RNA Profiling of Laser Microdissected Human Trophoblast Subtypes at Mid-Gestation Reveals a Role for Cannabinoid Signaling in Invasion

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Disclosure: SJF is a consultant for Novo Nordisk.

Key words: human, placenta, trophoblast, transcriptomics, proteomics, cannabinoid signaling

Summary statement

Laser captured human trophoblasts were profiled (transcriptomic and proteomic), which showed that placental cells lining uterine arteries express CANNABINOID RECEPTOR 1. Functional analyses suggest that endogenous/exogenous cannabinoids could affect placentation.

Abstract

Human placental architecture is complex. Its surface epithelium, specialized for transport, forms by fusion of cytotrophoblast progenitors into multinucleated syncytiotrophoblasts. Near the uterine surface, these progenitors assume a different fate, becoming cancer-like cells that invade its lining and blood vessels. The latter process physically connects the placenta to the mother and shunts uterine blood to the syncytiotrophoblasts. Isolation of trophoblast subtypes is technically challenging. Upon removal, syncytiotrophoblasts disintegrate and invasive cytotrophoblasts are admixed with uterine cells. We used laser capture to circumvent these obstacles. This enabled isolation of syncytiotrophoblasts and two subpopulations of invasive cytotrophoblasts from cell columns and the endovascular compartment of spiral arteries. Transcriptional profiling revealed numerous genes whose placental or trophoblast expression was not known, including neurotensin and *C4ORF36*. Using mass spectrometry, discovery of differentially expressed mRNAs was extended to the protein level. We also found that invasive cytotrophoblasts expressed cannabinoid receptor 1. Unexpectedly, screening agonists and antagonists showed signals from this receptor promote invasion. Together these results revealed novel gene expression patterns that translate to the protein level. Our data also suggested that endogenous and exogenous cannabinoids can affect human placental development.

Introduction

At birth, the human placenta is the newborn's largest organ (Pryce et al., 2014) compared to those of the body, its weight is approximately double that of the heaviest, the brain (Boyd and Hamilton, 1967). During the last six months of pregnancy, placental weight increases over seven-fold (Boyd and Hamilton, 1967) while simultaneously supporting over a thirty-fold increase in that of the fetus (Armitage et al., 1967).

The placenta's ability to transport the very substantial resources that are needed for its own growth and that of the embryo/fetus is enabled by its unique structure. Its surface area is increased by many orders of macroscopically visible branches—the chorionic villi. At term the total area in direct contact with maternal blood is estimated to be ~12 m^2 (Boyd, 1984). At an electron microscopic level, the syncytiotrophoblasts that form the outer surface of the villi are covered with branched microvilli, which substantially add to the surface area, by our estimate producing at least a 10-fold increase (Wislocki and Dempsey, 1955). Furthermore, the human placenta is hemochorial, *i.e.*, in direct contact with uterine blood, minimizing the cellular barriers between the maternal source of nutrients and oxygen, and the placental vasculature that carries these substances to the embryo/fetus.

At a cellular level, human placental structure is established by differentiation of its progenitor population, villous cytotrophoblasts (CTBs; diagrammed in **Fig. 1A and B;** reviewed in Maltepe and Fisher (Maltepe and Fisher, 2015)). In one pathway, the cells fuse producing multi-nucleated syncytiotrophoblasts (STBs). In the other pathway, the cells leave the placenta, forming bridges, termed cell columns, that connect to the uterus and are the conduit for CTBs that invade its wall. The process is accompanied by a dramatic phenotypic switch in which the formerly epithelial cells adopt many vascular properties (Damsky and Fisher, 1998). Remarkably, these cells also breach uterine vessels that lie in their path. They penetrate the end of veins and migrate in a retrograde fashion up spiral arteries whose walls they occupy throughout much of their intrauterine segments. The latter process establishes the funnel-like structure of spiral arteries that reduces the flow rate and increases the volume of maternal blood perfusing the placenta.

The cellular structure of the human placenta makes isolation of the various trophoblast subtypes difficult-to-impossible. Upon enzyme dissociation, the syncytium disintegrates and extravillous CTBs are only a small fraction of the mononuclear cells that can be isolated. To solve this problem, we used laser microdissection (LMD) to capture STBs and column, endovascular or smooth CTBs as well as decidual cells for RNA profiling in the context of severe preeclampsia (Garrido-Gomez et al., 2017; Gormley et al., 2017). Here we used this approach to study the cells' gene expression during the 2nd trimester of normal pregnancy. The results revealed numerous molecules that were not previously known to be expressed by STBs and/or CTBs. Among them was the cannabinoid receptor 1 (CNR1), which was highly expressed by the endovascular CTB subpopulation. We went on to show that the downstream signals can influence invasion.

Results

RNA profiling of human trophoblast subtypes at mid-gestation

Blocks were prepared from biopsies of the 2nd trimester (15-20 weeks gestation) maternal-fetal interface. The focus was on areas that by macroscopic inspection included spiral arteries with dilated termini, a sign of CTB invasion. LMD enabled the capture of syncytium, cell columns and the endovascular compartment. The experimental strategy, which we used previously in an analysis of the same cell types from severe preeclampsia (Gormley et al., 2017), is depicted in **Fig. 1**. The dashed lines drawn on the photomicrographs to the left show the TB subpopulations that were targeted for removal as shown to the right: STBs (**Panels C and D**), cell column CTBs (CC; **Panels E and F**), and the endovascular compartment (ENDO), containing CTBs and other cell types in spiral arteries (SA; **Panels G and H**).

Global profiling of RNA isolated from the samples and pair-wise comparisons of the results revealed 2,986 genes that were differentially expressed (DE; adjP-value <0.05) by one of the TB subtypes. Principal component analysis (PCA; **Fig. S1**) showed that data from the same cell type clustered together separate from the other samples. Thus, consistent with their different functions, the various TB subtypes analyzed had distinct transcriptomes.

As compared to the two CTB subpopulations, 2708 genes were DE in STBs (**Fig. 2A**; see **Fig. S2** for entire heatmap and fold changes). As expected, the up regulated category included growth-promoting molecules (*e.g.*, *GH2, AREG, CSHL1, INSL4*), numerous transporters (*e.g., SLC27A2, SLC26A7*), ion channels (*e.g., TRPV6, SCN7A)* and SYNCYTIN-2 (*ERVFRD-1*)*.* The transcript for *MEOX2* was also DE in STBs, suggesting the possibility that this homeobox gene plays a role in fate specification or maintenance of this cell type. Unexpectedly, the expression of *LGR5*, a cell surface molecule that marks stem cells (*e.g.*, intestinal and colonic; (Leung et al., 2018), was unique to STBs. Of interest was detection of the mRNA encoding neurotensin (NTS), raising the possibility that this small neuropeptide is released from the surface of the placenta into maternal blood during pregnancy where it seems likely that enteric and other effects are possible (Bugni and Pothoulakis, 2013).

With regard to cell column CTBs, 2070 genes were DE in this subpopulation (**Fig. 2B**; see **Fig. S2** for entire heatmap and fold changes). Receptors for metabolites were the most highly up regulated. They included *FABP7*. We previously described CTB expression of this molecule at the maternal-fetal interface (Winn et al., 2007). The alpha-ketoglutarate receptor (*OXGR1*) was highly expressed. This result suggested that CTBs might be using metabolic products in the basal plate as an energy source, which could couple the initial stages of invasion to maternal metabolism. As shown by our previous work (reviewed in Maltepe and Fisher (Maltepe and Fisher, 2015), molecules that are involved in adhesion/de-adhesion were up regulated in columns (*ITGB6, COL17A1, ACAN, VIT*). An mRNA encoding troponin I (*TNNI2*), a protein involved in muscle contraction, was DE, possible evidence of its involvement in movement of these cells through the columns and into the uterus. In accord with the dramatic phenotypic changes the cells undergo, the DNA demethylase, *TET1*, was up regulated, suggesting that alterations at the level of the epigenome might play a role in specifying the fate of this CTB population.

Overall, 2753 genes were DE in the endovascular compartment (**Fig. 2C**; see **Fig. S2** for entire heatmap and fold changes). The most highly up regulated molecules included the BMP4 antagonist, *CHRDL1*, which mitigates migration and invasion of breast cancer cells (Cyr-Depauw et al., 2016), the secretory leukocyte peptidase inhibitor, *SLPI,* which plays a role in host defense (Majchrzak-Gorecka et al., 2016) and a calcium channel involved in cell signaling (*TRPC4*), which promotes vessel relaxation and permeability (Freichel et al., 2004). We detected expression of molecules that could control leakage of blood from modified spiral arteries (*FGG, CP*) and the complement cascade (*CFH*, *C3*). To the best of our knowledge, this list included novel identifications: *OMB, RORB* and *MEDAG*. *CANNABINOID RECEPTOR 1* (*CNR1*) was also in this category, which raised the possibility that endogenous and exogenous cannabinoids could impact CTB invasion and remodeling of the uterine vasculature.

Finally, we detected expression of mRNAs that were indicative of contamination with other cell types, not unexpected because endovascular CTBs lie adjacent to the decidua, which expresses *RELAXIN* (Goldsmith and Weiss, 2009) *and PRL* (Jones et al., 1998) which we detected. NK cells infiltrate the walls of spiral arteries (Moffett and Colucci, 2015), which we found evidence for in the expression of molecules these immune cells produce, including *GZMA, KLRC1* and *3*. We also detected molecules expressed by T cells (*TRDJ2, TRDC*).

In parallel, we have been developing a mass spectrometry (MS)-based proteomic method for analyzing the same TB subpopulations, captured by laser microdissection, which were the focus of the transcriptomic analysis. Given that typical estimates of correlations between mRNA and protein expression are below 50% (Maier et al., 2009; Vogel and Marcotte, 2012), we were interested in those that were significant at both levels, making them more likely to have functional effects. For these experiments, we employed a shotgun proteomic approach in which the number of times a peptide is identified enables relative quantification of the parent protein (*i.e.*, spectral counting; (Zhang et al., 2013). In all, we showed that 108 DE mRNAs had similar relative protein abundances within STB, CTB, or ENDO (**Fig. S3**).

Examples of these data are shown in **Fig. 3**. The upper left hand panel illustrates the labeling scheme, which was subsequently omitted for the sake of simplification. Data are organized in columns. Molecules that were up regulated in STB are shown to the left, CTB in the middle and ENDO to the right. Each cell type is designated by a different bisected symbol (square, circle or diamond). Left or right shading denotes RNA or protein values, respectively, which is colored (green, blue or red) to aid interpretation.

With regard to STBs (**Fig. 3; left column**), CSHL1 was the most highly expressed DE molecule at both mRNA and protein levels. We validated translation of an open reading frame (*CHROMOSOME 4 OPEN READING FRAME 36; C4ORF36*). High placental levels of this mRNA (ENSG00000163633) have been reported (Fagerberg et al., 2014). Its fungal protein analog (MGG_01005) is dynein light chain Tctex-type 1 (dynlt1/3) (Li et al., 2018), which transports various types of cellular cargo. CYP19A1 and GH2 were also expressed at higher levels in the syncytium.

With regard to cell column CTBs (**Fig. 3; middle column**), the highly-expressed DE molecules included several novel identifications that, to our knowledge, were not known to be produced by the placenta. They included PANNEXIN-1 (a major ATP release and nucleotide eflux channel;(Chekeni et al., 2010; Elliott et al., 2009), PYROGLUTAMYL-PEPTIDASE I (an exopeptidase;(Cummins and O'Connor, 1998)) and LYMPHOCYTE ANTIGEN 6K (a biomarker of lung and esophageal carcinomas; (Ishikawa et al., 2007). We were also interested to find a sialyltransferse (ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE 6; (Samyn-Petit et al., 2000) was up regulated in this CTB subpopulation. Its identification may be related to the observation that placental proteins carry unusual forms of glycosylation not found on the same molecules produced by other cell types (McMaster et al., 1998).

With regard to the endovascular compartment (**Fig. 3; right column**), the highly-expressed DE molecules included the hydrolase, ACYLPHOSPHATASE-2, and FIBULIN-2, a secreted extracellular matrix glycoprotein that can stabilize the basement membranes of epithelial cells (Ibrahim et al., 2018). We also confirmed the DE expression of immune molecules: BUTYROPHILIN 3A2, which can inhibit T-cell activity as do other members of this family (Messal et al., 2011; Rhodes et al., 2016) and GALECTIN 3, which has numerous other functions, including a role in cell adhesion (Pugliese et al., 2015) and epithelial-stromal signaling (AbuSamra et al., 2019).

Next, we used Ingenuity Pathways Analysis (IPA) to infer functional similarities and differences among the TB subtypes. Pathways were assigned a z-score based on the predicted impact of DE genes, either activation (+) or deactivation (-). Those shown in **Fig. 4** were significantly over-represented (either positively or negatively) in all of the trophoblast subpopulations. Again, there was significant overlap between the *in silico* predictions of the pathways that were activated in STB and ENDO vs. column CTBs. It seems possible that this convergence could be driven, in part, by the fact that these two regions are in direct contact with maternal blood. In keeping with this theory, many of the pathways identified as potentially activated were involved in responding to signals from circulating molecules: corticotropin releasing hormone, relaxin, renin, angiotensin, NO, adrenomedullin, fatty acids (via PPAR, RXR), purines and pyrimidines (via P2Y receptors) or growth hormone. We also found potential positive regulation of pathways that are involved in neuronal functions, including synaptogenesis and CREB signaling. The STB and column CTB data suggested that these cells may be able to respond to cannabinoids; cell columns and endovascular compartments up regulated the expression of genes that are involved in TH2 (tolerogenic) responses. A large number of unique pathways that were predicted to be activated solely by the endovascular trophoblasts and other cells types of the remodeled spiral arteries (ENDO). The putative pathways were involved in immune functions (acute phase signaling, dendritic cell maturation, IL-6, Tec kinase signaling or osteoarthritis), cell movement (colorectal cancer metastasis as well as G12/13, integrin and ILK signaling), MAPK signaling, vascular biology (cardiac hypertrophy) and prolactin responses.

Given that the gene expression data were specific to various trophoblast subtypes, we were interested in showing that the DE molecules had the expected immunolocalization patterns. With regard to STBs, we chose neurotensin, a small peptide gut hormone, with brain and nervous system effects including analgesia (Cordomi et al., 2016; Perez de Vega et al., 2018; Tschumi and Beckstead, 2019), which to our knowledge was not known to be produced by the human placenta. The immunolocalization signal for this molecule (**Fig. 5A-C**) was detected as a vesicular pattern in the syncytium at higher density in the apical region of the cells, suggesting possible release into the maternal circulation. Additionally, we were interested in the expression of C4orf36, also in STBs, whose peptide product was detected by mass spectrometry. Immunostaining revealed a dense punctate pattern in STBs (**Fig. 5D-F)**. Within in the cell columns, we confirmed the expression of the peptidase PGPEP1 by the cytotrophoblasts in that region **(Fig. 5G-I)**.

To begin to explore the role of CTB *CNR1*/CB1 within the uterine wall, we confirmed the cells' expression of this receptor by using antibody-based methods. Immunolocalization with an antibody that was specific for this antigen showed binding to a subset of CK-positive CTBs within the uterine wall and in the endovascular compartment **(Fig. 6A-C)**. Immunoblotting with the same antibody detected a band of the expected molecular weight in CTB lysates (**Fig. 6D)**.

Next, we measured the absolute amounts of the major mammalian endogenous cannabinoids, anandamide (AED) and 2-arachidonoylglycerol (2-AG), in isolated CTBs and biopsies of the maternal-fetal interface that included invasive CTBs (**Fig. 6E)**. AEA was detected (50-100 pg/10^6 cells) and 2-AG was present at much higher concentrations (1000-5000 pg/10^6 cells).

We then explored CB1 function in terms of CTB invasion. CB1 and 2 agonists and antagonists (see **Table S2**) were added to the assay. Among the compounds tested, only a CB1 agonist had a dose-dependent effect, increasing invasion (**Fig. 6F)**.

Discussion

Here we used a laser capture approach combined with analyses at RNA and protein levels to learn more about the biology of human trophoblast subtypes during the second trimester of pregnancy. Our focus was on cells that are difficult to isolate by other means. Thus, much of the existing data are from analysis of tissue samples in which the cell type of interest is only a relatively minor component (*e.g.*, biopsies of the placenta or placental bed) or from *in vitro* models (*e.g.*, cell lines) whose fidelity to the cognate cell type(s) *in vivo* is largely unproven. Global transcriptional profiling of microdissected syncytium, cell columns and endovascular compartments revealed many identifications that were expected in addition to those that were, to the best of our knowledge, novel.

With regard to STBs, we expected to detect, at RNA and protein levels, well known abundant products such as *CSHL1* (CHORIONIC SOMATOMAMMOTROPIN HORMONE-LIKE 1), *CYP19* (AROMATASE) and *GH2* (GROWTH HORMONE 2). We were also interested to find the expression of novel molecules such as neurotensin. Immunostaining for this molecule showed a vesicle-like pattern (**Fig. 5A-C**) with the stronger signal in the apical regions of the cells, suggesting release into maternal blood where the circulating molecule could induce systemic effects. Neurotensin was first isolated based on this peptide's ability to lower blood pressure (Carraway and Leeman, 1973). Later on, its role in promoting prolactin release and inhibiting LH secretion was discovered (McCann et al., 1982) . Since then, other effects on the gut and brain have been described, which could account for a portion of the physiologic changes that occur during pregnancy (Bugni et al., 2012; Cordomi et al., 2016; Perez de Vega et al., 2018; Tschumi and Beckstead, 2019). It would be very interesting to assay levels of this peptide in normal pregnancy and pregnancy complications with vascular (*e.g.*, preeclampsia) or GI (*e.g.*, hyperemesis gravidarum) signs**.**

With regard to column CTBs, the highly-expressed DE molecules included PANNEXIN-1. To our knowledge, placental expression has not been described. The structure and diverse roles of the three mammalian pannexins was recently reviewed (Makarenkova et al., 2018; Penuela et al., 2013; Whyte-Fagundes and Zoidl, 2018). These gap junction hemichannels release relatively small amounts of ATP under steady state conditions, which can substantially increase in pathological situations. In parallel, their roles vary from protective to harmful. Within these broad categories are many functions that are relevant to the initial stages of CTB invasion in which the cells form aggregates (*i.e.*, columns) that connect the placenta to the uterus. In parallel, they execute an unusual differentiation program in which they transition from an epithelial to a vascular/mesenchymal phenotype. In keeping with the structural and functional changes CTBs undergo in columns, PANNEXIN 1 has numerous physiologic functions, mediated by low levels of ATP release that could facilitate column formation such as promoting differentiation and survival. However, stressors such as mechanostimulation can ramp up these levels producing inflammation and pyroptotic cell death.

Other novel identifications, at mRNA and protein levels, were associated with column CTBs. They included PYROGLUTAMYL-PEPTIDASE I (*PGPEP1*), an exopeptidase (**Fig. 5G-I**) that cleaves N-terminal pyroglutamyl residues (Dando et al., 2003), a modification that protects many chemokines and peptide hormones (gastrin, thyrotropin releasing hormone and neurotensin) from degradation and inactivation. In this regard, it is interesting to note that column CTBs make an enzyme that degrades a STB product (*e.g.*, neurotensin), suggesting that they might be immune to its effects. Other novel mRNAs/proteins that were up regulated in this population included LYMPHOCYTE ANTIGEN 6K (LY6K), which marks the progression of many cancers and has been implicated in immune escape (Upadhyay, 2019).

Trophoblasts within the endovascular compartment was notable for the expression of CANNABINOID RECEPTOR 1 (CB1/*CNR1*). The history of the endocannabinoid signaling field was recently reviewed (Maccarrone et al., 2015). Establishing the lipid, Δ^9 - tetrahydrocannabinol, as the psychoactive ingredient in cannabis enabled identification of a receptor, CB1, which was the entre into the signaling pathways this ligand activates. Subsequently, a second receptor (CB2/*CNR2*) was described and there may be others. The existence of an exogenous ligand led to the discovery of endogenous lipids that bind these receptors, *e.g.*, AEA and 2-AG, which are produced from multiple membrane lipids whenever the need arises. In this regard, we used a mass spectrometry approach to quantify AED and 2-AG in isolated CTBs and biopsies of the maternal-fetal interface that included invasive CTBs. In both cases, 2-AG was the dominant species (**Fig. 6E)**.

Most of the work on endocannabinoid signaling during pregnancy has been done in the mouse (reviewed in Sun and Dey (Sun and Dey, 2012)). On the maternal side, deletion of *Cnr1* and *2* reduces fertility secondary to impaired implantation due to heightened edema around the implantation site (Li et al., 2019). In contrast, prolongation of endocannabinoid signaling results in premature decidual aging and preterm birth (Sun et al., 2016). On the embryo side, aberrant endocannabinoid signaling triggers premature trophoblast stem cell differentiation, and consequently, impairs trophoblast invasion. As a result, fetal development is retarded (Sun et al., 2010).

Together these results suggest that this signaling system could play an important role in human placentation. Thus, we were interested to find that endovascular CTBs expressed *CNR1*. Analyses at the protein level showed widespread expression of this receptor among invasive CTBs. As a result, we asked whether agonists or antagonists impacted invasion, assayed by an *in vitro* model of this process. Unexpectedly, we found that a CB1 agonist substantially increased invasion. Of the many molecules whose functions we have tested in this system, very few have had this effect. Notably, perturbing integrin $\alpha5/\beta1$ interactions with fibronectin also increased invasion suggesting that CTBs have systems for accelerating and braking invasion (Damsky et al., 1994). With regard to physiological regulators, we showed that uterine hypoxia, produced by aortic constriction, very significantly increases CTB invasion in the rhesus macaque (Zhou et al., 1993). Whether the parallel increases in cannabinoid signaling and invasion are related to either of these observations remains to be determined.

In summary, our laser microdissection/transcriptomic analysis of human STBs and invasive CTBs identified the expression of mRNAs encoding molecules known to be expressed by each cell type as well as novel transcripts that were also differentially expressed at the protein level. By using a mass spectrometry-based approach to validate DE molecules we also confirmed that *C4ORF36* is translated. Immunolocalization revealed a cytoplasmic staining pattern (**Fig. 5D-F)** that was consistent with the function of its fungal protein analog, dynein light chain, which is involved in intracellular transport (Li et al., 2018). We also showed that invasive CTBs express CB1/*CNR1*. Furthermore, endocannabinoid signaling in these cells appears to increase invasion, suggesting that this system may play the important role of facilitating deep placentation in human pregnancy. This finding raises the possibility that exogenous cannabinoids could also impact CTB invasion. Given the rapid rate of marijuana legalization in the US combined with the increased availability of synthetic cannabinoids with enhanced activity, the results of our study suggest that women should be cautioned against using these drugs during pregnancy.

Materials and methods

Tissue collection and preparation; CTB isolation

The UCSF Institutional Review Board (Committee on Human Research) approved this study. Written informed consent was obtained from all donors. Samples were processed within an hour of obtaining the tissue. Biopsies of the maternal-fetal interface were taken from four placentas with gestational ages stratified across the second trimester (15, 17, 18 and 20 weeks, respectively). Spiral arteries from the same cases were identified using a dissection microscope (Leica MZ16). Biopsied specimens (1 x 1 x 0.5 cm) were rinsed in ice-cold PBS, transferred to a 1:1 (v:v) PBS:OCT (Optimal Cutting Temperature compound, Thermo Scientific) semi-frozen slurry for 15 minutes, oriented in an OCT-filled peel-a-way disposable embedding mold (Thermo Scientific) and frozen over a mixture of dry ice and ethanol. For immunolocalization, biopsies were fixed (3% paraformaldehyde in PBS [wt/vol]) and passed through a sucrose gradient (5, 10 and 15% in PBS). Then they were placed in a mold and frozen in OCT as described above. For immunoblotting, unfixed specimens were frozen in a mortar over dry ice, pulverized, and stored at -80^{o}C.

CTBs were isolated from 2nd trimester placentas as previously described (Hunkapiller and Fisher, 2008). Briefly, chorionic villi were subjected to a series of enzymatic digestion steps that sequentially removed the outer STB layer and the underlying CTBs, which were isolated by centrifugation on a Percoll density gradient. Only cell preparations that were >80% pure as determined by cytokeratin staining were used in experiments.

Laser microdissection

Frozen blocks were sectioned (-20^{o}C) using a Leica CM3050 cryostat. Sections (20 µm) were mounted on different slides depending on the intended analysis. For subsequent RNA isolation, we used poly-L-lysine (Sigma Chemical Company) -coated, UV-treated, metal-frame, polyethylene naphthalate-membrane (PEN) slides (ThermoFisher Scientific). For subsequent protein isolation, we used poly-L-lysine treated DIRECTOR slides (Expression Pathology; (Hembrough et al., 2012). Slides with sections were kept under dry ice until LMD the same day. Sections on slides were manually defrosted in room air (30 sec), immersed in PBS until the OCT was completely removed (~2 min), dipped in 0.1% toluidine blue for 30 sec, washed in cold PBS, dehydrated (30 sec/treatment) in a graded ethanol series (75% x 2, 95%, 100%), then rapidly dried with compressed nitrogen. All solutions were made with nuclease-free reagents for RNA isolation or HPLC grade solutions for protein isolation in sterile single-use 50 mL conical tubes (Falcon). Regions of interest were identified using a 20x objective and circled on a touch-screen monitor (Wacom) coupled to a color camera (Leica DFC310 FX), which triggered a solid state UV laser (LMD 7000) enabling dissection (samples for RNA isolation) or rasterisation (samples for protein isolation) into a buffer-filled cap suspended immediately below. Buffer RLT Plus (Qiagen) was used for subsequent RNA isolation. An alkaline surfactant-containing solution (50 mM triethylammonium bicarbonate [Sigma], 5 mM tris[2-

carboxyethyl]phosphine [“Bond-Breaker,” ThermoFisher], and 0.1% [w/v] RapiGest SF [Waters]) was used for subsequent protein isolation.

For RNA, 10 slides with 4 sections per slide were prepared for each specimen. For protein, 5 slides with 8 sections per slide were prepared. To limit degradation, each slide used for RNA isolation was microdissected for no more than 30 minutes, which was extended to 1 hour for protein recovery. The regions of interest were collected into different caps and pooled across all 40 tissue sections.

RNA isolation

Total RNA was isolated according to the manufacturer’s protocol (Qiagen RNeasy Plus Micro kit) with the added step of an on-column DNase digestion of bound RNA to avoid any DNA contamination. The concentration of total RNA was measured photometrically (NanoDrop 2000c). RNA integrity was determined via microfluidic phoresis (Agilent Tapestation). The samples were stored at -80^{o}C prior to analysis.

Global RNA profiling

We used a microarray approach (Affymetrix GeneChip HuGene 2.0 ST) and protocols that were devised by the UCSF Gladstone (NHLBI) Genomics Core Facility. Gene expression data quality was confirmed, RMA normalized (Bolstad et al., 2003; Irizarry et al., 2003; Wu et al., 2004) and summarized (oligo package) (Carvalho and Irizarry, 2010) in R/Bioconductor (Ihaka and Gentleman, 1996; RCoreTeam, 2013). The data were modeled and contrasts between STB, CTB and ENDO determined using the limma package (Ritchie et al., 2015). Differentially expressed genes (DEGs) had an absolute linear fold change ≥ 2 and an adjusted p value < 0.05 for any pairwise comparison (STB versus CTB, STB versus ENDO, ENDO versus CTB). Four biological replicates of each subpopulation were analyzed (15, 17, 18 and 20 wks gestation). The data were deposited in GEO (accession number GSE156766).

Global protein profiling: trophoblast capture; protein isolation and digestion

Three biological replicates of each cell type (STB, CTB and ENDO; 17, 18, and 20 wks gestation) were isolated by LMD from the same placentas that were subjected to global transcriptional profiling (see previous section). The samples were incubated in the alkaline surfactant-containing solution described above at 60^{o}C with rigorous vortexing every 15 min for 1 h. Iodoacetamide (ThermoFisher) was added to 15 mM and incubated at room temperature in the dark for 30 min. Proteins were digested overnight at 37^{o}C with trypsin (20 ng/µL, Pierce), then centrifuged at 16,000 x g (Eppendorf) for 10 min. Trifluoroacetic acid (Pierce) was added to the supernatant such that the final concentration was 0.5%. Duplicate technical replicates were performed along with a control that consisted of a blank DIRECTOR slide that was carried through the entire sample preparation protocol.

Global protein profiling: identification, relative quantification and tandem assembly

Using published methods(Branson and Freitas, 2016), each trypsin digestion was analyzed by reversed phase high performance liquid chromatography tandem mass spectrometry (RP HPLC MS/MS) using a nanoLC Ultra system (Eksigent Technologies) interfaced with a LTQ Orbitrap Velos mass spectrometer (ThermoScientific). Peptides were separated using an Acclaim PepMap100 C18 column (75 µm i.d. x 15 cm, 3 µm particle size, 100 Å pores, ThermoFisher) via mobile phase A (acetonitrile/water, 2:98, v/v, 0.1% formic acid) and mobile phase B (acetonitrile/water, 98:2, v/v, 0.1% formic acid) in conjunction with a linear gradient of 2-40% B over 90 min. The mobile phase flow rate was 550 nL/min. Using electrospray ionization, the LTQ Orbitrap Velos was operated in data-dependent acquisition mode for MS and MS/MS data collection. An initial survey scan was acquired (m/z 300-1500) in the Orbitrap analyzer at mass resolution 30,000, followed by collision-induced dissociation of precursor ions in the ion trap to produce MS/MS spectra for the 20 most abundant precursor ions. The instrument was operated with an isolation width of 3.0, normalized collision energy of 35, an ActQ of 0.25, and an MS/MS activation time of 10 ms.

The DEGs observed in the mRNA data were used to create a FASTA database of reviewed, canonical protein sequences (Pundir et al., 2017). Protein identification was accomplished by searching this database with the peptide MS/MS spectra using MS Amanda 2.0 and Sequest HT search algorithms (Proteome Discoverer, v2.2). The false discovery rate (FDR) was controlled by Percolator, a semi-supervised machine learning algorithm (Kall et al., 2007), using a target-decoy database strategy (Elias and Gygi, 2010). Criteria for identified proteins (IPs) included a minimum of two unique corresponding peptide spectra counted at least twice each, in two or more biological replicates, at an FDR < 0.10% (Proteome Discoverer, v2.2).

All subsequent analyses were done in R (Ihaka and Gentleman, 1996; RCoreTeam, 2013). The spectral counts were quantified (Branson and Freitas, 2016) and modeled using negative binomials (Robinson and Smyth, 2008). The differentially expressed proteins (STB versus CTB, STB versus ENDO, ENDO versus CTB) were identified using the exact test in edgeR (Robinson et al., 2010)($p < 0.05$). The coordinately differentially expressed genes and proteins were termed tandems.

All raw files are uploaded to the Center for Computational Mass Spectrometry, MassIVE (https://massive.ucsd.edu), dataset MSV000085995. Data uploads include the protein identification details.

Ingenuity Pathway Analysis

The tandems for each trophoblast subtype were uploaded to Ingenuity Pathway Analysis (IPA) and a core expression analysis performed, followed by a comparison analysis of the results. A significant canonical pathway had a -log(p-value) > 1.3, an absolute z-score > 2, and contained at least 4 tandems in a unique combination (no pathway redundancy).

Immunolocalization

Portions of second trimester placentas that included anchoring chorionic villi were fixed in 3% paraformaldehyde for 30 min., washed three times in phosphate-buffered saline (PBS), infiltrated with 5 to 15% sucrose followed by OCT medium, and frozen in liquid nitrogen. Tissues were sectioned (10 μm) using a cryostat (Leica CM3050) and collected on charged glass slides (Fisher). The OCT was removed by washing in cold PBS. Nonspecific binding was inhibited by incubation for 30 min. with blocking buffer: 3% (w/v) bovine serum albumin (BSA), 0.1% cold fish skin gelatin, 0.1% Triton X-100 and 0.05% Tween 20 (Fisher Scientific) in PBS. Primary and secondary antibodies, their sources/catalogue numbers, the species in which they were raised and the concentrations used in the immunolocalization experiments are listed in **Table S1**. As to the general methods, a primary unconjugated antibody and rat anti-cytokeratin were diluted together in blocking buffer, incubated overnight with tissue sections in a humidified chamber at 4^{o}C, washed (3 x 10 min.) in PBS, incubated with species-specific fluorescently tagged secondary antibodies and washed again in PBS. Mounting medium with 4',6-diamidino-2-phenylindole (DAPI; Vector Laboratories) was applied and the sections were coverslipped. Controls included omission of the primary or secondary antibody. The tissue sections were examined and images captured by using a confocal Leica DM5000 B microscope. Z-stacks were created in 1μm increments at 1024 x 1024 pixel resolution and line averaged 3 times.

Immunoblotting

Proteins from isolated CTB cell pellets were solubilized in M-PER (Thermo) according to the manufacturer's protocol and protein concentrations determined spectrophotometrically (Shimadzu). Samples (5 µg) were electrophoretically separated on 4-12% Bis-Tris protein gels (1.5 mm, Invitrogen) and transferred to nitrocellulose membranes, followed by blocking for 1 h with 5% nonfat powdered milk in PBS-Tween-20 (0.1%) before incubating overnight at 4°C with primary antibody. Then the membranes were washed 3 times in PBS-Tween-20 and incubated with the appropriate species-specific secondary antibody for 1 h. Immunoreactive bands were detected with ECL 2 Western Blotting Substrate (Thermo Fisher Scientific, Pierce) and ECL high performance chemiluminescence film (Amersham, GE Healthcare). Equal sample loading in all the lanes was confirmed by anti-α-actin immunoreactivity.

Mass spectrometry quantification of endogenous cannabinoids (anandamide and 2-arachidonoylglycerol).

Cell or tissue (maternal-fetal interface) samples were prepared using a Precellys 24 homogenizer with a Cryolys cooling unit (Bertin Technologies). Individual samples were placed in 2-ml vials with 10 vol water (10-fold dilution) and seven homogenization beads. Homogenization was conducted for three cycles (20 sec. each) at 5,000 rpm (with 30-sec. breaks) at < 10°C. Then 50 µl of each homogenized sample was pipetted into 13 × 100 mm tubes after which 150 µl of a deuterated internal standard solution were added, prior to vortexing for 1 min. and centrifugation (3000 *xg*) for 10 min.

Then the supernatant (5 µl) was separated on a Shimadzu Prominence UFLC system equipped with a binary pump and a SIL-20AC autosampler. Separation was achieved on a XBridge C18 column (4.6 × 50 mm). A gradient separation was used consisting of mobile phase A (0.05% H_2O/5mM MNH_4 [15%]) and mobile phase B (ACN/2.5 mM MNH_4 [85%]) at a flow rate of 1.0 mL/min.

Mass spectrometric detection was performed using an Applied Biosystems/MDS SCIEX API 5000 triple quadrupole mass spectrometer, which was operated in multiple reaction monitoring (MRM) mode via the negative electrospray ionization interface using the transitions (*m/z*) 379.4→287.4 for 2-AG (2-Arachidonoylglycerol), 386.4→293.4 for 2-AG-d8, 348.5→62.2 for AEA (anandamide), and 356.5→163.2 for AEA-d8. Data acquisition and quantitative processing were accomplished using Applied Biosystems Analyst version 1.5.1 software.

Invasion Assay

Cytotrophoblasts (2^{nd} trimester) were isolated according to methods described above. The cells (250,000) were plated in 500 μl of DME H-21/2% Nutridoma on Matrigel-coated 24-well Transwell inserts (Costar) with 8.0 mm pores for 1 h. Nonadherent cells were removed by washing with warm medium before adding DME H-21/2% Nutridoma containing 1 or 10 ng/ml of a CB1 or CB2, agonist or antagonist, or the vehicle in which they were dissolved as a control (0.1% Tocrisolve, Tocris). The compounds and their activities are shown in **Table S2**. Each condition was tested in triplicate. After culturing for 72 h, the inserts were washed with PBS and fixed for 20 min in 3% PFA. They were stored at 4°C in PBS or immediately immunostained as described above with anti-cytokeratin 7. Then the membrane inserts were removed with surgical scissors and mounted on slides with DAPI-containing medium such that the underside of the membrane faced up. They were imaged with a fluorescent microscope (Leica DM3000B). The number of cytotrophoblast projections that reached the underside of the filter was counted and the data were expressed as experimental values relative to controls. The assay was done 3 times (biological replicates). Students t-test ($p < 0.05$) was used to determine significance.

Creation of graphics

Tables and heat maps were constructed in Excel (Microsoft) and scatter and parallel plots were generated in OriginPro (OriginLabs).

Author contributions

MG did the majority of the experiments, analyzed the data, prepared the figures and wrote a draft of the paper. OO helped with the laser capture of trophoblast subpopulation. MK isolated cytotrophoblasts. KO did a portion of the immunolocalization studies. SH helped with the mass spectrometry data analyses. SJF conceived of the study, designed the experiments, interpreted data and wrote the paper.

Acknowledgements

We thank the clinical research coordinators, the patient participants, Norma McCormack for administrative support, and Drs. Michael McMaster and Steve Hall for careful reading and help with editing this manuscript. We are grateful to Dr. SK Dey for valuable advice on the function perturbation experiments. We thank Dr. Yong Huang for the mass spectrometry-small molecule analysis.

Funding

This work was supported by the generosity of the National Institute of Health National Institute of Drug Abuse (NIDA) (1R21DA042951-01) to SJF.

Data availability

Raw and normalized microarray data were deposited in the Gene Expression Omnibus (accession no. GSE156766). Raw and normalized mass spectrometry data were deposited in MassIVE (https://massive.ucsd.edu), dataset MSV000085995.

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Figures

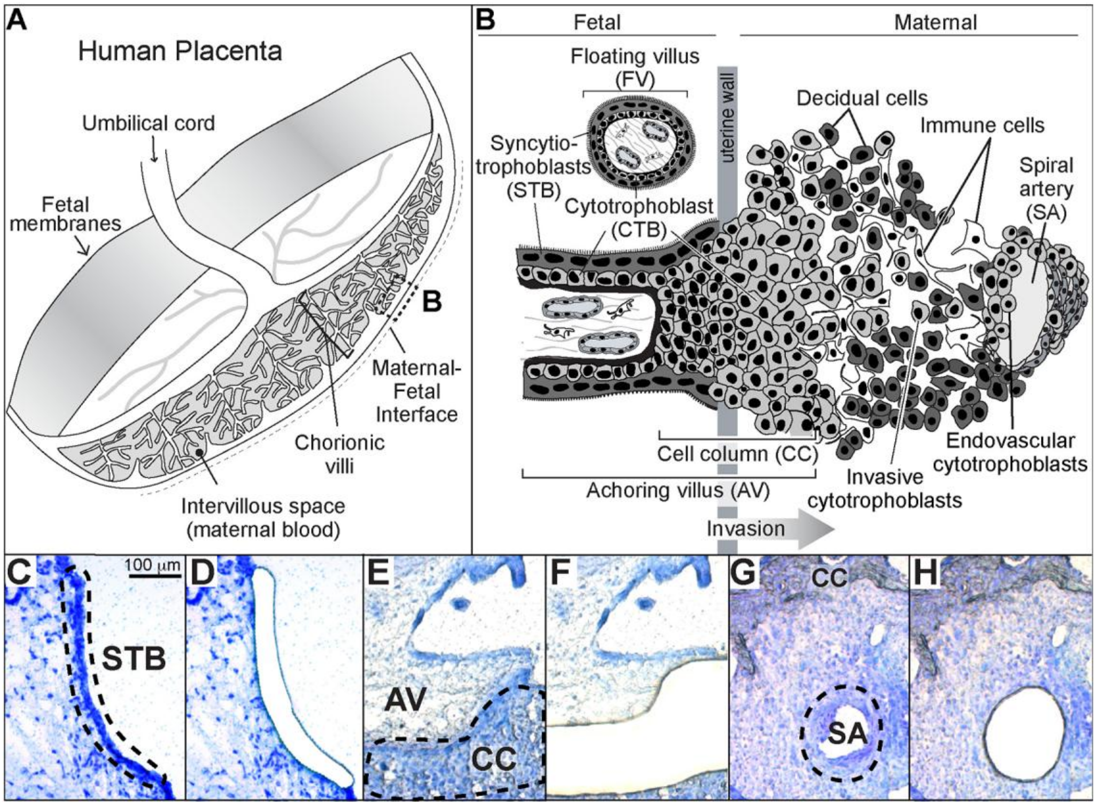


Fig 1. Diagram and photomicrographs of the human placenta highlighting the trophoblast subtypes targeted for laser microdissection. (A) Diagram of the human placenta in the second trimester of pregnancy. The *boxed area* indicates the region biopsied for these studies. (B) View of the maternal-fetal interface at the cellular level. Shown are the two classes of chorionic villi. Floating villi (FV), which are covered by multinucleated syncytiotrophoblasts (STB), transport substances between the mother and the embryo/fetus while producing growth factors and hormones essential to the unique symbiosis of pregnancy. Anchoring villi (AV), contain mononuclear cytotrophoblast progenitors that either fuse to form STBs or exit the placenta proper through cell columns (CCs) that attach the embryo/fetus to the uterus. Endovascular cytotrophoblasts mediate an increase in the terminal diameter of the maternal spiral arteries, enabling increase blood flow to the placenta. The arrow indicates the direction of trophoblast invasion (modified from Damsky *et al*.(Damsky et al., 1994)). (C-G) Photomicrographs taken before and after STB, CTB and ENDO were isolated using LMD. The sections were stained with toluidine blue, which enabled visualization of the cellular architecture. The dotted lines indicate the three trophoblast-containing regions that were targeted. Size bar = 100 µm.

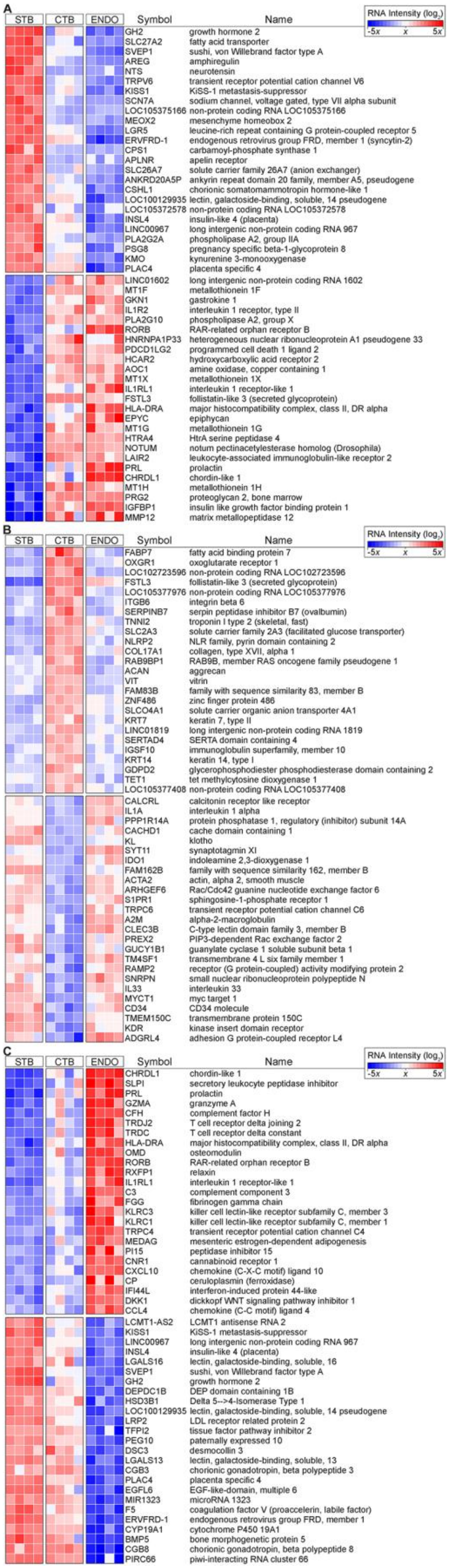

A
STB
CTB
ENDO
Symbol
Name
RNA Intensity ($\log_2$)
-5x
x
5x
GH2 growth hormone 2
SLC27A2 fatty acid transporter
SVEP1 sushi, von Willebrand factor type A
AREG amphiregulin
NTS neurotensin
TRPV6 transient receptor potential cation channel V6
KISS1 KiSS-1 metastasis-suppressor
SCN7A sodium channel, voltage gated, type VII alpha subunit
LOC105375166 non-protein coding RNA LOC105375166
MEOX2 mesenchyme homeobox 2
LGR5 leucine-rich repeat containing G protein-coupled receptor 5
ERVFRD-1 endogenous retrovirus group FRD, member 1 (syncytin-2)
CPS1 carbamoyl-phosphate synthase 1
APLNR apelin receptor
SLC26A7 solute carrier family 26A7 (anion exchanger)
ANKRD20A5P ankyrin repeat domain 20 family, member A5, pseudogene
CSHL1 chorionic somatomammotropin hormone-like 1
LOC100129935 lectin, galactoside-binding, soluble, 14 pseudogene
LOC105372578 non-protein coding RNA LOC105372578
INSL4 insulin-like 4 (placenta)
LINC00967 long intergenic non-protein coding RNA 967
PLA2G2A phospholipase A2, group IIA
PSG8 pregnancy specific beta-1-glycoprotein 8
KMO kynurenine 3-monooxygenase
PLAC4 placenta specific 4
LINC01602 long intergenic non-protein coding RNA 1602
MT1F metallothionein 1F
GKN1 gastrokine 1
IL1R2 interleukin 1 receptor, type II
PLA2G10 phospholipase A2, group X
RORB RAR-related orphan receptor B
HNRNPA1P33 heterogeneous nuclear ribonucleoprotein A1 pseudogene 33
PDCD1LG2 programmed cell death 1 ligand 2
HCAR2 hydroxycarboxylic acid receptor 2
AOC1 amine oxidase, copper containing 1
MT1X metallothionein 1X
IL1RL1 interleukin 1 receptor-like 1
FSTL3 follistatin-like 3 (secreted glycoprotein)
HLA-DRA major histocompatibility complex, class II, DR alpha
EPYC epiphycan
MT1G metallothionein 1G
HTRA4 HtrA serine peptidase 4
NOTUM notum pectinacetylesterase homolog (Drosophila)
LAIR2 leukocyte-associated immunoglobulin-like receptor 2
PRL prolactin
CHRDL1 chordin-like 1
MT1H metallothionein 1H
PRG2 proteoglycan 2, bone marrow
IGFBP1 insulin like growth factor binding protein 1
MMP12 matrix metallopeptidase 12
B
STB
CTB
ENDO
Symbol
Name
RNA Intensity ($\log_2$)
-5x
x
5x
FABP7 fatty acid binding protein 7
OXGR1 oxoglutarate receptor 1
LOC102723596 non-protein coding RNA LOC102723596
FSTL3 follistatin-like 3 (secreted glycoprotein)
LOC105377976 non-protein coding RNA LOC105377976
ITGB6 integrin beta 6
SERPINB7 serpin peptidase inhibitor B7 (ovalbumin)
TNNI2 troponin I type 2 (skeletal, fast)
SLC2A3 solute carrier family 2A3 (facilitated glucose transporter)
NLRP2 NLR family, pyrin domain containing 2
COL17A1 collagen, type XVII, alpha 1
RAB9BP1 RAB9B, member RAS oncogene family pseudogene 1
ACAN aggrecan
VIT vitrin
FAM83B family with sequence similarity 83, member B
ZNF486 zinc finger protein 486
SLCO4A1 solute carrier organic anion transporter 4A1
KRT7 keratin 7, type II
LINC01819 long intergenic non-protein coding RNA 1819
SERTAD4 SERTA domain containing 4
IGSF10 immunoglobulin superfamily, member 10
KRT14 keratin 14, type I
GDPD2 glycerophosphodiester phosphodiesterase domain containing 2
TET1 tet methylcytosine dioxygenase 1
LOC105377408 non-protein coding RNA LOC105377408
CALCRL calcitonin receptor like receptor
IL1A interleukin 1 alpha
PPP1R14A protein phosphatase 1, regulatory (inhibitor) subunit 14A
CACHD1 cache domain containing 1
KL klotho
SYT11 synaptotagmin XI
IDO1 indoleamine 2,3-dioxygenase 1
FAM162B family with sequence similarity 162, member B
ACTA2 actin, alpha 2, smooth muscle
ARHGEF6 Rac/Cdc42 guanine nucleotide exchange factor 6
S1PR1 sphingosine-1-phosphate receptor 1
TRPC6 transient receptor potential cation channel C6
A2M alpha-2-macroglobulin
CLEC3B C-type lectin domain family 3, member B
PREX2 PIP3-dependent Rac exchange factor 2
GUCY1B1 guanylate cyclase 1 soluble subunit beta 1
TM4SF1 transmembrane 4 L six family member 1
RAMP2 receptor (G protein-coupled) activity modifying protein 2
SNRPN small nuclear ribonucleoprotein polypeptide N
IL33 interleukin 33
MYCT1 myc target 1
CD34 CD34 molecule
TMEM150C transmembrane protein 150C
KDR kinase insert domain receptor
ADGRL4 adhesion G protein-coupled receptor L4
C
STB
CTB
ENDO
Symbol
Name
RNA Intensity ($\log_2$)
-5x
x
5x
CHRDL1 chordin-like 1
SLPI secretory leukocyte peptidase inhibitor
PRL prolactin
GZMA granzyme A
CFH complement factor H
TRDJ2 T cell receptor delta joining 2
TRDC T cell receptor delta constant
HLA-DRA major histocompatibility complex, class II, DR alpha
OMD osteomodulin
RORB RAR-related orphan receptor B
RXFP1 relaxin
IL1RL1 interleukin 1 receptor-like 1
C3 complement component 3
FGG fibrinogen gamma chain
KLRC3 killer cell lectin-like receptor subfamily C, member 3
KLRC1 killer cell lectin-like receptor subfamily C, member 1
TRPC4 transient receptor potential cation channel C4
MEDAG mesenteric estrogen-dependent adipogenesis
PI15 peptidase inhibitor 15
CNR1 cannabinoid receptor 1
CXCL10 chemokine (C-X-C motif) ligand 10
CP ceruloplasmin (ferroxidase)
IFI44L interferon-induced protein 44-like
DKK1 dickkopf WNT signaling pathway inhibitor 1
CCL4 chemokine (C-C motif) ligand 4
LCMT1-AS2 LCMT1 antisense RNA 2
KISS1 KiSS-1 metastasis-suppressor
LINC00967 long intergenic non-protein coding RNA 967
INSL4 insulin-like 4 (placenta)
LGALS16 lectin, galactoside-binding, soluble, 16
SVEP1 sushi, von Willebrand factor type A
GH2 growth hormone 2
DEPDC1B DEP domain containing 1B
HSD3B1 Delta 5-->4-Isomerase Type 1
LOC100129935 lectin, galactoside-binding, soluble, 14 pseudogene
LRP2 LDL receptor related protein 2
TFPI2 tissue factor pathway inhibitor 2
PEG10 paternally expressed 10
DSC3 desmocollin 3
LGALS13 lectin, galactoside-binding, soluble, 13
CGB3 chorionic gonadotropin, beta polypeptide 3
PLAC4 placenta specific 4
EGFL6 EGF-like-domain, multiple 6
MIR1323 microRNA 1323
F5 coagulation factor V (proaccelerin, labile factor)
ERVFRD-1 endogenous retrovirus group FRD, member 1
CYP19A1 cytochrome P450 19A1
BMP5 bone morphogenetic protein 5
CGB8 chorionic gonadotropin, beta polypeptide 8
PIRC66 piwi-interacting RNA cluster 66

Fig 2. Heat maps of differentially expressed STB, CTB and ENDO RNAs. (A) The 25 most highly up regulated and 25 most highly down regulated transcripts in syncytiotrophoblasts (STB) compared to cytotrophoblasts (CTB) and endovascular cytotrophoblasts (ENDO) (total = 2708, **Table S2**). (B) Heat map of the most highly differentially expressed transcripts in CTB (total = 2070, **Table S2**) relative to STB and ENDO. (C) Heat map of the most highly differentially expressed transcripts in ENDO (total = 2753, **Table S2**) relative to STB and CTB. The data are displayed as a heat map showing the relative RNA fold change as a variation in color from blue (decreased expression) to white (average expression) to red (increased expression). Cells captured from four placentas were analyzed.

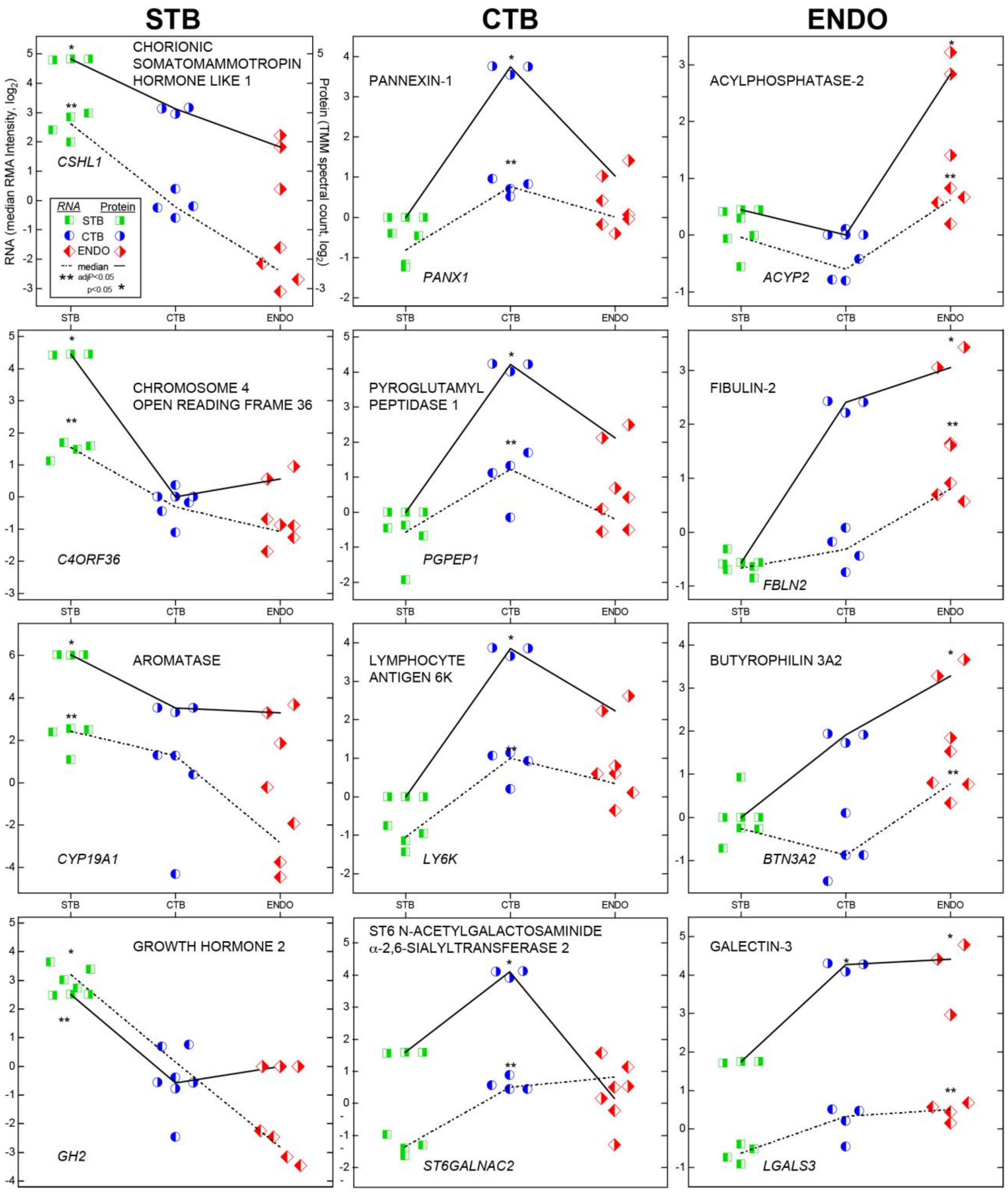

STB
CTB
ENDO
CHORIONIC SOMATOMAMMOTROPIN HORMONE LIKE 1
CSHL1
RNA (median RMA Intensity, $\log_2$)
Protein (TMM spectral count, $\log_2$)
RNA
Protein
STB
CTB
ENDO
median
** adjP<0.05
p<0.05 *
PANNEXIN-1
PANX1
ACYLPHOSPHATASE-2
ACYP2
CHROMOSOME 4 OPEN READING FRAME 36
C4ORF36
PYROGLUTAMYL PEPTIDASE 1
PGPEP1
FIBULIN-2
FBLN2
AROMATASE
CYP19A1
LYMPHOCYTE ANTIGEN 6K
LY6K
BUTYROPHILIN 3A2
BTN3A2
GROWTH HORMONE 2
GH2
ST6 N-ACETYLGALACTOSAMINIDE α-2,6-SIALYLTRANSFERASE 2
ST6GALNAC2
GALECTIN-3
LGALS3
STB
CTB
ENDO

Fig 3. Plots of relative RNA and protein abundances in the trophoblast subtypes analyzed. The upper left hand panel illustrates the labeling scheme. Data are organized in columns. Molecules that were up regulated in STBs are shown to the left, cell column CTBs in the middle and endovascular CTBs to the right. Each cell type is designated by a different bisected symbol (square, circle or diamond). Left or right shading denotes RNA or protein values, respectively, which is colored (green, blue or red) to aid interpretation. RNA data were from four biological replicates, protein data were from three biological replicates.

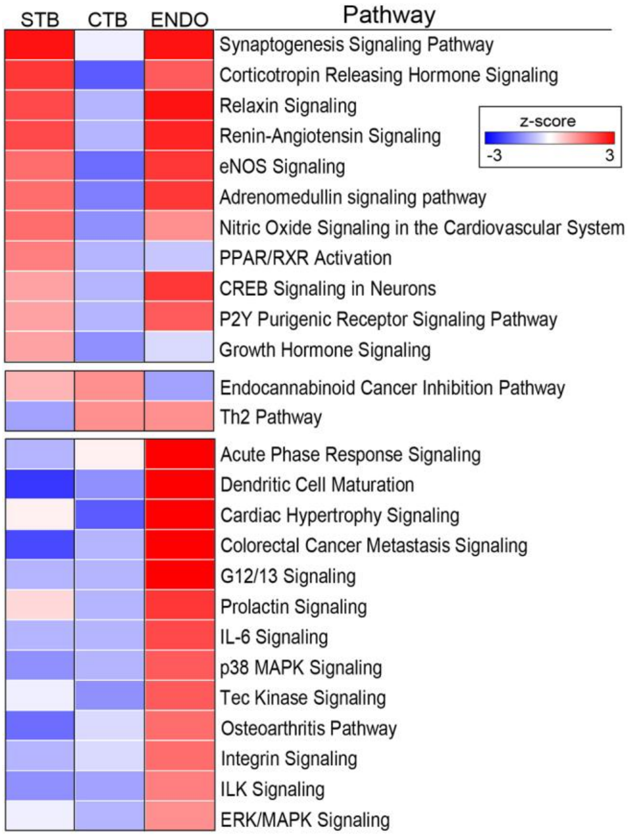


Fig 4. Ingenuity Pathway Analysis of the differentially expressed genes among trophoblast subpopulations. Pathways were assigned a z-score based on the predicted impact of DE genes, either activation (+) or deactivation (-). Significant pathways had a –log(p-value) > 1.3, an absolute z-score > 2, and contained at least 4 members in a unique combination. The data are displayed as a heat map showing the z-score as a variation in color from blue (decreased expression) to red (increased expression) for each trophoblast subtype. The results were notable for the number signaling pathways that were identified.

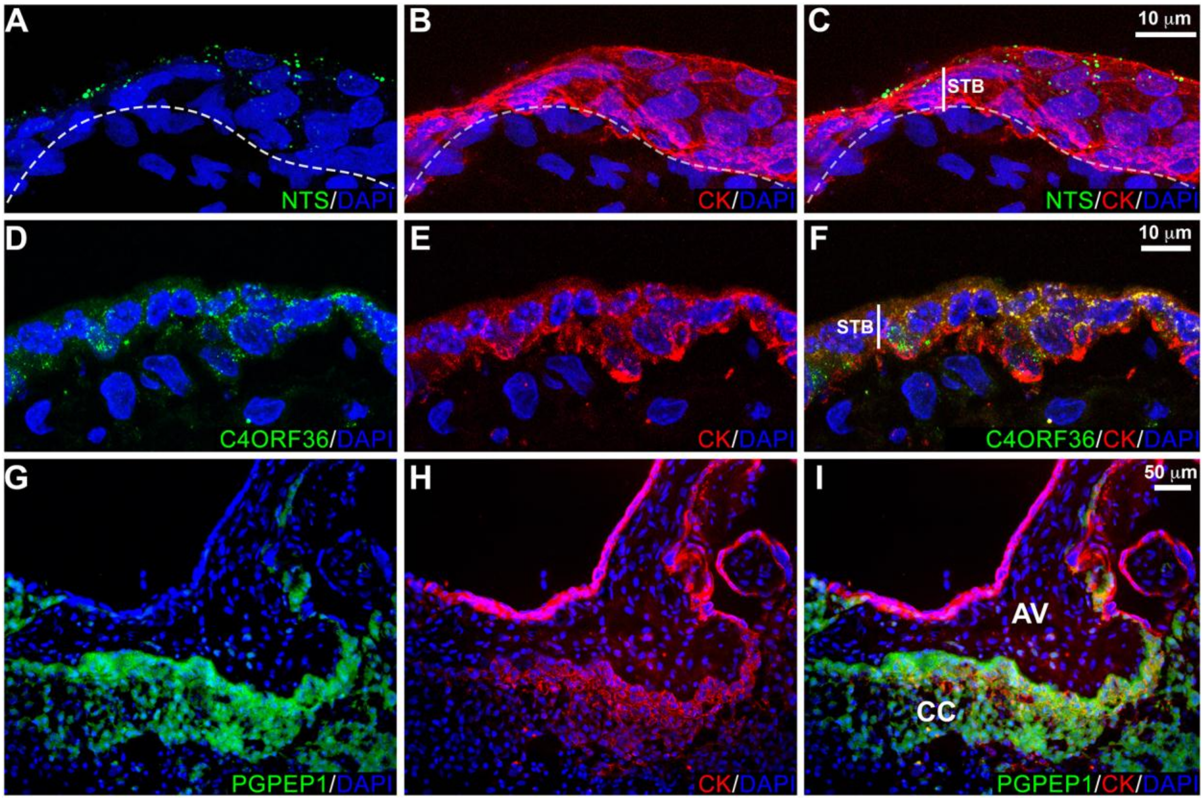


Fig 5. Immunolocalization of differentially expressed proteins: neurotensin (NTS), C4ORF36, and Pyroglutamyl-Peptidase I (PGPEP1). Tissue sections were immunostained for the antigen of interest and cytokeratin (CK), a trophoblast marker. Nuclei were localized with DAPI. Each panel was a confocal z-stack maximum intensity projection. (A-C) Neurotensin (NTS) was detected in a vesicular pattern localized to the apical region of syncytiotrophoblasts (STB). Within any one tissue section the vesicle density varied among regions although no areas lacked immunoreactivity. Furthermore, no differences based on gestational age were observed. (D-F) C4ORF36, which localized to STBs, had a uniformly dense punctate pattern. No variation was observed across the second trimester. (G-I) PGPEP1 was highly upregulated in cytotrophoblast columns (CC) of anchoring villi (AV). The results shown were represented of the immunostaining observed in a minimum of three biological replicates.

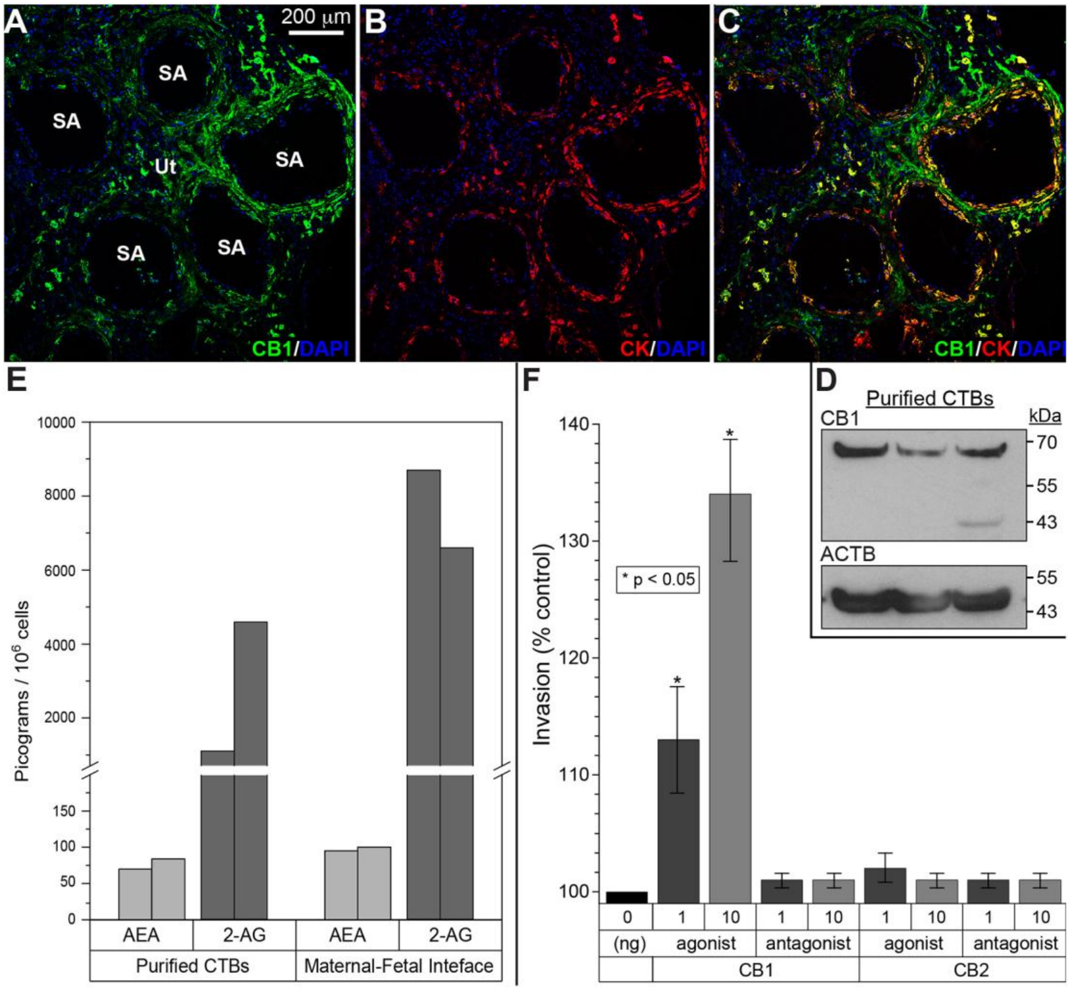


Fig 6. Expression of cannabinoid ligands and receptors at the maternal fetal interface and the functional consequences. (A-C) Tissue sections were immunostained for cannabinoid receptor 1 (CNR1)/CB1 and cytokeratin (CK), a trophoblast marker. Nuclei were localized with DAPI. Each panel was a confocal z-stack maximum intensity projection. Anti-CB1 specifically reacted with invasive/endovascular CTBs in the walls of uterine (Ut) spiral arteries (SA). Cytotrophoblasts in the cell columns showed variable CB1 expression, while syncytiotrophobasts were negative (data not shown). The results shown were representive of the immunostaining observed in a minimum of three biological replicates. (D) Immunoblotting with the same antibody detected a band of the expected molecular weight in CTB lysates. Protein loading was estimated by immunoblotting with anti-actin-B (ACTB). Cells from three placentas were analyzed. (E) Mass spectrometry enabled measuring the absolute amounts of the major mammalian endogenous cannabinoids, anandamide (AED) and 2-arachidonoylglycerol (2-AG), in isolated CTBs and biopsies of the maternal-fetal interface that included invasive CTBs. The results from replicate samples are shown. (F) Among the CB1 and CB2 agonists and antagonists assayed, only a CB1 agonist had a dose-dependent effect increasing invasion (n=3 biological replicates, * = significance $p < 0.05$).

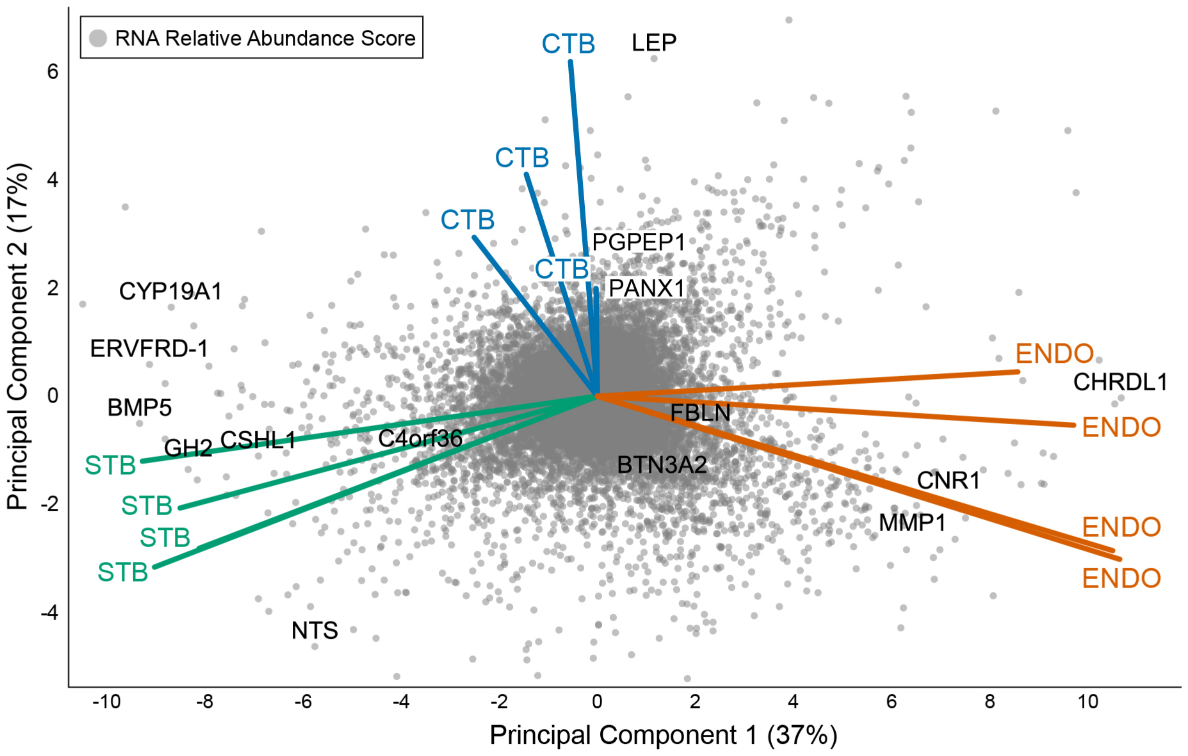
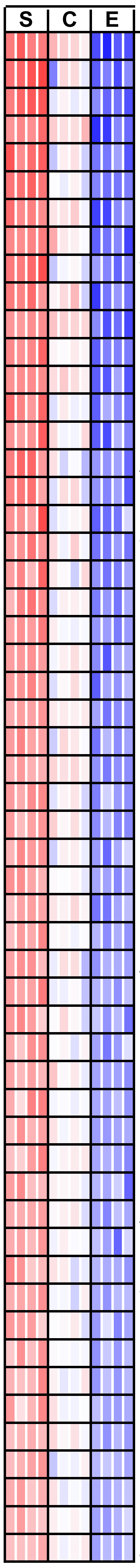

RNA Relative Abundance Score
Principal Component 2 (17%)
Principal Component 1 (37%)
6
4
2
0
-2
-4
-10
-8
-6
-4
-2
0
2
4
6
8
10
CTB
LEP
CTB
CTB
PGPEP1
CTB
PANX1
CYP19A1
ERVFRD-1
ENDO
CHRDL1
BMP5
FBLN
ENDO
GH2
CSHL1
C4orf36
STB
BTN3A2
CNR1
STB
MMP1
STB
ENDO
STB
ENDO
NTS

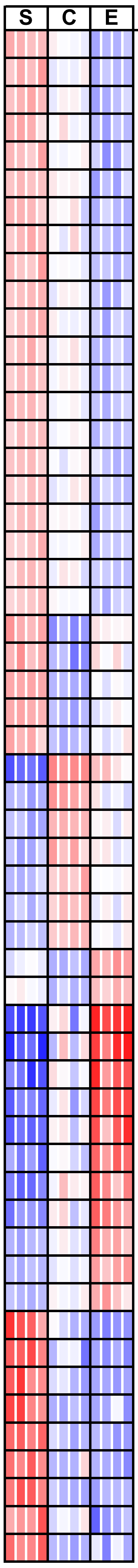
Fig. S1.



Linear Fold Change

(*ns*=no significant difference)

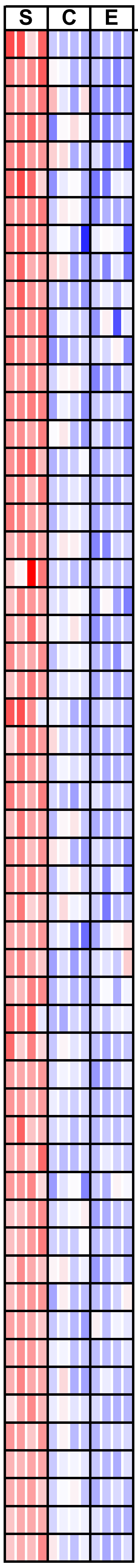
Symbol	Name	**S** vs **C**	**S** vs **E**	**E** vs **C**
ERVFRD-1	endogenous retrovirus group FRD, member 1	3.5	77.7	-21.9
GH2	growth hormone 2	11.6	64.7	-5.6
SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	9.3	57.8	-6.2
PLAC4	placenta specific 4	2.7	49.8	-18.1
KISS1	KiSS-1 metastasis-suppressor	9.0	44.5	-4.9
LGR5	leucine-rich repeat containing G protein-coupled receptor 5	8.1	41.2	-5.1
LOC100129935	lectin, galactoside-binding, soluble, 14 pseudogene	4.0	41.0	-10.2
LRP2	LDL receptor related protein 2	3.4	39.5	-11.5
TRPV6	transient receptor potential cation channel, subfamily V, member 6	10.3	39.5	-3.8
INSL4	insulin-like 4 (placenta)	4.3	37.9	-8.8
PEG10	paternally expressed 10	2.3	34.2	-15.0
LINC00967	long intergenic non-protein coding RNA 967	4.8	34.0	-7.1
DEPDC1B	DEP domain containing 1B	3.0	33.2	-11.2
CSHL1	chorionic somatomammotropin hormone-like 1	6.6	30.7	-4.7
LCMT1-AS2	LCMT1 antisense RNA 2	4.0	29.6	-7.4
ANKRD20A5P	ankyrin repeat domain 20 family, member A5, pseudogene	8.0	27.7	-3.5
KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	5.4	26.6	-5.0
PSG8	pregnancy specific beta-1-glycoprotein 8	5.4	26.5	-4.9
TCL6	T-cell leukemia	3.6	24.3	-6.8
GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon	4.2	21.2	-5.1
LOC100128988	uncharacterized LOC100128988	4.4	21.1	-4.8
SEMA6A	semaphorin 6A	4.4	18.5	-4.2
CRYBG1	crystallin beta-gamma domain containing 1	3.3	18.2	-5.5
PSG9	pregnancy specific beta-1-glycoprotein 9	4.2	17.3	-4.1
GPC3	glypican 3	2.8	16.2	-5.8
LOC102724687	uncharacterized LOC102724687	3.8	15.7	-4.1
FAM184A	family with sequence similarity 184, member A	2.1	15.0	-7.3
HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	4.4	14.4	-3.2
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	2.8	14.2	-5.1
ERV3-1	endogenous retrovirus group 3, member 1	4.3	13.5	-3.1
MPP7	membrane protein, palmitoylated 7	3.8	13.3	-3.5
EXPH5	exophilin 5	2.4	13.3	-5.6
IGSF5	immunoglobulin superfamily, member 5	3.4	12.1	-3.6
ABCG2	ATP binding cassette subfamily G member 2 (Junior blood group)	3.9	11.9	-3.1
SLC13A4	solute carrier family 13 (sodium	5.2	11.8	-2.3
MICU3	mitochondrial calcium uptake family, member 3	3.4	11.8	-3.4
SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	3.5	11.2	-3.2
LINC00845	long intergenic non-protein coding RNA 845	2.4	10.9	-4.6
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	3.8	10.9	-2.9
ESRRG	estrogen-related receptor gamma	2.9	10.8	-3.7
SLC43A2	solute carrier family 43 (amino acid system L transporter), member 2	2.6	10.7	-4.1
LOC105370058	uncharacterized LOC105370058	3.0	10.4	-3.5
ANK3	ankyrin 3, node of Ranvier (ankyrin G)	3.1	10.4	-3.4
LOC105369669	uncharacterized LOC105369669	3.3	10.4	-3.2
LOC105379298	uncharacterized LOC105379298	3.3	10.2	-3.1
TACC2	transforming, acidic coiled-coil containing protein 2	3.9	10.0	-2.6
PSG10P	pregnancy specific beta-1-glycoprotein 10, pseudogene	3.2	9.7	-3.0
SEMA6A-AS1	SEMA6A antisense RNA 1	3.2	9.5	-2.9
PLEKHA6	pleckstrin homology domain containing, family A member 6	2.9	9.3	-3.2
CKMT1B	creatine kinase, mitochondrial 1B	2.8	9.0	-3.2
RYBP	RING1 and YY1 binding protein	2.1	8.3	-4.0
LOC255187	uncharacterized LOC255187	3.8	8.1	-2.1
MIR503HG	MIR503 host gene	3.1	7.9	-2.6
LOC105370057	uncharacterized LOC105370057	2.4	7.3	-3.0
ZFAT	zinc finger and AT hook domain containing	2.2	7.2	-3.3



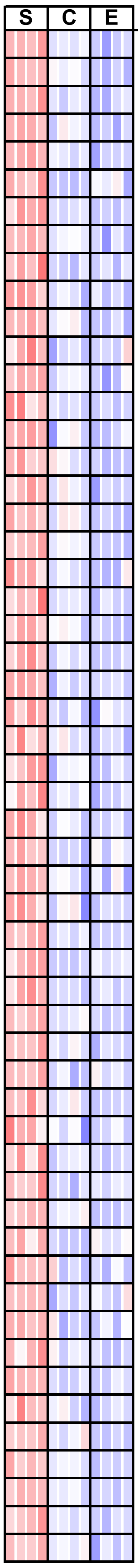
Linear Fold Change

(*ns*=no significant difference)

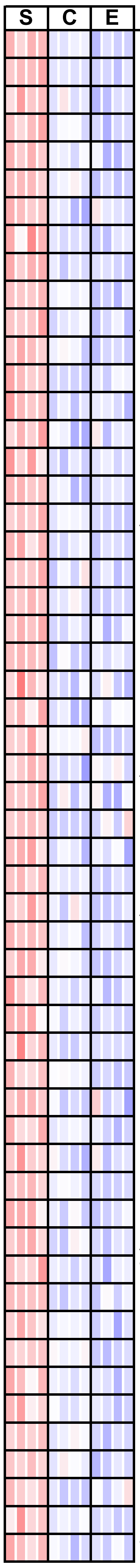
Symbol	Name	S vs C	S vs E	E vs C
PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	2.7	7.1	-2.6
ARHGAP26	Rho GTPase activating protein 26	3.1	7.0	-2.3
BPGM	2,3-bisphosphoglycerate mutase	2.9	6.8	-2.4
SLC22A3	solute carrier family 22 (organic cation transporter), member 3	2.4	6.7	-2.8
NHSL1	NHS-like 1	2.5	6.6	-2.6
PSG3	pregnancy specific beta-1-glycoprotein 3	2.1	6.1	-2.9
GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	2.5	6.1	-2.4
LOC105377029	uncharacterized LOC105377029	2.6	6.0	-2.3
SIAH1	siah E3 ubiquitin protein ligase 1	2.7	5.9	-2.2
POGLUT3	protein O-glucosyltransferase 3	2.5	5.6	-2.3
TBX3	T-box 3	2.5	5.2	-2.1
GULP1	GULP, engulfment adaptor PTB domain containing 1	2.2	5.2	-2.3
NECTIN3	nectin cell adhesion molecule 3	2.2	5.2	-2.4
KDM7A	lysine (K)-specific demethylase 7A	2.5	5.1	-2.0
GRIP1	glutamate receptor interacting protein 1	2.1	4.9	-2.3
ACADL	acyl-CoA dehydrogenase, long chain	2.3	4.8	-2.1
MAN1C1	mannosidase, alpha, class 1C, member 1	2.1	4.7	-2.3
ADRB1	adrenoceptor beta 1	2.1	4.7	-2.2
CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	2.1	4.7	-2.2
LNPEP	leucyl	2.3	4.6	-2.0
DUSP16	dual specificity phosphatase 16	2.1	4.3	-2.1
TMEM150C	transmembrane protein 150C	12.7	2.6	4.9
GUCY1B1	guanylate cyclase 1 soluble subunit beta 1	10.9	2.5	4.3
FAM162B	family with sequence similarity 162, member B	9.2	3.6	2.5
KL	klotho	8.4	3.4	2.5
DACH1	dachshund family transcription factor 1	6.5	2.9	2.3
FSTL3	follistatin-like 3 (secreted glycoprotein)	-38.5	-14.2	-2.7
SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-9.5	-2.3	-4.1
ZNF486	zinc finger protein 486	-7.4	-2.8	-2.7
SLCO4A1	solute carrier organic anion transporter family, member 4A1	-7.0	-2.6	-2.7
CLDN19	claudin 19	-5.5	-2.3	-2.4
CXCR6	chemokine (C-X-C motif) receptor 6	-5.1	-2.0	-2.5
IL1RAP	interleukin 1 receptor accessory protein	-5.0	-2.2	-2.3
SYT11	synaptotagmin XI	2.2	-4.3	9.4
HDGFL3	HDGF like 3	2.4	-2.4	5.8
CHRDL1	chordin-like 1	-8.7	-191.1	22.0
PRL	prolactin	-10.3	-150.8	14.7
HLA-DRA	major histocompatibility complex, class II, DR alpha	-7.8	-74.8	9.6
RORB	RAR-related orphan receptor B	-4.1	-63.4	15.7
IL1RL1	interleukin 1 receptor-like 1	-7.3	-59.9	8.2
IFI44L	interferon-induced protein 44-like	-3.4	-31.5	9.1
GKN1	gastrokine 1	-8.3	-29.7	3.6
F2R	coagulation factor II (thrombin) receptor	-4.2	-23.1	5.5
GPRC5B	G protein-coupled receptor, class C, group 5, member B	-2.3	-9.2	4.0
TMEM45A	transmembrane protein 45A	-2.1	-8.5	4.1
PDE6H	phosphodiesterase 6H, cGMP-specific, cone, gamma	-2.5	-6.2	2.4
AREG	amphiregulin	15.4	34.9	*ns*
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	18.4	31.6	*ns*
SCN7A	sodium channel, voltage gated, type VII alpha subunit	15.9	25.0	*ns*
NTS	neurotensin	23.3	21.1	*ns*
MEOX2	mesenchyme homeobox 2	17.0	23.2	*ns*
SLC26A7	solute carrier family 26 (anion exchanger), member 7	11.3	21.1	*ns*
LOC105375166	uncharacterized LOC105375166	19.4	20.4	*ns*
SH3TC2	SH3 domain and tetratricopeptide repeats 2	5.7	18.2	*ns*
APLNR	apelin receptor	18.1	14.2	*ns*



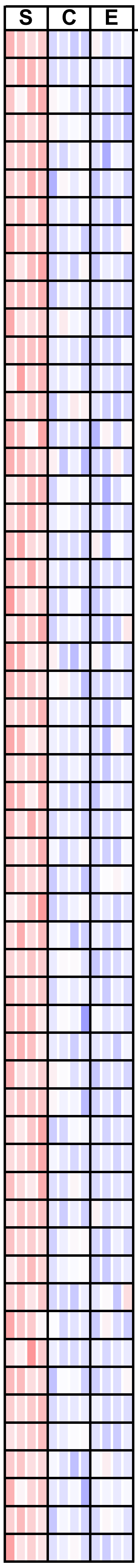
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
CPS1	carbamoyl-phosphate synthase 1	15.0	18.0	*ns*
PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	8.5	17.5	*ns*
MIR4713	microRNA 4713	4.3	16.9	*ns*
GSTA3	glutathione S-transferase alpha 3	6.2	16.5	*ns*
SNORD113-4	small nucleolar RNA, C	5.7	16.2	*ns*
LOC105372578	uncharacterized LOC105372578	10.8	15.2	*ns*
LOC105369382	uncharacterized LOC105369382	6.6	15.0	*ns*
P2RY1	purinergic receptor P2Y, G-protein coupled, 1	13.8	9.1	*ns*
SNORD113-5	small nucleolar RNA, C	6.3	13.1	*ns*
LOC101927482	uncharacterized LOC101927482	12.7	7.7	*ns*
LINC00474	long intergenic non-protein coding RNA 474	9.0	12.6	*ns*
HIGD1B	HIG1 hypoxia inducible domain family, member 1B	12.2	8.4	*ns*
USP27X	ubiquitin specific peptidase 27, X-linked	4.7	11.9	*ns*
ABCB1	ATP binding cassette subfamily B member 1	11.7	11.0	*ns*
SNORD113-1	small nucleolar RNA, C	6.9	11.4	*ns*
TTPA	tocopherol (alpha) transfer protein	8.4	11.3	*ns*
AGTR1	angiotensin II receptor, type 1	7.1	10.7	*ns*
LOC730101	uncharacterized LOC730101	6.9	10.7	*ns*
ZNF554	zinc finger protein 554	4.1	10.6	*ns*
MUCL1	mucin-like 1	10.1	9.9	*ns*
ISM1-AS1	ISM1 antisense RNA 1	4.3	9.9	*ns*
GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	4.1	9.8	*ns*
SMAGP	small cell adhesion glycoprotein	5.4	9.7	*ns*
ENDOU	endonuclease, polyU-specific	5.2	9.6	*ns*
CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	8.7	9.6	*ns*
MIR181B1	microRNA 181b-1	5.1	9.6	*ns*
LOC100128386	uncharacterized LOC100128386	5.4	9.5	*ns*
COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	9.5	8.5	*ns*
LOC100129345	uncharacterized LOC100129345	4.8	9.2	*ns*
SNHG24	small nucleolar RNA host gene 24	5.7	9.0	*ns*
PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like	5.3	8.9	*ns*
SNORD114-31	small nucleolar RNA, C	3.5	8.9	*ns*
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	8.8	4.1	*ns*
ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif 19	8.6	4.0	*ns*
PCDH11X	protocadherin 11 X-linked	8.5	6.3	*ns*
CRHBP	corticotropin releasing hormone binding protein	8.4	5.5	*ns*
IL22RA2	interleukin 22 receptor, alpha 2	4.9	8.3	*ns*
ZNF91	zinc finger protein 91	5.1	8.2	*ns*
FRAS1	Fraser extracellular matrix complex subunit 1	5.4	8.0	*ns*
COLEC10	collectin sub-family member 10 (C-type lectin)	6.4	7.9	*ns*
EGFEM1P	EGF-like and EMI domain containing 1, pseudogene	7.7	6.8	*ns*
GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2	7.7	5.1	*ns*
TRIM40	tripartite motif containing 40	3.6	7.7	*ns*
TBX5	T-box 5	5.5	7.7	*ns*
LOC105376429	uncharacterized LOC105376429	3.1	7.0	*ns*
LINC01336	long intergenic non-protein coding RNA 1336	6.9	6.1	*ns*
RAB38	RAB38, member RAS oncogene family	6.8	3.8	*ns*
EPHA3	EPH receptor A3	5.3	6.7	*ns*
SNORD114-28	small nucleolar RNA, C	6.3	6.7	*ns*
MINDY4B	MINDY family member 4B	3.4	6.6	*ns*
LOC100507661	uncharacterized LOC100507661	5.7	6.5	*ns*
SLC6A4	solute carrier family 6 (neurotransmitter transporter), member 4	4.1	6.4	*ns*
CLRN1	clarin 1	3.9	6.3	*ns*
MAP7D2	MAP7 domain containing 2	3.6	6.3	*ns*
MIR181A1HG	MIR181A1 host gene	4.0	6.3	*ns*



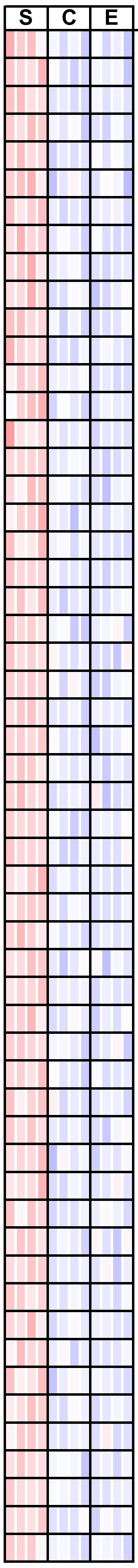
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
MTMR10	myotubularin related protein 10	3.7	6.2	*ns*
LINC01118	long intergenic non-protein coding RNA 1118	3.1	6.2	*ns*
ACSS1	acyl-CoA synthetase short-chain family member 1	4.5	6.1	*ns*
C4orf36	chromosome 4 open reading frame 36	3.5	6.1	*ns*
LINC02365	long intergenic non-protein coding RNA 2365	4.0	6.1	*ns*
CCDC102B	coiled-coil domain containing 102B	6.1	3.8	*ns*
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif 18	4.5	5.9	*ns*
MED12L	mediator complex subunit 12 like	3.2	5.9	*ns*
AFF2	AF4	5.8	5.7	*ns*
HSPA4L	heat shock 70kDa protein 4-like	5.2	5.8	*ns*
AHR	aryl hydrocarbon receptor	3.5	5.8	*ns*
NRCAM	neuronal cell adhesion molecule	5.7	3.7	*ns*
SLC20A1	solute carrier family 20 (phosphate transporter), member 1	3.8	5.7	*ns*
HS6ST2	heparan sulfate 6-O-sulfotransferase 2	4.9	5.7	*ns*
SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	5.0	5.6	*ns*
CROT	carnitine O-octanoyltransferase	2.9	5.6	*ns*
FAM3B	family with sequence similarity 3, member B	3.1	5.4	*ns*
TCHH	trichohyalin	2.7	5.4	*ns*
MEG3	maternally expressed 3 (non-protein coding)	2.9	5.4	*ns*
SLC16A12	solute carrier family 16, member 12	4.2	5.3	*ns*
CADM3	cell adhesion molecule 3	4.0	5.3	*ns*
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	3.0	5.3	*ns*
LOC105375161	uncharacterized LOC105375161	4.0	5.3	*ns*
ARHGAP42	Rho GTPase activating protein 42	5.3	4.9	*ns*
IGHA1	immunoglobulin heavy constant alpha 1	5.0	5.2	*ns*
WNT2	wingless-type MMTV integration site family member 2	3.0	5.2	*ns*
FLJ90680	FLJ90680 protein	3.7	5.1	*ns*
VXN	vexin	3.2	5.1	*ns*
TMEM133	transmembrane protein 133	4.2	5.0	*ns*
GPR183	G protein-coupled receptor 183	5.0	3.2	*ns*
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5	4.1	5.0	*ns*
TWIST1	twist family bHLH transcription factor 1	4.5	5.0	*ns*
ISM1	isthmin 1, angiogenesis inhibitor	3.8	4.9	*ns*
LOC101927139	uncharacterized LOC101927139	4.9	3.4	*ns*
MIR181A1	microRNA 181a-1	4.9	4.6	*ns*
SEMA3B	semaphorin 3B	3.2	4.8	*ns*
PART1	prostate androgen-regulated transcript 1 (non-protein coding)	3.3	4.8	*ns*
PTPRD	protein tyrosine phosphatase, receptor type, D	4.8	3.4	*ns*
OTOGL	otogelin-like	3.3	4.8	*ns*
CSTA	cystatin A (stefin A)	4.8	4.6	*ns*
NRAD1	non-coding RNA in the aldehyde dehydrogenase 1A pathway	3.8	4.8	*ns*
MPP1	membrane protein, palmitoylated 1	4.8	3.6	*ns*
AFF1	AF4	2.6	4.7	*ns*
ITGA9	integrin alpha 9	4.7	2.7	*ns*
BLID	BH3-like motif containing, cell death inducer	3.9	4.7	*ns*
SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	4.7	3.1	*ns*
ARHGAP28	Rho GTPase activating protein 28	4.7	4.3	*ns*
CKMT1A	creatine kinase, mitochondrial 1A	3.1	4.6	*ns*
RFX6	regulatory factor X, 6	4.6	4.6	*ns*
SNORD114-25	small nucleolar RNA, C	3.9	4.6	*ns*
MYLIP	myosin regulatory light chain interacting protein	2.5	4.6	*ns*
CCK	cholecystokinin	3.0	4.6	*ns*
HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1	3.3	4.5	*ns*
CADM3-AS1	CADM3 antisense RNA 1	3.3	4.5	*ns*
PRKCZ	protein kinase C, zeta	2.6	4.5	*ns*



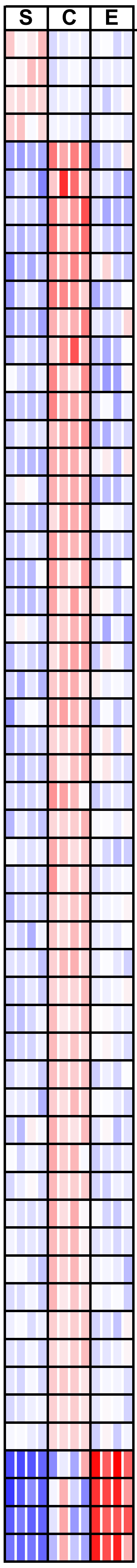
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
SH3BGRL2	SH3 domain binding glutamate-rich protein like 2	3.1	4.5	*ns*
FRMD6	FERM domain containing 6	3.6	4.5	*ns*
MIR30A	microRNA 30a	2.8	4.5	*ns*
USP46	ubiquitin specific peptidase 46	3.0	4.5	*ns*
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	3.0	4.5	*ns*
LRP8	LDL receptor related protein 8	2.7	4.5	*ns*
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	4.4	2.8	*ns*
SCNN1B	sodium channel, non voltage gated 1 beta subunit	4.0	4.4	*ns*
DYSF	dysferlin	4.1	4.4	*ns*
GSTA4	glutathione S-transferase alpha 4	2.5	4.4	*ns*
ANXA6	annexin A6	3.2	4.4	*ns*
SLC26A2	solute carrier family 26 (anion exchanger), member 2	2.9	4.4	*ns*
CA8	carbonic anhydrase VIII	4.3	3.3	*ns*
LINC01119	long intergenic non-protein coding RNA 1119	4.3	4.3	*ns*
PLAGL1	pleiomorphic adenoma gene-like 1	4.3	3.2	*ns*
GS1-594A7.3	uncharacterized LOC104798195	4.2	3.6	*ns*
CHN1	chimerin 1	4.2	3.6	*ns*
ADHFE1	alcohol dehydrogenase, iron containing 1	2.7	4.2	*ns*
MCOLN3	mucolipin 3	3.4	4.1	*ns*
PAPPA-AS2	PAPPA antisense RNA 2	3.0	4.1	*ns*
LOC101927354	uncharacterized LOC101927354	2.9	4.1	*ns*
KANK1	KN motif and ankyrin repeat domains 1	3.9	4.0	*ns*
IQGAP2	IQ motif containing GTPase activating protein 2	4.0	3.2	*ns*
MIR4659A	microRNA 4659a	4.0	4.0	*ns*
LINC00472	long intergenic non-protein coding RNA 472	4.0	2.4	*ns*
HSPB8	heat shock 22kDa protein 8	2.0	4.0	*ns*
ANKH	ANKH inorganic pyrophosphate transport regulator	4.0	2.4	*ns*
MIR30C2	microRNA 30c-2	3.4	4.0	*ns*
PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	4.0	2.4	*ns*
COLEC12	collectin sub-family member 12	4.0	3.9	*ns*
ELF5	E74-like factor 5 (ets domain transcription factor)	2.9	4.0	*ns*
ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4	2.8	4.0	*ns*
FAM171B	family with sequence similarity 171, member B	3.3	4.0	*ns*
OR2F1	olfactory receptor, family 2, subfamily F, member 1 (gene	2.7	3.9	*ns*
GALNT11	polypeptide N-acetylgalactosaminyltransferase 11	3.3	3.9	*ns*
LOC105370312	uncharacterized LOC105370312	3.1	3.9	*ns*
CNTN5	contactin 5	3.9	3.9	*ns*
SYT7	synaptotagmin VII	2.1	3.9	*ns*
MIR3120	microRNA 3120	3.9	3.5	*ns*
CDH3	cadherin 3, type 1, P-cadherin (placental)	2.7	3.9	*ns*
LINC00597	long intergenic non-protein coding RNA 597	3.8	3.2	*ns*
MPP5	membrane protein, palmitoylated 5	2.7	3.8	*ns*
LOC105378239	uncharacterized LOC105378239	3.5	3.8	*ns*
ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	3.1	3.8	*ns*
TGFB3	transforming growth factor beta 3	3.3	3.8	*ns*
GRB14	growth factor receptor bound protein 14	3.8	3.3	*ns*
CARD18	caspase recruitment domain family, member 18	2.4	3.7	*ns*
SERINC5	serine incorporator 5	2.0	3.7	*ns*
ISL1	ISL LIM homeobox 1	2.8	3.7	*ns*
LOC101929325	uncharacterized LOC101929325	2.7	3.7	*ns*
CEP85	centrosomal protein 85kDa	2.2	3.7	*ns*
CLRN1-AS1	CLRN1 antisense RNA 1	2.2	3.6	*ns*
LRP6	LDL receptor related protein 6	3.6	2.3	*ns*
PLCXD2-AS1	PLCXD2 antisense RNA 1	2.6	3.6	*ns*
TMEM88	transmembrane protein 88	3.6	3.6	*ns*



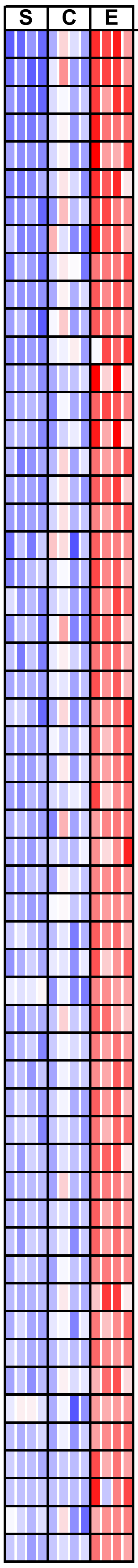
		Linear Fold Change (*ns*=no significant difference)		
Symbol	Name	S vs C	S vs E	E vs C
INTS6L	integrator complex subunit 6 like	3.5	2.5	*ns*
FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	3.1	3.5	*ns*
ARL4C	ADP-ribosylation factor like GTPase 4C	2.4	3.5	*ns*
CDKL5	cyclin-dependent kinase-like 5	2.0	3.5	*ns*
SORBS1	sorbin and SH3 domain containing 1	2.8	3.5	*ns*
NCMAP	noncompact myelin associated protein	2.8	3.5	*ns*
CD99P1	CD99 molecule pseudogene 1	2.7	3.4	*ns*
PNP	purine nucleoside phosphorylase	3.4	3.2	*ns*
TFCP2L1	transcription factor CP2-like 1	3.1	3.4	*ns*
ARHGAP17	Rho GTPase activating protein 17	3.3	3.4	*ns*
CECR2	cat eye syndrome chromosome region, candidate 2	2.1	3.4	*ns*
GABRA3	gamma-aminobutyric acid (GABA) A receptor, alpha 3	3.2	3.3	*ns*
LOC105378032	uncharacterized LOC105378032	2.9	3.3	*ns*
PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	2.2	3.3	*ns*
MAPK4	mitogen-activated protein kinase 4	3.3	3.1	*ns*
NOSTRIN	nitric oxide synthase trafficking	3.3	3.2	*ns*
C2CD3	C2 calcium-dependent domain containing 3	2.5	3.3	*ns*
AP1S3	adaptor-related protein complex 1 sigma 3 subunit	2.5	3.2	*ns*
PDE5A	phosphodiesterase 5A, cGMP-specific	3.2	2.6	*ns*
TMEM155	transmembrane protein 155	2.9	3.2	*ns*
LOC105369592	uncharacterized LOC105369592	3.2	3.0	*ns*
RALGAPA2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	3.1	3.2	*ns*
FREM2	FRAS1 related extracellular matrix protein 2	3.2	2.8	*ns*
BTG3	BTG family, member 3	2.6	3.2	*ns*
ELMO1	engulfment and cell motility 1	2.7	3.2	*ns*
LOC105369683	uncharacterized LOC105369683	2.5	3.2	*ns*
NOS3	nitric oxide synthase 3 (endothelial cell)	2.6	3.2	*ns*
SCN11A	sodium channel, voltage gated, type XI alpha subunit	3.1	3.1	*ns*
PP12613	uncharacterized LOC100192379	3.1	3.0	*ns*
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	2.4	3.1	*ns*
BMP2	bone morphogenetic protein 2	3.1	2.1	*ns*
FURIN	furin (paired basic amino acid cleaving enzyme)	2.7	3.1	*ns*
LOC105374693	spidroin-2-like	3.1	3.0	*ns*
AZIN1	antizyme inhibitor 1	2.1	3.1	*ns*
STARD4-AS1	STARD4 antisense RNA 1	2.6	3.1	*ns*
GCLM	glutamate-cysteine ligase, modifier subunit	3.1	2.6	*ns*
SLC16A12-AS1	SLC16A12 antisense RNA 1	3.1	3.0	*ns*
HOXA13	homeobox A13	2.1	3.1	*ns*
PHACTR2	phosphatase and actin regulator 2	2.5	3.0	*ns*
WWC1	WW and C2 domain containing 1	2.8	3.0	*ns*
NCBP3	nuclear cap binding subunit 3	2.8	3.0	*ns*
CTB-99A3.1	uncharacterized LOC105378215	2.6	3.0	*ns*
CHSY1	chondroitin sulfate synthase 1	3.0	2.3	*ns*
LOC102723465	uncharacterized LOC102723465	2.2	3.0	*ns*
LOC105369748	uncharacterized LOC105369748	2.1	2.9	*ns*
TMTC2	transmembrane and tetratricopeptide repeat containing 2	2.9	2.1	*ns*
GOLT1A	golgi transport 1A	2.6	2.9	*ns*
SLC4A4	solute carrier family 4 (sodium bicarbonate cotransporter), member 4	2.9	2.7	*ns*
LINC00882	long intergenic non-protein coding RNA 882	2.9	2.8	*ns*
SLC25A35	solute carrier family 25, member 35	2.7	2.9	*ns*
SCAPER	S-phase cyclin A-associated protein in the ER	2.0	2.9	*ns*
TSHZ1	teashirt zinc finger homeobox 1	2.9	2.0	*ns*
MIR4501	microRNA 4501	2.8	2.1	*ns*
LYPD8	LY6	2.8	2.3	*ns*
KDM7A-DT	KDM7A divergent transcript	2.4	2.8	*ns*



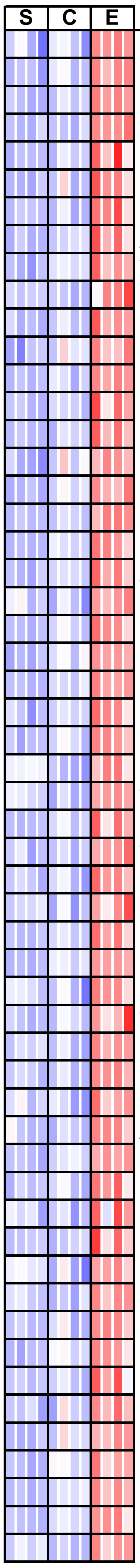
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
CRNDE	colorectal neoplasia differentially expressed (non-protein coding)	2.8	2.8	*ns*
CADM1	cell adhesion molecule 1	2.8	2.6	*ns*
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	2.8	2.4	*ns*
CALHM4	calcium homeostasis modulator family member 4	2.6	2.8	*ns*
MYLK	myosin light chain kinase	2.8	2.2	*ns*
GPR171	G protein-coupled receptor 171	2.8	2.7	*ns*
SLC18B1	solute carrier family 18, subfamily B, member 1	2.8	2.5	*ns*
MIR199A2	microRNA 199a-2	2.6	2.7	*ns*
ETFDH	electron-transferring-flavoprotein dehydrogenase	2.5	2.7	*ns*
FAM234B	family with sequence similarity 234, member B	2.4	2.7	*ns*
PRTG	protogenin	2.7	2.7	*ns*
ABCC2	ATP binding cassette subfamily C member 2	2.7	2.5	*ns*
STAT5B	signal transducer and activator of transcription 5B	2.0	2.7	*ns*
PRKCE	protein kinase C, epsilon	2.7	2.4	*ns*
C16orf74	chromosome 16 open reading frame 74	2.2	2.7	*ns*
CAST	calpastatin	2.1	2.6	*ns*
ETV5	ets variant 5	2.2	2.6	*ns*
NRP2	neuropilin 2	2.6	2.4	*ns*
LOC105370632	uncharacterized LOC105370632	2.1	2.6	*ns*
PARP1	poly(ADP-ribose) polymerase 1	2.4	2.6	*ns*
RYR2	ryanodine receptor 2 (cardiac)	2.6	2.3	*ns*
WFDC1	WAP four-disulfide core domain 1	2.6	2.2	*ns*
MRPS31P5	mitochondrial ribosomal protein S31 pseudogene 5	2.1	2.6	*ns*
MAGEA10	MAGE family member A10	2.3	2.6	*ns*
AK3	adenylate kinase 3	2.5	2.4	*ns*
CTDSPL	CTD small phosphatase like	2.3	2.5	*ns*
CASP4	caspase 4	2.2	2.5	*ns*
PNPO	pyridoxamine 5-phosphate oxidase	2.5	2.5	*ns*
BHLHE41	basic helix-loop-helix family, member e41	2.5	2.0	*ns*
JCAD	junctional cadherin 5 associated	2.5	2.2	*ns*
PGAP6	post-glycosylphosphatidylinositol attachment to proteins 6	2.3	2.5	*ns*
CATSPER2	cation channel, sperm associated 2	2.2	2.5	*ns*
NREP	neuronal regeneration related protein	2.4	2.5	*ns*
DOCK8	dedicator of cytokinesis 8	2.5	2.4	*ns*
DGKD	diacylglycerol kinase, delta 130kDa	2.1	2.5	*ns*
EID2	EP300 interacting inhibitor of differentiation 2	2.3	2.4	*ns*
RARB	retinoic acid receptor, beta	2.3	2.4	*ns*
BMP1	bone morphogenetic protein 1	2.4	2.3	*ns*
NPAS2	neuronal PAS domain protein 2	2.3	2.4	*ns*
ZSCAN12P1	zinc finger and SCAN domain containing 12 pseudogene 1	2.4	2.4	*ns*
CDYL2	chromodomain protein, Y-like 2	2.4	2.4	*ns*
SPRY4	sprouty RTK signaling antagonist 4	2.4	2.1	*ns*
COQ9	coenzyme Q9	2.4	2.1	*ns*
MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	2.4	2.2	*ns*
ELK1	ELK1, member of ETS oncogene family	2.3	2.3	*ns*
LOC105375423	uncharacterized LOC105375423	2.3	2.3	*ns*
LOC101928092	uncharacterized LOC101928092	2.3	2.3	*ns*
MMP16	matrix metallopeptidase 16 (membrane-inserted)	2.2	2.3	*ns*
LOC105379091	uncharacterized LOC105379091	2.2	2.3	*ns*
VSIR	V-set immunoregulatory receptor	2.2	2.3	*ns*
KIAA0319	KIAA0319	2.2	2.2	*ns*
ORMDL1	ORMDL sphingolipid biosynthesis regulator 1	2.1	2.2	*ns*
PDE4D	phosphodiesterase 4D, cAMP-specific	2.1	2.2	*ns*
CDK6	cyclin-dependent kinase 6	2.2	2.1	*ns*
NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	2.2	2.1	*ns*



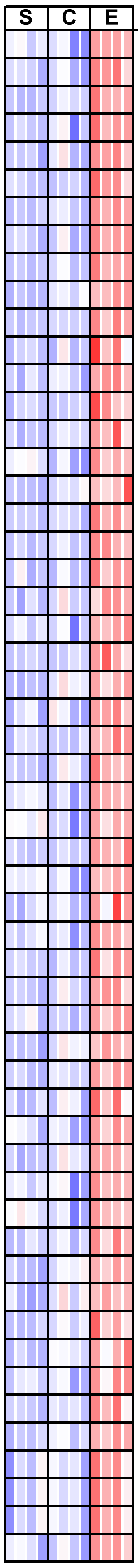
Symbol	Name	Linear Fold Change (*ns*=no significant difference) S vs C	S vs E	E vs C
NAV2-AS4	NAV2 antisense RNA 4	2.2	2.1	*ns*
ASB2	ankyrin repeat and SOCS box containing 2	2.1	2.1	*ns*
FNDC3A	fibronectin type III domain containing 3A	2.1	2.1	*ns*
LDHB	lactate dehydrogenase B	2.1	2.0	*ns*
OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	-15.0	*ns*	*-7.4*
FABP7	fatty acid binding protein 7, brain	-12.6	*ns*	*-9.7*
LOC102723596	uncharacterized LOC102723596	-9.3	*ns*	*-11.5*
LOC105377976	uncharacterized LOC105377976	-10.3	*ns*	*-8.0*
TNNI2	troponin I type 2 (skeletal, fast)	-10.1	*ns*	*-4.6*
ITGB6	integrin beta 6	-8.3	*ns*	*-7.0*
COL17A1	collagen, type XVII, alpha 1	-8.2	*ns*	*-3.7*
SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	-7.1	*ns*	*-7.3*
RAB9BP1	RAB9B, member RAS oncogene family pseudogene 1	-4.4	*ns*	*-6.9*
NLRP2	NLR family, pyrin domain containing 2	-6.8	*ns*	*-5.3*
ACAN	aggrecan	-4.6	*ns*	*-6.2*
SERTAD4	SERTA domain containing 4	-5.9	*ns*	*-3.0*
FAM83B	family with sequence similarity 83, member B	-3.4	*ns*	*-5.7*
LOC102723854	uncharacterized LOC102723854	-5.2	*ns*	*-3.4*
VIT	vitrin	-4.7	*ns*	*-5.1*
KRT7	keratin 7, type II	-5.0	*ns*	*-3.7*
LOC105377408	uncharacterized LOC105377408	-4.8	*ns*	*-2.7*
TET1	tet methylcytosine dioxygenase 1	-2.9	*ns*	*-4.7*
KRT14	keratin 14, type I	-4.7	*ns*	*-3.5*
SRI	sorcin	-4.6	*ns*	*-2.3*
IGSF10	immunoglobulin superfamily, member 10	-4.2	*ns*	*-4.1*
CMTM4	CKLF-like MARVEL transmembrane domain containing 4	-4.2	*ns*	*-2.3*
SEMA4C	semaphorin 4C	-4.0	*ns*	*-2.3*
GDPD2	glycerophosphodiester phosphodiesterase domain containing 2	-4.0	*ns*	*-3.8*
EFNA1	ephrin-A1	-3.8	*ns*	*-2.1*
LINC00456	long intergenic non-protein coding RNA 456	-2.9	*ns*	*-3.7*
CCDC81	coiled-coil domain containing 81	-3.6	*ns*	*-2.7*
PKP2	plakophilin 2	-3.6	*ns*	*-2.1*
BMS1P18	BMS1 ribosome biogenesis factor pseudogene 18	-3.6	*ns*	*-2.4*
VLDLR	very low density lipoprotein receptor	-3.5	*ns*	*-2.9*
PTBP3	polypyrimidine tract binding protein 3	-3.2	*ns*	*-2.0*
GATA3	GATA binding protein 3	-3.2	*ns*	*-2.0*
APOBR	apolipoprotein B receptor	-3.1	*ns*	*-2.2*
PPARG	peroxisome proliferator-activated receptor gamma	-3.1	*ns*	*-2.9*
INHA	inhibin alpha	-3.0	*ns*	*-2.4*
DLX3	distal-less homeobox 3	-2.8	*ns*	*-3.0*
CTSV	cathepsin V	-2.6	*ns*	*-3.0*
NOCT	nocturnin	-2.6	*ns*	*-2.9*
LOC101927431	uncharacterized LOC101927431	-2.8	*ns*	*-2.9*
GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)	-2.7	*ns*	*-2.8*
ZNF257	zinc finger protein 257	-2.7	*ns*	*-2.8*
TRABD2A	TraB domain containing 2A	-2.8	*ns*	*-2.3*
LOC105379110	uncharacterized LOC105379110	-2.3	*ns*	*-2.7*
SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-2.7	*ns*	*-2.3*
RFK	riboflavin kinase	-2.6	*ns*	*-2.3*
RTN2	reticulon 2	-2.3	*ns*	*-2.1*
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta	-2.0	*ns*	*-2.3*
SLPI	secretory leukocyte peptidase inhibitor	*ns*	*-157.1*	*24.7*
GZMA	granzyme A	*ns*	*-92.6*	*15.0*
CFH	complement factor H	*ns*	*-83.1*	*16.5*
TRDC	T cell receptor delta constant	*ns*	*-76.6*	*17.0*



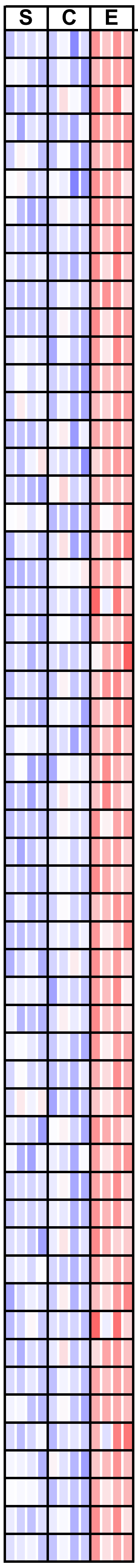
Symbol	Name	Linear Fold Change (*ns*=no significant difference) S vs C	 S vs E	 E vs C
TRDJ2	T cell receptor delta joining 2	*ns*	*-75.4*	*19.3*
OMD	osteomodulin	*ns*	*-64.4*	*14.7*
RXFP1	relaxin	*ns*	*-57.4*	*17.9*
C3	complement component 3	*ns*	*-44.8*	*15.5*
FGG	fibrinogen gamma chain	*ns*	*-35.1*	*18.2*
KLRC1	killer cell lectin-like receptor subfamily C, member 1	*ns*	*-34.8*	*14.2*
MEDAG	mesenteric estrogen-dependent adipogenesis	*ns*	*-34.7*	*12.1*
KLRC3	killer cell lectin-like receptor subfamily C, member 3	*ns*	*-33.6*	*16.2*
CXCL10	chemokine (C-X-C motif) ligand 10	*ns*	*-29.6*	*11.6*
CNR1	cannabinoid receptor 1 (brain)	*ns*	*-28.0*	*13.4*
DKK1	dickkopf WNT signaling pathway inhibitor 1	*ns*	*-27.5*	*9.5*
ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	*ns*	*-26.4*	*8.9*
CP	ceruloplasmin (ferroxidase)	*ns*	*-24.8*	*15.9*
TRPC4	transient receptor potential cation channel, subfamily C, member 4	*ns*	*-24.1*	*23.2*
PI15	peptidase inhibitor 15	*ns*	*-23.3*	*18.2*
CYP7B1	cytochrome P450, family 7, subfamily B, polypeptide 1	*ns*	*-22.9*	*9.8*
NKG7	natural killer cell granule protein 7	*ns*	*-22.7*	*11.1*
NDP	Norrie disease (pseudoglioma)	*ns*	*-21.0*	*9.2*
APOD	apolipoprotein D	*ns*	*-20.3*	*8.9*
CPXM1	carboxypeptidase X (M14 family), member 1	*ns*	*-19.4*	*13.0*
CCL4	chemokine (C-C motif) ligand 4	*ns*	*-19.2*	*16.3*
PROK1	prokineticin 1	*ns*	*-19.1*	*9.9*
HSPB6	heat shock protein, alpha-crystallin-related, B6	*ns*	*-18.6*	*8.1*
TRDJ1	T cell receptor delta joining 1	*ns*	*-17.8*	*11.1*
ALDH1A1	aldehyde dehydrogenase 1 family, member A1	*ns*	*-17.7*	*12.9*
PRUNE2	prune homolog 2 (Drosophila)	*ns*	*-16.6*	*9.0*
TRBV3-1	T cell receptor beta variable 3-1	*ns*	*-16.0*	*10.4*
RGS1	regulator of G-protein signaling 1	*ns*	*-15.9*	*7.6*
CTSK	cathepsin K	*ns*	*-15.2*	*9.6*
RBP4	retinol binding protein 4, plasma	*ns*	*-14.8*	*8.9*
GZMK	granzyme K	*ns*	*-14.7*	*9.3*
MAOB	monoamine oxidase B	*ns*	*-14.5*	*6.7*
ABCA8	ATP binding cassette subfamily A member 8	*ns*	*-11.2*	*14.4*
LOC100507639	uncharacterized LOC100507639	*ns*	*-14.4*	*8.9*
PALMD	palmdelphin	*ns*	*-5.0*	*14.1*
MACC1-AS1	MACC1 antisense RNA 1	*ns*	*-13.9*	*6.8*
MAP3K5	mitogen-activated protein kinase kinase kinase 5	*ns*	*-13.9*	*7.6*
FPR3	formyl peptide receptor 3	*ns*	*-13.9*	*10.1*
KLRC4-KLRK1	KLRC4-KLRK1 readthrough	*ns*	*-13.9*	*11.4*
IFI44	interferon-induced protein 44	*ns*	*-13.5*	*12.3*
TRGJP1	T cell receptor gamma joining P1	*ns*	*-13.4*	*12.6*
PGR	progesterone receptor	*ns*	*-13.3*	*9.8*
SULF2	sulfatase 2	*ns*	*-13.1*	*10.5*
PARM1	prostate androgen-regulated mucin-like protein 1	*ns*	*-13.0*	*12.1*
TRGJP2	T cell receptor gamma joining P2	*ns*	*-13.0*	*11.4*
CST11	cystatin 11	*ns*	*-12.9*	*9.3*
ABI3BP	ABI family, member 3 (NESH) binding protein	*ns*	*-12.8*	*8.4*
AOX1	aldehyde oxidase 1	*ns*	*-12.7*	*11.5*
XCL2	chemokine (C motif) ligand 2	*ns*	*-12.6*	*6.5*
SPARCL1	SPARC like 1	*ns*	*-3.9*	*12.5*
HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	*ns*	*-11.8*	*12.4*
IL15	interleukin 15	*ns*	*-12.4*	*11.8*
FGA	fibrinogen alpha chain	*ns*	*-11.2*	*12.2*
COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	*ns*	*-7.1*	*12.1*
CD96	CD96 molecule	*ns*	*-12.1*	*9.0*



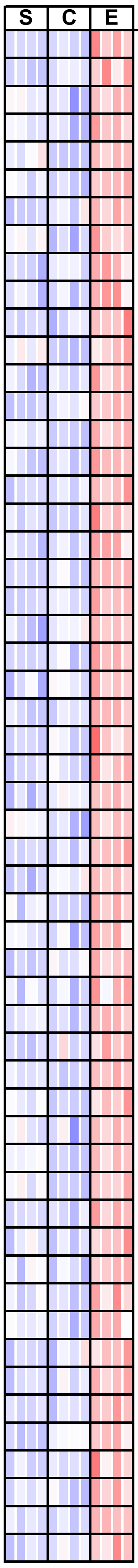
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
SQOR	sulfide quinone oxidoreductase	*ns*	-12.1	9.5
PLPP1	phospholipid phosphatase 1	*ns*	-11.7	7.4
GALNT15	polypeptide N-acetylgalactosaminyltransferase 15	*ns*	-11.6	8.7
CLIC2	chloride intracellular channel 2	*ns*	-11.6	10.9
FHL5	four and a half LIM domains 5	*ns*	-11.4	8.7
GZMB	granzyme B	*ns*	-11.4	7.5
STAP1	signal transducing adaptor family member 1	*ns*	-10.9	11.2
AVPR1A	arginine vasopressin receptor 1A	*ns*	-11.1	7.5
WT1	Wilms tumor 1	*ns*	-11.0	5.6
LOC105372762	uncharacterized LOC105372762	*ns*	-8.5	10.9
PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	*ns*	-10.8	8.8
CHI3L2	chitinase 3-like 2	*ns*	-10.6	4.4
IL2RG	interleukin 2 receptor, gamma	*ns*	-10.6	7.9
GPR174	G protein-coupled receptor 174	*ns*	-10.6	8.6
PDGFD	platelet derived growth factor D	*ns*	-10.5	8.3
MXRA7	matrix-remodelling associated 7	*ns*	-10.5	4.1
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	*ns*	-10.4	5.6
SULF1	sulfatase 1	*ns*	-10.3	8.5
PRF1	perforin 1 (pore forming protein)	*ns*	-10.1	6.2
ZNF727	zinc finger protein 727	*ns*	-10.1	6.9
FGF2	fibroblast growth factor 2 (basic)	*ns*	-5.9	10.0
PILRA	paired immunoglobin-like type 2 receptor alpha	*ns*	-10.0	6.7
CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	*ns*	-10.0	5.0
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	*ns*	-10.0	6.6
GZMH	granzyme H	*ns*	-9.7	6.9
IGFBP2	insulin like growth factor binding protein 2	*ns*	-9.7	6.6
PLN	phospholamban	*ns*	-3.7	9.7
TM6SF1	transmembrane 6 superfamily member 1	*ns*	-5.4	9.6
CABCOCO1	ciliary associated calcium binding coiled-coil 1	*ns*	-9.5	6.5
TMTC1	transmembrane and tetratricopeptide repeat containing 1	*ns*	-9.5	9.2
PTPRC	protein tyrosine phosphatase, receptor type, C	*ns*	-9.3	9.4
SEMA3A	semaphorin 3A	*ns*	-6.4	9.3
SCARA5	scavenger receptor class A, member 5	*ns*	-9.3	7.0
SPOCK1	sparc	*ns*	-9.3	5.1
CLEC2B	C-type lectin domain family 2, member B	*ns*	-5.7	9.3
TRAV20	T cell receptor alpha variable 20	*ns*	-9.3	7.4
CFI	complement factor I	*ns*	-6.8	9.2
SYNPO2	synaptopodin 2	*ns*	-8.5	9.2
PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	*ns*	-5.9	9.1
ABCA6	ATP binding cassette subfamily A member 6	*ns*	-7.7	9.1
PTHLH	parathyroid hormone-like hormone	*ns*	-9.1	5.6
CTSW	cathepsin W	*ns*	-9.0	7.7
SLC1A1	solute carrier family 1 (neuronal	*ns*	-7.0	9.0
FGB	fibrinogen beta chain	*ns*	-9.0	8.7
P2RY14	purinergic receptor P2Y, G-protein coupled, 14	*ns*	-4.1	8.9
PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1	*ns*	-6.6	8.9
IGFBP4	insulin like growth factor binding protein 4	*ns*	-8.8	7.3
IGFBP6	insulin like growth factor binding protein 6	*ns*	-8.8	4.4
GPR82	G protein-coupled receptor 82	*ns*	-8.7	8.2
RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	*ns*	-8.6	6.9
PDZK1IP1	PDZK1 interacting protein 1	*ns*	-8.6	4.5
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	*ns*	-8.4	4.2
DEPTOR	DEP domain containing MTOR-interacting protein	*ns*	-8.4	5.1
PTPRCAP	protein tyrosine phosphatase, receptor type, C-associated protein	*ns*	-8.2	5.4
NAV3	neuron navigator 3	*ns*	-5.3	8.2



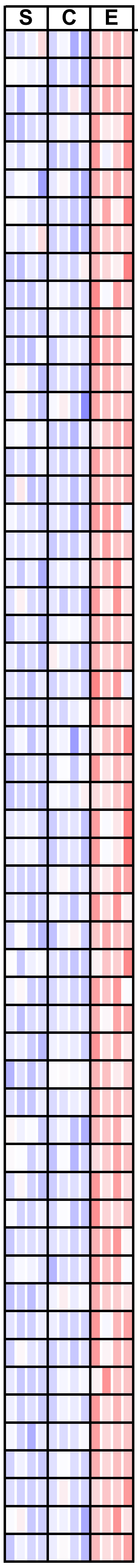
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PLCL1	phospholipase C-like 1	*ns*	-4.1	8.1
IGFBP7	insulin like growth factor binding protein 7	*ns*	-7.2	8.1
CD52	CD52 molecule	*ns*	-8.1	5.6
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif 5	*ns*	-7.9	8.0
GAS1	growth arrest-specific 1	*ns*	-8.0	5.8
LRRK2	leucine-rich repeat kinase 2	*ns*	-7.0	7.9
CCL4L2	chemokine (C-C motif) ligand 4-like 2	*ns*	-7.9	6.5
HAND2-AS1	HAND2 antisense RNA 1 (head to head)	*ns*	-7.8	7.6
PRDM1	PR domain containing 1, with ZNF domain	*ns*	-7.8	6.2
HAMP	hepcidin antimicrobial peptide	*ns*	-7.7	4.1
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3	*ns*	-7.7	6.4
REN	renin	*ns*	-7.7	6.8
MYL9	myosin light chain 9	*ns*	-7.5	6.6
CCL21	chemokine (C-C motif) ligand 21	*ns*	-7.5	7.2
LOC105379342	uncharacterized LOC105379342	*ns*	-7.4	5.0
ITGB8	integrin beta 8	*ns*	-3.2	7.4
HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	*ns*	-7.3	4.2
DOCK10	dedicator of cytokinesis 10	*ns*	-7.3	6.7
DTNA	dystrobrevin, alpha	*ns*	-7.3	6.1
CD226	CD226 molecule	*ns*	-6.7	7.2
ADRA2C	adrenoceptor alpha 2C	*ns*	-7.1	4.5
TLR4	toll-like receptor 4	*ns*	-4.9	7.1
TRDJ3	T cell receptor delta joining 3	*ns*	-7.1	6.6
PRR15	proline rich 15	*ns*	-7.0	3.0
ASPN	asporin	*ns*	-7.0	5.9
NPR3	natriuretic peptide receptor 3	*ns*	-6.9	7.0
CXCL13	chemokine (C-X-C motif) ligand 13	*ns*	-7.0	4.9
ZEB1	zinc finger E-box binding homeobox 1	*ns*	-3.9	7.0
TXNIP	thioredoxin interacting protein	*ns*	-2.6	7.0
TRGV10	T cell receptor gamma variable 10 (non-functional)	*ns*	-6.9	6.8
RGS2	regulator of G-protein signaling 2	*ns*	-3.4	6.9
TMEM47	transmembrane protein 47	*ns*	-6.9	6.8
EMILIN2	elastin microfibril interfacer 2	*ns*	-4.7	6.9
CD2	CD2 molecule	*ns*	-6.3	6.8
RGS22	regulator of G-protein signaling 22	*ns*	-6.8	5.1
DPYD	dihydropyrimidine dehydrogenase	*ns*	-5.0	6.8
OSGIN2	oxidative stress induced growth inhibitor family member 2	*ns*	-6.7	3.1
SAMD9L	sterile alpha motif domain containing 9-like	*ns*	-6.7	4.9
KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	*ns*	-6.6	5.6
RNASE6	ribonuclease, RNase A family, k6	*ns*	-4.7	6.6
CXCL16	chemokine (C-X-C motif) ligand 16	*ns*	-6.6	3.8
CD248	CD248 molecule, endosialin	*ns*	-4.3	6.6
PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	*ns*	-2.9	6.6
KCND2	potassium channel, voltage gated Shal related subfamily D, member 2	*ns*	-6.5	5.6
ANG	angiogenin, ribonuclease, RNase A family, 5	*ns*	-6.5	3.1
METRN	meteorin, glial cell differentiation regulator	*ns*	-6.5	2.9
GLB1L2	galactosidase beta 1 like 2	*ns*	-6.5	4.1
GPR155	G protein-coupled receptor 155	*ns*	-6.5	3.5
OGN	osteoglycin	*ns*	-5.3	6.4
KLRB1	killer cell lectin-like receptor subfamily B, member 1	*ns*	-6.4	5.0
EMP3	epithelial membrane protein 3	*ns*	-6.3	4.3
LOC102724994	putative POM121-like protein 1-like	*ns*	-6.3	5.5
LOC441081	POM121 membrane glycoprotein (rat) pseudogene	*ns*	-6.3	5.5
LOC728093	putative POM121-like protein 1-like	*ns*	-6.3	5.5
CTSS	cathepsin S	*ns*	-5.1	6.3



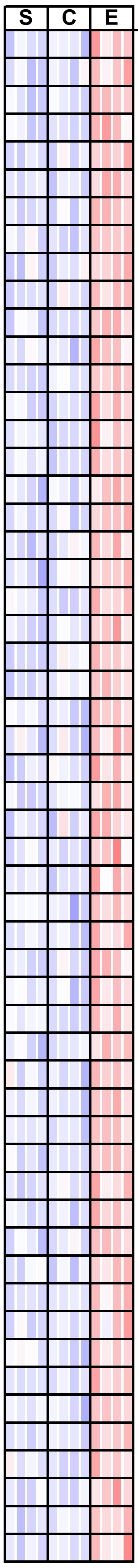
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LAPTM5	lysosomal protein transmembrane 5	*ns*	*-4.9*	*6.3*
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	*ns*	*-4.7*	*6.2*
TUBA3E	tubulin, alpha 3e	*ns*	*-6.2*	*3.9*
SCPEP1	serine carboxypeptidase 1	*ns*	*-5.8*	*6.1*
FGL2	fibrinogen-like 2	*ns*	*-4.2*	*6.1*
CCL2	chemokine (C-C motif) ligand 2	*ns*	*-3.5*	*6.1*
CERS6-AS1	CERS6 antisense RNA 1	*ns*	*-6.1*	*4.1*
GREB1	growth regulation by estrogen in breast cancer 1	*ns*	*-6.1*	*5.3*
APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	*ns*	*-4.5*	*6.0*
KLF9	Kruppel-like factor 9	*ns*	*-6.0*	*4.9*
EVA1C	eva-1 homolog C (C. elegans)	*ns*	*-5.9*	*5.2*
STAMBPL1	STAM binding protein-like 1	*ns*	*-4.1*	*5.9*
MCTP1	multiple C2 domains, transmembrane 1	*ns*	*-3.7*	*5.9*
MS4A7	membrane-spanning 4-domains, subfamily A, member 7	*ns*	*-3.5*	*5.9*
ISLR	immunoglobulin superfamily containing leucine-rich repeat	*ns*	*-5.8*	*4.1*
THBS1	thrombospondin 1	*ns*	*-3.6*	*5.8*
RBP1	retinol binding protein 1, cellular	*ns*	*-5.8*	*2.9*
MECOM	MDS1 and EVI1 complex locus	*ns*	*-2.6*	*5.7*
MGP	matrix Gla protein	*ns*	*-5.7*	*5.4*
DHRS3	dehydrogenase	*ns*	*-5.7*	*2.4*
KERA	keratocan	*ns*	*-5.7*	*4.8*
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	*ns*	*-5.7*	*4.1*
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	*ns*	*-5.7*	*5.2*
LOC105376125	uncharacterized LOC105376125	*ns*	*-5.7*	*5.1*
CAB39L	calcium binding protein 39-like	*ns*	*-5.7*	*4.8*
FCER1G	Fc fragment of IgE, high affinity I, receptor for gamma polypeptide	*ns*	*-3.5*	*5.6*
LYZ	lysozyme	*ns*	*-5.5*	*4.1*
CST7	cystatin F (leukocystatin)	*ns*	*-5.5*	*3.0*
MGST1	microsomal glutathione S-transferase 1	*ns*	*-5.5*	*3.6*
MFGE8	milk fat globule-EGF factor 8 protein	*ns*	*-5.5*	*3.8*
HAND2	heart and neural crest derivatives expressed 2	*ns*	*-5.5*	*4.2*
S100A3	S100 calcium binding protein A3	*ns*	*-5.5*	*4.6*
CD38	CD38 molecule	*ns*	*-5.5*	*3.6*
MACC1	metastasis associated in colon cancer 1	*ns*	*-5.5*	*3.7*
LMOD1	leiomodin 1 (smooth muscle)	*ns*	*-3.6*	*5.5*
CEP126	centrosomal protein 126kDa	*ns*	*-5.4*	*3.3*
CD53	CD53 molecule	*ns*	*-3.6*	*5.4*
MAP1LC3C	microtubule associated protein 1 light chain 3 gamma	*ns*	*-4.1*	*5.4*
BTBD3	BTB (POZ) domain containing 3	*ns*	*-2.4*	*5.3*
TLR1	toll-like receptor 1	*ns*	*-5.3*	*4.1*
CERS6	ceramide synthase 6	*ns*	*-5.3*	*4.4*
TYROBP	TYRO protein tyrosine kinase binding protein	*ns*	*-4.7*	*5.3*
AXL	AXL receptor tyrosine kinase	*ns*	*-5.0*	*5.2*
CCDC170	coiled-coil domain containing 170	*ns*	*-5.2*	*3.5*
LCP2	lymphocyte cytosolic protein 2	*ns*	*-3.5*	*5.2*
LINC00707	long intergenic non-protein coding RNA 707	*ns*	*-5.2*	*4.8*
TSPAN1	tetraspanin 1	*ns*	*-4.9*	*5.2*
LOC389033	placenta-specific 9 pseudogene	*ns*	*-5.1*	*3.5*
APOO	apolipoprotein O	*ns*	*-5.0*	*5.1*
OTULINL	OTU deubiquitinase with linear linkage specificity like	*ns*	*-4.6*	*5.0*
APCS	amyloid P component, serum	*ns*	*-4.5*	*5.0*
TLR7	toll-like receptor 7	*ns*	*-3.9*	*4.9*
MYO5A	myosin VA	*ns*	*-2.8*	*4.9*
C1QC	complement component 1, q subcomponent, C chain	*ns*	*-4.7*	*4.8*
GTF2A1L	general transcription factor IIA 1-like	*ns*	*-3.9*	*4.8*



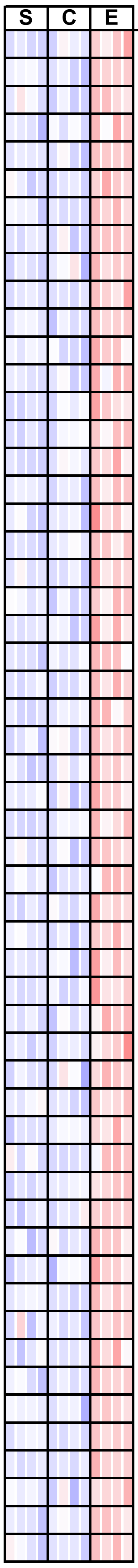
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PRPS2	phosphoribosyl pyrophosphate synthetase 2	*ns*	-4.7	4.8
NCAM1	neural cell adhesion molecule 1	*ns*	-4.8	3.5
SH3BGRL	SH3 domain binding glutamate-rich protein like	*ns*	-2.5	4.8
C1QA	complement component 1, q subcomponent, A chain	*ns*	-3.1	4.8
MSN	moesin	*ns*	-2.5	4.8
ODC1	ornithine decarboxylase 1	*ns*	-3.1	4.8
CD68	CD68 molecule	*ns*	-4.8	3.0
LONRF2	LON peptidase N-terminal domain and ring finger 2	*ns*	-2.3	4.8
SETDB2	SET domain, bifurcated 2	*ns*	-4.8	3.3
HOXA11	homeobox A11	*ns*	-4.5	4.7
GBP5	guanylate binding protein 5	*ns*	-4.6	4.7
ICAM2	intercellular adhesion molecule 2	*ns*	-2.2	4.7
C1GALT1C1L	C1GALT1-specific chaperone 1 like	*ns*	-4.7	3.8
TMEM132C	transmembrane protein 132C	*ns*	-4.7	2.9
SYTL4	synaptotagmin-like 4	*ns*	-3.0	4.6
C1S	complement component 1, s subcomponent	*ns*	-4.5	4.6
GPRIN3	GPRIN family member 3	*ns*	-4.6	3.8
EOMES	eomesodermin	*ns*	-4.0	4.6
C5AR1	complement component 5a receptor 1	*ns*	-4.6	4.0
C1QB	complement component 1, q subcomponent, B chain	*ns*	-4.6	4.1
C1R	complement component 1, r subcomponent	*ns*	-4.6	3.6
MTDH	metadherin	*ns*	-4.5	2.4
NNMT	nicotinamide N-methyltransferase	*ns*	-4.5	4.2
PLA2R1	phospholipase A2 receptor 1	*ns*	-4.5	2.8
EMCN	endomucin	*ns*	-4.5	3.9
CCN4	cellular communication network factor 4	*ns*	-4.5	3.6
TLR2	toll-like receptor 2	*ns*	-4.5	4.0
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	*ns*	-4.5	2.5
MAP1B	microtubule associated protein 1B	*ns*	-2.1	4.5
CD3D	CD3d molecule, delta (CD3-TCR complex)	*ns*	-4.5	4.3
FOXO1	forkhead box O1	*ns*	-4.4	2.3
HCST	hematopoietic cell signal transducer	*ns*	-3.2	4.4
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	*ns*	-3.0	4.4
ANOS1	anosmin 1	*ns*	-4.4	2.6
LOC105369863	uncharacterized LOC105369863	*ns*	-3.7	4.4
DDR2	discoidin domain receptor tyrosine kinase 2	*ns*	-3.3	4.4
LOC101926934	uncharacterized LOC101926934	*ns*	-4.4	3.2
CCL23	chemokine (C-C motif) ligand 23	*ns*	-3.4	4.4
VWF	von Willebrand factor	*ns*	-2.7	4.4
LOC101927414	uncharacterized LOC101927414	*ns*	-2.8	4.4
IFI16	interferon, gamma-inducible protein 16	*ns*	-2.4	4.4
EMP1	epithelial membrane protein 1	*ns*	-2.3	4.4
FBLN5	fibulin 5	*ns*	-4.3	4.4
MIR4263	microRNA 4263	*ns*	-3.5	4.3
PCBD1	pterin-4 alpha-carbinolamine dehydratase	*ns*	-3.0	4.3
STK39	serine threonine kinase 39	*ns*	-3.4	4.3
OLFML2B	olfactomedin like 2B	*ns*	-2.6	4.3
RNF144B	ring finger protein 144B	*ns*	-4.3	3.1
RGCC	regulator of cell cycle	*ns*	-4.2	3.8
LSAMP	limbic system-associated membrane protein	*ns*	-4.1	4.2
LOC100505851	uncharacterized LOC100505851	*ns*	-4.2	2.2
DPYD-AS1	DPYD antisense RNA 1	*ns*	-4.2	3.8
JUN	jun proto-oncogene	*ns*	-3.4	4.2
CCL4L1	chemokine (C-C motif) ligand 4-like 1	*ns*	-3.7	4.2
COPZ2	coatomer protein complex subunit zeta 2	*ns*	-4.2	3.0



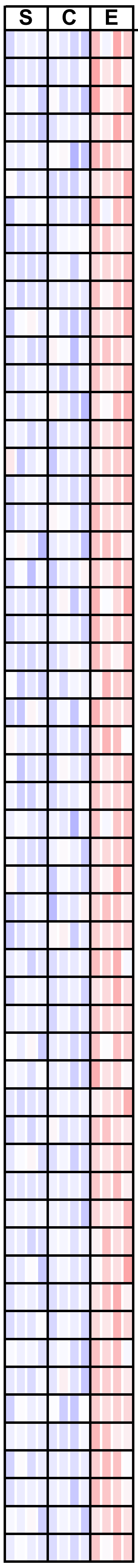
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs C	S vs E	E vs C
IFITM2	interferon induced transmembrane protein 2	*ns*	-2.4	4.2
LPAR1	lysophosphatidic acid receptor 1	*ns*	-2.4	4.2
IL13RA2	interleukin 13 receptor, alpha 2	*ns*	-4.2	3.9
ALDH1A2	aldehyde dehydrogenase 1 family, member A2	*ns*	-4.2	2.9
WNT5A	wingless-type MMTV integration site family, member 5A	*ns*	-3.1	4.2
TPST1	tyrosylprotein sulfotransferase 1	*ns*	-3.9	4.1
ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	*ns*	-2.9	4.1
PDGFRB	platelet-derived growth factor receptor, beta polypeptide	*ns*	-2.3	4.1
CXCL11	chemokine (C-X-C motif) ligand 11	*ns*	-4.1	3.0
PTGER4	prostaglandin E receptor 4 (subtype EP4)	*ns*	-4.1	3.3
ARL4D	ADP-ribosylation factor like GTPase 4D	*ns*	-4.1	3.3
PTGDR	prostaglandin D2 receptor (DP)	*ns*	-4.1	3.6
GNPDA2	glucosamine-6-phosphate deaminase 2	*ns*	-3.2	4.1
FAP	fibroblast activation protein alpha	*ns*	-3.7	4.1
ZNF667-AS1	ZNF667 antisense RNA 1 (head to head)	*ns*	-2.8	4.1
APCDD1	adenomatosis polyposis coli down-regulated 1	*ns*	-3.9	4.1
FYN	FYN proto-oncogene, Src family tyrosine kinase	*ns*	-3.7	4.1
CFD	complement factor D (adipsin)	*ns*	-3.5	4.0
ARMC9	armadillo repeat containing 9	*ns*	-3.3	4.0
RRAS	related RAS viral (r-ras) oncogene homolog	*ns*	-4.0	3.0
ARHGAP15	Rho GTPase activating protein 15	*ns*	-3.2	4.0
MSR1	macrophage scavenger receptor 1	*ns*	-4.0	2.9
INPP4B	inositol polyphosphate-4-phosphatase type II B	*ns*	-3.9	3.1
KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	*ns*	-3.9	3.8
CXCL12	chemokine (C-X-C motif) ligand 12	*ns*	-3.9	3.0
XGY2	Xg pseudogene, Y-linked 2	*ns*	-3.7	3.9
CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	*ns*	-3.9	3.1
SLC25A30	solute carrier family 25, member 30	*ns*	-3.9	2.3
TRGC2	T cell receptor gamma constant 2	*ns*	-3.2	3.9
TRGV9	T cell receptor gamma variable 9	*ns*	-3.2	3.9
TIMP4	TIMP metallopeptidase inhibitor 4	*ns*	-3.9	2.9
CCL3L3	chemokine (C-C motif) ligand 3-like 3	*ns*	-3.9	3.4
IL18	interleukin 18	*ns*	-3.9	3.4
PLA1A	phospholipase A1 member A	*ns*	-2.8	3.9
PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma	*ns*	-3.3	3.9
FAM155A	family with sequence similarity 155, member A	*ns*	-3.8	3.4
BIRC3	baculoviral IAP repeat containing 3	*ns*	-3.8	3.0
APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	*ns*	-3.8	2.1
SKAP1	src kinase associated phosphoprotein 1	*ns*	-3.8	3.2
CD58	CD58 molecule	*ns*	-2.6	3.8
FAM229B	family with sequence similarity 229, member B	*ns*	-2.7	3.8
CFAP300	cilia and flagella associated protein 300	*ns*	-3.7	3.8
AOAH	acyloxyacyl hydrolase (neutrophil)	*ns*	-3.2	3.8
CLECL1	C-type lectin-like 1	*ns*	-3.8	3.6
CD209	CD209 molecule	*ns*	-2.8	3.8
GADD45A	growth arrest and DNA-damage-inducible, alpha	*ns*	-3.8	2.1
SIPA1L2	signal-induced proliferation-associated 1 like 2	*ns*	-3.7	3.8
IL1B	interleukin 1 beta	*ns*	-3.1	3.8
P2RY10	purinergic receptor P2Y, G-protein coupled, 10	*ns*	-3.8	2.8
ZNF804A	zinc finger protein 804A	*ns*	-3.7	3.4
PYHIN1	pyrin and HIN domain family, member 1	*ns*	-3.7	3.1
NIPAL2	NIPA-like domain containing 2	*ns*	-3.7	3.2
LOC102723721	uncharacterized LOC102723721	*ns*	-3.7	3.1
GLIDR	glioblastoma down-regulated RNA	*ns*	-3.0	3.7
PAMR1	peptidase domain containing associated with muscle regeneration 1	*ns*	-3.7	3.4



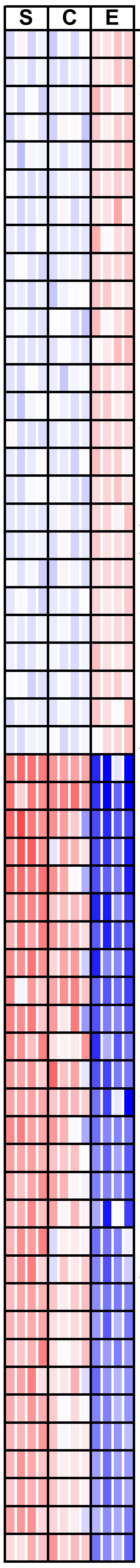
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LOC101928461	uncharacterized LOC101928461	*ns*	*-3.7*	*3.4*
IL18R1	interleukin 18 receptor 1	*ns*	*-3.7*	*2.8*
MNDA	myeloid cell nuclear differentiation antigen	*ns*	*-3.7*	*3.2*
SNORA78	small nucleolar RNA, H	*ns*	*-3.4*	*3.6*
UCHL1	ubiquitin C-terminal hydrolase L1	*ns*	*-3.6*	*3.1*
TPM2	tropomyosin 2 (beta)	*ns*	*-3.2*	*3.6*
CD48	CD48 molecule	*ns*	*-3.6*	*3.5*
ZNF25	zinc finger protein 25	*ns*	*-2.8*	*3.6*
CDA	cytidine deaminase	*ns*	*-3.6*	*2.9*
KCNH1	potassium channel, voltage gated eag related subfamily H, member 1	*ns*	*-3.6*	*3.0*
PWWP3B	PWWP domain containing 3B	*ns*	*-3.4*	*3.5*
NPR1	natriuretic peptide receptor 1	*ns*	*-2.7*	*3.5*
SOD2	superoxide dismutase 2, mitochondrial	*ns*	*-3.5*	*2.7*
TASL	TLR adaptor interacting with endolysosomal SLC15A4	*ns*	*-3.3*	*3.5*
TAGAP	T-cell activation RhoGTPase activating protein	*ns*	*-2.8*	*3.5*
DOCK2	dedicator of cytokinesis 2	*ns*	*-2.6*	*3.5*
SEMA3B-AS1	SEMA3B antisense RNA 1 (head to head)	*ns*	*-3.5*	*2.9*
MPZL2	myelin protein zero-like 2	*ns*	*-3.3*	*3.5*
RASD1	RAS, dexamethasone-induced 1	*ns*	*-3.5*	*2.6*
PRPS1	phosphoribosyl pyrophosphate synthetase 1	*ns*	*-3.5*	*2.3*
MDM1	Mdm1 nuclear protein	*ns*	*-2.7*	*3.5*
OXT	oxytocin	*ns*	*-3.5*	*2.9*
BRINP2	bone morphogenetic protein	*ns*	*-3.5*	*2.2*
TNC	tenascin C	*ns*	*-3.5*	*2.3*
C8orf88	chromosome 8 open reading frame 88	*ns*	*-2.6*	*3.5*
SLC46A3	solute carrier family 46, member 3	*ns*	*-3.2*	*3.4*
EMX2	empty spiracles homeobox 2	*ns*	*-3.4*	*2.8*
DNLZ	DNL-type zinc finger	*ns*	*-3.4*	*2.7*
ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	*ns*	*-3.4*	*3.1*
TAGLN	transgelin	*ns*	*-3.1*	*3.4*
SORL1	sortilin-related receptor, L(DLR class) A repeats containing	*ns*	*-2.8*	*3.4*
FOLR2	folate receptor 2 (fetal)	*ns*	*-2.2*	*3.4*
POLR1F	RNA polymerase I subunit F	*ns*	*-2.9*	*3.4*
TMSB4X	thymosin beta 4, X-linked	*ns*	*-3.4*	*3.3*
TRPS1	trichorhinophalangeal syndrome I	*ns*	*-2.4*	*3.4*
ZBTB20	zinc finger and BTB domain containing 20	*ns*	*-2.2*	*3.4*
WDR41	WD repeat domain 41	*ns*	*-3.4*	*2.9*
LOC101928100	uncharacterized LOC101928100	*ns*	*-2.7*	*3.3*
TP53I3	tumor protein p53 inducible protein 3	*ns*	*-3.0*	*3.3*
ADA2	adenosine deaminase 2	*ns*	*-2.7*	*3.3*
QPCT	glutaminyl-peptide cyclotransferase	*ns*	*-3.3*	*3.2*
PLAT	plasminogen activator, tissue	*ns*	*-3.3*	*2.7*
TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	*ns*	*-3.0*	*3.3*
SPAG1	sperm associated antigen 1	*ns*	*-3.3*	*2.9*
ABLIM3	actin binding LIM protein family, member 3	*ns*	*-2.7*	*3.2*
LINC00924	long intergenic non-protein coding RNA 924	*ns*	*-3.2*	*2.8*
GSTM5	glutathione S-transferase mu 5	*ns*	*-3.2*	*3.0*
ALCAM	activated leukocyte cell adhesion molecule	*ns*	*-2.1*	*3.2*
NCOA7	nuclear receptor coactivator 7	*ns*	*-3.2*	*3.2*
LCP1	lymphocyte cytosolic protein 1 (L-plastin)	*ns*	*-2.5*	*3.2*
PRSS23	protease, serine, 23	*ns*	*-3.2*	*3.1*
ACSL1	acyl-CoA synthetase long-chain family member 1	*ns*	*-2.3*	*3.2*
SMIM10	small integral membrane protein 10	*ns*	*-3.2*	*3.2*
LSAMP-AS1	uncharacterized LOC101926903	*ns*	*-3.2*	*2.6*
SNCAIP	synuclein alpha interacting protein	*ns*	*-3.2*	*2.9*



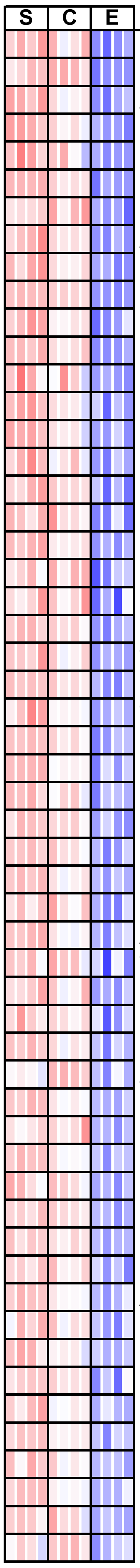
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
PLD1	phospholipase D1, phosphatidylcholine-specific	*ns*	-3.2	2.6
MCC	mutated in colorectal cancers	*ns*	-2.4	3.2
ARMCX1	armadillo repeat containing, X-linked 1	*ns*	-2.2	3.2
CLEC2D	C-type lectin domain family 2, member D	*ns*	-3.2	2.6
LGALS1	lectin, galactoside-binding, soluble, 1	*ns*	-2.7	3.2
UG0898H09	uncharacterized LOC643763	*ns*	-2.9	3.2
SAMHD1	SAM domain and HD domain 1	*ns*	-2.7	3.2
HLA-DMB	major histocompatibility complex, class II, DM beta	*ns*	-3.0	3.2
MANEA	mannosidase, endo-alpha	*ns*	-3.1	2.5
JAKMIP2	janus kinase and microtubule interacting protein 2	*ns*	-3.0	3.1
MEF2A	myocyte enhancer factor 2A	*ns*	-2.5	3.1
C2CD4B	C2 calcium-dependent domain containing 4B	*ns*	-2.4	3.1
MIR99AHG	mir-99a-let-7c cluster host gene	*ns*	-2.9	3.1
HLA-DPB1	major histocompatibility complex, class II, DP beta 1	*ns*	-3.1	2.4
WNT4	wingless-type MMTV integration site family, member 4	*ns*	-3.1	2.2
C1RL	complement component 1, r subcomponent-like	*ns*	-3.1	2.2
PRXL2A	peroxiredoxin like 2A	*ns*	-2.5	3.1
EVI2B	ecotropic viral integration site 2B	*ns*	-3.0	3.1
RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	*ns*	-3.1	2.3
KATNAL1	katanin p60 subunit A-like 1	*ns*	-2.5	3.1
MID2	midline 2	*ns*	-2.2	3.1
ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif 2	*ns*	-2.9	3.0
INE2	inactivation escape 2 (non-protein coding)	*ns*	-3.0	2.3
KCNK6	potassium channel, two pore domain subfamily K, member 6	*ns*	-2.8	3.0
GALNT13	polypeptide N-acetylgalactosaminyltransferase 13	*ns*	-3.0	2.4
PTGDS	prostaglandin D2 synthase 21kDa (brain)	*ns*	-3.0	2.3
RAI2	retinoic acid induced 2	*ns*	-3.0	2.3
SIGLEC7	sialic acid binding Ig-like lectin 7	*ns*	-2.3	3.0
EDNRB	endothelin receptor type B	*ns*	-3.0	2.2
MSANTD4	Myb	*ns*	-2.5	3.0
CLEC14A	C-type lectin domain family 14, member A	*ns*	-2.4	3.0
FBLN2	fibulin 2	*ns*	-3.0	2.4
S100A16	S100 calcium binding protein A16	*ns*	-2.3	3.0
CYBRD1	cytochrome b reductase 1	*ns*	-2.8	3.0
FAM155A-IT1	FAM155A intronic transcript 1	*ns*	-3.0	2.8
CORIN	corin, serine peptidase	*ns*	-2.9	3.0
MLLT11	myeloid	*ns*	-3.0	2.9
TMEM220	transmembrane protein 220	*ns*	-3.0	2.7
RGL1	ral guanine nucleotide dissociation stimulator-like 1	*ns*	-2.1	3.0
SAMD3	sterile alpha motif domain containing 3	*ns*	-3.0	2.1
EPHX4	epoxide hydrolase 4	*ns*	-2.3	3.0
DNASE1L3	deoxyribonuclease I-like 3	*ns*	-3.0	2.2
NFE2L1	nuclear factor, erythroid 2-like 1	*ns*	-2.9	2.4
KIR2DS3	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 3	*ns*	-2.9	2.5
ITGAX	integrin alpha X	*ns*	-2.9	2.8
HAVCR2	hepatitis A virus cellular receptor 2	*ns*	-2.2	2.9
CRYZ	crystallin zeta	*ns*	-2.4	2.9
NR1D1	nuclear receptor subfamily 1, group D, member 1	*ns*	-2.9	2.8
TTC30A	tetratricopeptide repeat domain 30A	*ns*	-2.9	2.9
EOGT	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	*ns*	-2.1	2.9
KALRN	kalirin, RhoGEF kinase	*ns*	-2.3	2.8
SMOX	spermine oxidase	*ns*	-2.8	2.8
OSBPL1A	oxysterol binding protein-like 1A	*ns*	-2.2	2.8
CFL2	cofilin 2 (muscle)	*ns*	-2.8	2.3
DNAAF4	dynein axonemal assembly factor 4	*ns*	-2.4	2.8



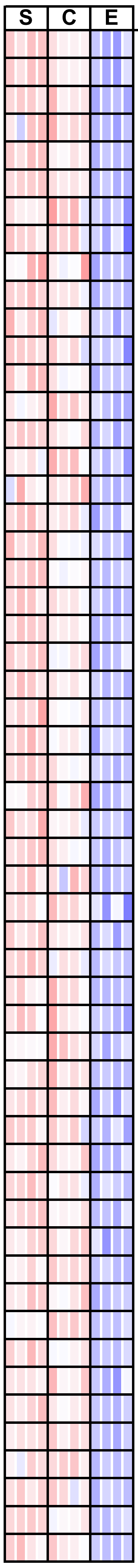
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
RNF138P1	ring finger protein 138, E3 ubiquitin protein ligase pseudogene 1	*ns*	*-2.5*	*2.8*
IRS2	insulin receptor substrate 2	*ns*	*-2.8*	*2.4*
LOC105376272	uncharacterized LOC105376272	*ns*	*-2.6*	*2.8*
ARL3	ADP-ribosylation factor like GTPase 3	*ns*	*-2.8*	*2.3*
CCL3	chemokine (C-C motif) ligand 3	*ns*	*-2.3*	*2.8*
S1PR4	sphingosine-1-phosphate receptor 4	*ns*	*-2.2*	*2.8*
FAM110C	family with sequence similarity 110, member C	*ns*	*-2.4*	*2.8*
HLA-DMA	major histocompatibility complex, class II, DM alpha	*ns*	*-2.7*	*2.0*
NIBAN1	niban apoptosis regulator 1	*ns*	*-2.7*	*2.2*
LOC100507195	uncharacterized LOC100507195	*ns*	*-2.7*	*2.4*
ZNF287	zinc finger protein 287	*ns*	*-2.2*	*2.7*
NUPR1	nuclear protein 1, transcriptional regulator	*ns*	*-2.7*	*2.3*
ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	*ns*	*-2.5*	*2.7*
TMEM98	transmembrane protein 98	*ns*	*-2.3*	*2.7*
TMEM35B	transmembrane protein 35B	*ns*	*-2.5*	*2.7*
C15orf65	chromosome 15 open reading frame 65	*ns*	*-2.1*	*2.7*
CELF2	CUGBP, Elav-like family member 2	*ns*	*-2.5*	*2.7*
CERK	ceramide kinase	*ns*	*-2.7*	*2.2*
TLR6	toll-like receptor 6	*ns*	*-2.5*	*2.7*
SLFN12	schlafen family member 12	*ns*	*-2.7*	*2.4*
GJA1	gap junction protein alpha 1	*ns*	*-2.7*	*2.6*
IL2RA	interleukin 2 receptor, alpha	*ns*	*-2.7*	*2.6*
ZNF438	zinc finger protein 438	*ns*	*-2.6*	*2.2*
HLA-A	major histocompatibility complex, class I, A	*ns*	*-2.6*	*2.2*
SOD3	superoxide dismutase 3, extracellular	*ns*	*-2.6*	*2.6*
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	*ns*	*-2.1*	*2.6*
ZNF516	zinc finger protein 516	*ns*	*-2.6*	*2.5*
RBKS	ribokinase	*ns*	*-2.6*	*2.3*
C1orf162	chromosome 1 open reading frame 162	*ns*	*-2.2*	*2.6*
MRPL33	mitochondrial ribosomal protein L33	*ns*	*-2.6*	*2.3*
CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	*ns*	*-2.1*	*2.6*
KANK2	KN motif and ankyrin repeat domains 2	*ns*	*-2.6*	*2.5*
GLB1L	galactosidase beta 1 like	*ns*	*-2.6*	*2.0*
CH25H	cholesterol 25-hydroxylase	*ns*	*-2.6*	*2.5*
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	*ns*	*-2.3*	*2.6*
PLXNC1	plexin C1	*ns*	*-2.3*	*2.5*
SELPLG	selectin P ligand	*ns*	*-2.1*	*2.5*
STAB1	stabilin 1	*ns*	*-2.0*	*2.5*
HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	*ns*	*-2.5*	*2.1*
CACNB2	calcium channel, voltage-dependent, beta 2 subunit	*ns*	*-2.5*	*2.2*
ALKBH3	alkB homolog 3, alpha-ketoglutarate-dependent dioxygenase	*ns*	*-2.1*	*2.5*
LY75-CD302	LY75-CD302 readthrough	*ns*	*-2.5*	*2.3*
TGFBR2	transforming growth factor beta receptor II	*ns*	*-2.0*	*2.5*
XG	Xg blood group	*ns*	*-2.5*	*2.1*
ZNF271P	zinc finger protein 271, pseudogene	*ns*	*-2.5*	*2.3*
GLIPR2	GLI pathogenesis-related 2	*ns*	*-2.4*	*2.5*
SCIMP	SLP adaptor and CSK interacting membrane protein	*ns*	*-2.3*	*2.5*
EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	*ns*	*-2.0*	*2.5*
ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	*ns*	*-2.4*	*2.4*
LARGE1	LARGE xylosyl- and glucuronyltransferase 1	*ns*	*-2.2*	*2.4*
ADCY1	adenylate cyclase 1 (brain)	*ns*	*-2.1*	*2.4*
LOC105372674	uncharacterized LOC105372674	*ns*	*-2.4*	*2.4*
SSC5D	scavenger receptor cysteine rich family, 5 domains	*ns*	*-2.3*	*2.4*
TMX4	thioredoxin-related transmembrane protein 4	*ns*	*-2.1*	*2.4*
PBX3	pre-B-cell leukemia homeobox 3	*ns*	*-2.1*	*2.4*



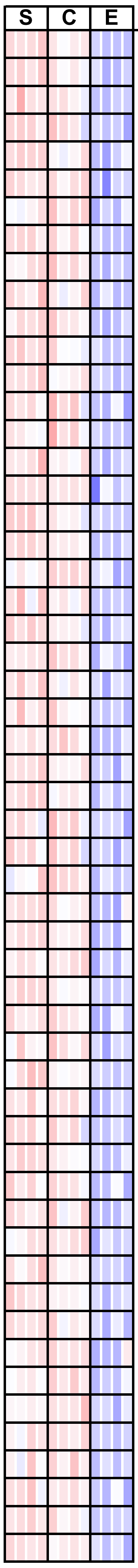
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
RIN2	Ras and Rab interactor 2	*ns*	*-2.3*	*2.4*
TCN2	transcobalamin II	*ns*	*-2.2*	*2.4*
TRGV8	T cell receptor gamma variable 8	*ns*	*-2.4*	*2.2*
IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	*ns*	*-2.3*	*2.4*
KRT37	keratin 37, type I	*ns*	*-2.4*	*2.3*
SIGLEC14	sialic acid binding Ig-like lectin 14	*ns*	*-2.3*	*2.1*
BMERB1	bMERB domain containing 1	*ns*	*-2.3*	*2.2*
SNAP91	synaptosome associated protein 91kDa	*ns*	*-2.2*	*2.3*
SGPL1	sphingosine-1-phosphate lyase 1	*ns*	*-2.3*	*2.3*
RNASET2	ribonuclease T2	*ns*	*-2.3*	*2.1*
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	*ns*	*-2.2*	*2.3*
DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	*ns*	*-2.3*	*2.2*
ICAM1	intercellular adhesion molecule 1	*ns*	*-2.3*	*2.3*
NECTIN2	nectin cell adhesion molecule 2	*ns*	*-2.3*	*2.1*
TARS3	threonyl-tRNA synthetase 3	*ns*	*-2.3*	*2.2*
CTSD	cathepsin D	*ns*	*-2.2*	*2.3*
CD83	CD83 molecule	*ns*	*-2.1*	*2.3*
ATL1	atlastin GTPase 1	*ns*	*-2.3*	*2.1*
AKAP6	A kinase (PRKA) anchor protein 6	*ns*	*-2.2*	*2.2*
PLLP	plasmolipin	*ns*	*-2.2*	*2.2*
GANC	glucosidase, alpha; neutral C	*ns*	*-2.2*	*2.0*
PRNP	prion protein	*ns*	*-2.1*	*2.1*
PLXND1	plexin D1	*ns*	*-2.1*	*2.1*
HCK	HCK proto-oncogene, Src family tyrosine kinase	*ns*	*-2.1*	*2.1*
PLXNA4	plexin A4	*ns*	*-2.1*	*2.1*
ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	*ns*	*-2.1*	*2.0*
PIRC66	piwi-interacting RNA cluster 66	*ns*	*151.3*	*-86.8*
CGB8	chorionic gonadotropin, beta polypeptide 8	*ns*	*89.1*	*-106.9*
BMP5	bone morphogenetic protein 5	*ns*	*86.0*	*-21.1*
F5	coagulation factor V (proaccelerin, labile factor)	*ns*	*74.3*	*-20.0*
EGFL6	EGF-like-domain, multiple 6	*ns*	*70.0*	*-15.5*
CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	*ns*	*61.7*	*-29.4*
MIR1323	microRNA 1323	*ns*	*47.1*	*-30.7*
LGALS13	lectin, galactoside-binding, soluble, 13	*ns*	*43.7*	*-16.5*
CGB3	chorionic gonadotropin subunit beta 3	*ns*	*23.5*	*-33.7*
LGALS16	lectin, galactoside-binding, soluble, 16	*ns*	*29.7*	*-12.0*
HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	*ns*	*29.7*	*-12.6*
DSC3	desmocollin 3	*ns*	*27.2*	*-21.8*
TFPI2	tissue factor pathway inhibitor 2	*ns*	*26.0*	*-18.3*
HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	*ns*	*24.1*	*-7.8*
PAGE4	P antigen family, member 4 (prostate associated)	*ns*	*19.2*	*-10.6*
DLK1	delta-like 1 homolog (Drosophila)	*ns*	*17.7*	*-9.6*
MUC15	mucin 15, cell surface associated	*ns*	*16.9*	*-10.2*
C21orf91-OT1	C21orf91 overlapping transcript 1	*ns*	*16.5*	*-4.3*
ANGPT2	angiopoietin 2	*ns*	*15.9*	*-6.4*
CDO1	cysteine dioxygenase type 1	*ns*	*15.4*	*-9.9*
SPTLC3	serine palmitoyltransferase, long chain base subunit 3	*ns*	*14.1*	*-7.7*
ERVW-1	endogenous retrovirus group W, member 1	*ns*	*13.6*	*-6.9*
OLAH	oleoyl-ACP hydrolase	*ns*	*13.3*	*-6.1*
STS	steroid sulfatase (microsomal), isozyme S	*ns*	*12.9*	*-5.5*
RHOBTB1	Rho-related BTB domain containing 1	*ns*	*12.7*	*-5.6*
RRS1-AS1	RRS1 antisense RNA 1 (head to head)	*ns*	*12.5*	*-6.0*
SLC19A3	solute carrier family 19 (thiamine transporter), member 3	*ns*	*12.3*	*-7.1*
KATNBL1	katanin p80 subunit B-like 1	*ns*	*12.1*	*-4.5*
SIGLEC6	sialic acid binding Ig-like lectin 6	*ns*	*9.8*	*-12.1*



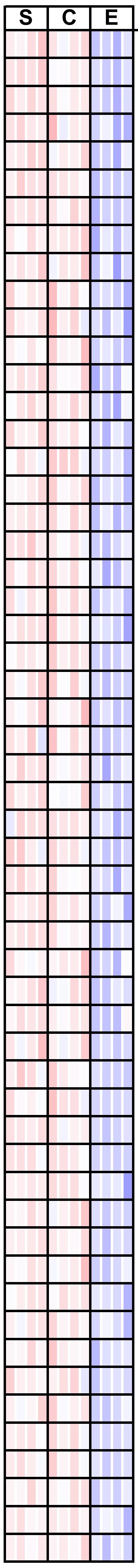
Symbol	Name	Linear Fold Change (*ns*=no significant difference) S vs C	 S vs E	 E vs C
LOC729739	peptidylprolyl isomerase A (cyclophilin A) pseudogene	*ns*	*11.9*	*-8.3*
PRSS12	protease, serine, 12 (neurotrypsin, motopsin)	*ns*	*9.0*	*-11.7*
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6	*ns*	*11.7*	*-4.7*
RADX	RPA1 related single stranded DNA binding protein, X-linked	*ns*	*11.6*	*-5.0*
PCDH10	protocadherin 10	*ns*	*11.5*	*-5.0*
LOC55338	uncharacterized LOC55338	*ns*	*11.1*	*-6.4*
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	*ns*	*7.0*	*-11.0*
ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	*ns*	*10.8*	*-6.0*
CSF3R	colony stimulating factor 3 receptor	*ns*	*10.8*	*-5.6*
PEG3-AS1	PEG3 antisense RNA 1	*ns*	*10.4*	*-7.8*
GLDN	gliomedin	*ns*	*10.4*	*-4.8*
PEG3	paternally expressed 3	*ns*	*10.0*	*-6.5*
C7	complement component 7	*ns*	*9.9*	*-5.5*
KYNU	kynureninase	*ns*	*9.9*	*-3.8*
LOC101927355	uncharacterized LOC101927355	*ns*	*9.5*	*-3.6*
LOC284561	uncharacterized LOC284561	*ns*	*9.5*	*-4.3*
SPINT1	serine peptidase inhibitor, Kunitz type 1	*ns*	*9.4*	*-6.8*
MIR498	microRNA 498	*ns*	*9.3*	*-7.8*
FOXO4	forkhead box O4	*ns*	*9.2*	*-4.7*
INHBA	inhibin beta A	*ns*	*6.2*	*-9.1*
ERVH48-1	endogenous retrovirus group 48, member 1	*ns*	*7.9*	*-8.3*
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	*ns*	*7.9*	*-5.6*
TP63	tumor protein p63	*ns*	*7.9*	*-4.8*
FHDC1	FH2 domain containing 1	*ns*	*7.9*	*-5.7*
TREML2	triggering receptor expressed on myeloid cells-like 2	*ns*	*7.8*	*-3.2*
KRT23	keratin 23, type I	*ns*	*7.5*	*-4.8*
PSG5	pregnancy specific beta-1-glycoprotein 5	*ns*	*7.5*	*-3.2*
PSG1	pregnancy specific beta-1-glycoprotein 1	*ns*	*6.9*	*-4.0*
LOC100505909	uncharacterized LOC100505909	*ns*	*6.8*	*-5.1*
LINC00470	long intergenic non-protein coding RNA 470	*ns*	*6.7*	*-4.9*
CMYA5	cardiomyopathy associated 5	*ns*	*6.5*	*-3.5*
LOC101927880	uncharacterized LOC101927880	*ns*	*6.3*	*-6.5*
ARHGAP32	Rho GTPase activating protein 32	*ns*	*6.5*	*-2.9*
TLR3	toll-like receptor 3	*ns*	*6.1*	*-6.4*
ERVK3-2	endogenous retrovirus group K3, member 2	*ns*	*6.4*	*-5.0*
SPDYA	speedy	*ns*	*6.3*	*-4.7*
RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	*ns*	*6.1*	*-3.5*
ZNF732	zinc finger protein 732	*ns*	*2.5*	*-6.0*
OPHN1	oligophrenin 1	*ns*	*5.9*	*-3.0*
PLEKHA8P1	pleckstrin homology domain containing, family A member 8 pseudogene 1	*ns*	*4.2*	*-5.9*
LOC105375403	uncharacterized LOC105375403	*ns*	*5.9*	*-2.9*
LOC105377871	uncharacterized LOC105377871	*ns*	*5.9*	*-5.0*
GLDC	glycine dehydrogenase (decarboxylating)	*ns*	*5.6*	*-4.8*
GDF15	growth differentiation factor 15	*ns*	*5.5*	*-4.3*
DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	*ns*	*5.5*	*-4.9*
ATP10D	ATPase, class V, type 10D	*ns*	*5.5*	*-2.7*
DOCK9-AS1	DOCK9 antisense RNA 1	*ns*	*5.4*	*-4.2*
BET1	Bet1 golgi vesicular membrane trafficking protein	*ns*	*5.4*	*-2.5*
CAPN6	calpain 6	*ns*	*5.4*	*-4.5*
SDC1	syndecan 1	*ns*	*5.2*	*-2.6*
FAM13A	family with sequence similarity 13, member A	*ns*	*5.1*	*-3.1*
LARGE2	LARGE xylosyl- and glucuronyltransferase 2	*ns*	*5.1*	*-3.3*
CEMIP2	cell migration inducing hyaluronidase 2	*ns*	*5.1*	*-2.3*
RNF128	ring finger protein 128, E3 ubiquitin protein ligase	*ns*	*5.1*	*-4.5*
GPR87	G protein-coupled receptor 87	*ns*	*2.9*	*-5.0*



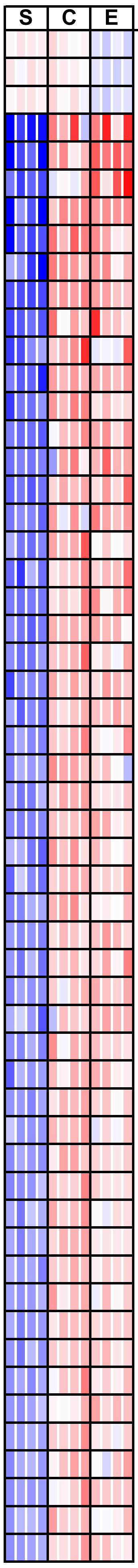
Symbol	Name	Linear Fold Change (*ns*=no significant difference) S vs C	 S vs E	 E vs C
SPDYE11	speedy	*ns*	4.9	-3.2
SPDYE8	speedy/RINGO cell cycle regulator family member E8	*ns*	4.9	-3.2
NEBL	nebulette	*ns*	4.9	-4.4
SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	*ns*	3.8	-4.8
SLC22A11	solute carrier family 22 (organic anion	*ns*	4.8	-3.0
MTARC1	mitochondrial amidoxime reducing component 1	*ns*	4.7	-3.5
CCNB1	cyclin B1	*ns*	3.4	-4.7
DEPDC1	DEP domain containing 1	*ns*	4.6	-4.2
TPRXL	tetra-peptide repeat homeobox-like	*ns*	4.6	-3.6
FDX1	ferredoxin 1	*ns*	4.5	-3.0
LOC101928408	uncharacterized LOC101928408	*ns*	4.5	-2.4
TOP2A	topoisomerase (DNA) II alpha	*ns*	4.4	-3.1
ATP6V1B1	ATPase, H+ transporting, lysosomal 56	*ns*	4.4	-2.6
DIAPH3	diaphanous-related formin 3	*ns*	2.8	-4.4
GAB1	GRB2-associated binding protein 1	*ns*	4.4	-3.2
ANLN	anillin actin binding protein	*ns*	2.9	-4.4
LOC105377872	uncharacterized LOC105377872	*ns*	3.0	-4.3
ST8SIA6-AS1	ST8SIA6 antisense RNA 1	*ns*	4.3	-2.9
TYMS	thymidylate synthetase	*ns*	4.3	-2.2
CLIP1	CAP-GLY domain containing linker protein 1	*ns*	4.3	-2.1
MBNL3	muscleblind-like splicing regulator 3	*ns*	4.2	-3.0
TMEM40	transmembrane protein 40	*ns*	4.2	-2.8
LOC105378019	uncharacterized LOC105378019	*ns*	4.2	-2.6
ZNF292	zinc finger protein 292	*ns*	4.2	-2.9
ZFAT-AS1	ZFAT antisense RNA 1	*ns*	4.2	-2.3
HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	*ns*	4.1	-2.3
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	*ns*	4.1	-2.5
TNS4	tensin 4	*ns*	3.4	-4.1
FXYD3	FXYD domain containing ion transport regulator 3	*ns*	4.0	-2.3
MEST	mesoderm specific transcript	*ns*	4.0	-2.4
LOC105376910	uncharacterized LOC105376910	*ns*	4.0	-3.2
MET	MET proto-oncogene, receptor tyrosine kinase	*ns*	3.6	-4.0
GRAMD2A	GRAM domain containing 2A	*ns*	4.0	-3.0
MB21D2	Mab-21 domain containing 2	*ns*	4.0	-2.2
SLC38A9	solute carrier family 38, member 9	*ns*	3.4	-4.0
LOC105379521	uncharacterized LOC105379521	*ns*	4.0	-3.8
LINC01194	long intergenic non-protein coding RNA 1194	*ns*	2.2	-3.9
ITGB4	integrin beta 4	*ns*	3.2	-3.9
TENM3	teneurin transmembrane protein 3	*ns*	3.9	-3.7
CCNA2	cyclin A2	*ns*	3.9	-3.0
CDK2	cyclin-dependent kinase 2	*ns*	3.8	-3.6
STK26	serine	*ns*	3.8	-2.3
SLC38A1	solute carrier family 38, member 1	*ns*	3.8	-2.6
SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	*ns*	3.7	-3.8
CCSAP	centriole, cilia and spindle-associated protein	*ns*	2.8	-3.8
CYP11A1	cytochrome P450, family 11, subfamily A, polypeptide 1	*ns*	3.7	-3.1
WEE1	WEE1 G2 checkpoint kinase	*ns*	2.1	-3.7
ZNF750	zinc finger protein 750	*ns*	3.7	-2.3
DPP4	dipeptidyl-peptidase 4	*ns*	3.1	-3.7
SLC5A6	solute carrier family 5 (sodium	*ns*	3.7	-2.8
FERMT1	fermitin family member 1	*ns*	3.4	-3.7
CLN3	ceroid-lipofuscinosis, neuronal 3	*ns*	2.8	-3.7
PCOLCE2	procollagen C-endopeptidase enhancer 2	*ns*	3.6	-2.9
NCOA3	nuclear receptor coactivator 3	*ns*	3.6	-2.2
LOC105377943	uncharacterized LOC105377943	*ns*	3.6	-3.0



Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
FIGN	fidgetin	*ns*	3.6	-2.7
EBLN2	endogenous Bornavirus-like nucleoprotein 2	*ns*	3.6	-2.5
TBX20	T-box 20	*ns*	3.6	-2.5
PGAP1	post-GPI attachment to proteins 1	*ns*	3.6	-2.8
PHLPP1	PH domain and leucine rich repeat protein phosphatase 1	*ns*	3.6	-2.3
GDA	guanine deaminase	*ns*	3.6	-3.6
SLC29A1	solute carrier family 29 (equilibrative nucleoside transporter), member 1	*ns*	2.3	-3.6
PARD6B	par-6 family cell polarity regulator beta	*ns*	3.5	-3.0
RFC3	replication factor C subunit 3	*ns*	3.0	-3.5
FAM156B	family with sequence similarity 156, member B	*ns*	3.4	-2.6
TFAP2A-AS1	TFAP2A antisense RNA 1	*ns*	3.4	-3.2
SMAD4	SMAD family member 4	*ns*	3.4	-2.1
ADAM12	ADAM metallopeptidase domain 12	*ns*	3.4	-2.4
KNL1	kinetochore scaffold 1	*ns*	3.2	-3.4
EXO1	exonuclease 1	*ns*	2.4	-3.4
IRF6	interferon regulatory factor 6	*ns*	3.4	-2.5
CGA	glycoprotein hormones, alpha polypeptide	*ns*	3.4	-3.0
TEX10	testis expressed 10	*ns*	3.4	-2.0
RASA1	RAS p21 protein activator (GTPase activating protein) 1	*ns*	3.4	-2.5
SNORD16	small nucleolar RNA, C	*ns*	2.2	-3.3
CCDC162P	coiled-coil domain containing 162, pseudogene	*ns*	3.3	-2.5
PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	*ns*	3.3	-2.0
TICRR	TOPBP1-interacting checkpoint and replication regulator	*ns*	2.9	-3.3
ST7-OT4	ST7 overlapping transcript 4	*ns*	3.3	-2.1
LOC105376501	uncharacterized LOC105376501	*ns*	3.2	-2.6
SLC52A1	solute carrier family 52 (riboflavin transporter), member 1	*ns*	2.9	-3.2
IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	*ns*	3.2	-2.5
MAN1A2	mannosidase, alpha, class 1A, member 2	*ns*	3.2	-2.2
ATAD5	ATPase family, AAA domain containing 5	*ns*	2.6	-3.2
SGO1	shugoshin 1	*ns*	3.2	-2.8
LOC105374160	uncharacterized LOC105374160	*ns*	2.2	-3.2
MYH10	myosin, heavy chain 10, non-muscle	*ns*	3.2	-2.5
COBLL1	cordon-bleu WH2 repeat protein like 1	*ns*	3.1	-2.7
LRRC1	leucine rich repeat containing 1	*ns*	2.6	-3.1
RGPD2	RANBP2-like and GRIP domain containing 2	*ns*	3.1	-2.1
CEP295NL	CEP295 N-terminal like	*ns*	3.1	-2.9
STC1	stanniocalcin 1	*ns*	2.4	-3.1
ATP7B	ATPase, Cu++ transporting, beta polypeptide	*ns*	3.1	-2.0
TDRP	testis development related protein	*ns*	3.0	-3.0
UBE2T	ubiquitin conjugating enzyme E2T	*ns*	3.0	-2.5
EML4	echinoderm microtubule associated protein like 4	*ns*	3.0	-2.1
CDC6	cell division cycle 6	*ns*	3.0	-2.8
RDH13	retinol dehydrogenase 13 (all-trans	*ns*	3.0	-3.0
NET1	neuroepithelial cell transforming 1	*ns*	2.4	-3.0
P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	*ns*	3.0	-2.3
LINC00540	long intergenic non-protein coding RNA 540	*ns*	3.0	-2.0
TPX2	TPX2, microtubule-associated	*ns*	3.0	-2.5
SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	*ns*	2.4	-3.0
CHML	choroideremia-like (Rab escort protein 2)	*ns*	2.1	-3.0
GRHL1	grainyhead-like transcription factor 1	*ns*	2.1	-3.0
S1PR2	sphingosine-1-phosphate receptor 2	*ns*	2.5	-2.9
CCDC169	coiled-coil domain containing 169	*ns*	2.3	-2.9
STEAP4	STEAP family member 4	*ns*	2.9	-2.7
WDR76	WD repeat domain 76	*ns*	2.9	-2.4
RFESD	Rieske (Fe-S) domain containing	*ns*	2.9	-2.4



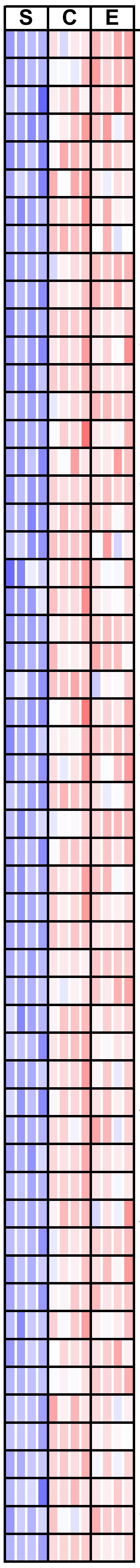
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
VGLL1	vestigial-like family member 1	*ns*	2.9	-2.6
PROSER1	proline and serine rich 1	*ns*	2.9	-2.1
ITIH5	inter-alpha-trypsin inhibitor heavy chain family, member 5	*ns*	2.9	-2.5
LOC101927853	uncharacterized LOC101927853	*ns*	2.9	-2.8
TENT5A	terminal nucleotidyltransferase 5A	*ns*	2.9	-2.4
MFSD4B	major facilitator superfamily domain containing 4B	*ns*	2.9	-2.5
LOC105377770	uncharacterized LOC105377770	*ns*	2.9	-2.8
LOC101926943	uncharacterized LOC101926943	*ns*	2.4	-2.9
GRHL2	grainyhead-like transcription factor 2	*ns*	2.8	-2.7
NUSAP1	nucleolar and spindle associated protein 1	*ns*	2.7	-2.8
CENPF	centromere protein F	*ns*	2.8	-2.8
NECTIN4	nectin cell adhesion molecule 4	*ns*	2.0	-2.8
DOCK9	dedicator of cytokinesis 9	*ns*	2.8	-2.6
TMC1	transmembrane channel like 1	*ns*	2.5	-2.8
PRC1	protein regulator of cytokinesis 1	*ns*	2.7	-2.4
SKA3	spindle and kinetochore associated complex subunit 3	*ns*	2.0	-2.7
TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	*ns*	2.4	-2.7
LOC105379715	uncharacterized LOC105379715	*ns*	2.6	-2.7
KIF2A	kinesin heavy chain member 2A	*ns*	2.7	-2.0
GTF2I	general transcription factor IIi	*ns*	2.7	-2.6
MCM5	minichromosome maintenance complex component 5	*ns*	2.3	-2.6
CENPI	centromere protein I	*ns*	2.6	-2.6
FMR1	fragile X mental retardation 1	*ns*	2.1	-2.6
EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit	*ns*	2.6	-2.6
EZR	ezrin	*ns*	2.5	-2.6
GPSM2	G-protein signaling modulator 2	*ns*	2.3	-2.6
AHSA2P	activator of HSP90 ATPase homolog 2, pseudogene	*ns*	2.6	-2.1
LIMK2	LIM domain kinase 2	*ns*	2.6	-2.1
LOC105370921	uncharacterized LOC105370921	*ns*	2.5	-2.6
IMMP2L	inner mitochondrial membrane peptidase subunit 2	*ns*	2.6	-2.4
GLCCI1	glucocorticoid induced 1	*ns*	2.6	-2.1
UBE2C	ubiquitin-conjugating enzyme E2C	*ns*	2.5	-2.5
RTTN	rotatin	*ns*	2.5	-2.1
MCTS2P	malignant T-cell amplified sequence 2, pseudogene	*ns*	2.1	-2.5
ATF3	activating transcription factor 3	*ns*	2.5	-2.2
MAST4	microtubule associated serine	*ns*	2.5	-2.2
DNMT1	DNA (cytosine-5-)-methyltransferase 1	*ns*	2.5	-2.2
MBTD1	mbt domain containing 1	*ns*	2.5	-2.3
SGO1-AS1	SGO1 antisense RNA 1	*ns*	2.0	-2.4
POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	*ns*	2.4	-2.1
DCP2	decapping mRNA 2	*ns*	2.4	-2.4
DKFZP586I1420	uncharacterized protein DKFZp586I1420	*ns*	2.2	-2.4
ANGPTL4	angiopoietin like 4	*ns*	2.2	-2.3
LGALS8	lectin, galactoside-binding, soluble, 8	*ns*	2.3	-2.2
PPP1R15B	protein phosphatase 1, regulatory subunit 15B	*ns*	2.1	-2.3
SCARNA9	small Cajal body-specific RNA 9	*ns*	2.2	-2.2
ERVMER34-1	endogenous retrovirus group MER34, member 1	*ns*	2.0	-2.2
DACT2	dishevelled-binding antagonist of beta-catenin 2	*ns*	2.0	-2.2
CDCA2	cell division cycle associated 2	*ns*	2.2	-2.0
SLC29A2	solute carrier family 29 (equilibrative nucleoside transporter), member 2	*ns*	2.0	-2.2
ADK	adenosine kinase	*ns*	2.0	-2.2
TBC1D3E	TBC1 domain family, member 3E	*ns*	2.0	-2.2
CYRIA	CYFIP related Rac1 interactor A	*ns*	2.1	-2.1
TMEM30B	transmembrane protein 30B	*ns*	2.0	-2.1
FAM117B	family with sequence similarity 117, member B	*ns*	2.0	-2.1



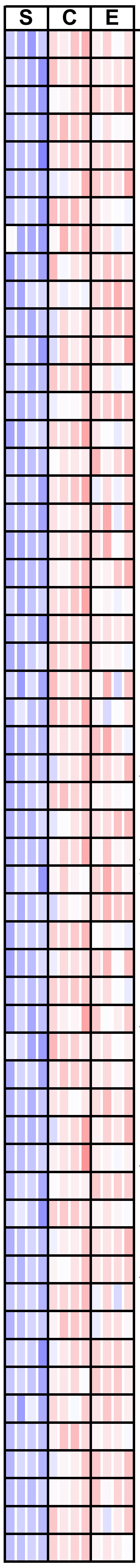
Linear Fold Change

(*ns*=no significant difference)

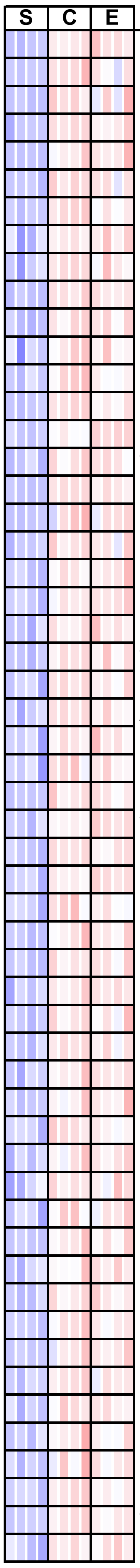
Symbol	Name	S vs C	S vs E	E vs C
ZNF808	zinc finger protein 808	*ns*	*2.1*	*-2.1*
SPC25	SPC25, NDC80 kinetochore complex component	*ns*	*2.0*	*-2.1*
KIF23	kinesin family member 23	*ns*	*2.0*	*-2.0*
MMP12	matrix metallopeptidase 12	-75.0	*-173.6*	*ns*
IGFBP1	insulin like growth factor binding protein 1	-53.3	*-151.0*	*ns*
EPYC	epiphycan	-11.1	*-74.0*	*ns*
PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	-66.5	*-73.7*	*ns*
MT1H	metallothionein 1H	-67.7	*-30.5*	*ns*
LAIR2	leukocyte-associated immunoglobulin-like receptor 2	-45.2	*-31.5*	*ns*
NOTUM	notum pectinacetylesterase homolog (Drosophila)	-44.8	*-31.3*	*ns*
MT1G	metallothionein 1G	-26.2	*-32.8*	*ns*
HNRNPA1P33	heterogeneous nuclear ribonucleoprotein A1 pseudogene 33	-32.1	*-10.2*	*ns*
HTRA4	HtrA serine peptidase 4	-30.0	*-28.7*	*ns*
HCAR2	hydroxycarboxylic acid receptor 2	-29.7	*-12.5*	*ns*
AOC1	amine oxidase, copper containing 1	-16.6	*-22.5*	*ns*
LINC01602	long intergenic non-protein coding RNA 1602	-9.7	*-22.4*	*ns*
MT1X	metallothionein 1X	-18.9	*-21.9*	*ns*
MAMDC2	MAM domain containing 2	-9.4	*-21.0*	*ns*
DIO2	deiodinase, iodothyronine, type II	-20.9	*-6.7*	*ns*
PDCD1LG2	programmed cell death 1 ligand 2	-16.0	*-20.7*	*ns*
IL1R2	interleukin 1 receptor, type II	-14.1	*-17.6*	*ns*
MT1F	metallothionein 1F	-17.2	*-14.0*	*ns*
RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	-17.1	*-8.7*	*ns*
PLA2G10	phospholipase A2, group X	-16.4	*-15.2*	*ns*
ISG15	ISG15 ubiquitin-like modifier	-11.9	*-14.0*	*ns*
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	-12.8	*-7.7*	*ns*
HAPLN3	hyaluronan and proteoglycan link protein 3	-12.6	*-4.3*	*ns*
PLAC8	placenta specific 8	-12.5	*-7.1*	*ns*
HSPG2	heparan sulfate proteoglycan 2	-12.3	*-11.0*	*ns*
DEPDC7	DEP domain containing 7	-12.3	*-7.1*	*ns*
GLIPR1	GLI pathogenesis-related 1	-11.7	*-9.4*	*ns*
SLC16A6	solute carrier family 16, member 6	-11.4	*-5.7*	*ns*
RFPL4B	ret finger protein-like 4B	-8.5	*-11.2*	*ns*
DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides	-8.7	*-11.0*	*ns*
MMP2	matrix metallopeptidase 2	-7.7	*-10.8*	*ns*
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	-5.2	*-10.4*	*ns*
GPR32	G protein-coupled receptor 32	-10.1	*-7.8*	*ns*
FAT2	FAT atypical cadherin 2	-9.8	*-8.1*	*ns*
NOG	noggin	-9.7	*-6.9*	*ns*
CST6	cystatin E	-9.6	*-4.4*	*ns*
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-9.4	*-6.9*	*ns*
TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	-9.3	*-6.0*	*ns*
SDC4	syndecan 4	-9.2	*-3.9*	*ns*
PTGES	prostaglandin E synthase	-9.1	*-4.8*	*ns*
CCR1	chemokine (C-C motif) receptor 1	-8.8	*-6.2*	*ns*
MYCNUT	MYCN upstream transcript (non-protein coding)	-8.7	*-5.2*	*ns*
JPT1	Jupiter microtubule associated homolog 1	-8.6	*-7.4*	*ns*
QSOX1	quiescin Q6 sulfhydryl oxidase 1	-8.5	*-7.6*	*ns*
REPS2	RALBP1 associated Eps domain containing 2	-8.5	*-6.3*	*ns*
SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	-4.9	*-8.3*	*ns*
FLNB	filamin B, beta	-8.3	*-4.5*	*ns*
UPK1B	uroplakin 1B	-8.3	*-5.2*	*ns*
IL2RB	interleukin 2 receptor, beta	-7.3	*-8.2*	*ns*
GREB1L	growth regulation by estrogen in breast cancer-like	-7.7	*-4.0*	*ns*
ADAM19	ADAM metallopeptidase domain 19	-7.6	*-6.2*	*ns*



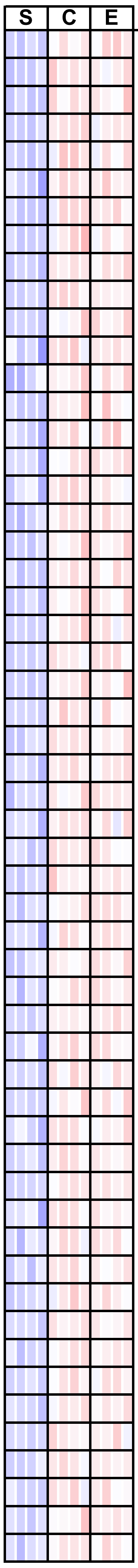
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PLAUR	plasminogen activator, urokinase receptor	-3.4	*-7.5*	*ns*
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	-3.3	*-7.5*	*ns*
SAMD9	sterile alpha motif domain containing 9	-5.2	*-7.4*	*ns*
SPRR2G	small proline-rich protein 2G	-6.6	*-7.3*	*ns*
GALNT3	polypeptide N-acetylgalactosaminyltransferase 3	-7.3	*-6.1*	*ns*
IL10RA	interleukin 10 receptor, alpha	-7.2	*-3.6*	*ns*
SNAI1	snail family zinc finger 1	-7.1	*-4.9*	*ns*
CCNE1	cyclin E1	-7.0	*-3.4*	*ns*
IFI27	interferon, alpha-inducible protein 27	-3.5	*-7.0*	*ns*
CITED2	Cbp	-5.3	*-7.0*	*ns*
FN1	fibronectin 1	-6.9	*-5.5*	*ns*
TGFB2	transforming growth factor beta 2	-6.8	*-6.3*	*ns*
C12orf75	chromosome 12 open reading frame 75	-6.8	*-5.4*	*ns*
HUNK	hormonally up-regulated Neu-associated kinase	-4.0	*-6.8*	*ns*
CLNK	cytokine-dependent hematopoietic cell linker	-6.7	*-4.7*	*ns*
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	-5.5	*-6.7*	*ns*
TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR	-5.9	*-6.6*	*ns*
GALNT7	polypeptide N-acetylgalactosaminyltransferase 7	-6.6	*-5.7*	*ns*
RAB6C-AS1	RAB6C antisense RNA 1	-6.6	*-3.7*	*ns*
HTRA1	HtrA serine peptidase 1	-6.5	*-4.4*	*ns*
TPM1	tropomyosin 1 (alpha)	-6.5	*-3.7*	*ns*
HLA-G	major histocompatibility complex, class I, G	-5.3	*-6.5*	*ns*
MXRA8	matrix-remodelling associated 8	-4.7	*-6.4*	*ns*
MIR181A2HG	MIR181A2 host gene	-6.4	*-2.7*	*ns*
GPRC5A	G protein-coupled receptor, class C, group 5, member A	-6.4	*-6.2*	*ns*
TIMP3	TIMP metallopeptidase inhibitor 3	-4.4	*-6.2*	*ns*
MX1	MX dynamin-like GTPase 1	-5.1	*-6.2*	*ns*
CHRM5	cholinergic receptor, muscarinic 5	-6.2	*-3.6*	*ns*
UBE2L6	ubiquitin-conjugating enzyme E2L 6	-2.8	*-5.9*	*ns*
KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-5.4	*-5.8*	*ns*
ISM2	isthmin 2	-5.8	*-4.9*	*ns*
LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	-5.7	*-4.3*	*ns*
EPSTI1	epithelial stromal interaction 1 (breast)	-5.7	*-4.8*	*ns*
LAMA4	laminin, alpha 4	-3.7	*-5.7*	*ns*
IFITM1	interferon induced transmembrane protein 1	-2.8	*-5.6*	*ns*
LVRN	laeverin	-5.5	*-4.5*	*ns*
UBL3	ubiquitin-like 3	-5.4	*-3.3*	*ns*
PTPRF	protein tyrosine phosphatase, receptor type, F	-5.4	*-3.7*	*ns*
ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	-5.3	*-4.8*	*ns*
HCG4	HLA complex group 4 (non-protein coding)	-4.5	*-5.2*	*ns*
SH3PXD2B	SH3 and PX domains 2B	-5.2	*-4.1*	*ns*
SOX4	SRY box 4	-5.2	*-3.3*	*ns*
ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	-5.2	*-3.5*	*ns*
UGDH	UDP-glucose 6-dehydrogenase	-3.6	*-5.2*	*ns*
PIPOX	pipecolic acid oxidase	-3.3	*-5.1*	*ns*
SOAT1	sterol O-acyltransferase 1	-3.9	*-5.1*	*ns*
GALNT6	polypeptide N-acetylgalactosaminyltransferase 6	-5.0	*-3.7*	*ns*
COL12A1	collagen, type XII, alpha 1	-4.2	*-5.0*	*ns*
NPC2	Niemann-Pick disease, type C2	-2.8	*-5.0*	*ns*
SCUBE1	signal peptide, CUB domain, EGF-like 1	-5.0	*-3.2*	*ns*
NRIP1	nuclear receptor interacting protein 1	-4.9	*-2.8*	*ns*
GPR78	G protein-coupled receptor 78	-4.9	*-3.1*	*ns*
IFIH1	interferon induced, with helicase C domain 1	-4.9	*-3.9*	*ns*
TIMP1	TIMP metallopeptidase inhibitor 1	-2.9	*-4.9*	*ns*
RAB8B	RAB8B, member RAS oncogene family	-4.8	*-3.7*	*ns*



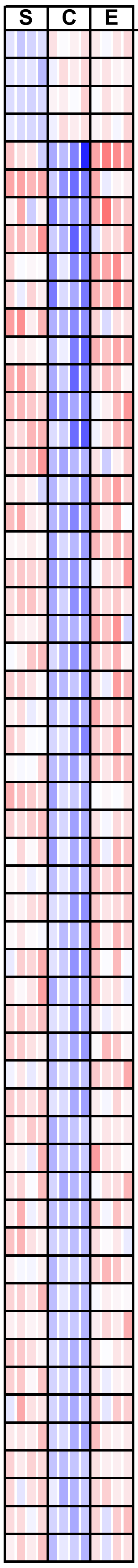
		Linear Fold Change (*ns*=no significant difference)		
Symbol	Name	**S** vs **C**	**S** vs **E**	**E** vs **C**
CD276	CD276 molecule	-4.7	-3.4	*ns*
GRK3	G protein-coupled receptor kinase 3	-4.7	-3.8	*ns*
PARP9	poly(ADP-ribose) polymerase family member 9	-3.5	-4.6	*ns*
LRRC32	leucine rich repeat containing 32	-4.6	-2.5	*ns*
MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	-4.6	-4.5	*ns*
LTBP1	latent transforming growth factor beta binding protein 1	-2.9	-4.6	*ns*
P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	-4.5	-2.5	*ns*
LOC105379311	uncharacterized LOC105379311	-4.5	-3.0	*ns*
GBP2	guanylate binding protein 2, interferon-inducible	-4.0	-4.5	*ns*
GAL	galanin	-2.3	-4.5	*ns*
LAYN	layilin	-3.0	-4.5	*ns*
CPED1	cadherin-like and PC-esterase domain containing 1	-3.2	-4.4	*ns*
LOC105377105	uncharacterized LOC105377105	-4.4	-2.5	*ns*
HLA-E	major histocompatibility complex, class I, E	-2.6	-4.4	*ns*
ITGA5	integrin alpha 5	-4.4	-2.4	*ns*
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	-2.9	-4.4	*ns*
GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	-4.4	-2.6	*ns*
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-3.3	-4.4	*ns*
FHOD3	formin homology 2 domain containing 3	-4.3	-4.4	*ns*
OAS1	2-5-oligoadenylate synthetase 1	-4.1	-4.4	*ns*
PXN	paxillin	-4.3	-2.2	*ns*
DNAPTP3	histone demethylase UTY-like	-4.3	-3.7	*ns*
MTSS2	MTSS I-BAR domain containing 2	-4.3	-2.4	*ns*
SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	-4.2	-3.4	*ns*
IGFBP3	insulin like growth factor binding protein 3	-4.2	-2.1	*ns*
ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	-3.8	-4.2	*ns*
ACSL5	acyl-CoA synthetase long-chain family member 5	-3.0	-4.2	*ns*
KRT19	keratin 19, type I	-4.2	-2.4	*ns*
HLA-C	major histocompatibility complex, class I, C	-2.6	-4.2	*ns*
ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	-4.2	-3.2	*ns*
TSPO	translocator protein (18kDa)	-2.9	-4.2	*ns*
PEA15	phosphoprotein enriched in astrocytes 15	-2.2	-4.1	*ns*
LPCAT1	lysophosphatidylcholine acyltransferase 1	-4.1	-2.1	*ns*
FBXO32	F-box protein 32	-3.1	-4.1	*ns*
PCSK6	proprotein convertase subtilisin	-4.1	-2.4	*ns*
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif 1	-4.1	-3.7	*ns*
LINC01296	long intergenic non-protein coding RNA 1296	-4.1	-2.9	*ns*
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-4.0	-3.0	*ns*
SEMA3C	semaphorin 3C	-3.0	-4.0	*ns*
PTGER3	prostaglandin E receptor 3 (subtype EP3)	-3.6	-4.0	*ns*
AFAP1	actin filament associated protein 1	-4.0	-2.4	*ns*
IL1R1	interleukin 1 receptor, type I	-2.5	-3.9	*ns*
PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	-3.9	-2.4	*ns*
STAT1	signal transducer and activator of transcription 1	-2.9	-3.8	*ns*
APOL6	apolipoprotein L, 6	-3.2	-3.8	*ns*
KAT14	lysine acetyltransferase 14	-3.8	-2.2	*ns*
LY6K	lymphocyte antigen 6 complex, locus K	-3.7	-2.5	*ns*
UGCG	UDP-glucose ceramide glucosyltransferase	-3.1	-3.7	*ns*
DHRS7	dehydrogenase	-2.8	-3.7	*ns*
CNN2	calponin 2	-3.3	-3.7	*ns*
HCAR1	hydroxycarboxylic acid receptor 1	-3.7	-2.4	*ns*
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	-2.5	-3.7	*ns*
PARP4	poly(ADP-ribose) polymerase family member 4	-2.8	-3.6	*ns*
PLSCR1	phospholipid scramblase 1	-3.6	-2.7	*ns*
MYADM	myeloid-associated differentiation marker	-3.6	-2.4	*ns*



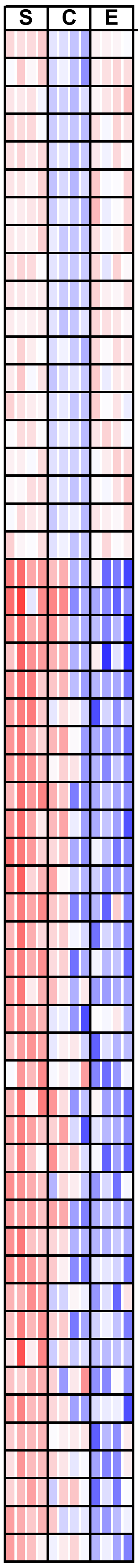
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PTPRS	protein tyrosine phosphatase, receptor type, S	-3.0	*-3.5*	*ns*
EXTL3	exostosin-like glycosyltransferase 3	-3.5	*-2.2*	*ns*
MACIR	macrophage immunometabolism regulator	-3.5	*-2.8*	*ns*
LIMA1	LIM domain and actin binding 1	-3.5	*-3.1*	*ns*
ETS2	v-ets avian erythroblastosis virus E26 oncogene homolog 2	-2.9	*-3.5*	*ns*
PDIA5	protein disulfide isomerase family A, member 5	-3.5	*-2.6*	*ns*
FHL2	four and a half LIM domains 2	-3.5	*-2.4*	*ns*
HLA-F-AS1	HLA-F antisense RNA 1	-2.8	*-3.5*	*ns*
MEX3D	mex-3 RNA binding family member D	-3.5	*-2.9*	*ns*
SLC2A10	solute carrier family 2 (facilitated glucose transporter), member 10	-3.5	*-3.1*	*ns*
GCH1	GTP cyclohydrolase 1	-3.4	*-3.4*	*ns*
COTL1	coactosin-like F-actin binding protein 1	-3.4	*-2.9*	*ns*
CRACDL	CRACD like	-3.4	*-2.1*	*ns*
SLC15A3	solute carrier family 15 (oligopeptide transporter), member 3	-3.4	*-2.6*	*ns*
PSMB8	proteasome subunit beta 8	-2.1	*-3.4*	*ns*
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	-3.4	*-3.1*	*ns*
CMTM3	CKLF-like MARVEL transmembrane domain containing 3	-3.3	*-2.8*	*ns*
RRAD	Ras-related associated with diabetes	-3.3	*-2.9*	*ns*
PLK2	polo-like kinase 2	-3.3	*-2.7*	*ns*
MEGF9	multiple EGF-like-domains 9	-2.6	*-3.3*	*ns*
SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	-2.5	*-3.2*	*ns*
ECE1	endothelin converting enzyme 1	-2.9	*-3.2*	*ns*
TUBB2A	tubulin, beta 2A class IIa	-3.2	*-3.2*	*ns*
SH3D19	SH3 domain containing 19	-3.2	*-2.8*	*ns*
ASCL2	achaete-scute family bHLH transcription factor 2	-3.2	*-2.7*	*ns*
LACTB	lactamase, beta	-2.7	*-3.2*	*ns*
CLN5	ceroid-lipofuscinosis, neuronal 5	-3.2	*-2.8*	*ns*
PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-3.2	*-2.8*	*ns*
WIPF1	WAS	-2.2	*-3.2*	*ns*
ERP27	endoplasmic reticulum protein 27	-3.2	*-2.7*	*ns*
IL13RA1	interleukin 13 receptor, alpha 1	-2.4	*-3.2*	*ns*
RPS27L	ribosomal protein S27-like	-3.2	*-2.2*	*ns*
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	-3.1	*-3.0*	*ns*
KCNK12	potassium channel, two pore domain subfamily K, member 12	-3.0	*-3.1*	*ns*
KLF6	Kruppel-like factor 6	-3.0	*-3.1*	*ns*
HEG1	heart development protein with EGF-like domains 1	-3.1	*-2.8*	*ns*
FAM110A	family with sequence similarity 110, member A	-3.0	*-2.6*	*ns*
PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	-3.0	*-3.0*	*ns*
MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	-2.6	*-3.0*	*ns*
SESTD1	SEC14 and spectrin domains 1	-3.0	*-2.2*	*ns*
PARP12	poly(ADP-ribose) polymerase family member 12	-2.8	*-3.0*	*ns*
CCN1	cellular communication network factor 1	-3.0	*-3.0*	*ns*
OCIAD2	OCIA domain containing 2	-3.0	*-2.9*	*ns*
RHOU	ras homolog family member U	-3.0	*-2.8*	*ns*
PIGT	phosphatidylinositol glycan anchor biosynthesis class T	-2.5	*-3.0*	*ns*
MMP14	matrix metallopeptidase 14 (membrane-inserted)	-3.0	*-2.9*	*ns*
CD9	CD9 molecule	-3.0	*-2.5*	*ns*
SYNE1	spectrin repeat containing, nuclear envelope 1	-2.6	*-3.0*	*ns*
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	-3.0	*-2.4*	*ns*
PGRMC1	progesterone receptor membrane component 1	-2.9	*-2.7*	*ns*
JAK1	Janus kinase 1	-2.9	*-2.3*	*ns*
GALM	galactose mutarotase (aldose 1-epimerase)	-2.9	*-2.7*	*ns*
STXBP5	syntaxin binding protein 5 (tomosyn)	-2.9	*-2.1*	*ns*
TRIM14	tripartite motif containing 14	-2.9	*-2.4*	*ns*
HACD4	3-hydroxyacyl-CoA dehydratase 4	-2.7	*-2.9*	*ns*



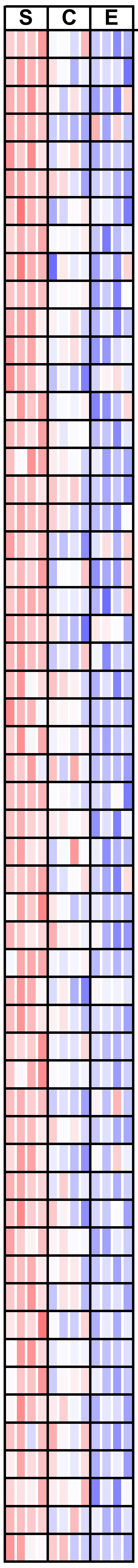
		Linear Fold Change (*ns*=no significant difference)		
Symbol	Name	**S** vs **C**	**S** vs **E**	**E** vs **C**
LINC00324	long intergenic non-protein coding RNA 324	-2.3	*-2.9*	*ns*
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	-2.8	*-2.4*	*ns*
EHBP1	EH domain binding protein 1	-2.8	*-2.8*	*ns*
TUBB6	tubulin, beta 6 class V	-2.8	*-2.2*	*ns*
C5orf46	chromosome 5 open reading frame 46	-2.8	*-2.3*	*ns*
PRDX4	peroxiredoxin 4	-2.8	*-2.8*	*ns*
RABAC1	Rab acceptor 1 (prenylated)	-2.8	*-2.7*	*ns*
EFNB1	ephrin-B1	-2.8	*-2.2*	*ns*
TES	testin LIM domain protein	-2.7	*-2.8*	*ns*
CDC42SE2	CDC42 small effector 2	-2.8	*-2.2*	*ns*
ZC3HAV1	zinc finger CCCH-type, antiviral 1	-2.3	*-2.8*	*ns*
GPR180	G protein-coupled receptor 180	-2.7	*-2.6*	*ns*
AIF1L	allograft inflammatory factor 1-like	-2.7	*-2.7*	*ns*
VASP	vasodilator-stimulated phosphoprotein	-2.7	*-2.4*	*ns*
RPL39L	ribosomal protein L39-like	-2.5	*-2.7*	*ns*
DTX3L	deltex 3 like, E3 ubiquitin ligase	-2.3	*-2.7*	*ns*
DENND1B	DENN	-2.7	*-2.0*	*ns*
ADA	adenosine deaminase	-2.6	*-2.6*	*ns*
SP110	SP110 nuclear body protein	-2.6	*-2.6*	*ns*
PLAAT4	phospholipase A and acyltransferase 4	-2.5	*-2.6*	*ns*
ATP11A	ATPase, class VI, type 11A	-2.6	*-2.6*	*ns*
P3H1	prolyl 3-hydroxylase 1	-2.6	*-2.3*	*ns*
KCTD12	potassium channel tetramerization domain containing 12	-2.2	*-2.6*	*ns*
NCOA1	nuclear receptor coactivator 1	-2.6	*-2.6*	*ns*
SLC50A1	solute carrier family 50 (sugar efflux transporter), member 1	-2.6	*-2.1*	*ns*
LPCAT4	lysophosphatidylcholine acyltransferase 4	-2.5	*-2.2*	*ns*
TMEM14A	transmembrane protein 14A	-2.5	*-2.5*	*ns*
GTPBP1	GTP binding protein 1	-2.4	*-2.5*	*ns*
GPX8	glutathione peroxidase 8 (putative)	-2.5	*-2.2*	*ns*
FYB1	FYN binding protein 1	-2.5	*-2.1*	*ns*
HSPA2	heat shock 70kDa protein 2	-2.5	*-2.4*	*ns*
ASPSCR1	alveolar soft part sarcoma chromosome region, candidate 1	-2.1	*-2.5*	*ns*
RARS2	arginyl-tRNA synthetase 2, mitochondrial	-2.2	*-2.5*	*ns*
GYS1	glycogen synthase 1 (muscle)	-2.0	*-2.4*	*ns*
FADS3	fatty acid desaturase 3	-2.3	*-2.4*	*ns*
CAPN2	calpain 2, (m	-2.0	*-2.4*	*ns*
CPM	carboxypeptidase M	-2.4	*-2.4*	*ns*
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	-2.4	*-2.2*	*ns*
IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	-2.3	*-2.4*	*ns*
PLS3	plastin 3	-2.3	*-2.2*	*ns*
IFNAR2	interferon (alpha, beta and omega) receptor 2	-2.3	*-2.1*	*ns*
FSTL1	follistatin like 1	-2.3	*-2.3*	*ns*
IFNAR1	interferon (alpha, beta and omega) receptor 1	-2.3	*-2.0*	*ns*
PSMB10	proteasome subunit beta 10	-2.2	*-2.3*	*ns*
APH1B	APH1B gamma secretase subunit	-2.3	*-2.1*	*ns*
CAPG	capping protein (actin filament), gelsolin-like	-2.3	*-2.2*	*ns*
ADAM9	ADAM metallopeptidase domain 9	-2.3	*-2.0*	*ns*
ADAM15	ADAM metallopeptidase domain 15	-2.2	*-2.2*	*ns*
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-2.2	*-2.2*	*ns*
ABRACL	ABRA C-terminal like	-2.2	*-2.2*	*ns*
DPP7	dipeptidyl-peptidase 7	-2.2	*-2.1*	*ns*
LOC100132215	uncharacterized LOC100132215	-2.2	*-2.1*	*ns*
POGLUT2	protein O-glucosyltransferase 2	-2.2	*-2.1*	*ns*
LASP1	LIM and SH3 protein 1	-2.2	*-2.2*	*ns*
SIK1	salt-inducible kinase 1	-2.2	*-2.0*	*ns*



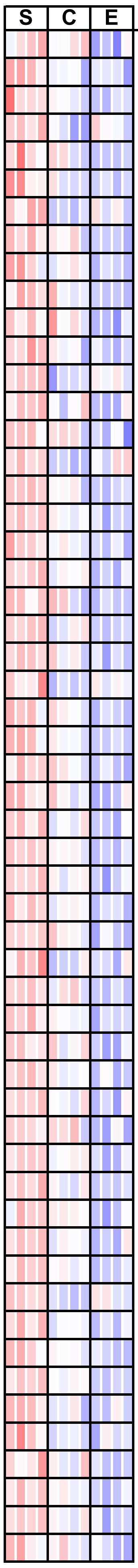
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
SP100	SP100 nuclear antigen	-2.1	*-2.2*	*ns*
CHIC2	cysteine rich hydrophobic domain 2	-2.1	*-2.1*	*ns*
MGLL	monoglyceride lipase	-2.1	*-2.1*	*ns*
PRCP	prolylcarboxypeptidase	-2.0	*-2.0*	*ns*
ADGRL4	adhesion G protein-coupled receptor L4	6.6	*ns*	*22.0*
KDR	kinase insert domain receptor	13.1	*ns*	*5.8*
SNRPN	small nuclear ribonucleoprotein polypeptide N	4.6	*ns*	*11.4*
CD34	CD34 molecule	10.1	*ns*	*5.9*
CLEC3B	C-type lectin domain family 3, member B	4.1	*ns*	*10.1*
TM4SF1	transmembrane 4 L six family member 1	4.8	*ns*	*10.0*
PREX2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	9.6	*ns*	*4.4*
A2M	alpha-2-macroglobulin	4.0	*ns*	*9.0*
IL33	interleukin 33	8.6	*ns*	*6.5*
MYCT1	myc target 1	8.2	*ns*	*7.0*
RAMP2	receptor (G protein-coupled) activity modifying protein 2	7.8	*ns*	*6.4*
CACHD1	cache domain containing 1	6.3	*ns*	*3.2*
CALCRL	calcitonin receptor like receptor	2.8	*ns*	*6.1*
TRPC6	transient receptor potential cation channel, subfamily C, member 6	6.1	*ns*	*5.9*
IL1A	interleukin 1 alpha	3.0	*ns*	*5.8*
S1PR1	sphingosine-1-phosphate receptor 1	5.8	*ns*	*5.7*
ARHGEF6	Rac	5.8	*ns*	*5.6*
PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	3.6	*ns*	*5.4*
ACTA2	actin, alpha 2, smooth muscle, aorta	4.4	*ns*	*5.3*
IDO1	indoleamine 2,3-dioxygenase 1	4.1	*ns*	*5.2*
DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	2.7	*ns*	*4.9*
GMFG	glia maturation factor, gamma	3.3	*ns*	*4.8*
MERTK	MER proto-oncogene, tyrosine kinase	2.7	*ns*	*4.8*
PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	4.8	*ns*	*2.5*
WLS	wntless Wnt ligand secretion mediator	4.7	*ns*	*3.4*
ZSWIM6	zinc finger, SWIM-type containing 6	3.3	*ns*	*4.6*
SDC2	syndecan 2	2.3	*ns*	*4.3*
IGF1	insulin-like growth factor 1 (somatomedin C)	3.5	*ns*	*4.3*
IRS1	insulin receptor substrate 1	2.4	*ns*	*4.3*
EBF1	early B-cell factor 1	4.2	*ns*	*3.9*
NID1	nidogen 1	4.2	*ns*	*3.7*
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	4.1	*ns*	*2.4*
VAMP5	vesicle associated membrane protein 5	4.1	*ns*	*4.0*
DOCK4	dedicator of cytokinesis 4	2.1	*ns*	*4.1*
SNAI2	snail family zinc finger 2	4.0	*ns*	*2.7*
ASS1	argininosuccinate synthase 1	3.9	*ns*	*2.9*
ABCC9	ATP binding cassette subfamily C member 9	3.1	*ns*	*3.8*
TCF4	transcription factor 4	3.8	*ns*	*3.7*
DEFB109A	defensin beta 109A (pseudogene)	3.5	*ns*	*3.7*
ICA1	islet cell autoantigen 1	3.7	*ns*	*2.3*
SPRY2	sprouty RTK signaling antagonist 2	2.1	*ns*	*3.7*
MTSS1	metastasis suppressor 1	3.7	*ns*	*2.2*
PTPRB	protein tyrosine phosphatase, receptor type, B	2.7	*ns*	*3.6*
FAT4	FAT atypical cadherin 4	3.5	*ns*	*2.9*
EPB41L2	erythrocyte membrane protein band 4.1-like 2	3.5	*ns*	*2.3*
PWAR5	Prader Willi	3.4	*ns*	*3.5*
MEIS1	Meis homeobox 1	3.4	*ns*	*3.3*
ANKRD44	ankyrin repeat domain 44	3.4	*ns*	*2.7*
CD93	CD93 molecule	2.9	*ns*	*3.2*
ETS1	v-ets avian erythroblastosis virus E26 oncogene homolog 1	2.9	*ns*	*3.2*
MEF2C	myocyte enhancer factor 2C	3.2	*ns*	*2.5*



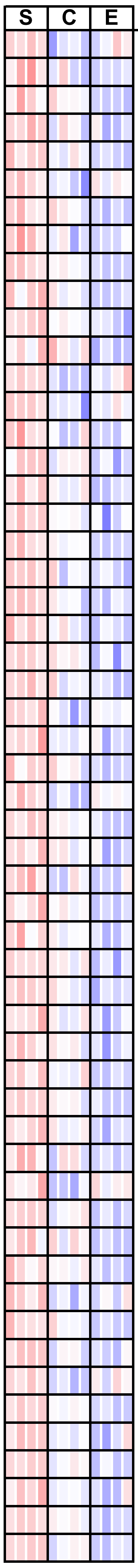
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
EML1	echinoderm microtubule associated protein like 1	3.2	*ns*	*2.1*
LOC105373192	uncharacterized LOC105373192	3.0	*ns*	*3.2*
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	2.4	*ns*	*3.0*
EAF2	ELL associated factor 2	2.9	*ns*	*2.8*
ZEB2	zinc finger E-box binding homeobox 2	2.8	*ns*	*2.2*
GLUL	glutamate-ammonia ligase	2.8	*ns*	*2.7*
ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	2.6	*ns*	*2.6*
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	2.6	*ns*	*2.4*
SSBP2	single-stranded DNA binding protein 2	2.5	*ns*	*2.2*
ARHGEF26	Rho guanine nucleotide exchange factor 26	2.4	*ns*	*2.5*
C1QTNF1	C1q and tumor necrosis factor related protein 1	2.2	*ns*	*2.5*
TEC	tec protein tyrosine kinase	2.3	*ns*	*2.5*
DEFB109B	defensin beta 109B	2.5	*ns*	*2.2*
RESF1	retroelement silencing factor 1	2.4	*ns*	*2.1*
PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	2.2	*ns*	*2.4*
FLI1	Fli-1 proto-oncogene, ETS transcription factor	2.1	*ns*	*2.4*
PCDH17	protocadherin 17	2.3	*ns*	*2.4*
PTPRJ	protein tyrosine phosphatase, receptor type, J	2.2	*ns*	*2.3*
LOC105375977	uncharacterized LOC105375977	2.3	*ns*	*2.1*
SNORD114-2	small nucleolar RNA, C	*ns*	*22.1*	*ns*
SNORD114-6	small nucleolar RNA, C	*ns*	*20.9*	*ns*
SNORD114-7	small nucleolar RNA, C	*ns*	*20.5*	*ns*
SNORD114-19	small nucleolar RNA, C	*ns*	*16.8*	*ns*
SNORD114-12	small nucleolar RNA, C	*ns*	*14.3*	*ns*
ERVV-2	endogenous retrovirus group V, member 2	*ns*	*14.1*	*ns*
CD36	CD36 molecule (thrombospondin receptor)	*ns*	*13.4*	*ns*
ZNF117	zinc finger protein 117	*ns*	*13.3*	*ns*
SNORD114-15	small nucleolar RNA, C	*ns*	*13.2*	*ns*
PABPC4L	poly(A) binding protein, cytoplasmic 4-like	*ns*	*13.0*	*ns*
SNORD114-13	small nucleolar RNA, C	*ns*	*12.2*	*ns*
SNORD114-17	small nucleolar RNA, C	*ns*	*12.2*	*ns*
SNORD114-11	small nucleolar RNA, C	*ns*	*11.6*	*ns*
ERVV-1	endogenous retrovirus group V, member 1	*ns*	*10.7*	*ns*
SNORD113-3	small nucleolar RNA, C	*ns*	*10.7*	*ns*
MIR503	microRNA 503	*ns*	*10.2*	*ns*
PCDH18	protocadherin 18	10.2	*ns*	*ns*
PLAC1	placenta specific 1	*ns*	*9.8*	*ns*
LOC105378624	uncharacterized LOC105378624	*ns*	*9.5*	*ns*
SNORD114-30	small nucleolar RNA, C	*ns*	*9.4*	*ns*
SNORD113-2	small nucleolar RNA, C	*ns*	*9.0*	*ns*
MIR1305	microRNA 1305	*ns*	*8.9*	*ns*
LINC01483	long intergenic non-protein coding RNA 1483	*ns*	*8.7*	*ns*
SNORD114-3	small nucleolar RNA, C	*ns*	*8.7*	*ns*
SNORD114-27	small nucleolar RNA, C	*ns*	*8.5*	*ns*
SNORD113-9	small nucleolar RNA, C	*ns*	*8.2*	*ns*
LOC105376127	uncharacterized LOC105376127	*ns*	*7.9*	*ns*
SNORD114-21	small nucleolar RNA, C	*ns*	*7.8*	*ns*
PCDH11Y	protocadherin 11 Y-linked	*ns*	*7.4*	*ns*
SNORD59A	small nucleolar RNA, C	*ns*	*7.3*	*ns*
SNORD114-1	small nucleolar RNA, C	*ns*	*7.2*	*ns*
PSG6	pregnancy specific beta-1-glycoprotein 6	*ns*	*7.1*	*ns*
CHODL-AS1	CHODL antisense RNA 1	*ns*	*7.1*	*ns*
PSG11	pregnancy specific beta-1-glycoprotein 11	*ns*	*6.9*	*ns*
TCF21	transcription factor 21	*ns*	*6.8*	*ns*
SCARNA2	small Cajal body-specific RNA 2	*ns*	*6.5*	*ns*



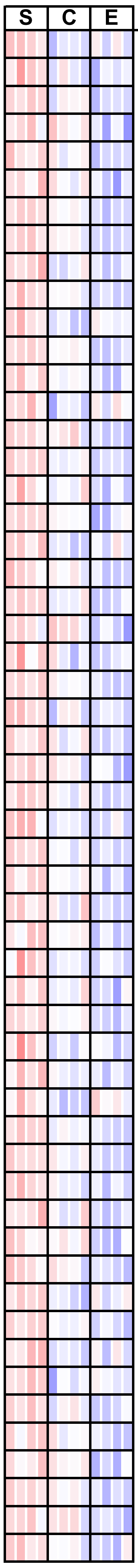
Symbol	Name	Linear Fold Change (*ns*=no significant difference) S vs C	 S vs E	 E vs C
ARHGAP26-IT1	ARHGAP26 intronic transcript 1	*ns*	6.4	*ns*
SNORD114-22	small nucleolar RNA, C	*ns*	6.4	*ns*
OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	*ns*	6.3	*ns*
ADGRL2	adhesion G protein-coupled receptor L2	6.2	*ns*	*ns*
LOC105375401	uncharacterized LOC105375401	*ns*	6.2	*ns*
LOC101927745	uncharacterized LOC101927745	*ns*	6.2	*ns*
MIR4659B	microRNA 4659b	*ns*	6.2	*ns*
CLIP4	CAP-GLY domain containing linker protein family, member 4	*ns*	6.1	*ns*
PLCE1-AS1	PLCE1 antisense RNA 1	*ns*	6.0	*ns*
MORC4	MORC family CW-type zinc finger 4	*ns*	6.0	*ns*
L1TD1	LINE-1 type transposase domain containing 1	*ns*	5.9	*ns*
LOC101929607	uncharacterized LOC101929607	*ns*	5.9	*ns*
GNG11	guanine nucleotide binding protein (G protein), gamma 11	5.8	*ns*	*ns*
LOC105370804	uncharacterized LOC105370804	*ns*	5.8	*ns*
LOC220729	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) pseudogene	*ns*	5.7	*ns*
CASC9	cancer susceptibility candidate 9 (non-protein coding)	*ns*	5.7	*ns*
HELLS	helicase, lymphoid-specific	*ns*	5.6	*ns*
SLIT2	slit guidance ligand 2	*ns*	5.6	*ns*
TLL1	tolloid like 1	5.5	*ns*	*ns*
RAB3B	RAB3B, member RAS oncogene family	*ns*	5.5	*ns*
FBN2	fibrillin 2	*ns*	5.5	*ns*
ENPEP	glutamyl aminopeptidase (aminopeptidase A)	5.5	*ns*	*ns*
LOC101927685	heat shock transcription factor, X-linked-like	*ns*	5.5	*ns*
LOC100508631	uncharacterized LOC100508631	*ns*	5.4	*ns*
MAEL	maelstrom spermatogenic transposon silencer	*ns*	5.3	*ns*
SIK3-IT1	SIK3 intronic transcript 1	*ns*	5.2	*ns*
SHANK2	SH3 and multiple ankyrin repeat domains 2	*ns*	5.2	*ns*
ACP3	acid phosphatase 3	*ns*	5.2	*ns*
NRK	Nik related kinase	*ns*	5.2	*ns*
LOC102725247	uncharacterized LOC102725247	*ns*	5.1	*ns*
CD200	CD200 molecule	*ns*	5.1	*ns*
MEG8	maternally expressed 8 (non-protein coding)	*ns*	5.1	*ns*
SNORD13P2	small nucleolar RNA, C	*ns*	5.0	*ns*
AKR1B15	aldo-keto reductase family 1, member B15	*ns*	4.9	*ns*
LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	4.9	*ns*	*ns*
SLC16A10	solute carrier family 16 (aromatic amino acid transporter), member 10	*ns*	4.9	*ns*
DLG5	discs, large homolog 5 (Drosophila)	*ns*	4.9	*ns*
DHRS2	dehydrogenase	*ns*	4.9	*ns*
GUCY1A2	guanylate cyclase 1, soluble, alpha 2	4.8	*ns*	*ns*
NFE2L3	nuclear factor, erythroid 2-like 3	*ns*	4.8	*ns*
SNORD116-21	small nucleolar RNA, C	4.7	*ns*	*ns*
MIRLET7F1	microRNA let-7f-1	*ns*	4.7	*ns*
SNORD113-7	small nucleolar RNA, C	*ns*	4.7	*ns*
LOC105376236	uncharacterized LOC105376236	*ns*	4.6	*ns*
RASSF6	Ras association (RalGDS	*ns*	4.6	*ns*
S100A9	S100 calcium binding protein A9	*ns*	4.6	*ns*
BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	*ns*	4.6	*ns*
PSG4	pregnancy specific beta-1-glycoprotein 4	*ns*	4.6	*ns*
OR52E6	olfactory receptor, family 52, subfamily E, member 6	*ns*	4.5	*ns*
HAPLN1	hyaluronan and proteoglycan link protein 1	*ns*	4.4	*ns*
LOC105377649	uncharacterized LOC105377649	*ns*	4.4	*ns*
LOC105371225	uncharacterized LOC105371225	*ns*	4.4	*ns*
LIPG	lipase, endothelial	*ns*	4.4	*ns*
GH1	growth hormone 1	*ns*	4.4	*ns*
SNORD114-8	small nucleolar RNA, C	*ns*	4.4	*ns*



		Linear Fold Change (*ns*=no significant difference)		
Symbol	Name	**S** vs **C**	**S** vs **E**	**E** vs **C**
OR7E91P	olfactory receptor, family 7, subfamily E, member 91 pseudogene	*ns*	4.3	*ns*
CCDC68	coiled-coil domain containing 68	*ns*	4.3	*ns*
XDH	xanthine dehydrogenase	*ns*	4.3	*ns*
COL6A3	collagen, type VI, alpha 3	4.3	*ns*	*ns*
LOC101927359	uncharacterized LOC101927359	*ns*	4.3	*ns*
LOC644919	uncharacterized LOC644919	*ns*	4.3	*ns*
NDNF	neuron-derived neurotrophic factor	4.2	*ns*	*ns*
TUSC3	tumor suppressor candidate 3	*ns*	4.2	*ns*
LOC105377196	uncharacterized LOC105377196	*ns*	4.2	*ns*
PDE3B	phosphodiesterase 3B, cGMP-inhibited	*ns*	4.2	*ns*
LOC101928794	uncharacterized LOC101928794	*ns*	4.2	*ns*
CXADRP2	coxsackie virus and adenovirus receptor pseudogene 2	*ns*	4.2	*ns*
ITGB3	integrin beta 3	4.2	*ns*	*ns*
MIR29C	microRNA 29c	*ns*	4.2	*ns*
CDS1	CDP-diacylglycerol synthase 1	*ns*	4.2	*ns*
GUCY1A1	guanylate cyclase 1 soluble subunit alpha 1	4.2	*ns*	*ns*
MAP3K13	mitogen-activated protein kinase kinase kinase 13	*ns*	4.1	*ns*
DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	*ns*	4.1	*ns*
NAALADL2-AS3	NAALADL2 antisense RNA 3	*ns*	4.1	*ns*
PSG2	pregnancy specific beta-1-glycoprotein 2	*ns*	4.0	*ns*
LOC102723920	uncharacterized LOC102723920	*ns*	4.0	*ns*
SLC30A2	solute carrier family 30 (zinc transporter), member 2	*ns*	4.0	*ns*
CKAP2L	cytoskeleton associated protein 2-like	*ns*	4.0	*ns*
FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	3.9	*ns*	*ns*
MIR3650	microRNA 3650	*ns*	3.9	*ns*
ZNF354B	zinc finger protein 354B	*ns*	3.9	*ns*
MIR17HG	miR-17-92 cluster host gene	*ns*	3.9	*ns*
LINC00622	long intergenic non-protein coding RNA 622	*ns*	3.9	*ns*
LOC100507487	uncharacterized LOC100507487	*ns*	3.9	*ns*
RHOBTB3	Rho-related BTB domain containing 3	*ns*	3.9	*ns*
LOC102723908	uncharacterized LOC102723908	*ns*	3.9	*ns*
PSCA	prostate stem cell antigen	*ns*	3.9	*ns*
C2orf81	chromosome 2 open reading frame 81	*ns*	3.8	*ns*
MGC12916	uncharacterized protein MGC12916	*ns*	3.7	*ns*
LOC105378300	uncharacterized LOC105378300	*ns*	3.8	*ns*
TCHHL1	trichohyalin like 1	*ns*	3.8	*ns*
LOC105369897	uncharacterized LOC105369897	*ns*	3.8	*ns*
IL1RAPL2	interleukin 1 receptor accessory protein-like 2	*ns*	3.7	*ns*
AGO2	argonaute RISC catalytic component 2	*ns*	3.7	*ns*
PBK	PDZ binding kinase	*ns*	3.7	*ns*
EMSY	EMSY BRCA2-interacting transcriptional repressor	*ns*	3.7	*ns*
SDHAP2	succinate dehydrogenase complex subunit A, flavoprotein pseudogene 2	*ns*	3.7	*ns*
PLGLB1	plasminogen-like B1	*ns*	3.7	*ns*
SEMA6D	semaphorin 6D	*ns*	3.7	*ns*
TMEM247	transmembrane protein 247	*ns*	3.7	*ns*
ZNF521	zinc finger protein 521	3.6	*ns*	*ns*
DUBR	DPPA2 upstream binding RNA	*ns*	3.6	*ns*
NAALADL2	N-acetylated alpha-linked acidic dipeptidase-like 2	*ns*	3.6	*ns*
TAB3	TGF-beta activated kinase 1	*ns*	3.6	*ns*
LRRN3	leucine rich repeat neuronal 3	*ns*	3.6	*ns*
SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	*ns*	3.6	*ns*
GTF2IP20	general transcription factor IIi pseudogene 20	*ns*	3.5	*ns*
RBMS3	RNA binding motif, single stranded interacting protein 3	*ns*	3.5	*ns*
PDZD2	PDZ domain containing 2	*ns*	3.5	*ns*
LOC100134868	uncharacterized LOC100134868	*ns*	3.5	*ns*

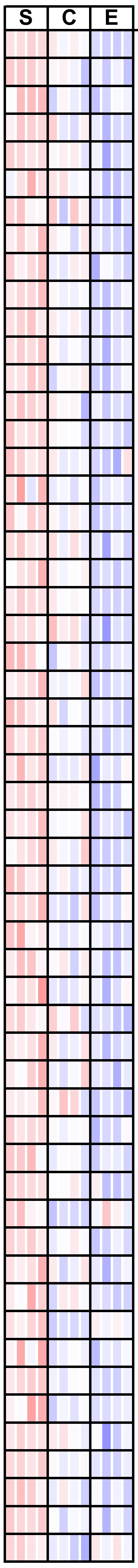


Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
ADIRF	adipogenesis regulatory factor	3.5	*ns*	*ns*
MIR487B	microRNA 487b	*ns*	3.5	*ns*
LOC102723439	uncharacterized LOC102723439	*ns*	3.5	*ns*
SNORA38B	small nucleolar RNA, H	*ns*	3.5	*ns*
KCNK5	potassium channel, two pore domain subfamily K, member 5	*ns*	3.5	*ns*
OGFRL1	opioid growth factor receptor-like 1	3.4	*ns*	*ns*
TFRC	transferrin receptor	*ns*	3.4	*ns*
SCN9A	sodium channel, voltage gated, type IX alpha subunit	*ns*	3.4	*ns*
LONP2	lon peptidase 2, peroxisomal	*ns*	3.4	*ns*
ATG9B	autophagy related 9B	*ns*	3.4	*ns*
SERPINF1	serpin peptidase inhibitor F1	*ns*	3.4	*ns*
MIRLET7G	microRNA let-7g	*ns*	3.4	*ns*
RAPGEF5	Rap guanine nucleotide exchange factor 5	3.4	*ns*	*ns*
EXOC6	exocyst complex component 6	3.4	*ns*	*ns*
CARD17	caspase recruitment domain family, member 17	*ns*	3.4	*ns*
FBXO9	F-box protein 9	*ns*	3.4	*ns*
MTNR1B	melatonin receptor 1B	*ns*	3.4	*ns*
LOC389765	kinesin family member 27 pseudogene	*ns*	3.4	*ns*
ZNF83	zinc finger protein 83	*ns*	3.3	*ns*
MIR581	microRNA 581	*ns*	3.3	*ns*
ARL15	ADP-ribosylation factor like GTPase 15	*ns*	3.3	*ns*
LINC01091	long intergenic non-protein coding RNA 1091	*ns*	3.3	*ns*
LOC102724917	uncharacterized LOC102724917	*ns*	3.3	*ns*
SDHAP1	succinate dehydrogenase complex subunit A, flavoprotein pseudogene 1	*ns*	3.3	*ns*
NFIB	nuclear factor I	3.3	*ns*	*ns*
RIMKLB	ribosomal modification protein rimK-like family member B	*ns*	3.3	*ns*
LOC101929787	uncharacterized LOC101929787	*ns*	3.3	*ns*
DUSP6	dual specificity phosphatase 6	3.3	*ns*	*ns*
RNF43	ring finger protein 43	*ns*	3.3	*ns*
LOC100133331	uncharacterized LOC100133331	*ns*	3.3	*ns*
XKRX	X-linked Kx blood group related, X-linked	*ns*	3.3	*ns*
LOC101926892	uncharacterized LOC101926892	*ns*	3.3	*ns*
LOC101928324	uncharacterized LOC101928324	*ns*	3.3	*ns*
CYTH3	cytohesin 3	*ns*	3.3	*ns*
ITGBL1	integrin beta like 1	*ns*	3.2	*ns*
NPIPB4	nuclear pore complex interacting protein family, member B4	*ns*	3.2	*ns*
LINC01355	long intergenic non-protein coding RNA 1355	*ns*	3.2	*ns*
CLMN	calmin (calponin-like, transmembrane)	*ns*	3.2	*ns*
ZFP2	ZFP2 zinc finger protein	*ns*	3.2	*ns*
DVL3	dishevelled segment polarity protein 3	*ns*	3.2	*ns*
NIPAL1	NIPA-like domain containing 1	*ns*	3.2	*ns*
WARS1	tryptophanyl-tRNA synthetase 1	3.2	*ns*	*ns*
TTBK2	tau tubulin kinase 2	*ns*	3.2	*ns*
SYCP2L	synaptonemal complex protein 2-like	*ns*	3.2	*ns*
SNAR-G1	small ILF3	*ns*	3.2	*ns*
HBA2	hemoglobin, alpha 2	3.2	*ns*	*ns*
LINC00939	long intergenic non-protein coding RNA 939	*ns*	3.2	*ns*
MMD	monocyte to macrophage differentiation-associated	*ns*	3.2	*ns*
CYYR1	cysteine	3.2	*ns*	*ns*
CLIP1-AS1	CLIP1 antisense RNA 1	*ns*	3.2	*ns*
SCIN	scinderin	*ns*	3.2	*ns*
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	*ns*	3.1	*ns*
ELMO1-AS1	ELMO1 antisense RNA 1	*ns*	3.1	*ns*
RGPD6	RANBP2-like and GRIP domain containing 6	*ns*	3.1	*ns*
IKZF2	IKAROS family zinc finger 2	*ns*	3.1	*ns*

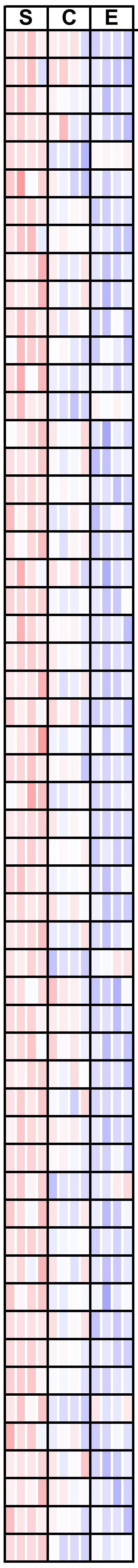


Linear Fold Change
(*ns*=no significant difference)

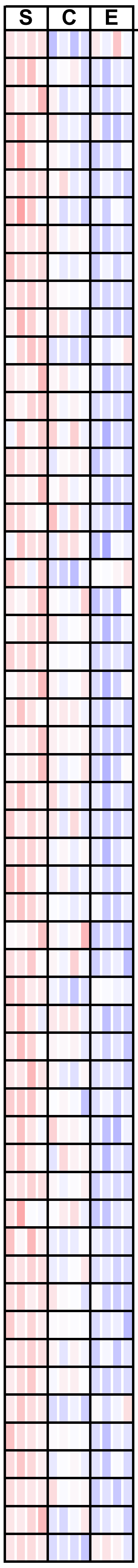
Symbol	Name	**S** vs **C**	**S** vs **E**	**E** vs **C**
SLC45A4	solute carrier family 45, member 4	3.1	*ns*	*ns*
FAM124B	family with sequence similarity 124 member B	*ns*	*3.1*	*ns*
BEX2	brain expressed X-linked 2	*ns*	*3.1*	*ns*
OCLN	occludin	*ns*	*3.1*	*ns*
SPIRE2	spire-type actin nucleation factor 2	*ns*	*3.1*	*ns*
LOC101928344	protein GVQW1-like	*ns*	*3.1*	*ns*
RGPD8	RANBP2-like and GRIP domain containing 8	*ns*	*3.1*	*ns*
SYNJ1	synaptojanin 1	*ns*	*3.1*	*ns*
DHCR24	24-dehydrocholesterol reductase	*ns*	*3.1*	*ns*
LOC100505938	uncharacterized LOC100505938	*ns*	*3.1*	*ns*
PLSCR4	phospholipid scramblase 4	3.1	*ns*	*ns*
C21orf91	chromosome 21 open reading frame 91	*ns*	*3.1*	*ns*
LRRTM2	leucine rich repeat transmembrane neuronal 2	*ns*	*3.1*	*ns*
GPNMB	glycoprotein (transmembrane) nmb	3.1	*ns*	*ns*
CCNE2	cyclin E2	*ns*	*3.0*	*ns*
SH3GLB2	SH3-domain GRB2-like endophilin B2	*ns*	*3.0*	*ns*
DHRSX	dehydrogenase	*ns*	*3.0*	*ns*
LOC101929494	uncharacterized LOC101929494	*ns*	*3.0*	*ns*
GJC1	gap junction protein gamma 1	3.0	*ns*	*ns*
ORC6	origin recognition complex subunit 6	*ns*	*3.0*	*ns*
STX3	syntaxin 3	*ns*	*3.0*	*ns*
CCNB2	cyclin B2	*ns*	*2.9*	*ns*
SLIT2-IT1	SLIT2 intronic transcript 1	*ns*	*3.0*	*ns*
CEP152	centrosomal protein 152kDa	*ns*	*3.0*	*ns*
SH3GL1P2	SH3-domain GRB2-like 1 pseudogene 2	*ns*	*3.0*	*ns*
LOC105371471	uncharacterized LOC105371471	*ns*	*3.0*	*ns*
SPDYE6	speedy	*ns*	*3.0*	*ns*
LOC105374911	uncharacterized LOC105374911	*ns*	*3.0*	*ns*
MIR223	microRNA 223	*ns*	*3.0*	*ns*
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	*ns*	*3.0*	*ns*
PAQR7	progestin and adipoQ receptor family member VII	*ns*	*3.0*	*ns*
CGB7	chorionic gonadotropin, beta polypeptide 7	*ns*	*2.9*	*ns*
ADGRG1	adhesion G protein-coupled receptor G1	*ns*	*2.9*	*ns*
MIR218-1	microRNA 218-1	*ns*	*2.9*	*ns*
ZNF250	zinc finger protein 250	*ns*	*2.9*	*ns*
AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	*ns*	*2.9*	*ns*
LOC101930100	uncharacterized LOC101930100	*ns*	*2.9*	*ns*
LOC100133091	uncharacterized LOC100133091	*ns*	*2.9*	*ns*
LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	2.9	*ns*	*ns*
LOC101929709	uncharacterized LOC101929709	*ns*	*2.9*	*ns*
EPHB4	EPH receptor B4	*ns*	*2.9*	*ns*
ANKRD20A2P	ankyrin repeat domain 20 family member A2, pseudogene	*ns*	*2.9*	*ns*
TRIM25	tripartite motif containing 25	*ns*	*2.9*	*ns*
PDXDC2P	pyridoxal-dependent decarboxylase domain containing 2, pseudogene	*ns*	*2.9*	*ns*
GGCT	gamma-glutamylcyclotransferase	*ns*	*2.9*	*ns*
LOC105369204	uncharacterized LOC105369204	2.9	*ns*	*ns*
ACADVL	acyl-CoA dehydrogenase, very long chain	*ns*	*2.9*	*ns*
BTG2	BTG family, member 2	2.9	*ns*	*ns*
BCL2	B-cell CLL	2.9	*ns*	*ns*
AUNIP	aurora kinase A and ninein interacting protein	*ns*	*2.9*	*ns*
SH2D4A	SH2 domain containing 4A	*ns*	*2.9*	*ns*
LIN28B	lin-28 homolog B (C. elegans)	*ns*	*2.9*	*ns*
MCM6	minichromosome maintenance complex component 6	*ns*	*2.9*	*ns*
AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	*ns*	*2.9*	*ns*
ARRDC3-AS1	ARRDC3 antisense RNA 1	*ns*	*2.9*	*ns*



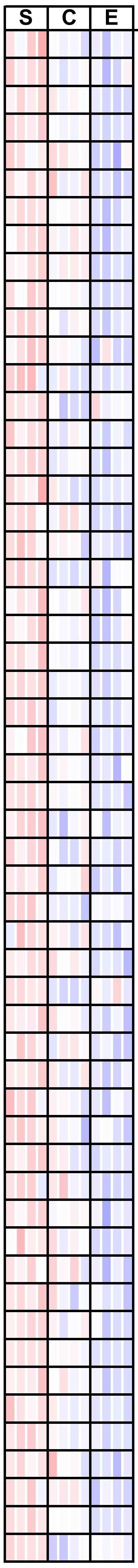
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
TOMM34	translocase of outer mitochondrial membrane 34	*ns*	2.9	*ns*
CNN3	calponin 3, acidic	*ns*	2.9	*ns*
VSTM5	V-set and transmembrane domain containing 5	*ns*	2.8	*ns*
LOC100506606	uncharacterized LOC100506606	*ns*	2.8	*ns*
RERG-AS1	RERG antisense RNA 1	*ns*	2.8	*ns*
LOC105376073	uncharacterized LOC105376073	*ns*	2.8	*ns*
MIR521-1	microRNA 521-1	*ns*	2.8	*ns*
LOC101930131	uncharacterized LOC101930131	*ns*	2.8	*ns*
PGF	placental growth factor	*ns*	2.8	*ns*
NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	*ns*	2.8	*ns*
SECISBP2L	SECIS binding protein 2-like	*ns*	2.8	*ns*
MAP3K4	mitogen-activated protein kinase kinase kinase 4	*ns*	2.8	*ns*
AKTIP	AKT interacting protein	*ns*	2.8	*ns*
ZC2HC1A	zinc finger, C2HC-type containing 1A	*ns*	2.8	*ns*
RPIA	ribose 5-phosphate isomerase A	*ns*	2.8	*ns*
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	*ns*	2.8	*ns*
HSD17B1P1	hydroxysteroid (17-beta) dehydrogenase 1 pseudogene 1	*ns*	2.8	*ns*
CRYBG2	crystallin beta-gamma domain containing 2	*ns*	2.8	*ns*
ADAM20	ADAM metallopeptidase domain 20	*ns*	2.8	*ns*
LOC105369468	uncharacterized LOC105369468	*ns*	2.8	*ns*
RGPD1	RANBP2-like and GRIP domain containing 1	*ns*	2.8	*ns*
NDC80	NDC80 kinetochore complex component	*ns*	2.8	*ns*
LOC101929570	uncharacterized LOC101929570	*ns*	2.8	*ns*
TTC7B	tetratricopeptide repeat domain 7B	*ns*	2.8	*ns*
LOC101928472	uncharacterized LOC101928472	*ns*	2.8	*ns*
ALDH7A1	aldehyde dehydrogenase 7 family, member A1	*ns*	2.8	*ns*
LOC105374895	uncharacterized LOC105374895	*ns*	2.8	*ns*
NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase	*ns*	2.8	*ns*
USP43	ubiquitin specific peptidase 43	*ns*	2.8	*ns*
EGFR	epidermal growth factor receptor	*ns*	2.8	*ns*
STARD4	StAR-related lipid transfer domain containing 4	*ns*	2.8	*ns*
PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 beta	*ns*	2.7	*ns*
RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	*ns*	2.7	*ns*
HERC2P4	hect domain and RLD 2 pseudogene 4	*ns*	2.7	*ns*
MRTFB	myocardin related transcription factor B	*ns*	2.7	*ns*
SHCBP1	SHC SH2-domain binding protein 1	*ns*	2.7	*ns*
NPIPB11	nuclear pore complex interacting protein family, member B11	*ns*	2.7	*ns*
BCORL1	BCL6 corepressor-like 1	*ns*	2.7	*ns*
SPATA9	spermatogenesis associated 9	*ns*	2.7	*ns*
RFX2	regulatory factor X, 2 (influences HLA class II expression)	*ns*	2.7	*ns*
MARVELD3	MARVEL domain containing 3	*ns*	2.7	*ns*
LOC101929461	uncharacterized LOC101929461	*ns*	2.7	*ns*
PCAT19	prostate cancer associated transcript 19 (non-protein coding)	2.7	*ns*	*ns*
ALDH4A1	aldehyde dehydrogenase 4 family, member A1	*ns*	2.7	*ns*
NPIPA1	nuclear pore complex interacting protein family member A1	*ns*	2.7	*ns*
LYPD5	LY6	*ns*	2.7	*ns*
TGM2	transglutaminase 2	2.7	*ns*	*ns*
OR6W1P	olfactory receptor, family 6, subfamily W, member 1 pseudogene	*ns*	2.7	*ns*
DCAF1	DDB1 and CUL4 associated factor 1	*ns*	2.7	*ns*
GAP43	growth associated protein 43	*ns*	2.7	*ns*
NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	*ns*	2.7	*ns*
ARGLU1	arginine and glutamate rich 1	*ns*	2.7	*ns*
CCL28	chemokine (C-C motif) ligand 28	*ns*	2.7	*ns*
LMO7	LIM domain 7	*ns*	2.7	*ns*
CAT	catalase	2.7	*ns*	*ns*



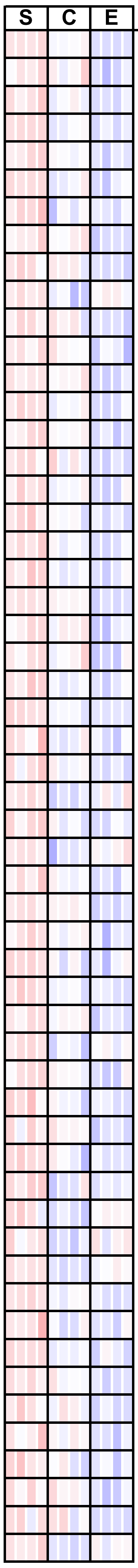
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
SOS2	SOS Ras	*ns*	2.7	*ns*
ZNF443	zinc finger protein 443	*ns*	2.7	*ns*
ZNRF3	zinc and ring finger 3	*ns*	2.7	*ns*
ZNF525	zinc finger protein 525	*ns*	2.7	*ns*
ECI2	enoyl-CoA delta isomerase 2	2.7	*ns*	*ns*
HYMAI	hydatidiform mole associated and imprinted (non-protein coding)	*ns*	2.6	*ns*
NEMP1	nuclear envelope integral membrane protein 1	*ns*	2.7	*ns*
RGPD3	RANBP2-like and GRIP domain containing 3	*ns*	2.6	*ns*
NPIPB3	nuclear pore complex interacting protein family, member B3	*ns*	2.6	*ns*
NPIPB9	nuclear pore complex interacting protein family, member B9	*ns*	2.6	*ns*
PCP4	Purkinje cell protein 4	*ns*	2.6	*ns*
FILIP1	filamin A interacting protein 1	*ns*	2.6	*ns*
ADAMTSL3	ADAMTS like 3	*ns*	2.6	*ns*
PEAK1	pseudopodium-enriched atypical kinase 1	2.6	*ns*	*ns*
H2BC21	H2B clustered histone 21	*ns*	2.6	*ns*
ATXN7	ataxin 7	*ns*	2.6	*ns*
PITX2	paired-like homeodomain 2	*ns*	2.6	*ns*
IL36RN	interleukin 36 receptor antagonist	*ns*	2.6	*ns*
CPPED1	calcineurin-like phosphoesterase domain containing 1	*ns*	2.6	*ns*
GRIK1	glutamate receptor, ionotropic, kainate 1	*ns*	2.6	*ns*
LARP4B	La ribonucleoprotein domain family, member 4B	*ns*	2.6	*ns*
LOC105379161	uncharacterized LOC105379161	*ns*	2.6	*ns*
DLG1	discs, large homolog 1 (Drosophila)	*ns*	2.6	*ns*
NPIPB5	nuclear pore complex interacting protein family, member B5	*ns*	2.6	*ns*
RMI2	RecQ mediated genome instability 2	*ns*	2.6	*ns*
STEAP3	STEAP family member 3, metalloreductase	*ns*	2.6	*ns*
CCDC125	coiled-coil domain containing 125	*ns*	2.6	*ns*
PCP4L1	Purkinje cell protein 4 like 1	*ns*	2.6	*ns*
TRIM33	tripartite motif containing 33	*ns*	2.6	*ns*
MTMR1	myotubularin related protein 1	*ns*	2.6	*ns*
RBM22	RNA binding motif protein 22	*ns*	2.6	*ns*
PPP1R9A	protein phosphatase 1, regulatory subunit 9A	*ns*	2.6	*ns*
SIK3	SIK family kinase 3	*ns*	2.6	*ns*
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	2.6	*ns*	*ns*
LINC00643	long intergenic non-protein coding RNA 643	*ns*	2.6	*ns*
TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	*ns*	2.6	*ns*
RBL1	retinoblastoma-like 1	*ns*	2.6	*ns*
KCNN4	potassium channel, calcium activated intermediate	*ns*	2.6	*ns*
LOC105374155	uncharacterized LOC105374155	*ns*	2.6	*ns*
ABCA5	ATP binding cassette subfamily A member 5	*ns*	2.6	*ns*
RBBP7	retinoblastoma binding protein 7	*ns*	2.6	*ns*
EFNB2	ephrin-B2	2.6	*ns*	*ns*
LINC01061	long intergenic non-protein coding RNA 1061	*ns*	2.6	*ns*
SMAD7	SMAD family member 7	*ns*	2.6	*ns*
LOC100288069	uncharacterized LOC100288069	*ns*	2.5	*ns*
GPD1L	glycerol-3-phosphate dehydrogenase 1-like	*ns*	2.5	*ns*
FAR2	fatty acyl-CoA reductase 2	*ns*	2.5	*ns*
KCTD3	potassium channel tetramerization domain containing 3	*ns*	2.5	*ns*
ACBD6	acyl-CoA binding domain containing 6	*ns*	2.5	*ns*
SLAIN1	SLAIN motif family member 1	2.5	*ns*	*ns*
TRIM55	tripartite motif containing 55	*ns*	2.5	*ns*
BAGE2	B melanoma antigen family, member 2	*ns*	2.5	*ns*
LOC100996442	uncharacterized LOC100996442	*ns*	2.5	*ns*
MCUB	mitochondrial calcium uniporter dominant negative subunit beta	*ns*	2.5	*ns*
UTRN	utrophin	2.5	*ns*	*ns*



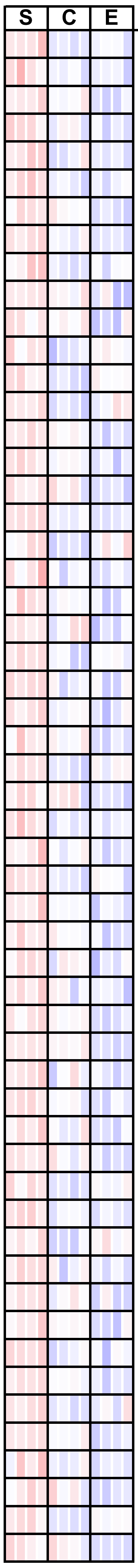
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
RFTN2	raftlin family member 2	2.5	*ns*	*ns*
MTM1	myotubularin 1	*ns*	2.5	*ns*
ENOSF1	enolase superfamily member 1	*ns*	2.5	*ns*
TBC1D32	TBC1 domain family, member 32	*ns*	2.5	*ns*
KCTD4	potassium channel tetramerization domain containing 4	*ns*	2.5	*ns*
DIO3	deiodinase, iodothyronine, type III	*ns*	2.5	*ns*
GAS2L3	growth arrest-specific 2 like 3	*ns*	2.5	*ns*
MCM3	minichromosome maintenance complex component 3	*ns*	2.5	*ns*
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	*ns*	2.5	*ns*
RGPD4	RANBP2-like and GRIP domain containing 4	*ns*	2.5	*ns*
FREM1	FRAS1 related extracellular matrix 1	*ns*	2.5	*ns*
ZNF22-AS1	ZNF22 antisense RNA 1	2.5	*ns*	*ns*
SPDYE2B	speedy	*ns*	2.5	*ns*
TKT	transketolase	*ns*	2.5	*ns*
YTHDC1	YTH domain containing 1	*ns*	2.5	*ns*
SLC2A11	solute carrier family 2 (facilitated glucose transporter), member 11	*ns*	2.5	*ns*
SPDYE2	speedy	*ns*	2.5	*ns*
GINS1	GINS complex subunit 1 (Psf1 homolog)	*ns*	2.5	*ns*
LOC100506514	uncharacterized LOC100506514	*ns*	2.5	*ns*
CAVIN2	caveolae associated protein 2	2.5	*ns*	*ns*
AMOTL1	angiomotin like 1	*ns*	2.5	*ns*
MDM4	MDM4, p53 regulator	*ns*	2.4	*ns*
SMS	spermine synthase	*ns*	2.4	*ns*
SMG1P2	SMG1 pseudogene 2	*ns*	2.4	*ns*
LARP1B	La ribonucleoprotein domain family, member 1B	*ns*	2.4	*ns*
AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	*ns*	2.4	*ns*
SMG1P3	SMG1 pseudogene 3	*ns*	2.4	*ns*
PAXBP1	PAX3 and PAX7 binding protein 1	*ns*	2.4	*ns*
LOC100128242	uncharacterized LOC100128242	*ns*	2.4	*ns*
PTPRK	protein tyrosine phosphatase, receptor type, K	*ns*	2.4	*ns*
LOC401585	uncharacterized LOC401585	*ns*	2.4	*ns*
HMGN2	high mobility group nucleosomal binding domain 2	*ns*	2.4	*ns*
GLI3	GLI family zinc finger 3	*ns*	2.4	*ns*
TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	*ns*	2.4	*ns*
NR2F1-AS1	NR2F1 antisense RNA 1	2.4	*ns*	*ns*
DIAPH2-AS1	DIAPH2 antisense RNA 1	*ns*	2.4	*ns*
TCAM1P	testicular cell adhesion molecule 1, pseudogene	*ns*	2.4	*ns*
KCTD1	potassium channel tetramerization domain containing 1	*ns*	2.4	*ns*
EXTL2	exostosin-like glycosyltransferase 2	*ns*	2.4	*ns*
LOC105379272	putative ankyrin repeat domain-containing protein 20A12 pseudogene	*ns*	2.4	*ns*
KLHL5	kelch-like family member 5	*ns*	2.4	*ns*
HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	*ns*	2.4	*ns*
SNORD51	small nucleolar RNA, C	*ns*	2.4	*ns*
LOC113230	uncharacterized protein LOC113230	*ns*	2.4	*ns*
CBX5	chromobox homolog 5	*ns*	2.4	*ns*
LINC01004	long intergenic non-protein coding RNA 1004	*ns*	2.4	*ns*
HEXIM1	hexamethylene bis-acetamide inducible 1	*ns*	2.4	*ns*
C4orf19	chromosome 4 open reading frame 19	*ns*	2.4	*ns*
ZNF507	zinc finger protein 507	*ns*	2.4	*ns*
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	2.4	*ns*	*ns*
CENATAC	centrosomal AT-AC splicing factor	*ns*	2.4	*ns*
MYO9A	myosin IXA	*ns*	2.4	*ns*
SPAG5	sperm associated antigen 5	*ns*	2.4	*ns*
HOPX	HOP homeobox	*ns*	2.4	*ns*
STOM	stomatin	2.4	*ns*	*ns*



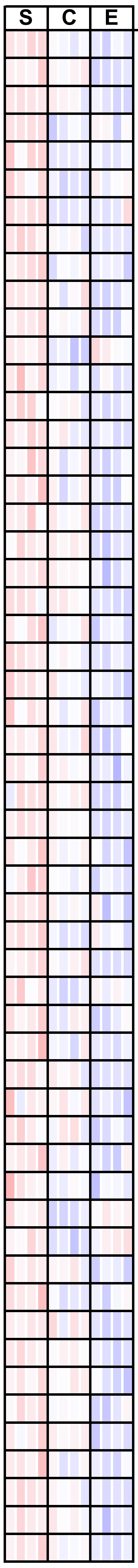
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
TBX4	T-box 4	*ns*	*2.4*	*ns*
SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1-like	*ns*	*2.4*	*ns*
MGST3	microsomal glutathione S-transferase 3	*ns*	*2.4*	*ns*
LOC553103	uncharacterized LOC553103	*ns*	*2.4*	*ns*
LOC400655	uncharacterized LOC400655	*ns*	*2.4*	*ns*
FER1L4	fer-1-like family member 4, pseudogene (functional)	*ns*	*2.4*	*ns*
MED13	mediator complex subunit 13	*ns*	*2.4*	*ns*
LOC105379520	uncharacterized LOC105379520	*ns*	*2.4*	*ns*
NRF1	nuclear respiratory factor 1	*ns*	*2.4*	*ns*
GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	*ns*	*2.4*	*ns*
MTMR7	myotubularin related protein 7	*ns*	*2.4*	*ns*
TLCD5	TLC domain containing 5	*ns*	*2.4*	*ns*
LOC101927391	uncharacterized LOC101927391	*ns*	*2.4*	*ns*
SIRPA	signal-regulatory protein alpha	2.4	*ns*	*ns*
TP53TG3D	TP53 target 3D	*ns*	*2.4*	*ns*
EXOC2	exocyst complex component 2	*ns*	*2.4*	*ns*
JAM3	junctional adhesion molecule 3	*ns*	*2.4*	*ns*
N4BP2	NEDD4 binding protein 2	*ns*	*2.4*	*ns*
RANBP17	RAN binding protein 17	*ns*	*2.4*	*ns*
CPEB4	cytoplasmic polyadenylation element binding protein 4	2.4	*ns*	*ns*
SMG1P5	SMG1 pseudogene 5	*ns*	*2.4*	*ns*
MVB12B	multivesicular body subunit 12B	*ns*	*2.4*	*ns*
CEP68	centrosomal protein 68kDa	*ns*	*2.4*	*ns*
BAZ2B	bromodomain adjacent to zinc finger domain 2B	*ns*	*2.4*	*ns*
AHCYL2	adenosylhomocysteinase-like 2	*ns*	*2.4*	*ns*
MFSD2A	major facilitator superfamily domain containing 2A	*ns*	*2.4*	*ns*
FDFT1	farnesyl-diphosphate farnesyltransferase 1	*ns*	*2.3*	*ns*
PLEKHA7	pleckstrin homology domain containing, family A member 7	*ns*	*2.3*	*ns*
GABARAPL1	GABA(A) receptor-associated protein like 1	*ns*	*2.3*	*ns*
HID1	HID1 domain containing	*ns*	*2.3*	*ns*
DDB1	damage-specific DNA binding protein 1	*ns*	*2.3*	*ns*
FAM135A	family with sequence similarity 135, member A	2.3	*ns*	*ns*
TSL	testis-expressed, seven-twelve, leukemia	*ns*	*2.3*	*ns*
PAK6	p21 protein (Cdc42	*ns*	*2.3*	*ns*
ILDR1	immunoglobulin-like domain containing receptor 1	2.3	*ns*	*ns*
TMEM63A	transmembrane protein 63A	*ns*	*2.3*	*ns*
TULP4	tubby like protein 4	*ns*	*2.3*	*ns*
YAP1	Yes-associated protein 1	*ns*	*2.3*	*ns*
BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	*ns*	*2.3*	*ns*
ZNF721	zinc finger protein 721	*ns*	*2.3*	*ns*
SH3D21	SH3 domain containing 21	*ns*	*2.3*	*ns*
CTHRC1	collagen triple helix repeat containing 1	*ns*	*2.3*	*ns*
LPCAT3	lysophosphatidylcholine acyltransferase 3	*ns*	*2.3*	*ns*
MIR548AL	microRNA 548al	*ns*	*2.3*	*ns*
CENPU	centromere protein U	*ns*	*2.3*	*ns*
LOC101059936	uncharacterized LOC101059936	*ns*	*2.3*	*ns*
LOC105374845	uncharacterized LOC105374845	*ns*	*2.3*	*ns*
ESRP2	epithelial splicing regulatory protein 2	*ns*	*2.3*	*ns*
SPDYE16	speedy	*ns*	*2.3*	*ns*
LENG8	leukocyte receptor cluster (LRC) member 8	*ns*	*2.3*	*ns*
LOC100289230	uncharacterized LOC100289230	*ns*	*2.3*	*ns*
LINC01036	long intergenic non-protein coding RNA 1036	*ns*	*2.3*	*ns*
TIGD2	tigger transposable element derived 2	*ns*	*2.3*	*ns*
BEX4	brain expressed X-linked 4	*ns*	*2.3*	*ns*
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	2.3	*ns*	*ns*



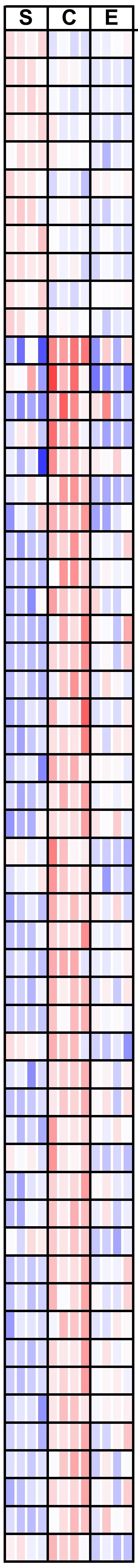
		Linear Fold Change (*ns*=no significant difference)		
Symbol	Name	S vs C	S vs E	E vs C
HP1BP3	heterochromatin protein 1, binding protein 3	*ns*	2.3	*ns*
KMT2C	lysine (K)-specific methyltransferase 2C	*ns*	2.3	*ns*
PITPNA	phosphatidylinositol transfer protein, alpha	*ns*	2.3	*ns*
NIN	ninein (GSK3B interacting protein)	*ns*	2.3	*ns*
MCM9	minichromosome maintenance 9 homologous recombination repair factor	*ns*	2.3	*ns*
DUS2	dihydrouridine synthase 2	*ns*	2.3	*ns*
STARD13	StAR-related lipid transfer domain containing 13	*ns*	2.3	*ns*
FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2	*ns*	2.3	*ns*
BRWD1	bromodomain and WD repeat domain containing 1	*ns*	2.3	*ns*
PMP22	peripheral myelin protein 22	2.3	*ns*	*ns*
RICTOR	RPTOR independent companion of MTOR, complex 2	*ns*	2.3	*ns*
WASH5P	WAS protein family homolog 5 pseudogene	*ns*	2.3	*ns*
MCM4	minichromosome maintenance complex component 4	*ns*	2.3	*ns*
SIAH2	siah E3 ubiquitin protein ligase 2	*ns*	2.3	*ns*
LOC100506314	uncharacterized LOC100506314	*ns*	2.3	*ns*
OMG	oligodendrocyte myelin glycoprotein	*ns*	2.3	*ns*
NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	*ns*	2.3	*ns*
ACER3	alkaline ceramidase 3	*ns*	2.3	*ns*
BRAF	B-Raf proto-oncogene, serine	*ns*	2.3	*ns*
GTF2IP4	general transcription factor IIi, pseudogene 4	*ns*	2.3	*ns*
TLK1	tousled-like kinase 1	*ns*	2.3	*ns*
CSRP2	cysteine and glycine-rich protein 2	*ns*	2.3	*ns*
PDE4DIP	phosphodiesterase 4D interacting protein	*ns*	2.2	*ns*
GTF2IP1	general transcription factor IIi pseudogene 1	*ns*	2.2	*ns*
HSPD1	heat shock 60kDa protein 1 (chaperonin)	*ns*	2.2	*ns*
RSKR	ribosomal protein S6 kinase related	*ns*	2.2	*ns*
GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	*ns*	2.2	*ns*
PIR	pirin	2.2	*ns*	*ns*
BLMH	bleomycin hydrolase	*ns*	2.2	*ns*
PTPN9	protein tyrosine phosphatase, non-receptor type 9	2.2	*ns*	*ns*
WSB1	WD repeat and SOCS box containing 1	*ns*	2.2	*ns*
STK3	serine	*ns*	2.2	*ns*
SIPA1L1	signal-induced proliferation-associated 1 like 1	*ns*	2.2	*ns*
LOC102723575	uncharacterized LOC102723575	*ns*	2.2	*ns*
TMEM168	transmembrane protein 168	*ns*	2.2	*ns*
LINC00885	long intergenic non-protein coding RNA 885	*ns*	2.2	*ns*
PELI1	pellino E3 ubiquitin protein ligase 1	2.2	*ns*	*ns*
SLC35B4	solute carrier family 35 (UDP-xylose	*ns*	2.2	*ns*
CPT2	carnitine palmitoyltransferase 2	*ns*	2.2	*ns*
MYORG	myogenesis regulating glycosidase (putative)	*ns*	2.2	*ns*
DIPK2A	divergent protein kinase domain 2A	*ns*	2.2	*ns*
TMEM139	transmembrane protein 139	*ns*	2.2	*ns*
ARL4A	ADP-ribosylation factor like GTPase 4A	2.2	*ns*	*ns*
ABHD4	abhydrolase domain containing 4	2.2	*ns*	*ns*
GSR	glutathione reductase	2.2	*ns*	*ns*
CCDC171	coiled-coil domain containing 171	*ns*	2.2	*ns*
SMARCA2	SWI	*ns*	2.2	*ns*
LOC157860	uncharacterized LOC157860	*ns*	2.2	*ns*
TOP1	topoisomerase (DNA) I	*ns*	2.2	*ns*
LOC105374417	uncharacterized LOC105374417	*ns*	2.2	*ns*
MCM7	minichromosome maintenance complex component 7	*ns*	2.2	*ns*
LOC105377601	uncharacterized LOC105377601	*ns*	2.2	*ns*
ZNF468	zinc finger protein 468	*ns*	2.2	*ns*
ASB4	ankyrin repeat and SOCS box containing 4	*ns*	2.2	*ns*
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1	2.2	*ns*	*ns*



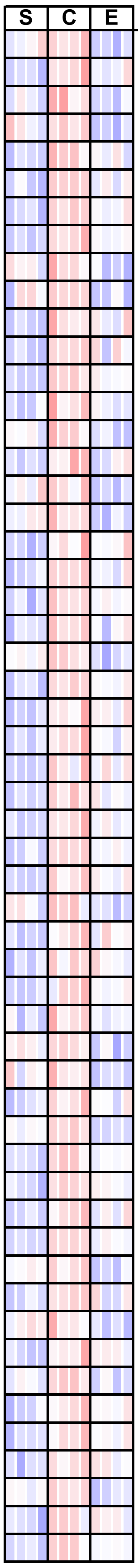
		Linear Fold Change (*ns*=no significant difference)		
Symbol	**Name**	**S** vs **C**	**S** vs **E**	**E** vs **C**
EGFLAM	EGF-like, fibronectin type III and laminin G domains	2.2	*ns*	*ns*
COL28A1	collagen, type XXVIII, alpha 1	*ns*	2.2	*ns*
HNRNPD	heterogeneous nuclear ribonucleoprotein D	*ns*	2.2	*ns*
TAPT1	transmembrane anterior posterior transformation 1	*ns*	2.2	*ns*
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	*ns*	2.2	*ns*
TCAF1	TRPM8 channel-associated factor 1	2.2	*ns*	*ns*
LRATD1	LRAT domain containing 1	*ns*	2.2	*ns*
NIBAN2	niban apoptosis regulator 2	*ns*	2.2	*ns*
ACO1	aconitase 1, soluble	2.2	*ns*	*ns*
TEAD3	TEA domain family member 3	*ns*	2.2	*ns*
ZNF587B	zinc finger protein 587B	*ns*	2.2	*ns*
FUCA1	fucosidase, alpha-L- 1, tissue	2.2	*ns*	*ns*
SNRK	SNF related kinase	2.2	*ns*	*ns*
ERG	v-ets avian erythroblastosis virus E26 oncogene homolog	2.2	*ns*	*ns*
RDX	radixin	*ns*	2.2	*ns*
LOC105375137	uncharacterized LOC105375137	*ns*	2.2	*ns*
HMGB2	high mobility group box 2	*ns*	2.2	*ns*
SNX27	sorting nexin family member 27	*ns*	2.2	*ns*
EMP2	epithelial membrane protein 2	2.2	*ns*	*ns*
TARID	TCF21 antisense RNA inducing promoter demethylation	*ns*	2.2	*ns*
RMC1	regulator of MON1-CCZ1	*ns*	2.2	*ns*
MXD1	MAX dimerization protein 1	*ns*	2.2	*ns*
CCND2	cyclin D2	2.2	*ns*	*ns*
LINC00894	long intergenic non-protein coding RNA 894	*ns*	2.2	*ns*
PSMD11	proteasome 26S subunit, non-ATPase 11	*ns*	2.2	*ns*
MIR551B	microRNA 551b	*ns*	2.2	*ns*
SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	2.2	*ns*	*ns*
ETFA	electron-transfer-flavoprotein, alpha polypeptide	*ns*	2.2	*ns*
SCML1	sex comb on midleg-like 1 (Drosophila)	2.1	*ns*	*ns*
SRSF4	serine	*ns*	2.1	*ns*
PRKG1	protein kinase, cGMP-dependent, type I	2.1	*ns*	*ns*
NT5DC3	5-nucleotidase domain containing 3	*ns*	2.1	*ns*
ANKRD10	ankyrin repeat domain 10	*ns*	2.1	*ns*
SLC16A4	solute carrier family 16, member 4	*ns*	2.1	*ns*
LINC01347	long intergenic non-protein coding RNA 1347	*ns*	2.1	*ns*
ALAS1	5-aminolevulinate synthase 1	*ns*	2.1	*ns*
AAK1	AP2 associated kinase 1	*ns*	2.1	*ns*
NOX5	NADPH oxidase, EF-hand calcium binding domain 5	*ns*	2.1	*ns*
CNOT6L	CCR4-NOT transcription complex subunit 6-like	*ns*	2.1	*ns*
SETD5	SET domain containing 5	*ns*	2.1	*ns*
LOC100132287	uncharacterized LOC100132287	*ns*	2.1	*ns*
PDE4B	phosphodiesterase 4B, cAMP-specific	2.1	*ns*	*ns*
HES1	hes family bHLH transcription factor 1	*ns*	2.1	*ns*
NUDT3	nudix hydrolase 3	2.1	*ns*	*ns*
AMBRA1	autophagy	*ns*	2.1	*ns*
TAS2R60	taste receptor, type 2, member 60	*ns*	2.1	*ns*
TGFBR3	transforming growth factor beta receptor III	*ns*	2.1	*ns*
C1QTNF1-AS1	C1QTNF1 antisense RNA 1	*ns*	2.1	*ns*
GRAMD2B	GRAM domain containing 2B	*ns*	2.1	*ns*
FXN	frataxin	2.1	*ns*	*ns*
DEDD	death effector domain containing	*ns*	2.1	*ns*
AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	*ns*	2.1	*ns*
ZNF552	zinc finger protein 552	*ns*	2.1	*ns*
MAP3K20	mitogen-activated protein kinase kinase kinase 20	2.1	*ns*	*ns*
FAM151B	family with sequence similarity 151, member B	*ns*	2.1	*ns*



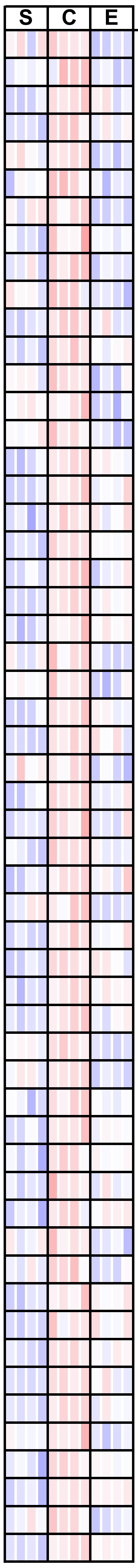
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
KLHL42	kelch-like family member 42	*ns*	2.1	*ns*
NASP	nuclear autoantigenic sperm protein (histone-binding)	*ns*	2.1	*ns*
CBWD5	COBW domain containing 5	*ns*	2.1	*ns*
CPT1A	carnitine palmitoyltransferase 1A (liver)	2.1	*ns*	*ns*
PTPN1	protein tyrosine phosphatase, non-receptor type 1	2.1	*ns*	*ns*
VSTM4	V-set and transmembrane domain containing 4	2.1	*ns*	*ns*
EPB41L3	erythrocyte membrane protein band 4.1-like 3	2.1	*ns*	*ns*
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	*ns*	2.1	*ns*
SQSTM1	sequestosome 1	*ns*	2.1	*ns*
MYO5B	myosin VB	*ns*	2.1	*ns*
TRA2B	transformer 2 beta homolog (Drosophila)	*ns*	2.1	*ns*
PSD3	pleckstrin and Sec7 domain containing 3	2.1	*ns*	*ns*
LOC100506504	uncharacterized LOC100506504	*ns*	2.1	*ns*
LRRC42	leucine rich repeat containing 42	*ns*	2.1	*ns*
NSG1	neuron specific gene family member 1	*ns*	2.1	*ns*
PGAP2	post-GPI attachment to proteins 2	*ns*	2.1	*ns*
NPIPA5	nuclear pore complex interacting protein family, member A5	*ns*	2.1	*ns*
MARVELD2	MARVEL domain containing 2	*ns*	2.1	*ns*
NUP58	nucleoporin 58kDa	*ns*	2.1	*ns*
HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	*ns*	2.1	*ns*
MCM8	minichromosome maintenance 8 homologous recombination repair factor	*ns*	2.1	*ns*
PCDH1	protocadherin 1	*ns*	2.1	*ns*
SLC19A1	solute carrier family 19 (folate transporter), member 1	*ns*	2.1	*ns*
C1orf21	chromosome 1 open reading frame 21	*ns*	2.1	*ns*
EPS8L1	EPS8-like 1	*ns*	2.1	*ns*
CHD2	chromodomain helicase DNA binding protein 2	*ns*	2.1	*ns*
HMGN1	high mobility group nucleosome binding domain 1	*ns*	2.1	*ns*
LCOR	ligand dependent nuclear receptor corepressor	*ns*	2.1	*ns*
NF1	neurofibromin 1	*ns*	2.1	*ns*
STRA6	stimulated by retinoic acid 6	*ns*	2.1	*ns*
HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	*ns*	2.1	*ns*
FGFR2	fibroblast growth factor receptor 2	*ns*	2.1	*ns*
KIRREL1	kirre like nephrin family adhesion molecule 1	2.1	*ns*	*ns*
MED12	mediator complex subunit 12	*ns*	2.1	*ns*
ANKRD44-IT1	ANKRD44 intronic transcript 1	2.1	*ns*	*ns*
LOC105376363	uncharacterized LOC105376363	*ns*	2.1	*ns*
NXF1	nuclear RNA export factor 1	*ns*	2.0	*ns*
TNPO1	transportin 1	*ns*	2.0	*ns*
LRP5	LDL receptor related protein 5	*ns*	2.0	*ns*
TCTEX1D4	Tctex1 domain containing 4	*ns*	2.0	*ns*
FAN1	FANCD2	*ns*	2.0	*ns*
LOC100288911	uncharacterized LOC100288911	*ns*	2.0	*ns*
ABI2	abl-interactor 2	2.0	*ns*	*ns*
MANSC1	MANSC domain containing 1	2.0	*ns*	*ns*
HPDL	4-hydroxyphenylpyruvate dioxygenase-like	*ns*	2.0	*ns*
APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	2.0	*ns*	*ns*
PLEKHA8	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	*ns*	2.0	*ns*
SCARNA7	small Cajal body-specific RNA 7	*ns*	2.0	*ns*
EP300-AS1	EP300 antisense RNA 1	*ns*	2.0	*ns*
RASAL2	RAS protein activator like 2	*ns*	2.0	*ns*
HMGA1	high mobility group AT-hook 1	*ns*	2.0	*ns*
NPIPA7	nuclear pore complex interacting protein family, member A7	*ns*	2.0	*ns*
ARID2	AT rich interactive domain 2 (ARID, RFX-like)	*ns*	2.0	*ns*
RBM39	RNA binding motif protein 39	*ns*	2.0	*ns*
SFPQ	splicing factor proline	*ns*	2.0	*ns*



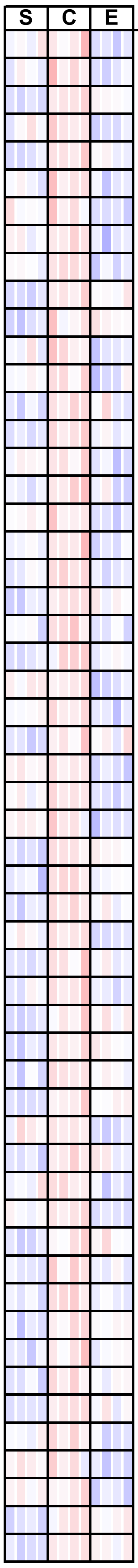
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LYPD6	LY6	2.0	*ns*	*ns*
EXOC6B	exocyst complex component 6B	*ns*	2.0	*ns*
DLG3	discs, large homolog 3 (Drosophila)	*ns*	2.0	*ns*
NEB	nebulin	*ns*	2.0	*ns*
AGFG1	ArfGAP with FG repeats 1	*ns*	2.0	*ns*
MOCS2	molybdenum cofactor synthesis 2	2.0	*ns*	*ns*
CASP3	caspase 3	*ns*	2.0	*ns*
LOC105370489	uncharacterized LOC105370489	*ns*	2.0	*ns*
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	*ns*	2.0	*ns*
HFE	hemochromatosis	2.0	*ns*	*ns*
CSTF2	cleavage stimulation factor, 3 pre-RNA, subunit 2	*ns*	2.0	*ns*
LEP	leptin	-19.5	*ns*	*ns*
OR5P2	olfactory receptor, family 5, subfamily P, member 2	*ns*	*ns*	-16.6
LOC105375837	uncharacterized LOC105375837	-12.4	*ns*	*ns*
LOC283299	uncharacterized LOC283299	*ns*	*ns*	-7.0
UCA1	urothelial cancer associated 1 (non-protein coding)	-6.4	*ns*	*ns*
LAMB4	laminin, beta 4	*ns*	*ns*	-6.4
AADACL2-AS1	AADACL2 antisense RNA 1	*ns*	*ns*	-5.8
ZFP42	ZFP42 zinc finger protein	-5.5	*ns*	*ns*
SLC17A8	solute carrier family 17 (vesicular glutamate transporter), member 8	-5.5	*ns*	*ns*
CA2	carbonic anhydrase II	-5.4	*ns*	*ns*
PPP4R4	protein phosphatase 4, regulatory subunit 4	-5.0	*ns*	*ns*
DOCK5	dedicator of cytokinesis 5	-5.0	*ns*	*ns*
ZNF300P1	zinc finger protein 300 pseudogene 1 (functional)	-4.9	*ns*	*ns*
LOC105370445	uncharacterized LOC105370445	-4.7	*ns*	*ns*
PLPP2	phospholipid phosphatase 2	-4.7	*ns*	*ns*
ARSK	arylsulfatase family, member K	-4.5	*ns*	*ns*
CNTNAP3	contactin associated protein-like 3	-4.4	*ns*	*ns*
FOS	FBJ murine osteosarcoma viral oncogene homolog	-4.3	*ns*	*ns*
LOC101927857	uncharacterized LOC101927857	*ns*	*ns*	-4.3
LOC102724484	uncharacterized LOC102724484	*ns*	*ns*	-4.2
LY6E	lymphocyte antigen 6 complex, locus E	-4.1	*ns*	*ns*
LOC100128979	uncharacterized LOC100128979	-4.0	*ns*	*ns*
HRAT17	heart tissue-associated transcript 17	-4.0	*ns*	*ns*
SFRP1	secreted frizzled-related protein 1	-4.0	*ns*	*ns*
BHLHE40	basic helix-loop-helix family, member e40	-4.0	*ns*	*ns*
TTK	TTK protein kinase	*ns*	*ns*	-3.9
NUAK2	NUAK family, SNF1-like kinase, 2	-3.9	*ns*	*ns*
BAIAP2L1	BAI1-associated protein 2-like 1	-3.8	*ns*	*ns*
LOC105372290	uncharacterized LOC105372290	-3.8	*ns*	*ns*
OR5E1P	olfactory receptor, family 5, subfamily E, member 1 pseudogene	*ns*	*ns*	-3.7
PRSS8	protease, serine, 8	-3.7	*ns*	*ns*
HCAR3	hydroxycarboxylic acid receptor 3	-3.7	*ns*	*ns*
SNORA3B	small nucleolar RNA, H	*ns*	*ns*	-3.7
LINC00294	long intergenic non-protein coding RNA 294	-3.7	*ns*	*ns*
EGLN3	egl-9 family hypoxia-inducible factor 3	-3.7	*ns*	*ns*
PGPEP1	pyroglutamyl-peptidase I	-3.6	*ns*	*ns*
SASH1	SAM and SH3 domain containing 1	-3.6	*ns*	*ns*
TET3	tet methylcytosine dioxygenase 3	-3.6	*ns*	*ns*
SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine transporter), member A3	-3.5	*ns*	*ns*
LINC00842	long intergenic non-protein coding RNA 842	-3.5	*ns*	*ns*
LOC102723446	uncharacterized LOC102723446	-3.5	*ns*	*ns*
F11R	F11 receptor	-3.5	*ns*	*ns*
NOS2	nitric oxide synthase 2, inducible	-3.5	*ns*	*ns*
COL21A1	collagen, type XXI, alpha 1	*ns*	*ns*	-3.5



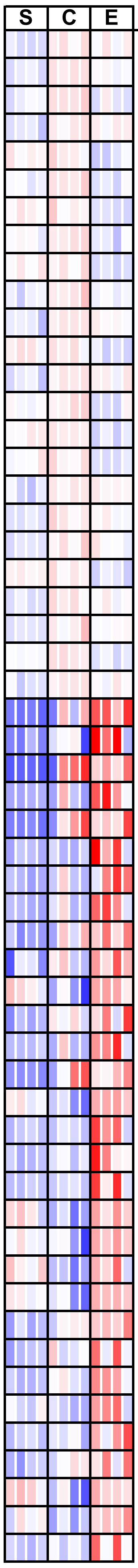
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
ACKR2	atypical chemokine receptor 2	*ns*	*ns*	*-3.5*
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-3.4	*ns*	*ns*
LOC105379109	uncharacterized LOC105379109	*ns*	*ns*	*-3.4*
MIG7	mig-7	*ns*	*ns*	*-3.4*
TGFB1	transforming growth factor beta 1	-3.4	*ns*	*ns*
ANKRD50	ankyrin repeat domain 50	-3.3	*ns*	*ns*
DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	-3.3	*ns*	*ns*
FLT1	fms-related tyrosine kinase 1	-3.3	*ns*	*ns*
ZNF726	zinc finger protein 726	*ns*	*ns*	*-3.3*
ADGRL3	adhesion G protein-coupled receptor L3	*ns*	*ns*	*-3.3*
LOC101927087	uncharacterized LOC101927087	-3.3	*ns*	*ns*
PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	-3.2	*ns*	*ns*
MAN2A1	mannosidase, alpha, class 2A, member 1	-3.2	*ns*	*ns*
BIRC7	baculoviral IAP repeat containing 7	-3.2	*ns*	*ns*
DSC2	desmocollin 2	*ns*	*ns*	*-3.2*
SLC1A6	solute carrier family 1 (high affinity aspartate	-3.1	*ns*	*ns*
CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1	*ns*	*ns*	*-3.1*
IGLJ2	immunoglobulin lambda joining 2	*ns*	*ns*	*-3.1*
RUSC2	RUN and SH3 domain containing 2	-3.1	*ns*	*ns*
GJA5	gap junction protein alpha 5	-3.1	*ns*	*ns*
LOC101928955	uncharacterized LOC101928955	-3.0	*ns*	*ns*
FBXO46	F-box protein 46	-3.0	*ns*	*ns*
LOC105376713	uncharacterized LOC105376713	*ns*	*ns*	*-3.0*
PANX1	pannexin 1	-3.0	*ns*	*ns*
TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	-3.0	*ns*	*ns*
ELF4	E74-like factor 4 (ets domain transcription factor)	-2.9	*ns*	*ns*
POTEG	POTE ankyrin domain family, member G	-2.9	*ns*	*ns*
PFKP	phosphofructokinase, platelet	-2.9	*ns*	*ns*
SH3BP5	SH3-domain binding protein 5 (BTK-associated)	-2.9	*ns*	*ns*
SLC6A8	solute carrier family 6 (neurotransmitter transporter), member 8	-2.9	*ns*	*ns*
TCP11L1	t-complex 11, testis-specific-like 1	-2.9	*ns*	*ns*
C18orf54	chromosome 18 open reading frame 54	*ns*	*ns*	*-2.9*
TCEA3	transcription elongation factor A (SII), 3	-2.9	*ns*	*ns*
SFN	stratifin	-2.9	*ns*	*ns*
SUGCT	succinyl-CoA:glutarate-CoA transferase	-2.9	*ns*	*ns*
LOC101929140	uncharacterized LOC101929140	-2.9	*ns*	*ns*
SLC44A5	solute carrier family 44, member 5	*ns*	*ns*	*-2.9*
RAB25	RAB25, member RAS oncogene family	*ns*	*ns*	*-2.9*
TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-2.9	*ns*	*ns*
SLC7A4	solute carrier family 7, member 4	*ns*	*ns*	*-2.9*
BMT2	base methyltransferase of 25S rRNA 2 homolog	-2.8	*ns*	*ns*
IPMK	inositol polyphosphate multikinase	-2.8	*ns*	*ns*
KIF21A	kinesin family member 21A	-2.8	*ns*	*ns*
TSC22D1	TSC22 domain family, member 1	-2.8	*ns*	*ns*
DSP	desmoplakin	*ns*	*ns*	*-2.8*
CORO2A	coronin, actin binding protein, 2A	-2.8	*ns*	*ns*
BRIP1	BRCA1 interacting protein C-terminal helicase 1	*ns*	*ns*	*-2.8*
SH3PXD2A	SH3 and PX domains 2A	-2.8	*ns*	*ns*
HYAL4	hyaluronoglucosaminidase 4	*ns*	*ns*	*-2.8*
LOC105378488	uncharacterized LOC105378488	-2.8	*ns*	*ns*
TAF5L	TAF5-like RNA polymerase II, p300	-2.7	*ns*	*ns*
LOC105376268	uncharacterized LOC105376268	-2.7	*ns*	*ns*
DSCR4	Down syndrome critical region 4	*ns*	*ns*	*-2.7*
ERO1A	endoplasmic reticulum oxidoreductase alpha	-2.7	*ns*	*ns*
SKIL	SKI-like proto-oncogene	-2.7	*ns*	*ns*



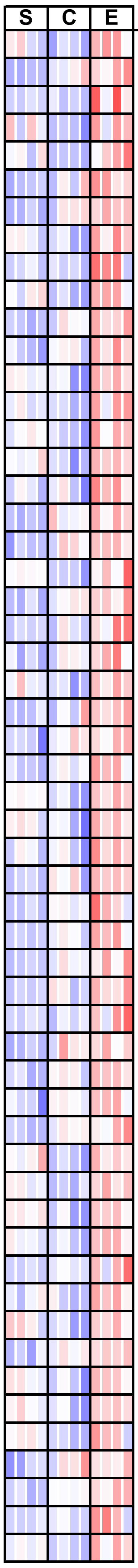
Symbol	Name	Linear Fold Change (*ns*=no significant difference)		
		S vs **C**	**S** vs **E**	**E** vs **C**
LOC100505918	uncharacterized LOC100505918	*ns*	*ns*	-2.7
LOC105370960	uncharacterized LOC105370960	*ns*	*ns*	-2.7
COL4A1	collagen, type IV, alpha 1	-2.7	*ns*	*ns*
CDK7	cyclin-dependent kinase 7	-2.7	*ns*	*ns*
LOC101927585	uncharacterized LOC101927585	*ns*	*ns*	-2.7
SUCNR1	succinate receptor 1	*ns*	*ns*	-2.7
LYPD3	LY6	*ns*	*ns*	-2.7
LOC105376938	uncharacterized LOC105376938	-2.7	*ns*	*ns*
LOC285500	uncharacterized LOC285500	*ns*	*ns*	-2.7
BRCA2	breast cancer 2, early onset	*ns*	*ns*	-2.7
SOWAHD	sosondowah ankyrin repeat domain family member D	-2.6	*ns*	*ns*
DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	-2.6	*ns*	*ns*
MME	membrane metallo-endopeptidase	*ns*	*ns*	-2.6
LOC102723985	uncharacterized LOC102723985	*ns*	*ns*	-2.6
ZNF90	zinc finger protein 90	*ns*	*ns*	-2.6
MFAP2	microfibrillar associated protein 2	-2.6	*ns*	*ns*
MBNL2	muscleblind-like splicing regulator 2	-2.6	*ns*	*ns*
LOC101927027	uncharacterized LOC101927027	-2.6	*ns*	*ns*
PRKD3	protein kinase D3	-2.6	*ns*	*ns*
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-2.6	*ns*	*ns*
VAV2	vav 2 guanine nucleotide exchange factor	-2.6	*ns*	*ns*
MOB3A	MOB kinase activator 3A	-2.5	*ns*	*ns*
OVOL1	ovo-like zinc finger 1	*ns*	*ns*	-2.5
ARHGAP24	Rho GTPase activating protein 24	*ns*	*ns*	-2.5
COL4A2	collagen, type IV, alpha 2	-2.5	*ns*	*ns*
GPX3	glutathione peroxidase 3	-2.5	*ns*	*ns*
ZNF662	zinc finger protein 662	*ns*	*ns*	-2.5
PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-2.5	*ns*	*ns*
PROSER2-AS1	PROSER2 antisense RNA 1	-2.5	*ns*	*ns*
ZNF100	zinc finger protein 100	-2.5	*ns*	*ns*
MFAP5	microfibrillar associated protein 5	-2.5	*ns*	*ns*
PLIN2	perilipin 2	*ns*	*ns*	-2.5
SLC10A7	solute carrier family 10, member 7	-2.5	*ns*	*ns*
SOWAHC	sosondowah ankyrin repeat domain family member C	-2.5	*ns*	*ns*
HYI	hydroxypyruvate isomerase (putative)	-2.5	*ns*	*ns*
PLAAT3	phospholipase A and acyltransferase 3	-2.4	*ns*	*ns*
HMGN3-AS1	HMGN3 antisense RNA 1	*ns*	*ns*	-2.4
PLCL2	phospholipase C-like 2	*ns*	*ns*	-2.4
SH3BP5-AS1	SH3BP5 antisense RNA 1	-2.4	*ns*	*ns*
JPT2	Jupiter microtubule associated homolog 2	-2.4	*ns*	*ns*
AP3S1	adaptor-related protein complex 3, sigma 1 subunit	-2.4	*ns*	*ns*
CHRDL2	chordin-like 2	-2.4	*ns*	*ns*
SCAMP1	secretory carrier membrane protein 1	-2.4	*ns*	*ns*
TK1	thymidine kinase 1, soluble	*ns*	*ns*	-2.4
CCSER1	coiled-coil serine rich protein 1	*ns*	*ns*	-2.4
NDST1	N-deacetylase	-2.4	*ns*	*ns*
PTH1R	parathyroid hormone 1 receptor	-2.4	*ns*	*ns*
ACTA1	actin, alpha 1, skeletal muscle	-2.4	*ns*	*ns*
PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	-2.4	*ns*	*ns*
ZBTB2	zinc finger and BTB domain containing 2	-2.4	*ns*	*ns*
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	*ns*	*ns*	-2.4
CCNG2	cyclin G2	-2.4	*ns*	*ns*
PARP14	poly(ADP-ribose) polymerase family member 14	-2.4	*ns*	*ns*
SLC27A6	solute carrier family 27 (fatty acid transporter), member 6	*ns*	*ns*	-2.4
B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	-2.3	*ns*	*ns*



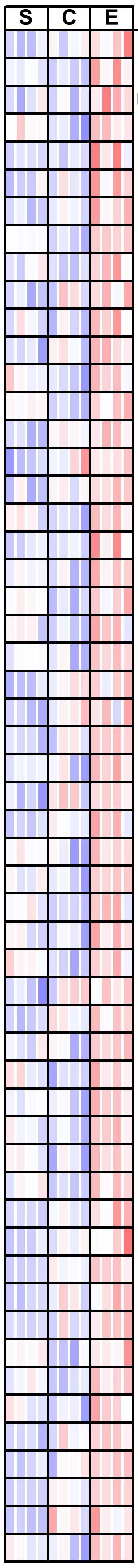
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PHKA2	phosphorylase kinase, alpha 2 (liver)	*ns*	*ns*	-2.3
ZNF93	zinc finger protein 93	*ns*	*ns*	-2.3
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	-2.3	*ns*	*ns*
IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	*ns*	*ns*	-2.3
GPR146	G protein-coupled receptor 146	-2.3	*ns*	*ns*
PLEKHA5	pleckstrin homology domain containing, family A member 5	*ns*	*ns*	-2.3
LMNB1	lamin B1	*ns*	*ns*	-2.3
BIRC5	baculoviral IAP repeat containing 5	*ns*	*ns*	-2.3
BZW2	basic leucine zipper and W2 domains 2	*ns*	*ns*	-2.3
MARVELD1	MARVEL domain containing 1	-2.3	*ns*	*ns*
LRP10	LDL receptor related protein 10	-2.3	*ns*	*ns*
LOC102723885	uncharacterized LOC102723885	*ns*	*ns*	-2.3
NR6A1	nuclear receptor subfamily 6, group A, member 1	*ns*	*ns*	-2.3
SLC16A3	solute carrier family 16 (monocarboxylate transporter), member 3	-2.3	*ns*	*ns*
FOXJ3	forkhead box J3	-2.3	*ns*	*ns*
RASL11B	RAS-like, family 11, member B	*ns*	*ns*	-2.3
FANCE	Fanconi anemia complementation group E	*ns*	*ns*	-2.3
LOC105373786	uncharacterized LOC105373786	*ns*	*ns*	-2.3
ESRP1	epithelial splicing regulatory protein 1	*ns*	*ns*	-2.3
RAB30	RAB30, member RAS oncogene family	*ns*	*ns*	-2.2
SLC39A11	solute carrier family 39, member 11	-2.2	*ns*	*ns*
ARL5B	ADP-ribosylation factor like GTPase 5B	*ns*	*ns*	-2.2
TAGLN2	transgelin 2	-2.2	*ns*	*ns*
CYB5R1	cytochrome b5 reductase 1	*ns*	*ns*	-2.2
DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	*ns*	*ns*	-2.2
MORF4L2	mortality factor 4 like 2	-2.2	*ns*	*ns*
MIR205HG	MIR205 host gene	*ns*	*ns*	-2.2
CENPJ	centromere protein J	*ns*	*ns*	-2.2
SORT1	sortilin 1	*ns*	*ns*	-2.2
CPVL	carboxypeptidase, vitellogenic-like	-2.2	*ns*	*ns*
NDFIP2	Nedd4 family interacting protein 2	-2.2	*ns*	*ns*
MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	-2.2	*ns*	*ns*
ITPRID2	ITPR interacting domain containing 2	*ns*	*ns*	-2.2
FAM78A	family with sequence similarity 78, member A	-2.2	*ns*	*ns*
KRT18P54	keratin 18 pseudogene 54	*ns*	*ns*	-2.2
NEK6	NIMA-related kinase 6	-2.2	*ns*	*ns*
LHX2	LIM homeobox 2	-2.2	*ns*	*ns*
CECR9	cat eye syndrome chromosome region, candidate 9 (non-protein coding)	-2.2	*ns*	*ns*
MAPK3	mitogen-activated protein kinase 3	-2.1	*ns*	*ns*
RPSAP58	ribosomal protein SA pseudogene 58	*ns*	*ns*	-2.1
NFIL3	nuclear factor, interleukin 3 regulated	-2.1	*ns*	*ns*
KCNQ1OT1	KCNQ1 opposite strand	*ns*	*ns*	-2.1
FAM120AOS	family with sequence similarity 120A opposite strand	*ns*	*ns*	-2.1
LOC100131262	uncharacterized LOC100131262	-2.1	*ns*	*ns*
LOC101929460	uncharacterized LOC101929460	-2.1	*ns*	*ns*
NKRF	NFKB repressing factor	-2.1	*ns*	*ns*
GPR150	G protein-coupled receptor 150	-2.1	*ns*	*ns*
DLK2	delta-like 2 homolog (Drosophila)	-2.1	*ns*	*ns*
HACD2	3-hydroxyacyl-CoA dehydratase 2	-2.1	*ns*	*ns*
ARHGAP10	Rho GTPase activating protein 10	-2.1	*ns*	*ns*
FAM83D	family with sequence similarity 83, member D	*ns*	*ns*	-2.1
KNTC1	kinetochore associated 1	*ns*	*ns*	-2.1
LOC105377606	uncharacterized LOC105377606	*ns*	*ns*	-2.1
CLDND1	claudin domain containing 1	-2.1	*ns*	*ns*
EDEM2	ER degradation enhancer, mannosidase alpha-like 2	-2.1	*ns*	*ns*



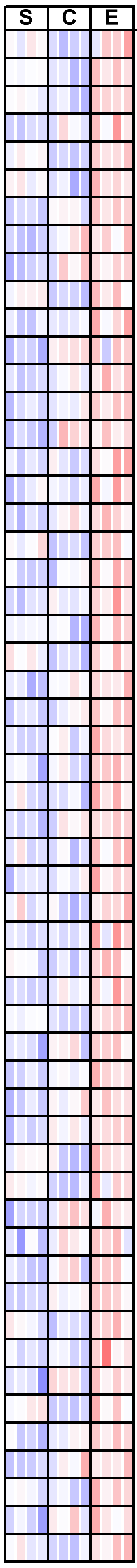
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LOC440461	Rho GTPase activating protein 27 pseudogene	-2.1	*ns*	*ns*
PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	-2.1	*ns*	*ns*
SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter), member 3	*ns*	*ns*	-2.1
EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	-2.1	*ns*	*ns*
ANXA3	annexin A3	*ns*	*ns*	-2.1
CSPP1	centrosome and spindle pole associated protein 1	*ns*	*ns*	-2.1
TRIM24	tripartite motif containing 24	*ns*	*ns*	-2.1
USP6NL	USP6 N-terminal like	*ns*	*ns*	-2.1
ACVR2B	activin A receptor type IIB	*ns*	*ns*	-2.1
ERBB3	erb-b2 receptor tyrosine kinase 3	-2.0	*ns*	*ns*
PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	-2.0	*ns*	*ns*
POLI	polymerase (DNA directed) iota	*ns*	*ns*	-2.0
RSPRY1	ring finger and SPRY domain containing 1	-2.0	*ns*	*ns*
PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	*ns*	*ns*	-2.0
SLC49A4	solute carrier family 49 member 4	*ns*	*ns*	-2.0
NEDD9	neural precursor cell expressed, developmentally down-regulated 9	*ns*	*ns*	-2.0
SNORA84	small nucleolar RNA, H	-2.0	*ns*	*ns*
LOXL1	lysyl oxidase-like 1	-2.0	*ns*	*ns*
GAA	glucosidase, alpha; acid	-2.0	*ns*	*ns*
ORC1	origin recognition complex subunit 1	*ns*	*ns*	-2.0
CDK17	cyclin-dependent kinase 17	-2.0	*ns*	*ns*
HK2	hexokinase 2	-2.0	*ns*	*ns*
PXDC1	PX domain containing 1	*ns*	*ns*	-2.0
KRTCAP3	keratinocyte associated protein 3	-2.0	*ns*	*ns*
CXCL9	chemokine (C-X-C motif) ligand 9	*ns*	-50.7	*ns*
PAEP	progestagen-associated endometrial protein	*ns*	-42.6	*ns*
OR5H14	olfactory receptor, family 5, subfamily H, member 14	*ns*	-25.9	*ns*
LOC100506530	uncharacterized LOC100506530	*ns*	-16.6	*ns*
TAC3	tachykinin 3	*ns*	-16.1	*ns*
LOC105374458	uncharacterized LOC105374458	*ns*	-15.4	*ns*
MYO16-AS1	MYO16 antisense RNA 1	*ns*	-12.6	*ns*
KLRF1	killer cell lectin-like receptor subfamily F, member 1	*ns*	-12.1	*ns*
SLAMF6	SLAM family member 6	*ns*	-11.3	*ns*
LOC105373334	uncharacterized LOC105373334	*ns*	-10.8	*ns*
C1orf54	chromosome 1 open reading frame 54	*ns*	*ns*	9.9
MMP3	matrix metallopeptidase 3	*ns*	-9.6	*ns*
SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	*ns*	-9.3	*ns*
LOC105379051	uncharacterized LOC105379051	*ns*	-9.2	*ns*
SRGN	serglycin	*ns*	*ns*	9.2
KLRF2	killer cell lectin-like receptor subfamily F, member 2	*ns*	-8.7	*ns*
KLRC2	killer cell lectin-like receptor subfamily C, member 2	*ns*	-8.6	*ns*
C4BPA	complement component 4 binding protein, alpha	*ns*	-8.6	*ns*
CAMK2D	calcium	*ns*	*ns*	8.0
CYBB	cytochrome b-245, beta polypeptide	*ns*	*ns*	7.3
CES1P1	carboxylesterase 1 pseudogene 1	*ns*	*ns*	7.0
VCAM1	vascular cell adhesion molecule 1	*ns*	*ns*	6.9
ANTXR1	anthrax toxin receptor 1	*ns*	-6.8	*ns*
AADAC	arylacetamide deacetylase	*ns*	-6.7	*ns*
GNLY	granulysin	*ns*	-6.7	*ns*
IGFBP5	insulin like growth factor binding protein 5	*ns*	*ns*	6.6
CCL8	chemokine (C-C motif) ligand 8	*ns*	-6.4	*ns*
TM4SF5	transmembrane 4 L six family member 5	*ns*	-6.3	*ns*
MS4A4A	membrane-spanning 4-domains, subfamily A, member 4A	*ns*	*ns*	6.3
GBP4	guanylate binding protein 4	*ns*	*ns*	6.3
MUC1	mucin 1, cell surface associated	*ns*	-6.2	*ns*



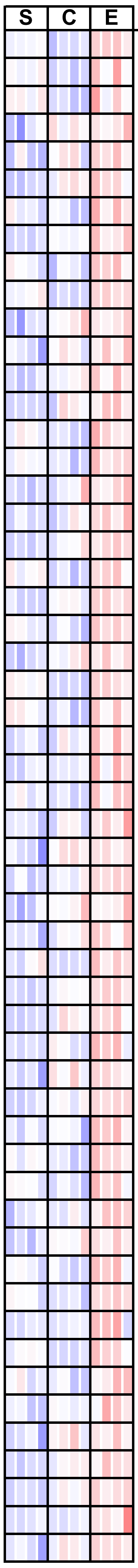
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
MMRN1	multimerin 1	*ns*	*ns*	*6.2*
OAS2	2-5-oligoadenylate synthetase 2	*ns*	*-6.2*	*ns*
NAPSB	napsin B aspartic peptidase, pseudogene	*ns*	*-5.6*	*ns*
ENPP4	ectonucleotide pyrophosphatase	*ns*	*ns*	*6.0*
TOX	thymocyte selection-associated high mobility group box	*ns*	*ns*	*5.9*
LINC01338	long intergenic non-protein coding RNA 1338	*ns*	*-5.9*	*ns*
NTN4	netrin 4	*ns*	*-5.8*	*ns*
C3AR1	complement component 3a receptor 1	*ns*	*ns*	*5.7*
CLTRN	collectrin, amino acid transport regulator	*ns*	*-5.3*	*ns*
EDNRA	endothelin receptor type A	*ns*	*ns*	*5.6*
ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	*ns*	*-5.4*	*ns*
S100A8	S100 calcium binding protein A8	*ns*	*-5.3*	*ns*
CD163	CD163 molecule	*ns*	*ns*	*5.3*
BICC1	BicC family RNA binding protein 1	*ns*	*ns*	*5.3*
LOC102724587	uncharacterized LOC102724587	*ns*	*ns*	*5.3*
VIM-AS1	VIM antisense RNA 1	*ns*	*ns*	*5.2*
GPR65	G protein-coupled receptor 65	*ns*	*-4.5*	*ns*
CLU	clusterin	*ns*	*-5.2*	*ns*
TDRD6	tudor domain containing 6	*ns*	*-5.1*	*ns*
ADGRF5	adhesion G protein-coupled receptor F5	*ns*	*ns*	*5.0*
EPHB2	EPH receptor B2	*ns*	*-5.0*	*ns*
LOC105374732	uncharacterized LOC105374732	*ns*	*-4.9*	*ns*
CRIP1	cysteine-rich protein 1 (intestinal)	*ns*	*-4.9*	*ns*
LOC100996713	uncharacterized LOC100996713	*ns*	*ns*	*4.8*
SEMA5A	semaphorin 5A	*ns*	*-4.7*	*ns*
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	*ns*	*-4.7*	*ns*
ITGAD	integrin alpha D	*ns*	*-4.7*	*ns*
VSIG4	V-set and immunoglobulin domain containing 4	*ns*	*ns*	*4.7*
PROS1	protein S (alpha)	*ns*	*ns*	*4.6*
F3	coagulation factor III (thromboplastin, tissue factor)	*ns*	*ns*	*4.6*
PLXDC2	plexin domain containing 2	*ns*	*-4.5*	*ns*
LEFTY2	left-right determination factor 2	*ns*	*-4.5*	*ns*
ECM2	extracellular matrix protein 2, female organ and adipocyte specific	*ns*	*-4.5*	*ns*
MYL10	myosin light chain 10	*ns*	*-4.5*	*ns*
LOC101929531	uncharacterized LOC101929531	*ns*	*-4.5*	*ns*
GSTA1	glutathione S-transferase alpha 1	*ns*	*-4.4*	*ns*
DAW1	dynein assembly factor with WDR repeat domains 1	*ns*	*-4.4*	*ns*
TTC39C	tetratricopeptide repeat domain 39C	*ns*	*-4.4*	*ns*
DUSP23	dual specificity phosphatase 23	*ns*	*-4.4*	*ns*
SMCO3	single-pass membrane protein with coiled-coil domains 3	*ns*	*-4.4*	*ns*
CD44	CD44 molecule (Indian blood group)	*ns*	*ns*	*4.3*
SLC12A2	solute carrier family 12 (sodium	*ns*	*ns*	*4.3*
MAGEH1	MAGE family member H1	*ns*	*ns*	*4.3*
RNF125	ring finger protein 125, E3 ubiquitin protein ligase	*ns*	*ns*	*4.2*
PZP	pregnancy-zone protein	*ns*	*-4.2*	*ns*
EHD2	EH domain containing 2	*ns*	*ns*	*4.2*
CD109	CD109 molecule	*ns*	*ns*	*4.2*
CCN2	cellular communication network factor 2	*ns*	*-4.1*	*ns*
ITGA4	integrin alpha 4	*ns*	*ns*	*4.1*
SLC9A9	solute carrier family 9, subfamily A (NHE9, cation proton antiporter 9), member 9	*ns*	*ns*	*4.1*
KLRD1	killer cell lectin-like receptor subfamily D, member 1	*ns*	*ns*	*4.0*
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	*ns*	*-4.0*	*ns*
CRLF1	cytokine receptor-like factor 1	*ns*	*-4.0*	*ns*
PGM5-AS1	PGM5 antisense RNA 1	*ns*	*-4.0*	*ns*
PRKD1	protein kinase D1	*ns*	*ns*	*4.0*



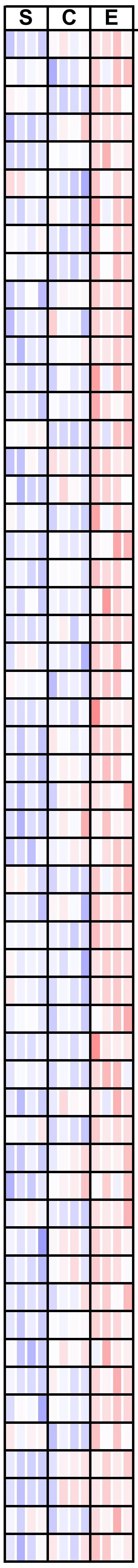
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker)	*ns*	-3.9	*ns*
TOB1	transducer of ERBB2, 1	*ns*	*ns*	3.9
LL22NC03-104C7.1	uncharacterized LOC105373004	*ns*	-3.7	*ns*
ACSS3	acyl-CoA synthetase short-chain family member 3	*ns*	*ns*	3.9
ADGRF1	adhesion G protein-coupled receptor F1	*ns*	-3.8	*ns*
KCNQ5-IT1	KCNQ5 intronic transcript 1	*ns*	-3.8	*ns*
CD69	CD69 molecule	*ns*	-3.8	*ns*
GIMAP7	GTPase, IMAP family member 7	*ns*	*ns*	3.8
MYH11	myosin, heavy chain 11, smooth muscle	*ns*	*ns*	3.7
LOC102724156	uncharacterized LOC102724156	*ns*	-3.7	*ns*
SNORA47	small nucleolar RNA, H	*ns*	*ns*	3.7
PMCH	pro-melanin-concentrating hormone	*ns*	-3.7	*ns*
MAP9	microtubule-associated protein 9	*ns*	*ns*	3.7
GIMAP4	GTPase, IMAP family member 4	*ns*	*ns*	3.7
LOC105377590	uncharacterized LOC105377590	*ns*	-3.7	*ns*
OAS3	2-5-oligoadenylate synthetase 3	*ns*	-3.7	*ns*
PSENEN	presenilin enhancer gamma secretase subunit	*ns*	-3.6	*ns*
PCGF5	polycomb group ring finger 5	*ns*	*ns*	3.6
CD82	CD82 molecule	*ns*	-3.6	*ns*
PLEK	pleckstrin	*ns*	*ns*	3.6
PRLR	prolactin receptor	*ns*	*ns*	3.6
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	*ns*	*ns*	3.6
GASK1B	golgi associated kinase 1B	*ns*	*ns*	3.6
XAF1	XIAP associated factor 1	*ns*	-3.6	*ns*
GPC4	glypican 4	*ns*	-3.5	*ns*
MORN2	MORN repeat containing 2	*ns*	-3.5	*ns*
MPEG1	macrophage expressed 1	*ns*	*ns*	3.5
ZNF675	zinc finger protein 675	*ns*	-3.5	*ns*
PODNL1	podocan-like 1	*ns*	-3.5	*ns*
CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	*ns*	*ns*	3.5
GDAP1	ganglioside induced differentiation associated protein 1	*ns*	*ns*	3.5
HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6	*ns*	*ns*	3.5
DYNC2LI1	dynein, cytoplasmic 2, light intermediate chain 1	*ns*	*ns*	3.5
ITM2A	integral membrane protein 2A	*ns*	*ns*	3.5
SLC30A4	solute carrier family 30 (zinc transporter), member 4	*ns*	-3.5	*ns*
KCNA4	potassium channel, voltage gated shaker related subfamily A, member 4	*ns*	-3.5	*ns*
ALOX5AP	arachidonate 5-lipoxygenase-activating protein	*ns*	*ns*	3.4
EDIL3	EGF-like repeats and discoidin I-like domains 3	*ns*	*ns*	3.4
BDH2	3-hydroxybutyrate dehydrogenase, type 2	*ns*	*ns*	3.4
CD86	CD86 molecule	*ns*	*ns*	3.4
RETREG1	reticulophagy regulator 1	*ns*	*ns*	3.4
PDE8B	phosphodiesterase 8B	*ns*	*ns*	3.4
LOC101928919	uncharacterized LOC101928919	*ns*	-3.4	*ns*
LRRC15	leucine rich repeat containing 15	*ns*	-3.4	*ns*
KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	*ns*	-3.4	*ns*
TSPAN8	tetraspanin 8	*ns*	-3.4	*ns*
ROS1	ROS proto-oncogene 1 , receptor tyrosine kinase	*ns*	-3.3	*ns*
TEK	TEK tyrosine kinase, endothelial	*ns*	*ns*	3.3
FKBP5	FK506 binding protein 5	*ns*	*ns*	3.3
PRTFDC1	phosphoribosyl transferase domain containing 1	*ns*	*ns*	3.3
HACD1	3-hydroxyacyl-CoA dehydratase 1	*ns*	-3.3	*ns*
GADD45B	growth arrest and DNA-damage-inducible, beta	*ns*	-3.3	*ns*
CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	*ns*	-3.3	*ns*
MAMDC2-AS1	MAMDC2 antisense RNA 1	*ns*	-3.3	*ns*
MAF	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog	*ns*	*ns*	3.3



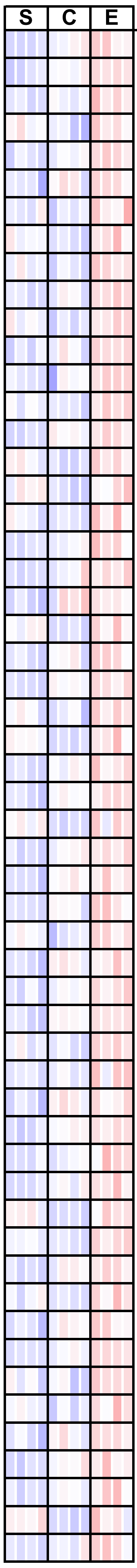
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
RHOJ	ras homolog family member J	*ns*	*ns*	3.3
VIM	vimentin	*ns*	*ns*	3.3
ZFAND4	zinc finger, AN1-type domain 4	*ns*	*ns*	3.3
WDR86-AS1	WDR86 antisense RNA 1	*ns*	-3.3	*ns*
ITPR1	inositol 1,4,5-trisphosphate receptor, type 1	*ns*	*ns*	3.3
ARRDC4	arrestin domain containing 4	*ns*	*ns*	3.3
ATP13A3	ATPase type 13A3	*ns*	-3.3	*ns*
MCAM	melanoma cell adhesion molecule	*ns*	-3.3	*ns*
SLC43A3	solute carrier family 43, member 3	*ns*	-3.3	*ns*
MIPOL1	mirror-image polydactyly 1	*ns*	*ns*	3.3
CCL5	chemokine (C-C motif) ligand 5	*ns*	-3.3	*ns*
APOC1	apolipoprotein C-I	*ns*	-3.2	*ns*
CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	*ns*	-3.2	*ns*
TTPAL	tocopherol (alpha) transfer protein-like	*ns*	-3.2	*ns*
STAB2	stabilin 2	*ns*	-3.2	*ns*
HSD17B14	hydroxysteroid (17-beta) dehydrogenase 14	*ns*	-3.2	*ns*
ZFP36	ZFP36 ring finger protein	*ns*	-3.2	*ns*
MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	*ns*	-3.2	*ns*
CDH13	cadherin 13	*ns*	*ns*	3.2
MIR3918	microRNA 3918	*ns*	-3.2	*ns*
PPDPF	pancreatic progenitor cell differentiation and proliferation factor	*ns*	-3.2	*ns*
LRP12	LDL receptor related protein 12	*ns*	*ns*	3.2
CADPS2	Ca++-dependent secretion activator 2	*ns*	*ns*	3.2
LOC105377134	uncharacterized LOC105377134	*ns*	-3.2	*ns*
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	*ns*	-3.2	*ns*
SLAMF8	SLAM family member 8	*ns*	-3.1	*ns*
RAB32	RAB32, member RAS oncogene family	*ns*	-3.1	*ns*
TREM2	triggering receptor expressed on myeloid cells 2	*ns*	*ns*	3.1
SMIM14	small integral membrane protein 14	*ns*	-3.1	*ns*
LINC01139	long intergenic non-protein coding RNA 1139	*ns*	*ns*	3.1
ABCC3	ATP binding cassette subfamily C member 3	*ns*	-3.1	*ns*
BTN3A2	butyrophilin, subfamily 3, member A2	*ns*	*ns*	3.1
ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	*ns*	-3.1	*ns*
TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	*ns*	*ns*	3.1
LINC00706	long intergenic non-protein coding RNA 706	*ns*	-3.1	*ns*
SRPX2	sushi-repeat containing protein, X-linked 2	*ns*	*ns*	3.1
PIGK	phosphatidylinositol glycan anchor biosynthesis class K	*ns*	-3.1	*ns*
IL15RA	interleukin 15 receptor, alpha	*ns*	-3.1	*ns*
PVR	poliovirus receptor	*ns*	-3.1	*ns*
SFT2D2	SFT2 domain containing 2	*ns*	-3.1	*ns*
FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	*ns*	*ns*	3.1
NID2	nidogen 2 (osteonidogen)	*ns*	*ns*	3.1
TMEM31	transmembrane protein 31	*ns*	-3.1	*ns*
LINC00484	long intergenic non-protein coding RNA 484	*ns*	-3.1	*ns*
PRXL2C	peroxiredoxin like 2C	*ns*	-3.1	*ns*
FLNA	filamin A, alpha	*ns*	-3.1	*ns*
C8orf48	chromosome 8 open reading frame 48	*ns*	*ns*	3.1
SERTM2	serine rich and transmembrane domain containing 2	*ns*	-3.1	*ns*
ANKRD36BP1	ankyrin repeat domain 36B pseudogene 1	*ns*	-3.1	*ns*
PLCB4	phospholipase C, beta 4	*ns*	*ns*	3.1
RPGRIP1L	RPGRIP1-like	*ns*	-3.1	*ns*
CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	*ns*	-3.0	*ns*
ATP8B4	ATPase, class I, type 8B, member 4	*ns*	*ns*	3.0
SAA1	serum amyloid A1	*ns*	-3.0	*ns*
PLCE1	phospholipase C, epsilon 1	*ns*	*ns*	3.0



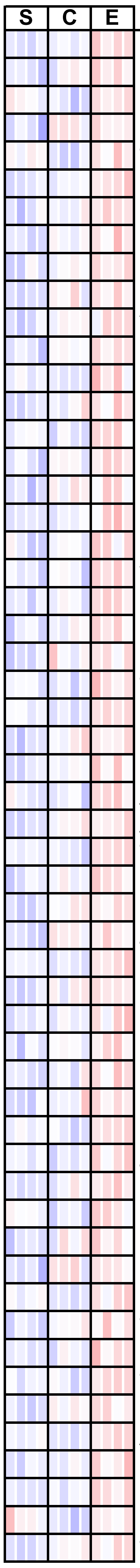
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
DEPP1	DEPP1 autophagy regulator	*ns*	*ns*	3.0
PKP4	plakophilin 4	*ns*	*ns*	3.0
ADGRD1	adhesion G protein-coupled receptor D1	*ns*	*ns*	3.0
GBP1	guanylate binding protein 1, interferon-inducible	*ns*	-3.0	*ns*
SNX16	sorting nexin 16	*ns*	-3.0	*ns*
OSR2	odd-skipped related transciption factor 2	*ns*	-3.0	*ns*
CHSY3	chondroitin sulfate synthase 3	*ns*	*ns*	3.0
IKZF3	IKAROS family zinc finger 3	*ns*	-3.0	*ns*
MED14OS	MED14 opposite strand	*ns*	*ns*	3.0
FGD5	FYVE, RhoGEF and PH domain containing 5	*ns*	*ns*	3.0
ZDHHC9	zinc finger, DHHC-type containing 9	*ns*	-3.0	*ns*
LINC01357	long intergenic non-protein coding RNA 1357	*ns*	-3.0	*ns*
DUSP1	dual specificity phosphatase 1	*ns*	-2.9	*ns*
LOC101927780	uncharacterized LOC101927780	*ns*	-2.9	*ns*
CACNA2D1	calcium channel, voltage-dependent, alpha 2	*ns*	*ns*	2.9
PAPSS2	3-phosphoadenosine 5-phosphosulfate synthase 2	*ns*	*ns*	2.9
BST2	bone marrow stromal cell antigen 2	*ns*	-2.9	*ns*
IRF8	interferon regulatory factor 8	*ns*	-2.9	*ns*
HLA-L	major histocompatibility complex, class I, L (pseudogene)	*ns*	-2.9	*ns*
CMTM7	CKLF-like MARVEL transmembrane domain containing 7	*ns*	*ns*	2.9
GNG4	guanine nucleotide binding protein (G protein), gamma 4	*ns*	-2.9	*ns*
AIF1	allograft inflammatory factor 1	*ns*	*ns*	2.9
DOP1B	DOP1 leucine zipper like protein B	*ns*	-2.9	*ns*
PYCARD	PYD and CARD domain containing	*ns*	*ns*	2.9
SPRED1	sprouty-related, EVH1 domain containing 1	*ns*	*ns*	2.9
KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	*ns*	-2.9	*ns*
PCDHB2	protocadherin beta 2	*ns*	-2.9	*ns*
NCKAP1L	NCK-associated protein 1-like	*ns*	*ns*	2.9
CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	*ns*	-2.9	*ns*
HLTF	helicase-like transcription factor	*ns*	-2.9	*ns*
LPCAT2	lysophosphatidylcholine acyltransferase 2	*ns*	-2.8	*ns*
TRIM21	tripartite motif containing 21	*ns*	-2.8	*ns*
RNF24	ring finger protein 24	*ns*	-2.8	*ns*
SLFN13	schlafen family member 13	*ns*	*ns*	2.8
SH3BGRL3	SH3 domain binding glutamate-rich protein like 3	*ns*	-2.8	*ns*
SELENOM	selenoprotein M	*ns*	-2.8	*ns*
CYBA	cytochrome b-245, alpha polypeptide	*ns*	-2.8	*ns*
ATP11C	ATPase, class VI, type 11C	*ns*	-2.8	*ns*
IFITM4P	interferon induced transmembrane protein 4 pseudogene	*ns*	-2.8	*ns*
CMC1	C-x(9)-C motif containing 1	*ns*	-2.8	*ns*
TUBA1A	tubulin, alpha 1a	*ns*	*ns*	2.8
LOC100506688	uncharacterized LOC100506688	*ns*	*ns*	2.8
LILRB4	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	*ns*	-2.7	*ns*
FOSL2	FOS-like antigen 2	*ns*	-2.7	*ns*
TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	*ns*	*ns*	2.7
ZNF32-AS1	ZNF32 antisense RNA 1	*ns*	*ns*	2.7
LOC101928047	uncharacterized LOC101928047	*ns*	-2.7	*ns*
ADAMTS9-AS2	ADAMTS9 antisense RNA 2	*ns*	*ns*	2.7
TENT5C	terminal nucleotidyltransferase 5C	*ns*	*ns*	2.7
STMN2	stathmin 2	*ns*	-2.7	*ns*
IFIT5	interferon-induced protein with tetratricopeptide repeats 5	*ns*	-2.7	*ns*
HABP4	hyaluronan binding protein 4	*ns*	-2.7	*ns*
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	*ns*	-2.7	*ns*
GGT2	gamma-glutamyltransferase 2	*ns*	-2.7	*ns*
CCDC80	coiled-coil domain containing 80	*ns*	-2.7	*ns*



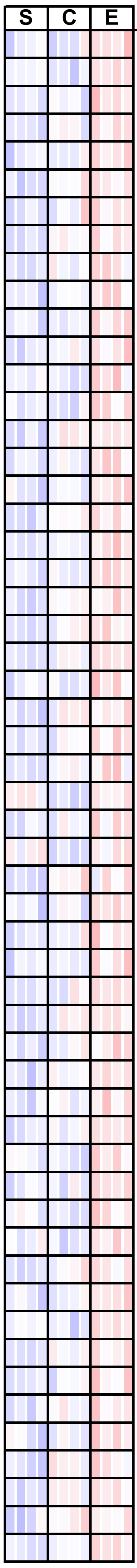
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	**S** vs **E**	**E** vs **C**
C12orf60	chromosome 12 open reading frame 60	*ns*	-2.7	*ns*
CLUAP1	clusterin associated protein 1	*ns*	*ns*	2.7
FNDC1	fibronectin type III domain containing 1	*ns*	*ns*	2.7
VAT1	vesicle amine transport 1	*ns*	-2.7	*ns*
TACR3	tachykinin receptor 3	*ns*	-2.7	*ns*
PIAS2	protein inhibitor of activated STAT 2	*ns*	*ns*	2.7
GRIA3	glutamate receptor, ionotropic, AMPA 3	*ns*	-2.7	*ns*
BICD1	bicaudal D homolog 1 (Drosophila)	*ns*	*ns*	2.7
CLIP3	CAP-GLY domain containing linker protein 3	*ns*	*ns*	2.6
SNX10	sorting nexin 10	*ns*	-2.6	*ns*
BST1	bone marrow stromal cell antigen 1	*ns*	-2.6	*ns*
C19orf53	chromosome 19 open reading frame 53	*ns*	-2.6	*ns*
MITF	microphthalmia-associated transcription factor	*ns*	-2.6	*ns*
CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	*ns*	-2.6	*ns*
KIF13B	kinesin family member 13B	*ns*	*ns*	2.6
LOX	lysyl oxidase	*ns*	-2.6	*ns*
MYDGF	myeloid-derived growth factor	*ns*	-2.6	*ns*
LACTB2	lactamase, beta 2	*ns*	*ns*	2.6
RSAD2	radical S-adenosyl methionine domain containing 2	*ns*	-2.6	*ns*
ERBIN	erbb2 interacting protein	*ns*	-2.6	*ns*
FBXO6	F-box protein 6	*ns*	-2.6	*ns*
TMEM176A	transmembrane protein 176A	*ns*	-2.6	*ns*
NAIP	NLR family, apoptosis inhibitory protein	*ns*	*ns*	2.6
CEP112	centrosomal protein 112kDa	*ns*	*ns*	2.6
C4A	complement component 4A (Rodgers blood group)	*ns*	-2.6	*ns*
RCN3	reticulocalbin 3, EF-hand calcium binding domain	*ns*	-2.6	*ns*
REX1BD	required for excision 1-B domain containing	*ns*	-2.6	*ns*
RECK	reversion-inducing-cysteine-rich protein with kazal motifs	*ns*	-2.6	*ns*
PTK2B	protein tyrosine kinase 2 beta	*ns*	-2.6	*ns*
AAMDC	adipogenesis associated, Mth938 domain containing	*ns*	-2.6	*ns*
ACOT9	acyl-CoA thioesterase 9	*ns*	*ns*	2.6
TMX3	thioredoxin-related transmembrane protein 3	*ns*	-2.6	*ns*
CD4	CD4 molecule	*ns*	*ns*	2.6
ADAP2	ArfGAP with dual PH domains 2	*ns*	*ns*	2.6
TMSB4XP4	thymosin beta 4, X-linked pseudogene 4	*ns*	*ns*	2.6
ATG4A	autophagy related 4A, cysteine peptidase	*ns*	*ns*	2.6
C4B	complement component 4B (Chido blood group)	*ns*	-2.6	*ns*
LOC100506388	uncharacterized LOC100506388	*ns*	*ns*	2.6
DIRAS2	DIRAS family, GTP-binding RAS-like 2	*ns*	-2.6	*ns*
SFMBT2	Scm-like with four mbt domains 2	*ns*	*ns*	2.6
ATRN	attractin	*ns*	-2.6	*ns*
ARHGAP31	Rho GTPase activating protein 31	*ns*	-2.5	*ns*
IQCK	IQ motif containing K	*ns*	*ns*	2.5
DRAM1	DNA-damage regulated autophagy modulator 1	*ns*	-2.5	*ns*
FKBP7	FK506 binding protein 7	*ns*	-2.5	*ns*
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	*ns*	-2.5	*ns*
SPSB1	splA	*ns*	-2.5	*ns*
CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	*ns*	-2.5	*ns*
APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	*ns*	-2.5	*ns*
TUBE1	tubulin, epsilon 1	*ns*	-2.5	*ns*
TRAF5	TNF receptor-associated factor 5	*ns*	*ns*	2.5
TCEAL1	transcription elongation factor A (SII)-like 1	*ns*	-2.5	*ns*
ENDOG	endonuclease G	*ns*	-2.5	*ns*
CRYAB	crystallin alpha B	*ns*	*ns*	2.5
PLBD2	phospholipase B domain containing 2	*ns*	-2.5	*ns*



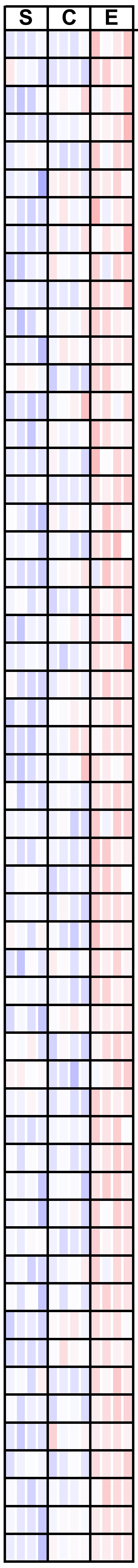
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
PLXNB2	plexin B2	*ns*	-2.5	*ns*
CAPNS1	calpain, small subunit 1	*ns*	-2.5	*ns*
CD300A	CD300a molecule	*ns*	-2.5	*ns*
HECTD2	HECT domain containing E3 ubiquitin protein ligase 2	*ns*	*ns*	2.5
CCDC107	coiled-coil domain containing 107	*ns*	-2.5	*ns*
HIF1A-AS2	HIF1A antisense RNA 2	*ns*	-2.5	*ns*
NPR2	natriuretic peptide receptor 2	*ns*	*ns*	2.5
RNF152	ring finger protein 152	*ns*	*ns*	2.5
CD84	CD84 molecule	*ns*	*ns*	2.5
TST	thiosulfate sulfurtransferase (rhodanese)	*ns*	-2.5	*ns*
EID1	EP300 interacting inhibitor of differentiation 1	*ns*	*ns*	2.5
TMEM176B	transmembrane protein 176B	*ns*	-2.5	*ns*
RGS10	regulator of G-protein signaling 10	*ns*	-2.5	*ns*
SOCS5	suppressor of cytokine signaling 5	*ns*	*ns*	2.5
SLC35B2	solute carrier family 35 (adenosine 3-phospho 5-phosphosulfate transporter), member B2	*ns*	-2.5	*ns*
LOC102724776	uncharacterized LOC102724776	*ns*	*ns*	2.5
CALHM5	calcium homeostasis modulator family member 5	*ns*	*ns*	2.5
TFEC	transcription factor EC	*ns*	*ns*	2.5
ABCC1	ATP binding cassette subfamily C member 1	*ns*	-2.5	*ns*
PARVA	parvin, alpha	*ns*	-2.5	*ns*
VWCE	von Willebrand factor C and EGF domains	*ns*	-2.3	*ns*
TNS1	tensin 1	*ns*	*ns*	2.4
WDR44	WD repeat domain 44	*ns*	-2.4	*ns*
GALC	galactosylceramidase	*ns*	-2.4	*ns*
ARL6	ADP-ribosylation factor like GTPase 6	*ns*	*ns*	2.4
CAVIN3	caveolae associated protein 3	*ns*	*ns*	2.4
PAPSS1	3-phosphoadenosine 5-phosphosulfate synthase 1	*ns*	-2.4	*ns*
JOSD2	Josephin domain containing 2	*ns*	-2.4	*ns*
ARHGAP20	Rho GTPase activating protein 20	*ns*	*ns*	2.4
TMEM219	transmembrane protein 219	*ns*	-2.4	*ns*
FAM8A1	family with sequence similarity 8, member A1	*ns*	-2.4	*ns*
PGM2L1	phosphoglucomutase 2-like 1	*ns*	-2.4	*ns*
CARD6	caspase recruitment domain family, member 6	*ns*	*ns*	2.4
ZNF699	zinc finger protein 699	*ns*	-2.4	*ns*
PCYOX1	prenylcysteine oxidase 1	*ns*	-2.4	*ns*
DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	*ns*	-2.4	*ns*
C2	complement component 2	*ns*	*ns*	2.4
ALPK2	alpha kinase 2	*ns*	-2.4	*ns*
CPEB2	cytoplasmic polyadenylation element binding protein 2	*ns*	-2.4	*ns*
IL17RA	interleukin 17 receptor A	*ns*	-2.4	*ns*
RGS4	regulator of G-protein signaling 4	*ns*	-2.4	*ns*
CTIF	CBP80	*ns*	-2.4	*ns*
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	*ns*	*ns*	2.4
PREPL	prolyl endopeptidase-like	*ns*	*ns*	2.4
TPGS2	tubulin polyglutamylase complex subunit 2	*ns*	-2.4	*ns*
TNS2	tensin 2	*ns*	*ns*	2.4
ZBTB8A	zinc finger and BTB domain containing 8A	*ns*	-2.4	*ns*
TXNDC15	thioredoxin domain containing 15	*ns*	-2.4	*ns*
CTSO	cathepsin O	*ns*	*ns*	2.4
RGS5	regulator of G-protein signaling 5	*ns*	*ns*	2.4
UBE2D1	ubiquitin conjugating enzyme E2D 1	*ns*	-2.4	*ns*
PLCD3	phospholipase C, delta 3	*ns*	-2.4	*ns*
SELENOW	selenoprotein W	*ns*	-2.4	*ns*
UST	uronyl-2-sulfotransferase	*ns*	*ns*	2.4
ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	*ns*	-2.4	*ns*



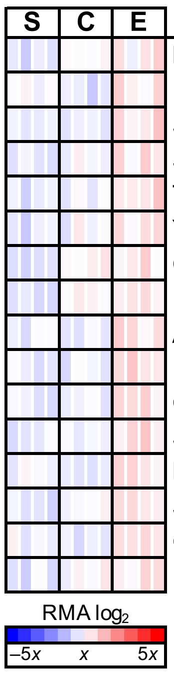
Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LRRN4CL	LRRN4 C-terminal like	*ns*	*-2.4*	*ns*
OTUD1	OTU deubiquitinase 1	*ns*	*-2.3*	*ns*
LIG4	ligase IV, DNA, ATP-dependent	*ns*	*ns*	*2.3*
GLS	glutaminase	*ns*	*-2.3*	*ns*
THRA	thyroid hormone receptor, alpha	*ns*	*ns*	*2.3*
HLA-F	major histocompatibility complex, class I, F	*ns*	*-2.3*	*ns*
LOC100287042	uncharacterized LOC100287042	*ns*	*-2.3*	*ns*
IFI35	interferon-induced protein 35	*ns*	*-2.3*	*ns*
SLC39A6	solute carrier family 39 (zinc transporter), member 6	*ns*	*-2.3*	*ns*
SLC66A3	solute carrier family 66 member 3	*ns*	*-2.3*	*ns*
VKORC1	vitamin K epoxide reductase complex subunit 1	*ns*	*-2.3*	*ns*
LNPK	lunapark, ER junction formation factor	*ns*	*-2.3*	*ns*
LRRC6	leucine rich repeat containing 6	*ns*	*ns*	*2.3*
MX2	MX dynamin-like GTPase 2	*ns*	*-2.3*	*ns*
GYPC	glycophorin C (Gerbich blood group)	*ns*	*ns*	*2.3*
SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2	*ns*	*-2.3*	*ns*
ODF3B	outer dense fiber of sperm tails 3B	*ns*	*-2.3*	*ns*
CA11	carbonic anhydrase XI	*ns*	*-2.3*	*ns*
LOC100996842	uncharacterized LOC100996842	*ns*	*-2.3*	*ns*
WASHC3	WASH complex subunit 3	*ns*	*-2.3*	*ns*
LOC102724094	uncharacterized LOC102724094	*ns*	*-2.3*	*ns*
OAF	out at first homolog	*ns*	*-2.3*	*ns*
FTH1	ferritin, heavy polypeptide 1	*ns*	*-2.3*	*ns*
TTC39B	tetratricopeptide repeat domain 39B	*ns*	*ns*	*2.3*
SLC9B2	solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	*ns*	*ns*	*2.3*
P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	*ns*	*-2.3*	*ns*
INHBB	inhibin beta B	*ns*	*-2.3*	*ns*
ACAT1	acetyl-CoA acetyltransferase 1	*ns*	*ns*	*2.3*
ATP6V0E1	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	*ns*	*-2.3*	*ns*
TMEM204	transmembrane protein 204	*ns*	*ns*	*2.3*
RAMP1	receptor (G protein-coupled) activity modifying protein 1	*ns*	*-2.3*	*ns*
RGS16	regulator of G-protein signaling 16	*ns*	*-2.3*	*ns*
ZNF562	zinc finger protein 562	*ns*	*-2.3*	*ns*
DDAH1	dimethylarginine dimethylaminohydrolase 1	*ns*	*ns*	*2.3*
MIR3622A	microRNA 3622a	*ns*	*-2.3*	*ns*
LY86	lymphocyte antigen 86	*ns*	*-2.3*	*ns*
POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	*ns*	*-2.3*	*ns*
S100A4	S100 calcium binding protein A4	*ns*	*-2.3*	*ns*
ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1	*ns*	*-2.3*	*ns*
RUNX3	runt-related transcription factor 3	*ns*	*ns*	*2.3*
ZNF330	zinc finger protein 330	*ns*	*ns*	*2.3*
PSMB9	proteasome subunit beta 9	*ns*	*-2.3*	*ns*
KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	*ns*	*ns*	*2.3*
SOCS3	suppressor of cytokine signaling 3	*ns*	*-2.2*	*ns*
C1GALT1C1	C1GALT1 specific chaperone 1	*ns*	*-2.2*	*ns*
DECR1	2,4-dienoyl-CoA reductase 1, mitochondrial	*ns*	*ns*	*2.2*
TPRG1L	tumor protein p63 regulated 1-like	*ns*	*-2.2*	*ns*
MAP1A	microtubule associated protein 1A	*ns*	*-2.2*	*ns*
TCTA	T-cell leukemia translocation altered	*ns*	*ns*	*2.2*
DNASE2	deoxyribonuclease II, lysosomal	*ns*	*-2.2*	*ns*
ARL2BP	ADP-ribosylation factor like GTPase 2 binding protein	*ns*	*ns*	*2.2*
CELF2-AS1	CELF2 antisense RNA 1	*ns*	*-2.2*	*ns*
CYTIP	cytohesin 1 interacting protein	*ns*	*-2.2*	*ns*
HHEX	hematopoietically expressed homeobox	*ns*	*ns*	*2.2*
THBS3	thrombospondin 3	*ns*	*-2.2*	*ns*



Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
TEX2	testis expressed 2	*ns*	-2.2	*ns*
RNF130	ring finger protein 130	*ns*	*ns*	2.2
FAM20A	family with sequence similarity 20, member A	*ns*	-2.2	*ns*
POT1-AS1	POT1 antisense RNA 1	*ns*	-2.2	*ns*
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	*ns*	-2.2	*ns*
SIAE	sialic acid acetylesterase	*ns*	-2.2	*ns*
AHNAK2	AHNAK nucleoprotein 2	*ns*	-2.2	*ns*
KLHL2	kelch-like family member 2	*ns*	-2.2	*ns*
ZYX	zyxin	*ns*	-2.2	*ns*
ZNHIT1	zinc finger, HIT-type containing 1	*ns*	-2.2	*ns*
LTA4H	leukotriene A4 hydrolase	*ns*	-2.2	*ns*
SLC37A3	solute carrier family 37, member 3	*ns*	-2.2	*ns*
TNXA	tenascin XA (pseudogene)	*ns*	*ns*	2.2
GGT3P	gamma-glutamyltransferase 3 pseudogene	*ns*	*ns*	2.2
ETHE1	ethylmalonic encephalopathy 1	*ns*	-2.2	*ns*
TWIST2	twist family bHLH transcription factor 2	*ns*	-2.2	*ns*
TUSC2	tumor suppressor candidate 2	*ns*	-2.2	*ns*
LITAF	lipopolysaccharide-induced TNF factor	*ns*	-2.2	*ns*
FKBP1B	FK506 binding protein 1B	*ns*	-2.2	*ns*
AKAP12	A kinase (PRKA) anchor protein 12	*ns*	-2.2	*ns*
LY6D	lymphocyte antigen 6 complex, locus D	*ns*	-2.2	*ns*
LHFPL6	LHFPL tetraspan subfamily member 6	*ns*	-2.2	*ns*
ASL	argininosuccinate lyase	*ns*	-2.2	*ns*
KREMEN1	kringle containing transmembrane protein 1	*ns*	-2.2	*ns*
PROCR	protein C receptor, endothelial	*ns*	-2.2	*ns*
MARCHF2	membrane associated ring-CH-type finger 2	*ns*	-2.2	*ns*
TWF2	twinfilin actin binding protein 2	*ns*	-2.2	*ns*
ADD3	adducin 3 (gamma)	*ns*	*ns*	2.2
ZBTB16	zinc finger and BTB domain containing 16	*ns*	-2.2	*ns*
RAB31	RAB31, member RAS oncogene family	*ns*	*ns*	2.2
IL17RE	interleukin 17 receptor E	*ns*	-2.1	*ns*
FUNDC1	FUN14 domain containing 1	*ns*	-2.2	*ns*
H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	*ns*	-2.2	*ns*
SPOCK2	sparc	*ns*	-2.2	*ns*
CLSTN2	calsyntenin 2	*ns*	-2.2	*ns*
LGALS3	lectin, galactoside-binding, soluble, 3	*ns*	-2.2	*ns*
MED11	mediator complex subunit 11	*ns*	-2.2	*ns*
ABR	active BCR-related	*ns*	-2.2	*ns*
GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	*ns*	-2.1	*ns*
ITGA3	integrin alpha 3	*ns*	-2.1	*ns*
CASP1	caspase 1	*ns*	*ns*	2.1
MR1	major histocompatibility complex, class I-related	*ns*	-2.1	*ns*
STX2	syntaxin 2	*ns*	*ns*	2.1
GPR4	G protein-coupled receptor 4	*ns*	*ns*	2.1
ABCA1	ATP binding cassette subfamily A member 1	*ns*	-2.1	*ns*
CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	*ns*	-2.1	*ns*
CYTH4	cytohesin 4	*ns*	*ns*	2.1
FKBP10	FK506 binding protein 10	*ns*	-2.1	*ns*
LRRC37A3	leucine rich repeat containing 37, member A3	*ns*	-2.1	*ns*
SLCO3A1	solute carrier organic anion transporter family, member 3A1	*ns*	-2.1	*ns*
TRG-AS1	T cell receptor gamma locus antisense RNA 1	*ns*	-2.1	*ns*
ODF2L	outer dense fiber of sperm tails 2-like	*ns*	-2.1	*ns*
LMAN2	lectin, mannose-binding 2	*ns*	-2.1	*ns*
IRF9	interferon regulatory factor 9	*ns*	-2.0	*ns*
CAPN5	calpain 5	*ns*	-2.1	*ns*

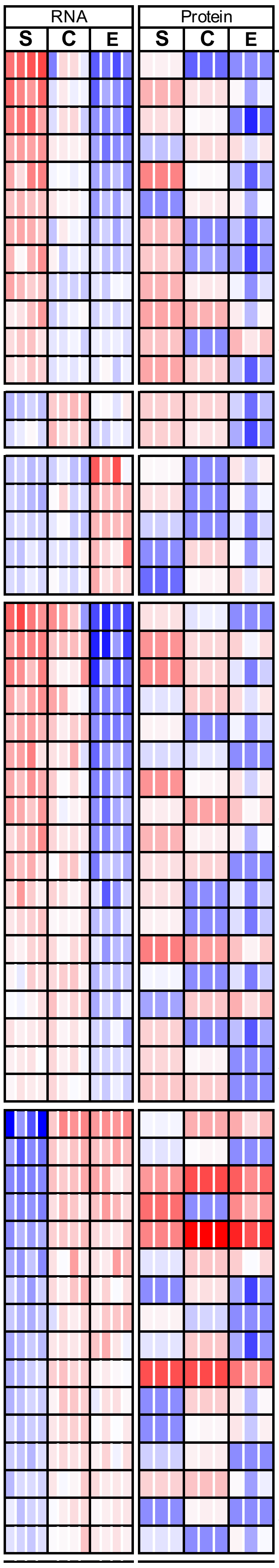


Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
NFASC	neurofascin	*ns*	-2.1	*ns*
METTL24	methyltransferase like 24	*ns*	*ns*	2.1
SNHG16	small nucleolar RNA host gene 16	*ns*	-2.1	*ns*
PPP1R7	protein phosphatase 1, regulatory subunit 7	*ns*	-2.1	*ns*
MFSD6	major facilitator superfamily domain containing 6	*ns*	*ns*	2.1
METTL23	methyltransferase like 23	*ns*	-2.1	*ns*
HOXA5	homeobox A5	*ns*	-2.1	*ns*
SLC31A1	solute carrier family 31 (copper transporter), member 1	*ns*	-2.1	*ns*
TNFRSF21	tumor necrosis factor receptor superfamily, member 21	*ns*	-2.1	*ns*
SPIRE1	spire-type actin nucleation factor 1	*ns*	-2.1	*ns*
HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	*ns*	-2.1	*ns*
BLOC1S6	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	*ns*	-2.1	*ns*
CNTN4	contactin 4	*ns*	*ns*	2.1
CARS1	cysteinyl-tRNA synthetase 1	*ns*	-2.1	*ns*
GPBAR1	G protein-coupled bile acid receptor 1	*ns*	-2.1	*ns*
LOC100506928	uncharacterized LOC100506928	*ns*	-2.1	*ns*
SLA	Src-like-adaptor	*ns*	*ns*	2.1
FAM98C	family with sequence similarity 98, member C	*ns*	-2.1	*ns*
BBS5	Bardet-Biedl syndrome 5	*ns*	*ns*	2.1
FZD8	frizzled class receptor 8	*ns*	-2.1	*ns*
SMAP2	small ArfGAP2	*ns*	*ns*	2.1
CYB5R3	cytochrome b5 reductase 3	*ns*	-2.1	*ns*
DST	dystonin	*ns*	*ns*	2.1
OXLD1	oxidoreductase-like domain containing 1	*ns*	-2.1	*ns*
LEPROTL1	leptin receptor overlapping transcript-like 1	*ns*	-2.1	*ns*
TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR	*ns*	-2.1	*ns*
IGF2R	insulin-like growth factor 2 receptor	*ns*	-2.1	*ns*
POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	*ns*	-2.1	*ns*
ZNF189	zinc finger protein 189	*ns*	*ns*	2.1
MASP1	mannan-binding lectin serine peptidase 1 (C4	*ns*	-2.1	*ns*
CDK14	cyclin-dependent kinase 14	*ns*	*ns*	2.1
RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	*ns*	*ns*	2.1
KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	*ns*	*ns*	2.1
FITM2	fat storage-inducing transmembrane protein 2	*ns*	-2.1	*ns*
RNLS	renalase, FAD-dependent amine oxidase	*ns*	*ns*	2.1
B2M	beta-2-microglobulin	*ns*	-2.1	*ns*
ACYP2	acylphosphatase 2, muscle type	*ns*	*ns*	2.1
RRN3P2	RRN3 homolog, RNA polymerase I transcription factor pseudogene 2	*ns*	*ns*	2.1
SLCO2B1	solute carrier organic anion transporter family, member 2B1	*ns*	*ns*	2.1
CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	*ns*	-2.1	*ns*
LYSMD2	LysM, putative peptidoglycan-binding, domain containing 2	*ns*	*ns*	2.0
NBN	nibrin	*ns*	-2.0	*ns*
ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	*ns*	-2.0	*ns*
ACE	angiotensin I converting enzyme	*ns*	*ns*	2.0
ABHD2	abhydrolase domain containing 2	*ns*	-2.0	*ns*
ENDOD1	endonuclease domain containing 1	*ns*	-2.0	*ns*
MPC1	mitochondrial pyruvate carrier 1	*ns*	-2.0	*ns*
FKBP11	FK506 binding protein 11	*ns*	-2.0	*ns*
SASH3	SAM and SH3 domain containing 3	*ns*	*ns*	2.0
RNASEH2C	ribonuclease H2, subunit C	*ns*	*ns*	2.0
PDCL3	phosducin like 3	*ns*	-2.0	*ns*
RDH10	retinol dehydrogenase 10 (all-trans)	*ns*	*ns*	2.0
RAB29	RAB29, member RAS oncogene family	*ns*	-2.0	*ns*
ATL3	atlastin GTPase 3	*ns*	-2.0	*ns*
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	*ns*	-2.0	*ns*

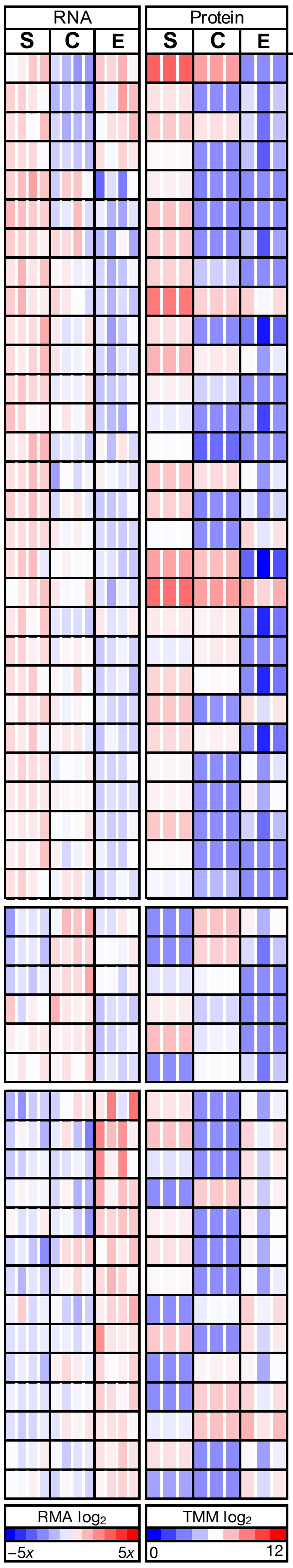


Symbol	Name	Linear Fold Change (*ns*=no significant difference) **S** vs **C**	 **S** vs **E**	 **E** vs **C**
LOC105376958	uncharacterized LOC105376958	*ns*	-2.0	*ns*
RASSF4	Ras association (RalGDS	*ns*	*ns*	2.0
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	*ns*	*ns*	2.0
SAP30	Sin3A associated protein 30kDa	*ns*	-2.0	*ns*
THYN1	thymocyte nuclear protein 1	*ns*	-2.0	*ns*
YBEY	ybeY metallopeptidase (putative)	*ns*	-2.0	*ns*
CD151	CD151 molecule (Raph blood group)	*ns*	-2.0	*ns*
DSTN	destrin (actin depolymerizing factor)	*ns*	-2.0	*ns*
ADGRG3	adhesion G protein-coupled receptor G3	*ns*	*ns*	2.0
PNMA1	paraneoplastic Ma antigen 1	*ns*	-2.0	*ns*
CFAP36	cilia and flagella associated protein 36	*ns*	-2.0	*ns*
SAPCD1-AS1	SAPCD1 antisense RNA 1	*ns*	-2.0	*ns*
PRICKLE2-AS1	PRICKLE2 antisense RNA 1	*ns*	*ns*	2.0
SDC3	syndecan 3	*ns*	-2.0	*ns*
GOLM1	golgi membrane protein 1	*ns*	*ns*	2.0
PDE4A	phosphodiesterase 4A, cAMP-specific	*ns*	-2.0	*ns*

Fig. S2. Syncytiotrophoblast (**S**), Cytotrophoblast (**C**), and Endovascular trophoblast (**E**) differentially expressed genes



		Linear Fold Change					
		RNA			Protein		
Symbol	Name	SvC	SvE	EvC	SvC	SvE	EvC
GH2	growth hormone 2	12	65	-6	7	42	-6
CSHL1	chorionic somatomammotropin hormone-like 1	7	5	-5	3	7	-3
KMO	kynurenine 3-monooxygenase	5	5	-5	2	10	-6
GPC3	glypican 3	3	4	-6	-5	-4	-1
HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	4	3	-3	19	58	-3
PSG3	pregnancy specific beta-1-glycoprotein 3	2	3	-3	-54	-32	-2
C4orf36	chromosome 4 open reading frame 36	4	3	-2	159	13	12
CKMT1A	creatine kinase, mitochondrial 1A	3	2	-1	10	12	-1
CA8	carbonic anhydrase VIII	4	2	1	4	9	-3
FURIN	furin (paired basic amino acid cleaving enzyme)	3	2	-1	1	8	-6
AK3	adenylate kinase 3	3	1	1	135	-1	148
ELK1	ELK1, member of ETS oncogene family	2	1	-1	3	23	-9
IL1RAP	interleukin 1 receptor accessory protein	-5	1	-2	-1	7	-7
NOCT	nocturnin	-3	0	-3	1	10	-7
GPR82	G protein-coupled receptor 82	-1	3	8	35	-1	44
RBP1	retinol binding protein 1, cellular	-2	3	3	64	2	28
C1QB	complement component 1, q subcomponent, B chain	-1	2	4	18	-1	21
CXCL11	chemokine (C-X-C motif) ligand 11	-1	2	3	-99	-25	-4
FBLN2	fibulin 2	-1	2	2	-7	-11	1
BMP5	bone morphogenetic protein 5	4	6	-21	2	62	-28
CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1	2	6	-29	5	6	-1
HSD3B1	isomerase 1	2	5	-13	6	30	-5
DLK1	delta-like 1 homolog (Drosophila)	2	4	-10	-6	-3	-2
CDO1	cysteine dioxygenase type 1	2	4	-10	40	2	22
OLAH	oleoyl-ACP hydrolase	2	4	-6	-1	21	-26
STS	steroid sulfatase (microsomal), isozyme S	2	4	-6	11	10	1
ADAMTS6	ADAM metallopeptidase with thrombospondin type S6	2	4	-5	-7	-2	-3
ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1C2	2	3	-6	4	6	-2
PSG1	pregnancy specific beta-1-glycoprotein 1	2	3	-4	-2	64	-100
SPDYA	speedy	1	3	-5	64	3	19
SLC38A1	solute carrier family 38, member 1	1	2	-3	42	2	17
SLC2A1	solute carrier family 2A1 (facilitated glucose transporter)	-1	2	-4	2	7	-4
CLN3	ceroid-lipofuscinosis, neuronal 3	-1	1	-4	28	2	18
SLC29A1	solute carrier family 29A1 (equilibrative nucleoside transporter)	-2	1	-4	-13	-17	1
UBE2C	ubiquitin-conjugating enzyme E2C	1	1	-2	93	8	12
ADK	adenosine kinase	-1	1	-2	2	82	-45
ZNF808	zinc finger protein 808	1	1	-2	-1	118	-119
PRG2	proteoglycan 2, bone marrow (natural killer cell activator)	-66	6	1	-10	-7	-1
ISG15	ISG15 ubiquitin-like modifier	-12	4	1	-2	23	-40
HSPG2	heparan sulfate proteoglycan 2	-12	3	-1	-9	-4	-2
RFPL4B	ret finger protein-like 4B	-8	3	1	1241	3	475
FN1	fibronectin 1	-7	2	-1	-35	-11	-3
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	-5	3	1	-6	-4	-2
CD276	CD276 molecule	-5	2	-1	-70	-9	-8
LAYN	layilin	-3	2	2	2	40	-21
ST6GALNAC2	ST6 N-Acetylgalactosaminide Alpha-2,6-Sialyltransferase 2	-4	2	1	-6	2	-15
KRT19	keratin 19, type I	-4	1	-2	-1	4	-5
LY6K	lymphocyte antigen 6 complex, locus K	-4	1	-2	-116	-36	-3
FHL2	four and a half LIM domains 2	-3	1	-1	-40	-44	1
FAM110A	family with sequence similarity 110, member A	-3	1	-1	-3	18	-52
GTPBP1	GTP binding protein 1	-2	1	1	-2	3	-6
ADAM15	ADAM metallopeptidase domain 15	-2	1	-1	-6	8	-47
LASP1	LIM and SH3 protein 1	-2	1	1	23	-1	31



Symbol	Name	Linear Fold Change RNA SvC	RNA SvE	RNA EvC	Protein SvC	Protein SvE	Protein EvC
ACTA2	actin, alpha 2, smooth muscle, aorta	4	0	5	4	1763	-397
IDO1	indoleamine 2,3-dioxygenase 1	4	0	5	59	3	17
TCF4	transcription factor 4	4	0	4	2	7	-4
EAF2	ELL associated factor 2	3	0	3	35	3	12
PSG11	pregnancy specific beta-1-glycoprotein 11	2	3	-3	5	45	-9
GH1	growth hormone 1	2	2	-2	138	138	-1
PBK	PDZ binding kinase	1	2	-3	113	10	11
RBMS3	RNA binding motif, single stranded interacting protein 3	2	2	-2	5	94	-20
TFRC	transferrin receptor	2	2	-2	8	12	-1
NPIPB4	nuclear pore complex interacting protein family B4	2	2	-2	66	11	6
DVL3	dishevelled segment polarity protein 3	2	2	-2	4	8	-2
STX3	syntaxin 3	2	2	-2	2	45	-22
PDXDC2P	pyridoxal-dependent decarboxylase domain containing 2, pseudogene	1	2	-2	25	3	9
BTG2	BTG family, member 2	3	1	1	5	30	-6
BCL2	B-cell CLL	3	1	1	2	5	-3
AUNIP	aurora kinase A and ninein interacting protein	2	2	-2	10	5	2
TOMM34	translocase of outer mitochondrial membrane 34	1	2	-2	30	-2	63
RGPD3	RANBP2-like and GRIP domain containing 3	1	1	-2	2	67	-38
H2BC21	H2B clustered histone 21	1	1	-2	3	5	-2
SLAIN1	SLAIN motif family member 1	3	1	2	-1	7	-8
SLC2A11	solute carrier family 2A11 (facilitated glucose transporter)	1	1	-2	-2	26	-54
TAF4B	TATA-Box Binding Protein Associated Factor 4b	1	1	-2	2	13	-6
MGST3	microsomal glutathione S-transferase 3	1	1	-2	12	2	6
TIGD2	tigger transposable element derived 2	1	1	-2	2	11	-7
SIAH2	siah E3 ubiquitin protein ligase 2	2	1	-1	37	2	24
TLK1	tousled-like kinase 1	1	1	-2	40	1	31
HNRNPD	heterogeneous nuclear ribonucleoprotein D	1	1	-2	118	8	15
NPIPA5	nuclear pore complex interacting protein family A5	2	1	-1	35	35	-1
TCTEX1D4	Tctex1 domain containing 4	1	1	-2	2	28	-15
PGPEP1	pyroglutamyl-peptidase I	-4	1	-2	-150	-34	-4
PANX1	pannexin 1	-3	1	-2	-108	-17	-7
ELF4	E74-like factor 4 (ets domain transcription factor)	-3	1	-2	-1	23	-34
RAB25	RAB25, member RAS oncogene family	-1	1	-3	2	47	-21
CYB5R1	cytochrome b5 reductase 1	-1	1	-2	5	152	-29
ACVR2B	activin A receptor type IIB	-1	1	-2	-36	-17	-2
TM4SF5	transmembrane 4 L six family member 5	-3	3	2	57	2	27
GPR65	G protein-coupled receptor 65	1	2	5	133	2	68
CD82	CD82 molecule	-1	2	4	23	-2	50
PLEK	pleckstrin	2	1	4	-129	-45	-3
GDAP1	ganglioside induced differentiation associated protein 1	2	1	4	45	1	33
SLC30A4	solute carrier family 30 (zinc transporter), member 4	-3	2	1	64	2	31
MGAT2	mannosyl (a-1,6-)-glycoprotein b-1,2-N-acetylglucosaminyltransferase	-2	2	2	35	1	26
BTN3A2	butyrophilin, subfamily 3, member A2	2	1	3	-31	-74	2
C4B	complement component 4B (Chido blood group)	-1	1	2	112	2	52
CPEB2	cytoplasmic polyadenylation element binding protein 2	-2	1	1	-46	-31	-1
CYTIP	cytohesin 1 interacting protein	-1	1	2	-126	-68	-2
LGALS3	lectin, galactoside-binding, soluble, 3	-2	1	1	-6	-6	1
GPR4	G protein-coupled receptor 4	1	1	2	62	2	27
ACYP2	acylphosphatase 2, muscle type	1	1	2	11	-5	55

Fig. S3. Syncytiotrophoblast (**S**), Cytotrophoblast (**C**), and Endovascular trophoblast (**E**) coordinately differentially expressed genes and proteins

Table S1. Antibodies

Antigen	Catalog number/ clone	Source	Species	Concentration (µg/ml)
NTS	ab172114	Abcam	Rabbit	10
C4ORF36	ab23703	Abcam	Rabbit	2
PGPEP1	ab220735	Abcam	Rabbit	0.5
CNR1	ab23703	Abcam	Rabbit	4
CK7	7D3	Damsky et al., 1992	Rat	26
FITC-conjugated anti-mouse secondary	715-095-151	Jackson ImmunoResearch	Donkey	15
FITC-conjugated anti-rabbit secondary	711-095-152	Jackson ImmunoResearch	Donkey	15
TRITC-conjugated anti-rat secondary	712-025-153	Jackson ImmunoResearch	Donkey	15

Table S2. Cannabinoid Receptor Agonists and Antagonists

Compound	CAS Registry No	Tocris Cat. No.	Target
(R)-(+)-Methanandamide	157182-49-5	1782	CB_1 Agonist
AM 251	183232-66-8	1117	CB_1 Receptor Antagonist
JWH 133	259869-55-1	1343	CB_2 Agonist
AM 630	164178-33-0	1120	CB_2 Inverse Agonist