -0.53   0.061   0.165190087   K11220   STAT1   signal transducer and activator of transcription 1   k004062 Chemokine signaling pathway; k004380 Osteoclast differentiation; k0046   -0.41   0.0277   0.223998.00   -0.49   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.143042222   0.001   0.001   0.143042222   0.001   0.001   0.001   0.001   0.001   0.143042222   0.001				
K11202   STAT1   signal transducer and activator of transcription 1   k004062 Chemokine signaling pathway; k004380 Osteoclast differentiation; k0046   0.41   0.027   0.22398206   0.481   0.027   0.23988206   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.43042222   0.49   0.0010   0.4304222   0.49   0.0010   0.4304222   0.49   0.0010   0.4304222   0.49   0.40   0.0010   0.4304222   0.49   0.40   0.4				
K11096   SNRPD2, SMD2   small nuclear ribonucleoprotein D2   k03040 Spliceosome   -0.49   0.010   0.143042222   0.125   0.12				
K11099 SNRPG, SMG         small nuclear ribonucleoprotein G         k03040 Spliceosome         -0.49         0.005         0.188745194           K02948 RP-S11, MRPS11, rpsK         small subunit ribosomal protein S11         k03010 Ribosome         -0.53         0.057         0.165190087           K02950 RP-S12, MRPS14, rpsN         small subunit ribosomal protein S12         k03010 Ribosome         -0.31         0.057         0.165190087           K02950 RP-S16, RP-S16         small subunit ribosomal protein S14         k03010 Ribosome         -0.47         0.019         0.02598506           K02950 RP-S16, RPS16         small subunit ribosomal protein S16e         k03010 Ribosome         -0.49         0.051         0.051510088           K16174 MRPS18B, MRPS18B, MRPS18B, VIA S10, RPS18B, VIA S10, RPS18B, VIA S10, RPS18B, VIA S10, RPS18B, VIA S10, RPS2B, RPS2B         K03010 Ribosome         -0.42         0.002         0.002         0.165190087           K02970 RP-S21, MRPS21, rpsU         small subunit ribosomal protein S2B         k03010 Ribosome         -0.42         0.009         0.180742394           K17404 MRPS25         small subunit ribosomal protein S2B         k03010 Ribosome         -0.42         0.009         0.180742394           K02976 RP-S25e, RPS25	K11096 SNRPD2, SMD2	small nuclear ribonucleoprotein D2	ko03040 Spliceosome	-0.49 0.0010 0.143042222
K02948 RP-511, MRP511, rpsk         small subunit ribosomal protein S11         k003010 Ribosome         — 0.68         0.066         0.165190087           K02954 RP-S12, mst, MRP512, rpst         small subunit ribosomal protein S12         k003010 Ribosome         — 0.73         0.0057         0.165190087           K02960 RP-S16e, RPS16         small subunit ribosomal protein S16e         k003010 Ribosome         — 0.49         0.003         0.165130468           K02962 RP-S17e, RPS17         small subunit ribosomal protein S16e         k003010 Ribosome         — 0.42         0.039         0.0259878           K02962 RP-S17e, RPS17         small subunit ribosomal protein S16e         k003010 Ribosome         — 0.42         0.039         0.165130468           K02960 RP-S20e, RPS20         small subunit ribosomal protein S20e         k003010 Ribosome         — 0.42         0.012         0.186740724           K02970 RP-S21, MRPS21, rpsU         small subunit ribosomal protein S20         k003010 Ribosome         — 0.42         0.090         0.180740724           K17404 MRPS25         small subunit ribosomal protein S25         NA         — 0.52         0.001         0.18040222           K02976 RP-S25e, RPS25         small subunit ribosomal protein S26e         k03010 Ribosome         — 0.50         0.001         0.18040222           K02976 RPS26         sm				
K02950 RP-512, MRP512, rpsL         small subunit ribosomal protein S12         k03010 Ribosome         — 0.53         0.057         0.165190087           K02954 RP-514, MRPS14, prsN         small subunit ribosomal protein S14         k03010 Ribosome         — 0.93         0.051         0.165133463           K02950 RP-516e, RPS16         small subunit ribosomal protein S16e         k03010 Ribosome         — 0.42         0.093         0.051         0.165133463           K02962 RP-517e, RPS17         small subunit ribosomal protein S17e         k009010 Ribosome         — 0.42         0.093         0.251981833           K02969 RP-520e, RPS20         small subunit ribosomal protein S20e         k03010 Ribosome         — 0.42         0.000         0.165190087           K02970 RP-521, MRPS21, rpsU         small subunit ribosomal protein S20e         k03010 Ribosome         — 0.42         0.000         0.165190087           K02970 RP-525, sps25         small subunit ribosomal protein S25         NA         — 0.52         0.001         0.180472394           K02976 RP-S25e, RPS25         small subunit ribosomal protein S26e         k03010 Ribosome         — 0.50         0.001         0.163642877           K02976 RPS26         small subunit ribosomal protein S26e         k03010 Ribosome         — 0.50         0.001         0.163642877           K02976 RPS26				
K02954 RP-516, MRP514, rpsN         small subunit ribosomal protein S14         k003010 Ribosome         — 0.47         0.090         0.020298808           K02956 RP-516, RP516 stopes         small subunit ribosomal protein S16e         k003010 Ribosome         — 0.42         0.093         0.051 313463           K16174 MRPS18, MRP518-2 stopes         small subunit ribosomal protein S18b, mitochondrial         k005203 Viral carcinogenesis         — 0.42         0.012         0.186740724           K02970 RP-520, RP520 stopes         small subunit ribosomal protein S20e         k003010 Ribosome         — 0.49         0.006         0.065100087           K17404 MRPS18, MRP51, rpsU         small subunit ribosomal protein S21         k003010 Ribosome         — 0.49         0.009         0.065100087           K17404 MRPS25         small subunit ribosomal protein S25         NA         — 0.52         0.001         0.143042222           K02976 RP-525e, RP525 stopes         small subunit ribosomal protein S25         NA         — 0.52         0.001         0.143042222           K02976 RP-526e, RP526 stopes         small subunit ribosomal protein S25         k03010 Ribosome         — 0.52         0.001         0.143042222           K02976 RP-526e, RP525 stopes         small subunit ribosomal protein S26         k03010 Ribosome         — 0.50         0.001         0.163642877				-0.53 0.0057 0.165190087
K02950, RP-517, RP517         small subunit ribosomal protein S17e         k03010 Ribosome         -0.42         0.033         0.51981833           K02969, RP-520e, RP520         small subunit ribosomal protein S18b, mitchondrial         k05203 Viral carcinogenesis         -0.42         0.030         0.186740724           K02959, RP-520e, RP520         small subunit ribosomal protein S20e         k063010 Ribosome         -0.42         0.009         0.185150088           K02970, RP-521, MRP521, rpSU         small subunit ribosomal protein S25         NA         -0.52         0.001         0.14027294           K02976, RP-525e, RP525         small subunit ribosomal protein S25e         k03010 Ribosome         -0.50         0.001         0.163642877           K02976, RP-526e, RP526         small subunit ribosomal protein S26e         k03010 Ribosome         -0.50         0.0021         0.168693932           K02976, RP-526e, RP526         small subunit ribosomal protein S26e         k03010 Ribosome         -0.50         0.0021         0.18689932           K02976, RP526         small subunit ribosomal protein S26e         k03010 Ribosome         -0.50         0.0021         0.18689932           K02976, RP526         small subunit ribosomal protein S26e         k03010 Ribosome         -0.50         0.0021         0.16869932           K02976, RP526         smal	K02954 RP-S14, MRPS14, rpsN	small subunit ribosomal protein S14	ko03010 Ribosome	-0.47 0.0190 0.202958509
K16174         MRP5188, MRP518-2         small subunit ribosomal protein S18b, mitochondrial         k005203 Viral carcinogenesis         — 0.42         0.012         0.186740724           K02969         RP-S20e, RP-S200         small subunit ribosomal protein S20e         k003010 Ribosome         — 0.49         0.009         0.165190083           K17404         MRPS12, MRPS21, rpsU         small subunit ribosomal protein S21         k03010 Ribosome         — 0.52         0.011         0.143042222           K02976         RP-S25e, RPS25         small subunit ribosomal protein S25e         k03010 Ribosome         — 0.50         0.001         0.143042222           K02976         RP-S26e, RPS26         small subunit ribosomal protein S26e         k03010 Ribosome         — 0.50         0.001         0.1685402877           K1741         MRPS34         small subunit ribosomal protein S26         k03010 Ribosome         — 0.50         0.001         0.1685402877           K1741         MRPS34         small subunit ribosomal protein S26         k03010 Ribosome         — 0.50         0.001         0.1685402877           K1741         MRPS34         small subunit ribosomal protein S26         k03010 Ribosome         — 0.50         0.001         0.168540287           K1741         MRPS34         small subunit ribosomal protein S34         NA				-0.39 0.0051 0.165133463
K02969 RP-S20e, RPS20         small subunit ribosomal protein S20e         ko03010 Ribosome         -0.49         0.060         0.165190087           K02970 RP-S21, MRPS21, prsU         small subunit ribosomal protein S21         ko03010 Ribosome         -0.42         0.099         0.180472394           K17404 MRPS25         small subunit ribosomal protein S25         NA         -0.52         0.001         0.1404072394           K02976 RP-S25e, RPS25         small subunit ribosomal protein S25e         ko03010 Ribosome         -0.50         0.003         0.163642877           K02976 RP-S26e, RPS26         small subunit ribosomal protein S26e         k003010 Ribosome         -0.50         0.012         0.186899392           K17412 MRPS34         small subunit ribosomal protein S34         NA         -0.59         0.051         0.165133463				
K02970         RP-S21, MRPS21, rpsU         small subunit ribosomal protein S21         k03010 Ribosome         — 0.42         0.009         0.180472394           K17404         MRPS25         small subunit ribosomal protein S25         NA         — 0.52         0.001         0.140402222           K02975         RP-S25e, RPS25         small subunit ribosomal protein S25e         k03010 Ribosome         — 0.50         0.001         0.186859932           K17412         MRPS34         small subunit ribosomal protein S34         NA         — 0.59         0.021         0.165133463				-0.49 0.0060 0.165190087
K02975 RP-525 small subunit ribosomal protein S26e         k03010 Ribosome         -0.50         0.0043         0.183642877           K02976 RP-526 small subunit ribosomal protein S26e         k03010 Ribosome         -0.56         0.012         0.186859932           K17412 MRP534         small subunit ribosomal protein S34         NA         -0.59         0.051         0.165133463	K02970 RP-S21, MRPS21, rpsU	small subunit ribosomal protein S21	ko03010 Ribosome	-0.42 0.0099 0.180472394
K02976 RP-526e, RP-526         small subunit ribosomal protein S26e         k003010 Ribosome         -0.56         0.021         0.186859932           K17412 MRPS34         small subunit ribosomal protein S34         NA         -0.59         0.051         0.165133463				
K17412 MRPS34 small subunit ribosomal protein S34 NA -0.59 0.0051 0.165133463				
			ko03010 Ribosome	-0.59 0.0050 0.165133463

# 1101 Supplementary File 4.

Additive	Limit
Vitamin A	No limit (for fish)
Vitamin D3	3000 I.U/kg or 0.075 mg/kg
Vitamin E	No limit
Vitamin K3	No limit
Vitamin B1	No limit
Vitamin B2	No limit
Vitamin B6	No limit
Vitamin B12	No limit
Vitamin B3 /Vitamin PP/ Niacin	No limit
Vitamin B5 (Calcium d-pantothenate)	No limit
Folic acid (vitamin B9)	No limit
Biotin	No limit
Vitamin C	No limit
Cobalt	No longer approved
Iodide and iodate	20 mg/kg
Selenium	0.5 mg/kg
Iron	max. 750 mg/kg
Manganese sulphate	100 mg/kg
Copper sulphate	25 mg/kg
Zinc sulphate monohydrate	180 mg/kg for salmonids, 150 mg/kg for other fish species
Taurine	No information
Histidine	No limit