

RNA profiling of laser microdissected human trophoblast subtypes at mid-gestation reveals a role for cannabinoid signaling in invasion

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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, the placental or trophoblast expression of which 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 that signals from this receptor promote invasion. Together, these results revealed previously unseen gene expression patterns that translate to the protein level. Our data also suggested that endogenous and exogenous cannabinoids can affect human placental development.

KEY WORDS: Human, Placenta, Trophoblast, Transcriptomics, Proteomics, Cannabinoid signaling

INTRODUCTION

At birth, the human placenta is the newborn's largest organ (Pryce et al., 2014), its weight being approximately double that of the

heaviest organ of the body, the brain (Boyd and Hamilton, 1967). During the last six months of pregnancy, placental weight increases over sevenfold (Boyd and Hamilton, 1967) while simultaneously supporting over a thirtyfold 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 m² (Boyd, 1984). At an electron microscopic level, the syncytiotrophoblasts (STBs) 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 tenfold 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; Fig. 1A,B; reviewed by Maltepe and Fisher, 2015). In one pathway, the cells fuse to produce multinucleated 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, the walls of which 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 have 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 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; also known as CB1), which was highly expressed by the

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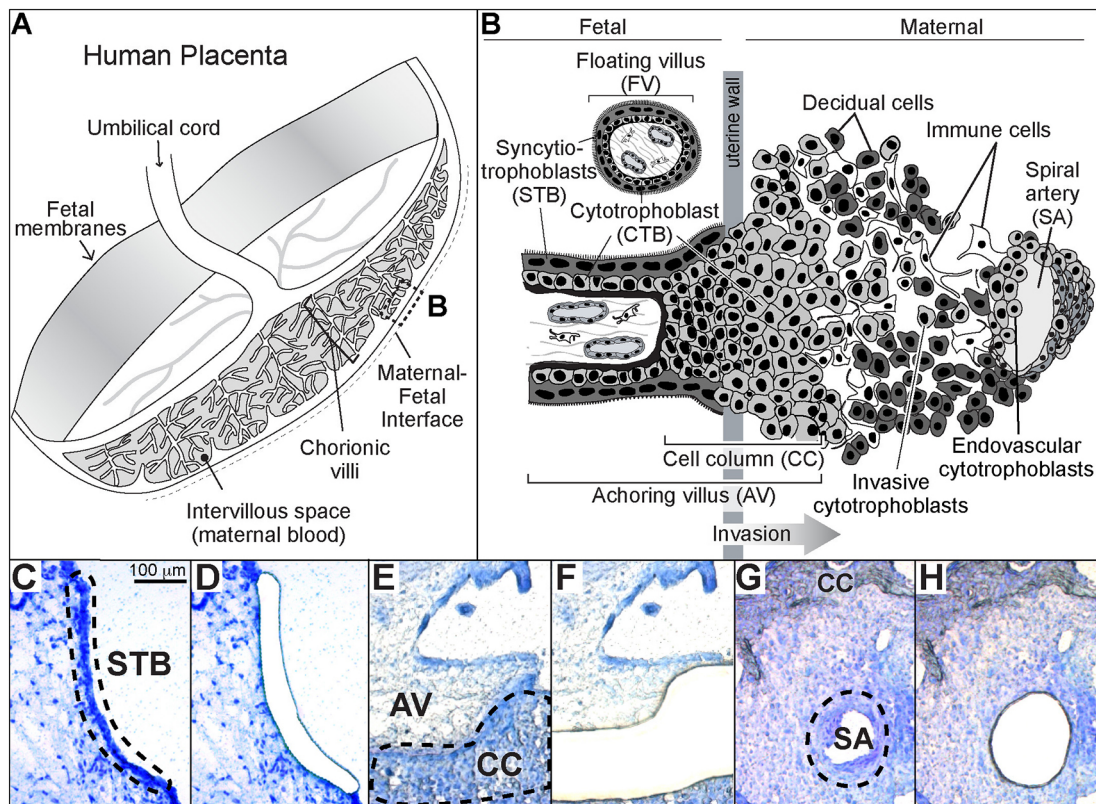


Fig. 1. Human placenta trophoblast subtypes targeted for laser microdissection. (A) Diagram of the human placenta in the second trimester of pregnancy. The boxed area (B) indicates the region biopsied for these studies. (B) View of the maternal-fetal interface at the cellular level. Shown are the two 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 increased blood flow to the placenta. The arrow indicates the direction of trophoblast invasion (modified from 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. SA, spiral artery.

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 trophoblast subpopulations that were targeted for removal as shown to the right: STBs (Fig. 1C,D), cell column CTBs (CC; Fig. 1E,F), and the endovascular compartment (ENDO), containing CTBs and other cell types in spiral arteries (SA; Fig. 1G,H).

Global profiling of RNA isolated from the samples and pair-wise comparisons of the results revealed 2986 genes that were differentially expressed (DE; $adjP$ -value <0.05) by one of the trophoblast 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 trophoblast subtypes analyzed had distinct transcriptomes.

Compared with the two CTB subpopulations, 2708 genes were differentially expressed in STBs (Fig. 2A; see Fig. S2 for entire heatmap and fold changes). As expected, the upregulated category included genes encoding 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 differentially expressed 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*, which encodes 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, following which it seems likely that enteric and other effects are possible (Bugni and Pothoulakis, 2013).

With regard to cell column CTBs, 2070 genes were differentially expressed in this subpopulation (Fig. 2B; see Fig. S2 for entire heatmap and fold changes). Receptors for metabolites were the most highly upregulated. They included *FABP7a*. We have previously described CTB expression of this molecule at the maternal-fetal interface (Winn et al., 2007). The alpha-ketoglutarate

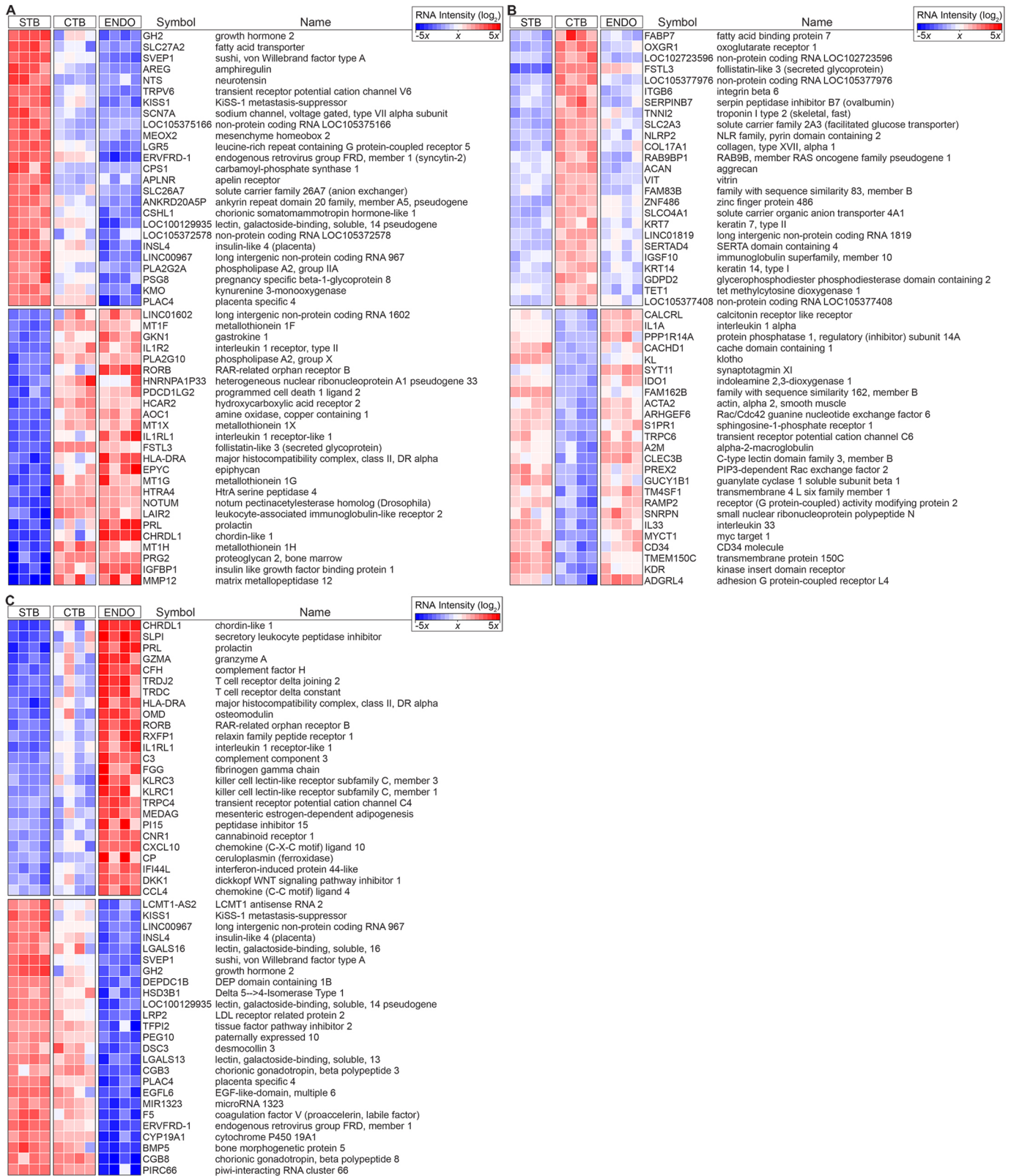


Fig. 2. Heatmaps of differentially expressed STB, CTB and ENDO RNAs. (A) The 25 most highly upregulated and 25 most highly downregulated transcripts in syncytiotrophoblasts (STB) compared with cytotrophoblasts (CTB) and endovascular cytotrophoblasts (ENDO) (total=2708, Table S2). (B) Heatmap of the most highly differentially expressed transcripts in CTB (total=2070, Table S2) relative to STB and ENDO. (C) Heatmap of the most highly differentially expressed transcripts in ENDO (total=2753, Table S2) relative to STB and CTB. The data are displayed as a heatmap 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.

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 by Maltepe and Fisher, 2015), molecules that are involved in adhesion/de-adhesion were upregulated in columns (*ITGB6*,

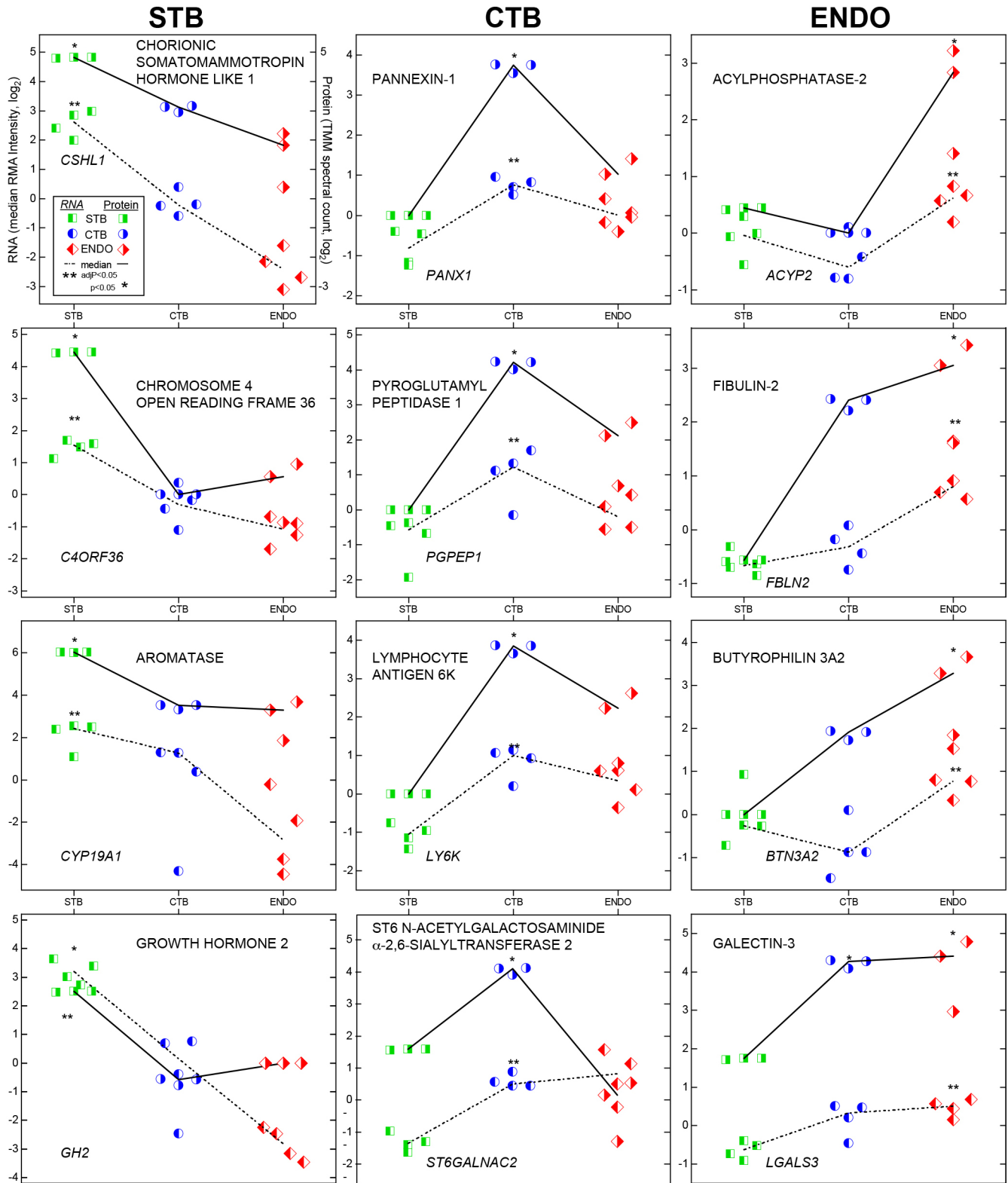


Fig. 3. Plots of relative RNA and protein abundances in trophoblast subtypes. The upper left hand panel illustrates the labeling scheme. Data are organized in columns. Molecules that were upregulated in STBs are shown to the left, cell column CTBs in the middle and endovascular CTBs to the right. Each 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.

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 upregulated, 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 differentially expressed in the endovascular compartment (Fig. 2C; see Fig. S2 for entire heatmap and fold changes). The most highly upregulated genes included the BMP4 antagonist *CHRD1*, 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 previously unseen identifications: *OMD*, *RORB* and *MEDAG*. *CNRI* 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 (*RLN1*) (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 *KLRC3*. 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 trophoblast subpopulations, captured by LMD, 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 differentially expressed 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 upregulated 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 differentially expressed 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

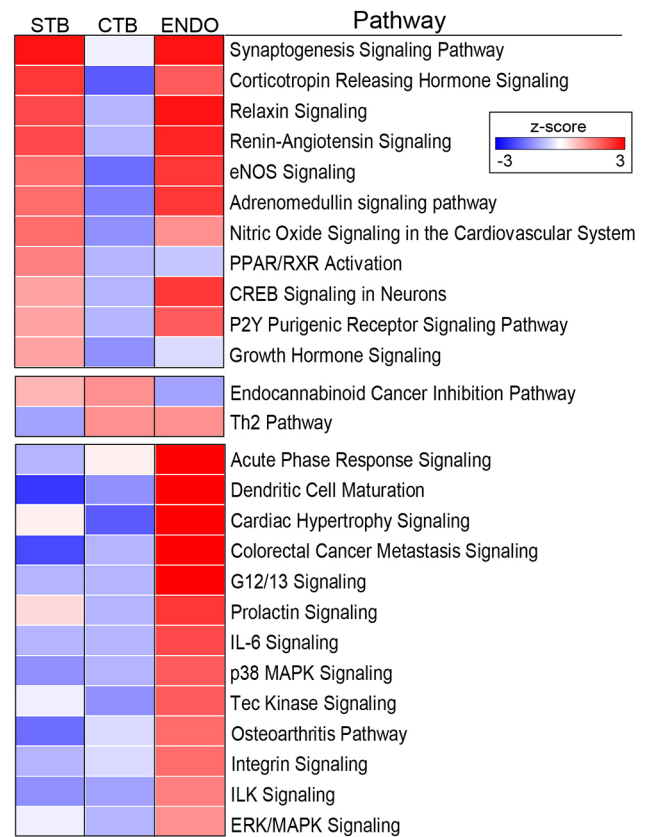


Fig. 4. Ingenuity Pathway Analysis of the differentially expressed genes among trophoblast subpopulations. Pathways were assigned a z-score based on the predicted impact of DEGs, either activation (+) or deactivation (-). Significant pathways had a $-\log(P\text{-value}) > 1.3$, an absolute z-score > 2 , and contained at least four members in a unique combination. The data are displayed as a heatmap 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.

(MGG_01005) is dynein light chain Tctex-type 1 (*dynlt1/3*; Li et al., 2018), which transports various types of cellular cargo. *CYP19A1* (aromatase) and *GH2* (growth hormone 2) were also expressed at higher levels in the syncytium.

With regards cell column CTBs (Fig. 3, middle column), the highly-expressed differentially expressed molecules included several identifications that, to our knowledge, were not known to be produced by the placenta. They included pannexin 1 (a major ATP release and nucleotide efflux channel; Chekeni et al., 2010; Elliott et al., 2009), pyroglutamyl-peptidase I (*PGPEPI*; an exopeptidase; Cummins and O'Connor, 1998) and lymphocyte antigen 6K (*LY6K*; a biomarker of lung and esophageal carcinomas; Ishikawa et al., 2007). We were also interested to find that a sialyltransferase (alpha-n-acetylgalactosaminide alpha-2,6-sialyltransferase 6; Samyn-Petit et al., 2000) was upregulated 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 differentially expressed 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

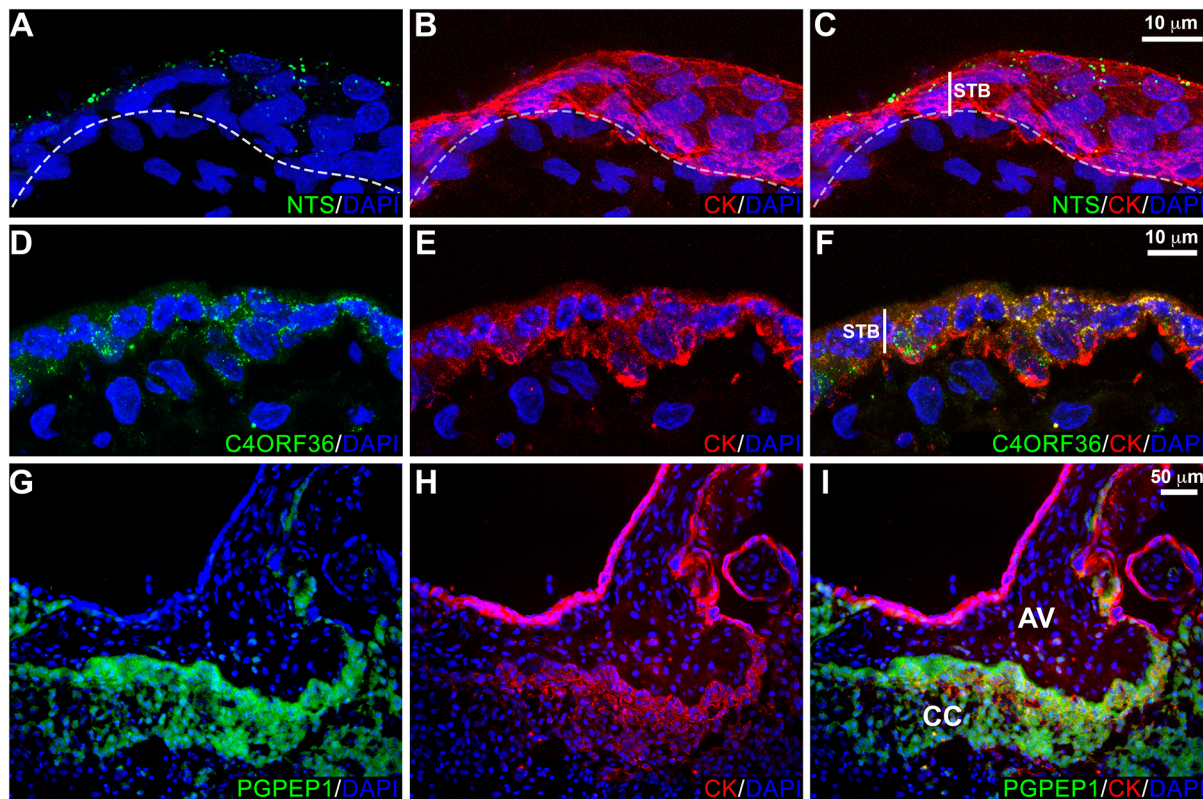


Fig. 5. Immunolocalization of differentially expressed proteins: NTS, C4ORF36 and PGPEP1. Tissue sections were immunostained for the antigen of interest and cytokeratin (CK), a trophoblast marker. Nuclei were localized with DAPI. Each panel was a confocal z-stack maximum intensity projection. (A-C) Neurotensin (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.

confirmed the differential 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 trophoblast subtypes. Pathways were assigned a z-score based on the predicted impact of differentially expressed genes (DEGs), 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 versus 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 upregulated the

expression of genes that are involved in TH2 (tolerogenic) responses. There were 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, IL6, 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 differentially expressed 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; Pérez 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. In addition, we were interested in the expression of C4orf36, also in STBs, the peptide product of which was detected by mass spectrometry. Immunostaining revealed a dense punctate pattern in STBs (Fig. 5D-F). Within the cell columns, we confirmed the expression of *PGPEP1* by the cytotrophoblasts in that region (Fig. 5G-I).

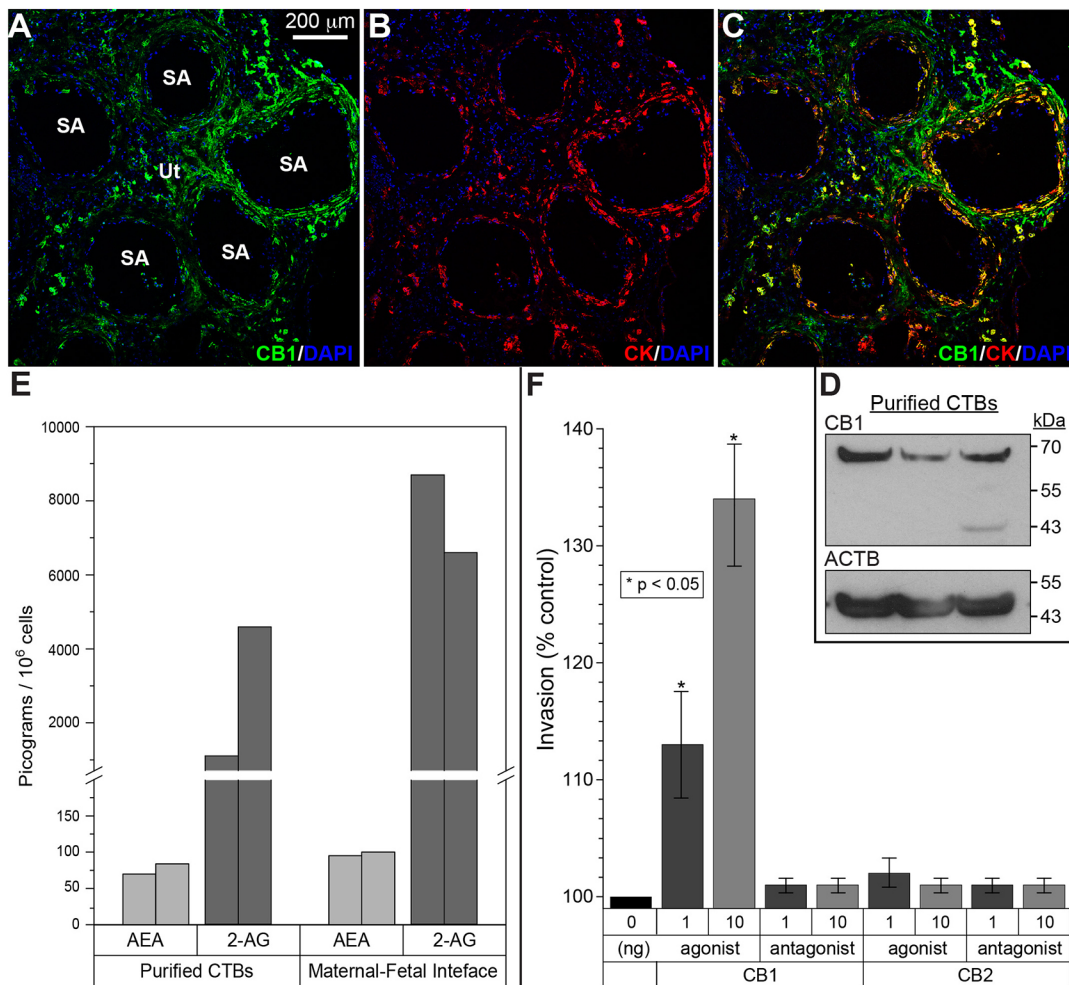


Fig. 6. Expression of cannabinoid ligands and receptors at the maternal-fetal interface and the functional consequences. (A-C) Tissue sections were immunostained for CNR1 (CB1) and cytokeratin (CK), a trophoblast marker. Nuclei were localized with DAPI. Each panel was a confocal z-stack maximum intensity projection. Anti-CNR1 specifically reacted with invasive/endothelial CTBs in the walls of uterine (Ut) spiral arteries (SA). Cytotrophoblasts (CTBs) in the cell columns showed variable CNR1 expression, while syncytiotrophoblasts were negative (data not shown). The results shown were representative 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- β (ACTB). Cells from three placentas were analyzed. (E) Mass spectrometry enabled measuring the absolute amounts of the major mammalian endogenous cannabinoids, anandamide (AEA) 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 CNR1 and CNR2 agonists and antagonists assayed, only a CNR1 agonist had a dose-dependent effect increasing invasion ($n=3$ biological replicates, * $P<0.05$, unpaired, two-tailed Student's t -test).

To begin to explore the role of CTB CNR1 within the uterine wall, we confirmed the cell 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 cytokeratin (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 (AEA) 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/10⁶ cells) and 2-AG was present at much higher concentrations (1000-5000 pg/10⁶ cells).

We then explored CNR1 function in terms of CTB invasion. CNR1 and CNR2 (CB2) agonists and antagonists (see Table S2) were added to the assay. Among the compounds tested, only a

CNR1 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 expected identifications as well as those that were, to the best of our knowledge, previously undescribed.

With regard to STBs, we expected to detect, at RNA and protein levels, well known abundant products such as *CSSL1* (chorionic somatomammotropin hormone-like 1), *CYP19A1* and *GH2*. 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 its ability to lower blood pressure (Carraway and Leeman, 1973). Later on, its role in promoting prolactin release and inhibiting luteinizing hormone 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; Pérez 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 gastrointestinal (e.g. hyperemesis gravidarum) signs.

With regard to column CTBs, the highly-expressed differentially expressed 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 PGPEP1, an exopeptidase (Fig. 5G-I) that cleaves N-terminal pyroglutamylic 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 an STB product (e.g. neurotensin), suggesting that they might be immune to its effects. Other novel mRNAs/proteins that were upregulated in this population included LY6K, which marks the progression of many cancers and has been implicated in immune escape (Upadhyay, 2019).

Trophoblasts within the endovascular compartment were notable for the expression of 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, CNR1, which was the entry into the signaling pathways this ligand activates. Subsequently, a second receptor (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 carried out in the mouse (reviewed by Sun and Dey, 2012). On the maternal side, deletion of *Cnr1* and *Cnr2* reduces fertility secondary to impaired implantation owing 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 CNR1 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 LMD/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 DEGs 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 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 University of California, San Francisco (UCSF) Institutional Review Board (Committee on Human Research) approved this study. Written informed consent was obtained from all donors. Samples were processed within 1 h 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). Spiral arteries from the same cases were identified using a dissection microscope (Leica MZ16). Biopsied specimens (1×1×0.5 cm) were rinsed in ice-cold PBS, transferred to a 1:1

(v:v) PBS:OCT (Optimal Cutting Temperature compound, Thermo Fisher Scientific) semi-frozen slurry for 15 min, oriented in an OCT-filled peel-a-way disposable embedding mold (Thermo Fisher 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°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 CK staining were used in experiments.

Laser microdissection

Frozen blocks were sectioned (-20°C) using a Leica CM3050 cryostat. Sections ($20\ \mu\text{m}$) 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 (Thermo Fisher 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 s), immersed in PBS until the OCT was completely removed (~ 2 min), dipped in 0.1% Toluidine Blue for 30 s, washed in ice-cold PBS, dehydrated (30 s/treatment) in a graded ethanol series (75% $\times 2$, 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 $20\times$ 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-Aldrich), 5 mM tris(2-carboxyethyl)phosphine (Bond-Breaker, Thermo Fisher Scientific), and 0.1% (w/v) RapiGest SF (Waters)] was used for subsequent protein isolation.

For RNA, ten slides with four sections per slide were prepared for each specimen. For protein, five slides with eight sections per slide were prepared. To limit degradation, each slide used for RNA isolation was microdissected for no more than 30 min, which was extended to 1 h 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°C before analysis.

Global RNA profiling

We used a microarray approach (Affymetrix GeneChip HuGene 2.0 ST) and protocols that were devised by the UCSF Gladstone (National Heart, Lung, and Blood Institute) Genomics Core Facility. Gene expression data quality was confirmed, robust multiarray averaging (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; R Core Team, 2013). The data were modeled and contrasts between STB, CTB and ENDO determined using the limma package (Ritchie et al., 2015). 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 weeks 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 weeks 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°C with rigorous vortexing every 15 min for 1 h. Iodoacetamide (Thermo Fisher Scientific) was added to 15 mM and incubated at room temperature in the dark for 30 min. Proteins were digested overnight at 37°C with trypsin (20 ng/ μl , Pierce), then centrifuged at 16,000 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 (Thermo Fisher Scientific). Peptides were separated using an Acclaim PepMap100 C18 column ($75\ \mu\text{m}$ i.d. $\times 15$ cm, $3\ \mu\text{m}$ particle size, 100 Å pores, Thermo Fisher Scientific) 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 (Käll 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 carried out in R (Ihaka and Gentleman, 1996; R Core Team, 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 have been 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 IPA and a core expression analysis performed, followed by a comparison analysis of the results. A significant canonical pathway had a $-\log(P\text{-value}) > 1.3$, an absolute z -score > 2 , and contained at least four 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 PBS, infiltrated with 5 to 15% sucrose followed by OCT medium, and frozen in liquid nitrogen. Tissues were sectioned (10 μ m) using a cryostat (Leica CM3050) and collected on charged glass slides (Thermo Fisher Scientific). The OCT was removed by washing in ice-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 (Thermo 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°C, washed (3 \times 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 using a confocal Leica DM5000 B microscope. Z-stacks were created in 1 μ m increments at 1024 \times 1024 pixel resolution and line averaged three times.

Immunoblotting

Proteins from isolated CTB cell pellets were solubilized in M-PER (Thermo Fisher Scientific) according to the manufacturer's protocol and protein concentrations determined spectrophotometrically (Shimadzu). Samples (5 μ g) 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 three 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 (AEA and 2-AG)

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 s each) at 5000 rpm (with 30 s breaks) at <10°C. Then 50 μ l of each homogenized sample was pipetted into 13 \times 100 mm tubes after which 150 μ l of a deuterated internal standard solution was added, before vortexing for 1 min and centrifugation (3000 g) for 10 min.

Then the supernatant (5 μ l) was separated on a Shimadzu Prominence UFLC system equipped with a binary pump and a SIL-20AC autosampler. Separation was achieved on an XBridge C18 column (4.6 \times 50 mm). A gradient separation was used consisting of mobile phase A [0.05% H₂O/5 mM MNH₄ (15%)] and mobile phase B [ACN/2.5 mM MNH₄ (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 \rightarrow 287.4 for 2-AG, 386.4 \rightarrow 293.4 for 2-AG-d8, 348.5 \rightarrow 62.2 for AEA, and 356.5 \rightarrow 163.2 for AEA-d8. Data acquisition and quantitative processing were accomplished using Applied Biosystems Analyst version 1.5.1 software.

Invasion assay

Cytotrophoblasts (2nd trimester) were isolated according to methods described above. The cells (250,000) were plated in 500 μ l 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 CNR1 or CNR2 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 carried out three times (biological replicates). An unpaired, two-tailed Student's *t*-test (*P*<0.05) was used to determine significance.

Creation of graphics

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

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Competing interests

S.J.F. is a consultant for Novo Nordisk.

Author contributions

Conceptualization: M.G., S.J.F.; Methodology: S.J.F.; Validation: K.O.; Formal analysis: M.G., S.H., S.J.F.; Investigation: M.G., O.O.; Resources: M.K.; Data curation: M.G.; Writing - original draft: S.J.F.; Writing - review & editing: M.G., S.J.F.; Visualization: M.G.; Supervision: S.J.F.; Project administration: M.G.; Funding acquisition: S.J.F.

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Data availability

Raw and normalized microarray data have been deposited in the Gene Expression Omnibus under accession number GSE156766. Raw and normalized mass spectrometry data have been deposited in MassIVE (<https://massive.ucsd.edu>), dataset MSV000085995.

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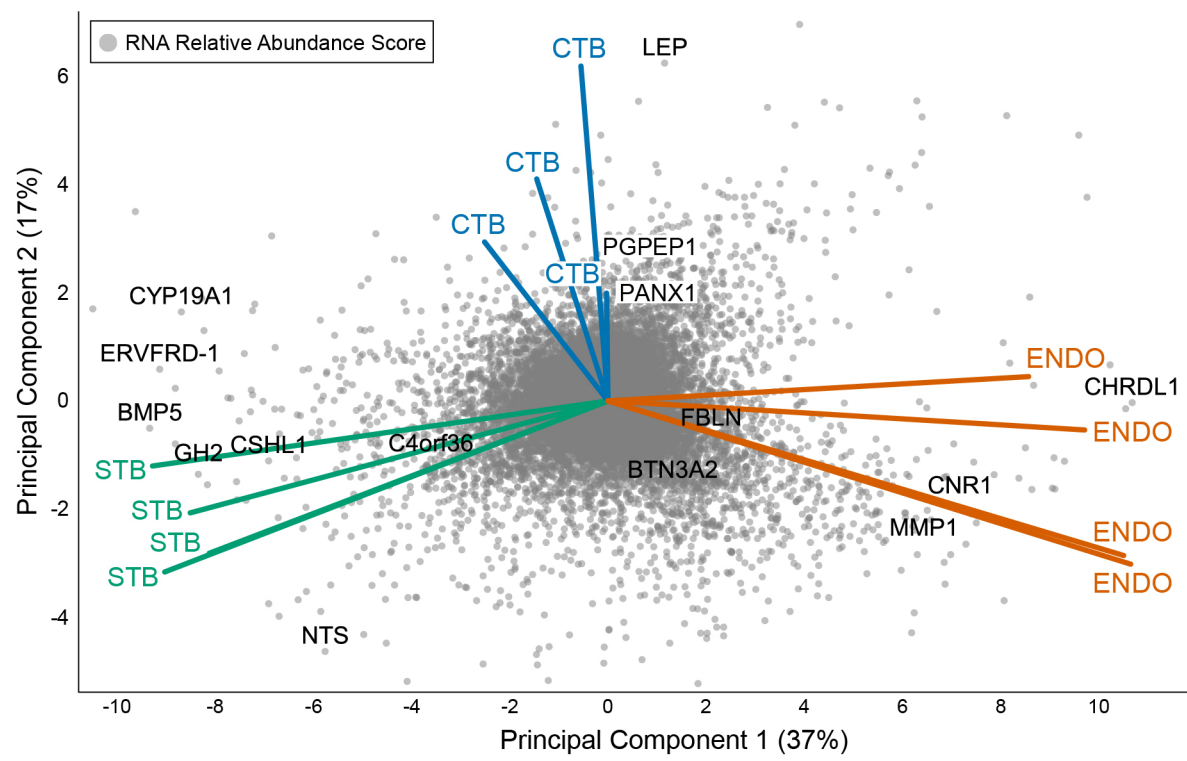


Fig. S1.

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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, foylpolypolyglutamyl 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
			CHRD1	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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	camitine 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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			PIP5K1	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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			P115	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 immunoglobulin-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
			PTH1H	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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 interfacier 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
			KCNB2	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

S	C	E	Symbol	Name	Linear Fold Change		
					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	leiomodulin 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

S	C	E	Symbol	Name	Linear Fold Change		
					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	coatamer protein complex subunit zeta 2	ns	-4.2	3.0

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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	glutamyl-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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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

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			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

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			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	plasmalipin	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

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					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 metalloproteinase 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

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					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	nebullette	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 metalloproteinase 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

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					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

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					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 metalloproteinase 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 pectinacetyltransferase 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 metalloproteinase 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 metalloproteinase domain 19	-7.6	-6.2	ns

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					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 metalloproteinase 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
			KDEL3	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
			ARHGDI3	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 metalloproteinase inhibitor 1	-2.9	-4.9	ns
			RAB8B	RAB8B, member RAS oncogene family	-4.8	-3.7	ns

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					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 metalloproteinase 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

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					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 metalloproteinase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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	folliculin 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 metalloproteinase domain 9	-2.3	-2.0	ns
			ADAM15	ADAM metalloproteinase domain 15	-2.2	-2.2	ns
			ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-2.2	-2.2	ns
			ABRA1	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

S	C	E	Symbol	Name	Linear Fold Change		
					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-acetylneuraminase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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 Ili 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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			NPIP4	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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			DHRX	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	progesterin 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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			REG-AS1	REG 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
			PSTIP2	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 metalloproteinase 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
			NPIP11	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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			NPIP3	nuclear pore complex interacting protein family, member B3	ns	2.6	ns
			NPIP3	nuclear pore complex interacting protein family, member B3	ns	2.6	ns
			NPIP9	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
			NPIP5	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, metalloredutase	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

S	C	E	Symbol	Name	Linear Fold Change		
					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	angiomin 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
			HMG2	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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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	camitine 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

S	C	E	Symbol	Name	Linear Fold Change		
					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-aminolevulinic acid 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

S	C	E	Symbol	Name	Linear Fold Change		
					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	camitine 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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			HMG3-AS1	HMG3 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
			CHRD2	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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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	progesterone-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 metalloproteinase 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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					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 transcription 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

S	C	E	Symbol	Name	Linear Fold Change		
					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
			ATRNL	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 adenyltransferase 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, contractin beta (yeast)	ns	-2.4	ns

S	C	E	Symbol	Name	Linear Fold Change		
					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
			LRR6	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

S	C	E	Symbol	Name	Linear Fold Change		
					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 acetyltransferase	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

S	C	E	Symbol	Name	Linear Fold Change		
					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

S	C	E	Symbol	Name	Linear Fold Change		
					S vs C	S vs E	E vs C
			LOC105376958	uncharacterized LOC105376958	<i>ns</i>	-2.0	<i>ns</i>
			RASSF4	Ras association (RalGDS	<i>ns</i>	<i>ns</i>	2.0
			ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	<i>ns</i>	<i>ns</i>	2.0
			SAP30	Sin3A associated protein 30kDa	<i>ns</i>	-2.0	<i>ns</i>
			THYN1	thymocyte nuclear protein 1	<i>ns</i>	-2.0	<i>ns</i>
			YBEY	ybeY metalloproteinase (putative)	<i>ns</i>	-2.0	<i>ns</i>
			CD151	CD151 molecule (Raph blood group)	<i>ns</i>	-2.0	<i>ns</i>
			DSTN	destrin (actin depolymerizing factor)	<i>ns</i>	-2.0	<i>ns</i>
			ADGRG3	adhesion G protein-coupled receptor G3	<i>ns</i>	<i>ns</i>	2.0
			PNMA1	paraneoplastic Ma antigen 1	<i>ns</i>	-2.0	<i>ns</i>
			CFAP36	cilia and flagella associated protein 36	<i>ns</i>	-2.0	<i>ns</i>
			SAPCD1-AS1	SAPCD1 antisense RNA 1	<i>ns</i>	-2.0	<i>ns</i>
			PRICKLE2-AS1	PRICKLE2 antisense RNA 1	<i>ns</i>	<i>ns</i>	2.0
			SDC3	syndecan 3	<i>ns</i>	-2.0	<i>ns</i>
			GOLM1	golgi membrane protein 1	<i>ns</i>	<i>ns</i>	2.0
			PDE4A	phosphodiesterase 4A, cAMP-specific	<i>ns</i>	-2.0	<i>ns</i>

(*ns*=no significant difference)

RMA log₂
-5x x 5x

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

RNA			Protein			Symbol	Name	Linear Fold Change					
S	C	E	S	C	E			RNA			Protein		
								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 metalloproteinase 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 metalloproteinase domain 15	-2	1	-1	-6	8	-47
						LASP1	LIM and SH3 protein 1	-2	1	1	23	-1	31

RNA			Protein			Symbol	Name	Linear Fold Change					
S	C	E	S	C	E			RNA			Protein		
								SvC	SvE	EvC	SvC	SvE	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
						NPIP4	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 (alpha-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

RMA log₂

-5x 5x

TMM log₂

0 12

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 ($\mu\text{g/ml}$)
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