

The Impact of Allergic Rhinitis and Asthma on Human Nasal and Bronchial Epithelial Gene Expression

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Abstract

Background: The link between upper and lower airways in patients with both asthma and allergic rhinitis is still poorly understood. As the biological complexity of these disorders can be captured by gene expression profiling we hypothesized that the clinical expression of rhinitis and/or asthma is related to differential gene expression between upper and lower airways epithelium.

Objective: Defining gene expression profiles of primary nasal and bronchial epithelial cells from the same individuals and examining the impact of allergic rhinitis with and without concomitant allergic asthma on expression profiles.

Methods: This cross-sectional study included 18 subjects (6 allergic asthma and allergic rhinitis; 6 allergic rhinitis; 6 healthy controls). The estimated false discovery rate comparing 6 subjects per group was approximately 5%. RNA was extracted from isolated and cultured epithelial cells from bronchial brushings and nasal biopsies, and analyzed by microarray (Affymetrix U133+ PM Genechip Array). Data were analysed using R and Bioconductor Limma package. For gene ontology GeneSpring GX12 was used.

Results: The study was successfully completed by 17 subjects (6 allergic asthma and allergic rhinitis; 5 allergic rhinitis; 6 healthy controls). Using correction for multiple testing, 1988 genes were differentially expressed between healthy lower and upper airway epithelium, whereas in allergic rhinitis with or without asthma this was only 40 and 301 genes, respectively. Genes influenced by allergic rhinitis with or without asthma were linked to lung development, remodeling, regulation of peptidases and normal epithelial barrier functions.

Conclusions: Differences in epithelial gene expression between the upper and lower airway epithelium, as observed in healthy subjects, largely disappear in patients with allergic rhinitis with or without asthma, whilst new differences emerge. The present data identify several pathways and genes that might be potential targets for future drug development.

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Introduction

Asthma and rhinitis are highly prevalent and interrelated diseases [1]. The nature of this relationship is still poorly understood, although similar mechanisms driving the inflammatory process have been postulated [2;3].

According to the updated Allergic Rhinitis and its Impact on Asthma (ARIA) – World Health Organisation (WHO) workshop, one of the main challenges in the field of allergic diseases such as rhinitis and asthma is to capture their complexity through unsupervised approaches [1]. Such approaches may identify mechanistic pathways that allow the development of personalized medicine in these co-morbid diseases. Although the majority of patients with asthma and rhinitis can be successfully treated with standard therapy, not all patients can be controlled with current

treatments. The efficacy of treatment might increase by developing new medications that specifically target mechanisms upstream to disease-specific pathways as opposed to current therapies that are mostly directed to downstream effector molecules and/or cells.

The airway epithelium is appreciated to play a key role in the regulation of airway inflammation and immune responses [4–6]. Epithelial cells are the first cells that encounter environmental triggers, including pathogens and allergens, and are targets for inhaled therapies. Therefore, thorough understanding of epithelial activity as intermediate between environment and immune system is needed in patients with allergic rhinitis, allergic asthma and controls [7].

Gene expression profiling is the most widespread application of unsupervised analysis of complex diseases [8;9]. Gene expression profiling is well suited for identifying genes involved in the

pathogenesis of inflammatory diseases such as asthma and rhinitis. Expression profiles of bronchial epithelial cells have already been used to classify subjects with asthma on the basis of high or low expression of IL-13-inducible genes [10], and similarly to identify genes involved in environmental determinants in asthma [11]. Furthermore, clear differences in expression pattern were found between nasal epithelial cells isolated from healthy and allergic individuals at baseline and between their responses to allergen exposure [12].

In this study we have analysed the expression profiles of airway epithelial cells of upper and lower airways in single individuals. We hypothesized that 1) differences in gene expression profiles between upper and lower airway epithelium provide insight into organ specific activity in allergic rhinitis and asthma, and that 2) defining the molecular processes in airway epithelia derived from patients with allergic rhinitis and/or allergic asthma will identify possible mechanisms of interaction. To that end, we compared the gene expression profiles between upper and lower airway epithelium in healthy individuals and studied the impact of allergic disease on these profiles by examining the differences of these profiles with those in patients with allergic rhinitis with or without concomitant allergic asthma.

Methods

See additional Methods information in File S1.

Ethics Statement

The study was approved by the hospital Medical Ethics Committee of the Academic Medical Centre in Amsterdam, and the study was registered in the Netherlands trial register (www.trialregister.nl) with identifier NTR2125. All patients gave written informed consent.

Subjects

This study included 18 subjects (>18 y) divided into three groups: 1) 6 patients with persistent, moderate to severe allergic rhinitis [13] and intermittent or mild persistent asthma [14], 2) 6 patients with persistent, moderate to severe allergic rhinitis [13] without asthma and 3) 6 healthy controls. Patients with allergic rhinitis had nasal symptoms for more than 4 days a week during more than 4 consecutive weeks [13]. Patients with asthma had episodic chest symptoms with airway hyperresponsiveness (PC_{20} methacholine ≤ 8 mg/mL) [15] according to the standardized tidal volume method [16]. Allergic status was based on the presence of a positive skin prick test response (>3 mm wheal) to common allergens. All patients with asthma and/or rhinitis were sensitized to at least one allergen. Patients had refrained from using any medication for their asthma, rhinitis or allergy in the four weeks prior to the visit when biopsies and brushings were taken. Healthy controls had no previous history of lung disease, had normal spirometric results without airway hyperresponsiveness (PC_{20} methacholine > 8 mg/mL) and were not allergic.

None of the subjects were current smokers, had smoked within 12 months prior to the study, nor had a smoking history of ≥ 5 pack years. Subjects did not have any signs of a respiratory infection at the time of study visits. In the case of a respiratory infection, a 6-week recovery period was taken into account.

Design

This study had a cross-sectional design with two study visits. At the first visit, subjects were screened for eligibility with inclusion and exclusion criteria. At the second visit, at least 14 days after the first visit, a fiberoptic bronchoscopy was performed using 1%

lignocaine for the local anaesthesia of the larynx and lower airways during which 4 bronchial brushings were taken. Subsequently, 4 nasal biopsies were taken from the lower edge of the inferior turbinate. Local anaesthesia was achieved by application of adrenalin and cocaine under the inferior turbinate without touching the biopsy site.

Primary epithelial cell culture and microarray Affymetrix

Primary nasal and bronchial epithelial cells were isolated from nasal biopsies and bronchial brushings and cultured. RNA was isolated and Human Genome U133+ PM Genechip Array (Affymetrix inc., Santa Clara, CA, USA) was used for microarray analysis of genes.

See additional Methods information in File S1 for a detailed description of the primary epithelial cell culture, RNA extraction, and Microarray Affymetrix U133+ PM.

Microarray data analysis and statistics

Array images were analyzed by Affymetrix Expression Console using the robust multichip analysis (RMA) algorithm. The normalized data were further analysed using R (version 2.9) and the Bioconductor Limma package [17]. Statistical analysis for assessing the differential gene expression was performed using the eBayes function to calculate moderated paired t-statistics after the linear model fit. All p-values were adjusted for false discovery rate correction [18]. All probe sets were included in the analysis. The full microarray data was uploaded to the Gene Expression Omnibus (GEO) with accession number GSE44037.

Gene ontology (GO) was done using GeneSpring GX12 (Agilent Technologies, Amstelveen, The Netherlands), which we used with subsets to investigate the overrepresentation of gene ontology groups (p-value < 0.05 , adjusted for multiple testing by Benjamini-Yekutieli [19]). Cluster analysis was done on all probe sets that were significantly differentially expressed between upper and lower airways (excluding probe sets that showed a lower than 2 fold difference in the healthy airway) by transforming the means of the expression values for a gene in the six groups (healthy, rhinitis, rhinitis and asthma, upper or lower airways) to Z-scores and using unsupervised K-means clustering. The latter was applied to differentiate patterns of gene expression between the six groups. Furthermore, network analysis was performed on the same set of genes using NLP Network Discovery (GeneSpring GX12, Agilent Technologies, Amstelveen, The Netherlands) that derives its relations from PubMed. A direct interaction network was built that captures relations based on regulation, connecting the genes entered into the programme.

The sample size was estimated with a custom made algorithm for microarray studies published previously [20]. In order to calculate the sample size, data from two studies were applied [12;21]. With 18 patients in total, comparing three groups of 6 subjects, and a significance level of 0.0001, this study had a False Discovery Rate of approximately 5% for detecting at least a 1.5-fold difference in gene expression.

Results

Nine differentially expressed genes identified from the results of these microarray experiments were validated by independent real time PCR on the same starting material used for the microarray analysis (see additional Results and Table S1 in File S1, and see Figure S1).

Differential gene expression in nasal and bronchial epithelium

Successful gene expression profiling was obtained in paired nasal and bronchial epithelium samples of 6 healthy controls, 5 patients with allergic rhinitis (1 patient was removed because of insufficient RNA in the nasal sample), and 6 patients with both allergic rhinitis and allergic asthma. The baseline characteristics of the subjects included in the study are presented in Table 1.

Using the p-value adjusted for multiple testing (< 0.05), we identified 1988 genes (2705 out of 41976 probe sets) of which differential expression was statistically significant between healthy nasal and healthy bronchial epithelium, 301 genes between nasal and bronchial epithelium of patients with allergic rhinitis, and 40 genes between nasal and bronchial epithelium from patients with allergic rhinitis and asthma (see additional Results, Table S2, Table S3, Table S4, Table S5, Table S6 and Table S7 in File S1).

Notably, in patients with allergic rhinitis, with or without concomitant asthma, significantly fewer genes were differentially expressed between upper and lower airways as compared to healthy controls (see Figure 1).

Functional characterization of expression differences between upper and lower airways

Among genes with significantly higher expression in healthy bronchial epithelial cells as compared to healthy nasal epithelial cells, there was significant enrichment of the Gene Ontology (GO)-classes *receptor activity*, *enzyme binding*, *cell communication*, and *developmental process* (see Table S8 in File S1). Among genes with higher expression in healthy nasal epithelium, the GO-classes *cell adhesion*, *calcium ion binding*, and *epithelial cell differentiation* (see Table S9 in File S1) were significantly enriched. In patients with allergic rhinitis alone, amongst the genes with higher expression in bronchial epithelial cells, the GO-class *regulation of signal transduction* was enriched (see Table S10 in File S1) and in the group of genes with higher expression in nasal epithelial cells, the GO-class *metal ion binding* was enriched (see Table S11 in File S1). None of the 40 genes that were differentially expressed between the upper and lower airways of patients with both allergic rhinitis and asthma could be assigned to any GO-class.

Refining the patterns of differential gene expression

The differences in expression of genes between upper and lower airways were less prominent in patients as compared to controls. By minimizing within-cluster variance and maximizing between-cluster variance, the K-means clustering grouped genes in 9 clusters based on their expression pattern in healthy, allergic

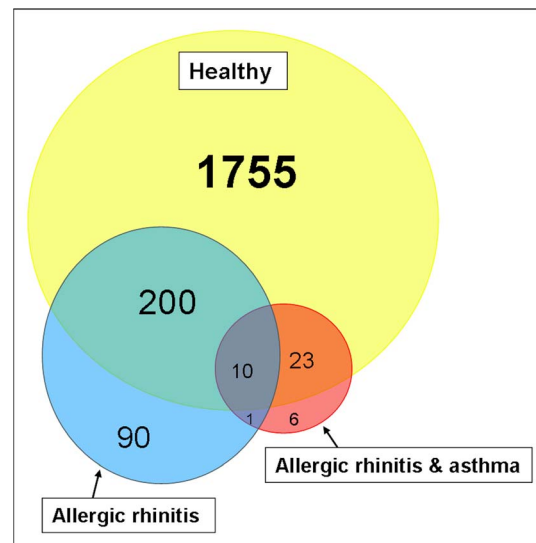


Figure 1. Venn diagram of the significantly differentially expressed genes between upper and lower airways.

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rhinitis and allergic asthma patients (see Figure 2). To get more insight whether these clusters were linked to specific molecular functions, we investigated whether the genes in these clusters were significantly enriched for any Gene Ontology-classes. See Table S12 File S1 for the following results. Clusters 1, 3, 7 and 9 consist mainly of genes that are differentially expressed in healthy controls. For genes in cluster 1 we found the GO-class *developmental process* enriched, for cluster 3 the classes *peptidase regulator activity* and *epidermis development*, and for cluster 7 *immune response*. Clusters 2, 4 and 5 consist of a mix of genes that are differentially expressed in healthy controls, in allergic rhinitis and overlap between these 2 groups. For genes within cluster 4 the GO-class *anatomical structure morphogenesis* was enriched and for cluster 5 we found several family members of UDP-glucuronosyltransferases belonging to the GO-class of *retinoic acid binding*. Finally, clusters 6 and 8 consist mainly of genes that are uniquely differentially expressed in patients with allergic rhinitis. No GO-class was significantly enriched among the genes belonging to clusters 2, 6, 8 and 9.

The regulatory network of the expression differences

Network analysis revealed a number of genes that were connected to more than 5% of the other genes in the network

Table 1. Baseline characteristics.

	Allergic Asthma & Rhinitis	Allergic Rhinitis	Healthy
	N = 6	N = 5	N = 6
Age*	24 (20–25)	24 (22–26)	26 (21–30)
Female gender (n)	6	3	5
Prebronchodilator FEV ₁ % predicted†	102 (11.4)	112 (12.8)	111 (9.3)
PC ₂₀ ‡	0.4 (0.3)	1.17 (0.05)	>16**

*Median (range).

†Mean (Standard Deviation).

‡Geometric Mean (Geometric Standard Deviation).

**No 20% drop in FEV₁ at highest concentration of Methacholine 16 mg/mL.

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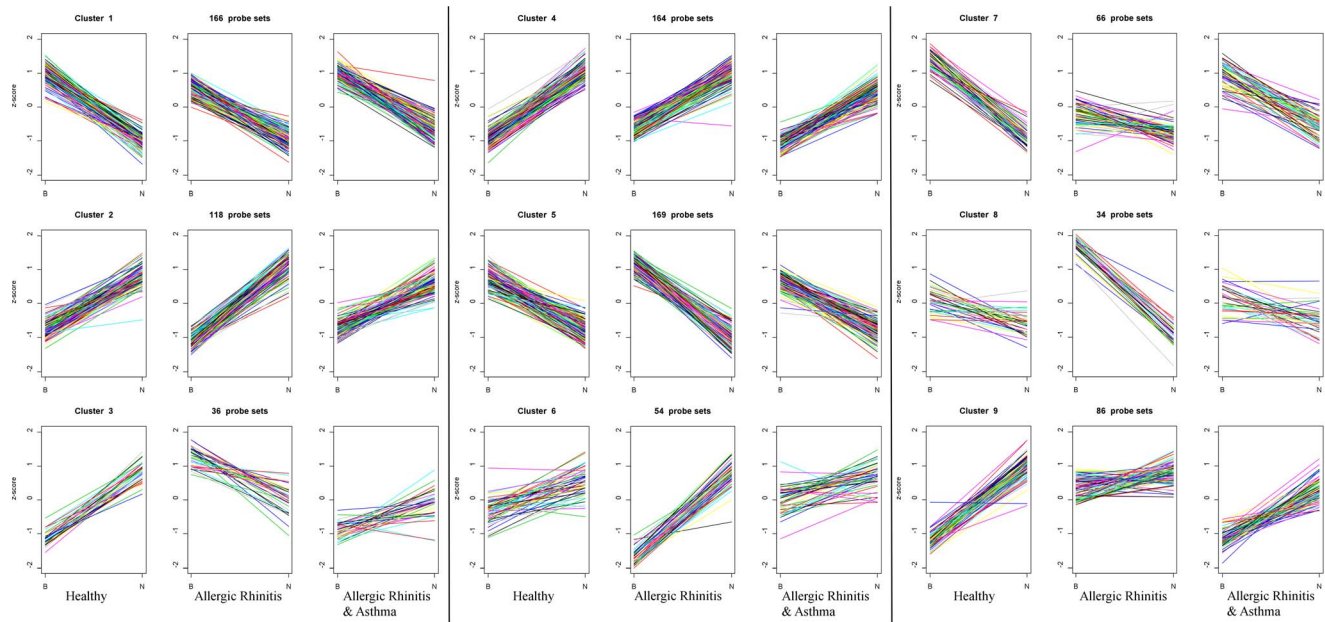


Figure 2. K-means clustering. Every three figures per row represent one cluster. The cluster is mentioned above the first figure. Every first figure are results for healthy subjects; every second figure for patients with rhinitis only; every third figure for patients with both asthma and rhinitis; **B** = expression level in bronchial epithelium, **N** = expression level in nasal epithelium.
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(hubs) (see Figure 3). This implies that a substantial part of the genes in the network are linked to hub genes that have been studied themselves in relation to signal transduction and remodeling in allergic asthma (EDN1, IL8, STAT1, JAK2), and genes that are involved in development and differentiation (RUNX2, WNT5A, EPHB2, CDKN2A) [22–28]. In the upper right-hand corner of the network, a group of linked transcription factors can be identified (FOXP2, FOXA1, FOXA2, NKX2-1, GATA6, SPDEF, FOXD1, CITED2, SFRP1), several of which are known to be involved in lung development [29]. Furthermore, surrounding hubs EDN1, JAK2 and IL8 a remarkable number of cytokines can be identified (CXCL1, CXCL2, CXCL5, CXCL10, CXCL11, CXCL17, IL11, IL24, IL33).

Discussion

This study shows that in healthy individuals substantial differences exist in gene expression between the epithelia from upper and lower airways but that these differences are smaller in patients with allergic rhinitis and almost disappear in those with concomitant allergic asthma. Hence, we observed influence of disease on the patterns of gene expression in upper and lower airways. Genes that are influenced by allergic rhinitis and asthma are linked to genes known to be involved in lung development, remodelling, regulation of peptidases, and normal epithelial barrier functions. Additionally, new players are identified. The gene expression patterns in the epithelia of upper and lower airways suggest that allergic inflammation of the upper airways also affects the lower airways.

To our knowledge, this is the first study that extensively profiles gene expression of the combined upper and lower airways epithelium by microarray in healthy individuals and patients with allergic rhinitis, either with or without allergic asthma. Some studies have investigated upper and lower airway epithelium but these have been limited to the impact of smoking [30;31] and cystic fibrosis [32]. Previously, our group has focused exclusively

on primary nasal epithelial cells from (house dust mite) allergic rhinitis patients [12] and on the effect of different allergens on a lung epithelial cell line [33;34]. Similar to these previous experiments, we chose to isolate and culture epithelial cells, thereby eliminating contamination of the gene expression profiles by other (inflammatory) cell-types.

Our study may have some limitations. Firstly, even though relative small sample sizes are commonly used in these kind of studies [35], it will affect the outcome of our study. Notwithstanding that our current application of a correction of multiple testing allowed the identification of many differentially expressed genes, a larger sample size would obviously have allowed capturing of even smaller differences. In addition, the group of patients with allergic rhinitis included five patients, whereas the other groups contained six patients. This leads to reduction of power of the paired t-test, and therefore the number of significantly differentially expressed genes in the allergic rhinitis group is underestimated as compared to the two other groups. Therefore, we randomly excluded one sample from each of the other two groups, resulting in a reduction of the number of significant probe sets by on average 700. When applying this correction to the results of the allergic rhinitis group, we might expect to have found 1081 probe sets if we had six samples. However, these results show that patients with allergic rhinitis still have significantly less genes differentially expressed between upper and lower airways as compared to healthy controls (1081 versus 2705 probe sets, respectively). To further mitigate these possible effects, we have used the power of our design to focus our analysis on paired differences between upper and lower airways in single individuals rather than differences between nose or lung between individuals of different groups. In addition to the original power calculation mentioned in the Method section, the Benjamini and Hochberg correction for multiple testing was applied because of the model used. This correction uses a smaller significance level, inevitably reducing the power of the analysis. But it primarily

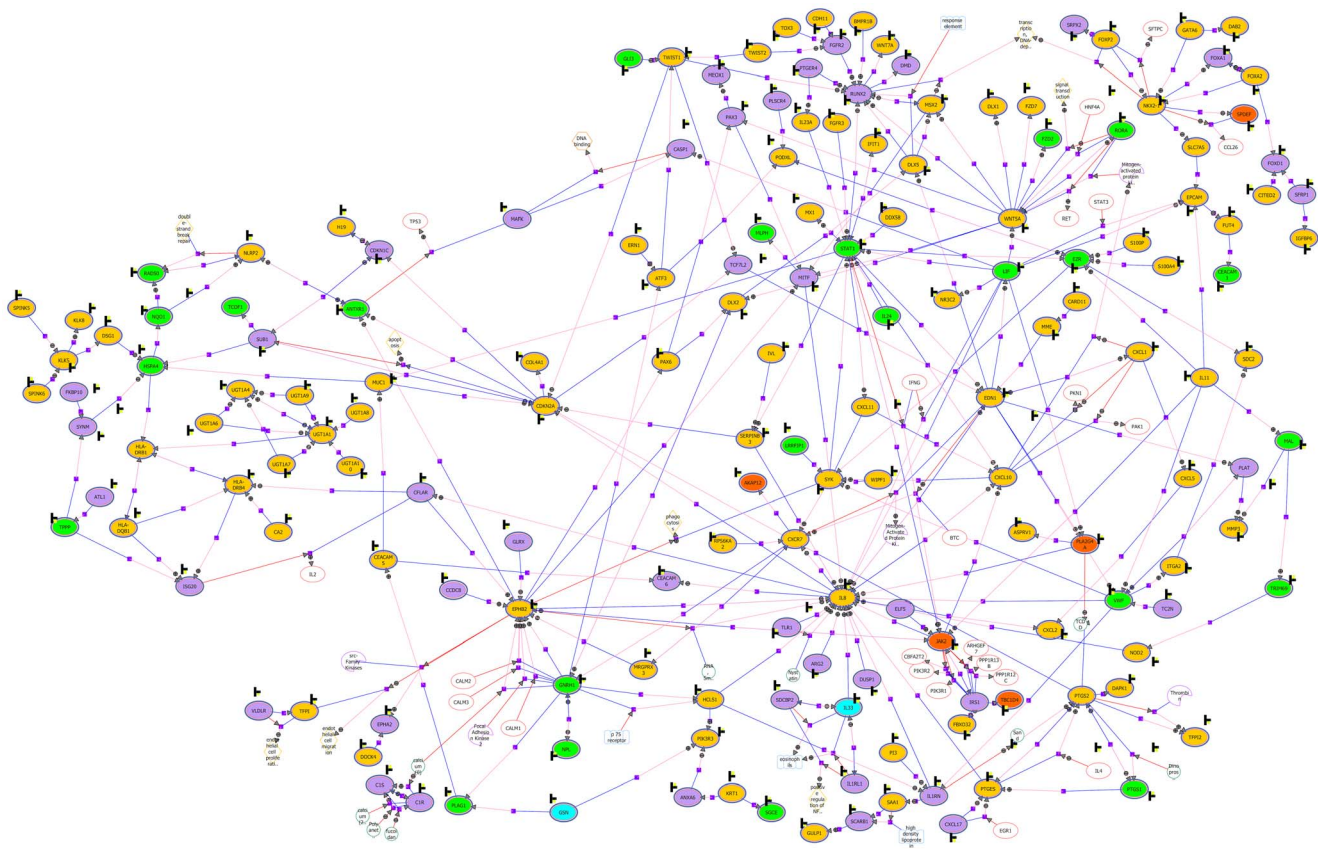


Figure 3. Regulation interaction network. Colours correspond to the Venn diagram (Figure 1): **yellow genes** = healthy specific; **green genes** = allergic rhinitis specific; **blue genes** = allergic rhinitis & asthma specific; **purple genes** = overlap healthy and allergic rhinitis; **red genes** = overlap healthy and allergic rhinitis & asthma.
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limits the risk of false positive differentially expressed genes between upper and lower airways.

Furthermore, there was a difference in the distribution of gender and age between the groups that may have had an effect on the results. Therefore, we re-analyzed the data for associations with gender and age. In nose and bronchial epithelium, expression of 50 and 42 probe sets, respectively, was significantly associated with sex and none of the probe sets was significantly associated with age for neither nose nor bronchial epithelium. Furthermore, the difference between nose and bronchial expression per probe was not significantly associated with neither sex nor age for any probe (data not shown). Finally, we cannot ensure that the expression profile observed after epithelial cell culturing was fully preserved as compared to the expression *in vivo*. Alternative procedures to obtain epithelial cells such as laser capture or direct measurement after isolation might mitigate these effects of cell culturing, but could introduce new biases introduced by contamination by other cell types and/or the (enzymatic) isolation procedure itself. However, as we compared epithelial cells from the same individuals, culturing of these cells has probably affected nose and lung epithelial cells in a similar fashion, thereby reducing a possible bias.

A major finding of our study is the impact of allergic disease, in particular allergic rhinitis, on the differences in epithelial gene expression between upper and lower airways. In the patients with allergic rhinitis, many of the differences between the epithelia of upper and lower airways have disappeared as is shown by Figure 1. This may be expected in case of increased variation of gene

expression in the nasal epithelium induced by either up or down regulation.

However, according to clusters 3, 6, 7, 8 and 9 of the K-means clustering the gene expression is altered in the lower airways of patients with allergic rhinitis. Hence, although allergic rhinitis is phenotypically restricted to the upper airways, it does impact the lower airways as well. As all of the allergic asthma patients in the present study suffered from allergic rhinitis as well, it is not surprising that also in these patients the majority of differences between upper and lower airways have disappeared as observed in Figure 1. A previous study by our group on changes in gene expression of upper airway epithelium in response to house dust mite showed less changes in patients with allergic rhinitis as compared to controls [12]. This absence of differentially expressed genes in allergic rhinitis was explained by the presence of an activated state before stimulation. Fewer differences in gene expression between upper and lower airway epithelium in allergic disease could also be explained by this principle, showing an activated state of genes in both upper and lower airways and thereby diminishing differences.

Genes belonging to K-means cluster 3 that were differentially expressed between healthy upper and lower airways are linked to the GO-class *regulation of peptidase activity*. This suggests that parts of the differences between healthy upper and lower airways is attributed to the genes of this cluster, and that both allergic rhinitis with or without asthma affect these healthy differences in gene expression between upper and lower airways. These results fit in with an imbalance between peptidase inhibitors and peptidases in

asthma that influence inflammation in the airways [36]. The peptidase inhibitor PI3 is one of these genes in cluster 3, which has previously been shown to preserve airway epithelium integrity during inflammation [37]. Furthermore, mutations in the serine peptidase inhibitor SPINK5 have been associated with asthma [38] and SPINK5 was suggested to play a role in mucin production [39].

UDP-glucuronosyltransferase genes in cluster 5 were differentially expressed between healthy upper and lower airways. These genes have not previously been linked to allergy. However, due to their ability to bind retinoic acid, they could be part of the mechanism by which retinoids influence immune regulation [40].

In our study, the regulation interaction network showed several interconnected transcription factors of which the Forkhead family members (FOXP2, FOXA1, FOXA2), NKX2-1, and GATA6 are known to be involved in lung development [29]. The majority of these transcription factors are only different in expression between healthy upper and lower airways (see Figure 3: yellow), and not in allergic rhinitis with or without asthma. These results support the hypothesis that the different embryologic origins of the nose and bronchi genes involved in the development might be responsible for the differences observed in remodelling between the nose and bronchi in asthma and rhinitis [41]. In the adult lung NKX2-1 was shown to inhibit aeroallergen-induced airway mucous cell metaplasia, in part, by the inhibition of SPDEF and by maintaining expression of FOXA2. Moreover, reduced expression of airway epithelial FOXA2 and NKX2-1 expression was observed in patients with asthma [42;43].

In the upper left-hand corner of the network (Figure 3) SPINK6, SPINK5, KLK5, and KLK8 are shown linked to each other, which have been suggested to be involved in the maintenance of normal epithelial barrier functions [44]. These genes are different in expression between healthy upper and lower airways alone, and therefore imply an altered expression in patients with allergic rhinitis with or without asthma.

Focusing on the genes that act as hubs in the gene interaction network, EDN1, IL8, WNT5A, EPHB2 and CDKN2A are all genes that attribute to the normal differences between healthy upper and lower airways (see Figure 3: yellow) Therefore, they are affected by allergic rhinitis with or without asthma. Previously, EDN1 was found increased in the airway epithelium of patients with asthma [45] where it may play a role in airway remodelling [22]. EPHB2 was found to be overexpressed in the lung in response to LPS and was suggested to contribute to the disruption of the epithelial barrier [46]. Our results confirm an influence of disease on the expression of EDN1 and EPHB2.

Although RUNX2 is a widely expressed transcription factor, RUNX2 might be a new gene in the field of allergy, since its function now is only well understood in bone development [23].

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Interestingly, IL33 is found in the network, which was differentially expressed between upper and lower airways of patients with allergic rhinitis with asthma. Like TSLP and IL25 (which were not differentially expressed between upper and lower airways), more recently IL33 is known to be an epithelial cytokine that induces T_H2-associated cytokines and is suggested to function as an endogenous ‘alarmin’, to alert the immune system in response to tissue injury or infection [47;48]. Previously, high levels of IL33 have been observed in the bronchial epithelium from patients with asthma when compared with healthy controls [49].

The currently observed disease-related differences in gene expression between upper and lower airways may have clinical implications. First, these results help to understand the mechanism of the mutual interaction between asthma and rhinitis, for which there is considerable clinical evidence. Secondly, the current analysis identified several new genes and pathways that might be potential targets for treatment of patients with combined upper and lower airway disease. It provides the opportunity to increase treatment efficacy by targeting the mechanisms upstream of the classic Th2-driven pathways.

In conclusion, we have shown that there are significant differences in gene expression between the upper and lower airway epithelium of healthy individuals and that the number of differences is significantly less in patients with allergic rhinitis with or without asthma. Moreover, allergic rhinitis seems to influence epithelial gene expression in both the upper and lower airways. Our unbiased approach has confirmed the role of some genes that have been previously described, but also identified new genes. This data represents the first step in understanding how epithelial differences (and similarities) may affect the interaction of local mucosal tissues with environmental factors, and the molecular link between the upper and lower airways in allergic rhinitis and asthma.

Supporting Information

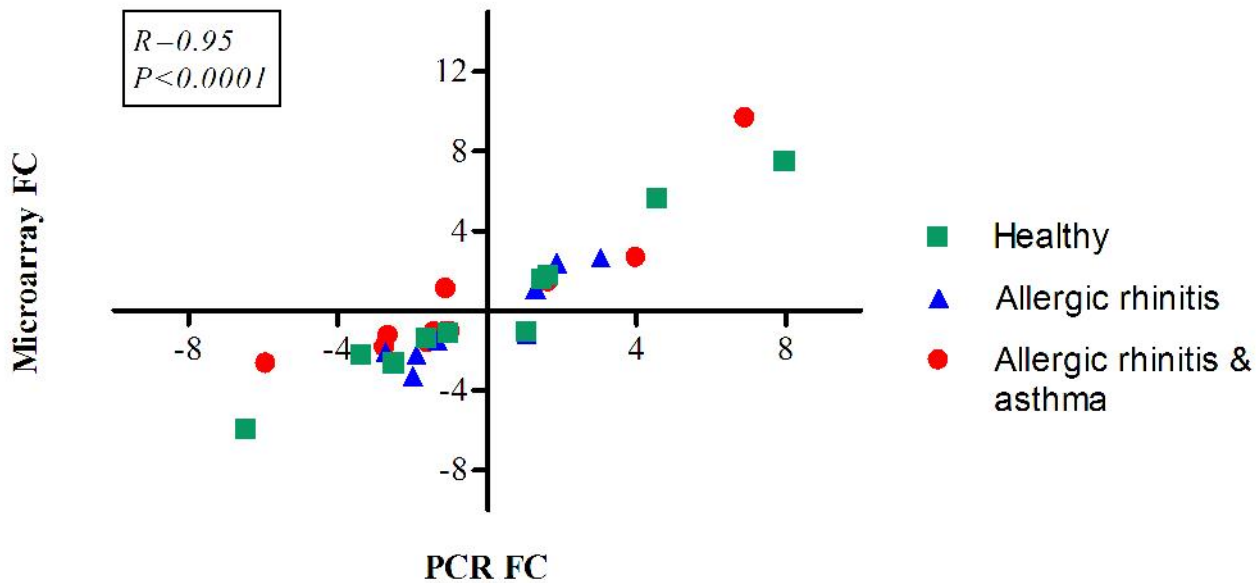
Figure S1 Correlation plot of real-time PCR data and microarray results. (TIF)

File S1 Supporting information methods, results, and tables. (DOC)

Author Contributions

Conceived and designed the experiments: AW EB WF PS CvD. Performed the experiments: AW SL. Analyzed the data: AW AZ. Contributed reagents/materials/analysis tools: AW SL AZ PS CvD. Wrote the paper: AW AZ SL WF EB PS CvD.

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SUPPORTING INFORMATION FILE S1

TITLE PAGE

Original Article

**The impact of allergic rhinitis and asthma on human nasal and
bronchial epithelial gene expression**

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METHODS

Primary epithelial cell culture

Primary cells were obtained by first digesting the biopsies and brushings with collagenase 4 (Worthington Biochemical Corp., Lakewood, NJ, USA) for 1 hour in Hanks' balanced salt 36 solution (Sigma-Aldrich, Zwijndrecht, The Netherlands). Subsequently cells were washed 37 with Hanks' balanced salt solution (HBSS) and resuspended in bronchial epithelial growth 38 medium (BEGM) (Invitrogen, Breda, The Netherlands) and seeded in one well of a 6 wells 39 plate. Cells were grown in fully humidified air containing 5% CO₂ at 37°C, and culture 40 medium was replaced every other day. Cells were cultured to 80% confluence and were pre- 41 incubated with bronchial epithelial basal medium (EBBM) for 48 hours prior to the 42 removal of supernatant and RNA extraction. For bronchial epithelial cells it took 14 days 43 on average, and for nasal epithelial cells it took 24 days on average to grow to 80% 44 confluence. There was no difference in time of culture between the three subject groups. 45

RNA extraction

Total RNA from each sample was extracted using Trizol (Life Technologies Inc., Gaithersburg, 48 MD, USA) using manufacturer's protocol, followed by purification by nucleospin RNA II 49 (Machery-Nagel, Düren, Germany). RNA concentration of all samples was measured on the 50 nanodrop ND-1000 (NanoDrop Technologies Inc., Wilmington, DE, USA). The quality of the 51 RNA was checked by using Agilent 2100 bio-analyser (Agilent Technologies, Palo Alto, CA, 52 USA). All RIN scores were ≥ 9.5 . 53

Microarray Affymetrix U133+ PM

Human Genome U133+ PM Genechip Array (Affymetrix inc., Santa Clara, CA, USA) 56 representing more than 47,000 transcripts and variants, including over 33,000 well- 57

characterized genes, was used in the analysis of the genes. The MicroArray Department (MAD) of the University of Amsterdam, a fully licensed microarray technologies centre for Affymetrix Genechip® platforms, performed the technical handling and the quality control of the microarray experiments. The quality of the images was checked by visual inspection and all raw data passed quality criteria based on borderplots, pseudocolor slide images, RNA degradation plots, box and density plots, RI plots (against a pseudoreference), correlation and PCA plots.

NLP network discovery

Network analysis was performed on the same set of genes using NLP Network Discovery (GeneSpring GX12, Agilent Technologies, Amstelveen, The Netherlands) that derives its relations from PubMed. A direct interaction network was built that captures relations based on regulation, connecting the genes entered into the programme. In more detail, the majority of relations in the GeneSpring Interaction database are derived using a Natural Language Processing (NLP) algorithm that runs on published Medline abstracts. NLP is based on a “deep parsing” method and is driven by an elaborate sentence grammar that maximizes accuracy and has control over different aspects of a sentence without compromising recall. The NLP system operates on a sentence-by-sentence manner and extracts only those relations that are completely within a sentence. There are four main phases:

- 1) Entity recognition by consulting entity dictionaries, taking into account that there are variations in how terms appear in literature.
- 2) Using a set of rules, the syntactic tree structure of the sentence is derived using context free grammar rules for English, breaking up the sentence into its underlying linguistic constituents and capturing the functional roles of different parts of the sentence.

3) A semantic analysis mapping all words of interest to semantic concepts and identifying which entity regulates another entity using the sentence structure imposed by the syntax tree. The relationships captured by the semantic tree are only direct relationships (finds relations that connect the selected entities by the previous NLP system).

4) Semantic interference: the semantic tree captures specific concepts from a sentence after which GeneSpring has to make inferences across these semantic concepts, using agents in one relationship to fill the missing holes in other relationships. GeneSpring extracts relations by searching the resulting semantic network for relation nodes that contain all the required arguments. A signature is created for each relation depending upon the participants, their roles, and their mechanisms, and references to the relation are added.

The relationships captured by the semantic tree are only direct relationships, which find relations that connect the selected entities by the NLP system that was previously explained.

The relation represents molecular interactions between the entities and is characterized by a set of participating entities. We used Regulation as relation, which is the most basic relation type. In GeneSpring an entity A “regulates” another entity B, if A has some influence on B. The participant entities in the Regulation relation are “regulator”, “target”, and “modulator”. Each participant either has a positive, negative, or unknown effect.

Depending on the source of the relation information, each relation is assigned a Relation score. This property indicates a confidence matrix on the quality of relations in the Interaction Database in GeneSpring. NLP-derived relations are graded on a scale of 1-9, the best being 9 and the weakest being 1. The score properties are internally calculated based on the number of references and the syntax of the sentences. We used 9 as Relation score for our network discovery.

Real-time polymerase chain reaction and analysis

107 Quantitative real-time PCR was used to validate the differential expression of selected genes.
 108 We chose a set of genes that represent a complete range of fold change values, capturing
 109 genes that were either higher expressed in the upper or lower airways. PCR was performed on
 110 Bio-Rad CFX96 real-time PCR detection system (Bio-Rad, Veenendaal, The Netherlands).
 111 SYBR® Green primer sequences for IL13-R α 2, EREG, PDE4D, IL1- β , IP-10, TIMP2, IL8, β
 112 -actin and GAPDH were obtained from Sigma-Aldrich (Sigma-Aldrich, Zwijndrecht, The
 113 Netherlands). The following primers were used: IL13-R α 2; sense: TGC-TCA-GAT-GAC-
 114 GGA-ATT-TGG, antisense: TGG-TAG-CCA-GAA-ACG-TAG-CAA-AG, EREG; sense:
 115 ATC-CTG-GCA-TGT-GCT-AGG-GT, antisense: GTG-CTC-CAG-AGG-TCA-GCC-AT,
 116 PDE4D; sense: GGC-CTC-CAA-CAA-GTT-TAA-AA, antisense: ACC-AGA-CAA-CTC-
 117 TGC-TAT-TCT, IL1- β ; sense: GGA-TAT-GGA-GCA-ACA-AGT-GG, antisense: ATG-
 118 TAC-CAG-TTG-GGG-AAC-TG, IP-10; sense: TGA-AAT-TAT-TCC-TGC-AAG-CCA-AT,
 119 antisense: CAG-ACA-TCT-CTT-CTC-ACC-CTT-CTT-T, TIMP2; sense: ATA-AGC-AGG-
 120 CCT-CCA-ACG-C, antisense: GAG-CTG-GAC-CAG-TCG-AAA-CC, IL8; sense: CCA-
 121 CAC-TGC-GCC-AAC-ACA-GAA-ATT-ATT-G, antisense: GCC-CTC-TTC-AAA-AAC-
 122 TTC-TCC-ACA-ACC-C, β -actin; sense: TGA-GCG-CGG-CTA-CAG-CTT, antisense:
 123 TCC-TTA-ATG-TCA-CGC-ACG-ATT-T, GAPDH; sense: GAA-GGT-GAA-GGT-CGG-
 124 AGT-C, antisense: GAA-GAT-GGT-GAT-GGG-ATT-TC. For ATF3 and DUSP1 we used
 125 TaqMan® gene expression assays from Applied Biosystems (Nieuwerkerk a/d IJssel, The
 126 Netherlands) with the following assay IDs: ATF3; HS00231069_M1, DUSP1;
 127 HS006102757_G1.
 128 Correlations between fold changes (FC) within the microarray data and the real-time PCR
 129 data were determined using Pearson's correlation.

RESULTS

Validation of microarray data

The results of this microarray experiment were validated by independent real time PCR on the same starting material used for the microarray analysis. We first determined the expression of the housekeeping genes (ACTB and GAPDH) which was not affected by type of tissue (upper or lower airway) or condition (healthy, asthma or rhinitis). A random selection of 9 genes was used that showed a significant different expression between upper and lower airways in at least one of the subject groups. Table S1 shows the ratios calculated from the microarray data and the real-time PCR-derived expression. Statistical analysis revealed a high level of correspondence ($R=0.92$, $P<0.0001$), pointing towards a correlation of 85% ($R^2=0.85$) between the microarray data and the real-time PCR (Figure S1).

Differential gene expression in nasal and bronchial epithelium

There were substantial differences in gene expression between the epithelia from upper and lower airways of healthy individuals. These differences were smaller in patients with allergic rhinitis and even smaller in those with concomitant allergic asthma. Using a cut-off of adjusted $p < 0.05$ we identified 2705 out of 41976 probe sets that were statistically differentially expressed between healthy nasal and healthy bronchial epithelium. These 2705 probe sets correspond to 1988 uniquely annotated genes, of which 979 genes [Table S2] were expressed higher in the bronchial epithelium as compared to the nasal epithelium and 1009 genes [Table S3] were expressed higher in the nasal epithelium as compared to the bronchial epithelium. In patients with allergic rhinitis we identified 381 probe sets that were statistically differentially expressed between nasal and bronchial epitheliums. These 381 probe sets correspond to 301 uniquely annotated genes, of which 138 genes [Table S4] were expressed higher in the bronchial epithelium as compared to the nasal epithelium, and 163 genes [Table

155 S5] were expressed higher in the nasal epithelium as compared to the bronchial epithelium.
156 Finally, we identified just 47 probe sets that were statistically differentially expressed between
157 nasal and bronchial epithelium from patients with allergic asthma and rhinitis. This original
158 set of 47 probe sets correspond to 40 uniquely annotated genes, of which 25 genes [Table S6]
159 were expressed higher in the bronchial epithelium as compared to the nasal epithelium, and 15
160 genes [Table S7] were expressed higher in the nasal epithelium as compared to the bronchial
161 epithelium.

162 **Table S1.** Validatory PCR of housekeeping genes and significantly different genes.

	Healthy		Allergic rhinitis		Allergic rhinitis & asthma	
	PCR FC	Microarray FC	PCR FC	Microarray FC	PCR FC	Microarray FC
ACTB	-1.1	-1.1	-1.3	-1.1	-1.0	-1.0
GAPDH	1.0	-1.0	1.3	1.1	-1.2	-1.0
ATF3	-3.4	-2.2	-2.7	-2.1	-2.8	-1.8
CXCL10	8.0	7.6	3.0	2.7	4.0	2.7
DUSP1	-2.5	-2.6	-2.0	-3.3	-1.6	-1.6
EREG	1.6	1.8	-1.9	-2.2	-1.1	1.2
IL13RA2	4.5	5.7	1.9	2.4	6.9	9.7
IL1B	1.4	1.6	1.3	1.1	-1.4	-1.0
IL8	-6.5	-5.9	1.0	-1.1	-6.0	-2.6
PDE4D	-1.6	-1.3	-1.3	-1.5	-2.7	-1.2
TIMP2	1.5	1.6	1.1	-1.2	1.6	1.5

163

164 PCR expression is given as fold change (FC) between upper and lower airways.

165 **Table S2.** Genes that were significantly higher expressed by healthy bronchial epithelial.

Gene alias	FC	Gene name/description	P-value	Gene ID
ABCG1	1.84	ATP-binding cassette, sub-family G (WHITE), member 1	8.17E-04	204567_PM_s_at
ABHD2	1.21	abhydrolase domain containing 2	4.84E-02	205566_PM_at
ABLIM3	1.93	actin binding LIM protein family, member 3	7.78E-03	205730_PM_s_at
ABR	1.52	active BCR-related gene	1.47E-02	212895_PM_s_at
ABT1	1.20	activator of basal transcription 1	4.91E-02	218405_PM_at
ABTB2	1.36	ankyrin repeat and BTB (POZ) domain containing 2	3.61E-02	213497_PM_at
ACACA	1.28	acetyl-CoA carboxylase alpha	2.29E-02	214358_PM_at
ACOT9	1.25	acyl-CoA thioesterase 9	4.49E-02	221641_PM_s_at
ACSL4	1.46	Acyl-CoA synthetase long-chain family member 4	4.94E-03	202422_PM_s_at
ACTA2	1.62	Actin, alpha 2, smooth muscle, aorta	5.47E-03	200974_PM_at
ACYP1	1.34	acylphosphatase 1, erythrocyte (common) type	4.88E-02	205260_PM_s_at
ADAM28	2.15	ADAM metalloproteinase domain 28	3.10E-02	205997_PM_at
ADAM9	1.72	ADAM metalloproteinase domain 9 (meltrin gamma)	2.93E-03	1555326_PM_a_at
ADAMTS1	2.42	ADAM metalloproteinase with thrombospondin type 1 motif, 1	3.87E-03	222486_PM_s_at
ADRB2	1.43	adrenergic, beta-2-, receptor, surface	1.21E-02	206170_PM_at
ADSSL1	1.74	Adenylosuccinate synthase like 1	4.77E-03	226325_PM_at
AFAP1L1	1.75	actin filament associated protein 1-like 1	7.81E-03	226955_PM_at
AFF1	1.40	AF4/FMR2 family, member 1	5.78E-03	201924_PM_at
AGFG1	1.35	ArfGAP with FG repeats 1	1.44E-02	226561_PM_at
AGR2	4.12	anterior gradient homolog 2 (Xenopus laevis)	1.58E-02	209173_PM_at
AHCTF1	1.27	AT hook containing transcription factor 1	4.83E-02	226115_PM_at
AHNAK2	1.23	AHNAK nucleoprotein 2	4.30E-02	1558378_PM_a_at
AKAP12	13.17	A kinase (PRKA) anchor protein 12	4.55E-06	227530_PM_at
AKT3	1.33	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	2.89E-02	212609_PM_s_at
ALG13	1.42	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	2.98E-02	219015_PM_s_at
ALOX5	1.40	arachidonate 5-lipoxygenase	3.71E-02	204446_PM_s_at
ANGPTL2	1.24	angiopoietin-like 2	2.96E-02	213001_PM_at
ANKRD20A1 ///				
ANKRD20A2 ///				
ANKRD20A3 ///				
ANKRD20A4 ///				
ANKRD20A5 ///				
ANKRD20A5 /// C21orf81				
/// LOC100132733 ///				
LOC644339	1.75	members of ankyrin repeat domain 20 family	1.26E-02	1569607_PM_s_at
ANKRD40	1.21	Ankyrin repeat domain 40	3.96E-02	227064_PM_at
ANKRD6	1.32	ankyrin repeat domain 6	1.37E-02	204672_PM_s_at
ANKRD9	1.32	Ankyrin repeat domain 9	3.91E-02	230972_PM_at
ANKS6	1.55	ankyrin repeat and sterile alpha motif domain containing 6	2.42E-03	235903_PM_at
ANO4	2.15	Anoctamin 4	4.94E-03	236420_PM_s_at
ANTXR2	1.82	anthrax toxin receptor 2	3.03E-02	228573_PM_at
ANXA11	1.49	annexin A11	3.84E-02	214783_PM_s_at
AOX1	1.87	aldehyde oxidase 1	9.95E-03	205083_PM_at
AP1S3	1.65	adaptor-related protein complex 1, sigma 3 subunit	2.56E-02	1555733_PM_s_at
AP2B1	1.28	adaptor-related protein complex 2, beta 1 subunit	1.76E-02	200615_PM_s_at
APAF1	1.40	apoptotic peptidase activating factor 1	3.35E-02	211554_PM_s_at
APLN	1.27	apelin	2.11E-02	244166_PM_at
APLP2	1.24	Amyloid beta (A4) precursor-like protein 2	2.45E-02	208703_PM_s_at
AR	1.22	androgen receptor	3.95E-02	226192_PM_at
ARAP2	1.85	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	1.63E-02	214102_PM_at
ARG2	1.64	arginase, type II	4.70E-03	203945_PM_at
ARHGAP29	1.31	Rho GTPase activating protein 29	2.09E-02	203910_PM_at
ARHGAP5	1.76	Rho GTPase activating protein 5	4.88E-02	235635_PM_at
ARHGEF10	1.31	Rho guanine nucleotide exchange factor (GEF) 10	2.09E-02	216620_PM_s_at
ARHGEF12	1.41	Rho guanine nucleotide exchange factor (GEF) 12	5.48E-03	201335_PM_s_at
ARHGEF16	1.39	Rho guanine nucleotide exchange factor (GEF) 16	2.02E-02	208009_PM_s_at
ARHGEF18	1.32	Rho/Rac guanine nucleotide exchange factor (GEF) 18	4.50E-02	213039_PM_at
ARID3B	1.45	AT rich interactive domain 3B (BRIGHT-like)	1.28E-02	218964_PM_at
ARMC8	1.32	Armadillo repeat containing 8	3.69E-02	1555281_PM_x_at
ARRDC1	1.23	arrestin domain containing 1	4.04E-02	226405_PM_s_at
ARSJ	1.51	arylsulfatase family, member J	3.39E-03	219973_PM_at
ASAP1	1.21	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	4.65E-02	224790_PM_at
ASB1	1.37	ankyrin repeat and SOCS box-containing 1	1.59E-02	212819_PM_at
ASPH	1.57	Aspartate beta-hydroxylase	7.20E-03	209135_PM_at
ASXL1	1.34	additional sex combs like 1 (Drosophila)	7.47E-03	242439_PM_s_at
ATF3	2.16	activating transcription factor 3	1.31E-02	202672_PM_s_at
ATF7IP2	1.38	activating transcription factor 7 interacting protein 2	3.81E-02	228381_PM_at
ATG5	1.34	ATG5 autophagy related 5 homolog (S. cerevisiae)	2.11E-02	202512_PM_s_at
ATL1	2.50	atlastin GTPase 1	1.81E-02	223340_PM_at

ATP12A	3.91	ATPase, H ⁺ /K ⁺ transporting, nongastric, alpha polypeptide	3.84E-02	207367_PM_at
ATP2C2	1.57	ATPase, Ca ⁺⁺ transporting, type 2C, member 2	3.81E-03	214798_PM_at
ATP8B1	1.30	ATPase, class I, type 8B, member 1	3.40E-02	238055_PM_at
ATXN2L	1.27	ataxin 2-like	2.09E-02	207798_PM_s_at
AXL	1.32	AXL receptor tyrosine kinase	6.91E-03	202686_PM_s_at
B4GALT1	1.55	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	2.38E-02	216627_PM_s_at
B4GALT6	1.36	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	1.76E-02	235333_PM_at
BAIAP2	1.42	BAI1-associated protein 2	2.86E-02	205294_PM_at
BCAR3	1.64	breast cancer anti-estrogen resistance 3	2.55E-03	204032_PM_at
BCL10	1.46	B-cell CLL/lymphoma 10	2.48E-03	205263_PM_at
BCL2L1	2.00	BCL2-like 1	1.04E-03	215037_PM_s_at
BCOR	1.31	BCL6 co-repressor	4.88E-02	219433_PM_at
BCR	1.32	breakpoint cluster region	4.75E-02	226602_PM_s_at
BEND7	1.64	BEN domain containing 7	4.48E-02	227341_PM_at
BHLHE40	1.43	basic helix-loop-helix family, member e40	5.51E-03	201170_PM_s_at
BIK	1.76	BCL2-interacting killer (apoptosis-inducing)	2.48E-02	205780_PM_at
BLMH	1.74	bleomycin hydrolase	1.21E-02	202179_PM_at
BLVRB	1.42	biliverdin reductase B (flavin reductase (NADPH))	1.66E-02	202201_PM_at
BMPRI1B	2.40	bone morphogenetic protein receptor, type IB	1.72E-03	229975_PM_at
BPGM	1.70	2,3-bisphosphoglycerate mutase	1.25E-02	203502_PM_at
BRF1	1.23	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	4.90E-02	215676_PM_at
BTG3	1.56	BTG family, member 3	7.58E-03	215425_PM_at
BTN2A1	1.28	butyrophilin, subfamily 2, member A1	3.56E-02	215493_PM_x_at
C10orf35	1.38	chromosome 10 open reading frame 35	2.06E-02	226313_PM_at
C10orf47	2.07	chromosome 10 open reading frame 47	3.35E-03	230051_PM_at
C11orf17 /// NUA2	1.53	chromosome 11 open reading frame 17 /// NUA2 family, SNF1-like kinase, 2	8.01E-03	220987_PM_s_at
C11orf75	1.86	chromosome 11 open reading frame 75	1.54E-02	219806_PM_s_at
C12orf39	1.41	chromosome 12 open reading frame 39	3.03E-02	229778_PM_at
C12orf49	1.39	chromosome 12 open reading frame 49	2.01E-02	222767_PM_s_at
C12orf54	1.62	chromosome 12 open reading frame 54	3.95E-02	240353_PM_s_at
C14orf139	2.39	chromosome 14 open reading frame 139	4.55E-03	219563_PM_at
C15orf39	1.38	chromosome 15 open reading frame 39	3.12E-02	204495_PM_s_at
C15orf48	2.66	chromosome 15 open reading frame 48	1.60E-04	223484_PM_at
C16orf45	2.00	chromosome 16 open reading frame 45	2.54E-04	212736_PM_at
C16orf52	1.28	Chromosome 16 open reading frame 52	4.83E-02	230721_PM_at
C16orf74	1.69	chromosome 16 open reading frame 74	1.26E-02	227806_PM_at
C17orf68	1.41	chromosome 17 open reading frame 68	1.82E-02	235523_PM_at
C18orf54	1.31	chromosome 18 open reading frame 54	3.25E-02	241733_PM_at
C19orf21	1.47	chromosome 19 open reading frame 21	8.01E-03	212925_PM_at
C19orf42	1.49	chromosome 19 open reading frame 42	4.57E-03	221988_PM_at
C19orf46	2.74	chromosome 19 open reading frame 46	3.87E-05	235515_PM_at
C19orf61	1.34	chromosome 19 open reading frame 61	4.27E-02	221335_PM_x_at
C1orf133	3.01	chromosome 1 open reading frame 133	1.60E-04	230121_PM_at
C1orf201	1.32	chromosome 1 open reading frame 201	4.35E-02	227694_PM_at
C1orf77	1.34	chromosome 1 open reading frame 77	2.54E-02	209927_PM_s_at
C1orf97	1.28	chromosome 1 open reading frame 97	4.59E-02	224444_PM_s_at
C3orf16	1.73	chromosome 3 open reading frame 16	2.24E-03	1561927_PM_at
C3orf52	2.05	chromosome 3 open reading frame 52	3.37E-04	219474_PM_at
C3orf67	1.63	chromosome 3 open reading frame 67	1.75E-02	239697_PM_x_at
C4orf19	1.91	chromosome 4 open reading frame 19	1.67E-02	219450_PM_at
C5orf32	1.36	chromosome 5 open reading frame 32	1.83E-02	224707_PM_at
C6orf106	1.20	chromosome 6 open reading frame 106	4.27E-02	217925_PM_s_at
C6orf168	1.78	chromosome 6 open reading frame 168	3.87E-03	232067_PM_at
C6orf211	1.20	chromosome 6 open reading frame 211	4.90E-02	218195_PM_at
C6orf223	1.81	chromosome 6 open reading frame 223	2.45E-02	230944_PM_at
C7orf46	1.44	chromosome 7 open reading frame 46	4.06E-02	228600_PM_x_at
C7orf47	1.25	chromosome 7 open reading frame 47	4.32E-02	226434_PM_at
C8orf4	1.25	chromosome 8 open reading frame 4	4.05E-02	218541_PM_s_at
C8orf73	1.28	chromosome 8 open reading frame 73	4.27E-02	227672_PM_at
C9orf125	1.41	chromosome 9 open reading frame 125	1.68E-02	224458_PM_at
C9orf167	1.37	chromosome 9 open reading frame 167	3.78E-02	233589_PM_x_at
C9orf30	1.50	chromosome 9 open reading frame 30	6.91E-03	1555841_PM_at
C9orf64	1.24	chromosome 9 open reading frame 64	4.65E-02	235940_PM_at
C9orf72	1.46	chromosome 9 open reading frame 72	3.10E-02	1553133_PM_at
CA9	1.37	carbonic anhydrase IX	2.86E-02	205199_PM_at
CADM1	1.61	cell adhesion molecule 1	2.38E-02	209031_PM_at
CADPS2	1.51	Ca ⁺⁺ -dependent secretion activator 2	1.72E-03	219572_PM_at
CALML4	2.36	calmodulin-like 4	1.64E-03	221879_PM_at
CAPN2	1.52	calpain 2, (m/II) large subunit	1.04E-02	214888_PM_at
CAPNS2	2.23	calpain, small subunit 2	5.89E-03	223832_PM_s_at
CAPRIN2	1.53	caprin family member 2	1.32E-02	218456_PM_at
CAPS	1.46	calcyphosine	5.54E-03	231729_PM_s_at

CARD11	2.08	caspase recruitment domain family, member 11	8.14E-04	223514_PM_at
CASKIN1	1.31	CASK interacting protein 1	2.99E-02	1569737_PM_a_at
CASP3	1.40	Caspase 3, apoptosis-related cysteine peptidase	7.36E-03	202763_PM_at
CAV2	1.24	Caveolin 2	2.82E-02	203323_PM_at
CCBE1	8.61	collagen and calcium binding EGF domains 1	7.41E-05	229641_PM_at
CCBL1	1.34	cysteine conjugate-beta lyase, cytoplasmic	3.00E-02	206037_PM_at
CCDC124	1.20	coiled-coil domain containing 124	4.91E-02	225454_PM_at
CCDC50	1.62	coiled-coil domain containing 50	1.49E-02	226713_PM_at
CCNG2	1.57	cyclin G2	8.41E-03	211559_PM_s_at
CCPG1	2.07	cell cycle progression 1	8.62E-03	222156_PM_x_at
CD274	1.62	CD274 molecule	3.69E-02	227458_PM_at
CD99	1.40	CD99 molecule	4.94E-02	201028_PM_s_at
CD99L2	1.60	CD99 molecule-like 2	5.38E-03	233825_PM_s_at
CDC42BPA	1.26	CDC42 binding protein kinase alpha (DMPK-like)	4.40E-02	214464_PM_at
CDC42EP2	1.90	CDC42 effector protein (Rho GTPase binding) 2	3.57E-03	214014_PM_at
CDC42SE2	1.25	CDC42 small effector 2	2.49E-02	229026_PM_at
CDH11	2.32	Cadherin 11, type 2, OB-cadherin (osteoblast)	1.70E-02	236179_PM_at
CDH26	6.00	cadherin 26	7.58E-06	232306_PM_at
CDK13	1.22	Cyclin-dependent kinase 13	3.04E-02	228991_PM_at
CDK17	1.55	cyclin-dependent kinase 17	1.53E-02	221918_PM_at
CDKN1C	4.21	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	7.87E-03	213348_PM_at
CDR2	1.34	cerebellar degeneration-related protein 2, 62kDa	6.18E-03	209501_PM_at
CDV3	1.28	CDV3 homolog (mouse)	3.88E-02	213548_PM_s_at
CEACAM5	4.14	carcinoembryonic antigen-related cell adhesion molecule 5	2.63E-02	201884_PM_at
		carcinoembryonic antigen-related cell adhesion molecule 6		
CEACAM6	3.76	(non-specific cross reacting antigen)	2.08E-02	211657_PM_at
CELF1	1.23	CUGBP, Elav-like family member 1	3.69E-02	1555467_PM_a_at
CEP135	1.42	centrosomal protein 135kDa	3.72E-02	206003_PM_at
CEP170	1.65	centrosomal protein 170kDa	3.00E-02	212746_PM_s_at
CERK	1.45	ceramide kinase	4.73E-02	218421_PM_at
CFLAR	1.81	CASP8 and FADD-like apoptosis regulator	2.38E-03	210564_PM_x_at
CGGBP1	1.39	CGG triplet repeat binding protein 1	3.45E-03	206861_PM_s_at
CGN	2.17	cingulin	2.19E-03	223232_PM_s_at
CHRNA1	1.64	cholinergic receptor, nicotinic, beta 1 (muscle)	5.23E-03	206703_PM_at
CHST9	3.26	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	1.18E-03	224400_PM_s_at
CIB1	1.36	calcium and integrin binding 1 (calmyrin)	1.74E-02	201953_PM_at
CLASP2	1.39	Cytoplasmic linker associated protein 2	1.55E-02	212308_PM_at
CLDN12	1.38	claudin 12	6.06E-03	223249_PM_at
CLDN4	1.96	Claudin 4	3.91E-03	201428_PM_at
CLDN7	1.68	claudin 7	9.70E-04	202790_PM_at
CLDN1	1.30	claudin domain containing 1	1.99E-02	208925_PM_at
CLEC11A	1.44	C-type lectin domain family 11, member A	1.05E-02	211709_PM_s_at
CLIC6	2.15	chloride intracellular channel 6	3.59E-02	227742_PM_at
		CAP-GLY domain containing linker protein family, member 4		
CLIP4	1.35		4.81E-02	219944_PM_at
CLK3	1.29	CDC-like kinase 3	1.49E-02	202140_PM_s_at
CMTM8	1.75	CKLF-like MARVEL transmembrane domain containing 8	1.74E-03	235099_PM_at
CNIH4	1.44	cornichon homolog 4 (Drosophila)	6.87E-03	222721_PM_at
CNOT4	1.36	CCR4-NOT transcription complex, subunit 4	3.71E-02	210203_PM_at
CNST	1.33	consortin, connexin sorting protein	2.10E-02	225550_PM_at
COBL	2.29	cordon-bleu homolog (mouse)	1.64E-02	213050_PM_at
COL13A1	1.83	collagen, type XIII, alpha 1	4.92E-02	211343_PM_s_at
COL4A4	1.63	Collagen, type IV, alpha 4	9.53E-03	229779_PM_at
COL4A6	2.10	collagen, type IV, alpha 6	7.67E-04	210945_PM_at
CORO1C	1.26	coronin, actin binding protein, 1C	2.04E-02	222409_PM_at
CORO2A	1.35	coronin, actin binding protein, 2A	2.07E-02	227177_PM_at
CPNE8	1.45	copine VIII	7.62E-03	241706_PM_at
CREB5	1.77	CAMP responsive element binding protein 5	7.48E-03	229228_PM_at
CRIP1	2.01	cysteine-rich protein 1 (intestinal)	5.85E-03	205081_PM_at
		colorectal neoplasia differentially expressed (non-protein coding)		
CRNDE	1.34		2.59E-02	238021_PM_s_at
CSGALNACT2	1.77	chondroitin sulfate N-acetylgalactosaminyltransferase 2	8.43E-03	218871_PM_x_at
		chondroitin sulfate N-acetylgalactosaminyltransferase 2 ///		
CSGALNACT2 ///		novel protein similar to chondroitin sulfate GalNAcT-2		
LOC644504	1.99	(GALNACT-2)	1.74E-03	222235_PM_s_at
CSNK1D	1.27	casein kinase 1, delta	1.76E-02	207945_PM_s_at
CSRNP1	1.82	cysteine-serine-rich nuclear protein 1	1.60E-02	225557_PM_at
CST6	1.43	cystatin E/M	2.23E-02	231248_PM_at
CTBP2	1.29	C-terminal binding protein 2	3.88E-02	201219_PM_at
		CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2		
CTDSP2	1.41		2.68E-02	208735_PM_s_at
CTNNA1	1.32	catenin (cadherin-associated protein), alpha 1, 102kDa	1.57E-02	1558214_PM_s_at
CTSS	2.36	cathepsin S	4.43E-02	232617_PM_at
CUL4A	1.34	Cullin 4A	1.69E-02	227757_PM_at
CUX2	2.54	cut-like homeobox 2	1.30E-02	213920_PM_at
CWC27	1.22	CWC27 spliceosome-associated protein homolog (S.	4.89E-02	223337_PM_at

		cerevisiae)		
CXADR	1.35	coxsackie virus and adenovirus receptor	4.31E-02	1555716_PM_a_at
		chemokine (C-X-C motif) ligand 1 (melanoma growth		
CXCL1	2.73	stimulating activity, alpha)	3.77E-03	204470_PM_at
CXCL17	16.06	chemokine (C-X-C motif) ligand 17	1.93E-05	226960_PM_at
CXCL2	2.49	chemokine (C-X-C motif) ligand 2	6.51E-03	209774_PM_x_at
		chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic		
CXCL6	1.45	protein 2)	2.17E-02	206336_PM_at
CXCR7	2.10	chemokine (C-X-C motif) receptor 7	2.01E-02	232746_PM_at
CXXC5	1.81	CXXC finger 5	1.63E-02	224516_PM_s_at
CYP2E1	2.73	Cytochrome P450, family 2, subfamily E, polypeptide 1	1.98E-02	209975_PM_at
CYP2S1	2.07	cytochrome P450, family 2, subfamily S, polypeptide 1	3.73E-04	223385_PM_at
CYR61	2.17	cysteine-rich, angiogenic inducer, 61	1.79E-04	210764_PM_s_at
DAPP1	1.35	dual adaptor of phosphotyrosine and 3-phosphoinositides	2.17E-02	222858_PM_s_at
DCAF7	1.26	DDB1 and CUL4 associated factor 7	2.34E-02	221745_PM_at
DDAH1	3.13	Dimethylarginine dimethylaminohydrolase 1	3.14E-05	209094_PM_at
DHRS3	1.57	dehydrogenase/reductase (SDR family) member 3	2.85E-02	202481_PM_at
DIP2A	1.28	DIP2 disco-interacting protein 2 homolog A (Drosophila)	1.39E-02	1561286_PM_a_at
DIP2C	2.35	DIP2 disco-interacting protein 2 homolog C (Drosophila)	4.50E-04	212503_PM_s_at
DISC1 /// TSNAX-DISC1	1.26	disrupted in schizophrenia 1 /// TSNAX-DISC1 gene	3.25E-02	206090_PM_s_at
DKK2	1.65	dickkopf homolog 2 (Xenopus laevis)	1.36E-02	219908_PM_at
DLG1	1.40	Discs, large homolog 1 (Drosophila)	4.59E-02	202515_PM_at
DMRT2	1.58	doublesex and mab-3 related transcription factor 2	4.41E-02	223704_PM_s_at
DMRTA2	3.61	DMRT-like family A2	1.02E-02	1558856_PM_at
DNAJA4	2.77	DnaJ (Hsp40) homolog, subfamily A, member 4	6.36E-04	225061_PM_at
DNAJB5	1.55	DnaJ (Hsp40) homolog, subfamily B, member 5	4.30E-02	207453_PM_s_at
DNAJC10	1.37	DnaJ (Hsp40) homolog, subfamily C, member 10	2.01E-02	221782_PM_at
DNAJC18	1.34	DnaJ (Hsp40) homolog, subfamily C, member 18	4.54E-02	227169_PM_at
DNMBP	1.41	dynamitin binding protein	5.21E-03	212838_PM_at
DOCK4	2.29	dedicator of cytokinesis 4	4.02E-03	205003_PM_at
DOCK5	1.42	Dedicator of cytokinesis 5	4.11E-03	230263_PM_s_at
DOK7	2.34	docking protein 7	2.06E-03	240633_PM_at
DPP9	1.84	dipeptidyl-peptidase 9	3.03E-03	231957_PM_s_at
DPY19L1	1.53	Dpy-19-like 1 (C. elegans)	1.25E-03	212792_PM_at
DPYSL3	2.01	dihydropyrimidinase-like 3	6.15E-03	201431_PM_s_at
DSG2	1.33	desmoglein 2	3.15E-02	1553105_PM_s_at
DST	1.57	dystonin	9.45E-03	216918_PM_s_at
DTNA	1.53	dystrobrevin, alpha	3.75E-02	205741_PM_s_at
DUSP1	2.59	dual specificity phosphatase 1	3.87E-03	201041_PM_s_at
DUSP5	1.76	dual specificity phosphatase 5	1.71E-02	209457_PM_at
DUSP6	1.53	dual specificity phosphatase 6	1.86E-02	208893_PM_s_at
DUSP7	1.29	dual specificity phosphatase 7	3.71E-02	214793_PM_at
ECE1	1.45	endothelin converting enzyme 1	4.92E-03	201749_PM_at
ECT2	1.60	Epithelial cell transforming sequence 2 oncogene	4.21E-03	234992_PM_x_at
EDIL3	3.16	EGF-like repeats and discoidin I-like domains 3	3.38E-02	225275_PM_at
EDN1	3.62	endothelin 1	6.06E-05	1564630_PM_at
		endonuclease/exonuclease/phosphatase family domain		
EEPDP1	1.33	containing 1	1.45E-02	225630_PM_at
EFHA2	1.23	EF-hand domain family, member A2	4.05E-02	238458_PM_at
EFHD2	1.30	EF-hand domain family, member D2	2.51E-02	217992_PM_s_at
EHBP1L1	1.42	EH domain binding protein 1-like 1	2.49E-02	91703_PM_at
EHD1	1.49	EH-domain containing 1	2.80E-02	222221_PM_x_at
EHF	1.37	ets homologous factor	4.79E-03	225645_PM_at
EIF1	1.48	Eukaryotic translation initiation factor 1	1.27E-02	228967_PM_at
EIF2C2	1.38	eukaryotic translation initiation factor 2C, 2	1.70E-02	225569_PM_at
ELF5	3.67	E74-like factor 5 (ets domain transcription factor)	3.61E-03	220625_PM_s_at
ELK4	1.22	ELK4, ETS-domain protein (SRF accessory protein 1)	4.57E-02	206919_PM_at
ELL2	1.33	elongation factor, RNA polymerase II, 2	2.50E-02	226982_PM_at
EML4	1.36	echinoderm microtubule associated protein like 4	2.24E-02	228674_PM_s_at
EMP3	1.82	epithelial membrane protein 3	6.59E-03	203729_PM_at
		egf-like module containing, mucin-like, hormone receptor-		
EMR2	1.75	like 2	1.24E-02	207610_PM_s_at
ENDOG	1.24	endonuclease G	3.00E-02	204824_PM_at
ENO2	2.80	enolase 2 (gamma, neuronal)	5.51E-03	201313_PM_at
EPB41L4A	1.33	erythrocyte membrane protein band 4.1 like 4A	9.79E-03	220119_PM_at
EPCAM	2.03	epithelial cell adhesion molecule	1.30E-02	201839_PM_s_at
EPHA2	1.74	EPH receptor A2	2.33E-03	203499_PM_at
EPHB2	2.82	EPH receptor B2	3.28E-03	209589_PM_s_at
EPS8	2.30	epidermal growth factor receptor pathway substrate 8	1.95E-02	202609_PM_at
		endoplasmic reticulum-golgi intermediate compartment		
ERGIC1	1.38	(ERGIC) 1	1.39E-02	223847_PM_s_at
ERN1	2.19	endoplasmic reticulum to nucleus signaling 1	3.41E-03	235745_PM_at
ESPN	1.53	espin	1.97E-03	223549_PM_s_at
ETV4	1.23	ets variant 4	3.53E-02	1554576_PM_a_at
		envoplakin-like /// similar to chromosome 2 open reading		
EVPLL /// LOC100132977	1.71	frame 27	3.71E-02	236933_PM_at

EYA1	1.63	eyes absent homolog 1 (Drosophila)	2.31E-02	214608_PM_s_at
EYA4	16.74	eyes absent homolog 4 (Drosophila)	1.56E-06	238877_PM_at
F11R	1.29	F11 receptor	2.52E-02	222354_PM_at
		coagulation factor VIII-associated (intronic transcript) 1 ///		
		coagulation factor VIII-associated (intronic transcript) 2 ///		
F8A1 /// F8A2 /// F8A3	1.40	coagulation factor VIII-associated (intronic transcript) 3	2.98E-02	203274_PM_at
FA2H	3.29	fatty acid 2-hydroxylase	1.13E-02	219429_PM_at
FAAH2	1.36	fatty acid amide hydrolase 2	8.70E-03	230792_PM_at
FAM102B	1.62	family with sequence similarity 102, member B	3.88E-02	226568_PM_at
FAM107B	3.22	family with sequence similarity 107, member B	5.68E-04	223058_PM_at
FAM119A	1.71	family with sequence similarity 119, member A	1.80E-03	235177_PM_at
FAM131A	1.33	family with sequence similarity 131, member A	3.45E-02	221904_PM_at
FAM155B	1.47	family with sequence similarity 155, member B	2.31E-02	206299_PM_at
FAM171A1	1.64	family with sequence similarity 171, member A1	9.13E-03	212771_PM_at
FAM174B	2.23	family with sequence similarity 174, member B	1.83E-04	221880_PM_s_at
FAM24B	1.78	family with sequence similarity 24, member B	2.20E-02	231146_PM_at
FAM65A	1.37	family with sequence similarity 65, member A	3.84E-02	45749_PM_at
FAM83A	1.56	family with sequence similarity 83, member A	1.73E-02	238460_PM_at
		family with sequence similarity 91, member A2 ///		
FAM91A2 /// FLJ39739 ///		hypothetical FLJ39739 /// similar to Neuroblastoma		
LOC100132057 ///		breakpoint family member 6-like protein /// hypothetical		
LOC100286793 ///		LOC100286793 /// hypothetical LOC728855 ///		
LOC728855 /// LOC728875	1.71	LOC728875	5.55E-03	1568609_PM_s_at
FAS	1.92	Fas (TNF receptor superfamily, member 6)	4.65E-04	204781_PM_s_at
FAT4	2.63	FAT tumor suppressor homolog 4 (Drosophila)	4.22E-03	219427_PM_at
FBXL14	1.46	F-box and leucine-rich repeat protein 14	6.13E-03	213145_PM_at
FBXL7	2.21	F-box and leucine-rich repeat protein 7	2.65E-04	213249_PM_at
FBXO33	1.22	F-box protein 33	4.63E-02	227521_PM_at
FERMT2	1.38	fermitin family homolog 2 (Drosophila)	3.71E-02	209210_PM_s_at
FGD6	1.59	FYVE, RhoGEF and PH domain containing 6	7.44E-03	1555137_PM_a_at
FGF13	1.45	fibroblast growth factor 13	2.30E-03	205110_PM_s_at
FGF18	1.33	fibroblast growth factor 18	1.67E-02	206986_PM_at
FGF5	3.56	fibroblast growth factor 5	4.67E-03	208378_PM_x_at
FGFR3	2.38	fibroblast growth factor receptor 3	9.08E-03	204379_PM_s_at
FHL1	1.70	four and a half LIM domains 1	3.39E-02	201539_PM_s_at
FIP1L1	1.35	FIP1 like 1 (S. cerevisiae)	6.15E-03	1554424_PM_at
		FK506 binding protein 1B, 12.6 kDa /// major facilitator		
FKBP1B /// MFSD2B	1.38	superfamily domain containing 2B	2.45E-02	209931_PM_s_at
FLJ10357	1.77	protein SOLO	9.88E-03	58780_PM_s_at
FLJ27352	1.75	hypothetical LOC145788	1.91E-02	243309_PM_at
FLJ35776	1.75	Hypothetical LOC649446	3.66E-03	238432_PM_at
FLJ37453	1.46	hypothetical LOC729614	3.83E-02	227593_PM_at
FLJ45340 /// FLJ45445 ///				
LOC100133150 ///		hypothetical LOC402483 /// hypothetical LOC399844 ///		
LOC100287274 ///		hypothetical LOC100133150 /// hypothetical LOC100287274		
LOC653340	1.46	/// hypothetical LOC653340	4.48E-02	225899_PM_x_at
FOSL1	1.60	FOS-like antigen 1	1.00E-02	204420_PM_at
FOXA1	4.68	Forkhead box A1	4.55E-06	204667_PM_at
FOXA2	2.37	forkhead box A2	8.19E-03	40284_PM_at
FOXD1	3.64	forkhead box D1	2.88E-02	206307_PM_s_at
FOXE1	3.16	forkhead box E1 (thyroid transcription factor 2)	1.49E-02	206912_PM_at
FOXL1	1.98	forkhead box L1	2.28E-02	243409_PM_at
FOXP2	2.54	forkhead box P2	5.08E-03	235201_PM_at
FRMD5	1.95	FERM domain containing 5	4.71E-03	230831_PM_at
FSTL3	1.53	folliculin-like 3 (secreted glycoprotein)	9.86E-03	203592_PM_s_at
FUCA1	2.06	fucosidase, alpha-L- 1, tissue	6.39E-04	202838_PM_at
FUT2	2.19	fucosyltransferase 2 (secretor status included)	1.27E-03	210608_PM_s_at
		fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-		
FUT4	2.25	specific)	8.01E-04	209892_PM_at
FUT6	2.01	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	4.23E-02	210399_PM_x_at
FUT8	1.36	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	2.77E-02	1554930_PM_a_at
FZD10	2.17	frizzled homolog 10 (Drosophila)	1.37E-02	219764_PM_at
FZD5	1.39	frizzled homolog 5 (Drosophila)	2.09E-02	221245_PM_s_at
G0S2	2.85	G0/G1switch 2	2.08E-02	213524_PM_s_at
G3BP2	1.26	GTPase activating protein (SH3 domain) binding protein 2	3.80E-02	208840_PM_s_at
GABRB3	1.86	gamma-aminobutyric acid (GABA) A receptor, beta 3	1.11E-02	229724_PM_at
GADD45B	1.54	Growth arrest and DNA-damage-inducible, beta	1.09E-02	207574_PM_s_at
GALC	1.38	galactosylceramidase	2.41E-02	204417_PM_at
GALM	1.45	galactose mutarotase (aldose 1-epimerase)	1.58E-02	234974_PM_at
GAS6	1.66	growth arrest-specific 6	3.01E-03	202177_PM_at
GATA6	2.63	GATA binding protein 6	1.36E-02	210002_PM_at
GBA2	1.40	glucosidase, beta (bile acid) 2	2.81E-02	224627_PM_at
GBGT1	1.42	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	1.26E-02	231780_PM_at
		glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I		
GCNT2	1.71	blood group)	1.55E-02	230788_PM_at
GDA	4.56	guanine deaminase	2.55E-03	224209_PM_s_at

GDE1	1.25	glycerophosphodiester phosphodiesterase 1	2.98E-02	226214_PM_at
GDI1	1.23	GDP dissociation inhibitor 1	3.15E-02	201864_PM_at
GIT2	1.82	G protein-coupled receptor kinase interacting ArfGAP 2	4.05E-03	204982_PM_at
GLB1L3	3.91	galactosidase, beta 1-like 3	2.35E-04	1569886_PM_a_at
GLRX	3.46	glutaredoxin (thioltransferase)	2.68E-04	206662_PM_at
GLUL	1.39	glutamate-ammonia ligase	1.10E-02	217202_PM_s_at
GNA15	1.45	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	5.78E-03	205349_PM_at
GNAS	1.52	GNAS complex locus	2.67E-02	229274_PM_at
GNG11	1.46	guanine nucleotide binding protein (G protein), gamma 11	2.66E-02	204115_PM_at
GOLM1	1.96	golgi membrane protein 1	1.72E-02	217771_PM_at
GPC4	1.84	glypican 4	1.50E-02	204984_PM_at
GPR110	2.41	G protein-coupled receptor 110	1.23E-02	236489_PM_at
GPR126	1.75	G protein-coupled receptor 126	6.33E-03	213094_PM_at
GPR153	1.26	G protein-coupled receptor 153	3.17E-02	64942_PM_at
GPR37	3.43	G protein-coupled receptor 37 (endothelin receptor type B-like)	1.69E-03	209631_PM_s_at
GPR39	2.44	G protein-coupled receptor 39	9.87E-05	229105_PM_at
GPRC5A	3.85	G protein-coupled receptor, family C, group 5, member A	2.24E-04	203108_PM_at
GPX3	1.54	glutathione peroxidase 3 (plasma)	3.44E-02	201348_PM_at
GRB10	2.17	growth factor receptor-bound protein 10	2.93E-03	209409_PM_at
GRK5	1.54	G protein-coupled receptor kinase 5	1.67E-02	204396_PM_s_at
GULP1	2.05	GULP, engulfment adaptor PTB domain containing 1	3.80E-04	204237_PM_at
H19	8.70	H19, imprinted maternally expressed transcript (non-protein coding)	2.32E-03	224646_PM_x_at
HCLS1	2.02	hematopoietic cell-specific Lyn substrate 1	3.05E-02	202957_PM_at
HDAC9	1.22	histone deacetylase 9	4.71E-02	205659_PM_at
HDGFRP3	1.31	hepatoma-derived growth factor, related protein 3	4.65E-02	209525_PM_at
HDHD1A	1.36	haloacid dehalogenase-like hydrolase domain containing 1A	5.66E-03	203974_PM_at
HEG1	1.45	HEG homolog 1 (zebrafish)	1.89E-03	213069_PM_at
HES4	1.38	hairy and enhancer of split 4 (Drosophila)	4.23E-02	227347_PM_x_at
HEY1	2.55	hairy/enhancer-of-split related with YRPW motif 1	5.31E-04	218839_PM_at
HIST2H4A /// HIST2H4B	1.50	histone cluster 2, H4a /// histone cluster 2, H4b	9.90E-03	207046_PM_at
HLA-DQB1	4.34	major histocompatibility complex, class II, DQ beta 1	4.66E-04	209480_PM_at
HLA-DQB1 /// HLA-DQB2		members of or similar to major histocompatibility complex, class II, DQ beta		
/// LOC100294318	2.29	major histocompatibility complex, class II, DQ beta 1 ///	1.09E-02	212999_PM_x_at
HLA-DQB1 ///		similar to major histocompatibility complex, class II, DQ beta 1		
LOC100294318	3.97	1	8.14E-04	212998_PM_x_at
HLA-DRB1 /// HLA-DRB3				
/// HLA-DRB4 /// HLA-DRB5		members of or similar to major histocompatibility complex, class II, DR beta		
/// LOC100133661 ///		members of major histocompatibility complex, class II, DR beta		
LOC100294036	2.40	1	4.84E-02	215193_PM_x_at
HLA-DRB1 /// HLA-DRB4	2.55	major histocompatibility complex, class I, G	2.31E-02	209312_PM_x_at
HLA-G	1.46	high-mobility group box 3	1.52E-02	211530_PM_x_at
HMGB3	2.04	high-mobility group box 3-like 1	1.58E-04	203744_PM_at
HMGB3L1	1.91	histocompatibility (minor) HA-1	1.32E-03	216548_PM_x_at
HMHA1	1.53	hematological and neurological expressed 1	6.17E-03	212873_PM_at
HN1	1.38	histamine N-methyltransferase	2.69E-02	222396_PM_at
HNMT	2.35	Heterogeneous nuclear ribonucleoprotein H1 (H)	5.14E-03	204112_PM_s_at
HNRNP1	1.28	hook homolog 3 (Drosophila)	3.50E-02	213470_PM_s_at
HOOK3	1.23	homeobox A1	3.95E-02	236192_PM_at
HOXA1	3.11	HRAS-like suppressor	6.98E-03	214639_PM_s_at
HRASLS	1.44	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.34E-02	219983_PM_at
HS3ST1	1.75	Heparan sulfate (glucosamine) 3-O-sulfotransferase 2	2.25E-02	205466_PM_s_at
HS3ST2	2.32	heparan sulfate 6-O-sulfotransferase 2	6.58E-03	219697_PM_at
HS6ST2	6.56	hydroxysteroid (11-beta) dehydrogenase 1	1.50E-04	230030_PM_at
HSD11B1	2.87	heat shock transcription factor 2 binding protein	4.87E-03	205404_PM_at
HSF2BP	1.36	islet cell autoantigen 1, 69kDa	4.37E-02	207020_PM_at
ICA1	2.68	intercellular adhesion molecule 2	2.50E-04	210547_PM_x_at
ICAM2	1.47	intercellular adhesion molecule 3	4.30E-02	213620_PM_s_at
ICAM3	1.34	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	2.97E-02	204949_PM_at
ICAM4	2.10	isopentenyl-diphosphate delta isomerase 1	8.43E-03	207194_PM_s_at
IDH1	1.30	immediate early response 3	1.84E-02	204615_PM_x_at
IER3	1.33	Interferon (alpha, beta and omega) receptor 1	6.37E-03	201631_PM_s_at
IFNAR1	1.28	interferon-related developmental regulator 1	4.32E-02	225661_PM_at
IFRD1	1.26	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	4.02E-02	202147_PM_s_at
IGF2 /// INS-IGF2	1.94	insulin-like growth factor 2 mRNA binding protein 2	2.56E-02	202409_PM_at
IGF2BP2	1.35	insulin-like growth factor binding protein 4	4.47E-02	223963_PM_s_at
IGFBP4	1.92	interleukin 11	1.01E-03	201508_PM_at
IL11	2.07	Interleukin 1 receptor-like 1	1.30E-02	206924_PM_at
IL1RL1	6.40	interleukin 1 receptor antagonist	4.66E-04	242809_PM_at
IL1RN	1.52		2.59E-03	212659_PM_s_at

IL23A	2.69	Interleukin 23, alpha subunit p19	9.36E-03	220054_PM_at
IL6ST	1.40	interleukin 6 signal transducer (gp130, oncostatin M receptor)	4.88E-02	212196_PM_at
IL8	5.88	interleukin 8	7.71E-03	211506_PM_s_at
ILK	1.33	integrin-linked kinase	2.79E-02	201234_PM_at
IMPDH1	1.29	IMP (inosine 5'-monophosphate) dehydrogenase 1	1.58E-02	204169_PM_at
INADL	1.25	InaD-like (Drosophila)	4.57E-02	239173_PM_at
INF2	1.61	inverted formin, FH2 and WH2 domain containing	1.86E-02	224469_PM_s_at
INPP4B	1.49	inositol polyphosphate-4-phosphatase, type II, 105kDa	2.55E-02	205376_PM_at
INPP5A	1.31	inositol polyphosphate-5-phosphatase, 40kDa	1.79E-02	203006_PM_at
INSIG1	1.40	insulin induced gene 1	3.68E-02	201626_PM_at
INSR	1.57	insulin receptor	8.26E-03	226216_PM_at
IQCD	1.57	IQ motif containing D	2.45E-02	1552540_PM_s_at
IRAK3	1.34	interleukin-1 receptor-associated kinase 3	3.03E-02	220034_PM_at
IRS1	1.70	insulin receptor substrate 1	6.98E-03	204686_PM_at
IRX5	1.35	iroquois homeobox 5	1.70E-02	210239_PM_at
ISG20	2.41	interferon stimulated exonuclease gene 20kDa	2.16E-02	204698_PM_at
ITGA2	2.02	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3.43E-03	205032_PM_at
ITGB1	1.28	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	2.46E-02	1553530_PM_a_at
ITPKC	1.26	inositol 1,4,5-trisphosphate 3-kinase C	2.87E-02	213076_PM_at
JAK2	1.53	Janus kinase 2	4.09E-03	205842_PM_s_at
JOSD1	1.35	Josephin domain containing 1	1.55E-02	201751_PM_at
JPH1	1.48	junctophilin 1	3.55E-02	229139_PM_at
JUB	1.46	Jub, ajuba homolog (Xenopus laevis)	1.22E-02	243446_PM_at
JUN	1.39	jun oncogene	2.07E-02	201465_PM_s_at
KAL1	1.75	Kallmann syndrome 1 sequence	3.28E-03	205206_PM_at
KANK2	1.61	KN motif and ankyrin repeat domains 2	1.09E-03	218418_PM_s_at
KBTBD2	1.23	kelch repeat and BTB (POZ) domain containing 2	3.71E-02	212447_PM_at
KCNJ15	2.40	potassium inwardly-rectifying channel, subfamily J, member 15	3.04E-04	210119_PM_at
KCNMA1	3.31	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1.52E-03	221584_PM_s_at
KCNQ1	1.71	potassium voltage-gated channel, KQT-like subfamily, member 1	6.51E-03	204487_PM_s_at
KCNQ5	1.42	potassium voltage-gated channel, KQT-like subfamily, member 5	4.83E-02	244623_PM_at
KCTD12	1.84	potassium channel tetramerisation domain containing 12	1.08E-03	212188_PM_at
KCTD5	1.31	Potassium channel tetramerisation domain containing 5	1.73E-02	222645_PM_s_at
KHDRBS3	1.52	KH domain containing, RNA binding, signal transduction associated 3	6.33E-03	209781_PM_s_at
KIAA0495	1.28	KIAA0495	2.61E-02	213340_PM_s_at
KIAA0649	1.51	KIAA0649	4.71E-03	203955_PM_at
KIAA1199	1.65	KIAA1199	1.00E-02	212942_PM_s_at
KIAA1217	1.26	KIAA1217	2.84E-02	232762_PM_at
KIAA1244	3.26	KIAA1244	1.06E-04	228051_PM_at
KISS1R	1.42	KISS1 receptor	4.85E-02	242517_PM_at
KLF12	1.48	Kruppel-like factor 12	2.73E-02	227261_PM_at
KLF7	1.45	Kruppel-like factor 7 (ubiquitous)	4.77E-02	238482_PM_at
KLHDC5	1.45	kelch domain containing 5	5.15E-03	225963_PM_at
KREMEN1	1.36	kringle containing transmembrane protein 1	3.08E-02	227250_PM_at
KRT13	5.16	keratin 13	4.85E-03	207935_PM_s_at
KRT18	1.95	keratin 18	6.05E-04	201596_PM_x_at
KRT19	7.71	keratin 19	5.68E-04	201650_PM_at
KRT31	1.95	keratin 31	1.36E-02	206677_PM_at
KRT8	1.68	keratin 8	1.31E-03	209008_PM_x_at
KRTCAP3	1.86	keratinocyte associated protein 3	4.73E-03	235148_PM_at
LACTB2	1.45	lactamase, beta 2	1.42E-02	218701_PM_at
LAMB3	1.26	laminin, beta 3	1.78E-02	209270_PM_at
LAMC2	2.00	laminin, gamma 2	2.33E-02	207517_PM_at
LARP1B	1.31	La ribonucleoprotein domain family, member 1B	3.33E-02	226750_PM_at
LARP6	1.34	La ribonucleoprotein domain family, member 6	3.24E-02	218651_PM_s_at
LASS2	1.30	LAG1 homolog, ceramide synthase 2	2.30E-02	222212_PM_s_at
LASS6	1.34	LAG1 homolog, ceramide synthase 6	2.65E-02	212446_PM_s_at
LBH	3.35	limb bud and heart development homolog (mouse)	6.42E-05	221011_PM_s_at
LBR	1.43	lamin B receptor	7.42E-03	201795_PM_at
LCORL	1.48	ligand dependent nuclear receptor corepressor-like	6.15E-03	232293_PM_at
LDLR	1.41	low density lipoprotein receptor	6.16E-03	217173_PM_s_at
LIFR	1.45	leukemia inhibitory factor receptor alpha	1.72E-02	225575_PM_at
LIMA1	1.57	LIM domain and actin binding 1	1.07E-02	222456_PM_s_at
LIMS3 /// LIMS3-LOC440895 /// LOC440895	2.51	LIM and senescent cell antigen-like domains 3 /// LIMS3-LOC440895 read-through /// LIM and senescent cell antigen-like domains 3-like	5.63E-03	229095_PM_s_at
LIX1L	1.61	Lix1 homolog (mouse)-like	2.60E-02	225793_PM_at
LLGL2	1.50	lethal giant larvae homolog 2 (Drosophila)	5.47E-03	1554006_PM_a_at
LMO2	1.99	LIM domain only 2 (rhombotin-like 1)	4.66E-04	204249_PM_s_at
LMO7	2.21	LIM domain 7	6.51E-03	242722_PM_at

LMTK2	1.29	lemur tyrosine kinase 2	2.15E-02	226375_PM_at
LOC100130175 ///		hypothetical protein LOC100130175 /// non-protein coding		
NCRNA00081	1.35	RNA 81	3.00E-02	213220_PM_at
LOC100130938	2.05	hypothetical LOC100130938	1.80E-03	230574_PM_at
LOC100132167	1.60	similar to hCG1993567	1.42E-02	224519_PM_at
LOC100132288	1.75	hypothetical protein LOC100132288	1.74E-03	229748_PM_x_at
		hypothetical protein LOC100132288 /// MAFF interacting		
LOC100132288 /// MAFIP	1.48	protein	4.33E-02	227330_PM_x_at
LOC100286909	1.74	Hypothetical protein LOC100286909	1.36E-02	228528_PM_at
LOC100287558	2.08	Hypothetical protein LOC100287558	5.85E-03	1569338_PM_at
LOC100288387	1.37	similar to c-jun	3.36E-02	213281_PM_at
		hypothetical protein LOC100293492 /// similar to		
LOC100293492 ///		Serine/threonine-protein kinase PRKX (Protein kinase PKX1)		
LOC389906 /// LOC441528		/// hypothetical protein LOC441528 /// similar to		
/// LOC729162	1.38	hCG1981372	2.90E-02	1558045_PM_a_at
		similar to single Ig IL-1R-related molecule /// single		
LOC100294402 /// SIGIRR	2.22	immunoglobulin and toll-interleukin 1 receptor (TIR) domain	4.92E-04	52940_PM_at
LOC158402	2.06	hypothetical protein LOC158402	5.04E-04	236769_PM_at
LOC202181	1.52	hypothetical protein LOC202181	1.96E-02	232309_PM_at
LOC284600	1.21	hypothetical protein LOC284600	4.32E-02	1559083_PM_x_at
LOC284900	1.52	hypothetical LOC284900	4.32E-03	244189_PM_at
LOC338620	1.75	hypothetical protein LOC338620	1.59E-03	230930_PM_at
		similar to solute carrier family 16 (monocarboxylic acid		
LOC346887	1.53	transporters), member 14	1.14E-02	235205_PM_at
LOC389834	1.58	ankyrin repeat domain 57 pseudogene	2.75E-02	226558_PM_at
LOC390940	1.68	similar to R28379_1	4.11E-03	213556_PM_at
LOC401074	2.27	hypothetical LOC401074	6.72E-03	1559827_PM_at
LOC439990	1.61	hypothetical gene supported by BC009626	1.06E-02	1569322_PM_at
LOC440335	1.84	hypothetical LOC440335	2.69E-03	229599_PM_at
LOC440894	1.84	hypothetical protein LOC440894	2.02E-02	242222_PM_at
LOC440895	1.25	LIM and senescent cell antigen-like domains 3-like	3.28E-02	215247_PM_at
LOC541471 ///				
NCRNA00152	1.25	hypothetical LOC541471 /// non-protein coding RNA 152	3.88E-02	225799_PM_at
LOC643008	1.70	hypothetical protein LOC643008	1.82E-02	229740_PM_at
LOC651250	1.43	hypothetical LOC651250	3.57E-03	225055_PM_at
		similar to solute carrier family 6 member 8 /// solute carrier		
LOC653562 /// SLC6A10P		family 6 (neurotransmitter transporter, creatine), member 10		
/// SLC6A8	1.37	(pseudogene) /// solute carrier family 6 (neurotransmitter		
LOC727820	1.56	transporter, creatine), member 8	2.09E-02	215812_PM_s_at
LOC728342	1.72	hypothetical protein LOC727820	3.96E-02	227383_PM_at
		Hypothetical protein LOC728342	7.70E-03	239319_PM_at
		hypothetical protein LOC728392 /// NLR family, pyrin		
LOC728392 /// NLRP1	1.78	domain containing 1	8.77E-03	218380_PM_at
LOC728613	1.67	programmed cell death 6 pseudogene	6.87E-03	1569110_PM_x_at
LOC728855	1.75	hypothetical LOC728855	1.93E-03	222001_PM_x_at
		similar to Myosin phosphatase Rho-interacting protein (Rho-		
LOC729143 /// MPRIP	1.31	interacting protein 3) (M-RIP) (RIP3) (p116Rip) /// myosin	2.73E-02	214694_PM_at
LOC729810	1.26	phosphatase Rho interacting protein	4.94E-02	229200_PM_at
LPAR1	2.09	hypothetical protein LOC729810	2.98E-03	204037_PM_at
LPCAT4	1.25	lysophosphatidic acid receptor 1	4.30E-02	239609_PM_s_at
LPPR1	1.70	lysophosphatidylcholine acyltransferase 4	3.72E-02	219732_PM_at
		lipid phosphate phosphatase-related protein type 1		
LRCH1	1.24	leucine-rich repeats and calponin homology (CH) domain	3.07E-02	226795_PM_at
LRG1	1.64	containing 1	1.11E-02	228648_PM_at
LRMP	2.21	leucine-rich alpha-2-glycoprotein 1	7.36E-03	204674_PM_at
LRRC8A	1.42	lymphoid-restricted membrane protein	8.55E-03	233487_PM_s_at
LRRC8C	1.96	leucine rich repeat containing 8 family, member A	5.84E-03	228314_PM_at
LTBP1	1.62	leucine rich repeat containing 8 family, member C	2.45E-02	202728_PM_s_at
		latent transforming growth factor beta binding protein 1		
MAFF	1.51	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F	5.14E-03	36711_PM_at
		(avian)		
MAFG	1.25	v-maf musculoaponeurotic fibrosarcoma oncogene homolog	2.39E-02	204970_PM_s_at
		G (avian)		
MAFK	1.65	v-maf musculoaponeurotic fibrosarcoma oncogene homolog	1.01E-02	226206_PM_at
		K (avian)		
MALT1	1.24	mucosa associated lymphoid tissue lymphoma translocation	2.38E-02	210018_PM_x_at
MAN2A1	1.36	gene 1	2.67E-02	226538_PM_at
MAP2K1	1.30	mannosidase, alpha, class 2A, member 1	2.21E-02	202670_PM_at
MAP3K9	1.61	mitogen-activated protein kinase kinase 1	1.29E-02	213927_PM_at
MAPK13	1.55	mitogen-activated protein kinase kinase kinase 9	2.12E-03	210058_PM_at
MAPK6	1.26	mitogen-activated protein kinase 13	2.63E-02	207121_PM_s_at
MATN3	1.60	mitogen-activated protein kinase 6	1.40E-02	206091_PM_at
MBOAT2	1.49	matrilin 3	1.40E-02	213288_PM_at
MCPH1	1.57	membrane bound O-acyltransferase domain containing 2	7.15E-03	228778_PM_at
MECOM	1.87	microcephalin 1	1.83E-02	226420_PM_at
		MDS1 and EVI1 complex locus		

MESDC1	1.49	mesoderm development candidate 1	1.03E-02	223264_PM_at
MET	1.41	met proto-oncogene (hepatocyte growth factor receptor)	4.98E-03	203510_PM_at
MFSD10	1.31	major facilitator superfamily domain containing 10	3.00E-02	209215_PM_at
MGAT2	1.28	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	3.03E-02	211061_PM_s_at
MGC16121	2.63	hypothetical protein MGC16121	2.23E-02	228235_PM_at
MGC16121 /// MIR503	2.37	hypothetical protein MGC16121 /// microRNA 503	4.75E-02	227488_PM_at
MGLL	1.28	monoglyceride lipase	4.44E-02	211026_PM_s_at
MIB1	1.24	Mindbomb homolog 1 (Drosophila)	4.58E-02	224722_PM_at
MIB2	1.71	mindbomb homolog 2 (Drosophila)	1.24E-02	228261_PM_at
MICALL2	1.57	MICAL-like 2	2.08E-02	1555862_PM_s_at
MID1	1.28	midline 1 (Opitz/BBB syndrome)	3.28E-02	203636_PM_at
MID1IP1	1.20	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	4.44E-02	218251_PM_at
MITF	2.07	microphthalmia-associated transcription factor	6.47E-03	226066_PM_at
MOCS1	1.23	molybdenum cofactor synthesis 1	4.56E-02	213181_PM_s_at
MPZL2	1.31	myelin protein zero-like 2	2.34E-02	203779_PM_s_at
MST1R	2.21	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	2.26E-03	205455_PM_at
MSTO1	1.31	misato homolog 1 (Drosophila)	2.96E-02	222584_PM_at
MSTO1 /// MSTO2P	1.44	misato homolog 1 (Drosophila) /// misato homolog 2 pseudogene	1.91E-02	224233_PM_s_at
MSX1	1.34	Msh homeobox 1	1.78E-02	205932_PM_s_at
MT1E	1.33	metallothionein 1E	1.69E-02	216336_PM_x_at
MT1F	1.37	metallothionein 1F	1.73E-02	217165_PM_x_at
MT1G	1.39	Metallothionein 1G	3.34E-02	204745_PM_x_at
MT1H /// MT1P2	1.35	metallothionein 1H /// metallothionein 1 pseudogene 2	1.23E-02	206461_PM_x_at
MT1P2	1.27	metallothionein 1 pseudogene 2	2.52E-02	211456_PM_x_at
MT1X	1.27	metallothionein 1X	3.24E-02	204326_PM_x_at
MT2A	1.28	metallothionein 2A	1.89E-02	212185_PM_x_at
MTP18	1.63	mitochondrial protein 18 kDa	2.14E-02	223172_PM_s_at
MUC1	3.10	mucin 1, cell surface associated	2.24E-02	213693_PM_s_at
MUC3B	1.23	mucin 3B, cell surface associated	3.88E-02	214898_PM_x_at
MUM1L1	2.98	melanoma associated antigen (mutated) 1-like 1	1.09E-02	229160_PM_at
MUS81	1.22	MUS81 endonuclease homolog (S. cerevisiae)	3.21E-02	218463_PM_s_at
MXD1	1.50	MAX dimerization protein 1	1.51E-02	228846_PM_at
MYADM	1.46	myeloid-associated differentiation marker	7.11E-03	225673_PM_at
MYEOV	1.95	myeloma overexpressed	4.29E-02	227342_PM_s_at
MYH14	1.66	myosin, heavy chain 14, non-muscle	9.73E-03	234290_PM_x_at
MYLIP	1.64	myosin regulatory light chain interacting protein	2.98E-02	228098_PM_s_at
MYO10	1.76	myosin X	2.17E-02	1554026_PM_a_at
MYO5B	1.46	myosin VB	4.53E-02	225299_PM_at
MYO5C	2.49	myosin VC	5.93E-03	218966_PM_at
N4BP2L2	1.27	NEDD4 binding protein 2-like 2	2.27E-02	202258_PM_s_at
NAGS	1.75	N-acetylglutamate synthase	6.24E-03	229432_PM_at
NAMPT	1.26	Nicotinamide phosphoribosyltransferase	2.68E-02	1555167_PM_s_at
NAT14	1.29	N-acetyltransferase 14 (GCN5-related, putative)	3.28E-02	223284_PM_at
NAT6	1.29	N-acetyltransferase 6 (GCN5-related)	4.23E-02	210874_PM_s_at
NCEH1	1.86	neutral cholesterol ester hydrolase 1	1.79E-02	225847_PM_at
NCF2	2.63	neutrophil cytosolic factor 2	2.24E-04	209949_PM_at
NDST1	1.29	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.99E-02	1554010_PM_at
NDUFA4L2	2.03	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	2.80E-02	218484_PM_at
NEIL1	1.37	nei endonuclease VIII-like 1 (E. coli)	1.21E-02	219396_PM_s_at
NET1	1.53	neuroepithelial cell transforming 1	6.58E-03	201829_PM_at
NEURL1B	2.86	neuralized homolog 1B (Drosophila)	8.91E-04	225355_PM_at
NFATC1	1.41	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.85E-02	211105_PM_s_at
NFYB	1.24	nuclear transcription factor Y, beta	3.53E-02	218129_PM_s_at
NHS	1.31	Nance-Horan syndrome (congenital cataracts and dental anomalies)	3.26E-02	228933_PM_at
NIPA1	1.43	non imprinted in Prader-Willi/Angelman syndrome 1	5.85E-03	225752_PM_at
NIPAL3	1.34	NIPA-like domain containing 3	4.79E-02	214579_PM_at
NKX2-1	3.76	NK2 homeobox 1	4.19E-04	231315_PM_at
NKX2-8	1.40	NK2 homeobox 8	2.38E-02	207451_PM_at
NKX3-1	1.28	NK3 homeobox 1	4.60E-02	209706_PM_at
NLRP1	2.20	NLR family, pyrin domain containing 1	6.35E-03	211824_PM_x_at
NLRP2	5.58	NLR family, pyrin domain containing 2	1.21E-02	221690_PM_s_at
NPC1	1.28	Niemann-Pick disease, type C1	2.97E-02	202679_PM_at
NR3C2	2.71	nuclear receptor subfamily 3, group C, member 2	1.97E-02	205259_PM_at
NRAS	1.40	neuroblastoma RAS viral (v-ras) oncogene homolog	5.57E-03	202647_PM_s_at
NRIP3	2.04	nuclear receptor interacting protein 3	1.23E-02	219557_PM_s_at
NRP2	1.34	neuropilin 2	2.51E-02	210842_PM_at
NRXN3	1.91	neurexin 3	4.53E-02	229649_PM_at
NT5E	2.36	5'-nucleotidase, ecto (CD73)	2.77E-04	203939_PM_at
NTHL1	1.31	nth endonuclease III-like 1 (E. coli)	4.16E-02	209731_PM_at

NTNG1	1.82	netrin G1	3.84E-02	236088_PM_at
OAF	1.50	OAF homolog (Drosophila)	4.11E-03	225510_PM_at
OCEL1	1.26	occludin/ELL domain containing 1	3.88E-02	205441_PM_at
OCIAD2	1.28	OCIA domain containing 2	2.35E-02	225314_PM_at
ODC1	1.98	Ornithine decarboxylase 1	4.58E-02	200790_PM_at
ODF2L	1.49	outer dense fiber of sperm tails 2-like	4.31E-02	230926_PM_s_at
OSBPL3	1.52	oxysterol binding protein-like 3	7.74E-03	209626_PM_s_at
OSMR	1.39	oncostatin M receptor	3.74E-02	1554008_PM_at
OTUD7B	1.33	OTU domain containing 7B	2.03E-02	227436_PM_at
OXTR	2.61	oxytocin receptor	2.35E-03	206825_PM_at
P2RY2	1.72	purinergic receptor P2Y, G-protein coupled, 2	7.95E-03	206277_PM_at
PADI1	2.53	peptidyl arginine deiminase, type I	5.47E-03	223739_PM_at
PAFAH1B3	1.31	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	2.99E-02	203228_PM_at
PANK4	1.28	pantothenate kinase 4	2.39E-02	218771_PM_at
PANX2	1.31	Pannexin 2	2.44E-02	239067_PM_s_at
PAPOLA	1.26	poly(A) polymerase alpha	4.83E-02	212720_PM_at
PAQR8	1.57	progesterone and adipoQ receptor family member VIII	2.09E-02	227626_PM_at
PARD6B	1.79	par-6 partitioning defective 6 homolog beta (C. elegans)	7.14E-03	235165_PM_at
PAWR	1.55	PRKC, apoptosis, WT1, regulator	2.88E-03	229515_PM_at
PAX9	1.50	paired box 9	2.63E-02	207059_PM_at
PCDH20	2.32	protocadherin 20	2.69E-02	232054_PM_at
PCDH7	4.14	protocadherin 7	1.44E-05	228640_PM_at
PCDHA1 /// PCDHA10 ///				
PCDHA11 /// PCDHA12 ///				
PCDHA13 /// PCDHA2 ///				
PCDHA3 /// PCDHA4 ///				
PCDHA5 /// PCDHA6 ///				
PCDHA7 /// PCDHA8 ///				
PCDHA9 /// PCDHAC1 ///				
PCDHAC2	2.94	members of protocadherin alpha	1.62E-03	223435_PM_s_at
PCGF3	1.56	polycomb group ring finger 3	1.41E-02	238084_PM_at
PDE4D	1.34	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3)		
PDE9A	2.71	dunce homolog, Drosophila)	2.17E-02	204491_PM_at
PDK3	1.44	phosphodiesterase 9A	2.31E-03	205593_PM_s_at
PDLIM5	1.40	pyruvate dehydrogenase kinase, isozyme 3	6.49E-03	228959_PM_at
PEAR1	1.88	PDZ and LIM domain 5	1.98E-02	211681_PM_s_at
PELO	1.55	platelet endothelial aggregation receptor 1	4.75E-02	228618_PM_at
PENK	1.21	pelota homolog (Drosophila)	3.57E-02	226731_PM_at
PGK1	1.34	proenkephalin	3.52E-02	213791_PM_at
PHACTR3	10.19	phosphoglycerate kinase 1	3.74E-02	200737_PM_at
PHC2	1.37	phosphatase and actin regulator 3	3.28E-05	227949_PM_at
PHF10	1.25	polyhomeotic homolog 2 (Drosophila)	1.47E-02	200919_PM_at
PHF19	1.37	PHD finger protein 10	4.96E-02	219126_PM_at
PHKA1	1.27	PHD finger protein 19	2.49E-02	227211_PM_at
PHLDA2	1.47	phosphorylase kinase, alpha 1 (muscle)	4.46E-02	205450_PM_at
PHTF2	1.53	pleckstrin homology-like domain, family A, member 2	5.00E-03	209803_PM_s_at
PIM1	1.28	putative homeodomain transcription factor 2	1.65E-02	215286_PM_s_at
PKIA	2.21	pim-1 oncogene	3.19E-02	209193_PM_at
PKIB	1.91	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	2.32E-03	204612_PM_at
PLAGL2	1.25	protein kinase (cAMP-dependent, catalytic) inhibitor beta	2.75E-02	223551_PM_at
PLAUR	1.60	pleiomorphic adenoma gene-like 2	3.03E-02	202925_PM_s_at
PLCB1	2.31	plasminogen activator, urokinase receptor	1.85E-02	214866_PM_at
PLCXD2	1.93	phospholipase C, beta 1 (phosphoinositide-specific)	5.78E-03	213222_PM_at
PLEC	1.55	phosphatidylinositol-specific phospholipase C, X domain		
PLEK2	1.43	containing 2	1.80E-02	235230_PM_at
PLEKHA2	1.41	plectin	4.54E-03	216971_PM_s_at
PLEKHG2	1.22	pleckstrin 2	2.82E-02	218644_PM_at
PLEKHG3	1.27	pleckstrin homology domain containing, family A		
PLEKHO1	2.08	(phosphoinositide binding specific) member 2	3.96E-02	238013_PM_at
PLK3	1.36	pleckstrin homology domain containing, family G (with		
PLLP	3.41	RhoGef domain) member 2	3.77E-02	233986_PM_s_at
PLS1	1.92	pleckstrin homology domain containing, family G (with		
PLXNA2	1.69	RhoGef domain) member 3	2.98E-02	212823_PM_s_at
PM20D2	1.53	pleckstrin homology domain containing, family O member 1	6.88E-03	218223_PM_s_at
PMEPA1	2.24	Polo-like kinase 3 (Drosophila)	1.99E-02	204958_PM_at
PODXL	10.45	plasma membrane proteolipid (plasmolipin)	1.83E-04	204519_PM_s_at
POLD4	1.25	plastin 1	1.28E-03	205190_PM_at
PORCN	1.57	plexin A2	6.57E-04	213030_PM_s_at
PP14571	1.91	Peptidase M20 domain containing 2	6.72E-03	225421_PM_at
PPAPDC1B	1.28	prostate transmembrane protein, androgen induced 1	1.68E-03	222449_PM_at
		podocalyxin-like	5.03E-03	201578_PM_at
		polymerase (DNA-directed), delta 4	3.73E-02	202996_PM_at
		porcupine homolog (Drosophila)	2.57E-02	219483_PM_s_at
		similar to hCG1777210	1.31E-02	214858_PM_at
		phosphatidic acid phosphatase type 2 domain containing 1B	2.08E-02	226150_PM_at

PPARD	1.65	peroxisome proliferator-activated receptor delta	1.11E-03	210636_PM_at
PPARG	1.44	peroxisome proliferator-activated receptor gamma	1.88E-02	208510_PM_s_at
PPFIA4	1.38	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	3.00E-02	214978_PM_s_at
PPP1R15A	1.62	protein phosphatase 1, regulatory (inhibitor) subunit 15A	1.61E-03	37028_PM_at
PPP1R16A	1.26	protein phosphatase 1, regulatory (inhibitor) subunit 16A	4.50E-02	225203_PM_at
PPP1R1C	1.76	protein phosphatase 1, regulatory (inhibitor) subunit 1C	2.73E-03	228646_PM_at
PPP2R1B	1.22	protein phosphatase 2, regulatory subunit A, beta	4.50E-02	222351_PM_at
PPP2R2A	1.28	protein phosphatase 2, regulatory subunit B, alpha	3.25E-02	228013_PM_at
PPP3CB	1.27	protein phosphatase 3, catalytic subunit, beta isozyme	3.84E-02	202432_PM_at
PPP3CC	1.73	protein phosphatase 3, catalytic subunit, gamma isozyme	1.02E-03	32541_PM_at
PPP4R4	1.68	protein phosphatase 4, regulatory subunit 4	8.26E-03	220673_PM_s_at
PPTC7	1.37	PTC7 protein phosphatase homolog (S. cerevisiae)	2.55E-02	235744_PM_at
PRDM16	1.66	PR domain containing 16	3.77E-03	232424_PM_at
PRKAA1	1.22	protein kinase, AMP-activated, alpha 1 catalytic subunit	4.81E-02	225985_PM_at
PRKAA2	2.90	protein kinase, AMP-activated, alpha 2 catalytic subunit	1.93E-03	227892_PM_at
PRKCD	1.25	protein kinase C, delta	2.50E-02	202545_PM_at
PRMT2	1.39	protein arginine methyltransferase 2	4.72E-02	228722_PM_at
PRR5L	1.56	proline rich 5 like	2.54E-03	219383_PM_at
PRSS23	1.63	Protease, serine, 23	1.00E-02	202458_PM_at
PSD3	1.51	pleckstrin and Sec7 domain containing 3	1.67E-02	218613_PM_at
PSG1	1.68	pregnancy specific beta-1-glycoprotein 1	1.14E-03	208257_PM_x_at
PSG7	1.35	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	2.79E-02	205602_PM_x_at
psiTPTE22	2.74	TPTE pseudogene	3.75E-03	1569348_PM_at
PSMD2	1.31	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	3.46E-02	200830_PM_at
PSMD7	1.38	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	2.63E-02	238738_PM_at
PSME4	1.22	Proteasome (prosome, macropain) activator subunit 4	4.29E-02	212219_PM_at
PTAFR	3.11	platelet-activating factor receptor	4.90E-03	227184_PM_at
PTAR1	1.37	protein prenyltransferase alpha subunit repeat containing 1	3.40E-02	235484_PM_at
PTGER4	2.49	prostaglandin E receptor 4 (subtype EP4)	3.77E-04	204897_PM_at
PTGS2	2.93	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	2.12E-03	204748_PM_at
PTK2	1.31	PTK2 protein tyrosine kinase 2	3.88E-02	241453_PM_at
PTK6	3.86	PTK6 protein tyrosine kinase 6	4.57E-03	206482_PM_at
PTN	1.76	pleiotrophin	1.32E-03	209466_PM_x_at
PTPLA	1.54	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	3.75E-03	219654_PM_at
PTPRD	1.32	protein tyrosine phosphatase, receptor type, D	2.09E-02	214043_PM_at
PVRL3	1.64	poliovirus receptor-related 3	1.55E-03	213325_PM_at
QSOX1	1.77	quiescin Q6 sulfhydryl oxidase 1	7.35E-04	201482_PM_at
RAB11FIP1	2.19	RAB11 family interacting protein 1 (class I)	4.22E-03	225177_PM_at
RAB11FIP4	1.33	RAB11 family interacting protein 4 (class II)	7.42E-03	224482_PM_s_at
RAB3B	1.82	RAB3B, member RAS oncogene family	4.57E-03	205924_PM_at
RAD18	1.41	RAD18 homolog (S. cerevisiae)	3.46E-02	238670_PM_at
RAF1	1.25	v-raf-1 murine leukemia viral oncogene homolog 1	3.88E-02	1557675_PM_at
RAP1GAP2	1.75	RAP1 GTPase activating protein 2	2.50E-02	213280_PM_at
RAPH1	1.57	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	3.29E-02	231075_PM_x_at
RARA	1.42	retinoic acid receptor, alpha	5.47E-03	203749_PM_s_at
RASA2	1.55	RAS p21 protein activator 2	1.78E-02	206636_PM_at
RASA3	1.54	RAS p21 protein activator 3	6.47E-03	225562_PM_at
RASAL2	1.46	RAS protein activator like 2	2.55E-03	227036_PM_at
RASD1	1.99	RAS, dexamethasone-induced 1	3.25E-02	223467_PM_at
RASGEF1A	6.75	RasGEF domain family, member 1A	2.07E-02	230563_PM_at
RASSF5	1.32	Ras association (RalGDS/AF-6) domain family member 5	1.84E-02	1554834_PM_a_at
RBM47	1.51	RNA binding motif protein 47	4.63E-03	218035_PM_s_at
RBPJ	1.36	recombination signal binding protein for immunoglobulin kappa J region	5.46E-03	211974_PM_x_at
RFX3	1.64	kappa J region	9.32E-03	230403_PM_at
RGMB	3.01	regulatory factor X, 3 (influences HLA class II expression)	3.45E-04	227339_PM_at
RGNEF	1.35	RGM domain family, member B	1.18E-02	1554003_PM_at
RGS12	1.44	190 kDa guanine nucleotide exchange factor	1.00E-02	209637_PM_s_at
RGS2	1.46	regulator of G-protein signaling 12	4.05E-02	202388_PM_at
RHBDL2	1.50	regulator of G-protein signaling 2, 24kDa	2.45E-02	1554897_PM_s_at
RHOBTB3	2.93	rhomboid, veinlet-like 2 (Drosophila)	2.26E-03	225202_PM_at
RHOC	1.24	Rho-related BTB domain containing 3	4.76E-02	200885_PM_at
RHOF	2.49	Ras homolog gene family, member C	3.33E-02	219045_PM_at
RHPN2	1.57	ras homolog gene family, member F (in filopodia)	8.26E-03	227196_PM_at
RICH2	1.89	rhopilin, Rho GTPase binding protein 2	1.80E-03	205414_PM_s_at
RIMS2	2.00	Rho-type GTPase-activating protein RICH2	6.79E-03	206137_PM_at
RIT1	1.28	regulating synaptic membrane exocytosis 2	1.62E-02	236224_PM_at
RND1	1.71	Ras-like without CAAX 1	3.29E-02	210056_PM_at
RNF114	1.26	Rho family GTPase 1	1.75E-02	200867_PM_at
RNF128	5.56	ring finger protein 114	5.58E-04	219263_PM_at
		ring finger protein 128		

RNF138	1.35	ring finger protein 138	2.50E-02	239143_PM_x_at
RNF144B	1.52	ring finger protein 144B	4.32E-02	239704_PM_at
RNF24	1.31	ring finger protein 24	3.80E-02	210706_PM_s_at
RNF7	1.29	Ring finger protein 7	3.84E-02	224394_PM_at
ROBO2	1.76	roundabout, axon guidance receptor, homolog 2 (Drosophila)	3.91E-03	226766_PM_at
ROD1	1.19	ROD1 regulator of differentiation 1 (S. pombe)	4.77E-02	224617_PM_at
RPH3AL	1.52	rabphilin 3A-like (without C2 domains)	4.22E-03	221614_PM_s_at
RPS16P5	1.32	ribosomal protein S16 pseudogene 5	4.32E-02	1566079_PM_at
RRAS	1.31	related RAS viral (r-ras) oncogene homolog	2.80E-02	212647_PM_at
RUFY2	1.32	RUN and FYVE domain containing 2	2.17E-02	235345_PM_at
RUNX2	2.67	runt-related transcription factor 2	9.15E-04	232231_PM_at
RUSC2	1.35	RUN and SH3 domain containing 2	3.89E-02	213066_PM_at
S100A13	1.25	S100 calcium binding protein A13	3.00E-02	202598_PM_at
S100A4	2.15	S100 calcium binding protein A4	1.21E-02	203186_PM_s_at
S100P	2.32	S100 calcium binding protein P	2.45E-02	204351_PM_at
SAMD4A	1.99	sterile alpha motif domain containing 4A	7.17E-03	215495_PM_s_at
SAMD5	2.41	sterile alpha motif domain containing 5	6.58E-03	228653_PM_at
SAT1	1.27	spermidine/spermine N1-acetyltransferase 1	3.10E-02	213988_PM_s_at
SATB1	1.82	SATB homeobox 1	4.09E-03	203408_PM_s_at
SATB2	1.54	SATB homeobox 2	5.85E-03	213435_PM_at
SBF1	1.25	SET binding factor 1	4.29E-02	212393_PM_at
SCCPDH	1.82	saccharopine dehydrogenase (putative)	2.90E-02	201825_PM_s_at
SCHIP1	1.57	schwannomin interacting protein 1	1.24E-02	204030_PM_s_at
SCNN1A	1.70	sodium channel, nonvoltage-gated 1 alpha	1.02E-02	203453_PM_at
SDC2	2.38	syndecan 2	1.27E-03	212154_PM_at
SDCBP2	1.57	syndecan binding protein (syntenin) 2	2.97E-02	233565_PM_s_at
SDCCAG8	2.29	Serologically defined colon cancer antigen 8	1.32E-02	227785_PM_at
SEC62	1.29	SEC62 homolog (S. cerevisiae)	2.46E-02	225352_PM_at
SEL1L3	1.56	Sel-1 suppressor of lin-12-like 3 (C. elegans)	2.31E-03	212311_PM_at
SEMA3A	2.75	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	7.39E-04	206805_PM_at
SEMA4D	1.48	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D semaphorin 7A, GPI membrane anchor (John Milton Hagen	1.72E-02	203528_PM_at
SEMA7A	2.01	blood group)	6.61E-03	230345_PM_at
SEPP1	10.92	Selenoprotein P, plasma, 1	4.96E-06	201427_PM_s_at
SEPT10	1.33	septin 10	3.91E-02	214720_PM_x_at
SERTAD4	3.48	SERTA domain containing 4	8.27E-05	230660_PM_at
SESTD1	1.43	SEC14 and spectrin domains 1	5.94E-03	227041_PM_at
SETBP1	2.35	SET binding protein 1	5.68E-04	227478_PM_at
SFRS12IP1	1.62	SFRS12-interacting protein 1	5.24E-03	235390_PM_at
SFTA3	4.39	surfactant associated 3	3.05E-03	228979_PM_at
SGCB	1.35	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	1.67E-02	226112_PM_at
SGPP2	1.64	sphingosine-1-phosphate phosphatase 2	1.67E-02	244780_PM_at
SH2D3A	1.55	SH2 domain containing 3A	4.77E-03	219513_PM_s_at
SH3D20	1.97	SH3 domain containing 20	2.31E-03	1554594_PM_at
SH3KBP1	1.29	SH3-domain kinase binding protein 1	1.21E-02	235692_PM_at
SH3RF3	1.37	SH3 domain containing ring finger 3	3.84E-02	228461_PM_at
SHANK2	2.03	SH3 and multiple ankyrin repeat domains 2	7.89E-04	213307_PM_at
SIPA1	1.24	signal-induced proliferation-associated 1	3.93E-02	204164_PM_at
SIX1	1.63	SIX homeobox 1	1.99E-02	205817_PM_at
SIX4	1.46	SIX homeobox 4	1.67E-02	229796_PM_at
SKAP2	2.96	Src kinase associated phosphoprotein 2	4.26E-04	204362_PM_at
SLAMF9	2.86	SLAM family member 9	1.23E-02	1553769_PM_at
SLC12A7	2.19	solute carrier family 12 (potassium/chloride transporters), member 7	1.83E-03	218066_PM_at
SLC1A1	2.10	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, (neuron Xag), member 1	1.71E-02	213664_PM_at
SLC1A4	2.39	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	7.82E-04	212810_PM_s_at
SLC25A37	1.50	solute carrier family 25, member 37	7.54E-03	222528_PM_s_at
SLC2A8	1.22	Solute carrier family 2 (facilitated glucose transporter), member 8	3.71E-02	218985_PM_at
SLC30A7	1.41	solute carrier family 30 (zinc transporter), member 7	1.69E-02	239596_PM_at
SLC36A4	1.40	solute carrier family 36 (proton/amino acid symporter), member 4	9.23E-03	234978_PM_at
SLC38A4	2.06	solute carrier family 38, member 4	1.72E-02	220786_PM_s_at
SLC40A1	1.58	Solute carrier family 40 (iron-regulated transporter), member 1	4.94E-02	223044_PM_at
SLC44A2	1.38	solute carrier family 44, member 2	2.72E-02	224609_PM_at
SLC44A4	2.10	solute carrier family 44, member 4	1.79E-03	205597_PM_at
SLC44A5	2.78	solute carrier family 44, member 5	8.53E-03	235763_PM_at
SLC4A11	2.69	solute carrier family 4, sodium borate transporter, member 11	1.61E-03	223748_PM_at
SLC4A7	1.45	solute carrier family 4, sodium bicarbonate cotransporter, member 7	9.03E-03	209884_PM_s_at
SLC7A6OS	1.25	solute carrier family 7, member 6 opposite strand	4.43E-02	229153_PM_at

		solute carrier family 9 (sodium/hydrogen exchanger), member		
SLC9A3R1	1.49	3 regulator 1	1.12E-02	201349_PM_at
SLFN11	4.62	schlafen family member 11	3.46E-03	226743_PM_at
SLFN12	2.34	schlafen family member 12	9.06E-03	219885_PM_at
SLMAP	1.26	sarcolemma associated protein	4.03E-02	222924_PM_at
SMAD3	1.53	SMAD family member 3	1.09E-03	218284_PM_at
SMAD4	1.29	SMAD family member 4	4.41E-02	235725_PM_at
		SWI/SNF related, matrix associated, actin dependent		
SMARCA1	1.46	regulator of chromatin, subfamily a, member 1	5.52E-03	203875_PM_at
SMCR7	1.39	Smith-Magenis syndrome chromosome region, candidate 7	3.14E-02	235896_PM_s_at
SMOC2	1.63	SPARC related modular calcium binding 2	2.44E-02	223235_PM_s_at
SMURF1	1.26	SMAD specific E3 ubiquitin protein ligase 1	1.49E-02	212666_PM_at
SMURF2	1.70	SMAD specific E3 ubiquitin protein ligase 2	2.93E-03	227489_PM_at
SNAP23	1.55	Synaptosomal-associated protein, 23kDa	4.89E-02	209131_PM_s_at
SNAPC1	1.90	small nuclear RNA activating complex, polypeptide 1, 43kDa	9.78E-03	205443_PM_at
SNCA	1.60	synuclein, alpha (non A4 component of amyloid precursor)	1.78E-02	236081_PM_at
SNX9	1.24	sorting nexin 9	3.10E-02	223027_PM_at
SOBP	8.37	sine oculis binding protein homolog (Drosophila)	4.54E-05	218974_PM_at
SOX4	1.23	SRY (sex determining region Y)-box 4	3.36E-02	213665_PM_at
SOX7	1.31	SRY (sex determining region Y)-box 7	2.45E-02	224013_PM_s_at
SPAG4	1.68	sperm associated antigen 4	4.44E-02	219888_PM_at
SPATA13	1.61	spermatogenesis associated 13	1.13E-02	225564_PM_at
SPATS2	1.50	spermatogenesis associated, serine-rich 2	1.84E-02	222594_PM_s_at
SPATS2L	1.42	Spermatogenesis associated, serine-rich 2-like	2.48E-02	222154_PM_s_at
SPDEF	7.03	SAM pointed domain containing ets transcription factor	2.68E-04	220192_PM_x_at
SPESP1	2.53	sperm equatorial segment protein 1	2.59E-02	229352_PM_at
		sparc/osteonectin, cwcv and kazal-like domains proteoglycan		
SPOCK1	3.21	(testican) 1	2.39E-03	202363_PM_at
		sparc/osteonectin, cwcv and kazal-like domains proteoglycan		
SPOCK3	3.37	(testican) 3	6.12E-03	235342_PM_at
SPRED1	1.37	sprouty-related, EVH1 domain containing 1	3.48E-02	235074_PM_at
SPRN	1.21	Shadow of prion protein homolog (zebrafish)	2.90E-02	238331_PM_at
SPTBN1	1.52	spectrin, beta, non-erythrocytic 1	2.26E-02	200672_PM_x_at
SRCAP	1.35	Snf2-related CREBBP activator protein	4.75E-02	213667_PM_at
SRPX2	2.91	sushi-repeat-containing protein, X-linked 2	9.93E-03	205499_PM_at
SSFA2	1.60	sperm specific antigen 2	4.24E-03	229744_PM_at
SSH1	1.36	slingshot homolog 1 (Drosophila)	2.69E-02	221752_PM_at
ST3GAL5	2.01	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	6.51E-04	203217_PM_s_at
		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-		
ST6GALNAC1	11.21	acetylglucosaminide alpha-2,6-sialyltransferase 1	3.16E-06	227725_PM_at
		signal transducing adaptor molecule (SH3 domain and ITAM		
STAM	1.29	motif) 1	1.21E-02	203544_PM_s_at
		signal transducing adaptor molecule (SH3 domain and ITAM		
STAM2	1.24	motif) 2	3.63E-02	208194_PM_s_at
STAMBPL1	1.91	STAM binding protein-like 1	6.08E-04	227607_PM_at
STARD3NL	1.28	STARD3 N-terminal like	1.37E-02	223065_PM_s_at
STK17A	1.51	serine/threonine kinase 17a	2.10E-02	202694_PM_at
STK17B	2.68	serine/threonine kinase 17b	2.55E-03	205214_PM_at
STK39	1.32	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	4.02E-02	202786_PM_at
STOM	1.57	stomatin	1.08E-03	201061_PM_s_at
STRA13	1.22	stimulated by retinoic acid 13 homolog (mouse)	4.32E-02	209478_PM_at
STS	1.43	steroid sulfatase (microsomal), isozyme S	3.03E-02	203769_PM_s_at
STX1A	1.85	syntaxin 1A (brain)	1.18E-03	204729_PM_s_at
STX2	1.40	syntaxin 2	4.41E-02	213434_PM_at
SUPT6H	1.25	suppressor of Ty 6 homolog (S. cerevisiae)	4.32E-02	1554311_PM_a_at
SUSD1	1.69	sushi domain containing 1	1.67E-02	226264_PM_at
SYK	2.07	spleen tyrosine kinase	1.52E-03	226068_PM_at
SYNPO	1.87	synaptopodin	2.32E-03	235914_PM_at
SYT17	1.57	synaptotagmin XVII	2.15E-02	205613_PM_at
SYTL4	2.17	Synaptotagmin-like 4	3.15E-02	229991_PM_s_at
TACC1	1.51	transforming, acidic coiled-coil containing protein 1	5.47E-03	1554690_PM_a_at
TAGLN3	2.92	transgelin 3	1.52E-03	204743_PM_at
TBRG1	1.33	transforming growth factor beta regulator 1	8.95E-03	225819_PM_at
TBX1	1.61	T-box 1	2.60E-03	236926_PM_at
TC2N	1.42	tandem C2 domains, nuclear	3.57E-03	234970_PM_at
TFF3	1.94	trefoil factor 3 (intestinal)	3.95E-03	204623_PM_at
		tissue factor pathway inhibitor (lipoprotein-associated		
TFPI	7.57	coagulation inhibitor)	3.47E-05	213258_PM_at
TFPI2	2.21	tissue factor pathway inhibitor 2	8.16E-04	209277_PM_at
TFPT	1.32	TCF3 (E2A) fusion partner (in childhood Leukemia)	1.58E-02	218996_PM_at
TGFA	1.35	transforming growth factor, alpha	1.93E-02	205015_PM_s_at
TGFBR1	1.23	transforming growth factor, beta receptor 1	4.16E-02	224793_PM_s_at
TGFBR2	1.57	transforming growth factor, beta receptor II (70/80kDa)	6.38E-03	208944_PM_at
TGFBR3	3.29	transforming growth factor, beta receptor III	6.05E-04	226625_PM_at
		transglutaminase 2 (C polypeptide, protein-glutamine-		
TGM2	1.90	gamma-glutamyltransferase)	3.95E-02	211003_PM_x_at

TICAM2 /// TMED7-TICAM2		toll-like receptor adaptor molecule 2 /// TMED7-TICAM2 readthrough	4.71E-02	239431_PM_at
TIMM50	1.38	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	3.15E-02	217612_PM_at
TIPARP	1.42	TCDD-inducible poly(ADP-ribose) polymerase	9.32E-03	212665_PM_at
TLL2	1.57	tolloid-like 2	3.54E-02	215008_PM_at
TM9SF3	1.26	Transmembrane 9 superfamily member 3	2.30E-02	224755_PM_at
TMC4	1.47	transmembrane channel-like 4	2.11E-02	226403_PM_at
TMC6	1.52	Transmembrane channel-like 6	9.42E-03	204328_PM_at
TMC7	1.31	transmembrane channel-like 7	2.69E-02	220021_PM_at
TMCC1	1.31	transmembrane and coiled-coil domain family 1	4.75E-02	213352_PM_at
TMCO3	1.45	Transmembrane and coiled-coil domains 3	2.85E-03	226050_PM_at
TMED5	1.46	transmembrane emp24 protein transport domain containing 5	5.47E-03	242263_PM_at
TMEM136	1.34	transmembrane protein 136	4.59E-02	1554076_PM_s_at
TMEM170A	1.24	Transmembrane protein 170A	3.79E-02	227586_PM_at
TMEM171	1.34	transmembrane protein 171	4.79E-02	240770_PM_at
TMEM191A	1.33	transmembrane protein 191A	3.81E-02	223628_PM_at
TMEM22	1.45	transmembrane protein 22	4.32E-02	219569_PM_s_at
TMEM223	1.41	transmembrane protein 223	1.32E-02	220934_PM_s_at
TMEM30B	1.27	transmembrane protein 30B	2.22E-02	213285_PM_at
TMEM40	1.76	transmembrane protein 40	7.47E-03	219503_PM_s_at
TMEM41B	1.35	transmembrane protein 41B	3.15E-02	212623_PM_at
TMEM55A	1.26	transmembrane protein 55A	2.18E-02	226338_PM_at
TMEM61	1.70	transmembrane protein 61	1.24E-03	230822_PM_at
TMEM71	1.37	transmembrane protein 71	4.96E-02	238429_PM_at
TMEM8A	1.59	transmembrane protein 8A	1.74E-03	222718_PM_at
TMEM92	2.09	transmembrane protein 92	2.00E-02	235245_PM_at
TMPRSS11D	3.10	transmembrane protease, serine 11D	4.97E-03	207602_PM_at
TMPRSS4	2.68	transmembrane protease, serine 4	1.18E-03	218960_PM_at
TNC	1.30	tenascin C	2.49E-02	201645_PM_at
TNFAIP3	1.80	tumor necrosis factor, alpha-induced protein 3	2.54E-02	202643_PM_s_at
TNFRSF10A	1.37	tumor necrosis factor receptor superfamily, member 10a	3.25E-02	231775_PM_at
TNFRSF10B	1.46	tumor necrosis factor receptor superfamily, member 10b	8.83E-03	209294_PM_x_at
TNFRSF12A	1.28	tumor necrosis factor receptor superfamily, member 12A	2.63E-02	218368_PM_s_at
TNFRSF21	1.51	tumor necrosis factor receptor superfamily, member 21	2.55E-03	218856_PM_at
TNFSF12-TNFSF13 ///		TNFSF12-TNFSF13 readthrough ///		
TNFSF13	1.34	(ligand) superfamily, member 13	4.86E-02	209500_PM_x_at
TNFSF9	1.75	tumor necrosis factor (ligand) superfamily, member 9	2.82E-03	206907_PM_at
TOMM34	1.43	translocase of outer mitochondrial membrane 34	1.67E-02	201870_PM_at
TOR1AIP1	1.34	torsin A interacting protein 1	5.47E-03	240310_PM_at
TOX3	3.64	TOX high mobility group box family member 3	6.89E-03	214774_PM_x_at
TP53TG3 ///	1.37	TP53 target 3 ///	1.55E-02	220167_PM_s_at
TP53TG3B		TP53 target 3B		
TPCN1	1.54	two pore segment channel 1	4.83E-02	217914_PM_at
TPM3	1.38	tropomyosin 3	8.86E-03	238065_PM_at
TRAF4	1.36	TNF receptor-associated factor 4	2.93E-02	242473_PM_at
TRIB1	1.48	tribbles homolog 1 (Drosophila)	6.49E-03	202241_PM_at
TRIM61	1.74	tripartite motif-containing 61	6.13E-03	238990_PM_x_at
TRIM7	1.81	tripartite motif-containing 7	2.42E-03	239694_PM_at
TRPC6	1.84	transient receptor potential cation channel, subfamily C, member 6	4.71E-02	217287_PM_s_at
TSC22D1	1.48	TSC22 domain family, member 1	5.74E-03	235315_PM_at
TSPAN1	5.22	tetraspanin 1	1.74E-05	209114_PM_at
TSPAN12	2.26	tetraspanin 12	1.36E-02	219274_PM_at
TSPAN13	1.49	tetraspanin 13	5.48E-03	217979_PM_at
TSPAN14	1.35	tetraspanin 14	8.52E-03	221002_PM_s_at
TSPAN15	1.84	tetraspanin 15	9.03E-04	218693_PM_at
TSPAN3	1.40	tetraspanin 3	5.31E-03	200973_PM_s_at
TTBK2	1.49	Tau tubulin kinase 2	7.49E-03	1554294_PM_s_at
TTC7A	1.32	tetratricopeptide repeat domain 7A	1.45E-02	224923_PM_at
TTC9	2.71	tetratricopeptide repeat domain 9	1.40E-03	213172_PM_at
TWIST1	9.30	twist homolog 1 (Drosophila)	1.56E-06	213943_PM_at
TWIST2	3.70	twist homolog 2 (Drosophila)	7.17E-03	229404_PM_at
TXNRD1	1.56	thioredoxin reductase 1	1.72E-02	201266_PM_at
UBASH3B	1.21	ubiquitin associated and SH3 domain containing B	4.14E-02	238462_PM_at
UBL3	1.46	ubiquitin-like 3	4.07E-03	201535_PM_at
UCK2	1.91	uridine-cytidine kinase 2	1.44E-02	209825_PM_s_at
UEVLD	1.29	UEV and lactate/malate dehydrogenase domains	3.87E-02	1554397_PM_s_at
UGT1A1 ///				
UGT1A10 ///				
UGT1A3 ///				
UGT1A4 ///				
UGT1A5 ///				
UGT1A6 ///				
UGT1A7 ///				
UGT1A8 ///				
UGT1A9	3.52	members of UDP glucuronosyltransferase 1 family, polypeptide A	7.87E-03	215125_PM_s_at
UGT1A1 ///				
UGT1A10 ///				
UGT1A4 ///				
UGT1A6 ///				
UGT1A8 ///				
UGT1A9	3.49	members of UDP glucuronosyltransferase 1 family, polypeptide A	5.47E-03	204532_PM_x_at
UGT1A6	3.39	UDP glucuronosyltransferase 1 family, polypeptide A6	7.49E-03	206094_PM_x_at

UHRF2	1.37	ubiquitin-like with PHD and ring finger domains 2	2.27E-02	225610_PM_at
USP25	1.32	ubiquitin specific peptidase 25	1.90E-02	223167_PM_s_at
VAV3	3.58	vav 3 guanine nucleotide exchange factor	3.95E-03	218807_PM_at
VEZF1	1.69	vascular endothelial zinc finger 1	9.11E-04	202172_PM_at
VILL	2.45	villin-like	5.85E-03	209950_PM_s_at
VLDLR	1.57	very low density lipoprotein receptor	1.09E-02	209822_PM_s_at
VOPP1	1.41	vesicular, overexpressed in cancer, prosurvival protein 1	2.85E-03	208091_PM_s_at
VPS37B	1.33	vacuolar protein sorting 37 homolog B (S. cerevisiae)	3.88E-02	221704_PM_s_at
VPS37C	1.24	vacuolar protein sorting 37 homolog C (S. cerevisiae)	2.17E-02	1560060_PM_s_at
VSIG10	1.27	V-set and immunoglobulin domain containing 10	4.09E-02	1553991_PM_s_at
VSTM2L	1.29	V-set and transmembrane domain containing 2 like	4.86E-02	226973_PM_at
VWDE	1.54	von Willebrand factor D and EGF domains	3.63E-02	239552_PM_at
WBP4	1.25	WW domain binding protein 4 (formin binding protein 21)	4.23E-02	203598_PM_s_at
WDR26	1.20	WD repeat domain 26	4.37E-02	224898_PM_at
WDR35	1.61	WD repeat domain 35	5.51E-03	226890_PM_at
WHSC1	1.44	Wolf-Hirschhorn syndrome candidate 1	3.90E-02	223472_PM_at
WIPF1	3.90	WAS/WASL interacting protein family, member 1	3.23E-03	202664_PM_at
WNT7A	2.27	wingless-type MMTV integration site family, member 7A	5.26E-05	210248_PM_at
WNT7B	1.30	wingless-type MMTV integration site family, member 7B	4.96E-02	238105_PM_x_at
WNT9A	1.80	wingless-type MMTV integration site family, member 9A	1.42E-02	223042_PM_at
WSB2	1.26	WD repeat and SOCS box-containing 2	1.37E-02	213734_PM_at
WWC1	1.34	WW and C2 domain containing 1	1.13E-02	241950_PM_at
XBP1	1.23	X-box binding protein 1	4.44E-02	200670_PM_at
YIF1B	1.22	Yip1 interacting factor homolog B (S. cerevisiae)	4.07E-02	231211_PM_s_at
ZBED2	1.88	zinc finger, BED-type containing 2	1.36E-02	219836_PM_at
ZBTB10	2.64	zinc finger and BTB domain containing 10	6.41E-04	219312_PM_s_at
ZBTB38	1.41	zinc finger and BTB domain containing 38	4.94E-02	225512_PM_at
ZDHHC2	2.04	zinc finger, DHHC-type containing 2	5.04E-04	222731_PM_at
ZEB1	1.37	zinc finger E-box binding homeobox 1	2.27E-02	221764_PM_at
ZFAND2A	1.25	zinc finger, AN1-type domain 2A	3.61E-02	226650_PM_at
ZFH3	1.51	Zinc finger homeobox 3	1.62E-02	226137_PM_at
ZFP36L1	1.82	zinc finger protein 36, C3H type-like 1	1.01E-03	211965_PM_at
ZFPM2	1.93	zinc finger protein, multitype 2	1.36E-02	219778_PM_at
ZG16B	1.78	zymogen granule protein 16 homolog B (rat)	1.57E-02	228058_PM_at
ZKSCAN5	1.33	zinc finger with KRAB and SCAN domains 5	3.03E-02	203730_PM_s_at
ZMYM6	1.31	zinc finger, MYM-type 6	4.94E-02	213698_PM_at
ZNF143	1.40	zinc finger protein 143	6.15E-03	221873_PM_at
ZNF148	1.47	zinc finger protein 148	2.23E-02	230821_PM_at
ZNF165	1.54	zinc finger protein 165	4.57E-03	206683_PM_at
ZNF193	1.45	zinc finger protein 193	4.26E-03	205181_PM_at
ZNF219	1.30	Zinc finger protein 219	4.98E-02	222864_PM_s_at
ZNF280B	1.40	zinc finger protein 280B	3.81E-02	229360_PM_at
ZNF354A	1.29	zinc finger protein 354A	4.29E-02	205427_PM_at
ZNF468	1.25	zinc finger protein 468	3.29E-02	214751_PM_at
ZNF655	1.74	zinc finger protein 655	1.20E-03	223302_PM_s_at
ZNF702P	2.41	zinc finger protein 702 (pseudogene)	9.07E-03	206557_PM_at
ZNF711	1.44	zinc finger protein 711	4.86E-02	228988_PM_at
ZPLD1	1.58	zona pellucida-like domain containing 1	2.67E-02	1561969_PM_at
ZSCAN18	1.29	zinc finger and SCAN domain containing 18	3.76E-02	232866_PM_at
ZSWIM6	1.34	zinc finger, SWIM-type containing 6	1.17E-02	226208_PM_at
ZXDA	1.39	zinc finger, X-linked, duplicated A	2.07E-02	243521_PM_at
ZXDB	1.88	zinc finger, X-linked, duplicated B	4.22E-03	228005_PM_at
ZXDC	1.68	ZX D family zinc finger C	4.31E-02	230209_PM_at

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167 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*168 *name/description), P-value, and probe ID (Gene ID).*

169 **Table S3.** Genes that were significantly higher expressed by healthy nasal epithelial cells.

Gene alias	FC	Gene name/description	P-value	Gene ID
AASDH	1.35	aminoadipate-semialdehyde dehydrogenase	1.18E-02	228041_PM_at
ABCA12	3.04	ATP-binding cassette, sub-family A (ABC1), member 12	7.67E-04	215465_PM_at
ABHD14B	1.37	abhydrolase domain containing 14B	1.26E-02	224821_PM_at
ABHD6	1.41	abhydrolase domain containing 6	2.37E-02	221552_PM_at
ACAA2	3.61	acetyl-CoA acyltransferase 2	3.75E-03	202003_PM_s_at
ACP2	1.38	acid phosphatase 2, lysosomal	3.57E-02	202767_PM_at
ACP5	2.16	acid phosphatase 5, tartrate resistant	6.49E-04	204638_PM_at
ACPP	1.60	acid phosphatase, prostate	2.69E-03	204393_PM_s_at
ACTG2	6.16	actin, gamma 2, smooth muscle, enteric	2.60E-03	202274_PM_at
ADAMTSL4	1.51	ADAMTS-like 4	2.09E-02	220578_PM_at
ADAP2	2.25	ArfGAP with dual PH domains 2	3.04E-04	222876_PM_s_at
ADARB1	2.48	Adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	3.51E-03	203865_PM_s_at
ADCY7	1.73	adenylate cyclase 7	2.95E-02	203741_PM_s_at
ADH7	2.49	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	1.52E-02	210505_PM_at
ADM	1.54	adrenomedullin	2.99E-02	202912_PM_at
AEBP1	3.08	AE binding protein 1	2.34E-02	201792_PM_at
AFAP1L2	1.29	actin filament associated protein 1-like 2	1.12E-02	226829_PM_at
AHCYL2	1.41	adenosylhomocysteinase-like 2	3.80E-03	212814_PM_at
AHR	1.39	aryl hydrocarbon receptor	4.32E-02	202820_PM_at
AJAP1	1.47	adherens junctions associated protein 1	1.69E-02	206460_PM_at
AKR1C3	1.82	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	1.98E-02	209160_PM_at
ALDH18A1	1.23	aldehyde dehydrogenase 18 family, member A1	3.88E-02	222416_PM_at
ALDH1L2	3.57	aldehyde dehydrogenase 1 family, member L2	2.38E-03	231202_PM_at
ALDH3B2	2.97	aldehyde dehydrogenase 3 family, member B2	1.52E-03	204942_PM_s_at
ALDH4A1	1.32	aldehyde dehydrogenase 4 family, member A1	4.43E-02	203722_PM_at
ALDH6A1	1.36	aldehyde dehydrogenase 6 family, member A1	1.00E-02	221589_PM_s_at
ALG10	1.34	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pombe)	2.56E-02	1552306_PM_at
ALKBH2	1.34	alkB, alkylation repair homolog 2 (E. coli)	1.22E-02	225625_PM_at
ALOX12B	2.23	arachidonate 12-lipoxygenase, 12R type	4.86E-02	207381_PM_at
ALOX15B	2.81	arachidonate 15-lipoxygenase, type B	5.54E-03	206714_PM_at
ANAPC5	1.22	anaphase promoting complex subunit 5	4.09E-02	211036_PM_x_at
ANAPC7	1.35	anaphase promoting complex subunit 7	1.81E-02	225521_PM_at
ANGEL2	1.25	angel homolog 2 (Drosophila)	3.88E-02	221826_PM_at
ANK3	1.78	ankyrin 3, node of Ranvier (ankyrin G)	5.30E-03	209442_PM_x_at
ANKH	1.34	ankylosis, progressive homolog (mouse)	1.84E-02	223092_PM_at
ANKRD22	1.60	ankyrin repeat domain 22	1.30E-02	238439_PM_at
ANO1	3.34	anoctamin 1, calcium activated chloride channel	2.45E-02	218804_PM_at
ANPEP	1.98	Alanyl (membrane) aminopeptidase	8.01E-03	202888_PM_s_at
ANUBL1	1.30	AN1, ubiquitin-like, homolog (Xenopus laevis)	2.44E-02	223624_PM_at
ANXA6	3.28	annexin A6	8.85E-03	200982_PM_s_at
APOE	1.88	apolipoprotein E	5.30E-03	203382_PM_s_at
APOO	1.40	apolipoprotein O	8.47E-03	221620_PM_s_at
ARHGAP1	1.26	Rho GTPase activating protein 1	3.30E-02	202117_PM_at
ARHGAP18	1.90	Rho GTPase activating protein 18	4.90E-04	225173_PM_at
ARHGAP28	1.63	Rho GTPase activating protein 28	1.67E-02	227911_PM_at
ARHGEF37	1.60	Rho guanine nucleotide exchange factor (GEF) 37	6.33E-03	227717_PM_at
ARHGEF9	1.55	Cdc42 guanine nucleotide exchange factor (GEF) 9	4.08E-03	203264_PM_s_at
ARID1B	1.24	AT rich interactive domain 1B (SWI1-like)	3.61E-02	225181_PM_at
ARMCX1	1.83	armadillo repeat containing, X-linked 1	1.52E-03	218694_PM_at
ARRDC3	1.56	arrestin domain containing 3	1.34E-02	224797_PM_at
ARSI	3.09	arylsulfatase family, member I	2.00E-04	230275_PM_at
ARV1	1.46	ARV1 homolog (S. cerevisiae)	5.07E-03	223223_PM_at
ASAH1	1.31	N-acylsphingosine amidohydrolase (acid ceramidase) 1	3.09E-02	213902_PM_at
ASAM	8.12	adipocyte-specific adhesion molecule	1.50E-04	228082_PM_at
ASAP3	1.43	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	3.74E-02	222236_PM_s_at
ASMTL	1.37	acetylserotonin O-methyltransferase-like	8.53E-03	36553_PM_at
ASPRV1	6.49	aspartic peptidase, retroviral-like 1	5.43E-03	235514_PM_at
ATG9B	1.34	ATG9 autophagy related 9 homolog B (S. cerevisiae)	1.68E-02	229252_PM_at
ATL2	1.26	atlastin GTPase 2	4.02E-02	222700_PM_at
ATMIN	1.29	ATM interactor	1.05E-02	201855_PM_s_at
ATP1A1	1.29	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.82E-02	220948_PM_s_at
ATP2B1	1.35	ATPase, Ca++ transporting, plasma membrane 1	7.44E-03	215716_PM_s_at
ATP2B4	1.30	ATPase, Ca++ transporting, plasma membrane 4	3.02E-02	212135_PM_s_at
ATP2C1	1.20	ATPase, Ca++ transporting, type 2C, member 1	4.58E-02	212255_PM_s_at
ATP6V1C2	1.94	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	1.09E-02	1553989_PM_a_at
B3GNT4	1.22	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	4.47E-02	221240_PM_s_at
B4GALNT3	1.71	beta-1,4-N-acetyl-galactosaminyl transferase 3	5.47E-03	229909_PM_at
BACE1	1.59	beta-site APP-cleaving enzyme 1	2.35E-02	217904_PM_s_at

BAG1	1.61	BCL2-associated athanogene	2.07E-02	229720_PM_at
BBOX1	5.51	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	1.88E-03	205363_PM_at
BC036928	1.24	hypothetical protein BC036928	4.77E-02	231260_PM_at
BCAM	1.37	basal cell adhesion molecule (Lutheran blood group)	2.78E-02	40093_PM_at
BCAT1	4.44	branched chain amino-acid transaminase 1, cytosolic	1.62E-05	226517_PM_at
BCKDHB	1.49	branched chain keto acid dehydrogenase E1, beta polypeptide	1.54E-02	210653_PM_s_at
BCL11A	1.36	B-cell CLL/lymphoma 11A (zinc finger protein)	2.73E-02	219497_PM_s_at
BCL11B	2.02	B-cell CLL/lymphoma 11B (zinc finger protein)	2.64E-03	222895_PM_s_at
BCL2L11	1.42	BCL2-like 11 (apoptosis facilitator)	3.43E-02	225606_PM_at
BCL2L13	1.34	BCL2-like 13 (apoptosis facilitator)	8.41E-03	217955_PM_at
BCL2L2	1.28	BCL2-like 2	3.81E-02	209311_PM_at
BCL7A	1.29	B-cell CLL/lymphoma 7A	3.25E-02	203796_PM_s_at
BEX1	3.17	brain expressed, X-linked 1	6.72E-03	218332_PM_at
BEX2	1.33	brain expressed X-linked 2	3.23E-02	224367_PM_at
BGN	1.29	biglycan	3.19E-02	201261_PM_x_at
BIVM	1.27	basic, immunoglobulin-like variable motif containing	4.09E-02	222761_PM_at
BPIL2	2.88	bactericidal/permeability-increasing protein-like 2 brain and reproductive organ-expressed (TNFRSF1A modulator)	8.36E-04	1555773_PM_at
BRE	1.30	modulator)	2.48E-02	205550_PM_s_at
BTBD11	1.56	BTB (POZ) domain containing 11	7.58E-03	228570_PM_at
BVES	2.05	blood vessel epicardial substance	1.32E-03	228783_PM_at
C10orf125	1.68	chromosome 10 open reading frame 125	1.86E-02	230259_PM_at
C10orf57	1.40	chromosome 10 open reading frame 57	1.96E-02	218174_PM_s_at
C10orf99	3.62	chromosome 10 open reading frame 99	1.11E-03	227736_PM_at
C12orf28	2.61	chromosome 12 open reading frame 28	1.98E-02	1556267_PM_at
C14orf1	1.25	chromosome 14 open reading frame 1	3.08E-02	217188_PM_s_at
C14orf101	1.32	chromosome 14 open reading frame 101	2.60E-02	225675_PM_at
C14orf128	1.51	chromosome 14 open reading frame 128	9.78E-03	228889_PM_at
C14orf45	1.65	chromosome 14 open reading frame 45	1.67E-02	220173_PM_at
C16orf70	1.30	chromosome 16 open reading frame 70	4.05E-02	223440_PM_at
C18orf10	1.34	chromosome 18 open reading frame 10	1.86E-02	212055_PM_at
C18orf21	1.25	chromosome 18 open reading frame 21	3.43E-02	223526_PM_at
C1orf107	1.58	chromosome 1 open reading frame 107	3.06E-02	220251_PM_at
C1orf131	1.27	chromosome 1 open reading frame 131	2.96E-02	226242_PM_at
C1orf163	1.54	chromosome 1 open reading frame 163	4.45E-02	222883_PM_at
C1orf216	1.41	chromosome 1 open reading frame 216	3.28E-02	212791_PM_at
C1orf59	1.43	chromosome 1 open reading frame 59	1.15E-02	225841_PM_at
C1R	4.60	complement component 1, r subcomponent	4.67E-03	212067_PM_s_at
C1S	7.12	complement component 1, s subcomponent	9.28E-03	208747_PM_s_at
C20orf108	1.49	chromosome 20 open reading frame 108	5.81E-03	224690_PM_at
C21orf33	1.22	chromosome 21 open reading frame 33	3.75E-02	202217_PM_at
C21orf63	1.89	chromosome 21 open reading frame 63	3.07E-04	227188_PM_at
C21orf91	1.33	chromosome 21 open reading frame 91	2.36E-02	220941_PM_s_at
C21orf96	9.85	chromosome 21 open reading frame 96	2.68E-04	220918_PM_at
C2CD4A	1.40	C2 calcium-dependent domain containing 4A	2.23E-02	241031_PM_at
C2orf18	1.59	chromosome 2 open reading frame 18	6.17E-03	225695_PM_at
C2orf74	1.33	chromosome 2 open reading frame 74	2.54E-02	1568658_PM_at
C3	3.30	complement component 3	2.21E-02	217767_PM_at
C3orf1	1.23	chromosome 3 open reading frame 1	2.86E-02	223004_PM_s_at
C3orf14	1.32	chromosome 3 open reading frame 14	2.38E-02	219288_PM_at
C3orf34	1.47	chromosome 3 open reading frame 34	2.89E-02	230860_PM_at
C4orf32	1.25	chromosome 4 open reading frame 32	3.44E-02	227856_PM_at
C4orf33	1.33	chromosome 4 open reading frame 33	2.29E-02	1552370_PM_at
C4orf48	1.24	chromosome 4 open reading frame 48	3.88E-02	229860_PM_x_at
C4orf49	2.97	chromosome 4 open reading frame 49	1.88E-03	223734_PM_at
C5orf33	1.31	chromosome 5 open reading frame 33	2.76E-02	228594_PM_at
C5orf46	7.41	chromosome 5 open reading frame 46	4.22E-03	1554195_PM_a_at
C5orf62	2.61	chromosome 5 open reading frame 62	5.51E-03	223276_PM_at
C6orf105	2.30	chromosome 6 open reading frame 105	1.18E-03	229070_PM_at
C6orf192	1.57	chromosome 6 open reading frame 192	6.13E-03	226301_PM_at
C7orf60	1.55	chromosome 7 open reading frame 60	5.84E-03	228149_PM_at
C8orf48	2.04	chromosome 8 open reading frame 48	9.56E-03	236634_PM_at
C9orf3	1.58	Chromosome 9 open reading frame 3	6.62E-03	212848_PM_s_at
C9orf40	1.28	chromosome 9 open reading frame 40	4.91E-02	218904_PM_s_at
C9orf91	1.27	chromosome 9 open reading frame 91	2.31E-02	221865_PM_at
C9orf95	1.51	chromosome 9 open reading frame 95	3.08E-03	219147_PM_s_at
CA2	2.81	carbonic anhydrase II	1.86E-02	209301_PM_at
CABC1	1.38	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	1.70E-02	218168_PM_s_at
CALB2	1.34	calbindin 2	2.15E-02	205428_PM_s_at
CALCOCO2	1.23	calcium binding and coiled-coil domain 2	2.13E-02	235076_PM_at
CALHM2	1.32	calcium homeostasis modulator 2	2.89E-02	221565_PM_s_at
CALML5	2.44	calmodulin-like 5	2.20E-02	220414_PM_at
CAMK1D	1.40	calcium/calmodulin-dependent protein kinase ID	4.83E-02	235626_PM_at
CAMK2D	1.58	calcium/calmodulin-dependent protein kinase II delta	5.89E-03	224994_PM_at

CAPN12	1.35	calpain 12	4.98E-02	228705_PM_at
CARD16	1.87	caspase recruitment domain family, member 16	3.22E-02	1552701_PM_a_at
		caspase recruitment domain family, member 16 /// caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.54E-03	1552703_PM_s_at
CARD16 /// CASP1	2.27			
CARD18	18.20	caspase recruitment domain family, member 18	1.40E-04	231733_PM_at
CARS2	1.34	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	2.97E-02	218153_PM_at
		caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	1.78E-04	206011_PM_at
CASP1	2.81			
CASP4	1.90	caspase 4, apoptosis-related cysteine peptidase	8.10E-04	213596_PM_at
CAT	1.39	Catalase	3.57E-02	201432_PM_at
CBR1	1.28	carbonyl reductase 1	4.91E-02	209213_PM_at
CBS	1.41	cystathionine-beta-synthase	4.79E-02	1553972_PM_a_at
CBX2	2.05	chromobox homolog 2 (Pc class homolog, Drosophila)	3.97E-03	226473_PM_at
CBX6	1.56	chromobox homolog 6	1.21E-02	202047_PM_s_at
CC2D2A	1.65	coiled-coil and C2 domain containing 2A	3.98E-02	234936_PM_s_at
CCBL2	1.25	cysteine conjugate-beta lyase 2	2.64E-02	209472_PM_at
CCDC115	1.36	coiled-coil domain containing 115	1.06E-02	224946_PM_s_at
CCDC41	1.30	coiled-coil domain containing 41	4.83E-02	219644_PM_at
CCDC51	1.37	coiled-coil domain containing 51	1.88E-02	218722_PM_s_at
CCDC8	3.71	coiled-coil domain containing 8	5.63E-03	223495_PM_at
CD109	1.31	CD109 molecule	3.97E-02	226545_PM_at
CD36	1.82	CD36 molecule (thrombospondin receptor)	3.93E-02	209555_PM_s_at
CDC25B	1.77	cell division cycle 25 homolog B (S. pombe)	6.72E-03	201853_PM_s_at
CDHR1	1.26	cadherin-related family member 1	4.27E-02	1555019_PM_at
CDK20	1.30	cyclin-dependent kinase 20	2.17E-02	205271_PM_s_at
		cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	5.30E-03	207039_PM_at
CDKN2A	4.04			
CDSN	2.34	corneodesmosin	1.69E-02	206192_PM_at
		cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	2.07E-02	36499_PM_at
CELSR2	1.42			
CEMP1	1.39	Cementum protein 1	2.31E-02	227841_PM_at
CGNL1	2.12	cingulin-like 1	1.33E-02	225817_PM_at
CHCHD10	1.40	coiled-coil-helix-coiled-coil-helix domain containing 10	6.72E-03	224932_PM_at
CHD2	1.23	Chromodomain helicase DNA binding protein 2	3.75E-02	244443_PM_at
		Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	5.38E-04	209357_PM_at
CITED2	2.74			
CLCA2	1.80	chloride channel accessory 2	4.57E-03	206166_PM_s_at
CLDN11	7.58	claudin 11	7.42E-03	228335_PM_at
CLDN17	2.24	claudin 17	3.54E-02	221328_PM_at
CLIC3	1.30	chloride intracellular channel 3	1.05E-02	219529_PM_at
CLIC4	1.54	chloride intracellular channel 4	6.62E-03	201560_PM_at
CLIP3	1.35	CAP-GLY domain containing linker protein 3	1.89E-02	212358_PM_at
CLPX	1.25	ClpX caseinolytic peptidase X homolog (E. coli)	1.81E-02	223507_PM_at
CNFN	3.26	cornifelin	4.29E-04	224329_PM_s_at
CNKSR2	1.41	connector enhancer of kinase suppressor of Ras 2	3.55E-02	229116_PM_at
CNKSR3	1.51	CNKSR family member 3	2.54E-02	227481_PM_at
CNP	1.30	2',3'-cyclic nucleotide 3' phosphodiesterase	2.50E-02	208912_PM_s_at
CNTN1	2.26	Contactin 1	4.55E-03	227202_PM_at
CNTN3	2.12	contactin 3 (plasmacytoma associated)	3.19E-02	229831_PM_at
CNTNAP3	1.71	contactin associated protein-like 3	3.32E-02	223796_PM_at
COL12A1	3.21	collagen, type XII, alpha 1	6.49E-03	225664_PM_at
COL4A1	4.39	collagen, type IV, alpha 1	1.93E-03	211981_PM_at
COL4A2	4.29	collagen, type IV, alpha 2	9.63E-03	211964_PM_at
COL6A1	9.89	collagen, type VI, alpha 1	1.41E-04	213428_PM_s_at
COMTD1	1.47	catechol-O-methyltransferase domain containing 1	2.37E-02	226870_PM_at
COX5B	1.28	Cytochrome c oxidase subunit Vb	2.15E-02	202343_PM_x_at
COX7A1	1.95	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	4.81E-02	204570_PM_at
CPA4	3.01	carboxypeptidase A4	4.57E-02	205832_PM_at
CPE	3.69	carboxypeptidase E	3.66E-03	201116_PM_s_at
CPS1	2.83	carbamoyl-phosphate synthase 1, mitochondrial	6.14E-05	204920_PM_at
CPT1A	1.40	carnitine palmitoyltransferase 1A (liver)	3.52E-02	203633_PM_at
CPT2	1.50	carnitine palmitoyltransferase 2	2.26E-03	204263_PM_s_at
CRBN	1.28	cereblon	2.05E-02	222533_PM_at
CREG1	2.53	cellular repressor of E1A-stimulated genes 1	7.67E-04	201200_PM_at
CRISPLD1	1.57	cysteine-rich secretory protein LCCL domain containing 1	3.00E-02	223475_PM_at
CRNN	2.48	cornulin	4.83E-02	220090_PM_at
CRYAB	6.83	crystallin, alpha B	1.39E-04	209283_PM_at
CSAD	1.34	cysteine sulfinic acid decarboxylase	3.38E-02	221139_PM_s_at
CSGALNACT1	2.24	chondroitin sulfate N-acetylgalactosaminyltransferase 1	3.27E-02	219049_PM_at
CSPG4	3.27	chondroitin sulfate proteoglycan 4	6.51E-03	214297_PM_at
CSRNP3	1.40	cysteine-serine-rich nuclear protein 3	4.66E-02	235355_PM_at
CSRP2BP	1.83	CSRP2 binding protein	4.66E-04	225432_PM_s_at
CSTF1	1.24	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	2.38E-02	202190_PM_at
CTSC	2.71	cathepsin C	5.20E-03	225646_PM_at
CTSK	2.02	cathepsin K	7.58E-03	202450_PM_s_at

CTSL1	1.42	cathepsin L1	5.16E-03	202087_PM_s_at
CWH43	4.20	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	5.85E-05	220724_PM_at
CXCL10	7.56	chemokine (C-X-C motif) ligand 10	2.44E-02	204533_PM_at
CXCL11	8.28	chemokine (C-X-C motif) ligand 11	2.42E-03	211122_PM_s_at
CXCL14	1.31	chemokine (C-X-C motif) ligand 14	3.90E-02	237038_PM_at
CXCL5	2.45	chemokine (C-X-C motif) ligand 5	1.80E-03	214974_PM_x_at
CYB5D1	1.37	cytochrome b5 domain containing 1	3.81E-02	226833_PM_at
CYB5R1	1.43	cytochrome b5 reductase 1	1.14E-02	202263_PM_at
CYB5R2	2.72	cytochrome b5 reductase 2	3.77E-04	220230_PM_s_at
CYBRD1	2.29	cytochrome b reductase 1	6.88E-03	222453_PM_at
CYGB	2.97	cytoglobin	4.37E-03	226632_PM_at
CYP1B1	2.80	cytochrome P450, family 1, subfamily B, polypeptide 1	3.00E-02	202437_PM_s_at
CYP26B1	3.13	cytochrome P450, family 26, subfamily B, polypeptide 1	2.74E-03	219825_PM_at
CYP39A1	1.40	cytochrome P450, family 39, subfamily A, polypeptide 1	4.72E-02	1553977_PM_a_at
D4S234E /// FOXP1	1.67	DNA segment on chromosome 4 (unique) 234 expressed sequence /// forkhead box P1	4.61E-03	213533_PM_at
DAB2	2.26	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	1.01E-03	201280_PM_s_at
DAPK1	3.53	death-associated protein kinase 1	1.61E-03	203139_PM_at
DBC1	4.04	deleted in bladder cancer 1	7.79E-04	205818_PM_at
DBI	1.39	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	1.02E-02	209389_PM_x_at
DCAF6	1.26	DDB1 and CUL4 associated factor 6	3.08E-02	217908_PM_s_at
DCBLD1	1.75	discoidin, CUB and LCCL domain containing 1	6.45E-03	226609_PM_at
DDX58	2.12	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.21E-02	242961_PM_x_at
DEM1	1.31	defects in morphology 1 homolog (S. cerevisiae)	1.58E-02	222902_PM_s_at
DENND1A	1.38	DENN/MADD domain containing 1A	1.95E-02	219763_PM_at
DEPDC7	3.53	DEP domain containing 7	1.48E-03	228293_PM_at
DGAT2	1.54	diacylglycerol O-acyltransferase homolog 2 (mouse)	1.77E-02	224327_PM_s_at
DGCR14	1.27	DiGeorge syndrome critical region gene 14	3.81E-02	204383_PM_at
DHDH	1.58	dihydrodiol dehydrogenase (dimeric)	1.01E-02	231416_PM_at
DHRS1	1.54	dehydrogenase/reductase (SDR family) member 1	3.01E-03	213279_PM_at
DHRS4 /// DHRS4L2	1.23	dehydrogenase/reductase (SDR family) member 4 /// dehydrogenase/reductase (SDR family) member 4 like 2	4.98E-02	218021_PM_at
DIRC2	1.39	disrupted in renal carcinoma 2	1.90E-02	226026_PM_at
DIXDC1	1.65	DIX domain containing 1	3.25E-02	214724_PM_at
DLK2	1.81	delta-like 2 homolog (Drosophila)	1.14E-02	220262_PM_s_at
DLX1	2.24	distal-less homeobox 1	6.79E-03	242138_PM_at
DLX2	2.27	distal-less homeobox 2	1.08E-03	207147_PM_at
DLX5	3.27	distal-less homeobox 5	1.41E-04	213707_PM_s_at
DLX6	1.55	distal-less homeobox 6	7.87E-03	239309_PM_at
DLX6AS	1.33	DLX6 antisense RNA (non-protein coding)	4.37E-02	230882_PM_at
DMD	2.16	Dystrophin	7.90E-04	203881_PM_s_at
DMKN	1.50	dermokine	4.54E-03	226926_PM_at
DNAH5	4.25	dynein, axonemal, heavy chain 5	7.17E-03	243938_PM_x_at
DNER	1.88	delta/notch-like EGF repeat containing	2.75E-02	226281_PM_at
DOCK11	2.41	dedicator of cytokinesis 11	1.01E-03	226875_PM_at
DPH5	1.44	DPH5 homolog (S. cerevisiae)	3.44E-02	222360_PM_at
DSC1	1.88	desmocollin 1	9.68E-03	207324_PM_s_at
DSC2	2.35	desmocollin 2	1.08E-03	204750_PM_s_at
DSC3	1.47	desmocollin 3	8.28E-03	206033_PM_s_at
DSG1	37.49	desmoglein 1	1.47E-05	206642_PM_at
DSG3	1.96	desmoglein 3 (pemphigus vulgaris antigen)	1.13E-02	205595_PM_at
DTWD1	1.47	DTW domain containing 1	1.00E-02	219291_PM_at
DUS2L	1.32	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	1.98E-02	219486_PM_at
DUSP28	1.56	dual specificity phosphatase 28	1.78E-02	229211_PM_at
DYRK2	1.32	dual specificity tyrosine-(Y)-phosphorylation regulated kinase 2	4.81E-02	202971_PM_s_at
DYX1C1	1.31	dyslexia susceptibility 1 candidate 1	4.57E-02	241713_PM_s_at
DZIP1	2.87	DAZ interacting protein 1	4.02E-04	204557_PM_s_at
ECHDC3	2.34	enoyl CoA hydratase domain containing 3	1.39E-02	219298_PM_at
ECM2	1.32	extracellular matrix protein 2, female organ and adipocyte specific	2.17E-02	206101_PM_at
EDC3	1.25	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	3.37E-02	226042_PM_at
EEF2K	1.23	eukaryotic elongation factor-2 kinase	4.50E-02	225545_PM_at
EFNB3	1.31	ephrin-B3	3.15E-02	205031_PM_at
EFS	1.46	embryonal Fyn-associated substrate	3.83E-02	204400_PM_at
EGFL6	4.00	EGF-like-domain, multiple 6	8.02E-03	219454_PM_at
EHHADH	1.35	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	1.55E-02	205222_PM_at
EIF3K	1.26	eukaryotic translation initiation factor 3, subunit K	2.18E-02	221494_PM_x_at
ELAC1	1.53	elaC homolog 1 (E. coli)	4.08E-02	222869_PM_s_at
ELAVL2	21.73	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	1.40E-05	228260_PM_at
ELOVL4	1.79	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	2.85E-03	219532_PM_at

ELOVL7	1.32	ELOVL family member 7, elongation of long chain fatty acids (yeast)	3.99E-02	227180_PM_at
EME2	1.28	essential meiotic endonuclease 1 homolog 2 (S. pombe)	2.09E-02	1556024_PM_at
ENAH	1.29	Enabled homolog (Drosophila)	2.86E-02	222433_PM_at
ENDOD1	1.74	endonuclease domain containing 1	9.84E-03	212573_PM_at
ENDOU	1.75	endonuclease, polyU-specific	1.34E-02	206605_PM_at
ENOSF1	1.36	enolase superfamily member 1	2.19E-02	204143_PM_s_at
EPB41L3	1.65	erythrocyte membrane protein band 4.1-like 3	1.45E-02	212681_PM_at
EPHA4	3.00	EPH receptor A4	5.31E-04	206114_PM_at
EPHB3	1.70	EPH receptor B3	5.51E-03	1438_PM_at
EPHX2	1.44	epoxide hydrolase 2, cytoplasmic	8.16E-03	209368_PM_at
EPHX3	1.94	epoxide hydrolase 3	2.40E-03	220013_PM_at
EPM2AIP1	1.60	EPM2A (laforin) interacting protein 1	7.71E-03	227847_PM_at
EPRS	1.23	glutamyl-prolyl-tRNA synthetase	4.32E-02	200842_PM_s_at
EPS15L1	1.40	epidermal growth factor receptor pathway substrate 15-like 1	2.96E-02	231926_PM_at
EPS8L2	1.23	EPS8-like 2	4.24E-02	218180_PM_s_at
ERBB2	1.35	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	3.71E-02	216836_PM_s_at
EREG	1.79	epiregulin	1.74E-03	205767_PM_at
ERP27	3.04	endoplasmic reticulum protein 27	2.73E-04	227450_PM_at
ESR1	1.27	estrogen receptor 1	2.31E-02	205225_PM_at
ESYT3	1.41	extended synaptotagmin-like protein 3	8.01E-03	239770_PM_at
ETFB	1.26	electron-transfer-flavoprotein, beta polypeptide	3.13E-02	202942_PM_at
ETFDH	1.38	electron-transferring-flavoprotein dehydrogenase	2.29E-02	205530_PM_at
ETS2	1.32	V-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	1.93E-02	201328_PM_at
EVL	1.45	Enah/Vasp-like	1.14E-02	217838_PM_s_at
EXOG	1.35	endo/exonuclease (5'-3'), endonuclease G-like	4.17E-02	205521_PM_at
EXOSC5	1.37	exosome component 5	1.11E-02	218481_PM_at
EXPH5	1.67	Exophilin 5	2.89E-02	213929_PM_at
FABP3	1.46	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	3.08E-02	205738_PM_s_at
FABP5	3.31	fatty acid binding protein 5 (psoriasis-associated)	2.65E-04	202345_PM_s_at
FAH	1.42	Fumarylacetoacetate hydrolase (fumarylacetoacetase)	2.25E-02	202862_PM_at
FAM110B	1.44	family with sequence similarity 110, member B	5.85E-03	221959_PM_at
FAM134B	1.44	family with sequence similarity 134, member B	3.93E-02	218510_PM_x_at
FAM135A	1.23	family with sequence similarity 135, member A	3.69E-02	223497_PM_at
FAM156A /// FAM156B	1.29	members of family with sequence similarity 156	9.96E-03	223203_PM_at
FAM167A	1.50	Family with sequence similarity 167, member A	2.55E-02	226614_PM_s_at
FAM169A	1.60	family with sequence similarity 169, member A	1.99E-03	235048_PM_at
FAM19A2	1.21	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	4.31E-02	241399_PM_at
FAM200B	1.23	family with sequence similarity 200, member B	3.77E-02	227466_PM_at
FAM21A /// FAM21B ///				
FAM21C	1.28	members of family with sequence similarity 21	4.89E-02	212370_PM_x_at
FAM21A /// FAM21B ///				
FAM21C /// FAM21D	1.24	members of family with sequence similarity 21	4.37E-02	212929_PM_s_at
FAM21A /// FAM21C ///				
FAM21D	1.25	members of family with sequence similarity 21	4.82E-02	214946_PM_x_at
FAM21C /// FAM21D	1.30	members of family with sequence similarity 21	1.54E-02	211068_PM_x_at
FAM46B	1.66	family with sequence similarity 46, member B	1.56E-02	229518_PM_at
FAM49A	1.65	family with sequence similarity 49, member A	2.74E-02	209683_PM_at
FAM83B	1.57	family with sequence similarity 83, member B	3.85E-03	1563900_PM_at
FAM84A	1.65	Family with sequence similarity 84, member A	1.37E-02	231439_PM_at
FAM89A	1.85	family with sequence similarity 89, member A	4.17E-03	226448_PM_at
FAM8A1	1.28	family with sequence similarity 8, member A1	1.86E-02	203420_PM_at
FAP	12.49	fibroblast activation protein, alpha	8.27E-05	209955_PM_s_at
FAT1	1.35	FAT tumor suppressor homolog 1 (Drosophila)	2.40E-02	201579_PM_at
FAT2	1.99	FAT tumor suppressor homolog 2 (Drosophila)	1.42E-03	208153_PM_s_at
FBLN2	1.53	fibulin 2	4.61E-03	203886_PM_s_at
FBXO32	2.43	F-box protein 32	4.17E-02	225803_PM_at
FBXO4	1.43	F-box protein 4	2.64E-02	223493_PM_at
FCHSD2	1.39	FCH and double SH3 domains 2	3.75E-02	203620_PM_s_at
FECH	1.34	ferrochelatase	9.16E-03	203116_PM_s_at
FGF2	1.91	fibroblast growth factor 2 (basic)	1.18E-02	204422_PM_s_at
FGFR2	1.70	fibroblast growth factor receptor 2	1.92E-02	203639_PM_s_at
FIBIN	1.64	fin bud initiation factor homolog (zebrafish)	2.31E-02	226769_PM_at
FIGN	1.47	fidgetin	2.21E-02	238964_PM_at
FKBP10	1.75	FK506 binding protein 10, 65 kDa	9.32E-03	219249_PM_s_at
FLI1	2.42	Friend leukemia virus integration 1	2.72E-02	204236_PM_at
FLJ13744	1.76	hypothetical FLJ13744	2.39E-02	1553413_PM_at
FLJ22536	1.27	hypothetical locus LOC401237	4.12E-02	229280_PM_s_at
FMO4	1.42	flavin containing monooxygenase 4	2.49E-02	206263_PM_at
FOXC2	2.70	Forkhead box C2 (MFH-1, mesenchyme forkhead 1)	1.32E-03	239058_PM_at
FOXG1	96.51	forkhead box G1	5.33E-07	206018_PM_at
FOXRED2	1.31	FAD-dependent oxidoreductase domain containing 2	4.32E-02	231846_PM_at
FRAS1	1.65	Fraser syndrome 1	1.51E-02	226145_PM_s_at

FRMD8	1.62	FERM domain containing 8	9.75E-03	227964_PM_at
FST	1.73	follistatin	5.12E-03	207345_PM_at
FXN	1.39	frataxin	3.03E-02	205565_PM_s_at
FXYP3	1.54	FXYP domain containing ion transport regulator 3	1.90E-02	202488_PM_s_at
FYN	1.94	FYN oncogene related to SRC, FGR, YES	1.31E-03	212486_PM_s_at
FZD7	2.89	frizzled homolog 7 (Drosophila)	1.59E-03	203706_PM_s_at
GAA	1.50	glucosidase, alpha	1.05E-02	202812_PM_at
GAB1	1.37	GRB2-associated binding protein 1	3.46E-02	225998_PM_at
GABRE	1.49	gamma-aminobutyric acid (GABA) A receptor, epsilon	1.32E-02	204537_PM_s_at
GAS1	10.88	growth arrest-specific 1	3.14E-05	204457_PM_s_at
GATA3	3.64	GATA binding protein 3	4.39E-03	209604_PM_s_at
GCSH /// LOC100329108	1.26	glycine cleavage system protein H (aminomethyl carrier) ///		
GDAP1	1.82	glycine cleavage system protein H pseudogene	3.95E-02	213129_PM_s_at
		ganglioside-induced differentiation-associated protein 1	2.97E-02	226269_PM_at
		golgi-associated, gamma adaptin ear containing, ARF binding		
GGA2	1.34	protein 2	9.01E-03	213772_PM_s_at
GGCT	1.26	gamma-glutamylcyclotransferase	4.67E-02	215380_PM_s_at
GJA5	2.41	gap junction protein, alpha 5, 40kDa	1.42E-02	226701_PM_at
GJC1	3.60	gap junction protein, gamma 1, 45kDa	3.28E-02	228776_PM_at
GLIPR2	2.47	GLI pathogenesis-related 2	2.93E-03	225602_PM_at
GLS	1.68	glutaminase	1.01E-02	203158_PM_s_at
GLT8D2	2.26	glycosyltransferase 8 domain containing 2	3.29E-02	227070_PM_at
GLTP	1.74	glycolipid transfer protein	1.83E-03	219267_PM_at
		guanine nucleotide binding protein (G protein), beta		
GNB4	1.25	polypeptide 4	3.98E-02	225710_PM_at
GOLGA1	1.31	golgin A1	2.22E-02	203383_PM_s_at
GOLGA7B	1.68	golgin A7 family, member B	1.10E-02	228068_PM_at
GOPC	1.61	Golgi-associated PDZ and coiled-coil motif containing	1.47E-03	227215_PM_at
GPC6	4.57	glypican 6	1.16E-03	227059_PM_at
GPM6B	2.10	glycoprotein M6B	9.08E-03	209170_PM_s_at
GPNNMB	5.52	glycoprotein (transmembrane) nmb	5.50E-03	201141_PM_at
GPR56	1.33	G protein-coupled receptor 56	4.41E-02	212070_PM_at
GPR85	1.56	G protein-coupled receptor 85	2.31E-02	224303_PM_s_at
GPSM1	1.33	G-protein signaling modulator 1 (AGS3-like, C. elegans)	1.45E-02	226043_PM_at
GPSM2	1.26	G-protein signaling modulator 2 (AGS3-like, C. elegans)	4.69E-02	230002_PM_at
GPX7	1.29	glutathione peroxidase 7	4.63E-02	213170_PM_at
GRAMD2	1.73	GRAM domain containing 2	1.39E-02	229616_PM_s_at
GRB14	1.56	growth factor receptor-bound protein 14	1.21E-02	206204_PM_at
GRHL1	1.42	grainyhead-like 1 (Drosophila)	2.43E-02	222830_PM_at
GTF2H1	1.32	General transcription factor IIH, polypeptide 1, 62kDa	2.42E-02	202451_PM_at
GUCY1A3	3.14	guanylate cyclase 1, soluble, alpha 3	3.44E-03	227235_PM_at
GXYLT2	1.60	glucoside xylosyltransferase 2	2.09E-02	235371_PM_at
GYG1	1.35	glycogenin 1	1.25E-02	201554_PM_x_at
H2BFS	1.43	H2B histone family, member S	3.84E-02	208579_PM_x_at
HAS3	1.30	hyaluronan synthase 3	4.75E-02	223541_PM_at
HERC6	3.06	Hect domain and RLD 6	2.38E-02	219352_PM_at
HIGD1A	1.28	HIG1 hypoxia inducible domain family, member 1A	2.51E-02	242317_PM_at
		huntingtin interacting protein 1 related /// similar to		
HIP1R /// LOC100294412	1.30	KIAA0655 protein	3.73E-02	209558_PM_s_at
HIPK2	1.25	homeodomain interacting protein kinase 2	3.43E-02	225368_PM_at
HIST1H2AJ	1.25	histone cluster 1, H2aj	3.98E-02	208583_PM_x_at
HIST1H2BF	1.41	histone cluster 1, H2bf	3.51E-02	208490_PM_x_at
HIST1H2BI	1.32	histone cluster 1, H2bi	2.66E-02	208523_PM_x_at
HIST1H2BK	1.42	histone cluster 1, H2bk	4.37E-02	209806_PM_at
HIST1H4J	1.36	histone cluster 1, H4j	1.46E-02	214463_PM_x_at
HIST1H4J /// HIST1H4K	1.36	members of histone cluster 1	3.51E-02	208580_PM_x_at
HMGN3	1.60	high mobility group nucleosomal binding domain 3	4.39E-02	209377_PM_s_at
HR	3.15	hairless homolog (mouse)	1.57E-03	241355_PM_at
HRSP12	1.22	Heat-responsive protein 12	4.32E-02	203790_PM_s_at
HSD17B2	2.37	hydroxysteroid (17-beta) dehydrogenase 2	9.80E-04	204818_PM_at
HSD17B4	1.30	hydroxysteroid (17-beta) dehydrogenase 4	2.81E-02	201413_PM_at
HSPA12A	2.28	heat shock 70kDa protein 12A	2.47E-04	214434_PM_at
HSPB1	1.51	heat shock 27kDa protein 1	1.31E-02	201841_PM_s_at
HSPB2	1.51	heat shock 27kDa protein 2	2.82E-03	205824_PM_at
HSPC159	1.56	galectin-related protein	1.50E-02	226188_PM_at
HTRA1	2.33	HtrA serine peptidase 1	3.21E-03	201185_PM_at
		inhibitor of DNA binding 2, dominant negative helix-loop-		
ID2	1.93	helix protein	5.31E-03	201565_PM_s_at
		inhibitor of DNA binding 3, dominant negative helix-loop-		
ID3	1.72	helix protein	4.36E-03	207826_PM_s_at
IFI30	1.87	interferon, gamma-inducible protein 30	2.55E-03	201422_PM_at
IFI6	6.41	interferon, alpha-inducible protein 6	3.44E-02	204415_PM_at
IFIT1	9.17	interferon-induced protein with tetratricopeptide repeats 1	4.26E-02	203153_PM_at
IFNA4	1.19	interferon, alpha 4	4.95E-02	207964_PM_x_at
IFT122	1.44	intraflagellar transport 122 homolog (Chlamydomonas)	2.82E-03	220744_PM_s_at
IFT46	1.28	intraflagellar transport 46 homolog (Chlamydomonas)	2.07E-02	218483_PM_s_at

IGF2BP3	4.89	insulin-like growth factor 2 mRNA binding protein 3	1.78E-03	203819_PM_s_at
IGF2R	1.28	insulin-like growth factor 2 receptor	4.94E-02	201392_PM_s_at
IGFBP6	3.60	insulin-like growth factor binding protein 6	2.45E-02	203851_PM_at
IGFL1	2.97	IGF-like family member 1	6.51E-03	239430_PM_at
IGFL2	5.75	IGF-like family member 2	3.44E-02	231148_PM_at
IGSF3	1.49	immunoglobulin superfamily, member 3	5.28E-03	202421_PM_at
IL15	1.58	interleukin 15	4.32E-02	205992_PM_s_at
IL17RA	1.39	interleukin 17 receptor A	8.12E-03	229101_PM_at
IL17RD	1.54	interleukin 17 receptor D	1.88E-03	227997_PM_at
IL1B	1.60	interleukin 1, beta	1.18E-02	39402_PM_at
IL1F5	3.00	interleukin 1 family, member 5 (delta)	4.77E-04	222223_PM_s_at
IL20	1.52	interleukin 20	2.21E-02	224071_PM_at
IL20RB	1.51	interleukin 20 receptor beta	1.78E-02	228575_PM_at
IL22RA1	1.53	interleukin 22 receptor, alpha 1	1.10E-02	220056_PM_at
IMPA2	3.03	inositol(myo)-1(or 4)-monophosphatase 2	4.32E-03	203126_PM_at
IMPACT	1.52	Impact homolog (mouse)	3.74E-03	218637_PM_at
ING4	1.26	inhibitor of growth family, member 4	3.25E-02	218234_PM_at
IRX1	3.38	iroquois homeobox 1	6.36E-04	230472_PM_at
IRX4	19.69	iroquois homeobox 4	1.56E-06	220225_PM_at
ITGA4	2.30	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	1.58E-02	213416_PM_at
ITGBL1	1.83	Integrin, beta-like 1 (with EGF-like repeat domains)	5.16E-03	205422_PM_s_at
IVL	2.61	involucrin	2.69E-03	214599_PM_at
IVNS1ABP	1.49	influenza virus NS1A binding protein	4.00E-02	201362_PM_at
JAK1	1.24	Janus kinase 1	4.02E-02	201648_PM_at
JAM3	6.72	junctional adhesion molecule 3	1.33E-03	212813_PM_at
JAZF1	1.47	JAZF zinc finger 1	1.13E-02	225798_PM_at
JMJD7-PLA2G4B /// PLA2G4B	1.76	JMJD7-PLA2G4B readthrough /// phospholipase A2, group IVB (cytosolic)	6.35E-03	219095_PM_at
JMY	1.35	junction mediating and regulatory protein, p53 cofactor	4.13E-02	226352_PM_at
JPH2	1.84	junctophilin 2	5.14E-03	229578_PM_at
JUP	1.25	junction plakoglobin	2.72E-02	201015_PM_s_at
KANK4	11.68	KN motif and ankyrin repeat domains 4	4.11E-03	229125_PM_at
KAZ	1.74	kazrin	5.47E-03	213478_PM_at
KBTBD6	1.35	kelch repeat and BTB (POZ) domain containing 6	3.79E-02	226479_PM_at
KCNG1	1.60	potassium voltage-gated channel, subfamily G, member 1	4.59E-03	214595_PM_at
KCTD1	1.50	potassium channel tetramerisation domain containing 1	1.94E-02	226246_PM_at
KCTD18	1.29	potassium channel tetramerisation domain containing 18	1.73E-02	226493_PM_at
KCTD4	3.43	potassium channel tetramerisation domain containing 4	2.40E-03	239787_PM_at
KDELC1	1.46	KDEL (Lys-Asp-Glu-Leu) containing 1	1.13E-02	219479_PM_at
KDSR	1.28	3-ketodihydrosphingosine reductase	3.19E-02	229850_PM_at
KIAA0141	1.28	KIAA0141	4.75E-02	227056_PM_at
KIAA0528	1.31	KIAA0528	1.78E-02	212943_PM_at
KIAA0922	1.37	KIAA0922	1.60E-02	209760_PM_at
KIAA1609	1.38	KIAA1609	2.29E-02	65438_PM_at
KIAA1644	1.92	KIAA1644	4.22E-03	221901_PM_at
KIAA1737	1.41	KIAA1737	6.38E-03	225623_PM_at
KIAA1919	1.34	KIAA1919	1.59E-02	242851_PM_at
KIF1C	1.58	kinesin family member 1C	1.55E-02	238477_PM_at
KIF7	1.35	kinesin family member 7	1.36E-02	229405_PM_at
KIFAP3	1.27	kinesin-associated protein 3	2.82E-02	203333_PM_at
KLC3	1.57	kinesin light chain 3	2.59E-03	239853_PM_at
KLHDC8B	1.51	kelch domain containing 8B	2.02E-02	225755_PM_at
KLK10	2.18	kallikrein-related peptidase 10	1.67E-02	215808_PM_at
KLK5	4.24	kallikrein-related peptidase 5	1.08E-03	222242_PM_s_at
KLK8	2.25	kallikrein-related peptidase 8	5.84E-03	1552319_PM_a_at
KLK8 /// KLK9	2.24	kallikrein-related peptidase 8 /// kallikrein-related peptidase 9	1.56E-02	233687_PM_s_at
KLRG2	1.74	killer cell lectin-like receptor subfamily G, member 2	1.02E-02	244264_PM_at
KMO	3.38	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	2.09E-02	205306_PM_x_at
KRCC1	1.44	lysine-rich coiled-coil 1	5.31E-03	233329_PM_s_at
KRT1	16.08	keratin 1	5.17E-04	205900_PM_at
KRT10	1.67	keratin 10	2.45E-02	210633_PM_x_at
KRT14	1.44	keratin 14	2.64E-03	209351_PM_at
KRT15	1.58	keratin 15	2.31E-02	204734_PM_at
KRT16	1.67	keratin 16	5.29E-03	209800_PM_at
KRT23	4.30	keratin 23 (histone deacetylase inducible)	5.71E-04	218963_PM_s_at
KRT6B	1.65	keratin 6B	2.54E-03	213680_PM_at
KRT75	4.96	keratin 75	7.36E-03	207065_PM_at
KRT81	11.69	keratin 81	4.22E-04	213711_PM_at
KRTDAP	25.43	keratinocyte differentiation-associated protein	5.80E-05	230835_PM_at
KSR1	1.42	kinase suppressor of ras 1	8.08E-03	235252_PM_at
KTELC1	1.35	KTEL (Lys-Tyr-Glu-Leu) containing 1	7.17E-03	218587_PM_s_at
L1TD1	5.92	LINE-1 type transposase domain containing 1	1.03E-03	219955_PM_at
LACTB	1.46	lactamase, beta	4.51E-02	1552485_PM_at
LAMA1	24.93	laminin, alpha 1	1.47E-06	227048_PM_at
LAMP2	1.46	lysosomal-associated membrane protein 2	6.10E-03	203041_PM_s_at

LANCL1	1.38	LanC lantibiotic synthetase component C-like 1 (bacterial)	2.78E-03	202020_PM_s_at
LAPTM4A	1.29	lysosomal protein transmembrane 4 alpha	2.02E-02	200673_PM_at
LASS3	4.52	LAG1 homolog, ceramide synthase 3	1.79E-04	1554252_PM_a_at
LCE3D	3.64	late cornified envelope 3D	2.51E-02	224328_PM_s_at
LCP1	6.91	lymphocyte cytosolic protein 1 (L-plastin)	3.05E-03	208885_PM_at
LDLRAD3	1.33	Low density lipoprotein receptor class A domain containing 3	4.65E-02	234985_PM_at
LEPROTL1	1.31	leptin receptor overlapping transcript-like 1	8.95E-03	202595_PM_s_at
LETM2	2.63	leucine zipper-EF-hand containing transmembrane protein 2	4.22E-03	1552546_PM_a_at
LHFPL2	2.18	lipoma HMGIC fusion partner-like 2	6.90E-03	212658_PM_at
LIAS	1.65	lipoic acid synthetase	3.00E-02	214045_PM_at
LINS1	1.37	lines homolog 1 (Drosophila)	2.54E-02	1554455_PM_at
LIPA	1.44	lipase A, lysosomal acid, cholesterol esterase	2.23E-02	201847_PM_at
LITAF	1.24	lipopolysaccharide-induced TNF factor	2.89E-02	200704_PM_at
LMCD1	1.85	LIM and cysteine-rich domains 1	1.24E-02	218574_PM_s_at
LOC100129502	1.43	hypothetical protein LOC100129502	6.38E-03	228791_PM_at
LOC100132891	2.12	hypothetical protein LOC100132891	3.98E-02	228438_PM_at
LOC100133660	1.81	Hypothetical LOC100133660	1.54E-02	230082_PM_at
LOC100144603	1.34	hypothetical transcript	2.44E-02	238557_PM_at
LOC100287482	1.46	Similar to hCG2038584	1.01E-02	235736_PM_at
LOC100288152	1.50	Hypothetical protein LOC100288152	1.49E-02	226125_PM_at
LOC100288294	1.24	Hypothetical protein LOC100288294	2.92E-02	243328_PM_at
LOC100288911	1.48	hypothetical protein LOC100288911	4.12E-02	236657_PM_at
LOC134466	2.69	zinc finger protein 300 pseudogene	1.24E-02	244289_PM_at
LOC150166	1.73	hypothetical protein LOC150166	2.01E-02	229295_PM_at
LOC1518	1.41	cathepsin L1 pseudogene	1.24E-02	1563445_PM_x_at
LOC203274	1.77	Hypothetical protein LOC203274	1.45E-02	232034_PM_at
LOC253039	1.78	hypothetical LOC253039	2.40E-03	231828_PM_at
LOC283267	1.69	hypothetical LOC283267	2.32E-03	226793_PM_at
LOC284023	1.74	hypothetical protein LOC284023	3.17E-03	238096_PM_at
LOC339290	1.39	hypothetical LOC339290	4.44E-02	228160_PM_at
LOC400931	1.49	hypothetical LOC400931	1.36E-03	241464_PM_s_at
LOC441259 /// PMS2L1 ///				
PMS2L14 /// PMS2L2 ///				
PMS2L5	1.27	PMS2 postmeiotic segregation increased 2-like cluster	3.33E-02	215667_PM_x_at
LOC642852	1.51	hypothetical LOC642852	1.70E-02	226995_PM_at
LOC645323	1.39	hypothetical LOC645323	1.27E-02	230272_PM_at
LOC646014	1.59	Hypothetical protein LOC646014	2.65E-02	238715_PM_at
LOX	1.43	lysyl oxidase	1.10E-02	215446_PM_s_at
LPCAT2	1.53	lysophosphatidylcholine acyltransferase 2	1.07E-02	227889_PM_at
LPHN2	1.77	latrophilin 2	5.75E-03	206953_PM_s_at
LRRC10B	1.34	leucine rich repeat containing 10B	1.98E-02	236666_PM_s_at
LRRC16A	1.61	leucine rich repeat containing 16A	9.54E-03	219573_PM_at
LRRC57	1.26	leucine rich repeat containing 57	2.22E-02	229232_PM_at
LRRC8D	1.47	leucine rich repeat containing 8 family, member D	1.64E-03	218684_PM_at
LRRC8E	1.51	leucine rich repeat containing 8 family, member E	2.69E-02	220174_PM_at
LRRFIP2	1.30	Leucine rich repeat (in FLII) interacting protein 2	1.72E-02	218364_PM_at
LTB4R	1.54	leukotriene B4 receptor	3.43E-02	236172_PM_at
LTBP3	1.41	latent transforming growth factor beta binding protein 3	2.17E-02	219922_PM_s_at
LY6G6C	1.52	lymphocyte antigen 6 complex, locus G6C	3.45E-02	207114_PM_at
LYPD3	2.01	LY6/PLAUR domain containing 3	8.03E-03	204952_PM_at
LYPD5	1.43	LY6/PLAUR domain containing 5	4.52E-02	236039_PM_at
LYPD6B	1.54	LY6/PLAUR domain containing 6B	1.51E-02	228360_PM_at
LYPLAL1	1.30	lysophospholipase-like 1	2.63E-02	226851_PM_at
LYRM2	1.22	LYR motif containing 2	3.07E-02	227712_PM_at
LYSMD4	1.37	LysM, putative peptidoglycan-binding, domain containing 4	8.26E-03	228954_PM_at
MAB21L1	1.77	mab-21-like 1 (C. elegans)	1.96E-02	206163_PM_at
MAEA	1.36	macrophage erythroblast attacher	2.53E-02	207922_PM_s_at
MAFB	2.18	B (avian)	5.78E-03	218559_PM_s_at
MALAT1	1.38	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	5.69E-03	223578_PM_x_at
MAML3	1.46	mastermind-like 3 (Drosophila)	1.36E-02	242794_PM_at
MANSC1	1.43	MANSC domain containing 1	3.40E-02	220945_PM_x_at
MAP2K5	1.22	Mitogen-activated protein kinase kinase 5	4.22E-02	211370_PM_s_at
MAP3K1	1.32	mitogen-activated protein kinase kinase kinase 1	7.81E-03	225927_PM_at
MARCH3	2.11	membrane-associated ring finger (C3HC4) 3	1.15E-02	213256_PM_at
MARCH8	1.36	membrane-associated ring finger (C3HC4) 8	3.16E-02	221824_PM_s_at
MATR3	1.78	Matrin 3	3.42E-03	242260_PM_at
MBD4	1.30	methyl-CpG binding domain protein 4	1.17E-02	209579_PM_s_at
MBNL3	1.37	muscleblind-like 3 (Drosophila)	3.91E-02	229498_PM_at
MCEE	1.47	methylmalonyl CoA epimerase	1.29E-02	226238_PM_at
MCOLN3	1.35	Mucolipin 3	3.72E-02	220484_PM_at
MDM1	1.30	Mdm1 nuclear protein homolog (mouse)	3.00E-02	213761_PM_at
MED12	1.26	mediator complex subunit 12	2.57E-02	211342_PM_x_at
MEG3	2.86	maternally expressed 3 (non-protein coding)	1.24E-02	210794_PM_s_at
MEGF9	1.79	multiple EGF-like-domains 9	1.93E-03	212830_PM_at

MEOX1	2.50	mesenchyme homeobox 1	2.81E-02	205619_PM_s_at
MEST	2.60	mesoderm specific transcript homolog (mouse)	3.87E-03	202016_PM_at
METTL8	1.39	methyltransferase like 8	1.87E-02	220007_PM_at
MFAP2	2.16	microfibrillar-associated protein 2	1.11E-02	203417_PM_at
MFAP3L	2.13	microfibrillar-associated protein 3-like	7.83E-03	205442_PM_at
MFAP5	4.23	microfibrillar associated protein 5	2.80E-03	213765_PM_at
MGC87042	1.70	STEAP family protein MGC87042	3.73E-02	217553_PM_at
MGC9913	1.83	hypothetical protein MGC9913	4.93E-03	244740_PM_at
MIA	1.92	melanoma inhibitory activity	4.57E-03	206560_PM_s_at
MINK1	1.25	misshapen-like kinase 1 (zebrafish)	2.15E-02	214246_PM_x_at
		myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	3.15E-02	230122_PM_at
MLLT10	1.36		3.43E-02	236347_PM_at
MMAA	1.24	methylmalonic aciduria (cobalamin deficiency) cblA type	9.57E-03	203434_PM_s_at
MME	3.56	membrane metallo-endopeptidase	6.84E-03	239272_PM_at
MMP28	2.92	matrix metallopeptidase 28	1.08E-02	205828_PM_at
MMP3	5.73	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	7.67E-04	209708_PM_at
MOXD1	1.91	monooxygenase, DBH-like 1	1.43E-02	233651_PM_s_at
MPND	1.32	MPN domain containing	1.20E-02	202974_PM_at
MPP1	1.47	membrane protein, palmitoylated 1, 55kDa	1.70E-02	206538_PM_at
MRAS	1.42	muscle RAS oncogene homolog	1.22E-03	37408_PM_at
MRC2	2.74	mannose receptor, C type 2	2.04E-02	1553293_PM_at
MRGPRX3	3.07	MAS-related GPR, member X3	1.78E-02	218773_PM_s_at
MSRB2	1.28	methionine sulfoxide reductase B2	2.97E-02	225782_PM_at
MSRB3	1.57	methionine sulfoxide reductase B3	2.12E-03	210319_PM_x_at
MSX2	2.32	msh homeobox 2	4.19E-02	217546_PM_at
MT1M	2.00	metallothionein 1M	4.91E-02	223311_PM_s_at
MTA3	1.28	metastasis associated 1 family, member 3	2.19E-02	222403_PM_at
MTCH2	1.25	mitochondrial carrier homolog 2 (C. elegans)	1.77E-02	225346_PM_at
MTERFD3	1.49	MTERF domain containing 3	3.10E-02	212767_PM_at
MTG1	1.25	mitochondrial GTPase 1 homolog (S. cerevisiae)	3.71E-02	239576_PM_at
MTUS1	1.29	Microtubule associated tumor suppressor 1	3.59E-02	1553602_PM_at
MUCL1	1.63	mucin-like 1		
		myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	4.76E-02	202086_PM_at
MX1	6.30		2.17E-02	213067_PM_at
MYH10	1.34	myosin, heavy chain 10, non-muscle	1.59E-03	224823_PM_at
MYLK	12.36	myosin light chain kinase	3.44E-02	202039_PM_at
MYO18A /// TIAF1	1.21	myosin XVIII A /// TGFB1-induced anti-apoptotic factor 1	4.36E-02	33197_PM_at
MYO7A	1.22	myosin VIIA	2.55E-03	209272_PM_at
NAB1	1.68	NGFI-A binding protein 1 (EGR1 binding protein 1)	4.02E-02	232946_PM_s_at
NADSYN1	1.22	NAD synthetase 1	1.27E-02	228063_PM_s_at
NAPIL5	2.41	nucleosome assembly protein 1-like 5	4.10E-02	208751_PM_at
NAPA	1.28	N-ethylmaleimide-sensitive factor attachment protein, alpha	7.15E-03	224772_PM_at
NAV1	1.58	neuron navigator 1	1.64E-02	244487_PM_at
NCK1	1.49	NCK adaptor protein 1	3.83E-02	207700_PM_s_at
NCOA3	1.20	nuclear receptor coactivator 3	6.13E-03	1559254_PM_at
NCRNA00162	3.79	non-protein coding RNA 162		
		NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	3.91E-02	201966_PM_at
NDUFS2	1.20		2.30E-03	33767_PM_at
NEFH	1.79	neurofilament, heavy polypeptide	1.24E-02	221805_PM_at
NEFL	4.84	neurofilament, light polypeptide	7.19E-03	205113_PM_at
NEFM	2.66	neurofilament, medium polypeptide	3.95E-03	209290_PM_s_at
NFIB	1.43	Nuclear factor I/B	3.98E-02	202007_PM_at
NID1	1.61	nidogen 1	1.55E-03	204114_PM_at
NID2	2.76	nidogen 2 (osteonidogen)	3.13E-03	230188_PM_at
NIPAL4	1.97	NIPA-like domain containing 4	2.63E-02	224436_PM_s_at
NIPSNAP3A	1.40	nipsnap homolog 3A (C. elegans)	3.77E-03	229340_PM_at
NKAPL	1.44	NFKB activating protein-like	2.19E-03	219680_PM_at
NLRX1	1.55	NLR family member X1	1.50E-02	1556029_PM_s_at
NMNAT2	1.39	nicotinamide nucleotide adenyltransferase 2	2.32E-03	223206_PM_s_at
NMRAL1	1.50	NmrA-like family domain containing 1	2.56E-05	202237_PM_at
NNMT	15.80	Nicotinamide N-methyltransferase	2.24E-04	220066_PM_at
NOD2	3.52	nucleotide-binding oligomerization domain containing 2	7.81E-03	202443_PM_x_at
NOTCH2	1.32	Notch homolog 2 (Drosophila)	6.68E-03	203238_PM_s_at
NOTCH3	1.45	Notch homolog 3 (Drosophila)	1.39E-04	213462_PM_at
NPAS2	2.12	neuronal PAS domain protein 2	3.73E-03	225911_PM_at
NPNT	1.61	nephronectin	1.52E-03	221803_PM_s_at
NRBF2	1.53	nuclear receptor binding factor 2	3.80E-02	221795_PM_at
NTRK2	1.22	neurotrophic tyrosine kinase, receptor, type 2	1.21E-02	220183_PM_s_at
NUDT6	1.71	nudix (nucleoside diphosphate linked moiety X)-type motif 6	6.51E-03	238327_PM_at
ODF3B	1.63	outer dense fiber of sperm tails 3B	1.34E-02	231867_PM_at
ODZ2	1.38	odx, odd Oz/ten-m homolog 2 (Drosophila)	5.28E-03	219523_PM_s_at
ODZ3	1.82	Odz, odd Oz/ten-m homolog 3 (Drosophila)	1.24E-02	219582_PM_at
OGFRL1	1.35	opioid growth factor receptor-like 1	8.01E-03	226019_PM_at
OMA1	1.47	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)		
		olfactory receptor, family 2, subfamily L, member 1 pseudogene	2.65E-02	1567242_PM_at
OR2L1P	1.23			

OSBPL10	1.70	oxysterol binding protein-like 10	2.32E-03	219073_PM_s_at
OSR2	2.38	odd-skipped related 2 (Drosophila)	6.55E-04	213568_PM_at
OXER1	1.22	oxoeicosanoid (OXE) receptor 1	3.56E-02	1553222_PM_at
PABPC4L	1.79	poly(A) binding protein, cytoplasmic 4-like	2.31E-02	238865_PM_at
PANK1	1.47	pantothenate kinase 1	1.01E-02	226649_PM_at
PAQR3	1.32	progesterin and adipoQ receptor family member III	3.92E-02	213372_PM_at
PARP12	1.89	poly (ADP-ribose) polymerase family, member 12	3.47E-02	218543_PM_s_at
PARVB	1.63	parvin, beta	7.09E-03	37966_PM_at
PAX3	5.49	paired box 3	1.62E-05	231666_PM_at
PAX6	10.29	paired box 6	3.16E-06	235795_PM_at
PCBP4	1.38	poly(rC) binding protein 4	5.24E-03	209361_PM_s_at
PCDH18	1.63	protocadherin 18	2.60E-03	225975_PM_at
PCDHB10	1.39	protocadherin beta 10	2.45E-02	223854_PM_at
PCDHB14	1.81	protocadherin beta 14	3.03E-02	231726_PM_at
PCDHGA1 /// PCDHGA10				
/// PCDHGA11 ///				
PCDHGA12 /// PCDHGA2				
/// PCDHGA3 /// PCDHGA4				
/// PCDHGA5 /// PCDHGA6				
/// PCDHGA7 /// PCDHGA8				
/// PCDHGA9 /// PCDHGB1				
/// PCDHGB2 /// PCDHGB3				
/// PCDHGB4 /// PCDHGB5				
/// PCDHGB6 /// PCDHGB7				
/// PCDHGC3 /// PCDHGC4				
/// PCDHGC5	1.34	protocadherin gamma subfamily	1.70E-02	211066_PM_x_at
PCDHGA11 /// PCDHGA12				
/// PCDHGA6 /// PCDHGB3				
/// PCDHGB4 /// PCDHGB5				
/// PCDHGB6 /// PCDHGB7				
/// PCDHGC3 /// PCDHGC4				
/// PCDHGC5	1.44	protocadherin gamma subfamily	2.97E-02	205717_PM_x_at
PCLO	1.53	piccolo (presynaptic cytomatrix protein)	4.02E-03	213558_PM_at
PCNT	1.21	pericentrin	4.32E-02	203660_PM_s_at
PCSK5	1.71	Proprotein convertase subtilisin/kexin type 5	2.19E-03	205559_PM_s_at
PCSK6	1.62	Proprotein convertase subtilisin/kexin type 6	3.07E-02	210553_PM_x_at
PCYOX1L	1.71	prenylcysteine oxidase 1 like	9.52E-04	218953_PM_s_at
PCYT1A	1.38	Phosphate cytidyltransferase 1, choline, alpha	2.98E-02	204210_PM_s_at
PDE4DIP	1.75	phosphodiesterase 4D interacting protein	2.76E-02	212390_PM_at
PDGFD	1.44	platelet derived growth factor D	4.02E-03	219304_PM_s_at
PK2	1.43	pyruvate dehydrogenase kinase, isozyme 2	1.42E-02	213724_PM_s_at
PDPR	1.31	pyruvate dehydrogenase phosphatase regulatory subunit	3.69E-02	224902_PM_at
PDZRN3	1.39	PDZ domain containing ring finger 3	9.14E-03	212915_PM_at
PEG10	2.26	paternally expressed 10	2.98E-02	212094_PM_at
PEPD	1.49	peptidase D	1.46E-02	202108_PM_at
PERP	1.33	PERP, TP53 apoptosis effector	3.80E-02	236009_PM_at
PEX12	1.25	peroxisomal biogenesis factor 12	4.23E-02	205094_PM_at
PEX3	1.55	peroxisomal biogenesis factor 3	6.87E-03	203972_PM_s_at
PEX5	1.21	peroxisomal biogenesis factor 5	4.25E-02	203244_PM_at
PFKFB2	1.41	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	7.37E-03	209992_PM_at
PGAP2	1.38	post-GPI attachment to proteins 2	2.63E-02	215293_PM_s_at
PGLYRP4	1.70	peptidoglycan recognition protein 4	6.98E-03	220944_PM_at
PGM2	1.55	phosphoglucomutase 2	5.06E-03	225366_PM_at
PGRMC2	1.56	progesterone receptor membrane component 2	5.78E-03	213227_PM_at
PHACTR2	1.31	phosphatase and actin regulator 2	2.76E-02	244774_PM_at
PHLPP1	1.38	PH domain and leucine rich repeat protein phosphatase 1	1.45E-02	212719_PM_at
PI15	1.80	peptidase inhibitor 15	5.00E-03	229947_PM_at
PI3	3.74	peptidase inhibitor 3, skin-derived	1.95E-02	203691_PM_at
PIGX	1.46	phosphatidylinositol glycan anchor biosynthesis, class X	1.14E-02	1552291_PM_at
PIK3C2B	1.81	phosphoinositide-3-kinase, class 2, beta polypeptide	1.45E-02	204484_PM_at
PIK3R3	2.05	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	2.60E-02	202743_PM_at
PILRB	1.38	paired immunoglobulin-like type 2 receptor beta	9.69E-03	220954_PM_s_at
PION	1.76	Pigeon homolog (Drosophila)	4.92E-03	213142_PM_x_at
PKP1	1.46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	2.17E-02	221854_PM_at
PKP3	1.43	plakophilin 3	4.55E-03	209873_PM_s_at
PL-5283	1.23	PL-5283 protein	3.13E-02	224752_PM_at
PLA2G4A	1.91	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1.01E-02	210145_PM_at
		phospholipase A2, group VII (platelet-activating factor		
PLA2G7	1.67	acetylhydrolase, plasma)	5.12E-03	206214_PM_at
PLAC2	2.72	placenta-specific 2 (non-protein coding)	6.97E-04	229385_PM_s_at
PLAT	6.48	plasminogen activator, tissue	5.38E-03	201860_PM_s_at
PLCD1	1.35	phospholipase C, delta 1	2.51E-02	205125_PM_at
PLCG2	1.50	phospholipase C, gamma 2 (phosphatidylinositol-specific)	7.81E-03	204613_PM_at
		phosphatidylinositol-specific phospholipase C, X domain		
PLCXD1	1.37	containing 1	1.24E-02	218951_PM_s_at
PLD1	1.39	phospholipase D1, phosphatidylcholine-specific	3.15E-02	226636_PM_at

PLD2	1.33	phospholipase D2	3.81E-02	209643_PM_s_at
PLD5	5.25	phospholipase D family, member 5	1.24E-03	1563933_PM_a_at
PLEKHF1	2.06	pleckstrin homology domain containing, family F (with		
PLIN2	2.97	FYVE domain) member 1	3.73E-04	219566_PM_at
PLK1S1	1.26	Perilipin 2	3.77E-04	209122_PM_at
PLSCR4	1.83	polo-like kinase 1 substrate 1	3.71E-02	228290_PM_at
PLXDC2	3.19	phospholipid scramblase 4	2.64E-03	218901_PM_at
PMP22	1.35	plexin domain containing 2	1.66E-03	227276_PM_at
PNLIPRP3	9.51	peripheral myelin protein 22	4.98E-02	210139_PM_s_at
PNMAL1	2.49	pancreatic lipase-related protein 3	1.79E-04	1558846_PM_at
PNPLA3	1.46	PNMA-like 1	1.75E-03	218824_PM_at
PNPO	1.43	patatin-like phospholipase domain containing 3	4.97E-02	220675_PM_s_at
POLR3G	1.82	pyridoxamine 5'-phosphate oxidase	5.51E-03	222653_PM_at
		Polymerase (RNA) III (DNA directed) polypeptide G (32kD)	3.88E-02	206653_PM_at
		polymerase (RNA) III (DNA directed) polypeptide H		
POLR3H	1.35	(22.9kD)	2.80E-02	225682_PM_s_at
POPDC3	2.42	popeye domain containing 3	6.72E-03	219926_PM_at
POU2AF1	1.38	POU class 2 associating factor 1	7.20E-03	205267_PM_at
PPAP2A	1.24	phosphatidic acid phosphatase type 2A	1.87E-02	209147_PM_s_at
		peroxisome proliferator-activated receptor gamma,		
PPARGC1B	1.76	coactivator 1 beta	2.10E-02	232181_PM_at
PPFIBP2	1.68	PTPRF interacting protein, binding protein 2 (liprin beta 2)	7.78E-03	212841_PM_s_at
PPIC	1.25	peptidylprolyl isomerase C (cyclophilin C)	2.95E-02	204517_PM_at
PPM1D	1.20	protein phosphatase, Mg2+/Mn2+ dependent, 1D	4.71E-02	204566_PM_at
PPM1F	1.25	protein phosphatase, Mg2+/Mn2+ dependent, 1F	4.94E-02	203063_PM_at
PPP1R14A	4.41	protein phosphatase 1, regulatory (inhibitor) subunit 14A	6.06E-05	227006_PM_at
PPP1R3C	2.86	protein phosphatase 1, regulatory (inhibitor) subunit 3C	6.45E-03	204284_PM_at
PRCD	1.42	progressive rod-cone degeneration	5.85E-03	230015_PM_at
PREPL	1.53	prolyl endopeptidase-like	1.41E-02	212216_PM_at
PRICKLE1	2.67	Prickle homolog 1 (Drosophila)	1.36E-02	226065_PM_at
PRICKLE2	2.88	prickle homolog 2 (Drosophila)	1.01E-03	225968_PM_at
PRKXP1	1.44	protein kinase, X-linked, pseudogene 1	2.27E-02	235987_PM_at
PRMT8	1.98	protein arginine methyltransferase 8	2.51E-03	230839_PM_at
PRR16	2.17	proline rich 16	7.89E-04	220014_PM_at
PRR9	5.28	proline rich 9	2.80E-02	237732_PM_at
PRRG4	2.05	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	1.83E-03	207291_PM_at
PSORS1C2	1.92	psoriasis susceptibility 1 candidate 2	2.05E-02	220635_PM_at
PSTPIP2	1.49	proline-serine-threonine phosphatase interacting protein 2	1.47E-02	219938_PM_s_at
PTCD2	1.48	pentatricopeptide repeat domain 2	3.17E-02	1555910_PM_at
PTER	1.48	phosphotriesterase related	4.37E-02	222798_PM_at
PTGES	2.93	prostaglandin E synthase	1.18E-03	210367_PM_s_at
PTK7	1.34	PTK7 protein tyrosine kinase 7	1.99E-02	207011_PM_s_at
		protein tyrosine phosphatase-like (proline instead of catalytic		
PTPLB	1.50	arginine), member b	3.80E-02	227741_PM_at
		protein tyrosine phosphatase, non-receptor type 4		
PTPN4	1.41	(megakaryocyte)	8.43E-03	205171_PM_at
PTPRZ1	13.11	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	6.06E-05	204469_PM_at
PVRL4	1.46	poliovirus receptor-related 4	1.72E-02	223540_PM_at
PXDNL	1.26	peroxidasin homolog (Drosophila)-like	2.44E-02	241942_PM_at
PXMP4	1.44	peroxisomal membrane protein 4, 24kDa	4.90E-03	238746_PM_at
PYGB	1.33	phosphorylase, glycogen	4.30E-02	201481_PM_s_at
QDPR	1.39	Quinoid dihydropteridine reductase	1.38E-02	209123_PM_at
RAB38	1.58	RAB38, member RAS oncogene family	1.22E-02	219412_PM_at
RAB3IP	1.56	RAB3A interacting protein (rabin3)	1.88E-02	231399_PM_at
RAB4A	1.23	RAB4A, member RAS oncogene family	4.35E-02	203581_PM_at
		RAB4A, member RAS oncogene family /// S-phase response		
RAB4A /// SPHAR	1.28	(cyclin related)	3.10E-02	206272_PM_at
RAB6B	1.35	RAB6B, member RAS oncogene family	4.47E-02	225259_PM_at
RAB7B	1.68	RAB7B, member RAS oncogene family	3.00E-02	230266_PM_at
RAB9A	1.36	RAB9A, member RAS oncogene family	9.11E-03	221808_PM_at
RAET1E	1.36	retinoic acid early transcript 1E	2.25E-02	1552777_PM_a_at
RAGE	1.54	renal tumor antigen	3.14E-02	205130_PM_at
RALGPS2	1.22	Ral GEF with PH domain and SH3 binding motif 2	4.81E-02	232112_PM_at
RAPGEF5	1.46	Rap guanine nucleotide exchange factor (GEF) 5	2.79E-02	204681_PM_s_at
RASGRP2	1.62	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	4.55E-03	214369_PM_s_at
RASL11B	1.50	RAS-like, family 11, member B	2.94E-02	219142_PM_at
RAVER2	1.44	ribonucleoprotein, PTB-binding 2	1.65E-02	231851_PM_at
RBKS	1.52	ribokinase	5.85E-03	57540_PM_at
RBM43	1.89	RNA binding motif protein 43	2.81E-02	228304_PM_at
RBMXL1	1.57	RNA binding motif protein, X-linked-like 1	6.15E-03	227748_PM_at
RCAN1	1.36	regulator of calcineurin 1	4.91E-02	208370_PM_s_at
RDH12	2.28	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	2.22E-02	242998_PM_at
RECK	1.65	reversion-inducing-cysteine-rich protein with kazal motifs	2.44E-02	205407_PM_at
REEP4	1.32	receptor accessory protein 4	1.21E-02	218777_PM_at
RFX2	1.68	regulatory factor X, 2 (influences HLA class II expression)	1.23E-02	226872_PM_at
RFXANK	1.29	regulatory factor X-associated ankyrin-containing protein	2.45E-02	202758_PM_s_at

RHCG	2.18	Rh family, C glycoprotein	3.50E-02	219554_PM_at
RHOJ	2.06	ras homolog gene family, member J	1.70E-02	235489_PM_at
RIN2	1.21	Ras and Rab interactor 2	3.81E-02	209684_PM_at
RMND5A	1.33	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	1.56E-02	212482_PM_at
RNF135	1.57	ring finger protein 135	4.99E-03	223591_PM_at
RNF144A	1.40	ring finger protein 144A	3.75E-02	204040_PM_at
RNF217	1.46	ring finger protein 217	4.13E-02	235492_PM_at
RNPC3	1.29	RNA-binding region (RNP1, RRM) containing 3	2.73E-02	226975_PM_at
RPL22L1	1.27	ribosomal protein L22-like 1	3.80E-02	225541_PM_at
RPP40	1.48	ribonuclease P/MRP 40kDa subunit	4.23E-02	213427_PM_at
RPS6KA2	4.14	ribosomal protein S6 kinase, 90kDa, polypeptide 2	5.68E-04	212912_PM_at
RPTN	4.68	repetin	4.61E-03	1553454_PM_at
RRN3P1	1.30	RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene 1	2.52E-02	215211_PM_at
RSU1	1.24	Ras suppressor protein 1	3.37E-02	201980_PM_s_at
RUNDC3B	1.83	RUN domain containing 3B	1.15E-02	241703_PM_at
RUNX3	1.69	runt-related transcription factor 3	1.52E-02	204198_PM_s_at
RWDD2B	1.31	RWD domain containing 2B	3.95E-02	218377_PM_s_at
S100A12	5.17	S100 calcium binding protein A12	1.29E-04	205863_PM_at
S100A7	16.15	S100 calcium binding protein A7	5.52E-03	205916_PM_at
S100A8	1.83	S100 calcium binding protein A8	1.42E-02	202917_PM_s_at
S100A9	1.75	S100 calcium binding protein A9	1.69E-02	203535_PM_at
SAA1 /// SAA2	4.05	serum amyloid A1 /// serum amyloid A2	3.76E-02	208607_PM_s_at
SASH1	1.76	SAM and SH3 domain containing 1	6.88E-03	226022_PM_at
SBSN	3.12	suprabasin	7.60E-04	235272_PM_at
SC65	1.58	synaptonemal complex protein SC65	1.93E-03	204078_PM_at
SCARB1	1.84	Scavenger receptor class B, member 1	4.67E-03	201819_PM_at
SCRN1	1.26	secernin 1	2.68E-02	201462_PM_at
SDK2	1.28	Sidekick homolog 2 (chicken)	4.42E-02	242064_PM_at
SDR9C7	2.04	short chain dehydrogenase/reductase family 9C, member 7	5.74E-03	1553077_PM_at
SDSL	1.54	serine dehydratase-like	4.79E-03	228274_PM_at
SELM	3.77	selenoprotein M	4.38E-03	226051_PM_at
SEMA5B	1.45	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	1.52E-02	223610_PM_at
SERPINA3	1.82	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	3.15E-02	202376_PM_at
SERPINB13	1.90	serpin peptidase inhibitor, clade B (ovalbumin), member 13	3.75E-02	211362_PM_s_at
SERPINB3	2.93	serpin peptidase inhibitor, clade B (ovalbumin), member 3	2.68E-02	209719_PM_x_at
SERPINH1	1.50	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	1.03E-02	207714_PM_s_at
SESN1	1.65	sestrin 1	5.81E-03	218346_PM_s_at
SETDB2	1.31	SET domain, bifurcated 2	3.35E-02	235339_PM_at
SETMAR	1.56	SET domain and mariner transposase fusion gene	5.24E-03	206554_PM_x_at
SEZ6L2	1.44	seizure related 6 homolog (mouse)-like 2	1.47E-02	233337_PM_s_at
SF3B3	1.57	splicing factor 3b, subunit 3, 130kDa	1.01E-02	200688_PM_at
SFRP1	17.30	Secreted frizzled-related protein 1	3.70E-05	202037_PM_s_at
SFRS2B	1.34	splicing factor, arginine/serine-rich 2B	1.42E-02	238929_PM_at
SFRS6	1.33	splicing factor, arginine/serine-rich 6	4.71E-02	206108_PM_s_at
SH3BP5	1.68	SH3-domain binding protein 5 (BTK-associated)	1.25E-03	201811_PM_x_at
SHROOM1	1.39	shroom family member 1	1.40E-02	239435_PM_x_at
SIDT2	1.65	SID1 transmembrane family, member 2	2.26E-03	56256_PM_at
SIK2	1.24	salt-inducible kinase 2	4.64E-02	213221_PM_s_at
SIRPA	1.22	signal-regulatory protein alpha	3.72E-02	202896_PM_s_at
SIX3	10.36	SIX homeobox 3	8.41E-06	206634_PM_at
SKP2	1.37	S-phase kinase-associated protein 2 (p45)	6.98E-03	203625_PM_x_at
SLC12A8	1.30	solute carrier family 12 (potassium/chloride transporters), member 8	2.88E-02	219874_PM_at
SLC13A5	1.51	solute carrier family 13 (sodium-dependent citrate transporter), member 5	4.51E-02	228844_PM_at
SLC16A1	1.42	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	8.58E-03	202236_PM_s_at
SLC16A6	1.32	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	3.25E-02	230748_PM_at
SLC16A7	1.72	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	5.47E-03	207057_PM_at
SLC1A3	3.65	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.88E-04	202800_PM_at
SLC24A3	1.49	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	4.37E-03	57588_PM_at
SLC25A12	1.32	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	3.99E-02	203339_PM_at
SLC25A20	1.52	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	1.09E-02	203658_PM_at
SLC26A2	1.45	solute carrier family 26 (sulfate transporter), member 2	4.63E-02	205097_PM_at

SLC28A3	1.28	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	2.33E-02	220475_PM_at
SLC2A1	1.37	solute carrier family 2 (facilitated glucose transporter), member 1	4.43E-02	201249_PM_at
SLC2A12	1.89	solute carrier family 2 (facilitated glucose transporter), member 12	6.68E-03	235050_PM_at
SLC2A14 /// SLC2A3	3.77	members of solute carrier family 2 (facilitated glucose transporter)	2.45E-02	222088_PM_s_at
SLC2A3	3.27	solute carrier family 2 (facilitated glucose transporter), member 3	2.64E-02	202498_PM_s_at
SLC30A1	1.32	solute carrier family 30 (zinc transporter), member 1	2.69E-02	212907_PM_at
SLC35A1	1.44	solute carrier family 35 (CMP-sialic acid transporter), member A1	1.70E-02	203306_PM_s_at
SLC35D1	1.48	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	8.73E-03	209713_PM_s_at
SLC35F3	4.54	Solute carrier family 35, member F3	2.37E-04	229065_PM_at
SLC35F5	1.29	solute carrier family 35, member F5	2.97E-02	225872_PM_at
SLC39A14	1.47	solute carrier family 39 (zinc transporter), member 14	1.90E-02	212110_PM_at
SLC39A2	1.92	solute carrier family 39 (zinc transporter), member 2	1.54E-02	220413_PM_at
SLC39A6	1.30	solute carrier family 39 (zinc transporter), member 6	1.49E-02	202088_PM_at
SLC3A2	1.79	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	1.34E-03	200924_PM_s_at
SLC46A3	2.61	solute carrier family 46, member 3	1.87E-02	214719_PM_at
SLC48A1	1.48	solute carrier family 48 (heme transporter), member 1	7.36E-03	48106_PM_at
SLC5A6	1.51	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	7.36E-03	204087_PM_s_at
SLC6A15	1.54	solute carrier family 6 (neutral amino acid transporter), member 15	9.13E-03	239352_PM_at
SLC6A2	2.05	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	1.50E-04	215715_PM_at
SLC7A1	1.42	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	3.49E-02	212290_PM_at
SLC7A5	2.70	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	7.94E-05	201195_PM_s_at
SLC7A8	2.43	solute carrier family 7 (amino acid transporter, L-type), member 8	6.97E-04	216092_PM_s_at
SLC9A9	1.61	solute carrier family 9 (sodium/hydrogen exchanger), member 9	1.81E-02	227791_PM_at
SLCO3A1	1.82	solute carrier organic anion transporter family, member 3A1	3.73E-03	229776_PM_at
SLPI	1.47	secretory leukocyte peptidase inhibitor	4.52E-02	203021_PM_at
SMOC1	1.51	SPARC related modular calcium binding 1	1.97E-02	222784_PM_at
SMPDL3A	1.36	sphingomyelin phosphodiesterase, acid-like 3A	3.03E-02	213624_PM_at
SNX2	1.24	sorting nexin 2	3.36E-02	202113_PM_s_at
SNX21	1.36	sorting nexin family member 21	2.90E-02	1553960_PM_at
SNX5	1.24	sorting nexin 5	3.57E-02	222417_PM_s_at
SORL1	2.62	sortilin-related receptor, L(DLR class) A repeats-containing	2.54E-03	203509_PM_at
SOX9	1.71	SRY (sex determining region Y)-box 9	3.37E-04	202935_PM_s_at
SP110	2.05	SP110 nuclear body protein	2.58E-02	209762_PM_x_at
SP8	8.78	Sp8 transcription factor	7.78E-06	237449_PM_at
SPAG16	1.37	sperm associated antigen 16	6.98E-03	219109_PM_at
SPARC	2.14	secreted protein, acidic, cysteine-rich (osteonectin)	7.78E-03	212667_PM_at
SPATA20	1.41	spermatogenesis associated 20	1.39E-02	218164_PM_at
SPINK5	2.83	serine peptidase inhibitor, Kazal type 5	1.36E-02	205185_PM_at
SPINK6	10.55	serine peptidase inhibitor, Kazal type 6	3.80E-03	1553973_PM_a_at
SPNS3	1.21	spinster homolog 3 (Drosophila)	4.19E-02	235900_PM_at
SPPL3	1.24	signal peptide peptidase 3	1.93E-02	224640_PM_at
SPRR1A	1.27	small proline-rich protein 1A	4.88E-02	213796_PM_at
SPRR1B	1.29	small proline-rich protein 1B (cornifin)	3.74E-02	205064_PM_at
SPRR2G	17.24	small proline-rich protein 2G	6.19E-04	236119_PM_s_at
SPRR4	2.45	small proline-rich protein 4	5.47E-03	1552620_PM_at
SPTLC3	3.32	serine palmitoyltransferase, long chain base subunit 3	5.47E-03	227752_PM_at
SRD5A1	1.78	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	2.10E-03	204675_PM_at
SRGAP2	1.21	SLIT-ROBO Rho GTPase activating protein 2	4.88E-02	1556202_PM_at
SRGAP3	1.67	SLIT-ROBO Rho GTPase activating protein 3	4.16E-03	209794_PM_at
SRGN	7.77	serglycin	1.88E-04	201859_PM_at
SRPX	1.88	sushi-repeat-containing protein, X-linked	9.52E-04	204955_PM_at
SS18	1.32	synovial sarcoma translocation, chromosome 18	1.74E-02	202816_PM_s_at
SSPN	1.34	sarcospan (Kras oncogene-associated gene)	2.38E-02	204964_PM_s_at
ST13	1.25	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	4.93E-02	208666_PM_s_at
ST5	1.32	suppression of tumorigenicity 5	2.38E-02	202440_PM_s_at
ST6GALNAC2	1.29	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	2.55E-02	204542_PM_at
STAC	1.68	SH3 and cysteine rich domain	1.92E-02	205743_PM_at
STAG3L1	1.46	stromal antigen 3-like 1	8.00E-03	221191_PM_at

STAG3L1 /// STAG3L2	1.48	stromal antigen 3-like 1 /// stromal antigen 3-like 2	2.73E-03	223724_PM_s_at
STARD5	1.60	StAR-related lipid transfer (START) domain containing 5	2.02E-02	213820_PM_s_at
STK19	1.21	serine/threonine kinase 19	4.54E-02	204090_PM_at
STYX	1.36	serine/threonine/tyrosine interacting protein	7.71E-03	228853_PM_at
SUB1	1.70	SUB1 homolog (S. cerevisiae)	2.59E-03	224587_PM_at
SYCE1L	1.34	synaptonemal complex central element protein 1-like	2.43E-02	1559960_PM_x_at
SYNM	2.33	synemin, intermediate filament protein	2.86E-02	212730_PM_at
SYT2	1.25	synaptotagmin II	3.48E-02	214903_PM_at
SYTL1	1.32	synaptotagmin-like 1	2.17E-02	227134_PM_at
TAGAP	2.08	T-cell activation RhoGTPase activating protein	5.46E-03	229723_PM_at
TARBP1	1.36	TAR (HIV-1) RNA binding protein 1	1.47E-02	202813_PM_at
TBC1D4	1.71	TBC1 domain family, member 4	1.08E-03	203386_PM_at
TCEA2	1.30	transcription elongation factor A (SII), 2	3.97E-02	203919_PM_at
TCEAL4	1.28	transcription elongation factor A (SII)-like 4	3.72E-02	202371_PM_at
TCF25	1.25	transcription factor 25 (basic helix-loop-helix)	2.54E-02	221495_PM_s_at
TCF7L1	1.83	transcription factor 7-like 1 (T-cell specific, HMG-box)	1.33E-02	221016_PM_s_at
TCF7L2	1.53	Transcription factor 7-like 2 (T-cell specific, HMG-box)	3.77E-03	216035_PM_x_at
TCFL5	1.32	Transcription factor-like 5 (basic helix-loop-helix)	3.68E-02	204849_PM_at
TCP11L1	1.83	t-complex 11 (mouse)-like 1	2.64E-03	205796_PM_at
TEX9	1.60	testis expressed 9	7.15E-03	243198_PM_at
TFAP2C	1.67	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	2.79E-03	205286_PM_at
TFCP2	1.24	transcription factor CP2	2.54E-02	227637_PM_at
TFCP2L1	1.52	transcription factor CP2-like 1	6.58E-03	219735_PM_s_at
TFRC	1.27	Transferrin receptor (p90, CD71)	1.78E-02	207332_PM_s_at
TGFBRAP1	1.35	transforming growth factor, beta receptor associated protein 1	2.29E-02	205210_PM_at
THBS1	1.39	thrombospondin 1	4.67E-02	201107_PM_s_at
THBS2	3.79	thrombospondin 2	2.25E-02	203083_PM_at
THEM4	1.69	thioesterase superfamily member 4	1.81E-02	229253_PM_at
THY1	18.97	Thy-1 cell surface antigen	1.74E-05	208850_PM_s_at
TIAM1	1.25	T-cell lymphoma invasion and metastasis 1	3.57E-02	213135_PM_at
TIMP2	1.60	TIMP metalloproteinase inhibitor 2	7.87E-03	224560_PM_at
TLCD2	1.89	TLC domain containing 2	7.71E-03	241359_PM_at
TLE1	1.31	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	3.55E-02	203222_PM_s_at
TLR1	1.75	toll-like receptor 1	1.81E-02	210176_PM_at
TLR5	1.79	toll-like receptor 5	2.45E-02	210166_PM_at
TLR6	1.33	toll-like receptor 6	3.00E-02	239021_PM_at
TMED3	1.28	transmembrane emp24 protein transport domain containing 3	2.80E-02	208837_PM_at
TMEM117	1.92	transmembrane protein 117	1.78E-02	223594_PM_at
TMEM139	3.12	transmembrane protein 139	3.13E-04	227753_PM_at
TMEM19	1.38	transmembrane protein 19	2.78E-02	226860_PM_at
TMEM47	2.01	transmembrane protein 47	9.44E-03	209656_PM_s_at
TMEM54	1.36	transmembrane protein 54	3.88E-02	225536_PM_at
TMEM79	1.87	transmembrane protein 79	3.77E-04	223544_PM_at
TMEM86A	1.73	transmembrane protein 86A	2.46E-02	242103_PM_at
TMPRSS13	1.56	transmembrane protease, serine 13	1.56E-02	223659_PM_at
TMTC1	6.29	transmembrane and tetratricopeptide repeat containing 1	2.34E-04	226322_PM_at
TNIP1	1.70	TNFAIP3 interacting protein 1	1.38E-02	243423_PM_at
TPD52L1	1.78	tumor protein D52-like 1	1.83E-03	210372_PM_s_at
TPM1	1.42	Tropomyosin 1 (alpha)	4.30E-02	210987_PM_x_at
TPRG1L	1.28	tumor protein p63 regulated 1-like	3.74E-02	224871_PM_at
TPST1	2.29	tyrosylprotein sulfotransferase 1	8.01E-03	204140_PM_at
TRAM1L1	1.32	translocation associated membrane protein 1-like 1	3.84E-02	244334_PM_at
TRDMT1	1.24	tRNA aspartic acid methyltransferase 1	3.08E-02	206308_PM_at
TRIM14	1.95	tripartite motif-containing 14	6.25E-03	203147_PM_s_at
TRIM29	1.53	tripartite motif-containing 29	5.46E-03	202504_PM_at
TRIM59	1.58	tripartite motif-containing 59	1.93E-02	235476_PM_at
TRIM6	1.74	tripartite motif-containing 6	2.09E-03	223599_PM_at
TRPS1	1.58	trichorhinophalangeal syndrome I	2.94E-02	224218_PM_s_at
TSPAN9	1.24	tetraspanin 9	4.51E-02	220968_PM_s_at
TSTA3	1.22	tissue specific transplantation antigen P35B	2.52E-02	36936_PM_at
TTC39A	1.58	tetratricopeptide repeat domain 39A	2.50E-02	210652_PM_s_at
TTC39B	1.31	tetratricopeptide repeat domain 39B	1.58E-02	232000_PM_at
TTC39C	1.45	tetratricopeptide repeat domain 39C	2.45E-02	238480_PM_at
TTL12	1.24	tubulin tyrosine ligase-like family, member 12	4.34E-02	216251_PM_s_at
TLL7	1.50	tubulin tyrosine ligase-like family, member 7	2.48E-02	219882_PM_at
TTYH2	1.55	tweety homolog 2 (Drosophila)	9.78E-03	223741_PM_s_at
TUBB2A	1.48	tubulin, beta 2A	3.82E-02	204141_PM_at
UBAC1	1.29	UBA domain containing 1	2.77E-02	202151_PM_s_at
UNG	1.33	uracil-DNA glycosylase	2.02E-02	202330_PM_s_at
URGCP	1.35	upregulator of cell proliferation	3.71E-02	244046_PM_at
UROS	1.27	uroporphyrinogen III synthase	3.15E-02	203031_PM_s_at
USP11	1.20	ubiquitin specific peptidase 11	4.65E-02	208723_PM_at
USP13	1.85	ubiquitin specific peptidase 13 (isopeptidase T-3)	6.57E-04	205356_PM_at
USP40	1.55	ubiquitin specific peptidase 40	6.98E-03	225089_PM_at

		UTP14, U3 small nucleolar ribonucleoprotein, homolog A		
UTP14A	1.34	(yeast)	4.39E-02	221514_PM_at
VANGL1	1.47	vang-like 1 (van gogh, Drosophila)	2.31E-02	229134_PM_at
VDR	1.44	Vitamin D (1,25- dihydroxyvitamin D3) receptor	1.23E-02	204254_PM_s_at
VGLL3	1.99	vestigial like 3 (Drosophila)	9.49E-04	227399_PM_at
VIPR1	1.84	vasoactive intestinal peptide receptor 1	4.39E-03	205019_PM_s_at
VNN1	2.60	vanin 1	1.25E-02	205844_PM_at
VPS36	1.32	vacuolar protein sorting 36 homolog (S. cerevisiae)	9.23E-03	222478_PM_at
WDR41	1.32	WD repeat domain 41	1.82E-02	218055_PM_s_at
WDR55	1.26	WD repeat domain 55	4.83E-02	219809_PM_at
WDR63	1.41	WD repeat domain 63	3.81E-02	243087_PM_at
WDR91	1.42	WD repeat domain 91	3.42E-02	218971_PM_s_at
WFDC12	3.84	WAP four-disulfide core domain 12	7.74E-03	1553081_PM_at
WFDC5	3.65	WAP four-disulfide core domain 5	5.78E-03	242204_PM_at
WNT5A	3.45	Wingless-type MMTV integration site family, member 5A	6.14E-03	213425_PM_at
XAF1	4.20	XIAP associated factor 1	4.76E-02	228617_PM_at
XG	3.70	Xg blood group	2.32E-03	1554062_PM_at
XYLT1	1.67	xylosyltransferase I	2.78E-03	213725_PM_x_at
ZAK	1.59	sterile alpha motif and leucine zipper containing kinase AZK	1.09E-03	222757_PM_s_at
ZBED1	1.30	zinc finger, BED-type containing 1	2.56E-02	203043_PM_at
ZFP42	2.06	zinc finger protein 42 homolog (mouse)	5.31E-03	243161_PM_x_at
ZHX1	1.36	zinc fingers and homeoboxes 1	2.48E-02	223213_PM_s_at
ZNF10	1.39	zinc finger protein 10	1.26E-02	235366_PM_at
ZNF114	1.26	zinc finger protein 114	3.83E-02	1552946_PM_at
ZNF12	1.28	zinc finger protein 12	3.19E-02	226015_PM_at
ZNF226	1.35	zinc finger protein 226	2.67E-02	233461_PM_x_at
ZNF232	1.31	zinc finger protein 232	2.88E-02	219123_PM_at
ZNF235	1.30	zinc finger protein 235	2.63E-02	220350_PM_at
ZNF253	1.27	zinc finger protein 253	2.21E-02	206900_PM_x_at
ZNF30	1.68	zinc finger protein 30	4.39E-03	232014_PM_at
ZNF300	1.48	zinc finger protein 300	9.05E-03	228144_PM_at
ZNF311	1.46	zinc finger protein 311	6.79E-03	236551_PM_at
ZNF32	1.23	zinc finger protein 32	4.23E-02	209538_PM_at
ZNF320	1.44	zinc finger protein 320	2.31E-02	229614_PM_at
ZNF331	1.44	zinc finger protein 331	6.15E-03	227613_PM_at
ZNF362	1.87	zinc finger protein 362	3.87E-03	226820_PM_at
ZNF436	1.28	zinc finger protein 436	2.50E-02	226113_PM_at
ZNF44	1.48	zinc finger protein 44	2.18E-02	228718_PM_at
ZNF471	1.37	zinc finger protein 471	2.75E-02	232117_PM_at
ZNF506	1.36	zinc finger protein 506	5.57E-03	238493_PM_at
ZNF567	1.33	zinc finger protein 567	1.24E-02	242429_PM_at
ZNF606	1.26	zinc finger protein 606	4.84E-02	219635_PM_at
ZNF615	1.35	zinc finger protein 615	2.66E-02	241827_PM_at
ZNF618	1.23	zinc finger protein 618	4.43E-02	226592_PM_at
ZNF626	1.32	zinc finger protein 626	4.12E-02	1552643_PM_at
ZNF642	1.27	zinc finger protein 642	3.32E-02	1569107_PM_s_at
ZNF667	1.84	zinc finger protein 667	1.18E-02	236635_PM_at
ZNF70	1.34	Zinc finger protein 70	3.13E-02	243816_PM_at
ZNF706	1.26	zinc finger protein 706	4.97E-02	227132_PM_at
ZNF770	1.38	zinc finger protein 770	1.11E-02	225517_PM_at
ZNF813	1.45	zinc finger protein 813	2.50E-02	217665_PM_at
ZNF827	1.39	Zinc finger protein 827	9.28E-03	228046_PM_at
ZNF879	1.46	zinc finger protein 879	2.75E-02	230421_PM_at
ZNF883	1.91	zinc finger protein 883	2.31E-03	230876_PM_at

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171 Given are abbreviation (Gene alias), fold change (FC), short description (Gene

172 name/description), P-value, and probe ID (Gene ID).

Table S4. Genes that were significantly higher expressed by bronchial epithelial cells from patients with allergic rhinitis.

Gene alias	FC	Gene name/description	P-value	Gene ID
ABCG1	4.20	ATP-binding cassette, sub-family G (WHITE), member 1	2.70E-02	204567_PM_s_at
ABLM3	6.36	actin binding LIM protein family, member 3	3.03E-02	205730_PM_s_at
AFAP1L1	2.10	actin filament associated protein 1-like 1	3.87E-02	226955_PM_at
AHNAK	2.05	AHNAK nucleoprotein	4.82E-02	220016_PM_at
ANKRD9	1.77	ankyrin repeat domain 9	2.57E-02	230972_PM_at
ARG2	2.12	arginase, type II	4.81E-02	203945_PM_at
ASAP1	1.57	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	4.40E-02	236533_PM_at
ATL1	2.00	atlastin GTPase 1	1.60E-02	223340_PM_at
ATP12A	25.66	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	3.82E-02	207367_PM_at
ATP2C2	6.02	ATPase, Ca++ transporting, type 2C, member 2	4.60E-02	206043_PM_s_at
C10orf47	1.76	chromosome 10 open reading frame 47	4.60E-02	230051_PM_at
C11orf17 /// NUAKE2	1.70	chromosome 11 open reading frame 17 /// NUAKE family, SNF1-like kinase, 2	1.65E-02	220987_PM_s_at
C14orf139	3.15	chromosome 14 open reading frame 139	4.81E-02	219563_PM_at
C14orf34	2.05	chromosome 14 open reading frame 34	1.64E-02	1555786_PM_s_at
C1orf133	2.15	chromosome 1 open reading frame 133	3.74E-02	230121_PM_at
C4orf10	1.74	chromosome 4 open reading frame 10	2.43E-02	214123_PM_s_at
CALML4	2.66	calmodulin-like 4	2.92E-02	221879_PM_at
CAMK2N1	2.35	calcium/calmodulin-dependent protein kinase II inhibitor 1	3.61E-02	229163_PM_at
CAPS	1.72	calcyphosine	3.48E-02	226424_PM_at
CDH26	9.65	cadherin 26	1.38E-02	233663_PM_s_at
CDKN1C	3.63	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	4.08E-02	219534_PM_x_at
CEACAM1	2.97	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	3.03E-02	211883_PM_x_at
CEACAM6	5.55	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	3.95E-02	211657_PM_at
CFLAR	2.31	CASP8 and FADD-like apoptosis regulator	1.38E-02	211317_PM_s_at
CMTM8	2.13	CKLF-like MARVEL transmembrane domain containing 8	2.08E-02	235099_PM_at
CXCL17	10.77	chemokine (C-X-C motif) ligand 17	4.58E-02	226960_PM_at
CXXC5	2.92	CXXC finger 5	3.74E-02	222996_PM_s_at
DAPP1	1.57	dual adaptor of phosphotyrosine and 3-phosphoinositides	3.85E-02	219290_PM_x_at
DCDC2	1.62	doublecortin domain containing 2	4.14E-02	222925_PM_at
DIDO1	1.50	death inducer-obliterator 1	3.91E-02	213213_PM_at
DLG1	1.75	Discs, large homolog 1 (Drosophila)	2.92E-02	217208_PM_s_at
DUSP1	3.26	dual specificity phosphatase 1	4.58E-02	201041_PM_s_at
ECM1	4.21	extracellular matrix protein 1	2.08E-02	209365_PM_s_at
EHF	1.81	ets homologous factor	3.63E-02	232360_PM_at
ELF5	7.61	E74-like factor 5 (ets domain transcription factor)	2.61E-02	220625_PM_s_at
ELK3	1.58	ELK3, ETS-domain protein (SRF accessory protein 2)	4.48E-02	206127_PM_at
EPHA2	1.95	EPH receptor A2	4.48E-02	203499_PM_at
EZR	1.72	ezrin	3.90E-02	208621_PM_s_at
FA2H	7.44	fatty acid 2-hydroxylase	4.52E-02	219429_PM_at
FAM107B	3.30	family with sequence similarity 107, member B	1.16E-02	223059_PM_s_at
FAM155B	2.46	family with sequence similarity 155, member B	4.13E-02	206299_PM_at
FGD4	1.54	FYVE, RhoGEF and PH domain containing 4	3.71E-02	227948_PM_at
FOXA1	3.31	forkhead box A1	3.14E-02	204667_PM_at
FOXD1	3.95	forkhead box D1	4.14E-02	206307_PM_s_at
FUT2	2.31	fucosyltransferase 2 (secretor status included)	1.60E-02	210608_PM_s_at
GALE	1.63	UDP-galactose-4-epimerase	3.72E-02	202528_PM_at
GDA	13.96	guanine deaminase	4.12E-02	224209_PM_s_at
GIT2	1.78	G protein-coupled receptor kinase interacting ArfGAP 2	3.85E-02	204982_PM_at
GLB1L3	2.33	galactosidase, beta 1-like 3	3.74E-02	1569886_PM_a_at
GLRX	4.14	glutaredoxin (thioltransferase)	2.68E-02	209276_PM_s_at
GNRH1	1.53	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	4.58E-02	235540_PM_at
GPRC5A	3.41	G protein-coupled receptor, family C, group 5, member A	1.83E-02	203108_PM_at
HERPUD2	1.70	HERPUD family member 2	4.14E-02	1552628_PM_a_at
HES4	1.77	hair cell enhancer of split 4 (Drosophila)	3.14E-02	227347_PM_x_at
HEY1	5.27	hair cell enhancer-of-split related with YRPW motif 1	3.59E-02	44783_PM_s_at
IDS	1.66	iduronate 2-sulfatase	4.60E-02	206342_PM_x_at
IL1RL1	9.14	interleukin 1 receptor-like 1	4.48E-02	242809_PM_at
IL1RN	3.62	interleukin 1 receptor antagonist	4.81E-02	216244_PM_at
INADL	2.04	InaD-like (Drosophila)	1.38E-02	239173_PM_at
IRS1	1.78	insulin receptor substrate 1	4.42E-02	242979_PM_at
ISG20	3.69	interferon stimulated exonuclease gene 20kDa	3.51E-02	204698_PM_at
KIAA1199	2.52	KIAA1199	1.60E-02	212942_PM_s_at
KRT18	1.91	keratin 18	2.92E-02	201596_PM_x_at
LMO7	4.94	LIM domain 7	4.60E-02	242722_PM_at

LOC100129406	1.68	hypothetical protein LOC100129406	4.14E-02	240868_PM_at
LOC100130938	2.31	hypothetical LOC100130938	3.74E-02	230574_PM_at
LOC100294402 /// SIGIRR	1.68	similar to single Ig IL-1R-related molecule /// single		
LOC284454	1.64	immunoglobulin and toll-interleukin 1 receptor (TIR) domain	4.29E-02	52940_PM_at
LOC440335	1.64	hypothetical protein LOC284454	3.75E-02	1555847_PM_a_at
LRRFIP1	2.25	hypothetical LOC440335	1.60E-02	229599_PM_at
	1.65	leucine rich repeat (in FLII) interacting protein 1	2.92E-02	227513_PM_s_at
MAFF	1.91	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	4.29E-02	205193_PM_at
MAFK	1.94	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	2.20E-02	226206_PM_at
MAL	9.05	mal, T-cell differentiation protein	2.92E-02	204777_PM_s_at
MALAT1	2.95	Metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	4.99E-02	228582_PM_x_at
MAP3K9	2.49	mitogen-activated protein kinase kinase kinase 9	4.82E-02	213927_PM_at
MAPK13	2.09	mitogen-activated protein kinase 13	1.60E-02	210058_PM_at
MIB2	2.11	Mindbomb homolog 2 (Drosophila)	3.98E-02	228261_PM_at
MITF	1.88	microphthalmia-associated transcription factor	1.60E-02	207233_PM_s_at
MLPH	2.27	melanophilin	4.99E-02	218211_PM_s_at
MYO5C	3.42	myosin VC	3.10E-02	218966_PM_at
NCF2	3.64	neutrophil cytosolic factor 2	4.48E-02	209949_PM_at
NLRP1	2.46	NLR family, pyrin domain containing 1	4.87E-02	210113_PM_s_at
NT5E	2.15	5'-nucleotidase, ecto (CD73)	1.83E-02	227486_PM_at
PADI1	8.60	peptidyl arginine deiminase, type I	3.51E-02	223739_PM_at
PCDH7	4.10	protocadherin 7	3.75E-02	228640_PM_at
PDCD5	1.69	programmed cell death 5	4.14E-02	227751_PM_at
PHACTR3	21.25	phosphatase and actin regulator 3	1.29E-02	227949_PM_at
PIK3C2A	1.52	Phosphoinositide-3-kinase, class 2, alpha polypeptide	2.92E-02	1569022_PM_a_at
PLAG1	2.37	pleiomorphic adenoma gene 1	1.60E-02	205372_PM_at
PLCB4	1.89	Phospholipase C, beta 4	3.74E-02	203896_PM_s_at
PLEKHG5	1.79	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	3.74E-02	227142_PM_at
PTGER4	1.88	prostaglandin E receptor 4 (subtype EP4)	2.69E-02	204897_PM_at
PTK6	5.20	PTK6 protein tyrosine kinase 6	1.38E-02	1553114_PM_a_at
QSOX1	1.99	quiescin Q6 sulfhydryl oxidase 1	4.52E-02	201482_PM_at
RASAL2	1.59	RAS protein activator like 2	2.92E-02	227036_PM_at
RASSF6	1.95	Ras association (RalGDS/AF-6) domain family member 6	1.83E-02	233463_PM_at
RGS12	1.53	regulator of G-protein signaling 12	3.04E-02	209637_PM_s_at
RHBDL2	2.38	rhomboid, veinlet-like 2 (Drosophila)	1.60E-02	1552502_PM_s_at
RIT1	1.48	Ras-like without CAAX 1	3.74E-02	243463_PM_s_at
RORA	3.29	RAR-related orphan receptor A	3.44E-02	210479_PM_s_at
RUNX2	2.50	runt-related transcription factor 2	2.88E-02	232231_PM_at
SDCBP2	3.58	syndecan binding protein (syntenin) 2	2.43E-02	233565_PM_s_at
SDR16C5	2.54	short chain dehydrogenase/reductase family 16C, member 5	2.20E-02	238017_PM_at
SEL1L3	1.42	Sel-1 suppressor of lin-12-like 3 (C. elegans)	4.99E-02	212314_PM_at
SEMA3A	2.36	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	1.60E-02	206805_PM_at
SERTAD4	3.22	SERTA domain containing 4	2.08E-02	230660_PM_at
SFRS12IP1	1.85	SFRS12-interacting protein 1	2.43E-02	235390_PM_at
SHANK2	3.43	SH3 and multiple ankyrin repeat domains 2	1.60E-02	213308_PM_at
SLAMF9	2.73	SLAM family member 9	4.14E-02	1553769_PM_at
SLC44A4	1.90	solute carrier family 44, member 4	4.86E-02	205597_PM_at
SLC4A11	2.54	solute carrier family 4, sodium borate transporter, member 11	1.60E-02	223748_PM_at
SRPX2	4.05	sushi-repeat-containing protein, X-linked 2	2.58E-02	205499_PM_at
SSFA2	2.52	Sperm specific antigen 2	2.68E-02	236207_PM_at
SSH3	1.60	slingshot homolog 3 (Drosophila)	4.14E-02	219241_PM_x_at
ST3GAL1	1.66	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	3.38E-02	225033_PM_at
STK17B	2.76	serine/threonine kinase 17b	1.60E-02	205214_PM_at
TANC2	1.87	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	3.22E-02	208425_PM_s_at
TC2N	1.51	tandem C2 domains, nuclear	4.99E-02	234970_PM_at
TEAD3	1.60	TEA domain family member 3	4.14E-02	209454_PM_s_at
TMC6	1.68	transmembrane channel-like 6	4.40E-02	204328_PM_at
TMEM191A	1.63	transmembrane protein 191A	3.67E-02	223628_PM_at
TMEM40	1.66	transmembrane protein 40	2.68E-02	222892_PM_s_at
TMEM61	1.79	transmembrane protein 61	2.68E-02	230822_PM_at
TMPPRSS11D	4.66	transmembrane protease, serine 11D	2.08E-02	207602_PM_at
TPCN1	2.10	two pore segment channel 1	4.59E-02	217914_PM_at
TPPP	1.87	Tubulin polymerization promoting protein	4.60E-02	230104_PM_s_at
TRIB1	2.29	Tribbles homolog 1 (Drosophila)	3.54E-02	202241_PM_at
TTBK2	1.62	Tau tubulin kinase 2	4.36E-02	231610_PM_at
TTC9	4.96	tetratricopeptide repeat domain 9	4.98E-02	213172_PM_at
VLDLR	2.20	very low density lipoprotein receptor	4.14E-02	209822_PM_s_at
VWF	1.88	von Willebrand factor	4.38E-02	202112_PM_at
WSB1	5.82	WD repeat and SOCS box-containing 1	1.83E-02	201294_PM_s_at
ZBED2	2.71	zinc finger, BED-type containing 2	1.60E-02	219836_PM_at

ZBTB34	1.46	zinc finger and BTB domain containing 34	4.66E-02	227111_PM_at
ZBTB38	1.48	zinc finger and BTB domain containing 38	4.87E-02	236557_PM_at
ZDHHC2	1.73	zinc finger, DHHC-type containing 2	3.74E-02	222730_PM_s_at
ZFAND6	1.71	Zinc finger, AN1-type domain 6	1.83E-02	222186_PM_at
ZNF655	1.99	zinc finger protein 655	3.32E-02	223302_PM_s_at

175

176 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*

177 *name/description), P-value, and probe ID (Gene ID).*

Table S5. Genes that were significantly higher expressed by nasal epithelial cells from patients with allergic rhinitis.

Gene alias	FC	Gene name/description	P-value	Gene ID
AEBP1	4.95	AE binding protein 1	2.00E-02	201792_PM_at
ANTXR1	2.13	Anthrax toxin receptor 1	4.52E-02	220092_PM_s_at
ANXA6	5.04	annexin A6	1.66E-02	200982_PM_s_at
ARHGAP18	2.69	Rho GTPase activating protein 18	2.82E-02	225171_PM_at
ARSI	3.04	arylsulfatase family, member I	1.16E-02	230275_PM_at
ARV1	1.52	ARV1 homolog (S. cerevisiae)	3.78E-02	223223_PM_at
ATP1A1	1.50	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	4.13E-02	220948_PM_s_at
BCAT1	3.10	branched chain amino-acid transaminase 1, cytosolic	1.60E-02	226517_PM_at
BCKDHB	2.05	branched chain keto acid dehydrogenase E1, beta polypeptide	2.08E-02	210653_PM_s_at
BCL11A	1.52	B-cell CLL/lymphoma 11A (zinc finger protein)	4.60E-02	219497_PM_s_at
BCL11B	1.94	B-cell CLL/lymphoma 11B (zinc finger protein)	3.91E-02	222895_PM_s_at
BEX1	5.33	brain expressed, X-linked 1	4.14E-02	218332_PM_at
BVES	3.39	blood vessel epicardial substance	2.61E-02	228783_PM_at
C16orf5	1.89	chromosome 16 open reading frame 5	3.15E-02	223960_PM_s_at
C18orf10	1.59	chromosome 18 open reading frame 10	4.58E-02	212055_PM_at
C1orf124	1.57	chromosome 1 open reading frame 124	4.56E-02	223511_PM_at
C1orf38	2.07	chromosome 1 open reading frame 38	2.88E-02	207571_PM_x_at
C1R	6.27	complement component 1, r subcomponent	2.70E-02	212067_PM_s_at
C1S	10.89	complement component 1, s subcomponent	1.50E-02	208747_PM_s_at
C21orf96	10.63	chromosome 21 open reading frame 96	3.90E-02	220918_PM_at
C3orf34	1.71	chromosome 3 open reading frame 34	4.66E-02	230860_PM_at
C4orf49	4.59	chromosome 4 open reading frame 49	4.85E-03	223734_PM_at
C5orf62	2.62	chromosome 5 open reading frame 62	1.60E-02	223276_PM_at
C6orf114	1.64	chromosome 6 open reading frame 114	3.74E-02	1554486_PM_a_at
C6orf192	1.71	chromosome 6 open reading frame 192	2.88E-02	226301_PM_at
		caspase recruitment domain family, member 16 /// caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	4.56E-02	1552703_PM_s_at
CARD16 /// CASP1	2.13	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.55E-02	206011_PM_at
CASP1	2.60	coiled-coil domain containing 15	4.29E-02	220466_PM_at
CCDC15	1.60	coiled-coil domain containing 8	4.63E-02	223496_PM_s_at
CCDC8	4.66	choline phosphotransferase 1	4.66E-02	230364_PM_at
CHPT1	1.89	claudin 11	2.92E-02	228335_PM_at
CLDN11	16.71	Collagen, type XII, alpha 1	3.90E-02	225664_PM_at
COL12A1	3.38	collagen, type IV, alpha 2	1.83E-02	211966_PM_at
COL4A2	3.56	Collagen, type VI, alpha 1	4.34E-02	213428_PM_s_at
COL6A1	11.49	carbamoyl-phosphate synthase 1, mitochondrial	2.38E-02	217564_PM_s_at
CPS1	2.75	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	3.72E-02	219913_PM_s_at
CRNKL1	1.48	chondroitin sulfate proteoglycan 4	8.30E-03	214297_PM_at
CSPG4	3.14	cytochrome b reductase 1	2.58E-02	222453_PM_at
CYBRD1	1.83	cytochrome c, somatic	3.08E-02	229415_PM_at
CYCS	1.91	cytochrome P450, family 26, subfamily B, polypeptide 1	2.41E-02	219825_PM_at
CYP26B1	5.20	deleted in bladder cancer 1	3.22E-02	205818_PM_at
DBC1	4.11	DEP domain containing 7	2.88E-02	228293_PM_at
DEPDC7	4.99	dystrophin	4.14E-02	203881_PM_s_at
DMD	1.86	DnaJ (Hsp40) homolog, subfamily B, member 4	4.14E-02	203811_PM_s_at
DNAJB4	1.75	DNA (cytosine-5-)-methyltransferase 3 beta	2.18E-02	220668_PM_s_at
DNMT3B	1.70	dystonin	3.74E-02	212254_PM_s_at
DST	2.01	deoxyuridine triphosphatase	4.58E-02	208955_PM_at
DUT	1.83	DAZ interacting protein 1	4.25E-02	204557_PM_s_at
DZIP1	2.91	DAZ interacting protein 3, zinc finger	4.58E-02	213186_PM_at
DZIP3	1.61	enoyl CoA hydratase domain containing 1	4.59E-02	223087_PM_at
ECHDC1	1.49	EGF-like-domain, multiple 6	3.22E-02	219454_PM_at
EGFL6	6.20	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	2.80E-02	228260_PM_at
ELAVL2	13.23	family with sequence similarity 110, member B	4.48E-02	228790_PM_at
FAM110B	1.53	family with sequence similarity 120C	4.48E-02	229512_PM_at
FAM120C	1.69	family with sequence similarity 198, member B	1.10E-03	223204_PM_at
FAM198B	4.47	fibroblast activation protein, alpha	1.60E-02	209955_PM_s_at
FAP	12.99	FAT tumor suppressor homolog 2 (Drosophila)	2.43E-02	208153_PM_s_at
FAT2	2.12	fibroblast growth factor receptor 2	3.71E-02	203639_PM_s_at
FGFR2	2.28	FK506 binding protein 10, 65 kDa	4.14E-02	219249_PM_s_at
FKBP10	1.83	hypothetical FLJ13744	4.46E-02	1553413_PM_at
FLJ13744	2.70	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	1.83E-02	239058_PM_at
FOXC2	2.13	FERM domain containing 4A	3.52E-02	225167_PM_at
FRMD4A	2.12	fragile X mental retardation, autosomal homolog 1	4.63E-02	201635_PM_s_at
FXR1	1.74	frizzled homolog 2 (Drosophila)	2.43E-02	210220_PM_at
FZD2	1.90			

GALNT5	1.62	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	4.08E-02	236129_PM_at
GAS1	11.22	growth arrest-specific 1	2.57E-02	204457_PM_s_at
GDAP1	2.30	ganglioside-induced differentiation-associated protein 1	4.14E-02	226269_PM_at
GGA2	1.63	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	4.63E-02	208913_PM_at
GLI3	1.65	GLI family zinc finger 3	3.79E-02	227376_PM_at
GLIPR2	2.84	GLI pathogenesis-related 2	2.08E-02	225604_PM_s_at
GLT8D2	3.08	glycosyltransferase 8 domain containing 2	4.24E-03	221447_PM_s_at
GPR85	2.71	G protein-coupled receptor 85	4.52E-02	234303_PM_s_at
GXYLT2	1.95	glucoside xylosyltransferase 2	4.56E-02	235371_PM_at
HFE	1.75	hemochromatosis	2.61E-02	235754_PM_at
HMGN3	2.33	high mobility group nucleosomal binding domain 3	3.74E-02	209377_PM_s_at
HSPA12A	2.21	heat shock 70kDa protein 12A	1.60E-02	214434_PM_at
HSPA4	1.67	heat shock 70kDa protein 4	4.14E-02	208814_PM_at
IFT74	1.70	intraflagellar transport 74 homolog (Chlamydomonas)	4.56E-02	219174_PM_at
IL24	2.56	interleukin 24	1.64E-02	206569_PM_at
IPO4	1.43	importin 4	4.29E-02	218305_PM_at
JAM3	8.70	junctional adhesion molecule 3	4.19E-03	212813_PM_at
KANK4	11.55	KN motif and ankyrin repeat domains 4	3.12E-02	229125_PM_at
KDEL1	2.28	KDEL (Lys-Asp-Glu-Leu) containing 1	1.60E-02	219479_PM_at
KRT75	2.41	keratin 75	3.78E-02	207065_PM_at
L1TD1	5.21	LINE-1 type transposase domain containing 1	2.16E-02	219955_PM_at
LCP1	7.96	lymphocyte cytosolic protein 1 (L-plastin)	8.46E-03	208885_PM_at
LIF	2.19	leukemia inhibitory factor (cholinergic differentiation factor)	4.33E-02	205266_PM_at
LOC100127983	1.83	hypothetical protein LOC100127983	4.80E-02	228107_PM_at
LOC100132891	4.06	hypothetical protein LOC100132891	3.03E-02	228438_PM_at
LOC642852	2.02	hypothetical LOC642852	2.20E-02	226995_PM_at
LOC653501 /// ZNF658 ///		zinc finger protein 658 pseudogene /// zinc finger protein 658		
ZNF658B	2.35	/// zinc finger protein 658B	3.44E-02	231950_PM_at
MDM1	2.28	Mdm1 nuclear protein homolog (mouse)	4.82E-02	213761_PM_at
MEOX1	2.26	mesenchyme homeobox 1	3.22E-02	205619_PM_s_at
MGC21881	1.56	hypothetical locus MGC21881	4.66E-02	228040_PM_at
MMP28	2.09	matrix metalloproteinase 28	3.74E-02	219909_PM_at
MRC2	2.56	Mannose receptor, C type 2	3.03E-02	37408_PM_at
MTUS1	1.80	microtubule associated tumor suppressor 1	2.70E-02	212095_PM_s_at
MYLK	11.94	myosin light chain kinase	1.64E-02	202555_PM_s_at
NAP1L5	3.29	nucleosome assembly protein 1-like 5	1.85E-02	228062_PM_at
NAPEPLD	1.74	N-acyl phosphatidylethanolamine phospholipase D	4.46E-02	226041_PM_at
NNMT	14.31	nicotinamide N-methyltransferase	6.85E-03	202237_PM_at
NPL	1.58	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	2.88E-02	223405_PM_at
NQO1	1.59	NAD(P)H dehydrogenase, quinone 1	4.89E-02	201468_PM_s_at
OSGEPL1	1.58	O-sialoglycoprotein endopeptidase-like 1	3.74E-02	220631_PM_at
PAX3	4.64	paired box 3	1.60E-02	231666_PM_at
PCLO	1.83	piccolo (presynaptic cytomatrix protein)	4.56E-02	213558_PM_at
PHOSPHO2	1.72	phosphatase, orphan 2	3.08E-02	230434_PM_at
PI15	1.95	peptidase inhibitor 15	2.82E-02	229947_PM_at
PLAT	12.97	plasminogen activator, tissue	2.08E-02	201860_PM_s_at
PLEKHF2	1.46	pleckstrin homology domain containing, family F (with FYVE domain) member 2	4.59E-02	222699_PM_s_at
PLSCR4	2.47	phospholipid scramblase 4	2.48E-02	218901_PM_at
POLR3G	2.45	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	4.85E-02	206653_PM_at
PRICKLE2	3.42	prickle homolog 2 (Drosophila)	1.83E-02	225968_PM_at
PTGS1	1.86	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1.60E-02	215813_PM_s_at
PURB	1.64	purine-rich element binding protein B	4.14E-02	226762_PM_at
RAD50	1.64	RAD50 homolog (S. cerevisiae)	3.08E-02	209349_PM_at
RAD54B	1.79	RAD54 homolog B (S. cerevisiae)	4.66E-02	219494_PM_at
RBM43	2.22	RNA binding motif protein 43	4.08E-02	228304_PM_at
RUNDC3B	1.56	RUN domain containing 3B	4.52E-02	215321_PM_at
SCARB1	2.15	scavenger receptor class B, member 1	2.48E-02	201819_PM_at
SELM	2.32	selenoprotein M	3.90E-02	226051_PM_at
SEPX1	1.49	selenoprotein X, 1	4.99E-02	217977_PM_at
SERPINH1	2.46	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	1.64E-02	207714_PM_s_at
SFRP1	5.58	secreted frizzled-related protein 1	2.00E-02	202036_PM_s_at
SGCE	2.09	sarcoglycan, epsilon	1.60E-02	204688_PM_at
SIX3	6.47	SIX homeobox 3	2.88E-02	206634_PM_at
SLC1A3	3.05	solute carrier family 1 (glial high affinity glutamate transporter), member 3	4.59E-02	202800_PM_at
SLC25A20	1.71	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	3.44E-02	203658_PM_at
SLC35D1	1.71	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	2.68E-02	209712_PM_at
SLC39A14	1.97	solute carrier family 39 (zinc transporter), member 14	4.30E-02	212110_PM_at

SLC39A6	1.57	solute carrier family 39 (zinc transporter), member 6	2.68E-02	202089_PM_s_at
SLC5A6	1.70	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	4.59E-02	204087_PM_s_at
SLCO3A1	1.58	solute carrier organic anion transporter family, member 3A1	3.22E-02	227367_PM_at
SNHG5 /// SNORD50A ///		small nucleolar RNA host gene 5 (non-protein coding) ///		
SNORD50B	1.95	small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	1.83E-02	244669_PM_at
SP110	1.74	SP110 nuclear body protein	3.34E-02	208392_PM_x_at
SPARC	4.22	secreted protein, acidic, cysteine-rich (osteonectin)	3.51E-02	200665_PM_s_at
SRD5A1	1.98	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	1.83E-02	210959_PM_s_at
SRPRB	1.51	signal recognition particle receptor, B subunit	3.92E-02	222532_PM_at
STAT1	1.77	signal transducer and activator of transcription 1, 91kDa	3.06E-02	AFFX-5_5_at
STEAP3	1.51	STEAP family member 3	3.85E-02	HUMISGF3A/M9793
SUB1	1.80	SUB1 homolog (S. cerevisiae)	2.66E-02	218424_PM_s_at
SYNM	3.01	synemin, intermediate filament protein	3.10E-02	221727_PM_at
TAF15	1.66	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	3.15E-02	212730_PM_at
TCF7L2	1.81	transcription factor 7-like 2 (T-cell specific, HMG-box)	2.00E-02	202840_PM_at
TCOF1	1.78	Treacher Collins-Franceschetti syndrome 1	2.66E-02	212761_PM_at
THBS2	6.82	thrombospondin 2	2.66E-02	202385_PM_s_at
THY1	18.03	Thy-1 cell surface antigen	3.08E-02	203083_PM_at
TLR1	2.42	toll-like receptor 1	4.63E-04	208850_PM_s_at
TMEM5	1.68	transmembrane protein 5	3.74E-02	210176_PM_at
TNIP1	2.02	TNFAIP3 interacting protein 1	3.74E-02	204807_PM_at
TRIM59	2.59	tripartite motif-containing 59	3.10E-02	243423_PM_at
TRIM69	1.93	tripartite motif-containing 69	1.60E-02	235476_PM_at
USP13	2.38	ubiquitin specific peptidase 13 (isopeptidase T-3)	3.22E-02	1568592_PM_at
VGLL3	1.95	vestigial like 3 (Drosophila)	3.10E-02	205356_PM_at
WDR67	2.02	WD repeat domain 67	4.13E-02	220327_PM_at
ZMAT3	1.60	zinc finger, matrin type 3	3.74E-02	214061_PM_at
ZNF124	2.20	zinc finger protein 124	3.63E-02	1555609_PM_a_at
ZNF30	1.73	zinc finger protein 30	3.22E-02	206928_PM_at
ZNF300	2.03	zinc finger protein 300	4.48E-02	232014_PM_at
ZNF362	1.95	zinc finger protein 362	4.29E-02	228144_PM_at
ZNF37A	1.59	zinc finger protein 37A	4.14E-02	226820_PM_at
ZNF827	1.95	Zinc finger protein 827	2.88E-02	228711_PM_at
ZNF879	1.86	Zinc finger protein 879	4.14E-02	228046_PM_at
			2.82E-02	230421_PM_at

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181 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*182 *name/description), P-value, and probe ID (Gene ID).*

183 **Table S6.** Genes that were significantly higher expressed by bronchial epithelial cells from
 184 patients with allergic rhinitis and asthma.

Gene alias	FC	Gene name/description	P-value	Gene ID
AKAP12	7.37	A kinase (PRKA) anchor protein 12	4.74E-02	227530_PM_at
BST2	3.29	bone marrow stromal cell antigen 2	4.74E-02	201641_PM_at
C16orf45	1.73	Chromosome 16 open reading frame 45	4.35E-02	212736_PM_at
C1orf133	2.36	chromosome 1 open reading frame 133	1.60E-02	230121_PM_at
CHST9	2.53	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	4.54E-02	223737_PM_x_at
DPYSL3	1.86	dihydropyrimidinase-like 3	4.54E-02	201431_PM_s_at
FOXA2	1.68	forkhead box A2	3.33E-02	210103_PM_s_at
FOXE1	3.63	forkhead box E1 (thyroid transcription factor 2)	4.74E-02	206912_PM_at
FUT2	1.87	fucosyltransferase 2 (secretor status included)	3.28E-02	208505_PM_s_at
GSN	1.71	Gelsolin (amyloidosis, Finnish type)	2.97E-02	214040_PM_s_at
HOXA1	2.61	homeobox A1	2.78E-02	214639_PM_s_at
IL33	3.39	interleukin 33	4.54E-02	209821_PM_at
JAK2	1.84	Janus kinase 2	4.73E-02	205842_PM_s_at
NCF2	2.67	neutrophil cytosolic factor 2	4.54E-02	209949_PM_at
NLRP1	2.24	NLR family, pyrin domain containing 1	4.74E-02	211822_PM_s_at
PCDH7	2.61	protocadherin 7	1.16E-02	205535_PM_s_at
PLCB1	2.24	phospholipase C, beta 1 (phosphoinositide-specific)	1.16E-02	213222_PM_at
PSD3	1.59	pleckstrin and Sec7 domain containing 3	4.14E-02	218613_PM_at
RIMS2	2.16	regulating synaptic membrane exocytosis 2	4.70E-02	206137_PM_at
SERTAD4	2.52	SERTA domain containing 4	4.54E-02	230660_PM_at
SKAP2	2.74	Src kinase associated phosphoprotein 2	3.28E-02	204361_PM_s_at
SPDEF	5.31	SAM pointed domain containing ets transcription factor ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-	1.16E-02	220192_PM_x_at
ST6GALNAC1	9.13	acetylgalactosaminide alpha-2,6-sialyltransferase 1	1.16E-02	227725_PM_at
STOM	1.67	stomatin	4.74E-02	201061_PM_s_at
TSPAN1	4.74	tetraspanin 1	4.54E-02	209114_PM_at

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186 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*

187 *name/description), P-value, and probe ID (Gene ID).*

188 **Table S7.** Genes that were significantly higher expressed by nasal epithelial cells from
 189 patients with allergic rhinitis and asthma.

Gene alias	FC	Gene name/description	P-value	Gene ID
AHI1	1.71	Abelson helper integration site 1	4.54E-02	221569_PM_at
ARMCX1	1.74	armadillo repeat containing, X-linked 1	3.01E-02	218694_PM_at
C1orf38	2.05	chromosome 1 open reading frame 38	4.54E-02	210785_PM_s_at
CTSC	2.10	cathepsin C	3.30E-02	225646_PM_at
ELAVL2	3.83	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	4.74E-02	208427_PM_s_at
GLIPR2	1.87	GLI pathogenesis-related 2	4.74E-02	225604_PM_s_at
HR	2.41	hairless homolog (mouse)	3.20E-02	241355_PM_at
IL13RA2	9.72	interleukin 13 receptor, alpha 2	4.54E-02	206172_PM_at
IL1R2	3.15	interleukin 1 receptor, type II	4.14E-02	211372_PM_s_at
IRX4	15.72	iroquois homeobox 4	4.54E-02	220225_PM_at
PLA2G4A	2.11	phospholipase A2, group IVA (cytosolic, calcium-dependent)	4.74E-02	210145_PM_at
PNMAL1	2.28	PNMA-like 1	4.74E-02	218824_PM_at
SELM	2.87	selenoprotein M	1.16E-02	226051_PM_at
TBC1D4	1.85	TBC1 domain family, member 4	4.54E-02	203387_PM_s_at
VGLL3	2.34	vestigial like 3 (Drosophila)	4.54E-02	227399_PM_at

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191 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*
 192 *name/description), P-value, and probe ID (Gene ID).*

193 **Table S8.** Genes that were significantly higher expressed by healthy bronchial epithelial cells
 194 sorted by ontology analysis in functional groups.

Gene alias	FC	Gene name/description	P-value	Gene ID
<i>receptor activity</i>				
HLA-DQB1	4.34	major histocompatibility complex, class II, DQ beta 1	4.66E-04	209480_PM_at
HLA-DQB1 /// HLA-DQB2		<i>major histocompatibility complex, class II, DQ family</i>		
/// LOC100294318	2.29		1.09E-02	212999_PM_x_at
HLA-DQB1 ///		major histocompatibility complex, class II, DQ beta 1		
LOC100294318	3.97		8.14E-04	212998_PM_x_at
HLA-DRB1 /// HLA-DRB3		<i>major histocompatibility complex, class II, DR family</i>		
/// HLA-DRB4 /// HLA-DRB5				
/// LOC100133661 ///				
LOC100294036	2.40		4.84E-02	215193_PM_x_at
HLA-DRB1 /// HLA-DRB4	2.55	<i>major histocompatibility complex, class II, DR family</i>	2.31E-02	209312_PM_x_at
<i>metabolism / enzyme binding</i>				
UGT1A1 /// UGT1A10 ///		<i>UDP glucuronosyltransferase 1 family</i>		
UGT1A4 /// UGT1A6 ///				
UGT1A8 /// UGT1A9	3.49		5.47E-03	204532_PM_x_at
UGT1A6	3.39	UDP glucuronosyltransferase 1 family, polypeptide A6	7.49E-03	206094_PM_x_at
UGT1A1 /// UGT1A10 ///		<i>UDP glucuronosyltransferase 1 family</i>		
UGT1A3 /// UGT1A4 ///				
UGT1A5 /// UGT1A6 ///				
UGT1A7 /// UGT1A8 ///				
UGT1A9	3.52		7.87E-03	215125_PM_s_at
<i>cell communication</i>				
ABR	1.52	active BCR-related gene	1.47E-02	212895_PM_s_at
ADAM28	2.15	ADAM metalloproteinase domain 28	3.10E-02	205997_PM_at
ADAM9	1.72	ADAM metalloproteinase domain 9 (meltrin gamma)	2.93E-03	1555326_PM_a_at
ADAMTS1	2.42	ADAM metalloproteinase with thrombospondin type 1 motif, 1	3.87E-03	222486_PM_s_at
ADRB2	1.43	adrenergic, beta-2-, receptor, surface	1.21E-02	206170_PM_at
AKAP12	13.17	A kinase (PRKA) anchor protein 12	4.55E-06	227530_PM_at
AKT3	1.33	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	2.89E-02	212609_PM_s_at
ANGPTL2	1.24	angiopoietin-like 2	2.96E-02	213001_PM_at
AP2B1	1.28	adaptor-related protein complex 2, beta 1 subunit	1.76E-02	200615_PM_s_at
APLN	1.27	Apelin	2.11E-02	244166_PM_at
APLP2	1.24	amyloid beta (A4) precursor-like protein 2	2.45E-02	208703_PM_s_at
AR	1.22	androgen receptor	3.95E-02	226192_PM_at
ARAP2	1.85	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	1.63E-02	214102_PM_at
ARHGAP29	1.31	Rho GTPase activating protein 29	2.09E-02	203910_PM_at
ARHGAP5	1.76	Rho GTPase activating protein 5	4.88E-02	235635_PM_at
ARHGEF12	1.41	Rho guanine nucleotide exchange factor (GEF) 12	5.48E-03	201335_PM_s_at
ARHGEF18	1.32	Rho/Rac guanine nucleotide exchange factor (GEF) 18	4.50E-02	213039_PM_at
ASAP1	1.21	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	4.65E-02	224790_PM_at
ASB1	1.37	ankyrin repeat and SOCS box-containing 1	1.59E-02	212819_PM_at
AXL	1.32	AXL receptor tyrosine kinase	6.91E-03	202686_PM_s_at
BAIAP2	1.42	BAI1-associated protein 2	2.86E-02	205294_PM_at
BCAR3	1.64	breast cancer anti-estrogen resistance 3	2.55E-03	204032_PM_at
BCL10	1.46	B-cell CLL/lymphoma 10	2.48E-03	205263_PM_at
BCL2L1	2.00	BCL2-like 1	1.04E-03	215037_PM_s_at
BCR	1.32	breakpoint cluster region	4.75E-02	226602_PM_s_at
BMPRI1B	2.40	bone morphogenetic protein receptor, type IB	1.72E-03	229975_PM_at
CAPS	1.46	calcyphosine	5.54E-03	231729_PM_s_at
CARD11	2.08	caspase recruitment domain family, member 11	8.14E-04	223514_PM_at
CASP3	1.40	caspase 3, apoptosis-related cysteine peptidase	7.36E-03	202763_PM_at
CAV2	1.24	caveolin 2	2.82E-02	203323_PM_at
CD274	1.62	CD274 molecule	3.69E-02	227458_PM_at
CEACAM6	3.76	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	2.08E-02	211657_PM_at
CERK	1.45	ceramide kinase	4.73E-02	218421_PM_at
CHRN1	1.64	cholinergic receptor, nicotinic, beta 1 (muscle)	5.23E-03	206703_PM_at
CLDN4	1.96	claudin 4	3.91E-03	201428_PM_at
CORO1C	1.26	coronin, actin binding protein, 1C	2.04E-02	222409_PM_at
CORO2A	1.35	coronin, actin binding protein, 2A	2.07E-02	227177_PM_at
CSNK1D	1.27	casein kinase 1, delta	1.76E-02	207945_PM_s_at
CSRNP1	1.82	cysteine-serine-rich nuclear protein 1	1.60E-02	225557_PM_at
CXCL1	2.73	chemokine (C-X-C motif) ligand 1 (melanoma growth	3.77E-03	204470_PM_at

		stimulating activity, alpha)		
		chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	2.17E-02	206336_PM_at
CXCL6	1.45			
CXCR7	2.10	Chemokine (C-X-C motif) receptor 7	2.01E-02	232746_PM_at
CXXC5	1.81	CXXC finger 5	1.63E-02	224516_PM_s_at
DAPP1	1.35	dual adaptor of phosphotyrosine and 3-phosphoinositides	2.17E-02	222858_PM_s_at
DDAH1	3.13	dimethylarginine dimethylaminohydrolase 1	3.14E-05	209094_PM_at
DISC1 /// TSNAX-DISC1	1.26	disrupted in schizophrenia 1 /// TSNAX-DISC1 gene	3.25E-02	206090_PM_s_at
DKK2	1.65	dickkopf homolog 2 (Xenopus laevis)	1.36E-02	219908_PM_at
DPYSL3	2.01	dihydropyrimidinase-like 3	6.15E-03	201431_PM_s_at
DST	1.57	dystonin	9.45E-03	216918_PM_s_at
DTNA	1.53	dystrobrevin, alpha	3.75E-02	205741_PM_s_at
ECT2	1.60	epithelial cell transforming sequence 2 oncogene	4.21E-03	234992_PM_x_at
EDN1	3.62	endothelin 1	6.06E-05	1564630_PM_at
EML4	1.36	echinoderm microtubule associated protein like 4	2.24E-02	228674_PM_s_at
		egf-like module containing, mucin-like, hormone receptor-like 2	1.24E-02	207610_PM_s_at
EMR2	1.75			
EPHA2	1.74	EPH receptor A2	2.33E-03	203499_PM_at
EPHB2	2.82	EPH receptor B2	3.28E-03	209589_PM_s_at
EPS8	2.30	epidermal growth factor receptor pathway substrate 8	1.95E-02	202609_PM_at
ERN1	2.19	endoplasmic reticulum to nucleus signaling 1	3.41E-03	235745_PM_at
FAS	1.92	Fas (TNF receptor superfamily, member 6)	4.65E-04	204781_PM_s_at
FGF13	1.45	fibroblast growth factor 13	2.30E-03	205110_PM_s_at
FGF18	1.33	fibroblast growth factor 18	1.67E-02	206986_PM_at
FGF5	3.56	fibroblast growth factor 5	4.67E-03	208378_PM_x_at
FGFR3	2.38	fibroblast growth factor receptor 3	9.08E-03	204379_PM_s_at
FIP1L1	1.35	FIP1 like 1 (S. cerevisiae)	6.15E-03	1554424_PM_at
		FK506 binding protein 1B /// major facilitator superfamily domain containing 2B	2.45E-02	209931_PM_s_at
FKBP1B /// MFSD2B	1.38			
FOXA1	4.68	forkhead box A1	4.55E-06	204667_PM_at
FOXA2	2.37	forkhead box A2	8.19E-03	40284_PM_at
FOXL1	1.98	forkhead box L1	2.28E-02	243409_PM_at
FUT8	1.36	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	2.77E-02	1554930_PM_a_at
FZD10	2.17	frizzled homolog 10 (Drosophila)	1.37E-02	219764_PM_at
FZD5	1.39	frizzled homolog 5 (Drosophila)	2.09E-02	221245_PM_s_at
G3BP2	1.26	GTPase activating protein (SH3 domain) binding protein 2	3.80E-02	208840_PM_s_at
GABRB3	1.86	gamma-aminobutyric acid (GABA) A receptor, beta 3	1.11E-02	229724_PM_at
GAS6	1.66	growth arrest-specific 6	3.01E-03	202177_PM_at
GDI1	1.23	GDP dissociation inhibitor 1	3.15E-02	201864_PM_at
		guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	5.78E-03	205349_PM_at
GNA15	1.45			
GNAS	1.52	GNAS complex locus	2.67E-02	229274_PM_at
GNG11	1.46	guanine nucleotide binding protein (G protein), gamma 11	2.66E-02	204115_PM_at
GPR110	2.41	G protein-coupled receptor 110	1.23E-02	236489_PM_at
GPR126	1.75	G protein-coupled receptor 126	6.33E-03	213094_PM_at
GPR153	1.26	G protein-coupled receptor 153	3.17E-02	64942_PM_at
		G protein-coupled receptor 37 (endothelin receptor type B-like)	1.69E-03	209631_PM_s_at
GPR37	3.43			
GPR39	2.44	G protein-coupled receptor 39	9.87E-05	229105_PM_at
GPRC5A	3.85	G protein-coupled receptor, family C, group 5, member A	2.24E-04	203108_PM_at
GRB10	2.17	growth factor receptor-bound protein 10	2.93E-03	209409_PM_at
GRK5	1.54	G protein-coupled receptor kinase 5	1.67E-02	204396_PM_s_at
GULP1	2.05	GULP, engulfment adaptor PTB domain containing 1	3.80E-04	204237_PM_at
HCLS1	2.02	hematopoietic cell-specific Lyn substrate 1	3.05E-02	202957_PM_at
HEY1	2.55	hairy/enhancer-of-split related with YRPW motif 1	5.31E-04	218839_PM_at
HIST2H4A /// HIST2H4B	1.50	histone cluster 2, H4a /// histone cluster 2, H4b	9.90E-03	207046_PM_at
HLA-G	1.46	major histocompatibility complex, class I, G	1.52E-02	211530_PM_x_at
HMHA1	1.53	histocompatibility (minor) HA-1	6.17E-03	212873_PM_at
IFNAR1	1.28	interferon (alpha, beta and omega) receptor 1	4.32E-02	225661_PM_at
		insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	2.56E-02	202409_PM_at
IGF2 /// INS-IGF2	1.94			
IGFBP4	1.92	insulin-like growth factor binding protein 4	1.01E-03	201508_PM_at
IL11	2.07	interleukin 11	1.30E-02	206924_PM_at
IL1RL1	6.40	interleukin 1 receptor-like 1	4.66E-04	242809_PM_at
IL1RN	1.52	interleukin 1 receptor antagonist	2.59E-03	212659_PM_s_at
IL23A	2.69	interleukin 23, alpha subunit p19	9.36E-03	220054_PM_at
IL6ST	1.40	interleukin 6 signal transducer (gp130, oncostatin M receptor)	4.88E-02	212196_PM_at
IL8	5.88	interleukin 8	7.71E-03	211506_PM_s_at
ILK	1.33	integrin-linked kinase	2.79E-02	201234_PM_at
INADL	1.25	InaD-like (Drosophila)	4.57E-02	239173_PM_at
INPP4B	1.49	inositol polyphosphate-4-phosphatase, type II	2.55E-02	205376_PM_at
INSIG1	1.40	insulin induced gene 1	3.68E-02	201626_PM_at
INSR	1.57	insulin receptor	8.26E-03	226216_PM_at
IRAK3	1.34	interleukin-1 receptor-associated kinase 3	3.03E-02	220034_PM_at
IRS1	1.70	insulin receptor substrate 1	6.98E-03	204686_PM_at
ITGA2	2.02	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3.43E-03	205032_PM_at

ITGB1	1.28	integrin, beta 1 (fibronectin receptor, beta polypeptide,	2.46E-02	1553530_PM_a_at
JAK2	1.53	antigen CD29 includes MDF2, MSK12)	4.09E-03	205842_PM_s_at
JUN	1.39	Janus kinase 2	2.07E-02	201465_PM_s_at
KCNMA1	3.31	jun oncogene	1.52E-03	221584_PM_s_at
KCNQ5	1.42	potassium large conductance calcium-activated channel,	4.83E-02	244623_PM_at
KISS1R	1.42	subfamily M, alpha member 1	4.85E-02	242517_PM_at
KREMEN1	1.36	potassium voltage-gated channel, KQT-like subfamily,	3.08E-02	227250_PM_at
LDLR	1.41	member 5	6.16E-03	217173_PM_s_at
LIFR	1.45	kringle containing transmembrane protein 1	1.72E-02	225575_PM_at
LOC100288387	1.37	low density lipoprotein receptor	3.36E-02	213281_PM_at
LOC100294402 /// SIGIRR	2.22	leukemia inhibitory factor receptor alpha	4.92E-04	52940_PM_at
LPAR1	2.09	similar to c-jun	2.98E-03	204037_PM_at
LTBP1	1.62	similar to single Ig IL-1R-related molecule /// single	2.45E-02	202728_PM_s_at
MALT1	1.24	immunoglobulin and toll-interleukin 1 receptor (TIR) domain	2.38E-02	210018_PM_x_at
MAP2K1	1.30	lysophosphatidic acid receptor 1	2.21E-02	202670_PM_at
MAP3K9	1.61	latent transforming growth factor beta binding protein 1	1.29E-02	213927_PM_at
MAPK13	1.55	mucosa associated lymphoid tissue lymphoma translocation	2.12E-03	210058_PM_at
MAPK6	1.26	gene 1	2.63E-02	207121_PM_s_at
MET	1.41	mitogen-activated protein kinase kinase 1	4.98E-03	20510_PM_at
MIB1	1.24	mitogen-activated protein kinase kinase kinase 9	4.58E-02	224722_PM_at
MIB2	1.71	mitogen-activated protein kinase 13	1.24E-02	228261_PM_at
MITF	2.07	mitogen-activated protein kinase 6	6.47E-03	226066_PM_at
MST1R	2.21	met proto-oncogene (hepatocyte growth factor receptor)	2.26E-03	205455_PM_at
MSX1	1.34	mindbomb homolog 1 (Drosophila)	1.78E-02	205932_PM_s_at
MT1H /// MT1P2	1.35	mindbomb homolog 2 (Drosophila)	1.23E-02	206461_PM_x_at
MYO10	1.76	microphthalmia-associated transcription factor	2.17E-02	1554026_PM_a_at
NAMPT	1.26	macrophage stimulating 1 receptor (c-met-related tyrosine	2.68E-02	1555167_PM_s_at
NDST1	1.29	kinase)	2.99E-02	1554010_PM_at
NET1	1.53	msh homeobox 1	6.58E-03	201829_PM_at
NFATC1	1.41	metallothionein 1H /// metallothionein 1 pseudogene 2	1.85E-02	211105_PM_s_at
NKX2-1	3.76	myosin X	4.19E-04	231315_PM_at
NKX3-1	1.28	nicotinamide phosphoribosyltransferase	4.60E-02	209706_PM_at
NPC1	1.28	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.97E-02	202679_PM_at
NR3C2	2.71	neuroepithelial cell transforming 1	1.97E-02	205259_PM_at
NRAS	1.40	nuclear factor of activated T-cells, cytoplasmic, calcineurin-	5.57E-03	202647_PM_s_at
NRP2	1.34	dependent 1	2.51E-02	210842_PM_at
NRXN3	1.91	NK2 homeobox 1	4.53E-02	229649_PM_at
OSMR	1.39	NK3 homeobox 1	3.74E-02	1554008_PM_at
OXTR	2.61	Niemann-Pick disease, type C1	2.35E-03	206825_PM_at
P2RY2	1.72	nuclear receptor subfamily 3, group C, member 2	7.95E-03	206277_PM_at
PANX2	1.31	neuroblastoma RAS viral (v-ras) oncogene homolog	2.44E-02	239067_PM_s_at
PDE4D	1.34	neuropilin 2	2.17E-02	204491_PM_at
PDE9A	2.71	neurexin 3	2.31E-03	205593_PM_s_at
PDK3	1.44	oncostatin M receptor	6.49E-03	228959_PM_at
PDLIM5	1.40	oxytocin receptor	1.98E-02	211681_PM_s_at
PELO	1.55	purinergic receptor P2Y, G-protein coupled, 2	3.57E-02	226731_PM_at
PENK	1.21	pannexin 2	3.52E-02	213791_PM_at
PLAUR	1.60	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3	1.85E-02	214866_PM_at
PLCB1	2.31	dunce homolog, Drosophila)	5.78E-03	213222_PM_at
PLCXD2	1.93	phosphodiesterase 9A	1.80E-02	235230_PM_at
PLEK2	1.43	pyruvate dehydrogenase kinase, isozyme 3	2.82E-02	218644_PM_at
PLK3	1.36	PDZ and LIM domain 5	1.99E-02	204958_PM_at
PLL	3.41	Pelota homolog (Drosophila)	1.83E-04	204519_PM_s_at
PLXNA2	1.69	proenkephalin	6.57E-04	213030_PM_s_at
PMEPA1	2.24	plasminogen activator, urokinase receptor	1.68E-03	222449_PM_at
PORCN	1.57	phospholipase C, beta 1 (phosphoinositide-specific)	2.57E-02	219483_PM_s_at
PPAD	1.65	phosphatidylinositol-specific phospholipase C, X domain	1.11E-03	210636_PM_at
PPARG	1.44	containing 2	1.88E-02	208510_PM_s_at
PPP1R15A	1.62	pleckstrin 2	1.61E-03	37028_PM_at
PPP1R1C	1.76	polo-like kinase 3 (Drosophila)	2.73E-03	228646_PM_at
PPP2R2A	1.28	plasma membrane proteolipid (plasmolipin)	3.25E-02	228013_PM_at
PPP3CB	1.27	plexin A2	3.84E-02	202432_PM_at
PRKAA1	1.22	prostate transmembrane protein, androgen induced 1	4.81E-02	225985_PM_at
PRKAA2	2.90	porcupine homolog (Drosophila)	1.93E-03	227892_PM_at
PRKCD	1.25	peroxisome proliferator-activated receptor delta	2.50E-02	202545_PM_at
PRMT2	1.39	peroxisome proliferator-activated receptor gamma	4.28E-02	228722_PM_at
PTAFR	3.11	protein phosphatase 1, regulatory (inhibitor) subunit 15A	4.90E-03	227184_PM_at
		protein phosphatase 1, regulatory (inhibitor) subunit 1C		
		protein phosphatase 2, regulatory subunit B, alpha		
		protein phosphatase 3, catalytic subunit, beta isozyme		
		protein kinase, AMP-activated, alpha 1 catalytic subunit		
		protein kinase, AMP-activated, alpha 2 catalytic subunit		
		protein kinase C, delta		
		protein arginine methyltransferase 2		
		platelet-activating factor receptor		

PTGER4	2.49	prostaglandin E receptor 4 (subtype EP4)	3.77E-04	204897_PM_at
PTK2	1.31	PTK2 protein tyrosine kinase 2	3.88E-02	241453_PM_at
PTN	1.76	pleiotrophin	1.32E-03	209466_PM_x_at
PTPLA	1.54	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	3.75E-03	219654_PM_at
PTPRD	1.32	protein tyrosine phosphatase, receptor type, D	2.09E-02	214043_PM_at
RAB3B	1.82	RAB3B, member RAS oncogene family	4.57E-03	205924_PM_at
RAF1	1.25	V-raf-1 murine leukemia viral oncogene homolog 1	3.88E-02	1557675_PM_at
RAPH1	1.57	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	3.29E-02	231075_PM_x_at
RARA	1.42	retinoic acid receptor, alpha	5.47E-03	203749_PM_s_at
RASA2	1.55	RAS p21 protein activator 2	1.78E-02	206636_PM_at
RASA3	1.54	RAS p21 protein activator 3	6.47E-03	225562_PM_at
RASAL2	1.46	RAS protein activator like 2	2.55E-03	227036_PM_at
RASD1	1.99	RAS, dexamethasone-induced 1	3.25E-02	223467_PM_at
RASGEF1A	6.75	RasGEF domain family, member 1A	2.07E-02	230563_PM_at
RASSF5	1.32	Ras association (RalGDS/AF-6) domain family member 5 recombination signal binding protein for immunoglobulin kappa J region	1.84E-02	1554834_PM_a_at
RBPJ	1.36	kappa J region	5.46E-03	211974_PM_x_at
RGBM	3.01	RGM domain family, member B	3.45E-04	227339_PM_at
RGS12	1.44	regulator of G-protein signaling 12	1.00E-02	209637_PM_s_at
RGS2	1.46	regulator of G-protein signaling 2	4.05E-02	202388_PM_at
RHBDL2	1.50	rhomboid, veinlet-like 2 (Drosophila)	2.45E-02	1554897_PM_s_at
RHOC	1.24	ras homolog gene family, member C	4.76E-02	200885_PM_at
RHOF	2.49	ras homolog gene family, member F (in filopodia)	3.33E-02	219045_PM_at
RHPN2	1.57	rhophilin, Rho GTPase binding protein 2	8.26E-03	227196_PM_at
RICH2	1.89	Rho-type GTPase-activating protein RICH2	1.80E-03	205414_PM_s_at
RIT1	1.28	Ras-like without CAAX 1	1.62E-02	236224_PM_at
RND1	1.71	Rho family GTPase 1	3.29E-02	210056_PM_at
RNF138	1.35	ring finger protein 138	2.50E-02	239143_PM_x_at
ROBO2	1.76	roundabout, axon guidance receptor, homolog 2 (Drosophila)	3.91E-03	226766_PM_at
RRAS	1.31	related RAS viral (r-ras) oncogene homolog	2.80E-02	212647_PM_at
SDCBP2	1.57	syndecan binding protein (syntenin) 2	2.97E-02	233565_PM_s_at
SH2D3A	1.55	SH2 domain containing 3A	4.77E-03	219513_PM_s_at
SH3D20	1.97	SH3 domain containing 20	2.31E-03	1554594_PM_at
SH3KBP1	1.29	SH3-domain kinase binding protein 1	1.21E-02	235692_PM_at
SHANK2	2.03	SH3 and multiple ankyrin repeat domains 2	7.89E-04	213307_PM_at
SIPA1	1.24	signal-induced proliferation-associated 1	3.93E-02	204164_PM_at
SIX1	1.63	SIX homeobox 1	1.99E-02	205817_PM_at
SKAP2	2.96	src kinase associated phosphoprotein 2	4.26E-04	204362_PM_at
SLC1A1	2.10	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	1.71E-02	213664_PM_at
SLC1A4	2.39	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	7.82E-04	212810_PM_s_at
SLC2A8	1.22	solute carrier family 2 (facilitated glucose transporter), member 8	3.71E-02	218985_PM_at
SLC44A2	1.38	solute carrier family 44, member 2	2.72E-02	224609_PM_at
SLC9A3R1	1.49	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	1.12E-02	201349_PM_at
SMAD3	1.53	SMAD family member 3	1.09E-03	218284_PM_at
SMAD4	1.29	SMAD family member 4	4.41E-02	235725_PM_at
SMURF1	1.26	SMAD specific E3 ubiquitin protein ligase 1	1.49E-02	212666_PM_at
SMURF2	1.70	SMAD specific E3 ubiquitin protein ligase 2	2.93E-03	227489_PM_at
SNCA	1.60	synuclein, alpha (non A4 component of amyloid precursor)	1.78E-02	236081_PM_at
SOX4	1.23	SRY (sex determining region Y)-box 4	3.36E-02	213665_PM_at
SPOCK1	3.21	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	2.39E-03	202363_PM_at
SPTBN1	1.52	spectrin, beta, non-erythrocytic 1	2.26E-03	200672_PM_x_at
STAM	1.29	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	1.21E-02	203544_PM_s_at
STK17A	1.51	serine/threonine kinase 17a	2.10E-02	202694_PM_at
STK17B	2.68	serine/threonine kinase 17b	2.55E-03	205214_PM_at
STK39	1.32	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	4.02E-02	202786_PM_at
STX1A	1.85	syntaxin 1A (brain)	1.18E-03	204729_PM_s_at
STX2	1.40	syntaxin 2	4.41E-02	213434_PM_at
SYK	2.07	spleen tyrosine kinase	1.52E-03	226068_PM_at
TGFA	1.35	transforming growth factor, alpha	1.93E-02	205015_PM_s_at
TGFBR1	1.23	transforming growth factor, beta receptor 1	4.16E-02	224793_PM_s_at
TGFBR2	1.57	transforming growth factor, beta receptor II	6.38E-03	208944_PM_at
TGFBR3	3.29	transforming growth factor, beta receptor III	6.05E-04	226625_PM_at
TGM2	1.90	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	3.95E-02	211003_PM_x_at
TICAM2 /// TMED7-		toll-like receptor adaptor molecule 2 /// TMED7-TICAM2		
TICAM2	1.38	readthrough	4.71E-02	239431_PM_at
TIMM50	1.26	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	3.15E-02	217612_PM_at

TIPARP	1.42	TCDD-inducible poly(ADP-ribose) polymerase	9.32E-03	212665_PM_at
TNC	1.30	tenascin C	2.49E-02	201645_PM_at
TNFRSF10A	1.37	tumor necrosis factor receptor superfamily, member 10a	3.25E-02	231775_PM_at
TNFRSF10B	1.46	tumor necrosis factor receptor superfamily, member 10b	8.83E-03	209294_PM_x_at
TNFRSF21	1.51	tumor necrosis factor receptor superfamily, member 21	2.55E-03	218856_PM_at
TNFSF12-TNFSF13 ///		TNFSF12-TNFSF13 readthrough /// tumor necrosis factor		
TNFSF13	1.34	(ligand) superfamily, member 13	4.86E-02	209500_PM_x_at
TNFSF9	1.75	tumor necrosis factor (ligand) superfamily, member 9	2.82E-03	206907_PM_at
TRAF4	1.36	TNF receptor-associated factor 4	2.93E-02	242473_PM_at
TRIB1	1.48	tribbles homolog 1 (Drosophila)	6.49E-03	202241_PM_at
TSpan12	2.26	tetraspanin 12	1.36E-02	219274_PM_at
TXNRD1	1.56	thioredoxin reductase 1	1.72E-02	210266_PM_at
VAV3	3.58	vav 3 guanine nucleotide exchange factor	3.95E-03	218807_PM_at
VLDLR	1.57	very low density lipoprotein receptor	1.09E-02	209822_PM_s_at
VOPPI	1.41	vesicular, overexpressed in cancer, prosurvival protein 1	2.85E-03	208091_PM_s_at
WNT7A	2.27	wingless-type MMTV integration site family, member 7A	5.26E-05	210248_PM_at
WNT7B	1.30	wingless-type MMTV integration site family, member 7B	4.96E-02	238105_PM_x_at
WNT9A	1.80	wingless-type MMTV integration site family, member 9A	1.42E-02	230643_PM_at
WSB2	1.26	WD repeat and SOCS box-containing 2	1.37E-02	213734_PM_at
ZMYM6	1.31	zinc finger, MYM-type 6	4.94E-02	213698_PM_at
ZNF219	1.30	zinc finger protein 219	4.98E-02	222864_PM_s_at

developmental process

ABT1	1.20	activator of basal transcription 1	4.91E-02	218405_PM_at
ACSL4	1.46	acyl-CoA synthetase long-chain family member 4	4.94E-03	202422_PM_s_at
ACTA2	1.62	actin, alpha 2, smooth muscle, aorta	5.47E-03	200974_PM_at
AGFG1	1.35	ArfGAP with FG repeats 1	1.44E-02	226561_PM_at
APAF1	1.40	apoptotic peptidase activating factor 1	3.35E-02	211554_PM_s_at
ARG2	1.64	arginase, type II	4.70E-03	203945_PM_at
ASPH	1.57	aspartate beta-hydroxylase	7.20E-03	209135_PM_at
ATL1	2.50	atlastin GTPase 1	1.81E-02	223340_PM_at
B4GALT1	1.55	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	2.38E-02	216627_PM_s_at
BCOR	1.31	BCL6 co-repressor	4.88E-02	219433_PM_at
BIK	1.76	BCL2-interacting killer (apoptosis-inducing)	2.48E-02	205780_PM_at
BPGM	1.70	2,3-bisphosphoglycerate mutase	1.25E-02	203502_PM_at
C19orf46	2.74	chromosome 19 open reading frame 46	3.87E-05	235515_PM_at
CA9	1.37	carbonic anhydrase IX	2.86E-02	205199_PM_at
CADM1	1.61	cell adhesion molecule 1	2.38E-02	209031_PM_at
CAPN2	1.52	calpain 2, (m/II) large subunit	1.04E-02	214888_PM_at
CCBE1	8.61	collagen and calcium binding EGF domains 1	7.41E-05	229641_PM_at
CDH11	2.32	cadherin 11, type 2, OB-cadherin (osteoblast)	1.70E-02	236179_PM_at
CDK13	1.22	cyclin-dependent kinase 13	3.04E-02	228991_PM_at
CDKN1C	4.21	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	7.87E-03	213348_PM_at
CELF1	1.23	CUGBP, Elav-like family member 1	3.69E-02	1555467_PM_a_at
CIB1	1.36	calcium and integrin binding 1 (calmyrin)	1.74E-02	201953_PM_at
CLASP2	1.39	cytoplasmic linker associated protein 2	1.55E-02	212308_PM_at
COBL	2.29	cordon-bleu homolog (mouse)	1.64E-02	213050_PM_at
COL13A1	1.83	collagen, type XIII, alpha 1	4.92E-02	211343_PM_s_at
COL4A4	1.63	collagen, type IV, alpha 4	9.53E-03	229779_PM_at
CST6	1.43	Cystatin E/M	2.23E-02	231248_PM_at
CTBP2	1.29	C-terminal binding protein 2	3.88E-02	201219_PM_at
CTNNA1	1.32	catenin (cadherin-associated protein), alpha 1	1.57E-02	1558214_PM_s_at
CXADR	1.35	coxsackie virus and adenovirus receptor	4.31E-02	1555716_PM_a_at
CXCL17	16.06	chemokine (C-X-C motif) ligand 17	1.93E-05	226960_PM_at
CYR61	2.17	cysteine-rich, angiogenic inducer, 61	1.79E-04	210764_PM_s_at
DCAF7	1.26	DDB1 and CUL4 associated factor 7	2.34E-02	221745_PM_at
DIP2A	1.28	DIP2 disco-interacting protein 2 homolog A (Drosophila)	1.39E-02	1561286_PM_a_at
DLG1	1.40	discs, large homolog 1 (Drosophila)	4.59E-02	202515_PM_at
DMRT2	1.58	doublesex and mab-3 related transcription factor 2	4.41E-02	223704_PM_s_at
DMRTA2	3.61	DMRT-like family A2	1.02E-02	1558856_PM_at
DUSP6	1.53	dual specificity phosphatase 6	1.86E-02	208893_PM_s_at
ECE1	1.45	endothelin converting enzyme 1	4.92E-03	201749_PM_at
EDIL3	3.16	EGF-like repeats and discoidin I-like domains 3	3.38E-02	225275_PM_at
EHF	1.37	Ets homologous factor	4.79E-03	225645_PM_at
ELF5	3.67	E74-like factor 5 (ets domain transcription factor)	3.61E-03	220625_PM_s_at
ENDOG	1.24	endonuclease G	3.00E-02	204824_PM_at
EPCAM	2.03	epithelial cell adhesion molecule	1.30E-02	201839_PM_s_at
ETV4	1.23	ets variant 4	3.53E-02	1554576_PM_a_at
EYA1	1.63	eyes absent homolog 1 (Drosophila)	2.31E-02	214608_PM_s_at
EYA4	16.74	eyes absent homolog 4 (Drosophila)	1.56E-06	238877_PM_at
F11R	1.29	F11 receptor	2.52E-02	222354_PM_at
FHL1	1.70	four and a half LIM domains 1	3.39E-02	201539_PM_s_at
FOXD1	3.64	forkhead box D1	2.88E-02	206307_PM_s_at
FOXE1	3.16	forkhead box E1 (thyroid transcription factor 2)	1.49E-02	206912_PM_at

FOXP2	2.54	forkhead box P2	5.08E-03	235201_PM_at
FSTL3	1.53	follistatin-like 3 (secreted glycoprotein)	9.86E-03	203592_PM_s_at
GADD45B	1.54	growth arrest and DNA-damage-inducible, beta	1.09E-02	207574_PM_s_at
GATA6	2.63	GATA binding protein 6	1.36E-02	210002_PM_at
GCNT2	1.71	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	1.55E-02	230788_PM_at
GDA	4.56	guanine deaminase	2.55E-03	224209_PM_s_at
GPC4	1.84	glypican 4	1.50E-02	204984_PM_at
HDAC9	1.22	histone deacetylase 9	4.71E-02	205659_PM_at
HES4	1.38	hairy and enhancer of split 4 (Drosophila)	4.23E-02	227347_PM_x_at
HMGB3	2.04	high-mobility group box 3	1.58E-04	203744_PM_at
HOOK3	1.23	hook homolog 3 (Drosophila)	3.95E-02	236192_PM_at
HOXA1	3.11	homeobox A1	6.98E-03	214639_PM_s_at
HSD11B1	2.87	hydroxysteroid (11-beta) dehydrogenase 1	4.87E-03	205404_PM_at
IER3	1.33	immediate early response 3	6.37E-03	201631_PM_s_at
IFRD1	1.26	interferon-related developmental regulator 1	4.02E-02	202147_PM_s_at
IGF2BP2	1.35	insulin-like growth factor 2 mRNA binding protein 2	4.47E-02	223963_PM_s_at
IRX5	1.35	iroquois homeobox 5	1.70E-02	210239_PM_at
JPH1	1.48	junctophilin 1	3.55E-02	229139_PM_at
KAL1	1.75	Kallmann syndrome 1 sequence	3.28E-03	205206_PM_at
KIAA1217	1.26	KIAA1217	2.84E-02	232762_PM_at
KLF7	1.45	Kruppel-like factor 7 (ubiquitous)	4.77E-02	238482_PM_at
KRT18	1.95	keratin 18	6.05E-04	201596_PM_x_at
KRT19	7.71	keratin 19	5.68E-04	201650_PM_at
KRT31	1.95	keratin 31	1.36E-02	206677_PM_at
LAMB3	1.26	laminin, beta 3	1.78E-02	209270_PM_at
LAMC2	2.00	laminin, gamma 2	2.33E-02	207517_PM_at
LBH	3.35	limb bud and heart development homolog (mouse)	6.42E-05	221011_PM_s_at
LMO2	1.99	LIM domain only 2 (rhombotin-like 1)	4.66E-04	204249_PM_at
LPFR1	1.70	lipid phosphate phosphatase-related protein type 1	3.72E-02	219732_PM_at
LRG1	1.64	leucine-rich alpha-2-glycoprotein 1	1.11E-02	228648_PM_at
LRR8A	1.42	leucine rich repeat containing 8 family, member A	8.55E-03	233487_PM_s_at
MAFF	1.51	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	5.14E-03	36711_PM_at
MAFG	1.25	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	2.39E-02	204970_PM_s_at
MAFK	1.65	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	1.01E-02	226206_PM_at
MAN2A1	1.36	mannosidase, alpha, class 2A, member 1	2.67E-02	226538_PM_at
MATN3	1.60	matrilin 3	1.40E-02	206091_PM_at
MECOM	1.87	MDS1 and EVI1 complex locus	1.83E-02	226420_PM_at
MID1	1.28	midline 1 (Opitz/BBB syndrome)	3.28E-02	203636_PM_at
MPZL2	1.31	myelin protein zero-like 2	2.34E-02	203779_PM_s_at
MXD1	1.50	MAX dimerization protein 1	1.51E-02	228846_PM_at
MYLIP	1.64	myosin regulatory light chain interacting protein	2.98E-02	228098_PM_s_at
NCF2	2.63	neutrophil cytosolic factor 2	2.24E-04	209949_PM_at
NHS	1.31	Nance-Horan syndrome (congenital cataracts and dental anomalies)	3.26E-02	228933_PM_at
NKX2-8	1.40	NK2 homeobox 8	2.38E-02	207451_PM_at
NTNG1	1.82	netrin G1	3.84E-02	236088_PM_at
ODC1	1.98	ornithine decarboxylase 1	4.58E-02	200790_PM_at
PAFAH1B3	1.31	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3	2.99E-02	203228_PM_at
PAQR8	1.57	progesterin and adipoQ receptor family member VIII	2.09E-02	227626_PM_at
PARD6B	1.79	par-6 partitioning defective 6 homolog beta (C. elegans)	7.14E-03	235165_PM_at
PAX9	1.50	paired box 9	2.63E-02	207059_PM_at
PCDHA1 /// PCDHA10 ///		<i>protocadherin alpha</i> family and <i>protocadherin alpha</i>		
PCDHA11 /// PCDHA12 ///		<i>subfamily C</i>		
PCDHA13 /// PCDHA2 ///				
PCDHA3 /// PCDHA4 ///				
PCDHA5 /// PCDHA6 ///				
PCDHA7 /// PCDHA8 ///				
PCDHA9 /// PCDHAC1 ///				
PCDHAC2	2.94		1.62E-03	223435_PM_s_at
PHC2	1.37	polyhomeotic homolog 2 (Drosophila)	1.47E-02	200919_PM_at
PHF10	1.25	PHD finger protein 10	4.96E-02	219126_PM_at
PHLDA2	1.47	pleckstrin homology-like domain, family A, member 2	5.00E-03	209803_PM_s_at
PIM1	1.28	pim-1 oncogene	3.19E-02	209193_PM_at
PODXL	10.45	podocalyxin-like	5.03E-03	201578_PM_at
PRDM16	1.66	PR domain containing 16	3.77E-03	232424_PM_at
PSME4	1.22	proteasome (prosome, macropain) activator subunit 4	4.29E-02	212219_PM_at
PTGS2	2.93	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	2.12E-03	204748_PM_at
PVRL3	1.64	poliovirus receptor-related 3	1.55E-03	213325_PM_at
RFX3	1.64	regulatory factor X, 3 (influences HLA class II expression)	9.32E-03	230403_PM_at
RGNEF	1.35	guanine nucleotide exchange factor	1.18E-02	1554003_PM_at

RNF114	1.26	ring finger protein 114	1.75E-02	200867_PM_at
ROD1	1.19	ROD1 regulator of differentiation 1 (S. pombe)	4.77E-02	224617_PM_at
RUNX2	2.67	runt-related transcription factor 2	9.15E-04	232231_PM_at
S100A4	2.15	S100 calcium binding protein A4	1.21E-02	203186_PM_s_at
SATB1	1.82	SATB homeobox 1	4.09E-03	203408_PM_s_at
SATB2	1.54	SATB homeobox 2	5.85E-03	213435_PM_at
SDC2	2.38	syndecan 2	1.27E-03	212154_PM_at
SEMA3A	2.75	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	7.39E-04	206805_PM_at
SEMA4D	1.48	sema domain, immunoglobulin domain (Ig), transmembrane domain TM , short cytoplasmic domain, (semaphorin) 4D semaphorin 7A, GPI membrane anchor (John Milton Hagen	1.72E-02	203528_PM_at
SEMA7A	2.01	blood group)	6.61E-03	230345_PM_at
SGCB	1.35	sarcoglycan, beta (dystrophin-associated glycoprotein)	1.67E-02	226112_PM_at
SIX4	1.46	SIX homeobox 4	1.67E-02	229796_PM_at
SLC40A1	1.58	solute carrier family 40 (iron-regulated transporter), member 1	4.94E-02	223044_PM_at
SMARCA1	1.46	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	5.52E-03	203875_PM_at
SOBP	8.37	sine oculis binding protein homolog (Drosophila)	4.54E-05	218974_PM_at
SOX7	1.31	SRY (sex determining region Y)-box 7	2.45E-02	224013_PM_s_at
SPDEF	7.03	SAM pointed domain containing ets transcription factor	2.68E-04	220192_PM_x_at
SPESP1	2.53	sperm equatorial segment protein 1	2.59E-02	229352_PM_at
SPRED1	1.37	sprouty-related, EVH1 domain containing 1	3.48E-02	235074_PM_at
SRPX2	2.91	sushi-repeat-containing protein, X-linked 2	9.93E-03	205499_PM_at
SSH1	1.36	slingshot homolog 1 (Drosophila)	2.69E-02	221752_PM_at
STS	1.43	steroid sulfatase (microsomal), isozyme S	3.03E-02	203769_PM_s_at
TACC1	1.51	transforming, acidic coiled-coil containing protein 1	5.47E-03	1554690_PM_a_at
TAGLN3	2.92	transgelin 3	1.52E-03	204743_PM_at
TBX1	1.61	T-box 1	2.60E-03	236926_PM_at
TLL2	1.57	tolloid-like 2	3.54E-02	215008_PM_at
TNFRSF12A	1.28	tumor necrosis factor receptor superfamily, member 12A	2.63E-02	218368_PM_s_at
TPM3	1.38	tropomyosin 3	8.86E-03	238065_PM_at
TTC7A	1.32	tetratricopeptide repeat domain 7A	1.45E-02	224923_PM_at
TWIST1	9.30	twist homolog 1 (Drosophila)	1.56E-06	213943_PM_at
TWIST2	3.70	twist homolog 2 (Drosophila)	7.17E-03	229404_PM_at
UHRF2	1.37	ubiquitin-like with PHD and ring finger domains 2	2.27E-02	225610_PM_at
VEZF1	1.69	vascular endothelial zinc finger 1	9.11E-04	202172_PM_at
WHSC1	1.44	Wolf-Hirschhorn syndrome candidate 1	3.90E-02	223472_PM_at
ZEB1	1.37	zinc finger E-box binding homeobox 1	2.27E-02	212764_PM_at
ZFH3	1.51	zinc finger homeobox 3	1.62E-02	226137_PM_at
ZFP36L1	1.82	zinc finger protein 36, C3H type-like 1	1.01E-03	211965_PM_at
ZFPM2	1.93	zinc finger protein, multitype 2	1.36E-02	219778_PM_at
ZNF354A	1.29	zinc finger protein 354A	4.29E-02	205427_PM_at

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196 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*197 *name/description), P-value, and probe ID (Gene ID).*

Table S9. Genes that were significantly higher expressed by healthy nasal epithelial cells sorted by ontology analysis in functional groups.

Gene alias	FC	Gene name/description	P-value	Gene ID
<i>Cell adhesion</i>				
AEBP1	3.08	AE binding protein 1	2.34E-02	201792_PM_at
AJAP1	1.47	adherens junctions associated protein 1	1.69E-02	206460_PM_at
ATP2C1	1.20	ATPase, Ca++ transporting, type 2C, member 1	4.58E-02	212255_PM_s_at
BCAM	1.37	basal cell adhesion molecule (Lutheran blood group)	2.78E-02	40093_PM_at
BCL2L11	1.42	BCL2-like 11 (apoptosis facilitator)	3.43E-02	225606_PM_at
BVES	2.05	blood vessel epicardial substance	1.32E-03	228783_PM_at
CD36	1.82	CD36 molecule (thrombospondin receptor)	3.93E-02	209555_PM_s_at
CDHR1	1.26	cadherin-related family member 1	4.27E-02	1555019_PM_at
CDSN	2.34	corneodesmosin	1.69E-02	206192_PM_at
CELSR2	1.42	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	2.07E-02	36499_PM_at
CLCA2	1.80	chloride channel accessory 2	4.57E-03	206166_PM_s_at
CLDN11	7.58	claudin 11	7.42E-03	228335_PM_at
CLDN17	2.24	claudin 17	3.54E-02	221328_PM_at
CNTN1	2.26	Contactin 1	4.55E-03	227202_PM_at
CNTN3	2.12	contactin 3 (plasmacytoma associated)	3.19E-02	229831_PM_at
CNTNAP3	1.71	contactin associated protein-like 3	3.32E-02	223796_PM_at
COL12A1	3.21	collagen, type XII, alpha 1	6.49E-03	225664_PM_at
COL6A1	9.89	collagen, type VI, alpha 1	1.41E-04	213428_PM_s_at
CRNN	2.48	cornulin	4.83E-02	220090_PM_at
DCBLD1	1.75	discoidin, CUB and LCCL domain containing 1	6.45E-03	226609_PM_at
DSC1	1.88	desmocollin 1	9.68E-03	207324_PM_s_at
DSC2	2.35	desmocollin 2	1.08E-03	204750_PM_s_at
DSC3	1.47	desmocollin 3	8.28E-03	206033_PM_s_at
DSG1	37.49	desmoglein 1	1.47E-05	206642_PM_at
DSG3	1.96	desmoglein 3 (pemphigus vulgaris antigen)	1.13E-02	205595_PM_at
ECM2	1.32	extracellular matrix protein 2, female organ and adipocyte specific	2.17E-02	206101_PM_at
EFS	1.46	embryonal Fyn-associated substrate	3.83E-02	204400_PM_at
EGFL6	4.00	EGF-like-domain, multiple 6	8.02E-03	219454_PM_at
FAT1	1.35	FAT tumor suppressor homolog 1 (Drosophila)	2.40E-02	201579_PM_at
FAT2	1.99	FAT tumor suppressor homolog 2 (Drosophila)	1.42E-03	208153_PM_s_at
GPNNMB	5.52	glycoprotein (transmembrane) nmb	5.50E-03	201141_PM_at
GPR56	1.33	G protein-coupled receptor 56	4.41E-02	212070_PM_at
ITGA4	2.30	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	1.58E-02	213416_PM_at
ITGBL1	1.83	integrin, beta-like 1 (with EGF-like repeat domains)	5.16E-03	205422_PM_s_at
JUP	1.25	junction plakoglobin	2.72E-02	210115_PM_s_at
LAMA1	24.93	laminin, alpha 1	1.47E-06	227048_PM_at
LYPD3	2.01	LY6/PLAUR domain containing 3	8.03E-03	204952_PM_at
MAEA	1.36	macrophage erythroblast attacher	2.53E-02	207922_PM_s_at
MIA	1.92	melanoma inhibitory activity	4.57E-03	206560_PM_s_at
NID1	1.61	nidogen 1	3.98E-02	202007_PM_at
NID2	2.76	nidogen 2 (osteonidogen)	1.55E-03	204114_PM_at
NPNT	1.61	nephronectin	3.73E-03	225911_PM_at
PARVB	1.63	parvin, beta	7.09E-03	37966_PM_at
PCDH18	1.63	protocadherin 18	2.60E-03	225975_PM_at
PCDHB10	1.39	protocadherin beta 10	2.45E-02	223854_PM_at
PCDHB14	1.81	protocadherin beta 14	3.03E-02	231726_PM_at
PCDHGA1 /// PCDHGA10 /// PCDHGA11 ///	1.34	<i>protocadherin gamma subfamily A, B, and C</i>	1.70E-02	211066_PM_x_at
PCDHGA12 /// PCDHGA2 /// PCDHGA3 ///				
PCDHGA4 /// PCDHGA5 /// PCDHGA6 ///				
PCDHGA7 /// PCDHGA8 /// PCDHGA9 ///				
PCDHGB1 /// PCDHGB2 /// PCDHGB3 ///				
PCDHGB4 /// PCDHGB5 /// PCDHGB6 ///				
PCDHGB7 /// PCDHGC3 /// PCDHGC4 ///				
PCDHGA11 /// PCDHGA12 /// PCDHGA6 /// PCDHGB3 ///	1.44	<i>protocadherin gamma subfamily A, B, and C</i>	2.97E-02	205717_PM_x_at
PCDHGB4 /// PCDHGB5				

/// PCDHGB6 ///
 PCDHGB7 /// PCDHGC3
 /// PCDHGC4 ///
 PCDHGC5

PERP	1.33	PERP, TP53 apoptosis effector	3.80E-02	236009_PM_at
PKP1	1.46	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	2.17E-02	221854_PM_at
PKP3	1.43	plakophilin 3	4.55E-03	209873_PM_s_at
PTK7	1.34	PTK7 protein tyrosine kinase 7	1.99E-02	207011_PM_s_at
PVRL4	1.46	poliovirus receptor-related 4	1.72E-02	223540_PM_at
SCARB1	1.84	scavenger receptor class B, member 1	4.67E-03	201819_PM_at
SDK2	1.28	sidekick homolog 2 (chicken)	4.42E-02	242064_PM_at
SIRPA	1.22	signal-regulatory protein alpha	3.72E-02	202896_PM_s_at
SOX9	1.71	SRY (sex determining region Y)-box 9	3.37E-04	202935_PM_s_at
SRPX	1.88	sushi-repeat-containing protein, X-linked	9.52E-04	204955_PM_at
SSPN	1.34	sarcospan (Kras oncogene-associated gene)	2.38E-02	204964_PM_s_at
THBS1	1.39	thrombospondin 1	4.67E-02	201107_PM_s_at
THBS2	3.79	thrombospondin 2	2.25E-02	203083_PM_at
THY1	18.97	Thy-1 cell surface antigen	1.74E-05	208850_PM_s_at
TSTA3	1.22	tissue specific transplantation antigen P35B	2.52E-02	36936_PM_at
VNN1	2.60	vanin 1	1.25E-02	205844_PM_at

calcium-ion binding

ANXA6	3.28	annexin A6	8.85E-03	200982_PM_s_at
C1R	4.60	complement component 1, r subcomponent	4.67E-03	212067_PM_s_at
C1S	7.12	complement component 1, s subcomponent	9.28E-03	208747_PM_s_at
CALB2	1.34	calbindin 2	2.15E-02	205428_PM_s_at
CALML5	2.44	calmodulin-like 5	2.20E-02	220414_PM_at
CAPN12	1.35	calpain 12	4.98E-02	228705_PM_at
DLK2	1.81	delta-like 2 homolog (Drosophila)	1.14E-02	220262_PM_s_at
DNER	1.88	delta/notch-like EGF repeat containing	2.75E-02	226281_PM_at
EEF2K	1.23	eukaryotic elongation factor-2 kinase	4.50E-02	225545_PM_at
EPS15L1	1.40	epidermal growth factor receptor pathway substrate 15-like 1	2.96E-02	231926_PM_at
FBLN2	1.53	fibulin 2	4.61E-03	203886_PM_s_at
FKBP10	1.75	FK506 binding protein 10	9.32E-03	219249_PM_s_at
JMJD7-PLA2G4B /// PLA2G4B	1.76	JMJD7-PLA2G4B readthrough /// phospholipase A2, group IVB (cytosolic)	6.35E-03	219095_PM_at
LCP1	6.91	lymphocyte cytosolic protein 1 (L-plastin)	3.05E-03	208885_PM_at
LPCAT2	1.53	lysophosphatidylcholine acyltransferase 2	1.07E-02	227889_PM_at
LTBP3	1.41	latent transforming growth factor beta binding protein 3	2.17E-02	219922_PM_s_at
MEGF9	1.79	multiple EGF-like-domains 9	1.93E-03	212830_PM_at
MMP28	2.92	matrix metalloproteinase 28	6.84E-03	239272_PM_at
MMP3	5.73	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	1.08E-02	205828_PM_at
NOTCH2	1.32	Notch homolog 2 (Drosophila)	7.81E-03	202443_PM_x_at
NOTCH3	1.45	Notch homolog 3 (Drosophila)	6.68E-03	203238_PM_s_at
PCLO	1.53	piccolo (presynaptic cytomatrix protein)	4.02E-03	213558_PM_at
PLA2G4A	1.91	phospholipase A2, group IVA (cytosolic, calcium- dependent)	1.01E-02	210145_PM_at
PLCD1	1.35	phospholipase C, delta 1	2.51E-02	205125_PM_at
PLSCR4	1.83	phospholipid scramblase 4	2.64E-03	218901_PM_at
PRRG4	2.05	proline rich Gla (G-carboxylglutamic acid) 4 (transmembrane)	1.83E-03	207291_PM_at
RASGRP2	1.62	RAS guanyl releasing protein 2 (calcium and DAG- regulated)	4.55E-03	214369_PM_s_at
RPTN	4.68	repetin	4.61E-03	1553454_PM_at
S100A12	5.17	S100 calcium binding protein A12	1.29E-04	205863_PM_at
S100A7	16.15	S100 calcium binding protein A7	5.52E-03	205916_PM_at
S100A8	1.83	S100 calcium binding protein A8	1.42E-02	202917_PM_s_at
S100A9	1.75	S100 calcium binding protein A9	1.69E-02	203535_PM_at
SLC25A12	1.32	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	3.99E-02	203339_PM_at
SMOC1	1.51	SPARC related modular calcium binding 1	1.97E-02	222784_PM_at
SPARC	2.14	secreted protein, acidic, cysteine-rich (osteonectin)	7.78E-03	212667_PM_at
SYT2	1.25	synaptotagmin II	3.48E-02	214903_PM_at

epithelial cell differentiation

CLIC4	1.54	chloride intracellular channel 4	6.62E-03	201560_PM_at
CNFN	3.26	cornifelin	4.29E-04	224329_PM_s_at
COL4A1	4.39	collagen, type IV, alpha 1	1.93E-03	211981_PM_at
DLX5	3.27	distal-less homeobox 5	1.41E-04	213707_PM_s_at
DLX6	1.55	distal-less homeobox 6	7.87E-03	239309_PM_at
EREG	1.79	epiregulin	1.74E-03	205767_PM_at
ESR1	1.27	estrogen receptor 1	2.31E-02	205225_PM_at
FGF2	1.91	fibroblast growth factor 2 (basic)	1.18E-02	204422_PM_s_at
FGFR2	1.70	fibroblast growth factor receptor 2	1.92E-02	203639_PM_s_at
FZD7	2.89	frizzled homolog 7 (Drosophila)	1.59E-03	203706_PM_s_at

ID3	1.72	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	4.36E-03	207826_PM_s_at
IVL	2.61	involucrin	2.69E-03	214599_PM_at
KAZ	1.74	kazrin	5.47E-03	213478_PM_at
KRT14	1.44	keratin 14	2.64E-03	209351_PM_at
LCE3D	3.64	late cornified envelope 3D	2.51E-02	224328_PM_s_at
PAX6	10.29	paired box 6	3.16E-06	235795_PM_at
RHCG	2.18	Rh family, C glycoprotein	3.50E-02	219554_PM_at
SPINK5	2.83	serine peptidase inhibitor, Kazal type 5	1.36E-02	205185_PM_at
SPRR1A	1.27	small proline-rich protein 1A	4.88E-02	213796_PM_at
SPRR1B	1.29	small proline-rich protein 1B (cornifin)	3.74E-02	205064_PM_at
SPRR2G	17.24	small proline-rich protein 2G	6.19E-04	236119_PM_s_at
SPRR4	2.45	small proline-rich protein 4	5.47E-03	1552620_PM_at
TFCP2L1	1.52	transcription factor CP2-like 1	6.58E-03	219735_PM_s_at
WNT5A	3.45	wingless-type MMTV integration site family, member 5A	6.14E-03	213425_PM_at

200

201 *Given are abbreviation (Gene alias), fold change (FC), short description (Gene*202 *name/description), P-value, and probe ID (Gene ID).*

Table S10. The genes that were significantly higher expressed by bronchial epithelial cells from patients with allergic rhinitis, sorted by ontology analysis in functional groups.

Gene alias	FC	Gene name/description	P-value	Gene ID
<i>regulation of signal transduction</i>				
TRIB1	2.29	tribbles homolog 1 (Drosophila)	3.54E-02	202241_PM_at
LOC100294402 /// SIGIRR	1.68	similar to single Ig IL-1R-related molecule /// single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	4.29E-02	52940_PM_at

Given are abbreviation (*Gene alias*), fold change (*FC*), short description (*Gene name/description*), *P*-value, and probe ID (*Gene ID*).

Table S11. The genes that were significantly higher expressed by nasal epithelial cells from patients with allergic rhinitis, sorted by ontology analysis in functional groups.

Gene alias	FC	Gene name/description	P-value	Gene ID
<i>metal ion binding</i>				
AEBP1	4.95	AE binding protein 1	2.00E-02	201792_PM_at
ANTXR1	2.13	anthrax toxin receptor 1	4.52E-02	220092_PM_s_at
ANXA6	5.04	annexin A6	1.66E-02	200982_PM_s_at
ARSI	3.04	arylsulfatase family, member I	1.16E-02	230275_PM_at
ATP1A1	1.50	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	4.13E-02	220948_PM_s_at
BCL11A	1.52	B-cell CLL/lymphoma 11A (zinc finger protein)	4.60E-02	219497_PM_s_at
BCL11B	1.94	B-cell CLL/lymphoma 11B (zinc finger protein)	3.91E-02	222895_PM_s_at
C1orf124	1.57	chromosome 1 open reading frame 124	4.56E-02	223511_PM_at
C1R	6.27	complement component 1, r subcomponent	2.70E-02	212067_PM_s_at
C1S	10.89	complement component 1, s subcomponent	1.50E-02	208747_PM_s_at
CHPT1	1.89	choline phosphotransferase 1	4.66E-02	230364_PM_at
CYBRD1	1.83	cytochrome b reductase 1	2.58E-02	222453_PM_at
CYCS	1.91	cytochrome c, somatic	3.08E-02	229415_PM_at
CYP26B1	5.20	cytochrome P450, family 26, subfamily B, polypeptide 1	2.41E-02	219825_PM_at
DMD	1.86	dystrophin	4.14E-02	203881_PM_s_at
DNMT3B	1.70	DNA (cytosine-5-)-methyltransferase 3 beta	2.18E-02	220668_PM_s_at
DST	2.01	dystonin	3.74E-02	212254_PM_s_at
DZIP1	2.91	DAZ interacting protein 1	4.25E-02	204557_PM_s_at
DZIP3	1.61	DAZ interacting protein 3, zinc finger	4.58E-02	213186_PM_at
EGFL6	6.20	EGF-like-domain, multiple 6	3.22E-02	219454_PM_at
FAT2	2.12	FAT tumor suppressor homolog 2 (Drosophila)	2.43E-02	208153_PM_s_at
FKBP10	1.83	FK506 binding protein 10	4.14E-02	219249_PM_s_at
GLI3	1.65	GLI family zinc finger 3	3.79E-02	227376_PM_at
LCP1	7.96	lymphocyte cytosolic protein 1 (L-plastin)	8.46E-03	208885_PM_at
LOC653501 /// ZNF658 ///	2.35	family members of zinc finger protein 658		
ZNF658B			3.44E-02	231950_PM_at
MMP28	2.09	matrix metalloproteinase 28	3.74E-02	219909_PM_at
MYLK	11.94	myosin light chain kinase	1.64E-02	202555_PM_s_at
NAPEPLD	1.74	N-acyl phosphatidylethanolamine phospholipase D	4.46E-02	226041_PM_at
OSGEPL1	1.58	O-sialoglycoprotein endopeptidase-like 1	3.74E-02	220631_PM_at
PCLO	1.83	piccolo (presynaptic cytomatrix protein)	4.56E-02	213558_PM_at
PHOSPHO2	1.72	phosphatase, orphan 2	3.08E-02	230434_PM_at
PLEKHF2	1.46	pleckstrin homology domain containing, family F (with FYVE domain) member 2	4.59E-02	222699_PM_s_at
PLSCR4	2.47	phospholipid scramblase 4	2.48E-02	218901_PM_at
PRICKLE2	3.42	prickle homolog 2 (Drosophila)	1.83E-02	225968_PM_at
PTGS1	1.86	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1.60E-02	215813_PM_s_at
RAD50	1.64	RAD50 homolog (S. cerevisiae)	3.08E-02	209349_PM_at
SEPX1	1.49	selenoprotein X, 1	4.99E-02	217977_PM_at
SGCE	2.09	sarcoglycan, epsilon	1.60E-02	204688_PM_at
SP110	1.74	SP110 nuclear body protein	3.34E-02	208392_PM_x_at
SPARC	4.22	secreted protein, acidic, cysteine-rich (osteonectin)	3.51E-02	200665_PM_s_at
STAT1	1.77	signal transducer and activator of transcription 1	3.06E-02	A/M97935_5_at
STEAP3	1.51	STEAP family member 3	3.85E-02	218424_PM_s_at
TAF15	1.66	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	3.15E-02	202840_PM_at
THBS2	6.82	thrombospondin 2	3.08E-02	203083_PM_at
TRIM59	2.59	tripartite motif-containing 59	1.60E-02	235476_PM_at
TRIM69	1.93	tripartite motif-containing 69	3.22E-02	1568592_PM_at
USP13	2.38	ubiquitin specific peptidase 13 (isopeptidase T-3)	3.10E-02	205356_PM_at
ZMAT3	1.60	zinc finger, matrin type 3	3.63E-02	1555609_PM_a_at
ZNF124	2.20	zinc finger protein 124	3.22E-02	206928_PM_at
ZNF30	1.73	zinc finger protein 30	4.48E-02	232014_PM_at
ZNF300	2.03	zinc finger protein 300	4.29E-02	228144_PM_at
ZNF362	1.95	zinc finger protein 362	4.14E-02	226820_PM_at
ZNF37A	1.59	zinc finger protein 37A	2.88E-02	228711_PM_at
ZNF827	1.95	Zinc finger protein 827	4.14E-02	228046_PM_at
ZNF879	1.86	zinc finger protein 879	2.82E-02	230421_PM_at

210

211 Given are abbreviation (Gene alias), fold change (FC), short description (Gene

212 name/description), P-value, and probe ID (Gene ID).

213 **Table S12.** Gene ontology analysis of the genes from the different clusters resulted by the K-
 214 means clustering.

Gene alias	Gene name/description
Cluster 1:	
<i>developmental process</i>	
ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1
ATL1	atlastin GTPase 1
BMPRI1B	bone morphogenetic protein receptor, type IB
C19orf46	chromosome 19 open reading frame 46
CARD11	caspase recruitment domain family, member 11
CCBE1	collagen and calcium binding EGF domains 1
CDH11	Cadherin 11, type 2, OB-cadherin (osteoblast)
COBL	cordon-bleu homolog
CXCL17	chemokine (C-X-C motif) ligand 17
CYR61	cysteine-rich, angiogenic inducer, 61
EDIL3	EGF-like repeats and discoidin I-like domains 3
EDN1	endothelin 1
EPHB2	EPH receptor B2
EYA4	eyes absent homolog 4 (Drosophila)
FGFR3	fibroblast growth factor receptor 3
FOXA1	Forkhead box A1
FOXE1	forkhead box E1 (thyroid transcription factor 2)
FOXP2	forkhead box P2
GATA6	GATA binding protein 6
HLA-DQB1 /// HLA-DQB2 ///	<i>major histocompatibility complex, class II, DR beta family</i>
LOC100133583 /// LOC100293977	
HMGB3	high-mobility group box 3
HOXA1	homeobox A1
IRS1	insulin receptor substrate 1
ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
JAK2	Janus kinase 2
KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1
KRT18	keratin 18
KRT19	Keratin 19
MITF	microphthalmia-associated transcription factor
NKX2-1	NK2 homeobox 1
OXTR	oxytocin receptor
PLLP	plasma membrane proteolipid (plasmolipin)
PODXL	podocalyxin-like
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
RUNX2	runx-related transcription factor 2
SDC2	syndecan 2
SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
SOBP	sine oculis binding protein homolog (Drosophila)
SPDEF	SAM pointed domain containing ets transcription factor
SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
TAGLN3	transgelin 3
TGFBR3	transforming growth factor, beta receptor III
TSPAN12	tetraspanin 12
TWIST1	twist homolog 1 (Drosophila)
TWIST2	twist homolog 2 (Drosophila)
VAV3	vav 3 guanine nucleotide exchange factor
Cluster 3:	
<i>epidermis development</i>	
ALOX12B	arachidonate 12-lipoxygenase, 12R type
CALML5	calmodulin-like 5
CDSN	corneodesmosin
CNFN	cornifelin
IVL	involucrin
LCE3D	late cornified envelope 3D
<i>peptidase regulator activity</i>	
PI3	peptidase inhibitor 3, skin-derived
SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
SPINK5	serine peptidase inhibitor, Kazal type 5
WFDC12	WAP four-disulfide core domain 12
WFDC5	WAP four-disulfide core domain 5
Cluster 4:	

anatomical structure
morphogenesis

ACP5	acid phosphatase 5, tartrate resistant
BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
CARD16 /// CASP1	caspase recruitment domain family, member 16 /// caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
COL4A1	collagen, type IV, alpha 1
COL4A2	collagen, type IV, alpha 2
CSPG4	chondroitin sulfate proteoglycan 4
DLX1	distal-less homeobox 1
DMD	Dystrophin
EPHA4	EPH receptor A4
FLI1	Friend leukemia virus integration 1
FOXP1	forkhead box G1
GAS1	growth arrest-specific 1
GATA3	GATA binding protein 3
GJC1	gap junction protein, gamma 1, 45kDa
IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
LAMA1	laminin, alpha 1
MEOX1	mesenchyme homeobox 1
MSX2	msh homeobox 2
OSR2	odd-skipped related 2 (Drosophila)
PAX3	paired box 3
PAX6	paired box 6
S100A7	S100 calcium binding protein A7
SFRP1	Secreted frizzled-related protein 1
SIX3	SIX homeobox 3
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
SP8	Sp8 transcription factor
TCF7L2	Transcription factor 7-like 2 (T-cell specific, HMG-box)
THY1	Thy-1 cell surface antigen

Cluster 5:

retinoic acid binding

UGT1A1 /// UGT1A10 /// UGT1A3	<i>UDP glucuronosyltransferase 1 family</i>
/// UGT1A4 /// UGT1A5 ///	
UGT1A6 /// UGT1A7 /// UGT1A8	
/// UGT1A9	<i>UDP glucuronosyltransferase 1 family</i>
UGT1A1 /// UGT1A10 /// UGT1A4	
/// UGT1A6 /// UGT1A8 ///	
UGT1A9	<i>UDP glucuronosyltransferase 1 family, polypeptide A6</i>
UGT1A6	

Cluster 7:

immune response

BST2	bone marrow stromal cell antigen 2
CTSS	cathepsin S
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
HLA-DQB1 /// LOC100133583	major histocompatibility complex, class II, DQ beta 1
HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 ///	<i>major histocompatibility complex, class II, DR family</i>
LOC100133661 /// LOC100294036	<i>major histocompatibility complex, class II, DR family</i>
/// LOC100509582 ///	
LOC100510495 /// LOC100510519	
HLA-DRB1 /// HLA-DRB4	<i>interleukin 23, alpha subunit p19</i>
IL23A	
IL8	interleukin 8
PTAFR	platelet-activating factor receptor
SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
SYK	spleen tyrosine kinase

215

216 Given are abbreviation (Gene alias), and short description (Gene name/description).

217 **Supporting Information Figure Legends**

218 **Figure S1.** Correlation plot of real-time PCR data and microarray results.