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Original Article

Discovery of a stem-like multipotent cell fate

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Abstract: Adipose derived stem cells (ASCs) can be obtained from lipoaspirates and induced *in vitro* to differentiate into bone, cartilage, and fat. Using this powerful model system we show that after *in vitro* adipose differentiation a population of cells retain stem-like qualities including multipotency. They are lipid (-), retain the ability to propagate, express two known stem cell markers, and maintain the capacity for trilineage differentiation into chondrocytes, adipocytes, and osteoblasts. However, these cells are not traditional stem cells because gene expression analysis showed an overall expression profile similar to that of adipocytes. In addition to broadening our understanding of cellular multipotency, our work may be particularly relevant to obesity-associated metabolic disorders. The adipose expandability hypothesis proposes that inability to differentiate new adipocytes is a primary cause of metabolic syndrome in obesity, including diabetes and cardiovascular disease. Here we have defined a differentiation-resistant stem-like multipotent cell population that may be involved in regulation of adipose expandability *in vivo* and may therefore play key roles in the comorbidities of obesity.

Keywords: Adipose-derived stem cells, multipotency, adipocyte, chondrocyte, osteoblast

Introduction

Currently 35% of adults in the United States are obese [1], a condition associated with comorbidities including cardiovascular disease [2], diabetes [3], and even cancer [4]. Obesity comes in two forms, distinguished by the ability of subcutaneous fat depots to grow by the differentiation of new fat cells (hyperplasia) or alternatively, by the enlargement of existing adipocytes to accommodate greater lipid storage (hypertrophy) [5]. In hypertrophic obesity, lipids are also stored as ectopic visceral fat causing lipotoxicity, which contributes to adverse health outcomes and comorbidities including diabetes and cardiovascular disease [6].

The adipose tissue expandability hypothesis states that when excess energy cannot be stored in subcutaneous fat depots (i.e., more adipocytes cannot be formed), the existing adipocytes compensate by becoming larger (storing more lipid per cell), and lipids are also stored in other body regions (ectopically). The ability to differentiate new adipocytes from preadipocytes determines the limit on subcutaneous adipose tissue expandability [7]. Here we use adipose-derived stem cells (ASCs) [8] as a model system to investigate adipose differentiation *in vitro.*

ASCs are adult stem cells of the mesodermal lineage that can easily be purified from subcutaneous fat obtained from liposuction aspirates and can be differentiated into chondrocytes, adipocytes, and osteoblasts by adding the appropriate cocktail of hormones to the culture media [8, 9]. However, we found that adipose differentiation always appears incomplete-a substantial subpopulation of lipid (-) cells is always present. Here we investigate these cells to determine whether they represent *bona fide* stem cells. The International Society for Cellular Therapy (ISCT) defines ASCs based on the following criteria: cells must adhere to plastic; cells must express three surface markers CD73, CD90, and CD105; and cells must have trilineage differentiation potential to produce bone, cartilage and fat [10]. Here we show that the lipid (-) cells satisfy most of these criteria:

they adhere to plastic, they express two of the three markers, and they retain trilineage differentiation capacity. Surprisingly, however, their gene expression profile strongly resembles that of adipocytes, suggesting that multipotency can be retained in previously unknown cell populations that may exist on a continuum between classical stem cells and differentiated fates.

Material and methods

Cell culture

Cell lines were grown in plastic 6-well dishes with growth media maintained in a humidified 5% CO_2 incubator at 37°C. The growth media consist of Dulbecco's Modified Eagle Medium (DMEM, ThermoFisher #11965118) supplemented with 10% fetal bovine serum (ThermoFisher #10082147), 1X Penicillin/Streptomycin (ThermoFisher #15140122), and 1X Glutamax (ThermoFisher #35050061). Cell washes were performed with DPBS (ThermoFisher #14190144) and passages with Trypsin-EDTA 0.25% (ThermoFisher #25200056). Media was always changed every 72-96 hours under sterile hood for both growth and differentiation.

Culture volumes for 6-well dishes (VWR Cat #10062-892) was 2 ml/well. For 16-chamber slides (VWR Cat #62407-350), 200 ul was used, but to avoid contamination and evaporation during 2-3 week differentiations slides were housed inside a sterile plastic petri dish.

Adipocyte differentiation

For adipocyte differentiation, cells were cultured to confluence. Then, the growth media was removed and replaced with adipogenic differentiation media consisting of 10% FBS, 1% Penicillin/Streptomycin, 1X Glutamax, 1.0 μM Dexamethasone, 0.5 mM IBMX (3-isobutyl-1-methylxanthine), 0.2 mM Indomethacin, and 10.0 μM Insulin.

Chondrocyte differentiation

For chondrocyte differentiation, cells were cultured to confluence in 6-well dishes. Then, the growth media was removed, cells trypsinized and concentrated at 200 g for 5 minutes into 2-3 micromass 10 μL droplets in a new dish (i.e., one well was concentrated to 3 drops). They were allowed to adhere at 37°C in an atmosphere of 5% CO_2 for 45 minutes, followed by gentle flooding of the new well with chondrocyte differentiation media (2 mL). Chondrocyte media is composed of 1% FBS, 1% PenStrep, 6.25 μg/mL Insulin, 10 ng/mL TGF-β1, and 50 nM Ascorbate-2-Phosphate.

Osteoblast differentiation

For osteoblast differentiation, cells were cultured to confluence. Then, the growth media was removed and replaced with osteoblast differentiation media consisting of 10% FBS, 1% PenStrep, 50 μM ascorbate-2-phosphate, 0.1 μM dexamethasone, and 10 mM β-glycerophosphate.

Trilineage differentiation

Confluent cells grown in plastic 6-well dishes were treated with adipogenic differentiation media (day 0). Media changes were performed under a sterile hood every 72-96 hours for 27 days. These adipocyte cells were then trypsinized and centrifuged at 200 g for 5 minutes. The floating lipid (+) cells were discarded, and the lipid (-) cells were re-plated and placed into standard growth media. Once again, these cells were grown to confluency with regular media changes every 72-96 hours. On day 45, the trilineage differentiation was initiated by placing an individual population of cells (2 wells) into either chondrogenic differentiation media, adipogenic differentiation media, or osteogenic differentiation media. These cell populations were permitted to differentiate with regular media changes every 72-96 hours, for 26 days. On day 66, the cells were fixed and stained using Alcian Blue, Oil Red O, and Von Kossa and imaged. In brief, cells were washed twice with DPBS, fixed in 4% paraformaldehyde (diluted from 20%, Electron Microscopy Sciences #15713-S) in PBS for 1 hour (for adipocytes, supplemented with 1% calcium chloride).

For adipocytes, cells were stained with Oil Red O (ORO; Santa Cruz Biotechnology #sc-203749) working solution for 5 minutes, then washed in 60% ethanol for 5 minutes and rinsed 3 times with diH_2O and imaged immediately under DIC microscopy on an inverted microscope. The ORO working solution was prepared by dissolving 0.1% w/v OrO powder directly into 99% Isopropanol; this was then diluted to 60% isopropanol in diH_2O and filtered through a 0.2 μm filter prior to use.

For osteoblasts, fixed cells were rinsed twice in DPBS, and then incubated in 2% Silver Nitrate Solution (5 ml diH_2O with 0.1 g silver nitrate powder, Sigma-Aldrich #209139) for 30 min in the dark. After a DPBS wash, cells were air dried and imaged on an inverted DIC microscope; sufficient darkening occurred spontaneously without use of UV light to further develop the signal.

For chondrocytes, fixed cells were washed in diH_2O twice and then incubated with 1% wt/vol Alcian Blue (Sigma-Aldrich #A3157) in 0.1N HCl (pH 1.0) for 30 min; they were then washed in 0.1N HCl for 5 minutes to remove excess stain, and imaged under DIC microscopy.

Surface marker immunofluorescence and oil red O (ORO) staining

ASCs were cultured in chamber slides to ~95% confluency and analyzed. For differentiated cells, ASCs were cultured in growth media in chamber slides until confluent, and differentiated in adipocyte media for 18-21 days. Protocol A is described in Koopman et al. 2001 [11]. Briefly, media was aspirated and cells were fixed in 3.7% formaldehyde (VWR #97064-888) in PBS. After 1 hr the cells were rinsed 3x in diH_2O before permeabilization in 0.5% Triton X-100 in PBS for 5 min, followed by rinsing 3x in PBS and incubation with primary antibodies in PBS overnight at 4°C. The cells were then rinsed 3x in PBS, then incubated with secondary antibodies in PBS for 1 hr, and rinsed again 3x in PBS. Cells were then incubated in Oil Red O working solution (see below) for 30 min at room temperature, then rinsed 3x in diH_2O and then in gently flowing tap water for 10 minutes before mounting in Prolong Gold Antifade Reagent with DAPI (Cell Signaling #8961S). Negative controls lacking primary antibodies were included in all experiments. Protocol B is published on the Cell Signaling website (https://www.cellsignal.com/contents/resources-protocols/immunofluorescence-general-protocol/if). Briefly, cells are fixed in 4% methanol-free formaldehyde (Polysciences, Inc #18814-10) in PBS for 15 min at room temperature, followed by 3 rinses in PBS, blocking for 1 hour (1X PBS/5% Goat serum albumin/0.3% Triton^{TM} X-100), then incubated with primary antibodies overnight. Samples were then incubated with secondary antibodies and washed as in Protocol A, followed by mounting in Prolong Gold Antifade Reagent with DAPI.

Primary antibodies: CD90, BD Pharmingen 55-0402 used at 1:100 dilution; CD105, Thermo-Fisher PA5-16895 used at 1:50 dilution. Secondary (FITC) antibody was Santa Cruz sc-2010, used at 1:1000 dilution.

For the Oil Red O working solution, a stock was prepared as follows: 10 mg of ORO powder (Santa Cruz Biotechnology #sc-203749) was dissolved in 2 ml of 60% Triethyl phosphate (Santa Cruz #sc-251322). This was then further diluted to a 36% Triethyl-phosphate solution by combining 1.2 ml of this stock with 0.8 ml diH_2O, and filtered through a 0.2 μm vacuum filter (VWR #10040-460) to generate the working solution used in cell staining.

Laser confocal microscopy

Imaging and z-stack construction were performed using an Olympus FV1200 Laser Scanning Microscope equipped with FV10-ASW Viewer software (Olympus).

FACS sorting & microarray

ASC080414AF2 clonal cells (passage 12) were grown to confluency and differentiated in adipocyte media (AM) for 23 days. After trypsin treatment cells were FACS separated based on side scatter (SSC) using gates from 'high SSC' (lipid +) to 'low SSC' (lipid -). ASC080414AF2 stem cells were grown in parallel in growth media to approx. 70% confluency and then FACS sorted using the 'low SSC' gate to control for effects of sorting and gating. All cells were directly sorted into DNA/RNA Shield Buffer from the Zymo Duet DNA/RNA MiniPrep Plus kit (Zymo #D7003), followed by RNA extraction as per provided protocol. RNA was submitted to the Johns Hopkins University Microarray Core for Human PrimeView Gene Expression Array (Affymetrix) analysis.

Principal component analysis & hierarchical clustering analysis

Microarray data was processed using the Expression Console 1.4.1.46 for PCA and Transcriptome Array Console v3.1 for Hierarchical

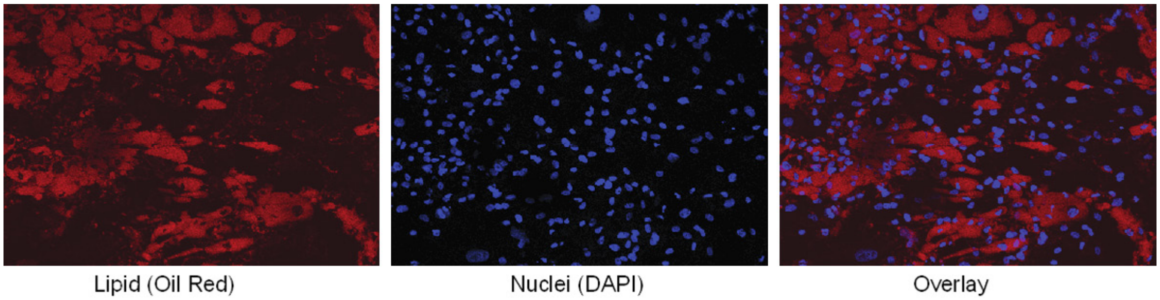


Figure 1. Fixed differentiated cells stained with Oil Red O (ORO) and nuclei counterstained with DAPI to demonstrate the existence of two populations: lipid-positive adipocytes and lipid-minus cells.

Clustering Analysis plus differential gene expression analysis.

Go analysis

The goatools v. 0.7.11 python package was used, with the 'find_enrichment.py' command using defaults (propagation of counts to parent terms). The PrimeView probe set and associated GO terms were used as the population data while Tables S1 and S2 were used as study data.

Cells used in the study

Cell Line	Source	BMI	Depot	Sex	Donor Age	Passage at Experiment	Figure
ASC100610B	Zen-Bio, Inc.	23.3	Abdomen	F	40	p6	**Figure 5B, 5C**
ASC021606	Zen-Bio, Inc.	32.1	Abdomen	F	46	p4	**Figures 4, 5A**
ASC080414A-derived clonal line	Zen-Bio, Inc.	25.1	Abdomen	F	39	p12	**Figures 2, 3, 6**
0912	DeCicco-Skinner lab, AU	31.6	Breast	M	27	p5	**Figure 1**

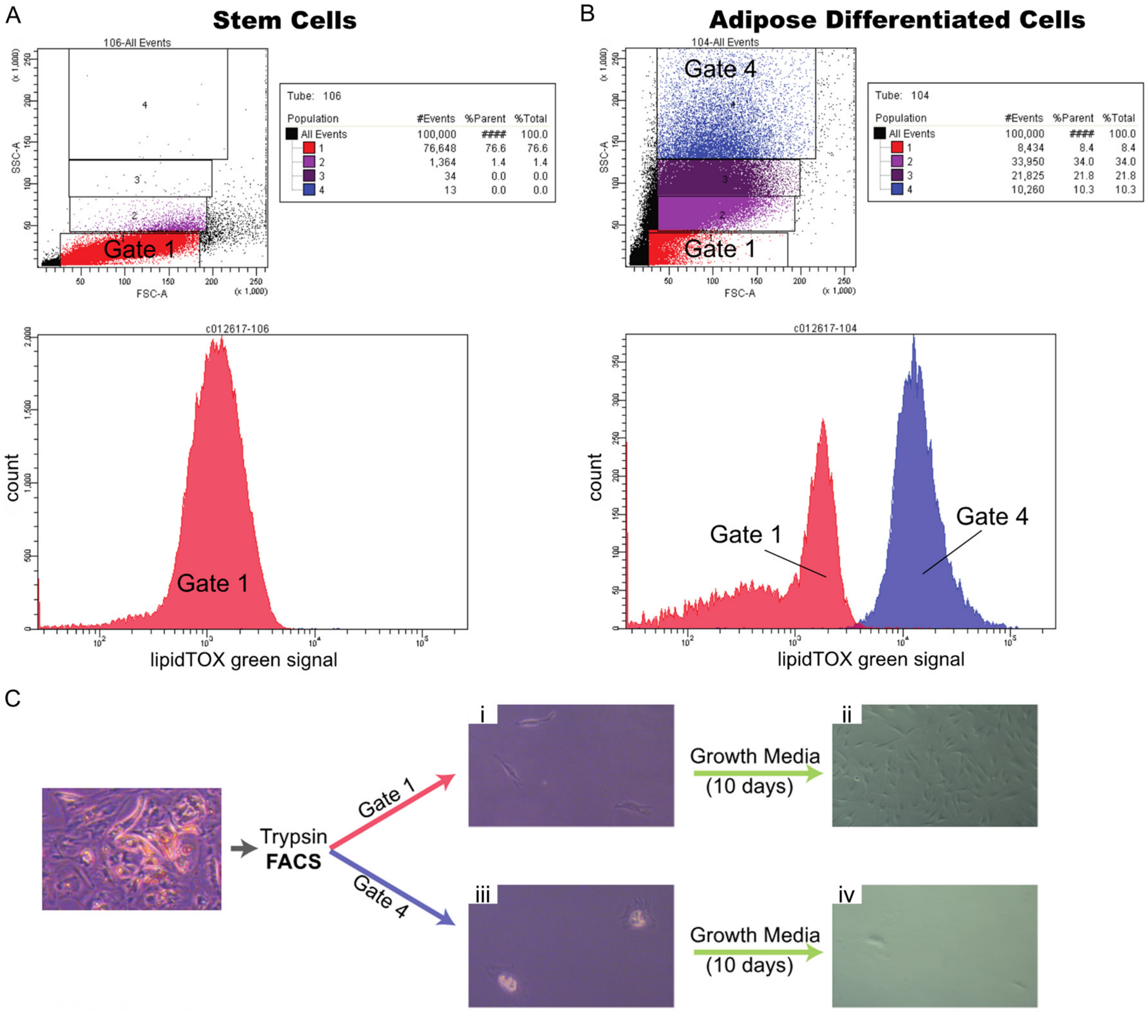
Results

We observed that adipose-differentiated human ASCs always result in two apparently distinct populations, lipid (+) adipocytes and lipid (-) cells (**Figure 1**). We hypothesized these lipid (-) cells might represent a previously unknown population of quiescent stem cells maintained even during culture in differentiation-inducing conditions, but to study them further we needed to isolate them.

We found that by FACS sorting on side scatter alone we were able to cleanly separate lipid (-) from lipid (+) cells as measured both by lipidTOX dye and by visual inspection of sorted cells (**Figure 2**). Consistent with their quiescent stem-cell status, the lipid (-) population demonstrated good replicative ability while the lipid (+) cells do not appreciably replicate (**Figure 2C**). We extracted RNA from differentiated FACS-sorted lipid (+), lipid (-), and matching stem cells (~70% confluent, collected through the same gate as lipid (-) on FACS), in triplicate. Because the FACS-sorted lipid (-) population yielded very low RNA levels, we pooled all three replicates and obtained seven total PrimeView microarray gene expression profiles covering over 49,000 individual loci and all annotated human genes.

We used Principal Component Analysis (PCA) to evaluate relative gene expression profile differences. PCA captures the variation between extremely large complex datasets into new variables (components) that capture the between-dataset variation [12]. Plotting the top three components as axes on a 3D graph and locating individual datasets within that space graphically represents the relative similarity of datasets, with more similar samples clustering together [12]. In the case of our FACS-sorted cells, the top three PCA components capture 97.4% of the variation between the datasets, with PC1 alone capturing 78.8%. This component represents a clear differentiation axis with stem cells at one end and adipocytes at the other; the lipid (-) cells lie between them but closer to the adipocyte samples (**Figure 3A**).

Based on this, we conclude that the lipid (-) population does not represent traditional stem cells at least by gene expression analysis. However, the lack of lipid accumulation suggests lipid (-) cells may be at least partly undifferentiated, so we searched for genes that might contribute to this shift of the lipid (-) cells toward stem cells and away from adipocytes in



Tube: 106

Population	#Events	%Parent	%Total
■ All Events	100,000	####	100.0
🟥 1	76,648	76.6	76.6
■ 2	1,364	1.4	1.4
■ 3	34	0.0	0.0
🟦 4	13	0.0	0.0

Tube: 104

Population	#Events	%Parent	%Total
■ All Events	100,000	####	100.0
🟥 1	8,434	8.4	8.4
■ 2	33,950	34.0	34.0
■ 3	21,825	21.8	21.8
🟦 4	10,260	10.3	10.3

Figure 2. Demonstration that FACS can effectively separate lipid (-) from lipid (+) cells. (A) FACS-sorted stem cells showing Gate 1 captures stem cells. (B) FACS of adipose differentiated cells on side scatter (SSC) and forward scatter (FSC). Gates 1 and 4 cleanly separate two populations, lipid (+) and lipid (-), as shown by lipidTOX green dye readout, and by visual inspection in (C). (C) FACS sorted differentiated cells were visually inspected (i) and (iii) and allowed to propagate 10 days in growth media, (ii) vs. (iv). After 10 days only the lipid (-) cells had propagated, (ii) vs. (iv).

PCA space (**Figure 3A**). In total 39 genes are statistically upregulated in lipid (-) relative to adipocytes by ANOVA ($p < 0.05$) and at least twofold expression change (**Figure 3B**; Table S1). Using unsupervised hierarchical clustering [13] to group the samples based on the gene expression profiles of these 39 genes produced a consistent grouping of lipid (-) cells with adipocytes, rather than stem cells (**Figure 3B**) similar to the result seen with PCA analysis (**Figure 3A**). These genes give insight into the mechanisms by which these quiescent stem cells are maintained in the population: they overexpress PTGS2/COX-2, which is a direct target of dexamethasone [14], a differentiation-inducing glucocorticoid hormone added to the adipocyte-differentiation media [8, 9]. Furthermore, lipid (-) cells upregulate Gremlin-1 and Gremlin-2, which are antagonists of BMP signaling [15]. Gremlin-1 has been reported to be highly expressed in undifferentiated adipose stem cells or preadipocytes [16] consistent with its expression here in a quiescent stem cell population. Therefore, this lipid (-) cell population has specific mechanisms for counteracting the differentiation-inducing effects of adipose-differentiation media. Additionally, lipid (-) upregulated genes include CD1d, an

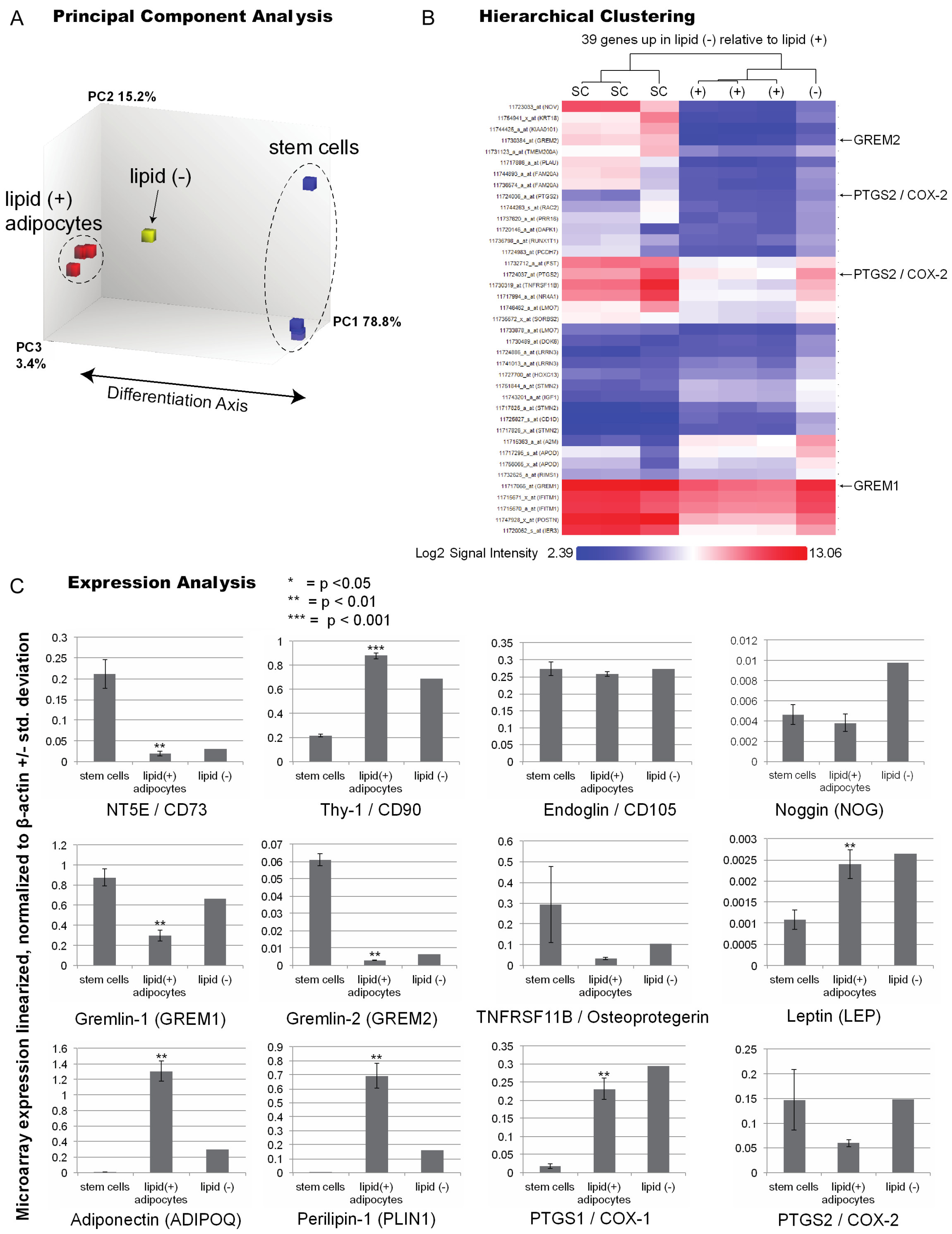


Figure 3. Analysis of gene expression data from FACS-sorted stem cells and lipid-minus cells. A. Principal Component Analysis (PCA) used to characterize gene expression profiles of FACS-separated adipocytes (red), actively growing stem cells (blue) and lipid-minus cells (yellow). B. Hierarchical clustering of 39 genes statistically up-regulated ($P < 0.05$ by ANOVA and over 2-fold change) in lipid-minus relative to adipocytes. Arrows indicate probes for Gremlin-1 and -2, and PTGS2/COX-2. C. Individual gene expression data from microarray. Microarray data for each gene was normalized to β-actin and displayed on a linear scale. Error bars represent standard deviation of three replicate microarrays; due to limited RNA yield the lipid (-) replicates were pooled into a single microarray. Student's 2-tailed T-test was used to compare adipocytes to stem cells, with * = $P < 0.05$, ** = $P < 0.01$, *** = $P < 0.001$.

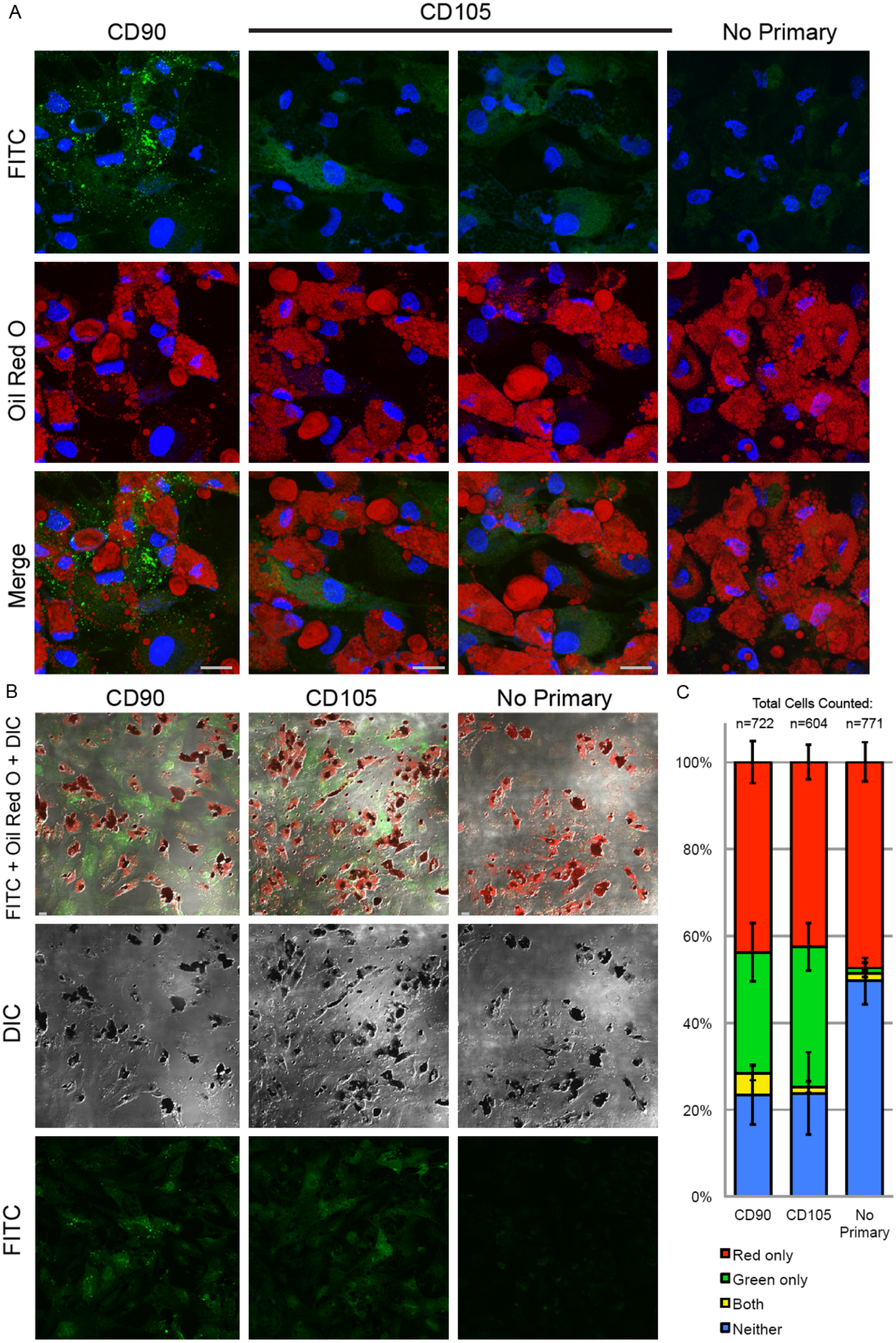

A
CD90
CD105
No Primary
FITC
Oil Red O
Merge
B
CD90
CD105
No Primary
FITC + Oil Red O + DIC
DIC
FITC
C
Total Cells Counted:
n=722
n=604
n=771
100%
80%
60%
40%
20%
0%
CD90
CD105
No Primary
🟥 Red only
🟩 Green only
🟨 Both
🟦 Neither

Figure 4. CD90 and CD105 surface markers are detected by immunofluorescence in differentiated cell line ASC021606 (BMI = 32.1). A. Cells were fixed and stained using Protocol A (Koopman, et al., 2001 [11]), with FITC signal (green) for surface markers and counterstained with Oil Red O for lipid content. No primary controls: identically processed samples but only stained with secondary (FITC) antibodies to control for background. All panels represent compressed Z-stacks taken and displayed under identical conditions. Scale bars = 20 μm. B. DIC images (planar single images, not stacks) showing that surface marker signal is co-located with membrane. Scale bars = 20 μm. C. Quantitation of green and red cells observed after CD90 or CD105 immunofluorescence with Oil Red O staining. Data represent the average and standard deviation of three fields.

MHC class I molecule that presents lipid antigens; tumor necrosis factor member 11 (TNFRSF11B, or Osteoprotegerin), involved in bone development; FAM20A, involved in hematopoiesis and tooth development; and Homeobox C13 (HOXC13), involved in hair development (Table S1). Interestingly, HOXC13 has recently emerged in meta-analysis of GWAS studies as a gene affecting fat distribution [17], suggesting it plays unappreciated adipose-related functions, and highlighting the value of our microarray data. The BMP antagonist Noggin was higher in lipid (-) than in either stem cells or lipid (+) adipocytes (**Figure 3C**) but due to its low overall expression this was not scored as statistically significant and is not included in Table S1.

These data suggest that lipid (-) cells may be primed toward non-adipose lineages including bone. Gene Ontology (GO) analysis of Table S1 confirms this, as GO:0031214, 'biomineral tissue development' was statistically over-represented after Bonferroni correction (Table S3). In addition, two smooth-muscle-related terms appear in this list: GO:0048660, 'regulation of smooth muscle cell proliferation' and GO: 2000097, 'regulation of smooth muscle cell-matrix adhesion' suggesting that the lipid (-) cells may be poised between mesodermal fates known to be within the differentiating range of these cells [8, 9]. These data support the idea that lipid (-) cells occupy a different fate space than adipocytes, as suggested by our PCA analysis (**Figure 3A**).

Genes upregulated in adipocytes relative to lipid (-) cells are generally adipocyte-specific lipid or glucose metabolism genes (Table S2). For example, adiponectin (ADIPOQ) and perilipin-1 (PLIN1) were significantly up, as was adipogenesis regulatory factor (ADRIF) (Table S2; **Figure 3C**). The most strongly upregulated genes include mitochondrial glycerol-3-phosphate dehydrogenase 1 (GPD1), a metabolic link between glucose and lipid metabolism [18] and a known adipocyte-specific gene [19], and glycerol-3-phosphate acyltransferase, (GAPM), a gene linked to a congenital lipidistrophy disorder [20]. The top adipocyte upregulated gene was phosphoenolpyruvate carboxykinase 1 (PCK1), which regulates the critical step in adipocyte glyceroneogenesis [21]. In total 141 genes were statistically upregulated in adipocytes relative to lipid (-) cells (Table S2). Gene Ontology (GO) analysis of Table S2 confirmed this: statistically enriched are GO:0019432, 'triglyceride biosynthetic process', GO:0046460, 'neutral lipid biosynthetic process', GO: 0032868, 'response to insulin', and strikingly, GO:0005811, 'lipid droplet' (Table S4).

We observed that expression of two of the three classical stem-cell markers [10] were not apparently decreased upon adipose differentiation: CD90 expression appears to increase upon differentiation while CD105 is relatively unaffected (**Figure 3C**). To confirm this we performed immunofluorescence against these three markers, enabling us to examine both their differentiation behavior and their expression in lipid (-) cells. We found that both CD90 and CD105 are detected in lipid (-) cells after differentiation (**Figure 4A**), while CD73 was not reliably detected by immunofluorescence and thus is not shown. Consistent with our observation that lipid (-) cells are relatively undifferentiated (**Figure 3A**), both CD90 and CD105 are depleted in (differentiated) lipid (+) adipocytes, being predominantly detected in lipid (-) cells (**Figure 4A-C**). The staining pattern of CD90 was highly punctate, raising the concern that it might be marking cytoplasmic structures, so we performed DIC imaging along with immunofluorescence to confirm that signal is indeed co-planar with cell membranes (**Figure 4B**). Quantitation showed that cells generally express either a stem cell surface marker (green) or Oil Red O, but rarely both, and that similar proportions of cells are positive for CD90 and CD105 (**Figure 4C**).

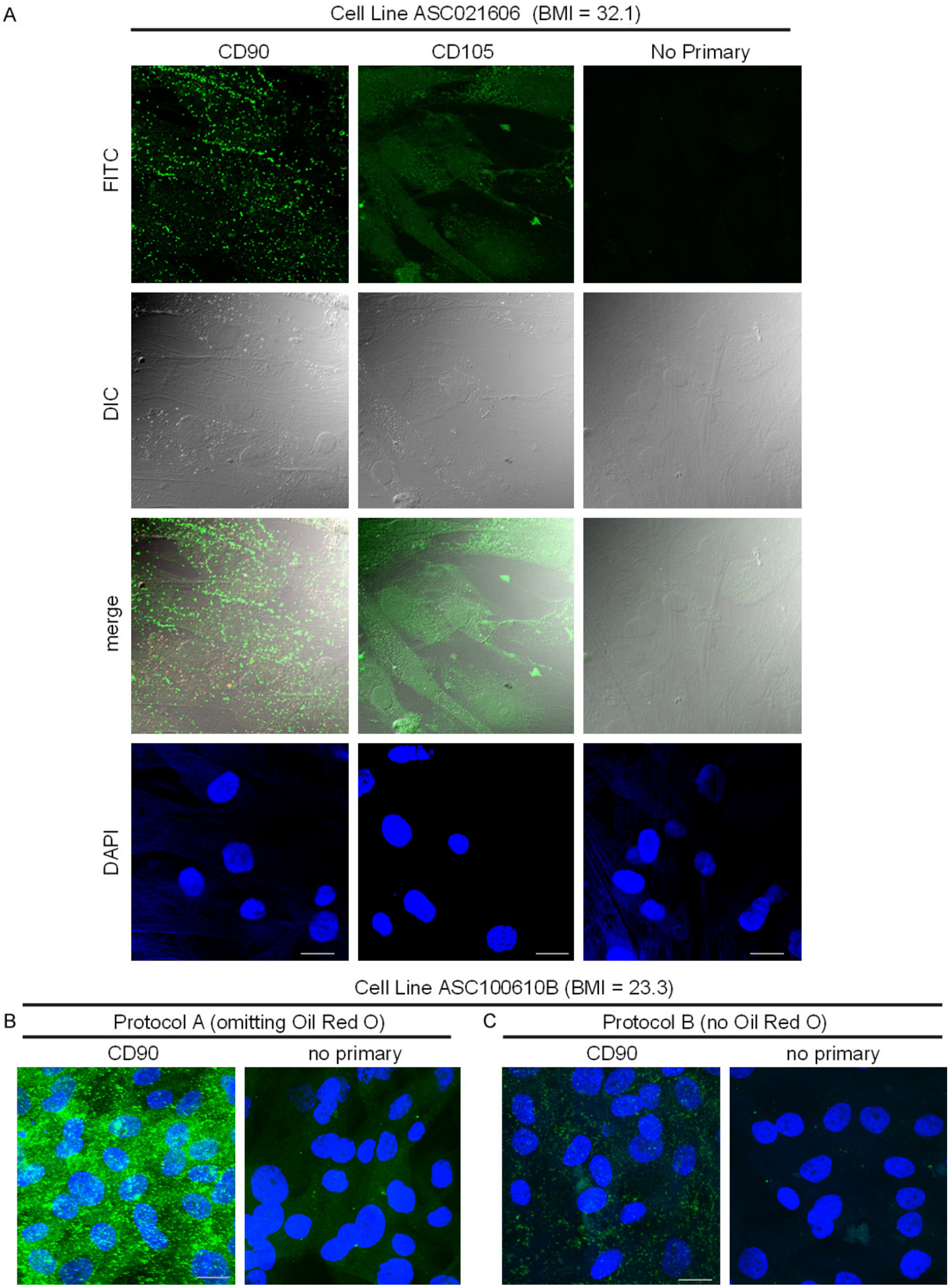


Figure 5. CD90 and CD105 surface markers are detectable by immunofluorescence in stem cells. A. Stem cells (line ASC021606, BMI = 32.1) processed using Protocol A, imaged from a single plane to show membranes by DIC. B, C. Controls to verify punctate CD90 signal is still evident without Oil Red O treatment and in a different cell line (ASC100610B, BMI = 23.3); two fixing and staining protocols used (see Methods). B. Protocol A, (Koopman et al. 2001 [11]) omitting ORO gives much stronger signal than with ORO (compare to A). C. Protocol B gives fainter signal but has lower background. All panels in B and C represent compressed Z-stacks taken and displayed under identical conditions. Scale bars = 20 μm.

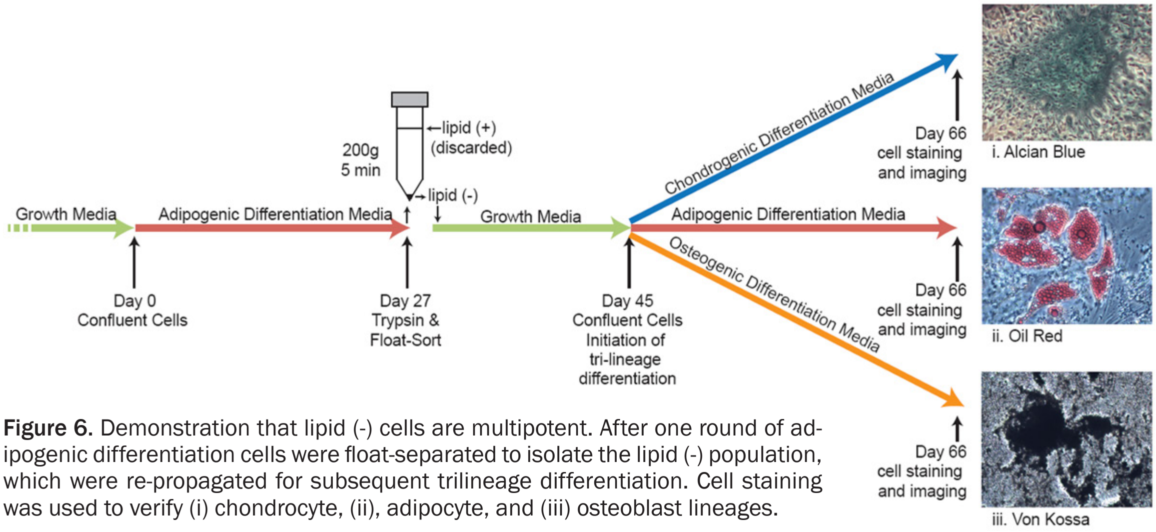


Figure 6. Demonstration that lipid (-) cells are multipotent. After one round of adipogenic differentiation cells were float-separated to isolate the lipid (-) population, which were re-propagated for subsequent trilineage differentiation. Cell staining was used to verify (i) chondrocyte, (ii), adipocyte, and (iii) osteoblast lineages.

We confirmed both stem cell markers are detectable in stem cells and that the signal is also co-planar with the membrane as revealed by DIC imaging (**Figure 5A**). We observed a consistent punctate CD90 pattern and tested whether it was potentially an artifact of fixation method or use of Oil Red O in our staining protocol. While omitting Oil Red O increased CD90 signal intensity, the signal was still punctate (**Figure 5B**); similarly using a different (Oil Red O-free) protocol (see Methods) also revealed the punctate pattern (**Figure 5C**). We therefore conclude that the CD90 pattern observed here is not caused by treatment of samples with Oil Red O, nor is it limited to a single cell type or BMI since samples from both obese (**Figure 5A**) and normal (**Figure 5B**, **5C**) donors produce a consistent pattern. Both Protocols A and B use formaldehyde (one is methanol-free and the other is not): methanol fixation did not yield good immunofluorescence signal so we cannot rule out the possibility that formaldehyde fixation induces punctate CD90 signals. However, we consider this unlikely because the CD105 signal was relatively more diffuse in both stem and differentiated cells imaged on the same slides and treated the same as CD90 (**Figures 4A**, **4B**, **5A**).

Given that the lipid (-) cells were not apparently 'true' stem cells based on their gene expression profile, we queried their multi-lineage stem potential. ASCs are considered stem cells if they retain ability to differentiate into bone, cartilage, and fat [10] so we devised an experiment to first differentiate, then isolate lipid (-) cells, re-grow them, and perform multi-lineage differentiation. We found that lipid (-) cells retain full multi-lineage potential and thus are functional stem cells (**Figure 6**). This finding fundamentally broadens our understanding of stem potential and quiescence, suggesting that a broader array of cells may retain multipotency than previously appreciated.

Discussion

In this study we show that a previously overlooked lipid (-) population continues to display two of three stem-cell markers even after adipose differentiation (**Figure 4**), and although its gene expression profile is relatively adipocyte-like (**Figure 3**) these cells are multipotent (**Figure 6**). Since they adhere to plastic, these cells satisfy the ISCT criteria for multipotent stem cells [10], with the exception of CD73 expression (**Figure 3**), suggesting that they are not 'canonical' stem cells. Therefore we have elucidated a novel stem-like multipotent fate that does not require other cell types for specification, instead being established by adipose-intrinsic cell fate determination *in vitro*. While quiescent stem cells have been reported in skin [22, 23], gut [24], blood [25], and neurons [26], they have yet to be defined in adipose tissue [27], although active adipose stem cell depots have been reported in the adipose perivasculature [28-31]. Here we describe a population of quiescent stem cells that may constitute a source of ASCs from lipoaspiration [8, 9] and under physiological regulation *in vivo* may activate into more classical stem-cell states (bearing the three surface markers [10]) specifically at times when new terminally differentiated adipocytes are needed by the organism.

This quiescent stem-like fate may be one mechanism used by the body to preserve adipose expandability. According to the adipose expandability hypothesis, when excess energy cannot be stored in subcutaneous fat depots through differentiation of new adipocytes, the existing adipocytes compensate by becoming larger (storing more lipid per cell), and lipids are also stored in other body regions (ectopically) [6, 7]. Ectopic lipid accumulation in turn causes lipotoxic effects, leading to insulin resistance, apoptosis and inflammation. The ability to differentiate new adipocytes is limited by an unknown mechanism [7]; here we have defined an apparent cell-intrinsic mechanism determining efficiency of adipose cell differentiation *in vitro*. We hypothesize that when the lipid (-) stem-like multipotent cells are depleted or not adequately maintained, adipose expandability is lost and hypertrophic obesity results. Alternatively, if a stem cell population over-commits to lipid (-) cells, it may fail to differentiate new adipocytes when they are needed, thereby limiting adipose expandability at the other extreme: retaining too many differentiation-resistant quiescent stem cells.

In vivo data appears to support this general model. One study found an inverse relationship between Body Mass Index (BMI) and lipoaspirate-derived stem cells yields, consistent with a depletion in the stem-cell population under obese conditions [32]. In diabetic patients (generally also more obese) fewer pre-adipocytes are found in adipose tissues compared to the control (non-diabetic) population [33]. Even those stem cells retained in obese individuals may be compromised: the ability of preadipocytes to differentiate into mature adipocytes was impaired in hypertrophic obesity [34, 35] and in both diabetes-predisposed [36] and diabetic [33, 37] individuals. Taken together, these mechanisms would severely limit the ability of hypertrophically obese individuals to generate new adipocytes, which may drive ectopic lipid deposition.

Our discovery of a quiescent stem-like cell population in adult adipose tissue fundamentally expands our understanding of cellular multipotency. In light of the link between BMI and stem cell abundance and behavior, future studies are necessary to investigate the relative role of a stem-like fate in comorbidities of obesity.

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Disclosure of conflict of interest

None.

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Table S1. Genes overexpressed in lipid (-) cells relative to adipocytes

Microarray Probe ID	Fold Change Lipid-minus vs. Adipocytes	ANOVA *p*-value	Gene Symbol	Description
11717825_a_at	4.52	0.010824	STMN2	Stathmin 2
11730319_at	3.75	0.035059	TNFRSF11B	Tumor necrosis factor receptor superfamily, member 11b
11754941_x_at	3.16	0.007474	KRT18	Keratin 18, type I
11717826_x_at	3.11	0.003881	STMN2	Stathmin 2
11756065_x_at	2.95	0.037153	APOD	Apolipoprotein D
11724037_at	2.85	0.029635	PTGS2	Prostaglandin-endoperoxide synthase 2
11736574_a_at	2.84	0.033771	FAM20A	Family with sequence similarity 20, member A
11730384_at	2.8	0.029845	GREM2	Gremlin 2, DAN family BMP antagonist
11717066_at	2.78	0.038987	GREM1	Gremlin 1, DAN family BMP antagonist
11744425_a_at	2.74	0.015785	KIAA0101	KIAA0101
11720062_s_at	2.66	0.00313	IER3	Immediate early response 3
11735572_x_at	2.53	0.035121	SORBS2	Sorbin and SH3 domain containing 2
11751844_a_at	2.52	0.01612	STMN2	Stathmin 2
11744893_a_at	2.5	0.031829	FAM20A	Family with sequence similarity 20, member A
11725827_s_at	2.48	0.029583	CD1D	CD1d molecule
11715363_a_at	2.47	0.031502	A2M	Alpha-2-macroglobulin
11741013_a_at	2.46	0.049384	LRRN3	Leucine rich repeat neuronal 3
11747928_x_at	2.39	0.025965	POSTN	Periostin, osteoblast specific factor
11717994_a_at	2.37	0.003252	NR4A1	Nuclear receptor subfamily 4, group A, member 1
11744263_s_at	2.36	0.03441	RAC2	Ras-related C3 botulinum toxin substrate 2
11723033_at	2.26	0.044371	NOV	Nephroblastoma overexpressed
11731123_a_at	2.26	0.046164	TMEM200A	Transmembrane protein 200A
11736798_a_at	2.25	0.037736	RUNX1T1	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
11724983_at	2.24	0.047928	PCDH7	Protocadherin 7
11737620_a_at	2.23	0.042455	PRR16	Proline rich 16
11715670_a_at	2.22	0.016909	IFITM1	Interferon induced transmembrane protein 1
11715671_x_at	2.21	0.019455	IFITM1	Interferon induced transmembrane protein 1
11730489_at	2.19	0.023307	DOK6	Docking protein 6
11743201_a_at	2.17	0.009703	IGF1	Insulin-like growth factor 1 (somatomedin C)
11733878_a_at	2.17	0.013165	LMO7	LIM domain 7
11746462_a_at	2.15	0.047996	LMO7	LIM domain 7
11732625_a_at	2.12	0.00284	RIMS1	Regulating synaptic membrane exocytosis 1
11724886_a_at	2.1	0.000834	LRRN3	Leucine rich repeat neuronal 3
11717886_a_at	2.08	0.028685	PLAU	Plasminogen activator, urokinase
11727700_at	2.07	0.013777	HOXC13	Homeobox C13
11717295_s_at	2.05	0.042684	APOD	Apolipoprotein D
11720146_a_at	2.04	0.029523	DAPK1	Death-associated protein kinase 1
11732712_a_at	2.03	0.048684	FST	Follistatin
11724036_a_at	2.02	0.001676	PTGS2	Prostaglandin-endoperoxide synthase 2

Table S2. Genes overexpressed in adipocytes relative to lipid (-) cells

Microarray Probe	Fold Change, Lipid-minus vs. Adipocytes	ANOVA *p*-value	Gene Symbol	Description
11749273_a_at	-14.54	0.01793	PCK1	Phosphoenolpyruvate carboxykinase 1 (soluble)
11726274_x_at	-12.58	0.003274	PCK1	Phosphoenolpyruvate carboxykinase 1 (soluble)
11726273_a_at	-11.33	0.026183	PCK1	Phosphoenolpyruvate carboxykinase 1 (soluble)
11734560_x_at	-8.12	0.000481	ADIPOQ	Adiponectin, C1Q and collagen domain containing
11748917_a_at	-7.21	0.029367	GPD1	Glycerol-3-phosphate dehydrogenase 1
11730626_at	-6.66	0.002294	KLB	Klotho beta
11756200_a_at	-5.55	0.011108	CHI3L2	Chitinase 3-like 2
11734558_a_at	-5.49	0.003365	ADIPOQ	Adiponectin, C1Q and collagen domain containing
11721708_at	-5.44	0.01845	GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial
11736704_a_at	-5.07	0.010859	C6	Complement component 6
11756201_x_at	-4.92	0.008297	CHI3L2	Chitinase 3-like 2
11718869_x_at	-4.89	0.005407	PALMD	Palmdelphin
11731765_a_at	-4.82	0.025649	LGALS12	Lectin, galactoside-binding, soluble, 12
11730261_a_at	-4.73	0.001618	PRKAR2B	Protein kinase, cAMP-dependent, regulatory, type II, beta
11719660_at	-4.71	0.012403	ATP1A2	ATPase, Na^+/K^+ transporting, alpha 2 polypeptide
11720460_x_at	-4.66	0.04504	F11R	F11 receptor
11730474_at	-4.58	0.002888	PDE3B	Phosphodiesterase 3B, cGMP-inhibited
11757277_x_at	-4.51	0.014964	HP	Haptoglobin
11730624_at	-4.47	0.020697	KLB	Klotho beta
11719736_s_at	-4.37	0.00931	FAM134B	Family with sequence similarity 134, member B
11722061_a_at	-4.36	0.003957	PPP1R1A	Protein phosphatase 1, regulatory (inhibitor) subunit 1A
11730600_s_at	-4.24	0.008796	AQP7	Aquaporin 7
11756585_a_at	-4.23	0.036684	AQP3	Aquaporin 3
11744311_a_at	-4.21	0.009522	PLIN1	Perilipin 1
11728791_at	-4.19	0.020129	THRSP	Thyroid hormone responsive
11730473_at	-4.11	0.003943	PDE3B	Phosphodiesterase 3B, cGMP-inhibited
11729504_a_at	-4.08	0.034752	AOC2	Amine oxidase, copper containing 2 (retina-specific)
11753179_s_at	-4.07	0.018173	FAM134B	Family with sequence similarity 134, member B
11719737_a_at	-4.02	0.003364	FAM134B	Family with sequence similarity 134, member B
11717913_at	-3.93	0.004761	CDO1	Cysteine dioxygenase type 1
11755284_s_at	-3.85	0.008887	TSPAN13	Tetraspanin 13
11717305_a_at	-3.81	0.005562	ADIRF	Adipogenesis regulatory factor
11720472_a_at	-3.62	0.0212	GPD1	Glycerol-3-phosphate dehydrogenase 1
11744649_x_at	-3.61	0.024874	HP	Haptoglobin
11757654_x_at	-3.55	0.014368	UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)
11718132_at	-3.52	0.013413	RBP4	Retinol binding protein 4, plasma
11734559_x_at	-3.5	0.013538	ADIPOQ	Adiponectin, C1Q and collagen domain containing
11723947_a_at	-3.46	0.000148	ACSL5	Acyl-CoA synthetase long-chain family member 5
11730472_a_at	-3.44	0.018038	PDE3B	Phosphodiesterase 3B, cGMP-inhibited
11754235_a_at	-3.42	0.020277	PTPRF	Protein tyrosine phosphatase, receptor type, F
11756138_a_at	-3.41	0.038808	HK2	Hexokinase 2
11725300_a_at	-3.39	0.007817	AOC3	Amine oxidase, copper containing 3
11754282_s_at	-3.35	0.005121	GYG2	Glycogenin 2
11717306_x_at	-3.26	0.013094	ADIRF	Adipogenesis regulatory factor
11719035_a_at	-3.24	0.023552	ACSF2	Acyl-CoA synthetase family member 2
11739899_a_at	-3.23	0.032559	SLC19A3	Solute carrier family 19 (thiamine transporter), member 3
11739900_at	-3.22	0.000729	SLC19A3	Solute carrier family 19 (thiamine transporter), member 3
11721377_x_at	-3.12	0.023981	BCL2	B-cell CLL/lymphoma 2
11723946_a_at	-3.09	0.002151	ACSL5	Acyl-CoA synthetase long-chain family member 5
11721706_at	-3.07	0.007087	GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial
11758374_s_at	-3.06	0.014918	PLIN1	Perilipin 1
11718491_x_at	-3.04	0.002341	FABP5	Fatty acid binding protein 5 (psoriasis-associated)
11719393_a_at	-2.99	0.046251	NR1H3	Nuclear receptor subfamily 1, group H, member 3

11733829_x_at	-2.99	0.048646	HP	Haptoglobin
11759041_x_at	-2.96	0.000912	VKORC1L1	Vitamin K epoxide reductase complex subunit 1 like 1
11743088_s_at	-2.91	0.044214	PDE8B	Phosphodiesterase 8B
11721707_at	-2.85	0.004401	GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial
11731029_a_at	-2.83	0.000794	SLC25A18	Solute carrier family 25 (glutamate carrier), member 18
11718490_s_at	-2.81	0.003057	FABP5	Fatty acid binding protein 5 (psoriasis-associated)
11724966_s_at	-2.78	0.039935	BLOC1S1-RDH5	BLOC1S1-RDH5 readthrough; retinol dehydrogenase 5 (11-cis/9-cis)
11738185_s_at	-2.75	0.049529	PDE8B	Phosphodiesterase 8B
11750186_a_at	-2.71	0.007644	ALDH1A3	Aldehyde dehydrogenase 1 family, member A3
11722641_s_at	-2.69	0.044612	DGAT2	Diacylglycerol O-acyltransferase 2
11741154_s_at	-2.69	0.04753	LIMS1	LIM and senescent cell antigen-like domains 1
11725510_a_at	-2.68	0.008325	SLC7A6	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 6
11720885_at	-2.68	0.00946	ACACB	Acetyl-CoA carboxylase beta
11752995_a_at	-2.66	0.001083	DLAT	Dihydrolipoamide S-acetyltransferase
11756668_x_at	-2.65	0.00001	FAM213A	Family with sequence similarity 213, member A
11724975_a_at	-2.61	0.049723	HRASLS5	HRAS-like suppressor family, member 5
11739975_at	-2.6	0.002636	ZNF117	Zinc finger protein 117
11750801_a_at	-2.57	0.005918	DLAT	Dihydrolipoamide S-acetyltransferase
11719162_a_at	-2.57	0.014797	GPT2	Glutamic pyruvate transaminase (alanine aminotransferase) 2
11754461_s_at	-2.56	0.013038	UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)
11746395_x_at	-2.54	0.010077	NRCAM	Neuronal cell adhesion molecule
11758535_s_at	-2.53	0.006139	GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial
11747765_a_at	-2.53	0.03328	PPP2R5A	Protein phosphatase 2, regulatory subunit B', alpha
11748266_a_at	-2.5	0.012293	RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)
11726445_at	-2.49	0.034881	KCNK3	Potassium channel, two pore domain subfamily K, member 3
11754074_s_at	-2.48	0.019157	G0S2	G0/G1 switch 2
11727791_s_at	-2.47	0.012585	DLAT	Dihydrolipoamide S-acetyltransferase
11733025_at	-2.46	0.030736	CLCA2	Chloride channel accessory 2
11723372_a_at	-2.45	0.005907	DOCK11	Dedicator of cytokinesis 11
11727793_x_at	-2.42	0.003051	DLAT	Dihydrolipoamide S-acetyltransferase
11720544_x_at	-2.42	0.015428	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2
11753749_x_at	-2.42	0.024656	ANP32A	Acidic nuclear phosphoprotein 32 family member A
11715845_s_at	-2.42	0.034979	PTPRF	Protein tyrosine phosphatase, receptor type, F
11751002_x_at	-2.39	0.002185	DLAT	Dihydrolipoamide S-acetyltransferase
11750636_a_at	-2.39	0.0043	ACACB	Acetyl-CoA carboxylase beta
11747494_a_at	-2.36	0.046886	AQP3	Aquaporin 3 (Gill blood group)
11727268_at	-2.34	0.012087	ZBED3	Zinc finger, BED-type containing 3
11727792_at	-2.3	0.001832	DLAT	Dihydrolipoamide S-acetyltransferase
11758661_s_at	-2.29	0.031902	CDKN2C	Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
11730222_x_at	-2.27	0.028685	PNPLA2	Patatin-like phospholipase domain containing 2
11731778_a_at	-2.26	0.043886	_MARC1	Mitochondrial amidoxime reducing component 1
11741273_a_at	-2.25	0.002843	KCNAB1	Potassium channel, voltage gated subfamily A regulatory beta subunit 1
11723707_a_at	-2.25	0.009042	AIFM2	Apoptosis-inducing factor, mitochondrion-associated, 2
11718243_a_at	-2.25	0.016552	ITGA7	Integrin alpha 7
11758204_s_at	-2.25	0.018638	PPP2R5A	Protein phosphatase 2, regulatory subunit B', alpha
11733969_a_at	-2.22	0.041275	SHMT1	Serine hydroxymethyltransferase 1 (soluble)
11750103_a_at	-2.21	0.020146	HADH	Hydroxyacyl-CoA dehydrogenase
11746281_a_at	-2.21	0.024441	LPCAT3	Lysophosphatidylcholine acyltransferase 3
11756274_a_at	-2.21	0.032888	ALDH1L1	Aldehyde dehydrogenase 1 family, member L1
11723793_s_at	-2.21	0.036813	OSBPL11	Oxysterol binding protein-like 11
11752376_a_at	-2.2	0.004207	GHR	Growth hormone receptor
11755235_a_at	-2.19	0.049406	FAR2	Fatty acyl-CoA reductase 2
11722555_s_at	-2.18	0.014651	HADH	Hydroxyacyl-CoA dehydrogenase
11744199_a_at	-2.18	0.014988	RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)
11750700_a_at	-2.17	0.011831	ACSL1	Acyl-CoA synthetase long-chain family member 1
11721248_s_at	-2.16	0.022478	GNG2	Guanine nucleotide binding protein (G protein), gamma 2

11744219_at	-2.15	0.005351	G0S2	G0/G1 switch 2
11724515_a_at	-2.15	0.008529	GPD1L	Glycerol-3-phosphate dehydrogenase 1-like
11745789_a_at	-2.13	0.007056	TMEM135	Transmembrane protein 135
11725902_s_at	-2.12	0.020885	TMEM135	Transmembrane protein 135
11723857_at	-2.12	0.038597	TXNDC16	Thioredoxin domain containing 16
11757044_x_at	-2.1	0.018464	HILPDA	Hypoxia inducible lipid droplet-associated
11753466_a_at	-2.1	0.027933	ACSS2	Acyl-CoA synthetase short-chain family member 2
11760128_x_at	-2.1	0.044822	LIMS1	LIM and senescent cell antigen-like domains 1
11716839_a_at	-2.09	0.024405	RASD1	RAS, dexamethasone-induced 1
11738228_s_at	-2.09	0.028728	ERV3-1	Endogenous retrovirus group 3, member 1; zinc finger protein 117
11726294_s_at	-2.08	0.018005	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha
11760127_at	-2.08	0.045872	LIMS1	LIM and senescent cell antigen-like domains 1
11717732_s_at	-2.07	0.005879	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
11748543_a_at	-2.07	0.008322	TXNIP	Thioredoxin interacting protein
11716208_s_at	-2.07	0.029398	GLUD1	Glutamate dehydrogenase 1
11749685_a_at	-2.07	0.035662	FAM13A	Family with sequence similarity 13, member A
11758259_s_at	-2.06	0.001493	SLCO2B1	Solute carrier organic anion transporter family, member 2B1
11718974_at	-2.05	0.004884	LPL	Lipoprotein lipase
11723666_a_at	-2.04	0.00285	SEMA3C	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
11754184_a_at	-2.04	0.009235	ALDH1A3	Aldehyde dehydrogenase 1 family, member A3
11718988_s_at	-2.03	0.007514	RNASE4	Ribonuclease, RNase A family, 4
11749276_a_at	-2.03	0.01553	C14orf180	Chromosome 14 open reading frame 180
11748017_a_at	-2.03	0.023613	PECR	Peroxisomal trans-2-enoyl-CoA reductase
11721688_at	-2.03	0.029344	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
11759061_at	-2.02	0.005548	SIK2	Salt-inducible kinase 2
11759042_at	-2.02	0.00731	VKORC1L1	Vitamin K epoxide reductase complex subunit 1 like 1
11752681_s_at	-2.02	0.017965	TMEM135	Transmembrane protein 135
11751628_a_at	-2.02	0.038806	TMEM140	Transmembrane protein 140
11730454_at	-2.02	0.040689	GLYCTK	Glycerate kinase
11746394_a_at	-2.02	0.044968	NRCAM	Neuronal cell adhesion molecule
11727564_a_at	-2.01	0.018057	GYG2	Glycogenin 2
11755688_a_at	-2.01	0.049214	ADAMTSL4	ADAMTS like 4

Table S3. Gene Ontology (GO) analysis of Table S1

#GO	NS	Enrichment	Name	Ratio_in_ study	Ratio_in_ pop	Study_ count	P_bonferroni	Study_items
GO:2000097	BP	e	Regulation of smooth muscle cell-matrix adhesion	3/39	9/49395	3	0.000706456	11717295_s_at, 11717886_a_at, 11756065_x_at
GO:0031117	BP	e	Positive regulation of microtubule depolymerization	3/39	12/49395	3	0.00184721	11717825_a_at, 11717826_x_at, 11751844_a_at
GO:0046822	BP	e	Regulation of nucleocytoplasmic transport	7/39	591/49395	7	0.00693447	11717066_at, 11717295_s_at, 11720062_s_at, 11724036_a_at, 11724037_at, 11743201_a_at, 11756065_x_at
GO:0031214	BP	e	Biomineral tissue development	5/39	196/49395	5	0.008942598	11724036_a_at, 11724037_at, 11736574_a_at, 11743201_a_at, 11744893_a_at
GO:0042306	BP	e	Regulation of protein import into nucleus	6/39	455/49395	6	0.027647086	11717066_at, 11717295_s_at, 11724036_a_at, 11724037_at, 11743201_a_at, 11756065_x_at
GO:1904589	BP	e	Regulation of protein import	6/39	455/49395	6	0.027647086	11717066_at, 11717295_s_at, 11724036_a_at, 11724037_at, 11743201_a_at, 11756065_x_at
GO:0048660	BP	e	Regulation of smooth muscle cell proliferation	5/39	252/49395	5	0.030776574	11717295_s_at, 11724036_a_at, 11724037_at, 11743201_a_at, 11756065_x_at
GO:2000405	BP	e	Negative regulation of T cell migration	2/39	3/49395	2	0.033775264	11717295_s_at, 11756065_x_at
GO:0060588	BP	e	Negative regulation of lipoprotein lipid oxidation	2/39	3/49395	2	0.033775264	11717295_s_at, 11756065_x_at
GO:0035633	BP	e	Maintenance of permeability of blood-brain barrier	2/39	3/49395	2	0.033775264	11724036_a_at, 11724037_at
GO:0090271	BP	e	Positive regulation of fibroblast growth factor production	2/39	3/49395	2	0.033775264	11724036_a_at, 11724037_at
GO:0051241	BP	e	Negative regulation of multicellular organismal process	11/39	2432/49395	11	0.034805044	11717066_at, 11717295_s_at, 11717825_a_at, 11717826_x_at, 11717886_a_at, 11724036_a_at, 11724037_at, 11730319_at, 11732712_a_at, 11751844_a_at, 11756065_x_at
GO:1900180	BP	e	Regulation of protein localization to nucleus	6/39	481/49395	6	0.038084368	11717066_at, 11717295_s_at, 11724036_a_at, 11724037_at, 11743201_a_at, 11756065_x_at

Table S4. Gene Ontology (GO) analysis of Table S2

#GO	NS	Enrichment	Name	Ratio_ in_study	Ratio_in_pop	Study_ count	P_bonferroni	Study_items
GO:0070236	BP	e	Negative regulation of activation-induced cell death of T cells	4/141	10/49395	4	0.000244454	11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:1900121	BP	e	Negative regulation of receptor binding	5/141	27/49395	5	0.000251151	11715845_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754235_a_at
GO:0005967	CC	e	Mitochondrial pyruvate dehydrogenase complex	6/141	11/49395	6	0.00038329	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:2000295	BP	e	Regulation of hydrogen peroxide catabolic process	3/141	3/49395	3	0.000422224	11733829_x_at, 11744649_x_at, 11757277_x_at
GO:2000296	BP	e	Negative regulation of hydrogen peroxide catabolic process	3/141	3/49395	3	0.000422224	11733829_x_at, 11744649_x_at, 11757277_x_at
GO:0055089	BP	e	Fatty acid homeostasis	5/141	33/49395	5	0.000728256	11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11758535_s_at
GO:0042762	BP	e	Regulation of sulfur metabolic process	6/141	67/49395	6	0.000779413	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0019432	BP	e	Triglyceride biosynthetic process	13/141	116/49395	13	0.000886525	11718974_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11748917_a_at, 11750700_a_at, 11758535_s_at
GO:0004366	MF	e	Glycerol-3-phosphate O-acyltransferase activity	4/141	14/49395	4	0.001154928	11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:0046463	BP	e	Acylglycerol biosynthetic process	14/141	121/49395	14	0.001186332	11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11748917_a_at, 11750700_a_at, 11758535_s_at
GO:0046460	BP	e	Neutral lipid biosynthetic process	14/141	121/49395	14	0.001186332	11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11748917_a_at, 11750700_a_at, 11758535_s_at
GO:0035384	BP	e	Thioester biosynthetic process	12/141	72/49395	12	0.00120604	11720885_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0071616	BP	e	Acyl-CoA biosynthetic process	12/141	72/49395	12	0.00120604	11720885_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:1900120	BP	e	Regulation of receptor binding	5/141	37/49395	5	0.001325316	11715845_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754235_a_at
GO:0010510	BP	e	Regulation of acetyl-CoA biosynthetic process from pyruvate	6/141	37/49395	6	0.001325316	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0014823	BP	e	Response to activity	8/141	124/49395	8	0.001404306	11722555_s_at, 11726273_a_at, 11726274_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11750103_a_at
GO:0072350	BP	e	Tricarboxylic acid metabolic process	8/141	125/49395	8	0.001484089	11716208_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at
GO:0046888	BP	e	Negative regulation of hormone secretion	9/141	127/49395	9	0.001655185	11722555_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0016417	MF	e	S-acyltransferase activity	6/141	76/49395	6	0.001671838	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0070994	BP	e	Detection of oxidative stress	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at

GO:2000590	BP	e	Negative regulation of metanephric mesenchymal cell migration	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:0070543	BP	e	Response to linoleic acid	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000583	BP	e	Regulation of platelet-derived growth factor receptor-alpha signaling pathway	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000584	BP	e	Negative regulation of platelet-derived growth factor receptor-alpha signaling pathway	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000534	BP	e	Positive regulation of renal albumin absorption	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000477	BP	e	Regulation of metanephric glomerular visceral epithelial cell development	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000478	BP	e	Positive regulation of metanephric glomerular visceral epithelial cell development	3/141	4/49395	3	0.001685356	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:0001523	BP	e	Retinoid metabolic process	8/141	194/49395	8	0.001840518	11718132_at, 11718974_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748266_a_at, 11750186_a_at, 11754184_a_at
GO:0070542	BP	e	Response to fatty acid	9/141	130/49395	9	0.0019429	11721248_s_at, 11722641_s_at, 11724966_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750700_a_at, 11754461_s_at, 11757654_x_at
GO:0070235	BP	e	Regulation of activation-induced cell death of T cells	4/141	16/49395	4	0.002090567	11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:0032868	BP	e	Response to insulin	15/141	369/49395	15	0.002306506	11718132_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0006090	BP	e	Pyruvate metabolic process	11/141	200/49395	11	0.00232523	11717732_s_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11749273_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11756138_a_at
GO:0046676	BP	e	Negative regulation of insulin secretion	6/141	81/49395	6	0.002452976	11722555_s_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0045254	CC	e	Pyruvate dehydrogenase complex	6/141	17/49395	6	0.002727758	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0006720	BP	e	Isoprenoid metabolic process	9/141	286/49395	9	0.002870933	11718132_at, 11718974_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11750186_a_at, 11754184_a_at
GO:0016024	BP	e	CDP-diacylglycerol biosynthetic process	5/141	43/49395	5	0.002886719	11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:0071375	BP	e	Cellular response to peptide hormone stimulus	11/141	379/49395	11	0.002951421	11721248_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0016747	MF	e	Transferase activity, transferring acyl groups other than amino-acyl groups	14/141	594/49395	14	0.002964072	11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11746281_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11758535_s_at
GO:0050812	BP	e	Regulation of acyl-CoA biosynthetic process	6/141	44/49395	6	0.003249351	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at

GO:0046486	BP	e	Glycerolipid metabolic process	21/141	856/49395	21	0.003492527	11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11730222_x_at, 11744311_a_at, 11746281_a_at, 11748917_a_at, 11750700_a_at, 11758374_s_at, 11758535_s_at
GO:0006085	BP	e	Acetyl-CoA biosynthetic process	7/141	18/49395	7	0.003499342	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0006631	BP	e	Fatty acid metabolic process	21/141	727/49395	21	0.003575015	11718974_at, 11719035_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748017_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11753466_a_at, 11758535_s_at
GO:0070403	MF	e	NAD+ binding	5/141	45/49395	5	0.003647148	11716208_s_at, 11722555_s_at, 11750103_a_at, 11750186_a_at, 11754184_a_at
GO:0090278	BP	e	Negative regulation of peptide hormone secretion	6/141	87/49395	6	0.003763597	11722555_s_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0046341	BP	e	CDP-diacylglycerol metabolic process	5/141	46/49395	5	0.004082551	11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:0050796	BP	e	Regulation of insulin secretion	13/141	498/49395	13	0.004119128	11716208_s_at, 11718132_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0031968	CC	e	Organelle outer membrane	16/141	499/49395	16	0.004201813	11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11731778_a_at, 11744199_a_at, 11748266_a_at, 11750636_a_at, 11750700_a_at, 11756138_a_at, 11758535_s_at
GO:0046327	BP	e	Glycerol biosynthetic process from pyruvate	3/141	5/49395	3	0.004204563	11726273_a_at, 11726274_x_at, 11749273_a_at
GO:0070970	BP	e	Interleukin-2 secretion	4/141	5/49395	4	0.004204563	11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:0033500	BP	e	Carbohydrate homeostasis	13/141	394/49395	13	0.004215876	11718132_at, 11726273_a_at, 11726274_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11754461_s_at, 11756138_a_at, 11757654_x_at
GO:0042593	BP	e	Glucose homeostasis	13/141	394/49395	13	0.004215876	11718132_at, 11726273_a_at, 11726274_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11754461_s_at, 11756138_a_at, 11757654_x_at
GO:0019216	BP	e	Regulation of lipid metabolic process	18/141	740/49395	18	0.004370365	11719393_a_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11730222_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11747765_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11758204_s_at
GO:0016101	BP	e	Diterpenoid metabolic process	9/141	218/49395	9	0.004490928	11718132_at, 11718974_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11750186_a_at, 11754184_a_at
GO:0051048	BP	e	Negative regulation of secretion	10/141	398/49395	10	0.004624598	11719393_a_at, 11722555_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0032869	BP	e	Cellular response to insulin stimulus	9/141	219/49395	9	0.004650074	11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0045017	BP	e	Glycerolipid biosynthetic process	18/141	620/49395	18	0.004676233	11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748917_a_at, 11750700_a_at, 11758535_s_at

GO:0001101	BP	e	Response to acid chemical	14/141	879/49395	14	0.004802089	11717913_at, 11718132_at, 11721248_s_at, 11721377_x_at, 11722641_s_at, 11724966_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11747494_a_at, 11750700_a_at, 11754461_s_at, 11756585_a_at, 11757654_x_at
GO:0051046	BP	e	Regulation of secretion	22/141	1485/49395	22	0.004995234	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0008610	BP	e	Lipid biosynthetic process	25/141	1489/49395	25	0.005194365	11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748017_a_at, 11748917_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11753466_a_at, 11754184_a_at, 11755235_a_at, 11758535_s_at
GO:0005996	BP	e	Monosaccharide metabolic process	22/141	627/49395	22	0.005267172	11717732_s_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11720472_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11754282_s_at, 11756138_a_at
GO:0031966	CC	e	Mitochondrial membrane	20/141	1491/49395	20	0.005296626	11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11730261_a_at, 11731029_a_at, 11731778_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11754461_s_at, 11756138_a_at, 11757654_x_at, 11758535_s_at
GO:1990204	CC	e	Oxidoreductase complex	9/141	223/49395	9	0.005335969	11720472_a_at, 11724515_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11748917_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:1901653	BP	e	Cellular response to peptide	11/141	407/49395	11	0.005673692	11721248_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0019217	BP	e	Regulation of fatty acid metabolic process	11/141	225/49395	11	0.005710243	11719393_a_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0008654	BP	e	Phospholipid biosynthetic process	13/141	632/49395	13	0.005729108	11718490_s_at, 11718491_x_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748917_a_at, 11758535_s_at
GO:1901652	BP	e	Response to peptide	18/141	762/49395	18	0.006083449	11717913_at, 11718132_at, 11721248_s_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0051186	BP	e	Cofactor metabolic process	25/141	897/49395	25	0.006119223	11717732_s_at, 11720472_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11733969_a_at, 11748917_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at, 11755235_a_at, 11756138_a_at, 11756274_a_at, 11758535_s_at
GO:0006084	BP	e	Acetyl-CoA metabolic process	9/141	50/49395	9	0.006252755	11720885_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0046473	BP	e	Phosphatidic acid metabolic process	8/141	95/49395	8	0.006357319	11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11724515_a_at, 11748917_a_at, 11758535_s_at

GO:0006654	BP	e	Phosphatidic acid biosynthetic process	8/141	95/49395	8	0.006357319	11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11724515_a_at, 11748917_a_at, 11758535_s_at
GO:0006091	BP	e	Generation of precursor metabolites and energy	16/141	1049/49395	16	0.006889956	11717732_s_at, 11720885_at, 11721248_s_at, 11722061_a_at, 11726294_s_at, 11727564_a_at, 11730261_a_at, 11730600_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750636_a_at, 11754282_s_at, 11754461_s_at, 11756138_a_at, 11757654_x_at
GO:1903530	BP	e	Regulation of secretion by cell	22/141	1358/49395	22	0.007059608	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0019867	CC	e	Outer membrane	16/141	526/49395	16	0.007068626	11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11731778_a_at, 11744199_a_at, 11748266_a_at, 11750636_a_at, 11750700_a_at, 11756138_a_at, 11758535_s_at
GO:0010565	BP	e	Regulation of cellular ketone metabolic process	11/141	417/49395	11	0.007079135	11719393_a_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0006732	BP	e	Coenzyme metabolic process	25/141	645/49395	25	0.007103477	11717732_s_at, 11720472_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11733969_a_at, 11748917_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at, 11755235_a_at, 11756138_a_at, 11756274_a_at, 11758535_s_at
GO:0032880	BP	e	Regulation of protein localization	26/141	2046/49395	26	0.007246392	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724515_a_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11747765_a_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758204_s_at, 11758535_s_at
GO:0050708	BP	e	Regulation of protein secretion	19/141	912/49395	19	0.007456145	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:1901700	BP	e	Response to oxygen-containing compound	35/141	3016/49395	35	0.007470786	11717913_at, 11718132_at, 11719393_a_at, 11720472_a_at, 11721248_s_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744649_x_at, 11747494_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750700_a_at, 11752376_a_at, 11754461_s_at, 11756585_a_at, 11757277_x_at, 11757654_x_at, 11758535_s_at
GO:0006006	BP	e	Glucose metabolic process	22/141	420/49395	22	0.007556334	11717732_s_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11720472_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11754282_s_at, 11756138_a_at

GO:0044429	CC	e	Mitochondrial part	29/141	2239/49395	29	0.00774118	11716208_s_at, 11719162_a_at, 11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730261_a_at, 11731029_a_at, 11731778_a_at, 11748543_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11754461_s_at, 11756138_a_at, 11757654_x_at, 11758535_s_at
GO:0005975	BP	e	Carbohydrate metabolic process	29/141	1875/49395	29	0.007769698	11717732_s_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11720472_a_at, 11722061_a_at, 11722641_s_at, 11724515_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730624_at, 11730626_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11754282_s_at, 11756138_a_at, 11756200_a_at, 11756201_x_at
GO:0042493	BP	e	Response to drug	17/141	1060/49395	17	0.007853988	11718974_at, 11720885_at, 11721377_x_at, 11722555_s_at, 11723666_a_at, 11724966_s_at, 11726445_at, 11730261_a_at, 11730600_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11754461_s_at
GO:0032787	BP	e	Monocarboxylic acid metabolic process	34/141	1213/49395	34	0.008026799	11717732_s_at, 11718974_at, 11719035_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748017_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754184_a_at, 11756138_a_at, 11758535_s_at
GO:0048878	BP	e	Chemical homeostasis	26/141	2060/49395	26	0.008093016	11718132_at, 11718974_at, 11719393_a_at, 11719660_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11726273_a_at, 11726274_x_at, 11726445_at, 11730472_a_at, 11730473_at, 11730474_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744649_x_at, 11749273_a_at, 11754461_s_at, 11756138_a_at, 11757277_x_at, 11757654_x_at, 11758535_s_at
GO:0071639	BP	e	Positive regulation of monocyte chemotactic protein-1 production	3/141	6/49395	3	0.008391509	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:2000532	BP	e	Regulation of renal albumin absorption	3/141	6/49395	3	0.008391509	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:0004742	MF	e	Dihydrolipoyllysine-residue acetyltransferase activity	6/141	6/49395	6	0.008391509	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0004119	MF	e	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity	3/141	6/49395	3	0.008391509	11730472_a_at, 11730473_at, 11730474_at
GO:0030523	MF	e	Dihydrolipoamide s-acyltransferase activity	6/141	6/49395	6	0.008391509	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0006641	BP	e	Triglyceride metabolic process	17/141	237/49395	17	0.008463019	11718974_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11730222_x_at, 11744311_a_at, 11748917_a_at, 11750700_a_at, 11758374_s_at, 11758535_s_at
GO:0009749	BP	e	Response to glucose	10/141	326/49395	10	0.008605527	11721706_at, 11721707_at, 11721708_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at

GO:0005811	CC	e	Lipid droplet	8/141	162/49395	8	0.008685699	11722641_s_at, 11723707_a_at, 11730222_x_at, 11744219_at, 11744311_a_at, 11754074_s_at, 11757044_x_at, 11758374_s_at
GO:0070201	BP	e	Regulation of establishment of protein localization	23/141	1714/49395	23	0.008764384	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0042592	BP	e	Homeostatic process	28/141	3044/49395	28	0.008902791	11718132_at, 11718974_at, 11718988_s_at, 11719393_a_at, 11719660_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723857_at, 11726273_a_at, 11726274_x_at, 11726445_at, 11730472_a_at, 11730473_at, 11730474_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744649_x_at, 11749273_a_at, 11754461_s_at, 11756138_a_at, 11757277_x_at, 11757654_x_at, 11758535_s_at
GO:0009743	BP	e	Response to carbohydrate	10/141	429/49395	10	0.009161327	11721706_at, 11721707_at, 11721708_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0043436	BP	e	Oxoacid metabolic process	41/141	2649/49395	41	0.009301411	11716208_s_at, 11717732_s_at, 11717913_at, 11718974_at, 11719035_a_at, 11719162_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730261_a_at, 11731778_a_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748017_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754184_a_at, 11756138_a_at, 11756274_a_at, 11758535_s_at
GO:0046883	BP	e	Regulation of hormone secretion	16/141	663/49395	16	0.009489284	11716208_s_at, 11718132_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0005741	CC	e	Mitochondrial outer membrane	14/141	431/49395	14	0.009556055	11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11731778_a_at, 11750636_a_at, 11750700_a_at, 11756138_a_at, 11758535_s_at
GO:0019318	BP	e	Hexose metabolic process	22/141	544/49395	22	0.009833685	11717732_s_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11720472_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11754282_s_at, 11756138_a_at
GO:0035383	BP	e	Thioester metabolic process	18/141	166/49395	18	0.010238456	11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at, 11755235_a_at, 11758535_s_at
GO:0006637	BP	e	Acyl-coa metabolic process	18/141	166/49395	18	0.010238456	11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at, 11755235_a_at, 11758535_s_at
GO:0016746	MF	e	Transferase activity, transferring acyl groups	15/141	668/49395	15	0.010267503	11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724966_s_at, 11724975_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11746281_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11758535_s_at

GO:0010817	BP	e	Regulation of hormone levels	21/141	1236/49395	21	0.010274905	11716208_s_at, 11718132_at, 11722555_s_at, 11722641_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11744199_a_at, 11748266_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at, 11754461_s_at, 11757654_x_at
GO:0005739	CC	e	Mitochondrion	40/141	4369/49395	40	0.010502283	11716208_s_at, 11719035_a_at, 11719162_a_at, 11720472_a_at, 11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730454_at, 11731029_a_at, 11731765_a_at, 11731778_a_at, 11733969_a_at, 11744219_at, 11748017_a_at, 11748917_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11754074_s_at, 11754461_s_at, 11756138_a_at, 11756274_a_at, 11756668_x_at, 11757654_x_at, 11758535_s_at
GO:0006790	BP	e	Sulfur compound metabolic process	22/141	939/49395	22	0.010539383	11717913_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11739899_a_at, 11739900_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11755235_a_at, 11758535_s_at
GO:0051287	MF	e	NAD binding	8/141	168/49395	8	0.01109831	11716208_s_at, 11720472_a_at, 11722555_s_at, 11724515_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at
GO:0035336	BP	e	Long-chain fatty-acyl-CoA metabolic process	5/141	56/49395	5	0.01111885	11722641_s_at, 11723946_a_at, 11723947_a_at, 11750700_a_at, 11755235_a_at
GO:0090276	BP	e	Regulation of peptide hormone secretion	13/141	552/49395	13	0.011342515	11716208_s_at, 11718132_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0006099	BP	e	Tricarboxylic acid cycle	6/141	105/49395	6	0.011499874	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0016054	BP	e	Organic acid catabolic process	11/141	554/49395	11	0.011750241	11716208_s_at, 11717913_at, 11719162_a_at, 11722555_s_at, 11724966_s_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750103_a_at, 11756274_a_at
GO:0046395	BP	e	Carboxylic acid catabolic process	11/141	554/49395	11	0.011750241	11716208_s_at, 11717913_at, 11719162_a_at, 11722555_s_at, 11724966_s_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750103_a_at, 11756274_a_at
GO:0051188	BP	e	Cofactor biosynthetic process	12/141	441/49395	12	0.011761562	11720885_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0006082	BP	e	Organic acid metabolic process	41/141	2685/49395	41	0.011825624	11716208_s_at, 11717732_s_at, 11717913_at, 11718974_at, 11719035_a_at, 11719162_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730261_a_at, 11731778_a_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748017_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754184_a_at, 11756138_a_at, 11756274_a_at, 11758535_s_at
GO:1901615	BP	e	Organic hydroxy compound metabolic process	15/141	1096/49395	15	0.011921289	11718132_at, 11721377_x_at, 11722641_s_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11729504_a_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11749273_a_at, 11750186_a_at, 11753466_a_at, 11754184_a_at

GO:0033211	BP	e	Adiponectin-activated signaling pathway	4/141	24/49395	4	0.011990944	11734558_a_at, 11734559_x_at, 11734560_x_at, 11750700_a_at
GO:0006198	BP	e	cAMP catabolic process	5/141	57/49395	5	0.012160073	11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at
GO:0055114	BP	e	Oxidation-reduction process	35/141	2692/49395	35	0.012384448	11716208_s_at, 11717913_at, 11720472_a_at, 11720885_at, 11721248_s_at, 11722061_a_at, 11722555_s_at, 11723707_a_at, 11724515_a_at, 11724966_s_at, 11725300_a_at, 11727564_a_at, 11729504_a_at, 11730261_a_at, 11731778_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11753466_a_at, 11754184_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11756274_a_at, 11756668_x_at, 11757654_x_at, 11759041_x_at, 11759042_at
GO:0046474	BP	e	Glycerophospholipid biosynthetic process	13/141	557/49395	13	0.012386088	11718490_s_at, 11718491_x_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748917_a_at, 11758535_s_at
GO:0006721	BP	e	Terpenoid metabolic process	9/141	250/49395	9	0.012655943	11718132_at, 11718974_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11750186_a_at, 11754184_a_at
GO:1901698	BP	e	Response to nitrogen compound	21/141	1935/49395	21	0.012676843	11717913_at, 11718132_at, 11720472_a_at, 11721248_s_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0051223	BP	e	Regulation of protein transport	22/141	1586/49395	22	0.012894182	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0006639	BP	e	Acylglycerol metabolic process	18/141	251/49395	18	0.013041408	11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11730222_x_at, 11744311_a_at, 11748917_a_at, 11750700_a_at, 11758374_s_at, 11758535_s_at
GO:0009746	BP	e	Response to hexose	10/141	343/49395	10	0.013126457	11721706_at, 11721707_at, 11721708_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0044283	BP	e	Small molecule biosynthetic process	17/141	1105/49395	17	0.013197719	11716208_s_at, 11717913_at, 11718132_at, 11718974_at, 11719162_a_at, 11720472_a_at, 11720885_at, 11726273_a_at, 11726274_x_at, 11733969_a_at, 11748017_a_at, 11748917_a_at, 11749273_a_at, 11750186_a_at, 11750636_a_at, 11753466_a_at, 11754184_a_at
GO:0009719	BP	e	Response to endogenous stimulus	28/141	2125/49395	28	0.013347551	11717913_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11720472_a_at, 11721248_s_at, 11721377_x_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11741154_s_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at, 11760127_at, 11760128_x_at
GO:0040018	BP	e	Positive regulation of multicellular organism growth	6/141	108/49395	6	0.013578092	11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11752376_a_at, 11758535_s_at
GO:1903531	BP	e	Negative regulation of secretion by cell	10/141	345/49395	10	0.013773823	11719393_a_at, 11722555_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at

GO:0006650	BP	e	Glycerophospholipid metabolic process	13/141	689/49395	13	0.014192066	11718490_s_at, 11718491_x_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748917_a_at, 11758535_s_at
GO:0034308	BP	e	Primary alcohol metabolic process	9/141	109/49395	9	0.014335495	11718132_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11750186_a_at, 11753466_a_at, 11754184_a_at
GO:0042572	BP	e	Retinol metabolic process	7/141	59/49395	7	0.014472926	11718132_at, 11722641_s_at, 11724966_s_at, 11744199_a_at, 11748266_a_at, 11750186_a_at, 11754184_a_at
GO:0002791	BP	e	Regulation of peptide secretion	19/141	965/49395	19	0.014545306	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0005743	CC	e	Mitochondrial inner membrane	14/141	965/49395	14	0.014545306	11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11730261_a_at, 11731029_a_at, 11731778_a_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0031838	CC	e	Haptoglobin-hemoglobin complex	3/141	7/49395	3	0.01465438	11733829_x_at, 11744649_x_at, 11757277_x_at
GO:0016418	MF	e	S-acetyltransferase activity	6/141	7/49395	6	0.01465438	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752995_a_at
GO:0004367	MF	e	Glycerol-3-phosphate dehydrogenase [NAD+] activity	3/141	7/49395	3	0.01465438	11720472_a_at, 11724515_a_at, 11748917_a_at
GO:0004613	MF	e	Phosphoenolpyruvate carboxykinase (GTP) activity	3/141	7/49395	3	0.01465438	11726273_a_at, 11726274_x_at, 11749273_a_at
GO:0004611	MF	e	Phosphoenolpyruvate carboxykinase activity	3/141	7/49395	3	0.01465438	11726273_a_at, 11726274_x_at, 11749273_a_at
GO:0050662	MF	e	Coenzyme binding	12/141	569/49395	12	0.015243612	11716208_s_at, 11720472_a_at, 11722555_s_at, 11723707_a_at, 11724515_a_at, 11731778_a_at, 11748017_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at, 11755235_a_at
GO:1904950	BP	e	Negative regulation of establishment of protein localization	10/141	455/49395	10	0.015592615	11719393_a_at, 11722555_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0051224	BP	e	Negative regulation of protein transport	10/141	455/49395	10	0.015592615	11719393_a_at, 11722555_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0071868	BP	e	Cellular response to monoamine stimulus	5/141	60/49395	5	0.015752513	11721248_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754461_s_at
GO:0071870	BP	e	Cellular response to catecholamine stimulus	5/141	60/49395	5	0.015752513	11721248_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754461_s_at
GO:0048037	MF	e	Cofactor binding	18/141	830/49395	18	0.015812558	11716208_s_at, 11719162_a_at, 11720472_a_at, 11722555_s_at, 11723707_a_at, 11724515_a_at, 11725300_a_at, 11729504_a_at, 11731778_a_at, 11733969_a_at, 11748017_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at, 11755235_a_at, 11759041_x_at, 11759042_at

GO:0044281	BP	e	Small molecule metabolic process	74/141	6064/49395	74	0.016002283	11716208_s_at, 11717732_s_at, 11717913_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11719035_a_at, 11719162_a_at, 11719660_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721248_s_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730222_x_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11731778_a_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11739899_a_at, 11739900_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11746281_a_at, 11748017_a_at, 11748266_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754074_s_at, 11754184_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11756138_a_at, 11756274_a_at, 11757654_x_at, 11758374_s_at, 11758535_s_at, 11759041_x_at, 11759042_at
GO:0019752	BP	e	Carboxylic acid metabolic process	40/141	2339/49395	40	0.016024087	11716208_s_at, 11717732_s_at, 11717913_at, 11718974_at, 11719035_a_at, 11719162_a_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11723946_a_at, 11723947_a_at, 11724966_s_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730261_a_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748017_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754184_a_at, 11756138_a_at, 11756274_a_at, 11758535_s_at
GO:0006638	BP	e	Neutral lipid metabolic process	18/141	258/49395	18	0.016031403	11718974_at, 11718988_s_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11730222_x_at, 11744311_a_at, 11748917_a_at, 11750700_a_at, 11758374_s_at, 11758535_s_at
GO:0043648	BP	e	Dicarboxylic acid metabolic process	8/141	258/49395	8	0.016031403	11716208_s_at, 11719162_a_at, 11726273_a_at, 11726274_x_at, 11733969_a_at, 11749273_a_at, 11752376_a_at, 11756274_a_at
GO:0044255	BP	e	Cellular lipid metabolic process	42/141	2534/49395	42	0.016120862	11718132_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719393_a_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11730222_x_at, 11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11746281_a_at, 11748017_a_at, 11748266_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11753466_a_at, 11754074_s_at, 11754184_a_at, 11755235_a_at, 11758374_s_at, 11758535_s_at
GO:1905954	BP	e	Positive regulation of lipid localization	7/141	178/49395	7	0.016363425	11718974_at, 11719393_a_at, 11723793_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11757044_x_at
GO:0043434	BP	e	Response to peptide hormone	18/141	699/49395	18	0.016490749	11717913_at, 11718132_at, 11721248_s_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0009725	BP	e	Response to hormone	23/141	1448/49395	23	0.017026892	11717913_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721248_s_at, 11721377_x_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at

GO:0065008	BP	e	Regulation of biological quality	53/141	8111/49395	53	0.017323326	11716208_s_at, 11717913_at, 11718132_at, 11718243_a_at, 11718869_x_at, 11718974_at, 11718988_s_at, 11719393_a_at, 11719660_at, 11720460_x_at, 11721248_s_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723372_a_at, 11723793_s_at, 11723857_at, 11724515_a_at, 11724966_s_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11726445_at, 11727268_at, 11730222_x_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11744199_a_at, 11744649_x_at, 11746394_a_at, 11746395_x_at, 11748266_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at, 11754461_s_at, 11756138_a_at, 11757044_x_at, 11757277_x_at, 11757654_x_at, 11758535_s_at
GO:0008374	MF	e	O-acyltransferase activity	8/141	113/49395	8	0.017719505	11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724966_s_at, 11746281_a_at, 11758535_s_at
GO:0014070	BP	e	Response to organic cyclic compound	20/141	1800/49395	20	0.01816201	11717913_at, 11719393_a_at, 11720472_a_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11724966_s_at, 11726294_s_at, 11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11747494_a_at, 11748543_a_at, 11748917_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11754461_s_at, 11756585_a_at
GO:0006629	BP	e	Lipid metabolic process	47/141	3163/49395	47	0.018303745	11718132_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719393_a_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11728791_at, 11730222_x_at, 11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11746281_a_at, 11748017_a_at, 11748266_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11753466_a_at, 11754074_s_at, 11754184_a_at, 11755235_a_at, 11758374_s_at, 11758535_s_at
GO:0006644	BP	e	Phospholipid metabolic process	14/141	845/49395	14	0.019279592	11718490_s_at, 11718491_x_at, 11718974_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724515_a_at, 11730222_x_at, 11746281_a_at, 11748917_a_at, 11758535_s_at
GO:0031406	MF	e	Carboxylic acid binding	14/141	466/49395	14	0.019327539	11716208_s_at, 11718490_s_at, 11718491_x_at, 11720885_at, 11726273_a_at, 11726274_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11739899_a_at, 11739900_at, 11749273_a_at, 11750636_a_at
GO:0009108	BP	e	Coenzyme biosynthetic process	12/141	265/49395	12	0.019587964	11720885_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0006101	BP	e	Citrate metabolic process	7/141	115/49395	7	0.019641459	11727791_s_at, 11727792_at, 11727793_x_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at
GO:2000479	BP	e	Regulation of cAMP-dependent protein kinase activity	4/141	27/49395	4	0.019673018	11730261_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at
GO:0034284	BP	e	Response to monosaccharide	10/141	361/49395	10	0.020026201	11721706_at, 11721707_at, 11721708_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748543_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0043177	MF	e	Organic acid binding	14/141	468/49395	14	0.020084635	11716208_s_at, 11718490_s_at, 11718491_x_at, 11720885_at, 11726273_a_at, 11726274_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11739899_a_at, 11739900_at, 11749273_a_at, 11750636_a_at

GO:0044272	BP	e	Sulfur compound biosynthetic process	13/141	469/49395	13	0.020472802	11717913_at, 11720885_at, 11723946_a_at, 11723947_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752995_a_at, 11753466_a_at
GO:0042221	BP	e	Response to chemical	52/141	5848/49395	52	0.021035704	11717305_a_at, 11717306_x_at, 11717913_at, 11718132_at, 11718974_at, 11718988_s_at, 11719393_a_at, 11719660_at, 11720472_a_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723666_a_at, 11724966_s_at, 11725300_a_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11726445_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11730600_s_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11741154_s_at, 11744649_x_at, 11747494_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11754461_s_at, 11756585_a_at, 11757277_x_at, 11757654_x_at, 11758535_s_at, 11759041_x_at, 11759042_at, 11760127_at, 11760128_x_at
GO:0090087	BP	e	Regulation of peptide transport	22/141	1642/49395	22	0.02111555	11716208_s_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11724966_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at, 11758535_s_at
GO:0071417	BP	e	Cellular response to organonitrogen compound	13/141	852/49395	13	0.021118061	11720472_a_at, 11721248_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0044242	BP	e	Cellular lipid catabolic process	10/141	364/49395	10	0.021437774	11718974_at, 11722555_s_at, 11724966_s_at, 11730222_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744311_a_at, 11750103_a_at, 11758374_s_at
GO:0019637	BP	e	Organophosphate metabolic process	22/141	2004/49395	22	0.021729957	11717732_s_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11719660_at, 11720472_a_at, 11720544_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11724515_a_at, 11730222_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11746281_a_at, 11748917_a_at, 11756138_a_at, 11758535_s_at
GO:0010243	BP	e	Response to organonitrogen compound	21/141	1824/49395	21	0.022079149	11717913_at, 11718132_at, 11720472_a_at, 11721248_s_at, 11722555_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at
GO:0006114	BP	e	Glycerol biosynthetic process	3/141	8/49395	3	0.0233979	11726273_a_at, 11726274_x_at, 11749273_a_at
GO:0019401	BP	e	Alditol biosynthetic process	3/141	8/49395	3	0.0233979	11726273_a_at, 11726274_x_at, 11749273_a_at
GO:0006066	BP	e	Alcohol metabolic process	13/141	724/49395	13	0.023743904	11718132_at, 11722641_s_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11749273_a_at, 11750186_a_at, 11753466_a_at, 11754184_a_at
GO:0071495	BP	e	Cellular response to endogenous stimulus	16/141	1320/49395	16	0.024173684	11720472_a_at, 11721248_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11741154_s_at, 11748917_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at, 11760127_at, 11760128_x_at
GO:1901136	BP	e	Carbohydrate derivative catabolic process	10/141	480/49395	10	0.025195002	11720472_a_at, 11724515_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11748917_a_at, 11756200_a_at, 11756201_x_at

GO:0070887	BP	e	Cellular response to chemical stimulus	26/141	3010/49395	26	0.025428059	11717305_a_at, 11717306_x_at, 11719393_a_at, 11720472_a_at, 11721248_s_at, 11721377_x_at, 11722641_s_at, 11724966_s_at, 11726294_s_at, 11726445_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11741154_s_at, 11748917_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at, 11759041_x_at, 11759042_at, 11760127_at, 11760128_x_at
GO:0006107	BP	e	Oxaloacetate metabolic process	4/141	29/49395	4	0.026506334	11726273_a_at, 11726274_x_at, 11749273_a_at, 11752376_a_at
GO:0009214	BP	e	Cyclic nucleotide catabolic process	5/141	67/49395	5	0.027412234	11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at
GO:0016491	MF	e	Oxidoreductase activity	21/141	2039/49395	21	0.028296809	11716208_s_at, 11717913_at, 11720472_a_at, 11722555_s_at, 11723707_a_at, 11724515_a_at, 11724966_s_at, 11725300_a_at, 11729504_a_at, 11731778_a_at, 11744199_a_at, 11748017_a_at, 11748266_a_at, 11748917_a_at, 11750103_a_at, 11750186_a_at, 11754184_a_at, 11755235_a_at, 11756274_a_at, 11759041_x_at, 11759042_at
GO:0006793	BP	e	Phosphorus metabolic process	46/141	5594/49395	46	0.02851311	11715845_s_at, 11717732_s_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11719660_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11726273_a_at, 11726274_x_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11746281_a_at, 11748917_a_at, 11749273_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11754235_a_at, 11755235_a_at, 11756138_a_at, 11758535_s_at, 11758661_s_at, 11759061_at
GO:0003676	MF	p	Nucleic acid binding	9/141	11325/49395	9	0.029265552	11718988_s_at, 11719393_a_at, 11721377_x_at, 11723707_a_at, 11726294_s_at, 11727268_at, 11738228_s_at, 11739975_at, 11753749_x_at
GO:1901618	MF	e	Organic hydroxy compound transmembrane transporter activity	5/141	68/49395	5	0.029520122	11718132_at, 11730600_s_at, 11747494_a_at, 11756585_a_at, 11758259_s_at
GO:0010033	BP	e	Response to organic substance	39/141	4658/49395	39	0.029757851	11717913_at, 11718132_at, 11718988_s_at, 11719393_a_at, 11720472_a_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11724966_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11741154_s_at, 11747494_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11752376_a_at, 11754461_s_at, 11756585_a_at, 11757654_x_at, 11758535_s_at, 11760127_at, 11760128_x_at
GO:0034383	BP	e	Low-density lipoprotein particle clearance	4/141	30/49395	4	0.030516494	11722641_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at

GO:0071704	BP	e	Organic substance metabolic process	98/141	23587/49395	98	0.030822794	11715845_s_at, 11716208_s_at, 11717305_a_at, 11717306_x_at, 11717732_s_at, 11717913_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719162_a_at, 11719393_a_at, 11719660_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722061_a_at, 11722555_s_at, 11722641_s_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11725300_a_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11729504_a_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11730624_at, 11730626_at, 11731778_a_at, 11733829_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11736704_a_at, 11738185_s_at, 11738228_s_at, 11739899_a_at, 11739900_at, 11739975_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11744649_x_at, 11746281_a_at, 11748017_a_at, 11748266_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11753749_x_at, 11754074_s_at, 11754184_a_at, 11754235_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11755688_a_at, 11756138_a_at, 11756200_a_at, 11756201_x_at, 11756274_a_at, 11757277_x_at, 11758374_s_at, 11758535_s_at, 11759041_x_at, 11759042_at, 11759061_at
GO:1901575	BP	e	Organic substance catabolic process	29/141	3919/49395	29	0.032748906	11716208_s_at, 11717732_s_at, 11717913_at, 11718974_at, 11719162_a_at, 11720472_a_at, 11722555_s_at, 11724515_a_at, 11724966_s_at, 11727564_a_at, 11730222_x_at, 11730472_a_at, 11730473_at, 11730474_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11743088_s_at, 11744311_a_at, 11748917_a_at, 11750103_a_at, 11754282_s_at, 11756138_a_at, 11756200_a_at, 11756201_x_at, 11756274_a_at, 11758374_s_at
GO:2000481	BP	e	Positive regulation of cAMP-dependent protein kinase activity	3/141	9/49395	3	0.035023351	11734558_a_at, 11734559_x_at, 11734560_x_at
GO:0030492	MF	e	Hemoglobin binding	3/141	9/49395	3	0.035023351	11733829_x_at, 11744649_x_at, 11757277_x_at
GO:0009605	BP	e	Response to external stimulus	26/141	3277/49395	26	0.035243147	11718132_at, 11718974_at, 11719393_a_at, 11719660_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11724966_s_at, 11726294_s_at, 11733829_x_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11744649_x_at, 11747494_a_at, 11748543_a_at, 11750186_a_at, 11750700_a_at, 11752376_a_at, 11754184_a_at, 11754461_s_at, 11756585_a_at, 11757277_x_at, 11757654_x_at, 11758535_s_at

GO:0008150	BP	e	Biological_process	138/141	41633/49395	138	0.037189472	11715845_s_at, 11716208_s_at, 11716839_a_at, 11717305_a_at, 11717306_x_at, 11717732_s_at, 11717913_at, 11718132_at, 11718243_a_at, 11718490_s_at, 11718491_x_at, 11718869_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719162_a_at, 11719393_a_at, 11719660_at, 11719736_s_at, 11719737_a_at, 11720460_x_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11721688_at, 11721706_at, 11721707_at, 11721708_at, 11722061_a_at, 11722555_s_at, 11722641_s_at, 11723372_a_at, 11723666_a_at, 11723707_a_at, 11723793_s_at, 11723857_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11724975_a_at, 11725300_a_at, 11725510_a_at, 11725902_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11726445_at, 11727268_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11729504_a_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11730600_s_at, 11730624_at, 11730626_at, 11731029_a_at, 11731765_a_at, 11731778_a_at, 11733025_at, 11733829_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11736704_a_at, 11738185_s_at, 11738228_s_at, 11739899_a_at, 11739900_at, 11739975_at, 11741154_s_at, 11741273_a_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11744649_x_at, 11745789_a_at, 11746281_a_at, 11746394_a_at, 11746395_x_at, 11747494_a_at, 11747765_a_at, 11748017_a_at, 11748266_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11749685_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752681_s_at, 11752995_a_at, 11753179_s_at, 11753466_a_at, 11753749_x_at, 11754074_s_at, 11754184_a_at, 11754235_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11755688_a_at, 11756138_a_at, 11756200_a_at, 11756201_x_at, 11756274_a_at, 11756585_a_at, 11756668_x_at, 11757044_x_at, 11757277_x_at, 11757654_x_at, 11758204_s_at, 11758259_s_at, 11758374_s_at, 11758535_s_at, 11758661_s_at, 11759041_x_at, 11759042_at, 11759061_at, 11760127_at, 11760128_x_at
GO:0044444	CC	e	Cytoplasmic part	96/141	21134/49395	96	0.038238965	11716208_s_at, 11716839_a_at, 11717732_s_at, 11717913_at, 11718132_at, 11719035_a_at, 11719162_a_at, 11719660_at, 11719736_s_at, 11719737_a_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722555_s_at, 11722641_s_at, 11723372_a_at, 11723707_a_at, 11723793_s_at, 11723857_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11725902_s_at, 11726273_a_at, 11726274_x_at, 11727268_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11731029_a_at, 11731765_a_at, 11731778_a_at, 11733829_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11738185_s_at, 11741154_s_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11744649_x_at, 11745789_a_at, 11746281_a_at, 11747765_a_at, 11748017_a_at, 11748266_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11749685_a_at, 11750103_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752681_s_at, 11752995_a_at, 11753179_s_at, 11753466_a_at, 11753749_x_at, 11754074_s_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11756138_a_at, 11756274_a_at, 11756668_x_at, 11757044_x_at, 11757277_x_at, 11757654_x_at, 11758204_s_at, 11758374_s_at, 11758535_s_at, 11758661_s_at, 11759041_x_at, 11759042_at, 11759061_at, 11760127_at, 11760128_x_at

GO:0006635	BP	e	Fatty acid beta-oxidation	6/141	130/49395	6	0.040194222	11722555_s_at, 11724966_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11750103_a_at
GO:0046434	BP	e	Organophosphate catabolic process	8/141	292/49395	8	0.040309478	11720472_a_at, 11724515_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11738185_s_at, 11743088_s_at, 11748917_a_at
GO:0033993	BP	e	Response to lipid	18/141	1720/49395	18	0.040525468	11717913_at, 11718132_at, 11719393_a_at, 11721248_s_at, 11721377_x_at, 11722641_s_at, 11724966_s_at, 11726294_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11747494_a_at, 11748543_a_at, 11750700_a_at, 11752376_a_at, 11754461_s_at, 11756585_a_at, 11757654_x_at
GO:0044464	CC	e	Cell part	135/141	40029/49395	135	0.044167296	11715845_s_at, 11716208_s_at, 11716839_a_at, 11717305_a_at, 11717306_x_at, 11717732_s_at, 11717913_at, 11718132_at, 11718243_a_at, 11718490_s_at, 11718491_x_at, 11718869_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719162_a_at, 11719393_a_at, 11719660_at, 11719736_s_at, 11719737_a_at, 11720460_x_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11721688_at, 11721706_at, 11721707_at, 11721708_at, 11722061_a_at, 11722555_s_at, 11722641_s_at, 11723372_a_at, 11723707_a_at, 11723793_s_at, 11723857_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11725300_a_at, 11725510_a_at, 11725902_s_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11726445_at, 11727268_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11729504_a_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11730600_s_at, 11730624_at, 11730626_at, 11731029_a_at, 11731765_a_at, 11731778_a_at, 11733025_at, 11733829_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11736704_a_at, 11738185_s_at, 11738228_s_at, 11739899_a_at, 11739900_at, 11739975_at, 11741154_s_at, 11741273_a_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11744649_x_at, 11745789_a_at, 11746281_a_at, 11746394_a_at, 11746395_x_at, 11747494_a_at, 11747765_a_at, 11748017_a_at, 11748266_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11749276_a_at, 11749685_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752681_s_at, 11752995_a_at, 11753179_s_at, 11753466_a_at, 11753749_x_at, 11754074_s_at, 11754184_a_at, 11754235_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11755284_s_at, 11756138_a_at, 11756274_a_at, 11756585_a_at, 11756668_x_at, 11757044_x_at, 11757277_x_at, 11757654_x_at, 11758204_s_at, 11758259_s_at, 11758374_s_at, 11758535_s_at, 11758661_s_at, 11759041_x_at, 11759042_at, 11759061_at, 11760127_at, 11760128_x_at
GO:0071867	BP	e	Response to monoamine	5/141	74/49395	5	0.044995994	11721248_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754461_s_at
GO:0071869	BP	e	Response to catecholamine	5/141	74/49395	5	0.044995994	11721248_s_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11754461_s_at
GO:0055091	BP	e	Phospholipid homeostasis	4/141	33/49395	4	0.045263913	11721706_at, 11721707_at, 11721708_at, 11758535_s_at
GO:1901699	BP	e	Cellular response to nitrogen compound	13/141	916/49395	13	0.046681343	11720472_a_at, 11721248_s_at, 11730261_a_at, 11730472_a_at, 11730473_at, 11730474_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11748917_a_at, 11752376_a_at, 11754461_s_at, 11757654_x_at

GO:0008152	BP	e	Metabolic process	105/141	26281/49395	105	0.046984993	11715845_s_at, 11716208_s_at, 11717305_a_at, 11717306_x_at, 11717732_s_at, 11717913_at, 11718132_at, 11718490_s_at, 11718491_x_at, 11718974_at, 11718988_s_at, 11719035_a_at, 11719162_a_at, 11719393_a_at, 11719660_at, 11720472_a_at, 11720544_x_at, 11720885_at, 11721248_s_at, 11721377_x_at, 11721706_at, 11721707_at, 11721708_at, 11722061_a_at, 11722555_s_at, 11722641_s_at, 11723707_a_at, 11723946_a_at, 11723947_a_at, 11724515_a_at, 11724966_s_at, 11724975_a_at, 11725300_a_at, 11725510_a_at, 11726273_a_at, 11726274_x_at, 11726294_s_at, 11727564_a_at, 11727791_s_at, 11727792_at, 11727793_x_at, 11728791_at, 11729504_a_at, 11730222_x_at, 11730261_a_at, 11730454_at, 11730472_a_at, 11730473_at, 11730474_at, 11730600_s_at, 11730624_at, 11730626_at, 11731778_a_at, 11733829_x_at, 11733969_a_at, 11734558_a_at, 11734559_x_at, 11734560_x_at, 11736704_a_at, 11738185_s_at, 11738228_s_at, 11739899_a_at, 11739900_at, 11739975_at, 11743088_s_at, 11744199_a_at, 11744219_at, 11744311_a_at, 11744649_x_at, 11746281_a_at, 11748017_a_at, 11748266_a_at, 11748543_a_at, 11748917_a_at, 11749273_a_at, 11750103_a_at, 11750186_a_at, 11750636_a_at, 11750700_a_at, 11750801_a_at, 11751002_x_at, 11752376_a_at, 11752995_a_at, 11753466_a_at, 11753749_x_at, 11754074_s_at, 11754184_a_at, 11754235_a_at, 11754282_s_at, 11754461_s_at, 11755235_a_at, 11755688_a_at, 11756138_a_at, 11756200_a_at, 11756201_x_at, 11756274_a_at, 11756668_x_at, 11757277_x_at, 11757654_x_at, 11758374_s_at, 11758535_s_at, 11758661_s_at, 11759041_x_at, 11759042_at, 11759061_at
GO:0050709	BP	e	Negative regulation of protein secretion	7/141	209/49395	7	0.047627942	11719393_a_at, 11722555_s_at, 11738185_s_at, 11743088_s_at, 11750103_a_at, 11754461_s_at, 11757654_x_at
GO:0035337	BP	e	Fatty-acyl-CoA metabolic process	5/141	75/49395	5	0.048099747	11722641_s_at, 11723946_a_at, 11723947_a_at, 11750700_a_at, 11755235_a_at