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BAL Cell Gene Expression is indicative of Outcome and Airway Basal Cell involvement in IPF

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At a Glance Commentary

What is the current scientific knowledge on this subject?

Although multiple peripheral blood derived biomarkers have been shown to predict mortality in IPF, there is no information which alveolar molecular changes are indicative of disease progression and outcome. To test this, we studied the transcriptome of BAL cells. Airway basal cells are the progenitor cells of the airway epithelium and recent murine studies suggested a pathogenic role of these cells in IPF. So far these cells were not known to be present in BAL and indicative of high mortality in IPF.

What does this study add to the field?

Using gene expression microarrays we identified transcripts of BAL cells that were associated with mortality in patients with IPF. A 9 gene expression signature that predicted mortality in IPF patients from a discovery cohort, performed well in two replication cohorts and could be used in future as a new biomarker. The obtained gene expression data allow insights which tissue derived signal pathways are associated with mortality in IPF. Unexpectedly the genes predictive of mortality were significantly enriched for genes expressed in airway basal cells. This led to the discovery that these cells are indeed increased in the BAL and tissue of patients with IPF.

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Abstract

Rationale. Idiopathic pulmonary fibrosis (IPF) is a fatal disease with a variable and unpredictable course.

Objective. We designed this study to determine whether bronchoalveolar lavage (BAL) cell gene expression is predictive of survival in IPF.

Methods. Retrospective study analyzing the BAL transcriptome of three independent IPF cohorts: Freiburg (Germany), Siena (Italy) and Leuven (Belgium) including 212 patients. BAL cells from 20 healthy volunteers, 26 patients with sarcoidosis stage III and IV and 29 patients with COPD were used as controls. Survival analysis was performed by Cox models and component-wise boosting. Presence of airway basal cells was tested by immunohistochemistry and flow cytometry.

Measurements and Main Results. 1582 genes were predictive of mortality in the IPF derivation cohort in univariate analyses adjusted for age and sex at FDR<0.05. A nine-gene signature, derived from the discovery cohort (Freiburg), performed well in both replication cohorts, Siena ($p<0.0032$) and Leuven ($p=0.0033$). nCounter® expression analysis confirmed the array results ($p<0.0001$). The genes associated with mortality in BAL cells were significantly enriched for genes expressed in airway basal cells. Further analyses by gene expression, flow cytometry and immunohistochemistry showed an increase in airway basal cells in BAL and tissues of IPF compared to controls, but not in COPD or sarcoidosis.

Conclusions. Our results identify and validate a BAL signature that predicts mortality in IPF and improves the accuracy of outcome prediction based on clinical parameters. The BAL signature associated with mortality unmasks a potential role for airway basal cells in IPF.

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Introduction

Idiopathic pulmonary fibrosis (IPF) is a fatal disease with an estimated median survival time of 3 years and a variable course.[1,2] Although there has been significant progress in predicting outcome in IPF using clinical disease staging systems,[2,3] peripheral blood biomarkers[4-6] and gene variants[7], very little is known whether molecular events in the lung milieu are predictive of outcome in IPF.

Ideally, research aiming to identify molecular markers in patients with IPF would focus on lung biopsies obtained at diagnosis. However, lung biopsies are invasive and indicated in less than 30% of patients and thus are limited in their utility. Bronchoalveolar lavage (BAL), a procedure in which saline is injected and then collected through a bronchoscope, samples the cells residing on the external layer of the alveolus.[8] While BAL is not absolutely required for the diagnosis of IPF, it can be used in the routine diagnostic work-up, most often to exclude infections as well as other inflammatory conditions commonly associated with an UIP pattern on HRCT.[9] Multiple studies suggested that the alveolar molecular environment is altered in IPF.[10,11]

Considering that the cells obtained in BAL reside in the alveolar compartment we hypothesized that changes in gene expression of BAL cells will be predictive of IPF outcome. Some of the results of these studies have been previously reported in the form of an abstract.[12]

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Methods

A comprehensive description of all methods is available in the supplement

Study population

BAL was obtained from 212 IPF patients in three independent cohorts obtained at 3 referral centers: Freiburg (Germany) - derivation, Siena (Italy) and Leuven (Belgium) - replication (Table 1 and Figure S1). IPF diagnosis was established by a multidisciplinary board at each institution according to the ATS/ ERS criteria[13] and later determined to be consistent with recent guidelines.[14,15] BAL cells from 20 healthy donors served as control for IPF (Table S1). For active disease controls we used gene expression data of 2 additional studies testing BAL-cells from 26 patients with sarcoidosis stage III and IV versus 20 healthy volunteers and BAL-cells from 29 currently smoking COPD patients versus 28 currently smoking controls (Table S2-3). All studies were approved by local ethics committees. In all three centres pulmonary function tests were routinely performed with a standard methodology, according to the ATS/ERS recommendations using a body-plethysmograph. Survival status was obtained from follow-up visits and telephone interviews. Patients who had not been seen within 3 months were called to confirm their vitality. Ten patients underwent a lung transplant. None of the patients received pirfenidone or nintedanib prior to BAL examination, however during follow-up, patients were treated with varied treatment regimens including corticosteroids, azathioprine, N-acetylcysteine or pirfenidone. All patients were Caucasians except one patient of the Leuven cohort. For further details, see Table 1 and online-only supplement.

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Microarray

For detailed description see supplement and our recent publication.[5] Gene expression was detected using Whole Human Genome arrays. All MIAME compliant raw data have been deposited in the Gene Expression Omnibus (GEO) with the accession GSE70867.

nCounter® expression analysis

To validate the microarray data of IPF samples we applied multiplexed, color-coded probe pairs using the nCounter® expression analysis system (Nanostring). Detailed information is given in the supplement.

Determining the gene expression profile of airway basal cells

Airway basal cells were isolated from bronchial brushes of sub-segmental bronchi of the right lower lobe as recently described.[16] Detailed information regarding cell isolation and gene expression profiling is given in the supplement.

Immuno-cytology and immuno-histochemistry

Cell smears of BALs from 20 patients with IPF, 20 patients with sarcoidosis and 10 healthy volunteers were evaluated by immune-cytology. Immuno-histochemistry of lung tissues from 15 patients with IPF (7 wedge biopsies and 8 explants), 3 patients with sarcoidosis and 3 healthy lung donors (transplants) was performed. A monoclonal mouse-anti human cytokeratin-5/6 antibody (DAKO clone D5/16 B4, Hamburg, Germany) and polyclonal rabbit anti-human ΔNP63 antibody (Calbiochem PC373, Schwalbach, Germany) were used.

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Gender Age Physiology (GAP)- Index

The GAP index, a staging system for patients with IPF, was calculated as recently described using age, gender, FVC and DLCO.[2]

Statistical analysis

In the IPF Freiburg (derivation) cohort, univariate Cox proportional hazards models were calculated for each gene separately adjusted for age and gender using false discovery rate (FDR) < 0.05. Median survival was calculated, censoring at the time of transplant.

We used componentwise likelihood-based boosting[17] for developing a multivariable risk prediction signature, considering all genes simultaneously in a Cox model, adjusted for age and gender. The number of boosting steps, which determines the number of genes to be selected for the signature, was chosen by 10-fold cross-validation. For identifying high- and low-risk groups, we considered for each patient and each signature gene, whether the expression level of the gene for this patient was above the median expression level of all patients. Genes with risk-increasing effect, i.e. positive coefficient, being above the median were counted as one point in the risk score, and reversely for genes with risk-decreasing effect. Patients were divided at the median of the resulting risk score, and differences were evaluated by logrank tests.

Stable selection of genes was performed using cross validation and resampling. Genes from the signature obtained from the original data were considered for further validation by nCounter® if they were selected in at least 20% of these resamplings. Prediction error curves, which indicate the mean squared error in predicting patient survival in the course of time, were used to evaluate the signature alone, and the signature in addition to the GAP index.[2] In addition to prediction accuracy (as evaluated e.g. by ROC curves), these prediction error curves also indicate calibration.[18]

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Results

Patients' characteristics

The clinical characteristics of the IPF patients in the three cohorts are provided in Table 1 and indicate that the cohorts differed slightly. The information about 20 old healthy volunteers as well as the cohorts of patients with sarcoidosis or COPD and their controls is available in Tables S1-3.

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BAL cell transcriptome is predictive of mortality in IPF

After adjustment for age and gender, 1582 genes were associated with mortality (FDR < 0.05, Table S4) in the derivation cohort of IPF patients. A multivariate prediction model consisting of 9 genes was generated by componentwise likelihood-based boosting in the derivation cohort (Figure 1A, Table S5). Prediction performance on the replication cohorts was evaluated by considering for these 9 genes whether the expression level is above or below the median expression level, adding up a risk score accordingly. High- and low-risk groups were determined by splitting this score at the median. This multivariate prediction model performed well in the Siena cohort (p=0.0032; c-index = 0.63, CI: 0.54 - 0.72; Figure 1B) and the Leuven cohort (p=0.0033; c-index = 0.66, CI: 0.55 - 0.76; Figure 1C). Combining the information from the GAP index and the expression signature resulted in better prediction performance than using the GAP index alone (see supplementary Table S6)

A stable 6 gene signature confirms microarray results and accurately predicts outcome in the combined cohort

As it is well known that risk prediction signatures can be unstable,[18] we used a resampling approach for identifying a stable subset of the signature for further validation. Six

of the 9 genes were selected stably (using selection in at least 20% of the resampling data sets as a cutoff) and were considered for further validation (Tables S4, S5, S7). Using the nCounter® digital expression system we confirmed that this signature is significantly predictive of mortality in the total cohort of 168 IPF patients ($p<0.00001$; HR= 3.951; CI: 2.132 – 7.323; c-index = 0.67, 95% CI: 0.62 - 0.71; Figure 2A). Impressively, this stable 6-gene signature alone performed better than the GAP index (Figure 2B; c-index = 0.63, 95% CI: 0.58 - 0.69). More importantly, when the 6-gene signature and the GAP index were combined, the outcome prediction error rate was reduced, indicating a significant added value (Figure 2B; c-index = 0.72, 95% CI: 0.66 - 0.77).

Network analysis

Network analysis using Ingenuity revealed that the processes associated with mortality in IPF are similar to cancer, organismal injury and stem cells (reproductive system disease). Processes involved are important for cell proliferation and migration (Table S8).

Enrichment for ABC derived genes in the BAL signature associated with mortality

Surprisingly, while 98% of the cells seen in the BAL pellet were of hematopoietic origin, 10% of the genes in the BAL signature were known to be specifically up-regulated in cultured airway basal cells (ABC).[16] We generated an empiric ABCs signature by comparing gene expression of isolated ABC with alveolar macrophages and bronchial epithelial cells (Figure S3). The overlap between our signature and the one recently described by Hackett and colleagues is 38%.[16] We identified 921 genes that were increased in ABCs and listed in the BAL IPF microarray dataset (Table S9). Impressively, 165 of these 921 ABC genes were among the 1582 genes associated with mortality, indicating significant enrichment ($p<0.0001$). ABC genes were overexpressed in patients with short survival. Because the

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signatures were all developed in cultured cells, we also analyzed whether our ABC signature was representative of ABCs in vivo utilizing a recently published single cell RNAseq dataset.[19] The genes we identified were significantly enriched in airway basal cells compared to alveolar type II cells ($p<0.0001$, two tail Fisher Exact test).

To investigate whether ABCs genes could predict mortality, we derived a survival signature based only on ABCs genes, again using componentwise likelihood-based boosting. The resulting model contains 16 ABC genes (Table S10). This multivariate prediction model based on ABC genes performed well in all three cohorts: the Freiburg cohort ($p<0.00001$, c-index = 0.73, 95% CI: 0.68 - 0.77, Figure 3A), the Siena cohort ($p=0.000512$, c-index = 0.66, 95% CI: 0.57 - 0.74 , Figure 3B) and the Leuven cohort ($p=0.00508$, c-index = 0.67, 95% CI: 0.56 - 0.76, Figure 3C). Combining the information from the GAP index and the expression signature resulted in better prediction performance than using the GAP index alone (see supplementary Table S11).

Presence of ABCs in the BAL of IPF patients

To evaluate the presence of ABCs in BAL, we stained BAL cell smears for the expression of ΔNP63 and cytokeratin 5 and 6 (CK5/6) and cytokeratin 5 alone (CK5).[20] We found clusters of CK5/6+ cells and $CK5^{+}$ cells within the BAL of IPF patients consistent with the presence of ABCs in IPF lavages (Figure 4A and B, Figure S4). Ciliated cells did not stain for CK5/6 (Figure 4C). ABCs were rarely observed in BAL of controls or patients with sarcoidosis (Figure 4C and D).

ABCs are increased in BAL of IPF patients compared to healthy volunteers, but not in BAL from patients with sarcoidosis or COPD

ABC genes were significantly ($p=0.0156$) enriched in BAL obtained from IPF patients compared to healthy volunteers, but not in the BAL of patients with sarcoidosis ($p=0.3527$) or

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COPD (p=0.1326). Flow cytometry revealed that 0.26% of BAL cells were EPCAM+ CK5/6+ in IPF (Figure 4E and F), compared to 0.05% in age matched controls (p=0.001) and 0.07% in patients with sarcoidosis (p=0.008).

ABCs are enriched in the alveolar compartment of IPF tissues

To localize ABCs in the alveolar compartment we stained lung tissues from healthy donors patients with sarcoidosis and patients with IPF for CK5/6 and ΔNP63. In normal and sarcoid tissues, cells expressing CK5/6 and ΔNP63 were found only in the airways, but not in the alveolar compartments (Figure 4G and H). In contrast in IPF, ABCs frequently covered fibroblast foci (Figure 4I-L), were within fibrotic lesions and occasionally formed hollow structures (Figure 4M). In some patients, alveolar epithelium was replaced by multiple layers of ABCs resembling ABC hyperplasia and squamous metaplasia (Figure 4L-M). In addition, we performed immunohistochemistry for S100A14, a gene that was shown to be highly expressed by ABCs and that was included in the described predictive 9-gene signature of the microarray experiment and the predictive 6-gene signature of the nanostring experiment. We found S100A14 highly expressed by airway basal cells and epithelial cells covering honeycomb cysts and fibroblast foci, but not in normal lung tissues (Figure S5). The pattern of S100A14 staining was very similar to the described CK5/6 and ΔNP63 staining (Figure 4).

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Discussion

In this paper we identified BAL gene expression patterns associated with increased mortality in IPF patients and then developed a gene expression signature predictive of mortality. This signature was derived in one cohort and validated in two additional independent cohorts. Although BAL cells are comprised nearly entirely of hematopoietic cells, the genes associated with mortality were enriched for genes highly expressed in ABCs. Immuno-cytology, flow cytometry and immuno-histochemistry confirmed enrichment of ABCs within the BAL and tissues of IPF patients.

In recent years there has been an increased recognition that molecular and genetic changes may be informative about distinct outcomes in IPF. The majority of these studies focused on the peripheral blood and identified proteins or changes in gene expression in PBMCs that predict mortality[4-7] but did not directly investigate the alveolar compartment. Gene expression of lung tissues from IPF patients has been extensively studied.[21,22] However, these studies rarely attempted to correlate gene expression with disease severity, were all hampered by missing mortality data and did not develop outcome prediction models. Although BAL is reflective of the alveolar milieu and relatively easy to obtain, very few studies tried to identify molecular biomarkers in BAL. Most recently high BAL neutrophil counts[23] and changes in BAL bacterial burden[24] have been shown to be associated with changed mortality. We used the BAL transcriptome data of IPF patients from Freiburg as a derivation cohort and found 1582 genes to be significantly associated with mortality. Based on these data we generated a multivariate prediction model consisting of 9 genes which performed well in the independent replication cohorts, despite differences in lavage procedure and patient characteristics. For further validation we tested the 6 most stably selected genes from the signature by nCounter® expression analysis in the total cohort. Using this second

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method we confirmed the signature derived from the microarray data. Impressively, our gene expression signatures improved the performance of accepted clinical predictors such as the GAP index.[2] Thus, our study, the first comprehensive study of BAL gene expression patterns and their relevance to outcome in IPF, differs from previous studies not only by the focus on BAL and the novelty of the results, but also by the size of the cohort, the incorporation of a derivation and two replication cohorts, and the comparison to accepted clinical predictors of outcome, making it a significant advance over previous biomarker studies in IPF. This is important, because improvement of outcome prediction over what is currently available, may have significant implications on timing and prioritization of lung transplantation. The nCounter® expression analysis system is a robust technology which is used for molecular diagnostics and even has FDA approval for some assays and thus would be ideal for use in future prospective studies.

One of the most surprising aspects of our study was that many of the genes associated with mortality were epithelial genes described by Hackett and colleagues[16] to be expressed in ABCs, an airway progenitor population that give rise to all types of airway epithelial cells and is capable of proliferation and self-renewal.[20] The specific ABC gene expression signature we obtained was similar to the previously described by Hackett and colleagues[16] and significantly enriched among 1582 genes associated with mortality. Both signatures were derived from ABCs isolated from an outgrow of bronchial epithelial cells and thereby cultured for 21 days. The genes highly expressed by cultured ABCs were over-expressed in BAL of patients with poor survival. Importantly, a similar enrichment was also found with genes identified in ABCs by single cell RNAseq.[19] indicating that this is not solely an *in-vitro* signature. Of course, many of the top ABC genes associated with early mortality such as S100A14, stratifin are not only expressed by airway basal cells but also by metaplastic

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epithelial lesions, non-small cell lung and other cancers; especially the so-called basal-like breast cancer. Indeed, our network analysis revealed similarities with mechanisms present in cancer. Similarly, some of the ABC genes associated with mortality indicate a phenotype to squamous differentiation which may in vivo promoted by TGF-β signaling.[25]

The possibility that this finding is caused by bronchoscopy technique or a patient population peculiarity is ruled out because it was found in three independent cohorts, in IPF BAL samples obtained by different investigators, but not in samples obtained from patients with COPD or sarcoidosis. Applying immuno-cytology and flow cytometry we demonstrated that these findings were not limited to changes in gene expression. CK5/6 double and CK5 positive cells were present in BAL of IPF patients but very rarely in BAL of old healthy volunteers or patients with sarcoidosis. Immuno-histochemical analysis of IPF lungs demonstrated abundance of ABCs expressing CK5/6 and ΔNP63 around fibroblast foci, within fibrotic lesions and occasionally forming hollow structures similar to early honeycomb cysts. In normal histology controls such cells were observed in the airways, but never in the alveolar compartment. Our results are consistent with previous findings by Chilosi and colleagues[26] that detected ΔNP63 expressing cells in the abnormal bronchiolization that characterizes the IPF lung. This is of particular interest, IPF is characterized by fibroblast foci, honeycomb cyst formation and bronchiolization of the alveolar space.[13,14,26-29] In the current model of disease pathogenesis the bronchiolization and honeycomb cysts formation occur after the formation of myofibroblast foci.[30] However, recent data from animal models suggest that CK5/6+ ΔNP63+ cells may have important roles in the early response to fibrosis. In a model of influenza virus induced pulmonary fibrosis, Kumar et al.[31] showed that a bronchoalveolar subpopulation of ABCs accumulates in fibrotic lesions and that this response may be part of regeneration in healthy mice.[31] More recently, Vaughan et al.[32] demonstrated

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that migration and proliferation of a CK5/6+ ΔNP63+ progenitor cell population is an early and key event in the evolution of pulmonary fibrosis. Together with the work by Kumar[31] and Vaughan[32], our results suggest that ABCs are recruited potentially in response to alveolar epithelial cell injury and their proliferation and invasion determine the distortion of the alveolar structure that we typically associate with IPF. Very recently, single cell RNA sequencing of epithelial cells in IPF revealed that normal alveolar type II cells were very rare in the IPF lung.[19] Instead, epithelial cells derived from IPF tissues consisted of three major populations: airway basal cells, goblet cells and indeterminate cells. This study also demonstrated an abnormal differentiation program in the tissue microenvironment of IPF in which the proximal-peripheral patterns of cell differentiation are disrupted, with many respiratory epithelial cells acquiring aberrant, multilineage-like states.[19] Impressively, many of the genes that characterized IPF epithelial genes in this study are in our BAL signature.[19] Thus, our results concur and enhance previous observations, but adding to previous observations we demonstrate that the airway basal cell is clinically relevant that may suggest an involvement of this cell type in the pathophysiology of this disease, but definitely need further evaluation.

Our study has several limitations. First, we studied the gene expression profile of a cellular admixture and therefore cannot clarify the exact cellular sources of each change in gene expression. While this is a significant limitation, it is also the foundation for our unexpected finding. Based on our knowledge we had no reason to look for epithelial cells, thus a more targeted experiment at lymphocytes or macrophages would probably have resulted in us missing this most novel finding. However, this limitation is still an important consideration. Airway epithelial progenitors are a heterogeneous population of cells[32] and our study was not aimed to identify the exact regional source and subtype of the CK5/6+ cells in the BAL of IPF patients which needs to be defined in future single cell based studies. A

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further limitation is that we used cultured ABCs to retrieve their cell specific signature. We compared cultured ABCs, alveolar macrophages and bronchial epithelial cells. Our ABC gene list may therefore contain genes highly expressed by other cell types not studied because we found them enriched in cultured ABCs compared to macrophages and bronchial epithelial cells. The described signature of ABCs is influenced by the culture conditions of the cells in our experiment, but the fact that it was also enriched applying a signature retrieved from naïve ABCs of IPF lung tissues by single cell RNAseq reduces the likelihood of culture conditions being a major confounder. Moreover, the described list of ABC genes is not exclusively expressed by ABCs rather also expressed by metaplastic lesions and cancers derived from airway basal cells and basal cells from other organs. However, what is important, is that we found using unbiased approaches a significant enrichment of these genes in uncultured BAL of IPF patients and an association of this signature with early mortality. We believe that our findings warrant a detailed characterization of CK5/6+ ΔNP63+ basal-like epithelial cells in IPF and follow up studies to dissect their role in the pathogenesis of fibrosis.

In conclusion, our foray into the BAL transcriptome was very productive. We identified a gene expression signature that predicts mortality in IPF. This signature was validated in three cohorts and has been shown to improve the accuracy of outcome prediction based on clinical parameters suggesting that it should be considered for transplant prioritization and clinical trial design. Our unexpected finding that genes from ABCs were highly enriched in the BAL of patients likely to progress adds to recently published murine data and may suggest an unexpected role of ABCs in the pathogenesis of IPF. Our results should have significant impact on reconsideration of BAL as part of the evaluation of patients with IPF, as well as on further studies addressing ABCs as potential therapeutic targets in this devastating disease.

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Acknowledgements

We thank S. Hahn, H. Rhode-Wagner and N. Wehrle for skillful technical assistance.

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Table 1. Baseline Characteristics of IPF Patients

Characteristic	All IPF N=176	Freiburg N=62	Leuven N=64	Siena N=50	p value*
Age -yr	68.1 ± 9.5	67.4 ± 9.1	68.2 ± 8.5	68.7 ± 11.2	0.768
Male sex -%	82	85	80	80	0.648
FVC percent predicted value -%	71 ± 21	66 ± 20	78 ± 18	67 ± 23	< 0.001
DLCO					
Percent predicted value -%	43 ± 14	44 ± 16	45 ± 12	40 ± 15	0.396
Could not perform DLCO -No.	20	7	1	12	
Deaths – No. (%)	100 (51)	45 (73)	24 (37)	31 (62)	
Transplants – No. (%)	10 (6)	3 (5)	3 (5)	4 (8)	0.704
Median observation time- months		20	18	16	
Smoking Status - %					0.156
Never smoked	33	42	23	34	
Former smoker	64	56	70	64	
Current smoker	3	2	6	2	
HRCT UIP – No. (%)					0.208
Definite	134 (76)	43 (69)	53 (83)	38 (76)	
Possible	42 (24)	19 (31)	11 (17)	12 (24)	
HRCT Emphysema present -No.	24 (16)	5 (8)	16 (26)	3 (6)	
Bronchoalveolar Lavage (BAL)					
Cell count –$\times 10^6$ cells ±SD	13.0 ± 7.7	12.1 ± 7.2	13.3 ± 8.8	13.7 ± 6.9	0.518
Alveolar macrophages ±SD -%	74 ± 17	71 ± 17	80 ± 17	71 ± 16	0.006
Lymphocytes ±SD -%	10 ± 9	11 ± 9	9 ± 10	10 ± 9	0.358
Neutrophils ±SD -%	11 ± 14	12 ± 14	9 ± 14	13 ± 14	0.192
Eosinophils ±SD -%	4 ± 5	4 ± 5	3 ± 4	5 ± 6	0.128

* group comparison by ANOVA for continuous and chi-squared test for categorical characteristics

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Figure 1

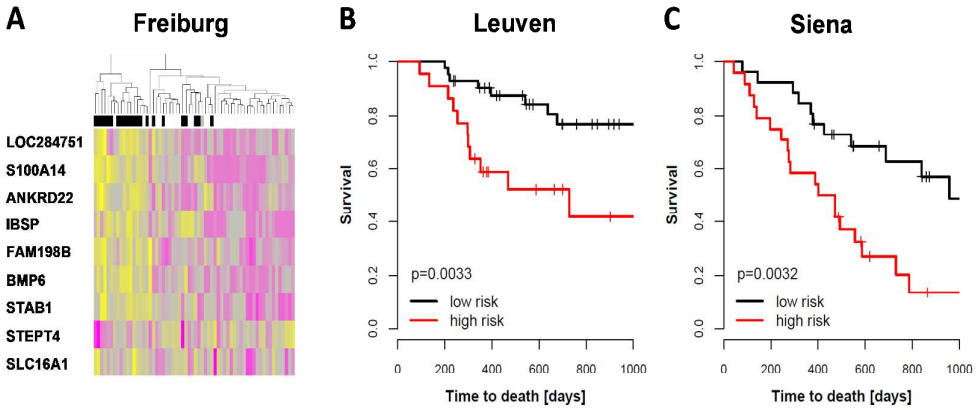

Figure 1. The BAL cell transcriptome is predictive of mortality in IPF. *Based on the microarray data from the Freiburg cohort we found 1582 genes predictive of mortality. We developed a prediction signature consisting out of 9 genes by componentwise likelihood-based boosting. The expression levels of the 9 genes in the Freiburg cohort are depicted in Panel A. Every row represents a gene, and every column, a patient. Yellow denotes increase over the mean of samples, and purple, decrease. Black denotes patients who died within 18 months, grey patients censored before 18 months and white patients who survived 18 months. The prediction model based on the gene expression data of 9 genes was validated in the Leuven cohort (B) and in the Siena cohort (C) and statistically significantly separated between mortality in both cohorts.*

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Figure 2

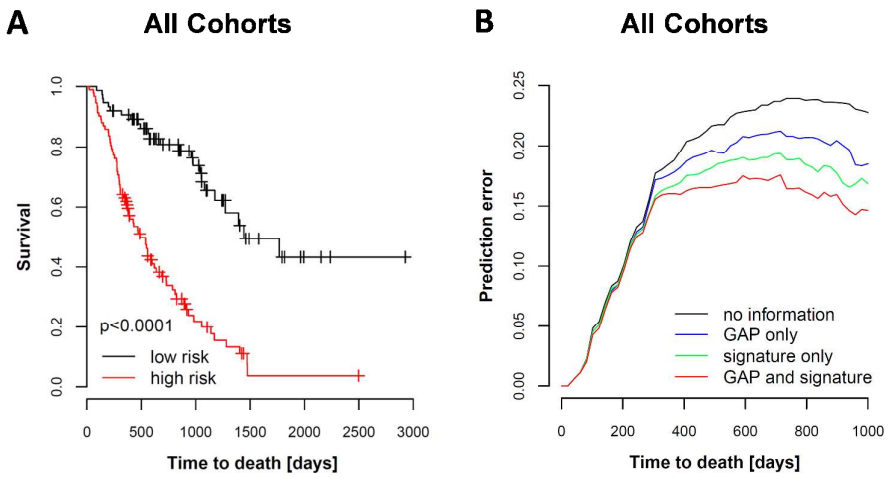

Figure 2. The BAL gene signature is predictive of mortality in IPF. *The microarray data were validated by nCounter® expression analysis. Panel A: Based on inclusion frequency data from the resampling we further reduced the signature to 6 genes. The 6 gene signature measured by nCounter® expression analysis predicted mortality in all cohorts. Panel B: Prediction error curves (indicating mean squared error in predicting survival status) were calculated for the signature of 6 genes (green) and GAP (blue). The 6 gene signature was superior to the GAP score in predicting mortality in IPF. Combining the 6 gene signature with GAP score (red) reduced prediction errors and resulted in better prediction (p<0.01).*

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Figure 3

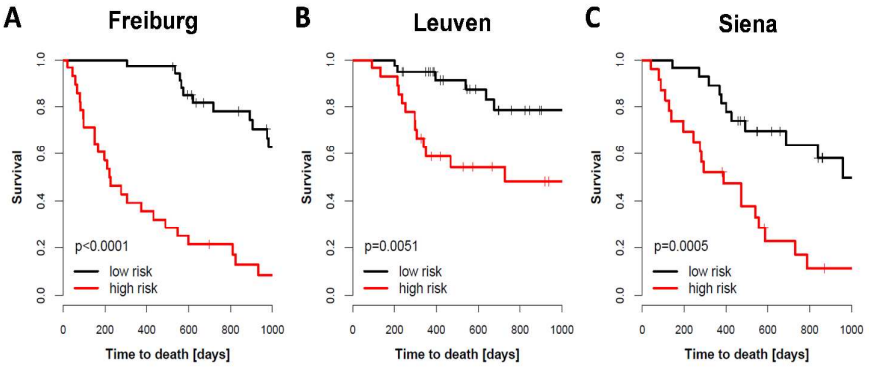

Figure 3. Genes derived from airway basal cells are associated with high mortality in IPF. *Based on the gene expression data from the Freiburg cohort we found 165 genes highly expressed by airway basal cells predictive of mortality. By componentwise likelihood-based boosting we developed a prediction model in the Freiburg cohort (Panel A). The prediction model based on the gene expression data of airway basal cell genes was validated in the Leuven cohort (Panel B) and in the Siena cohort (Panel C) and statistically significantly separated between mortality in both cohorts.*

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Figure 4

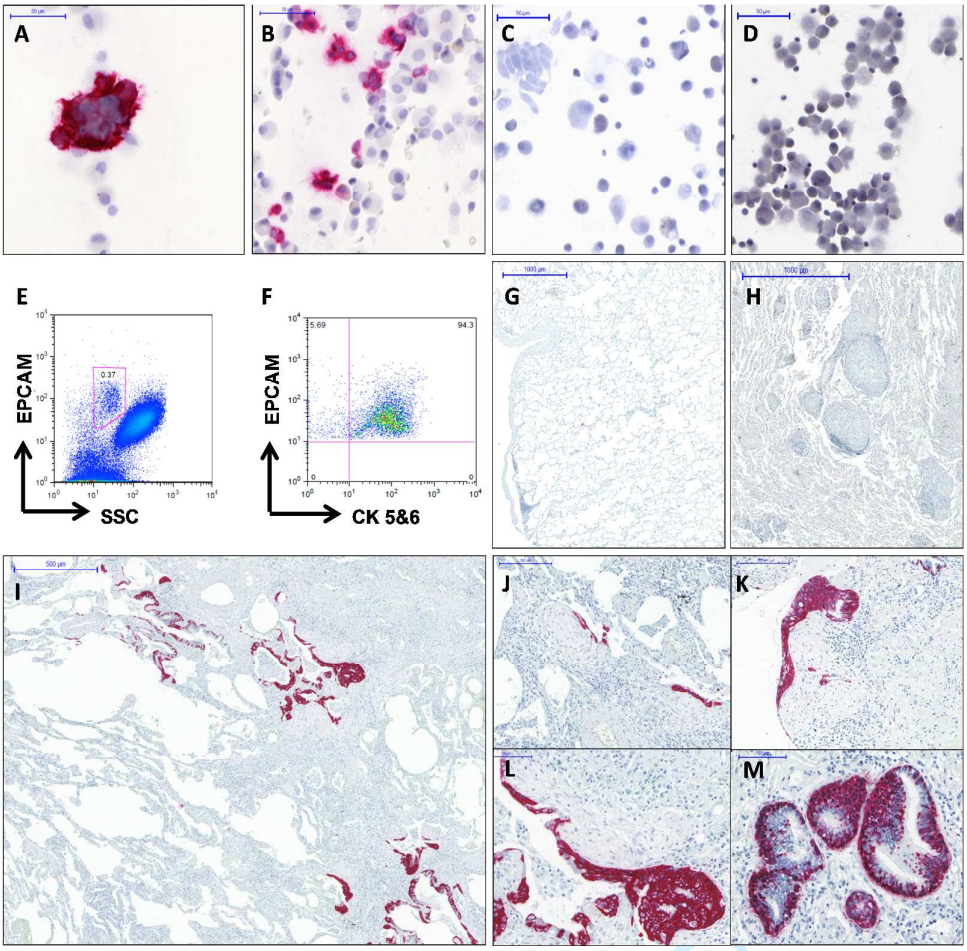

Figure 4. Increase in CK5/6+ ΔNP63+ Airway Basal Cells in BAL and Alveolar Tissue of IPF Patients. Panel A-D: *Cytokeratin (CK) 5/6+ airway basal cells (ABC, stained in red) were found frequently in cell smears of BAL from IPF patients (**Panel A and B**) and often formed cell clusters. In contrast, CK5/6+ ABC were found only rarely in the BAL of old healthy volunteers (**Panel C**) and patients with COPD (**Panel D**). Flow cytometry revealed presence of EPCAM+ epithelial cells in the BAL of IPF patients and most of them co-expressed CK5/6 identifying these cells as ABC (**Panel E-F**). Immuno-histochemistry of lung tissues stained for CK5/6 (red) and ΔNp63 (nuclear turquois) showed ABCs in the basal layer of airway epithelium but not in the alveolar compartment of normal lung tissue (**Panel G**) and sarcoid tissue (**Panel H**). In contrast, in IPF tissues we observed an enrichment of ABCs within the alveolar compartment (**Panel I-M**). ABCs frequently covered fibroblast foci (**Panel J -L**), and occasionally formed hollow structures (**Panel M**). In some patients, alveolar epithelium was replaced by multiple layers of ABCs consistent with basal cell hyperplasia and squamous metaplasia (**Panel L-M**).*

Supplement

BAL Cell Gene Expression is indicative of Outcome and Airway Basal Cell involvement in IPF

Prasse A et al.

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SUPPLEMENTARY METHODS

Study population

Bronchoalveolar lavage was obtained from 212 consecutive patients at 3 different tertiary referral centers: Freiburg (Germany), Siena (Italy) and Leuven (Belgium) (Figure S1). All patients signed informed consent prior to inclusion and the studies were approved by the respective local ethic committee and were registered at the German Clinical Trials Register; DRKS00000017 and DRKS00000620). IPF diagnosis was established by a multidisciplinary board at each institution according to the American Thoracic Society/European Respiratory Society criteria[1,2] and was later determined to be consistent with recent guidelines.[3] Only patients with an idiopathic UIP and HRCT consistent with a "definite" or "possible" UIP pattern were included. In patients with possible UIP at HRCT an UIP confirming histology was warranted. A lung biopsy was obtained in 33% of affected subjects. In all three centres pulmonary function tests were routinely performed with a standard methodology, according to the ATS/ERS recommendations using a body-plethysmograph.[4] Survival status was obtained from follow-up visits and telephone interviews. Patients who had not been seen within 3 months were called to confirm their vitality. Ten patients underwent a lung transplant. None of the patients received pirfenidone or nintedanib prior to BAL examination, however during follow-up, patients were treated with varied treatment regimens including corticosteroids, azathioprine, N-acetylcysteine and pirfenidone. All patients were Caucasians except one patient of the Leuven cohort. Twenty healthy volunteers (HV) were recruited as controls at the University Medical Center Freiburg, Germany. All these volunteers were apparently healthy and lung disease was ruled out by pulmonary function test and clinical examination (Table S1).

BAL cells from 26 patients with sarcoidosis, 20 with stage III and 6 with stage IV disease, and 20 healthy volunteers were harvested in an additional study at the University Mecial Center Freiburg and gene expression analysed in a collaborative project with Stromedix/ Biogen Idec Inc (Table S2).

Furthermore, BAL cells from 29 patients with COPD and 28 healthy volunteers were harvested in a collaborative study with Boehringer Ingelheim Pharma at the Fraunhofer Institute ITEM, Hannover, Germany. All patients and healthy volunteers were current smoker (Table S3).

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BAL sampling

Regarding the IPF cohort, in each of the 3 center BAL was performed in the middle lobe using a standardized procedure. Sterile, pre-warmed saline (37°C) was instilled by 20ml aliquots with immediate aspiration by gentle suction after each aliquot. There were a few differences between the centers; the first fraction was discarded in Leuven and Siena but not in Freiburg. Similarly the lavage volume was usually 300ml in Freiburg, but in Siena and in Leuven 150 ml. In all cases BAL cells were immediately isolated and frozen in TRIzol (#15596018, life technologies, Santa Clara, CA) at -80°C until RNA isolation.

Bronchoscopy, BAL and BAL cell isolation of the study comparing sarcoid patients with healthy volunteers were performed at the University Medical Center Freiburg using the same protocol as described for IPF patients.

Bronchoscopy and BAL of the study comparing patients with COPD with healthy volunteers were performed at the Fraunhofer institute ITEM at Hannover. BAL cells were isolated in accordance to a standardized protocol and harvested in 0.6 ml Qiazol.

BAL cell isolation and differential counts of IPF patients

The retrieved BAL was immediately processed in the respective local laboratories. The fluid was pooled, filtered through two layers of gauze, and centrifuged at 500 g for 10 minutes at 4°C. The cells were counted and cell smears were stained with May-Grunwald-Giemsa stain (Merck, Darmstadt, Germany), and counted for the cell differentials.

RNA isolation

Total RNA was extracted using a modified version of the TRIzol method, in which RNA is purified directly from the aqueous phase (RNeasy Mini Kit, #217004, Qiagen, Valencia, CA). RNA integrity was determined by assessing an aliquot of each RNA sample on an Agilent Bioanalyzer (Agilent Technologies, Palo Alto, CA). The concentration was determined using a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE). High quality RNA with a sufficient yield was extracted from 184 BAL samples.

Microarray of IPF samples and respective controls

Labeling of IPF samples and respective controls was performed using the Agilent Low RNA Input Linear Amplification Kit PLUS, one color (Agilent Technologies). Briefly, first-strand cDNA synthesis was performed using an oligo(dT) 24 primer containing a T7 RNA polymerase promoter site. The cDNA was used as a template to generate Cy3-labeled cRNA that was used for hybridization. After purification and fragmentation, aliquots of each sample were hybridized to Agilent SurePrint G3 Human Gene Expression 8 × 60K microarray kits (Agilent Technologies) with the only exception of the BAL samples from Leuven which were hybridized to Agilent SurePrint G3 Human Gene Expression 8 × 60K version 2 microarray kits (Agilent Technologies). After hybridization, each array was sequentially washed and scanned by Agilent microarray scanner. Arrays were individually visually inspected for hybridization defects, and quality control procedures were applied as recommended by the manufacturer of the arrays. For array readout, Agilent Feature Extraction 9.5.3 Software was used, and microarray data were imported, log2-transformed and quantile normalized using robust multi-array average (RMA), and expression levels were summarized on a transcript level using average gene expression values of the replicated probes, as recently described.[5] Non-expressed and invariant transcripts were removed using a median variance filter resulting in a final dataset of 20330 transcript measurements across 176 samples.

Microarray of sarcoid patients and respective controls

Gene expression of BAL cells from 26 patients with sarcoidosis and 20 healthy volunteers was detected using Affymetrix Whole-Transcript Human Gene 1.0 ST array on an Affymetrix platform. Microarray data were normalized, log2-transformed and quantile normalized using robust multi-array average (RMA).

Microarray of COPD patients and respective controls

Gene expression of BAL cells from 29 patients with COPD and 28 healthy volunteers was detected using Affymetrix Human Genome U133 Plus 2.0 array on an Affymetrix platform. Microarray data were normalized, log2-transformed and quantile normalized using robust multi-array average (RMA).

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nCounter® expression analysis

To validate the microarray data we applied multiplexed, color-coded probe pairs using the nCounter® expression analysis system (Nanostring).[6] After re-evaluation of RNA quality, 100 ng of total RNA per sample were hybridized with a custom code set generated based on the 6 stably selected genes and the endogenous controls ACTB, GAPDH, GUSB and B2M. After hybridization, gene transcript counts were obtained using the Nanostring preparation station and digital analyzer. Gene expression values of the genes which built up the signature associated with mortality were normalized to an average of positive, spiked-in and endogenous controls as recommended by the manufacturer using the nSolver analysis software. Normalized, log2 transformed gene expression values were used for statistical analyses.

GAP Index

The GAP index, a staging system for patients with IPF, was calculated as recently described using age, gender, FVC and DLCO.[7]

Network analysis

Network analysis, based on the false discovery rates from the (age and gender adjusted) univariate analysis with respect to mortality, using Ingenuity (version 21901358) are depicted in Table S7.

Determining the gene expression profile of airway basal cells

Alveolar macrophages were sorted from BAL of healthy volunteers by flow cytometry on a Moflo Astrios / Beckman Coulter cell sorter (sort strategy Figure S2). Cell pellet of 1 $\times 10^6$ sorted alveolar macrophages were solved in Quiazol (Quiagen, #79306) and immediately frozen at -80°C. RNA of alveolar macrophages was isolated accordingly to the protocol described for BAL cells.

Bronchial epithelial cells from healthy volunteers were harvested by bronchial brushes of sub-segmental bronchi of the right lower lobe during flexible bronchoscopy. Brushes were immediately placed in RNAprotect and cells were detached from each brush by flicking the brush in the RNAprotect cell reagent (Quiagen, #76526). Remaining solution was frozen at -80°C. RNA was isolated by RNeasy Protect Mini Kit (Qiagen, #74126).

Airway basal cells from healthy volunteers were isolated from bronchial brushes of sub-segmental bronchi of the right lower lobe as recently described.[8] Therefore bronchial brushes were placed in 2ml of pre-warmed (37°C) Clonetics™ Bronchial Epithelium Cell Growth Medium (BEGM, Lonza, Basel, Switzerland). Cells were detached from the brush by flicking the brush. Then, airway epithelial cells were pelleted by centrifugation (250×g, 5 min) and disaggregated by resuspension in 0.05% trypsin-ethylenediaminetetraacetic acid (EDTA) for 5 min at 37°C. Trypsinization was stopped by addition of HEPES buffered saline (Lonza, Basel, Switzerland) supplemented with 15% fetal bovine serum (FBS; GIBCO-Invitrogen, Carlsbad, CA), and the cells were again pelleted at 250×g, 5 min. The pellet was washed once with 5 ml of phosphate buffered saline (PBS). Afterwards, the cell pellet was resuspended in 5 ml of BEGM and cultured in T25 flasks in BEGM, supplemented with growth factors according to the manufacturer's instructions. The antibiotics supplied by the manufacturer of BEGM were used and additionally (50 mg/ ml; Sigma, St Louis, MO), 0.1% amphotericin B (BioWhittaker Amphotericin B Antifungal Lonza/ USA), and 1% penicillin-streptomycin (10000 U/ml Biochrom GmbH, Germany). Cultures were maintained in a humidified atmosphere of 5% CO_2 at 37°C. Unattached cells were removed by changing medium after 18 hr. Thereafter, media was changed every 3 days and cells were harvested at 21 days. Therefore, cells were trypsinized, harvested and counted. Purity of the airway basal cell population was detected by immunocytology (cytokeratin 5/6) of cytospins and always

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exceeded 98%. Directly, after harvesting cells, 500000 airway basal cells were pelleted, solved in TRIzol and stored at -80°C. RNA of airway basal cells was isolated accordingly to the same protocol as for BAL cells.
Microarray data of 11 airway basal cell lines, of alveolar macrophages flow-sorted from 7 healthy donors and samples of bronchial epithelial cells derived from 4 healthy volunteers were obtained with the same method as described for BAL cells. The transcriptome of the three different cell types was compared using per-gene ANOVA resulting in 8874 genes significantly differently expressed between the three cell types ($p<0.0001$). The data of these 8874 transcripts were used for a clustering approach applying Cluster 3.0 software. The samples were hierarchically clustered with median normalization of the genes and centroid linkage, and the similarity metric used was Pearson correlation.

Immuno-cytology and Immuno-histochemistry
Cell smears of BALs from 20 IPF patients, 10 patients with COPD and 10 healthy volunteers were evaluated by immmuno-cytology. Cytological smears of bronchoalveolar lavages were air dried. In addition, immuno-histochemistry of formalin fixed lung tissues from 15 patients with IPF (7 wedge biopsies and 8 explants), 3 patients with sarcoidosis and 3 healthy lung donors (transplants) was performed. Three micrometer thick sections of paraffinblocks were deparaffinized in xylol and rehydrated using a descending alcohol row. Heat induced antigen retrieval was performed at 110°C for 2 minutes in citrate buffer (pH 6.0) using a pressure cooker. For double staining procedure monoclonal mouse anti-human antibody directed against CK5/6 (DAKO clone D5/16 B4, Hamburg, Germany) was incubated for 30 minutes at room temperature. Incubation time of the biotinilated secondary antibody (DAKO REAL AB2) was 20 minutes at room temperature. Activation was done using alkaline phosphatase (DAKO REAL Streptavidin Alkaline Phosphatase) for 15 minutes and visualization was performed by DAKO REAL Chromogen Red (incubation time 10 minutes). Prior to incubation with the second primary antibody, endogenous peroxidase was deactivated by H_2O_2 for 10 minutes. Incubation time for the second primary antibody was 30 minutes (ΔNP63: polyclonal rabbit anti-human antibody Calbiochem PC373, Schwalbach, Germany). Peroxidase coupled secondary antibody (DAKO EnVision FLEX/HRP) was incubated for 20 minutes and visualization was performed using DAKO FLEX HRP Green Chromogen for 10 minutes. In addition, using the same immunohistochemistry protocol staining for S100A14 (ThermoFisher Scientific, #PA5-50783) and CK5 (ThermoFisher Scientific, #MA5-17057) was performed. Finally, all slides were counterstained by hematoxilin and coverslipped.

Statistical analysis

For continuous baseline characteristics frequencies, mean values, and standard deviations were calculated, and chi-squared tests and ANOVAs were performed.

For BAL gene expression, heatmaps were built, using hierarchical clustering according to Euclidean distance and complete linkage.

For the endpoints of interest, univariate analyses were performed as a first step. Median was survival was calculated, censoring at the time of transplant. In the Freiburg (derivation) cohort, univariate Cox proportional hazards models were calculated for each gene separately adjusted for age and gender using a cutoff of 0.05 on the false discovery rate (FDR).[9] To avoid batch effects, comparison of IPF to healthy control BAL was done only in samples from Freiburg. For this we used logistic regression models, adjusted for age and gender, and FDR values were calculated as above. For enrichment analysis we used global tests based on (adjusted) univariate models according to Goeman and colleagues.[10] This approach to test

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whether the effects of a group of genes are significantly different from zero was also used for all other enrichment analyses, using univariate Cox models for analyses with respect to mortality (adjusted for age and gender), and univariate logistic regression models for enrichment analyses in group comparisons, i.e. for comparison of Freiburg IPF patients to healthy controls (adjusted for age and gender), of sarcoidosis patients to healthy volunteers (adjusted for age, gender, % neutrophils, and % lymphocytes), and of COPD patients to healthy volunteers.

Component-wise likelihood based boosting for variable selection

We used componentwise likelihood-based boosting[11] for developing a multivariable risk prediction signature, considering all genes simultaneously in a Cox model, adjusted for age and gender.

Similar to the LASSO,[12] the size of the regression coefficients is penalized so that only coefficients for genes are estimated whose expression is strongly associated with survival. This results in a model, where the coefficients of most genes are zero. On the other hand genes with non-zero coefficient are termed selected since they improve the model fit. In contrast to the LASSO, in component-wise likelihood based boosting the coefficients are estimated in a stage-wise procedure. During a number of boosting steps, which is determined by cross validation, the coefficient of the regressor which, given the so far estimated regression model, most strongly improves the model fit, receives an update. For example, in a linear regression model, at boosting step m with non-zero regression coefficients for gene x and y, the coefficient of gene z would be updated if regressing the residuals of the so far estimated model over z would increase the model fit. The size of the update is controlled by a penalty term, which can be set individually for each regressor. By restricting the penalty to zero, the procedure allows for the inclusion of mandatory covariates, such as age or gender.

The number of boosting steps, which determines the number of genes to be selected for the signature, was chosen by 10-fold cross-validation. For identifying high- and low-risk groups, we considered for each patient and each signature gene, whether the expression level of the gene for this patient was above the median expression level of all patients. Genes with risk-increasing effect, i.e. positive coefficient, being above the median were counted as one point in the risk score, and reversely for genes with risk-decreasing effect. Patients were divided at the median of the resulting risk score, and differences were evaluated by logrank tests.

Stably selected genes were identified from signature building in 100 resampling data sets. Genes from the signature obtained from the original data were considered for further validation in the nCounter® expression data if they were selected in at least 20% of these resampling data sets (using the results from[13] as an orientation for the cutoff). The high/low risk indicator derived from the gene expression signature (transferred to the nCounter® expression data by counting the number of over-expressed signature genes per patients and splitting at the median) was entered into a multivariable Cox regression model together with the GAP staging information to test for added value. Prediction error curves[14], which indicate the mean squared error in predicting patient survival in the course of time, were used to evaluate the signature alone, and the signature in addition to the GAP index. In addition to prediction accuracy (as evaluated e.g. by ROC curves), these prediction error curves also indicate calibration.[14]

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Table S1. Baseline Characteristics of IPF Patients and HV

Table S1. Baseline Characteristics of IPF Patients and HV*		
Characteristic	**IPF Freiburg** N=62	**HV Freiburg** N=20
Age -yr	67.4 ± 9.1	61.9 ± 7.6
Male sex -%	85	75
FVC percent predicted value -%	66 ± 20	96 ± 19
Smoking Status		
Never smoked -%	42	30
Former smoker-%	56	70
Current smoker-%	2	0
Bronchoalveolar Lavage (BAL)		
Cell count –×10^6 cells	12.1 ± 7.2	9.3 ± 4.6
Alveolar macrophages -%	71 ± 17	76 ± 13
Lymphocytes -%	11 ± 9	20 ± 13
Neutrophils -%	12 ± 14	3 ± 4
Eosinophils -%	4 ± 5	0 ± 1

* Plus–minus values are means ±SD. FVC denotes for forced vital capacity. HV denotes for healthy volunteers. IPF denotes for idiopathic pulmonary fibrosis.

Table S2. Baseline Characteristics of Sarcoid Patients and additional HV

Table S2. Baseline Characteristics of Sarcoid Patients and HV*		
Characteristic	**SARC Freiburg** N=26	**HV Freiburg** N=20
Age -yr	48.5 ± 13.8	31.8 ± 15.7
Male sex -%	65	60
FVC percent predicted value -%	68 ± 19	112 ± 10
Smoking Status		
Never smoked -%	85	80
Former smoker-%	15	20
Current smoker-%	0	0
Bronchoalveolar Lavage (BAL)		
Cell count –×10^6 cells	10.9 ± 5.8	10.4 ± 9.6
Alveolar macrophages -%	66 ± 16	87 ± 7
Lymphocytes -%	28 ± 15	10 ± 6
Neutrophils -%	4 ± 6	2 ± 2
Eosinophils -%	1 ± 1	0 ± 1

* Plus–minus values are means ±SD. FVC denotes for forced vital capacity. HV denotes for healthy volunteers. SARC denotes for sarcoidosis.

Table S3. Baseline Characteristics of COPD Patients and respective HV

Table S3. Baseline Characteristics of COPD Patients and HV*			
Characteristic	**HV Hannover** N=28	**COPD Hannover** N=29	**p-value**
Age -yr	53.4 ± 6.9	54.5 ± 7.0	0.54
Male sex -%	68	59	
FVC percent predicted value -%	119 ± 14	97 ± 9	5.7E-09
FEV percent predicted value -%	109 ± 14	63 ± 9	3.8E-21
Smoking Status			
Never smoked -%	na	na	
Former smoker-%	na	na	
Current smoker-%	100	100	
Pack years	36 ± 13	54 ± 24	0.0008
Bronchoalveolar Lavage (BAL)			
Cell count –$\times 10^6$ cells	36.6 ± 20.0	32.2 ± 18.8	0.39
Alveolar macrophages -%	96 ± 3	95 ± 4	0.43
Lymphocytes -%	2 ± 2	2 ± 2	0.47
Neutrophils -%	2 ± 2	2 ± 2	0.97
Eosinophils -%	0 ± 0	1 ± 1	0.18

* Plus–minus values are means ±SD. FVC denotes for forced vital capacity. FEV1 denotes for forced exspiratory volume. HV denotes for healthy volunteers. COPD denotes for chronic obstructive pulmonary disease.

Table S4. BAL cell Genes related to Mortality in IPF

Table S4. BAL cell Genes related to Mortality in IPF with FDR<0.05							
	Symbol	Gene Name	p-value	FDR*	HR	CI	Freq**
1	BMP6	bone morphogenetic protein 6	8.34553E-10	9.54573E-06	2.04	0.764	0.54
2	S100A14	S100 calcium binding protein A14	9.39078E-10	9.54573E-06	1.85	0.748	0.47
3	STAB1	stabilin 1	2.3319E-09	1.58025E-05	2.53	0.758	0.37
4	LOC284751	cDNA FLJ33286 fis, clone ASTRO2014174	1.77482E-08	3.3665E-05	2.04	0.704	0.34
5	TPST1	tyrosylprotein sulfotransferase 1	1.24212E-08	3.3665E-05	1.62	0.744	0.24
6	LOC388210	similar to GM17625	1.93611E-08	3.3665E-05	2.38	0.684	0.14
7	HTRA1	HtrA serine peptidase 1	8.90271E-09	3.3665E-05	2.35	0.768	0.11
8	TM4SF1	transmembrane 4 L six family member 1	1.98711E-08	3.3665E-05	1.57	0.740	0.05
9	MMP25	matrix metallopeptidase 25	1.80271E-08	3.3665E-05	1.97	0.737	0.05
10	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	1.75388E-08	3.3665E-05	5.57	0.732	0.01
11	SLC36A1	solute carrier family 36 (proton/amino acid symporter), member 1	1.00546E-08	3.3665E-05	5.13	0.724	0
12	TLR2	toll-like receptor 2	9.60861E-09	3.3665E-05	3.44	0.730	0
13	IBSP	integrin-binding sialoprotein	2.66835E-08	4.17289E-05	2.04	0.747	0.54
14	FAM198B	family with sequence similarity 198, member B	3.1409E-08	4.56104E-05	2.11	0.725	0.03
15	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	3.77246E-08	5.11295E-05	1.92	0.717	0.09
16	SLC34A2	solute carrier family 34	4.0942E-08	5.20219E-05	1.54	0.735	0.02
17	ENAH	enabled homolog	5.15147E-08	6.16056E-05	2.39	0.689	0.05
18	ADM	adrenomedullin	6.21741E-08	6.8816E-05	1.93	0.708	0.02
19	DLGAP3	discs, large (Drosophila) homolog-associated protein 3	6.43141E-08	6.8816E-05	4.50	0.749	0
20	S100A12	S100 calcium binding protein A12	6.83934E-08	6.95219E-05	1.40	0.715	0.09
21	MRVI1	murine retrovirus integration site 1 homolog	7.44406E-08	7.20656E-05	1.76	0.749	0.16
22	MTSS1	metastasis suppressor 1	8.87837E-08	7.8477E-05	1.64	0.720	0.05
23	MUC21	mucin 21, cell surface associated	8.62643E-08	7.8477E-05	1.56	0.704	0.02
24	FAM40B	family with sequence similarity 40, member B	1.01435E-07	8.59242E-05	2.37	0.709	0.02
25	BCL6	B-cell CLL/lymphoma 6	1.09437E-07	8.89942E-05	5.96	0.683	0
26	JPH4	junctophilin 4	1.17378E-07	9.17807E-05	0.40	0.722	0
27	CAMK1	calcium/calmodulin-dependent protein kinase I	1.28903E-07	9.5842E-05	2.92	0.738	0.02
28	DYSF	dysferlin, limb girdle muscular dystrophy 2B	1.32001E-07	9.5842E-05	2.02	0.711	0
29	NRG1	neuregulin 1	1.71539E-07	0.000108639	1.75	0.719	0.16
30	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	1.9696E-07	0.000108639	2.58	0.740	0.14
31	RAB3IL1	RAB3A interacting protein	1.97719E-07	0.000108639	2.52	0.737	0.07
32	MAL2	mal, T-cell differentiation protein 2	1.67131E-07	0.000108639	1.53	0.696	0.05
33	FAM57A	family with sequence similarity 57, member A	1.66678E-07	0.000108639	2.31	0.728	0.04
34	SLC25A37	solute carrier family 25, member 37	1.85113E-07	0.000108639	2.58	0.698	0
35	CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	1.82659E-07	0.000108639	1.59	0.718	0
36	GPR110	G protein-coupled receptor 110	1.58541E-07	0.000108639	1.91	0.671	0
37	F5	coagulation factor V	1.93673E-07	0.000108639	1.90	0.697	0
38	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	2.30293E-07	0.000111473	1.70	0.702	0.05
39	SLCO4A1	solute carrier organic anion transporter family, member 4A1	2.08897E-07	0.000111473	1.77	0.692	0.02
40	PRSS8	protease, serine, 8	2.18964E-07	0.000111473	1.67	0.723	0
41	C17orf76	chromosome 17 open reading frame 76	2.21776E-07	0.000111473	0.40	0.692	0
42	CYR61	cysteine-rich, angiogenic inducer, 61	2.30244E-07	0.000111473	1.51	0.698	0
43	MYO1B	myosin IB	2.42438E-07	0.000112017	1.91	0.673	0.02
44	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6	2.38535E-07	0.000112017	1.44	0.725	0.01
45	CXCL14	chemokine (C-X-C motif) ligand 14	2.53543E-07	0.000114545	1.52	0.726	0.17
46	SFTA3	surfactant associated 3	2.86533E-07	0.000119968	1.59	0.676	0.02
47	MET	met proto-oncogene	3.00953E-07	0.000119968	1.58	0.715	0.01
48	S1PR3	sphingosine-1-phosphate receptor 3	2.92768E-07	0.000119968	1.55	0.702	0.01
49	MARCKS	myristoylated alanine-rich protein kinase C substrate	3.00124E-07	0.000119968	2.42	0.733	0
50	ASB13	ankyrin repeat and SOCS box-containing 13	2.73898E-07	0.000119968	0.22	0.689	0
51	CRB3	crumbs homolog 3	2.97047E-07	0.000119968	1.80	0.696	0
52	RAB3D	RAB3D, member RAS oncogene family	3.13679E-07	0.000120323	2.36	0.736	0.01
53	TIMP1	TIMP metallopeptidase inhibitor 1	3.11884E-07	0.000120323	3.35	0.704	0
54	MXD1	MAX dimerization protein 1	3.38175E-07	0.000127317	3.00	0.689	0
55	AATK	apoptosis-associated tyrosine kinase	3.61342E-07	0.000128879	1.91	0.715	0.05

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56	RGL1	ral guanine nucleotide dissociation stimulator-like 1	3.6079E-07	0.000128879	2.13	0.734	0.01
57	NCKAP1	NCK-associated protein 1	3.60153E-07	0.000128879	2.27	0.659	0.01
58	CCNJL	cyclin J-like	3.70647E-07	0.000129518	2.36	0.691	0.09
59	SFN	stratifin	3.75876E-07	0.000129518	1.79	0.694	0
60	METTL7B	methyltransferase like 7B	3.83466E-07	0.000129931	1.99	0.711	0
61	ANKRD22	ankyrin repeat domain 22	4.38317E-07	0.000133129	1.63	0.719	0.22
62	AGR3	anterior gradient homolog 3	4.04675E-07	0.000133129	1.60	0.732	0.05
63	MERTK	c-mer proto-oncogene tyrosine kinase	4.42453E-07	0.000133129	1.95	0.745	0.04
64	CREB5	cAMP responsive element binding protein 5	4.1408E-07	0.000133129	4.66	0.704	0
65	LOC100132707	hypothetical LOC100132707	4.44656E-07	0.000133129	0.08	0.707	0
66	TPCN1	two pore segment channel 1	4.44161E-07	0.000133129	1.83	0.725	0
67	LOC100131733	hypothetical LOC100131733	4.45864E-07	0.000133129	0.26	0.710	0
68	CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	4.5184E-07	0.000133129	2.20	0.698	0
69	PRSS23	protease, serine, 23	4.16236E-07	0.000133129	1.64	0.698	0
70	LCP2	lymphocyte cytosolic protein 2	4.73558E-07	0.000137535	4.96	0.701	0
71	SCHIP1	schwannomin interacting protein 1	5.38759E-07	0.000154267	2.07	0.700	0
72	ANTXR2	anthrax toxin receptor 2	5.5269E-07	0.000156058	2.95	0.707	0
73	CXCR7	chemokine (C-X-C motif) receptor 7	6.66807E-07	0.000176428	0.49	0.716	0.03
74	SFTPB	surfactant protein B	6.54617E-07	0.000176428	1.45	0.730	0.03
75	PROK2	prokineticin 2	6.41857E-07	0.000176428	1.57	0.721	0.03
76	SFTA2	surfactant associated 2	6.68224E-07	0.000176428	1.64	0.696	0
77	MEF2C	myocyte enhancer factor 2C	6.556E-07	0.000176428	2.62	0.708	0
78	FA2H	fatty acid 2-hydroxylase	6.86837E-07	0.000179018	1.81	0.691	0.02
79	PLA2G7	phospholipase A2, group VII	7.2124E-07	0.000185605	2.13	0.724	0
80	ALPL	alkaline phosphatase, liver/bone/kidney	7.95627E-07	0.000202117	1.77	0.704	0.12
81	LOC100132234	similar to hCG2020055	8.38103E-07	0.000202117	0.31	0.716	0.03
82	PELI1	pellino homolog 1	8.45052E-07	0.000202117	3.49	0.708	0
83	SUSD2	sushi domain containing 2	8.40738E-07	0.000202117	1.61	0.720	0
84	SCGB3A2	secretoglobin, family 3A, member 2	8.20491E-07	0.000202117	2.19	0.699	0
85	IFNAR1	interferon –alpha receptor 1	8.28761E-07	0.000202117	10.84	0.709	0
86	SPRY2	sprouty homolog 2	8.67126E-07	0.000204469	3.04	0.723	0
87	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	8.75003E-07	0.000204469	1.91	0.679	0
88	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	9.26103E-07	0.000213951	2.71	0.704	0
89	CD24	CD24 molecule	9.68321E-07	0.000221191	2.02	0.707	0
90	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	1.03482E-06	0.000233755	1.63	0.682	0.01
91	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	1.05201E-06	0.000235026	1.52	0.709	0
92	FAM20A	family with sequence similarity 20, member A	1.1584E-06	0.000249807	2.06	0.724	0
93	LAMB3	laminin, beta 3	1.16732E-06	0.000249807	1.93	0.703	0
94	TRPM6	transient receptor potential cation channel, subfamily M, member 6	1.14138E-06	0.000249807	2.15	0.677	0
95	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B	1.16668E-06	0.000249807	3.44	0.695	0
96	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B)	1.21525E-06	0.0002563	5.40	0.666	0
97	CLIC6	chloride intracellular channel 6	1.22288E-06	0.0002563	1.65	0.669	0
98	SLC30A1	solute carrier family 30 (zinc transporter), member 1	1.25685E-06	0.000258703	3.65	0.685	0
99	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	1.25979E-06	0.000258703	0.24	0.682	0
100	SLC44A1	solute carrier family 44, member 1	1.31531E-06	0.000267378	3.27	0.674	0
101	PLEKHG2	pleckstrin homology domain containing, family G	1.32834E-06	0.000267378	2.61	0.714	0
102	LAPTM4B	lysosomal protein transmembrane 4 beta	1.37861E-06	0.000274776	2.79	0.733	0.05
103	RASSF2	Ras association	1.40342E-06	0.000277005	1.99	0.705	0
104	KANK1	KN motif and ankyrin repeat domains 1	1.43783E-06	0.000281067	1.91	0.740	0.03
105	SLC39A8	solute carrier family 39	1.47447E-06	0.000285485	2.59	0.698	0.01
106	SOD3	superoxide dismutase 3, extracellular	1.5802E-06	0.000303071	1.50	0.722	0.07
107	EPCAM	epithelial cell adhesion molecule	1.709E-06	0.000315559	1.54	0.700	0
108	SCEL	sciellin	1.71544E-06	0.000315559	1.67	0.672	0
109	CXCL17	chemokine (C-X-C motif) ligand 17	1.71167E-06	0.000315559	1.66	0.686	0
110	PAK1	p21 protein	1.72292E-06	0.000315559	7.73	0.683	0
111	DDHD1	DDHD domain containing 1	1.66597E-06	0.000315559	0.42	0.701	0
112	AKAP5	A kinase	1.74327E-06	0.000316434	0.57	0.693	0.02
113	GPR84	G protein-coupled receptor 84	1.82432E-06	0.000325338	2.40	0.696	0.01
114	CCL7	chemokine (C-C motif) ligand 7	1.82056E-06	0.000325338	1.64	0.717	0
115	FBLN5	fibulin 5	1.90667E-06	0.000331543	1.68	0.726	0.08
116	IRX2	iroquois homeobox 2	1.90805E-06	0.000331543	1.61	0.694	0

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117	EFNB1	ephrin-B1	1.89596E-06	0.000331543	0.33	0.665	0
118	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	1.96388E-06	0.000338353	1.87	0.689	0.01
119	LRRC70	leucine rich repeat containing 70	2.02443E-06	0.000343009	2.03	0.663	0.03
120	CHSY1	chondroitin sulfate synthase 1	2.02465E-06	0.000343009	4.17	0.694	0
121	CTTN	cortactin	2.08999E-06	0.000348275	1.76	0.711	0.01
122	PIM3	pim-3 oncogene	2.07622E-06	0.000348275	4.67	0.698	0
123	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	2.13682E-06	0.000353183	2.25	0.732	0
124	IER3	immediate early response 3	2.20683E-06	0.000353266	2.35	0.708	0
125	MYO1A	myosin IA	2.19298E-06	0.000353266	0.41	0.708	0
126	MGAM	maltase-glucoamylase (alpha-glucosidase)	2.18766E-06	0.000353266	1.96	0.669	0
127	TNNC1	troponin C type 1	2.16218E-06	0.000353266	2.28	0.696	0
128	KCNK1	potassium channel, subfamily K, member 1	2.23507E-06	0.000354991	1.92	0.701	0
129	F13A1	coagulation factor XIII, A1 polypeptide	2.32224E-06	0.000365977	1.86	0.702	0.03
130	FAM110C	family with sequence similarity 110, member C	2.34502E-06	0.000366724	2.51	0.654	0
131	TCEA3	transcription elongation factor A (SII), 3	2.4601E-06	0.000381785	0.48	0.703	0.04
132	LOC257358	hypothetical LOC257358	2.49079E-06	0.00038362	2.03	0.686	0
133	CLEC4G	C-type lectin domain family 4, member G	2.55824E-06	0.000391038	1.66	0.707	0.03
134	C3orf62	chromosome 3 open reading frame 62	2.57742E-06	0.000391038	0.25	0.693	0
135	CXCL1	chemokine (C-C motif) ligand 1	2.62174E-06	0.000392043	1.85	0.696	0
136	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa	2.62262E-06	0.000392043	12.88	0.673	0
137	FAM157A	family with sequence similarity 157, member A	2.65053E-06	0.000392771	2.16	0.656	0
138	NKX2-1	NK2 homeobox 1	2.66613E-06	0.000392771	1.53	0.662	0
139	RAB25	RAB25, member RAS oncogene family	2.68594E-06	0.000392843	1.77	0.687	0
140	ATP13A3	ATPase type 13A3	2.81343E-06	0.00040855	3.72	0.680	0
141	LOC151438	cDNA FLJ31315 fis, clone LIVER1000303	2.88507E-06	0.000415982	1.73	0.714	0.02
142	S1PR1	sphingosine-1-phosphate receptor 1	2.91347E-06	0.000417119	1.45	0.699	0.05
143	NLRP3	NLR family, pyrin domain containing 3	3.11331E-06	0.000442612	2.17	0.691	0
144	GABARAPL1	GABA (A) receptor-associated protein like 1	3.17631E-06	0.000446987	0.21	0.716	0
145	EMR2	egf-like module containing, mucin-like, hormone receptor-like 2	3.21004E-06	0.000446987	2.89	0.713	0
146	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	3.20288E-06	0.000446987	1.55	0.688	0
147	ADAM8	ADAM metallopeptidase domain 8	3.35166E-06	0.000456054	1.92	0.712	0
148	CSF3R	colony stimulating factor 3 receptor	3.36489E-06	0.000456054	2.29	0.674	0
149	PDE2A	phosphodiesterase 2A, cGMP-stimulated	3.32935E-06	0.000456054	2.40	0.701	0
150	ODC1	ornithine decarboxylase 1	3.3056E-06	0.000456054	12.27	0.687	0
151	SPON2	spondin 2, extracellular matrix protein	3.6292E-06	0.000485405	1.37	0.698	0
152	GJA1	gap junction protein, alpha 1, 43kDa	3.60857E-06	0.000485405	1.91	0.670	0
153	PLIN4	perilipin 4	3.66511E-06	0.000487005	1.79	0.686	0
154	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	3.95358E-06	0.000521924	1.79	0.705	0.01
155	MYO5C	myosin VC	3.98907E-06	0.000523211	1.68	0.661	0.02
156	PXN	paxillin	4.07267E-06	0.000527372	1.62	0.703	0
157	CDKL1	cyclin-dependent kinase-like 1	4.0622E-06	0.000527372	0.14	0.692	0
158	CCL2	chemokine (C-C motif) ligand 2	4.17565E-06	0.000533906	1.69	0.743	0.02
159	TMEM30B	transmembrane protein 30B	4.16236E-06	0.000533906	1.80	0.664	0
160	TRIM47	tripartite motif-containing 47	4.24196E-06	0.000538835	2.33	0.730	0
161	CD300E	CMRF35-like molecule 2 Precursor	4.26722E-06	0.000538835	2.12	0.680	0
162	TBC1D14	TBC1 domain family, member 14	4.35707E-06	0.000546785	5.47	0.702	0
163	MATK	megakaryocyte-associated tyrosine kinase	4.38984E-06	0.000547518	2.19	0.711	0
164	NOV	nephroblastoma overexpressed gene	4.4781E-06	0.000555121	1.84	0.709	0
165	IL1R2	interleukin 1 receptor, type II	5.10483E-06	0.000617072	1.48	0.720	0.03
166	EPHA4	EPH receptor A4	5.01837E-06	0.000617072	1.95	0.697	0.03
167	PDCD1LG2	programmed cell death 1 ligand 2	5.05752E-06	0.000617072	0.57	0.702	0
168	PTPRF	protein tyrosine phosphatase, receptor type, F	5.12962E-06	0.000617072	1.63	0.711	0
169	ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	5.12386E-06	0.000617072	3.06	0.696	0
170	PTPRE	protein tyrosine phosphatase, receptor type, E	5.1782E-06	0.000619252	2.48	0.676	0
171	TCEB1	transcription elongation factor B (SIII), polypeptide 1	5.40519E-06	0.000638881	11.77	0.683	0
172	TMEM2	transmembrane protein 2	5.39491E-06	0.000638881	3.16	0.686	0
173	FNBP1L	formin binding protein 1-like	5.53398E-06	0.000650322	1.75	0.686	0.03
174	WWC1	WW and C2 domain containing 1	5.65886E-06	0.000661176	1.82	0.674	0
175	TDG	thymine-DNA glycosylase	5.90095E-06	0.000685521	8.20	0.696	0
176	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	5.9825E-06	0.00068779	1.71	0.684	0.01
177	COX15	COX15 homolog, cytochrome c oxidase assembly protein	5.98814E-06	0.00068779	0.39	0.696	0

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178	FNIP2	folliculin interacting protein 2	6.21284E-06	0.000708866	3.57	0.694	0
179	PAWR	PRKC, apoptosis, WT1, regulator	6.24137E-06	0.000708866	1.91	0.698	0
180	FJX1	four jointed box 1	6.34685E-06	0.000716842	2.08	0.705	0
181	ANXA3	annexin A3	6.44205E-06	0.000723574	1.90	0.703	0.01
182	SNAI1	snail homolog 1	6.48829E-06	0.000724763	1.83	0.690	0.02
183	TMEM98	transmembrane protein 98	6.57185E-06	0.000730085	1.58	0.676	0
184	TMEM125	transmembrane protein 125	6.61312E-06	0.000730677	1.68	0.706	0
185	ZBTB4	zinc finger and BTB domain containing 4	6.69227E-06	0.000735427	0.06	0.727	0
186	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	6.86525E-06	0.000746367	0.39	0.669	0
187	TREML2	triggering receptor expressed on myeloid cells-like 2	6.844E-06	0.000746367	2.00	0.711	0
188	HIF1A	hypoxia inducible factor 1, alpha subunit	7.10063E-06	0.000764846	3.76	0.654	0
189	ACPP	acid phosphatase, prostate	7.11047E-06	0.000764846	1.73	0.673	0
190	WIF1	WNT inhibitory factor 1	7.19373E-06	0.000769729	1.57	0.665	0
191	SPP1	secreted phosphoprotein 1	7.35129E-06	0.00078247	1.68	0.741	0.01
192	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A	7.47319E-06	0.000783144	1.88	0.696	0
193	PPIF	peptidylprolyl isomerase F	7.47046E-06	0.000783144	4.30	0.667	0
194	CTSE	cathepsin E	7.45685E-06	0.000783144	1.73	0.681	0
195	HOMER3	homer homolog 3	7.79689E-06	0.000808729	3.37	0.727	0
196	F2RL1	coagulation factor II (thrombin) receptor-like 1	7.76966E-06	0.000808729	1.73	0.681	0
197	ZNF570	zinc finger protein 570	8.05592E-06	0.000831354	0.23	0.679	0
198	MMP24	matrix metallopeptidase 24	8.30412E-06	0.00085264	1.63	0.668	0
199	STEAP4	STEAP family member 4	8.58155E-06	0.000864992	1.54	0.738	0.09
200	SLC16A1	solute carrier family 16, member 1	8.50399E-06	0.000864992	2.77	0.702	0.08
201	PRKCB	protein kinase C, beta	8.51983E-06	0.000864992	1.68	0.684	0.01
202	OASL	2'-5'-oligoadenylate synthetase-like	8.61643E-06	0.000864992	0.42	0.703	0
203	VAV3	vav 3 guanine nucleotide exchange factor	8.64866E-06	0.000864992	3.13	0.667	0
204	FZD2	frizzled homolog 2	8.6797E-06	0.000864992	3.96	0.703	0
205	AMPD3	adenosine monophosphate deaminase	8.75046E-06	0.00086774	1.95	0.692	0
206	C5orf62	chromosome 5 open reading frame 62	8.83533E-06	0.00086774	2.48	0.668	0
207	MEX3A	mex-3 homolog A	8.8347E-06	0.00086774	2.01	0.643	0
208	C9orf89	chromosome 9 open reading frame 89	9.35221E-06	0.000914088	4.14	0.690	0
209	RTCD1	RNA terminal phosphate cyclase domain 1	9.41524E-06	0.000915846	9.29	0.706	0
210	FCAR	Fc fragment of IgA, receptor for	9.55356E-06	0.000918051	1.69	0.713	0.07
211	SELL	selectin L	9.49608E-06	0.000918051	1.49	0.676	0.02
212	LOC388780	hypothetical LOC388780	9.57338E-06	0.000918051	1.69	0.675	0
213	NPL	N-acetylneuraminate pyruvate lyase	9.62989E-06	0.000919134	5.49	0.683	0
214	FERMT2	fermitin family homolog 2	9.77173E-06	0.000928314	1.68	0.685	0
215	CECR6	cat eye syndrome chromosome region, candidate 6	9.94253E-06	0.000935795	2.05	0.716	0.01
216	SPINT2	serine peptidase inhibitor, Kunitz type, 2	9.91908E-06	0.000935795	0.16	0.704	0
217	SLC7A2	solute carrier family 7	9.99032E-06	0.000935959	2.56	0.653	0
218	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	1.02391E-05	0.000952112	2.39	0.701	0.01
219	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	1.02564E-05	0.000952112	1.83	0.683	0
220	TRIM21	tripartite motif-containing 21	1.03378E-05	0.00095531	0.28	0.668	0
221	UCK2	uridine-cytidine kinase 2	1.04892E-05	0.000964914	3.64	0.713	0
222	NIPAL4	NIPA-like domain containing 4	1.06427E-05	0.000974624	1.80	0.640	0.02
223	SH3D19	SH3 domain containing 19	1.07889E-05	0.00098358	1.75	0.694	0.01
224	SEPT4	septin 4	1.09386E-05	0.000987911	0.51	0.705	0.18
225	HS3ST3B1	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1	1.09194E-05	0.000987911	1.67	0.706	0.01
226	FBLIM1	filamin binding LIM protein 1	1.09822E-05	0.000987911	2.23	0.659	0
227	HAMP	hepcidin antimicrobial peptide	1.13217E-05	0.001011312	2.09	0.692	0
228	VSTM2L	V-set and transmembrane domain containing 2 like	1.13418E-05	0.001011312	1.85	0.644	0
229	SLC20A1	solute carrier family 20	1.19543E-05	0.001052085	3.88	0.685	0
230	RGL4	ral guanine nucleotide dissociation stimulator-like 4	1.19091E-05	0.001052085	1.51	0.692	0
231	ST6GALNAC1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1	1.19455E-05	0.001052085	1.68	0.673	0
232	BRD4	bromodomain containing 4	1.20435E-05	0.001055368	2.17	0.676	0.01
233	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8	1.21409E-05	0.001059335	0.23	0.665	0
234	MGC4859	hypothetical protein MGC4859 similar to HSPA8	1.25519E-05	0.001088665	0.24	0.697	0
235	C1orf182	chromosome 1 open reading frame 182	1.25842E-05	0.001088665	0.37	0.685	0
236	ZNF32	zinc finger protein 32	1.26659E-05	0.00109109	0.19	0.681	0
237	MMP1	matrix metallopeptidase 1	1.30717E-05	0.001107281	1.68	0.693	0.01
238	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.29382E-05	0.001107281	3.20	0.722	0

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239	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	1.30017E-05	0.001107281	2.14	0.667	0
240	GGCT	gamma-glutamyl cyclotransferase	1.30238E-05	0.001107281	5.61	0.662	0
241	ZNF814	zinc finger protein 814	1.31909E-05	0.001112739	0.16	0.663	0
242	BASP1	brain abundant, membrane attached signal protein 1	1.33681E-05	0.001123028	2.52	0.685	0
243	ANO5	anoctamin 5	1.38112E-05	0.001155479	0.58	0.664	0
244	C6orf154	chromosome 6 open reading frame 154	1.44798E-05	0.001206455	1.91	0.676	0.01
245	SSTR2	somatostatin receptor 2	1.49259E-05	0.001238547	1.79	0.729	0.08
246	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	1.54398E-05	0.001275981	2.61	0.679	0
247	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	1.59254E-05	0.001300251	0.50	0.715	0.11
248	MYBPH	myosin binding protein H	1.59154E-05	0.001300251	1.91	0.690	0
249	MYC	v-myc myelocytomatosis viral oncogene homolog	1.58965E-05	0.001300251	2.52	0.704	0
250	CCL4	chemokine (CC-motif) ligand 4	1.62314E-05	0.001317579	1.91	0.687	0
251	TMEM154	transmembrane protein 154	1.62672E-05	0.001317579	1.70	0.697	0
252	SERPING1	serpin peptidase inhibitor, clade G	1.64413E-05	0.001325522	0.69	0.664	0.01
253	FSTL1	follistatin-like 1	1.64957E-05	0.001325522	1.83	0.677	0
254	TKTL1	transketolase-like 1	1.66409E-05	0.001326702	1.61	0.663	0.03
255	PLA2G16	phospholipase A2, group XVI	1.66013E-05	0.001326702	0.39	0.688	0
256	FDFT1	farnesyl-diphosphate farnesyltransferase 1	1.70953E-05	0.001352327	0.24	0.674	0
257	MRS2	MRS2 magnesium homeostasis factor homolog	1.70895E-05	0.001352327	0.15	0.678	0
258	SH3RF1	SH3 domain containing ring finger 1	1.76644E-05	0.001391924	1.89	0.719	0.05
259	CLEC6A	C-type lectin domain family 6, member A	1.79663E-05	0.001404829	0.62	0.703	0.03
260	SGK1	serum/glucocorticoid regulated kinase 1	1.79441E-05	0.001404829	3.29	0.678	0
261	C6orf192	chromosome 6 open reading frame 192	1.81992E-05	0.001417583	2.03	0.678	0
262	ELF3	E74-like factor 3	1.82695E-05	0.001417632	1.60	0.680	0
263	PARVA	parvin, alpha	1.85266E-05	0.001432117	2.49	0.654	0
264	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	1.88501E-05	0.001451604	0.46	0.677	0
265	EGR3	early growth response 3	1.90237E-05	0.001453955	1.65	0.722	0.2
266	LOC100132344	cDNA FLJ43495 fis, clone PEBLM2000338.	1.90136E-05	0.001453955	2.13	0.698	0
267	ARID5B	AT rich interactive domain 5B	1.94663E-05	0.001482209	1.77	0.710	0.01
268	LOC730227	cDNA FLJ14231 fis, clone NT2RP3004470	1.9764E-05	0.001499264	2.58	0.648	0
269	FABP4	fatty acid binding protein 4, adipocyte	2.0209E-05	0.001527318	0.72	0.664	0.01
270	SPAG9	sperm associated antigen 9	2.07135E-05	0.001559647	5.13	0.685	0
271	ARHGAP20	Rho GTPase activating protein 20	2.17676E-05	0.001632973	2.84	0.637	0
272	KRT23	keratin 23	2.27313E-05	0.001688739	1.57	0.674	0
273	PDE3A	phosphodiesterase 3A, cGMP-inhibited	2.26062E-05	0.001688739	2.43	0.632	0
274	MBOAT7	membrane bound O-acyltransferase domain containing 7	2.27602E-05	0.001688739	2.72	0.679	0
275	MRO	maestro	2.30366E-05	0.001697552	1.97	0.689	0.15
276	ASPRV1	aspartic peptidase, retroviral-like 1	2.3046E-05	0.001697552	1.94	0.693	0
277	KRT19	keratin 19	2.33242E-05	0.001711844	1.50	0.697	0
278	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	2.36583E-05	0.001730117	1.75	0.637	0.03
279	ASB10	ankyrin repeat and SOCS box-containing 10	2.40608E-05	0.001734597	0.48	0.697	0
280	MPP6	membrane protein, palmitoylated 6	2.40236E-05	0.001734597	2.12	0.679	0
281	LOC100130633	ZMYM6 proteinZinc finger, MYM-type 6, isoform CRA_a	2.39418E-05	0.001734597	0.23	0.678	0
282	MUC1	mucin 1, cell surface associated	2.39842E-05	0.001734597	1.53	0.682	0
283	ANGPTL4	angiopoietin-like 4	2.43277E-05	0.001736212	1.52	0.699	0.01
284	SELENBP1	selenium binding protein 1	2.45102E-05	0.001736212	1.54	0.680	0.01
285	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	2.42934E-05	0.001736212	1.70	0.682	0
286	CD93	CD93 molecule	2.4472E-05	0.001736212	1.75	0.677	0
287	PGM5	phosphoglucomutase 5	2.43612E-05	0.001736212	0.47	0.689	0
288	ADORA3	adenosine A3 receptor	2.46788E-05	0.00174208	1.87	0.693	0.02
289	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	2.49417E-05	0.001754552	2.27	0.690	0
290	ZNF124	zinc finger protein 124	2.51169E-05	0.001760784	0.28	0.687	0
291	CYBA	cytochrome b-245, alpha polypeptide	2.54225E-05	0.001776083	0.11	0.637	0
292	GPR125	G protein-coupled receptor 125	2.5756E-05	0.001793218	1.80	0.670	0
293	LHFPL2	lipoma HMGIC fusion partner-like 2	2.64189E-05	0.00183309	5.11	0.722	0
294	CD177	CD177 molecule	2.71023E-05	0.001874117	1.52	0.646	0
295	PEBP1	phosphatidylethanolamine binding protein 1	2.73508E-05	0.001884886	0.15	0.654	0
296	TRAF5	TNF receptor-associated factor 5	2.74658E-05	0.001886418	2.05	0.676	0
297	TMEM158	transmembrane protein 158	2.7822E-05	0.001904447	1.83	0.695	0
298	MMP9	matrix metallopeptidase 9	2.85712E-05	0.001929745	1.50	0.681	0
299	MYO1D	myosin ID	2.84006E-05	0.001929745	1.70	0.691	0

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300	SEC14L1	SEC14-like 1	2.85149E-05	0.001929745	4.24	0.665	0
301	INHBB	inhibin, beta B	2.83124E-05	0.001929745	1.55	0.681	0
302	MMP10	matrix metallopeptidase 10	2.95449E-05	0.001982333	1.36	0.664	0
303	BCL2L13	BCL2-like 13	2.95151E-05	0.001982333	0.24	0.700	0
304	PARK2	Parkin	2.99155E-05	0.002000597	0.46	0.686	0
305	ITGB4	integrin, beta 4	3.02366E-05	0.002015443	1.77	0.667	0
306	RGS2	regulator of G-protein signaling 2, 24kDa	3.05761E-05	0.002031412	1.65	0.671	0
307	LIMCH1	LIM and calponin homology domains 1	3.15663E-05	0.002090367	1.63	0.687	0
308	ICAM1	intercellular adhesion molecule 1	3.19361E-05	0.002104759	2.32	0.669	0
309	ASS1	argininosuccinate synthetase 1	3.19907E-05	0.002104759	1.58	0.667	0
310	DBN1	drebrin 1	3.30089E-05	0.002157783	1.72	0.716	0
311	LOC100293193	hypothetical LOC100293193	3.30071E-05	0.002157783	1.76	0.688	0
312	TBC1D4	TBC1 domain family, member 4	3.35403E-05	0.002185492	0.50	0.686	0
313	PCDH20	protocadherin 20	3.49331E-05	0.002268979	2.39	0.621	0
314	CGNL1	cingulin-like 1	3.57374E-05	0.002313827	1.57	0.647	0
315	MGC16703	tubulin, alpha pseudogene	3.60628E-05	0.002315387	0.36	0.692	0.05
316	RNASE2	ribonuclease, RNase A family, 2	3.61032E-05	0.002315387	1.90	0.691	0
317	CD163	CD163 molecule	3.60982E-05	0.002315387	3.09	0.713	0
318	HES4	hairy and enhancer of split 4	3.66033E-05	0.002340082	1.78	0.668	0
319	BTN2A2	butyrophilin, subfamily 2, member A2	3.69664E-05	0.002355886	0.18	0.678	0
320	CNN3	calponin 3, acidic	3.78961E-05	0.002407587	1.61	0.649	0
321	SYNJ2	synaptojanin 2	3.80925E-05	0.002412522	2.23	0.672	0
322	GHRL	ghrelin/obestatin prepropeptide	3.89487E-05	0.002436394	2.02	0.701	0
323	PTPRK	protein tyrosine phosphatase, receptor type, K	3.88557E-05	0.002436394	1.55	0.673	0
324	SDCCAG3	serologically defined colon cancer antigen 3	3.88124E-05	0.002436394	11.83	0.702	0
325	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	3.87964E-05	0.002436394	0.21	0.705	0
326	DCLK1	doublecortin-like kinase 1	3.96816E-05	0.002473092	2.02	0.647	0
327	FAM83E	family with sequence similarity 83, member E	3.97787E-05	0.002473092	1.84	0.682	0
328	SLPI	secretory leukocyte peptidase inhibitor	4.06496E-05	0.002511748	1.56	0.700	0.01
329	LRG1	leucine-rich alpha-2-glycoprotein 1	4.08947E-05	0.002511748	1.90	0.676	0
330	ABCB6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	4.08818E-05	0.002511748	2.58	0.690	0
331	C7orf58	chromosome 7 open reading frame 58	4.0843E-05	0.002511748	0.63	0.659	0
332	FBXL13	F-box and leucine-rich repeat protein 13	4.1022E-05	0.002511982	2.23	0.660	0
333	SLC43A1	solute carrier family 43, member 1	4.21551E-05	0.002573615	1.91	0.704	0
334	TMEM54	transmembrane protein 54	4.27579E-05	0.002602597	2.03	0.658	0
335	CLDN4	claudin 4	4.42822E-05	0.002687335	1.43	0.685	0
336	CRYBB1	crystallin, beta B1	4.47193E-05	0.002705785	1.69	0.676	0.04
337	COL1A1	collagen, type I, alpha 1	4.4927E-05	0.002710285	1.50	0.713	0.13
338	TMEM71	transmembrane protein 71	4.51247E-05	0.002714157	1.98	0.670	0
339	CREM	cAMP responsive element modulator	4.57204E-05	0.002725792	2.48	0.705	0
340	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	4.56568E-05	0.002725792	1.71	0.663	0
341	LOC644231	similar to WAS protein homolog associated with actin, golgi membranes	4.56396E-05	0.002725792	0.33	0.700	0
342	C4BPA	complement component 4 binding protein, alpha	4.67291E-05	0.002777782	1.80	0.680	0
343	RGNEF	Rho-guanine nucleotide exchange factor	4.73732E-05	0.002807863	0.72	0.648	0
344	MPO	myeloperoxidase	4.80811E-05	0.002828107	1.60	0.675	0
345	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	4.81321E-05	0.002828107	2.68	0.696	0
346	LCN2	lipocalin 2	4.79111E-05	0.002828107	1.48	0.662	0
347	GRAMD1C	GRAM domain containing 1C	4.84162E-05	0.002836602	1.89	0.663	0
348	VNN3	vanin 3	5.01877E-05	0.002931944	1.71	0.658	0
349	CH25H	cholesterol 25-hydroxylase	5.06436E-05	0.002950097	1.78	0.684	0
350	HGF	hepatocyte growth factor	5.09702E-05	0.002960642	1.88	0.656	0
351	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	5.1362E-05	0.0029749	1.76	0.671	0.01
352	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	5.16538E-05	0.002983301	0.57	0.682	0
353	ANKRD58	ankyrin repeat domain 58	5.18507E-05	0.002986189	0.28	0.666	0
354	EMP1	epithelial membrane protein 1	5.23494E-05	0.002999008	1.95	0.698	0
355	WDR70	WD repeat domain 70	5.23683E-05	0.002999008	0.11	0.670	0
356	RHOBTB3	Rho-related BTB domain containing 3	5.2855E-05	0.003018379	1.88	0.701	0.02
357	ECM1	extracellular matrix protein 1	5.30201E-05	0.003019322	2.13	0.687	0
358	FOLR3	folate receptor 3	5.33751E-05	0.00303105	0.53	0.714	0.05
359	SFTPA1	surfactant protein A1	5.39447E-05	0.003038217	1.44	0.680	0
360	RBM28	RNA binding motif protein 28	5.40991E-05	0.003038217	19.24	0.680	0

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361	IFT20	intraflagellar transport 20 homolog	5.39904E-05	0.003038217	0.23	0.679	0
362	UBE2G2	ubiquitin-conjugating enzyme E2G 2	5.39257E-05	0.003038217	0.11	0.688	0
363	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	5.44377E-05	0.003040434	8.79	0.656	0
364	GPR56	G protein-coupled receptor 56	5.43706E-05	0.003040434	1.42	0.692	0
365	MYLIP	myosin regulatory light chain interacting protein	5.49383E-05	0.003059987	2.36	0.681	0
366	EGR4	early growth response 4	5.68633E-05	0.003158554	2.37	0.654	0
367	ABHD14A	abhydrolase domain containing 14A	5.70827E-05	0.003158695	0.11	0.659	0
368	CMKLR1	chemokine-like receptor 1	5.7332E-05	0.003158695	1.96	0.722	0
369	FAM20C	family with sequence similarity 20, member C	5.7263E-05	0.003158695	2.72	0.681	0
370	C2orf80	chromosome 2 open reading frame 80	5.81267E-05	0.003185216	1.62	0.657	0.03
371	IGFBP7	insulin-like growth factor binding protein 7	5.80442E-05	0.003185216	2.66	0.682	0
372	SOBP	sine oculis binding protein homolog	5.88709E-05	0.003214025	0.59	0.652	0
373	LOC283454	cDNA FLJ37411 fis, clone BRAMY2028682	5.89686E-05	0.003214025	1.75	0.619	0
374	CFI	complement factor I	5.95914E-05	0.003239288	1.62	0.652	0.01
375	MT1G	metallothionein 1G	5.99001E-05	0.003247385	1.94	0.682	0
376	FANCD2	Fanconi anemia, complementation group D2	6.03229E-05	0.003261605	0.39	0.674	0
377	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	6.07168E-05	0.0032742	1.89	0.647	0
378	ADORA2A	adenosine A2a receptor	6.16498E-05	0.003306967	1.57	0.674	0.01
379	RIBC2	RIB43A domain with coiled-coils 2	6.14988E-05	0.003306967	1.77	0.676	0.01
380	QPCT	glutaminyl-peptide cyclotransferase	6.31314E-05	0.003359845	2.64	0.680	0
381	LAMA3	laminin, alpha 3	6.31062E-05	0.003359845	1.64	0.646	0
382	NGEF	neuronal guanine nucleotide exchange factor	6.29942E-05	0.003359845	2.40	0.672	0
383	CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	6.39957E-05	0.003396949	2.29	0.673	0
384	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	6.44431E-05	0.003397916	3.19	0.662	0
385	MREG	melanoregulin	6.45153E-05	0.003397916	2.28	0.672	0
386	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	6.42701E-05	0.003397916	4.07	0.671	0
387	PLEKHB1	pleckstrin homology domain containing, family B	6.49593E-05	0.003401715	0.32	0.674	0
388	C6orf108	chromosome 6 open reading frame 108	6.53824E-05	0.003401715	6.14	0.714	0
389	CLEC12A	C-type lectin domain family 12, member A	6.52923E-05	0.003401715	0.34	0.696	0
390	PLIN5	perilipin 5	6.5424E-05	0.003401715	1.50	0.648	0
391	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	6.53105E-05	0.003401715	1.73	0.673	0
392	PIPOX	pipecolic acid oxidase	6.56588E-05	0.003405211	0.24	0.691	0
393	LOC100128697	cDNA FLJ42049 fis, clone SPLEN2041720.	6.60324E-05	0.003415875	2.60	0.630	0
394	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	6.6201E-05	0.003415906	5.31	0.667	0
395	TMEM55A	transmembrane protein 55A	6.72446E-05	0.00346097	2.29	0.662	0
396	FOXA2	forkhead box A2	6.79982E-05	0.003490916	1.67	0.646	0
397	RNF145	ring finger protein 145	6.94399E-05	0.003555953	3.05	0.665	0
398	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	6.99301E-05	0.00357206	0.47	0.668	0
399	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	7.07514E-05	0.00358915	1.39	0.668	0.05
400	TRPM2	transient receptor potential cation channel, subfamily M, member 2	7.09709E-05	0.00358915	2.27	0.667	0
401	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	7.07892E-05	0.00358915	1.86	0.678	0
402	SHQ1	SHQ1 homolog	7.09167E-05	0.00358915	0.38	0.676	0
403	GALM	galactose mutarotase (aldose 1-epimerase)	7.16655E-05	0.003602155	3.41	0.648	0
404	VENTX	VENT homeobox homolog	7.16021E-05	0.003602155	1.75	0.696	0
405	ATL1	atlastin GTPase 1	7.17596E-05	0.003602155	0.60	0.647	0
406	MALL	mal, T-cell differentiation protein-like	7.23711E-05	0.003615404	1.54	0.689	0
407	PKN2	protein kinase N2	7.23792E-05	0.003615404	0.53	0.699	0
408	PDZK1IP1	PDZK1 interacting protein 1	7.35631E-05	0.003656573	1.60	0.682	0
409	LOC729040	hypothetical LOC729040	7.35498E-05	0.003656573	1.55	0.661	0
410	TMEM107	transmembrane protein 107	7.42695E-05	0.003682682	0.06	0.680	0
411	TUBB3	tubulin, beta 3	7.53284E-05	0.003717054	1.44	0.684	0
412	HIC1	hypermethylated in cancer 1	7.52797E-05	0.003717054	1.74	0.660	0
413	BCL3	B-cell CLL/lymphoma 3	7.61682E-05	0.003749395	2.18	0.674	0
414	AXL	AXL receptor tyrosine kinase	7.70072E-05	0.003781539	0.60	0.657	0
415	ASGR2	asialoglycoprotein receptor 2	7.76713E-05	0.003804958	1.46	0.667	0
416	RTN3	reticulon 3	7.81058E-05	0.003817045	0.46	0.651	0
417	PHLDA3	pleckstrin homology-like domain, family A, member 3	7.92432E-05	0.003863345	0.66	0.681	0
418	NLRP6	NLR family, pyrin domain containing 6	8.42153E-05	0.004095927	1.81	0.653	0.01
419	FERMT1	fermitin family homolog 1	8.50126E-05	0.004124834	1.93	0.684	0
420	SULF2	sulfatase 2	8.66136E-05	0.00418255	1.53	0.676	0
421	MOGAT1	monoacylglycerol O-acyltransferase 1	8.64988E-05	0.00418255	0.72	0.653	0

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422	PRODH	proline dehydrogenase (oxidase) 1	8.81372E-05	0.004246041	1.77	0.674	0
423	PERP	PERP, TP53 apoptosis effector	8.84171E-05	0.004249453	1.61	0.707	0
424	OR5F1	olfactory receptor, family 5, subfamily F, member 1	9.021E-05	0.004325401	0.42	0.665	0
425	PTEN	phosphatase and tensin homolog	9.15451E-05	0.004379085	3.68	0.669	0
426	TUSC3	tumor suppressor candidate 3	9.20431E-05	0.004392574	2.03	0.661	0
427	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	9.24713E-05	0.004402675	2.01	0.655	0
428	NOTCH3	Notch homolog 3	9.28344E-05	0.004405319	1.93	0.673	0
429	LBR	lamin B receptor	9.29602E-05	0.004405319	2.30	0.674	0
430	PBLD	phenazine biosynthesis-like protein domain containing	9.42122E-05	0.004435263	0.45	0.666	0.01
431	MRPL49	mitochondrial ribosomal protein L49	9.41747E-05	0.004435263	0.07	0.668	0
432	LEP	leptin	9.42466E-05	0.004435263	1.79	0.681	0
433	PHC2	polyhomeotic homolog 2	9.5298E-05	0.004466215	3.43	0.676	0
434	STARD7	StAR-related lipid transfer (START) domain containing 7	9.55634E-05	0.004466215	0.17	0.641	0
435	CLDN3	claudin 3	9.54944E-05	0.004466215	1.46	0.675	0
436	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	9.65371E-05	0.004482609	1.93	0.702	0.01
437	DSP	desmoplakin	9.63708E-05	0.004482609	1.54	0.654	0
438	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	9.65756E-05	0.004482609	1.58	0.682	0
439	HSPA4	heat shock 70kDa protein 4	9.89049E-05	0.004580265	6.24	0.654	0
440	CXCR4	chemokine (C-X-C motif) receptor 4	0.000100242	0.004629405	1.91	0.670	0
441	MPZL2	myelin protein zero-like 2	0.000100421	0.004629405	0.43	0.629	0
442	MT1X	metallothionein 1X	0.000100966	0.004643214	2.52	0.645	0
443	C20orf96	chromosome 20 open reading frame 96	0.000101178	0.004643214	0.51	0.671	0
444	TRIM7	tripartite motif-containing 7	0.000102908	0.004711999	2.03	0.679	0
445	FRMD4B	FERM domain containing 4B	0.000104751	0.00475512	3.76	0.685	0
446	OAF	OAF homolog	0.00010557	0.00475512	1.58	0.674	0
447	MAPK13	mitogen-activated protein kinase 13	0.000105369	0.00475512	2.97	0.663	0
448	FAM65B	family with sequence similarity 65, member B	0.000104423	0.00475512	1.47	0.673	0
449	IFITM2	interferon induced transmembrane protein 2 (1-8D)	0.000104147	0.00475512	1.88	0.660	0
450	CYSLTR1	cysteinyl leukotriene receptor 1	0.000105807	0.00475512	0.39	0.682	0
451	LOC440335	hypothetical LOC440335	0.000106189	0.00475512	1.53	0.673	0
452	PCDH12	protocadherin 12	0.000105092	0.00475512	2.17	0.648	0
453	MYL6B	myosin, light chain 6B, alkali, smooth muscle and non-muscle	0.000105525	0.00475512	4.74	0.672	0
454	SMAD4	SMAD family member 4	0.000106097	0.00475512	0.26	0.680	0
455	PON3	paraoxonase 3	0.000106883	0.004775668	1.79	0.662	0
456	SAT1	spermidine/spermine N1-acetyltransferase 1	0.000107529	0.004794002	4.89	0.661	0
457	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3	0.000109196	0.004857662	6.11	0.663	0
458	FOXQ1	forkhead box Q1	0.000110141	0.004889013	1.55	0.670	0
459	PTS	6-pyruvoyltetrahydropterin synthase	0.000110618	0.004899477	6.88	0.671	0
460	GPRIN2	G protein regulated inducer of neurite outgrowth 2	0.000110917	0.004902055	1.76	0.644	0
461	FIG4	FIG4 homolog, SAC1 lipid phosphatase domain containing	0.000111464	0.004915546	0.38	0.650	0
462	KIF1B	kinesin family member 1B	0.000112497	0.004939676	4.23	0.672	0
463	CGN	cingulin	0.000112309	0.004939676	1.52	0.654	0
464	SNN	stannin	0.000113578	0.004976401	2.62	0.667	0
465	NTNG2	netrin G2	0.000114493	0.005005687	1.76	0.663	0
466	PIGY	phosphatidylinositol glycan anchor biosynthesis, class Y	0.000114756	0.005006405	0.31	0.663	0
467	PI3	peptidase inhibitor 3, skin-derived	0.000115273	0.005018206	1.45	0.680	0
468	TIMP4	TIMP metallopeptidase inhibitor 4	0.000117956	0.005117366	1.64	0.672	0
469	BCL2L15	BCL2-like 15	0.00011848	0.005117366	0.44	0.705	0
470	KRT6A	keratin 6A	0.000118558	0.005117366	1.82	0.642	0
471	HTR7	5-hydroxytryptamine	0.00011819	0.005117366	3.91	0.677	0
472	NR2F2	nuclear receptor subfamily 2, group F, member 2	0.000119397	0.005133264	1.86	0.657	0.01
473	S1PR2	sphingosine-1-phosphate receptor 2	0.000119431	0.005133264	3.24	0.671	0
474	DBR1	debranching enzyme homolog 1	0.000120647	0.005174568	0.45	0.660	0
475	GPD1	glycerol-3-phosphate dehydrogenase 1	0.000121103	0.005183196	0.70	0.654	0
476	MSRB3	methionine sulfoxide reductase B3	0.000121658	0.005196043	2.35	0.633	0
477	CIB1	calcium and integrin binding 1	0.00012253	0.005216959	0.15	0.689	0
478	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)	0.000122661	0.005216959	2.24	0.683	0
479	TPD52L2	tumor protein D52-like 2	0.00012404	0.005264596	3.37	0.669	0
480	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	0.000124331	0.005265934	1.40	0.706	0
481	SPNS2	spinster homolog 2	0.000125317	0.005296647	1.88	0.663	0
482	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	0.000126267	0.005325734	0.54	0.633	0

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483	SLC26A9	solute carrier family 26, member 9	0.00012653	0.005325782	2.03	0.639	0
484	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.000126894	0.005330061	2.64	0.657	0
485	TMEM132A	transmembrane protein 132A	0.000127583	0.005347964	1.81	0.682	0
486	PRCD	progressive rod-cone degeneration	0.000128222	0.005363706	0.41	0.660	0
487	C6orf47	chromosome 6 open reading frame 47	0.000128571	0.005367258	0.35	0.638	0
488	C19orf33	chromosome 19 open reading frame 33	0.000129899	0.005411585	1.80	0.671	0
489	DNAH5	dynein, axonemal, heavy chain 5	0.000130295	0.005416974	1.93	0.633	0
490	IL1RN	interleukin 1 receptor antagonist	0.000131642	0.005445567	2.40	0.676	0
491	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	0.000131786	0.005445567	1.79	0.655	0
492	DGKD	diacylglycerol kinase, delta 130kDa	0.000131738	0.005445567	2.00	0.665	0
493	PLK3	polo-like kinase 3	0.000135638	0.005593367	3.26	0.679	0
494	APCDD1	adenomatosis polyposis coli down-regulated 1	0.000137224	0.0056473	1.84	0.650	0
495	LY6E	lymphocyte antigen 6 complex, locus E	0.000137806	0.005658479	0.46	0.657	0
496	RAB21	RAB21, member RAS oncogene family	0.000138052	0.005658479	13.04	0.653	0
497	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	0.000138961	0.005684261	7.56	0.663	0
498	OLFML2B	olfactomedin-like 2B	0.000139421	0.005687297	2.24	0.663	0
499	UBXN8	UBX domain protein 8	0.000139595	0.005687297	5.22	0.662	0
500	TTYH3	tweety homolog 3	0.000140301	0.005693247	2.51	0.651	0
501	ABHD5	abhydrolase domain containing 5	0.00014021	0.005693247	0.43	0.658	0
502	MGC4473	hypothetical LOC79100	0.000141132	0.005704218	0.42	0.684	0
503	IFITM4P	interferon induced transmembrane protein 4 pseudogene	0.000140874	0.005704218	1.83	0.662	0
504	AQP9	aquaporin 9	0.00014155	0.005709756	4.09	0.682	0
505	BPHL	biphenyl hydrolase-like	0.000142344	0.005730414	0.34	0.672	0
506	CCBL2	cysteine conjugate-beta lyase 2	0.00014478	0.005816952	0.26	0.658	0
507	POGZ	pogo transposable element with ZNF domain	0.00014627	0.00586521	0.38	0.653	0
508	GPA33	glycoprotein A33	0.00014777	0.005913695	0.58	0.670	0.01
509	B3GNT8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	0.000153685	0.00613835	2.07	0.679	0
510	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	0.000155748	0.006156778	1.74	0.693	0.01
511	LOC100130506	hypothetical LOC100130506	0.000155418	0.006156778	0.63	0.668	0
512	STAC3	SH3 and cysteine rich domain 3	0.000154717	0.006156778	0.27	0.656	0
513	FHL1	four and a half LIM domains 1	0.000155443	0.006156778	0.42	0.672	0
514	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	0.000155692	0.006156778	9.74	0.676	0
515	LOC100240734	hypothetical LOC100240734	0.000155964	0.006156778	2.71	0.625	0
516	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	0.000156659	0.006172224	2.93	0.681	0
517	BCAT1	branched chain aminotransferase 1, cytosolic	0.000157833	0.006206453	2.61	0.671	0
518	UBQLN2	ubiquilin 2	0.000164554	0.006436091	6.79	0.675	0
519	ASRGL1	asparaginase like 1	0.000164577	0.006436091	0.26	0.665	0
520	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	0.000164622	0.006436091	0.21	0.658	0
521	ZNF445	zinc finger protein 445	0.000166397	0.006492986	2.70	0.645	0
522	KCNA3	potassium voltage-gated channel, shaker-related subfamily, member 3	0.000167156	0.006510105	0.28	0.674	0
523	SLC37A3	solute carrier family 37 member 3	0.000167922	0.00652743	1.54	0.686	0
524	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	0.000169699	0.006583915	6.57	0.663	0
525	FAM129B	family with sequence similarity 129, member B	0.00017143	0.006625801	3.11	0.679	0
526	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.000171141	0.006625801	4.14	0.648	0
527	SIRPD	signal-regulatory protein delta	0.000174549	0.006733534	0.40	0.669	0
528	ZNF703	zinc finger protein 703	0.000176928	0.006812396	1.68	0.643	0
529	FBXO25	F-box protein 25	0.000178919	0.006876055	0.07	0.665	0
530	FBXL17	F-box and leucine-rich repeat protein 17	0.000180007	0.006904779	0.35	0.676	0
531	MT1H	metallothionein 1H	0.000180559	0.006912911	2.47	0.648	0
532	ABCB4	ATP-binding cassette, sub-family B	0.000181824	0.006916909	1.82	0.667	0.01
533	HLA-DPB2	major histocompatibility complex, class II, DP beta 2	0.000182114	0.006916909	0.37	0.695	0
534	NGLY1	N-glycanase 1	0.000182364	0.006916909	6.72	0.667	0
535	CD5L	CD5 molecule-like	0.00018171	0.006916909	0.71	0.647	0
536	ZNF542	zinc finger protein 542	0.000181785	0.006916909	0.34	0.671	0
537	CSF3	colony stimulating factor 3	0.000185357	0.006950684	1.85	0.627	0.02
538	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0.000184581	0.006950684	1.75	0.659	0
539	C5orf30	chromosome 5 open reading frame 30	0.000184679	0.006950684	2.88	0.676	0
540	CYYR1	cysteine/tyrosine-rich 1	0.000183602	0.006950684	1.75	0.618	0
541	CTPS	CTP synthase	0.000184181	0.006950684	4.85	0.688	0
542	LOC729799	SEC14-like 1 pseudogene	0.000184982	0.006950684	3.61	0.656	0
543	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.000185648	0.006950684	0.24	0.665	0

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544	BLM	Bloom syndrome, RecQ helicase-like	0.000186765	0.006962801	1.99	0.691	0.01
545	LARP1B	La ribonucleoprotein domain family, member 1B	0.000186604	0.006962801	4.38	0.658	0
546	REM2	RAS (RAD and GEM)-like GTP binding 2	0.000186999	0.006962801	1.63	0.669	0
547	GRB10	growth factor receptor-bound protein 10	0.000188183	0.006979496	2.38	0.666	0
548	MME	membrane metallo-endopeptidase	0.000187881	0.006979496	0.70	0.647	0
549	CAMSAP1	calmodulin regulated spectrin-associated protein 1	0.000188477	0.006979496	0.44	0.667	0
550	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0.000189908	0.007012813	1.78	0.691	0
551	ZNF658	zinc finger protein 658	0.000190067	0.007012813	0.37	0.694	0
552	COL18A1	collagen, type XVIII, alpha 1	0.000196072	0.00722129	1.86	0.667	0
553	DDR1	discoidin domain receptor tyrosine kinase 1	0.00019675	0.007233147	1.93	0.686	0
554	CCL8	chemokine (CC motif) ligand 8	0.000201674	0.007387452	1.30	0.672	0
555	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	0.00020133	0.007387452	0.17	0.665	0
556	OLIG1	oligodendrocyte transcription factor 1	0.000203533	0.007428788	1.38	0.680	0
557	DUSP14	dual specificity phosphatase 14	0.000203286	0.007428788	2.40	0.675	0
558	WDR63	WD repeat domain 63	0.000204964	0.007467578	1.97	0.662	0
559	SLC46A3	solute carrier family 46, member 3	0.000207518	0.00754713	0.42	0.684	0
560	FAM162A	family with sequence similarity 162, member A	0.000208066	0.007553535	0.18	0.660	0
561	DEXI	Dexi homolog	0.000214953	0.007789661	2.59	0.668	0
562	SMAD3	SMAD family member 3	0.000216751	0.007840828	1.48	0.680	0
563	KRTAP9L1	Putative keratin-associated protein 9-2-like 1	0.000220148	0.007949556	0.47	0.656	0
564	FAM89A	family with sequence similarity 89, member A	0.000220545	0.007949789	0.57	0.655	0
565	MEX3C	mex-3 homolog C	0.000221049	0.007953854	1.98	0.676	0
566	JUB	jub, ajuba homolog	0.00022209	0.007977194	1.88	0.622	0
567	MMP8	matrix metallopeptidase 8	0.00022254	0.007979246	2.27	0.617	0
568	LOC100129363	cDNA FLJ46623 fis, clone TLUNG2001810.	0.000224191	0.008010185	1.81	0.671	0
569	EIF2C2	eukaryotic translation initiation factor 2C, 2	0.000224026	0.008010185	6.10	0.665	0
570	CDRT4	CMT1A duplicated region transcript 4	0.000225846	0.00804569	0.51	0.671	0.01
571	NFU1	NFU1 iron-sulfur cluster scaffold homolog	0.000225976	0.00804569	0.16	0.680	0
572	DENND3	DENN/MADD domain containing 3	0.000226392	0.008046413	2.64	0.664	0
573	RAB34	RAB34, member RAS oncogene family	0.000228511	0.008107549	0.34	0.663	0
574	CKB	creatine kinase, brain	0.000229405	0.00811817	1.69	0.676	0
575	FHOD1	formin homology 2 domain containing 1	0.000229609	0.00811817	3.83	0.676	0
576	AQP4	aquaporin 4	0.000230654	0.008131424	1.41	0.684	0.01
577	VRK2	vaccinia related kinase 2	0.000230784	0.008131424	0.44	0.680	0
578	LOC541472	hypothetical LOC541472	0.000232476	0.008176886	2.13	0.641	0
579	AMICA1	adhesion molecule, interacts with CXADR antigen 1	0.000234522	0.008234607	0.31	0.671	0
580	E2F3	E2F transcription factor 3	0.000235908	0.008268967	2.64	0.649	0
581	PLBD1	phospholipase B domain containing 1	0.00023654	0.008276867	0.28	0.665	0
582	BCAS1	breast carcinoma amplified sequence 1	0.00023699	0.008278368	1.74	0.649	0
583	CCL3	chemokine (C-C motif) ligand 3	0.000238327	0.008288119	1.66	0.657	0
584	IQSEC3	IQ motif and Sec7 domain 3	0.000238492	0.008288119	0.70	0.642	0
585	ECHDC3	enoyl Coenzyme A hydratase domain containing 3	0.000238077	0.008288119	0.51	0.635	0
586	C1orf133	chromosome 1 open reading frame 133	0.000239696	0.008315744	1.92	0.620	0
587	GATA1	GATA binding protein 1	0.000242959	0.008402737	1.77	0.662	0
588	LCE1D	late cornified envelope 1D	0.00024303	0.008402737	0.53	0.630	0
589	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	0.000243566	0.008406948	3.11	0.628	0
590	DACH1	dachshund homolog 1	0.000244197	0.008414437	1.58	0.684	0
591	NTSR1	neurotensin receptor 1	0.000247237	0.008504789	1.64	0.650	0
592	AMIGO2	adhesion molecule with Ig-like domain 2	0.000248723	0.008541457	0.56	0.650	0
593	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	0.000249162	0.008542101	1.47	0.678	0
594	MIDN	midnolin	0.000250561	0.008575608	3.77	0.676	0
595	STX8	syntaxin 8	0.000253954	0.00867713	0.27	0.664	0
596	CYTL1	cytokine-like 1	0.000255323	0.008679134	1.82	0.705	0.01
597	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	0.000255566	0.008679134	1.75	0.649	0
598	MFSD6L	major facilitator superfamily domain containing 6-like	0.000256148	0.008679134	1.75	0.670	0
599	ZNF20	zinc finger protein 20	0.000254928	0.008679134	0.40	0.683	0
600	TSNARE1	t-SNARE domain containing 1	0.000256007	0.008679134	0.25	0.670	0
601	CALR	calreticulin	0.000258983	0.008760613	10.52	0.663	0
602	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A	0.000262607	0.008868432	10.37	0.645	0
603	OSM	oncostatin M	0.000263916	0.008897858	1.90	0.660	0
604	ECE1	endothelin converting enzyme 1	0.00026496	0.008918282	1.63	0.681	0

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605	METRNL	meteorin, glial cell differentiation regulator-like	0.000267771	0.008997977	4.01	0.662	0
606	CRLF1	cytokine receptor-like factor 1	0.000269619	0.009045137	1.96	0.662	0
607	STAMBP	STAM binding protein	0.000270305	0.009053216	0.32	0.654	0
608	CHKA	choline kinase alpha	0.000271012	0.009061964	3.48	0.683	0
609	CEP135	centrosomal protein 135kDa	0.000276026	0.009199673	2.42	0.654	0
610	CCL3L3	chemokine (C-C motif) ligand 3-like 3	0.000276035	0.009199673	1.58	0.655	0
611	KRT24	keratin 24	0.000279188	0.009289514	4.05	0.638	0
612	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	0.000281076	0.009337047	2.57	0.673	0
613	FBRSL1	fibrosin-like 1	0.000283355	0.009397407	0.63	0.631	0
614	LGMN	legumain	0.000288283	0.009545275	1.81	0.664	0.02
615	ZNF595	zinc finger protein 595	0.00028921	0.009560403	0.35	0.675	0
616	ZFP36	zinc finger protein 36, C3H type, homolog	0.000290307	0.009581073	2.21	0.675	0
617	RPL6	ribosomal protein L6	0.000291301	0.009587538	6.31	0.666	0
618	USP33	ubiquitin specific peptidase 33	0.000291446	0.009587538	0.35	0.672	0
619	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	0.000292084	0.009593002	2.21	0.671	0
620	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	0.000293172	0.009613188	6.53	0.693	0
621	SIK2	salt-inducible kinase 2	0.000293802	0.009618355	0.40	0.642	0
622	DUSP10	dual specificity phosphatase 10	0.000295069	0.009644311	0.46	0.654	0
623	C20orf106	chromosome 20 open reading frame 106	0.000295796	0.009652537	3.37	0.654	0
624	C5orf44	chromosome 5 open reading frame 44	0.00029823	0.009716377	0.32	0.687	0
625	MS4A6E	membrane-spanning 4-domains, subfamily A, member 6E	0.000300856	0.009776978	1.68	0.700	0
626	TPSG1	tryptase gamma 1	0.000301052	0.009776978	0.47	0.633	0
627	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0.000303547	0.009842276	1.81	0.668	0
628	WFIKKN2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	0.000305967	0.009873506	0.73	0.678	0
629	LOC727721	cDNA clone TRACH3034794 5'	0.000305602	0.009873506	0.52	0.664	0
630	CORO2A	coronin, actin binding protein, 2A	0.000305069	0.009873506	0.39	0.630	0
631	CMTM2	CKLF-like MARVEL transmembrane domain containing 2	0.000309017	0.009932269	1.64	0.667	0
632	LOC286058	cDNA DKFZp686J2011	0.000309742	0.009932269	1.74	0.621	0
633	ARHGAP6	Rho GTPase activating protein 6	0.000308348	0.009932269	0.63	0.638	0
634	PLD6	phospholipase D family, member 6	0.000309437	0.009932269	1.80	0.682	0
635	KIAA0247	KIAA0247	0.000310372	0.009936796	6.99	0.660	0
636	CYBRD1	cytochrome b reductase 1	0.000311876	0.009969249	2.09	0.659	0
637	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein,	0.000318454	0.010163539	6.64	0.650	0
638	C17orf108	chromosome 17 open reading frame 108	0.000320156	0.010201837	0.30	0.687	0
639	GPRC5C	G protein-coupled receptor, family C, group 5, member C	0.000321086	0.010215454	2.38	0.668	0
640	UBE2E2	ubiquitin-conjugating enzyme E2E 2	0.000325685	0.010345591	0.31	0.645	0
641	GGT5	gamma-glutamyltransferase 5	0.000327643	0.010390394	1.87	0.675	0
642	EGR1	early growth response 1	0.000328118	0.010390394	1.88	0.677	0
643	ANUBL1	AN1, ubiquitin-like, homolog	0.000330879	0.01046155	0.38	0.658	0
644	SLC2A1	solute carrier family 2	0.000332501	0.010496485	1.81	0.668	0
645	KLF10	Kruppel-like factor 10	0.000333422	0.010509244	4.06	0.672	0
646	INE2	inactivation escape 2	0.000334525	0.010527695	2.03	0.615	0
647	PTPN9	protein tyrosine phosphatase, non-receptor type 9	0.000339574	0.010653602	0.25	0.651	0
648	NAALADL2	N-acetylated alpha-linked acidic dipeptidase-like 2	0.000339126	0.010653602	0.38	0.681	0
649	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	0.000342699	0.010735081	1.75	0.673	0
650	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	0.000343422	0.010741173	1.31	0.659	0
651	H2AFB2	H2A histone family, member B2	0.000346583	0.010823411	0.46	0.676	0
652	CDH1	cadherin 1, type 1, E-cadherin	0.000349756	0.010905745	1.38	0.667	0.01
653	ANKRD29	ankyrin repeat domain 29	0.000353035	0.010988388	2.13	0.665	0
654	C12orf62	chromosome 12 open reading frame 62	0.000353533	0.010988388	0.07	0.671	0
655	SCG5	secretogranin V	0.000355109	0.010988388	1.50	0.620	0
656	ITGA3	integrin, alpha 3	0.000355068	0.010988388	1.54	0.682	0
657	ZNF181	zinc finger protein 181	0.000354466	0.010988388	0.34	0.664	0
658	BEX4	brain expressed, X-linked 4	0.000356675	0.011020071	0.38	0.660	0
659	LIMD1	LIM domains containing 1	0.000358401	0.011039845	3.03	0.652	0
660	ACSBG2	acyl-CoA synthetase bubblegum family member 2	0.000358364	0.011039845	0.49	0.670	0
661	ADAMTSL3	ADAMTS-like 3	0.000360592	0.011090538	12.64	0.578	0
662	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B	0.000362816	0.011142054	3.42	0.660	0
663	SHISA4	shisa homolog 4	0.00036566	0.011212478	0.41	0.673	0
664	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2	0.000366821	0.011231119	1.66	0.668	0
665	ZNF385B	zinc finger protein 385B	0.00037225	0.011366232	5.43	0.643	0

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666	KLHL33	kelch-like 33	0.000372352	0.011366232	0.49	0.660	0
667	UCP3	uncoupling protein 3	0.000373559	0.011385989	0.64	0.634	0
668	EMP2	epithelial membrane protein 2	0.00037425	0.011389972	1.66	0.658	0
669	PRDM8	PR domain containing 8	0.000377085	0.01145911	1.49	0.674	0
670	LSM1	LSM1 homolog, U6 small nuclear RNA associated	0.000381408	0.011573163	10.00	0.677	0
671	ZNF28	zinc finger protein 28	0.000382189	0.011579583	0.32	0.672	0
672	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	0.000386097	0.011680583	1.83	0.668	0
673	CDA	cytidine deaminase	0.000387493	0.011705388	1.76	0.673	0
674	TTR	transthyretin	0.000390419	0.011741438	1.53	0.608	0
675	ARHGAP12	Rho GTPase activating protein 12	0.000390053	0.011741438	2.25	0.677	0
676	NINJ1	ninjurin 1	0.000390384	0.011741438	1.87	0.647	0
677	SKP2	S-phase kinase-associated protein 2	0.000391511	0.011756898	0.44	0.633	0
678	BNIPL	BCL2/adenovirus E1B 19kD interacting protein like	0.000392707	0.011775411	1.69	0.665	0
679	KCNAB1	potassium voltage-gated channel shaker-related subfamily beta member 1	0.000393659	0.011786573	0.73	0.659	0
680	CAT	catalase	0.000394396	0.011791288	0.41	0.654	0
681	ZC4H2	zinc finger, C4H2 domain containing	0.000398038	0.01186748	0.44	0.663	0
682	IL10	interleukin 10	0.000398112	0.01186748	1.77	0.677	0
683	DNAJC5B	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	0.000399542	0.011875283	0.64	0.669	0
684	HNRNPCL1	heterogeneous nuclear ribonucleoprotein C-like 1	0.000399211	0.011875283	0.39	0.647	0
685	LOC732160	similar to NADH dehydrogenase	0.000404093	0.011975511	0.22	0.658	0
686	YRDC	yrdC domain containing	0.000403793	0.011975511	4.34	0.662	0
687	ACR	acrosin	0.000406044	0.012015834	0.51	0.693	0.02
688	KREMEN1	kringle containing transmembrane protein 1	0.000408937	0.012082647	2.04	0.664	0
689	KRT83	keratin 83	0.000410044	0.012082647	1.72	0.694	0
690	HSPA6	heat shock 70kDa protein 6	0.000410085	0.012082647	2.21	0.647	0
691	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	0.000411874	0.012117803	1.71	0.675	0
692	PDSS1	prenyl	0.000413855	0.012130926	4.98	0.672	0
693	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	0.000413578	0.012130926	2.38	0.709	0
694	IRX1	iroquois homeobox 1	0.00041411	0.012130926	1.94	0.617	0
695	MPP1	membrane protein, palmitoylated 1, 55kDa	0.000416849	0.012193583	6.65	0.641	0
696	BAIAP2L1	BAI1-associated protein 2-like 1	0.000417947	0.012208128	1.72	0.633	0
697	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	0.000421487	0.012285202	3.57	0.684	0
698	ZNF354C	zinc finger protein 354C	0.000421794	0.012285202	0.54	0.676	0
699	C5orf13	chromosome 5 open reading frame 13	0.000424305	0.012306204	3.40	0.658	0
700	HSPG2	heparan sulfate proteoglycan 2	0.000424331	0.012306204	1.58	0.673	0
701	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	0.000424297	0.012306204	1.53	0.633	0
702	LY86	lymphocyte antigen 86	0.000427059	0.012367683	0.47	0.641	0
703	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	0.000431658	0.012418287	1.69	0.666	0
704	CD244	CD244 molecule, natural killer cell receptor 2B4	0.000431777	0.012418287	1.46	0.670	0
705	TINAGL1	tubulointerstitial nephritis antigen-like 1	0.000432472	0.012418287	0.64	0.626	0
706	HHIP	hedgehog interacting protein	0.000431825	0.012418287	1.96	0.638	0
707	COQ2	coenzyme Q2 homolog, prenyltransferase	0.00043199	0.012418287	0.37	0.638	0
708	PSMG2	proteasome (prosome, macropain) assembly chaperone 2	0.000430021	0.012418287	0.27	0.666	0
709	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	0.000433123	0.01241945	1.91	0.678	0
710	CCDC125	coiled-coil domain containing 125	0.000433924	0.012424898	0.34	0.668	0
711	CES1	carboxylesterase 1	0.000434577	0.012426091	0.64	0.656	0.02
712	ANO6	anoctamin 6	0.000436033	0.012450202	3.19	0.665	0
713	HPSE	heparanase	0.000437592	0.012477202	2.43	0.632	0
714	DIABLO	diablo homolog, nuclear gene encoding mitochondrial protein	0.000439337	0.012509407	0.55	0.622	0
715	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0.000443441	0.012599584	1.61	0.682	0
716	LRRC8A	leucine rich repeat containing 8 family, member A	0.000443743	0.012599584	4.03	0.663	0
717	ZNF226	zinc finger protein 226	0.000444463	0.012602417	0.16	0.670	0
718	SDS	serine dehydratase	0.000446574	0.012639899	1.46	0.662	0
719	C8G	complement component 8, gamma polypeptide	0.000447028	0.012639899	0.40	0.648	0
720	TST	thiosulfate sulfurtransferase	0.000451217	0.012740609	0.30	0.636	0
721	NLN	neurolysin	0.000453211	0.01275596	3.30	0.646	0
722	PM20D2	peptidase M20 domain containing 2	0.00045347	0.01275596	2.23	0.683	0
723	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	0.000453643	0.01275596	0.45	0.653	0
724	CARD10	caspase recruitment domain family, member 10	0.000455229	0.012782879	1.66	0.669	0
725	KDM1A	lysine	0.000457932	0.012841044	0.39	0.642	0
726	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.000460646	0.012899349	1.49	0.688	0

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727	PRDM1	PR domain containing 1, with ZNF domain	0.000466613	0.01301476	1.52	0.672	0
728	RBPMS	RNA binding protein with multiple splicing	0.000466328	0.01301476	1.60	0.619	0
729	CRYZL1	crystallin, zeta (quinone reductase)-like 1	0.000466688	0.01301476	0.20	0.657	0
730	NT5C3L	5'-nucleotidase, cytosolic III-like	0.000468013	0.013033847	0.56	0.637	0.02
731	TCTEX1D2	Tctex1 domain containing 2	0.000470173	0.013076095	2.03	0.661	0
732	FAM184A	family with sequence similarity 184, member A	0.000471947	0.013092371	1.86	0.649	0
733	TRPM5	transient receptor potential cation channel, subfamily M, member 5	0.000472047	0.013092371	0.43	0.675	0
734	ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2	0.000480784	0.01331654	1.55	0.666	0.01
735	GPR114	G protein-coupled receptor 114	0.000482632	0.013331397	1.51	0.644	0.07
736	CNKSR1	connector enhancer of kinase suppressor of Ras 1	0.000482007	0.013331397	1.62	0.652	0
737	PGC	progastricsin	0.0004837	0.013342768	1.76	0.661	0
738	SNHG3	small nucleolar RNA host gene 3	0.000485521	0.013356754	2.29	0.674	0
739	DDAH1	dimethylarginine dimethylaminohydrolase 1	0.000485364	0.013356754	1.45	0.655	0
740	ZNF419	zinc finger protein 419	0.000488177	0.013411666	0.47	0.638	0
741	ZFP82	zinc finger protein 82 homolog	0.000489889	0.013424953	0.49	0.646	0
742	METTL1	methyltransferase like 1	0.000490641	0.013424953	3.36	0.689	0
743	SEZ6L2	seizure related 6 homolog	0.000490638	0.013424953	1.68	0.683	0
744	FAM27A	family with sequence similarity 27, member A	0.000495512	0.013540004	2.44	0.658	0
745	FSTL3	follistatin-like 3	0.000498793	0.013611345	2.52	0.679	0
746	TNNI1	troponin I type 1	0.000500361	0.013615491	0.31	0.680	0
747	SPPL2B	signal peptide peptidase-like 2B	0.000500954	0.013615491	0.40	0.687	0
748	FOXP1	forkhead box P1	0.00050014	0.013615491	0.35	0.669	0
749	SPRN	shadow of prion protein homolog	0.000505592	0.013704907	0.57	0.657	0
750	TCEAL1	transcription elongation factor A	0.000505408	0.013704907	0.33	0.648	0
751	CNR1	cannabinoid receptor 1	0.000508969	0.013778095	4.63	0.637	0
752	SLC22A17	solute carrier family 22, member 17	0.000510213	0.013793396	0.42	0.669	0
753	LOC100133161	hypothetical LOC100133161	0.00051662	0.013948049	0.50	0.620	0
754	PGLYRP1	peptidoglycan recognition protein 1	0.000519338	0.014002838	1.53	0.643	0
755	GLT1D1	glycosyltransferase 1 domain containing 1	0.000522626	0.014058863	1.91	0.629	0
756	TIGD3	tigger transposable element derived 3	0.000522799	0.014058863	2.37	0.625	0
757	SOAT1	sterol O-acyltransferase 1	0.00052827	0.014187221	3.43	0.671	0
758	EHD2	EH-domain containing 2	0.000529601	0.014196894	1.49	0.673	0.01
759	KIAA1143	KIAA1143	0.000530027	0.014196894	0.41	0.676	0
760	LOC100128607	cDNA FLJ45251 fis, clone BRHIP2009177.	0.00053311	0.014241957	1.72	0.653	0
761	PSD	pleckstrin and Sec7 domain containing	0.000533109	0.014241957	0.43	0.665	0
762	GKN2	gastrokine 2	0.000540447	0.014400118	1.62	0.630	0
763	ARSK	arylsulfatase family, member K	0.000540322	0.014400118	0.40	0.676	0
764	GNL3	guanine nucleotide binding protein-like 3	0.000542421	0.014433787	9.98	0.654	0
765	TMED4	transmembrane emp24 protein transport domain containing 4	0.00054484	0.014479205	0.35	0.642	0
766	STYK1	serine/threonine/tyrosine kinase 1	0.000548207	0.014549662	1.54	0.672	0
767	LOC93444	cDNA FLJ20168 fis, clone COL09525	0.000555787	0.014731606	2.07	0.657	0
768	HIF3A	HIF-3A4 mRNA for hypoxia-inducible factor-3 alpha 4	0.00055725	0.014732998	0.60	0.635	0
769	SH2D1B	SH2 domain containing 1B	0.000557289	0.014732998	1.37	0.638	0
770	SNCA	synuclein, alpha	0.000558991	0.014758807	1.96	0.669	0
771	EXD2	exonuclease 3'-5' domain containing 2	0.000561904	0.014812232	0.58	0.642	0
772	PARP15	poly (ADP-ribose) polymerase family, member 15	0.000562471	0.014812232	0.49	0.667	0
773	IFITM1	interferon induced transmembrane protein 1 (9-27)	0.000564407	0.014824787	1.43	0.671	0
774	KLK6	kallikrein-related peptidase 6	0.000564176	0.014824787	2.08	0.653	0
775	LRRN2	leucine rich repeat neuronal 2	0.00057081	0.014973628	0.33	0.668	0
776	LOC644962	cDNA FLJ46065 fis, clone TBAES2007862.	0.00057553	0.015077991	0.33	0.679	0
777	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.000576991	0.015096827	2.19	0.643	0
778	TMEM27	transmembrane protein 27	0.000586073	0.015255907	2.49	0.612	0
779	NAV2	neuron navigator 2	0.00058599	0.015255907	1.51	0.671	0
780	MARCKSL1	MARCKS-like 1	0.000584791	0.015255907	1.53	0.669	0
781	DHRS9	dehydrogenase/reductase	0.000584044	0.015255907	2.08	0.662	0
782	KCTD9	potassium channel tetramerisation domain containing 9	0.000589658	0.015329591	4.28	0.676	0
783	H3F3B	H3 histone, family 3B (H3.3B)	0.000593492	0.015409559	8.95	0.648	0
784	LOC100134229	hypothetical protein LOC100134229	0.000594475	0.015415405	1.99	0.678	0
785	EXOG	endo/exonuclease (5'-3'), endonuclease G-like	0.000596297	0.015442941	0.29	0.675	0
786	AES	amino-terminal enhancer of split	0.000598549	0.015461919	0.14	0.683	0
787	SCARNA2	small Cajal body-specific RNA 2	0.000599235	0.015461919	0.55	0.633	0

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788	CAPN8	calpain 8	0.000599311	0.015461919	1.98	0.647	0
789	AUTS2	autism susceptibility candidate 2	0.000600943	0.015484373	1.41	0.674	0
790	GABPB2	GA binding protein transcription factor, beta subunit 2	0.000602966	0.015516826	7.50	0.653	0
791	LILRB4	leukocyte immunoglobulin-like receptor, subfamily B	0.000604879	0.015546377	1.92	0.656	0
792	TACC2	transforming, acidic coiled-coil containing protein 2	0.000608638	0.015623257	1.66	0.634	0
793	RASGRP3	RAS guanyl releasing protein 3	0.000618612	0.015682948	3.17	0.643	0
794	C16orf89	chromosome 16 open reading frame 89	0.000618486	0.015682948	1.68	0.679	0
795	MYO7A	myosin VIIA	0.00061614	0.015682948	1.81	0.669	0
796	OXCT1	3-oxoacid CoA transferase 1	0.000617721	0.015682948	1.59	0.668	0
797	AFMID	arylformamidase	0.000613856	0.015682948	0.42	0.641	0
798	LOC100129387	hypothetical LOC100129387	0.000618678	0.015682948	1.68	0.672	0
799	LOC441025	Homo sapiens cDNA clone IMAGE:5164155	0.000614674	0.015682948	0.44	0.690	0
800	AZIN1	antizyme inhibitor 1	0.000613471	0.015682948	3.53	0.660	0
801	SMAD5	SMAD family member 5	0.000615475	0.015682948	0.18	0.664	0
802	SP140	SP140 nuclear body protein	0.000616321	0.015682948	0.31	0.655	0
803	SIGLEC10	sialic acid binding Ig-like lectin 10	0.000621428	0.015733039	1.52	0.660	0
804	IRAK2	interleukin-1 receptor-associated kinase 2	0.000623886	0.015756026	1.69	0.631	0
805	PTPDC1	protein tyrosine phosphatase domain containing 1	0.000623687	0.015756026	0.56	0.636	0
806	WHAMM	WAS protein homolog associated with actin, golgi membranes and microtubules	0.000627533	0.015828472	0.41	0.669	0
807	SH3KBP1	SH3-domain kinase binding protein 1	0.000630055	0.01585637	2.38	0.634	0
808	ZNF684	zinc finger protein 684	0.000630199	0.01585637	0.35	0.648	0
809	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	0.000630987	0.015856567	1.99	0.666	0
810	SPINK1	serine peptidase inhibitor, Kazal type 1	0.000635938	0.015961264	1.36	0.688	0.02
811	FAM161B	family with sequence similarity 161, member B	0.000638926	0.016010938	0.46	0.673	0
812	DYTN	dystrotelin	0.000639492	0.016010938	0.47	0.671	0
813	FAM66D	family with sequence similarity 66, member D	0.000640333	0.016012267	0.39	0.693	0
814	PHF19	PHD finger protein 19	0.000644317	0.016052651	3.07	0.667	0
815	SIAH1	seven in absentia homolog 1	0.000642811	0.016052651	0.16	0.668	0
816	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog	0.000644247	0.016052651	4.13	0.674	0
817	DEFA3	defensin, alpha 3, neutrophil-specific	0.000647178	0.016083911	1.21	0.652	0
818	EHD3	EH-domain containing 3	0.000647945	0.016083911	1.64	0.655	0
819	MYL9	myosin, light chain 9, regulatory	0.000647406	0.016083911	1.92	0.666	0
820	MEST	mesoderm specific transcript homolog	0.000649607	0.016105495	2.12	0.672	0
821	AGRP	agouti related protein homolog	0.000654284	0.016201696	0.74	0.639	0
822	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	0.000661167	0.016352221	2.10	0.675	0
823	C10orf116	chromosome 10 open reading frame 116	0.00066697	0.016475693	1.46	0.681	0
824	PPCS	phosphopantothenoylcysteine synthetase	0.000675177	0.016658197	0.20	0.660	0
825	PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	0.000676851	0.016679246	3.09	0.653	0
826	ABLIM3	actin binding LIM protein family, member 3	0.000685738	0.016837032	2.04	0.663	0
827	CPLX2	complexin 2	0.000684897	0.016837032	0.49	0.668	0
828	MPP7	membrane protein, palmitoylated 7	0.000685702	0.016837032	1.61	0.648	0
829	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.000689597	0.016911337	2.00	0.681	0
830	DUSP12	dual specificity phosphatase 12	0.000690471	0.016912373	5.14	0.655	0
831	PLS1	plastin 1	0.000696425	0.017037687	2.11	0.628	0
832	ZNF717	zinc finger protein 717	0.000699508	0.017092542	0.46	0.650	0
833	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3	0.000703586	0.017134564	3.15	0.649	0
834	PRDM14	PR domain containing 14	0.000703756	0.017134564	2.20	0.619	0
835	CYGB	cytoglobin	0.000702295	0.017134564	0.55	0.637	0
836	G0S2	G0/G1switch 2	0.000704767	0.01713864	1.39	0.655	0
837	IL1B	interleukin 1, beta	0.000706314	0.01715576	2.17	0.616	0
838	SLC6A17	solute carrier family 6, member 17	0.000710264	0.017190074	0.69	0.655	0.02
839	ITGAL	integrin, alpha L	0.000708575	0.017190074	0.29	0.684	0
840	C17orf105	chromosome 17 open reading frame 105	0.000709942	0.017190074	0.51	0.664	0
841	IL18R1	interleukin 18 receptor 1	0.000715445	0.017294891	1.48	0.665	0
842	PYDC1	PYD (pyrin domain) containing 1	0.00072241	0.017421823	0.21	0.629	0
843	ARHGEF3	Rho guanine nucleotide exchange factor	0.00072203	0.017421823	0.35	0.625	0
844	CLIC3	chloride intracellular channel 3	0.000727674	0.01752798	1.41	0.683	0
845	AHNAK2	AHNAK nucleoprotein 2	0.000729654	0.017539869	1.68	0.671	0.01
846	CCDC115	coiled-coil domain containing 115	0.00073251	0.017539869	0.11	0.676	0
847	RGS12	regulator of G-protein signaling 12	0.000732973	0.017539869	0.48	0.657	0
848	TTLL11	tubulin tyrosine ligase-like family, member 11	0.000731681	0.017539869	0.50	0.666	0

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849	SBNO2	strawberry notch homolog 2	0.000733174	0.017539869	3.14	0.662	0
850	LILRA4	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain),	0.000733344	0.017539869	2.71	0.657	0
851	FLRT2	fibronectin leucine rich transmembrane protein 2	0.000738215	0.017635618	1.59	0.647	0
852	RRAD	Ras-related associated with diabetes	0.000740516	0.017669825	1.50	0.657	0
853	DOT1L	DOT1-like, histone H3 methyltransferase	0.000744473	0.017743426	2.18	0.652	0
854	GPR143	G protein-coupled receptor 143	0.000749795	0.017849335	2.09	0.638	0
855	SLC6A9	solute carrier family 6	0.000755728	0.017969538	1.71	0.649	0
856	GGTLC1	gamma-glutamyltransferase light chain 1	0.000758604	0.018016834	3.26	0.675	0
857	RPL22L1	ribosomal protein L22-like 1	0.00076113	0.018034711	4.49	0.660	0
858	GNG2	guanine nucleotide binding protein (G protein), gamma 2	0.000760977	0.018034711	1.42	0.670	0
859	LIPH	lipase, member H	0.000767233	0.01811863	1.53	0.656	0.01
860	AGR2	anterior gradient homolog 2	0.000767601	0.01811863	1.43	0.673	0
861	PHLDA2	pleckstrin homology-like domain, family A, member 2	0.000768237	0.01811863	1.98	0.681	0
862	CCPG1	cell cycle progression 1	0.000766329	0.01811863	0.42	0.677	0
863	ZNF626	zinc finger protein 626	0.000769745	0.018133162	0.44	0.663	0
864	SYNPO2L	synaptopodin 2-like	0.000772576	0.018178789	1.70	0.615	0
865	RPL13AP17	ribosomal protein L13a pseudogene 17	0.000773794	0.018186389	0.30	0.651	0
866	DONSON	downstream neighbor of SON	0.000775327	0.018201389	2.44	0.657	0
867	ZNF493	zinc finger protein 493	0.00077853	0.018255489	0.29	0.662	0
868	MT1E	metallothionein 1E	0.000780722	0.018285794	2.55	0.634	0
869	BMP2	bone morphogenetic protein 2	0.000782016	0.018295043	1.54	0.627	0
870	ANK3	ankyrin 3, node of Ranvier	0.000785292	0.018350554	1.51	0.657	0
871	HEY1	hairy/enhancer-of-split related with YRPW motif 1	0.000788797	0.018411305	1.74	0.614	0
872	CLDN18	claudin 18	0.000791122	0.018444392	1.33	0.660	0
873	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12	0.000795152	0.018517123	0.57	0.633	0
874	NAT8L	N-acetyltransferase 8-like (GCN5-related, putative)	0.000797244	0.018544599	0.55	0.668	0
875	TMEM25	transmembrane protein 25	0.000799369	0.018572761	1.47	0.644	0
876	MARVELD2	MARVEL domain containing 2	0.00080431	0.018644948	2.07	0.662	0
877	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D	0.000803933	0.018644948	1.99	0.651	0
878	KRT14	keratin 14	0.000805373	0.018648331	1.43	0.663	0
879	HEXIM2	hexamthylene bis-acetamide inducible 2	0.000806915	0.018662784	0.31	0.680	0
880	GAS6	growth arrest-specific 6	0.000808018	0.018667049	1.71	0.648	0
881	NFIB	nuclear factor I/B	0.000809122	0.018671345	1.93	0.638	0
882	SFTPC	surfactant protein C	0.000817494	0.01884315	1.33	0.680	0
883	AHCTF1	AT hook containing transcription factor 1	0.000824667	0.018986965	2.28	0.666	0.02
884	CTSF	cathepsin F	0.000831003	0.019033789	0.38	0.664	0
885	SLC6A8	solute carrier family 6	0.000829792	0.019033789	1.99	0.650	0
886	DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1)	0.000829612	0.019033789	0.19	0.671	0
887	SHISA3	shisa homolog 3	0.000829503	0.019033789	16.61	0.604	0
888	C8orf4	chromosome 8 open reading frame 4	0.000831382	0.019033789	1.53	0.635	0
889	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	0.000833996	0.019072138	4.26	0.671	0
890	PID1	phosphotyrosine interaction domain containing 1	0.000835825	0.019090355	1.45	0.670	0
891	MAT2B	methionine adenosyltransferase II, beta	0.00083667	0.019090355	0.48	0.615	0
892	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.000839032	0.019095327	1.56	0.662	0.04
893	TLR6	toll-like receptor 6	0.000839706	0.019095327	1.72	0.699	0.01
894	NPC1	Niemann-Pick disease, type C1	0.000838859	0.019095327	3.04	0.622	0
895	LMO4	LIM domain only 4	0.000842346	0.019116751	0.24	0.656	0
896	VMO1	vitelline membrane outer layer 1 homolog	0.00084535	0.019116751	0.68	0.646	0
897	SYK	spleen tyrosine kinase	0.000843719	0.019116751	0.19	0.636	0
898	SCGBL	secretoglobin-like	0.000844316	0.019116751	0.38	0.661	0
899	TLR1	toll-like receptor 1	0.000844718	0.019116751	3.99	0.644	0
900	C19orf21	chromosome 19 open reading frame 21	0.000850923	0.019221409	1.55	0.636	0
901	LOC649201	similar to paraneoplastic antigen MA1	0.00085366	0.019240466	1.69	0.646	0.01
902	TIMP3	TIMP metallopeptidase inhibitor 3	0.000853276	0.019240466	1.57	0.667	0
903	NPR2	natriuretic peptide receptor B/guanylate cyclase B	0.00085766	0.019287853	0.38	0.647	0
904	LOC642826	hypothetical LOC642826	0.000857561	0.019287853	0.25	0.656	0
905	PRR7	proline rich 7	0.000869384	0.019529923	2.17	0.636	0
906	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0.000871106	0.019547004	0.55	0.645	0
907	GAL3ST4	galactose-3-O-sulfotransferase 4	0.00087874	0.019654058	1.89	0.705	0
908	PLEKHA5	pleckstrin homology domain containing, family A member 5	0.000878689	0.019654058	1.63	0.649	0
909	FAM120C	family with sequence similarity 120C	0.000878777	0.019654058	0.26	0.627	0

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910	PGBD2	piggyBac transposable element derived 2	0.000886647	0.019808268	0.19	0.645	0
911	EDN2	endothelin 2	0.000895892	0.019992853	1.74	0.618	0
912	DRD5	dopamine receptor D5	0.000899311	0.020047148	0.56	0.656	0
913	MT1B	metallothionein 1B	0.000905712	0.020167717	2.51	0.641	0
914	LOC375196	hypothetical protein LOC375196	0.000908491	0.020207457	1.71	0.646	0
915	ZNF720	zinc finger protein 720	0.000912141	0.020266477	0.28	0.643	0
916	MYBPHL	myosin binding protein H-like	0.00092377	0.02049227	1.63	0.616	0
917	CD300A	CD300a molecule	0.000924319	0.02049227	2.01	0.649	0
918	GOLGA7B	golgi autoantigen, golgin subfamily a, 7B	0.000925542	0.020497034	1.78	0.653	0
919	CYP4B1	cytochrome P450, family 4, subfamily B, polypeptide 1	0.000928662	0.020543736	1.47	0.643	0
920	POLD3	polymerase (DNA-directed), delta 3, accessory subunit	0.000930342	0.020558527	0.27	0.635	0
921	IRX5	iroquois homeobox 5	0.000933711	0.020588231	1.75	0.639	0
922	MOCS2	molybdenum cofactor synthesis 2	0.000932957	0.020588231	0.26	0.639	0
923	FGFBP1	fibroblast growth factor binding protein 1	0.000934965	0.020593546	1.85	0.615	0
924	SGPP2	sphingosine-1-phosphate phosphotase 2	0.000939448	0.020669886	1.59	0.628	0
925	DCST2	DC-STAMP domain containing 2	0.000945667	0.020758771	0.40	0.659	0
926	C4orf34	chromosome 4 open reading frame 34	0.0009456	0.020758771	0.31	0.659	0
927	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	0.000946551	0.020758771	0.60	0.626	0
928	IL1A	interleukin 1, alpha	0.00095169	0.020829267	0.52	0.663	0
929	YIPF5	Yip1 domain family, member 5	0.000951815	0.020829267	0.38	0.642	0
930	AIMP2	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	0.000952977	0.020832277	3.74	0.659	0
931	LOC100129869	hypothetical protein LOC100129869	0.000955407	0.020862966	1.70	0.629	0.01
932	WFDC2	WAP four-disulfide core domain 2	0.000967141	0.021073929	1.41	0.668	0
933	CTRC	chymotrypsin C (caldecrin)	0.000966674	0.021073929	1.61	0.629	0
934	XAGE2B	X antigen family, member 2B	0.000974836	0.021204331	1.42	0.645	0
935	FOSL1	FOS-like antigen 1	0.000975211	0.021204331	1.83	0.657	0
936	ZNF846	zinc finger protein 846	0.000977217	0.021225241	0.60	0.646	0
937	TTC30B	tetratricopeptide repeat domain 30B	0.000980886	0.021282188	0.34	0.637	0
938	ATHL1	ATH1, acid trehalase-like 1	0.000987897	0.021411448	1.64	0.644	0
939	ZC3H12C	zinc finger CCCH-type containing 12C	0.000993806	0.02151296	1.53	0.665	0
940	SNORA28	small nucleolar RNA, H/ACA box 28	0.000994697	0.02151296	0.68	0.668	0
941	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	0.00099612	0.021520842	0.60	0.666	0
942	LOC727993	cDNA FLJ33362 fis, clone BRACE2005337	0.001004567	0.021543097	0.52	0.663	0.01
943	CCR5	chemokine (CC-motif) receptor type 5	0.00100454	0.021543097	2.21	0.669	0
944	SOD2	superoxide dismutase 2, mitochondrial	0.000999313	0.021543097	2.28	0.608	0
945	TMEM14A	transmembrane protein 14A	0.000998826	0.021543097	0.46	0.677	0
946	KIR2DS2	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic	0.001003494	0.021543097	1.56	0.654	0
947	CD300LB	CD300 molecule-like family member b	0.001002781	0.021543097	2.11	0.650	0
948	SLC1A4	solute carrier family 1	0.001001826	0.021543097	1.89	0.667	0
949	NPDC1	neural proliferation, differentiation and control, 1	0.001010193	0.021640918	1.52	0.660	0
950	CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6	0.001018029	0.021740051	0.44	0.662	0
951	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.001017487	0.021740051	1.87	0.616	0
952	IL6	interleukin 6 (interferon, beta 2)	0.00101644	0.021740051	1.40	0.651	0
953	FSCN1	fascin homolog 1, actin-bundling protein	0.001020908	0.021778663	2.00	0.651	0
954	SAP30	Sin3A-associated protein, 30kDa	0.001023756	0.02181651	2.21	0.653	0
955	POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	0.001025251	0.0218255	0.19	0.630	0
956	ZNF852	Putative zinc finger protein FLJ16720	0.001030065	0.021905054	0.55	0.643	0
957	OPN3	opsin 3	0.001032121	0.02192584	0.49	0.639	0
958	LOC338620	hypothetical protein LOC338620	0.001034615	0.021932977	1.74	0.662	0.01
959	TTC8	tetratricopeptide repeat domain 8	0.001034496	0.021932977	0.52	0.642	0
960	RGS3	regulator of G-protein signaling 3	0.001040077	0.022025803	0.46	0.648	0
961	TFPI	tissue factor pathway inhibitor	0.001042811	0.022060722	1.40	0.652	0
962	SPG21	spastic paraplegia 21	0.001044386	0.022071058	0.27	0.649	0
963	LYPD5	LY6/PLAUR domain containing 5	0.001045485	0.022071353	0.69	0.657	0
964	SGPP1	sphingosine-1-phosphate phosphatase 1	0.001051346	0.022172056	0.56	0.657	0
965	KLF9	Kruppel-like factor 9	0.001056774	0.022217232	2.18	0.653	0
966	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	0.001056899	0.022217232	0.28	0.632	0
967	NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	0.001055695	0.022217232	1.97	0.647	0
968	NUAK1	NUAK family, SNF1-like kinase, 1	0.001057859	0.022217232	1.55	0.644	0
969	RHOBTB1	Rho-related BTB domain containing 1	0.001062695	0.022295754	3.09	0.648	0
970	LOC100130152	cDNA FLJ45869 fis, clone OCBBF3004908.	0.001065137	0.022323964	0.52	0.673	0

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971	C3orf52	chromosome 3 open reading frame 52	0.001068792	0.022377499	1.88	0.620	0
972	IVD	isovaleryl Coenzyme A dehydrogenase	0.001071871	0.022408152	0.34	0.652	0
973	LOC100129447	cDNA FLJ30384 fis, clone BRACE2008114.	0.001072461	0.022408152	0.65	0.632	0
974	HIST3H2A	histone cluster 3, H2a	0.001075608	0.022450829	1.77	0.648	0
975	LOC100130298	similar to hCG1816373	0.001080086	0.022521176	1.58	0.668	0
976	MLLT4	myeloid/lymphoid or mixed-lineage leukemia	0.001082257	0.02254333	0.39	0.673	0
977	CCDC101	coiled-coil domain containing 101	0.001089724	0.022675631	0.29	0.679	0
978	STX11	syntaxin 11	0.001097705	0.022786526	0.25	0.643	0
979	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	0.001098416	0.022786526	1.67	0.685	0
980	RRP15	ribosomal RNA processing 15 homolog	0.001097653	0.022786526	2.95	0.644	0
981	HMGB2	high-mobility group box 2	0.001099683	0.022789552	2.02	0.663	0
982	C7orf70	chromosome 7 open reading frame 70	0.001102818	0.022808018	0.19	0.664	0
983	MPHOSPH9	M-phase phosphoprotein 9	0.001102214	0.022808018	0.38	0.665	0
984	SELM	selenoprotein M	0.001113056	0.022990236	0.42	0.645	0
985	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B	0.001115021	0.022990236	3.70	0.640	0
986	C5orf56	chromosome 5 open reading frame 56	0.001114909	0.022990236	0.60	0.655	0
987	TPPP3	tubulin polymerization-promoting protein family member 3	0.001116219	0.022991623	1.52	0.663	0
988	LOC100131700	similar to mCG15963	0.00111999	0.023045939	0.56	0.638	0
989	RSPH3	radial spoke 3 homolog	0.001125378	0.023119142	0.32	0.657	0
990	RNF207	cDNA FLJ46380 fis, clone THYMU2008207.	0.001126705	0.023119142	1.66	0.650	0
991	OR4A15	olfactory receptor, family 4, subfamily A, member 15	0.001126959	0.023119142	0.47	0.671	0
992	NRAS	neuroblastoma RAS viral	0.001132107	0.02317503	4.93	0.674	0
993	ADRB1	adrenergic, beta-1-, receptor	0.001133076	0.02317503	1.53	0.659	0
994	PPM1K	protein phosphatase 1K (PP2C domain containing)	0.001133103	0.02317503	0.44	0.647	0
995	GNLY	granulysin	0.001141732	0.023328059	1.28	0.656	0.02
996	RIMS3	regulating synaptic membrane exocytosis 3	0.001150769	0.023489084	1.69	0.704	0
997	KGFLP2	keratinocyte growth factor-like protein 2	0.001158984	0.023633039	0.52	0.660	0
998	CSTA	cystatin A (stefin A)	0.001163626	0.023675032	0.33	0.655	0
999	ICOS	inducible T-cell co-stimulator	0.001163926	0.023675032	0.62	0.650	0
1000	C22orf36	chromosome 22 open reading frame 36	0.001164537	0.023675032	1.87	0.674	0
1001	FARP2	FERM, RhoGEF and pleckstrin domain protein 2	0.001167206	0.023680869	0.58	0.668	0
1002	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	0.001168251	0.023680869	2.05	0.634	0
1003	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S member 3	0.001168318	0.023680869	1.55	0.645	0
1004	NPNT	nephronectin	0.001171407	0.02369895	1.77	0.655	0
1005	SCPEP1	serine carboxypeptidase 1	0.001171542	0.02369895	0.31	0.624	0
1006	RAB15	RAB15, member RAS onocogene family	0.001183253	0.023908262	1.39	0.671	0
1007	LHFP	lipoma HMGIC fusion partner	0.001184241	0.023908262	1.65	0.640	0
1008	PYY2	peptide YY, 2 (seminalplasmin)	0.001189741	0.023982298	0.64	0.639	0
1009	ST13	suppression of tumorigenicity 13 (Hsp70 interacting protein)	0.001190268	0.023982298	0.33	0.656	0
1010	MFSD1	major facilitator superfamily domain containing 1	0.001195721	0.024068322	6.28	0.648	0
1011	TM4SF19	transmembrane 4 L six family member 19	0.001201847	0.024108111	1.46	0.666	0
1012	SH3BP4	SH3-domain binding protein 4	0.001202441	0.024108111	0.70	0.653	0
1013	SLC44A3	solute carrier family 44, member 3	0.00120081	0.024108111	1.66	0.640	0
1014	TSNAX	translin-associated factor X	0.001199445	0.024108111	0.51	0.665	0
1015	ST6GALNAC6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	0.001206275	0.024161151	0.34	0.635	0
1016	ZNF382	zinc finger protein 382	0.001214257	0.024297099	0.50	0.668	0
1017	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	0.001215916	0.024306364	1.83	0.659	0
1018	CCDC75	coiled-coil domain containing 75	0.001219079	0.02434566	0.52	0.653	0
1019	CCDC126	coiled-coil domain containing 126	0.001227187	0.024483515	0.31	0.653	0
1020	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	0.001233811	0.024591548	5.48	0.661	0
1021	OLFML3	olfactomedin-like 3	0.001244965	0.024741097	1.71	0.643	0.01
1022	MLF1	myeloid leukemia factor 1	0.00124327	0.024741097	0.60	0.621	0
1023	ANKMY2	ankyrin repeat and MYND domain containing 2	0.001244942	0.024741097	0.36	0.650	0
1024	ADAMDEC1	ADAM-like, decysin 1	0.00125316	0.024879638	1.56	0.601	0
1025	AADACL2	arylacetamide deacetylase-like 2	0.001255761	0.024906945	0.00	0.650	0
1026	BANP	BTG3 associated nuclear protein	0.001268734	0.025139725	3.87	0.657	0
1027	FKBP3	FK506 binding protein 3, 25kDa	0.00127351	0.025209796	6.55	0.668	0
1028	ETV5	ets variant 5	0.001275613	0.025226854	1.98	0.608	0
1029	ZNF614	zinc finger protein 614	0.001277418	0.025238012	0.36	0.664	0
1030	NT5DC2	5'-nucleotidase domain containing 2	0.001280119	0.025266806	1.62	0.681	0
1031	TLR10	toll-like receptor 10	0.001284528	0.025313455	1.58	0.664	0.01

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1032	ZNF737	zinc finger protein 737	0.001284972	0.025313455	0.55	0.671	0
1033	ARHGAP26	Rho GTPase activating protein 26	0.001291467	0.025318725	2.60	0.651	0
1034	DUOX1	dual oxidase 1	0.001287321	0.025318725	1.44	0.656	0
1035	TMEM86A	transmembrane protein 86A	0.001290647	0.025318725	0.59	0.658	0
1036	ZC3HAV1	zinc finger CCCH-type, antiviral 1	0.001290887	0.025318725	2.23	0.663	0
1037	FCGR1B	Fc fragment of IgG, high affinity Ib, receptor	0.001289047	0.025318725	0.45	0.634	0
1038	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	0.00129474	0.025358447	2.23	0.673	0
1039	AREG	amphiregulin	0.001302871	0.025493133	1.36	0.661	0
1040	RAP2B	RAP2B, member of RAS oncogene family	0.001306977	0.025548894	2.63	0.665	0
1041	CAV2	caveolin 2	0.001310971	0.025602351	1.62	0.652	0
1042	GIN1	gypsy retrotransposon integrase 1	0.001316166	0.025679128	0.55	0.641	0
1043	LOC100131283	hypothetical LOC100131283	0.0013289	0.025720081	2.01	0.634	0
1044	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	0.001330916	0.025720081	1.85	0.639	0
1045	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and	0.00132775	0.025720081	1.65	0.660	0
1046	CDK9	cyclin-dependent kinase 9	0.001326111	0.025720081	0.21	0.672	0
1047	FAM110B	family with sequence similarity 110, member B	0.001326407	0.025720081	0.51	0.640	0
1048	FLNB	filamin B, beta	0.001330852	0.025720081	2.29	0.645	0
1049	ZNF365	zinc finger protein 365	0.001328844	0.025720081	0.74	0.626	0
1050	ACCN2	amiloride-sensitive cation channel 2, neuronal	0.001323206	0.025720081	1.69	0.665	0
1051	LOC100128219	cDNA FLJ38606 fis, clone HEART2004940.	0.001320868	0.025720081	0.51	0.670	0
1052	SSX5	synovial sarcoma, X breakpoint 5	0.001325206	0.025720081	0.56	0.642	0
1053	GPATCH4	G patch domain containing 4	0.001332441	0.025725094	3.44	0.661	0
1054	PNMA6A	paraneoplastic antigen like 6A	0.001334942	0.025748938	1.69	0.665	0
1055	HPGDS	hematopoietic prostaglandin D synthase	0.001339003	0.02577319	0.67	0.650	0
1056	LMO3	LIM domain only 3	0.001338263	0.02577319	1.56	0.629	0
1057	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.001340003	0.02577319	2.46	0.667	0
1058	DAPL1	death associated protein-like 1	0.001346196	0.025867836	2.42	0.604	0
1059	TMC5	transmembrane channel-like 5	0.001358986	0.02606561	1.47	0.649	0
1060	LOC100132483	hypothetical LOC100132483	0.001359053	0.02606561	0.51	0.665	0
1061	TMEM45B	transmembrane protein 45B	0.001361123	0.026080698	1.39	0.688	0.02
1062	LOC389834	ankyrin repeat domain 57 pseudogene	0.001368263	0.026146065	0.28	0.661	0
1063	FAM174B	family with sequence similarity 174, member B	0.001368392	0.026146065	1.81	0.648	0
1064	PKD1	polycystic kidney disease 1	0.001366072	0.026146065	0.58	0.633	0
1065	RNF217	ring finger protein 217	0.001372201	0.02619422	0.42	0.659	0
1066	BCAR3	breast cancer anti-estrogen resistance 3	0.001377709	0.026256072	0.65	0.647	0
1067	COG3	component of oligomeric golgi complex 3	0.001379316	0.026256072	2.88	0.663	0
1068	ZNF675	zinc finger protein 675	0.001378552	0.026256072	0.52	0.666	0
1069	NCF4	neutrophil cytosolic factor 4, 40kDa	0.001387859	0.026257915	0.29	0.640	0
1070	WWOX	WW domain containing oxidoreductase	0.001388508	0.026257915	0.52	0.635	0
1071	MYB	v-myb myeloblastosis viral oncogene homolog	0.001388258	0.026257915	0.50	0.639	0
1072	PRR5L	proline rich 5 like	0.001389542	0.026257915	1.58	0.661	0
1073	C10orf128	chromosome 10 open reading frame 128	0.001387592	0.026257915	0.62	0.646	0
1074	C9orf102	chromosome 9 open reading frame 102	0.001389745	0.026257915	0.54	0.640	0
1075	WDR90	WD repeat domain 90	0.001384922	0.026257915	0.58	0.651	0
1076	TNIP1	TNFAIP3 interacting protein 1	0.001383514	0.026257915	2.95	0.638	0
1077	ZNF697	zinc finger protein 697	0.001392622	0.026274226	2.59	0.630	0
1078	CPNE5	copine V	0.001393193	0.026274226	1.39	0.633	0
1079	AMDHD1	amidohydrolase domain containing 1	0.001403962	0.026452779	1.51	0.657	0.01
1080	NAIP	NLR family, apoptosis inhibitory protein	0.001407714	0.026498914	1.96	0.636	0
1081	PHF23	PHD finger protein 23	0.001416196	0.026633922	4.79	0.675	0
1082	ORMDL1	ORM1-like 1	0.00141934	0.026668379	4.31	0.652	0
1083	PSMD12	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	0.001423808	0.026702973	5.33	0.666	0
1084	CACNA1I	calcium channel, voltage-dependent, T type, alpha 1I subunit	0.001423097	0.026702973	0.37	0.650	0
1085	MITD1	MIT, microtubule interacting and transport, domain containing 1	0.001434469	0.026828655	3.31	0.638	0
1086	EFCAB3	EF-hand calcium binding domain 3	0.001432168	0.026828655	0.65	0.625	0
1087	ADAM12	ADAM metallopeptidase domain 12	0.001433674	0.026828655	0.48	0.673	0
1088	RASAL2	RAS protein activator like 2	0.001439205	0.026892495	0.74	0.651	0
1089	SVIL	supervillin	0.001444187	0.026960808	0.51	0.646	0
1090	DAZAP2	DAZ associated protein 2	0.001447733	0.027002222	4.05	0.638	0
1091	MEX3D	mex-3 homolog D	0.001452432	0.027065023	0.37	0.679	0
1092	SRI	sorcin	0.001463092	0.027238698	0.33	0.645	0

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1093	CCND1	cyclin D1	0.001471241	0.027365354	1.64	0.639	0
1094	LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	0.001474831	0.027382019	1.66	0.646	0
1095	POLB	polymerase (DNA directed), beta	0.00147454	0.027382019	0.27	0.656	0
1096	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	0.001485427	0.027503389	1.57	0.639	0
1097	ANP32D	acidic (leucine-rich) nuclear phosphoprotein 32 family, member D	0.001483084	0.027503389	0.56	0.629	0
1098	LOC284749	hypothetical LOC284749	0.001484788	0.027503389	0.43	0.658	0
1099	SMOX	spermine oxidase	0.001496886	0.027523334	1.42	0.671	0.01
1100	MCTP2	multiple C2 domains, transmembrane 2	0.001503516	0.027523334	1.58	0.619	0
1101	LOC440356	hypothetical LOC440356	0.00149689	0.027523334	0.41	0.668	0
1102	PGP	phosphoglycolate phosphatase	0.001504452	0.027523334	0.24	0.665	0
1103	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	0.001505872	0.027523334	3.75	0.658	0
1104	C1R	complement component 1, r subcomponent	0.001498466	0.027523334	1.72	0.671	0
1105	TGFBI	transforming growth factor, beta-induced, 68kDa	0.001494832	0.027523334	3.59	0.650	0
1106	PECAM1	platelet/endothelial cell adhesion molecule	0.001488325	0.027523334	0.26	0.660	0
1107	IAPP	islet amyloid polypeptide	0.001493011	0.027523334	0.50	0.667	0
1108	SNX29	sorting nexin 29	0.001506811	0.027523334	4.05	0.661	0
1109	C1orf21	chromosome 1 open reading frame 21	0.001497772	0.027523334	1.48	0.647	0
1110	KLHL21	kelch-like 21	0.001504885	0.027523334	3.54	0.631	0
1111	WTIP	Wilms tumor 1 interacting protein	0.001504436	0.027523334	1.79	0.656	0
1112	LOC100128843	similar to DNA polymerase epsilon catalytic subunit protein	0.001501461	0.027523334	0.40	0.662	0
1113	LOC728323	hypothetical LOC728323	0.001499559	0.027523334	0.40	0.648	0
1114	LMNB1	lamin B1	0.001516506	0.02767556	2.30	0.638	0
1115	C8orf38	chromosome 8 open reading frame 38	0.001519032	0.027696787	3.23	0.640	0
1116	TM6SF1	transmembrane 6 superfamily member 1	0.001520582	0.027700217	0.35	0.650	0
1117	TPP1	tripeptidyl peptidase I	0.001522369	0.027707935	0.59	0.629	0
1118	CASP6	caspase 6, apoptosis-related cysteine peptidase	0.001535989	0.027930816	0.20	0.674	0
1119	RWDD2A	RWD domain containing 2A	0.00153841	0.027949849	0.33	0.640	0
1120	SPRED1	sprouty-related, EVH1 domain containing 1	0.001540604	0.02795349	2.70	0.687	0
1121	KLF8	Kruppel-like factor 8	0.001541361	0.02795349	0.49	0.644	0
1122	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2	0.001552521	0.028086871	1.58	0.650	0
1123	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	0.001550608	0.028086871	2.21	0.662	0
1124	C12orf24	chromosome 12 open reading frame 24	0.001554241	0.028086871	2.14	0.646	0
1125	C17orf57	chromosome 17 open reading frame 57	0.001553086	0.028086871	0.61	0.660	0
1126	ISG20	interferon stimulated exonuclease gene 20kDa	0.001564192	0.028204202	1.46	0.660	0
1127	SCARNA17	small Cajal body-specific RNA 17	0.001564587	0.028204202	0.44	0.663	0
1128	ADARB1	adenosine deaminase, RNA-specific, B1	0.001564896	0.028204202	1.61	0.674	0
1129	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	0.001567123	0.028219316	1.51	0.647	0
1130	C20orf24	chromosome 20 open reading frame 24	0.001569473	0.02823663	7.68	0.633	0
1131	C1orf187	chromosome 1 open reading frame 187	0.001577881	0.028256778	2.00	0.661	0.01
1132	HOPX	HOP homeobox	0.001576157	0.028256778	1.33	0.692	0.01
1133	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	0.001574327	0.028256778	2.64	0.669	0
1134	CCDC40	coiled-coil domain containing 40	0.001576414	0.028256778	0.59	0.642	0
1135	LEPROT	leptin receptor overlapping transcript	0.00157473	0.028256778	0.41	0.633	0
1136	MACC1	metastasis associated in colon cancer 1	0.001578933	0.028256778	0.72	0.629	0
1137	CPE	carboxypeptidase E	0.001583254	0.028309191	0.79	0.645	0
1138	VPS53	vacuolar protein sorting 53 homolog	0.001590922	0.028421312	0.45	0.676	0
1139	TMEM170A	transmembrane protein 170A	0.001597198	0.028433475	0.21	0.661	0
1140	DUT	deoxyuridine triphosphatase	0.001596097	0.028433475	0.29	0.644	0
1141	SCARNA7	small Cajal body-specific RNA 7	0.001594428	0.028433475	0.52	0.658	0
1142	LOC441666	zinc finger protein 91 pseudogene	0.001594935	0.028433475	0.53	0.668	0
1143	ZNF141	zinc finger protein 141	0.001606583	0.028575536	0.55	0.653	0
1144	FBXO8	F-box protein 8	0.001612896	0.028662734	0.25	0.645	0
1145	BATF	basic leucine zipper transcription factor, ATF-like	0.001617344	0.028679267	1.64	0.668	0
1146	VTCN1	V-set domain containing T cell activation inhibitor 1	0.001618058	0.028679267	2.01	0.643	0
1147	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	0.001617284	0.028679267	1.88	0.647	0
1148	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	0.001620252	0.028693142	2.92	0.621	0
1149	PRR15	proline rich 15	0.001623698	0.028729141	0.41	0.640	0
1150	CT47A11	cancer/testis antigen family 47, member A11	0.001625965	0.028744228	0.37	0.648	0
1151	C8orf34	chromosome 8 open reading frame 34	0.001638072	0.028872446	0.55	0.666	0
1152	CRYM	crystallin, mu	0.001638898	0.028872446	1.70	0.657	0
1153	APIP	APAF1 interacting protein	0.001635843	0.028872446	0.50	0.629	0

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1154	ZNF85	zinc finger protein 85	0.001637154	0.028872446	0.55	0.657	0
1155	PEX11A	peroxisomal biogenesis factor 11 alpha	0.001642411	0.028884264	0.53	0.637	0
1156	SRBD1	S1 RNA binding domain 1	0.001641814	0.028884264	0.31	0.648	0
1157	CLEC4A	C-type lectin domain family 4, member A	0.001645248	0.028893511	3.41	0.639	0
1158	EGLN1	egl nine homolog 1	0.001645779	0.028893511	0.26	0.646	0
1159	SYT7	synaptotagmin VII	0.001647849	0.028904893	2.20	0.641	0
1160	FLJ38717	FLJ38717 protein	0.001649287	0.028905182	0.59	0.646	0
1161	AP1M2	adaptor-related protein complex 1, mu 2 subunit	0.00165631	0.029000721	1.83	0.641	0
1162	NOP16	NOP16 nucleolar protein homolog	0.001657592	0.029000721	3.08	0.654	0
1163	RBM20	RNA binding motif protein 20	0.001662732	0.02906565	0.30	0.663	0
1164	FBXO32	F-box protein 32	0.001669109	0.029152051	0.36	0.623	0
1165	RHOB	ras homolog gene family, member B	0.001671254	0.029164466	0.41	0.665	0
1166	RNU2-2	RNA, U2 small nuclear 2	0.001673928	0.029186069	0.70	0.623	0
1167	GGTLC2	gamma-glutamyltransferase light chain 2	0.001685244	0.029358195	2.95	0.669	0
1168	psiTPTE22	TPTE pseudogene	0.001694316	0.029490955	0.61	0.647	0
1169	OR5P3	olfactory receptor, family 5, subfamily P, member 3	0.001699348	0.029553247	2.61	0.603	0
1170	PAGE2	P antigen family, member 2	0.001710973	0.029729984	2.14	0.634	0
1171	OMA1	OMA1 homolog, zinc metallopeptidase	0.001720861	0.029876271	0.34	0.655	0
1172	CCR3	chemokine (C-C motif) receptor 3	0.001732321	0.02999212	1.46	0.672	0
1173	UBA5	ubiquitin-like modifier activating enzyme 5	0.001733435	0.02999212	3.20	0.627	0
1174	C17orf28	chromosome 17 open reading frame 28	0.001730759	0.02999212	1.49	0.655	0
1175	ZBTB7B	zinc finger and BTB domain containing 7B	0.001731288	0.02999212	2.84	0.643	0
1176	POLG2	polymerase (DNA directed), gamma 2, accessory subunit	0.001737278	0.030012631	2.39	0.650	0
1177	SGMS2	sphingomyelin synthase 2	0.001737573	0.030012631	0.54	0.625	0
1178	PANX3	pannexin 3	0.001740085	0.030030496	0.47	0.660	0
1179	SUMF2	sulfatase modifying factor 2	0.001744628	0.03008336	0.49	0.643	0
1180	ALKBH8	alkB, alkylation repair homolog 8	0.001750251	0.030129215	0.42	0.650	0
1181	BYSL	bystin-like	0.001749064	0.030129215	5.47	0.657	0
1182	FGFBP2	fibroblast growth factor binding protein 2	0.001756435	0.030210081	1.27	0.641	0.01
1183	C17orf46	chromosome 17 open reading frame 46	0.001764243	0.03029347	0.45	0.637	0
1184	EHF	ets homologous factor	0.001764263	0.03029347	1.58	0.629	0
1185	RAI14	retinoic acid induced 14	0.001774114	0.030436901	1.58	0.638	0
1186	FAM101B	family with sequence similarity 101, member B	0.001779284	0.030499867	1.38	0.664	0
1187	SLC35F2	solute carrier family 35, member F2	0.001780982	0.03050326	1.73	0.652	0
1188	SLC24A4	solute carrier family 24	0.001783131	0.030514354	0.51	0.651	0
1189	CDK6	cyclin-dependent kinase 6	0.001791046	0.03062402	1.64	0.686	0
1190	IL1RAP	interleukin 1 receptor accessory protein	0.001799462	0.030742061	2.51	0.676	0
1191	SHPRH	SNF2 histone linker PHD RING helicase	0.001805602	0.030821064	0.41	0.647	0
1192	IGFALS	insulin-like growth factor binding protein, acid labile subunit	0.00181061	0.030880618	1.49	0.646	0.01
1193	C21orf88	chromosome 21 open reading frame 88	0.001819754	0.03096481	0.40	0.649	0
1194	ZCCHC7	zinc finger, CCHC domain containing 7	0.001821639	0.03096481	0.50	0.633	0
1195	LRRC25	leucine rich repeat containing 25	0.00181952	0.03096481	2.74	0.643	0
1196	ZNF782	zinc finger protein 782	0.001820781	0.03096481	0.44	0.662	0
1197	OSGIN1	oxidative stress induced growth inhibitor 1	0.00184244	0.031292236	1.89	0.623	0
1198	IL8	interleukin 8	0.001844318	0.031297991	1.38	0.659	0
1199	IL1RL1	interleukin 1 receptor-like 1	0.001858062	0.031485306	1.61	0.655	0
1200	SPIRE2	spire homolog 2	0.001858454	0.031485306	0.74	0.639	0
1201	FXYD3	FXYD domain containing ion transport regulator 3	0.001863601	0.031528115	1.58	0.651	0
1202	NSL1	NSL1, MIND kinetochore complex component, homolog	0.001865633	0.031528115	0.36	0.643	0
1203	XYLB	xylulokinase homolog	0.001864195	0.031528115	1.88	0.642	0
1204	PMM2	phosphomannomutase 2	0.001869327	0.031564299	4.07	0.626	0
1205	CD46	CD46 molecule, complement regulatory protein	0.001874136	0.031619245	0.53	0.670	0
1206	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	0.001880594	0.031659039	2.40	0.651	0
1207	CAMP	cathelicidin antimicrobial peptide	0.001887279	0.031659039	0.61	0.653	0
1208	MIF4GD	MIF4G domain containing	0.00187829	0.031659039	0.47	0.631	0
1209	PTPN7	protein tyrosine phosphatase, non-receptor type 7	0.0018863	0.031659039	1.53	0.664	0
1210	TEX14	testis expressed 14	0.001885407	0.031659039	0.70	0.659	0
1211	ZNF585B	zinc finger protein 585B	0.001881686	0.031659039	0.36	0.646	0
1212	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.001887396	0.031659039	0.40	0.656	0
1213	LOC550112	hypothetical LOC550112	0.001891464	0.031701122	0.33	0.644	0
1214	KLHL15	kelch-like 15	0.001906641	0.031929166	0.64	0.663	0.01

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1215	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	0.00190928	0.031932176	3.03	0.658	0
1216	TRPC6	transient receptor potential cation channel, subfamily C, member 6	0.001911533	0.031932176	0.49	0.665	0
1217	CRELD2	cysteine-rich with EGF-like domains 2	0.001910735	0.031932176	7.10	0.673	0
1218	ZCCHC14	zinc finger, CCHC domain containing 14	0.001915075	0.031965094	3.20	0.663	0
1219	TMEM220	transmembrane protein 220	0.001917538	0.031979933	4.43	0.638	0
1220	HMHB1	histocompatibility (minor) HB-1	0.001921548	0.032020551	0.58	0.645	0
1221	ZMYND15	zinc finger, MYND-type containing 15	0.001924168	0.032037942	0.58	0.644	0
1222	ZNF546	zinc finger protein 546	0.001930934	0.032124287	0.43	0.659	0
1223	TNNI2	troponin I type 2	0.001932734	0.032127948	0.51	0.647	0
1224	TFB2M	transcription factor B2, mitochondrial	0.001939506	0.032186632	3.59	0.634	0
1225	ASB1	ankyrin repeat and SOCS box-containing 1	0.001941891	0.032186632	4.05	0.644	0
1226	LOC645553	cDNA clone IMAGE:5478640, partial cds	0.001939474	0.032186632	0.61	0.633	0
1227	MRPL1	mitochondrial ribosomal protein L1	0.001942597	0.032186632	0.47	0.648	0
1228	ZNF728	zinc finger protein 728	0.001952219	0.032319716	0.55	0.650	0
1229	NCOA6	nuclear receptor coactivator 6	0.001955681	0.032350691	2.73	0.668	0
1230	GRAMD4	GRAM domain containing 4	0.001958064	0.032363774	3.41	0.640	0
1231	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	0.001975315	0.032569464	0.65	0.622	0
1232	RAB35	RAB35, member RAS oncogene family	0.001973886	0.032569464	5.91	0.659	0
1233	ACOXL	acyl-Coenzyme A oxidase-like	0.001972412	0.032569464	1.58	0.641	0
1234	PARD3	par-3 partitioning defective 3 homolog	0.001984243	0.032690156	1.48	0.674	0
1235	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	0.001986555	0.032701758	2.34	0.672	0
1236	CCDC90A	coiled-coil domain containing 90A	0.001990923	0.032747138	5.00	0.644	0
1237	DSG2	desmoglein 2	0.001993393	0.032761269	1.82	0.648	0
1238	MAPK8	mitogen-activated protein kinase 8	0.001999347	0.032832577	0.58	0.646	0
1239	RPL23AP32	ribosomal protein L23a pseudogene 32	0.002013606	0.033003038	1.58	0.643	0
1240	TMEM63C	transmembrane protein 63C	0.002014598	0.033003038	1.43	0.643	0
1241	RNF24	ring finger protein 24	0.00201451	0.033003038	2.80	0.647	0
1242	CCL1	chemokine (C-C motif) ligand 1	0.002024151	0.033132849	1.61	0.643	0
1243	C5orf4	chromosome 5 open reading frame 4	0.002027467	0.033150065	0.46	0.643	0
1244	ANGPT4	angiopoietin 4	0.002028464	0.033150065	0.63	0.658	0
1245	LAYN	layilin	0.002030142	0.03315084	1.61	0.642	0
1246	AMN	amnionless homolog	0.002038695	0.033263781	0.62	0.632	0
1247	RASL10B	RAS-like, family 10, member B	0.002043449	0.033314615	0.56	0.654	0
1248	C15orf38	chromosome 15 open reading frame 38	0.002053445	0.033450752	0.49	0.653	0
1249	DCHS1	dachsous 1	0.002056103	0.033467232	1.74	0.655	0
1250	SERPINA1	serpin peptidase inhibitor, clade A	0.00206701	0.033590984	0.48	0.661	0
1251	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.002066026	0.033590984	4.97	0.655	0
1252	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	0.00206877	0.033592727	6.12	0.652	0
1253	SRPX2	sushi-repeat-containing protein, X-linked 2	0.002072219	0.033621881	1.53	0.669	0
1254	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	0.002074572	0.033633211	3.21	0.642	0
1255	RBM3	RNA binding motif (RNP1, RRM) protein 3	0.002082092	0.033728226	0.50	0.601	0
1256	ITGA7	integrin, alpha 7	0.002083834	0.033729576	2.40	0.639	0
1257	ZNF479	zinc finger protein 479	0.002086396	0.033744184	0.58	0.665	0
1258	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	0.002090355	0.033781326	1.54	0.655	0
1259	DUSP13	dual specificity phosphatase 13	0.002105339	0.033977305	1.65	0.635	0
1260	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	0.002105824	0.033977305	0.24	0.639	0
1261	PTP4A2	protein tyrosine phosphatase type IVA, member 2	0.002130127	0.034342169	0.45	0.610	0
1262	SRPK1	SFRS protein kinase 1	0.002135729	0.034405204	4.10	0.649	0
1263	CDH23	cadherin-like 23	0.002145683	0.034426095	0.57	0.660	0
1264	SLAMF7	SLAM family member 7	0.002144693	0.034426095	1.39	0.641	0
1265	TDRD1	tudor domain containing 1	0.002140613	0.034426095	0.58	0.656	0
1266	PLA2G2D	phospholipase A2, group IID	0.002149959	0.034426095	1.61	0.668	0
1267	AKAP4	A kinase	0.002150573	0.034426095	0.48	0.666	0
1268	PLAGL2	pleiomorphic adenoma gene-like 2	0.002143436	0.034426095	2.31	0.649	0
1269	TMED7-TICAM2	TMED7-TICAM2 read-through transcript	0.002150221	0.034426095	0.40	0.662	0
1270	CCNC	cyclin C	0.002139385	0.034426095	0.44	0.659	0
1271	DLG1	discs, large homolog 1	0.002153894	0.03445213	0.55	0.649	0
1272	KIAA0368	KIAA0368	0.002161475	0.034546222	0.30	0.635	0
1273	DOK4	docking protein 4	0.002164049	0.034560189	1.62	0.620	0
1274	MYO6	myosin VI	0.0021671	0.034576445	0.64	0.635	0
1275	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	0.002170169	0.034576445	2.60	0.644	0

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1276	IPO4	importin 4	0.002168676	0.034576445	2.65	0.638	0
1277	BCL2L11	BCL2-like 11	0.002172023	0.034578886	2.42	0.668	0
1278	SEMA3B	sema domain, immunoglobulin domain	0.002187378	0.034796082	1.90	0.632	0
1279	RMRP	RNA component of mitochondrial RNA processing endoribonuclease	0.002189835	0.034807933	0.70	0.648	0
1280	TBC1D10A	TBC1 domain family, member 10A	0.002198849	0.034923905	0.17	0.667	0
1281	RGS20	regulator of G-protein signaling 20	0.002206527	0.034963916	1.65	0.623	0
1282	C8B	complement component 8, beta polypeptide	0.002205251	0.034963916	0.81	0.651	0
1283	ZNF808	zinc finger protein 808	0.0022035	0.034963916	0.43	0.650	0
1284	TRIM2	tripartite motif-containing 2	0.002212455	0.035012453	1.77	0.606	0
1285	ZNF676	zinc finger protein 676	0.002213035	0.035012453	0.60	0.655	0
1286	DNAJC17	DnaJ (Hsp40) homolog, subfamily C, member 17	0.002222846	0.0351203	0.50	0.624	0
1287	GRID1	glutamate receptor, ionotropic, delta 1	0.002225034	0.0351203	1.54	0.612	0
1288	UOX	urate oxidase	0.002224117	0.0351203	2.14	0.609	0
1289	CTSA	cathepsin A	0.0022292	0.03515876	3.34	0.641	0
1290	NPHP1	nephronophthisis 1	0.002234197	0.035210252	0.54	0.633	0
1291	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	0.002237993	0.035242755	0.74	0.642	0
1292	FLRT3	fibronectin leucine rich transmembrane protein 3	0.002242823	0.035291485	1.72	0.610	0
1293	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	0.002250054	0.035350547	1.74	0.664	0.01
1294	C10orf47	chromosome 10 open reading frame 47	0.002248412	0.035350547	1.67	0.648	0
1295	TNK1	tyrosine kinase, non-receptor, 1	0.002256254	0.035420578	0.43	0.629	0
1296	PDLIM3	PDZ and LIM domain 3	0.00225923	0.035439922	1.40	0.627	0
1297	ANXA8L2	annexin A8-like 2	0.002266176	0.03552148	1.60	0.660	0
1298	ZNF701	zinc finger protein 701	0.00228276	0.035753855	0.45	0.658	0
1299	FOLR2	folate receptor 2	0.00229784	0.035962348	1.92	0.644	0
1300	DYDC2	DPY30 domain containing 2	0.002306256	0.036066302	1.94	0.615	0
1301	MS4A15	membrane-spanning 4-domains, subfamily A, member 15	0.002309737	0.036092976	1.64	0.619	0
1302	SLC39A14	solute carrier family 39	0.002314336	0.036137064	1.58	0.651	0
1303	C14orf181	chromosome 14 open reading frame 181	0.002323247	0.036248352	0.62	0.622	0
1304	OSBPL6	oxysterol binding protein-like 6	0.002334966	0.036403268	1.92	0.670	0
1305	KIAA1841	KIAA1841	0.002339277	0.036442528	0.52	0.652	0
1306	IGBP1	immunoglobulin (CD79A) binding protein 1	0.002351148	0.036496953	0.16	0.659	0
1307	CLCN4	chloride channel 4	0.00234757	0.036496953	0.58	0.640	0
1308	MOCS3	molybdenum cofactor synthesis 3	0.00235249	0.036496953	0.68	0.631	0
1309	NBPF3	neuroblastoma breakpoint family, member 3	0.002353542	0.036496953	0.50	0.645	0
1310	FAM132A	family with sequence similarity 132, member A	0.002349582	0.036496953	1.76	0.640	0
1311	TOMM20L	translocase of outer mitochondrial membrane 20 homolog	0.00235005	0.036496953	0.47	0.642	0
1312	ZIK1	zinc finger protein interacting with K protein 1 homolog	0.002355796	0.036504057	0.32	0.638	0
1313	KRTAP23-1	keratin associated protein 23-1	0.002359246	0.036514267	0.55	0.643	0
1314	MEGF11	multiple EGF-like-domains 11	0.002360047	0.036514267	0.40	0.644	0
1315	KLHL5	kelch-like 5	0.002363188	0.03653506	2.39	0.661	0
1316	FFAR3	free fatty acid receptor 3	0.002366625	0.036540517	1.38	0.661	0
1317	TRIB1	tribbles homolog 1	0.002371321	0.036540517	3.02	0.639	0
1318	C10orf35	chromosome 10 open reading frame 35	0.002372274	0.036540517	0.39	0.669	0
1319	RNF168	ring finger protein 168	0.002372527	0.036540517	0.35	0.639	0
1320	LOC728208	hypothetical protein LOC728208	0.002368468	0.036540517	0.53	0.657	0
1321	MAP2K3	mitogen-activated protein kinase kinase 3	0.002376354	0.036571739	2.70	0.643	0
1322	EPM2AIP1	EPM2A (laforin) interacting protein 1	0.002412419	0.037070654	1.45	0.645	0.01
1323	CDK5R2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	0.00241235	0.037070654	0.57	0.662	0
1324	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	0.002417043	0.037085652	0.26	0.672	0
1325	ZNF562	zinc finger protein 562	0.002415704	0.037085652	3.56	0.649	0
1326	SCARNA10	small Cajal body-specific RNA 10	0.002420775	0.037114893	0.60	0.654	0
1327	TSHZ3	teashirt zinc finger homeobox 3	0.002434309	0.037294272	1.55	0.649	0
1328	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	0.002437639	0.037309461	0.58	0.648	0
1329	C7orf40	chromosome 7 open reading frame 40	0.002438971	0.037309461	3.08	0.660	0
1330	IGLL1	immunoglobulin lambda-like polypeptide 1	0.00245677	0.037507418	1.34	0.653	0
1331	NUAK2	NUAK family, SNF1-like kinase, 2	0.002455443	0.037507418	1.68	0.674	0
1332	FRRS1	ferric-chelate reductase 1	0.002457446	0.037507418	0.62	0.639	0
1333	ZNF876P	zinc finger protein 876	0.002464628	0.037588817	0.36	0.652	0
1334	LOC222070	cDNA FLJ32004 fis, clone NT2RP7009429	0.002471075	0.037630679	0.26	0.659	0
1335	HLA-B	major histocompatibility complex, class I, B	0.002470729	0.037630679	0.35	0.652	0
1336	HM13	histocompatibility (minor) 13	0.002475327	0.037639042	2.82	0.649	0

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1337	TRIM25	tripartite motif-containing 25	0.002473791	0.037639042	2.55	0.631	0
1338	HSPD1	heat shock 60kDa protein 1 (chaperonin) (HSPD1), nuclear gene encoding	0.002477538	0.037644512	3.83	0.636	0
1339	HOXA10	homeobox A10	0.002480018	0.037654042	0.56	0.623	0
1340	FLJ30698	cDNA FLJ30698 fis, clone FCBBF2000825	0.002484587	0.037695258	0.39	0.648	0
1341	SFTPA2	surfactant protein A2	0.002486946	0.037702911	1.68	0.639	0
1342	CASP3	caspase 3, apoptosis-related cysteine peptidase	0.002491747	0.037747554	3.85	0.662	0
1343	CDK3	cyclin-dependent kinase 3	0.002497287	0.037803308	0.62	0.633	0
1344	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	0.002500774	0.037827929	0.32	0.656	0
1345	COMT	catechol-O-methyltransferase	0.002502936	0.037832477	0.42	0.654	0
1346	RBMS2	RNA binding motif, single stranded interacting protein 2	0.002518622	0.038041294	0.43	0.645	0
1347	FAM26F	family with sequence similarity 26, member F	0.002523003	0.038079179	1.51	0.657	0
1348	ARF6	ADP-ribosylation factor 6	0.002531966	0.038157793	2.39	0.636	0
1349	HOXA9	homeobox A9	0.002530254	0.038157793	0.59	0.628	0
1350	ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	0.002545188	0.03832864	2.02	0.642	0
1351	CFH	complement factor H	0.0025582	0.038467606	1.49	0.668	0
1352	PDCL	phosducin-like	0.002556578	0.038467606	0.52	0.626	0
1353	ZNF804A	zinc finger protein 804A	0.002562881	0.038477526	0.42	0.665	0.02
1354	TBC1D10C	TBC1 domain family, member 10C	0.002563784	0.038477526	0.34	0.624	0
1355	ULBP1	UL16 binding protein 1	0.002565514	0.038477526	1.55	0.655	0
1356	SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	0.00256643	0.038477526	2.18	0.665	0
1357	CDKN1C	cyclin-dependent kinase inhibitor 1C	0.002578418	0.038628769	1.39	0.633	0
1358	FN3K	fructosamine 3 kinase	0.00258097	0.038638525	0.61	0.646	0
1359	UBFD1	ubiquitin family domain containing 1	0.002585203	0.038644978	3.45	0.655	0
1360	JPH1	junctophilin 1	0.002584008	0.038644978	1.79	0.623	0
1361	LIM2	lens intrinsic membrane protein 2, 19kDa	0.002597314	0.038797501	1.56	0.624	0
1362	SAMHD1	SAM domain and HD domain 1	0.002603353	0.03885915	0.41	0.659	0
1363	VWCE	von Willebrand factor C and EGF domains	0.002610849	0.038942446	0.31	0.671	0
1364	DDA1	DET1 and DDB1 associated 1	0.002615142	0.038961277	0.28	0.633	0
1365	VSIG10	V-set and immunoglobulin domain containing 10	0.002615944	0.038961277	0.60	0.627	0
1366	LY6G6D	lymphocyte antigen 6 complex, locus G6D	0.002619979	0.038992804	0.63	0.634	0
1367	TP53BP2	tumor protein p53 binding protein, 2	0.002625617	0.038998815	2.24	0.663	0
1368	RHPN2	rhophilin, Rho GTPase binding protein 2	0.002624705	0.038998815	1.72	0.633	0
1369	SNORD3B-1	small nucleolar RNA, C/D box 3B-1	0.002626138	0.038998815	0.58	0.634	0
1370	GLTP	glycolipid transfer protein	0.002630428	0.039034015	0.53	0.631	0
1371	UIMC1	ubiquitin interaction motif containing 1	0.002643361	0.039197319	2.99	0.646	0
1372	FCRL1	Fc receptor-like 1	0.002646122	0.039209662	0.63	0.628	0
1373	DAPK2	death-associated protein kinase 2	0.002664215	0.039449016	1.40	0.675	0
1374	APC	adenomatous polyposis coli	0.002666679	0.03945675	0.52	0.646	0
1375	ICOSLG	ICOS ligand Precursor (B7 homolog 2)(B7-H2)(B7-like protein GI50)(B7-related protein 1)(B7RP-1)(CD275 antigen)	0.00266941	0.039468442	1.84	0.673	0
1376	ACO1	aconitase 1, soluble	0.002679776	0.039578058	0.66	0.640	0
1377	EVX1	even-skipped homeobox 1	0.002682664	0.039578058	0.62	0.639	0
1378	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	0.002680791	0.039578058	0.55	0.638	0
1379	ACER2	alkaline ceramidase 2	0.002688696	0.039638278	0.52	0.623	0
1380	TPD52L1	tumor protein D52-like 1	0.002697657	0.039741564	0.73	0.652	0
1381	ECSCR	endothelial cell-specific chemotaxis regulator	0.002700469	0.039754184	0.73	0.620	0
1382	EHD4	EH-domain containing 4	0.002713165	0.039895777	0.41	0.631	0
1383	GNAO1	guanine nucleotide binding protein	0.002714012	0.039895777	0.65	0.624	0
1384	MT1L	metallothionein 1L	0.00273797	0.040218879	2.31	0.629	0
1385	S100A13	S100 calcium binding protein A13	0.002741597	0.040243087	0.60	0.608	0
1386	MAP4	microtubule-associated protein 4	0.00274498	0.04026367	0.51	0.617	0
1387	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	0.002747521	0.040271884	0.46	0.641	0
1388	N4BP2L1	NEDD4 binding protein 2-like 1	0.002754932	0.04035142	0.42	0.647	0
1389	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0.002766516	0.040491913	5.70	0.631	0
1390	TP53TG3	TP53 target 3	0.002784331	0.040723349	0.53	0.641	0
1391	DUSP5	dual specificity phosphatase 5	0.002796377	0.040811443	1.84	0.650	0
1392	C8A	complement component 8, alpha polypeptide	0.002792537	0.040811443	0.72	0.651	0
1393	MACROD2	MACRO domain containing 2	0.002795306	0.040811443	1.75	0.614	0
1394	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0.002799204	0.040823403	1.59	0.634	0
1395	CDH5	cadherin 5, type 2	0.002813523	0.040914825	0.28	0.643	0
1396	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	0.002812687	0.040914825	1.78	0.640	0
1397	EXOC4	exocyst complex component 4	0.002812729	0.040914825	0.45	0.635	0

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1398	PTCD3	Pentatricopeptide repeat domain 3	0.002811668	0.040914825	0.50	0.642	0
1399	DYX1C1	dyslexia susceptibility 1 candidate 1	0.002817543	0.040943997	0.62	0.617	0
1400	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	0.002822824	0.040991432	0.63	0.635	0
1401	ZNF799	zinc finger protein 799	0.002828718	0.041047712	0.39	0.641	0
1402	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial	0.002835674	0.041080564	4.79	0.646	0
1403	C7orf53	chromosome 7 open reading frame 53	0.002837208	0.041080564	1.66	0.692	0
1404	HOXA5	homeobox A5	0.002839065	0.041080564	0.58	0.627	0
1405	HIST2H2AC	histone cluster 2, H2ac	0.002835032	0.041080564	0.59	0.641	0
1406	NKG7	natural killer cell group 7 sequence	0.002842954	0.041107581	1.33	0.651	0
1407	ZNF486	zinc finger protein 486	0.002856034	0.041267361	0.63	0.662	0
1408	TSPAN19	tetraspanin 19	0.002859083	0.041282075	1.80	0.625	0
1409	LOC100128551	cDNA FLJ43158 fis, clone ERLTF2000324.	0.002862844	0.041307036	2.07	0.616	0
1410	BTD	biotinidase	0.00287339	0.041373051	0.56	0.638	0
1411	RPAP2	RNA polymerase II associated protein 2	0.00287298	0.041373051	0.25	0.645	0
1412	NR2C1	nuclear receptor subfamily 2, group C, member 1	0.002873524	0.041373051	0.41	0.650	0
1413	C14orf167	chromosome 14 open reading frame 167	0.002894626	0.041602499	0.26	0.675	0
1414	OR2A9P	olfactory receptor, family 2, subfamily A, member 9 pseudogene	0.002894729	0.041602499	0.70	0.629	0
1415	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	0.002895599	0.041602499	3.30	0.640	0
1416	ACER1	alkaline ceramidase 1	0.002899879	0.041634564	0.59	0.665	0
1417	MAGEA6	melanoma antigen family A, 6	0.002908261	0.041696016	0.62	0.637	0
1418	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog	0.002906335	0.041696016	2.01	0.635	0
1419	C9orf152	chromosome 9 open reading frame 152	0.002917365	0.041797064	1.34	0.633	0
1420	JAK3	Janus kinase 3	0.002928813	0.041902021	1.37	0.648	0
1421	ZCCHC17	zinc finger, CCHC domain containing 17	0.002927265	0.041902021	0.37	0.634	0
1422	BCL7A	B-cell CLL/lymphoma 7A	0.002931023	0.041904153	1.71	0.646	0
1423	FIBCD1	fibrinogen C domain containing 1	0.002937669	0.041914522	0.38	0.655	0
1424	HTATSF1	HIV-1 Tat specific factor 1	0.002937934	0.041914522	3.11	0.636	0
1425	SNRK	SNF related kinase	0.002934559	0.041914522	2.32	0.627	0
1426	SLC17A9	solute carrier family 17, member 9	0.002955244	0.042102389	1.86	0.652	0
1427	IFITM3	interferon induced transmembrane protein 3 (1-8U)	0.002953263	0.042102389	1.68	0.646	0
1428	C7orf23	chromosome 7 open reading frame 23	0.002962581	0.042151613	0.34	0.659	0
1429	BAGE4	B melanoma antigen family, member 4	0.002962846	0.042151613	0.59	0.647	0
1430	AKR1B1	aldo-keto reductase family 1, member B1 (aldose reductase)	0.002965535	0.04216037	0.49	0.657	0
1431	LOC100132207	cDNA FLJ41345 fis, clone BRAWH2002761.	0.002983356	0.042384081	0.35	0.648	0
1432	CD14	CD14 molecule	0.002985751	0.042388496	2.86	0.637	0
1433	LOC100130238	hypothetical LOC100130238	0.00300663	0.042655121	0.58	0.626	0
1434	SPATA6	spermatogenesis associated 6	0.0030132	0.042718515	0.43	0.626	0
1435	KRTAP5-5	keratin associated protein 5-5	0.0030164	0.042734087	0.49	0.655	0
1436	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	0.003020734	0.042735919	0.68	0.614	0
1437	OR52M1	olfactory receptor, family 52, subfamily M, member 1	0.003018674	0.042735919	0.49	0.659	0
1438	VEZT	vezatin, adherens junctions transmembrane protein	0.003023573	0.042738657	3.17	0.636	0
1439	ZNF2	zinc finger protein 2	0.003029002	0.042738657	0.53	0.659	0
1440	TAS1R3	Taste receptor type 1 member 3 Precursor	0.003031438	0.042738657	0.59	0.638	0
1441	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	0.003028731	0.042738657	7.99	0.661	0
1442	FBXO9	F-box protein 9	0.003030672	0.042738657	0.28	0.637	0
1443	ZNF326	zinc finger protein 326	0.003052272	0.042943033	3.07	0.630	0
1444	CSF1R	colony stimulating factor 1 receptor	0.003051046	0.042943033	3.12	0.635	0
1445	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.003051198	0.042943033	0.78	0.625	0
1446	CENPT	centromere protein T	0.003057475	0.042986493	0.63	0.646	0
1447	GPR176	G protein-coupled receptor 176	0.003064431	0.043054509	0.53	0.667	0
1448	THAP10	THAP domain containing 10	0.003069257	0.043073756	0.66	0.631	0
1449	SPOP	speckle-type POZ protein	0.003070038	0.043073756	0.28	0.628	0
1450	TSPAN8	tetraspanin 8	0.003083629	0.04323461	1.45	0.659	0
1451	IGSF6	immunoglobulin superfamily, member 6	0.003087091	0.043253317	2.22	0.662	0
1452	TACR2	tachykinin receptor 2	0.003092215	0.043295268	0.33	0.616	0
1453	OLAH	oleoyl-ACP hydrolase	0.003094366	0.043295572	1.44	0.643	0
1454	PATE3	prostate and testis expressed 3	0.003097871	0.043314798	0.48	0.626	0
1455	CCR1	chemokine (C-C motif) receptor 1	0.003119312	0.043534081	2.88	0.649	0
1456	ABHD4	abhydrolase domain containing 4	0.003120894	0.043534081	0.30	0.642	0
1457	LOC153577	cDNA FLJ30091 fis, clone BNGH41000017	0.003126335	0.043534081	2.10	0.650	0
1458	ETNK2	ethanolamine kinase 2	0.003124998	0.043534081	1.59	0.634	0

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1459	ARHGAP9	Rho GTPase activating protein 9	0.003126402	0.043534081	2.55	0.636	0
1460	GCC2	GRIP and coiled-coil domain containing 2	0.00312222	0.043534081	0.57	0.640	0
1461	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14	0.003128685	0.043536047	0.46	0.657	0
1462	OSBPL7	oxysterol binding protein-like 7	0.00314262	0.04367017	1.52	0.657	0
1463	TRIM34	tripartite motif-containing 34	0.003140641	0.04367017	0.51	0.641	0
1464	LOC399715	cDNA FLJ46311 fis, clone TESTI4040197	0.003148636	0.043694041	1.58	0.633	0
1465	C17orf89	chromosome 17 open reading frame 89	0.003147738	0.043694041	4.68	0.632	0
1466	C1orf95	chromosome 1 open reading frame 95	0.003162899	0.043842586	1.76	0.624	0
1467	LOC644189	similar to peroxisomal long-chain acyl-coA thioesterase	0.00316581	0.043842586	0.61	0.646	0
1468	NANOG	Nanog homeobox	0.003165368	0.043842586	0.67	0.675	0
1469	ZNF185	zinc finger protein 185 (LIM domain)	0.003175674	0.04389897	0.37	0.702	0
1470	SYPL2	synaptophysin-like 2	0.003176359	0.04389897	1.86	0.594	0
1471	MAD2L2	MAD2 mitotic arrest deficient-like 2	0.003173755	0.04389897	4.41	0.656	0
1472	ALAS2	aminolevulinate, delta-, synthase 2	0.00318381	0.043972043	1.27	0.657	0.01
1473	PODXL	podocalyxin-like	0.003187064	0.043987112	2.18	0.628	0
1474	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2	0.003197488	0.044101034	2.60	0.625	0
1475	ZNF324B	zinc finger protein 324B	0.003200858	0.044117584	0.27	0.650	0
1476	LOC729770	hypothetical protein LOC729770	0.003204248	0.044134391	0.56	0.666	0
1477	APOLD1	apolipoprotein L domain containing 1	0.003224209	0.044359088	0.54	0.650	0
1478	ZNF257	zinc finger protein 257	0.003224925	0.044359088	0.41	0.649	0
1479	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	0.003229988	0.044398683	2.15	0.640	0
1480	ATP8B3	ATPase, class I, type 8B, member 3	0.00323631	0.044455532	0.70	0.627	0
1481	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7	0.003238558	0.044456374	2.38	0.653	0
1482	TAS2R50	taste receptor, type 2, member 50	0.003243464	0.044463671	0.64	0.658	0.01
1483	LOC100131043	cDNA FLJ42228 fis, clone THYMU2041252.	0.003242177	0.044463671	1.48	0.657	0
1484	MURC	muscle-related coiled-coil protein	0.003246413	0.04447411	0.70	0.662	0
1485	RELB	v-rel reticuloendotheliosis viral oncogene homolog B	0.003255352	0.044546594	1.97	0.634	0
1486	SV2B	synaptic vesicle glycoprotein 2B	0.003256087	0.044546594	1.56	0.625	0
1487	POT1	POT1 protection of telomeres 1 homolog	0.003258827	0.0445541	0.66	0.628	0
1488	OXER1	oxoeicosanoid (OXE) receptor 1	0.003288111	0.044924261	2.00	0.621	0
1489	CLCN1	chloride channel 1, skeletal muscle	0.003292601	0.044955385	0.52	0.632	0
1490	BRSK2	BR serine/threonine kinase 2	0.003311756	0.04518658	0.47	0.661	0
1491	PRDM2	PR domain containing 2, with ZNF domain	0.003319819	0.045243999	3.01	0.651	0
1492	KRTAP4-2	keratin associated protein 4-2	0.003320415	0.045243999	0.51	0.650	0
1493	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	0.003323347	0.045253615	1.63	0.603	0
1494	TBC1D16	TBC1 domain family, member 16	0.003337403	0.04541459	2.08	0.662	0
1495	C3orf39	chromosome 3 open reading frame 39	0.003345094	0.045428034	0.34	0.643	0
1496	PRELID1	PRELI domain containing 1	0.003342902	0.045428034	0.26	0.644	0
1497	FAM81B	family with sequence similarity 81, member B	0.003344567	0.045428034	1.52	0.624	0
1498	LOC100129292	cDNA FLJ46168 fis, clone TESTI4003279.	0.003349729	0.045460609	0.54	0.651	0
1499	LOC92659	hypothetical LOC92659	0.003358796	0.04549256	0.44	0.657	0
1500	DPYSL3	dihydropyrimidinase-like 3	0.003354718	0.04549256	1.46	0.661	0
1501	PAX4	paired box 4	0.003357624	0.04549256	0.38	0.653	0
1502	FLJ11235	hypothetical FLJ11235	0.003363595	0.045527219	0.72	0.634	0
1503	HLA-A	major histocompatibility complex, class I, A	0.003368562	0.045564111	0.22	0.646	0
1504	ZNF706	zinc finger protein 706	0.003382752	0.045636766	1.32	0.625	0.01
1505	PGM1	phosphoglucomutase 1	0.003376962	0.045636766	0.33	0.644	0
1506	B3GNT9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	0.003382912	0.045636766	1.66	0.649	0
1507	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	0.003379505	0.045636766	0.61	0.652	0
1508	FLJ40434	hypothetical FLJ40434	0.003385509	0.045641514	0.49	0.651	0
1509	FAM138A	family with sequence similarity 138, member A	0.00338828	0.045648599	0.44	0.660	0
1510	PDLIM4	PDZ and LIM domain 4	0.003393891	0.04566367	1.89	0.607	0
1511	LCN9	lipocalin 9	0.003392935	0.04566367	0.43	0.671	0
1512	RNF166	ring finger protein 166	0.003397823	0.045686338	0.43	0.650	0
1513	BBS2	Bardet-Biedl syndrome 2	0.003402441	0.045718191	0.28	0.639	0
1514	HPRT1	hypoxanthine phosphoribosyltransferase 1	0.003410594	0.04579747	5.14	0.633	0
1515	MYCNOS	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) opposite strand	0.003433549	0.04595946	0.63	0.620	0
1516	LOC100128276	hypothetical LOC100128276	0.003432056	0.04595946	1.71	0.630	0
1517	ASNS	asparagine synthetase	0.003433433	0.04595946	1.96	0.640	0
1518	ZNF248	zinc finger protein 248	0.003425669	0.04595946	0.49	0.634	0
1519	GLUD1	glutamate dehydrogenase 1	0.003433961	0.04595946	0.36	0.639	0

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1520	GNRH1	gonadotropin-releasing hormone 1	0.003444669	0.046072452	1.88	0.659	0
1521	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	0.003451913	0.046129274	1.94	0.665	0
1522	ZNF273	zinc finger protein 273	0.003453456	0.046129274	0.49	0.644	0
1523	TSPAN10	tetraspanin 10	0.003457828	0.046157348	0.44	0.641	0
1524	MRC2	mannose receptor, C type 2	0.003480702	0.046432205	1.76	0.645	0
1525	RNU12	RNA, U12 small nuclear	0.003486984	0.046455041	0.58	0.631	0
1526	HSF1	heat shock transcription factor 1	0.003486825	0.046455041	0.39	0.637	0
1527	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	0.003500955	0.046610614	0.59	0.688	0
1528	SBDS	Shwachman-Bodian-Diamond syndrome	0.003510682	0.046709537	0.52	0.633	0
1529	ACSF2	acyl-CoA synthetase family member 2	0.003515491	0.046742921	0.49	0.638	0
1530	PSD4	pleckstrin and Sec7 domain containing 4	0.003524261	0.046828901	0.66	0.622	0
1531	FYB	FYN binding protein	0.003530457	0.046849997	1.80	0.638	0
1532	E2F6	E2F transcription factor 6	0.003530216	0.046849997	4.19	0.635	0
1533	PRINS	psoriasis associated RNA induced by stress	0.003548294	0.047055983	2.57	0.617	0
1534	SPINK7	serine peptidase inhibitor, Kazal type 7	0.003555991	0.047127317	0.39	0.665	0
1535	OR2AG2	olfactory receptor, family 2, subfamily AG, member 2	0.003558672	0.047132124	0.62	0.657	0
1536	EPDR1	ependymin related protein 1	0.003561151	0.047134249	1.63	0.664	0
1537	POLQ	polymerase (DNA directed), theta	0.003566951	0.04718029	1.81	0.668	0
1538	MAK	male germ cell-associated kinase	0.003589899	0.047429929	1.72	0.647	0
1539	SLFN13	schlafen family member 13	0.00359049	0.047429929	1.43	0.632	0
1540	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	0.003608181	0.04763267	0.47	0.651	0
1541	CTSK	cathepsin K	0.003612282	0.047655872	1.43	0.610	0
1542	RAB5A	RAB5A, member RAS oncogene family	0.003616627	0.047682243	3.44	0.639	0
1543	KRTAP4-12	keratin associated protein 4-12	0.003620221	0.047698697	0.57	0.660	0
1544	TTC1	tetratricopeptide repeat domain 1	0.003634576	0.047856814	0.35	0.640	0
1545	C1orf93	chromosome 1 open reading frame 93	0.003638634	0.047879246	1.99	0.631	0
1546	MEGF6	multiple EGF-like-domains 6	0.003651254	0.047966597	1.51	0.670	0
1547	CA4	carbonic anhydrase IV	0.003652351	0.047966597	1.49	0.634	0
1548	ZNF430	zinc finger protein 430	0.003651783	0.047966597	0.52	0.650	0
1549	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	0.003657695	0.048005773	0.40	0.644	0
1550	ZNF583	zinc finger protein 583	0.003671035	0.048149767	0.36	0.633	0
1551	BACE1	beta-site APP-cleaving enzyme 1	0.003676002	0.048183836	0.59	0.614	0
1552	TTYH1	tweety homolog 1	0.003679278	0.048195698	0.61	0.639	0
1553	TARS2	threonyl-tRNA synthetase 2, mitochondrial	0.003686481	0.048258953	0.31	0.643	0
1554	PNPLA2	patatin-like phospholipase domain containing 2	0.003706409	0.048488602	0.54	0.621	0
1555	FAM21C	family with sequence similarity 21, member C	0.003718072	0.048609912	0.60	0.626	0
1556	NEK11	NIMA	0.003733912	0.048785618	0.46	0.627	0
1557	SIGLEC8	sialic acid binding Ig-like lectin 8	0.003747401	0.048853379	1.64	0.606	0
1558	CRY2	cryptochrome 2	0.003748096	0.048853379	0.26	0.631	0
1559	TRIM5	tripartite motif-containing 5	0.00374871	0.048853379	0.42	0.648	0
1560	LRRC33	leucine rich repeat containing 33	0.003744438	0.048853379	1.71	0.651	0
1561	LOC642587	NPC-A-5	0.003752786	0.048875163	1.73	0.652	0
1562	ZNF709	zinc finger protein 709	0.003756889	0.048897285	0.38	0.657	0
1563	SULF1	sulfatase 1	0.00376885	0.048991304	6.57	0.593	0
1564	S100A8	S100 calcium binding protein A8	0.003768933	0.048991304	1.99	0.621	0
1565	PPID	peptidylprolyl isomerase D	0.00377282	0.049010496	2.32	0.650	0
1566	RNF208	ring finger protein 208	0.003791424	0.049189306	0.46	0.676	0
1567	UTP3	UTP3, small subunit (SSU) processome component, homolog	0.00379022	0.049189306	4.82	0.635	0
1568	ZHX3	zinc fingers and homeoboxes 3	0.003794561	0.049198613	0.37	0.630	0
1569	ASB18	ankyrin repeat and SOCS box-containing 18	0.003808053	0.049303187	0.61	0.640	0
1570	ZNF138	zinc finger protein 138	0.003809645	0.049303187	0.63	0.624	0
1571	ZNF625	zinc finger protein 625	0.003809902	0.049303187	0.50	0.643	0
1572	WDFY3	WD repeat and FYVE domain containing 3	0.00381588	0.049349134	2.44	0.647	0
1573	LOC283050	hypothetical LOC283050	0.003833121	0.049509118	1.41	0.652	0
1574	CXorf26	chromosome X open reading frame 26	0.003830995	0.049509118	0.54	0.643	0
1575	VSNL1	visinin-like 1	0.003847134	0.049600738	1.29	0.641	0.03
1576	ZNF688	zinc finger protein 688	0.003847397	0.049600738	0.16	0.632	0
1577	DCLRE1A	DNA cross-link repair 1A	0.003849974	0.049600738	2.45	0.644	0
1578	PRKCA	protein kinase C, alpha	0.003847804	0.049600738	2.04	0.644	0
1579	UNC119B	unc-119 homolog B	0.003854622	0.04962917	2.75	0.657	0
1580	EIF2C1	eukaryotic translation initiation factor 2C, 1	0.003861461	0.049685755	0.44	0.650	0

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1581	PECR	peroxisomal trans-2-enoyl-CoA reductase	0.003866247	0.049711376	0.53	0.667	0
1582	ADNP2	ADNP homeobox 2	0.003868342	0.049711376	0.49	0.612	0

*Hazard Ratio (HR), p-value and FDR computed for association with mortality in the Freiburg cohort. For each gene the relative frequency of inclusion into the signature (the resampling inclusion frequency (Freq) from 100 resampling data sets) was recorded.

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Table S5. 9- Gene Signature picked by Componentwise Boosting

Table S5. 9- Gene Signature developed by Componentwise Boosting				
Gene Symbol	**Gene Name**	**Beta-value***	**FDR**	**Frequency****
BMP6	Bone morphogenetic protein 6	0.185910087	9.54573E-06	0.54
IBSP	Integrin-binding sialoprotein	0.106645031	4.17289E-05	0.54
S100A14	S100 calcium binding protein A14	0.132209853	9.54573E-06	0.47
STAB1	Stabilin 1	0.173815731	1.58025E-05	0.37
LOC284751	cDNA FLJ33286 fis	0.087142377	3.3665E-05	0.34
ANKRD22	Ankyrin repeat domain 22	0.035989823	0.000133129	0.22
SEPT4	Septin 4	-0.09270581	0.000987911	0.18
SLC16A1	Solute carrier family 16, member 1	0.101123344	0.000864992	0.08
FAM198B	Family with sequence similarity 198	0.029617883	4.56104E-05	0.03

*Estimated multivariable regression parameters (Beta-value), i.e., conditional log-hazard ratios, from componentwise boosting and univariate FDR computed for association with mortality in the Freiburg cohort. **For each gene the relative frequency of inclusion into the signature (the resampling inclusion frequency (Freq) from 100 resampling data sets) was recorded.

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Table S6. C-Indices and confidence intervals for the survival models

Table S6. C-Indices and confidence intervals for the survival models			
	c-index*	**2.5%**	**97.5%**
Freiburg Signature + GAP	0.755	0.709	0.813
Freiburg Signature	0.733	0.688	0.772
Freiburg GAP	0.602	0.526	0.686
Leuven Signature + GAP	0.779	0.658	0.879
Leuven Signature	0.656	0.546	0.762
Leuven GAP	0.709	0.606	0.801
Siena Signature + GAP	0.713	0.643	0.811
Siena Signature	0.634	0.542	0.724
Siena GAP	0.639	0.559	0.747

* C-indices and 95% confidence interval for models that predict patient survival either using the GAP index only, the grouping of patients based on the inferred gene expression signature or a combination of both. The gene expression signature was inferred using all expressed genes.

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Table S7. 6- Gene Signature picked by Componentwise Boosting

Table S6. 6- Gene Signature developed by Componentwise Boosting			
Gene Symbol	**Gene Name**	**FDR***	**Frequency****
BMP6	Bone morphogenetic protein 6	9.54573E-06	0.54
IBSP	Integrin-binding sialoprotein	4.17289E-05	0.54
S100A14	S100 calcium binding protein A14	9.54573E-06	0.47
STAB1	Stabilin 1	1.58025E-05	0.37
LOC284751	cDNA FLJ33286 fis, clone ASTRO2014174	3.3665E-05	0.34
ANKRD22	Ankyrin repeat domain 22	0.000133129	0.22

*Univariate FDR computed for association with mortality in the Freiburg cohort. **For each gene the relative frequency of inclusion into the signature (the resampling inclusion frequency (Freq) from 100 resampling data sets) was recorded.

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Table S8. Ingenuity Network Analysis of the BAL Signature related to Mortality

Top Networks		
ID	Associated Network Functions	Score
1	Cancer, Organismal Injury and Abnormalities, Reproductive System Disease	41
2	Dermatological Diseases and Conditions, Hereditary Disorder, Cell-To-Cell Signaling and Interaction	37
3	Cell Cycle, Cancer, Organismal Injury and Abnormalities	35
4	Cellular Movement, Cancer, Organismal Injury and Abnormalities	35
5	Carbohydrate Metabolism, Small Molecule Biochemistry, Skeletal and Muscular System Development and Function	33

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Table S9. The Airway Basal Cell (ABC) Signature

Table S8. List of ABC Genes and Association with Mortality in IPF

	Symbol	Gene Name	p-value	FDR*
1	S100A14	S100 calcium binding protein A14	9.39E-10	8.65E-07
2	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	3.77E-08	1.74E-05
3	ADM	adrenomedullin	6.22E-08	1.91E-05
4	NRG1	neuregulin 1	1.72E-07	3.95E-05
5	CYR61	cysteine-rich, angiogenic inducer, 61	2.30E-07	4.24E-05
6	RAB3D	RAB3D, member RAS oncogene family	3.14E-07	4.33E-05
7	CCNJL	cyclin J-like	3.71E-07	4.33E-05
8	SFN	stratifin	3.76E-07	4.33E-05
9	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	1.33E-06	0.00014
10	SCEL	sciellin	1.72E-06	0.00016
11	IER3	immediate early response 3	2.21E-06	0.00018
12	FAM110C	family with sequence similarity 110, member C	2.35E-06	0.00018
13	GJA1	gap junction protein, alpha 1, 43kDa	3.61E-06	0.00026
14	TRIM47	tripartite motif containing 47	4.24E-06	0.00028
15	FJX1	four jointed box 1 (Drosophila)	6.35E-06	0.00037
16	ANXA3	annexin A3	6.44E-06	0.00037
17	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	7.10E-06	0.00038
18	HOMER3	homer homolog 3 (Drosophila)	7.80E-06	0.00040
19	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	8.50E-06	0.00041
20	MEX3A	mex-3 homolog A (C. elegans)	8.83E-06	0.00041
21	C9orf89	chromosome 9 open reading frame 89	9.35E-06	0.00041
22	UCK2	uridine-cytidine kinase 2	1.05E-05	0.00042
23	NIPAL4	NIPA-like domain containing 4	1.06E-05	0.00042
24	FBLIM1	filamin binding LIM protein 1	1.10E-05	0.00042
25	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	1.59E-05	0.00059
26	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	2.37E-05	0.00080
27	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	2.40E-05	0.00080
28	ANGPTL4	angiopoietin-like 4	2.43E-05	0.00080
29	DBN1	drebrin 1	3.30E-05	0.00105
30	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	4.81E-05	0.00148
31	ECM1	extracellular matrix protein 1	5.30E-05	0.00158
32	LAMA3	laminin, alpha 3	6.31E-05	0.00182
33	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	6.53E-05	0.00182
34	TUBB3	tubulin, beta 3 class III	7.53E-05	0.00204
35	FERMT1	fermitin family member 1	8.50E-05	0.00224
36	MT1X	metallothionein 1X	0.00010	0.00256
37	TRIM7	tripartite motif containing 7	0.00010	0.00256
38	OAF	OAF homolog (Drosophila)	0.00011	0.00256
39	HTR7	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	0.00012	0.00273
40	KRT6A	keratin 6A	0.00012	0.00273
41	TMEM132A	transmembrane protein 132A	0.00013	0.00287
42	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	0.00016	0.00344
43	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	0.00017	0.00357
44	FAM129B	family with sequence similarity 129, member B	0.00017	0.00357
45	ZNF703	zinc finger protein 703	0.00018	0.00357
46	MT1H	metallothionein 1H	0.00018	0.00357
47	LARP1B	La ribonucleoprotein domain family, member 1B	0.00019	0.00357
48	GRB10	growth factor receptor-bound protein 10	0.00019	0.00357
49	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0.00019	0.00357
50	COL18A1	collagen, type XVIII, alpha 1	0.00020	0.00361
51	MEX3C	mex-3 homolog C (C. elegans)	0.00022	0.00393
52	JUB	jub, ajuba homolog (Xenopus laevis)	0.00022	0.00393
53	ECE1	endothelin converting enzyme 1	0.00026	0.00460
54	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	0.00036	0.00606
55	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	0.00039	0.00636

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56	YRDC	yrdC domain containing (E. coli)	0.00040	0.00636
57	KRT83	keratin 83	0.00041	0.00636
58	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	0.00041	0.00636
59	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	0.00041	0.00636
60	IRX1	iroquois homeobox 1	0.00041	0.00636
61	ZNF354C	zinc finger protein 354C	0.00042	0.00637
62	LRRC8A	leucine rich repeat containing 8 family, member A	0.00044	0.00659
63	CARD10	caspase recruitment domain family, member 10	0.00046	0.00666
64	SNHG3	small nucleolar RNA host gene 3 (non-protein coding)	0.00049	0.00699
65	FSTL3	follistatin-like 3 (secreted glycoprotein)	0.00050	0.00707
66	EHD2	EH-domain containing 2	0.00053	0.00739
67	KLK6	kallikrein-related peptidase 6	0.00056	0.00776
68	MARCKSL1	MARCKS-like 1	0.00058	0.00792
69	LOC100129387	uncharacterized LOC100129387	0.00062	0.00826
70	MYL9	myosin, light chain 9, regulatory	0.00065	0.00852
71	ABLIM3	actin binding LIM protein family, member 3	0.00069	0.00882
72	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.00069	0.00882
73	CLIC3	chloride intracellular channel 3	0.00073	0.00908
74	AHNAK2	AHNAK nucleoprotein 2	0.00073	0.00908
75	PHLDA2	pleckstrin homology-like domain, family A, member 2	0.00077	0.00935
76	MT1E	metallothionein 1E	0.00078	0.00935
77	BMP2	bone morphogenetic protein 2	0.00078	0.00935
78	KRT14	keratin 14	0.00081	0.00942
79	GAS6	growth arrest-specific 6	0.00081	0.00942
80	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0.00083	0.00948
81	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	0.00083	0.00948
82	TIMP3	TIMP metallopeptidase inhibitor 3	0.00085	0.00952
83	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	0.00086	0.00952
84	MT1B	metallothionein 1B	0.00091	0.00993
85	FGFBP1	fibroblast growth factor binding protein 1	0.00093	0.01013
86	FOSL1	FOS-like antigen 1	0.00098	0.01044
87	CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6	0.00102	0.01068
88	FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	0.00102	0.01068
89	LOC338620	uncharacterized protein LOC338620	0.00103	0.01071
90	RIMS3	regulating synaptic membrane exocytosis 3	0.00115	0.01170
91	C22orf36	chromosome 22 open reading frame 36	0.00116	0.01170
92	KCNS3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	0.00117	0.01170
93	LHFP	lipoma HMGIC fusion partner	0.00118	0.01173
94	NT5DC2	5'-nucleotidase domain containing 2	0.00128	0.01254
95	AREG	amphiregulin	0.00130	0.01258
96	CAV2	caveolin 2	0.00131	0.01258
97	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.00133	0.01261
98	SMOX	spermine oxidase	0.00150	0.01400
99	KLHL21	kelch-like 21 (Drosophila)	0.00150	0.01400
100	ADARB1	adenosine deaminase, RNA-specific, B1	0.00156	0.01437
101	HOPX	HOP homeobox	0.00158	0.01437
102	SYT7	synaptotagmin VII	0.00165	0.01488
103	FBXO32	F-box protein 32	0.00167	0.01492
104	SLC35F2	solute carrier family 35, member F2	0.00178	0.01577
105	OSGIN1	oxidative stress induced growth inhibitor 1	0.00184	0.01616
106	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	0.00199	0.01716
107	DSG2	desmoglein 2	0.00199	0.01716
108	SRPX2	sushi-repeat containing protein, X-linked 2	0.00207	0.01767
109	DOK4	docking protein 4	0.00216	0.01829
110	SEMA3B	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	0.00219	0.01831
111	RGS20	regulator of G-protein signaling 20	0.00221	0.01831
112	C10orf47	chromosome 10 open reading frame 47	0.00225	0.01849
113	SLC39A14	solute carrier family 39 (zinc transporter), member 14	0.00231	0.01886
114	TSHZ3	teashirt zinc finger homeobox 3	0.00243	0.01967
115	TPD52L1	tumor protein D52-like 1	0.00270	0.02160
116	MT1L	metallothionein 1L (gene/pseudogene)	0.00274	0.02174

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117	DUSP5	dual specificity phosphatase 5	0.00280	0.02201
118	VEZT	vezatin, adherens junctions transmembrane protein	0.00302	0.02344
119	PPP2R2A	protein phosphatase 2, regulatory subunit B, alpha	0.00303	0.02344
120	ETNK2	ethanolamine kinase 2	0.00312	0.02398
121	ASNS	asparagine synthetase (glutamine-hydrolyzing)	0.00343	0.02613
122	MRC2	mannose receptor, C type 2	0.00348	0.02628
123	VSNL1	visinin-like 1	0.00385	0.02881
124	DVL1	dishevelled, dsh homolog 1 (Drosophila)	0.00390	0.02895
125	C14orf34	chromosome 14 open reading frame 34	0.00402	0.02963
126	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	0.00409	0.02988
127	PLSCR3	phospholipid scramblase 3	0.00428	0.03101
128	ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	0.00439	0.03160
129	PDCD5	programmed cell death 5	0.00447	0.03179
130	PHLDA1	pleckstrin homology-like domain, family A, member 1	0.00449	0.03179
131	IPO9	importin 9	0.00456	0.03183
132	PGAM1	phosphoglycerate mutase 1 (brain)	0.00456	0.03183
133	FAM46B	family with sequence similarity 46, member B	0.00463	0.03203
134	CDH3	cadherin 3, type 1, P-cadherin (placental)	0.00470	0.03229
135	TMEM159	transmembrane protein 159	0.00482	0.03289
136	MAPK6	mitogen-activated protein kinase 6	0.00487	0.03297
137	SLC39A13	solute carrier family 39 (zinc transporter), member 13	0.00493	0.03317
138	PPP1R12B	protein phosphatase 1, regulatory subunit 12B	0.00500	0.03335
139	LAMC2	laminin, gamma 2	0.00514	0.03380
140	NFYA	nuclear transcription factor Y, alpha	0.00514	0.03380
141	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	0.00525	0.03427
142	KRT17	keratin 17	0.00535	0.03467
143	MICALL1	MICAL-like 1	0.00541	0.03482
144	DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila)	0.00546	0.03491
145	TEAD4	TEA domain family member 4	0.00575	0.03653
146	FHDC1	FH2 domain containing 1	0.00580	0.03653
147	HMGA1	high mobility group AT-hook 1	0.00583	0.03653
148	SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	0.00590	0.03673
149	ITGA6	integrin, alpha 6	0.00620	0.03818
150	TRIB3	tribbles homolog 3 (Drosophila)	0.00622	0.03818
151	ZNF281	zinc finger protein 281	0.00631	0.03846
152	CRABP2	cellular retinoic acid binding protein 2	0.00637	0.03861
153	FAM83G	family with sequence similarity 83, member G	0.00654	0.03935
154	GPRC5A	G protein-coupled receptor, family C, group 5, member A	0.00662	0.03957
155	PLXNA1	plexin A1	0.00685	0.04073
156	ATP13A2	ATPase type 13A2	0.00706	0.04170
157	PSAT1	phosphoserine aminotransferase 1	0.00735	0.04311
158	GTPBP4	GTP binding protein 4	0.00746	0.04323
159	FASN	fatty acid synthase	0.00746	0.04323
160	ELMO3	engulfment and cell motility 3	0.00759	0.04370
161	C10orf10	chromosome 10 open reading frame 10	0.00779	0.04452
162	TSPAN5	tetraspanin 5	0.00787	0.04452
163	STRAP	serine/threonine kinase receptor associated protein	0.00788	0.04452
164	MFGE8	milk fat globule-EGF factor 8 protein	0.00839	0.04710
165	ANKRD9	ankyrin repeat domain 9	0.00879	0.04908
166	EXT1	exostosin 1	0.00902	0.05004
167	AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	0.00907	0.05004
168	MAFA	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	0.00915	0.05018
169	KCNQ3	potassium voltage-gated channel, KQT-like subfamily, member 3	0.00934	0.05093
170	ZXDB	zinc finger, X-linked, duplicated B	0.00940	0.05093
171	DST	dystonin	0.00948	0.05108
172	LY6D	lymphocyte antigen 6 complex, locus D	0.00958	0.05130
173	AKAP2	A kinase (PRKA) anchor protein 2	0.00965	0.05139
174	XDH	xanthine dehydrogenase	0.01043	0.05521
175	IL6R	interleukin 6 receptor	0.01050	0.05527
176	RP9	retinitis pigmentosa 9 (autosomal dominant)	0.01099	0.05731
177	CTSL2	cathepsin L2	0.01101	0.05731

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178	TNKS1BP1	tankyrase 1 binding protein 1, 182kDa	0.01109	0.05739
179	STXBP1	syntaxin binding protein 1	0.01160	0.05933
180	PDPN	podoplanin	0.01160	0.05933
181	PXDN	peroxidasin homolog (Drosophila)	0.01173	0.05968
182	VCL	vinculin	0.01185	0.05986
183	PFKP	phosphofructokinase, platelet	0.01189	0.05986
184	LOC100132240	hypothetical LOC100132240	0.01203	0.06007
185	PRSS2	protease, serine, 2 (trypsin 2)	0.01207	0.06007
186	RAB38	RAB38, member RAS oncogene family	0.01217	0.06028
187	NCCRP1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	0.01242	0.06118
188	MT1A	metallothionein 1A	0.01256	0.06151
189	GK5	glycerol kinase 5 (putative)	0.01262	0.06151
190	SPINK5	serine peptidase inhibitor, Kazal type 5	0.01287	0.06241
191	IARS	isoleucyl-tRNA synthetase	0.01319	0.06358
192	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.01360	0.06526
193	EDN1	endothelin 1	0.01390	0.06630
194	TRAF3IP2	TRAF3 interacting protein 2	0.01413	0.06630
195	TMEM189	transmembrane protein 189	0.01414	0.06630
196	TUBA8	tubulin, alpha 8	0.01414	0.06630
197	AIG1	androgen-induced 1	0.01418	0.06630
198	RHBDF1	rhomboid 5 homolog 1 (Drosophila)	0.01508	0.07015
199	HDAC7	histone deacetylase 7	0.01532	0.07063
200	JAG1	jagged 1	0.01541	0.07063
201	NIPSNAP1	nipsnap homolog 1 (C. elegans)	0.01546	0.07063
202	ADA	adenosine deaminase	0.01549	0.07063
203	SBF1	SET binding factor 1	0.01563	0.07064
204	IL20RB	interleukin 20 receptor beta	0.01565	0.07064
205	CCDC85C	coiled-coil domain containing 85C	0.01575	0.07077
206	STX1A	syntaxin 1A (brain)	0.01588	0.07098
207	PAMR1	peptidase domain containing associated with muscle regeneration 1	0.01606	0.07143
208	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	0.01644	0.07280
209	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	0.01671	0.07362
210	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0.01724	0.07563
211	IGFBP4	insulin-like growth factor binding protein 4	0.01762	0.07693
212	SDCBP2	syndecan binding protein (syntenin) 2	0.01833	0.07925
213	FLJ13744	uncharacterized FLJ13744	0.01838	0.07925
214	TMSB15B	thymosin beta 15B	0.01841	0.07925
215	COL7A1	collagen, type VII, alpha 1	0.01996	0.08537
216	DGKA	diacylglycerol kinase, alpha 80kDa	0.02002	0.08537
217	TPM1	tropomyosin 1 (alpha)	0.02023	0.08587
218	TTPAL	tocopherol (alpha) transfer protein-like	0.02133	0.09013
219	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	0.02210	0.09296
220	GJB2	gap junction protein, beta 2, 26kDa	0.02221	0.09300
221	STC2	stanniocalcin 2	0.02356	0.09801
222	LOC645937	zinc finger protein 598 pseudogene	0.02363	0.09801
223	LTBP4	latent transforming growth factor beta binding protein 4	0.02386	0.09855
224	GARS	glycyl-tRNA synthetase	0.02470	0.10125
225	EPS8L2	EPS8-like 2	0.02474	0.10125
226	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	0.02512	0.10238
227	LOC100134237	uncharacterized LOC100134237	0.02579	0.10465
228	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	0.02831	0.11436
229	SLC38A2	solute carrier family 38, member 2	0.02888	0.11615
230	FAM83F	family with sequence similarity 83, member F	0.02939	0.11717
231	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0.02950	0.11717
232	GPR126	G protein-coupled receptor 126	0.02967	0.11717
233	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	0.02975	0.11717
234	EHBP1	EH domain binding protein 1	0.02982	0.11717
235	ADAM9	ADAM metallopeptidase domain 9	0.02990	0.11717
236	ULK1	unc-51-like kinase 1 (C. elegans)	0.03027	0.11812
237	KLK5	kallikrein-related peptidase 5	0.03096	0.12030
238	ARG2	arginase, type II	0.03115	0.12054

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239	HSD17B1	hydroxysteroid (17-beta) dehydrogenase 1	0.03135	0.12082
240	GUCA1B	guanylate cyclase activator 1B (retina)	0.03155	0.12107
241	PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	0.03190	0.12190
242	LEPREL1	leprecan-like 1	0.03233	0.12306
243	CLASP1	cytoplasmic linker associated protein 1	0.03364	0.12740
244	FAM45A	family with sequence similarity 45, member A	0.03375	0.12740
245	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.03473	0.13057
246	PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	0.03500	0.13104
247	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.03528	0.13156
248	ZNF219	zinc finger protein 219	0.03596	0.13354
249	DUSP7	dual specificity phosphatase 7	0.03645	0.13384
250	LAMC1	laminin, gamma 1 (formerly LAMB2)	0.03649	0.13384
251	CRYAB	crystallin, alpha B	0.03653	0.13384
252	ARHGEF16	Rho guanine nucleotide exchange factor (GEF) 16	0.03662	0.13384
253	NPAS2	neuronal PAS domain protein 2	0.03730	0.13579
254	PLCD1	phospholipase C, delta 1	0.03771	0.13675
255	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.03848	0.13838
256	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	0.03870	0.13838
257	CKAP4	cytoskeleton-associated protein 4	0.03875	0.13838
258	LOC100289600	hypothetical protein LOC100289600	0.03876	0.13838
259	MFF	mitochondrial fission factor	0.03946	0.14032
260	VEGFA	vascular endothelial growth factor A	0.04005	0.14187
261	PYCR1	pyrroline-5-carboxylate reductase 1	0.04022	0.14192
262	HAS3	hyaluronan synthase 3	0.04068	0.14301
263	MORC4	MORC family CW-type zinc finger 4	0.04084	0.14301
264	CERCAM	cerebral endothelial cell adhesion molecule	0.04135	0.14361
265	SOX4	SRY (sex determining region Y)-box 4	0.04139	0.14361
266	NELF	nasal embryonic LHRH factor	0.04148	0.14361
267	PHLDB1	pleckstrin homology-like domain, family B, member 1	0.04210	0.14522
268	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	0.04322	0.14851
269	IMPDH2	IMP (inosine 5'-monophosphate) dehydrogenase 2	0.04347	0.14883
270	GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon	0.04477	0.15256
271	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.04494	0.15256
272	EIF4H	eukaryotic translation initiation factor 4H	0.04513	0.15256
273	TMEM8B	transmembrane protein 8B	0.04528	0.15256
274	LTBP1	latent transforming growth factor beta binding protein 1	0.04539	0.15256
275	DOCK6	dedicator of cytokinesis 6	0.04604	0.15419
276	LOC100129532	hypothetical LOC100129532	0.04712	0.15725
277	ATL2	atlastin GTPase 2	0.04757	0.15815
278	ENO2	enolase 2 (gamma, neuronal)	0.04811	0.15890
279	SEC14L2	SEC14-like 2 (S. cerevisiae)	0.04814	0.15890
280	SCRIB	scribbled homolog (Drosophila)	0.04854	0.15965
281	ARL4C	ADP-ribosylation factor-like 4C	0.04972	0.16298
282	SLC16A2	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	0.05129	0.16698
283	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	0.05131	0.16698
284	CAV1	caveolin 1, caveolae protein, 22kDa	0.05149	0.16698
285	C5orf38	chromosome 5 open reading frame 38	0.05218	0.16825
286	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	0.05225	0.16825
287	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	0.05244	0.16829
288	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	0.05327	0.17034
289	RPL27A	ribosomal protein L27a	0.05383	0.17154
290	RASL11B	RAS-like, family 11, member B	0.05404	0.17164
291	TRIP10	thyroid hormone receptor interactor 10	0.05512	0.17402
292	MKNK2	MAP kinase interacting serine/threonine kinase 2	0.05517	0.17402
293	PTPLB	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	0.05759	0.18083
294	PAQR6	progestin and adipoQ receptor family member VI	0.05791	0.18083
295	AVEN	apoptosis, caspase activation inhibitor	0.05792	0.18083
296	CCND2	cyclin D2	0.05837	0.18162
297	PTP4A1	protein tyrosine phosphatase type IVA, member 1	0.05930	0.18390
298	SAMD5	sterile alpha motif domain containing 5	0.05989	0.18508
299	IL17RD	interleukin 17 receptor D	0.06033	0.18583

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300	WBP5	WW domain binding protein 5	0.06091	0.18700
301	RBBP8	retinoblastoma binding protein 8	0.06157	0.18839
302	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	0.06215	0.18954
303	PPA1	pyrophosphatase (inorganic) 1	0.06267	0.18994
304	SH3GL1	SH3-domain GRB2-like 1	0.06270	0.18994
305	MAP3K6	mitogen-activated protein kinase kinase kinase 6	0.06375	0.19250
306	LOC613126	uncharacterized LOC613126	0.06540	0.19684
307	LAMB2	laminin, beta 2 (laminin S)	0.06612	0.19796
308	DFNA5	deafness, autosomal dominant 5	0.06620	0.19796
309	RCN1	reticulocalbin 1, EF-hand calcium binding domain	0.06645	0.19805
310	NLE1	notchless homolog 1 (Drosophila)	0.06768	0.20108
311	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	0.06855	0.20301
312	ARPP19	cAMP-regulated phosphoprotein, 19kDa	0.06907	0.20370
313	ZBED2	zinc finger, BED-type containing 2	0.06934	0.20370
314	KCNG1	potassium voltage-gated channel, subfamily G, member 1	0.06945	0.20370
315	BCS1L	BCS1-like (S. cerevisiae)	0.06997	0.20428
316	LSR	lipolysis stimulated lipoprotein receptor	0.07009	0.20428
317	ZNF812	zinc finger protein 812	0.07037	0.20446
318	TNS4	tensin 4	0.07062	0.20452
319	GNB5	guanine nucleotide binding protein (G protein), beta 5	0.07104	0.20511
320	TSPAN9	tetraspanin 9	0.07264	0.20850
321	NDRG1	N-myc downstream regulated 1	0.07267	0.20850
322	BDNF	brain-derived neurotrophic factor	0.07382	0.21115
323	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	0.07526	0.21460
324	ULBP2	UL16 binding protein 2	0.07648	0.21740
325	GLRX3	glutaredoxin 3	0.07781	0.21983
326	NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0.07794	0.21983
327	THSD1	thrombospondin, type I, domain containing 1	0.07823	0.21983
328	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	0.07829	0.21983
329	PLEK2	pleckstrin 2	0.07963	0.22291
330	PLXNA2	plexin A2	0.08212	0.22868
331	ANKH	ankylosis, progressive homolog (mouse)	0.08219	0.22868
332	KIRREL	kin of IRRE like (Drosophila)	0.08276	0.22915
333	CAPRIN2	caprin family member 2	0.08285	0.22915
334	PTGFRN	prostaglandin F2 receptor negative regulator	0.08389	0.23132
335	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	0.08462	0.23264
336	BEX2	brain expressed X-linked 2	0.08537	0.23400
337	TOR1AIP2	torsin A interacting protein 2	0.08614	0.23504
338	DAB2IP	DAB2 interacting protein	0.08626	0.23504
339	FBLN1	fibulin 1	0.08694	0.23619
340	RAB18	RAB18, member RAS oncogene family	0.08793	0.23820
341	ALS2CL	ALS2 C-terminal like	0.08987	0.24274
342	POLH	polymerase (DNA directed), eta	0.09096	0.24495
343	SYNPO	synaptopodin	0.09196	0.24692
344	GPC1	glypican 1	0.09301	0.24901
345	BCL9L	B-cell CLL/lymphoma 9-like	0.09353	0.24916
346	BICD1	bicaudal D homolog 1 (Drosophila)	0.09373	0.24916
347	RPL18A	ribosomal protein L18a	0.09387	0.24916
348	RTTN	rotatin	0.09516	0.25184
349	SLC47A2	solute carrier family 47, member 2	0.09561	0.25231
350	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	0.09661	0.25423
351	SLC38A5	solute carrier family 38, member 5	0.09763	0.25619
352	CBX1	chromobox homolog 1	0.09968	0.26082
353	SLC4A3	solute carrier family 4, anion exchanger, member 3	0.10201	0.26615
354	ITPR3	inositol 1,4,5-trisphosphate receptor, type 3	0.10240	0.26641
355	FKBP1B	FK506 binding protein 1B, 12.6 kDa	0.10335	0.26739
356	PPP1R3C	protein phosphatase 1, regulatory subunit 3C	0.10335	0.26739
357	MORN4	MORN repeat containing 4	0.10374	0.26762
358	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	0.10540	0.27116
359	ACSL3	acyl-CoA synthetase long-chain family member 3	0.10629	0.27268
360	NANOS1	nanos homolog 1 (Drosophila)	0.10791	0.27578

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361	FYN	FYN oncogene related to SRC, FGR, YES	0.10809	0.27578
362	SBSN	suprabasin	0.10904	0.27667
363	TMEM41B	transmembrane protein 41B	0.10905	0.27667
364	LOXL2	lysyl oxidase-like 2	0.11128	0.28155
365	MT2A	metallothionein 2A	0.11403	0.28734
366	ALDH3B2	aldehyde dehydrogenase 3 family, member B2	0.11512	0.28734
367	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.11540	0.28734
368	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	0.11565	0.28734
369	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	0.11573	0.28734
370	GAMT	guanidinoacetate N-methyltransferase	0.11603	0.28734
371	ISL1	ISL LIM homeobox 1	0.11605	0.28734
372	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)	0.11606	0.28734
373	C17orf96	chromosome 17 open reading frame 96	0.11955	0.29519
374	SH3PXD2A	SH3 and PX domains 2A	0.11997	0.29529
375	RAN	RAN, member RAS oncogene family	0.12023	0.29529
376	GSK3B	glycogen synthase kinase 3 beta	0.12067	0.29558
377	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.12147	0.29675
378	CLDND1	claudin domain containing 1	0.12401	0.30162
379	LAMA5	laminin, alpha 5	0.12412	0.30162
380	SLC29A4	solute carrier family 29 (nucleoside transporters), member 4	0.12535	0.30380
381	RARG	retinoic acid receptor, gamma	0.12659	0.30542
382	ERMP1	endoplasmic reticulum metallopeptidase 1	0.12668	0.30542
383	C12orf54	chromosome 12 open reading frame 54	0.12777	0.30664
384	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.12785	0.30664
385	USP46	ubiquitin specific peptidase 46	0.12958	0.30925
386	FTSJ1	FtsJ homolog 1 (E. coli)	0.12961	0.30925
387	ZP3	zona pellucida glycoprotein 3 (sperm receptor)	0.13152	0.31299
388	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	0.13370	0.31737
389	ZNF692	zinc finger protein 692	0.13409	0.31748
390	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	0.13546	0.31975
391	COL17A1	collagen, type XVII, alpha 1	0.13575	0.31975
392	NME4	non-metastatic cells 4, protein expressed in	0.13765	0.32340
393	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	0.13833	0.32418
394	AFF4	AF4/FMR2 family, member 4	0.13894	0.32477
395	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	0.13945	0.32507
396	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	0.13977	0.32507
397	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.14099	0.32709
398	NUMBL	numb homolog (Drosophila)-like	0.14332	0.33165
399	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	0.14460	0.33378
400	EFNA3	ephrin-A3	0.14582	0.33512
401	PHF13	PHD finger protein 13	0.14642	0.33512
402	SOX15	SRY (sex determining region Y)-box 15	0.14654	0.33512
403	C17orf69	chromosome 17 open reading frame 69	0.14664	0.33512
404	GJB5	gap junction protein, beta 5, 31.1kDa	0.14719	0.33512
405	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	0.14737	0.33512
406	BARX2	BARX homeobox 2	0.14820	0.33576
407	SCAND3	SCAN domain containing 3	0.14838	0.33576
408	OLA1	Obg-like ATPase 1	0.15061	0.33998
409	DKK3	dickkopf homolog 3 (Xenopus laevis)	0.15271	0.34329
410	C22orf43	chromosome 22 open reading frame 43	0.15282	0.34329
411	LOC100128320	uncharacterized protein LOC100128320	0.15445	0.34610
412	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	0.15510	0.34673
413	MTA3	metastasis associated 1 family, member 3	0.15573	0.34729
414	RHOD	ras homolog gene family, member D	0.15662	0.34841
415	BTBD11	BTB (POZ) domain containing 11	0.16133	0.35803
416	FRZB	frizzled-related protein	0.16203	0.35824
417	ANO4	anoctamin 4	0.16220	0.35824
418	PODNL1	podocan-like 1	0.16332	0.35984
419	LOC100129781	hypothetical LOC100129781	0.16406	0.36013
420	TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	0.16423	0.36013
421	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	0.16499	0.36093

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422	EPHA2	EPH receptor A2	0.16630	0.36295
423	PLP2	proteolipid protein 2 (colonic epithelium-enriched)	0.16727	0.36419
424	TP63	tumor protein p63	0.16907	0.36725
425	HES2	hairy and enhancer of split 2 (Drosophila)	0.17231	0.37341
426	KIF1C	kinesin family member 1C	0.17345	0.37499
427	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	0.17391	0.37510
428	RPL7A	ribosomal protein L7a	0.17531	0.37724
429	CGB	chorionic gonadotropin, beta polypeptide	0.17595	0.37774
430	MPST	mercaptopyruvate sulfurtransferase	0.17734	0.37984
431	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	0.17843	0.38129
432	UBAP1	ubiquitin associated protein 1	0.17911	0.38186
433	KRT7	keratin 7	0.18055	0.38403
434	CDH16	cadherin 16, KSP-cadherin	0.18330	0.38817
435	CLDN7	claudin 7	0.18334	0.38817
436	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	0.18392	0.38852
437	MGC57346	uncharacterized LOC401884	0.18639	0.39282
438	BAG3	BCL2-associated athanogene 3	0.18894	0.39730
439	RPL39L	ribosomal protein L39-like	0.19011	0.39735
440	LAD1	ladinin 1	0.19027	0.39735
441	FKBP9	FK506 binding protein 9, 63 kDa	0.19047	0.39735
442	SCARNA12	small Cajal body-specific RNA 12	0.19069	0.39735
443	RPF2	ribosome production factor 2 homolog (S. cerevisiae)	0.19317	0.40161
444	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	0.19489	0.40426
445	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	0.19593	0.40550
446	CAPN12	calpain 12	0.19709	0.40700
447	PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	0.19969	0.41143
448	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	0.20100	0.41321
449	TYRO3	TYRO3 protein tyrosine kinase	0.20221	0.41478
450	CIB2	calcium and integrin binding family member 2	0.20333	0.41614
451	TM7SF2	transmembrane 7 superfamily member 2	0.20384	0.41627
452	KRT13	keratin 13	0.20647	0.42071
453	TMEM38A	transmembrane protein 38A	0.21241	0.43137
454	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	0.21264	0.43137
455	CDH13	cadherin 13, H-cadherin (heart)	0.21675	0.43875
456	BCAS4	breast carcinoma amplified sequence 4	0.21860	0.44151
457	DTD1	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae)	0.21972	0.44280
458	SIK1	salt-inducible kinase 1	0.22108	0.44350
459	RIMS2	regulating synaptic membrane exocytosis 2	0.22126	0.44350
460	ARL4D	ADP-ribosylation factor-like 4D	0.22151	0.44350
461	CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	0.22430	0.44811
462	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	0.22608	0.45070
463	PRSS3	protease, serine, 3	0.22845	0.45444
464	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	0.22922	0.45460
465	DAPK3	death-associated protein kinase 3	0.22986	0.45460
466	SPTBN1	spectrin, beta, non-erythrocytic 1	0.23002	0.45460
467	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	0.23362	0.46074
468	PHACTR3	phosphatase and actin regulator 3	0.23496	0.46173
469	PGF	placental growth factor	0.23513	0.46173
470	LOC100128252	uncharacterized LOC100128252	0.23578	0.46203
471	CALD1	caldesmon 1	0.23676	0.46296
472	GLIS2	GLIS family zinc finger 2	0.23827	0.46446
473	PCBP4	poly(rC) binding protein 4	0.23885	0.46446
474	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	0.23904	0.46446
475	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0.23955	0.46447
476	PCDHGB7	protocadherin gamma subfamily B, 7	0.24133	0.46463
477	EFEMP2	EGF containing fibulin-like extracellular matrix protein 2	0.24205	0.46463
478	CSRP2	cysteine and glycine-rich protein 2	0.24213	0.46463
479	S100A2	S100 calcium binding protein A2	0.24225	0.46463
480	GJB3	gap junction protein, beta 3, 31kDa	0.24251	0.46463
481	SERPINB7	serpin peptidase inhibitor, clade B (ovalbumin), member 7	0.24266	0.46463
482	MICALCL	MICAL C-terminal like	0.24614	0.47033

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483	YDJC	YdjC homolog (bacterial)	0.24718	0.47134
484	COPZ2	coatomer protein complex, subunit zeta 2	0.24905	0.47391
485	BMS1	BMS1 homolog, ribosome assembly protein (yeast)	0.25267	0.47982
486	CEACAM20	carcinoembryonic antigen-related cell adhesion molecule 20	0.25436	0.48179
487	ZNF286B	zinc finger protein 286B	0.25476	0.48179
488	STK24	serine/threonine kinase 24	0.25702	0.48506
489	CCNB1IP1	cyclin B1 interacting protein 1, E3 ubiquitin protein ligase	0.25972	0.48917
490	PTPN14	protein tyrosine phosphatase, non-receptor type 14	0.26029	0.48925
491	ZNF57	zinc finger protein 57	0.26101	0.48959
492	FBXL16	F-box and leucine-rich repeat protein 16	0.26259	0.49060
493	ZDBF2	zinc finger, DBF-type containing 2	0.26261	0.49060
494	VEGFC	vascular endothelial growth factor C	0.26368	0.49159
495	PCDHGA8	protocadherin gamma subfamily A, 8	0.26493	0.49293
496	STON2	stonin 2	0.26576	0.49348
497	RDX	radixin	0.26956	0.49953
498	PHGDH	phosphoglycerate dehydrogenase	0.27133	0.50180
499	KRT16	keratin 16	0.27300	0.50250
500	VAV2	vav 2 guanine nucleotide exchange factor	0.27337	0.50250
501	IGFBP6	insulin-like growth factor binding protein 6	0.27377	0.50250
502	NAGS	N-acetylglutamate synthase	0.27389	0.50250
503	ALOX15B	arachidonate 15-lipoxygenase, type B	0.27477	0.50311
504	C8orf42	chromosome 8 open reading frame 42	0.27742	0.50487
505	TRIM46	tripartite motif containing 46	0.27788	0.50487
506	CERK	ceramide kinase	0.27793	0.50487
507	SPATS2	spermatogenesis associated, serine-rich 2	0.27844	0.50487
508	CFL2	cofilin 2 (muscle)	0.27848	0.50487
509	TPBG	trophoblast glycoprotein	0.27947	0.50489
510	KCTD15	potassium channel tetramerisation domain containing 15	0.27958	0.50489
511	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	0.28295	0.50997
512	UBE2E1	ubiquitin-conjugating enzyme E2E 1	0.28415	0.51076
513	C15orf41	chromosome 15 open reading frame 41	0.28449	0.51076
514	PPM1J	protein phosphatase, Mg2+/Mn2+ dependent, 1J	0.28569	0.51190
515	LGALS7	lectin, galactoside-binding, soluble, 7	0.28644	0.51225
516	C14orf33	chromosome 14 open reading frame 33	0.28761	0.51268
517	GRHL3	grainyhead-like 3 (Drosophila)	0.28852	0.51268
518	RNF152	ring finger protein 152	0.28861	0.51268
519	TNFAIP8L3	tumor necrosis factor, alpha-induced protein 8-like 3	0.28894	0.51268
520	AGRN	agrin	0.28946	0.51268
521	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	0.29176	0.51577
522	SREBF2	sterol regulatory element binding transcription factor 2	0.29957	0.52856
523	ANKIB1	ankyrin repeat and IBR domain containing 1	0.30024	0.52872
524	LOC648149	uncharacterized protein LOC648149	0.30139	0.52973
525	GRHL1	grainyhead-like 1 (Drosophila)	0.30255	0.53076
526	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	0.30344	0.53131
527	KRT5	keratin 5	0.30435	0.53190
528	NCKAP5	NCK-associated protein 5	0.30499	0.53200
529	BTG3	BTG family, member 3	0.30711	0.53385
530	TMEM79	transmembrane protein 79	0.30829	0.53385
531	WNT7B	wingless-type MMTV integration site family, member 7B	0.30868	0.53385
532	UCN2	urocortin 2	0.30925	0.53385
533	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.30934	0.53385
534	TNC	tenascin C	0.30953	0.53385
535	MARS2	methionyl-tRNA synthetase 2, mitochondrial	0.31225	0.53643
536	TFPI2	tissue factor pathway inhibitor 2	0.31275	0.53643
537	FAM83H	family with sequence similarity 83, member H	0.31277	0.53643
538	F2R	coagulation factor II (thrombin) receptor	0.31403	0.53758
539	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	0.31590	0.53864
540	VDAC2	voltage-dependent anion channel 2	0.31623	0.53864
541	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	0.31682	0.53864
542	SLC16A14	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	0.31699	0.53864
543	PVRL3	poliovirus receptor-related 3	0.31803	0.53886

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544	SMTN	smoothelin	0.31902	0.53886
545	PEAR1	platelet endothelial aggregation receptor 1	0.31917	0.53886
546	SEC1	secretory blood group 1	0.31950	0.53886
547	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	0.32021	0.53886
548	RPSAP52	ribosomal protein SA pseudogene 52	0.32063	0.53886
549	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0.32195	0.53949
550	CYP27C1	cytochrome P450, family 27, subfamily C, polypeptide 1	0.32307	0.53949
551	HYAL1	hyaluronoglucosaminidase 1	0.32362	0.53949
552	FAM189B	family with sequence similarity 189, member B	0.32432	0.53949
553	GTF2IRD1	GTF2I repeat domain containing 1	0.32445	0.53949
554	MRPL36	mitochondrial ribosomal protein L36	0.32453	0.53949
555	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	0.32510	0.53949
556	SKA2	spindle and kinetochore associated complex subunit 2	0.32674	0.54123
557	GPR87	G protein-coupled receptor 87	0.33006	0.54576
558	FOXL1	forkhead box L1	0.33168	0.54745
559	DPH5	DPH5 homolog (S. cerevisiae)	0.33421	0.55059
560	LRRC42	leucine rich repeat containing 42	0.33539	0.55059
561	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	0.33635	0.55059
562	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	0.33659	0.55059
563	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0.33691	0.55059
564	KIF3C	kinesin family member 3C	0.33717	0.55059
565	ACTN4	actinin, alpha 4	0.33806	0.55092
566	ZNF323	zinc finger protein 323	0.33861	0.55092
567	TMPRSS11F	transmembrane protease, serine 11F	0.33917	0.55092
568	VASN	vasorin	0.34339	0.55681
569	JAG2	jagged 2	0.34645	0.56078
570	EPHA1	EPH receptor A1	0.34808	0.56242
571	CARS	cysteinyl-tRNA synthetase	0.34892	0.56279
572	GLS2	glutaminase 2 (liver, mitochondrial)	0.35010	0.56370
573	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	0.35179	0.56545
574	C16orf5	chromosome 16 open reading frame 5	0.35252	0.56563
575	ELOVL4	ELOVL fatty acid elongase 4	0.35595	0.56935
576	SPRR1A	small proline-rich protein 1A	0.35609	0.56935
577	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.35670	0.56935
578	MACROD1	MACRO domain containing 1	0.35754	0.56971
579	ZFYVE9	zinc finger, FYVE domain containing 9	0.35948	0.57181
580	RPL18	ribosomal protein L18	0.36127	0.57238
581	XYLT2	xylosyltransferase II	0.36157	0.57238
582	RPL8	ribosomal protein L8	0.36170	0.57238
583	EGFR	epidermal growth factor receptor	0.36247	0.57262
584	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.36381	0.57375
585	MARK1	MAP/microtubule affinity-regulating kinase 1	0.36537	0.57523
586	TCEA2	transcription elongation factor A (SII), 2	0.36941	0.58058
587	GPX3	glutathione peroxidase 3 (plasma)	0.37118	0.58135
588	TMC7	transmembrane channel-like 7	0.37132	0.58135
589	PTK7	PTK7 protein tyrosine kinase 7	0.37319	0.58135
590	PCDHB8	protocadherin beta 8	0.37347	0.58135
591	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	0.37384	0.58135
592	BNC1	basonuclin 1	0.37516	0.58135
593	CHPF	chondroitin polymerizing factor	0.37534	0.58135
594	DDIT4	DNA-damage-inducible transcript 4	0.37543	0.58135
595	C11orf80	chromosome 11 open reading frame 80	0.37557	0.58135
596	GRPEL2	GrpE-like 2, mitochondrial (E. coli)	0.37698	0.58254
597	DGCR2	DiGeorge syndrome critical region gene 2	0.38309	0.59100
598	S1PR5	sphingosine-1-phosphate receptor 5	0.38405	0.59149
599	FKBP10	FK506 binding protein 10, 65 kDa	0.38963	0.59908
600	LOC100131067	uncharacterized LOC100131067	0.39246	0.59972
601	ALDOC	aldolase C, fructose-bisphosphate	0.39252	0.59972
602	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	0.39309	0.59972
603	KRT6B	keratin 6B	0.39315	0.59972
604	HES1	hairy and enhancer of split 1, (Drosophila)	0.39330	0.59972

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605	LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	0.39491	0.60117
606	IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	0.39757	0.60340
607	ARPC5L	actin related protein 2/3 complex, subunit 5-like	0.39776	0.60340
608	WASF1	WAS protein family, member 1	0.39833	0.60340
609	RAB11FIP5	RAB11 family interacting protein 5 (class I)	0.40090	0.60628
610	FAM25A	family with sequence similarity 25, member A	0.40351	0.60923
611	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.40482	0.60984
612	RAG1	recombination activating gene 1	0.40524	0.60984
613	MPZL1	myelin protein zero-like 1	0.40616	0.61024
614	C5orf23	chromosome 5 open reading frame 23	0.40778	0.61070
615	NOB1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	0.40779	0.61070
616	TEAD2	TEA domain family member 2	0.40945	0.61132
617	RILPL1	Rab interacting lysosomal protein-like 1	0.40999	0.61132
618	HSPB1	heat shock 27kDa protein 1	0.41020	0.61132
619	NXN	nucleoredoxin	0.41341	0.61447
620	SPRR1B	small proline-rich protein 1B	0.41365	0.61447
621	POLR1D	polymerase (RNA) I polypeptide D, 16kDa	0.41596	0.61645
622	LEMD1	LEM domain containing 1	0.41632	0.61645
623	HDGFRP3	hepatoma-derived growth factor, related protein 3	0.42016	0.62113
624	SPRR2E	small proline-rich protein 2E	0.42166	0.62228
625	KLHL23	kelch-like 23 (Drosophila)	0.42228	0.62228
626	IGSF9B	immunoglobulin superfamily, member 9B	0.42798	0.62924
627	SERF1A	small EDRK-rich factor 1A (telomeric)	0.42838	0.62924
628	EDNRA	endothelin receptor type A	0.43165	0.63305
629	VLDLR	very low density lipoprotein receptor	0.43284	0.63367
630	BRMS1L	breast cancer metastasis-suppressor 1-like	0.43346	0.63367
631	LPIN3	lipin 3	0.43726	0.63821
632	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	0.43838	0.63883
633	E2F7	E2F transcription factor 7	0.44335	0.64419
634	OR6B3	olfactory receptor, family 6, subfamily B, member 3	0.44345	0.64419
635	OCA2	oculocutaneous albinism II	0.44428	0.64438
636	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	0.44593	0.64575
637	PLCG1	phospholipase C, gamma 1	0.44702	0.64632
638	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	0.45164	0.65198
639	FLJ32224	uncharacterized LOC440584	0.45437	0.65420
640	DSG3	desmoglein 3	0.45475	0.65420
641	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)	0.45531	0.65420
642	FRMD6	FERM domain containing 6	0.45887	0.65829
643	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	0.45964	0.65837
644	PORCN	porcupine homolog (Drosophila)	0.46749	0.66857
645	C1QTNF6	C1q and tumor necrosis factor related protein 6	0.46849	0.66896
646	TUFT1	tuftelin 1	0.47009	0.67020
647	SIGMAR1	sigma non-opioid intracellular receptor 1	0.47094	0.67037
648	SHROOM2	shroom family member 2	0.47491	0.67498
649	TMEM22	transmembrane protein 22	0.47583	0.67525
650	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	0.47694	0.67579
651	MMP15	matrix metallopeptidase 15 (membrane-inserted)	0.48006	0.67916
652	C1orf74	chromosome 1 open reading frame 74	0.48093	0.67936
653	RHCG	Rh family, C glycoprotein	0.48188	0.67965
654	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	0.48592	0.68430
655	LYPD3	LY6/PLAUR domain containing 3	0.48706	0.68485
656	C6orf168	chromosome 6 open reading frame 168	0.48983	0.68711
657	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	0.49055	0.68711
658	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	0.49090	0.68711
659	GRB14	growth factor receptor-bound protein 14	0.49637	0.69371
660	KCNJ5	potassium inwardly-rectifying channel, subfamily J, member 5	0.49975	0.69622
661	FBXO17	F-box protein 17	0.50028	0.69622
662	EVC2	Ellis van Creveld syndrome 2	0.50103	0.69622
663	MXRA5	matrix-remodelling associated 5	0.50119	0.69622
664	RPL35	ribosomal protein L35	0.50410	0.69863
665	RTKN	rhotekin	0.50489	0.69863

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666	SMO	smoothened, frizzled family receptor	0.50520	0.69863
667	BMP1	bone morphogenetic protein 1	0.50781	0.70120
668	DEPDC7	DEP domain containing 7	0.51332	0.70716
669	C6orf141	chromosome 6 open reading frame 141	0.51441	0.70716
670	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	0.51444	0.70716
671	CLSTN3	calsyntenin 3	0.51742	0.70880
672	CATSPERB	cation channel, sperm-associated, beta	0.51755	0.70880
673	ACBD6	acyl-CoA binding domain containing 6	0.51868	0.70880
674	SPAG4	sperm associated antigen 4	0.51871	0.70880
675	RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	0.52155	0.71163
676	SEMA5B	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	0.52249	0.71186
677	C17orf100	chromosome 17 open reading frame 100	0.52332	0.71193
678	FST	follistatin	0.52435	0.71228
679	HSPA4L	heat shock 70kDa protein 4-like	0.53335	0.72344
680	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	0.53630	0.72637
681	PHF21A	PHD finger protein 21A	0.53807	0.72721
682	C19orf48	chromosome 19 open reading frame 48	0.53879	0.72721
683	CCDC64	coiled-coil domain containing 64	0.53929	0.72721
684	MTUS1	microtubule associated tumor suppressor 1	0.54032	0.72754
685	TES	testis derived transcript (3 LIM domains)	0.54159	0.72818
686	AIM1L	absent in melanoma 1-like	0.54278	0.72872
687	CAPN14	calpain 14	0.54805	0.73430
688	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	0.54853	0.73430
689	EI24	etoposide induced 2.4 mRNA	0.55409	0.73895
690	SDC1	syndecan 1	0.55436	0.73895
691	BTBD10	BTB (POZ) domain containing 10	0.55442	0.73895
692	MRPL12	mitochondrial ribosomal protein L12	0.56087	0.74648
693	GGN	gametogenetin	0.56256	0.74679
694	ZP2	zona pellucida glycoprotein 2 (sperm receptor)	0.56273	0.74679
695	RPS16	ribosomal protein S16	0.56355	0.74680
696	GJB6	gap junction protein, beta 6, 30kDa	0.56486	0.74747
697	TMEM156	transmembrane protein 156	0.56656	0.74864
698	IRS1	insulin receptor substrate 1	0.56891	0.74979
699	SMAGP	small cell adhesion glycoprotein	0.56909	0.74979
700	CCNA1	cyclin A1	0.56987	0.74979
701	EMD	emerin	0.57095	0.75013
702	GPSM2	G-protein signaling modulator 2	0.57380	0.75281
703	ADAM15	ADAM metallopeptidase domain 15	0.57573	0.75426
704	LOC100131820	uncharacterized protein LOC100131820	0.57763	0.75568
705	ZNF827	zinc finger protein 827	0.58194	0.76024
706	NXPH4	neurexophilin 4	0.58630	0.76464
707	MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	0.58778	0.76464
708	ZNF862	zinc finger protein 862	0.58780	0.76464
709	POMT2	protein-O-mannosyltransferase 2	0.59110	0.76785
710	RAPGEFL1	Rap guanine nucleotide exchange factor (GEF)-like 1	0.59223	0.76823
711	C5orf28	chromosome 5 open reading frame 28	0.59432	0.76986
712	ELOVL6	ELOVL fatty acid elongase 6	0.59586	0.77076
713	SNHG8	small nucleolar RNA host gene 8 (non-protein coding)	0.59744	0.77172
714	DQX1	DEAQ box RNA-dependent ATPase 1	0.60001	0.77291
715	GNG8	guanine nucleotide binding protein (G protein), gamma 8	0.60003	0.77291
716	AKTIP	AKT interacting protein	0.60267	0.77477
717	C16orf88	chromosome 16 open reading frame 88	0.60316	0.77477
718	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	0.60461	0.77556
719	ARTN	artemin	0.60779	0.77855
720	SYT12	synaptotagmin XII	0.60981	0.77988
721	DKFZP586K1520	DKFZP586K1520 protein	0.61052	0.77988
722	AMN1	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	0.61139	0.77991
723	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.61382	0.78161
724	GCAT	glycine C-acetyltransferase	0.61443	0.78161
725	ZFP64	zinc finger protein 64 homolog (mouse)	0.61667	0.78338
726	MDFI	MyoD family inhibitor	0.61898	0.78421

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727	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	0.61982	0.78421
728	FKBP14	FK506 binding protein 14, 22 kDa	0.61988	0.78421
729	PLCD3	phospholipase C, delta 3	0.62165	0.78537
730	B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	0.62275	0.78569
731	CLTB	clathrin, light chain B	0.62472	0.78645
732	UQCC	ubiquinol-cytochrome c reductase complex chaperone	0.62584	0.78645
733	RNF187	ring finger protein 187	0.62638	0.78645
734	ARL5B	ADP-ribosylation factor-like 5B	0.62738	0.78645
735	SFXN1	sideroflexin 1	0.62762	0.78645
736	KIAA1609	KIAA1609	0.62973	0.78798
737	LOC284219	uncharacterized protein LOC284219	0.63056	0.78798
738	MTX2	metaxin 2	0.63450	0.79183
739	LOC100130938	hypothetical LOC100130938	0.63801	0.79513
740	SPRR2A	small proline-rich protein 2A	0.63963	0.79608
741	GPR68	G protein-coupled receptor 68	0.64195	0.79788
742	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	0.64851	0.80495
743	ZNF618	zinc finger protein 618	0.64957	0.80519
744	IGF2	insulin-like growth factor 2 (somatomedin A)	0.65452	0.80907
745	ENDOD1	endonuclease domain containing 1	0.65497	0.80907
746	GBE1	glucan (1,4-alpha-), branching enzyme 1	0.65534	0.80907
747	ARSJ	arylsulfatase family, member J	0.66057	0.81282
748	PLS3	plastin 3	0.66068	0.81282
749	LOC100130580	uncharacterized protein LOC100130580	0.66103	0.81282
750	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	0.66424	0.81568
751	WASF3	WAS protein family, member 3	0.67083	0.82268
752	PPP1R13L	protein phosphatase 1, regulatory subunit 13 like	0.67336	0.82392
753	UGT1A8	UDP glucuronosyltransferase 1 family, polypeptide A8	0.67427	0.82392
754	TPI1	triosephosphate isomerase 1	0.67452	0.82392
755	MGST1	microsomal glutathione S-transferase 1	0.67778	0.82581
756	CLDND2	claudin domain containing 2	0.67803	0.82581
757	MRPS2	mitochondrial ribosomal protein S2	0.67876	0.82581
758	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	0.68053	0.82688
759	TCERG1	transcription elongation regulator 1	0.68422	0.82982
760	FGF11	fibroblast growth factor 11	0.68476	0.82982
761	ZNF665	zinc finger protein 665	0.68739	0.83064
762	A2ML1	alpha-2-macroglobulin-like 1	0.68920	0.83064
763	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	0.68969	0.83064
764	C6orf125	chromosome 6 open reading frame 125	0.68971	0.83064
765	NTF4	neurotrophin 4	0.68995	0.83064
766	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	0.69349	0.83382
767	ITGB6	integrin, beta 6	0.69604	0.83579
768	ERRFI1	ERBB receptor feedback inhibitor 1	0.70460	0.84374
769	SERINC2	serine incorporator 2	0.70525	0.84374
770	MTSS1L	metastasis suppressor 1-like	0.70541	0.84374
771	S100A16	S100 calcium binding protein A16	0.70741	0.84504
772	RAB6A	RAB6A, member RAS oncogene family	0.71092	0.84684
773	RAET1E	retinoic acid early transcript 1E	0.71134	0.84684
774	CLCA4	chloride channel accessory 4	0.71187	0.84684
775	FAM83B	family with sequence similarity 83, member B	0.71260	0.84684
776	MBD5	methyl-CpG binding domain protein 5	0.71657	0.85047
777	ADCY6	adenylate cyclase 6	0.72122	0.85488
778	TMEM184A	transmembrane protein 184A	0.72243	0.85522
779	PTHLH	parathyroid hormone-like hormone	0.72600	0.85689
780	RPAIN	RPA interacting protein	0.72736	0.85689
781	TUBA3C	tubulin, alpha 3c	0.72828	0.85689
782	TTLL12	tubulin tyrosine ligase-like family, member 12	0.72861	0.85689
783	CA12	carbonic anhydrase XII	0.73024	0.85689
784	C17orf98	chromosome 17 open reading frame 98	0.73108	0.85689
785	GSDMC	gasdermin C	0.73132	0.85689
786	FANCE	Fanconi anemia, complementation group E	0.73391	0.85689
787	GADD45A	growth arrest and DNA-damage-inducible, alpha	0.73468	0.85689

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788	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	0.73472	0.85689
789	KRT6C	keratin 6C	0.73562	0.85689
790	PHKA1	phosphorylase kinase, alpha 1 (muscle)	0.73595	0.85689
791	PHPT1	phosphohistidine phosphatase 1	0.73635	0.85689
792	RNF112	ring finger protein 112	0.73703	0.85689
793	THOC3	THO complex 3	0.73861	0.85689
794	RPL4	ribosomal protein L4	0.73873	0.85689
795	NMT2	N-myristoyltransferase 2	0.74102	0.85846
796	METTL5	methyltransferase like 5	0.74419	0.86105
797	KLC3	kinesin light chain 3	0.75122	0.86788
798	AFAP1	actin filament associated protein 1	0.75235	0.86788
799	NMU	neuromedin U	0.75292	0.86788
800	MED21	mediator complex subunit 21	0.75699	0.86986
801	PHEX	phosphate regulating endopeptidase homolog, X-linked	0.75741	0.86986
802	EGLN3	egl nine homolog 3 (C. elegans)	0.75746	0.86986
803	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	0.76014	0.87067
804	RPL10L	ribosomal protein L10-like	0.76112	0.87067
805	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	0.76135	0.87067
806	ABCA12	ATP-binding cassette, sub-family A (ABC1), member 12	0.76195	0.87067
807	KRT75	keratin 75	0.76616	0.87439
808	SARS	seryl-tRNA synthetase	0.76780	0.87446
809	POPDC3	popeye domain containing 3	0.76876	0.87446
810	DSC3	desmocollin 3	0.76992	0.87446
811	UQCRH	ubiquinol-cytochrome c reductase hinge protein	0.77091	0.87446
812	PRMT1	protein arginine methyltransferase 1	0.77136	0.87446
813	GAS5	growth arrest-specific 5 (non-protein coding)	0.77502	0.87446
814	LOC100216001	uncharacterized LOC100216001	0.77505	0.87446
815	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	0.77512	0.87446
816	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	0.77521	0.87446
817	ADK	adenosine kinase	0.77571	0.87446
818	TEPP	testis, prostate and placenta expressed	0.77840	0.87641
819	PMEPA1	prostate transmembrane protein, androgen induced 1	0.78171	0.87667
820	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein	0.78181	0.87667
821	LOC729242	similar to keratin 17	0.78186	0.87667
822	C18orf56	chromosome 18 open reading frame 56	0.78381	0.87667
823	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	0.78410	0.87667
824	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	0.78433	0.87667
825	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	0.78750	0.87914
826	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	0.79129	0.88229
827	GALE	UDP-galactose-4-epimerase	0.79475	0.88473
828	KLK7	kallikrein-related peptidase 7	0.79540	0.88473
829	FAM83A	family with sequence similarity 83, member A	0.79800	0.88656
830	CAPNS2	calpain, small subunit 2	0.79995	0.88766
831	DNAH14	dynein, axonemal, heavy chain 14	0.80361	0.89064
832	ARMC10	armadillo repeat containing 10	0.80675	0.89305
833	IFNE	interferon, epsilon	0.81110	0.89641
834	RPL29P2	ribosomal protein L29 pseudogene 2	0.81173	0.89641
835	PRRG2	proline rich Gla (G-carboxyglutamic acid) 2	0.81489	0.89882
836	COL4A6	collagen, type IV, alpha 6	0.81587	0.89883
837	C14orf176	chromosome 14 open reading frame 176	0.81691	0.89890
838	FNDC4	fibronectin type III domain containing 4	0.82131	0.90266
839	C9orf169	chromosome 9 open reading frame 169	0.82541	0.90533
840	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	0.82571	0.90533
841	RCOR2	REST corepressor 2	0.82752	0.90624
842	KRT33B	keratin 33B	0.83019	0.90808
843	LOC100133089	uncharacterized protein LOC100133089	0.83536	0.91056
844	ARF5	ADP-ribosylation factor 5	0.83588	0.91056
845	WNT7A	wingless-type MMTV integration site family, member 7A	0.83641	0.91056
846	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.83738	0.91056
847	EDA2R	ectodysplasin A2 receptor	0.83740	0.91056
848	FRMD5	FERM domain containing 5	0.84405	0.91671

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849	KIAA0391	KIAA0391	0.85156	0.92282
850	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	0.85168	0.92282
851	HRSP12	heat-responsive protein 12	0.85641	0.92685
852	IGSF3	immunoglobulin superfamily, member 3	0.85930	0.92883
853	TM7SF3	transmembrane 7 superfamily member 3	0.86025	0.92883
854	EDIL3	EGF-like repeats and discoidin I-like domains 3	0.86397	0.93072
855	CTNND1	catenin (cadherin-associated protein), delta 1	0.86402	0.93072
856	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	0.86543	0.93114
857	RBP1	retinol binding protein 1, cellular	0.86685	0.93158
858	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	0.86962	0.93337
859	AKR1B15	aldo-keto reductase family 1, member B15	0.87211	0.93337
860	DCTN2	dynactin 2 (p50)	0.87324	0.93337
861	RSL24D1	ribosomal L24 domain containing 1	0.87350	0.93337
862	TMEM147	transmembrane protein 147	0.87358	0.93337
863	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0.88014	0.93929
864	ERO1L	ERO1-like (S. cerevisiae)	0.88247	0.93971
865	LOXL1	lysyl oxidase-like 1	0.88423	0.93971
866	PADI1	peptidyl arginine deiminase, type I	0.88520	0.93971
867	S100A3	S100 calcium binding protein A3	0.88541	0.93971
868	RPS3	ribosomal protein S3	0.88625	0.93971
869	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	0.88818	0.93971
870	KLK8	kallikrein-related peptidase 8	0.88911	0.93971
871	FAM160A1	family with sequence similarity 160, member A1	0.89054	0.93971
872	STK32A	serine/threonine kinase 32A	0.89162	0.93971
873	RPL10	ribosomal protein L10	0.89162	0.93971
874	RRP1B	ribosomal RNA processing 1 homolog B (S. cerevisiae)	0.89175	0.93971
875	HDAC11	histone deacetylase 11	0.89298	0.93992
876	PRR5-ARHGAP8	PRR5-ARHGAP8 readthrough	0.89504	0.94102
877	C14orf2	chromosome 14 open reading frame 2	0.90062	0.94580
878	ZNF251	zinc finger protein 251	0.90194	0.94584
879	CA11	carbonic anhydrase XI	0.90484	0.94584
880	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	0.90548	0.94584
881	EPHX4	epoxide hydrolase 4	0.90577	0.94584
882	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	0.90579	0.94584
883	LRRC16A	leucine rich repeat containing 16A	0.90823	0.94731
884	H2BFM	H2B histone family, member M	0.90982	0.94790
885	RIN1	Ras and Rab interactor 1	0.91197	0.94907
886	SOX7	SRY (sex determining region Y)-box 7	0.91606	0.95018
887	KHDC1	KH homology domain containing 1	0.91609	0.95018
888	RHOC	ras homolog gene family, member C	0.91727	0.95018
889	RAD52	RAD52 homolog (S. cerevisiae)	0.91907	0.95018
890	TSPAN7	tetraspanin 7	0.91911	0.95018
891	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	0.91923	0.95018
892	AASS	aminoadipate-semialdehyde synthase	0.92305	0.95217
893	CAV3	caveolin 3	0.92322	0.95217
894	PNLIPRP3	pancreatic lipase-related protein 3	0.92473	0.95266
895	LYSMD1	LysM, putative peptidoglycan-binding, domain containing 1	0.92714	0.95408
896	EPHB4	EPH receptor B4	0.93778	0.96336
897	NLGN4X	neuroligin 4, X-linked	0.93826	0.96336
898	C1orf210	chromosome 1 open reading frame 210	0.93944	0.96350
899	RNF167	ring finger protein 167	0.94292	0.96436
900	ANO9	anoctamin 9	0.94428	0.96436
901	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	0.94465	0.96436
902	SLC2A4RG	SLC2A4 regulator	0.94562	0.96436
903	FBXO27	F-box protein 27	0.94574	0.96436
904	PTGR1	prostaglandin reductase 1	0.94696	0.96436
905	EIF3L	eukaryotic translation initiation factor 3, subunit L	0.94761	0.96436
906	B4GALNT4	beta-1,4-N-acetyl-galactosaminyl transferase 4	0.95251	0.96825
907	PTK6	PTK6 protein tyrosine kinase 6	0.95353	0.96825
908	OLFML2A	olfactomedin-like 2A	0.95606	0.96975
909	NOXO1	NADPH oxidase organizer 1	0.96061	0.97316

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910	ANTXR1	anthrax toxin receptor 1	0.96154	0.97316
911	AFAP1L2	actin filament associated protein 1-like 2	0.96606	0.97629
912	ZNF532	zinc finger protein 532	0.96674	0.97629
913	MARVELD3	MARVEL domain containing 3	0.96995	0.97845
914	DKK1	dickkopf homolog 1 (Xenopus laevis)	0.97434	0.98180
915	VSTM2A	V-set and transmembrane domain containing 2A	0.97642	0.98283
916	ARHGAP21	Rho GTPase activating protein 21	0.97835	0.98284
917	PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	0.97857	0.98284
918	EIF2B2	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	0.98537	0.98859
919	NT5M	5',3'-nucleotidase, mitochondrial	0.99460	0.99588
920	CA9	carbonic anhydrase IX	0.99480	0.99588
921	C16orf74	chromosome 16 open reading frame 74	0.99652	0.99652

* P-value and FDR computed for univariate analysis of association with mortality in the Freiburg cohort adjusted for age and gender

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Table S10. ABC Signature picked by Componentwise Boosting

Table S9. ABC Gene Signature developed by Componentwise Boosting

Gene Symbol	Gene Name	Beta-value*	FDR	Freq**
S100A14	S100 calcium binding protein A14	0.264564775	8.65E-07	0.98
SLC16A1	Solute carrier family 16, member 1	0.459126634	0.00041	0.61
NRG1	Neuregulin 1	0.110035791	3.95E-05	0.58
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14	0.088291498	1.74E-05	0.55
ADM	Adrenomedullin	0.088018716	1.91E-05	0.47
RAB3D	RAB3D, member RAS oncogene family	0.148806164	4.33E-05	0.39
ANXA3	Annexin A3	0.018785012	0.00037	0.31
CCNJL	Cyclin J-like	0.074435128	4.33E-05	0.29
SLC7A11	Solute carrier family 7 member 11	0.023982017	0.00080	0.23
KLK6	kallikrein-related peptidase 6	0.04082356	0.00776	0.20
ZNF703	zinc finger protein 703	0.062170248	0.00357	0.08
MRC2	mannose receptor, C type 2	0.070080375	0.02628	0.06
SOX4	SRY (sex determining region Y)-box 4	-0.01388770	0.14361	0.05
RGS20	regulator of G-protein signaling 20	0.010046361	0.01831	0.03
CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6	-0.05261972	0.01068	0.02
NDUFA4L2	NADH dehydrogenase 1 alpha subcomplex, 4-like 2	0.09780996	0.21983	0.01

*Estimated multivariable regression parameters (Beta-value), i.e., conditional log-hazard ratios, from componentwise boosting and univariate FDR computed for association with mortality in the Freiburg cohort. **For each gene the relative frequency of inclusion into the signature (the resampling inclusion frequency (Freq) from 100 resampling data sets) was recorded.

Table S11. C-Indices and confidence intervals for the ABC survival models

Table S11. C-Indices and confidence intervals for the ABC survival models			
	c-index*	**2.5%**	**97.5%**
Freiburg Signature + GAP	0.728	0.661	0.805
Freiburg Signature	0.688	0.622	0.752
Freiburg GAP	0.602	0.526	0.686
Leuven Signature + GAP	0.791	0.698	0.880
Leuven Signature	0.712	0.610	0.805
Leuven GAP	0.709	0.606	0.801
Siena Signature + GAP	0.749	0.654	0.847
Siena Signature	0.674	0.588	0.754
Siena GAP	0.639	0.559	0.747

* C-indices and 95% confidence interval for models that predict patient survival either using the GAP index only, the grouping of patients based on the inferred gene expression signature or a combination of both. The gene expression signature was inferred using only the ABC genes.

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Figure S1. Study Design

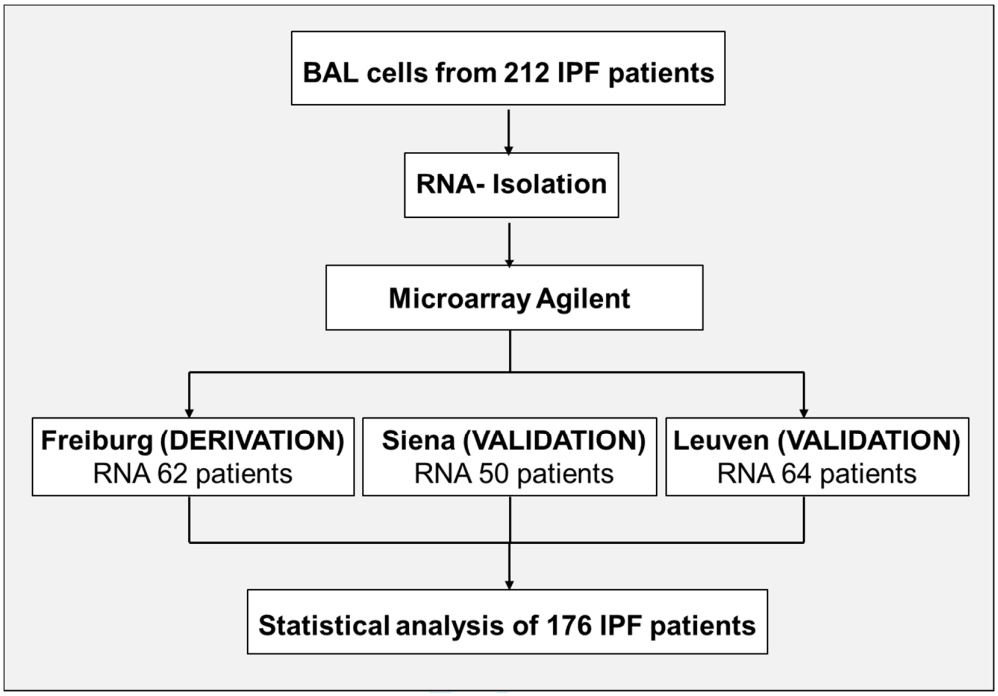

Figure S1. Study design. BAL cells from 212 IPF patients were harvested in TRIzol at 3 different tertiary referral centers: Freiburg (Germany), Siena (Italy) and Leuven (Belgium). Next, RNA was isolated and RNA yield and integrity measured. This resulted in 184 RNA samples with good quality which were labelled and hybridized to 8 x 60K Agilent Whole Human Genome arrays. After quality control a final data set of 176 patients were used for statistical analysis.

Figure S2. Sorting Strategy for Alveolar Macrophages

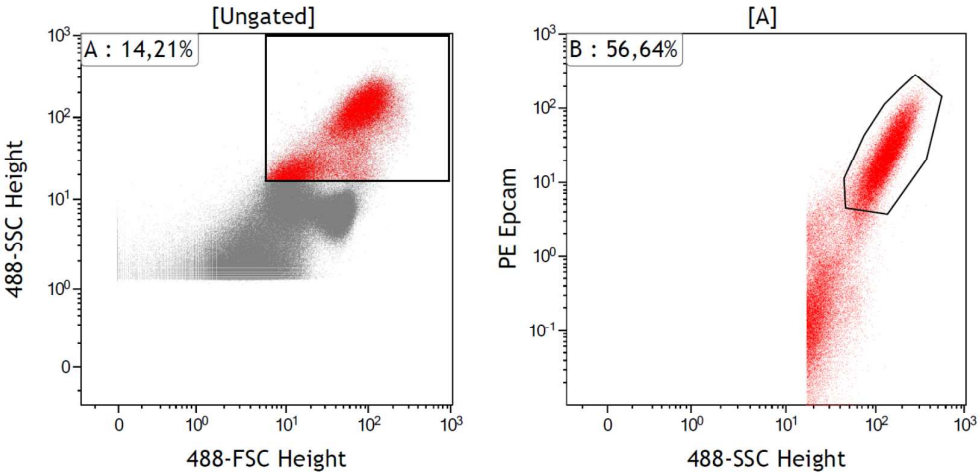

Figure S2. Sorting strategy for alveolar macrophages. Alveolar macrophages were sorted from BAL of healthy subjects using cell characteristics in the Forward Scatter (FSC) and Sideward Scatter. Gated cells are shown in red (Panel A). Next, these gated cells were depicted in a plot for SSC and PE staining and alveolar macrophages were delineated on the basis of autofluorescence and negative staining for EPCAM.

Figure S3. Determination of the Airway Basal Cell Signature

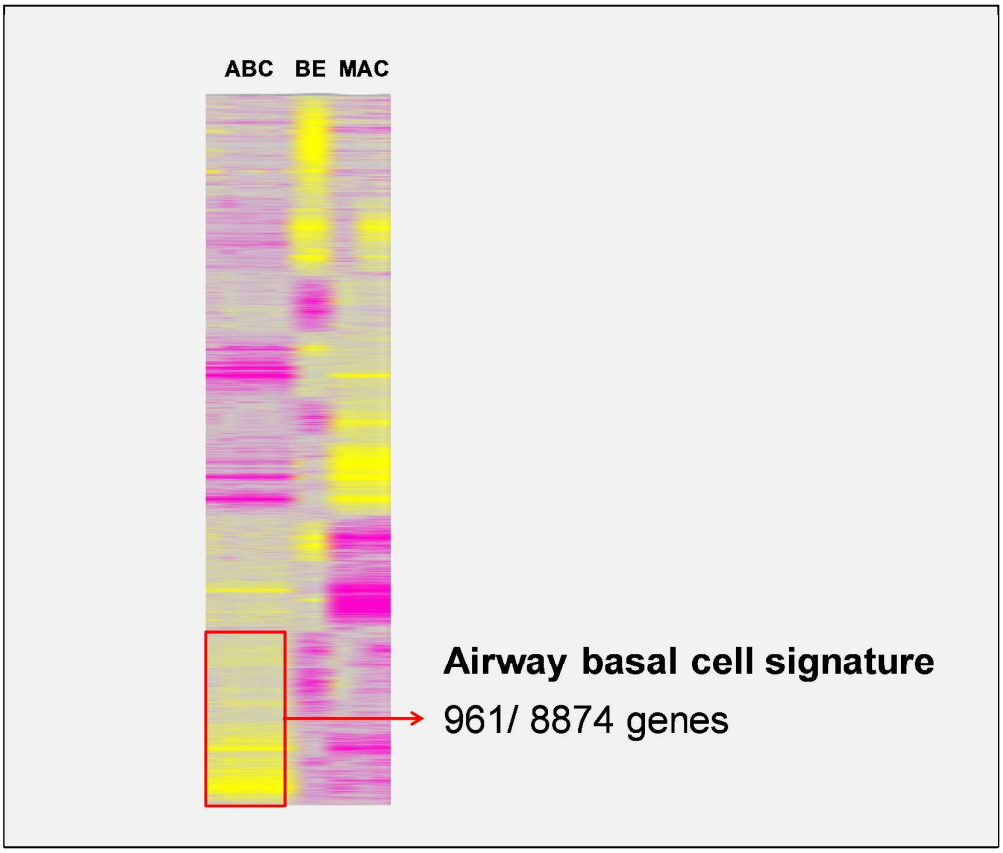

Figure S3. Determination of the airway basal cell signature. *Gene expression of isolated airway basal cells (ABC), bronchial epithelial cells (BE) and alveolar macrophages (MAC) were obtained by microarray. Univariate F-test resulted in 8874 significantly expressed genes ($p<0.0001$). By cluster analysis of the 8874 differentially expressed genes we identified 961 genes highly expressed by airway basal cells and not expressed by bronchial epithelial cells and alveolar macrophages. Of these 961 ABC genes the BAL dataset of all 3 IPF patient cohorts contained 921 ABC genes which were used for further analysis (Table S8).*

Figure S4. Increase in CK5+ Airway Basal Cells in BAL of IPF Patients.

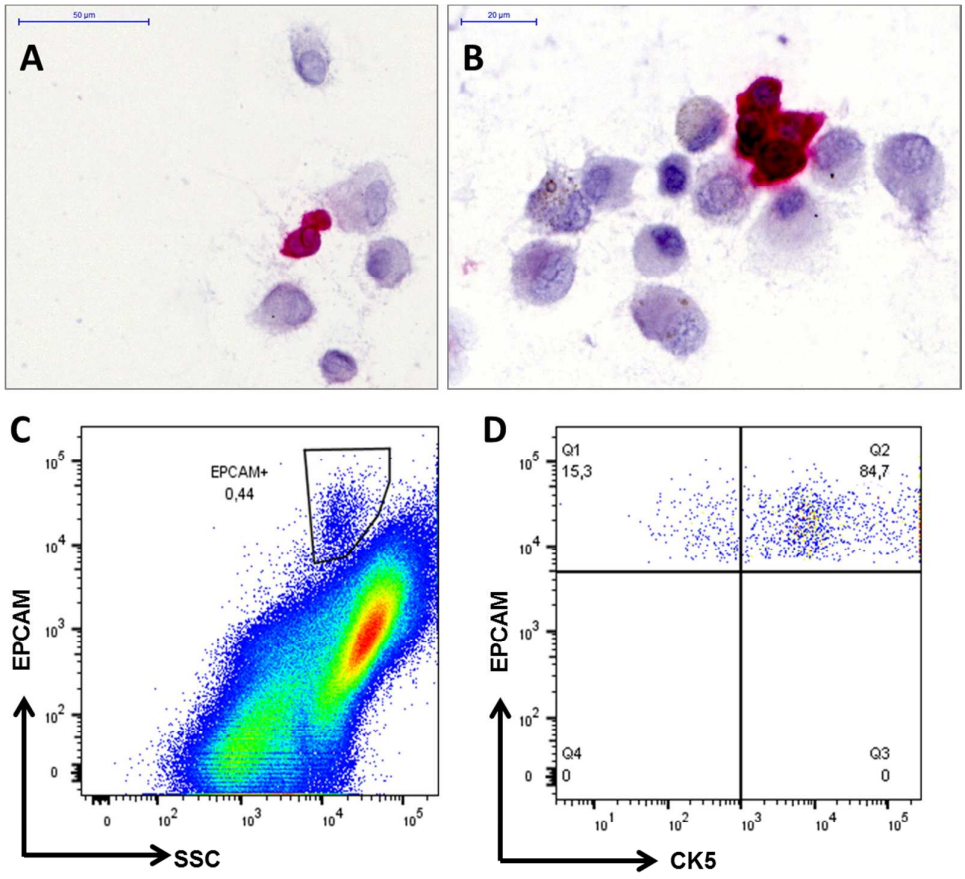

Figure S4. Increase in CK5+ Airway Basal Cells in BAL of IPF Patients. *Panel A-D: Similar to the cytokeratin CK5/6 double staining (Figure 4) also CK5+ airway basal cells (ABC, stained in red) were found frequently in cell smears of BAL from IPF patients (Panel A and B). Flow cytometry revealed presence of EPCAM+ epithelial cells in the BAL of IPF patients and most of them co-expressed CK5 identifying these cells as ABC (Panel C-D).*

Figure S5. S100A14 Immunostaining

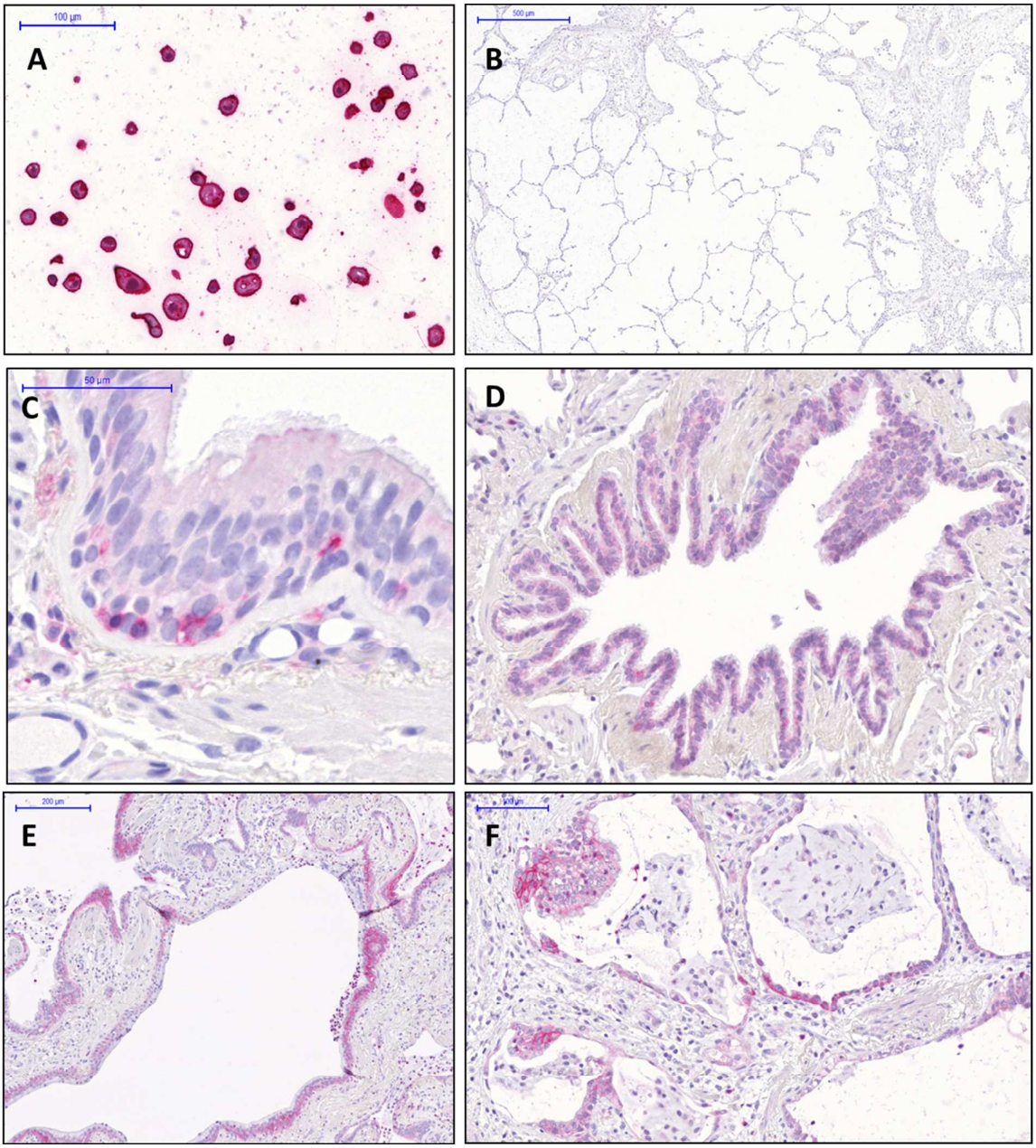

Figure S5. S100A14 immohistochemistry. *S100A14 immunohistochemistry of isolated airway basal cells (Panel A), normal lung tissue (Panel B,C,D) and lung tissues from two different IPF patients (Panel E and F). Panel A: Isolated airway basal cells and airway basal cells of normal healthy airways (Panel C and D) highly express S100A14 in line with our microarray experiment (Table S8 and S9). Similar to the CK5/6 and p40 staining in normal alveolar epithelium hardly any cells are stained by S100A14 (Panel B) while in IPF tissues (Panel E and F) epithelial cells covering honeycomb cysts and the epithelium covering fibroblast foci expressed S100A14.*

Supplementary References

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