ERJ Express. Published on August 30, 2018 as doi: 10.1183/13993003.00564-2018

EUROPEAN RESPIRATORY *journal*

FLAGSHIP SCIENTIFIC JOURNAL OF ERS

Original article

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Please cite this article as: Kwapiszewska G, Gungl A, Wilhelm J, *et al*. Transcriptome profiling reveals the complexity of pirfenidone effects in IPF. *Eur Respir J* 2018; in press (https://doi.org/10.1183/13993003.00564-2018).

Transcriptome profiling reveals the complexity of pirfenidone effects in IPF

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Keywords: CEMIP/KIAA1199, pulmonary fibrosis, IPF, fibroblast

Word count: 3771

Take home message: Pirfenidone mode of action in human lungs involves a complex interactome comprising genes related to inflammation and extracellular matrix architecture.

Abstract

Despite the beneficial effects of pirfenidone in treating idiopathic pulmonary fibrosis (IPF) patients, it remains unclear if lung fibroblasts are the main therapeutic target. To resolve this question, we employed a comparative transcriptomic approach and analyzed lung homogenates (LH) and lung fibroblasts (FB) derived from IPF patients treated with or without pirfenidone. In FB, pirfenidone therapy predominantly affected growth and cell division pathways indicating a major cellular metabolic shift. In LH samples, pirfenidone treatment was mostly associated with inflammation-related processes. In FB and LH, regulated genes were over-represented in the Gene Ontology node “extracellular matrix (ECM)”. We identified lower expression of cell migration-inducing and hyaluronan-binding protein (CEMIP) in both LH and FB from pirfenidone-treated patients. Plasma levels of CEMIP were elevated in IPF patients compared to healthy controls and decreased after 7 months of pirfenidone treatment. CEMIP expression in FB was downregulated in a glioma-associated oncogene homolog (GLI)-dependent manner and CEMIP silencing in IPF FB reduced collagen production and attenuated cell proliferation and migration. Cumulatively, our approach indicates that pirfenidone exerts the beneficial effects via its action on multiple pathways in both fibroblasts and other pulmonary cells, through its ability to control ECM architecture and inflammatory reactions.

Introduction

Idiopathic pulmonary fibrosis (IPF) is a devastating disease with a median survival of less than five years following diagnosis and a mortality rate that exceeds many types of cancer. An IPF diagnosis leads to a high burden of morbidity with poor quality of life. In spite of recently approved medical therapies, lung transplantation still remains the only definitive treatment option [1].

The basic pathologic mechanisms in IPF are characterized by injury and activation of alveolar epithelial cells, (myo)-fibroblast proliferation and dysregulated transcriptional and posttranslational control of extracellular matrix (ECM) components such as collagen and hyaluronan (HA) in the lung. As a result, there are changes reminiscent of excessive scar formation, with irreversible damage of the lung architecture causing disturbance in ventilation, perfusion and gas exchange and eventually death from cardio-respiratory failure [2].

Despite inhibitory effects on lung fibroblast proliferation and collagen production, several treatment strategies failed to show a positive effect in IPF patients; these include interferon gamma [3], the tyrosine kinase inhibitor imatinib [4] and the selective endothelin receptor antagonists bosentan [5] and ambrisentan [6]. Accordingly, a strong or conditional negative recommendation has been attributed to these therapeutic concepts in the current international clinical practice guidelines for IPF [7]. Currently, there are only two approved drugs for the treatment of IPF, pirfenidone and nintedanib [7]. Pirfenidone (5-Methyl-1-Phenyl-2-(1H)-Pyridon) is an orally available synthetic drug, which was approved in 2011 in Europe and in 2014 in the United States for the treatment of mild to moderate IPF. To date, four randomized placebo-controlled phase III studies demonstrated that pirfenidone significantly slows down disease progression by reducing the decline in forced vital capacity (FVC) [8-11]. Combined data from the CAPACITY 1 and 2 as well as ASCEND trials showed a significant benefit with respect to progression-free survival, six-minute walking test distance and dyspnea score [8, 9]. Furthermore, pooled analysis of data from four phase III trials demonstrated a reduction in all-cause mortality under pirfenidone treatment [12]. In real-world observational studies of pirfenidone treatment in IPF patients, the effects of pirfenidone on FVC decline were consistent with the findings from the clinical trials [13].

Although recent findings demonstrated that pirfenidone exerts pleiotropic effects on numerous cell types [14, 15], the mechanisms by which pirfenidone slows IPF progression is not well understood. Here, by applying a complex unbiased transcriptomic approach employing 1) lung tissue from IPF patients with or without pirfenidone treatment, 2) isolated fibroblasts from the same patients, and 3) cultured fibroblasts from IPF patients treated *in vitro* with pirfenidone, we found that pirfenidone exerts most of its effects on the lung by regulating expression of genes involved in inflammation and ECM architecture.

Material and Methods

A description of methodologies is provided in the supplement; here only information about the IPF patients is given.

Human lungs

Human lung samples were obtained from patients with IPF who underwent lung transplantation at the Department of Surgery, Division of Thoracic Surgery, Medical University of Vienna, Vienna, Austria. The protocol and tissue usage were approved by the institutional ethics committee (976/2010) and patient consent was obtained before lung transplantation. Microscopic sections were prepared and Hematoxylin-Eosin-stained to assess the morphology of the fibrotic lungs.

Results

Study population

Transplanted lungs from 14 clinically well-characterized patients with IPF were used in this study. Demographic characteristics and clinical data of the IPF patient experimental and validation cohort, including pirfenidone (ESBRIET®/PIRFENEX) medication, are reported in Table 1. These parameters did not show significant differences between the treated and non-treated groups. All lungs possessed classical characteristics of parenchymal remodeling with the typical pattern of usual interstitial pneumonia (UIP) (Supplementary Figure S1).

Effects of pirfenidone on the expression profiles in lung homogenates and isolated fibroblasts

To determine the effects of pirfenidone treatment on the molecular signature *in situ*, we performed gene expression profiling on i) lung homogenate (LH) samples and ii) isolated human lung fibroblasts (FB) from IPF patients treated with or without pirfenidone (P). Lung homogenates are heterogeneous tissue samples that can be used to identify individual genes with a strong treatment-associated average change in gene expression pointing to processes that are either directly or indirectly changed by pirfenidone. In contrast, the analysis of isolated fibroblasts could identify cell-type specific responses to pirfenidone treatment. The experimental design is presented in Figure 1A.

The comparison of the entire gene expression profile by principal component analysis (PCA) revealed only minor global changes between LH samples from pirfenidone treated patients

(IPF+P(LH)) to those without pirfenidone treatment (IPF(LH)) (Figure 1Ba). Global gene set tests using the Kyoto Encyclopedia of Gene and Genomes (KEGG) showed several significantly perturbed pathways (Figure 1Bb). These included inflammatory processes and changes in cell-cell contact (e.g. tight junction, endocytosis). The global distribution of all genes according to the respective log fold changes and p-values are depicted in the volcano plot in Figure 1Bc, and Figure 1Bd shows the expression levels of top 20 regulated genes at single patient level.

The expression profiles of FB isolated from pirfenidone treated (IPF+P(FB)) and untreated patients (IPF(FB)) were distinct and gave good separation in PCA (Figure 1Ca). The most significantly altered pathways in FB indicated that cells possessed general metabolic alterations related to growth and cell division (e.g. DNA replication, cell cycle) and modified protein turnover (e.g. proteasome) (Figure 1Cb). The top 20 regulated genes according to the p-value ranking are highlighted in the volcano plot in Figure 1Cc, and shown on single-patient-level expression in Figure 1Cd.

Comparison of lung homogenate (IPF(LH), IPF+P(LH)) and fibroblast (IPF(FB), IPF+P(FB)) samples by PCA, gave a clear separation that primarily discriminated between LH and FB (Figure 1D). Global gene set tests showed a larger number of significantly perturbed pirfenidone-induced pathways in FB than in LH (Figure 1E). This is expected as the profiles obtained from LH represent a mixture of the responses of many cell types, so that the cell-type specific perturbation of defined pathways is more difficult to ascertain. Analysis of the 100 genes with the largest differences showed clear separation of LH and FB expression profiles in a hierarchical cluster analysis (Euclidean distance and complete linkage; Figure 1F). Gene clustering revealed several groups of genes with a source-specific regulation associated with pirfenidone treatment (regulated in LH but not in FB (blue cluster); regulated in FB but not in LH (yellow cluster), concurrently regulated in LH and FB (green cluster) and oppositely regulated in LH and in FB (grey cluster; Figure 1F and Supplementary Table S1).

Pirfenidone induces distinct gene regulation in lung homogenates and isolated fibroblasts

To understand the transcriptional repertoire being specifically regulated in response to pirfenidone in either compartment, we selected genes regulated only in one group, either LH or FB. For this purpose, the threshold was set to a log fold change (LFC) higher than $|1.41|$ to define upregulated genes and lower than $|0.5|$ to define not regulated genes (coloured dots in Figure 2A and listed as “only in LH/only in FB” in Supplementary Table

S1). This way we focused on genes either induced by at least 2-fold change or repressed to at least 50%. Over-representation analysis of these selectively regulated genes with Gene Ontology (GO) nodes revealed that in FB, the selected genes were contained within the “extracellular matrix”, “cytosol” and “nucleus” nodes. In LH, the selected genes were over-represented in “extracellular matrix” and “immune response” nodes (Figure 2B, C). Due to their strong abundance in our analysis, we first explored the molecular interactions within the ECM and inflammatory response nodes. The interaction network together with parallel expressional annotation of genes regulated in LH and FB once more highlighted differences between LH and FB (Figure 2D and E, Supplementary Figure S2). We also explored representative inflammatory and ECM KEGG pathways and colour-mapped the expressional change after pirfenidone treatment (B- and T-cell receptor signalling and ECM-receptor interaction; Supplementary Figure S3).

Additionally, the five most downregulated genes in LH pointed towards a dysbalanced immune system: defensin beta 4A (DEFB4A), chemokine ligand 6 (CXCL6), serum amyloid A2 (SAA2), serum amyloid A1 (SAA1); BPI fold containing family A member 1 (BPIFA1) (Supplementary Table S2). In FB, pirfenidone downregulated genes involved in: transcription: homeobox C9 (HOXC8), cell signalling: sulfatase 2 (SULF2) and osteogenic differentiation: stimulator of chondrogenesis 1 (SCRG1) (Supplementary Table S3).

Convergently regulated genes in lung homogenates and isolated fibroblasts due to pirfenidone treatment

Applying a cutoff of LFC>$|1|$, we found 1) 803 (393 up and 410 down) genes being regulated in LH (Supplementary Table S2) and 2) 557 (282 up and 275 down) genes that were differentially regulated in FB after pirfenidone treatment in comparison to the respective controls (Supplementary Table S3). Eleven annotated genes had the same direction of regulation (4 up and 7 down) in both comparison groups (Figure 2F and G). The individual patient-to-patient variations of these genes are shown in Figure 2H. The functional involvements of these 11 commonly regulated annotated genes are given in Supplementary Table S4.

Cell migration-inducing and hyaluronan-binding protein (CEMIP) as a target of pirfenidone

CEMIP was strongly downregulated by pirfenidone treatment in both our approaches (Figure 2G and H) and has previously been implicated in several processes relevant to lung fibrosis, namely ECM production, inflammation, and cell proliferation (Supplementary Table S4) [16]. Thus we explored the role of CEMIP in more detail. The decrease in CEMIP mRNA expression in IPF+P(LH) and IPF+P(FB), observed in the microarray experiments, was confirmed using a validation cohort (Figure 3A and C). Furthermore, IPF+P(LH) and IPF+P(FB) exhibited reduced CEMIP protein expression as compared to IPF patients without the therapy (Figure 3B and D). Importantly, CEMIP was elevated on both mRNA and protein levels in IPF(LH) and IPF(FB) in comparison to donor samples (Figure 3A-D). These results were corroborated by immunohistochemistry, which showed increased staining intensity for CEMIP in the lungs of pirfenidone naïve IPF patients as compared to donors and pirfenidone treated patients (Figure 3E and F). CEMIP immunoreactivity was mainly observed in alveolar type II cells and (myo)-fibroblasts (as identified by the expression of prosurfactant protein C (proSP-C) and α-smooth muscle actin (SMA), respectively) in donor and IPF lungs. Positive staining for CEMIP was also observed in endothelial cells (as identified by the expression of von Willebrand factor (vWF)) in donor lungs (Figure 3F). These findings indicate that fibroblasts are not the exclusive producers of CEMIP in human lungs.

Analysis of circulating CEMIP revealed significantly elevated levels in IPF samples as compared to age and sex-matched healthy controls (Figure 4A and Table 2). As pirfenidone decreased CEMIP expression in our array analysis, we analyzed circulating CEMIP levels in IPF patients before and during pirfenidone treatment. The mean treatment period of these patients was 7.1±2.5 months (Figure 4B). In 6 from 7 patients pirfenidone treatment was associated with a marked decrease in CEMIP levels (Figure 4C).

CEMIP is involved in invasive properties of IPF fibroblasts

We recently demonstrated that pirfenidone inhibits the Hedgehog (Hh) signaling pathway by targeting GLI proteins [14]. The promotor analysis of the *CEMIP* gene revealed the presence of the GLI consensus sequence GAACACCCA at the -820 bp position (Supplementary Figure 4A). In line with this observation, SAG, a synthetic Hh pathway agonist, induced CEMIP protein expression in donor FB. This effect was blocked by pirfenidone and the potent GLI1/2 inhibitor, JQ1. Importantly, no additive inhibitory effect was observed when pirfenidone and JQ1 were used simultaneously (Supplementary Figure 4B) suggesting that pirfenidone itself blocks SAG-triggered CEMIP expression by interfering with GLI transcription factors.

Next we investigated the functional relevance of CEMIP in IPF(FB) via depletion experiments. Knockdown of CEMIP decreased the proliferation under basal conditions as well as following stimulation with platelet derived growth factor (PDGF)-BB or epidermal growth factor (EGF) (Figure 5A), but did not affect apoptosis (Figure 5B). Furthermore, silencing of CEMIP inhibited migration and increased the time for wound closure (Figure 5C). In addition, knockdown impaired stress fiber formation (Figure 5D) and reduced expression of collagen I but did not affect the expression of fibronectin (FN), matrix metalloprotease (MMP)-2 or α-SMA (Figure 5E-G). The mRNA levels of the senescence markers, p21 and p53, were downregulated following CEMIP depletion, however, on the protein level no changes were apparent (Figure 5E-G). Given that CEMIP is implicated in the catabolism of hyaluronan (HA), we examined whether pirfenidone treatment affects deposition of HA in the lungs of IPF patients. As depicted in Figure 5H, more prominent accumulation of HA was observed in IPF patients who received pirfenidone as compared to the IPF patients with no treatment. Furthermore, our microarray analysis revealed that pirfenidone differently regulated the HA-mediated motility receptor (HMMR) and HA and proteoglycan link protein 4 (HAPLN4) in both IPF(LH) and IPF(FB). Additionally, pirfenidone significantly affected the expression of HA synthase 1 (HAS1) and HA binding protein 2 (HABP2) specifically in IPF(LH), while the expression of inter-alpha-trypsin inhibitor heavy chain 3 (ITIH3), a HA binding protein essential for ECM stabilization, and CD44 molecule was changed in IPF(FB) only (Supplementary Table S5 and S6).

Effects of pirfenidone *in vitro*

In the final set of experiments, we extended our transcriptomic analysis to genes that are dysregulated in IPF FB, kept in culture for several passages, and then treated with pirfenidone *in vitro*. The rationale behind this was: i) to have a complementary *in vitro* experimental setting of pirfenidone action and ii) to single out the specific signaling mechanisms of pirfenidone in FB without the effects of the global response to pirfenidone when FB are in their natural microenvironment. To this end, we performed a comparative study between i) FB isolated from treated (IPF+P(FB)) *vs* non-treated (IPF(FB)) IPF patients and ii) lung fibroblasts isolated from IPF patients, cultured and exposed to pirfenidone *in vitro* (IPF(FB+P) (Figure 6A). Applying a LFC>│1│, we found a total of 743 genes that were regulated in *in vitro* pirfenidone-treated fibroblasts (Supplementary Table S7). Hierarchical clustering of the top 100 regulated genes showed complete separation of the transcription profiles from fibroblasts, treated both *in vivo* as well as *in vitro* (Figure 6B). Of note, we found that the gene expression considerably varied between fibroblasts from *in vivo* and *in vitro* settings underlining the influence of *in vitro* culturing on fibroblasts. Nevertheless, the comparison of pirfenidone-regulated genes from IPF(FB+P) and IPF+P(FB) revealed 23 genes with the same expression pattern (17 up and 6 down; Figure 6C and D and Supplementary Table S8). Among the down-regulated genes were: endothelin 1 (EDN1) and 5-hydroxytryptamine receptor 2B (HTR2B), both being part of the G protein-coupled receptor signal transduction pathways. On the other hand, the upregulated genes were annotated to the following biological processes: TGF-β receptor signaling pathway, transcription from RNA polymerase II promoter and cellular lipid metabolic process. The heat-maps represent the individual patient-to-patient variations of commonly regulated genes in both settings (Figure 6E).

Discussion

The clinical success of pirfenidone in the treatment of IPF patients is attributed to its pleiotropic mode of action. Numerous *in vitro* and *in vivo* studies demonstrated that pirfenidone exhibits anti-fibrotic, anti-inflammatory, and anti-oxidant effects [15], however, it still remains unclear which of these effects occur at the therapeutic doses achieved in humans.

In the present study, we performed gene expression profiling analysis to identify the pirfenidone mode of action. The analysis was performed on multiple levels using lung homogenate samples and freshly isolated fibroblasts derived from IPF patients who were or were not treated with pirfenidone. This *in situ* approach was further corroborated by our *in vitro* study, where fibroblasts isolated from IPF patients were exposed to pirfenidone in cell culture. Pirfenidone treatment was associated with major changes in inflammatory processes and cell-cell contacts in lung homogenates, while in fibroblasts the most significantly perturbed pathways were related to metabolic reprogramming, growth and cell division. Genes regulated in both specimens primarily belonged to the extracellular matrix.

Interactions between ECM molecules and inflammatory cells/mediators ensure proper response of the lung to insults and their dysregulation may lead to an aberrant damage response and finally to fibrosis. The mutual relationship between ECM producing fibroblasts and different subpopulations of inflammatory cells in lung fibrosis is supported by numerous studies. For instance, degradation products of HA were found to stimulate B cells to produce various profibrogenic cytokines, including potent activators of fibroblasts such as TGF-β1, IL-6, and IL-4 [17]. Interestingly, abnormal B and T cell aggregates were shown in IPF lungs and diverse IgG autoantibodies have been reported in IPF plasma [2, 18-20].

The close interplay between the ECM and the immune responses is supported by our data demonstrating that among the genes significantly downregulated by pirfenidone in the lung homogenate were those involved in the regulation of innate and adaptive immunity, including e.g. CXCL6, and tumor necrosis factor receptor superfamily member 17 (TNFRSF17). Strikingly, TNFRSF17 was shown to control the development of B cells and thereby the autoimmune responses [21]. In pulmonary fibroblasts, pirfenidone therapy mainly suppressed the expression of sulfatase 2 (SULF2), an enzyme involved in posttranslational modification of ECM components [22]. Increased sulfation of ECM heparan sulfate proteoglycans has already been described in the lungs of IPF patients suggesting altered structural and growth factor binding capacity of the fibrotic matrix [23].

In both pulmonary fibroblasts and lung homogenates derived from pirfenidone-treated patients one of the most upregulated genes was gremlin 2 (*GREM2)* while one of the most significantly downregulated genes was *CEMIP*. The role of gremlin in fibrogenesis remains controversial, with studies demonstrating its pro- and anti-fibrotic activities [24, 25]. Anti-fibrotic properties of gremlin are associated with its ability to upregulate fibroblast growth factor (FGF) 10 and thus to facilitate the repair of injured alveolar epithelium [26, 27]. The contribution of CEMIP to the pathogenesis of IPF has not been acknowledged to date, thus our study is the first one to demonstrate its potent pro-fibrotic actions.

CEMIP influences the extracellular environment by participating in the catabolism of HA [28], which not only alters the strength, lubrication and hydration of ECM but also regulates adhesion, migration, proliferation and differentiation of a variety of cells [29]. We found a marked increase in CEMIP mRNA and protein expression in lung homogenates and fibroblasts of IPF patients as compared to donors. Most importantly, CEMIP expression was suppressed by pirfenidone treatment in both the primary and the validation cohort of our IPF patients. Furthermore, pirfenidone therapy resulted in a sharp decrease of CEMIP plasma levels in IPF patients who had high CEMIP plasma levels at baseline. These findings strongly encourage further investigations and suggest that CEMIP could be used as a predictive biomarker that identifies IPF patients with profound alterations in ECM architecture and inflammation who are most likely to respond favorably to this treatment.

Although *in vivo* studies are needed to delineate the contribution of CEMIP to the development of lung fibrosis, our results suggest that CEMIP depletion suppresses proliferation of IPF lung fibroblasts in response to different pro-fibrotic stimuli, impairs migration of these cells and lowers collagen I production. Furthermore, the decreased CEMIP expression may stabilize HA fibers, as suggested from our stainings. HA can differentially promote or suppress fibrosis depending on the length of its carbohydrate chain. In the lungs of bleomycin-treated mice low-molecular-weight HA exerts potent pro-inflammatory effects and exacerbates inflammatory responses, which consequently lead to the progression of lung fibrosis [30, 31]. In contrast, high-molecular-weight HA, which is mainly produced by HA synthase (HAS) 1 and HAS2, was found to be crucial for regenerative tissue repair. In the skin, IL-10-triggered increase in HAS1 and HAS2 expression and decrease in hyaluronidase (HYAL) 1, HYAL2 and CEMIP expression reduced scar formation in different wound models [32]. In the lung, depletion of HAS2 in alveolar type II cells (ATIIC) impaired the renewal capacity of ATIIC and exacerbated lung fibrosis upon bleomycin instillation [33]. Thus, our data support an important role of an HA-rich wound ECM for proper tissue regeneration and suggest CEMIP as a potential therapeutic target in diseases in which dysregulated inflammation and HA intersect [23, 29, 34].

The direct comparison of gene profile changes of IPF pulmonary fibroblasts upon *in vitro* treatment with pirfenidone with pulmonary fibroblasts isolated from IPF patients that received pirfenidone as IPF treatment revealed only 23 genes with the matching expression change. Among these, only two protein-coding genes, EDN1 and 5-HTR2B, were downregulated. EDN1 and 5-HTR2B are involved in the pathogenesis of IPF; EDN1 through the induction of fibroblast proliferation and transdifferentiation [35] and 5-HTR2B *via* the regulation of TGF-β1-triggered collagen production [36]. Although, the contribution of EDN1 and 5-HTR2B to the development of lung fibrosis has been examined in experimental models of lung fibrosis, the role of these molecules in the pathogenesis of human IPF is still unclear.

Even though valuable insights can be gained from *in vitro* experiments on the direct effects of pirfenidone, our results demonstrate that these experiments do not provide a full picture of the biological complexity of pirfenidone action in IPF and should be regarded with caution. *In vitro* results can be influenced by culture conditions, cell passage and direct exposure of a single cell type to a pharmalogical compound at non-physiological levels. Our previous findings demonstrated that pirfenidone inhibits profibrotic activities of cultured lung fibroblasts only when it is used in the concentration strongly exceeding its levels observed in IPF plasma [14]. We cannot exclude that the high pirfenidone concentrations *in vitro* could lead to additional off target effects, explaining the small overlap between IPF+P(FB) and IPF(FB+P) groups. Thus, *in vitro* studies might be used to generate a hypothesis, which then has to be tested in *in situ* and *in vivo* approaches.

The main limitation of this study is that our lung samples do not represent a random sample from a prospective randomized controlled study where pirfenidone was compared to placebo. In fact we used tissue samples from explanted end-stage lungs of IPF patients who were or were not treated with pirfenidone. Therefore, it is possible that this patient selection may have biased the results. Although all patients suffered from end-stage lung disease, we found highly significant differences associated with pirfenidone treatment. Further, the low number of patients used for the analysis could limit the reliability of the results; however, two independent approaches increased the robustness of the results. By combining the analysis of biomaterial from IPF patients who received or did not receive pirfenidone treatment and that of isolated lung fibroblasts, which were treated with pifenidone *in vitro*, we were able to identify a consistent pattern of pirfenidone-induced changes in the gene expression profiles.

Although we are far away from fully understanding the pathogenesis of IPF and the effects of pirfenidone, our results point to an important role of innate and adaptive immune responses as well as ECM organization in the progressive and irreversible lung tissue scarring. Our approach provides a basis for new combination-based therapeutic strategies improving the effectiveness of pirfenidone in IPF.

Research support: the German Research Foundation (DFG: WY119/1-3 to M.W.), the Else Kröner-Fresenius-Foundation (to M.W.), the Excellence Cluster “Cardiopulmonary System” (ECCPS to M.W.), the German Center for Lung Research (to M.W.), the University Medical Center Giessen and Marburg (UKGM to M.W.), the Austrian Science Fund (FWF: P27848-B28 to G.K.) and the Jubilee Foundation of the Austrian National Bank (16187 to G.K.), and the Austrian Research Promotion Agency (FFG: 858308 to G.K. and H.T.P).

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Figure legends:

Figure 1: Transcriptomic profiling of human lung homogenates and human lung fibroblasts derived from IPF patients treated with pirfenidone. A) Schematic overview of the experimental design. IPF: idiopathic pulmonary fibrosis; LH: lung homogenate; FB: lung fibroblasts; P: pirfenidone. B) Transcriptome profiling of IPF LH: a) Principal component analysis (PCA) showing the separation between pirfenidone treated and non-treated IPF LH samples. b) Kyoto Encyclopedia of Gene and Genomes (KEGG) based gene function analysis showing the top ten most affected pathways after pirfenidone treatment in IPF LH. c) Volcano plot indicating global distribution of log2 (fold change in expression) and p-value. Highlighted are the 20 genes with the highest significance. d) The heatmap shows the clustering between treated and non-treated samples for the top 20 regulated genes as in c. C) Transcriptome profiling of IPF FB: a) PCA plot showing clear separation between pirfenidone treated and non-treated IPF FB. b) KEGG analysis showing the ten most significantly perturbed pathways in IPF FB after pirfenidone treatment. c) Volcano plot depicting the global distribution of log2 (fold change in expression) and p-value. The labelling shows the 20 genes with the highest significance. d) Heatmap representing expression at single patient level for the top 20 genes as in c. D) PCA of LH and FB from IPF patients with and without pirfenidone treatment. E) KEGG pathway analysis comparing pathway enrichment between FB and LH samples. F) Heat-map representation of significant changes in gene expression with colour coded grouping (left hand side) of the top 100 differentially regulated genes between FB and LH.

Figure 2: Differentially and commonly regulated genes between lung homogenates and lung fibroblasts upon pirfenidone treatment. A) Scatter plot presenting the values of $\log_2$ (fold change in expression) for each gene in the IPF(LH) samples (x-axis) versus the IPF(FB) samples (y-axis). Coloured spots represent divergent genes being regulated by pirfenidone only in one of the groups. Genes were considered exclusively regulated in either FB or LH when their point on the scatterplot was outside the dotted circle (radius 1.41) and remained within ± 0.5 for one of the groups (indicated by the horizontal and vertical dotted lines, respectively). B) Spider (radar) chart displays core Gene Ontology (GO) nodes being regulated in IPF(LH) (red colour) and/or in IPF(FB) (green colour), and C) shows the top 7 single GO nodes significant for each group. D, E) Representation of minimum network analysis as performed by NetworkAnalyst showing core protein-protein interactions within the most abundant GO nodes, ECM (D, expression shown for FB) and immune cell response (E, expression shown for LH). F) Venn diagrams representing the number of common up- and

down-regulated genes between LH and FB from patients without compared to patients with pirfenidone (IPF+P) treatment. G) Scatter plot presenting the values of log2 (fold change in expression) for each gene regulated upon pirfenidone treatment in the IPF(LH) samples (x-axis) versus the IPF(FB) samples (y-axis). Marked spots represent convergent genes. G) The heat-maps represent the individual patient-to-patient variations of commonly regulated genes.

Figure 3: CEMIP regulation in lung fibrosis upon pirfenidone treatment. A) CEMIP expression in LH of an independent validation cohort (n=20 for donor; n=18 for IPF and n=7 for IPF+P). B) CEMIP protein levels in LH of donors and IPF patients with and without pirfenidone treatment (n=8 for donor; n=9 for IPF and n=7 for IPF+P). C) CEMIP expression in lung FB isolated from donor lungs and untreated and pirfenidone treated IPF patients of an independent validation cohort (n=11 for donor; n=5 for IPF and n=7 for IPF+P). D) CEMIP protein levels in FB isolated from lungs of donors, IPF patients without pirfenidone treatment and IPF patients with pirfenidone treatment (n=8 for donor; n=8 for IPF and n=7 for IPF+P). mRNA levels were assessed by qPCR, whereas proteins levels by western blotting. *PBGD* was used as a reference gene in qPCR and HSP70 as a loading control in western blotting. Biological replicates are shown. For statistical analysis one-way ANOVA with Tukey's multiple comparisons test was used. *$p<0.05$, **$p<0.01$. ***$p<0.001$. E) Overview images of CEMIP immunoreactivity in lungs of donors, IPF patients untreated and treated with pirfenidone. Isotype control antibody was used to confirm the specificity of the staining; Scale bar = 200 µm. F) High magnification images of CEMIP, prosurfactant protein C (proSP-C), α-smooth muscle actin (α-SMA), CD45 and von Willebrand factor (vWF) immunostainings on serial sections of lungs from donor, untreated IPF patients and IPF patients treated with pirfenidone; Scale bar = 50 µm.

Figure 4: CEMIP levels in the plasma of healthy controls and IPF patients with and without pirfenidone treatment. A) CEMIP plasma levels of healthy control subjects and IPF patients with and without pirfenidone treatment. Kruskal-Wallis test with Dunn's multiple comparison test. *$p<0.05$. B) Schematic of follow-up in IPF patients before and duringpirfenidone treatment. C) CEMIP plasma levels at baseline and after 7.1±2.5 months of pirfenidone treatment. Wilcoxon matched pairs test.

Figure 5: Effects of knockdown of CEMIP on IPF pulmonary fibroblasts. A) Proliferation of IPF(FB) treated with *CEMIP* siRNA (siCEMIP) or non-targeting control siRNA (siCtrl) at basal conditions and upon stimulation with PDGF-BB or EGF. B) Apoptosis of IPF(FB) measured by AnnexinV-FITC and propidium iodide (PI) staining. A

minimum of 5,000 cells were measured. C) Representative pictures and quantification of IPF(FB) migration after 24 hours of siCEMIP or siCtrl treatment. D) α-SMA (green) and Phalloidin (red) fluorescence staining of IPF(FB) after treatment with siCEMIP or siCtrl. A-D) Combined data of 2 independent experiments with n=4 biological replicates. E) mRNA and F) protein levels of markers for ECM production/turnover (Col1, FN, MMP2), FB differentiation (α-SMA) and FB senescence (p53, p21). mRNA levels were assessed by qPCR (n=6) and protein levels by western blotting (n=4). *PBGD* was used as a reference gene in qPCR and HSP70 as a loading control in western blotting. G) Quantification of F. For statistical analysis a Mann Whitney test were used. $^*p<0.05$, $^{**}p<0.01$. $^{***}p<0.001$. H) Affinity-histochemical staining and quantification of hyaluronan on IPF lungs of patients with and without pirfenidone treatment. Upper panel scale bar = 100 µm, inset/lower panel scale bar = 50 µm. Sections pre-treated with hyaluronidase were used as a staining control.

Figure 6: Transcriptomic profiling of human lung fibroblasts treated with pirfenidone *in vitro*. A) Schematic overview of the experimental design. FB used for the first transcriptomic profiling (*in situ*) were used immediately after isolation (passage one). In the *in vitro* settings, FB were used between passage three to five (second transcriptomic profiling). B) Heat-map representation of significant changes in gene expression between *in situ* (IPF+P(FB)) and *in vitro* (IPF(FB+P)) treated fibroblasts. C) Venn diagrams showing the number of common up- and down-regulated genes between IPF+P(FB) and IPF(FB+P). D) Scatter plot presenting the values of log2 (fold change in expression) for each gene in the IPF+P(FB) samples (x-axis) versus the *in vitro* treated fibroblasts (IPF(FB+P)) (y-axis). Marked spots represent genes with an absolute log2 fold change of more than one in both experimental approaches (*in situ* and *in vitro*). E) The heat-maps represent the individual patient-to-patient variations of commonly regulated genes.

Table 1. Demographic characteristics and clinical data of donors and IPF patients in the transcriptome cohort and the validation cohort.

	Cohort used for transcriptome profiling		Validation cohort		
Variable	**[*]IPF**	**IPF+[♯]P**	**Donor**	**IPF**	**IPF+P**
Subjects [n]	7	7	31	23	7
Age, years [mean±SD]	56.8±9.0	55.4±7.5	51.4±14.7	61.8±12.9	58.0±5.4
Sex, male/female [n]	4/3	5/2	12/19	16/7	4/3
Smoking status, never/former/current [n]	0/7/0	2/5/0	-	7/16/0	2/5/0
[†]FVC, % predicted [mean±SD]	39.6±16.7	49.5±11.2	-	49.1±13.0	48.1±10.2
Histological confirmation of a [‡]UIP pattern, [%]	100	100	-	100	100
Daily dose of pirfenidone [g]	-	2.0 ± 0.7	-	-	1.9±0.6
Duration of pirfenidone treatment [month]	-	8.4 ± 4.8	-	-	11.2 ± 3.8

[*]IPF, idiopathic pulmonary fibrosis; [♯]P, Pirfenidone; [†]FVC, forced vital capacity; [‡]UIP, usual interstitial pneumonia

Table 2. Demographic characteristics and clinical data of the IPF patients whose plasma was used to measure CEMIP levels.

Variable	**Healthy**	**[*]IPF baseline**	**IPF+[♯]P**
CEMIP plasma levels [ng/mL]	0.83±0.6	1.49±0.7	1.13±0.4
Subjects [n]	7	8	11
Age, years [mean±SD]	58.5±6.6	59.4±12.7	61.6±10.8
Sex, male/female [n]	5/2	5/3	9/2
Smoking status, never/former/current [n]	2/2/3	1/7/0	2/9/0
[†]FVC, % predicted [mean±SD]	-	60.1±12.5	61.1±9.9
Histological confirmation of a [‡]UIP pattern, [%]	-	100	100
Daily dose of pirfenidone [g]	-	-	2.4±0.0
Duration of pirfenidone treatment [month]	-	-	7.1±2.5

[*]IPF, idiopathic pulmonary fibrosis; [♯]P, Pirfenidone; [†]FVC, forced vital capacity; [‡]UIP, usual interstitial pneumonia

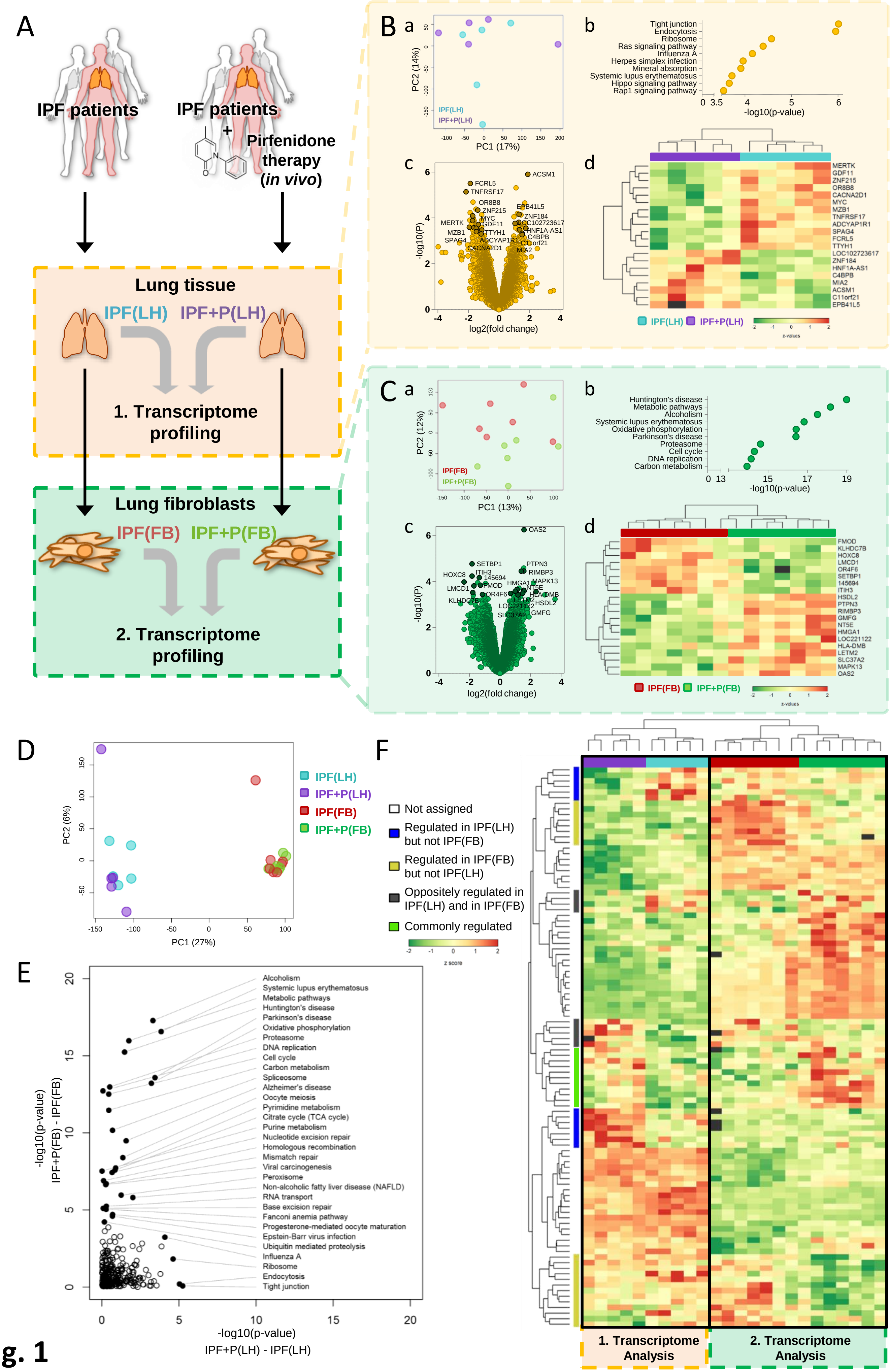
A
IPF patients
IPF patients
+
Pirfenidone
therapy
(in vivo)
Lung tissue
IPF(LH)
IPF+P(LH)
1. Transcriptome
profiling
Lung fibroblasts
IPF(FB)
IPF+P(FB)
2. Transcriptome
profiling
B
a
PC1 (17%)
PC2 (14%)
IPF(LH)
IPF+P(LH)
b
Tight junction
Endocytosis
Ribosome
Ras signaling pathway
Influenza A
Herpes simplex infection
Mineral absorption
Systemic lupus erythematosus
Hippo signaling pathway
Rap1 signaling pathway
-log10(p-value)
c
ACSM1
FCRL5
TNFRSF17
OR8B8
ZNF215
MYC
GDF11
EPB41L5
ZNF184
LOC102723617
HNF1A-AS1
C4BPB
C11orf21
MIA2
MERTK
MZB1
SPAG4
TTYH1
ADCYAP1R1
CACNA2D1
-log10(P)
log2(fold change)
d
MERTK
GDF11
ZNF215
OR8B8
CACNA2D1
MYC
MZB1
TNFRSF17
ADCYAP1R1
SPAG4
FCRL5
TTYH1
LOC102723617
ZNF184
HNF1A-AS1
C4BPB
MIA2
ACSM1
C11orf21
EPB41L5
IPF(LH)
IPF+P(LH)
z-values
C
a
PC1 (13%)
PC2 (12%)
IPF(FB)
IPF+P(FB)
b
Huntington's disease
Metabolic pathways
Alcoholism
Systemic lupus erythematosus
Oxidative phosphorylation
Parkinson's disease
Proteasome
Cell cycle
DNA replication
Carbon metabolism
-log10(p-value)
c
OAS2
SETBP1
PTPN3
RIMBP3
HOXC8
ITIH3
145694
HMGA1
MAPK13
LMCD1
FMOD
NT5E
OR4F6
HLA-DMB
KLHDC7B
LETM2
LOC221122
HSDL2
SLC37A2
GMFG
-log10(P)
log2(fold change)
d
FMOD
KLHDC7B
HOXC8
LMCD1
OR4F6
SETBP1
145694
ITIH3
HSDL2
PTPN3
RIMBP3
GMFG
NT5E
HMGA1
LOC221122
HLA-DMB
LETM2
SLC37A2
MAPK13
OAS2
IPF(FB)
IPF+P(FB)
z-values
D
PC1 (27%)
PC2 (6%)
IPF(LH)
IPF+P(LH)
IPF(FB)
IPF+P(FB)
E
Alcoholism
Systemic lupus erythematosus
Metabolic pathways
Huntington's disease
Parkinson's disease
Oxidative phosphorylation
Proteasome
DNA replication
Cell cycle
Carbon metabolism
Spliceosome
Alzheimer's disease
Oocyte meiosis
Pyrimidine metabolism
Citrate cycle (TCA cycle)
Purine metabolism
Nucleotide excision repair
Homologous recombination
Mismatch repair
Viral carcinogenesis
Peroxisome
Non-alcoholic fatty liver disease (NAFLD)
RNA transport
Base excision repair
Fanconi anemia pathway
Progesterone-mediated oocyte maturation
Epstein-Barr virus infection
Ubiquitin mediated proteolysis
Influenza A
Ribosome
Endocytosis
Tight junction
-log10(p-value)
IPF+P(FB) - IPF(FB)
-log10(p-value)
IPF+P(LH) - IPF(LH)
F
Not assigned
Regulated in IPF(LH) but not IPF(FB)
Regulated in IPF(FB) but not IPF(LH)
Oppositely regulated in IPF(LH) and in IPF(FB)
Commonly regulated
z score
1. Transcriptome Analysis
2. Transcriptome Analysis

Fig. 1

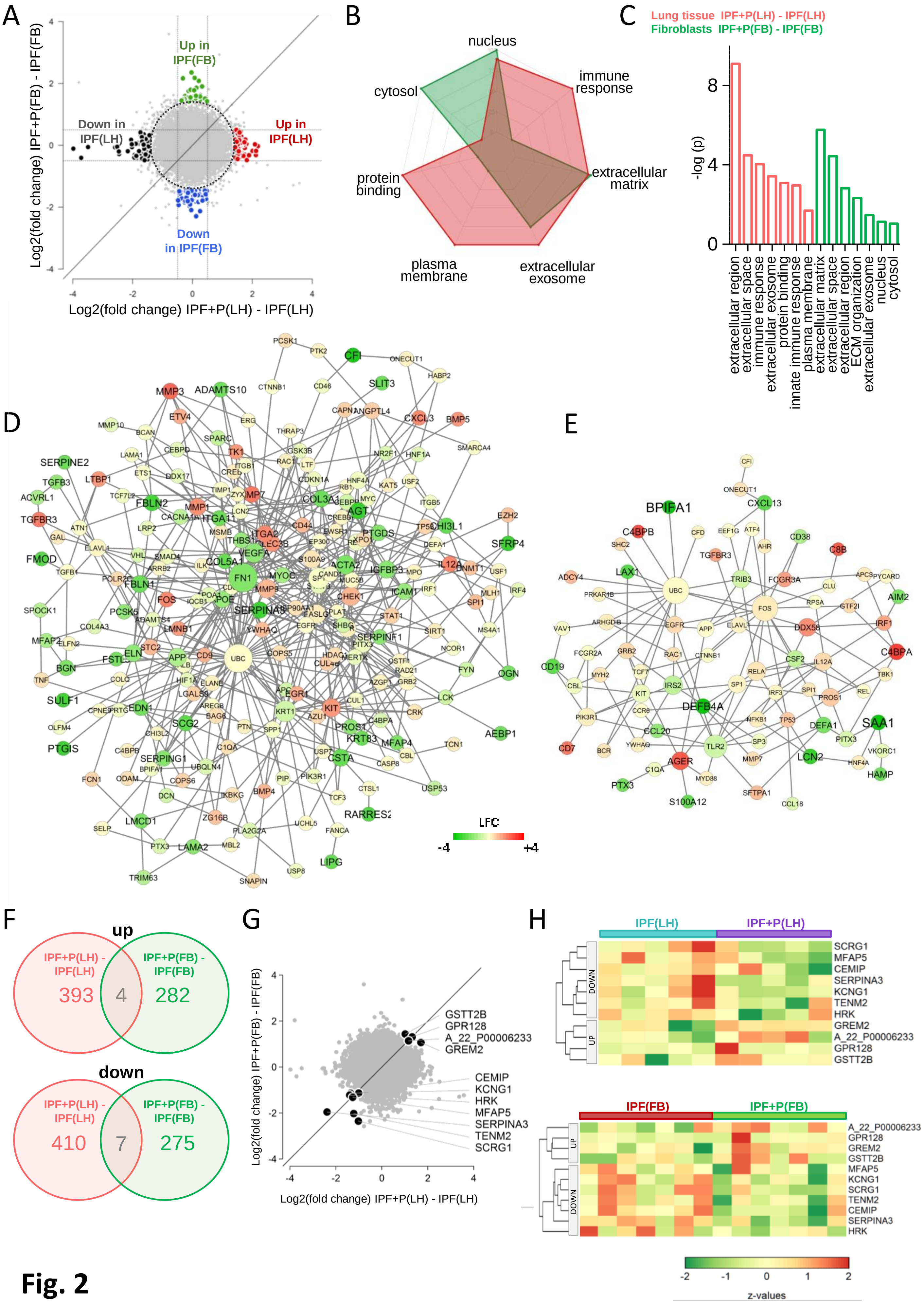
A
Log2(fold change) IPF+P(FB) - IPF(FB)
Log2(fold change) IPF+P(LH) - IPF(LH)
Up in IPF(FB)
Down in IPF(LH)
Up in IPF(LH)
Down in IPF(FB)
4
2
0
-2
-4
-4
-2
0
2
4
B
nucleus
immune response
extracellular matrix
extracellular exosome
plasma membrane
protein binding
cytosol
C
Lung tissue IPF+P(LH) - IPF(LH)
Fibroblasts IPF+P(FB) - IPF(FB)
-log (p)
8
4
0
extracellular region
extracellular space
immune response
extracellular exosome
protein binding
innate immune response
plasma membrane
extracellular matrix
extracellular space
extracellular region
ECM organization
extracellular exosome
nucleus
cytosol
D
PCSK1
PTK2
CFI
ONECUT1
HABP2
SLIT3
MMP3
ADAMTS10
CTNNB1
CD46
CAPN1
ANGPTL4
CXCL3
BMP5
MMP10
ETV4
ERG
THRAP3
SMARCA4
BCAN
SPARC
GSK3B
NR2F1
HNF1A
SERPINE2
LAMA1
CEBPD
TK1
RAC1
LTF
TGFB3
ETS1
ITGB1
CREB
DDX17
CDKN1A
HNF4A
KAT5
USF2
ACVRL1
LTBP1
TIMP1
ZYX
MMP7
COL3A1
RB1
CEBPB
MYC
ITGB5
TGFBR3
TCF7L2
FBLN2
MMP1
AGT
EZH2
ATN1
CACNA1A
ITGA11
LCN2
CD44
TP53
CHI3L1
GAL
LRP2
MSMB
EWSR1
ITGA2
PTGDS
SFRP4
ELAVL1
THBS1
LEC3B
EP300
XPO1
DEFA1
VHL
SMAD4
VEGFA
S100A9
FMOD
ACTA2
IL12A
DNMT1
USF1
TGFB1
ARRB2
ILK
COL5A1
FN1
MYOC
SP1
CAND1
IGFBP3
MPO
POLR2C
FBLN1
MUC5B
IRF1
IRF4
SPOCK1
FOS
MMP9
CHEK1
ICAM1
MLH1
PCSK6
APOE
SPI1
SERPINA3
HSP90AA1
FASLG
PLAT
STAT1
ADAMTS4
COL4A3
LMNB1
YWHAQ
EGFR
SHBG
SIRT1
MS4A1
MFAP2
ELFN2
SERPINF1
PITX3
NCOR1
STC2
HDAC1
ERTK
FSTL1
ELN
APP
CD9
UBC
CUL4B
OSTF1
FYN
OGN
BGN
HIF1A
ELANE
RAD21
TNF
COL6
AZGP1
GRB2
LGALS9
APC
EGR1
SULF1
EDN1
AREGB
KRT1
CUL1
LCK
CPNE
PRTG
BAG6
KIT
CRK
OLFM4
SCG2
PTN
AZU1
C4BPA
AEBP1
CHI3L2
SPP1
PROS1
PTGIS
KRT83
MFAP4
TCN1
C4BPB
C1QA
CBL
SERPING1
USP7
CSTA
CASP8
BPIFA1
UBQLN4
FCN1
ODAM
COPS6
PIP
PIK3R1
CTSL1
USP53
DCN
IKBKG
BMP4
TCF3
RARRES2
LMCD1
ZG16B
UCHL5
SELP
PLA2G2A
FANCA
PTX3
LAMA2
MBL2
LIPG
TRIM63
SNAPIN
USP8
COPS5
LFC
-4
+4
E
CFI
ONECUT1
CXCL13
BPIFA1
C4BPB
CFD
EEF1G
ATF4
CD38
SHC2
AHR
C8B
TGFBR3
ADCY4
LAX1
UBC
TRIB3
FCGR3A
APCS
PYCARD
CLU
AIM2
PRKAR1B
FOS
RPSA
GTF2I
VAV1
ARHGDIB
EGFR
APP
ELAVL1
DDX58
IRF1
FCGR2A
GRB2
RAC1
CTNNB1
CSF2
IL12A
C4BPA
CD19
MYH2
TCF7
RELA
TBK1
CBL
KIT
IRS2
SP1
IRF3
SPI1
PROS1
REL
PIK3R1
CCR6
DEFB4A
NFKB1
TP53
DEFA1
SAA1
CCL20
PITX3
CD7
BCR
YWHAQ
TLR2
SP3
VKORC1
AGER
MMP7
LCN2
HNF4A
C1QA
MYD88
HAMP
PTX3
SFTPA1
S100A12
CCL18
F
up
IPF+P(LH) - IPF(LH)
IPF+P(FB) - IPF(FB)
393
4
282
down
IPF+P(LH) - IPF(LH)
IPF+P(FB) - IPF(FB)
410
7
275
G
Log2(fold change) IPF+P(FB) - IPF(FB)
Log2(fold change) IPF+P(LH) - IPF(LH)
4
2
0
-2
-4
-4
-2
0
2
4
GSTT2B
GPR128
A_22_P00006233
GREM2
CEMIP
KCNG1
HRK
MFAP5
SERPINA3
TENM2
SCRG1
H
IPF(LH)
IPF+P(LH)
DOWN
UP
SCRG1
MFAP5
CEMIP
SERPINA3
KCNG1
TENM2
HRK
GREM2
A_22_P00006233
GPR128
GSTT2B
IPF(FB)
IPF+P(FB)
UP
DOWN
A_22_P00006233
GPR128
GREM2
GSTT2B
MFAP5
KCNG1
SCRG1
TENM2
CEMIP
SERPINA3
HRK
-2
-1
0
1
2
z-values

Fig. 2

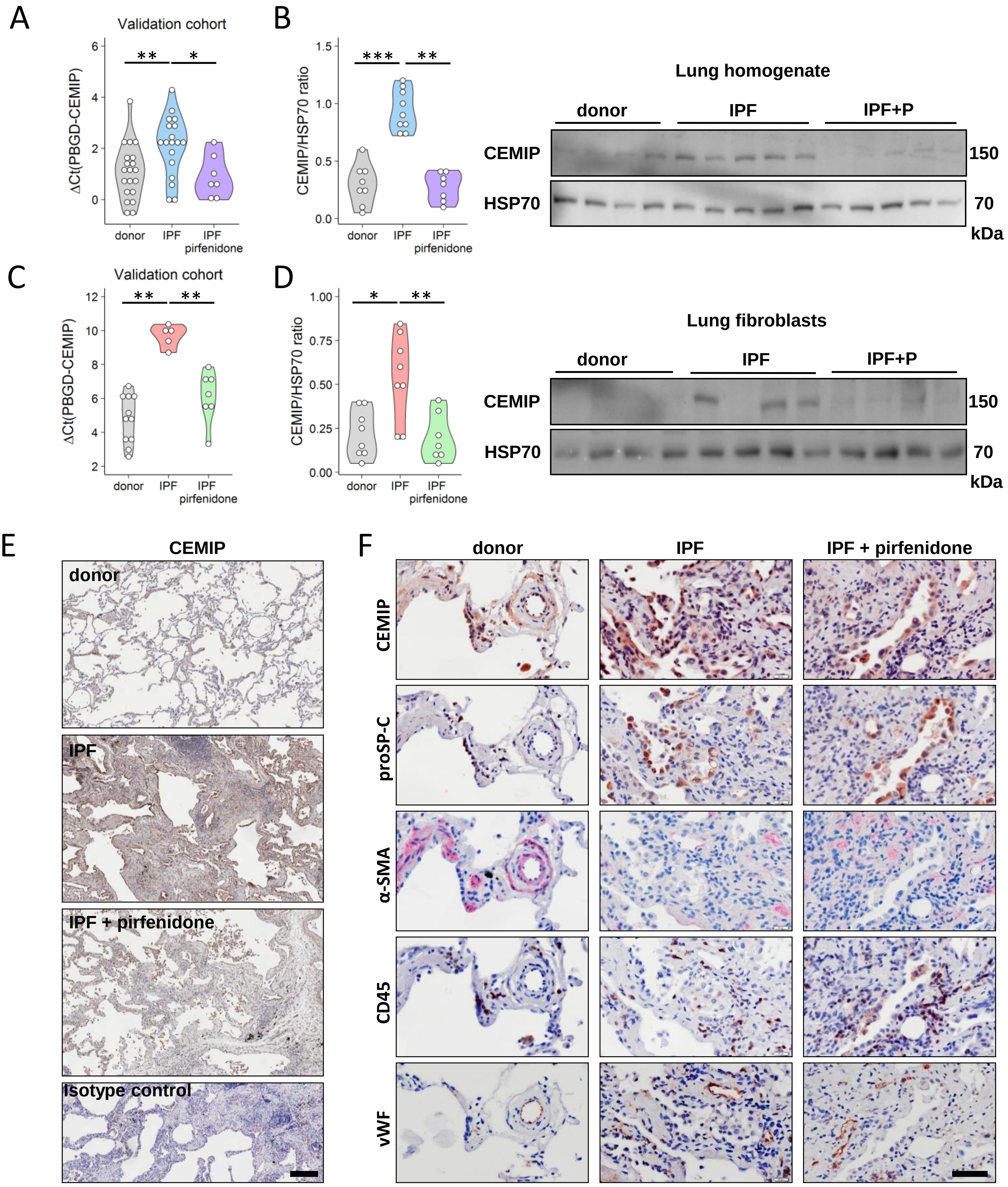
A
Validation cohort
ΔCt(PBGD-CEMIP)
6
4
2
0
**
*
donor
IPF
IPF pirfenidone
B
CEMIP/HSP70 ratio
1.5
1.0
0.5
0.0
***
**
donor
IPF
IPF pirfenidone
Lung homogenate
donor
IPF
IPF+P
CEMIP
HSP70
150
70
kDa
C
Validation cohort
ΔCt(PBGD-CEMIP)
12
10
8
6
4
2
**
**
donor
IPF
IPF pirfenidone
D
CEMIP/HSP70 ratio
1.00
0.75
0.50
0.25
0.00
*
**
donor
IPF
IPF pirfenidone
Lung fibroblasts
donor
IPF
IPF+P
CEMIP
HSP70
150
70
kDa
E
CEMIP
donor
IPF
IPF + pirfenidone
Isotype control
F
donor
IPF
IPF + pirfenidone
CEMIP
proSP-C
α-SMA
CD45
vWF

Fig. 3

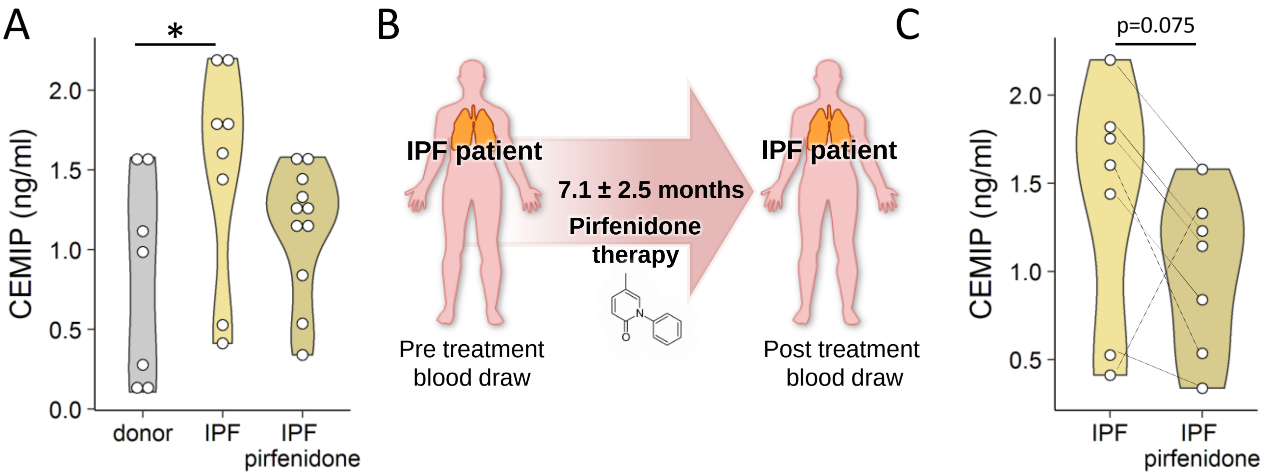
A
*
CEMIP (ng/ml)
0.0
0.5
1.0
1.5
2.0
donor
IPF
IPF pirfenidone
B
IPF patient
7.1 ± 2.5 months
Pirfenidone therapy
IPF patient
Pre treatment blood draw
Post treatment blood draw
C
p=0.075
CEMIP (ng/ml)
0.5
1.0
1.5
2.0
IPF
IPF pirfenidone

Fig. 4

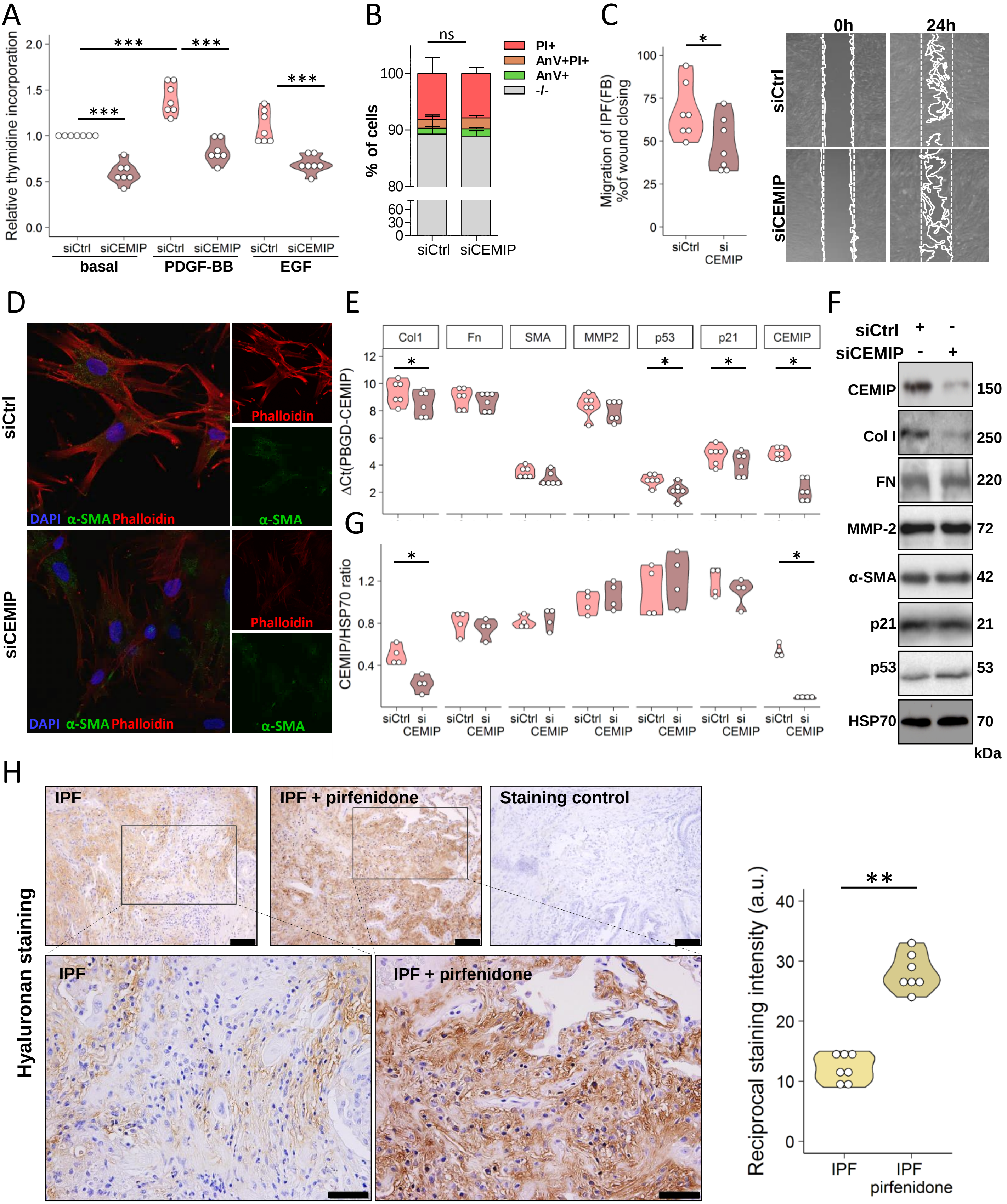
A
Relative thymidine incorporation
2.0
1.5
1.0
0.5
0.0
***
***
***
***
siCtrl siCEMIP siCtrl siCEMIP siCtrl siCEMIP
basal
PDGF-BB
EGF
B
ns
% of cells
100
90
80
60
30
0
siCtrl siCEMIP
PI+
AnV+PI+
AnV+
-/-
C
*
Migration of IPF(FB) %of wound closing
100
75
50
25
0
siCtrl
si CEMIP
0h
24h
siCtrl
siCEMIP
D
siCtrl
siCEMIP
DAPI α-SMA Phalloidin
Phalloidin
α-SMA
E
Col1
Fn
SMA
MMP2
p53
p21
CEMIP
ΔCt(PBGD-CEMIP)
12
10
8
6
4
2
*
*
*
*
G
CEMIP/HSP70 ratio
1.2
0.8
0.4
*
*
siCtrl si CEMIP
F
siCtrl + -
siCEMIP - +
CEMIP 150
Col I 250
FN 220
MMP-2 72
α-SMA 42
p21 21
p53 53
HSP70 70
kDa
H
Hyaluronan staining
IPF
IPF + pirfenidone
Staining control
IPF
IPF + pirfenidone
**
Reciprocal staining intensity (a.u.)
40
30
20
10
0
IPF
IPF pirfenidone

Fig. 5

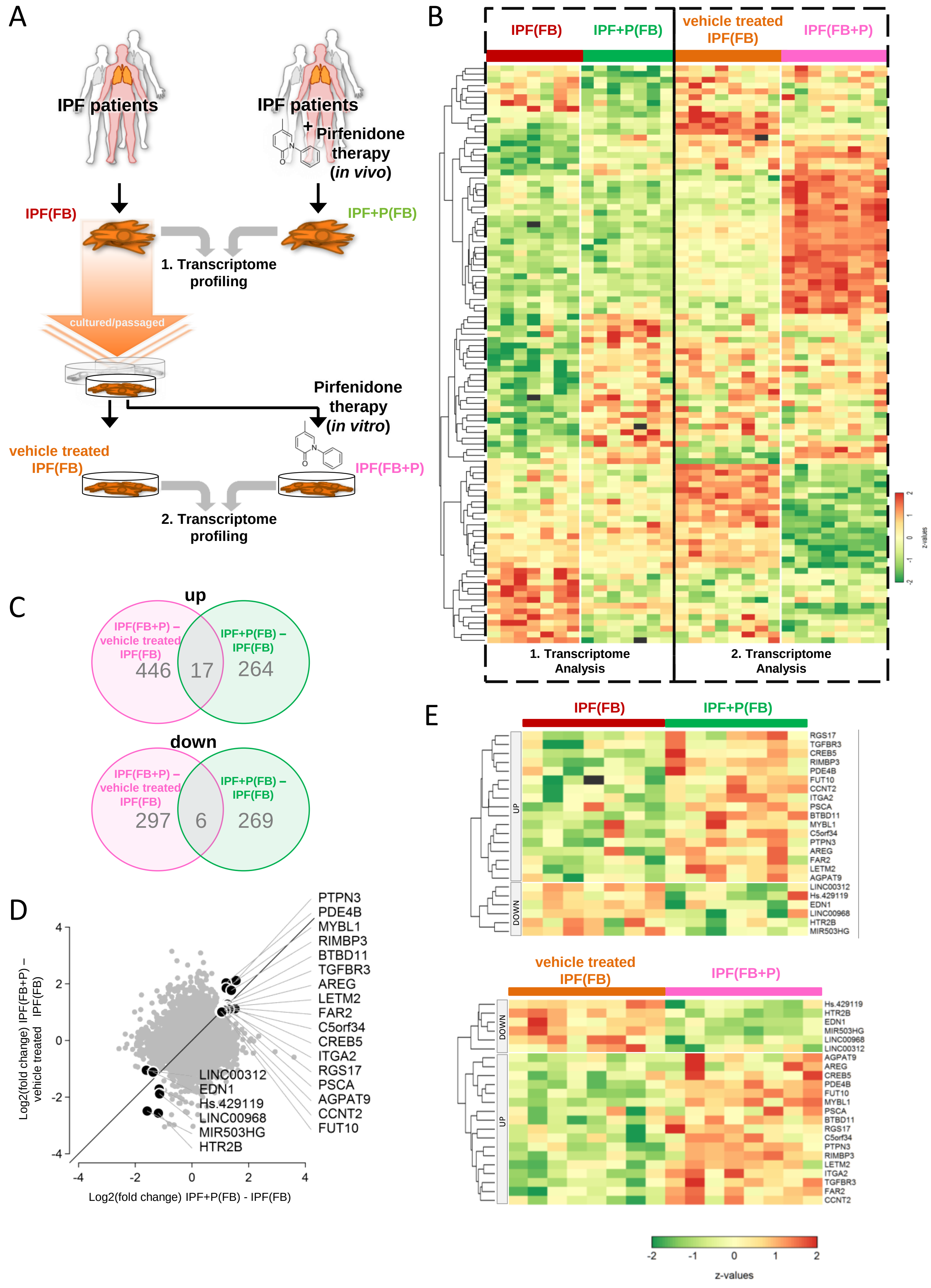
A
IPF patients
IPF patients
+ Pirfenidone therapy (in vivo)
IPF(FB)
IPF+P(FB)
1. Transcriptome profiling
cultured/passaged
Pirfenidone therapy (in vitro)
vehicle treated IPF(FB)
IPF(FB+P)
2. Transcriptome profiling
B
IPF(FB)
IPF+P(FB)
vehicle treated IPF(FB)
IPF(FB+P)
1. Transcriptome Analysis
2. Transcriptome Analysis
z-values
-2
-1
0
1
2
C
up
IPF(FB+P) – vehicle treated IPF(FB)
IPF+P(FB) – IPF(FB)
446
17
264
down
IPF(FB+P) – vehicle treated IPF(FB)
IPF+P(FB) – IPF(FB)
297
6
269
D
Log2(fold change) IPF(FB+P) – vehicle treated IPF(FB)
Log2(fold change) IPF+P(FB) - IPF(FB)
4
2
0
-2
-4
-4
-2
0
2
4
PTPN3
PDE4B
MYBL1
RIMBP3
BTBD11
TGFBR3
AREG
LETM2
FAR2
C5orf34
CREB5
ITGA2
RGS17
PSCA
AGPAT9
CCNT2
FUT10
LINC00312
EDN1
Hs.429119
LINC00968
MIR503HG
HTR2B
E
IPF(FB)
IPF+P(FB)
UP
DOWN
RGS17
TGFBR3
CREB5
RIMBP3
PDE4B
FUT10
CCNT2
ITGA2
PSCA
BTBD11
MYBL1
C5orf34
PTPN3
AREG
FAR2
LETM2
AGPAT9
LINC00312
Hs.429119
EDN1
LINC00968
HTR2B
MIR503HG
vehicle treated IPF(FB)
IPF(FB+P)
DOWN
UP
Hs.429119
HTR2B
EDN1
MIR503HG
LINC00968
LINC00312
AGPAT9
AREG
CREB5
PDE4B
FUT10
MYBL1
PSCA
BTBD11
RGS17
C5orf34
PTPN3
RIMBP3
LETM2
ITGA2
TGFBR3
FAR2
CCNT2
-2
-1
0
1
2
z-values

Fig. 6

Supplementary material

Transcriptome profiling reveals the complexity of pirfenidone effect in human lungs

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Supplementary material and methods

Fibroblast isolation

Human lung samples (1cm^2) without apparent vessels, bronchi or pleural structures were isolated and cut into small pieces. After centrifugation, the supernatant was discarded and the pellet was resuspended in DMEM-F12 (1:1) medium (Gibco, Fisher Scientific, MA, USA) supplemented with 10% fetal calf serum (FCS), 0.2% Penicillin/Streptomycin (Gibco) and 1% Glutamin (Sigma-Aldrich, Hamburg, Germany), seeded in T_{75} Flasks and incubated in humidified atmosphere of 5% CO_2 at 37°C and left for 7 days until cell outgrowth. The purity of isolated human lung fibroblasts (FB) was verified by positive staining for vimentin and fibronectin.

In vitro experiments

Human lung fibroblasts were stimulated with 100nM smoothened agonist (SAG; Calbiochem, Darmstadt, Germany) in the absence or presence of 1.2mg/ml pirfenidone (Sigma-Aldrich) and/or 1µM JQ1 (kindly provided by Dr. M. Lauth, Institute of Molecular Biology and Tumor Research, Center for Tumor- and Immunobiology, Marburg, Germany) and the cells were collected 24 hours thereafter. In other experiments IPF(FB) were treated with 1.2mg/ml pirfenidone for 8 hours and subsequently harvested for global gene profiling. IPF(FB) were transfected with 50nM siRNA (SMARTpool: ON-TARGETplus CEMIP siRNA or Non-targeting siRNA; Dharmacon, Lafayette, CO) using the Effectene Transfection Reagent (Qiagen, Hilden, Germany) according to manufacturer’s instruction. To measure proliferation, 10,000 siRNA-transfected cells were seeded onto 96-well plates. After a 24 hours regeneration period, cells were starved in basal medium DMEM-F12 (1:1) medium (Gibco) supplemented with 0.2% penicillin/streptomycin (Gibco) for 6 hours. Afterwards cells were stimulated for 24 hours with 10ng/ml PDGF-BB (Sigma-Aldrich) or 15ng/ml EGF (Peprotech, London, UK) and proliferation was determined by [^{3}H]thymidine incorporation. Migration of IPF(FB) after knock-down of CEMIP was investigated by seeding 20,000 siRNA-transfected cells in two wells of a Wound Healing assay Cell Culture Insert (Ibidi, Munich, Germany). Cells were allowed to grow confluent for one day before removing the insert. Pictures were taken after 0, and 24 hours and images were analysed using the Image J software. To measure apoptosis, 40,000 siRNA-transfected IPF(FB) were seeded in 12-well plates for 48 hours. Supernatant and cells were collected and washed with binding buffer (10mM HEPES, 2.5mM $CaCl_2$, 140mM NaCl, pH 7.4). Cells were stained with AnnexinV-FITC (1:50, eBioscience/Thermo Fisher Sicentific, Waltham, MA) for 15 min at 4°C, followed by additional washing. One minute before measurement, 0.5µg/ml propidium iodide was added. Apoptosis was measured on a CytoFLEX flow cytometer (Beckman Coulter, Brea, CA) on a minimum of 5,000 events gated on single cells.

RNA isolation and reverse-transcription real-time quantitative RT-PCR

RNA isolation and reverse-transcription real-time quantitative PCR (RT-qPCR) were performed as previously described [1]. The following oligonucleotide primers were used: CEMIP forward 5′- AGCAAACACTTCCTGCACCT-3′, CEMIP reverse 5′-CAGA-GCCTCGATGTCCATGAT-3′; PBGD/HMBS forward 5′-ACCCTAGAAACCCTGCC-AGAGAA-3′, PBGD/HMBS reverse 5′-GCCGGGTGTTGAGGTTTCCCC-3, Collagen

(COL) IA1 forward 5´- CCAAGAGGAAGGCCAAGTC-3´, COLIA1 reverse 5´-CTCGGG-TTTCCACACGTC -3´; Fibronectin (FN) forward 5´-CACCTCTGTGCAGACCACATC-3´, FN reverse 5´-GTCTCTTGGCAGCTGACTCCG-3´; α-smooth muscle actin (SMA) forward 5´-GGGACTAAGACGGGAA-TCCT-3´, α-SMA reverse 5´-CAAAGCCGGCCT-TACAGAG-3´; matrix metalloprotease (MMP) 2 forward 5'-CTTCCAAGTCTGGAGC-GATGT-3', MMP2 reverse 5'-TACCGTCAAAGGGGTATCCAT-3'; p21 forward 5'-ACTCTCAGGGTCGAAAACGG-3', p21 reverse 5'-GATGTAGAGCGGGCCTTTGA-3', p53 forward 5'-GCCTTGGAACTCAAGGATGC-3', p53 reverse 5'-GGCTGTCAGTGG-GGAACAAG-3'. PBGD served as a reference gene. Cycling conditions were 95°C for 6 min, followed by 45 cycles of 95°C for 20 s, 55°C for 30 s, and 73°C for 30 s. Melting curve analysis and gel electrophoresis was performed to confirm the exclusive amplification of the expected PCR product. Results are expressed as ΔCt (Ct_{PBGD}-$Ct_{target\ gene}$).

Western blot analysis

Ten µg cell/lung lysates were separated on a SDS polyacrylamide gel, followed by electrotransfer to a polyvinylidene difluoride (PVDF) membrane. After blocking with 5% non-fat dry milk in TBS-T buffer (25mM Tris-Cl, 150mM NaCl, 0.1% Tween 20, pH 7.5), the membrane was incubated overnight at 4°C with rabbit anti-CEMIP (Biozol, Eching, Germany), rabbit anti-p21 (Cell Signaling Technology, Frankfurt am Main, Germany), rabbit anti-COL I (Sigma-Aldrich), goat anti-MMP2 (R&D Systems, Wiesbaden, Germany), mouse anti-α-SMA (Merck Millipore, Darmstadt, Germany), mouse anti-FN (Enzo Life Sciences, Lörrach, Germany) and mouse anti-p53 (Santa Cruz Biotechnology, Heidelberg, Germany) antibodies. Afterwards, the membrane was incubated with peroxidase-labelled secondary antibody (Dako, Gostrup, Denmark). Final detection of proteins was performed using an ECL Plus Kit (Amersham Biosciences, Freiburg, Germany). As a loading control HSP70 (detected with a mouse anti-HSP70 antibody; Sigma-Aldrich) was used.

Enzyme-linked immunosorbent assay for CEMIP

Detection of CEMIP antigens in plasma from pirfenidone-treated and non-treated IPF patients was performed using Human CEMIP/KIAA1199 ELISA Kit (LifeSpan BioSciences, Vienna, Austria) according to the manufacturer´s instructions. The optical density was determined using a microplate reader at 450 nm.

Immunohistochemistry

Lung tissue specimens were fixed with 4% formaldehyde in PBS and embedded in paraffin. Three µm sections were deparaffinized in xylene and rehydrated through graded ethanol washes. Immunohistochemistry was performed using ImmPressTM Kit with NovaRed Substrate (Vector Laboratories, Eching, Germany) according to the manufacturer´s instruction. The following primary antibodies were used: rabbit anti-CEMIP (Bioss, Woburn, CA), rabbit anti-proSP-C (Millipore, Burlington, MA), rabbit anti-αSma (Thermo Fisher Scientific, Waltham, MA), rabbit anti-CD45 (Abcam, Cambridge, UK) and rabbit anti-vWF (DAKO/Agilent, Santa-Clara, CA). Negative control was performed by replacing the primary antibody with a species-matched isotype control. Images were captured using an Olympus VS120 slide scanning microscope at 40× magnification.

Immunofluorescence

20,000 siRNA transfected IPF(FB) cells were seeded in 8-well chamber slides and cultured for 48 hours. Cells were washed with PBS and fixed with 1% PFA for 20 minutes on ice prior to blocking and permeabilization with 0.02% TritonX and 3% BSA in PBS for 60 minutes. The chamber slides were incubated overnight at 4°C with mouse anti-αSma antibody (Sigma-Aldrich, Vienna, Austria) followed by AlexaFluor 488-anti-mouse secondary antibody for one hour and AlexaFluor 555-Phalloidin (Invitrogen, Carlsbad, CA) for 20 minutes at room temperature. Slides were mounted with DAPI mounting medium (Vectorshield) and sealed.

Affinity-histochemical staining of hyaluronan

Four µm paraffin sections from pirfenidone-treated and non-treated IPF patients (n=7, each group) were deparaffinized in xylene, rehydrated and blocked in 3% H_2O_2 for 10 minutes at room temperature. Next, sections were incubated in 50mM Tris, 150mM NaCl, pH 7.4 buffer containing 5µg/ml biotinylated HA-binding protein (bHABP, Merck Millipore) at 4°C overnight. Afterwards, sections were incubated with horseradish peroxidase-conjugated ExtrAvidin (Sigma-Aldrich). Staining was visualized with 3,3-diaminobenzidine peroxidase substrate (Vector Laboratories, Eching, Germany). To ensure specificity of staining, control sections were incubated with 100U hyaluronidase (Sigma-Aldrich) for 30 minutes at 37°C prior to incubation with bHABP. Finally, the sections were counterstained with hematoxylin (AppliChem, Darmstadt, Germany). Histological examinations were performed in a blinded fashion by two independent observers. For histological examinations, HA staining was determined by DAB signal quantification of at least 5 high-power fields (magnification,

×200) per section for each sample utilizing the Fiji Colour Deconvolution plugin (NIH, Bethesda, MD; https://imagej.net/Fiji/Downloads) which implements stain separation using Ruifrok & Johnston's method [2].

In silico transcription factor binding site analysis

Transcription factor binding site analysis was performed with the ConTra v3 web server [3]. The CEMIP promoter region, up to 1kb upstream of transcription start site (NCBI reference sequence: NM_018689) was analyzed. The positional weight matrix motif V$GLI1_Q2,M01042 (TRANSFAC20113 database) was selected for visualization with a core stringency of 0.90 and similarity stringency of 0.75.

Gene expression profiling

Purified total RNA was amplified and Cy3-labeled using the LIRAK kit (Agilent) following the kit instructions. Per reaction, 200 ng of total RNA was used. The Cy-labeled aRNA was hybridized overnight to 8x60K 60-mer oligonucleotide spotted microarray slides (Agilent Technologies, design ID 074809). Hybridization and subsequent washing and drying of the slides was performed following the Agilent hybridization protocol as described [4]. The dried slides were scanned at 2 µm/pixel resolution using the InnoScan 900 (Innopsys, Carbonne, France). Image analysis was performed with Mapix 6.5.0 software, and calculated values for all spots were saved as GenePix results files. Stored data were evaluated using the R software [5] and the limma package [6] from BioConductor [7]. Log mean spot signals were taken for further analysis. Data was background corrected using the NormExp procedure on the negative control spots and quantile-normalized [6, 8] before averaging. Genes were ranked for differential expression using a moderated t-statistic [6]. Pathway analyses were done using gene set tests on the ranks of the t-values [6].

Statistics

The statistical analysis was performed in GraphPad Prism 5.02 (GraphPad Software Inc., La Jolla, CA). Data are presented as mean±SD. Data from multiple groups were compared for statistical significance using the Kruskal-Wallis test Dunn’s post-hoc test. All tests were performed with an undirected hypothesis. The level of statistical significance was set at 5%.

Supplementary references

1. Wygrecka M, Marsh LM, Morty RE, Henneke I, Guenther A, Lohmeyer J, Markart P, Preissner KT. Enolase-1 promotes plasminogen-mediated recruitment of monocytes to the acutely inflamed lung. Blood 2009: 113(22): 5588-5598.

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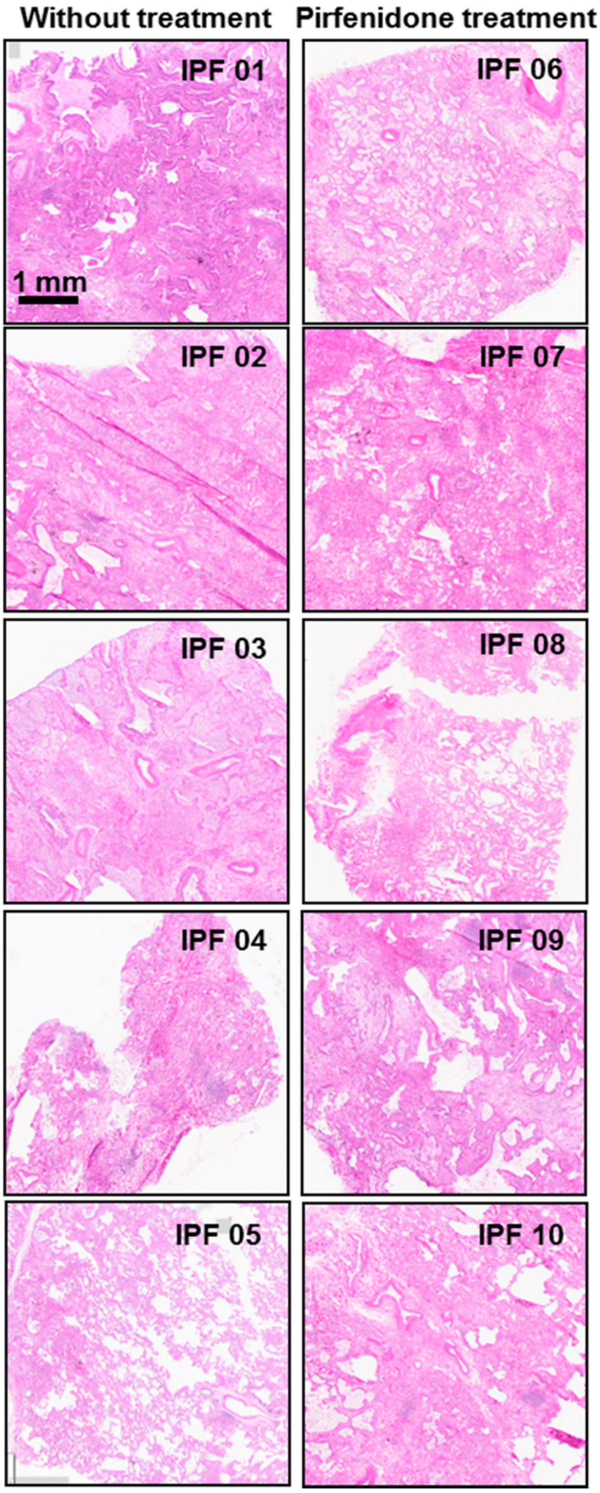
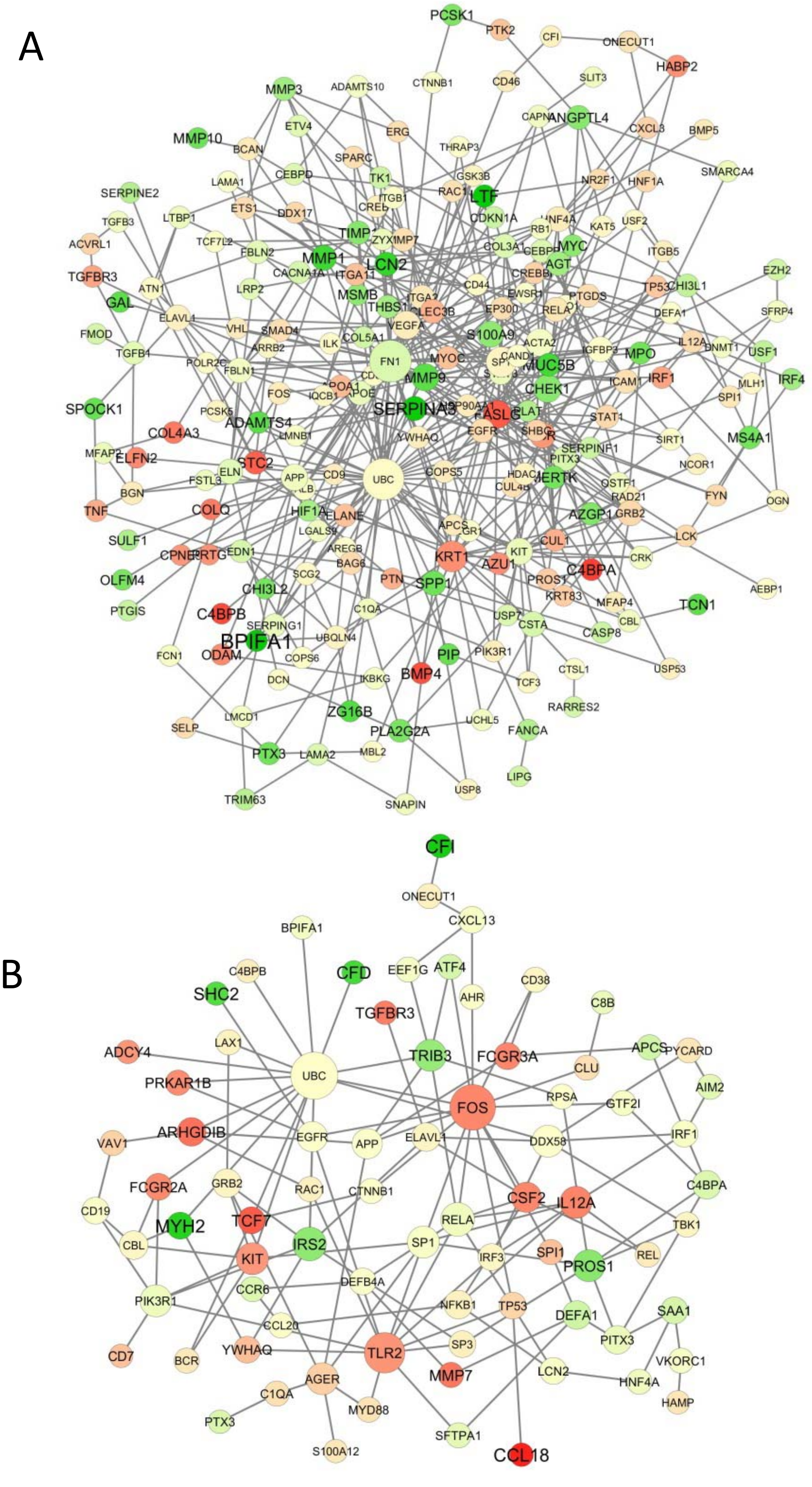
Supplementary figures and tables

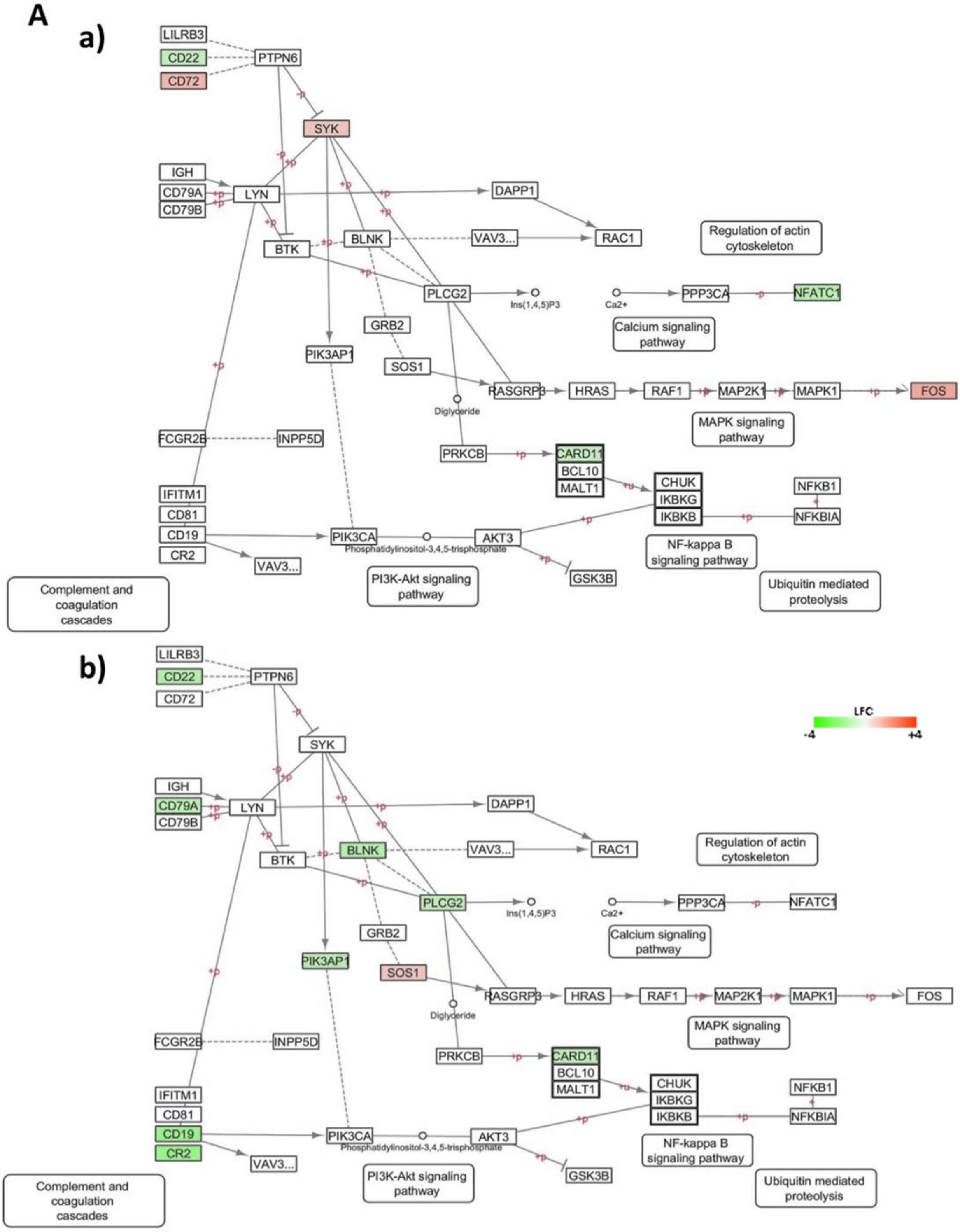
Supplementary Figure S1. Lung tissue sections obtained from idiopathic pulmonary fibrosis (IPF) patients untreated or treated with pirfenidone. Haematoxylin and eosin stained human lung tissues depicting morphological characteristics (from five patients treated and five not treated with pirfenidone).



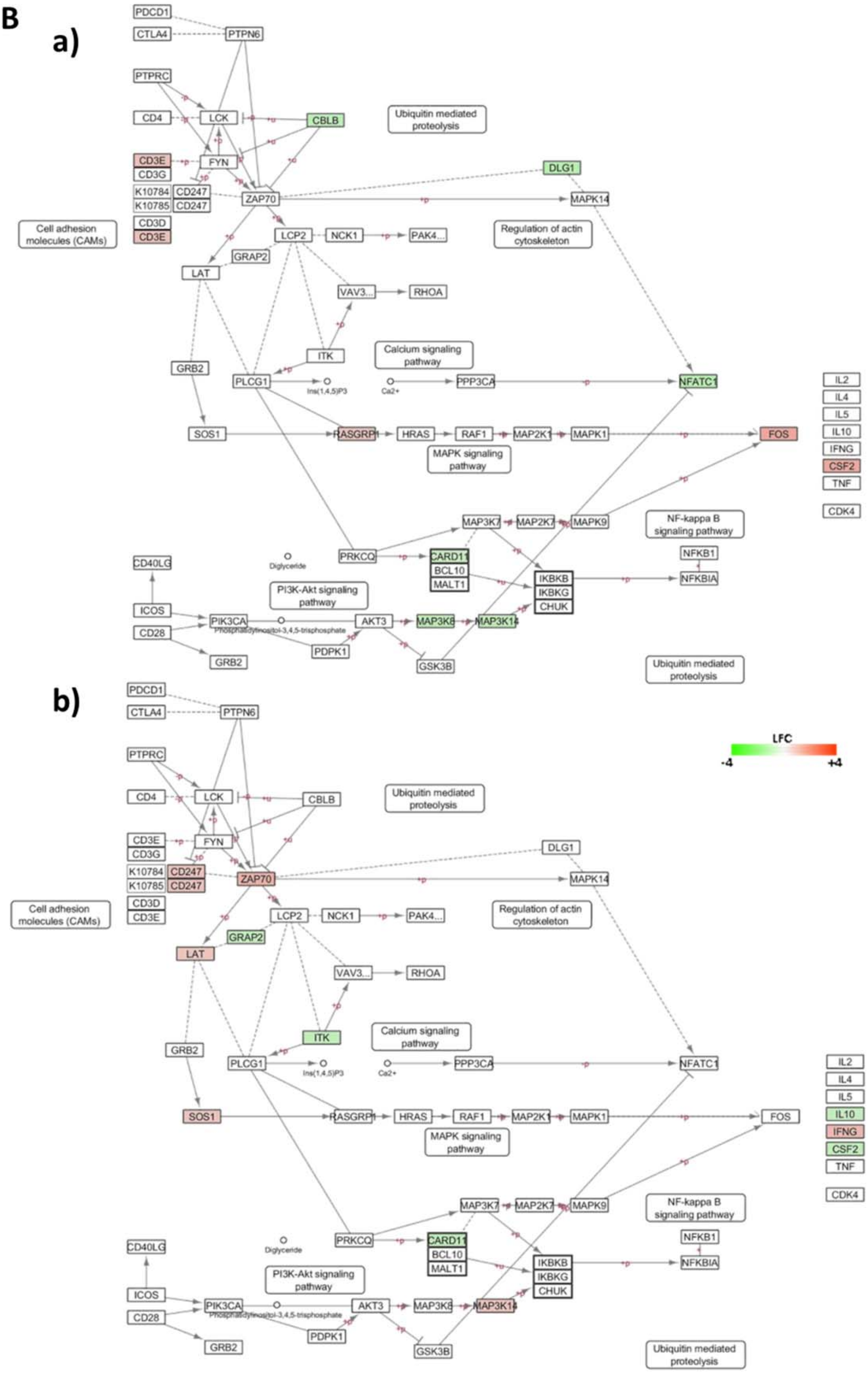
Supplementary Figure S2: Protein-protein interactions in GO nodes ECM and immune cell response. Representation of minimum network analysis showing core protein-protein interactions within the GO nodes, immune cell response and ECM, with expressional annotation for LH in ECM network (A) and for FB in immune cell response (B) (complementary network to figure 2D and E).

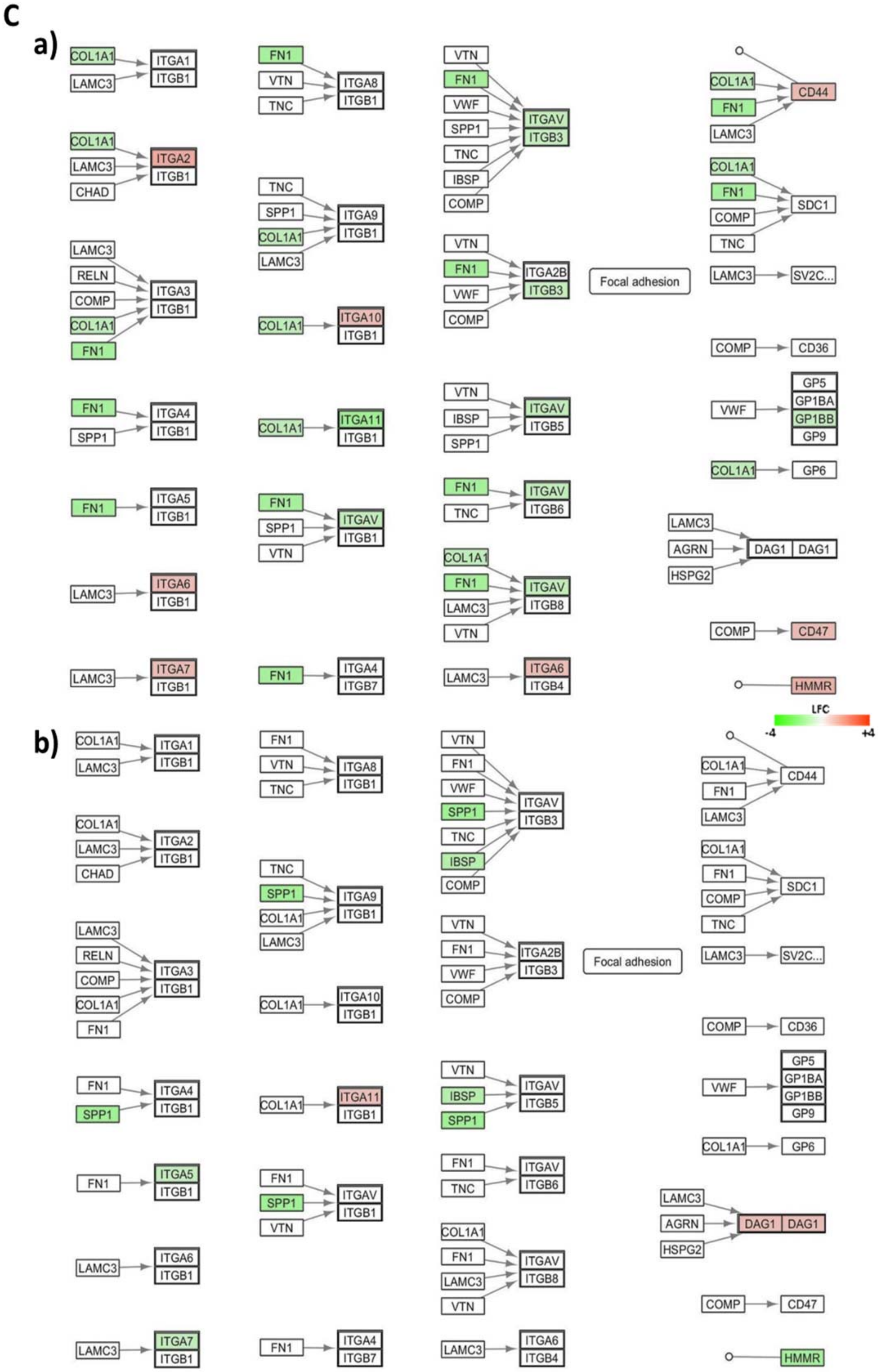


Supplementary Figure S3. Regulation of genes in representative inflammatory and ECM KEGG pathway maps. Gene expression data for the LH samples (**a**) and FB (**b**) samples are depicted in color coding for **A**) B cell receptor signaling pathway (04662), **B**) T cell receptor signaling pathway (04660) and **C**) ECM-receptor interaction (04512).

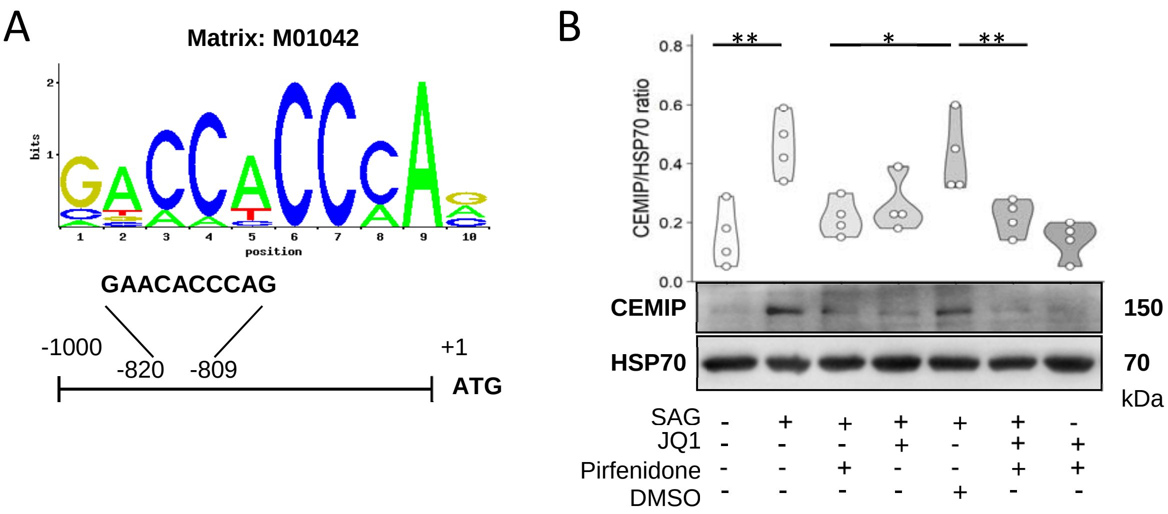

A
a)
LILRB3
CD22
CD72
PTPN6
SYK
IGH
CD79A
CD79B
LYN
DAPP1
RAC1
BTK
BLNK
VAV3...
Regulation of actin cytoskeleton
PLCG2
Ins(1,4,5)P3
Ca2+
PPP3CA
NFATC1
Calcium signaling pathway
GRB2
PIK3AP1
SOS1
RASGRP3
HRAS
RAF1
MAP2K1
MAPK1
FOS
Diglyceride
MAPK signaling pathway
FCGR2B
INPP5D
PRKCB
CARD11
BCL10
MALT1
CHUK
IKBKG
IKBKB
NFKB1
NFKBIA
IFITM1
CD81
CD19
CR2
PIK3CA
AKT3
Phosphatidylinositol-3,4,5-trisphosphate
VAV3...
GSK3B
NF-kappa B signaling pathway
PI3K-Akt signaling pathway
Ubiquitin mediated proteolysis
Complement and coagulation cascades
+p
-p
+u
b)
LILRB3
CD22
CD72
PTPN6
SYK
IGH
CD79A
CD79B
LYN
DAPP1
RAC1
BTK
BLNK
VAV3...
Regulation of actin cytoskeleton
PLCG2
Ins(1,4,5)P3
Ca2+
PPP3CA
NFATC1
Calcium signaling pathway
GRB2
PIK3AP1
SOS1
RASGRP3
HRAS
RAF1
MAP2K1
MAPK1
FOS
Diglyceride
MAPK signaling pathway
FCGR2B
INPP5D
PRKCB
CARD11
BCL10
MALT1
CHUK
IKBKG
IKBKB
NFKB1
NFKBIA
IFITM1
CD81
CD19
CR2
PIK3CA
AKT3
Phosphatidylinositol-3,4,5-trisphosphate
VAV3...
GSK3B
NF-kappa B signaling pathway
PI3K-Akt signaling pathway
Ubiquitin mediated proteolysis
Complement and coagulation cascades
LFC
-4
+4

B


a)
PDCD1
CTLA4
PTPN6
PTPRC
CD4
LCK
CBLB
Ubiquitin mediated proteolysis
CD3E
FYN
CD3G
DLG1
K10784
CD247
K10785
CD247
ZAP70
MAPK14
CD3D
CD3E
Cell adhesion molecules (CAMs)
LCP2
NCK1
PAK4...
Regulation of actin cytoskeleton
LAT
GRAP2
VAV3...
RHOA
ITK
Calcium signaling pathway
GRB2
PLCG1
Ins(1,4,5)P3
Ca2+
PPP3CA
NFATC1
IL2
IL4
IL5
IL10
IFNG
CSF2
TNF
CDK4
SOS1
RASGRP1
HRAS
RAF1
MAP2K1
MAPK1
FOS
MAPK signaling pathway
MAP3K7
MAP2K7
MAPK9
NF-kappa B signaling pathway
NFKB1
NFKBIA
PRKCQ
CARD11
BCL10
MALT1
IKBKB
IKBKG
CHUK
Diglyceride
CD40LG
PI3K-Akt signaling pathway
ICOS
CD28
PIK3CA
Phosphatidylinositol-3,4,5-trisphosphate
AKT3
MAP3K8
MAP3K14
PDPK1
GRB2
GSK3B
Ubiquitin mediated proteolysis
+p
+u
b)
LFC
-4
+4


C
a)
COL1A1
LAMC3
ITGA1
ITGB1
CHAD
ITGA2
RELN
COMP
FN1
ITGA3
SPP1
ITGA4
ITGA5
ITGA6
ITGA7
VTN
TNC
ITGA8
ITGA9
ITGA10
ITGA11
ITGAV
ITGB7
VWF
IBSP
ITGB3
ITGA2B
Focal adhesion
ITGB5
ITGB6
ITGB8
ITGB4
CD44
SDC1
SV2C...
CD36
GP5
GP1BA
GP1BB
GP9
GP6
AGRN
HSPG2
DAG1
CD47
HMMR
LFC
-4
+4
b)

Supplementary Figure S4. Regulation of CEMIP by Hedgehog signalling. A) *In silico CEMIP* gene promoter analysis with GLI consensus binding using the TRANSFAC20113 position weight matrix M01042. B) CEMIP expression in donor FB treated with the Hedgehog agonist SAG in the absence or presence of the GLI1/2 inhibitor JQ1 and/or pirfenidone. DMSO was used as a vehicle. HSP70 was used as a loading control. n=4, for statistical analysis Mann Whitney or One-way ANOVA with Tukey's multiple comparisons test was used. *p<0.05, **p<0.01.



Supplementary Table S1. Annotated genes with log2(fold-change) |> 1| in at least one contrast. Oppositely regulated genes were defined having a LFC > 1.41 in one sample type and LFC<0.5 in the other. Numbers represent mean log2(fold-change) ± the half width of the 95% confidence interval. Values in brackets are significances as -log10(P-value).

GENE SYMBOL	GENE NAME	ENTREZ ID	SPOT ID	IPF+P(LH) - IPF(LH)	IPF+P(FB) - IPF(FB)	Regulation
XIST	X inactive specific transcript (non-protein coding)	7503	A_19_P00323692	-3.80 ± 4.03 (1.20)	2.03 ± 3.54 (0.61)	opposite
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	4312	A_23_P1691	-1.87 ± 2.58 (0.83)	1.07 ± 2.18 (0.49)	opposite
SPC25	SPC25, NDC80 kinetochore complex component	57405	A_23_P51085	-1.52 ± 1.05 (2.20)	1.09 ± 0.89 (1.74)	opposite
CDKN3	cyclin-dependent kinase inhibitor 3	1033	A_23_P48669	-1.41 ± 0.96 (2.25)	1.38 ± 0.81 (2.76)	opposite
ANLN	anillin, actin binding protein	54443	A_23_P356684	-1.28 ± 1.15 (1.52)	1.01 ± 0.97 (1.37)	opposite
SHCBP1	SHC SH2-domain binding protein 1	79801	A_32_P96719	-1.18 ± 0.93 (1.81)	1.08 ± 0.79 (2.02)	opposite
BIRC5	baculoviral IAP repeat containing 5	332	A_23_P118815	-1.16 ± 1.01 (1.59)	1.03 ± 0.85 (1.71)	opposite
BLM	Bloom syndrome, RecQ helicase-like	641	A_23_P88630	-1.07 ± 0.99 (1.46)	1.08 ± 0.84 (1.88)	opposite
CXCL8	chemokine (C-X-C motif) ligand 8	3576	A_32_P87013	-1.03 ± 1.52 (0.76)	1.32 ± 1.28 (1.36)	opposite
METTL7B	methyltransferase like 7B	196410	A_24_P64653	-1.02 ± 1.01 (1.31)	1.07 ± 0.85 (1.80)	opposite
AREG	amphiregulin	374	A_23_P259071	-1.00 ± 1.38 (0.83)	1.24 ± 1.17 (1.42)	opposite
RPS4Y1	ribosomal protein S4, Y-linked 1	6192	A_23_P259314	3.57 ± 4.92 (0.83)	-1.23 ± 4.16 (0.26)	opposite
RPS4Y2	ribosomal protein S4, Y-linked 2	140032	A_23_P324384	3.37 ± 4.88 (0.78)	-1.29 ± 4.12 (0.28)	opposite
TTTY15	testis-specific transcript, Y-linked 15 (non-protein coding)	64595	A_21_P0006594	2.49 ± 2.72 (1.15)	-1.39 ± 2.39 (0.62)	opposite
DDX3Y	DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked	8653	A_33_P3224331	2.17 ± 2.99 (0.83)	-1.78 ± 2.63 (0.75)	opposite
TNNT2	troponin T type 2 (cardiac)	7139	A_23_P34700	1.62 ± 1.69 (1.23)	-1.93 ± 1.43 (2.00)	opposite
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	3357	A_23_P16953	1.23 ± 1.62 (0.88)	-1.18 ± 1.37 (1.06)	opposite
LOC100128288	uncharacterized LOC100128288		A_24_P256415	1.05 ± 0.91 (1.58)	-1.14 ± 0.77 (2.27)	opposite
GREM2	gremlin 2, DAN family BMP antagonist	64388	A_24_P40626	1.70 ± 1.56 (1.48)	1.07 ± 1.32 (0.97)	both up
GPR128	G protein-coupled receptor 128	84873	A_23_P40919	1.32 ± 2.23 (0.63)	1.31 ± 1.88 (0.78)	both up
GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)	653689	A_33_P3289045	1.01 ± 1.82 (0.58)	1.43 ± 1.54 (1.18)	both up

SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	12	A_33_P3399788	-2.39 ± 1.60 (2.30)	-1.96 ± 1.35 (2.20)	both down
HRK	harakiri, BCL2 interacting protein	8739	A_23_P25194	-1.40 ± 1.74 (0.96)	-1.22 ± 1.47 (1.00)	both down
KCNG1	potassium channel, voltage gated modifier subfamily G, member 1	3755	A_22_P00005343	-1.37 ± 1.26 (1.47)	-1.14 ± 1.06 (1.43)	both down
MFAP5	microfibrillar associated protein 5	8076	A_33_P3708413	-1.27 ± 2.00 (0.69)	-1.32 ± 1.69 (0.92)	both down
TENM2	teneurin transmembrane protein 2	57451	A_24_P299474	-1.23 ± 2.34 (0.54)	-2.02 ± 1.98 (1.34)	both down
SCRG1	stimulator of chondrogenesis 1	11341	A_23_P167159	-1.02 ± 2.12 (0.48)	-2.35 ± 1.79 (1.92)	both down
CEMIP	cell migration inducing protein, hyaluronan binding	57214	A_23_P324754	-1.01 ± 1.17 (1.06)	-1.13 ± 0.99 (1.58)	both down
BPIFA1	BPI fold containing family A, member 1	51297	A_33_P3245228	-3.98 ± 2.35 (2.74)	-0.11 ± 1.99 (0.04)	only in LH
SAA1	serum amyloid A1	6288	A_24_P335092	-3.72 ± 2.35 (2.49)	-0.40 ± 1.99 (0.17)	only in LH
SAA2	serum amyloid A2	6289	A_33_P3408918	-3.49 ± 2.21 (2.49)	-0.06 ± 1.86 (0.02)	only in LH
CXCL6	chemokine (C-X-C motif) ligand 6	6372	A_23_P155755	-2.59 ± 1.46 (2.91)	-0.07 ± 1.24 (0.04)	only in LH
DEFB4A	defensin, beta 4A	1673	A_23_P157628	-2.52 ± 1.66 (2.35)	-0.05 ± 1.40 (0.02)	only in LH
SAA4	serum amyloid A4, constitutive	6291	A_23_P87238	-2.46 ± 1.55 (2.50)	-0.20 ± 1.31 (0.12)	only in LH
PI15	peptidase inhibitor 15	51050	A_33_P3254096	-2.45 ± 1.71 (2.17)	-0.28 ± 1.44 (0.16)	only in LH
TNFRSF17	tumor necrosis factor receptor superfamily, member 17	608	A_23_P37736	-2.16 ± 0.79 (5.14)	-0.19 ± 0.67 (0.25)	only in LH
USP9Y	ubiquitin specific peptidase 9, Y-linked	8287	A_33_P3217700	2.12 ± 2.48 (1.04)	-0.31 ± 2.10 (0.12)	only in LH
SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	3053	A_33_P3241511	2.12 ± 1.42 (2.30)	-0.18 ± 1.20 (0.12)	only in LH
CLDN18	claudin 18	51208	A_33_P3240752	2.09 ± 2.92 (0.82)	0.03 ± 2.47 (0.01)	only in LH
MT1H	metallothionein 1H	4496	A_33_P3368313	-2.03 ± 1.34 (2.34)	0.03 ± 1.13 (0.02)	only in LH
LCN2	lipocalin 2	3934	A_23_P169437	-2.02 ± 1.23 (2.62)	-0.06 ± 1.04 (0.04)	only in LH
MZB1	marginal zone B and B1 cell-specific protein	51237	A_23_P84596	-1.94 ± 0.94 (3.59)	-0.40 ± 0.79 (0.50)	only in LH
KRT5	keratin 5, type II	3852	A_23_P218047	-1.93 ± 2.47 (0.92)	-0.31 ± 2.09 (0.12)	only in LH
ACSM1	acyl-CoA synthetase medium-chain family member 1	116285	A_23_P106933	1.89 ± 0.61 (5.90)	-0.32 ± 0.54 (0.64)	only in LH
FCRL5	Fc receptor-like 5	83416	A_23_P201211	-1.88 ± 0.65 (5.50)	-0.34 ± 0.55 (0.68)	only in LH
BPIFB1	BPI fold containing family B, member 1	92747	A_23_P154784	-1.87 ± 1.92 (1.25)	-0.41 ± 1.62 (0.22)	only in LH
IRF5	interferon regulatory factor 5	3663	A_23_P500271	-1.87 ± 1.43 (1.91)	0.04 ± 1.21 (0.03)	only in LH

C4BPA	complement component 4 binding protein, alpha	722	A_23_P97541	1.87 ± 1.05 (2.95)	-0.34 ± 0.89 (0.36)	only in LH
MUC5B	mucin 5B, oligomeric mucus/gel-forming	727897	A_24_P102650	-1.84 ± 1.47 (1.79)	0.08 ± 1.24 (0.05)	only in LH
GDF10	growth differentiation factor 10	2662	A_23_P52227	1.80 ± 2.29 (0.93)	0.04 ± 1.94 (0.02)	only in LH
KLK12	kallikrein-related peptidase 12	43849	A_23_P500010	-1.79 ± 1.93 (1.17)	-0.19 ± 1.63 (0.09)	only in LH
C4BPB	complement component 4 binding protein, beta	725	A_23_P319598	1.77 ± 0.86 (3.54)	0.18 ± 0.73 (0.22)	only in LH
IL1R2	interleukin 1 receptor, type II	7850	A_24_P63019	-1.74 ± 1.10 (2.48)	0.41 ± 0.93 (0.43)	only in LH
KRT6A	keratin 6A, type II	3853	A_33_P3292886	-1.73 ± 3.34 (0.53)	-0.26 ± 2.82 (0.07)	only in LH
CLIC3	chloride intracellular channel 3	9022	A_33_P3336686	1.73 ± 1.66 (1.39)	-0.30 ± 1.40 (0.18)	only in LH
GDF11	growth differentiation factor 11	10220	A_23_P76102	-1.73 ± 0.79 (3.88)	0.33 ± 0.67 (0.49)	only in LH
ZNF215	zinc finger protein 215	7762	A_23_P53057	-1.72 ± 0.75 (4.09)	0.07 ± 0.64 (0.08)	only in LH
CA4	carbonic anhydrase IV	762	A_23_P4096	1.71 ± 1.55 (1.49)	0.01 ± 1.31 (0.01)	only in LH
SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	6318	A_23_P502413	-1.69 ± 1.56 (1.46)	-0.17 ± 1.32 (0.10)	only in LH
LAX1	lymphocyte transmembrane adaptor 1	54900	A_23_P438	-1.68 ± 0.94 (2.94)	0.12 ± 0.80 (0.12)	only in LH
CA3	carbonic anhydrase III	761	A_23_P20316	-1.67 ± 1.12 (2.27)	0.02 ± 0.95 (0.01)	only in LH
UCN3	urocortin 3	114131	A_33_P3241369	1.65 ± 0.88 (3.14)	0.06 ± 0.74 (0.06)	only in LH
SOSTDC1	sclerostin domain containing 1	25928	A_23_P145841	1.64 ± 1.72 (1.22)	0.01 ± 1.45 (0.01)	only in LH
CHRM1	cholinergic receptor, muscarinic 1	1128	A_33_P3367860	1.64 ± 1.70 (1.24)	0.09 ± 1.44 (0.05)	only in LH
SPAG4	sperm associated antigen 4	6676	A_23_P132027	-1.64 ± 0.80 (3.57)	-0.02 ± 0.67 (0.03)	only in LH
PRB2	proline-rich protein BstNI subfamily 2	653247	A_23_P139434	-1.63 ± 1.73 (1.20)	0.02 ± 1.46 (0.01)	only in LH
CXCL13	chemokine (C-X-C motif) ligand 13	10563	A_23_P121695	-1.63 ± 1.29 (1.83)	-0.06 ± 1.09 (0.04)	only in LH
ZNF300P1	zinc finger protein 300 pseudogene 1 (functional)		A_24_P300302	1.63 ± 1.11 (2.25)	-0.21 ± 0.94 (0.19)	only in LH
CNTN6	contactin 6	27255	A_33_P3329378	1.63 ± 1.01 (2.57)	0.30 ± 0.85 (0.32)	only in LH
LOC100652999	uncharacterized LOC100652999	100652999	A_22_P00023251	1.62 ± 1.07 (2.32)	0.43 ± 0.91 (0.48)	only in LH
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	3248	A_24_P71904	1.61 ± 1.60 (1.31)	-0.36 ± 1.35 (0.23)	only in LH
FASLG	Fas ligand (TNF superfamily, member 6)	356	A_23_P369815	1.61 ± 0.92 (2.87)	0.18 ± 0.77 (0.20)	only in LH
FCRL1	Fc receptor-like 1	115350	A_33_P3294504	-1.61 ± 0.87 (3.12)	-0.11 ± 0.73 (0.12)	only in LH
KRT6C	keratin 6C, type II	286887	A_23_P366936	-1.60 ± 1.96 (0.98)	-0.48 ± 1.65 (0.26)	only in LH
AGER	advanced glycosylation end product-specific receptor	177	A_23_P93360	1.60 ± 1.78 (1.12)	0.46 ± 1.51 (0.27)	only in LH

ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	9507	A_23_P360754	-1.60 ± 1.47 (1.46)	-0.20 ± 1.24 (0.13)	only in LH
CD19	CD19 molecule	930	A_23_P113572	-1.60 ± 1.22 (1.89)	-0.03 ± 1.04 (0.02)	only in LH
WIF1	WNT inhibitory factor 1	11197	A_32_P216520	1.59 ± 1.71 (1.18)	0.43 ± 1.45 (0.26)	only in LH
GAL	galanin/GMAP prepropeptide	51083	A_23_P374844	-1.58 ± 1.57 (1.31)	0.19 ± 1.33 (0.12)	only in LH
ZBED2	zinc finger, BED-type containing 2	79413	A_23_P113793	1.58 ± 1.28 (1.75)	0.47 ± 1.08 (0.43)	only in LH
C8B	complement component 8, beta polypeptide	732	A_33_P3423854	1.58 ± 1.20 (1.92)	-0.20 ± 1.02 (0.16)	only in LH
MED4-AS1	MED4 antisense RNA 1	100873965	A_22_P00011103	1.57 ± 1.21 (1.88)	0.41 ± 1.02 (0.38)	only in LH
CADM3-AS1	CADM3 antisense RNA 1		A_33_P3359953	-1.57 ± 0.77 (3.51)	-0.30 ± 0.65 (0.45)	only in LH
TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	6947	A_23_P64372	-1.56 ± 1.36 (1.58)	0.20 ± 1.15 (0.14)	only in LH
SCTR	secretin receptor	6344	A_23_P28139	1.56 ± 1.16 (1.98)	-0.28 ± 0.98 (0.25)	only in LH
SLC5A5	solute carrier family 5 (sodium/iodide cotransporter), member 5	6528	A_23_P101774	1.56 ± 0.86 (3.02)	0.23 ± 0.72 (0.29)	only in LH
BANCR	BRAF-activated non-protein coding RNA		A_22_P00001400	1.56 ± 0.83 (3.16)	0.17 ± 0.73 (0.19)	only in LH
CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	1572	A_23_P89981	-1.55 ± 1.65 (1.19)	0.10 ± 1.40 (0.05)	only in LH
S100A12	S100 calcium binding protein A12	6283	A_23_P74001	-1.54 ± 0.99 (2.43)	0.23 ± 0.84 (0.24)	only in LH
TPTE2P3	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 3		A_32_P48134	1.54 ± 0.86 (2.98)	-0.19 ± 0.72 (0.23)	only in LH
C11orf21	chromosome 11 open reading frame 21	29125	A_33_P3377229	1.52 ± 0.79 (3.27)	-0.14 ± 0.69 (0.17)	only in LH
MIA2	melanoma inhibitory activity 2	117153	A_23_P117387	1.52 ± 0.77 (3.32)	0.37 ± 0.68 (0.57)	only in LH
MUCL1	mucin-like 1	118430	A_23_P150979	-1.51 ± 1.77 (1.04)	0.14 ± 1.50 (0.07)	only in LH
ECEL1P2	endothelin converting enzyme-like 1, pseudogene 2	347694	A_33_P3610406	1.51 ± 1.26 (1.68)	-0.26 ± 1.07 (0.21)	only in LH
ARL14	ADP-ribosylation factor-like 14	80117	A_23_P92161	1.51 ± 0.90 (2.69)	-0.44 ± 0.79 (0.59)	only in LH
LOC101928794	uncharacterized LOC101928794		A_21_P0014149	1.51 ± 0.71 (3.72)	0.03 ± 0.60 (0.04)	only in LH
C12orf80	chromosome 12 open reading frame 80		A_22_P00008937	-1.51 ± 0.63 (4.38)	-0.46 ± 0.53 (1.06)	only in LH
NCKAP5	NCK-associated protein 5	344148	A_23_P360079	1.50 ± 1.42 (1.41)	-0.25 ± 1.24 (0.16)	only in LH
SEPSECS-AS1	SEPSECS antisense RNA 1 (head to head)		A_21_P0000709	1.50 ± 0.73 (3.55)	0.03 ± 0.62 (0.04)	only in LH
IHH	indian hedgehog	3549	A_33_P3338698	1.49 ± 0.80 (3.09)	0.01 ± 0.68 (0.01)	only in LH
SPRR1B	small proline-rich protein 1B	6699	A_23_P159406	-1.48 ± 2.00 (0.85)	0.08 ± 1.76 (0.03)	only in LH

S100P	S100 calcium binding protein P	6286	A_23_P58266	-1.48 ± 1.23 (1.70)	-0.08 ± 1.04 (0.06)	only in LH
FPR2	formyl peptide receptor 2	2358	A_23_P55649	-1.48 ± 1.19 (1.78)	-0.04 ± 1.05 (0.03)	only in LH
LOC101928152	uncharacterized LOC101928152		A_21_P0014466	-1.48 ± 0.89 (2.67)	-0.34 ± 0.75 (0.45)	only in LH
CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	781	A_23_P82379	-1.48 ± 0.75 (3.40)	0.04 ± 0.63 (0.05)	only in LH
PIP	prolactin-induced protein	5304	A_23_P8702	-1.47 ± 1.86 (0.94)	-0.16 ± 1.57 (0.08)	only in LH
SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	6317	A_23_P55632	-1.47 ± 1.53 (1.23)	-0.43 ± 1.29 (0.30)	only in LH
TXLNGY	taxilin gamma pseudogene, Y-linked		A_23_P96658	1.47 ± 1.20 (1.74)	-0.28 ± 1.01 (0.24)	only in LH
TRIM49	tripartite motif containing 49	57093	A_23_P1575	1.46 ± 1.30 (1.53)	0.05 ± 1.10 (0.03)	only in LH
HAMP	hepcidin antimicrobial peptide	57817	A_33_P3336720	-1.44 ± 0.94 (2.39)	0.24 ± 0.79 (0.26)	only in LH
SP2-AS1	SP2 antisense RNA 1		A_21_P0014351	-1.44 ± 0.68 (3.69)	-0.04 ± 0.58 (0.06)	only in LH
SLC6A4	solute carrier family 6 (neurotransmitter transporter), member 4	6532	A_23_P152995	1.43 ± 2.52 (0.59)	0.16 ± 2.13 (0.06)	only in LH
S100A2	S100 calcium binding protein A2	6273	A_33_P3376249	-1.43 ± 2.35 (0.66)	0.31 ± 1.98 (0.13)	only in LH
SMR3A	submaxillary gland androgen regulated protein 3A	26952	A_23_P41365	-1.43 ± 1.21 (1.66)	-0.21 ± 1.02 (0.17)	only in LH
GPA33	glycoprotein A33 (transmembrane)	10223	A_24_P319374	1.43 ± 1.16 (1.76)	0.11 ± 0.98 (0.09)	only in LH
RBP2	retinol binding protein 2, cellular	5948	A_23_P80491	1.43 ± 0.90 (2.51)	-0.06 ± 0.79 (0.06)	only in LH
MMP10	matrix metallopeptidase 10 (stromelysin 2)	4319	A_23_P13094	-1.42 ± 2.05 (0.78)	-0.25 ± 1.73 (0.11)	only in LH
HAS1	hyaluronan synthase 1	3036	A_33_P3295203	-1.42 ± 1.39 (1.35)	0.31 ± 1.17 (0.22)	only in LH
SPP1	secreted phosphoprotein 1	6696	A_23_P7313	-1.41 ± 2.58 (0.57)	-0.10 ± 2.18 (0.03)	only in LH
PRB3	proline-rich protein BstNI subfamily 3	5544	A_23_P116890	-1.41 ± 1.49 (1.21)	-0.02 ± 1.26 (0.01)	only in LH
ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	479	A_23_P87982	-1.41 ± 1.35 (1.38)	-0.23 ± 1.14 (0.17)	only in LH
DPCR1	diffuse panbronchiolitis critical region 1	135656	A_23_P122508	1.41 ± 1.28 (1.49)	0.32 ± 1.09 (0.26)	only in LH
RORC	RAR-related orphan receptor C	6097	A_33_P3386671	1.41 ± 0.90 (2.45)	-0.05 ± 0.76 (0.05)	only in LH

NPTX1	neuronal pentraxin I	4884	A_23_P124905	-0.79 ± 2.23 (0.32)	3.60 ± 1.88 (3.23)	only in FB
SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	6563	A_23_P55616	0.90 ± 1.74 (0.52)	2.93 ± 1.47 (3.42)	only in FB
SULF2	sulfatase 2	55959	A_23_P154605	-0.78 ± 1.67 (0.46)	-2.58 ± 1.41 (3.03)	only in FB
HLA-DMB	major histocompatibility complex, class II, DM	3109	A_32_P351968	-0.03 ± 1.36 (0.02)	2.36 ± 1.15 (3.56)	only in FB

	beta					
HOXC8	homeobox C8	3224	A_24_P124558	-0.52 ± 1.25 (0.40)	-2.35 ± 1.05 (3.98)	only in FB
CFI	complement factor I	3426	A_23_P7212	0.12 ± 1.87 (0.05)	-2.29 ± 1.58 (2.20)	only in FB
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	6362	A_23_P55270	-0.32 ± 2.91 (0.09)	2.17 ± 2.46 (1.09)	only in FB
MYH2	myosin, heavy chain 2, skeletal muscle, adult	4620	A_23_P38271	0.25 ± 2.20 (0.09)	-2.13 ± 1.93 (1.49)	only in FB
HOXC9	homeobox C9	3225	A_23_P25150	-0.04 ± 1.55 (0.02)	-2.09 ± 1.31 (2.53)	only in FB
FOXQ1	forkhead box Q1	94234	A_32_P164246	0.21 ± 2.00 (0.08)	2.08 ± 1.69 (1.75)	only in FB
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	183	A_23_P115261	-0.89 ± 2.11 (0.41)	-1.99 ± 1.79 (1.52)	only in FB
PTGIS	prostaglandin I2 (prostacyclin) synthase	5740	A_24_P48723	-0.53 ± 1.58 (0.30)	-1.96 ± 1.34 (2.24)	only in FB
FRAS1	Fraser extracellular matrix complex subunit 1	80144	A_32_P107876	0.70 ± 1.56 (0.44)	-1.96 ± 1.32 (2.27)	only in FB
SFRP4	secreted frizzled-related protein 4	6424	A_21_P0011967	-0.10 ± 1.54 (0.05)	-1.96 ± 1.30 (2.33)	only in FB
POSTN	periostin, osteoblast specific factor	10631	A_33_P3511265	-0.46 ± 2.11 (0.18)	-1.93 ± 1.78 (1.46)	only in FB
SULF1	sulfatase 1	23213	A_23_P43164	-0.79 ± 1.72 (0.45)	-1.91 ± 1.45 (1.92)	only in FB
SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	6445	A_23_P423237	0.50 ± 1.71 (0.26)	-1.91 ± 1.44 (1.93)	only in FB
KCND2	potassium channel, voltage gated Shal related subfamily D, member 2	3751	A_23_P259251	-0.08 ± 1.23 (0.05)	-1.91 ± 1.04 (3.08)	only in FB
CPZ	carboxypeptidase Z	8532	A_23_P58251	0.65 ± 1.59 (0.39)	-1.86 ± 1.34 (2.07)	only in FB
LPXN	leupaxin	9404	A_23_P87150	0.13 ± 1.16 (0.09)	1.86 ± 0.98 (3.21)	only in FB
FBLN2	fibulin 2	2199	A_23_P143981	-0.26 ± 1.41 (0.15)	-1.85 ± 1.19 (2.41)	only in FB
BEX2	brain expressed X-linked 2	84707	A_33_P3245178	-0.05 ± 1.37 (0.02)	-1.85 ± 1.16 (2.52)	only in FB
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3	3699	A_33_P3313145	0.53 ± 0.92 (0.61)	-1.83 ± 0.78 (4.24)	only in FB
SETBP1	SET binding protein 1	26040	A_23_P4551	0.20 ± 0.84 (0.20)	-1.83 ± 0.71 (4.77)	only in FB
CFD	complement factor D (adipsin)	1675	A_23_P119562	0.10 ± 1.39 (0.05)	-1.81 ± 1.18 (2.40)	only in FB
LOC284561	uncharacterized LOC284561		A_33_P3672756	-0.16 ± 1.33 (0.09)	-1.81 ± 1.12 (2.54)	only in FB
GSTM4	glutathione S-transferase mu 4	2948	A_23_P217917	0.54 ± 1.15 (0.47)	1.81 ± 0.97 (3.13)	only in FB
SPON1	spondin 1, extracellular matrix protein	10418	A_32_P133072	-0.24 ± 1.44 (0.13)	-1.80 ± 1.22 (2.26)	only in FB
B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	8707	A_33_P3286958	0.33 ± 1.63 (0.17)	-1.79 ± 1.37 (1.89)	only in FB

CTTNBP2	cortactin binding protein 2	83992	A_23_P215744	-0.06 ± 1.29 (0.04)	1.79 ± 1.09 (2.64)	only in FB
TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	7292	A_23_P126836	-0.48 ± 2.06 (0.20)	-1.78 ± 1.74 (1.35)	only in FB
KLHDC7B	kelch domain containing 7B	113730	A_24_P117410	0.30 ± 1.03 (0.26)	-1.78 ± 0.87 (3.52)	only in FB
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	23460	A_23_P500400	-0.02 ± 1.69 (0.01)	-1.77 ± 1.43 (1.77)	only in FB
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	54566	A_23_P216556	-0.13 ± 1.19 (0.09)	1.76 ± 1.00 (2.87)	only in FB
PLXDC2	plexin domain containing 2	84898	A_23_P161424	0.01 ± 1.09 (0.01)	-1.76 ± 0.92 (3.23)	only in FB
PKP2	plakophilin 2	5318	A_33_P3405728	-0.56 ± 1.26 (0.43)	-1.75 ± 1.07 (2.62)	only in FB
APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	54518	A_23_P401700	-0.15 ± 1.04 (0.12)	-1.75 ± 0.88 (3.41)	only in FB
CCND2	cyclin D2	894	A_24_P278747	0.46 ± 1.48 (0.28)	-1.74 ± 1.25 (2.08)	only in FB
MEST	mesoderm specific transcript		A_23_P156970	-0.36 ± 1.66 (0.18)	-1.72 ± 1.40 (1.73)	only in FB
RARRES2	retinoic acid receptor responder (tazarotene induced) 2	5919	A_23_P134237	-0.43 ± 1.83 (0.20)	-1.71 ± 1.55 (1.50)	only in FB
FMOD	fibromodulin	2331	A_23_P114883	-0.40 ± 0.93 (0.41)	-1.71 ± 0.79 (3.81)	only in FB
ARHGAP26	Rho GTPase activating protein 26	23092	A_33_P3228305	-0.20 ± 1.32 (0.12)	-1.69 ± 1.11 (2.35)	only in FB
SHC2	SHC (Src homology 2 domain containing) transforming protein 2	25759	A_32_P205624	0.31 ± 1.19 (0.22)	-1.69 ± 1.01 (2.69)	only in FB
HOXC6	homeobox C6	3223	A_33_P3300965	0.02 ± 1.62 (0.01)	-1.62 ± 1.37 (1.65)	only in FB
SLC51B	solute carrier family 51, beta subunit	123264	A_23_P436284	-0.64 ± 1.54 (0.39)	1.62 ± 1.36 (1.67)	only in FB
KLHL13	kelch-like family member 13	90293	A_23_P159974	0.26 ± 1.04 (0.22)	1.62 ± 0.88 (3.09)	only in FB
ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	A_23_P83098	0.39 ± 1.86 (0.17)	-1.61 ± 1.58 (1.34)	only in FB
LINC00312	lincRNA 312		A_23_P166779	0.18 ± 1.06 (0.14)	-1.61 ± 0.90 (2.98)	only in FB
LINC01444	lincRNA 1444	101927642	A_22_P00012170	0.12 ± 1.47 (0.06)	1.60 ± 1.24 (1.87)	only in FB
SCG2	secretogranin II	7857	A_24_P88696	0.08 ± 1.42 (0.04)	-1.60 ± 1.20 (1.97)	only in FB
AKR1C8P	aldo-keto reductase family 1, member C8, pseudogene	340811	A_21_P0010854	-0.95 ± 1.20 (0.93)	1.60 ± 1.02 (2.47)	only in FB
LRRD1	leucine-rich repeats and death domain containing 1	401387	A_33_P3420446	-0.25 ± 2.31 (0.08)	1.59 ± 1.95 (0.98)	only in FB
KRT18	keratin 18, type I	3875	A_32_P151544	0.13 ± 2.18 (0.04)	-1.59 ± 1.84 (1.06)	only in FB
TCF7	transcription factor 7 (T-cell specific, HMG-box)	6932	A_23_P7582	0.09 ± 0.99 (0.07)	1.59 ± 0.88 (2.99)	only in FB

LAMP3	lysosomal-associated membrane protein 3	27074	A_23_P29773	0.22 ± 1.92 (0.09)	-1.58 ± 1.62 (1.25)	only in FB
C10orf99	chromosome 10 open reading frame 99	387695	A_33_P3392405	0.44 ± 1.73 (0.22)	-1.58 ± 1.46 (1.46)	only in FB
LOC102725254	uncharacterized LOC102725254		A_22_P00010091	0.25 ± 1.15 (0.18)	1.58 ± 1.02 (2.42)	only in FB
MIR503HG	MIR503 host gene (non-protein coding)	84848	A_33_P3402329	0.47 ± 1.11 (0.40)	-1.58 ± 0.94 (2.71)	only in FB
CD52	CD52 molecule	1043	A_23_P85800	0.19 ± 2.47 (0.06)	1.57 ± 2.09 (0.87)	only in FB
GMFG	glia maturation factor, gamma	9535	A_23_P208866	0.09 ± 0.90 (0.08)	1.57 ± 0.76 (3.58)	only in FB
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	4939	A_33_P3225522	-0.02 ± 0.57 (0.03)	1.57 ± 0.48 (6.26)	only in FB
GPR133	G protein-coupled receptor 133	283383	A_23_P415706	0.55 ± 1.17 (0.46)	-1.56 ± 0.99 (2.49)	only in FB
LINC01503	lincRNA 1503	100506119	A_19_P00319981	-0.41 ± 1.09 (0.35)	-1.56 ± 0.92 (2.72)	only in FB
NT5E	5'-nucleotidase, ecto (CD73)	4907	A_24_P354715	-0.21 ± 0.89 (0.21)	1.56 ± 0.75 (3.62)	only in FB
PTPN3	protein tyrosine phosphatase, non-receptor type 3	5774	A_22_P00025093	0.21 ± 0.75 (0.24)	1.56 ± 0.64 (4.46)	only in FB
WBSCR27	Williams Beuren syndrome chromosome region 27	155368	A_23_P381017	-0.13 ± 1.67 (0.06)	1.55 ± 1.41 (1.49)	only in FB
FAM20A	family with sequence similarity 20, member A	54757	A_32_P108254	0.02 ± 1.32 (0.01)	-1.55 ± 1.16 (1.96)	only in FB
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	5570	A_23_P145529	-0.15 ± 1.15 (0.10)	-1.54 ± 0.97 (2.50)	only in FB
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	1116	A_23_P137665	-0.60 ± 1.84 (0.29)	-1.53 ± 1.55 (1.27)	only in FB
CREB5	cAMP responsive element binding protein 5	9586	A_23_P157117	0.10 ± 0.98 (0.08)	1.52 ± 0.83 (3.06)	only in FB
NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	56901	A_23_P9614	0.55 ± 1.37 (0.38)	-1.51 ± 1.16 (1.88)	only in FB
COL5A1	collagen, type V, alpha 1	1289	A_33_P3629678	-0.46 ± 1.29 (0.33)	-1.51 ± 1.09 (2.07)	only in FB
CSTA	cystatin A (stefin A)	1475	A_23_P41114	-0.39 ± 1.13 (0.31)	-1.51 ± 0.99 (2.36)	only in FB
LAMP5	lysosomal-associated membrane protein family, member 5	24141	A_23_P40295	-0.27 ± 2.47 (0.08)	1.50 ± 2.09 (0.82)	only in FB
IGSF10	immunoglobulin superfamily, member 10	285313	A_23_P333683	0.76 ± 1.45 (0.54)	-1.50 ± 1.23 (1.72)	only in FB
NUAK1	NUAK family, SNF1-like kinase, 1	9891	A_23_P348257	-0.25 ± 1.38 (0.15)	-1.50 ± 1.16 (1.87)	only in FB
KIF26B	kinesin family member 26B	55083	A_33_P3382565	-0.69 ± 1.26 (0.57)	-1.50 ± 1.07 (2.12)	only in FB
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	5270	A_23_P50919	-0.72 ± 1.55 (0.45)	-1.49 ± 1.31 (1.56)	only in FB
LIPG	lipase, endothelial	9388	A_24_P125469	-0.44 ± 1.17 (0.35)	-1.49 ± 1.03 (2.18)	only in FB
CLIC6	chloride intracellular channel 6	54102	A_23_P385067	0.12 ± 1.18 (0.08)	1.49 ± 1.00 (2.31)	only in FB

PCOLCE2	procollagen C-endopeptidase enhancer 2	26577	A_23_P57709	-0.01 ± 1.70 (0.01)	1.48 ± 1.43 (1.35)	only in FB
KRT83	keratin 83, type II	3889	A_33_P3273552	0.48 ± 1.54 (0.28)	-1.48 ± 1.30 (1.55)	only in FB
MGP	matrix Gla protein	4256	A_33_P3361636	0.16 ± 1.26 (0.10)	-1.48 ± 1.06 (2.08)	only in FB
CCDC80	coiled-coil domain containing 80	151887	A_23_P58082	-0.64 ± 1.00 (0.70)	-1.48 ± 0.85 (2.86)	only in FB
SLC37A2	solute carrier family 37 (glucose-6-phosphate transporter), member 2	219855	A_33_P3474319	-0.34 ± 0.87 (0.37)	1.48 ± 0.73 (3.49)	only in FB
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	2354	A_23_P429998	-0.21 ± 1.69 (0.10)	1.47 ± 1.43 (1.36)	only in FB
TPD52L1	tumor protein D52-like 1	7164	A_23_P31143	-0.38 ± 1.38 (0.24)	-1.47 ± 1.16 (1.82)	only in FB
GPM6B	glycoprotein M6B	2824	A_23_P378416	0.50 ± 1.35 (0.35)	1.47 ± 1.14 (1.86)	only in FB
DHRS3	dehydrogenase/reductase (SDR family) member 3	9249	A_23_P33759	0.21 ± 1.12 (0.16)	-1.47 ± 0.99 (2.30)	only in FB
FAM64A	family with sequence similarity 64, member A	54478	A_33_P3276918	-0.83 ± 1.04 (0.95)	1.47 ± 0.88 (2.68)	only in FB
SUSD3	sushi domain containing 3	203328	A_23_P401076	-0.28 ± 1.04 (0.24)	1.47 ± 0.88 (2.67)	only in FB
CDKN2A-AS1	CDKN2A antisense RNA 1 (head to head)		A_23_P307502	-0.03 ± 0.92 (0.02)	-1.47 ± 0.78 (3.18)	only in FB
KRT18P55	keratin 18 pseudogene 55	284085	A_23_P373708	0.11 ± 2.44 (0.03)	-1.46 ± 2.06 (0.80)	only in FB
PRSS36	protease, serine, 36	146547	A_24_P412734	0.24 ± 2.23 (0.08)	1.46 ± 1.89 (0.91)	only in FB
CACNG7	calcium channel, voltage-dependent, gamma subunit 7	59284	A_24_P365349	-0.02 ± 2.14 (0.01)	-1.46 ± 1.81 (0.96)	only in FB
ITGA11	integrin, alpha 11	22801	A_23_P206022	0.61 ± 1.89 (0.29)	-1.46 ± 1.60 (1.14)	only in FB
FBLN1	fibulin 1	2192	A_23_P211631	-0.12 ± 1.35 (0.07)	-1.46 ± 1.14 (1.84)	only in FB
CDC25C	cell division cycle 25C	995	A_23_P70249	-0.60 ± 1.33 (0.44)	1.46 ± 1.12 (1.90)	only in FB
ISLR	immunoglobulin superfamily containing leucine-rich repeat	3671	A_23_P3312	-0.26 ± 1.20 (0.18)	-1.46 ± 1.02 (2.18)	only in FB
KIF20A	kinesin family member 20A	10112	A_23_P256956	-0.74 ± 1.02 (0.84)	1.46 ± 0.86 (2.75)	only in FB
MAOB	monoamine oxidase B	4129	A_23_P85015	0.50 ± 0.96 (0.54)	1.46 ± 0.81 (2.97)	only in FB
MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	4314	A_23_P161698	-0.90 ± 2.12 (0.41)	1.45 ± 1.80 (0.96)	only in FB
COL3A1	collagen, type III, alpha 1	1281	A_24_P935491	-0.33 ± 1.49 (0.19)	-1.45 ± 1.26 (1.60)	only in FB
EYA2	EYA transcriptional coactivator and phosphatase 2	2139	A_23_P319859	-0.57 ± 1.46 (0.36)	1.45 ± 1.23 (1.63)	only in FB
CPE	carboxypeptidase E	1363	A_23_P259442	-0.13 ± 1.40 (0.07)	-1.45 ± 1.18 (1.75)	only in FB
GACAT2	gastric cancer associated transcript 2 (non-protein coding)	100287082	A_21_P0014365	-0.37 ± 0.99 (0.34)	1.45 ± 0.84 (2.82)	only in FB

DSP	desmoplakin	1832	A_32_P157945	-0.15 ± 2.20 (0.05)	-1.44 ± 1.86 (0.90)	only in FB
SLIT3	slit homolog 3 (Drosophila)	6586	A_23_P58588	-0.13 ± 1.08 (0.09)	-1.44 ± 0.91 (2.48)	only in FB
S100A3	S100 calcium binding protein A3	6274	A_23_P104073	0.53 ± 0.95 (0.59)	1.43 ± 0.80 (2.95)	only in FB
KRTAP19-2	keratin associated protein 19-2	337969	A_33_P3311267	-0.12 ± 2.22 (0.04)	1.42 ± 1.87 (0.88)	only in FB
SOX11	SRY (sex determining region Y)-box 11	6664	A_24_P302584	0.49 ± 1.43 (0.31)	1.42 ± 1.21 (1.64)	only in FB
NCAM2	neural cell adhesion molecule 2	4685	A_33_P3239884	0.95 ± 1.42 (0.75)	-1.42 ± 1.20 (1.65)	only in FB
ADM2	adrenomedullin 2	79924	A_33_P3413905	-0.82 ± 1.32 (0.67)	-1.42 ± 1.12 (1.84)	only in FB
ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	81794	A_33_P3223056	-0.10 ± 1.10 (0.07)	-1.42 ± 0.93 (2.35)	only in FB
THAP10	THAP domain containing 10	56906	A_23_P106391	0.77 ± 1.05 (0.84)	1.42 ± 0.89 (2.53)	only in FB
ERICH2	glutamate-rich 2		A_32_P197340	0.37 ± 1.54 (0.20)	-1.41 ± 1.31 (1.45)	only in FB
AEBP1	AE binding protein 1	165	A_23_P157299	0.01 ± 1.07 (0.01)	-1.41 ± 0.90 (2.45)	only in FB
TSPO2	translocator protein 2	222642	A_33_P3234222	-0.91 ± 1.03 (1.10)	-1.41 ± 0.87 (2.59)	only in FB

Supplementary Table S2. Annotated genes regulated in the lung homogenate samples after pirfenidone treatment.

GENE_SYMBOL	GENE_NAME	ENTREZ_ID	SPOT_ID	mean log2(fold-change) ± the half width of the 95% confidence interval	-log10(P-value)
BPIFA1	BPI fold containing family A, member 1	51297	A_33_P3245228	-3.98 ± 2.35	2.74
XIST	X inactive specific transcript (non-protein coding)	7503	A_19_P00323692	-3.80 ± 4.03	1.20
SAA1	serum amyloid A1	6288	A_24_P335092	-3.72 ± 2.35	2.49
RPS4Y1	ribosomal protein S4, Y-linked 1	6192	A_23_P259314	3.57 ± 4.92	0.83
SAA2	serum amyloid A2	6289	A_33_P3408918	-3.49 ± 2.21	2.49
RPS4Y2	ribosomal protein S4, Y-linked 2	140032	A_23_P324384	3.37 ± 4.88	0.78
CXCL6	chemokine (C-X-C motif) ligand 6	6372	A_23_P155755	-2.59 ± 1.46	2.91
DEFB4A	defensin, beta 4A	1673	A_23_P157628	-2.52 ± 1.66	2.35
RTKN2	rhotekin 2	219790	A_24_P13041	2.51 ± 1.51	2.66
TTTY15	testis-specific transcript, Y-linked 15 (non-protein coding)	64595	A_21_P0006594	2.49 ± 2.72	1.15

SAA4	serum amyloid A4, constitutive	6291	A_23_P87238	-2.46 ± 1.55	2.50
PI15	peptidase inhibitor 15	51050	A_33_P3254096	-2.45 ± 1.71	2.17
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	12	A_33_P3399788	-2.39 ± 1.60	2.30
DDX3Y	DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked	8653	A_33_P3224331	2.17 ± 2.99	0.83
TNFRSF17	tumor necrosis factor receptor superfamily, member 17	608	A_23_P37736	-2.16 ± 0.79	5.14
KDM5D	lysine (K)-specific demethylase 5D	8284	A_23_P137238	2.14 ± 2.04	1.40
USP9Y	ubiquitin specific peptidase 9, Y-linked	8287	A_33_P3217700	2.12 ± 2.48	1.04
SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	3053	A_33_P3241511	2.12 ± 1.42	2.30
CLDN18	claudin 18	51208	A_33_P3240752	2.09 ± 2.92	0.82
MT1H	metallothionein 1H	4496	A_33_P3368313	-2.03 ± 1.34	2.34
LCN2	lipocalin 2	3934	A_23_P169437	-2.02 ± 1.23	2.62
HIST1H2AI	histone cluster 1, H2ai	8329	A_33_P3360216	-1.98 ± 1.15	2.82
MZB1	marginal zone B and B1 cell-specific protein	51237	A_23_P84596	-1.94 ± 0.94	3.59
KRT5	keratin 5, type II	3852	A_23_P218047	-1.93 ± 2.47	0.92
ACSM1	acyl-CoA synthetase medium-chain family member 1	116285	A_23_P106933	1.89 ± 0.61	5.90
FCRL5	Fc receptor-like 5	83416	A_23_P201211	-1.88 ± 0.65	5.50
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	4312	A_23_P1691	-1.87 ± 2.58	0.83
BPIFB1	BPI fold containing family B, member 1	92747	A_23_P154784	-1.87 ± 1.92	1.25
IRF5	interferon regulatory factor 5	3663	A_23_P500271	-1.87 ± 1.43	1.91
C4BPA	complement component 4 binding protein, alpha	722	A_23_P97541	1.87 ± 1.05	2.95
MUC5B	mucin 5B, oligomeric mucus/gel-forming	727897	A_24_P102650	-1.84 ± 1.47	1.79
PRB4	proline-rich protein BstNI subfamily 4	5545	A_33_P3216150	-1.82 ± 1.85	1.26
GDF10	growth differentiation factor 10	2662	A_23_P52227	1.80 ± 2.29	0.93
KLK12	kallikrein-related peptidase 12	43849	A_23_P500010	-1.79 ± 1.93	1.17
C4BPB	complement component 4 binding protein, beta	725	A_23_P319598	1.77 ± 0.86	3.54
IL1R2	interleukin 1 receptor, type II	7850	A_24_P63019	-1.74 ± 1.10	2.48
KRT6A	keratin 6A, type II	3853	A_33_P3292886	-1.73 ± 3.34	0.53

CLIC3	chloride intracellular channel 3	9022	A_33_P3336686	1.73 ± 1.66	1.39
GDF11	growth differentiation factor 11	10220	A_23_P76102	-1.73 ± 0.79	3.88
BMP4	bone morphogenetic protein 4	652	A_23_P54144	1.72 ± 1.70	1.32
ZNF215	zinc finger protein 215	7762	A_23_P53057	-1.72 ± 0.75	4.09
CA4	carbonic anhydrase IV	762	A_23_P4096	1.71 ± 1.55	1.49
CHRDL2	chordin-like 2	25884	A_23_P13548	-1.71 ± 1.20	2.15
GREM2	gremlin 2, DAN family BMP antagonist	64388	A_24_P40626	1.70 ± 1.56	1.48
SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	6318	A_23_P502413	-1.69 ± 1.56	1.46
MST1P2	macrophage stimulating 1 (hepatocyte growth factor-like) pseudogene 2		A_21_P0010518	1.69 ± 0.67	4.65
LAX1	lymphocyte transmembrane adaptor 1	54900	A_23_P438	-1.68 ± 0.94	2.94
ZG16B	zymogen granule protein 16B	124220	A_23_P118203	-1.67 ± 1.39	1.70
CA3	carbonic anhydrase III	761	A_23_P20316	-1.67 ± 1.12	2.27
UCN3	urocortin 3	114131	A_33_P3241369	1.65 ± 0.88	3.14
SOSTDC1	sclerostin domain containing 1	25928	A_23_P145841	1.64 ± 1.72	1.22
CHRM1	cholinergic receptor, muscarinic 1	1128	A_33_P3367860	1.64 ± 1.70	1.24
SPAG4	sperm associated antigen 4	6676	A_23_P132027	-1.64 ± 0.80	3.57
PRB2	proline-rich protein BstNI subfamily 2	653247	A_23_P139434	-1.63 ± 1.73	1.20
CXCL13	chemokine (C-X-C motif) ligand 13	10563	A_23_P121695	-1.63 ± 1.29	1.83
ZNF300P1	zinc finger protein 300 pseudogene 1 (functional)		A_24_P300302	1.63 ± 1.11	2.25
CNTN6	contactin 6	27255	A_33_P3329378	1.63 ± 1.01	2.57
TNNT2	troponin T type 2 (cardiac)	7139	A_23_P34700	1.62 ± 1.69	1.23
LOC100652999	uncharacterized LOC100652999	100652999	A_22_P00023251	1.62 ± 1.07	2.32
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	3248	A_24_P71904	1.61 ± 1.60	1.31
SNAR-F	small ILF3/NF90-associated RNA F		A_21_P0000492	1.61 ± 1.30	1.76
FASLG	Fas ligand (TNF superfamily, member 6)	356	A_23_P369815	1.61 ± 0.92	2.87
FCRL1	Fc receptor-like 1	115350	A_33_P3294504	-1.61 ± 0.87	3.12
MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	4318	A_23_P40174	-1.60 ± 2.70	0.63
KRT6C	keratin 6C, type II	286887	A_23_P366936	-1.60 ± 1.96	0.98

AGER	advanced glycosylation end product-specific receptor	177	A_23_P93360	1.60 ± 1.78	1.12
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	9507	A_23_P360754	-1.60 ± 1.47	1.46
CD19	CD19 molecule	930	A_23_P113572	-1.60 ± 1.22	1.89
WIF1	WNT inhibitory factor 1	11197	A_32_P216520	1.59 ± 1.71	1.18
GAL	galanin/GMAP prepropeptide	51083	A_23_P374844	-1.58 ± 1.57	1.31
ZBED2	zinc finger, BED-type containing 2	79413	A_23_P113793	1.58 ± 1.28	1.75
C8B	complement component 8, beta polypeptide	732	A_33_P3423854	1.58 ± 1.20	1.92
SNAR-H	small ILF3/NF90-associated RNA H		A_21_P0000511	1.57 ± 1.40	1.52
MED4-AS1	MED4 antisense RNA 1	100873965	A_22_P00011103	1.57 ± 1.21	1.88
CADM3-AS1	CADM3 antisense RNA 1		A_33_P3359953	-1.57 ± 0.77	3.51
TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	6947	A_23_P64372	-1.56 ± 1.36	1.58
SCTR	secretin receptor	6344	A_23_P28139	1.56 ± 1.16	1.98
SLC5A5	solute carrier family 5 (sodium/iodide cotransporter), member 5	6528	A_23_P101774	1.56 ± 0.86	3.02
BANCR	BRAF-activated non-protein coding RNA		A_22_P00001400	1.56 ± 0.83	3.16
CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	1572	A_23_P89981	-1.55 ± 1.65	1.19
STC2	stanniocalcin 2	8614	A_23_P416395	1.54 ± 1.01	2.37
S100A12	S100 calcium binding protein A12	6283	A_23_P74001	-1.54 ± 0.99	2.43
TPTE2P3	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 3		A_32_P48134	1.54 ± 0.86	2.98
SPC25	SPC25, NDC80 kinetochore complex component	57405	A_23_P51085	-1.52 ± 1.05	2.20
C11orf21	chromosome 11 open reading frame 21	29125	A_33_P3377229	1.52 ± 0.79	3.27
MIA2	melanoma inhibitory activity 2	117153	A_23_P117387	1.52 ± 0.77	3.32
MUCL1	mucin-like 1	118430	A_23_P150979	-1.51 ± 1.77	1.04
ECEL1P2	endothelin converting enzyme-like 1, pseudogene 2	347694	A_33_P3610406	1.51 ± 1.26	1.68
ARL14	ADP-ribosylation factor-like 14	80117	A_23_P92161	1.51 ± 0.90	2.69
RASD1	RAS, dexamethasone-induced 1	51655	A_23_P118392	-1.51 ± 0.87	2.84

LOC101928794	uncharacterized LOC101928794		A_21_P0014149	1.51 ± 0.71	3.72
C12orf80	chromosome 12 open reading frame 80		A_22_P00008937	-1.51 ± 0.63	4.38
NCKAP5	NCK-associated protein 5	344148	A_23_P360079	1.50 ± 1.42	1.41
SEPSECS-AS1	SEPSECS antisense RNA 1 (head to head)		A_21_P0000709	1.50 ± 0.73	3.55
IHH	indian hedgehog	3549	A_33_P3338698	1.49 ± 0.80	3.09
ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	117	A_23_P157109	-1.49 ± 0.73	3.54
SPRR1B	small proline-rich protein 1B	6699	A_23_P159406	-1.48 ± 2.00	0.85
SNAR-D	small ILF3/NF90-associated RNA D		A_21_P0000508	1.48 ± 1.36	1.46
SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	6695	A_24_P354689	-1.48 ± 1.29	1.58
S100P	S100 calcium binding protein P	6286	A_23_P58266	-1.48 ± 1.23	1.70
FPR2	formyl peptide receptor 2	2358	A_23_P55649	-1.48 ± 1.19	1.78
LOC101928152	uncharacterized LOC101928152		A_21_P0014466	-1.48 ± 0.89	2.67
CACNA2D1	calcium channel, voltage-dependent, alpha 2/delta subunit 1	781	A_23_P82379	-1.48 ± 0.75	3.40
PIP	prolactin-induced protein	5304	A_23_P8702	-1.47 ± 1.86	0.94
SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	6317	A_23_P55632	-1.47 ± 1.53	1.23
TCL1A	T-cell leukemia/lymphoma 1A	8115	A_23_P357717	-1.47 ± 1.20	1.74
TXLNGY	taxilin gamma pseudogene, Y-linked		A_23_P96658	1.47 ± 1.20	1.74
RGS9	regulator of G-protein signaling 9	8787	A_23_P66881	1.47 ± 1.18	1.78
LINC01436	lincRNA 1436		A_22_P00019460	1.46 ± 1.52	1.23
TRIM49	tripartite motif containing 49	57093	A_23_P1575	1.46 ± 1.30	1.53
TXLNGY	taxilin gamma pseudogene, Y-linked	246126	A_23_P364792	1.45 ± 1.48	1.26
HJURP	Holliday junction recognition protein	55355	A_33_P3807062	-1.45 ± 0.98	2.27
MEDAG	mesenteric estrogen-dependent adipogenesis	84935	A_23_P99515	-1.44 ± 1.26	1.57
HAMP	hepcidin antimicrobial peptide	57817	A_33_P3336720	-1.44 ± 0.94	2.39
SP2-AS1	SP2 antisense RNA 1		A_21_P0014351	-1.44 ± 0.68	3.69
SLC6A4	solute carrier family 6 (neurotransmitter transporter), member 4	6532	A_23_P152995	1.43 ± 2.52	0.59
S100A2	S100 calcium binding protein A2	6273	A_33_P3376249	-1.43 ± 2.35	0.66

FGFBP1	fibroblast growth factor binding protein 1	9982	A_23_P30126	-1.43 ± 1.62	1.10
SMR3A	submaxillary gland androgen regulated protein 3A	26952	A_23_P41365	-1.43 ± 1.21	1.66
GPA33	glycoprotein A33 (transmembrane)	10223	A_24_P319374	1.43 ± 1.16	1.76
ABHD2	abhydrolase domain containing 2	11057	A_23_P395172	1.43 ± 1.15	1.77
RBP2	retinol binding protein 2, cellular	5948	A_23_P80491	1.43 ± 0.90	2.51
MMP10	matrix metallopeptidase 10 (stromelysin 2)	4319	A_23_P13094	-1.42 ± 2.05	0.78
HAS1	hyaluronan synthase 1	3036	A_33_P3295203	-1.42 ± 1.39	1.35
SPP1	secreted phosphoprotein 1	6696	A_23_P7313	-1.41 ± 2.58	0.57
PRB3	proline-rich protein BstNI subfamily 3	5544	A_23_P116890	-1.41 ± 1.49	1.21
ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	479	A_23_P87982	-1.41 ± 1.35	1.38
SNAR-G2	small ILF3/NF90-associated RNA G2		A_21_P0000509	1.41 ± 1.31	1.45
DPCR1	diffuse panbronchiolitis critical region 1	135656	A_23_P122508	1.41 ± 1.28	1.49
CDKN3	cyclin-dependent kinase inhibitor 3	1033	A_23_P48669	-1.41 ± 0.96	2.25
RORC	RAR-related orphan receptor C	6097	A_33_P3386671	1.41 ± 0.90	2.45
HRK	harakiri, BCL2 interacting protein	8739	A_23_P25194	-1.40 ± 1.74	0.96
LOC285889	uncharacterized LOC285889	285889	A_21_P0013359	1.40 ± 1.25	1.53
SRPX2	sushi-repeat containing protein, X-linked 2	27286	A_23_P136978	-1.40 ± 1.11	1.82
ZDHHC11B	zinc finger, DHHC-type containing 11B		A_33_P3345643	1.40 ± 1.02	2.02
LINC00622	lincRNA 622	644242	A_21_P0000663	1.40 ± 0.92	2.36
ANKRD20A9P	ankyrin repeat domain 20 family, member A9, pseudogene		A_21_P0012182	1.40 ± 0.83	2.70
ZNF287	zinc finger protein 287	57336	A_23_P4416	1.40 ± 0.75	3.15
SNAR-B2	small ILF3/NF90-associated RNA B2		A_21_P0000507	1.39 ± 1.34	1.37
HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	3128	A_24_P169013	-1.39 ± 1.24	1.52
MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	23209	A_23_P211680	1.39 ± 1.14	1.73
FAM3D	family with sequence similarity 3, member D	131177	A_23_P41145	-1.39 ± 0.97	2.16
GPR39	G protein-coupled receptor 39	2863	A_23_P79155	1.39 ± 0.95	2.25
GGACT	gamma-glutamylamine cyclotransferase	87769	A_32_P110872	-1.39 ± 0.91	2.38

RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	65059	A_33_P3421571	-1.39 ± 0.89	2.45
OR8B8	olfactory receptor, family 8, subfamily B, member 8	26493	A_23_P1819	-1.39 ± 0.58	4.34
ITLN2	intelectin 2	142683	A_24_P53778	1.38 ± 1.77	0.92
STRA6	stimulated by retinoic acid 6	64220	A_33_P3307495	-1.38 ± 1.56	1.10
MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	245802	A_23_P416238	-1.38 ± 1.20	1.59
VPREB3	pre-B lymphocyte 3	29802	A_33_P3299254	-1.38 ± 0.94	2.25
KCNG1	potassium channel, voltage gated modifier subfamily G, member 1	3755	A_22_P00005343	-1.37 ± 1.26	1.47
PTX3	pentraxin 3, long	5806	A_23_P121064	-1.37 ± 1.12	1.74
MPO	myeloperoxidase	4353	A_23_P141173	-1.37 ± 0.85	2.54
MS4A1	membrane-spanning 4-domains, subfamily A, member 1	931	A_33_P3406567	-1.36 ± 1.36	1.31
NUDT9P1	nudix (nucleoside diphosphate linked moiety X)-type motif 9 pseudogene 1		A_32_P40463	1.36 ± 0.86	2.48
LGALS7	lectin, galactoside-binding, soluble, 7	3963	A_24_P238250	-1.35 ± 2.05	0.73
SPRR2A	small proline-rich protein 2A	6700	A_33_P3260430	-1.35 ± 1.22	1.50
HNF1A-AS1	HNF1A antisense RNA 1	283460	A_24_P314515	1.35 ± 0.67	3.48
MERTK	MER proto-oncogene, tyrosine kinase	10461	A_33_P3402091	-1.35 ± 0.64	3.71
CCL7	chemokine (C-C motif) ligand 7	6354	A_23_P78037	-1.34 ± 1.84	0.84
GALNT14	polypeptide N-acetylgalactosaminyltransferase 14	79623	A_23_P67847	-1.34 ± 1.77	0.88
SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	5268	A_33_P3310104	-1.34 ± 1.74	0.91
HIST1H2AG	histone cluster 1, H2ag	8969	A_21_P0000197	-1.34 ± 1.29	1.38
PROK2	prokineticin 2	60675	A_24_P97342	-1.34 ± 1.04	1.85
FBN3	fibrillin 3	84467	A_33_P3300430	1.34 ± 0.81	2.64
PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	7941	A_23_P145096	-1.33 ± 1.66	0.95
HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	A_23_P70007	-1.33 ± 0.97	2.05
LMO7DN-IT1	LMO7DN intronic transcript 1	104326189	A_22_P00023866	1.33 ± 0.89	2.30
ASB18	ankyrin repeat and SOCS box containing 18	401036	A_33_P3290162	-1.33 ± 0.88	2.35

GPR128	G protein-coupled receptor 128	84873	A_23_P40919	1.32 ± 2.23	0.63
CCDC85A	coiled-coil domain containing 85A	114800	A_23_P349566	1.32 ± 1.73	0.89
SPRR2E	small proline-rich protein 2E	6704	A_33_P3325704	-1.32 ± 1.35	1.26
MS4A15	membrane-spanning 4-domains, subfamily A, member 15	219995	A_33_P3312499	1.32 ± 1.16	1.57
CHI3L2	chitinase 3-like 2	1117	A_23_P12082	-1.32 ± 1.13	1.62
CD7	CD7 molecule	924	A_33_P3226995	1.32 ± 0.89	2.28
AIM2	absent in melanoma 2	9447	A_32_P44394	-1.32 ± 0.75	2.88
EPB41L5	erythrocyte membrane protein band 4.1 like 5	57669	A_24_P944640	1.32 ± 0.57	4.15
DEFA3	defensin, alpha 3, neutrophil-specific	1667	A_23_P31816	-1.31 ± 1.78	0.85
MT1G	metallothionein 1G	4495	A_33_P3233645	-1.31 ± 1.41	1.18
SP5	Sp5 transcription factor	389058	A_23_P135381	1.31 ± 1.15	1.56
ZDHHC11	zinc finger, DHHC-type containing 11	79844	A_33_P3344204	1.31 ± 1.09	1.70
CYS1	cystin 1	192668	A_33_P3398156	1.31 ± 0.96	2.01
NR1D1	nuclear receptor subfamily 1, group D, member 1	9572	A_24_P250227	-1.31 ± 0.93	2.11
PNOC	prepronociceptin	5368	A_23_P253321	-1.31 ± 0.93	2.11
CYTL1	cytokine-like 1	54360	A_23_P10647	-1.31 ± 0.90	2.23
CXCR4	chemokine (C-X-C motif) receptor 4	7852	A_23_P102000	-1.31 ± 0.82	2.50
SIGLEC5	sialic acid binding Ig-like lectin 5	8778	A_24_P48539	-1.31 ± 0.80	2.60
LINC01500	lincRNA 1500	102723742	A_22_P00004890	-1.31 ± 0.77	2.78
SCN3A	sodium channel, voltage gated, type III alpha subunit	6328	A_23_P67896	1.31 ± 0.76	2.79
KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2	202559	A_23_P366453	1.30 ± 0.98	1.96
GXYLT1P3	glucoside xylosyltransferase 1 pseudogene 3		A_33_P3244369	1.30 ± 0.94	2.06
TIMP4	TIMP metallopeptidase inhibitor 4	7079	A_32_P70315	-1.30 ± 0.88	2.27
CCR10	chemokine (C-C motif) receptor 10	2826	A_33_P3221303	-1.30 ± 0.72	3.01
OLFM4	olfactomedin 4	10562	A_24_P181254	-1.29 ± 1.47	1.08
COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	1285	A_23_P170679	1.29 ± 1.18	1.48
LOC100240735	uncharacterized LOC100240735	100240735	A_32_P170481	1.29 ± 1.16	1.51
EFCC1	EF-hand and coiled-coil domain containing 1	79825	A_23_P166566	1.29 ± 1.15	1.54

PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	5320	A_23_P321949	-1.29 ± 1.13	1.57
SLC41A2	solute carrier family 41 (magnesium transporter), member 2	84102	A_23_P204801	-1.29 ± 0.95	2.01
TAL1	T-cell acute lymphocytic leukemia 1	6886	A_23_P63371	1.29 ± 0.95	2.01
PI3	peptidase inhibitor 3, skin-derived	5266	A_23_P210465	-1.29 ± 0.93	2.07
LOC283710	uncharacterized LOC283710		A_33_P3336587	-1.29 ± 0.88	2.22
AQP4	aquaporin 4	361	A_33_P3420757	1.29 ± 0.86	2.30
ZNF184	zinc finger protein 184	7738	A_23_P156620	1.29 ± 0.60	3.81
NRXN3	neurexin 3	9369	A_33_P3851023	1.28 ± 1.76	0.84
PRB1	proline-rich protein BstNI subfamily 1	5542	A_33_P3258593	-1.28 ± 1.48	1.06
ANXA3	annexin A3	306	A_23_P121716	1.28 ± 1.20	1.43
ANLN	anillin, actin binding protein	54443	A_23_P356684	-1.28 ± 1.15	1.52
LOC90246	uncharacterized LOC90246		A_24_P532180	1.28 ± 1.12	1.57
ARHGEF26	Rho guanine nucleotide exchange factor (GEF) 26	26084	A_32_P5276	1.28 ± 1.11	1.60
FKBP5	FK506 binding protein 5	2289	A_24_P38081	-1.28 ± 1.07	1.68
LOC101927542	uncharacterized LOC101927542		A_21_P0013388	1.28 ± 0.93	2.04
MFAP5	microfibrillar associated protein 5	8076	A_33_P3708413	-1.27 ± 2.00	0.69
DAPK2	death-associated protein kinase 2	23604	A_24_P10233	1.27 ± 1.35	1.20
TTTY16	testis-specific transcript, Y-linked 16 (non-protein coding)	252948	A_33_P3349495	1.27 ± 1.04	1.71
LINC00346	lincRNA 346	283487	A_23_P368909	-1.27 ± 1.01	1.79
LOC101928075	uncharacterized LOC101928075	101928075	A_22_P00009780	-1.27 ± 0.84	2.35
COLQ	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	8292	A_23_P212126	1.27 ± 0.82	2.40
KCNK12	potassium channel, two pore domain subfamily K, member 12	56660	A_33_P3256510	-1.26 ± 1.36	1.17
PCSK1	proprotein convertase subtilisin/kexin type 1	5122	A_24_P174793	-1.26 ± 1.01	1.78
ZAN	zonadhesin (gene/pseudogene)	7455	A_23_P82286	1.26 ± 0.81	2.44
LMO7	LIM domain 7	4008	A_33_P3280801	1.26 ± 0.81	2.42
CDH16	cadherin 16, KSP-cadherin	1014	A_23_P100240	1.26 ± 0.74	2.78
SSTR1	somatostatin receptor 1	6751	A_24_P244706	1.25 ± 1.39	1.12

GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	2999	A_23_P128993	1.25 ± 1.26	1.29
SPRR2F	small proline-rich protein 2F	6705	A_33_P3274811	-1.25 ± 1.12	1.51
ANKRD20A2	ankyrin repeat domain 20 family, member A2	441425	A_21_P0010771	1.25 ± 1.11	1.53
LOC100130691	uncharacterized LOC100130691	100130691	A_19_P00315584	1.25 ± 1.08	1.61
TMEM38B	transmembrane protein 38B	55151	A_23_P60259	-1.25 ± 0.90	2.07
ARL13B	ADP-ribosylation factor-like 13B	200894	A_23_P10081	1.25 ± 0.87	2.18
GLB1L3	galactosidase, beta 1-like 3	112937	A_32_P741851	1.25 ± 0.80	2.48
KIAA1683	KIAA1683	80726	A_23_P130974	1.24 ± 1.08	1.58
ADIRF	adipogenesis regulatory factor	10974	A_23_P161439	1.24 ± 1.04	1.67
RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	6036	A_23_P151637	-1.24 ± 0.85	2.23
TENM2	teneurin transmembrane protein 2	57451	A_24_P299474	-1.23 ± 2.34	0.54
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	3357	A_23_P16953	1.23 ± 1.62	0.88
KRT6B	keratin 6B, type II	3854	A_23_P76249	-1.23 ± 1.55	0.94
TNNC1	troponin C type 1 (slow)	7134	A_23_P166823	1.23 ± 1.30	1.20
FPR1	formyl peptide receptor 1	2357	A_23_P38795	-1.23 ± 0.98	1.81
MYOZ1	myozenin 1	58529	A_23_P1320	1.23 ± 0.98	1.78
C20orf166-AS1	C20orf166 antisense RNA 1		A_33_P3423853	1.23 ± 0.84	2.22
HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	57520	A_33_P3270311	1.22 ± 1.79	0.77
RHOV	ras homolog family member V	171177	A_23_P424561	-1.22 ± 1.51	0.97
CXCL14	chemokine (C-X-C motif) ligand 14	9547	A_33_P3590259	-1.22 ± 1.51	0.96
SLC22A18AS	solute carrier family 22 (organic cation transporter), member 18 antisense	5003	A_33_P3316587	-1.22 ± 1.04	1.63
KLHL22	kelch-like family member 22	84861	A_24_P117323	1.22 ± 0.87	2.10
LINC00935	lincRNA 935	255411	A_32_P161994	1.22 ± 0.70	2.87
XCL1	chemokine (C motif) ligand 1	6375	A_24_P45476	1.21 ± 1.07	1.53
LOC344887	NmrA-like family domain containing 1 pseudogene		A_24_P68908	-1.21 ± 1.02	1.66
GYG2P1	glycogenin 2 pseudogene 1		A_33_P3253598	1.21 ± 1.00	1.73
IGLL1	immunoglobulin lambda-like polypeptide 1	3543	A_24_P239076	-1.21 ± 0.93	1.89

TSHB	thyroid stimulating hormone, beta	7252	A_23_P12128	1.21 ± 0.93	1.89
PNLIPRP3	pancreatic lipase-related protein 3	119548	A_33_P3368193	-1.21 ± 0.92	1.93
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	6507	A_24_P286114	-1.21 ± 0.72	2.68
MRAP	melanocortin 2 receptor accessory protein	56246	A_24_P126210	-1.20 ± 1.64	0.83
LINC01116	lincRNA 1116		A_23_P302787	-1.20 ± 1.46	0.98
AZGP1	alpha-2-glycoprotein 1, zinc-binding	563	A_23_P71270	-1.20 ± 1.38	1.06
NDNF	neuron-derived neurotrophic factor	79625	A_23_P110266	1.20 ± 1.28	1.20
C1orf116	chromosome 1 open reading frame 116	79098	A_23_P897	1.20 ± 0.98	1.73
DDIT4	DNA-damage-inducible transcript 4	54541	A_23_P104318	-1.20 ± 0.82	2.24
CDH15	cadherin 15, type 1, M-cadherin (myotubule)	1013	A_32_P25357	-1.20 ± 0.75	2.52
LOC100133286	uncharacterized LOC100133286	100133286	A_33_P3235117	-1.20 ± 0.65	3.06
KREMEN2	kringle containing transmembrane protein 2	79412	A_33_P3396214	-1.19 ± 1.16	1.35
CREB3L3	cAMP responsive element binding protein 3-like 3	84699	A_23_P108082	1.19 ± 1.10	1.45
VTRNA2-1	vault RNA 2-1	100126299	A_21_P0000584	-1.19 ± 1.08	1.49
PODNL1	podocan-like 1	79883	A_23_P433798	-1.19 ± 1.01	1.65
CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	51302	A_23_P133712	1.19 ± 1.01	1.63
FXYD4	FXYD domain containing ion transport regulator 4	53828	A_23_P98121	1.19 ± 0.98	1.72
CPNE5	copine V	57699	A_23_P360804	-1.19 ± 0.91	1.90
LOC100996660	uncharacterized LOC100996660		A_21_P0011598	1.19 ± 0.86	2.05
PPP1R2P9	protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 9		A_23_P34007	-1.19 ± 0.84	2.11
PLVAP	plasmalemma vesicle associated protein	83483	A_23_P56328	-1.19 ± 0.76	2.47
LOC389641	uncharacterized LOC389641	389641	A_22_P00004017	-1.19 ± 0.75	2.52
LINC00293	lincRNA 293	497634	A_33_P3237859	-1.19 ± 0.74	2.52
GGT8P	gamma-glutamyltransferase 8 pseudogene		A_24_P375322	1.19 ± 0.68	2.86
LINC01506	lincRNA 1506	101927015	A_21_P0006079	-1.19 ± 0.64	3.13
OXTR	oxytocin receptor	5021	A_33_P3413741	-1.18 ± 2.44	0.48
PEBP4	phosphatidylethanolamine-binding protein 4	157310	A_33_P3627001	1.18 ± 1.67	0.80
EDNRB	endothelin receptor type B	1910	A_24_P330263	1.18 ± 1.53	0.90

CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	1577	A_23_P8801	1.18 ± 1.24	1.22
TLE6	transducin-like enhancer of split 6	79816	A_23_P208937	1.18 ± 1.00	1.63
SHCBP1	SHC SH2-domain binding protein 1	79801	A_32_P96719	-1.18 ± 0.93	1.81
LOC101927311	uncharacterized LOC101927311	101927311	A_22_P00011483	1.18 ± 0.91	1.89
MT1X	metallothionein 1X	4501	A_33_P3236868	-1.18 ± 0.88	1.97
ANKRD30BP2	ankyrin repeat domain 30B pseudogene 2		A_24_P917819	-1.18 ± 0.83	2.13
C2CD4B	C2 calcium-dependent domain containing 4B	388125	A_24_P788878	1.18 ± 0.79	2.27
CLEC1B	C-type lectin domain family 1, member B	51266	A_33_P3332955	1.18 ± 0.74	2.53
BLK	BLK proto-oncogene, Src family tyrosine kinase	640	A_23_P31725	-1.17 ± 1.41	0.99
CLCA2	chloride channel accessory 2	9635	A_23_P397248	-1.17 ± 1.33	1.09
FAM167A	family with sequence similarity 167, member A	83648	A_23_P334955	1.17 ± 1.06	1.49
SHISA2	shisa family member 2	387914	A_32_P55241	1.17 ± 1.05	1.52
UBE2C	ubiquitin-conjugating enzyme E2C	11065	A_24_P297539	-1.17 ± 0.91	1.87
SUN5	Sad1 and UNC84 domain containing 5	140732	A_33_P3292198	1.17 ± 0.91	1.87
CSH2	chorionic somatomammotropin hormone 2	1443	A_23_P207174	-1.17 ± 0.90	1.88
DDIAS	DNA damage-induced apoptosis suppressor	220042	A_23_P429491	-1.17 ± 0.89	1.93
TIMP1	TIMP metallopeptidase inhibitor 1	7076	A_23_P62115	-1.17 ± 0.86	2.02
KCNE2	potassium voltage-gated channel, Isk-related family, member 2	9992	A_23_P120694	1.17 ± 0.67	2.84
C3orf67-AS1	C3orf67 antisense RNA 1	101929238	A_22_P00008596	1.16 ± 1.36	1.04
FCRLA	Fc receptor-like A	84824	A_23_P46039	-1.16 ± 1.06	1.47
BIRC5	baculoviral IAP repeat containing 5	332	A_23_P118815	-1.16 ± 1.01	1.59
SCN3B	sodium channel, voltage gated, type III beta subunit	55800	A_33_P3402404	-1.16 ± 0.97	1.66
NUCB1-AS1	NUCB1 antisense RNA 1	100874085	A_22_P00017074	-1.16 ± 0.86	2.00
SLC25A30-AS1	SLC25A30 antisense RNA 1	100874259	A_22_P00025147	1.16 ± 0.83	2.09
NYX	nyctalopin	60506	A_23_P137046	-1.16 ± 0.83	2.08
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	9700	A_23_P32707	-1.16 ± 0.73	2.49
TTYH1	tweety family member 1	57348	A_23_P50815	-1.16 ± 0.60	3.30
TNS4	tensin 4	84951	A_23_P207850	-1.15 ± 2.12	0.56

KRT23	keratin 23, type I	25984	A_23_P78248	-1.15 ± 1.68	0.76
ANGPTL4	angiopoietin-like 4	51129	A_33_P3295358	-1.15 ± 1.56	0.85
SNORD83A	small nucleolar RNA, C/D box 83A	116937	A_21_P0000224	-1.15 ± 1.52	0.89
E2F2	E2F transcription factor 2	1870	A_23_P408955	-1.15 ± 1.13	1.34
ERP44	endoplasmic reticulum protein 44	23071	A_23_P373927	1.15 ± 1.04	1.49
L3MBTL4	l(3)mbt-like 4 (Drosophila)	91133	A_23_P326474	1.15 ± 0.87	1.91
LOC101929066	uncharacterized LOC101929066	101929066	A_22_P00011609	1.15 ± 0.71	2.58
LRRC31	leucine rich repeat containing 31	79782	A_24_P240259	1.15 ± 0.71	2.57
CHEK1	checkpoint kinase 1	1111	A_33_P3349536	-1.15 ± 0.68	2.76
ZFY	zinc finger protein, Y-linked	7544	A_24_P942743	1.14 ± 1.58	0.82
MMP24	matrix metallopeptidase 24 (membrane-inserted)	10893	A_33_P3398331	1.14 ± 1.34	1.03
TXNDC2	thioredoxin domain containing 2 (spermatozoa)	84203	A_24_P125434	1.14 ± 1.24	1.16
AGTR1	angiotensin II receptor, type 1	185	A_23_P166616	1.14 ± 1.18	1.23
LPPR4	lipid phosphate phosphatase-related protein type 4	9890	A_32_P148538	1.14 ± 1.07	1.43
PLA2R1	phospholipase A2 receptor 1, 180kDa	22925	A_23_P142830	1.14 ± 0.97	1.64
SNAI3-AS1	SNAI3 antisense RNA 1	197187	A_23_P406227	-1.14 ± 0.91	1.79
LOC101928195	monofunctional C1-tetrahydrofolate synthase, mitochondrial-like		A_21_P0013573	1.14 ± 0.91	1.79
GLS2	glutaminase 2 (liver, mitochondrial)	27165	A_24_P326739	1.14 ± 0.87	1.93
SIGLEC15	sialic acid binding Ig-like lectin 15	284266	A_23_P50146	-1.14 ± 0.75	2.37
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	2919	A_23_P7144	-1.13 ± 2.38	0.47
SLC4A5	solute carrier family 4 (sodium bicarbonate cotransporter), member 5	57835	A_33_P3241393	1.13 ± 1.19	1.21
SNAR-G1	small ILF3/NF90-associated RNA G1		A_21_P0000491	1.13 ± 1.17	1.25
DIRAS3	DIRAS family, GTP-binding RAS-like 3	9077	A_23_P149121	1.13 ± 1.14	1.29
ODAM	odontogenic, ameloblast asssociated	54959	A_23_P58228	1.13 ± 1.01	1.52
ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	114794	A_32_P219279	1.13 ± 0.91	1.77
LINC01060	lincRNA 1060	401164	A_21_P0000610	-1.13 ± 0.64	2.92
MYC	v-myc avian myelocytomatosis viral oncogene	4609	A_23_P215956	-1.13 ± 0.56	3.47

	homolog				
RARRES1	retinoic acid receptor responder (tazarotene induced) 1	5918	A_23_P18078	-1.12 ± 1.96	0.60
SNORD114-20	small nucleolar RNA, C/D box 114-20	767598	A_21_P0000417	-1.12 ± 1.30	1.05
CBX2	chromobox homolog 2	84733	A_33_P3423949	1.12 ± 0.93	1.70
TNN	tenascin N	63923	A_32_P480177	1.12 ± 0.91	1.73
FOXD4	forkhead box D4	2298	A_32_P119248	1.12 ± 0.85	1.93
OR4F21	olfactory receptor, family 4, subfamily F, member 21	441308	A_33_P3316147	1.12 ± 0.85	1.91
CAV1	caveolin 1, caveolae protein, 22kDa	857	A_23_P134454	1.12 ± 0.84	1.97
TBR1	T-box, brain, 1	10716	A_22_P00014844	1.12 ± 0.75	2.31
LOC101927902	uncharacterized LOC101927902		A_21_P0005196	-1.12 ± 0.74	2.33
IL12RB1	interleukin 12 receptor, beta 1	3594	A_23_P399156	1.12 ± 0.68	2.63
MSMB	microseminoprotein, beta-	4477	A_24_P146683	-1.11 ± 2.13	0.53
MEG9	maternally expressed 9 (non-protein coding)	100507257	A_21_P0011281	-1.11 ± 1.32	1.03
LINC01164	lincRNA 1164	399827	A_33_P3362034	-1.11 ± 0.96	1.59
LOC100129931	uncharacterized LOC100129931	100129931	A_22_P00003503	-1.11 ± 0.88	1.82
SELL	selectin L	6402	A_33_P3400273	-1.11 ± 0.74	2.31
CACNG4	calcium channel, voltage-dependent, gamma subunit 4	27092	A_24_P70303	1.11 ± 0.66	2.73
ZNF252P-AS1	ZNF252P antisense RNA 1	286103	A_32_P935906	1.11 ± 0.62	2.99
FJX1	four jointed box 1 (Drosophila)	24147	A_23_P150693	-1.11 ± 0.60	3.12
SNORA2B	small nucleolar RNA, H/ACA box 2B	677794	A_21_P0000307	1.10 ± 2.71	0.39
TSPAN19	tetraspanin 19	144448	A_23_P2322	-1.10 ± 1.60	0.78
CAPN13	calpain 13	92291	A_23_P101972	-1.10 ± 1.60	0.77
HTR3C	5-hydroxytryptamine (serotonin) receptor 3C, ionotropic	170572	A_23_P124402	1.10 ± 1.45	0.88
CADM1	cell adhesion molecule 1	23705	A_33_P3421913	1.10 ± 1.31	1.01
TG	thyroglobulin	7038	A_23_P32454	-1.10 ± 1.25	1.09
HIST1H3B	histone cluster 1, H3b	8358	A_23_P93258	-1.10 ± 1.21	1.13
XAGE2	X antigen family, member 2	9502	A_23_P34031	1.10 ± 1.16	1.21

EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	2015	A_33_P3215803	1.10 ± 1.06	1.37
LOC101929450	uncharacterized LOC101929450	101929450	A_19_P00321279	-1.10 ± 0.97	1.55
RNLS	renalase, FAD-dependent amine oxidase	55328	A_23_P202501	1.10 ± 0.96	1.59
GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	79153	A_23_P26511	1.10 ± 0.95	1.61
LOC101928906	uncharacterized LOC101928906		A_21_P0006270	1.10 ± 0.95	1.60
NOVA1-AS1	NOVA1 antisense RNA 1 (head to head)	102725045	A_21_P0008504	-1.10 ± 0.91	1.71
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	23586	A_33_P3372910	1.10 ± 0.89	1.78
SH3GL3	SH3-domain GRB2-like 3	6457	A_23_P48988	1.10 ± 0.89	1.78
TSC22D3	TSC22 domain family, member 3	1831	A_33_P3237634	-1.10 ± 0.85	1.88
MURC	muscle-related coiled-coil protein	347273	A_33_P3335147	1.10 ± 0.78	2.15
PMPCB	peptidase (mitochondrial processing) beta	9512	A_33_P3294162	1.10 ± 0.77	2.14
OR4F29	olfactory receptor, family 4, subfamily F, member 29	81399	A_33_P3268582	1.10 ± 0.73	2.32
KRT1	keratin 1, type II	3848	A_33_P3379396	1.09 ± 1.18	1.16
STAR	steroidogenic acute regulatory protein	6770	A_23_P8981	-1.09 ± 1.07	1.34
AADAC	arylacetamide deacetylase	13	A_23_P80570	1.09 ± 1.01	1.43
INSC	inscuteable homolog (Drosophila)	387755	A_33_P3814721	1.09 ± 0.99	1.49
LOC101930162	uncharacterized LOC101930162		A_22_P00012430	1.09 ± 0.92	1.66
LOC391322	D-dopachrome tautomerase-like		A_33_P3379341	-1.09 ± 0.91	1.67
SIGLEC10	sialic acid binding Ig-like lectin 10	89790	A_23_P208182	-1.09 ± 0.74	2.25
SNORD59B	small nucleolar RNA, C/D box 59B		A_21_P0000374	1.09 ± 0.72	2.34
AZU1	azurocidin 1	566	A_33_P3279353	1.09 ± 0.69	2.49
ZNF792	zinc finger protein 792	126375	A_23_P67618	1.09 ± 0.67	2.55
LINC01119	lincRNA 1119	100134259	A_21_P0001773	-1.09 ± 0.65	2.70
ACAN	aggrecan	176	A_23_P307310	-1.08 ± 2.24	0.48
S100A9	S100 calcium binding protein A9	6280	A_23_P23048	-1.08 ± 1.40	0.90
SPNS3	spinster homolog 3 (Drosophila)	201305	A_23_P100963	1.08 ± 0.93	1.61
PSAT1	phosphoserine aminotransferase 1	29968	A_23_P259692	-1.08 ± 0.88	1.75
FOXA2	forkhead box A2	3170	A_24_P365515	1.08 ± 0.74	2.21

ZNF503-AS1	ZNF503 antisense RNA 1	253264	A_21_P0010924	1.07 ± 1.46	0.84
SBF2-AS1	SBF2 antisense RNA 1	283104	A_22_P00015662	-1.07 ± 1.29	1.00
B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	10331	A_23_P78980	-1.07 ± 1.22	1.08
SLC29A4	solute carrier family 29 (equilibrative nucleoside transporter), member 4	222962	A_23_P168551	1.07 ± 1.12	1.21
BLM	Bloom syndrome, RecQ helicase-like	641	A_23_P88630	-1.07 ± 0.99	1.46
TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	23495	A_23_P84705	-1.07 ± 0.89	1.71
HABP2	hyaluronan binding protein 2	3026	A_23_P1173	1.07 ± 0.80	1.96
C15orf27	chromosome 15 open reading frame 27	123591	A_23_P88678	-1.07 ± 0.76	2.11
KIAA1958	KIAA1958		A_33_P3314341	1.07 ± 0.74	2.19
IFT57	intraflagellar transport 57	55081	A_24_P362881	1.07 ± 0.66	2.60
HTRA4	HtrA serine peptidase 4	203100	A_23_P44421	-1.06 ± 1.40	0.88
SAMD3	sterile alpha motif domain containing 3	154075	A_23_P93524	1.06 ± 1.35	0.93
LOC440040	glutamate receptor, metabotropic 5 pseudogene	440040	A_23_P150198	1.06 ± 1.21	1.08
VMO1	vitelline membrane outer layer 1 homolog (chicken)	284013	A_23_P55356	-1.06 ± 1.15	1.17
GGTLC1	gamma-glutamyltransferase light chain 1	92086	A_23_P57199	1.06 ± 1.07	1.28
CATSPER3	cation channel, sperm associated 3	347732	A_23_P393749	1.06 ± 0.86	1.74
ZNF483	zinc finger protein 483	158399	A_33_P3620832	1.06 ± 0.79	1.98
UBASH3A	ubiquitin associated and SH3 domain containing A	53347	A_33_P3385909	-1.06 ± 0.75	2.14
OTOS	otospiralin	150677	A_23_P90997	-1.06 ± 0.69	2.40
ADAM12	ADAM metallopeptidase domain 12	8038	A_22_P00000010	-1.05 ± 1.56	0.75
ALOX15B	arachidonate 15-lipoxygenase, type B	247	A_23_P60627	-1.05 ± 1.33	0.94
CCL20	chemokine (C-C motif) ligand 20	6364	A_23_P17065	-1.05 ± 1.33	0.94
C1orf94	chromosome 1 open reading frame 94	84970	A_23_P160297	-1.05 ± 1.23	1.05
FOXM1	forkhead box M1	2305	A_23_P151150	-1.05 ± 1.06	1.28
ZNF519	zinc finger protein 519	162655	A_23_P328766	1.05 ± 0.92	1.57
LOC100128288	uncharacterized LOC100128288		A_24_P256415	1.05 ± 0.91	1.58
DNASE2B	deoxyribonuclease II beta	58511	A_23_P126677	-1.05 ± 0.90	1.62

FLT4	fms-related tyrosine kinase 4	2324	A_23_P356070	1.05 ± 0.79	1.97
PRTG	protogenin	283659	A_33_P3234657	1.05 ± 0.77	2.02
LSP1	lymphocyte-specific protein 1	4046	A_22_P00025404	-1.05 ± 0.76	2.06
SNORD114-10	small nucleolar RNA, C/D box 114-10	767588	A_21_P0000407	-1.05 ± 0.76	2.06
LINC00260	lincRNA 260		A_33_P3210810	1.05 ± 0.75	2.09
ANKRD20A5P	ankyrin repeat domain 20 family, member A5, pseudogene		A_21_P0012183	1.05 ± 0.73	2.16
GLRA4	glycine receptor, alpha 4	441509	A_24_P404868	1.05 ± 0.70	2.28
FKBP11	FK506 binding protein 11, 19 kDa	51303	A_33_P3267296	-1.05 ± 0.66	2.51
EGFLAM-AS4	EGFLAM antisense RNA 4	100852408	A_22_P00025440	-1.05 ± 0.57	3.07
LOC102723617	uncharacterized LOC102723617	102723617	A_21_P0011769	1.05 ± 0.49	3.76
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	3294	A_23_P118065	-1.04 ± 1.95	0.55
CALB2	calbindin 2	794	A_23_P21092	-1.04 ± 1.51	0.77
GATA5	GATA binding protein 5	140628	A_23_P371835	1.04 ± 1.41	0.85
FSIP1	fibrous sheath interacting protein 1	161835	A_22_P00006743	1.04 ± 1.09	1.22
MOGAT1	monoacylglycerol O-acyltransferase 1	116255	A_23_P142574	1.04 ± 1.06	1.27
HCN3	hyperpolarization activated cyclic nucleotide gated potassium channel 3	57657	A_23_P34827	1.04 ± 0.91	1.56
CRISP2	cysteine-rich secretory protein 2	7180	A_32_P173662	-1.04 ± 0.89	1.62
GFPT2	glutamine-fructose-6-phosphate transaminase 2	9945	A_23_P144916	-1.04 ± 0.87	1.69
FAM198A	family with sequence similarity 198, member A	729085	A_23_P69154	-1.04 ± 0.87	1.68
CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	494143	A_32_P194264	-1.04 ± 0.87	1.67
LINC01554	lincRNA 1554		A_32_P128209	-1.04 ± 0.85	1.74
C10orf90	chromosome 10 open reading frame 90	118611	A_32_P191441	-1.04 ± 0.70	2.30
LINC01490	lincRNA 1490	101928420	A_22_P00010372	-1.04 ± 0.70	2.30
KCNJ13	potassium channel, inwardly rectifying subfamily J, member 13	3769	A_33_P3314857	1.04 ± 0.60	2.82
LCN15	lipocalin 15	389812	A_33_P3263938	1.04 ± 0.58	2.94
LOC388780	uncharacterized LOC388780		A_33_P3241661	-1.03 ± 1.55	0.74
CXCL8	chemokine (C-X-C motif) ligand 8	3576	A_32_P87013	-1.03 ± 1.52	0.76

ZNF683	zinc finger protein 683	257101	A_33_P3208970	1.03 ± 1.37	0.88
BDKRB1	bradykinin receptor B1	623	A_23_P128744	-1.03 ± 1.29	0.95
LRRIQ3	leucine-rich repeats and IQ motif containing 3	127255	A_33_P3292387	-1.03 ± 1.20	1.05
LLPH-AS1	LLPH antisense RNA 1 (head to head)	103625681	A_22_P00008226	1.03 ± 1.11	1.17
ADORA1	adenosine A1 receptor	134	A_23_P74299	1.03 ± 1.09	1.21
LOC102724851	uncharacterized LOC102724851		A_21_P0004864	1.03 ± 1.06	1.24
LINC01268	lincRNA 1268	285758	A_33_P3867584	1.03 ± 1.02	1.33
PRR35	proline rich 35	146325	A_33_P3420633	-1.03 ± 0.96	1.45
SEC62	SEC62 homolog (S. cerevisiae)	7095	A_23_P357860	1.03 ± 0.96	1.45
SOCS1	suppressor of cytokine signaling 1	8651	A_23_P420196	-1.03 ± 0.89	1.61
IGLL5	immunoglobulin lambda-like polypeptide 5	100423062	A_33_P3379039	-1.03 ± 0.80	1.85
TET3	tet methylcytosine dioxygenase 3	200424	A_22_P00015990	-1.03 ± 0.66	2.46
SCRG1	stimulator of chondrogenesis 1	11341	A_23_P167159	-1.02 ± 2.12	0.48
ERN2	endoplasmic reticulum to nucleus signaling 2	10595	A_33_P3213645	-1.02 ± 1.54	0.74
VSIG1	V-set and immunoglobulin domain containing 1	340547	A_32_P163147	1.02 ± 1.46	0.79
KRT13	keratin 13, type I	3860	A_24_P228149	-1.02 ± 1.38	0.85
HSPA12B	heat shock 70kD protein 12B	116835	A_23_P91334	1.02 ± 1.19	1.04
FAM162B	family with sequence similarity 162, member B	221303	A_23_P145054	1.02 ± 1.12	1.13
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	3791	A_24_P71973	1.02 ± 1.10	1.18
METTL7B	methyltransferase like 7B	196410	A_24_P64653	-1.02 ± 1.01	1.31
GPR19	G protein-coupled receptor 19	2842	A_33_P3236813	-1.02 ± 0.95	1.44
TNRC18	trinucleotide repeat containing 18	84629	A_33_P3321507	-1.02 ± 0.90	1.57
GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	2562	A_33_P3277075	1.02 ± 0.87	1.64
SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	79723	A_23_P202392	-1.02 ± 0.85	1.69
LOC286178	uncharacterized LOC286178	286178	A_22_P00006024	-1.02 ± 0.85	1.69
RASL10B	RAS-like, family 10, member B	91608	A_24_P322229	1.02 ± 0.85	1.69
GPM6A	glycoprotein M6A	2823	A_23_P121545	1.02 ± 0.84	1.70
FLJ41200	uncharacterized LOC401492	401492	A_33_P3266739	-1.02 ± 0.82	1.80

PDK1	pyruvate dehydrogenase kinase, isozyme 1	5163	A_24_P37441	-1.02 ± 0.79	1.88
SLC39A3	solute carrier family 39 (zinc transporter), member 3	29985	A_24_P382467	-1.02 ± 0.75	1.99
LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	9227	A_32_P113066	1.02 ± 0.55	3.10
GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)	653689	A_33_P3289045	1.01 ± 1.82	0.58
ALDH1L1	aldehyde dehydrogenase 1 family, member L1	10840	A_23_P258887	-1.01 ± 1.55	0.72
CLDN2	claudin 2	9075	A_33_P3249046	1.01 ± 1.39	0.83
CCNO	cyclin O	10309	A_23_P92860	-1.01 ± 1.34	0.87
KRT15	keratin 15, type I	3866	A_23_P27133	-1.01 ± 1.22	1.00
CEMIP	cell migration inducing protein, hyaluronan binding	57214	A_23_P324754	-1.01 ± 1.17	1.06
SLC16A6	solute carrier family 16, member 6	9120	A_23_P152791	-1.01 ± 1.13	1.11
SIGLEC12	sialic acid binding Ig-like lectin 12 (gene/pseudogene)	89858	A_23_P164596	-1.01 ± 1.11	1.13
FAM189A1	family with sequence similarity 189, member A1	23359	A_32_P143000	1.01 ± 1.07	1.20
ZNF155	zinc finger protein 155	7711	A_24_P301629	-1.01 ± 0.96	1.40
DHRS2	dehydrogenase/reductase (SDR family) member 2	10202	A_23_P321501	1.01 ± 0.94	1.45
CPNE9	copine family member IX	151835	A_23_P57829	1.01 ± 0.88	1.57
MEIS3	Meis homeobox 3	56917	A_23_P78795	-1.01 ± 0.85	1.65
FLNC	filamin C, gamma	2318	A_21_P0013349	-1.01 ± 0.81	1.78
C8orf37-AS1	C8orf37 antisense RNA 1		A_21_P0000720	1.01 ± 0.77	1.92
OR5A1	olfactory receptor, family 5, subfamily A, member 1	219982	A_23_P75764	-1.01 ± 0.71	2.13
SNORD116-28	small nucleolar RNA, C/D box 116-28		A_21_P0000455	1.01 ± 0.70	2.16
GYPE	glycophorin E (MNS blood group)	2996	A_23_P41304	1.01 ± 0.63	2.57
TM4SF19	transmembrane 4 L six family member 19	116211	A_23_P372946	-1.00 ± 1.54	0.72
SNX22	sorting nexin 22	79856	A_33_P3212172	1.00 ± 1.44	0.79
AREG	amphiregulin	374	A_23_P259071	-1.00 ± 1.38	0.83
UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	7345	A_23_P132956	-1.00 ± 1.24	0.96

AXDND1	axonemal dynein light chain domain containing 1	126859	A_23_P356425	1.00 ± 1.07	1.18
TYRP1	tyrosinase-related protein 1	7306	A_23_P94403	1.00 ± 1.03	1.25
LINC00861	lincRNA 861	100130231	A_21_P0000807	-1.00 ± 0.99	1.33
GBP4	guanylate binding protein 4	115361	A_24_P45446	1.00 ± 0.91	1.50
LHFPL3-AS1	LHFPL3 antisense RNA 1	645591	A_32_P394491	1.00 ± 0.86	1.63
SPATA13-AS1	SPATA13 antisense RNA 1	100874231	A_22_P00023937	1.00 ± 0.83	1.71
LRRC52	leucine rich repeat containing 52	440699	A_33_P3292043	1.00 ± 0.81	1.77
EMP2	epithelial membrane protein 2	2013	A_23_P106682	1.00 ± 0.71	2.11
LOC101928445	uncharacterized LOC101928445	101928445	A_22_P00007787	-1.00 ± 0.70	2.17
ZNF230	zinc finger protein 230	7773	A_24_P370096	-1.00 ± 0.64	2.48

Supplementary Table S3. Annotated genes regulated in the lung fibroblast samples after pirfenidone treatment.

GENE SYMBOL	GENE NAME	ENTREZ ID	SPOT ID	mean log2(fold-change) ± the half width of the 95% confidence interval	-log10(P-value)
NPTX1	neuronal pentraxin I	4884	A_23_P124905	3.60 ± 1.88	3.23
SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	6563	A_23_P55616	2.93 ± 1.47	3.42
SULF2	sulfatase 2	55959	A_23_P154605	-2.58 ± 1.41	3.03
HLA-DMB	major histocompatibility complex, class II, DM beta	3109	A_32_P351968	2.36 ± 1.15	3.56
SCRG1	stimulator of chondrogenesis 1	11341	A_23_P167159	-2.35 ± 1.79	1.92
HOXC8	homeobox C8	3224	A_24_P124558	-2.35 ± 1.05	3.98
CFI	complement factor I	3426	A_23_P7212	-2.29 ± 1.58	2.20
CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	6362	A_23_P55270	2.17 ± 2.46	1.09
MYH2	myosin, heavy chain 2, skeletal muscle, adult	4620	A_23_P38271	-2.13 ± 1.93	1.49
HOXC9	homeobox C9	3225	A_23_P25150	-2.09 ± 1.31	2.53
FOXQ1	forkhead box Q1	94234	A_32_P164246	2.08 ± 1.69	1.75
XIST	X inactive specific transcript (non-protein coding)	7503	A_19_P00323692	2.03 ± 3.54	0.61
TENM2	teneurin transmembrane protein 2	57451	A_24_P299474	-2.02 ± 1.98	1.34
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	183	A_23_P115261	-1.99 ± 1.79	1.52
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	12	A_33_P3399788	-1.96 ± 1.35	2.20
PTGIS	prostaglandin I2 (prostacyclin) synthase	5740	A_24_P48723	-1.96 ± 1.34	2.24
FRAS1	Fraser extracellular matrix complex subunit 1	80144	A_32_P107876	-1.96 ± 1.32	2.27
SFRP4	secreted frizzled-related protein 4	6424	A_21_P0011967	-1.96 ± 1.30	2.33
POSTN	periostin, osteoblast specific factor	10631	A_33_P3511265	-1.93 ± 1.78	1.46
TNNT2	troponin T type 2 (cardiac)	7139	A_23_P34700	-1.93 ± 1.43	2.00
SULF1	sulfatase 1	23213	A_23_P43164	-1.91 ± 1.45	1.92
SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	6445	A_23_P423237	-1.91 ± 1.44	1.93

KCND2	potassium channel, voltage gated Shal related subfamily D, member 2	3751	A_23_P259251	-1.91 ± 1.04	3.08
CPZ	carboxypeptidase Z	8532	A_23_P58251	-1.86 ± 1.34	2.07
LPXN	leupaxin	9404	A_23_P87150	1.86 ± 0.98	3.21
FBLN2	fibulin 2	2199	A_23_P143981	-1.85 ± 1.19	2.41
BEX2	brain expressed X-linked 2	84707	A_33_P3245178	-1.85 ± 1.16	2.52
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3	3699	A_33_P3313145	-1.83 ± 0.78	4.24
SETBP1	SET binding protein 1	26040	A_23_P4551	-1.83 ± 0.71	4.77
CFD	complement factor D (adipsin)	1675	A_23_P119562	-1.81 ± 1.18	2.40
LOC284561	uncharacterized LOC284561		A_33_P3672756	-1.81 ± 1.12	2.54
GSTM4	glutathione S-transferase mu 4	2948	A_23_P217917	1.81 ± 0.97	3.13
SPON1	spondin 1, extracellular matrix protein	10418	A_32_P133072	-1.80 ± 1.22	2.26
B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	8707	A_33_P3286958	-1.79 ± 1.37	1.89
CTTNBP2	cortactin binding protein 2	83992	A_23_P215744	1.79 ± 1.09	2.64
DDX3Y	DEAD (Asp-Glu-Ala-Asp) box helicase 3, Y-linked	8653	A_33_P3224331	-1.78 ± 2.63	0.75
TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	7292	A_23_P126836	-1.78 ± 1.74	1.35
KLHDC7B	kelch domain containing 7B	113730	A_24_P117410	-1.78 ± 0.87	3.52
ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	23460	A_23_P500400	-1.77 ± 1.43	1.77
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	54566	A_23_P216556	1.76 ± 1.00	2.87
PLXDC2	plexin domain containing 2	84898	A_23_P161424	-1.76 ± 0.92	3.23
PKP2	plakophilin 2	5318	A_33_P3405728	-1.75 ± 1.07	2.62
APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein	54518	A_23_P401700	-1.75 ± 0.88	3.41
CCND2	cyclin D2	894	A_24_P278747	-1.74 ± 1.25	2.08
MEST	mesoderm specific transcript		A_23_P156970	-1.72 ± 1.40	1.73
RARRES2	retinoic acid receptor responder (tazarotene induced) 2	5919	A_23_P134237	-1.71 ± 1.55	1.50
FMOD	fibromodulin	2331	A_23_P114883	-1.71 ± 0.79	3.81
ARHGAP26	Rho GTPase activating protein 26	23092	A_33_P3228305	-1.69 ± 1.11	2.35

SHC2	SHC (Src homology 2 domain containing) transforming protein 2	25759	A_32_P205624	-1.69 ± 1.01	2.69
HOXC6	homeobox C6	3223	A_33_P3300965	-1.62 ± 1.37	1.65
SLC51B	solute carrier family 51, beta subunit	123264	A_23_P436284	1.62 ± 1.36	1.67
KLHL13	kelch-like family member 13	90293	A_23_P159974	1.62 ± 0.88	3.09
ALDH1A1	aldehyde dehydrogenase 1 family, member A1	216	A_23_P83098	-1.61 ± 1.58	1.34
LINC00312	lincRNA 312		A_23_P166779	-1.61 ± 0.90	2.98
LINC01444	lincRNA 1444	101927642	A_22_P00012170	1.60 ± 1.24	1.87
SCG2	secretogranin II	7857	A_24_P88696	-1.60 ± 1.20	1.97
AKR1C8P	aldo-keto reductase family 1, member C8, pseudogene	340811	A_21_P0010854	1.60 ± 1.02	2.47
LRRD1	leucine-rich repeats and death domain containing 1	401387	A_33_P3420446	1.59 ± 1.95	0.98
KRT18	keratin 18, type I	3875	A_32_P151544	-1.59 ± 1.84	1.06
TCF7	transcription factor 7 (T-cell specific, HMG-box)	6932	A_23_P7582	1.59 ± 0.88	2.99
LAMP3	lysosomal-associated membrane protein 3	27074	A_23_P29773	-1.58 ± 1.62	1.25
C10orf99	chromosome 10 open reading frame 99	387695	A_33_P3392405	-1.58 ± 1.46	1.46
LOC102725254	uncharacterized LOC102725254		A_22_P00010091	1.58 ± 1.02	2.42
MIR503HG	MIR503 host gene (non-protein coding)	84848	A_33_P3402329	-1.58 ± 0.94	2.71
CD52	CD52 molecule	1043	A_23_P85800	1.57 ± 2.09	0.87
GMFG	glia maturation factor, gamma	9535	A_23_P208866	1.57 ± 0.76	3.58
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	4939	A_33_P3225522	1.57 ± 0.48	6.26
GPR133	G protein-coupled receptor 133	283383	A_23_P415706	-1.56 ± 0.99	2.49
LINC01503	lincRNA 1503	100506119	A_19_P00319981	-1.56 ± 0.92	2.72
NT5E	5'-nucleotidase, ecto (CD73)	4907	A_24_P354715	1.56 ± 0.75	3.62
PTPN3	protein tyrosine phosphatase, non-receptor type 3	5774	A_22_P00025093	1.56 ± 0.64	4.46
WBSCR27	Williams Beuren syndrome chromosome region 27	155368	A_23_P381017	1.55 ± 1.41	1.49
FAM20A	family with sequence similarity 20, member A	54757	A_32_P108254	-1.55 ± 1.16	1.96
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	5570	A_23_P145529	-1.54 ± 0.97	2.50
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	1116	A_23_P137665	-1.53 ± 1.55	1.27
CREB5	cAMP responsive element binding protein 5	9586	A_23_P157117	1.52 ± 0.83	3.06

NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	56901	A_23_P9614	-1.51 ± 1.16	1.88
COL5A1	collagen, type V, alpha 1	1289	A_33_P3629678	-1.51 ± 1.09	2.07
CSTA	cystatin A (stefin A)	1475	A_23_P41114	-1.51 ± 0.99	2.36
LAMP5	lysosomal-associated membrane protein family, member 5	24141	A_23_P40295	1.50 ± 2.09	0.82
IGSF10	immunoglobulin superfamily, member 10	285313	A_23_P333683	-1.50 ± 1.23	1.72
NUAK1	NUAK family, SNF1-like kinase, 1	9891	A_23_P348257	-1.50 ± 1.16	1.87
KIF26B	kinesin family member 26B	55083	A_33_P3382565	-1.50 ± 1.07	2.12
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	5270	A_23_P50919	-1.49 ± 1.31	1.56
LIPG	lipase, endothelial	9388	A_24_P125469	-1.49 ± 1.03	2.18
CLIC6	chloride intracellular channel 6	54102	A_23_P385067	1.49 ± 1.00	2.31
PCOLCE2	procollagen C-endopeptidase enhancer 2	26577	A_23_P57709	1.48 ± 1.43	1.35
KRT83	keratin 83, type II	3889	A_33_P3273552	-1.48 ± 1.30	1.55
MGP	matrix Gla protein	4256	A_33_P3361636	-1.48 ± 1.06	2.08
CCDC80	coiled-coil domain containing 80	151887	A_23_P58082	-1.48 ± 0.85	2.86
SLC37A2	solute carrier family 37 (glucose-6-phosphate transporter), member 2	219855	A_33_P3474319	1.48 ± 0.73	3.49
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	2354	A_23_P429998	1.47 ± 1.43	1.36
TPD52L1	tumor protein D52-like 1	7164	A_23_P31143	-1.47 ± 1.16	1.82
GPM6B	glycoprotein M6B	2824	A_23_P378416	1.47 ± 1.14	1.86
DHRS3	dehydrogenase/reductase (SDR family) member 3	9249	A_23_P33759	-1.47 ± 0.99	2.30
FAM64A	family with sequence similarity 64, member A	54478	A_33_P3276918	1.47 ± 0.88	2.68
SUSD3	sushi domain containing 3	203328	A_23_P401076	1.47 ± 0.88	2.67
CDKN2A-AS1	CDKN2A antisense RNA 1 (head to head)		A_23_P307502	-1.47 ± 0.78	3.18
KRT18P55	keratin 18 pseudogene 55	284085	A_23_P373708	-1.46 ± 2.06	0.80
PRSS36	protease, serine, 36	146547	A_24_P412734	1.46 ± 1.89	0.91
CACNG7	calcium channel, voltage-dependent, gamma subunit 7	59284	A_24_P365349	-1.46 ± 1.81	0.96
ITGA11	integrin, alpha 11	22801	A_23_P206022	-1.46 ± 1.60	1.14
FBLN1	fibulin 1	2192	A_23_P211631	-1.46 ± 1.14	1.84

CDC25C	cell division cycle 25C	995	A_23_P70249	1.46 ± 1.12	1.90
ISLR	immunoglobulin superfamily containing leucine-rich repeat	3671	A_23_P3312	-1.46 ± 1.02	2.18
KIF20A	kinesin family member 20A	10112	A_23_P256956	1.46 ± 0.86	2.75
MAOB	monoamine oxidase B	4129	A_23_P85015	1.46 ± 0.81	2.97
MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	4314	A_23_P161698	1.45 ± 1.80	0.96
COL3A1	collagen, type III, alpha 1	1281	A_24_P935491	-1.45 ± 1.26	1.60
EYA2	EYA transcriptional coactivator and phosphatase 2	2139	A_23_P319859	1.45 ± 1.23	1.63
CPE	carboxypeptidase E	1363	A_23_P259442	-1.45 ± 1.18	1.75
GACAT2	gastric cancer associated transcript 2 (non-protein coding)	100287082	A_21_P0014365	1.45 ± 0.84	2.82
DSP	desmoplakin	1832	A_32_P157945	-1.44 ± 1.86	0.90
SLIT3	slit homolog 3 (Drosophila)	6586	A_23_P58588	-1.44 ± 0.91	2.48
GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)	653689	A_33_P3289045	1.43 ± 1.54	1.18
S100A3	S100 calcium binding protein A3	6274	A_23_P104073	1.43 ± 0.80	2.95
KRTAP19-2	keratin associated protein 19-2	337969	A_33_P3311267	1.42 ± 1.87	0.88
SOX11	SRY (sex determining region Y)-box 11	6664	A_24_P302584	1.42 ± 1.21	1.64
NCAM2	neural cell adhesion molecule 2	4685	A_33_P3239884	-1.42 ± 1.20	1.65
ADM2	adrenomedullin 2	79924	A_33_P3413905	-1.42 ± 1.12	1.84
ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif, 10	81794	A_33_P3223056	-1.42 ± 0.93	2.35
THAP10	THAP domain containing 10	56906	A_23_P106391	1.42 ± 0.89	2.53
ERICH2	glutamate-rich 2		A_32_P197340	-1.41 ± 1.31	1.45
AEBP1	AE binding protein 1	165	A_23_P157299	-1.41 ± 0.90	2.45
TSPO2	translocator protein 2	222642	A_33_P3234222	-1.41 ± 0.87	2.59
RASL12	RAS-like, family 12	51285	A_24_P150580	1.40 ± 1.51	1.17
KCTD16	potassium channel tetramerization domain containing 16	57528	A_24_P409800	-1.40 ± 1.46	1.23
ADRB2	adrenoceptor beta 2, surface	154	A_23_P145024	1.40 ± 1.18	1.66
FOXC2-AS1	FOXC2 antisense RNA 1	103752587	A_22_P00010265	1.40 ± 0.88	2.50

TTTY15	testis-specific transcript, Y-linked 15 (non-protein coding)	64595	A_21_P0006594	-1.39 ± 2.39	0.62
SEL1L2	sel-1 suppressor of lin-12-like 2 (C. elegans)	80343	A_33_P3283430	-1.39 ± 1.59	1.08
KIF15	kinesin family member 15	56992	A_23_P80902	1.39 ± 0.86	2.58
ALDH1L2	aldehyde dehydrogenase 1 family, member L2	160428	A_33_P3282634	-1.39 ± 0.80	2.84
RIMBP3	RIMS binding protein 3	85376	A_23_P154962	1.39 ± 0.57	4.45
CDC20	cell division cycle 20	991	A_23_P149200	1.38 ± 0.86	2.54
CDKN3	cyclin-dependent kinase inhibitor 3	1033	A_23_P48669	1.38 ± 0.81	2.76
FSTL3	follistatin-like 3 (secreted glycoprotein)	10272	A_33_P3318796	-1.38 ± 0.80	2.80
SCARNA20	small Cajal body-specific RNA 20	677681	A_21_P0000350	1.37 ± 1.59	1.05
RHOJ	ras homolog family member J	57381	A_24_P82032	-1.37 ± 1.13	1.70
EDN1	endothelin 1	1906	A_23_P214821	-1.37 ± 1.09	1.80
RBP1	retinol binding protein 1, cellular	5947	A_23_P257649	-1.37 ± 1.07	1.85
NXPH4	neurexophilin 4	11247	A_33_P3363245	-1.37 ± 0.97	2.13
DEPDC1B	DEP domain containing 1B	55789	A_23_P361419	1.37 ± 0.94	2.21
DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)		A_22_P00015351	1.37 ± 0.87	2.49
ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	397	A_23_P151075	1.37 ± 0.86	2.51
RIBC2	RIB43A domain with coiled-coils 2	26150	A_23_P166526	1.35 ± 1.22	1.51
ELOVL2	ELOVL fatty acid elongase 2	54898	A_33_P3231739	1.35 ± 0.81	2.69
CEND1	cell cycle exit and neuronal differentiation 1	51286	A_33_P3323945	1.35 ± 0.81	2.66
ULBP1	UL16 binding protein 1	80329	A_33_P3422802	-1.34 ± 1.48	1.14
KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	3738	A_33_P3415032	1.34 ± 1.02	1.92
CENPA	centromere protein A	1058	A_24_P413884	1.34 ± 1.00	1.97
GPR56	G protein-coupled receptor 56	9289	A_23_P206280	1.34 ± 0.85	2.47
AMPH	amphiphysin	273	A_23_P31273	1.34 ± 0.76	2.88
OGN	osteoglycin	4969	A_23_P82990	-1.33 ± 1.29	1.36
MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	4316	A_23_P52761	1.32 ± 1.92	0.77
MFAP5	microfibrillar associated protein 5	8076	A_33_P3708413	-1.32 ± 1.69	0.92
CXCL8	chemokine (C-X-C motif) ligand 8	3576	A_32_P87013	1.32 ± 1.28	1.36

KCNE3	potassium channel, voltage gated subfamily E regulatory beta subunit 3	10008	A_23_P24948	-1.32 ± 0.77	2.78
GPR128	G protein-coupled receptor 128	84873	A_23_P40919	1.31 ± 1.88	0.78
SCN4B	sodium channel, voltage gated, type IV beta subunit	6330	A_23_P303833	1.31 ± 1.44	1.14
GRB14	growth factor receptor-bound protein 14	2888	A_23_P154526	1.31 ± 1.18	1.51
TBX2-AS1	TBX2 antisense RNA 1	103689912	A_24_P896205	1.31 ± 1.05	1.78
LOC101928143	uncharacterized LOC101928143		A_21_P0008460	1.31 ± 0.96	2.01
SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	10371	A_24_P192301	1.31 ± 0.94	2.08
STRIP2	striatin interacting protein 2	57464	A_32_P213831	1.31 ± 0.74	2.91
C16orf46	chromosome 16 open reading frame 46	123775	A_22_P00002490	-1.30 ± 1.40	1.17
TMEM35	transmembrane protein 35	59353	A_23_P45324	1.30 ± 1.34	1.24
RGS17	regulator of G-protein signaling 17	26575	A_23_P156861	1.30 ± 0.99	1.92
PALMD	palmdelphin	54873	A_23_P23669	1.30 ± 0.81	2.55
NR3C2	nuclear receptor subfamily 3, group C, member 2	4306	A_23_P392470	1.30 ± 0.74	2.87
RPS4Y2	ribosomal protein S4, Y-linked 2	140032	A_23_P324384	-1.29 ± 4.12	0.28
HOPX	HOP homeobox	84525	A_23_P254507	1.29 ± 1.50	1.05
WWC2-AS2	WWC2 antisense RNA 2	152641	A_24_P354496	1.29 ± 0.91	2.15
WDFY4	WDFY family member 4	57705	A_32_P30905	1.29 ± 0.89	2.20
HBD	hemoglobin, delta	3045	A_24_P75190	-1.28 ± 1.57	0.98
MFAP4	microfibrillar-associated protein 4	4239	A_23_P164057	-1.28 ± 1.13	1.55
THBS2	thrombospondin 2	7058	A_33_P3227375	-1.28 ± 1.10	1.61
EDIL3	EGF-like repeats and discoidin I-like domains 3	10085	A_23_P401606	-1.28 ± 1.06	1.70
ACTA2	actin, alpha 2, smooth muscle, aorta	59	A_23_P150053	-1.28 ± 1.02	1.79
LMCD1	LIM and cysteine-rich domains 1	29995	A_23_P6771	-1.28 ± 0.59	3.84
LRRC15	leucine rich repeat containing 15	131578	A_24_P827037	-1.27 ± 1.49	1.04
NALCN	sodium leak channel, non selective	259232	A_33_P3230166	-1.27 ± 1.03	1.74
MXRA5	matrix-remodelling associated 5	25878	A_23_P258136	-1.26 ± 1.61	0.93
TGFBR3	transforming growth factor, beta receptor III	7049	A_23_P200780	1.26 ± 1.19	1.41
CCDC144A	coiled-coil domain containing 144A		A_33_P3390580	-1.26 ± 1.13	1.52

BGN	biglycan	633	A_23_P34126	-1.26 ± 0.98	1.84
CCPG1	cell cycle progression 1	9236	A_23_P346006	-1.26 ± 0.85	2.28
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	23327	A_24_P108311	1.26 ± 0.71	2.93
NEK2	NIMA-related kinase 2	4751	A_23_P35219	1.26 ± 0.71	2.92
TUBBP5	tubulin, beta pseudogene 5		A_33_P3409518	1.25 ± 1.45	1.05
TRPA1	transient receptor potential cation channel, subfamily A, member 1	8989	A_24_P235338	1.25 ± 1.11	1.54
RAB26	RAB26, member RAS oncogene family	25837	A_33_P3209229	1.25 ± 1.02	1.75
C7orf69	chromosome 7 open reading frame 69		A_23_P168368	-1.25 ± 0.99	1.82
TMSB15A	thymosin beta 15a	11013	A_23_P137173	1.25 ± 0.89	2.12
TOP2A	topoisomerase (DNA) II alpha 170kDa	7153	A_23_P118834	1.25 ± 0.89	2.10
MMP23B	matrix metallopeptidase 23B	8510	A_23_P74088	-1.25 ± 0.86	2.22
PRR11	proline rich 11	55771	A_33_P3403075	1.25 ± 0.74	2.75
CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	1551	A_23_P358917	-1.24 ± 1.46	1.04
C4B	complement component 4B (Chido blood group)	721	A_23_P42282	-1.24 ± 1.25	1.30
AREG	amphiregulin	374	A_23_P259071	1.24 ± 1.17	1.42
DNER	delta/notch-like EGF repeat containing	92737	A_23_P362148	1.24 ± 0.99	1.80
PHLDA1	pleckstrin homology-like domain, family A, member 1	22822	A_24_P915692	1.24 ± 0.87	2.17
HES4	hes family bHLH transcription factor 4	57801	A_33_P3342628	-1.24 ± 0.76	2.61
SVIL	supervillin	6840	A_23_P35349	1.24 ± 0.75	2.62
GTSE1	G-2 and S-phase expressed 1	51512	A_23_P57588	1.24 ± 0.72	2.81
STXBP5-AS1	STXBP5 antisense RNA 1		A_19_P00322407	1.24 ± 0.58	3.71
RPS4Y1	ribosomal protein S4, Y-linked 1	6192	A_23_P259314	-1.23 ± 4.16	0.26
PTGDS	prostaglandin D2 synthase 21kDa (brain)	5730	A_33_P3298159	-1.23 ± 1.52	0.97
ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	3400	A_33_P3229370	-1.23 ± 1.52	0.96
C11orf96	chromosome 11 open reading frame 96	387763	A_32_P74409	-1.23 ± 1.16	1.43
MDFI	MyoD family inhibitor	4188	A_33_P3246418	-1.23 ± 1.12	1.48
CCND2-AS1	CCND2 antisense RNA 1	103752584	A_22_P00006494	-1.23 ± 0.95	1.89

SCARA3	scavenger receptor class A, member 3	51435	A_23_P215900	1.23 ± 0.90	2.02
HRK	harakiri, BCL2 interacting protein	8739	A_23_P25194	-1.22 ± 1.47	1.00
SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	6839	A_23_P422193	1.22 ± 1.02	1.68
MSC	musculin	9242	A_23_P256948	-1.22 ± 0.94	1.87
PTTG3P	pituitary tumor-transforming 3, pseudogene	26255	A_23_P60016	1.22 ± 0.92	1.94
DUSP10	dual specificity phosphatase 10	11221	A_24_P182494	1.22 ± 0.87	2.10
BTBD11	BTB (POZ) domain containing 11	121551	A_23_P419714	1.22 ± 0.72	2.73
CHN1	chimerin 1	1123	A_33_P3325723	1.22 ± 0.65	3.15
LRRC17	leucine rich repeat containing 17	10234	A_23_P253958	-1.21 ± 1.33	1.14
THBD	thrombomodulin	7056	A_23_P91390	1.21 ± 1.15	1.41
MYBL1	v-myb avian myeloblastosis viral oncogene homolog-like 1	4603	A_23_P43157	1.21 ± 1.00	1.70
SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	9056	A_23_P99642	-1.21 ± 0.88	2.06
FN1	fibronectin 1	2335	A_24_P334130	-1.21 ± 0.82	2.27
FAM46C	family with sequence similarity 46, member C	54855	A_33_P3314176	1.21 ± 0.77	2.45
PDE4B	phosphodiesterase 4B, cAMP-specific	5142	A_23_P74278	1.20 ± 1.19	1.32
SLC22A15	solute carrier family 22, member 15	55356	A_23_P388900	-1.20 ± 0.87	2.04
HRCT1	histidine rich carboxyl terminus 1	646962	A_23_P94434	1.20 ± 0.73	2.61
IL12A	interleukin 12A	3592	A_23_P91943	1.20 ± 0.61	3.31
ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	81849	A_23_P33093	-1.19 ± 1.37	1.06
CDH2	cadherin 2, type 1, N-cadherin (neuronal)	1000	A_33_P3214159	-1.19 ± 1.09	1.47
FAM65B	family with sequence similarity 65, member B	9750	A_24_P941359	1.19 ± 0.90	1.92
FOS	FBJ murine osteosarcoma viral oncogene homolog	2353	A_23_P106194	1.18 ± 1.87	0.69
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	2214	A_23_P200728	1.18 ± 1.77	0.74
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	3357	A_23_P16953	-1.18 ± 1.37	1.06
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	1437	A_23_P133408	1.18 ± 1.18	1.29

RSPO3	R-spondin 3	84870	A_24_P106542	-1.18 ± 1.08	1.49
GPX3	glutathione peroxidase 3 (plasma)	2878	A_23_P133474	1.18 ± 1.06	1.51
KCTD15	potassium channel tetramerization domain containing 15	79047	A_24_P373844	-1.18 ± 0.75	2.47
LINC01144	lincRNA 1144	400752	A_33_P3239317	1.18 ± 0.72	2.65
LAMA2	laminin, alpha 2	3908	A_23_P70719	-1.18 ± 0.65	3.01
LETM2	leucine zipper-EF-hand containing transmembrane protein 2	137994	A_23_P348264	1.18 ± 0.59	3.42
IGFBP3	insulin-like growth factor binding protein 3	3486	A_23_P215634	-1.17 ± 1.01	1.61
CAMK1G	calcium/calmodulin-dependent protein kinase IG	57172	A_23_P97402	1.17 ± 0.97	1.70
PSCA	prostate stem cell antigen	8000	A_23_P71379	1.16 ± 1.72	0.75
ECM2	extracellular matrix protein 2, female organ and adipocyte specific	1842	A_23_P303671	-1.16 ± 1.15	1.31
PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	5732	A_23_P151710	1.16 ± 1.05	1.49
SKA3	spindle and kinetochore associated complex subunit 3	221150	A_33_P3216008	1.16 ± 0.98	1.65
KLHDC9	kelch domain containing 9	126823	A_23_P86100	1.16 ± 0.95	1.71
FAR2	fatty acyl CoA reductase 2	55711	A_23_P150903	1.16 ± 0.87	1.96
C5orf34	chromosome 5 open reading frame 34	375444	A_23_P403081	1.16 ± 0.85	2.04
CNTFR-AS1	CNTFR antisense RNA 1		A_22_P00005289	-1.16 ± 0.85	2.01
LOC81691	exonuclease NEF-sp	81691	A_23_P49459	1.16 ± 0.80	2.20
CENPH	centromere protein H	64946	A_23_P110802	1.16 ± 0.75	2.41
MPHOSPH9	M-phase phosphoprotein 9	10198	A_24_P398500	1.16 ± 0.74	2.44
DGUOK-AS1	DGUOK antisense RNA 1		A_22_P00002126	1.16 ± 0.60	3.30
CXCL3	chemokine (C-X-C motif) ligand 3	2921	A_24_P183150	1.15 ± 1.62	0.81
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	5176	A_23_P100660	-1.15 ± 1.31	1.08
CLDN23	claudin 23	137075	A_23_P134854	1.15 ± 1.22	1.19
PRRX2	paired related homeobox 2	51450	A_23_P83298	1.15 ± 1.08	1.42
ERCC6L	excision repair cross-complementation group 6-like	54821	A_23_P96325	1.15 ± 0.96	1.68
RAB33A	RAB33A, member RAS oncogene family	9363	A_23_P147025	-1.15 ± 0.78	2.25

BUB1	BUB1 mitotic checkpoint serine/threonine kinase	699	A_23_P124417	1.15 ± 0.63	3.02
OR4F6	olfactory receptor, family 4, subfamily F, member 6	390648	A_33_P3344454	-1.15 ± 0.57	3.44
PROS1	protein S (alpha)	5627	A_23_P73114	-1.14 ± 1.18	1.24
RSPO4	R-spondin 4	343637	A_33_P3251552	-1.14 ± 1.14	1.30
KCNG1	potassium channel, voltage gated modifier subfamily G, member 1	3755	A_22_P00005343	-1.14 ± 1.06	1.43
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	2212	A_23_P85716	1.14 ± 1.00	1.56
LINC00968	lincRNA 968	100507632	A_21_P0000731	-1.14 ± 0.91	1.79
ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif, 12	81792	A_23_P44648	-1.14 ± 0.90	1.82
ZMAT4	zinc finger, matrin-type 4	79698	A_32_P164593	-1.14 ± 0.89	1.83
DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	56521	A_33_P3225066	-1.14 ± 0.87	1.91
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3673	A_32_P178800	1.14 ± 0.83	2.05
GINS2	GINS complex subunit 2 (Psf2 homolog)	51659	A_23_P118246	1.14 ± 0.77	2.28
LOC100128288	uncharacterized LOC100128288		A_24_P256415	-1.14 ± 0.77	2.27
CHD7	chromodomain helicase DNA binding protein 7	55636	A_24_P289383	-1.14 ± 0.73	2.46
DMKN	dermokine	93099	A_23_P320261	-1.13 ± 1.33	1.04
CEMIP	cell migration inducing protein, hyaluronan binding	57214	A_23_P324754	-1.13 ± 0.99	1.58
AURKA	aurora kinase A	6790	A_23_P131866	1.13 ± 0.90	1.81
PSMC3IP	PSMC3 interacting protein	29893	A_24_P287941	1.13 ± 0.90	1.81
NOV	nephroblastoma overexpressed	4856	A_23_P82929	1.13 ± 0.90	1.80
ZNF571	zinc finger protein 571	51276	A_23_P108342	1.13 ± 0.89	1.83
DPF1	D4, zinc and double PHD fingers family 1	8193	A_33_P3317277	1.13 ± 0.81	2.09
TTK	TTK protein kinase	7272	A_23_P259586	1.13 ± 0.77	2.22
PITX1	paired-like homeodomain 1	5307	A_33_P3240328	1.12 ± 1.95	0.61
NOX4	NADPH oxidase 4	50507	A_23_P47148	-1.12 ± 1.28	1.08
PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	5575	A_33_P3360675	1.12 ± 1.19	1.20
ACHE	acetylcholinesterase (Yt blood group)	43	A_24_P60845	-1.12 ± 1.15	1.25
APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	9582	A_24_P66027	1.12 ± 0.96	1.60

SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	6536	A_33_P3402615	-1.12 ± 0.91	1.74
SPC24	SPC24, NDC80 kinetochore complex component	147841	A_24_P314571	1.12 ± 0.86	1.90
RDH10	retinol dehydrogenase 10 (all-trans)	157506	A_32_P25050	-1.12 ± 0.86	1.89
SGOL1	shugoshin-like 1 (S. pombe)	151648	A_24_P225970	1.12 ± 0.85	1.90
CACNG8	calcium channel, voltage-dependent, gamma subunit 8	59283	A_23_P420218	-1.12 ± 0.83	2.01
SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	56606	A_23_P213014	-1.12 ± 0.77	2.21
GALNT5	polypeptide N-acetylgalactosaminyltransferase 5	11227	A_24_P408736	1.12 ± 0.75	2.28
CRLF1	cytokine receptor-like factor 1	9244	A_33_P3252286	-1.11 ± 1.15	1.24
TIMP3	TIMP metallopeptidase inhibitor 3	7078	A_23_P399078	-1.11 ± 1.08	1.35
CLDN4	claudin 4	1364	A_33_P3285545	1.11 ± 1.05	1.41
LOC101928812	uncharacterized LOC101928812		A_21_P0007435	1.11 ± 0.99	1.55
TSLP	thymic stromal lymphopoietin	85480	A_33_P3221783	1.11 ± 0.88	1.80
LINC00856	lincRNA 856	100132987	A_33_P6806243	1.11 ± 0.82	2.00
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	50515	A_23_P139919	1.11 ± 0.81	2.04
AXIN2	axin 2	8313	A_23_P148015	-1.11 ± 0.73	2.37
TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	7133	A_24_P54174	1.11 ± 0.71	2.48
HMGA1	high mobility group AT-hook 1	3159	A_23_P42331	1.11 ± 0.53	3.66
MAPK13	mitogen-activated protein kinase 13	5603	A_24_P406132	1.11 ± 0.53	3.65
AIM1	absent in melanoma 1	202	A_23_P70785	1.10 ± 0.95	1.60
VEGFA	vascular endothelial growth factor A	7422	A_23_P70398	-1.10 ± 0.81	2.00
ERV3-1	endogenous retrovirus group 3, member 1	2086	A_33_P3228355	1.10 ± 0.70	2.46
MYH10	myosin, heavy chain 10, non-muscle	4628	A_33_P3235004	-1.10 ± 0.60	3.02
ELN	elastin	2006	A_23_P215454	-1.09 ± 1.46	0.86
LOC400958	uncharacterized LOC400958	400958	A_19_P00800206	-1.09 ± 1.33	0.98
HOXC-AS2	HOXC cluster antisense RNA 2	100874364	A_22_P00015030	-1.09 ± 0.91	1.70
SPC25	SPC25, NDC80 kinetochore complex component	57405	A_23_P51085	1.09 ± 0.89	1.74
SCARNA5	small Cajal body-specific RNA 5	677775	A_33_P3363082	-1.09 ± 0.77	2.13

TMEM59L	transmembrane protein 59-like	25789	A_33_P3302245	-1.09 ± 0.76	2.18
ZNF669	zinc finger protein 669	79862	A_33_P3339687	1.09 ± 0.72	2.33
UNC5B	unc-5 homolog B (C. elegans)	219699	A_23_P52336	-1.09 ± 0.70	2.42
PTTG1	pituitary tumor-transforming 1	9232	A_23_P7636	1.09 ± 0.70	2.40
IRS2	insulin receptor substrate 2	8660	A_24_P154037	-1.09 ± 0.60	3.03
C10orf120	chromosome 10 open reading frame 120	399814	A_33_P3287477	1.09 ± 0.57	3.25
GSTT2	glutathione S-transferase theta 2	2953	A_23_P109427	1.08 ± 1.34	0.96
FOXS1	forkhead box S1	2307	A_33_P3283833	-1.08 ± 1.32	0.98
FSCN3	fascin actin-bundling protein 3, testicular	29999	A_23_P93898	-1.08 ± 1.06	1.33
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	59269	A_32_P59302	-1.08 ± 0.90	1.67
CIT	citron rho-interacting serine/threonine kinase	11113	A_23_P420551	1.08 ± 0.85	1.82
BLM	Bloom syndrome, RecQ helicase-like	641	A_23_P88630	1.08 ± 0.84	1.88
SFXN2	sideroflexin 2	118980	A_24_P175612	1.08 ± 0.84	1.88
SOX9	SRY (sex determining region Y)-box 9	6662	A_23_P26847	1.08 ± 0.84	1.88
SHCBP1	SHC SH2-domain binding protein 1	79801	A_32_P96719	1.08 ± 0.79	2.02
IQGAP3	IQ motif containing GTPase activating protein 3	128239	A_33_P3321293	1.08 ± 0.78	2.07
SNORD12	small nucleolar RNA, C/D box 12	692057	A_21_P0000365	-1.08 ± 0.74	2.20
GXYLT1	glucoside xylosyltransferase 1	283464	A_23_P336796	1.08 ± 0.73	2.28
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	4312	A_23_P1691	1.07 ± 2.18	0.49
SLITRK6	SLIT and NTRK-like family, member 6	84189	A_23_P65307	1.07 ± 1.82	0.63
NEURL1	neuralized E3 ubiquitin protein ligase 1	9148	A_33_P3293524	1.07 ± 1.48	0.83
GREM2	gremlin 2, DAN family BMP antagonist	64388	A_24_P40626	1.07 ± 1.32	0.97
PTPRB	protein tyrosine phosphatase, receptor type, B	5787	A_23_P53390	-1.07 ± 1.30	0.99
SLC4A3	solute carrier family 4 (anion exchanger), member 3	6508	A_23_P39647	-1.07 ± 0.92	1.62
ASF1B	anti-silencing function 1B histone chaperone	55723	A_23_P119254	1.07 ± 0.87	1.75
METTL7B	methyltransferase like 7B	196410	A_24_P64653	1.07 ± 0.85	1.80
TP53INP2	tumor protein p53 inducible nuclear protein 2	58476	A_24_P357465	1.07 ± 0.80	1.98
SYNPO2L	synaptopodin 2-like	79933	A_23_P355517	-1.06 ± 1.76	0.64
TMEM130	transmembrane protein 130	222865	A_23_P349966	-1.06 ± 1.29	0.99

KCNMB4	potassium channel subfamily M regulatory beta subunit 4	27345	A_23_P64792	-1.06 ± 1.07	1.28
ZSWIM5	zinc finger, SWIM-type containing 5	57643	A_23_P383118	1.06 ± 0.96	1.51
PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	8497	A_23_P420692	-1.06 ± 0.93	1.57
FUCA1	fucosidase, alpha-L- 1, tissue	2517	A_23_P11543	1.06 ± 0.92	1.58
PITX2	paired-like homeodomain 2	5308	A_23_P167367	1.06 ± 0.88	1.71
TGFB3	transforming growth factor, beta 3	7043	A_23_P88404	-1.06 ± 0.88	1.69
GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon	2564	A_23_P159775	-1.06 ± 0.82	1.87
NRGN	neurogranin (protein kinase C substrate, RC3)	4900	A_23_P116264	1.06 ± 0.75	2.14
ZDHHC23	zinc finger, DHHC-type containing 23	254887	A_23_P350689	1.06 ± 0.72	2.26
KIAA0101	KIAA0101	9768	A_23_P117852	1.06 ± 0.68	2.45
PCSK5	proprotein convertase subtilisin/kexin type 5	5125	A_23_P257003	-1.06 ± 0.63	2.74
CLEC3B	C-type lectin domain family 3, member B	7123	A_23_P69497	1.05 ± 1.40	0.87
SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	10924	A_23_P72117	-1.05 ± 1.05	1.30
OR10G2	olfactory receptor, family 10, subfamily G, member 2	26534	A_33_P3225507	-1.05 ± 1.01	1.39
DCLK1	doublecortin-like kinase 1	9201	A_23_P369994	-1.05 ± 1.00	1.39
SLC38A5	solute carrier family 38, member 5	92745	A_23_P84929	-1.05 ± 0.98	1.43
FXYD1	FXYD domain containing ion transport regulator 1		A_33_P3228435	-1.05 ± 0.98	1.43
PLK1	polo-like kinase 1	5347	A_23_P118174	1.05 ± 0.92	1.59
CCNT2	cyclin T2	905	A_24_P174341	1.05 ± 0.87	1.71
PITPNM2	phosphatidylinositol transfer protein, membrane-associated 2	57605	A_23_P401361	1.05 ± 0.82	1.85
CDCA3	cell division cycle associated 3	83461	A_24_P218979	1.05 ± 0.81	1.88
FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	84750	A_33_P3748714	1.05 ± 0.78	1.98
RGS20	regulator of G-protein signaling 20	8601	A_23_P73097	1.05 ± 0.75	2.11
PALM	paralemmin	5064	A_33_P3384287	-1.05 ± 0.72	2.22
MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	84057	A_23_P133123	1.05 ± 0.67	2.50
LOC101929484	uncharacterized LOC101929484	101929484	A_21_P0004807	-1.04 ± 1.07	1.26

CCDC74A	coiled-coil domain containing 74A	90557	A_33_P3303212	-1.04 ± 1.01	1.37
ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	10351	A_33_P3342305	-1.04 ± 0.97	1.44
CYB5RL	cytochrome b5 reductase-like	606495	A_33_P3353263	1.04 ± 0.88	1.65
TLR2	toll-like receptor 2	7097	A_23_P92499	1.04 ± 0.88	1.63
PLCB4	phospholipase C, beta 4	5332	A_33_P3353502	1.04 ± 0.86	1.70
ZNF365	zinc finger protein 365	22891	A_24_P226970	-1.04 ± 0.86	1.69
NCAPG	non-SMC condensin I complex, subunit G	64151	A_33_P3230254	1.04 ± 0.82	1.83
NEURL1B	neuralized E3 ubiquitin protein ligase 1B	54492	A_32_P198731	1.04 ± 0.73	2.15
PTTG2	pituitary tumor-transforming 2	10744	A_23_P18579	1.04 ± 0.72	2.19
PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	25894	A_23_P345460	1.04 ± 0.64	2.61
DDO	D-aspartate oxidase	8528	A_23_P30603	1.04 ± 0.57	3.08
RHOBTB1	Rho-related BTB domain containing 1	9886	A_33_P3348288	-1.04 ± 0.52	3.40
APOE	apolipoprotein E	348	A_33_P3223592	-1.03 ± 1.60	0.71
TRIM55	tripartite motif containing 55	84675	A_23_P123402	1.03 ± 1.46	0.81
BMP5	bone morphogenetic protein 5	653	A_23_P19723	1.03 ± 1.45	0.81
PBK	PDZ binding kinase	55872	A_32_P62997	1.03 ± 1.07	1.24
GAA	glucosidase, alpha; acid	2548	A_23_P153026	-1.03 ± 1.06	1.26
FBP1	fructose-1,6-bisphosphatase 1	2203	A_23_P257111	1.03 ± 1.06	1.26
HIST1H1A	histone cluster 1, H1a	3024	A_23_P70448	1.03 ± 0.99	1.37
RNF112	ring finger protein 112	7732	A_23_P107116	1.03 ± 0.98	1.40
AKR1C1	aldo-keto reductase family 1, member C1	1645	A_23_P257971	1.03 ± 0.92	1.53
VLDLR-AS1	VLDLR antisense RNA 1	401491	A_19_P00315804	-1.03 ± 0.91	1.55
ERO1LB	ERO1-like beta (S. cerevisiae)	56605	A_33_P3350703	-1.03 ± 0.89	1.60
USP18	ubiquitin specific peptidase 18	11274	A_23_P132159	1.03 ± 0.89	1.58
PGM5P4-AS1	PGM5P4 antisense RNA 1	101929127	A_21_P0012084	1.03 ± 0.87	1.66
BIRC5	baculoviral IAP repeat containing 5	332	A_23_P118815	1.03 ± 0.85	1.71
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	A_23_P163481	1.03 ± 0.80	1.88
MPP1	membrane protein, palmitoylated 1, 55kDa	4354	A_23_P171296	1.03 ± 0.64	2.55

PKNOX2	PBX/knotted 1 homeobox 2	63876	A_23_P75529	-1.02 ± 1.15	1.09
DOK6	docking protein 6	220164	A_32_P160561	-1.02 ± 1.03	1.30
LOC101928076	uncharacterized LOC101928076		A_32_P4626	-1.02 ± 1.02	1.29
PAQR5	progestin and adipoQ receptor family member V	54852	A_33_P3368750	1.02 ± 0.98	1.38
LINC00578	lincRNA 578		A_21_P0014129	-1.02 ± 0.94	1.46
CKAP2L	cytoskeleton associated protein 2-like	150468	A_23_P388812	1.02 ± 0.89	1.57
QRICH2	glutamine rich 2	84074	A_23_P141142	1.02 ± 0.89	1.57
MYO1D	myosin ID	4642	A_23_P389102	-1.02 ± 0.87	1.64
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	84803	A_23_P69810	1.02 ± 0.84	1.70
FXYD6	FXYD domain containing ion transport regulator 6	53826	A_23_P150394	-1.02 ± 0.82	1.77
RAD51AP1	RAD51 associated protein 1	10635	A_23_P99292	1.02 ± 0.77	1.95
CCNA2	cyclin A2	890	A_23_P58321	1.02 ± 0.76	1.98
LOC100130417	uncharacterized LOC100130417		A_19_P00320067	-1.02 ± 0.74	2.03
CCNB1	cyclin B1	891	A_23_P122197	1.02 ± 0.73	2.11
TPX2	TPX2, microtubule-associated	22974	A_23_P68610	1.02 ± 0.71	2.17
EML1	echinoderm microtubule associated protein like 1	2009	A_23_P205746	1.02 ± 0.69	2.29
LTBP1	latent transforming growth factor beta binding protein 1	4052	A_23_P43810	1.02 ± 0.69	2.26
VLDLR	very low density lipoprotein receptor	7436	A_23_P43476	-1.02 ± 0.53	3.27
PI16	peptidase inhibitor 16	221476	A_33_P3215640	-1.01 ± 1.94	0.53
ICAM1	intercellular adhesion molecule 1	3383	A_23_P153320	-1.01 ± 1.10	1.14
SAMD5	sterile alpha motif domain containing 5	389432	A_24_P602871	1.01 ± 1.08	1.19
C10orf107	chromosome 10 open reading frame 107	219621	A_32_P8156	1.01 ± 1.03	1.26
ADCY4	adenylate cyclase 4	196883	A_23_P381261	1.01 ± 1.00	1.30
FAM180A	family with sequence similarity 180, member A	389558	A_32_P204218	1.01 ± 0.98	1.36
ANLN	anillin, actin binding protein	54443	A_23_P356684	1.01 ± 0.97	1.37
LRCOL1	leucine rich colipase-like 1	100507055	A_32_P49867	1.01 ± 0.94	1.43
POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	5427	A_23_P163099	1.01 ± 0.92	1.49
CENPL	centromere protein L	91687	A_23_P126120	1.01 ± 0.92	1.49

MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	58538	A_33_P3404480	1.01 ± 0.88	1.57
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	A_23_P110253	1.01 ± 0.83	1.71
TRIB3	tribbles pseudokinase 3	57761	A_23_P210690	-1.01 ± 0.71	2.15
CORO2B	coronin, actin binding protein, 2B	10391	A_23_P117694	1.01 ± 0.70	2.16
ARHGAP44	Rho GTPase activating protein 44	9912	A_23_P26854	1.01 ± 0.64	2.47
OXTR	oxytocin receptor	5021	A_33_P3413741	-1.00 ± 2.06	0.48
PEG10	paternally expressed 10	23089	A_23_P82503	1.00 ± 0.97	1.35
SNORD116-11	small nucleolar RNA, C/D box 116-11	100033423	A_21_P0000447	1.00 ± 0.78	1.86
DLGAP5	discs, large (Drosophila) homolog-associated protein 5	9787	A_23_P88331	1.00 ± 0.75	1.97
CCNB2	cyclin B2	9133	A_23_P65757	1.00 ± 0.70	2.18
CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1439	A_23_P120899	-1.00 ± 0.68	2.24
LOC221122	uncharacterized LOC221122	221122	A_33_P3347887	1.00 ± 0.49	3.57

Supplementary Table S4. Functional involvement of genes commonly regulated in lung homogenates and fibroblasts after pirfenidone treatment.

Gene name		**Functional involvement**
A_22_P00006233	-	not known
GPR128	G protein-coupled receptor 128	orphan receptor
GREM2	Gremlin-2	regulation of BMP2/4 activity, embryonic morphogenesis, progesterone production in granulosa cells
GSTT2	Glutathione S-transferase theta-2B	glutathione transferase activity, sulfatase activity
AGRG7	Adhesion G-protein coupled receptor G7	orphan receptor
CEMIP	Cell migration-inducing and hyaluronan-binding protein	interaction with hyaluronic acid (HA), hyaluronan catabolism, positive regulator of epithelial-mesenchymal transistion, tumor cell growth, invasion, migration and cancer dissemination
KCNG1	Potassium voltage-gated channel subfamily G member 1	potassium channel subunit, modulates potassium channel activation and deactivation rates of KCNB1
MFAP5	Microfibrillar-associated protein 5	hematopoiesis, regulation of growth factors and cell signaling in cardiovascular system, component of the elastin-associated microfibrils
TEN2	Teneurin-2	neural development, homophilic cell-cell adhesion, cellular signal transducer
SCRG1	Scrapie-responsive protein 1	acts against the prion protein, scrapie
HRK	Activator of apoptosis harakiri	apoptosis

Supplementary Table S5. Genes related to hyaluronic acid metabolism and signaling being regulated in IPF LH after pirfenidone treatment.

GENE SYMBOL	GENE NAME	ENTREZ ID	SPOT ID	mean log2(fold-change) ± the half width of the 95% confidence interval	-log10(P-value)
HAS1	hyaluronan synthase 1	3036	A_33_P3295203	-1.42 ± 1.39	1.35
HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	A_23_P70007	-1.33 ± 0.97	2.05
HAPLN4	hyaluronan and proteoglycan link protein 4	404037	A_23_P430842	-0.68 ± 0.59	1.62
HABP2	hyaluronan binding protein 2	3026	A_23_P1173	1.07 ± 0.80	1.96

Supplementary Table S6. Genes related to hyaluronic acid metabolism and signaling being regulated in IPF FB after pirfenidone treatment.

GENE SYMBOL	GENE NAME	ENTREZ ID	SPOT ID	mean log2(fold-change) ± the half width of the 95% confidence interval	-log10(P-value)
ITIH3	inter-alpha-trypsin inhibitor heavy chain 3	3699	A_33_P3313145	-1.83 ± 0.78	4.24
CEMIP	cell migration inducing protein, hyaluronan binding	57214	A_23_P324754	-1.13 ± 0.99	1.58
HAPLN4	hyaluronan and proteoglycan link protein 4	404037	A_23_P430842	-0.60 ± 0.50	1.70
CD44	CD44 molecule (Indian blood group)	960	A_33_P3294509	0.69 ± 0.46	2.31
HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	A_23_P70007	0.98 ± 0.82	1.67

Supplementary Table S7. Annotated genes regulated in IPF FB upon pirfenidone treatment *in vitro*.

GENE SYMBOL	GENE NAME	ENTREZ ID	SPOT ID	mean log2(fold-change) ± the half width of the 95% confidence interval	-log10(P-value)
MYCL	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	4610	A_33_P3306068	3.15 ± 1.11	5.21
NGFR	nerve growth factor receptor	4804	A_23_P389897	3.09 ± 0.66	8.78

LOC101927057	uncharacterized LOC101927057		A_21_P0014360	-3.05 ± 1.60	3.18
CYR61	cysteine-rich, angiogenic inducer, 61	3491	A_23_P46429	-3.03 ± 0.77	7.48
C10orf10	chromosome 10 open reading frame 10	11067	A_24_P329795	-2.98 ± 0.57	9.69
EGR2	early growth response 2	1959	A_23_P46936	-2.95 ± 0.93	5.93
RRAD	Ras-related associated with diabetes	6236	A_24_P262127	-2.84 ± 0.62	8.72
PDE4D	phosphodiesterase 4D, cAMP-specific	5144	A_33_P3389653	2.81 ± 0.57	9.29
RNF150	ring finger protein 150	57484	A_24_P350589	2.75 ± 0.90	5.71
KCNE4	potassium channel, voltage gated subfamily E regulatory beta subunit 4	23704	A_33_P3246448	2.66 ± 1.00	4.85
MIR143HG	MIR143 host gene (non-protein coding)		A_19_P00324470	-2.62 ± 0.82	6.03
BMF	Bcl2 modifying factor	90427	A_23_P379649	-2.62 ± 0.70	7.13
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	3357	A_23_P16953	-2.57 ± 1.02	4.55
KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2	3759	A_23_P329261	-2.54 ± 0.75	6.43
MIR503HG	MIR503 host gene (non-protein coding)	84848	A_33_P3402329	-2.49 ± 0.66	7.22
COX8C	cytochrome c oxidase subunit VIIIC	341947	A_33_P3372069	2.44 ± 0.90	4.97
FRMD6-AS2	FRMD6 antisense RNA 2	100874185	A_22_P00013581	2.38 ± 0.61	7.41
HSPA4L	heat shock 70kDa protein 4-like	22824	A_23_P363936	2.37 ± 0.86	5.06
SLC16A14	solute carrier family 16, member 14	151473	A_24_P342829	2.36 ± 1.19	3.36
SLC16A9	solute carrier family 16, member 9	220963	A_23_P115726	2.35 ± 0.68	6.58
EGR3	early growth response 3	1960	A_23_P216225	-2.34 ± 0.83	5.20
KRTAP1-5	keratin associated protein 1-5	83895	A_23_P118842	-2.30 ± 1.53	2.30
ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	245972	A_23_P146146	2.29 ± 0.66	6.55
SLC6A13	solute carrier family 6 (neurotransmitter transporter), member 13	6540	A_21_P0000624	2.24 ± 0.54	7.88
HSPB3	heat shock 27kDa protein 3	8988	A_23_P92730	-2.22 ± 1.37	2.53
CTGF	connective tissue growth factor	1490	A_23_P19663	-2.22 ± 0.92	4.31
CRB1	crumbs family member 1, photoreceptor morphogenesis associated	23418	A_24_P196528	2.22 ± 0.49	8.53
MAT2A	methionine adenosyltransferase II, alpha	4144	A_23_P401568	-2.21 ± 0.49	8.50
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	3815	A_23_P110253	-2.19 ± 1.20	3.00
FMO2	flavin containing monooxygenase 2 (non-functional)	2327	A_33_P3275702	-2.17 ± 1.54	2.10
GAREM	GRB2 associated, regulator of MAPK1	64762	A_23_P66948	2.14 ± 0.68	5.90
PTPN3	protein tyrosine phosphatase, non-receptor type 3	5774	A_22_P00025093	2.12 ± 0.87	4.34

MADCAM1	mucosal vascular addressin cell adhesion molecule 1	8174	A_23_P153616	2.12 ± 0.48	8.39
ACVR1C	activin A receptor, type IC	130399	A_23_P397455	2.11 ± 0.66	6.02
HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	3157	A_24_P63522	-2.08 ± 0.75	5.05
ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	126	A_23_P81158	-2.07 ± 1.55	1.95
FBXL14	F-box and leucine-rich repeat protein 14	144699	A_23_P36724	2.05 ± 0.53	7.38
PDE4B	phosphodiesterase 4B, cAMP-specific	5142	A_23_P74278	2.03 ± 0.60	6.38
CACNB2	calcium channel, voltage-dependent, beta 2 subunit	783	A_33_P3363271	2.01 ± 0.57	6.72
EPS8L1	EPS8-like 1	54869	A_33_P3220698	-2.00 ± 0.76	4.77
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	7130	A_23_P165624	1.96 ± 0.81	4.35
LAMB2P1	laminin, beta 2 pseudogene 1		A_33_P3413815	1.93 ± 0.75	4.68
ARID5A	AT rich interactive domain 5A (MRF1-like)	10865	A_23_P143016	-1.91 ± 0.56	6.48
ATE1-AS1	ATE1 antisense RNA 1 (head to head)	100130887	A_33_P3340752	1.90 ± 1.46	1.87
FABP3	fatty acid binding protein 3, muscle and heart	2170	A_24_P62783	-1.90 ± 1.18	2.53
LINC00968	lincRNA 968	100507632	A_21_P0000731	-1.89 ± 1.23	2.35
CMTM8	CKLF-like MARVEL transmembrane domain containing 8	152189	A_23_P40880	1.88 ± 0.59	6.00
LINC01569	lincRNA 1569	100507501	A_21_P0009120	1.87 ± 0.49	7.20
TUBE1	tubulin, epsilon 1	51175	A_33_P3240538	1.87 ± 0.42	8.34
LOC101927067	uncharacterized LOC101927067	101927067	A_21_P0014218	1.86 ± 0.65	5.31
LINC00473	lincRNA 473	90632	A_32_P8546	1.85 ± 0.99	3.07
EGR1	early growth response 1	1958	A_23_P214080	-1.85 ± 0.87	3.67
MYBL1	v-myb avian myeloblastosis viral oncogene homolog-like 1	4603	A_23_P43157	1.85 ± 0.80	4.04
BMP6	bone morphogenetic protein 6	654	A_23_P19624	1.85 ± 0.77	4.26
LINC00622	lincRNA 622	644242	A_21_P0000663	1.84 ± 0.58	6.00
WWTR1	WW domain containing transcription regulator 1	25937	A_23_P29769	1.84 ± 0.54	6.48
NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	4810	A_32_P126375	1.83 ± 0.57	6.05
SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	8140	A_24_P335620	1.82 ± 0.74	4.42
NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	57532	A_24_P791829	-1.81 ± 0.32	10.56
ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	124	A_24_P291658	-1.80 ± 1.43	1.78
RBM26-AS1	RBM26 antisense RNA 1	100505538	A_33_P6815667	1.80 ± 0.81	3.86

FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2526	A_33_P3286536	-1.80 ± 0.73	4.38
NCOA7	nuclear receptor coactivator 7	135112	A_24_P12435	1.80 ± 0.39	8.78
ZNF433	zinc finger protein 433	163059	A_23_P27649	1.79 ± 0.63	5.24
TSPYL4	TSPY-like 4	23270	A_23_P110882	-1.79 ± 0.49	6.98
SEC1P	secretory blood group 1, pseudogene	653677	A_33_P3548860	1.78 ± 0.84	3.67
C17orf51	chromosome 17 open reading frame 51	339263	A_24_P59607	1.78 ± 0.41	8.28
GOLGA6L6	golgin A6 family-like 6	727832	A_24_P50972	1.77 ± 0.84	3.63
RIMBP3	RIMS binding protein 3	85376	A_23_P154962	1.77 ± 0.78	3.95
C11orf96	chromosome 11 open reading frame 96	387763	A_32_P74409	1.75 ± 0.82	3.66
ARRDC3	arrestin domain containing 3	57561	A_24_P274615	1.74 ± 0.52	6.33
DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	4189	A_23_P258944	1.74 ± 0.37	8.80
FAM227B	family with sequence similarity 227, member B	196951	A_33_P3361758	1.72 ± 0.73	4.19
HMGB2	high mobility group box 2	3148	A_23_P155765	1.72 ± 0.43	7.59
DDIT4L	DNA-damage-inducible transcript 4-like	115265	A_33_P3372099	-1.70 ± 0.50	6.42
HSPA1A	heat shock 70kDa protein 1A	3303	A_23_P111132	-1.70 ± 0.48	6.79
ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein	85450	A_23_P340333	1.69 ± 0.66	4.67
LOC101927571	uncharacterized LOC101927571	101927571	A_22_P00004635	1.68 ± 0.58	5.37
OSBPL6	oxysterol binding protein-like 6	114880	A_23_P108823	1.67 ± 0.34	9.23
FGD4	FYVE, RhoGEF and PH domain containing 4	121512	A_24_P158946	-1.66 ± 0.85	3.30
NEAT1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	283131	A_19_P00321332	-1.66 ± 0.65	4.63
CCR1	chemokine (C-C motif) receptor 1	1230	A_24_P148717	-1.65 ± 0.99	2.65
FRMPD4	FERM and PDZ domain containing 4	9758	A_24_P672240	1.65 ± 0.91	2.99
NIM1K	NIM1 serine/threonine protein kinase	167359	A_23_P254863	1.65 ± 0.74	3.87
TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	51330	A_23_P49338	-1.65 ± 0.65	4.57
CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	10435	A_23_P1602	-1.64 ± 0.39	8.01
PLEKHA6	pleckstrin homology domain containing, family A member 6	22874	A_23_P431268	-1.63 ± 0.76	3.70
USP3-AS1	USP3 antisense RNA 1		A_22_P00007632	1.63 ± 0.66	4.48
FRMD4A	FERM domain containing 4A	55691	A_23_P22352	-1.62 ± 0.98	2.60
HIC1	hypermethylated in cancer 1	3090	A_23_P129856	-1.62 ± 0.64	4.57
LINC01301	lincRNA 1301		A_21_P0005840	1.62 ± 0.63	4.63

HEXIM1	hexamethylene bis-acetamide inducible 1	10614	A_24_P356601	-1.62 ± 0.43	7.09
TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	7292	A_23_P126836	1.61 ± 0.51	5.93
IER2	immediate early response 2	9592	A_32_P36235	-1.61 ± 0.47	6.46
NUPR1L	nuclear protein, transcriptional regulator, 1-like	389493	A_32_P42964	1.61 ± 0.33	9.05
HEY1	hes-related family bHLH transcription factor with YRPW motif 1	23462	A_32_P83845	1.60 ± 0.82	3.27
OSGIN2	oxidative stress induced growth inhibitor family member 2	734	A_23_P82859	1.59 ± 0.80	3.36
SNRNP35	small nuclear ribonucleoprotein 35kDa (U11/U12)	11066	A_23_P159101	-1.59 ± 0.32	9.28
FOSL1	FOS-like antigen 1	8061	A_23_P161624	-1.58 ± 0.99	2.49
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	2982	A_23_P69573	-1.58 ± 0.97	2.58
ADORA2B	adenosine A2b receptor	136	A_23_P55477	1.58 ± 0.69	4.01
MIR4458HG	MIR4458 host gene (non-protein coding)	100505738	A_22_P00010295	-1.58 ± 0.65	4.34
GATAD2B	GATA zinc finger domain containing 2B	57459	A_33_P3323822	-1.58 ± 0.64	4.40
SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	6617	A_22_P00019571	1.58 ± 0.48	6.24
FAM43A	family with sequence similarity 43, member A	131583	A_33_P3410589	-1.57 ± 0.67	4.12
NCK1-AS1	NCK1 antisense RNA 1 (head to head)		A_21_P0014119	1.57 ± 0.59	4.88
LOC101927895	uncharacterized LOC101927895		A_22_P00010200	1.57 ± 0.54	5.34
ASB2	ankyrin repeat and SOCS box containing 2	51676	A_23_P205370	-1.56 ± 0.76	3.49
LOC100289495	uncharacterized LOC100289495		A_21_P0013047	1.56 ± 0.54	5.31
KCNG1	potassium channel, voltage gated modifier subfamily G, member 1	3755	A_22_P00005343	1.55 ± 0.57	5.02
SLC22A18AS	solute carrier family 22 (organic cation transporter), member 18 antisense	5003	A_33_P3316587	1.54 ± 1.15	1.94
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	83716	A_23_P106602	1.54 ± 0.87	2.87
RAB39B	RAB39B, member RAS oncogene family	116442	A_24_P408603	1.54 ± 0.77	3.38
C18orf65	chromosome 18 open reading frame 65		A_33_P3311165	1.54 ± 0.44	6.55
STX19	syntaxin 19	415117	A_33_P3269208	1.53 ± 0.81	3.12
ADAP2	ArfGAP with dual PH domains 2	55803	A_23_P49816	1.53 ± 0.69	3.86
PSAT1	phosphoserine aminotransferase 1	29968	A_23_P259692	1.53 ± 0.60	4.58
KLHL9	kelch-like family member 9	55958	A_23_P83159	-1.53 ± 0.37	7.97
ADCY10P1	adenylate cyclase 10 (soluble) pseudogene 1	221442	A_24_P303420	1.52 ± 0.79	3.20
ZNF441	zinc finger protein 441	126068	A_33_P3397323	1.52 ± 0.45	6.36

MCTP1	multiple C2 domains, transmembrane 1	79772	A_23_P133293	1.51 ± 0.88	2.74
DENND5B	DENN/MADD domain containing 5B	160518	A_24_P541919	1.51 ± 0.57	4.86
C17orf82	chromosome 17 open reading frame 82		A_33_P3417195	-1.51 ± 0.57	4.80
PCDH18	protocadherin 18	54510	A_33_P3250348	-1.50 ± 0.86	2.81
ZCCHC2	zinc finger, CCHC domain containing 2		A_22_P00017844	1.49 ± 0.95	2.42
CARD8-AS1	CARD8 antisense RNA 1	100505812	A_22_P00017991	-1.49 ± 0.62	4.31
ZSCAN20	zinc finger and SCAN domain containing 20	7579	A_23_P23102	-1.49 ± 0.62	4.26
SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	9197	A_33_P3251108	1.49 ± 0.57	4.77
MAP2K6	mitogen-activated protein kinase kinase 6	5608	A_23_P207445	1.49 ± 0.55	4.99
MYBPH	myosin binding protein H	4608	A_23_P148737	-1.48 ± 1.07	2.04
SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	6509	A_24_P191312	1.48 ± 0.65	3.99
LOC100505912	uncharacterized LOC100505912		A_21_P0000697	1.48 ± 0.62	4.27
NEXN	nexilin (F actin binding protein)	91624	A_23_P200001	-1.48 ± 0.39	7.13
ZNF784	zinc finger protein 784	147808	A_33_P3230399	-1.48 ± 0.31	9.09
TMPRSS4	transmembrane protease, serine 4	56649	A_33_P3296846	-1.47 ± 2.04	0.80
FAM169A	family with sequence similarity 169, member A	26049	A_23_P423074	1.47 ± 0.69	3.63
TBC1D31	TBC1 domain family, member 31	93594	A_23_P334218	1.47 ± 0.52	5.22
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	55454	A_23_P149892	1.47 ± 0.41	6.74
PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	285755	A_23_P111361	1.45 ± 0.92	2.47
FAM46C	family with sequence similarity 46, member C	54855	A_33_P3314176	-1.45 ± 0.62	4.14
ZNF33B	zinc finger protein 33B	7582	A_33_P3296871	-1.45 ± 0.36	7.65
KCNK1	potassium channel, two pore domain subfamily K, member 1	3775	A_23_P126075	1.44 ± 0.87	2.63
C3orf52	chromosome 3 open reading frame 52	79669	A_23_P58009	-1.44 ± 0.67	3.71
TRIM47	tripartite motif containing 47	91107	A_33_P3235053	-1.44 ± 0.61	4.19
KLF4	Kruppel-like factor 4 (gut)	9314	A_23_P32233	1.44 ± 0.60	4.33
C4orf46	chromosome 4 open reading frame 46	201725	A_33_P3344243	-1.44 ± 0.36	7.63
GLI1	GLI family zinc finger 1	2735	A_23_P105251	-1.43 ± 1.02	2.07
NOTCH4	notch 4	4855	A_23_P365614	-1.43 ± 0.72	3.37
CCNO	cyclin O	10309	A_23_P92860	1.43 ± 0.68	3.60

TMEM170A	transmembrane protein 170A	124491	A_23_P100517	1.42 ± 0.70	3.40
LOC100507291	uncharacterized LOC100507291	100507291	A_22_P00010168	1.42 ± 0.62	4.02
THBS1	thrombospondin 1	7057	A_24_P142118	-1.42 ± 0.62	4.01
MESP1	mesoderm posterior basic helix-loop-helix transcription factor 1	55897	A_33_P3214466	1.42 ± 0.49	5.40
LOC100507437	uncharacterized LOC100507437		A_21_P0014544	1.42 ± 0.44	6.00
SDSL	serine dehydratase-like	113675	A_33_P3227472	1.42 ± 0.42	6.47
TUBA1A	tubulin, alpha 1a	7846	A_23_P139547	-1.42 ± 0.29	9.14
RTKN2	rhotekin 2	219790	A_24_P13041	-1.41 ± 0.80	2.86
ZNF285	zinc finger protein 285	26974	A_23_P101319	1.41 ± 0.75	3.14
SSR4P1	signal sequence receptor, delta pseudogene 1	728039	A_33_P3676515	1.41 ± 0.74	3.18
VLDLR-AS1	VLDLR antisense RNA 1	401491	A_19_P00315804	1.41 ± 0.68	3.54
ZBED8	zinc finger, BED-type containing 8	63920	A_24_P166311	1.41 ± 0.49	5.38
UHRF1BP1	UHRF1 binding protein 1	54887	A_33_P3313421	1.41 ± 0.40	6.68
ELL2	elongation factor, RNA polymerase II, 2	22936	A_23_P58506	-1.41 ± 0.31	8.63
LRRC32	leucine rich repeat containing 32	2615	A_24_P389916	-1.40 ± 0.98	2.14
CRYGN	crystallin, gamma N	155051	A_33_P3461948	1.40 ± 0.74	3.12
PSMD6-AS2	PSMD6 antisense RNA 2	100507062	A_21_P0000751	1.40 ± 0.69	3.45
MEIG1	meiosis/spermiogenesis associated 1	644890	A_32_P175715	1.40 ± 0.61	4.06
TMEM79	transmembrane protein 79	84283	A_23_P149259	1.40 ± 0.53	4.77
PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	160760	A_23_P306933	1.40 ± 0.51	5.01
LOC100507291	uncharacterized LOC100507291		A_21_P0014120	1.40 ± 0.44	6.05
BANP	BTG3 associated nuclear protein	54971	A_23_P22263	1.40 ± 0.29	9.05
ACKR4	atypical chemokine receptor 4	51554	A_23_P6909	-1.39 ± 1.48	1.19
KLHL30	kelch-like family member 30	377007	A_33_P3243702	-1.39 ± 0.78	2.87
KLLN	killin, p53-regulated DNA replication inhibitor	100144748	A_33_P3267410	1.39 ± 0.75	3.04
DUSP1	dual specificity phosphatase 1	1843	A_23_P110712	1.39 ± 0.74	3.11
HSPA1B	heat shock 70kDa protein 1B	3304	A_33_P3415430	-1.39 ± 0.61	4.01
ASNS	asparagine synthetase (glutamine-hydrolyzing)	440	A_23_P145694	1.39 ± 0.54	4.63
ETNK1	ethanolamine kinase 1	55500	A_33_P3351559	1.39 ± 0.35	7.51
LOC101060091	uncharacterized LOC101060091		A_22_P00014756	1.38 ± 1.03	1.96

TDO2	tryptophan 2,3-dioxygenase	6999	A_23_P80974	1.38 ± 0.92	2.27
UNC5B	unc-5 homolog B (C. elegans)	219699	A_23_P52336	1.38 ± 0.77	2.92
CEBPB-AS1	CEBPB antisense RNA 1		A_33_P3781228	1.38 ± 0.67	3.50
ASH1L-AS1	ASH1L antisense RNA 1		A_24_P272225	-1.38 ± 0.52	4.86
TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	6877	A_23_P52311	1.38 ± 0.50	5.03
SPRY4-IT1	SPRY4 intronic transcript 1	100642175	A_22_P00000104	-1.37 ± 0.99	2.03
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	490	A_33_P3267186	1.37 ± 0.80	2.74
MIAT	myocardial infarction associated transcript (non-protein coding)	440823	A_24_P854492	-1.37 ± 0.74	3.02
GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	284161	A_23_P84666	1.37 ± 0.50	5.02
ANKRD37	ankyrin repeat domain 37	353322	A_24_P237586	1.37 ± 0.46	5.58
PPP1R10	protein phosphatase 1, regulatory subunit 10	5514	A_23_P156667	1.37 ± 0.34	7.59
MEDAG	mesenteric estrogen-dependent adipogenesis	84935	A_23_P99515	1.36 ± 1.45	1.19
ARL6	ADP-ribosylation factor-like 6	84100	A_24_P354337	1.36 ± 0.83	2.60
ARSK	arylsulfatase family, member K	153642	A_33_P3273664	1.36 ± 0.67	3.45
EAF2	ELL associated factor 2	55840	A_23_P252201	1.36 ± 0.67	3.42
PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	5563	A_32_P94160	1.36 ± 0.58	4.16
USP12	ubiquitin specific peptidase 12	219333	A_24_P237613	1.36 ± 0.57	4.30
ETS2	v-ets avian erythroblastosis virus E26 oncogene homolog 2	2114	A_24_P314179	-1.36 ± 0.54	4.48
FICD	FIC domain containing	11153	A_23_P128246	1.36 ± 0.45	5.64
ODC1	ornithine decarboxylase 1	4953	A_23_P165840	1.36 ± 0.34	7.48
ZHX1-C8orf76	ZHX1-C8orf76 readthrough	100533106	A_33_P3373214	1.36 ± 0.33	7.79
LINC01436	lincRNA 1436		A_22_P00019460	1.35 ± 1.12	1.69
RCAN2	regulator of calcineurin 2	10231	A_32_P156851	-1.35 ± 0.83	2.56
SOCS1	suppressor of cytokine signaling 1	8651	A_23_P420196	-1.35 ± 0.53	4.58
ZNF397	zinc finger protein 397	84307	A_23_P304511	1.35 ± 0.42	6.01
GPR180	G protein-coupled receptor 180	160897	A_24_P942481	1.35 ± 0.41	6.17
TIMM10B	translocase of inner mitochondrial membrane 10 homolog B (yeast)	26515	A_33_P3243657	-1.35 ± 0.34	7.53
GADD45A	growth arrest and DNA-damage-inducible, alpha	1647	A_23_P23221	1.34 ± 0.52	4.72
RORA	RAR-related orphan receptor A	6095	A_23_P26124	1.34 ± 0.48	5.09

TATDN3	TatD DNase domain containing 3	128387	A_33_P3249773	1.34 ± 0.43	5.88
ZNF668	zinc finger protein 668	79759	A_33_P3290487	-1.34 ± 0.30	8.59
SNAR-B2	small ILF3/NF90-associated RNA B2		A_21_P0000507	-1.33 ± 1.53	1.06
TUBD1	tubulin, delta 1	51174	A_23_P26895	1.33 ± 0.69	3.24
ARL5B	ADP-ribosylation factor-like 5B	221079	A_24_P943997	1.33 ± 0.63	3.61
TLR6	toll-like receptor 6	10333	A_23_P256561	1.33 ± 0.58	4.02
PRELID2	PRELI domain containing 2	153768	A_24_P346101	-1.33 ± 0.58	4.01
MFHAS1	malignant fibrous histiocytoma amplified sequence 1	9258	A_33_P3256680	1.33 ± 0.54	4.45
LBH	limb bud and heart development	81606	A_23_P120227	-1.33 ± 0.45	5.51
SLC43A2	solute carrier family 43 (amino acid system L transporter), member 2	124935	A_24_P296508	1.33 ± 0.35	7.22
SNAR-F	small ILF3/NF90-associated RNA F		A_21_P0000492	-1.32 ± 1.54	1.03
TPPP	tubulin polymerization promoting protein	11076	A_33_P3371999	1.32 ± 1.28	1.35
ERICH2	glutamate-rich 2		A_32_P197340	1.32 ± 1.18	1.52
BTBD11	BTB (POZ) domain containing 11	121551	A_23_P419714	1.32 ± 0.74	2.93
CABLES1	Cdk5 and Abl enzyme substrate 1	91768	A_23_P422851	1.32 ± 0.64	3.52
C9orf91	chromosome 9 open reading frame 91	203197	A_24_P915196	1.32 ± 0.54	4.39
ZNF677	zinc finger protein 677	342926	A_33_P3231705	-1.32 ± 0.45	5.39
SMIM12	small integral membrane protein 12	113444	A_33_P3325467	-1.32 ± 0.40	6.16
CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	120227	A_23_P202860	1.32 ± 0.37	6.79
OTUD7A	OTU deubiquitinase 7A	161725	A_33_P3262376	1.32 ± 0.37	6.76
SNAR-H	small ILF3/NF90-associated RNA H		A_21_P0000511	-1.31 ± 1.53	1.04
SNAR-G2	small ILF3/NF90-associated RNA G2		A_21_P0000509	-1.31 ± 1.45	1.12
ZSCAN31	zinc finger and SCAN domain containing 31	64288	A_23_P214533	-1.31 ± 1.19	1.49
ZNF341-AS1	ZNF341 antisense RNA 1	101929746	A_22_P00012654	1.31 ± 0.66	3.38
HDAC4	histone deacetylase 4	9759	A_23_P210048	1.31 ± 0.66	3.32
ANKRD11	ankyrin repeat domain 11	29123	A_33_P3280044	1.31 ± 0.50	4.80
FAM49A	family with sequence similarity 49, member A	81553	A_23_P21560	1.31 ± 0.41	5.93
FAM107B	family with sequence similarity 107, member B	83641	A_23_P149975	1.31 ± 0.40	6.20
CCAR1	cell division cycle and apoptosis regulator 1	55749	A_23_P115842	-1.31 ± 0.27	9.15
SNAR-D	small ILF3/NF90-associated RNA D		A_21_P0000508	-1.30 ± 1.55	1.01

BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	701	A_23_P163481	-1.30 ± 1.10	1.63
SOCS7	suppressor of cytokine signaling 7	30837	A_24_P367211	1.30 ± 0.68	3.18
LINC00565	lincRNA 565	100861555	A_22_P00006915	1.30 ± 0.67	3.21
CCIN	calicin	881	A_23_P60227	-1.30 ± 0.54	4.32
TSGA10	testis specific, 10	80705	A_23_P17103	1.30 ± 0.54	4.28
WDR6	WD repeat domain 6	11180	A_33_P3815560	-1.30 ± 0.33	7.52
ATXN3	ataxin 3	4287	A_22_P00001843	-1.30 ± 0.31	8.07
GDF10	growth differentiation factor 10	2662	A_23_P52227	-1.29 ± 1.36	1.20
CTH	cystathionine gamma-lyase	1491	A_23_P126103	1.29 ± 0.66	3.30
FRY	furry homolog (Drosophila)	10129	A_23_P105862	-1.29 ± 0.56	4.05
TYSND1	trypsin domain containing 1	219743	A_33_P3351101	1.29 ± 0.55	4.16
INTS2	integrator complex subunit 2	57508	A_23_P420269	1.29 ± 0.48	4.91
PLK3	polo-like kinase 3	1263	A_23_P51646	-1.29 ± 0.43	5.61
TUBB4B	tubulin, beta 4B class IVb	10383	A_23_P312863	-1.29 ± 0.42	5.77
LRRN4CL	LRRN4 C-terminal like	221091	A_33_P3221129	-1.28 ± 0.99	1.86
TGFBR3	transforming growth factor, beta receptor III	7049	A_23_P200780	1.28 ± 0.95	1.97
LAMTOR5-AS1	LAMTOR5 antisense RNA 1		A_21_P0010545	1.28 ± 0.48	4.89
EAF1	ELL associated factor 1	85403	A_24_P941930	1.28 ± 0.46	5.16
HDAC5	histone deacetylase 5	10014	A_24_P125283	-1.28 ± 0.42	5.65
ILF3-AS1	ILF3 antisense RNA 1 (head to head)	147727	A_33_P3601163	-1.28 ± 0.34	7.05
INMT	indolethylamine N-methyltransferase	11185	A_33_P3347291	-1.27 ± 1.05	1.70
FLJ42351	uncharacterized LOC400999		A_21_P0002674	1.27 ± 1.04	1.70
DKK1	dickkopf WNT signaling pathway inhibitor 1	22943	A_23_P24129	-1.27 ± 0.82	2.38
PRMT3	protein arginine methyltransferase 3	10196	A_23_P9894	1.27 ± 0.64	3.36
C4orf29	chromosome 4 open reading frame 29	80167	A_23_P167358	1.27 ± 0.62	3.47
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	3156	A_23_P30495	-1.27 ± 0.55	4.07
BTG1	B-cell translocation gene 1, anti-proliferative	694	A_22_P00013430	1.27 ± 0.44	5.29
IP6K2	inositol hexakisphosphate kinase 2	51447	A_23_P301138	-1.27 ± 0.41	5.84
RAP2B	RAP2B, member of RAS oncogene family	5912	A_33_P3303121	-1.27 ± 0.40	5.95
HTR2A	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	3356	A_24_P355967	1.26 ± 1.06	1.65

NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	4776	A_33_P3250083	-1.26 ± 0.66	3.15
RSRP1	arginine/serine-rich protein 1	57035	A_23_P34396	1.26 ± 0.38	6.28
HEIH	hepatocellular carcinoma up-regulated EZH2-associated long non-coding RNA	100859930	A_22_P00009905	1.26 ± 0.28	8.56
TMEM100	transmembrane protein 100	55273	A_23_P15450	1.25 ± 0.85	2.21
ZNF391	zinc finger protein 391	346157	A_33_P3220090	1.25 ± 0.80	2.44
TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	8148	A_23_P159305	-1.25 ± 0.71	2.85
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	2650	A_33_P3282489	-1.25 ± 0.61	3.53
WEE1	WEE1 G2 checkpoint kinase	7465	A_33_P3290567	-1.25 ± 0.48	4.75
MBLAC2	metallo-beta-lactamase domain containing 2	153364	A_33_P3415663	1.25 ± 0.42	5.50
SNRNP48	small nuclear ribonucleoprotein 48kDa (U11/U12)	154007	A_33_P3404448	1.25 ± 0.40	5.75
CCDC102B	coiled-coil domain containing 102B	79839	A_23_P44466	-1.24 ± 1.01	1.72
CCDC13-AS1	CCDC13 antisense RNA 1	100874114	A_22_P00008465	-1.24 ± 0.97	1.74
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	3397	A_23_P252306	1.24 ± 0.81	2.35
PNMA6A	paraneoplastic Ma antigen family member 6A	84968	A_33_P3233436	-1.24 ± 0.65	3.15
CENPJ	centromere protein J	55835	A_32_P219116	-1.24 ± 0.47	4.86
PTP4A1	protein tyrosine phosphatase type IVA, member 1	7803	A_23_P81770	1.24 ± 0.43	5.37
ADM	adrenomedullin	133	A_23_P127948	-1.24 ± 0.43	5.31
SRXN1	sulfiredoxin 1	140809	A_23_P320113	1.24 ± 0.40	5.82
MAP3K4	mitogen-activated protein kinase kinase kinase 4	4216	A_33_P3245922	1.24 ± 0.34	6.82
MKX-AS1	MKX antisense RNA 1		A_22_P00012696	-1.23 ± 0.85	2.18
MTX3	metaxin 3	345778	A_33_P3356846	1.23 ± 0.77	2.48
CCDC121	coiled-coil domain containing 121	79635	A_23_P5742	1.23 ± 0.71	2.81
C9orf47	chromosome 9 open reading frame 47	286223	A_33_P3379061	-1.23 ± 0.71	2.78
DUSP5	dual specificity phosphatase 5	1847	A_23_P150018	-1.23 ± 0.62	3.35
DUSP19	dual specificity phosphatase 19	142679	A_23_P90933	1.23 ± 0.54	3.96
ST7-AS1	ST7 antisense RNA 1	93653	A_32_P181297	-1.23 ± 0.31	7.56
SNAR-A3	small ILF3/NF90-associated RNA A3		A_33_P3587376	-1.22 ± 1.48	0.99
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	9507	A_23_P360754	1.22 ± 1.47	0.99

KIAA0226L	KIAA0226-like	80183	A_23_P53763	-1.22 ± 1.22	1.29
SLCO4A1	solute carrier organic anion transporter family, member 4A1	28231	A_23_P5903	1.22 ± 0.73	2.65
KLF10	Kruppel-like factor 10	7071	A_23_P168828	-1.22 ± 0.67	3.02
DDIT3	DNA-damage-inducible transcript 3	1649	A_23_P21134	1.22 ± 0.61	3.36
CEP19	centrosomal protein 19kDa	84984	A_32_P212058	1.22 ± 0.55	3.92
DGKD	diacylglycerol kinase, delta 130kDa	8527	A_23_P210253	1.22 ± 0.54	3.94
FNDC3A	fibronectin type III domain containing 3A	22862	A_23_P25503	1.22 ± 0.53	4.05
RFESD	Rieske (Fe-S) domain containing	317671	A_23_P251647	1.21 ± 0.85	2.13
LOC101928424	uncharacterized LOC101928424	101928424	A_32_P110016	1.21 ± 0.69	2.83
C10orf35	chromosome 10 open reading frame 35	219738	A_23_P369328	1.21 ± 0.59	3.48
RBM12	RNA binding motif protein 12	10137	A_23_P502832	-1.21 ± 0.45	4.88
LINC01003	lincRNA 1003		A_32_P6172	-1.21 ± 0.38	5.90
SPRYD4	SPRY domain containing 4	283377	A_23_P411612	-1.21 ± 0.37	6.11
SNORD12C	small nucleolar RNA, C/D box 12C		A_21_P0000238	-1.20 ± 0.76	2.46
MTM1	myotubularin 1	4534	A_23_P62133	1.20 ± 0.75	2.52
IP6K3	inositol hexakisphosphate kinase 3	117283	A_23_P168130	-1.20 ± 0.72	2.64
BEST1	bestrophin 1	7439	A_23_P104996	1.20 ± 0.59	3.45
LOC100270746	uncharacterized LOC100270746		A_32_P232035	-1.20 ± 0.56	3.69
INSIG1	insulin induced gene 1	3638	A_33_P3219090	-1.20 ± 0.48	4.55
AREG	amphiregulin	374	A_23_P259071	1.19 ± 1.31	1.14
STOX2	storkhead box 2	56977	A_24_P163237	1.19 ± 0.89	1.95
SCARNA20	small Cajal body-specific RNA 20	677681	A_21_P0000350	-1.19 ± 0.79	2.30
VWCE	von Willebrand factor C and EGF domains	220001	A_23_P52986	-1.19 ± 0.64	3.07
IRAK2	interleukin-1 receptor-associated kinase 2	3656	A_33_P3352970	1.19 ± 0.59	3.39
CDNF	cerebral dopamine neurotrophic factor	441549	A_24_P93309	1.19 ± 0.56	3.65
LOC100129361	chromosome X open reading frame 69-like	100129361	A_21_P0000666	-1.19 ± 0.53	3.89
HIST1H4J	histone cluster 1, H4j	8363	A_23_P30805	1.19 ± 0.52	3.99
EFCAB3	EF-hand calcium binding domain 3	146779	A_33_P3264042	1.19 ± 0.49	4.35
PDE7B	phosphodiesterase 7B	27115	A_33_P3301940	1.19 ± 0.45	4.74
C12orf73	chromosome 12 open reading frame 73	728568	A_24_P769672	1.19 ± 0.33	6.82

STC1	stanniocalcin 1	6781	A_23_P314755	1.18 ± 1.12	1.39
LOC729950	uncharacterized LOC729950	729950	A_22_P00023603	-1.18 ± 1.04	1.55
LETM2	leucine zipper-EF-hand containing transmembrane protein 2	137994	A_23_P348264	1.18 ± 0.64	3.04
ZNRF3	zinc and ring finger 3	84133	A_24_P162373	1.18 ± 0.58	3.40
VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	7421	A_23_P162589	-1.18 ± 0.51	4.09
KIAA1958	KIAA1958	158405	A_33_P3404744	1.18 ± 0.50	4.24
MCOLN1	mucolipin 1	57192	A_23_P27571	-1.18 ± 0.50	4.15
USP35	ubiquitin specific peptidase 35	57558	A_23_P116602	-1.18 ± 0.44	4.92
CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	1050	A_24_P224727	1.18 ± 0.41	5.28
GTF2IRD2	GTF2I repeat domain containing 2	84163	A_23_P59616	-1.18 ± 0.39	5.74
CASP9	caspase 9, apoptosis-related cysteine peptidase	842	A_23_P97309	1.18 ± 0.39	5.67
CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	1577	A_23_P8801	1.17 ± 1.34	1.06
IL11	interleukin 11	3589	A_33_P3243887	-1.17 ± 0.72	2.52
FAR2	fatty acyl CoA reductase 2	55711	A_23_P150903	1.17 ± 0.71	2.60
PRKAR2A-AS1	PRKAR2A antisense RNA 1	100506637	A_21_P0002702	1.17 ± 0.70	2.69
JUN	jun proto-oncogene	3725	A_33_P3323298	-1.17 ± 0.64	3.00
AVPI1	arginine vasopressin-induced 1	60370	A_23_P1492	1.17 ± 0.55	3.69
PDE5A	phosphodiesterase 5A, cGMP-specific	8654	A_33_P3378514	-1.17 ± 0.50	4.17
AP5S1	adaptor-related protein complex 5, sigma 1 subunit	55317	A_23_P57137	-1.17 ± 0.34	6.59
LOC100506844	uncharacterized LOC100506844		A_33_P6822486	1.17 ± 0.33	6.75
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	6507	A_24_P286114	1.16 ± 1.00	1.60
CLDN4	claudin 4	1364	A_33_P3285545	-1.16 ± 0.88	1.91
FAM167A	family with sequence similarity 167, member A	83648	A_23_P334955	1.16 ± 0.78	2.26
BHLHE40	basic helix-loop-helix family, member e40	8553	A_24_P268676	-1.16 ± 0.61	3.21
ITIH4	inter-alpha-trypsin inhibitor heavy chain family, member 4	3700	A_23_P109881	1.16 ± 0.59	3.33
HIST1H4F	histone cluster 1, H4f	8361	A_23_P359540	1.16 ± 0.58	3.41
MDN1	MDN1, midasin homolog (yeast)	23195	A_23_P365060	1.16 ± 0.56	3.53
ZSCAN12	zinc finger and SCAN domain containing 12		A_21_P0000037	-1.16 ± 0.55	3.57
PICK1	protein interacting with PRKCA 1	9463	A_33_P3398697	-1.16 ± 0.47	4.45

TUBGCP4	tubulin, gamma complex associated protein 4	27229	A_23_P3450	1.16 ± 0.42	5.12
SRSF6	serine/arginine-rich splicing factor 6	6431	A_33_P3220530	-1.16 ± 0.36	5.96
TXLNG	taxilin gamma	55787	A_23_P146997	1.16 ± 0.36	5.96
DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	25822	A_23_P112241	-1.16 ± 0.35	6.33
ZNF844	zinc finger protein 844	284391	A_33_P3247838	1.16 ± 0.33	6.54
PPP4R2	protein phosphatase 4, regulatory subunit 2	151987	A_32_P228775	1.16 ± 0.32	6.80
SLBP	stem-loop binding protein	7884	A_23_P7101	1.16 ± 0.30	7.23
LOC100505501	uncharacterized LOC100505501		A_21_P0014222	-1.15 ± 0.90	1.84
KIF23	kinesin family member 23	9493	A_23_P48835	-1.15 ± 0.89	1.86
CSRP2	cysteine and glycine-rich protein 2	1466	A_23_P44724	-1.15 ± 0.81	2.12
C5orf34	chromosome 5 open reading frame 34	375444	A_23_P403081	1.15 ± 0.76	2.32
LINC01431	lincRNA 1431		A_22_P00019189	1.15 ± 0.71	2.53
CDK17	cyclin-dependent kinase 17	5128	A_33_P3341224	1.15 ± 0.70	2.56
SRP14-AS1	SRP14 antisense RNA1 (head to head)		A_19_P00320723	1.15 ± 0.59	3.25
PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	5775	A_33_P3265920	1.15 ± 0.53	3.74
BICD1	bicaudal D homolog 1 (Drosophila)	636	A_33_P3256425	1.15 ± 0.50	4.08
PYGO1	pygopus family PHD finger 1	26108	A_33_P3782469	-1.15 ± 0.48	4.20
PPAT	phosphoribosyl pyrophosphate amidotransferase	5471	A_24_P123347	1.15 ± 0.46	4.45
SCHIP1	schwannomin interacting protein 1	29970	A_32_P62863	-1.15 ± 0.40	5.30
SLC39A14	solute carrier family 39 (zinc transporter), member 14	23516	A_23_P59950	1.15 ± 0.38	5.62
RASD1	RAS, dexamethasone-induced 1	51655	A_23_P118392	-1.14 ± 0.91	1.79
LINC00629	lincRNA 629		A_21_P0006516	1.14 ± 0.89	1.83
TMEM44-AS1	TMEM44 antisense RNA 1		A_22_P00006209	1.14 ± 0.60	3.16
MYCBPAP	MYCBP associated protein	84073	A_33_P3361388	1.14 ± 0.43	4.75
SLC3A2	solute carrier family 3 (amino acid transporter heavy chain), member 2	6520	A_23_P75811	1.14 ± 0.42	5.02
LOC101927789	putative ubiquitin-like protein FUBI-like protein ENSP00000310146		A_21_P0010979	-1.14 ± 0.42	4.94
NUBP1	nucleotide binding protein 1	4682	A_33_P3413053	-1.14 ± 0.29	7.50
SIAH2	siah E3 ubiquitin protein ligase 2	6478	A_33_P3358342	1.14 ± 0.28	7.82
KLHL41	kelch-like family member 41	10324	A_23_P17190	-1.13 ± 1.10	1.34
KIF18A	kinesin family member 18A	81930	A_33_P3242649	-1.13 ± 0.98	1.57

CNIH3	cornichon family AMPA receptor auxiliary protein 3	149111	A_23_P384044	-1.13 ± 0.86	1.91
ATOH8	atonal homolog 8 (Drosophila)	84913	A_23_P142878	-1.13 ± 0.63	2.89
CGRRF1	cell growth regulator with ring finger domain 1	10668	A_23_P37283	1.13 ± 0.59	3.18
HIST2H4B	histone cluster 2, H4b	554313	A_23_P436281	1.13 ± 0.56	3.43
TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	944	A_23_P169257	-1.13 ± 0.54	3.56
ACAT2	acetyl-CoA acetyltransferase 2	39	A_23_P31135	-1.13 ± 0.49	4.12
ST3GAL4-AS1	ST3GAL4 antisense RNA 1 (head to head)		A_21_P0000607	1.13 ± 0.42	4.86
PELI1	pellino E3 ubiquitin protein ligase 1	57162	A_33_P3316928	1.13 ± 0.35	6.08
RIPK2	receptor-interacting serine-threonine kinase 2	8767	A_23_P252106	1.13 ± 0.34	6.33
ABHD6	abhydrolase domain containing 6	57406	A_23_P211850	1.13 ± 0.34	6.23
CREB5	cAMP responsive element binding protein 5	9586	A_23_P157117	1.12 ± 1.20	1.18
FAM26F	family with sequence similarity 26, member F	441168	A_23_P7827	1.12 ± 0.99	1.55
GOLGA2P2Y	golgin A2 pseudogene 2, Y-linked	84559	A_24_P314554	-1.12 ± 0.83	1.99
EDN1	endothelin 1	1906	A_23_P214821	-1.12 ± 0.79	2.11
PGM5P3-AS1	PGM5P3 antisense RNA 1	572558	A_32_P157208	-1.12 ± 0.79	2.11
SLC25A40	solute carrier family 25, member 40	55972	A_23_P432626	1.12 ± 0.78	2.16
JUNB	jun B proto-oncogene	3726	A_24_P241815	-1.12 ± 0.68	2.61
ZNF138	zinc finger protein 138	7697	A_23_P59855	1.12 ± 0.64	2.87
IER3	immediate early response 3	8870	A_23_P42257	-1.12 ± 0.62	2.97
NEK7	NIMA-related kinase 7	140609	A_23_P353574	1.12 ± 0.55	3.46
OPA3	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	80207	A_24_P475814	-1.12 ± 0.36	5.87
CNNM4	cyclin and CBS domain divalent metal cation transport mediator 4	26504	A_23_P119923	1.12 ± 0.36	5.76
FNBP4	formin binding protein 4	23360	A_23_P395595	1.12 ± 0.35	6.06
RBM4B	RNA binding motif protein 4B	83759	A_23_P1638	-1.12 ± 0.30	7.03
THBD	thrombomodulin	7056	A_23_P91390	-1.11 ± 0.97	1.56
CRLF3	cytokine receptor-like factor 3	51379	A_24_P56894	1.11 ± 0.92	1.68
BMP4	bone morphogenetic protein 4	652	A_23_P54144	-1.11 ± 0.87	1.81
CTAGE10P	CTAGE family, member 10, pseudogene		A_33_P3340007	1.11 ± 0.81	2.02
VTRNA1-3	vault RNA 1-3	56662	A_21_P0000515	-1.11 ± 0.76	2.21
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3673	A_32_P178800	1.11 ± 0.64	2.76

CUTC	cutC copper transporter	51076	A_23_P98015	1.11 ± 0.62	2.93
SCML2	sex comb on midleg-like 2 (Drosophila)	10389	A_33_P3320010	1.11 ± 0.61	3.00
MESP2	mesoderm posterior basic helix-loop-helix transcription factor 2	145873	A_33_P3214463	1.11 ± 0.56	3.37
AMOTL2	angiomotin like 2	51421	A_23_P166686	-1.11 ± 0.52	3.72
DLEU1	deleted in lymphocytic leukemia 1 (non-protein coding)		A_23_P151337	1.11 ± 0.52	3.71
HOMER1	homer homolog 1 (Drosophila)	9456	A_33_P3372257	1.11 ± 0.52	3.69
TMEM169	transmembrane protein 169	92691	A_24_P929388	1.11 ± 0.49	3.96
PNMA5	paraneoplastic Ma antigen family member 5	114824	A_23_P352950	-1.11 ± 0.46	4.32
FLJ37035	uncharacterized LOC399821	399821	A_22_P00002248	1.11 ± 0.43	4.65
ZNF846	zinc finger protein 846	162993	A_21_P0011721	-1.11 ± 0.36	5.85
TUBB2A	tubulin, beta 2A class IIa	7280	A_23_P19291	-1.11 ± 0.30	7.07
PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	5739	A_23_P340848	-1.10 ± 1.04	1.40
LOC101926967	uncharacterized LOC101926967		A_22_P00016533	1.10 ± 0.77	2.14
RGS17	regulator of G-protein signaling 17	26575	A_23_P156861	1.10 ± 0.67	2.57
HIP1R	huntingtin interacting protein 1 related	9026	A_23_P398294	-1.10 ± 0.66	2.62
SCARNA11	small Cajal body-specific RNA 11	677780	A_21_P0000356	-1.10 ± 0.60	2.99
SCARNA13	small Cajal body-specific RNA 13	677768	A_33_P3338360	-1.10 ± 0.58	3.11
HIST1H4K	histone cluster 1, H4k	8362	A_33_P3299865	1.10 ± 0.51	3.77
FAM127C	family with sequence similarity 127, member C	441518	A_33_P3296707	-1.10 ± 0.49	3.92
RHPN2	rhophilin, Rho GTPase binding protein 2	85415	A_33_P3387621	1.10 ± 0.42	4.80
PEX12	peroxisomal biogenesis factor 12	5193	A_24_P416411	1.10 ± 0.42	4.76
SLC25A30	solute carrier family 25, member 30	253512	A_33_P3380417	1.10 ± 0.37	5.62
LHFPL2	lipoma HMGIC fusion partner-like 2	10184	A_23_P255104	1.10 ± 0.34	6.16
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	259266	A_23_P52017	-1.09 ± 1.15	1.20
LOC284561	uncharacterized LOC284561		A_33_P3672756	1.09 ± 0.99	1.48
LOC101926941	uncharacterized LOC101926941	101926941	A_21_P0012956	1.09 ± 0.96	1.54
RNA5-8S5	RNA, 5.8S ribosomal 5	100008587	A_33_P3399064	-1.09 ± 0.95	1.57
C6orf52	chromosome 6 open reading frame 52	347744	A_23_P410224	1.09 ± 0.77	2.14
SAMD8	sterile alpha motif domain containing 8	142891	A_23_P63870	1.09 ± 0.69	2.44
TMEM97	transmembrane protein 97	27346	A_24_P190168	-1.09 ± 0.65	2.65

C11orf70	chromosome 11 open reading frame 70	85016	A_24_P364057	1.09 ± 0.64	2.74
RHCE	Rh blood group, CcEe antigens	6006	A_23_P62634	1.09 ± 0.64	2.72
GEMIN5	gem (nuclear organelle) associated protein 5	25929	A_23_P336513	1.09 ± 0.59	3.05
PRR19	proline rich 19	284338	A_33_P3403107	-1.09 ± 0.58	3.12
SNORA11D	small nucleolar RNA, H/ACA box 11D	100124541	A_21_P0000479	-1.09 ± 0.53	3.54
TBC1D22B	TBC1 domain family, member 22B	55633	A_23_P58983	1.09 ± 0.46	4.28
C17orf58	chromosome 17 open reading frame 58	284018	A_24_P49190	1.09 ± 0.46	4.16
TUBB8	tubulin, beta 8 class VIII	347688	A_24_P813147	-1.09 ± 0.40	4.98
RHBDD1	rhomboid domain containing 1	84236	A_24_P134834	1.09 ± 0.31	6.62
CLEC2B	C-type lectin domain family 2, member B	9976	A_33_P3332970	-1.08 ± 1.24	1.07
FRZB	frizzled-related protein	2487	A_23_P363778	-1.08 ± 1.11	1.25
LOC101928907	uncharacterized LOC101928907	101928907	A_21_P0008557	1.08 ± 1.09	1.27
ASAP1-IT1	ASAP1 intronic transcript 1 (non-protein coding)		A_23_P146325	-1.08 ± 0.92	1.62
SOX9-AS1	SOX9 antisense RNA 1	400618	A_24_P497464	1.08 ± 0.86	1.79
TMEM217	transmembrane protein 217	221468	A_23_P334870	1.08 ± 0.82	1.93
PRPS1L1	phosphoribosyl pyrophosphate synthetase 1-like 1	221823	A_32_P192823	-1.08 ± 0.80	1.96
CHAC1	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	79094	A_33_P3376971	1.08 ± 0.73	2.24
LOC102724528	uncharacterized LOC102724528		A_21_P0014060	1.08 ± 0.68	2.45
MGC16275	uncharacterized protein MGC16275	85001	A_22_P00024329	1.08 ± 0.65	2.62
MALT1	MALT1 paracaspase	10892	A_24_P116909	1.08 ± 0.61	2.89
BNC1	basonuclin 1	646	A_23_P22134	1.08 ± 0.56	3.25
EPT1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	85465	A_24_P940803	1.08 ± 0.46	4.22
SQLE	squalene epoxidase	6713	A_23_P146284	-1.08 ± 0.42	4.60
DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	1601	A_33_P3338928	-1.08 ± 0.40	5.02
N4BP2L2	NEDD4 binding protein 2-like 2	10443	A_23_P53856	-1.08 ± 0.40	4.88
LOC102723919	uncharacterized LOC102723919		A_22_P00023080	1.08 ± 0.38	5.19
ZNF425	zinc finger protein 425	155054	A_24_P941166	1.08 ± 0.37	5.44
SPTBN4	spectrin, beta, non-erythrocytic 4	57731	A_24_P293114	-1.07 ± 0.87	1.73
FAM46B	family with sequence similarity 46, member B	115572	A_23_P12199	-1.07 ± 0.79	1.97
MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B	9935	A_33_P3220837	-1.07 ± 0.78	2.01

IDI1	isopentenyl-diphosphate delta isomerase 1	3422	A_24_P103886	-1.07 ± 0.73	2.21
PTGER4	prostaglandin E receptor 4 (subtype EP4)	5734	A_23_P148047	-1.07 ± 0.70	2.36
SLC16A13	solute carrier family 16, member 13	201232	A_23_P118741	1.07 ± 0.70	2.36
ARMC9	armadillo repeat containing 9	80210	A_23_P209731	-1.07 ± 0.65	2.60
NT5DC2	5'-nucleotidase domain containing 2	64943	A_23_P44836	-1.07 ± 0.58	3.06
SHROOM3	shroom family member 3	57619	A_33_P3336700	-1.07 ± 0.53	3.43
IPO9	importin 9	55705	A_33_P3360917	-1.07 ± 0.53	3.41
PNPLA7	patatin-like phospholipase domain containing 7	375775	A_33_P3666884	-1.07 ± 0.53	3.38
CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	80777	A_22_P00010686	-1.07 ± 0.46	4.12
C3orf17	chromosome 3 open reading frame 17	25871	A_24_P921155	-1.07 ± 0.34	5.97
ARMC5	armadillo repeat containing 5	79798	A_33_P3221563	-1.07 ± 0.32	6.24
XPO1	exportin 1	7514	A_23_P40078	1.07 ± 0.28	7.25
CARD6	caspase recruitment domain family, member 6	84674	A_23_P41854	-1.07 ± 0.28	7.15
PSCA	prostate stem cell antigen	8000	A_23_P71379	1.06 ± 1.45	0.83
CCL2	chemokine (C-C motif) ligand 2	6347	A_23_P89431	-1.06 ± 1.27	1.01
DLGAP5	discs, large (Drosophila) homolog-associated protein 5	9787	A_23_P88331	-1.06 ± 1.17	1.12
PTHLH	parathyroid hormone-like hormone	5744	A_23_P2271	1.06 ± 0.87	1.72
C1QTNF2	C1q and tumor necrosis factor related protein 2	114898	A_33_P3403153	-1.06 ± 0.75	2.13
C1orf109	chromosome 1 open reading frame 109	54955	A_23_P45970	1.06 ± 0.67	2.45
DCT	dopachrome tautomerase	1638	A_23_P76622	1.06 ± 0.66	2.50
MMD	monocyte to macrophage differentiation-associated	23531	A_23_P164047	1.06 ± 0.62	2.74
C1QTNF9B-AS1	C1QTNF9B antisense RNA 1		A_33_P3531204	-1.06 ± 0.55	3.22
TRMT10A	tRNA methyltransferase 10 homolog A (S. cerevisiae)	93587	A_23_P398637	1.06 ± 0.50	3.64
HS6ST1	heparan sulfate 6-O-sulfotransferase 1	9394	A_24_P8220	1.06 ± 0.50	3.62
RIN2	Ras and Rab interactor 2	54453	A_24_P305570	-1.06 ± 0.39	4.94
DCAF10	DDB1 and CUL4 associated factor 10	79269	A_23_P217054	1.06 ± 0.38	5.08
LOC286437	uncharacterized LOC286437		A_33_P3807593	-1.06 ± 0.37	5.36
KCTD11	potassium channel tetramerization domain containing 11	147040	A_23_P354027	-1.06 ± 0.34	5.75
HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible,	9709	A_23_P54846	1.06 ± 0.32	6.25

	ubiquitin-like domain member 1				
RC3H1	ring finger and CCCH-type domains 1	149041	A_32_P96807	-1.06 ± 0.30	6.63
SLC51B	solute carrier family 51, beta subunit	123264	A_23_P436284	-1.05 ± 1.38	0.89
LINC00312	lincRNA 312		A_23_P166779	-1.05 ± 0.93	1.53
PEX5L	peroxisomal biogenesis factor 5-like	51555	A_23_P259003	1.05 ± 0.74	2.12
LOC101928236	uncharacterized LOC101928236		A_22_P00009053	1.05 ± 0.73	2.14
PHLPP1	PH domain and leucine rich repeat protein phosphatase 1	23239	A_23_P89762	1.05 ± 0.71	2.27
DPY19L2P1	DPY19L2 pseudogene 1		A_33_P3626301	1.05 ± 0.71	2.23
GPATCH1	G patch domain containing 1	55094	A_23_P27822	1.05 ± 0.56	3.12
MYLIP	myosin regulatory light chain interacting protein	29116	A_33_P3255914	1.05 ± 0.52	3.39
TBL1X	transducin (beta)-like 1X-linked	6907	A_33_P3347168	1.05 ± 0.47	3.86
MRM1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	79922	A_23_P15603	1.05 ± 0.44	4.23
CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	9469	A_24_P269779	1.05 ± 0.44	4.23
LOC100499489	uncharacterized LOC100499489		A_21_P0000660	-1.05 ± 0.40	4.82
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	3613	A_23_P50081	1.05 ± 0.39	4.95
KSR1	kinase suppressor of ras 1	8844	A_23_P207774	1.05 ± 0.38	5.04
C12orf65	chromosome 12 open reading frame 65	91574	A_32_P11894	1.05 ± 0.37	5.26
FAM199X	family with sequence similarity 199, X-linked	139231	A_23_P45294	1.05 ± 0.32	6.21
FAM220A	family with sequence similarity 220, member A	84792	A_23_P42738	1.05 ± 0.31	6.47
ZNF25	zinc finger protein 25	219749	A_24_P69691	1.05 ± 0.28	7.13
LOC101928716	uncharacterized LOC101928716		A_22_P00022529	-1.04 ± 1.05	1.27
CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	4435	A_23_P73526	1.04 ± 1.04	1.28
NAMA	non-protein coding RNA, associated with MAP kinase pathway and growth arrest	100996569	A_21_P0013736	-1.04 ± 0.93	1.50
ITIH1	inter-alpha-trypsin inhibitor heavy chain 1	3697	A_23_P18223	-1.04 ± 0.92	1.55
PDCD6	programmed cell death 6		A_21_P0003089	1.04 ± 0.84	1.75
ODF3L1	outer dense fiber of sperm tails 3-like 1	161753	A_32_P468743	1.04 ± 0.84	1.75
OR51A2	olfactory receptor, family 51, subfamily A, member 2	401667	A_33_P3268060	-1.04 ± 0.74	2.08
CLEC18B	C-type lectin domain family 18, member B	283971	A_23_P206501	1.04 ± 0.69	2.29

ZNF780A	zinc finger protein 780A	284323	A_33_P3255631	1.04 ± 0.66	2.48
ARIH2OS	ariadne homolog 2 opposite strand	646450	A_24_P76018	1.04 ± 0.64	2.60
ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	25841	A_23_P356616	1.04 ± 0.53	3.30
AVL9	AVL9 homolog (S. cerevisiase)	23080	A_23_P122947	1.04 ± 0.45	4.13
CREB3L2	cAMP responsive element binding protein 3-like 2	64764	A_33_P3211739	1.04 ± 0.40	4.75
SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	11000	A_24_P179816	-1.04 ± 0.40	4.64
CABIN1	calcineurin binding protein 1	23523	A_24_P336113	-1.04 ± 0.37	5.21
MTURN	maturin, neural progenitor differentiation regulator homolog (Xenopus)	222166	A_32_P100439	-1.04 ± 0.35	5.49
UBE2O	ubiquitin-conjugating enzyme E2O	63893	A_24_P172993	1.04 ± 0.32	6.14
FMO3	flavin containing monooxygenase 3	2328	A_23_P155596	-1.03 ± 1.90	0.56
IL1RN	interleukin 1 receptor antagonist	3557	A_33_P3246833	1.03 ± 1.54	0.75
LIF	leukemia inhibitory factor	3976	A_24_P122137	-1.03 ± 1.18	1.07
ZNF700	zinc finger protein 700	90592	A_23_P27636	1.03 ± 0.78	1.89
TRIM21	tripartite motif containing 21	6737	A_23_P47691	-1.03 ± 0.68	2.35
INTU	inturned planar cell polarity protein	27152	A_32_P118372	1.03 ± 0.65	2.46
GLYATL1	glycine-N-acyltransferase-like 1	92292	A_23_P370666	1.03 ± 0.65	2.44
ZNF81	zinc finger protein 81	347344	A_33_P3372285	1.03 ± 0.54	3.15
CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	23283	A_24_P941051	-1.03 ± 0.44	4.11
MFSD6	major facilitator superfamily domain containing 6	54842	A_33_P3272209	-1.03 ± 0.44	4.09
LOC100630918	uncharacterized LOC100630918		A_21_P0000847	-1.03 ± 0.43	4.19
NCOR1	nuclear receptor corepressor 1	9611	A_24_P204214	1.03 ± 0.42	4.38
ZFAT	zinc finger and AT hook domain containing	57623	A_32_P109922	-1.03 ± 0.41	4.55
KLF6	Kruppel-like factor 6	1316	A_23_P63798	-1.03 ± 0.40	4.75
EEF2K	eukaryotic elongation factor 2 kinase	29904	A_33_P3342410	-1.03 ± 0.38	4.99
LMO4	LIM domain only 4	8543	A_23_P380181	1.03 ± 0.38	4.96
CRTC3	CREB regulated transcription coactivator 3	64784	A_23_P77228	1.03 ± 0.31	6.24
DDX42	DEAD (Asp-Glu-Ala-Asp) box helicase 42	11325	A_23_P152651	-1.03 ± 0.31	6.20
DUSP26	dual specificity phosphatase 26 (putative)	78986	A_23_P146134	-1.02 ± 1.00	1.33
SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8	23428	A_23_P205489	-1.02 ± 0.89	1.56

FAM196B	family with sequence similarity 196, member B	100131897	A_33_P3375636	1.02 ± 0.88	1.60
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	84803	A_23_P69810	1.02 ± 0.80	1.83
LOC102723505	uncharacterized LOC102723505	102723505	A_22_P00014813	1.02 ± 0.74	2.04
PRPS1	phosphoribosyl pyrophosphate synthetase 1	5631	A_23_P95764	-1.02 ± 0.68	2.30
IPMK	inositol polyphosphate multikinase	253430	A_23_P380371	1.02 ± 0.65	2.42
TCP10L	t-complex 10-like	140290	A_23_P350555	1.02 ± 0.64	2.47
TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	26517	A_33_P3413845	-1.02 ± 0.57	2.89
C10orf32	chromosome 10 open reading frame 32	119032	A_23_P305140	-1.02 ± 0.52	3.34
JMJD1C	jumonji domain containing 1C	221037	A_23_P427217	1.02 ± 0.44	4.06
NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	123606	A_33_P3250840	1.02 ± 0.41	4.49
MTMR12	myotubularin related protein 12	54545	A_24_P354615	1.02 ± 0.39	4.80
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	57678	A_24_P227069	1.02 ± 0.32	6.07
XBP1	X-box binding protein 1	7494	A_23_P120845	1.02 ± 0.29	6.80
TENM2	teneurin transmembrane protein 2	57451	A_24_P299474	1.01 ± 1.33	0.88
FAM225B	family with sequence similarity 225, member B (non-protein coding)	100128385	A_32_P99347	1.01 ± 1.15	1.08
PPL	periplakin	5493	A_23_P106906	-1.01 ± 0.83	1.70
PCSK9	proprotein convertase subtilisin/kexin type 9	255738	A_32_P142440	-1.01 ± 0.78	1.86
FAR2P1	fatty acyl CoA reductase 2 pseudogene 1		A_24_P508103	1.01 ± 0.71	2.14
ATP6V1E2	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E2	90423	A_23_P143047	1.01 ± 0.67	2.30
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	2683	A_23_P135271	1.01 ± 0.53	3.15
DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	9149	A_23_P90296	-1.01 ± 0.51	3.32
SNORD52	small nucleolar RNA, C/D box 52	26797	A_21_P0000284	-1.01 ± 0.50	3.45
CSDC2	cold shock domain containing C2, RNA binding	27254	A_24_P177279	-1.01 ± 0.47	3.71
UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1	91373	A_23_P135164	-1.01 ± 0.46	3.79
BET1	Bet1 golgi vesicular membrane trafficking protein	10282	A_24_P269432	1.01 ± 0.44	4.01
SERTAD3	SERTA domain containing 3	29946	A_23_P141960	-1.01 ± 0.41	4.37
C14orf159	chromosome 14 open reading frame 159	80017	A_23_P48771	-1.01 ± 0.38	4.86
ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	9828	A_23_P76015	-1.01 ± 0.37	4.99
BCDIN3D	BCDIN3 domain containing	144233	A_23_P338233	1.01 ± 0.34	5.58
CCNT2	cyclin T2	905	A_24_P174341	1.00 ± 0.82	1.71

NUP50-AS1	NUP50 antisense RNA 1 (head to head)		A_22_P00008681	1.00 ± 0.72	2.04
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	6541	A_24_P253251	1.00 ± 0.71	2.12
KLHDC9	kelch domain containing 9	126823	A_23_P86100	1.00 ± 0.70	2.13
LINC00938	lincRNA 938		A_24_P661641	-1.00 ± 0.68	2.23
DLX2	distal-less homeobox 2	1746	A_23_P28598	1.00 ± 0.56	2.91
PAXIP1-AS1	PAXIP1 antisense RNA 1 (head to head)	202781	A_21_P0005447	1.00 ± 0.55	2.95
XPOT	exportin, tRNA	11260	A_23_P340722	1.00 ± 0.49	3.46
FUT10	fucosyltransferase 10 (alpha (1,3) fucosyltransferase)	84750	A_33_P3748714	1.00 ± 0.43	4.12
HSPA13	heat shock protein 70kDa family, member 13	6782	A_24_P134392	1.00 ± 0.31	6.07

Supplementary Table S8. Common genes regulated by pirfenidone in fibroblasts *in vivo* and *in vitro*. Numbers represent mean log2(fold-change) ± the half width of the 95% confidence interval. Values in brackets are significances as -log10(P-value).

GENE_SYMBOL	GENE_NAME	ENTREZ_ID	SPOT_ID	IPF+P(FB) - IPF(FB)	IPF(FB+P) – vehicle treated IPF(FB)	Regulation
PDE4B	phosphodiesterase 4B, cAMP-specific	5142	A_23_P74278	1.20 ± 1.19 (1.32)	2.03 ± 0.60 (6.38)	both up
PTPN3	protein tyrosine phosphatase, non-receptor type 3	5774	A_22_P00025093	1.56 ± 0.64 (4.46)	2.12 ± 0.87 (4.34)	both up
MYBL1	v-myb avian myeloblastosis viral oncogene homolog-like 1	4603	A_23_P43157	1.21 ± 1.00 (1.70)	1.85 ± 0.80 (4.04)	both up
RIMBP3	RIMS binding protein 3	85376	A_23_P154962	1.39 ± 0.57 (4.45)	1.77 ± 0.78 (3.95)	both up
BTBD11	BTB (POZ) domain containing 11	121551	A_23_P419714	1.22 ± 0.72 (2.73)	1.32 ± 0.74 (2.93)	both up
TGFBR3	transforming growth factor, beta receptor III	7049	A_23_P200780	1.26 ± 1.19 (1.41)	1.28 ± 0.95 (1.97)	both up
AREG	amphiregulin	374	A_23_P259071	1.24 ± 1.17 (1.42)	1.19 ± 1.31 (1.14)	both up
LETM2	leucine zipper-EF-hand containing transmembrane protein 2	137994	A_23_P348264	1.18 ± 0.59 (3.42)	1.18 ± 0.64 (3.04)	both up
FAR2	fatty acyl CoA reductase 2	55711	A_23_P150903	1.16 ± 0.87 (1.96)	1.17 ± 0.71 (2.60)	both up
C5orf34	chromosome 5 open reading frame 34	375444	A_23_P403081	1.16 ± 0.85 (2.04)	1.15 ± 0.76 (2.32)	both up

CREB5	cAMP responsive element binding protein 5	9586	A_23_P157117	1.52 ± 0.83 (3.06)	1.12 ± 1.20 (1.18)	both up
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3673	A_32_P178800	1.14 ± 0.83 (2.05)	1.11 ± 0.64 (2.76)	both up
RGS17	regulator of G-protein signaling 17	26575	A_23_P156861	1.30 ± 0.99 (1.92)	1.10 ± 0.67 (2.57)	both up
PSCA	prostate stem cell antigen	8000	A_23_P71379	1.16 ± 1.72 (0.75)	1.06 ± 1.45 (0.83)	both up
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	84803	A_23_P69810	1.02 ± 0.84 (1.70)	1.02 ± 0.80 (1.83)	both up
CCNT2	cyclin T2	905	A_24_P174341	1.05 ± 0.87 (1.71)	1.00 ± 0.82 (1.71)	both up
KLHDC9	kelch domain containing 9	126823	A_23_P86100	1.16 ± 0.95 (1.71)	1.00 ± 0.70 (2.13)	both up
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B, G protein-coupled	3357	A_23_P16953	-1.18 ± 1.37 (1.06)	-2.57 ± 1.02 (4.55)	both down
MIR503HG	MIR503 host gene (non-protein coding)	84848	A_33_P3402329	-1.58 ± 0.94 (2.71)	-2.49 ± 0.66 (7.22)	both down
LINC00968	lincRNA 968	100507632	A_21_P0000731	-1.14 ± 0.91 (1.79)	-1.89 ± 1.23 (2.35)	both down
EDN1	endothelin 1	1906	A_23_P214821	-1.37 ± 1.09 (1.80)	-1.12 ± 0.79 (2.11)	both down
LINC00312	lincRNA 312		A_23_P166779	-1.61 ± 0.90 (2.98)	-1.05 ± 0.93 (1.53)	both down