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1 **Protein signatures of spontaneous lipolysis and lipoprotein lipase**
2 **activity in cow's milk**

3

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19

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37 The experiment was conducted in accordance with the French legislation on animal
38 experimentation and was approved by the French National Committee for
39 Consideration of Ethics in Animal Experimentation (Authorization: APAFiS #17944-
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41

42 **Conflict of interest statement**

43 The authors declare that they have no conflict of interest.

44

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55 **Author's contributions :**

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57 curation, Formal analysis, Visualization, Writing – original draft.

58 L. Bernard: Conceptualization and management of the Lipomec project, Resources,
59 Supervision, Visualization, Writing – original draft.

60 C. Hurtaud: Conceptualization and management of the Lipomec project, Resources,
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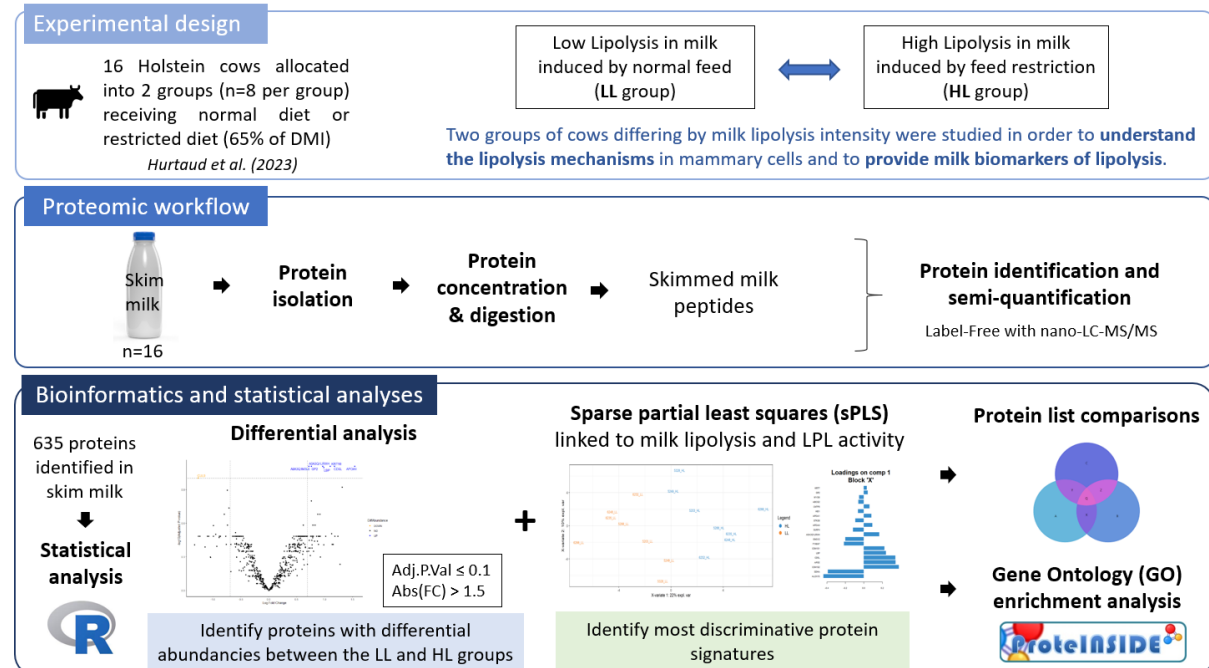
64 D. Viala: Proteome Analysis, Data Curation, Writing – review & editing.

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67 M. Bonnet: Conceptualization of the proteome methodology, conceptualization of the
68 data analysis, data curation, Supervision, Visualization, Writing– original draft.
69 C. Cebo: Conceptualization and management of the Lipomec project, Funding
70 acquisition, Supervision, Data curation, Visualization, Writing – original draft.
71 All authors agree to be accountable for the content of the work.
72

Highlights

- A specific protein signature is associated with high lipolysis levels in cow milk
- CD5L and GP2 in skim milk are putative biomarkers of lipolysis
- CUL9, SURF4 and HID1 are associated with low levels of lipolysis in skim milk
- LPL inhibitors contribute to explaining low lipolysis levels observed in cow milk

Graphical abstract



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Abstract

Spontaneous milk lipolysis refers to the breakdown of triacylglycerols in milk. Lipolysis impacts the organoleptic value of milk by causing off-flavours and reduces the technological properties of milk. Lipolysis is caused by lipoprotein lipase (LPL), a tightly regulated enzyme in milk. Our objective was to identify robust biomarkers of lipolysis and putative regulators of LPL enzyme in bovine milk. To achieve this goal, we used feed restriction as a lever to generate highly contrasted samples with regard to milk lipolysis. We combined statistical methods on proteomics data, milk lipolysis and LPL activity values. Following this strategy, we identified CD5L and GP2 as robust biomarkers of high lipolysis in cow milk. We also identified HID1, SURF4 and CUL9 as putative inhibitors of the lipolytic process in the milk. We thus proposed 5 putative biomarkers to be considered in future tools to manage milk lipolysis.

Keywords

Dairy cows, lipolysis, lipoprotein lipase, milk fat, milk proteins, biomarkers

Introduction

Fat is present in milk as fat globules, a supra-molecular structure made of a triglyceride core surrounded by a complex membrane called the Milk Fat Globule Membrane (MFGM). In freshly secreted milk, the MFGM is intact and forms an effective barrier that protects fat from the action of milk lipases, with an efficiency that can vary according to the molecular composition of the membrane [1]. In addition, in some cases such as agitation, pumping or homogenization of milk, this membrane is damaged and lipases are able to reach the triglyceride core causing lipolysis [2]. Milk lipolysis, that is, enzymatic degradation of milk triglycerides into free fatty acids by the lipoprotein lipase (LPL; EC:3.1.1.34), severely impairs milk quality from both the organoleptic and the technological points of view. Off-flavours originating from free fatty acids and their oxidation products in milk are not appreciated by consumers. Moreover, the presence of partial triglycerides in milk impairs its technological properties, like foaming and creaming abilities [3]. Controlling milk lipolysis is therefore an economic issue for dairy producers. Spontaneous lipolysis of milk results from a complex interplay between farming practices, animal physiology and animal genetics [4,5], but underlying mechanisms

35 are still poorly understood. At the molecular level, the lipolytic system is constituted
36 by the lipoprotein lipase, cofactors (activators and inhibitors) and substrate (milk
37 triglycerides), and the resulting products are free fatty acids and partial glycerides. In
38 the native bovine milk, the skim fraction is the richest source of LPL mainly
39 associated with the casein micelle through electrostatic interactions [3] and upon
40 cooling the proportion of LPL linked to the MFGM increases [6,7]. Inactive LPL can
41 refold into active LPL dimers in the presence of calcium ions and this phenomenon is
42 potentiated by the presence of activators, namely serum albumin, lipoproteins,
43 heparin or glycerol [8], which are mainly located in skim milk. The presence of LPL
44 inhibitors has also been documented in milk. A component of the milk proteose-
45 peptone fraction PP3, also known as lactophorin, has been identified as a potential
46 LPL inhibitor [9]. The skim milk proteose-peptone component 5 (PP5, residues 1–105
47 and 1–107 of β -casein) has been identified in some studies as an activator of LPL
48 [10] and in other studies, as an inhibitor of LPL [9]. However, most of these studies
49 dealing with the identification of milk and skim milk lipase activity regulators were
50 conducted in the 1980s [9,11–13] and need to be reassessed in view of the major
51 advances in proteomics that have occurred over the past decade, especially with
52 regard to the analysis of milk protein fractions [14,15].

53 The aim of the present study is to discover biomarkers of lipolysis in skim milk by
54 using a model of feed restriction as a lever to produce milk samples with contrasted
55 lipolysis rates [16]. To achieve this outcome, we combined statistical methods on our
56 proteomics data with milk lipolysis values and LPL enzyme activities to identify
57 robustly discriminant proteins of lipolysis in milk. Following this strategy, we further
58 describe the protein signatures of spontaneous lipolysis or LPL activity in skim milk.
59 We acknowledge some limitations in our approach. In order to perform satisfactory
60 proteomic analysis of skim milk, milk fat was removed with skimming, but part of the
61 LPL is located in the fat phase. However, our results help to better understand the
62 biological mechanisms of milk fat degradation through the identification of putative
63 regulators of lipase activity in milk, which is a prerequisite to design a test to detect
64 lipolysis in milk samples.

65

66 **1. Material and methods**

67 **1.1 Animals and experimental design**

68 The experiment was conducted at the Installation Expérimentale Production Laitière,
69 INRAE, Dairy nutrition and physiology (IE PL, 35650 Le Rheu, France;
70 <https://doi.org/10.15454/yk9q-pf68>) with agreement for animal housing number C-35–
71 275-23. This study was realized on samples from sixteen primiparous and
72 multiparous Holstein cows at 156 ± 20 days in milk fed with diet treatments based on
73 corn silage and differing by the level of feeding. These cows are a subsample of the
74 44 cows included in a reverse design on feeding level during 4 weeks split into 2 two-
75 week periods in March 2019 [16]. Two feeding levels were considered: “non-
76 restricted”, with cows fed a corn silage-based diet at 100% of ad libitum dry matter
77 intake (DMI), and “restricted”, corresponding to a corn silage-based diet at 65% of ad
78 libitum DMI. For omics studies, 8 cows in each two-week period were used. During
79 period 1, each group of cows first received the non-restricted diet, followed by the
80 restricted diet. During period 2, the order of feeding levels was reversed. Further
81 details about the feed offered in the two diets can be found in [16]. The animals had
82 access to fresh water *ad libitum*.

83

84 **1.2 Milk processing and lipolysis determination**

85 The milk yields of individual animals were recorded over 6 milkings at 8:00 and 16:30
86 each week. Milk samples were collected individually on morning milking on the last
87 day of each experimental period, with one part immediately treated with bronopol-B2
88 preservative (LIAL, Aurillac, France) to measure fat, protein and lactose content
89 (MyLab, Chateaugiron, France). The other part of milk (unpreserved) was used to
90 determine the milk lipolysis level using the copper soap method (mEq/100g fat) [5,17]
91 as described in detail in [16]. The morning lipolysis levels of milk collected on the last
92 day of the period were used to define groups of low and high lipolysis cows based on
93 a threshold of 0.5 mEq/100 g fat: Low Lipolysis (LL group with mean of 0.32 ± 0.12
94 mEq/100 g fat) vs High Lipolysis (HL group, 0.84 ± 0.33 mEq/100 g fat). Unpreserved
95 milk was also stored at -80°C for protein extraction and identification analyses and
96 LPL activity determination (nmol/mn/ml) measured in vitro using a radiolabelled
97 substrate [18].

98 **1.3 Major protein identification using LC-ESI-MS**

99 Major milk proteins, namely the four caseins (α s1-caseins, α s2 caseins, β -caseins
100 and κ -caseins), α -lactalbumin, and β -lactoglobulin and all their isoforms were

101 identified and quantified using our improved method combining reverse-phase high
102 performance liquid chromatography (Ultimate LC 3 000 system, Thermo Fisher
103 Scientific, Waltham, MA) with an ESI-TOF mass spectrometer micrOTOF II focus
104 (Bruker Daltonics, Wissembourg, France) [19]. Briefly, milk samples were placed on
105 dry ice immediately after milking and stored at -80°C for further analyses. Milk
106 samples were rapidly thawed at 37°C then skimmed by centrifugation at 2 000 g and
107 4°C for 10 min. The cream was removed by means of a spatula and the skimmed
108 milk was aliquoted into fractions of 20 and 100 µL, frozen at -20°C and kept under
109 these conditions until analysis by Liquid Chromatography-Electro Spray Ionization-
110 Mass Spectrometry (LC-ESI-MS). Identification of the main milk protein isoforms was
111 performed using our in-house mass database of bovine milk proteins containing
112 nearly 3 000 theoretical masses, corresponding to the multiple isoforms of milk
113 proteins including genetic and splicing variants, post-translationally modified proteins
114 (phosphorylated and glycosylated) and main known plasmin hydrolysis products.

115

116 **1.4 Minor protein identification using nano-LC-MS/MS**

117 ***1.4.1 Skim milk protein isolation, concentration and digestion***

118 All reagents were purchased from Sigma-Aldrich (Saint Louis (MO)) except when
119 otherwise specified. The raw milk was slightly defrosted during one night at 4°C and
120 milk components equilibrated by incubation during 1 h at 37°C. The equilibrated raw
121 milk was centrifuged at 3 500 g for 15 min at 4°C to separate the cream from the
122 skimmed milk (SM). Acetic acid was added to the SM reaching pH 4.6 to precipitate
123 the caseins. The homogenate was centrifuged at 10 000 g for 10 min at 4°C to
124 discard caseins and supernatant recovered until protein concentration determination.
125 Enrichment of minor or low-abundance SM proteins was performed using the
126 ProteoMiner Small-Capacity columns (#163-3006, Bio-Rad Laboratories, Hercules
127 (CA)) according to the manufacturer's instructions. Column was washed twice, and
128 10 mg of proteins from SM were deposited on column and incubated 2 h at room
129 temperature (RT) under agitation. Then, spin columns were washed with buffer twice
130 and with purified milli-Q water once (1 min at RT) followed by a 1 000 g centrifugation
131 in order to eliminate unbound proteins. Proteins enriched from medium- and low-
132 abundance were incubated for two runs of 15 min in 20 µL of elution buffer (RT) and
133 centrifuged at 1 000 g. Supernatant was recovered until protein concentration

134 determination using Pierce™ BCA protein assay kit (Fisher Scientific, Hampton
135 (NH)).

136 Twenty µg of proteins were mixed with reducing sodium dodecylsulfate buffer (4%)
137 with dithiothreitol (20 mM) and incubated 10 min boiling in order to reduce disulphide
138 bonds. Then proteins were alkylated in iodoacetamide (50 mM) during 45 min
139 protected from light. After acidification with phosphoric acid (1.2%), S-Trap® buffer
140 (triethylammonium bicarbonate 100 mM; in ethanol 90%) was added and proteins
141 were deposit on S-Trap® column (Protifi, Fairport, NY). Columns containing proteins
142 were centrifuged at 4 000 g during 10 min, washed with S-Trap® buffer and this step
143 was repeated 3 times.

144 SM protein digestion was performed with sequencing grade trypsin (Promega,
145 Madison (WI)) 1:50 [w/w] enzyme/protein ratio in triethylammonium bicarbonate (50
146 mM) with overnight incubation at 37°C. Tryptic peptides were extracted by adding 60
147 µL of 0.2% formic acid in acetonitrile (50%) followed by centrifugation at 4 000 g
148 during 10 min repeated twice. Supernatants containing peptides were dried by
149 SpeedVac vacuum concentrator (ThermoScientific, Illkirch (FR)). Peptides were
150 recovered in 100 µL of 5% acetonitrile and 0.05% trifluoroacetic acid (TFA) solution
151 with sonication during 5 min and transferred into glass vials (Interchim, Montluçon
152 (FR)) prior to nano-LC-MS/MS analysis.

153 **1.4.2 Peptide analysis on nano-LC-MS/MS**

154 Peptide mixtures were analysed by nano-LC-MS/MS using an Ultimate 3 000 system
155 coupled to a QExactive HF-X mass spectrometer (MS) (Thermo Fisher Scientific). A
156 volume of 6 µl of peptide extract was first concentrated and desalted at a flow rate of
157 30 µl/min on a C18 pre-column 5 cm length x 100 µm (Acclaim PepMap 100 C18, 5
158 µm, 100A nanoViper) equilibrated with Trifluoroacetic Acid 0.05% in water. Then this
159 preconcentration column was switched online with a nanoflow analytical C18 column
160 (Acclaim PepMap 100 - 75 µm inner diameter x 25 cm length; C18 - 3 µm -100Å - SN
161 10719167) equilibrated at a flow rate of 300 nL/min with a 95% solvent A (99.9%
162 H₂O, 0.1% formic acid). The peptides were separated according to their
163 hydrophobicity using a gradient of solvent B (99.9% acetonitrile, 0.1% formic acid)
164 from 5 to 32% during 50 min. For MS analysis, eluted peptides were electrosprayed
165 in positive-ion mode at 1.6 kV through a nanoelectrospray ion source heated to
166 250°C. The MS operated in data dependent mode: the parent ion was selected in the

167 orbitrap cell (FTMS) at a resolution of 120 000 and each MS analysis was followed by
168 18 MS/MS with analysis of the MS/MS fragments at a resolution of 15 000.

169 At the end of the LC-MS/MS analysis, the raw data processing of peptide MS/MS
170 spectra was carried out with Progenesis Q1 software (version 4.2, Nonlinear
171 Dynamics, Newcastle upon Tyne, UK). The software defined a reference run used to
172 perform an automatic alignment of all other runs considering a maximum allowable
173 ion charged set to 5. The detected ions were grouped in a file (mgf) directly exported
174 to the Mascot v2.5 (<http://www.matrixscience.com>) interrogation engine and searched
175 against a *Bos taurus* decoy database (i.e. ref_bos_taurus, 37 513 sequences) with
176 the following parameters during the request: precursor mass tolerance of 10 ppm and
177 fragment mass tolerance of 0.05 Da, a maximum of two missed cleavage sites of
178 trypsin, carbamidomethylation (C), oxidation (M) and deamidation (NQ) set as
179 variable modifications. Protein identification was validated when at least two peptides
180 from one protein showed statistically significant identity above Mascot scores with a
181 false discovery rate (FDR) of 1%. For label-free protein quantification analysis, the
182 identified peptides from the database search were imported back to Progenesis Q1
183 software. All unique validated peptides of an identified protein were included and the
184 total cumulative abundance was calculated by summing the abundances of all
185 peptides allocated to the respective protein. Consequently, proteins were quantified
186 based on the intensities of the specific validated peptides.

187

188 **1.5 Statistical analysis**

189 Statistical analyses were performed using R (version 4.2.1). All data came from 2
190 groups of 8 animals forming a part of the reverse design experiment (full details in
191 Hurtaud et al., 2023). As cited earlier, the milk lipolysis level was used to constitute
192 the Low Lipolysis (LL) group with a mean of 0.32 ± 0.12 mEq/100 g fat and the High
193 Lipolysis (HL) group with a mean of 0.84 ± 0.33 mEq/100 g fat. Thus, the
194 experimental design consists of the following fixed effects: period (P1 vs P2, differing
195 by 15 d of lactation), sequence (order of feed restriction treatment), and lipolysis level
196 (LL vs HL). We note that as both diets (restricted and unrestricted) were fed in
197 succession to each cow, repeated measurements were available for each cow in this
198 design.

199 Animal parameters (such as DMI, milk production and composition) and major
200 proteins from milk containing 0.3% missing variables were imputed by the k-nearest
201 neighbour method (k=5) using the impute package (version 1.70.0).

202 A linear mixed model with fixed effects (period, sequence and lipolysis) and a random
203 animal effect was fit for animal parameters using the lme4 package (version 1.1.31),
204 and statistical significance was evaluated using Type II sums of squares in the Anova
205 function from the car package (version 3.1.1; $p < 0.05$). The sequence effect was not
206 significant and was thus removed from the model.

207 Raw minor protein abundances from SM containing 0.4% missing variables were
208 imputed by the k-nearest neighbour method (k=5) using the impute package.

209 Abundances were then log-transformed. We applied two complementary statistical
210 analyses to identify a proteomic signature that discriminates the LL and HL groups: i)
211 a parametric univariate differential analysis (Diff-A) to identify significant proteins one
212 by one based on their abundances; and to go further ii) a sparse multi-level
213 multivariate analysis to identify a concise signature of proteins strongly linked to
214 either lipolysis (sPLS-lipolysis) or LPL activity (sPLS-LPL-activity). The parametric
215 univariate differential analysis (Diff-A) was performed by fitting to each protein an
216 empirical Bayes linear model including lipolysis, sequence and period fixed effects
217 and a random animal effect using the limma package (version 3.52.2). As no
218 significant effect was observed across proteins for period and sequence, these were
219 removed from the model. P-values were adjusted to control the FDR (adj.P.Val) using
220 the Benjamini-Hochberg approach. Statistical significance was considered at
221 $\text{adj.P.Val} < 0.1$ and an absolute fold change threshold of 1.5.

222 Sparse multi-level partial least square analyses (sPLS) were performed in regression
223 mode with paired observations on cows using the mixOmics package (version 6.20.0,
224 Rohart et al., 2017). Predictor variables (X) corresponded to the log protein
225 abundances, and the response variable (Y) to either the milk lipolysis (sPLS-lipolysis)
226 or the milk LPL activity (sPLS-LPL-activity). For each sPLS model, we retained 2
227 components, both including a total of 30 proteins with non-zero loadings. A posteriori,
228 the first sPLS component for each model was found to be highly discriminative
229 between the LL and HL groups. The proteins with non-zero loadings in the first
230 component were compiled into lists of milk lipolysis related proteins and LPL activity
231 related proteins with their respective contributions. Contributions correspond to the

232 weight assigned to each protein to define each component; larger absolute values
233 mean that a given protein has a greater importance for a given component.
234 Lists of proteins were mined for biological meaning by a gene ontology (GO)
235 enrichment analysis, performed using the ProteINSIDE webservice online tool
236 version 2.0 (available at [https://umrh-](https://umrh-bioinfo.clermont.inrae.fr/ProteINSIDE_2/index.php?page=upload.php)
237 [bioinfo.clermont.inrae.fr/ProteINSIDE_2/index.php?page=upload.php](https://umrh-bioinfo.clermont.inrae.fr/ProteINSIDE_2/index.php?page=upload.php), [20]) based on
238 *Bos taurus* and a search of biological reactions on Reactome based on *Homo*
239 *sapiens*.

240

241 **2. Results**

242 **2.1 Highly contrasted milk samples with regard to spontaneous lipolysis levels**

243 We used feed restriction of the cows as a lever to generate two groups of 8 cows with
244 contrasted milk in terms of lipolysis levels for use in omics studies. The performance
245 data of these 8 dairy cows were comparable with those on the full set of 44 cows in
246 the original study [16].

247 The parameters relative to the ingestion of the 8 dairy cows from the LL group (fed an
248 unrestricted diet) and the HL group (fed a restricted diet) are reported in
249 Supplementary Table S1. As expected, the milk yield and composition are
250 dramatically divergent between LL and HL groups (Table 1). The milk production
251 decreased by 9.7% in the HL compared with LL group ($P < 0.05$). The total milk
252 protein content was reduced by 16.7% in the HL group compared to the LL group
253 (583.4 g and 486.1 g secreted in morning milk, respectively). Both the casein and
254 soluble protein content were divergent between LL and HL groups (-6.5% and -9.6%,
255 respectively). At the same time, milk lipolysis increased by a factor of 2.6 in the HL
256 group compared with the LL group ($P < 0.05$). Interestingly, the milk LPL activity
257 increased by a factor of only 1.4 in the HL group ($P < 0.05$). Although the correlation
258 between LPL activity and lipolysis in milk is high ($r = 0.69$; $P = 0.003$; Figure 1), the
259 increase in the milk LPL activity (+44.5%) cannot solely explain the dramatic increase
260 in lipolysis levels we observed in the HL group (+162.5%), thus suggesting that
261 regulators may amplify the lipolytic response in milk.

262

263 **2.2 Spontaneous lipolysis modulates the abundances of skimmed milk proteins**

264 635 proteins were identified in our study and raw abundances for each protein are
265 reported in Supplementary Table S3. Among these 635 proteins, the spontaneous

266 lipolysis significantly impacts the milk abundances of eight proteins. The volcano plot
267 (Figure 2), resulting from the parametric univariate analysis, displays the seven
268 proteins with higher abundance (A0A3Q1M3L6, CD5L, A0A3Q1LRW4, KRT10, GP2,
269 APOA4, LBP) and the one with lower abundance (CUL9) in the HL compared with LL
270 group (Table 2). Interestingly, the LPL protein (P11151) was 1.9 times more
271 abundant in HL compared with LL group, but this increase was not statistically
272 significant.

273

274 **2.3 Milk protein signature of lipolysis in milk**

275 The sPLS multivariate analysis of milk lipolysis (Y) and log protein abundances (X)
276 reveals a component that is highly discriminative between the HL and LL groups
277 (Supplementary Figure S1). The corresponding milk proteins implicated in lipolysis
278 are reported in Table 3. Among the 15 proteins associated with the HL group, the ten
279 with the largest weights corresponded to two caseins (CSN1S2, CSN1S1), 3
280 apolipoproteins (APOE, APOA4, APOA1), CD5L, LBP, A0A3Q1LRW4, CNTFR and
281 GP2. Among the 15 proteins associated with the LL group, the ten with the largest
282 weights are ALOX15, SDHA, FASN, GNG12, SURF4, STK38, HID1, ABCG2, MYO6
283 and UQCRC2 (Table 3).

284 The 15 proteins associated with HL are annotated by terms within the biological
285 process (BP) ontology related to the “positive regulation of cholesterol esterification”,
286 the “steroid esterification” and the “very-low-density lipoprotein particle remodelling”
287 for APOA1, APOA4 and APOE (Supplementary Table S3). Similarly, the 15 proteins
288 associated with the LL group were annotated by terms within the BP ontology
289 highlighting the “positive regulation of protein lipidation” and “lipoprotein metabolic
290 process” and the “establishment of protein localization at the membrane of reticulum
291 endoplasmic” for both RAB3GAP1 and RAB3GAP2 (Supplementary Table S3).

292

293 **2.4 Milk protein signature of LPL activity**

294 The first component of the sPLS multivariate analysis of milk LPL activity (Y) and log
295 protein abundances (X) similarly discriminated between the HL and LL groups
296 (Supplementary Figure S2). SM proteins related to the level of milk LPL activity are
297 listed in Table 4. Seventeen proteins were strongly associated with the HL group (i.e.,
298 positive loadings for component 1 of the sPLS) with GP2, BSPRY, KRT10, ANXA7,
299 MARCKS, CD5L, SLC5A9, SLC6A8, A0A3Q1M3L6 and IDH1 in the top 10. Among

300 the 13 proteins associated with the LL group, HID1, SQLE, CUL9, VAT1, PHB2,
301 ACSL3, NDRG4, ATP13A3, FASN and ANKRD13A were in the top 10 (Table 4).
302 The 17 proteins associated with HL were significantly annotated by terms within the
303 BP category that emphasized “localization” for CD5L, GP2, NAPA, SH3GLB1,
304 SLC5A9, SLC6A8, the “negative regulation of cholesterol metabolic process” for
305 ERLIN2 the “isocitrate metabolic process”, the “glyoxylate cycle” and “tricarboxylic
306 acid metabolic process” for IDH1. Moreover, 13 proteins among the 17 were
307 annotated by the “membrane” term within the CC category (Supplementary Table
308 S3).

309 The 13 proteins associated with the LL group were annotated by terms within the BP
310 category that highlight the “regulation of phospholipid metabolic process”, particularly
311 phosphatidylcholine, for ACSL3 and PHB2 and “negative regulation of protein
312 localization to endosome” for ANKRD13A (Supplementary Table S3).

313

314 **2.5 Putative milk biomarkers of milk lipolysis**

315 Crossing the protein lists resulting from the univariate and multivariate statistical
316 analyses highlights the CD5 molecule like (CD5L) and the Glycoprotein 2 (GP2).
317 These are therefore putative biomarkers of high lipolysis in milk (Figure 3). CD5L and
318 GP2 skim milk abundances correlated positively with milk lipolysis ($r = 0.69$; $P =$
319 0.003 and $r = 0.5$; $P = 0.04$) and milk LPL activity ($r = 0.68$; $P = 0.003$ and $r = 0.6$; $P =$
320 0.01) (Supplementary Table S4).

321 Focusing on protein lists associated with the LL group, the Surfeit locus protein 4
322 (SURF4) and Chromosome 17 open reading frame 28 ortholog (HID1) are common
323 proteins linked to milk lipolysis (sPLS-lipolysis) and milk LPL activity (sPLS-LPL
324 activity) (Figure 4). SURF4, HID1 and CUL9 are negatively correlated with both
325 lipolysis ($r = -0.63$, $P = 0.008$; $r = -0.4$, $P = 0.1$ and $r = -0.48$, $P = 0.06$) and LPL
326 activity in milk ($r = -0.74$, $P = 0.0009$; $r = -0.6$, $P = 0.01$ and $r = -0.59$, $P = 0.01$)
327 (Supplementary Table S4). These proteins are therefore good candidates that may
328 be indicative of low lipolysis in the milk of dairy cows.

329

330 **3. Discussion**

331 As expected, the feed restriction of dairy cows dramatically induced lipolysis in milk
332 (+162.5%; HL group) compared with cows fed with normal diet (LL group) [16,21].

333 Noticeably, while lipolysis increased 2.6 times in the HL compared to LL group, the
334 activity of the LPL enzyme only increased 1.4 times, thus suggesting that molecules
335 may act as regulators of the enzyme in skim milk (Table 1). However, the LPL activity
336 measured in vitro in optimal conditions represents the potential LPL activity and not
337 the in vivo activity. Furthermore, previous studies in cows showed that milk lipolysis
338 was poorly correlated to LPL activity [22], which is probably due at least in part to the
339 major cellular location of the LPL in the casein micelle fraction of milk in cows. These
340 considerations support giving more weight to the molecules identified as a signature
341 of lipolysis within the skim milk.

342 The feed restriction necessarily impacts the milk proteome [21,23]. Our aim was to
343 identify robust biomarkers of milk lipolysis and a list of putative regulators of lipolysis
344 in skim milk to better understand the lipolytic processes. To achieve this goal, we first
345 performed a classical univariate statistical analysis on our proteomics data to identify
346 differentially abundant proteins between lipolysis treatments while accounting for
347 other experimental factors. We then performed two multivariate statistical analyses
348 on the proteomics abundance data to identify proteins forming signatures of lipolysis
349 and milk LPL enzyme activity. sPLS is a powerful tool that seeks to maximize the
350 covariance between the proteomic abundances and response variable of interest
351 (lipolysis, LPL activity) using a set of latent components, where a lasso penalization
352 is used to focus interest on a concise set of predictive biomarkers. Finally, we
353 compared differential proteins and those forming signatures of lipolysis and LPL
354 activity to identify proteins involved in the regulation of the lipolytic process in milk.
355 Following this 3-step strategy, we identified CD5L and GP2 as robust biomarkers and
356 putative regulators of lipolysis in milk (Figure 3). These proteins were consistently
357 identified in the differential analysis, as well as sPLS-lipolysis and sPLS-LPL activity
358 analyses, highlighting them as key molecules involved in the lipolytic pathway in
359 bovine milk. CD5L, also called Apoptosis inhibitor of macrophage (AIM) or apoptosis
360 inhibitor 6 (Api6), is a soluble member of the scavenger receptor cysteine-rich
361 superfamily, which is secreted by mature tissue macrophages in mouse in the
362 context of inflammation and obesity. Kurokawa et al. [24,25] reported that the
363 AIM/Api6/CD5L protein is incorporated into adipocytes via CD36-mediated
364 endocytosis, and induces lipolysis by suppressing the activity of fatty acid synthase
365 (FASN). In our study, CD5L negatively correlates ($r = -0.75$; $P = 0.0007$) with FASN,
366 the latter of which was strongly associated with the LL group for both sPLS-lipolysis

367 and sPLS-LPL-activity (Tables 3 and 4). As proposed earlier by Iwamura et al. [26] in
368 adipocytes of mice, we further suggest that in bovine mammary epithelial cells, the
369 highly abundant CD5L binds to cytosolic FASN, inhibiting its enzymatic activity and
370 thus lowering the milk short and medium chain FA from *de novo* mammary synthesis.
371 In other words, CD5L may act by repressing *de novo* synthesis by FASN, favouring a
372 higher fatty acid uptake by both the mammary LPL and NEFA transporters for milk
373 lipid synthesis [27]. The latter being favoured by the high plasma NEFA concentration
374 observed due to adipose mobilization which was associated with lipolysis in milk [21].
375 GP2 was identified in the heat- and acid-stable fraction of ovine milk [28] and was
376 recently listed in all the fractions of bovine milk throughout lactation [15]. The heat-
377 and acid-stable fraction of bovine milk belongs to the proteose-peptone fraction,
378 which contain potential activators or inhibitors of LPL enzyme [29]. Most of the
379 component of proteose-peptone fraction are fragments of caseins produced by the
380 action of endogenous plasmin and the main constituents are recognized as
381 components 3, 5, 8 [30,31]. Peptone protease (PP) 5 have been identified both as an
382 activator [10] or an inhibitor of LPL enzyme [9,21] and remain controversial. Among
383 this PP fraction, the potential GP2 role in the lipolysis process has not been yet
384 addressed. However, given its structure of glycosylphosphatidylinositol-anchored
385 glycoprotein, GP2 may be involved in the link of LPL with the MFGM. This hypothesis
386 remains to be investigated and is based on the observations that
387 glycosylphosphatidylinositol-anchored glycoprotein such as GPIHBP1 is involved in
388 the binding of LPL and chylomicrons in mice [32]. Moreover, GP2 is highly positively
389 correlated with the glypican-1 protein (GPC1) in an sPLS discriminant analysis
390 between the LL and HL groups (Supplementary Figure S3 reports the circle plot of
391 component 1 and 2). GPC1 is a cell surface proteoglycan carrying an heparan sulfate
392 moiety, which facilitates or inhibits the interaction of proteins with lipid-rafts. Heparin-
393 like glycosaminoglycans have been identified as potential activators of LPL [29,33].
394 Among research focusing on the interactions between LPL and MFGM allowing its
395 access to its substrates, LPL is known to bind to heparan sulfate-type
396 glycosaminoglycans present on the surface of MFG [6]. All these assumptions justify
397 analyzing the involvement of GP2 in the localization of LPL close to its substrate,
398 supported by GP2 positive correlation with milk LPL activity ($r = 0.60$; $P = 0.01$)
399 (Supplementary Table S4).

400 Three proteins were both differentially abundant and related to lipolysis. APOA4,
401 A0A3Q1LRW4 and LBP were identified in the milk from the HL group as strongly
402 associated proteins (Table 3, Figure 3). APOA4 is a known actor in lipolysis, since it
403 is required for efficient activation of LPL by APOC-II [3,34]. A0A3Q1LRW4 protein is
404 an immunoglobulin fragment, but not well described. Lastly, the LBP protein
405 addressing the HL group indicates modification of the immune response and lipid
406 transport in the cows in line with adaptive response to feed restriction [35].

407

408 Dairy cows fed diets covering requirements present low lipolysis levels in milk despite
409 the presence of LPL, thus suggesting that the LPL enzyme is tightly regulated. It is
410 therefore of interest to identify not only proteins associated with high levels of
411 lipolysis in milk, but also proteins associated with low levels of lipolysis, the latter of
412 which may be putative inhibitors of lipolysis in milk. The cullin 9 protein (CUL9) was
413 identified in the milk of the LL group both in our differential analysis and sPLS-LPL
414 activity analysis (Figure 4). CUL9 belongs to the cullin family of proteins, molecular
415 scaffolds that have crucial roles in the homeostasis of cellular proteins through the
416 ubiquitin-proteasome system [36]. Cullins work in concert with RING proteins as
417 docking proteins to add ubiquitin to specific proteins, targeting them for destruction.
418 Such a regulation of lipase activity through ubiquitination has been recently
419 demonstrated for the adipose triglyceride lipase in hepatic cells [37].

420 Two additional proteins were strongly associated with reduced lipolysis levels in milk:
421 SURF4 (Surfeit locus protein 4) and HID1 (Chromosome 17 open reading frame 28
422 ortholog protein) (Figure 4). SURF4 is an endoplasmic reticulum (ER) cargo receptor
423 that mediates the selective export of lipoproteins to facilitate their secretion, thus
424 playing a crucial role for the maintenance of lipid homeostasis [38].

425 As well as SURF4, HID1 protein is associated with low levels of LPL activity and
426 lipolysis (Figure 4). HID-1 controls formation of large dense core vesicles by
427 influencing cargo sorting of neuropeptides and peptide hormones through
428 acidification of the trans Golgi network [39]. HID1 is thus involved in the release of
429 insulin by pancreatic cells through the processing of proinsulin to functionally active
430 hormone [40]. Moreover, in our study, the expression of HID1 is positively correlated
431 with the expression of FASN in the LL group ($r = 0.72$; $P = 0.001$; Supplementary
432 Table S4), thus favouring the mammary *de novo* FA pathway in the case of a
433 sufficient feeding level.

434

435 **4. Conclusions**

436 In this study, we used feed restriction as a lever to produce highly contrasted
437 samples with regard to lipolysis levels in bovine milk. Following proteomic studies, we
438 combined uni- and multivariate statistical analyses with milk lipolysis values and/or
439 LPL enzyme activities measured in milk to identify key regulators of lipolysis in bovine
440 milk. We identified the CD5L and GP2 proteins as robust biomarkers of high lipolysis
441 in cow milk. HID1, SURF4 and CUL9 are putative inhibitors of the lipolytic process in
442 the milk. The data provided here constitute a robust basis for further tests on a larger
443 population to design a quick on-farm diagnosis tool such as strip tests to monitor
444 lipolysis levels in cow milk.

445

446 **References**

- 447 [1] C. Lopez, M.-N. Madec, R. Jimenez-Flores, Lipid rafts in the bovine milk fat
448 globule membrane revealed by the lateral segregation of phospholipids and
449 heterogeneous distribution of glycoproteins, *FOOD Chem.* 120 (2010) 22–33.
450 <https://doi.org/10.1016/j.foodchem.2009.09.065>.
- 451 [2] M.C. Michalski, R. Cariou, F. Michel, C. Garnier, Native vs. damaged milk fat
452 globules: membrane properties affect the viscoelasticity of milk gels, *J. Dairy*
453 *Sci.* 85 (2002) 2451–2461. [https://doi.org/10.3168/jds.S0022-0302\(02\)74327-0](https://doi.org/10.3168/jds.S0022-0302(02)74327-0).
- 454 [3] H.C. Deeth, Lipoprotein lipase and lipolysis in milk, *Int. Dairy J.* 16 (2006) 555.
- 455 [4] E. Vanbergue, L. Delaby, J.L. Peyraud, S. Colette, Y. Gallard, C. Hurtaud,
456 Effects of breed, feeding system, and lactation stage on milk fat characteristics
457 and spontaneous lipolysis in dairy cows., *J. Dairy Sci.* 100 (2017) 4623–4636.
458 <https://doi.org/10.3168/jds.2016-12094>.
- 459 [5] E. Vanbergue, J.L. Peyraud, J. Guinard-Flament, C. Charton, S. Barbey, R.
460 Lefebvre, Y. Gallard, C. Hurtaud, Effects of DGAT1 K232A polymorphism and
461 milking frequency on milk composition and spontaneous lipolysis in dairy cows,
462 *J. Dairy Sci.* 99 (2016) 5739–5749. <https://doi.org/10.3168/jds.2015-10731>.
- 463 [6] J.A. Dickow, L.B. Larsen, M. Hammershøj, L. Wiking, Cooling causes changes
464 in the distribution of lipoprotein lipase and milk fat globule membrane proteins
465 between the skim milk and cream phase, *J. Dairy Sci.* 94 (2011) 646–656.
466 <https://doi.org/10.3168/jds.2010-3549>.

- 467 [7] G. Sundheim, G. Bengtsson-Olivecrona, Lipolysis in milk induced by cooling or
468 by heparin - comparisons of amount of lipoprotein-lipase in the cream fraction
469 and degree of lipolysis, *J. Dairy Sci.* 68 (1985) 589–593.
470 [https://doi.org/10.3168/jds.S0022-0302\(85\)80862-6](https://doi.org/10.3168/jds.S0022-0302(85)80862-6).
- 471 [8] L. Zhang, A. Lookene, G. Wu, G. Olivecrona, Calcium triggers folding of
472 lipoprotein lipase into active dimers, *J. Biol. Chem.* 280 (2005) 42580–42591.
473 <https://doi.org/10.1074/jbc.M507252200>.
- 474 [9] M. Anderson, Inhibition of lipolysis in bovine milk by proteose peptone, *J. Dairy*
475 *Res.* 48 (1981) 247–252. <https://doi.org/10.1017/s002202990002166x>.
- 476 [10] P. Cartier, Y. Chilliard, Effects of different skim milk fractions on activity of cow
477 milk purified lipoprotein lipase, *J. Dairy Sci.* 69 (1986) 951–955.
478 [https://doi.org/10.3168/jds.S0022-0302\(86\)80486-6](https://doi.org/10.3168/jds.S0022-0302(86)80486-6).
- 479 [11] G. Sundheim, G. Bengtsson-Olivecrona, Hydrolysis of bovine and caprine milk-
480 fat globules by lipoprotein-lipase - effects of heparin and of skim milk on lipase
481 distribution and on lipolysis, *J. Dairy Sci.* 70 (1987) 2467–2475.
482 [https://doi.org/10.3168/jds.S0022-0302\(87\)80313-2](https://doi.org/10.3168/jds.S0022-0302(87)80313-2).
- 483 [12] G. Sundheim, G. Bengtsson-Olivecrona, Hydrolysis of bovine-milk fat globules
484 by lipoprotein-lipase - inhibition by proteins extracted from milk-fat globule-
485 membrane, *J. Dairy Sci.* 70 (1987) 1815–1821.
486 [https://doi.org/10.3168/jds.S0022-0302\(87\)80219-9](https://doi.org/10.3168/jds.S0022-0302(87)80219-9).
- 487 [13] Chilliard, Y., Variations physiologiques des activités lipasiques et de la lipolyse
488 spontanée dans les laits de vache, de chèvre et de femme : revue
489 bibliographique (suite), *Lait.* 62 (1982) 126–154.
490 <https://doi.org/10.1051/lait:1982613-6148>.
- 491 [14] M. Delosière, J.A.A. Pires, L. Bernard, I. Cassar-Malek, M. Bonnet, Dataset
492 reporting 4654 cow milk proteins listed according to lactation stages and milk
493 fractions, *Data Brief.* 29 (2020) 105105.
494 <https://doi.org/10.1016/j.dib.2019.105105>.
- 495 [15] M. Delosière, J. Pires, L. Bernard, I. Cassar-Malek, M. Bonnet, Milk proteome
496 from in silico data aggregation allows the identification of putative biomarkers of
497 negative energy balance in dairy cows, *Sci. Rep.* 9 (2019).
498 <https://doi.org/10.1038/s41598-019-46142-7>.

- 499 [16] C. Hurtaud, L. Bernard, M. Boutinaud, C. Cebo, Feed restriction as a tool for
500 further studies describing the mechanisms underlying lipolysis in milk in dairy
501 cows., *Anim. Open Space.* (2023).
- 502 [17] W. Shipe, G. Senyk, K. Fountain, Modified copper soap solvent-extraction
503 method for measuring free fatty acids in milk, *J. Dairy Sci.* 63 (1980) 193–198.
504 [https://doi.org/10.3168/jds.S0022-0302\(80\)82913-4](https://doi.org/10.3168/jds.S0022-0302(80)82913-4).
- 505 [18] L. Bernard, J. Rouel, C. Leroux, A. Ferlay, Y. Faulconnier, P. Legrand, Y.
506 Chilliard, Mammary Lipid Metabolism and Milk Fatty Acid Secretion in Alpine
507 Goats Fed Vegetable Lipids, *J. Dairy Sci.* 88 (2005) 1478–1489.
508 [https://doi.org/10.3168/jds.S0022-0302\(05\)72816-2](https://doi.org/10.3168/jds.S0022-0302(05)72816-2).
- 509 [19] G. Miranda, L. Bianchi, Z. Krupova, P. Trossat, P. Martin, An improved LC-MS
510 method to profile molecular diversity and quantify the six main bovine milk
511 proteins, including genetic and splicing variants as well as post-translationally
512 modified isoforms, *Food Chem. X.* 5 (2020) 100080.
513 <https://doi.org/10.1016/j.fochx.2020.100080>.
- 514 [20] N. Kaspric, B. Picard, M. Reichstadt, J. Tournayre, M. Bonnet, ProteINSIDE to
515 Easily Investigate Proteomics Data from Ruminants: Application to Mine
516 Proteome of Adipose and Muscle Tissues in Bovine Foetuses, *Plos One.* 10
517 (2015). <https://doi.org/10.1371/journal.pone.0128086>.
- 518 [21] E. Vanbergue, J.L. Peyraud, A. Ferlay, G. Miranda, P. Martin, C. Hurtaud,
519 Effects of feeding level, type of forage and milking time on milk lipolytic system
520 in dairy cows, *Livest. Sci.* 217 (2018) 116–126.
521 <https://doi.org/10.1016/j.livsci.2018.09.019>.
- 522 [22] Y. Chilliard, A. Ferlay, J. Rouel, G. Lamberett, A review of nutritional and
523 physiological factors affecting goat milk lipid synthesis and lipolysis, *J. Dairy Sci.*
524 86 (2003) 1751–1770. [https://doi.org/10.3168/jds.S0022-0302\(03\)73761-8](https://doi.org/10.3168/jds.S0022-0302(03)73761-8).
- 525 [23] A. Leduc, S. Le Guillou, L. Bianchi, L.O. Correia, M. Gelé, J. Pires, P. Martin, C.
526 Leroux, F. Le Provost, M. Boutinaud, Milk proteins as a feed restriction signature
527 indicating the metabolic adaptation of dairy cows, *Sci. Rep.* 12 (2022) 18886.
528 <https://doi.org/10.1038/s41598-022-21804-1>.
- 529 [24] J. Kurokawa, H. Nagano, O. Ohara, N. Kubota, T. Kadowaki, S. Arai, T.
530 Miyazaki, Apoptosis inhibitor of macrophage (AIM) is required for obesity-
531 associated recruitment of inflammatory macrophages into adipose tissue, *Proc.*

532 Natl. Acad. Sci. U. S. A. 108 (2011) 12072–12077.
533 <https://doi.org/10.1073/pnas.1101841108>.

534 [25] J. Kurokawa, S. Arai, K. Nakashima, H. Nagano, A. Nishijima, K. Miyata, R. Ose,
535 M. Mori, N. Kubota, T. Kadowaki, Y. Oike, H. Koga, M. Febbraio, T. Iwanaga, T.
536 Miyazaki, Macrophage-derived AIM is endocytosed into adipocytes and
537 decreases lipid droplets via inhibition of fatty acid synthase activity, *Cell Metab.*
538 11 (2010) 479–492. <https://doi.org/10.1016/j.cmet.2010.04.013>.

539 [26] Y. Iwamura, M. Mori, K. Nakashima, T. Mikami, K. Murayama, S. Arai, T.
540 Miyazaki, Apoptosis inhibitor of macrophage (AIM) diminishes lipid droplet-
541 coating proteins leading to lipolysis in adipocytes, *Biochem. Biophys. Res.*
542 *Commun.* 422 (2012) 476–481. <https://doi.org/10.1016/j.bbrc.2012.05.018>.

543 [27] L. Bernard, C. Leroux, Y. Chilliard, Expression and Nutritional Regulation of
544 Lipogenic Genes in the Ruminant Lactating Mammary Gland, in: Z. Bösze (Ed.),
545 *Bioact. Compon. Milk*, Springer New York, New York, NY, 2008: pp. 67–108.
546 https://doi.org/10.1007/978-0-387-74087-4_2.

547 [28] E. Alichanidis, A. Michaelidou, Glycoproteins in the heat-stable and acid-stable
548 fraction of ovine milk, *J. Dairy Res.* 57 (1990) 507–515.
549 <https://doi.org/10.1017/S0022029900029551>.

550 [29] E. Vanbergue, J.-L. Poulet, J.-L. Peyraud, C. Hurtaud, Cow milk lipolysis
551 updates: determining factors and biochemical mechanisms, *INRA Prod. Anim.*
552 33 (2020) 41–51. <https://doi.org/10.20870/productions-animales.2020.33.1.3178>.

553 [30] C. Kolar, J. Brunner, Proteose-peptone fraction of bovine milk - lacteal serum
554 components-5 and component-8 - casein-associated glycoproteins, *J. Dairy Sci.*
555 53 (1970) 997-. [https://doi.org/10.3168/jds.S0022-0302\(70\)86335-4](https://doi.org/10.3168/jds.S0022-0302(70)86335-4).

556 [31] C. Kolar, J. Brunner, Pproteose-peptone fraction of bovine milk - distribution in
557 protein system, *J. Dairy Sci.* 52 (1969) 1541-. [https://doi.org/10.3168/jds.S0022-0302\(69\)86789-5](https://doi.org/10.3168/jds.S0022-0302(69)86789-5).

558

559 [32] A.P. Beigneux, M.M. Weinstein, B.S. Davies, P. Gin, A. Bensadoun, L.G. Fong,
560 S.G. Young, GPIHBP1 and lipolysis: an update, *Curr. Opin. Lipidol.* 20 (2009).
561 [https://journals.lww.com/co-](https://journals.lww.com/co-lipidology/Fulltext/2009/06000/GPIHBP1_and_lipolysis__an_update.11.aspx)
562 [lipidology/Fulltext/2009/06000/GPIHBP1_and_lipolysis__an_update.11.aspx](https://journals.lww.com/co-lipidology/Fulltext/2009/06000/GPIHBP1_and_lipolysis__an_update.11.aspx).

563 [33] P. Iverius, A. Ostlund-Linqvist, Lipoprotein-lipase from bovine milk - Isolation
564 procedue, chemical characteriztion, and molecular-weight analysis, *J. Biochem.*
565 *Chem.* 251 (1976) 7791–7795.

- 566 [34] G. Bengtsson, T. Olivecrona, Activation of lipoprotein-lipase by apolipoprotein-CII
567 - Demonstration of an effect of the activator on the binding of the enzyme to
568 milk-fat globules, *FEBS Lett.* 147 (1982) 183–187. [https://doi.org/10.1016/0014-](https://doi.org/10.1016/0014-5793(82)81038-7)
569 [5793\(82\)81038-7](https://doi.org/10.1016/0014-5793(82)81038-7).
- 570 [35] E.A. Horst, E.J. Mayorga, M. Al-Qaisi, S. Rodriguez-Jimenez, B.M. Goetz, M.A.
571 Abeyta, P.J. Gordon, S.K. Kvidera, L.H. Baumgard, Evaluating effects of zinc
572 hydroxychloride on biomarkers of inflammation and intestinal integrity during
573 feed restriction, *J. DAIRY Sci.* 103 (2020) 11911–11929.
574 <https://doi.org/10.3168/jds.2020-18860>.
- 575 [36] A. Sarikas, T. Hartmann, Z.-Q. Pan, The cullin protein family, *Genome Biol.* 12
576 (2011) 220. <https://doi.org/10.1186/gb-2011-12-4-220>.
- 577 [37] L. Ding, W. Sun, M. Balaz, A. He, M. Klug, S. Wieland, R. Caiazzo, V. Raverdy,
578 F. Pattou, P. Lefebvre, I.J. Lodhi, B. Staels, M. Heim, C. Wolfrum, Peroxisomal
579 β -oxidation acts as a sensor for intracellular fatty acids and regulates lipolysis,
580 *Nat. Metab.* 3 (2021) 1648–1661. <https://doi.org/10.1038/s42255-021-00489-2>.
- 581 [38] X. Wang, H. Wang, B. Xu, D. Huang, C. Nie, L. Pu, G.J.M. Zajac, H. Yan, J.
582 Zhao, F. Shi, B.T. Emmer, J. Lu, R. Wang, X. Dong, J. Dai, W. Zhou, C. Wang,
583 G. Gao, Y. Wang, C. Willer, X. Lu, Y. Zhu, X.-W. Chen, Receptor-Mediated ER
584 Export of Lipoproteins Controls Lipid Homeostasis in Mice and Humans, *Cell*
585 *Metab.* 33 (2021) 350-366.e7. <https://doi.org/10.1016/j.cmet.2020.10.020>.
- 586 [39] B.H. Hummer, N.F. de Leeuw, C. Burns, L. Chen, M.S. Joens, B. Hosford, J.A.J.
587 Fitzpatrick, C.S. Asensio, HID-1 controls formation of large dense core vesicles
588 by influencing cargo sorting and trans-Golgi network acidification, *Mol. Biol.*
589 *CELL.* 28 (2017) 3870–3880. <https://doi.org/10.1091/mbc.E17-08-0491>.
- 590 [40] W. Du, M. Zhou, W. Zhao, D. Cheng, L. Wang, J. Lu, E. Song, W. Feng, Y. Xue,
591 P. Xu, T. Xu, HID-1 is required for homotypic fusion of immature secretory
592 granules during maturation, *ELife.* 5 (2016) e18134.
593 <https://doi.org/10.7554/eLife.18134>.

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Table 1: Morning milk parameters in LL and HL groups.

	LL	HL	SEM	p-val lipolysis	Significa nce of lipolysis	Signific ance of period
Milk yield and gross composition						
Milk yield (kg)	18.5	16.7	0.62	0.031	*	NS
Milk fat content (g secreted)	710.7	611.5	31.8	0.056	NS	NS
Milk protein content (g secreted)	583.4	486.1	24.2	0.0004	***	NS
Milk lactose content (g secreted)	908.1	825.3	31	0.044	*	NS
Somatic Cell Count (x10 ³ /mL)	34.3	33.5	8	0.967	NS	NS
Milk fat characteristics						
Lipolysis (mEq/100g fat)	0.32	0.84	0.09	0.002	**	NS
Lipoprotein Lipase activity (nmol/min/ml)	514.8	744.2	35.7	0.002	**	NS
Milk fat globule diameter (d _{4,3} [*]) (µm)	3.74	3.65	0.09	0.587	NS	NS
Milk fat globule diameter (d _{3,2} [*]) (µm)	3.31	3.13	0.07	0.185	NS	NS
Milk fat globule area (S [*]) (m ²)	1.97	2.11	0.05	0.147	NS	NS
Milk proteins characteristics						
Protein content (g/kg)	31.2	29	0.5	0.011	*	NS
Nitrogen content (g/kg)	32.5	30.3	0.5	0.01	**	NS
Non-casein nitrogen (g/kg)	6.4	6	0.1	0.046	*	*
Non-protein nitrogen (g/kg)	1.25	1.32	0.04	0.215	NS	NS
Casein content (g/kg)	26	24.3	0.5	0.008	**	NS
Soluble protein content (g/kg)	5.2	4.7	0.2	0.011	*	NS
Casein/protein ratio (%)	82.8	83.6	0.5	0.054	NS	NS

* $d_{4,3} = \frac{\sum(N_i \times d_i^4)}{\sum(N_i \times d_i^3)}$

* $d_{3,2} = \frac{\sum(N_i \times d_i^3)}{\sum(N_i \times d_i^2)}$

* $S = \frac{6}{\rho} \times d_{3,2}$ (with N_i the number of MFG in diameter class d_i and ρ the density of the particle considered (0.92 for fat))

P-values were significant at <0.001 (***) ; <0.01 (**) and <0.05 (*)

NS = not significant

Table 2: Differentially regulated proteins in HL group compared with LL group from the parametric univariate differential analysis (Diff-A).

Accession	Gene name	Protein name	Raw abundance ratio (HL/LL)	FC	RSD	Adjusted-Pvalue
A0A3Q1M3L6	Uncharacterized protein	Immunoglobulin heavy constant mu	2.0	1.6	0.262	0.078
A6QNW7	CD5L	CD5 molecule like	3.1	2.2	0.624	0.078
A0A3Q1LRW4	Uncharacterized protein	Immunoglobulin heavy constant mu	2.7	1.9	0.470	0.078
P06394	KRT10	Keratin, type I cytoskeletal 10	2.7	2.1	0.590	0.078
A0A3Q1M193	GP2	Glycoprotein 2	2.1	1.7	0.315	0.078
Q32PJ2	APOA4	Apolipoprotein A-IV	5.6	2.9	0.739	0.078
Q2TBI0	LBP	Lipopolysaccharide-binding protein	2.6	1.9	0.521	0.080
E1BM39	CUL9	Cullin 9	0.3	-2.4	0.760	0.099

Table 3: List of 30 proteins from component 1 of sparse multi-level multivariate analysis (sPLS – milk lipolysis) contributing to LL or HL group

Accession	Gene Name	Protein Name	Importance of contribution to comp1	
			HL	LL
P02663	CSN1S2	Alpha-S2-casein	0.338	.
Q03247	APOE	Apolipoprotein E	0.314	.
A6QNW7	CD5L	CD5 molecule like	0.313	.
Q2TBI0	LBP	Lipopolysaccharide-binding protein	0.242	.
P02662	CSN1S1	Alpha-S1-casein	0.231	.
A0A3Q1LRW4	Uncharacterized protein	Immunoglobulin heavy constant mu	0.192	.
Q32PJ2	APOA4	Apolipoprotein A-IV	0.140	.
P15497	APOA1	Apolipoprotein A-I	0.133	.
A0A3Q1LQY1	CNTFR	Ciliary neurotrophic factor receptor	0.119	.
A0A3Q1M193	GP2	Glycoprotein 2	0.105	.
Q29S21	KRT7	Keratin, type II cytoskeletal 7	0.099	.
P17697	CLU	Clusterin	0.070	.
P11017	GNB2	Guanine nucleotide-binding protein G	0.065	.
P81265	PIGR	Polymeric immunoglobulin receptor	0.054	.
F1MKU3	BSPRY	B-box and SPRY domain containing Polyunsaturated fatty acid lipoxigenase	0.032	.
P27479	ALOX15	ALOX15	.	-0.378
P31039	SDHA	Succinate dehydrogenase	.	-0.345
F1N647	FASN	Fatty acid synthase	.	-0.224
Q28024	GNG12	Guanine nucleotide-binding protein G	.	-0.214
A7YY49	SURF4	Surfeit locus protein 4	.	-0.158
A2VDV2	STK38	Serine/threonine-protein kinase 38	.	-0.139
Q08E22	HID1	Chromosome 17 open reading frame 28 ortholog	.	-0.120
Q4GZT4	ABCG2	Broad substrate specificity ATP-binding cassette transporter ABCG2	.	-0.117
E1BPK6	MYO6	Unconventional myosin-VI	.	-0.111
P23004	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	.	-0.076
A3KMV5	UBA1	Ubiquitin-like modifier-activating enzyme 1	.	-0.048
A3KN04	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	.	-0.036
A0A3Q1MSN7	COASY	Coenzyme A synthase	.	-0.033
A0A3Q1LTV4	RAB3GAP2	RAB3 GTPase activating non-catalytic protein subunit 2	.	-0.030
A0A3Q1MFP2	RAB3GAP1	Rab3 GTPase-activating protein catalytic subunit	.	-0.023

Table 4: List of 30 proteins from component 1 of sparse multi-level multivariate analysis (sPLS – LPL activity) contributing to LL or HL group

Accession	Gene name	Protein name	Importance of contribution to comp1	
			HL	LL
A0A3Q1M193	GP2	Glycoprotein 2	0.442	.
F1MKU3	BSPRY	B-box and SPRY domain containing	0.305	.
P06394	KRT10	Keratin, type I cytoskeletal 10	0.244	.
P20072	ANXA7	Annexin A7	0.208	.
P12624	MARCKS	Myristoylated alanine-rich C-kinase substrate	0.191	.
A6QNW7	CD5L	CD5 molecule like	0.164	.
E1B749	SLC5A9	Solute carrier family 5 member 9	0.147	.
O18875	SLC6A8	Sodium- and chloride-dependent creatine transporter 1	0.126	.
A0A3Q1M3L6	Uncharacterized protein	Immunoglobulin heavy constant mu	0.106	.
Q9XSG3	IDH1	Isocitrate dehydrogenase	0.104	.
Q29S21	KRT7	Keratin, type II cytoskeletal 7	0.079	.
E1BEH7	TC2N	Tandem C2 domains, nuclear	0.079	.
A0A3Q1LQY1	CNTFR	Ciliary neurotrophic factor receptor	0.063	.
P09487	ALPL	Alkaline phosphatase, tissue-nonspecific isozyme	0.056	.
Q32LM0	SH3GLB1	Endophilin-B1	0.046	.
Q1RMU4	ERLIN2	Erlin-2	0.036	.
P81125	NAPA	Alpha-soluble NSF attachment protein	0.015	.
Q08E22	HID1	Chromosome 17 open reading frame 28 ortholog	.	-0.344
A5D9A8	SQLE	Squalene monooxygenase	.	-0.327
E1BM39	CUL9	Cullin 9	.	-0.275
F1MUP9	VAT1	Vesicle amine transport 1	.	-0.271
Q2HJ97	PHB2	Prohibitin-2	.	-0.215
F1MEX9	ACSL3	Acyl-CoA synthetase long chain family member 3	.	-0.136
A0A3Q1LVG9	NDRG4	NDRG family member 4	.	-0.100
A0A3Q1LMJ5	ATP13A3	ATPase 13A3	.	-0.083
Q71SP7	FASN	Fatty acid synthase	.	-0.081
F1N545	ANKRD13A	Ankyrin repeat domain 13A	.	-0.032
P63009	AP2B1	AP-2 complex subunit beta	.	-0.020
Q1RMP9	CMTM8	CKLF-like MARVEL transmembrane domain-containing protein 8	.	-0.018
A7YY49	SURF4	Surfeit locus protein 4	.	-0.010

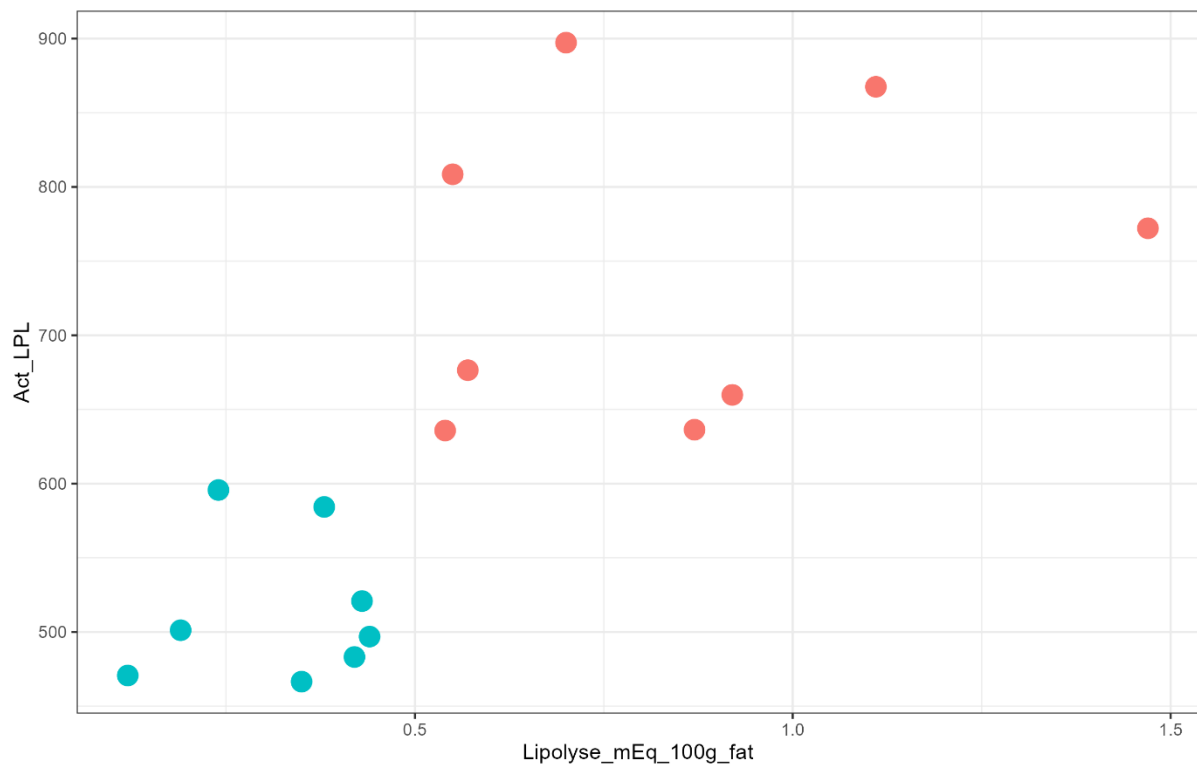


Figure 1: Plot regression between lipolysis (mEq/100g of fat) and LPL activity in milk (nmol/mn/ml). Blue dots are from LL group and red dots are from HL group.

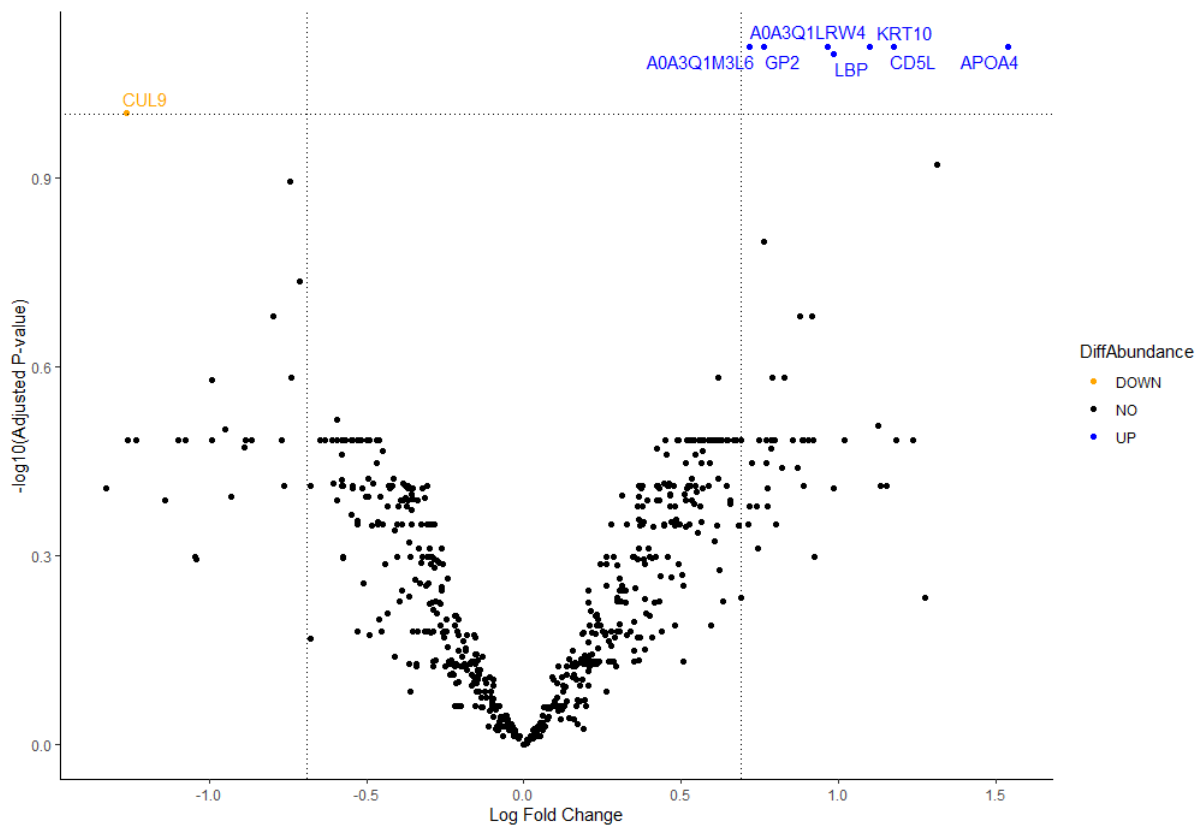


Figure 2: Volcano plot displays log fold changes on the x-axis versus a measure of statistical significance (Adjusted P-value) on the y-axis from the parametric univariate differential analysis (Diff-A). Gene Name of proteins with a higher abundance in HL than LL group are in blue. Gene Name of proteins with a lower abundance in HL than in LL group are in orange.

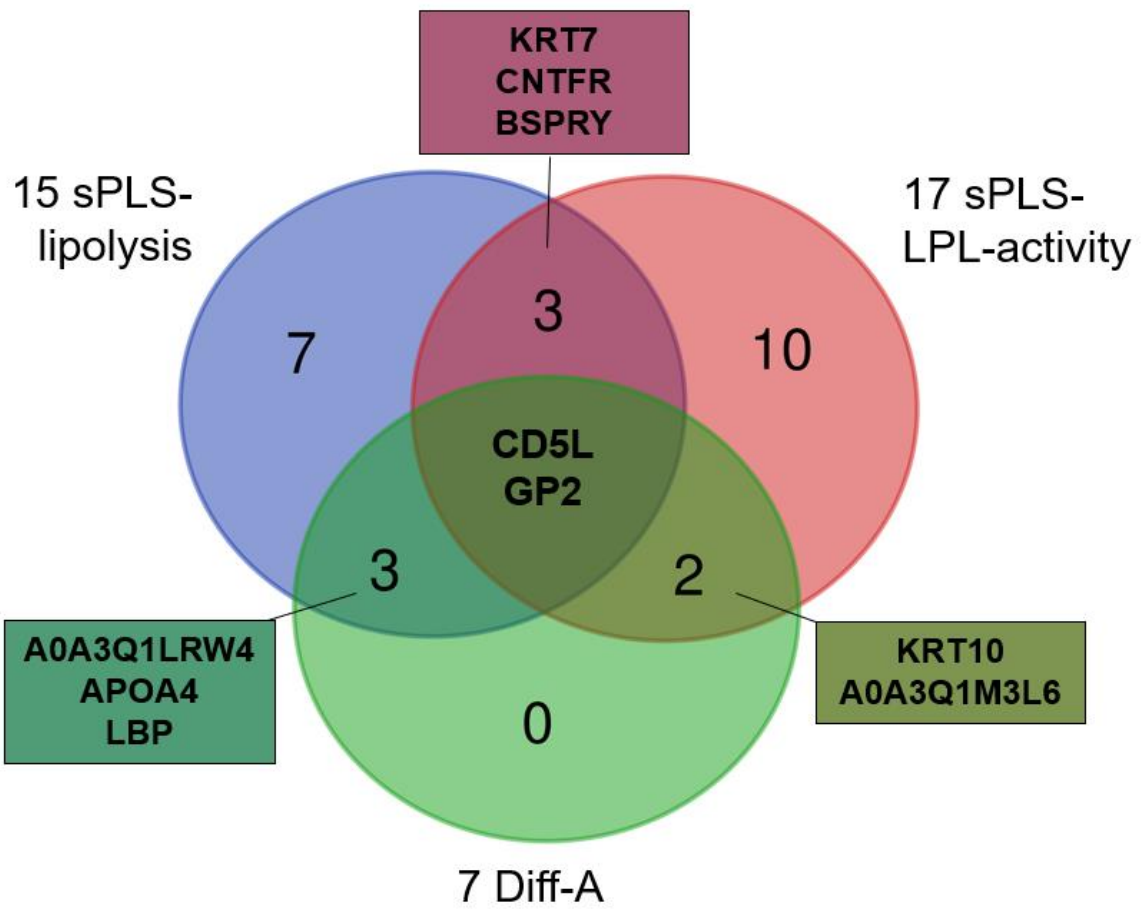


Figure 3: Venn diagram comparing proteins lists addressing HL group from sPLS-lipolysis (n=15), sPLS-LPL-activity (n=17) and differential analysis (n=7).

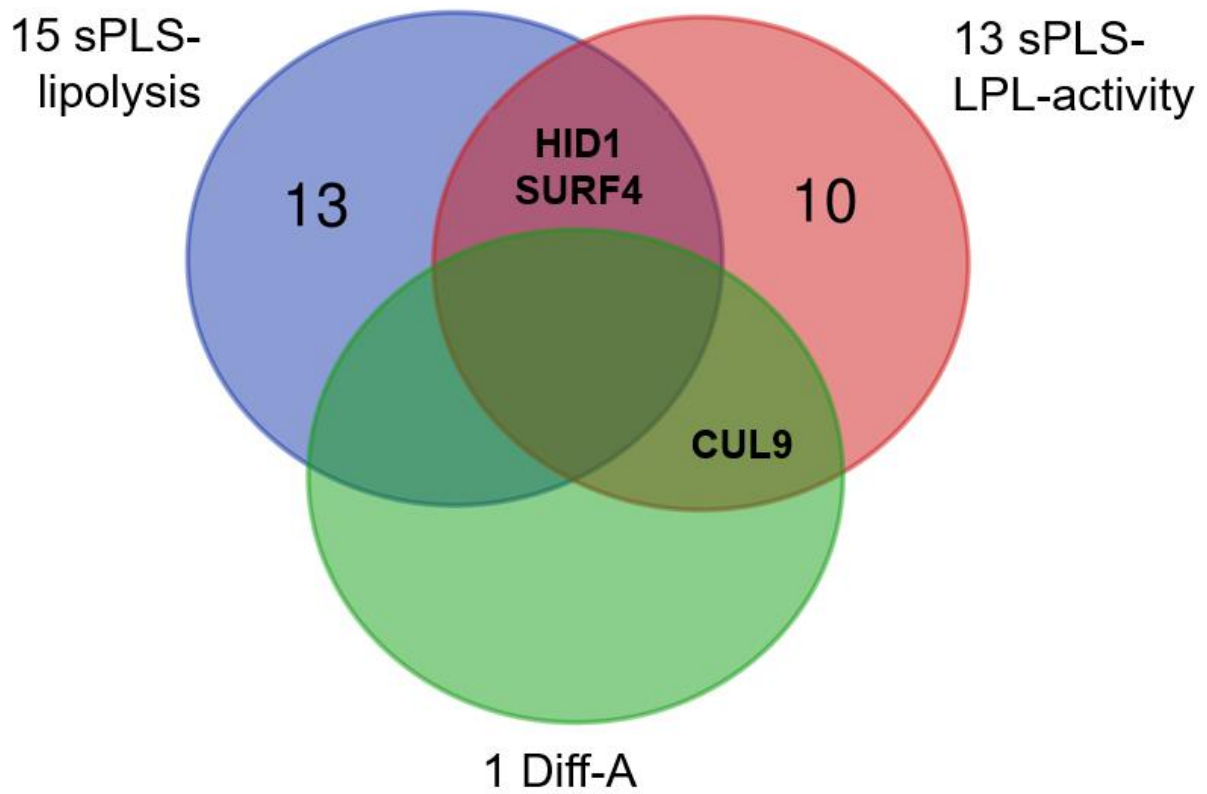


Figure 4: Venn diagram comparing proteins lists addressing LL group from sPLS-lipolysis (n=15), sPLS-LPL-activity (n=13) and differential analysis (n=1).

Supplementary Table S1: Dry matter, protein and energy intakes, energy balance and efficiency of protein digestible in intestine for LL and HL groups of cows

	LL	HL	SEM	p-val lipolysis	Signifi cance of lipolysi s	Signific ance of period
DMI (kg/d)	21,1	15,8	0,8	0,000	***	NS
PDI* (g/d)	1761,6	1306,1	74,9	0,000	***	NS
NEL requirements (MJ/d)	19,69	17,56	0,65	0,016	*	NS
PDI efficiency**	0,83	0,84	0,01	0,023	*	**
NEL balance (MJ/kg DM)	-5,7	-21,9	2,8	0,003	**	NS

*PDI = protein digestible in the intestine (INRA, 2018)

**PDI efficiency = $(67,5 - 0,52 \times (\text{PDI} - 100) + 0,014 \times (\text{MilkProteins} - 1000)) / 100$ (INRA, 2018)

Accession	Peptide count	Unique peptides	Confiden score	Enova (p value)	Max fold	Change Power	Highest mean condition		Lowest mean condition		Mass	Description	c8_HL	c6_HL	c5_HL	c3_HL	c4_HL	c1_HL	c7_HL	c2_HL	c8_LL	c6_LL	c5_LL	c3_LL	c4_LL	c1_LL	c7_LL	c2_LL	
							HL	LL	HL	LL																			
A0A031M3L6 A0A031M3L3	3	3	288.6	0.00015	0.07954	2.20488	0.99405	LL	LL	40450	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1	3226518	2621250	4618716	4488874	3744970	4456664	3369445	4974398	2228555	1349347	1586230	2537017	2647998	1919380	2153799	1202398		
P81265 PIGR_BOVIN;F1MR	9	8	775.38	0.00033	0.07954	3.27159	0.85556	LL	LL	82383	Polymeric immunoglobulin receptor OS=Bos taurus OX=9913 GN=PIGR PE	18491661	17827337	16234862	5688932	24959464	13957555	22436900	24789977	6311510	16559764	5968600	10893410	16724890	9121268	7368834	17332609		
E1BM39 E1BM39_BOVIN	3	2	167.06	0.00048	0.07954	4.08048	0.97886	LL	LL	280394	Cullin 9 OS=Bos taurus OX=9913 GN=CU9 PE=3 SV=3	57721	42068	57630	12035	63371	155657	32947	24046	106520	228090	731736	61953	262431	136179	78939	66437		
A5D9A8 A5D9A8_BOVIN	3	3	234.75	0.00055	0.07954	2.7695	0.97575	LL	LL	63250	Squalene epoxidase OS=Bos taurus OX=9913 GN=SQLE PE=2 SV=1	267138	333860	222873	348292	513451	176116	265883	319247	492317	1316786	1651862	620758	482820	269110	337201	1066616		
A6QNW7 A6QNW7_BOVIN	2	2	154.21	0.00059	0.07954	3.25975	0.97403	LL	LL	50179	D5 molecule like OS=Bos taurus OX=9913 GN=D5L PE=3 SV=5	643807	592909	562089	266766	338739	337445	131201	310142	127599	26711	80848	104284	129637	207537	127133	226291		
P62935 PPIA_BOVIN;GX3E	5	2	453.78	0.00066	0.07954	1.91686	0.97125	LL	LL	17858	Phenylprolyl-tRNA trans isomerase A OS=Bos taurus OX=9913 GN=PP1A PE	4100575	2290016	3584617	6517901	4244459	2079380	4202181	6021004	7403051	8048892	6802231	6978896	4898127	8894638	7140479	1253203		
Q0E822 Q0E822_BOVIN	2	2	115.78	0.00078	0.07954	2.21171	0.9662	LL	LL	88424	Chromidome 17 open reading frame 28 ortholog OS=Bos taurus OX=9913	1500079	194259	380989	341137	135199	186125	185060	946040	562788	336053	359689	236875	380311	254266	361512			
A0A031LRW4 A0A031LRW3	3	3	219.5	0.00085	0.07954	2.97963	0.96359	LL	LL	47130	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1	4893882	5780402	4429250	9578073	1570842	5224401	9815090	6730173	1070669	6179313	1070669	1817993	1951621	2026944	2145015	1817171	2387631	4305990
A6QNZ7 A6QNZ7_BOVIN;A1	4	4	749.45	0.00097	0.08093	2.95267	0.9589	LL	LL	54816	Keratin 10 (Epidermolytic hyperkeratosis; keratosis palmaris et plantaris) C	882223	963247	211321	391108	584185	724840	913247	6701319	194422	127432	142178	206594	386029	949395	241266	361512		
Q14814 Q14814_BOVIN;A0	9	9	738.22	0.00273	0.18811	1.6784	0.90436	LL	LL	20837	RAB2A, member RAS oncogene family OS=Bos taurus OX=9913 GN=RAB2F	10535272	3974009	7852213	4848207	7005446	4912477	11433578	9508143	7763388	9786634	10670024	6609125	12262340	18545996	12715467	15876130		
E1BNW4 E1BNW4_BOVIN	4	4	260.94	0.00275	0.18811	1.61707	0.90393	LL	LL	78539	Transmembrane channel-like protein OS=Bos taurus OX=9913 GN=TMCA F	1392826	1674433	2569599	1110141	1160836	938296	1818823	1389589	1368477	671131	780583	794407	807036	1223767	1257034	516457		
A0A031M193 A0A031M191	3	3	174.07	0.00307	0.19262	2.89491	0.8958	LL	LL	58427	Glycoprotein 2 OS=Bos taurus OX=9913 GN=GP2 PE=1 SV=1	4238810	7983325	6800899	7208158	5478408	6206673	5097694	10608024	2424584	3124936	1604835	2466313	4036523	3978824	2995935	4722875		
A0A031LK80 A0A031LK80	2	2	66.53	0.00364	0.20491	3.14467	0.88234	LL	LL	53280	Lipopolysaccharide-binding protein OS=Bos taurus OX=9913 GN=LB PE=4	423454	250408	120660	126822	145365	106415	143257	227590	39144	162852	91116	79247	55110	38138	298319	96054		
Q3ZC65 Q3ZC65_BOVIN	6	6	543.39	0.00411	0.20491	1.89149	0.87184	LL	LL	40573	AUP1, lipid droplet-regulating VLDL assembly factor OS=Bos taurus OX=99	7645294	7534288	7454262	6163405	6756025	7592812	7761627	3795844	6607011	10030098	11771302	8395895	9106829	7845246	7614252	1306290		
Q28024 GBG12_BOVIN	3	3	168.18	0.00426	0.20491	1.66504	0.86675	LL	LL	7852	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=	769263	514114	879234	596975	948293	1372805	813274	2282752	1951921	2157106	1366973	1337010	1375231	3103622	2503532	1936831		
A0A031MB37 A0A031MB35	5	5	334.19	0.00622	0.24533	1.92418	0.83157	LL	LL	82007	AcyL-CoA synthetase short chain family member 2 OS=Bos taurus OX=9913	2114252	1577784	2816705	4837036	4059671	4029825	2611713	2284668	4298939	6310487	10846871	6608888	4959270	2152739	2854309	9948758		
P09487 P9BT_BOVIN	5	5	355.76	0.00634	0.24533	2.15142	0.82958	LL	LL	57156	Alkaline phosphatase, tissue-nonspecific isozyme OS=Bos taurus OX=9913	8423425	5029499	3210044	4136854	2849111	3978422	1041247	1426687	2338748	403245	2313361	1715647	4093220	3497860	3559427	1783223		
A0A031ME17 A0A031ME17	2	2	258.92	0.00652	0.24533	1.87271	0.82648	LL	LL	52267	Presenilin OS=Bos taurus OX=9913 GN=PSN1 PE=3 SV=1	521189	478065	302372	1005377	251318	870944	869947	939459	708107	1510679	1229433	1757367	540016	828499	580572	2039818		
A0A031MKC8 A0A031MKC4	4	3	244.33	0.00757	0.26146	1.61746	0.80978	LL	LL	50852	Keratin, type II cytoskeletal 7 OS=Bos taurus OX=9913 GN=KR17 PE=1 SV=	348587	603401	418522	326480	350165	185414	216983	479894	147272	216983	99392	253901	203872	181963	273669	180700		
A0A031LQY1 A0A031LQY1	4	4	395.17	0.00902	0.26146	1.88002	0.78854	LL	LL	42982	Ciliary neurotrophic factor receptor OS=Bos taurus OX=9913 GN=CNTRF P	4635077	1967033	1984517	1919417	2108630	2407122	3502870	2446000	930868	528658	360485	796890	3732271	1873800	2069573	667784		
A0A031M3N0 A0A031M3F9	8	7	574.94	0.00955	0.26146	4.76744	0.78136	LL	LL	43051	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1	3104310	1776546	302598	495812	393613	511824	1920270	606006	323928	259873	122680	55187	376609	179461	155496	134563		
F1MH40 F1MH40_BOVIN	3	3	134.93	0.01004	0.26146	2.05099	0.77494	LL	LL	26318	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=2	1730097	1772626	1371175	776731	263100	960929	1278585	1693129	280019	432583	334291	512970	1446930	717647	1189429	396489		
A9YX73 SEF15_BOVIN	2	2	145.18	0.01054	0.26146	1.95847	0.76865	LL	LL	17964	Selenenoprotein F OS=Bos taurus OX=9913 GN=SELENOF PE=2 SV=2	239484	187935	500675	679423	220178	325444	449553	739840	482334	903434	806062	491656	791788	786816	526637	2228024		
P12624 MARCS_BOVIN	3	3	252.76	0.01059	0.26146	2.4738	0.75468	LL	LL	31546	Myristoylated alanine-rich C-kalivase substrate OS=Bos taurus OX=9913 GN	1356703	1202599	833963	385107	570318	938623	639730	628274	63097	53917	63097	122707	133779	635756	921401	465568	48135	
Q18875 GSG6_BOVIN;A0	10	10	541	0.01204	0.26146	1.74348	0.73059	LL	LL	155250	RAB7 GTPase-activating non-catalytic protein subunit 2 OS=Bos taurus OX=	819971	684956	841835	455899	1248151	384673	852648	748010	2727916	662038	1127075	1137708	1309198	1421875	1540285	695999		
O15671 GSE6A_BOVIN	3	3	220.18	0.0132	0.26146	1.47092	0.73774	LL	LL	70629	Sodium- and chloride-dependent creatine transporter 1 OS=Bos taurus OX=	924262	1028489	1345651	892580	531101	805669	1020297	853460	6072041	298207	556840	547517	568751	903711	950356	46262		
A0A031MK38 A0A031MK3	10	10	641.79	0.01327	0.26266	1.74728	0.73692	LL	LL	81483	Thyestine cytochrome b5/putase family member OS=Bos taurus OX=9913 GN=	4018389	3277247	38666579	44694265	31218702	19000071	40310361	24919069	45001505	7982774	113951178	61645104	37061194	34428648	32789309	6750557		
A0A14T831 A0A14T831_1	3	3	245.17	0.01364	0.26312	1.65172	0.73294	LL	LL	16384	Cypene B OS=Bos taurus OX=9913 GN=CSTB PE=3 SV=2	1170879	758225	778259	2115827	957953	722953	1490000	931657	1206587	1049224	1505295	1573080	1161361	2091382	1484808	4207306		
Q28065 C4BPB_BOVIN;A0	4	4	182.09	0.01423	0.26366	3.87951	0.72686	LL	LL	68841	Cab-binding protein alpha chain OS=Bos taurus OX=9913 GN=C4BPB PE=2	384050	498445	288435	66578	10100	465844	297912	85171	36782	129449	69469	15268	20536	48367	29628	228893		
A0A031M1J5 A0A031M1J5	8	8	638.27	0.01437	0.26366	1.69107	0.72537	LL	LL	141962	Cation-transporting ATPase OS=Bos taurus OX=9913 GN=ATP13A3 PE=3 S	2184290	2765134	2924505	2993222	2740416	3158788	2806095	2177996	3893128	10147833	679569	4910873	3032263	2236400	2576470	3629961		
A0A14T897 A0A14T897_5	5	5	391.07	0.01559	0.27168	1.86065	0.70953	LL	LL	69278	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=3 SV=2	552810	512617	891593	498733	648380	876041	918869	1342093	393748	511213	759848	246604	488320	673436	347039	211724		
G5E6N4 G5E6N4_BOVIN	2	2	102.95	0.01694	0.27168	1.74547	0.70131	LL	LL	41723	Palmitoyltransferase OS=Bos taurus OX=9913 GN=PDHHC18 PE=3 SV=2	59117	17238	76560	72388	47171	24136	28068	76055	119161	38027	76692	42220	70203	81234	136189	129260		
A0A031MKJ0 A0A031MKJ4	4	4	450.07	0.0171	0.27168	1.41322	0.69928	LL	LL	49429	FAS-associated factor 2 OS=Bos taurus OX=9913 GN=FA2 PE=4 SV=1	3354205	4065670	3689523	3827263	2264581	3137224	3433115	2683479	3256532	4356339	5737916	2979207	3517992					

A0A3Q1L1U2 A0A3Q1L1U2_2	4	2	383.54	0.06263	0.35191	1.38472	0.46813	HL	LL	55488	Anxrer OS-Bos taurus OX-9913 GN-ANXAK7 PE=1 SV=1	1529932	1369942	1369675	1447517	1518536	1217346	1548335	1860984	1173251	456663	600472	1114488	1390209	1271622	1225384	790708
A0A3Q1LVG9 A0A3Q1LVG9_2	4	2	121.14	0.06335	0.35191	2.58146	0.46589	HL	LL	44909	NRDG family member 4 OS-Bos taurus OX-9913 GN-NDRG4 PE=4 SV=1	1012123	103263	31975	703719	46246	206094	49559	92051	61904	905120	484882	840211	1119490	1363691	1416567	447577
F1MLB8 F1MLB8_BOVIN.P1	7	7	581.16	0.06364	0.35191	1.81508	0.465	HL	LL	59653	AT synthase subunit alpha OS-Bos taurus OX-9913 GN-ATPSF1A PE=1 SV=1	121706	177294	261886	1711626	1653075	253816	471179	1258970	300185	1879162	858949	1253484	1213581	782053	1383566	3598483
A0A3Q1LYB4 A0A3Q1LYB4_6	6	6	372.76	0.06511	0.35239	1.36006	0.46052	HL	LL	37563	Syntaxin 3 OS-Bos taurus OX-9913 GN-STX3 PE=3 SV=1	7210758	7375898	8748547	5303185	5933924	9480739	10677219	4958598	4475666	762761	1912742	5025278	8691792	9510499	9093374	4678475
F1N116 F1N116_BOVIN.A0	8	8	494.54	0.06583	0.35239	1.46587	0.45837	HL	LL	92027	Gelsolin OS-Bos taurus OX-9913 GN-GSN PE=1 SV=2	2067625	2999108	1296172	1032635	2821905	2544757	3860350	2576334	2307605	336645	697902	1130886	2563257	1799801	3296721	991957
E1BM99 E1BM99_BOVIN_3	3	3	236.14	0.0661	0.35239	1.5496	0.47557	HL	LL	37783	Retinol dehydrogenase 11 OS-Bos taurus OX-9913 GN-RDH11 PE=3 SV=2	1043871	589269	729724	3948281	839921	744151	1271219	948889	872171	1193689	871779	506683	1876601	873333	1063431	1853488
F1MXE4 F1MXE4_BOVIN_2	2	2	151.91	0.06969	0.35654	1.71274	0.44722	HL	LL	45562	26S proteasome non-ATPase regulatory subunit 6 OS-Bos taurus OX-9913	40571	87417	34102	17438	183269	100301	108902	289243	78429	30111	2598	8830	69989	55934	230717	83966
F2Z411 F2Z411_BOVIN.A0A3	8	8	498.18	0.0707	0.35771	1.57195	0.4444	HL	LL	20467	GTP-binding protein Rho5 OS-Bos taurus OX-9913 GN-RHEB PE=4 SV=1	2380743	1437415	2265168	1667086	1701305	2230678	3003353	3087500	1801138	1465418	2733900	2349452	3889256	4033726	5235709	3496704
A0A3Q1LRL7 A0A3Q1LRL7_2	2	2	148.23	0.07171	0.35823	1.55363	0.4416	HL	LL	58225	Ytuclose kinase OS-Bos taurus OX-9913 GN-YX1L PE=1 SV=1	53699	140234	47949	222436	140691	62876	50632	111240	117543	344329	175150	125250	98612	51628	109363	170065
Q7YR99 Q7YR99_BOVIN_2	2	2	148.23	0.07233	0.35823	1.58128	0.43991	HL	LL	22381	Reticulon OS-Bos taurus OX-9913 GN-RTN4 PE=1 SV=2	247792	124823	295099	113434	136066	219166	240349	469420	287262	126951	408224	389983	460577	527452	157465	
A0A3Q1LYE7 A0A3Q1LYE7_2	3	3	478.43	0.07274	0.35823	1.42011	0.43879	HL	LL	21837	RAB1A, member RAS oncogene family OS-Bos taurus OX-9913 GN-RAB1A	14940887	9712159	7951142	10667764	12095728	12704552	17995602	14063890	11940108	29309739	19392814	16287263	14941062	10903186	15066166	38407563
F7YY49 SURFA_BOVIN.F1N1	2	2	112.26	0.0747	0.36263	1.29762	0.43558	HL	LL	30402	Surfactin locus protein A OS-Bos taurus OX-9913 GN-SURFA PE=2 SV=1	117251	117251	221837	301517	242422	171663	508244	263762	470282	507171	485628	348935	224617	317948	3680570	
A0A3Q1MWL7 A0A3Q1MW_3	3	3	128.76	0.07518	0.36263	1.57695	0.43231	HL	LL	184220	DENN domain containing 3 OS-Bos taurus OX-9913 GN-DENND3 PE=4 SV=1	39488	70264	110654	12484	116151	89540	81965	134694	67434	4160	36761	19186	95669	102169	94591	914
P80195 GLCM1_BOVIN.Q3	10	9	953.3	0.07632	0.36263	2.84178	0.42935	HL	LL	17141	GENY domain-dependent cell adhesion molecule 1 OS-Bos taurus OX-9913	64078449	24245386	86826587	87166225	53667656	77562767	586199525	4472289	6305077	23829553	27257874	22508319	145523200	128892789	68494225	69182238
A0A3QLUE9 A0A3QLUE9_2	2	2	123.14	0.07709	0.36263	1.46781	0.42737	HL	LL	16698	lg-like domain-containing protein OS-Bos taurus OX-9913 PE=1 SV=1	2644865	754844	428806	2186592	1657844	1675448	1209995	2546179	379475	453927	310222	707284	2832810	1937601	1542230	449475
Q6WQDS Q6WQDS_BOVIN_4	4	4	174.38	0.07733	0.36263	1.678	0.42676	HL	LL	95954	Toll-like receptor 4 OS-Bos taurus OX-9913 GN-TLR4 PE=2 SV=1	164078	483004	580606	106237	25025	147774	127766	260131	460603	507700	760006	371219	96261	262055	256146	220370
A0A498U20 A0A498U20_2	3	2	135.02	0.07811	0.36263	1.36614	0.42379	HL	LL	148566	Unconventional myosin-VI OS-Bos taurus OX-9913 GN-MYO6 PE=3 SV=1	10037	36362	51343	38681	126248	38441	84672	73291	68853	51807	135122	52344	74541	66021	83872	52634
Q08D98 FLOT1_BOVIN_3	6	6	445.71	0.07859	0.36263	1.32567	0.42478	HL	LL	47324	Flotillin-1 OS-Bos taurus OX-9913 GN-FLOT1 PE=2 SV=1	2196855	2122085	1457094	125120	118278	1964580	2694993	905866	1196429	688761	1503148	1176841	1525996	2426115	843140	1237744
F6R1D7 F6R1D7_BOVIN_5	5	5	152.16	0.08001	0.36482	1.38467	0.42006	HL	LL	35020	Family with sequence similarity B4 member 8 OS-Bos taurus OX-9913 GN	404112	425610	588836	316533	398223	338138	300993	476470	357534	57484	160508	285475	342439	375874	519711	161509
A0A3Q1LN63 A0A3Q1LN63_2	2	2	116.56	0.08113	0.36482	2.75765	0.41732	HL	LL	45688	Kelch-like ectodomain inhibitor OS-Bos taurus OX-9913 GN-SERPIN1 PE=1	120431	204428	38950	23959	197351	67274	779375	104698	62872	90506	50674	92014	24480	81284	50539	
A0A3Q1M9B5 A0A3Q1M9B_2	2	2	97.06	0.08154	0.36482	2.2036	0.41632	HL	LL	139145	High density lipoprotein binding protein OS-Bos taurus OX-9913 GN-HDL3	1569	8009	21257	27533	77523	11207	1087	47539	87557	217640	43219	27968	39762	23359	27224	144271
E1BA10 E1BA10_BOVIN_2	2	2	118.44	0.08198	0.36482	1.38786	0.41526	HL	LL	26648	RAB23, member RAS oncogene family OS-Bos taurus OX-9913 GN-RAB23	500542	101029	212222	93537	199398	250703	709665	291320	187317	323184	498487	221829	507317	239977	259495	69935
Q9BG11 PROXS_BOVIN_3	3	3	106.61	0.08405	0.36874	1.511	0.41034	HL	LL	23238	Peroxiredoxin-5, mitochondrial OS-Bos taurus OX-9913 GN-PRDX5 PE=2	340574	227004	258731	62862	246892	166897	436131	431683	373428	296688	230150	161448	569433	609873	541697	33361
Q68B55 TKT_BOVIN_4	4	4	124.92	0.08433	0.36874	1.576	0.40968	HL	LL	67963	Transketolase OS-Bos taurus OX-9913 GN-TKT PE=1 SV=1	209182	292677	129892	139294	384939	214666	305124	183141	229630	17514	26791	150783	232777	166914	239208	55588
F1N545 F1N545_BOVIN_5	4	4	278.28	0.08641	0.37349	1.59042	0.40488	HL	LL	67456	Ankyrin repeat domain 13A OS-Bos taurus OX-9913 GN-ANKRD13A PE=4	519344	581017	378113	897372	462972	448416	409824	506996	571214	1675867	1735123	1140098	331211	507913	472645	859738
A0A452D16 A0A452D16_B	5	5	378.72	0.08814	0.37391	1.54732	0.40286	HL	LL	60941	Glycyl-protein OS-Bos taurus OX-9913 GN-GPC PE=3 SV=1	473572	473572	372440	27496	389935	36822	80763	816994	309868	86762	378606	101973	552167	83217	108966	
Q5E555 GOGA7_BOVIN_4	4	4	221.82	0.08814	0.37391	1.54774	0.40966	HL	LL	15814	Glycyl-protein OS-Bos taurus OX-9913 GN-GOLGA7 PE=4	974466	666227	852003	845499	8118466	7020891	1238811	1295535	1011604	694390	732419	863795	1571765	1676718	2158993	1539000
A0A3Q1N1P7 A0A3Q1N1P7_2	2	2	72.63	0.08981	0.37458	1.50297	0.39726	HL	LL	26672	Rfx-related protein Rab-26 OS-Bos taurus OX-9913 GN-RAB26 PE=4 SV=1	161174	235850	125151	20896	125027	63844	209473	149828	149754	37753	10110	32979	21608	67056	177152	27039
A0A3Q1M253 A0A3Q1M25_2	2	2	82.96	0.09015	0.37458	1.47822	0.39652	HL	LL	53868	DENN domain containing 20 OS-Bos taurus OX-9913 GN-DENND20 PE=1	71074	157383	15051	12092	12077	176421	117990	194314	16773	537824	307252	165969	245393	15185	169426	101026
Q3S201 SH2Y1_BOVIN_2	2	2	77.72	0.09124	0.37585	1.48751	0.39415	HL	LL	37042	SH3 domain-containing YSC84-like protein OS-Bos taurus OX-9913 GN	907923	562947	427045	1039315	437571	604473	958450	462324	548349	1378049	818808	1371408	542812	349999	675506	1293101
Q2SCT1 STX19_BOVIN_6	6	6	603.36	0.09158	0.37585	1.39927	0.43942	HL	LL	33868	Syntaxin 19 OS-Bos taurus OX-9913 GN-STX19 PE=2 SV=1	3828347	2366125	2439429	1141314	1909137	3221951	298117	3060400	1339222	864736	912557	905172	1216524	3300412	3194500	864734
Q3S321 Q3S321_BOVIN_10	10	10	816.26	0.09209	0.37585	1.61157	0.39233	HL	LL	47573	Perilipin OS-Bos taurus OX-9913 GN-PLIN3 PE=2 SV=1	32280411	33982030	28701724	9185170	10800805	16603890	44578771	7996659	14203313	971467	11643635	13055652	11915010	16573899	12481725	9936007
G5E6P3 G5E6P3_BOVIN_3	3	3	640.36	0.09273	0.379	1.31273	0.38883	HL	LL	43919	G protein subunit alpha 13 OS-Bos taurus OX-9913 GN-GNA13 PE=4 SV=2	1627876	14217482	1275914	7165327	1060935	13524548	14913620	16412466	8965266	5116959	5128256	14166120	10774540	16737467	5923403	4607740
Q0V829 MRP_BOVIN_3	3	2	222.11	0.09794	0.3859	1.48599	0.38017	HL	LL	19813	MARCKS-related protein OS-Bos taurus OX-9913 GN-MARCKSL1 PE=2 SV	289266	349559	265223	45403	205010	302786	158752	127783	384397	11158	73272	28886	54641	483386	215261	38605
A0A3Q1MG04 A0A3Q1MG_4	4	4	243.56	0.098	0.3859	1.34136	0.38006	HL	LL	57430	Fibrinogen beta chain OS-Bos taurus OX-9913 GN-FGB PE=4 SV=1	1034499	823341	843464	122246	129581	343169	346117	540492	132729	905105	1546809	73612	237632	67796	225215	414569
F6RW2D F6RW2D_BOVIN_2	2	2	169.44	0.098	0.3859	2.24956	0.38004	HL	LL	38573	AK1 transferase OS-Bos taurus OX-9913 GN-DHDDS PE=3 SV=1	276697	291111	358534	758436	290931	517221	95986	312007	454158	3285128	134720	820564	99453	359121	301906	122445
Q0I059 PDXK_BOVIN_4	4	4	260.54	0.10091	0.391	1.43056	0.37429	HL	LL	34795	Pyrroldoxin kinase OS-Bos taurus OX-9913 GN-PDK PE=2 SV=1	2457007	3291746	2746430	901539	2984866	6988500	6112051	3116123	1390050	350028	805661	5736861	2963651	5890834	297865	
A0A3Q1M3X3 A0A3Q1M3X_2	2	2	70.6	0.10091	0.391	1.46255	0.37429	HL	LL	23663	Syndecan OS-Bos taurus OX-9913 GN-SDC PE=1 SV=1	455212	416237	379602	153620	472827	621689	395570</									

ASD7E1 ASD7_F1_BOVIN;F1	4	2	284.31	0.16498	0.44659	1.35474	0.2791	HL	LL	60893	Eth domain containing 3 OS=Bo... tous OX=9913 GN=EHND3 PE=2 SV=1	388266	373334	823949	402997	480448	269928	436708	396840	381803	180416	172987	371462	394255	301959	491493	208385
Q3Z7H1 G3X74 BOVIN;A03	10	9	925.33	0.16509	0.44659	1.22977	0.27898	HL	LL	77965	Sodium-dependent phosphate... transport protein 2B OS=Bo... tous OX=9913 GN=NP2B PE=3 SV=1	23682767	26417800	32626369	15217928	17492790	205031360	221108685	198664912	269477265	132267518	142303132	254054532	235955165	178840270	122697477	
G3X74 G3X74_BOVIN;Q3	3	2	83.39	0.16658	0.44659	2.21473	0.27726	HL	LL	13364	40S ribosomal protein S20 OS=... Bo... tous OX=9913 GN=RP20 PE=3 SV=1	53703	45417	49147	21633	229529	32185	80825	552194	217073	141263	26627	7854	503340	369633	588528	517646
G3X74 G3X74_BOVIN;Q3	3	2	281.22	0.16705	0.44659	1.52806	0.27766	HL	LL	85403	AP complex subunit beta OS=... Bo... tous OX=9913 GN=APB21 PE=3 SV=1	89733	92852	71691	325738	21895	131727	45657	151768	176539	453444	279422	426343	168785	74954	123723	266445
AOA3Q1MH4 AOA3Q1MH	8	8	585.21	0.16993	0.44659	1.48802	0.27354	HL	LL	99047	Cytoplasmic aconitate hydratase OS=... Bo... tous OX=9913 GN=ACO1 PE=3 SV=1	5236061	5900219	4579988	4653283	6186644	5873100	6079265	534314	7482555	27110242	7702839	8151194	5095960	4677056	4385329	6345141
F1MFK7 F1MFK7_BOVIN;F	11	11	667.45	0.17127	0.44726	1.35953	0.27207	HL	LL	81875	Uncharacterized protein OS=... Bo... tous OX=9913 PE=3 SV=3	178592227	205986210	26796620	11965117	14147042	2874865	15658807	16805477	14841586	4936340	19615399	9511297	5096932	26293399	18216028	5501633
AOA3Q1M2B2 AOA3Q1M2E	19	19	1428.75	0.17445	0.45297	1.12567	0.26863	HL	LL	183629	Complement C3 OS=Bo... tous OX=9913 GN=C3 PE=1 SV=1	6275450	3322776	4891430	3608629	6512458	5408736	8289953	2624170	6154900	1075971	1033389	1305611	15867058	3137885	5048533	3620283
ASD7E8 ASD7_BOVIN	9	9	510.82	0.17467	0.45297	1.33577	0.2884	HL	LL	56894	Protein disulfide-isomerase OS=... Bo... tous OX=9913 GN=PDIA3 PE=2 SV=1	6157546	123751	776943	438247	1617206	788404	1004802	2651387	1506315	467421	369818	263689	1641598	930938	1441347	388235
Q2TAD8 BAG5_BOVIN;Q	4	4	306.09	0.17548	0.45353	1.40528	0.26753	HL	LL	50923	BAG family major chaperone regulat... or OS=Bo... tous OX=9913 GN=1	438172	451076	436828	559754	51341	738319	419470	326362	725838	1327022	1359468	750837	500416	314293	278323	916519
F1MX05 F1MX05_BOVIN;Q	3	2	122.63	0.17632	0.45412	1.21686	0.26664	HL	LL	47285	Saccharopine dehydrogenase-like... oxidoreductase OS=Bo... tous OX=9913 GN=1	19449379	832076	1538013	1003695	495205	740794	999799	1054294	890523	387647	580334	1173098	888230	896274	619222	916519
Q3ZB69 PLS2_BOVIN	2	2	94.17	0.17951	0.45676	1.48955	0.26331	HL	LL	32555	Phospholipid scramblase 2 OS=... Bo... tous OX=9913 GN=PLSCR2 PE=2 SV=1	968816	890374	785301	529104	498366	1041543	1269158	1106113	765364	443522	1308440	783408	925692	2495199	2004299	1912983
F1MDM4 F1MDM4_BOVIN	2	2	84.84	0.17957	0.45676	3.39223	0.2631	HL	LL	21415	Protein expression-enhancing pro... tein OS=Bo... tous OX=9913 GN=REEP	15017	13248	69335	14239	3085	144779	24212	134361	24360	3435	318473	14927	37645	279249	433198	78696
AOA4S2D82 AOA4S2D82_	4	4	584.09	0.17973	0.45676	1.2666	0.26308	HL	LL	32777	Rho GTP-dissociation inhibitor 1 OS=... Bo... tous OX=9913 GN=RHGDIA PE=3 SV=1	3546552	1968444	1335978	4235984	1379554	1397954	3224491	2119936	3520288	1317391	4091810	3809350	2339273	4232623	2155949	3348550
F1MU09 F1MU09_BOVIN	8	8	458.87	0.17807	0.45676	1.37499	0.26203	HL	LL	42803	Vesicle amino transport 1 OS=Bo... tous OX=9913 GN=VAT1 PE=3 SV=1	10683860	1138399	2556670	22451491	10202879	9543891	10162690	11011629	12772956	19477049	45692138	288266209	10304753	12874906	10682221	1734497
AOA3Q1MF5 AOA3Q1MF5	4	4	255.91	0.18099	0.45676	1.75391	0.26178	HL	LL	32700	ADP/ATP translocase 2 OS=Bo... tous OX=9913 GN=SLC25A5 PE=3 SV=1	364375	539780	974434	427704	1878378	1222199	1294868	1963788	606459	561916	844783	1043525	2076412	1875274	6359310	2662317
F1MFK8 F1MFK8_BOVIN	2	2	86.51	0.1831	0.4583	1.38426	0.25963	HL	LL	87698	Lysine-tRNA ligase OS=Bo... tous OX=9913 GN=KARS1 PE=1 SV=2	400994	118513	74484	318825	1158356	1128843	616816	466341	667652	255026	113082	311365	790585	794724	942427	188168
E1BA29 E1BA29_BOVIN	9	8	352.84	0.18504	0.4583	1.38806	0.25768	HL	LL	42115	G protein subunit alpha h OS=Bo... tous OX=9913 GN=GNAQ PE=4 SV=1	4594396	4262714	6873066	1947814	4445113	6041295	4620980	3641487	3149972	1985573	1794414	1821387	5037695	5784925	6844290	1727543
F1MX6E F1MX6E_BOVIN;Q	17	17	2190.48	0.18517	0.4583	1.34179	0.25754	HL	LL	47815	Lactadherin OS=Bo... tous OX=9913 GN=MFE6 PE=4 SV=1	180771536	146468265	1032113700	333084349	180240486	157109540	1836718502	1139725437	123798834	298170000	178554000	275867645	180189721	1160338996	143095966	2402746864
E1BCP6 E1BCP6_BOVIN	4	4	204.05	0.18561	0.4583	1.21804	0.25711	HL	LL	130797	Thyrosine-protein kinase OS=Bo... tous OX=9913 GN=JAK2 PE=3 SV=2	260198	479129	561701	193854	542150	476332	170066	544992	496301	118129	405342	246409	124267	37473	53598	191653
PO4896 GNAS2_BOVIN;AO3	5	5	320.32	0.18586	0.4583	1.29193	0.25673	HL	LL	45680	Guanine nucleotide-binding protein... (G) subunit alpha isoforms short OS=...	21084159	15160228	19932104	35071183	15593337	15177219	20121086	16224557	1284366	29582469	23613599	2812029	1857997	20152080	16095891	24529900
Q2HJ65 VPS35_BOVIN	7	7	499.96	0.18647	0.4583	1.28623	0.25626	HL	LL	91693	Adenoviral protein sorting-associated... protein 35 OS=Bo... tous OX=9913 GN=3	714657	2403559	1588423	4466373	3372195	2571700	2606410	2108498	2516700	4102247	6006971	6701251	2607912	2578172	2114870	4357828
AOA3Q1LK2 AOA3Q1LK2_	9	8	64.15	0.18716	0.45849	1.15878	0.25558	HL	LL	53662	Aldehyde dehydrogenase oxidore... ductase OS=Bo... tous OX=9913 GN=LOC508879 PE=3 S	3270466	4814507	5046585	1026347	8147996	7563720	4652339	4111998	7294153	6330672	6743299	5800215	5192421	4358015	7614948	6203017
ASD7R9 ASD7R9_BOVIN	4	4	356.81	0.18817	0.45947	1.29696	0.25459	HL	LL	21216	NRAS protein OS=Bo... tous OX=9913 GN=NRAS PE=2 SV=1	2682940	1543656	1298583	1832355	1343744	1060450	2475544	1923018	1505098	3200305	1904262	1523229	1342653	1958572	1970253	542598
AOA3Q1MD5 AOA3Q1MD	4	4	160.02	0.19007	0.46123	1.59244	0.25278	HL	LL	119134	Ubiquitin-conjugation factor E4 A OS=... Bo... tous OX=9913 GN=UBE4A PE=1 SV=1	193644	250075	358604	503068	368822	525232	243346	246634	617233	1344191	838662	773927	167933	29098	207301	588511
F1MDG6 F1MDG6_BOVIN	3	3	126.65	0.19011	0.46123	1.40359	0.25269	HL	LL	54477	Annexin OS=Bo... tous OX=9913 GN=ANXA1 PE=3 SV=3	211466	236161	75980	34923	216863	17133	221993	160047	245901	21388	2336	21189	276040	84758	123323	9976
F1M077 F1M077_BOVIN	2	2	115.91	0.19127	0.46106	1.36567	0.25079	HL	LL	48941	Eukaryotic translation initiation fac... tor 5 OS=Bo... tous OX=9913 GN=EIF5	87932	151226	104312	144857	259144	108349	110439	331793	316793	103071	131753	20786	151750	306839	320362	150908
E1B1M5 E1B1M5_BOVIN	3	3	279.66	0.19321	0.46306	1.45723	0.24972	HL	LL	55584	Family with sequence similarity 83 m... ember F OS=Bo... tous OX=9913 GN=1	682599	1635705	1556176	551227	1307626	498712	1570645	489451	874989	1315810	1973576	9094468	5447084	411962	366453	1867358
AOA3Q1LH1 AOA3Q1LH1_	2	2	85.8	0.19441	0.46306	1.18015	0.24859	HL	LL	18957	Uncharacterized protein OS=Bo... tous OX=9913 PE=4 SV=1	86675	102971	83721	191144	350771	111768	155988	445277	160283	211416	115689	105754	215133	14442	24639	273817
AOA3Q1LH7 AOA3Q1LH7_	3	3	190.34	0.19432	0.46306	1.45117	0.24854	HL	LL	51584	Neuropilin OS=Bo... tous OX=9913 GN=NPTN PE=4 SV=1	449957	860296	956124	41231	463975	65283	320945	679940	323480	296325	125374	282990	522411	74795	485178	61465
E1B1M0 E1B1M0_BOVIN;A	10	10	548.18	0.19828	0.46306	1.15028	0.24499	HL	LL	93979	RAS protein activator-like 1 OS=Bo... tous OX=9913 GN=RASAL1 PE=4 SV=1	2309013	1510912	2325345	1924669	2064227	1859592	2762977	1709027	2395714	1764372	2657297	1727932	1011255	845065	1745466	1030778
F1M203 F1M203_BOVIN;A	5	5	265.17	0.20129	0.46306	1.44616	0.24225	HL	LL	63768	ArFGAP with coiled-coil, links rep... eat and PH domains 2 OS=Bo... tous OX=9913 GN=2	271190	414706	556870	136664	478001	293433	272418	330473	454268	104495	114698	393288	391569	366682	61775	
E1BAV3 E1BAV3_BOVIN;A	2	2	128.63	0.20242	0.46306	1.54835	0.24123	HL	LL	42806	Stomatin like 1 OS=Bo... tous OX=9913 GN=STOML1 PE=4 SV=2	78333	92223	107195	161774	206179	147933	107836	50060	208818	805729	203117	170463	83441	77819	109772	250517
E1BIQ7 E1BIQ7_BOVIN;A	4	4	380.63	0.20251	0.46306	1.22656	0.24115	HL	LL	35943	GIPC PDZ domain containing family m... ember 1 OS=Bo... tous OX=9913 GN=1	387432	470827	1040538	378534	481578	955434	527344	558280	297402	73232	159673	330996	522953	547100	897742	231976
AOA3Q1LJ2 AOA3Q1LJ2_	6	6	463.48	0.20265	0.46306	1.46574	0.24103	HL	LL	48251</																	

A0A031LYU3 A0A031LYU3	3	248.67	0.29651	0.51527	1.38401	0.17531	LL	HL	60027	Atlantin GTPase 3 OS=Bes taurus OX=9913 GN=ATL3 PE=4 SV=1	227119	282151	261322	102667	314103	100179	303988	345889	397388	227084	281091	126279	786595	107988	303589	69662	
F1M6E5 F1M6E5_BOVIN	2	126.02	0.29876	0.51527	1.46757	0.17408	LL	HL	64491	Cytoskeleton associated protein 4 OS=Bes taurus OX=9913 GN=CKAP4 PE=	25907	73147	25547	80960	71386	114264	56295	81575	74050	60812	28961	20112	71210	141481	101391	63046	19476
F1M2Q4 F1M2Q4_BOVIN	8	638.71	0.29885	0.51527	1.3278	0.17408	LL	HL	51914	Myotubularin subfamily 1 member A1 OS=Bes taurus OX=9913 GN=BTN1A1	8641352	6634432	1164288	729871	8209064	6794326	1137136	2151752	9116541	2055057	3155260	1329236	7317347	3139222	1059446	1965588	
Q3MHW6 MOT1_BOVIN	10	875.91	0.29911	0.51527	1.18261	0.17408	LL	HL	54262	Biotin carboxyl transferase 1 OS=Bes taurus OX=9913 GN=SLC16A1 PE=	5605344	4966618	6925547	1531535	3836553	4212298	5908878	4152466	5916354	517022	2527484	1236596	4917209	5504892	4988356	1509889	
A0A031MZJ6 A0A031MZJ6	2	189.44	0.30016	0.51527	1.17094	0.17331	LL	HL	32326	Dnal heat shock protein family (Hsp40) member B2 OS=Bes taurus OX=99	217888	143746	345770	94889	169246	178210	174983	252780	150320	50409	68047	80866	144100	280193	302984	141106	
E1BA03 E1BA03_BOVIN	2	75.34	0.30052	0.51787	1.23447	0.17107	LL	HL	74332	Non-specific serine/threonine protein kinase OS=Bes taurus OX=9913 GN=	181806	190974	169532	104077	177646	126016	232199	300733	225971	150800	146657	183656	262407	303849	345332	77818	
F1N261 F1N261_BOVIN	4	270.21	0.30466	0.51787	1.26755	0.17093	HL	HL	58698	Tyrosine-protein kinase OS=Bes taurus OX=9913 GN=LYN PE=1 SV=1	1981253	1158525	1960883	824808	1162780	739253	936299	1320093	1134146	1284359	620119	782700	916942	757986	1120555	778441	
Q2H94 DNJ2_BOVIN;AOA	4	225.75	0.30471	0.51787	1.19419	0.17093	HL	HL	45733	Dnal homolog subfamily A member 2 OS=Bes taurus OX=9913 GN=DNJ2	1048825	1008853	1023074	322828	1602201	1267523	439795	841476	760329	90973	326929	270961	632641	1145527	1270410	283089	
A0A031N9J9 A0A031N9J9	2	126.13	0.30711	0.51787	1.08012	0.16965	HL	HL	36482	Cycl cell control protein OS=Bes taurus OX=9913 GN=TMEM304 PE=3 SV	609763	434018	637305	494838	978193	488004	379555	517195	568213	78431	144008	444100	1248816	505704	728808	246075	
AOA452DIU9 AOA452DIU9	2	125	0.30711	0.51787	1.16265	0.16964	HL	HL	86811	Protein transport protein SEC23 OS=Bes taurus OX=9913 GN=SEC23B PE=	73134	117899	75445	134147	274324	137933	113270	180389	273992	377507	184873	297758	184284	109015	134752	59755	
F1N2L5 F1N2L5_BOVIN	2	92.65	0.31026	0.51844	1.2559	0.16801	LL	HL	76275	Maestro heat like repeat family member 6 OS=Bes taurus OX=9913 GN=M	10051	12427	15677	12165	45543	35694	21664	22985	60975	11994	42470	69239	21634	12332	36628	16784	
Q3T056 RL8_BOVIN	2	82.81	0.31056	0.51844	1.02864	0.16785	HL	HL	28007	60S ribosomal protein L8 OS=Bes taurus OX=9913 GN=RL8 PE=2 SV=3	145464	144645	156296	72168	227810	299441	283282	410831	206569	26275	47258	35033	550544	335623	376694	154071	
A2VDZ9 VAPB_BOVIN;AOA	2	292.41	0.31068	0.51844	1.54374	0.16779	HL	HL	27141	Vesicle-associated membrane protein-associated protein 8 OS=Bes taurus	349727	95078	200437	118529	268524	373327	442807	462325	160843	129575	145447	172638	701982	1235039	986834	384648	
A0A031M9B3 A0A031M9B	2	183.39	0.31368	0.51844	1.85498	0.16629	HL	HL	22994	60S ribosomal protein L18 OS=Bes taurus OX=9913 GN=RL18 PE=1 SV=1	29631	63394	85477	93889	254267	14932	53041	454444	177852	43071	54641	5167	184455	220821	561944	521253	
A0A031LW82 A0A031LW8	5	438.73	0.31407	0.51844	1.33676	0.16606	HL	HL	45191	Protein NDRG1 beta OS=Bes taurus OX=9913 GN=NDRG1 PE=3 SV=1	1375195	1000759	1223182	2827323	1625616	2628271	1542422	1393787	936259	2742518	1260219	4525181	909093	1856084	1891984	1644000	
AOA140T894 AOA140T894	2	480.95	0.31462	0.51844	1.0699	0.16578	HL	HL	28065	14-3-3 domain beta/alpha OS=Bes taurus OX=9913 GN=YVHAB PE=3 SV=1	1089141	28065	14433	189887	389103	942859	935249	1295263	606270	75045	397944	349574	1600872	1586896	1975873	645504	
A0A031MHG7 A0A031MH	2	206.43	0.31503	0.51844	1.20953	0.16558	HL	HL	35882	Annexin OS=Bes taurus OX=9913 GN=ANXA4 PE=1 SV=1	225423	89208	311080	82784	191829	70734	162431	318152	51539	68781	20653	31449	172410	197481	305335	84948	
A0A031M3N4 A0A031M3	9	503.18	0.31779	0.52071	1.16445	0.16442	HL	HL	121004	Unconventional myosin-c1 OS=Bes taurus OX=9913 GN=MYO1C PE=1 SV=1	852127	868665	987446	322778	985405	767737	1012381	1161523	1047165	283304	296186	359860	967473	1279058	1111295	265081	
A0A031MM65 A0A031M	4	162.79	0.31876	0.52116	1.17269	0.16371	LL	HL	43243	60S ribosomal protein L4 OS=Bes taurus OX=9913 GN=RL4 PE=1 SV=1	273106	414242	325270	578463	1389707	583095	335969	1248214	698080	1490632	269655	382992	1019701	687278	831350	816913	
A0A031LU44 A0A031LU4	6	524.79	0.32167	0.52365	1.32174	0.16278	LL	HL	132545	Calcium-transferring ATPase OS=Bes taurus OX=9913 GN=ATP2B2 PE=3 S	1816583	2649842	1647297	4855848	1736805	1827225	565354	2080490	1552601	3424533	3313724	4045983	1594532	1641218	1331404	1720929	
G3N0Q8 G3N0Q8_BOVIN	3	129.58	0.32379	0.52595	1.40423	0.16125	LL	HL	26488	Axistrodin 1 OS=Bes taurus OX=9913 GN=A2U1 PE=1 SV=2	354	47892	5562	14299	7905	1410	321597	5313	0	96767	0	1727	49785	1567	10529	255942	
A0A031M588 A0A031M58	2	113.11	0.32512	0.52698	1.46409	0.16101	HL	HL	15289	Histone domain-containing protein OS=Bes taurus OX=9913 GN=PE3 SV=3	234820	861385	199173	324298	624285	120927	4437917	448780	34070	249957	13605	271235	2110094	278126	552106	1235442	
F1MFD9 F1MFD9_BOVIN;G	4	286.86	0.32629	0.52773	1.08321	0.16005	HL	HL	83988	Oxytetrodoxin-binding protein OS=Bes taurus OX=9913 GN=OSPL10 PE=5 S	541939	332800	1082105	461549	774991	922942	772661	1057246	669208	96431	474106	369480	457419	1103624	1340495	289230	
AOA452DJA8 AOA452DJA8	2	105.44	0.32847	0.52965	1.36612	0.15919	LL	HL	36450	Purine nucleoside phosphorylase OS=Bes taurus OX=9913 GN=PMP PE=3 S	84079	19604	59378	201749	42648	249896	82477	78759	81404	240322	423022	225019	31752	158831	64004	263891	
A0A031M463 A0A031M46	4	92.71	0.33019	0.52965	1.41424	0.15819	HL	HL	33814	ERM domain-containing protein 2 OS=Bes taurus OX=9913 GN=ERM1/OD2	157083	107342	443249	746952	180750	633550	183452	550768	142633	831273	114457	776473	165913	734743	380594	785866	
A0A031M049 BOVIN;BOV	4	296.97	0.33136	0.5297	1.42405	0.15795	HL	HL	60767	ERM domain-containing protein OS=Bes taurus OX=9913 GN=RT6A PE=	24483	31707	298069	285459	432738	79533	86104	90863	161629	379957	709289	109863	161629	379957	90324	206592	
A0A031LPS9 A0A031LPS9	3	258.08	0.33678	0.52977	1.15919	0.15652	HL	HL	44594	Unclear-activated protein OS=Bes taurus OX=9913 GN=TMEM43 PE=1 SV=1	302670	367523	379725	887189	4552466	460630	607329	633427	456102	469976	560239	590297	836357	780494	412207	1072325	
A0A031M9K4 A0A031M9K	4	250.37	0.33378	0.52987	1.08512	0.15551	LL	HL	31145	Elongation factor 1 delta OS=Bes taurus OX=9913 GN=EF1D PE=4 SV=1	287156	344821	307316	209184	801745	370983	345030	610244	223583	125408	98606	97883	611213	665479	890822	239867	
A0A031N7N1 A0A031N7N	2	119.17	0.33455	0.52987	1.2147	0.15616	HL	HL	95782	ARFGAP with SH3 domain, ankyrin repeat and PH domain 3 OS=Bes taur	54238	70504	170977	32453	133137	107999	49916	105613	76497	8831	35497	31410	83475	92159	141404	27541	
E1BP13 E1BP13_BOVIN	3	146.2	0.33882	0.53205	1.22773	0.15443	HL	HL	59243	Tyrosine-protein kinase OS=Bes taurus OX=9913 GN=FRK PE=3 SV=2	49923	39324	53936	12957	79120	3153	16285	40601	86160	15970	9088	26793	79429	44773	60561	30695	
E18K13 LRCRC_BOVIN	7	793.86	0.33872	0.53205	1.26627	0.15425	HL	HL	92260	Volume-regulated anion channel subunit LRCRC3 OS=Bes taurus OX=9913	8987201	9242699	8846242	22096903	9506391	6728047	11103416	6137405	11708237	23506665	18010766	19868175	9462428	11013968	5901637	2226692	
A0A031M2A1 A0A031M2A	2	90.32	0.33886	0.53205	1.33436	0.15418	HL	HL	56759	Tissue specific transplantation antigen P35B OS=Bes taurus OX=9913 GN=I	107717	192241	103937	78530	209406	143426	94091	152769	112164	47791	60579	93874	126993	172230	108966	24873	
A6QLG5 RS9_BOVIN;AOA	2	169.6	0.34466	0.53557	1.58216	0.15158	HL	HL	22578	40S ribosomal protein S9 OS=Bes taurus OX=9913 GN=RP59 PE=2 SV=1	148083	70304	17820	21804	215527	38473	179315	425463	220387	131559	35407	30300	482865	321616	415206	50895	
A0A031LU04 A0A031LU0	2	98.95	0.34658	0.53744	1.41469	0.15073	HL	HL	86592	Inositol polyphosphate 5-phosphatase B OS=Bes taurus OX=9913 GN=INP1	130455	126270	94920	145487	158984	91003	121505	122221	116694	261334	230036	244223	69980	56879	82594	187917	
Q27965 H5718_BOVIN;PC	13	691.23	0.34741	0.53762	1.16816	0.15037	HL	HL	70185	Heat shock 70 kDa protein B18 OS=Bes taurus OX=9913 GN=HSPA1B PE=2 S	1601916	1371376	1876003	700347	1352462	5900125	694484	1401270	2113130	547440	718786	728455	848800	1638971	1607648	366297	
F1MYX6 F1MYX6_BOVIN	2	110.06	0.35101	0.54095	1.14154	0.14881	HL	HL	57657	Solute carrier family 7 member 8 OS=Bes taurus OX=9913 GN=SLC7A8 PE=	288069	185696	886623	116293	139555	354301	216480	242889	239249	106337	274444	38919	163716	262407	197809	241010	
F1MY82 F1MY82_BOVIN	4	415.35	0.35507	0.54479	1.15186	0.14707	HL	HL	77698	Protein kinase C eta type OS=Bes taurus OX=9913 GN=PKCXB PE=3 SV=1	1187404	1138957	1209542	564779	1303424	726763	1190745	773684	997500	162122	282704	543047	1838958	552035	1343101	498511	
A0A031M912 A0A031M91	2	79.72	0.35857	0.54811	1.35093	0.1456	LL	HL	37276	Abhydrolase domain containing 5 OS=Bes taurus OX=9913 GN=ABHD05 PE=	128100	242204	219494	104783	279575	157602	207060	304114	200806	104231	429915	97314	389483	192900	307753	370415	
Q3ZCA1 LRAT1_BOVIN	2	151.51	0.35967	0.54867	1.23573	0.14514	HL	HL	33104	Protein LRATD1 OS=Bes taurus OX=9913 GN=LRATD1 PE=2 SV=1	128786	116101	134176	15621	53979	31817	45734	181993									

QDR86 GLPKS_BOVIN	3	3	109.3	0.45261	57282	1.30663	011284	LL	HL	24757	Putative glycerol kinase OS=Bos taurus OX-9913 GN=GKS PE=2 SV=1	858581	813651	573714	1714239	1051665	1831005	1248348	1552208	1033541	2369053	1658108	1727776	4892988	424095	1248130	1839194
AOA3Q1M8R8 AOA3Q1M8F	5	5	372.78	0.4563	57282	1.10558	011273	LL	HL	58774	Transmembrane protein 263 OS=Bos taurus OX-9913 GN=TM263 PE=4	4365100	2776695	2439239	1697100	1684194	2387345	4822262	2858689	3605403	2881585	1962143	2196738	4163800	5083917	4118984	1810357
AOA3Q1MSN7 AOA3Q1MS	2	2	93.82	0.4553	57282	1.06481	011207	LL	HL	65636	Coenzyme A synthase OS=Bos taurus OX-9913 GN=COASY PE=3 SV=1	21913	75814	38538	18784	147496	52422	44116	108370	91278	92964	50495	53711	124427	39965	51381	91176
G3N254 G3N254_BOVIN	4	3	235.87	0.45963	57282	1.18199	011084	HL	LL	34398	Leucine rich repeat containing 26 OS=Bos taurus OX-9913 GN=LRRC26 PE=3	236635	174593	137979	203269	598702	542356	542942	522597	149805	203084	36228	332823	603233	157288	317048	411297
Q76LV2 HS90A_BOVIN;AOA	13	5	1003.46	0.60807	57282	1.23238	011049	HL	LL	84678	Heat shock protein HSP 90-alpha OS=Bos taurus OX-9913 GN=HSP90AA1	1937635	1722759	2079211	739589	3109930	1837118	1658066	4094833	2977991	546055	1385644	630653	3747236	2343857	3023382	1075135
F1M6G8 F1M6G8_BOVIN	2	2	110.69	0.4615	57282	1.27328	011031	HL	LL	42140	Oncostatin M receptor OS=Bos taurus OX-9913 GN=OSMR PE=4 SV=3	164731	283606	238046	165856	201750	51483	207272	160098	166637	271266	299603	298064	2347844	31847	227994	316985
PE8138 ACTS_BOVIN;G81KJ	2	5	1005.34	0.4643	57282	1.28879	010954	HL	LL	42024	Actin, alpha skeletal muscle OS=Bos taurus OX-9913 GN=ACTA1 PE=1 SV=1	135446638	18357958	8733833	1417265	18661697	22708149	17049528	19785706	13167524	20504513	22083120	18712142	10109555	10950581	15293174	14260464
AOA3Q1N4J5 AOA3Q1N45	2	2	137.42	0.46574	57282	1.1348	010914	HL	LL	43081	Palmitoyl thioesterase OS=Bos taurus OX-9913 GN=ZDHHC20 PE=3 SV=3	515885	200719	355325	321219	155605	206603	339736	345997	389484	56216	140563	310469	133885	470197	336620	339469
AOA3Q1MS82 AOA3Q1MS8	5	5	467.76	0.46677	57282	1.17863	010886	LL	HL	71015	Dolichyl-diphosphoglycosyltransferase subunit 2	526441	986431	290805	1227976	1062458	924048	956911	1581004	1243013	2543871	1183404	1083310	1623092	432264	63551	1434047
A3KNS1 A3KNS1_BOVIN	3	3	204.55	0.46743	57282	1.03201	010868	LL	HL	44027	TSG101 protein OS=Bos taurus OX-9913 GN=TSG101 PE=1 SV=1	566273	418514	136968	197476	341710	316711	634837	357776	385279	510092	382486	407463	462706	303094	238688	299903
AOA5S2DW1 AOA5S2DW1	3	3	233.07	0.46938	57282	1.32962	010814	LL	HL	34517	60S ribosomal protein L10 OS=Bos taurus OX-9913 GN=RLP10 PE=4 SV=1	274831	215779	271668	173178	460338	185417	398478	768417	347318	303035	144108	153118	1896783	609645	929757	685518
Q1QQD4 GIP2C_BOVIN;AOA	12	12	1008.21	0.46991	57282	1.07667	010814	HL	LL	34478	PAD domain-containing protein GIP2C OS=Bos taurus OX-9913 GN=GIP2C	24155675	18731553	20683868	9702983	1317844	15738149	23520110	20193277	13428170	5699257	12742010	9841077	26400686	18034396	29824976	1068852
AOA3Q1M656 AOA3Q1M65	2	2	98.88	0.47071	57282	1.08345	010778	LL	HL	30395	40S ribosomal protein S2 OS=Bos taurus OX-9913 GN=RP52 PE=3 SV=1	66272	64431	51362	19798	168852	30718	85331	242330	101640	178548	62056	39129	193035	125812	191307	289971
F1N480 F1N480_BOVIN	2	2	57.32	0.47074	57282	1.1371	010778	HL	LL	30837	Tetratricopeptide repeat domain 39C OS=Bos taurus OX-9913 GN=TRC39C	6828	20401	84733	16547	79683	15671	13475	73255	52552	3217	2917	19580	32961	17083	84217	3713
AOA407856 AOA407856_BO	8	8	474.54	0.47111	57282	1.16385	010758	LL	HL	138257	Coatomer subunit alpha OS=Bos taurus OX-9913 GN=COPA PE=4 SV=1	103988	141755	86453	122843	569718	137075	125764	616257	620108	451255	381540	191345	385307	128308	261083	157587
Q6E407 JF5A1_BOVIN;F1A	2	2	175.18	0.47146	57282	1.30664	010758	HL	LL	16821	Eukaryotic translation initiation factor 5A-1 OS=Bos taurus OX-9913 GN=E	2037412	1684866	1481287	929881	2187940	1668968	1778909	2361375	1927601	1149145	792417	776689	3052732	3562657	3758783	1520208
Q17QZ0 Q17QZ0_BOVIN;A	3	3	186.21	0.47498	57609	1.04658	010637	HL	LL	64244	Non-specific serine/threonine protein kinase OS=Bos taurus OX-9913 GN=	722137	540243	644082	253066	446644	734355	767010	567182	535008	36894	136196	333370	708469	701997	1306522	172270
F6R0H3 F6R0H3_BOVIN	4	4	194.09	0.47565	57609	1.36124	010637	HL	LL	68692	Syntaxin-binding protein 1 OS=Bos taurus OX-9913 GN=STXB1 PE=3 SV=1	79266	247037	128278	154547	390088	140678	79702	130159	87839	142066	40968	145516	127410	117576	277698	31115
Q2KJ46 PSMD3_BOVIN	4	4	236.99	0.47925	57761	1.11244	010552	HL	LL	60919	26S proteasome non-ATPase regulatory subunit 3 OS=Bos taurus OX-9913	113075	156298	80040	280821	511390	160373	267055	791264	364975	298997	286559	222471	419829	133026	435775	343803
A8E4P3 A8E4P3_BOVIN;F1J	9	9	812.36	0.48031	57797	1.20073	010524	HL	LL	31268	STOM protein OS=Bos taurus OX-9913 GN=STOM PE=1 SV=1	60373522	93149651	48503924	43134514	39847355	25209479	144435301	93181780	19864269	81614509	30327742	31838312	67066260	56682200	98576100	69267585
ASPM14 AFM2_BOVIN;AOA	2	2	155.65	0.4843	58184	1.11643	010421	HL	LL	40451	Apoptosis-inducing factor 2 OS=Bos taurus OX-9913 GN=AIFM2 PE=2 SV=1	140791	313468	202998	75011	271145	64003	225860	177576	128856	4932	11869	83330	204921	142099	493155	100302
Q58DW6 RAB25_BOVIN	6	5	303.63	0.4855	58227	1.05376	010319	HL	LL	23522	Ras-related protein Rab-25 OS=Bos taurus OX-9913 GN=RAB25 PE=2 SV=1	5047864	1783318	3110348	1868010	2112387	1669386	4357330	3551078	1960337	836751	1237432	2080896	4922255	3521649	5000819	2101448
AOA3Q1LMX0 AOA3Q1LMX	13	13	1031.05	0.49617	59134	1.16706	010122	HL	LL	31587	NADH-cytochrome b5 reductase OS=Bos taurus OX-9913 GN=CYB5R3 PE=3	4894574	2246784	2483603	1280985	15500960	20073457	44447368	18138008	22848967	9369769	15504552	12491978	29857573	2111300	3260264	12730610
AOA1407886 AOA1407886	5	5	198.42	0.50173	59186	1.15597	009987	HL	LL	93737	Coatomer subunit gamma OS=Bos taurus OX-9913 GN=COPG1 PE=3 SV=1	11553	41931	66704	87039	294607	53841	36794	263784	167074	63856	76644	100806	66541	127465	155327	25560
Q3T077 SAR1_BOVIN	3	3	504.39	0.50176	59186	1.32393	009986	HL	LL	22395	GTP-binding protein SAR1a OS=Bos taurus OX-9913 GN=SAR1A PE=3 SV=1	6168849	3370327	5310904	805108	253967	1740227	7643300	4739220	4901527	2012760	1896708	1508192	7998505	9629022	8519503	2941069
AOA3Q1ML89 AOA3Q1ML8	6	6	1057.69	0.50176	59186	1.04839	009979	HL	LL	138573	Uncharacterized protein OS=Bos taurus OX-9913 GN=LOC10291810 PE=1	1531101	234523	1064929	1373230	2323867	346551	958416	1174177	234557	105337	142763	105337	266770	3413401	1223265	800798
AOA1407885 AOA3Q1ML5	13	10	1094.98	0.50385	59206	1.04587	009936	HL	LL	71720	Heat shock cognate 71 kDa protein OS=Bos taurus OX-9913 GN=HSP71K	14052058	11078066	6117322	14415107	3626280	11445394	12064999	17904668	3651848	3025182	10533983	14311828	14837619	1242865	3998545	
AOA1407883 AOA1407883	3	3	150.06	0.50504	59206	1.33858	009831	HL	LL	235129	Phosphatidylinositol 4-kinase alpha OS=Bos taurus OX-9913 GN=PI4KA PE=1	112336	45241	103300	81442	179310	61323	158581	161870	157659	129863	359770	164380	203565	144480	44482	264051
FPKRX5 FPKRX_BOVIN	7	7	450.19	0.50828	59295	1.10906	009301	HL	LL	99376	Toll like receptor 5 OS=Bos taurus OX-9913 GN=TLR5 PE=4 SV=1	655318	385181	127402	472366	857929	342672	440053	1433428	7906460	1700510	131342	684928	336954	561783	1552446	112707
Q17QES CIB1_BOVIN;AOA3	5	5	291.96	0.50937	59301	1.11349	009805	HL	LL	21715	Calcium and integrin-binding protein 1 OS=Bos taurus OX-9913 GN=CIB1 F	265167	183733	417259	482224	248885	354553	631412	571397	297206	666838	143540	478029	422136	499233	790716	1026173
AOA3Q1MF86 AOA3Q1MF8	2	2	96.1	0.51261	5944	1.15497	009713	HL	LL	41429	Actin related protein 1A OS=Bos taurus OX-9913 GN=ACTR1A PE=1 SV=1	191938	107710	232921	252069	452020	135794	183952	262743	390726	249434	165431	108231	173004	120625	224291	213771
Q3ZC84 CNDP2_BOVIN;AOA	6	6	258.27	0.51293	5944	1.04325	009723	HL	LL	51622	Cytosolic non-specific dipeptidase OS=Bos taurus OX-9913 GN=CNDP2 PE=1	1282737	894065	806696	481506	2155611	685900	1067291	1620978	956320	1397613	821232	751984	1272702	855639	1746161	824225
F1MX65 F1MX65_BOVIN	2	2	134.64	0.51517	59537	1.13158	009671	HL	LL	74218	Protein OS-9 OS=Bos taurus OX-9913 GN=OS9 PE=4 SV=2	45008	67773	58630	11090	151594	5891	39569	218347	90686	13223	6389	18021	166875	108513	143356	5305
Q3SWY3 IMHD2_BOVIN	2	2	120.64	0.51635	59537	1.33092	009644	HL	LL	55728	Inosine 5'-monophosphate dehydrogenase 2 OS=Bos taurus OX-9913 GN=	76659	164622	31652	38016	639270	10468	81030	796480	26784	40862	6508	11796	574528	237172	219263	4392
AOA3Q1LRW8 AOA3Q1LRW	4	4	304.59	0.51671	59537	1.48841	009636	HL	LL	49223	60S ribosomal protein L3 OS=Bos taurus OX-9913 GN=RLP3 PE=1 SV=1	33139	257138	130663	54578	779114	273887	95626	274769	336010	15209	59873	29794	301483	339901	636034	194924
Q6QRN7 Q6QRN_BOVIN	2	2	207.5	0.51975	5956	1.30879	009567	HL	LL	33926	PP1201 protein OS=Bos taurus OX-9913 GN=TM1B1 PE=3 SV=1	3370472	3089234	5843383	6582117	3466058	4106714	3428231	3065683	3264034	4091763	1067616	5215582	2099299	4647346	5113864	
AOA3Q1MIY5 AOA3Q1MIY5	2	2	126.39	0.52015	5956	1.24572	009558	HL	LL	45486	Arrestin domain containing 1 OS=Bos taurus OX-9913 GN=ARRDC1 PE=4 S	280237	244679	537735	85660	275558	317503	409023	28169	206709	80911	94129	108331	273063	391600	301144	61788
AOA3Q1LM10 AOA3Q1LM1	2	2	111.72	0.52031	5956	1.05693	009554	LL	HL	77068	Erythrocyte membrane protein band 4.1 like 4A OS=Bos taurus OX-9913 C	27676	29560	93351	24527	39395	56816										

A0A0Q1MSA1 A0A03Q1MSA	3	2	242.87	0.64148	0.63286	1.25754	0.07353	HL	LL	58122	Lectin, mannoside binding 1 OS=	Bos taurus OX=9913 GN=LMMAN1 PE=1 SV=1	1019398	2209016	437660	182709	924559	1615876	1082359	911079	984176	128320	734779	273637	1849892	1621659	915736	277342
E1B1E4 E1B1E4_BOVIN.F1M	2	2	115.6	0.64241	0.63286	1.25041	0.07339	HL	LL	108212	EPH receptor B4 OS=	Bos taurus OX=9913 GN=EPHB4 PE=3 SV=3	62003	26439	63411	15340	90882	39863	34012	50250	98053	28880	77943	63871	45680	19568	91158	27983
A0A052PZB0 A0A052PZB0	3	2	287.37	0.64348	0.63286	1.12383	0.07324	HL	LL	55620	Fructose-bisphosphate aldolase OS=	Bos taurus OX=9913 GN=ALDOPC PE=1 SV=1	294849	257525	110672	302863	506334	368105	246247	296909	362698	382851	241463	422968	190030	118613	264872	269578
Q5E9R3 EH01_BOVIN	3	2	275.11	0.64374	0.63286	1.07833	0.0732	HL	LL	60644	EH domain-containing protein 1 OS=	Bos taurus OX=9913 GN=EH01 PE=1 SV=1	474422	751860	1150308	600971	744703	470674	283198	679234	546653	793411	787700	610581	317755	737550	869415	489004
A0A031MXV0 A0A031MXV	2	2	248.21	0.64662	0.63442	1.11948	0.0728	HL	LL	42486	IgV domain-containing protein OS=	Bos taurus OX=9913 GN=CECAM19 PI=1	80191	62369	541125	37566	116481	133248	258103	122835	71753	5153	237968	46132	127386	297094	188152	106242
Q0I1G7 RABA_BOVIN	4	2	347.17	0.64768	0.63442	1.06083	0.07265	HL	LL	23674	Ras-related protein Rab-5A OS=	Bos taurus OX=9913 GN=RAB5A PE=1 SV=1	3115387	1354030	1895250	747012	1308026	910916	3292361	1958250	2111636	261155	503270	800937	2531574	4128671	2953947	987443
Q6B3B3 SND1_BOVIN.A0A1	11	11	636.96	0.64785	0.63442	1.11948	0.07262	HL	LL	101926	Staphylococcal nuclease domain-containing protein 1 OS=	Bos taurus OX=9913 GN=	942955	2133009	2008000	1455160	2916953	1716543	997474	2434240	2936626	988732	628475	1290278	2025929	2126604	1981271	1005702
FQH949 FQH94_BOVIN	2	2	211.75	0.65465	0.6393	1.25707	0.07168	HL	LL	48111	Protein disulfide isomerase family A member 6 OS=	Bos taurus OX=9913 GN=	1602125	463261	225664	849714	131067	310769	177599	599070	324504	564994	432198	273673	128857	144232	1052149	
Q3SVU2 EF2_BOVIN.A0A3C	14	14	939.4	0.65486	0.6393	1.04808	0.07165	HL	LL	95307	Elongation factor 2 OS=	Bos taurus OX=9913 GN=EEF2 PE=2 SV=3	718375	1107385	8917337	4414080	148781514	5831716	9421023	11444934	13042671	4797582	5294546	5309297	13935176	9690355	14420427	369152
Q1RMI2 Q1RMI2_BOVIN	5	5	257.04	0.65563	0.6393	1.54067	0.07155	HL	LL	21267	Ras homolog family member G OS=	Bos taurus OX=9913 GN=RHOG PE=1 SV=1	1254600	368131	542606	591257	447326	511550	918334	975234	526847	86182	249525	750629	1370005	1919086	1601750	1076456
Q3SV24 SYDC_BOVIN.F1M.3	3	3	121.6	0.65633	0.6393	1.1471	0.07145	HL	LL	57000	Aspartate-tRNA ligase, cytoplasmic OS=	Bos taurus OX=9913 GN=DARS PE=1 SV=1	27315	93996	41923	74142	312847	56223	46981	277443	150630	134112	52900	53982	211317	83717	92014	96520
A0A031M273 A0A031M27	2	2	135.19	0.65822	0.63958	1.02046	0.07142	HL	LL	91024	Pre-B cell leukemia transcription factor-interacting protein 1 OS=	Bos taurus OX=9913 GN=	29341	71834	91420	182268	100253	147240	20845	90650	122127	25139	68697	112129	80233	36145	74241	182893
Q0A031LMR8 A0A031LMR8	3	3	107.66	0.6593	0.6398	1.10981	0.07105	HL	LL	38351	Prostaglandin reductase 2 OS=	Bos taurus OX=9913 GN=PTRG2 PE=1 SV=1	544899	693297	383030	127473	946078	287700	797223	820865	682592	509093	269110	582592	714746	1159435	711861	248653
Q0VCV9 Q0VCV9_BOVIN	2	2	201.77	0.66408	0.64057	1.46738	0.07042	HL	LL	17199	GLI pathogenesis-related 2 OS=	Bos taurus OX=9913 GN=GLIPR2 PE=2 SV=1	141033	11677	386839	36081	133448	246730	2287819	97279	201858	70665	199307	106681	196681	558397	68684	497167
Q3ZB8A NDRG2_BOVIN.F11	3	3	369.09	0.66538	0.64057	1.26215	0.07025	HL	LL	39183	Protein NDRG2 OS=	Bos taurus OX=9913 GN=NDRG2 PE=2 SV=1	2333883	682471	1393652	171935	833607	837400	1734455	114999	2023888	298733	723413	144302	983302	633829	222615	619059
E1BL67 E1BL67_BOVIN	2	2	126.78	0.66586	0.64057	1.09577	0.07018	HL	LL	54949	Oxyester-binding protein OS=	Bos taurus OX=9913 GN=OSBPL2 PE=3 SV=1	32349	374619	250156	144199	177377	122468	30986	171947	136336	249397	149173	739985	25209	88888	331334	75283
F1MSF7 F1MSF7_BOVIN	5	5	320.05	0.66712	0.64057	1.07161	0.07002	HL	LL	89996	Sushi domain containing 2 OS=	Bos taurus OX=9913 GN=SUSD2 PE=4 SV=1	158551	195537	347221	280605	846752	556197	80794	183068	110795	751923	169304	511767	162094	121958	103655	174264
Q2YD14 HINT3_BOVIN	2	2	110.12	0.66741	0.64057	1.0373	0.06998	HL	LL	20457	Histidine triad nucleotide-binding protein 3 OS=	Bos taurus OX=9913 GN=H	29539	201209	434973	139148	335674	437000	103143	389797	270610	230963	334989	150060	352161	491461	527973	250820
A0A031MWU8 A0A031MW	3	3	131.67	0.66801	0.64057	1.34485	0.06983	HL	LL	64422	Syntaxin-binding protein 3 OS=	Bos taurus OX=9913 GN=STXBP3 PE=3 SV=1	160725	305100	132936	56564	100523	183203	39490	65944	192979	23927	91639	70758	120671	151923	119118	74551
E1BEV7 E1BEV7_BOVIN	2	2	84.01	0.67169	0.64213	1.07428	0.06951	HL	LL	111699	Metalloendopeptidase OS=	Bos taurus OX=9913 GN=BMP1 PE=4 SV=3	66928	60412	95830	14067	126131	21564	101184	109824	50604	12551	8263	17160	60824	24712	184111	27884
F1M096 F1M096_BOVIN	2	2	107.69	0.67449	0.64457	1.25388	0.06908	HL	LL	68255	Transmembrane protein C OS=	Bos taurus OX=9913 GN=PRKI PE=3 SV=3	103502	192313	104102	268296	133938	234838	113392	102955	241154	443085	113873	319185	69749	76646	64509	179062
A4FV45 TM214_BOVIN	2	2	104.53	0.6772	0.64633	1.04106	0.06874	HL	LL	76967	Transmembrane protein 214 OS=	Bos taurus OX=9913 GN=TMEM214 PE=1 SV=1	4177	6362	13160	21602	70236	8546	3696	71197	28354	71521	0	9631	32381	56696	29117	0
Q279M8 Q279M8_BOVIN.F	6	6	684.79	0.67896	0.64719	1.12313	0.06852	HL	LL	23212	Synaptosomal-associated protein OS=	Bos taurus OX=9913 GN=SNAP23 PE=1 SV=1	5635039	2962404	5496460	3220168	2939193	3113544	5632162	4761244	2848959	1991414	3153270	3155983	4754673	6689147	7723499	4016365
Q2XWV9 KCY_BOVIN.A0A45	3	3	247.43	0.68549	0.65113	1.04336	0.06772	HL	LL	22265	UMP-CMP kinase OS=	Bos taurus OX=9913 GN=CMPK1 PE=2 SV=2	1125244	596455	1316237	483015	820209	825639	1320489	1318510	1772124	193981	450097	336912	1101597	1739813	1808461	557426
A0A031S5ES A0A031S5ES	2	2	92.35	0.68569	0.65113	1.12262	0.0677	HL	LL	84546	N-ethylmaleimide sensitive factor, vesicle fusing ATPase OS=	Bos taurus OX=9913 GN=	54974	81617	140568	37598	135405	87283	75086	139627	115425	3761	50602	40325	171927	103212	116182	11782
F1N3M3 F1N3M3_BOVIN.F1	2	2	137.25	0.68793	0.65123	1.10207	0.06747	HL	LL	136855	Butyrophilin subfamily 1 member A1 OS=	Bos taurus OX=9913 GN=FCMB	285705	22171	238006	484800	223905	158829	108337	274475	224702	153833	80733	202418	256981	246988	183799	133229
F18892 BT1A1_BOVIN	2	2	469.3	0.68793	0.65123	1.12178	0.06747	HL	LL	52239	Myosin heavy chain 9 OS=	Bos taurus OX=9913 GN=BTM1A1	2385504	30476226	36477221	960154	25580665	12476234	14429006	26775166	38693052	21363211	15328411	9191386	14775898	20626318	21159283	6420978
A6Q0P5 DHR12_BOVIN.A0D	2	2	126.8	0.69236	0.65127	1.10059	0.06659	HL	LL	35043	Dehydrogenase/reductase SDR family class 12 OS=	Bos taurus OX=9913 GN=	31436	158335	3174429	18184	192237	188002	32123	252307	152999	21589	58128	37591	121796	254150	301663	62510
A6Q9P6 A6Q9P6_BOVIN	3	3	174.53	0.69334	0.65127	1.16029	0.06679	HL	LL	49135	LANCL2 protein OS=	Bos taurus OX=9913 GN=LANCL2 PE=1 SV=1	437356	466958	414240	907142	915640	559646	710054	547767	1340027	791427	919434	1116700	526165	477632	52903	
A6QLS9 A6QLS9_BOVIN	3	3	319.73	0.69407	0.65127	1.15893	0.06667	HL	LL	22527	RAB10 protein OS=	Bos taurus OX=9913 GN=RAB10 PE=1 SV=1	2517363	1620866	2818424	820249	1829274	203900	274059	3199170	1777649	276385	963052	894774	2692800	4984169	4519566	2017678
A6Q1MNH4 A0A031M1N5	5	5	264.16	0.69535	0.65127	1.06086	0.06655	HL	LL	30512	Ethylmalonyl-CoA decarboxylase OS=	Bos taurus OX=9913 GN=ECHDC1 PE=1 SV=1	419891	250109	278907	182138	604808	428155	786045	401083	307388	146584	159046	314325	406623	714886	473729	425423
E1BK9J E1BK9J_BOVIN	2	2	105.12	0.69584	0.65127	1.00728	0.0665	HL	LL	66734	Retinol saturated OS=	Bos taurus OX=9913 GN=RETSAT PE=4 SV=1	23081	242591	223142	111365	172421	133223	93929	21742	97741	10440	91752	112030	213787	199944	74471	123870
A5PKP12 A5PKP12_BOVIN.A0	5	4	285.2	0.69882	0.65288	1.05106	0.06615	HL	LL	23385	Ras related 2 OS=	Bos taurus OX=9913 GN=RRAS2 PE=2 SV=1	2741323	990606	2271980	688917	1109513	1732519	3143845	2314035	1232046	447457	867922	602520	2000524	3910900	3318367	1116200
A0A031LTG9 A0A031LTG9	3	3	185.19	0.70178	0.6537	1.03397	0.06582	HL	LL	139251	TBC1 domain family member 9B OS=	Bos taurus OX=9913 GN=TB1C09B PE=1 SV=1	45371	58930	156802	17417	110323	231218	68138	69461	107644	14398	73412	27254	5594	289054	94815	29583
P63103 I43Z3_BOVIN.E1B	6	6	422.8	0.70223	0.6537	1.02774	0.06577	HL	LL	27728	14-3-3 protein zeta/delta OS=	Bos taurus OX=9913 GN=YYWAZ PE=1 SV=1	2798671	1926326	2484904	1805951	3176037	2594877	3668015	3916035	2316213	2805288	2528040	1953337	4257735	3766574	4947371	3843039
A0A031LZC0 A0A031LZC0	2	2	87.71	0.70309	0.6537	1.02879	0.06567	HL	LL	62944	Glycerol kinase OS=	Bos taurus OX=9913 GN=GK PE=3 SV=1	67728	36274	12562	3112	44804	6130	95229	29228	42162	11954	52014	19360	94762	14140	23114	30932
A0A031M591 A0A031M59	4	2	206.47	0.70724	0.65586	1.06564	0.06521	HL	LL	23074	Uncharacterized protein OS=	Bos taurus OX=9913 GN=RAB43 PE=4 SV=1	791780	490001	651421	205050	388318	557607	733671	446795	481652	84128	201891	264686	736038	1044985	966638	466431
A0A452DIW4 A0A452DIW4	2	2	102.34	0.71103	0.65669	1.05141</																						

A04452D134 A04452D134_	2	2	116.57	0.81941	0.68028	1.24076	0.05558	LL	HL	22938	60S ribosomal protein L28 OS=Bos taurus OX=9913 GN=RPL28 PE=4 SV=1	8937	18182	14399	5956	80567	23316	152985	165286	83630	4548	7199	4869	133367	134032	150070	18806	
A4FV54 RAB8A_BOVIN;A0A	7	5	637.52	0.82001	0.68028	1.17785	0.05554	LL	HL	23669	Ras-related protein Rab-8A OS=Bos taurus OX=9913 GN=RAB8A PE=2 SV=1	1490281	907426	1271873	333318	994427	1022840	1588174	2020224	938181	250822	594694	282298	1471683	3388392	2640053	1199162	
F1MSQ2 F1MSQ2_BOVIN;A	2	2	91.04	0.82014	0.68028	1.05969	0.05553	HL	LL	56740	Receptor protein serine/threonine kinase OS=Bos taurus OX=9913 GN=AC	169023	186168	99195	55660	78266	26293	125870	118622	123760	131741	84480	32835	94223	37115	67110	119890	
Q08D15 RAP2C_BOVIN;A0	4	2	345.03	0.82039	0.68028	1.04255	0.05552	HL	LL	20731	Ras-related protein Rap-2c OS=Bos taurus OX=9913 GN=RAP2C PE=2 SV=1	770145	250712	133633	180723	237494	143674	441792	512193	185701	135390	177824	98861	589205	585319	475241	200393	
A0A3Q1NH16 A0A3Q1NH16	4	4	276.05	0.82132	0.68028	1.22051	0.05546	HL	HL	55258	Protein FAM114A2 OS=Bos taurus OX=9913 GN=FAM114A1 PE=4 SV=1	385053	633316	645274	1072746	476738	884263	331244	369591	377278	2182461	750876	808763	144027	690262	410456	655837	
A0A3Q1M7E0 A0A3Q1M7E	2	2	81.8	0.82357	0.68028	1.28064	0.05532	HL	LL	63777	24-dehydrocholesterol reductase OS=Bos taurus OX=9913 GN=DHCR24 PE	807266	315761	126758	49241	310788	61224	516800	160040	290376	197820	171021	171211	114973	173262	294184	274404	180272
P20000 ALDH2_BOVIN	5	5	268.42	0.82403	0.68028	1.03049	0.05529	HL	HL	56617	Aldehyde dehydrogenase, mitochondrial OS=Bos taurus OX=9913 GN=ALD	213332	478263	240601	512626	2267689	221503	1206959	1265348	345277	814012	221667	821377	1356782	388795	1383149	1721024	
A0A3Q1LQ52 A0A3Q1LQ5	2	2	107.1	0.82561	0.68042	1.0557	0.0552	HL	HL	26217	SEA domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=1	292622	141514	720866	992525	316867	796311	274160	266025	177304	1076566	811606	567345	257698	568999	151494	947605	
A0A3Q1M10 A0A3Q1M10	4	3	173.45	0.83335	0.68439	1.14292	0.05473	HL	HL	40626	Calcium-binding protein 39 OS=Bos taurus OX=9913 GN=CAL39 PE=4 SV=1	684473	246652	452742	235328	221905	104893	787744	374600	246607	178320	173100	164042	395802	446636	553261	215646	
A0A452DIP2 A0A452DIP_1	3	3	132.06	0.83346	0.68439	1.0131	0.05473	HL	HL	54619	UDP-glucose 4-epimerase OS=Bos taurus OX=9913 GN=GALE PE=3 SV=1	320420	372030	221721	370036	539211	319069	468201	296443	472684	895673	623137	713483	310971	289607	209266		
F6QJH8 F6QJH8_BOVIN	2	2	90.21	0.83356	0.68439	1.17622	0.05472	HL	HL	26046	Progesterone receptor membrane component 2 OS=Bos taurus OX=9913	34917	3755	110523	11905	41522	43927	28922	56056	5679	44316	11914	14508	26410	38282	114449	60648	
A0A3Q1LKB7 A0A3Q1LKB	7	2	180.45	0.83508	0.68439	1.09729	0.05463	HL	HL	21628	H1Ras proto-oncogene, GTPase OS=Bos taurus OX=9913 GN=HRAS PE=4 SV	410253	189053	359557	166697	570103	292610	401637	437495	261525	257619	143754	188979	501192	623364	530861	206110	
A0A3Q1M1B0 A0A3Q1M1B	3	3	248.28	0.83738	0.68603	1.03632	0.0545	HL	HL	180725	IQ motif containing GTPase activating protein 1 OS=Bos taurus OX=9913 G	131747	186543	93591	519818	480190	166164	288076	479448	425475	804512	355905	253022	215985	139587	130530	363143	
A0A3Q1LPA4 A0A3Q1LPA	4	2	63.56	0.8431	0.68942	1.22637	0.05419	HL	HL	93089	Ras GTPase-activating protein 3 OS=Bos taurus OX=9913 GN=RASA3 PE=4 SV	27329	44426	18150	7423	17708	28970	65589	8335	18117	898	7723	15079	78527	176529	58163	8502	
Q95M18 ENPL_BOVIN	8	7	585.57	0.84335	0.68942	1.1232	0.05417	HL	HL	92369	Endoplasmic OS=Bos taurus OX=9913 GN=HSP90B1 PE=2 SV=1	324611	554279	649159	357148	981346	403395	471066	1319702	1049491	250192	257521	239592	771545	611369	967063	249244	
Q3B7M5 LASP1_BOVIN	4	4	243.19	0.85142	0.69225	1.11134	0.05375	HL	HL	29658	LIM and SH3 domain protein 1 OS=Bos taurus OX=9913 GN=LASP1 PE=2 S	119759	111410	264082	81575	273862	150272	231530	326495	1059491	45056	70018	93527	176529	386139	581560	128711	
A0A3Q1LZU8 A0A3Q1LZU	4	4	191.12	0.85431	0.69311	1.0630	0.0536	HL	HL	106854	Glycosidase II alpha subunit OS=Bos taurus OX=9913 GN=GANAB PE=1 SV-	139449	186525	83304	230058	203364	78014	153500	323274	263977	224245	362232	151625	249835	161510	102580	61475	
Q58DQ3 RL6_BOVIN;GN3N	5	5	262.74	0.8603	0.69664	1.05234	0.05331	HL	HL	32670	60S ribosomal protein L6 OS=Bos taurus OX=9913 GN=RPL6 PE=2 SV=3	387265	335045	406913	331498	999404	369817	684778	1096756	816912	279599	91580	212189	1330441	651008	1078816	506048	
A0A140T841 A0A140T84_1	4	4	373.14	0.86052	0.69676	1.27744	0.0533	HL	HL	21467	Prostamide/prostaglandin F synthase OS=Bos taurus OX=9913 GN=PRXL2E	6248782	2637485	3800557	1846621	2124678	3839946	6912701	4068192	2491000	488719	988879	1963505	7099213	8246535	9887084	3101203	
A0A3Q1LXR2 A0A3Q1LXR	5	3	353.68	0.86283	0.69676	1.04341	0.05319	HL	HL	23476	Ras-related G botulinum toxin substrate 1 OS=Bos taurus OX=9913 GN=RT	9740090	2437959	3411918	3591959	2734789	3567453	9582643	4084509	2521678	1834414	1728057	1748809	7436962	7668816	9057702	2291821	
A0A3Q1MTL6 A0A3Q1MTU	2	2	90.93	0.86462	0.69817	1.35656	0.0531	HL	HL	54654	T-complex protein 1 subunit theta OS=Bos taurus OX=9913 GN=CTCF PE=1	21417	233118	58958	5414	60276	45169	26916	64857	24490	5589	10221	2528	39776	78643	66439	8069	
ASD7A4 ASD7A4_BOVIN	4	4	163.86	0.86519	0.69817	1.08255	0.05308	HL	HL	25040	RIT1 protein OS=Bos taurus OX=9913 GN=RIT1 PE=2 SV=1	1109904	645938	1326735	256724	537245	765463	2125604	954201	586207	219290	783076	409312	1162747	1449375	1427861	451956	
A0A3Q1LMG1 A0A3Q1LMC	3	3	188.6	0.8822	0.70519	1.16063	0.05251	HL	HL	39508	Fructose-bisphosphate aldolase OS=Bos taurus OX=9913 GN=ALDOA PE=1	295743	506708	78493	191423	467996	130242	460598	340944	415221	192709	73116	249471	402306	203777	246143	293013	
Q3S2A1 RHOF_BOVIN	5	5	372.32	0.8876	0.70519	1.15967	0.05241	HL	HL	23825	Rho-related GTP-binding protein RhoF OS=Bos taurus OX=9913 GN=RHO	3375029	1583328	2845201	1265063	1674675	1679096	2320999	3660588	1680545	1058245	1135924	959840	3317892	3968358	5341940	1731751	
QXN25 PSD12_BOVIN	2	2	93.12	0.88279	0.70519	1.20444	0.05232	HL	LL	53019	26S proteasome non-ATPase regulatory subunit 12 OS=Bos taurus OX=9913	0	0	5989	8137	37584	8671	0	40453	0	469	0	0	0	25161	36834	2716	
A0A3Q1M7S9 A0A3Q1M73	3	3	118.54	0.88408	0.70519	1.05789	0.05227	HL	HL	67779	Tyrosine-protein phosphatase non-receptor type OS=Bos taurus OX=9913	56719	92241	121019	45564	132961	79047	40000	188034	92066	117571	31737	94746	33462	52328	155608	70073	
A0A3Q1M9J5 A0A3Q1M9J	6	6	419.89	0.88504	0.70519	1.11895	0.05222	HL	HL	140481	Glutathione S-transferase A TPase OS=Bos taurus OX=9913 GN=ATP8B1 PE	454764	140481	277805	1319248	521579	416568	239745	663339	456912	410222	764338	405337	513167	453139	377330		
F1MZT7 F1MZT7_BOVIN;A	6	6	218.15	0.88515	0.70519	1.08233	0.05213	HL	HL	76703	Glutamine-fructose-6-phosphate transaminase 1 OS=Bos taurus OX=9913	55455	117881	185983	59506	341457	239019	40198	391702	311519	51673	37635	67627	133122	286250	403260	92120	
A0A452DID1 A0A452DID_1	3	3	273.13	0.88629	0.70536	1.13476	0.05218	HL	HL	24628	Translationaly-controlled tumor protein OS=Bos taurus OX=9913 GN=TP	431286	311146	486583	238400	427007	512377	481505	597364	246037	162577	409937	396252	359634	475533	1069283	445596	
F1M9V9 F1M9V9_BOVIN	2	2	104.27	0.88825	0.70571	1.10315	0.05211	HL	HL	57891	Oxidative stress responsive kinase 1 OS=Bos taurus OX=9913 GN=OXSR1 P	115377	57891	219305	76397	140033	162147	47550	200694	110520	338761	118404	75929	38196	176839	266903	184882	18453
A0A3Q1LIQ7 A0A3Q1LIQ	2	2	86.67	0.8946	0.70748	1.17773	0.05187	HL	HL	51288	Adenylyl cyclase-associated protein OS=Bos taurus OX=9913 GN=AC	70516	144102	52609	480607	207999	262399	268729	229411	368043	564526	98333	254781	172199	130410	157418	476481	
A0A3Q1LQ87 A0A3Q1LQ8	3	3	142.5	0.89576	0.70765	1.67341	0.05183	HL	HL	19061	40S ribosomal protein S16 OS=Bos taurus OX=9913 GN=RPS16 PE=3 SV=1	20396	32992	49158	37092	144561	64666	84890	393074	164076	164076	2945	9204	24551	439754	323666	464472	107181
ASD7E0 ASD7E0_BOVIN;A	6	5	481.07	0.90207	0.70985	1.14577	0.05161	HL	HL	23011	RAB35 protein OS=Bos taurus OX=9913 GN=RAB35 PE=1 SV=1	5413842	3558884	5514725	1795402	3570426	3573476	5403875	6933327	4616260	2162631	2974771	1946661	5908627	10062452	8601597	2822409	
Q3T0U2 RL14_BOVIN;G8IK	2	2	144.5	0.90215	0.70985	1.20481	0.05161	HL	HL	23421	60S ribosomal protein L14 OS=Bos taurus OX=9913 GN=RPL14 PE=2 SV=3	29627	73115	143426	163139	279116	179708	148641	347918	159993	45466	44637	81970	294250	298108	528606	187002	
E1B7R4 E1B7R4_BOVIN	3	3	185.83	0.90502	0.71016	1.82774	0.05152	HL	HL	165948	Eukaryotic translation initiation factor 3 subunit A OS=Bos taurus OX=9913	13353	37855	9630	3629	130891	744	16844	166066	47155	26765	5240	5735	79087	3255	41888	3273	
A0A3Q1NNJ3 A0A3Q1NNJ	2	2	150.21	0.9077	0.71185	1.16084	0.05143	HL	HL	20498	Flavin reductase (NADPH) OS=Bos taurus OX=9913 GN=BLVRB PE=1 SV=1	450904	448480	1171736	252787	442653	319550	637190	437625	117079	270789	197254	660097	797974	902811	542319		
A0A3Q1MRR6 A0A3Q1MRF	2	2	85.42	0.90957	0.71257	1.02747	0.05138	HL	HL	77769	Protein kinase C delta type OS=Bos taurus OX=9913 GN=PKCDB PE=3 SV=1	79148	85209	117088	20149	254761	170606	74863	160431	31924	310910	31696	47749	184726	229141	230753	46307	
F1ML75 F1ML75_BOVIN	3	3	211.43	0.91837	0.7165	1.00355	0.05112	HL	HL	65789	Interleukin 1 receptor type 1 OS=Bos taurus OX=9913 GN=IL1R1 PE=4 SV-	745598	215630	380301	58361	397289	106366	388639	705519	243777	100494	155919	313782	338021	722993	670409	80670	
P50227 ST1A1_BOVIN	2	2	269.91</																									

sPLS_Lipolysis_Enrichment_GO_BP_of_15prot_contributing_to_HL_group

GO_BP	Name	Function	Gene Name	Term frequency v	Term frequency	P-value (fdr)	Query with no gene names
GO:0010873	positive regulation of cholesterol esterification	Any process that increases the frequency, rate or extent of cholest	APOA1 APOA4 APOE	23.08 3/13	37.50 3/8	6,0673E-06	
GO:0034433	steroid esterification	A lipid modification process in which a steroid ester is formed by	tr APOA1 APOA4 APOE	23.08 3/13	25.00 3/12	6,0673E-06	
GO:0034372	very-low-density lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a	tr APOA1 APOA4 APOE	23.08 3/13	30.00 3/10	6,0673E-06	
GO:0034370	triglyceride-rich lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a	tr APOA1 APOA4 APOE	23.08 3/13	30.00 3/10	6,0673E-06	
GO:0034434	sterol esterification	A lipid modification process in which a sterol ester is formed by	tr APOA1 APOA4 APOE	23.08 3/13	25.00 3/12	6,0673E-06	
GO:0010872	regulation of cholesterol esterification	Any process that modulates the frequency, rate or extent of cholest	APOA1 APOA4 APOE	23.08 3/13	33.33 3/9	6,0673E-06	
GO:0034435	cholesterol esterification	A lipid modification process in which a sterol ester is formed by	tr APOA1 APOA4 APOE	23.08 3/13	25.00 3/12	6,0673E-06	
GO:0043691	reverse cholesterol transport	The directed movement of peripheral cell cholesterol, cholest-5-en	APOA1 APOA4 APOE	23.08 3/13	27.27 3/11	6,0673E-06	
GO:0033700	phospholipid efflux	The directed movement of a phospholipid out of a cell or organelle	APOA1 APOA4 APOE	23.08 3/13	23.08 3/13	7,00849E-06	
GO:0045940	positive regulation of steroid metabolic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE	23.08 3/13	15.79 3/19	2,13232E-05	
GO:0065005	protein-lipid complex assembly	The aggregation, arrangement and bonding together of proteins ar	APOA1 APOA4 APOE	23.08 3/13	15.00 3/20	2,27971E-05	
GO:0034369	plasma lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a	pl APOA1 APOA4 APOE	23.08 3/13	13.64 3/22	2,60387E-05	
GO:0034368	protein-lipid complex remodeling	The acquisition, loss or modification of a protein or lipid within a	pl APOA1 APOA4 APOE	23.08 3/13	13.64 3/22	2,60387E-05	
GO:1903494	response to dehydroepiandrosterone	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	100.00 2/2	2,69778E-05	
GO:1903496	response to 11-deoxycorticosterone	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	100.00 2/2	2,69778E-05	
GO:0034367	protein-containing complex remodeling	The acquisition, loss, or modification of macromolecules within a	co APOA1 APOA4 APOE	23.08 3/13	12.50 3/24	2,77849E-05	
GO:0071827	plasma lipoprotein particle organization	A protein-lipid complex subunit organization process that results	in APOA1 APOA4 APOE	23.08 3/13	9.68 3/31	5,79248E-05	
GO:1902995	positive regulation of phospholipid efflux	Any process that activates or increases the frequency, rate or exte	APOA1 APOE	15.38 2/13	66.67 2/3	5,95205E-05	
GO:1902994	regulation of phospholipid efflux	Any process that modulates the frequency, rate or extent of phosph	APOA1 APOE	15.38 2/13	66.67 2/3	5,95205E-05	
GO:0071825	protein-lipid complex subunit organization	Any process in which macromolecules aggregate, disaggregate, or	APOA1 APOA4 APOE	23.08 3/13	8.82 3/34	5,95205E-05	
GO:0010033	response to organic substance	Any process that results in a change in state or activity of a cell	or a APOA1 APOA4 APOE BSI	69.23 9/13	0.41 9/2222	5,95205E-05	
GO:0090207	regulation of triglyceride metabolic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4 APOE	23.08 3/13	8.82 3/34	5,95205E-05	
GO:0032374	regulation of cholesterol transport	Any process that modulates the frequency, rate or extent of the di	APOA1 APOA4 APOE	23.08 3/13	6.82 3/44	0,000115493	
GO:0033344	cholesterol efflux	The directed movement of cholesterol, cholest-5-en-3-beta-ol, out	APOA1 APOA4 APOE	23.08 3/13	6.98 3/43	0,000115493	
GO:0032371	regulation of sterol transport	Any process that modulates the frequency, rate or extent of the di	APOA1 APOA4 APOE	23.08 3/13	6.82 3/44	0,000115493	
GO:0120009	intermembrane lipid transfer	The transport of lipids between membranes in which a lipid molecu	APOA1 APOA4 APOE	23.08 3/13	6.52 3/46	0,000121789	
GO:0097006	regulation of plasma lipoprotein particle levels	Any process involved in the maintenance of internal levels of plas	pln APOA1 APOA4 APOE	23.08 3/13	6.25 3/48	0,000139447	
GO:0032489	regulation of Cdc42 protein signal transduction	Any process that modulates the frequency, rate or extent of Cdc4	2 APOA1 APOE	15.38 2/13	33.33 2/6	0,00021647	
GO:0046889	positive regulation of lipid biosynthetic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE	23.08 3/13	5.17 3/58	0,000230753	
GO:0051385	response to mineralocorticoid	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	28.57 2/7	0,000282751	
GO:0042632	cholesterol homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1 APOA4 APOE	23.08 3/13	4.62 3/65	0,000304784	
GO:0050592	sterol homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1 APOA4 APOE	23.08 3/13	4.55 3/66	0,000309204	
GO:0034380	high-density lipoprotein particle assembly	The non-covalent aggregation and arrangement of proteins and lip	APOA1 APOE	15.38 2/13	25.00 2/8	0,000335406	
GO:0051129	negative regulation of cellular component organization	Any process that stops, prevents, or reduces the frequency, rate	or APOA1 APOA4 APOE CLI	38.46 5/13	0.99 5/507	0,000335406	
GO:0019218	regulation of steroid metabolic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4 APOE	23.08 3/13	4.23 3/71	0,000352439	
GO:0051006	positive regulation of lipoprotein lipase activity	Any process that activates or increases the activity of the enzyme	lip APOA1 APOA4	15.38 2/13	22.22 2/9	0,000392726	
GO:2001140	positive regulation of phospholipid transport	Any process that activates or increases the frequency, rate or exte	APOA1 APOE	15.38 2/13	22.22 2/9	0,000392726	
GO:0010898	positive regulation of triglyceride catabolic process	Any process that increases the frequency, rate, or extent of the ch	APOA1 APOA4	15.38 2/13	20.00 2/10	0,000422255	
GO:0061365	positive regulation of triglyceride lipase activity	Any process that increases the activity of triglyceride lipase.	APOA1 APOA4	15.38 2/13	20.00 2/10	0,000422255	
GO:2001138	regulation of phospholipid transport	Any process that modulates the frequency, rate or extent of phosph	APOA1 APOE	15.38 2/13	20.00 2/10	0,000422255	
GO:0030301	cholesterol transport	The directed movement of cholesterol, cholest-5-en-3-beta-ol, int	APOA1 APOA4 APOE	23.08 3/13	3.80 3/79	0,000422255	
GO:0042221	response to chemical	Any process that results in a change in state or activity of a cell	or a APOA1 APOA4 APOE BSI	76.92 10/13	0.25 10/4056	0,000422255	
GO:1905907	negative regulation of amyloid fibril formation	Any process that stops, prevents or reduces the frequency, rate	or APOE CLU	15.38 2/13	20.00 2/10	0,000422255	
GO:0006641	triglyceride metabolic process	The chemical reactions and pathways involving triglyceride, any tri	APOA1 APOA4 APOE	23.08 3/13	3.61 3/83	0,000448668	
GO:0032368	regulation of lipid transport	Any process that modulates the frequency, rate or extent of the di	APOA1 APOA4 APOE	23.08 3/13	3.57 3/84	0,000454776	
GO:0032488	Cdc42 protein signal transduction	A series of molecular signals within the cell that are mediated by	tr APOA1 APOE	15.38 2/13	18.18 2/11	0,000482255	
GO:0034375	high-density lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a	hi APOA1 APOE	15.38 2/13	16.67 2/12	0,000543077	
GO:0032570	response to progesterone	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	16.67 2/12	0,000543077	
GO:1905906	regulation of amyloid fibril formation	Any process that modulates the frequency, rate or extent of amylo	APOE CLU	15.38 2/13	16.67 2/12	0,000543077	
GO:0098869	cellular oxidant detoxification	Any process carried out at the cellular level that reduces or remov	APOA4 APOE CSN151	23.08 3/13	3.23 3/93	0,000555447	
GO:0015918	sterol transport	The directed movement of sterols into, out of or within a cell, or	bc APOA1 APOA4 APOE	23.08 3/13	3.19 3/94	0,000562399	
GO:0010896	regulation of triglyceride catabolic process	Any process that modulates the frequency, rate, or extent of the c	APOA1 APOA4	15.38 2/13	15.38 2/13	0,000582178	
GO:0051004	regulation of lipoprotein lipase activity	Any process that modulates the activity of the enzyme lipoprotein	APOA1 APOA4	15.38 2/13	15.38 2/13	0,000582178	
GO:0008203	cholesterol metabolic process	The chemical reactions and pathways involving cholesterol, cholest	APOA1 APOA4 APOE	23.08 3/13	3.12 3/96	0,000582178	
GO:0015914	phospholipid transport	The directed movement of phospholipids into, out of or within a	ce APOA1 APOA4 APOE	23.08 3/13	3.03 3/99	0,000609081	
GO:1902652	secondary alcohol metabolic process	The chemical reactions and pathways involving secondary alcohol.	APOA1 APOA4 APOE	23.08 3/13	2.97 3/101	0,00063511	
GO:0016125	sterol metabolic process	The chemical reactions and pathways involving sterols, steroids	wit APOA1 APOA4 APOE	23.08 3/13	2.91 3/103	0,000661667	
GO:1902903	regulation of supramolecular fiber organization	Any process that modulates the frequency, rate or extent of sup	rap APOA1 APOE CLU CSN151	30.77 4/13	1.27 4/315	0,000665794	
GO:0045834	positive regulation of lipid metabolic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4 APOE	23.08 3/13	2.88 3/104	0,000665794	
GO:1990748	cellular detoxification	Any process carried out at the cellular level that reduces or remov	APOA4 APOE CSN151	23.08 3/13	2.86 3/105	0,000665794	
GO:1905952	regulation of lipid localization	Any process that modulates the frequency, rate or extent of lipid	lc APOA1 APOA4 APOE	23.08 3/13	2.73 3/110	0,000740408	
GO:0097237	cellular response to toxic substance	Any process that results in a change in state or activity of a cell	(in l APOA4 APOE CSN151	23.08 3/13	2.73 3/110	0,000740408	
GO:0034377	plasma lipoprotein particle assembly	The non-covalent aggregation and arrangement of proteins and lip	APOA1 APOE	15.38 2/13	12.50 2/16	0,000760008	
GO:0006869	lipid transport	The directed movement of lipids into, out of or within a cell, or	bet APOA1 APOA4 APOE LBI	30.77 4/13	1.20 4/332	0,000760008	
GO:0006639	acylglycerol metabolic process	The chemical reactions and pathways involving acylglycerol, any m	AP APOA1 APOA4 APOE	23.08 3/13	2.65 3/113	0,000765313	
GO:0006638	neutral lipid metabolic process	The chemical reactions and pathways involving neutral lipids, lipids	APOA1 APOA4 APOE	23.08 3/13	2.63 3/114	0,000773799	
GO:1990000	amyloid fibril formation	The generation of amyloid fibrils, insoluble fibrous protein aggrega	APOE CLU	15.38 2/13	11.76 2/17	0,000793252	
GO:0031331	positive regulation of cellular catabolic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4 APOE CLI	30.77 4/13	1.17 4/342	0,000793252	
GO:0010875	positive regulation of cholesterol efflux	Any process that increases the frequency, rate or extent of cholest	APOA1 APOE	15.38 2/13	11.76 2/17	0,000793252	
GO:0098754	detoxification	Any process that reduces or removes the toxicity of a toxic subst	an APOA4 APOE CSN151	23.08 3/13	2.54 3/118	0,000808629	
GO:0055088	lipid homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1 APOA4 APOE	23.08 3/13	2.50 3/120	0,000838202	
GO:0046890	regulation of lipid biosynthetic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4 APOE	23.08 3/13	2.42 3/124	0,000911385	
GO:0045723	positive regulation of fatty acid biosynthetic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4	15.38 2/13	10.00 2/20	0,001020122	
GO:0010876	lipid localization	Any process in which a lipid is transported to, or maintained in, a	sj APOA1 APOA4 APOE LBI	30.77 4/13	1.07 4/373	0,001020122	
GO:0060416	response to growth hormone	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	10.00 2/20	0,001020122	
GO:0042157	lipoprotein metabolic process	The chemical reactions and pathways involving any conjugated, w	APOA1 APOA4 APOE	23.08 3/13	2.24 3/134	0,00108753	
GO:0092028	positive regulation of triglyceride metabolic process	Any process that increases the frequency, rate or extent of the ch	APOA1 APOA4	15.38 2/13	9.52 2/21	0,001096015	
GO:0002385	mucosal immune response	An immune response taking place in mucosal tissues, including tho	APOA4 PIGR	15.38 2/13	9.09 2/22	0,001145662	
GO:0055090	acylglycerol homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1 APOE	15.38 2/13	9.09 2/22	0,001145662	
GO:0070328	triglyceride homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1 APOE	15.38 2/13	9.09 2/22	0,001145662	
GO:1902904	negative regulation of supramolecular fiber organization	Any process that stops, prevents or reduces the frequency, rate	or APOE CLU CSN151	23.08 3/13	2.16 3/139	0,001145662	
GO:0009896	positive regulation of catabolic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4 APOE CLI	30.77 4/13	1.00 4/400	0,001208571	
GO:0015748	organophosphate ester transport	The directed movement of organophosphate esters into, out of	or APOA1 APOA4 APOE	23.08 3/13	2.10 3/143	0,001208571	
GO:0050996	positive regulation of lipid catabolic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4	15.38 2/13	8.70 2/23	0,001209518	
GO:0050821	protein stabilization	Any process involved in maintaining the structure and integrity of	z APOA1 CLU CSN151	23.08 3/13	2.04 3/147	0,001280069	
GO:0002376	immune system process	Any process involved in the development or functioning of the inm	un APOA1 APOA4 APOE CLI	53.85 7/13	0.34 7/2045	0,001338684	
GO:0009636	response to toxic substance	Any process that results in a change in state or activity of a cell	or a APOA4 APOE CSN151	23.08 3/13	1.99 3/151	0,00135265	
GO:0002251	organ or tissue specific immune response	An immune response taking place in an organ or tissues such as th	APOA4 PIGR	15.38 2/13	8.00 2/25	0,00135265	
GO:0010874	regulation of cholesterol efflux	Any process that modulates the frequency, rate or extent of cholest	APOA1 APOE	15.38 2/13	8.00 2/25	0,00135265	
GO:0032376	positive regulation of cholesterol transport	Any process that activates or increases the frequency, rate or exte	r APOA1 APOE	15.38 2/13	7.69 2/26	0,001432643	
GO:0032373	positive regulation of sterol transport	Any process that activates or increases the frequency, rate or exte	r APOA1 APOE	15.38 2/13	7.69 2/26	0,001432643	
GO:0019433	triglyceride catabolic process	The chemical reactions and pathways resulting in the breakdown	o APOA1 APOA4	15.38 2/13	7.41 2/27	0,001529878	
GO:0045923	positive regulation of fatty acid metabolic process	Any process that activates or increases the frequency, rate or exte	r APOA1 APOA4	15.38 2/13	6.67 2/30	0,001873565	
GO:0033993	response to lipid	Any process that results in a change in state or activity of a cell	or a APOA4 CSN151 CSN152	30.77 4/13	0.86 4/464	0,001891867	
GO:0032355	response to estradiol	Any process that results in a change in state or activity of a cell	or a CSN151 CSN152	15.38 2/13	6.25 2/32	0,002089795	
GO:0030258	lipid modification	The covalent alteration of one or more fatty acids in a lipid, resul	tr APOA1 APOA4 APOE	23.08 3/13	1.60 3/187	0,002308728	
GO:0046461	neutral lipid catabolic process	The chemical reactions and pathways resulting in the breakdown	o APOA1 APOA4	15.38 2/13	5.56 2/36	0,002493052	
GO:1902653	secondary alcohol biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	5.56 2/36	0,002493052	
GO:0042304	regulation of fatty acid biosynthetic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4	15.38 2/13	5.56 2/36	0,002493052	
GO:0006695	cholesterol biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	5.56 2/36	0,002493052	

GO:0019216	regulation of lipid metabolic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4 APOE	23.08 3/13	1.22 3/246	0.004346252
GO:0031329	regulation of cellular catabolic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4 APOE CLI	30.77 4/13	0.65 4/613	0.004476717
GO:0060191	regulation of lipase activity	Any process that modulates the frequency, rate or extent of lipase	APOA1 APOA4	15.38 2/13	3.85 2/52	0.004503354
GO:0032370	positive regulation of lipid transport	Any process that activates or increases the frequency, rate or exte	APOA1 APOE	15.38 2/13	3.85 2/52	0.004503354
GO:0046503	glycerolipid catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOA1 APOA4	15.38 2/13	3.70 2/54	0.004815256
GO:0097435	supramolecular fiber organization	A process that is carried out at the cellular level which results in th	APOA1 APOE CLU CSN11	30.77 4/13	0.63 4/636	0.004972967
GO:0006066	alcohol metabolic process	The chemical reactions and pathways involving alcohols, any of a c	APOA1 APOA4 APOE	23.08 3/13	1.13 3/266	0.004986179
GO:1903000	regulation of lipid transport across blood-brain barrier	Any process that modulates the frequency, rate or extent of lipid tr	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:1905853	regulation of heparan sulfate binding	Any process that modulates the frequency, rate or extent of hepar	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:1905855	positive regulation of heparan sulfate binding	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:1905858	regulation of heparan sulfate proteoglycan binding	Any process that modulates the frequency, rate or extent of hepar	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0060265	positive regulation of respiratory burst involved in infla	Any process that increases the rate, frequency or extent of a phase	LBP	7.69 1/13	100.00 1/1	0.004986179
GO:0090731	cellular response to very-low-density lipoprotein partic	Any process that results in a change in state or activity of a cell (in	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0045919	positive regulation of cytolysis	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	100.00 1/1	0.004986179
GO:1903002	positive regulation of lipid transport across blood-brain	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:1905890	regulation of cellular response to very-low-density lipop	Any process that modulates the frequency, rate or extent of cellula	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0006952	defense response	Reactions, triggered in response to the presence of a foreign body	APOA1 APOA4 APOE CSI	38.46 5/13	0.43 5/1172	0.004986179
GO:0042268	regulation of cytolysis	Any process that modulates the frequency, rate or extent of the ru	LBP	7.69 1/13	100.00 1/1	0.004986179
GO:1502001	positive regulation of transport across blood-brain barr	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0150200	regulation of transport across blood-brain barrier	Any process that modulates the frequency, rate or extent of transp	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0032805	positive regulation of low-density lipoprotein particle n	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:1905860	positive regulation of heparan sulfate proteoglycan bin	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0071831	intermediate-density lipoprotein particle clearance	The process in which a intermediate-density lipoprotein particle is	APOE	7.69 1/13	100.00 1/1	0.004986179
GO:0016042	lipid catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOA1 APOA4 APOE	23.08 3/13	1.06 3/284	0.00549518
GO:0051241	negative regulation of multicellular organismal process	Any process that stops, prevents, or reduces the frequency, rate or	APOA1 APOA4 APOE LBI	30.77 4/13	0.58 4/686	0.005703479
GO:0045807	positive regulation of endocytosis	Any process that activates or increases the frequency, rate or exte	APOE CLU	15.38 2/13	3.12 2/64	0.005737915
GO:0016192	vesicle-mediated transport	A cellular transport process in which transported substances are m	APOA1 APOE CDSL CLU	38.46 5/13	0.39 5/1276	0.006401248
GO:0019217	regulation of fatty acid metabolic process	Any process that modulates the frequency, rate or extent of the ch	APOA1 APOA4	15.38 2/13	2.90 2/69	0.006524187
GO:0019915	lipid storage	The accumulation and maintenance in cells or tissues of lipids, corr	APOA1 APOE	15.38 2/13	2.90 2/69	0.006524187
GO:0006955	immune response	Any immune system process that functions in the calibrated respon	APOA1 APOA4 APOE LBI	38.46 5/13	0.39 5/1288	0.006540511
GO:1905954	positive regulation of lipid localization	Any process that activates or increases the frequency, rate or exte	APOA1 APOE	15.38 2/13	2.82 2/71	0.006809794
GO:0009894	regulation of catabolic process	Any process that modulates the frequency, rate, or extent of the c	APOA1 APOA4 APOE CLI	30.77 4/13	0.55 4/732	0.006923904
GO:0035023	regulation of Rho protein signal transduction	Any process that modulates the frequency, rate or extent of Rho p	APOA1 APOE	15.38 2/13	2.63 2/76	0.007689011
GO:1901654	response to ketone	A response that results in a state of tolerance to ketone.	CSN151 CSN152	15.38 2/13	2.60 2/77	0.007837493
GO:0034444	regulation of plasma lipoprotein oxidation	Any process that modulates the frequency, rate or extent of lipopr	APOA4	7.69 1/13	50.00 1/2	0.008421342
GO:1903365	regulation of fear response	Any process that modulates the frequency, rate or extent of fear r	APOE	7.69 1/13	50.00 1/2	0.008421342
GO:2000822	regulation of behavioral fear response	Any process that modulates the frequency, rate or extent of behav	APOE	7.69 1/13	50.00 1/2	0.008421342
GO:0002434	immune complex clearance	A process directed at removing immune complexes from the body.	CLU	7.69 1/13	50.00 1/2	0.008421342
GO:0050896	response to stimulus	Any process that results in a change in state or activity of a cell or	APOA1 APOA4 APOE BSI	84.62 11/13	0.14 11/7978	0.008421342
GO:0034445	negative regulation of plasma lipoprotein oxidation	Any process that stops, prevents, or reduces the frequency, rate or	APOA4	7.69 1/13	50.00 1/2	0.008421342
GO:0006982	response to lipid hydroperoxide	Any process that results in a change in state or activity of a cell or	APOA4	7.69 1/13	50.00 1/2	0.008421342
GO:0046486	glycerolipid metabolic process	The chemical reactions and pathways involving glycerolipids, any li	APOA1 APOA4 APOE	23.08 3/13	0.86 3/347	0.008421342
GO:0002415	immunoglobulin transcytosis in epithelial cells mediate	The process of transporting polymeric IgA and polymeric IgM immu	PIGR	7.69 1/13	50.00 1/2	0.008421342
GO:0015920	lipopolysaccharide transport	The directed movement of lipopolysaccharides into, out of or withi	LBP	7.69 1/13	50.00 1/2	0.008421342
GO:0010877	lipid transport involved in lipid storage	The directed movement of lipids into cells that is part of their accu	APOE	7.69 1/13	50.00 1/2	0.008421342
GO:0002414	immunoglobulin transcytosis in epithelial cells	The process of transporting immunoglobulin, via transcytosis, from	PIGR	7.69 1/13	50.00 1/2	0.008421342
GO:0097114	NMDA glutamate receptor clustering	The receptor clustering process in which N-methyl-D-aspartate (N	APOE	7.69 1/13	50.00 1/2	0.008421342
GO:1902952	positive regulation of dendritic spine maintenance	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	50.00 1/2	0.008421342
GO:0062013	positive regulation of small molecule metabolic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4	15.38 2/13	2.33 2/86	0.008854576
GO:0097305	response to alcohol	Any process that results in a change in state or activity of a cell or	CSN151 CSN152	15.38 2/13	2.30 2/87	0.009000436
GO:0098542	defense response to other organism	Reactions triggered in response to the presence of another organis	APOA4 APOE CSN152 LB	30.77 4/13	0.49 4/812	0.009009757
GO:0043534	blood vessel endothelial cell migration	The orderly movement of an endothelial cell into the extracellular	APOA1 APOE	15.38 2/13	2.22 2/90	0.009512196
GO:0050728	negative regulation of inflammatory response	Any process that stops, prevents, or reduces the frequency, rate or	APOA1 APOE	15.38 2/13	2.20 2/91	0.009636812
GO:0031347	regulation of defense response	Any process that modulates the frequency, rate or extent of a defe	APOA1 APOE LBP	23.08 3/13	0.80 3/376	0.010133214
GO:0042158	lipoprotein biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	2.08 2/96	0.010550927
GO:1990266	neutrophil migration	The movement of a neutrophil within or between different tissues	GP2 LBP	15.38 2/13	2.08 2/96	0.010550927
GO:0060627	regulation of vesicle-mediated transport	Any process that modulates the rate, frequency, or extent of vesic	APOA1 APOE	23.08 3/13	0.78 3/385	0.01065243
GO:0010565	regulation of cellular ketone metabolic process	Any process that modulates the chemical reactions and pathways i	APOA1 APOA4	15.38 2/13	2.04 2/98	0.010860945
GO:0061771	response to caloric restriction	A change in state or activity of a cell or an organism (in terms of	APOE	7.69 1/13	33.33 1/3	0.011551973
GO:0071830	triglyceride-rich lipoprotein particle clearance	The process in which a triglyceride-rich lipoprotein particle is rem	APOE	7.69 1/13	33.33 1/3	0.011551973
GO:1901615	organic hydroxy compound metabolic process	The chemical reactions and pathways involving organic hydroxy co	APOA1 APOA4 APOE	23.08 3/13	0.75 3/398	0.011551973
GO:0034382	chylomicron remnant clearance	The process in which a chylomicron remnant is removed from the i	APOE	7.69 1/13	33.33 1/3	0.011551973
GO:0034441	plasma lipoprotein particle oxidation	The modification of a lipid or protein within a plasma lipoprotein p	APOA4	7.69 1/13	33.33 1/3	0.011551973
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a cell (in	APOA1 APOA4 APOE BSI	76.92 10/13	0.15 10/6878	0.012172433
GO:0080134	regulation of response to stress	Any process that modulates the frequency, rate or extent of a resp	APOA1 APOE CLU LBP	30.77 4/13	0.44 4/909	0.012591759
GO:0046165	alcohol biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	1.83 2/109	0.012797411
GO:1903364	positive regulation of cellular protein catabolic process	Any process that activates or increases the frequency, rate or exte	APOE CLU	15.38 2/13	1.75 2/114	0.013748188
GO:0001935	endothelial cell proliferation	The multiplication or reproduction of endothelial cells, resulting i	APOA1 APOE	15.38 2/13	1.75 2/114	0.013748188
GO:0007266	Rho protein signal transduction	A series of molecular signals within the cell that are mediated by a	APOA1 APOE	15.38 2/13	1.75 2/114	0.013748188
GO:0003360	brainstem development	The progression of the brainstem from its formation to the mature	CNTFR	7.69 1/13	25.00 1/4	0.013826807
GO:0032802	low-density lipoprotein particle receptor catabolic proc	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0097530	granulocyte migration	The movement of a granulocyte within or between different tissue	GP2 LBP	15.38 2/13	1.69 2/118	0.013826807
GO:0045541	negative regulation of cholesterol biosynthetic process	Any process that stops, prevents, or reduces the frequency, rate or	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:1900223	positive regulation of amyloid-beta clearance	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0090206	negative regulation of cholesterol metabolic process	Any process that decreases the rate, frequency, or extent of chole	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0032799	low-density lipoprotein receptor particle metabolic pro	The chemical reactions and pathways involving low-density lipoppr	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0010903	negative regulation of very-low-density lipoprotein par	Any process that decreases the rate, frequency or extent of very-lo	APOA1	7.69 1/13	25.00 1/4	0.013826807
GO:0060264	regulation of respiratory burst involved in inflammator	Any process that modulates the rate, frequency or extent of a phas	LBP	7.69 1/13	25.00 1/4	0.013826807
GO:0044283	small molecule biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4 APOE	23.08 3/13	0.69 3/437	0.013826807
GO:0006694	steroid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	1.72 2/116	0.013826807
GO:0106119	negative regulation of sterol biosynthetic process	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:2000646	positive regulation of receptor catabolic process	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0032803	regulation of low-density lipoprotein particle receptor i	Any process that modulates the frequency, rate or extent of the ch	APOE	7.69 1/13	25.00 1/4	0.013826807
GO:0002252	immune effector process	Any process of the immune system that executes a component of a	APOA1 CLU LBP	23.08 3/13	0.66 3/454	0.014705774
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4	15.38 2/13	1.61 2/124	0.014907769
GO:0006897	endocytosis	A vesicle-mediated transport process in which cells take up extern	APOE CDSL CLU	23.08 3/13	0.64 3/466	0.015675041
GO:0006954	inflammatory response	The immediate defensive reaction (by vertebrate tissue) to infecti	APOA1 APOE LBP	23.08 3/13	0.64 3/472	0.016031837
GO:0045088	regulation of innate immune response	Any process that modulates the frequency, rate or extent of the in	APOE LBP	15.38 2/13	1.54 2/130	0.016031837
GO:0030100	regulation of endocytosis	Any process that modulates the frequency, rate or extent of endoc	APOE CLU	15.38 2/13	1.54 2/130	0.016031837
GO:0097688	glutamate receptor clustering	The neurotransmitter-gated ion channel clustering process in whic	APOE	7.69 1/13	20.00 1/5	0.016203623
GO:0010901	regulation of very-low-density lipoprotein particle rem	Any process that modulates the rate, frequency or extent of very-l	APOA1	7.69 1/13	20.00 1/5	0.016203623
GO:1990379	lipid transport across blood-brain barrier	The directed movement of lipid molecules passing through the blo	APOE	7.69 1/13	20.00 1/5	0.016203623
GO:0034447	very-low-density lipoprotein particle clearance	The process in which a very-low-density lipoprotein particle is rem	APOE	7.69 1/13	20.00 1/5	0.016203623
GO:0097113	AMPA glutamate receptor clustering	The glutamate receptor clustering process in which alpha-amino-3-	APOE	7.69 1/13	20.00 1/5	0.016203623
GO:0002536	respiratory burst involved in inflammatory response	A phase of elevated metabolic activity, during which oxygen consu	LBP	7.69 1/13	20.00 1/5	0.016203623
GO:0060354	negative regulation of cell adhesion molecule productio	Any process that decreases the rate, frequency or extent of cell ad	APOA1	7.69 1/13	20.00 1/5	0.016203623
GO:1901700	response to oxygen-containing compound	Any process that results in a change in state or activity of a cell or	APOA4 CSN151 CSN152	30.77 4/13	0.39 4/1028	0.016724838
GO:0051128	regulation of cellular component organization	Any process that modulates the frequency, rate or extent of a proc	APOA1 APOA4 APOE CLI	38.46 5/13	0.29 5/1732	0.016729878
GO:0051707	response to other organism	Any process that results in a change in state or activity of a cell or	APOA4 APOE CSN152 LB	30.77 4/13	0.38 4/1066	0.016839074
GO:0002232	leukocyte chemotaxis involved in inflammatory respon	The movement of an immune cell in response to an external stimu	LBP	7.69 1/13	16.67 1/6	0.016839074
GO:1902950	regulation of dendritic spine maintenance	Any process that modulates the frequency, rate or extent of dendr	APOE	7.69 1/13	16.67 1/6	0.016839074
GO:0034115	negative regulation of heterotypic cell-cell adhesion	Any process that stops, prevents, or reduces the frequency, rate o	APOA1	7.69 1/13	16.67 1/6	0.016839074
GO:0031348	negative regulation of defense response	Any process that stops, prevents, or reduces the frequency, rate or	APOA1 APOE	15.38 2/13	1.37 2/146	0.016839074
GO:0060267	positive regulation of respiratory burst	Any process that increases the rate frequency or extent of a phase	LBP	7.69 1/13	16.67 1/6	0.016839074
GO:0090209	negative regulation of triglyceride metabolic process	Any process that decreases the frequency, rate or extent of the ch	APOE	7.69 1/13	16.67 1/6	0.016839074
GO:0070587	regulation of cell-cell adhesion involved in gastrulation	Any process that modulates the frequency, rate, or extent of attach	APOA1	7.69 1/13	16.67 1/6	0.016839074
GO:0043207	response to external biotic stimulus	Any process that results in a change in state or activity of a cell or	APOA4 APOE CSN152 LB	30.77 4/13	0.37 4/1068	0.016839074
GO:1900272	negative regulation of long-term synaptic potentiation	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	16.67 1/6	0.016839074
GO:0002682	regulation of immune system process	Any process that modulates the frequency, rate, or extent of an im	APOA1 APOE LBP PIGR	30.77 4/13	0.37 4/1077	0.016839074
GO:0008610	lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4 APOE	23.08 3/13	0.57 3/525	0.019579555
GO:0048545	response to steroid hormone	Any process that results in a change in state or activity of a cell or	CSN151 CSN152	15.38 2/13	1.32 2/152	0.019628779
GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4	15.38 2/13	1.31 2/153	0.01963209
GO:0061136	regulation of proteasomal protein catabolic process	Any process that modulates the rate, frequency, or extent of the c	APOE CLU	15.38 2/13	1.31 2/153	0.01963209
GO:0009607	response to biotic stimulus	Any process that results in a change in state or activity of a cell or	APOA4 APOE CSN152 LB	30.77 4/13	0.36 4/1098	0.01963209
GO:1904729	regulation of intestinal lipid absorption	Any process that modulates the frequency, rate or extent of intesti	APOA1	7.69 1/13	14.29 1/7	0.020249368

GO:0070391	response to lipoteichoic acid	Any process that results in a change in state or activity of an organi	LBP	7.69 1/13	14.29 1/7	0,020249368
GO:2000644	regulation of receptor catalytic process	Any process that modulates the frequency, rate or extent of recept	APOE	7.69 1/13	14.29 1/7	0,020249368
GO:0070586	cell-cell adhesion involved in gastrulation	The attachment of one cell to another cell affecting gastrulation.	APOA1	7.69 1/13	14.29 1/7	0,020249368
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	A series of molecular signals initiated by the binding of a ciliary neu	CNTFR	7.69 1/13	14.29 1/7	0,020249368
GO:0030300	regulation of intestinal cholesterol absorption	Any process that modulates the frequency, rate or extent of absorp	APOA1	7.69 1/13	14.29 1/7	0,020249368
GO:0071223	cellular response to lipoteichoic acid	Any process that results in a change in state or activity of a cell (in	LBP	7.69 1/13	14.29 1/7	0,020249368
GO:0046578	regulation of Ras protein signal transduction	Any process that modulates the frequency, rate or extent of Ras pr	APOA1 APOE	15.38 2/13	1.25 2/160	0,020677805
GO:0045087	innate immune response	Innate immune responses are defense responses mediated by gen	APOA4 APOE LBP	23.08 3/13	0.54 3/558	0,021945498
GO:0097529	myeloid leukocyte migration	The movement of a myeloid leukocyte within or between different	GP2 LBP	15.38 2/13	1.20 2/166	0,022026717
GO:0044093	positive regulation of molecular function	Any process that activates or increases the rate or extent of a mole	APOA1 APOA4 APOE CLU	30.77 4/13	0.35 4/1149	0,022040865
GO:0043542	endothelial cell migration	The orderly movement of an endothelial cell into the extracellular	APOA1 APOE	15.38 2/13	1.18 2/169	0,02261672
GO:0009967	positive regulation of signal transduction	Any process that activates or increases the frequency, rate or exte	APOA1 APOE CLU LBP	30.77 4/13	0.34 4/1161	0,022685293
GO:0042180	cellular ketone metabolic process	The chemical reactions and pathways involving any of a class of or	APOA1 APOA4	15.38 2/13	1.18 2/170	0,022687777
GO:0006950	response to stress	Any process that results in a change in state or activity of a cell or	APOA1 APOA4 APOE CLU	46.15 6/13	0.21 6/2809	0,022750495
GO:0044419	biological process involved in interspecies interaction	Any process evolved to enable an interaction with an organism of	APOA4 APOE CSN152 LB	30.77 4/13	0.34 4/1167	0,022822023
GO:0006898	receptor-mediated endocytosis	An endocytosis process in which cell surface receptors ensure spec	APOE CLU	15.38 2/13	1.16 2/173	0,023098847
GO:0051050	positive regulation of transport	Any process that activates or increases the frequency, rate or exte	APOA1 APOE CLU	23.08 3/13	0.52 3/576	0,023098847
GO:1903050	regulation of proteolysis involved in cellular protein cat	Any process that modulates the frequency, rate or extent of protec	APOE CLU	15.38 2/13	1.15 2/174	0,023392718
GO:0055089	fatty acid homeostasis	Any process involved in the maintenance of an internal steady stat	APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0035376	sterol import	The directed movement of a sterol into a cell or organelle. Sterols	APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0001818	negative regulation of cytokine production	Any process that stops, prevents, or reduces the rate of productio	APOA1 LBP	15.38 2/13	1.10 2/181	0,023392718
GO:0032490	detection of molecule of bacterial origin	The series of events in which a stimulus from a molecule of bacteri	LBP	7.69 1/13	11.11 1/9	0,023392718
GO:0070508	cholesterol import	The directed movement of cholesterol into a cell or organelle.	APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0034384	high-density lipoprotein particle clearance	The process in which a high-density lipoprotein particle is removed	APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0016127	sterol catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	11.11 1/9	0,023392718
GO:1901617	organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOE	15.38 2/13	1.14 2/175	0,023392718
GO:0045732	positive regulation of protein catabolic process	Any process that activates or increases the frequency, rate or exte	APOE CLU	15.38 2/13	1.11 2/180	0,023392718
GO:0051049	regulation of transport	Any process that modulates the frequency, rate or extent of the dir	APOA1 APOA4 APOE CLU	30.77 4/13	0.33 4/1201	0,023392718
GO:0002679	respiratory burst involved in defense response	A phase of elevated metabolic activity, during which oxygen consu	LBP	7.69 1/13	11.11 1/9	0,023392718
GO:0001967	suckling behavior	Specific behavior of a newborn or infant mammal that results in th	CNTFR	7.69 1/13	11.11 1/9	0,023392718
GO:1904478	regulation of intestinal absorption	Any process that modulates the frequency, rate or extent of intesti	APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0006707	cholesterol catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0016477	cell migration	The controlled self-propelled movement of a cell from one site to	APOA1 APOE GP2 LBP	30.77 4/13	0.33 4/1202	0,023392718
GO:0006810	transport	The directed movement of substances (such as macromolecules, si	APOA1 APOA4 APOE CD	53.85 7/13	0.18 7/3886	0,023392718
GO:0060353	regulation of cell adhesion molecule production	Any process that modulates the rate, frequency or extent of cell ad	APOA1	7.69 1/13	11.11 1/9	0,023392718
GO:0072578	neurotransmitter-gated ion channel clustering	The receptor clustering process in which neurotransmitter-gated ic	APOE	7.69 1/13	11.11 1/9	0,023392718
GO:0034374	low-density lipoprotein particle remodeling	The acquisition, loss or modification of a protein or lipid within a	lo APOE	7.69 1/13	10.00 1/10	0,023955793
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a cell or	APOA1 APOA4 APOE CSI	38.46 5/13	0.25 5/2004	0,024955793
GO:0044242	cellular lipid catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOA1 APOA4	15.38 2/13	1.06 2/188	0,024955793
GO:0034145	positive regulation of toll-like receptor 4 signaling path	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	10.00 1/10	0,024955793
GO:1900221	regulation of amyloid-beta clearance	Any process that modulates the frequency, rate or extent of amylo	APOE	7.69 1/13	10.00 1/10	0,024955793
GO:0106118	regulation of sterol biosynthetic process	Any process that modulates the frequency, rate or extent of a ster	APOE	7.69 1/13	10.00 1/10	0,024955793
GO:0045540	regulation of cholesterol biosynthetic process	Any process that modulates the frequency, rate or extent of the ch	APOE	7.69 1/13	10.00 1/10	0,024955793
GO:0050776	regulation of immune response	Any process that modulates the frequency, rate or extent of the im	APOE LBP PIGR	23.08 3/13	0.49 3/616	0,02507701
GO:0061024	membrane organization	A process which results in the assembly, arrangement of constitue	APOA1 APOA4 APOE	23.08 3/13	0.48 3/620	0,025437538
GO:0051056	regulation of small GTPase mediated signal transductio	Any process that modulates the frequency, rate or extent of small	APOA1 APOE	15.38 2/13	1.04 2/193	0,025523705
GO:0032879	regulation of localization	Any process that modulates the frequency, rate or extent of any pr	APOA1 APOA4 APOE CLU	38.46 5/13	0.24 5/2055	0,0261192
GO:0044794	positive regulation by host of viral process	A process in which a host organism activates or increases the freq	APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0002523	leukocyte migration involved in inflammatory response	The movement of a leukocyte within or between different tissues	LBP	7.69 1/13	9.09 1/11	0,0261192
GO:0033194	response to hydroperoxide	Any process that results in a change in state or activity of a cell or	APOA4	7.69 1/13	9.09 1/11	0,0261192
GO:1902931	negative regulation of alcohol biosynthetic process	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0051234	establishment of localization	Any process that localizes a substance or cellular component. This	APOA1 APOA4 APOE CD	53.85 7/13	0.17 7/4033	0,0261192
GO:1903362	regulation of cellular protein catabolic process	Any process that modulates the frequency, rate or extent of cellula	APOE CLU	15.38 2/13	1.02 2/196	0,0261192
GO:0097062	dendritic spine maintenance	The organization process that preserves a dendritic spine in a stabl	APOE	7.69 1/13	9.09 1/11	0,0261192
GO:0030269	intestinal cholesterol absorption	Uptake of cholesterol into the blood by absorption from the small	APOA1	7.69 1/13	9.09 1/11	0,0261192
GO:0060263	regulation of respiratory burst	Any process that modulates the rate frequency or extent of a phas	LBP	7.69 1/13	9.09 1/11	0,0261192
GO:0018206	peptidyl-methionine modification	The modification of peptidyl-methionine.	APOA1	7.69 1/13	9.09 1/11	0,0261192
GO:0032101	regulation of response to external stimulus	Any process that modulates the frequency, rate or extent of a resp	APOA1 APOE LBP	23.08 3/13	0.47 3/642	0,026741073
GO:0010647	positive regulation of cell communication	Any process that increases the frequency, rate or extent of cell con	APOA1 APOE CLU LBP	30.77 4/13	0.31 4/1286	0,027281672
GO:0060352	cell adhesion molecule production	The appearance of a cell adhesion molecule due to biosynthesis or	APOA1	7.69 1/13	8.33 1/12	0,027681859
GO:0051044	positive regulation of membrane protein ectodomain p	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	8.33 1/12	0,027681859
GO:0043117	positive regulation of vascular permeability	Any process that increases the extent to which blood vessels can b	APOE	7.69 1/13	8.33 1/12	0,027681859
GO:1902430	negative regulation of amyloid-beta formation	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	8.33 1/12	0,027681859
GO:0023056	regulation of signaling	Any process that activates, maintains or increases the frequency, r	APOA1 APOE CLU LBP	30.77 4/13	0.31 4/1293	0,027681859
GO:0038093	Fc receptor signaling pathway	A series of molecular signals initiated by the binding of the Fc porti	PIGR	7.69 1/13	8.33 1/12	0,027681859
GO:0010243	response to organonitrogen compound	Any process that results in a change in state or activity of a cell or	APOE CSN151 CSN152	23.08 3/13	0.46 3/658	0,027842254
GO:0071345	cellular response to cytokine stimulus	Any process that results in a change in state or activity of a cell (in	APOA1 BSPRY CNTFR	23.08 3/13	0.45 3/660	0,027808979
GO:0002831	regulation of response to biotic stimulus	Any process that modulates the frequency, rate, or extent of a resp	APOE LBP	15.38 2/13	0.95 2/211	0,028067229
GO:0035641	locomotory exploration behavior	The specific movement from place to place of an organism in resp	APOE	7.69 1/13	7.69 1/13	0,029182936
GO:0044241	lipid digestion	The whole of the physical, chemical, and biochemical processes ca	APOA1	7.69 1/13	7.69 1/13	0,029182936
GO:0018158	protein oxidation	The modification of a protein amino acid by oxidation.	APOA1	7.69 1/13	7.69 1/13	0,029182936
GO:0098856	intestinal lipid absorption	Any process in which lipids are taken up from the contents of the i	APOA1	7.69 1/13	7.69 1/13	0,029182936
GO:0010544	negative regulation of platelet activation	Any process that decreases the rate or frequency of platelet activa	APOE	7.69 1/13	7.69 1/13	0,029182936
GO:0010232	vascular transport	The directed movement of substances, into, out of or within a cell,	APOE	7.69 1/13	7.14 1/14	0,030604986
GO:0150104	transport across blood-brain barrier	The directed movement of substances (e.g. macromolecules, small	APOE	7.69 1/13	7.14 1/14	0,030604986
GO:0055091	phospholipid homeostasis	Any process involved in the maintenance of an internal steady stat	APOA1	7.69 1/13	7.14 1/14	0,030604986
GO:0048870	cell motility	Any process involved in the controlled self-propelled movement of	APOA1 APOE GP2 LBP	30.77 4/13	0.30 4/1350	0,030604986
GO:0032691	negative regulation of interleukin-1 beta production	Any process that stops, prevents, or reduces the frequency, rate, o	APOA1	7.69 1/13	7.14 1/14	0,030604986
GO:0051000	positive regulation of nitric-oxide synthase activity	Any process that activates or increases the activity of the enzyme	APOE	7.69 1/13	7.14 1/14	0,030604986
GO:0051674	localization of cell	Any process in which a cell is transported to, and/or maintained in,	APOA1 APOE GP2 LBP	30.77 4/13	0.30 4/1350	0,030604986
GO:0045056	transcytosis	The directed movement of endocytosed material through the cell	PIGR	7.69 1/13	7.14 1/14	0,030604986
GO:0051179	localization	Any process in which a cell, a substance, or a cellular entity, such	APOA1 APOA4 APOE CD	61.54 8/13	0.15 8/5413	0,030904237
GO:0043434	response to peptide hormone	Any process that results in a change in state or activity of a cell or	CSN151 CSN152	15.38 2/13	0.87 2/229	0,031271859
GO:0010804	negative regulation of tumor necrosis factor-mediated	Any process that decreases the rate or extent of the tumor necrosi	APOA1	7.69 1/13	6.67 1/15	0,032055113
GO:0002281	macrophage activation involved in immune response	A change in morphology and behavior of a macrophage resulting fr	LBP	7.69 1/13	6.67 1/15	0,032055113
GO:0043032	positive regulation of macrophage activation	Any process that stimulates, induces or increases the rate of macr	LBP	7.69 1/13	6.67 1/15	0,032055113
GO:0030325	adrenal gland development	The process whose specific outcome is the progression of the adre	APOA1	7.69 1/13	6.67 1/15	0,032055113
GO:1902992	negative regulation of amyloid precursor protein catab	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	6.67 1/15	0,032055113
GO:0034097	response to cytokine	Any process that results in a change in state or activity of a cell or	APOA1 BSPRY CNTFR	23.08 3/13	0.42 3/713	0,032140446
GO:0010631	epithelial cell migration	The orderly movement of an epithelial cell from one site to anothe	APOA1 APOE	15.38 2/13	0.85 2/235	0,032140446
GO:0090132	epithelium migration	The process in which the population of cells that make up an epith	APOA1 APOE	15.38 2/13	0.84 2/237	0,032564831
GO:0046394	carboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4	15.38 2/13	0.84 2/239	0,032990424
GO:0007263	nitric oxide mediated signal transduction	Any intracellular signal transduction in which the signal is passed	o APOE	7.69 1/13	6.25 1/16	0,033065378
GO:0002719	negative regulation of cytokine production involved in	Any process that stops, prevents, or reduces the frequency, rate, o	APOA1	7.69 1/13	6.25 1/16	0,033065378
GO:0002227	innate immune response in mucosa	Any process of the innate immune response that takes place in the	APOA4	7.69 1/13	6.25 1/16	0,033065378
GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1 APOA4	15.38 2/13	0.83 2/242	0,033065378
GO:0008283	cell population proliferation	The multiplication or reproduction of cells, resulting in the expansi	APOA1 APOE CLU CNTFR	30.77 4/13	0.28 4/1409	0,033065378
GO:0019430	removal of superoxide radicals	Any process, acting at the cellular level, involved in removing super	APOA4	7.69 1/13	6.25 1/16	0,033065378
GO:0006656	phosphatidylcholine biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOA1	7.69 1/13	6.25 1/16	0,033065378
GO:0090130	tissue migration	The process in which the population of cells that make up a tissue	APOA1 APOE	15.38 2/13	0.82 2/243	0,033226039
GO:0007166	cell surface receptor signaling pathway	A series of molecular signals initiated by activation of a receptor or	APOA1 APOE CNTFR LBF	38.46 5/13	0.22 5/2259	0,033649856
GO:1902533	positive regulation of intracellular signal transduction	Any process that activates or increases the frequency, rate or exte	APOA1 APOE CLU	23.08 3/13	0.40 3/741	0,034146314
GO:0042159	lipoprotein catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	5.88 1/17	0,034146314
GO:1901698	response to nitrogen compound	Any process that results in a change in state or activity of a cell or	APOE CSN151 CSN152	23.08 3/13	0.40 3/741	0,034146314
GO:0071450	cellular response to oxygen radical	Any process that results in a change in state or activity of a cell (in	APOA4	7.69 1/13	5.88 1/17	0,034146314
GO:0071451	cellular response to superoxide	Any process that results in a change in state or activity of a cell (in	APOA4	7.69 1/13	5.88 1/17	0,034146314
GO:0051043	regulation of membrane protein ectodomain proteolys	Any process that modulates the frequency, rate or extent of the pr	APOE	7.69 1/13	5.88 1/17	0,034146314
GO:0090023	positive regulation of neutrophil chemotaxis	Any process that increases the frequency, rate, or extent of neutro	LBP	7.69 1/13	5.88 1/17	0,034146314
GO:0002697	regulation of immune effector process	Any process that modulates the frequency, rate, or extent of an im	APOA1 LBP	15.38 2/13	0.79 2/252	0,034669907
GO:0034114	regulation of heterotypic cell-cell adhesion	Any process that modulates the frequency, rate, or extent of heter	APOA1	7.69 1/13	5.56 1/18	0,035718919
GO:0032692	negative regulation of interleukin-1 production	Any process that stops, prevents, or reduces the frequency, rate, o	APOA1	7.69 1/13	5.56 1	

GO:0006650	glycerophospholipid metabolic process	The chemical reactions and pathways involving glycerophospholipid	APOA1 APOA4	15.38 2/13	0.76 2/262	0.036585695
GO:0040011	locomotion	Self-propelled movement of a cell or organism from one location to another	APOA1 APOE GP2 LBP	30.77 4/13	0.27 4/1476	0.036726162
GO:0000303	response to superoxide	Any process that results in a change in state or activity of a cell or organelle	APOA4	7.69 1/13	5.26 1/19	0.036825582
GO:0035640	exploration behavior	The specific behavior of an organism in response to a novel environment	APOE	7.69 1/13	5.26 1/19	0.036825582
GO:0034143	regulation of toll-like receptor 4 signaling pathway	Any process that modulates the frequency, rate, or extent of toll-like receptor signaling	LBP	7.69 1/13	5.26 1/19	0.036825582
GO:0032102	negative regulation of response to external stimulus	Any process that stops, prevents, or reduces the frequency, rate or extent of response to external stimulus	APOA1 APOE	15.38 2/13	0.75 2/266	0.037119143
GO:0000305	response to oxygen radical	Any process that results in a change in state or activity of a cell or organelle	APOA4	7.69 1/13	5.00 1/20	0.037669754
GO:0033036	macromolecule localization	Any process in which a macromolecule is transported to, or maintained in, a specific location	APOA1 APOA4 APOE LBP	38.46 5/13	0.21 5/2363	0.037669754
GO:0045939	negative regulation of steroid metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of steroid metabolism	APOE	7.69 1/13	5.00 1/20	0.037669754
GO:0010894	negative regulation of steroid biosynthetic process	Any process that decreases the frequency, rate or extent of the biosynthesis of steroids	APOE	7.69 1/13	5.00 1/20	0.037669754
GO:0008211	glucocorticoid metabolic process	The chemical reactions and pathways involving glucocorticoids, hormones	APOA1	7.69 1/13	5.00 1/20	0.037669754
GO:0060999	positive regulation of dendritic spine development	Any process that increases the rate, frequency, or extent of dendritic spine development	APOE	7.69 1/13	5.00 1/20	0.037669754
GO:0071624	positive regulation of granulocyte chemotaxis	Any process that increases the rate, frequency or extent of granulocyte chemotaxis	LBP	7.69 1/13	5.00 1/20	0.037669754
GO:0006706	steroid catabolic process	The chemical reactions and pathways resulting in the breakdown of steroids	APOE	7.69 1/13	5.00 1/20	0.037669754
GO:0090181	regulation of cholesterol metabolic process	Any process that modulates the rate, frequency, or extent of cholesterol metabolism	APOE	7.69 1/13	5.00 1/20	0.037669754
GO:0042742	defense response to bacterium	Reactions triggered in response to the presence of a bacterium	CSN152 LBP	15.38 2/13	0.73 2/273	0.03791638
GO:1901652	response to peptide	Any process that results in a change in state or activity of a cell or organelle	CSN151 CSN152	15.38 2/13	0.73 2/274	0.038075223
GO:0006979	response to oxidative stress	Any process that stops, prevents, or reduces the frequency, rate or extent of oxidative stress	APOA4 APOE	15.38 2/13	0.73 2/275	0.038128387
GO:0045862	positive regulation of proteolysis	Any process that activates or increases the frequency, rate or extent of proteolysis	APOE CLU	15.38 2/13	0.73 2/275	0.038128387
GO:0007265	Ras protein signal transduction	A series of molecular signals within the cell that are mediated by the Ras protein	APOA1 APOE	15.38 2/13	0.72 2/276	0.038286961
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway	Any process that stops, prevents or reduces the frequency, rate or extent of intrinsic apoptotic signaling	CLU	7.69 1/13	4.76 1/21	0.038783126
GO:0055094	response to lipoprotein particle	Any process that results in a change in state or activity of a cell or organelle	APOE	7.69 1/13	4.76 1/21	0.038783126
GO:1900271	regulation of long-term synaptic potentiation	Any process that modulates the frequency, rate or extent of long-term synaptic potentiation	APOE	7.69 1/13	4.55 1/22	0.03985352
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency, rate or extent of a biological process	APOA1 APOA4 APOE CLU	53.85 7/13	0.15 7/4543	0.03985352
GO:0050999	regulation of nitric-oxide synthase activity	Any process that modulates the activity of the enzyme nitric-oxide synthase	APOE	7.69 1/13	4.55 1/22	0.03985352
GO:0071402	cellular response to lipoprotein particle stimulus	Any process that results in a change in state or activity of a cell in response to lipoprotein particle	APOE	7.69 1/13	4.55 1/22	0.03985352
GO:0051788	response to misfolded protein	Any process that results in a change in state or activity of a cell or organelle	CLU	7.69 1/13	4.55 1/22	0.03985352
GO:0032801	receptor catabolic process	The chemical reactions and pathways resulting in the breakdown of receptors	APOE	7.69 1/13	4.55 1/22	0.03985352
GO:0002021	response to dietary excess	The physiological process in which dietary excess is sensed by the organism	APOE	7.69 1/13	4.55 1/22	0.03985352
GO:0050900	leukocyte migration	The movement of a leukocyte within or between different tissues	GP2 LBP	15.38 2/13	0.69 2/289	0.040667112
GO:0019934	cGMP-mediated signaling	Any intracellular signal transduction in which the signal is passed on by cGMP	APOE	7.69 1/13	4.35 1/23	0.041319408
GO:0007616	long-term memory	The memory process that deals with the storage, retrieval and modification of information	APOE	7.69 1/13	4.35 1/23	0.041319408
GO:0002701	negative regulation of production of molecular mediator	Any process that stops, prevents, or reduces the frequency, rate, or extent of production of a molecular mediator	APOA1	7.69 1/13	4.17 1/24	0.042447919
GO:0034123	positive regulation of toll-like receptor signaling pathway	Any process that activates or increases the frequency, rate, or extent of toll-like receptor signaling	LBP	7.69 1/13	4.17 1/24	0.042447919
GO:1902624	positive regulation of neutrophil migration	Any process that activates or increases the frequency, rate or extent of neutrophil migration	LBP	7.69 1/13	4.17 1/24	0.042447919
GO:0043085	positive regulation of catalytic activity	Any process that activates or increases the activity of an enzyme	APOA1 APOA4 APOE	23.08 3/13	0.36 3/845	0.042447919
GO:0019835	cytolysis	The rupture of cell membranes and the loss of cytoplasm	LBP	7.69 1/13	4.17 1/24	0.042447919
GO:0045730	respiratory burst	A phase of elevated metabolic activity, during which oxygen consumption is increased	LBP	7.69 1/13	4.17 1/24	0.042447919
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as carried out in a cell	APOA1 APOA4 APOE	23.08 3/13	0.35 3/852	0.043284516
GO:0002764	immune response-regulating signaling pathway	The cascade of processes by which a signal interacts with a receptor to regulate an immune response	LBP PIGR	15.38 2/13	0.66 2/303	0.043321258
GO:0090022	regulation of neutrophil chemotaxis	Any process that modulates the frequency, rate, or extent of neutrophil chemotaxis	LBP	7.69 1/13	4.00 1/25	0.043381743
GO:0032770	positive regulation of monooxygenase activity	Any process that activates or increases the activity of a monooxygenase	APOE	7.69 1/13	4.00 1/25	0.043381743
GO:0001662	behavioral fear response	An acute behavioral change resulting from a perceived external threat	APOE	7.69 1/13	4.00 1/25	0.043381743
GO:0034381	plasma lipoprotein particle clearance	The process in which a lipoprotein particle is removed from the bloodstream	APOE	7.69 1/13	4.00 1/25	0.043381743
GO:0050892	intestinal absorption	Any process in which nutrients are taken up from the contents of the intestine	APOA1	7.69 1/13	4.00 1/25	0.043381743
GO:0042176	regulation of protein catabolic process	Any process that modulates the frequency, rate or extent of protein catabolism	APOE CLU	15.38 2/13	0.65 2/310	0.043860115
GO:0042311	vasodilation	An increase in the internal diameter of blood vessels, especially arteries	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:0050673	epithelial cell proliferation	The multiplication or reproduction of epithelial cells, resulting in the formation of a new epithelium	APOA1 APOE	15.38 2/13	0.65 2/308	0.043860115
GO:0044788	modulation by host of viral process	A process in which a host organism modulates the frequency, rate or extent of a viral process	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:0043537	negative regulation of blood vessel endothelial cell migration	Any process that stops, prevents, or reduces the frequency, rate or extent of blood vessel endothelial cell migration	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:0048584	positive regulation of response to stimulus	Any process that activates, maintains or increases the rate of response to a stimulus	APOA1 APOE CLU LBP	30.77 4/13	0.25 4/1617	0.043860115
GO:0044058	regulation of digestive system process	Any process that modulates the frequency, rate or extent of a digestive system process	APOA1	7.69 1/13	3.85 1/26	0.043860115
GO:1902003	regulation of amyloid-beta formation	Any process that modulates the frequency, rate or extent of amyloid-beta formation	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:0002209	behavioral defense response	A behavioral response seeking to protect an organism from an external threat	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:0006953	acute-phase response	An acute inflammatory response that involves non-antibody proteins	LBP	7.69 1/13	3.85 1/26	0.043860115
GO:0097242	amyloid-beta clearance	The process in which amyloid-beta is removed from extracellular spaces	APOE	7.69 1/13	3.85 1/26	0.043860115
GO:1902930	regulation of alcohol biosynthetic process	Any process that modulates the frequency, rate or extent of alcohol biosynthesis	APOE	7.69 1/13	3.70 1/27	0.044858905
GO:0006631	fatty acid metabolic process	The chemical reactions and pathways involving fatty acids, aliphatic	APOA1 APOA4	15.38 2/13	0.63 2/316	0.044858905
GO:0009595	detection of biotic stimulus	The series of events in which a biotic stimulus, one caused or produced by a living organism, is detected	LBP	7.69 1/13	3.70 1/27	0.044858905
GO:0042744	hydrogen peroxide catabolic process	The chemical reactions and pathways resulting in the breakdown of hydrogen peroxide	APOA4	7.69 1/13	3.70 1/27	0.044858905
GO:0001941	postsynaptic membrane organization	A process which results in the assembly, arrangement or modification of a postsynaptic membrane	APOE	7.69 1/13	3.70 1/27	0.044858905
GO:0043114	regulation of vascular permeability	Any process that modulates the extent to which blood vessels can be permeable	APOE	7.69 1/13	3.70 1/27	0.044858905
GO:0048662	negative regulation of smooth muscle cell proliferation	Any process that stops, prevents or reduces the rate or extent of smooth muscle cell proliferation	APOE	7.69 1/13	3.57 1/28	0.046277957
GO:0060998	regulation of dendritic spine development	Any process that modulates the rate, frequency, or extent of dendritic spine development	APOE	7.69 1/13	3.57 1/28	0.046277957
GO:0048878	chemical homeostasis	Any biological process involved in the maintenance of an internal environment	APOA1 APOA4 APOE	23.08 3/13	0.33 3/900	0.046277957
GO:0043254	regulation of protein-containing complex assembly	Any process that modulates the frequency, rate or extent of protein-containing complex assembly	APOE CLU	15.38 2/13	0.61 2/330	0.047334955
GO:0035025	positive regulation of Rho protein signal transduction	Any process that activates or increases the frequency, rate or extent of Rho protein signal transduction	APOA1	7.69 1/13	3.45 1/29	0.047334955
GO:0019068	virion assembly	A late phase of the viral life cycle during which all the components of a virion are assembled	APOE	7.69 1/13	3.45 1/29	0.047334955
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to stress	Any process that modulates the frequency, rate or extent of intrinsic apoptotic signaling	APOE	7.69 1/13	3.45 1/29	0.047334955
GO:0010543	regulation of platelet activation	Any process that modulates the rate or frequency of platelet activation	APOE	7.69 1/13	3.33 1/30	0.04836565
GO:0044057	regulation of system process	Any process that modulates the frequency, rate or extent of a system process	APOA1 APOE	15.38 2/13	0.60 2/335	0.04836565
GO:0050795	regulation of behavior	Any process that modulates the frequency, rate or extent of behavior	APOE	7.69 1/13	3.33 1/30	0.04836565
GO:0042596	fear response	The response of an organism to a perceived external threat	APOE	7.69 1/13	3.33 1/30	0.04836565
GO:1902991	regulation of amyloid precursor protein catabolic process	Any process that modulates the frequency, rate or extent of amyloid precursor protein catabolism	APOE	7.69 1/13	3.33 1/30	0.04836565
GO:0001667	ameboid-type cell migration	Cell migration that is accomplished by extension and retraction of pseudopodia	APOA1 APOE	15.38 2/13	0.59 2/337	0.04851437
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipids, any	APOA1 APOA4	15.38 2/13	0.59 2/338	0.048699334
GO:0006928	movement of cell or subcellular component	The directed, self-propelled movement of a cell or subcellular component	APOA1 APOE GP2 LBP	30.77 4/13	0.23 4/1707	0.049543195
GO:1900026	positive regulation of substrate adhesion-dependent cell-cell adhesion	Any process that activates or increases the frequency, rate or extent of substrate adhesion-dependent cell-cell adhesion	APOA1	7.69 1/13	3.12 1/32	0.05106943
GO:0048260	positive regulation of receptor-mediated endocytosis	Any process that activates or increases the frequency, rate or extent of receptor-mediated endocytosis	CLU	7.69 1/13	3.03 1/33	0.052031715
GO:0001580	detection of chemical stimulus involved in sensory perception of taste	The series of events required for a bitter taste stimulus to be received by taste buds	PIGR	7.69 1/13	3.03 1/33	0.052031715
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	Any process that modulates the rate or extent of the tumor necrosis factor signaling pathway	APOA1	7.69 1/13	3.03 1/33	0.052031715
GO:0030195	negative regulation of blood coagulation	Any process that stops, prevents, or reduces the frequency, rate or extent of blood coagulation	APOE	7.69 1/13	3.03 1/33	0.052031715
GO:0034205	amyloid-beta formation	The generation of amyloid-beta by cleavage of the amyloid precursor protein	APOE	7.69 1/13	3.03 1/33	0.052031715
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breakdown of organic substances	APOA1 APOA4 APOE CLU	30.77 4/13	0.16 6/3856	0.05853875
GO:1900047	negative regulation of hemostasis	Any process that stops, prevents or reduces the frequency, rate or extent of hemostasis	APOE	7.69 1/13	2.94 1/34	0.053093937
GO:0001937	negative regulation of endothelial cell proliferation	Any process that stops, prevents, or reduces the rate or extent of endothelial cell proliferation	APOE	7.69 1/13	2.94 1/34	0.053093937
GO:0034142	toll-like receptor 4 signaling pathway	Any series of molecular signals generated as a consequence of binding of ligand to toll-like receptor 4	LBP	7.69 1/13	2.94 1/34	0.053093937
GO:0009968	negative regulation of signal transduction	Any process that stops, prevents, or reduces the frequency, rate or extent of signal transduction	APOA1 APOE CLU	23.08 3/13	0.31 3/964	0.053290293
GO:1902622	regulation of neutrophil migration	Any process that modulates the frequency, rate or extent of neutrophil migration	LBP	7.69 1/13	2.86 1/35	0.054011214
GO:0032768	regulation of monooxygenase activity	Any process that modulates the activity of a monooxygenase	APOE	7.69 1/13	2.86 1/35	0.054011214
GO:0062208	positive regulation of pattern recognition receptor signaling pathway	Any process that increases the rate, frequency or extent of pattern recognition receptor signaling	LBP	7.69 1/13	2.86 1/35	0.054011214
GO:0043030	regulation of macrophage activation	Any process that modulates the frequency or rate of macrophage activation	LBP	7.69 1/13	2.86 1/35	0.054011214
GO:0050819	negative regulation of coagulation	Any process that stops, prevents, or reduces the frequency, rate or extent of coagulation	APOE	7.69 1/13	2.78 1/36	0.055283676
GO:0050913	sensory perception of bitter taste	The series of events required to receive a bitter taste stimulus, on the tongue	PIGR	7.69 1/13	2.78 1/36	0.055283676
GO:0006509	membrane protein ectodomain proteolysis	The proteolytic cleavage of transmembrane proteins and release of ectodomains	APOE	7.69 1/13	2.70 1/37	0.056672733
GO:0007264	small GTPase mediated signal transduction	Any series of molecular signals in which a small monomeric GTPase is involved	APOA1 APOE	15.38 2/13	0.53 2/378	0.057276578
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the breakdown of cellular components	APOA1 APOA4 APOE CLU	30.77 4/13	0.22 4/1814	0.057824709
GO:0050912	detection of chemical stimulus involved in sensory perception of taste	The series of events involved in the perception of taste in which a stimulus is detected	PIGR	7.69 1/13	2.63 1/38	0.057824709
GO:0048523	negative regulation of cellular process	Any process that stops, prevents, or reduces the frequency, rate or extent of a cellular process	APOA1 APOA4 APOE CLU	46.15 6/13	0.16 6/3856	0.05853875
GO:0034113	heterotypic cell-cell adhesion	The attachment of a cell to a cell of a different type via adhesion molecules	APOA1	7.69 1/13	2.56 1/39	0.059026748
GO:0050709	negative regulation of protein secretion	Any process that stops, prevents, or reduces the frequency, rate or extent of protein secretion	APOE	7.69 1/13	2.50 1/40	0.05929432
GO:0051055	negative regulation of lipid biosynthetic process	Any process that stops, prevents, or reduces the frequency, rate or extent of lipid biosynthesis	APOE	7.69 1/13	2.50 1/40	0.05929432
GO:0010648	negative regulation of cell communication	Any process that decreases the frequency, rate or extent of cell-cell communication	APOA1 APOE CLU	23.08 3/13	0.29 3/1021	0.05929432
GO:0050435	amyloid-beta metabolic process	The chemical reactions and pathways involving amyloid-beta, a glycoprotein	APOE	7.69 1/13	2.50 1/40	0.05929432
GO:0023057	negative regulation of signaling	Any process that stops, prevents, or reduces the frequency, rate or extent of signaling	APOA1 APOE CLU	23.08 3/13	0.29 3/1023	0.05929432
GO:0071310	cellular response to organic substance	Any process that results in a change in state or activity of a cell in response to an organic substance	APOA1 BSPRY CNTFR LBP	30.77 4/13	0.22 4/1848	0.060402842
GO:0046164	alcohol catabolic process	The chemical reactions and pathways resulting in the breakdown of alcohols	APOE	7.69 1/13	2.44 1/41	0.060647805
GO:0010596	negative regulation of endothelial cell migration	Any process that decreases the rate, frequency, or extent of the migration of endothelial cells	APOE	7.69 1/13	2.44 1/41	0.060647805
GO:0042743	hydrogen peroxide metabolic process	The chemical reactions and pathways involving hydrogen peroxide	APOA4	7.69 1/13	2.44 1/41	0.060647805
GO:0032720	negative regulation of tumor necrosis factor production	Any process that stops, prevents, or reduces the frequency, rate, or extent of tumor necrosis factor production	LBP	7.69 1/13	2.44 1/41	0.060647805
GO:0071622	regulation of granulocyte chemotaxis	Any process that modulates the rate, frequency or extent of granulocyte chemotaxis	LBP	7.69 1/13	2.38 1/42	0.061430492
GO:0043407	negative regulation of MAP kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of MAP kinase activity	APOE	7.69 1/13	2.38 1/42	0.061430492
GO:1903556	negative regulation of tumor necrosis factor superfamily member-mediated signaling pathway	Any process that stops, prevents or reduces the frequency, rate or extent of tumor necrosis factor superfamily member-mediated signaling	LBP	7.69 1/13	2.38 1/42	0.061430492
GO:0042981	regulation of apoptotic process	Any process that modulates the occurrence or rate of cell death by apoptosis	APOE CLU CNTFR	23.08 3/13	0.29 3/1039	0.061430492
GO:0051496	positive regulation of stress fiber assembly	Any process that activates or increases the frequency, rate or extent of stress fiber assembly	APOA1	7.69 1/13	2.38 1/42	0.061430492

GO:0010629	negative regulation of gene expression	Any process that decreases the frequency, rate or extent of gene e	APOA1 APOE LBP	23.08 3/13	0.29 3/1043	0.061528017
GO:0051353	positive regulation of oxidoreductase activity	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	2.33 1/43	0.062330041
GO:0042987	amyloid precursor protein catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	2.33 1/43	0.062330041
GO:0051180	vitamin transport	The directed movement of vitamins into, out of or within a cell, o	APOA1	7.69 1/13	2.33 1/43	0.062330041
GO:0019221	cytokine-mediated signaling pathway	A series of molecular signals initiated by the binding of a cytokine t	APOA1 CNTRF	15.38 2/13	0.49 2/408	0.062596225
GO:0043954	cellular component maintenance	The organization process that preserves a cellular component in a	APOE	7.69 1/13	2.27 1/44	0.063079338
GO:0032757	positive regulation of interleukin-8 production	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	2.27 1/44	0.063079338
GO:0031663	lipopolysaccharide-mediated signaling pathway	A series of molecular signals initiated by the binding of a lipopolys	LBP	7.69 1/13	2.27 1/44	0.063079338
GO:1900024	regulation of substrate adhesion-dependent cell spread	Any process that modulates the frequency, rate or extent of substr	APOA1	7.69 1/13	2.27 1/44	0.063079338
GO:0043067	regulation of programmed cell death	Any process that modulates the frequency, rate or extent of progr	APOE CLU CNTRF	23.08 3/13	0.28 3/1065	0.063716124
GO:1902532	negative regulation of intracellular signal transduction	Any process that stops, prevents or reduces the frequency, rate or	APOE CLU	15.38 2/13	0.48 2/415	0.063774319
GO:0050919	negative chemotaxis	The directed movement of a motile cell or organism towards a low	APOA1	7.69 1/13	2.22 1/45	0.064808681
GO:0009719	response to endogenous stimulus	Any process that results in a change in state or activity of a cell o	APOE CSN1S1 CSN1S2	23.08 3/13	0.28 3/1076	0.064885454
GO:0051345	positive regulation of hydrolase activity	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4	15.38 2/13	0.48 2/420	0.064885454
GO:0007610	behavior	The internally coordinated responses (actions or inactions) of anim	APOE CNTRF	15.38 2/13	0.48 2/421	0.064937264
GO:0097061	dendritic spine organization	A process that is carried out at the cellular level which results in th	APOE	7.69 1/13	2.13 1/47	0.066324433
GO:0033619	membrane protein proteolysis	The proteolytic cleavage of a transmembrane protein leading to th	APOE	7.69 1/13	2.08 1/48	0.0670086
GO:0050766	positive regulation of phagocytosis	Any process that activates or increases the frequency, rate or exte	APOA1	7.69 1/13	2.08 1/48	0.0670086
GO:0060801	superoxide metabolic process	The chemical reactions and pathways involving superoxide, the sup	APOA4	7.69 1/13	2.08 1/48	0.0670086
GO:0051239	regulation of multicellular organismal process	Any process that modulates the frequency, rate or extent of a mult	APOA1 APOA4 APOE LBI	30.77 4/13	0.21 4/1943	0.0670086
GO:0030193	regulation of blood coagulation	Any process that modulates the frequency, rate or extent of blood	APOE	7.69 1/13	2.08 1/48	0.0670086
GO:0061045	negative regulation of wound healing	Any process that decreases the rate, frequency, or extent of the se	APOE	7.69 1/13	2.04 1/49	0.0682418
GO:0046579	positive regulation of Ras protein signal transduction	Any process that activates or increases the frequency, rate or exte	APOA1	7.69 1/13	2.00 1/50	0.068332543
GO:0048844	artery morphogenesis	The process in which the anatomical structures of arterial blood ve	APOE	7.69 1/13	2.00 1/50	0.068332543
GO:0065008	regulation of biological quality	Any process that modulates a qualitative or quantitative trait of a	APOA1 APOA4 APOE CLU	38.46 5/13	0.17 5/2959	0.068332543
GO:0001960	negative regulation of cytokine-mediated signaling path	Any process that stops, prevents, or reduces the frequency, rate o	APOA1	7.69 1/13	2.00 1/50	0.068332543
GO:0033555	multicellular organismal response to stress	Any process that results in a change in state or activity of a multic	APOE	7.69 1/13	2.00 1/50	0.068332543
GO:0010770	positive regulation of cell morphogenesis involved in di	Any process that increases the frequency, rate or extent of cell mo	APOA1	7.69 1/13	2.00 1/50	0.068332543
GO:0050810	regulation of steroid biosynthetic process	Any process that modulates the frequency, rate or extent of the ch	APOE	7.69 1/13	2.00 1/50	0.068332543
GO:1900046	regulation of hemostasis	Any process that modulates the frequency, rate or extent of hemo:	APOE	7.69 1/13	2.00 1/50	0.068332543
GO:0071702	organic substance transport	The directed movement of organic substances into, out of or withi	APOA1 APOA4 APOE LBI	30.77 4/13	0.20 4/1968	0.068332543
GO:2001244	positive regulation of intrinsic apoptotic signaling path	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	1.96 1/51	0.068973218
GO:0019935	cyclic-nucleotide-mediated signaling	Any intracellular signal transduction in which the signal is passed o	APOE	7.69 1/13	1.96 1/51	0.068973218
GO:0106027	neuron projection organization	A process that is carried out at the cellular level which results in th	APOE	7.69 1/13	1.96 1/51	0.068973218
GO:0099175	regulation of postsynapse organization	Any process that modulates the physical form of a postsynapse.	APOE	7.69 1/13	1.96 1/51	0.068973218
GO:0060761	negative regulation of response to cytokine stimulus	Any process that decreases the rate, frequency, or extent of a resp	APOA1	7.69 1/13	1.96 1/51	0.068973218
GO:0048583	regulation of response to stimulus	Any process that modulates the frequency, rate or extent of a resp	APOA1 APOE CLU LBP PI	38.46 5/13	0.17 5/2982	0.069120741
GO:0006629	lipid metabolic process	The chemical reactions and pathways involving lipids, compounds	APOA1 APOA4 APOE	23.08 3/13	0.27 3/1124	0.069125283
GO:0050818	regulation of coagulation	Any process that modulates the frequency, rate or extent of coagu	APOE	7.69 1/13	1.92 1/52	0.069880346
GO:0032233	positive regulation of actin filament bundle assembly	Any process that activates or increases the frequency, rate or exte	APOA1	7.69 1/13	1.89 1/53	0.070917637
GO:0010633	negative regulation of epithelial cell migration	Any process that stops, prevents, or reduces the frequency, rate o	APOE	7.69 1/13	1.89 1/53	0.070917637
GO:0060996	dendritic spine development	The process whose specific outcome is the progression of the dend	APOE	7.69 1/13	1.85 1/54	0.070954481
GO:0032611	interleukin-1 beta production	The appearance of interleukin-1 beta due to biosynthesis or secret	APOA1	7.69 1/13	1.85 1/54	0.070954481
GO:0032651	regulation of interleukin-1 beta production	Any process that modulates the frequency, rate, or extent of interl	APOA1	7.69 1/13	1.85 1/54	0.070954481
GO:0010941	regulation of cell death	Any process that modulates the rate or frequency of cell death. Cel	APOE CLU CNTRF	23.08 3/13	0.26 3/1142	0.070954481
GO:0042982	amyloid precursor protein metabolic process	The chemical reactions and pathways involving amyloid precursor p	APOE	7.69 1/13	1.85 1/54	0.070954481
GO:0051057	positive regulation of small GTPase mediated signal tra	Any process that activates or increases the frequency, rate or exte	APOA1	7.69 1/13	1.85 1/54	0.070954481
GO:0032722	positive regulation of chemokine production	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	1.85 1/54	0.070954481
GO:0051851	production by host of symbiont process	The process in which an organism effects a change in the structure	APOE	7.69 1/13	1.85 1/54	0.070954481
GO:0002532	modulation of molecular mediator involved in inflamme	The synthesis or release of any molecular mediator of the inflamme	LBP	7.69 1/13	1.85 1/54	0.070954481
GO:0010498	proteasomal protein catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE CLU	15.38 2/13	0.43 2/464	0.072181144
GO:0009893	positive regulation of metabolic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE CLU	38.46 5/13	0.16 5/3040	0.072184268
GO:0042127	regulation of cell population proliferation	Any process that modulates the frequency, rate or extent of cell pr	APOE CLU CNTRF	23.08 3/13	0.26 3/1156	0.072184268
GO:0032787	monocarboxylic acid metabolic process	The chemical reactions and pathways involving monocarboxylic aci	APOA1 APOA4	15.38 2/13	0.43 2/470	0.073467859
GO:0072657	protein localization to membrane	A process in which a protein is transported to, or maintained in, a	APOE PIGR	15.38 2/13	0.42 2/473	0.073752568
GO:0034121	regulation of toll-like receptor signaling pathway	Any process that modulates the frequency, rate, or extent of toll-li	LBP	7.69 1/13	1.75 1/57	0.073752568
GO:0060291	long-term synaptic potentiation	A process that modulates synaptic plasticity such that synapses ar	APOE	7.69 1/13	1.75 1/57	0.073752568
GO:0050865	regulation of cell activation	Any process that modulates the frequency, rate or extent of cell ac	APOE LBP	15.38 2/13	0.42 2/472	0.073752568
GO:0002526	acute inflammatory response	Inflammation which comprises a rapid, short-lived, relatively unif	LBP	7.69 1/13	1.72 1/58	0.074650289
GO:1901616	organic hydroxy compound catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE	7.69 1/13	1.72 1/58	0.074650289
GO:0015909	long-chain fatty acid transport	The directed movement of long-chain fatty acids into, out of or wit	APOE	7.69 1/13	1.69 1/59	0.075189028
GO:0032677	regulation of interleukin-8 production	Any process that modulates the frequency, rate, or extent of interl	LBP	7.69 1/13	1.69 1/59	0.075189028
GO:0031638	zymogen activation	The proteolytic processing of an inactive enzyme to an active form.	CD5L	7.69 1/13	1.69 1/59	0.075189028
GO:0050909	sensory perception of taste	The series of events required for an organism to receive a gustator	PIGR	7.69 1/13	1.69 1/59	0.075189028
GO:0032637	interleukin-8 production	The appearance of interleukin-8 due to biosynthesis or secretion f	LBP	7.69 1/13	1.69 1/59	0.075189028
GO:0042116	macrophage activation	A change in morphology and behavior of a macrophage resulting fr	LBP	7.69 1/13	1.67 1/60	0.076294813
GO:0009725	response to hormone	Any process that results in a change in state or activity of a cell o	CSN1S1 CSN1S2	15.38 2/13	0.41 2/488	0.076447669
GO:0014070	response to organic cyclic compound	Any process that results in a change in state or activity of a cell o	CSN1S1 CSN1S2	15.38 2/13	0.40 2/495	0.077874217
GO:1903035	negative regulation of response to wounding	Any process that stops, prevents or reduces the frequency, rate o	APOE	7.69 1/13	1.61 1/62	0.077874217
GO:0032760	positive regulation of tumor necrosis factor production	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	1.61 1/62	0.077874217
GO:0002367	cytokine production involved in immune response	The appearance of a cytokine due to biosynthesis or secretion foll	APOA1	7.69 1/13	1.61 1/62	0.077874217
GO:0061077	chaperone-mediated protein folding	The process of inhibiting aggregation and assisting in the covalen	CLU	7.69 1/13	1.61 1/62	0.077874217
GO:0002718	regulation of cytokine production involved in immune r	Any process that modulates the frequency, rate, or extent of cytot	APOA1	7.69 1/13	1.61 1/62	0.077874217
GO:0009056	catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOA1 APOA4 APOE CLU	30.77 4/13	0.19 4/2106	0.078066328
GO:0048259	regulation of receptor-mediated endocytosis	Any process that modulates the frequency, rate or extent of recept	CLU	7.69 1/13	1.59 1/63	0.078100545
GO:0032652	regulation of interleukin-1 production	Any process that modulates the frequency, rate, or extent of interl	APOA1	7.69 1/13	1.59 1/63	0.078100545
GO:0010769	regulation of cell morphogenesis involved in differenti	Any process that modulates the frequency, rate or extent of cell m	APOA1	7.69 1/13	1.59 1/63	0.078100545
GO:0032612	interleukin-1 production	The appearance of interleukin-1 due to biosynthesis or secretion f	APOA1	7.69 1/13	1.59 1/63	0.078100545
GO:0007631	feeding behavior	Behavior associated with the intake of food.	CNTRF	7.69 1/13	1.59 1/63	0.078100545
GO:0006935	chemotaxis	The directed movement of a motile cell or organism, or the directe	APOA1 LBP	15.38 2/13	0.40 2/503	0.079137945
GO:1903557	positive regulation of tumor necrosis factor superfamily	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	1.54 1/65	0.079789134
GO:0002275	myeloid cell activation involved in immune response	A change in the morphology or behavior of a myeloid cell resultin	LBP	7.69 1/13	1.54 1/65	0.079789134
GO:2001021	negative regulation of response to DNA damage stimul	Any process that stops, prevents or reduces the frequency, rate o	CLU	7.69 1/13	1.54 1/65	0.079789134
GO:0042330	taxi	The directed movement of a motile cell or organism in response to	APOA1 LBP	15.38 2/13	0.40 2/506	0.080949821
GO:0048585	negative regulation of response to stimulus	Any process that stops, prevents, or reduces the frequency, rate o	APOA1 APOE CLU	23.08 3/13	0.24 3/1236	0.080949821
GO:0022600	digestive system process	A physical, chemical, or biochemical process carried out by living o	APOA1	7.69 1/13	1.52 1/66	0.080949821
GO:0009617	response to bacterium	Any process that results in a change in state or activity of a cell o	CSN1S2 LBP	15.38 2/13	0.39 2/514	0.081254242
GO:0001817	regulation of cytokine production	Any process that modulates the frequency, rate, or extent of prod.	APOA1 LBP	15.38 2/13	0.39 2/515	0.081254242
GO:0050829	defense response to Gram-negative bacterium	Reactions triggered in response to the presence of a Gram-negati	LBP	7.69 1/13	1.49 1/67	0.081254242
GO:0050764	regulation of phagocytosis	Any process that modulates the frequency, rate or extent of phago	APOA1	7.69 1/13	1.49 1/67	0.081254242
GO:0043535	regulation of blood vessel endothelial cell migration	Any process that modulates the frequency, rate or extent of the mi	APOE	7.69 1/13	1.47 1/68	0.082184286
GO:0051492	regulation of stress fiber assembly	Any process that modulates the frequency, rate or extent of the as	APOA1	7.69 1/13	1.47 1/68	0.082184286
GO:0032602	chemokine production	The appearance of a chemokine due to biosynthesis or secretion f	LBP	7.69 1/13	1.45 1/69	0.082320393
GO:0001816	cytokine production	The appearance of a cytokine due to biosynthesis or secretion foll	APOA1 LBP	15.38 2/13	0.38 2/522	0.082320393
GO:0062014	negative regulation of small molecule metabolic proces	Any process that stops, prevents or reduces the frequency, rate o	APOE	7.69 1/13	1.45 1/69	0.082320393
GO:0060840	artery development	The progression of the artery over time, from its initial formatio	n APOE	7.69 1/13	1.45 1/69	0.082320393
GO:0032642	regulation of chemokine production	Any process that modulates the frequency, rate, or extent of chem	LBP	7.69 1/13	1.45 1/69	0.082320393
GO:0030168	platelet activation	A series of progressive, overlapping events triggered by exposure c	APOE	7.69 1/13	1.45 1/69	0.082320393
GO:0007613	memory	The activities involved in the mental information processing system	APOE	7.69 1/13	1.45 1/69	0.082320393
GO:0032755	positive regulation of interleukin-6 production	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	1.43 1/70	0.08318993
GO:0051341	regulation of oxidoreductase activity	Any process that modulates the frequency, rate or extent of oxidor	APOE	7.69 1/13	1.43 1/70	0.08318993
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to trigger a chang	APOA1 APOE CLU CNTRF	53.85 7/13	0.12 7/5642	0.08325862
GO:1902531	regulation of intracellular signal transduction	Any process that modulates the frequency, rate or extent of intrac	APOA1 APOE CLU	23.08 3/13	0.24 3/1270	0.083444285
GO:0015908	fatty acid transport	The directed movement of fatty acids into, out of or within a cell, o	APOE	7.69 1/13	1.41 1/71	0.08345751
GO:0048660	regulation of smooth muscle cell proliferation	Any process that modulates the frequency, rate or extent of smoo	APOE	7.69 1/13	1.41 1/71	0.08345751
GO:0045833	negative regulation of lipid metabolic process	Any process that stops, prevents, or reduces the frequency, rate o	APOE	7.69 1/13	1.41 1/71	0.08345751
GO:0051702	biological process involved in interaction with symbion	An interaction between two organisms living together in more or l	APOE	7.69 1/13	1.41 1/71	0.08345751
GO:0032436	positive regulation of proteasomal ubiquitin-dependen	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	1.39 1/72	0.084458335
GO:1901264	carbohydrate derivative transport	The directed movement of a carbohydrate derivative into, out of a	LBP	7.69 1/13	1.37 1/73	0.085154604
GO:0048659	smooth muscle cell proliferation	The multiplication or reproduction of smooth muscle cells, resulti	n APOE	7.69 1/13	1.37 1/73	0.085154604
GO:0032092	positive regulation of protein binding	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	1.37 1/73	0.085154604
GO:0051668	localization within membrane	Any process in which a substance or cellular entity, such as a prote	APOE PIGR	15.38 2/13	0.37 2/541	0.085236353
GO:0033209						

GO:0010976	positive regulation of neuron projection development	Any process that increases the rate, frequency or extent of neuron	APOE	7.69 1/13	1.33 1/75	0,086674025
GO:0043086	negative regulation of catalytic activity	Any process that stops or reduces the activity of an enzyme.	APOA1 APOE	15.38 2/13	0.36 2/555	0,088470115
GO:0002690	positive regulation of leukocyte chemotaxis	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	1.30 1/77	0,088470115
GO:0045089	positive regulation of innate immune response	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	1.30 1/77	0,088470115
GO:0048522	positive regulation of cellular process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE CLU	46.15 6/13	0.13 6/4480	0,08855188
GO:0002698	negative regulation of immune effector process	Any process that stops, prevents, or reduces the frequency, rate,	APOA1	7.69 1/13	1.28 1/78	0,088975658
GO:0050729	positive regulation of inflammatory response	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	1.28 1/78	0,088975658
GO:0030593	neutrophil chemotaxis	The directed movement of a neutrophil cell, the most numerous p	LBP	7.69 1/13	1.28 1/78	0,088975658
GO:0007173	epidermal growth factor receptor signaling pathway	A series of molecular signals initiated by binding of a ligand to the	PIGR	7.69 1/13	1.27 1/79	0,089934828
GO:0030038	contractile actin filament bundle assembly	Assembly of actin filament bundles in which the filaments are loos	APOA1	7.69 1/13	1.25 1/80	0,09027069
GO:0051224	negative regulation of protein transport	Any process that stops, prevents, or reduces the frequency, rate o	APOE	7.69 1/13	1.25 1/80	0,09027069
GO:2000060	positive regulation of ubiquitin-dependent protein cata	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	1.25 1/80	0,09027069
GO:0062207	regulation of pattern recognition receptor signaling pat	Any process that modulates the rate, frequency or extent of a patt	LBP	7.69 1/13	1.25 1/80	0,09027069
GO:0043149	stress fiber assembly	The aggregation, arrangement and bonding together of a set of coi	APOA1	7.69 1/13	1.25 1/80	0,09027069
GO:0009966	regulation of signal transduction	Any process that modulates the frequency, rate or extent of signal	APOA1 APOE CLU LBP	30.77 4/13	0.18 4/2282	0,091127281
GO:0012501	programmed cell death	A process which begins when a cell receives an internal or external	APOE CLU CNTRF	23.08 3/13	0.22 3/1343	0,091432903
GO:2001243	negative regulation of intrinsic apoptotic signaling path	Any process that stops, prevents or reduces the frequency, rate or	CLU	7.69 1/13	1.22 1/82	0,092002344
GO:0032231	regulation of actin filament bundle assembly	Any process that modulates the frequency, rate or extent of the as	APOA1	7.69 1/13	1.20 1/83	0,092469774
GO:0042592	homeostatic process	Any biological process involved in the maintenance of an internal	APOA1 APOA4 APOE	23.08 3/13	0.22 3/1352	0,092469774
GO:1904950	negative regulation of establishment of protein localiza	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	1.20 1/83	0,092469774
GO:0007586	digestion	The whole of the physical, chemical, and biochemical processes ca	APOA1	7.69 1/13	1.20 1/83	0,092469774
GO:0071901	negative regulation of protein serine/threonine kinase	Any process that decreases the rate, frequency, or extent of protei	APOE	7.69 1/13	1.19 1/84	0,093242151
GO:1998030	cellular response to leukemia inhibitory factor	Any process that results in a change in state or activity of a cell (i	n l BSPRY	7.69 1/13	1.19 1/84	0,093242151
GO:0010977	negative regulation of neuron projection development	Any process that decreases the rate, frequency or extent of neuron	APOE	7.69 1/13	1.18 1/85	0,094008716
GO:1998023	response to leukemia inhibitory factor	Any process that results in a change in state or activity of a cell o	r z BSPRY	7.69 1/13	1.18 1/85	0,094008716
GO:0038127	ERBB signaling pathway	A series of molecular signals initiated by binding of a ligand to a me	PIGR	7.69 1/13	1.16 1/86	0,094927738
GO:1903531	negative regulation of secretion by cell	Any process that stops, prevents or reduces the frequency, rate or	APOE	7.69 1/13	1.15 1/87	0,095843053
GO:0007229	integrin-mediated signaling pathway	A series of molecular signals initiated by the binding of extracellula	APOA1	7.69 1/13	1.14 1/88	0,09675468
GO:0050830	defense response to Gram-positive bacterium	Reactions triggered in response to the presence of a Gram-positive	LBP	7.69 1/13	1.12 1/89	0,097662638
GO:0035296	regulation of tube diameter	Any process that modulates the diameter of a tube.	APOE	7.69 1/13	1.11 1/90	0,098078989
GO:0061041	regulation of wound healing	Any process that modulates the rate, frequency, or extent of the se	APOE	7.69 1/13	1.11 1/90	0,098078989
GO:0010811	negative regulation of cell-substrate adhesion	Any process that increases the frequency, rate or extent of cell-sub	APOA1	7.69 1/13	1.11 1/90	0,098078989
GO:0097746	blood vessel diameter maintenance	Any process that modulates the diameter of blood vessels.	APOE	7.69 1/13	1.11 1/90	0,098078989
GO:0035150	regulation of tube size	Ensuring that a tube is of the correct length and diameter. Tube siz	APOE	7.69 1/13	1.10 1/91	0,098813226
GO:0008630	intrinsic apoptotic signaling pathway in response to DN	A series of molecular signals in which an intracellular signal is con	CLU	7.69 1/13	1.10 1/91	0,098813226
GO:0034446	substrate adhesion-dependent cell spreading	The morphogenetic process that results in flattening of a cell as a	c APOA1	7.69 1/13	1.09 1/92	0,099705469
GO:1901800	positive regulation of proteasomal protein catabolic pr	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	1.08 1/93	0,100919155
GO:0030162	regulation of proteolysis	Any process that modulates the frequency, rate or extent of the hy	APOE CLU	15.38 2/13	0.32 2/620	0,101345243
GO:0002224	tol-l like receptor signaling pathway	Any series of molecular signals generated as a consequence of binc	LBP	7.69 1/13	1.06 1/94	0,101345243
GO:0034614	cellular response to reactive oxygen species	Any process that results in a change in state or activity of a cell (i	n l APOA4	7.69 1/13	1.05 1/95	0,102193945
GO:0008219	cell death	Any biological process that results in permanent cessation of all vit	APOE CLU CNTRF	23.08 3/13	0.21 3/1432	0,102814184
GO:0050806	positive regulation of synaptic transmission	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	1.03 1/97	0,103944398
GO:0071621	granulocyte chemotaxis	The movement of a granulocyte in response to an external stimulu	LBP	7.69 1/13	1.02 1/98	0,104814427
GO:0023052	signaling	The entirety of a process in which information is transmitted withi	APOA1 APOE CLU CNTRF	53.85 7/13	0.12 7/6020	0,104815771
GO:0035270	endocrine system development	Progression of the endocrine system over time, from its formation	APOA1	7.69 1/13	1.01 1/99	0,105339557
GO:0051048	negative regulation of secretion	Any process that stops, prevents, or reduces the frequency, rate or	APOE	7.69 1/13	1.01 1/99	0,105339557
GO:1903052	positive regulation of proteolysis involved in cellular pr	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	1.00 1/100	0,10593642
GO:0065009	regulation of molecular function	Any process that modulates the frequency, rate or extent of a mol	APOA1 APOA4 APOE CLU	30.77 4/13	0.16 4/2439	0,10593642
GO:0002688	regulation of leukocyte chemotaxis	Any process that modulates the frequency, rate, or extent of leuko	LBP	7.69 1/13	1.00 1/100	0,10593642
GO:0001959	regulation of cytokine-mediated signaling pathway	Any process that modulates the frequency, rate or extent of the cy	APOA1	7.69 1/13	0.99 1/101	0,106202928
GO:0050680	negative regulation of epithelial cell proliferation	Any process that stops, prevents or reduces the rate or extent of e	APOE	7.69 1/13	0.99 1/101	0,106202928
GO:0044281	small molecule metabolic process	The chemical reactions and pathways involving small molecules, ar	APOA1 APOA4 APOE	23.08 3/13	0.21 3/1460	0,106202928
GO:0001936	regulation of endothelial cell proliferation	Any process that modulates the frequency, rate, or extent of endot	APOE	7.69 1/13	0.99 1/101	0,106202928
GO:0043066	negative regulation of apoptotic process	Any process that stops, prevents, or reduces the frequency, rate or	CLU CNTRF	15.38 2/13	0.31 2/646	0,106391557
GO:0007154	cell communication	Any process that mediates interactions between a cell and its surr	APOA1 APOE CLU CNTRF	53.85 7/13	0.12 7/6065	0,106849976
GO:0002833	positive regulation of response to biotic stimulus	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	0.97 1/103	0,107725513
GO:0043524	negative regulation of neuron apoptotic process	Any process that stops, prevents, or reduces the frequency, rate or	CNTRF	7.69 1/13	0.96 1/104	0,108052023
GO:0032640	tumor necrosis factor production	The appearance of tumor necrosis factor due to biosynthesis or sei	LBP	7.69 1/13	0.96 1/104	0,108052023
GO:0032680	regulation of tumor necrosis factor production	Any process that modulates the frequency, rate or extent of tumor	LBP	7.69 1/13	0.96 1/104	0,108052023
GO:0086609	cell-cell adhesion	The attachment of one cell to another cell via adhesion molecules.	APOA1 APOA4	15.38 2/13	0.31 2/655	0,108052023
GO:0032635	interleukin-6 production	The appearance of interleukin-6 due to biosynthesis or secretion fr	LBP	7.69 1/13	0.94 1/106	0,109545519
GO:0032675	regulation of Interleukin-6 production	Any process that modulates the frequency, rate, or extent of interl	LBP	7.69 1/13	0.94 1/106	0,109545519
GO:0099173	postsynapse organization	A process that is carried out at the cellular level which results in th	APOE	7.69 1/13	0.94 1/106	0,109545519
GO:0043069	negative regulation of programmed cell death	Any process that stops, prevents, or reduces the frequency, rate or	CLU CNTRF	15.38 2/13	0.30 2/663	0,109632964
GO:0060759	regulation of response to cytokine stimulus	Any process that modulates the rate, frequency, or extent of a resp	APOA1	7.69 1/13	0.93 1/107	0,109683911
GO:1903555	regulation of tumor necrosis factor superfamily cytokin	Any process that modulates the frequency, rate or extent of tumor	LBP	7.69 1/13	0.93 1/107	0,109683911
GO:0071706	tumor necrosis factor superfamily cytokine production	The appearance of any member of the TNF superfamily due to bios	LBP	7.69 1/13	0.93 1/107	0,109683911
GO:2001235	positive regulation of apoptotic signaling pathway	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	0.93 1/107	0,109683911
GO:0002687	positive regulation of leukocyte migration	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	0.92 1/109	0,111493948
GO:0032434	regulation of proteasomal ubiquitin-dependent protein	Any process that modulates the frequency, rate or extent of the br	CLU	7.69 1/13	0.91 1/110	0,112134172
GO:0033002	muscle cell proliferation	The expansion of a muscle cell population by cell division.	APOE	7.69 1/13	0.91 1/110	0,112134172
GO:0065003	protein-containing complex assembly	The aggregation, arrangement and bonding together of a set of ma	APOA1 APOA4 APOE CLU	30.77 4/13	0.16 4/2520	0,112906094
GO:1903034	regulation of response to wounding	Any process that modulates the frequency, rate or extent of respon	APOE	7.69 1/13	0.89 1/112	0,113752085
GO:0050921	positive regulation of chemotaxis	Any process that activates or increases the frequency, rate or exte	LBP	7.69 1/13	0.88 1/113	0,114379623
GO:0035966	response to topologically incorrect protein	Any process that results in a change in state or activity of a cell	or a CLU	7.69 1/13	0.88 1/113	0,114379623
GO:0031345	negative regulation of cell projection organization	Any process that stops, prevents, or reduces the frequency, rate or	APOE	7.69 1/13	0.87 1/115	0,116155859
GO:0051603	proteolysis involved in cellular protein catabolic proces	The hydrolysis of a peptide bond or bonds within a protein as part	APOE CLU	15.38 2/13	0.29 2/696	0,117004369
GO:0030334	regulation of cell migration	Any process that modulates the frequency, rate or extent of cell m	APOE LBP	15.38 2/13	0.29 2/697	0,117118434
GO:0002700	regulation of production of molecular mediator of immu	Any process that modulates the frequency, rate, or extent of the pi	APOA1	7.69 1/13	0.85 1/117	0,11721475
GO:0010646	regulation of cell communication	Any process that modulates the frequency, rate or extent of cell co	APOA1 APOE CLU LBP	30.77 4/13	0.16 4/2562	0,11721475
GO:0010605	negative regulation of macromolecule metabolic proces	Any process that decreases the frequency, rate or extent of the chl	APOA1 APOE CLU LBP	30.77 4/13	0.16 4/2563	0,11721475
GO:0023051	regulation of signaling	Any process that modulates the frequency, rate or extent of a sign	APOA1 APOE CLU LBP	30.77 4/13	0.16 4/2573	0,118422427
GO:0031333	negative regulation of protein-containing complex asse	Any process that stops, prevents, or reduces the frequency, rate or	CLU	7.69 1/13	0.83 1/120	0,119553112
GO:0090090	negative regulation of canonical Wnt signaling pathway	Any process that decreases the rate, frequency, or extent of the W	APOE	7.69 1/13	0.83 1/120	0,119553112
GO:0000302	response to reactive oxygen species	Any process that results in a change in state or activity of a cell	or a APOA4	7.69 1/13	0.83 1/121	0,120330555
GO:0048518	positive regulation of biological process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE CLU	46.15 6/13	0.12 6/4958	0,120330683
GO:0060548	negative regulation of cell death	Any process that decreases the rate or frequency of cell death. Cell	CLU CNTRF	15.38 2/13	0.28 2/719	0,121959776
GO:0048167	regulation of synaptic plasticity	A process that modulates synaptic plasticity, the ability of synapse	APOE	7.69 1/13	0.79 1/126	0,123987015
GO:0031328	positive regulation of cellular biosynthetic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE	23.08 3/13	0.19 3/1596	0,123987015
GO:0051017	actin filament bundle assembly	The assembly of actin filament bundles; actin filaments are on the	APOA1	7.69 1/13	0.79 1/126	0,123987015
GO:0051092	positive regulation of NF-kappaB transcription factor ac	Any process that activates or increases the frequency, rate or exte	CLU	7.69 1/13	0.79 1/126	0,123987015
GO:0043409	negative regulation of MAPK cascade	Any process that stops, prevents, or reduces the frequency, rate or	APOE	7.69 1/13	0.79 1/127	0,124499498
GO:0031325	positive regulation of cellular metabolic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE CLU	30.77 4/13	0.15 4/2631	0,124499498
GO:0044257	cellular protein catabolic process	The chemical reactions and pathways resulting in the breakdown o	APOE CLU	15.38 2/13	0.27 2/732	0,124499498
GO:0061572	actin filament bundle organization	A process that results in the assembly, arrangement of constituent	APOA1	7.69 1/13	0.78 1/128	0,124939733
GO:0010594	regulation of endothelial cell migration	Any process that modulates the rate, frequency, or extent of the oi	APOE	7.69 1/13	0.78 1/128	0,124939733
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic acids, an	APOA1 APOA4	15.38 2/13	0.27 2/736	0,125120083
GO:0060538	skeletal muscle organ development	The progression of a skeletal muscle organ over time from its initia	CNTRF	7.69 1/13	0.78 1/129	0,125130411
GO:0071222	cellular response to lipopolysaccharide	Any process that results in a change in state or activity of a cell (i	n l LBP	7.69 1/13	0.78 1/129	0,125130411
GO:0003018	vascular process in circulatory system	A circulatory process that occurs at the level of the vasculature.	APOE	7.69 1/13	0.78 1/129	0,125130411
GO:1901215	negative regulation of neuron death	Any process that stops, prevents or reduces the frequency, rate or	CNTRF	7.69 1/13	0.77 1/130	0,125318278
GO:0009891	positive regulation of biosynthetic process	Any process that activates or increases the frequency, rate or exte	APOA1 APOA4 APOE	23.08 3/13	0.19 3/1617	0,125318278
GO:2000058	regulation of ubiquitin-dependent protein catabolic pr	Any process that modulates the frequency, rate or extent of ubiqui	CLU	7.69 1/13	0.77 1/130	0,125318278
GO:0043112	receptor metabolic process	The chemical reactions and pathways involving a receptor molecu	APOE	7.69 1/13	0.77 1/130	0,125318278
GO:2000145	regulation of cell motility	Any process that modulates the frequency, rate or extent of cell m	APOE LBP	15.38 2/13	0.27 2/742	0,125396873
GO:0051099	positive regulation of binding	Any process that activates or increases the rate or extent of bindi	APOE	7.69 1/13	0.76 1/131	0,125503385
GO:0002221	pattern recognition receptor signaling pathway	Any series of molecular signals generated as a consequence of a p	LBP	7.69 1/13	0.76 1/131	0,125503385
GO:0007596	blood coagulation	The sequential process in which the multiple coagulation factors of	APOE	7.69 1/13	0.76 1/131	0,125503385
GO:0043436	oxoacid metabolic process	The chemical reactions and pathways involving any oxoacid; an ox	APOA1 APOA4	15.38 2/13	0.27 2/745	0,12555906
GO:0043523	regulation of neuron apoptotic process	Any process that modulates the occurrence or rate of cell death by	CNTRF	7.69 1/13	0.76 1/132	0,126053821
GO:0007599	hemostasis	The stopping of bleeding (loss of body fluid) or the arrest of the ci	APOE	7.69 1/13	0.75 1/133	0,126785581
GO:0043933	protein-containing complex organization	Any process in which mac				

GO:0022408	negative regulation of cell-cell adhesion	Any process that stops, prevents or reduces the rate or extent of cell-cell adhesion	7.69 1/13	0.73 1/137	0,129497658
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. Includes APOA1 APOA4 APOE BSI	46.15 6/13	0.12 6/5108	0,130185757
GO:0009892	negative regulation of metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of a metabolic process	30.77 4/13	0.15 4/2707	0,130364418
GO:2001242	regulation of intrinsic apoptotic signaling pathway	Any process that modulates the frequency, rate or extent of intrinsic apoptosis	7.69 1/13	0.72 1/139	0,130364418
GO:0058007	regulation of synapse organization	Any process that modulates the physical form of a synapse, the junction between two neurons	7.69 1/13	0.72 1/139	0,130364418
GO:0043405	regulation of MAP kinase activity	Any process that modulates the frequency, rate or extent of MAP kinase activity	7.69 1/13	0.72 1/139	0,130364418
GO:0040012	regulation of locomotion	Any process that modulates the frequency, rate or extent of locomotion	15.38 2/13	0.26 2/773	0,131292122
GO:0006082	organic acid metabolic process	The chemical reactions and pathways involving organic acids, any	15.38 2/13	0.26 2/774	0,131395627
GO:0007369	gastrulation	A complex and coordinated series of cellular movements that occur during embryonic development	7.69 1/13	0.71 1/141	0,131593151
GO:0006508	proteolysis	The hydrolysis of proteins into smaller polypeptides and/or amino acids	23.08 3/13	0.18 3/1674	0,131834103
GO:1902905	positive regulation of molecular biological process	Any process that activates or increases the frequency, rate or extent of a molecular biological process	7.69 1/13	0.70 1/142	0,132108189
GO:0002440	production of molecular mediator of immune response	The synthesis or release of any molecular mediator of the immune response	7.69 1/13	0.70 1/143	0,132809921
GO:0034249	negative regulation of cellular amide metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of cellular amide metabolic processes	7.69 1/13	0.69 1/144	0,133317515
GO:0058003	regulation of synapse structure or activity	Any process that modulates the physical form or the activity of a synapse	7.69 1/13	0.69 1/144	0,133317515
GO:0051270	regulation of cellular component movement	Any process that modulates the frequency, rate or extent of cellular component movement	15.38 2/13	0.25 2/788	0,134158391
GO:0030178	negative regulation of Wnt signaling pathway	Any process that stops, prevents, or reduces the frequency, rate or extent of Wnt signaling	7.69 1/13	0.68 1/146	0,134705499
GO:0019637	organophosphate metabolic process	The chemical reactions and pathways involving organophosphates	15.38 2/13	0.25 2/793	0,134822032
GO:0001775	cell activation	A change in the morphology or behavior of a cell resulting from external stimuli	15.38 2/13	0.25 2/793	0,134822032
GO:0058066	negative regulation of cell activation	Any process that stops, prevents, or reduces the frequency, rate or extent of cell activation	7.69 1/13	0.68 1/147	0,134822032
GO:0070374	positive regulation of ERK1 and ERK2 cascade	Any process that activates or increases the frequency, rate or extent of ERK1 and ERK2 cascade	7.69 1/13	0.68 1/147	0,134822032
GO:0002274	myeloid leukocyte activation	A change in the morphology or behavior of a myeloid leukocyte resulting from external stimuli	7.69 1/13	0.67 1/149	0,136190891
GO:0043393	regulation of protein binding	Any process that modulates the frequency, rate or extent of protein binding	7.69 1/13	0.67 1/149	0,136190891
GO:0071356	cellular response to tumor necrosis factor	Any process that results in a change in state or activity of a cell in response to tumor necrosis factor	7.69 1/13	0.66 1/151	0,137743424
GO:0007626	locomotory behavior	The specific movement from place to place of an organism in response to external stimuli	7.69 1/13	0.65 1/153	0,138899335
GO:0050708	regulation of protein secretion	Any process that modulates the frequency, rate or extent of protein secretion	7.69 1/13	0.65 1/153	0,138899335
GO:1901701	cellular response to oxygen-containing compound	Any process that results in a change in state or activity of a cell in response to an oxygen-containing compound	15.38 2/13	0.25 2/811	0,138899335
GO:0044092	negative regulation of molecular function	Any process that stops or reduces the rate or extent of a molecular function	15.38 2/13	0.25 2/816	0,140029785
GO:0016358	dendrite development	The process whose specific outcome is the progression of the development of a dendrite	7.69 1/13	0.65 1/155	0,140043497
GO:0010810	regulation of cell-substrate adhesion	Any process that modulates the frequency, rate or extent of cell-substrate adhesion	7.69 1/13	0.65 1/155	0,140043497
GO:0051336	regulation of hydrolase activity	Any process that modulates the frequency, rate or extent of hydrolase activity	15.38 2/13	0.24 2/819	0,140320408
GO:0046474	glycerophospholipid biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerophospholipids	7.69 1/13	0.64 1/156	0,140513436
GO:0031032	actin cytoskeleton organization	A process that is carried out at the cellular level which results in the organization of the actin cytoskeleton	7.69 1/13	0.64 1/157	0,141176059
GO:0006469	negative regulation of protein kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of protein kinase activity	7.69 1/13	0.63 1/158	0,141639878
GO:0051495	positive regulation of cytoskeleton organization	Any process that activates or increases the frequency, rate or extent of cytoskeleton organization	7.69 1/13	0.63 1/158	0,141639878
GO:0071216	cellular response to biotic stimulus	Any process that results in a change in state or activity of a cell in response to a biotic stimulus	7.69 1/13	0.63 1/159	0,142100623
GO:0031349	positive regulation of defense response	Any process that activates or increases the frequency, rate or extent of defense response	7.69 1/13	0.63 1/159	0,142100623
GO:0007611	learning or memory	The acquisition and processing of information and/or the storage and retrieval of information	7.69 1/13	0.62 1/161	0,143604767
GO:0051248	negative regulation of protein metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of protein metabolic processes	15.38 2/13	0.24 2/839	0,144590764
GO:0007186	G protein-coupled receptor signaling pathway	A series of molecular signals that proceeds with an activated G protein-coupled receptor	23.08 3/13	0.17 3/1776	0,145417166
GO:0051402	neuron apoptotic process	Any apoptotic process in a neuron, the basic cellular unit of nervous tissue	7.69 1/13	0.61 1/164	0,145548879
GO:0072593	reactive oxygen species metabolic process	The chemical reactions and pathways involving a reactive oxygen species	7.69 1/13	0.60 1/167	0,147877068
GO:0030163	protein catabolic process	The chemical reactions and pathways resulting in the breakdown of proteins	15.38 2/13	0.23 2/855	0,148478489
GO:0002685	regulation of leukocyte migration	Any process that modulates the frequency, rate, or extent of leukocyte migration	7.69 1/13	0.59 1/169	0,148743611
GO:0034612	response to tumor necrosis factor	Any process that results in a change in state or activity of a cell or organism in response to tumor necrosis factor	7.69 1/13	0.59 1/169	0,148743611
GO:0002699	positive regulation of immune effector process	Any process that activates or increases the frequency, rate, or extent of immune effector processes	7.69 1/13	0.59 1/169	0,148743611
GO:0033673	negative regulation of kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of kinase activity	7.69 1/13	0.58 1/172	0,150983994
GO:0001932	regulation of protein phosphorylation	Any process that modulates the frequency, rate or extent of protein phosphorylation	15.38 2/13	0.23 2/867	0,150983994
GO:2001234	negative regulation of apoptotic signaling pathway	Any process that stops, prevents or reduces the frequency, rate or extent of apoptotic signaling	7.69 1/13	0.57 1/174	0,152295279
GO:0010632	regulation of epithelial cell migration	Any process that modulates the frequency, rate or extent of epithelial cell migration	7.69 1/13	0.57 1/176	0,153746068
GO:0051651	maintenance of location in cell	Any process in which a substance or cellular entity, such as a protein, remains in a specific location	7.69 1/13	0.56 1/177	0,154364585
GO:0050920	regulation of chemotaxis	Any process that modulates the frequency, rate or extent of chemotaxis	7.69 1/13	0.56 1/178	0,154980931
GO:1901214	regulation of neuron death	Any process that modulates the frequency, rate or extent of neuron death	7.69 1/13	0.56 1/179	0,155385135
GO:0006457	protein folding	The process of assisting in the covalent and noncovalent assembly of a protein	7.69 1/13	0.56 1/179	0,155385135
GO:0017038	protein import	The targeting and directed movement of proteins into a cell or organelle	7.69 1/13	0.55 1/181	0,156817033
GO:0044403	biological process involved in symbiotic interaction	A process carried out by gene products in an organism that enables it to interact with another organism	7.69 1/13	0.55 1/182	0,157424785
GO:0030595	leukocyte chemotaxis	The movement of a leukocyte in response to an external stimulus	7.69 1/13	0.55 1/183	0,158030411
GO:0002768	immune response-regulating cell surface receptor signaling pathway	A series of molecular signals initiated by the binding of an extracellular ligand to a cell surface receptor	7.69 1/13	0.54 1/184	0,158421274
GO:2001020	regulation of response to DNA damage stimulus	Any process that modulates the frequency, rate or extent of response to DNA damage	7.69 1/13	0.54 1/184	0,158421274
GO:0008654	phospholipid biosynthetic process	The chemical reactions and pathways resulting in the formation of phospholipids	7.69 1/13	0.54 1/185	0,158601739
GO:0050790	regulation of catalytic activity	Any process that modulates the activity of an enzyme	23.08 3/13	0.16 3/1868	0,158601739
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	The attachment of one cell to another cell via adhesion molecules	7.69 1/13	0.54 1/185	0,158601739
GO:0006909	phagocytosis	A vesicle-mediated transport process that results in the engulfment of a particle	7.69 1/13	0.53 1/188	0,160384562
GO:0034599	cellular response to oxidative stress	Any process that results in a change in state or activity of a cell in response to oxidative stress	7.69 1/13	0.53 1/188	0,160384562
GO:0032496	response to lipopolysaccharide	Any process that results in a change in state or activity of an organism in response to lipopolysaccharide	7.69 1/13	0.53 1/188	0,160384562
GO:0032268	regulation of cellular protein metabolic process	Any process that modulates the frequency, rate or extent of cellular protein metabolic processes	23.08 3/13	0.16 3/1884	0,160762609
GO:0050890	cognition	The operation of the mind by which an organism becomes aware of and responds to its environment	7.69 1/13	0.53 1/189	0,160762609
GO:0045017	glycerolipid biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerolipids	7.69 1/13	0.53 1/190	0,161351601
GO:0016485	protein processing	Any protein maturation process achieved by the cleavage of a polypeptide	7.69 1/13	0.52 1/192	0,162738445
GO:0051348	negative regulation of transferase activity	Any process that stops or reduces the rate of transferase activity	7.69 1/13	0.51 1/196	0,165714026
GO:0030336	negative regulation of cell migration	Any process that stops, prevents, or reduces the frequency, rate or extent of cell migration	7.69 1/13	0.51 1/197	0,166290792
GO:0051094	positive regulation of developmental process	Any process that activates or increases the rate or extent of developmental processes	15.38 2/13	0.21 2/946	0,169194999
GO:0002237	response to molecule of bacterial origin	Any process that results in a change in state or activity of an organism in response to a molecule of bacterial origin	7.69 1/13	0.49 1/204	0,171392867
GO:0007548	sex differentiation	The establishment of the sex of an organism by physical differentiation	7.69 1/13	0.49 1/205	0,171956085
GO:0019932	second-messenger-mediated signaling	Any intracellular signal transduction in which the signal is passed on through second messengers	7.69 1/13	0.49 1/206	0,172291246
GO:0010720	positive regulation of cell development	Any process that increases the rate, frequency or extent of cell development	7.69 1/13	0.49 1/206	0,172291246
GO:2000146	negative regulation of cell motility	Any process that stops, prevents, or reduces the frequency, rate or extent of cell motility	7.69 1/13	0.48 1/207	0,17285013
GO:0007162	negative regulation of cell adhesion	Any process that stops, prevents, or reduces the frequency, rate or extent of cell adhesion	7.69 1/13	0.48 1/208	0,173407081
GO:0070372	regulation of ERK1 and ERK2 cascade	Any process that modulates the frequency, rate or extent of ERK1 and ERK2 cascade	7.69 1/13	0.47 1/211	0,17506641
GO:0031346	positive regulation of cell projection organization	Any process that activates or increases the frequency, rate or extent of cell projection organization	7.69 1/13	0.47 1/211	0,17506641
GO:0051271	negative regulation of cellular component movement	Any process that stops, prevents, or reduces the frequency, rate or extent of cellular component movement	7.69 1/13	0.47 1/211	0,17506641
GO:0070997	neuron death	The process of cell death in a neuron	7.69 1/13	0.47 1/213	0,176163105
GO:0060828	regulation of canonical Wnt signaling pathway	Any process that modulates the rate, frequency, or extent of the canonical Wnt signaling pathway	7.69 1/13	0.47 1/213	0,176163105
GO:0051091	positive regulation of DNA-binding transcription factor activity	Any process that activates or increases the frequency, rate or extent of DNA-binding transcription factor activity	7.69 1/13	0.47 1/215	0,177482151
GO:0044265	cellular macromolecule catabolic process	The chemical reactions and pathways resulting in the breakdown of macromolecules	15.38 2/13	0.20 2/985	0,177823505
GO:0042325	regulation of phosphorylation	Any process that modulates the frequency, rate or extent of phosphorylation	15.38 2/13	0.20 2/986	0,177901885
GO:0019058	viral life cycle	A set of processes which all viruses follow to ensure survival and replication	7.69 1/13	0.46 1/217	0,178333911
GO:0002366	leukocyte activation involved in immune response	A change in morphology and behavior of a leukocyte resulting from immune response	7.69 1/13	0.45 1/222	0,181705455
GO:0062197	cellular response to chemical stress	Any process that results in a change in state or activity of a cell in response to chemical stress	7.69 1/13	0.45 1/222	0,181705455
GO:0007517	muscle organ development	The process whose specific outcome is the progression of the development of a muscle	7.69 1/13	0.45 1/224	0,182529035
GO:0070371	ERK1 and ERK2 cascade	An intracellular protein kinase cascade containing at least ERK1 and ERK2	7.69 1/13	0.45 1/224	0,182529035
GO:0002263	cell activation involved in immune response	A change in the morphology or behavior of a cell resulting from immune response	7.69 1/13	0.45 1/224	0,182529035
GO:0051246	regulation of protein metabolic process	Any process that modulates the frequency, rate or extent of protein metabolic processes	23.08 3/13	0.15 3/2025	0,182785027
GO:0022604	regulation of cell morphogenesis	Any process that modulates the frequency, rate or extent of cell morphogenesis	7.69 1/13	0.44 1/228	0,185094999
GO:0009306	protein secretion	The controlled release of proteins from a cell	7.69 1/13	0.44 1/229	0,185614539
GO:0051240	positive regulation of multicellular organismal process	Any process that activates or increases the frequency, rate or extent of multicellular organismal processes	15.38 2/13	0.20 2/1022	0,186265341
GO:0110053	regulation of actin filament organization	Any process that modulates the frequency, rate or extent of actin filament organization	7.69 1/13	0.43 1/231	0,18641051
GO:0035592	establishment of protein localization to extracellular region	The directed movement of a protein to a specific location within an extracellular region	7.69 1/13	0.43 1/231	0,18641051
GO:0040013	negative regulation of locomotion	Any process that stops, prevents, or reduces the frequency, rate or extent of locomotion	7.69 1/13	0.43 1/232	0,186924371
GO:0071692	protein localization to extracellular region	Any process in which a protein is transported from one specific location to another	7.69 1/13	0.42 1/236	0,189682612
GO:0097193	intrinsic apoptotic signaling pathway	A series of molecular signals in which an intracellular signal is converted into an apoptotic signal	7.69 1/13	0.42 1/237	0,190188758
GO:0001933	negative regulation of protein phosphorylation	Any process that stops, prevents or reduces the rate of addition of phosphate groups	7.69 1/13	0.41 1/242	0,193670523
GO:0035556	intracellular signal transduction	The process in which a signal is passed on to downstream components	23.08 3/13	0.14 3/2097	0,195003374
GO:0050878	regulation of body fluid levels	Any process that modulates the levels of body fluids	7.69 1/13	0.41 1/246	0,196143493
GO:0032270	positive regulation of cellular protein metabolic process	Any process that activates or increases the frequency, rate or extent of cellular protein metabolic processes	15.38 2/13	0.19 2/1072	0,199004659
GO:0031667	response to nutrient levels	Any process that results in a change in state or activity of a cell or organism in response to nutrient levels	7.69 1/13	0.40 1/252	0,20006821
GO:0051604	protein maturation	Any process leading to the attainment of the full functional capacity of a protein	7.69 1/13	0.39 1/254	0,20128396
GO:0015849	organic acid transport	The directed movement of organic acids, any acidic compound	7.69 1/13	0.39 1/255	0,201763048
GO:0007155	cell adhesion	The attachment of a cell, either to another cell or to an underlying substrate	15.38 2/13	0.18 2/1087	0,201984547
GO:0050678	regulation of epithelial cell proliferation	Any process that modulates the frequency, rate or extent of epithelial cell proliferation	7.69 1/13	0.39 1/256	0,201984547
GO:1901564	organonitrogen compound metabolic process	The chemical reactions and pathways involving organonitrogen compounds	15.38 2/13	0.10 6/5915	0,201984547
GO:0022610	biological adhesion	The attachment of a cell or organism to a substrate, another cell, or a molecule	15.38 2/13	0.18 2/1092	0,203227085
GO:0051174	regulation of phosphorus metabolic process	Any process that modulates the frequency, rate or extent of phosphorus metabolism	15.38 2/13	0.18 2/1094	0,203316999
GO:0019220	regulation of phosphate metabolic process	Any process that modulates the frequency, rate or extent of phosphate metabolism	15.38 2/13	0.18 2/1094	0,203316999
GO:0060070	canonical Wnt signaling pathway	The series of molecular signals initiated by binding of a Wnt protein to its receptor	7.69 1/13	0.38 1/260	0,203371287
GO:0042060	wound healing	The series of events that restore integrity to a damaged tissue	7.69 1/13	0.38 1/260	0,203371287

GO:0009593	detection of chemical stimulus	The series of events in which a chemical stimulus is received by a cell	LBP PIGR	15.38	2/13	0.18	2/1107	0.206436292
GO:0051098	regulation of binding	Any process that modulates the frequency, rate or extent of binding	APOE	7.69	1/13	0.37	1/267	0.207900797
GO:0031589	cell-substrate adhesion	The attachment of a cell to the underlying substrate via adhesion molecules	APOA1	7.69	1/13	0.26	1/268	0.208359481
GO:0030111	regulation of Wnt signaling pathway	Any process that modulates the frequency, rate or extent of the Wnt signaling pathway	APOE	7.69	1/13	0.37	1/269	0.208816595
GO:0051051	negative regulation of transport	Any process that stops, prevents, or reduces the frequency, rate or extent of transport	APOE	7.69	1/13	0.37	1/272	0.209920074
GO:0031326	regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent of the biosynthesis of a cell	APOA1 APOA4 APOE CLU	30.77	4/13	0.12	4/3385	0.209920074
GO:0042326	negative regulation of phosphorylation	Any process that stops, prevents or decreases the rate of addition of a phosphate group to a protein	APOE	7.69	1/13	0.37	1/271	0.209920074
GO:0050794	regulation of cellular process	Any process that modulates the frequency, rate or extent of a cellular process	APOA1 APOA4 APOE CLU	69.23	9/13	0.09	9/10398	0.209920074
GO:0009991	response to extracellular stimulus	Any process that results in a change in state or activity of a cell or its parts	APOE	7.69	1/13	0.37	1/273	0.210370081
GO:1901565	organotinogen compound catabolic process	The chemical reactions and pathways resulting in the breakdown of organotinogen compounds	APOE CLU	15.38	2/13	0.12	6/71129	0.210677743
GO:0060326	cell chemotaxis	The directed movement of a motile cell guided by a specific chemical gradient	LBP	7.69	1/13	0.36	1/275	0.211266796
GO:0016032	viral process	A multi-organism process in which a virus is a participant. The other organisms are hosts	APOE	7.69	1/13	0.36	1/276	0.211712862
GO:0009057	macromolecule catabolic process	The chemical reactions and pathways resulting in the breakdown of macromolecules	APOE CLU	15.38	2/13	0.18	2/1142	0.213766539
GO:0002696	positive regulation of leukocyte activation	Any process that activates or increases the frequency, rate, or extent of leukocyte activation	LBP	7.69	1/13	0.36	1/280	0.214004591
GO:0051247	positive regulation of protein metabolic process	Any process that activates or increases the frequency, rate or extent of protein metabolism	APOE CLU	15.38	2/13	0.17	2/1145	0.21413537
GO:0010975	regulation of neuron projection development	Any process that modulates the rate, frequency or extent of neuron projection development	APOE	7.69	1/13	0.16	1/281	0.214181715
GO:0071900	regulation of protein serine/threonine kinase activity	Any process that modulates the rate, frequency, or extent of protein serine/threonine kinase activity	APOE	7.69	1/13	0.35	1/282	0.214618966
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent of the biosynthesis of a cell	APOA1 APOA4 APOE CLU	30.77	4/13	0.12	4/3433	0.215348593
GO:0050867	positive regulation of cell activation	Any process that activates or increases the frequency, rate or extent of cell activation	LBP	7.69	1/13	0.35	1/286	0.216616035
GO:2001233	regulation of apoptotic signaling pathway	Any process that modulates the frequency, rate or extent of apoptotic signaling	LBP	7.69	1/13	0.35	1/286	0.216616035
GO:0032103	positive regulation of response to external stimulus	Any process that activates, maintains or increases the rate of response to an external stimulus	LBP	7.69	1/13	0.35	1/287	0.217046107
GO:0044282	small molecule catabolic process	The chemical reactions and pathways resulting in the breakdown of small molecules	APOE	7.69	1/13	0.35	1/289	0.218165997
GO:0002683	negative regulation of immune system process	Any process that stops, prevents, or reduces the frequency, rate or extent of immune system processes	APOA1	7.69	1/13	0.34	1/294	0.221347817
GO:0050808	synapse organization	A process that is carried out at the cellular level which results in the formation of a synapse	APOE	7.69	1/13	0.34	1/296	0.222185296
GO:0032956	regulation of actin cytoskeleton organization	Any process that modulates the frequency, rate or extent of the organization of the actin cytoskeleton	APOA1	7.69	1/13	0.34	1/296	0.222185296
GO:0007159	leukocyte cell-cell adhesion	The attachment of a leukocyte to another cell via adhesion molecules	APOA4	7.69	1/13	0.34	1/298	0.223017081
GO:0050804	modulation of chemical synaptic transmission	Any process that modulates the frequency or amplitude of synaptic transmission	APOE	7.69	1/13	0.34	1/298	0.223017081
GO:0099177	regulation of trans-synaptic signaling	Any process that modulates the frequency, rate or extent of trans-synaptic signaling	APOE	7.69	1/13	0.33	1/299	0.223430852
GO:0031399	regulation of protein modification process	Any process that modulates the frequency, rate or extent of protein modification	APOA1 APOE	15.38	2/13	0.17	2/1192	0.224361059
GO:0010035	response to inorganic substance	Any process that results in a change in state or activity of a cell or its parts	APOA4	7.69	1/13	0.33	1/304	0.226290751
GO:0048732	gland development	The process whose specific outcome is the progression of a gland	APOA1	7.69	1/13	0.33	1/306	0.227373454
GO:0003008	system process	A multicellular organismal process carried out by any of the organs	APOA1 APOE PIGR	23.08	3/13	0.13	3/2314	0.228258451
GO:0051606	detection of stimulus	The series of events in which a stimulus is received by a cell or organism	LBP PIGR	15.38	2/13	0.16	2/1215	0.230084939
GO:0051223	regulation of protein transport	Any process that modulates the frequency, rate or extent of protein transport	APOE	7.69	1/13	0.32	1/314	0.231938893
GO:0051346	negative regulation of hydrolase activity	Any process that stops or reduces the rate of hydrolase activity	APOA1	7.69	1/13	0.32	1/317	0.233392136
GO:0006874	cellular calcium ion homeostasis	Any process involved in the maintenance of an internal steady state of calcium ion concentration	APOE	7.69	1/13	0.32	1/317	0.233392136
GO:0008015	blood circulation	The flow of blood through the body of an animal, enabling the transport of substances	APOE	7.69	1/13	0.31	1/320	0.235114394
GO:0045936	negative regulation of phosphate metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of phosphate metabolism	APOE	7.69	1/13	0.31	1/321	0.23522024
GO:0010563	negative regulation of phosphorus metabolic process	Any process that decreases the frequency, rate or extent of the phosphate cycle	APOE	7.69	1/13	0.31	1/321	0.23522024
GO:0032970	regulation of actin filament-based process	Any process that modulates the frequency, rate or extent of an actin filament-based process	APOA1	7.69	1/13	0.31	1/324	0.236929371
GO:0009611	response to wounding	Any process that results in a change in state or activity of a cell or its parts	APOE	7.69	1/13	0.31	1/326	0.237970511
GO:0050574	calcium ion homeostasis	Any process involved in the maintenance of an internal steady state of calcium ion concentration	APOE	7.69	1/13	0.30	1/328	0.239007586
GO:0034248	regulation of cellular amide metabolic process	Any process that modulates the frequency, rate or extent of cellular amide metabolism	APOE	7.69	1/13	0.30	1/329	0.239383041
GO:0001819	positive regulation of cytokine production	Any process that activates or increases the frequency, rate or extent of cytokine production	LBP	7.69	1/13	0.30	1/330	0.239757211
GO:0051090	regulation of DNA-binding transcription factor activity	Any process that modulates the frequency, rate or extent of the activity of a DNA-binding transcription factor	CLU	7.69	1/13	0.30	1/333	0.24144015
GO:0070201	regulation of establishment of protein localization	Any process that modulates the frequency, rate or extent of protein localization	APOE	7.69	1/13	0.30	1/336	0.242957053
GO:0006796	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the phosphate cycle	APOA1 APOA4 APOE	23.08	3/13	0.12	3/2404	0.242957053
GO:0003013	cellular system process	A organ system process carried out by any of the organs or tissues	APOE	7.69	1/13	0.29	1/342	0.246154629
GO:0022607	cellular component assembly	The aggregation, arrangement and bonding together of a cellular component	APOA1 APOA4 APOE CLU	30.77	4/13	0.11	4/3663	0.246154629
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the nonmetallic element phosphorus	APOA1 APOA4 APOE	23.08	3/13	0.12	3/2425	0.246532915
GO:0045785	positive regulation of cell adhesion	Any process that activates or increases the frequency, rate or extent of cell adhesion	APOA1	7.69	1/13	0.29	1/345	0.247515849
GO:0022407	regulation of cell-cell adhesion	Any process that modulates the frequency, rate or extent of cell-cell adhesion	APOA1	7.69	1/13	0.29	1/346	0.247870716
GO:0071396	cellular response to lipid	Any process that results in a change in state or activity of a cell in response to a lipid	LBP	7.69	1/13	0.29	1/347	0.24793472
GO:0072503	cellular divalent inorganic cation homeostasis	Any process involved in the maintenance of an internal steady state of a divalent inorganic cation	APOE	7.69	1/13	0.29	1/347	0.24793472
GO:0043065	positive regulation of apoptotic process	Any process that activates or increases the frequency, rate or extent of apoptosis	CLU	7.69	1/13	0.29	1/349	0.248928016
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicellular organism	APOA1 APOA4 APOE CN	46.15	6/13	0.09	6/6399	0.250398406
GO:0016055	Wnt signaling pathway	The series of molecular signals initiated by binding of a Wnt protein to its receptor	APOE	7.69	1/13	0.28	1/355	0.252177649
GO:1903530	regulation of secretion by cell	Any process that modulates the frequency, rate or extent of secretory activity	APOE	7.69	1/13	0.25	1/357	0.252862676
GO:198738	cell-cell signaling by wnt	Any process that mediates the transfer of information from one cell to another	APOE	7.69	1/13	0.28	1/357	0.252862676
GO:0043068	positive regulation of programmed cell death	Any process that activates or increases the frequency, rate or extent of programmed cell death	LBP	7.69	1/13	0.28	1/360	0.254469765
GO:0060284	regulation of cell development	Any process that modulates the rate, frequency or extent of cell development	APOA1	7.69	1/13	0.28	1/361	0.254807102
GO:0072507	divalent inorganic cation homeostasis	Any process involved in the maintenance of an internal steady state of a divalent inorganic cation	APOE	7.69	1/13	0.27	1/364	0.256403624
GO:0006468	protein phosphorylation	The process of introducing a phosphate group onto a protein	APOA1 APOE	15.38	2/13	0.15	2/1340	0.258358008
GO:0043410	positive regulation of MAPK cascade	Any process that activates or increases the frequency, rate or extent of the MAPK cascade	APOE	7.69	1/13	0.27	1/373	0.261451749
GO:0090066	regulation of anatomical structure size	Any process that modulates the size of an anatomical structure	APOE	7.69	1/13	0.26	1/379	0.264888846
GO:0044089	positive regulation of cellular component biogenesis	Any process that activates or increases the frequency, rate or extent of cellular component biogenesis	APOA1	7.69	1/13	0.26	1/382	0.266445924
GO:1901361	organic cyclic compound catabolic process	The chemical reactions and pathways resulting in the breakdown of organic cyclic compounds	APOE	7.69	1/13	0.26	1/386	0.268614067
GO:0010942	positive regulation of cell death	Any process that increases the rate or frequency of cell death	CLU	7.69	1/13	0.26	1/388	0.269230092
GO:0031400	negative regulation of protein modification process	Any process that stops, prevents, or reduces the frequency, rate or extent of protein modification	APOE	7.69	1/13	0.26	1/388	0.269230092
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakdown of proteins	CLU	7.69	1/13	0.26	1/391	0.27076494
GO:0030335	regulation of cell migration	Any process that activates or increases the frequency, rate or extent of cell migration	LBP	7.69	1/13	0.25	1/393	0.271680698
GO:0007015	actin filament organization	A process that is carried out at the cellular level which results in the formation of actin filaments	APOA1	7.69	1/13	0.25	1/396	0.272891771
GO:0050778	positive regulation of immune response	Any process that activates or increases the frequency, rate or extent of an immune response	LBP	7.69	1/13	0.25	1/396	0.272891771
GO:0010638	positive regulation of organelle organization	Any process that increases the frequency, rate or extent of organelle organization	APOA1	7.69	1/13	0.25	1/398	0.273798258
GO:0051046	regulation of secretion	Any process that modulates the frequency, rate or extent of the secretory process	APOE	7.69	1/13	0.25	1/400	0.274701
GO:0044085	cellular component biogenesis	A process that results in the biosynthesis of constituent macromolecules	APOA1 APOA4 APOE CLU	30.77	4/13	0.10	4/3907	0.280759789
GO:0034613	cellular protein localization	Any process in which a protein is transported to, and/or maintained in, a particular cellular location	APOE PIGR	15.38	2/13	0.14	2/1432	0.280980247
GO:2000147	positive regulation of cell motility	Any process that activates or increases the frequency, rate or extent of cell motility	LBP	7.69	1/13	0.24	1/412	0.280998782
GO:0070727	cellular macromolecule localization	Any process in which a macromolecule is transported to, and/or maintained in, a particular cellular location	APOE PIGR	15.38	2/13	0.14	2/1438	0.282093234
GO:0051272	positive regulation of cellular component movement	Any process that activates or increases the frequency, rate or extent of cellular component movement	LBP	7.69	1/13	0.24	1/417	0.283353704
GO:0034645	cellular macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formation of macromolecules	APOA1 APOE	15.38	2/13	0.14	2/1449	0.2846592
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent of a biological process	APOA1 APOA4 APOE CLU	69.23	9/13	0.08	9/11175	0.285250534
GO:1905114	cell surface receptor signaling pathway involved in cell-cell communication	Any cell surface receptor signaling pathway that is involved in cell-cell communication	APOE	7.69	1/13	0.24	1/424	0.286552791
GO:0040017	positive regulation of locomotion	Any process that activates or increases the frequency, rate or extent of locomotion	LBP	7.69	1/13	0.24	1/425	0.286821692
GO:0033554	cellular response to stress	Any process that results in a change in state or activity of a cell in response to stress	APOA4 CLU	15.38	2/13	0.14	2/1463	0.287441725
GO:0120035	regulation of plasma membrane bounded cell projectile	Any process that modulates the frequency, rate or extent of a projectile	APOE	7.69	1/13	0.23	1/433	0.290888498
GO:0006875	cellular metal ion homeostasis	Any process involved in the maintenance of an internal steady state of a metal ion	APOE	7.69	1/13	0.23	1/435	0.291734768
GO:0051493	regulation of cytoskeleton organization	Any process that modulates the frequency, rate or extent of cytoskeleton organization	APOA1	7.69	1/13	0.23	1/437	0.292577709
GO:0090407	organophosphate biosynthetic process	The chemical reactions and pathways resulting in the biosynthesis of organophosphates	APOA1	7.69	1/13	0.23	1/439	0.293417335
GO:0031344	regulation of cell projection organization	Any process that modulates the frequency, rate or extent of a projection	APOE	7.69	1/13	0.23	1/441	0.294253657
GO:0002694	regulation of leukocyte activation	Any process that modulates the frequency, rate, or extent of leukocyte activation	LBP	7.69	1/13	0.23	1/444	0.295667245
GO:0061061	muscle structure development	The progression of a muscle structure over time, from its formation to its maintenance	CNTFR	7.69	1/13	0.22	1/445	0.295916443
GO:0048514	blood vessel morphogenesis	The process in which the anatomical structures of blood vessels are formed	APOE	7.69	1/13	0.22	1/448	0.29732078
GO:0007190	apoptotic signaling pathway	A series of molecular signals which triggers the apoptotic death of a cell	CLU	7.69	1/13	0.22	1/459	0.303315344
GO:0008285	negative regulation of cell population proliferation	Any process that stops, prevents or reduces the rate or extent of cell population proliferation	APOE	7.69	1/13	0.21	1/469	0.308685376
GO:0010604	positive regulation of macromolecule metabolic process	Any process that increases the frequency, rate or extent of the metabolism of macromolecules	APOE CLU LBP	23.08	3/13	0.11	3/2795	0.311072191
GO:1901566	organotinogen compound biosynthetic process	The chemical reactions and pathways resulting in the formation of organotinogen compounds	APOA1 APOE	15.38	2/13	0.13	2/1575	0.315851788
GO:0030003	cellular cation homeostasis	Any process involved in the maintenance of an internal steady state of a cation	APOE	7.69	1/13	0.20	1/491	0.320051181
GO:0048468	cell development	The process whose specific outcome is the progression of the cell	APOA1 APOE	15.38	2/13	0.13	2/1592	0.320052147
GO:0048598	embryonic morphogenesis	The process in which anatomical structures are generated and organized	APOA1	7.69	1/13	0.20	1/494	0.321015759
GO:0055065	metal ion homeostasis	Any process involved in the maintenance of an internal steady state of a metal ion	APOE	7.69	1/13	0.20</		

GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent of gene	AP0A1 APOE CLU LBP	30.77 4/13	0.09 4/4340	0.345279159
GO:0000904	cell morphogenesis involved in differentiation	The change in form (cell shape and size) that occurs when relative	AP0A1	7.69 1/13	0.18 1/552	0.346253185
GO:0050580	cation homeostasis	Any process involved in the maintenance of an internal steady state	APOE	7.69 1/13	0.18 1/556	0.347983958
GO:0098771	inorganic ion homeostasis	Any process involved in the maintenance of an internal steady state	APOE	7.69 1/13	0.18 1/565	0.352322678
GO:0030155	regulation of cell adhesion	Any process that modulates the frequency, rate or extent of attach	AP0A1	7.69 1/13	0.17 1/573	0.356106743
GO:0050582	cellular chemical homeostasis	Any biological process involved in the maintenance of an internal	APOE	7.69 1/13	0.17 1/586	0.362439936
GO:0140352	export from cell	The directed movement of some substance from a cell, into the ext	APOE	7.69 1/13	0.17 1/587	0.362562147
GO:0043549	regulation of kinase activity	Any process that modulates the frequency, rate or extent of kinase	APOE	7.69 1/13	0.17 1/588	0.363683779
GO:0006511	ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakdown o	CLU	7.69 1/13	0.17 1/589	0.362804833
GO:0000165	MAPK cascade	An intracellular protein kinase cascade containing at least a MAPK, APOE		7.69 1/13	0.17 1/591	0.363436429
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific protein, r	AP0A1 APOE BSPRY CLU	30.77 4/13	0.09 4/4461	0.363621939
GO:0032880	regulation of protein localization	Any process that modulates the frequency, rate or extent of any pr	APOE	7.69 1/13	0.17 1/594	0.363791845
GO:0045597	positive regulation of cell differentiation	Any process that activates or increases the frequency, rate or exte	AP0A1	7.69 1/13	0.17 1/594	0.363791845
GO:0050801	ion homeostasis	Any process involved in the maintenance of an internal steady stat	APOE	7.69 1/13	0.17 1/602	0.367454167
GO:0019941	modification-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakdown o	CLU	7.69 1/13	0.17 1/603	0.367564965
GO:0030036	actin cytoskeleton organization	A process that is carried out at the cellular level which results in th	AP0A1	7.69 1/13	0.16 1/611	0.370796073
GO:0043632	modification-dependent macromolecule catabolic proc	The chemical reactions and pathways resulting in the breakdown o	CLU	7.69 1/13	0.16 1/611	0.370796073
GO:0065007	biological regulation	Any process that modulates a measurable attribute of any biolog	AP0A1 APOA4 APOE CLU	69.23 9/13	0.08 9/11905	0.371110441
GO:0050793	regulation of developmental process	Any process that modulates the frequency, rate or extent of devel	AP0A1 APOE	15.38 2/13	0.11 2/1822	0.37196899
GO:0050877	nervous system process	A organ system process carried out by any of the organs or tissues	APOE PIGR	15.38 2/13	0.11 2/1827	0.372955229
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent of the ch	AP0A1 APOA4 APOE CLU	38.46 5/13	0.08 5/5976	0.376657959
GO:0046903	secretion	The controlled release of a substance by a cell or a tissue.	APOE	7.69 1/13	0.16 1/645	0.385588701
GO:0035239	tube morphogenesis	The process in which the anatomical structures of a tube are gener	APOE	7.69 1/13	0.15 1/646	0.385666206
GO:0008284	positive regulation of cell population proliferation	Any process that activates or increases the rate or extent of cell p	CNTFR	7.69 1/13	0.15 1/651	0.387686058
GO:0036211	protein modification process	The covalent alteration of one or more amino acids occurring in pr	AP0A1 APOE BSPRY	23.08 3/13	0.09 3/3236	0.388693709
GO:0006464	cellular protein modification process	The covalent alteration of one or more amino acids occurring in pr	AP0A1 APOE BSPRY	23.08 3/13	0.09 3/3236	0.388693709
GO:0019725	cellular homeostasis	Any process involved in the maintenance of an internal steady stat	APOE	7.69 1/13	0.15 1/660	0.390795323
GO:0003006	developmental process involved in reproduction	A developmental process in which a progressive change in the stat	CNTFR	7.69 1/13	0.15 1/666	0.393259156
GO:0006974	cellular response to DNA damage stimulus	Any process that results in a change in state or activity of a cell (n	CLU	7.69 1/13	0.15 1/668	0.393799491
GO:0022603	regulation of anatomical structure morphogenesis	Any process that modulates the frequency, rate or extent of anato	AP0A1	7.69 1/13	0.15 1/671	0.394813775
GO:0051172	negative regulation of nitrogen compound metabolic p	Any process that stops, prevents, or reduces the frequency, rate or	APOE CLU	15.38 2/13	0.10 2/1924	0.395060766
GO:0030029	actin filament-based process	Any cellular process that depends upon or alters the actin cytoskel	AP0A1	7.69 1/13	0.15 1/675	0.395880714
GO:0051338	regulation of transferase activity	Any process that modulates the frequency, rate or extent of trans	APOE	7.69 1/13	0.15 1/676	0.395937736
GO:0002684	positive regulation of immune system process	Any process that activates or increases the frequency, rate, or exte	LBP	7.69 1/13	0.15 1/677	0.395994347
GO:0008104	protein localization	Any process in which a protein is transported to, or maintained in,	APOE PIGR	15.38 2/13	0.10 2/1967	0.405004369
GO:0031175	neuron projection development	The process whose specific outcome is the progression of a neuror	APOE	7.69 1/13	0.14 1/701	0.406393709
GO:0016567	protein ubiquitination	The process in which one or more ubiquitin groups are added to a	BSPRY	7.69 1/13	0.14 1/702	0.406431971
GO:0045321	leukocyte activation	A change in morphology and behavior of a leukocyte resulting from	LBP	7.69 1/13	0.14 1/713	0.411084482
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units in a poly	AP0A1 APOE BSPRY	23.08 3/13	0.09 3/3413	0.420547459
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent of the ch	AP0A1 APOA4 APOE CLU	30.77 4/13	0.08 4/4857	0.42410368
GO:0032446	protein modification by small protein conjugation	A protein modification process in which one or more groups of a sr	BSPRY	7.69 1/13	0.13 1/758	0.430150421
GO:0016043	cellular component organization	A process that results in the assembly, arrangement of constituent	AP0A1 APOA4 APOE CLU	38.46 5/13	0.08 5/6354	0.430796145
GO:0007167	enzyme linked receptor protein signaling pathway	Any series of molecular signals initiated by the binding of an extrac	PIGR	7.69 1/13	0.13 1/778	0.438101381
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated and org	AP0A1 APOE	15.38 2/13	0.09 2/2107	0.43827074
GO:0032269	negative regulation of cellular protein metabolic proces	Any process that stops, prevents, or reduces the frequency, rate or	APOE	7.69 1/13	0.13 1/792	0.443306075
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of	AP0A1 APOE CLU	23.08 3/13	0.08 3/3552	0.446397462
GO:0035295	tube development	The process whose specific outcome is the progression of a tube or	APOE	7.69 1/13	0.12 1/804	0.446649717
GO:0000902	cell morphogenesis	The developmental process in which the size or shape of a cell is g	AP0A1	7.69 1/13	0.12 1/802	0.446649717
GO:0072359	circulatory system development	The process whose specific outcome is the progression of the circ	APOE	7.69 1/13	0.12 1/804	0.446649717
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent of the ch	AP0A1 APOA4 APOE CLU	30.77 4/13	0.08 4/5027	0.450445619
GO:0048731	system development	The process whose specific outcome is the progression of an organ	AP0A1 APOE CNTFR	23.08 3/13	0.08 3/3612	0.456320018
GO:0048666	neuron development	The process whose specific outcome is the progression of a neuror	APOE	7.69 1/13	0.12 1/830	0.456320018
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent macromol	AP0A1 APOA4 APOE CLU	38.46 5/13	0.08 5/6564	0.460658644
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the formation of	AP0A1 APOA4 APOE CLU	30.77 4/13	0.08 4/5094	0.460658644
GO:0010628	positive regulation of gene expression	Any process that increases the frequency, rate or extent of gene ex	LBP	7.69 1/13	0.12 1/857	0.466167228
GO:0009790	embryo development	The process whose specific outcome is the progression of an embr	AP0A1	7.69 1/13	0.11 1/874	0.472186037
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the formation of	AP0A1 APOA4 APOE CLU	30.77 4/13	0.08 4/5165	0.472186037
GO:0070647	protein modification by small protein conjugation or re	A protein modification process in which one or more groups of a sr	BSPRY	7.69 1/13	0.11 1/877	0.472924217
GO:0006518	peptide metabolic process	The chemical reactions and pathways involving peptides, compound	APOE	7.69 1/13	0.11 1/897	0.480520167
GO:0009058	biosynthetic process	The chemical reactions and pathways resulting in the formation of	AP0A1 APOA4 APOE CLU	30.77 4/13	0.08 4/5231	0.481937985
GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent of a proc	AP0A1	7.69 1/13	0.11 1/903	0.481937985
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, a	AP0A1 APOE BSPRY CLU	30.77 4/13	0.08 4/5305	0.494496024
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progression c	AP0A1 APOE CNTFR	23.08 3/13	0.08 3/3871	0.520093785
GO:0051641	cellular localization	A cellular localization process whereby a substance or cellular entit	APOE PIGR	15.38 2/13	0.08 2/2418	0.507309426
GO:0051173	positive regulation of nitrogen compound metabolic pr	Any process that activates or increases the frequency, rate or exte	APOE CLU	15.38 2/13	0.08 2/2473	0.520095882
GO:0030182	neuron differentiation	The process in which a relatively unspecialized cell acquires special	APOE	7.69 1/13	0.10 1/1022	0.524497076
GO:0022414	reproductive process	A biological process that directly contributes to the process of proc	CNTFR	7.69 1/13	0.10 1/1021	0.524497076
GO:0000003	reproduction	The production of new individuals that contain some portion of ge	CNTFR	7.69 1/13	0.10 1/1024	0.524700345
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent of the ch	AP0A1 APOE CLU LBP	30.77 4/13	0.07 4/5552	0.534251272
GO:0050907	detection of chemical stimulus involved in sensory perc	The series of events in which a chemical stimulus is received and c	PIGR	7.69 1/13	0.09 1/1085	0.545578724
GO:0048513	animal organ development	Development of a tissue or tissues that work together to perform	AP0A1 CNTFR	15.38 2/13	0.08 2/2612	0.549636105
GO:0043603	cellular amide metabolic process	The chemical reactions and pathways involving an amide, any deriv	APOE	7.69 1/13	0.09 1/1112	0.553902636
GO:0045595	regulation of cell differentiation	Any process that modulates the frequency, rate or extent of cell di	AP0A1	7.69 1/13	0.09 1/1123	0.557134281
GO:0018193	peptidyl-amino acid modification	The alteration of an amino acid residue in a peptide.	AP0A1	7.69 1/13	0.09 1/1125	0.55725833
GO:0050906	detection of stimulus involved in sensory perception	The series of events involved in sensory perception in which a sens	PIGR	7.69 1/13	0.09 1/1133	0.559428443
GO:0007267	cell-cell signaling	Any process that mediates the transfer of information from one ce	APOE	7.69 1/13	0.09 1/1138	0.560563984
GO:0048699	generation of neurons	The process in which nerve cells are generated. This includes the p	APOE	7.69 1/13	0.09 1/1146	0.562704087
GO:0007606	sensory perception of chemical stimulus	The series of events required for an organism to receive a sensory	PIGR	7.69 1/13	0.09 1/1156	0.565495908
GO:0120036	plasma membrane bounded cell projection organizatio	A process that is carried out at the cellular level which results in th	APOE	7.69 1/13	0.09 1/1160	0.566264143
GO:0030030	cell projection organization	A process that is carried out at the cellular level which results in th	APOE	7.69 1/13	0.08 1/1190	0.575595382
GO:0015031	protein transport	The directed movement of proteins into, out of or within a cell, or	APOE	7.69 1/13	0.08 1/1193	0.575997775
GO:0009059	macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formation of	AP0A1 APOE CLU	23.08 3/13	0.07 3/4337	0.582048203
GO:0048856	anatomical structure development	The biological process whose specific outcome is the progression c	AP0A1 APOE CNTFR	23.08 3/13	0.07 3/4373	0.588043902
GO:0007010	cytoskeleton organization	A process that is carried out at the cellular level which results in th	AP0A1	7.69 1/13	0.08 1/1245	0.590303082
GO:0022008	neurogenesis	Generation of cells within the nervous system.	APOE	7.69 1/13	0.08 1/1245	0.590303082
GO:0010467	gene expression	The process in which a gene's sequence is converted into a mature	AP0A1 APOE CDSL CLU	38.46 5/13	0.07 5/7489	0.592935623
GO:1903506	regulation of nucleic acid-templated transcription	Any process that modulates the frequency, rate or extent of nuclei	APOE CLU	15.38 2/13	0.07 2/2881	0.598834421
GO:0006355	regulation of transcription, DNA-templated	Any process that modulates the frequency, rate or extent of cellula	APOE CLU	15.38 2/13	0.07 2/2881	0.598834421
GO:0009890	negative regulation of biosynthetic process	Any process that stops, prevents, or reduces the rate of the chemi	APOE	7.69 1/13	0.08 1/1277	0.598834421
GO:2001141	regulation of RNA biosynthetic process	Any process that modulates the frequency, rate or extent of RNA b	APOE CLU	15.38 2/13	0.07 2/2884	0.598873483
GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location.	APOE	7.69 1/13	0.08 1/1286	0.599425856
GO:1902680	positive regulation of RNA biosynthetic process	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	0.07 1/1360	0.619564812
GO:0045893	positive regulation of transcription, DNA-templated	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	0.07 1/1358	0.619564812
GO:1903508	positive regulation of nucleic acid-templated transcript	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	0.07 1/1358	0.619564812
GO:0006351	transcription, DNA-templated	The cellular synthesis of RNA on a template of DNA.	APOE CLU	15.38 2/13	0.07 2/3019	0.623076713
GO:0097659	nucleic acid-templated transcription	The cellular synthesis of RNA on a template of nucleic acid (DNA or	APOE CLU	15.38 2/13	0.07 2/3019	0.623076713
GO:0032774	RNA biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOE CLU	15.38 2/13	0.07 2/3030	0.624671372
GO:0030154	cell differentiation	The process in which relatively unspecialized cells, e.g. embryonic	AP0A1 APOE	15.38 2/13	0.06 2/3098	0.637526399
GO:0051171	regulation of nitrogen compound metabolic process	Any process that modulates the frequency, rate or extent of the ch	AP0A1 APOE CLU	23.08 3/13	0.06 3/4722	0.639275541
GO:0007600	sensory perception	The series of events required for an organism to receive a sensory	PIGR	7.69 1/13	0.07 1/1454	0.642140251
GO:0051252	regulation of RNA metabolic process	Any process that modulates the frequency, rate or extent of the ch	APOE CLU	15.38 2/13	0.06 2/3134	0.642229693
GO:0051254	positive regulation of RNA metabolic process	Any process that activates or increases the frequency, rate or exte	APOE	7.69 1/13	0.07 1/1459	0.642229693
GO:0032502	developmental process	A biological process whose specific outcome is the progression of	AP0A1 APOE CNTFR	23.08 3/13	0.06 3/4755	0.642240252
GO:0043170	macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, a	AP0A1 APOA4 APOE BSI	53.85 7/13	0.06 7/10935	0.642971788
GO:0048869	cellular developmental process	A biological process whose specific outcome is the progression of	AP0A1 APOE	15.38 2/13	0.06 2/3162	0.645488616
GO:0010557	positive regulation of macromolecule biosynthetic proc	Any process that increases the rate, frequency or extent of the ch	APOE	7.69 1/13	0.07 1/1528	0.657829223
GO:0010556	regulation of macromolecule biosynthetic process	Any process that modulates the rate, frequency or extent of the ch	APOE CLU	15.38 2/13	0.06 2/3278	0.665862095
GO:0071705	nitrogen compound transport	The directed movement of nitrogen-containing compounds into, or	APOE	7.69 1/13	0.06 1/1587	0.671363035
GO:0045935	positive regulation of nucleobase-containing compound	Any cellular process that activates or increases the frequency, rate	APOE	7.69 1/13	0.06 1/1597	0.673163562
GO:0019219	regulation of nucleobase-containing compound metabi	Any cellular process that modulates the frequency, rate or exte	APOE CLU	15.38 2/13	0.06 2/3342	0.675453838
GO:0034654	nucleobase-containing compound biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOE CLU	15.38 2/13	0.06 2/3364	0.678698589
GO:0018130	heterocycle biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOE CLU	15.38 2/13	0.06 2/3434	0.680236036
GO:0019438	aromatic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of	APOE CLU	15.38 2/13	0.06 2/3441	0.690767929
GO:0007399	nervous system development	The process whose specific outcome is the progression of nervous	APOE	7.69 1/13	0.06 1/1710	0.696425723
GO:1901360	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyclic comp	AP0A1 APOA4 APOE CLU	30.77 4/13	0.06 4/7066	0.736495369

GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency, rate or APOE	7.69 1/13	0.05 1/2035	0,761153639
GO:0044271	cellular nitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formation of APOE CLU	15.38 2/13	0.05 2/4213	0,801554622
GO:0071704	organic substance metabolic process	The chemical reactions and pathways involving an organic substani APOA1 APOA4 APOE BSI	53.85 7/13	0.06 7/12360	0,813612225
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or inorgani APOA1 APOA4 APOE BSI	46.15 6/13	0.05 6/10926	0,817432796
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those compounds v APOA1 APOA4 APOE BSI	46.15 6/13	0.05 6/11429	0,863735743
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism and cat APOA1 APOA4 APOE BSI	53.85 7/13	0.05 7/12915	0,865498758
GO:0006996	organelle organization	A process that is carried out at the cellular level which results in th APOA1	7.69 1/13	0.03 1/3330	0,9128581
GO:0016070	RNA metabolic process	The cellular chemical reactions and pathways involving RNA, riboni APOE CLU	15.38 2/13	0.03 2/5843	0,934248931
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not necessa APOA1 APOA4 APOE BSI	84.62 11/13	0.06 11/18706	0,949011927
GO:0090304	nucleic acid metabolic process	Any cellular metabolic process involving nucleic acids. APOE CLU	15.38 2/13	0.03 2/6311	0,953583437
GO:0044237	cellular metabolic process	The chemical reactions and pathways by which individual cells tran APOA1 APOA4 APOE BSI	38.46 5/13	0.04 5/11581	0,95708073
GO:0006139	nucleobase-containing compound metabolic process	Any cellular metabolic process involving nucleobases, nucleosides, APOE CLU	15.38 2/13	0.03 2/6721	0,965715164
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocyclic compc APOE CLU	15.38 2/13	0.03 2/6828	0,967847786
GO:0006725	cellular aromatic compound metabolic process	The chemical reactions and pathways involving aromatic compoun APOE CLU	15.38 2/13	0.03 2/6891	0,968619603
GO:0034641	cellular nitrogen compound metabolic process	The chemical reactions and pathways involving various organic anc APOE CLU	15.38 2/13	0.03 2/7596	0,982311673
GO:0008150	biological_process	A biological process represents a specific objective that the organis APOA1 APOA4 APOE BSI	100.00 13/13	0.06 13/20110	1

sPLS_Lipolysis_Enrichment_GO_BP_of_15prot_contributing_to_LL_group	GO_BP	Name	Function	Gene Name	Term frequency	Term frequen	P-value (fdr)	Query with no gene names
GO:1903061	GO:1903061	positive regulation of protein lipidation	Any process that activates or increases the frequency, rate or extent of protein lipidation	RAB3GAP1 RAB3GAP2	14.29/2/14	66.67/2/3	0.00023238	
GO:0097051	GO:0097051	establishment of protein localization to endoplasmic reticulum membrane	The directed movement of a protein to a specific location in the endoplasmic reticulum	RAB3GAP1 RAB3GAP2	14.29/2/14	66.67/2/3	0.00023238	
GO:0050747	GO:0050747	positive regulation of lipoprotein metabolic process	Any process that activates or increases the frequency, rate or extent of the chemical	RAB3GAP1 RAB3GAP2	14.29/2/14	66.67/2/3	0.00023238	
GO:1903373	GO:1903373	positive regulation of endoplasmic reticulum tubular network organization	Any process that activates or increases the frequency, rate or extent of endoplasmic	RAB3GAP1 RAB3GAP2	14.29/2/14	50.00/1/4	0.000348068	
GO:1903059	GO:1903059	regulation of protein lipidation	Any process that modulates the frequency, rate or extent of protein lipidation.	RAB3GAP1 RAB3GAP2	14.29/2/14	33.33/2/6	0.000579652	
GO:1903371	GO:1903371	regulation of endoplasmic reticulum tubular network organization	Any process that modulates the frequency, rate or extent of endoplasmic reticulum t	RAB3GAP1 RAB3GAP2	14.29/2/14	33.33/2/6	0.000579652	
GO:0050746	GO:0050746	regulation of lipoprotein metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions a	RAB3GAP1 RAB3GAP2	14.29/2/14	20.00/1/20	0.001488163	
GO:2000786	GO:2000786	positive regulation of autophagosome assembly	Any process that activates or increases the frequency, rate or extent of autophagic v	RAB3GAP1 RAB3GAP2	14.29/2/14	13.33/2/15	0.002695373	
GO:0071786	GO:0071786	endoplasmic reticulum tubular network organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1 RAB3GAP2	14.29/2/14	13.33/2/15	0.002695373	
GO:0040490	GO:0040490	positive regulation of vacuole organization	Any process that activates or increases the frequency, rate or extent of a process inv	RAB3GAP1 RAB3GAP2	14.29/2/14	11.11/2/18	0.003505372	
GO:0010638	GO:0010638	positive regulation of organelle organization	Any process that increases the frequency, rate or extent of a process involved in the	ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57/4/14	1.01/4/398	0.000606322	
GO:2000785	GO:2000785	regulation of autophagosome assembly	Any process that modulates the frequency, rate or extent of autophagosome assemb	RAB3GAP1 RAB3GAP2	14.29/2/14	5.00/2/40	0.014868471	
GO:0044088	GO:0044088	regulation of vacuole organization	Any process that modulates the frequency, rate or extent of a process involved in the	RAB3GAP1 RAB3GAP2	14.29/2/14	4.55/2/44	0.016619188	
GO:0016239	GO:0016239	positive regulation of macroautophagy	Any process that activates or increases the frequency, rate or extent of the process i	ALOX15 RAB3GAP1 RAB3GAP2	28.57/4/14	3.57/2/56	0.025002424	
GO:0072599	GO:0072599	establishment of protein localization to endoplasmic reticulum	The directed movement of a protein to a specific location in the endoplasmic reticu	RAB3GAP1 RAB3GAP2	14.29/2/14	3.45/2/58	0.02502797	
GO:1901074	GO:1901074	regulation of engulfment of apoptotic cell	Any process that modulates the frequency, rate or extent of engulfment of apoptotic	ALOX15	7.14/1/4	50.00/1/2	0.031226796	
GO:0035963	GO:0035963	cellular response to interleukin-13	Any process that results in a change in state or activity of a cell (in terms of movem	ALOX15	7.14/1/4	50.00/1/2	0.031226796	
GO:1902117	GO:1902117	positive regulation of organelle assembly	Any process that activates or increases the frequency, rate or extent of organelle ass	RAB3GAP1 RAB3GAP2	14.29/2/14	2.99/2/67	0.031226796	
GO:0070972	GO:0070972	protein localization to endoplasmic reticulum	A process in which a protein is transported to, or maintained in, a location within the	RAB3GAP1 RAB3GAP2	14.29/2/14	2.56/2/78	0.031226796	
GO:0035962	GO:0035962	response to interleukin-13	Any process that results in a change in state or activity of a cell or organism (in t	ALOX15	7.14/1/4	50.00/1/2	0.031226796	
GO:1909062	GO:1909062	xenobiotic transport across blood-brain barrier	The directed movement of a xenobiotic through the blood-brain barrier.	ABCG2	7.14/1/4	50.00/1/2	0.031226796	
GO:0007029	GO:0007029	endoplasmic reticulum organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1 RAB3GAP2	14.29/2/14	2.67/2/75	0.031226796	
GO:0097744	GO:0097744	renal urate salt excretion	The elimination of urate salt or uric acid from peritubular capillaries (or surroundin	ABCG2	7.14/1/4	50.00/1/2	0.031226796	
GO:0051130	GO:0051130	positive regulation of cellular component organization	Any process that activates or increases the frequency, rate or extent of a process inv	ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57/4/14	0.52/4/763	0.032631168	
GO:0042158	GO:0042158	lipoprotein biosynthetic process	The chemical reactions and pathways resulting in the formation of any conjugated, w	RAB3GAP1 RAB3GAP2	14.29/2/14	2.08/2/96	0.034158726	
GO:0016241	GO:0016241	regulation of macroautophagy	Any process that modulates the frequency, rate or extent of macroautophagy.	RAB3GAP1 RAB3GAP2	14.29/2/14	2.17/2/92	0.034158726	
GO:0044089	GO:0044089	positive regulation of cellular component biogenesis	Any process that activates or increases the frequency, rate or extent of cellular comp	ALOX15 RAB3GAP1 RAB3GAP2	21.43/3/14	0.79/3/82	0.034158726	
GO:0006497	GO:0006497	protein lipidation	The covalent attachment of lipid groups to an amino acid in a protein.	RAB3GAP1 RAB3GAP2	14.29/2/14	2.20/2/91	0.034158726	
GO:0000045	GO:0000045	autophagosome assembly	The formation of a double membrane-bounded structure, the autophagosome, that i	RAB3GAP1 RAB3GAP2	14.29/2/14	2.15/2/93	0.034158726	
GO:2001303	GO:2001303	lipoxin A4 biosynthetic process	The chemical reactions and pathways resulting in the formation of lipoxin A4. Lipoxi	ALOX15	7.14/1/4	33.33/1/3	0.034158726	
GO:2001302	GO:2001302	lipoxin A4 metabolic process	The chemical reactions and pathways involving lipoxin A4. Lipoxin A4 is a C20 hydro	ALOX15	7.14/1/4	33.33/1/3	0.034158726	
GO:1905037	GO:1905037	autophagosome organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1 RAB3GAP2	14.29/2/14	2.04/2/98	0.034158726	
GO:2001301	GO:2001301	lipoxin biosynthetic process	The chemical reactions and pathways involving lipoxin. A lipoxin is a non-classic et	ALOX15	7.14/1/4	25.00/1/4	0.039277551	
GO:0033043	GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent of a process involved in the	ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57/4/14	0.44/4/903	0.039277551	
GO:2001300	GO:2001300	lipoxin metabolic process	The chemical reactions and pathways involving lipoxin. A lipoxin is a non-classic et	ALOX15	7.14/1/4	25.00/1/4	0.039277551	
GO:0010256	GO:0010256	endomembrane system organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1 RAB3GAP2 SURF4	21.43/3/14	0.73/3/409	0.039277551	
GO:0010508	GO:0010508	positive regulation of autophagy	Any process that activates, maintains or increases the rate of autophagy. Autophagy i	RAB3GAP1 RAB3GAP2	14.29/2/14	1.75/2/114	0.039277551	
GO:0006633	GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of a fatty acid, any o	ALOX15 FASN	14.29/2/14	1.61/2/124	0.044398803	
GO:0032218	GO:0032218	riboflavin transport	The directed movement of riboflavin into, out of or within a cell, or between cells, b	ABCG2	7.14/1/4	20.00/1/5	0.045994882	
GO:0042157	GO:0042157	lipoxin metabolic process	The chemical reactions and pathways involving any conjugated, water-soluble protei	RAB3GAP1 RAB3GAP2	14.29/2/14	1.49/2/134	0.047892584	
GO:0006897	GO:0006897	endocytosis	A vesicle-mediated transport process in which cells take up external materials (or m	ALOX15 MYO6 SURF4	21.43/3/14	0.64/3/466	0.047892584	
GO:0015747	GO:0015747	urate transport	The directed movement of urate into, out of or within a cell, or between cells, by me	ABCG2	7.14/1/4	16.67/1/6	0.051234879	
GO:0044509	GO:0044509	glycerol ether biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerol ethers, ar	FASN	7.14/1/4	12.50/1/8	0.054099999	
GO:0008611	GO:0008611	ether lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of ether lipids, lipids	FASN	7.14/1/4	12.50/1/8	0.054099999	
GO:0007033	GO:0007033	vacuole organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1 RAB3GAP2	14.29/2/14	1.25/2/160	0.054099999	
GO:0051122	GO:0051122	hepoxilin biosynthetic process	The chemical reactions and pathways resulting in the formation of hepoxilins, a class	ALOX15	7.14/1/4	14.29/1/7	0.054099999	
GO:0030223	GO:0030223	neutrophil differentiation	The process in which a myeloid precursor cell acquires the specialized features of a	FASN	7.14/1/4	12.50/1/8	0.054099999	
GO:0051121	GO:0051121	hepoxilin metabolic process	The chemical reactions and pathways involving hepoxilins, a class of bioactive icosa	ALOX15	7.14/1/4	14.29/1/7	0.054099999	
GO:0097384	GO:0097384	cellular lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of lipids, as carried o	FASN	7.14/1/4	12.50/1/8	0.054099999	
GO:1905153	GO:1905153	regulation of membrane invagination	Any process that modulates the frequency, rate or extent of membrane invagination.	ALOX15	7.14/1/4	12.50/1/8	0.054099999	
GO:0072330	GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of monocarboxylic ac	ALOX15 FASN	14.29/2/14	1.31/2/153	0.054099999	
GO:0006099	GO:0006099	regulation of phagocytosis, engulfment	Any process that modulates the frequency, rate or extent of the internalization of ba	ALOX15	7.14/1/4	12.50/1/8	0.054099999	
GO:0043651	GO:0043651	linoleic acid metabolic process	The chemical reactions and pathways involving linoleic acid, an unsaturated omega-6	ALOX15	7.14/1/4	12.50/1/8	0.054099999	
GO:1902115	GO:1902115	regulation of organelle assembly	Any process that modulates the frequency, rate or extent of organelle assembly.	RAB3GAP1 RAB3GAP2	14.29/2/14	1.20/2/166	0.055119087	
GO:0090557	GO:0090557	establishment of endothelial intestinal barrier	The establishment of a barrier between endothelial cell layers of the intestine to exe	FASN	7.14/1/4	11.11/1/9	0.057583388	
GO:1901503	GO:1901503	ether biosynthetic process	The chemical reactions and pathways resulting in the formation of ether.	FASN	7.14/1/4	11.11/1/9	0.057583388	
GO:0015937	GO:0015937	coenzyme A biosynthetic process	The chemical reactions and pathways resulting in the formation of coenzyme A, 3'-ph	COASY	7.14/1/4	10.00/1/10	0.060708626	
GO:0019372	GO:0019372	lipoygenase pathway	The chemical reactions and pathways by which an unsaturated fatty acid (such as ara	ALOX15	7.14/1/4	10.00/1/10	0.060708626	
GO:0006646	GO:0006646	phosphatidylethanolamine biosynthetic process	The chemical reactions and pathways resulting in the formation of phosphatidyletha	ALOX15	7.14/1/4	10.00/1/10	0.060708626	
GO:0021854	GO:0021854	hypothalamus development	The progression of the hypothalamus region of the forebrain, from its initial format	RAB3GAP1	7.14/1/4	8.33/1/2	0.068180864	
GO:0046415	GO:0046415	urate metabolic process	The chemical reactions and pathways involving urate, the anion of uric acid, 2,6,8-tri	ABCG2	7.14/1/4	8.33/1/2	0.068180864	
GO:0046416	GO:0046416	ether lipid metabolic process	The chemical reactions and pathways involving ether lipids, lipids that contain (norm	FASN	7.14/1/4	8.33/1/2	0.068180864	
GO:0097254	GO:0097254	retinoid biosynthetic process	The elimination of substances from peritubular capillaries (or surrounding hemolym	ABCG2	7.14/1/4	8.33/1/2	0.068180864	
GO:0016236	GO:0016236	macroautophagy	The major inducible pathway for the general turnover of cytoplasmic constituents i	RAB3GAP1 RAB3GAP2	14.29/2/14	0.98/2/105	0.06999336	
GO:0033538	GO:0033538	regulation of peroxisome proliferator activated receptor signaling pathway	Any process that modulates the frequency, rate or extent of the peroxisome prolifer	ALOX15	7.14/1/4	7.69/1/3	0.071566786	
GO:0090150	GO:0090150	establishment of protein localization to membrane	The directed movement of a protein to a specific location in a membrane.	RAB3GAP1 RAB3GAP2	14.29/2/14	0.94/2/122	0.072397073	
GO:0045184	GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location.	MYO6 RAB3GAP1 RAB3GAP2 SURF4	28.57/4/14	0.31/4/1286	0.072487065	
GO:0010232	GO:0010232	vascular transport	The directed movement of substances, into, out of or within a cell, either in a vascu	ABCG2	7.14/1/4	7.14/1/4	0.072487065	
GO:0042759	GO:0042759	long-chain fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formation of long-chain fatty a	ALOX15	7.14/1/4	6.67/1/15	0.072487065	
GO:0042953	GO:0042953	lipoprotein transport	The directed movement of any conjugated, water-soluble protein in which the nonpr	SURF4	7.14/1/4	6.67/1/15	0.072487065	
GO:0006662	GO:0006662	glycerol ether metabolic process	The chemical reactions and pathways involving glycerol ethers, any anhydride forme	FASN	7.14/1/4	6.67/1/15	0.072487065	
GO:0015014	GO:0015014	transport across blood-brain barrier	The directed movement of substances (e.g. macromolecules, small molecules, ions) fr	FASN	7.14/1/4	7.14/1/4	0.072487065	
GO:0015993	GO:0015993	coenzyme A biosynthetic process	The chemical reactions and pathways involving coenzyme A, 3'-phosphatidylethanol	COASY	7.14/1/4	7.14/1/4	0.072487065	
GO:0044872	GO:0044872	lipoprotein localization	Any process in which a lipoprotein is transported to, or maintained in, a specific loc	SURF4	7.14/1/4	6.67/1/15	0.072487065	
GO:0010506	GO:0010506	regulation of autophagy	Any process that modulates the frequency, rate or extent of autophagy. Autophagy i	RAB3GAP1 RAB3GAP2	14.29/2/14	0.87/2/129	0.073862879	
GO:0046394	GO:0046394	carboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of carboxylic acids, a	ALOX15 FASN	14.29/2/14	0.84/2/239	0.07906213	
GO:0016053	GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the formation of organic acids, any	ALOX15 FASN	14.29/2/14	0.83/2/242	0.079950159	
GO:0018279	GO:0018279	protein N-linked glycosylation via asparagine	The glycosylation of protein via the N4 atom of peptidyl-asparagine forming N4-gly	RPN1	7.14/1/4	5.26/1/19	0.085894731	
GO:0033537	GO:0033537	peroxisome proliferator activated receptor signaling pathway	The series of molecular signals initiated by binding of a ligand to any of the peroxis	ALOX15	7.14/1/4	5.26/1/19	0.085894731	
GO:0018196	GO:0018196	peptidyl-asparagine modification	The modification of peptidyl-asparagine.	RPN1	7.14/1/4	5.00/1/20	0.086030352	
GO:0018904	GO:0018904	ether metabolic process	The chemical reactions and pathways involving organic ethers, any anhydride of the f	FASN	7.14/1/4	5.00/1/20	0.086030352	
GO:0043652	GO:0043652	engulfment of apoptotic cell	The removal of the apoptotic cell by phagocytosis, by a neighboring cell or by a ph	ALOX15	7.14/1/4	5.00/1/20	0.086030352	
GO:0034389	GO:0034389	lipid droplet organization	A process that is carried out at the cellular level which results in the assembly, arr	RAB3GAP1	7.14/1/4	5.00/1/20	0.086030352	
GO:0071353	GO:0071353	cellular response to interleukin-4	Any process that results in a change in state or activity of a cell (in terms of movem	FASN	7.14/1/4	4.76/1/21	0.087152618	
GO:0044087	GO:0044087	regulation of cellular component biogenesis	Any process that modulates the frequency, rate or extent of cellular component biog	ALOX15 RAB3GAP1 RAB3GAP2	21.43/3/14	0.39/3/762	0.087152618	
GO:1901570	GO:1901570	fatty acid derivative biosynthetic process	The chemical reactions and pathways resulting in the formation of fatty acid derivati	ALOX15	7.14/1/4	4.76/1/21	0.087152618	
GO:0002068	GO:0002068	glandular epithelial cell development	The process whose specific outcome is the progression of a glandular epithelial cell	FASN	7.14/1/4	4.55/1/22	0.088085295	
GO:0070670	GO:0070670	response to interleukin-4	Any process that results in a change in state or activity of a cell or organism (in t	FASN	7.14/1/4	4.55/1/22	0.088085295	
GO:0006082	GO:0006082	organic acid metabolic process	The chemical reactions and pathways involving organic acids, any acidic compound c	ABCG2 ALOX15 FASN	21.43/3/14	0.39/3/774	0.088085295	
GO:								

GO:0006911	phagocytosis, engulfment	The internalization of bacteria, immune complexes and other particulate matter or o ALOX15	7.14 1/14	1.61 1/62	0.162969827
GO:0006487	protein N-linked glycosylation	A protein glycosylation process in which a carbohydrate or carbohydrate derivative u RPN1	7.14 1/14	1.59 1/63	0.163110603
GO:2000112	regulation of cellular macromolecule biosynthetic process	Any process that modulates the frequency, rate or extent of cellular macromolecule i RAB3GAP1 RAB3GAP2	14.29 2/14	0.42 2/480	0.163110603
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the formation of an organic substal ALOX15 COASY FASN MYO6 RAB3GAP1	50.00 7/14	0.14 7/1565	0.165118173
GO:0051234	establishment of localization	Any process that localizes a substance or cellular component. This may occur via mo ABCG2 ALOX15 MYO6 RAB3GAP1 RAB3	42.86 6/14	0.15 6/4033	0.165746843
GO:0021761	limbic system development	The progression of the limbic system over time from its initial formation until its mat RAB3GAP1	7.14 1/14	1.49 1/67	0.167845322
GO:0031399	regulation of protein modification process	Any process that modulates the frequency, rate or extent of the covalent alteration c RAB3GAP1 RAB3GAP2 STK38	21.43 3/14	0.25 3/1192	0.167845322
GO:0003014	renal system process	A organ system process carried out by any of the organs or tissues of the renal syste ABCG2	7.14 1/14	1.45 1/69	0.167845322
GO:0001676	long-chain fatty acid metabolic process	The chemical reactions and pathways involving long-chain fatty acids, A long-chain fa ALOX15	7.14 1/14	1.47 1/68	0.167845322
GO:0009058	biochemical process	The chemical reactions and pathways resulting in the formation of substances; typica ALOX15 COASY FASN MYO6 RAB3GAP1	50.00 7/14	0.13 7/5231	0.167845322
GO:0050764	regulation of phagocytosis	Any process that modulates the frequency, rate or extent of phagocytosis, the proces ALOX15	7.14 1/14	1.49 1/67	0.167845322
GO:0051049	regulation of transport	Any process that modulates the frequency, rate or extent of the directed movement ALOX15 MYO6 SURF4	21.43 3/14	0.25 3/1201	0.167845322
GO:0099024	plasma membrane invagination	An infolding of the plasma membrane. ALOX15	7.14 1/14	1.43 1/70	0.168444318
GO:0032273	positive regulation of protein polymerization	Any process that activates or increases the frequency, rate or extent of the process o ALOX15	7.14 1/14	1.41 1/71	0.168444318
GO:0012777	cellular response to calcium ion	Any process that results in a change in state or activity of a cell (in terms of moveme ALOX15	7.14 1/14	1.41 1/71	0.168444318
GO:0002065	columns/subodil epithelial cell differentiation	The process in which a relatively unspecialized cell acquires specialized features of a FASN	7.14 1/14	1.39 1/72	0.169653974
GO:1901137	carbohydrate derivative biosynthetic process	The chemical reactions and pathways resulting in the formation of carbohydrate deri COASY RPN1	14.29 2/14	0.38 2/521	0.170716373
GO:0008610	lipid biosynthetic process	The chemical reactions and pathways resulting in the formation of lipids, compounds ALOX15 FASN	14.29 2/14	0.38 2/525	0.170799473
GO:0043408	regulation of MAPK cascade	Any process that modulates the frequency, rate or extent of signal transduction me ALOX15 STK38	14.29 2/14	0.38 2/524	0.170799473
GO:0010324	membrane invagination	The infolding of a membrane. ALOX15	7.14 1/14	1.32 1/76	0.17417539
GO:0051668	localization within membrane	Any process in which a substance or cellular entity, such as a protein complex or orgi RAB3GAP1 RAB3GAP2	14.29 2/14	0.37 2/541	0.177896317
GO:0045446	endothelial cell differentiation	The process in which a mesodermal, bone marrow or neural crest cell acquires speci FASN	7.14 1/14	1.23 1/81	0.181772047
GO:0016192	vesicle-mediated transport	A cellular transport process in which transported substances are moved in membran ALOX15 MYO6 SURF4	21.43 3/14	0.24 3/1276	0.181772047
GO:0033875	ribonucleoside bisphosphate metabolic process	The chemical reactions and pathways involving a ribonucleoside bisphosphate, a conr COASY	7.14 1/14	1.16 1/86	0.184448033
GO:0012935	fatty acid catabolism	The removal of one or more electrons from a fatty acid, with or without the concomit ALOX15	7.14 1/14	1.19 1/84	0.184448033
GO:0006692	icosanoid metabolic process	The chemical reactions and pathways involving icosanoids, any of a group of C20 poly ALOX15	7.14 1/14	1.16 1/86	0.184448033
GO:0032368	regulation of lipid transport	Any process that modulates the frequency, rate or extent of the directed movement SURF4	7.14 1/14	1.19 1/84	0.184448033
GO:0034032	purine nucleoside bisphosphate metabolic process	The chemical reactions and pathways involving a purine nucleoside bisphosphate, a c COASY	7.14 1/14	1.16 1/86	0.184448033
GO:0033865	nucleoside bisphosphate metabolic process	The chemical reactions and pathways involving a nucleoside bisphosphate, a compou COASY	7.14 1/14	1.16 1/86	0.184448033
GO:0071901	negative regulation of protein serine/threonine kinase activity	Any process that decreases the rate, frequency, or extent of protein serine/threonin STK38	7.14 1/14	1.19 1/84	0.184448033
GO:0036211	protein modification process	The covalent alteration of one or more amino acids occurring in proteins, peptides at RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	35.71 5/14	0.15 5/3236	0.188120909
GO:0010811	positive regulation of cell-substrate adhesion	Any process that increases the frequency, rate or extent of cell-substrate adhesion. C ALOX15	7.14 1/14	1.11 1/90	0.188120909
GO:0003158	endothelium development	The process whose specific outcome is the progression of an endothelium over time, FASN	7.14 1/14	1.12 1/89	0.188120909
GO:0006464	cellular protein modification process	The covalent alteration of one or more amino acids occurring in proteins, peptides at RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	35.71 5/14	0.15 5/3236	0.188120909
GO:0014440	lipid oxidation	The removal of one or more electrons from a lipid, with or without the concomitant ALOX15	7.14 1/14	1.10 1/91	0.190918224
GO:0001655	MAPK cascade	An intracellular protein kinase cascade containing at least a MAPK, a MAPKK and a M ALOX15 STK38	14.29 2/14	0.34 2/591	0.189706905
GO:0033559	unsaturated fatty acid metabolic process	The chemical reactions and pathways involving an unsaturated fatty acid, any fatty ac ALOX15	7.14 1/14	1.08 1/93	0.190777301
GO:0030282	bone mineralization	The deposition of hydroxyapatite, a form of calcium phosphate with the formula Ca1 ALOX15	7.14 1/14	1.05 1/95	0.193616032
GO:0031329	regulation of cellular catabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions a RAB3GAP1 RAB3GAP2	14.29 2/14	0.33 2/613	0.198814088
GO:0051592	response to calcium ion	Any process that results in a change in state or activity of a cell or an organism (in ter ALOX15	7.14 1/14	0.96 1/104	0.208903999
GO:1990748	cellular detoxification	Any process carried out at the cellular level that reduces or removes the toxicity of a ABCG2	7.14 1/14	0.95 1/105	0.209633292
GO:0097237	cellular response to toxic substance	Any process that results in a change in state or activity of a cell (in terms of moveme ABCG2	7.14 1/14	0.91 1/110	0.21050944
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism and catabolism, by which ABCG2 ALOX15 COASY FASN MYO6 RAE	85.71 12/14	0.09 12/1291	0.21050944
GO:1909592	regulation of lipid localization	Any process that modulates the frequency, rate or extent of lipid localization. SURF4	7.14 1/14	0.91 1/110	0.21050944
GO:0034645	cellular macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formation of a macromolecule RAB3GAP1 RAB3GAP2 RPN1	21.43 3/14	0.21 3/449	0.21050944
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units in a polypeptide, polynucle RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	35.71 5/14	0.15 5/3413	0.21050944
GO:0071345	cellular response to cytokine stimulus	Any process that results in a change in state or activity of a cell (in terms of moveme ALOX15 FASN	14.29 2/14	0.30 2/660	0.21050944
GO:0120254	olefinic compound metabolic process	The chemical reactions and pathways involving an olefinic compound, any compound ALOX15	7.14 1/14	0.89 1/112	0.21050944
GO:0070730	Golgi organization	A process that is carried out at the cellular level which results in the assembly, arrang SURF4	7.14 1/14	0.88 1/113	0.21050944
GO:0072331	signal transduction by p53 class mediator	An intracellular signaling process that is induced by the cell cycle regulator phospho MYO6	7.14 1/14	0.90 1/111	0.21050944
GO:0033036	macromolecule localization	Any process in which a macromolecule is transported to, or maintained in, a specific MYO6 RAB3GAP1 RAB3GAP2 SURF4	28.57 4/14	0.17 2/363	0.21050944
GO:0030879	mammary gland development	The process whose specific outcome is the progression of the mammary gland over t FASN	7.14 1/14	0.89 1/112	0.21050944
GO:0050777	negative regulation of immune response	Any process that stops, prevents, or reduces the frequency, rate or extent of the immr ALOX15	7.14 1/14	0.88 1/113	0.21050944
GO:0035554	cellular response to stress	Any process that results in a change in state or activity of a cell (in terms of moveme ALOX15 MYO6 UBA1	21.43 3/14	0.21 3/463	0.211100224
GO:0006974	cellular response to DNA damage stimulus	Any process that results in a change in state or activity of a cell (in terms of moveme MYO6 UBA1	14.29 2/14	0.30 2/668	0.211936623
GO:0098754	detoxification	Any process that reduces or removes the toxicity of a toxic substance. These may incl ABCG2	7.14 1/14	0.85 1/118	0.215988336
GO:0050588	lipid homeostasis	Any process involved in the maintenance of an internal steady state of lipid within ar SURF4	7.14 1/14	0.83 1/120	0.21835313
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those compounds which are formed i ALOX15 COASY FASN MYO6 RAB3GAP1	78.57 11/14	0.10 11/1142	0.22137561
GO:0031214	biomineral tissue development	Formation of hard tissues that consist mainly of inorganic compounds, and also cont ALOX15	7.14 1/14	0.80 1/125	0.22355731
GO:0007605	sensory perception of sound	The series of events required for an organism to receive an auditory stimulus, conver MYO6	7.14 1/14	0.80 1/125	0.22355731
GO:1901564	organonitrogen compound metabolic process	The chemical reactions and pathways involving organonitrogen compound. COASY RAB3GAP1 RAB3GAP2 RPN1 STK	50.00 7/14	0.12 7/5915	0.223755991
GO:0110148	biomineralization	The process where mineral crystals are formed and deposited in an organized fashio ALOX15	7.14 1/14	0.79 1/127	0.223755991
GO:0043409	negative regulation of MAPK cascade	Any process that stops, prevents, or reduces the frequency, rate or extent of signal t STK38	7.14 1/14	0.79 1/127	0.223755991
GO:0034097	response to cytokine	Any process that results in a change in state or activity of a cell or an organism (in ter ALOX15 FASN	14.29 2/14	0.28 2/713	0.224681351
GO:0003015	vascular smooth muscle contractile system	A circulatory process that occurs at the level of the vasculature. ABCG2	7.14 1/14	0.78 1/129	0.24681351
GO:0031010	regulation of endocytosis	Any process that modulates the frequency, rate or extent of endocytosis. ALOX15	7.14 1/14	0.77 1/130	0.251128826
GO:0071248	cellular response to metal ion	Any process that results in a change in state or activity of a cell (in terms of moveme ALOX15	7.14 1/14	0.76 1/131	0.225654031
GO:0030833	regulation of actin filament polymerization	Any process that modulates the frequency, rate or extent of the assembly of actin fil ALOX15	7.14 1/14	0.76 1/132	0.22617294
GO:0022900	electron transport chain	A process in which a series of electron carriers operate together to transfer electrons SDHA	7.14 1/14	0.75 1/133	0.22668565
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic acids, any organic acid con ALOX15 FASN	14.29 2/14	0.27 2/736	0.226949411
GO:0044237	cellular metabolic process	The chemical reactions and pathways by which individual cells transform chemical su ABCG2 ALOX15 COASY FASN MYO6 RAE	78.57 11/14	0.09 11/1158	0.226949411
GO:0050954	sensory perception of mechanical stimulus	The series of events required for an organism to receive a sensory mechanical stimul MYO6	7.14 1/14	0.74 1/136	0.226949411
GO:0033365	protein localization to organelle	A process in which a protein is transported to, or maintained in, a location within a RAB3GAP1 RAB3GAP2	14.29 2/14	0.27 2/729	0.226949411
GO:0009894	regulation of catabolic process	Any process that modulates the frequency, rate, or extent of the chemical reactions i RAB3GAP1 RAB3GAP2	14.29 2/14	0.27 2/729	0.226949411
GO:0071700	nitrogen compound transport	The directed movement of nitrogen-containing compounds into, out of or within a ce ABCG2 MYO6 SURF4	21.43 3/14	0.19 1/267	0.228405969
GO:0043436	oxoacid metabolic process	The chemical reactions and pathways involving any oxoacid: an oxoacid is a compou ALOX15 FASN	14.29 2/14	0.27 2/745	0.228405969
GO:0043405	regulation of MAP kinase activity	Any process that modulates the frequency, rate or extent of MAP kinase activity. STK38	7.14 1/14	0.72 1/139	0.228405969
GO:1902905	positive regulation of supramolecular fiber organization	Any process that activates or increases the frequency, rate or extent of supramolecul ALOX15	7.14 1/14	0.70 1/142	0.229327675
GO:0071241	cellular response to inorganic substance	Any process that results in a change in state or activity of a cell (in terms of moveme ALOX15	7.14 1/14	0.70 1/143	0.229327675
GO:0031328	positive regulation of cellular biosynthetic process	Any process that activates or increases the frequency, rate or extent of the chemical MYO6 RAB3GAP1 RAB3GAP2	21.43 3/14	0.19 3/1596	0.229327675
GO:0042770	signal transduction in response to DNA damage	A cascade of processes induced by the detection of DNA damage within a cell. MYO6	7.14 1/14	0.70 1/143	0.229327675
GO:0070734	positive regulation of ERK1 and ERK2 cascade	Any process that activates or increases the frequency, rate or extent of signal transd ALOX15	7.14 1/14	0.68 1/147	0.230065715
GO:0008064	regulation of actin polymerization or depolymerization	Any process that modulates the frequency, rate or extent of the assembly or disasse ALOX15	7.14 1/14	0.68 1/147	0.230065715
GO:0003152	purine ribonucleotide biosynthetic process	The chemical reactions and pathways resulting in the formation of a purine ribonucle COASY	7.14 1/14	0.68 1/146	0.230065715
GO:0008981	positive regulation of biosynthetic process	Any process that activates or increases the frequency, rate or extent of the chemical MYO6 RAB3GAP1 RAB3GAP2	21.43 3/14	0.19 3/1617	0.230065715
GO:0030832	regulation of actin filament length	Any process that controls the length of actin filaments in a cell. ALOX15	7.14 1/14	0.68 1/147	0.230065715
GO:0031334	positive regulation of protein-containing complex assembly	Any process that activates or increases the frequency, rate or extent of protein comp ALOX15	7.14 1/14	0.68 1/148	0.230504212
GO:0030041	actin filament polymerization	Assembly of actin filaments by the addition of actin monomers to a filament. ALOX15	7.14 1/14	0.67 1/149	0.230576642
GO:0031401	positive regulation of protein modification process	Any process that activates or increases the frequency, rate or extent of the covalent i RAB3GAP1 RAB3GAP2	14.29 2/14	0.26 2/774	0.230576642
GO:0002819	regulation of adaptive immune response	Any process that modulates the frequency, rate, or extent of an adaptive immune re ALOX15	7.14 1/14	0.66 1/151	0.230756068
GO:0009636	response to toxic substance	Any process that results in a change in state or activity of a cell or an organism (in ter ABCG2	7.14 1/14	0.66 1/151	0.230756068
GO:0006469	negative regulation of protein kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of protein STK38	7.14 1/14	0.63 1/158	0.232606043
GO:0051495	positive regulation of cytokinesis organization	Any process that activates or increases the frequency, rate or extent of the formation ALOX15	7.14 1/14	0.63 1/158	0.232606043
GO:0070921	organellar arrangement and bonding together of a set of components to form ALOX15	The aggregation, arrangement and bonding together of a set of components to form ALOX15 RAB3GAP1 RAB3GAP2	14.29 2/14	0.24 2/785	0.232606043
GO:0046474	glycerophospholipid biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerophospholip ALOX15	7.14 1/14	0.64 1/156	0.232606043
GO:0009260	ribonucleoside bisphosphate synthesis	The chemical reactions and pathways resulting in the formation of a ribonucleoside, i COASY	7.14 1/14	0.63 1/158	0.232606043
GO:0010810	regulation of cell-substrate adhesion	Any process that modulates the frequency, rate or extent of cell-substrate adhesion. ALOX15	7.14 1/14	0.65 1/155	0.232606043
GO:0002573	myeloid leukocyte differentiation	The process in which a relatively unspecialized myeloid precursor cell acquires the sp FASN	7.14 1/14	0.64 1/157	0.232606043
GO:0019637	organophosphate metabolic process	The chemical reactions and pathways involving organophosphates, any phosphate-co ALOX15 COASY	14.29 2/14	0.25 2/793	0.232606043
GO:0002064	epithelial cell development	The process whose specific outcome is the progression of an epithelial cell over time FASN	7.14 1/14	0.62 1/161	0.2357793
GO:0006164	purine nucleotide biosynthetic process	The chemical reactions and pathways resulting in the formation of a purine nucleotic COASY	7.14 1/14	0.61 1/163	0.237536347
GO:0051336	regulation of hydrolase activity	Any process that modulates the frequency, rate or extent of hydrolase activity, the c RAB3GAP1 RAB3GAP2	14.29 2/14	0.24 2/819	0.238615353
GO:0046390	ribose phosphate biosynthetic process	The chemical reactions and pathways resulting in the formation of ribose phosphate, COASY	7.14 1/14	0.61 1/165	0.238615353
GO:0009060	aerobic respiration	The enzymatic release of energy from inorganic and organic compounds (especially i SDHA	7.14 1/14	0.59 1/169	0.242657197
GO:0072522	purine-containing compound biosynthetic process	The chemical reactions and pathways resulting in the formation of a purine-containi COASY	7.14 1/14	0.58 1/172	0.244704036
GO:0033673	negative regulation of kinase activity	Any process that stops, prevents, or reduces the frequency, rate or extent of kinase t STK38	7.14 1/14	0.58 1/172	0.244704036
GO:0008154	actin polymerization or depolymerization	Assembly or disassembly of actin filaments by the addition or removal of actin mono ALOX15	7.14 1/14	0.57 1/174	0.246360704
GO:1901617	organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the formation of organic hydroxy c ALOX15	7.14 1/14	0.57 1/175	0.246669939
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as carried out by individual cell ALOX15 FASN	14.29 2/14	0.23 2/852	0.248595335
GO:0032271	regulation of protein polymerization	Any process that modulates the frequency, rate or extent of the process of creating a ALOX15	7.14 1/14	0.56 1/178	0.248595335
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. Includes protein modifiat RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	42.86 6/14	0.12 6/5108	0.251179609
GO:1901335	carbohydrate derivative metabolic process	The chemical reactions and pathways involving carbohydrate derivative. COASY RPN1	14.29 2/14	0.23 2/870	0.254247743
GO:0008654	phosphoglipid biosynthetic process	The chemical reactions and pathways resulting in the formation of a phosphoglipid, a ALOX15	7.14 1/14	0.54 1/185	0.254651631
GO:0030258	lipid modification	The covalent alteration of one or more fatty acids in a lipid, resulting in a change in ALOX15	7.14 1/14	0.53 1/187	0.254651631
GO:0006909	phagocytosis	A vesicle-mediated transport process that results in the engulfment of external parti ALOX15	7.14 1/14	0.53 1/188	0.256448824
GO:0045017	glycerolipid biosynthetic process	The chemical reactions and pathways resulting in the formation of glycerolipids, any ALOX15	7.14 1/14	0.53 1/190	0.257971654
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the breakdown of substances, carri RAB3GAP1 RAB3GAP2 UBA1	21.43 3/14	0.17 3/1814	0.26021517
GO:0010038	response to metal ion	Any process that results in a change in state or activity of a cell or an organism (in ter ALOX15	7.14 1/14	0.52 1/194	0.260971001
GO:0051348	negative regulation of transferase activity	Any process that stops or reduces the rate of transferase activity, the catalysis of the STK38	7.14 1/14	0.51 1/196	0.262447894
GO:0043413	macromolecule glycosylation	The covalent attachment of a glycosyl residue to one or more monomeric units in a p RPN1	7.14 1/14	0.49 2/203	0.269802663
GO:0006486	protein glycosylation	A protein modification process that results in the addition of a carbohydrate or carb RPN1	7.14 1/14	0.49 2/203	0.269802663
GO:00					

GO:0110053	regulation of actin filament organization	Any process that modulates the frequency, rate or extent of actin filament organization	ALOX15	7.14 1/14	0.43 1/231	0.2865579
GO:0051258	protein polymerization	The process of creating protein polymers, compounds composed of a large number of	C ALOX15	7.14 1/14	0.43 2/234	0.28786274
GO:0071702	organic substance transport	The directed movement of organic substances into, out of or within a cell, or between	ABCG2 MYO6 SURF4	21.43 3/14	0.15 3/1968	0.28786274
GO:0001933	negative regulation of protein phosphorylation	Any process that stops, prevents or reduces the rate of addition of phosphate groups	STK38	7.14 1/14	0.41 1/242	0.295857355
GO:0051246	regulation of protein metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions a	RAB3GAP1 RAB3GAP2 STK38	21.43 3/14	0.15 5/2025	0.30377112
GO:0030900	forebrain development	The process whose specific outcome is the progression of the forebrain over time	RAB3GAP1	7.14 1/14	0.38 1/260	0.310489732
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a cell (in terms of movem	ABCG2 ALOX15 FASN GNG12 MYO6 STK	50.00 7/14	0.10 7/6878	0.310489732
GO:0042060	wound healing	The series of events that restore integrity to a damaged tissue, following an injury.	ALOX15	7.14 1/14	0.38 2/260	0.310489732
GO:0032879	regulation of localization	Any process that modulates the frequency, rate or extent of any process in which a	C ALOX15 MYO6 SURF4	21.43 3/14	0.15 5/2025	0.310489732
GO:0006650	glycerophospholipid metabolic process	The chemical reactions and pathways involving glycerophospholipids, any deriva	ALOX15	7.14 1/14	0.38 2/262	0.31060407
GO:0043010	camera-type eye development	The process whose specific outcome is the progression of the camera-type eye o	RAB3GAP1	7.14 1/14	0.38 1/264	0.31106407
GO:0032270	positive regulation of cellular protein metabolic process	Any process that activates or increases the frequency, rate or extent of the chemi	RAB3GAP1 RAB3GAP2	14.29 2/14	0.19 1/1072	0.31106407
GO:0009101	glycoprotein biosynthetic process	The chemical reactions and pathways resulting in the formation of glycoproteins, a	p RPN1	7.14 1/14	0.38 2/263	0.31106407
GO:0031589	cell-substrate adhesion	The attachment of a cell to the underlying substrate via adhesion molecules.	ALOX15	7.14 1/14	0.37 1/268	0.313430852
GO:0042326	negative regulation of phosphorylation	Any process that stops, prevents or decreases the rate of addition of phosphate gro	STK38	7.14 1/14	0.37 1/271	0.314677943
GO:0035555	intracellular signal transduction	The process in which a signal is passed on to downstream components within the cell	ALOX15 MYO6 STK38	21.43 3/14	0.14 3/2097	0.314677943
GO:0000956	catabolic process	The chemical reactions and pathways resulting in the breakdown of substances, inclu	RAB3GAP1 RAB3GAP2 UBA1	21.43 3/14	0.14 3/2106	0.316443963
GO:0015980	energy derivation by oxidation of organic compounds	The chemical reactions and pathways by which a cell derives energy from organic c	SDHA	7.14 1/14	0.36 1/280	0.321660933
GO:0032535	regulation of cellular component size	A process that modulates the size of a cellular component.	ALOX15	7.14 1/14	0.35 1/289	0.321965047
GO:0071900	regulation of protein serine/threonine kinase activity	Any process that modulates the rate, frequency, or extent of protein serine/threoni	STK38	7.14 1/14	0.35 1/282	0.321965047
GO:0030099	myeloid cell differentiation	The process in which a relatively unspecialized myeloid precursor cell acquires the	sp FASN	7.14 1/14	0.34 1/290	0.321965047
GO:0006629	lipid metabolic process	The chemical reactions and pathways involving lipids, compounds soluble in an org	ALOX15 FASN	14.29 2/14	0.18 2/1124	0.321965047
GO:0018193	peptidyl-amino acid modification	The alteration of an amino acid residue in a peptide.	RPN1 STK38	14.29 2/14	0.18 2/1125	0.321965047
GO:0018105	peptidyl-serine phosphorylation	The phosphorylation of peptidyl-serine to form peptidyl-O-phospho-L-serine.	STK38	7.14 1/14	0.35 1/284	0.321965047
GO:0048522	positive regulation of cellular process	Any process that activates or increases the frequency, rate or extent of a cellular	pro ALOX15 MYO6 RAB3GAP1 RAB3GAP2 S	35.71 5/14	0.11 5/4480	0.321965047
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific protein, rather than of pro	RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	35.71 5/14	0.11 5/4464	0.321965047
GO:0015003	ossification	The formation of bone or of a bony substance, or the conversion of fibrous tissue o	ALOX15	7.14 1/14	0.35 1/289	0.321965047
GO:0002683	negative regulation of immune system process	Any process that stops, prevents, or reduces the frequency, rate, or extent of an im	ALOX15	7.14 1/14	0.34 1/294	0.324892169
GO:0051247	positive regulation of protein metabolic process	Any process that activates or increases the frequency, rate or extent of the chemi	RAB3GAP1 RAB3GAP2	14.29 2/14	0.17 2/1145	0.325252644
GO:0032956	regulation of actin cytoskeleton organization	Any process that modulates the frequency, rate or extent of the formation, arrang	ALOX15	7.14 1/14	0.34 1/296	0.325252644
GO:0006996	organelle organization	A process that is carried out at the cellular level which results in the assembly, arr	ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57 4/14	0.12 4/3330	0.327557611
GO:0009150	purine ribonucleotide metabolic process	The chemical reactions and pathways involving a purine ribonucleotide, a compound	COASY	7.14 1/14	0.33 1/301	0.327557611
GO:0015711	organic anion transport	The directed movement of organic anions into, out of or within a cell, or between	ABCG2	7.14 1/14	0.33 1/306	0.328008547
GO:0048732	gland development	The process whose specific outcome is the progression of a gland over time, from its	FASN	7.14 1/14	0.33 1/306	0.328008547
GO:0010035	response to inorganic substance	Any process that decreases the frequency, rate or extent of the chemical reactions	AT STK38	7.14 1/14	0.31 1/321	0.328008547
GO:0018209	peptidyl-serine modification	The modification of peptidyl-serine.	STK38	7.14 1/14	0.33 1/306	0.328008547
GO:0001654	eye development	The process whose specific outcome is the progression of the eye over time, from	its RAB3GAP1	7.14 1/14	0.32 1/309	0.329825804
GO:0015063	visual system development	The process whose specific outcome is the progression of the visual system over t	ime RAB3GAP1	7.14 1/14	0.32 1/312	0.331625508
GO:0045936	negative regulation of phosphate metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of the	che STK38	7.14 1/14	0.31 1/321	0.332874665
GO:0002250	adaptive immune response	An immune response mediated by cells expressing specific receptors for antigen	pro ALOX15	7.14 1/14	0.31 1/325	0.332874665
GO:1902903	regulation of supramolecular fiber organization	Any process that modulates the frequency, rate or extent of supramolecular fib	or ALOX15	7.14 1/14	0.32 1/315	0.332874665
GO:0019693	ribose phosphate metabolic process	The chemical reactions and pathways involving ribose phosphate, any phosphoryla	te COASY	7.14 1/14	0.31 1/327	0.332874665
GO:0006163	purine nucleotide metabolic process	The chemical reactions and pathways involving a purine nucleotide, a compound con	COASY	7.14 1/14	0.31 1/323	0.332874665
GO:0009611	response to wounding	Any process that results in a change in state or activity of a cell or an organism (in	ter ALOX15	7.14 1/14	0.31 1/326	0.332874665
GO:0010563	negative regulation of phosphorus metabolic process	Any process that decreases the frequency, rate or extent of the chemical reactions	AT STK38	7.14 1/14	0.31 1/321	0.332874665
GO:0032970	regulation of actin filament-based process	Any process that modulates the frequency, rate or extent of any cellular process th	at ALOX15	7.14 1/14	0.31 1/324	0.332874665
GO:0048880	sensory system development	The process whose specific outcome is the progression of a sensory system over t	ime RAB3GAP1	7.14 1/14	0.32 1/317	0.332874665
GO:0009100	glycoprotein metabolic process	The chemical reactions and pathways involving glycoproteins, a protein that conta	ins RPN1	7.14 1/14	0.31 1/325	0.332874665
GO:0015031	protein transport	The directed movement of proteins into, out of or within a cell, or between cells,	by MYO6 SURF4	14.29 2/14	0.17 2/1193	0.332874665
GO:0009259	ribonucleotide metabolic process	The chemical reactions and pathways involving a ribonucleotide, a compound consi	st COASY	7.14 1/14	0.31 1/318	0.332874665
GO:0043254	regulation of protein-containing complex assembly	Any process that modulates the frequency, rate or extent of protein complex assem	bl ALOX15	7.14 1/14	0.30 1/330	0.334559013
GO:0006869	lipid transport	The directed movement of lipids into, out of or within a cell, or between cells, b	y SURF4	7.14 1/14	0.30 1/332	0.335324138
GO:0048585	negative regulation of response to stimulus	Any process that stops, prevents, or reduces the frequency, rate or extent of a res	po ALOX15 STK38	14.29 2/14	0.16 2/1236	0.338624273
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipids, any lipid containi	ng ALOX15	7.14 1/14	0.30 1/338	0.338624273
GO:0003013	circulatory system process	A organ system process carried out by any of the organs or tissues of the circula	tory ABCG2	7.14 1/14	0.29 1/342	0.341139127
GO:0045785	positive regulation of cell adhesion	Any process that activates or increases the frequency, rate or extent of cell adhe	sion ALOX15	7.14 1/14	0.29 1/345	0.342402026
GO:0046486	glycerolipid metabolic process	The chemical reactions and pathways involving glycerolipids, any lipid with a	glycerol ALOX15	7.14 1/14	0.29 1/347	0.342402026
GO:0072521	purine-containing compound metabolic process	The chemical reactions and pathways involving a purine-containing compound, i.e.	at COASY	7.14 1/14	0.29 1/346	0.342402026
GO:1903131	mononuclear cell differentiation	The process in which a relatively unspecialized cell acquires the specialized fe	atures FASN	7.14 1/14	0.29 1/349	0.343106388
GO:1902531	regulation of intracellular signal transduction	Any process that modulates the frequency, rate or extent of intracellular signal	trans ALOX15 STK38	14.29 2/14	0.16 2/1270	0.346325081
GO:0070887	cellular response to chemical stimulus	Any process that results in a change in state or activity of a cell (in terms of	movem ABCG2 ALOX15 FASN	21.43 3/14	0.13 3/2376	0.351908037
GO:0010876	lipid localization	Any process in which a lipid is transported to, or maintained in, a specific locali	ty SURF4	7.14 1/14	0.27 1/373	0.358463952
GO:0043410	positive regulation of MAPK cascade	Any process that activates or increases the frequency, rate or extent of signal tra	ns ALOX15	7.14 1/14	0.27 1/373	0.358463952
GO:0006796	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the phosphate group, the anion or	ate ALOX15 COASY STK38	21.43 3/14	0.12 3/2404	0.358463952
GO:0031341	regulation of immune response	Any process that modulates the frequency, rate or extent of a defense respons	e ALOX15	7.14 1/14	0.29 1/342	0.351908037
GO:0090966	regulation of anatomical structure size	Any process that modulates the size of an anatomical structure.	ALOX15	7.14 1/14	0.26 1/379	0.360289038
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the nonmetallic element phosph	orus ALOX15 COASY STK38	21.43 3/14	0.12 3/2425	0.360289038
GO:0065009	regulation of molecular function	Any process that modulates the frequency, rate or extent of a molecular functio	n, an RAB3GAP1 RAB3GAP2 STK38	21.43 3/14	0.12 3/2439	0.362888591
GO:0060627	regulation of vesicle-mediated transport	Any process that modulates the rate, frequency, or extent of vesicle-mediated	transp ALOX15	7.14 1/14	0.26 1/385	0.362888591
GO:0006091	generation of precursor metabolites and energy	The chemical reactions and pathways resulting in the formation of precursor met	abolo SDHA	7.14 1/14	0.26 1/386	0.362888591
GO:0031400	negative regulation of protein modification process	Any process that stops, prevents, or reduces the frequency, rate or extent of the	cov STK38	7.14 1/14	0.26 1/388	0.36346474
GO:0007015	actin filament organization	A process that is carried out at the cellular level which results in the assembly,	arrang ALOX15	7.14 1/14	0.25 1/396	0.367859268
GO:0051173	organic regulation of nitrogen compound metabolic process	Any process that activates or increases the frequency, rate or extent of the chemi	cal ALOX15 RAB3GAP1 RAB3GAP2	21.43 3/14	0.12 3/2473	0.367859268
GO:0016515	organic hydroxy compound metabolic process	The chemical reactions and pathways involving organic hydroxy compound.	ALOX15	7.14 1/14	0.25 1/398	0.368465099
GO:0051047	regulation of enzyme response	Any process that modulates the frequency, rate or extent of the controlled rele	ase of MYO6	7.14 1/14	0.25 1/402	0.368465099
GO:0009117	nucleotide metabolic process	The chemical reactions and pathways involving a nucleotide, a nucleoside that is	este COASY	7.14 1/14	0.25 1/402	0.368465099
GO:0048518	positive regulation of biological process	Any process that activates or increases the frequency, rate or extent of a biolog	ical pr ALOX15 MYO6 RAB3GAP1 RAB3GAP2 S	35.71 5/14	0.10 5/4958	0.371419844
GO:0006753	nucleoside phosphate metabolic process	The chemical reactions and pathways involving any phosphorylated nucleoside.	COASY	7.14 1/14	0.24 1/412	0.37530594
GO:1902532	negative regulation of intracellular signal transduction	Any process that stops, prevents or reduces the frequency, rate or extent of intr	acell STK38	7.14 1/14	0.24 1/415	0.375695525
GO:0051345	positive regulation of hydrolase activity	Any process that activates or increases the frequency, rate or extent of hydrolase	act RAB3GAP1	7.14 1/14	0.24 1/420	0.379443534
GO:0051493	regulation of cytoskeleton organization	Any process that modulates the frequency, rate or extent of the formation, arrang	er ALOX15	7.14 1/14	0.23 1/437	0.387147008
GO:0009888	tissue development	The process whose specific outcome is the progression of a tissue over time, from	its ALOX15 FASN	14.29 2/14	0.14 2/1431	0.387147008
GO:0002521	leukocyte differentiation	The process in which a relatively unspecialized hemopoietic precursor cell acq	uires th FASN	7.14 1/14	0.23 1/437	0.387147008
GO:0070727	cellular macromolecule localization	Any process in which a macromolecule is transported to, and/or maintained in, a	spe RAB3GAP1 RAB3GAP2	14.29 2/14	0.14 2/1438	0.387147008
GO:0034613	cellular protein localization	Any process in which a protein is transported to, and/or maintained in, a specifi	loc RAB3GAP1 RAB3GAP2	14.29 2/14	0.14 2/1432	0.387147008
GO:0048513	animal organ development	Development of a tissue or tissues that work together to perform a specific func	tion ALOX15 FASN RAB3GAP1	21.43 3/14	0.11 3/2612	0.393979871
GO:0006820	anion transport	The directed movement of anions, atoms or small molecules with a net negative	char ABCG2	7.14 1/14	0.22 1/449	0.394057858
GO:0031325	positive regulation of cellular metabolic process	Any process that activates or increases the frequency, rate or extent of the chemi	cal MYO6 RAB3GAP1 RAB3GAP2	21.43 3/14	0.11 3/2631	0.397235582
GO:0007420	brain development	The process whose specific outcome is the progression of the brain over time, fr	om RAB3GAP1	7.14 1/14	0.22 1/463	0.401731499
GO:0006810	transport	The directed movement of substances (such as macromolecules, small molecules,	ion ABCG2 ALOX15 MYO6 SURF4	28.57 4/14	0.10 4/3886	0.401731499
GO:0007423	sensory organ development	The process whose specific outcome is the progression of sensory organs over t	ime RAB3GAP1	7.14 1/14	0.21 1/472	0.404447914
GO:0006954	inflammatory response	The immediate defensive reaction (by vertebrate tissue) to infection or injury caus	ed ALOX15	7.14 1/14	0.21 1/472	0.404447914
GO:0030855	epithelial cell differentiation	The process in which a relatively unspecialized cell acquires specialized featur	es of FASN	7.14 1/14	0.21 1/470	0.404447914
GO:0050986	nucleoside-containing small molecule metabolic process	The chemical reactions and pathways involving a nucleoside-containing small	molecule ALOX15	7.14 1/14	0.21 1/471	0.404960959
GO:0045859	regulation of protein kinase activity	Any process that modulates the frequency, rate or extent of protein kinase activi	ty STK38	7.14 1/14	0.20 1/496	0.419526731
GO:0050896	response to stimulus	Any process that results in a change in state or activity of a cell or an organism	(in ter ABCG2 ALOX15 FASN GNG12 MYO6 ST	50.00 7/14	0.09 7/9798	0.422196861
GO:0060322	head development	The biological process whose specific outcome is the progression of a head from	an RAB3GAP1	7.14 1/14	0.20 1/503	0.422196861
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, any molecule of	hig RAB3GAP1 RAB3GAP2 RPN1 STK38 UBA	35.71 5/14	0.09 5/5305	0.422907028
GO:0010604	positive regulation of macromolecule metabolic process	Any process that increases the frequency, rate or extent of the chemical reactio	ns ALOX15 MYO6 RAB3GAP1 RAB3GAP2	21.43 3/14	0.11 3/2795	0.431608859
GO:0006950	response to stress	Any process that results in a change in state or activity of a cell or an organis	(in ter ALOX15 MYO6 UBA1	21.43 3/14	0.11 3/2809	0.433232234
GO:0016310	phosphorylation	The process of introducing a phosphate group into a molecule, usually with the	form COASY STK38	14.29 2/14	0.12 2/1608	0.433232234
GO:0043086	negative regulation of catalytic activity	Any process that stops or reduces the activity of an enzyme.	STK38	7.14 1/14	0.18 1/555	0.452200249
GO:0006508	proteolysis	The hydrolysis of proteins into smaller polypeptides and/or amino acids by cleav	age UBA1 UQCRC2	14.29 2/14	0.12 2/1674	0.452200249
GO:0030155	regulation of cell adhesion	Any process that modulates the frequency, rate or extent of attachment of a cell	to ALOX15	7.14 1/14	0.17 1/573	0.461780117
GO:0043549	regulation of kinase activity	Any process that modulates the frequency, rate or extent of kinase activity, the	catal STK38	7.14 1/14	0.17 1/588	0.469810606
GO:0006511	ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the breakdown of a protein or	pept UBA1	7.14 1/14	0.17 1/589	0.469810606
GO:0019941	modification-dependent protein catabolic process	The				

GO:0051248	negative regulation of protein metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of chemical	STK38	7.14	1/14	0.12	1/839	0.572619405
GO:008090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	A MYO6 RAB3GAP1 RAB3GAP2 STK38	28.57	4/14	0.08	4/4857	0.572619405
GO:0043085	positive regulation of catalytic activity	Any process that activates or increases the activity of an enzyme.	RAB3GAP1	7.14	1/14	0.12	1/845	0.574253899
GO:0030163	protein catabolic process	The chemical reactions and pathways resulting in the breakdown of a protein by the	UBA1	7.14	1/14	0.12	1/855	0.577878039
GO:0001932	regulation of protein phosphorylation	Any process that modulates the frequency, rate or extent of addition of phosphate g	STK38	7.14	1/14	0.12	1/867	0.582444353
GO:0060429	epithelium development	The process whose specific outcome is the progression of an epithelium over time, f	FA5N	7.14	1/14	0.11	1/875	0.584527663
GO:0070647	protein modification by small protein conjugation or removal	A protein modification process in which one or more groups of a small protein, such	UBA1	7.14	1/14	0.11	1/877	0.584527663
GO:0010033	response to organic substance	Any process that results in a change in state or activity of a cell or an organism (in	ter ALOX15 FASN	14.29	2/14	0.09	2/2232	0.587962578
GO:0048878	chemical homeostasis	Any biological process involved in the maintenance of an internal steady state of a	ch SURF4	7.14	1/14	0.11	1/900	0.591401095
GO:0048731	system development	The process whose specific outcome is the progression of an organismal system over	ALOX15 FASN RAB3GAP1	21.43	3/14	0.08	3/3612	0.591401095
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicellular organism, pertain	to ABCG2 ALOX15 FASN MYO6 RAB3GAP1	35.71	5/14	0.08	5/6399	0.592544291
GO:0080134	regulation of response to stress	Any process that modulates the frequency, rate or extent of a response to stress.	Res ALOX15	7.14	1/14	0.11	1/909	0.592834959
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	A MYO6 RAB3GAP1 RAB3GAP2 STK38	28.57	4/14	0.08	4/5027	0.593641032
GO:0022607	cellular component assembly	The aggregation, arrangement and bonding together of a cellular component.	ALOX15 RAB3GAP1 RAB3GAP2	21.43	3/14	0.08	3/3663	0.596201656
GO:0009966	regulation of signal transduction	Any process that modulates the frequency, rate or extent of signal transduction.	ALOX15 STK38	14.29	2/14	0.09	2/2282	0.596201656
GO:0003008	system process	A multicellular organismal process carried out by any of the organs or tissues in an	or ABCG2 MYO6	14.29	2/14	0.09	2/2314	0.604252389
GO:0009968	negative regulation of signal transduction	Any process that stops, prevents, or reduces the frequency, rate or extent of signal	tr STK38	7.14	1/14	0.10	1/964	0.611088163
GO:0042325	regulation of phosphorylation	Any process that modulates the frequency, rate or extent of addition of phosphate g	STK38	7.14	1/14	0.10	1/986	0.618008138
GO:0042665	cellular macromolecule catabolic process	The chemical reactions and pathways resulting in the breakdown of a macromolecu	l UBA1	7.14	1/14	0.10	1/985	0.618008138
GO:0051641	cellular localization	A cellular localization process whereby a substance or cellular entity, such as a protei	n RAB3GAP1 RAB3GAP2	14.29	2/14	0.08	2/2418	0.628623981
GO:0010648	negative regulation of cell communication	Any process that decreases the frequency, rate or extent of cell communication. Cell	STK38	7.14	1/14	0.10	1/1021	0.629712767
GO:0023057	negative regulation of signaling	Any process that stops, prevents, or reduces the frequency, rate or extent of a signal	STK38	7.14	1/14	0.10	1/1023	0.629712767
GO:0045944	positive regulation of transcription by RNA polymerase II	Any process that activates or increases the frequency, rate or extent of transcription	MYO6	7.14	1/14	0.10	1/1036	0.63254333
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progression of a multicellu	lar or ALOX15 FASN RAB3GAP1	21.43	3/14	0.08	3/3871	0.63254333
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or inorganic compounds that	COASY MYO6 RAB3GAP1 RAB3GAP2 RP	57.14	9/14	0.07	8/1026	0.633883678
GO:0044085	macromolecule metabolic process	A process that results in the biosynthesis of constituent macromolecules, assembly,	or ALOX15 RAB3GAP1 RAB3GAP2	21.43	3/14	0.08	3/3907	0.637886152
GO:0002682	regulation of immune system process	Any process that modulates the frequency, rate, or extent of an immune system pro	cess ALOX15	7.14	1/14	0.09	1/1077	0.644860067
GO:0007155	cell adhesion	The attachment of a cell, either to another cell or to an underlying substrate such	as ALOX15	7.14	1/14	0.09	1/1087	0.645757013
GO:0022610	biological adhesion	The attachment of a cell or organism to a substrate, another cell, or other organ	ism. ALOX15	7.14	1/14	0.09	1/1092	0.645757013
GO:0019220	regulation of phosphate metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	a STK38	7.14	1/14	0.09	1/1094	0.645757013
GO:0051174	regulation of phosphorus metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	a STK38	7.14	1/14	0.09	1/1094	0.645757013
GO:0010646	regulation of cell communication	Any process that modulates the frequency, rate or extent of cell communication. Cell	ALOX15 STK38	14.29	2/14	0.08	2/2562	0.650470638
GO:0023051	regulation of signaling	Any process that modulates the frequency, rate or extent of a signaling process.	ALOX15 STK38	14.29	2/14	0.08	2/2573	0.651899554
GO:1901565	organonitrogen compound catabolic process	The chemical reactions and pathways resulting in the breakdown of organonitrogen	UBA1	7.14	1/14	0.09	1/1129	0.655063989
GO:0042221	response to chemical	Any process that results in a change in state or activity of a cell or an organism (in	ter ABCG2 ALOX15 FASN	21.43	3/14	0.07	3/4056	0.657076932
GO:0009057	macromolecule catabolic process	The chemical reactions and pathways resulting in the breakdown of a macromolecu	l UBA1	7.14	1/14	0.09	1/1142	0.657076932
GO:0044093	positive regulation of molecular function	Any process that activates or increases the rate or extent of a molecular function,	or RAB3GAP1	7.14	1/14	0.09	1/1149	0.65824996
GO:0009967	positive regulation of signal transduction	Any process that activates or increases the frequency, rate or extent of signal trans	d. ALOX15	7.14	1/14	0.09	1/1161	0.661288298
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	a MYO6 RAB3GAP1 RAB3GAP2 STK38	28.57	4/14	0.07	4/5552	0.662404929
GO:0006952	defense response	Reactions, triggered in response to the presence of a foreign body or the occurrence	of ALOX15	7.14	1/14	0.09	1/1172	0.662404929
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to trigger a change in the activi	ty on ALOX15 GNG12 MYO6 STK38	28.57	4/14	0.07	4/5642	0.677536177
GO:0007010	cytoskeleton organization	A process that is carried out at the cellular level which results in the assembly,	arrang ALOX15	7.14	1/14	0.08	1/1245	0.685760136
GO:0006955	immune response	Any immune system process that functions in the calibrated response of an organ	ism ALOX15	7.14	1/14	0.08	1/1288	0.69752737
GO:0010647	positive regulation of cell communication	Any process that increases the frequency, rate or extent of cell communication. Cell	ALOX15	7.14	1/14	0.08	1/1286	0.69752737
GO:0021305	positive regulation of signaling	Any process that activates, maintains or increases the frequency, rate or extent of	a ALOX15	7.14	1/14	0.08	1/1293	0.697636325
GO:0048856	anatomical structure development	The biological process whose specific outcome is the progression of an anatomical	s. ALOX15 FASN RAB3GAP1	21.43	3/14	0.07	3/4373	0.707007445
GO:1903508	positive regulation of nucleic acid-templated transcription	Any process that activates or increases the frequency, rate or extent of nucleic acid- <i>t</i>	MYO6	7.14	1/14	0.07	1/1358	0.708717817
GO:0042592	homeostatic process	Any biological process involved in the maintenance of an internal steady state.	SURF4	7.14	1/14	0.07	1/1352	0.708717817
GO:1902680	positive regulation of RNA biosynthetic process	Any process that activates or increases the frequency, rate or extent of RNA biosynth	esis MYO6	7.14	1/14	0.07	1/1360	0.708717817
GO:0045893	positive regulation of transcription, DNA-templated	Any process that activates or increases the frequency, rate or extent of cellular DNA- <i>t</i>	MYO6	7.14	1/14	0.07	1/1358	0.708717817
GO:0006811	ion transport	The directed movement of charged atoms or small charged molecules into, out of or	ABCG2	7.14	1/14	0.07	1/1347	0.708717817
GO:0006468	protein phosphorylation	The process of introducing a phosphate group on to a protein.	STK38	7.14	1/14	0.07	1/1340	0.708717817
GO:0006008	regulation of biological quality	Any process that modulates a qualitative or quantitative trait of a biological quality.	f ALOX15 SURF4	14.29	2/14	0.07	2/2959	0.715381414
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent of the chemical reactions	a MYO6 RAB3GAP1 RAB3GAP2 STK38	28.57	4/14	0.07	4/5976	0.71649446
GO:0051585	transmembrane transport	The process in which a solute is transported across a lipid bilayer, from one side of	a ABCG2	7.14	1/14	0.07	1/1405	0.71649446
GO:0048583	regulation of response to stimulus	Any process that modulates the frequency, rate or extent of a response to a stimuli	s. ALOX15 STK38	14.29	2/14	0.07	2/2982	0.71649446
GO:0023052	signaling	The entirety of a process in which information is transmitted within a biological syste	m ALOX15 GNG12 MYO6 STK38	28.57	4/14	0.07	4/6020	0.721192617
GO:0007154	cell communication	Any process that mediates interactions between a cell and its surroundings. Encomp	s. ALOX15 GNG12 MYO6 STK38	28.57	4/14	0.07	4/6065	0.726342259
GO:0007600	sensory perception	The series of events required for an organism to receive a sensory stimulus, convert i	t MYO6	7.14	1/14	0.07	1/1454	0.726342259
GO:0051254	positive regulation of RNA metabolic process	Any process that activates or increases the frequency, rate or extent of the chemica	l MYO6	7.14	1/14	0.07	1/1459	0.726342259
GO:0050794	regulation of cellular process	Any process that modulates the frequency, rate or extent of a cellular process, any	of ALOX15 GNG12 MYO6 RAB3GAP1 RAB3	50.00	7/14	0.07	1/10398	0.727114876
GO:0010557	developmental regulation of macromolecule biosynthetic process	Any process that increases the rate, frequency or extent of the chemical reactions	a MYO6	7.14	1/14	0.07	1/1528	0.742766646
GO:0032502	positive regulation of process	A biological process whose specific outcome is the progression of an integrated livi	ng ALOX15 FASN RAB3GAP1	21.43	3/14	0.06	3/4755	0.759096813
GO:0049325	positive regulation of nucleobase-containing compound metabolic	Any cellular process that activates or increases the frequency, rate or extent of the	l MYO6	7.14	1/14	0.06	1/1597	0.756512816
GO:0049468	cell development	The process whose specific outcome is the progression of the cell over time, from its	FASN	7.14	1/14	0.06	1/1592	0.756512816
GO:0016043	cellular component organization	A process that results in the assembly, arrangement of constituent parts, or disasse	m ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57	4/14	0.06	6/6354	0.759661517
GO:0048584	positive regulation of response to stimulus	Any process that activates, maintains or increases the rate of a response to a stimuli	s. ALOX15	7.14	1/14	0.06	1/1617	0.759661517
GO:0034654	nucleobase-containing compound biosynthetic process	The chemical reactions and pathways resulting in the formation of nucleobases, nucl	eo COASY MYO6	14.29	2/14	0.06	2/3364	0.773838427
GO:0007399	nervous system development	The process whose specific outcome is the progression of nervous tissue over time, f	RAB3GAP1	7.14	1/14	0.06	1/1710	0.778295517
GO:0019438	aromatic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of aromatic compou	COASY MYO6	14.29	2/14	0.06	2/3441	0.781020446
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breakdown of an organic subst	UBA1	7.14	1/14	0.06	1/1742	0.781020446
GO:0018130	cellular biosynthetic process	The chemical reactions and pathways resulting in the formation of heterocyclic comp	COASY MYO6	14.29	2/14	0.06	2/3434	0.781020446
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent macromolecules, assembly,	or ALOX15 RAB3GAP1 RAB3GAP2 SURF4	28.57	4/14	0.06	6/6564	0.781266538
GO:0007186	G protein-coupled receptor signaling pathway	A series of molecular signals that proceeds with an activated receptor promoting the	GNG12	7.14	1/14	0.06	1/1716	0.783789594
GO:0001670	macromolecule metabolic process	The chemical reactions and pathways involving macromolecules, any molecule of hig	h MYO6 RAB3GAP1 RAB3GAP2 RTP1 STK	50.00	7/14	0.06	1/10935	0.783789594
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the formation of organic cyclic com	COASY MYO6	14.29	2/14	0.06	2/3552	0.791862207
GO:0050877	nervous system process	A organ system process carried out by any of the organs or tissues of neurological	s; MYO6	7.14	1/14	0.05	1/1827	0.791862207
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not necessarily restricted	to a ABCG2 ALOX15 COASY FASN GNG12 MY	92.86	13/14	0.05	13/1870	0.798722877
GO:0051172	negative regulation of nitrogen compound metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of the che	STK38	7.14	1/14	0.05	1/1924	0.807079065
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent of a biological process. Biol	ALOX15 GNG12 MYO6 RAB3GAP1 RAB3	50.00	7/14	0.06	7/11175	0.807079065
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a cell or an organism (in	ter ALOX15	7.14	1/14	0.05	1/2004	0.821021545
GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of the che	STK38	7.14	1/14	0.05	1/2035	0.825128758
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated and organized. Morphogen	e RAB3GAP1	7.14	1/14	0.05	1/2107	0.836886121
GO:0006357	regulation of transcription by RNA polymerase II	Any process that modulates the frequency, rate or extent of transcription mediated	by MYO6	7.14	1/14	0.05	1/2147	0.841565107
GO:0006366	transcription by RNA polymerase II	The synthesis of RNA from a DNA template by RNA polymerase II (RNAP II), originar	ly MYO6	7.14	1/14	0.04	1/2234	0.854141339
GO:0044271	cellular nitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formation of organic and inorg	COASY MYO6	14.29	2/14	0.05	2/4213	0.87037813
GO:0065007	cellular regulation	Any process that modulates a measurable attribute of any biological process, quali	ty ALOX15 GNG12 MYO6 RAB3GAP1 RAB3	50.00	7/14	0.06	7/11905	0.879094619
GO:0065003	protein-containing complex assembly	The aggregation, arrangement and bonding together of a set of macromolecules to	flo ALOX15	7.14	1/14	0.04	1/2520	0.889763164
GO:0010605	negative regulation of macromolecule metabolic process	Any process that decreases the frequency, rate or extent of the chemical reactions	at STK38	7.14	1/14	0.04	1/2563	0.893374164
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency, rate or extent of a biolo	g ALOX15 STK38	14.29	2/14	0.04	2/4543	0.899092454
GO:0043933	protein-containing complex organization	Any process in which macromolecules aggregate, disaggregate, or are modified, resu	ALOX15	7.14	1/14	0.04	1/2678	0.903374055
GO:0009892	negative regulation of metabolic process	Any process that stops, prevents, or reduces the frequency, rate or extent of the che	STK38	7.14	1/14	0.04	1/2707	0.904796064
GO:0006355	regulation of transcription, DNA-templated	Any process that modulates the frequency, rate or extent of cellular DNA-templated	MYO6	7.14	1/14	0.03	1/2881	0.917593805
GO:1903506	regulation of nucleic acid-templated transcription	Any process that modulates the frequency, rate or extent of nucleic acid-templated	I MYO6	7.14	1/14	0.03	1/2881	0.917593805
GO:2001141	regulation of RNA biosynthetic process	Any process that modulates the frequency, rate or extent of RNA biosynthetic proces	MYO6	7.14	1/14	0.03	1/2884	0.917593805
GO:0032774	RNA biosynthetic process	The chemical reactions and pathways resulting in the formation of RNA, ribonuclei	c MYO6	7.14	1/14	0.03	1/3030	0.925341895
GO:0006351	transcription, DNA-templated	The cellular synthesis of RNA as a result of DNA.	MYO6					

sPLS_LPLactivity_Enrichment_GO_BP_of_17prot_contributing_to_HL_group

GO_BP	Name	Function	Gene Name	Term frequ	Term frequ	P-value (fdr)
GO:009206	negative regulation of cholesterol metabolic process	Any process that decreases the rate, frequency, or extent of	ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:0006102	isocitrate metabolic process	The chemical reactions and pathways involving isocitrate,	IDH1	7.14 1/14	33.33 1/3	0,079087858
GO:0006097	glyoxylate cycle	A modification of the TCA cycle occurring in some plants	IDH1	7.14 1/14	50.00 1/2	0,079087858
GO:0006081	cellular aldehyde metabolic process	The chemical reactions and pathways involving aldehydes,	ALPL IDH1	14.29 2/14	3.85 2/52	0,079087858
GO:1903778	protein localization to vacuolar membrane	A process in which a protein is transported to, or maintain	SH3GLB1	7.14 1/14	100.00 1/1	0,079087858
GO:1903527	positive regulation of membrane tubulation	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	25.00 1/4	0,079087858
GO:0045541	negative regulation of cholesterol biosynthetic process	Any process that stops, prevents, or reduces the frequency	ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:0106119	negative regulation of sterol biosynthetic process	Any process that stops, prevents or reduces the frequency	ERLIN2	7.14 1/14	25.00 1/4	0,079087858
GO:1901615	organic hydroxy compound metabolic process	The chemical reactions and pathways involving organic hydr	ALPL ERLIN2 IDH1	21.43 3/14	0.75 3/398	0,079087858
GO:1902652	secondary alcohol metabolic process	The chemical reactions and pathways involving secondary	ERLIN2 IDH1	14.29 2/14	1.98 2/101	0,079087858
GO:0003360	brainstem development	The progression of the brainstem from its formation to the	CNTFR	7.14 1/14	25.00 1/4	0,079087858
GO:0042822	pyridoxal phosphate metabolic process	The chemical reactions and pathways involving pyridoxal p	ALPL	7.14 1/14	25.00 1/4	0,079087858
GO:0015881	creatine transmembrane transport	The directed movement of creatine across a membrane.	SLC6A8	7.14 1/14	50.00 1/2	0,079087858
GO:0042816	vitamin B6 metabolic process	The chemical reactions and pathways involving any of the	ALPL	7.14 1/14	25.00 1/4	0,079087858
GO:0046890	regulation of lipid biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2 IDH1	14.29 2/14	1.61 2/124	0,08647439
GO:0060696	regulation of phospholipid catabolic process	Any process that modulates the rate, frequency, or extent	IDH1	7.14 1/14	20.00 1/5	0,08647439
GO:0046487	glyoxylate metabolic process	The chemical reactions and pathways involving glyoxylate,	IDH1	7.14 1/14	14.29 1/7	0,092179749
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	A series of molecular signals initiated by the binding of a ci	CNTFR	7.14 1/14	14.29 1/7	0,092179749
GO:1903525	regulation of membrane tubulation	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	14.29 1/7	0,092179749
GO:0090148	membrane fission	A process that is carried out at the cellular level which res	SH3GLB1	7.14 1/14	14.29 1/7	0,092179749
GO:0048102	autophagic cell death	A form of programmed cell death that is accompanied by t	SH3GLB1	7.14 1/14	16.67 1/6	0,092179749
GO:0106118	regulation of sterol biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	10.00 1/10	0,103534823
GO:0001967	suckling behavior	Specific behavior of a newborn or infant mammal that res	CNTFR	7.14 1/14	11.11 1/9	0,103534823
GO:1902931	negative regulation of alcohol biosynthetic process	Any process that stops, prevents or reduces the frequency	ERLIN2	7.14 1/14	9.09 1/11	0,103534823
GO:0006103	2-oxoglutarate metabolic process	The chemical reactions and pathways involving oxoglutarat	IDH1	7.14 1/14	10.00 1/10	0,103534823
GO:0072350	tricarboxylic acid metabolic process	The chemical reactions and pathways involving dicarboxyli	IDH1	7.14 1/14	9.09 1/11	0,103534823
GO:0071071	regulation of phospholipid biosynthetic process	Any process that modulates the frequency, rate or extent	IDH1	7.14 1/14	8.33 1/12	0,103534823
GO:0006814	sodium ion transport	The directed movement of sodium ions (Na+) into, out of c	SLC5A9 SLC6A8	14.29 2/14	1.00 2/200	0,103534823
GO:0051764	actin crosslink formation	The process in which two or more actin filaments are conn	MARCKS	7.14 1/14	9.09 1/11	0,103534823
GO:0045540	regulation of cholesterol biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	10.00 1/10	0,103534823
GO:0045717	negative regulation of fatty acid biosynthetic process	Any process that stops, prevents, or reduces the frequenc	ERLIN2	7.14 1/14	8.33 1/12	0,103534823
GO:0051290	protein heterotetramerization	The formation of a protein heterotetramer, a macromolecu	KRT10	7.14 1/14	10.00 1/10	0,103534823
GO:0071501	cellular response to sterol depletion	Any process that results in a change in state or activity of	ERLIN2	7.14 1/14	7.69 1/13	0,103530823
GO:0032933	SREBP signaling pathway	A series of molecular signals from the endoplasmic reticul	ERLIN2	7.14 1/14	7.69 1/13	0,103530823
GO:1903729	regulation of plasma membrane organization	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	7.14 1/14	0,107300105
GO:0006991	response to sterol depletion	Any process that results in a change in state or activity of	ERLIN2	7.14 1/14	7.14 1/14	0,107300105
GO:2000786	positive regulation of autophagosome assembly	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	6.67 1/15	0,111821131
GO:0033280	response to vitamin D	Any process that results in a change in state or activity of	ALPL	7.14 1/14	6.25 1/16	0,116099533
GO:0031667	response to nutrient levels	Any process that results in a change in state or activity of	ALPL SH3GLB1	14.29 2/14	0.79 2/252	0,119730648
GO:0019216	regulation of lipid metabolic process	Any process that modulates the frequency, rate or extent	ERLIN2 IDH1	14.29 2/14	0.81 2/246	0,119730648
GO:0090181	regulation of cholesterol metabolic process	Any process that modulates the rate, frequency, or extent	ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0045939	negative regulation of steroid metabolic process	Any process that stops, prevents, or reduces the frequenc	ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0097320	plasma membrane tubulation	A membrane tubulation process occurring in a plasma mer	SH3GLB1	7.14 1/14	5.26 1/19	0,119730648
GO:0010894	negative regulation of steroid biosynthetic process	Any process that decreases the frequency, rate or extent	ERLIN2	7.14 1/14	5.00 1/20	0,119730648
GO:0044090	positive regulation of vacuole organization	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	5.56 1/18	0,119730648
GO:0051291	protein heterooligomerization	The process of creating protein oligomers, compounds cor	KRT10	7.14 1/14	5.56 1/18	0,119730648
GO:0006066	alcohol metabolic process	The chemical reactions and pathways involving alcohols, a	ERLIN2 IDH1	14.29 2/14	0.75 2/266	0,120950404
GO:0009991	response to extracellular stimulus	Any process that results in a change in state or activity of	ALPL SH3GLB1	14.29 2/14	0.73 2/273	0,12108921
GO:0045922	negative regulation of fatty acid metabolic process	Any process that stops, prevents, or reduces the frequenc	ERLIN2	7.14 1/14	4.55 1/22	0,12108921
GO:0032801	receptor catabolic process	The chemical reactions and pathways resulting in the brea	SH3GLB1	7.14 1/14	4.55 1/22	0,12108921
GO:0033273	response to vitamin	Any process that results in a change in state or activity of	ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0001958	endochondral ossification	Replacement ossification wherein bone tissue replaces car	ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0072337	modified amino acid transport	The directed movement of modified amino acids into, out	SLC6A8	7.14 1/14	4.35 1/23	0,121119324
GO:0006767	water-soluble vitamin metabolic process	The chemical reactions and pathways involving any of a di	ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0036075	replacement ossification	Ossification that requires the replacement of a preexisting	ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:0046677	response to antibiotic	Any process that results in a change in state or activity of	ALPL	7.14 1/14	4.35 1/23	0,121119324
GO:0018149	peptide cross-linking	The formation of a covalent cross-link between or within p	KRT10	7.14 1/14	4.00 1/25	0,121119324
GO:0072524	pyridine-containing compound metabolic process	The chemical reactions and pathways involving a pyridine-	ALPL	7.14 1/14	3.85 1/26	0,121119324
GO:1903725	regulation of phospholipid metabolic process	Any process that modulates the frequency, rate or extent	IDH1	7.14 1/14	4.00 1/25	0,121119324
GO:1902930	regulation of alcohol biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	3.70 1/27	0,121614649
GO:0006739	NADP metabolic process	The chemical reactions and pathways involving nicotinami	IDH1	7.14 1/14	3.70 1/27	0,121614649
GO:0006099	tricarboxylic acid cycle	A nearly universal metabolic pathway in which the acetyl g	IDH1	7.14 1/14	3.57 1/28	0,124044689
GO:0007584	response to nutrient	Any process that results in a change in state or activity of	ALPL	7.14 1/14	2.94 1/34	0,147948184
GO:0042304	regulation of fatty acid biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:0006695	cholesterol biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:1902653	secondary alcohol biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	2.78 1/36	0,149434108
GO:0009395	phospholipid catabolic process	The chemical reactions and pathways resulting in the brea	IDH1	7.14 1/14	2.44 1/41	0,151545566
GO:2000785	regulation of autophagosome assembly	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	2.50 1/40	0,151545566
GO:0042149	cellular response to glucose starvation	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	2.50 1/40	0,151545566
GO:0061919	process utilizing autophagic mechanism	A cellular process involving delivery of a portion of the cy	ANXA7 SH3GLB1	14.29 2/14	0.52 2/382	0,151545566
GO:0051055	negative regulation of lipid biosynthetic process	Any process that stops, prevents, or reduces the frequenc	ERLIN2	7.14 1/14	2.50 1/40	0,151545566
GO:0006914	autophagy	The cellular catabolic process in which cells digest parts	ANXA7 SH3GLB1	14.29 2/14	0.52 2/382	0,151545566
GO:0016126	sterol biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	2.56 1/39	0,151545566
GO:0006984	ER-nucleus signaling pathway	Any series of molecular signals that conveys information fr	ERLIN2	7.14 1/14	2.63 1/38	0,151545566
GO:0034198	cellular response to amino acid starvation	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	2.38 1/42	0,153122546
GO:1990928	response to amino acid starvation	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	2.33 1/43	0,154655727
GO:0044088	regulation of vacuole organization	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	2.27 1/44	0,156146816
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the bre	ANXA7 ERLIN2 IDH	28.57 4/14	0.22 4/181	0,161534441
GO:0050994	regulation of lipid catabolic process	Any process that modulates the frequency, rate, or extent	IDH1	7.14 1/14	2.04 1/49	0,169215648
GO:0050810	regulation of steroid biosynthetic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	2.00 1/50	0,170455749
GO:0060350	endochondral bone morphogenesis	The process in which bones are generated and organized	ALPL	7.14 1/14	1.96 1/51	0,171663082
GO:0006766	vitamin metabolic process	The chemical reactions and pathways involving vitamins.	ALPL	7.14 1/14	1.89 1/53	0,176105947
GO:0006749	glutathione metabolic process	The chemical reactions and pathways involving glutathion	IDH1	7.14 1/14	1.85 1/54	0,177209833
GO:0016239	positive regulation of macroautophagy	Any process, such as recognition of nutrient depletion, tha	SH3GLB1	7.14 1/14	1.79 1/56	0,181468483
GO:0072665	protein localization to vacuole	A process in which a protein is transported to, or maintain	SH3GLB1	7.14 1/14	1.67 1/60	0,184241808
GO:0031638	zymogen activation	The proteolytic processing of an inactive enzyme to an act	CD5L	7.14 1/14	1.69 1/59	0,184241808
GO:0030855	epithelial cell differentiation	The process in which a relatively unspecialized cell acquire	ANXA7 KRT10	14.29 2/14	0.43 2/470	0,184241808

GO:0032787	monocarboxylic acid metabolic process	The chemical reactions and pathways involving monocarb	ERLIN2 IDH1	14.29 2/14	0.43 2/470	0,184241808
GO:0043648	dicarboxylic acid metabolic process	The chemical reactions and pathways involving dicarboxyly	IDH1	7.14 1/14	1.67 1/60	0,184241808
GO:0120162	positive regulation of cold-induced thermogenesis	Any process that activates or increases the frequency, rate	ALPL	7.14 1/14	1.61 1/62	0,187155616
GO:0007631	feeding behavior	Behavior associated with the intake of food.	CNTFR	7.14 1/14	1.59 1/63	0,18802391
GO:0062014	negative regulation of small molecule metabolic process	Any process that stops, prevents or reduces the frequency	ERLIN2	7.14 1/14	1.45 1/69	0,196879758
GO:0051262	protein tetramerization	The formation of a protein tetramer, a macromolecular str	KRT10	7.14 1/14	1.45 1/69	0,196879758
GO:1902117	positive regulation of organelle assembly	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	1.49 1/67	0,196879758
GO:0019217	regulation of fatty acid metabolic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	1.45 1/69	0,196879758
GO:0019218	regulation of steroid metabolic process	Any process that modulates the frequency, rate or extent	ERLIN2	7.14 1/14	1.41 1/71	0,198281792
GO:0045833	negative regulation of lipid metabolic process	Any process that stops, prevents, or reduces the frequenc	ERLIN2	7.14 1/14	1.41 1/71	0,198281792
GO:0008610	lipid biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2 IDH1	14.29 2/14	0.38 2/525	0,202907868
GO:0009056	catabolic process	The chemical reactions and pathways resulting in the breal	ANXA7 ERLIN2 IDH1	28.57 4/14	0.19 4/210	0,202907868
GO:0032465	regulation of cytokinesis	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	1.33 1/75	0,202907868
GO:1904659	glucose transmembrane transport	The process in which glucose is transported across a memb	SLC5A9	7.14 1/14	1.27 1/79	0,211341563
GO:0060349	bone morphogenesis	The process in which bones are generated and organized.	ALPL	7.14 1/14	1.20 1/83	0,21422839
GO:1990823	response to leukemia inhibitory factor	Any process that results in a change in state or activity of	BSPRY	7.14 1/14	1.18 1/85	0,21422839
GO:0008645	hexose transmembrane transport	The process in which hexose is transported across a memb	SLC5A9	7.14 1/14	1.23 1/81	0,21422839
GO:0030433	ubiquitin-dependent ERAD pathway	The series of steps necessary to target endoplasmic reticul	ERLIN2	7.14 1/14	1.20 1/83	0,21422839
GO:0015718	monocarboxylic acid transport	The directed movement of monocarboxylic acids into, out	SLC6A8	7.14 1/14	1.18 1/85	0,21422839
GO:1990830	cellular response to leukemia inhibitory factor	Any process that results in a change in state or activity of	BSPRY	7.14 1/14	1.19 1/84	0,21422839
GO:0015749	monosaccharide transmembrane transport	The process in which a monosaccharide is transported acr	SLC5A9	7.14 1/14	1.15 1/87	0,217099264
GO:0034219	carbohydrate transmembrane transport	The process in which a carbohydrate is transported across	SLC5A9	7.14 1/14	1.12 1/89	0,217912025
GO:0010033	response to organic substance	Any process that results in a change in state or activity of	ALPL BSPRY CNTFR	28.57 4/14	0.18 4/222	0,217912025
GO:0016241	regulation of macroautophagy	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	1.09 1/92	0,21798349
GO:0008203	cholesterol metabolic process	The chemical reactions and pathways involving cholesterol	ERLIN2	7.14 1/14	1.04 1/96	0,21798349
GO:0030216	keratinocyte differentiation	The process in which a relatively unspecialized cell acquir	KRT10	7.14 1/14	1.05 1/95	0,21798349
GO:0030282	bone mineralization	The deposition of hydroxyapatite, a form of calcium phosph	ALPL	7.14 1/14	1.05 1/95	0,21798349
GO:0010565	regulation of cellular ketone metabolic process	Any process that modulates the chemical reactions and pa	ERLIN2	7.14 1/14	1.02 1/98	0,21798349
GO:0031329	regulation of cellular catabolic process	Any process that modulates the frequency, rate or extent	IDH1 SH3GLB1	14.29 2/14	0.33 2/613	0,21798349
GO:0106106	cold-induced thermogenesis	The process by which heat is generated by increasing meta	ALPL	7.14 1/14	1.08 1/93	0,21798349
GO:0000045	autophagosome assembly	The formation of a double membrane-bound structure,	SH3GLB1	7.14 1/14	1.08 1/93	0,21798349
GO:1990266	neutrophil migration	The movement of a neutrophil within or between differen	GP2	7.14 1/14	1.04 1/96	0,21798349
GO:1905037	autophagosome organization	A process that is carried out at the cellular level which res	SH3GLB1	7.14 1/14	1.02 1/98	0,21798349
GO:0120161	regulation of cold-induced thermogenesis	Any process that modulates the frequency, rate or extent	ALPL	7.14 1/14	1.08 1/93	0,21798349
GO:1990845	adaptive thermogenesis	The regulated production of heat in response to short term	ALPL	7.14 1/14	0.98 1/102	0,22271412
GO:0016125	sterol metabolic process	The chemical reactions and pathways involving sterols, ste	ERLIN2	7.14 1/14	0.97 1/103	0,22271412
GO:0036503	ERAD pathway	The protein catabolic pathway which targets endoplasmic	ERLIN2	7.14 1/14	0.97 1/103	0,22271412
GO:0043524	negative regulation of neuron apoptotic process	Any process that stops, prevents, or reduces the frequenc	CNTFR	7.14 1/14	0.96 1/104	0,223005828
GO:0009888	tissue development	The process whose specific outcome is the progression of	ALPL ANXA7 KRT10	21.43 3/14	0.21 3/143	0,229156697
GO:0046165	alcohol biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	0.92 1/109	0,229677896
GO:0010508	positive regulation of autophagy	Any process that activates, maintains or increases the rate	SH3GLB1	7.14 1/14	0.88 1/114	0,231020925
GO:0071345	cellular response to cytokine stimulus	Any process that results in a change in state or activity of	BSPRY CNTFR	14.29 2/14	0.30 2/660	0,231020925
GO:0003006	developmental process involved in reproduction	A developmental process in which a progressive change in	ALPL CNTFR	14.29 2/14	0.30 2/666	0,231020925
GO:0044281	small molecule metabolic process	The chemical reactions and pathways involving small mole	ALPL ERLIN2 IDH1	21.43 3/14	0.21 3/146	0,231020925
GO:0001659	temperature homeostasis	A homeostatic process in which an organism modulates its	ALPL	7.14 1/14	0.88 1/114	0,231020925
GO:0008643	carbohydrate transport	The directed movement of carbohydrate into, out of or wi	SLC5A9	7.14 1/14	0.86 1/116	0,231139951
GO:0006694	steroid biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	0.86 1/116	0,231139951
GO:0097530	granulocyte migration	The movement of a granulocyte within or between differe	GP2	7.14 1/14	0.85 1/118	0,233233916
GO:0060538	skeletal muscle organ development	The progression of a skeletal muscle organ over time from	CNTFR	7.14 1/14	0.78 1/129	0,23507163
GO:0007009	plasma membrane organization	A process that is carried out at the cellular level which res	SH3GLB1	7.14 1/14	0.80 1/125	0,23507163
GO:0043112	receptor metabolic process	The chemical reactions and pathways involving a receptor	SH3GLB1	7.14 1/14	0.77 1/130	0,23507163
GO:0031214	biomineral tissue development	Formation of hard tissues that consist mainly of inorganic	ALPL	7.14 1/14	0.80 1/125	0,23507163
GO:0051017	actin filament bundle assembly	The assembly of actin filament bundles; actin filaments are	MARCKS	7.14 1/14	0.79 1/126	0,23507163
GO:0061572	actin filament bundle organization	A process that results in the assembly, arrangement of con	MARCKS	7.14 1/14	0.78 1/128	0,23507163
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	0.81 1/124	0,23507163
GO:0034097	response to cytokine	Any process that results in a change in state or activity of	BSPRY CNTFR	14.29 2/14	0.28 2/713	0,23507163
GO:0046434	organophosphate catabolic process	The chemical reactions and pathways resulting in the breal	IDH1	7.14 1/14	0.79 1/126	0,23507163
GO:0110148	biomineralization	The process where mineral crystals are formed and deposi	ALPL	7.14 1/14	0.79 1/127	0,23507163
GO:1901215	negative regulation of neuron death	Any process that stops, prevents or reduces the frequency	CNTFR	7.14 1/14	0.77 1/130	0,23507163
GO:0030001	metal ion transport	The directed movement of metal ions, any metal ion with	SLC5A9 SLC6A8	14.29 2/14	0.28 2/708	0,23507163
GO:0043523	regulation of neuron apoptotic process	Any process that modulates the occurrence or rate of cell	CNTFR	7.14 1/14	0.76 1/132	0,236923618
GO:0000910	cytokinesis	The division of the cytoplasm and the plasma membrane o	SH3GLB1	7.14 1/14	0.75 1/134	0,238746302
GO:0009267	cellular response to starvation	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	0.73 1/137	0,23904417
GO:0009894	regulation of catabolic process	Any process that modulates the frequency, rate, or extent	IDH1 SH3GLB1	14.29 2/14	0.27 2/732	0,23904417
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic	ERLIN2 IDH1	14.29 2/14	0.27 2/736	0,23904417
GO:0051302	regulation of cell division	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	0.72 1/138	0,239138704
GO:0043436	oxoacid metabolic process	The chemical reactions and pathways involving any oxoaci	ERLIN2 IDH1	14.29 2/14	0.27 2/745	0,240236722
GO:0006575	cellular modified amino acid metabolic process	The chemical reactions and pathways involving compound	IDH1	7.14 1/14	0.65 1/153	0,24920429
GO:0031334	positive regulation of protein-containing complex assembl	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	0.68 1/148	0,24920429
GO:0006836	neurotransmitter transport	The directed movement of a neurotransmitter into, out of	SLC6A8	7.14 1/14	0.67 1/149	0,24920429
GO:0006082	organic acid metabolic process	The chemical reactions and pathways involving organic aci	ERLIN2 IDH1	14.29 2/14	0.26 2/774	0,24920429
GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	0.65 1/153	0,24920429
GO:0035725	sodium ion transmembrane transport	A process in which a sodium ion is transported from one si	SLC6A8	7.14 1/14	0.67 1/149	0,24920429
GO:0042594	response to starvation	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	0.66 1/151	0,24920429
GO:0009913	epidermal cell differentiation	The process in which a relatively unspecialized cell acquir	KRT10	7.14 1/14	0.65 1/153	0,24920429
GO:0019637	organophosphate metabolic process	The chemical reactions and pathways involving organophos	ALPL IDH1	14.29 2/14	0.25 2/793	0,252377521
GO:0031669	cellular response to nutrient levels	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	0.62 1/161	0,256809463
GO:0007033	vacuole organization	A process that is carried out at the cellular level which res	SH3GLB1	7.14 1/14	0.62 1/160	0,256809463
GO:0097529	myeloid leukocyte migration	The movement of a myeloid leukocyte within or between	GP2	7.14 1/14	0.60 1/166	0,259641729
GO:1902115	regulation of organelle assembly	Any process that modulates the frequency, rate or extent	SH3GLB1	7.14 1/14	0.60 1/166	0,259641729
GO:0051402	neuron apoptotic process	Any apoptotic process in a neuron, the basic cellular unit	CNTFR	7.14 1/14	0.61 1/164	0,259641729
GO:0009060	aerobic respiration	The enzymatic release of energy from inorganic and organi	IDH1	7.14 1/14	0.59 1/169	0,262434639
GO:0042180	cellular ketone metabolic process	The chemical reactions and pathways involving any of a cl	ERLIN2	7.14 1/14	0.59 1/170	0,262434639
GO:0060348	bone development	The process whose specific outcome is the progression of	ALPL	7.14 1/14	0.57 1/175	0,265045347
GO:1901617	organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the form	ERLIN2	7.14 1/14	0.57 1/175	0,265045347
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breal	ERLIN2 IDH1 SH3GLB1	21.43 3/14	0.17 3/174	0,265045347
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as	ERLIN2 IDH1	14.29 2/14	0.23 2/852	0,266687742
GO:1901214	regulation of neuron death	Any process that modulates the frequency, rate or exten	CNTFR	7.14 1/14	0.56 1/179	0,267663455
GO:0031668	cellular response to extracellular stimulus	Any process that results in a change in state or activity of	SH3GLB1	7.14 1/14	0.55 1/181	0,268944706

GO:008654	phospholipid biosynthetic process	The chemical reactions and pathways resulting in the form IDH1	7.14 1/14	0.54 1/185	0,272499475
GO:0060429	epithelium development	The process whose specific outcome is the progression of ANXA7 KRT10	14.29 2/14	0.23 2/875	0,272499475
GO:0044242	cellular lipid catabolic process	The chemical reactions and pathways resulting in the break IDH1	7.14 1/14	0.53 1/188	0,274051847
GO:0016485	protein processing	Any protein maturation process achieved by the cleavage of CD5L	7.14 1/14	0.52 1/192	0,277973286
GO:0048705	skeletal system morphogenesis	The process in which the anatomical structures of the skeletal ALPL	7.14 1/14	0.50 1/199	0,285877842
GO:0071310	cellular response to organic substance	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR	21.43 3/14	0.16 3/184	0,287438919
GO:0007548	sex differentiation	The establishment of the sex of an organism by physical IDH1	7.14 1/14	0.49 1/205	0,288890774
GO:0045333	cellular respiration	The enzymatic release of energy from inorganic and organic IDH1	7.14 1/14	0.49 1/206	0,288890774
GO:0016236	macroautophagy	The major inducible pathway for the general turnover of cellular SH3GLB1	7.14 1/14	0.49 1/205	0,288890774
GO:0051259	protein complex oligomerization	The process of creating protein oligomers, compounds or KRT10	7.14 1/14	0.48 1/209	0,291243947
GO:0043588	skin development	The process whose specific outcome is the progression of KRT10	7.14 1/14	0.47 1/212	0,293286893
GO:0070997	neuron death	The process of cell death in a neuron. CNTFR	7.14 1/14	0.47 1/213	0,293286893
GO:0071496	cellular response to external stimulus	Any process that results in a change in state or activity of a SH3GLB1	7.14 1/14	0.45 1/222	0,301249335
GO:0007517	muscle organ development	The process whose specific outcome is the progression of CNTFR	7.14 1/14	0.45 1/224	0,301249335
GO:0051179	localization	Any process in which a cell, a substance, or a cellular entity CD5L GP2 NAPA SH	42.86 6/14	0.11 6/541	0,301249335
GO:0008202	steroid metabolic process	The chemical reactions and pathways involving steroids, or ERLIN2	7.14 1/14	0.44 1/229	0,301249335
GO:0010506	regulation of autophagy	Any process that modulates the frequency, rate or extent of SH3GLB1	7.14 1/14	0.44 1/229	0,301249335
GO:0046942	carboxylic acid transport	The directed movement of carboxylic acids into, out of or into SLC6A8	7.14 1/14	0.44 1/228	0,301249335
GO:0044262	cellular carbohydrate metabolic process	The chemical reactions and pathways involving carbohydrates IDH1	7.14 1/14	0.44 1/229	0,301249335
GO:0043976	response to endoplasmic reticulum stress	Any process that results in a change in state or activity of a ERLIN2	7.14 1/14	0.45 1/224	0,301249335
GO:0071702	organic substance transport	The directed movement of organic substances into, out of or into NAPA SLC5A9 SLC6A	21.43 3/14	0.15 3/196	0,301725763
GO:0006812	cation transport	The directed movement of cations, atoms or small molecules SLC5A9 SLC6A8	14.29 2/14	0.20 2/999	0,301725763
GO:0008544	epidermis development	The process whose specific outcome is the progression of KRT10	7.14 1/14	0.42 1/236	0,301725763
GO:0098656	anion transmembrane transport	The process in which an anion is transported across a membrane SLC6A8	7.14 1/14	0.43 1/232	0,301725763
GO:0062012	regulation of small molecule metabolic process	Any process that modulates the rate, frequency or extent of ERLIN2	7.14 1/14	0.42 1/236	0,301725763
GO:0046394	carboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	0.42 1/239	0,303759134
GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	0.41 1/242	0,305746757
GO:0000003	reproduction	The production of new individuals that contain some portion of ALPL CNTFR	14.29 2/14	0.20 2/102	0,305746757
GO:0022414	reproductive process	A biological process that directly contributes to the process of ALPL CNTFR	14.29 2/14	0.20 2/102	0,305746757
GO:0051604	protein maturation	Any process leading to the attainment of the full functional CD5L	7.14 1/14	0.39 1/254	0,315052273
GO:0048856	anatomical structure development	The biological process whose specific outcome is the progression of ALPL ANXA7 CNTFR	35.71 5/14	0.11 5/473	0,32699463
GO:0006790	sulfur compound metabolic process	The chemical reactions and pathways involving the nonmetal IDH1	7.14 1/14	0.37 1/272	0,33234638
GO:0006979	response to oxidative stress	Any process that results in a change in state or activity of a IDH1	7.14 1/14	0.36 1/275	0,333974491
GO:0015980	energy derivation by oxidation of organic compounds	The chemical reactions and pathways by which a cell derives IDH1	7.14 1/14	0.36 1/280	0,337892402
GO:0016042	lipid catabolic process	The chemical reactions and pathways resulting in the break IDH1	7.14 1/14	0.35 1/284	0,34066382
GO:0006629	lipid metabolic process	The chemical reactions and pathways involving lipids, compounds ERLIN2 IDH1	14.29 2/14	0.18 2/112	0,341261655
GO:0001503	ossification	The formation of bone or of a bony substance, or the conversion ALPL	7.14 1/14	0.35 1/289	0,341261655
GO:0050900	leukocyte migration	The movement of a leukocyte within or between different GP2	7.14 1/14	0.35 1/289	0,341261655
GO:0009057	macromolecule catabolic process	The chemical reactions and pathways resulting in the break ERLIN2 SH3GLB1	14.29 2/14	0.18 2/114	0,346305827
GO:0015711	organic anion transport	The directed movement of organic anions into, out of or into SLC6A8	7.14 1/14	0.33 1/306	0,356072443
GO:0006631	fatty acid metabolic process	The chemical reactions and pathways involving fatty acids, ERLIN2	7.14 1/14	0.32 1/316	0,364860904
GO:1901564	organonitrogen compound metabolic process	The chemical reactions and pathways involving organonitrogen ALPL BSPRY CD5L EF	42.86 6/14	0.10 6/591	0,373962119
GO:0043254	regulation of protein-containing complex assembly	Any process that modulates the frequency, rate or extent of SH3GLB1	7.14 1/14	0.30 1/330	0,37588299
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipids IDH1	7.14 1/14	0.30 1/338	0,38228067
GO:0031331	positive regulation of cellular catabolic process	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	0.29 1/342	0,384569779
GO:0032502	developmental process	A biological process whose specific outcome is the progression of ALPL ANXA7 CNTFR	35.71 5/14	0.11 5/475	0,394007027
GO:0016192	vesicle-mediated transport	A cellular transport process in which transported substances CD5L NAPA	14.29 2/14	0.16 2/127	0,395703715
GO:0070887	cellular response to chemical stimulus	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR	21.43 3/14	0.13 3/237	0,398667135
GO:0006915	apoptotic process	A programmed cell death process which begins when a cell CNTFR SH3GLB1	14.29 2/14	0.15 2/129	0,402320032
GO:0048871	multicellular organismal homeostasis	Any process involved in the maintenance of an internal state ALPL	7.14 1/14	0.27 1/369	0,402320032
GO:0051301	cell division	The process resulting in division and partitioning of components SH3GLB1	7.14 1/14	0.27 1/373	0,40438132
GO:0048731	system development	The process whose specific outcome is the progression of ALPL CNTFR KRT10	128.57 4/14	0.11 4/361	0,408178997
GO:0071407	cellular response to organic cyclic compound	Any process that results in a change in state or activity of a ALPL	7.14 1/14	0.26 1/383	0,408522312
GO:0044089	positive regulation of cellular component biogenesis	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	0.26 1/382	0,408522312
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolism	The chemical reactions and pathways resulting in the break ERLIN2	7.14 1/14	0.26 1/391	0,408898892
GO:0012501	programmed cell death	A process which begins when a cell receives an internal or external CNTFR SH3GLB1	14.29 2/14	0.15 2/134	0,408898892
GO:0006091	generation of precursor metabolites and energy	The chemical reactions and pathways resulting in the form IDH1	7.14 1/14	0.26 1/386	0,408898892
GO:0006811	ion transport	The directed movement of charged atoms or small molecules SLC5A9 SLC6A8	14.29 2/14	0.15 2/134	0,408898892
GO:0009896	positive regulation of catabolic process	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	0.25 1/400	0,410121831
GO:0016311	dephosphorylation	The process of removing one or more phosphoric (ester) or ALPL	7.14 1/14	0.25 1/399	0,410121831
GO:0007015	actin filament organization	A process that is carried out at the cellular level which results MARCKS	7.14 1/14	0.25 1/396	0,410121831
GO:0010638	positive regulation of organelle organization	Any process that increases the frequency, rate or extent of SH3GLB1	7.14 1/14	0.25 1/398	0,410121831
GO:0001501	skeletal system development	The process whose specific outcome is the progression of ALPL	7.14 1/14	0.25 1/405	0,412863711
GO:0019221	cytokine-mediated signaling pathway	A series of molecular signals initiated by the binding of a cytokine CNTFR	7.14 1/14	0.25 1/408	0,412963669
GO:0010256	endomembrane system organization	A process that is carried out at the cellular level which results SH3GLB1	7.14 1/14	0.24 1/409	0,412963669
GO:0055085	transmembrane transport	The process in which a solute is transported across a lipid bilayer SLC5A9 SLC6A8	14.29 2/14	0.14 2/140	0,420001124
GO:0007610	behavior	The internally coordinated responses (actions or inactions) CNTFR	7.14 1/14	0.24 1/421	0,420001124
GO:0008219	cell death	Any biological process that results in permanent cessation of SH3GLB1	14.29 2/14	0.14 2/143	0,42672106
GO:0044283	small molecule biosynthetic process	The chemical reactions and pathways resulting in the form ERLIN2	7.14 1/14	0.23 1/437	0,42672106
GO:0070727	cellular macromolecule localization	Any process in which a macromolecule is transported to, or NAPA SH3GLB1	14.29 2/14	0.14 2/143	0,42672106
GO:0034613	cellular protein localization	Any process in which a protein is transported to, and/or from NAPA SH3GLB1	14.29 2/14	0.14 2/143	0,42672106
GO:0090407	organophosphate biosynthetic process	The chemical reactions and pathways resulting in the biosynthesis IDH1	7.14 1/14	0.23 1/439	0,42672106
GO:0033554	cellular response to stress	Any process that results in a change in state or activity of a ERLIN2 SH3GLB1	14.29 2/14	0.14 2/146	0,428211624
GO:0006820	anion transport	The directed movement of anions, atoms or small molecules SLC6A8	7.14 1/14	0.22 1/449	0,428211624
GO:0061061	muscle structure development	The progression of a muscle structure over time, from its formation CNTFR	7.14 1/14	0.22 1/445	0,428211624
GO:0048513	animal organ development	Development of a tissue or tissues that work together to perform ALPL CNTFR KRT10	21.43 3/14	0.11 3/261	0,428211624
GO:0006810	transport	The directed movement of substances (such as macromolecules) CD5L NAPA SLC5A9	28.57 4/14	0.10 4/388	0,433436809
GO:0006897	endocytosis	A vesicle-mediated transport process in which cells take up CD5L	7.14 1/14	0.21 1/466	0,433436809
GO:0033993	response to lipid	Any process that results in a change in state or activity of a ALPL	7.14 1/14	0.22 1/464	0,433436809
GO:0010498	proteasomal protein catabolic process	The chemical reactions and pathways resulting in the break ERLIN2	7.14 1/14	0.22 1/464	0,433436809
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progression of ALPL CNTFR KRT10	28.57 4/14	0.10 4/387	0,433436809
GO:0072657	protein localization to membrane	A process in which a protein is transported to, or maintained on SH3GLB1	7.14 1/14	0.21 1/473	0,437287783
GO:0005975	carbohydrate metabolic process	The chemical reactions and pathways involving carbohydrates IDH1	7.14 1/14	0.21 1/484	0,444205924
GO:0014070	response to organic cyclic compound	Any process that results in a change in state or activity of a ALPL	7.14 1/14	0.20 1/495	0,451008587
GO:0051234	establishment of localization	Any process that localizes a substance or cellular component CD5L NAPA SLC5A9	28.57 4/14	0.10 4/403	0,462048459
GO:0071705	nitrogen compound transport	The directed movement of nitrogen-containing compound NAPA SLC6A8	14.29 2/14	0.13 2/158	0,462048459
GO:0010564	regulation of cell cycle process	Any process that modulates a cellular process that is involved in SH3GLB1	7.14 1/14	0.19 1/520	0,463737395
GO:0042221	response to chemical	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR	28.57 4/14	0.10 4/405	0,463737395
GO:0006950	response to stress	Any process that results in a change in state or activity of a ERLIN2 IDH1 SH3GLB1	21.43 3/14	0.11 3/280	0,465301685

GO:0051668	localization within membrane	Any process in which a substance or cellular entity, such as SH3GLB1	7.14 1/14	0.18 1/541	0,474974404
GO:006508	proteolysis	The hydrolysis of proteins into smaller polypeptides and/or CD5L ERLIN2	14.29 2/14	0.12 2/167	0,487900758
GO:006511	ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.17 1/589	0,505700048
GO:0019941	modification-dependent protein catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.17 1/503	0,513574642
GO:0043632	modification-dependent macromolecule catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.16 1/611	0,515276864
GO:0030036	actin cytoskeleton organization	A process that is carried out at the cellular level which res MARCKS	7.14 1/14	0.16 1/611	0,515276864
GO:0061024	membrane organization	A process which results in the assembly, arrangement of c SH3GLB1	7.14 1/14	0.16 1/620	0,519503943
GO:0097435	supramolecular fiber organization	A process that is carried out at the cellular level which res MARCKS	7.14 1/14	0.16 1/636	0,528353733
GO:0007417	central nervous system development	The process whose specific outcome is the progression of MARCKS	7.14 1/14	0.15 1/649	0,532479195
GO:0008284	positive regulation of cell population proliferation	Any process that activates or increases the rate or extent c CNTFR	7.14 1/14	0.15 1/651	0,532479195
GO:0043066	negative regulation of apoptotic process	Any process that stops, prevents, or reduces the frequency CNTFR	7.14 1/14	0.15 1/646	0,532479195
GO:0010243	response to organonitrogen compound	Any process that results in a change in state or activity of a ERLIN2	7.14 1/14	0.15 1/658	0,535111914
GO:0043069	negative regulation of programmed cell death	Any process that stops, prevents, or reduces the frequency CNTFR	7.14 1/14	0.15 1/663	0,536415959
GO:0098662	inorganic cation transmembrane transport	A process in which an inorganic cation is transported from SLC6A8	7.14 1/14	0.15 1/673	0,540234846
GO:0030029	actin filament-based process	Any cellular process that depends upon or alters the actin MARCKS	7.14 1/14	0.15 1/675	0,540234846
GO:0051603	proteolysis involved in cellular protein catabolic process	The hydrolysis of a peptide bond or bonds within a protein ERLIN2	7.14 1/14	0.14 1/696	0,551506482
GO:0016567	protein ubiquitination	The process in which one or more ubiquitin groups are adt BSPRY	7.14 1/14	0.14 1/702	0,553273348
GO:0060548	negative regulation of cell death	Any process that decreases the rate or frequency of cell de CNTFR	7.14 1/14	0.14 1/719	0,56174767
GO:0098660	inorganic ion transmembrane transport	The process in which an inorganic ion is transported across SLC6A8	7.14 1/14	0.14 1/736	0,562127217
GO:0044257	cellular protein catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.14 1/732	0,562127217
GO:0008104	protein localization	Any process in which a protein is transported to, or maint NAPA SH3GLB1	14.29 2/14	0.10 2/196	0,562127217
GO:0033365	protein localization to organelle	A process in which a protein is transported to, or maintain SH3GLB1	7.14 1/14	0.14 1/729	0,562127217
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent c ALPL ANXA7 ERLIN2	35.71 5/14	0.08 5/597	0,562127217
GO:1901698	response to nitrogen compound	Any process that results in a change in state or activity of a ERLIN2	7.14 1/14	0.13 1/741	0,562360499
GO:0006886	intracellular protein transport	The directed movement of proteins in a cell, including the NAPA	7.14 1/14	0.13 1/743	0,562360499
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a ALPL SH3GLB1	14.29 2/14	0.10 2/200	0,565704898
GO:0044087	regulation of cellular component biogenesis	Any process that modulates the frequency, rate or extent c SH3GLB1	7.14 1/14	0.13 1/762	0,566188013
GO:0032446	protein modification by small protein conjugation	A protein modification process in which one or more group BSPRY	7.14 1/14	0.13 1/758	0,566188013
GO:0051130	positive regulation of cellular component organization	Any process that activates or increases the frequency, rate SH3GLB1	7.14 1/14	0.13 1/763	0,566188013
GO:0070925	organelle assembly	The aggregation, arrangement and bonding together of a s SH3GLB1	7.14 1/14	0.13 1/786	0,577235731
GO:0051726	regulation of cell cycle	Any process that modulates the rate or extent of progress SH3GLB1	7.14 1/14	0.13 1/790	0,577512781
GO:0098655	cation transmembrane transport	The process in which a cation is transported across a membr SLC6A8	7.14 1/14	0.13 1/794	0,577781997
GO:0009887	animal organ morphogenesis	Morphogenesis of an animal organ. An organ is defined as ALPL	7.14 1/14	0.12 1/817	0,588414518
GO:0030163	protein catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.12 1/855	0,606726245
GO:0070647	protein modification by small protein conjugation or remc	A protein modification process in which one or more group BSPRY	7.14 1/14	0.11 1/877	0,616170698
GO:0006518	peptide metabolic process	The chemical reactions and pathways involving peptides, c IDH1	7.14 1/14	0.11 1/897	0,624366921
GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent c SH3GLB1	7.14 1/14	0.11 1/903	0,62533545
GO:0022607	cellular component assembly	The aggregation, arrangement and bonding together of a c KRT10 MARCKS SH3	21.43 3/14	0.08 3/366	0,634395658
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. I BSPRY CD5L ERLIN2	28.57 4/14	0.08 4/510	0,645112565
GO:0022402	cell cycle process	The cellular process that ensures successive accurate and c SH3GLB1	7.14 1/14	0.10 1/965	0,649542338
GO:0044265	cellular macromolecule catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.10 1/985	0,652646283
GO:0050896	response to stimulus	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR	14.28 6/14	0.08 6/797	0,652646283
GO:0033036	macromolecule localization	Any process in which a macromolecule is transported to, o NAPA SH3GLB1	14.29 2/14	0.08 2/236	0,652646283
GO:0006796	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the phospho ALPL IDH1	14.29 2/14	0.08 2/240	0,657397925
GO:0034220	ion transmembrane transport	A process in which an ion is transported across a membrar SLC6A8	7.14 1/14	0.10 1/100	0,657397925
GO:0051240	positive regulation of multicellular organismal process	Any process that activates or increases the frequency, rate ALPL	7.14 1/14	0.10 1/102	0,659059358
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the nonme ALPL IDH1	14.29 2/14	0.08 2/242	0,659059358
GO:0051641	cellular localization	A cellular localization process whereby a substance or cell. NAPA SH3GLB1	14.29 2/14	0.08 2/241	0,659059358
GO:1901700	response to oxygen-containing compound	Any process that results in a change in state or activity of a ALPL	7.14 1/14	0.10 1/102	0,659642725
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromole BSPRY ERLIN2 KRT1	28.57 4/14	0.08 4/530	0,661370354
GO:0042981	regulation of apoptotic process	Any process that modulates the occurrence or rate of cell c CNTFR	7.14 1/14	0.10 1/103	0,661370354
GO:0010629	negative regulation of gene expression	Any process that decreases the frequency, rate or extent o ANXA7	7.14 1/14	0.10 1/104	0,661370354
GO:0044085	cellular component biogenesis	A process that results in the biosynthesis of constituent m: KRT10 MARCKS SH3	21.43 3/14	0.08 3/390	0,663732525
GO:0043067	regulation of programmed cell death	Any process that modulates the frequency, rate or extent c CNTFR	7.14 1/14	0.09 1/106	0,665348444
GO:0065003	protein-containing complex assembly	The aggregation, arrangement and bonding together of a s KRT10 SH3GLB1	14.29 2/14	0.08 2/252	0,670212347
GO:0019220	regulation of phosphate metabolic process	Any process that modulates the frequency, rate or extent c IDH1	7.14 1/14	0.09 1/109	0,67133047
GO:0051174	regulation of phosphorus metabolic process	Any process that modulates the frequency, rate or extent c IDH1	7.14 1/14	0.09 1/109	0,67133047
GO:0043603	cellular amide metabolic process	The chemical reactions and pathways involving an amide, c IDH1	7.14 1/14	0.09 1/111	0,676669002
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a ALPL BSPRY CNTFR	135.71 5/14	0.07 5/687	0,67838709
GO:1901565	organonitrogen compound catabolic process	The chemical reactions and pathways resulting in the brea ERLIN2	7.14 1/14	0.09 1/112	0,679383777
GO:0010941	regulation of cell death	Any process that modulates the rate or frequency of cell d CNTFR	7.14 1/14	0.09 1/114	0,682490344
GO:0042127	regulation of cell population proliferation	Any process that modulates the frequency, rate or extent c CNTFR	7.14 1/14	0.09 1/115	0,685924626
GO:0043933	protein-containing complex organization	Any process in which macromolecules aggregate, disaggre KRT10 SH3GLB1	14.29 2/14	0.07 2/267	0,69600714
GO:0015031	protein transport	The directed movement of proteins into, out of or within a NAPA	7.14 1/14	0.08 1/119	0,69600714
GO:0016477	cell migration	The controlled self-propelled movement of a cell from one GP2	7.14 1/14	0.08 1/120	0,697300013
GO:0009892	negative regulation of metabolic process	Any process that stops, prevents, or reduces the frequency ANXA7 ERLIN2	14.29 2/14	0.07 2/270	0,697698405
GO:0007010	cytoskeleton organization	A process that is carried out at the cellular level which res MARCKS	7.14 1/14	0.08 1/124	0,70896947
GO:0031327	negative regulation of cellular biosynthetic process	Any process that stops, prevents, or reduces the frequency ERLIN2	7.14 1/14	0.08 1/125	0,711891578
GO:0009890	negative regulation of biosynthetic process	Any process that stops, prevents, or reduces the rate of th ERLIN2	7.14 1/14	0.08 1/127	0,716163988
GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location. NAPA	7.14 1/14	0.08 1/128	0,717188907
GO:0007049	cell cycle	The progression of biochemical and morphological phases SH3GLB1	7.14 1/14	0.08 1/130	0,721647353
GO:0042592	homeostatic process	Any biological process involved in the maintenance of an ii ALPL	7.14 1/14	0.07 1/135	0,728911121
GO:0046907	intracellular transport	The directed movement of substances within a cell. NAPA	7.14 1/14	0.07 1/133	0,728911121
GO:0051674	localization of cell	Any process in which a cell is transported to, and/or maint GP2	7.14 1/14	0.07 1/135	0,728911121
GO:0048870	cell motility	Any process involved in the controlled self-propelled move GP2	7.14 1/14	0.07 1/135	0,728911121
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific p BSPRY ERLIN2 KRT1	21.43 3/14	0.07 3/446	0,735627158
GO:0008283	cell population proliferation	The multiplication or reproduction of cells, resulting in the CNTFR	7.14 1/14	0.07 1/140	0,742970078
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency ANXA7 CNTFR ERLIN	21.43 3/14	0.07 3/454	0,747280672
GO:0009893	positive regulation of metabolic process	Any process that activates or increases the frequency, rate ALPL SH3GLB1	14.29 2/14	0.07 2/304	0,749650637
GO:0040011	locomotion	Self-propelled movement of a cell or organism from one lo GP2	7.14 1/14	0.07 1/147	0,7569576
GO:0030154	cell differentiation	The process in which relatively unspecialized cells, e.g. emi ANXA7 KRT10	14.29 2/14	0.06 2/309	0,75795121
GO:0048869	cellular developmental process	A biological process whose specific outcome is the progres ANXA7 KRT10	14.29 2/14	0.06 2/316	0,769346524
GO:0006464	cellular protein modification process	The covalent alteration of one or more amino acids occur BSPRY KRT10	14.29 2/14	0.06 2/323	0,780132201
GO:0036211	protein modification process	The covalent alteration of one or more amino acids occur BSPRY KRT10	14.29 2/14	0.06 2/323	0,780132201
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicell ALPL CNTFR KRT1	128.57 4/14	0.06 4/639	0,793981459
GO:0006996	organelle organization	A process that is carried out at the cellular level which res MARCKS SH3GLB1	14.29 2/14	0.06 2/333	0,794239542
GO:0051128	regulation of cellular component organization	Any process that modulates the frequency, rate or extent c SH3GLB1	7.14 1/14	0.06 1/173	0,79698703
GO:0006928	movement of cell or subcellular component	The directed, self-propelled movement of a cell or subcell GP2	7.14 1/14	0.06 1/170	0,79698703
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent c ERLIN2 IDH1	14.29 2/14	0.06 2/343	0,79698703

GO:0048518	positive regulation of biological process	Any process that activates or increases the frequency, rate	ALPL CNTFR SH3GLE	21.43 3/14	0.06 3/495	0,79698703
GO:0007399	nervous system development	The process whose specific outcome is the progression of	MARCKS	7.14 1/14	0.06 1/171	0,79698703
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units	ir BSPRY KRT10	14.29 2/14	0.06 2/341	0,79698703
GO:0031326	regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent	of ERLIN2 IDH1	14.29 2/14	0.06 2/338	0,79698703
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent	of ERLIN2 IDH1 SH3GL	21.43 3/14	0.06 3/502	0,79698703
GO:0051649	establishment of localization in cell	Any process, occurring in a cell, that localizes a substance	in NAPA	7.14 1/14	0.06 1/178	0,804324588
GO:0071704	organic substance metabolic process	The chemical reactions and pathways involving an organic	ALPL ANXA7 BSPRY	57.14 8/14	0.06 8/123	0,8067419
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not	ALPL ANXA7 BSPRY	92.86 13/14	0.07 13/18	0,81858918
GO:0051239	regulation of multicellular organismal process	Any process that modulates the frequency, rate or extent	of ALPL	7.14 1/14	0.05 1/194	0,832200855
GO:0002376	immune system process	Any process involved in the development or functioning of	GP2	7.14 1/14	0.05 1/204	0,847565399
GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency	of ERLIN2	7.14 1/14	0.05 1/203	0,847565399
GO:0048523	negative regulation of cellular process	Any process that stops, prevents, or reduces the frequency	of CNTFR ERLIN2	14.29 2/14	0.05 2/385	0,848931299
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated	by ALPL	7.14 1/14	0.05 1/210	0,854299974
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism	ALPL ANXA7 BSPRY	57.14 8/14	0.06 8/129	0,864376958
GO:004237	cellular metabolic process	The chemical reactions and pathways by which individual	of ALPL ANXA7 BSPRY	50.00 7/14	0.06 7/115	0,864687819
GO:0007166	cell surface receptor signaling pathway	A series of molecular signals initiated by activation of a	receptor CNTFR	7.14 1/14	0.04 1/225	0,872935767
GO:0007154	cell communication	Any process that mediates interactions between a cell and	CNTFR ERLIN2 SH3G	21.43 3/14	0.05 3/606	0,903627165
GO:0010605	negative regulation of macromolecule metabolic process	Any process that decreases the frequency, rate or extent	of ANXA7	7.14 1/14	0.04 1/256	0,910119162
GO:0048522	positive regulation of cellular process	Any process that activates or increases the frequency, rate	CNTFR SH3GLB1	14.29 2/14	0.04 2/448	0,910119162
GO:0031325	positive regulation of cellular metabolic process	Any process that activates or increases the frequency, rate	SH3GLB1	7.14 1/14	0.04 1/263	0,914830252
GO:0006807	nitrogen compound metabolic process	The chemical reactions and pathways involving organic or	inorganic ALPL BSPRY CD5L EF	42.86 6/14	0.05 6/109	0,919988415
GO:0016043	cellular component organization	A process that results in the assembly, arrangement of	constituents KRT10 MARCKS SH3	21.43 3/14	0.05 3/635	0,919988415
GO:0043170	macromolecule metabolic process	The chemical reactions and pathways involving macromole	cules ANXA7 BSPRY CD5L	42.86 6/14	0.05 6/109	0,919988415
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent	of ERLIN2 IDH1	14.29 2/14	0.04 2/485	0,930689335
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent	molecules KRT10 MARCKS SH3	21.43 3/14	0.05 3/656	0,930689335
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent	of ALPL ANXA7 CNTFR	42.86 6/14	0.05 6/111	0,931829975
GO:0065008	regulation of biological quality	Any process that modulates a qualitative or quantitative	trait ALPL	7.14 1/14	0.03 1/295	0,932184262
GO:0042429	cellular biosynthetic process	The chemical reactions and pathways resulting in the form	of ERLIN2 IDH1	14.29 2/14	0.04 2/509	0,941637763
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the form	of ERLIN2 IDH1	14.29 2/14	0.04 2/516	0,944150782
GO:0009058	biosynthetic process	The chemical reactions and pathways resulting in the form	of ERLIN2 IDH1	14.29 2/14	0.04 2/523	0,94611299
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to	trigger CNTFR ERLIN2	14.29 2/14	0.04 2/564	0,96237207
GO:0065007	biological regulation	Any process that modulates a measurable attribute of any	ALPL ANXA7 CNTFR	42.86 6/14	0.05 6/119	0,96237207
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the form	of ERLIN2	7.14 1/14	0.03 1/355	0,96237207
GO:0023052	signaling	The entirety of a process in which information is transmit	ted CNTFR ERLIN2	14.29 2/14	0.03 2/602	0,97662684
GO:004238	primary metabolic process	The chemical reactions and pathways involving those com	ponents BSPRY CD5L ERLIN2	35.71 5/14	0.04 5/114	0,988590329
GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent	of ANXA7	7.14 1/14	0.02 1/434	0,988590329
GO:1901360	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyc	lic ALPL ERLIN2	14.29 2/14	0.03 2/706	0,995002214
GO:0050794	regulation of cellular process	Any process that modulates the frequency, rate or extent	of CNTFR ERLIN2 IDH1	28.57 4/14	0.04 4/103	0,995002214
GO:0010467	gene expression	The process in which a gene's sequence is converted into a	transcript ANXA7 CD5L	14.29 2/14	0.03 2/748	0,996675729
GO:0034641	cellular nitrogen compound metabolic process	The chemical reactions and pathways involving various org	anic ALPL IDH1	14.29 2/14	0.03 2/759	0,996675729
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent	of ANXA7	7.14 1/14	0.02 1/555	0,996675729
GO:0006725	cellular aromatic compound metabolic process	The chemical reactions and pathways involving aromatic co	mpounds ALPL	7.14 1/14	0.01 1/689	0,99970648
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocycli	c ALPL	7.14 1/14	0.01 1/682	0,99970648
GO:0008150	biological_process	A biological process represents a specific objective that th	e ALPL ANXA7 BSPRY	100.00 14/14	0.07 14/20	1

sPLS_LPLactivity_Enrichment_GO_BP_of_13prot_contributing_to_LL_group

GO_BP	Name	Function	Gene Name	Term frequen	Term frequen	P-value (fdr)
GO:1903725	regulation of phospholipid metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67 2/12	8.00 2/25	0.0635563
GO:1905667	negative regulation of protein localization to endosome	Any process that stops, prevents or reduces the frequency, rate or extent of	ANKRD13A	8.33 1/12	100.00 1/1	0.0650423
GO:0150173	positive regulation of phosphatidylcholine metabolic process	Any process that activates or increases the frequency, rate or extent of	ACSL3	8.33 1/12	100.00 1/1	0.0650423
GO:2001247	positive regulation of phosphatidylcholine biosynthetic process	Any process that activates or increases the frequency, rate or extent of	ACSL3	8.33 1/12	100.00 1/1	0.0650423
GO:0051049	regulation of transport	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A NDRG4 PHB2 SURF4	41.67 5/12	0.42 5/1201	0.0650423
GO:0016192	vesicle-mediated transport	A cellular transport process in which transported substances	ACSL3 ANKRD13A AP2B1 NDRG4 SURF4	41.67 5/12	0.39 5/1276	0.0650423
GO:0033600	negative regulation of mammary gland epithelial cell proliferation	Any process that stops, prevents or reduces the rate or extent of	PHB2	8.33 1/12	25.00 1/4	0.0677404
GO:0032879	regulation of localization	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A NDRG4 PHB2 SURF4	41.67 5/12	0.24 5/2055	0.0677404
GO:0097384	cellular lipid biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	12.50 1/8	0.0677404
GO:1904732	regulation of electron transfer activity	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	14.29 1/7	0.0677404
GO:1904959	regulation of cytochrome-c oxidase activity	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	16.67 1/6	0.0677404
GO:0060341	regulation of cellular localization	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A NDRG4	25.00 3/12	0.53 3/565	0.0677404
GO:0042695	telarche	The beginning of development of the breasts in the female.	PHB2	8.33 1/12	20.00 1/5	0.0677404
GO:0033036	macromolecule localization	Any process in which a macromolecule is transported to, or r	ACSL3 ANKRD13A AP2B1 PHB2 SQLE SURF4	50.00 6/12	0.25 6/2363	0.0677404
GO:0010637	negative regulation of mitochondrial fusion	Any process that decreases the frequency, rate or extent of	VAT1	8.33 1/12	14.29 1/7	0.0677404
GO:0042996	regulation of Golgi to plasma membrane protein transport	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	12.50 1/8	0.0677404
GO:0042998	positive regulation of Golgi to plasma membrane protein transport	Any process that activates or increases the frequency, rate or ACSL3		8.33 1/12	20.00 1/5	0.0677404
GO:0098876	vesicle-mediated transport to the plasma membrane	The directed movement of substances to the plasma membr	ACSL3 NDRG4	16.67 2/12	1.72 2/116	0.0677404
GO:0060744	mammary gland branching involved in telarche	The process in which the branching structure of the mamma	PHB2	8.33 1/12	20.00 1/5	0.0677404
GO:2001245	regulation of phosphatidylcholine biosynthetic process	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	50.00 1/2	0.0677404
GO:0034379	very-low-density lipoprotein particle assembly	The non-covalent aggregation and arrangement of proteins a	ACSL3	8.33 1/12	16.67 1/6	0.0677404
GO:0060627	regulation of vesicle-mediated transport	Any process that modulates the rate, frequency, or extent of	ACSL3 ANKRD13A NDRG4	25.00 3/12	0.78 3/385	0.0677404
GO:1990051	activation of protein kinase C activity	Any process that initiates the activity of the inactive enzyme	PHB2	8.33 1/12	25.00 1/4	0.0677404
GO:0008611	ether lipid biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	12.50 1/8	0.0677404
GO:0006629	lipid metabolic process	The chemical reactions and pathways involving lipids, compo	ACSL3 FASN PHB2 SQLE	33.33 4/12	0.36 4/1124	0.0677404
GO:0060762	regulation of branching involved in mammary gland duct morphogen	Any process that modulates the rate, frequency, or extent of	PHB2	8.33 1/12	25.00 1/4	0.0677404
GO:0006898	receptor-mediated endocytosis	An endocytosis process in which cell surface receptors ensur	ANKRD13A AP2B1	16.67 2/12	1.16 2/173	0.0677404
GO:0046504	glycerol ether biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	12.50 1/8	0.0677404
GO:0006897	endocytosis	A vesicle-mediated transport process in which cells take up e	ANKRD13A AP2B1 SURF4	25.00 3/12	0.64 3/466	0.0677404
GO:0008104	protein localization	Any process in which a protein is transported to, or maintain	ACSL3 ANKRD13A AP2B1 PHB2 SURF4	41.67 5/12	0.25 5/1967	0.0677404
GO:0002091	negative regulation of receptor internalization	Any process that stops, prevents, or reduces the frequency, r	ANKRD13A	8.33 1/12	12.50 1/8	0.0677404
GO:0070374	positive regulation of ERK1 and ERK2 cascade	Any process that activates or increases the frequency, rate o	NDRG4 PHB2	16.67 2/12	1.36 2/147	0.0677404
GO:0006010	transport	The directed movement of substances (such as macromolecu	ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PH	58.33 7/12	0.18 7/3886	0.0677404
GO:0015031	protein transport	The directed movement of proteins into, out of or within a c	ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.34 4/1193	0.0677404
GO:0030223	neutrophil differentiation	The process in which a myeloid precursor cell acquires the s	FASN	8.33 1/12	12.50 1/8	0.0677404
GO:0071073	positive regulation of phospholipid biosynthetic process	Any process that activates or increases the frequency, rate o	ACSL3	8.33 1/12	14.29 1/7	0.0677404
GO:0150172	regulation of phosphatidylcholine metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	16.67 1/6	0.0677404
GO:0008610	lipid biosynthetic process	The chemical reactions and pathways resulting in the formati	ACSL3 FASN SQLE	25.00 3/12	0.57 3/525	0.0677404
GO:0045136	development of secondary sexual characteristics	The process whose specific outcome is the progression of the	PHB2	8.33 1/12	12.50 1/8	0.0677404
GO:1900208	regulation of cardioliipin metabolic process	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	33.33 1/3	0.0677404
GO:0051179	localization	Any process in which a cell, a substance, or a cellular entity, s	ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PH	66.67 8/12	0.15 8/5413	0.0677404
GO:0051234	establishment of localization	Any process that localizes a substance or cellular component	ACSL3 ANKRD13A AP2B1 ATP13A3 NDRG4 PH	58.33 7/12	0.17 7/4033	0.0677404
GO:0031536	positive regulation of exit from mitosis	Any process that activates or increases the rate of progressio	PHB2	8.33 1/12	20.00 1/5	0.0677404
GO:0030879	mammary gland development	The process whose specific outcome is the progression of the	FASN PHB2	16.67 2/12	1.79 2/112	0.0677404
GO:0046543	development of secondary female sexual characteristics	The process whose specific outcome is the progression of the	PHB2	8.33 1/12	16.67 1/6	0.0677404
GO:0010876	lipid localization	Any process in which a lipid is transported to, or maintained	ACSL3 SQLE SURF4	25.00 3/12	0.80 3/373	0.0677404
GO:0045184	establishment of protein localization	The directed movement of a protein to a specific location.	ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.31 4/1286	0.0697581
GO:1905666	regulation of protein localization to endosome	Any process that modulates the frequency, rate or extent of	ANKRD13A	8.33 1/12	11.11 1/9	0.0697581
GO:0090557	establishment of endothelial intestinal barrier	The establishment of a barrier between endothelial cell layer	FASN	8.33 1/12	11.11 1/9	0.0697581
GO:1901503	ether biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	11.11 1/9	0.0697581
GO:0140042	lipid droplet formation	A process that results in the assembly, arrangement of consti	SQLE	8.33 1/12	11.11 1/9	0.0697581
GO:0033147	negative regulation of intracellular estrogen receptor signaling pathw	Any process that stops, prevents, or reduces the frequency, r	PHB2	8.33 1/12	10.00 1/10	0.0707808
GO:1903727	positive regulation of phospholipid metabolic process	Any process that activates or increases the frequency, rate o	ACSL3	8.33 1/12	10.00 1/10	0.0707808
GO:0010635	regulation of mitochondrial fusion	Any process that modulates the frequency, rate or extent of	VAT1	8.33 1/12	10.00 1/10	0.0707808
GO:0010642	negative regulation of platelet-derived growth factor receptor signal	Any process that stops, prevents, or reduces the frequency, r	NDRG4	8.33 1/12	10.00 1/10	0.0707808
GO:0007096	regulation of exit from mitosis	Any process involved in the progression from anaphase/teloe	PHB2	8.33 1/12	9.09 1/11	0.0751064
GO:0140374	antiviral innate immune response	A defense response against viruses mediated through an inn	PHB2	8.33 1/12	9.09 1/11	0.0751064
GO:0014912	negative regulation of smooth muscle cell migration	Any process that stops, prevents, or reduces the frequency, r	NDRG4	8.33 1/12	8.33 1/12	0.0753061
GO:0007202	activation of phospholipase C activity	The initiation of the activity of the inactive enzyme phosphol	PHB2	8.33 1/12	8.33 1/12	0.0753061
GO:0070372	regulation of ERK1 and ERK2 cascade	Any process that modulates the frequency, rate or extent of	NDRG4 PHB2	16.67 2/12	0.95 2/211	0.0753061
GO:0071071	regulation of phospholipid biosynthetic process	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	8.33 1/12	0.0753061
GO:0046485	ether lipid metabolic process	The chemical reactions and pathways involving ether lipids, l	FASN	8.33 1/12	8.33 1/12	0.0753061
GO:0007071	ERK1 and ERK2 cascade	An intracellular protein kinase cascade containing at least ER	NDRG4 PHB2	16.67 2/12	0.89 2/224	0.0786281
GO:0023035	CD40 signaling pathway	A series of molecular signals initiated by the binding of the	PHB2	8.33 1/12	7.69 1/13	0.0790106
GO:0007072	cellular macromolecule localization	Any process in which a macromolecule is transported to, and	ACSL3 ANKRD13A AP2B1 PHB2	33.33 4/12	0.28 4/1438	0.0791132
GO:0034613	cellular protein localization	Any process in which a protein is transported to, and/or main	ACSL3 ANKRD13A AP2B1 PHB2	33.33 4/12	0.28 4/1432	0.0791132
GO:0019216	regulation of lipid metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67 2/12	0.81 2/246	0.0791132
GO:0034377	plasma lipoprotein particle assembly	The non-covalent aggregation and arrangement of proteins a	ACSL3	8.33 1/12	6.25 1/16	0.0791132
GO:0006662	glycerol ether metabolic process	The chemical reactions and pathways involving glycerol ether	FASN	8.33 1/12	6.67 1/15	0.0791132
GO:0006656	phosphatidylcholine biosynthetic process	The chemical reactions and pathways resulting in the formati	ACSL3	8.33 1/12	6.25 1/16	0.0791132
GO:0033599	regulation of mammary gland epithelial cell proliferation	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	6.25 1/16	0.0791132
GO:0060973	cell migration involved in heart development	The orderly movement of a cell from one site to another th	NDRG4	8.33 1/12	6.67 1/15	0.0791132
GO:0035336	long-chain fatty-acyl-CoA metabolic process	The chemical reactions and pathways involving long-chain fat	ACSL3	8.33 1/12	6.25 1/16	0.0791132
GO:0140014	mitotic nuclear division	A mitotic cell cycle process comprising the steps by which the	CUL9 PHB2	16.67 2/12	0.81 2/248	0.0791132
GO:0010155	regulation of proton transport	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	6.25 1/16	0.0791132
GO:0042953	lipoprotein transport	The directed movement of any conjugated, water-soluble pr	SURF4	8.33 1/12	6.67 1/15	0.0791132
GO:0044872	lipoprotein localization	Any process in which a lipoprotein is transported to, or main	SURF4	8.33 1/12	6.67 1/15	0.0791132
GO:0048261	negative regulation of receptor-mediated endocytosis	Any process that stops, prevents, or reduces the frequency, r	ANKRD13A	8.33 1/12	6.67 1/15	0.0791132
GO:0051641	cellular localization	A cellular localization process whereby a substance or cellula	ACSL3 ANKRD13A AP2B1 NDRG4 PHB2	41.67 5/12	0.21 5/2418	0.0791132
GO:2001135	regulation of endocytic recycling	Any process that modulates the frequency, rate or extent of	NDRG4	8.33 1/12	5.88 1/17	0.0815475
GO:0032048	cardiolipin metabolic process	The chemical reactions and pathways involving cardiolipin, 1	PHB2	8.33 1/12	5.88 1/17	0.0815475
GO:0006650	glycerophospholipid metabolic process	The chemical reactions and pathways involving glycerophosph	ACSL3 PHB2	16.67 2/12	0.76 2/262	0.0816634
GO:0060749	mammary gland alveolus development	The progression of the mammary gland alveolus over time, fr	PHB2	8.33 1/12	5.26 1/19	0.0826025
GO:0065005	protein-lipid complex assembly	The aggregation, arrangement and bonding together of prot	ACSL3	8.33 1/12	5.00 1/20	0.0826025
GO:0034389	lipid droplet organization	A process that is carried out at the cellular level which resu	SQLE	8.33 1/12	5.00 1/20	0.0826025
GO:0018904	ether metabolic process	The chemical reactions and pathways involving organic ether	FASN	8.33 1/12	5.00 1/20	0.0826025
GO:0140354	lipid import into cell	The directed movement of a lipid from outside of a cell into	ACSL3	8.33 1/12	5.26 1/19	0.0826025
GO:0036010	protein localization to endosome	A process in which a protein is transported to, or maintained	ANKRD13A	8.33 1/12	5.26 1/19	0.0826025
GO:0010863	positive regulation of phospholipase C activity	Any process that increases the rate of phospholipase C activi	PHB2	8.33 1/12	5.00 1/20	0.0826025
GO:0010458	exit from mitosis	The cell cycle transition where a cell leaves M phase and entr	PHB2	8.33 1/12	5.00 1/20	0.0826025
GO:0039529	RIG-I signaling pathway	Any series of molecular signals generated as a consequence c	PHB2	8.33 1/12	5.00 1/20	0.0826025
GO:0044539	long-chain fatty acid import into cell	The directed movement of a long-chain fatty acid from outsid	ACSL3	8.33 1/12	5.56 1/18	0.0826025
GO:0061377	mammary gland lobule development	The progression of the mammary gland lobule over time, fro	PHB2	8.33 1/12	5.26 1/19	0.0826025
GO:0071705	nitrogen compound transport	The directed movement of nitrogen-containing compounds in	ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.25 4/1587	0.0826025
GO:0010640	regulation of platelet-derived growth factor receptor signaling pathw	Any process that modulates the frequency, rate or extent of	NDRG4	8.33 1/12	4.76 1/21	0.0826635
GO:1900274	regulation of phospholipase C activity	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	4.76 1/21	0.0826635
GO:0060444	branching involved in mammary gland duct morphogenesis	The process in which the branching structure of the mamma	PHB2	8.33 1/12	4.76 1/21	0.0826635
GO:0044255	cellular lipid metabolic process	The chemical reactions and pathways involving lipids, as car	ACSL3 FASN PHB2	25.00 3/12	0.35 3/852	0.0826635
GO:0071353	cellular response to interleukin-4	Any process that results in a change in state or activity of a	ci FASN	8.33 1/12	4.76 1/21	0.0826635
GO:0035337	fatty-acyl-CoA metabolic process	The chemical reactions and pathways involving fatty-acyl-C	ACSL3	8.33 1/12	4.55 1/22	0.0836905
GO:0070670	response to interleukin-4	Any process that results in a change in state or activity of a	ci FASN	8.33 1/12	4.55 1/22	0.0836905
GO:0002068	glandular epithelial cell development	The process whose specific outcome is the progression of a	g FASN	8.33 1/12	4.55 1/22	0.0836905
GO:0048732	gland development	The process whose specific outcome is the progression of a	g FASN PHB2	16.67 2/12	0.65 2/306	0.0874493
GO:0004423	mitophagy	The selective autophagy process in which a mitochondrion is	PHB2	8.33 1/12	4.17 1/24	0.0886417
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in respor	Any series of molecular signals generated as a consequence c	PHB2	8.33 1/12	4.17 1/24	0.0886417
GO:0006631	fatty acid metabolic process	The chemical reactions and pathways involving fatty acids, al	ACSL3 FASN	16.67 2/12	0.63 2/316	0.0895066
GO:0033043	regulation of organelle organization	Any process that modulates the frequency, rate or extent of	CUL9 SURF4 VAT1	25.00 3/12	0.33 3/903	0.0895066

GO:0006869	lipid transport	The directed movement of lipids into, out of or within a cell, ACSL3 SURF4	16.67 2/12	0.60 2/332	0,0906447
GO:0033598	mammary gland epithelial cell proliferation	The multiplication or reproduction of mammary gland epithelium PHB2	8.33 1/12	3.70 1/27	0,0906447
GO:0014910	regulation of smooth muscle cell migration	Any process that modulates the frequency, rate or extent of NDRG4	8.33 1/12	3.85 1/26	0,0906447
GO:0033146	regulation of intracellular estrogen receptor signaling pathway	Any process that modulates the frequency, rate or extent of PHB2	8.33 1/12	3.85 1/26	0,0906447
GO:0006603	mammary gland duct morphogenesis	The process in which anatomical structures of the mammary PHB2	8.33 1/12	3.70 1/27	0,0906447
GO:0046471	phosphatidylglycerol metabolic process	The chemical reactions and pathways involving phosphatidylglycerol PHB2	8.33 1/12	3.70 1/27	0,0906447
GO:0030224	monocyte differentiation	The process in which a relatively unspecialized myeloid precursor FASN	8.33 1/12	3.70 1/27	0,0906447
GO:0008053	mitochondrial fusion	Merging of two or more mitochondria within a cell to form a VAT1	8.33 1/12	3.85 1/26	0,0906447
GO:0051128	regulation of cellular component organization	Any process that modulates the frequency, rate or extent of ANKRD13A CUL9 SURF4 VAT1	33.33 4/12	0.23 4/1732	0,0906447
GO:0048662	negative regulation of smooth muscle cell proliferation	Any process that stops, prevents or reduces the rate or extent NDRG4	8.33 1/12	3.57 1/28	0,0914053
GO:0006644	phospholipid metabolic process	The chemical reactions and pathways involving phospholipid: ACSL3 PHB2	16.67 2/12	0.59 2/338	0,0914053
GO:0030851	granulocyte differentiation	The process in which a myeloid precursor cell acquires the specific FASN	8.33 1/12	3.57 1/28	0,0914053
GO:0045806	negative regulation of endocytosis	Any process that stops, prevents, or reduces the frequency, rate or extent ANKRD13A	8.33 1/12	3.45 1/29	0,0928188
GO:0043001	Golgi to plasma membrane protein transport	The directed movement of proteins from the Golgi to the plasma membrane ACSL3	8.33 1/12	3.45 1/29	0,0928188
GO:0046486	glycerolipid metabolic process	The chemical reactions and pathways involving glycerolipids, ACSL3 PHB2	16.67 2/12	0.58 2/347	0,0936966
GO:0033144	negative regulation of intracellular steroid hormone receptor signaling pathway	Any process that stops, prevents, or reduces the frequency, rate or extent PHB2	8.33 1/12	3.33 1/30	0,0944323
GO:0008542	visual learning	Any process in an organism in which a change in behavior of NDRG4	8.33 1/12	3.23 1/31	0,0944809
GO:0007346	regulation of mitotic cell cycle	Any process that modulates the rate or extent of progress through the cell cycle CUL9 PHB2	16.67 2/12	0.57 2/353	0,0944809
GO:0010518	positive regulation of phospholipase activity	Any process that increases the frequency, rate or extent of phospholipase activity PHB2	8.33 1/12	3.23 1/31	0,0944809
GO:0071827	plasma lipoprotein particle organization	A protein-lipid complex subunit organization process that results in the formation of ACSL3	8.33 1/12	3.23 1/31	0,0944809
GO:0014909	smooth muscle cell migration	The orderly movement of a smooth muscle cell from one site to another NDRG4	8.33 1/12	3.12 1/32	0,0967403
GO:0000280	nuclear division	The division of a cell nucleus into two nuclei, with DNA and organelles CUL9 PHB2	16.67 2/12	0.54 2/372	0,0988684
GO:0007632	visual behavior	The behavior of an organism in response to a visual stimulus. NDRG4	8.33 1/12	3.03 1/33	0,0988684
GO:0043410	positive regulation of MAPK cascade	Any process that activates or increases the frequency, rate or extent of NDRG4 PHB2	16.67 2/12	0.54 2/373	0,0988684
GO:0010823	negative regulation of mitochondrion organization	Any process that decreases the frequency, rate or extent of a VAT1	8.33 1/12	2.94 1/34	0,0988684
GO:0071825	protein-lipid complex subunit organization	Any process in which macromolecules aggregate, disaggregate or assemble ACSL3	8.33 1/12	2.94 1/34	0,0988684
GO:0002090	regulation of receptor internalization	Any process that modulates the frequency, rate or extent of internalization ANKRD13A	8.33 1/12	2.78 1/36	0,1015722
GO:0002066	columnar/cuboidal epithelial cell development	The process whose specific outcome is the progression of a cell to become a columnar epithelial cell FASN	8.33 1/12	2.78 1/36	0,1015722
GO:1902808	positive regulation of cell cycle G1/S phase transition	Any signaling pathway that activates or increases the activity of PHB2	8.33 1/12	2.78 1/36	0,1015722
GO:0010517	regulation of phospholipase activity	Any process that modulates the frequency, rate or extent of phospholipase activity PHB2	8.33 1/12	2.78 1/36	0,1015722
GO:0061028	establishment of endothelial barrier	The establishment of a barrier between endothelial cell layers FASN	8.33 1/12	2.56 1/39	0,1046019
GO:0060443	mammary gland morphogenesis	The process in which anatomical structures of the mammary gland PHB2	8.33 1/12	2.56 1/39	0,1046019
GO:0016126	sterol biosynthetic process	The chemical reactions and pathways resulting in the formation of cholesterol SQLE	8.33 1/12	2.56 1/39	0,1046019
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	Any series of molecular signals generated as a consequence of the binding of a ligand to a cytoplasmic pattern recognition receptor PHB2	8.33 1/12	2.56 1/39	0,1046019
GO:0019568	fatty acid derivative metabolic process	The chemical reactions and pathways involving fatty acid derivatives ACSL3	8.33 1/12	2.63 1/38	0,1046019
GO:0030520	intracellular estrogen receptor signaling pathway	Any series of molecular signals generated as a consequence of the binding of a ligand to an intracellular estrogen receptor PHB2	8.33 1/12	2.63 1/38	0,1046019
GO:0002639	positive regulation of immunoglobulin production	Any process that activates or increases the frequency, rate or extent of immunoglobulin production PHB2	8.33 1/12	2.63 1/38	0,1046019
GO:0006688	regulation of morphogenesis of a branching structure	Any process that modulates the rate, frequency, or extent of branching PHB2	8.33 1/12	2.50 1/40	0,106515
GO:0071702	organic substance transport	The directed movement of organic substances into, out of or within a cell ACSL3 AP2B1 PHB2 SURF4	33.33 4/12	0.20 4/1968	0,1066871
GO:0048285	organelle fission	The creation of two or more organelles by division of one organelle CUL9 PHB2	16.67 2/12	0.48 2/414	0,1075817
GO:0072583	clathrin-dependent endocytosis	An endocytosis process that begins when material is taken up by a clathrin-coated vesicle AP2B1	8.33 1/12	2.44 1/41	0,1075817
GO:0060193	positive regulation of lipase activity	Any process that increases the frequency, rate or extent of lipase activity PHB2	8.33 1/12	2.33 1/43	0,1113385
GO:0002067	glandular epithelial cell differentiation	The process in which a relatively unspecialized cell acquires the characteristics of a glandular epithelial cell FASN	8.33 1/12	2.27 1/44	0,1123881
GO:0006893	Golgi to plasma membrane transport	The directed movement of substances from the Golgi to the plasma membrane ACSL3	8.33 1/12	2.27 1/44	0,1123881
GO:0014812	muscle cell migration	The orderly movement of a muscle cell from one site to another NDRG4	8.33 1/12	2.22 1/45	0,1141551
GO:0007005	mitochondrion organization	A process that is carried out at the cellular level which results in the formation of mitochondria PHB2 VAT1	16.67 2/12	0.45 2/444	0,1170456
GO:1903078	positive regulation of protein localization to plasma membrane	Any process that activates or increases the frequency, rate or extent of protein localization to the plasma membrane ACSL3	8.33 1/12	2.08 1/48	0,1170456
GO:0061951	establishment of protein localization to plasma membrane	The directed movement of a protein to a specific location on the plasma membrane ACSL3	8.33 1/12	2.13 1/47	0,1170456
GO:0009706	regulation of plasma lipoprotein particle levels	Any process involved in the maintenance of internal levels of lipoproteins ACSL3	8.33 1/12	2.08 1/48	0,1170456
GO:1905330	regulation of morphogenesis of an epithelium	Any process that modulates the frequency, rate or extent of morphogenesis PHB2	8.33 1/12	2.08 1/48	0,1170456
GO:0042127	regulation of cell population proliferation	Any process that modulates the frequency, rate or extent of cell population proliferation NDRG4 PHB2 SQLE	25.00 3/12	0.26 3/1156	0,1170456
GO:0046470	phosphatidylcholine metabolic process	The chemical reactions and pathways involving phosphatidylcholine ACSL3	8.33 1/12	2.04 1/49	0,1179583
GO:0048856	anatomical structure development	The biological process whose specific outcome is the progression of an anatomical structure ACSL3 CMTM8 FASN NDRG4 PHB2 VAT1	50.00 6/12	0.14 6/4373	0,1179583
GO:0048278	vesicle docking	The initial attachment of a transport vesicle membrane to a target membrane NDRG4	8.33 1/12	2.00 1/50	0,1188472
GO:0048008	platelet-derived growth factor receptor signaling pathway	The series of molecular signals generated as a consequence of the binding of a ligand to a platelet-derived growth factor receptor NDRG4	8.33 1/12	2.00 1/50	0,1188472
GO:0008306	associative learning	Learning by associating a stimulus (the cause) with a particular response NDRG4	8.33 1/12	1.96 1/51	0,1197131
GO:0007062	sister chromatid cohesion	The cell cycle process in which the sister chromatids of a replicated chromosome remain together PHB2	8.33 1/12	1.96 1/51	0,1197131
GO:0032787	monocarboxylic acid metabolic process	The chemical reactions and pathways involving monocarboxylic acids FASN	16.67 2/12	0.43 2/470	0,120659
GO:0008285	negative regulation of cell population proliferation	Any process that stops, prevents or reduces the rate or extent of cell population proliferation NDRG4 PHB2	16.67 2/12	0.43 2/469	0,120659
GO:0060191	regulation of lipase activity	Any process that modulates the frequency, rate or extent of lipase activity PHB2	8.33 1/12	1.92 1/52	0,120659
GO:0001885	endothelial cell development	The progression of an endothelial cell over time, from its formation FASN	8.33 1/12	1.89 1/53	0,1213794
GO:1904377	positive regulation of protein localization to cell periphery	Any process that activates or increases the frequency, rate or extent of protein localization to the cell periphery ACSL3	8.33 1/12	1.85 1/54	0,1229043
GO:0098586	cellular response to virus	Any process that results in a change in state or activity of a cell in response to a virus PHB2	8.33 1/12	1.82 1/55	0,12441
GO:0002637	regulation of immunoglobulin production	Any process that modulates the frequency, rate, or extent of immunoglobulin production PHB2	8.33 1/12	1.79 1/56	0,125165
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	Any process that modulates the frequency, rate or extent of intracellular steroid hormone receptor signaling pathway PHB2	8.33 1/12	1.79 1/56	0,125165
GO:1901224	positive regulation of NIK/NF-kappaB signaling	Any process that activates or increases the frequency, rate or extent of NIK/NF-kappaB signaling PHB2	8.33 1/12	1.75 1/57	0,1266291
GO:0046889	positive regulation of lipid biosynthetic process	Any process that activates or increases the frequency, rate or extent of lipid biosynthesis ACSL3	8.33 1/12	1.72 1/58	0,1280752
GO:0015909	long-chain fatty acid transport	The directed movement of long-chain fatty acids into, out of or within a cell ACSL3	8.33 1/12	1.69 1/59	0,1293036
GO:0006996	organelle organization	A process that is carried out at the cellular level which results in the formation of an organelle CUL9 PHB2 SQLE SURF4 VAT1	41.67 5/12	0.15 5/3330	0,130146
GO:0061180	mammary gland epithelium development	The process whose specific outcome is the progression of the mammary gland PHB2	8.33 1/12	1.67 1/60	0,130146
GO:0051129	negative regulation of cellular component organization	Any process that stops, prevents, or reduces the frequency, rate or extent of cellular component organization ANKRD13A VAT1	16.67 2/12	0.39 2/507	0,130146
GO:0061912	selective autophagy	The macroautophagy process in which specific structures are targeted for degradation PHB2	8.33 1/12	1.64 1/61	0,1308302
GO:0010564	regulation of cell cycle process	Any process that modulates a cellular process that is involved in the cell cycle CUL9 PHB2	16.67 2/12	0.38 2/520	0,1340659
GO:0048259	regulation of receptor-mediated endocytosis	Any process that modulates the frequency, rate or extent of receptor-mediated endocytosis ANKRD13A	8.33 1/12	1.59 1/63	0,1340659
GO:0043408	regulation of MAPK cascade	Any process that modulates the frequency, rate or extent of MAPK cascade NDRG4 PHB2	16.67 2/12	0.38 2/524	0,1352119
GO:0000422	autophagy of mitochondrion	The autophagic process in which mitochondria are delivered to lysosomes PHB2	8.33 1/12	1.52 1/66	0,1375199
GO:0061726	mitochondrion disassembly	The disassembly of a mitochondrion into its constituent components PHB2	8.33 1/12	1.52 1/66	0,1375199
GO:1901992	positive regulation of mitotic cell cycle phase transition	Any process that activates or increases the frequency, rate or extent of mitotic cell cycle phase transition PHB2	8.33 1/12	1.49 1/67	0,1380196
GO:0001676	long-chain fatty acid metabolic process	The chemical reactions and pathways involving long-chain fatty acids ACSL3	8.33 1/12	1.47 1/68	0,1380196
GO:0051668	localization within membrane	Any process in which a substance or cellular entity, such as a protein, is localized to a membrane ACSL3 NDRG4	16.67 2/12	0.37 2/541	0,1380196
GO:0032456	endocytic recycling	The directed movement of membrane-bounded vesicles from the plasma membrane back to the plasma membrane NDRG4	8.33 1/12	1.47 1/68	0,1380196
GO:0140056	organelle localization by membrane tethering	The process by which an organelle membrane interacts with another membrane NDRG4	8.33 1/12	1.49 1/67	0,1380196
GO:0019915	lipid storage	The accumulation and maintenance in cells or tissues of lipid droplets SQLE	8.33 1/12	1.45 1/69	0,1391169
GO:0046907	intracellular transport	The directed movement of substances within a cell. ACSL3 NDRG4 PHB2	25.00 3/12	0.22 3/1335	0,1396249
GO:0051341	regulation of oxidoreductase activity	Any process that modulates the frequency, rate or extent of oxidoreductase activity PHB2	8.33 1/12	1.43 1/70	0,1396249
GO:0002065	columnar/cuboidal epithelial cell differentiation	The process in which a relatively unspecialized cell acquires the characteristics of a columnar epithelial cell FASN	8.33 1/12	1.39 1/72	0,1398364
GO:0032502	developmental process	A biological process whose specific outcome is the progression of an organism ACSL3 CMTM8 FASN NDRG4 PHB2 VAT1	50.00 6/12	0.13 6/4755	0,1398364
GO:0035383	thioester metabolic process	The chemical reactions and pathways involving thioesters, ACSL3	8.33 1/12	1.39 1/72	0,1398364
GO:0015908	fatty acid transport	The directed movement of fatty acids into, out of or within a cell ACSL3	8.33 1/12	1.41 1/71	0,1398364
GO:0006637	acyl-CoA metabolic process	The chemical reactions and pathways involving acyl-CoAs, ACSL3	8.33 1/12	1.39 1/72	0,1398364
GO:0048660	regulation of smooth muscle cell proliferation	Any process that modulates the frequency, rate or extent of smooth muscle cell proliferation NDRG4	8.33 1/12	1.41 1/71	0,1398364
GO:0048659	smooth muscle cell proliferation	The multiplication or reproduction of smooth muscle cells, resulting in the formation of smooth muscle NDRG4	8.33 1/12	1.37 1/73	0,1403721
GO:0022406	membrane docking	The initial attachment of a membrane or protein to a target membrane NDRG4	8.33 1/12	1.35 1/74	0,141545
GO:1905477	positive regulation of protein localization to membrane	Any process that activates or increases the frequency, rate or extent of protein localization to the membrane ACSL3	8.33 1/12	1.32 1/76	0,1438528
GO:0006892	post-Golgi vesicle-mediated transport	The directed movement of substances from the Golgi to other parts of the cell ACSL3	8.33 1/12	1.32 1/76	0,1438528
GO:1903047	mitotic cell cycle process	A process that is part of the mitotic cell cycle. CUL9 PHB2	16.67 2/12	0.34 2/584	0,147802
GO:0000165	MAPK cascade	An intracellular protein kinase cascade containing at least one MAPK NDRG4 PHB2	16.67 2/12	0.34 2/591	0,147802
GO:1901222	regulation of NIK/NF-kappaB signaling	Any process that modulates the frequency, rate or extent of NIK/NF-kappaB signaling PHB2	8.33 1/12	1.23 1/81	0,147802
GO:0008283	cell population proliferation	The multiplication or reproduction of cells, resulting in the formation of a population NDRG4 PHB2 SQLE	25.00 3/12	0.21 3/1409	0,147802
GO:0032880	regulation of protein localization	Any process that modulates the frequency, rate or extent of protein localization ACSL3 ANKRD13A	16.67 2/12	0.34 2/594	0,147802
GO:0045446	endothelial cell differentiation	The process in which a mesodermal, bone marrow or neural epithelial cell acquires the characteristics of an endothelial cell FASN	8.33 1/12	1.23 1/81	0,147802
GO:0002377	immunoglobulin production	The appearance of immunoglobulin due to biosynthesis or secretion PHB2	8.33 1/12	1.23 1/81	0,147802
GO:0032368	regulation of lipid transport	Any process that modulates the frequency, rate or extent of lipid transport SURF4	8.33 1/12	1.19 1/84	0,149056
GO:0048731	system development	The process whose specific outcome is the progression of an organism ACSL3 CMTM8 FASN NDRG4 PHB2	41.67 5/12	0.14 5/3612	0,149056
GO:0030518	intracellular steroid hormone receptor signaling pathway	A series of molecular signals generated as a consequence of the binding of a ligand to an intracellular steroid hormone receptor PHB2	8.33 1/12	1.19 1/84	0,149056
GO:0034032	purine nucleoside diphosphate metabolic process	The chemical reactions and pathways involving purine nucleoside diphosphates ACSL3	8.33 1/12	1.16 1/86	0,149056
GO:0007088	regulation of mitotic nuclear division	Any process that modulates the frequency, rate or extent of mitotic nuclear division CUL9	8.33 1/12	1.18 1/85	0,149056
GO:1903076	regulation of protein localization to plasma membrane	Any process that modulates the frequency, rate or extent of protein localization to the plasma membrane ACSL3	8.33 1/12	1.16 1/86	0,149056
GO:0033865	nucleoside diphosphate metabolic process	The chemical reactions and pathways involving nucleoside diphosphates ACSL3	8.33 1/12	1.16 1/86	0,149056

GO:1901989	positive regulation of cell cycle phase transition	Any process that activates or increases the frequency, rate or	8.33 1/12	1.18 1/85	0.149056
GO:0002702	positive regulation of production of molecular mediator of immune response	Any process that activates or increases the frequency, rate, o	8.33 1/12	1.20 1/83	0.149056
GO:0033875	ribonucleoside bisphosphate metabolic process	The chemical reactions and pathways involving a ribonucleos	8.33 1/12	1.16 1/86	0.149056
GO:0031623	receptor internalization	A receptor-mediated endocytosis process that results in the	8.33 1/12	1.19 1/84	0.149056
GO:0016043	cellular component organization	A process that results in the assembly, arrangement of const	58.33 7/12	0.11 7/6354	0.1495738
GO:0044281	small molecule metabolic process	The chemical reactions and pathways involving small molecu	25.00 3/12	0.21 3/1460	0.1509158
GO:0003158	endothelium development	The process whose specific outcome is the progression of an	8.33 1/12	1.12 1/89	0.1520562
GO:0040011	locomotion	Self-propelled movement of a cell or organism from one loca	25.00 3/12	0.20 3/1476	0.153326
GO:2000027	regulation of animal organ morphogenesis	Any process that modulates the frequency, rate or extent of	8.33 1/12	1.10 1/91	0.153326
GO:1903008	organelle disassembly	The disaggregation of an organelle into its constituent comp	8.33 1/12	1.10 1/91	0.153326
GO:0045931	positive regulation of mitotic cell cycle	Any process that activates or increases the rate or extent of	8.33 1/12	1.08 1/93	0.1545588
GO:0042552	myelination	The process in which myelin sheaths are formed and maintai	8.33 1/12	1.08 1/93	0.1545588
GO:0007612	learning	Any process in an organism in which a relatively long-lasting	8.33 1/12	1.08 1/93	0.1545588
GO:0008366	axon ensheathment	Any process in which the axon of a neuron is insulated, and t	8.33 1/12	1.05 1/95	0.1564306
GO:0007272	ensheathment of neurons	The process in which glial cells envelop neuronal cell bodies	8.33 1/12	1.05 1/95	0.1564306
GO:0032147	activation of protein kinase activity	Any process that initiates the activity of an inactive protein	8.33 1/12	1.04 1/96	0.1566777
GO:0008203	cholesterol metabolic process	The chemical reactions and pathways involving cholesterol, c	8.33 1/12	1.04 1/96	0.1566777
GO:0043401	steroid hormone mediated signaling pathway	A series of molecular signals mediated by a steroid hormone	8.33 1/12	1.01 1/99	0.1593899
GO:0038061	NIK/NF-kappaB signaling	The process in which a signal is passed on to downstream cor	8.33 1/12	1.01 1/99	0.1593899
GO:0022612	gland morphogenesis	The process in which the anatomical structures of a gland are	8.33 1/12	1.01 1/99	0.1593899
GO:0050680	negative regulation of epithelial cell proliferation	Any process that stops, prevents or reduces the rate or exten	8.33 1/12	0.99 1/101	0.1602184
GO:0022603	regulation of anatomical structure morphogenesis	Any process that modulates the frequency, rate or extent of	16.67 2/12	0.30 2/671	0.1602184
GO:0016125	sterol metabolic process	The chemical reactions and pathways involving sterols, steroi	8.33 1/12	0.97 1/103	0.1602184
GO:0071840	cellular component organization or biogenesis	A process that results in the biosynthesis of constituent macr	58.33 7/12	0.11 7/6564	0.1602184
GO:0010821	regulation of mitochondrion organization	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.98 1/102	0.1602184
GO:0043467	regulation of generation of precursor metabolites and energy	Any process that modulates the frequency, rate or extent of	8.33 1/12	1.00 1/100	0.1602184
GO:1902806	regulation of cell cycle G1/S phase transition	Any signalling pathway that modulates the activity of a cell	8.33 1/12	0.97 1/103	0.1602184
GO:1902652	secondary alcohol metabolic process	The chemical reactions and pathways involving secondary alc	8.33 1/12	0.99 1/101	0.1602184
GO:1904375	regulation of protein localization to cell periphery	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.96 1/104	0.1604151
GO:0045834	positive regulation of lipid metabolic process	Any process that activates or increases the frequency, rate o	8.33 1/12	0.96 1/104	0.1604151
GO:0010562	positive regulation of phosphorus metabolic process	Any process that increases the frequency, rate or extent of	16.67 2/12	0.29 2/698	0.1653601
GO:0051783	regulation of nuclear division	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.91 1/110	0.1653601
GO:0033002	muscle cell proliferation	The expansion of a muscle cell population by cell division.	8.33 1/12	0.91 1/110	0.1653601
GO:0045937	positive regulation of phosphate metabolic process	Any process that activates or increases the frequency, rate o	16.67 2/12	0.29 2/698	0.1653601
GO:0007275	multicellular organism development	The biological process whose specific outcome is the progres	41.67 5/12	0.13 5/3871	0.1653601
GO:1905952	regulation of lipid localization	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.91 1/110	0.1653601
GO:0007030	Golgi organization	A process that is carried out at the cellular level which result	8.33 1/12	0.88 1/113	0.1690606
GO:0000278	mitotic cell cycle	Progression through the phases of the mitotic cell cycle, the	16.67 2/12	0.28 2/717	0.1702816
GO:0006694	steroid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.86 1/116	0.1720475
GO:0002700	regulation of production of molecular mediator of immune response	Any process that modulates the frequency, rate, or extent of	8.33 1/12	0.85 1/117	0.1728058
GO:0033365	protein localization to organelle	A process in which a protein is transported to, or maintained	16.67 2/12	0.27 2/729	0.1732908
GO:0050588	lipid homeostasis	Any process involved in the maintenance of an internal stead	8.33 1/12	0.83 1/120	0.1743679
GO:0048284	organelle fusion	The creation of a single organelle from two or more organel	8.33 1/12	0.83 1/120	0.1743679
GO:0019752	carboxylic acid metabolic process	The chemical reactions and pathways involving carboxylic aci	16.67 2/12	0.27 2/736	0.1743679
GO:1902533	positive regulation of intracellular signal transduction	Any process that activates or increases the frequency, rate o	16.67 2/12	0.27 2/741	0.1756061
GO:0006886	intracellular protein transport	The directed movement of proteins in a cell, including the m	16.67 2/12	0.27 2/743	0.1757661
GO:0043436	oxoacid metabolic process	The chemical reactions and pathways involving any oxoacid;	16.67 2/12	0.27 2/745	0.1758757
GO:0043433	negative regulation of DNA-binding transcription factor activity	Any process that stops, prevents, or reduces the frequency, r	8.33 1/12	0.81 1/123	0.1758757
GO:0046890	regulation of lipid biosynthetic process	Any process that modulates the frequency, rate, or extent of	8.33 1/12	0.81 1/124	0.1759247
GO:0006633	fatty acid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.81 1/124	0.1759247
GO:0006507	biological regulation	Any process that modulates a measurable attribute of any bio	83.33 10/12	0.08 10/1190	0.1798833
GO:0007399	nervous system development	The process whose specific outcome is the progression of nei	25.00 3/12	0.18 3/1710	0.1798833
GO:0030100	regulation of endocytosis	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.77 1/130	0.1798833
GO:0002221	pattern recognition receptor signaling pathway	Any series of molecular signals generated as a consequence	8.33 1/12	0.76 1/131	0.1798833
GO:0048754	branching morphogenesis of an epithelial tube	The process in which the anatomical structures of branches i	8.33 1/12	0.77 1/130	0.1798833
GO:0006082	organic acid metabolic process	The chemical reactions and pathways involving organic acids,	16.67 2/12	0.26 2/774	0.1798833
GO:0006606	protein import into nucleus	The directed movement of a protein from the cytoplasm to t	8.33 1/12	0.78 1/128	0.1798833
GO:0071383	cellular response to steroid hormone stimulus	Any process that results in a change in state or activity of a	8.33 1/12	0.77 1/130	0.1798833
GO:0043112	receptor metabolic process	The chemical reactions and pathways involving a receptor m	8.33 1/12	0.77 1/130	0.1798833
GO:0051170	import into nucleus	The directed movement of substances into the nucleus.	8.33 1/12	0.76 1/132	0.1800977
GO:1903828	negative regulation of protein localization	Any process that stops, prevents or reduces the frequency, r	8.33 1/12	0.75 1/134	0.1820676
GO:1905475	regulation of protein localization to membrane	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.74 1/135	0.1827169
GO:0051726	regulation of cell cycle	Any process that modulates the rate or extent of progression	16.67 2/12	0.25 2/790	0.1837433
GO:0019637	organophosphate metabolic process	The chemical reactions and pathways involving organophosph	16.67 2/12	0.25 2/793	0.1840459
GO:0098655	cation transmembrane transport	The process in which a cation is transported across a membr	16.67 2/12	0.25 2/794	0.1840459
GO:0009755	hormone-mediated signaling pathway	A series of molecular signals mediated by the detection of a	8.33 1/12	0.70 1/142	0.1891055
GO:0002440	production of molecular mediator of immune response	The synthesis or release of any molecular mediator of the im	8.33 1/12	0.70 1/143	0.1891058
GO:0044843	cell cycle G1/S phase transition	The cell cycle process by which a cell in G1 phase commits to	8.33 1/12	0.69 1/144	0.1903151
GO:0051649	establishment of localization in cell	Any process, occurring in a cell, that localizes a substance	25.00 3/12	0.17 3/1783	0.1916847
GO:0050821	protein stabilization	Any process involved in maintaining the structure and integri	8.33 1/12	0.68 1/147	0.1927645
GO:1902600	proton transmembrane transport	The directed movement of a proton across a membrane.	8.33 1/12	0.67 1/149	0.1946008
GO:0048545	response to steroid hormone	Any process that results in a change in state or activity of a	8.33 1/12	0.66 1/152	0.1976688
GO:0072330	monocarboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.65 1/153	0.198227
GO:0061138	morphogenesis of a branching epithelium	The process in which the anatomical structures of a branche	8.33 1/12	0.64 1/156	0.2005615
GO:0046474	glycerophospholipid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.64 1/156	0.2005615
GO:0002573	myeloid leukocyte differentiation	The process in which a relatively unspecialized myeloid prec	8.33 1/12	0.64 1/157	0.2010114
GO:0050794	regulation of cellular process	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.62 1/161	0.2028349
GO:0007611	learning or memory	The acquisition and processing of information and/or the sto	8.33 1/12	0.62 1/161	0.2039067
GO:0002064	epithelial cell development	The process whose specific outcome is the progression of an	8.33 1/12	0.62 1/161	0.2039067
GO:0060429	epithelium development	The process whose specific outcome is the progression of an	16.67 2/12	0.23 2/875	0.2066201
GO:0002699	positive regulation of immune effector process	Any process that activates or increases the frequency, rate, o	8.33 1/12	0.59 1/169	0.2107181
GO:0001763	morphogenesis of a branching structure	The process in which the anatomical structures of branches a	8.33 1/12	0.60 1/168	0.2107181
GO:0032412	regulation of ion transmembrane transporter activity	Any process that modulates the activity of an ion transporter	8.33 1/12	0.59 1/169	0.2107181
GO:0048878	chemical homeostasis	Any biological process involved in the maintenance of an int	16.67 2/12	0.22 2/900	0.2139191
GO:1901617	organic hydroxy compound biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.57 1/175	0.2163975
GO:0000819	sister chromatid segregation	The cell cycle process in which sister chromatids are organiz	8.33 1/12	0.56 1/178	0.2184768
GO:0022898	regulation of transmembrane transporter activity	Any process that modulates the frequency, rate or extent of	8.33 1/12	0.56 1/178	0.2184768
GO:0090068	positive regulation of cell cycle process	Any process that increases the rate, frequency or extent of	8.33 1/12	0.55 1/181	0.2205231
GO:0017038	protein import	The targeting and directed movement of proteins into a cell	8.33 1/12	0.55 1/181	0.2205231
GO:0051222	positive regulation of protein transport	Any process that activates or increases the frequency, rate o	8.33 1/12	0.54 1/184	0.2232642
GO:0008654	phospholipid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.54 1/185	0.2236859
GO:0051047	positive regulation of secretion	Any process that activates or increases the frequency, rate o	8.33 1/12	0.53 1/187	0.2252481
GO:0032409	regulation of transporter activity	Any process that modulates the activity of a transporter.	8.33 1/12	0.53 1/188	0.2256587
GO:0050890	cognition	The operation of the mind by which an organism becomes av	8.33 1/12	0.53 1/189	0.226066
GO:0045017	glycerolipid biosynthetic process	The chemical reactions and pathways resulting in the formati	8.33 1/12	0.53 1/190	0.2264701
GO:0009968	negative regulation of signal transduction	Any process that stops, prevents, or reduces the frequency, r	16.67 2/12	0.21 2/964	0.2307464
GO:0022402	cell cycle process	The cellular process that ensures successive accurate and cor	16.67 2/12	0.21 2/965	0.2307464
GO:0030336	negative regulation of cell migration	Any process that stops, prevents, or reduces the frequency, r	8.33 1/12	0.51 1/197	0.2321305
GO:1904951	positive regulation of establishment of protein localization	Any process that activates or increases the frequency, rate o	8.33 1/12	0.50 1/199	0.2336164
GO:0098657	import into cell	The directed movement of some substance from outside of a	8.33 1/12	0.50 1/200	0.2339884
GO:0016197	endosomal transport	The directed movement of substances mediated by an endos	8.33 1/12	0.50 1/201	0.2343488
GO:0016236	macroautophagy	The major inducible pathway for the general turnover of cytc	8.33 1/12	0.49 1/205	0.2372573
GO:0030522	intracellular receptor signaling pathway	Any series of molecular signals initiated by a ligand binding	8.33 1/12	0.49 1/205	0.2372573
GO:0006812	cation transport	The directed movement of cations, atoms or small molecules	16.67 2/12	0.20 2/999	0.2384555
GO:2000146	negative regulation of cell motility	Any process that stops, prevents, or reduces the frequency, r	8.33 1/12	0.48 1/207	0.2384555
GO:0140546	defense response to symbiont	Reactions triggered in response to the presence of a symbior	8.33 1/12	0.48 1/210	0.2389703
GO:0034220	ion transmembrane transport	A process in which an ion is transported across a membrane.	16.67 2/12	0.20 2/1004	0.2389703
GO:0051607	defense response to virus	Reactions triggered in response to the presence of a virus th	8.33 1/12	0.48 1/210	0.2389703
GO:0051271	negative regulation of cellular component movement	Any process that stops, prevents, or reduces the frequency, r	8.33 1/12	0.47 1/211	0.2393048

GO:0090150	establishment of protein localization to membrane	The directed movement of a protein to a specific location in	ACSL3	8.33 1/12	0.47 1/212	0.2396367
GO:0010648	negative regulation of cell communication	Any process that decreases the frequency, rate or extent of	NDRG4 PHB2	16.67 2/12	0.20 2/1021	0.2420058
GO:0051091	positive regulation of DNA-binding transcription factor activity	Any process that activates or increases the frequency, rate or	PHB2	8.33 1/12	0.47 1/215	0.2420058
GO:0023057	negative regulation of signaling	Any process that stops, prevents, or reduces the frequency, r	NDRG4 PHB2	16.67 2/12	0.20 2/1023	0.2420576
GO:0032386	regulation of intracellular transport	Any process that modulates the frequency, rate or extent of	NDRG4	8.33 1/12	0.45 1/220	0.245135
GO:1901990	regulation of mitotic cell cycle phase transition	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.24 1/221	0.2454391
GO:0009416	response to light stimulus	Any process that results in a change in state or activity of a	ci NDRG4	8.33 1/12	0.44 1/229	0.250745
GO:0008202	steroid metabolic process	The chemical reactions and pathways involving steroids, com	SQLE	8.33 1/12	0.44 1/229	0.250745
GO:1904062	regulation of cation transmembrane transport	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.44 1/228	0.250745
GO:0034504	protein localization to nucleus	A process in which a protein transports or maintains the loca	PHB2	8.33 1/12	0.44 1/229	0.250745
GO:0031647	regulation of protein stability	Any process that affects the structure and integrity of a prote	PHB2	8.33 1/12	0.43 1/231	0.2512982
GO:0072659	protein localization to plasma membrane	A process in which a protein is transported to, or maintained	ACSL3	8.33 1/12	0.43 1/231	0.2512982
GO:0040013	negative regulation of locomotion	Any process that stops, prevents, or reduces the frequency, r	NDRG4	8.33 1/12	0.43 1/232	0.2515714
GO:0042113	B cell activation	The change in morphology and behavior of a mature or immu	PHB2	8.33 1/12	0.43 1/235	0.2538673
GO:0046394	carboxylic acid biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	0.42 1/239	0.2571514
GO:0016053	organic acid biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	0.41 1/242	0.2586473
GO:0045787	positive regulation of cell cycle	Any process that activates or increases the rate or extent of	PHB2	8.33 1/12	0.41 1/242	0.2586473
GO:0019220	regulation of phosphate metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67 2/12	0.18 2/1094	0.258661
GO:0051174	regulation of phosphorus metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67 2/12	0.18 2/1094	0.258661
GO:0048193	Golgi vesicle transport	The directed movement of substances into, out of or within t	ACSL3	8.33 1/12	0.40 1/247	0.2613431
GO:0098813	nuclear chromosome segregation	The process in which genetic material, in the form of nuclear	PHB2	8.33 1/12	0.40 1/248	0.2615723
GO:0002697	regulation of immune effector process	Any process that modulates the frequency, rate, or extent of	PHB2	8.33 1/12	0.40 1/252	0.2647397
GO:0015849	organic acid transport	The directed movement of organic acids, any acidic compou	ACSL3	8.33 1/12	0.39 1/255	0.2669057
GO:0050678	regulation of epithelial cell proliferation	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.39 1/256	0.2671126
GO:0050789	regulation of biological process	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A CMTM8 CUL9 NDRG4 PHB2	75.00 9/12	0.08 9/11175	0.2675604
GO:0051235	maintenance of location	Any process in which a cell, substance or cellular entity, such	SQLE	8.33 1/12	0.38 1/262	0.2713765
GO:0060562	epithelial tube morphogenesis	The process in which the anatomical structures of a tube are	PHB2	8.33 1/12	0.38 1/265	0.273483
GO:0060666	alcohol metabolic process	The chemical reactions and pathways involving alcohols, any	SQLE	8.33 1/12	0.38 1/266	0.2736637
GO:0009615	response to virus	Any process that results in a change in state or activity of a	ci PHB2	8.33 1/12	0.37 1/269	0.2741964
GO:0006913	nucleocytoplasmic transport	The directed movement of molecules between the nucleus a	PHB2	8.33 1/12	0.37 1/269	0.2741964
GO:0051169	nuclear transport	The directed movement of substances into, out of, or within	PHB2	8.33 1/12	0.37 1/269	0.2741964
GO:0009967	positive regulation of signal transduction	Any process that activates or increases the frequency, rate o	NDRG4 PHB2	16.67 2/12	0.17 2/1161	0.2746106
GO:0051051	negative regulation of transport	Any process that stops, prevents, or reduces the frequency, r	ANKRD13A	8.33 1/12	0.37 1/272	0.2747156
GO:0006790	sulfur compound metabolic process	The chemical reactions and pathways involving the nonmetal	ACSL3	8.33 1/12	0.37 1/272	0.2747156
GO:1990778	protein localization to cell periphery	A process in which a protein is transported to, or maintained	ACSL3	8.33 1/12	0.36 1/274	0.2758183
GO:0010639	negative regulation of organelle organization	Any process that decreases the frequency, rate or extent of a	VAT1	8.33 1/12	0.36 1/279	0.279697
GO:0016477	cell migration	The controlled self-propelled movement of a cell from one si	NDRG4 PHB2	16.67 2/12	0.17 2/1202	0.2864115
GO:0030099	myeloid cell differentiation	The process in which a relatively unspecialized myeloid prec	FASN	8.33 1/12	0.34 1/290	0.2882686
GO:1901987	regulation of cell cycle phase transition	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.34 1/298	0.2947726
GO:0045860	positive regulation of protein kinase activity	Any process that activates or increases the frequency, rate o	PHB2	8.33 1/12	0.33 1/299	0.2948722
GO:0009150	purine ribonucleotide metabolic process	The chemical reactions and pathways involving purine riboi	ACSL3	8.33 1/12	0.33 1/301	0.2954114
GO:0048585	negative regulation of response to stimulus	Any process that stops, prevents, or reduces the frequency, r	NDRG4 PHB2	16.67 2/12	0.16 2/1236	0.2954114
GO:0002764	immune response-regulating signaling pathway	The cascade of processes by which a signal interacts with a	ci PHB2	8.33 1/12	0.33 1/303	0.2960626
GO:0007059	chromosome segregation	The process in which genetic material, in the form of chrom	PHB2	8.33 1/12	0.33 1/304	0.2961552
GO:1903829	positive regulation of protein localization	Any process that activates or increases the frequency, rate o	ACSL3	8.33 1/12	0.33 1/305	0.2962468
GO:0050673	epithelial cell proliferation	The multiplication or reproduction of epithelial cells, resulti	PHB2	8.33 1/12	0.32 1/308	0.2981114
GO:0044772	mitotic cell cycle phase transition	The cell cycle process by which a cell commits to entering th	PHB2	8.33 1/12	0.32 1/311	0.2999668
GO:0009314	response to radiation	Any process that results in a change in state or activity of a	ci NDRG4	8.33 1/12	0.32 1/314	0.3009983
GO:0051223	regulation of protein transport	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	0.32 1/314	0.3009983
GO:1902531	regulation of intracellular signal transduction	Any process that modulates the frequency, rate or extent of	NDRG4 PHB2	16.67 2/12	0.16 2/1270	0.3018567
GO:0006874	cellular calcium ion homeostasis	Any process involved in the maintenance of an internal stead	ATP13A3	8.33 1/12	0.32 1/317	0.3020144
GO:0009259	ribonucleotide metabolic process	The chemical reactions and pathways involving a ribonucleot	ACSL3	8.33 1/12	0.31 1/318	0.3020824
GO:0006163	purine nucleotide metabolic process	The chemical reactions and pathways involving a purine nucl	ACSL3	8.33 1/12	0.31 1/323	0.3048038
GO:0010647	positive regulation of cell communication	Any process that increases the frequency, rate or extent of	ci NDRG4 PHB2	16.67 2/12	0.16 2/1286	0.3048038
GO:0023056	positive regulation of signaling	Any process that activates, maintains or increases the frequ	NDRG4 PHB2	16.67 2/12	0.15 2/1293	0.3049732
GO:0022411	cellular component disassembly	A cellular process that results in the breakdown of a cellular	PHB2	8.33 1/12	0.31 1/325	0.3049732
GO:0034765	regulation of ion transmembrane transport	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.31 1/326	0.3049732
GO:0019693	ribose phosphate metabolic process	The chemical reactions and pathways involving ribose phospl	ACSL3	8.33 1/12	0.31 1/327	0.3050282
GO:0055074	calcium ion homeostasis	Any process involved in the maintenance of an internal stead	ATP13A3	8.33 1/12	0.30 1/328	0.3050824
GO:0007049	cell cycle	The progression of biochemical and morphological phases an	CUL9 PHB2	16.67 2/12	0.15 2/1305	0.3069113
GO:0051090	regulation of DNA-binding transcription factor activity	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.30 1/333	0.3077154
GO:0070201	regulation of establishment of protein localization	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	0.30 1/336	0.3094363
GO:0048523	negative regulation of cellular process	Any process that stops, prevents, or reduces the frequency, r	ANKRD13A NDRG4 PHB2 VAT1	33.33 4/12	0.10 4/3856	0.309986
GO:0140694	non-membrane-bounded organelle assembly	The aggregation, arrangement and bonding together of a set	SQLE	8.33 1/12	0.28 1/351	0.314588
GO:0042592	homeostatic process	Any biological process involved in the maintenance of an inte	ATP13A3 SURF4	16.67 2/12	0.15 2/1352	0.314588
GO:0048870	cell motility	Any process involved in the controlled self-propelled movem	NDRG4 PHB2	16.67 2/12	0.15 2/1350	0.314588
GO:1903131	mononuclear cell differentiation	The process in which a relatively unspecialized cell acquires t	FASN	8.33 1/12	0.29 1/349	0.314588
GO:0071396	cellular response to lipid	Any process that results in a change in state or activity of a	ci PHB2	8.33 1/12	0.29 1/347	0.314588
GO:0051674	localization of cell	Any process in which a cell is transported to, and/or maintai	NDRG4 PHB2	16.67 2/12	0.15 2/1350	0.314588
GO:0006811	ion transport	The directed movement of charged atoms or small charged r	ATP13A3 PHB2	16.67 2/12	0.15 2/1347	0.314588
GO:0072521	purine-containing compound metabolic process	The chemical reactions and pathways involving a purine-cont	ACSL3	8.33 1/12	0.29 1/346	0.314588
GO:0072503	cellular divalent inorganic cation homeostasis	Any process involved in the maintenance of an internal stead	ATP13A3	8.33 1/12	0.29 1/347	0.314588
GO:0072594	establishment of protein localization to organelle	The directed movement of a protein to a specific location on	PHB2	8.33 1/12	0.28 1/357	0.3178959
GO:0072507	divalent inorganic cation homeostasis	Any process involved in the maintenance of an internal stead	ATP13A3	8.33 1/12	0.27 1/364	0.3217928
GO:0033674	positive regulation of kinase activity	Any process that activates or increases the frequency, rate o	PHB2	8.33 1/12	0.27 1/364	0.3217928
GO:0048513	animal organ development	Development of a tissue or tissues that work together to per	FASN NDRG4 PHB2	25.00 3/12	0.11 3/2612	0.3217928
GO:0055085	transmembrane transport	The process in which a solute is transported across a lipid bil	ATP13A3 PHB2	16.67 2/12	0.14 2/1405	0.3297505
GO:0061919	process utilizing autophagic mechanism	A cellular process involving delivery of a portion of the cytop	PHB2	8.33 1/12	0.26 1/382	0.3328304
GO:0071407	cellular response to organic cyclic compound	Any process that results in a change in state or activity of a	ci PHB2	8.33 1/12	0.26 1/383	0.3328304
GO:0006914	autophagy	The cellular catabolic process in which cells digest parts of	PHB2	8.33 1/12	0.26 1/382	0.3328304
GO:0006091	generation of precursor metabolites and energy	The chemical reactions and pathways resulting in the formati	PHB2	8.33 1/12	0.26 1/386	0.3335216
GO:0034762	regulation of transmembrane transport	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.26 1/386	0.3335216
GO:0009888	tissue development	The process whose specific outcome is the progression of a ti	FASN PHB2	16.67 2/12	0.14 2/1431	0.3341879
GO:0044770	cell cycle phase transition	The cell cycle process by which a cell commits to entering th	PHB2	8.33 1/12	0.26 1/391	0.335741
GO:1901615	organic hydroxy compound metabolic process	The chemical reactions and pathways involving organic hydr	SQLE	8.33 1/12	0.25 1/398	0.3394535
GO:0010638	positive regulation of organelle organization	Any process that increases the frequency, rate or extent of a	SURF4	8.33 1/12	0.25 1/398	0.3394535
GO:0002009	morphogenesis of an epithelium	The process in which the anatomical structures of epithelia a	PHB2	8.33 1/12	0.25 1/404	0.3398845
GO:0009117	nucleotide metabolic process	The chemical reactions and pathways involving a nucleotide,	ACSL3	8.33 1/12	0.25 1/402	0.3398845
GO:0007507	heart development	The process whose specific outcome is the progression of the	NDRG4	8.33 1/12	0.25 1/401	0.3398845
GO:0051046	regulation of secretion	Any process that modulates the frequency, rate or extent of	ACSL3	8.33 1/12	0.25 1/400	0.3398845
GO:0032870	cellular response to hormone stimulus	Any process that results in a change in state or activity of a	ci PHB2	8.33 1/12	0.25 1/404	0.3398845
GO:0010256	endomembrane system organization	A process that is carried out at the cellular level which result	SURF4	8.33 1/12	0.24 1/409	0.3428081
GO:0006753	nucleoside phosphate metabolic process	The chemical reactions and pathways involving any phospho	ACSL3	8.33 1/12	0.24 1/412	0.3442209
GO:0051345	positive regulation of hydrolase activity	Any process that activates or increases the frequency, rate o	PHB2	8.33 1/12	0.24 1/420	0.349226
GO:0007610	behavior	The internally coordinated responses (actions or inactions) o	NDRG4	8.33 1/12	0.24 1/421	0.349226
GO:0051347	positive regulation of transferase activity	Any process that activates or increases the frequency, rate o	PHB2	8.33 1/12	0.23 1/428	0.3535291
GO:0044283	small molecule biosynthetic process	The chemical reactions and pathways resulting in the formati	FASN	8.33 1/12	0.23 1/437	0.3575507
GO:0002521	leukocyte differentiation	The process in which a relatively unspecialized hemopoietic	ci FASN	8.33 1/12	0.23 1/437	0.3575507
GO:0006875	cellular metal ion homeostasis	Any process involved in the maintenance of an internal stead	ATP13A3	8.33 1/12	0.23 1/435	0.3575507
GO:0090407	organophosphate biosynthetic process	The chemical reactions and pathways resulting in the biosynt	ACSL3	8.33 1/12	0.23 1/439	0.3581511
GO:0051640	organelle localization	Any process in which an organelle is transported to, and/or n	NDRG4	8.33 1/12	0.23 1/443	0.3593387
GO:0043269	regulation of ion transport	Any process that modulates the frequency, rate or extent of	PHB2	8.33 1/12	0.23 1/442	0.3593387
GO:0002252	immune effector process	Any process of the immune system that executes a compone	PHB2	8.33 1/12	0.22 1/454	0.3663269
GO:0033993	response to lipid	Any process that results in a change in state or activity of a	ci PHB2	8.33 1/12	0.22 1/464	0.3716645
GO:0007420	brain development	The process whose specific outcome is the progression of the	NDRG4	8.33 1/12	0.22 1/463	0.3716645
GO:0030855	epithelial cell differentiation	The process in which a relatively unspecialized cell acquires	FASN	8.33 1/12	0.21 1/470	0.3749985
GO:0072657	protein localization to membrane	A process in which a protein is transported to, or maintained	ACSL3	8.33 1/12	0.21 1/473	0.3762184
GO:0055086	nucleobase-containing small molecule metabolic process	The cellular chemical reactions and pathways involving a nuc	ACSL3	8.33 1/12	0.21 1/477	0.3775412
GO:0048584	positive regulation of response to stimulus	Any process that activates, maintains or increases the rate of	NDRG4 PHB2	16.67 2/12	0.12 2/1617	0.3775412

GO:0048729	tissue morphogenesis	The process in which the anatomical structures of a tissue are	PHB2	8.33	1/12	0.21	1/486	0.3816918
GO:0065008	regulation of biological quality	Any process that modulates a qualitative or quantitative trait	ATP13A3 PHB2 SURF4	25.00	3/12	0.10	3/2959	0.3816918
GO:0009725	response to hormone	Any process that results in a change in state or activity of a	cr PHB2	8.33	1/12	0.20	1/488	0.3821825
GO:0055065	metal ion homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.20	1/495	0.383239
GO:0030003	cellular cation homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.20	1/491	0.383239
GO:0045859	regulation of protein kinase activity	Any process that modulates the frequency, rate or extent of	phosphorylation	8.33	1/12	0.20	1/496	0.383239
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	A series of molecular signals initiated by the binding of an	extracellular ligand	8.33	1/12	0.20	1/496	0.383239
GO:0014070	response to organic cyclic compound	Any process that results in a change in state or activity of a	cr PHB2	8.33	1/12	0.20	1/495	0.383239
GO:0006873	cellular ion homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.20	1/504	0.385975
GO:0006935	chemotaxis	The directed movement of a motile cell or organism, or the	chemotactic stimulus	8.33	1/12	0.20	1/503	0.385975
GO:0060322	head development	The biological process whose specific outcome is the	progression of head development	8.33	1/12	0.20	1/503	0.385975
GO:0042330	taxis	The directed movement of a motile cell or organism in	response to a stimulus	8.33	1/12	0.20	1/506	0.3864328
GO:0048522	positive regulation of cellular process	Any process that activates or increases the frequency, rate or	extent of a cellular process	33.33	4/12	0.09	4/4480	0.393603
GO:0006928	movement of cell or subcellular component	The directed, self-propelled movement of a cell or subcellular	component	16.67	2/12	0.12	2/1707	0.3958285
GO:0048519	negative regulation of biological process	Any process that stops, prevents, or reduces the frequency, rate	or extent of a biological process	33.33	4/12	0.09	4/4543	0.405219
GO:0055080	cation homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.18	1/556	0.4153099
GO:0045087	innate immune response	Innate immune responses are defense responses mediated by	pattern recognition receptors	8.33	1/12	0.18	1/558	0.4156599
GO:0098771	inorganic ion homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.18	1/565	0.4191672
GO:0000226	microtubule cytoskeleton organization	A process that is carried out at the cellular level which results	in the organization of microtubules	8.33	1/12	0.18	1/569	0.4207582
GO:0051050	positive regulation of transport	Any process that activates or increases the frequency, rate or	extent of a transport process	8.33	1/12	0.17	1/576	0.4242116
GO:0044248	cellular catabolic process	The chemical reactions and pathways resulting in the	breakdown of macromolecules	16.67	2/12	0.11	2/1814	0.4250981
GO:0050793	regulation of developmental process	Any process that modulates the frequency, rate or extent of	a developmental process	16.67	2/12	0.11	2/1822	0.4258722
GO:0001934	positive regulation of protein phosphorylation	Any process that activates or increases the frequency, rate or	extent of phosphorylation	8.33	1/12	0.17	1/583	0.4258722
GO:0006511	ubiquitin-dependent protein catabolic process	The chemical reactions and pathways resulting in the	breakdown of proteins	8.33	1/12	0.17	1/589	0.4266619
GO:0055082	cellular chemical homeostasis	Any biological process involved in the maintenance of an	internal steady state	8.33	1/12	0.17	1/586	0.4266619
GO:0043549	regulation of kinase activity	Any process that modulates the frequency, rate or extent of	phosphorylation	8.33	1/12	0.17	1/588	0.4266619
GO:0071310	cellular response to organic substance	Any process that results in a change in state or activity of a	cr FASN PHB2	16.67	2/12	0.11	2/1848	0.430665
GO:0050801	ion homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.17	1/602	0.4323745
GO:0019941	modification-dependent protein catabolic process	The chemical reactions and pathways resulting in the	breakdown of proteins	8.33	1/12	0.17	1/603	0.4323745
GO:0046649	lymphocyte activation	A change in morphology and behavior of a lymphocyte	resulting in an immune response	8.33	1/12	0.17	1/605	0.4326457
GO:0043632	modification-dependent macromolecule catabolic process	The chemical reactions and pathways resulting in the	breakdown of macromolecules	8.33	1/12	0.16	1/611	0.4353083
GO:0050776	regulation of immune response	Any process that modulates the frequency, rate or extent of	an immune response	8.33	1/12	0.16	1/616	0.4373526
GO:0043066	negative regulation of apoptotic process	Any process that stops, prevents, or reduces the frequency, rate	or extent of apoptosis	8.33	1/12	0.15	1/646	0.4511908
GO:0035239	tube morphogenesis	The process in which the anatomical structures of a tube are	formed	8.33	1/12	0.15	1/646	0.4511908
GO:0032501	multicellular organismal process	Any biological process, occurring at the level of a multicellular	organism	41.67	5/12	0.08	5/6399	0.4511908
GO:0007417	central nervous system development	The process whose specific outcome is the progression of the	development of the central nervous system	8.33	1/12	0.15	1/649	0.4511908
GO:0042327	positive regulation of phosphorylation	Any process that activates or increases the frequency, rate or	extent of phosphorylation	8.33	1/12	0.15	1/647	0.4511908
GO:0051093	negative regulation of developmental process	Any process that stops, prevents or reduces the rate or extent	of a developmental process	8.33	1/12	0.15	1/651	0.4511908
GO:0046903	secretion	The controlled release of a substance by a cell or a tissue		8.33	1/12	0.16	1/645	0.4511908
GO:0071345	cellular response to cytokine stimulus	Any process that results in a change in state or activity of a	cr FASN	8.33	1/12	0.15	1/660	0.4544275
GO:0019725	cellular homeostasis	Any process involved in the maintenance of an internal steady	state ATP13A3	8.33	1/12	0.15	1/660	0.4544275
GO:0043069	negative regulation of programmed cell death	Any process that stops, prevents, or reduces the frequency, rate	or extent of apoptosis	8.33	1/12	0.15	1/663	0.4551756
GO:0003006	developmental process involved in reproduction	A developmental process in which a progressive change in the	development of an organism	8.33	1/12	0.15	1/666	0.4559176
GO:0030097	hemopoiesis	The process whose specific outcome is the progression of the	FASN	8.33	1/12	0.15	1/670	0.4572163
GO:0098662	inorganic cation transmembrane transport	A process in which an inorganic cation is transported from one	side of a membrane to the other	8.33	1/12	0.15	1/673	0.4579443
GO:0002684	positive regulation of immune system process	Any process that activates or increases the frequency, rate, or	extent of an immune system process	8.33	1/12	0.15	1/677	0.4582698
GO:0051338	regulation of transferase activity	Any process that modulates the frequency, rate or extent of	phosphorylation	8.33	1/12	0.15	1/676	0.4582698
GO:0009605	response to external stimulus	Any process that results in a change in state or activity of a	cr CMTM8 PHB2	16.67	2/12	0.10	2/2004	0.4603966
GO:0048518	positive regulation of biological process	Any process that activates or increases the frequency, rate or	extent of a biological process	33.33	4/12	0.08	4/4958	0.4603966
GO:0051241	negative regulation of multicellular organismal process	Any process that stops, prevents, or reduces the frequency, rate	or extent of a multicellular organismal process	8.33	1/12	0.15	1/686	0.4603966
GO:0030334	regulation of cell migration	Any process that modulates the frequency, rate or extent of	cell migration	8.33	1/12	0.14	1/697	0.4641036
GO:0051603	proteolysis involved in cellular protein catabolic process	The hydrolysis of a peptide bond or bonds within a protein	is carried out	8.33	1/12	0.14	1/696	0.4641036
GO:0009628	response to abiotic stimulus	Any process that results in a change in state or activity of a	cr NDRG4	8.33	1/12	0.14	1/698	0.4641036
GO:0031324	negative regulation of cellular metabolic process	Any process that stops, prevents, or reduces the frequency, rate	or extent of a cellular metabolic process	16.67	2/12	0.10	2/2035	0.4643665
GO:0016567	protein ubiquitination	The process in which one or more ubiquitin groups are added	to a protein	8.33	1/12	0.14	1/702	0.4643665
GO:0048534	hematopoietic or lymphoid organ development	The process whose specific outcome is the progression of the	development of a hematopoietic or lymphoid organ	8.33	1/12	0.14	1/705	0.4645733
GO:0002376	immune system process	Any process involved in the development or functioning of the	immune system	16.67	2/12	0.10	2/2045	0.4645733
GO:0045321	leukocyte activation	A change in morphology and behavior of a leukocyte	resulting in an immune response	8.33	1/12	0.14	1/713	0.4664732
GO:0034097	response to cytokine	Any process that results in a change in state or activity of a	cr FASN	8.33	1/12	0.14	1/713	0.4664732
GO:0060548	negative regulation of cell death	Any process that decreases the rate or frequency of cell death		8.33	1/12	0.14	1/719	0.4687105
GO:0044257	cellular protein catabolic process	The chemical reactions and pathways resulting in the	breakdown of proteins	8.33	1/12	0.14	1/732	0.4747603
GO:0035556	intracellular signal transduction	The process in which a signal is passed on to downstream	components	16.67	2/12	0.10	2/2097	0.4747603
GO:0098660	inorganic ion transmembrane transport	The process in which an inorganic ion is transported across a	membrane	8.33	1/12	0.14	1/736	0.4747833
GO:0009056	catabolic process	The chemical reactions and pathways resulting in the	breakdown of macromolecules	16.67	2/12	0.09	2/2106	0.4750372
GO:2000145	regulation of cell motility	Any process that modulates the frequency, rate or extent of	cell motility	8.33	1/12	0.13	1/742	0.4750372
GO:0009653	anatomical structure morphogenesis	The process in which anatomical structures are generated		16.67	2/12	0.09	2/2107	0.4750372
GO:0002520	immune system development	The process whose specific outcome is the progression of an	immune system	8.33	1/12	0.13	1/758	0.4813342
GO:0032446	protein modification by small protein conjugation	A protein modification process in which one or more groups	are added to a protein	8.33	1/12	0.13	1/758	0.4813342
GO:0051130	positive regulation of cellular component organization	Any process that activates or increases the frequency, rate or	extent of cellular component organization	8.33	1/12	0.13	1/763	0.4829162
GO:1901576	organic substance biosynthetic process	The chemical reactions and pathways resulting in the	formation of organic substances	33.33	4/12	0.08	4/5165	0.4833261
GO:0031401	positive regulation of protein modification process	Any process that activates or increases the frequency, rate or	extent of a protein modification process	8.33	1/12	0.13	1/774	0.4855804
GO:0040012	regulation of locomotion	Any process that modulates the frequency, rate or extent of	locomotion	8.33	1/12	0.13	1/773	0.4855804
GO:0007167	enzyme linked receptor protein signaling pathway	Any series of molecular signals initiated by the binding of an	extracellular ligand	8.33	1/12	0.13	1/778	0.4866201
GO:0007925	organelle assembly	The aggregation, arrangement and bonding together of a set	of organelles	8.33	1/12	0.13	1/786	0.4896355
GO:0051270	regulation of cellular component movement	Any process that modulates the frequency, rate or extent of	cellular component movement	8.33	1/12	0.13	1/788	0.4896226
GO:0009058	biosynthetic process	The chemical reactions and pathways resulting in the	formation of macromolecules	33.33	4/12	0.08	4/5231	0.4902026
GO:0001775	cell activation	A change in the morphology or behavior of a cell resulting	in an immune response	8.33	1/12	0.13	1/793	0.4902026
GO:0072359	circulatory system development	The process whose specific outcome is the progression of the	development of the circulatory system	8.33	1/12	0.12	1/804	0.4936551
GO:0035295	tube development	The process whose specific outcome is the progression of a	tube	8.33	1/12	0.12	1/804	0.4936551
GO:0007017	microtubule-based process	Any cellular process that depends upon or alters the	microtubule cytoskeleton	8.33	1/12	0.12	1/809	0.4941496
GO:0010033	response to organic substance	Any process that results in a change in state or activity of a	cr FASN PHB2	16.67	2/12	0.09	2/2222	0.4941496
GO:0098542	defense response to other organism	Reactions triggered in response to the presence of another	organism	8.33	1/12	0.12	1/812	0.4946353
GO:0051336	regulation of hydrolase activity	Any process that modulates the frequency, rate or extent of	hydrolysis	8.33	1/12	0.12	1/819	0.4951148
GO:0009887	animal organ morphogenesis	Morphogenesis of an animal organ. An organ is defined as a	functional unit	8.33	1/12	0.12	1/817	0.4951148
GO:0044092	negative regulation of molecular function	Any process that stops or reduces the rate or extent of a	molecular function	8.33	1/12	0.12	1/816	0.4951148
GO:0007166	cell surface receptor signaling pathway	A series of molecular signals initiated by activation of a	receptor	16.67	2/12	0.09	2/2259	0.499612
GO:0043085	positive regulation of catalytic activity	Any process that activates or increases the activity of an	enzyme	8.33	1/12	0.12	1/845	0.5044835
GO:0009966	regulation of signal transduction	Any process that modulates the frequency, rate or extent of	signal transduction	16.67	2/12	0.09	2/2282	0.5044835
GO:0030163	protein catabolic process	The chemical reactions and pathways resulting in the	breakdown of proteins	8.33	1/12	0.12	1/855	0.5081131
GO:0010628	positive regulation of gene expression	Any process that increases the frequency, rate or extent of	gene expression	8.33	1/12	0.12	1/857	0.5081131
GO:0001932	regulation of protein phosphorylation	Any process that modulates the frequency, rate or extent of	phosphorylation	8.33	1/12	0.12	1/867	0.5117368
GO:1901135	carbohydrate derivative metabolic process	The chemical reactions and pathways involving carbohydrate	derivatives	8.33	1/12	0.11	1/870	0.5121337
GO:0070647	protein modification by small protein conjugation or removal	A protein modification process in which one or more groups	are added to or removed from a protein	8.33	1/12	0.11	1/877	0.5143428
GO:0051276	chromosome organization	A process that is carried out at the cellular level that results	in chromosome organization	8.33	1/12	0.11	1/881	0.5151772
GO:0009987	cellular process	Any process that is carried out at the cellular level, but not	involving the nucleus	100.00	12/12	0.06	12/1870	0.5186106
GO:0070887	cellular response to chemical stimulus	Any process that results in a change in state or activity of a	cr FASN PHB2	16.67	2/12	0.08	2/2376	0.52229
GO:0006796	phosphate-containing compound metabolic process	The chemical reactions and pathways involving the	phosphorylation of macromolecules	16.67	2/12	0.08	2/2404	0.5288993
GO:0006793	phosphorus metabolic process	The chemical reactions and pathways involving the	nonmetabolic phosphorylation of macromolecules	16.67	2/12	0.08	2/2425	0.5355686
GO:0051173	positive regulation of nitrogen compound metabolic process	Any process that activates or increases the frequency, rate or	extent of a nitrogen compound metabolic process	16.67	2/12	0.08	2/2473	0.5454193
GO:0042221	response to chemical	Any process that results in a change in state or activity of a	cr CMTM8 FASN PHB2	25.00	3/12	0.07	3/4056	0.5482549
GO:0071495	cellular response to endogenous stimulus	Any process that results in a change in state or activity of a	cr PHB2	8.33	1/12	0.10	1/988	0.5526274
GO:0042325	regulation of phosphorylation	Any process that modulates the frequency, rate or extent of	phosphorylation	8.33	1/12	0.10	1/986	0.5526274
GO:0044265	cellular macromolecule catabolic process	The chemical reactions and pathways resulting in the	breakdown of macromolecules	8.33	1/12	0.10	1/985	0.5526274
GO:0010646	regulation of cell communication	Any process that modulates the frequency, rate or extent of	cell communication	16.67	2/12	0.08	2/2562	0.5613355
GO:0000003	reproduction	The production of new individuals that contain some portion	of the parent	8.33	1/12	0.10	1/1024	0.5613355
GO:0010605	negative regulation of macromolecule metabolic process	Any process that decreases the frequency, rate or extent of	macromolecule metabolic process	16.67	2/12	0.08	2/2563	

GO:0045892	negative regulation of transcription, DNA-templated	Any process that stops, prevents, or reduces the frequency, r	PHB2	8.33	1/12	0.10	1/1044	0.5655129
GO:0042981	regulation of apoptotic process	Any process that modulates the occurrence or rate of cell de	PHB2	8.33	1/12	0.10	1/1039	0.5655129
GO:1902679	negative regulation of RNA biosynthetic process	Any process that stops, prevents or reduces the frequency, r	PHB2	8.33	1/12	0.10	1/1045	0.5655129
GO:1903507	negative regulation of nucleic acid-templated transcription	Any process that stops, prevents or reduces the frequency, r	PHB2	8.33	1/12	0.10	1/1045	0.5655129
GO:0031325	positive regulation of cellular metabolic process	Any process that activates or increases the frequency, rate or	ACSL3 PHB2	16.67	2/12	0.08	2/2631	0.5704059
GO:0043067	regulation of programmed cell death	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.09	1/1065	0.5704059
GO:0043207	response to external biotic stimulus	Any process that results in a change in state or activity of a	ci PHB2	8.33	1/12	0.09	1/1068	0.5704059
GO:0051707	response to other organism	Any process that results in a change in state or activity of a	ci PHB2	8.33	1/12	0.09	1/1066	0.5704059
GO:0009719	response to endogenous stimulus	Any process that results in a change in state or activity of a	ci PHB2	8.33	1/12	0.09	1/1076	0.5707868
GO:0002682	regulation of immune system process	Any process that modulates the frequency, rate, or extent of	PHB2	8.33	1/12	0.09	1/1077	0.5707868
GO:0032270	positive regulation of cellular protein metabolic process	Any process that activates or increases the frequency, rate or	PHB2	8.33	1/12	0.09	1/1072	0.5707868
GO:0009607	response to biotic stimulus	Any process that results in a change in state or activity of a	ci PHB2	8.33	1/12	0.09	1/1098	0.5777702
GO:0043603	cellular amide metabolic process	The chemical reactions and pathways involving an amide, am	ACSL3	8.33	1/12	0.09	1/1112	0.580964
GO:0009892	negative regulation of metabolic process	Any process that stops, prevents, or reduces the frequency, r	ANKRD13A PHB2	16.67	2/12	0.07	2/2707	0.580964
GO:0051253	negative regulation of RNA metabolic process	Any process that stops, prevents, or reduces the frequency, r	PHB2	8.33	1/12	0.09	1/1131	0.5859421
GO:1901565	organonitrogen compound catabolic process	The chemical reactions and pathways resulting in the breakd	CUL9	8.33	1/12	0.09	1/1129	0.5859421
GO:0009057	macromolecule catabolic process	The chemical reactions and pathways resulting in the breakd	CUL9	8.33	1/12	0.09	1/1142	0.5872562
GO:0010941	regulation of cell death	Any process that modulates the rate or frequency of cell dea	PHB2	8.33	1/12	0.09	1/1142	0.5872562
GO:0051247	positive regulation of protein metabolic process	Any process that activates or increases the frequency, rate or	PHB2	8.33	1/12	0.09	1/1145	0.5872562
GO:0048699	generation of neurons	The process in which nerve cells are generated. This includes	ACSL3	8.33	1/12	0.09	1/1146	0.5872562
GO:0044093	positive regulation of molecular function	Any process that activates or increases the rate or extent of	PHB2	8.33	1/12	0.09	1/1149	0.5873028
GO:0044419	biological process involved in interspecies interaction between organ	Any process evolved to enable an interaction with an organis	PHB2	8.33	1/12	0.09	1/1167	0.592739
GO:0006952	defense response	Reactions, triggered in response to the presence of a foreign	PHB2	8.33	1/12	0.09	1/1172	0.5934754
GO:0031399	regulation of protein modification process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.08	1/1192	0.5994922
GO:0010558	negative regulation of macromolecule biosynthetic process	Any process that decreases the rate, frequency or extent of	PHB2	8.33	1/12	0.08	1/1221	0.6081521
GO:0045934	negative regulation of nucleobase-containing compound metabolic p	Any cellular process that stops, prevents, or reduces the freq	PHB2	8.33	1/12	0.08	1/1223	0.6081521
GO:0022008	neurogenesis	Generation of cells within the nervous system.	ACSL3	8.33	1/12	0.08	1/1245	0.6135148
GO:0007010	cytoskeleton organization	A process that is carried out at the cellular level which result	CUL9	8.33	1/12	0.08	1/1245	0.6135148
GO:0031327	negative regulation of cellular biosynthetic process	Any process that stops, prevents, or reduces the frequency, r	PHB2	8.33	1/12	0.08	1/1259	0.6171524
GO:0009890	negative regulation of biosynthetic process	Any process that stops, prevents, or reduces the rate of the	PHB2	8.33	1/12	0.08	1/1277	0.6220644
GO:0006955	immune response	Any immune system process that functions in the calibrated	PHB2	8.33	1/12	0.08	1/1288	0.6246035
GO:0048583	regulation of response to stimulus	Any process that modulates the frequency, rate or extent of	NDRG4 PHB2	16.67	2/12	0.07	2/2982	0.625435
GO:0006915	apoptotic process	A programmed cell death process which begins when a cell r	PHB2	8.33	1/12	0.08	1/1299	0.6262018
GO:0009893	positive regulation of metabolic process	Any process that activates or increases the frequency, rate or	ACSL3 PHB2	16.67	2/12	0.07	2/3040	0.6360302
GO:0012501	programmed cell death	A process which begins when a cell receives an internal or ex	PHB2	8.33	1/12	0.07	1/1343	0.6368246
GO:0006468	protein phosphorylation	The process of introducing a phosphate group on to a protei	PHB2	8.33	1/12	0.07	1/1340	0.6368246
GO:0030154	cell differentiation	The process in which relatively unspecialized cells, e.g. emb	ACSL3 FASN	16.67	2/12	0.06	2/3098	0.6452496
GO:0048869	cellular developmental process	A biological process whose specific outcome is the progressi	ACSL3 FASN	16.67	2/12	0.06	2/3162	0.6576973
GO:0008219	cell death	Any biological process that results in permanent cessation of	PHB2	8.33	1/12	0.07	1/1432	0.6607283
GO:0006464	cellular protein modification process	The covalent alteration of one or more amino acids occurri	CUL9 PHB2	16.67	2/12	0.06	2/3236	0.6696226
GO:0036211	protein modification process	The covalent alteration of one or more amino acids occurri	CUL9 PHB2	16.67	2/12	0.06	2/3236	0.6696226
GO:0031323	regulation of cellular metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A PHB2	25.00	3/12	0.06	3/5027	0.6811726
GO:0044249	cellular biosynthetic process	The chemical reactions and pathways resulting in the formati	ACSL3 FASN PHB2	25.00	3/12	0.06	3/5094	0.6914526
GO:1901566	organonitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formati	ACSL3	8.33	1/12	0.06	1/1575	0.6947104
GO:0031326	regulation of cellular biosynthetic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67	2/12	0.06	2/3385	0.6947104
GO:0031328	positive regulation of cellular biosynthetic process	Any process that activates or increases the frequency, rate or	ACSL3	8.33	1/12	0.06	1/1596	0.6965817
GO:0043412	macromolecule modification	The covalent alteration of one or more monomeric units in a	CUL9 PHB2	16.67	2/12	0.06	2/3413	0.6965817
GO:0048468	cell development	The process whose specific outcome is the progression of the	FASN	8.33	1/12	0.06	1/1592	0.6965817
GO:0009889	regulation of biosynthetic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67	2/12	0.06	2/3433	0.6968717
GO:0016310	phosphorylation	The process of introducing a phosphate group into a molecu	PHB2	8.33	1/12	0.06	1/1608	0.6968717
GO:0051716	cellular response to stimulus	Any process that results in a change in state or activity of a	ci CMTM8 FASN NDRG4 PHB2	33.33	4/12	0.06	4/6878	0.6968717
GO:0009891	positive regulation of biosynthetic process	Any process that activates or increases the frequency, rate or	ACSL3	8.33	1/12	0.06	1/1617	0.6972951
GO:0006508	proteolysis	The hydrolysis of proteins into smaller polypeptides and/or	CUL9	8.33	1/12	0.06	1/1674	0.7107193
GO:0044260	cellular macromolecule metabolic process	The chemical reactions and pathways involving macromolecu	ANKRD13A CUL9 PHB2	25.00	3/12	0.06	3/5305	0.7130572
GO:1901362	organic cyclic compound biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2 SQLE	16.67	2/12	0.06	2/3552	0.7142344
GO:1901575	organic substance catabolic process	The chemical reactions and pathways resulting in the breakd	CUL9	8.33	1/12	0.06	1/1742	0.723849
GO:0022607	cellular component assembly	The aggregation, arrangement and bonding together of a cell	ACSL3 SQLE	16.67	2/12	0.05	2/3663	0.7315838
GO:0005077	nervous system process	A organ system process carried out by any of the organs or ti	NDRG4	8.33	1/12	0.05	1/1827	0.7413014
GO:0050790	regulation of catalytic activity	Any process that modulates the activity of an enzyme.	PHB2	8.33	1/12	0.05	1/1868	0.7492779
GO:0032268	regulation of cellular protein metabolic process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.05	1/1884	0.7515515
GO:0007165	signal transduction	The cellular process in which a signal is conveyed to trigger	a CMTM8 NDRG4 PHB2	25.00	3/12	0.05	3/5642	0.7556332
GO:0051172	negative regulation of nitrogen compound metabolic process	Any process that stops, prevents, or reduces the frequency, r	PHB2	8.33	1/12	0.05	1/1924	0.7577161
GO:0051239	regulation of multicellular organismal process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.05	1/1943	0.7604901
GO:0044085	cellular component biogenesis	A process that results in the biosynthesis of constituent macr	ACSL3 SQLE	16.67	2/12	0.05	2/3907	0.7635171
GO:0051246	regulation of protein metabolic process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.05	1/2025	0.7747789
GO:1901564	organonitrogen compound metabolic process	The chemical reactions and pathways involving organonitro	ACSL3 CUL9 PHB2	25.00	3/12	0.05	3/5915	0.787099
GO:0019222	regulation of metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 ANKRD13A PHB2	25.00	3/12	0.05	3/5976	0.7938144
GO:0023052	signaling	The entirety of a process in which information is transmitted	CMTM8 NDRG4 PHB2	25.00	3/12	0.05	3/6020	0.7981898
GO:0007154	cell communication	Any process that mediates interactions between a cell and its	CMTM8 NDRG4 PHB2	25.00	3/12	0.05	3/6065	0.802601
GO:0050896	response to stimulus	Any process that results in a change in state or activity of a	ci CMTM8 FASN NDRG4 PHB2	33.33	4/12	0.05	4/7978	0.8190301
GO:0003008	system process	A multicellular organismal process carried out by any of the	c NDRG4	8.33	1/12	0.04	1/2314	0.8195921
GO:0044267	cellular protein metabolic process	The chemical reactions and pathways involving a specific pro	CUL9 PHB2	16.67	2/12	0.04	2/4461	0.8317141
GO:0065009	regulation of molecular function	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.04	1/2439	0.8367886
GO:0065003	protein-containing complex assembly	The aggregation, arrangement and bonding together of a set	ACSL3	8.33	1/12	0.04	1/2520	0.84748
GO:0051171	regulation of nitrogen compound metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67	2/12	0.04	2/4722	0.8586972
GO:0043933	protein-containing complex organization	Any process in which macromolecules aggregate, disaggregat	ACSL3	8.33	1/12	0.04	1/2678	0.8664832
GO:0080090	regulation of primary metabolic process	Any process that modulates the frequency, rate or extent of	ACSL3 PHB2	16.67	2/12	0.04	2/4857	0.8705709
GO:0010604	positive regulation of macromolecule metabolic process	Any process that increases the frequency, rate or extent of	PHB2	8.33	1/12	0.04	1/2795	0.8784046
GO:0006950	response to stress	Any process that results in a change in state or activity of a	ci PHB2	8.33	1/12	0.04	1/2809	0.8786781
GO:0006355	regulation of transcription, DNA-templated	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.03	1/2881	0.8831973
GO:1903506	regulation of nucleic acid-templated transcription	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.03	1/2881	0.8831973
GO:2001141	regulation of RNA biosynthetic process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.03	1/2884	0.8831973
GO:0019538	protein metabolic process	The chemical reactions and pathways involving a protein. Inc	CUL9 PHB2	16.67	2/12	0.04	2/5108	0.8869735
GO:1901360	organic cyclic compound metabolic process	The chemical reactions and pathways involving organic cyclic	ACSL3 PHB2 SQLE	25.00	3/12	0.04	3/7066	0.8877152
GO:0097659	nucleic acid-templated transcription	The cellular synthesis of RNA on a template of nucleic acid	(C PHB2	8.33	1/12	0.03	1/3019	0.8919133
GO:0006351	transcription, DNA-templated	The cellular synthesis of RNA on a template of DNA.	PHB2	8.33	1/12	0.03	1/3019	0.8919133
GO:0032774	RNA biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.03	1/3030	0.8919133
GO:0071704	organic substance metabolic process	The chemical reactions and pathways involving an organic su	ACSL3 ANKRD13A CUL9 FASN PHB2 SQLE	50.00	6/12	0.05	6/12360	0.8979909
GO:0051252	regulation of RNA metabolic process	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.03	1/3134	0.8993919
GO:0010556	regulation of macromolecule biosynthetic process	Any process that modulates the rate, frequency or extent of	PHB2	8.33	1/12	0.03	1/3278	0.9111134
GO:0060255	regulation of macromolecule metabolic process	Any process that modulates the frequency, rate or extent of	ANKRD13A PHB2	16.67	2/12	0.04	2/5552	0.9124633
GO:0019219	regulation of nucleobase-containing compound metabolic process	Any cellular process that modulates the frequency, rate or e	PHB2	8.33	1/12	0.03	1/3342	0.9136827
GO:0034654	nucleobase-containing compound biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.03	1/3364	0.9140608
GO:0019438	aromatic compound biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.03	1/3441	0.9173246
GO:0018130	heterocycle biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.03	1/3434	0.9173246
GO:0008152	metabolic process	The chemical reactions and pathways, including anabolism ar	ACSL3 ANKRD13A CUL9 FASN PHB2 SQLE	50.00	6/12	0.05	6/12915	0.9271546
GO:0044238	primary metabolic process	The chemical reactions and pathways involving those compo	ACSL3 CUL9 FASN PHB2 SQLE	41.67	5/12	0.04	5/11429	0.93122
GO:0044237	cellular metabolic process	The chemical reactions and pathways by which individual cel	ACSL3 ANKRD13A CUL9 FASN PHB2	41.67	5/12	0.04	5/11581	0.9383581
GO:0044271	cellular nitrogen compound biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.02	1/4213	0.9580875
GO:0006139	nucleobase-containing compound metabolic process	Any cellular metabolic process involving nucleobases, nucleo	ACSL3 PHB2	16.67	2/12	0.03	2/6721	0.9599763
GO:0010468	regulation of gene expression	Any process that modulates the frequency, rate or extent of	PHB2	8.33	1/12	0.02	1/4340	0.9599763
GO:0009059	macromolecule biosynthetic process	The chemical reactions and pathways resulting in the formati	PHB2	8.33	1/12	0.02	1/4337	0.9599763
GO:0046483	heterocycle metabolic process	The chemical reactions and pathways involving heterocyclic c	ACSL3 PHB2	16.67	2/12	0.03	2/6828	0.9624271
GO:0006725	cellular aromatic compound metabolic process	The chemical reactions and pathways involving aromatic comp	ACSL3 PHB2	16.67	2/12	0.03	2/6891	0.9631

GO:0010467 gene expression
GO:0008150 biological_process

The process in which a gene's sequence is converted into a r PHB2 8.33 1/12 0.01 1/7489 0,9977989
A biological process represents a specific objective that the o ACSL3 ANKRD13A AP2B1 ATP13A3 CMTM8 Cl. 100.00 12/12 0.06 12/2011 1

Diet	animal	A0A3Q1M3L	PIGR	CUL9	SQLE	CD5L	PPIA	HID1	A0A3Q1LRW	KRT10	RAB2A	TMC4	GP2	LBP	AUP1	GNG12	ACSS2	ALPL
HL	c8	3226518	18491661	55721	267138	643807	4010575	150009	4893882	883223	10535572	1392806	4238810	423454	7645294	769263	2114252	8423425
HL	c6	2621250	17827237	42068	333860	592909	2290016	369420	5780402	963247	3997409	1674433	7983325	250048	7533428	514114	1577784	5029499
HL	c5	4618716	16234862	57630	222873	562089	3584617	149259	4249250	1133275	7852213	2569959	6800899	120660	7454262	879234	2816705	7231044
HL	c3	4488714	56889382	12035	348292	266766	6517901	308098	9587083	391108	4848207	1110141	7208158	126822	6136405	596975	4387306	4136854
HL	c4	3744970	24959346	63371	513451	338739	4244459	341137	1750842	584185	7005446	1160836	5478408	145365	6756025	948293	4059671	2849111
HL	c1	4456646	13957555	155657	176116	337455	2079380	135199	5222401	748431	4912477	938296	6206673	106415	7592812	1372805	4092851	3978422
HL	c7	3369445	22436490	32947	265883	131201	4202181	186125	9810590	913247	11433758	1818823	5097694	143527	7761627	813274	2617173	10412417
HL	c2	4974398	24789977	24046	319247	310142	6021004	185060	6730173	1961319	9508143	1839859	10608024	227590	3795844	2282752	2284696	4162687
LL	c8	2228555	6311510	106520	492317	127599	3740351	414099	1070669	194422	7763388	1386477	2424584	39144	6607011	1951921	4289839	2338748
LL	c6	1349347	16559764	228090	1316786	26711	8048892	946040	1817993	127432	9786634	671131	3124936	168252	10030098	2157106	6310487	403245
LL	c5	1586230	5968660	731736	1651682	80848	6802231	652788	1951621	142178	10670042	780583	1604835	91116	11771302	1636973	10846871	2313361
LL	c3	2537017	10893410	91953	620758	104284	6978896	336053	2026944	406512	6609125	794407	2466313	79247	8395895	1337010	6608888	1715647
LL	c4	2647998	16724980	263421	482820	129637	4898127	359689	2145015	386029	12262340	807036	4036523	55110	9106829	1375231	4509270	4935284
LL	c1	1919380	9122168	136179	269110	207537	8894368	236875	1817171	943935	18548596	1223767	3978824	38138	7854526	3103622	2152739	3497869
LL	c7	2153799	7368834	78939	337201	127133	7140479	380311	2387631	241266	12715467	1257034	2995935	32871	7614252	2503532	2854309	3559427
LL	c2	1202398	17332069	66437	1060616	226291	12533023	435730	4305990	361512	15876310	514567	4722875	96054	13062908	1936831	9948758	1783223
	Moy HL	3937582	24448314	55434	305857	397889	4118767	228038	6003078	947255	7511653	1563144	6702749	192985	6834462	1022089	2993805	5777932
	ET HL	820307	13699246	44184	101893	180727	1567416	95400	2697027	470424	2805219	528410	1983806	106494	1346504	571266	1051570	2625892
	Moy LL	1953090	11285174	212910	778911	128755	7379546	470198	2190379	350411	11778988	929375	3169353	74991	9305352	2000278	5940145	2568350
	ET LL	535030	4886573	221425	504298	64400	2652578	225777	935964	263530	3996034	315560	1024651	45090	2198626	593319	3147948	1393739
	Ratio HL/LL	2,0	2,2	0,3	0,4	3,1	0,6	0,5	2,7	2,7	0,6	1,7	2,1	2,6	0,7	0,5	0,5	2,2
	Ratio LL/HL	0,5	0,5	3,8	2,5	0,3	1,8	2,1	0,4	0,4	1,6	0,6	0,5	0,4	1,4	2,0	2,0	0,4

PSEN1	KRT7	CNTFR	APOA4	F1MH40	SELENOF	MARCKS	RAB3GAP2	SLC6A8	LSS	CSTB	C4BPA	ATP13A3	ALB	ZDHC18	FAF2	FASN	SEC22B	RAB13
521189	348587	4635077	3104310	1730907	239484	1356703	819917	924262	40183899	1170879	384050	2184290	552810	59117	3354205	4144732	352640	608319
470865	683041	1967503	1776546	1772626	187035	1200599	684956	1028849	32772747	758225	498445	2756134	512617	17238	4056370	3426255	309229	261969
302372	415822	1984517	302598	1371175	500675	853963	841835	1354651	36866579	778259	288435	2924505	891593	76560	3685925	5003815	381666	786305
1005377	326480	1919417	459812	776731	638425	385107	456899	892850	44694265	2115827	66578	2993222	498733	72388	3287263	12529573	329112	272913
251318	350165	2108630	393613	263100	202178	570318	1248151	531101	31218702	957953	10100	2740416	648380	47171	2264581	22749906	671157	448751
870944	185141	2407122	511824	960929	325442	899710	384583	805669	19000071	722954	465844	3158768	876041	24136	1312724	18893801	221413	422625
869947	216983	3502870	1920270	1278585	449553	938623	852648	1032097	40310361	1490040	297912	2080695	918869	28068	3433115	3743940	533578	744490
593459	479894	2446000	606006	1693129	793840	658359	748010	853460	24919069	931657	85171	2177796	1342093	76055	2683479	9727860	1192359	696952
708107	147272	930868	323928	280019	482354	628734	2727916	602041	45001505	1206587	36782	3893128	393748	111961	3526532	15144389	621532	551656
1510679	224216	528658	259873	432583	903434	63997	682038	298207	79828774	1049224	129449	10147833	511213	38027	4356340	80382645	931684	637171
1229433	99932	360485	122680	334921	806062	116997	1227056	556840	113957118	1509295	69469	6705968	759848	76692	5737916	39515881	755999	727681
1757367	253901	796890	55187	512970	491656	129379	1113708	547517	61645104	1753080	15268	4910873	246604	42220	2979207	16972339	275161	354147
540016	203872	3732271	376609	1446930	791788	376576	1389198	568751	37061194	1613617	20536	3032263	488320	70203	3157992	18101400	1084932	942710
892899	184163	1873800	179461	717647	786618	921401	1421875	903711	34428648	2093182	48367	2236400	674346	81234	2982014	19271271	1466128	1449530
580572	273669	2069573	155496	1189429	526637	465689	1540285	950536	32278390	1484308	29628	2576470	347039	136189	3688504	5895740	1564941	1101374
2039818	180670	667784	134563	396489	2228024	48188	695999	446262	67655057	4203706	228893	3629961	211724	129260	6214712	16435192	437020	1057936
610684	375764	2621392	1134372	1230898	417079	857923	754625	927867	33745712	1115724	262067	2626978	780142	50092	3009708	10027485	498894	530290
278463	156861	963437	1019315	533837	219749	320843	266060	233708	8592617	477806	187942	419382	286968	24495	883916	7461568	313665	207629
1157361	195962	1370041	200975	663873	877072	343870	1349759	609233	58981974	1864125	72299	4641612	454105	85723	4080402	26464857	892175	852776
567493	56343	1137975	109388	430215	569889	314832	642140	218680	28109712	997696	73078	2642403	193954	37111	1259765	23727909	462974	352447
0,5	1,9	1,9	5,6	1,9	0,5	2,5	0,6	1,5	0,6	0,6	3,6	0,6	1,7	0,6	0,7	0,4	0,6	0,6
1,9	0,5	0,5	0,2	0,5	2,1	0,4	1,8	0,7	1,7	1,7	0,3	1,8	0,6	1,7	1,4	2,6	1,8	1,6

SACM1L	MUC15	ANKRD22	SCAMP2	CSN1S1	STK26	REEP6	ARF4	FABP3	FGG	PGD	SEC14L1	IMMT	PFN1	TC2N	TMEM120B	IDH1	ACTB	PHB2
326960	25843723	2291745	8378051	161025009	518338	401554	12389670	120510636	2805032	10054736	159418	20233	471111	57289	633832	1960074	9387976	24101
262467	15816447	904395	7153414	44936046	640270	314594	4717871	89246663	1921266	6641776	93606	6714	258068	42467	558013	1789382	11076102	63091
217194	13939732	2172792	1983184	46322973	504866	173301	7849047	150313686	1828229	12415049	135498	10030	613479	106359	646845	1668287	7641346	1674
450825	5291420	681096	1526808	111661782	1738375	130999	7445385	125251540	548270	8789050	85439	41886	416788	11735	706073	705714	6466282	120489
486318	15021924	2157662	2980145	36995023	372233	239592	7546355	77807444	485152	20652379	259066	219950	396919	58920	782901	2304733	11028798	163133
287094	12135382	1502431	5224795	37737358	425815	131499	6926538	183975063	1151472	10897343	179623	46374	361165	106406	587792	2194203	7383537	20708
611780	13836104	3209587	6514626	76215672	184188	208868	12784481	228480112	7546779	12661578	158798	71597	846161	75919	1284593	2217150	11784602	59706
594868	12234034	1952154	1663009	52489829	362193	319564	13513925	220308398	1453435	15311257	140695	94989	973792	37261	1337892	2093191	12667531	136018
626100	12185499	2119462	947656	20555789	422672	479905	7465823	124709129	546856	4665172	185468	20052	875670	41379	953628	1279630	9287169	37510
398469	689047	2630031	246255	43708857	1426413	385261	9261434	144277778	1105455	13169664	183872	99555	974451	8087	1375209	390133	880221	392101
1748787	4159545	2829724	3360519	30167063	2125087	265245	8443344	183334593	2008564	17590860	290153	26173	624776	6771	1591442	451894	1493721	39418
814410	5562389	2308755	1206023	63020894	1805481	158140	9353538	184228358	504073	5952254	124066	144090	435757	11576	975275	631123	5333149	81226
556407	9853067	6982344	2750893	37541099	523826	616112	19118788	295301610	814441	10182792	155439	224086	1056945	73992	1125357	1516842	9539225	516736
440818	11253964	2478720	4753553	33671378	473108	488483	20588024	512545569	581835	5153470	251223	107735	1020348	24937	1530180	3017134	9371053	39482
357876	12111773	4652210	3950952	52384591	474466	535379	19832858	310699131	805344	6726724	129365	185653	1025505	53519	897881	1786878	8998890	165170
575303	3874178	2803099	1170866	52396524	5342356	306931	14817677	277180804	296796	7591456	236408	142857	1455522	15177	2156269	666095	5725931	1012445
404688	14264846	1858983	4428004	70922961	593285	239996	9146659	149486693	2217454	12177896	151518	63972	542185	62045	817242	1866592	9679522	73615
152643	5688607	813595	2729604	44205190	481745	97882	3262472	56870198	2283270	4312863	54203	69947	250468	33134	312947	517576	2298016	59564
689771	7461183	3350543	2298339	41680774	1574176	404432	13610186	254034621	832921	8879049	194499	118775	933622	29430	1325655	1217466	6328670	285511
451819	4428610	1661985	1629723	13882315	1666002	153354	5614964	125880069	534250	4511857	59818	71311	305154	24553	429140	892422	3582960	344771
0,6	1,9	0,6	1,9	1,7	0,4	0,6	0,7	0,6	2,7	1,4	0,8	0,5	0,6	2,1	0,6	1,5	1,5	0,3
1,7	0,5	1,8	0,5	0,6	2,7	1,7	1,5	1,7	0,4	0,7	1,3	1,9	1,7	0,5	1,6	0,7	0,7	3,9

ALG1	ATP13A4	ACSL3	SLC39A8	RAB3GAP1	UBA1	RAB3D	GPAM	GSE513	DGKD	ARL1	SSR4	BSPRY	GSE5T5	CHP1	Q3ZC78	RNH1	KRT1	RACK1
283061	11301660	10970286	39827879	540560	273060	1884006	10929563	19033541	325786	28304	73165	2603496	275850	2553243	384360	1780243	840334	687339
190849	17431189	9600273	49597974	365804	274384	759378	16147365	23036916	267298	98878	128637	977136	395094	2146141	108718	1057732	564739	280690
248658	10039576	15584159	46462100	382879	157084	1582352	11576359	30939797	442505	139888	142304	1294897	1826588	3812724	127835	1665154	824825	76821
166397	37907607	17631092	32248307	459335	172117	3393771	19521772	49477999	976442	303395	228682	1001547	964891	1574298	110635	693359	374332	740057
274814	13228619	8916733	32306141	669911	449520	1027487	16217480	22155140	338529	70112	226760	1744865	343250	4200723	112657	1810069	580871	290168
252561	23050734	8645180	38176620	698710	110861	862387	11640787	20557234	172945	131509	150741	724930	426722	3713656	412938	1024037	604052	111840
455966	12129888	10191715	49590814	457234	196528	1921571	14336045	23502086	291913	33129	187570	3807036	266075	7288614	551312	1871270	406581	673797
217948	10911521	8924628	39781710	410208	315133	1480311	12911469	46776018	190298	150325	590834	1263800	548859	2871096	187739	1789602	930043	469158
138538	14897056	12679894	31850057	1274081	454241	1038555	19624499	9177365	376220	98541	268760	665228	181523	2824948	387792	1531308	345046	297874
443816	46385969	24335161	5058191	472865	438996	2044450	56683811	58483052	543537	497425	460091	51885	452720	2178195	401344	2374688	62326	620871
271809	44070442	48193756	14768271	1240601	348356	3748496	28776539	19444731	1615914	282695	191669	137041	1193891	4121978	100053	3525612	293226	876437
344802	48814806	21521470	29966372	988401	285284	3350960	20606123	18244026	715445	207570	98481	547652	244244	2669685	204383	2010586	449041	715176
424717	16243829	8633362	51150168	867857	401517	1629244	16724728	18977867	394362	125304	472872	2436890	265675	9113256	663209	2112486	461258	984408
243969	15643876	9786557	25408522	736963	241697	1338772	8795682	13158740	304655	229757	472785	506567	132523	6013110	243859	1161833	761826	393153
353104	11872096	10582010	36322096	1166341	192039	2305639	16250200	11500995	331011	163196	464423	1538631	27307	6559770	349759	1217596	267928	473354
514535	31600251	20307125	25017637	282998	285953	2539981	31798545	20641626	681998	1128077	837856	503908	307305	7613262	419447	3062571	480632	414743
261282	17000099	11308008	40998943	498080	243586	1613908	14160105	29434841	375714	119442	216087	1677213	630916	3520062	249524	1461433	640722	416234
88347	9485740	3402367	6975126	127191	108078	844585	2975582	12076148	257317	87805	160049	1039868	532802	1765461	174207	460524	204915	264473
341911	28691041	19504917	27442664	878763	331010	2249512	24907516	21203550	620393	341570	408367	798475	350649	5136775	346231	2124585	390160	597002
121327	15862708	13038006	13827548	362893	95266	946445	14736248	15631336	431599	341103	227114	799980	363049	2562152	169797	846833	203080	245601
0,8	0,6	0,6	1,5	0,6	0,7	0,7	0,6	1,4	0,6	0,3	0,5	2,1	1,8	0,7	0,7	0,7	1,6	0,7
1,3	1,7	1,7	0,7	1,8	1,4	1,4	1,8	0,7	1,7	2,9	1,9	0,5	0,6	1,5	1,4	1,5	0,6	1,4

ESYT2	A0A3Q1MAC CD36		CALR	ESYT1	ABCG2	A0A3Q1LSB7 GNB2		KPNB1	CSN1S2	RAP2B	CLU	RALA	TMC5	RAB9A	STK38	RPL27	ANXA7	NDRG4
252726	1414293	143997448	523566	347326	424107538	512996	40399240	81326	68732759	340528	288187	2319529	2112956	204756	142392	43557	1529932	101213
172319	476607	149497712	931652	580287	461975398	402973	23310644	182891	31098216	95591	76744	1073963	1884604	118524	214231	49334	1369942	103263
143362	1372027	182819900	890090	513852	668353352	622600	30192318	109470	41767609	188510	265258	999288	1644183	437663	352131	20118	1369675	31975
73471	2854271	83497265	506204	572999	488077770	316503	23220382	259132	161472957	255029	405674	1371778	564614	155676	119747	113972	1447517	703719
198040	373019	97663915	1333057	498439	479930166	99962	23274841	185854	20987921	92890	292720	751487	928720	137264	235029	195814	1518536	46246
124239	855774	83961123	401319	340351	486354649	126843	25213570	198606	28320301	126794	367063	758656	1488567	40271	147636	34023	1217346	206094
228712	528278	100327738	807130	163441	418876367	285278	37696047	285029	39679872	191976	143813	1360987	2025285	102645	155020	87870	1548335	49559
244149	1013709	82265905	1857495	883319	423358218	377126	25947838	241734	29867499	173925	223661	1203761	1704571	260923	307738	389209	1860894	92051
337043	624914	99143455	1357902	802442	690853813	468454	16629770	189836	10305392	227064	55493	703850	1144658	142924	277404	165507	1173251	61904
345377	2595561	61634168	130628	1133274	1158483830	269096	8605381	500764	15672696	383963	79907	1464020	509800	223822	424892	240162	454663	905120
370038	1246285	115136234	146462	1533512	1051269989	259263	11997878	436592	15127098	231484	127540	3368133	451640	272606	666730	69842	600472	484582
339694	2045653	54075464	226906	701471	832837543	415424	18469106	406919	50720013	279424	139680	1329147	798961	96323	227751	46689	1114488	840211
321314	439518	77953662	759699	309018	477209303	901794	31729017	276931	24510735	192541	32435	1090928	1228386	195225	201154	492780	1390209	119490
192705	1819953	110618413	551179	588742	419380640	548339	27465899	103418	29665800	222668	152802	1918756	1128225	404524	198329	292201	1271622	163691
237160	1474259	103384136	1100984	528497	482422490	488485	31008681	222706	30454229	333280	247781	1426424	1483802	378151	235595	313085	1225384	141667
121413	3321064	35028991	587882	468217	513711745	1710821	15251271	311477	39601644	717266	113589	2528991	820244	545616	213024	194816	790708	447577
179627	1110997	115503876	906314	487502	481379182	343035	28656860	193005	52740892	183156	257890	1229931	1544187	182215	209241	116737	1482772	166765
63201	807143	38119403	486856	213716	81029667	177949	6847800	70560	46237923	83765	108853	500534	540901	122601	84534	123872	188222	223673
283093	1695901	82121815	607705	758147	703271169	632709	20144625	306081	27007201	323461	118653	1728781	945715	282399	305610	226885	1002600	395530
88990	968434	29484329	450106	398981	283263657	479363	8819273	134970	13599676	171477	66880	857110	361295	150509	163615	143677	342413	332472
0,6	0,7	1,4	1,5	0,6	0,7	0,5	1,4	0,6	2,0	0,6	2,2	0,7	1,6	0,6	0,7	0,5	1,5	0,4
1,6	1,5	0,7	0,7	1,6	1,5	1,8	0,7	1,6	0,5	1,8	0,5	1,4	0,6	1,5	1,5	1,9	0,7	2,4

ATP5F1A	STX3	GSN	RDH11	PSMD6	RHEB	XYLB	RTN4	RAB1A	SURF4	DENND3	GLYCAM1	A0A3Q1LUE9	TLR4	MYO6	FLOT1	LRATD2	SERPIN1	HDLBP
121706	7210758	2067625	1043871	40571	2380743	53699	247792	14940887	117251	39488	640784409	2644865	160478	10037	2196855	404112	120431	1569
177294	7375898	2999108	589269	87418	1437415	140234	124823	9712159	119801	70264	242453861	754844	183403	36362	2122085	425610	204428	8500
261886	8748547	1296172	729724	34102	2265168	47949	295099	7951142	176909	110654	86826587	853854	228006	51343	1457094	588836	38950	21257
1711626	5303185	1043635	392841	17438	1667086	222436	113434	10677674	221837	12484	87166125	2186592	106237	38681	1257120	316533	23599	27533
1653075	5933924	2821905	839921	183269	1701305	140692	316306	12095728	301517	116151	53667656	1657844	250525	126248	1118278	398223	197351	77523
253816	9480739	2544757	744151	100301	2230678	62876	219166	12704576	242422	89540	77562767	1675448	174774	38441	1964580	338138	67724	11207
471179	10677219	3860350	1271219	108902	3003353	50632	240349	17995602	176613	81965	586199525	1209995	127766	84672	2694993	300993	779375	1087
1258790	8954598	2576334	948898	289243	3087500	111240	469420	14063890	508244	134694	44722289	2546179	260131	73291	905866	476470	104698	47539
300185	4475666	2307605	872171	78429	1801138	117543	287262	11940108	263762	67434	63050707	379475	460603	68853	1196429	357354	62872	87557
1879162	762761	336645	1193689	30111	1465418	344329	476120	29309739	470282	4160	23829553	453927	507700	51807	688761	57484	90506	217640
858949	1912742	697902	871779	2598	2733390	175150	323432	19392814	507171	36761	27257874	310222	965086	135122	1503148	160508	43994	43219
1253484	5025278	1130886	505683	8830	2349452	125250	196951	16287264	485828	19186	22508319	707284	372129	52344	1176841	285475	56616	27968
1213581	8691792	2563257	1876601	69989	3889256	98612	408224	14941060	348935	95669	145525320	2832810	96261	74541	1525996	342439	92014	39762
782053	9591049	1799801	873333	55934	4033726	51628	389383	10903186	224167	102169	128982789	1937601	262055	66021	2426115	375874	24480	23359
1383566	9093376	3296721	1063431	230717	5235709	109363	460577	15066166	317948	94591	68494225	1542230	256146	83872	843140	517911	81284	27224
3598483	4678745	991957	1885348	83966	3496704	177452	520065	38407563	368502	914	69182238	449475	220370	52634	1237744	161509	55039	14275
738671	7960608	2401236	819987	107656	2221656	103720	253299	12517707	233074	81905	227422902	1691202	186415	57385	1714609	406114	192069	24527
684841	1827299	917312	272641	90401	607262	62048	113299	3175647	127169	40705	246484447	726706	56010	36191	621924	94476	246450	26373
1408683	5528926	1640597	1142754	70072	3125599	149916	382752	19530988	373324	52610	68603878	1076628	392544	73149	1324772	282319	63351	60125
1000214	3318537	1023565	496265	71883	1268564	88467	107890	9528547	105498	42562	46953987	928372	267040	27610	530185	148080	23546	67437
0,5	1,4	1,5	0,7	1,5	0,7	0,7	0,7	0,6	0,6	1,6	3,3	1,6	0,5	0,8	1,3	1,4	3,0	0,4
1,9	0,7	0,7	1,4	0,7	1,4	1,4	1,5	1,6	1,6	0,6	0,3	0,6	2,1	1,3	0,8	0,7	0,3	2,5

RAB23	PRDX5	TKT	ANKRD13A	GPC1	GOLGA7	RAB26	DENND2D	SH3YL1	STX19	PLIN3	GNA13	MARCKSL1	FGF	DHDDS	PDXK	SDC2	F1N647	NSDHL
500542	340574	209182	519344	485916	947646	161174	71074	907923	3828347	32280411	16278876	289266	1034499	276697	2457007	455212	6343805	24169884
101029	227004	292677	581017	473572	666227	235850	153783	562947	2366125	33982030	14217482	349559	823341	291111	3291746	416237	5384548	19651208
212222	258731	129892	378113	372440	852003	125151	154501	427045	2439429	28701724	17257914	265223	843464	358534	2746430	379602	7994487	25683347
93537	68562	123294	893732	272496	845599	20896	120902	1039315	1141314	9481570	7165632	45403	122246	758436	901539	153620	2343877	33739170
199398	246892	384939	462972	388935	811846	125027	220772	437571	1909137	10800805	10600935	205010	129581	290931	2984866	472827	27096882	23890793
250073	166897	214666	448416	368220	702891	63844	176421	604473	3221951	16603809	13524458	302786	343169	517221	6988500	621689	14995535	20018493
709665	436131	305124	409824	867623	1238811	209473	117990	958450	2981171	44578771	14913602	158752	3461117	95986	6121051	395570	7336711	22542889
291320	431683	183141	506996	816994	1259535	149828	149413	426234	3060404	7996695	16412466	172783	540492	312007	3116123	553437	11784053	16802076
187317	373428	229630	571214	309868	1011604	149754	167737	548349	1339322	14203313	8966526	384397	132729	454158	1390050	248855	21894506	21794291
323184	296688	17514	1675867	249384	694390	37753	537824	1378049	864736	9171467	3695555	11158	905105	3285128	199859	52127	16040376	69614069
498487	230150	26791	1735123	378606	732416	10110	307252	818808	912557	11643365	5116959	73272	1546809	1374270	350028	146785	20685331	58232331
221829	161448	150783	1140098	101973	863795	32979	169354	1371408	905172	13055652	5128256	28886	73612	820556	805641	137179	6017149	30503505
507317	569433	232777	331211	552167	1571765	215039	147686	542812	2116524	11915010	14166120	54641	237632	99453	5736861	459480	39034625	23097801
233977	609873	166914	507913	83227	1676718	67056	159115	349999	3300412	16573889	20774540	483383	65796	359121	2963651	437595	23755405	20454811
259495	541697	239208	472645	284686	2158893	177152	169426	675506	3194500	12481725	16737467	215261	225215	301906	5890834	505045	13152755	25930674
699311	333361	55588	859738	108966	1539000	27039	101026	1293101	864374	9936007	5923403	38605	414569	1224345	297865	206585	4301034	62497121
294723	272059	230364	525052	505775	915570	136405	145607	670495	2618485	23053227	13796421	223598	912239	362615	3575908	431024	10409987	23312232
210588	126720	90907	162134	218434	223902	70595	44220	257579	839704	13640486	3394661	97883	1083845	197078	1994895	138741	7778160	5107968
366365	389510	139900	911726	258610	1281073	89610	219927	872254	1687199	12372554	10063603	161200	450183	989867	2204349	274206	18110147	39015575
182027	166273	94316	551045	161092	530510	78970	141204	415737	1051861	2342350	6367541	181532	520568	1031683	2401071	170652	11061178	20684897
0,8	0,7	1,6	0,6	2,0	0,7	1,5	0,7	0,8	1,6	1,9	1,4	1,4	2,0	0,4	1,6	1,6	0,6	0,6
1,2	1,4	0,6	1,7	0,5	1,4	0,7	1,5	1,3	0,6	0,5	0,7	0,7	0,5	2,7	0,6	0,6	1,7	1,7

SLC7A4	UQCRC2	TUBA4A	APOE	CMTM8	MICALL2	SDHA	STXBP2	SIRT2	GSTM3	INPP5A	SELENBP1	SLC1A2	FERMT2	FGR	GNAI1	ALOX15	G3MYK6	ARL15
25223615	4773	588859	13748865	88956	461981	2605	4054254	927585	1001450	263340	9776895	126469	137698	6120610	323860	2174792	163480	2395654
37964137	67436	1010508	5625880	226500	667860	19084	4451862	808541	241378	177199	9926574	173714	103452	6952135	521368	3930796	35747	2363790
19233095	66840	659014	11954768	106486	668829	11388	2029059	442946	448729	346572	2229867	173607	173493	14187891	445607	2009879	432674	2027140
24177642	825992	440858	4008162	1230897	232350	18668	2235943	326967	741248	131277	2421743	110825	90886	4223641	1418556	2387425	221844	1082544
33556536	759368	1455352	6083109	90493	887124	187389	5525779	946021	415349	256275	5058559	128950	231851	8837368	589757	3515277	143187	1392692
20099670	69011	932122	4986925	142552	654627	13155	4040743	971216	623578	309077	4492427	152462	145494	6616310	1520796	1685146	148825	968736
30897255	271146	581053	9082569	14509	732247	53364	4022576	780906	1122663	126440	7252831	87946	78517	6258043	299026	2235020	347343	2620773
44699868	320730	1325079	3543134	201463	803946	77281	5726599	591149	857684	251518	4191776	333202	198122	6470083	574647	2622905	248590	1944480
21929177	59220	929266	3304198	109424	501466	38431	3816512	512204	840941	165220	6995236	75749	382541	10597130	442257	5264626	97579	1449870
11320834	170757	642424	2604502	992816	73383	57157	1870031	207413	856641	42903	5803778	21611	205859	3086429	2789335	6948884	206411	1176698
12385278	198782	484508	3811198	1149724	155746	34149	2469318	476424	1092684	73364	1650338	15576	161746	11640203	2197748	3977529	111021	1190792
18877015	676294	333724	2933654	660626	202138	55257	3293017	407992	1049478	146188	4012829	133320	259707	7783530	1495118	3661055	331300	1156246
40047583	554661	851406	4229353	217536	652964	97185	3772571	390248	615509	161345	3825984	195029	109718	11323497	340110	4588021	281348	2642501
13762609	233346	949138	5718625	245108	704707	26821	2699685	666404	945031	219791	5565690	83482	77886	10172703	461961	2411678	879576	2573302
38348174	435239	916070	4335363	86556	783146	107660	4665076	874145	756688	306783	3687680	373810	186520	10674532	541464	2218614	634679	3352329
16948873	1790133	569602	5019579	1732033	158252	110546	1877907	195943	1053648	59743	2685111	24703	215702	7125732	2243657	1642964	606779	3053159
29481477	298162	874106	7379177	262732	638621	47867	4010852	724416	681510	232712	5668834	160897	144939	7458260	711702	2570155	217711	1849476
8956029	324673	371177	3797860	396907	205681	61676	1337054	243931	305587	80451	3019501	75707	53858	2995807	480429	769652	125547	629156
21702443	514804	709517	3994559	649228	403975	65901	3058014	466347	901328	146917	4278331	115410	199960	9050469	1313956	3839171	393587	2074362
11350794	556196	234348	1053046	597471	287287	34217	1000193	226112	165587	88833	1749879	121312	94017	2904234	991814	1764780	282524	924460
1,4	0,6	1,2	1,8	0,4	1,6	0,7	1,3	1,6	0,8	1,6	1,3	1,4	0,7	0,8	0,5	0,7	0,6	0,9
0,7	1,7	0,8	0,5	2,5	0,6	1,4	0,8	0,6	1,3	0,6	0,8	0,7	1,4	1,2	1,8	1,5	1,8	1,1

GNAI3	APOA1	CNP	PARK7	SH3GLB2	RPN1	FGA	COPB1	EEF1A1	PRKAA2	TPRG1L	ACTN1	GPX4	TBC1D24	AOA0A0MPA	ANXA2	CANX	MELTF	TMCO4
2368901	13946364	1253189	525352	252623	274628	1162652	53475	215216457	68197	3546593	530621	1628370	375847	34641	10998032	152377	809505	103109
1795272	4838576	1244795	221632	348154	620148	417219	75970	137618376	79556	2384652	875156	1244502	438867	30150	6521406	415563	54071	49699
1635343	3586474	1152208	84059	316273	246058	321102	62219	120797101	94542	2440162	226098	1196636	323336	10894	9225836	536907	74760	55946
3885368	3736069	305209	240364	114516	329935	35740	141463	106756877	33251	4004585	761647	295762	865782	27007	4045465	266950	150999	37360
1756668	2879454	702365	254354	293313	950186	103920	343005	185143076	166108	1494247	643257	914755	508481	139987	6385136	868591	44509	97911
2409988	4374234	732093	377975	583752	233800	105310	211898	158814188	42010	2915596	565853	864085	115670	32743	7364266	559993	151586	44926
2240896	10652807	1021783	1074901	248279	391650	3898346	42397	251558921	27763	6128790	880590	1877287	325145	82929	13242106	146802	146542	161810
2102046	4682469	511600	209013	535443	1272988	309869	474038	154729579	86512	2189501	742017	1799777	409965	238312	10157105	811071	94599	66183
1742458	1171033	1310668	96561	247615	999182	174584	261164	125109688	126095	2338464	858705	1539932	410742	94481	5895738	919279	180422	126999
7942804	3846005	136064	12486	65454	2744369	248729	443788	35434343	145019	16351548	372443	785390	395662	104348	1714534	465996	405	45156
4391313	2186233	327892	18186	112761	797707	819838	286956	38072623	86226	6290093	402375	1395462	749495	20243	5380451	733906	38905	104328
3460764	1247671	363868	513210	84459	266715	45557	140645	96784381	30789	6465232	271928	819868	981717	21002	3466061	295586	63825	75578
2575034	4047976	411431	284737	251516	972580	309395	192208	307158946	73925	1774903	544470	2570101	449887	285877	9675035	459076	98903	110011
2451715	4922640	745973	291933	457707	584607	87625	161167	171739984	99155	2384320	329271	3042912	240350	202086	8849687	705618	251384	72776
1642277	4598667	662405	547872	510148	611043	88467	230789	162146596	119317	2379185	500926	2569271	511164	259349	8266358	574174	71151	45794
5029675	4254443	473539	80724	57875	593233	30952	156607	70490490	75925	12583712	204173	686895	579096	194978	6284617	569288	14527	132589
2274310	6087056	865405	373456	336544	539924	794270	175558	166329322	74742	3138016	653155	1227647	420387	74583	8492419	469782	190821	77118
713078	3984773	355442	311874	154558	383343	1303748	158119	48763867	44632	1442631	215735	535814	213780	78189	2964561	277054	253741	41777
3654505	3284333	553980	230714	223442	946180	225643	234165	125867131	94556	6320932	435537	1676229	539764	147796	6191560	590365	89940	89154
2110449	1515214	360535	213924	178242	764230	259512	99513	89511498	36023	5443452	204200	931012	232014	102651	2718487	193604	85919	34336
0,6	1,9	1,6	1,6	1,5	0,6	3,5	0,7	1,3	0,8	0,5	1,5	0,7	0,8	0,5	1,4	0,8	2,1	0,9
1,6	0,5	0,6	0,6	0,7	1,8	0,3	1,3	0,8	1,3	2,0	0,7	1,4	1,3	2,0	0,7	1,3	0,5	1,2

TXNDC5	ZW10	RAB7A	OSBPL9	SLC29A1	RHPN2	GOLPH3	NUP155	LPL	DDX3X	VPS4A	SFT2D2	DNAJB9	LRRC47	ZDHC9	GPD1	EHD3	SLC34A2	RPS20
536003	234761	7388429	1876188	694370	73081	1856989	65969	45131818	23318	826829	2080625	473424	78062	972463	2650714	388266	236827348	53703
444914	163262	2911712	1636604	637600	69972	1130089	115944	22847767	68795	844869	1068752	496464	124726	805326	2440579	373334	264178040	45418
731413	225368	5109179	2064111	1174429	130143	572663	89125	7187396	41559	159295	1375136	574656	37706	1122859	4094920	823949	326263369	49147
642012	375936	2146192	1077032	597091	164054	880790	41444	10134553	57777	34403	2965373	926670	198586	489086	1539737	402997	152179283	21633
1386506	526895	3471770	2496570	1018246	161556	1300402	80776	6435015	79798	237278	1376708	470104	277719	711827	3258004	480448	174927907	226525
733597	681014	2720806	1843618	775790	38206	1261917	127940	7962983	42730	72876	653270	369705	58316	1020538	5307256	269928	205031360	32185
866988	334689	6366472	2428092	773644	107782	668294	42141	15727714	43673	374211	2132566	955479	106420	1433248	2123351	436708	221108685	80825
1335869	352741	4589272	3133709	856207	61523	2182337	47323	7242363	61449	239781	2001051	814908	194579	866737	3038443	396840	198664912	552194
1116928	550210	3867841	1681219	530771	97067	1563214	109677	6280426	104621	203805	1197879	426795	229163	591398	1670288	381803	269477265	271703
3343514	667382	5389077	1123951	1608978	320260	1527115	201939	16324052	311007	143079	1754243	609703	132068	121120	1092902	180416	52990663	141263
1310041	1211303	4266396	2866147	1131294	141740	934217	468825	12960547	62812	56734	2189602	450443	199395	270324	1139512	172987	132256718	26627
590508	830467	3271934	1667393	519424	153098	799803	170009	6537403	35447	55427	3320316	916910	329797	960953	1548186	371462	142303132	78854
1371660	367855	6314539	1710952	698444	89850	732888	53556	6920828	57308	267780	1727979	642064	283366	1636794	2009825	394255	254054352	503340
737490	246489	6925502	1302443	711731	70522	753436	151023	5626937	46811	194848	1930019	1070165	92214	860818	4674866	301959	235955165	369633
884398	407015	7799347	2215774	800663	89932	593137	37849	2969959	51764	211781	992610	1652413	193696	975602	4810394	491493	178840270	588528
1167076	685121	5111146	1031319	278707	155106	944983	65793	6415555	35771	31126	5869917	1264608	94184	368151	1662555	208385	122697477	517646
834663	361833	4337979	2069491	815922	100790	1231685	76333	15333701	52388	348693	1706685	635176	134514	927760	3056626	446559	222397613	132704
349668	170855	1862474	621557	196012	47481	558768	33276	13292971	17981	318581	729736	228866	82350	283338	1189268	163880	54500842	181560
1315202	620730	5368223	1699900	785001	139697	981099	157334	8004464	88192	145572	2372821	879138	194235	723145	2326066	312845	173571881	312199
863799	305600	1565572	605271	414636	79811	365926	138829	4368731	92647	88042	1578471	431220	86066	490605	1520937	116412	75030863	215559
0,6	0,6	0,8	1,2	1,0	0,7	1,3	0,5	1,9	0,6	2,4	0,7	0,7	0,7	1,3	1,3	1,4	1,3	0,4
1,6	1,7	1,2	0,8	1,0	1,4	0,8	2,1	0,5	1,7	0,4	1,4	1,4	1,4	0,8	0,8	0,7	0,8	2,4

AP2B1	ACO1	F1MPK7	C3	PDIA3	BAG5	SCCPDH	PLSCR2	REEP5	ARHGDI	VAT1	SLC25A5	KARS1	GNAQ	MFGE8	JAK2	GNAS	VPS35	LOC508879
89733	5236061	17859227	6728540	547516	438172	1449379	968816	15017	3545652	10683860	364375	400994	4594396	1807715376	260198	21084159	1674657	3270466
92852	5930019	19548280	3322776	1237351	451076	832315	890374	13248	1968444	11383993	539780	1118513	4226714	1464682655	479129	15160228	2403559	4814507
71691	4579988	20691620	4891430	776943	436828	1538013	785301	69335	1353978	25566700	974434	743484	6873066	1032113700	561701	19932104	1588423	5046585
325738	4653283	11960517	3608629	438247	559754	1003695	529104	14239	4235984	22451491	427704	318825	1947814	3330843349	193854	35071183	4496673	1623347
218915	6168644	14147042	6512458	1617207	415341	959205	498366	30585	1379554	10202879	1878378	1158356	4445113	1802404868	542150	15594337	3372195	8149796
131727	5873107	27374865	5408736	788404	738319	740794	1041543	144779	1397954	9543991	1222199	1128843	6461293	1571095540	476332	15177219	2571700	7563720
45657	6097265	16568307	8298953	1004802	419470	999799	1269158	24212	3224491	10160930	1294868	616816	4620980	1836718502	170066	20121086	2606410	4652539
151768	5334314	16805477	2624170	2615387	326362	1045294	1106113	134361	2119936	11011629	1963788	466341	6431487	1139725437	544992	16224557	2108498	4111958
176539	7482555	14841569	6175490	1506315	725838	890523	765365	24360	3530288	12772956	606459	667562	3149972	1237389842	496301	12843660	2516700	7294153
453444	27110242	4936340	1075971	467421	1327022	387647	443522	3415	1317391	19477049	561916	255026	1985573	2981670009	118129	29582469	4102247	6330672
279422	7730289	16915539	1303389	369818	1359468	583034	1308440	318473	4091810	45692138	844783	113082	1794414	1785543040	405342	23613590	6006971	6743299
426343	8151194	9511297	1305611	263689	750837	699722	783408	14927	3809350	28826269	1043525	311365	1821387	2755876345	246409	28182029	6702151	5380471
168785	5095960	19609325	15867058	1641596	500416	1173098	925692	37645	2339273	10048573	2076412	790585	5037695	1801897921	124267	18579977	2607912	5192421
74954	4677056	22693939	3137885	930938	314293	888230	2495199	279249	4232623	12874906	1875274	794724	5784925	1160338996	377473	20152080	2571872	4385015
123723	4385329	18216028	3504853	1441347	278323	896274	2004299	433198	2155949	10628221	6359310	942427	6844290	1430965956	535998	16095891	2114870	7614948
266445	6345141	5501633	3620283	388235	916519	861527	1912983	78696	3348550	17344947	2663217	188168	1772543	2402746864	191653	24529970	4357828	6203017
141010	5484085	18119417	5174462	1128232	473165	1071062	886097	55722	2403249	13875684	1083191	744022	4950108	1748162428	403553	19795609	2602764	4904115
91995	630915	4663431	1945228	710137	124565	280315	271005	54912	1119139	6334439	623972	348825	1612579	708503926	166593	6636990	952751	2130034
246207	8872221	14028209	4498817	876170	771590	797507	1329864	148745	3103154	19708133	2003862	507867	3523850	1944553622	311946	21697458	3872569	6143000
137367	7509597	6639136	4895818	578430	414660	237652	728951	168397	1046366	12156647	1916997	324514	2066467	693673091	164211	5828402	1734914	1099774
0,6	0,6	1,3	1,2	1,3	0,6	1,3	0,7	0,4	0,8	0,7	0,5	1,5	1,4	0,9	1,3	0,9	0,7	0,8
1,7	1,6	0,8	0,9	0,8	1,6	0,7	1,5	2,7	1,3	1,4	1,8	0,7	0,7	1,1	0,8	1,1	1,5	1,3

NRAS	UBE4A	ANXA11	EIF5	FAM83F	A0A3Q1LLH1	NPTN	RASAL1	ACAP2	STOML1	GIPC1	FLOT2	MYH9	FCGR2B	ANXA5	NAPA	PGLS	VDAC2	SLC5A9
2682940	193644	211466	87832	682599	86075	449957	2309013	271190	75833	387432	2380852	177287	11052162	13195648	2810925	234556	74478	3368735
1543656	250075	236161	151226	1635705	102971	860296	1510912	414706	92223	470827	2200792	316550	2233687	6092051	1867567	99953	188207	3355511
1429853	358604	75980	194312	156176	83271	675515	2325345	556870	107195	1040538	898329	97675	2485288	8933596	3562338	291014	139289	6004460
1832535	503068	34923	148557	551227	191144	412317	1392469	136664	161774	378534	944843	90412	1669942	4932989	1289745	63921	407913	1060345
1343744	368822	216863	259144	1307626	350771	463975	2064227	407801	206179	481578	751818	611496	1985562	10015976	1496409	176612	809766	2795337
1064054	525323	17133	108349	498712	111768	652823	1859592	293433	147933	953543	714755	170802	4196682	7631467	2909201	173601	84206	3389908
2457544	243346	221993	110429	1570645	155988	320945	2762977	272418	107836	527344	2677846	273185	2272822	8132045	2854346	180297	791787	3706915
1923018	246634	160647	331759	489451	445277	679940	1709027	530473	50060	558280	747766	277588	6720757	20399137	2308121	161953	610566	2640027
1505098	617233	245901	316793	874989	160283	323480	2395714	454628	208818	297042	1108403	107153	9223405	3209101	1538034	94028	122064	2898400
3200305	1344191	21388	103071	1315810	211416	296325	1764372	26687	805729	72322	307399	312035	232981	6676038	436830	48524	438790	1261759
1904262	838562	23046	105786	1973756	115689	125374	2657297	104495	203117	159673	559027	92935	410062	5407506	1758097	20520	394743	2047990
1523229	779907	21189	151750	909448	105754	282990	1722932	114698	170463	339096	442221	120904	1056561	4561266	1108957	45819	437918	883008
1342563	167933	276040	310159	1547084	315133	522411	1011355	349286	83441	522953	1544272	311927	2136419	10607811	1705971	173309	1127000	3312032
1955872	290958	84758	360829	411962	144422	747955	845065	391569	77819	547100	1458039	157104	1494340	5658814	2916148	320505	527932	2476218
1970253	207301	123323	320362	366453	242639	485178	1745466	366682	109772	877432	634237	190094	4890220	8857657	2192256	174922	1240971	2276753
5442598	588511	9976	150908	1867358	273817	64165	1030778	61775	250517	231976	443682	238362	741218	4220032	1589731	101098	268058	859426
1784668	336189	146896	173951	861518	190908	564471	1991695	360444	118629	599760	1414625	251874	4077113	9916614	2387332	172739	388276	3290155
557900	125107	90449	84085	560243	135252	179941	462868	142910	50516	253836	845870	167592	3273511	4920539	786074	70851	312415	1373270
2355523	604324	100703	227457	1158358	196144	355985	1646622	233727	238710	380949	812160	191314	2523151	6149778	1655753	122341	569685	2001948
1373083	392752	106548	108961	617591	76710	222426	658720	172397	237573	258972	487567	88014	3087778	2483387	726282	98239	399895	920231
0,8	0,6	1,5	0,8	0,7	1,0	1,6	1,2	1,5	0,5	1,6	1,7	1,3	1,6	1,6	1,4	1,4	0,7	1,6
1,3	1,8	0,7	1,3	1,3	1,0	0,6	0,8	0,6	2,0	0,6	0,6	0,8	0,6	0,6	0,7	0,7	1,5	0,6

PARVA	MOB1A	CIDEA	SYPL1	TAX1BP1	RNPEP	PDCD10	GDI2	CLIC4	LOC1003374:RRBP1	CADPS2	C4A	LAP3	AKR1A1	KRT14	DYNC1H1	LTF	ADAM9	
220150	637739	254221616	3140724	376309	85621	1308150	5259054	716320	207092	159902	53027	150069	48982	416475	686361	58024	4168335	72553
71368	218889	89732855	2044049	323683	294912	529158	4515261	514966	3981215	614816	34514	139371	38551	416412	488307	21429	2643051	1281
75355	335285	117581919	1788271	562483	221567	716889	1315036	1141488	3059184	467004	97538	352314	35270	206961	611359	21898	1156651	1218360
351692	113863	73887543	2124580	159893	412503	437578	6401667	643879	1081630	162189	46428	84126	41048	144224	560198	53511	5284606	1110054
106232	407195	112245315	2106227	474670	363663	568518	7814903	667654	575638	807162	237903	50321	103306	300532	807411	438593	1026528	476090
42911	314721	97707817	2007548	714155	217055	407265	3803855	929933	1971493	469213	203104	122325	65568	378973	282768	257612	842460	455184
206506	786573	285878442	3505816	689623	118006	624285	4923081	618531	1249024	352380	69408	188042	58644	695763	807046	248831	5251915	30189
143524	448489	163126554	3255214	207747	290800	873293	3370085	1477478	6788053	1196113	197450	87149	14794	309000	1372127	152617	1063843	373722
73655	326264	149748471	2395637	632967	255110	249841	3596017	466812	325822	692321	280328	97739	27383	217541	487779	225706	647901	458641
161641	276633	113752545	1923435	132471	974834	88715	8325308	171262	943632	62894	51703	405989	16379	95580	256205	252773	3430734	2118172
324537	304196	159733476	1527258	489528	558015	273822	3317223	295961	1053212	92849	528462	1297906	3910	37013	499295	148621	2259074	499738
284798	327918	97898627	2509897	466026	458393	324807	7926111	347101	933520	112259	127191	116019	80284	148197	678328	80212	2216261	1369367
194644	362543	266576901	2661144	628883	150827	734407	2756353	635551	479366	618510	106605	157512	30001	374081	471465	510466	877979	63558
102601	1055834	145161392	1406183	556109	164321	969662	1894332	1334857	3805604	595996	67741	62940	36962	604627	496652	475159	412168	1322772
118712	984169	262873708	2739706	551752	258993	1019784	2158919	1343912	4401199	859309	180434	156871	17376	428915	388621	124755	428348	616045
344702	376949	215963443	1274759	454319	272554	302023	2857906	523278	571990	162643	94788	537690	15178	189158	97837	29876	6023158	370383
152217	407844	149297758	2496554	438570	250516	683142	4675368	838781	2364166	528597	117421	146714	50770	358543	701947	156564	2679674	467179
102772	218438	79399094	680903	208274	112974	293903	1964674	325907	2189687	346239	81961	93653	26248	167148	320982	148808	1951494	470603
200661	501813	176463570	2054752	489007	386631	495383	4104021	639842	1564293	399598	179657	354083	28434	261889	422023	230946	2036953	852334
105012	321916	64615242	595790	159275	275716	358232	2545021	454474	1595142	322865	158560	416086	23328	191373	176356	177071	1942538	684583
0,8	0,8	0,8	1,2	0,9	0,6	1,4	1,1	1,3	1,5	1,3	0,7	0,4	1,8	1,4	1,7	0,7	1,3	0,5
1,3	1,2	1,2	0,8	1,1	1,5	0,7	0,9	0,8	0,7	0,8	1,5	2,4	0,6	0,7	0,6	1,5	0,8	1,8

SPHK2	P4HB	ARHGAP1	PTPRJ	GALM	CYB5A	EIF3H	EZR	MVK	RDH14	WDR1	YWHAE	GAPDH	AACS	PRDX1	GPAT4	WARS1	YWHAQ	RAB21
201655	757019	103338	2121873	2155125	123300	21589	746908	36816	171181	263755	3426483	1735669	1028030	1934709	7329314	955311	496456	4269504
107147	1184551	114434	2538274	1906724	73846	51671	394763	72235	218426	583423	2112376	705252	1033128	807439	6548366	1208735	284010	2669470
435459	908435	179349	2960369	2163833	246463	5652	502947	57363	177016	214718	2346892	1046240	1522822	936085	12856352	681372	590079	1855555
125890	552323	50213	619779	624998	91673	123876	168099	13941	56551	264100	1140915	575491	306951	574787	6338846	337407	236620	939244
254788	1274873	208056	1662603	2226785	294420	115409	318630	171026	145583	561300	2591909	774839	2317461	1202437	11345946	1665677	405244	1533810
217699	686640	172562	3063373	3245281	191047	0	247212	59958	160532	92647	2671535	527800	1001822	727298	9123932	1246558	394443	1540699
146111	1310318	87625	2056944	1862554	281304	7	569383	56896	225421	462881	4327958	1461664	961745	2429135	9899607	1393198	763064	4081923
294241	2790518	180553	1744437	2963621	439769	201869	568751	96108	152868	395682	4077090	1156006	1736724	2440444	5901378	1097585	677170	2473018
211327	837129	110716	1884802	2271767	178510	57847	516535	25346	100600	622974	2088479	996678	2367948	1738087	10157908	897146	284862	2322875
312171	246976	50417	483142	711414	77835	3254	97215	4553	52591	250140	331204	136466	978777	700931	6626837	112496	61420	2133850
229676	451406	57397	1175193	2683539	81766	20288	94541	20242	22016	144155	535800	110968	1965317	571219	13119993	197086	189372	4738884
155928	813814	68619	983494	1411791	77868	19498	176975	3301	47296	58369	1036323	454513	926314	996490	7614234	464308	190366	2322450
42088	1415290	116814	1496263	1777157	471800	73874	470819	111190	168622	272819	4084237	1183960	1873902	2794102	12936811	1291040	664313	3436102
113333	807366	124636	2460533	1420004	939427	1234	586452	57387	225217	414401	4243732	1282043	2148430	3893387	8841076	1651961	709997	3180766
156062	1150948	190967	3256487	2643868	729317	110415	507452	156313	202411	309117	4850493	1335076	2016876	3150882	7227995	1920220	733154	2373607
97491	466915	33881	913118	958486	749321	803	76489	49542	90758	21984	1405166	946455	510725	1456290	15135326	333336	353208	1071172
222874	1183085	137016	2095957	2143615	217728	65009	439586	70543	163447	354813	2836895	4997870	1238585	1381542	8667968	1073230	480886	2420403
107219	708090	55570	790244	786933	123214	74426	192482	47157	52063	174490	1058146	434501	607112	771243	2557971	415978	185910	1214051
164760	773731	94181	1581629	1734753	413231	35901	315810	53484	113689	261745	2321929	805770	1598536	1912673	10207522	858449	398337	2697463
84924	384735	51601	914437	743548	355186	40511	222834	54437	76129	196020	1808459	501479	686508	1229360	3173741	693911	266008	1088569
1,4	1,5	1,5	1,3	1,2	0,5	1,8	1,4	1,3	1,4	1,4	1,2	1,2	0,8	0,7	0,8	1,3	1,2	0,9
0,7	0,7	0,7	0,8	0,8	1,9	0,6	0,7	0,8	0,7	0,7	0,8	0,8	1,3	1,4	1,2	0,8	0,8	1,1

FKBP4	NTSE	PALS1	VCP	ABHD4	A0A3Q1MQ9 CSN3	SPPL2A	ENPP3	PLIN2	LOC782884	SLC5A1	SYT4	PYCR3	UBXN6	ATL3	CKAP4	F1M2Q4	SLC16A1	
24789	4243928	20403	1061286	309460	890995	47148359	18021	16859508	3320453595	117378	6665715	1861486	132526	242671	227119	25907	8641352	5605344
31058	2385241	76119	1286799	224704	986857	30412557	185924	13819687	3170644059	3650	4901714	1873431	115511	580515	282151	73147	6634432	4966618
89046	11254490	147911	510414	496260	506725	41321917	241668	29087672	2322576722	11710	11225281	2551187	59453	885259	261322	25547	1146288	6925547
24952	7071548	123324	880626	361458	318779	117699649	506231	31269029	4541495610	53628	9047344	1625530	21755	455211	102667	80960	729871	1535135
77311	3252225	158414	1096980	487154	170695	39154554	173152	14986517	2404907347	2712	7921977	2081646	83242	672854	314103	71386	8209046	3036553
163605	5009836	83740	811035	390922	1031090	53771033	254724	25036971	2245905773	24723	5706859	2057834	111259	334627	100179	114264	6794326	4212299
55167	11961192	47437	1111561	384696	122735	88484445	30778	15763760	2835317002	59114	5575202	2372014	113178	197200	303898	56295	1137136	5908878
52433	5690714	207236	734010	409802	506581	35487387	272514	15858877	2277998048	96845	9741337	3073017	131201	630603	345889	81575	2151752	4152466
42445	1490580	49518	1868138	331291	1124895	16038459	303979	21252691	2195808929	21731	6225515	1882269	72119	527061	397388	74050	9116541	5916135
2384	681090	233059	2798644	462124	893169	28703738	242159	74176507	6350759763	0	2916786	589337	5342	165078	227084	60812	2055057	517022
16966	7982956	339825	1519544	238523	1170084	50796962	357552	54778235	4353991487	40053	4150599	731006	21285	340684	281091	28961	3155260	2527484
22603	5877164	145116	1399923	321245	478209	53400384	407241	32639309	3754120600	8871	8816407	1416712	12440	322245	126279	20112	1329236	1236596
44346	7989894	36517	1004545	307721	357765	30309807	35239	12727895	2854750807	0	6824252	2496184	332527	142852	786595	71210	7317347	4917209
152864	8245212	160482	491024	248885	1485830	21038012	220616	16496263	1743488392	2387427	8316539	2771991	339267	753689	107398	141841	3139222	5504892
78595	7032739	149815	755958	431221	458937	35097057	192427	14530595	2287868285	35904	9821116	3929984	274551	654309	303589	63064	10979446	4898356
6289	6293246	82769	1159637	403283	282530	72532227	300010	33491221	3254647525	29631	3994024	1340362	536	199512	69662	19476	1956588	1509889
64795	6358647	108073	936589	383057	566807	56684988	210376	20335252	2889912270	46220	7598179	2187018	96016	499868	242166	66135	4430525	4542855
46414	3546453	62293	249599	88954	362523	30510775	153798	6993235	787506655	43434	2260337	462787	38716	235767	93775	29794	3442867	1708328
45812	5699110	149638	1374677	343037	781427	38489581	257403	32511590	3349429474	315452	6383155	1894731	132259	388179	287386	59941	4881087	3378448
49810	2976138	100399	721081	82146	447537	18956703	114412	21813197	1486673810	837347	2518663	1125540	154436	231723	230218	40050	3707748	2159050
1,4	1,1	0,7	0,7	1,1	0,7	1,5	0,8	0,6	0,9	0,1	1,2	1,2	0,7	1,3	0,8	1,1	0,9	1,3
0,7	0,9	1,4	1,5	0,9	1,4	0,7	1,2	1,6	1,2	6,8	0,8	0,9	1,4	0,8	1,2	0,9	1,1	0,7

DNAJB2	PAK6	LYN	DNAJA2	TMEM30A	SEC23B	MROHG	RPL8	VAPB	RPL18	NDRG1	YWHAB	ANXA4	MYO1C	RPL4	ATP2B2	AZU1	A0A3Q1M58	OSBPL10
217888	181306	1981523	824820	609763	73134	10051	154894	349727	29631	1375195	1089141	225423	852127	273106	1816583	354	234820	541593
143746	190975	1158525	1008853	434018	117989	32427	144645	95078	63394	1000759	656148	89208	868865	414242	2649842	47892	861385	332080
345770	169532	1960883	1023074	637305	75445	15677	156296	200437	85477	1223182	1289887	131080	987446	325270	1647297	5562	199173	1082105
94889	104077	824080	332828	494838	134147	12165	77428	118529	93889	2827323	389105	82784	322778	578463	4855848	14299	324296	461549
169246	177646	1162780	967021	978193	274324	45543	227810	268524	254267	1652561	948259	191829	985405	1389707	1736805	7905	624285	774981
178210	126016	739253	1267523	488004	137933	35694	299441	373327	14932	2628271	935249	70734	767737	583095	1827257	1410	120927	922942
174983	232199	936299	439795	379555	113270	21664	283282	442807	53041	1542422	1715704	162431	1012381	335969	565354	321597	4437917	772661
252780	300733	1320093	841476	517195	180389	22985	410312	462357	454444	1393787	1592363	316152	1181523	1243814	2082049	5313	448780	1057246
150320	225971	1134146	760329	568213	273992	60975	206569	160843	177852	936259	606720	51539	1047165	698080	1552601	0	34070	669208
50409	150800	1284359	90973	78431	377507	11994	26275	129575	43071	2742518	75045	67871	283304	1490632	5645133	96767	249957	96431
68047	146657	620119	326929	144008	184873	42470	47258	145447	54641	2610219	397944	20653	296186	269655	3313724	0	13605	474106
80966	138656	782700	270961	444100	297758	69239	35033	172638	5167	4525181	349574	31449	359860	382992	4045983	1727	271235	369480
144100	262407	916942	632641	1248816	184284	21634	550544	701982	184455	909093	1600872	172410	967473	1019701	1594532	49785	2110094	457419
280193	303849	757986	1145527	505704	109015	12332	335635	1235039	220821	1856084	1586896	197481	1279058	687728	1614218	1567	278126	1103624
302984	345332	1120555	1270410	728808	134752	36682	372694	986834	561944	1891984	1978573	305335	1111295	831350	1331404	10529	552106	1340495
141106	77818	778441	283089	246075	59755	16784	154071	384648	521253	1640000	445941	84948	265081	816913	1720929	255942	1235442	289230
197189	185310	1260429	838174	567359	138329	24526	219263	288848	131134	1705437	1076982	158705	872283	642958	2147629	50541	906448	743145
76112	60935	478267	311340	186164	64948	12422	107500	141137	150074	662781	448170	84047	254845	432711	1237850	110590	1447641	276885
152266	206436	924406	597607	495519	202742	34014	216010	489626	221150	2138917	880196	116461	701178	774632	2602315	52040	593079	599999
93982	92660	231072	433614	376005	106342	22205	189709	433532	212304	1172875	722198	99530	437212	377873	1573664	89283	725499	421941
1,3	0,9	1,4	1,4	1,1	0,7	0,7	1,0	0,6	0,6	0,8	1,2	1,4	1,2	0,8	0,8	1,0	1,5	1,2
0,8	1,1	0,7	0,7	0,9	1,5	1,4	1,0	1,7	1,7	1,3	0,8	0,7	0,8	1,2	1,2	1,0	0,7	0,8

PNP	ELMOD2	KRT6A	TMEM43	EEF1D	ASAP3	FRK	LRRC8C	GFUS	RPS9	INPP5B	HSPA1B	SLC7A8	PRKCH	ABHD5	LRATD1	RAB1B	GOLPH3L	CNNM3
84079	157083	244853	302607	287156	54238	49932	8987201	107717	148083	130455	1601916	288069	1187404	128100	128786	2931030	1565718	1077884
19604	107342	31707	367253	344821	70504	39324	9242699	192241	70304	126270	1371376	185696	1138957	242204	116101	1142091	827981	905895
59378	443249	298069	379725	307316	170977	53936	8846242	103937	17820	94920	1876003	386623	1209542	219494	134176	2602037	981815	689993
201749	746952	285459	887189	209184	32453	12957	22096903	78530	21804	145488	700347	116293	564779	104783	15621	1313001	2244341	306999
42648	180750	432738	455246	801745	132317	79120	9506391	209406	215527	159894	1352462	139555	1303424	279575	53979	1895323	1477568	856773
249896	633550	79553	460530	370983	70909	3153	6728047	143426	38473	91903	900125	354301	726763	157602	31817	1918133	1774472	375802
82477	183452	86104	602790	345030	49916	16285	11103416	90491	179315	121505	694484	216480	1190745	207060	45734	3211462	1292330	1694754
78759	550768	753886	633427	610244	105613	40601	6137406	153759	425463	122221	1401270	242889	773684	304114	181983	2638486	1639223	1021932
81404	142633	109863	456102	223583	76497	88160	11708237	112164	220387	166794	2111315	239249	997500	220806	90602	1355772	1246630	773540
240333	831273	161629	469976	125408	8831	15970	23509665	47791	131559	261334	547440	106337	188212	104231	110814	1481812	3554343	394756
423022	114457	379957	566037	96806	35947	9088	18016076	60579	35407	230036	718786	274444	282704	429915	159608	2372936	2534271	406272
225019	776473	709289	590279	97883	31410	26793	19868175	93874	30300	242423	728155	38919	543407	97314	29699	1495974	2342337	240401
31752	165913	109307	836357	611213	83475	79429	9462428	126993	482865	69980	848800	163716	1838958	389483	106025	3461535	1477326	1483226
158813	734743	90324	380194	665479	92159	44773	11013986	172230	321616	56879	1638971	262407	552035	192900	99357	4530849	1184270	794868
64004	380594	38546	412207	898022	141404	60561	5901637	108966	415206	82594	1607648	197809	1341301	307754	109579	4825124	1114635	1090788
263891	758566	206592	1072325	239867	27541	30695	22266962	24873	50895	187917	366297	241010	498511	370415	19203	3543662	2655321	227939
102323	375393	276546	511096	409560	85866	36913	10331038	134938	139599	124082	1237248	241238	1011912	205367	88525	2206445	1475431	866254
80350	249084	235680	189703	196219	46900	25069	5006785	47980	137771	22935	430227	96927	277989	70898	59468	754912	449127	437766
186030	488081	225689	597935	369783	62158	44434	15218396	93434	211030	162245	1070926	190486	780329	261602	90611	2883458	2013642	676474
129326	318306	221179	239453	309649	43939	29170	6522558	47495	178631	82360	627299	82787	569267	130288	45751	1400928	889351	445559
0,6	0,8	1,2	0,9	1,1	1,4	0,8	0,7	1,4	0,7	0,8	1,2	1,3	1,3	0,8	1,0	0,8	0,7	1,3
1,8	1,3	0,8	1,2	0,9	0,7	1,2	1,5	0,7	1,5	1,3	0,9	0,8	0,8	1,3	1,0	1,3	1,4	0,8

ERLIN2	CHMP6	DHRS3	LRRCSA	PCBP2	CARMIL1	CEMIP2	ASNS	PNPLA2	TOM1L1	MAPK13	TMEM63A	RP2	CHMP7	NCSTN	SNX9	ITCH	RPL12	HSD17B12
511341	431935	7355212	3101283	343792	48775	643306	705043	3011037	706070	968187	168836	2662179	597289	710934	430682	84157	34126	71265
511856	374567	3304955	2694355	217411	240458	591511	882389	3532769	811580	811913	237737	3048154	1153600	608373	581075	122723	32202	98971
415864	529266	3081445	1721895	373015	138913	582491	975750	2395467	315890	914154	423525	4611882	488726	927554	442893	153392	14828	69154
164387	247420	1083571	2310617	405435	955907	399490	274863	352697	744687	341797	79887	1183261	206140	1397805	1077067	41918	26652	26318
256060	398233	2769045	3831847	465414	568197	406151	1415487	1050195	640185	653854	290365	3242550	512983	405069	622040	87873	98506	253948
559721	352738	864777	2194458	392060	78529	410708	622329	1701234	229595	559780	364817	3285045	481807	590173	528809	164027	49991	99432
516709	425226	6336392	4104028	355272	67071	202037	1033421	3545251	613206	975546	392753	3077082	1058043	1259397	411839	169614	136175	352028
358533	442378	4120168	2521656	594113	446320	759960	1306495	758703	455717	799397	339155	4232105	766405	401980	597469	87833	265041	283615
340478	246810	2781260	3653899	290779	358415	859364	1013541	1300822	702051	642834	225401	1996615	1289409	546273	609460	80413	79042	151730
45373	101464	1019701	3292744	274531	317582	288301	421775	1032894	730733	369556	18080	812435	740534	955878	1716090	11499	188338	57325
72730	111393	1297842	4116490	281000	356820	169261	436088	606766	564971	346212	87628	1700868	1291862	1746305	821430	38493	4270	97226
127516	324312	762488	3263449	342514	419463	160131	308480	494695	903577	531476	166591	1250684	697627	2561913	890746	35507	20269	35109
540899	326741	4351180	3880344	598298	308297	329667	1687107	1940568	497355	907742	209320	3147671	1080154	729400	436537	140696	265529	610499
266587	420075	6762955	2597524	314106	179420	532595	876696	1339258	141230	651523	319333	3834301	658528	647946	333892	72268	144798	293118
305099	608304	4374762	2681827	389780	355975	705832	1080508	2147901	491358	1025929	439292	4998354	536603	788430	355836	99003	230972	397010
131176	87601	865542	1923321	368287	211627	76687	289137	898017	728364	269151	125713	1413434	158810	303636	1059981	9456	250696	258034
411809	400220	3614446	2810017	393314	318021	499457	901972	2043419	564616	753079	287135	3167782	658124	787661	586484	113942	82190	156841
141990	81351	2290311	820478	107518	320015	176860	370461	1261887	209578	221578	118258	1031922	317580	375412	214078	45790	84585	120885
228732	278337	2776966	3176200	357412	313450	390230	764166	1220115	594955	593053	198920	2394295	806691	1034972	777997	60917	147989	237506
166870	181247	2200866	734685	105855	80468	281348	490614	590615	229899	270421	133406	1455704	391720	748467	462073	45612	103241	195866
1,8	1,4	1,3	0,9	1,1	1,0	1,3	1,2	1,7	0,9	1,3	1,4	1,3	0,8	0,8	0,8	1,9	0,6	0,7
0,6	0,7	0,8	1,1	0,9	1,0	0,8	0,8	0,6	1,1	0,8	0,7	0,8	1,2	1,3	1,3	0,5	1,8	1,5

UBTD1	SRPRA	RAB18	GNAI2	PABPC1	GC	PTBP1	A0A3Q1LQDI	FBXL20	PSMD5	ALDH3A2	PLPP1	ATP5F1B	MAP2K2	STK38L	LOC10190271	MAP2K1	RPSA	SH3GLB1
1208316	878980	86889952	2610103	14624	193888	12873	123765	692766	18844	140353	584146	428718	1340658	344610	32063131	216322	123439	35428
794827	859229	41644239	1561623	23819	61756	85483	91205	603649	77801	163984	324914	985397	1646129	497765	25420589	417698	163295	16871
480485	687500	55294414	2278230	51213	76868	26997	22623	614787	66359	57028	1141752	744464	2746069	658496	38960640	859034	119487	285946
129138	107658	37893521	3871594	35007	154352	8471	37530	171952	8457	44422	308658	1002386	662909	549027	14941353	265268	134956	11726
521642	926286	51988411	4039050	182128	115559	144844	189149	481754	160446	266463	499778	3306460	718161	398430	26841077	763784	247196	70659
423591	534638	52538875	2657625	23627	106845	102093	8970	650119	50034	188110	509295	524057	3112468	290815	23084397	405863	137331	30375
1129702	645249	82784605	2447274	2224	35442	109196	227469	733836	43606	185744	672983	1514109	2596888	398337	29532599	264121	160176	93528
975505	857997	70450944	2949237	157358	188439	169919	260678	365601	123992	323442	794543	2758033	568109	403362	27352362	456611	628860	58277
828027	1277436	60094696	4022541	39049	88795	108385	103486	379850	80773	181127	608335	915406	873793	451384	31394633	351107	241397	11365
272306	227777	33160127	6783303	91722	148108	52783	35424	177311	41071	75240	72522	832516	640855	650063	5122200	140052	294522	321
846262	195688	48793998	4129759	0	143711	10880	1509	155480	18684	325693	238545	540749	3281537	228354	22610205	116578	180576	20772
540525	170633	44029210	4466256	5379	216517	4138	23011	149428	2635	173148	148140	1381678	744503	568658	14672450	244224	86011	8932
1301811	1028977	98665403	4106389	111105	12598	139534	98665403	822700	3653	390086	709589	3390757	1899490	371401	33838597	333306	374046	51866
776017	914551	107225748	2016788	105809	39253	35264	20525	760801	132031	99861	819171	1809383	3408710	254147	39439830	570272	202551	17177
1003845	895834	118876544	2731777	146361	79076	161562	400968	772149	131087	214723	1058023	3137438	692228	437143	40000537	889421	219380	137605
202912	125633	42672067	4668808	15632	33565	18262	19893	271052	9070	96305	338910	1610202	938980	231369	13591545	91068	321559	14392
707901	687192	59935620	2801842	61250	116644	82485	120173	539308	68692	171193	604509	1407953	1673924	442605	27274519	456088	214342	75351
379795	270874	18201349	818742	68777	58345	60996	96788	189715	51625	94764	271394	1066486	1024072	118967	6947664	236580	172352	89506
721463	604566	69189724	4115703	64382	95203	66351	124908	436096	52376	194523	499155	1702266	1560012	399065	25083750	342004	240005	32804
368360	469138	33631213	1407864	56076	69615	61642	171072	299076	55205	112967	352495	1052764	1172062	158105	13039117	271520	89973	44975
1,0	1,1	0,9	0,7	1,0	1,2	1,2	1,0	1,2	1,3	0,9	1,2	0,8	1,1	1,1	1,1	1,3	0,9	2,3
1,0	0,9	1,2	1,5	1,1	0,8	0,8	1,0	0,8	0,8	1,1	0,8	1,2	0,9	0,9	0,9	0,7	1,1	0,4

PKN1	LPO	CD47	PRDX6	MSRA	ACACA	EIF3L	IST1	LOC10084871	CAB39L	ATP5F1C	GNAO1	CAPG	DHRS1	GK5	TMEM263	COASY	LRRC26	HSP90AA1
51332	799751	4126832	387499	167940	20454389	3583	9061	1563686	136921	4946	8565907	215195	4002119	885881	4365100	21913	326635	1937635
87194	751902	5466289	156460	7441	39590692	29838	89826	1995186	122863	8321	5069006	217069	1061026	813651	2776695	75815	174593	1722759
84417	777468	6775698	291026	74223	22588704	45502	16800	964482	121081	19534	7276419	206219	2369728	573714	2439239	38538	137979	2072921
55309	1245440	9060640	162015	101721	8165981	6051	62329	75236	16255	1675	4364126	192291	3314348	1714239	1699710	18784	203269	739589
313068	1427445	2162107	149295	50547	48701261	46092	13766	1056287	115579	70365	5880222	644624	4137221	1051665	1684194	147496	598702	3109930
140825	794097	2104076	164945	30752	51716730	23496	69434	1847226	61388	16472	3769010	318870	5111220	1831005	2387345	52472	432356	1837118
62616	2389125	4527530	219399	77976	26388899	9439	0	347025	117121	60313	8352418	233987	4974180	1248348	4822262	44116	542942	1658066
213707	1828835	2577275	413213	101326	23409615	63591	28669	1154033	140550	76250	7049364	511108	5967995	1552208	2858689	108370	522597	4094833
248868	830184	4359214	199078	13105	22234935	36927	40066	2471067	58785	19113	6492314	285343	4334056	1033541	3065403	91278	149805	2977991
104754	3851284	6120957	196798	53966	34940222	5201	38111	1441159	39821	1582	1377770	87724	6839259	2369053	2881585	92964	203084	546055
48477	1888942	7682398	84367	86016	21825629	2513	31367	1210484	53425	3584	3977906	65095	3730257	1658108	2961243	50495	36228	1385644
111478	1356978	8812878	126803	60269	8468522	9910	4534	203920	35202	7600	3883009	160247	4531327	1727776	2196388	53711	332823	630653
232393	1206807	3431524	372170	72992	32663474	25847	13142	1534192	148196	156855	7790202	402490	2643759	892988	4163800	124427	603233	3747236
60697	703902	3523605	377796	122171	28016578	45610	107193	2252619	97816	80128	11139010	276548	7727021	424095	5083917	39965	157288	2343857
138614	439768	2725248	574512	191262	21805362	40644	10643	1431337	156874	143411	8240092	555740	6964703	1248130	4118984	51381	317048	3023382
16086	2094564	5820995	513839	135905	6691112	8079	23873	231406	58113	28091	4199868	104457	6354844	1839194	1810357	91176	411297	1075135
126058	1251758	4600056	242981	76491	30127034	28449	36235	1125395	103970	32234	6290809	317420	3867230	1208839	2879154	63438	367384	2146606
93145	603099	2445840	107992	49507	15082863	21860	33050	677164	42909	31259	1801035	169066	1590154	455215	1149474	44832	181671	1018856
120171	1546554	5309602	305670	91961	22080729	21841	33616	1347023	81029	55046	5887521	242206	5390653	1399111	3285209	74425	276351	1966244
83939	1090800	2175251	181036	55762	10246201	17502	32443	819801	47997	63895	3115616	172362	1817437	617924	1094098	29589	178536	1218172
1,0	0,8	0,9	0,8	0,8	1,4	1,3	1,1	0,8	1,3	0,6	1,1	1,3	0,7	0,9	0,9	0,9	1,3	1,1
1,0	1,2	1,2	1,3	1,2	0,7	0,8	0,9	1,2	0,8	1,7	0,9	0,8	1,4	1,2	1,1	1,2	0,8	0,9

OSMR	ACTA1	ZDHC20	RPN2	TSG101	RPL10	GIPC2	RPS2	TTC39C	COPA	EIF5A	PAK4	STXBP1	PSMD3	STOM	AIFM2	RAB25	CYB5R3	COPG1
164731	13544638	551885	526441	656273	274831	24156575	66272	6828	109388	2037412	722137	79266	113075	60373522	140791	5047864	48945774	11533
283606	18355798	309176	986431	418514	215779	18731553	64431	20401	141755	1684866	540243	247073	156298	91349651	313468	1783318	22467884	41491
238046	8733833	355325	290805	136968	271668	20683868	51362	84733	86453	1481287	644082	128278	80040	45803924	202998	3110348	24836033	66704
165856	14172765	321219	1227796	179476	173178	9702983	19798	16547	122843	928981	253066	154547	280821	43134514	75011	1868010	12809855	87039
201750	18661697	155605	1062458	341710	460338	13178444	168852	79683	569718	2187940	446464	390088	511390	39847355	271145	2112387	15500960	294607
51483	22708149	206603	924048	316171	185417	15738149	30718	15671	137057	1668968	734355	140678	160373	25209749	64003	1669386	20073457	53841
207227	17045928	339736	956911	634837	398478	23520110	85331	13475	125764	1778909	767010	97902	267055	144435301	225860	4357330	44437268	36794
160098	19785706	345997	1581004	353776	768417	20193277	242330	73253	615257	2361375	567182	310519	791264	93181780	177576	3551078	18138008	263784
168637	13167254	389484	1243013	385280	347318	13428170	101640	52552	620108	1927061	535008	87839	364975	19864629	128856	1960337	22849867	160704
271266	20504513	56216	2543871	510092	303035	5699257	178548	3217	451255	1149145	36894	142066	298997	81614509	4932	836751	9369769	63856
299063	22083120	140563	1183404	382486	144108	12742010	62056	2917	381540	792417	136196	40968	286559	30327742	11869	1237432	15504552	76644
298064	18712412	310469	1083130	407463	153118	9841077	39129	19580	191345	776689	333370	145516	222471	31838312	83330	2080896	12491978	100806
238344	10109555	133885	1623092	462706	896783	26400686	193035	32961	383507	3052732	708649	127410	419829	67066620	204921	4922255	29385753	66541
31847	10950581	470197	432264	303094	606945	18034936	125812	17083	128308	3562657	701998	171756	133036	56668220	149209	3521649	21111300	127465
227994	15293174	333620	633551	238658	929757	29829476	191307	84217	261083	3758783	1306522	277698	435775	98576100	491355	5000819	32602674	155327
316985	14260464	339469	1434047	299903	685518	10688852	289971	3713	157587	1520208	172270	31115	343803	69267585	100302	2100148	12730610	25560
184100	16626064	323193	944487	379716	343513	18238120	91137	38824	238529	1766217	584317	193544	295040	67916975	183856	2937465	25901155	106974
68169	4343934	117111	397084	188321	199075	5038056	76145	33807	219472	447851	172966	110815	242237	39305264	88363	1289561	13423532	108864
231525	15635134	271738	1272047	373710	508323	15833058	147687	27030	321842	2067462	491363	128046	313181	56902965	146847	2707536	19505813	97113
93927	4396933	144334	646343	89876	315441	8390653	81830	28794	168283	1225985	417037	78743	101146	27541831	154433	1594986	8424013	47730
0,8	1,1	1,2	0,7	1,0	0,7	1,2	0,6	1,4	0,7	0,9	1,2	1,5	0,9	1,2	1,3	1,1	1,3	1,1
1,3	0,9	0,8	1,3	1,0	1,5	0,9	1,6	0,7	1,3	1,2	0,8	0,7	1,1	0,8	0,8	0,9	0,8	0,9

SAR1A	LOC10029911	HSPA8	PI4KA	TLR5	CIB1	ACTR1A	CNDP2	OS9	IMPDH2	RPL3	TMBIM1	ARRDC1	EPB41L4A	HP	PHB	SPCS2	EFR3A	LOC523126
6168849	1531101	14052058	112336	656318	265167	191938	1282737	45008	76659	33139	3370472	280237	27676	20091	11874	135671	178347	1065745
3370327	2346252	11078066	45241	385818	183733	107710	894065	67773	164622	257138	3089234	244679	29560	285530	20584	159671	118961	1477946
5310904	1064929	11955207	103300	1274207	417259	232921	806696	58630	31652	130663	5843183	357735	93351	0	1839	117867	295706	646204
805108	1373230	6117322	81442	427366	428224	252069	481506	11090	38016	54578	6582117	85660	24527	22740	0	15647	257086	196696
2583967	2252867	14415107	179310	857929	248885	452020	2155611	151594	639270	779114	3440695	267558	39395	83954	66227	39631	357917	1989193
1740227	3462122	6326820	61323	349742	354553	135794	685300	5891	10468	273887	4106714	317503	56816	2843	17803	325063	174148	1739839
7634330	349561	11445384	185851	440053	631412	183952	1067291	39569	81030	59626	3422831	409323	13149	743480	106700	0	268779	407895
4739220	958416	12064999	161970	1433580	571397	262743	1620978	218347	796480	724769	3065683	189169	29033	3290	118644	143388	405775	620399
4901527	1177477	17909468	175769	706510	297206	308385	956320	90686	276784	336010	3264034	206970	6631	0	10659	131922	332612	855817
2012760	2324857	3651884	129863	313342	666838	249434	1397613	13223	40862	15209	4091763	80911	3299	144280	4938	907	281574	191091
1896708	1421763	4215081	359770	684928	143540	165431	821232	6389	6508	59783	10676616	94130	95426	0	1886	53421	490639	227373
1508192	1063437	10563883	203565	336954	478809	108231	751984	18021	11796	29794	5215582	108331	67610	3744	9056	16593	568182	221424
7998505	2569770	14311828	144380	661733	422136	173004	1272702	166857	574528	301483	2099299	273063	21765	88792	194518	3589	216912	2969060
9629022	3413401	14816749	31431	754843	499323	120645	855639	108513	237172	339901	4647436	391600	92212	0	47652	223570	103423	1651339
8519503	1223265	12424865	44482	1552446	790716	224291	1746161	143356	219263	636034	2161232	301144	46755	10667	180651	163739	157656	748959
2941069	800798	3998545	264051	112707	1026173	213771	824225	5305	4392	194924	5113864	61788	23792	718876	77754	37337	199377	103564
4044116	1667310	10931871	116347	728126	387579	227393	1124273	74738	229775	289114	4115116	268983	39188	145241	42959	117117	257090	1017990
2326161	980676	3136676	53938	422859	157045	105698	547518	73436	307705	299869	1347735	100444	25258	260088	47762	104269	97145	656961
4925911	1749346	10236538	169164	640433	540593	195399	1078234	69044	171413	239142	4658728	189742	44686	120795	65889	78884	293797	871078
3332899	914542	5604644	109045	435765	280491	67022	356043	66358	199223	210117	2719956	122114	36812	247525	79535	83625	162697	993791
0,8	1,0	1,1	0,7	1,1	0,7	1,2	1,0	1,1	1,3	1,2	0,9	1,4	0,9	1,2	0,7	1,5	0,9	1,2
1,2	1,0	0,9	1,5	0,9	1,4	0,9	1,0	0,9	0,7	0,8	1,1	0,7	1,1	0,8	1,5	0,7	1,1	0,9

SCD	DNAJCS	A0A3Q1LYA8	SMAD5	MUC1	PSMC1	OSBP	TUBB2B	PSMC5	LOC782057	MYH1	ACSL1	DNAJA1	GRTP1	DCTN1	BACL2	SYTL2	HSP90AB1	PSMD2	
3630632	1308176	2201329	340383	32937354	59095	1646903	681639	18156	589526	219688	92232224	3466014	448727	130694	2679941	89064	2165964	82766	
2946491	984098	2714295	505609	12212498	89539	2377610	872258	67535	1029517	308099	105966818	3488045	216549	62027	3367688	163110	2656053	162162	
5747437	832374	2773410	684289	12342770	54810	2174433	957848	49881	535552	84714	78487739	967006	242263	61723	4161972	195946	2799471	158205	
1492075	367905	2002752	1028252	10262314	61317	658696	1086801	43	258840	43202	123208931	735815	79668	14415	1891451	13144	1343856	71007	
5180964	858664	3894743	415659	36385894	124732	2271451	1636525	191671	721975	221273	70911409	2052796	228427	201754	3656691	173887	4322433	463441	
3113087	1291355	4953606	172371	29800963	107824	993770	1024024	95938	872046	257751	86602355	726195	121464	88971	3671687	89647	2075867	40064	
4626246	1474264	3081049	443834	15946485	160777	2314284	1027509	12560	761289	140525	97695277	3160813	220258	119593	2867332	124358	3825603	161964	
7881150	972871	2639453	334296	13838021	234246	2038215	1341839	208420	494787	150592	42901902	1999955	457108	140183	3335340	113923	4976140	910576	
4043073	681640	1939456	513613	8006172	154404	2124947	1151152	137921	521161	280402	94441569	3058838	287997	207501	3045523	157282	6162502	395577	
1727600	58893	7800893	297640	16694669	198816	270630	2741698	89870	183042	74573	227854949	380588	121730	37106	1754831	142829	2218059	49597	
2442522	431983	8487524	713664	30610284	247658	1177295	1459779	60778	246167	84034	109786938	1309565	115806	35706	4229038	55231	4335561	87125	
2836704	329303	3852569	1057811	14781640	107550	761870	1292178	13177	297012	98772	132747080	308439	114901	23110	2460065	162103	1235108	100279	
8153637	1742903	2708286	600635	54134426	216988	3048370	854334	98196	733106	357329	57151521	3569657	342954	246947	4409893	172904	6363572	440528	
8443483	1889869	783261	260854	16145773	14011	2170336	886810	104504	876485	161677	56516954	2080061	433123	84366	3728225	91504	3574515	185191	
8810477	2496823	2423449	668248	31338311	156556	2951380	794909	99262	840218	174831	44491906	2265210	517048	128207	2046348	113761	3578425	450104	
2158846	483664	4186404	371562	16658913	146183	560370	1347549	53798	263016	92328	146211325	238723	189416	13400	776452	74609	1408769	67204	
4327260	1011213	3032580	490587	20465788	111542	1809420	1078555	80525	657941	178231	87250832	2074580	251808	102420	3204013	120385	3020673	256273	
1977355	348955	964407	262646	10681745	61695	653850	293006	80216	240313	89382	24166655	1192660	136499	58065	706721	58409	1241147	295097	
4827043	1014385	4022730	560503	23546273	155271	1633150	1316051	82188	495026	165493	108650280	1651385	265372	97043	2806297	121278	3609564	221950	
3093783	895123	2761581	262073	14705258	72267	1085308	626886	38243	286440	103381	60816731	1295714	155575	89140	1277617	44039	1965748	176458	
	0,9	1,0	0,8	0,9	0,9	0,7	1,1	0,8	1,0	1,3	1,1	0,8	1,3	0,9	1,1	1,1	1,0	0,8	1,2
	1,1	1,0	1,3	1,1	1,2	1,4	0,9	1,2	1,0	0,8	0,9	1,2	0,8	1,1	0,9	0,9	1,0	1,2	0,9

PPA1	LIFR	WBP2	GNA11	EIF3F	ABHD14B	TMED4	METTL9	PTP4A2	VPS37B	RHOA	EEF1G	CSNK1G3	SQSTM1	RALB	ANXA1	ARF2	DCTN2	RPL13
41568	80314	261250	9231667	95198	494414	763787	3713559	563233	163797	9007613	480627	48721	729260	1352498	811366	838085	194442	215655
7860	182319	148292	5623221	229111	202528	800943	1734740	231016	75320	2094431	855513	106741	615425	407678	1455216	1787873	285525	166744
86278	137762	342326	9390527	11596	198543	474037	2108129	306735	154212	3871108	802553	73195	1042975	526221	400520	1059829	170277	281849
41249	68447	70697	17653929	66360	25550	684733	667701	384929	42180	2831882	780845	83812	200782	210060	1291154	714753	98716	575558
213498	152320	207201	9913264	375510	310280	733847	2395410	238453	92066	1946600	2112237	156274	367462	390626	1066584	969110	600917	613284
283072	142748	312973	11891035	73886	300221	504022	1592340	462597	136297	1515539	557363	69826	617165	381684	382265	2724549	77500	235244
53469	136395	247910	9051586	204906	463073	1313519	4978480	1448922	16202	7883258	780569	25366	1400582	561780	4694573	685343	220662	143688
104013	106952	248405	16463690	609717	591464	778044	2754483	325287	149988	3702601	2391456	158083	258186	752652	792913	1654886	386566	679708
49540	99097	176004	7909995	428141	406555	870832	2661607	198355	78464	2146164	1047386	106586	942148	548400	206252	1144034	400244	348312
281129	27171	10710	49210929	293005	301688	346928	1264056	217317	8951	1927163	992930	167759	428215	77895	3788864	502683	17275	185857
43734	40672	153189	21594494	213237	194495	1285175	2312600	120784	34623	545277	447287	47750	397438	475404	932980	612362	93240	117169
186330	55973	150893	22167875	121052	172564	801930	1519000	240189	31343	2148576	431051	145247	123575	294633	740594	677118	35096	383522
4068	100107	187912	6049802	547658	597399	1250542	4998346	295518	101379	5866321	1435238	13467	908422	1019645	1420121	752419	470129	598449
145724	138121	327338	6937945	49719	256183	597192	3418642	736064	232099	3726098	1237736	116528	628696	706688	151405	2853352	617642	658411
139921	185714	300270	7374048	274499	910275	705421	3271728	522412	127544	4356393	1573634	140262	658112	680788	465353	3753320	618796	942082
27462	31528	144044	19836901	141072	146706	209906	1531519	529546	43887	3362180	623739	82519	569347	114478	4186541	1503067	42070	321015
103876	125907	229882	11152365	208285	323259	756616	2493105	495146	103758	4106629	1095145	90252	653980	572900	1361824	1304303	254326	363966
95620	38086	87596	4041559	199728	185255	256893	1342240	401344	55741	2817159	729238	47684	407321	352770	1399919	706501	171486	220179
109738	84798	181295	17635249	258548	373233	758491	2622187	357523	82286	3009771	973625	102515	581994	489741	1486514	1474794	286811	444352
95141	56572	98384	14573062	165683	262440	384184	1256462	213382	72300	1662349	437934	52166	270517	319937	1600113	1198166	267131	272372
0,9	1,5	1,3	0,6	0,8	0,9	1,0	1,0	1,4	1,3	1,4	1,1	0,9	1,1	1,2	0,9	0,9	0,9	0,8
1,1	0,7	0,8	1,6	1,2	1,2	1,0	1,1	0,7	0,8	0,7	0,9	1,1	0,9	0,9	1,1	1,1	1,1	1,2

RPL23	OLA1	ABCE1	PGK1	NBR1	QARS1	EHD4	NAPG	LYPLA2	HSPA5	EIF4A1	VAPA	CAPN6	LMAN1	EPHB4	ALDOC	EHD1	CEACAM19	RAB5A
205423	204674	19667	64886	725055	9125	20782693	3109396	133861	572346	548097	178971	9421357	1019399	62003	294489	472442	80191	3115387
156713	150110	36566	109210	423251	17771	25265097	2270925	82438	346232	1098919	130463	9327532	2209016	26439	255725	751860	62369	1354030
48648	173984	22577	34133	827888	21113	19100907	2121419	94761	573653	768564	277847	21992351	437660	63411	110672	1153038	541125	1892520
104326	259423	1231	77255	129377	16657	8939703	802806	68519	895422	562083	73129	8510289	182709	15340	302863	600971	37566	747012
288197	520722	65729	183540	363285	392414	23245075	2935738	168048	964068	1416528	178945	2847652	924559	90882	506334	744703	116481	1308026
386139	157134	21710	30151	1459334	8406	16082108	2105415	154098	566072	777638	300340	1779080	1615876	39863	368105	470674	133248	910916
2690124	198615	29896	151309	493895	40495	20009907	2308264	202149	412065	707458	163803	2319491	1082359	34012	246247	283198	258103	3292361
713347	493076	73185	75846	273242	177775	17368036	3388547	186544	2126841	1335992	236805	1589652	911079	50250	296909	679234	122835	1958250
491479	302142	189151	113644	736727	154189	23239360	1741199	124630	499580	1150066	150646	14297110	984176	98053	362698	546653	71753	2111636
247233	215928	0	130237	75683	43624	10527622	1066506	133529	1377908	631810	52763	4303160	128320	28880	382851	793411	5153	261155
109906	151903	0	28558	177415	16094	21946354	708769	43497	824625	912882	189999	30605756	734779	77943	241463	787700	237968	503270
192173	427437	1733	75044	460163	14723	12926388	1811629	96780	386661	376135	115539	16206766	273637	63871	422968	610511	46132	800937
917804	319609	215226	36491	303598	217939	21811025	2189561	142859	692921	1478776	308993	3661400	1849892	45680	190030	317755	127386	2531574
312708	170072	41731	68298	825400	57496	11648266	5264303	206606	703074	634533	777450	3085590	1621569	19568	118613	737550	297094	4128671
525596	315580	67962	56537	712589	110372	20294485	4025204	326373	680818	1109567	544498	2607850	915736	91158	264872	869415	188152	2953947
165267	151118	7704	54502	311098	3247	9475827	674711	102646	686967	827065	136026	1182414	277342	27983	269578	438904	106242	987443
574114	269717	33820	90791	586916	85470	18849191	2380314	136302	807087	901910	192538	7223426	1047832	47775	297668	644515	168990	1822313
880011	150442	24279	54207	419429	136269	4981182	802218	49874	574495	338858	75749	6903535	635573	24114	112066	260120	164367	950728
370271	256724	65438	70414	450334	77210	16483666	2185235	147115	731569	890104	284489	9493756	848181	56642	281634	637737	134985	1784829
266886	99955	88047	35500	279626	76957	5843226	1643868	85881	294246	351114	251379	10228606	633768	30470	102677	193214	99531	1367621
1,6	1,1	0,5	1,3	1,3	1,1	1,1	1,1	0,9	1,1	1,0	0,7	0,8	1,2	0,8	1,1	1,0	1,3	1,0
0,6	1,0	1,9	0,8	0,8	0,9	0,9	0,9	1,1	0,9	1,0	1,5	1,3	0,8	1,2	0,9	1,0	0,8	1,0

SND1	PDIA6	EEF2	RHOG	DARS1	PBXIP1	PTGR2	GLIPR2	NDRG2	OSBPL2	SUSD2	HINT3	STXBP3	BMP1	PRKCI	TMEM214	SNAP23	CMPK1	NSF
942955	160215	7183725	1254600	27316	29341	544989	141033	2333883	32349	58551	219539	160725	66958	103502	4177	5635039	1125244	54974
2133009	436321	11073785	368131	93996	71834	693297	161777	682471	374619	195537	201209	305100	60412	192313	6362	2962044	596455	81617
2008000	225664	8917337	542606	41923	91420	383030	386839	1393652	250156	347221	434973	132936	95830	104102	13160	5496460	1316237	140568
1455160	849714	4414080	591257	74142	182268	172473	36081	171935	144199	280605	139148	56564	14067	268296	21602	3220168	483015	37598
2916953	351756	14781514	447326	312847	100253	946078	133448	833607	177377	846752	335674	100523	126131	113938	70236	2939193	820209	135405
1716543	310769	5831716	511550	56223	147240	287700	54638	837400	122468	556197	437000	183203	21561	234838	8546	3113544	825639	87283
997474	177599	9421023	918334	46981	20845	797223	227819	1734455	30986	80794	103143	39490	101184	113392	3696	5632162	1320489	75086
2434240	599070	11144934	975324	277443	90650	820865	97279	114999	171947	183068	389797	65944	109824	102955	71197	4761244	1318510	139627
2936626	324504	13042671	528647	150630	122127	682592	201858	2028388	136336	110795	270610	192979	55064	241154	28354	2848559	772124	115425
988732	1129740	4797582	86182	134112	25139	509093	76665	298733	249397	751923	203963	23927	12551	443085	71521	1991414	193981	3761
628475	564994	5294546	249528	52900	68967	269110	193907	723413	149173	169304	334989	91639	8263	113873	0	3153270	450097	50602
1290278	432198	5303297	759617	53982	112129	582592	23681	144302	149985	151767	300170	70758	17160	319185	9631	3155983	336912	40325
2025929	273673	13935176	1370005	211317	80233	714746	196681	983302	25209	162094	352161	120671	68824	69749	32381	4754673	1011597	171927
2162604	188857	9690355	1919086	83717	36145	1154935	569137	633629	88888	121958	491461	151923	24712	76646	56696	6689147	1739813	103212
1981271	144232	14420427	1601750	92014	74241	711861	68684	222615	313314	103565	527973	119118	181411	64509	29117	7723499	1808461	116182
1005702	1052149	3619512	1076456	96520	182893	248653	497167	619059	75283	174264	250820	24551	7784	179062	0	4016365	557426	11782
1825542	388888	9096014	701141	116359	91731	580707	154864	1012800	163013	318591	282560	130561	74496	154167	24872	4219982	975725	94020
686943	235992	3312425	311020	112591	54334	278667	111678	764964	112858	266016	133497	87012	41041	67576	28878	1274231	339745	40045
1627452	513793	8762946	948909	109399	87734	609198	228473	706680	148448	218209	341518	99446	46971	188408	28463	4291614	858801	76652
773718	380628	4537356	655408	53571	50714	288166	200599	604003	93816	217348	114199	59204	58822	137482	25751	1991948	618883	59001
1,1	0,8	1,0	0,7	1,1	1,0	1,0	0,7	1,4	1,1	1,5	0,8	1,3	1,6	0,8	0,9	1,0	1,1	1,2
0,9	1,3	1,0	1,4	0,9	1,0	1,0	1,5	0,7	0,9	0,7	1,2	0,8	0,6	1,2	1,1	1,0	0,9	0,8

PCDHGA3	BTN1A1	DHRS12	LANCL2	RAB10	ECHDC1	RETSAT	RRAS2	TBC1D9B	YWHAZ	GK	RAB43	MDH1	ENG	LOC521224	SNX3	SNAP29	ERGIC1	G3N059	
295705	23855104	31436	437356	2517363	419891	23081	2741323	45371	2798671		67728	791780	244939	344426	478878	81215	3865041	36175	817105
22171	30476236	158335	446958	1620866	250109	242591	990606	58930	1926326		36274	490001	209534	597720	105466	39803	2847702	104828	90012
238006	33642721	177439	414240	2818424	278907	223142	2271980	156802	2484904		12562	651421	236543	318736	96514	87406	1999560	231925	121416
484890	9601544	18184	907155	802049	182138	111365	688917	17417	1805951		3112	205050	97465	832466	18636	15020	646371	37023	42479
222996	25590865	192237	661142	1829274	604808	172421	1109513	110323	3176037		44804	388318	375100	383772	353905	54389	1881200	298555	32318
168269	12476234	188002	915640	2033900	428155	137323	1325179	213128	2594787		6130	557607	362242	570628	20113	69629	816867	236697	20972
109037	14429006	23123	559646	2474059	786045	93929	3143845	68138	3668015		95229	733671	349548	400056	280787	86064	4787441	11888	551920
274675	22677516	252307	710054	3199170	401083	21742	2314053	69461	3916035		29228	446795	177802	315105	303974	93060	3315317	516088	106752
224702	38693052	159299	744277	1777649	307388	97741	1232406	107464	2316213		42162	481652	158091	385809	532258	49232	2922785	196932	27982
153833	21363211	21589	1340277	276385	164584	10440	447457	14398	2805288		11954	84128	105591	2153397	38451	43654	428001	112711	87583
907333	15328410	58128	919434	963052	159046	91752	867922	73412	2528040		52014	201891	145162	613432	322937	21404	1456492	72153	25466
202618	9191386	37591	1116700	894774	314325	112030	602520	27254	1953337		19360	264686	208699	566092	63805	16601	648661	40607	24510
259681	14773589	121796	262090	2692080	406623	213787	2000524	5594	4257735		94762	736038	312422	297657	341056	123793	3779502	145035	108116
246998	20692618	254150	562165	4984169	714886	199944	3910900	289054	3766574		14140	1044985	435970	207687	266666	245745	3866978	207911	39791
183797	21159283	301663	477632	4519566	473729	74471	3318367	94815	4947371		23114	966638	358336	182310	207439	205120	4980381	333148	85810
139229	6420978	62510	529013	2017678	425423	123870	1116200	29583	3843039		30932	466431	284229	825449	69652	58105	964713	43604	578168
226969	21593653	130133	631524	2161888	418892	128199	1823177	92446	2796341		36883	533080	256647	470364	207284	65823	2519937	184147	222872
137818	8657096	91722	202796	755899	197812	82790	907633	64491	759052		31971	192587	98654	182361	170407	27405	1453096	172306	295787
289774	18452816	127091	743948	2265669	370751	115504	1687037	80197	3302200		36055	530806	251063	653979	230283	95457	2380939	144012	122178
253072	9887344	104028	360100	1710689	180409	65980	1288482	92493	1053269		27444	354871	115498	644488	170799	87287	1727510	99696	187158
0,8	1,2	1,0	0,8	1,0	1,1	1,1	1,1	1,2	0,8		1,0	1,0	1,0	0,7	0,9	0,7	1,1	1,3	1,8
1,3	0,9	1,0	1,2	1,0	0,9	0,9	0,9	0,9	1,2		1,0	1,0	1,0	1,4	1,1	1,5	0,9	0,8	0,5

PKM	MYO1D	RPL7A	A0A3Q1MBN CSNK1G1	CDC42	CPNE3	RAB14	CYRIA	HSD17B7	MPO	SLC1A1	RAB33B	EPRS1	BSG	GSTM2	CHMP3	LDAH	CCT3	
123790	1461534	193130	420842	89885	4077034	188728	341238	1037847	4962324	15407	2831521	455706	13034	2010134	389879	874397	405270	12852
411282	1630468	283287	1963123	638	1753022	462502	590218	487809	3696485	391865	3728189	339733	14018	2792154	108779	807021	112425	49613
97051	1241404	139807	336584	100447	2500532	31086	545780	1933182	6128516	25313	4396202	181125	2253	1896139	321291	723362	717586	46812
94245	636448	106496	233942	8320	1012253	58583	92522	572840	2206093	0	3186340	23192	79729	502689	212354	348624	124126	7944
628817	1274442	608888	1755583	164973	1888460	192329	753316	509401	3621906	100721	1729950	107518	215505	638822	211678	541504	1041998	103303
250152	949143	150123	375631	49385	2192863	128938	655183	518362	3350091	4415	5850055	168794	74188	1654447	177468	793973	947063	10267
289976	795602	471547	8892989	2033	4135801	77097	537925	494971	3637504	951076	3037712	370756	1934	2129458	332968	1029538	276093	92556
323055	1160826	683561	1443285	141177	4001035	156793	871584	750545	4193835	16397	2176220	190843	128428	820467	274244	692706	1110573	195586
358627	1100105	305388	211272	3335	1938440	332496	974139	612951	3020610	2352	4401816	223536	20851	2212628	294864	645600	255448	112663
148425	712253	170836	1989644	40528	597471	39393	277543	482816	649793	256193	7935890	24720	77326	1114246	251288	212735	298263	44908
233003	981609	101781	62946	47551	936132	164126	429444	1143939	2087957	0	5829210	72041	23394	2029907	153178	362652	669797	22673
166248	778238	105109	631062	126431	776171	76650	229401	458992	3040388	6081	9566377	35048	55497	416514	338614	472312	681450	1661
439593	1230195	739830	4716116	6441	3139481	159495	464381	624875	5422342	167866	1379657	533853	50595	2078416	180402	1087237	254730	132550
218792	1435321	476210	965530	146709	5881261	112518	1922231	1466821	5495813	0	1917516	538581	42545	2073633	619870	839617	1043458	48493
164524	1215905	809728	1540189	188424	4765304	42819	1332841	824444	6898964	9243	1888047	468349	13701	959751	448923	1112242	2278955	76782
36042	309549	279173	3327804	13863	1804314	138541	416330	1211189	5092902	644540	4091772	95846	32417	754208	417063	346887	173274	15433
277296	1143733	329605	1927747	69607	2695125	162007	548471	788120	3974594	188149	3367024	229708	66136	1555539	253583	726390	591892	64867
182862	334071	227476	2899773	64440	1216029	135276	242147	499695	1164721	335136	1302798	145522	75763	817683	92665	208021	413491	64162
220657	970397	373507	1680570	71660	2479822	133255	755789	853253	3963596	135784	4626286	248997	39541	1454913	338025	634910	706922	56895
126793	358799	276591	1622672	71792	1956908	94104	603999	376541	2091076	227368	2988480	228226	21186	717816	154172	345629	701698	46881
1,3	1,2	0,9	1,1	1,0	1,1	1,2	0,7	0,9	1,0	1,4	0,7	0,9	1,7	1,1	0,8	1,1	0,8	1,1
0,8	0,8	1,1	0,9	1,0	0,9	0,8	1,4	1,1	1,0	0,7	1,4	1,1	0,6	0,9	1,3	0,9	1,2	0,9

STXBP6	AGPAT1	AIDA	S100A9	JAK1	UGP2	RAB11B	CYSTM1	TMED10	PAEP	MVP	CD109	TLR2	CSNK1A1	PRKG2	VAMP8	TOLLIP	A0A3Q1LP69 HSPB1	
898737	32281	335265	95719	345805	1967407	5866819	745966	389517	878264	1087311	5497286	10231176	189037	14783733	696088	2802123	22073	2982691
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UBXN4	SH3BP4	SERPINB6	RPS3	GGT1	XDH	ATP11B	AP2A2	RRAS	LOC521568	SLC28A3	MINDY1	RPL28	RAB8A	ACVR1B	RAP2C	FAM114A1	DHCR24	ALDH2
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652448	193153	338362	36144	11300138	2994314532	187026	0	3842957	668263	61231348	270547	4869	282298	32835	98861	808763	114973	821377
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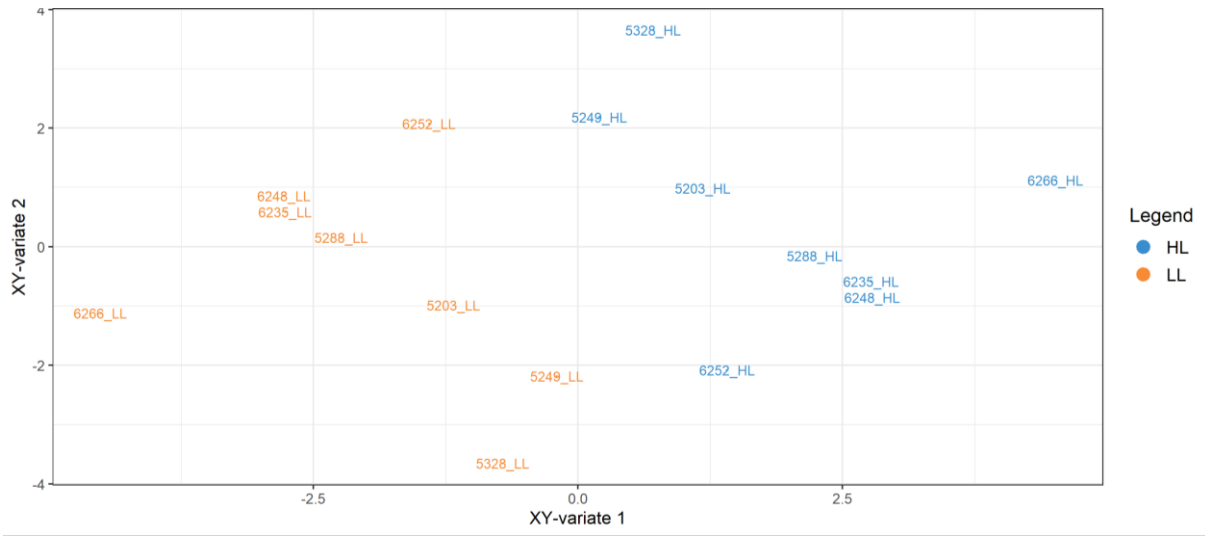
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796311	104893	319069	43927	292610	166164	28970	403395	150272	78014	369817	3839946	3567453	45169	765463	130242	1679069	8671	79947
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ATP8B1	GFPT1	TPT1	OXSRI	A0A3Q1LJQ7 RPS16	RAB35	RPL14	EIF3A	BLVRB	PRKCD	IL1R1	SULT1A1	YKT6	BZW1	RPLP0	APMAP	DNAJC12	PATJ	
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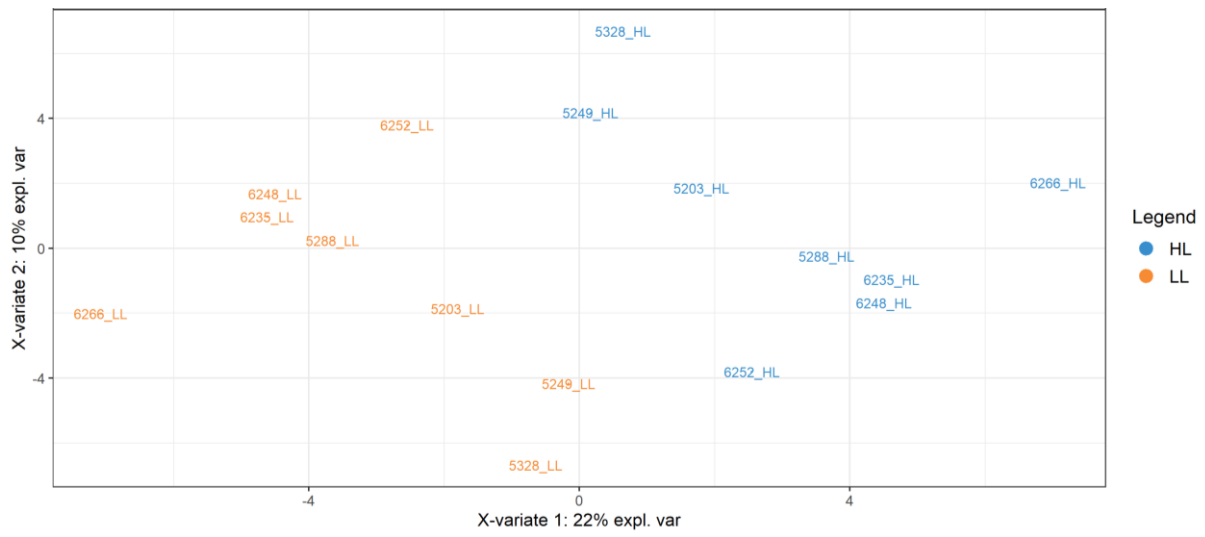
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151113	198376	120430	5623698	49111	3075637	90762	1336737	565489	281266	6587055	141601	472619	5586580	1973690	1807431	990672	284511	68015
76555	125304	89643	2453059	38829	1220798	45501	1762515	420116	187532	3796636	375910	176066	1846297	761358	963479	1233953	154135	24955
1,0	0,8	1,2	0,9	1,2	1,0	1,1	1,1	0,9	0,9	0,8	0,4	1,1	1,0	1,3	1,0	0,9	0,9	1,1
1,0	1,3	0,8	1,1	0,8	1,0	0,9	0,9	1,1	1,1	1,2	2,4	0,9	1,0	0,8	1,0	1,1	1,1	0,9

GSE554	PSMC2	DDOST	ARCN1	RAB22A	PSAT1	NIBAN2	PCBP1	SPTLC1	NAPRT
4793513	3600	51961	35966	195070	80313	871954	997824	107179	33144
6228737	50048	113448	74370	43918	46529	1100561	909816	125574	12172
15400107	15709	108693	119247	159602	156080	1254262	1230730	142391	45777
1015592	33818	98704	44273	21279	116223	986809	932879	24067	250927
2941278	169754	258141	234543	103915	524678	1226313	1399949	172365	82458
7128657	26723	68664	83092	56065	181109	1632583	1434999	232817	42776
4638224	19832	54090	66364	272525	52626	638203	1245714	63842	0
1755639	178531	318902	419635	153791	706548	1219310	1358635	222425	31851
3264784	96385	86374	209732	86511	169052	1163000	737544	203438	56365
1058100	186655	281946	145015	9402	123403	2900082	902494	131112	109542
6639682	9801	44904	24489	14464	52925	1520525	1062392	134511	238539
2174398	6150	72910	23190	41777	150437	1442623	991519	23838	130442
3010860	126389	157183	223152	237571	241532	729229	1439026	116656	0
18757204	24696	123894	172022	283158	288585	747887	1381778	261579	51928
7503241	62067	165928	246187	299011	478508	705079	1204509	200954	42123
3507820	112224	64108	37425	28058	17079	1047508	1037876	29690	12311
5487718	62252	134075	134686	125771	233013	1116249	1188818	136332	62388
4521591	70410	99494	131091	85544	245587	296068	213421	72585	80011
5739511	78046	124656	135152	124994	190190	1281992	1094642	137722	80156
5689053	63881	77156	93674	126125	146746	726410	236780	83491	77749
1,0	0,8	1,1	1,0	1,0	1,2	0,9	1,1	1,0	0,8
1,0	1,3	0,9	1,0	1,0	0,8	1,1	0,9	1,0	1,3

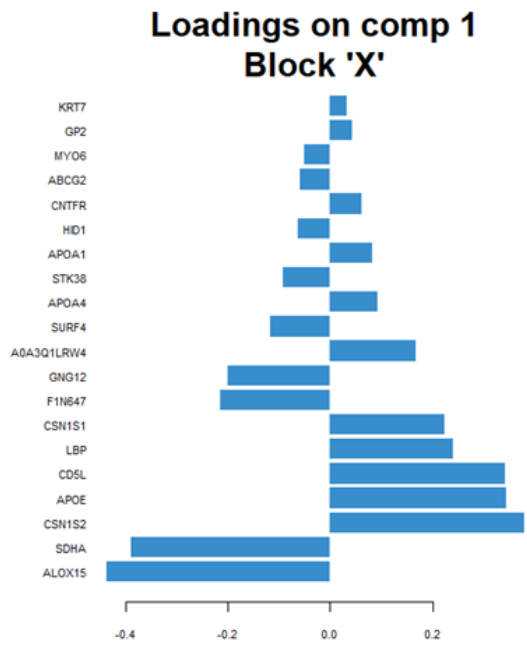
A.



B.

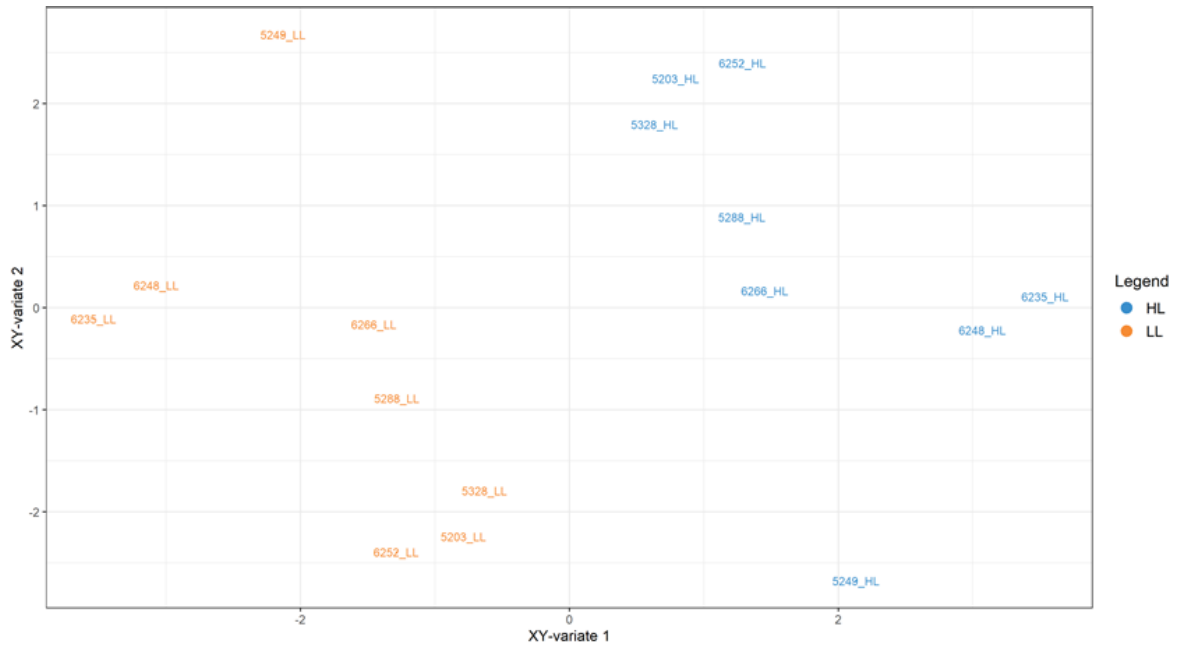


C.

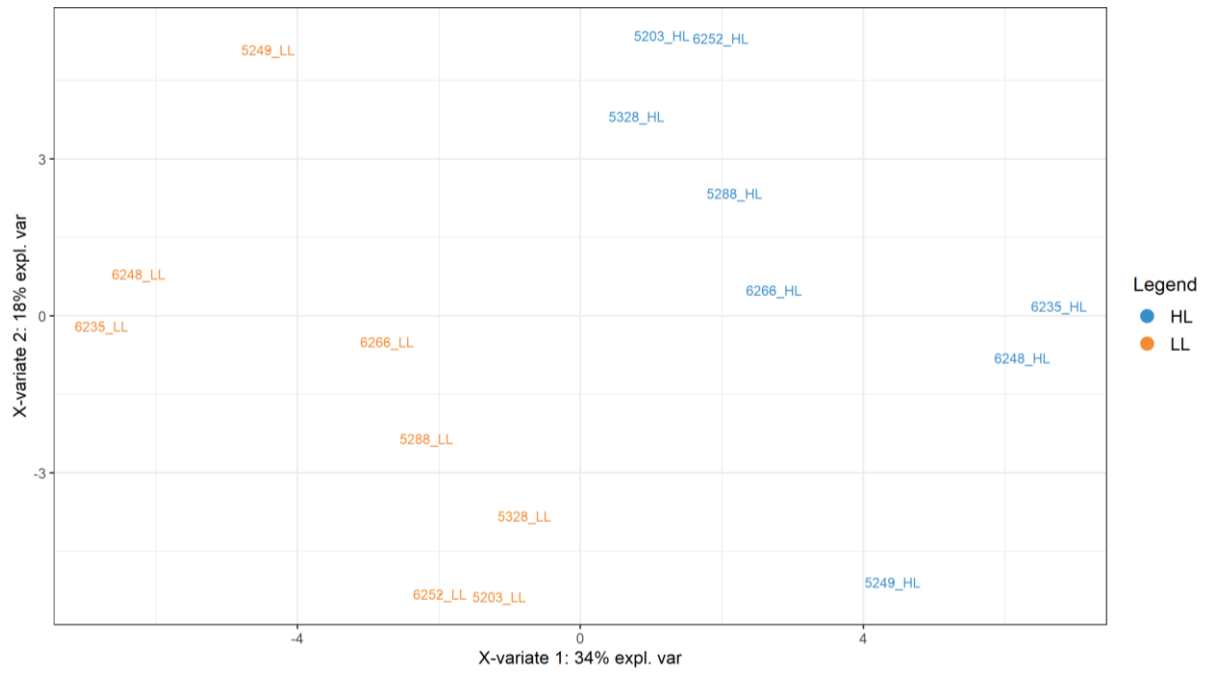


Supplementary Figure S1: sPLS - lipolysis results: A. Plot of the XY space, B. Plot of the X space, C. Loadings on component 1 of Block X.

A.

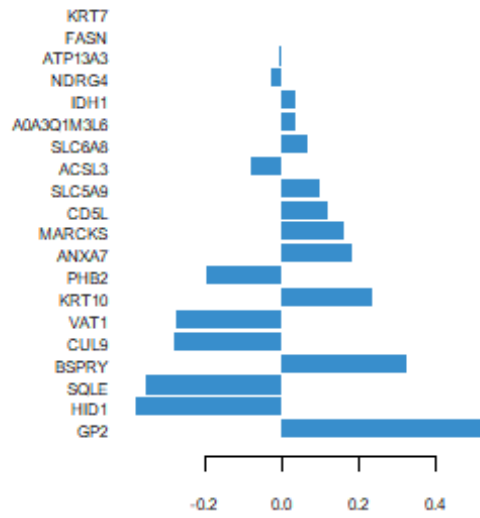


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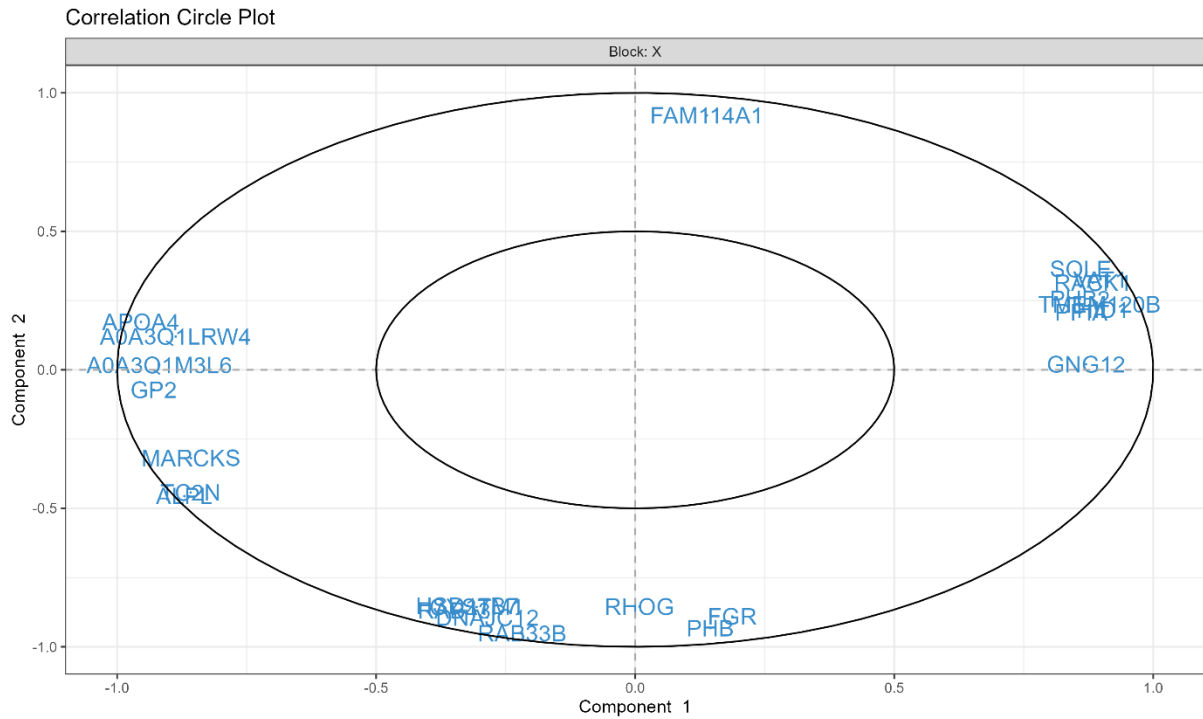


C.

Loadings on comp 1 Block 'X'



Supplementary Figure S2: sPLs – milk LPL activity results: A. Plot of the XY space, B. Plot of the X space, C. Loadings on component 1 of Block X.



Supplementary Figure S3: Correlation circle plot representing the proteins selected by sPLS-DA with a cut-off at $r > 0.85$. Only the proteins selected by sPLS-DA (corresponding to 20% of the total protein dataset) are shown in components 1 and 2 (details of sPLS-DA analysis not shown).