

TNO report

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Transcriptome analysis of effects of Fenofibrate or PFOS in intestine of ApoE3L.CETP mice

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1 Introduction

In a previous study performed for 3M, 3M#03 (project number: 031.12685), the mechanism responsible for the lipid lowering effects of three perfluoralkyl sulfonates, including transcriptome analysis of liver, was investigated in APOE*3-Leiden/huCETP transgenic mice. The test compounds were the potassium salts of perfluorobutanesulfonate, perfluorohexanesulfonate, and perfluorooctanesulfonate (PFOS). Fenofibrate (FF), a known hypolipidemic drug that works via activation of xenosensor nuclear receptor NR1C1 (PPAR α), was included as a positive control. In addition to collecting liver tissue, total small intestines were collected, snap frozen and stored at -80°C.

The study reported herein analyzed the mRNA transcription patterns associated with intestinal transport processes and lipid metabolism from the small intestines of mice fed PFOS and FF that were obtained from the 3M#03 study. The genomic transcription expression patterns in small intestine were then compared to those in obtained for liver in the 3M#03 study. The information obtained is of value in understanding the differential effects of PFOS and FF on lipid homeostasis in the APOE*3Leiden/huCETP transgenic mouse model.

1.1 Aim

To investigate the expression patterns of genes involved in intestinal transport and lipid metabolism in samples of small intestines from male ApoE3L.CETP transgenic mice fed PFOS or FF using the Affymetrix technology platform and Affmetrix GeneChip® mouse genome MOE430-2.0 arrays and to compare these intestinal expression pattern to those previously analyzed from liver samples obtained from the same study.

2 Methods

2.1 Study design

Microarray and transcriptome analysis was performed on isolated RNA from intestines collected from group 1, 2 and 5 of experiment 3 of the 3M-03 study (n=5 per group). See also figure 1 for the study design.

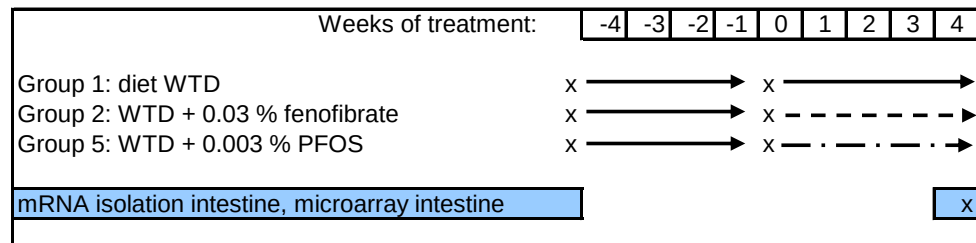


Figure 1. Study design for transcriptome analysis on intestines

2.2 Mice

Male heterozygous APOE*3Leiden.CETP mice, 7-10 weeks of age, from the SPF breeding stock at TNO-Biosciences (Leiden) were used. Mice were housed during the experiment in macrolon cages (maximum 4 mice per cage), in clean-conventional animal rooms at TNO-Leiden (relative humidity 50-60%, temperature ~21°C, light cycle 7 am to 7 pm). Individual animals were marked by ear punch-holes. Mice were supplied with food and acidified tap water *ad libitum*.

2.3 Animal welfare

Experiments performed conformed to the rules and regulations set forward by the Netherlands Law on Animal Experiments. Experiments were approved by the Animal Experiment Committee of TNO under registration number 2483. The study director was entitled to terminate experiments in case of serious, unexpected animal discomfort.

2.4 Diets

Mice received Western type diet (WTD; semi synthetic diet containing 14% beef tallow, 1% corn oil and 0.25% of cholesterol), purchased from ABdiets (Woerden, The Netherlands). This diet resulted in baseline total cholesterol (TC) plasma levels of about 8 mmol/L and triglyceride levels of about 2 mmol/L. Diets were renewed once per week.

2.5 Treatment

FF or PFOS were incorporated into the Western type diet as a food admix at the following concentrations: 0.003% w/w PFOS in the diet (nominally 3.0 mg/kg bw/day); 0.03% w/w FF (nominally 30 mg/kg bw/day).

2.6 Groups

- | | |
|---|-------|
| 1) Control group: diet WTD | (n=5) |
| 2) WTD + 0.03% FF (30 mg/kg bw/day) | (n=5) |
| 5) WTD + 0.003% PFOS (3.0 mg/kg bw/day) | (n=5) |

2.7 Small intestines; storage and homogenization

After sacrifice of the animals, total small intestines were collected, snap frozen in liquid nitrogen and stored at -80 °C (storage since 25 September 2008) until RNA isolation. The intestines were homogenized under liquid nitrogen using a RNaseaway pre-treated mortar and pestle, which were placed on dry ice during the whole procedure. Not all the intestinal tissue was used for RNA isolation. Intestinal tissue not used for transcriptional analysis was stored after homogenization at -80°C for protein expression levels of intestinal and/or liver transporters (mRNA expression levels do not always parallel protein expression levels).

2.8 RNA isolation and microarray hybridization

RNA was isolated from homogenized small intestines using RNABee (Tel-Test, Inc) and NucleoSpin® RNA II kit (Machery Nagel). After quality control of the RNA, microarray analysis was carried out at Service XS B.V. (Leiden, The Netherlands) using the Affymetrix technology platform and Affymetrix GeneChip® mouse genome MOE430-2.0 arrays. Data were sent to TNO.

2.9 Gene expression data analysis

Preprocessing and quality control of the microarray data was performed using the ArrayAnalysis.org pipeline, which combines BioConductor packages for Affymetrix analysis (simpleaffy, affyPLM, affyQCReport). All samples passed the QC (see also appendix 5.1 for the QC and pre-processing evaluation report). Raw signal intensities were normalized using the GCRMA algorithm applied across all arrays in the dataset. Probe-level signals were summarized to gene-level intensities using the custom MNBI CDF-file (Entrez Gene annotation, version 15.0.0). This resulted in expression values for 17370 genes, represented by unique Entrez Gene identifiers. Normalized intensities were log transformed (base2).

Statistical analysis was performed using the moderated t-test (empirical Bayes method) as implemented in the Bioconductor package limma (<http://bioinf.wehi.edu.au/limma/>). Resulting p-values were corrected for multiple testing using the Benjamini-Hochberg procedure. The cut-off for statistically significant changes was set at multiple testing adjusted p-value <0.05.

To provide an overview of affected processes, a T-profiler analysis (<http://www.t-profiler.org>) was performed using expression values corrected for mean expression in the control group. This analysis resulted in scores (t-scores) and significance values for pathways and biological processes. A positive score means that the majority of the genes in the pathway are up-regulated; a negative score means that the majority of the genes in the pathway are down-regulated. Pathways and biological processes with significant scores (absolute score > 4) in at least 3 animals were selected. A hierarchical clustering (complete linkage, pearson-based distance) of these biological processes was generated in R (<http://www.r-project.org>) and visualized as heatmap using the heatmap package.

To identify affected transcription factors, upstream regulator analysis was performed using the Ingenuity Pathway Analysis (IPA) software. This analysis determines activation state of transcription factors based on the observed differential gene expression. This results in an overlap p-value and activation z-score for each transcription factor in the IPA knowledgebase. The overlap p-value indicates the significance of the overlap between the target genes of the transcription factor and the differentially expressed genes. The activation z-score indicates the significance of the activation (positive z-score) or inhibition (negative z-score) of the transcription factor, based on how well the expected response of the target gene expression matches the measured differential gene expression.

To further investigate processes specifically related to intestinal transport, gene ontology (GO) analysis was performed on GO terms categorized under the term "Transport" (GO:0006810) in the Biological Process ontology. This resulted in 1303 terms related to different types of transport. This list of terms contained several transport processes not directly relevant for intestinal transport: vesicle-mediated transport (GO:0016192), intracellular transport (GO:0046907), and nucleobase-containing compound transport (GO:0015931). These terms and their offspring were excluded. Note that although vesicle-mediated transport was excluded, genes relevant to cholesterol vesicle-mediated transport process are still included in the analysis because they are present in the more generic cholesterol transport term. Overrepresentation analysis was performed on the filtered list of GO terms using the TopGO Bioconductor package. This resulted in a p-value per term that indicates enrichment of the genes in each term with significant genes, based on how many significant genes were expected to occur by chance alone.

3 Results

3.1 Differentially expressed genes

In the statistical analysis the PFOS and FF groups were compared to the control group. FF resulted in 247 differentially expressed genes, PFOS resulted in 2531 differentially expressed genes (figure 2).

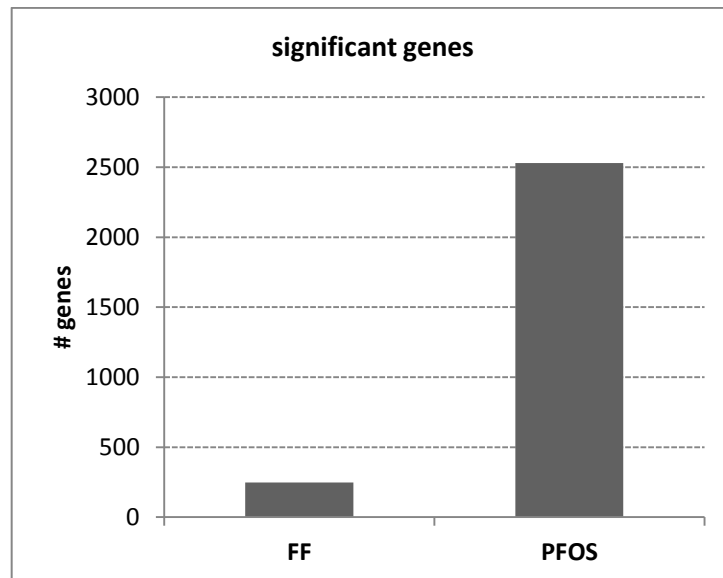


Figure 2. Number of differentially expressed genes for FF and PFOS compared to control.

The overlap in differentially expressed genes between FF and PFOS is shown in figure 3. Of the 247 significant genes for FF, 113 (45.7%) are also regulated by PFOS.

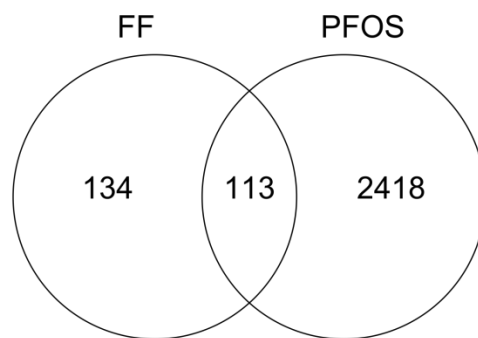


Figure 3. Venn diagram of the overlap between differentially expressed genes for FF and PFOS.

3.2 Pathway analysis

Figure 4 gives an overview of functional gene sets (based on gene ontology annotation) regulated by FF or PFOS. The clustered heatmap shows a number of groups of gene sets with a similar response profile. The first cluster contains processes related to immune response, and is down-regulated specifically by FF.

The second cluster contains processes related to cell-cell interaction (e.g. chemotaxis, extracellular matrix) and is down-regulated by both FF and PFOS. The third cluster contains translation-related processes and is down-regulated specifically by PFOS. In addition, the fourth cluster, related to cell division is also down-regulated by PFOS. Both the fifth and sixth clusters, containing gene sets related to cholesterol transport and intercellular signalling respectively, are specifically up-regulated by PFOS. Finally, the seventh cluster, comprising mostly processes related to oxidative phosphorylation is up-regulated by both FF and PFOS.

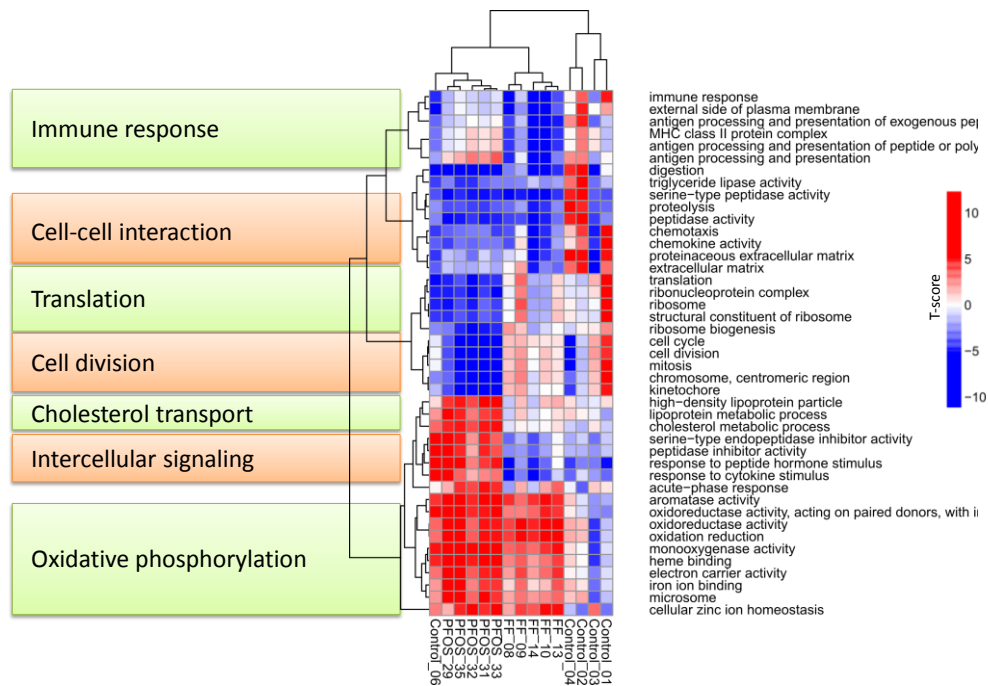


Figure 4. Clustered heatmap of scores for functional gene sets (based on Gene Ontology) that are significantly affected in at least 3 animals. Boxes are colored by scores, where red indicates a positive score (majority of genes up-regulated) and blue a negative score (majority of genes down-regulated).

The main overlap in regulated processes between FF and PFOS is oxidative phosphorylation, which is significantly up-regulated by both treatments. Also in cell-cell interaction processes there is overlap between FF and PFOS. Immune response is significantly down-regulated by FF alone, while cholesterol transport is significantly up-regulated by PFOS alone.

3.3 Transcription factors

In addition to the affected processes, we aimed to identify activated or inhibited transcription factors relevant in regulating these processes, focusing on transcription factors involved in lipid metabolism in particular. Table 1 shows the top five activated or inhibited transcription factors for FF and PFOS, based on Ingenuity upstream regulator analysis. For each transcription factor, the table lists its differential expression (as log2 ratio), and an activation state prediction based on the expression of its known target genes. This prediction is based on two scores listed in the table, the activation z-score and overlap p-value. The activation z-score

indicates how well the measured up or down-regulation matches the known effects of the transcription factor on its targets. The overlap p-value indicates how well the set of known targets overlaps with the measured differentially expressed genes.

Fenofibrate				
Transcription Factor	Log Ratio	Predicted Activation	Activation z-score	Overlap p-value
TRIM24	0.056	Activated	5.144	2.03E-29
STAT1	-0.589	Inhibited	-4.315	1.40E-14
NKX2-3	-0.029	Activated	4.025	8.68E-13
NR1H2	-0.242		1.911	1.96E-10
IRF1	-0.133	Inhibited	-3.569	2.62E-09
PFOS				
Transcription Factor	Log Ratio	Predicted Activation	Activation z-score	Overlap p-value
HNF4A	-0.052	Activated	5.382	2.10E-21
PPARA	0.443	Activated	2.253	2.57E-11
E2F4	0.048		-0.271	9.08E-08
RORA	-0.213	Activated	2.887	3.94E-07
MYC	-0.191	Inhibited	-5.313	5.76E-07

Table 1. Top five transcription factors resulting from the Ingenuity upstream regulator analysis for Fenofibrate and PFOS. A z-score ≥ 2.0 or ≤ -2.0 is considered significantly changed.

These data highlight several transcription factors that connect to the observations based on pathway analysis as described in section 2.2. For example, MYC (c-MYC), a transcription factor driving proliferation, is predicted to be inhibited by PFOS specifically. This is in line with the down-regulation of proliferation-related processes “Cell division” and “Translation” upon PFOS treatment as observed in the pathway analysis (Figure 3). In addition, STAT1, which is part of a family of nuclear proteins mediating the action several cytokines and known to play a role in the immune system is inhibited by FF specifically, linking to the down-regulated “Immune response” cluster in the pathway analysis. Focusing on lipid metabolism, data for transcription factors of interest related to lipid metabolism are listed in Table 2. These data show that both FF and PFOS activate several lipid metabolism related transcription factors or complexes containing these transcription factors. In the case of FF, four transcription factors are significantly activated, and, for PFOS, six transcription factors are significantly activated. The main difference between FF and PFOS in these transcription factors is the absence of significant activation of PPAR α , PPAR γ , and LXR after FF treatment. Although the activation z-scores for PPAR α and PPAR γ are positive, they do not reach the required significance level.

Fenofibrate					
TF	Protein/complex	Log Ratio	Predicted Activation	Activation z-score	Overlap p-value
PPAR α	PPARA	0.322		1.715	2.92E-09
PPAR γ	PPARG	0.144		1.819	2.81E-02
RXR	RXRA	0.083	Activated	2.791	3.83E-05
LXR	NR1H2	-0.114			3.25E-02
PXR	PXR ligand-PXR-Retinoic acid-RXR α	-	Activated	2.777	3.19E-08
	NR1I2	-0.242		1.911	1.96E-10
	Ncoa-Nr1i2-Rxra	-	Activated	2.000	6.82E-05
CAR	NR1I3	0.328	Activated	2.934	4.05E-08
PFOS					
TF	Protein/complex	Log Ratio	Predicted Activation	Activation z-score	Overlap p-value
PPAR α	PPARA	0.443	Activated	2.253	2.57E-11
PPAR γ	PPARG	-0.430	Activated	5.320	3.74E-05
RXR	RXRA	0.161		1.516	2.36E-02
	PPAR α -RXR α	-	Activated	2.236	1.42E-02
LXR	NR1H3	0.550	Activated	2.135	5.36E-02
PXR	PXR ligand-PXR-Retinoic acid-RXR α	-	Activated	2.236	1.26E-01
	NR1I2	0.229		-0.558	3.62E-04
CAR	NR1I3	0.179	Activated	2.624	1.86E-02

Table 2. Results from the Ingenuity upstream regulator analysis of transcription factors relevant for lipid metabolism. A z-score ≥ 2.0 or ≤ -2.0 is considered significantly changed.

3.4 Lipid metabolism genes

A set of genes of interest related to lipid metabolism was defined, based on the list used in the previous study investigating gene expression changes in liver (3M#03). The expression changes as a result of FF and PFOS intervention are listed in the excel file added to this report (Suppl. table 1, see also table 4-7 for comparison between small intestine and liver expression), grouped by specific processes (e.g. lipolysis, beta oxidation, uptake). Of the 95 genes for which a mouse gene identifier could be found, 91 were found to be expressed. Intervention with FF resulted in 6 significantly regulated pre-selected genes, of which 4 were down and 2 were up-regulated. The PFOS intervention resulted in 31 significantly regulated pre-selected genes, of which 26 were up and 5 were down-regulated. Of the 6 pre-selected genes regulated by FF, 5 were also regulated by PFOS (SCD1, Acsl6, Acox2, Acaa1b, CD36).

3.5 Transporters based on GO

In addition to the global pathway and transcription factor analysis, we zoomed in to transporter processes more specifically. Based on the Gene Ontology functional annotation, we defined a list of transport processes and genes playing a role in transport. Excel file Supplementary table 2 (see also appendix 5.2) provides a full list of 211 genes related to transport processes that were found to be significantly regulated in FF or PFOS. To provide an overview of affected transport processes, we performed enrichment analysis on the transport GO terms. Supplementary table 3 (see also appendix 5.3) lists terms that were significantly enriched with differentially expressed genes. For both FF and PFOS these include fatty acid

transport, carbohydrate transport, and organic cation transport. For PFOS, but not for FF, cholesterol and steroid transport were also found to be significantly enriched with up-regulated genes. Table 3 lists the significantly regulated genes for lipid, fatty acid, and cholesterol transport. Overall, PFOS has a more extensive effect on both fatty acid and cholesterol transport. For PFOS, 43 genes related to these transport processes are significantly regulated of which 35 are up-regulated, while FF regulates only 5 genes. Only one gene (Slco3a1) is significantly regulated by FF but not by PFOS. This gene, which is down-regulated by FF, is part of the solute carrier organic anion transporter family and is involved in transport of prostaglandins. The other 4 genes regulated by FF are also regulated by PFOS in the same direction.

Gene	GO Term	Log ratio FF	Log ratio PFOS	adj. p-value FF	adj. p-value PFOS
Abca1	Cholesterol transport	0.399656498	0.443072493	0.062922264	0.009227433
Apoa1	Cholesterol transport	-0.013288054	0.173022994	0.966169442	0.021628587
Apoa2	Cholesterol transport	-0.015664843	1.930995618	0.996523819	0.005313706
Apoa4	Cholesterol transport	0.020732206	0.148084	0.940374602	0.045425502
Apoc1	Cholesterol transport	0.157078306	2.892596171	0.937047146	0.000401783
Apoc2	Cholesterol transport	0.053058232	0.201098616	0.832105695	0.021869206
Lrp6	Cholesterol transport	0.114634192	0.478049359	0.762021683	0.005140573
Pon1	Cholesterol transport	0.174067816	1.396351251	0.865544216	0.001486693
Soat1	Cholesterol transport	-0.30075352	-0.368232718	0.264580815	0.035739568
Nr1h3	Cholesterol transport	0.403793146	0.549647293	0.130927537	0.007424532
Stard3	Cholesterol transport	0.331645073	0.416774058	0.018252518	0.00189498
Npc1l1	Cholesterol transport	-0.038333172	0.396216094	0.939331136	0.007570549
ApoB	Cholesterol transport	0.02962116	0.22312843	0.937047146	0.027931954
Ace	Fatty acid transport	0.784504955	0.727528929	0.00621252	0.003035417
Plin2	Fatty acid transport	0.206782996	0.521267518	0.42001136	0.003347215
Fabp2	Fatty acid transport	0.044312676	0.17663018	0.852409611	0.026935752
Pla2g4a	Fatty acid transport	-0.299450267	-0.773886139	0.584626097	0.008605923
Pparg	Fatty acid transport	0.144238673	-0.429813179	0.75574906	0.022559948
Slc25a17	Fatty acid transport	-0.138422212	-0.621176806	0.775853991	0.004386132
Slc2a1	Fatty acid transport	-0.003232584	0.276017563	0.99667172	0.048332391
Slc27a2	Fatty acid transport	0.217371068	0.321086678	0.225444714	0.010855195
Slc27a4	Fatty acid transport	0.079582	0.491262696	0.881634889	0.007497354
AcsL4	Fatty acid transport	-0.181161325	-0.361629619	0.557141061	0.024669412
Slco3a1	Fatty acid transport	-0.352662435	0.165143781	0.019098564	0.133439813
AcsL6	Fatty acid transport	-1.089101021	-0.909807239	0.04007155	0.023157133
Irs2	Fatty acid transport	0.091281184	0.725427648	0.895840566	0.003301897
AcsL5	Fatty acid transport	0.063527376	0.199618908	0.76081509	0.018621682
Cd36	Fatty acid transport, Cholesterol transport	0.902175972	0.362311736	0.000330286	0.027625836
Pla2g10	Fatty acid transport, Cholesterol transport	0.156001682	-0.791892031	0.859851753	0.010252283
ApoH	Lipid transport	0.151326465	1.007759024	0.873732013	0.004206667
Atp8a1	Lipid transport	0.010815546	0.218925917	0.977072624	0.025805131
Atp9a	Lipid transport	-0.046226118	0.408690367	0.947515973	0.024435828
Mtttp	Lipid transport	0.133672906	0.19549194	0.319022268	0.022372955
Ppara	Lipid transport	0.321692959	0.44323114	0.161773479	0.009227433
Rbp4	Lipid transport	0.261885841	1.015488235	0.85662955	0.032792997
Ncor1	Lipid transport	-0.087039968	0.20055416	0.643859039	0.024887407
Abca7	Lipid transport	-0.00093738	0.650276019	0.999068508	0.009291023
Atp9b	Lipid transport	-0.042787572	0.386668953	0.940319582	0.015203566
Osbp1a	Lipid transport	0.513281719	0.927176281	0.132895066	0.002158091
Osbp13	Lipid transport	0.049679582	0.539486384	0.942016181	0.006742039
Spns1	Lipid transport	0.032927194	0.314080719	0.954223013	0.025464131
Osbp	Lipid transport	-0.077245556	0.403201078	0.848015564	0.006588983
Osbp16	Lipid transport	0.316647745	0.304845396	0.081215497	0.022992524
Atp11c	Lipid transport	-0.042425327	-0.212064254	0.893349246	0.025998398

Table 3. Genes annotated to GO terms "Lipid transport", "Fatty acid transport", or "Cholesterol transport" that are significantly regulated by FF or PFOS. The log ratio column is colored according to the direction of regulation (red is up-regulated, blue is down-regulated). Significant p-values are marked with bold font type

3.6 Comparison with liver gene expression

In a previous analysis in this experiment (3M#03 study), liver gene expression was analysed. In comparison to liver, there are less significantly regulated genes involved in lipid metabolism, especially for FF. For the set of preselected lipid metabolism related genes more than 50% was regulated for both FF and PFOS in liver, but only 6.6% and 34% respectively in intestine (for comparison of gene expression of preselected lipid metabolism related genes between liver and intestine see table 4, 5, 6 and 7).

Pathway	common name	Average expression (Zlog)						Fenofibrate vs control				PFOS vs Control			
		Liver			small intestine			Liver		small intestine		Liver		small intestine	
		Control	Fenofibrate	PFOS	Control	Fenofibrate	PFOS	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value
TG metabolism	lipolysis														
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	FXR	9.78	9.82	10.06	9.04	8.82	8.86	1.03	0.436	-1.16	0.596	1.21	0.028	-1.13	0.398
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	PPARg	5.58	5.28	6.18	6.41	6.56	5.98	-1.23	0.256	1.11	0.756	1.52	0.042	-1.35	0.023
	LPL	8.92	11.13	10.01	7.03	7.23	6.71	4.63	0.000	1.15	0.866	2.13	0.000	-1.25	0.410
	HL	10.82	10.42	10.33	1.77	1.78	1.81	-1.32	0.000	1.01	0.983	-1.40	0.000	1.03	0.839
	ApoC3	14.10	13.98	14.08	13.47	13.38	13.54	-1.08	0.011	-1.07	0.510	-1.01	0.370	1.05	0.359
	ApoC1	13.81	13.77	13.71	3.25	3.41	6.14	-1.03	0.235	1.12	0.937	-1.07	0.020	7.43	0.000
	ApoC2	12.49	12.54	12.11	13.62	13.67	13.82	1.04	0.402	1.04	0.832	-1.30	0.003	1.15	0.022
	ApoA5	13.14	12.94	12.45	2.79	2.84	3.10	-1.15	0.064	1.03	0.955	-1.61	0.000	1.24	0.079
	GPIHBP1	7.41	7.52	7.85	2.59	2.47	2.44	1.08	0.344	-1.09	0.727	1.36	0.012	-1.11	0.295
	FA/TG synthesis														
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	FXR	9.78	9.82	10.06	9.04	8.82	8.86	1.03	0.436	-1.16	0.596	1.21	0.028	-1.13	0.398
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	PPARg	5.58	5.28	6.18	6.41	6.56	5.98	-1.23	0.256	1.11	0.756	1.52	0.042	-1.35	0.023
	SREBP1a/c	11.05	10.90	10.03	10.10	10.37	11.09	-1.11	0.350	1.20	0.305	-2.03	0.000	1.98	0.000
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051
	FAS	10.06	10.99	9.89	6.23	6.85	6.58	1.90	0.068	1.54	0.095	-1.13	0.374	1.28	0.185
	DGAT1	5.99	6.56	6.44	12.28	12.32	12.58	1.48	0.002	1.03	0.904	1.37	0.008	1.23	0.004
	DGAT2	9.25	9.02	9.04	8.51	8.68	8.73	-1.17	0.046	1.13	0.410	-1.16	0.042	1.17	0.066
	SCD1	13.15	13.47	13.10	11.39	12.10	11.99	1.24	0.207	1.63	0.008	-1.03	0.420	1.51	0.006
	SCD2	1.98	2.10	2.30	7.40	7.66	8.03	1.09	0.247	1.19	0.592	1.25	0.013	1.55	0.011
	ACLY	11.10	11.02	9.79	9.15	9.23	9.04	-1.05	0.476	1.06	0.832	-2.47	0.003	-1.09	0.375
	s14	12.36	12.75	12.53	5.33	6.32	6.37	1.31	0.326	1.99	0.268	1.12	0.389	2.05	0.070
	ACS, Acs1	11.68	12.79	12.48	7.22	7.36	7.29	2.15	0.000	1.10	0.513	1.73	0.000	1.05	0.586
	ACS, Acs3	6.89	8.51	7.67	9.00	9.33	9.33	3.07	0.000	1.26	0.107	1.71	0.016	1.25	0.026
	ACS, Acs4	8.29	8.95	8.78	4.34	4.16	3.98	1.58	0.000	-1.13	0.557	1.40	0.001	-1.28	0.025
	ACS, Acs5	11.73	12.31	11.76	13.29	13.35	13.49	1.49	0.001	1.05	0.761	1.03	0.407	1.15	0.019
	ACS, Acs1	2.04	2.03	2.28	8.91	8.93	9.04	-1.01	0.487	1.01	0.973	1.18	0.057	1.09	0.333
	ACS, Acs2	10.77	11.58	10.43	8.59	8.77	8.40	1.76	0.068	1.13	0.507	-1.26	0.257	-1.14	0.189
	ACS, Acsm1	11.23	10.89	11.18	1.97	1.91	2.04	-1.27	0.000	-1.04	0.927	-1.04	0.305	1.05	0.704
	ACS, Acsm2	2.09	1.95	2.05	1.60	1.63	1.59	-1.10	0.130	1.02	0.897	-1.02	0.371	-1.01	0.935
	ACS, Acsm3	9.74	9.92	9.25	5.07	5.03	4.26	1.13	0.168	-1.03	0.954	-1.40	0.001	-1.76	0.001
	ACS, Acsm5	9.85	9.77	9.94	5.38	5.43	5.36	-1.06	0.373	1.03	0.968	1.06	0.300	-1.02	0.941
	ACS, Acs6	measured, but not expressed			5.80	4.71	4.89			-2.13	0.040			-1.88	0.023
	SCD3	measured, but not expressed			1.98	1.93	1.94			-1.03	0.858			-1.03	0.675
	SCD4	not measured (not on array)													
	ACC, Acaca	not measured (not on array)			6.57	6.82	7.24			1.19	0.660			1.60	0.014
	ACC, Acacb	not measured (not on array)			2.89	2.97	3.29			1.06	0.858			1.32	0.013
	ACS, Acsm4	not measured (not on array)													
	ACS, Acs3	not measured (not on array)													
	S34-THRSP-SPOT34	12.36	12.75	12.53				1.31	0.326			1.12	0.389		
	beta oxidation														
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	PCC1alpha	6.40	6.50	5.12	10.01	9.90	10.00	0.11	0.436	-1.08	0.579	-1.27	0.000	-1.01	0.933
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051
	CAR	7.46	7.86	8.32	6.63	6.96	6.81	1.32	0.172	1.26	0.332	1.82	0.007	1.13	0.406
	CPT1a	10.89	11.25	10.74	10.12	10.10	9.83	1.28	0.010	-1.01	0.976	-1.12	0.143	-1.22	0.014
	CPT1b	2.60	5.20	3.84				6.08	0.000			2.37	0.000		
	ACO, Acox1	13.55	14.14	14.03	11.48	11.62	11.76	1.51	0.000	1.10	0.484	1.39	0.000	1.21	0.016
	ACO, Acox2	10.85	10.99	11.26	5.71	7.28	7.14	1.10	0.108	2.97	0.005	1.33	0.000	2.69	0.003
	ACO, Acox3	2.18	2.05	2.07	2.63	2.45	2.43	-1.10	0.243	-1.14	0.674	-1.08	0.240	-1.15	0.328
	bifunctional enzym	12.71	14.33	14.24	11.11	10.96	10.72	3.08	0.000	-1.10	0.811	2.89	0.000	-1.31	0.063
	thiolase, Acaa1a	10.26	11.17	11.12	10.41	10.84	10.74	1.89	0.000	1.35	0.019	1.82	0.000	1.26	0.018
	thiolase, Acaa1b	14.31	14.68	14.62	12.33	12.66	12.69	1.29	0.000	1.26	0.124	1.24	0.000	1.28	0.019
	thiolase, Acaa2	12.74	13.02	12.82	11.30	11.46	11.29	1.21	0.000	1.11	0.647	1.06	0.107	-1.01	0.937
	ACS, Acs1	11.68	12.79	12.48	7.22	7.36	7.29	2.15	0.000	1.10	0.513	1.73	0.000	1.05	0.586
	ACS, Acs3	6.89	8.51	7.67	9.00	9.33	9.33	3.07	0.000	1.26	0.107	1.71	0.016	1.25	0.026
	ACS, Acs4	8.29	8.95	8.78	4.34	4.16	3.98	1.58	0.000	-1.13	0.557	1.40	0.001	-1.28	0.025
	ACS, Acs5	11.73	12.31	11.76	13.29	13.35	13.49	1.49	0.001	1.05	0.761	1.03	0.407	1.15	0.019
	ACS, Acs1	2.04	2.03	2.28	8.91	8.93	9.04	-1.01	0.487	1.01	0.973	1.18	0.057	1.09	0.333
	ACS, Acs2	10.77	11.58	10.43	8.59	8.77	8.40	1.76	0.068	1.13	0.507	-1.26	0.257	-1.14	0.189
	ACS, Acsm1	11.23	10.89	11.18	1.97	1.91	2.04	-1.27	0.000	-1.04	0.927	-1.04	0.305	1.05	0.704
	ACS, Acsm2	2.09	1.95	2.05	1.60	1.63	1.59	-1.10	0.130	1.02	0.897	-1.02	0.371	-1.01	0.935
	ACS, Acsm3	9.74	9.92	9.25	5.07	5.03	4.26	1.13	0.168	-1.03	0.954	-1.40	0.001	-1.76	0.001
	ACS, Acsm5	9.85	9.77	9.94	5.38	5.43	5.36	-1.06	0.373	1.03	0.968	1.06	0.300	-1.02	0.941
	ACS, Acs6	measured, but not expressed			5.80	4.71	4.89			-2.13	0.040			-1.88	0.023
	CPT1c	measured, but not expressed			2.34	2.38	2.46			1.02	0.958			1.09	0.440
	HNF3b-FoxA-2	8.58	8.37	7.68				-1.16	0.322			-1.87	0.003		
	HNF4a	9.02	8.77	8.77				-1.19	0.025			-1.19	0.019		
	TR	3.53	3.33	3.39				-1.15	0.099			-1.10	0.161		

Table 4. Gene expression data of triglyceride metabolism pathway in liver and intestine with transcription factors and genes involved. Continued on next page.

Pathway	common name	Average expression (2log)						Fenofibrate vs control				PFOS vs Control				
		Liver			small intestine			Liver		small intestine		Liver		small intestine		
		Control	Fenofibrate	PFOS	Control	Fenofibrate	PFOS	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value	
TG metabolism	FA uptake, transport, binding															
	SREBP2	3.32	3.50	3.09	4.63	4.46	4.90	1.13	0.165	-1.12	0.698	-1.17	0.077	1.20	0.155	
	SREBP1a/c	11.05	10.90	10.03	10.10	10.37	11.09	-1.11	0.350	1.20	0.305	-2.03	0.000	1.98	0.000	
	PPARq	5.58	5.28	6.18	6.41	6.56	5.98	-1.23	0.256	1.11	0.756	1.52	0.042	-1.35	0.023	
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051	
	FABP, Fabp1	14.47	14.61	14.55	14.19	14.26	14.14	1.10	0.012	1.05	0.727	1.06	0.087	-1.04	0.604	
	FABP, Fabp2	11.78	12.22	10.64	14.05	14.09	14.22	1.36	0.006	1.03	0.852	-2.20	0.000	1.13	0.027	
	FABP, Fabp4	9.16	10.29	10.31	10.70	10.78	10.62	2.19	0.000	1.06	0.935	2.21	0.000	-1.06	0.787	
	FABP, Fabp6	2.32	2.40	2.22	14.31	14.06	14.24	1.05	0.412	-1.19	0.256	-1.08	0.303	-1.05	0.670	
	FABP, Fabp7	7.51	5.71	7.07	3.21	2.71	2.86	-3.48	0.000	-1.41	0.183	-1.35	0.169	-1.27	0.167	
	FATP, Slc27a1	2.82	5.01	4.04	2.70	2.74	2.65	4.59	0.000	1.03	0.920	2.33	0.000	-1.04	0.706	
	FATP, Slc27a2	13.86	14.06	13.96	11.96	12.18	12.28	1.15	0.001	1.16	0.225	1.07	0.043	1.25	0.011	
	FATP, Slc27a3	measured, but not expressed														
	FATP, Slc27a4	4.48	6.20	5.53	10.57	10.65	11.06	3.30	0.000	1.06	0.882	2.08	0.000	1.41	0.007	
	FATP, Slc27a5	13.16	13.06	13.06	2.24	2.20	2.46	-1.07	0.181	-1.03	0.926	-1.08	0.127	1.16	0.069	
	CD36	9.45	11.23	11.22	9.96	10.86	10.32	3.42	0.000	1.87	0.000	3.40	0.000	1.29	0.028	
	LDLR	6.51	7.11	6.21	6.36	6.32	6.25	1.52	0.016	-1.03	0.930	-1.23	0.137	-1.08	0.397	
	PCSK9	5.42	6.14	4.86	5.10	4.70	5.18	1.64	0.110	-1.32	0.487	-1.48	0.142	1.06	0.841	
	Fabp9	measured, but not expressed					1.76	1.81	1.78		1.03	0.913			1.02	0.888
	VLDL assemblage/formation															
	ApoB	14.19	14.15	14.04	12.44	12.47	12.67	-1.02	0.374	1.02	0.937	-1.11	0.012	1.17	0.028	
	ApoBEC	6.06	6.06	6.10	9.42	9.38	9.70	1.00	0.515	-1.03	0.951	1.03	0.413	1.21	0.063	
	MTTP	8.67	9.18	8.96	12.17	12.30	12.36	1.42	0.000	1.10	0.319	1.22	0.020	1.15	0.022	
	ApoBec2	measured, but not expressed					3.25	3.23	3.26		-1.02	0.976			1.01	0.979
	ApoBec3	measured, but not expressed					2.79	2.67	2.82		-1.09	0.822			1.02	0.893
	ApoBec4	measured, but not expressed					1.73	1.61	1.84		-1.09	0.790			1.08	0.521
	PL excretion															
MDR2	10.85	11.20	11.05	2.32	2.48	2.54	1.27	0.003	1.12	0.733	1.14	0.055	1.17	0.244		

Table 4. Gene expression data of triglyceride metabolism pathway in liver and intestine with transcription factors and genes involved. The fold change column is colored according to the direction of regulation (red is up-regulated, blue is down-regulated). Significant q-values (or multiple testing adjusted p-values) are marked with bold font type.

Interestingly, for PFOS a number of genes, which were significantly regulated in the liver, were also significantly regulated in the small intestine but in opposite direction (LXRa, PPARa, PPARg, ApoC1, ApoC2, SREBP1a/c, Acsl4, Fabp2, ApoB).

Pathway	common name	Average expression (2log)						Fenofibrate vs control				PFOS vs Control				
		Liver			small intestine			Liver		small intestine		Liver		small intestine		
		Control	Fenofibrate	PFOS	Control	Fenofibrate	PFOS	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value	
Cholesterol	cholesterol synthesis, storage, uptake and metabolism															
	SREBP2	3.32	3.50	3.09	4.63	4.46	4.90	1.13	0.165	-1.12	0.698	-1.17	0.077	1.20	0.155	
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007	
	SREBP1a/c	11.05	10.90	10.03	10.10	10.37	11.09	-1.11	0.350	1.20	0.305	-2.03	0.000	1.98	0.000	
	synthesis															
	ACLY	11.10	11.02	9.79	9.15	9.23	9.04	-1.05	0.476	1.06	0.832	-2.47	0.003	-1.09	0.375	
	HMG CoA reductase	7.69	8.48	7.33	8.73	8.73	8.51	1.73	0.039	1.00	0.998	-1.28	0.204	-1.17	0.192	
	HMG CoA synthase	12.45	12.83	12.53	8.34	7.68	7.84	1.29	0.000	-1.58	0.500	1.05	0.244	-1.42	0.355	
	squalene synthase	8.64	9.50	8.53	8.40	8.23	8.41	1.83	0.003	-1.13	0.859	-1.08	0.360	1.01	0.983	
	HMGCS	not measured (not on array)														
	storage															
	ACAT1	11.40	11.88	11.54	11.03	10.94	10.88	1.39	0.000	-1.06	0.738	1.10	0.034	-1.11	0.158	
	ACAT2	9.41	10.33	9.37	8.48	7.88	8.28	1.89	0.004	-1.52	0.006	-1.03	0.429	-1.14	0.212	
	uptake															
	SREBP2	3.32	3.50	3.09	4.63	4.46	4.90	1.13	0.165	-1.12	0.698	-1.17	0.077	1.20	0.155	
	SREBP1a/c	11.05	10.90	10.03	10.10	10.37	11.09	-1.11	0.350	1.20	0.305	-2.03	0.000	1.98	0.000	
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007	
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447	
	LDLR	6.51	7.11	6.21	6.36	6.32	6.25	1.52	0.016	-1.03	0.930	-1.23	0.137	-1.08	0.397	
	PCSK9	5.42	6.14	4.86	5.10	4.70	5.18	1.64	0.110	-1.32	0.487	-1.48	0.142	1.06	0.841	
	NPC1-like1	not measured (not on array)														
	metabolism															
	FXR	9.78	9.82	10.06	9.04	8.82	8.86	1.03	0.436	-1.16	0.596	1.21	0.028	-1.13	0.398	
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007	
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447	
	CAR	7.46	7.86	8.32	6.63	6.96	6.81	1.32	0.172	1.26	0.332	1.82	0.007	1.13	0.406	
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051	
	CYP7A	7.82	7.77	5.90	1.76	1.70	1.72	-1.04	0.506	-1.04	0.833	-3.78	0.021	-1.02	0.747	
	IBAT	5.01	4.15	3.52	10.05	10.36	9.88	-1.81	0.062	1.24	0.879	-2.80	0.002	-1.12	0.833	
	bsep	11.12	10.67	10.32	1.56	1.52	1.69	-1.37	0.004	-1.03	0.937	-1.74	0.000	1.09	0.355	
	ntcp	12.19	12.02	11.77	1.49	1.46	1.58	-1.13	0.242	-1.02	0.951	-1.34	0.014	1.06	0.527	
	excretion															
LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007		
LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447		
ABCG5	11.00	10.65	10.13	11.99	11.80	12.09	-1.28	0.049	-1.14	0.203	-1.83	0.000	1.08	0.293		
ABCG8	7.20	7.05	5.95	7.45	7.40	7.72	-1.11	0.369	-1.03	0.954	-2.38	0.000	1.20	0.188		

Table 5. Gene expression data of cholesterol metabolism pathway in liver and intestine with transcription factors and genes involved. The fold change column is colored according to the direction of regulation (red is up-regulated, blue is down-regulated). Significant q-values (or multiple testing adjusted p-values) are marked with bold font type.

Pathway	common name	Average expression (2log)						Fenofibrate vs control				PFOS vs Control			
		Liver			small intestine			Liver		small intestine		Liver		small intestine	
		Control	Fenofibrate	PFOS	Control	Fenofibrate	PFOS	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value
HDL metabolism															
HDL formation															
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051
	ApoA1	14.38	14.34	13.85				-1.03	0.365			-1.45	0.000		
	APOA2	14.52	14.55	14.50	4.64	4.63	6.58	1.03	0.310	-1.01	0.997	-1.01	0.373	3.81	0.005
HDL maturation															
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	ABCA1	5.14	5.06	5.01	4.60	5.00	5.04	-1.06	0.244	1.32	0.063	-1.09	0.092	1.36	0.009
	LCAT	10.98	10.82	10.55	2.23	2.14	2.15	-1.12	0.080	-1.06	0.700	-1.35	0.000	-1.06	0.456
HDL modelling/destabilisation															
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447
	PLTP	7.65	9.38	8.05	3.72	3.62	3.59	3.32	0.000	-1.07	0.841	1.31	0.171	-1.09	0.465
	endothelial lipase	2.90	3.41	2.65	2.51	2.55	2.42	1.42	0.045	1.03	0.916	-1.19	0.185	-1.06	0.483
	HL	10.82	10.42	10.33	1.77	1.78	1.81	-1.32	0.000	1.01	0.983	-1.40	0.000	1.03	0.839
	GPIHBP1	7.41	7.52	7.85	2.59	2.47	2.44	1.08	0.344	-1.09	0.727	1.36	0.012	-1.11	0.295
	CETP	not measured (not on array)													
HDL uptake															
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009
	FXR	9.78	9.82	10.06	9.04	8.82	8.86	1.03	0.436	-1.16	0.596	1.21	0.028	-1.13	0.398
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051
	SRB1	9.50	8.99	8.68	4.70	4.42	4.46	-1.42	0.001	-1.21	0.790	-1.76	0.000	-1.18	0.571
	ATPsynth	13.07	13.20	13.05				1.10	0.064			-1.01	0.424		

Table 6. Gene expression data of HDL metabolism pathway in liver and intestine with transcription factors and genes involved. The fold change column is colored according to the direction of regulation (red is up-regulated, blue is down-regulated). Significant q-values (or multiple testing adjusted p-values) are marked with bold font type.

In the small intestine, PFOS treatment resulted in up-regulation of a number of genes involved in HDL formation and maturation (APOA2, ABCA1, LXRa, PPARa).

Pathway	common name	Average expression (2log)						Fenofibrate vs control				PFOS vs Control				
		Liver			small intestine			Liver		small intestine		Liver		small intestine		
		Control	Fenofibrate	PFOS	Control	Fenofibrate	PFOS	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value	
Safety and transcription factors																
	safety															
	ALAT	9.58	9.64	9.80	9.95	10.09	10.52	1.04	0.368	1.11	0.688	1.17	0.039	1.49	0.003	
	transcription factors															
	LXRa	6.77	6.76	6.42	5.52	5.93	6.07	-1.01	0.505	1.32	0.131	-1.27	0.008	1.46	0.007	
	LXRb	4.48	4.33	4.37	5.48	5.37	5.58	-1.11	0.271	-1.08	0.683	-1.08	0.277	1.07	0.447	
	PPARa	11.03	11.33	10.55	8.53	8.85	8.97	1.23	0.055	1.25	0.162	-1.40	0.003	1.36	0.009	
	PPARq	5.58	5.28	6.18	6.41	6.56	5.98	-1.23	0.256	1.11	0.756	1.52	0.042	-1.35	0.023	
	CAR	7.46	7.86	8.32	6.63	6.96	6.81	1.32	0.172	1.26	0.332	1.82	0.007	1.13	0.406	
	FXR	9.78	9.82	10.06	9.04	8.82	8.86	1.03	0.436	-1.16	0.596	1.21	0.028	-1.13	0.398	
	PXR	6.74	7.10	7.41	7.96	7.72	8.19	1.28	0.010	-1.18	0.161	1.59	0.000	1.17	0.051	
	PGC1alpha	6.40	6.50	5.12	10.01	9.90	10.00	0.11	0.436	-1.08	0.579	-1.27	0.000	-1.01	0.933	
	PGC1beta	7.00	6.84	6.55	9.04	8.87	9.04	-0.16	0.405	-1.12	0.271	-0.44	0.139	-1.00	0.999	
	PPARd	measured, but not expressed					3.17	2.98	3.08		-1.14	0.172			-1.06	0.381
	CYP3A11	13.53	13.39	13.73	12.87	12.90	13.10	-1.10	0.100	1.02	0.947	1.15	0.013	1.17	0.018	

Table 7. Gene expression data of transcription factors and safety parameters in liver and intestine. The fold change column is colored according to the direction of regulation (red is up-regulated, blue is down-regulated). Significant q-values (or multiple testing adjusted p-values) are marked with bold font type.

At the level of pathways and processes, energy metabolism was observed to be activated by FF and PFOS in liver, and this was also observed in intestine ("Oxidative phosphorylation" cluster in section 2.2). In addition, a down-regulation of inflammation by FF was observed in liver and a similar response was seen in intestine, by inactivation of STAT1 and down-regulation of immune response related processes. At the level of transcription factors relevant for lipid metabolism, the observed LXR activation by both PFOS and FF in liver could also be observed in intestine by PFOS. The main difference with the observations in liver was the apparent lack of strong activation of PPAR α and PPAR γ by FF in intestine.

4 Conclusion

- PFOS has a more extensive effect than FF on the intestinal transcriptome in ApoE3L.CETP mice.
- Oxidative phosphorylation is up-regulated by both FF and PFOS.
- Fatty acid transport is up-regulated by both FF and PFOS, while cholesterol transport is up-regulated by PFOS, but not by FF.
- For the set of preselected lipid metabolism related genes, there are less significantly regulated genes in the intestine as compared to the liver, especially for FF. For PFOS, a number of genes, which were significantly regulated in the liver, were also significantly regulated in the small intestine, but in opposite direction. In the intestine PFOS treatment resulted in up-regulation of a number of genes involved in HDL formation and maturation (APOA2, ABCA1, LXRA, PPARa).
- Several lipid metabolism related transcription factors are activated by both FF and PFOS. PPAR α , PPAR γ and LXR are only activated by PFOS.

5 Appendices

5.1 Quality control & pre-processing evaluation report

Quality Control & Pre-processing Evaluation
of
3M_intestine_microarray
REPORT

Array names and grouping

ArrayDataFile	SourceName	FactorValue
Control-intestine-03.CEL	Control-intestine-03	Control-intestine
Control-intestine-04.CEL	Control-intestine-04	Control-intestine
Control-intestine-06.CEL	Control-intestine-06	Control-intestine
FF-intestine-05.CEL	FF-intestine-05	FF-intestine
FF-intestine-09.CEL	FF-intestine-09	FF-intestine
FF-intestine-10.CEL	FF-intestine-10	FF-intestine
FF-intestine-13.CEL	FF-intestine-13	FF-intestine
FF-intestine-14.CEL	FF-intestine-14	FF-intestine
PFOS-intestine-29.CEL	PFOS-intestine-29	PFOS-intestine
PFOS-intestine-31.CEL	PFOS-intestine-31	PFOS-intestine
PFOS-intestine-32.CEL	PFOS-intestine-32	PFOS-intestine
PFOS-intestine-33.CEL	PFOS-intestine-33	PFOS-intestine
PFOS-intestine-35.CEL	PFOS-intestine-35	PFOS-intestine
Control-intestine-01.CEL	Control-intestine-01	Control-intestine
Control-intestine-02.CEL	Control-intestine-02	Control-intestine

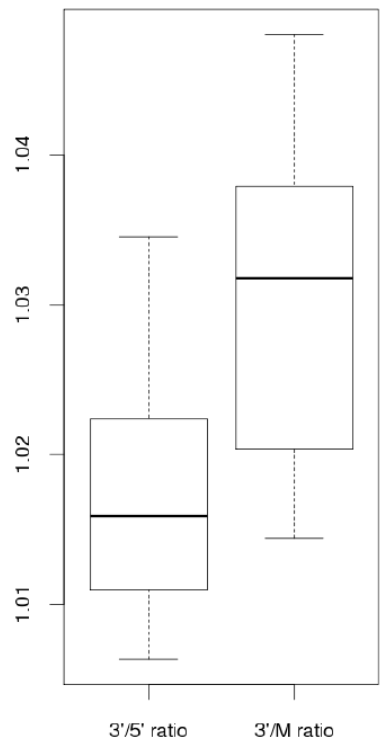
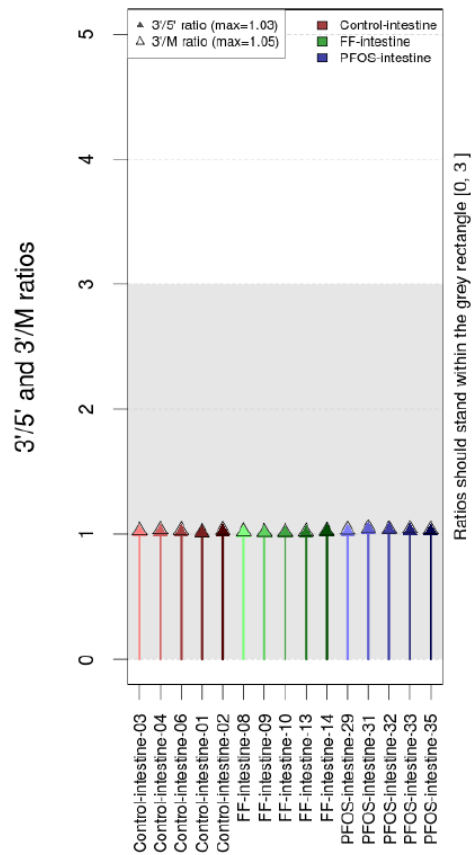
Summary of raw data quality indicators

blue = "within" / red = "out of" recommended cut-off

	3'/5' beta-actin (cut-off=3)	3'/5' GAPDH (cut-off=1.25)	Hybridization BioB-BioC-BioD-CreX	Hybridization BioB- <u>Present</u>	Percent Present spread<=10%	Background spread<=20%	Log Scale Factor spread<=3
Control-intestine-03	1.02	1.02	T	P	56 %	41	-0.8
Control-intestine-04	1.02	0.99	T	P	58 %	48	-1.14
Control-intestine-06	1.01	1.02	T	P	59 %	43	-1.08
Control-intestine-01	1.01	0.99	T	P	59 %	44	-1.32
Control-intestine-02	1.02	1	T	P	58 %	40	-1.05
FF-intestine-08	1.01	1	T	P	58 %	41	-1.15
FF-intestine-09	1.01	1	T	P	58 %	38	-1.05
FF-intestine-10	1.01	1.01	T	P	58 %	44	-1.24
FF-intestine-13	1.01	1.01	T	P	58 %	44	-1.18
FF-intestine-14	1.02	1	T	P	57 %	38	-1.01
PFOS-intestine-29	1.02	1.02	T	P	60 %	41	-0.96
PFOS-intestine-31	1.03	1.02	T	P	57 %	42	-0.65
PFOS-intestine-32	1.03	1.03	T	P	57 %	44	-0.67
PFOS-intestine-33	1.03	1.01	T	P	56 %	50	-0.66
PFOS-intestine-35	1.02	1.01	T	P	58 %	42	-0.76

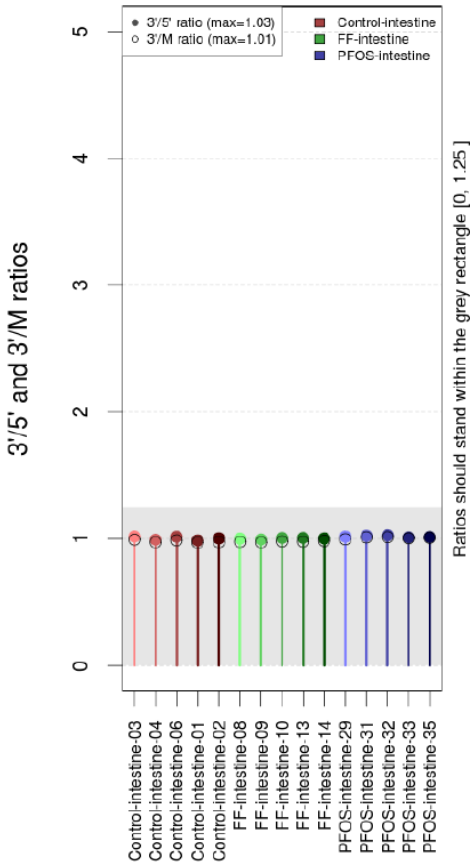
RNA degradation of beta-actin

Boxplot of beta-actin ratios

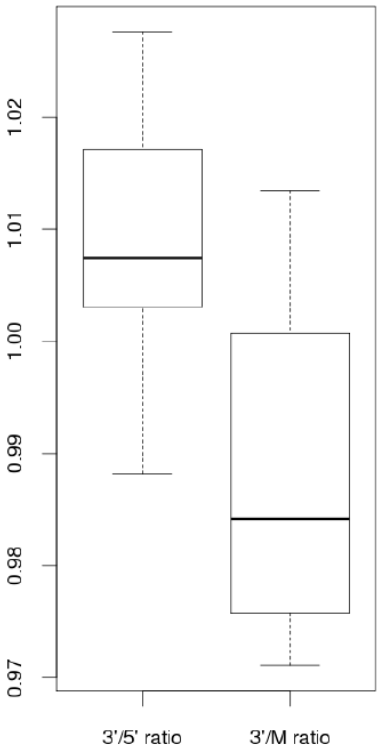


beta-actin QC: OK (all 3'/5' ratios < 3)

RNA degradation of GAPDH

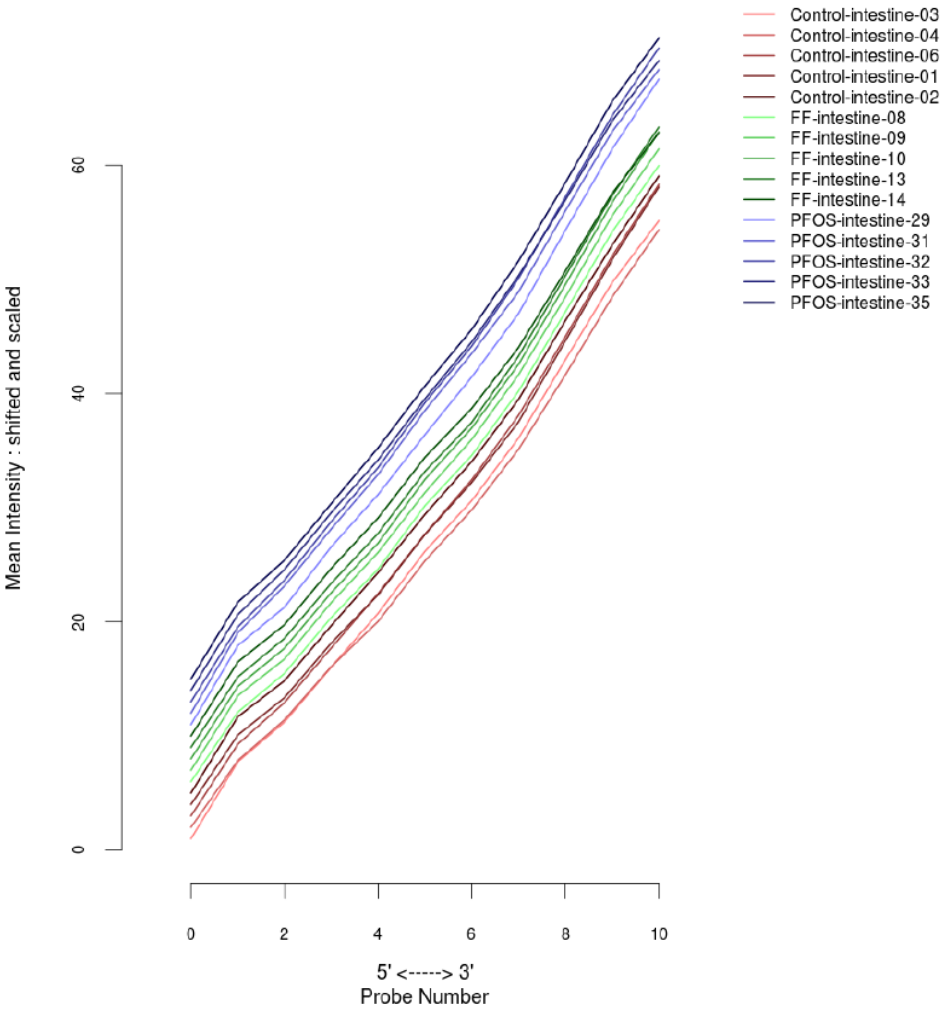


Boxplot of GAPDH ratios

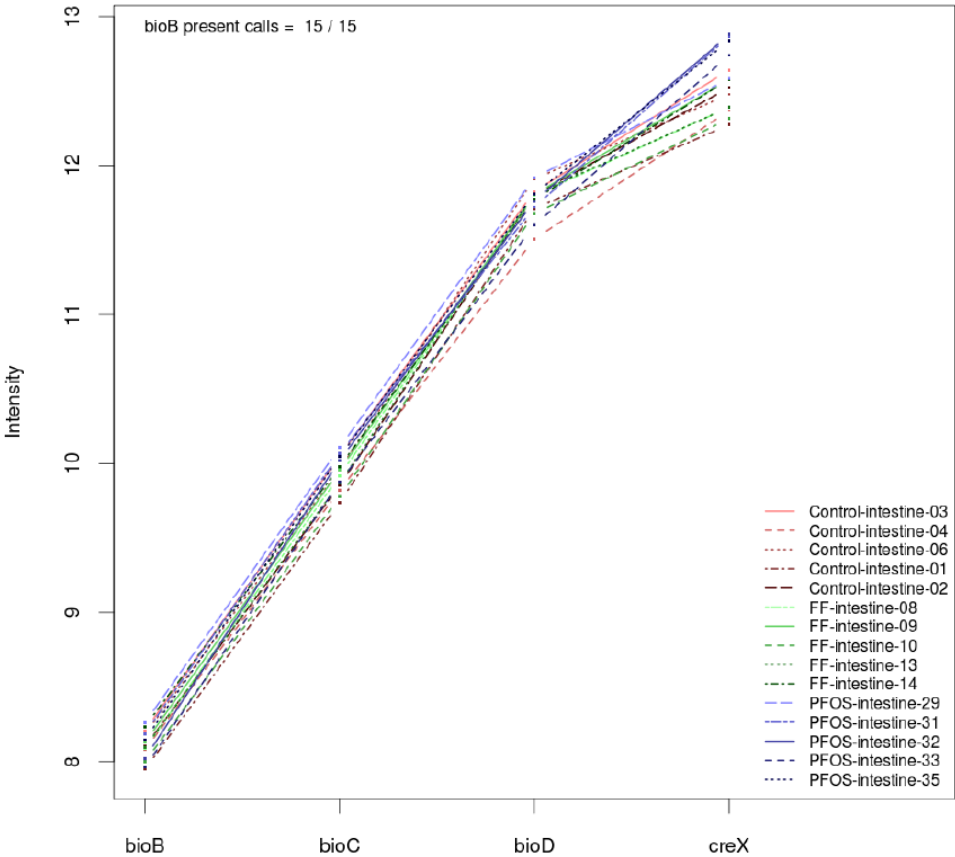


GAPDH QC: OK (all 3'/5' ratios < 1.25)

RNA degradation plot

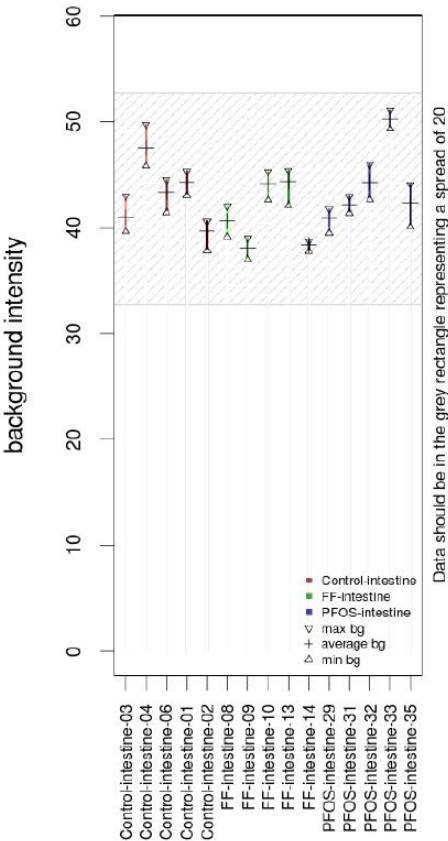


Spike-in Hybridization controls intensities and calls

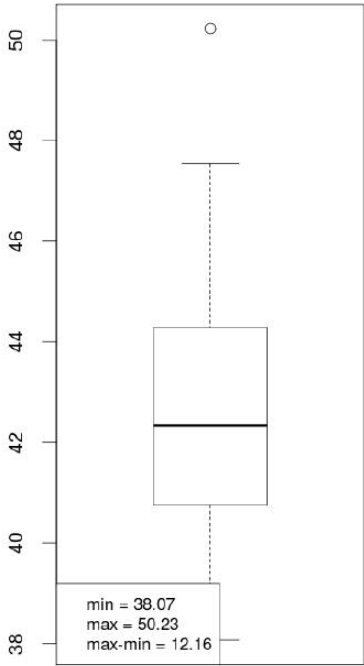


Intensities: OK (bioB < bioC < bioD < creX for all arrays)
BioB Present calls: OK (indeed all bioB are called present)

Plot of background intensity

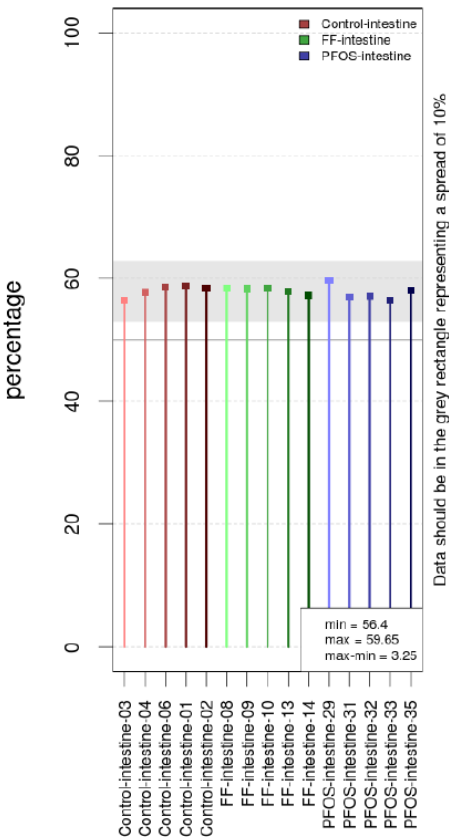


Average background intensity

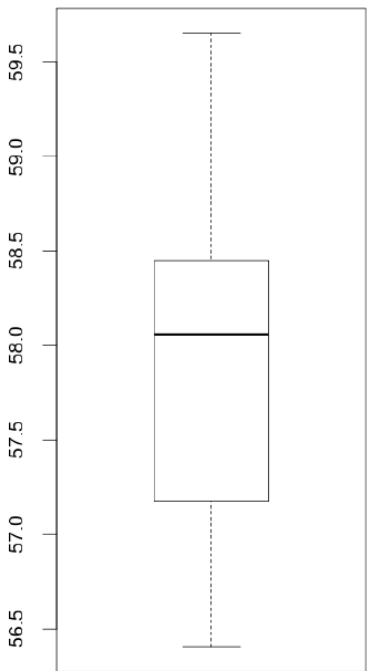


Background QC: OK (spread <= 20)

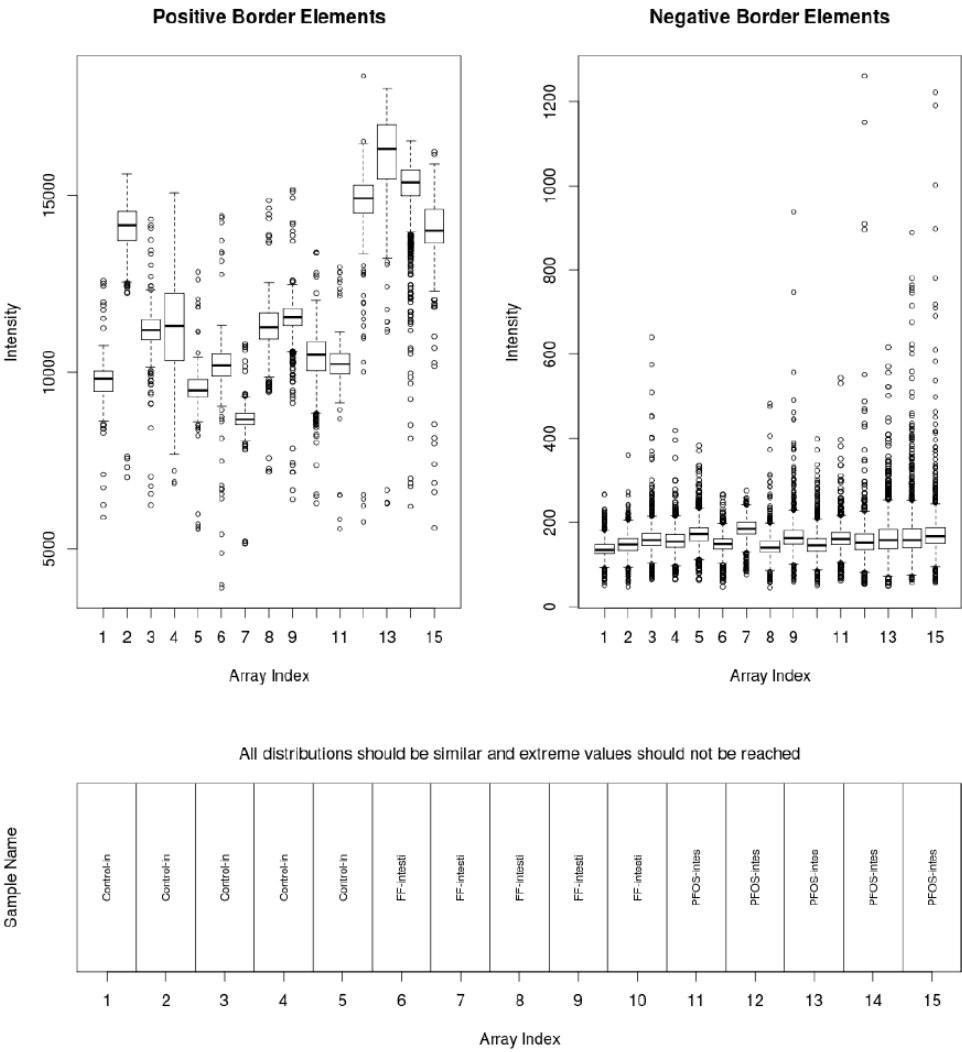
Plot of percent present



Boxplot of percent present

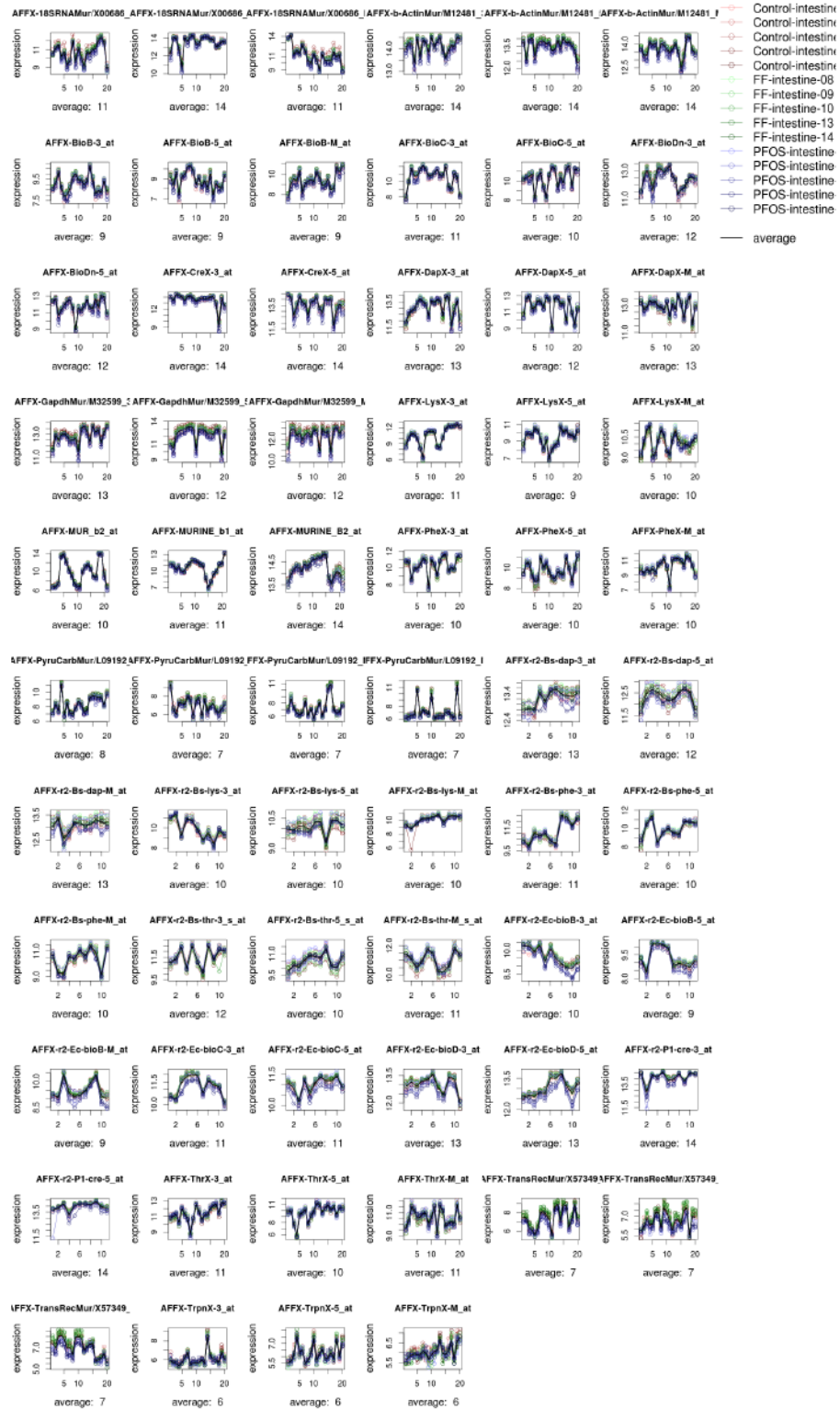


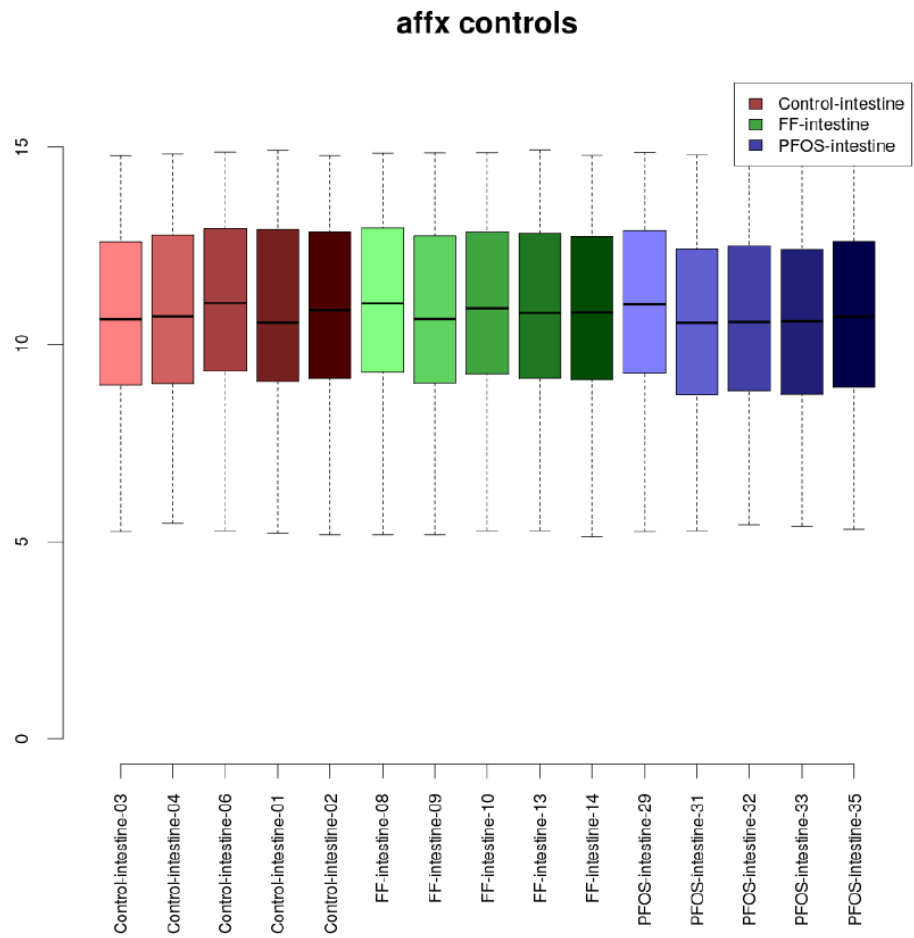
Percent present QC: OK (spread <= 10%)



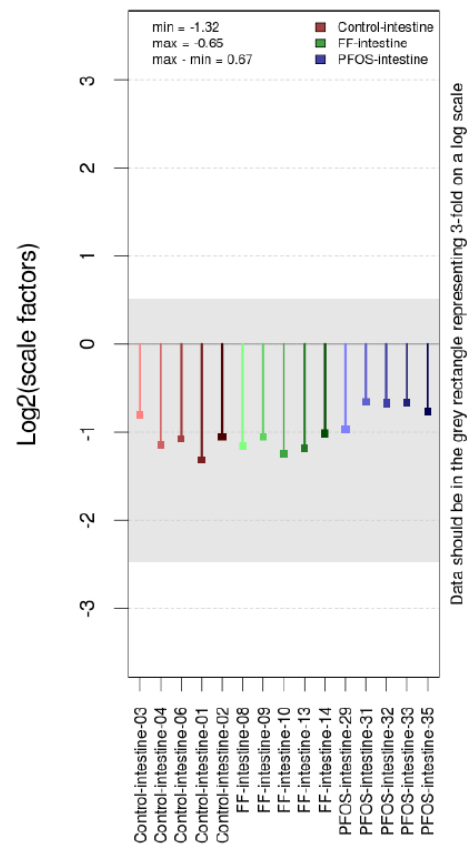
Sample Name

affx control profiles

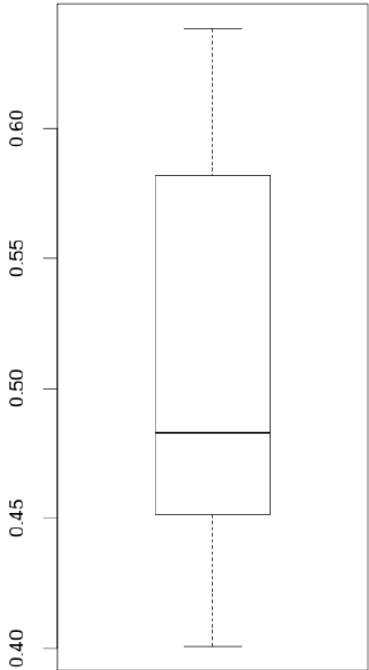




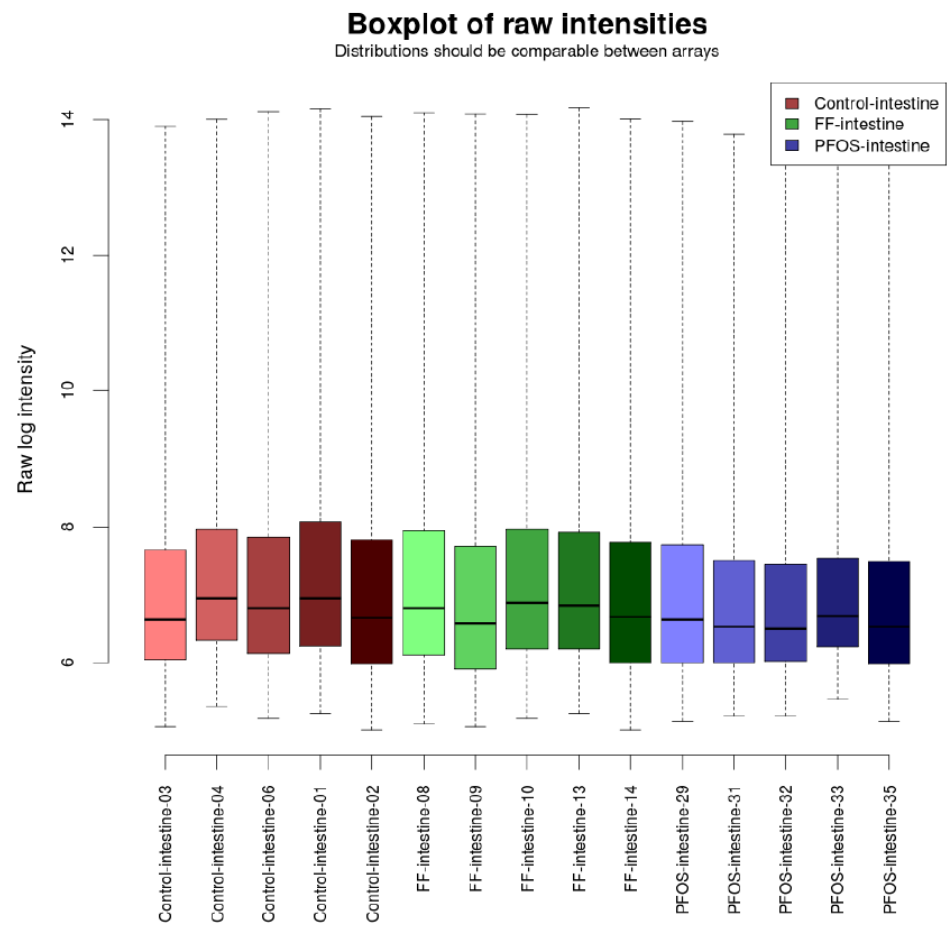
Plot of Log scale factors



Boxplot of scale factors
(natural scale)

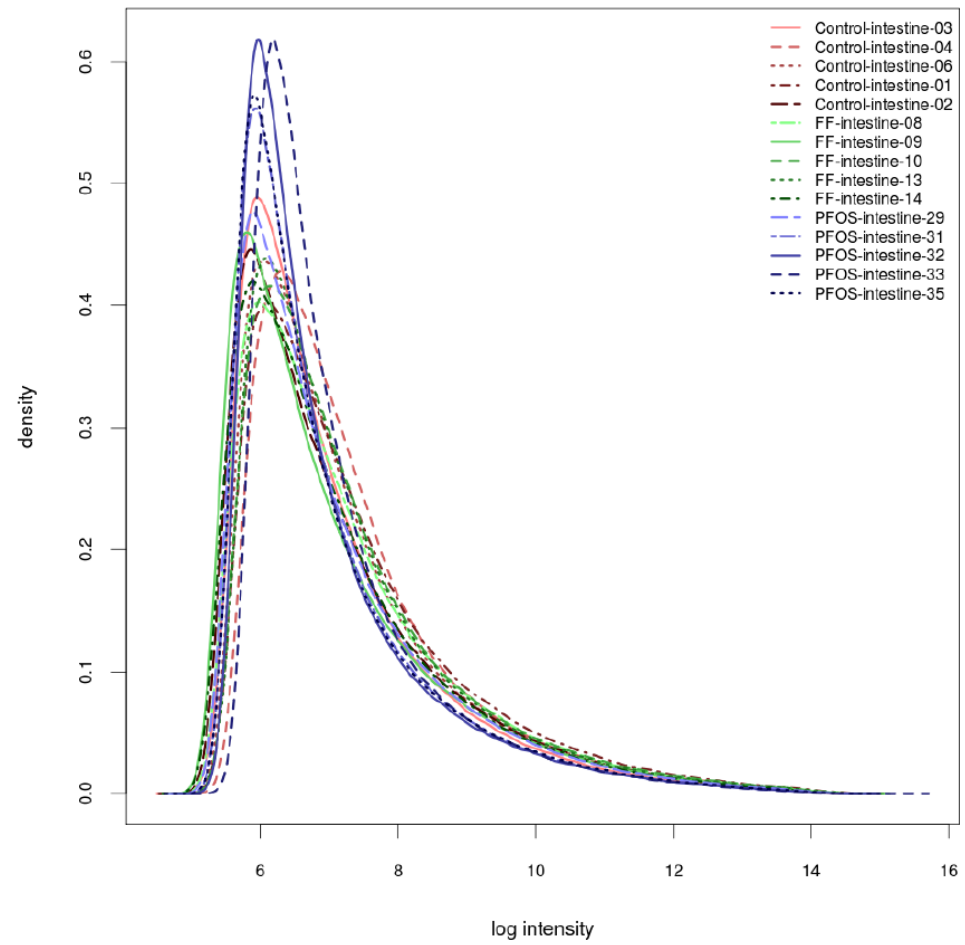


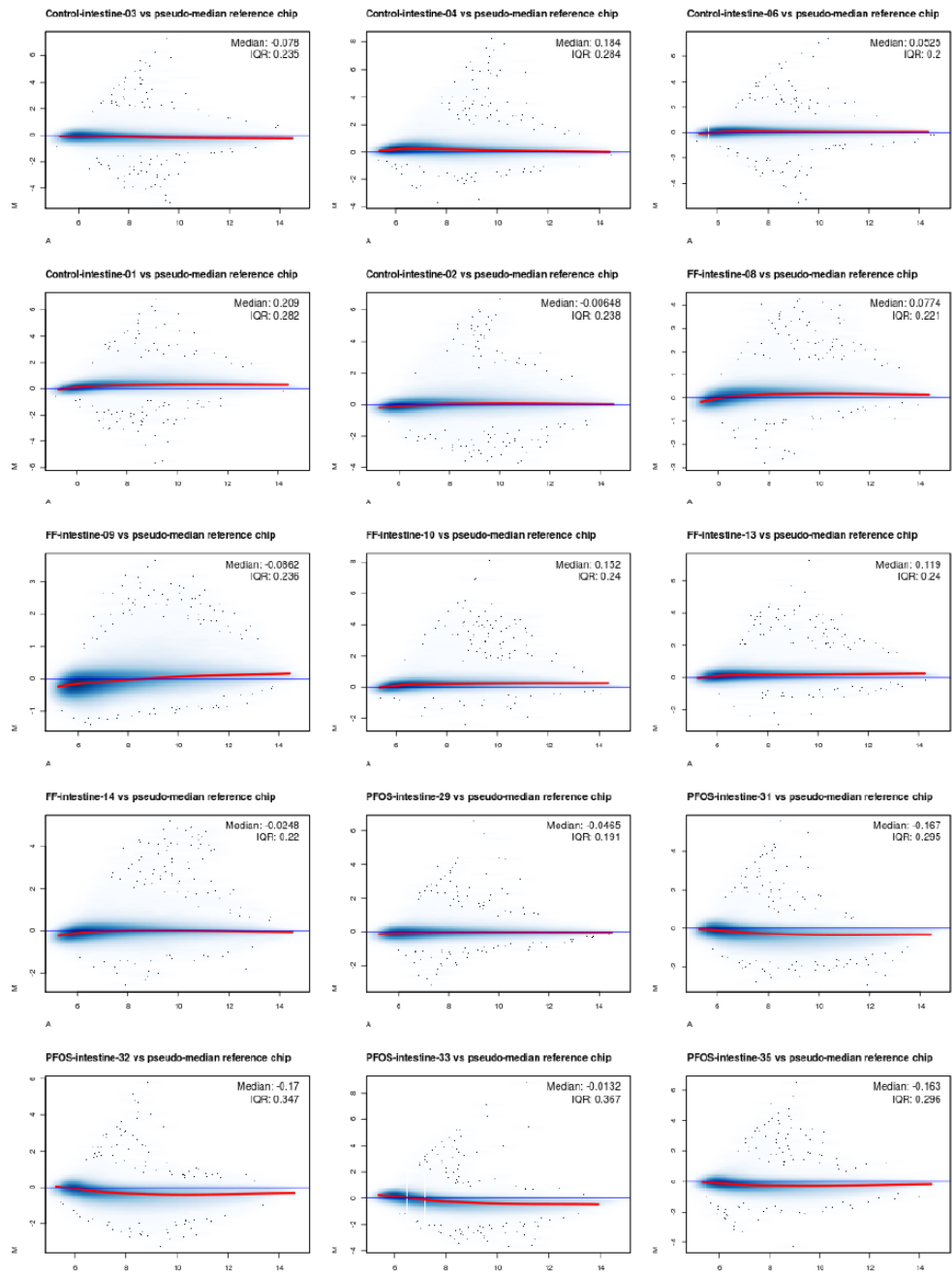
Scale factors QC: OK (spread < 3-fold)



Density histogram of raw intensities

Curves should be comparable between arrays



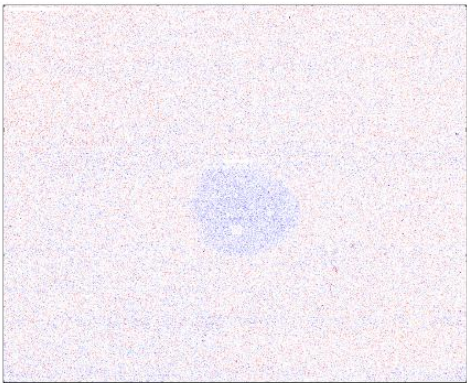
MA plots of raw data

2D virtual PLM image for model characteristic: resids 1 / 3

Control-intestine-03



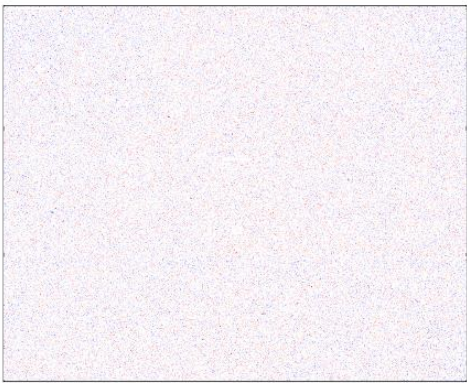
Control-intestine-04



Control-intestine-06



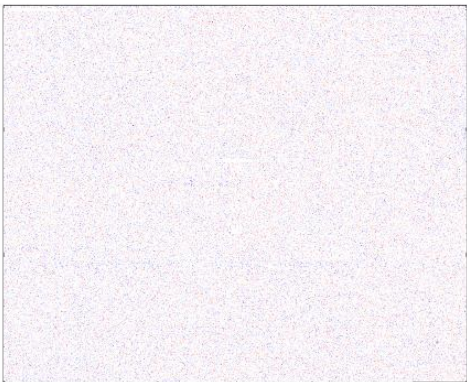
Control-intestine-01

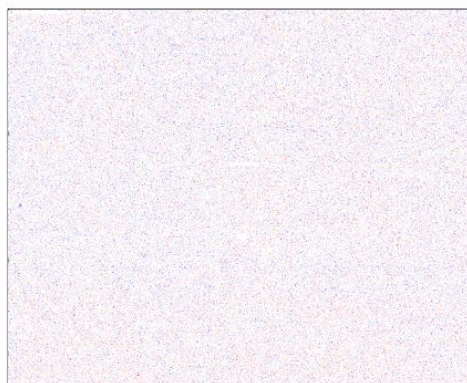
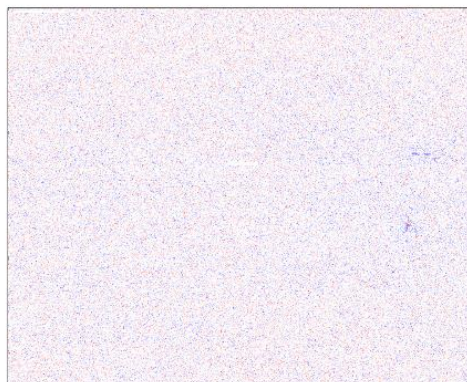


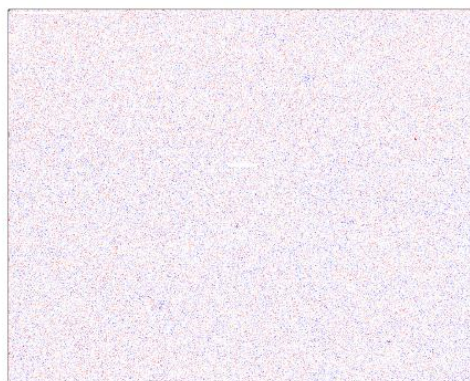
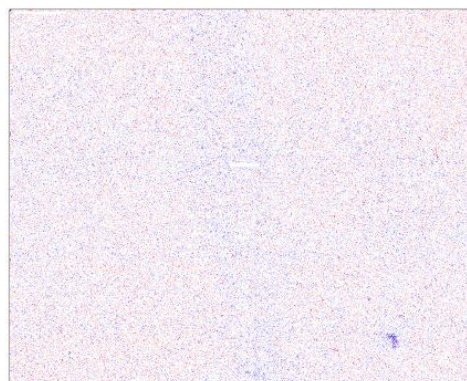
Control-intestine-02



FF-intestine-08

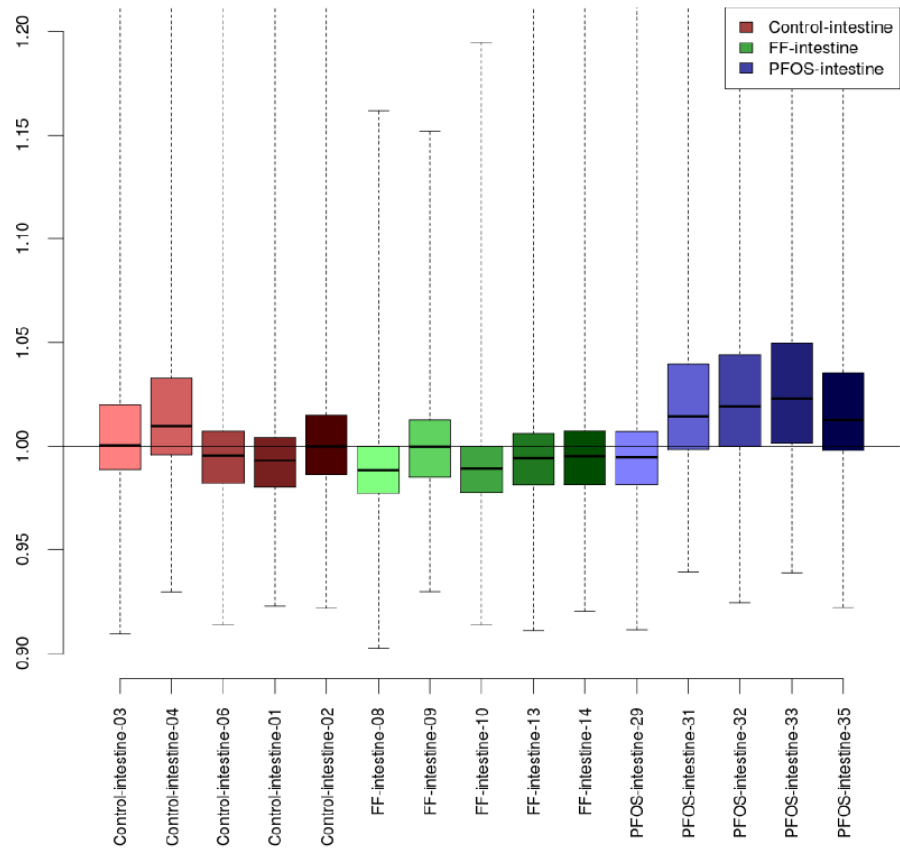


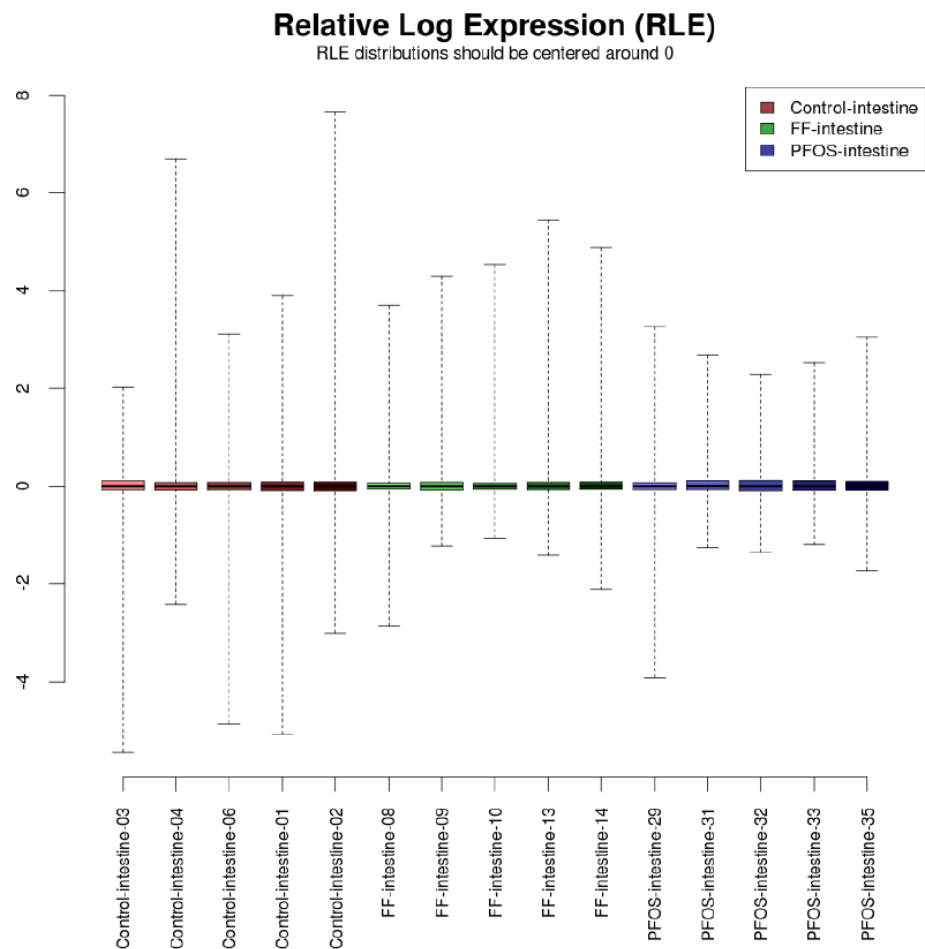
2D virtual PLM image for model characteristic: resids 2 / 3**FF-intestine-09****FF-intestine-10****FF-intestine-13****FF-intestine-14****PFOS-intestine-29****PFOS-intestine-31**

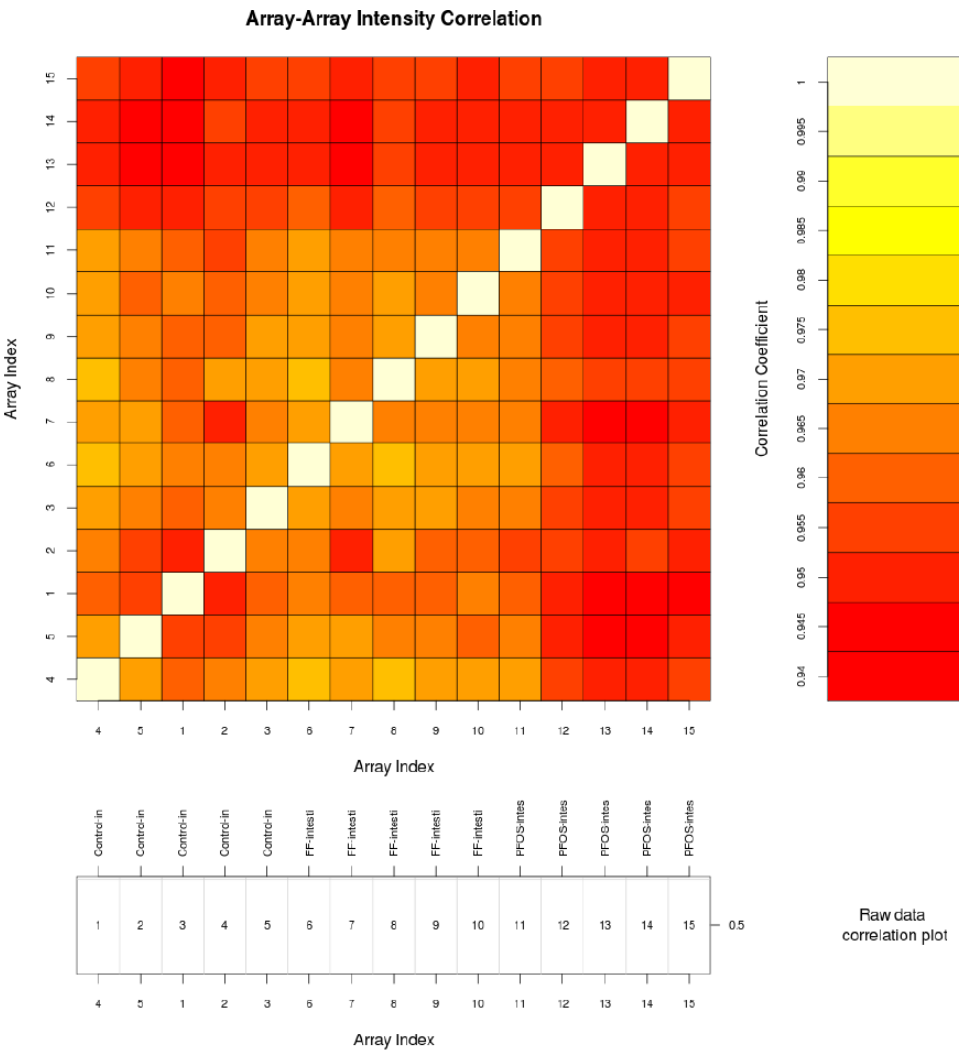
2D virtual PLM image for model characteristic: resids 3 / 3**PFOS-intestine-32****PFOS-intestine-33****PFOS-intestine-35**

Normalized Unscaled Standard Errors (NUSE)

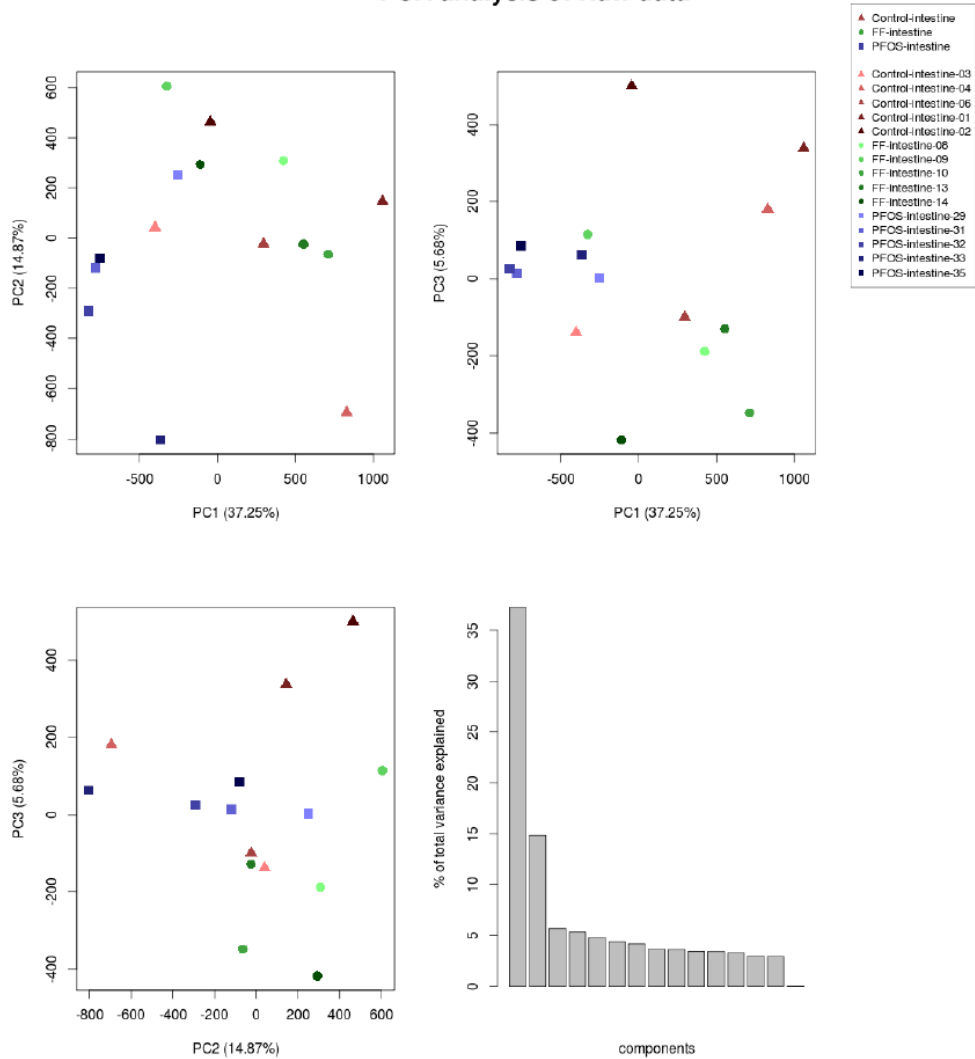
NUSE median value should be < 1.1

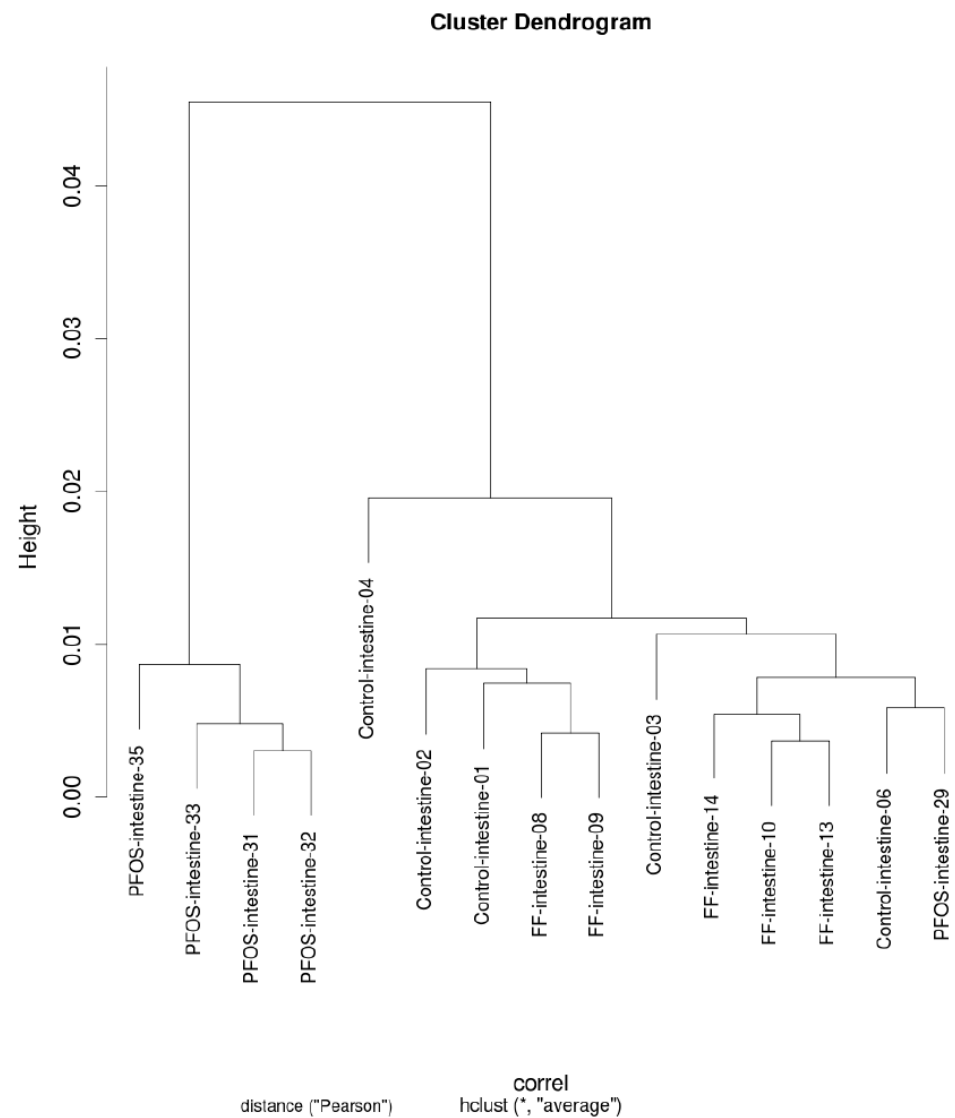






PCA analysis of Raw data

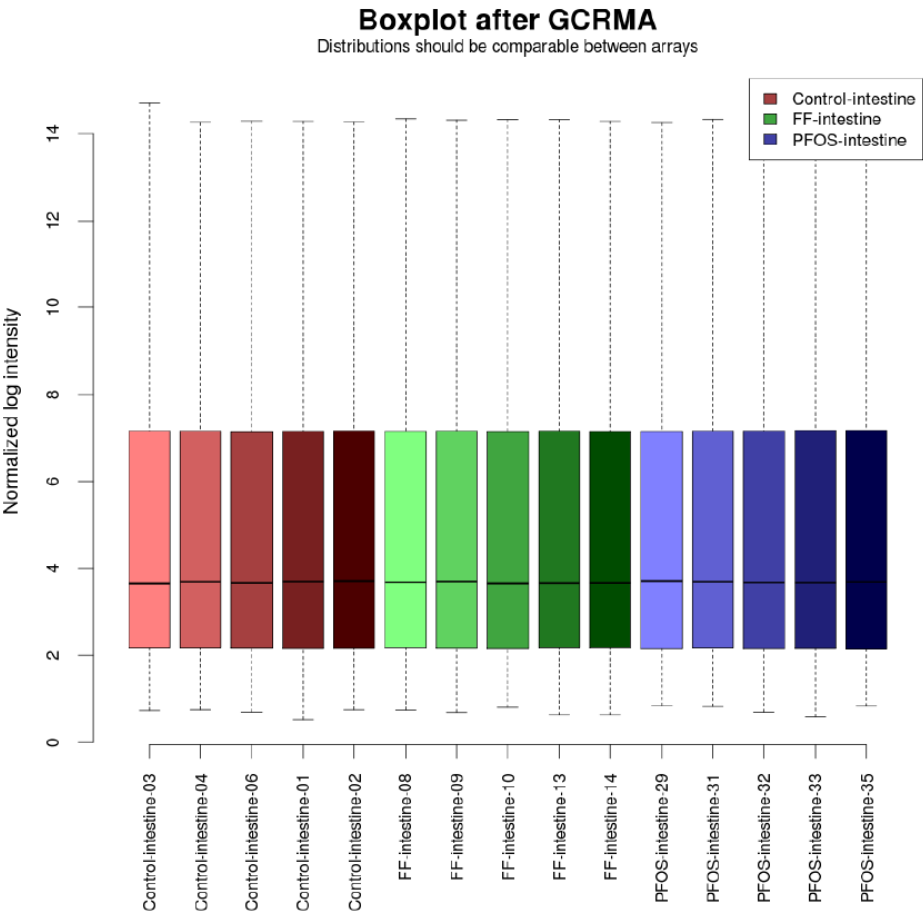




Pre-processing of Raw Data

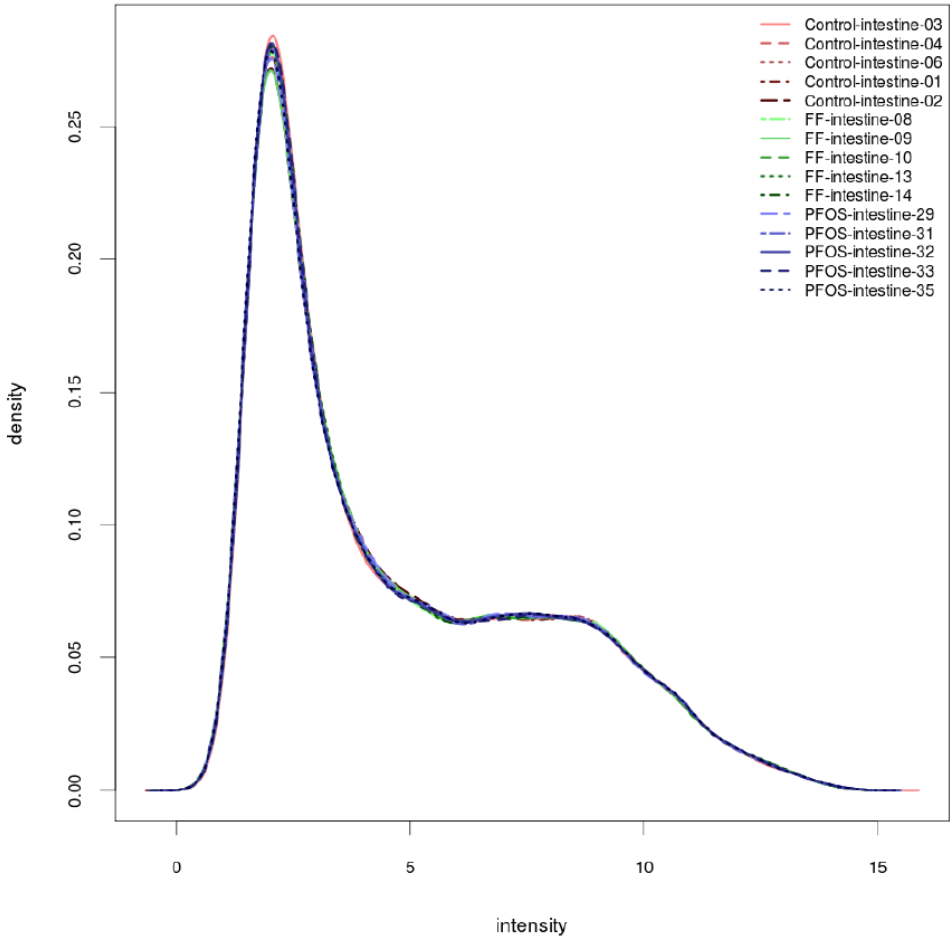
Method: GCRMA

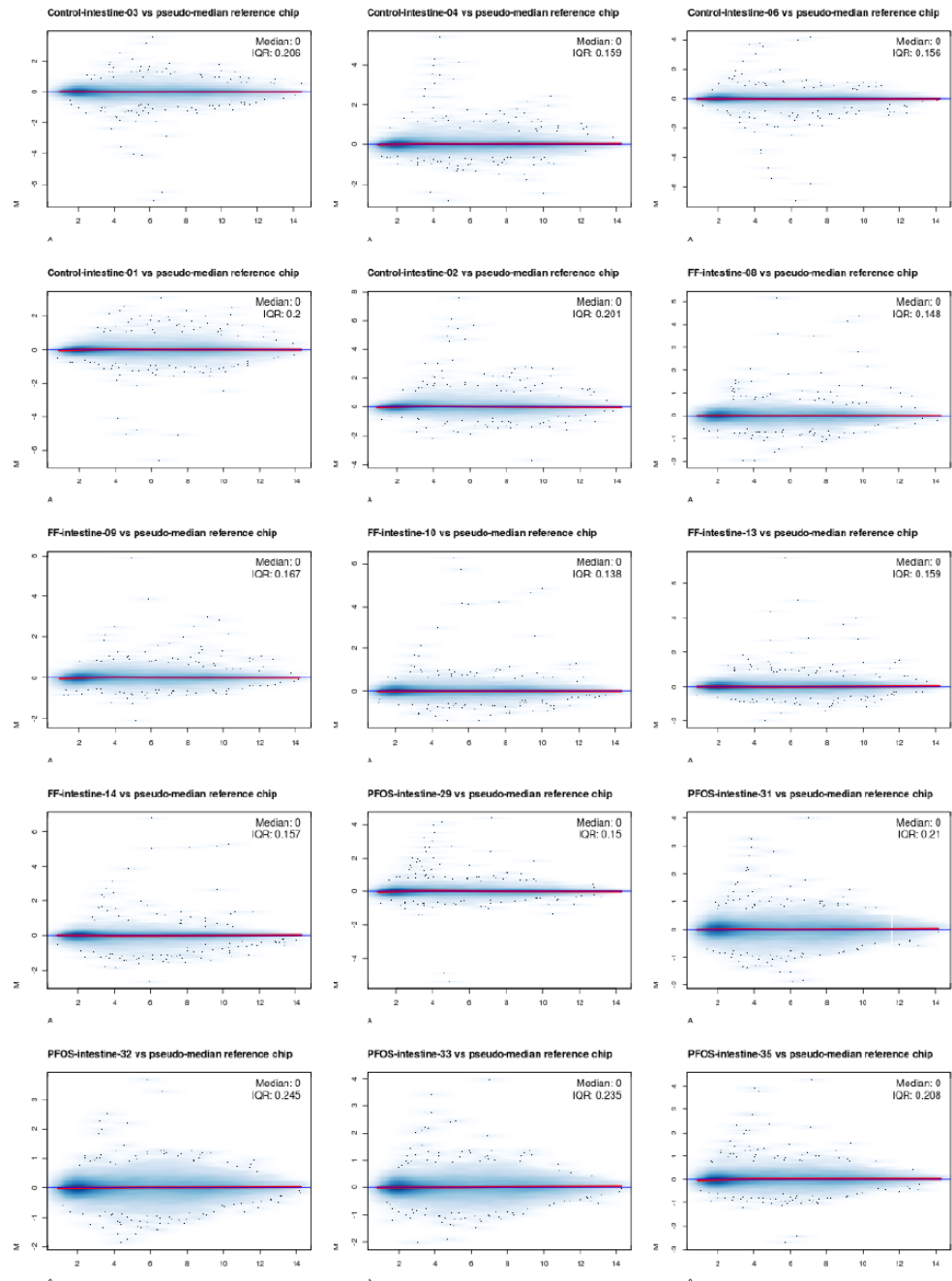
Annotation: mouse4302_Mm_ENTREZG

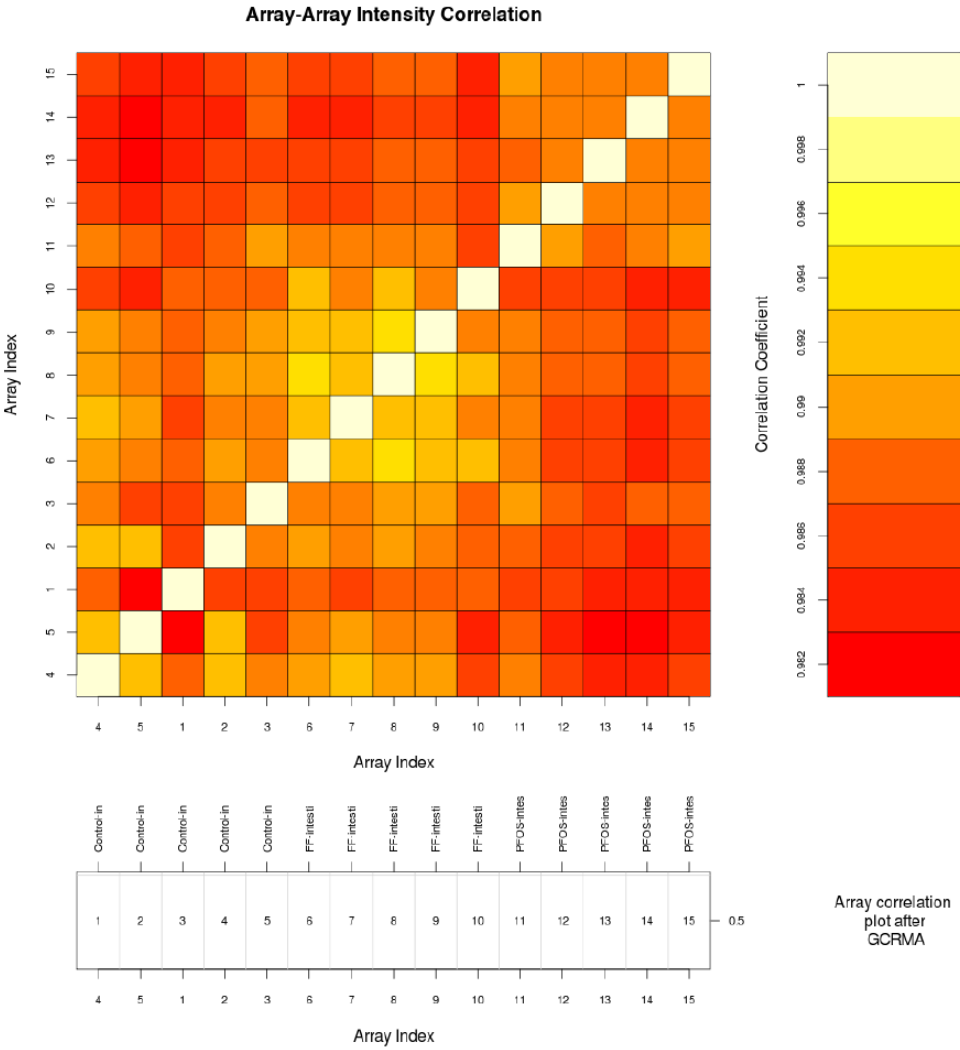


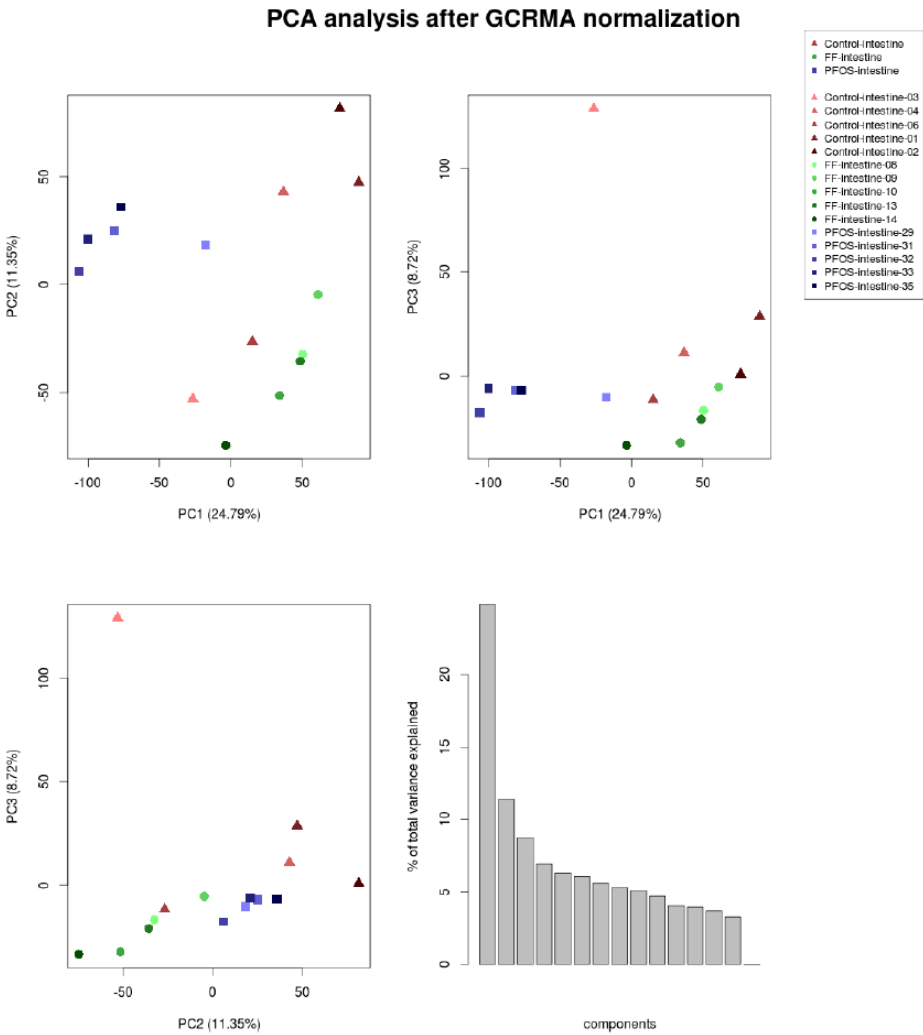
Density histogram after GCRMA

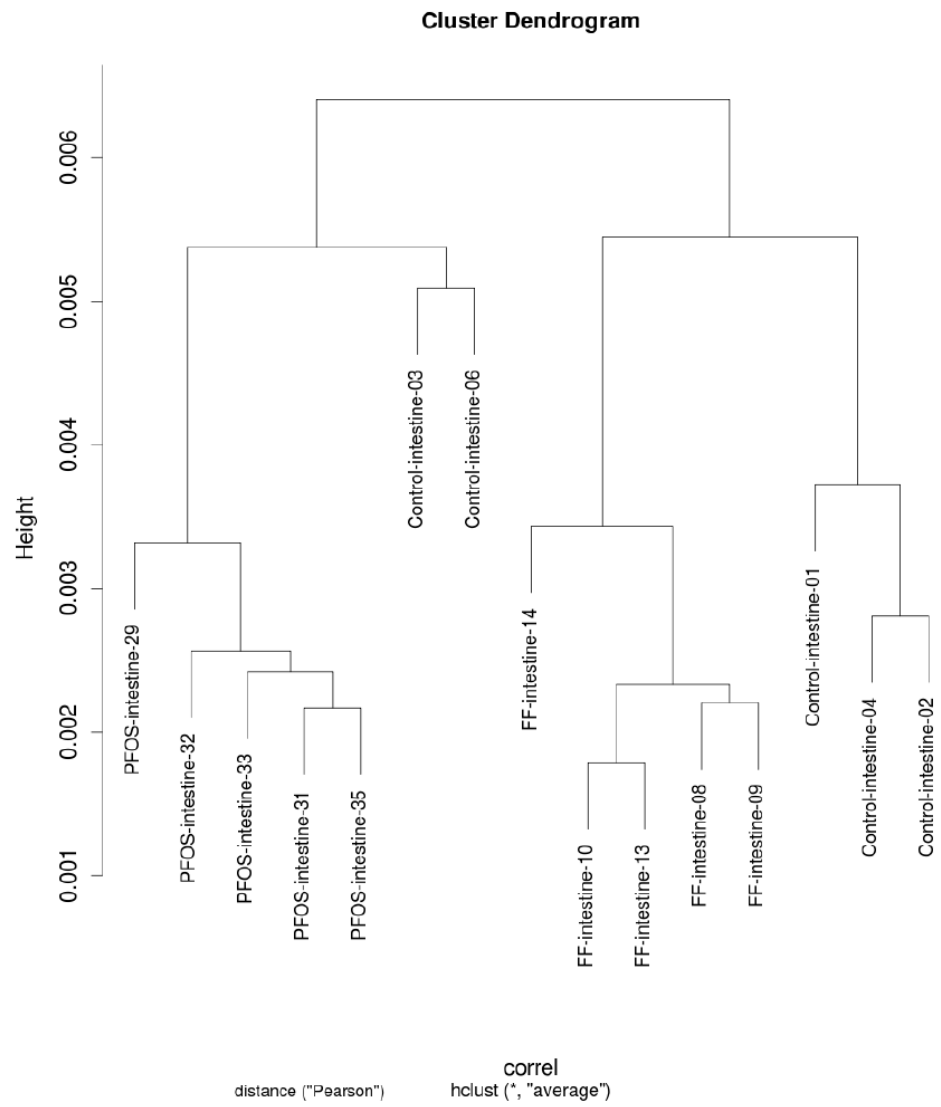
Curves should be comparable between arrays



MA plots afterGCRMANormalization







5.2

Full list of genes related to transport processes that are significantly regulated by FF or PFOS

symbol	entrezid	geneName	NTerms	NrgTermsF	NrgTermsPOS	logFC_Fintestine - ControlIntestine	logFC_POSIntestine - ControlIntestine	adj.p.value_Fintestine - ControlIntestine	adj.p.value_POSIntestine - ControlIntestine
Abca1	11303	ATP-binding cassette, sub-family A (ABC1), member 1	32	1	2	0.399656	0.443072	0.062922	0.009227
Abca7	27403	ATP-binding cassette, sub-family A (ABC1), member 7	4	1	0	-0.00094	0.650276	0.999069	0.009291
Abcb1a	18671	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	3	2	2	0.647908	0.325517	0.022998	0.121306
Abcb6	74104	ATP-binding cassette, sub-family B (MDR/TAP), member 6	11	0	1	0.183483	0.531006	0.749729	0.024208
Abcc3	76408	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	10	6	3	0.190597	0.429963	0.497141	0.009291
Abcc6	27421	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	1	0	1	0.302609	0.759864	0.366495	0.002501
Abcc9	20928	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	10	0	1	0.044795	0.415312	0.937047	0.010117
Abp1	76507	amiloride binding protein 1 (amine oxidase, copper-containing)	8	3	1	0.161802	0.479711	0.727145	0.016058
Accn2	11419	amiloride-sensitive cation channel 2, neuronal	24	1	2	0.152625	0.409895	0.592576	0.007644
Ace	11421	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	12	6	1	0.784505	0.727529	0.006213	0.003035
Acs14	50790	acyl-CoA synthetase long-chain family member 4	6	5	1	-0.18116	-0.36163	0.557141	0.024669
Acs15	433256	acyl-CoA synthetase long-chain family member 5	21	8	4	0.063527	0.199619	0.760815	0.018622
Acs16	216739	acyl-CoA synthetase long-chain family member 6	21	8	4	1.0891	-0.90881	0.040072	0.023157
Acvr1c	269275	activin A receptor, type IC	21	0	1	0.063323	-0.47373	0.833871	0.000929
Acvr2b	11481	activin receptor IIB	8	0	1	0.153941	0.698501	0.799134	0.005582
Adipor2	68465	adiponectin receptor 2	12	2	1	-0.06442	0.230315	0.770504	0.011298
Ahcy1	229709	S-adenosylhomocysteine hydrolase-like 1	21	1	3	-0.37372	-0.42173	0.190859	0.030787
Al317395	215929	expressed sequence Al317395	8	3	2	0.111607	0.211313	0.550928	0.030787
Ano6	105722	anoctamin 6	6	0	1	0.175448	0.611481	0.783741	0.015336
Apoa1	11806	apolipoprotein A-I	40	1	1	-0.01329	0.173023	0.966169	0.021629
Apoa2	11807	apolipoprotein A-II	50	2	1	-0.01566	1.580966	0.996524	0.005314
Apoa4	11808	apolipoprotein A-IV	14	1	0	0.020732	0.148084	0.940375	0.045426
ApoB	238055	apolipoprotein B	5	1	0	0.029621	0.223128	0.937047	0.027932
ApoC1	11812	apolipoprotein C-I	15	1	0	0.157078	2.462546	0.937047	0.004042
ApoC2	11813	apolipoprotein C-II	16	1	0	0.053058	0.201099	0.832106	0.021869
ApoH	11818	apolipoprotein H	4	1	0	0.151326	1.007759	0.873732	0.04207
Aqp11	66333	aquaporin 11	12	10	4	0.318079	0.102976	0.007666	0.233873
Aqp3	11828	aquaporin 3	13	10	4	0.995629	0.098848	0.004761	0.727164
Aqp8	11833	aquaporin 8	9	6	2	-0.67865	-0.66762	0.073379	0.018359
Arg1	11846	arginase, liver	18	5	2	0.048994	0.559133	0.959328	0.017292
Arr1	56327	ADP-ribosylation factor-like 2	5	3	1	0.050604	0.352622	0.931033	0.025478
Arrb1	109689	arrestin, beta 1	24	0	1	-0.49137	-0.14646	0.005644	0.234627
Atp11c	320940	ATPase, class VI, type 11C	7	1	1	-0.04243	-0.21206	0.893349	0.025998
Atp13a1	170759	ATPase type 13A1	4	0	1	-0.06755	0.464935	0.896673	0.006346
Atp1a1	11928	ATPase, Na+/K+ transporting, alpha 1 polypeptide	17	2	4	-0.02663	0.227368	0.937499	0.016509
Atp2a2	11938	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	9	0	1	-0.15996	0.293949	0.30994	0.007105
Atp6ap1	54411	ATPase, H+ transporting, lysosomal accessory protein 1	9	0	2	-0.02095	0.267693	0.965148	0.021688
Atp6v0a1	11975	ATPase, H+ transporting, lysosomal V0 subunit A1	9	0	2	-0.04705	0.258139	0.89016	0.015642
Atp6v0b	114143	ATPase, H+ transporting, lysosomal V0 subunit B	9	0	2	0.169058	0.402685	0.51217	0.008013
Atp8a1	11980	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	7	1	1	0.010816	0.218926	0.977073	0.025805
Atp9a	11981	ATPase, class II, type 9A	7	1	1	-0.04623	0.40869	0.947516	0.024436
Atp9b	50771	ATPase, class II, type 9B	7	1	1	-0.04279	0.386669	0.94032	0.015204
Casp1	12362	caspase 1	23	0	1	-0.10122	-0.4163	0.738429	0.042229
Cd209d	170779	CD209d antigen	14	0	1	0.153148	-0.2469	0.486298	0.04105
Cd36	12491	CD36 antigen	20	7	3	0.902176	0.362312	0.00033	0.027626
Cdk1	12534	cyclin-dependent kinase 1	7	0	1	0.017304	-0.49792	0.981254	0.009501
Chd7	320790	chromodomain helicase DNA binding protein 7	15	0	1	0.009645	0.385672	0.989581	0.012078
Clcc1	229725	chloride channel CLIC-like 1	6	0	1	-0.00513	-0.4766	0.994731	0.003985
Clcn2	12724	chloride channel 2	11	0	1	0.266597	0.485785	0.497141	0.025734
Clcn6	209195	chloride intracellular channel 6	11	0	1	-0.20646	-0.5004	0.712674	0.037156
Cln8	26889	ceroid-lipofuscinosis, neuronal 8	19	5	1	0.325705	0.555563	0.283398	0.00833
Cox6b2	333182	cytochrome c oxidase subunit VIb polypeptide 2	7	0	2	0.753322	0.390843	0.018151	0.092848
Cox8a	12868	cytochrome c oxidase, subunit VIIIa	7	0	2	-0.07609	0.308031	0.87596	0.045084
Cpt1a	12894	carnitine palmitoyltransferase 1a, liver	15	0	1	-0.01444	-0.28829	0.975637	0.013998
Crym	12971	crystallin, mu	9	5	1	-0.79748	-0.6698	0.042898	0.023736
Dab2ip	69601	disabled homolog 2 (Drosophila) interacting protein	8	0	1	-0.00689	0.447806	0.994515	0.013981
Dgat1	13350	diacylglycerol O-acyltransferase 1	8	0	1	0.037053	0.304442	0.904421	0.003941
Ect2	13605	ect2 oncogene	8	0	1	0.141677	-0.70672	0.749423	0.002025
Edn1	13614	endothelin 1	32	5	3	0.176555	0.765875	0.715584	0.00265
Ednra	13617	endothelin receptor type A	30	4	3	-0.0406	-0.25499	0.934754	0.047703
Eif2ak3	13666	eukaryotic translation initiation factor 2 alpha kinase 3	10	0	1	0.045459	0.20845	0.857987	0.015369
Ensa	56205	endosulfine alpha	15	0	1	0.208171	0.366669	0.271678	0.006687
F2	14061	coagulation factor II	20	0	1	-0.06089	0.529375	0.937419	0.014676
F2r11	14063	coagulation factor II (thrombin) receptor-like 1	35	0	1	0.297781	0.381454	0.311549	0.039481
Fabp2	14079	fatty acid binding protein 2, intestinal	7	6	1	0.044313	0.17663	0.85241	0.026936
Fgf15	14170	fibroblast growth factor 15	12	2	1	2.54446	-1.20891	0.044856	0.267921
Flna	192176	filamin, alpha	11	0	1	-0.1137	0.530728	0.866314	0.017623
Fxyd1	56188	FXYD domain-containing ion transport regulator 1	6	0	1	0.036859	0.232738	0.933788	0.044598
G6pc	14377	glucose-6-phosphatase, catalytic	7	4	3	-1.14837	-0.37791	0.007171	0.21849
Gc	14473	group specific component	2	0	1	-0.45751	3.119747	0.841228	0.001793
Gcg	14526	glucagon	45	0	3	-0.09799	-0.75361	0.930566	0.014711
Glud1	14661	glutamate dehydrogenase 1	21	0	1	0.425597	0.272193	0.007666	0.022478
Grid1	14803	glutamate receptor, ionotropic, delta 1	3	0	1	-0.18859	-0.30674	0.429515	0.027416
Hiat1	15247	hippocampus abundant gene transcript 1	3	2	1	-0.01918	-0.28194	0.966169	0.012361
Hnf1b	21410	HNF1 homeobox B	8	0	1	0.087007	0.290049	0.735501	0.010307
Hyal2	15587	hyaluronoglucosaminidase 2	8	0	1	0.023106	0.482602	0.979805	0.035606
Inpp5k	19062	inositol polyphosphate 5-phosphatase K	28	4	2	0.079199	0.35521	0.861179	0.018917
Ins2	16334	insulin II	32	2	3	-0.21908	0.783639	0.777905	0.012778
Irs2	384783	insulin receptor substrate 2	50	8	5	0.091281	0.725428	0.895841	0.003302
Itln1	16429	interlectin 1 (galactofuranose binding)	12	2	1	-0.35147	-1.15251	0.797986	0.025478
Jak2	16452	Janus kinase 2	26	0	2	0.192332	0.248992	0.317905	0.039033
Kcne3	57442	potassium voltage-gated channel, Isk-related subfamily, gene 3	15	0	2	-0.01238	-0.54301	0.987636	0.005582
Kcnj13	1E+08	potassium inwardly-rectifying channel, subfamily J, member 13	13	0	1	0.532385	1.229739	0.695929	0.039302
Kcnk1	16525	potassium channel, subfamily K, member 1	13	0	1	-0.39943	-0.47967	0.295787	0.046719
Kcnk2	16526	potassium channel, subfamily K, member 2	13	0	1	-0.13396	-0.37865	0.669314	0.011706
Kcnmb4	58802	potassium large conductance calcium-activated channel, subfamily M, beta member 4	9	0	1	-0.13078	-0.33273	0.753024	0.045317
Kcns3	238076	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	13	0	1	-0.16044	-0.4995	0.735686	0.014497
Kctd12	239217	potassium channel tetramerisation domain containing 12	13	0	1	-0.16122	-0.36113	0.509127	0.010645
Kctd14	233529	potassium channel tetramerisation domain containing 14	3	0	1	-0.89441	-0.77891	0.014797	0.008225

symbol	entrezid	geneName	NTerms	NsigTermsF	NsigTermsP	adj.p.value_Fintestine - ControlIntestine	adj.p.value_Fintestine - ControlIntestine	adj.p.value_Fintestine - ControlIntestine	adj.p.value_Fintestine - ControlIntestine
Kctd2	70382	potassium channel tetramerisation domain containing 2	3	0	1	0.047733	0.298621	0.925083	0.028887
Kctd3	226823	potassium channel tetramerisation domain containing 3	13	0	1	0.069391	-0.40473	0.788429	0.001624
Kctd5	69259	potassium channel tetramerisation domain containing 5	13	0	1	0.19762	0.429141	0.691295	0.048482
Lrp6	16974	low density lipoprotein receptor-related protein 6	4	1	0	0.114634	0.478049	0.762022	0.005141
Ly6e	17069	lymphocyte antigen 6 complex, locus E	12	6	2	-1.28866	-0.37615	0.046399	0.454807
Maob	109731	monoamine oxidase B	16	5	3	0.440557	0.317027	0.008297	0.013554
Mcoln1	94178	mucolin 1	8	0	1	-0.02106	0.497028	0.974988	0.00504
Mfsd2a	76574	major facilitator superfamily domain containing 2A	1	0	1	0.125095	0.596174	0.60803	0.000608
Mfsd4	213006	major facilitator superfamily domain containing 4	1	0	1	-0.79317	-0.79339	0.005225	0.001793
Mfsd7b	226844	major facilitator superfamily domain containing 7B	3	1	1	0.3956	0.10223	0.006213	0.006527
Mfsd7c	217721	major facilitator superfamily domain containing 7C	3	0	1	-0.08691	0.573341	0.936613	0.045945
Micu1	216001	mitochondrial calcium uptake 1	10	0	1	-0.01441	0.377713	0.982402	0.018464
Mtpp	17777	microsomal triglyceride transfer protein	3	1	0	0.133673	0.195492	0.319022	0.022373
Ncor1	20185	nuclear receptor co-repressor 1	6	1	0	-0.08704	0.200554	0.643859	0.024887
Nisch	64652	nischarin	11	6	2	-0.02737	0.324073	0.960015	0.016271
Npc1l1	237636	NPC1-like 1	5	1	0	-0.03833	0.396216	0.939331	0.007571
Nr1h3	22259	nuclear receptor subfamily 1, group H, member 3	33	1	0	0.403793	0.549647	0.130928	0.007425
Osbp	76303	oxysterol binding protein	2	1	0	-0.07725	0.403201	0.848016	0.006589
Osbpl1a	64291	oxysterol binding protein-like 1A	2	1	0	0.513282	0.927176	0.132895	0.002158
Osbpl3	71720	oxysterol binding protein-like 3	2	1	0	0.04968	0.539486	0.942016	0.007642
Osbpl6	99031	oxysterol binding protein-like 6	2	1	0	0.316648	0.304845	0.081215	0.022993
Oxct1	67041	3-oxoacid CoA transferase 1	21	0	1	-0.25651	-0.59546	0.311599	0.002626
Panx1	55991	pannexin 1	32	0	2	-0.00984	0.495011	0.993677	0.033467
Pde2a	207728	phosphodiesterase 2A, cGMP-stimulated	7	0	1	-0.09359	0.433702	0.902368	0.048423
Pdx1	18609	pancreatic and duodenal homeobox 1	21	0	1	-0.33146	-0.42615	0.3534	0.048006
Pdzk1	59020	PDZ domain containing 1	22	6	3	0.056647	0.413572	0.856599	0.001793
Pex6	224824	peroxisomal biogenesis factor 6	3	0	1	-0.02275	0.27801	0.958978	0.012196
Pla2g10	26565	phospholipase A2, group X	43	6	1	0.156002	-0.79189	0.859852	0.010252
Pla2g4a	18783	phospholipase A2, group IVA (cytosolic, calcium-dependent)	14	6	1	-0.29945	-0.77389	0.584626	0.008606
Plin2	11520	perilipin 2	7	6	1	0.206783	0.521268	0.420011	0.003347
Pon1	18979	paraoxonase 1	17	1	0	0.174068	1.396351	0.865544	0.001487
Ppara	19013	peroxisome proliferator activated receptor alpha	6	1	0	0.321693	0.443231	0.161773	0.009227
Pparg	19016	peroxisome proliferator activated receptor gamma	8	6	1	0.144239	-0.42981	0.755749	0.02256
Ppp3ca	19055	protein phosphatase 3, catalytic subunit, alpha isoform	28	0	1	0.06944	0.273893	0.87504	0.048738
Prdx1	18477	peroxiredoxin 1	5	0	1	0.095605	-0.44139	0.81134	0.005837
Prkcz	18762	protein kinase C, zeta	33	2	2	0.112041	0.334825	0.759278	0.023398
Psmd10	53380	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	9	0	1	0.000135	-0.21582	0.999681	0.027748
Ptger4	19219	prostaglandin E receptor 4 (subtype EP4)	19	0	1	-0.42468	-0.25817	0.008533	0.03101
Pycard	66824	PYD and CARD domain containing	20	0	1	-0.08654	-0.26571	0.67821	0.008606
Rbp4	19662	retinol binding protein 4, plasma	36	1	1	0.261886	1.015488	0.85663	0.032793
Rhbg	58176	Rhesus blood group-associated B glycoprotein	9	1	2	-0.03312	0.498486	0.973937	0.035606
Scamp5	56807	secretory carrier membrane protein 5	15	0	1	-0.29237	-0.06228	0.043992	0.59737
Sfxn1	14057	sideroflexin 1	7	0	1	0.096887	0.206911	0.520767	0.01421
Sfxn5	94282	sideroflexin 5	11	3	1	-0.2318	-0.24992	0.102012	0.016639
Slc12a2	20496	solute carrier family 12, member 2	16	2	3	-0.14407	-0.31648	0.437249	0.00691
Slc12a6	107723	solute carrier family 12, member 6	10	0	1	0.158669	0.472627	0.635663	0.006901
Slc12a7	20499	solute carrier family 12, member 7	10	0	1	0.08958	0.457203	0.86703	0.011783
Slc13a2	20500	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	6	1	2	0.662521	0.904854	0.148608	0.008425
Slc16a1	20501	solute carrier family 16 (monocarboxylic acid transporters), member 1	8	4	2	-0.09417	-0.2736	0.580741	0.004918
Slc16a10	72472	solute carrier family 16 (monocarboxylic acid transporters), member 10	1	0	1	0.379794	0.502903	0.045538	0.003147
Slc16a11	216867	solute carrier family 16 (monocarboxylic acid transporters), member 11	1	0	1	-0.29782	-0.29748	0.155371	0.039955
Slc18a1	110877	solute carrier family 18 (vesicular monoamine), member 1	36	8	4	0.514958	0.515259	0.139547	0.034486
Slc22a1	20517	solute carrier family 22 (organic cation transporter), member 1	21	9	5	-0.01417	0.302727	0.977017	0.016451
Slc22a13	102570	solute carrier family 22 (organic cation transporter), member 13	1	0	1	-0.30979	-0.29999	0.088739	0.024436
Slc22a23	73102	solute carrier family 22, member 23	2	0	1	0.052406	0.826259	0.975637	0.042495
Slc22a3	20519	solute carrier family 22 (organic cation transporter), member 3	17	8	4	0.665486	0.729751	0.030273	0.005138
Slc22a4	30805	solute carrier family 22 (organic cation transporter), member 4	18	7	4	0.253032	0.404957	0.371938	0.019995
Slc23a1	20522	solute carrier family 23 (nucleobase transporters), member 1	17	7	3	1.139962	0.927103	0.000125	0.000608
Slc24a3	94249	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	10	1	2	-0.02189	0.472493	0.977017	0.01291
Slc25a10	27376	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	19	3	1	0.023601	0.375093	0.972916	0.018359
Slc25a16	73132	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	1	0	1	0.109637	-0.34273	0.616876	0.004781
Slc25a17	20524	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	9	6	2	-0.13842	-0.62118	0.775854	0.004386
Slc25a22	68267	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	14	5	2	-0.15293	0.737301	0.76407	0.002852
Slc25a26	67582	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	13	5	2	-0.1203	-0.28226	0.660718	0.026022
Slc25a42	73095	solute carrier family 25, member 42	1	0	1	-0.04183	0.276754	0.925738	0.023938
Slc27a2	26458	solute carrier family 27 (fatty acid transporter), member 2	6	5	1	0.217371	0.321087	0.225445	0.010855
Slc27a4	26569	solute carrier family 27 (fatty acid transporter), member 4	8	6	1	0.079582	0.491263	0.881635	0.007497
Slc2a1	20525	solute carrier family 2 (facilitated glucose transporter), member 1	11	2	2	0.012268	-0.5242	0.983279	0.002758
Slc2a3	20527	solute carrier family 2 (facilitated glucose transporter), member 3	11	2	2	0.021012	0.262763	0.956601	0.008225
Slc30a10	226781	solute carrier family 30, member 10	9	0	1	-0.69182	-0.67669	0.050554	0.013554
Slc35a4	67843	solute carrier family 35, member A4	10	2	2	0.079278	0.384182	0.879309	0.022068
Slc36a1	215335	solute carrier family 36 (proton/amino acid symporter), member 1	20	5	3	0.741176	0.663291	0.018705	0.008913
Slc36a2	246049	solute carrier family 36 (proton/amino acid symporter), member 2	20	5	3	0.18978	0.266081	0.120984	0.005832
Slc37a2	56857	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	7	5	3	-0.36103	-0.61588	0.55464	0.049481
Slc37a4	14385	solute carrier family 37 (glucose-6-phosphate transporter), member 4	10	4	4	-0.23316	0.282136	0.213191	0.025845
Slc39a1	30791	solute carrier family 39 (zinc transporter), member 1	10	0	1	0.071215	0.27199	0.85162	0.03222
Slc39a4	72027	solute carrier family 39 (zinc transporter), member 4	9	0	1	-0.16834	0.497856	0.683397	0.010855
Slc39a5	72002	solute carrier family 39 (metal ion transporter), member 5	9	0	1	0.36306	1.092576	0.479434	0.002215
Slc39a9	328133	solute carrier family 39 (zinc transporter), member 9	9	0	1	-0.12697	0.507317	0.649849	0.002101
Slc3a1	20532	solute carrier family 3, member 1	6	5	1	0.241014	0.488538	0.467846	0.012144
Slc46a3	71706	solute carrier family 46, member 3	1	0	1	0.581066	0.709336	0.083594	0.007713
Slc47a1	67473	solute carrier family 47, member 1	10	3	4	0.355041	0.554435	0.04899	0.00159
Slc4a2	20535	solute carrier family 4 (anion exchanger), member 2	6	0	1	-0.11995	0.569789	0.901871	0.04273
Slc4a3	20536	solute carrier family 4 (anion exchanger), member 3	4	0	1	0.190836	0.245286	0.261251	0.027903
Slc5a11	233836	solute carrier family 5 (sodium/glucose cotransporter), member 11	8	3	2	0.543223	0.773285	0.024227	0.001366
Slc5a12	241612	solute carrier family 5 (sodium/glucose cotransporter), member 12	6	1	2	0.738422	0.652507	0.000265	0.000608
Slc5a3	53881	solute carrier family 5 (inositol transporters), member 3	10	4	3	-0.06889	0.44887	0.914221	0.014825
Slc5a4a	64452	solute carrier family 5, member 4a	5	1	1	0.158238	0.475505	0.782661	0.030614
Slc5a4b	64454	solute carrier family 5 (neutral amino acid transporters, system A), member 4b	5	1	1	0.850079	0.79096	0.000828	0.000812
Slc5a9	230612	solute carrier family 5 (sodium/glucose cotransporter), member 9	6	1	2	0.349414	0.578876	0.134107	0.003161
Slc6a14	56774	solute carrier family 6 (neurotransmitter transporter), member 14	16	7	4	1.394426	0.405794	0.007666	0.29182
Slc6a3	13162	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	20	8	5	0.731049	0.732603	0.005839	0.001989
Slc6a4	15567	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	17	6	5	0.241102	0.414416	0.295787	0.008781
Slc6a8	102857	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	24	9	5	0.098875	0.437797	0.81134	0.007259
Slc7a15	328059	solute carrier family 7 (cationic amino acid transporter, y+ system), member 15	6	5	1	0.421986	0.872956	0.525714	0.016885

symbol	entrezid	gene Name	Wormis	logFC_Fitness	logFC_Fitness - Control	adj.p-value_Fitness	adj.p-value_Fitness - Control	adj.p-value_Fitness - Control	adj.p-value_Fitness - Control
Slc7a8	50934	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	13	6	3	0.531801	0.350535	0.017941	0.036414
Slc9a3r1	26941	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	45	7	6	0.115663	0.337808	0.70098	0.013748
Slco1b2	28253	solute carrier organic anion transporter family, member 1b2	11	7	4	0.067659	0.391533	0.858281	0.005413
Slco2a1	24059	solute carrier organic anion transporter family, member 2a1	8	5	1	-0.00323	0.276018	0.996672	0.048332
Slco3a1	108116	solute carrier organic anion transporter family, member 3a1	13	6	2	-0.35266	0.165144	0.019099	0.13344
Smpd3	58994	sphingomyelin phosphodiesterase 3, neutral	7	0	1	0.148041	0.315599	0.636098	0.033745
Soat1	20652	sterol O-acyltransferase 1	5	1	0	-0.30075	-0.36823	0.264581	0.03574
Spns1	73658	spinster homolog 1 (Drosophila)	3	1	1	0.032927	0.314081	0.954223	0.025464
Src	20779	Rous sarcoma oncogene	14	0	1	0.007178	0.329356	0.990685	0.011707
Srebf1	20787	sterol regulatory element binding transcription factor 1	21	0	1	0.265679	0.986098	0.305233	0.000181
Stard3	59045	START domain containing 3	4	1	0	0.331645	0.416774	0.018253	0.001895
Stk39	53416	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	12	0	1	-0.19001	-0.51966	0.719267	0.022274
Stxbp3a	20912	syntaxin binding protein 3A	17	2	2	0.005758	-0.33149	0.991461	0.007058
Tap1	21354	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	4	2	3	-0.36692	0.08503	0.044402	0.559903
Tap2	21355	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	5	3	4	-0.51802	0.086131	0.040609	0.68688
Thra	21833	thyroid hormone receptor alpha	9	0	1	0.007307	0.651091	0.996253	0.013998
Tlr3	142980	toll-like receptor 3	8	0	1	-0.27877	-0.33529	0.070098	0.0069
Tmem38b	52076	transmembrane protein 38B	9	0	1	-0.09279	-0.32961	0.705536	0.005708
Tnfrsf1a	21937	tumor necrosis factor receptor superfamily, member 1a	7	0	1	0.076318	0.427609	0.910479	0.02595
Tomm22	223696	translocase of outer mitochondrial membrane 22 homolog (yeast)	2	0	1	-0.10449	-0.60714	0.894998	0.013377
Trf	22041	transferrin	10	0	1	0.29867	1.080709	0.760798	0.009525
Trpm4	68667	transient receptor potential cation channel, subfamily M, member 4	8	0	1	0.034791	0.447356	0.96923	0.032203
Ttyh1	57776	tweety homolog 1 (Drosophila)	6	0	1	-0.10579	-0.29194	0.623932	0.008663
Ttyh2	117160	tweety homolog 2 (Drosophila)	6	0	1	-0.02759	0.305529	0.953114	0.011541
Vdac1	22333	voltage-dependent anion channel 1	14	0	1	-0.03196	0.246724	0.947344	0.044179
Vdr	22337	vitamin D receptor	27	0	2	0.01063	0.282215	0.977017	0.006346
Wfs1	22393	Wolfram syndrome 1 homolog (human)	13	0	1	-0.3523	-0.36017	0.032424	0.007469

5.3

Overview of affected transport processes (enrichment analysis on the transport GO terms)

FF affected transporter terms

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0071702	organic substance transport	444	19	6.69	26	4.40E-05	1	0.100483257	0.010990863	Ace; Aqp3; Cd36; Slc6a3; Slc22a3; Slc23a1; Slc7a8; Slc6a14; Stard3; Aqp11; Maob; Slc36a1; Slc5a11	Crym; Fgf15; G6pc; Ly6e; Slco3a1; Acsf6
GO:0071705	nitrogen compound transport	200	10	3.01	45	0.00092	1	0.373205729	0.033806831	Aqp3; Slc6a3; Slc22a3; Slc7a8; Slc6a14; Aqp11; Maob; Slc36a1	Crym; Ly6e
GO:0046942	carboxylic acid transport	172	9	2.59	48	0.0012	1	0.36164469	0.032399751	Ace; Cd36; Slc23a1; Slc7a8; Slc6a14; Slc36a1	Crym; Slco3a1; Acsf6
GO:0015849	organic acid transport	174	9	2.62	49	0.0013	1	0.36164469	0.032261902	Ace; Cd36; Slc23a1; Slc7a8; Slc6a14; Slc36a1	Crym; Slco3a1; Acsf6
GO:0035672	oligopeptide transmembrane transport	4	2	0.06	51	0.00133	0.00133	-0.442469599	-0.220967149		Tap1; Tap2
GO:0006857	oligopeptide transport	15	3	0.23	59	0.00134	0.15259	-0.412533878	-0.060796858		Tap1; Tap2; Slco3a1
GO:0015850	organic alcohol transport	60	5	0.9	68	0.00207	1	0.284315526	0.051034293	Aqp3; Slc6a3; Slc22a3; Aqp11	Ly6e
GO:0015793	glycerol transport	6	2	0.09	76	0.00325	0.00325	0.656853976	0.228404527	Aqp3; Aqp11	
GO:0015840	urea transport	6	2	0.09	77	0.00325	0.00325	0.656853976	0.258955314	Aqp3; Aqp11	
GO:0015695	organic cation transport	21	3	0.32	81	0.00367	0.00592	0.517442443	0.12366709	Slc22a3; Slc7a8; Slc47a1	
GO:0015908	fatty acid transport	45	4	0.68	94	0.0046	1	0.061229368	0.00860675	Ace; Cd36	Slco3a1; Acsf6
GO:0015837	amine transport	176	8	2.65	98	0.00524	1	0.302293667	0.03031946	Slc6a3; Slc22a3; Slc7a8; Slc6a14; Maob; Slc36a1	Crym; Ly6e
GO:0015791	polyol transport	8	2	0.12	104	0.00596	1	0.656853976	0.170390262	Aqp3; Aqp11	
GO:0015911	plasma membrane long-chain fatty acid tr...	9	2	0.14	118	0.00758	0.04433	-0.093462524	-0.054484156	Cd36	Acsf6
GO:0042886	amide transport	9	2	0.14	119	0.00758	1	0.656853976	0.176985002	Aqp3; Aqp11	
GO:0015909	long-chain fatty acid transport	30	3	0.45	126	0.01014	1	0.199193302	0.02061467	Ace; Cd36	Acsf6
GO:0015844	monoamine transport	59	4	0.89	134	0.01195	1	0.137106723	0.015309	Slc6a3; Slc22a3; Maob	Ly6e
GO:0046968	peptide antigen transport	1	1	0.02	162	0.01506	0.01506	-0.518023528	-0.518023528		Tap2
GO:0051615	histamine uptake	1	1	0.02	164	0.01506	0.01506	0.665485622	0.665485622	Slc22a3	
GO:0097037	heme export	1	1	0.02	173	0.01506	0.01506	0.395600194	0.395600194	Mfsd7b	
GO:0015718	monocarboxylic acid transport	66	4	0.99	202	0.01745	1	0.061229368	0.009615049	Ace; Cd36	Slco3a1; Acsf6
GO:0008643	carbohydrate transport	101	5	1.52	210	0.01829	0.28109	-0.44513846	-0.016144287	Aqp3; Aqp11; Slc5a11	Fgf15; G6pc
GO:0006833	water transport	16	2	0.24	218	0.02358	0.14031	0.656853976	0.093939831	Aqp3; Aqp11	
GO:0006855	drug transmembrane transport	17	2	0.26	228	0.02646	0.02646	0.501474803	0.129370458	Abcb1a; Slc47a1	
GO:0006814	sodium ion transport	154	6	2.32	238	0.02918	0.11129	0.899526936	0.054131504	Slc6a3; Slc23a1; Slc6a14; Slc5a4b; Slc5a11; Slc5a12	
GO:0010747	positive regulation of plasma membrane L...	2	1	0.03	258	0.02989	0.02989	-1.089101021	-0.512786822		Acsf6
GO:0070904	transepithelial L-ascorbic acid transpor...	2	1	0.03	272	0.02989	0.02989	1.139962295	0.519896547	Slc23a1	
GO:0015882	L-ascorbic acid transport	2	1	0.03	279	0.02989	1	1.139962295	0.519896547	Slc23a1	
GO:0071436	sodium ion export	47	3	0.71	296	0.03364	0.03364	1.088479139	0.103437408	Slc6a3; Slc23a1; Slc6a14	
GO:0051937	catecholamine transport	47	3	0.71	298	0.03364	1	0.035956559	0.031210524	Slc6a3; Slc22a3	Ly6e
GO:0042044	fluid transport	20	2	0.3	306	0.0359	1	0.656853976	0.091515534	Aqp3; Aqp11	
GO:0015893	drug transport	21	2	0.32	312	0.03929	1	0.501474803	0.107768997	Abcb1a; Slc47a1	
GO:0014063	negative regulation of serotonin secreti...	3	1	0.05	329	0.0445	0.0445	0.440557216	0.14071944	Maob	
GO:0015760	glucose-6-phosphate transport	3	1	0.05	330	0.0445	0.0445	-1.148366805	-0.476239121		G6pc
GO:0015712	hexose phosphate transport	3	1	0.05	348	0.0445	1	-1.148366805	-0.476239121		G6pc
GO:0055085	transmembrane transport	895	20	13.48	372	0.05044	0.02839	0.358793992	0.000358302	Aqp3; Cd36; Slc6a3; Abcb1a; Slc22a3; Slc23a1; Slc7a8; Slc6a14; Aqp11; Slc47a1; Slc16a10; Slc36a1; Slc5a11; Slc5a12; Cox6b2	Tap1; Tap2; Mfsd4; Acsf6; Kctd14
GO:0015872	dopamine transport	25	2	0.38	373	0.05398	0.05398	0.698267297	0.076938554	Slc6a3; Slc22a3	
GO:0071715	icosanoid transport	25	2	0.38	375	0.05398	1	0.21592126	0.004818963	Ace	Slco3a1
GO:0070295	renal water absorption	4	1	0.06	399	0.05889	0.05889	0.99562939	0.388835353	Aqp3	
GO:0070837	dehydroascorbic acid transport	4	1	0.06	400	0.05889	0.05889	1.139962295	0.247530904	Slc23a1	
GO:0015886	heme transport	4	1	0.06	404	0.05889	1	0.395600194	0.016995759	Mfsd7b	
GO:0046717	acid secretion	27	2	0.41	424	0.06195	1	2.734049798	0.198799151	Ace; Tff2	
GO:0006865	amino acid transport	101	4	1.52	434	0.06624	0.36355	0.467480611	0.046291452	Slc7a8; Slc6a14; Slc36a1	Crym
GO:0015808	L-alanine transport	5	1	0.08	449	0.07307	0.07307	0.74117569	0.229237028	Slc36a1	
GO:0015816	glycine transport	5	1	0.08	450	0.07307	0.07307	0.74117569	0.243092893	Slc36a1	
GO:0015824	proline transport	5	1	0.08	451	0.07307	0.07307	0.74117569	0.22962435	Slc36a1	
GO:0060455	negative regulation of gastric acid secr...	5	1	0.08	461	0.07307	0.07307	4.80359464	0.919581863	Tff2	
GO:0070327	thyroid hormone transport	5	1	0.08	462	0.07307	0.07307	-0.797479908	-0.11737469		Crym
GO:0014062	regulation of serotonin secretion	5	1	0.08	468	0.07307	1	0.440557216	0.076147292	Maob	
GO:0060453	regulation of gastric acid secretion	5	1	0.08	483	0.07307	1	4.80359464	0.919581863	Tff2	
GO:0015833	peptide transport	151	5	2.27	492	0.07826	1	-0.260675528	-0.02014092	Glut1	Tap1; Tap2; Slco3a1; Arrb1
GO:0015672	monovalent inorganic cation transport	346	9	5.21	493	0.07885	1	0.805188912	0.02866912	Slc6a3; Slc23a1; Slc6a14; Slc5a4b; Slc47a1; Slc36a1; Slc5a11; Slc5a12; Cox6b2	
GO:0003097	renal water transport	6	1	0.09	526	0.08703	1	0.99562939	0.262518806	Aqp3	
GO:0010746	regulation of plasma membrane long-chain...	6	1	0.09	528	0.08703	1	-1.089101021	-0.220994103		Acsf6
GO:0032328	alanine transport	6	1	0.09	530	0.08703	1	0.74117569	0.184499402	Slc36a1	
GO:0006869	lipid transport	159	5	2.39	547	0.0926	1	0.115312509	0.001954209	Ace; Cd36; Stard3	Slco3a1; Acsf6
GO:0015807	L-amino acid transport	37	2	0.56	607	0.10674	0.38375	0.6364881	0.047071432	Slc7a8; Slc36a1	
GO:0035725	sodium ion transmembrane transport	76	3	1.14	611	0.10689	1	1.088479139	0.076731617	Slc6a3; Slc23a1; Slc6a14	
GO:0015992	proton transport	77	3	1.16	614	0.11005	0.11005	0.616512864	0.032801066	Slc47a1; Slc36a1; Cox6b2	
GO:0006818	hydrogen transport	78	3	1.17	620	0.11325	1	0.616512864	0.032839164	Slc47a1; Slc36a1; Cox6b2	
GO:0035774	positive regulation of insulin secretion...	8	1	0.12	624	0.11433	0.11433	-0.491372673	-0.049291186		Arrb1
GO:0048242	epinephrine secretion	8	1	0.12	630	0.11433	0.11433	-1.288664917	-0.18183245		Ly6e
GO:0032024	positive regulation of insulin secretion	41	2	0.62	663	0.1265	0.39307	-0.032888004	-0.022740597	Glut1	Arrb1
GO:0001696	gastric acid secretion	9	1	0.14	681	0.12767	1	4.80359464	0.5162938	Tff2	
GO:0048241	epinephrine transport	9	1	0.14	686	0.12767	1	-1.288664917	-0.163202766		Ly6e
GO:0050715	positive regulation of cytokine secretio...	45	2	0.68	723	0.14704	0.14704	-0.358521808	-0.006204047		Ptger4; Scamp5
GO:0015732	prostaglandin transport	11	1	0.17	731	0.15376	0.15376	-0.352662435	-0.021803379		Slco3a1
GO:0001820	serotonin secretion	11	1	0.17	739	0.15376	1	0.440557216	-0.089367921	Maob	
GO:0051181	cofactor transport	11	1	0.17	749	0.15376	1	0.395600194	-0.030699299	Mfsd7b	
GO:0051608	histamine transport	11	1	0.17	750	0.15376	1	0.665485622	0.056130993	Slc22a3	
GO:0000193	positive regulation of fatty acid transp...	11	1	0.17	755	0.15376	1	-1.089101021	-0.108156531		Acsf6
GO:0090277	positive regulation of peptide hormone s...	48	2	0.72	765	0.16286	1	-0.032888004	-0.017811486	Glut1	Arrb1
GO:0070633	transepithelial transport	12	1	0.18	783	0.16651	1	1.139962295	0.10538884	Slc23a1	
GO:0003333	amino acid transmembrane transport	50	2	0.75	788	0.17356	0.17356	0.6364881	0.048611882	Slc7a8; Slc36a1	
GO:0002793	positive regulation of peptide secretion	50	2	0.75	791	0.17356	1	-0.032888004	-0.016376406	Glut1	Arrb1
GO:0051051	negative regulation of transport	251	6	3.78	795	0.1786	1	0.817731767	0.021707034	Cd36; Tff2; Maob	Cnn2; Ptger4; Scamp5
GO:0015697	quaternary ammonium group transport	13	1	0.2	807	0.17907	0.17907	0.665485622	0.12714319	Slc22a3	
GO:0030301	cholesterol transport	52	2	0.78	825	0.18438	0.18438	0.616910523	0.011290148	Cd36; Stard3	
GO:0015918	sterol transport	52	2	0.78	828	0.18438	1	0.616910523	0.011290148	Cd36; Stard3	
GO:0042953	lipoprotein transport	14	1	0.21	843	0.19144	0.19144	0.902175972	0.071181783	Cd36	

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0001504	neurotransmitter uptake	14	1	0.21	845	0.19144	1	0.665485622	0.164748516 Slc22a3	
GO:0072337	modified amino acid transport	14	1	0.21	860	1.91E-01	1.00E+00	-0.797479908	0.000508433	Crym
GO:0050482	arachidonic acid secretion	15	1	0.23	880	0.20363	0.20363	0.784504955	0.034420861 Ace	
GO:0006812	cation transport	667	13	10.04	897	0.20705	1	0.591090921	0.00189613 Slc6a3; Slc22a3; Slc23a1; Slc7a8; Slc6a14; Slc5a4b; Slc47a1; Slc36a1; Slc5a11; Slc5a12; Cox6b2	Lck; Wfs1
GO:0050710	negative regulation of cytokine secretio...	16	1	0.24	911	0.21563	0.21563	-0.424675473	-0.072495153	Ptger4
GO:0006837	serotonin transport	16	1	0.24	917	0.21563	1	0.440557216	0.006732017 Maob	
GO:0032892	positive regulation of organic acid tran...	16	1	0.24	918	0.21563	1	-1.089101021	-0.060417133	Acs16
GO:2000191	regulation of fatty acid transport	16	1	0.24	924	0.21563	1	-1.089101021	-0.102474889	Acs16
GO:0006811	ion transport	858	16	12.92	927	0.22274	0.28138	0.42219945	-0.001040409 Slc6a3; Slc22a3; Slc23a1; Slc7a8; Slc6a14; Slc5a4b; Aqp11; Slc47a1; Slc36a1; Slc5a11; Slc5a12; Cox6b2	Lck; Wfs1; Slco3a1; Kctd14
GO:0051180	vitamin transport	17	1	0.26	952	0.22746	1	1.139962295	-0.000183721 Slc23a1	
GO:0050707	regulation of cytokine secretion	60	2	0.9	958	0.22844	1	-0.358521808	-0.031973477	Ptger4; Scamp5
GO:0006836	neurotransmitter transport	114	3	1.72	990	0.2463	0.44423	0.930320248	0.063166245 Slc6a3; Slc22a3; Slc6a14	
GO:0051953	negative regulation of amine transport	19	1	0.29	1006	0.25057	1	0.440557216	0.069396732 Maob	
GO:0015804	neutral amino acid transport	20	1	0.3	1019	0.26187	1	0.74117569	0.077459524 Slc36a1	
GO:0035773	insulin secretion involved in cellular r...	20	1	0.3	1022	0.26187	1	-0.491372673	-0.07443549	Arrb1
GO:0061178	regulation of insulin secretion involved...	20	1	0.3	1027	0.26187	1	-0.491372673	-0.07443549	Arrb1
GO:0046903	secretion	585	11	8.81	1036	0.26787	0.08656	0.342108649	-0.005678135 Ace; Slc6a3; Glud1; Tff2; Maob	Hck; Ly6e; Ptger4; Scamp5; Arrb1; Car9
GO:0051048	negative regulation of secretion	122	3	1.84	1060	0.2788	1	1.606492128	0.045713081 Tff2; Maob	Ptger4
GO:0032309	icosanoid secretion	22	1	0.33	1075	0.28396	1	0.784504955	0.01193389 Ace	
GO:0050714	positive regulation of protein secretion	70	2	1.05	1083	0.2843	1	-0.358521808	-0.009232102	Ptger4; Scamp5
GO:0015758	glucose transport	71	2	1.07	1087	0.28988	1	-0.041311808	-0.054791047	Fgf15; G6pc
GO:0050663	cytokine secretion	71	2	1.07	1088	0.28988	1	-0.358521808	-0.030923031	Ptger4; Scamp5
GO:0032370	positive regulation of lipid transport	23	1	0.35	1099	0.29476	1	-1.089101021	-0.007247522	Acs16
GO:0008645	hexose transport	72	2	1.08	1106	0.29546	1	-0.041311808	-0.05349307	Fgf15; G6pc
GO:0046887	positive regulation of hormone secretion	72	2	1.08	1109	0.29546	1	-0.032888004	-0.002380361 Glud1	Arrb1
GO:0015749	monosaccharide transport	73	2	1.1	1113	0.30104	1	-0.041311808	-0.050273839	Fgf15; G6pc
GO:0009914	hormone transport	188	4	2.83	1147	0.31441	1	-0.537980208	-0.020243207 Glud1	Crym; Ly6e; Arrb1
GO:0046326	positive regulation of glucose import	25	1	0.38	1150	0.31587	0.31587	-0.930256811	-0.105440932	Fgf15
GO:0051224	negative regulation of protein transport	77	2	1.16	1163	0.32324	1	0.23875025	0.008361067 Cd36	Ptger4
GO:0051050	positive regulation of transport	432	8	6.51	1177	0.32637	1	-0.53203738	-0.020787438 Cd36; Glud1	Fgf15; Ptger4; Wfs1; Scamp5; Arrb1; Acs16
GO:0007595	lactation	27	1	0.41	1187	0.33635	0.33635	0.731048972	0.017829995 Slc6a3	
GO:0032890	regulation of organic acid transport	28	1	0.42	1206	0.34636	1	-1.089101021	-0.029569065	Acs16
GO:0050709	negative regulation of protein secretion	28	1	0.42	1211	0.34636	1	-0.424675473	-0.011619358	Ptger4
GO:0010828	positive regulation of glucose transport	30	1	0.45	1241	0.36593	1	-0.330256811	-0.092512402	Fgf15
GO:0051047	positive regulation of secretion	207	4	3.12	1269	0.37931	1	-0.195704906	0.00129152 Glud1	Ptger4; Scamp5; Arrb1
GO:0050796	regulation of insulin secretion	91	2	1.37	1312	0.39921	1	-0.032888004	-0.023529061 Glud1	Arrb1
GO:0046324	regulation of glucose import	36	1	0.54	1349	0.42122	1	-0.930256811	-0.074746981	Fgf15
GO:0050432	catecholamine secretion	38	1	0.57	1389	0.43856	1	-1.288664917	-0.002091313	Ly6e
GO:0046323	glucose import	39	1	0.59	1403	0.44703	1	-0.930256811	-0.072342694	Fgf15
GO:0050708	regulation of protein secretion	101	2	1.52	1409	0.45099	1	-0.358521808	-0.017494262	Ptger4; Scamp5
GO:0090276	regulation of peptide hormone secretion	101	2	1.52	1410	0.45099	1	-0.032888004	-0.021955426 Glud1	Arrb1
GO:0002791	regulation of peptide secretion	104	2	1.57	1443	0.46604	1	-0.032888004	-0.02799769 Glud1	Arrb1
GO:0090087	regulation of peptide transport	104	2	1.57	1445	0.46604	1	-0.032888004	-0.02799769 Glud1	Arrb1
GO:0034763	negative regulation of transmembrane tra...	43	1	0.65	1466	0.47968	1	0.902175972	-0.000471057 Cd36	
GO:0051209	release of sequestered calcium ion into ...	46	1	0.69	1502	0.50289	0.50289	-0.407506809	-0.048797144	Lck
GO:0010827	regulation of glucose transport	46	1	0.69	1503	0.50289	1	-0.930256811	-0.065097081	Fgf15
GO:0051046	regulation of secretion	378	6	5.69	1513	0.50594	1	0.743555372	0.011454212 Glud1; Tff2; Maob	Ptger4; Scamp5; Arrb1
GO:0034220	ion transmembrane transport	579	9	8.72	1515	0.50928	0.76667	0.601983914	0.00116547 Slc6a3; Slc22a3; Slc23a1; Slc7a8; Slc6a14; Slc47a1; Slc36a1; Cox6b2	Kctd14
GO:0032368	regulation of lipid transport	47	1	0.71	1520	0.5104	1	-1.089101021	-0.013741391	Acs16
GO:0030073	insulin secretion	114	2	1.72	1529	0.51437	1	-0.032888004	-0.01838202 Glud1	Arrb1
GO:0051952	regulation of amine transport	52	1	0.78	1600	0.54628	1	0.440557216	0.047004834 Maob	
GO:0015711	organic anion transport	54	1	0.81	1619	0.55988	0.55988	-0.352662435	-0.000948054	Slco3a1
GO:0007589	body fluid secretion	57	1	0.86	1647	0.57954	1	0.731048972	0.002722554 Slc6a3	
GO:0009306	protein secretion	130	2	1.96	1656	0.58548	1	-0.358521808	-0.022878888	Ptger4; Scamp5
GO:0030072	peptide hormone secretion	131	2	1.97	1661	0.58966	1	-0.032888004	-0.009892523 Glud1	Arrb1
GO:0030001	metal ion transport	551	8	8.3	1663	0.59208	1	0.579669657	-0.004866413 Slc6a3; Slc23a1; Slc6a14; Slc5a4b; Slc5a11; Slc5a12	Lck; Wfs1
GO:0034764	positive regulation of transmembrane tra...	59	1	0.89	1668	0.59215	1	-1.089101021	-0.043097621	Acs16
GO:0051222	positive regulation of protein transport	133	2	2	1675	0.59793	1	-0.358521808	-0.011013216	Ptger4; Scamp5
GO:0017038	protein import	206	3	3.1	1687	0.60263	1	-0.233314074	-0.006903163 Cd36	Arnt1; Pik3r1
GO:0060402	calcium ion transport into cytosol	61	1	0.92	1694	0.60439	1	-0.407506809	-0.045915008	Lck
GO:0002790	peptide secretion	136	2	2.05	1699	0.6101	1	-0.032888004	-0.01565681 Glud1	Arrb1
GO:0051928	positive regulation of calcium ion trans...	62	1	0.93	1700	0.61037	0.61037	-0.352297554	-0.061905284	Wfs1
GO:0060401	cytosolic calcium ion transport	62	1	0.93	1704	0.61037	1	-0.407506809	-0.055690201	Lck
GO:0046883	regulation of hormone secretion	138	2	2.08	1714	0.61805	1	-0.032888004	-0.009455802 Glud1	Arrb1
GO:0032940	secretion by cell	513	7	7.72	1767	0.65731	1	-0.288521848	-0.013368838 Glud1; Maob	Hck; Ly6e; Ptger4; Scamp5; Arrb1
GO:0051223	regulation of protein transport	227	3	3.42	1791	0.66778	1	0.061710785	-0.006567485 Cd36	Ptger4; Scamp5
GO:0051049	regulation of transport	913	12	13.75	1883	0.72731	1	0.0063528	-0.011303427 Cd36; Glud1; Tff2; Maob	Cnn2; Fgf15; Hck; Ptger4; Wfs1; Scamp5; Arrb1; Acs16
GO:0043270	positive regulation of ion transport	87	1	1.31	1897	0.73384	1	-0.352297554	-0.060963281	Wfs1
GO:0046879	hormone secretion	179	2	2.7	1935	0.7546	1	-0.032888004	-0.009241103 Glud1	Arrb1
GO:0051924	regulation of calcium ion transport	126	1	1.9	2084	0.85331	1	-0.352297554	-0.043542243	Wfs1
GO:0006816	calcium ion transport	225	2	3.39	2086	0.85581	1	-0.379902181	-0.040595916	Lck; Wfs1
GO:0070838	divalent metal ion transport	259	2	3.9	2142	0.90442	1	-0.379902181	-0.036095931	Lck; Wfs1
GO:0072511	divalent inorganic cation transport	262	2	3.95	2146	0.90788	1	-0.379902181	-0.034708385	Lck; Wfs1
GO:0006820	anion transport	163	1	2.45	2160	0.91676	1	-0.352662435	-0.009093361	Slco3a1
GO:0010959	regulation of metal ion transport	164	1	2.47	2163	0.91803	1	-0.352297554	-0.039960757	Wfs1
GO:0034762	regulation of transmembrane transport	319	2	4.8	2208	0.95503	1	-0.093462524	-0.019639294 Cd36	Acs16
GO:0043269	regulation of ion transport	320	1	4.82	2256	0.99259	1	-0.352297554	-0.024473997	Wfs1

PFOS affected transporter terms

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0006869	lipid transport	159	43	23.96	52	6.50E-05	0.51128	0.362733997	0.096860004	Abca1; Ace; Plin2; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Apoh; Atp8a1; Atp9a; Cd36; Fabp2; Lrp6; Mttp; Pon1; Ppara; Rbp4; Ncor1; Nr1h3; Slco2a1; Slc27a2; Slc27a4; Abca7; Atp9b; Stard3; Osbpl1a; Osbpl3; Spns1; Osbp; Osbpl6; Npc11; Apob; Irs2;	Pla2g4a; Pparg; Slc25a17; Soat1; Pla2g10; Acsf4; Acsf6; Atp11c
GO:0033700	phospholipid efflux	11	7	1.66	64	0.00033	0.00033	0.919877987	0.608530335	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2;	
GO:0015908	fatty acid transport	45	15	6.78	92	0.00175	0.02675	-0.005803544	0.007075959	Ace; Plin2; Cd36; Fabp2; Slco2a1; Slc27a2; Slc27a4;	Pla2g4a; Pparg; Slc25a17; Pla2g10; Acsf4; Acsf6
GO:0015695	organic cation transport	21	9	3.16	97	0.00207	0.02263	0.37508621	0.217967999	Slc22a1; Slc22a3; Slc22a4; Slc7a8; Rhbg; Pdck1;	Slc12a2
GO:0015914	phospholipid transport	33	12	4.97	98	0.00215	0.28116	0.537456239	0.197316775	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Atp8a1; Atp9a; Abca7; Atp9b	Pla2g10; Atp11c
GO:0071702	organic substance transport	444	89	66.91	102	0.00248	1	0.303656829	0.068369276	Abca1; Ace; Plin2; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Apoh; Arg1; Atp8a1; Atp9a; Cd36; Slc6a3; Edn1; Fabp2; Slc37a4; Slc6a4; Ins2; Lrp6; Mttp; Prkcz; Pon1; Ppara; Inpp5k; Rbp4; Ncor1; Slc22a1; Slc22a3; Slc23a1; Slc2a3; Slc3a1; Nr1h3; Slco2a1; Slc27a2; Slc27a4; Cln8; Slc9a3r1; Slc25a10; Abca7; Slco1b2; Slc22a4; Atp9b; Slc7a8; Slc5a3; Arl2; Pdck1; Stard3; Osbpl1a; Nisch; Slc35a4; Slc25a22; Adipor2; Osbpl3; Spns1; Osbp; Abcc3; Osbpl6;	Aqp8; Crym; Ednra; Hiat1; Itln1; Pla2g4a; Pparg; Slc16a1; Slc25a17; Slc2a1; Soat1; Stxbp3a; Pla2g10; Acsf4; Slc37a2; Slc25a26; Sfxn5; Acsf6; Atp11c
GO:0051181	cofactor transport	11	6	1.66	107	0.00271	0.16571	0.189717335	0.108594319	Abcb6; Slc6a8; Mfsd7c; Mfsd7b	Ppt1; Slc25a26
GO:0015909	long-chain fatty acid transport	30	11	4.52	111	0.00303	0.00595	0.027149911	0.019051173	Ace; Plin2; Cd36; Fabp2; Slco2a1; Slc27a2; Slc27a4;	Pla2g4a; Pparg; Pla2g10; Acsf6
GO:0015718	monocarboxylic acid transport	66	19	9.95	115	0.00317	0.7279	-0.010883355	0.024439122	Ace; Plin2; Cd36; Fabp2; Slco2a1; Slc27a2; Slc27a4;	Aqp8; Pla2g4a; Pparg; Slc16a1; Slc25a17; Pla2g10; Acsf4; Acsf6
GO:0032368	regulation of lipid transport	47	14	7.08	150	0.00764	1	0.543000073	0.186690716	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Pon1; Ppara; Ncor1; Nr1h3; Irs2; Acsf5	Pla2g10; Acsf6
GO:0030301	cholesterol transport	52	15	7.84	155	0.0081	0.14156	0.563414891	0.141509419	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Cd36; Lrp6; Pon1; Nr1h3; Stard3; Npc11; Apob	Soat1; Pla2g10
GO:0015918	sterol transport	52	15	7.84	156	0.0081	1	0.563414891	0.141509419	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Cd36; Lrp6; Pon1; Nr1h3; Stard3; Npc11; Apob	Soat1; Pla2g10
GO:0070837	dehydroascorbic acid transport	4	3	0.6	202	0.01213	0.01213	0.221889155	0.106809068	Slc23a1; Slc2a3	Slc2a1
GO:0015886	heme transport	4	3	0.6	203	0.01213	0.06123	0.471523026	0.302861491	Abcb6; Mfsd7c; Mfsd7b	
GO:0032371	regulation of sterol transport	27	9	4.07	220	0.01416	1	0.771441823	0.304947718	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Pon1;	Pla2g10
GO:0032374	regulation of cholesterol transport	27	9	4.07	221	0.01416	1	0.771441823	0.304947718	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Pon1;	Pla2g10
GO:0050702	interleukin-1 beta secretion	15	6	2.26	234	0.01714	0.06117	0.135092102	0.040317193	Abca1; Apoa1; F2r1; Panx1	Casp1; Pycard
GO:0033344	cholesterol efflux	33	10	4.97	241	0.01997	0.03237	0.657474369	0.255529165	Abca1; Apoa1; Apo2; Apo4; Apoc1; Apoc2; Pon1;	Soat1; Pla2g10
GO:0010747	positive regulation of plasma membrane l...	2	2	0.3	264	0.0227	0.0227	-0.355094166	-0.355094166	Acsf5	Acsf6
GO:0046942	carboxylic acid transport	172	36	25.92	290	0.02348	1	0.166137969	0.055125634	Ace; Plin2; Arg1; Cd36; Fabp2; Slc23a1; Slc3a1; Slco2a1; Slc27a2; Slc27a4; Cln8; Slc9a3r1; Slc25a10; Slco1b2; Slc22a4; Slc7a8; Pdck1; Slc25a22; Abcc3; Slc6a8; Slc36a1; Slc36a2; Slc7a15; Irs2; Acsf5	Aqp8; Crym; Pla2g4a; Pparg; Slc16a1; Slc25a17; Pla2g10; Acsf4; Slc25a26; Sfxn5; Acsf6
GO:0015849	organic acid transport	174	36	26.22	327	0.02761	1	0.166137969	0.055081743	Ace; Plin2; Arg1; Cd36; Fabp2; Slc23a1; Slc3a1; Slco2a1; Slc27a2; Slc27a4; Cln8; Slc9a3r1; Slc25a10; Slco1b2; Slc22a4; Slc7a8; Pdck1; Slc25a22; Abcc3; Slc6a8; Slc36a1; Slc36a2; Slc7a15; Irs2; Acsf5	Aqp8; Crym; Pla2g4a; Pparg; Slc16a1; Slc25a17; Pla2g10; Acsf4; Slc25a26; Sfxn5; Acsf6
GO:0050701	interleukin-1 secretion	17	6	2.56	343	0.03247	1	0.135092102	0.043226758	Abca1; Apoa1; F2r1; Panx1	Casp1; Pycard
GO:0015911	plasma membrane long-chain fatty acid tr...	9	4	1.36	352	0.03443	0.38714	0.094387763	0.111914439	Cd36; Irs2; Acsf5	Acsf6
GO:0030299	intestinal cholesterol absorption	9	4	1.36	353	0.03443	0.38714	0.662079676	0.098661768	Apoa1; Apo2; Apo4; Npc1l1	
GO:0015697	quaternary ammonium group transport	13	5	1.96	359	0.03473	0.0612	0.457760803	0.229133964	Slc22a1; Slc22a3; Slc22a4; Pdck1; Slc6a8	
GO:0032369	negative regulation of lipid transport	18	6	2.71	376	0.04266	0.47932	0.917978886	0.367191536	Apoa2; Apoc1; Apoc2; Nr1h3; Irs2	Pla2g10
GO:0042953	lipoprotein transport	14	5	2.11	392	0.0475	0.0475	0.110443509	0.171081516	Apoc2; Cd36; Mttp; Apob	Pparg
GO:0030300	regulation of intestinal cholesterol abs...	6	3	0.9	400	0.04789	0.04789	0.750700871	0.396660363	Apoa1; Apo2; Apo4	
GO:0002374	cytokine secretion involved in immune re...	6	3	0.9	411	0.04789	1	0.828490939	0.408877306	Apoa1; Apo2; F2r1	
GO:0002739	regulation of cytokine secretion involve...	6	3	0.9	412	0.04789	1	0.828490939	0.408877306	Apoa1; Apo2; F2r1	
GO:0010746	regulation of plasma membrane long-chain...	6	3	0.9	413	0.04789	1	0.005079772	0.062755268	Irs2; Acsf5	Acsf6
GO:0032375	negative regulation of cholesterol trans...	10	4	1.51	425	0.05067	0.11033	1.058199593	0.48734686	Apoa2; Apoc1; Apoc2	Pla2g10
GO:0032372	negative regulation of sterol transport	10	4	1.51	427	0.05067	1	1.058199593	0.48734686	Apoa2; Apoc1; Apoc2	Pla2g10
GO:0050717	positive regulation of interleukin-1 alp...	3	2	0.45	472	0.06128	0.06128	0.039358143	-0.003411506	Panx1	Casp1
GO:0070634	transperithecium ammonium transport	3	2	0.45	474	0.06128	0.06128	0.091000915	0.091818923	Rhbg	Slc12a2
GO:0072608	interleukin-10 secretion	3	2	0.45	483	0.06128	0.15066	0.358139819	0.314897105	F2r1; Prkcz	
GO:0050705	regulation of interleukin-1 alpha secret...	3	2	0.45	497	0.06128	1	0.039358143	-0.003411506	Panx1	Casp1
GO:0072367	regulation of lipid transport by regulat...	3	2	0.45	500	0.06128	1	0.32189265	0.303203622	Ppara; Ncor1	
GO:0043691	reverse cholesterol transport	11	4	1.66	525	0.07039	0.07039	0.673793776	0.216203108	Abca1; Apoa1; Apo2; Apo4	
GO:0017038	protein import	206	39	31.05	561	0.07502	1	0.012348286	0.008478946	Bcl6; Cd36; Cry2; Dag1; Hyal2; Jak2; Jun; Ppp3a; Stat3; Thra; Tnfrsf1a; Ing1; Mapk1; Pex14; Tomm34; Dab2ip; Flna; Pde2a; Pex6; Ipo13	Arnt1; Cdk1; Ect2; Hspa4; Kpnb1; Kpna3; Prdx1; Ran; Timm9; Mtx2; Psmd10; Nop58; Pex3; Snupn; Ipo5; Ipo4; Pex12; Tlr3; Tomm22
GO:0007589	body fluid secretion	57	13	8.59	564	0.07869	0.68311	0.170693349	0.027798518	Arpt; Copa; Slc6a3; Edn1; Eif2ak3; Guca2b; Nr1h3;	Usf2; Agr2; Sytl2; Socs2
GO:0015893	drug transport	21	6	3.16	582	0.08414	1	0.445604666	0.167997547	Slc22a1; Slco1b2; Slc47a1; Abcc3; Abp1; Slc18a1	
GO:0050706	regulation of interleukin-1 beta secreti...	12	4	1.81	614	0.09342	1	-0.003493521	-0.010193696	Apoa1; Panx1	Casp1; Pycard
GO:0006855	drug transmembrane transport	17	5	2.56	624	0.10018	0.10018	0.43878341	0.169664733	Slc22a1; Slco1b2; Slc47a1; Abcc3; Slc18a1	
GO:0051180	vitamin transport	17	5	2.56	627	0.10018	0.83386	0.960180547	0.310159195	Gc; Rbp4; Slc23a1; Slc2a3	Slc2a1
GO:0007595	lactation	27	7	4.07	630	0.10035	0.10035	0.161059023	0.035149992	Aprt; Slc6a3; Eif2ak3; Vdr; Vegfa	Usf2; Socs2
GO:0002740	xenobiotic transport	4	2	0.6	684	0.11042	0.11042	1.052009306	0.526373286	Apoa1; Apo2	
GO:0042908	xenobiotic transport	4	2	0.6	698	0.11042	0.11042	-0.047117924	0.046634724	Abcc3	Slc2a1
GO:0015682	ferric iron transport	4	2	0.6	712	0.11042	0.15067	0.752813216	0.37756298	Trf; Lmtk2	
GO:0051610	serotonin uptake	4	2	0.6	713	0.11042	0.15067	0.464837234	0.275670563	Slc6a4; Slc18a1	
GO:0050703	interleukin-1 alpha secretion	4	2	0.6	737	0.11042	1	0.039358143	0.002002211	Panx1	Casp1
GO:0050709	negative regulation of protein secretion	28	7	4.22	749	0.11726	0.50999	0.466843209	0.111341507	Apoa1; Apo2; F2r1; Ins2; Nr1h3	Ptger4; Dph3
GO:0050704	regulation of interleukin-1 secretion	13	4	1.96	769	0.11951	1	-0.003493521	-0.00080544	Apoa1; Panx1	Casp1; Pycard
GO:0032370	positive regulation of lipid transport	23	6	3.47	776	0.12079	1	0.147831779	0.058968623	Abca1; Pon1; Nr1h3; Acsf5	Pla2g10; Acsf6
GO:0015693	magnesium ion transport	9	3	1.36	831	0.14232	0.14232	-0.397761623	-0.066123593		Tusc3; Nipa2; Nipa1
GO:0035428	hexose transmembrane transport	9	3	1.36	833	0.14232	0.14232	0.006899869	0.001007298	Slc37a4; Slc2a3	Slc2a1
GO:0001504	neurotransmitter uptake	14	4	2.11	879	0.14831	1	0.553746962	0.183657642	Slc6a4; Slc22a3; Cln8; Slc18a1	
GO:0072337	modified amino acid transport	14	4	2.11	895	0.14831	1	-0.04411408	0.048066156	Slc9a3r1; Slc6a8	Crym; Slc25a26
GO:0003096	renal sodium ion transport	1	1	0.15	918	0.15071	0.15071	0.337808006	0.337808006	Slc9a3r1	
GO:0015709	thiosulfate transport	1	1	0.15	953	0.15071	0.15071	0.375093168	0.375093168	Slc25a10	
GO:0015759	beta-glucoside transport	1	1	0.15	954	0.15071	0.15071	1.930995618	1.930995618	Apoa2	
GO:0015794	glycerol-3-phosphate transport	1	1	0.15	955	0.15071	0.15071	-0.61587845	-0.61587845		Slc37a2
GO:0015798	myo-inositol transport	1	1	0.15	956	0.15071	0.15071	0.448870105	0.448870105	Slc5a3	
GO:0015881	creatine transport	1	1	0.15	958	0.15071	0.15071	0.43779731	0.43779731	Slc6a8	
GO:0015898	amiloride transport	1	1	0.15	959	0.15071	0.15071	0.479710944	0.479710944	Abp1	
GO:0032782	bile acid secretion	1	1	0.15	987	0.15071	0.15071	0.337808006	0.337808006	Slc9a3r1	
GO:0034197	triglyceride transport	1	1	0.15	996	0.15071	0.15071	1.007759024	1.007759024	Apoh	
GO:0034633	retinol transport	1	1	0.15	1002	0.15071	0.15071	1.015488235	1.015488235	Rbp4	
GO:0035926	chemokine (C-C motif) ligand 2 secretion	1	1	0.15	1015	0.15071	0.15071	0.381454205	0.381454205	F2r1	

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0050713	negative regulation of interleukin-1 bet...	1	1	0.15	1044	0.15071	0.15071	0.173022994	0.173022994	Apoa1	
GO:0051615	histamine uptake	1	1	0.15	1049	0.15071	0.15071	0.729750694	0.729750694	Slc22a3	
GO:0051977	lysophospholipid transport	1	1	0.15	1052	0.15071	0.15071	-0.791892031	-0.791892031		Pla2g10
GO:0060695	negative regulation of cholesterol trans...	1	1	0.15	1060	0.15071	0.15071	1.930995618	1.930995618	Apoa2	
GO:0071423	malate transmembrane transport	1	1	0.15	1079	0.15071	0.15071	0.375093168	0.375093168	Slc25a10	
GO:0072369	regulation of lipid transport by positiv...	1	1	0.15	1088	0.15071	0.15071	0.44323114	0.44323114	Ppara	
GO:0072512	trivalent inorganic cation transport	1	1	0.15	1090	0.15071	0.15071	1.080709288	1.080709288	Trf	
GO:0090198	negative regulation of chemokine secreti...	1	1	0.15	1092	0.15071	0.15071	0.381454205	0.381454205	F2r1	
GO:0090341	negative regulation of secretion of lyso...	1	1	0.15	1096	0.15071	0.15071	0.549647293	0.549647293	Nr1h3	
GO:0097037	heme export	1	1	0.15	1097	0.15071	0.15071	0.310222504	0.310222504	Mfsd7b	
GO:2001153	positive regulation of renal water trans...	1	1	0.15	1119	0.15071	0.15071	0.355209957	0.355209957	Inpp5k	
GO:2001181	positive regulation of interleukin-10 se...	1	1	0.15	1120	0.15071	0.15071	0.334825433	0.334825433	Prkc	
GO:0015743	malate transport	1	1	0.15	1152	0.15071	1	0.375093168	0.375093168	Slc25a10	
GO:0034196	acylglycerol transport	1	1	0.15	1173	0.15071	1	1.007759024	1.007759024	ApoH	
GO:0046864	isoprenoid transport	1	1	0.15	1199	0.15071	1	1.015488235	1.015488235	Rbp4	
GO:0046865	terpenoid transport	1	1	0.15	1200	0.15071	1	1.015488235	1.015488235	Rbp4	
GO:0060694	regulation of cholesterol transporter ac...	1	1	0.15	1217	0.15071	1	1.930995618	1.930995618	Apoa2	
GO:0071938	vitamin A transport	1	1	0.15	1224	0.15071	1	1.015488235	1.015488235	Rbp4	
GO:2001151	regulation of renal water transport	1	1	0.15	1252	0.15071	1	0.355209957	0.355209957	Inpp5k	
GO:0006829	zinc ion transport	25	6	3.77	1269	0.16397	0.06273	0.336229424	0.070506453	Ap3d1; Slc39a1; Slc39a5; Slc39a4; Slc39a9	Slc30a10
GO:0010107	potassium ion import	5	2	0.75	1289	0.16607	0.16607	0.321339985	0.142466707	Atp1a1; Abcc9	
GO:0015722	canalicular bile acid transport	5	2	0.75	1293	0.16607	0.16607	-0.118830782	-0.008056536	Abcc3	Aqp8
GO:0015808	L-alanine transport	5	2	0.75	1294	0.16607	0.16607	0.464685718	0.156034409	Slc36a1; Slc36a2	
GO:0015816	glycine transport	5	2	0.75	1295	0.16607	0.16607	0.464685718	0.183975282	Slc36a1; Slc36a2	
GO:0015879	carnitine transport	5	2	0.75	1296	0.16607	0.16607	0.409264589	0.266599321	Slc22a4; Pdzk1	
GO:0015824	proline transport	5	2	0.75	1312	0.16607	0.27865	0.464685718	0.247950948	Slc36a1; Slc36a2	
GO:0015838	betaine transport	5	2	0.75	1321	0.16607	1	0.409264589	0.266599321	Slc22a4; Pdzk1	
GO:0000041	transition metal ion transport	65	13	9.8	1332	0.17211	1	0.335807235	0.055578637	Ap3d1; Sfxn1; Trf; Slc39a1; Slc25a37; Slc39a5; Slc39a4; Abcb6; Lmtk2; Slc39a9	Ltf; Sco1; Slc30a10
GO:0051224	negative regulation of protein transport	77	15	11.6	1336	0.17586	0.38704	0.409654317	0.099048063	Apoa1; Apoa2; Cd36; F2r1; Ins2; Inpp5k; Thra; Nr1h3; Ndfip1; Dab2ip; Flna; Pde2a	Ptger4; Psmd10; Dph3
GO:0050710	negative regulation of cytokine secretio...	16	4	2.41	1439	0.21251	0.80455	0.556824477	0.123605488	Apoa1; Apoa2; F2r1	Ptger4
GO:0010874	regulation of cholesterol efflux	16	4	2.41	1444	0.21251	1	0.399294751	0.176080072	Abca1; Pon1; Nr1h3	Pla2g10
GO:2000191	regulation of fatty acid transport	16	4	2.41	1446	0.21251	1	-0.194163179	-0.051360731	Irs2; Acs15	Pla2g10; Acs16
GO:0010875	positive regulation of cholesterol efflu...	11	3	1.66	1475	0.22329	0.22329	0.796357012	0.310664809	Abca1; Pon1; Nr1h3	
GO:0050718	positive regulation of interleukin-1 bet...	11	3	1.66	1479	0.22329	0.22329	-0.06233236	-0.026849759	Panx1	Casp1; Pycard
GO:0050716	positive regulation of interleukin-1 sec...	11	3	1.66	1496	0.22329	1	-0.06233236	-0.026849759	Panx1	Casp1; Pycard
GO:0051608	histamine transport	11	3	1.66	1498	0.22329	1	0.41354418	0.127303966	Edn1; Slc22a3	Ednra
GO:2000193	positive regulation of fatty acid transp...	11	3	1.66	1500	0.22329	1	-0.500693454	-0.179730209	Acs15	Pla2g10; Acs16
GO:0070508	cholesterol import	6	2	0.9	1528	0.22516	0.38735	1.052009306	0.303282605	Apoa1; Apoa2	
GO:0015696	ammonium transport	6	2	0.9	1540	0.22516	1	0.091000915	0.115602732	Rhhg	Slc12a2
GO:0032328	alanine transport	6	2	0.9	1541	0.22516	1	0.464685718	0.157187041	Slc36a1; Slc36a2	
GO:0035376	sterol import	6	2	0.9	1544	0.22516	1	1.052009306	0.303282605	Apoa1; Apoa2	
GO:0035382	sterol transmembrane transport	6	2	0.9	1545	0.22516	1	1.052009306	0.303282605	Apoa1; Apoa2	
GO:0006826	iron ion transport	22	5	3.32	1564	0.22903	0.64575	0.440988956	0.053147189	Sfxn1; Trf; Slc25a37; Lmtk2	Ltf
GO:0050715	positive regulation of cytokine secretio...	45	9	6.78	1567	0.22904	0.6545	0.126355918	0.038450614	F2r1; Ins2; Prkc; Src; Panx1	Casp1; Ptger4; Pycard; Cd209d
GO:0050714	positive regulation of protein secretion	70	13	10.55	1607	0.24977	0.56151	0.207413441	0.033123589	F2r1; Ins2; Prkc; Rbp4; Src; Panx1; Zfp384; Exph5	Casp1; Ptger4; Pycard; Dnm1; Cd209d
GO:0008643	carbohydrate transport	101	18	15.22	1618	0.25631	0.26623	0.215497325	0.055301511	Apoa2; Edn1; Slc37a4; Ins2; Prkc; Inpp5k; Slc2a3; Slc5a4; Adipor2; Al317395; Slc5a11; Irs2	Ednra; Hiat1; Itln1; Slc2a1; Stxbp3a; Slc37a2
GO:0050708	regulation of protein secretion	101	18	15.22	1619	0.25631	0.55777	0.294825217	0.049983812	Apoa1; Apoa2; F2r1; Ins2; Prkc; Rbp4; Src; Nr1h3; Panx1; Arfip1; Zfp384; Exph5	Casp1; Ptger4; Pycard; Dnm1; Dph3; Cd209d
GO:0032274	gonadotropin secretion	12	3	1.81	1636	0.26658	0.15069	0.240437036	0.014823659	Acrv2a; Meg3; Tbx3	
GO:0032373	positive regulation of sterol transport	12	3	1.81	1650	0.26658	1	0.796357012	0.277775885	Abca1; Pon1; Nr1h3	
GO:0032376	positive regulation of cholesterol trans...	12	3	1.81	1651	0.26658	1	0.796357012	0.277775885	Abca1; Pon1; Nr1h3	
GO:0070633	transcellular transport	12	3	1.81	1652	0.26658	1	0.369701734	0.107584767	Slc23a1; Rhhg	Slc12a2
GO:0001579	medium-chain fatty acid transport	2	1	0.3	1672	0.27871	0.27871	0.491262696	0.219633179	Slc27a4	
GO:0002741	positive regulation of cytokine secretio...	2	1	0.3	1683	0.27871	0.27871	0.381454205	0.173885348	F2r1	
GO:0010963	regulation of L-arginine import	2	1	0.3	1712	0.27871	0.27871	0.559132869	0.21459813	Arg1	
GO:0030185	nitric oxide transport	2	1	0.3	1732	0.27871	0.27871	0.765874959	0.524408121	Edn1	
GO:0032416	negative regulation of sodium:hydrogen a...	2	1	0.3	1740	0.27871	0.27871	0.337808006	0.198242882	Slc9a3r1	
GO:0046881	positive regulation of follicle-stimulat...	2	1	0.3	1787	0.27871	0.27871	0.208364366	0.080134572	Acrv2a	
GO:0051935	glutamate uptake involved in synaptic tr...	2	1	0.3	1798	0.27871	0.27871	0.555562684	0.254886241	Cln8	
GO:0060621	negative regulation of cholesterol impor...	2	1	0.3	1809	0.27871	0.27871	1.930995618	1.001284885	Apoa2	
GO:0070904	transcellular L-ascorbic acid transport...	2	1	0.3	1821	0.27871	0.27871	0.927103373	0.509960251	Slc23a1	
GO:0072368	regulation of lipid transport by negativ...	2	1	0.3	1833	0.27871	0.27871	0.20055416	0.233189862	Ncor1	
GO:0072643	interferon-gamma secretion	2	1	0.3	1835	0.27871	0.27871	0.381454205	0.183757539	F2r1	
GO:0090238	positive regulation of arachidonic acid ...	2	1	0.3	1839	0.27871	0.27871	-0.791892031	-0.530566544		Pla2g10
GO:2000664	positive regulation of interleukin-5 sec...	2	1	0.3	1848	0.27871	0.27871	0.334825433	0.160443153	Prkc	
GO:2000667	positive regulation of interleukin-13 se...	2	1	0.3	1849	0.27871	0.27871	0.334825433	0.160443153	Prkc	
GO:0010958	regulation of amino acid import	2	1	0.3	1869	0.27871	1	0.559132869	0.21459813	Arg1	
GO:0015882	L-ascorbic acid transport	2	1	0.3	1872	0.27871	1	0.927103373	0.509960251	Slc23a1	
GO:0032278	positive regulation of gonadotropin secr...	2	1	0.3	1876	0.27871	1	0.208364366	0.080134572	Acrv2a	
GO:0042946	glucoside transport	2	1	0.3	1891	0.27871	1	1.930995618	0.958597678	Apoa2	
GO:0050711	negative regulation of interleukin-1 sec...	2	1	0.3	1905	0.27871	1	0.173022994	0.142438311	Apoa1	
GO:0051182	coenzyme transport	2	1	0.3	1908	0.27871	1	-0.282258057	0.212132226		Slc25a26
GO:0051933	amino acid uptake involved in synaptic t...	2	1	0.3	1911	0.27871	1	0.555562684	0.254886241	Cln8	
GO:0071806	protein transmembrane transport	2	1	0.3	1945	0.27871	1	0.278010243	0.217989898	Pex6	
GO:0072603	interleukin-5 secretion	2	1	0.3	1949	0.27871	1	0.334825433	0.160443153	Prkc	
GO:0072611	interleukin-13 secretion	2	1	0.3	1950	0.27871	1	0.334825433	0.160443153	Prkc	
GO:0090182	regulation of secretion of lysosomal enz...	2	1	0.3	1952	0.27871	1	0.549647293	0.324317618	Nr1h3	
GO:2000650	negative regulation of sodium ion transm...	2	1	0.3	1957	0.27871	1	0.337808006	0.198242882	Slc9a3r1	
GO:2000662	regulation of interleukin-5 secretion	2	1	0.3	1958	0.27871	1	0.334825433	0.160443153	Prkc	
GO:2000665	regulation of interleukin-13 secretion	2	1	0.3	1959	0.27871	1	0.334825433	0.160443153	Prkc	
GO:2000910	negative regulation of sterol import	2	1	0.3	1960	0.27871	1	1.930995618	1.001284885	Apoa2	
GO:2001179	regulation of interleukin-10 secretion	2	1	0.3	1961	0.27871	1	0.334825433	0.281618555	Prkc	
GO:0006821	chloride transport	78	14	11.76	1964	0.2814	0.3015	0.107005754	0.002904326	Cln2; Slc12a7; Slc4a2; Fxyd1; Clca6; Ano6; Slc12a6;	Clns1a; Slc12a2; Clca3; Ttyh1; Cltc6; Clctc1
GO:0034219	carbohydrate transmembrane transport	18	4	2.71	1974	0.28272	0.76995	0.101220458	0.00429701	Slc37a4; Slc2a3; Slc35a4	Slc2a1
GO:0070254	mucus secretion	7	2	1.05	1980	0.28539	0.1507	-0.431506919	-0.057078807		Agtr2; Sytl2
GO:0050707	regulation of cytokine secretion	60	11	9.04	2057	0.28882	1	0.294656534	0.065116848	Apoa1; Apoa2; F2r1; Ins2; Prkc; Src; Panx1	Casp1; Ptger4; Pycard; Cd209d
GO:0015721	bile acid and bile salt transport	13	3	1.96	2091	0.31071	0.7292	0.051290596	0.028146812	Slc10b2; Abcc3	Aqp8
GO:0046326	positive regulation of glucose import	25	5	3.77	2132	0.32153	0.32153	0.184339608	0.064201374	Ins2; Prkc; Adipor2; Irs2	Itln1
GO:0034767	positive regulation of ion transmembrane...	8	2	1.21	2158	0.34507	0.15071	-0.17001841	-0.03539898	Pdzk1	Gcg
GO:0046884	follicle-stimulating hormone secretion	8	2	1.21	2161	0.34507	0.2787	0.217264102	-0.012757309	Acrv2a; Tbx3	
GO:0030157	pancreatic juice secretion	8	2	1.21	2186	0.34507	0.47971	0.470032091	-0.04212087		

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0051589	negative regulation of neurotransmitter ...	8	2	1.21	2216	0.34507	1	0.46257697	0.100458884	Accn2; Slc18a1	
GO:0051222	positive regulation of protein transport	133	22	20.04	2232	0.35253	1	0.135763383	0.03304736	F2r1; Hyal2; Ins2; Jak2; Mdm2; Prkcz; Rbp4; Src; Tnfrsf1a; Panx1; Flna; Zfp384; Exph5	Casp1; Cdk1; Ect2; Ptger4; Pycard; Tmem30a; Dnm1; Tlr3; Cd209d
GO:0015758	glucose transport	71	12	10.7	2295	0.38157	0.319	0.123082989	0.035427633	Edn1; Slc37a4; Ins2; Prkcz; Inpp5k; Slc2a3; Adipor2;	Ednra; Itln1; Slc2a1; Stxbp3a
GO:0050663	cytokine secretion	71	12	10.7	2297	0.38157	1	0.307024531	0.054703679	Abca1; Apoa1; Apoa2; F2r1; Ins2; Prkcz; Src; Panx1	Casp1; Ptger4; Pycard; Cd209d
GO:0046717	acid secretion	27	5	4.07	2310	0.38537	1	0.829551982	0.137987452	Ace; Tff2; Slc9a3r1	Pla2g4a; Pla2g10
GO:0010248	establishment or maintenance of transmem...	3	1	0.45	2348	0.38743	0.38743	0.302726832	0.191018731	Slc22a1	
GO:0014063	negative regulation of serotonin secreti...	3	1	0.45	2353	0.38743	0.38743	0.31702691	0.066678505	Maob	
GO:0015760	glucose-6-phosphate transport	3	1	0.45	2355	0.38743	0.38743	0.282135517	-0.034676127	Slc37a4	
GO:0033572	transferrin transport	3	1	0.45	2380	0.38743	0.38743	0.424917145	0.143180877	Lmtk2	
GO:0034635	glutathione transport	3	1	0.45	2383	0.38743	0.38743	0.337808006	0.107977187	Slc9a3r1	
GO:0035524	proline transmembrane transport	3	1	0.45	2387	0.38743	0.38743	0.266080627	0.13634755	Slc36a2	
GO:0051612	negative regulation of serotonin uptake	3	1	0.45	2410	0.38743	0.38743	0.515258897	0.229422227	Slc18a1	
GO:0071422	succinate transmembrane transport	3	1	0.45	2432	0.38743	0.38743	0.375093168	0.128091359	Slc25a10	
GO:0072488	ammonium transmembrane transport	3	1	0.45	2436	0.38743	0.38743	0.498485991	0.240978928	Rhbq	
GO:0090188	negative regulation of pancreatic juice ...	3	1	0.45	2440	0.38743	0.38743	0.549647293	0.240035744	Nr1h3	
GO:0020484	positive regulation of interleukin-8 sec...	3	1	0.45	2448	0.38743	0.38743	0.381454205	0.027715962	F2r1	
GO:2000778	positive regulation of interleukin-6 sec...	3	1	0.45	2450	0.38743	0.38743	0.381454205	0.079739856	F2r1	
GO:0015712	hexose phosphate transport	3	1	0.45	2491	0.38743	1	0.282135517	-0.034676127	Slc37a4	
GO:0015740	C4-dicarboxylate transport	3	1	0.45	2492	0.38743	1	0.375093168	0.128091359	Slc25a10	
GO:0015744	succinate transport	3	1	0.45	2493	0.38743	1	0.375093168	0.128091359	Slc25a10	
GO:0042939	tripeptide transport	3	1	0.45	2526	0.38743	1	0.337808006	0.107977187	Slc9a3r1	
GO:0043091	L-arginine import	3	1	0.45	2527	0.38743	1	0.559132869	0.062061004	Arg1	
GO:0051581	negative regulation of neurotransmitter ...	3	1	0.45	2546	0.38743	1	0.515258897	0.229422227	Slc18a1	
GO:0051611	regulation of serotonin uptake	3	1	0.45	2547	0.38743	1	0.515258897	0.229422227	Slc18a1	
GO:0060620	regulation of cholesterol import	3	1	0.45	2553	0.38743	1	0.930995618	0.667015821	Apoa2	
GO:0072604	interleukin-6 secretion	3	1	0.45	2570	0.38743	1	0.381454205	0.079739856	F2r1	
GO:0072606	interleukin-8 secretion	3	1	0.45	2571	0.38743	1	0.381454205	0.027715962	F2r1	
GO:0090237	regulation of arachidonic acid secretion	3	1	0.45	2574	0.38743	1	-0.791892031	-0.330864141		Pla2g10
GO:2000482	regulation of interleukin-8 secretion	3	1	0.45	2581	0.38743	1	0.381454205	0.027715962	F2r1	
GO:2000909	regulation of sterol import	3	1	0.45	2584	0.38743	1	0.930995618	0.667015821	Apoa2	
GO:0051220	cytoplasmic sequestering of protein	15	3	2.26	2611	0.39888	0.3874	0.321998496	0.063858982	Thra; Flna	Psmid10
GO:0050482	arachidonic acid secretion	15	3	2.26	2617	0.39888	0.55924	-0.279416414	-0.072894182	Ace	Pla2g4a; Pla2g10
GO:0008645	hexose transport	72	12	10.85	2635	0.40108	1	0.123082989	0.035533048	Edn1; Slc37a4; Ins2; Prkcz; Inpp5k; Slc2a3; Adipor2;	Ednra; Itln1; Slc2a1; Stxbp3a
GO:0009306	protein secretion	130	21	19.59	2637	0.40123	0.76993	0.31157029	0.039813514	Abca1; Apoa1; Apoa2; F2r1; Ins2; Jak2; Mdm2; Prkcz; Rbp4; Src; Tnfrsf1a; Panx1; Mon1a; Arfip1; Traf3ip2; Zfp384;	Casp1; Ptger4; Pycard; Dnm1; Dph3; Cd209d
GO:0001821	histamine secretion	9	2	1.36	2640	0.40299	0.40299	0.255440923	0.079610903	Edn1	Ednra
GO:0032890	regulation of organic acid transport	28	5	4.22	2699	0.41726	1	-0.043503969	-0.005565351	Arg1; Irs2; Acsf5	Pla2g10; Acsf5
GO:0015749	monosaccharide transport	73	12	11	2702	0.42064	1	0.123082989	0.039973069	Edn1; Slc37a4; Ins2; Prkcz; Inpp5k; Slc2a3; Adipor2;	Ednra; Itln1; Slc2a1; Stxbp3a
GO:0032024	positive regulation of insulin secretion	41	7	6.18	2707	0.42453	0.37862	0.069555023	0.010916789	Glud1; Jak2; Rbp4; Irs2	Gcg; Pdx1; Oxtct1
GO:0006837	serotonin transport	16	3	2.41	2745	0.44189	1	0.415567126	0.03961791	Slc6a4; Maob; Slc18a1	
GO:0032892	positive regulation of organic acid tran...	16	3	2.41	2749	0.44189	1	-0.500693454	-0.126955819	Acsf5	Pla2g10; Acsf6
GO:0015870	acetylcholine transport	10	2	1.51	2779	0.45835	0.45835	0.327674443	0.060196964	Slc22a1; Arl2	
GO:0051223	regulation of protein transport	227	35	34.21	2834	0.47005	1	0.214344706	0.043783179	Mdm2; Prkcz; Inpp5k; Rbp4; Src; Thra; Tnfrsf1a; Nr1h3; Panx1; Ndfip1; Dab2ip; Arfip1; Flna; Pde2a;	Casp1; Cdk1; Ect2; Prdx1; Ptger4; Psmid10; Pycard; Tmem30a; Dnm1; Dph3; Tlr3; Cd209d
GO:0010748	negative regulation of plasma membrane l...	4	1	0.6	2862	0.47977	0.47977	0.725427648	0.271679984	Irs2	
GO:0010766	negative regulation of sodium ion transp...	4	1	0.6	2863	0.47977	0.47977	0.337808006	0.105767788	Slc9a3r1	
GO:0015746	citrate transport	4	1	0.6	2868	0.47977	0.47977	-0.249915875	-0.078966939		Sfxn5
GO:0034755	iron ion transmembrane transport	4	1	0.6	2891	0.47977	0.47977	1.080709288	0.1186739	Trf	
GO:0042045	epithelial fluid transport	4	1	0.6	2898	0.47977	0.47977	0.765874959	0.112331529	Edn1	
GO:0045332	phospholipid translocation	4	1	0.6	2902	0.47977	0.47977	0.443072493	0.096898987	Abca1	
GO:0046929	negative regulation of neurotransmitter ...	4	1	0.6	2910	0.47977	0.47977	0.409895043	0.021361768	Accn2	
GO:0070257	positive regulation of mucus secretion	4	1	0.6	2928	0.47977	0.47977	-0.294739539	0.042046801		Sylt2
GO:0070574	cadmium ion transmembrane transport	4	1	0.6	2929	0.47977	0.47977	0.531005774	0.019872509	Abcb6	
GO:0072321	chaperone-mediated protein transport	4	1	0.6	2935	0.47977	0.47977	-0.966215967	-0.208367243		Timm9
GO:0090370	negative regulation of cholesterol efflu...	4	1	0.6	2936	0.47977	0.47977	-0.791892031	-0.149627359		Pla2g10
GO:0006842	tricarboxylic acid transport	4	1	0.6	2947	0.47977	1	-0.249915875	-0.078966939		Sfxn5
GO:0015691	cadmium ion transport	4	1	0.6	2959	0.47977	1	0.531005774	0.019872509	Abcb6	
GO:0032415	regulation of sodium:hydrogen antiporter...	4	1	0.6	2967	0.47977	1	0.337808006	0.090612226	Slc9a3r1	
GO:0034204	lipid translocation	4	1	0.6	2974	0.47977	1	0.443072493	0.096898987	Abca1	
GO:0090186	regulation of pancreatic juice secretion	4	1	0.6	3028	0.47977	1	0.549647293	0.204773793	Nr1h3	
GO:2000192	negative regulation of fatty acid transp...	4	1	0.6	3033	0.47977	1	0.725427648	0.271679984	Irs2	
GO:0010828	positive regulation of glucose transport	30	5	4.52	3038	0.47999	1	0.184339608	0.052670513	Ins2; Prkcz; Adipor2; Irs2	Itln1
GO:0002790	peptide secretion	136	21	20.5	3056	0.48859	0.27873	0.211032853	0.003711908	Abca1; Acvr2b; Dgat1; Edn1; Elf2ak3; Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Hnf1b; Ensa; Smpd3; Chd7;	Cpt1a; Gcg; Pdx1; Stxbp3a; Oxtct1; Acvr1c
GO:0015807	L-amino acid transport	37	6	5.58	3063	0.49216	0.84688	0.521983829	0.080572107	Arg1; Cln8; Slc7a8; Slc25a22; Slc36a1; Slc36a2	
GO:0015732	prostaglandin transport	11	2	1.66	3097	0.51058	0.38746	-0.257937234	-0.035847686	Slc2a1	Pla2g10
GO:0043092	L-amino acid import	11	2	1.66	3139	0.51058	1	0.557347777	0.080913737	Arg1; Cln8	
GO:0072530	purine-containing compound transmembrane...	11	2	1.66	3146	0.51058	1	-0.451717431	-0.110510744		Slc25a17; Slc25a26
GO:0030072	peptide hormone secretion	131	20	19.74	3150	0.51248	0.34518	0.199430871	0.011202935	Acvr2b; Dgat1; Edn1; Elf2ak3; Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Hnf1b; Ensa; Smpd3; Chd7; Irs2	Cpt1a; Gcg; Pdx1; Stxbp3a; Oxtct1; Acvr1c
GO:0015833	peptide transport	151	23	22.76	3151	0.51296	1	0.224392664	0.013155888	Abca1; Acvr2b; Dgat1; Edn1; Elf2ak3; Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Hnf1b; Slc9a3r1; Slco1b2;	Cpt1a; Gcg; Pdx1; Stxbp3a; Oxtct1; Acvr1c
GO:0032410	negative regulation of transporter activ...	18	3	2.71	3161	0.52383	0.62476	0.86023032	0.180593119	Apoa2; Slc9a3r1; Ndfip1	
GO:0015872	dopamine transport	25	4	3.77	3194	0.53297	0.10652	0.570084842	0.090692186	Slc6a3; Slc22a1; Slc22a3; Slc18a1	
GO:0044070	regulation of anion transport	25	4	3.77	3196	0.53297	0.53297	-0.047404069	0.003388886	Cln2; Vdac1	Clc6; Ahcy1
GO:0071715	icosanoid transport	25	4	3.77	3205	0.53297	1	-0.14055792	-0.02783381	Ace; Slco2a1	Pla2g4a; Pla2g10
GO:0046323	glucose import	39	6	5.88	3220	0.54646	0.38749	0.197410172	0.058610479	Ins2; Prkcz; Slc2a3; Adipor2; Irs2	Itln1
GO:0015871	choline transport	5	1	0.75	3247	0.55819	0.55819	0.43779731	0.135747862	Slc6a8	
GO:0030321	trans epithelial chloride transport	5	1	0.75	3254	0.55819	0.55819	-0.316484162	-0.150355534		Slc12a2
GO:0060455	negative regulation of gastric acid secr...	5	1	0.75	3293	0.55819	0.55819	4.648201148	0.946079795	Tff2	
GO:0070327	thyroid hormone transport	5	1	0.75	3298	0.55819	0.55819	-0.669803581	-0.108904565		Crym
GO:0014062	regulation of serotonin secretion	5	1	0.75	3320	0.55819	1	0.31702691	0.045780073	Maob	
GO:0060453	regulation of gastric acid secretion	5	1	0.75	3361	0.55819	1	4.648201148	0.946079795	Tff2	
GO:2000649	regulation of sodium ion transmembrane t...	5	1	0.75	3374	0.55819	1	0.337808006	0.055135824	Slc9a3r1	
GO:0030073	insulin secretion	114	17	17.18	3379	0.55928	0.2596	0.148321835	-0.002475154	Acvr2b; Dgat1; Elf2ak3; Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Hnf1b; Ensa; Irs2	Cpt1a; Gcg; Pdx1; Stxbp3a; Oxtct1; Acvr1c
GO:0043090	amino acid import	12	2	1.81	3412	0.55938	1	0.557347777	0.087060011	Arg1; Cln8	
GO:0051048	negative regulation of secretion	122	18	18.39	3468	0.57809	1	0.624033644	0.092421127	Accn2; Apoa1; Apoa2; Edn1; F2r1; Ins2; Anpep; Ppp3ca; Srebf1; Tff2; Nr1h3; Maob; Abi; Bcr	Ptger4; Stxbp3a; Dph3; Acvr1c
GO:0044062	regulation of excretion	20	3	3.01	3498	0.59867	0.38751	0.59849968	0.036232632	Edn1; Anpep; Slc9a3r1	
GO:0042044	fluid transport	20	3	3.01	3511	0.59867	1	0.151153433	0.005377736	Edn1; Inpp5k	Aqp8
GO:0090277	positive regulation of peptide hormone s...	48	7	7.23	3521	0.59945	1	0.069555023	0.012832857	Glud1; Jak2; Rbp4; Irs2	Gcg; Pdx1; Oxtct1
GO:0015793	glycerol transport	6	1	0.9	3615	0.6248	0.6248	-0.61587845	0.012836579		Slc37a2
GO:0032275	luteinizing hormone secretion	6	1	0.9	3624	0.6248	0.6248	0.2261			

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0046880	regulation of follicle-stimulating hormo...	6	1	0.9	3711	0.6248	1	0.208364366	-0.047411983	Acrv2a	
GO:0051580	regulation of neurotransmitter uptake	6	1	0.9	3714	0.6248	1	0.515258897	0.174885286	Sic18a1	
GO:0070255	regulation of mucus secretion	6	1	0.9	3738	0.6248	1	-0.294739539	0.028120442		Sytl2
GO:0072348	sulfur compound transport	6	1	0.9	3741	0.6248	1	-0.282258057	-0.097499803		Sic25a26
GO:0015991	ATP hydrolysis coupled proton transport	21	3	3.16	3763	0.63306	0.63306	0.309505712	0.097801402	Atp6v0a1; Atp6ap1; Atp6v0b	
GO:0015988	energy coupled proton transport, against...	21	3	3.16	3768	0.63306	1	0.309505712	0.097801402	Atp6v0a1; Atp6ap1; Atp6v0b	
GO:0003333	amino acid transmembrane transport	50	7	7.54	3783	0.64421	0.73122	0.368243366	0.076347265	Sic22a4; Sic7a8; Sic25a22; Sic6a8; Sic36a1; Sic36a2	Sic25a26
GO:0002793	positive regulation of peptide secretion	50	7	7.54	3784	0.64421	1	0.069555023	0.016129831	Glud1; Jak2; Rbp4; Irs2	Gcg; Pdx1; Oxtt1
GO:0034763	negative regulation of transmembrane tra...	43	6	6.48	3819	0.64623	1	0.650301415	0.10665727	Apoa2; Cd36; Thr; Dab2ip; Irs2	Psmid10
GO:0046324	regulation of glucose import	36	5	5.43	3828	0.64966	1	0.184339608	0.055329255	Ins2; Prkc; Adipor2; Irs2	Itln1
GO:0015698	inorganic anion transport	107	15	16.13	3845	0.6609	1	0.124878249	0.010009267	Cln2; Sic12a7; Sic4a2; Sic25a10; Fxyd1; Clca6; Ano6; Sic12a6; Ttyh2	Clns1a; Sic12a2; Clca3; Ttyh1; Clc6; Clcc1
GO:0032309	icosanoid secretion	22	3	3.32	3857	0.66534	1	-0.279416414	-0.059051073	Ace	Pla2g4a; Pla2g10
GO:0006820	anion transport	163	23	24.57	3861	0.66791	0.28584	0.137211921	0.013232335	Abca1; Cln2; Sic12a7; Sic4a2; Sic4a3; Vdac1; Cln8; Sic25a10; Fxyd1; Sic25a22; Clca6; Ano6; Sic12a6; Arg1; Sic3a1; Cln8; Sic9a3r1; Sic22a4; Sic7a8; Pdzk1; Sic25a22; Sic6a8; Sic36a1; Sic36a2; Sic7a15	Clns1a; Sic12a2; Sic16a1; Clca3; Ttyh1; Sfxn5; Clc6; Ahcy1; Clcc1
GO:0006865	amino acid transport	101	14	15.22	3871	0.67538	0.68447	0.366819283	0.078306356	Sic18a1	Crym; Sic25a26
GO:0036303	positive regulation of dopamine secretio...	7	1	1.05	3908	0.68136	0.68136	0.515258897	0.05985866	Sic18a1	
GO:0051024	positive regulation of immunoglobulin se...	7	1	1.05	3919	0.68136	0.68136	0.105488235	0.171740998	Rbp4	
GO:0002080	positive regulation of calcium ion impor...	7	1	1.05	3931	0.68136	0.68136	-0.753609108	-0.099537732		Gcg
GO:0015809	arginine transport	7	1	1.05	3949	0.68136	1	0.559132869	0.030255914	Arg1	
GO:0051938	L-glutamate import	7	1	1.05	3971	0.68136	1	0.555562684	0.086918421	Cln8	
GO:000195	chemokine secretion	7	1	1.05	3989	0.68136	1	0.381454205	0.041860271	F2r1	
GO:0090196	regulation of chemokine secretion	7	1	1.05	3990	0.68136	1	0.381454205	0.041860271	F2r1	
GO:0034764	positive regulation of transmembrane tra...	59	8	8.89	4009	0.68241	1	-0.134863426	-0.003635108	Hyal2; Pdzk1; Flna; Acsi5	Ect2; Gcg; Tlr3; Acsi6
GO:0051281	positive regulation of release of seques...	15	2	2.26	4014	0.68424	0.68424	0.137191025	0.001746686	F2	Ednra
GO:0006857	oligopeptide transport	15	2	2.26	4018	0.68424	0.85921	0.364670679	0.098781308	Sic9a3r1; Sico1b2	
GO:0015850	organic alcohol transport	60	8	9.04	4061	0.70101	1	0.359400205	0.065004013	Sic6a3; Sic22a1; Sic22a3; Sic5a3; Nisch; Sic6a8;	Sic37a2
GO:0010827	regulation of glucose transport	46	6	6.93	4074	0.7116	1	0.212818	0.047870739	Ins2; Prkc; Inpp5k; Adipor2; Irs2	Itln1
GO:0009914	hormone transport	188	26	28.33	4080	0.71405	1	0.148977927	0.012946703	Meg3; Ppp3ca; Rbp4; Sic22a1; Srebf1; Tbx3; Hnf1b; Ensa; Smpd3; Chd7; Irs2	Cpt1a; Crym; Gcg; Pdx1; Scg5; Stxbp3a; Oxtt1; Acvr1c
GO:0015813	L-glutamate transport	16	2	2.41	4089	0.71886	0.77022	0.646431772	0.078081099	Cln8; Sic25a22	
GO:0006833	water transport	16	2	2.41	4090	0.71886	0.80485	-0.15620733	0.004860816	Inpp5k	Aqp8
GO:0032308	positive regulation of prostaglandin sec...	8	1	1.21	4137	0.72941	0.72941	-0.791892031	-0.124700363		Pla2g10
GO:0035435	phosphate ion transmembrane transport	8	1	1.21	4145	0.72941	0.72941	0.375093168	0.116639144	Sic25a10	
GO:0035774	positive regulation of insulin secretion...	8	1	1.21	4146	0.72941	0.72941	-0.753609108	-0.074789283		Gcg
GO:0043268	positive regulation of potassium ion tra...	8	1	1.21	4149	0.72941	0.72941	-0.519664949	-0.056492909		Stk39
GO:0032306	regulation of prostaglandin secretion	8	1	1.21	4184	0.72941	1	-0.791892031	-0.124700363		Pla2g10
GO:0032310	prostaglandin secretion	8	1	1.21	4185	0.72941	1	-0.791892031	-0.124700363		Pla2g10
GO:0015837	amine transport	176	24	26.52	4221	0.73445	1	0.388951209	0.065235266	Arg1; Sic6a3; Edn1; Sic6a4; Sic22a1; Sic22a3; Sic3a1; Cln8; Sic9a3r1; Sic22a4; Sic7a8; Arl2; Pdzk1; Nisch; Sic25a22; Sic6a8; Maob; Sic18a1; Sic36a1; Sic36a2;	Crym; Ednra; Sic25a26
GO:0050796	regulation of insulin secretion	91	12	13.71	4222	0.73583	0.71916	0.11262697	-0.008116635	Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Ensa; Irs2	Cpt1a; Gcg; Pdx1; Oxtt1; Acvr1c
GO:0048305	immunoglobulin secretion	17	2	2.56	4245	0.75022	0.55832	0.637529939	0.084017377	Rbp4; Traf3ip2	
GO:0035813	regulation of renal sodium excretion	17	2	2.56	4263	0.75022	1	0.728845517	0.029363661	Edn1; Anpep	
GO:0046879	hormone secretion	179	24	26.98	4292	0.764	1	0.176687618	0.018737507	Acvr2a; Acvr2b; Dgat1; Edn1; Eif2ak3; Glud1; Jak2; Meg3; Ppp3ca; Rbp4; Srebf1; Tbx3; Hnf1b; Ensa;	Cpt1a; Gcg; Pdx1; Scg5; Stxbp3a; Oxtt1; Acvr1c
GO:0048241	epinephrine transport	9	1	1.36	4319	0.77021	0.77021	0.302726832	0.002906824	Sic22a1	
GO:0001696	gastric acid secretion	9	1	1.36	4329	0.77021	1	0.646201148	0.491201598	Tff2	
GO:0032276	regulation of gonadotropin secretion	9	1	1.36	4342	0.77021	1	0.208364366	-0.032368047	Acvr2a	
GO:0032305	positive regulation of icosanoid secreti...	9	1	1.36	4343	0.77021	1	-0.791892031	-0.14076044		Pla2g10
GO:0042886	amide transport	9	1	1.36	4352	0.77021	1	0.479710944	0.135745368	Abp1	
GO:0090276	regulation of peptide hormone secretion	101	13	15.22	4372	0.77203	1	0.133630472	-0.004158215	Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Ensa; Chd7; Irs2	Cpt1a; Gcg; Pdx1; Oxtt1; Acvr1c
GO:0046887	positive regulation of hormone secretion	72	9	10.85	4394	0.7766	0.97256	0.162347165	0.037935299	Acvr2a; Edn1; Glud1; Jak2; Rbp4; Irs2	Gcg; Pdx1; Oxtt1
GO:0015874	norepinephrine transport	18	2	2.71	4399	0.77852	0.3876	0.313400071	0.035007691	Sic22a1; Nisch	
GO:0055085	transmembrane transport	895	127	134.88	4426	0.78905	0.16434	0.233361798	0.03557095	Abca1; Accn2; Apoa1; Apoa2; Atp1a1; Atp2a2; Atp6v0a1; Atp8a1; Atp9a; Cd36; Cln2; Cox8a; Sic6a3; Sfxn1; Sic37a4; Gc; Sic6a4; Hyal2; Ins2; Jak2; Sic12a7; Sic13a2; Sic22a1; Sic22a3; Sic23a1; Sic2a3; Sic4a2; Sic4a3; Abcc9; Thr; Tnfrsf1a; Trf; Vdac1; Vdr; Sic9a3r1; Sic25a10; Abcc6; Sico1b2; Sic39a1; Sic22a4; Atp9b; Sic7a8; Sic5a3; Atp6ap1; Panx1; Fxyd1; Rhb; Pdzk1; Sic47a1; Sic35a4; Sic25a22; Trpm4; Kctd5; Dab2ip; Kctd2; Sic46a3; Sic39a5; Sic39a4; Sic16a10; Sic25a22; Sic22a23; Spns1; Abcc6; Abcc3; Abp1; Mfsd2a; Mcoln1; Sic22a3; Sic6a8; Ano6; Sic12a6; Sic18a1; Atp6v0b; Ttyh2;	Aqp8; Cdk1; Ect2; Gcg; Grid1; Hiat1; Kcnk1; Kcnk2; Prdx1; Sic12a2; Sic16a1; Sic25a17; Sic2a1; Tmem38b; Psmid10; Sic37a2; Kcne3; Ttyh1; Kcnmb4; Sic25a26; Sic25a16; Sfxn5; Sic22a13; Tlr3; Clc6; Mfsd4; Acsi6; Sic16a11; Tomm22; Sic30a10; Kctd3; Ahcy1; Clcc1; Kctd14; Kcns3; Kctd12; Atp11c
GO:0015800	acidic amino acid transport	19	2	2.86	4475	0.80397	1	0.646431772	0.070087354	Cln8; Sic25a22	
GO:0051953	negative regulation of amine transport	19	2	2.86	4479	0.80397	1	0.416142903	0.046698326	Maob; Sic18a1	
GO:0035815	positive regulation of renal sodium excr...	10	1	1.51	4497	0.80486	0.80486	0.765874959	-0.002099359	Edn1	
GO:0051929	positive regulation of calcium ion trans...	10	1	1.51	4502	0.80486	0.80486	0.282215436	-0.10985619	Vdr	
GO:0060123	regulation of growth hormone secretion	10	1	1.51	4503	0.80486	0.80486	0.385672496	0.049067447	Chd7	
GO:0071577	zinc ion transmembrane transport	10	1	1.51	4504	0.80486	0.80486	0.271989996	0.034007786	Sic39a1	
GO:0010155	regulation of proton transport	10	1	1.51	4518	0.80486	1	0.337808006	-0.014318114	Sic9a3r1	
GO:0015802	basic amino acid transport	10	1	1.51	4524	0.80486	1	0.559132869	0.014010969	Arg1	
GO:0032303	regulation of icosanoid secretion	10	1	1.51	4529	0.80486	1	-0.791892031	-0.11983033		Pla2g10
GO:0032891	negative regulation of organic acid tran...	10	1	1.51	4531	0.80486	1	0.725427648	0.12605561	Irs2	
GO:0015844	monoamine transport	59	7	8.89	4551	0.80576	1	0.476550737	0.04566338	Sic6a3; Sic6a4; Sic22a1; Sic22a3; Nisch; Maob;	
GO:0002791	regulation of peptide secretion	104	13	15.67	4554	0.80665	1	0.133630472	-0.001378986	Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Ensa; Chd7; Irs2	Cpt1a; Gcg; Pdx1; Oxtt1; Acvr1c
GO:0090087	regulation of peptide transport	104	13	15.67	4555	0.80665	1	0.133630472	-0.001378986	Glud1; Jak2; Ppp3ca; Rbp4; Srebf1; Ensa; Chd7; Irs2	Cpt1a; Gcg; Pdx1; Oxtt1; Acvr1c
GO:0051050	positive regulation of transport	432	59	65.11	4566	0.81545	1	0.105793507	0.012978322	Abca1; Acvr2a; C3; Cd36; Edn1; F2; F2r1; Glud1; Hyal2; Ins2; Cd47; Jak2; Mbl2; Mdm2; Prkc; Pon1; Inpp5k; Rbp4; Src; Tnfrsf1a; Nr1h3; Vdr; Vtn;	Casp1; Cdk1; Ect2; Ednra; Ptkc; Gcg; Itln1; Pdx1; Pla2g4a; Ppt1; Ptger4; Wfs1; Pla2g10; Stk39; Pycard; Oxtt1; Dnm1; Steap2; Clk1; Scfd1; Rab27b; Sytl2; Tlr3; Cd209d; Acsi6; Ahcy1
GO:0071705	nitrogen compound transport	200	26	30.14	4585	0.82131	1	0.35359089	0.058537896	Cln8; Sic9a3r1; Sic22a4; Sic7a8; Arl2; Pdzk1; Nisch; Sic25a22; Abp1; Sic6a8; Maob; Sic18a1; Sic36a1;	Crym; Ednra; Sic25a17; Sic25a26
GO:0070509	calcium ion import	20	2	3.01	4599	0.82678	0.68152	-0.187948215	-0.035294091	Micu1	Gcg
GO:0015804	neutral amino acid transport	20	2	3.01	4611	0.82678	1	0.464685718	0.052806221	Sic36a1; Sic36a2	
GO:0051051	negative regulation of transport	251	33	37.83	4615	0.8279	1	0.539133874	0.088388694	Accn2; Apoa1; Apoa2; Apoc1; Apoc2; Cd36; Edn1; F2r1; Ins2; Anpep; Ppp3ca; Inpp5k; Srebf1; Tff2; Thr; Nr1h3; Sic9a3r1; Ndfip1; Dab2ip; Maob; Abp;	Pten; Ptger4; Stxbp3a; Pla2g10; Psmid10; Dph3; Acvr1c
GO:0008272	sulfate transport	11	1	1.66	4633	0.83429	0.83429	0.375093168	0.043571617	Sic25a10	
GO:0001820	serotonin secretion	11	1	1.66	4655	0.83429	1	0.31702691	-0.045341182	Maob	
GO:0032413	negative regulation of ion transmembrane...	11	1	1.66	4670	0.83429	1	0.337808006	0.031617009	Sic9a3r1	
GO:0060986	endocrine hormone secretion	29	3	4.37	4695	0.83436	1	0.240437036	-0.001304325	Acvr2a; Meg3; Tbx3	
GO:0015992	proton transport	77	9	11.6	4702	0.83951	0.84332	0.382482794	0.041612376	Atp6v0a1; Cox8a; Sic9a3r1; Atp6ap1; Sic47a1; Sic35a4; Atp6v0b; Sic36a1; Sic36a2	
GO:0046903	secretion	585	80	88.16	4719	0.84643	0.55963	0.199184664	0.012787417	Abca1; Accn2; Ace; Acvr2a; Acvr2b; Apoa1; Apoa2; Aprt; Copa; Sic6a3; Dgat1; Dvl1; Edn1; Eif2ak3; F2r1; Glud1; Guca2b; Ins2; Jak2; Anpep; Ugl1; Meg3; Pdpk1; Prkc; Ppp3ca; Rbp4; Src; Srebf1; Stx4a; Stxbp2; Tbx3; Hnf1b; Tff2; Nr1h3; Vdr; Vegfa; Sic9a3r1; Panx1; Ensa; Smpd3; Rab3; Nisch;	Casp1; Cpt1a; Ednra; Gcg; Pdx1; Pla2g4a; Ppt1; Ptger4; Scg5; Stxbp3a; Usf2; Agr2; Pla2g10; Rala; Pycard; Oxtt1; Dnm1; Steap2; Clk1; Scfd1; Rab27b; Sytl2; Dph3; Cd209d; Socs2; Car9; Acvr1c

GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0006818	hydrogen transport	78	9	11.76	4730	0.85026	1	0.382482794	0.043249771	Atp6v0a1; Cox8a; Slc9a3r1; Atp6ap1; Slc47a1; Slc35a4; Atp6v0b; Slc36a1; Slc36a2	
GO:0046676	negative regulation of insulin secretion	30	3	4.52	4732	0.85125	0.85125	0.26208732	-0.021015743	Ppp3ca; Sreb1	Acvr1c
GO:0071436	sodium ion export	47	5	7.08	4745	0.85643	0.85643	0.547857463	0.092593653	Atp1a1; Slc6a3; Slc6a4; Slc23a1; Slc6a8	
GO:0051937	catecholamine transport	47	5	7.08	4747	0.85643	1	0.520882536	0.05725291	Slc6a3; Slc22a1; Slc22a3; Nisch; Slc18a1	
GO:0006814	sodium ion transport	154	19	23.21	4749	0.85788	0.12465	0.445389435	0.07091268	Slc9a3r1; Slc22a4; Slc5a3; Slc5a4a; Slc5a4b; Slc24a3; Slc6a8; Al1317395; Slc5a9; Slc5a11; Slc5a12	Slc12a2; Ahcy1
GO:0010829	negative regulation of glucose transport	12	1	1.81	4755	0.85928	0.85928	0.355209957	0.052811349	Inpp5k	
GO:0030252	growth hormone secretion	12	1	1.81	4778	0.85928	1	0.385672496	0.046666589	Chd7	
GO:0051023	regulation of immunoglobulin secretion	12	1	1.81	4786	0.85928	1	1.015488235	0.08982852	Rbp4	
GO:0043266	regulation of potassium ion transport	22	2	3.32	4811	0.86535	0.89855	-0.531337464	-0.043801524		Stk39; Kcne3
GO:0006817	phosphate ion transport	13	1	1.96	4878	0.8805	1	0.375093168	0.0513248	Slc25a10	
GO:0033605	positive regulation of catecholamine sec...	13	1	1.96	4881	0.8805	1	0.515258897	0.075794411	Slc18a1	
GO:0051955	regulation of amino acid transport	13	1	1.96	4885	0.8805	1	0.559132869	0.044383927	Arg1	
GO:0090279	regulation of calcium ion import	13	1	1.96	4893	0.8805	1	-0.753609108	-0.083232558		Gcg
GO:0020208	regulation of sodium ion transport	32	3	4.82	4896	0.88056	0.80505	0.047816325	0.004748011	Atp1a1; Slc9a3r1	Ahcy1
GO:0010524	positive regulation of calcium ion trans...	23	2	3.47	4912	0.88153	1	0.137191025	0.013172605	F2	Ednra
GO:0051046	regulation of secretion	378	49	56.97	4939	0.89283	1	0.257490386	0.031323124	Accn2; Acvr2a; Apoa1; Apoa2; Edn1; F2r1; Glud1; Ins2; Jak2; Anpep; Pdpk1; Prkcz; Ppp3ca; Rbp4; Src; Sreb1; Stxbp2; Tff2; Nr1h3; Slc9a3r1; Panx1; Ensa; Ralb; Arfip1; Maob; Abr; Bcr; Slc18a1; Zfp384; Cyt12; Dph3; Cd209d; Acvr1c	Casp1; Cpt1a; Gcg; Pdx1; Ptger4; Scg5; Stxbp3a; Pla2g10; Rala; Pycard; Oxt1; Dnm1l; Rab27b; Sytl2; Dph3; Cd209d; Acvr1c
GO:0090278	negative regulation of peptide hormone s...	33	3	4.97	4944	0.89319	1	0.26208732	-0.019012456	Ppp3ca; Sreb1	Acvr1c
GO:0010765	positive regulation of sodium ion transp...	14	1	2.11	4979	0.89653	0.89653	-0.421727144	-0.052029931		Ahcy1
GO:0006835	dicarboxylic acid transport	14	1	2.11	4995	0.89653	1	0.375093168	-0.055628848	Slc25a10	
GO:0046883	regulation of hormone secretion	138	16	20.8	5016	0.90083	0.27931	0.140125611	0.014085866	Acvr2a; Edn1; Glud1; Jak2; Ppp3ca; Rbp4; Sreb1; Ensa; Chd7; Irs2	Cpt1a; Gcg; Pdx1; Scg5; Oxt1; Acvr1c
GO:0002792	negative regulation of peptide secretion	34	3	5.12	5028	0.90461	1	0.26208732	-0.015922361	Ppp3ca; Sreb1	Acvr1c
GO:0051047	positive regulation of secretion	207	25	31.2	5043	0.90795	1	0.075977913	0.012833919	Acvr2a; Edn1; F2r1; Glud1; Ins2; Jak2; Prkcz; Rbp4; Src; Panx1; Slc18a1; Zfp384; Exph5; Irs2	Casp1; Gcg; Pdx1; Ptger4; Pla2g10; Pycard; Oxt1; Dnm1l; Rab27b; Sytl2; Cd209d
GO:0032411	positive regulation of transporter activ...	25	2	3.77	5044	0.90861	0.4801	0.839283343	-0.016117276	Pon1; Vdr	
GO:0051279	regulation of release of sequestered cal...	25	2	3.77	5054	0.90861	1	0.137191025	0.00998921	F2	Ednra
GO:0006825	copper ion transport	15	1	2.26	5075	0.91383	0.91383	-0.387833043	-0.035438906		Sco1
GO:0048243	norepinephrine secretion	15	1	2.26	5076	0.91383	0.91383	0.32407331	0.021006721	Nisch	
GO:0015711	organic anion transport	54	5	8.14	5140	0.92539	0.99546	0.228887692	0.013556441	Cln8; Slc25a10; Slc25a22	Slc16a1; Sfxn5
GO:0032409	regulation of transporter activity	71	7	10.7	5146	0.92572	1	0.660167095	0.050213317	Apoa2; Ins2; Pon1; Vdr; Slc9a3r1; Ndfip1	Ahcy1
GO:0014046	dopamine secretion	17	1	2.56	5220	0.938E-01	1.00E+00	0.515258897	0.022861105	Slc18a1	
GO:0014059	regulation of dopamine secretion	17	1	2.56	5221	0.93787	1	0.515258897	0.022861105	Slc18a1	
GO:0006836	neurotransmitter transport	114	12	17.18	5231	0.93806	0.90907	0.365846137	0.058658321	Accn2; Slc6a3; Dvl1; Slc6a4; Slc22a1; Slc22a3; Stx4a; Cln8; Arl2; Slc6a8; Slc18a1	Ppt1
GO:0006813	potassium ion transport	154	17	23.21	5253	0.94054	0.24898	-0.027135703	0.006481497	Atp1a1; Slc12a7; Abcc9; Kctd5; Slc24a3; Slc12a6; Kcnj13	Kcnk1; Kcnk2; Slc12a2; Tmem38b; Stk39; Kcne3; Kcnmb4; Kctd3; Kcns3; Kctd12
GO:0006812	cation transport	667	87	100.52	5257	0.94166	0.53412	0.229596253	0.031514753	Accn2; Ap3d1; Atp1a1; Atp2a2; Atp6v0a1; Atp8a1; Atp9a; Cox8a; Slc6a3; Sfxn1; F2; Slc6a4; Pkd1; Ppp3ca; Inpp5k; Psen2; Slc12a7; Slc13a2; Slc22a1; Slc22a3; Slc23a1; Abcc9; Trf; Vdac1; Vdr; Slc9a3r1; Slc39a1; Slc22a4; Atp9b; Slc7a8; Slc5a3; Atp6ap1; Panx1; Rhhg; Pdzk1; Slc5a4a; Slc5a4b; Slc47a1; Slc25a37; Slc35a4; Trpm4; Kctd5; Slc39a5; Slc39a4; Abcb6; Abp1; Mcoln1; Slc24a3; Slc6a8; Slc12a6; Slc39a1; Slc22a4; Atp9b; Slc7a8; Slc5a3; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc5a4a; Slc5a4b; Slc47a1; Slc25a37; Slc35a4; Slc25a22; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; Abp1; Mcoln1; Cnmm4; Slc24a3; Clca6; Abca1; Accn2; Acvr2a; Acvr2b; Apoa1; Apoa2; Dgat1; Dvl1; Edn1; Elf2ak3; F2r1; Glud1; Ins2; Jak2; Slc22a4; Atp9b; Slc7a8; Atp6ap1; Panx1; Fxyd1; Rhhg; Pdzk1; Slc47a1; Slc35a4; Trpm4; Kctd5; Kctd2; Slc39a5; Slc39a4; Slc22a23; Abcb6; 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GO.ID	Term	Annotated	Significant	Expected	Rank in classic	classic	weight	avgFC.sig	avgFC	sigGenesUp	sigGenesDown
GO:0043271	negative regulation of ion transport	37	2	5.58	5626	0.98215	1	0.346508982	0.011633046	Inpp5k; Slc9a3r1	
GO:0050432	catecholamine secretion	38	2	5.73	5642	0.98449	1	0.419666103	0.022085704	Nisch; Slc18a1	
GO:0022898	regulation of transmembrane transporter ...	62	4	9.34	5693	0.98881	0.55912	0.245483865	-0.012781733	Ins2; Vdr; Slc9a3r1	Ahcy1
GO:0051952	regulation of amine transport	52	3	7.84	5701	0.98945	1	0.463806225	0.039399158	Arg1; Maob; Slc18a1	
GO:0051588	regulation of neurotransmitter transport	41	2	6.18	5714	0.98986	1	0.46257697	0.037266261	Accn2; Slc18a1	
GO:0051049	regulation of transport	913	114	137.6	5720	0.99043	1	0.184494592	0.024950357	Abca1; Accn2; Acvr2a; Apoa1; Apoa2; Apoa4; Apoc1; Apoc2; Arg1; Atp1a1; C3; Cd36; Clcn2; Edn1; F2; F2r1; Gas1; Glud1; Hyal2; Ins2; Cd47; Jak2; Anpep; Mbl2; Mdm2; Ppp1r12a; Pdpk1; Prkcz; Pon1; Ppara; Ppp3ca; Inpp5k; Rbp4; Ncor1; Src; Srebf1; Stxbp2; Tff2; Thra; Tnfrsf1a; Nr1h3; Vdac1; Vdr; Vtn; Synj2bp; Slc9a3r1; Panx1; Ensa; Pdzk1; Actn4; Ralb; Ndfip1; Adipor2; Kctd5; Dab2ip; Apoa2; Cd36; Clcn2; Hyal2; Ins2; Jak2; Thra; Tnfrsf1a; Vdac1; Vdr; Slc9a3r1; Pdzk1; Kctd5; Dab2ip; Flna; Pde2a; Irs2; Acs15; Kcnj13	Casp1; Cd2ap; Cdk1; Cpt1a; Ect2; Ednra; Ptk2; Gcg; Itln1; Kcnk1; Kcnk2; Prdx1; Pdx1; Pla2g4a; Ppt1; Pten; Ptger4; Scg5; Stxbp3a; Wfs1; Pla2g10; Psmd10; Stk39; Rala; Kcne3; Pycard; Oxct1; Tmem30a; Dnm1; Scfd1; Rab27b; Sytl2; Dph3; Prkaa1; Tlr3; Cd209d; Clic6; Acs16; Kctd3; Ahcy1; Kcns3; Kctd12; Acvr1c
GO:0034762	regulation of transmembrane transport	319	34	48.08	5737	0.99168	1	0.094120936	0.011484913	Apoa2; Cd36; Clcn2; Hyal2; Ins2; Jak2; Thra; Tnfrsf1a; Vdac1; Vdr; Slc9a3r1; Pdzk1; Kctd5; Dab2ip; Flna; Pde2a; Irs2; Acs15; Kcnj13	Cdk1; Ect2; Gcg; Kcnk1; Kcnk2; Prdx1; Psmd10; Kcne3; Tlr3; Clic6; Acs16; Kctd3; Ahcy1; Kcns3; Kctd12
GO:0032412	regulation of ion transmembrane transpor...	57	3	8.59	5777	0.99451	0.62576	0.066098766	-0.026110371	Vdr; Slc9a3r1	Ahcy1
GO:0051209	release of sequestered calcium ion into ...	46	2	6.93	5797	0.99505	1	0.137191025	-0.011698853	F2	Ednra
GO:0070588	calcium ion transmembrane transport	81	5	12.21	5811	0.99604	0.99679	0.164591748	0.015885684	Accn2; Atp2a2; Panx1; Micu1	Gcg
GO:0050433	regulation of catecholamine secretion	34	1	5.12	5815	0.99615	1	0.515258897	0.025542743	Slc18a1	
GO:0007269	neurotransmitter secretion	72	4	10.85	5828	0.99672	0.77984	0.087354163	0.010885382	Accn2; Dvl1; Stx4a	Ppt1
GO:0046928	regulation of neurotransmitter secretion	35	1	5.27	5829	0.99673	1	0.409895043	0.013942694	Accn2	
GO:0051925	regulation of calcium ion transport via ...	38	1	5.73	5853	0.998	1	0.282215436	-0.012995545	Vdr	
GO:0006816	calcium ion transport	225	19	33.91	5882	0.99902	0.32458	0.186608061	-0.003325024	Accn2; Atp2a2; F2; Pkd1; Ppp3ca; Inpp5k; Psen2; Vdac1; Vdr; Panx1; Trpm4; Mcoln1; Slc24a3; Micu1	Ednra; Gcg; Wfs1; Clca3; Sri
GO:0060402	calcium ion transport into cytosol	61	2	9.19	5911	0.99945	1	0.137191025	0.002437118	F2	Ednra
GO:0060401	cytosolic calcium ion transport	62	2	9.34	5916	0.99953	1	0.137191025	0.001346232	F2	Ednra
GO:0034765	regulation of ion transmembrane transpor...	207	16	31.2	5918	0.99955	0.99641	-0.057340702	-0.009844496	Clcn2; Vdac1; Vdr; Slc9a3r1; Pdzk1; Kctd5; Kcnj13	Gcg; Kcnk1; Kcnk2; Kcne3; Clic6; Kctd3; Ahcy1; Ednra; Gcg; Wfs1; Stk39; Kcne3; Ahcy1
GO:0010959	regulation of metal ion transport	164	11	24.72	5930	0.9997	1	-0.101927093	-0.023236013	Atp1a1; F2; Inpp5k; Vdr; Slc9a3r1	Ednra; Gcg; Wfs1; Stk39; Kcne3; Ahcy1
GO:0051924	regulation of calcium ion transport	126	6	18.99	5952	0.99994	1	-0.033662012	-0.022696587	F2; Inpp5k; Vdr	Ednra; Gcg; Wfs1
GO:0043269	regulation of ion transport	320	22	48.23	5965	1	1	-0.042742112	-0.011947785	Atp1a1; Clcn2; F2; Inpp5k; Vdac1; Vdr; Slc9a3r1; Pdzk1; Kctd5; Kcnj13	Ednra; Gcg; Kcnk1; Kcnk2; Wfs1; Stk39; Kcne3; Clic6; Kctd3; Ahcy1; Kcns3; Kctd12